Autoantigen Processing. How immunodominant thyroglobulin peptides are generated and presented by HLA-DR molecules

TESIS DOCTORAL

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"*Las ideas no duran mucho.*

Hay que hacer algo con ellas"

Santiago Ramón y Cajal

Premio Nobel de Medicina (1906)

ABBREVIATIONS

ADAM13:A disintegrin
like and metalloprotease
with thrombospondin type 1 motif 13

AEP: asparagine endopeptidase

AIRE: autoimmune regulator

AITD: autoimmune thyroid diseases

APC: antigen presenting cell

cDC: conventional DCs

CFS: Cell-free system

CII: type II collagen

CIITA: MHC class II transactivator

CLIP: Class II-associated invariant chain peptide

cTEC: cortical thymus epithelial cells

DC: dendritic cell

EAT: experimental autoimmune thyroiditis

EBV: Epstein Barr virus

ER: endoplasmic reticulum

GD: Graves' disease

FVIII: coagulation factor VIII

HB: high binder

HLA: Human Leucocyte Antigen

HSA: human serum albumin

HT: Hashimoto's thyroiditis

IFN: interferon

IB: intermediate binder

Ii: Invariant chain

LB: low binder

MALDI: Matrix-Assisted Laser Desorption/Ionization

MBP: myelin basic protein

MHC: Major Histocompatibility Complex

MHC-I: MHC class I

MHC-II: MHC class II

MIIC: MHC-II-rich compartments

MoDC: monocyte-derived dendritic cells

mTEC: medullary thymus epithelial cells

MS: mass spectrometry

NA: non-associated

PBMC: Peripheral blood mononuclear cells

pDC: plasmacytoid DCs

PFR: peptide flanking residues

pGE: "promiscuous" gene expression

pMHC: peptide-MHC-II complexes

PTM: Post-translational modifications

RA: rheumatoid arthritis

RT: room temperature

SE: shared epitope

SNP: single nucleotide polymorphism

T1D: type 1 diabetes

TAP: transporter associated with antigen processing

TCR: T cell receptor

TNF: Tissue Necrotic Factor

TTCF: tetanus toxin C fragment

TTP: Thrombotic thrombocytopenic purpura

TFC: thyroid follicular cells

TGFβ: Transforming Growth Factor β

TPO: thyroid peroxidase

Tregs: T regulatory cells

TRA: tissue restricted antigen

TSHR: thyroid stimulating hormone receptor

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INTRODUCTION

i. Antigen presentation

The main role of antigen presentation by Major Histocompatibility Complex (MHC) molecules is to activate or enhance the T cell adaptive responses to pathogens. Virtually all cells in the body express MHC class I (MHC-I) molecules that present intracellular proteins to CD8+ T cell. In healthy cells, self-peptides are presented to signal normal cell state. When foreign or ectopic proteins are expressed in cytosol (due to virus infection or tumors), derived peptides associate to MHC-I to be presented on the surface, targeting for cell destruction by cytotoxic T cells. Sometimes infections or tumor processes inhibit the surface expression of MHC-I molecules to escape the immune response, but NK cells are able to sense MHC-I absence and kill the cells. Conversely, professional antigen presenting cells (APC), dendritic cells (DC), macrophages and B cells are specialized in taking up exogenous material for MHC class II (MHC-II) antigen presentation to CD4+ T cells. Nevertheless, MHC-II is expressed by non-professional APC such thymus epithelial cells, and also by other cells such as fibroblasts, epithelial cells and other cells in inflammatory conditions. Cross-presentation mechanisms are also available for exogenous material to be presented by MHC-I, mostly by DCs (1-3).

MHC is a polygenic complex with a very high gene density. In humans, it is called Human Leucocyte Antigen (HLA) whereas in the mouse it is referred as H-2. The human HLA complex (4000kb) are located in chromosome 6 and comprise three major regions containing class I, class II and class III genes. Class I loci encode the α chain of HLA-A, HLA-B and HLA-C, the classic presenting molecules. Non-classic (class Ib) molecules such HLA-E, HLA-G, MICA and MICB and many others are also clustered in this region. Class II loci encode the α and β chains of the classic presenting molecules HLA-DP, HLA-DQ and HLA-DR. MHC-I and MHC-II pathway-associated molecules are also encoded in this region: the transporter associated with antigen processing (TAP), two subunits of the immuneproteasome, HLA-DM and HLA-DO. Class III region genes encode a variety of proteins, some related to the immune response including complement factors, Tissue Necrotic Factor (TNF) α and β or transcription factors like NOTCH (4). MHC-II gene expression is controlled by the MHC class II transactivator (CIITA), encoded in chromosome 16 (5).

Classic MHC-I and MHC-II molecules are structurally different but homologous glycoproteins. Crystal structures of many of these molecules have shown the particularities of the class I and II heterodimers (6-11). MHC-I heterodimers are constituted by a transmembrane glycoprotein (α chain) that associate to the soluble molecule β2 microglobulin, which is encoded by chromosome 15. The α chain has three extracellular domains (α1, α2 and α3), a transmembrane domain and a cytoplasmic tail. The β2 microglobulin interacts directly with the α3 domain, both being immunoglobulin-like domains, whereas α1 and α2 are the structural support for peptide binding, forming the peptide-binding cleft or groove. The MHC-II αβ heterodimer structure is specular, each chain being formed by a cytoplasmic tail, a transmembrane domain and two extracellular domains. The distal domains of each chain configure the peptide binding cleft. In both types of molecules, the binding groove, where the

peptide is allocated, is conformed by two α helix and eight β sheets. The residues that constitute the binding groove form a succession of structural pockets, where the peptide is anchored. Additional hydrogen bonds between the peptide backbone and the HLA chains help peptide stabilization. Physicochemical properties of the peptide residues will determine these interactions and thus, the affinity of the peptide for the MHC molecule. Peptide residues oriented outside the binding groove contact directly with the T cell receptor (TCR) (12) (Fig.1).

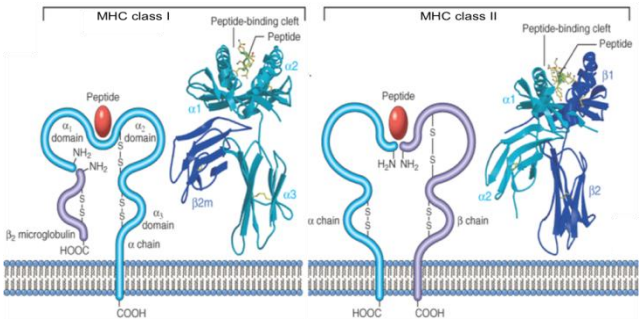

Figure 1. Heterodimers and tridimensional structure of MHC class I and class II molecules. Lechler and Warrens: HLA in health and disease (Elsevier 2005, London).

MHC-I molecules have an end-closed binding groove that limit the size of the presented peptides to around 9 residues. This characteristic makes N- and C-terminal residues of the peptide of special relevance (13). In contrast, MHC-II groove ends are open, allowing the binding of longer peptides (around 12-30 residues). However, only an internal 9-residue core binds directly to the anchor pockets. The rest N- and C-terminal regions of the peptide are known as the peptide flanking residues (PFR). These regions may also interact with outer residues of the HLA heterodimer for peptide stabilization and TCR recognition (12, 14). Because of the open binding cleft, MHC-II peptides are often clustered in nested sets i.e. peptides with the same binding core but different length of the PFRs. High polymorphism of classic MHC molecules make differences in the nature of peptide binding for each allele because they are located in the binding groove. The high degree of polymorphism shows the evolution pressure over these genes to adapt the immune response to diverse pathogens. In general, the binding positions P1, P4, P6, P7 and P9 of the core are the most important positions for peptide binding, but there are allele-dependent variations. The allowed amino acids in each of these core positions for the different alleles are known as the binding motif, which have been defined for several MHC-I and MHC-II alleles (6, 15-30). Of the HLA-II molecules, HLA-DRβ chain is the most polymorphic, which makes HLA-DR the most diverse molecule for MHC-II antigen presentation (1364 proteins are codified according to the IMGT/HLA database).

MHC-II transmembrane α and β chains are synthetized in the endoplasmic reticulum (ER)-associated ribosomes towards the ER lumen. $\alpha\beta$ heterodimer conformation is mediated by calnexin to prevent degradation of single chains and also the dimer exit to the secretory pathway (31). However, the $\alpha\beta$ heterodimer *per se* is unstable and requires the association of a peptide for complete stability. Here, the Invariant chain (Ii) binds to the empty dimer, occupying the binding groove, thus preventing the binding of peptides in the ER (32). Trimerized Ii molecules bind three $\alpha\beta$ MHC-II heterodimers. Stable (Ii- $\alpha\beta)_3$ complexes are sent directly to the

cell surface and then re-internalized (33) or are driven through the Golgi apparatus to the secretory pathway (34). Which of these two pathways is dominant depends mostly on the cell type. Ii-MHC-II complexes accumulate into the MHC-II-rich compartments (MIIC) of the endocytic pathway. MIIC are mostly multi-vesicular or multi-laminar bodies where antigen processing takes place at acid pH and where the peptide-editing chaperone HLA-DM is localized. This compartments belong to the late endosomal pathway and they are where the binding of the endocytic-generated peptides to MHC-II mostly takes place (35). In MIIC, Ii must be partially degraded to release functional MHC-II dimers. The trimerization domain of the C-terminal region is first cut to release the Lip22 peptide. Lip22 is further degraded to Lip10 peptides and finally a peptide named Class II-associated invariant chain peptide (CLIP) is the only Ii fragment that remains bound to the binding groove. This sequential degradation is mediated by MHC-II-related proteases cathepsin S, L, F and asparagine endopeptidase (AEP), depending on the cellular type (36-38). Once antigenic peptides are available, the chaperone HLA-DM releases CLIP, editing the peptide repertoire. Empty heterodimers are degraded in lysosomes whereas stable peptide-MHC-II complexes (pMHC) are transported to the cellular surface to be recognized by CD4+ T cells (Fig.2).

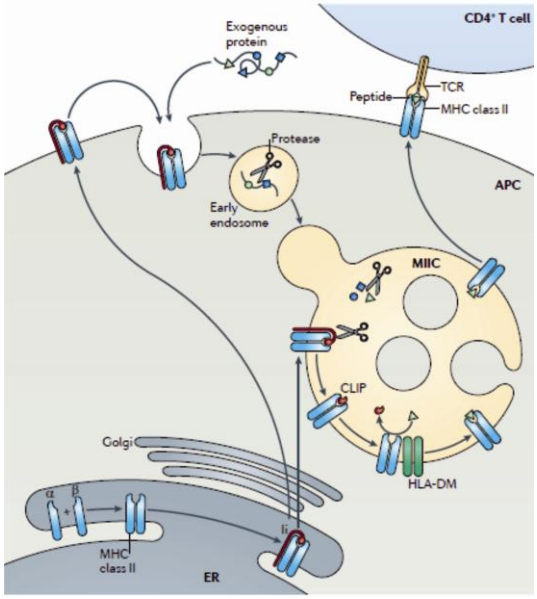

Figure 2. The MHC-II antigen presentation pathway. MHC-II α- and β-chains assemble in the endoplasmic reticulum (ER) and form a complex with the invariant chain (Ii). The Ii–MHC-II heterotrimer is transported through the Golgi to the MHC class II compartment (MIIC), either directly and/or via the plasma membrane. Endocytosed proteins and Ii are degraded by resident proteases in the MIIC. CLIP remains in the peptide-binding groove of the MHC-II and is exchanged for an antigenic peptide with the help of the chaperone HLA-DM. MHC-II molecules are then transported to the plasma membrane to present antigenic peptides to CD4+ T cells. Adapted from Neefjes et al. (3)

ii. T cell education: this is self, don't fight it

In absence of infection, MHC present peptides derived from self-proteins to keep functional and stable MHC complexes. Lymphocytes must be "educated" in the thymus during maturation to avoid responses against self-antigens. The result of this process is called central tolerance.

Once T cells with a functional TCR are positively selected in the thymus cortex by their capacity of recognizing MHC-peptide complexes, they migrate to the medulla. There, single positive (CD4+ or CD8+) T cells are tested to recognize peptides derived from self-proteins in the context of MHC-I or MHC-II, depending on the expressed co-receptor, in what is called negative

selection. During this process, any T cell capable of recognizing a self-peptide with high or intermediate affinity is eliminated. In addition to thymus DCs, medullary thymus epithelial cells (mTECs) are the major antigen presenting cells in the medulla. These cells express tissue restricted antigens (TRAs) by a mechanism designated “promiscuous” gene expression (pGE) that generates peptides from virtually any molecule to be presented by MHC to the T cells (39). pGE studies have focused on the mTEC transcriptome while data on the mTEC proteome are scarce. The autoimmune regulator (AIRE) controls the expression of many genes encoding TRAs in the mTECs (40), although promiscuously expressed TRAs (e.g. GAD1) can also be AIRE-independent (41), implying the involvement of additional factors regulating pGE. Thymus B cells have been reported recently to express *Aire* in the mouse (42). There is only a limited number of native TRA that have been unambiguously detected at the protein level in the thymus (41, 43-45). Likewise, only a limited number of peptides from ubiquitous putative autoantigens have been reported as part of the MHC peptidome of thymus APC (46). We recently reported TRA peptides identified within the HLA-DR thymus peptidome from two peripheral antigens that were targets of autoimmunity: prostate-specific semenogelin-1 (an autoantigen in autoimmune chronic prostatitis/chronic pelvic pain syndrome) and central nervous system-specific contactin-2 (an autoantigen in multiple sclerosis). Thymus expression of both genes was restricted to mTECs (47). In addition, resident and migratory DCs and B cells also contribute to antigen presentation for negative selection (42, 48, 49).

Beside the expression of TRAs by mTEC, the thymus can generate a large variety of MHC ligands for display through activities like highly activated thymocyte proliferation and apoptosis, constitutive levels of autophagy by mTECs (50, 51) and antigen exchange between mTEC and DCs (52). The resulting peptides would compete for *de novo* synthesized MHC molecules. This constant competition should presumably favor the presentation of the highest affinity ligands, displacing those peptides with lower affinities for the binding groove. High-stability peptides form long-life pMHC at the APC surface, increasing the possibility of recognition by self-reacting thymocytes and improving negative selection efficiency. In contrast, low-stability complexes are short-lived, so they may be ignored or only be recognized by a small number of thymocytes, increasing the probability of escaping selection (53). Finally, autoreactive T cells that recognize MHC-peptide complexes with intermediate or high affinity are deleted, anergized or directed towards a regulatory phenotype, always depending on TCR interactions with MHC-self antigen-peptide complexes (54). Major mechanisms for TRAs presentation in thymus are summarized in Fig.3.

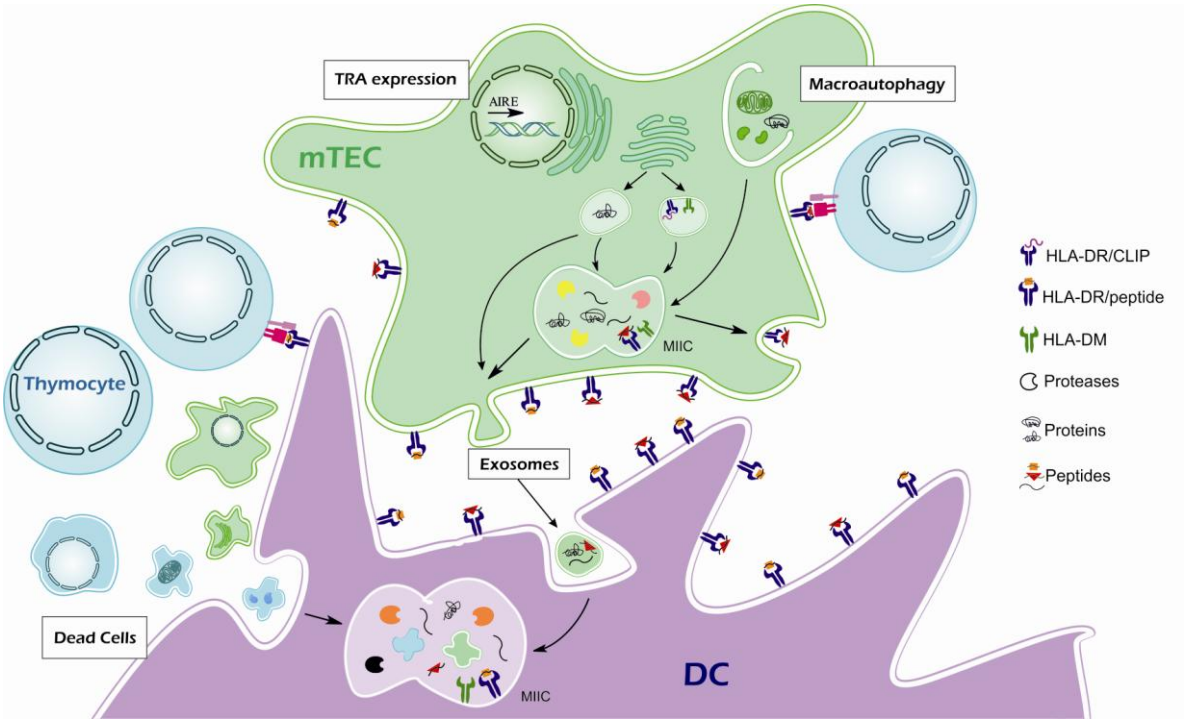

Figure 3. Thymus mechanisms involved in antigen processing. Tissue restricted antigens (TRAs) are expressed by medullary epithelial cells (mTECs) for negative selection. Secretory TRAs are processed by self-proteases and peptides (orange squares and red triangles) are loaded onto MHC II molecules once exocytic vesicles reach the MIIC compartment. Peptide exchange is mediated by HLA-DM. Macroautophagy permits the access of cytosolic TRAs and other proteins into the MIIC compartment so their processing and presentation via MHC-II can take place. Besides their own proteome, thymus dendritic cells (DC) are expected to present antigens via the uptake of apoptotic thymocytes and mTECs, exosomes delivered by mTECs and other extracellular material. Thymus-specific and conventional proteases generate high affinity peptides. Adapted from Collado et al. (53)

Low affinity self-reactive T cells, with high affinity for some foreign peptide, leave the thymus to act as the main actors of the adaptive immune response in the periphery. T cell maturation in the thymus continues until puberty when thymus degenerate. At any time, circulating *naïve* T cells and memory T cells are responsible of the adaptive immune response. It has been described that *naïve* T cell homeostasis is dependent on the recognition of self-pMHC (55) because T cells are stimulated below the minimal signal for TCR activation but enough to keep them in a “ready-to-response” state (54, 56, 57).

The maintenance of tolerance will correspond to peripheral tolerance, that takes place in secondary lymphoid organs (spleen and lymph nodes), essentially by DCs but also other APC, where MHC molecules should present much the same peptides as those presented in thymus (58). Our analysis of a spleen HLA-DR repertoire showed many common peptides with an HLA-DR-matched thymus, and with slight differences related to the spleen function such as a large number of peptides from blood proteins (59, Collado *et al.*, in preparation). However, few studies are available concerning the peptide repertoires associated to MHC-II in healthy lymphoid tissue in mice (60, 61).

iii. Autoimmunity: when tolerance fails

Up to date there is not a clear explanation of how tolerance is broken to generate the autoimmune response that, if pathologic, develops into autoimmune diseases. *Naïve* T cells do not infiltrate the tissues. It is though that tissue alterations or damage due to infections, injury, stress or diet changes would start an inflammatory response and tissue resident APCs would capture autoantigens and present them to T cells in secondary lymphoid organs (62). Antigen mimicry has been proposed as a mechanism for autoimmunity since many autoimmune diseases correlate with bacterial and virus infections (63). In addition, exacerbated cytokine secretion during infection could hyper activate self-reactive cells. The development of the autoimmune processes is usually slow, becoming chronic. Target tissue may also be essential to expand and maintain the response by expressing MHC and presenting antigens to T cells and by the generation of lymph follicles (64, 65). Over time, available autoantigens increase in an epitope expansion mechanism which amplifies the response (66). There are some organ-specific autoimmune diseases where cellular and humoral responses are directed against three or four antigens. In type 1 diabetes (T1D) insulin is the major autoantigen once there is pancreatic islet destruction but the starting antigen is still unknown (67). In autoimmune thyroid diseases (AITD), autoantibodies and specific T cells against thyroglobulin, thyroid stimulating hormone receptor (TSHR) and thyroid peroxidase (TPO) are found in patients with all types of AITD (68, 69).

Autoimmune diseases are multifactorial diseases. Age, sex and thus hormones, diet, environmental factors and genetic factors may influence in the development of the autoimmune response. Some MHC alleles, mostly class II, are highly associated to autoimmune diseases (Table 1) (70, 71).

Miyadera *et al*. (71) have recently reviewed the two main mechanisms to explain this association: a) selective presentation of disease-relevant self-peptides by the disease susceptible HLA alleles, or b) intrinsically unstable HLA proteins form unstable HLA-peptide complex through the presentation of diverse self-peptides, confer a risk for autoimmune diseases.

There are data describing the MHC-II peptidome from non-lymphoid peripheral tissues affected by autoimmunity (72-74). Albeit most peptides belonged from ubiquitous proteins, there were sequences derived from tissue-restricted proteins potentially related to the disease. We were the first to demonstrate the *in vivo* presentation thyroglobulin peptides by HLA-DR in thyroid glands affected by Graves' disease (GD) (72). In later reports, myelin basic protein (MBP) and other autoantigens peptides were identified in central nervous system samples from multiple sclerosis patients (73). Peptides from collagen, vimentin and others were detected in synovial samples from rheumatoid arthritis (RA) patients (74). Potential affinity analysis of peptides from autoimmune thyroid tissue showed that only one third of the sequences corresponded to peptides with predicted high affinity for HLA-DR. The affinity of peptides from Multiple Sclerosis

patients showed less than 20% of the peptides with high affinity and around 65% low affinity peptides. So, contrary to thymus, where low-affinity peptides appeared to be relatively unavailable for presentation by HLA-DR, these peptides were abundant in the affected tissues (53). Considering these differences, specific processes in peripheral tissues may modify the outcome of antigen processing and presentation *in situ*, favoring the generation of peptides that would have been ignored or not generated in the thymus.

Table 1. MHC-II association to autoimmune diseases.

	HLA-DR3	HLA-DR4	HLA-DR8	HLA-DR15	HLA-DQ2	HLA-DQ8
Autoimmune thyroid diseases	Yes					
Type 1 Diabetes	Yes	Yes	Yes		Yes	Yes
Rheumatoid arthritis		Yes				
Multiple Sclerosis			Yes	Yes		
Systemic lupus erythematosus	Yes		Yes			
Celiac disease					Yes	

a) Proteolysis

Detailed cathepsin expression by each particular cell subset of the human thymus has been reported (75). Cathepsin V is expressed only in the cortex, while cathepsin L is expressed by few cells distributed throughout the thymus, including mTECs (76). Cortical thymus epithelial cells (cTEC) and mTEC also express common proteases such cathepsin B, D, H, S and X and GILT. The importance of cathepsins in tolerance is evidenced when autoantigen processing is studied. Cathepsin S processes MBP in thymus DCs generating an immunodominant epitope that is destroyed by cathepsin G in peripheral blood DCs (77). Cathepsin S cleavage of proinsulin can also destroy insulin T cell epitopes (75). Moreover, NOD mice deficient in cathepsin B, S, or L are protected from type I diabetes development (78).

Normal turn-over of tissue-specific proteins, cell death, extracellular processing and different tissue proteases may provide a source of peptides in peripheral tissues that will not be found in thymus. In AITD, the thyroglobulin antigen is secreted and stored in the colloid. Solubilization and pre-cleavage of thyroglobulin are necessary prior to endocytosis by thyroid follicular cells (TFC) to generate T3 and T4 hormones in a process mediated by cathepsin B, L, S, K present both in colloid and in the TFC's endocytic vesicles (79). Similarly, extracellular matrix remodeling occurs in other autoimmune diseases, such as RA, where cathepsin S, K, B and L are secreted to synovial fluid and tissue (80, 81). A wide range of different peptides can be generated in the affected tissue, leading to the activation of autoreactive T cells that were not negatively selected, causing and maintaining the autoimmune process.

b) Differential dose of antigen in peripheral tissue vs. thymus

The expression of TRAs in the thymus is temporally regulated and is much weaker than in the corresponding peripheral tissue (47, 82-84). In a mouse model of thyroid autoimmunity, transgenic BALB/c mice were generated with the human TSHR A-subunit targeted to the thyroid and thymus. Two types of mice were obtained, low and high TSHR expressors. When these mice were immunized with a human TSHR construct and T regulatory cells (Tregs) were depleted, the low expressors suffered the disease (thyroid infiltration and damage) while the high expressors remained tolerant. Presumably, THSR peptides presented in the high expressors' thymus were enough to induce tolerance to all possible epitopes, whereas low-expressors presented insufficient TSHR peptides or presented them with low efficiency. These peptides would be presented in periphery and responsible for the *in situ* reactivity (69). This suggests that to generate tolerance, peptides from all relevant antigens should be presented at an adequate concentration in thymus to prevent autoimmunity. Interestingly, a recent work analyzing the MHC-I peptide repertoire of HLA-B27 allelic variants associated to ankylosing spondylitis addressed this question. They proposed that quantitative rather than qualitative changes in presented peptides may be relevant to reach the threshold of antigen required for the selection or activation of autoreactive T cells (85).

c) Post-translational modifications in the tissue

Post-translational modifications (PTM) are common processes for most mammalian proteins that allow the generation of neo-self epitopes (86, 87). PTMs can occur spontaneously or arise by enzymatic modifications, altering the protein structure and biological functions. Modifications of the proteolytic degradation can also occur. PTMs that generate neo-self peptides include enzyme-dependent glycosilation (88), deamidation (89), citrullination (90, 91), iodination (92), phosphorylation (93), methylation (94) or chemical modifications such as disulphide bridge formation, oxidative modifications or nitration, and many others (95). In Multiple Sclerosis, citrulination increases the sensitivity of MBP to cleavage by cathepsin D, allowing epitope destruction or neo-epitope generation (96-98). In RA, associated HLA-DR molecules share a consensus sequence in the peptide binding groove, named the "shared epitope" (SE) (99), that contains a positively charged P4 peptide binding pocket. Citrullination will remove a positively charged arginine residue from any peptide, enhancing its ability to bind to SE-MHC-II molecules. Iodinated thyroglobulin epitopes in mice are highly immunogenic and can trigger thyroid autoreactive T cells (92, 100).

d) Expression of HLA-DR and HLA-DM in autoimmunity affected tissue

In organs affected by autoimmune diseases, cell targets of the tissue damage often overexpress MHC-I and ectopically express MHC-II molecules (101-106). The importance of this expression in the pathology may vary for the different tissues. There is very high expression of MHC-II in autoimmune TFCs, whereas MHC-II expression in pancreatic islets in diabetes is not so high, despite the stronger association to HLA-DR and -DQ alleles with T1D compared to thyroid

autoimmunity (107). HLA-DM is also expressed by autoimmune TFC, although at lower levels than in conventional APCs (108). In the absence of HLA-DM or if HLA-DM is insufficient, high affinity peptides may be outcompeted by low-affinity peptides. A recent report related HLA-DM editing-susceptibility and cathepsin digestion resistance of a series of immunodominant peptides derived from autoantigens. This model proposes that some immunodominant peptides may be resistant to cathepsin digestion. In such a situation, even if HLA-DM displaces the peptides from the binding groove, epitopes would not be destroyed and can rebind HLA-DR molecules increasing the complex density at the surface (109). Additionally, HLA-DR3 has low affinity for CLIP (110), thus it may not so strictly require HLA-DM to ensure peptide presentation, avoiding efficient peptide selection and allowing the binding of low-stability peptides (111). HLA-DQ2 also interacts poorly with HLA-DM (111-112) (Fig 4),

e) Unique T cell recognition of tissue-derived antigens

Therefore, peptides from antigens expressed in tissues can be presented by local APC activating self-reactive T cells. Evidence comes from studies that show that APCs stimulate a subset of T cells only when they are loaded with soluble peptide but not with the whole protein (113). These so-called type B T cells recognize pMHC complexes that are different from those generated when peptide is derived from intracellular processing of native proteins. One reasonable explanation is that peptides can bind MHC-II molecules on the plasma membrane or in recycling vesicles, avoiding the effects of HLA-DM, so less-stable complexes are available for presentation. Moreover, register shifting of peptides at the binding groove might be relevant since loading of exogenous peptide could lead to different conformations. Such T cells have been reported to infiltrate islets of pre-diabetic NOD mice (114-115) and to escape from tolerance in experimental autoimmune thyroiditis (EAT) (116).

iv. DCs in autoimmunity

The mechanisms underlying the role of DCs in antigen presentation by MHC-II have been recently reviewed (2). Immature DCs internalize exogenous material through nonspecific processes (macropinocytosis), receptor-mediated endocytosis (FcγRs and lectin receptors), pathogen or apoptotic body phagocytosis and incorporation of endogenous material by autophagy. After activation, mature DCs mobilize the antigenic pMHC to the surface and increase their stability to improve the recognition by T cells and induce the adaptive immune response.

Human DCs are diverse according to phenotype, “specialization” and tissue residence. In general, DCs have been divided into two main groups: plasmacytoid DCs (pDC) and “myeloid” or “conventional” DCs (cDCs). cDCs can be further separated into two subsets: cDC1 (BDCA3/CD141+) and cDC2 (BDCA1/CD1c+). In skin, liver, lung, and intestine, two main DCs populations, CD1c+CD1a+ and CD141+Clec9A+, have been identified. Additional DC subsets

have been described in mucosal tissues: Langerhans cells and CD14+ DCs in skin and vaginal mucosa, and CD103-CD172a+ DCs in the intestine (117).

DCs are important in central and peripheral tolerance by presenting self-peptides to CD4+ and CD8+ T cells that are generated in thymus and non-lymphoid tissues (58, 118). In thymus, DCs represent 0.5% of total cellularity. These thymus DCs are resident cells generated from thymus precursors that present mTEC-derived and serum-borne antigens. Those resident DCs are particularly efficient in cross-presentation and are located in the medulla. Migratory DCs, pDCs and cDCs, can be loaded with peripheral antigens and home from their original tissue to the thymus. Migratory cDCs can also be found in the thymus cortex for positive selection (119).

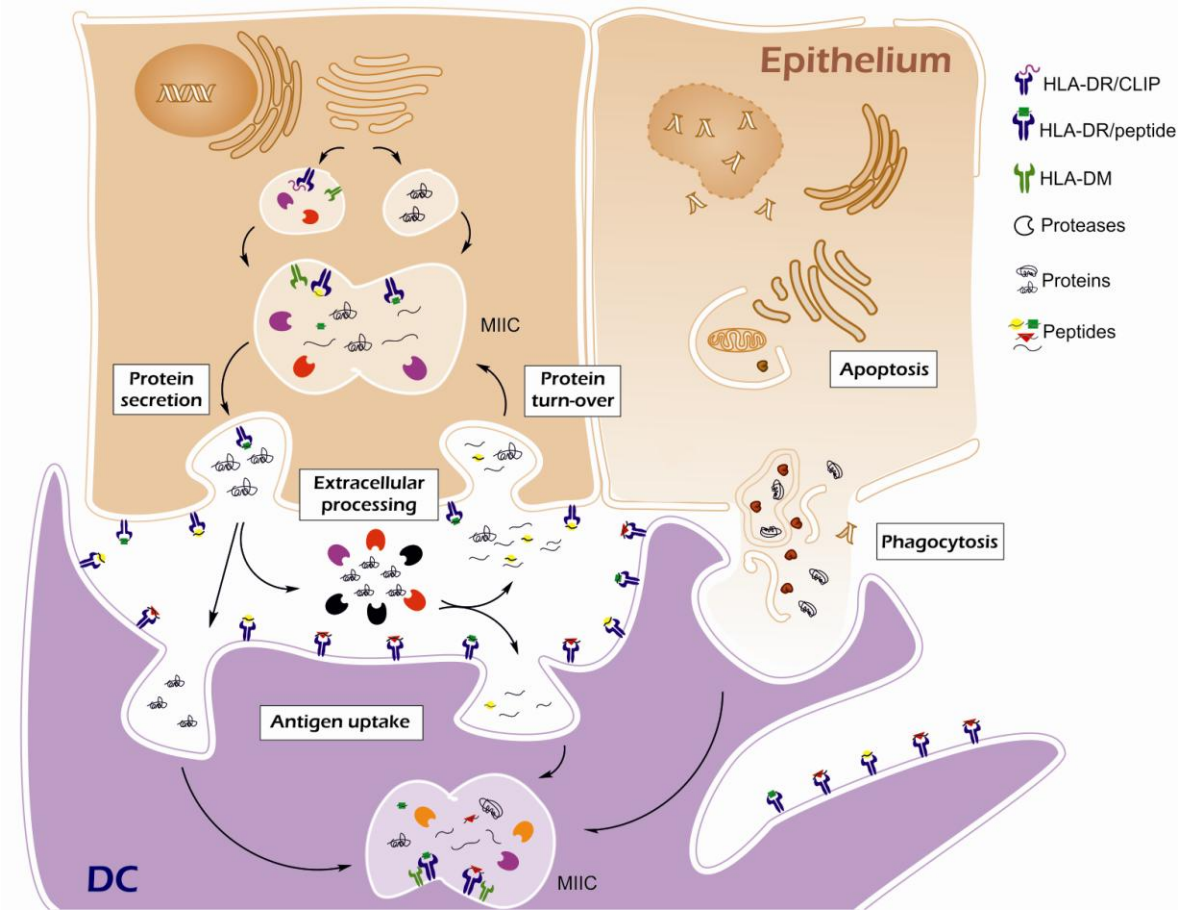

Figure 4. Peripheral tissue mechanisms involved in antigen processing. In peripheral tissues, specific proteases may be essential for peptide generation. A protein can generate peptides for MHC-II in the secretory pathway. Tissue-specific posttranslational modifications may result in modified antigenic peptides (orange squares from thymus are represented as green squares in periphery) or even prevent the generation of some peptides. Once in the extracellular environment, proteases could partially degrade the protein into smaller fragments (yellow circles) that would be potential binders for MHC-II molecules. In some cases protein storage outside the cells (e.g. thyroglobulin in thyroid colloid) is followed by protein turn-over into the cells. Proteins or their cleavage products contained in endosomes can be processed again in the MIIC compartment to generate MHC-II ligands. During inflammation, infiltrating DCs can uptake the antigenic proteins or their fragments for processing with their specific proteases. They can also phagocyte apoptotic epithelial cells. Compared with thymus, events in periphery may result in a set of presented peptides that were not used in negative selection. Lack of competition with high affinity peptides and low or absent expression of HLA-DM may result in the presentation of peptides with low affinity for MHC-II molecules. Adapted from Collado et al. (53)

DCs are also important in maintaining steady-state immune homeostasis by presenting tissue-derived self-antigens to T cells in the absence of inflammatory signals, leading to tolerance against those self-antigens in secondary lymph tissues. However, DCs in autoimmunity can either induce or suppress autoreactive T cell responses. DCs exhibit alterations in phenotype or function that could be due to underlying genetic defects or to the chronic inflammatory environment, and can affect the initiation of disease and later failure of tolerance mechanisms that lead to tissue destruction (118, 120). A tolerogenic microenviroment is necessary to control their steady-state to prevent the secretion of pro-inflammatory cytokines required for T cell activation. Actually, self-reactive T cells recognizing antigens from DCs die or become Tregs in absence of the relevant cytokine signal (58, 121). In addition, Tregs may regulate the behavior of the DCs by secreting inhibitory molecules (IL-10, IL-35 and Transforming Growth Factor β (TGFβ)) (122), cytolysis suppression (123) or proliferation inhibition (124).

Most studies concerning the role of DCs in autoimmunity focused on mouse models, where antigen pulsed-DCs have been used extensively (118). It is thought that mouse $CD8\alpha^+$ cDC1 more efficiently cross-present antigens to CD8+ T cells, while cDC2 stimulate CD4+ T cells (125). pDCs would contribute secreting type I interferons (IFN) (126). Several studies have shown different mechanisms by which DCs modulate antigen presentation and T cell response polarization, although how the autoimmune response begins is still unclear. Interestingly, both mice and human studies have agreed that I IFN production by pDCs might represent common mechanisms that lead to pathogenesis in autoimmune diseases as distinct as psoriasis, systemic lupus erythematosus (SLE) or T1D. The tolerogenic role of DCs is less robust in most diseases other than experimental autoimmune encephalomyelitis, which is an inducible model in which T cells are primed in the periphery but function in an immuno-privileged tissue (120).

v. Autoimmune Thyroid Diseases (AITD): an accessible model of autoimmunity

Most prevalent autoimmune diseases target essential tissues that cannot be removed from patients: T1D target pancreas, multiple sclerosis the central nervous system, RA the joints, celiac disease the small intestine, etc (4). However, treatment for AITD sometimes includes surgery removal of the gland and hormone treatment replacement. As said before, particularities of the autoimmune target thyroglobulin processing in thyroid may play an important role in the evolution of autoimmunity. The availability of tissue glands have permitted us to study the characteristics of T cell infiltrates, the role of TFC in disease progression, the influence of recent thymus emigrants in thyroid autoimmunity and the characterization of HLA-DR associated peptides derived from thyroglobulin (65, 72, 108, 127-130). Thus, AITD is a good model for the study of autoimmune diseases allowing the development of new *in vitro* and *ex vivo* technics that can be applied to the antigen processing and presentation studies of non-easily accessible autoimmune material.

AITD are endocrine autoimmune diseases affecting the thyroid gland, characterized by the generation of auto-antibodies against thyroglobulin, TSHR and TPO, and CD4+ and CD8+ T cell and B cell infiltration of the tissue (68, 69). AITD affect over 2% of the population in one of the two main and opposite syndromes: Graves' Disease (GD) characterized by the hyper-stimulation of the gland and Hashimoto thyroiditis (HT) characterized by thyroid hypo-stimulation (69).

In GD the agonist auto-antibodies specific of the TSHR simulate the activation of the receptor in the TFCs by hypophysis-secreted TSH, resulting in the excessive secretion of the metabolism-regulator hormones T3 and T4. Hyperplasia and hypertrophy of the tissue is observed due to the activation (131). Although this disease in mainly meditated by the humoral response against TSHR, thyroglobulin and TPO are found to be important autoantigens in 75% of patients (132). On the other hand, HT, where cytotoxic antibodies against TPO and thyroglobulin are common, is characterized by the destruction of the thyroid follicular cells by cytotoxic response-induced apoptosis and subsequently, gland destruction (133).

Concerning the antigens, TSHR is a glycosylated receptor expressed at the basal membrane of TFCs. The extracellular domain is known as subunit A whereas the transmembrane domain and cytosolic tail are called subunit C. Both subunits are covalently linked by the peptide C region which can be split, releasing the soluble subunit A. Thyroglobulin is an heterodimer protein (330kDa each subunit) that is found posttranslationally modified by iodination (134), glycosylation (135) and phosphorylation (136). As mentioned before, thyroglobulin is secreted by TFC to the thyroid colloid where it is stored. In the colloid, thyroglobulin represents 70-80% of all protein content (137). After TSHR activation, thyroglobulin is taken up by TFC to release T3 and T4 hormones from it structure (131). This antigen is not recruited in thyroid exclusively but can also be found in blood (138). TPO is the transmembrane enzyme on the apical side of TFCs that catalyze the iodination of thyroglobulin in the colloid lumen.

Genetic susceptibility has been described for both main types of AITD. Not only HLA genes, mostly HLA-DR are associated to the disease but also polymorphisms of the genes encoding thyroid antigens TSHR and thyroglobulin genes have also been associated (68, 139). The HLA-DR3 (HLA-DRB1*0301) allele have been associated to GD in 40-50% of patients (140), specially because there is a arginine in position 74 of the HLA-DRβ chain, very characteristic of this allele, that influence in the acid residues preference in the anchor pocket P4 of the binding groove (141-143). HLA-DQA*0501 is also associated to GD (144-145). In contrast, HLA-DR15 (HLA-DRB1*1501) and HLA-DR4 (HLA-DRB1*0401) have been reported as conferring resistance to thyroiditis (146- 148). Sequencing the thyroglobulin gene, a single nucleotide polymorphism (SNP) resulting in amino acid substitution has been identified as associated to AITD (141). TSHR SNPs have been described to give RNA splice variants, that result in less transcripts in thymus (139). In addition, other genes related to immune response such *CTLA-4*,

CD40 and FOXP3 polymorphism have been described to confer susceptibility for GD in some populations (149-151).

HYPOTHESIS AND OBJECTIVES

Immunodominance was originally defined as a restricted T cell response to a **single peptide** sequence derived from a given protein. According to Sercatz and Maverakis (152), an epitope generated by "the first endocytic cut" of an antigen is likely to be the first to bind MHC and if the affinity is high enough, this determinant will be immunodominant respect to other determinants from the same antigen, creating a **hierarchy** of epitopes. Abundance, affinity to MHC, sensitivity to proteases and dependence of HLA-DM are within the factors that define this hierarchy.

We propose that tissue-specific proteases influence canonical APC-processing events, modifying the hierarchy of epitopes presented in situ by HLA-DR and thus resulting in the presentation of peptides that were not generated in the thymus

Objectives

1 - Definition of the HLA-DR-associated self peptidome generated by professional APC in the absence of infection

2 - Processing of thyroid autoantigen thyroglobulin and epitope generation by monocyte-derived DCs pulsed with purified antigen or thyroid tissue extract

3 - Use of a minimalist cell-free system (CFS) to define the influence of tissue-specific proteases in the generation of HLA-DR3-associated thyroglobulin epitopes

4 - Comparison of the two in vitro approaches for the evaluation of thyroglobulin immunodominant epitope presentation

MATERIALS AND METHODS

M1. Tissue and blood samples

Thyroid surgery samples from patients with GD were used after the patients' informed consent, using a protocol approved by the ethical committee of University Hospital Germans Trias i Pujol and Vall d'Hebron. Samples from GD patients were used due to the follicular structure remains intact, instead of HT where there is severe tissue damage. Diagnosis was done based on the presence of two or more of the clinical parameters: hyperthyroidism symptoms (sweating, loss of weight, nervousness), ophthalmopathy and goiter. T3, T4, free T4 and TSH plasma levels as well as thyroidal autoantibodies were also tested. MHC-II typing was obtained by exon 2 sequencing at the Laboratori d'Immunologia per la Recerca i les Aplicacions Diagnostiques (LIRAD) of the Banc de Sang i Teixits, Barcelona . MHC-II expression by TFC was assessed by immunofluorescence staining on cryostat sections and by flow cytometry, as described (72). Thyroid TB449 belonged to a 35-years old female and typed for DRB1*0301, 1501 DQB1*0201, 0602.

Blood was drawn from HLA-typed healthy volunteers in accordance with Dutch regulations and following approval from Sanquin Blood Supply Ethical Advisory Board in accordance with the Declaration of Helsinki.

M1.1 Tissue extracts

Tissue pieces of 0.5 cm^3 were cut and frozen in cold isopentane. Tissue blocks were stored at − 80°C until use. Thyroid extracts were obtained by mechanic disaggregation of 0.3g of thyroid blocks in sterile extraction buffer (50mM Tris-HCl, 100mM NaCl, pH 7.4) in absence of detergent and proteases inhibitors.

M1.2 Blood processing

M1.2.1 Peripheral blood mononuclear cells (PBMC) purification.

PBMCs were isolated from freshly drawn EDTA anticoagulated blood. Blood was diluted 1:2 in phosphate buffer (PBS, 2mM NaH_2PO4, 8mM Na_2HPO4, 150mM NaCl). PBMCs were separated over a Ficoll-Paque PLUS gradient (GE Healthcare, Buckinghamshire, UK) by centrifugation 30min 600g at room temperature (RT), then removed from their phase and washed two times with MACS buffer (0.5% human serum albumin (HSA), 2mM EDTA in PBS) by centrifugation 5min 600g. Cell count and viability were then determined.

M1.2.2 Monocyte isolation and monocyte-derived dendritic cells (MoDC) generation

Monocytes were purified by magnetic separation with anti-CD14+ magnetic beads (MACS, Miltenyi Biotec, Bergisch Gladbach, Germany). For immature DCs differentiation, monocytes were plated in 6-well plates at $2.5x10^6$ cell/well in CellGro medium (CellGenix, Freiburg, Germany), supplemented with 1000 U/ml of IL-4 and 800

U/ml GM-CSF (CellGenix, Freiburg, Germany). After 5 days, the immature MoDCs were collected and seeded at $5x10^6$ cells/well in 24-well plates in conditioned medium and were maturated using 1 µg/ml LPS (Sigma-Aldrich, St. Louis, USA) for 24 h in the presence of 1% human serum. The adherent maturated MoDCs were detached with PBS.

M2. Cell cultures

M2.1 Hybridomas

Hybridoma HB55 (American Type Culture Collection, ATCC) was used to produce HLA-DR-specific antibodies. The IgG2a mouse monoclonal antibody L243 recognizes a monomorfic epitope of HLA-DR dependent of dimer αβ. Cells were cultured in Hybridoma medium (Invitrogen, Waltham, MA, USA) supplemented with 2mM L-glutamine, 0.1 mg/ml streptomycin and 100U/ml penicillin at 37ºC and 5% CO_2 in absence of serum. Cell culture was scaled-up to 500ml and when mortality reached 80%, supernatant was collected and cleared up of cells by centrifugation 1000g. Supernatants were filtered through a 0.45µm membrane (Merck Millipore, Billerica, MA, USA) and stored at -20ºC.

M2.2 Lymphoblastoid cell line HOM-2

HOM-2 (European Collection of Cell Cultures, ECACC) is an Epstein-Barr Virus (EBV) transformed lymphoblastoid line that express the HLA-DR1 molecules. Cell were cultured in RPMI 1640 medium (Sigma-Aldrich, St. Louis, USA), supplemented with 2mM L-glutamine, 10% Fetal Bovine Serum, 0.1 mg/ml streptomycin and 100U/ml penicillin. Cells were maintained in a concentration of $3x10^5$ - $2x10^6$ cells/ml at 37ºC and 5% CO_2.

M2.3 Sf9 insect cell line

Spodoptera frugiperda cell line Sf9 was used for recombinant protein production using baculovirus (see M3.2). Cells were cultured in Insect-XPRESS™ medium (Lonza, Basel, Switzerland) in suspension grown at 27ºC and final concentration $0.5x10^6$ cells/ml.

M3. Protein production and purification

M3.1 L243 Antibodies

For antibody purification, 3ml of Protein G sepharose (GE Healthcare, Buckinghamshire, UK) was packed into chromatography columns and washed with 10 volumes of 20mM phosphate buffer. Hybridoma supernatant was passed through the column at 4ºC twice and then washed again with 20ml of 20mM phosphate buffer. Elution was done with 20ml of 0.1M citric acid pH 2.7-3-0. Fractions of 1ml were collected, neutralized with 1M Tris buffer pH 8.0 and kept on ice until concentration evaluation. Column was washed with 20mM phosphate buffer and stored in 0.02% sodium azide in phosphate buffer. The presence of protein in each fraction was determined by Bradford method. Selected fractions were pooled and dialyzed with 500ml of

coupler buffer (0.1M $NaHCO_3$, 0.5M NaCl, pH 8.3) 4h 4 times. Protein quantification was determined using DC Protein Assay Kit (Bio-Rad, Hercules, California, USA) using a standard curve of bovine serum albumin. Antibodies were stored at -20ºC until use.

M3.2 Recombinant HLA-DM

Extracellular domains of the genes encoding the human HLA-DMα and β chains were cloned into pAcUW51 plasmid. The truncated α and β chains were genetically modified to contain the Flag epitope (DYKDDDDK) for protein purification and the c-Myc epitope (EQKLISEEDL) respectively, at their C termini. Construct was kindly provided by Prof. Sadegh-Nasseri. Baculovirus generation and protein production were carried out by the Platform of Protein Production (Ciber-bbn, UAB). pAcUW51-DMαβ was cotransfected together with BD BaculoGold Baculovirus DNA using BD BaculoGold Transfection Buffer A and B Set (Thermo Fisher Scientific, Waltham, MA, USA) into Sf9 cells. Best baculovirus clone was selected for high scale production.

Sf9 cell culture was scaled-up to $1x10^6$ cells/ml for baculovirus infection (MOI=5). Total volume of 1.5-3L of cell culture was infected during 72h. Supernatant was collected by centrifugation 10000g 10min at 4ºC. Supernatant was filtered through a 0.45µm membrane (Merck Millipore, Billerica, MA, USA) before be frozen until purification.

For protein purification, 6ml of 50% slurry anti-Flag M2 resin (Sigma-Aldrich, St. Louis, USA) were packed into a chromatography column for gravity flow purification. To clear up the glycerol, the column was washed with two volumes of Tris buffer saline (TBS, 50mM Tris, 150mM NaCl, pH 7.4), three volumes of 0.1M Glycine pH 3.5 and three volumes of TBS. Affinity column was placed into a cold chamber to work at 4ºC. Supernatants were passed through the M2 affinity column twice. Then, column was washed with 200 ml of citric phosphate buffer (18mM citric acid, 64mM Na_2HPO_4, pH 6.0) and let run out until the fluid level reached approximately the resin level. For elution, 20ml solution of 0.1mg/ml Flag peptide (Sigma-Aldrich, St. Louis, USA) was prepared in citric phosphate buffer pH 6.0. Once loaded with elution solution, column was let rest for 5min prior to elution. Fractions of 5ml were collected and placed on ice until validation. To regenerate the column, Glycine-HCl pH 3.5 was passed through for 15min and then washed with 200ml of TBS. Resin was regenerated in TBS-50% Glycerol-0.02% sodium azide and stored at 4ºC.

Protein quantification of each fraction was determined as described in section M3.1, and fractions were pooled at convenience. For sample concentration, Centriprep Ultracel YM-10 devices (Merck Millipore, Billerica, MA, USA) were used. Filters were conditioned first with citric phosphate buffer pH 6.0 by sequential centrifugations (30, 15 and 5min) at 2500g and then samples were concentrated following the same centrifugation procedure. Protein concentration was measured again and working fractions were frozen at -80ºC until use. Recombinant HLA-DM functionality was tested as described in section M17.2.

M3.3 Recombinant HLA-DR3

Soluble HLA-DR3 was purified from insect cell culture supernatants by affinity chromatography and dialyzed against phosphate storage buffer (pH 6.0), as previously described (153). Material was provided by the Tetramer Core Laboratory (Benaroya Research Institute, Seattle, USA).

M4. Commercial available proteins and peptides

Human thyroglobulin (Sigma-Aldrich, St. Louis, USA) and recombinant subunit A of the TSHR (CheasePeake PERL, Savage, MD, USA) antigens were purchased. The human proteases cathepsin B, cathepsin L, cathepsin H and recombinant cathepsin S were purchased from Merk-Millipore and human cathepsin D from Sigma-Aldrich.

The reference myoglobin peptide $Myo_{137–148}$ (LFRKDIAAKYKE) with or without the N-terminal biotin label, thyroglobulin-derived peptides (VPESKVIFDANAPVA, LSSVVVDPSIRHFDV, VVVDPSIRH, SSVVVDPSIRHF, SVVVDPSIRHFDVAH, SLALSSVVVDPSIRHFDV, LSSVVVDPSIRHF. SVVVDPSIRHFD, LSSVVVDPSIRHFDVAH, SVVVDPSIRHFDV) and hemagglutinin A peptide $HA_{306-318}$ (PKYVKQNTLKLAT) were synthesized by GenScript Inc. with >90-95% purity. Peptides were dissolved in DMSO at 10 mg/ml and subsequently diluted as needed.

$CLIP_{89-105}$ KMRMATPLLMQALPM peptide was synthetized with an extra cysteine residue at N-ter for peptide labelling. 1-2mg peptide was dissolved in cold PBS and incubated for 3h at RT with 20 µl of 75mM fluorescein-5-maleimide (Thermo Fisher Scientific, Waltham, MA, USA). Samples were concentrated to 100-200µl a SpeedVac unbound fluorescein was removed from the sample by passing through a Sephadex G10 column (Sigma-Aldrich, St. Louis, USA). Concentration of labeled peptide was determined by spectrophotometry according to extinction coefficient of fluorescein-5-maleimide (83 $mM^{-1}cm^{-1}$).

M5. Endocytosis experiments

Immature MoDCs were pulsed with purified thyroglobulin, thyroid extract or PBS. Antigen were diluted in sterile PBS to pulse with 10-200nM final concentration and several incubation times (5-120min) were used for flow cytometry and confocal microscopy experiments. For HLA-DR peptide isolation experiments, cells were pulsed with 100nM commercial thyroglobulin, 1500ug thyroid extract (1000nM thyroglobulin) or PBS for 5h prior the maturation LPS. Cells were detached with PBS and washed before analysis.

In blocking experiments, cells were pre-incubated with 1mg/ml mannan, 10nM mannose, 10nM galactose, 10nM lactose or 10nM N-acetyl-D-glucosamine for 30min at 37ºC prior thyroglobulin pulsing.

M6. Flow cytometry

M6.1 L243 antibody titration

Serial dilutions of the dialyzed antibodies (1:50 to 1:1600) were tested for HLA-DR recognition using a HLA-DR^+ cell line HOM-2. $2x10^5$ cells were incubated with 50µl of the diluted antibody for 30min at 4ºC to prevent the HLA reinternalization. Supernatant of a previous purification was used as positive control and mouse anti-human IgG2a isotype for negative control. After washing with PBS, secondary antibody goat anti-mouse IgG Alexa488 (Invitrogen, Waltham, MA, USA) was added and incubated for additional 20min on ice. Fluorescence was measured with FACsCanto flow cytometer and analyzed with FACsDiva software (BD, San Jose, CA, USA).

M6.2 MoDCs cell surface phenotype

Conjugated antibodies anti-CD83-APC, anti-CD86-APC, anti-CD206-APC (Mannose receptor 6) (BD Biosciences, CA, USA), anti-CD209-PE (DCSIGN) (AbD Serotec, Düsseldorf, Germany) and anti-CD14-PE (Sanquin Reagents, Amsterdam, The Netherlands) and their corresponding isotype controls were used for phenotype studies.

Monocyte, immature MoDCs or mature MoDCs were washed with TBS containing 0.5% human serum albumin (HSA) (Sanquin Reagents, Amsterdam, The Netherlands). Cells were incubated with 50 µl of 1 µg/ml mAb or appropriate isotype controls diluted in TBS/0.5% HSA for 30 min at 4 °C. Cells were washed twice and resuspended in TBS/0.5% HSA. Cells were analyzed on a Fortesa flow cytometer (BD, San Jose, CA, USA) and analyzed with Flowjo software version 8.6 (Tree Star, Inc, Ashland, OR, USA).

M6.3 Thyroglobulin uptake measurement

Immature MoDCs were washed with TBS/0.5% HSA and fixed in 1% paraformaldehyde in TBS for 15min. Then, 50mM NH_4Cl in TBS/0.2% saponin was added for 15 min to quench unspecific fluorescence. Fc receptors were blocked (human FcR blocking reagent, MACS, Miltenyi Biotec, Bergisch Gladbach, Germany) at 4ºC overnight (O/N). Cells were incubated with 50 µl of 1 µg/ml anti-thyroglobulin antibodies TGB04 and TGB05 cocktail (IgG1) (abcam, Cambridge, UK) or the appropriate isotype controls diluted in TBS/0.5% HSA for 1h at 4°C. Cells were washed twice and resuspended in TBS/0.5% HSA and incubated with goat anti-mouse IgG1 conjugated to Alexa488. Cells were analyzed on a Fortesa flow cytometer (BD, San Jose, CA, USA) and analyzed with Flowjo software version 8.6 (Tree Star, Inc, Ashland, OR, USA).

M7. Confocal microscopy

Cells were washed with TBS/0.5% HSA and fixed in 4% paraformaldehyde in TBS for 15min. Then, 50mM NH_4Cl in TBS/0.2% saponin was added for 15min and Fc receptors were blocked at 4ºC O/N. Cells were incubated with 1µg/ml of anti-HLA-DR and anti-thyroglobulin antibodies

for 1h at 4ºC and after washing, with goat anti-mouse IgG1 conjugated to Alexa488 and goat anti-mouse IgG2a conjugated to Alexa568 (Invitrogen, Waltham, MA, USA) for 45min at 4°C. Cells were mounted with Mowiol-Hoerstch (Polysciences, Warrington, PA, USA). Preparations were visualized in a Leica TCS SP8 confocal microscope (Leica Microsystems, Wetzlar, Germany) and images analyzed with LAS X software (Leica Microsystems, Wetzlar, Germany).

M8. RNA extraction and retrotranscription

RNeasy Plus Mini Kit (Qiagen, Venlo, The Netherlands) was used for total RNA extraction following the recommended procedure. Cells ($1x10^6$) were manually disrupted using a 1ml syringe in presence of lysis buffer and β-mercaptoethanol. Extracted RNA was quantified using NanoDrop 1000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). For each sample, a maximum of 2µg of RNA was transcribed to cDNA in presence of 200 units of SuperScript III retrotranscriptase (Invitrogen, Waltham, MA, USA), 0.5µg oligo(dT)s, 0.5mM dNTPs, 5mM DTT and 40 units of RNase OUT (Invitrogen, Waltham, MA, USA) for 20µl final volume per reaction. cDNA was quantified using NanoDrop 1000.

M9. Conventional PCR

The housekeeping of Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) expression was used as control for retrotranscription and to compare other genes expression. Cathepsin primers used were published by Stoeckle *et al*.(75). Additionally. CD86, CD1a and CD1c were studied. Primers are summarized in Table 2. For reactions, final concentration 0.5µM of forward and reverse primers were used for amplification in presence of cDNA sample, 1x reaction buffer, 0.2mM MgCl2, 0.25mM dNTP's, 0.04 unit of Taq Polimerase (Biotools, Madrid, Spain). Reaction procedure for GAPDH expression was: one step at 95ºC for 3min, 28 amplification steps (95ºC 30'', annealing 65ºC 30'', 72ºC 30'') and a final step of 7' at 72ºC. Reaction procedure was as follows: one step at 95ºC for 3min, 30 amplification steps (95ºC 30'', annealing at 58ºC 30'', 72ºC 30'') and a final step of 7' at 72ºC. 2% agarose gels in Tris-Acetate-EDTA (TAE) buffer were used for electrophoresis. Gel Doc XR system and QuantityOne software was used for imaging acquisition.

Table 2. Primer sequences used for PCR

Gene	Forward (5'-3')	Reverse (5'-3')
GAPDH	CTTCTTTTGCGTCGCCAG	AGCCCCAGCCTTCTCCA
Cathepsin B	CTGTGTATTCGGACTTCCTGC	CTGGTTGCCAACTCCTGG
Cathepsin D	AACTGCTGGACATCGCTTG	CAGCCTCTCCGGGTACCT
Cathepsin H	ACTGGCTGTTGGGTATGGAG	GGAAAGAACATGTGTGGCCT
Cathepsin L	CTTATCTCACTGAGTGAGCA	TGAGGCAACAGAAGAATCC
Cathepsin S	ACTCAGAATGTGAATCATGGTG	GGATATATTCGGATGGCAAGAA
Cathepsin V	CAGAAATTCAGGAAGGGGAA	TGGTGCTCTTGAAGGACA
CD86	ATTCTGAACTGTCAGTGCTTGC	CGGTTACCCAGAACCTAAGAAG
CD1a	TGTTAGCTGTTCTCCCAGGTGA	AGGATGCGATCCAGATGACAT
CD1c	TGGTGACAATGCAGACGCA	GGTTGACAAATGAGAAGATCTGGA

M10. Protein gel electrophoresis

M10.1 Polyacrylamide gels

Different gels were used depending on the finality of the analysis. To test recombinant protein integrity and for western blot, 10% SDS-PAGE polyacrylamide homemade gels were used. To test stability of peptide-HLA-DR3 complexes, Criterion™ Tris-HCl Precast 12% gels (Bio-Rad, Hercules, California, USA) were used. Gradient gels, NuPAGE® Novex® 4-12% Bis-Tris gels (Invitrogen, Waltham, MA, USA), were necessary to run cathepsin-digested proteins due to the smaller fragments generated.

M10.2 Electrophoresis

In denaturing electrophoresis, samples were boiled in presence of 1x sample buffer (62.5mM Tris-HCl pH 6.8, 0.02% bromophenol blue, 10% glycerol, 0.1% SDS and 12.5% β-mercaptoethanol). Electrophoresis was run in running buffer (35mM Tris, 1.32mM Glycine, 0.1% SDS) for handmade and Bio-Rad gels and MOPS running buffer (Invitrogen, Waltham, MA, USA) for Invitrogen gels at recommended voltage by manufacturer or 200V for handmade gels.

In gentle electrophoresis, samples were not boiled to preserve the protein conformation and were run as described above. For native electrophoresis, samples were not boiled and SDS was not used in running buffer.

M10.3 Gel staining

For coomassie blue staining, gels were incubated with colloidal coomassie blue (Sigma-Aldrich, St. Louis, USA) O/N at RT.

For silver staining, gels were fixed in 2% Trichloroacetic acid (TCA), 50% ethanol and 0.1% formaldehyde for 10min. Gels were washed with distilled water and 50% ethanol twice. Sensitization was done using 0.02% $Na_2S_2O_3$ 1min. Gels were rinsed with distilled water and stained with 0.2% AgNO and 0.1% formaldehyde for 10min. After rinse, gels were revealed with 0.625 Na_2CO_3, 0.04% and 0.0005% $Na_2S_2O_3$ for 5min.

M11. Tissue extracts analysis

M11.1 Western blot

Tissue extracts were electrophoretically separated in 10% SDS-PAGE as described in M10. Proteins were transferred to polyvinylidene difluoride (PVDF) membranes for 90min at 300mA. After washing, membranes were incubated with 1µg/ml of anti-thyroglobulin antibody (see M6.3) O/N at 4ºC. Membranes were washed and sheep anti-mouse IgG conjugated to horseradish peroxidase (GE Healthcare, Buckinghamshire, UK) was added and incubated for 2h at RT. Clarity Western ECL Blotting Substrate kit (Bio-Rad, Hercules, California, USA) was used to

reveal the membrane. Gel Doc XR system and QuantityOne software was used for imaging acquisition.

M11.2 Thyroglobulin quantification

Thyroglobulin content of the tissue extracts was determined by ELISA in duplicate experiments. 96-well plates were coated with 0.5µg/ml of anti-thyroglobulin antibody (see M6.3) and incubated O/N at 4ºC. Serial dilutions of commercial-available thyroglobulin or extracts dilutions were incubated in those plates for 4h at RT. After washing, sheep anti-mouse IgG conjugated to horseradish peroxidase (GE Healthcare, Buckinghamshire, UK) was added and incubated for 2h at RT. SIGMAFAST™ OPD tablets (Sigma-Aldrich, St. Louis, USA) were used for HRP-substrate colorimetric reaction. Reaction was stopped with 3M H_2SO_4 solution and absorbance measured at 492 nm.

M12. Cell free system (CFS) for antigen processing *in vitro*

Protocol was optimized based on the previously described by Hartman *et al*.(154). Intact thyroglobulin or pre-digested thyroglobulin with human cathepsins B, L and S (Calbiochem, Merck Millipore, Billerica, MA, USA) at neutral pH (pH 7.4.) were used as antigen. HLA-DR3, antigen, and HLA-DM were incubated in citrate phosphate buffer (24mM citric acid, 50mM Na2HPO4, pH 5.0) at 37 °C for 2h, after which the selected cathepsin combination (B, H and S or B, H and L) were added with 6mM L-Cysteine and 4mM EDTA for an additional 1h. In thyroid-like condition, thyroglobulin was predigested in PBS at neutral pH by cathepsin B, S and L before it inclusion in the system. After incubation, the pH was adjusted to 7.5 and 10 mM iodoacetamide was added to inactivate the cathepsins.

M13. Peptide elution from HLA-DR molecules

M13.1 Preparation of L243-coupled sepharose

L243 was coupled to CNBr activated sepharose 4B (GE Healthcare, Buckinghamshire, UK) to obtain 2-4mg/ml of antibody in 1ml final volume. First, sepharose beads were weighed and resuspended in 1mM HCl. Hydrated beads were washed with 1mM HCl and coupling buffer (0.1 M NaHCO3; 0.5 M NaCl; pH 8.3). Beads were incubated with the antibody solution for 4h at RT in rotation. As control, absorbance at 280nm was measured after incubation to determine the antibody coupling. Two wash steps were then done with blocking buffer (0.1M Tris-HCl, pH 8.0) and beads blocked for 2h in rotation in blocking buffer. Beads were then washed again alternatively with wash buffer pH 4.0 (0.1M NaAC, 0.5M NaCl) and 30 ml of wash buffer pH 8.0 (0.1M Tris-HCl, 0.5M NaCl), three times each. Antibody-coupled sepharose was stored at 4ºC in 0.02% sodium azide in wash buffer pH 8.0.

M13.2 Peptide purification from MoDCs samples

Peptide-HLA-DR complexes were purified as described (155-157). Mature MoDCs cell pellets were resuspended in 50mM Tris-HCl pH 7.0, containing 4% MS-grade NP-40 (Thermo Fisher Scientific, Waltham, MA, USA) and protease inhibitor cocktail (Halt Protease and Phosphatase Inhibitor cocktail, EDTA free, Thermo Fisher Scientific, Waltham, MA, USA) by end-over-end incubation at 4 °C for 1h. Cell lysates were cleared by centrifugation for 15 min at 4°C at 14.000 rpm. The HLA-DR–peptide complexes were purified from the soluble fraction by immunoaffinity chromatography using L243-coupled CNBr Sepharose 4B in O/N incubation at 4°C. Subsequently, L243 sepharose was washed 3 times with 10 mM Tris-HCl pH 7.0 supplemented with the protease inhibitor cocktail and 5 times with 10 mM Tris-HCl pH 7.0 without protease inhibitor cocktail. Peptides were eluted from HLA-DR by adding 10% acetic acid for 15 min at 70°C. In parallel experiments, cell lysates were incubated with non-coupled CNBr Sepharose 4B to identify the non-specific-bound peptides.

M13.3 Peptide purification from CFS samples

HLA-DR3-peptide complexes were immunoprecipitated with L243-coupled CNBr Sepharose 4B. Bound peptides were eluted with 1% trifluoroacetic acid, filtered through 10kDa molecular weight cut-off Centriprep Ultracel YM-10 devices (Merck Millipore, Billerica, MA, USA) and lyophilized until analysis. In parallel experiments, samples with all the components except for HLA-DR3 were incubated with L234-sepharose to identify the non-specific-thyroglobulin peptides.

M14. Peptide digestion

Thyroglobulin peptides VPESKVIFDANAPVA and LSSVVVDPSIRHFDV were digested *in vitro* in 20mM ammonium formiate buffer at pH 5.0 as follows: a) cathepsin B (0.36μM), cathepsin H (0.36μM) and cathepsin S (0.14μM) 1h at 37ºC, b) cathepsin B (0.36μM), cathepsin H (0.36μM) and cathepsin L (0.2μM) and 1h at 37ºC and c) cathepsin B (0.36μM), cathepsin H (0.36μM) , cathepsin L (0.2μM) and cathepsin D (0.2μM) and 1h at 37ºC. Proteases were inactivated with 10mM iodoacetamide and then samples were frozen at -20ºC until analysis.

M15. Mass spectrometry (MS) analysis

M15.1 Matrix-Assisted Laser Desorption/Ionization (MALDI)-TOF

AB Sciex 4800 MALDI-TOF/TOF mass spectrometer using AB Sciex 4000 Series Data Explorer control and processing software (V3.7.1 Build 1, AB Scix) was used for analysis. A 0.5μL sample fraction was loaded onto a 348-well SB Sciex MALDI plate and mixed with 0.5μL of matrix (3mg/mL α-ciano-4-hidroxicinamic acid in ACN/H2O 2/1 v/v 0.1% TFA) and was let to dry. Each duplicate spectrum acquired was a composite of 800 laser shots. Spectra were externally calibrated using a two standard mixture (Peptide calibration standards, Bruker). Spectra were analyzed with FindPept (http://web.expasy.org/findpept/) to identify the peptide

sequences based on the mass of relevant peaks. Only peaks with relative intensity over 10% were considered.

M15.2 Liquid chromatography–tandem mass spectrometry (LC-MS/MS)

Eluted peptides from MoDCs samples were analyzed at the Department of Plasma Proteins (Sanquin Blood Supply, Amsterdam, The Netherlands). Peptides were purified from the acetic acid eluate and desalted using C18 stage-tips prepared in-house (3M, Neuss, Germany) and then separated using a reverse-phase C18 column made in-house from a Silica tip emitter (New objective, Woburn, MA, USA) filled with 1.9um C18 particles (Dr. Maisch, Ammerbuch-Entringen, Germany) at a flow rate of 300 nL/min with a gradient from 0% to 80% (vol/vol) acetonitrile with 1% HAc. Separated peptides were sprayed directly into the LTQ Orbitrap XL mass spectrometer (Thermo Fisher Scientific, Waltham, MA, USA) using a nanoelectrospray source with a spray voltage of 2.1 kV. A collision-induced dissociation was performed for the 5 most intense precursor ions selected from each full scan in the Orbitrap (350 to 2000 m/z, resolving power 60 000). An isolation width of 2 Da was used for the selected ions (charge ≥2) and an activation time of 30 ms. Dynamic exclusion was activated for the MS/MS scan with a repeat count of 1 and exclusion duration of 60 s.

MS analysis of CFS samples was performed using also a LTQ Orbitrap XL mass spectrometer (Thermo Fisher Scientific, Waltham, MA, USA) equipped with the Protana interface (Protana A/S, Denmark) at the Proteomic facility (CSIC/UAB, Bellatera, Spain). The instrument was operated in the positive-ion mode with a 2 kV spray voltage. The scan range for full MS was *m*/*z* 2000. The analysis was performed in an automatic dependent scan mode. A full MS scan followed by eight MS/MS scans for the most abundant signals were acquired. The resolution was set to 6000 full MS. To minimize the redundant selection of precursor ions, dynamic exclusion was set to 1 MS/MS scan for each time window of 5 min.

M15.3 Database search

Peptides were identified based on the MS/MS fragmentation spectra in a Sequest search algorithm against the UniprotKB human non-redundant protein database 25.H_sapiens.fasta, using Proteome Discoverer release version 1.4 software (Thermo Fisher Scientific, Waltham, MA, USA*).* The search parameters allowed a peptide mass tolerance of 10 ppm, a fragment tolerance of 0.6 Da, no enzyme restriction and variable modifications for oxidized methionine (+16 Da) iodination (+125.89 Da). A false discovery rate (FDR) of 1% was used as filter for MoDCs samples and 0.01% for CFS samples.

M15.4 SIEVE™ Software for differential analysis

SIEVE 2.2 software (Thermo Fisher Scientific, Waltham, MA, USA*)* was used for semi-quantitative differential analysis of the LC-MS data sets. This software uses the MS intensities from raw data to find statistical differences between samples and determined a p-value for the

expression ratio of each putative biomarker, so at least duplicates of each condition are needed. ChromAlign algorithm reduces the effect of chromatographic variability between samples but a high degree of similarity iss still needed for comparison. Frame parameters were adjusted as described for MoDCs Proteome Discoverer analysis. A threshold of $1x10^5$ units were determined as basal peak intensity.

M16. Theoretical binding assignment

Three evaluation methods where used to assign each peptide to the corresponding allele: Propred (www.intech. res.in/raghava/propred/index.html), NetMHCII (www.cbs.dtu.dk/services/netmhcIIpan) and an in-house software, *LaiaMotifs* (www.proteomica.uab.cat), based on the binding motifs published in SYFPEITHY database (www.syfpeithy.de) except for HLA-DR10 (DRB1*1001), HLA-DR4 (DRB1*0401) and HLA-DR3 (DRB1*0301) for which the revised binding motif were studied in our laboratory (29, 158, Guitart *et al*. in preparation). This methodology has been previously tested experimentally (59). NetMHCII tool uses an Artificial Neural Network (ANN) that takes into account the residues in the anchor pockets of MHC-II molecule as well as peptide core and flanking residues. With this system, high binder (HB) peptides (corresponding to IC50 < 50) and intermediate binders (IB) (50 < IC50 < 500) were assigned to one of the two DRB1 expressed alleles of each sample. Propred tool contains a database of binding matrixes for 51 HLA-DR alleles and assigns a core sequence based on the presence of at least a correct P1 residue according to the allele's binding motif and a low or high threshold depending on the other anchor residues (generally P4, P6, P9). The threshold is defined as the 'percentage of best scoring natural peptides'. We used the following criteria: a peptide was considered HB if a core was assigned to the alleles at threshold ≤3 and IB if a core was assigned at a threshold between 9 and 3. For validation, we performed a manual analysis based on the described allele-binding motifs. All possible nine-residue cores were identified from each sequence, by fixing the P1 residue for each allele's motif. From the resultant cores, we chose the one best complying with an allele-binding motif, based on the rest of positions. A core with ≥3 coincidences with the motif was considered HB, 2 coincidences were IB and the remaining sequences, low binders (LB). Finally, to assign a peptide to a given allele, at least two out of the three methods must define the same binding core for each peptide and the same degree of affinity for the allele. If more than one core were acceptable, the one with higher affinity was considered. If a peptide could be associated to two alleles with the same affinity, it was noted as double-binder. Peptides were defined as not assigned (NA) due to discrepancy between the three methods.

M17. Experimental binding assays

M17.1 Direct binding assays

For binding assays, HLA-DR3 (1.5μM) was incubated for various times in the presence or absence of 1μM DM together with 50μM fluorescence-labeled peptides in citrate phosphate

buffer (pH 5.0) at 37 °C. Unbound peptide was removed by Sephadex G50 spin columns (GE Healthcare, Buckinghamshire, UK) at pH 7.4. Fluorescence emission of the FITC–peptide–DR complexes was measured at 25°C and 514–516 nm with excitation at 492 nm on a Fluoromax3 spectrofluorometer (Horiba Jobin-Yvon, Kyoto, Japan) with a slit width of 2nm.

M17.2 Indirect binding assays

For competitive binding assays, increasing concentrations of each non-biotinylated test peptide (1, 10, 100, 1000, $1x10^4$ and $1x10^5$nM) were incubated in competition with 250nM biotinylated $Myo_{137–148}$ peptide. Binding assays were carried out as previously described with some modifications (153) Briefly, peptides were incubated during 48h in the presence of 50nM of recombinant HLA-DR3 protein and 100nM of recombinant HLA-DM in binding buffer (citrate phosphate buffer pH 5.4, 0.02% n-dodecyl-β-maltoside). Reaction was neutralized with 50mM Tris-HCl and complexes were then transferred into wells coated with anti-HLA-DR antibodies for pMHC capture O/N at 4ºC. After washing, residual biotinylated reference peptide was labelled using europium-conjugated streptavidin (PerkinElmer, Waltham, MA, USA) and quantified using a Victor2 D time resolved fluorimeter (PerkinElmer, Waltham, MA, USA). Peptide binding curves were simulated by non-linear regression with GraphPad Prism 5 software (GraphPad Software, San Diego, CA, USA) using a sigmoidal dose–response curve. EC50 binding values in the presence or absence of HLA-DM were calculated from the resulting curves as the peptide concentration needed for 50% inhibition of reference peptide binding.

M18. Statistical analysis

Statistical analysis was performed using the GraphPad Prism version 5.0 for Windows (GraphPad Software, San Diego, CA, USA). Variance was calculated with the two-way ANOVA method followed by Bonferroni correction or t-test, depending on the analysis. A p value <0.05 was considered significant.

CHAPTER 1

Processing self-proteins by human monocyte-derived dendritic cells (MoDCs): an analysis of the peptide repertoires presented by HLA-DR alleles

1.1 BACKGROUND

For the last 25 years, the study of the MHC-II peptide repertoires has been used to describe the allele-specific peptide binding motifs of human (HLA-DR, HLA-DQ and HLA-DP) and mouse (IA and IE) MHC-II molecules and to analyze the general and the specific mechanisms of antigen processing and presentation. From the beginning, tumor or EBV-transformed B lymphoblastoid cell lines were used for mouse and human studies. In early reports, the relative inefficiency of sequencing methods was compensated by the use of very high numbers of cells to isolate the pMHC, usually between 10^8-10^{10} cells (23, 159-163). Other approaches such as cells transfected with MHC-II molecules have been used to study the importance of accessory molecules in the generation of peptide repertoires (158, 164). An interesting comparison of MHC-II repertoires from human T cell clones and B lymphoblastoid cell lines derived from peripheral blood of the same donors showed that only ~10% of the peptides belonged to cell-type specific proteins, the remaining peptides were common to both cell types (165).

Besides the data from transformed cell lines, MHC-II peptide repertoires have been analyzed from several lymphoid tissues and primary cell cultures. MHC-II peptidomes from thymus and spleen have been described for both human (59) and mouse (60, Guitart *et al*.. in preparation). From our work on the thymus HLA-DR peptidome, we were first to report peptides derived from tissue restricted antigens related to autoimmune diseases (47). Mouse MHC-II peptide repertoires have also been studied from splenic B cells and activated macrophages (61, 166). However, for DCs, the high numbers of cells needed and the moderate yield of peptides obtained have been a barrier difficult to overcome. There are limited data available on MHC-II peptide repertoires from DCs in mouse, sheep and human. *In vivo* enriched splenic DCs were used to study the mouse MHC-II peptidome (61). In our study (167), sheep DCs migrating from skin to draining lymph nodes were collected via the cannulation of the pseudo-afferent lymph duct. Interestingly, one sheep-specific cytokeratin peptide was identified, suggesting the active processing of epithelium-derived antigens. In a recent work, a total of 115 non-redundant HLA-DR-associated peptides were obtained from thymus resident DCs (46).

Small numbers of human *in vitro* monocyte-derived DCs (MoDCs) have been used to identify the HLA-DR peptidome from professional antigen presenting cells. More than 200 peptides associated to HLA-DR4 were isolated from $5x10^6$ cells to analyze the influence of CLIP in the HLA-DR repertoire of immature and mature MoDCs (168). Later works used a similar approach to study the presentation of antigens involved in hemophilia A and thrombotic thrombocytopenic purpura (TTP) by MoDCs (155-157). In the present work, using a small number of mature MoDCs and a highly efficient sequencing method by MS/MS, we have performed an exhaustive analysis of the endogenous HLA-DR peptidome from MoDCs expressing different HLA-DR alleles.

1.2 RESULTS

1.2.1 Characteristics of the HLA-DR-associated peptide repertoires in mature MoDCs

Mature MoDCs from HLA-typed healthy donors were used to analyze their endogenous HLA-DR-associated peptidome as previously described (155-157). Phenotype of immature and mature MoDCs was analyzed by flow cytometry and confocal microcopy. Mature MoDCs expressed higher levels of co-stimulatory molecules (CD80 and CD86) than monocytes and immature MoDCs (Fig.5A). HLA-DR molecules were expressed at the intracellular compartments in immature MoDCs and delivered to the membrane surface in mature MoDCs (Fig.5B). Only *bona fide* identifiable sequences and non-redundant peptides were included in the analysis. Thus, peptides derived from skin proteins (e.g. keratins) as possible handling contaminations, peptides from proteins non-specifically bound to sepharose controls, sequences unidentifiable in the databases and redundant peptides were discarded. The complete list of accepted sequences, their source protein and its most likely cellular localization are included in Annex 1.

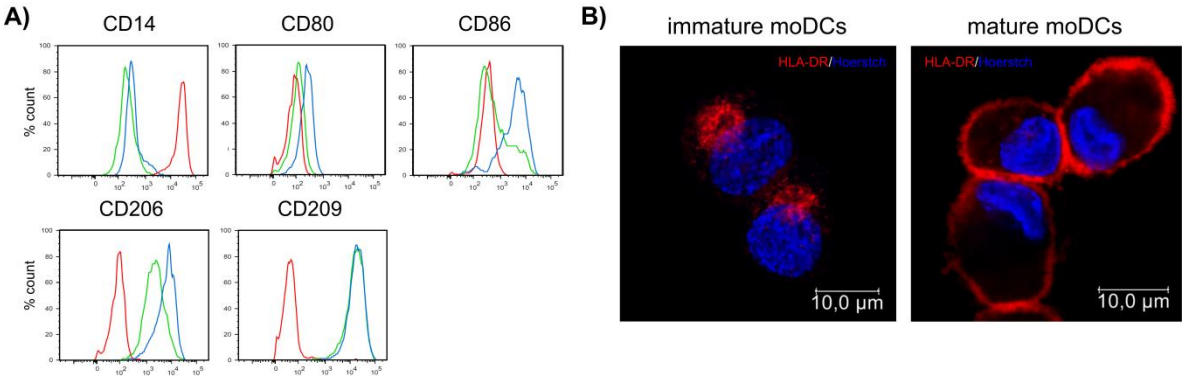

Figure 5. Phenotype analysis of the human monocytes, immature and mature monocyte-derived dendritic cells (MoDCs). A) FACS histograms represent the surface expression of CD14, CD80, CD83, CD206 (mannose receptor 6) and CD209 (DC-SIGN) of monocytes (red line), immature MoDCs (green line) and mature MoDCs (blue line). B) Immunofluorescence detection of HLA-DR molecules (L243 antibody) and nucleus (Hoerstch) in immature and mature MoDCs. HLA-DR molecules are retained in the intracellular compartments and delivered to the cell surface after the maturation stimulus.

The analysis of HLA-DR-associated peptides from mature MoDCs derived from seven HLA-DR-typed donors yielded 1319 peptides. Donor G typed DRB1*0701 and DRB1*1501. In the DRB1*1501 haplotype the HLA-DRB5*0101 gene is expressed, generating a second HLA-DR molecule (HLA-DR51), as capable as those encoded by DRB1 to present peptides with a well-defined motif (21). Therefore HLA-DR51 was also included within the molecules analyzed. To increase the number of peptides associated to each allele, donor G samples were prepared and analyzed by mass spectrometry in two parallel experiments and the resulting peptides were then pooled.

Peptide analysis data are summarized in Table 3. Peptide size followed a normal distribution (Fig.6A) with an average length of 16 residues, as described for peptides associated to human MHC-II alleles (169). Another classical feature of MHC-II-associated peptides is that they are often clustered in nested sets, i.e., peptide families with a common core sequence but different length along C- and N-termini, allowing long peptides to bind the MHC-II molecules (169). In our analysis, between 44 and 73.5% of the peptides were grouped in nested sets comprised of 2-20 peptides, whereas only a single variant was found for an average of 42% of the peptides.

Table 3. Characteristics of the MoDCs samples and description of peptides and source proteins

	Donor A	Donor B	Donor C	Donor D	Donor E	Donor F	Donor G
HLA-DR type	DRB1*0301 DRB1*1101	DRB1*0301 DRB1*1301	DRB1*0401 DRB1*1301	DRB1*0101 DRB1*0701	DRB1*0101 DRB1*1101	DRB1*0901 DRB1*1001	DRB1*0701 DRB1*1501 DRB5*0101
Non redundant peptides	140	85	106	219	194	213	362
Proteins	79	57	70	98	89	85	138
Unique peptides	66 (47.1%)	47 (55.3%)	70 (66%)	69 (31.5%)	74 (38.1%)	65 (30.5%)	96 (26.5%)
Peptides in nested sets	74 (52.5%)	38 (44.7%)	36 (44%)	150 (68.5%)	120 (61.9%)	148 (69.5%)	266 (73.5%)
Nested sets	25	16	12	39	35	44	80
Peptides per protein	1-11	1-6	1-5	1-20	1-31	1-14	1-21
Peptides per nested set	2-7	2-6	2-5	2-20	2-20	2-14	2-15

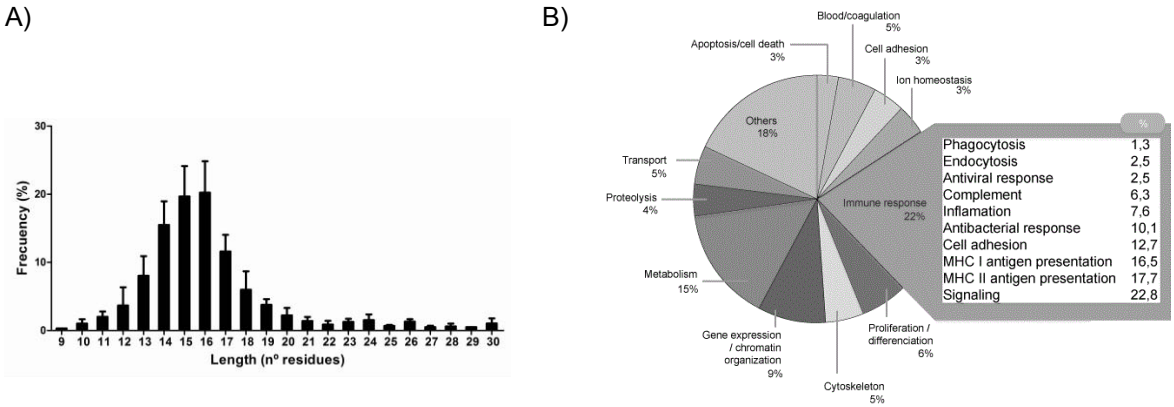

Figure 6. Size and functional distribution of the peptides associated to HLA-DR in mature MoDCs. A) Size of MHC-II peptides followed a normal distribution, with an average size of 16 residues. Bars represent frequency (%) of the samples ± Standard Deviation (SD). B) Functional clustering of the parental proteins based on the annotation in Gene Ontology Database.

Between 85 and 362 peptides were analyzed per sample. They all derived from a total of 353 proteins, from which many were shared by two or more samples. Only 5 proteins were common to all samples: human serum albumin, present in the human serum used for cell culture medium supplementation, serine-tRNA ligase, 60S ribosomal protein L22, prolow-density lipoprotein receptor-related 1 and low affinity immunoglobulin Fcε receptor. Proteins related to antigen processing and presentation such as HLA-DRα chain, HLA-Bα chain and cathepsin B were found in more than 5 samples. Peptides from DCs and other myeloid cells-specific proteins,

such as myeloperoxidase and the macrophage mannose receptor, were shared by 6 from 7 samples. The CLIP peptide was found in samples from donors A, F and G. Other Ii-derived peptides were identified from the same donors and donor D. Peptides from shared proteins were abundant; for instance, 31, 20, 15 and 11 peptides from serum albumin were identified from donor E, D, G and A samples, respectively.

Location and function of the 353 parental proteins were determined, based on their annotation in the Gene Ontology database. A variety of cellular processes were represented by the source proteins (Fig.6B). As expected, ubiquitously expressed proteins belonging to processes such as basic metabolism, cell proliferation or gene expression were found to be predominant. However, a wide range of proteins related to the immune response (22%) were also identified, mostly MHC-I and II antigen presentation-related proteins and molecules from the immune system signaling pathways.

1.2.2 Mature MoDCs mostly present high affinity peptides from the endocytic pathway

Because of the large size of MHC-II peptides, up to 46% were assigned to more than one allele in some of the samples and most of them were high binders for both alleles. For HLA-DR1 or HLA-DR4 positive donors C, D, and E there was a clear prevalence of peptides assigned to these alleles (47.2%, 47.5% and 68.3%) vs. the partner alleles (17.9%, 5% and 5.7%), when discarding the double-binder peptides. Looking to the peptides exclusively associated to one allele from DR15 positive donor G, more peptides were assigned to HLA-DR51 (DRA1*0101/DRB5*0101) than to HLA-DR15 (DRA1*0101/DRB1*1501), 15.2% vs. 11%, confirming the contribution of DRB5 alleles to the HLA-DR peptide repertoires.

To study the affinity of analyzed peptides for each HLA-DR allele in the context of professional APCs, we pooled all the peptides from different samples assigned to the same allele. Double-binder peptides were included for the analysis of both alleles. More than 75% of the peptides were high binders (HB) for their respective allele (Fig.7), whereas over 20% were assigned as intermediate (IB) or low binders (LB). We did not find significant differences in predicted affinity between alleles.

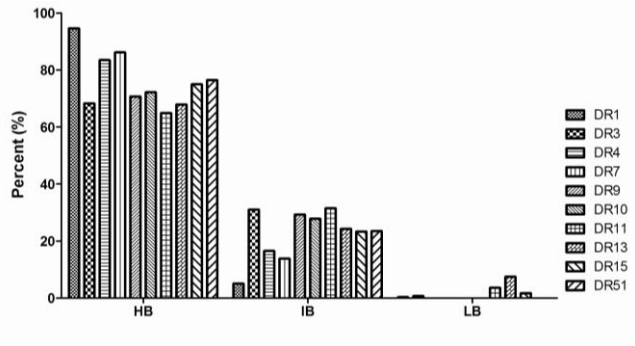

Figure 7. Theoretical affinity assignment. Peptides assigned to the same allele were pooled together, independently of the donor. Double-binder peptides were included for the analysis in both alleles. Around 5% of total peptides were not assigned to any allele due to discrepancy in the analysis. For the rest, an average of 76% were assigned as high binders (HB), 22.6% as intermediate binders (IB) and 1.4% as low binders (LB). Bar graph represents average percent of each allele.

In a standard location definition, proteins secreted and from the extracellular matrix, ER and Golgi apparatus, lysosomes/endosomes and cellular membrane component proteins are considered to be degraded in the endocytic pathway for antigen processing and presented by MHC-II molecules. Instead, mitochondrial, cytosolic and nuclear proteins are associated to the cytosolic pathway. As expected for MHC-II peptides, the endocytic pathway was predominant (~80% of peptides) over the cytosolic pathway (~20%) (Fig.8A) (162, 170). When focused on the specific compartments, the cellular membrane showed to be the main source of proteins, followed by the extracellular or secreted proteins and the lysosomal/endosomal components (Fig.8B). This was expected in cells derived from cell culture conditions, where the extracellular milieu only contains serum and some secreted proteins. Interestingly, even in these culture conditions, significant differences were observed for HLA-DR51, compared to the other HLA-DR molecules. HLA-DR51 only bound 25% of the peptides from the cellular membrane, as many as from extracellular environment and from lysosome/endosome proteins. In contrast, the cytosolic pathway appeared to be favored in HLA-DR15, in detriment of extracellular and lysosomal/endosomal components, although this was not statistically significant.

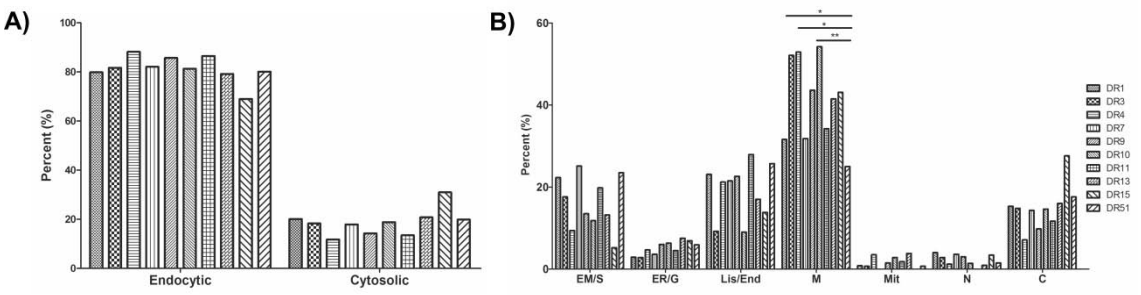

Figure 8. Degradative pathway and Intracellular distribution of the HLA-DR-associated peptide parental proteins according to the assigned allele. Endocytic pathway of protein degradation included membrane (M), extracellular matrix or secreted proteins (EM/S), endoplasmic reticulum/Golgi (ER/G) and lysosome/endosome (Lys/End). Mitochondrial (Mit), cytosolic (C) and nuclear (N) proteins were included in the cytosolic pathway of degradation. A) Average percent of HLA-DR ligands derived from each degradative pathway. B) Subcellular location of the parental proteins. Contribution of membrane components to HLA-DR peptidome is significantly lower in HLA-DR51 (HLA-DRB5*0101) subset when compared to HLA-DR4, HLA-DR10 and HLA-DR3. Bars represent average percent of each allele (*P<0.05, **P<0.01. Two-way ANOVA. Bonferroni post-test)

1.2.3 Peptide flanking residues are restricted in some HLA-DR alleles

Peptide flanking residues (PFR) of the MHC-II peptides are defined as the residues adjacent to the binding core, in their N- and C-terminus. They are described as capable of influencing the peptide binding to MHC and by T Cell Receptor (TCR) recognition (12, 14). Peptide binding is mediated by hydrogen bonds between the side chain of these residues and of residues located at the MHC-II α and β chains. We analyzed the PFR length for each HLA-DR allele repertoire. Because the length of the PFR is dependent on the assigned binding core, doubled-binder peptides were excluded from this particular study. The analysis showed that the average length

for N-terminus PFR was of 4 residues, except for HLA-DR9 and HLA-DR51 peptides where it was 5 and 3 residues, respectively. For C-terminus PFR, the average length was of 3 residues, except for HLA-DR13 associated peptides, with an average of 4 residues, and HLA-DR9 and HLA-DR7 peptides, with 2 residues. When N-terminus PFR length were sorted out by their predicted affinity, no significant differences in peptide length were found, but IB peptides seemed to have shorter PFR than HB peptides (data not shown). This supports the idea that PFR stabilize the peptides in the binding groove.

To compare the biochemical characteristics of peptide repertoires associated to each HLA-DR allele, amino acids were classified according to the physicochemical properties of their side chains into aliphatic (G, A, V, L, M, I), aromatic (F, Y, W), polar-uncharged (S, T, C, P, N, Q), acid (D, E) or basic (H, K, R). As expected, amino acids at P1 anchor position were equally distributed into aliphatic and aromatic (Fig.9A), with variable proportions between alleles. Hydrophobicity is a shared feature for the residues occupying the P1 anchor position of HLA-DR peptides (169). For the N-terminus PFR, a higher frequency of basic, acid and polar amino acids in P-1 and P-2 compared to P1, was remarkable for most alleles. For example, 32% of HLA-DR15 peptides had Glu in P-1 and 33% Lys in P-2. Other alleles such as HLA-DR9 and HLA-DR51 also had preferred residues in both positions. For HLA-DR9, 29% of P-1 residues were Val and Ser represented 26% of all amino acids in P-2. In HLA-DR51, 27% Asn and 22% Val occupied P-1 and Gly constituted 27% of residues in P-2. Other alleles were more permissive (data not shown). These frequencies were the same, independent of the predicted affinity of the peptides (data not shown).

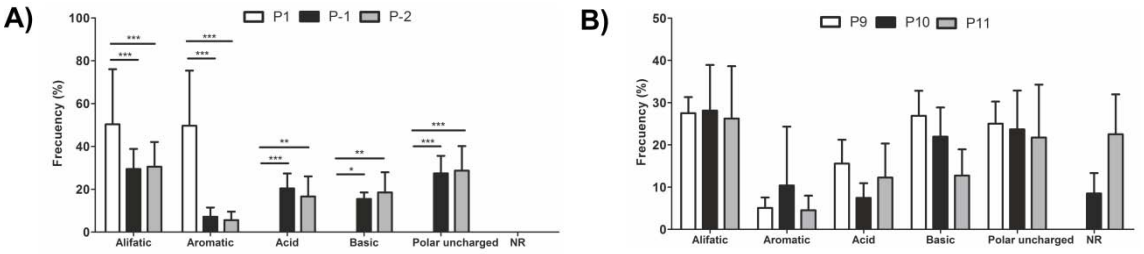

Figure 9. N- and C-terminus peptide flanking residues (PFR) grouped by the physicochemical properties of their side group in aliphatic (G, A, V, L, M, I), aromatics (F, Y, W), polar-uncharged (S, T, C, P, N, Q), acid (D, E) or basic (H, K, R). No residue was considered as NR. (a) Anchor position P1 (white boxes) were preferentially hydrophobic residues (aliphatic and aromatic), while in P-1 (black boxes) and P-2 (grey boxes) there was an increment of basic, acid and uncharged polar residues. (b) Similar preference for aliphatic, basic and uncharged polar amino acids were found in anchor position P9 and adjacent P10 and P11. Bars represent average percent of each group ± SD (*P<0.05, **P<0.01, ***P<0.001. Two-way ANOVA. Bonferroni post- test)

For C-terminus PFR, anchor position P9 and the adjacent positions P10 and P11 were analyzed (Fig.9B). As described above, C-terminus PFR were shorter than N-terminus PFR and up to 25% of the peptides were so short that there was no residue in position P11, especially those assigned to HLA-DR9, HLA-DR3, HLA-DR13 and HLA-DR7. Residues occupying all the three positions were mostly aliphatic, basic or polar-uncharged. HLA-DR9 seemed to be more

restrictive at position P10 (28% Pro). HLA-DR15 also had a preference for Trp in P10 (25%) and Leu in P11 (25%). These data indicate that HLA-DR9 and HLA-DR15 are within the most restrictive alleles for both N- and C-terminus PFR. In contrast, HLA-DR1 and HLA-DR4 molecules were very permissive in their PFR composition (data not shown)

1.2.4 Peptides derived from the N- and C-terminal part of the protein are preferentially generated from cytosolic and nuclear proteins

To determine the importance of the protein structure in peptide generation, we studied the location of the peptides along the parental protein sequence. Peptides located in the first 30 residues were considered as N-terminal (N-ter) peptides and those located in the last 30 residues, as C-terminal (C-ter) peptides. In mature MoDCs peptidomes, most peptides (82.4%) were located in the middle of the parental protein sequence (internal peptides) (Fig.10A) whereas N- and C-ter peptides constituted an average of 5% to 12%, respectively, without any apparent differences between alleles (data not shown). To note, all C-ter peptides were located at the very end of the protein whereas only 25% of the N-ter peptides began in the first or second residue of the protein. Most terminal peptides (62% N-ter and 76% C-ter peptides) were unique and corresponded to unique regions of the parental protein being presented and most were high binders (Fig.10B). Taking into account the antigen processing route, it was evident that the degradation of proteins by the cytosolic pathway favored the presentation of terminal peptides (Fig.10C).

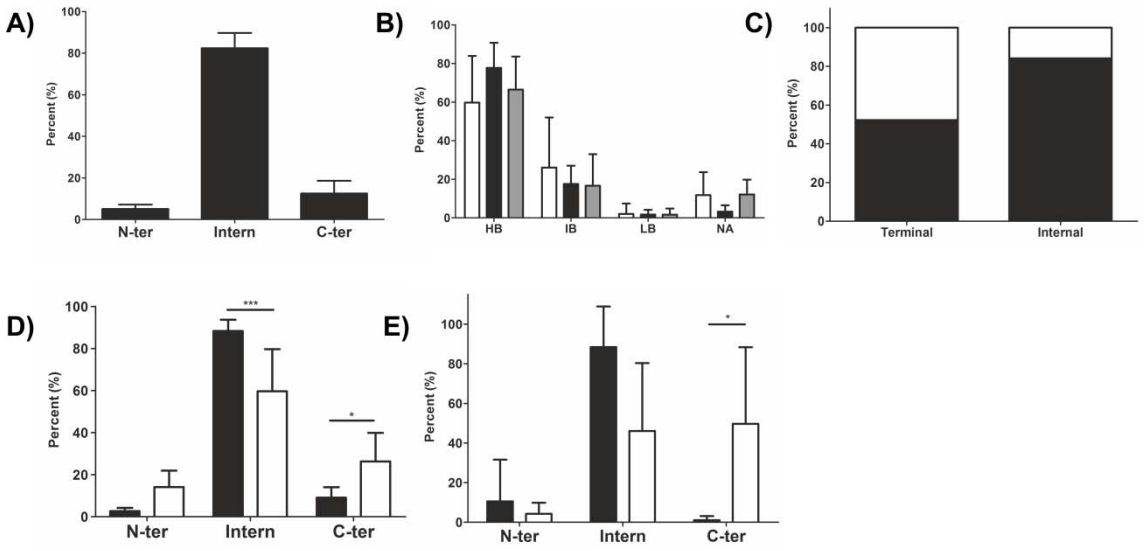

Figure 10. Peptide location in the parental protein sequence. The 30 first residues were considered as the N-ter side of the protein and the last 30 residues as C-ter side (n=1319). A) A general overview showed that an average of 82.4% derived from the internal part of the protein whereas nearly 18% were considered terminal peptides. B) Affinity analysis of the N-ter peptides (white boxes), intern peptides (black boxes) and C-ter peptides (grey boxes) showed no differences between terminal and internal peptides, the majority were HB peptides independently of the location in the protein. C) Contribution of the cytosolic pathway (white boxes) and the endocytic pathway (black boxes) to the generation of terminal or intern peptides. D) Terminal peptides, especially C-ter peptides, were significantly favored in proteins degraded in the cytosolic pathway (white boxes) when compared to the endocytic pathway (black boxes). E) Analysis of the HLA-DR peptides from thymus DCs (46) according to the location of the peptide in the protein and the route of degradation (n=115). As shown in MoDCs, C-ter peptides came preferentially from the cytosolic pathway (white boxes) when compared to the endocytic pathway. Bars represent average percent ± SD (*P<0.05, **P<0.01, ***P<0.001. Two-way ANOVA. Bonferroni post-test)

A significantly reduced frequency of internal peptides processed by the cytosolic pathway was observed (Fig10D). Similar data were obtained when the HLA-DR peptide repertoire from thymus DCs (46) was re-analyzed. The published list of peptides was revised, redundant peptides from each sample were discarded and finally 115 accepted peptides were subjected to the same analysis. As shown in our data, C-ter peptides were preferentially generated in the cytosolic degradation pathway (Fig.10E).

The terminal peptides generated by the cytosolic pathway came principally from proteins related to gene expression and chromatin organization (34%), cytoskeleton (14%) and cell metabolism (14%). On the other hand, the less abundant terminal peptides generated by the endocytic pathway were mainly from proteins related to the immune response (25%, mainly antigen presentation) and cell metabolism (15%).

1.2.5 Different cleavage motifs are found depending on the peptide location in the protein

In contrast to MHC-I, the influence of individual proteases in the generation of MHC-II peptide repertoires has not been fully studied. For a further understanding of the role of MHC-II pathway-associated proteases, we studied the amino acids in the first (N-terminus) and last position (C-terminus) of all non-redundant peptides. The adjacent sequences in their parental protein were also analyzed to try to identify one or more cleavage motifs. According to the literature for MHC-II proteases (171), four residues were analyzed (R2, R1, R´1 and R´2) from each terminus, and proteases were described to cut between R1 and R´1. Residues at the N-terminus were referred to as NR, and CR for C-terminal residues. Amino acids were grouped as described above.

Different proteases should take part in antigen processing depending on the degradation route of the source protein, endocytic or cytosolic. Expected differences were observed in peptides derived from proteins presumably degraded by the endocytic pathway, compared to cytosolic processing (Fig.1). Endocytic peptides required Pro (17%) in position NR´2 for the generation of the N-terminus side of the peptide (Fig. 11A) whereas cytosolic peptides preferred Asp (20%) in the position immediately before the cut, NR1 (Fig.11C). For C-terminus generation, the pattern was similar for both pathways (Fig.11B, 11D), i.e. a basic residue (Lys or Arg, up to 12.2% and 10.8%, respectively) was preferred at CR1, followed by a hydrophobic residue. Despite the similarity, endocytic peptides frequently had (15.8%) Pro at CR2 (Fig.11B).

Significant differences in the cleavage motifs were also shown when the location of the peptide in the protein sequence was included in the analysis. Internal peptides showed a similar distribution of amino acids at their N- and C-terminal cleavage regions, where mostly aliphatic and uncharged polar amino acids were found. Some preference for Asp in NR´1, Asp and Pro in

NR´2, Pro in CR2 and Lys in CR1 was observed (up to 15%), although it was not significant in all cases (Fig.12A-B).

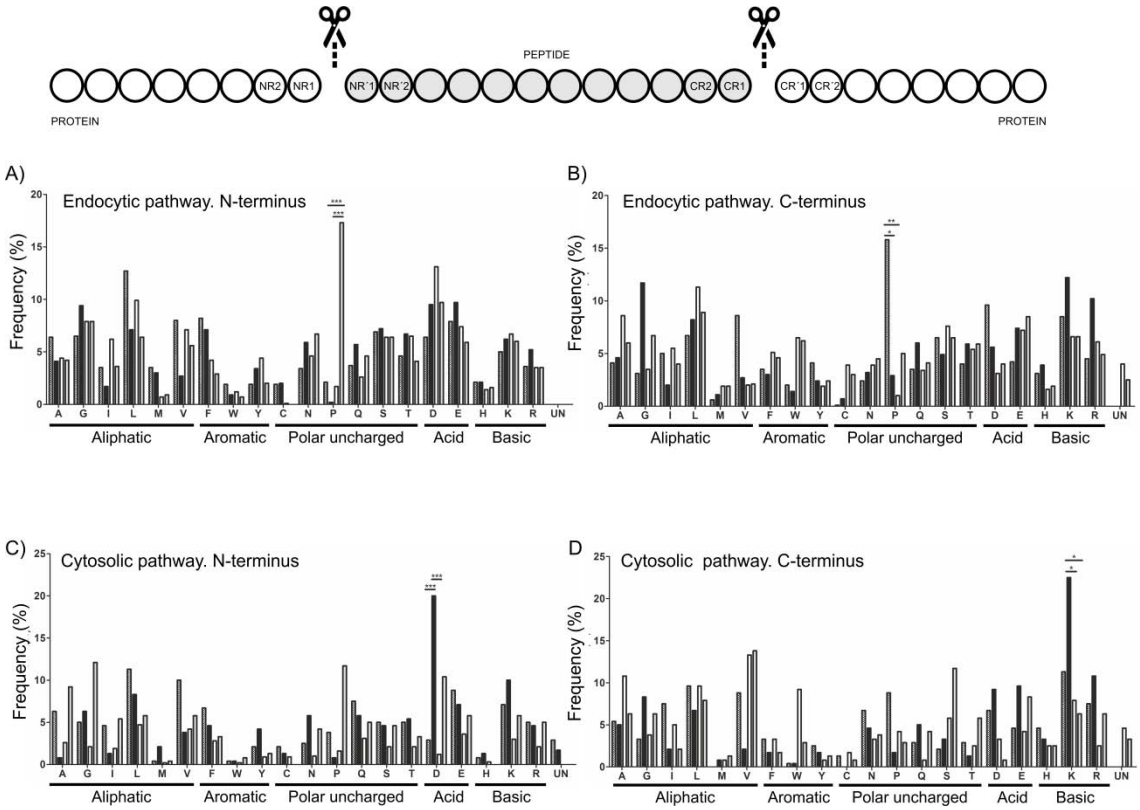

Figure 11. Amino acid frequency in the catalytic positions involved in N- and C-terminus generation of peptides associated to the endocytic (A, B) and cytosolic (C, D) pathways of protein degradation. Pattern in the endocytic pathway was studied for N-terminus (A) and C-terminus (B), and cytosolic pathway for N-terminus (C) and C-terminus (D) generation. N-terminus pattern was analyzed in positions NR2 (dotted boxes), NR1 (black boxes), NR´1 (white boxes) and NR´2 (grey boxes). C-terminus pattern was analyzed in positions CR2 (dotted boxes), CR1 (black boxes), CR´1 (white boxes) and CR´2 (grey boxes). Bars represent the individual amino acid frequency (%). If none amino acid was found in a given position was considered as undefined (UN). (*P<0.05, **P<0.01, ***P<0.001. Two-way ANOVA. Bonferroni post-test)

For the generation of N-ter peptides, the protease activity is focused on the C-terminus of the peptide, the side from which the peptide would be released from the protein backbone. Similarly, for C-ter peptides, protease activity is focused on the N-terminus of the peptide. The data for the terminal peptides showed some clear patterns. In N-ter peptides, positions CR2 and CR1 were markedly different from the rest with an increment of Lys (22%) and Pro (20%) in CR2 and Asp (22%) in CR1 (Fig.12C), both residues located just before the cleavage site. On the other hand, C-ter peptides that are cut by their N-terminus showed a strong preference for Asp (48%) in the catalytic position NR1 while Pro was significantly high (30%) in the next residue, NR´1 (Fig.12D). In addition, 20% of the residues in NR´2 were Pro (Fig.12D). Thus, these data show that Asp and Pro seem to be highly important for the cleavage motif recognition by the proteases generating terminal peptides.

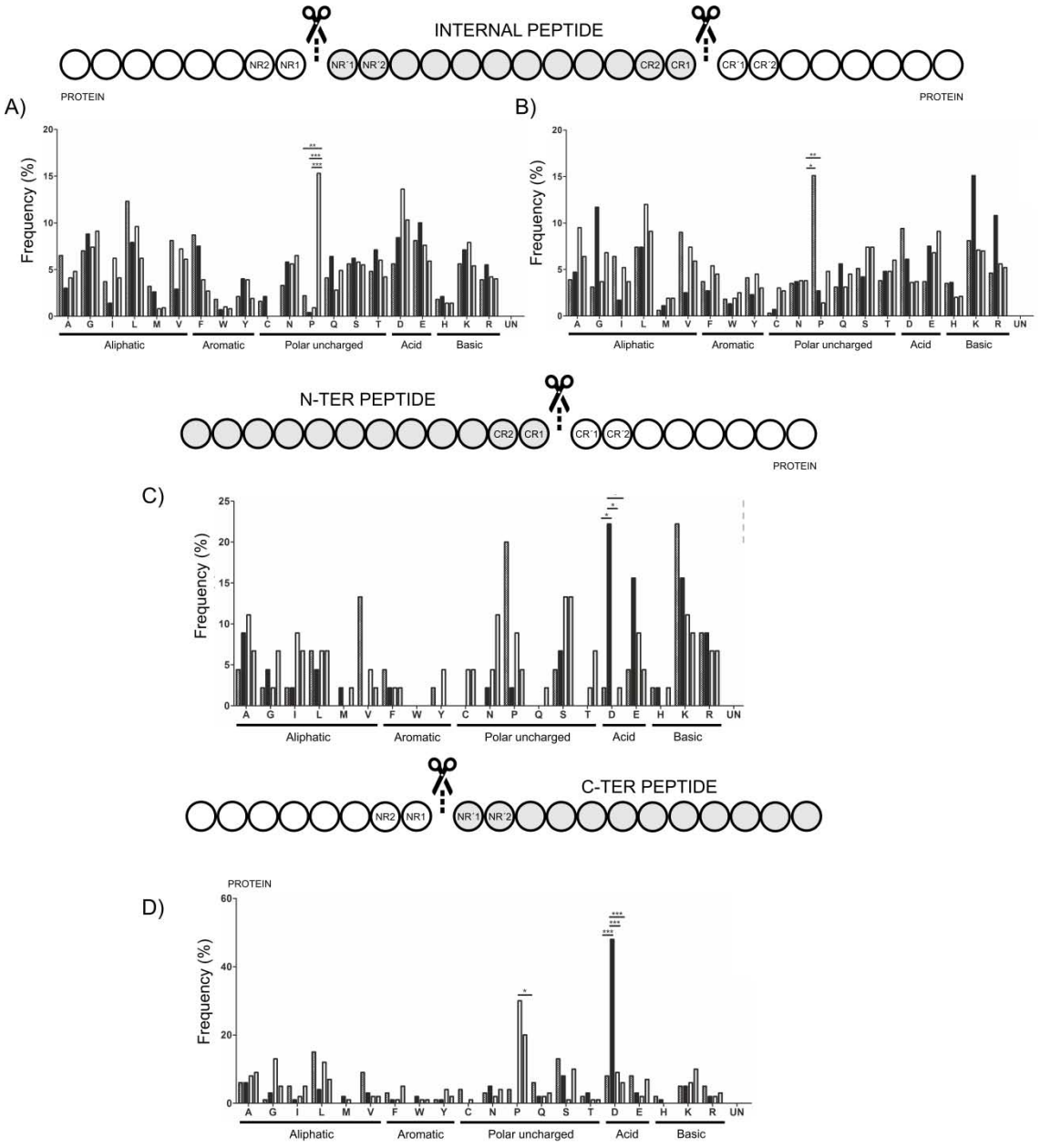

Figure 12. Amino acid frequency in the catalytic positions involved in N- and C-terminus generation of peptides according to their location in the parental protein. Pattern of the internal peptides was studied for N-terminus (A) and C-terminus (B) genertation. N-ter peptides (C) were analyzed in their C-termini ends and the C-ter peptides (D) were analyzed for the N-terminus generation. N-terminus pattern was analyzed in positions NR2 (dotted boxes), NR1 (black boxes), NR´1 (white boxes) and NR´2 (grey boxes). C-terminus pattern was analyzed in positions CR2 (dotted boxes), CR1 (black boxes), CR´1 (white boxes) and CR´2 (grey boxes). Panels represent the individual amino acid frequency (%). If none amino acid was found in a given position was considered as undefined (UN). Bars represent residue frequency (%). (*P<0.05, **P<0.01, ***P<0.001. Two-way ANOVA. Bonferroni post-test)

1.3 DISCUSSION

The deep analysis of human MHC-II peptide repertoires in physiological conditions using professional APCs has been an arduous and difficult task, because an adequate number of cells was not easily obtainable. To date, only the natural HLA-DR peptidome of human thymus DCs has been analyzed (46). Thymus DCs were isolated by their expression of CD11c, and separated from other thymus cell subsets. A total of 115 non-redundant HLA-DR-associated peptides were identified from 4 donors. The starting material for the study was 30-66x10^6 DCs, yielding up to 48 peptides per sample, a big step in the identification of natural DC-presented peptides, considering that the thymus plays a major role in T cell development and tolerance. Pending higher-efficiency methods to isolate DCs from thymus and other tissues, we have used MoDCs to complete the characterization of antigen processing and presentation by mature DCs.

In this report we have used mature MoDCs from seven different donors to yield 1319 peptides associated to 9 different HLA-DR alleles. Isolated peptides had standard size and were mostly grouped in nested sets (44-73.5%), similar to thymus DCs (46-80%). A high representation of parental proteins involved in cellular growth, differentiation processes and metabolism was observed, coinciding with the proteomic profile of similarly matured MoDCs (172). An over-representation of proteins related to the immune system was also found, mostly proteins involved in MHC pathways and receptor signaling, likely related to the high specialization of DCs on antigen presentation. A large proportion of the source proteins identified in our study (40-55%) were also found in previous studies on DCs (46, 168). CLIP peptides derived from Ii were also found, assigned to HLA-DR3, HLA-DR7, HLA-DR9, HLA-DR10 and HLA-DR51 molecules, but not to others, confirming allele-specific differences in the affinity of HLA-DR-CLIP interaction. The presentation of HLA-DR-CLIP complexes at the cell surface of mature MoDCs was reported to be increased respect to immature MoDCs (168). The authors proposed that after LPS stimulus, HLA-DM expression and catalytic activity would be reduced in the APCs to avoid peptide exchange. Peptide-MHC complexes would then be quickly delivered to the surface, where the presence of CLIP-HLA-DR complexes may play a role in T cell activation.

MHC-II peptides are usually large peptides that may be potential binders for more than one allele, because their sequence may include several binding cores. Up to 46% of peptides from our samples were assigned to both HLA-DR alleles expressed. The re-analysis of the published DC peptidome data confirmed this and also that most self-peptides were high binders for their corresponding alleles (~75%). As highly specialized APCs, DCs have an active machinery of antigen processing. In our case, no foreign antigen was used to pulse the cells, so HLA-DM would favor the binding of high affinity self-peptides to HLA-DR, prior to the maturation and surface delivery of the peptide-MHC complexes. When MoDCs were pulsed with antigen (155-157), most antigen-derived peptides were also high binders. However, our analysis of peptides from HLA-DR11, HLA-DR8, HLA-DR3 and HLA-DR4 lymphoblastoid cell lines (53, 158, 164, 165) and rat insulinoma cells transfected with HLA-DR4 (164) showed a different distribution,

where the intermediate and low affinity peptides represented between 40 and 60% of the total repertoire. Thus, the preference for high affinity peptides appears to be related to the cell type, suggesting that the intrinsic machinery of DCs may favor the generation and presentation of high affinity peptides, although a certain influence of the allele must be considered.

Peptide length and PFRs have been proposed to help in peptide stabilization and TCR interaction with the peptide-MHC II complexes (12, 173, 174). A published *in silico* analysis correlated peptide length with their experimental affinity, using data from 19 MHC-II allele ligands from the AntiJen database (175). This analysis showed a point (~19 residues) beyond which the increment of the peptide length did not result in higher affinity, although they did not conclude that 19 amino acids was the optimal length for high affinity peptides because characteristics of the MHC alleles must also be taken into account.

We looked at the number of residues that comprised the N- and C-terminus PFR as determined by the position of the allele-dependent assigned binding core. In general, the average size of the N-terminal PFR was 4 residues and 3 for C-terminal PFR, but small differences were observed depending on the allele. When affinity was considered, the data showed that for some alleles, PFRs of intermediate binding peptides were slightly shorter than those of high binders. However, more than 80% of peptides were high binders and thus the number of intermediate or low affinity peptides was low. We also studied each amino acid frequency in PFRs, described as key positions for peptide stabilization (14, 176) but also for TCR recognition (12). Previous studies were centered on peptides from some well-known antigens, such as HIV Gag (p24) or influenza HA, to describe the alterations in stability and T cell stimulation by peptide modifications (177, 178). So far, only two studies of HLA-DR repertoires focused on this particularity. The first one used tandem mass spectrometry to analyze the frequencies of the residues, only focusing on the peptides belonging to the most abundant nested sets associated to HLA-DR4 (179). The second work relied on Edman sequencing of peptides associated to 11 HLA-DR alleles, revealing the enrichment of acid residues and proline at the N-terminus and the preference for basic residues at the C-terminus of the flanking sequences (180). In contrast, our data showed a clear preference for hydrophobic amino acids in the N-terminal P1 anchor position, as expected for HLA-DR molecules, but also for reactive residues in the adjacent positions P-1 and P-2 that could interact with conserved HLA-DRα51 Phe, HLA-DRα53 Ser and HLA-DRβ81 His residues, via hydrogen bonds (176). No relevant amino acid preferences were observed for the C-terminus PFRs. In addition, there were differences in PFR amino acid frequencies when individual HLA alleles were compared, showing that HLA-DR9 and HLA-DR15 were the most restrictive alleles at both sides (data not shown). These data contrasts with those published by Godkin *et al*. (180) that presented a high homology between the PFRs of different alleles. The number of peptides analyzed may explain this difference.

As described, nearly 80% of HLA-DR-associated peptides derived from the endocytic pathway of antigen processing and 20% from the cytosolic pathway (170). Autophagy is probably the

most common provider of degraded cytosolic material to the endo-lysosomal pathway. All cytosolic material, including mitochondria or secretory granules can be degraded in autophagosomes that fuse with the MIIC, allowing the association of peptides to the MHC-II molecules (181). Other form of autophagy involve the recognition of target sequence motifs by chaperones, such as the KFERQ-like motif recognized by Hsc70, that delivers proteins directly to lysosomes with the help of LAMP-2A (182). Additionally, phagocytosis of material from dead or damaged cells is another source of cytosolic and nuclear material (183).

The vast majority of peptides were internal sequences of the parental proteins, suggesting that most peptides were generated in a late degrading milieu where partial degradation of the source proteins would have already happened. However, around 20% of the peptides were directly derived from the N- and mostly C-terminal ends of the source protein. These terminal peptides were unique peptides from their parental protein, i.e. they did not form nested sets, as if they were dominant for each particular protein. Interestingly, when comparing the terminal peptides from proteins degraded by the endocytic or cytosolic pathways, the results changed. A high percentage of cytosolic (50%) but not of endocytic peptides, belonged to the N- or C-terminal ends of the proteins. In particular, the proportion of C-terminal peptides derived from cytosolic proteins was very large (62% of all terminal peptides). We had previously described a similar phenomenon in cells expressing transfected HLA-DR in the absence of HLA-DM and Ii (164), where single peptides from the terminal regions of cytoplasmic proteins were eluted from HLA-DR4-transfected cells. A recent work, while reviewing how immunodominant CD4 T-cell epitopes were generated and selected (184) they noted that several immunodominant peptides from antigens such as fibrinogen, MBP, GAD65 and cytochrome c were located at the N- or C-terminal ends of the proteins.

The C-ter peptides that we isolated had a marked preference for Asp residue in the position before the cleavage site (R1) and some peptides suggested a possible cleavage pattern with Asp in position R1 and Pro in R'1. Asn and to a lesser extent Asp are allowed as a pre-cleavage residues for AEP, although there is no data concerning the post cleavage residue (171, 185). A contribution of the MHC-I antigen processing machinery may be relevant in this context. For instance, MHC-II self and non-self peptide repertoires are strongly affected in TAP and ERAP deficient mice (186). Also, MHC-I processing components have been found in DC endosomes and are considered important for cross-presentation (187, 188). And interestingly, an MHC-I pathway-related protease, the signal peptide protease (SPP) of the ER, generates N- and C-ter peptides from transmembrane proteins (189). These and other MHC-I proteases, that may end into endosomes and lysosomes, can participate in shaping the MHC-II peptidome, including the generation of terminal peptides.

The internal peptides from all proteins also showed some preferential cleavage residues, with Pro as a dominant amino acid for as many peptides. However, terminal trimming must be considered as a mechanism of peptide alteration that is consistent with the common presence

of nested sets in the MHC-II repertoires (190, 179). Internal peptides mostly belonged to nested sets. High frequency of Pro in the N-terminal position has been described in HLA-DR repertoires (191). But it is known that some aminopeptidases cannot cleave the Pro bonds and that Pro is an unfavorable cut residue for most MHC-II related cathepsins (171). Therefore the preferential presence of Pro at both ends of the internal peptides may be more related to its own capacity to stop cleavage by many proteases than to being the specific target of a single enzyme. This may not apply so much to the C-ter peptides since most of them did not form nested sets and were unique sequences.

CHAPTER 2

Thyroglobulin and thyroid extracts processing and presentation by MoDCs. Identification of dominant peptides associated to HLA-DR

2.1 Background

Thyroglobulin, one of the main autoantigens in AITD, is highly expressed in the thymus during maturation (192) so a high level of tolerance to this molecule is expected in the periphery. The identification of thyroglobulin peptides as natural ligands in the HLA-DR repertoire of GD-affected thyroids indicates that these pMHC must be relatively abundant (72). This putative high ligand density in the inflamed tissue may be a reason for otherwise ignorant T cells to become stimulated. A wealth of evidence has demonstrated the role of thyroglobulin in the etiology of AITD: anti-thyroglobulin antibodies are detected in most patients with AITD and EAT can be induced in susceptible animals by both mouse and human thyroglobulin immunization, generating both B and T cell autoimmune responses (68).

DC loaded with self-proteins or peptides have been well known to induce organ-specific autoimmune diseases (118, 120). The role of DCs in AITD has been recently reviewed (193, 194). But an exhaustive analysis of DC resident populations is a methodological problem due to the low number of cells. In human, a few thyroid DCs were reported to be positioned outside the follicular epithelium in healthy glands (195). Later quantification of DCs in normal pig thyroids suggested that only 2-3% of the total cells were DCs both in tissue sections and isolated cells (196). These thyroid DCs would function as a clearance mechanism to eliminate foreign and damaged thyroid material, and would migrate to the lymph nodes to induce immune responses or maintain peripheral tolerance.

DCs also infiltrate the thyroid gland during the autoimmune response (197). Most authors have focused on the increased DCs infiltrating the thyroid both in GD and in HT studying a large cohort of AITD patients. Immature and mature DCs were found outside the thyroid follicles, connective tissue close to the venules and also in the periphery of lymphoid follicles in thyroid (129, 198). Interestingly, immunofluorescence analysis of GD-affected thyroids showed the presence of immature pDCs ($CD303^{+}CD123^{+}CD83^{-}$) as well as cDCs (CD11c+) (199). In GD, these pDCs were significantly increased in untreated GD patients as compared with chronic GD and healthy subjects (200). Similar increment in thyroid pDCs was observed in HT patients but independently of the clinical stage (201). Additional studies of the peripheral blood and thyroid DCs showed that the peripheral blood pDC population was significantly lower in both HT and GD patients than in healthy controls, cDC population was similar. In contrast, the percentage of pDCs was significantly higher in thyroid tissue than in peripheral blood of the same AITD patients (202).

In pig, the cultured thyroid-derived DCs have been shown to endocytose thyroglobulin (196). Actually, mouse EAT has been induced with thyroglobulin but also with necrotic thyrocytes-pulsed DCs (203-205). Similarly, adoptive transfer of DCs isolated from animals with EAT induced by thyroglobulin immunization, were able to initiate thyroid-specific immune reactions in healthy animals (203). Although some T cell epitopes from thyroglobulin have been described in mouse EAT (206,), very little is known about the specific human anti-thyroglobulin response (72,

207). In this chapter, we propose the use of MoDCs from different HLA-DR types to elicit the nature of thyroglobulin-derived peptides that can be presented to the CD4+T cells. A similar method was successfully used to study the presentation of autoantigens involved in hemophilia A and thrombotic thrombocytopenic purpura by *in vitro*-derived MoDCs (155-157).

As mentioned above, total autoimmune tissues have been used before to describe the associated HLA-DR repertoires, including thyroid glands from GD patients (72-74). However, these data did not allow to discriminate whether these peptides were presented by HLA-DR molecules expressed by epithelial cells, B cells, DCs, or macrophages, all present in GD infiltrates. Peptide identification from a single cell population in the infiltrated tissue is at the moment very difficult because of the high amount of material needed. So far, only human DCs from thymus have been successfully isolated for MHC peptidome analysis (46). Additionally, thyroglobulin is found in blood so capture and processing by splenic DCs should be also considered. Knowing that there are differences in lysosomal proteases and their activity between human MoDCs and peripheral CD1c-DCs (77), in this chapter, we propose to use MoDCs to analyze the antigen processing and presentation of thyroglobulin by HLA-DR molecules.

2.2 RESULTS

2.2.1 Thyroglobulin is endocytosed by immature MoDCs cells when pulsed with purified antigen or thyroid extract

Thyroglobulin endocytosis by APCs was studied using human immature MoDCs (iDCs). Phenotype was analyzed by FACS, as shown in chapter 1. Commercial purified thyroglobulin and thyroid extract from GD patients were used as antigen source. First, the optimal concentration for the uptake of purified thyroglobulin was determined by dose-response experiments. Immature DCs were pulsed with the antigen at 10-200nM final concentration for 2h, prior to intracellular antigen staining. A concentration of 100mM was considered optimal because more than 60% of thyroglobulin was endocytosed (Fig.13A). Time-course experiments showed that most thyroglobulin was taken up within 5min (Fig.13B).

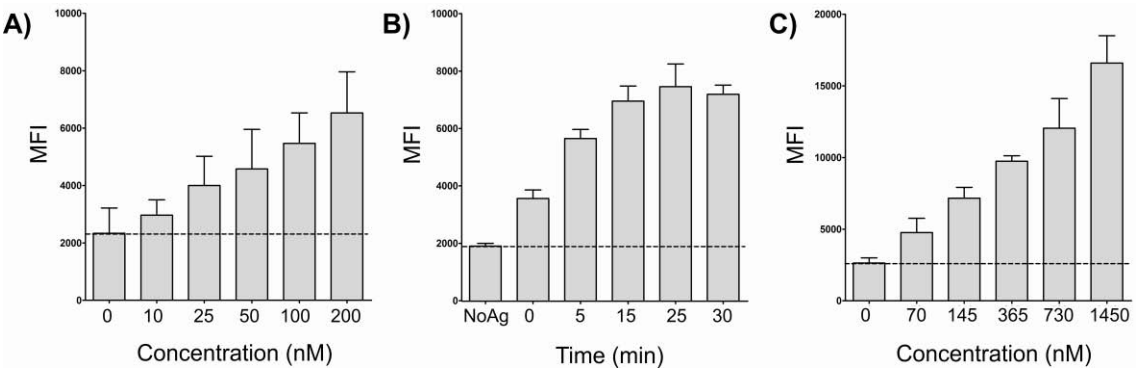

Figure 13. Immature moDCs (iDCs) take up thyroglobulin independently of the antigen source. A) Dose response: iDCs were pulsed with different concentrations of commercial purified thyroglobulin for 2h and intracellular antigen was analyzed by FACS. Uptake of thyroglobulin was dose-dependent. A concentration of 100nM was used for further experiments. B) Time course: iDCs were pulsed with 100nM of purified thyroglobulin in short-time incubations and antigen uptake was measured by FACS. The maximum uptake (100%) was measured 25min after pulse. An average of 60% thyroglobulin was endocytosed within the first 5 minutes. C) iDCs were pulsed with thyroid extracts containing different concentrations of thyroglobulin for 2h and intracellular antigen was analyzed by FACS. For all experiments, bars represent mean fluorescence intensity (MFI) of the samples ± Standard Deviation (SD) (n=3).

Tissue blocks from one HLA-DR3^{+} thyroid previously analyzed for HLA-DR peptide identification (72), were used to purify the components of colloid. Protease inhibitors and detergent were not included in the extraction buffer to prevent blocking proteolysis in iDCs. Western blot of thyroid extract showed the presence of thyroglobulin (data not shown) but also of fragments from partial degradation of thyroglobulin both in the tissue extract and purified thyroglobulin. Antigen content was quantified by ELISA, yielding an average 48% thyroglobulin in the total tissue extract samples. Because thyroglobulin can be partially degraded in the colloid and some fragments were still detected by the antibody, iDCs were pulsed with tissue extract with a range of thyroglobulin concentrations wider than that of the purified protein. The iDCs efficiently captured thyroglobulin when they were incubated with tissue extracts, in a concentration dependent manner (Fig.13C). Confocal microscopy confirmed that iDCs endocytosed the thyroglobulin independently of the source (Figure 14).

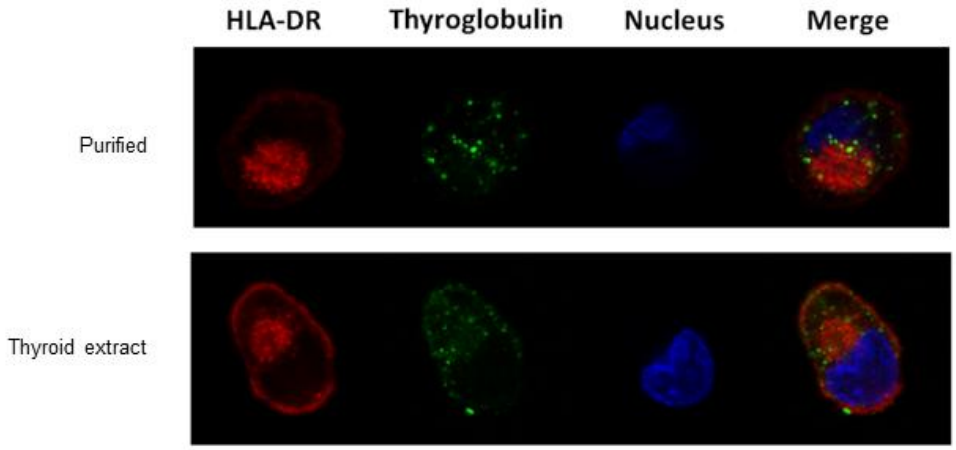

Figure 14. Confocal microscopy of iDCs showed uptake of thyroglobulin from thyroid extract (800nM) in a similar manner than purified antigen (100nM) after 30min of incubation. HLA-DR molecules (in red) were retained in the intracellular compartments but there was not much colocalization of HLA-DR with thyroglobulin (in green) at this time point.

As a high glycosylated protein, thyroglobulin uptake could be mediated by sugar receptors. Actually, when iDCs were pulsed with thyroid extract and surface staining was carried out, thyroglobulin was detected on the surface (Fig.15A). However, blocking sugar receptors with n-acetil-glucosamide, mannose, mannan, lactose or galactose did not result in an altered antigen capture (Fig.15B).

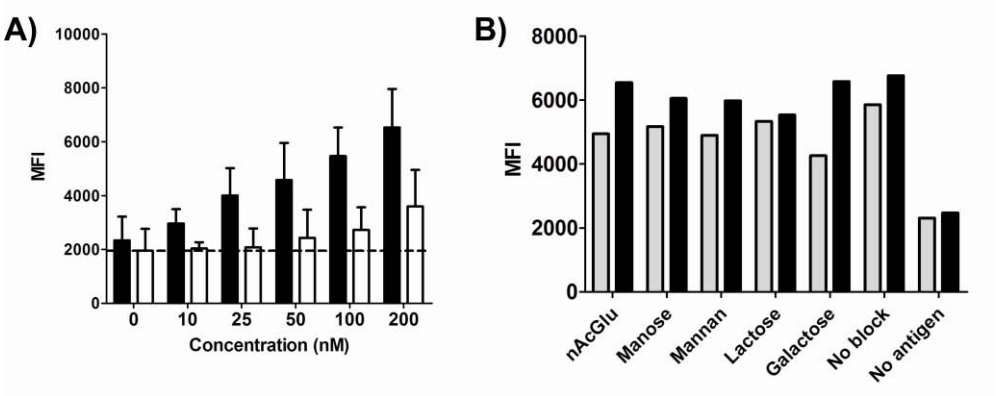

Figure 15. Thyroglobulin uptake by Immature moDCs (iDCs) is sugar receptors independent. A) iDCs take up thyroglobulin (black bars) but also there is some thyroglobulin in the membrane surface (white bars). B) iDCs take up thyroglobulin efficiently (black bars) even if some sugar receptors are blocked. Negative control is luciferase yellow (grey bars). For all experiments, bars represent mean fluorescence intensity (MFI) of the samples ± Standard Deviation (SD) (n=3).

2.2.2 Mature MoDCs (mDCs) successfully present thyroglobulin-derived peptides bound to their HLA-DR molecules

A total of eight HLA-typed donors were used for MoDCs generation. Donor A to E typed for the AITD-associated allele HLA-DR3 to which naturally presented peptides were isolated from GD patients' thyroids (72). Donors F and G shared the allele HLA-DR15, also expressed in thyroids from which HLA-DR peptides were isolated (72). In addition, donors G and H typed for HLA-DR7, an allele proposed as protective in AITD (68). The iDCs were pulsed with antigen and then matured (mDCs), after which peptide-HLA-DR complexes were purified. For mass spectrometry experiments, 100nM of purified thyroglobulin, 1500ug of thyroid extract (1000nM thyroglobulin) or PBS were used for cell pulsing.

Two control experiments were carried out. First, thyroglobulin-derived peptides that non-specifically bound to CNBr sepharose were identified from mDCs samples when non-coupled sepharose instead of L243-sepharose was used and compared with the L243-precipitated peptides. Technical replicates of each condition were performed because of the impossibility to obtain biological replicates. The relative abundance of peptides was determined using their peak intensity by SIEVE 2.2 differential analysis software (Fig.16A). A baseline of 10^5 units of intensity was defined in the chromatogram from which the peaks were compared. Results showed that most peptides had a L243-sepharose: uncoupled sepharose ratio higher than 1, meaning that these peptides were more abundantly present when samples were immunoprecipitated with L243-sepharose than with uncoupled-sepharose. Non-specific peptides were reproducible independently of the donor, so they were discarded in further analyses. Second, the peptide repertoire of antigen pulsed cells was compared with that of PBS-pulsed cells. As expected, no thyroglobulin-derived peptide was identified in PBS samples, validating the correct identification of thyroglobulin peptides (Fig.16B).

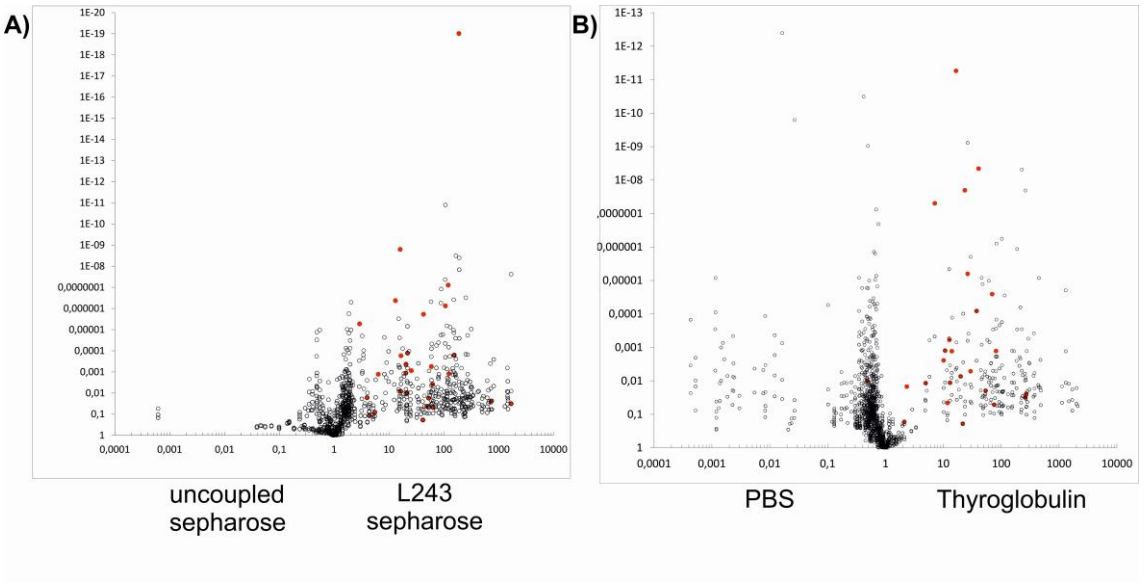

Figure 16. Identification and relative quantification of HLA-DR-bound thyroglobulin peptides in duplicate samples using SIEVE 2.2 (ThermoScientific). A) iDCs from donor E (DRB1*0301, 1501) were pulsed with 100nM of thyroglobulin, matured with LPS and HLA-DR complexes purified with L243-coupled sepharose or uncoupled sepharose. Volcano plot represents the ratio between L243 and uncoupled samples (X axis) and the p-value (Y axis). All thyroglobulin-derived peptides, labeled in red, showed a ratio >1 meaning that they were more abundant in L243-purified samples. B) iDCs from donor E (DRB1*0301, 1501) were pulsed with 100nM of thyroglobulin or PBS and pMHC-II were purified with L243-coupled sepharose. Volcano plot represents the ratio between PBS and thyroglobulin-pulsed samples (X axis) and the p-value (Y axis). All thyroglobulin-derived peptides, labeled in red, showed a ratio >1 meaning that they were more abundant in thyroglobulin-pulsed samples

An average of 25 and 42 unique thyroglobulin-derived peptides were isolated from HLA-DR3^{+} and non-HLA-DR3+ donors, respectively, when pulsed with the purified antigen (Table 4). Interestingly, an average of 21 and 26 peptides were identified in HLA-DR3^{+} and non-HLA-DR3+ donors, respectively, when iDCs were pulsed with thyroid extract, although the amount of antigen was 10-fold higher than in the purified thyroglobulin samples (Table 5). From donor C, 17/21 thyroglobulin peptides derived from the tissue extract were common with the purified antigen-pulsed cells. For donor D, the ratio was 6/10 common peptides and for donor E 30/31.

Table 4. Summary of the thyroglobulin peptides isolated from mature MoDCs when pulsed with commercial thyroglobulin

	Donor A	**Donor B**	**Donor C**	**Donor D**	**Donor E**	**Donor F**	**Donor G**
HLA-DRB1 type	*0301	*0301 *1301	*0301 *0901	*0301 *1101	*0301 *1501	*0701 *1501	*1101 *1501
Antigen source	Purified	Purified	Purified	Purified	Purified	Purified	Purified
Tg unique peptides	22	22	33	11	36	58	25
Single peptides	1	2	1	0	2	2	3
Nested sets	3	4	6	2	3	8	3
Max Size nested sets	15	10	12	9	18	21	13

Table 5. Summary of the thyroglobulin peptides isolated from mature MoDCs when pulsed with thyroid extract

	Donor C	Donor D	Donor E	Donor H
HLA-DRB1 type	*0301 *0901	*0301 *1101	*0301 *1501	*0101 *0701
Antigen source	Tissue extract	Tissue extract	Tissue extract	Tissue extract
Tg unique peptides	21	10	31	26
Single peptides	1	1	2	5
Nested sets	5	1	4	4
Max Size nested sets	7	10	14	10

There were no differences in the source protein function when iDCs were pulsed with tissue extract or purified antigen (Fig.17A). However, there were significant differences if their potential degradation route (endocytic or cytosolic) was considered. Peptides from cytosol-degraded proteins were more abundant when iDCs were pulsed with thyroid extract (Fig.17B). Interestingly, one peptide derived from carboxypeptidase Q, an enzyme that may play a role in the liberation of thyroxine hormone from its thyroglobulin precursor, was isolated from donor D when pulsed with tissue extract. Data can be found in Annex 2.

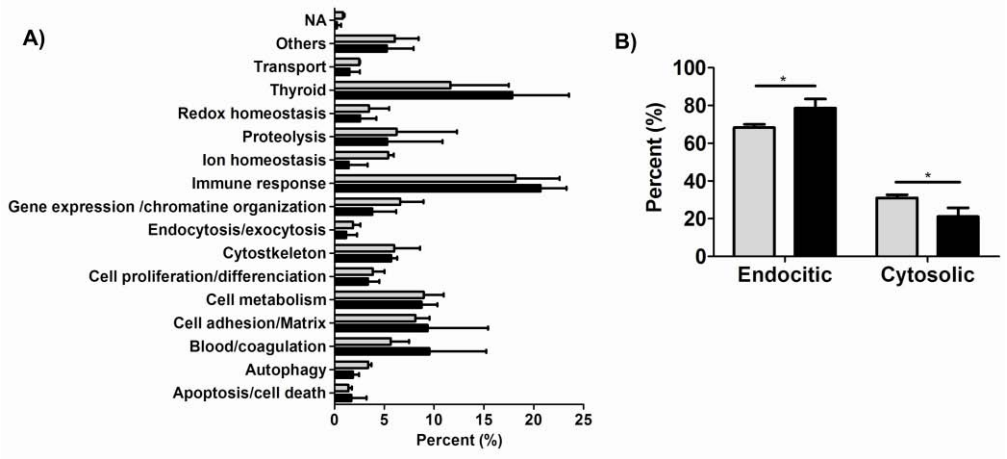

Figure 17. Function and degradative pathway associated to the parental protein of the peptides isolated from thyroglobulin or thyroid extracts-pulsed MoDCs of donors C (DRB1*0301, DRB1*0901, DRB1*0301, DRB1*1101), D (DRB1*0301, DRB1*1501 and E.. Bars represent mean fluorescence intensity (MFI) of the thyroid extract-pulsed (grey bars) and thyroglobulin-pulsed (black bars) samples ± Standard Deviation (SD) (n=3).

We quantified the abundance of thyroglobulin-derived peptides from this donor when pulsed with thyroid extract or purified antigen. According to the SIEVE analysis of technical duplicates for each condition, there were no significant differences between these two conditions of antigen pulsing for most peptides. However, 5 peptides showed significant differences ($p<0.05$) (Fig.18A). Peptides LSSVVVDPSIRHFD, PIIDMASAWAKR and SLKIMQYFSHFIRSGN were more abundant in samples pulsed with the tissue extract, 1.8, 2.3 and 1.4-fold respectively. In contrast, peptides LKIMQYFSHFIR and LSLKIMQYFSHFIR were increased 3.9 and 4.3-fold in

samples pulsed with purified thyroglobulin. The lack of substantial differences between number of peptides and relative abundance are hard to explain considering that iDCs were pulsed with 10-fold more thyroglobulin when tissue extract was used instead of the purified antigen. Misfolded thyroglobulin could be generated during mechanical tissue extraction so we analyzed if structure conformational state could influence thyroglobulin capture and presentation. As shown in Fig.18B, iDCs efficiently captured heat-denatured thyroglobulin and similar numbers of peptides were generated to be presented (data not shown).

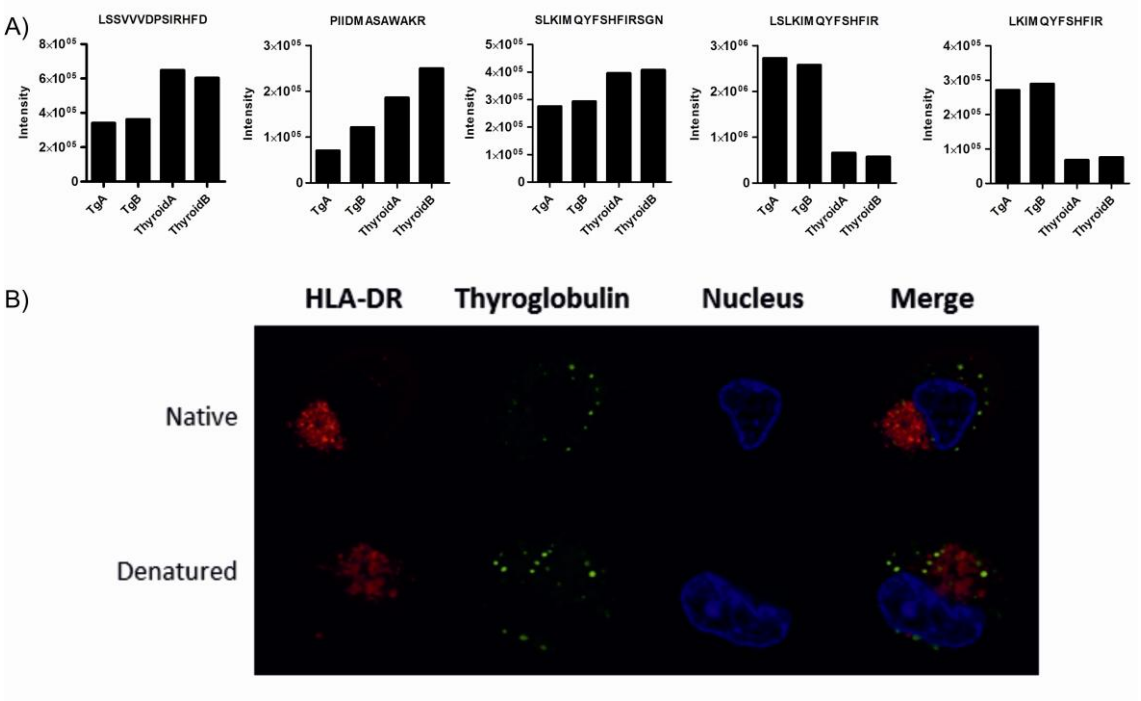

Figure 18. A) Identification and relative quantification of HLA-DR-bound thyroglobulin peptides in duplicate samples using SIEVE 1.4 . Peptides with significant differences ($p<0.05$) in peak intensity when iDCs from donor E (DRB1*0301, DRB1*1501) were pulsed with purified thyroglobulin (100nM) or thyroid extract (1000nM). Panels show the peak intensity per duplicates of each condition. Peptides LSSVVVDPSIRHFD, PIIDMASAWAKR and SLKIMQYFSHFIRSGN were more abundant in samples pulsed with the tissue extract and peptides LKIMQYFSHFIR and LSLKIMQYFSHFIR were more abundant in samples pulsed with the purified thyroglobulin. B) Confocal microscopy of thyroglobulin uptake. iDCs captured the antigen (100nM) independently of the conformational state.

2.2.3 Most HLA-DR associated thyroglobulin peptides in mDCs are part of nested sets

MHC II peptides are often grouped in nested sets, i.e. peptide families with a common core sequence but different length at the N- and C-termini. We have proposed an approach for core and theoretical affinity assignation based on the combination of bioinformatics tools and manual analysis and confirmed by experimental binding assays (59). As described in chapter 1, in the DRB1*1501 haplotype, the HLA-DRB5*0101 gene is also expressed, generating a second HLA-DR molecule (HLA-DR51), as capable to present peptides (21). HLA-DR51 was also included within the alleles but no thyroglobulin peptide was potentially assignable to this molecule.

			Thyroglobulin							Thyroid extracts			
			Donor A	Donor B	Donor C	Donor D	Donor E	Donor F	Donor G	Donor C	Donor D	Donor E	Donor H
Binding core/s	**Alelle/s**	**Affinity**	*0301	*0301 *1301	*0301 *0901	*0301 *1101	*0301 *1501	*0701 *1501	*1101 *1501	*0301 *0901	*0301 *1101	*0301 *1501	*0101 *0701
MIFDLVHSY/VHSYNRFPD	DR3/DR15	HB											
FTETTLYRI	DR7	HB											
ETTLYRILQ	DR11	HB											
FLAVQSVIS(VQSVISGRF)	DR7/DR9	HB (IB)											
FTTNPKRLQ	DR11	HB											
WQILNGQLS	DR1	HB											
FLVAKGIRL	DR1/DR7/DR15	HB											
VDPASGEEL	DR13	IB											
VGKDLLGRF	DR3	HB											
LIQSGSFQL	DR7/DR15	HB											
FCVDGEGRR	DR3	HB											
VIFDANAPV	DR3 (DR15)	HB (IB)											
LRCQVKVRS/FGSLRCQVK	DR3/DR11	IB											
FIKSLTPLE	DR3/DR9	IB											
ILEDKVKNF	DR3	HB											
FQKLMGISI	DR1/DR7	HB											
VVVDPSIRH	DR3	HB											
FLAAVGNLI	DR7/DR9	HB (IB)											
IVVTASYRV	DR1/DR7/DR15	HB											
LTWVQTHIR	DR3	IB											
IHLLTARAT	DR1	HB											
FLREPPARA	DR1	HB											
FYPAYEGQF	DR9	IB											
IDMASAWAK/IIDMASAWA	DR3/DR15	IB											
FYPAYEGQF	DR9	IB											
IMQYFSHFI/FSHFIRSGN	DR15/DR13	HB											

Figure 19. Analysis of the thyroglobulin peptides clustered in nested sets. Peptides were grouped in nested sets defined by the core sequence, the HLA-DR allele assigned and the theoretical affinity: high binders (HB) or intermediate binders (HB). Some peptides were potential binder for more than one allele but sometimes with the same predicted binding core. Black boxes represent nested sets predicted to bind to HLA-DR3, grey boxes peptides that can be associated to HLA-DR3 and the other allele with the same theoretical affinity, and white boxes represent peptides associated to other HLA-DR alleles. iDCs from donors C (DRB1*0301, 0901), D (DRB1*0301, 1101) and E (DRB1*0301, 1501) were pulsed with purified thyroglobulin or thyroid extract. As shown, most nested sets were generated independently of the antigen source

Independently of the antigen source, most thyroglobulin-derived peptides from each sample were grouped in 1 or 2 dominant nested set. The core sequence was dependent on the HLA-DR alleles expressed by the DCs (Fig.19). The complete list of thyroglobulin-derived peptides in each donor can be found in Annex 2. Although the presence of most nested sets was consistent in samples with the same HLA-DR type, the peptide length was variable. Thyroglobulin peptides preferentially bound HLA-DR3 and HLA-DR15 molecules, compared to other alleles expressed by our samples. A major nested set was associated to each allele. For HLA-DR3, the group defined by the core VVVDPSIRH ranged between 7 and 15 peptides, depending on the donor. The already defined immunodominant peptide Tg2098 (LSSVVVDPSIRHFDV) (72, 207) is part of this nested set and its exact sequence was identified in all HLA-DR3^{+} donors except for donor C (DRB1*0301, DRB1*0901), if pulsed with thyroid extract (Table 6) For HLA-DR15, the set with the IMQYFSHFI core varied between 13 and 21 peptides (Table 7). If one of these HLA-DR

alleles was expressed, they dominated the antigen presentation compared to the partner allele (see Annex 3). In donor E, positive for both alleles, HLA-DR15 was preferred for thyroglobulin presentation over HLA-DR3. This dominance was shown in the number of unique peptides (17 vs 9) but also in the abundance of these peptides in the sample, measured by the peak intensity as shown before (Fig.20A). Interestingly, most thyroglobulin peptides, specially the dominant nested sets, were assigned as high binders for their corresponding allele (Fig.20B).

Table 6. Peptides included in the nested set defined by the HLA-DR3 core VVVDPSIRH.

	Thyroglobulin							Thyroid extracts			
	Donor A	Donor B	Donor C	Donor D	Donor E	Donor F	Donor G	Donor C	Donor D	Donor E	Donor H
Peptide sequence	*0301	*0301 *1301	*0301 *0901	*0301 *1101	*0301 *1501	*0701 *1501	*1101 *1501	*0301 *0901	*0301 *1101	*0301 *1501	*0101 *0701
ALSSVVVDPSIRHFD	X										
ALSSVVVDPSIRHFDV	X	X			X				X	X	
ALSSVVVDPSIRHFDVA	X	X	X	X	X			X	X	X	
ALSSVVVDPSIRHFDVAH			X							X	
DSWQSLALSSVVVDPSIRHFDVAH				X							
LALSSVVVDPSIRHFDV	X	X	X	X				X			
LALSSVVVDPSIRHFDVA	X		X	X	X			X	X	X	
LALSSVVVDPSIRHFDVAH	X	X	X	X	X			X	X		
LDSWQSLALSSVVVDPSIRHFDVAH			X	X	X						
LSSVVVDPSIRHFD	X	X	X		X				X	X	
LSSVVVDPSIRHFDV	X	X	X	X	X				X	X	
LSSVVVDPSIRHFDVA	X	X	X		X			X	X	X	
LSSVVVDPSIRHFDVAH	X	X									
SLALSSVVVDPSIRHFDV	X	X						X			
SLALSSVVVDPSIRHFDVA	X		X	X				X	X		
SLALSSVVVDPSIRHFDVAH	X	X	X	X	X				X	X	
SSVVVDPSIRHFD	X										
SVVVDPSIRHFDV	X										
SWQSLALSSVVVDPSIRHFDVAH			X								

Table 7. Peptides included in the nested set defined by the HLA-DR15 core IMQYFSHFI.

	Thyroglobulin							Thyroid extracts			
	Donor A	Donor B	Donor C	Donor D	Donor E	Donor F	Donor G	Donor C	Donor D	Donor E	Donor H
Peptide sequence	*0301	*0301 *1301	*0301 *0901	*0301 *1101	*0301 *1501	*0701 *1501	*1101 *1501	*0301 *0901	*0301 *1101	*0301 *1501	*0101 *0701
EKSLSLKIMQYFSHFIR					X	X	X				
EKSLSLKIMQYFSHFIRSGNPN					X	X	X			X	
KIMQYFSHFIR					X	X				X	
KIMQYFSHFIRS						X					
KIMQYFSHFIRSG					X	X					
KIMQYFSHFIRSGN						X					
KIMQYFSHFIRSGNPN		X			X	X				X	
KSLSLKIMQYFSHFIR							X				
KSLSLKIMQYFSHFIRSGNPN							X				
LKIMQYFSHFIR					X	X	X			X	
LKIMQYFSHFIRS					X	X					
LKIMQYFSHFIRSG					X	X	X			X	
LKIMQYFSHFIRSGN						X					
LKIMQYFSHFIRSGNPN		X			X	X	X			X	
LSLKIMQYFSHFIR					X	X	X			X	
LSLKIMQYFSHFIRS					X	X	X			X	
LSLKIMQYFSHFIRSG					X	X	X			X	
LSLKIMQYFSHFIRSGN					X	X				X	
SLKIMQYFSHFIRS					X	X	X			X	
SLKIMQYFSHFIRSGN					X	X				X	
SLKIMQYFSHFIRSGNPN		X			X	X	X			X	
SLSLKIMQYFSHFIR					X	X					
SLSLKIMQYFSHFIRSGNPN					X	X	X			X	

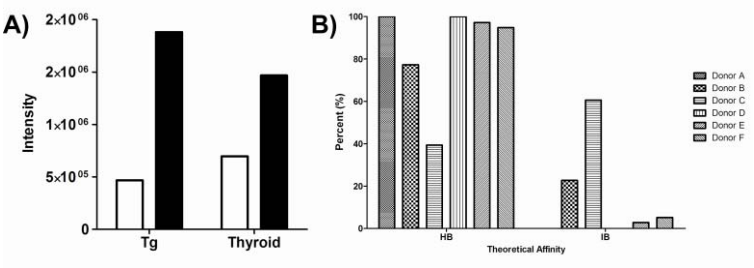

Figure 20. Analysis of the thyroglobulin peptides clustered in nested sets. A) Average peak intensity of peptides grouped in the nested sets defined by the core VVVDPSIRH (white boxes) and IMQYFSHFI (black boxes), isolated from donor E when pulsed with thyroglobulin (Tg) or thyroid extract. B) Predicted binding affinity of the thyroglobulin peptides in samples pulsed with thyroglobulin. Except for donor C, most peptides were assigned as high binders.

2.3 DISCUSSON

In healthy donors' thyroid glands DCs are located interstitially (195), but there are evidences of perifollicular DCs in GD thyroids with long protrusions capable of penetrating the junctions between the TFCs (197), which can sense and capture colloid material. In HT, were tissue destruction is important, DCs may take up material from necrotic cells. DCs that have captured necrotic thyrocytes can undergo maturation though a series of danger signals. This maturation enables the immunogenic presentation of thyroid antigens. This model leads to the development of EAT with thyroglobulin-specific T and B cell responses (205). Interestingly, in this study, necrotic TFCs-pulsed DCs induced greater response than thyroglobulin-pulsed cells, probably because of the presentation of T-cell epitopes from other antigens in addition that maturation with necrotic material induces imflammatory DCs.

In this work we have shown that thyroglobulin is successfully endocytosed by iDCs independently on the antigen source, being it purified thyroglobulin or thyroid extract containing ~50% thyroglobulin. In surface staining experiments, thyroglobulin was detected to be associated to the cellular membrane. The capture of this antigen by TFCs has been reported as preferentially mediated by micropinocytosis but also by endocytosis to clathrin-coated-vesicles and other receptors (208). However, as a glycosylated protein (~10% of the thryroglobulin mass correspond to carbohydrates, (209)), thyroglobulin uptake could also be mediated by sugar receptors. C-lectin receptors expressed by DCs such as mannose receptor and asialoglycoprotein receptor have also been described to bind thyroglobulin in the thyroid (208, 210, 211). However in our samples, when receptors were blocked with n-acetilglucosamine, mannose, mannan, lactose or galactose, no effect was observed on thyroglobulin capture. Therefore our data suggest that sugar receptor binding is not the mechanism for thyroglobulin internalization by iDCs.

Confocal microscopy did perfectly show Tg uptake by iDCs but low co-localization of thyroglobulin with HLA-DR molecules. In immature DCs, most HLA-DR molecules are confined in internal compartments. Interestingly, iDCs are able to present antigenic peptides from

coagulation factor VIII (FVIII) on MHC-II, albeit less efficiently than LPS-matured MoDCs, probably because the rapid turn-over of surface-expressed MHC-II in immature DCs (156). Despite the low expression levels of co-stimulatory molecules such as CD80, CD83 and CD86, immature DCs would not be completely unable of presenting peptides to CD4+ T cells, at least those that can be digested rapidly. Actually, immature DCs are thought to be the major players in peripheral tolerance whereas mature DCs would lead to immunity (212). Nevertheless, mature DCs can also be tolerogenic after maturation under immflamatory signals in the absence of pathogen-associated molecular pattern signals (213).

To our knowledge this is the first analysis of HLA-DR-associated peptides derived from the uptake of tissue material by DCs. We used samples of the thyroid gland of a patient with autoimmune thyroid disease because thyroglobulin-derived peptides were identified from HLA-DR molecules, expressed by thyroid samples from the same donor (72). In both tissue and purified thyroglobulin-pulsed DCs, the identified sequences constituted up to 24% of the total of peptide pool and in all cases, thyroglobulin was the most represented protein within the HLA-DR peptidome. Similar numbers of thyroglobulin-derived peptides were identified in mDCs samples independently of the antigen source (purified antigen or tissue extract) except for DCs from one of the donors (donor F, DRB1*0701/DRB1*1501), that yielded 58 peptides when pulsed with purified thyroglobulin.

Even though cells were pulsed with 10-fold more thyroglobulin when tissue extract was used, non-significant changes were observed in terms of numbers of thyroglobulin peptides. A quantitative analysis using the peak intensity of the peptides in HLA-DR3donor E showed significant differences only in 5 peptides, comparing both peptide sources. Taking into account that the content of thyroglobulin in tissue extract-pulsed cells was 10-fold higher than in purified antigen-pulsed cells, the similarity is notable. Once the native or denatured structure of thyroglobulin was discarded to influence in antigen capture and presentation, one can suggest that fragments detected by the antibody in the ELISA test may not result in peptide presentation. Peptides derived from other soluble thyroid antigens were not identified. TPO and TSHR are transmembrane proteins, and the membrane fraction was discarded from the thyroid extract prior to DCs pulsing. Moreover, although the TSHR subunit A can be found in a soluble state, being a very low-expression molecule, it would be highly diluted in the final protein composition of the enriched colloid extract. On the other hand, TSHR is an extremely very low-expression molecule that is only expressed at the basal membrane of TFCs. To differentiate from experiments with necrotic thyrocytes (205), it must be said that the extract used in the present work may contain colloid-enriched and soluble intracellular material from TFCs that might be absent in necrotic cells or vice-versa.

Two major nested sets of thyroglobulin were found in HLA-DR3+ and/or HLA-DR15+ samples. The first one, defined by the binding core VVVDPSIRH, comprised 7-15 peptides depending on the sample. The VVVDPSIRH included the Tg2098 peptide that was isolated from the thyroid samples used in this work (72) and that was shown to be immunodominant in thyroglobulin-

induced EAT in HLA-DR3 transgenic mice (207). A detailed analysis of the peptides presented by HLA-DR3 is discussed in chapters 3 and 4. The association of HLA-DR3 with AITD is proposed to be due to the presence of a basic amino acid in position 74 of the HLA-DRβ chain. This amino acid makes the anchor pocket P4 restrictive to acid residues (68). The nested set VVVDPSIRH has an aspartic acid in this position which allows this set to bind HLA-DR3 rather than other alleles. HLA-DR1, HLA-DR11, HLA-DR13 and HLA-DR15 have an alanine in β74, HLA-DR7 a glutamine and HLA-DR9 a glutamic acid. Not only this position but the entire P4 binding pocket in these alleles are, in general, negatively charged, what would prevent the anchoring of acid residues. The second major nested set, defined by the IMQYFSHFI core, ranged between 13-21 peptides. Interestingly, the HLA-DR15-associated IMQYFSHFI nested set was predominant in terms of percentage of thyroglobulin peptides in all samples expressing this allele, even if HLA-DR3 was also expressed. It is important to note that the work that analyzed the HLA-DR peptidome of GD thyroids, included two glands that typed for HLA-DRB1*1501: TB449 (HLA-DRB1*0301/HLA-DRB1*1501), the one used in this work for tissue extract, and TB448 (HLA-DRB1*0407/HLA-DRB1*1501). From TB448, two similar peptides (CPTPCQLQAEQAFLRTV and PTPCQLQAEQAFLRTVQ) were isolated and predicted to bind HLA-DR51 with higher affinity than to HLA-DR15. HLA-DR15-associated peptides described in our samples were not found in these thyroid samples. In any case, transgenic HLA-DR15 mice tested for induction of EAT after thyroglobulin did not reproduce thyroiditis, infiltration or T cell responses, whereas HLA-DR3+ transgenic mice did (214, 215). Therefore, we can hypothesize that the combined expression of HLA-DR3 and HLA-DR15 may attenuate the autoimmune process if, as our data suggest, HLA-DR15 is the preferred molecule for thyroglobulin peptide binding. In such case, molecules displayed at the cell surface would be mostly HLA-DR15 with its dominant peptides. Thus, central tolerance to HLA-DR15-presented thyroglobulin peptides would be more efficient than to HLA-DR3 presented peptides in the thymus. The study of ADAM13-pulsed MoDCs, showed the preferred presentation by HLA-DR11 molecules of peptides with antigenic properties. Despite this preference, some promiscuous antigenic-peptides were also associated to other alleles. In our samples, some peptides were assigned with the same affinity to both alleles but the major nested sets, where the HLA-DR3 immunodominant peptide is included, were exclusive binders for one allele. This may be explained by the restrictive P4 of the binding motif to this allele, a feature unshared with most other HLA-DR molecules (68).

The HLA-DR thymus peptidome showed that most peptides derived from one single region of each protein (59) while MoDCs present peptides from up to 9 different regions of the thyroglobulin, although not in the same proportion. This suggests that a wide range of peptides derived from the same protein may be generated and presented in the autoimmune target tissue by infiltrating DCs, whereas efficient tolerization in the thymus may be only directed against the dominant epitope/s of each protein. It also must be considered that despite its relatively high expression, the availability of thyroglobulin for presentation in the thymus would be much lower

that in thyroid. The role of tissue and thymus in the differential generation of peptides is discussed in chapter 3.

Except for donor C (HLA-DRB1*0301/HLA-DRB1*0901), thyroglobulin derived peptides were preferentially assigned as high binders for their respective allele. It must be said that HLA-DR9 binding motif is not fully studied (153) and the conservative method we used for affinity assignation may loose some high affinity peptides. As shown in chapter 1, MoDCs favor the generation and presentation of high affinity peptides. The studies of antigen presentation of FVIII or ADAM13-pulsed MoDCs (Simon, Niki, Simon) revealed that most antigen-derived peptides were also high binders. In contrast, the analysis of peptides repertories from total autoimmune affected tissues showed a lower frequency of high affinity peptides than in thymus or in MoDCs (collado review). That might be a consequence of the antigen presentation by the non-professional APCs, such as TFCs, that would not be as regulated as APC to present high affinity peptides.

Thyroglobulin is a large autoantigen of 2749 residues that is extensively modified by iodination and other posttranslational events. Some iodinated thyroglobulin peptides are highly immunogenic and can trigger thyroid autoreactive T cells in mouse EAT (216). Iodination has been proposed as capable of modifying the processing of thyroglobulin by APCs, resulting in the generation of pathogenic epitopes in mouse models (217). However, no human thyroglobulin peptide was found to have iodinated Tyr from our samples nor in the work with thyroids from GD patients (72) or in the HLA-DR3+ mouse model data (216). Additionally, as a highly glycosylated protein, thyroglobulin-derived peptides could be modified by glycosilation or even the glycosylation could interfere with peptide generation by blocking the access to thyroglobulin of some proteases (218, 219). Human thyroglobulin is modified with the addition of several oligosaccharide units of different kinds, among which the N-linked type A (high-mannose) and type B (complex) units have been characterized to modify asparagine (218). Type C units are linked to serine and threonine by O-glycosidic bonds and contain D-galactosamine and also D-glucuronic acid-N-acetyl-D-galactosamine (219) N-glycosylation motif consists of Asn followed by an irrelevant amino acid and serine or threonine (NXS/T). Only three nested sets were found near N-glycosylation sites (<15 residues from P1 or P9 to the Asn): MIFDLVHSY, LVAKGIRLR, VVVDPSIRH. Interestingly, in the MIFDLVHSY nested set, identified in donors E, F and G, four peptides began with one amino acid that is part of a NTT glycosylation site (in bold): **T**DMMIFDLVHSYNRFPD, **T**DMMIFDLVHSYNRFPDA, **T**TDMMIFDLVHSYNRFPD and **T**TDMMIFDLVHSYNRFPDA. These peptides were found in samples pulsed with purified thyroglobulin and tissue extract. Data suggest that this site was not glycosylated, so the glycosylation was removed prior to protease activity or it does not affect the proteolysis. For the other two nested sets, there were at least 4 residues between the modified Asn and the N- or C-terminal of the peptides. In contrast, no peptide was located near O-glycosilation sites described for human thyroglobulin.

On the other hand, fourteen single nucleotide polymorphisms (SNPs) in the thyroglobulin gene have been also associated to AITD (141). Only six of them resulted in amino acid substitutions. A polymorphism in exon 33, which resulted in the substitution of arginine by tryptophan in position 1980, was the most associated SNP to the disease. Patients with the exon 33 SNP mostly expressed HLA-DR3. We have not been able to find the described polymorphism or at least no peptide with the Trp^{1980} was found presented by HLA-DR3 in our data. We just found a set of peptides located in the affected region from donor H (DRB1*0101/ DRB1*0701) Thyroid extract-pulsed DCs from this donor generated a nested set derived from the polymorphic region, but these peptides contained Arg^{1980} and not Trp. Thus, the association of this SNP to autoimmunity is not related to any modification of the peptide repertoire of HLA-DR3.

Our data demonstrate that immunodominant tissue-specific peptides are presented by MoDCs via HLA-DR so DCs must be involved in the autoimmune thyroid process. Nevertheless, different processing machinery may also influence MHC-II peptide repertoires *in situ*. Thus, the influence of other APCs and epithelial cells in antigen presentation should be analyzed. A recent work analyzed the ability to internalize and present FVIII peptides by *in vitro* derived MoDCs and macrophages (156). Both cell types internalized the antigen, but MoDCs were more efficient in presentation. Even so, macrophage-presented peptides were different to those presented by MoDCs. In GD infiltrates, B cells are abundant, where they form autoantigen-specific germinal centers (64). High levels of anti-thyroglobulin antibodies in GD patients suggest that this antigen could be internalized and processed by B cells *in situ* or even that DC can interact directly with naïve B cells via antigen transfer. Another important player to be considered in this disease are the TFCs. As mentioned before, these cells ectopically express HLA-DR and HLA-DM molecules and have been reported to interact with T cells (65, 108, 127-130). In GD thyroid there is not much tissue destruction and TFCs are hyperfunctional, constantly producing thyroid hormones by the interaction with agonistic anti-TSHR antibodies and therefore require continuous endocytosis of thyroglobulin. Interestingly, in the work where thyroid glands were used for pMHC isolation two thyroglobulin peptides associated to HLA-DR15 were identified that were not found in our HLA-DR15+ DCs samples (72). Thus, these MHC-II-expressing TFC, B cells or macrophages with high acces to thyroglobulin, may be maintaining autoimmune responses by presenting extra peptides in the thyroid that were not presented in the thymus.

CHAPTER 3

Application of a minimalist cell-free system in the study of thyroid antigen processing

3.1 BACKGROUND

A determinant of the fragments resulting from “the first endocytic cut” of an antigen is likely to be the first to bind MHC and, if the affinity is high enough, this determinant will be immunodominant respect to other determinants from the same antigen, creating a hierarchy of epitopes (152). High binding to MHC is necessary but not sufficient for immunodominance, because an immunodominant peptide is the one from the peptide hierarchy that is preferentially recognized by antigen-specific T cells. The identification of immunodominant peptides from a given antigen has so far required the stimulation of antigen-specific T cells with large panels of synthetic overlapping peptides, but this methodology is expensive and may be unreliable. Predicted binding affinity to MHC by computer-assisted algorithms has been used to reduce the peptides in study. However, none of these approaches take into account the processing of the studied antigen.

The methodology applied in this chapter to identify immunodominant peptides was set up as a minimalist cell-free system (CFS) of antigen processing and presentation for the well-studied HLA-DR1 molecule and some well-known antigens (154). They selected a minimum number of essential components to recreate the MIIC: soluble HLA-DR, soluble HLA-DM and cathepsins B, H and S. HLA-DM was included in the system because of its essential role in peptide editing. The combination of cathepsins B, H, and S was considered sufficient. Cathepsin S is the major endoprotease involved in MHC-II antigen processing in DCs and B cells (220). APC also constitutively express the exopeptidases cathepsin B (carboxypeptidase) and cathepsin H (aminopeptidase), the activity of which is important for trimming long fragments bound to MHC-II molecules (171, 221, 222). This mixture is incubated, pMHC are purified and the bound peptides analyzed by MS/MS. In addition, using this CFS method, the sequence of steps necessary to generate the immunodominant peptides from exogenous or self-antigens could be analyzed (109). It was concluded that if an antigen was first digested by cathepsins, the capture of the immunodominant peptide by HLA-DR was abrogated. On the other hand, when antigen was captured by HLA-DR in the presence of HLA-DM, the immunodominant peptides were protected and therefore presented. Interestingly, some epitopes from autoantigens appeared to be less sensitive to cathepsin degradation than those from exogenous antigens.

However, normal turnover of tissue-specific proteins, extracellular processing and different tissue proteases may provide a source of peptides specific of the target tissue, for MHC-II presentation, that will not be found in thymus (53). The processing of thyroglobulin in the thyroid is a good example. Solubilization and pre-cleavage of thyroglobulin are necessary prior to endocytosis by TFC to generate T3 and T4 hormones. Cathepsins B, L, S, K present both in colloid and in the TFC’s endocytic vesicles cleave thyroglobulin at different pH (neutral and acid pH, respectively) (79), probably giving a different pattern of cleavage in each condition. By using the CFS method, we have performed a detailed study of how peptides from thyroid antigens

thyroglobulin and TSHR, are generated and presented by HLA-DR3 in different processing conditions.

3.2 RESULTS

3.2.1 Recombinant HLA-DR3 and HLA-DM function analysis

The ability of purified soluble HLA-DR3 molecules to generate peptide-MHC-II complexes was tested by polyacrylamide gel electrophoresis and binding assays (Fig.21). Electrophoresis of unboiled samples in the absence of detergent (native) showed peptide-MHC-II complexed with $CLIP_{89-105}$ but not with the hemagglutinin A peptide ($HA_{306-318}$) which is not a good binder for HLA-DR3. Intermediate conformations were observed for empty HLA-DR3 and HLA-DR3-$HA_{306-318}$ complexes, whereas an unique band was detected for $CLIP_{89-105}$ complexes (Fig.21A). Then, HLA-DR3 molecules were incubated with or without peptides for 72h at 37ºC and complexes were not boiled before electrophoresis. HLA-DR3- $CLIP_{89-105}$ complexes were SDS-sensitive, generating dissociated α and β chains (Fig.21B). Direct binding assays were performed to test the HLA-DM function using fluorescein-labeled CLIP peptide (Fig.21C). Fluorescence of bound peptide was measured in short-time association experiments. HLA-DM improved the binding of CLIP to HLA-DR3 but the peptide was released, independently of the HLA-DM presence, with a $t_{1/2}$≈3h. Thus, purified proteins HLA-DR3 and HLA-DM functioned as expected.

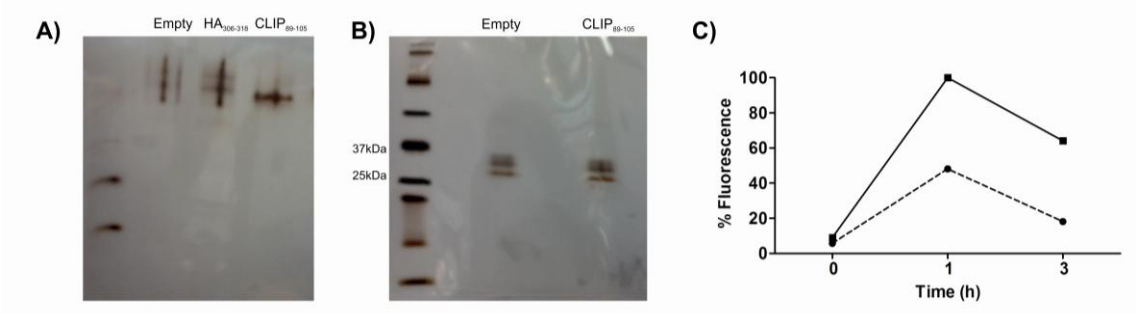

Figure 21. Recombinant HLA-DR and HLA-DM functional assay. A) HLA-DR3 complexes were analyzed in a native gel. Empty HLA-DR3 molecules and HLA-DR3-$HA_{306-318}$ complexes were dissociated but HLA-DR3-CLIP complexes were visualized as a single band. B) Empty HLA-DR3 molecules and HLA-DR3-CLIP complexes were analyzed in gentle SDS-PAGE gels. These complexes were SDS-sensitive and dissociated in HLA-DR αand βchains and free peptide when present. C) Direct binding assay of CLIP peptide and HLA-DR3 in the presence (black line) or absence of HLA-DM (dotted line). HLA-DM improved the binding of CLIP but with a t1/2≈3h. These data are representative of 4 experiments.

3.2.2 Optimization of thyroglobulin digestion

Cathepsins B, H and S were used as the main proteases involved in antigen processing by APCs (109) at pH 5.0. In addition, cathepsins L and D were included because of their role in thyroglobulin degradation in the thyroid (79). First, thyroglobulin was exposed to different concentrations of cathepsins for 1h and optimal concentrations were determined as follows: 0.36μM for cathepsins B and H, 0.2μM for cathepsins L and D and 0.14μM for cathepsin S (data

not shown). We then used these optimal concentrations and digested thyroglobulin with each enzyme plus combinations of them (Fig.22). Cathepsins B, H and S at pH 5.0 simulated the processing compartment of APCs (109); cathepsins B, L and S at pH 7.4 mimicked the colloid degradation environment (79); cathepsins B, H and L at pH 5.0 simulated the thymus mTECs processing machinery (75, 223); and cathepsins B, H, L and D at pH 5.0, the processing by TFCs (224, 225). Endopeptidase cathepsin S appeared to be crutial for thyroglobulin degradation both alone and in combination with other cathepsins, even at neutral pH. Of the other enthymes, endopeptidases cathepsin B and D mildly degraded the protein and cathepsin L showed a higher cleavage capacity. Exopeptidase cathepsin H was inefficient for whole thyroglobulin digestion.

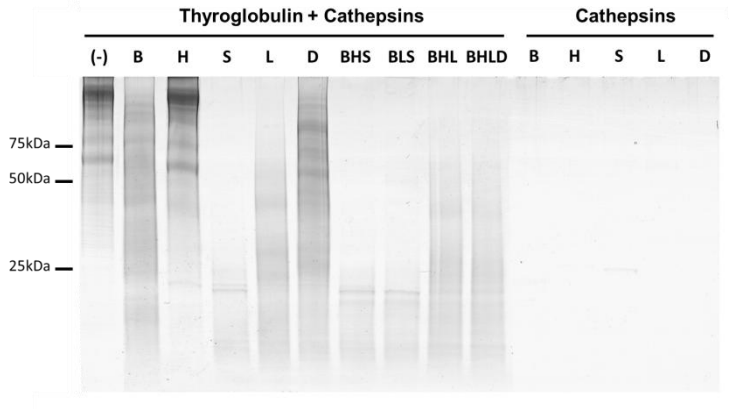

Figure 22. 4-12% SDS-PAGE gel of thyroglobulin digestion with different cathepsins alone or in combination. Lane 1: 1ug of thyroglobulin. Lanes 2-5: 1ug of thyroglobulin digested with cathepsin B, H, S, L and D at optimal concentration and pH 5.0. Lanes 6-9: combinations of cathepsins at pH 5.0 (BHS, BHL and BHLD) or pH 7.4 (BLS). Lanes 10-14: cathepsins alone.

The CFS method established that the antigen must be incubated with the HLA-DR molecule before the addition of proteases, to protect the immunodominant and other epitopes and the pMHCII from degradation. Thus, HLA-DR3-CLIP complexes were exposed to the same concentrations of cathepsins as thyroglobulin and complex degradation was analyzed by SDS-PAGE. The SDS gels showed that proteases slightly degraded the HLA-DR3 empty molecules. Degradation was prevented if HLA-DR3 was complexed with a peptide (Fig. 23).

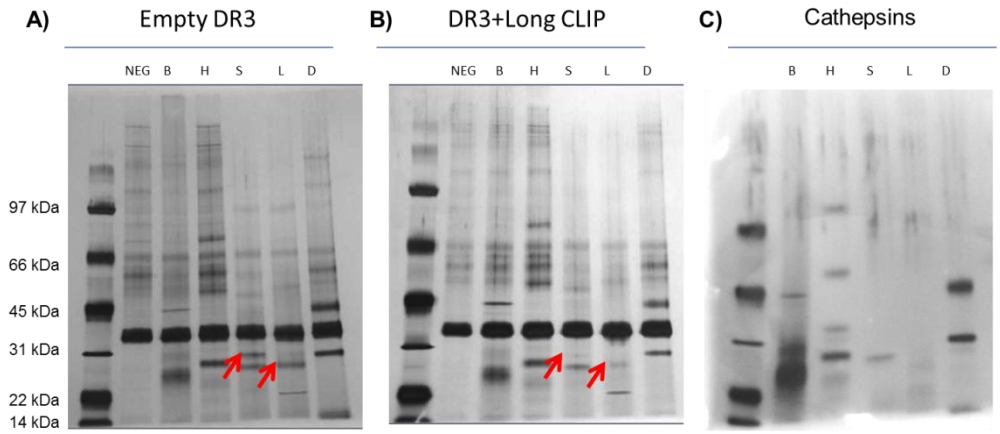

Figure 23. 4-12% SDS-PAGE of HLA-DR3-CLIP complex digestion with different cathepsins. HLA-DR3-CLIP complexes or empty HLA-DR3 molecules were incubated overnight and digested with the cathepsins (B, H, S, L or D) for 1h or nor digested (NEG). A) Some bands showed up after the digestion with cathepsin S or L when empty HLA-DR3 was analyzed (red arrows). B) Complexes seemed to be protected from degradation by the cathepsins S and L. C) Control gel with cathepsins alone.

3.2.3 Influence of colloid degradation in thyroglobulin processing and presentation

Cathepsins B, L and S are found in the colloid of normal thyroid glands and process thyroglobulin to facilitate its uptake by TFCs (79). We wanted to analyze whether the thyroglobulin epitopes were generated or destroyed by the proteases found in colloid prior the capture of these fragments by DCs. To address that, two experimental conditions for thyroglobulin degradation were selected. 1) thyroglobulin endocytosed and processed by infiltrating DCs (digestion with cathepsin B, H and S at pH 5.0) and 2) thyroglobulin partially degraded in colloid at pH 7.4 and then processed by DCs (sequential digestion by cathepsin B, L and S at pH 7.4 followed by digestion with cathepsin B, H and S at pH 5.0). (Fig.24).

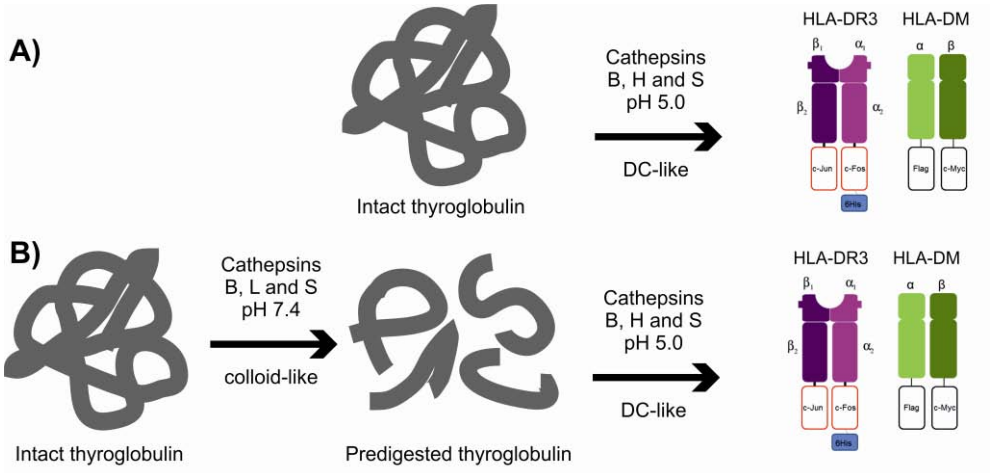

Figure 24. Schematic representation of the experimental conditions. A) Condition 1: simulation of thyroglobulin capture and processing by infiltrating DCs (digestion with cathepsin B, H and S at pH 5.0)- B) Condition 1: simulation of antigen processing by DCs if thyroglobulin is partially degraded in colloid conditions at pH 7.4 prior to capture (sequential digestion by cathepsin B, L and S at pH 7.4 followed by digestion with cathepsin B, H and S at pH 5.0)

Peptides bound to HLA-DR3 were immunopurified and analyzed by mass spectrometry. Non-specific binding peptides were identified in parallel experiments and excluded from the analysis. MALDI-TOF spectra showed both qualitative (m/z species) and quantitative (intensity) differences in peptide generation between both conditions (Fig.25).

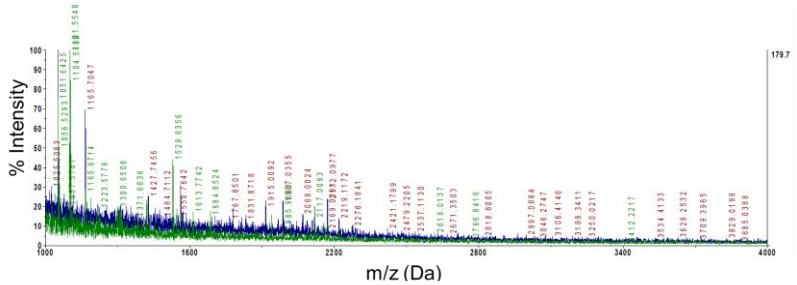

Figure 25. MALDI-TOF spectra of CFS samples represented according to their mass/charge (m/z) and intensity. The green spectrum corresponds to the digestion of the intact thyroglobulin by cathepsins B, H and S at pH 5.0 (condition 1). The blue spectrum corresponds to the digestion of the pre-digested thyroglobulin by cathepsins B, S and L at pH 7.4 prior the a second digestion with cathepsins B, H and S (condition 2). Green annotations correspond to m/z species were the intensity was higher in condition 1 and red annotations correspond to m/z species were the intensity was higher in condition 2. Peaks below m/z 1000Da were not shown in the X axis because they were matrix-derived.

Thyroglobulin peptides sequenced from each sample had an average size of 15 residues, within the standard range for MHC-II peptides (Fig.26A, 26B). For DC-like processing, 106 peptides were identified and 123 peptides when thyroglobulin was pre-digested in colloid-like conditions. Core sequence and theoretical binding affinity were assigned and then peptides were clustered in nested sets. All data is annotated in in Annex 3. Interestingly, the simulation of intact thyroglobulin processing by DCs yielded a higher percent of intermediate binders (38.7%) than of high binders (29.2%) whereas the pre-digestion of thyroglobulin favored HB (37.4%) in front of IB (33.3%) (Fig.26C, 26D).

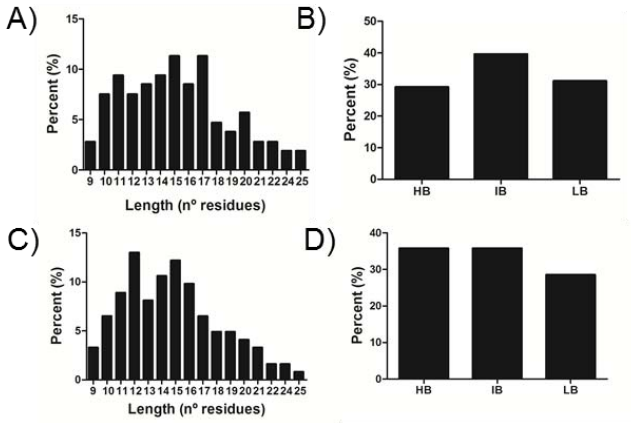

Figure 26. Size distribution and theoretical affinity of the peptides identified using the cell-free system for the study of antigen processing and presentation. Panels A and B represent characteristic of HLA-DR3-associated peptides derived from thyroglobulin when antigen was processed by cathepsins B, H and S at pH 5.0. Panels C and D represent the characteristics of the peptides when thyroglobulin was predigested with cathepsin B, L and S at pH 7.4 prior to the processing by cathepsins B, H and S, simulating the colloid degradative conditions. A, C show size distribution and B and D show theoretical affinity: high binder (HB), intermediate binder (IB) and low binder (LB)

Predigested thyroglobulin generated 18 unique nested sets and shared 40 nested sets with those from intact thyroglobulin: 10 HB, 13 IB and 17 LB (Fig.27). There were two dominant nested sets in both conditions, defined by the VIFDANAPV and VVVDPSIRH peptide-binding cores. The VVVDPSIRH core defines the group in which the immunodominant peptide Tg2098 is clustered. The pre-digestion generated two other well-represented groups (LQCDQNGQY and LQFTTNPKR) that were less represented in samples from intact thyroglobulin. In terms of peptides, 56 sequences were identical in both samples. The number of unique peptides in these nested sets was similar in both conditions but there were quantitative differences as represented by the number of peptide spectral match (PSM). PSM is a parameter that counts the number of times a single sequence is identified from different fragmentation spectra, meaning redundancy in peptide identification, i.e., a quantification of the fragmented peptides. Using PSM instead of SIEVE 1.4 (see chapter 2) was needed because the chromatograms were not strictly comparable in these type of experiments. PSM data showed that pre-digestion of thyroglobulin reduced the presentation of some peptides from the major VVVDPSIRH and VIFDANAPV nested sets (Tables 8-9). Different processing also affected the nature of the peptides. For example, in the nested set VIFDANAPV peptides preferentially started with a lysine if thyroglobulin was intact (6/11 peptides) whereas in the pre-digested sample only 2/8 peptides started with this amino acid (Table 9).

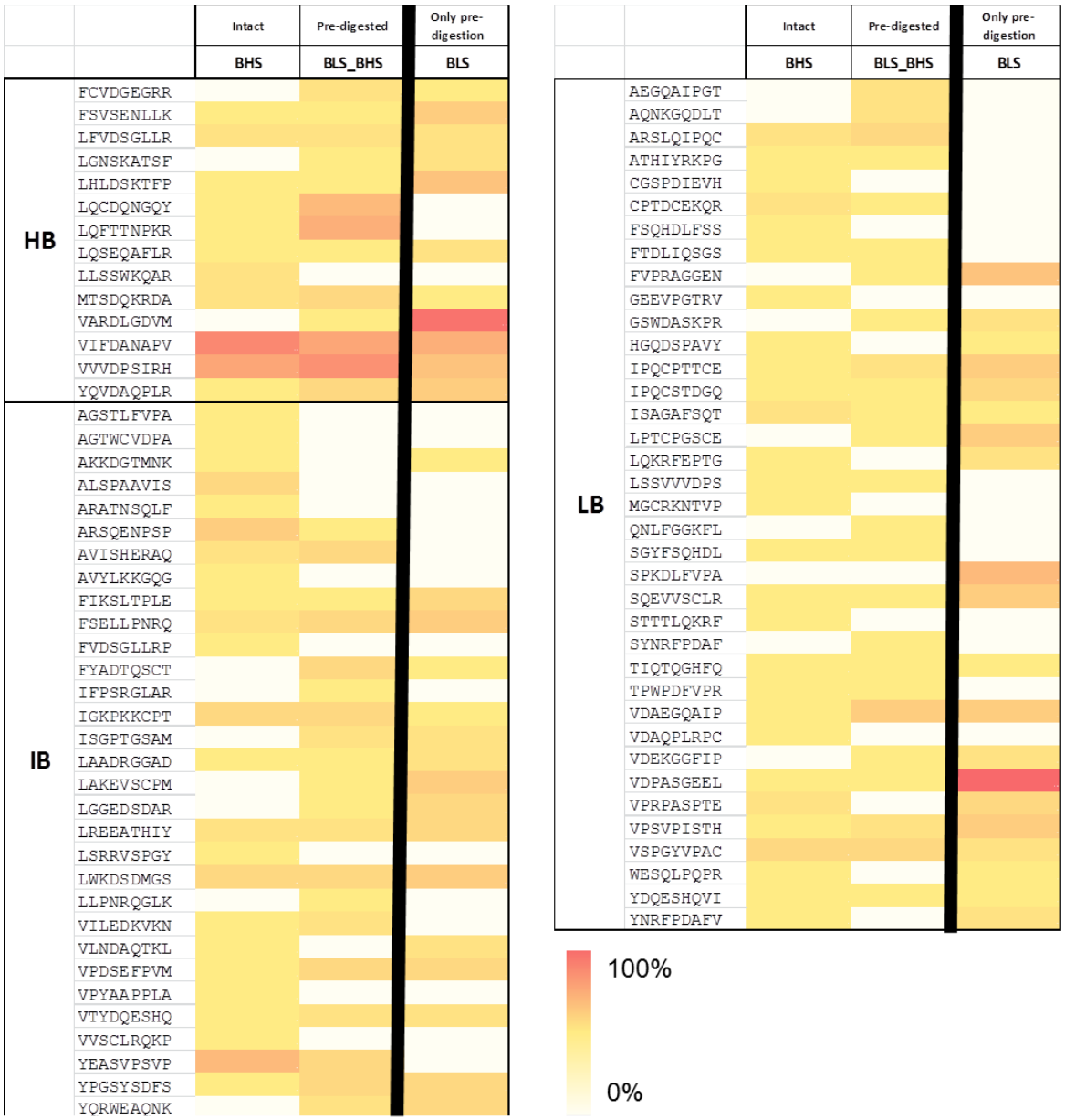

Figure 27. Relative abundance of the nested sets identified in samples where intact thyroglobulin was digested by cathepsins B, H and S at pH 5.0 (first column), where the thyroglobulin was pre-digested by cathepsins B, S and L at pH 7.4 prior to a second digestion with cathepsins B, H and S (second column) and the fragments generated by the pre-digestion and predicted to bind HLA-DR3 (third column). Left panel shows the high and intermediate binder (HB, IB) nested set cores and the right panel the low binders (LB). Results in different colors represent the percent peptides forming each nested set. The most abundant nested set was considered 100%.

The contribution of the pre-digestion to the generation of potential binding peptides was established by mass spectrometry sequencing of the fragments after digestion with cathepsin B, L, and S at pH 7.4 in the absence of HLA-DR and HLA-DM (Fig.27). The two major nested sets defined by VVVDPSIRH and VIFDANAPV cores, were generated in this control experiments. As shown above, cathepsin S leaded the degradation of thyroglobulin at acid and neutral pH whereas cathepsin B and L mildly degraded this protein (see Fig.22). These data suggested that the generation of the most abundant nested sets was mediated by cathepsin S and that

their cores were resistant to degradation. There also were two highly represented groups, VDPASGEEL (LB) and VARDLGDVM (HB) that were less abundant in the two conditions established (Fig.27). These two groups of peptides might be sensitive to cathepsin B, H and S digestion at pH 5.0. Thus, some epitopes generated in the pre-digestion would be destroyed and not presented by HLA-DR3.

Table 8. Number of peptide spectral match (PSM) for each peptide of the nested set with VVVDPSIRH core.

Peptide sequence	Intact thyroglobulin	Predigested thyroglobulin
LSSVVVDPSIRH	2	1
LSSVVVDPSIRHF		1
LSSVVVDPSIRHFDV		1
LSSVVVDPSIRHFDVAH	2	1
LSSVVVDPSIRHFDVAHVS	2	1
SLALSSVVVDPSIRHFDVAH	2	
SSVVVDPSIRHF		1
SSVVVDPSIRHFDVAH	2	1
SVVVDPSIRH	2	
SVVVDPSIRHFDV	2	1
SVVVDPSIRHFDVAH	2	1
SVVVDPSIRHFDVAHVS		1

Table 9. Number of peptide spectral match (PSM) for each peptide of the nested set with VIFDANAPV core.

Peptide sequence	Intact thyroglobulin	Predigested thyroglobulin
EKVPESKVIFDANAPVA		1
KVPESKVIFDANAPVA	2	1
KVPESKVIFDANAPVAVR	2	1
KVPESKVIFDANAPVAVRS	2	
KVPESKVIFDANAPVAVRSK	2	
KVPESKVIFDANAPVAVRSKVPDS	2	
KVPESKVIFDANAPVAVRSKVPDSE	2	
MQKFEKVPESKVIFDANAPVA	2	2
QKFEKVPESKVIFDANAPVA		1
QKFEKVPESKVIFDANAPVAVR	2	1
QKFEKVPESKVIFDANAPVAVRSK	2	
SKVIFDANAPVA		1
VPESKVIFDANAPVA	2	1
VPESKVIFDANAPVAVR		
VPESKVIFDANAPVAVRS	2	

As shown in chapter 2, posttranslational modifications may affect the thyroglobulin derived peptide repertoire. We analyzed the isolated peptides within the thyroglobulin sequence and their glycosylation and iodination sites. Some peptides contained residues that might have been modified by iodination (Tyr^{24}, Tyr^{785}, Tyr^{883}, Tyr^{2184}, Tyr^{2697}) but no iodinated peptide was identified by MS. Additionally, 3 glycosylation regions (positions 1774-1776, 2250-2251, 2617-2619) were closely located to some of the identified peptides but they did not appear to influence thyroglobulin processing.. Some regions seemed to be predominant for peptide generation in both cases although there were frequency differences. However, pre-digestion at neutral pH generated 9 new regions generating peptides.

3.2.4 Differential processing of thyroglobulin in thyroid and thymus-like conditions

The induction of tolerance to thyroglobulin in the thymus, would require presentation of the antigen by mTECs or thymus DCs. The mechanisms for antigen processing would be different because of the source of protein for each cell type. mTECs express thyroglobulin (192) and their own machinery, presumably autophagy, would degrade and present the antigen, whereas DCs would take up cellular material from mTECs from which they would obtain the thyroglobulin or circulating DCs loaded with the antigen in the periphery could migrate to thymus. Contrary to mTECs, thymus DCs overexpress cathepsin S instead of cathepsin L (75). Thus, DC-like conditions (cathepsins B, H and S at pH 5.0) was compared to mTEC-like conditions

(cathepsins B, H and L at pH 5.0) that generated 44 non-redundant peptides derived from thyroglobulin. Size average was as expected for MHC-II peptides (14 residues) but surprisingly most peptides were low binders (50%) and only 20.5% were high binders (Fig 28).

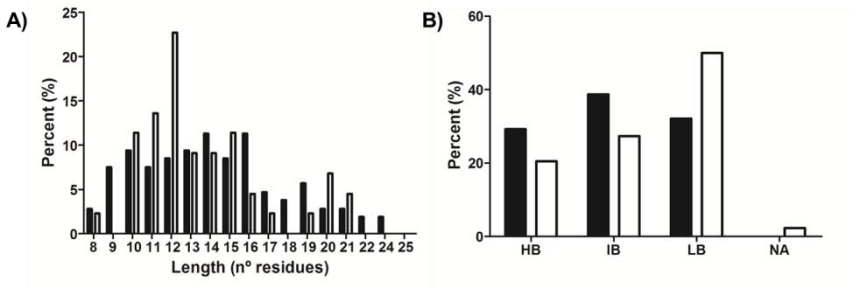

Figure 28. Size distribution (A) and predicted affinity (B) of the peptides isolated in cell-free system samples simulating DCs (cathepsins B, H and S at pH 5.0) (black bars) and mTECs (cathepsins B, H and L at pH 5.0) (white bars). Peptides were considered high binders (HB), intermediate binders (IB), low binders (LB) or non-assigned (NA).

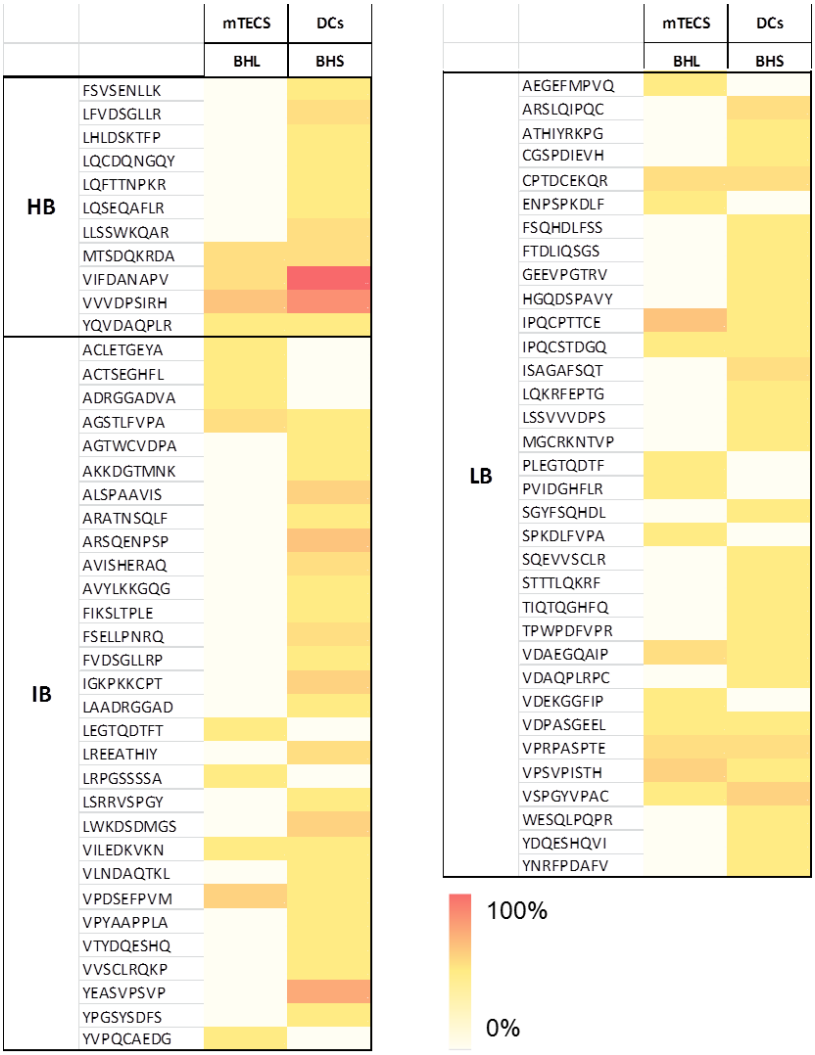

Figure 29. Relative abundance of the nested sets identified in samples where intact thyroglobulin was digested simulating mTECS by cathepsins B, H and L at pH 5.0 (first column) and where the thyroglobulin was digested simulating DCs by cathepsins B, H andS at pH 5 (second column) Left panel shows the high and intermediate binder (HB, IB) nested set cores and the right panel the low binders (LB). Results in different colors represent the percent peptides forming each nested set. The most abundant nested set was considered 100%.

Compared to DC-like conditions, the mTEC-like processing generated less peptides (44 vs 106) grouped in 12 unique nested sets and 15 shared nested sets: 4 HB, 3 IB and 8 LB (Fig,29). In mTEC-like conditions, the nested sets defined by VVVDPSIRH and VIFDANAPV cores were also generated but the variety of peptides was considerably lower than in DC-like condition. For the VIFDANAPV group, only 2 different sequences were found (4 PSMs) and 4 for the VVVDPSIRH nested set (8 PSMs). These data suggested that the mTECs-like condition poorly contributed to the generation of thyroglobulin peptides. It would be very interesting to identify which of the two cell types are more responsible for the generation of central tolerance for thyroglobulin.

3.3 DISCUSSION

The influence of tissue-specific degradative processes has been proposed as a mechanism to generate potential T cell epitopes that may not be presented during central tolerance (53). A major evidence came from the discovery of “type B” CD4+ T cells in the NOD mouse model (226, 227). These cells responded to peptides generated exogenously but were not responders to the same peptide if generated from the protein processing in the MHC-II pathway. Mohan *et al*. proposed that MHC-II molecules would bind peptides, fragments or denatured proteins at the cell surface or in early recycling compartments where the chaperone HLA-DM is not found. Excluding posttranslational modifications, they also suggested that different binding registers within the groove may have been involved in differential recognition by T cells. Such differential behavior of type B T cells has also been observed in myasthenia gravis (228) and multiple sclerosis (229).

The study of thyroid autoimmunity in HLA-DR3 transgenic mice showed a thyroglobulin peptide that induced mild EAT when challenged with the peptide, but if the lymph node APCs were primed with the entire protein, T cells were unable to respond to this epitope (230). Thus, tissues with highly activated proteolysis processes may play an important role in autoimmune peptide generation. In RA, type II collagen (CII) is a major component of cartilage and the main suspected autoantigen for HLA-DR1 individuals. It has been shown that CII undergoes extracellular processing with matrix metalloproteinase 9 (MMP9), before the resulting fragments are further processed by APC to generate the immunodominant peptide $CII_{280–294}$ CAGFKGEQGPKGEPGP (231). In agreement with these data, Hartman *et al*. (154), only reproduced the generation of this peptide after predigestion of CII with MMP9 using the *in vitro* CFS.

In thyroid autoimmune diseases, thyroglobulin proteolysis in the colloid may display a source of peptides or fragments that could then be processed by APCs. An elegant work by Jordans *et al*. studied the role of cathepsins B, L, S and K, pH and redox potential in thyroglobulin degradation (79). The presence of cathepsins in the colloid is necessary to produce some fragments that are easly endocytosed by TFCs to release the hormones. In our *in vitro* digestion experiments, cathepsin S was shown to be the most degradative protease for thyroglobulin, even at neutral

pH. Although most cathepsins are highly unstable at the neutral colloid pH, cathepsin S and K are stable and active. Jordans *et al*. proved that cathepsin S is the most degradative protease at neutral pH by measuring the release of T4 hormone. They found the endopeptidase cathepsin L to be the most degradative protease at lysosomal-like condition, pH 5.0 (79). In our hands, cathepsin L was less degradative at pH 5.0 than cathepsin S, although the conditions used were very different. Cathepsin B was partially degradative in both studies.

Cathepsin D was considered dispensable to recreate the processing by DCs in CFS, as was demonstrated by the unaffected antigen processing in knock-out mice (109, 154, 232). However, the inhibition of cathepsin D with pepstatin A in mice improved the presentation of a myoglobin peptide to T cells by DCs (233). In addition, cathepsin D is overexpressed by TFCs in GD patients and also exhibited a high activity in patients, so it was proposed to have a role in thyroid antigen processing (225, 226). By in vitro digestion experiments, we observed that cathepsin D had a medium impact in thyroglobulin digestion, similar to that of cathepsin B.

Despite the importance of cathepsins in thyroid, only a few works about AITD included them as potential generators of T cell epitopes. Jacobson et at (142) examined the individual cleavage of thyroglobulin by cathepsin B, L and D at pH 3.5 as they proposed for TFC's lysosomes. Fragments were sequenced by MS and their theoretical affinity for HLA-DR3 was assigned in order to use them in experimental assays. Another study defined cleavage sites for cathepsins B, L and D in rabbit and mouse thyroglobulin (224, 234). Kolypetri *et al*. l related the cleavage sites with described T cell epitopes and also analyzed the thyroglobulin sequence adjacent to cleavage sites to find new epitopes. They found two new peptides capable of inducing mild EAT near cathepsin L cleavage sites. Interestingly, these epitopes were clustered close to known pathogenic thyroglobulin epitopes in mouse and human (230, 235). Thus, this is the first time that a combined analysis of both processing and presentation are used to evaluate HLA-DR3-associated thyroglobulin peptides.

Our data show that pre-digestion of thyroglobulin at colloid-like conditions prior to processing by DC-like conditions, increased the number of HLA-DR3 associated peptides, especially those of high affinity. However, a large number of nested sets were common in both conditions (40/68), such as the two major nested sets defined by cores VIFDANAPV and VVVDPSIRH and assigned as high binders. If peptide redundancy was included in the analysis, less peptides were generated when thyroglobulin was predigested in both nested sets. These groups were also found in HLA-DR3+ DCs pulsed with thyroglobulin and is discussed in chapter 4. Fragments of the pre-digestion were sequenced to determine whether this proteolysis would be enough to generate potential binders. Analysis showed that the two major nested sets were also found but were not as abundant as VDPASGEEL and VARDLGDVM groups. Interestingly, these pre-digestion-derived nested sets were poorly represented when a second digestion was performed in DCs-like conditions. Additionally, peptides from 9 exclusive regions were generated when thyroglobulin was predigested.

Therefore, pre-digestion in colloid conditions favors the proteolysis of some regions that can be further degraded or protected by DC-like processing. In a recent report, cathepsin resistance of given epitopes, together with their degree of sensitivity to HLA-DM was related to peptide presentation (109, 154). Authors suggested that if antigens bind first to MHC-II and are later trimmed by proteases, this binding would be protective for some epitopes. In addition, most MHC molecules will end up with epitopes that are bound to MHC-II very tightly or not so tightly, but because of resistance to digestion by the cathepsins, even if they are dislodged by HLA-DM, they can rebind, so some epitopes would gain in relative abundance. Neutral pH may also interfere in proteolytic activity reducing the efficient generation of other fragments. However, one might conclude that there is not a clear contribution of colloid-specific proteolysis to the generation or destruction of the peptides included in the nested set VVVDPSIRH, where the immunodominant Tg2098 is clustered. A putative role for peptides specifically generated in TFC remains to be demonstrated.

In a second experimental situation, we simulated and compared the processing of thyroglobulin by mTECs (with cathepsins B, H and L) and DCs (with cathepsins B, H and S). Both L and S are important in antigen processing and presentation, being the key enzymes involved in the processing of Ii (236, 237). On the other hand, cathepsin S knock-out mice, although phenotypically normal, are partially resistant to experimental autoimmune T1D, myasthenia gravis and collagen-induced arthritis, while their wild type counterparts are susceptible (78, 238, 239). Cathepsin S has been found to be dominating in thymus DCs (75). Authors showed that cathepsin S can destroy T cell epitopes of MBP and insulin, which would explain why some autoreactive T cells can escape from central tolerance. Cathepsin L is required for the positive selection of CD4+ T cells in the mouse (223), but human cortical epithelial cells express cathepsin V and not cathepsin L, that is expressed by human mTECs. Thus, we set up experimental conditions for thyroglobulin processing where cathepsin L substituted cathepsin S for mTEC-like condition.

Digestion of thyroglobulin with cathepsins B, H and L reduced the number of peptides associated to HLA-DR3 when compared to DC-like condition (cathepsins B, H and S). Moreover, many peptides were low binders (50%) and few were high binders (20%), compared to what we found in DC simulation (30%). Only 15/27 groups of peptides were shared with DCs condition but they included the major HLA-DR3 nested sets, VVVDPSIRH and VIFDANAPV with only 4 and 2 different peptides sequences for each group, respectively. Therefore cathepsin S generates the highest number of different thyroglobulin-derived peptides to be presented by HLA-DR3 molecules.

As discussed in previous chapters, the thymus HLA-DR peptidome has been reported to be mostly constituted by high affinity peptides (59). However, here we show how simulation of mTECs processing did not generate many HB peptides for this particular antigen and this particular allele. A study of this same antigen in CFS with a "protective" allele such as HLA-DR15 may solve some of the questions generated by these data.

Finally, the method presented in this chapter was initially set up to study antigens presented by HLA-DR1 (154). This allele, together HLA-DR4, is very well studied. Many cells lines have been used to describe their peptides repertoires (6, 15, 16, 19, 158 190) and also the role of MHC-II associated molecules such as Ii and HLA-DM in antigen presentation (164, 176, 240). Despite its association to autoimmune diseases, HLA-DR3 has not been fully characterized in relation to antigen presentation (17, 241, 242). Soluble HLA-DR3 molecules are unstable in SDS and the $t_{1/2}$ of CLIP binding is ~3h, although the X-ray crystal structure of HLA-DR3 was the first described with CLIP bound to the cleft (8). Our data demostrate that CFS is a robust method because using HLA-DR3 as presentation molecule, it works for the identification of immunodominant peptides.

CHAPTER 4

Evaluation of two different approaches for the identification of thyroglobulin-derived immunodominant peptides

4.1 BACKGROUND

Different strategies have been used to analyze the impact of MHC-II proteases in antigen processing and presentation: knock-out mice for specific proteases, cell lines expressing the selected protease and specific inhibition of proteases in *ex vivo* experiments. For example, NOD mice deficient in cathepsin B, S, or L are protected from type I diabetes development (78). Hsieh *et al*. (243) used mouse embryonic fibroblast lines that expressed cathepsin L, S or neither to study their role in antigen presentation. The presentation of several peptides from IgM, HEL and OVA was augmented by cathepsin L or S expression but diminished for one of the IgM peptides especially in cathepsin S-expressing cells. DCs and B cells incubated with the cathepsin D and E-inhibitor pepstatin A or from cathepsin D-null mice improved the presentation of a myoglobin peptide to T-cells (233).

Some other authors have used the lysosomal content from diverse APCs to analyze the crucial proteases involved in the degradation of some antigens *in vitro*. Exposition of TTCF to disrupted lysosomes purified from a human B-cell line showed that the dominant processing activity that allowed TTCF-derived peptide presentation was mediated by AEP (244). Similarly, differential MBP processing has been analyzed in B cell lines (245-247) and in MoDCs and primary CD1c-DCs (77). Interestingly, the processing of proinsulin by human thymus DCs lysosome components was also analyzed (75). However, the antigen presentation readout of most of those experiments relied on the recognition of the T cell epitopes by well-stablish antigen-specific T cell clones or newly-generated reactive T cells with unknown epitopes.

In this chapter, we evaluate two different approaches for the study of both antigen processing and presentation using a cellular-based method and a cell-free system based on the minimal players involved in both processes. This would allow us to establish whether different processing conditions result in changes in the peptide pool presented from a given antigen, opening the possibility to identify new T cell epitopes for known antigens but also from new antigens. Here, we focused on thyroglobulin processing because of its special degradation in the thyroid as part of its function, its role in autoimmune thyroiditis and also because several thyroglobulin-derived peptides have been analyzed as potential T cell epitopes in autoimmunity. Although most studies described T cell epitopes in EAT-susceptible mice (e.g. CBA/J, SJL, AKR/J, NOD) in association to murine MHC-II (205, 234, 248, 249), some others used HLA-DR3 transgenic mice (207, 230) and human material (72, 143) to dissect the T cell responses in autoimmune thyroiditis.

4.2 RESULTS

4.2.1 The reductionist cell-free system reproduces the major findings of thyroglobulin processing in HLA-DR3 mature moDCs

To evaluate the similarity between DC-like conditions of CFS with thyroglobulin processing by MoDCs we compared the repertoires obtained by both methods. For the CFS method, the cathepsins used to mimic DCs machinery were Cat B, H and S. As an indication of expression, we did conventional PCR for cathepsin genes in monocytes, iDCs and mDCs. As shown in Fig.30A, iDCs showed the highest expression of all cathepsins tested compared to monocytes and mature DCs (cathepsin B, H, S and L), except for cathepsin D that was predominant in monocytes and Cat V, specific of cTECs, that was not expressed by any of the samples.

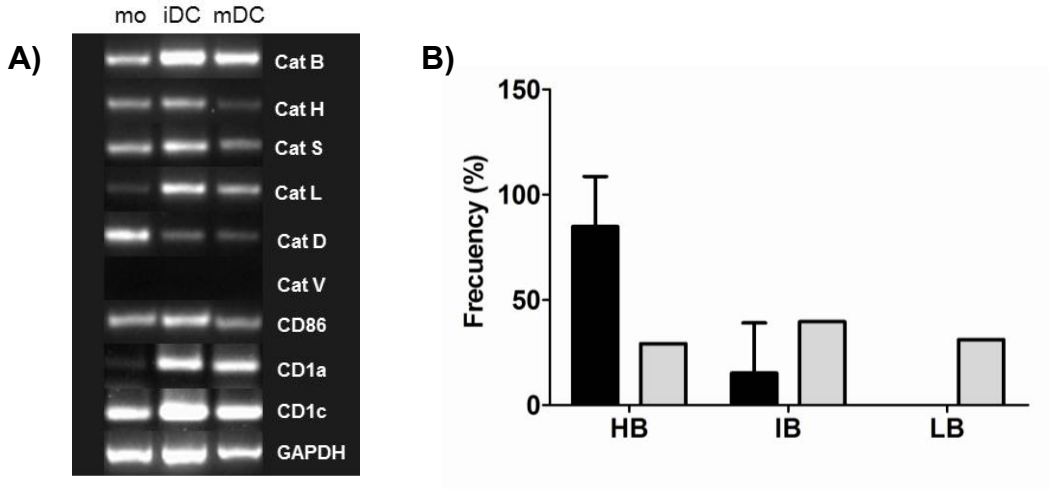

Figure 30. A) Conventional PCR for cathepsin (Cat) expression in monocytes (mo), immature MoDCs (iDCs) and LPS-matured MoDCs (mDCs). GAPDH, CD86, CD1a and CD1c were used as control. B) Comparative of the affinity of thyroglobulin-derived peptides by HLA-DR3 if isolated from mDCs (black bars) or from the DC-like condition of the cell-free method

Using the CFS method, intermediate and low affinity peptides derived from thyroglobulin were presented and isolated in a similar proportion to the high binders (Fig.30B). As show in chapter 1, mature DCs preferentially presented high binders (75%) including those derived from thyroglobulin (chapter 2). However there were two dominant HLA-DR3-associated nested sets in both peptide pools, and these were the most numerous and all high binders. In the CFS samples, 11 peptides defined by the VIFDANAPV core group but only 5 different peptides constituted the same nested set in the pool obtained from HLA-DR3+ mDCs, 1 to 4 different peptide sequences per sample. In contrast, the other dominant nested set around the VVVDPSIRH core, generated 8 peptides in CFS whereas 19 different sequences were clustered for the same group in mDCs (Table 10-11). It must be said that for the VVVDPSIRH core group, 7-15 different peptide sequences were isolated from each HLA-DR3^{+} donor.

Table 10. Comparative of the HLA-DR3 nested set with VVVDPSIRH core in mDCs samples and DC-like condition in CFS. Intact thyroglobulin was used in both cases.

Peptide sequence	mDCs	DC-like CFS
ALSSVVVDPSIRHFD	X	
ALSSVVVDPSIRHFDV	X	
ALSSVVVDPSIRHFDVA	X	
ALSSVVVDPSIRHFDVAH	X	
DSWQSLALSSVVVDPSIRHFDVAH	X	
LALSSVVVDPSIRHFDV	X	
LALSSVVVDPSIRHFDVA	X	
LALSSVVVDPSIRHFDVAH	X	
LDSWQSLALSSVVVDPSIRHFDVAH	X	
LSSVVVDPSIRH		X
LSSVVVDPSIRHF		
LSSVVVDPSIRHFD	X	
LSSVVVDPSIRHFDV	X	
LSSVVVDPSIRHFDVA	X	
LSSVVVDPSIRHFDVAH	X	X
LSSVVVDPSIRHFDVAHVS		X
SLALSSVVVDPSIRHFDV	X	
SLALSSVVVDPSIRHFDVA	X	
SLALSSVVVDPSIRHFDVAH	X	X
SSVVVDPSIRHF		
SSVVVDPSIRHFD	X	
SSVVVDPSIRHFDVAH		X
SVVVDPSIRH		X
SVVVDPSIRHFDV	X	X
SVVVDPSIRHFDVAH		X
SVVVDPSIRHFDVAHVS		
SWQSLALSSVVVDPSIRHFDVAH	X	

Table 11. Comparative of the HLA-DR3 nested set with VIFDANAPV core in mDCs samples and DC-like condition in CFS. Intact thyroglobulin was used in both cases.

Peptide sequence	mDCs	DC-like CFS
EKVPESKVIFDANAPVA	X	
KVPESKVIFDANAPVA	X	X
KVPESKVIFDANAPVAVR		X
KVPESKVIFDANAPVAVRS		X
KVPESKVIFDANAPVAVRSK		X
KVPESKVIFDANAPVAVRSKVPDS		X
KVPESKVIFDANAPVAVRSKVPDSE		X
KVPESKVIFDANAPVAVRSKVPDSEFPVM	X	
MQKFEKVPESKVIFDANAPVA		X
QKFEKVPESKVIFDANAPVA		
QKFEKVPESKVIFDANAPVAVR		X
QKFEKVPESKVIFDANAPVAVRSK		X
SKVIFDANAPVA		
VPESKVIFDANAPV	X	
VPESKVIFDANAPVA	X	X
VPESKVIFDANAPVAVRSK		X

In terms of individual peptides, 4 identical sequences were identified in both sample types, two for each dominant nested set (VPESKVIFDANAPVA, KVPESKVIFDANAPVA, SLALSSVVVDPSIRHFDVAH, SVVVDPSIRHFDV). For the VVVDPSIRH set, the peptides were slightly shorter in the CFS sample compared to mDCs (15aa vs 18aa average) whereas for the VIFDANAPV group CFS peptides were larger (20aa vs 18aa).

As shown in chapter 2, MoDCs pulsed with tissue extract did not produce differences in the thyroglobulin peptides associated to HLA-DR molecules, despite a 10-fold higher concentration of thyroglobulin in these samples. The quantification may not be totally exact because the antibody used for ELISA quantification can recognize fragments of partially degraded thyroglobulin. These fragments might be processed differentially and not result in antigen presentation.

To check this point, immature moDCs were pulsed with cathepsin B, L and S-pre-digested thyroglobulin at neutral pH, simulating colloid conditions. The digestion was first stopped with iodoacetamide that was then degraded with light to prevent the inhibition of iDCs proteases.

Three concentrations of initial antigen (100, 300 and 450nM) and two time points for uptake prior to maturation (1 and 5h) were used. The HLA-DR-peptides isolation was successful but only 2 and 5 thyroglobulin peptide were identified when pulsed with 450nM of pre-digested antigen for 1h or 5h, respectively. These data suggested that the digested fragments may be totally degraded without reaching the MIIC for antigen presentation, or that the relevant epitopes are destroyed by the MIIC proteases before binding to MHC-II. The only peptide generated by the pre-digestion that was still isolated in mDCs pulsed with thyroglobulin fragments, suggesting resistance to degradation, was the Tg1574 peptide (VPESKVIFDANAPVA). Pre-digestion *per se* generated peptides clustered in high binding nested sets that were the same as those associated to HLA-DR3 in mature moDCs, i.e. sets with VVVDPSIRH, VIDAFNAPV, FIKSLTPLE, ILEDKVKNF and FCVDGEGRR cores (see Annex 4). Although little information was gathered from pulsing MoDCs with thyroglobulin fragments, the CFS applied to identically pre-digested thyroglobulin allowed us to analyze the effect of the pre-digestion and confirmed that the dominant epitopes were not destroyed and that different HLA-DR3-binding peptides were generated (chapter 3).

Pre-digestion also generated peptides capable to binding non-HLA-DR3 alleles that were detected from MoDCs after pulsing with whole thyroglobulin or tissue extract. For instance, peptides from nested sets corresponding to cores WQILNGQLS, FYPAYEGQF, VDPASGEEL, VIDAFNAPV and FIKSLTPLE, predicted to bind HLA-DR1, HLA-DR9, HLA-DR13, DR15 and HLA-DR9 respectively, were identified (see Annex 4).

4.2.2 Non-immunodominant peptide Tg1574 (VPESKVIFDANAPVA) is more resistant to cathepsin degradation than the immunodominant peptide Tg2098 (LSSVVVDPSIRHFDV)

Tg1574 (VPESKVIFDANAPVA) and Tg2098 (LSSVVVDPSIRHFDV) peptides from the major HLA-DR3-associated nested sets were identified from DCs samples and also in CFS experiments, independently of the condition. Flynn *et al*. (207) used these two peptides as predicted binders for HLA-DR3 in the EAT model of HLA-DR3-transgenic mice immunized with human thyroglobulin. Later, Tg1574 peptide immunization slightly stimulated $CD4^+$ T cells, but Tg2098 induced a high immune response and it also recreated a severe thyroiditis. As discussed before, mechanisms underlying immunodominance may be influenced by the resistance to HLA-DM and/or to cathepsin digestion of antigenic peptides (109).

Thus, the two peptides were generated and presented by HLA-DR3 using our methods but after thyroglobulin immunization, only one (Tg2098) had been able to induce disease in HLA-DR3-transgenic mice (207). To understand this difference, we exposed each peptide to CFS-like digestion using different combinations of cathepsins: a) cathepsins B, H and S simulating DCs; b) cathepsins B, H and L simulating mTECs, and c) cathepsins B, H, L and D, simulating TFCs. Digestion was carried out for 1h at 37ºC and analyzed by MALDI-TOF.

As shown in Fgure 31, Tg1574 (VPESKVIFDANAPVA, m/z 1556.80 Da) was more resistant to digestion than Tg2098 (Fig.31). The VPESKVIFDANAPVA peak intensity was 2-fold lower after digestion in DC- and mTEC-like conditions (Fig.31B-C) compared to the undigested peptide (Fig.31A) but no shorter peptides were generated, indicating that the other half of the peptide was fully degraded. The conditions simulating TFCs did not produce any peptide degradation. The Tg1574 peptide was therefore cathepsin resistant.

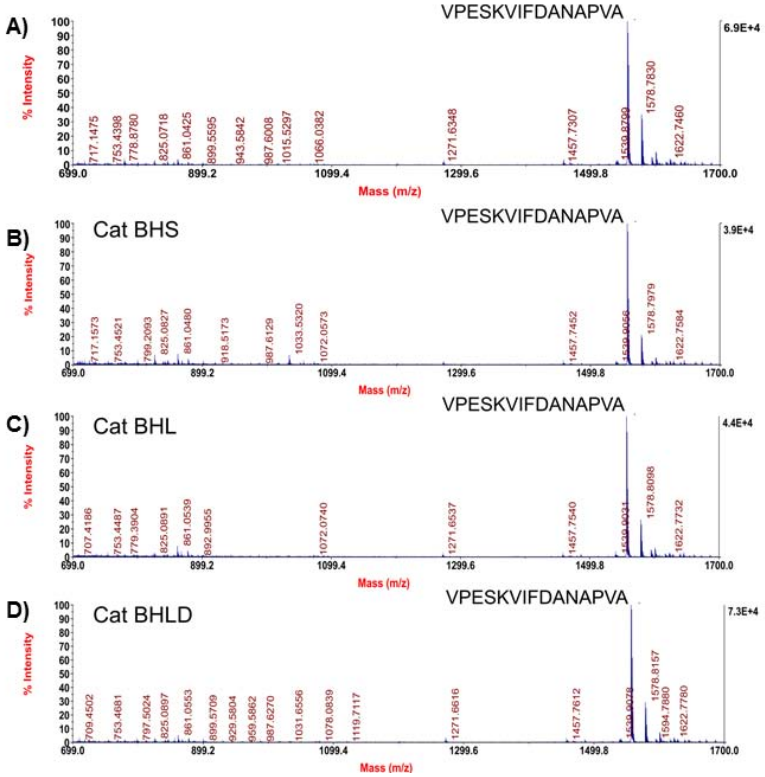

Figure 31. *In vitro* digestion of the synthetic peptide Tg1574 (VPESKVIFDANAPVA, m/z 1556.80 Da) with different combinations of cathepsin (Cat) simulating A) no digestion, B) DC-like processing, C) mTEC-like processing and TFC-like processing.

In contrast, under DC-like conditions (Fig.32A), Tg2098 (LSSVVVDPSIRHFDV, m/z 1669.93 Da) generated a high intensity peak that corresponded to the shorter SVVVDPSIRHFDV peptide (m/z 1469.79 Da) and other peaks with less intensity that were identified as SSVVVDPSIRHFDV (m/z 1556.82 Da) and LSSVVVDPSIR (m/z 1171.68 Da). This condition yielded 20-fold less intensity of the intact Tg2098 peptide. In mTEC-like conditions (Fig.32B), the degradation of Tg2098 peptide was lower than in DC simulation (the peak for intact Tg2098 was only 4-fold lower), leading to less intense peaks for SSVVVDPSIRHFDV (m/z 1556.82 Da) and LSSVVVDPSIR (m/z 1171.68 Da) peptides. TFC-conditions generated an 8-fold lower intact Tg2098 peak and another high intensity peak corresponding to the LSSVVVDPSIR peptide (m/z 1171.68 Da) (Fig.32C). Therefore cathepsins partially degraded the whole peptide but the binding core appeared to be cathepsin resistant.

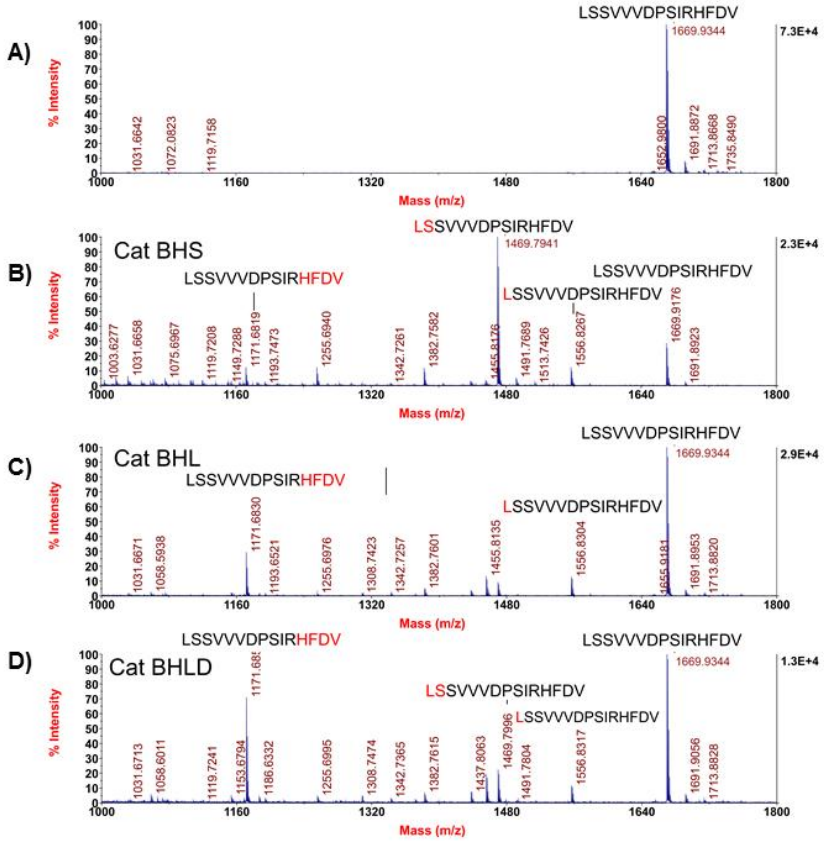

Figure 32. *In vitro* digestion of the synthetic peptide Tg2098 (LSSVVVDPSIRHFDV, m/z 1669.93 Da) with different combinations of cathepsin (Cat) simulating A) no digestion, B) DC-like processing, C) mTEC-like processing and TFC-like processing. This peptide is partially degraded by all cathepsin combinations

The experimental binding affinity of both peptides to soluble HLA-DR3 was measured as EC50 in a competitive binding assay in the presence or absence of soluble HLA-DM. EC50 represent the concentration of the studied peptide at which the reporter peptide is displaced to 50% of its maximum binding capacity. Biotinylated myoglobulin peptide LFRKDIAAKYKE (Myo137-148) was used as reporter peptide (153) in competition with 1-1x10^5nM of thyroglobulin peptides. Control experiments testing $Myo_{137-148}$ sensitivity to HLA-DM were carried out. As shown in Fig.33A, when the unbiotinylated $Myo_{137-148}$ was co-incubated with biotinylated $Myo_{137-148}$ in the absence of HLA-DM, $Myo_{137-148}$ was more easily removed from the binding groove than when HLA-DM was present. This corresponded to a 6-fold decrease in affinity. Thus, $Myo_{137-148}$ was considered a HLA-DM-dependent peptide.

For thyroglobulin peptides, an interesting phenomenon was observed. In the absence of HLA-DM, both major peptides had high affinity for HLA-DR3 (Fig.33B) with an EC50 of 140nM and 260nM for Tg2098 and Tg1574, respectively. However, the presence of HLA-DM did not affect the binding of Tg2098 (EC50 105nM), whereas Tg1574 was less capable to displace the reported peptide in the presence of HLA-DM (EC50 614nM, i.e., 2.3-fold affinity decrease in the presence of HLA-DM) (Fig.33C). In these experimental settings, the lower concentration of peptide needed to displace the reporter peptide corresponded to better affinity of the test peptide. Thus, HLA-DM holds the reported peptide in the groove and the peptide Tg1574 show

less affinity for HLA-DR3 in its presence, whereas Tg2098 is equally capable of displacing the reporter peptide in the presence or in the absence of HLA-DM. Tg2098 is then a HLA-DM-independent peptide, whereas the Tg1574 appears to be at least partially dependent on HLA-DM.

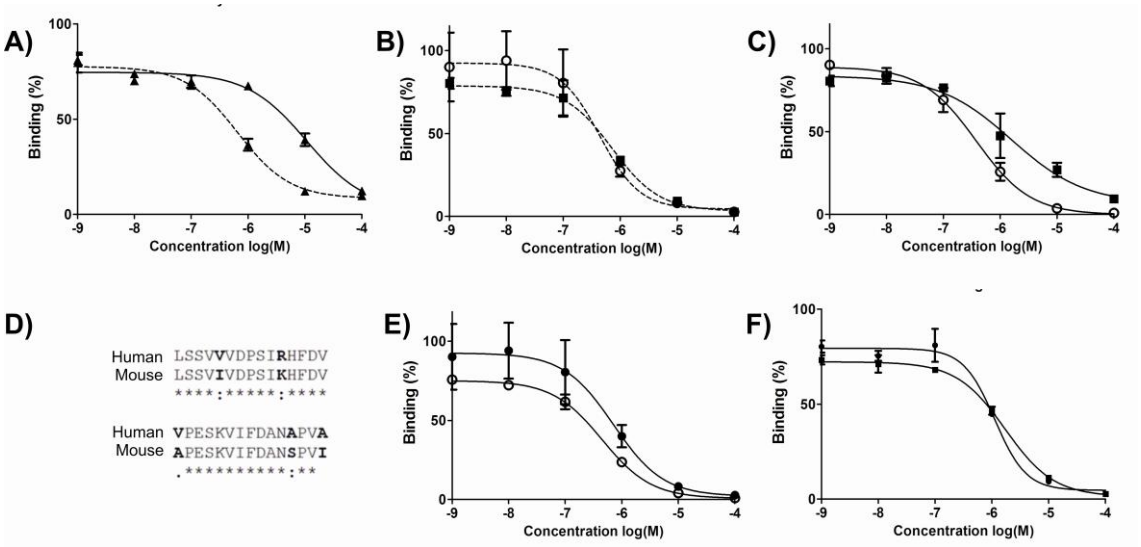

Figure 33. Competitive binding assays using biotinylated $Myo_{137-148}$ peptide as reporter to determine the affinity for HLA-DR3 of thyroglobulin peptides Tg2098 (LSSVVVDPSIRHFDV) and Tg1574 (VPESKVIFDANAPVA). A) Binding of unbiotinylated peptide in the presence (dotted line) or absence (black line) of HLA-DM. This peptide is HLA-DM sensitive. B) Binding of Tg2098 (white circles) and Tg1574 (black squares) in the absence of HLA-DM. C) Binding of Tg2098 (white circles) and Tg1574 (black squares) in the presence of HLA-DM. D) Alignment of the human and mouse versions of Tg209and Tg1574 peptides. Asterisk (*) indicates positions which have a single, fully conserved residue. Colon (:) indicates conservation between groups of strongly similar properties. Period(.) indicates conservation between groups of weakly similar properties E) Comparative between the human (black circles) and the mouse (white circles) version of the peptide 2098, in absence of HLA-DM. F) Comparative between the human (black squares) and the mouse (white squares) version of the peptide 2098, in the absence of HLA-DM. X axis shows the logarithm of the concentration (M) of each point in duplicate experiments ± SD. Points were adjusted to variable slope lines using GraphPad

On the other hand, sequence variations between human and mouse thyroglobulin may condition the binding of the peptides for HLA-DR3 or their recognition by T cells, in the developing of EAT in HLA-DR3-transgenic mice. Both proteins share 74.1% homology. For the corresponding sequence of human peptides Tg1574 and Tg2098 there are amino acid substitutions affecting the binding core and PFRs when compared to mice thyroglobulin. For Tg2098 peptide (Fig.33D) there are two conservative changes in human respect to mouse thyroglobulin, Val instead of Ile in P2 and Arg instead of Lys in P8. In Tg1574, the binding core is affected only in P7 by the presence of Ala in the place of Ser, a conservative substitution. Interestingly, this peptide differs with its mouse counterpart in the first and last residue of the peptide sequence, Val to Ala and Ala to Ile respectively. These changes modify the PFRs. Experimental binding assays to HLA-DR3 of the human and mouse peptides showed slight

differences between the human and mouse version of Tg2098 (Fig.33E-F), in which the mouse peptide showed ~2.5-fold greater affinity for HLA-DR3 (EC50=58nM) than the human peptide. APESKVIFDANSPVI, the mouse version of Tg1574, also had better affinity for HLA-DR3 (EC50=124nM) than its human counterpart. As shown for human peptides, the mouse variant of Tg2098 is the best binder of all four peptides.

4.2.3 Tg2098 and the other components of the VVVDPSIRH nested set have similar affinity for HLA-DR3

The nested-set with the core VVVDPSIRH was further studied to analyze whether small differences in the peptide length could influence the binding affinity to HLA-DR3 (174). The peptides analyzed were 4 identified using both the CFS (HLA-DM and no HLA-DM samples) and the DC processing, including the Tg2098 peptide and 4 that were exclusively isolated from mDCs processing, in addition to the positive control peptide ($Myo_{137-148}$) and the 9-mer core sequence. All showed high affinity for HLA-DR3 except for the 9-mer core peptide which did not bind. EC50 for the core peptide was over $1x10^5$nM (Table 12). The experimental affinity (EC50) ranged between 53 and 484nM in the absence of HLA-DM. The maximum difference (~10-fold) was between peptides SSVVVDPSIRHF and SVVVDPSIRHFDV. Peptide SSVVVDPSIRHF, the best binder in this condition, had short N- and C-ter PFRs, 2 and 1 residues, respectively. In the presence of HLA-DM, EC50 ranged between 46-270nM. In general, HLA-DM improved the binding affinity of these peptides with the exceptions of SSVVVDPSIRHF and SVVVDPSIRHFDVAH. Although these differences were not statistically significant, the presence of HLA-DM appeared to equalize the binding affinity of the nested set components, showing a less wide range of affinities. Looking at the data, HLA-DM improved the affinity of the worst binders.

Table 12. Binding affinity of peptides from the VVVDPSIRH nested set represented by the EC_{50} (M) in presence or absence of HLA-DM.

			EC50 (nM)		
	Method/ Reference	**Antigen source**	**(-)HLA-DM**	**(+)HLA-DM**	**Ratio (-)DM/ (+)DM**
LFRKDIAAKYKE ($_{Myo137-148}$)	---	---	132	749	-5.7
VVVDPSIRH	---	---	$>1x10^5$	$>1x10^5$	---
SSVVVDPSIRHF	CFS	pre-Tg	53	170	-3.2
SVVVDPSIRHFDVAH	CFS	Tg, pre-Tg	79	153	-1.9
SLALSSVVVDPSIRHFDV	mDCs	Tg, thyoid extract	138	46	+3
LSSVVVDPSIRHFDV	mDCS, CFS (72, 142, 143, 146)	Tg, pre-Tg, thyroid extract	140	105	+1.3
LSSVVVDPSIRHF	CFS	pre-Tg	156	106	+1.5
SVVVDPSIRHFD	(142)	---	181	127	+1.4
LSSVVVDPSIRHFDVAH	mDCs, CFS	Tg, pre-Tg	383	122	+3.1
SVVVDPSIRHFDV	mDCs, CFS	Tg, pre-Tg	484	270	+1.8

4.3 DISCUSSION

MoDCs have been used as a model to study the mechanisms involved in DCs maturation, MHC-II antigen presentation and endocytic transport (1). Concerning antigen processing and presentation, differential expression and activity of proteases in the different DC types must be taken in account. Burster *et al.* (77) showed differences between MoDCs and primary peripheral CD1c-DCs in protease expression at RNA and protein level in lysosomes, as well as in their activity. MoDCs expressed mature isoforms for cathepsins S, L, B, D, H, and Z and AEP, whereas CD1c-DC lacked mature cathepsin L, B, H, C and Z. Despite similar quantities of cathepsin S protein in both cell types, its activity was lower in peripheral DCs, suggesting that it was more controlled. The immature and mature MoDCs analyzed in the present work did express cathepsins B, H and S, the chosen minimal combination of cathepsins used in the CFS.

The results from thyroglobulin processing and presentation using the CFS method reproduced those observed with thyroglobulin-pulsed HLA-DR3+ MoDCs. However, when affinity was analyzed, we clearly showed that mDCs favored high affinity peptides from self and exogenous proteins whereas in CFS samples high, intermediate and low binders were identified. This phenomenon may be explained by the experimental method itself. In CFS peptides derived mainly from the antigen in study, although some cathepsin and HLA molecules-derived peptides were also found. The experimental set up included an excess of HLA-DR molecules to improve the immunoaffinity purification. This could explain that once all the generated HB peptides occupied HLA-DR3 molecules, IB and LB could bind to the “free” molecules. Even if HLA-DM removed them, they could always rebind if there was no competition with higher affinity peptides.

The two predominant nested sets associated to this allele, VIFDANAPV and VVVDPSIRH, were found using both experimental procedures. Nevertheless, the number of nested set components varied differentially between one and the other group. VVVDPSIRH was comprised by 8 peptides in the CFS sample but 7-15 in mDCs samples. In contrast, VIFDANAPV was more represented in CFS (11 different sequences) than in mDCs (1-4 peptides). Two explanations can be proposed. First, the MoDCs machinery for antigen capture, processing and presentation is more complex so some steps in epitope selection may be lost in CFS. Second, and in particular for the VIFDANAPV nested set, other cathepsins beside B, H and S may have their role in epitope selection. This group of peptides has an Asn residue in their sequence that may make them a target for AEP (244). AEP have been described to be essential in MBP processing, selectively destructing its dominant epitope in MoDCs and B-lymphoplastoid cells lines (77, 246). Since the CFS did not include this protease, more peptides would be available for association to HLA-DR3, whereas in MoDCs those peptides would be degraded. On the other hand, it is important to note that even if relatively abundant in both conditions, these nested sets were composed by different peptides variants, depending on the method used. Actually, only 4 peptides were common in both methods: VPESKVIFDANAPVA,

KVPESKVIFDANAPVA, SLALSSVVVDPSIRHFDVAH, SVVVDPSIRHFDV. Here again, the relevance of other peptidases expressed by MoDCs but not included in the reductionist system must be considered.

Uptake of thyroglobulin by MoDCs in conditions simulating the colloid proteolysis prevented the presentation of any peptide. After 5h pulsing of MoDcs with 450nM of cathepsin B, L and S pre-digested thyroglobulin at pH 7.4, only five peptides, one of which was peptide VPESKVIFDANAPVA were identified. The other four peptides were: two truncated peptides of the VVVDPSIRH nested set, one that could not bind HLA-DR3 or HLA-DR15 and one that associated to HLA-DR15. None had been identified in any previous experiment. However, pulsing the same cells with tissue extracts, where colloid contents were enriched, generated the presentation of thyroglobulin peptides with as much efficiency as when purified thyroglobulin was used. These extracts contained predigested thyroglobulin but also intact protein. Therefore it is likely that the predigested antigen was nearly completely degraded by MoDCs. Contrary to MoDCs, CFS allowed us to analyze the colloid-like conditions by which thyroglobulin is normally degraded prior to internalization (see chapter 3). In addition, the digestion of thyroglobulin *per se* with cathepsins B, L and S at neutral pH resulted in the generation of potential HLA-DR3 binding peptides (nested sets VVVDPSIRH, VIDAFNAPV, FIKSLTPLE, ILEDKVKNF and FCVDGEGRR) but also to HLA-DR1 (WQILNGQLS), HLA-DR9 (FYPAYEGQF), HLA-DR13 (VDPASGEEL) and HLA-DR15 (VIDAFNAPV and FIKSLTPLE nested sets).

Using both procedures, we have identified two peptides associated to HLA-DR3, whose sequence had previously been described in literature: LSSVVVDPSIRHFDV (72, 142, 146, 207) and VPESKVIFDANAPVA (207). A nested set with the VPESKVIFDANAPVA binding core was found in our samples. This peptide was described as a potential HLA-DR3 binder using an algorithm-based program (Flynn) and a peptide described as cathepsin D-generated (EKVPESKVIFDANAPVAVRSKVPDSEF) was found to be a good binder for HLA-DR3 (142). However, Tg1574 peptide (VPESKVIFDANAPVA) did not stimulate high thyroglobulin-specific HLA-DR3-restricted T cells *in vitro* and also failed to induce EAT in HLA-DR3-transgenic mice (207). In contrast, Tg2098 (LSSVVVDPSIRHFDV) was isolated from HLA-DR3 in thyroid from GD patient (72). This peptide has been described as immunodominant in HLA-DR3+ transgenic mice both for T cells stimulation and induction of thyroiditis (207). In addition this peptide was capable of stimulating T cells from four AITD patients (only one HLA-DR3) with high titer of anti-thyroglobulin antibodies (143). The Tg2098 peptide has also been described as HLA-DM-independent and cathepsin B, H and S-cleavage resistant in a collaboration work recently published (109). The degradation resistance was established as the prevention of epitope destruction, even if partial degradation occurred. We extended the analysis to degradation by different combination of cathepsins B, H and L (mTECs-like condition) and cathepsins B, H, L, D (TFCs-like condition). Tg2098 was partially degraded in all three conditions but always leading to the generation of other peptides that are part of the nested set, indicating that the binding core is cathepsin-resistant. Moreover, cathepsin S seemed to be the critical for the generation of

at least one variant peptide producing a peak of high intensity, SVVVDPSIRHFDV (m/z 1669.93 Da). This was also the case for the entire thyroglobulin, as seen in chapter 3.

In contrast, Tg1574 was resistant to the analyzed cathepsins thought AEP should be also checked, as mentioned before. Additionally, the affinity of this peptide for HLA-DR3 was affected by the presence of HLA-DM, contrary to Tg2098. According to our data and Sadegh-Nasseri *et al.* (250), this would be one example of how immunodominant peptides are selected. Pending to solve AEP degradation and despite the experimental high affinity to HLA-DR3 of the Tg1574 peptide, its removal from the binding groove by HLA-DM appeared to be favored. In contrast, Tg2098 would gain access to HLA-DR3 in an HLA-DM independent way. Partial degradation of Tg2098 generated a larger nested set of peptides (19 peptides vs. 4 for the VIDAFNAPV set) that showed very small differences in peptide affinity to HLA-DR3. One of the peptides from the same nested set (SVVVDPSIRHFD) was previously reported as a non-binder by Jacobson *et al*. (142) but in our data it showed as high affinity as the other peptides. As claimed in their report, Jacobson *et al*. used biotinylated peptides to measure the affinity so the two amino acid N-terminal truncation could place the biotin group much closer to the binding groove and thus sterically prevent binding. Despite similarities in binding to HLA-DR3, differences in T cell stimulation could not be excluded for some of these peptides, because PFRs may modify the interaction with TCR and hence alter the immune response (12).

Transgenic HLA-DR3+ mice have been used for EAT induction with human thyroglobulin. Since human and mouse thyroglobulin shared 74.1% sequence, autoreactive CD4+ T cells recognizing shared peptides would be deleted during thymus selection then a smaller repertoire of anti-human thyroglobulin reactive cells would be expected (207). We analyzed the affinity of human and mouse Tg2098 and VPESKVIFDANAPVA peptide equivalents to HLA-DR3. Interestingly, both mouse peptides showed greater affinity for HLA-DR3 than their human counterparts. As in human, the mouse version of Tg2098 was a better HLA-DR3-binder than the mouse version of VPESKVIFDANAPVA. Thus, if generated in thymus, mouse peptides should be presented for tolerance since they are good binders for HLA-DR3. However, the CFS data suggest that some peptides may be poorly generated in thymus.

Both by mDCs and CFS, we have identified several nested sets associated to HLA-DR3 from which some thyroglobulin-derived peptides were analyzed by other groups (72, 142, 146, 207, 230). Interestingly, two peptides clustered around the IB core VPYAAPPLA were isolated from a GD-affected thyroid (QVDQFLGVPYAAPPLAE and VDQFLGVPYAAPPLAER) (72) and one similar peptide was generated in our CFS samples (VPYAAPPLAERRFQ) but not in MoDCs, where intermediate binders are not favoured. Jacobson *et al.* (142) identified a predicted cathepsin B- and D-generated peptide FRKKVILEDKVKNF as a better binder for HLA-DR3 than Tg2098. We identified two similar peptides (KKVILEDKVKN and KKVILEDKVKNFYTR) in CFS samples. Flynne e*t al.* (207) used a panel of overlapping peptides, analyzed their affinity by HLA-DR3 and finally, 40 good binder peptides were tested to induce stimulate T cells in HLA-DR3+ transgenic mice. 10/40 of the predicted peptides were found in our samples, DCs or CFS,

some clustered in HB nested sets MIFDLVHSY, LFVDSGLLR, FCVDGEGRR, VARDLGDVM, LQCDQNGQY, some from IB nested sets LKEAIRAIF, IDMASAWAK and the previously commented, VVVDPSIRH, VIDAFNAPV. As discussed before, only Tg2098 stimulated a cellular proliferative response and expanded thyroglobulin primed cells both of the B10 and NOD background. Additionally Tg2098 generated thyroid infiltration not only following the adoptive transfer of thyroglobulin-primed, Tg2098-activated cells, but also after direct immunization with only Tg2098 (207).

Since thyroglobulin-primed cells were stimulated by Tg2098, this epitope is a naturally processed peptide by APCs. It is therefore not a ‘‘cryptic’’ epitope (i.e., epitopes not stimulatory for intact Tg-primed cells and revealed only by direct immunization with the peptide). In addition, the peptide-primed cells also responded to thyroglobulin stimulation *in vitro*, indicating that this peptide is presented by and detected on HLA-DR3+ APCs (251, 207). Actually, we showed in chapter 2 that also peptides grouped in nested sets MIFDLVHSY, FCVDGEGRR, IDMASAWAK are presented by *in vitro* matured MoDCs. However these nested sets are less represented than the dominant VVVDPSIRH. All these data suggest that, in spite of the differences with freshly isolated DCs, there are peptides generated and presented by human APCs but they do not lead into the experimental disease. Thus, those peptides should be efficiently presented for T cell tolerance, including Tg2098, at least considering that presentation of soluble thyroglobulin by thymus DCs is highly likely. How this peptide is then recognized by T cells in the thyroid is still to be elucidated but a possible high expression of the HLA-DR3-Tg2098 complexes thus increasing the density of ligands for reactive T cells could be thought of, having into account the resistance of Tg2098 to be degraded in TFC-like conditions.

In summary, we believe that the use of CFS in different proteolytic conditions may provide answers to subtle differences between the presentation of peptides in the thymus and in peripheral tissues. These systems would allow us to deeply analyze the role of proteases, pH and also the recently reported HLA-DM polymorphisms (240) in peptide generation and presentation. But its major interest, in our opinion, is its application to the study of many other autoantigens that are difficult to study *ex vivo*. These include TSHR, insulin, collagen, that we are already starting to study and many other antigens known to be presented in autoimmune conditions.

FINAL DISCUSSION

Once established that the peptidome from unpulsed professional APC can be studied without having to resort to cell lines, we can conclude that contrary to the cell lines used before, DCs tend to select very high affinity peptides forming nested sets as a norm. This may be important when studying non-professional APCs or even conventional APCs in unconventional sites such as inflammed tissues. DCs are the most capable APCs, express all the necessary machinery and in this set up, showed their capacity of efficient presentation.

However, in all their efficiency, they also presented unconventional peptides. 20% of the peptides presented by all alleles were N-terminal or, most frequently, C-terminal peptides. Some defined immunodominant peptides are terminal peptides and are considered to be the "first cut" and hence the most accessible to MHC-II (184). However, in our data, most C-terminal peptides were located at the very extreme of the protein and pertained to cytosolic proteins. These would not be digested in early compartments of the endocytic route, rather in deeper compartments where proteases are not limited. They could also be generated by the class I pathway. On the other hand, these peptides were unique and did not form nested sets, which again modifies the idea of "first bind then trimmed" of most MHC-II peptides, even having classical class II peptide size between 10 and 30aa that could be easily trimmed. Finally, they appeared to have preferential cleavage residues at the peptide end where they are cut from the protein backbone. More experiments are needed to fully understand the sites and enzimes where they are generated and also their possible importance in immune responses.

The analysis of thyroglobulin processing generated some interesting questions and answers. Native or denatured purified thyroglobulin captured by MoDC generated a large number of peptides, with dominant nested sets and no peptide derived from the N- or C-terminus of the protein. Very similar pattern was obtained wen MoDC were pulsed with colloid-enriched thyroid tissue extracts. This surprised us because it appeared that the colloid-specific proteolysis of thyroglobulin did not affect the final presentation by DCs, going directly against our own hypothesis. Yet, if thyroglobulin was digested by the colloid cathepsins (B, L and S) at pH 7.4 prior to pulsing, MoDCs presentation of thyroglobulin peptides was almost completely abrogated. We thought that the large amount of intact thyroglobulin in the tissue extract preparation would be accountable for these data and that the pre-digestion must have destroyed any thyroglobulin epitope that could be presented. However, when we did the same experiment using the CFS, the predigested thyroglobulin was as efficiently presented as the purified protein. Therefore, pre-digestion did not destroy epitopes, but the fragments may have been degraded before reaching the MIIC in MoDCs. Thus, the state of the antigen is extremely relevant for its presentation by MoDCs but, at the same time, the CFS method may help identifying steps of the processing events that may be lost when analyzing DC-presented peptides.

Two abundant and high affinity dominant nested sets were identified from thyroglobulin. One, associated to HLA-DR3 with the VVVDPSIRH core and the other associated to HLA-DR15 with the core IMQYFSHFI. No other really dominant nested set was identified associated to any of

the other alleles studied. The VVVDPSIRH set contains the peptide Tg2098, defined as immunodominant in an *in vivo* model of thyroiditis induced in HLA-DR3 transgenic mice (207). The same peptide was identified in the analysis of an HLA-DR3+ thyroid sample from a GD patient (72). HLA-DR15 is not negatively associated to AITD but in a similar mouse model, HLA-DR15 transgenic mice did not develop the disease using the same conditions as the HLA-DR3 mice. Interestingly, in HLA-DR15/DR3 MoDCs, most thyroglobulin peptides were presented by HLA-DR15 but peptides with this core were not identified in HLA-DR15+ thyroid samples affected by GD (72). A second nested set associated to HLA-DR3 was also found, independent of the source of antigen or the processing method. This second HLA-DR3 nested set, around the VIFDANAPV core, was not as abundant as the VVVDPSIRH and contained a peptide (Tg1574), known not to generate T cell responses in the same EAT model as the Tg2098 peptide (207).

The functional difference between these two peptides correlated with two characteristics that are important in the definition of immunodominance (109), i.e. sensitivity to cathepsins and to HLA-DM. Tg1574 was cathepsin-resistant whereas Tg2098 was partially sensitive. Upon digestion with several combinations of cathepsins, Tg1574 did not generate any intermediate variants, only part of it was degraded and between 45 and 100% remained intact, depending on the conditions. In contrast, Tg2098 was trimmed at the peptide ends generating a number of variants, its core was maintained resistant to cleavage and only between 6 and 26% remained intact. In addition, Tg1574 was much more sensitive to HLA-DM than Tg2098.

When studying the thymus peptidome, peptides were grouped into nested sets and most represented a single region of the parental protein, at the expense of the rest of the sequence (59). This contrasted with our study of thyroglobulin, where up to 9 regions generated peptides presented by HLA-DR in the same donor. Thus, one of the major thyroglobulin peptides must be preferentially presented in the thymus to generate tolerance. Having into account the small number of thyroglobulin peptides presented in mTEC simulation, the resistance of the Tg1574 peptide set to cathepsins, we could presume that this peptide was favored by mTEC presentation, thus tolerance to this peptide would be efficiently generated. In addition, abundance of T cell precursors in the thymus may condition the escape of self-reactive T cells. In mouse, the magnitude of the T cell responses correlated to their initial frequency (252). Being that, if Tg2098-reactive T cells were more abundant than Tg1574-reactive precursors but the presentation of the antigenic peptides is balanced in favor of Tg1574, Tg2098-reactive T cells group would not be fully tolerized, allowing the exit to periphery of some Tg2098-reactive T cells. In the thyroid, the available antigen is much more abundant than in thymus and thyroid DC would present a large number of variants of Tg2098 and only a few of Tg1574. This difference in efficiency of tolerization together with the higher density in the periphery could be a possible explanation of the final immunodominance of the Tg2098 peptide. TFC are also presumably able to present Tg2098 (72). However, the effect of TFC presentation must be studied in depth

and the thyroglobulin peptides presented in the thymus must be known before we can draw any major conclusion around our hypothesis.

CONCLUSIONS

1 - Low numbers of MoDCs allowed the study the HLA-DR peptidome in professional APCs. Most peptides presented by any allele were part of high-affinity nested sets.

2 - Around 20% were individual peptides from the N- and C-terminal regions of cytosolic proteins. Asp and Pro were favored in positions next to the cleavage site of these terminal peptides.

3 - HLA-DR3 and HLA-DR15 are prefered alleles for thyroglobulin presentation. In DR15/DR3^{+} donors, thyroglobulin peptides were mostly presented by DR15, in contrast to the presentation of only the HLA-DR3 set in a DR15/DR3^{+} autoimmune thyroid.

4 - Cathepsin S at neutral pH is able to cleave thyroglobulin more efficiently than the other colloid cathepsins B and L. Pre-digested thyroglobulin generates more peptides than intact thyroglobulin when processed in DC-like conditions.

5 - MoDCs do not present Tg peptides after uptake of colloid-like digested thyroglobulin.

6 - The CFS reproduces the major findings of thyroglobulin processing and presentation by MoDCs: two major nested were preferentially presented by HLA-DR3. Of these, one included an immunodominant peptide (Tg2098) and the second a peptide that does not generate T cell responses (Tg1574).

7 - Tg1574 is cathepsin-resistant whereas Tg2098 is partially sensitive to cathepsins with a cleavage-resistant core. Tg1574 is more sensitive to DM than Tg2098. Thus, the peptide loading site may also influence the final peptides presented by HLA-DR molecules.

8 - Data from CFS using mTEC-like conditions suggested that many peptides may not be generated or be less abundant in the thymus. However, no definite conclusion can be drawn unless the thyroglobulin peptides presented in the thymus are actually identified.

ANNEXES

ANNEX 1. LIST OF HLA-DR PEPTIDES ISOLATED FROM MONOCYTE-DERIVED DENDRITIC CELLS

Donor A (DRB1*0301, DRB1*1101)

Sequence	Uniprot AC	Protein name	Length	Cellular Location (a)	Location in Sequence (b)	Binding Core/s (c)	Allele/s (d)	Theoretical Affinity (e)
PSGWWKGRLHGQEGLFPGNYVEKI	O00160	Unconventional myosin-If	24	C	C-ter	NA	NA	NA
PRVPWVKMILNKLSQ	O00626	C-C motif chemokine 22	15	EM	C-ter	WVKMILNKL	DR11	IB
APEEIIMDRPFLFVVR	P05121	Plasminogen activator inhibitor 1	16	EM	C-ter	IIMDRPFLF	DR3	HB
APEEIIMDRPFLFVVRH	P05121	Plasminogen activator inhibitor 1	17	EM	C-ter	IIMDRPFLF	DR3	HB
PKENWVQRVVEKFLKRAENS	P10145	Interleukin-8	20	EM	C-ter	VEKFLKRAE	DR3	IB
PFSVTEALIRTCLLNETGDEPFQYKN	P15104	Glutamine synthetase	26	C	C-ter	FSVTEALIR	DR3	HB
PKFEVIEKPQA	P18859	ATP synthase-coupling factor 6, mitochondrial	11	Mit	C-ter	FEVIEKPQA	DR11	HB
NPKVMNLISKLSAKFG	P50502	Hsc70-interacting protein	16	C	C-ter	ISKLSAKFG	DR3	IB
GYEPPVQESV	P61247	40S ribosomal protein S3a	10	C	C-ter	NA	NA	NA
RYISKMFLRGDSVIVVLRNPLIAGK	P62316	Small nuclear ribonucleoprotein Sm D2	25	C	C-ter	LRGDSVIVV	DR3	IB
QTWVKYIVRLLSKK	P78556	C-C motif chemokine 20	14	EM	C-ter	WVKYIVRLL	DR11	IB
PKERWVRDSMKHLDQIFQNLKP	P80075	C-C motif chemokine 8	22	EM	C-ter	VRDSMKHLD	DR3	HB
PSGWWTGRLRGKQGLFPNNYVTKI	Q12965	Unconventional myosin-Ie	24	C	C-ter	WTGRLRGKQ	DR11	IB
PRRGGVPSWFGL	Q16540	39S ribosomal protein L23, mitochondrial	12	Mit	C-ter	NA	NA	NA
PNNKRVKNAVKYLQSLERS	Q92583	C-C motif chemokine 17	19	EM	C-ter	VKNAVKYLQ	DR11	IB
PDTILKALFKSSGASVTTQPTEFKIKL	Q9BY77	Polymerase delta-interacting protein 3	27	N	C-ter	FKSSGASVT	DR3	HB
GSSFVVARYFPAGNVVNEGFFEENVLPPKK	Q9H4G4	Golgi-associated plant pathogenesis-related protein 1	30	ER/G	C-ter	FVVARYFPA	DR11	IB
HVGFIFKNGKITSIVK	O00560	Syntenin-1	16	M	Internal	IFKNGKITS	DR3	HB
ITSIVKDSSAARNGLL	O00560	Syntenin-1	16	M	Internal	IVKDSSAAR	DR3	HB
RGFYCNDESIKYPL	O14495	Lipid phosphate phosphohydrolase 3	14	ER/G	Internal	YCNDESIKY	DR3	IB
FSSKFQVDNNNRLL	P01023	Alpha-2-macroglobulin	14	EM	Internal	FQVDNNNRL	DR3	IB
SSKFQVDNNNRLL	P01023	Alpha-2-macroglobulin	13	EM	Internal	FQVDNNNRL	DR3	IB
KSWITFDLKNKEVS	P01730	T-cell surface glycoprotein CD4	14	M	Internal	ITFDLKNKE/FDLKNKEVS	DR3/DR11	HB
KSWITFDLKNKEVSVK	P01730	T-cell surface glycoprotein CD4	16	M	Internal	ITFDLKNKE/FDLKNKEVS	DR3/DR11	HB
SKSWITFDLKNKEVSVK	P01730	T-cell surface glycoprotein CD4	17	M	Internal	ITFDLKNKE/FDLKNKEVS	DR3/DR11	HB
LANIAVDKANLEIM	P01903	HLA class II histocompatibility antigen, DR alpha chain	14	M	Internal	IAVDKANLE	DR3	HB
NALLVRYTKKVPQVS	P02768	Serum albumin	15	EM	Internal	VRYTKKVPQ/YTKKVPQVS	DR3/DR11	IB
APELLFFAKRYKAA	P02768	Serum albumin	14	EM	Internal	LFFAKRYKA	DR11	HB
STPTLVEVSRNLGKVG	P02768	Serum albumin	16	EM	Internal	VEVSRNLGK/LVEVSRNLG	DR3/DR11	HB
APELLFFAKRYKAAF	P02768	Serum albumin	15	EM	Internal	LFFAKRYKA	DR11	HB
APELLFFAKRYKAAFT	P02768	Serum albumin	16	EM	Internal	LFFAKRYKA	DR11	HB
APELLFFAKRYKAAFTE	P02768	Serum albumin	17	EM	Internal	LFFAKRYKA	DR11	HB
TPTLVEVSRNLGK	P02768	Serum albumin	13	EM	Internal	VEVSRNLGK/LVEVSRNLG	DR3/DR11	HB
TPTLVEVSRNLGKVG	P02768	Serum albumin	15	EM	Internal	VEVSRNLGK/LVEVSRNLG	DR3/DR11	HB
TPTLVEVSRNLGKVGS	P02768	Serum albumin	16	EM	Internal	VEVSRNLGK/LVEVSRNLG	DR3/DR11	HB
TPTLVEVSRNLGKVGSK	P02768	Serum albumin	17	EM	Internal	VEVSRNLGK/LVEVSRNLG	DR3/DR11	HB
NALLVRYTKKVPQVSTPTL	P02768	Serum albumin	19	EM	Internal	VRYTKKVPQ/YTKKVPQVS	DR3/DR11	IB
SSALRWLGRYYCFQ	P02790	Hemopexin	14	EM	Internal	ALRWLGRYY/LRWLGRYYC	DR3/DR11	IB
SSALRWLGRYYCFQG	P02790	Hemopexin	15	EM	Internal	ALRWLGRYY/LRWLGRYYC	DR3/DR11	IB
SSALRWLGRYYCFQGN	P02790	Hemopexin	16	EM	Internal	ALRWLGRYY/LRWLGRYYC	DR3/DR11	IB
IEGNLIFDPNNYL	P04114	Apolipoprotein B-100	13	C	Internal	LIFDPNNYL	DR3	HB
LPKPPKPVSKMRMATPLLMQALPM	P04233	HLA class II histocompatibility antigen gamma chain	24	ER/G	Internal	MRMATPLLM	DR3	IB

IDWKVFESWMHH	P04233	HLA class II histocompatibility antigen gamma chain	12	ER/G	Internal	WKVFESWMH	DR11	IB
LPVNGEFSLDDLQPWH	P05067	Amyloid beta A4 protein	16	M	Internal	FSLDDLQPW	DR3	IB
NGEFSLDDLQPWH	P05067	Amyloid beta A4 protein	13	M	Internal	FSLDDLQPW	DR3	IB
DPDSIRCDTRPQLLM	P05107	Integrin beta-2	15	M	Internal	IRCDTRPQL	DR3	IB
LLVFATDDGFHFA	P05107	Integrin beta-2	13	M	Internal	FATDDGFHF	DR3	IB
GPGDPDSIRCDTRPQL	P05107	Integrin beta-2	16	M	Internal	IRCDTRPQL	DR3	IB
SLPRIICDNTGITT	P05164	Myeloperoxidase	14	Lis/End	Internal	IICDNTGIT	DR3	IB
ISLPRIICDNTGITT	P05164	Myeloperoxidase	15	Lis/End	Internal	IICDNTGIT	DR3	IB
LLWHWDTTQSLKQ	P06734	Low affinity immunoglobulin epsilon Fc receptor	13	M	Internal	WHWDTTQSL	DR3	IB
YPRISVNNVLPVFDN	P07339	Cathepsin D	15	Lis/End	Internal	YPRISVNNV	DR11	LB
SHRGILIDTSRHYLPV	P07686	Beta-hexosaminidase subunit beta	16	Lis/End	Internal	ILIDTSRHY	DR3	HB
APGTIVEVWKDSAYPE	P07686	Beta-hexosaminidase subunit beta	16	Lis/End	Internal	VWKDSAYPE	DR3	HB
YNVDMSYLKRLCGTF	P07858	Cathepsin B	15	Lis/End	Internal	MSYLKRLCG	DR11	HB
DFDNRLVNHFVEEFKR	P0DMV8	Heat shock 70 kDa protein 1A	16	C	Internal	LVNHFVEEF	DR3	IB
KPFHPKFIKELRVIESGPH	P10145	Interleukin-8	19	EM	Internal	FIKELRVIE	DR11	IB
GSFQFGYNTGVINAPE	P11169	Solute carrier family 2, facilitated glucose transporter member 3	16	M	Internal	NA	NA	NA
GSFQFGYNTGVINAPEKI	P11169	Solute carrier family 2, facilitated glucose transporter member 3	18	M	Internal	NA	NA	NA
IGSFQFGYNTGVINAPEKI	P11169	Solute carrier family 2, facilitated glucose transporter member 3	19	M	Internal	NA	NA	NA
SFQFGYNTGVINAPE	P11169	Solute carrier family 2, facilitated glucose transporter member 3	15	M	Internal	NA	NA	NA
FKEFQNNPNPRSLVKP	P11215	Integrin alpha-M	16	M	Internal	FQNNPNPRS	DR3	HB
SDIAFLIDGSGSIIPH	P11215	Integrin alpha-M	16	M	Internal	FLIDGSGSI	DR3	IB
KEFQNNPNPRSLVKP	P11215	Integrin alpha-M	15	M	Internal	FQNNPNPRS	DR3	HB
TFKEFQNNPNPRSLVKP	P11215	Integrin alpha-M	17	M	Internal	FQNNPNPRS	DR3	HB
TFKEFQNNPNPRSLVKPI	P11215	Integrin alpha-M	18	M	Internal	FQNNPNPRS	DR3	HB
LNTILPDARDPAFK	P11279	Lysosome-associated membrane glycoprotein 1	14	Lis/End	Internal	NA	NA	NA
TNPDFYINICQPLNPM	P11717	Cation-independent mannose-6-phosphate receptor	16	Lis/End	Internal	YINICQPLN	DR11	LB
PQGEAEFARIMSIVD	P12814	Alpha-actinin-1	15	C	Internal	FARIMSIVD	DR11	LB
LTDEIVKDVKQTYLAR	P13726	Tissue factor	16	M	Internal	IVKDVKQTY	DR3	HB
RPRAPIIAVTRNPQ	P14618	Pyruvate kinase PKM	14	C	Internal	IIAVTRNPQ	DR11	IB
DENILWLDYKNICK	P14618	Pyruvate kinase PKM	14	C	Internal	LWLDYKNIC	DR3	HB
RPRAPIIAVTRNPQTA	P14618	Pyruvate kinase PKM	16	C	Internal	IIAVTRNPQ	DR11	IB
DENILWLDYKNICKVVE	P14618	Pyruvate kinase PKM	17	C	Internal	LWLDYKNIC	DR3	HB
LPTMAQMEKALSIG	P16070	CD44 antigen	14	M	Internal	MAQMEKALS	DR11	HB
GPPYVSWLIDANHNMQ	P17813	Endoglin	16	M	Internal	VSWLIDANH	DR3	LB
FPLDTLIPDGKRIIWDSR	P17948	Vascular endothelial growth factor receptor 1	18	M	Internal	LIPDGKRII	DR3	HB
EMFYVDLDKKETVWHL	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	16	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR11	HB
FYVDLDKKETVWH	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	13	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR11	HB
FYVDLDKKETVWHLE	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	15	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR11	HB
MFYVDLDKKETVWHLE	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	16	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR11	HB
YVDLDKKETVWH	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	12	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR11	HB
EMFYVDLDKKETVWH	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	15	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR11	HB
MFYVDLDKKETVWH	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	14	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR11	HB
DRYFYNQEEYVRFD	P20039	HLA class II histocompatibility antigen, DP alpha 1 chain	14	M	Internal	NA	NA	NA
FLDRYFYNQEEYVRFD	P20039	HLA class II histocompatibility antigen, DP alpha 1 chain	16	M	Internal	NA	NA	NA
LDRYFYNQEEYVR	P20039	HLA class II histocompatibility antigen, DP alpha 1 chain	13	M	Internal	NA	NA	NA
LDRYFYNQEEYVRFD	P20039	HLA class II histocompatibility antigen, DP alpha 1 chain	15	M	Internal	NA	NA	NA
LDRYFYNQEEYVRFDS	P20039	HLA class II histocompatibility antigen, DP alpha 1 chain	16	M	Internal	NA	NA	NA
SEKELALVKRLKPL	P20645	Cation-dependent mannose-6-phosphate receptor	14	Lis/End	Internal	LALVKRLKP	DR11	HB
SEKELALVKRLKPLF	P20645	Cation-dependent mannose-6-phosphate receptor	15	Lis/End	Internal	LVKRLKPLF/LALVKRLKP	DR3/DR11	HB
EETVITVDTKAAGKGK	P21333	Filamin-A	16	C	Internal	ITVDTKAAG	DR3	HB

NPAEFVVNTSNAGAG	P21333	Filamin-A	15	C	Internal	NA	NA	NA
IGEETVITVDTKAAGKGK	P21333	Filamin-A	18	C	Internal	ITVDTKAAG	DR3	HB
RRPIIVISDKMLRSLE	P21580	Tumor necrosis factor alpha-induced protein 3	16	C	Internal	IVISDKMLR/IVISDKMLR	DR3/DR11	HB
EGWNFYSNKCFKIFG	P22897	Macrophage mannose receptor 1	15	M	Internal	FYSNKCFKI	DR11	IB
IGLLISLDKKFAWM	P22897	Macrophage mannose receptor 1	14	M	Internal	ISLDKKFAW/LISLDKKFA	DR3/DR11	HB
WDVLKCDEKAKFV	P22897	Macrophage mannose receptor 1	13	M	Internal	LKCDEKAKF	DR3	HB
GWNFYSNKCFKIFG	P22897	Macrophage mannose receptor 1	14	M	Internal	FYSNKCFKI	DR11	IB
IGLLISLDKKFAWMDG	P22897	Macrophage mannose receptor 1	16	M	Internal	ISLDKKFAW/LISLDKKFA	DR3/DR11	HB
WDVLKCDEKAKFVC	P22897	Macrophage mannose receptor 1	14	M	Internal	LKCDEKAKF	DR3	HB
APNRTITVDDKMSLRL	P23458	Tyrosine-protein kinase JAK1	16	M	Internal	ITVDDKMSL	DR3	HB
TPAAPPKAVLKLEPQWINVLQED	P31994	Low affinity immunoglobulin gamma Fc region receptor II-b	23	M	Internal	VLKLEPQWI	DR3	IB
VPSILINKAQGSKL	P36269	Gamma-glutamyltransferase 5	14	M	Internal	ILINKAQGS	DR3	HB
IEEYLKDPTQPILE	P38484	Interferon gamma receptor 2	14	M	Internal	YLKDPTQPI	DR3	IB
DGYILCLNRIPHG	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	LCLNRIPHG/YILCLNRIP	DR3/DR11	IB
DGYILCLNRIPHGR	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	LCLNRIPHG/YILCLNRIP	DR3/DR11	IB
EDGYILCLNRIPHG	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	LCLNRIPHG/YILCLNRIP	DR3/DR11	IB
EDGYILCLNRIPHGR	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	LCLNRIPHG/YILCLNRIP	DR3/DR11	IB
EDGYILCLNRIPHGRK	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	16	Lis/End	Internal	LCLNRIPHG/YILCLNRIP	DR3/DR11	IB
GYILCLNRIPHGR	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	LCLNRIPHG/YILCLNRIP	DR3/DR11	IB
TDRFLVNLVKLKHELTD	P43652	Afamin	17	EM	Internal	LVNLVKLKH	DR11	HB
WPEALAISQRWQQQDK	P55899	IgG receptor FcRn large subunit p51	16	M	Internal	LAISQRWQQ	DR3	IB
VAQFMWIIRKRIQLPS	P60520	Gamma-aminobutyric acid receptor-associated protein-like 2	16	ER/G	Internal	FMWIIRKRI	DR11	HB
LVREIAQDFKTDLRFQ	P68431	Histone H3.1	16	N	Internal	IAQDFKTDL	DR3	HB
DKYATVSSPSKSKKLE	Q01804	OTU domain-containing protein 4	16	C	Internal	YATVSSPSK	DR11	IB
TPNGLAIDHRAEKLYF	Q07954	Prolow-density lipoprotein receptor-related protein 1	16	M	Internal	LAIDHRAEK	DR3	IB
DVYGIVYDLRMHRP	Q12913	Receptor-type tyrosine-protein phosphatase eta	14	M	Internal	IVYDLRMHR	DR3	HB
DVYGIVYDLRMHRPL	Q12913	Receptor-type tyrosine-protein phosphatase eta	15	M	Internal	IVYDLRMHR	DR3	HB
QINRYGHFQATITIVEG	Q14956	Transmembrane glycoprotein NMB	17	M	Internal	YGHFQATIT	DR11	IB
PNTEENLTYLQLMERCITD	Q15149	Plectin	19	C	Internal	YLQLMERCI	DR11	IB
GGIGALVRLKSLQGD	Q15582	Transforming growth factor-beta-induced protein ig-h3	15	EM	Internal	IGALVRLKS	DR11	HB
DIMRVNVDKVLERDQK	Q15836	Vesicle-associated membrane protein 3	16	M	Internal	VNVDKVLER	DR3	HB
DIMRVNVDKVLERDQKL	Q15836	Vesicle-associated membrane protein 3	17	M	Internal	VNVDKVLER	DR3	HB
DMAVVQRLFCM	Q6NY19	KN motif and ankyrin repeat domain-containing protein 3	11	C	Internal	MAVVQRLFC	DR11	IB
PKSLATLGGKII	Q7Z589	Protein EMSY	12	N	Internal	NA	NA	NA
DSIKLDDDSERKVVKM	Q86VP6	Cullin-associated NEDD8-dissociated protein 1	16	C	Internal	IKLDDDSER	DR3	HB
HTKFWVVDQTHFY	Q8IV08	Phospholipase D3	13	ER/G	Internal	WVVDQTHFY/FWVVDQTHF	DR3/DR11	IB
SVLITFDNKAHSGRIPI	Q9GZU1	Mucolipin-1	17	M	Internal	ITFDNKAHS	DR3	HB
IRTIELDGKTIKLQ	Q9H0U4	Ras-related protein Rab-1B	14	C	Internal	IELDGKTIK	DR3	HB
KIRTIELDGKTIKLQ	Q9H0U4	Ras-related protein Rab-1B	15	C	Internal	IELDGKTIK	DR3	HB
KIRTIELDGKTIKLQIW	Q9H0U4	Ras-related protein Rab-1B	17	C	Internal	IELDGKTIK	DR3	HB
VVLKGDAKKLQLY	Q9H9V4	RING finger protein 122	13	ER/G	Internal	LKGDAKKLQ	DR3	HB
LPGGIVTDETLSFIQK	Q9NPH3	Interleukin-1 receptor accessory protein	16	M	Internal	IVTDETLSF	DR3	HB
VDSIVWTFNTTPLVT	Q9NQ25	SLAM family member 7	15	M	Internal	IVWTFNTTP	DR3	IB
DVTEIDILVKNRGVLR	Q9NU53	Glycoprotein integral membrane protein 1	16	M	Internal	LVKNRGVLR/IDILVKNRG	DR3/DR11	HB
PIHGHIELHPLLVRIID	Q9Y3Z3	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	17	M	Internal	LHPLLVRII	DR11	LB
APVKKLVVKGGKKKKQVLKFTLD	P35268	60S ribosomal protein L22	23	C	N-ter	VKKLVVKGG	DR11	IB
MLMPKKNRIAIYELLFKEGVMVAKKD	P46783	40S ribosomal protein S10	26	C	N-ter	YELLFKEGV	DR11	HB
VLDLDLFRVDKGGD	P49591	Serine--tRNA ligase, cytoplasmic	14	C	N-ter	LDLDLFRVD	DR3	IB

Donor B (DRB1*0301, DRB1*1301)

Sequence	Uniprot AC	Protein name	Length	Cellular Location (a)	Location in Sequence (b)	Binding Core/s (c)	Allele/s (d)	Theoretical Affinity (e)
HLIMEMILQALGKSYHPGCFRCSVCN	A6NIX2	Wilms tumor protein 1-interacting protein	26	C	Internal	LQALGKSYH	DR13	HB
DLEKDIISDTSGDFRK	A6NMY6	Putative annexin A2-like protein	16	EM	Internal	IISDTSGDF	DR3	HB
ITSIVKDSSAARNGLL	O00560	Syntenin-1	16	M	Internal	IVKDSSAAR/ITSIVKDSS	DR3/DR13	HB
PRVPWVKMILNKLSQ	O00626	C-C motif chemokine 22	15	EM	C-ter	VKMILNKLS/VKMILNKLS	DR3/DR13	IB
FSENLLADVKGARAAL	O75558	Syntaxin-11	16	M	Internal	LLADVKGAR/LADVKGARA	DR3/DR13	HB
FSSKFQVDNNNRLL	P01023	Alpha-2-macroglobulin	14	EM	Internal	FQVDNNNRL	DR3	IB
SSKFQVDNNNRLL	P01023	Alpha-2-macroglobulin	13	EM	Internal	FQVDNNNRL	DR3	IB
SKSWITFDLKNKEVSVK	P01730	T-cell surface glycoprotein CD4	17	M	Internal	ITFDLKNKE/FDLKNKEVS	DR3/DR13	HB
PENFRLLGNVL	P02042	Hemoglobin subunit delta	11	EM	Internal	NA	NA	NA
APELLFFAKRYKAAF	P02768	Serum albumin	15	EM	Internal	LFFAKRYKA	DR13	HB
TPTLVEVSRNLGKVG	P02768	Serum albumin	15	EM	Internal	LVEVSRNLG	DR13	HB
KYLYEIARRHPYFY	P02768	Serum albumin	14	EM	Internal	YEIARRHPY	DR13	HB
DSAQNSVIIVDKNGRL	P02786	Transferrin receptor protein 1	16	M	Internal	IIVDKNGRL/VIIVDKNGR	DR3/DR13	HB
NSVIIVDKNGRL	P02786	Transferrin receptor protein 1	12	M	Internal	IIVDKNGRL/VIIVDKNGR	DR3/DR13	HB
GDREWFWDLATGTMK	P02790	Hemopexin	15	EM	Internal	FWDLATGTM/WFWDLATGT	DR3/DR13	IB
IEGNLIFDPNNYL	P04114	Apolipoprotein B-100	13	C	Internal	LIFDPNNYL	DR3	HB
NGEFSLDDLQPWH	P05067	Amyloid beta A4 protein	13	M	Internal	FSLDDLQPW	DR3	IB
DPDSIRCDTRPQLLM	P05107	Integrin beta-2	15	M	Internal	IRCDTRPQL/IRCDTRPQL	DR3/DR13	IB
GPGDPDSIRCDTRPQLLM	P05107	Integrin beta-2	18	M	Internal	IRCDTRPQL/IRCDTRPQL	DR3/DR13	IB
APEEIIMDRPFLFVVR	P05121	Plasminogen activator inhibitor 1	16	EM	C-ter	IIMDRPFLF	DR3	HB
APEEIIMDRPFLFVVRH	P05121	Plasminogen activator inhibitor 1	17	EM	C-ter	IIMDRPFLF	DR3	HB
VSNEIVRFPTDQLTPDQ	P05164	Myeloperoxidase	17	Lis/End	Internal	VRFPTDQLT	DR13	IB
SLPRIICDNTGITT	P05164	Myeloperoxidase	14	Lis/End	Internal	IICDNTGIT	DR3	IB
LLLWHWDTTQSLKQ	P06734	Low affinity immunoglobulin epsilon Fc receptor	14	M	Internal	LWHWDTTQS	DR13	HB
LLWHWDTTQSLKQ	P06734	Low affinity immunoglobulin epsilon Fc receptor	13	M	Internal	LWHWDTTQS	DR13	HB
LARDIMNDSNYIVK	P07333	Macrophage colony-stimulating factor 1 receptor	14	M	Internal	IMNDSNYIV	DR3	HB
YPAEAWNFWTRKGLVSGG	P07858	Cathepsin B	18	Lis/End	Internal	WNFWTRKGL	DR13	HB
GHPQYLLDSNSWIEEMPS	P0C0L4	Complement C4-A	18	EM	Internal	YLLDSNSWI	DR3	HB
HPQYLLDSNSWIEE	P0C0L4	Complement C4-A	14	EM	Internal	YLLDSNSWI	DR3	HB
GLAVLAVVVIGAVVATVMC	P10319	HLA class I histocompatibility antigen, B-58 alpha chain	19	M	Internal	VVVIGAVVA/VLAVVVIGA	DR3/DR13	HB
LNTILPDARDPAFK	P11279	Lysosome-associated membrane glycoprotein 1	14	Lis/End	Internal	ILPDARDPA/LPDARDPAF	DR3/DR13	HB
LTDEIVKDVKQTYLAR	P13726	Tissue factor	16	M	Internal	IVKDVKQTY/IVKDVKQTY	DR3/DR13	HB
GPPKLDIRKEEKQIMIDIFHP	P15260	Interferon gamma receptor 1	21	M	Internal	IRKEEKQIM	DR3	HB
RYGFIEGHVVIPRIHPN	P16070	CD44 antigen	17	M	Internal	IEGHVVIPR	DR13	LB
YGFIEGHVVIPRIHPN	P16070	CD44 antigen	16	M	Internal	IEGHVVIPR	DR13	LB
GPPYVSWLIDANHNMQ	P17813	Endoglin	16	M	Internal	NA	NA	NA
PKFEVIEKPQA	P18859	ATP synthase-coupling factor 6, mitochondrial	11	Mit	C-ter	FEVIEKPQA	DR13	HB
EMFYVDLDKKETVWH	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	15	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR13	HB
EMFYVDLDKKETVWHLE	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	17	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR13	HB
MFYVDLDKKETVWH	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	14	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR13	HB
MFYVDLDKKETVWHLE	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	16	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR13	HB
YVDLDKKETVWH	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	12	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR13	HB
YVDLDKKETVWHLEE	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	15	M	Internal	VDLDKKETV/YVDLDKKET	DR3/DR13	HB
IGEETVITVDTKAAGKGK	P21333	Filamin-A	18	C	Internal	ITVDTKAAG/VITVDTKAA	DR3/DR13	HB
PATEKDLAED	P21333	Filamin-A	10	C	N-ter	NA	NA	NA

DGVIKVFNDMKVRKSSTPE	P23528	Cofilin-1	19	C	N-ter	VFNDMKVRK/FNDMKVRKS	DR3/DR13	HB
KPDDWDEDAPAKIPDE	P27824	Calnexin	16	ER/G	Internal	WDEDAPAKI	DR13	LB
KPDDWDEDAPAKIPDEE	P27824	Calnexin	17	ER/G	Internal	WDEDAPAKI	DR13	LB
RGLFIIDPNGVIK	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	13	Mit	Internal	FIIDPNGVI	DR3	HB
APVKKLVVKGGKKKKQVLKFTLD	P35268	60S ribosomal protein L22	23	C	N-ter	VKKLVVKGG	DR13	IB
IDQINTDLNLERSH	P35579	Myosin-9	14	C	Internal	INTDLNLER	DR3	HB
IDQINTDLNLERSHAQ	P35579	Myosin-9	16	C	Internal	INTDLNLER	DR3	HB
IDQINTDLNLERSHAQK	P35579	Myosin-9	17	C	Internal	INTDLNLER	DR3	HB
IEEYLKDPTQPILE	P38484	Interferon gamma receptor 2	14	M	Internal	IEEYLKDPT	DR13	HB
GGHDWLADVYDVNIL	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	LADVYDVNI	DR13	IB
VLDLDLFRVDKGGD	P49591	Serine--tRNA ligase, cytoplasmic	14	C	N-ter	LFRVDKGGD	DR13	HB
DNIADAVACAKRVVRDPQ	P61626	Lysozyme C	18	EM	C-ter	VACAKRVVR	DR13	HB
DNIADAVACAKRVVRDPQG	P61626	Lysozyme C	19	EM	C-ter	VACAKRVVR	DR13	HB
IADAVACAKRVVRDPQG	P61626	Lysozyme C	17	EM	C-ter	VACAKRVVR	DR13	HB
TPKIQVYSRHPA	P61769	Beta-2-microglobulin	12	M	N-ter	IQVYSRHPA	DR13	HB
TPKIQVYSRHPAE	P61769	Beta-2-microglobulin	13	M	N-ter	IQVYSRHPA	DR13	HB
GDGQVNYEEFVQMMTAK	P62158	Calmodulin	17	C	C-ter	YEEFVQMMT	DR13	IB
PPAENSSAPEAEQGGAE	P67809	Nuclease-sensitive element-binding protein 1	17	C	C-ter	NA	NA	NA
LVREIAQDFKTDLRFQ	P68431	Histone H3.1	16	N	Internal	IAQDFKTDL	DR3	HB
PLIAKADAQESRL	Q00722	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2	13	C	C-ter	AKADAQESR	DR13	HB
TPNGLAIDHRAEKLY	Q07954	Prolow-density lipoprotein receptor-related protein 1	15	M	Internal	LAIDHRAEK	DR3	HB
EPRALVVDVQNGYL	Q07954	Prolow-density lipoprotein receptor-related protein 1	14	M	Internal	LVVDVQNGY	DR3	HB
TPNGLAIDHRAEKLYF	Q07954	Prolow-density lipoprotein receptor-related protein 1	16	M	Internal	LAIDHRAEK	DR3	HB
DVYGIVYDLRMHRP	Q12913	Receptor-type tyrosine-protein phosphatase eta	14	M	Internal	IVYDLRMHR	DR3	HB
PAGKLKYFDKLN	Q13162	Peroxiredoxin-4	12	C	C-ter	NA	NA	NA
AQNVGTTHDLLD	Q13867	Bleomycin hydrolase	12	C	N-ter	VGTTHDLLD	DR13	LB
VDKVLERDQKLSELDDR	Q15836	Vesicle-associated membrane protein 3	17	M	Internal	LERDQKLSE	DR3	HB
DIMRVNVDKVLERDQKL	Q15836	Vesicle-associated membrane protein 3	17	M	Internal	VNVDKVLER	DR3	HB
FQTLVMLETVPRSGEV	Q5Y7A7	HLA class II histocompatibility antigen, DRB1-13 beta chain	16	M	Internal	LETVPRSGE	DR13	HB
KDILEDERAAVDT	Q5Y7A7	HLA class II histocompatibility antigen, DRB1-13 beta chain	13	M	Internal	ILEDERAAV	DR3	HB
SQKDILEDERAAVDT	Q5Y7A7	HLA class II histocompatibility antigen, DRB1-13 beta chain	15	M	Internal	ILEDERAAV	DR3	HB
PKRIITYNEAMDSPDQ	Q7Z417	Nuclear fragile X mental retardation-interacting protein 2	16	N	C-ter	ITYNEAMDS	DR3	HB
HTKFWVVDQTHFY	Q8IV08	Phospholipase D3	13	ER/G	Internal	FWVVDQTHF	DR13	HB
TKFWVVDQTHFY	Q8IV08	Phospholipase D3	12	ER/G	Internal	FWVVDQTHF	DR13	HB
NNQWMIVDYKAFIPGGPSPG	Q8NHP8	Putative phospholipase B-like 2	20	Lis/End	Internal	WMIVDYKAF	DR13	HB
PNNKRVKNAVKYLQSLERS	Q92583	C-C motif chemokine 17	19	EM	C-ter	VKNAVKYLQ	DR13	HB
DLRFDNIYATQQ	Q9BR26	Osteoclast stimulatory transmembrane protein	12	M	Internal	LRFDNIYAT/LRFDNIYAT	DR3/DR13	IB
LPGGIVTDETLSFIQK	Q9NPH3	Interleukin-1 receptor accessory protein	16	M	Internal	IVTDETLSF	DR3	HB
EDDAWSYDINRAVDE	Q9NZM1	Myoferlin	15	M	Internal	YDINRAVDE	DR3	HB
AIRQELSGISTT	Q9UI08	Ena/VASP-like protein	12	C	C-ter	IRQELSGIS	DR13	IB

Donor C (DRB1*0301, DRB1*1301)

Sequence	Uniprot AC	Protein name	Length	Cellular Location (a)	Location in Sequence (b)	Binding Core/s (c)	Allele/s (d)	Theoretical Affinity (e)
DVPKWISIMTERSVPH	A6NMY6	Putative annexin A2-like protein	16	EM	Internal	WISIMTERS/VPKWISIMT	DR4/DR13	HB
FNRYSFDITNVVRDV	O00462	Beta-mannosidase	15	Lis/End	Internal	YSFDITNVV/FNRYSFDIT	DR4/DR13	HB
IPSVFIGESSANSLK	O43567	E3 ubiquitin-protein ligase RNF13	15	ER/G	Internal	FIGESSANS/IPSVFIGES	DR4/DR13	HB
NPRKFNLDATELSIRK	O43752	Syntaxin-6	16	ER/G	Internal	FNLDATELS	DR4	HB
REDSWLKSLFVRKVD	O75323	Protein NipSnap homolog 2	15	M	Internal	LKSLFVRKV	DR4	HB
VPGTYKITASARGYNPV	O75976	Carboxypeptidase D	17	M	Internal	YKITASARG/VPGTYKITA	DR4/DR13	HB
SKFRLLQETLYMCVGIMDRFLQVQPVSRKK	O95067	G2/mitotic-specific cyclin-B2	30	C	Internal	FLQVQPVSR/VGIMDRFLQ	DR4/DR13	HB
DTQFVRFDSDAASPR	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	15	M	Internal	FVRFDSDAA	DR4	HB
TQFVRFDSDAASPR	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	14	M	Internal	VRFDSDAAS	DR4	HB
VDDTQFVRFDSDAASPR	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	17	M	Internal	VRFDSDAAS	DR4	HB
DLRSWTAADTAAQITQ	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	16	M	Internal	WTAADTAAQ/LRSWTAADT	DR4/DR13	HB
LRSWTAADTAAQITQ	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	15	M	Internal	WTAADTAAQ/LRSWTAADT	DR4/DR13	HB
DTQFVRFDSDAASQR	P01891	HLA class I histocompatibility antigen, A-68 alpha chain	15	M	Internal	FVRFDSDAA	DR4	HB
DTQFVRFDSDAASQRM	P01891	HLA class I histocompatibility antigen, A-68 alpha chain	16	M	Internal	FVRFDSDAA	DR4	HB
DTQFVRFDSDAASQRMEP	P01891	HLA class I histocompatibility antigen, A-68 alpha chain	18	M	Internal	FVRFDSDAA	DR4	HB
DTQFVRFDSDAASQRMEPR	P01891	HLA class I histocompatibility antigen, A-68 alpha chain	19	M	Internal	FVRFDSDAA	DR4	HB
VDDTQFVRFDSDAASQRMEPR	P01891	HLA class I histocompatibility antigen, A-68 alpha chain	21	M	Internal	VRFDSDAAS	DR4	HB
QSGEFMFDFDGDEIFH	P01903	HLA class II histocompatibility antigen, DR alpha chain	16	M	Internal	FDFDGDEIF	DR13	IB
QGALANIAVDKANLE	P01903	HLA class II histocompatibility antigen, DR alpha chain	15	M	Internal	IAVDKANLE	DR4	HB
IQAEFYLNPDQSGEF	P01903	HLA class II histocompatibility antigen, DR alpha chain	15	M	Internal	FYLNPDQSG/LNPDQSGEF	DR4/DR13	IB
DHVKLVNEVTEFAKT	P02768	Serum albumin	15	EM	Internal	LVNEVTEFA	DR4	HB
ETYGEMADCCAKQEP	P02768	Serum albumin	15	EM	Internal	YGEMADCCA	DR4	HB
LGEYKFQNALLVRYT	P02768	Serum albumin	15	EM	Internal	YKFQNALLV/FQNALLVRY	DR4/DR13	HB
KEIKILNIFGVIK	P02786	Transferrin receptor protein 1	13	M	Internal	IKILNIFGV	DR13	IB
TGQFLYQDSNWASK	P02786	Transferrin receptor protein 1	14	M	Internal	LYQDSNWAS	DR4	HB
YPRDFVNCSTLPAL	P05164	Myeloperoxidase	14	Lis/End	C-ter	YPRDFVNCS/FVNCSTLPA	DR4/DR13	HB
YPRDFVNCSTLPALNL	P05164	Myeloperoxidase	16	Lis/End	C-ter	YPRDFVNCS/FVNCSTLPA	DR4/DR13	HB
AEQQRLKSQDLELSWNLNG	P06734	Low affinity immunoglobulin epsilon Fc receptor	19	M	Internal	LELSWNLNG	DR4	HB
LLWHWDTTQSLKQ	P06734	Low affinity immunoglobulin epsilon Fc receptor	13	M	Internal	WHWDTTQSL/LWHWDTTQS	DR4/DR13	HB
NIFSFYLSRDPDAQPG	P07339	Cathepsin D	16	Lis/End	Internal	FYLSRDPDA	DR13	HB
GPSYWCQNTETAAQ	P07602	Prosaposin	14	Lis/End	C-ter	YWCQNTETA	DR4	HB
WGPSYWCQNTETAAQ	P07602	Prosaposin	15	Lis/End	C-ter	YWCQNTETA	DR4	HB
YPAEAWNFWTRKGLVSG	P07858	Cathepsin B	17	Lis/End	Internal	WNFWTRKGL	DR13	HB
MQIFVKTLTGKTITLEVEPSD	P0CG48	Polyubiquitin-C	21	C	N-ter	FVKTLTGKT/FVKTLTGKT	DR4/DR13	HB
PKENWVQRVVEKFLKRAENS	P10145	Interleukin-8	20	EM	C-ter	VEKFLKRAE	DR13	IB
IADYFETSSQCSKPG	P10147	C-C motif chemokine 3	15	EM	Internal	YFETSSQCS/IADYFETSS	DR4/DR13	HB
DLSSWTAADTAAQITQ	P10319	HLA class I histocompatibility antigen, B-58 alpha chain	16	M	Internal	WTAADTAAQ/LSSWTAADT	DR4/DR13	HB
LSSWTAADTAAQIT	P10319	HLA class I histocompatibility antigen, B-58 alpha chain	14	M	Internal	WTAADTAAQ/LSSWTAADT	DR4/DR13	HB
LSSWTAADTAAQITQ	P10319	HLA class I histocompatibility antigen, B-58 alpha chain	15	M	Internal	WTAADTAAQ/LSSWTAADT	DR4/DR13	HB
EDLSSWTAADTAAQITQ	P10319	HLA class I histocompatibility antigen, B-58 alpha chain	17	M	Internal	WTAADTAAQ/LSSWTAADT	DR4/DR13	HB
VPMYIGEISPTALR	P11169	Solute carrier family 2, facilitated glucose transporter member 3	14	M	Internal	YIGEISPTA/VPMYIGEIS	DR4/DR13	HB
GSFQFGYNTGVINAPE	P11169	Solute carrier family 2, facilitated glucose transporter member 3	16	M	N-ter	FQFGYNTGV	DR4	IB
GSFQFGYNTGVINAPEKI	P11169	Solute carrier family 2, facilitated glucose transporter member 3	18	M	N-ter	FQFGYNTGV	DR4	IB
SFQFGYNTGVINAPE	P11169	Solute carrier family 2, facilitated glucose transporter member 3	15	M	N-ter	FQFGYNTGV	DR4	IB
FKEFQNNPNPRSLVKP	P11215	Integrin alpha-M	16	M	Internal	FQNNPNPRS	DR4	HB

TFKEFQNNPNPRSLV	P11215	Integrin alpha-M	15	M	Internal	FQNNPNPRS	DR4	HB
TFKEFQNNPNPRSLVKP	P11215	Integrin alpha-M	17	M	Internal	FQNNPNPRS	DR4	HB
PETEQVNGLF	P11586	C-1-tetrahydrofolate synthase, cytoplasmic	10	C	C-ter	NA	NA	NA
PSESWVQEYVYDLELN	P13236	C-C motif chemokine 4	16	EM	C-ter	WVQEYVYDL	DR4	HB
QPPHEYVPWVTVNGKPL	P13284	Gamma-interferon-inducible lysosomal thiol reductase	17	Lis/End	Internal	YVPWVTVNG	DR4	HB
HNLQYLQDENGVGYV	P13686	Tartrate-resistant acid phosphatase type 5	15	Lis/End	Internal	YLQDENGVG	DR4	HB
DTQFVRFDNDAASPR	P13747	HLA class I histocompatibility antigen, alpha chain E	15	M	Internal	FVRFDNDAA	DR4	HB
PFSVTEALIRTCLLNETGDEPFQYKN	P15104	Glutamine synthetase	26	C	C-ter	FSVTEALIR/IRTCLLNET	DR4/DR13	IB
ANIDLGPTILDIAGYDLNK	P15586	N-acetylglucosamine-6-sulfatase	19	Lis/End	Internal	LGPTILDIA	DR13	IB
YGFIEGHVVIPRIHPN	P16070	CD44 antigen	16	M	Internal	IEGHVVIPR	DR13	LB
TGNYRIESVLSSSG	P17900	Ganglioside GM2 activator	14	Lis/End	C-ter	YRIESVLSS	DR4	HB
PKFEVIEKPQA	P18859	ATP synthase-coupling factor 6, mitochondrial	11	Mit	C-ter	FEVIEKPQA/FEVIEKPQA	DR4/DR13	HB
NPAEFVVNTSNAGAG	P21333	Filamin-A	15	C	Internal	VVNTSNAGA	DR4	HB
SRGYEAMYTLLGNAN	P22897	Macrophage mannose receptor 1	15	M	Internal	YEAMYTLLG	DR4	HB
ENKWYADCTSAGRSDG	P22897	Macrophage mannose receptor 1	16	M	Internal	WYADCTSAG	DR4	HB
FENKWYADCTSAGRSDG	P22897	Macrophage mannose receptor 1	17	M	Internal	WYADCTSAG	DR4	HB
NKWYADCTSAGRSDG	P22897	Macrophage mannose receptor 1	15	M	Internal	WYADCTSAG	DR4	HB
SRGYEAMYTLLGNANG	P22897	Macrophage mannose receptor 1	16	M	Internal	YTLLGNANG	DR4	HB
TTAFQYIIDNKGID	P25774	Cathepsin S	14	Lis/End	Internal	FQYIIDNKG/YIIDNKGID	DR4/DR13	IB
NGKEYWLVKNSWGHN	P25774	Cathepsin S	15	Lis/End	Internal	YWLVKNSWG/YWLVKNSWG	DR4/DR13	IB
TTAFQYIIDNKGIDS	P25774	Cathepsin S	15	Lis/End	Internal	FQYIIDNKG/YIIDNKGID	DR4/DR13	IB
TTAFQYIIDNKGIDSD	P25774	Cathepsin S	16	Lis/End	Internal	FQYIIDNKG/YIIDNKGID	DR4/DR13	IB
DNPEYSPDPSIYAYDN	P27797	Calreticulin	16	ER/G	Internal	YSPDPSIYA	DR4	HB
DNLYDGIEDMIGYRPG	P31641	Sodium- and chloride-dependent taurine transporter	16	M	Internal	YDGIEDMIG	DR4	HB
KVGAENTITYSLLMHPDALEEPDDQNRI	P31994	Low affinity immunoglobulin gamma Fc region receptor II-b	28	M	C-ter	VGAENTITY/YSLLMHPDA	DR4/DR13	HB
TPAAPPKAVLKLEPQWINVLQED	P31994	Low affinity immunoglobulin gamma Fc region receptor II-b	23	M	Internal	VLKLEPQWI/VLKLEPQWI	DR4/DR13	IB
IAYQLSRSRNITYLPAGQSVLLQLPQ	P35232	Prohibitin	26	Mit	C-ter	YQLSRSRNI/ITYLPAGQS	DR4/DR13	HB
APVKKLVVKGGKKKKQVLKFTLD	P35268	60S ribosomal protein L22	23	C	N-ter	VKKLVVKGG	DR13	IB
RAKVNVNLLIFLLNKKFYGK	P46940	Ras GTPase-activating-like protein IQGAP1	20	M	C-ter	IFLLNKKFY	DR13	HB
VLDLDLFRVDKGGD	P49591	Serine--tRNA ligase, cytoplasmic	14	C	N-ter	LFRVDKGGD	DR13	HB
KKVVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	16	Lis/End	Internal	VVYLQKLDT	DR13	HB
YDHNFVKAINAIQKS	P53634	Dipeptidyl peptidase 1	15	Lis/End	Internal	FVKAINAIQ	DR4	HB
YDHNFVKAINAIQKSW	P53634	Dipeptidyl peptidase 1	16	Lis/End	Internal	FVKAINAIQ	DR4	HB
KVVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	15	Lis/End	Internal	VYLQKLDTA/VYLQKLDTA	DR4/DR13	HB
NVLRIINEPTAAAIAYG	P54652	Heat shock-related 70 kDa protein 2	17	M	Internal	IINEPTAAA	DR4	HB
VLRIINEPTAAAIA	P54652	Heat shock-related 70 kDa protein 2	14	M	Internal	IINEPTAAA	DR4	HB
GYEPPVQESV	P61247	40S ribosomal protein S3a	10	C	C-ter	YEPPVQESV	DR13	LB
IADAVACAKRVVRDPQ	P61626	Lysozyme C	16	EM	Internal	VACAKRVVR	DR13	HB
YLLYYTEFTPTEKDE	P61769	Beta-2-microglobulin	15	M	C-ter	YYTEFTPTE/YLLYYTEFT	DR4/DR13	HB
LKFLSDASVTAGGF	P98066	Tumor necrosis factor-inducible gene 6 protein	14	EM	Internal	FLSDASVTA	DR4	HB
IKGKINSITVDNCKK	Q01518	Adenylyl cyclase-associated protein 1	15	M	Internal	INSITVDNC	DR4	IB
DPFKPFIIFSNRHEIRR	Q07954	Prolow-density lipoprotein receptor-related protein 1	17	M	Internal	FIIFSNRHE/IIFSNRHEI	DR4/DR13	IB
PAGKLKYFDKLN	Q13162	Peroxiredoxin-4	12	C	C-ter	NA	NA	NA
PAKRPKFDMIVPILEKMQDK	Q13418	Integrin-linked protein kinase	20	M	C-ter	VPILEKMQD	DR13	HB
PAKRISINQALQHAFIQEKI	Q13523	Serine/threonine-protein kinase PRP4 homolog	20	N	C-ter	INQALQHAF	DR13	HB
LPSYEEALSLPSKTPE	Q13571	Lysosomal-associated transmembrane protein 5	16	Lis/End	C-ter	YEEALSLPS	DR4	HB
PETSVLVLRKPGINVASDWSIHLR	Q14697	Neutral alpha-glucosidase AB	24	ER/G	C-ter	INVASDWSI/VLVLRKPGI	DR4/DR13	HB
GELPVEDDIDLSDVELDDLGKDEL	Q15084	Protein disulfide-isomerase A6	24	ER/G	C-ter	LDDLGKDEL	DR13	HB
YRFTIVNLLKP	Q5U5Z8	Cytosolic carboxypeptidase 2	11	C	Internal	YRFTIVNLL/FTIVNLLKP	DR4/DR13	IB

PKRIITYNEAMDSPDQ	Q7Z417	Nuclear fragile X mental retardation-interacting protein 2	16	N	C-ter	ITYNEAMDS	DR4	HB
PLENQPLPLGR	Q96QH2	PML-RARA-regulated adapter molecule 1	11	M	C-ter	LENQPLPLG	DR13	LB
KPPSYNVATTLPSYDE	Q9BT67	NEDD4 family-interacting protein 1	16	Lis/End	Internal	YNVATTLPS/YNVATTLPS	DR4/DR13	HB
RSHSATAVDFLPVMVH	Q9BYV7	Beta,beta-carotene 9',10'-oxygenase	16	Mit	N-ter	VDFLPVMVH/VDFLPVMVH	DR4/DR13	IB
DGKRIQYQLVDISQDN	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	16	C	Internal	IQYQLVDIS	DR4	HB
FGGFLIDRVFGIR	Q9H3U5	Major facilitator superfamily domain-containing protein 1	13	M	Internal	FLIDRVFGI	DR4	HB
GSSFVVARYFPAGNVVNEGFFEENVLPPKK	Q9H4G4	Golgi-associated plant pathogenesis-related protein 1	30	ER/G	C-ter	FVVARYFPA	DR13	HB
DGTEYWIVRNSWGEPW	Q9UBR2	Cathepsin Z	16	Lis/End	Internal	YWIVRNSWG	DR4	HB
DAGDYKADINTQADPY	Q9UIB8	SLAM family member 5	16	M	Internal	YKADINTQA	DR4	HB
RIGNGKFSLSGGNWDNISD	Q9UK32	Ribosomal protein S6 kinase alpha-6	19	C	Internal	IGNGKFSLS	DR13	IB
CRDGWRMKNETSPTVEL	Q9Y5X9	Endothelial lipase	17	EM	C-ter	MKNETSPTV	DR4	HB
WPASWKQEDNPFSWK	Q9Y666	Solute carrier family 12 member 7	15	M	Internal	WKQEDNPFS	DR4	HB

Donor D (DRB1*0101, DRB1*0701)

Sequence	Uniprot AC	Protein name	Length	Cellular Location (a)	Location in Sequence (b)	Binding Core/s (c)	Allele/s (d)	Theoretical Affinity (e)
DAERDALNIETAIKTKGVDE	A6NMY6	Putative annexin A2-like protein	20	EM	Internal	LNIETAIKT	DR1	HB
RDALNIETAIKTKG	A6NMY6	Putative annexin A2-like protein	14	EM	Internal	LNIETAIKT	DR1	HB
RDALNIETAIKTKGVD	A6NMY6	Putative annexin A2-like protein	16	EM	Internal	LNIETAIKT	DR1	HB
RDALNIETAIKTKGVDE	A6NMY6	Putative annexin A2-like protein	17	EM	Internal	LNIETAIKT	DR1	HB
VDKVIQAQTAFSANPA	O00560	Syntenin-1	16	M	N-ter	IQAQTAFSA	DR1	HB
VDKVIQAQTAFSANPANPA	O00560	Syntenin-1	19	M	N-ter	IQAQTAFSA	DR1	HB
PRVPWVKMILNKLSQ	O00626	C-C motif chemokine 22	15	EM	C-ter	WVKMILNKL	DR1	HB
DTIHIWKTNSLPLR	O43157	Plexin-B1	14	M	Internal	IWKTNSLPL/IWKTNSLPL	DR1/DR7	HB
IHIWKTNSLPLR	O43157	Plexin-B1	12	M	Internal	IWKTNSLPL/IWKTNSLPL	DR1/DR7	HB
DTPDIRRFDPIPAQYVRVYPE	O60462	Neuropilin-2	21	M	Internal	FDPIPAQYV/IPAQYVRVY	DR1/DR7	HB
IRRFDPIPAQYVR	O60462	Neuropilin-2	13	M	Internal	FDPIPAQYV	DR1	HB
LLPIMFEVMLVSGVLY	O75027	ATP-binding cassette sub-family B member 7, mitochondrial	16	Mit	Internal	VMLVSGVLY	DR1	HB
ALATISTLEAVRGRPF	O75629	Protein CREG1	16	EM	Internal	LATISTLEA	DR1	HB
ALATISTLEAVRGRPFA	O75629	Protein CREG1	17	EM	Internal	LATISTLEA	DR1	HB
LATISTLEAVRGRPFA	O75629	Protein CREG1	16	EM	Internal	LATISTLEA	DR1	HB
NVNIFKFIIPNVVK	P00338	L-lactate dehydrogenase A chain	14	C	Internal	FKFIIPNVV/FKFIIPNVV	DR1/DR7	HB
MDFEVENAVLGKDFK	P00488	Coagulation factor XIII A chain	15	C	Internal	FEVENAVLG	DR1	IB
VDMDFEVENAVLGKDFK	P00488	Coagulation factor XIII A chain	17	C	Internal	FEVENAVLG	DR1	IB
ERPFLAILGGAKVADK	P00558	Phosphoglycerate kinase 1	16	C	Internal	LAILGGAKV	DR1	HB
SPERPFLAILGGAKVADK	P00558	Phosphoglycerate kinase 1	18	C	Internal	LAILGGAKV	DR1	HB
INEQWLLTTAKNL	P00739	Haptoglobin-related protein	13	EM	Internal	WLLTTAKNL/WLLTTAKNL	DR1/DR7	HB
GKPQYMVLVPSLLH	P01023	Alpha-2-macroglobulin	14	EM	C-ter	YMVLVPSLL	DR1	HB
GKPQYMVLVPSLLHTE	P01023	Alpha-2-macroglobulin	16	EM	C-ter	YMVLVPSLL	DR1	HB
GKPQYMVLVPSLLHTET	P01023	Alpha-2-macroglobulin	17	EM	C-ter	YMVLVPSLL	DR1	HB
KPQYMVLVPSLLHT	P01023	Alpha-2-macroglobulin	14	EM	C-ter	YMVLVPSLL	DR1	HB
KPQYMVLVPSLLHTE	P01023	Alpha-2-macroglobulin	15	EM	C-ter	YMVLVPSLL	DR1	HB
KPQYMVLVPSLLHTET	P01023	Alpha-2-macroglobulin	16	EM	C-ter	YMVLVPSLL	DR1	HB
KVDLSFSPSQSLPA	P01023	Alpha-2-macroglobulin	14	EM	Internal	FSPSQSLPA/LSFSPSQSL	DR1/DR7	HB
AENDVLHCVAFAVPKS	P01023	Alpha-2-macroglobulin	16	EM	Internal	VLHCVAFAV	DR1	HB
EFGRFASFEAQGALA	P01903	HLA class II histocompatibility antigen, DR alpha chain	15	M	Internal	FASFEAQGA	DR1	HB
EFGRFASFEAQGALAN	P01903	HLA class II histocompatibility antigen, DR alpha chain	16	M	Internal	FASFEAQGA	DR1	HB
GRFASFEAQGALAN	P01903	HLA class II histocompatibility antigen, DR alpha chain	14	M	Internal	FASFEAQGA	DR1	HB
EQLGEYKFQNALLVR	P02768	Serum albumin	15	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
EQLGEYKFQNALLVRY	P02768	Serum albumin	16	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
EQLGEYKFQNALLVRYT	P02768	Serum albumin	17	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
EQLGEYKFQNALLVRYTK	P02768	Serum albumin	18	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
EQLGEYKFQNALLVRYTKK	P02768	Serum albumin	19	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
EQLGEYKFQNALLVRYTKKVPQ	P02768	Serum albumin	22	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
EYKFQNALLVR	P02768	Serum albumin	11	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
EYKFQNALLVRY	P02768	Serum albumin	12	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
EYKFQNALLVRYT	P02768	Serum albumin	13	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
EYKFQNALLVRYTK	P02768	Serum albumin	14	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
GEYKFQNALLVRYT	P02768	Serum albumin	14	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
GEYKFQNALLVRYTK	P02768	Serum albumin	15	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
LFEQLGEYKFQNALLVRYTK	P02768	Serum albumin	20	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB

LGEYKFQNALLVR	P02768	Serum albumin	13	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
LGEYKFQNALLVRY	P02768	Serum albumin	14	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
LGEYKFQNALLVRYT	P02768	Serum albumin	15	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
LGEYKFQNALLVRYTK	P02768	Serum albumin	16	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
QLGEYKFQNALLVR	P02768	Serum albumin	14	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
QLGEYKFQNALLVRYT	P02768	Serum albumin	16	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
QLGEYKFQNALLVRYTK	P02768	Serum albumin	17	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR7	HB
RVEYHFLSPYVSPK	P02786	Transferrin receptor protein 1	14	M	Internal	YHFLSPYVS/YHFLSPYVS	DR1/DR7	HB
NPGGYVAYSKAATVTGKL	P02786	Transferrin receptor protein 1	18	M	Internal	VAYSKAATV/VAYSKAATV	DR1/DR7	HB
RVEYHFLSPYVSPKE	P02786	Transferrin receptor protein 1	15	M	Internal	YHFLSPYVS/YHFLSPYVS	DR1/DR7	HB
WDFWSLRPESLHQ	P04040	Catalase	13	Lis/End	Internal	FWSLRPESL	DR1	HB
SPDRIFFHLNAVALGDG	P04217	Alpha-1B-glycoprotein	17	EM	Internal	FFHLNAVAL/IFFHLNAVA	DR1/DR7	HB
ENGNYLPLQCYGSIG	P04233	HLA class II histocompatibility antigen gamma chain	15	ER/G	Internal	YLPLQCYGS/LPLQCYGSI	DR1/DR7	HB
GNYLPLQCYGSIG	P04233	HLA class II histocompatibility antigen gamma chain	13	ER/G	Internal	YLPLQCYGS/LPLQCYGSI	DR1/DR7	HB
LISWYDNEFGYSNR	P04406	Glyceraldehyde-3-phosphate dehydrogenase	14	C	C-ter	YDNEFGYSN/ISWYDNEFG	DR1/DR7	HB
KKGFKMEVGQYIFVK	P04839	Cytochrome b-245 heavy chain	15	M	Internal	FKMEVGQYI/FKMEVGQYI	DR1/DR7	HB
IPADLRIISANGCKVDN	P05023	Sodium/potassium-transporting ATPase subunit alpha-1	17	M	Internal	IISANGCKV	DR1	HB
KTYEKLTEIIPK	P05107	Integrin beta-2	12	M	Internal	NA	NA	NA
IKGNFHAVYRDDLKKL	P05109	Protein S100-A8	16	C	N-ter	IKGNFHAVY	DR7	HB
GPRSYTIAVASLGKG	P06280	Alpha-galactosidase A	15	Lis/End	Internal	YTIAVASLG	DR1	HB
KQIWRIEGSNKVPVDP	P06396	Gelsolin	16	C	Internal	WRIEGSNKV/WRIEGSNKV	DR1/DR7	HB
DAYVILKTVQLR	P06396	Gelsolin	12	C	Internal	YVILKTVQL	DR1	HB
KQIWRIEGSNKVPVDPA	P06396	Gelsolin	17	C	Internal	WRIEGSNKV/WRIEGSNKV	DR1/DR7	HB
DAYVILKTVQLRN	P06396	Gelsolin	13	C	Internal	YVILKTVQL	DR1	HB
DAYVILKTVQLRNG	P06396	Gelsolin	14	C	Internal	YVILKTVQL	DR1	HB
GDAYVILKTVQLRN	P06396	Gelsolin	14	C	Internal	YVILKTVQL	DR1	HB
GDAYVILKTVQLRNG	P06396	Gelsolin	15	C	Internal	YVILKTVQL	DR1	HB
TGDAYVILKTVQLRNG	P06396	Gelsolin	16	C	Internal	YVILKTVQL	DR1	HB
TGDAYVILKTVQLRNGN	P06396	Gelsolin	17	C	Internal	YVILKTVQL	DR1	HB
TGDAYVILKTVQLRNGNL	P06396	Gelsolin	18	C	Internal	YVILKTVQL	DR1	HB
DYPVVSIEDPFDQDDWGAWQK	P06733	Alpha-enolase	21	C	Internal	NA	NA	NA
AEQQRLKSQDLELSWNLNG	P06734	Low affinity immunoglobulin epsilon Fc receptor	19	M	Internal	LELSWNLNG	DR7	HB
RAGSSRQSIQKYIKSHYK	P07305	Histone H1.0	18	N	Internal	IQKYIKSHY	DR7	HB
TKDTYRHTFTLSLPR	P07333	Macrophage colony-stimulating factor 1 receptor	15	M	Internal	YRHTFTLSL/YRHTFTLSL	DR1/DR7	HB
LGGGTGSGMGTLLISKIREEYPD	P07437	Tubulin beta chain	23	C	Internal	MGTLLISKI/LISKIREEY	DR1/DR7	HB
SGPFGQIFRPDNFVFGQSGAGNNWAK	P07437	Tubulin beta chain	26	C	Internal	VFGQSGAGN/IFRPDNFVF	DR1/DR7	HB
EPVAVLKANRVWG	P07686	Beta-hexosaminidase subunit beta	13	Lis/End	Internal	VAVLKANRV	DR1	HB
VKEPVAVLKANRVWGAL	P07686	Beta-hexosaminidase subunit beta	17	Lis/End	Internal	VAVLKANRV	DR1	HB
ANRVWGALRGLETFSQ	P07686	Beta-hexosaminidase subunit beta	16	Lis/End	Internal	WGALRGLET	DR1	HB
DPASFRAAIGLLARH	P07741	Adenine phosphoribosyltransferase	15	C	Internal	FRAAIGLLA	DR1	HB
DNGFFKILRGQDH	P07858	Cathepsin B	13	Lis/End	C-ter	FKILRGQDH	DR1	HB
GDNGFFKILRGQDH	P07858	Cathepsin B	14	Lis/End	C-ter	FKILRGQDH	DR1	HB
GFFKILRGQDH	P07858	Cathepsin B	11	Lis/End	C-ter	FKILRGQDH	DR1	HB
GFFKILRGQDHCG	P07858	Cathepsin B	13	Lis/End	C-ter	FKILRGQDH	DR1	HB
KSGVYQHVTGEMMGGHA	P07858	Cathepsin B	17	Lis/End	Internal	YQHVTGEMM/YQHVTGEMM	DR1/DR7	HB
LVFDEYLKTTGKPIE	P08133	Annexin A6	15	C	Internal	YLKTTGKPI/YLKTTGKPI	DR1/DR7	HB
KGRLDYLSSLKVKG	P08195	4F2 cell-surface antigen heavy chain	14	M	Internal	LDYLSSLKV/LDYLSSLKV	DR1/DR7	HB
LKGRLDYLSSLKVKG	P08195	4F2 cell-surface antigen heavy chain	15	M	Internal	LDYLSSLKV/LDYLSSLKV	DR1/DR7	HB
PMPQAPALWIETTAYALLHLLLHEGK	P0C0L4	Complement C4-A	26	EM	Internal	ALWIETTAY/WIETTAYAL	DR1/DR7	HB
RPAGDGTFQKWASVVVPSG	P10314	HLA class I histocompatibility antigen, A-32 alpha chain	19	M	Internal	FQKWASVVV/FQKWASVVV	DR1/DR7	HB

TRPAGDGTFQKWASVVVPSG	P10314	HLA class I histocompatibility antigen, A-32 alpha chain	20	M	Internal	FQKWASVVV/FQKWASVVV	DR1/DR7	HB
TRPAGDRTFQKWAAVVVPSG	P10319	HLA class I histocompatibility antigen, B-58 alpha chain	20	M	Internal	FQKWAAVVV	DR1	HB
TRPAGDRTFQKWAAVVVPSGEE	P10319	HLA class I histocompatibility antigen, B-58 alpha chain	22	M	Internal	FQKWAAVVV	DR1	HB
FAYYHGLLGNRLWSS	P10619	Lysosomal protective protein	15	Lis/End	Internal	YHGLLGNRL/YHGLLGNRL	DR1/DR7	HB
FAYYHGLLGNRLWSSL	P10619	Lysosomal protective protein	16	Lis/End	Internal	YHGLLGNRL/YHGLLGNRL	DR1/DR7	HB
YFAYYHGLLGNRLWSS	P10619	Lysosomal protective protein	16	Lis/End	Internal	YHGLLGNRL/YHGLLGNRL	DR1/DR7	HB
YFAYYHGLLGNRLWSSL	P10619	Lysosomal protective protein	17	Lis/End	Internal	YHGLLGNRL/YHGLLGNRL	DR1/DR7	HB
YRRLYRSMNSQYLKLL	P10619	Lysosomal protective protein	16	Lis/End	Internal	YRSMNSQYL/YRSMNSQYL	DR1/DR7	HB
TPLSAFGNLRPVLAEDAQ	P11215	Integrin alpha-M	18	M	Internal	FGNLRPVLA	DR1	HB
GFGQSVVQLQGSRVVVG	P11215	Integrin alpha-M	17	M	Internal	VVQLQGSRV/VQLQGSRVV	DR1/DR7	HB
DSVFTLLPGQGAFVR	P11215	Integrin alpha-M	15	M	Internal	FTLLPGQGA	DR1	HB
AQGHVLLLRSQPVLR	P11215	Integrin alpha-M	15	M	Internal	VLLLRSQPV/VLLLRSQPV	DR1/DR7	HB
TPLSAFGNLRPVLAEDAQR	P11215	Integrin alpha-M	19	M	Internal	FGNLRPVLA	DR1	HB
GQSVVQLQGSRVVVG	P11215	Integrin alpha-M	15	M	Internal	VVQLQGSRV/VQLQGSRVV	DR1/DR7	HB
GNIGYTLFSSKPVT	P12318	Low affinity immunoglobulin gamma Fc region receptor II-a	14	M	Internal	YTLFSSKPV/YTLFSSKPV	DR1/DR7	HB
KALDFIASKGVKL	P12814	Alpha-actinin-1	13	C	Internal	FIASKGVKL/FIASKGVKL	DR1/DR7	HB
DNFYFTGVQDINDKR	P13686	Tartrate-resistant acid phosphatase type 5	15	Lis/End	Internal	FYFTGVQDI/FYFTGVQDI	DR1/DR7	HB
GDNFYFTGVQDINDKR	P13686	Tartrate-resistant acid phosphatase type 5	16	Lis/End	Internal	FYFTGVQDI/FYFTGVQDI	DR1/DR7	HB
LGDNFYFTGVQDINDK	P13686	Tartrate-resistant acid phosphatase type 5	16	Lis/End	Internal	FYFTGVQDI/FYFTGVQDI	DR1/DR7	HB
LGDNFYFTGVQDINDKR	P13686	Tartrate-resistant acid phosphatase type 5	17	Lis/End	Internal	FYFTGVQDI/FYFTGVQDI	DR1/DR7	HB
SDVGEYRAVTELGRPV	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	16	M	Internal	YRAVTELGR/VGEYRAVTE	DR1/DR7	IB
VGEYRAVTELGRPV	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	14	M	Internal	YRAVTELGR/VGEYRAVTE	DR1/DR7	IB
NAKYAISMARKIGAR	P13796	Plastin-2	15	C	Internal	YAISMARKI/YAISMARKI	DR1/DR7	HB
GQDSILSLPGNVGHQDV	P13798	Acylamino-acid-releasing enzyme	17	C	Internal	ILSLPGNVG	DR1	HB
YDWYTKVTSVVVD	P13798	Acylamino-acid-releasing enzyme	13	C	Internal	YTKVTSVVV/YTKVTSVVV	DR1/DR7	HB
IINDAFNLASAHKVPVT	P15144	Aminopeptidase N	17	M	Internal	FNLASAHKV/FNLASAHKV	DR1/DR7	HB
RPSEFNYVWIVPITS	P15144	Aminopeptidase N	15	M	Internal	FNYVWIVPI/FNYVWIVPI	DR1/DR7	HB
KQDATSTIISITNNVIG	P15144	Aminopeptidase N	17	M	Internal	IISITNNVI/IISITNNVI	DR1/DR7	HB
INDAFNLASAHKVPV	P15144	Aminopeptidase N	15	M	Internal	FNLASAHKV/FNLASAHKV	DR1/DR7	HB
INDAFNLASAHKVPVT	P15144	Aminopeptidase N	16	M	Internal	FNLASAHKV/FNLASAHKV	DR1/DR7	HB
FEPFFMMIATPAPH	P15586	N-acetylglucosamine-6-sulfatase	14	Lis/End	Internal	FFMMIATPA	DR1	HB
ELPSWLTTGNYRIES	P17900	Ganglioside GM2 activator	15	Lis/End	C-ter	LPSWLTTGN/WLTTGNYRI	DR1/DR7	HB
ELPSWLTTGNYRIESV	P17900	Ganglioside GM2 activator	16	Lis/End	C-ter	LPSWLTTGN/WLTTGNYRI	DR1/DR7	HB
DVNSEHTFLWTDGRGVHYT	P22897	Macrophage mannose receptor 1	19	M	Internal	FLWTDGRGV/FLWTDGRGV	DR1/DR7	HB
EEQQTIWRLITASGSYH	P22897	Macrophage mannose receptor 1	17	M	Internal	WRLITASGS	DR1	HB
VLGKFVSLEGFAQPV	P23141	Liver carboxylesterase 1	15	ER/G	Internal	FVSLEGFAQ	DR1	HB
TGKLVSLSAQNLVD	P25774	Cathepsin S	14	Lis/End	Internal	LVSLSAQNL/VSLSAQNLV	DR1/DR7	HB
TGKLVSLSAQNLVDC	P25774	Cathepsin S	15	Lis/End	Internal	LVSLSAQNL/VSLSAQNLV	DR1/DR7	HB
GVVYYRVQNATLAVAN	P27105	Erythrocyte band 7 integral membrane protein	16	M	Internal	YRVQNATLA/YYRVQNATL	DR1/DR7	HB
VVYYRVQNATLAVAN	P27105	Erythrocyte band 7 integral membrane protein	15	M	Internal	YRVQNATLA/YYRVQNATL	DR1/DR7	HB
YASFFAVMGASAAM	P27449	V-type proton ATPase 16 kDa proteolipid subunit	14	Lis/End	N-ter	FFAVMGASA	DR1	HB
APVKKLVVKGGKKKKQVLKFTLD	P35268	60S ribosomal protein L22	23	C	N-ter	VKKLVVKGG/LVVKGGKKK	DR1/DR7	IB
FRQRYEILTPNSIPK	P35579	Myosin-9	15	C	Internal	YEILTPNSI/YEILTPNSI	DR1/DR7	HB
EVNKYQYLLTGRVYDGK	P35625	Metalloproteinase inhibitor 3	17	EM	Internal	YQYLLTGRV/YQYLLTGRV	DR1/DR7	HB
LEVNKYQYLLTGRVYDGK	P35625	Metalloproteinase inhibitor 3	18	EM	Internal	YQYLLTGRV/YQYLLTGRV	DR1/DR7	HB
IKMFFALGPVAS	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	12	Lis/End	Internal	MFFALGPVA	DR1	HB
SVQNMLHWSQAVKFQKFQ	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	18	Lis/End	Internal	LHWSQAVKF/LHWSQAVKF	DR1/DR7	HB
VQNMLHWSQAVKF	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	LHWSQAVKF/LHWSQAVKF	DR1/DR7	HB
VQNMLHWSQAVKFQK	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	LHWSQAVKF/LHWSQAVKF	DR1/DR7	HB
VQNMLHWSQAVKFQKF	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	16	Lis/End	Internal	LHWSQAVKF/LHWSQAVKF	DR1/DR7	HB

VQNMLHWSQAVKFQKFQ	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	17	Lis/End	Internal	LHWSQAVKF/LHWSQAVKF	DR1/DR7	HB
NMLHWSQAVKF	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	11	Lis/End	Internal	LHWSQAVKF/LHWSQAVKF	DR1/DR7	HB
IKMFFALGPVASVA	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	MFFALGPVA	DR1	HB
RIKMFFALGPVASVA	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	MFFALGPVA	DR1	HB
NLHYFNSDSFASHPNYPYSDEY	P42330	Aldo-keto reductase family 1 member C3	22	C	C-ter	LHYFNSDSF/FASHPNYPY	DR1/DR7	HB
VLDLDLFRVDKGGD	P49591	Serine--tRNA ligase, cytoplasmic	14	C	N-ter	VLDLDLFRV	DR1	HB
KGNKYWKFNNQKLKVEPG	P50281	Matrix metalloproteinase-14	18	M	Internal	YWKFNNQKL/YWKFNNQKL	DR1/DR7	IB
LIPKFLMANGQLVK	P50395	Rab GDP dissociation inhibitor beta	14	C	Internal	FLMANGQLV/FLMANGQLV	DR1/DR7	HB
GGQFLRAVAQRCPSPP	P50897	Palmitoyl-protein thioesterase 1	16	Lis/End	Internal	FLRAVAQRC	DR1	HB
DIRSEYKRMYGKSLYHD	P50995	Annexin A11	17	C	C-ter	YKRMYGKSL	DR1	HB
GPRPEEYEFLTPVEEAPK	P52566	Rho GDP-dissociation inhibitor 2	18	C	Internal	YEFLTPVEE	DR1	HB
KKVVVYLQKLDTAYD	P53634	Dipeptidyl peptidase 1	15	Lis/End	Internal	YLQKLDTAY	DR7	HB
LPTSWDWRNVHGINF	P53634	Dipeptidyl peptidase 1	15	Lis/End	Internal	WRNVHGINF/WRNVHGINF	DR1/DR7	HB
KKVVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	16	Lis/End	Internal	YLQKLDTAY	DR7	HB
KVVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	15	Lis/End	Internal	YLQKLDTAY	DR7	HB
TPSYVAFTDTERLIG	P54652	Heat shock-related 70 kDa protein 2	15	M	Internal	VAFTDTERL/VAFTDTERL	DR1/DR7	HB
KNNLCPSGSNIISNL	P60033	CD81 antigen	15	M	Internal	LCPSGSNII/LCPSGSNII	DR1/DR7	HB
SRETYNSLAAWLTDAR	P61018	Ras-related protein Rab-4B	16	M	Internal	YNSLAAWLT	DR1	HB
DITRRSTYNHLSSWLTDARN	P61106	Ras-related protein Rab-14	20	Lis/End	Internal	YNHLSSWLT	DR1	HB
RRSTYNHLSSWLTDAR	P61106	Ras-related protein Rab-14	16	Lis/End	Internal	YNHLSSWLT	DR1	HB
GYEPPVQESV	P61247	40S ribosomal protein S3a	10	C	C-ter	NA	NA	NA
DFPEFLTMMARKMKDTD	P62158	Calmodulin	17	C	Internal	FLTMMARKM	DR1	HB
IDFPEFLTMMARKMKDTD	P62158	Calmodulin	18	C	Internal	FLTMMARKM	DR1	HB
IDFPEFLTMMARKMKDTDS	P62158	Calmodulin	19	C	Internal	FLTMMARKM	DR1	HB
DFQEFISLVAIALK	P80511	Protein S100-A12	14	C	C-ter	FISLVAIAL	DR1	HB
DFQEFISLVAIALKA	P80511	Protein S100-A12	15	C	C-ter	FISLVAIAL	DR1	HB
YPAYISIKAIESPN	Q00765	Receptor expression-enhancing protein 5	14	M	Internal	YISIKAIES	DR1	HB
DGSHRYVILKSEPVHPFG	Q07954	Prolow-density lipoprotein receptor-related protein 1	18	M	Internal	YVILKSEPV/YVILKSEPV	DR1/DR7	HB
GSHRYVILKSEPVHPF	Q07954	Prolow-density lipoprotein receptor-related protein 1	16	M	Internal	YVILKSEPV/YVILKSEPV	DR1/DR7	HB
GSHRYVILKSEPVHPFG	Q07954	Prolow-density lipoprotein receptor-related protein 1	17	M	Internal	YVILKSEPV/YVILKSEPV	DR1/DR7	HB
YDGSHRYVILKSEPVHPFG	Q07954	Prolow-density lipoprotein receptor-related protein 1	19	M	Internal	YVILKSEPV/YVILKSEPV	DR1/DR7	HB
PAGKLKYFDKLN	Q13162	Peroxiredoxin-4	12	C	C-ter	NA	NA	NA
DTSVYSQLPGQEAFMR	Q13349	Integrin alpha-D	16	M	Internal	YSQLPGQEA	DR1	HB
INEIRQMSGAQIKIA	Q15365	Poly(rC)-binding protein 1	15	C	Internal	IRQMSGAQI	DR1	HB
IDKVISTITNNIQQ	Q15582	Transforming growth factor-beta-induced protein ig-h3	14	EM	Internal	VISTITNNI	DR7	HB
APTNEAFEKIPSETLNR	Q15582	Transforming growth factor-beta-induced protein ig-h3	17	EM	Internal	FEKIPSETL	DR1	HB
LIDKVISTITNNIQQ	Q15582	Transforming growth factor-beta-induced protein ig-h3	15	EM	Internal	VISTITNNI	DR7	HB
QKSNLYCLKPTICSDQD	Q16553	Lymphocyte antigen 6E	17	M	C-ter	LYCLKPTIC/YCLKPTICS	DR1/DR7	HB
QNLIDELSKTLETAGY	Q5VZ66	Janus kinase and microtubule-interacting protein 3	16	ER/G	Internal	LIDELSKTL/LIDELSKTL	DR1/DR7	HB
ALDGEAPRGISSGYPFLK	Q6ZS27	Zinc finger protein 662	18	N	Internal	LDGEAPRGI	DR7	HB
NTDPYQLMNAVNTLDR	Q8IWU5	Extracellular sulfatase Sulf-2	16	ER/G	Internal	YQLMNAVNT	DR1	HB
TDPYQLMNAVNTLDR	Q8IWU5	Extracellular sulfatase Sulf-2	15	ER/G	Internal	YQLMNAVNT	DR1	HB
YVLQGLHLHIP	Q8IY34	Solute carrier family 15 member 3	11	Lis/End	Internal	YVLQGLHLH	DR1	HB
YVLQGLHLHIPN	Q8IY34	Solute carrier family 15 member 3	12	Lis/End	Internal	YVLQGLHLH	DR1	HB
QMCFFVLFIVLDSLLL	Q8NGA2	Putative olfactory receptor 7A2	16	M	Internal	FIVLDSLLL	DR1	HB
DGLGTLLVGSCPEVIIGHQS	Q8NHY0	Beta-1,4 N-acetylgalactosaminyltransferase 2	20	ER/G	Internal	LVGSCPEVI/LVGSCPEVI	DR1/DR7	HB
NSENLWKTALLAVKQ	Q92674	Centromere protein I	15	N	Internal	LWKTALLAV	DR7	IB
AEILELAGNAARDNK	Q96KK5	Histone H2A type 1-H	15	N	Internal	ILELAGNAA	DR1	HB
LTAEILELAGNAARDNK	Q96KK5	Histone H2A type 1-H	17	N	Internal	ILELAGNAA	DR1	HB

LTAEILELAGNAARDNKK	Q96KK5	Histone H2A type 1-H	18	N	Internal	ILELAGNAA	DR1	HB
TAEILELAGNAARDNK	Q96KK5	Histone H2A type 1-H	16	N	Internal	ILELAGNAA	DR1	HB
TAEILELAGNAARDNKK	Q96KK5	Histone H2A type 1-H	17	N	Internal	ILELAGNAA	DR1	HB
YLTAEILELAGNAARDNK	Q96KK5	Histone H2A type 1-H	18	N	Internal	ILELAGNAA	DR1	HB
YLTAEILELAGNAARDNKK	Q96KK5	Histone H2A type 1-H	19	N	Internal	ILELAGNAA	DR1	HB
LAKWVAIQSVSAWPE	Q96KP4	Cytosolic non-specific dipeptidase	15	C	N-ter	WVAIQSVSA	DR1	HB
NLGLTFLRGSQTQSHPD	Q96PD5	N-acetylmuramoyl-L-alanine amidase	17	EM	Internal	LTFLRGSQT/LRGSQTQSH	DR1	HB
LDHKFDLMYAKRAFVH	Q9BQE3	Tubulin alpha-1C chain	16	C	Internal	FDLMYAKRA	DR1	HB
IWHHTFYNELR	Q9BYX7	Putative beta-actin-like protein 3	11	C	Internal	WHHTFYNEL	DR7	IB
DGKRIQYQLVDISQDN	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	16	C	Internal	YQLVDISQD	DR1	IB
DGKRIQYQLVDISQDNA	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	17	C	Internal	YQLVDISQD	DR1	IB
KRIQYQLVDISQDNA	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	15	C	Internal	YQLVDISQD	DR1	IB
AGKYVPAIAHLIHSL	Q9H3G5	Probable serine carboxypeptidase CPVL	15	Lis/End	Internal	YVPAIAHLI	DR1	HB
KYVPAIAHLIHS	Q9H3G5	Probable serine carboxypeptidase CPVL	12	Lis/End	Internal	YVPAIAHLI	DR1	HB
LKVILGILLPP	Q9HCF6	ransient receptor potential cation channel subfamily M member 3	11	M	Internal	LKVILGILL	DR1	HB
IKVTDPQLLEL	Q9NP55	BPI fold-containing family A member 1	11	EM	Internal	IKVTDPQLL	DR1	HB
GGNDLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	19	Lis/End	Internal	YAHQHGIPD	DR1	HB
INHVVSVAGWGISDG	Q9UBR2	Cathepsin Z	15	Lis/End	Internal	VVSVAGWGI	DR1	HB
GGNDLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	20	Lis/End	Internal	YAHQHGIPD	DR1	HB
GNDLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	18	Lis/End	Internal	YAHQHGIPD	DR1	HB
GNDLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	19	Lis/End	Internal	YAHQHGIPD	DR1	HB
LSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	15	Lis/End	Internal	YAHQHGIPD	DR1	HB
NDLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	17	Lis/End	Internal	YAHQHGIPD	DR1	HB
NDLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	18	Lis/End	Internal	YAHQHGIPD	DR1	HB
PPVKTKFGYHIIMVEGRK	Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	18	N	C-ter	VKTKFGYHI/VKTKFGYHI	DR1/DR7	HB

Donor E (DRB1*0101, DRB1*1101)

Uniprot AC	Protein name	Length	Cellular Location (a)	Location in Sequence (b)	Binding Core/s (c)	Allele/s (d)	Theoretical Affinity (e)
O00160	Unconventional myosin-If	24	C	C-ter	LHGQEGLFP	DR1	HB
O00560	Syntenin-1	17	M	Internal	IFKNGKITS	DR11	HB
O00560	Syntenin-1	16	M	Internal	IFKNGKITS	DR11	HB
O00560	Syntenin-1	15	M	Internal	IFKNGKITS	DR11	HB
O00560	Syntenin-1	16	M	N-ter	IQAQTAFSA	DR1	HB
O00560	Syntenin-1	19	M	N-ter	IQAQTAFSA	DR1	HB
O00626	C-C motif chemokine 22	15	EM	C-ter	WVKMILNKL/WVKMILNKL	DR1/DR11	HB
O14773	Tripeptidyl-peptidase 1	15	Lis/End	Internal	LLAAGAQKC	DR1	HB
O14773	Tripeptidyl-peptidase 1	18	Lis/End	Internal	LLAAGAQKC	DR1	HB
O15235	28S ribosomal protein S12, mitochondrial	10	Mit	Internal	NA	NA	NA
O43567	E3 ubiquitin-protein ligase RNF13	13	ER/G	Internal	FTYEKGGHL	DR1	HB
O43567	E3 ubiquitin-protein ligase RNF13	15	ER/G	Internal	FTYEKGGHL	DR1	HB
O60462	Neuropilin-6	21	M	Internal	FDPIPAQYV	DR1	HB
O60462	Neuropilin-2	14	M	Internal	FDPIPAQYV	DR1	HB
O60462	Neuropilin-3	16	M	Internal	FDPIPAQYV	DR1	HB
O60462	Neuropilin-4	17	M	Internal	FDPIPAQYV	DR1	HB
O60462	Neuropilin-5	20	M	Internal	FDPIPAQYV	DR1	HB
O75629	Protein CREG1	17	EM	Internal	ISTLEAVRG	DR1	HB
O95400	CD2 antigen cytoplasmic tail-binding protein 2	18	C	C-ter	FYNSKRIDF	DR11	HB
P00488	Coagulation factor XIII A chain	17	C	Internal	FEVENAVLG	DR1	IB
P00558	Phosphoglycerate kinase 1	18	C	Internal	LAILGGAKV	DR1	HB
P01375	Tumor necrosis factor	16	M	C-ter	FQLEKGDRL	DR1	HB
P01589	Interleukin-2 receptor subunit alpha	16	M	Internal	YHFVVGQMV	DR1	HB
P01892	HLA class I histocompatibility antigen, A-2 alpha chain	14	M	Internal	WRFLRGYHQ	DR1	HB
P01892	HLA class I histocompatibility antigen, A-2 alpha chain	22	M	Internal	WRFLRGYHQ	DR1	HB
P01903	HLA class II histocompatibility antigen, DR alpha chain	17	M	Internal	VIIQAEFYL	DR1	HB
P01903	HLA class II histocompatibility antigen, DR alpha chain	16	M	Internal	FASFEAQGA/FGRFASFEA	DR1/DR11	HB
P02652	Apolipoprotein A-II	16	EM	C-ter	LIKKAGTEL	DR1	HB
P02768	Serum albumin	14	EM	Internal	LFFAKRYKA	DR1	HB
P02768	Serum albumin	15	EM	Internal	LLVRYTKKV	DR1	HB
P02768	Serum albumin	14	EM	Internal	YLYEIARRH	DR1	IB
P02768	Serum albumin	13	EM	Internal	LVEVSRNLG	DR1	IB
P02768	Serum albumin	15	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	16	EM	Internal	LFFAKRYKA	DR1	HB
P02768	Serum albumin	15	EM	Internal	LVEVSRNLG	DR1	IB
P02768	Serum albumin	16	EM	Internal	LVEVSRNLG	DR1	IB
P02768	Serum albumin	17	EM	Internal	LVEVSRNLG	DR1	IB
P02768	Serum albumin	18	EM	Internal	LLVRYTKKV	DR1	HB
P02768	Serum albumin	16	EM	Internal	VSRNLGKVG	DR1	HB
P02768	Serum albumin	16	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	17	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	18	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	19	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	13	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	14	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB

P02768	Serum albumin	20	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	12	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	14	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	15	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	13	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	14	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	15	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	16	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	14	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	15	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	16	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	17	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	18	EM	Internal	YKFQNALLV/YKFQNALLV	DR1/DR11	HB
P02768	Serum albumin	13	EM	Internal	YLYEIARRH	DR1	IB
P02786	Transferrin receptor protein 1	15	M	C-ter	WTIQGAANA	DR1	HB
P02786	Transferrin receptor protein 1	16	M	Internal	ISRAAAEKL	DR1	HB
P02786	Transferrin receptor protein 1	19	M	Internal	YHFLSPYVS/YHFLSPYVS	DR1/DR11	HB
P02786	Transferrin receptor protein 1	16	M	Internal	VARAAAEVA/LNKVARAAA	DR1/DR11	HB
P02786	Transferrin receptor protein 1	14	M	Internal	YHFLSPYVS/YHFLSPYVS	DR1/DR11	HB
P04040	Catalase	14	Lis/End	Internal	FWSLRPESL	DR1	HB
P04066	Tissue alpha-L-fucosidase	14	Lis/End	Internal	WLSINGEAI	DR1	HB
P04217	Alpha-1B-glycoprotein	17	EM	Internal	FFHLNAVAL	DR1	HB
P04406	Glyceraldehyde-3-phosphate dehydrogenase	15	C	Internal	VINGNPITI	DR1	HB
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	17	M	Internal	IISANGCKV	DR1	HB
P05109	Protein S100-A8	11	C	N-ter	NA	NA	NA
P05155	Plasma protease C1 inhibitor	18	EM	Internal	LVLLNAIYL	DR1	HB
P05164	Myeloperoxidase	18	Lis/End	Internal	WWENEGVFS	DR1	IB
P05387	60S acidic ribosomal protein P2	22	C	N-ter	MRYVASYLL	DR1	HB
P06702	Protein S100-A9	13	C	Internal	NA	NA	NA
P06734	Low affinity immunoglobulin epsilon Fc receptor	13	M	Internal	WIGLRNLDL	DR1	HB
P06734	Low affinity immunoglobulin epsilon Fc receptor	17	M	Internal	WIGLRNLDL	DR1	HB
P06734	Low affinity immunoglobulin epsilon Fc receptor	14	M	Internal	WIGLRNLDL	DR1	HB
P06734	Low affinity immunoglobulin epsilon Fc receptor	16	M	Internal	WIGLRNLDL	DR1	HB
P06865	Beta-hexosaminidase subunit alpha	15	Lis/End	Internal	WGALRGLET	DR1	HB
P07333	Macrophage colony-stimulating factor 1 receptor	18	M	Internal	YSIMQACWA/YSIMQACWA	DR1/DR11	HB
P07602	Prosaposin	16	Lis/End	Internal	LDIIKGEMS	DR1	HB
P07686	Beta-hexosaminidase subunit beta	18	Lis/End	Internal	VAVLKANRV	DR1	HB
P07686	Beta-hexosaminidase subunit beta	15	Lis/End	Internal	VAVLKANRV	DR1	HB
P07686	Beta-hexosaminidase subunit beta	17	Lis/End	Internal	VAVLKANRV	DR1	HB
P07741	Adenine phosphoribosyltransferase	15	C	Internal	FRAAIGLLA/FRAAIGLLA	DR1/DR11	HB
P07858	Cathepsin B	13	Lis/End	C-ter	FKILRGQDH	DR1	HB
P07858	Cathepsin B	16	Lis/End	C-ter	FKILRGQDH	DR1	HB
P07858	Cathepsin B	11	Lis/End	C-ter	FKILRGQDH	DR1	HB
P07858	Cathepsin B	17	Lis/End	Internal	YLKRLCGTF/MSYLKRLCG	DR1/DR11	HB
P07858	Cathepsin B	13	Lis/End	Internal	YLKRLCGTF/MSYLKRLCG	DR1/DR11	HB
P07858	Cathepsin B	15	Lis/End	Internal	YLKRLCGTF/MSYLKRLCG	DR1/DR11	HB
P08246	Neutrophil elastase	16	M	Internal	FAVQRIFEN	DR1	HB
P08670	Vimentin	15	C	C-ter	VINETSQHH	DR1	HB
P0DMV8	Heat shock 70 kDa protein 1A	14	C	Internal	ISWLDANTL	DR1	HB
P0DMV9	Heat shock 70 kDa protein 1A	15	C	Internal	ISWLDANTL	DR1	HB

P10145	Interleukin-8	20	EM	C-ter	VQRVVEKFL	DR1	HB
P10319	HLA class I histocompatibility antigen, B-58 alpha chain	19	M	Internal	VVVIGAVVA	DR1	HB
P10619	Lysosomal protective protein	14	Lis/End	Internal	YHGLLGNRL/FAYYHGLLG	DR1/DR11	HB
P10619	Lysosomal protective protein	15	Lis/End	Internal	YHGLLGNRL/FAYYHGLLG	DR1/DR11	HB
P10619	Lysosomal protective protein	16	Lis/End	Internal	YHGLLGNRL/FAYYHGLLG	DR1/DR11	HB
P10619	Lysosomal protective protein	16	Lis/End	Internal	YHGLLGNRL/FAYYHGLLG	DR1/DR11	HB
P10619	Lysosomal protective protein	17	Lis/End	Internal	YHGLLGNRL/FAYYHGLLG	DR1/DR11	HB
P11169	Solute carrier family 2, facilitated glucose transporter member 3	16	M	N-ter	FGYNTGVIN	DR1	HB
P11169	Solute carrier family 2, facilitated glucose transporter member 3	18	M	N-ter	FGYNTGVIN	DR1	HB
P11169	Solute carrier family 2, facilitated glucose transporter member 3	15	M	N-ter	FGYNTGVIN	DR1	HB
P11215	Integrin alpha-M	15	M	Internal	VVQLQGSRV	DR1	HB
P11215	Integrin alpha-M	15	M	Internal	FTLLPGQGA/FTLLPGQGA	DR1/DR11	HB
P11215	Integrin alpha-M	17	M	Internal	FGNLRPVLA/FGNLRPVLA	DR1/DR11	HB
P11215	Integrin alpha-M	18	M	Internal	FGNLRPVLA/FGNLRPVLA	DR1/DR11	HB
P11215	Integrin alpha-M	19	M	Internal	FGNLRPVLA/FGNLRPVLA	DR1/DR11	HB
P11215	Integrin alpha-M	16	M	Internal	FTLLPGQGA/FTLLPGQGA	DR1/DR11	HB
P14384	Carboxypeptidase M	20	M	Internal	FQYLAHTYA/FQYLAHTYA	DR1/DR11	HB
P15104	Glutamine synthetase	26	C	C-ter	ALIRTCLLN	DR1	HB
P15144	Aminopeptidase N	15	M	Internal	FNLASAHKV	DR1	HB
P15144	Aminopeptidase N	13	M	Internal	FKQGLASYL	DR1	HB
P15144	Aminopeptidase N	15	M	Internal	LIQAVTRRF	DR1	HB
P15144	Aminopeptidase N	14	M	Internal	WILNRYLSY	DR1	HB
P15144	Aminopeptidase N	16	M	Internal	FNLASAHKV	DR1	HB
P15144	Aminopeptidase N	19	M	Internal	VVHLKGSLV/YLVVHLKGS	DR1/DR11	HB
P15586	N-acetylglucosamine-6-sulfatase	14	Lis/End	Internal	FFMMIATPA/FFMMIATPA	DR1/DR11	HB
P15586	N-acetylglucosamine-6-sulfatase	15	Lis/End	Internal	FFMMIATPA/FFMMIATPA	DR1/DR11	HB
P16619	C-C motif chemokine 3-like 1	14	EM	C-ter	FLTKRGRQV	DR1	HB
P18859	ATP synthase-coupling factor 6, mitochondrial	11	Mit	C-ter	FEVIEKPQA/FEVIEKPQA	DR1/DR11	HB
P20039	HLA class II histocompatibility antigen, DP alpha 1 chain	16	M	Internal	YFYNQEEYV	DR1	IB
P20039	HLA class II histocompatibility antigen, DP alpha 1 chain	15	M	Internal	YFYNQEEYV	DR1	IB
P20701	Integrin alpha-L	16	M	Internal	IRYIIGIGK	DR1	HB
P22897	Macrophage mannose receptor 1	14	M	Internal	LISLDKKFA	DR1	HB
P22897	Macrophage mannose receptor 1	17	M	Internal	WRLITASGS	DR1	HB
P22897	Macrophage mannose receptor 1	14	M	Internal	FAWMDGSKV	DR1	HB
P22897	Macrophage mannose receptor 1	15	M	Internal	FYSNKCFKI	DR1	HB
P22897	Macrophage mannose receptor 1	16	M	Internal	LISLDKKFA	DR1	HB
P22897	Macrophage mannose receptor 1	14	M	Internal	WRLITASGS	DR1	HB
P22897	Macrophage mannose receptor 1	18	M	Internal	LNWLPGSPS/FRYLNWLPG	DR1/DR11	HB
P25774	Cathepsin S	13	Lis/End	Internal	LVSLSAQNL	DR1	HB
P25774	Cathepsin S	16	Lis/End	Internal	LVSLSAQNL	DR1	HB
P25774	Cathepsin S	17	Lis/End	Internal	LVSLSAQNL	DR1	HB
P25774	Cathepsin S	14	Lis/End	Internal	LVSLSAQNL	DR1	HB
P25774	Cathepsin S	15	Lis/End	Internal	LVSLSAQNL	DR1	HB
P35268	60S ribosomal protein L22	23	C	N-ter	NA	NA	NA
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	12	Lis/End	Internal	MFFALGPVA/FFALGPVAS	DR1/DR11	HB
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	MFFALGPVA/FFALGPVAS	DR1/DR11	HB
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	MFFALGPVA/FFALGPVAS	DR1/DR11	HB
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	YILCLNRIP	DR11	IB
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	YILCLNRIP	DR11	IB
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	YILCLNRIP	DR11	IB

P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	YILCLNRIP	DR11	IB
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	YILCLNRIP	DR11	IB
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	16	Lis/End	Internal	YILCLNRIP	DR11	IB
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	YILCLNRIP	DR11	IB
P47897	Glutamine--tRNA ligase	23	C	C-ter	LVFNRTVTL	DR1	HB
P48723	Heat shock 70 kDa protein 13	17	Lis/End	Internal	AKRFIGKIF	DR1	HB
P49591	Serine--tRNA ligase, cytoplasmic	14	C	N-ter	VLDLDLFRV	DR1	HB
P50897	Palmitoyl-protein thioesterase 1	16	Lis/End	Internal	FLRAVAQRC	DR1	HB
P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	22	Mit	C-ter	NA	NA	NA
P60520	Gamma-aminobutyric acid receptor-associated protein-like 2	16	ER/G	Internal	FMWIIRKRI/FMWIIRKRI	DR1/DR11	HB
P61247	40S ribosomal protein S3a	10	C	C-ter	NA	NA	NA
P62158	Calmodulin	17	C	C-ter	VNYEEFVQM	DR1	LB
P62805	Histone H4	10	N	Internal	NA	NA	NA
P63220	40S ribosomal protein S21	17	C	C-ter	LRLAKADGI	DR1	HB
P68366	Tubulin alpha-4A chain	16	C	Internal	FDLMYAKRA/FDLMYAKRA	DR1/DR11	HB
Q00722	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2	17	C	Internal	NA	NA	NA
Q07954	Prolow-density lipoprotein receptor-related protein 1	18	M	Internal	YVILKSEPV	DR1	HB
Q07954	Prolow-density lipoprotein receptor-related protein 1	17	M	Internal	YVILKSEPV	DR1	HB
Q13162	Peroxiredoxin-4	12	C	C-ter	NA	NA	NA
Q13349	Integrin alpha-D	16	M	Internal	YSQLPGQEA/YSQLPGQEA	DR1/DR11	HB
Q13418	Integrin-linked protein kinase	20	M	C-ter	FDMIVPILE	DR1	HB
Q13443	Disintegrin and metalloproteinase domain-containing protein 9	13	M	Internal	YEIITPWRL	DR1	HB
Q13443	Disintegrin and metalloproteinase domain-containing protein 9	15	M	Internal	YEIITPWRL	DR1	HB
Q14956	Transmembrane glycoprotein NMB	17	M	Internal	YGHFQATIT	DR1	HB
Q14956	Transmembrane glycoprotein NMB	26	M	Internal	YVVTDQIPV	DR1	HB
Q15084	Protein disulfide-isomerase A6	17	ER/G	C-ter	NA	NA	NA
Q15084	Protein disulfide-isomerase A6	24	ER/G	C-ter	NA	NA	NA
Q15084	Protein disulfide-isomerase A6	14	ER/G	C-ter	NA	NA	NA
Q15582	Transforming growth factor-beta-induced protein ig-h3	16	EM	Internal	FETLRAAVA/FETLRAAVA	DR1/DR11	HB
Q15843	NEDD8	14	N	C-ter	YKILGGSVL	DR1	HB
Q16572	Vesicular acetylcholine transporter	18	M	Internal	VIGASSCIV	DR1	HB
Q4G0N8	Sodium/hydrogen exchanger 10	18	M	Internal	LYILEALLK/FLTLYILEA	DR1/DR11	HB
Q5TAP6	U3 small nucleolar RNA-associated protein 14 homolog C	23	N	Internal	NA	NA	NA
Q5VVM6	Coiled-coil domain-containing protein 30	12	EM	N-ter	NA	NA	NA
Q6PI73	Leukocyte immunoglobulin-like receptor subfamily A member 6	15	M	Internal	LLTLQGPVL	DR1	HB
Q86WG3	Caytaxin	16	M	Internal	LHMIRPYMK	DR1	HB
Q8IWU5	Extracellular sulfatase Sulf-2	16	ER/G	Internal	YQLMNAVNT	DR1	HB
Q8N370	Large neutral amino acids transporter small subunit 4	17	M	Internal	FGSLTGLQS/FGSLTGLQS	DR1/DR11	HB
Q96KK5	Histone H2A type 1-H	17	N	Internal	ILELAGNAA	DR1	HB
Q96KK5	Histone H2A type 1-H	18	N	Internal	ILELAGNAA	DR1	HB
Q96KK5	Histone H2A type 1-H	16	N	Internal	ILELAGNAA	DR1	HB
Q96KK5	Histone H2A type 1-H	17	N	Internal	ILELAGNAA	DR1	HB
Q96KK5	Histone H2A type 1-H	19	N	Internal	ILELAGNAA	DR1	HB
Q9H2Y9	Solute carrier organic anion transporter family member 5A1	25	M	Internal	FITACAQPS/FITACAQPS	DR1/DR11	HB
Q9H3G5	Probable serine carboxypeptidase CPVL	15	Lis/End	Internal	YVPAIAHLI	DR1	HB
Q9H3G5	Probable serine carboxypeptidase CPVL	12	Lis/End	Internal	YVPAIAHLI	DR1	HB
Q9H3G5	Probable serine carboxypeptidase CPVL	13	Lis/End	Internal	YVPAIAHLI	DR1	HB
Q9NX14	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	29	Mit	Internal	APSAVAGKR	DR1	HB
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	18	N	C-ter	VKTKFGYHI	DR1	HB

Donor F (DRB1*0901, DRB1*1001)

Sequence	Uniprot AC	Protein name	Length	Cellular Location (a)	Location in Sequence (b)	Binding Core/s (c)	Allele/s (d)	Theoretical Affinity (e)
DVPKWISIMTERSVPH	A6NMY6	Putative annexin A2-like protein	16	EM	Internal	ISIMTERSV	DR9	IB
TDVPKWISIMTERSVPH	A6NMY6	Putative annexin A2-like protein	17	EM	Internal	ISIMTERSV	DR9	IB
VPKWISIMTERSVPH	A6NMY6	Putative annexin A2-like protein	15	EM	Internal	ISIMTERSV	DR9	IB
PSGWWKGRLHGQEGLFPGNYVEKI	O00160	Unconventional myosin-If	24	C	C-ter	LFPGNYVEK/FPGNYVEKI	DR9/DR10	IB
FDKFANIVPFDSWDQ	O00220	Tumor necrosis factor receptor superfamily member 10A	15	M	Internal	FANIVPFDS	DR10	HB
IDNGIFVQLVQANSPA	O00560	Syntenin-1	16	M	Internal	VQLVQANSP/FVQLVQANS	DR9/DR10	HB
NGIFVQLVQANSPA	O00560	Syntenin-1	14	M	Internal	VQLVQANSP/FVQLVQANS	DR9/DR10	HB
VDKVIQAQTAFSANPA	O00560	Syntenin-1	16	M	N-ter	IQAQTAFSA/IQAQTAFSA	DR9/DR10	IB
TGKNFVSQIVAENLHPK	O14657	Torsin-1B	17	ER/G	Internal	FVSQIVAEN	DR10	HB
EYDSILVEINKR	O15031	Plexin-B2	12	M	Internal	YDSILVEIN	DR10	HB
SEYDSILVEINKR	O15031	Plexin-B2	13	M	Internal	YDSILVEIN	DR10	HB
SSEYDSILVEINKR	O15031	Plexin-B2	14	M	Internal	YDSILVEIN	DR10	HB
SSEYDSILVEINKRVK	O15031	Plexin-B2	16	M	Internal	YDSILVEIN	DR10	HB
TPDGTSSEYDSILVEINKRVK	O15031	Plexin-B2	21	M	Internal	YDSILVEIN	DR10	HB
TSSEYDSILVEINKRVK	O15031	Plexin-B2	17	M	Internal	YDSILVEIN	DR10	HB
IPKTLEILDVSNNNL	O60603	Toll-like receptor 2	15	M	Internal	ILDVSNNNL	DR9	HB
IPKTLEILDVSNNNLN	O60603	Toll-like receptor 2	16	M	Internal	ILDVSNNNL	DR9	HB
IPKTLEILDVSNNNLNL	O60603	Toll-like receptor 2	17	M	Internal	ILDVSNNNL	DR9	HB
NEFSILKSPGSVVF	O75787	Renin receptor	14	M	N-ter	ILKSPGSVV/FSILKSPGS	DR9/DR10	HB
FNKPFVFLMIEQNTK	P01009	Alpha-1-antitrypsin	15	ER/G	C-ter	FVFLMIEQN	DR10	HB
SPMYSIITPNILR	P01024	Complement C3	13	EM	N-ter	YSIITPNIL/YSIITPNIL	DR9/DR10	IB
ELWWQAERASSSKSW	P01730	T-cell surface glycoprotein CD4	15	M	Internal	WWQAERASS/LWWQAERAS	DR9/DR10	IB
IQFHWKNSNQIKI	P01730	T-cell surface glycoprotein CD4	13	M	Internal	WKNSNQIKI	DR9	HB
GELWWQAERASSSKSW	P01730	T-cell surface glycoprotein CD4	16	M	Internal	WWQAERASS/LWWQAERAS	DR9/DR10	IB
DGKDYLALNEDLR	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	13	M	Internal	YLALNEDLR/YLALNEDLR	DR9/DR10	IB
VDDTQFVRFDSDAASPR	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	17	M	Internal	FVRFDSDAA	DR9	IB
YDGKDYIALNEDLRSW	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	16	M	Internal	YIALNEDLR	DR10	IB
HYLPFLPSTEDVYD	P01903	HLA class II histocompatibility antigen, DR alpha chain	14	M	Internal	FLPSTEDVY/LPFLPSTED	DR9/DR10	HB
AQGALANIAVDKANLE	P01903	HLA class II histocompatibility antigen, DR alpha chain	16	M	Internal	IAVDKANLE	DR10	HB
EFGRFASFEAQGALANIAVDK	P01903	HLA class II histocompatibility antigen, DR alpha chain	21	M	Internal	FEAQGALAN	DR10	HB
FASFEAQGALANIA	P01903	HLA class II histocompatibility antigen, DR alpha chain	14	M	Internal	FEAQGALAN	DR10	HB
RFASFEAQGALANIA	P01903	HLA class II histocompatibility antigen, DR alpha chain	15	M	Internal	FEAQGALAN	DR10	HB
RFASFEAQGALANIAVD	P01903	HLA class II histocompatibility antigen, DR alpha chain	17	M	Internal	FEAQGALAN	DR10	HB
RFASFEAQGALANIAVDK	P01903	HLA class II histocompatibility antigen, DR alpha chain	18	M	Internal	FEAQGALAN	DR10	HB
AQGALANIAVDKANLEI	P01903	HLA class II histocompatibility antigen, DR alpha chain	17	M	Internal	IAVDKANLE	DR10	HB
QGALANIAVDKANLE	P01903	HLA class II histocompatibility antigen, DR alpha chain	15	M	Internal	IAVDKANLE	DR10	HB
LPFLPSTEDVYD	P01903	HLA class II histocompatibility antigen, DR alpha chain	12	M	Internal	FLPSTEDVY/LPFLPSTED	DR9/DR10	HB
AFAQYLQQCPFEDHVK	P02768	Serum albumin	16	EM	Internal	YLQQCPFED	DR10	HB
NRRPCFSALEVDETYVPK	P02768	Serum albumin	18	EM	Internal	FSALEVDET/FSALEVDET	DR9/DR10	IB
FAQYLQQCPFEDHVK	P02768	Serum albumin	15	EM	Internal	YLQQCPFED	DR10	HB
RRPCFSALEVDETYVPK	P02768	Serum albumin	17	EM	Internal	FSALEVDET/FSALEVDET	DR9/DR10	IB
RVEYHFLSPYVSPK	P02786	Transferrin receptor protein 1	14	M	Internal	YHFLSPYVS	DR10	HB
KEIKILNIFGVIK	P02786	Transferrin receptor protein 1	13	M	Internal	IKILNIFGV	DR10	HB
RVEYHFLSPYVSPKE	P02786	Transferrin receptor protein 1	15	M	Internal	YHFLSPYVS	DR10	HB
VEYHFLSPYVSPK	P02786	Transferrin receptor protein 1	13	M	Internal	YHFLSPYVS	DR10	HB

VEYHFLSPYVSPKE	P02786	Transferrin receptor protein 1	14	M	Internal	YHFLSPYVS	DR10	HB
YLGYEYVTAIRNLRE	P02787	Serotransferrin	15	EM	Internal	YVTAIRNLR/YEYVTAIRN	DR9/DR10	HB
YLGYEYVTAIRNLREG	P02787	Serotransferrin	16	EM	Internal	YVTAIRNLR/YEYVTAIRN	DR9/DR10	HB
LEKKLNQALLDLHA	P02792	Ferritin light chain	14	C	Internal	LNQALLDLH	DR9	HB
KKLNQALLDLHA	P02792	Ferritin light chain	12	C	Internal	LNQALLDLH	DR9	HB
VGDEDFVHLRVFQSLPH	P04080	Cystatin-B	17	C	C-ter	FVHLRVFQS	DR10	HB
LRFFSLLSGSLNSHG	P04114	Apolipoprotein B-100	15	C	Internal	LSGSLNSHG/FSLLSGSLN	DR9/DR10	HB
STPEFTILNTFHIPS	P04114	Apolipoprotein B-100	15	C	Internal	FTILNTFHI	DR10	HB
DLHDLKIAIANIIDE	P04114	Apolipoprotein B-100	15	C	Internal	LKIAIANII	DR9	HB
SLRFFSLLSGSLNSHG	P04114	Apolipoprotein B-100	16	C	Internal	LSGSLNSHG/FSLLSGSLN	DR9/DR10	HB
LPYDYGALEPHINAQI	P04179	Superoxide dismutase [Mn], mitochondrial	16	Mit	Internal	YGALEPHIN	DR10	HB
LPYDYGALEPHINA	P04179	Superoxide dismutase [Mn], mitochondrial	14	Mit	Internal	YGALEPHIN	DR10	HB
ENGNYLPLQCYGSIG	P04233	HLA class II histocompatibility antigen gamma chain	15	ER/G	Internal	YLPLQCYGS	DR10	HB
ETIDWKVFESWMHH	P04233	HLA class II histocompatibility antigen gamma chain	14	ER/G	Internal	IDWKVFESW	DR9	IB
ATPLLMQALPMGALPQ	P04233	HLA class II histocompatibility antigen gamma chain	16	ER/G	Internal	LMQALPMGA	DR9	HB
GNYLPLQCYGSIG	P04233	HLA class II histocompatibility antigen gamma chain	13	ER/G	Internal	YLPLQCYGS	DR10	HB
MATPLLMQALPMGALPQ	P04233	HLA class II histocompatibility antigen gamma chain	17	ER/G	Internal	LMQALPMGA	DR9	HB
MATPLLMQALPMGALPQG	P04233	HLA class II histocompatibility antigen gamma chain	18	ER/G	Internal	LMQALPMGA	DR9	HB
IDWKVFESWMHH	P04233	HLA class II histocompatibility antigen gamma chain	12	ER/G	Internal	WKVFESWMH	DR9	IB
LPKPPKPVSKMRMATPLLMQALPM	P04233	HLA class II histocompatibility antigen gamma chain	24	ER/G	Internal	VSKMRMATP/LPKPPKPVS	DR9/DR10	IB
KLVFFAEDVGSNKG	P05067	Amyloid beta A4 protein	14	M	Internal	VFFAEDVGS	DR9	HB
DLSYSMLDDLRNVK	P05107	Integrin beta-2	14	M	Internal	LSYSMLDDL/YSMLDDLRN	DR9/DR10	HB
DLSYSMLDDLRNVKK	P05107	Integrin beta-2	15	M	Internal	LSYSMLDDL/YSMLDDLRN	DR9/DR10	HB
LSYSMLDDLRNVK	P05107	Integrin beta-2	13	M	Internal	LSYSMLDDL/YSMLDDLRN	DR9/DR10	HB
LSYSMLDDLRNVKK	P05107	Integrin beta-2	14	M	Internal	LSYSMLDDL/YSMLDDLRN	DR9/DR10	HB
LSYSMLDDLRNVKKLG	P05107	Integrin beta-2	16	M	Internal	LSYSMLDDL/YSMLDDLRN	DR9/DR10	HB
MDLSYSMLDDLRNVKK	P05107	Integrin beta-2	16	M	Internal	LSYSMLDDL/YSMLDDLRN	DR9/DR10	HB
DNGRALLPFDNLHDDP	P05164	Myeloperoxidase	16	Lis/End	Internal	LLPFDNLHD	DR10	IB
FPVALARAVSNEIVR	P05164	Myeloperoxidase	15	Lis/End	Internal	LARAVSNEI	DR9	HB
IRNQINALTSFVDAS	P05164	Myeloperoxidase	15	Lis/End	Internal	INALTSFVD/INALTSFVD	DR9/DR10	IB
VSNEIVRFPTDQLTPD	P05164	Myeloperoxidase	16	Lis/End	Internal	IVRFPTDQL/FPTDQLTPD	DR9/DR10	IB
VEKFDLVPVPTNLYG	P06396	Gelsolin	15	C	Internal	FDLVPVPTN	DR10	HB
AEQQRLKSQDLELSWNLNG	P06734	Low affinity immunoglobulin epsilon Fc receptor	19	M	Internal	LELSWNLNG	DR9	HB
IPVIEPSVPELVVK	P07333	Macrophage colony-stimulating factor 1 receptor	14	M	N-ter	IEPSVPELV	DR9	HB
IPVIEPSVPELVVKP	P07333	Macrophage colony-stimulating factor 1 receptor	15	M	N-ter	IEPSVPELV	DR9	HB
IPVIEPSVPELVVKPG	P07333	Macrophage colony-stimulating factor 1 receptor	16	M	N-ter	IEPSVPELV	DR9	HB
STFVQALVEHVKE	P07602	Prosaposin	13	Lis/End	N-ter	FVQALVEHV	DR9	HB
STFVQALVEHVKEE	P07602	Prosaposin	14	Lis/End	N-ter	FVQALVEHV	DR9	HB
EPTRQVFAVQRIFENGYD	P08246	Neutrophil elastase	18	M	Internal	VFAVQRIFE	DR9	HB
EPTRQVFAVQRIFENGYDP	P08246	Neutrophil elastase	19	M	Internal	VFAVQRIFE	DR9	HB
ASPEYVNLPINGNGKQ	P09211	Glutathione S-transferase P	16	C	C-ter	YVNLPINGN	DR10	HB
GNRDQVLLAARELRVPEA	P10074	Zinc finger and BTB domain-containing protein 48	18	N	Internal	LLAARELRV	DR9	HB
EKGPMFELLPGESNKIPR	P10124	Serglycin	18	C	Internal	FELLPGESN	DR10	HB
GPMFELLPGESNK	P10124	Serglycin	13	C	Internal	FELLPGESN	DR10	HB
GPMFELLPGESNKIPR	P10124	Serglycin	16	C	Internal	FELLPGESN	DR10	HB
KGPMFELLPGESNKIPR	P10124	Serglycin	17	C	Internal	FELLPGESN	DR10	HB
PKENWVQRVVEKFLKRAENS	P10145	Interleukin-8	20	EM	C-ter	VQRVVEKFL	DR9	HB
HPKFIKELRVIESGPH	P10145	Interleukin-8	16	EM	Internal	LRVIESGPH/IKELRVIES	DR9/DR10	IB
KPFHPKFIKELRVIESGPH	P10145	Interleukin-8	19	EM	Internal	LRVIESGPH/IKELRVIES	DR9/DR10	IB
GILNVSAVDKSTG	P11142	Heat shock cognate 71 kDa protein	13	C	Internal	NA	NA	NA

KNAFKILVVITDG	P11215	Integrin alpha-M	13	M	Internal	FKILVVITD	DR10	HB
VNNFEALKTIQNQ	P11215	Integrin alpha-M	13	M	Internal	FEALKTIQN	DR10	HB
YLGYAAAIILRNRVQ	P11215	Integrin alpha-M	15	M	Internal	YAAAIILRN/YAAAIILRN	DR9/DR10	HB
VNNFEALKTIQNQL	P11215	Integrin alpha-M	14	M	Internal	FEALKTIQN	DR10	HB
VNNFEALKTIQNQLR	P11215	Integrin alpha-M	15	M	Internal	FEALKTIQN	DR10	HB
QVNNFEALKTIQNQLR	P11215	Integrin alpha-M	16	M	Internal	FEALKTIQN	DR10	HB
RKNAFKILVVITDGE	P11215	Integrin alpha-M	15	M	Internal	FKILVVITD	DR10	HB
DAYLGYAAAIILRNRVQ	P11215	Integrin alpha-M	17	M	Internal	YLGYAAAII	DR10	HB
SDMNDAYLGYAAAIILRNRVQ	P11215	Integrin alpha-M	21	M	Internal	YLGYAAAII	DR10	HB
YLGYAAAIILRNRV	P11215	Integrin alpha-M	14	M	Internal	YLGYAAAII	DR10	HB
SSRFFLQGIQLNTI	P11279	Lysosome-associated membrane glycoprotein 1	14	Lis/End	Internal	FLQGIQLNT	DR10	HB
ENIYDMVVPFPDKP	P12821	Angiotensin-converting enzyme	14	M	Internal	YDMVVPFPD/YDMVVPFPD	DR9/DR10	HB
WENIYDMVVPFPDKP	P12821	Angiotensin-converting enzyme	15	M	Internal	YDMVVPFPD/YDMVVPFPD	DR9/DR10	HB
VDDTQFVRFDNDAASPR	P13747	HLA class I histocompatibility antigen, alpha chain E	17	M	Internal	FVRFDNDAA/FDNDAASPR	DR9/DR10	IB
DVGEYRAVTELGRPV	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	15	M	Internal	YRAVTELGR/YRAVTELGR	DR9/DR10	HB
ASDYLELDTIKNLVK	P14625	Endoplasmin	15	ER/G	Internal	YLELDTIKN	DR10	HB
EKRFEIIKEAYMRSL	P14735	Insulin-degrading enzyme	15	C	Internal	IKEAYMRSL/FEIIKEAYM	DR9/DR10	HB
PFSVTEALIRTCLLNETGDEPFQYKN	P15104	Glutamine synthetase	26	C	C-ter	VTEALIRTC	DR9	HB
AAPQYQKAFQNVFAPR	P15586	N-acetylglucosamine-6-sulfatase	16	Lis/End	Internal	YQKAFQNVF	DR9	HB
GIPVYRFVLPSKAFASPV	P16671	Platelet glycoprotein 4	18	M	Internal	YRFVLPSKA/YRFVLPSKA	DR9/DR10	HB
PKFEVIEKPQA	P18859	ATP synthase-coupling factor 6, mitochondrial	11	Mit	C-ter	FEVIEKPQA/FEVIEKPQA	DR9/DR10	IB
ANIAILNNNLNTL	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	13	M	Internal	IAILNNNLN	DR10	HB
HYLTFVPSAEDFYD	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	14	M	Internal	YLTFVPSAE	DR10	IB
GGLANIAILNNNLNTLIQ	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	18	M	Internal	IAILNNNLN	DR10	HB
GLANIAILNNNLNTL	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	15	M	Internal	IAILNNNLN	DR10	HB
GLANIAILNNNLNTLIQ	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	17	M	Internal	IAILNNNLN	DR10	HB
LANIAILNNNLNTLIQ	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	16	M	Internal	IAILNNNLN	DR10	HB
LANIAILNNNLNTL	P20036	HLA class II histocompatibility antigen, DP alpha 1 chain	14	M	Internal	IAILNNNLN	DR10	HB
NSWKELNDIASKPS	P20702	Integrin alpha-X	14	M	Internal	LNDIASKPS/LNDIASKPS	DR9/DR10	IB
EEQQTIWRLITASGSYH	P22897	Macrophage mannose receptor 1	17	M	Internal	LITASGSYH	DR9	HB
SAYFIGLLISLDKK	P22897	Macrophage mannose receptor 1	14	M	Internal	IGLLISLDK/FIGLLISLD	DR9/DR10	IB
INNKEEQQTIWRLITASGSYH	P22897	Macrophage mannose receptor 1	21	M	Internal	LITASGSYH	DR9	HB
QQTIWRLITASGSYH	P22897	Macrophage mannose receptor 1	15	M	Internal	LITASGSYH	DR9	HB
QTIWRLITASGSYH	P22897	Macrophage mannose receptor 1	14	M	Internal	LITASGSYH	DR9	HB
QTIWRLITASGSYHK	P22897	Macrophage mannose receptor 1	15	M	Internal	LITASGSYH	DR9	HB
SINNKEEQQTIWRLITASGSYH	P22897	Macrophage mannose receptor 1	22	M	Internal	LITASGSYH	DR9	HB
TIWRLITASGSYH	P22897	Macrophage mannose receptor 1	13	M	Internal	LITASGSYH	DR9	HB
QTIWRLITASGSYHKL	P22897	Macrophage mannose receptor 1	16	M	Internal	NA	NA	NA
EPTQQHFSVAQVFLNNYD	P24158	Myeloblastin	18	C	Internal	FSVAQVFLN	DR10	HB
QQHFSVAQVFLNNYD	P24158	Myeloblastin	15	C	Internal	FSVAQVFLN	DR10	HB
DEAAFQKLMSNLDSN	P26447	Protein S100-A4	15	EM	Internal	FQKLMSNLD	DR10	HB
NQQFVHFTQLDLSYLQ	P26572	Ipha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	16	ER/G	Internal	FTQLDLSYL	DR10	HB
GPEVVHPLVPLDNHIP	P31431	Syndecan-4	16	M	Internal	VVHPLVPLD/LVPLDNHIP	DR9/DR10	IB
GPEVVHPLVPLDNHIPE	P31431	Syndecan-4	17	M	Internal	VVHPLVPLD/LVPLDNHIP	DR9/DR10	IB
IGPEVVHPLVPLDNHIP	P31431	Syndecan-4	17	M	Internal	VVHPLVPLD/LVPLDNHIP	DR9/DR10	IB
IGPEVVHPLVPLDNHIPE	P31431	Syndecan-4	18	M	Internal	VVHPLVPLD/LVPLDNHIP	DR9/DR10	IB
IGPEVVHPLVPLDNHIPER	P31431	Syndecan-4	19	M	Internal	VVHPLVPLD/LVPLDNHIP	DR9/DR10	IB
APVKKLVVKGGKKKKQVLKFTLD	P35268	60S ribosomal protein L22	23	C	N-ter	LVVKGGKKK	DR10	IB
VQNMLHWSQAVKF	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	LHWSQAVKF	DR9	HB
DEFWAFSYDEMAK	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	WAFSYDEMA	DR9	HB

IKMFFALGPVAS	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	12	Lis/End	Internal	FFALGPVAS	DR10	HB
IKMFFALGPVASVA	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	FFALGPVAS	DR10	HB
RIKMFFALGPVAS	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	FFALGPVAS	DR10	HB
RIKMFFALGPVASVA	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	FFALGPVAS	DR10	HB
VQNMLHWSQAVKFQ	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	LHWSQAVKF	DR9	HB
EFWAFSYDEMAK	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	12	Lis/End	Internal	WAFSYDEMA	DR9	HB
IKMFFALGPVA	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	11	Lis/End	Internal	IKMFFALGP/IKMFFALGP	DR9/DR10	IB
DPNLSFDAVTTVGNKI	P39900	Macrophage metalloelastase	16	EM	Internal	FDAVTTVGN	DR9	HB
DDKYWLISNLRPEPNYPK	P39900	Macrophage metalloelastase	18	EM	Internal	WLISNLRPE/ISNLRPEPN	DR9/DR10	HB
DPNLSFDAVTTVGNKIF	P39900	Macrophage metalloelastase	17	EM	Internal	FDAVTTVGN	DR9	HB
DDKYWLISNLRPEPNYPKSI	P39900	Macrophage metalloelastase	20	EM	Internal	WLISNLRPE/ISNLRPEPN	DR9/DR10	HB
WLISNLRPEPNYPK	P39900	Macrophage metalloelastase	14	EM	Internal	WLISNLRPE/ISNLRPEPN	DR9/DR10	HB
YWLISNLRPEPNYPK	P39900	Macrophage metalloelastase	15	EM	Internal	WLISNLRPE/ISNLRPEPN	DR9/DR10	HB
KYWLISNLRPEPNYPK	P39900	Macrophage metalloelastase	16	EM	Internal	WLISNLRPE/ISNLRPEPN	DR9/DR10	HB
MTKLDFNTDEEKKMVEEV	P42285	Superkiller viralicidic activity 2-like 2	18	N	Internal	LDFNTDEEK/FNTDEEKKM	DR9/DR10	IB
VLDLDLFRVDKGGD	P49591	Serine--tRNA ligase, cytoplasmic	14	C	N-ter	LFRVDKGGD	DR9	HB
GPRPEEYEFLTPVEEAP	P52566	Rho GDP-dissociation inhibitor 2	17	C	Internal	YEFLTPVEE	DR10	HB
GPRPEEYEFLTPVEEAPK	P52566	Rho GDP-dissociation inhibitor 2	18	C	Internal	YEFLTPVEE	DR10	HB
KVVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	15	Lis/End	Internal	LQKLDTAYD/LQKLDTAYD	DR9/DR10	IB
NVHGINFVSPVRNQAS	P53634	Dipeptidyl peptidase 1	16	Lis/End	Internal	INFVSPVRN/INFVSPVRN	DR9/DR10	HB
KKVVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	16	Lis/End	Internal	LQKLDTAYD/LQKLDTAYD	DR9/DR10	IB
VVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	14	Lis/End	Internal	LQKLDTAYD/LQKLDTAYD	DR9/DR10	IB
IKGKINSITVDNCKK	Q01518	Adenylyl cyclase-associated protein 1	15	M	Internal	INSITVDNC	DR10	IB
LPGFEGSTCERNIDD	Q04721	Neurogenic locus notch homolog protein 2	15	M	Internal	FEGSTCERN/FEGSTCERN	DR9/DR10	HB
GSHRYVILKSEPVHPF	Q07954	Prolow-density lipoprotein receptor-related protein 1	16	M	Internal	ILKSEPVHP/YVILKSEPV	DR9/DR10	HB
DPFKPFIIFSNRHE	Q07954	Prolow-density lipoprotein receptor-related protein 1	14	M	Internal	FIIFSNRHE/FKPFIIFSN	DR9/DR10	IB
GSHRYVILKSEPVHPFG	Q07954	Prolow-density lipoprotein receptor-related protein 1	17	M	Internal	ILKSEPVHP/YVILKSEPV	DR9/DR10	HB
SHRYVILKSEPVHPF	Q07954	Prolow-density lipoprotein receptor-related protein 1	15	M	Internal	ILKSEPVHP/YVILKSEPV	DR9/DR10	HB
EIPYYAEVVATNNPD	Q08ET2	Sialic acid-binding Ig-like lectin 14	15	M	Internal	YAEVVATNN/YAEVVATNN	DR9/DR10	HB
EIPYYAEVVATNNPDR	Q08ET2	Sialic acid-binding Ig-like lectin 14	16	M	Internal	YAEVVATNN/YAEVVATNN	DR9/DR10	HB
IPYYAEVVATNNPD	Q08ET2	Sialic acid-binding Ig-like lectin 14	14	M	Internal	YAEVVATNN/YAEVVATNN	DR9/DR10	HB
KVEELEGEITTLNHK	Q10589	Bone marrow stromal antigen 2	15	M	Internal	LEGEITTLN	DR10	IB
PSGWWTGRLRGKQGLFPNNYVTKI	Q12965	Unconventional myosin-Ie	24	C	C-ter	FPNNYVTKI	DR10	IB
KLRVFENIVAVLNKEVE	Q13077	TNF receptor-associated factor 1	17	C	Internal	FENIVAVLN	DR10	HB
LRVFENIVAVLNKE	Q13077	TNF receptor-associated factor 1	14	C	Internal	FENIVAVLN	DR10	HB
PAKRPKFDMIVPILEKMQDK	Q13418	Integrin-linked protein kinase	20	M	C-ter	FDMIVPILE	DR10	HB
GDNRFSMLVAAIQS	Q15582	Transforming growth factor-beta-induced protein ig-h3	14	EM	Internal	FSMLVAAIQ	DR10	HB
EAGRALAGQAAGLGLVGKRLSLARNVL	Q15722	Leukotriene B4 receptor 1	27	M	Internal	LGLVGKRLS	DR9	HB
FQTLVMLETVPQSG	Q30167	HLA class II histocompatibility antigen, DRB1-10 beta chain	14	M	Internal	FQTLVMLET	DR10	IB
GLSLIGYLITKKNVFIGTGHLLAKIL	Q5S007	Leucine-rich repeat serine/threonine-protein kinase 2	26	Mit	Internal	FIGTGHLLA/YLITKKNVF	DR9/DR10	IB
KQVHALSPEENVIIK	Q6UX65	DNA damage-regulated autophagy modulator protein 2	15	C	Internal	NA	NA	NA
LLLLALLVLTCLVLALLAVYLSVL	Q8N112	Leucine-rich single-pass membrane protein 2	24	M	Internal	VLALLAVYL/LALLAVYLS	DR9/DR10	IB
MPLEFKTLNVLHNRG	Q92187	CMP-N-acetylneuraminate-poly-alpha-2,8-sialyltransferase	15	ER/G	C-ter	FKTLNVLHN	DR10	HB
PLENQPLPLGR	Q96QH2	PML-RARA-regulated adapter molecule 1	11	M	C-ter	LENQPLPLG	DR9	IB
GELILEELEVFKNHAPIT	Q99985	Semaphorin-3C	18	EM	Internal	LEELEVFKN	DR10	HB
DGKRIQYQLVDISQDN	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	16	C	Internal	YQLVDISQD	DR9	HB
KRIQYQLVDISQDN	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	14	C	Internal	YQLVDISQD	DR9	HB
KYVPAIAHLIHS	Q9H3G5	Probable serine carboxypeptidase CPVL	12	Lis/End	Internal	YVPAIAHLI	DR9	HB
GSSFVVARYFPAGNVVNEGFFEENVLPPKK	Q9H4G4	Golgi-associated plant pathogenesis-related protein 1	30	ER/G	C-ter	VARYFPAGN/YFPAGNVVN	DR9/DR10	IB

KGLQIDVGCPVKVQLRSGEE	Q9NQC7	Ubiquitin carboxyl-terminal hydrolase CYLD	20	C	Internal	IDVGCPVKV/IDVGCPVKV	DR9/DR10	IB
AGLLQFLRLDGFSVLMRAMQQQVQ	Q9NZL4	Hsp70-binding protein 1	24	C	Internal	LMRAMQQQV	DR9	HB
DLSVWDYAHQHGIPD	Q9UBR2	Cathepsin Z	15	Lis/End	Internal	WDYAHQHGI	DR9	HB
DLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	16	Lis/End	Internal	WDYAHQHGI	DR9	HB
DLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	17	Lis/End	Internal	WDYAHQHGI	DR9	HB
GGNDLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	19	Lis/End	Internal	WDYAHQHGI	DR9	HB
GGNDLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	20	Lis/End	Internal	WDYAHQHGI	DR9	HB
GNDLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	18	Lis/End	Internal	WDYAHQHGI	DR9	HB
GNDLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	19	Lis/End	Internal	WDYAHQHGI	DR9	HB
LSVWDYAHQHGIPD	Q9UBR2	Cathepsin Z	14	Lis/End	Internal	WDYAHQHGI	DR9	HB
LSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	15	Lis/End	Internal	WDYAHQHGI	DR9	HB
NDLSVWDYAHQHGIPD	Q9UBR2	Cathepsin Z	16	Lis/End	Internal	WDYAHQHGI	DR9	HB
NDLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	17	Lis/End	Internal	WDYAHQHGI	DR9	HB
NDLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	18	Lis/End	Internal	WDYAHQHGI	DR9	HB
SVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	14	Lis/End	Internal	WDYAHQHGI	DR9	HB
VWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	13	Lis/End	Internal	WDYAHQHGI	DR9	HB
VPVPEFADSDPANIVHD	Q9Y287	Integral membrane protein 2B	17	ER/G	Internal	FADSDPANI	DR9	HB
DIGTEMIITKAGRRMFPSVRVKVKGL	Q9Y458	T-box transcription factor TBX22	26	N	Internal	ITKAGRRMF/FPSVRVKVK	DR9/DR10	HB
VAAAATAGKEMDSNE	Q9Y467	Sal-like protein 2	15	N	Internal	VAAAATAGK	DR9	HB

Donor G (DRB1*0701, DRB1*1501, DRB5*0101)

Sequence	Uniprot AC	Protein name	Length	Cellular Location (a)	Location in Sequence (b)	Binding Core/s (c)	Allele/s (d)	Theoretical Affinity (e)
TPPSAYGSVKAYTNFDAERDA	A6NMY6	Putative annexin A2-like protein	21	EM	N-ter	VKAYTNFDA/VKAYTNFDA	DR7/DR15	HB
YGSVKAYTNFDAERD	A6NMY6	Putative annexin A2-like protein	15	EM	N-ter	VKAYTNFDA/VKAYTNFDA	DR7/DR15	HB
KNLLLPRGV	A9Z1Z3	Fer-1-like protein 4	9	M	Internal	NA	NA	NA
GNHQFAKYKSFKVADE	O00602	Ficolin-3	16	M	Internal	FAKYKSFKV/FAKYKSFKV	DR7/DR15	HB
HQFAKYKSFKVADE	O00602	Ficolin-1	14	M	Internal	FAKYKSFKV/FAKYKSFKV	DR7/DR15	HB
NHQFAKYKSFKVADE	O00602	Ficolin-2	15	M	Internal	FAKYKSFKV/FAKYKSFKV	DR7/DR15	HB
DVERDVFLYRAYLAQRK	O14579	Coatomer subunit epsilon	17	ER/G	Internal	VFLYRAYLA/LYRAYLAQR	DR15/DRB5	IB
RDVFLYRAYLAQR	O14579	Coatomer subunit epsilon	13	ER/G	Internal	VFLYRAYLA/LYRAYLAQR	DR15/DRB5	IB
SPERDVERDVFLYRAYLAQRK	O14579	Coatomer subunit epsilon	21	ER/G	Internal	VFLYRAYLA/LYRAYLAQR	DR15/DRB5	IB
VERDVFLYRAYLAQR	O14579	Coatomer subunit epsilon	15	ER/G	Internal	VFLYRAYLA/LYRAYLAQR	DR15/DRB5	IB
DTIHIWKTNSLPLR	O15031	Plexin-B2	14	M	Internal	IWKTNSLPL	DR7	HB
RVYGSFLVNPE	O15144	Actin-related protein 2/3 complex subunit 2	11	C	Internal	YGSFLVNPE	DR7	IB
AVPGALDYKSFSTALYGESDL	O43707	Alpha-actinin-4	21	C	C-ter	YKSFSTALY/YKSFSTALY/YKSFSTALY	DR7/DR15/DRB5	IB
YKSFSTALYGESDL	O43707	Alpha-actinin-4	14	C	C-ter	YKSFSTALY/YKSFSTALY/YKSFSTALY	DR7/DR15/DRB5	IB
AIDDIRISTDVPLE	O60462	Neuropilin-2	14	M	Internal	IRISTDVPL/IDDIRISTD	DR7/DR15	IB
NNRITYISNSDLQR	O60603	Toll-like receptor 2	14	M	Internal	ITYISNSDL	DR7	HB
SNNRITYISNSDLQR	O60603	Toll-like receptor 2	15	M	Internal	ITYISNSDL	DR7	HB
GNNFLYTNGKCVIL	O75083	WD repeat-containing protein 1	14	C	N-ter	FLYTNGKCV/FLYTNGKCV	DR7/DRB5	HB
PQGPSLEWLKKL	O95167	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	12	Mit	C-ter	NA	NA	NA
NVNIFKFIIPNVVK	P00338	L-lactate dehydrogenase A chain	14	C	Internal	FKFIIPNVV/VNIFKFIIP/FKFIIPNVV	DR7/DR15/DRB5	HB
NPVDILTYVAWKISGFPK	P00338	L-lactate dehydrogenase A chain	18	C	Internal	ILTYVAWKI	DR15	HB
VNIFKFIIPNVVK	P00338	L-lactate dehydrogenase A chain	13	C	Internal	FKFIIPNVV/VNIFKFIIP/FKFIIPNVV	DR7/DR15/DRB5	HB
EFLNVTSVHL	P00488	Coagulation factor XIII A chain	10	C	Internal	FLNVTSVHL	DR7	HB
INEQWLLTTAKNL	P00739	Haptoglobin-related protein	13	EM	Internal	WLLTTAKNL	DR7	HB
EQWLLTTAKNL	P00739	Haptoglobin-related protein	11	EM	Internal	WLLTTAKNL	DR7	HB
VGMLANFLGFRIYG	P01019	Angiotensinogen	14	EM	Internal	LANFLGFRI/LANFLGFRI	DR7/DR15	HB
KVDLSFSPSQSLPA	P01023	Alpha-2-macroglobulin	14	EM	Internal	LSFSPSQSL	DR7	HB
AENDVLHCVAFAVPK	P01023	Alpha-2-macroglobulin	15	EM	Internal	VLHCVAFAV/LHCVAFAVP	DR7/DRB5	IB
DMKGHFSISIPVK	P01023	Alpha-2-macroglobulin	13	EM	Internal	NA	NA	NA
VLPKFEVQVTVPKIIT	P01023	Alpha-2-macroglobulin	16	EM	Internal	FEVQVTVPK	DRB5	HB
KVDLSFSPSQSLPAS	P01023	Alpha-2-macroglobulin	15	EM	Internal	LSFSPSQSL	DR7	HB
AENDVLHCVAFAVPKS	P01023	Alpha-2-macroglobulin	16	EM	Internal	VLHCVAFAV/LHCVAFAVP	DR7/DRB5	IB
LPKFEVQVTVPKIIT	P01023	Alpha-2-macroglobulin	15	EM	Internal	FEVQVTVPK	DRB5	HB
VLPKFEVQVTVPKI	P01023	Alpha-2-macroglobulin	14	EM	Internal	FEVQVTVPK	DRB5	HB
EDMKGHFSISIPVK	P01023	Alpha-2-macroglobulin	14	EM	Internal	NA	NA	NA
DKDLFKAVDAALKK	P01042	Kininogen-1	14	EM	N-ter	FKAVDAALK	DRB5	HB
DKDLFKAVDAALKKYN	P01042	Kininogen-1	16	EM	N-ter	FKAVDAALK	DRB5	HB
ALYLVCGERGFFYTPKT	P01308	Insulin	17	EM	Internal	VCGERGFFY	DR7	HB
IQFHWKNSNQIKI	P01730	T-cell surface glycoprotein CD4	13	M	Internal	FHWKNSNQI	DR7	HB
DGKDYIALNEDLRSW	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	15	M	Internal	IALNEDLRS/YIALNEDLR	DR15/DRB5	IB
GDRTFQKWAAVVVPSG	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	16	M	Internal	FQKWAAVVV	DR7	IB
EEFGRFASFEAQG	P01903	HLA class II histocompatibility antigen, DR alpha chain	13	M	Internal	FGRFASFEA/FGRFASFEA	DR7/DR15	IB
LEEFGRFASFEAQG	P01903	HLA class II histocompatibility antigen, DR alpha chain	14	M	Internal	LEEFGRFAS	DR15	HB
LEEFGRFASFEAQGA	P01903	HLA class II histocompatibility antigen, DR alpha chain	15	M	Internal	LEEFGRFAS	DR15	HB
LEEFGRFASFEAQGAL	P01903	HLA class II histocompatibility antigen, DR alpha chain	16	M	Internal	LEEFGRFAS	DR15	HB

RLEEFGRFASFEAQG	P01903	HLA class II histocompatibility antigen, DR alpha chain	15	M	Internal	LEEFGRFAS	DR15	HB
RLEEFGRFASFEAQGAL	P01903	HLA class II histocompatibility antigen, DR alpha chain	17	M	Internal	LEEFGRFAS	DR15	HB
WRLEEFGRFASFEAQG	P01903	HLA class II histocompatibility antigen, DR alpha chain	16	M	Internal	LEEFGRFAS	DR15	HB
DVGEFRAVTELGRPD	P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain	15	M	Internal	VGEFRAVTE/FRAVTELGR	DR15/DRB5	HB
DVGEFRAVTELGRPDA	P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain	16	M	Internal	VGEFRAVTE/FRAVTELGR	DR15/DRB5	HB
SDVGEFRAVTELGRPD	P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain	16	M	Internal	VGEFRAVTE/FRAVTELGR	DR15/DRB5	HB
SDVGEFRAVTELGRPDA	P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain	17	M	Internal	VGEFRAVTE/FRAVTELGR	DR15/DRB5	HB
VGEFRAVTELGRPD	P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain	14	M	Internal	VGEFRAVTE/FRAVTELGR	DR15/DRB5	HB
ASLLSFMQGYMKHAT	P02656	Apolipoprotein C-III	15	Lis/End	C-ter	LSFMQGYMK	DRB5	HB
YPGPSGPLGARGIPGIKG	P02745	Complement C1q subcomponent subunit A	18	EM	Internal	LGARGIPGI	DR7	HB
EQLGEYKFQNALLVR	P02768	Serum albumin	15	EM	Internal	YKFQNALLV	DR7	HB
DNEETFLKKYLYEIARRHP	P02768	Serum albumin	19	EM	Internal	FLKKYLYEI/YLYEIARRH	DR7/DRB5	HB
RHPYFYAPELLFFAK	P02768	Serum albumin	15	EM	Internal	YFYAPELLF/YFYAPELLF	DR7/DRB5	IB
EQLGEYKFQNALLVRYT	P02768	Serum albumin	17	EM	Internal	YKFQNALLV	DR7	HB
EQLGEYKFQNALLVRYTK	P02768	Serum albumin	18	EM	Internal	YKFQNALLV	DR7	HB
LGEYKFQNALLVR	P02768	Serum albumin	13	EM	Internal	YKFQNALLV	DR7	HB
LGEYKFQNALLVRYT	P02768	Serum albumin	15	EM	Internal	YKFQNALLV	DR7	HB
QLGEYKFQNALLVR	P02768	Serum albumin	14	EM	Internal	YKFQNALLV	DR7	HB
DNEETFLKKYLYEIARRHPY	P02768	Serum albumin	20	EM	Internal	FLKKYLYEI/YLYEIARRH	DR7/DRB5	HB
DNEETFLKKYLYEIARRHPYF	P02768	Serum albumin	21	EM	Internal	FLKKYLYEI/YLYEIARRH	DR7/DRB5	HB
DNEETFLKKYLYEIARRHPYFY	P02768	Serum albumin	22	EM	Internal	FLKKYLYEI/YLYEIARRH	DR7/DRB5	HB
FLKKYLYEIARRHP	P02768	Serum albumin	14	EM	Internal	FLKKYLYEI/YLYEIARRH	DR7/DRB5	HB
FLKKYLYEIARRHPY	P02768	Serum albumin	15	EM	Internal	FLKKYLYEI/YLYEIARRH	DR7/DRB5	HB
LKKYLYEIARRHP	P02768	Serum albumin	13	EM	Internal	YLYEIARRH	DRB5	HB
LKKYLYEIARRHPY	P02768	Serum albumin	14	EM	Internal	YLYEIARRH	DRB5	HB
SPFRHVFWGSGSHTLPA	P02786	Transferrin receptor protein 1	17	M	Internal	FWGSGSHTL/FRHVFWGSG	DR7/DRB5	HB
LKDGFQPSRSIIF	P02786	Transferrin receptor protein 1	13	M	Internal	FQPSRSIIF	DR7	HB
NPGGYVAYSKAATVTG	P02786	Transferrin receptor protein 1	16	M	Internal	VAYSKAATV	DR7	HB
DGFQPSRSIIFASW	P02786	Transferrin receptor protein 1	14	M	Internal	FQPSRSIIF	DR7	HB
KDGFQPSRSIIF	P02786	Transferrin receptor protein 1	12	M	Internal	FQPSRSIIF	DR7	HB
NPGGYVAYSKAATVTGK	P02786	Transferrin receptor protein 1	17	M	Internal	VAYSKAATV	DR7	HB
NPGGYVAYSKAATVTGKL	P02786	Transferrin receptor protein 1	18	M	Internal	VAYSKAATV	DR7	HB
SPFRHVFWGSGSHTLPAL	P02786	Transferrin receptor protein 1	18	M	Internal	FWGSGSHTL/FRHVFWGSG	DR7/DRB5	HB
DPQTFYYAVAVVK	P02787	Serotransferrin	13	EM	Internal	FYYAVAVVK	DRB5	HB
DKSKEFQLFSSPHGKDL	P02787	Serotransferrin	17	EM	Internal	FQLFSSPHG	DR15	HB
EDPQTFYYAVAVVK	P02787	Serotransferrin	14	EM	Internal	FYYAVAVVK	DRB5	HB
DPQTFYYAVAVVKKDSG	P02787	Serotransferrin	17	EM	Internal	YYAVAVVKK	DRB5	HB
PQTFYYAVAVVKKDSG	P02787	Serotransferrin	16	EM	Internal	YYAVAVVKK	DRB5	HB
DPQTFYYAVAVVKK	P02787	Serotransferrin	14	EM	Internal	YYAVAVVKK	DRB5	HB
DPQTFYYAVAVVKKD	P02787	Serotransferrin	15	EM	Internal	YYAVAVVKK	DRB5	HB
KGGYTLVSGYPKRLE	P02790	Hemopexin	15	EM	Internal	YTLVSGYPK	DRB5	HB
KGGYTLVSGYPKR	P02790	Hemopexin	13	EM	Internal	YTLVSGYPK	DRB5	HB
GVSHFFRELAEEKREG	P02792	Ferritin light chain	16	C	Internal	VSHFFRELA/FFRELAEEK	DR15/DRB5	IB
TPDAMKAAMALEKKLNQ	P02792	Ferritin light chain	17	C	Internal	MKAAMALEK	DRB5	HB
KKLNQALLDLHA	P02792	Ferritin light chain	12	C	Internal	NA	NA	NA
VSHFFRELAEEKREG	P02792	Ferritin light chain	15	C	Internal	VSHFFRELA/FFRELAEEK	DR15/DRB5	IB
VSHFFRELAEEKREGY	P02792	Ferritin light chain	16	C	Internal	VSHFFRELA/FFRELAEEK	DR15/DRB5	IB
PAVGFLETISPGYSIHTYLWRRQ	P04062	Glucosylceramidase	23	Lis/End	C-ter	FLETISPGY	DR7	HB
YPKSLHMYANRLLDHR	P04114	Apolipoprotein B-100	16	C	Internal	LHMYANRLL	DR7	HB
VGEYRAVTELGRPD	P04229	HLA class II histocompatibility antigen, DRB1-1 beta chain	14	M	Internal	VGEYRAVTE/YRAVTELGR	DR15/DRB5	HB

FQTLVMLETVPRSG	P04229	HLA class II histocompatibility antigen, DRB1-1 beta chain	14	M	Internal	LVMLETVPR/LVMLETVPR/LVMLETVPR	DR7/DR15/DRB5	IB
DVGEYRAVTELGRPD	P04229	HLA class II histocompatibility antigen, DRB1-1 beta chain	15	M	Internal	VGEYRAVTE/YRAVTELGR	DR15/DRB5	HB
DVGEYRAVTELGRPDA	P04229	HLA class II histocompatibility antigen, DRB1-1 beta chain	16	M	Internal	VGEYRAVTE/YRAVTELGR	DR15/DRB5	HB
IDWKVFESWMHH	P04233	HLA class II histocompatibility antigen gamma chain	12	ER/G	Internal	WKVFESWMH	DR7	IB
NADPLKVYPPLKGSFPENLRH	P04233	HLA class II histocompatibility antigen gamma chain	21	ER/G	Internal	LKGSFPENL/LKVYPPLKG	DR7/DR15	HB
LPKPPKPVSKMRMATPLLMQALPMG	P04233	HLA class II histocompatibility antigen gamma chain	25	ER/G	Internal	LLMQALPMG/LLMQALPMG	DR7/DRB5	IB
TIDWKVFESWMHH	P04233	HLA class II histocompatibility antigen gamma chain	13	ER/G	Internal	WKVFESWMH	DR7	IB
APMFVMGVNHEKYDN	P04406	Glyceraldehyde-3-phosphate dehydrogenase	15	C	Internal	FVMGVNHEK	DRB5	IB
DAPMFVMGVNHEKYDN	P04406	Glyceraldehyde-3-phosphate dehydrogenase	16	C	Internal	FVMGVNHEK	DRB5	IB
DSDVGEFRAVTELGRPA	P04440	HLA class II histocompatibility antigen, DP beta 1 chain	17	M	Internal	VGEFRAVTE/FRAVTELGR	DR7/DRB5	HB
DVGEFRAVTELGRPA	P04440	HLA class II histocompatibility antigen, DP beta 1 chain	15	M	Internal	VGEFRAVTE/FRAVTELGR	DR7/DRB5	HB
SDVGEFRAVTELGRPA	P04440	HLA class II histocompatibility antigen, DP beta 1 chain	16	M	Internal	VGEFRAVTE/FRAVTELGR	DR7/DRB5	HB
VGEFRAVTELGRPA	P04440	HLA class II histocompatibility antigen, DP beta 1 chain	14	M	Internal	VGEFRAVTE/FRAVTELGR	DR7/DRB5	HB
NIQPIFAVTSRMVKT	P05107	Integrin beta-2	15	M	Internal	IFAVTSRMV/IQPIFAVTS	DR7/DR15	HB
NIQPIFAVTSRMVKTYE	P05107	Integrin beta-2	17	M	Internal	IFAVTSRMV/IQPIFAVTS	DR7/DR15	HB
VSNEIVRFPTDQLTPD	P05164	Myeloperoxidase	16	Lis/End	Internal	IVRFPTDQL	DR15	IB
FPVALARAVSNEIVR	P05164	Myeloperoxidase	15	Lis/End	Internal	LARAVSNEI	DR7	HB
LDNRYQPMEPNPRVPL	P05164	Myeloperoxidase	16	Lis/End	Internal	YQPMEPNPR	DRB5	HB
VSNEIVRFPTDQLTPDQ	P05164	Myeloperoxidase	17	Lis/End	Internal	IVRFPTDQL	DR15	IB
NPTVEVDLFTSKGLFR	P06733	Alpha-enolase	16	C	N-ter	VDLFTSKGL/VDLFTSKGL/LFTSKGLFR	DR7/DR15/DRB5	IB
AEQQRLKSQDLELSWNLNG	P06734	Low affinity immunoglobulin epsilon Fc receptor	19	M	Internal	LELSWNLNG	DR7	HB
EQQRLKSQDLELSWN	P06734	Low affinity immunoglobulin epsilon Fc receptor	15	M	Internal	LKSQDLELS	DR15	LB
QQRLKSQDLELSWN	P06734	Low affinity immunoglobulin epsilon Fc receptor	14	M	Internal	LKSQDLELS	DR15	LB
RSIHLFIDSLLNEENPS	P06858	Lipoprotein lipase	17	M	Internal	IHLFIDSLL	DR15	HB
NVNVFKFIIPQIVK	P07195	L-lactate dehydrogenase B chain	14	C	Internal	FKFIIPQIV/VNVFKFIIP/FKFIIPQIV	DR7/DR15/DRB5	HB
RAGSSRQSIQKYIKSHYK	P07305	Histone H1.0	18	N	Internal	IQKYIKSHY	DR15	IB
KSGVYQHVTGEMMGGHA	P07858	Cathepsin B	17	Lis/End	Internal	YQHVTGEMM	DR7	HB
DEYLKTTGKPIE	P08133	Annexin A6	12	C	Internal	YLKTTGKPI	DR7	HB
VFDEYLKTTGKPIE	P08133	Annexin A6	14	C	Internal	YLKTTGKPI	DR7	HB
VITYKCEESFVKIPG	P08174	Complement decay-accelerating factor	15	M	Internal	YKCEESFVK/YKCEESFVK	DR7/DRB5	HB
PPFEVRGANQWIKFKSVS	P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	18	Mit	C-ter	VRGANQWIK	DRB5	HB
VVDIFQVVKALRK	P08575	Receptor-type tyrosine-protein phosphatase C	13	M	Internal	FQVVKALRK	DRB5	HB
VVDIFQVVKALRKA	P08575	Receptor-type tyrosine-protein phosphatase C	14	M	Internal	FQVVKALRK	DRB5	HB
VVDIFQVVKALRKARPG	P08575	Receptor-type tyrosine-protein phosphatase C	17	M	Internal	FQVVKALRK	DRB5	HB
KVESLQEEIAFLKK	P08670	Vimentin	14	C	Internal	LQEEIAFLK	DRB5	IB
VESLQEEIAFLKKLHE	P08670	Vimentin	16	C	Internal	LQEEIAFLK	DRB5	IB
DGDLTLYQSNTILR	P09211	Glutathione S-transferase P	14	C	Internal	LTLYQSNTI/LTLYQSNTI	DR7/DR15	HB
DGDLTLYQSNTILRH	P09211	Glutathione S-transferase P	15	C	Internal	LTLYQSNTI/LTLYQSNTI	DR7/DR15	HB
GDLTLYQSNTILR	P09211	Glutathione S-transferase P	13	C	Internal	LTLYQSNTI/LTLYQSNTI	DR7/DR15	HB
QDGDLTLYQSNTILR	P09211	Glutathione S-transferase P	15	C	Internal	LTLYQSNTI/LTLYQSNTI	DR7/DR15	HB
QDGDLTLYQSNTILRH	P09211	Glutathione S-transferase P	16	C	Internal	LTLYQSNTI/LTLYQSNTI	DR7/DR15	HB
LPKFQDGDLTLYQSNTILRH	P09211	Glutathione S-transferase P	20	C	Internal	LTLYQSNTI/LTLYQSNTI	DR7/DR15	HB
GLEEELQFSLGSKINVK	P0C0L4	Complement C4-A	17	EM	Internal	LQFSLGSKI	DR7	HB
GDGTFQKWASVVVPSG	P10314	HLA class I histocompatibility antigen, A-32 alpha chain	16	M	Internal	FQKWASVVV	DR7	HB
GTFQKWASVVVPSG	P10314	HLA class I histocompatibility antigen, A-32 alpha chain	14	M	Internal	FQKWASVVV	DR7	HB
GLAVLAVVVIGAVVATVMC	P10319	HLA class I histocompatibility antigen, B-58 alpha chain	19	M	C-ter	VVVIGAVVA	DR15	HB
APDQDEIQRLPGLAKQPS	P10619	Lysosomal protective protein	18	Lis/End	N-ter	IQRLPGLAK	DRB5	HB
LPDNFIAACTEKKIPV	P10768	S-formylglutathione hydrolase	16	C	Internal	FIAACTEKK	DRB5	IB
NDAYLGYAAAIILR	P11215	Integrin alpha-M	14	M	Internal	LGYAAAIIL	DR7	HB
NDAYLGYAAAIILRNR	P11215	Integrin alpha-M	16	M	Internal	LGYAAAIIL	DR7	HB

EHVRVTKAFSVNIFK	P11279	Lysosome-associated membrane glycoprotein 1	15	Lis/End	Internal	VTKAFSVNI	DR7	HB
SPESDSIQWFHNGNLIPT	P12318	Low affinity immunoglobulin gamma Fc region receptor II-a	18	M	Internal	WFHNGNLIP	DR7	HB
GNIGYTLFSSKPVT	P12318	Low affinity immunoglobulin gamma Fc region receptor II-a	14	M	Internal	YTLFSSKPV	DR7	HB
SPESDSIQWFHNGNLIPTHT	P12318	Low affinity immunoglobulin gamma Fc region receptor II-a	20	M	Internal	WFHNGNLIP	DR7	HB
IGYTLFSSKPVTIT	P12318	Low affinity immunoglobulin gamma Fc region receptor II-a	14	M	Internal	YTLFSSKPV	DR7	HB
NIGYTLFSSKPVT	P12318	Low affinity immunoglobulin gamma Fc region receptor II-a	13	M	Internal	YTLFSSKPV	DR7	HB
ALDFIASKGVKLVS	P12814	Alpha-actinin-1	14	C	Internal	FIASKGVKL	DR7	HB
KALDFIASKGVKL	P12814	Alpha-actinin-1	13	C	Internal	FIASKGVKL	DR7	HB
KALDFIASKGVKLVS	P12814	Alpha-actinin-1	15	C	Internal	FIASKGVKL	DR7	HB
KALDFIASKGVKLVSIG	P12814	Alpha-actinin-1	17	C	Internal	FIASKGVKL	DR7	HB
APEYEKIANILKDKDPP	P13667	Protein disulfide-isomerase A4	17	ER/G	Internal	YEKIANILK	DRB5	HB
LGDNFYFTGVQDINDK	P13686	Tartrate-resistant acid phosphatase type 5	16	Lis/End	Internal	FYFTGVQDI	DR7	HB
LGDNFYFTGVQDINDKR	P13686	Tartrate-resistant acid phosphatase type 5	17	Lis/End	Internal	FYFTGVQDI	DR7	HB
DNFYFTGVQDINDK	P13686	Tartrate-resistant acid phosphatase type 5	14	Lis/End	Internal	FYFTGVQDI	DR7	HB
DNFYFTGVQDINDKR	P13686	Tartrate-resistant acid phosphatase type 5	15	Lis/End	Internal	FYFTGVQDI	DR7	HB
GDNFYFTGVQDINDK	P13686	Tartrate-resistant acid phosphatase type 5	15	Lis/End	Internal	FYFTGVQDI	DR7	HB
GDNFYFTGVQDINDKR	P13686	Tartrate-resistant acid phosphatase type 5	16	Lis/End	Internal	FYFTGVQDI	DR7	HB
FQTLVMLETVPRSGE	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	15	M	Internal	LVMLETVPR	DR7	HB
ERLFYNQEEFVRFD	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	14	M	Internal	FYNQEEFVR	DRB5	HB
DSDVGEYRAVTELGRPV	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	17	M	Internal	VGEYRAVTE/YRAVTELGR	DR15/DRB5	HB
DSDVGEYRAVTELGRPVA	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	18	M	Internal	VGEYRAVTE/YRAVTELGR	DR15/DRB5	HB
DVGEYRAVTELGRPV	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	15	M	Internal	VGEYRAVTE/YRAVTELGR	DR15/DRB5	HB
SDVGEYRAVTELGRPV	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	16	M	Internal	VGEYRAVTE/YRAVTELGR	DR15/DRB5	HB
SDVGEYRAVTELGRPVA	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	17	M	Internal	VGEYRAVTE/YRAVTELGR	DR15/DRB5	HB
VGEYRAVTELGRPV	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	14	M	Internal	VGEYRAVTE/YRAVTELGR	DR15/DRB5	HB
FQTLVMLETVPRSGEV	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	16	M	Internal	LVMLETVPR	DR7	HB
ERLFYNQEEFVRFDS	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	15	M	Internal	FYNQEEFVR	DRB5	HB
LERLFYNQEEFVRFDS	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	16	M	Internal	FYNQEEFVR	DRB5	HB
VNDDIIVNWVNETLRE	P13796	Plastin-2	16	C	Internal	IVNWVNETL	DR7	HB
AKYAISMARKIGAR	P13796	Plastin-2	14	C	Internal	YAISMARKI/YAISMARKI	DR7/DRB5	HB
DDIIVNWVNETLRE	P13796	Plastin-2	14	C	Internal	IVNWVNETL	DR7	HB
DIIVNWVNETLRE	P13796	Plastin-2	13	C	Internal	IVNWVNETL	DR7	HB
NDDIIVNWVNETLR	P13796	Plastin-2	14	C	Internal	IVNWVNETL	DR7	HB
NDDIIVNWVNETLRE	P13796	Plastin-2	15	C	Internal	IVNWVNETL	DR7	HB
NAKYAISMARKIGAR	P13796	Plastin-2	15	C	Internal	YAISMARKI/YAISMARKI	DR7/DRB5	HB
NNAKYAISMARKIGAR	P13796	Plastin-2	16	C	Internal	YAISMARKI/YAISMARKI	DR7/DRB5	HB
NAKYAISMARKIG	P13796	Plastin-2	13	C	Internal	YAISMARKI/YAISMARKI	DR7/DRB5	HB
NNAKYAISMARKIG	P13796	Plastin-2	14	C	Internal	YAISMARKI/YAISMARKI	DR7/DRB5	HB
RQVWVYTGASVLGPR	P14780	Matrix metalloproteinase-9	15	EM	Internal	VWVYTGASV/VWVYTGASV	DR7/DR15	HB
HPAFVNYSTSQKISRPG	P14866	Heterogeneous nuclear ribonucleoprotein L	17	N	Internal	VNYSTSQKI	DR7	HB
LWILNRYLSYTLNPDL	P15144	Aminopeptidase N	16	M	Internal	LNRYLSYTL	DR15	HB
DAFNLASAHKVPVT	P15144	Aminopeptidase N	14	M	Internal	FNLASAHKV/FNLASAHKV	DR7/DRB5	HB
WILNRYLSYTLNPDL	P15144	Aminopeptidase N	15	M	Internal	LNRYLSYTL	DR15	HB
RPSEFNYVWIVPITS	P15144	Aminopeptidase N	15	M	Internal	FNYVWIVPI	DR7	HB
INDAFNLASAHKVPV	P15144	Aminopeptidase N	15	M	Internal	FNLASAHKV/FNLASAHKV	DR7/DRB5	HB
INDAFNLASAHKVPVT	P15144	Aminopeptidase N	16	M	Internal	FNLASAHKV/FNLASAHKV	DR7/DRB5	HB
GDGTFQKWAAVVVPSG	P17693	HLA class I histocompatibility antigen, alpha chain G	16	M	Internal	FQKWAAVVV	DR7	IB
LPSWLTTGNYRI	P17900	Ganglioside GM2 activator	12	Lis/End	C-ter	WLTTGNYRI	DR7	HB
ELPSWLTTGNYRIES	P17900	Ganglioside GM2 activator	15	Lis/End	C-ter	WLTTGNYRI	DR7	HB
LPSWLTTGNYRIES	P17900	Ganglioside GM2 activator	14	Lis/End	C-ter	WLTTGNYRI	DR7	HB

LPSWLTTGNYRIESV	P17900	Ganglioside GM2 activator	15	Lis/End	C-ter	WLTTGNYRI	DR7	HB
PKFEVIEKPQA	P18859	ATP synthase-coupling factor 6, mitochondrial	11	Mit	C-ter	NA	NA	NA
TPEGHFGNVYSTPL	P20062	Transcobalamin-2	14	EM	Internal	FGNVYSTPL	DR7	HB
KGEYTLVVKWGDEHIPGSPYRVVVP	P21333	Filamin-A	25	C	C-ter	IPGSPYRVV	DR7	HB
SEHTFLWTDGRGVHYT	P22897	Macrophage mannose receptor 1	16	M	Internal	FLWTDGRGV	DR7	HB
EKNIMLYKGSGLWS	P22897	Macrophage mannose receptor 1	14	M	Internal	IMLYKGSGL	DR15	HB
KGTFQWTIEEEVR	P22897	Macrophage mannose receptor 1	13	M	Internal	FQWTIEEEV	DR7	HB
EKNIMLYKGSGLWSR	P22897	Macrophage mannose receptor 1	15	M	Internal	IMLYKGSGL	DR15	HB
KNIMLYKGSGLWSR	P22897	Macrophage mannose receptor 1	14	M	Internal	IMLYKGSGL	DR15	HB
NRQEKNIMLYKGSGLWSR	P22897	Macrophage mannose receptor 1	18	M	Internal	IMLYKGSGL	DR15	HB
QEKNIMLYKGSGLWS	P22897	Macrophage mannose receptor 1	15	M	Internal	IMLYKGSGL	DR15	HB
QEKNIMLYKGSGLWSR	P22897	Macrophage mannose receptor 1	16	M	Internal	IMLYKGSGL	DR15	HB
RQEKNIMLYKGSGLWSR	P22897	Macrophage mannose receptor 1	17	M	Internal	IMLYKGSGL	DR15	HB
RQEKNIMLYKGSGLWSRW	P22897	Macrophage mannose receptor 1	18	M	Internal	IMLYKGSGL	DR15	HB
DVNSEHTFLWTDGRGVHYT	P22897	Macrophage mannose receptor 1	19	M	Internal	FLWTDGRGV	DR7	HB
DVNSEHTFLWTDGRGVHYTN	P22897	Macrophage mannose receptor 1	20	M	Internal	FLWTDGRGV	DR7	HB
DGVIKVFNDMKVR	P23528	Cofilin-1	13	C	N-ter	IKVFNDMKV	DR15	HB
DGVIKVFNDMKVRK	P23528	Cofilin-1	14	C	N-ter	IKVFNDMKV	DR15	HB
DGVIKVFNDMKVRKS	P23528	Cofilin-1	15	C	N-ter	IKVFNDMKV	DR15	HB
GVIKVFNDMKVRK	P23528	Cofilin-1	13	C	N-ter	IKVFNDMKV	DR15	HB
SDGVIKVFNDMKVR	P23528	Cofilin-1	14	C	N-ter	IKVFNDMKV	DR15	HB
SDGVIKVFNDMKVRK	P23528	Cofilin-1	15	C	N-ter	IKVFNDMKV	DR15	HB
DDISLYKSFLQLG	P27449	V-type proton ATPase 16 kDa proteolipid subunit	13	Lis/End	Internal	ISLYKSFLQ/ISLYKSFLQ	DR7/DR15	HB
LNDDISLYKSFLQLG	P27449	V-type proton ATPase 16 kDa proteolipid subunit	15	Lis/End	Internal	ISLYKSFLQ/ISLYKSFLQ	DR7/DR15	HB
SPDPSIYAYDNFGVLG	P27797	Calreticulin	16	ER/G	Internal	IYAYDNFGV	DR15	HB
DVKIQWYKDSLLLDK	P27930	Interleukin-1 receptor type 2	15	M	Internal	IQWYKDSLL/IQWYKDSLL	DR7/DR15	IB
TDVKIQWYKDSLLLDK	P27930	Interleukin-1 receptor type 2	16	M	Internal	IQWYKDSLL/IQWYKDSLL	DR7/DR15	IB
TPEPSDIFSCIVTHEIDR	P28067	HLA class II histocompatibility antigen, DM alpha chain	18	Lis/End	Internal	FSCIVTHEI	DR7	HB
TPKDFTYCISFNK	P28068	HLA class II histocompatibility antigen, DM beta chain	13	Lis/End	Internal	FTYCISFNK	DRB5	HB
TPKDFTYCISFNKDL	P28068	HLA class II histocompatibility antigen, DM beta chain	15	Lis/End	Internal	YCISFNKDL/FTYCISFNK	DR7/DRB5	HB
TPKDFTYCISFNKDLL	P28068	HLA class II histocompatibility antigen, DM beta chain	16	Lis/End	Internal	YCISFNKDL/FTYCISFNK	DR7/DRB5	HB
FPTIYFSPANKKLNPK	P30101	Protein disulfide-isomerase A3	16	ER/G	Internal	IYFSPANKK	DRB5	HB
TPAAPPKAVLKLEPQWINVLQED	P31994	Low affinity immunoglobulin gamma Fc region receptor II-b	23	M	Internal	VLKLEPQWI/LEPQWINVL	DR7/DRB5	IB
APVKKLVVKGGKKKKQVLKFTLD	P35268	60S ribosomal protein L22	23	C	N-ter	LVVKGGKKK	DRB5	HB
NTKKVIQYLAYVASSHK	P35579	Myosin-9	17	C	Internal	LAYVASSHK	DRB5	HB
LAQLIRQQIDGRGD	P36269	Gamma-glutamyltransferase 5	14	M	Internal	LIRQQIDGR	DRB5	HB
VSEIISYWGFPSE	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	IISYWGFPS	DR15	HB
VQNMLHWSQAVKF	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	LHWSQAVKF	DR7	HB
DKEFLPQSAFLKW	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	FLPQSAFLK	DRB5	HB
VSEIISYWGFPSEE	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	IISYWGFPS	DR15	HB
VQNMLHWSQAVKFQK	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	LHWSQAVKF	DR7	HB
VQNMLHWSQAVKFQKF	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	16	Lis/End	Internal	LHWSQAVKF	DR7	HB
VSEIISYWGFPSEEY	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	YWGFPSEEY/IISYWGFPS	DR7/DR15	HB
DKEFLPQSAFLKWLG	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	FLPQSAFLK	DRB5	HB
DKEFLPQSAFLKWLGT	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	16	Lis/End	Internal	FLPQSAFLK	DRB5	HB
EFLPQSAFLKWLGT	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	FLPQSAFLK	DRB5	HB
FGDKEFLPQSAFLKW	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	FLPQSAFLK	DRB5	HB
FGDKEFLPQSAFLKWLG	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	17	Lis/End	Internal	FLPQSAFLK	DRB5	HB
FGDKEFLPQSAFLKWLGT	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	18	Lis/End	Internal	FLPQSAFLK	DRB5	HB
GDKEFLPQSAFLKW	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	FLPQSAFLK	DRB5	HB

GDKEFLPQSAFLKWL	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	15	Lis/End	Internal	FLPQSAFLK	DRB5	HB
GDKEFLPQSAFLKWLG	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	16	Lis/End	Internal	FLPQSAFLK	DRB5	HB
GDKEFLPQSAFLKWLGT	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	17	Lis/End	Internal	FLPQSAFLK	DRB5	HB
KEFLPQSAFLKW	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	12	Lis/End	Internal	FLPQSAFLK	DRB5	HB
KEFLPQSAFLKWLG	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	14	Lis/End	Internal	FLPQSAFLK	DRB5	HB
DLFGDKEFLPQSAFLKWLGTH	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	21	Lis/End	Internal	FLPQSAFLK	DRB5	HB
GDKEFLPQSAFLK	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase	13	Lis/End	Internal	FLPQSAFLK	DRB5	HB
KANVKIFKSQGAALDK	P40925	Malate dehydrogenase, cytoplasmic	16	C	Internal	VKIFKSQGA	DR15	HB
LKANVKIFKSQGAALDK	P40925	Malate dehydrogenase, cytoplasmic	17	C	Internal	VKIFKSQGA	DR15	HB
KTQYFHVKVFDINLK	P41218	Myeloid cell nuclear differentiation antigen	15	N	Internal	YFHVKVFDI	DRB5	HB
KGNLVYIIDFGLAKK	P48730	Casein kinase I isoform delta	15	C	Internal	LVYIIDFGL	DR15	HB
VLDLDLFRVDKGGD	P49591	Serine--tRNA ligase, cytoplasmic	14	C	N-ter	NA	NA	NA
ASPNIVIALAGNKADL	P51148	Ras-related protein Rab-5C	16	Lis/End	Internal	IVIALAGNK	DRB5	HB
SPNIVIALAGNKADL	P51148	Ras-related protein Rab-5C	15	Lis/End	Internal	IVIALAGNK	DRB5	HB
GVIQYYPAAPLPG	P51570	Galactokinase	13	C	Internal	IQYYPAAPL	DR15	HB
KGVIQYYPAAPLPG	P51570	Galactokinase	14	C	Internal	IQYYPAAPL	DR15	HB
VKGVIQYYPAAPLPG	P51570	Galactokinase	15	C	Internal	IQYYPAAPL	DR15	HB
LPTSWDWRNVHGINF	P53634	Dipeptidyl peptidase 1	15	Lis/End	Internal	WRNVHGINF	DR7	HB
KKVVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	16	Lis/End	Internal	YLQKLDTAY	DR7	HB
KKVVVYLQKLDTAYDDLG	P53634	Dipeptidyl peptidase 1	18	Lis/End	Internal	YLQKLDTAY	DR7	HB
KVVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	15	Lis/End	Internal	YLQKLDTAY	DR7	HB
VVVYLQKLDTAYDD	P53634	Dipeptidyl peptidase 1	14	Lis/End	Internal	YLQKLDTAY	DR7	HB
KVVVYLQKLDTAYD	P53634	Dipeptidyl peptidase 1	14	Lis/End	Internal	YLQKLDTAY	DR7	HB
LPTSWDWRNVHGINFVSPV	P53634	Dipeptidyl peptidase 1	19	Lis/End	Internal	WRNVHGINF/VHGINFVSP	DR7/DR15	HB
LPTSWDWRNVHGINFVSPVR	P53634	Dipeptidyl peptidase 1	20	Lis/End	Internal	WRNVHGINF/VHGINFVSP	DR7/DR15	HB
TPSYVAFTDTERL	P54652	Heat shock-related 70 kDa protein 2	13	M	Internal	VAFTDTERL	DR7	HB
TPSYVAFTDTERLIG	P54652	Heat shock-related 70 kDa protein 2	15	M	Internal	VAFTDTERL	DR7	HB
SDGSFHASSSLTVK	P55899	IgG receptor FcRn large subunit p51	14	M	Internal	FHASSSLTV	DR7	HB
SDGSFHASSSLTVKSG	P55899	IgG receptor FcRn large subunit p51	16	M	Internal	FHASSSLTV	DR7	HB
KNNLCPSGSNIIS	P60033	CD81 antigen	13	M	Internal	LCPSGSNII	DR7	HB
KNNLCPSGSNIISN	P60033	CD81 antigen	14	M	Internal	LCPSGSNII	DR7	HB
KNNLCPSGSNIISNL	P60033	CD81 antigen	15	M	Internal	LCPSGSNII	DR7	HB
EKIWHHTFYNELR	P60709	Actin, cytoplasmic 1	13	C	Internal	WHHTFYNEL	DR7	IB
NWDDMEKIWHHTFYNELR	P60709	Actin, cytoplasmic 1	18	C	Internal	WHHTFYNEL	DR7	IB
HSDLSFSKDWSFYL	P61769	Beta-2-microglobulin	14	M	Internal	NA	NA	NA
GQVNYEEFVQMMTAK	P62158	Calmodulin	15	C	C-ter	VNYEEFVQM	DR7	IB
ETRGVLKVFLENVIR	P62805	Histone H4	15	N	Internal	LKVFLENVI/LKVFLENVI	DR7/DR15	IB
RGVLKVFLENVIR	P62805	Histone H4	13	N	Internal	LKVFLENVI/LKVFLENVI	DR7/DR15	IB
RGVLKVFLENVIRDA	P62805	Histone H4	15	N	Internal	LKVFLENVI/LKVFLENVI	DR7/DR15	IB
AVRDMRQTVAVGVIK	P68104	Elongation factor 1-alpha 1	15	C	Internal	MRQTVAVGV	DR7	HB
GNASGTTLLEALD	P68104	Elongation factor 1-alpha 1	13	C	Internal	NA	NA	NA
RDMRQTVAVGVIK	P68104	Elongation factor 1-alpha 1	13	C	Internal	MRQTVAVGV	DR7	HB
IKGKINSITVDNCKK	Q01518	Adenylyl cyclase-associated protein 1	15	M	Internal	IKGKINSIT	DR7	HB
FIYFADTTSYLIGRQ	Q07954	Prolow-density lipoprotein receptor-related protein 1	15	M	Internal	FADTTSYLI	DR7	HB
PAGKLKYFDKLN	Q13162	Peroxiredoxin-4	12	C	C-ter	NA	NA	NA
YDQFYVANEFLKYR	Q14314	Fibroleukin	14	EM	Internal	YVANEFLKY/FYVANEFLK	DR7/DRB5	HB
PETSVLVLRKPGINVASDWSIHLR	Q14697	Neutral alpha-glucosidase AB	24	ER/G	C-ter	INVASDWSI/VLRKPGINV	DR7/DR15	IB
INEFLRELSFGRGST	Q15084	Protein disulfide-isomerase A6	15	ER/G	Internal	FLRELSFGR/FLRELSFGR	DR7/DRB5	HB
PEESHRLPVEVAYKRGLFDEEMNEILTD	Q15149	Plectin	28	C	Internal	FDEEMNEIL	DR7	HB
ELQDIIPFGNNPIFR	Q15392	Delta(24)-sterol reductase	15	ER/G	Internal	IIPFGNNPI/IIPFGNNPI	DR7/DR15	HB

ALEIFKQASAFSRASQ	Q15582	Transforming growth factor-beta-induced protein ig-h3	16	EM	C-ter	IFKQASAFS/FKQASAFSR	DR7/DRB5	HB
DSALEIFKQASAFSRASQR	Q15582	Transforming growth factor-beta-induced protein ig-h3	19	EM	C-ter	IFKQASAFS/FKQASAFSR	DR7/DRB5	HB
LEIFKQASAFSR	Q15582	Transforming growth factor-beta-induced protein ig-h3	12	EM	C-ter	IFKQASAFS/FKQASAFSR	DR7/DRB5	HB
LEIFKQASAFSRA	Q15582	Transforming growth factor-beta-induced protein ig-h3	13	EM	C-ter	IFKQASAFS/FKQASAFSR	DR7/DRB5	HB
LEIFKQASAFSRAS	Q15582	Transforming growth factor-beta-induced protein ig-h3	14	EM	C-ter	IFKQASAFS/FKQASAFSR	DR7/DRB5	HB
LEIFKQASAFSRASQ	Q15582	Transforming growth factor-beta-induced protein ig-h3	15	EM	C-ter	IFKQASAFS/FKQASAFSR	DR7/DRB5	HB
APTNEAFEKIPSETLNRI	Q15582	Transforming growth factor-beta-induced protein ig-h3	18	EM	Internal	FEKIPSETL	DR7	IB
GKKLRVFVYRNSLCIENS	Q15582	Transforming growth factor-beta-induced protein ig-h3	18	EM	Internal	FVYRNSLCI	DR7	HB
IDKVISTITNNIQ	Q15582	Transforming growth factor-beta-induced protein ig-h3	13	EM	Internal	VISTITNNI	DR7	HB
KKLRVFVYRNSLCIENS	Q15582	Transforming growth factor-beta-induced protein ig-h3	17	EM	Internal	FVYRNSLCI	DR7	HB
LRVFVYRNSLCIEN	Q15582	Transforming growth factor-beta-induced protein ig-h3	14	EM	Internal	FVYRNSLCI	DR7	HB
LRVFVYRNSLCIENS	Q15582	Transforming growth factor-beta-induced protein ig-h3	15	EM	Internal	FVYRNSLCI	DR7	HB
IDKVISTITNNIQQ	Q15582	Transforming growth factor-beta-induced protein ig-h3	14	EM	Internal	VISTITNNI	DR7	HB
IDKVISTITNNIQQII	Q15582	Transforming growth factor-beta-induced protein ig-h3	16	EM	Internal	VISTITNNI	DR7	HB
LIDKVISTITNNIQ	Q15582	Transforming growth factor-beta-induced protein ig-h3	14	EM	Internal	VISTITNNI	DR7	HB
APTNEAFEKIPSETLNR	Q15582	Transforming growth factor-beta-induced protein ig-h3	17	EM	Internal	FEKIPSETL/FEKIPSETL	DR7/DRB5	IB
EFPIGTYLNYECRPG	Q2VPA4	Complement component receptor 1-like protein	15	M	Internal	IGTYLNYEC	DR7	HB
FPIGTYLNYECRPG	Q2VPA4	Complement component receptor 1-like protein	14	M	Internal	IGTYLNYEC	DR7	HB
VDNIINSSAWVIR	Q5QGZ9	C-type lectin domain family 12 member A	13	M	Internal	IINSSAWVI	DR7	HB
EIRRYQKSTELLIRK	Q6NXT2	Histone H3.3C	15	N	Internal	YQKSTELLI	DR7	HB
RRYQKSTELLIRKLPFQR	Q6NXT2	Histone H3.3C	18	N	Internal	YQKSTELLI/LIRKLPFQR	DR7/DRB5	HB
DMAVVQRLFCM	Q6NY19	KN motif and ankyrin repeat domain-containing protein 3	11	C	Internal	NA	NA	NA
SNPHLLSFPSEPLE	Q6PI73	Leukocyte immunoglobulin-like receptor subfamily A member 6	14	M	Internal	LLSFPSEPL	DR7	HB
KIYWVNESAGFLF	Q86XX4	Extracellular matrix protein FRAS1	13	EM	Internal	YWVNESAGF	DR7	HB
PDNLEKYGFEPTQEGKLFQLYPRNFLR	Q8IXM3	39S ribosomal protein L41, mitochondrial	27	Mit	C-ter	YGFEPTQEG	DR7	HB
FEHVNGKYSTPDLIPEG	Q8TDI0	Chromodomain-helicase-DNA-binding protein 5	17	N	Internal	VNGKYSTPD	DR7	HB
PPILPLTHGPTGGFNWRETLLQE	Q8TF42	Ubiquitin-associated and SH3 domain-containing protein B	23	C	C-ter	LTHGPTGGF	DR7	HB
KPVPDQIINFYKSNYVQRF	Q92608	Dedicator of cytokinesis protein 2	19	C	Internal	INFYKSNYV/INFYKSNYV	DR7/DR15	HB
QIINFYKSNYVQR	Q92608	Dedicator of cytokinesis protein 2	13	C	Internal	INFYKSNYV/INFYKSNYV	DR7/DR15	HB
QIINFYKSNYVQRF	Q92608	Dedicator of cytokinesis protein 2	14	C	Internal	INFYKSNYV/INFYKSNYV	DR7/DR15	HB
DHVLLFWKSLALKE	Q92673	Sortilin-related receptor	14	M	Internal	LLFWKSLAL/VLLFWKSLA	DR7/DR15	HB
NDHVLLFWKSLALKE	Q92673	Sortilin-related receptor	15	M	Internal	LLFWKSLAL/VLLFWKSLA	DR7/DR15	HB
KDIILPFRVIPLVR	Q96CW1	AP-2 complex subunit mu	14	M	Internal	LPFRVIPLV/ILPFRVIPL	DR7/DR15	HB
RVHRLLRKGNYAERVG	Q96KK5	Histone H2A type 1-H	16	N	N-ter	LLRKGNYAE	DR7	HB
KVNGLPPEIAAVPELAK	Q96RS0	Trimethylguanosine synthase	17	C	Internal	NA	NA	NA
DHGSTGILVFPNEDLH	Q99538	Legumain	16	Lis/End	Internal	ILVFPNEDL/ILVFPNEDL	DR7/DR15	IB
DHGSTGILVFPNEDLHVK	Q99538	Legumain	18	Lis/End	Internal	ILVFPNEDL/ILVFPNEDL	DR7/DR15	IB
DHGSTGILVFPNEDLHVKD	Q99538	Legumain	19	Lis/End	Internal	ILVFPNEDL/ILVFPNEDL	DR7/DR15	IB
PIRTVGLGDAISAEGLFYSEVHPHY	Q9BRR6	ADP-dependent glucokinase	25	EM	C-ter	LFYSEVHPH/VGLGDAISA	DR7/DR15	IB
YVDKFYRSLNIRI	Q9H013	ADAM19	13	M	Internal	FYRSLNIRI	DR7	HB
PALPLDQLQITHKD	Q9H1I8	Activating signal cointegrator 1 complex subunit 2	14	N	N-ter	NA	NA	NA
DGKRIQYQLVDISQDN	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	16	C	Internal	NA	NA	NA
KRIQYQLVDISQDN	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	14	C	Internal	NA	NA	NA
DGKRIQYQLVDISQDNA	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	17	C	Internal	NA	NA	NA
KYVPAIAHLIH	Q9H3G5	Probable serine carboxypeptidase CPVL	11	Lis/End	Internal	VPAIAHLIH/YVPAIAHLI	DR15/DRB5	HB
KYVPAIAHLIHS	Q9H3G5	Probable serine carboxypeptidase CPVL	12	Lis/End	Internal	VPAIAHLIH/YVPAIAHLI	DR15/DRB5	HB
YAGKYVPAIAHLIHSL	Q9H3G5	Probable serine carboxypeptidase CPVL	16	Lis/End	Internal	VPAIAHLIH/YVPAIAHLI	DR15/DRB5	HB
VTFAGTLLERGPLVTAR	Q9HD36	Bcl-2-like protein 10	17	Mit	Internal	NA	NA	NA
MFLQYYLNEQGDRVYTLKKFD	Q9NPE3	H/ACA ribonucleoprotein complex subunit 3	21	N	N-ter	NA	NA	NA
AKHLIERSQVFNILR	Q9NZK5	Adenosine deaminase CECR1	15	EM	Internal	IERSQVFNI	DR7	HB

DLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	16	Lis/End	Internal	WDYAHQHGI/YAHQHGIPD	DR7/DRB5	IB
GGNDLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	19	Lis/End	Internal	WDYAHQHGI/YAHQHGIPD	DR7/DRB5	IB
GGNDLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	20	Lis/End	Internal	WDYAHQHGI/YAHQHGIPD	DR7/DRB5	IB
GNDLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	18	Lis/End	Internal	WDYAHQHGI/YAHQHGIPD	DR7/DRB5	IB
GNDLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	19	Lis/End	Internal	WDYAHQHGI/YAHQHGIPD	DR7/DRB5	IB
LSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	15	Lis/End	Internal	WDYAHQHGI/YAHQHGIPD	DR7/DRB5	IB
NDLSVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	17	Lis/End	Internal	WDYAHQHGI/YAHQHGIPD	DR7/DRB5	IB
NDLSVWDYAHQHGIPDET	Q9UBR2	Cathepsin Z	18	Lis/End	Internal	WDYAHQHGI/YAHQHGIPD	DR7/DRB5	IB
SVWDYAHQHGIPDE	Q9UBR2	Cathepsin Z	14	Lis/End	Internal	WDYAHQHGI/YAHQHGIPD	DR7/DRB5	IB
DGIFYEFRSYYLKPS	Q9UFN0	Protein NipSnap homolog 3A	15	C	Internal	FYEFRSYYL	DR7	HB
KNKSIICYYNTYQVVQ	Q9UHA4	Ragulator complex protein LAMTOR3	16	Lis/End	Internal	ICYYNTYQV/ICYYNTYQV	DR7/DR15	HB
IPLSIIAFTNHRIFR	Q9UNW8	Probable G-protein coupled receptor 132	15	M	Internal	IIAFTNHRI/IIAFTNHRI	DR7/DR15	HB
KNMKCLTFFLMLPETVKNRSKKS	Q9Y2F9	BTB/POZ domain-containing protein 3	23	C	N-ter	LTFFLMLPE/FFLMLPETV	DR15/DRB5	HB
DPDTLHIWKTNSLPLR	Q9Y4D7	Plexin-D1	16	M	Internal	IWKTNSLPL	DR7	HB
DTLHIWKTNSLPLR	Q9Y4D7	Plexin-D1	14	M	Internal	IWKTNSLPL	DR7	HB
HRKVILRFTDFKLDG	Q9Y561	Low-density lipoprotein receptor-related protein 12	15	M	Internal	VILRFTDFK/ILRFTDFKL	DR7/DR15	HB
EGNAIFTFPNTPVK	Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	14	Mit	Internal	IFTFPNTPV	DR7	HB

Cellular Location (a)	Location in Sequence (b)	Binding Core/s (c)	Allele/s (d)	Theoretical Affinity (e)

(a) Cellular location: membrane (M), extracellular matrix or secreted proteins (EM/S), endoplasmic reticulum/Golgi (ER/G), lysosome/endosome (Lys/End). Mitochondrial (Mit), cytosolic (C) and nuclear (N).
(b) Location in the sequence of the parental protein: the 30 first residues of the parental protein were considered as the N-ter, and the last 30 residues as C-ter and the rest as internal peptides.
(c) Binding core: / separates cores for different alleles. NA means non-assigned
(d) Allele: if more than one allele can assigned to a peptide, was noted as double binder. / separates alleles in the same order that the binding core is annotated
(e) Theoretical affinity: High binders (HB), Intermediate binders (IB), low binders (LB) or non-assigned (NA)

ANNEX 2. TOTAL HLA-DR PEPTIDOME FROM SAMPLES PULSED WITH THYROGLOBULIN OR THYROID EXTRACT

Donor C(DRB1 *0301, DRB1*0901)

AC	Description	Sequence	Sample	Source	Length	Cellular Location	Function
P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	GQVINETSQHHDDLE	Donor C	Extract	15	C	Apoptosis/cell death
P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]	GDGQVNYEEFVQMMTAK	Donor C	Extract	17	C	Apoptosis/cell death
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	LNTILPDARDPAFK	Donor C	Extract	14	Lys/End	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQ	Donor C	Extract	15	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIW	Donor C	Extract	17	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIWD	Donor C	Extract	18	C	Autophagy
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor C	Extract	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor C	Extract	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVRH	Donor C	Extract	17	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	LTDEIVKDVKQTYLARV	Donor C	Extract	17	EM/S	Blood/coagulation
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 - [HBA_HUMAN]	LPAEFTPAVHASLDK	Donor C	Extract	15	C	Blood/coagulation
O60716	Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN]	DSIKMEIVDHALHA	Donor C	Extract	14	C	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLLM	Donor C	Extract	15	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	GPGDPDSIRCDTRPQLLM	Donor C	Extract	18	M	Cell adhesion/Matrix
P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	GPPYVSWLIDANHNMQ	Donor C	Extract	16	M	Cell adhesion/Matrix
P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	GPPYVSWLIDANHNMQ	Donor C	Extract	16	M	Cell adhesion/Matrix
Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	SHDSIQISWKAPRGKF	Donor C	Extract	16	EM/S	Cell adhesion/Matrix
Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	SHDSIQISWKAPRGKFG	Donor C	Extract	17	EM/S	Cell adhesion/Matrix
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	DVYGIVYDLRMHRP	Donor C	Extract	14	M	Cell adhesion/Matrix
Q13418	Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 - [ILK_HUMAN]	PAKRPKFDMIVPILEKMQDK	Donor C	Extract	20	M	Cell adhesion/Matrix
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICKVVE	Donor C	Extract	17	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	PILYRPVAVALDTKGPEIR	Donor C	Extract	19	C	Cell metabolism
P15291	Beta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 PE=1 SV=5 - [B4GT1_HUMAN]	DGLNSLTYQVLDVQRYPL	Donor C	Extract	18	ER/G	Cell metabolism
P15586	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3 - [GNS_HUMAN]	AAPQYQKAFQNVFAPR	Donor C	Extract	16	Lys/End	Cell metabolism
P18859	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 - [ATP5J_HUMAN]	PKFEVIEKPQA	Donor C	Extract	11	Mit	Cell metabolism
Q13510	Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=5 - [ASAH1_HUMAN]	LDVYELDAKQGRWY	Donor C	Extract	14	Lys/End	Cell metabolism
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]	PETSVLVLRKPGINVASDWSIHLR	Donor C	Extract	24	ER/G	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	TKFWVVDQTHFY	Donor C	Extract	12	ER/G	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	HTKFWVVDQTHFY	Donor C	Extract	13	ER/G	Cell metabolism
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	VQNMLHWSQAVKF	Donor C	Extract	13	Lys/End	Cell proliferation/differenciation
Q92674	Centromere protein I OS=Homo sapiens GN=CENPI PE=1 SV=2 - [CENPI_HUMAN]	RKWNSLSVIPVLNSSSYT	Donor C	Extract	18	N	Cell proliferation/differenciation
Q9BYP7	Serine/threonine-protein kinase WNK3 OS=Homo sapiens GN=WNK3 PE=1 SV=2 - [WNK3_HUMAN]	KAVAKSIRDRVTPIK	Donor C	Extract	15	C	Cell proliferation/differenciation

O15143	Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3 - [ARC1B_HUMAN]	GGMSIWDVKSLESALKDLKIK	Donor C	Extract	21	C	Cytostkeleton
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	IGEETVITVDTKAAGKGK	Donor C	Extract	18	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVRKSSTPE	Donor C	Extract	19	C	Cytostkeleton
Q01518	Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 - [CAP1_HUMAN]	IKGKINSITVDNCKK	Donor C	Extract	15	M	Cytostkeleton
Q0JRZ9	FCH domain only protein 2 OS=Homo sapiens GN=FCHO2 PE=1 SV=2 - [FCHO2_HUMAN]	IHIKEIIGSLSNAIKE	Donor C	Extract	16	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	VDKVLERDQKLSELDDR	Donor C	Extract	17	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	VDIMRVNVDKVLERDQKL	Donor C	Extract	18	M	Endocytosis/exocytosis
P05388	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 - [RLA0_HUMAN]	PREDRATWKSNYFLKIIQLLD	Donor C	Extract	21	N	Gene expression /chromatine organization
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	APVKKLVVKGGKKKKQVLKFTLD	Donor C	Extract	23	C	Gene expression /chromatine organization
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	VPELPLVVEDKVEGYKK	Donor C	Extract	17	C	Gene expression /chromatine organization
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	GYEPPVQESV	Donor C	Extract	10	C	Gene expression /chromatine organization
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	LVREIAQDFKTDLRFQ	Donor C	Extract	16	N	Gene expression /chromatine organization
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	VGVLLRKLEAGIRGISH	Donor C	Extract	17	N	Gene expression /chromatine organization
Q9BY77	Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=1 SV=2 - [PDIP3_HUMAN]	PDTILKALFKSSGASVTTQPTEFKIKL	Donor C	Extract	27	N	Gene expression /chromatine organization
O00626	C-C motif chemokine 22 OS=Homo sapiens GN=CCL22 PE=1 SV=2 - [CCL22_HUMAN]	PRVPWVKMILNKLSQ	Donor C	Extract	15	EM/S	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	SKSWITFDLKNKEVSVK	Donor C	Extract	17	M	Immune response
P04233	HLA class II histocompatibility antigen gamma chain OS=Homo sapiens GN=CD74 PE=1 SV=3 - [HG2A_HUMAN]	TIDWKVFESWMHH	Donor C	Extract	13	Lys/End	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	EMFYVDLDKKETVWH	Donor C	Extract	15	M	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KVVVYLQKLDTAYD	Donor C	Extract	14	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	VVVYLQKLDTAYDD	Donor C	Extract	14	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KVVVYLQKLDTAYDD	Donor C	Extract	15	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KKVVVYLQKLDTAYDD	Donor C	Extract	16	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	VVVYLQKLDTAYDDLG	Donor C	Extract	16	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	EKKVVVYLQKLDTAYDD	Donor C	Extract	17	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KKVVVYLQKLDTAYDDL	Donor C	Extract	17	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KVVVYLQKLDTAYDDLG	Donor C	Extract	17	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KKVVVYLQKLDTAYDDLG	Donor C	Extract	18	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	EKKVVVYLQKLDTAYDDLG	Donor C	Extract	19	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	GPQEKKVVVYLQKLDTAYDD	Donor C	Extract	20	Lys/End	Immune response
Q9NPH3	Interleukin-1 receptor accessory protein OS=Homo sapiens GN=IL1RAP PE=1 SV=2 - [IL1AP_HUMAN]	LPGGIVTDETLSFIQK	Donor C	Extract	16	M	Immune response
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	KDLIADLKYELTGKF	Donor C	Extract	15	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTG	Donor C	Extract	15	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	KDLIADLKYELTGKFE	Donor C	Extract	16	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTGK	Donor C	Extract	16	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTGKF	Donor C	Extract	17	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTGKFE	Donor C	Extract	18	C	Ion homeostasis
Q99250	Sodium channel protein type 2 subunit alpha OS=Homo sapiens GN=SCN2A PE=1 SV=3 - [SCN2A_HUMAN]	RWKNVKVNFDNVGLGYLSLLQV	Donor C	Extract	22	M	Ion homeostasis

Q658L1	Protein FAM154B OS=Homo sapiens GN=FAM154B PE=2 SV=1 - [F154B_HUMAN]	KSIMKEDFPAWESCRQGLIKKQQQIPNP	Donor C	Extract	28	NA	NA
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	FSSKFQVDNNNRLL	Donor C	Extract	14	EM/S	Others
P30086	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 - [PEBP1_HUMAN]	WSGPLSLQEVDEQPQHPL	Donor C	Extract	18	C	Others
P30533	Alpha-2-macroglobulin receptor-associated protein OS=Homo sapiens GN=LRPAP1 PE=1 SV=1 - [AMRP_HUMAN]	LAELHADLKIQERDEL	Donor C	Extract	16	ER/G	Others
P43251	Biotinidase OS=Homo sapiens GN=BTD PE=1 SV=2 - [BTD_HUMAN]	DILFFDPAIRVLRD	Donor C	Extract	14	EM/S	Others
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]	DPANITLEPMEIRTFLASVQWK	Donor C	Extract	22	Lys/End	Proteolysis
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]	KYVPAIAHLIH	Donor C	Extract	11	Lys/End	Proteolysis
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]	KYVPAIAHLIHS	Donor C	Extract	12	Lys/End	Proteolysis
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]	KYVPAIAHLIHSL	Donor C	Extract	13	Lys/End	Proteolysis
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]	AGKYVPAIAHLIHSL	Donor C	Extract	15	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	SVWDYAHQHGIPDE	Donor C	Extract	14	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	LSVWDYAHQHGIPDE	Donor C	Extract	15	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	DLSVWDYAHQHGIPDE	Donor C	Extract	16	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	LSVWDYAHQHGIPDET	Donor C	Extract	16	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	DLSVWDYAHQHGIPDET	Donor C	Extract	17	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	NDLSVWDYAHQHGIPDE	Donor C	Extract	17	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	GNDLSVWDYAHQHGIPDE	Donor C	Extract	18	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	NDLSVWDYAHQHGIPDET	Donor C	Extract	18	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	GGNDLSVWDYAHQHGIPDE	Donor C	Extract	19	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	GNDLSVWDYAHQHGIPDET	Donor C	Extract	19	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	GGNDLSVWDYAHQHGIPDET	Donor C	Extract	20	Lys/End	Proteolysis
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	RGLFIIDPNGVIK	Donor C	Extract	13	Mit	Redox homeostasis
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	RGLFIIDDKGILRQ	Donor C	Extract	14	C	Redox homeostasis
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	RGLFIIDDKGILRQIT	Donor C	Extract	16	C	Redox homeostasis
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	ISFRGLFIIDDKGILRQ	Donor C	Extract	17	C	Redox homeostasis
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 - [SH3L3_HUMAN]	KRIQYQLVDISQDN	Donor C	Extract	14	C	Redox homeostasis
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 - [SH3L3_HUMAN]	DGKRIQYQLVDISQDN	Donor C	Extract	16	C	Redox homeostasis
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 - [SH3L3_HUMAN]	DGKRIQYQLVDISQDNA	Donor C	Extract	17	C	Redox homeostasis
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	GSFLAAVGNLI	Donor C	Extract	11	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	IDGSFLAAVGNLI	Donor C	Extract	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LPFYPAYEGQFSL	Donor C	Extract	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	RRFLAVQSVISGRF	Donor C	Extract	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SKTAFYQALQNSLG	Donor C	Extract	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LPFYPAYEGQFSLEE	Donor C	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	QRRFLAVQSVISGRF	Donor C	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SKTAFYQALQNSLGG	Donor C	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	VPESKVIFDANAPVA	Donor C	Extract	15	EM/S	Thyroid

P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDVA	Donor C	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	QRRFLAVQSVISGRFR	Donor C	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SKTAFYQALQNSLGGE	Donor C	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDVA	Donor C	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ILQRRFLAVQSVISGRF	Donor C	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDV	Donor C	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SKTAFYQALQNSLGGED	Donor C	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVA	Donor C	Extract	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDV	Donor C	Extract	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SSKTAFYQALQNSLGGED	Donor C	Extract	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVAH	Donor C	Extract	19	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDVA	Donor C	Extract	19	EM/S	Thyroid
P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3 - [MPRI_HUMAN]	GPLKFLHQDIDSGQGIR	Donor C	Extract	17	Lys/End	Transport
P61026	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 - [RAB10_HUMAN]	ISTIGIDFKIKTVEL	Donor C	Extract	15	ER/G	Transport
Q15751	Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens GN=HERC1 PE=1 SV=2 - [HERC1_HUMAN]	ARFRGLTASVLLDL	Donor C	Extract	14	M	Transport
P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	GQVINETSQHHDDLE	Donor C	Purified	15	C	Apoptosis/cell death
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	IRTIELDGKTIKLQ	Donor C	Purified	14	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQ	Donor C	Purified	15	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIWD	Donor C	Purified	18	C	Autophagy
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor C	Purified	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor C	Purified	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVRH	Donor C	Purified	17	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVRH	Donor C	Purified	17	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	LTDEIVKDVKQTYLAR	Donor C	Purified	16	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	DLTDEIVKDVKQTYLAR	Donor C	Purified	17	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	LTDEIVKDVKQTYLARV	Donor C	Purified	17	EM/S	Blood/coagulation
Q13093	Platelet-activating factor acetylhydrolase OS=Homo sapiens GN=PLA2G7 PE=1 SV=1 - [PAFA_HUMAN]	FADFTFATGKIIG	Donor C	Purified	13	EM/S	Blood/coagulation
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLLM	Donor C	Purified	15	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	GPGDPDSIRCDTRPQL	Donor C	Purified	16	M	Cell adhesion/Matrix
P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	GPPYVSWLIDANHNMQ	Donor C	Purified	16	M	Cell adhesion/Matrix
P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	GPPYVSWLIDANHNMQ	Donor C	Purified	16	M	Cell adhesion/Matrix
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	DVYGIVYDLRMHRP	Donor C	Purified	14	M	Cell adhesion/Matrix
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	DVYGIVYDLRMHRPLM	Donor C	Purified	16	M	Cell adhesion/Matrix
P01308	Insulin OS=Homo sapiens GN=INS PE=1 SV=1 - [INS_HUMAN]	HLVEALYLVCGERGFFYTPKT	Donor C	Purified	21	EM/S	Cell metabolism
P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 - [ODPA_HUMAN]	PPFEVRGANQWIKFKSVS	Donor C	Purified	18	Mit	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICK	Donor C	Purified	14	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICKVVE	Donor C	Purified	17	C	Cell metabolism

P15291	Beta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 PE=1 SV=5 - [B4GT1_HUMAN]	LNSLTYQVLDVQRYP	Donor C	Purified	15	ER/G	Cell metabolism
P15586	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3 - [GNS_HUMAN]	AAPQYQKAFQNVFAPR	Donor C	Purified	16	Lys/End	Cell metabolism
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	DLEKIHLDEKSFRWL	Donor C	Purified	15	C	Cell metabolism
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	DLEKIHLDEKSFRWLH	Donor C	Purified	16	C	Cell metabolism
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	DLEKIHLDEKSFRWLHN	Donor C	Purified	17	C	Cell metabolism
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]	PETSVLVLRKPGINVASDWSIHLR	Donor C	Purified	24	ER/G	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	TKFWVVDQTHFY	Donor C	Purified	12	ER/G	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	HTKFWVVDQTHFY	Donor C	Purified	13	ER/G	Cell metabolism
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	EFWAFSYDEMAK	Donor C	Purified	12	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	VQNMLHWSQAVKF	Donor C	Purified	13	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	VQNMLHWSQAVKFQK	Donor C	Purified	15	Lys/End	Cell proliferation/differenciation
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	ITSIVKDSSAARNGLL	Donor C	Purified	16	M	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	GVIKVFNDMKVRKSSTPE	Donor C	Purified	18	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVRKSSTPE	Donor C	Purified	19	C	Cytostkeleton
P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	MLMPKKNRIAIYELLFKEGVMVAKKD	Donor C	Purified	26	C	Cytostkeleton
P47755	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3 - [CAZA2_HUMAN]	FNEVFNDVRLLLNNDN	Donor C	Purified	16	C	Cytostkeleton
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	AEREIVRDIKEKLCY	Donor C	Purified	15	C	Cytostkeleton
Q01518	Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 - [CAP1_HUMAN]	IKGKINSITVDNCKK	Donor C	Purified	15	M	Cytostkeleton
P09525	Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4 - [ANXA4_HUMAN]	TPTVLYDVQELRRA	Donor C	Purified	14	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	DIMRVNVDKVLERDQKL	Donor C	Purified	17	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	DIMRVNVDKVLERDQKL	Donor C	Purified	17	M	Endocytosis/exocytosis
P26196	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2 - [DDX6_HUMAN]	LIKKGVAKVDHVQMIVLDE	Donor C	Purified	19	C	Gene expression /chromatine organization
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	APVKKLVVKGGKKKKQVLKFTLD	Donor C	Purified	23	C	Gene expression /chromatine organization
P61353	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2 - [RL27_HUMAN]	GKFMKPGKVVLVLAGRYSGRKAVIVKNIDD	Donor C	Purified	30	C	Gene expression /chromatine organization
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	RGVLKVFLENVIR	Donor C	Purified	13	N	Gene expression /chromatine organization
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	ETRGVLKVFLENVIR	Donor C	Purified	15	N	Gene expression /chromatine organization
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	LVREIAQDFKTDLRFQ	Donor C	Purified	16	N	Gene expression /chromatine organization
Q14191	Werner syndrome ATP-dependent helicase OS=Homo sapiens GN=WRN PE=1 SV=2 - [WRN_HUMAN]	QLTSISEEVMDLAKHLPHA	Donor C	Purified	19	N	Gene expression /chromatine organization
Q9NSI6	Bromodomain and WD repeat-containing protein 1 OS=Homo sapiens GN=BRWD1 PE=1 SV=4 - [BRWD1_HUMAN]	IEHNARTFNEPESVIAR	Donor C	Purified	17	C	Gene expression /chromatine organization
O00626	C-C motif chemokine 22 OS=Homo sapiens GN=CCL22 PE=1 SV=2 - [CCL22_HUMAN]	PRVPWVKMILNKLSQ	Donor C	Purified	15	EM/S	Immune response
O00626	C-C motif chemokine 22 OS=Homo sapiens GN=CCL22 PE=1 SV=2 - [CCL22_HUMAN]	PRVPWVKMILNKLSQ	Donor C	Purified	15	EM/S	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	IQFHWKNSNQIKI	Donor C	Purified	13	M	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	SKSWITFDLKNKEVSVK	Donor C	Purified	17	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	AQGALANIAVDKANLEI	Donor C	Purified	17	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	IKEEHVIIQAEFYLNPD	Donor C	Purified	17	M	Immune response
P04233	HLA class II histocompatibility antigen gamma chain OS=Homo sapiens GN=CD74 PE=1 SV=3 - [HG2A_HUMAN]	TIDWKVFESWMHH	Donor C	Purified	13	Lys/End	Immune response
P04233	HLA class II histocompatibility antigen gamma chain OS=Homo sapiens GN=CD74 PE=1 SV=3 - [HG2A_HUMAN]	LPKPPKPVSKMRMATPLLMQALPM	Donor C	Purified	24	Lys/End	Immune response

P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	LPRIICDNTGITT	Donor C	Purified	13	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	SLPRIICDNTGITT	Donor C	Purified	14	Lys/End	Immune response
P06734	Low affinity immunoglobulin epsilon Fc receptor OS=Homo sapiens GN=FCER2 PE=1 SV=1 - [FCER2_HUMAN]	EQQRLKSQDLELSWN	Donor C	Purified	15	M	Immune response
P06734	Low affinity immunoglobulin epsilon Fc receptor OS=Homo sapiens GN=FCER2 PE=1 SV=1 - [FCER2_HUMAN]	AEQQRLKSQDLELSWNLNG	Donor C	Purified	19	M	Immune response
P13686	Tartrate-resistant acid phosphatase type 5 OS=Homo sapiens GN=ACP5 PE=1 SV=3 - [PPA5_HUMAN]	YPVWSIAEHGPT	Donor C	Purified	12	Lys/End	Immune response
P15260	Interferon gamma receptor 1 OS=Homo sapiens GN=IFNGR1 PE=1 SV=1 - [INGR1_HUMAN]	GPPKLDIRKEEKQIMIDIFHP	Donor C	Purified	21	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	EMFYVDLDKKETVWH	Donor C	Purified	15	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	MFYVDLDKKETVWHLE	Donor C	Purified	16	M	Immune response
P38484	Interferon gamma receptor 2 OS=Homo sapiens GN=IFNGR2 PE=1 SV=2 - [INGR2_HUMAN]	IEEYLKDPTQPILE	Donor C	Purified	14	M	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	VVVYLQKLDTAYDD	Donor C	Purified	14	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KVVVYLQKLDTAYDD	Donor C	Purified	15	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KKVVVYLQKLDTAYDD	Donor C	Purified	16	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KVVVYLQKLDTAYDDL	Donor C	Purified	16	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	KKVVVYLQKLDTAYDDLG	Donor C	Purified	18	Lys/End	Immune response
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]	GPQEKKVVVYLQKLDTAYDD	Donor C	Purified	20	Lys/End	Immune response
Q92583	C-C motif chemokine 17 OS=Homo sapiens GN=CCL17 PE=1 SV=1 - [CCL17_HUMAN]	PNNKRVKNAVKYLQSLERS	Donor C	Purified	19	EM/S	Immune response
Q9NPH3	Interleukin-1 receptor accessory protein OS=Homo sapiens GN=IL1RAP PE=1 SV=2 - [IL1AP_HUMAN]	LPGGIVTDETLSFIQK	Donor C	Purified	16	M	Immune response
Q9Y3Z3	SAM domain and HD domain-containing protein 1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2 - [SAMH1_HUMAN]	AKPKVLLDVKLKAEDFI	Donor C	Purified	17	N	Immune response
Q93050	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3 - [VPP1_HUMAN]	RRKHLGTLNFGGIR	Donor C	Purified	14	M	Ion homeostasis
Q658Y4	Protein FAM91A1 OS=Homo sapiens GN=FAM91A1 PE=1 SV=3 - [F91A1_HUMAN]	HSSWKNVPSVNRLK	Donor C	Purified	14	NA	NA
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	SSKFQVDNNNRLL	Donor C	Purified	13	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	FSSKFQVDNNNRLL	Donor C	Purified	14	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	EDSLVFVQTDKSIYKP	Donor C	Purified	16	EM/S	Others
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]	DPANITLEPMEIRTFLASVQWK	Donor C	Purified	22	Lys/End	Proteolysis
P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	INDAFNLASAHKVPV	Donor C	Purified	15	M	Proteolysis
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]	KYVPAIAHLIHS	Donor C	Purified	12	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	LSVWDYAHQHGIPD	Donor C	Purified	14	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	SVWDYAHQHGIPDE	Donor C	Purified	14	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	LSVWDYAHQHGIPDE	Donor C	Purified	15	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	DLSVWDYAHQHGIPDE	Donor C	Purified	16	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	LSVWDYAHQHGIPDET	Donor C	Purified	16	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	DLSVWDYAHQHGIPDET	Donor C	Purified	17	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	GNDLSVWDYAHQHGIPD	Donor C	Purified	17	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	NDLSVWDYAHQHGIPDE	Donor C	Purified	17	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	GNDLSVWDYAHQHGIPDE	Donor C	Purified	18	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	NDLSVWDYAHQHGIPDET	Donor C	Purified	18	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	GGNDLSVWDYAHQHGIPDE	Donor C	Purified	19	Lys/End	Proteolysis

Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	GNDLSVWDYAHQHGIPDET	Donor C	Purified	19	Lys/End	Proteolysis
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	GGNDLSVWDYAHQHGIPDET	Donor C	Purified	20	Lys/End	Proteolysis
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	RGLFIIDPNGVIK	Donor C	Purified	13	Mit	Redox homeostasis
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	RGLFIIDPNGVIKH	Donor C	Purified	14	Mit	Redox homeostasis
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	RGLFIIDDKGILRQ	Donor C	Purified	14	C	Redox homeostasis
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 - [SH3L3_HUMAN]	DGKRIQYQLVDISQDN	Donor C	Purified	16	C	Redox homeostasis
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 - [SH3L3_HUMAN]	DGKRIQYQLVDISQDNA	Donor C	Purified	17	C	Redox homeostasis
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 - [SH3L3_HUMAN]	ILDGKRIQYQLVDISQDNAL	Donor C	Purified	20	C	Redox homeostasis
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LPFYPAYEGQFS	Donor C	Purified	12	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	GDQEFIKSLTPLE	Donor C	Purified	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	IDGSFLAAVGNLI	Donor C	Purified	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	KTAFYQALQNSLG	Donor C	Purified	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LPFYPAYEGQFSL	Donor C	Purified	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	RFLAVQSVISGRF	Donor C	Purified	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	IDGSFLAAVGNLIV	Donor C	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	KTAFYQALQNSLGG	Donor C	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LGDQEFIKSLTPLE	Donor C	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LPFYPAYEGQFSLE	Donor C	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFD	Donor C	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	RRFLAVQSVISGRF	Donor C	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SKTAFYQALQNSLG	Donor C	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDV	Donor C	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	QRRFLAVQSVISGRF	Donor C	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	VPESKVIFDANAPVA	Donor C	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	IDGSFLAAVGNLIVVT	Donor C	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LQRRFLAVQSVISGRF	Donor C	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDVA	Donor C	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	QRRFLAVQSVISGRFR	Donor C	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SKTAFYQALQNSLGGE	Donor C	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDVA	Donor C	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ILQRRFLAVQSVISGRF	Donor C	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDV	Donor C	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SKTAFYQALQNSLGGED	Donor C	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDVAH	Donor C	Purified	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVA	Donor C	Purified	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SSKTAFYQALQNSLGGED	Donor C	Purified	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVAH	Donor C	Purified	19	EM/S	Thyroid

P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDVA	Donor C	Purified	19	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDVAH	Donor C	Purified	20	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SWQSLALSSVVVDPSIRHFDVAH	Donor C	Purified	23	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LDSWQSLALSSVVVDPSIRHFDVAH	Donor C	Purified	25	EM/S	Thyroid

Donorr D (DRB1*0301, DRB1 *1101)

AC	Description	Sequence	Sample	Source	Length	Celullar Location	Function
P49773	Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2 - [HINT1_HUMAN]	IPAKIIFEDDRCLAFHDI	Donor D	Extract	18	C	Apoptosis/cell death
P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]	GDGQVNYEEFVQMMTAK	Donor D	Extract	17	C	Apoptosis/cell death
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN]	GQTLFAGYTDNLVRVWQVTIGTR	Donor D	Extract	23	M	Apoptosis/cell death
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	LNTILPDARDPAFK	Donor D	Extract	14	Lys/End	Autophagy
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	IQLNTILPDARDPAFK	Donor D	Extract	16	Lys/End	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	IRTIELDGKTIKLQ	Donor D	Extract	14	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQ	Donor D	Extract	15	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIW	Donor D	Extract	17	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIWD	Donor D	Extract	18	C	Autophagy
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	TPTLVEVSRNLGK	Donor D	Extract	13	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	APELLFFAKRYKAA	Donor D	Extract	14	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	NALLVRYTKKVPQVS	Donor D	Extract	15	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	TPTLVEVSRNLGKVG	Donor D	Extract	15	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	APELLFFAKRYKAAFT	Donor D	Extract	16	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	STPTLVEVSRNLGKVG	Donor D	Extract	16	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	TPTLVEVSRNLGKVGS	Donor D	Extract	16	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	TPTLVEVSRNLGKVGSK	Donor D	Extract	17	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	NALLVRYTKKVPQVSTPT	Donor D	Extract	18	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor D	Extract	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor D	Extract	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVRH	Donor D	Extract	17	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	LTDEIVKDVKQTYLAR	Donor D	Extract	16	EM/S	Blood/coagulation

P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	DLTDEIVKDVKQTYLAR	Donor D	Extract	17	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	LTDEIVKDVKQTYLARV	Donor D	Extract	17	EM/S	Blood/coagulation
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	LLVFATDDGFHFA	Donor D	Extract	13	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLL	Donor D	Extract	14	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLLM	Donor D	Extract	15	M	Cell adhesion/Matrix
P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	VPDDRDFEPSLGPVCPFR	Donor D	Extract	18	EM/S	Cell adhesion/Matrix
P10915	Hyaluronan and proteoglycan link protein 1 OS=Homo sapiens GN=HAPLN1 PE=2 SV=2 - [HPLN1_HUMAN]	KVGQIFAAWKILGYDR	Donor D	Extract	16	EM/S	Cell adhesion/Matrix
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2 - [ITAM_HUMAN]	FKEFQNNPNPRSLVKP	Donor D	Extract	16	M	Cell adhesion/Matrix
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2 - [ITAM_HUMAN]	SDIAFLIDGSGSIIPH	Donor D	Extract	16	M	Cell adhesion/Matrix
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2 - [ITAM_HUMAN]	SDIAFLIDGSGSIIPHD	Donor D	Extract	17	M	Cell adhesion/Matrix
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2 - [ITAM_HUMAN]	TFKEFQNNPNPRSLVKPI	Donor D	Extract	18	M	Cell adhesion/Matrix
P14780	Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=3 - [MMP9_HUMAN]	NQLYLFKDGKYWRFSEG	Donor D	Extract	17	EM/S	Cell adhesion/Matrix
P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	GPPYVSWLIDANHNMQ	Donor D	Extract	16	M	Cell adhesion/Matrix
Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	IPKVIVVITDGRSQ	Donor D	Extract	14	EM/S	Cell adhesion/Matrix
Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	SHDSIQISWKAPRGKF	Donor D	Extract	16	EM/S	Cell adhesion/Matrix
Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	SHDSIQISWKAPRGKFG	Donor D	Extract	17	EM/S	Cell adhesion/Matrix
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	DVYGIVYDLRMHRP	Donor D	Extract	14	M	Cell adhesion/Matrix
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	DVYGIVYDLRMHRPLM	Donor D	Extract	16	M	Cell adhesion/Matrix
Q13418	Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 - [ILK_HUMAN]	PAKRPKFDMIVPILEKMQDK	Donor D	Extract	20	M	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	GGIGALVRLKSLQGD	Donor D	Extract	15	EM/S	Cell adhesion/Matrix
Q9NQ25	SLAM family member 7 OS=Homo sapiens GN=SLAMF7 PE=1 SV=1 - [SLAF7_HUMAN]	SIVWTFNTTPLVT	Donor D	Extract	13	M	Cell adhesion/Matrix
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	NGKLVINGNPITIFQ	Donor D	Extract	15	C	Cell metabolism
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	SFQFGYNTGVINAPE	Donor D	Extract	15	M	Cell metabolism
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	GSFQFGYNTGVINAPE	Donor D	Extract	16	M	Cell metabolism
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	GSFQFGYNTGVINAPEKI	Donor D	Extract	18	M	Cell metabolism
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	IGSFQFGYNTGVINAPEKI	Donor D	Extract	19	M	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICK	Donor D	Extract	14	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	RPRAPIIAVTRNPQTA	Donor D	Extract	16	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICKVVE	Donor D	Extract	17	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	RPRAPIIAVTRNPQTAR	Donor D	Extract	17	C	Cell metabolism
P18859	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 - [ATP5J_HUMAN]	PKFEVIEKPQA	Donor D	Extract	11	Mit	Cell metabolism
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]	MNIVEAMERFGSR	Donor D	Extract	13	C	Cell metabolism
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]	MNIVEAMERFGSRNG	Donor D	Extract	15	C	Cell metabolism

Q16698	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1 - [DECR_HUMAN]	GHPNIVINNAAGNFISP	Donor D	Extract	17	Mit	Cell metabolism
Q16698	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1 - [DECR_HUMAN]	GHPNIVINNAAGNFISPT	Donor D	Extract	18	Mit	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	HTKFWVVDQTHFY	Donor D	Extract	13	ER/G	Cell metabolism
Q9NTX5	Enoyl-CoA hydratase domain-containing protein 1 OS=Homo sapiens GN=ECHDC1 PE=1 SV=2 - [ECHD1_HUMAN]	KVIELENWTEGKGLIVRGAKNTFS	Donor D	Extract	24	C	Cell metabolism
P17948	Vascular endothelial growth factor receptor 1 OS=Homo sapiens GN=FLT1 PE=1 SV=2 - [VGFR1_HUMAN]	FPLDTLIPDGKRIIWDSR	Donor D	Extract	18	M	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	DGYILCLNRIPHG	Donor D	Extract	13	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GYILCLNRIPHGR	Donor D	Extract	13	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	DGYILCLNRIPHGR	Donor D	Extract	14	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	DGYILCLNRIPHGRK	Donor D	Extract	15	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	EDGYILCLNRIPHGR	Donor D	Extract	15	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	EDGYILCLNRIPHGRK	Donor D	Extract	16	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	TEDGYILCLNRIPHGRK	Donor D	Extract	17	Lys/End	Cell proliferation/differenciation
P57059	Serine/threonine-protein kinase SIK1 OS=Homo sapiens GN=SIK1 PE=1 SV=2 - [SIK1_HUMAN]	TDPFRPALLCPQPQTLVQSVLQAEMDCE	Donor D	Extract	28	C	Cell proliferation/differenciation
O00160	Myosin-If OS=Homo sapiens GN=MYO1F PE=1 SV=3 - [MYO1F_HUMAN]	PSGWWKGRLHGQEGLFPGNYVEKI	Donor D	Extract	24	C	Cytostkeleton
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	VGFIFKNGKITSIV	Donor D	Extract	14	M	Cytostkeleton
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	HVGFIFKNGKITSIV	Donor D	Extract	15	M	Cytostkeleton
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	HVGFIFKNGKITSIVK	Donor D	Extract	16	M	Cytostkeleton
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	ITSIVKDSSAARNGLL	Donor D	Extract	16	M	Cytostkeleton
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	GHVGFIFKNGKITSIVK	Donor D	Extract	17	M	Cytostkeleton
O15143	Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3 - [ARC1B_HUMAN]	GGMSIWDVKSLESALKDLKIK	Donor D	Extract	21	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	GVIKVFNDMKVRKSSTPE	Donor D	Extract	18	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVRKSSTPE	Donor D	Extract	19	C	Cytostkeleton
P47755	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3 - [CAZA2_HUMAN]	FNEVFNDVRLLLNNDN	Donor D	Extract	16	C	Cytostkeleton
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	AEREIVRDIKEKLCY	Donor D	Extract	15	C	Cytostkeleton
Q12965	Myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2 - [MYO1E_HUMAN]	PSGWWTGRLRGKQGLFPNNYVTKI	Donor D	Extract	24	C	Cytostkeleton
Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN]	FPTIKIFQKGESPV	Donor D	Extract	14	ER/G	Others
Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN]	GFPTIKIFQKGESPVD	Donor D	Extract	16	ER/G	Others
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	DIMRVNVDKVLERDQK	Donor D	Extract	16	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	DIMRVNVDKVLERDQK	Donor D	Extract	16	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	DIMRVNVDKVLERDQKL	Donor D	Extract	17	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	VDKVLERDQKLSELDDR	Donor D	Extract	17	M	Endocytosis/exocytosis
O15516	Circadian locomoter output cycles protein kaput OS=Homo sapiens GN=CLOCK PE=1 SV=1 - [CLOCK_HUMAN]	GMSQFQFSAQLGAMQHL	Donor D	Extract	17	N	Gene expression /chromatine organization
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	NPTNTVFDAKRLIGRRFDD	Donor D	Extract	19	C	Gene expression /chromatine organization

P15923	Transcription factor E2-alpha OS=Homo sapiens GN=TCF3 PE=1 SV=1 - [TFE2_HUMAN]	VRERNLNPKAACLKRR	Donor D	Extract	16	N	Gene expression /chromatine organization
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	EILPTTPISEQKGGKPEPPAMPQPVPTA	Donor D	Extract	28	C	Gene expression /chromatine organization
P32969	60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 - [RL9_HUMAN]	GIYVSEKGTVQQADE	Donor D	Extract	15	C	Gene expression /chromatine organization
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	PVKKLVVKGGKKKKQVLKFTLD	Donor D	Extract	22	C	Gene expression /chromatine organization
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	APVKKLVVKGGKKKKQVLKFTLD	Donor D	Extract	23	C	Gene expression /chromatine organization
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	VPELPLVVEDKVEGYKK	Donor D	Extract	17	C	Gene expression /chromatine organization
P49591	Seryl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN]	VLDLDLFRVDKGGD	Donor D	Extract	14	C	Gene expression /chromatine organization
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	GYEPPVQESV	Donor D	Extract	10	C	Gene expression /chromatine organization
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	NTLVFIVDVKANKHQ	Donor D	Extract	15	C	Gene expression /chromatine organization
Q04837	Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1 - [SSBP_HUMAN]	ESETTTSLVLERSLNRVHLLGRVGQD	Donor D	Extract	26	Mit	Gene expression /chromatine organization
Q13347	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1 - [EIF3I_HUMAN]	PQYFEFEFEA	Donor D	Extract	10	C	Gene expression /chromatine organization
Q13523	Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens GN=PRPF4B PE=1 SV=3 - [PRP4B_HUMAN]	PAKRISINQALQHAFIQEKI	Donor D	Extract	20	N	Gene expression /chromatine organization
Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3 - [H2A1H_HUMAN]	RVHRLLRKGNYAERVG	Donor D	Extract	16	N	Gene expression /chromatine organization
Q99547	M-phase phosphoprotein 6 OS=Homo sapiens GN=MPHOSPH6 PE=1 SV=2 - [MPH6_HUMAN]	KLMLQMNAKHKAE	Donor D	Extract	13	N	Gene expression /chromatine organization
Q9BY77	Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=1 SV=2 - [PDIP3_HUMAN]	PDTILKALFKSSGASVTTQPTEFKIKL	Donor D	Extract	27	N	Gene expression /chromatine organization
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 OS=Homo sapiens GN=PIN4 PE=1 SV=1 - [PIN4_HUMAN]	PPVKTKFGYHIIMVEGRK	Donor D	Extract	18	N	Gene expression /chromatine organization
O00626	C-C motif chemokine 22 OS=Homo sapiens GN=CCL22 PE=1 SV=2 - [CCL22_HUMAN]	PRVPWVKMILNKLSQ	Donor D	Extract	15	EM/S	Immune response
O00626	C-C motif chemokine 22 OS=Homo sapiens GN=CCL22 PE=1 SV=2 - [CCL22_HUMAN]	PRVPWVKMILNKLSQ	Donor D	Extract	15	EM/S	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	SKSWITFDLKNKEVSVK	Donor D	Extract	17	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	LANIAVDKANLEIM	Donor D	Extract	14	M	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	SLPRIICDNTGITT	Donor D	Extract	14	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	ISLPRIICDNTGITT	Donor D	Extract	15	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	QNQIAVDEIRERLFE	Donor D	Extract	15	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	DGDRFWWENEGVFSMQQR	Donor D	Extract	18	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	YPRISVNNVLPVFD	Donor D	Extract	14	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	YPRISVNNVLPVFDN	Donor D	Extract	15	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	AYPRISVNNVLPVFDN	Donor D	Extract	16	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	YPRISVNNVLPVFDNL	Donor D	Extract	16	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	AYPRISVNNVLPVFDNL	Donor D	Extract	17	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	GPVDEVRELQKAIGAVPL	Donor D	Extract	18	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	YPRISVNNVLPVFDNLMQ	Donor D	Extract	18	Lys/End	Immune response
P08246	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1 - [ELNE_HUMAN]	EPTRQVFAVQRIFENG	Donor D	Extract	16	M	Immune response
P0CG48	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=2 - [UBC_HUMAN]	MQIFVKTLTGKTITLEVEPSD	Donor D	Extract	21	C	Immune response

P10145	Interleukin-8 OS=Homo sapiens GN=IL8 PE=1 SV=1 - [IL8_HUMAN]	PKENWVQRVVEKFLKRAENS	Donor D	Extract	20	EM/S	Immune response
P17693	HLA class I histocompatibility antigen, alpha chain G OS=Homo sapiens GN=HLA-G PE=1 SV=1 - [HLAG_HUMAN]	GKDYLALNEDLRSWTA	Donor D	Extract	16	ER/G	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	FYVDLDKKETVWH	Donor D	Extract	13	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	MFYVDLDKKETVWH	Donor D	Extract	14	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	EMFYVDLDKKETVWH	Donor D	Extract	15	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	EMFYVDLDKKETVWH	Donor D	Extract	15	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	EMFYVDLDKKETVWHLE	Donor D	Extract	17	M	Immune response
P20039	HLA class II histocompatibility antigen, DRB1-11 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=1 - [2B1B_HUMAN]	DRYFYNQEEYVRFD	Donor D	Extract	14	M	Immune response
P20039	HLA class II histocompatibility antigen, DRB1-11 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=1 - [2B1B_HUMAN]	LDRYFYNQEEYVRFD	Donor D	Extract	15	M	Immune response
P20039	HLA class II histocompatibility antigen, DRB1-11 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=1 - [2B1B_HUMAN]	FLDRYFYNQEEYVRFD	Donor D	Extract	16	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	WDVLKCDEKAKFV	Donor D	Extract	13	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	IGLLISLDKKFAWM	Donor D	Extract	14	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	WDVLKCDEKAKFVC	Donor D	Extract	14	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	IGLLISLDKKFAWMD	Donor D	Extract	15	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	IGLLISLDKKFAWMDG	Donor D	Extract	16	M	Immune response
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	KPDDWDEDAPAKIPDE	Donor D	Extract	16	ER/G	Immune response
P31994	Low affinity immunoglobulin gamma Fc region receptor II-b OS=Homo sapiens GN=FCGR2B PE=1 SV=2 - [FCG2B_HUMAN]	TPAAPPKAVLKLEPQWINVLQED	Donor D	Extract	23	M	Immune response
P38484	Interferon gamma receptor 2 OS=Homo sapiens GN=IFNGR2 PE=1 SV=2 - [INGR2_HUMAN]	IEEYLKDPTQPILE	Donor D	Extract	14	M	Immune response
Q92583	C-C motif chemokine 17 OS=Homo sapiens GN=CCL17 PE=1 SV=1 - [CCL17_HUMAN]	PNNKRVKNAVKYLQSLERS	Donor D	Extract	19	EM/S	Immune response
Q9NPH3	Interleukin-1 receptor accessory protein OS=Homo sapiens GN=IL1RAP PE=1 SV=2 - [IL1AP_HUMAN]	LPGGIVTDETLSFIQK	Donor D	Extract	16	M	Immune response
Q9Y3Z3	SAM domain and HD domain-containing protein 1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2 - [SAMH1_HUMAN]	PIHGHIELHPLLVRIID	Donor D	Extract	17	N	Immune response
P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	SSALRWLGRYYCFQ	Donor D	Extract	14	EM/S	Ion homeostasis
P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	SSALRWLGRYYCFQG	Donor D	Extract	15	EM/S	Ion homeostasis
P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	SSALRWLGRYYCFQGN	Donor D	Extract	16	EM/S	Ion homeostasis
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	HLTNLHRLGGPEAGLGEYLFERLTLKHD	Donor D	Extract	28	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTG	Donor D	Extract	15	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTGKF	Donor D	Extract	17	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTGKFE	Donor D	Extract	18	C	Ion homeostasis
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	DPIIEDRHGGYKP	Donor D	Extract	13	C	Ion homeostasis
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	FDPIIEDRHGGYKPS	Donor D	Extract	15	C	Ion homeostasis
Q8NET8	Transient receptor potential cation channel subfamily V member 3 OS=Homo sapiens GN=TRPV3 PE=1 SV=2 - [TRPV3_HUMAN]	QLAKEEQRRKKRRLKK	Donor D	Extract	16	M	Ion homeostasis
Q93050	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3 - [VPP1_HUMAN]	RRKHLGTLNFGGIR	Donor D	Extract	14	M	Ion homeostasis
Q8N9G6	Putative UPF0607 protein FLJ37424 OS=Homo sapiens PE=2 SV=1 - [YJ012_HUMAN]	VLSRISKFRRLRQLLRRRK	Donor D	Extract	19	NA	NA

Q9H4G4	Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3 - [GAPR1_HUMAN]	GSSFVVARYFPAGNVVNEGFFEENVLPPKK	Donor D	Extract	30	ER/G	NA
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	SSKFQVDNNNRLL	Donor D	Extract	13	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	FSSKFQVDNNNRLL	Donor D	Extract	14	EM/S	Others
P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	LPDPYQKQCDQFVAEYEPV	Donor D	Extract	19	Lys/End	Others
P08754	Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3 - [GNAI3_HUMAN]	IQSIIAIIRAMGRLK	Donor D	Extract	15	C	Others
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	NPKVMNLISKLSAKFG	Donor D	Extract	16	C	Others
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]	TPNGLAIDHRAEKLYF	Donor D	Extract	16	M	Others
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]	TPNGLAIDHRAEKLYFS	Donor D	Extract	17	M	Others
Q68CQ7	Glycosyltransferase 8 domain-containing protein 1 OS=Homo sapiens GN=GLT8D1 PE=1 SV=2 - [GL8D1_HUMAN]	WEKWYIPDPTGKFN	Donor D	Extract	14	M	Others
Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	NWDEVDPDPNQLRWKPFE	Donor D	Extract	18	C	Others
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	AKMMALDREVQYLLNK	Donor D	Extract	16	ER/G	Others
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	HDFNFHINYGDLGFLGPE	Donor D	Extract	18	ER/G	Others
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	HDFNFHINYGDLGFLGPED	Donor D	Extract	19	ER/G	Others
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	NPKATLRYFQHLLGKQADNPH	Donor D	Extract	21	ER/G	Others
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]	RKVNWMVRLPVSEG	Donor D	Extract	14	Lys/End	Proteolysis
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]	GRKVNWMVRLPVSEG	Donor D	Extract	15	Lys/End	Proteolysis
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]	DPANITLEPMEIRTFLASVQWK	Donor D	Extract	22	Lys/End	Proteolysis
P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 - [HEXB_HUMAN]	APGTIVEVWKDSAYPE	Donor D	Extract	16	Lys/End	Proteolysis
P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	KELWILNRYLSYT	Donor D	Extract	13	M	Proteolysis
P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	SKELWILNRYLSYT	Donor D	Extract	14	M	Proteolysis
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	RGLFIIDDKGILRQ	Donor D	Extract	14	C	Redox homeostasis
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	FRGLFIIDDKGILRQ	Donor D	Extract	15	C	Redox homeostasis
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	ISFRGLFIIDDKGILRQ	Donor D	Extract	17	C	Redox homeostasis
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	PAGKLKYFDKLN	Donor D	Extract	12	C	Redox homeostasis
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	RGLFIIDDKGILRQ	Donor D	Extract	14	C	Redox homeostasis
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFD	Donor D	Extract	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDV	Donor D	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDV	Donor D	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDVA	Donor D	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDVA	Donor D	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SFGSLRCQVKVRSHGQD	Donor D	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVA	Donor D	Extract	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVAH	Donor D	Extract	19	EM/S	Thyroid

P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDVA	Donor D	Extract	19	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDVAH	Donor D	Extract	20	EM/S	Thyroid
Q9Y646	Carboxypeptidase Q OS=Homo sapiens GN=CPQ PE=1 SV=1 [CBPQ_HUMAN]	LEKAIQIMYQNLQQDG	Donor D	Extract	16	ER/G	Thyroid
P20645	Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1 - [MPRD_HUMAN]	SEKELALVKRLKPLF	Donor D	Extract	15	Lys/End	Transport
P60520	Gamma-aminobutyric acid receptor-associated protein-like 2 OS=Homo sapiens GN=GABARAPL2 PE=1 SV=1 - [GBRL2_HUMAN]	VAQFMWIIRKRIQLPS	Donor D	Extract	16	ER/G	Transport
Q14108	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	IHVFRPDISPYFG	Donor D	Extract	13	Lys/End	Transport
Q14108	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	LIHVFRPDISPYFG	Donor D	Extract	14	Lys/End	Transport
Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens GN=ERGIC1 PE=1 SV=1 - [ERGI1_HUMAN]	FEGQFSINKVPGNFH	Donor D	Extract	15	ER/G	Transport
P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]	GDGQVNYEEFVQMMTAK	Donor D	Purified	17	C	Apoptosis/cell death
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN]	GQTLFAGYTDNLVRVWQVTIGTR	Donor D	Purified	23	M	Apoptosis/cell death
Q92542	Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2 - [NICA_HUMAN]	DSRSFFWNVAPGAES	Donor D	Purified	15	M	Apoptosis/cell death
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIWD	Donor D	Purified	18	C	Autophagy
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	TPTLVEVSRNLGK	Donor D	Purified	13	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	APELLFFAKRYKAA	Donor D	Purified	14	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	APELLFFAKRYKAAF	Donor D	Purified	15	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	TPTLVEVSRNLGKVG	Donor D	Purified	15	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	APELLFFAKRYKAAFT	Donor D	Purified	16	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	TPTLVEVSRNLGKVGS	Donor D	Purified	16	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	TPTLVEVSRNLGKVGSK	Donor D	Purified	17	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	NALLVRYTKKVPQVSTPT	Donor D	Purified	18	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	IPIGLLYCDLPEPRKPLE	Donor D	Purified	18	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor D	Purified	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor D	Purified	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVRH	Donor D	Purified	17	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	LTDEIVKDVKQTYLAR	Donor D	Purified	16	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	DLTDEIVKDVKQTYLAR	Donor D	Purified	17	EM/S	Blood/coagulation
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLL	Donor D	Purified	14	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	LLVFATDDGFHFAG	Donor D	Purified	14	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLLM	Donor D	Purified	15	M	Cell adhesion/Matrix
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2 - [ITAM_HUMAN]	SDIAFLIDGSGSIIPH	Donor D	Purified	16	M	Cell adhesion/Matrix
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2 - [ITAM_HUMAN]	SDIAFLIDGSGSIIPHD	Donor D	Purified	17	M	Cell adhesion/Matrix
P16070	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3 - [CD44_HUMAN]	LPTMAQMEKALSIG	Donor D	Purified	14	M	Cell adhesion/Matrix
P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	VSWLIDANHNMQ	Donor D	Purified	12	M	Cell adhesion/Matrix

P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	GPPYVSWLIDANHNMQ	Donor D	Purified	16	M	Cell adhesion/Matrix
P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	GPPYVSWLIDANHNMQ	Donor D	Purified	16	M	Cell adhesion/Matrix
P20701	Integrin alpha-L OS=Homo sapiens GN=ITGAL PE=1 SV=3 - [ITAL_HUMAN]	DIIRYIIGIGKHFQTKES	Donor D	Purified	18	M	Cell adhesion/Matrix
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	DVYGIVYDLRMHRP	Donor D	Purified	14	M	Cell adhesion/Matrix
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	DVYGIVYDLRMHRPL	Donor D	Purified	15	M	Cell adhesion/Matrix
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	DVYGIVYDLRMHRPLM	Donor D	Purified	16	M	Cell adhesion/Matrix
Q13418	Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 - [ILK_HUMAN]	PAKRPKFDMIVPILEKMQDK	Donor D	Purified	20	M	Cell adhesion/Matrix
P01308	Insulin OS=Homo sapiens GN=INS PE=1 SV=1 - [INS_HUMAN]	HLVEALYLVCGERGFFYTPKT	Donor D	Purified	21	EM/S	Cell metabolism
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	NGKLVINGNPITIFQ	Donor D	Purified	15	C	Cell metabolism
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	SFQFGYNTGVINAPE	Donor D	Purified	15	M	Cell metabolism
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	GSFQFGYNTGVINAPE	Donor D	Purified	16	M	Cell metabolism
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	GSFQFGYNTGVINAPEKI	Donor D	Purified	18	M	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICKVVE	Donor D	Purified	17	C	Cell metabolism
Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 - [UGPA_HUMAN]	RIDIPPGAVLENKIVSGNLRILDH	Donor D	Purified	24	C	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	TKFWVVDQTHFY	Donor D	Purified	12	ER/G	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	HTKFWVVDQTHFY	Donor D	Purified	13	ER/G	Cell metabolism
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GYILCLNRIPHGR	Donor D	Purified	13	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	DGYILCLNRIPHGR	Donor D	Purified	14	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	EDGYILCLNRIPHGR	Donor D	Purified	15	Lys/End	Cell proliferation/differenciation
O00160	Myosin-If OS=Homo sapiens GN=MYO1F PE=1 SV=3 - [MYO1F_HUMAN]	PSGWWKGRLHGQEGLFPGNYVEKI	Donor D	Purified	24	C	Cytostkeleton
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	NPAEFVVNTSNAGAG	Donor D	Purified	15	C	Cytostkeleton
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	IGEETVITVDTKAAGKGK	Donor D	Purified	18	C	Cytostkeleton
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	KGEYTLVVKWGDEHIPGSPYRVVVP	Donor D	Purified	25	C	Cytostkeleton
Q16586	Alpha-sarcoglycan OS=Homo sapiens GN=SGCA PE=1 SV=1 - [SGCA_HUMAN]	ALVTLLVPLL	Donor D	Purified	10	C	Cytostkeleton
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	LVREIAQDFKTDLRFQ	Donor D	Purified	16	N	Gene expression /chromatine organization
O00626	C-C motif chemokine 22 OS=Homo sapiens GN=CCL22 PE=1 SV=2 - [CCL22_HUMAN]	PRVPWVKMILNKLSQ	Donor D	Purified	15	EM/S	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	KSWITFDLKNKEVSVK	Donor D	Purified	16	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	VEHWGLDEPLLKHWEF	Donor D	Purified	16	M	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	ISLPRIICDNTGITT	Donor D	Purified	15	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	DGDRFWWENEGVFSMQQR	Donor D	Purified	18	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	AYPRISVNNVLPVFDN	Donor D	Purified	16	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	GPVDEVRELQKAIGAVP	Donor D	Purified	17	Lys/End	Immune response
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	GPVDEVRELQKAIGAVPL	Donor D	Purified	18	Lys/End	Immune response

P0DMV8	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	FDNRLVNHFVEEFKR	Donor D	Purified	15	C	Immune response
P20039	HLA class II histocompatibility antigen, DRB1-11 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=1 - [2B1B_HUMAN]	LDRYFYNQEEYVR	Donor D	Purified	13	M	Immune response
P20039	HLA class II histocompatibility antigen, DRB1-11 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=1 - [2B1B_HUMAN]	LDRYFYNQEEYVRFD	Donor D	Purified	15	M	Immune response
P20039	HLA class II histocompatibility antigen, DRB1-11 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=1 - [2B1B_HUMAN]	FLDRYFYNQEEYVRFD	Donor D	Purified	16	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	IGLLISLDKKFAWM	Donor D	Purified	14	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	IGLLISLDKKFAWMDG	Donor D	Purified	16	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	IGLLISLDKKFAWMDG	Donor D	Purified	16	M	Immune response
P80075	C-C motif chemokine 8 OS=Homo sapiens GN=CCL8 PE=1 SV=2 - [CCL8_HUMAN]	PKERWVRDSMKHLDQIFQNLKP	Donor D	Purified	22	EM/S	Immune response
Q9NPH3	Interleukin-1 receptor accessory protein OS=Homo sapiens GN=IL1RAP PE=1 SV=2 - [IL1AP_HUMAN]	LPGGIVTDETLSFIQK	Donor D	Purified	16	M	Immune response
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	FSSKFQVDNNNRLL	Donor D	Purified	14	EM/S	Others
P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	LPVILDIIKGEMSRPG	Donor D	Purified	16	Lys/End	Others
P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	LPVILDIIKGEMSRPG	Donor D	Purified	16	Lys/End	Others
P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	YLPVILDIIKGEMSRPG	Donor D	Purified	17	Lys/End	Others
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	NPKVMNLISKLSAKFG	Donor D	Purified	16	C	Others
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]	EPRALVVDVQNGYLYW	Donor D	Purified	16	M	Others
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]	DPANITLEPMEIRTFLASVQWK	Donor D	Purified	22	Lys/End	Proteolysis
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	PAGKLKYFDKLN	Donor D	Purified	12	C	Redox homeostasis
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDV	Donor D	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	VPESKVIFDANAPVA	Donor D	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDVA	Donor D	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDV	Donor D	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVA	Donor D	Purified	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVAH	Donor D	Purified	19	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDVA	Donor D	Purified	19	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDVAH	Donor D	Purified	20	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	DSWQSLALSSVVVDPSIRHFDVAH	Donor D	Purified	24	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LDSWQSLALSSVVVDPSIRHFDVAH	Donor D	Purified	25	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	KVPESKVIFDANAPVAVRSKVPDSEFPVM	Donor D	Purified	29	EM/S	Thyroid
Q14108	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	IHVFRPDISPYFG	Donor D	Purified	13	Lys/End	Transport

Donor E(DRB1*0301, DRB1*1501)

AC	Description	Sequence	Sample	Source	Length	Cellular Location	Function
P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	VESLQEEIAFLKKLHE	Donor E	Extract	16	C	Apoptosis/cell death
Q13501	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 - [SQSTM_HUMAN]	AMSYVKDDIFRIYIK	Donor E	Extract	15	C	Apoptosis/cell death
Q9NR09	Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens GN=BIRC6 PE=1 SV=2 - [BIRC6_HUMAN]	SLSYHPALNAILAVTSRG	Donor E	Extract	18	ER/G	Apoptosis/cell death
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	NTILPDARDPAFK	Donor E	Extract	13	Lys/End	Autophagy
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	LNTILPDARDPAFK	Donor E	Extract	14	Lys/End	Autophagy
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	LNTILPDARDPAFKA	Donor E	Extract	15	Lys/End	Autophagy
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	LNTILPDARDPAFKAA	Donor E	Extract	16	Lys/End	Autophagy
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	AVGGALAGLVLIVLIAYLVGRKR	Donor E	Extract	23	Lys/End	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	IRTIELDGKTIKLQ	Donor E	Extract	14	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQ	Donor E	Extract	15	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQI	Donor E	Extract	16	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	IRTIELDGKTIKLQIWD	Donor E	Extract	17	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIW	Donor E	Extract	17	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIWD	Donor E	Extract	18	C	Autophagy
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	LGEYKFQNALLVR	Donor E	Extract	13	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	LKKYLYEIARRHP	Donor E	Extract	13	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	FLKKYLYEIARRHP	Donor E	Extract	14	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	LKKYLYEIARRHPY	Donor E	Extract	14	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	FLKKYLYEIARRHPY	Donor E	Extract	15	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	DNEETFLKKYLYEIARRHP	Donor E	Extract	19	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	DNEETFLKKYLYEIARRHPY	Donor E	Extract	20	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	DPQTFYYAVAVVKK	Donor E	Extract	14	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	DPQTFYYAVAVVKKD	Donor E	Extract	15	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	DKSKEFQLFSSPHGKDL	Donor E	Extract	17	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	DPQTFYYAVAVVKKDSG	Donor E	Extract	17	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	EDPQTFYYAVAVVKKDSG	Donor E	Extract	18	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor E	Extract	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVRH	Donor E	Extract	17	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	LTDEIVKDVKQTYLAR	Donor E	Extract	16	EM/S	Blood/coagulation

P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQL	Donor E	Extract	13	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLL	Donor E	Extract	14	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLLM	Donor E	Extract	15	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	GPGDPDSIRCDTRPQL	Donor E	Extract	16	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	GPGDPDSIRCDTRPQLL	Donor E	Extract	17	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	NIQPIFAVTSRMVKTYE	Donor E	Extract	17	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	GPGDPDSIRCDTRPQLLM	Donor E	Extract	18	M	Cell adhesion/Matrix
P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	GPPYVSWLIDANHNMQ	Donor E	Extract	16	M	Cell adhesion/Matrix
P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	VPKEISPDTTLLDLQNN	Donor E	Extract	17	EM/S	Cell adhesion/Matrix
P28300	Protein-lysine 6-oxidase OS=Homo sapiens GN=LOX PE=1 SV=2 - [LYOX_HUMAN]	QVFSLLSLGSQYQPQRR	Donor E	Extract	17	EM/S	Cell adhesion/Matrix
Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	DSIQISWKAPRGKFG	Donor E	Extract	15	EM/S	Cell adhesion/Matrix
Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	SHDSIQISWKAPRGKF	Donor E	Extract	16	EM/S	Cell adhesion/Matrix
Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	SHDSIQISWKAPRGKFG	Donor E	Extract	17	EM/S	Cell adhesion/Matrix
Q13445	Transmembrane emp24 domain-containing protein 1 OS=Homo sapiens GN=TMED1 PE=1 SV=1 - [TMED1_HUMAN]	DGEFTFLLPAGRKQ	Donor E	Extract	14	M	Cell adhesion/Matrix
Q14050	Collagen alpha-3(IX) chain OS=Homo sapiens GN=COL9A3 PE=2 SV=2 - [CO9A3_HUMAN]	ISEQIAQLAAHLRKPLAPG	Donor E	Extract	19	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	KLRVFVYRNSLCIE	Donor E	Extract	14	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	LEIFKQASAFSRAS	Donor E	Extract	14	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	LEIFKQASAFSRASQ	Donor E	Extract	15	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	LNRILGDPEALRDLLN	Donor E	Extract	16	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	KKLRVFVYRNSLCIENS	Donor E	Extract	17	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	IPSETLNRILGDPEALRDLLN	Donor E	Extract	21	EM/S	Cell adhesion/Matrix
O94905	Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1 - [ERLN2_HUMAN]	LPFITSYKSVQTTL	Donor E	Extract	14	ER/G	Cell metabolism
O94905	Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1 - [ERLN2_HUMAN]	LPFITSYKSVQTTLQ	Donor E	Extract	15	ER/G	Cell metabolism
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	DAPMFVMGVNHEKYDN	Donor E	Extract	16	C	Cell metabolism
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	YDNSLKIISNASCTTN	Donor E	Extract	16	C	Cell metabolism
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]	TPILVDGKDVMPE	Donor E	Extract	13	C	Cell metabolism
P06858	Lipoprotein lipase OS=Homo sapiens GN=LPL PE=1 SV=1 - [LIPL_HUMAN]	HERSIHLFIDSLLNEENPS	Donor E	Extract	19	M	Cell metabolism
P08240	Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2 - [SRPR_HUMAN]	LAKLITVNTPDLVLFVG	Donor E	Extract	17	Lys/End	Cell metabolism
P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	DGDLTLYQSNTILR	Donor E	Extract	14	C	Cell metabolism
P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	DGDLTLYQSNTILRH	Donor E	Extract	15	C	Cell metabolism
P10768	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 - [ESTD_HUMAN]	LPDNFIAACTEKKIPV	Donor E	Extract	16	C	Cell metabolism
P10768	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 - [ESTD_HUMAN]	LPDNFIAACTEKKIPVV	Donor E	Extract	17	C	Cell metabolism
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1 - [COX41_HUMAN]	WSSLSMDEKVELYR	Donor E	Extract	14	Mit	Cell metabolism

P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	ENILWLDYKNICK	Donor E	Extract	13	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICK	Donor E	Extract	14	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	ENILWLDYKNICKVVE	Donor E	Extract	16	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICKVVE	Donor E	Extract	17	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	PILYRPVAVALDTKGPEIR	Donor E	Extract	19	C	Cell metabolism
P15289	Arylsulfatase A OS=Homo sapiens GN=ARSA PE=1 SV=3 - [ARSA_HUMAN]	DRPFFLYYASHHTHYPQ	Donor E	Extract	17	Lys/End	Cell metabolism
P18859	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 - [ATP5J_HUMAN]	PKFEVIEKPQA	Donor E	Extract	11	Mit	Cell metabolism
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	EPSKITKFENAFLSH	Donor E	Extract	15	Mit	Cell metabolism
P27449	V-type proton ATPase 16 kDa proteolipid subunit OS=Homo sapiens GN=ATP6V0C PE=1 SV=1 - [VATL_HUMAN]	DDISLYKSFLQLGAG	Donor E	Extract	15	Lys/End	Cell metabolism
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	DLEKIHLDEKSFRWLHN	Donor E	Extract	17	C	Cell metabolism
P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	KGVIQYYPAAPLPG	Donor E	Extract	14	C	Cell metabolism
P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	VKGVIQYYPAAPLPG	Donor E	Extract	15	C	Cell metabolism
Q13510	Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=5 - [ASAH1_HUMAN]	LDVYELDAKQGRWY	Donor E	Extract	14	Lys/End	Cell metabolism
Q13510	Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=5 - [ASAH1_HUMAN]	LDVYELDAKQGRWYVV	Donor E	Extract	16	Lys/End	Cell metabolism
Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 - [UGPA_HUMAN]	RIDIPPGAVLENKIVSGNLRILDH	Donor E	Extract	24	C	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	TKFWVVDQTHFY	Donor E	Extract	12	ER/G	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	HTKFWVVDQTHFY	Donor E	Extract	13	ER/G	Cell metabolism
Q9HAT2	Sialate O-acetylesterase OS=Homo sapiens GN=SIAE PE=1 SV=1 - [SIAE_HUMAN]	FPALIEDWRETFHRG	Donor E	Extract	15	Lys/End	Cell metabolism
Q9NX14	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial OS=Homo sapiens GN=NDUFB11 PE=1 SV=1 - [NDUBB_HUMAN]	ESSFSRTVVAPSAVAGKRPPEPTTPWQED	Donor E	Extract	29	Mit	Cell metabolism
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1 - [SQRD_HUMAN]	GNAIFTFPNTPVK	Donor E	Extract	13	Mit	Cell metabolism
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1 - [SQRD_HUMAN]	EGNAIFTFPNTPVK	Donor E	Extract	14	Mit	Cell metabolism
P15104	Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4 - [GLNA_HUMAN]	PFSVTEALIRTCLLNETGDEPFQYKN	Donor E	Extract	26	C	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	DKEFLPQSAFLKW	Donor E	Extract	13	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLK	Donor E	Extract	13	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLKW	Donor E	Extract	14	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	FGDKEFLPQSAFLKW	Donor E	Extract	15	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLKWL	Donor E	Extract	15	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	DKEFLPQSAFLKWLGT	Donor E	Extract	16	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLKWLG	Donor E	Extract	16	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLKWLGT	Donor E	Extract	17	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	FGDKEFLPQSAFLKWLGT	Donor E	Extract	18	Lys/End	Cell proliferation/differenciation
Q06889	Early growth response protein 3 OS=Homo sapiens GN=EGR3 PE=1 SV=1 - [EGR3_HUMAN]	GKLAEKLPVTMSSLLNQLPD	Donor E	Extract	20	N	Cell proliferation/differenciation
Q13642	Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1 PE=1 SV=4 - [FHL1_HUMAN]	YYCVDCYKNFVAK	Donor E	Extract	13	C	Cell proliferation/differenciation

Q13642	Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1 PE=1 SV=4 - [FHL1_HUMAN]	YYCVDCYKNFVAKK	Donor E	Extract	14	C	Cell proliferation/differenciation
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	ITSIVKDSSAARNGL	Donor E	Extract	15	M	Cytostkeleton
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	ITSIVKDSSAARNGLL	Donor E	Extract	16	M	Cytostkeleton
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	KITSIVKDSSAARNGLL	Donor E	Extract	17	M	Cytostkeleton
P07305	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3 - [H10_HUMAN]	RAGSSRQSIQKYIKSHYK	Donor E	Extract	18	N	Cytostkeleton
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN]	SNPQFIVDGATRTDI	Donor E	Extract	15	C	Cytostkeleton
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	EETVITVDTKAAGKGK	Donor E	Extract	16	C	Cytostkeleton
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	GEETVITVDTKAAGKGK	Donor E	Extract	17	C	Cytostkeleton
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	IGEETVITVDTKAAGKGK	Donor E	Extract	18	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVR	Donor E	Extract	13	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVRK	Donor E	Extract	14	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVRKS	Donor E	Extract	15	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	SDGVIKVFNDMKVRK	Donor E	Extract	15	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	VIKVFNDMKVRKSSTPE	Donor E	Extract	17	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVRKSSTPE	Donor E	Extract	19	C	Cytostkeleton
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	IDQINTDLNLERSH	Donor E	Extract	14	C	Cytostkeleton
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	IDQINTDLNLERSHAQ	Donor E	Extract	16	C	Cytostkeleton
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	IKALELDSNLYRIGQS	Donor E	Extract	16	C	Cytostkeleton
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	NTKKVIQYLAYVASSHK	Donor E	Extract	17	C	Cytostkeleton
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	REIVRDIKEKL	Donor E	Extract	11	C	Cytostkeleton
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	REIVRDIKEKLCY	Donor E	Extract	13	C	Cytostkeleton
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	AEREIVRDIKEKLCY	Donor E	Extract	15	C	Cytostkeleton
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	PRVPWVKMILNKLSQ	Donor E	Extract	15	C	Cytostkeleton
Q05D60	Coiled-coil domain-containing protein 67 OS=Homo sapiens GN=CCDC67 PE=2 SV=2 - [CCD67_HUMAN]	ELMEQIDIMVSNKKMD	Donor E	Extract	16	C	Cytostkeleton
Q12965	Myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2 - [MYO1E_HUMAN]	PSGWWTGRLRGKQGLFPNNYVTKI	Donor E	Extract	24	C	Cytostkeleton
Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	DKAYVERYANTLLSVK	Donor E	Extract	16	C	Cytostkeleton
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	SPDPSIYAYDNFGVLG	Donor E	Extract	16	ER/G	Others
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	DIMRVNVDKVLERDQK	Donor E	Extract	16	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	DIMRVNVDKVLERDQKL	Donor E	Extract	17	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	VDKVLERDQKLSELDDR	Donor E	Extract	17	M	Endocytosis/exocytosis
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	EILPTTPISEQKGGKPEPPAMPQPVPTA	Donor E	Extract	28	C	Gene expression /chromatine organization
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	NVQRLKEYRSKLILFPR	Donor E	Extract	17	C	Gene expression /chromatine organization
P32519	ETS-related transcription factor Elf-1 OS=Homo sapiens GN=ELF1 PE=1 SV=2 - [ELF1_HUMAN]	HTVTLQTVPLTTVIASTDP	Donor E	Extract	19	N	Gene expression /chromatine organization

P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	APVKKLVVKGGKKKKQVLKFTLD	Donor E	Extract	23	C	Gene expression /chromatine organization
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	VPELPLVVEDKVEGYKK	Donor E	Extract	17	C	Gene expression /chromatine organization
P49591	Seryl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN]	VLDLDLFRVDKGGD	Donor E	Extract	14	C	Gene expression /chromatine organization
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	TLVFIVDVKANKHQ	Donor E	Extract	14	C	Gene expression /chromatine organization
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	NTLVFIVDVKANKHQ	Donor E	Extract	15	C	Gene expression /chromatine organization
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	NTLVFIVDVKANKHQIK	Donor E	Extract	17	C	Gene expression /chromatine organization
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	VREIAQDFKTDLRFQ	Donor E	Extract	15	N	Gene expression /chromatine organization
P85037	Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 - [FOXK1_HUMAN]	KEEAPASPLRPLYPQISPL	Donor E	Extract	19	N	Gene expression /chromatine organization
Q8NFC6	Biorientation of chromosomes in cell division protein 1-like OS=Homo sapiens GN=BOD1L PE=1 SV=2 - [BOD1L_HUMAN]	EKTEKKFDHSKKSEDTQKVKDEKQAKEK	Donor E	Extract	28	N	Gene expression /chromatine organization
Q96DT7	Zinc finger and BTB domain-containing protein 10 OS=Homo sapiens GN=ZBTB10 PE=1 SV=2 - [ZBT10_HUMAN]	KTLLLRHHV	Donor E	Extract	9	N	Gene expression /chromatine organization
Q9BVI0	PHD finger protein 20 OS=Homo sapiens GN=PHF20 PE=1 SV=2 - [PHF20_HUMAN]	KKKKKKKTKPECP	Donor E	Extract	13	N	Gene expression /chromatine organization
O00602	Ficolin-1 OS=Homo sapiens GN=FCN1 PE=1 SV=2 - [FCN1_HUMAN]	NHQFAKYKSFKVADE	Donor E	Extract	15	EM/S	Immune response
O00602	Ficolin-1 OS=Homo sapiens GN=FCN1 PE=1 SV=2 - [FCN1_HUMAN]	GNHQFAKYKSFKVADE	Donor E	Extract	16	EM/S	Immune response
O00602	Ficolin-1 OS=Homo sapiens GN=FCN1 PE=1 SV=2 - [FCN1_HUMAN]	GNHQFAKYKSFKVADEA	Donor E	Extract	17	EM/S	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	KSWITFDLKNKEVS	Donor E	Extract	14	M	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	KSWITFDLKNKEVSVK	Donor E	Extract	16	M	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	SKSWITFDLKNKEVSVK	Donor E	Extract	17	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	LEEFGRFASFEAQG	Donor E	Extract	14	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	RLEEFGRFASFEAQG	Donor E	Extract	15	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	LEEFGRFASFEAQGAL	Donor E	Extract	16	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	VGEFRAVTELGRPD	Donor E	Extract	14	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	DVGEFRAVTELGRPD	Donor E	Extract	15	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	DVGEFRAVTELGRPDA	Donor E	Extract	16	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	FQTLVMLETVPRSGEV	Donor E	Extract	16	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	SDVGEFRAVTELGRPD	Donor E	Extract	16	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	DVGEFRAVTELGRPDAE	Donor E	Extract	17	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	SDVGEFRAVTELGRPDA	Donor E	Extract	17	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	SDVGEFRAVTELGRPDAE	Donor E	Extract	18	M	Immune response
P04440	HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens GN=HLA-DPB1 PE=1 SV=1 - [DPB1_HUMAN]	VGEFRAVTELGRPA	Donor E	Extract	14	M	Immune response
P04440	HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens GN=HLA-DPB1 PE=1 SV=1 - [DPB1_HUMAN]	DVGEFRAVTELGRPA	Donor E	Extract	15	M	Immune response
P04440	HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens GN=HLA-DPB1 PE=1 SV=1 - [DPB1_HUMAN]	SDVGEFRAVTELGRPA	Donor E	Extract	16	M	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	LPRIICDNTGITT	Donor E	Extract	13	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	SLPRIICDNTGITT	Donor E	Extract	14	Lys/End	Immune response

P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	QNQIAVDEIRERLFE	Donor E	Extract	15	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	LDNRYQPMEPNPRVPL	Donor E	Extract	16	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	RQNQIAVDEIRERLFE	Donor E	Extract	16	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	VSNEIVRFPTDQLTPD	Donor E	Extract	16	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	VSNEIVRFPTDQLTPDQ	Donor E	Extract	17	Lys/End	Immune response
P07814	Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=5 - [SYEP_HUMAN]	DGKIISLDAKLNLENK	Donor E	Extract	16	C	Immune response
P08575	Receptor-type tyrosine-protein phosphatase C OS=Homo sapiens GN=PTPRC PE=1 SV=2 - [PTPRC_HUMAN]	VDIFQVVKALRKARPG	Donor E	Extract	16	M	Immune response
P08575	Receptor-type tyrosine-protein phosphatase C OS=Homo sapiens GN=PTPRC PE=1 SV=2 - [PTPRC_HUMAN]	VVDIFQVVKALRKARPG	Donor E	Extract	17	M	Immune response
P10145	Interleukin-8 OS=Homo sapiens GN=IL8 PE=1 SV=1 - [IL8_HUMAN]	DGRELCLDPKENWVQ	Donor E	Extract	15	EM/S	Immune response
P10145	Interleukin-8 OS=Homo sapiens GN=IL8 PE=1 SV=1 - [IL8_HUMAN]	PKENWVQRVVEKFLKRAENS	Donor E	Extract	20	EM/S	Immune response
P10319	HLA class I histocompatibility antigen, B-58 alpha chain OS=Homo sapiens GN=HLA-B PE=2 SV=1 - [1B58_HUMAN]	GLAVLAVVVIGAVVATVMC	Donor E	Extract	19	M	Immune response
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	DDIIVNWVNETLRE	Donor E	Extract	14	C	Immune response
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	NDDIIVNWVNETLR	Donor E	Extract	14	C	Immune response
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	NDDIIVNWVNETLRE	Donor E	Extract	15	C	Immune response
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	VNDDIIVNWVNETLRE	Donor E	Extract	16	C	Immune response
P15260	Interferon gamma receptor 1 OS=Homo sapiens GN=IFNGR1 PE=1 SV=1 - [INGR1_HUMAN]	GPPKLDIRKEEKQIMIDIFH	Donor E	Extract	20	M	Immune response
P15260	Interferon gamma receptor 1 OS=Homo sapiens GN=IFNGR1 PE=1 SV=1 - [INGR1_HUMAN]	GPPKLDIRKEEKQIMIDIFHP	Donor E	Extract	21	M	Immune response
P18084	Integrin beta-5 OS=Homo sapiens GN=ITGB5 PE=1 SV=1 - [ITB5_HUMAN]	DDVPHIALDGKLGGLVQPH	Donor E	Extract	19	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	YVDLDKKETVWH	Donor E	Extract	12	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	MFYVDLDKKETVWH	Donor E	Extract	14	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	EMFYVDLDKKETVWH	Donor E	Extract	15	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	EKNIMLYKGSGLWS	Donor E	Extract	14	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	QEKNIMLYKGSGLWS	Donor E	Extract	15	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	WDVLKCDEKAKFVCK	Donor E	Extract	15	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	QEKNIMLYKGSGLWSR	Donor E	Extract	16	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	RQEKNIMLYKGSGLWS	Donor E	Extract	16	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	QEKNIMLYKGSGLWSRW	Donor E	Extract	17	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	RQEKNIMLYKGSGLWSRW	Donor E	Extract	18	M	Immune response
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	KPDDWDEDAPAKIPDE	Donor E	Extract	16	ER/G	Immune response
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	KPDDWDEDAPAKIPDEE	Donor E	Extract	17	ER/G	Immune response
P27930	Interleukin-1 receptor type 2 OS=Homo sapiens GN=IL1R2 PE=1 SV=1 - [IL1R2_HUMAN]	DVKIQWYKDSLLLDK	Donor E	Extract	15	M	Immune response
P27930	Interleukin-1 receptor type 2 OS=Homo sapiens GN=IL1R2 PE=1 SV=1 - [IL1R2_HUMAN]	TDVKIQWYKDSLLLDK	Donor E	Extract	16	M	Immune response
P28068	HLA class II histocompatibility antigen, DM beta chain OS=Homo sapiens GN=HLA-DMB PE=1 SV=1 - [DMB_HUMAN]	TPKDFTYCISFNK	Donor E	Extract	13	Lys/End	Immune response

P28068	HLA class II histocompatibility antigen, DM beta chain OS=Homo sapiens GN=HLA-DMB PE=1 SV=1 - [DMB_HUMAN]	TPKDFTYCISFNKDL	Donor E	Extract	15	Lys/End	Immune response
P28068	HLA class II histocompatibility antigen, DM beta chain OS=Homo sapiens GN=HLA-DMB PE=1 SV=1 - [DMB_HUMAN]	TPKDFTYCISFNKDLL	Donor E	Extract	16	Lys/End	Immune response
P31994	Low affinity immunoglobulin gamma Fc region receptor II-b OS=Homo sapiens GN=FCGR2B PE=1 SV=2 - [FCG2B_HUMAN]	SPESDSIQWFHNGNLIPT	Donor E	Extract	18	M	Immune response
P38484	Interferon gamma receptor 2 OS=Homo sapiens GN=IFNGR2 PE=1 SV=2 - [INGR2_HUMAN]	IEEYLKDPTQPILE	Donor E	Extract	14	M	Immune response
P79483	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 - [DRB3_HUMAN]	DRYFHNQEEFLRFDS	Donor E	Extract	15	M	Immune response
P79483	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 - [DRB3_HUMAN]	DVGEYRAVTELGRPV	Donor E	Extract	15	M	Immune response
P79483	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 - [DRB3_HUMAN]	DRYFHNQEEFLRFDSD	Donor E	Extract	16	M	Immune response
P79483	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 - [DRB3_HUMAN]	LDRYFHNQEEFLRFDS	Donor E	Extract	16	M	Immune response
Q9NPH3	Interleukin-1 receptor accessory protein OS=Homo sapiens GN=IL1RAP PE=1 SV=2 - [IL1AP_HUMAN]	LPGGIVTDETLSFIQK	Donor E	Extract	16	M	Immune response
P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	KGGYTLVSGYPKR	Donor E	Extract	13	EM/S	Ion homeostasis
P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	KGGYTLVSGYPKRLE	Donor E	Extract	15	EM/S	Ion homeostasis
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	LGEYLFERLTLKHD	Donor E	Extract	14	C	Ion homeostasis
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	VSHFFRELAEEKREG	Donor E	Extract	15	C	Ion homeostasis
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	GVSHFFRELAEEKREG	Donor E	Extract	16	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTGKF	Donor E	Extract	17	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTGKFE	Donor E	Extract	18	C	Ion homeostasis
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	DPIIEDRHGGYKP	Donor E	Extract	13	C	Ion homeostasis
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	DPIIEDRHGGYKPS	Donor E	Extract	14	C	Ion homeostasis
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	FDPIIEDRHGGYKP	Donor E	Extract	14	C	Ion homeostasis
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	FDPIIEDRHGGYKPS	Donor E	Extract	15	C	Ion homeostasis
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	FDPIIEDRHGGYKPSDE	Donor E	Extract	17	C	Ion homeostasis
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	LFDPIIEDRHGGYKPSDE	Donor E	Extract	18	C	Ion homeostasis
Q93050	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3 - [VPP1_HUMAN]	RRKHLGTLNFGGIR	Donor E	Extract	14	M	Ion homeostasis
Q86V87	Protein FAM160B2 OS=Homo sapiens GN=FAM160B2 PE=2 SV=2 - [F16B2_HUMAN]	LTSTALLTAMLRQL	Donor E	Extract	14	NA	NA
Q8IYT3	Coiled-coil domain-containing protein C6orf97 OS=Homo sapiens GN=C6orf97 PE=2 SV=3 - [CF097_HUMAN]	QKKVERLQKEL	Donor E	Extract	11	NA	NA
A6NMY6	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2 - [AXA2L_HUMAN]	DLEKDIISDTSGDFRK	Donor E	Extract	16	EM/S	Others
A6NMY6	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2 - [AXA2L_HUMAN]	TPPSAYGSVKAYTNFDAERDA	Donor E	Extract	21	EM/S	Others
O75170	Serine/threonine-protein phosphatase 6 regulatory subunit 2 OS=Homo sapiens GN=PPP6R2 PE=1 SV=2 - [PP6R2_HUMAN]	EGLVDSFSQGLERSYAVSSSVLHGIEPR	Donor E	Extract	28	C	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	SSKFQVDNNNRLL	Donor E	Extract	13	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	FSSKFQVDNNNRLL	Donor E	Extract	14	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	GNRIAQWQSFQLEG	Donor E	Extract	14	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	GNRIAQWQSFQLEGG	Donor E	Extract	15	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	LPKFEVQVTVPKIIT	Donor E	Extract	15	EM/S	Others

P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	GNRIAQWQSFQLEGGL	Donor E	Extract	16	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	VLPKFEVQVTVPKIIT	Donor E	Extract	16	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	DPKGNRIAQWQSFQLEG	Donor E	Extract	17	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	DPKGNRIAQWQSFQLEGG	Donor E	Extract	18	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	DPKGNRIAQWQSFQLEGGL	Donor E	Extract	19	EM/S	Others
Q01780	Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2 - [EXOSX_HUMAN]	RSDMYILNESLTDP	Donor E	Extract	14	C	Others
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	IGDRVFVHYTGWLLDGTK	Donor E	Extract	18	C	Others
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]	TPNGLAIDHRAEKLYF	Donor E	Extract	16	M	Others
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]	TPNGLAIDHRAEKLYFS	Donor E	Extract	17	M	Others
Q5VVM6	Coiled-coil domain-containing protein 30 OS=Homo sapiens GN=CCDC30 PE=2 SV=1 - [CCD30_HUMAN]	EKNEMFESEWSK	Donor E	Extract	12	EM/S	Others
Q68CQ7	Glycosyltransferase 8 domain-containing protein 1 OS=Homo sapiens GN=GLT8D1 PE=1 SV=2 - [GL8D1_HUMAN]	WEKWYIPDPTGKFN	Donor E	Extract	14	M	Others
Q7Z417	Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1 - [NUFP2_HUMAN]	PKRIITYNEAMDSPDQ	Donor E	Extract	16	N	Others
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]	DPANITLEPMEIRTFLASVQWK	Donor E	Extract	22	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GAFSVYSDFLLYK	Donor E	Extract	13	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GAFSVYSDFLLYKS	Donor E	Extract	14	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GAFSVYSDFLLYKSG	Donor E	Extract	15	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GPVEGAFSVYSDFLLYK	Donor E	Extract	17	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GPVEGAFSVYSDFLLYKS	Donor E	Extract	18	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GPVEGAFSVYSDFLLYKSG	Donor E	Extract	19	Lys/End	Proteolysis
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	RGLFIIDPNGVIK	Donor E	Extract	13	Mit	Redox homeostasis
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN]	FPTIYFSPANKKLNPK	Donor E	Extract	16	ER/G	Redox homeostasis
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN]	GFPTIYFSPANKKLNPK	Donor E	Extract	17	ER/G	Redox homeostasis
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	RGLFIIDGKGVLRQ	Donor E	Extract	14	C	Redox homeostasis
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	PAGKLKYFDKLN	Donor E	Extract	12	C	Redox homeostasis
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	RGLFIIDDKGILRQ	Donor E	Extract	14	C	Redox homeostasis
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	KIMQYFSHFIR	Donor E	Extract	11	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LKIMQYFSHFIR	Donor E	Extract	12	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	PIIDMASAWAKR	Donor E	Extract	12	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIR	Donor E	Extract	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LKIMQYFSHFIRSG	Donor E	Extract	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSLKIMQYFSHFIR	Donor E	Extract	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFD	Donor E	Extract	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	MIFDLVHSYNRFPD	Donor E	Extract	14	EM/S	Thyroid

P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIRS	Donor E	Extract	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ESFLVAKGIRLRNED	Donor E	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSLKIMQYFSHFIRS	Donor E	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDV	Donor E	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	MMIFDLVHSYNRFPD	Donor E	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIRSG	Donor E	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	VPESKVIFDANAPVA	Donor E	Extract	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDV	Donor E	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ESFLVAKGIRLRNEDL	Donor E	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	KIMQYFSHFIRSGNPN	Donor E	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSLKIMQYFSHFIRSG	Donor E	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDVA	Donor E	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	MMIFDLVHSYNRFPDA	Donor E	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIRSGN	Donor E	Extract	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDVA	Donor E	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	DMMIFDLVHSYNRFPDA	Donor E	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LKIMQYFSHFIRSGNPN	Donor E	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSLKIMQYFSHFIRSGN	Donor E	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	TDMMIFDLVHSYNRFPD	Donor E	Extract	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDVAH	Donor E	Extract	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVA	Donor E	Extract	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIRSGNPN	Donor E	Extract	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	TDMMIFDLVHSYNRFPDA	Donor E	Extract	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	TTDMMIFDLVHSYNRFPD	Donor E	Extract	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDVAH	Donor E	Extract	20	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLSLKIMQYFSHFIRSGNPN	Donor E	Extract	20	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	EKSLSLKIMQYFSHFIRSGNPN	Donor E	Extract	22	EM/S	Thyroid
O14579	Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3 - [COPE_HUMAN]	VERDVFLYRAYLAQR	Donor E	Extract	15	C	Transport
O14579	Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3 - [COPE_HUMAN]	VERDVFLYRAYLAQRK	Donor E	Extract	16	C	Transport
O14579	Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3 - [COPE_HUMAN]	DVERDVFLYRAYLAQRK	Donor E	Extract	17	C	Transport
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2 - [RAB5C_HUMAN]	SPNIVIALAGNKADL	Donor E	Extract	15	M	Transport
P62491	Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RB11A_HUMAN]	ATRSIQVDGKTIKAQIW	Donor E	Extract	17	M	Transport
Q14108	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	IHVFRPDISPYFG	Donor E	Extract	13	Lys/End	Transport

Q9H223	EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 - [EHD4_HUMAN]	TPGNALVVDPKKPFRK	Donor E	Extract	16	M	Transport
P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	GQVINETSQHHDDLE	Donor E	Purified	15	C	Apoptosis/cell death
Q13501	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 - [SQSTM_HUMAN]	AMSYVKDDIFRIYIK	Donor E	Purified	15	C	Apoptosis/cell death
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	LNTILPDARDPAFK	Donor E	Purified	14	Lys/End	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	IRTIELDGKTIKLQ	Donor E	Purified	14	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQ	Donor E	Purified	15	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIW	Donor E	Purified	17	C	Autophagy
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	KIRTIELDGKTIKLQIWD	Donor E	Purified	18	C	Autophagy
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	LGEYKFQNALLVR	Donor E	Purified	13	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	LKKYLYEIARRHP	Donor E	Purified	13	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	FLKKYLYEIARRHP	Donor E	Purified	14	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	FLKKYLYEIARRHPY	Donor E	Purified	15	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	DNEETFLKKYLYEIARRHP	Donor E	Purified	19	EM/S	Blood/coagulation
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	DNEETFLKKYLYEIARRHPY	Donor E	Purified	20	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	DPQTFYYAVAVVKK	Donor E	Purified	14	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	EDPQTFYYAVAVVK	Donor E	Purified	14	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	DPQTFYYAVAVVKKD	Donor E	Purified	15	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	DKSKEFQLFSSPHGKDL	Donor E	Purified	17	EM/S	Blood/coagulation
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	DPQTFYYAVAVVKKDSG	Donor E	Purified	17	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVR	Donor E	Purified	16	EM/S	Blood/coagulation
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	APEEIIMDRPFLFVVRH	Donor E	Purified	17	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	LTDEIVKDVKQTYLAR	Donor E	Purified	16	EM/S	Blood/coagulation
P13726	Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	DLTDEIVKDVKQTYLAR	Donor E	Purified	17	EM/S	Blood/coagulation
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQL	Donor E	Purified	13	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLL	Donor E	Purified	14	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	DPDSIRCDTRPQLLM	Donor E	Purified	15	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	GPGDPDSIRCDTRPQL	Donor E	Purified	16	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	GPGDPDSIRCDTRPQLL	Donor E	Purified	17	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	NIQPIFAVTSRMVKTYE	Donor E	Purified	17	M	Cell adhesion/Matrix
P05107	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 - [ITB2_HUMAN]	GPGDPDSIRCDTRPQLLM	Donor E	Purified	18	M	Cell adhesion/Matrix
P14780	Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=3 - [MMP9_HUMAN]	NQLYLFKDGKYWRFSEG	Donor E	Purified	17	EM/S	Cell adhesion/Matrix
P17813	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]	GPPYVSWLIDANHNMQ	Donor E	Purified	16	M	Cell adhesion/Matrix
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	DVYGIVYDLRMHRPLM	Donor E	Purified	16	M	Cell adhesion/Matrix

Q13445	Transmembrane emp24 domain-containing protein 1 OS=Homo sapiens GN=TMED1 PE=1 SV=1 - [TMED1_HUMAN]	DGEFTFLLPAGRKQ	Donor E	Purified	14	M	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	KLRVFVYRNSLCIE	Donor E	Purified	14	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	LEIFKQASAFSRAS	Donor E	Purified	14	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	LEIFKQASAFSRASQ	Donor E	Purified	15	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	LRVFVYRNSLCIENS	Donor E	Purified	15	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	KKLRVFVYRNSLCIENS	Donor E	Purified	17	EM/S	Cell adhesion/Matrix
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	IPSETLNRILGDPEALRDLLN	Donor E	Purified	21	EM/S	Cell adhesion/Matrix
P06858	Lipoprotein lipase OS=Homo sapiens GN=LPL PE=1 SV=1 - [LIPL_HUMAN]	RSIHLFIDSLLNEENPS	Donor E	Purified	17	M	Cell metabolism
P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	DGDLTLYQSNTILR	Donor E	Purified	14	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	ENILWLDYKNICK	Donor E	Purified	13	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICK	Donor E	Purified	14	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	ENILWLDYKNICKVVE	Donor E	Purified	16	C	Cell metabolism
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	DENILWLDYKNICKVVE	Donor E	Purified	17	C	Cell metabolism
P18859	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 - [ATP5J_HUMAN]	PKFEVIEKPQA	Donor E	Purified	11	Mit	Cell metabolism
P27449	V-type proton ATPase 16 kDa proteolipid subunit OS=Homo sapiens GN=ATP6V0C PE=1 SV=1 - [VATL_HUMAN]	DDISLYKSFLQLG	Donor E	Purified	13	Lys/End	Cell metabolism
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	DLEKIHLDEKSFRWLH	Donor E	Purified	16	C	Cell metabolism
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	DLEKIHLDEKSFRWLHN	Donor E	Purified	17	C	Cell metabolism
P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	KGVIQYYPAAPLPG	Donor E	Purified	14	C	Cell metabolism
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	HTKFWVVDQTHFY	Donor E	Purified	13	ER/G	Cell metabolism
Q9NX14	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial OS=Homo sapiens GN=NDUFB11 PE=1 SV=1 - [NDUBB_HUMAN]	ESSFSRTVVAPSAVAGKRPPEPTTPWQED	Donor E	Purified	29	Mit	Cell metabolism
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1 - [SQRD_HUMAN]	NAIFTFPNTPVK	Donor E	Purified	12	Mit	Cell metabolism
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1 - [SQRD_HUMAN]	GNAIFTFPNTPVK	Donor E	Purified	13	Mit	Cell metabolism
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1 - [SQRD_HUMAN]	EGNAIFTFPNTPVK	Donor E	Purified	14	Mit	Cell metabolism
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	DKEFLPQSAFLKW	Donor E	Purified	13	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLK	Donor E	Purified	13	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLKW	Donor E	Purified	14	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	VSEIISYWGFPSEE	Donor E	Purified	14	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	DKEFLPQSAFLKWLG	Donor E	Purified	15	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	FGDKEFLPQSAFLKW	Donor E	Purified	15	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLKWL	Donor E	Purified	15	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLKWLG	Donor E	Purified	16	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	SGGHDWLADVYDVNIL	Donor E	Purified	16	Lys/End	Cell proliferation/differenciation
P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	GDKEFLPQSAFLKWLGT	Donor E	Purified	17	Lys/End	Cell proliferation/differenciation

O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	ITSIVKDSSAARNGL	Donor E	Purified	15	M	Cytostkeleton
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	ITSIVKDSSAARNGLL	Donor E	Purified	16	M	Cytostkeleton
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 - [SDCB1_HUMAN]	KITSIVKDSSAARNGLL	Donor E	Purified	17	M	Cytostkeleton
O43307	Rho guanine nucleotide exchange factor 9 OS=Homo sapiens GN=ARHGEF9 PE=1 SV=3 - [ARHG9_HUMAN]	LSKLMKDSRYQHFFE	Donor E	Purified	15	C	Cytostkeleton
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	ISVLYGDEEVPRSPF	Donor E	Purified	15	C	Cytostkeleton
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	EETVITVDTKAAGKGK	Donor E	Purified	16	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVR	Donor E	Purified	13	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVRK	Donor E	Purified	14	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	VIKVFNDMKVRKSSTPE	Donor E	Purified	17	C	Cytostkeleton
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	DGVIKVFNDMKVRKSSTPE	Donor E	Purified	19	C	Cytostkeleton
P47755	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3 - [CAZA2_HUMAN]	FNEVFNDVRLLLNNDN	Donor E	Purified	16	C	Cytostkeleton
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	REIVRDIKEKLCY	Donor E	Purified	13	C	Cytostkeleton
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	AEREIVRDIKEKLCY	Donor E	Purified	15	C	Cytostkeleton
Q92608	Dedicator of cytokinesis protein 2 OS=Homo sapiens GN=DOCK2 PE=1 SV=2 - [DOCK2_HUMAN]	KPVPDQIINFYKSNYVQR	Donor E	Purified	18	C	Cytostkeleton
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	SPDPSIYAYDNFGVLG	Donor E	Purified	16	ER/G	Others
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	DIMRVNVDKVLERDQK	Donor E	Purified	16	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	DIMRVNVDKVLERDQKL	Donor E	Purified	17	M	Endocytosis/exocytosis
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	VDKVLERDQKLSELDDR	Donor E	Purified	17	M	Endocytosis/exocytosis
P06746	DNA polymerase beta OS=Homo sapiens GN=POLB PE=1 SV=3 - [DPOLB_HUMAN]	CGVLYFTGSDIFNKNMRA	Donor E	Purified	18	N	Gene expression /chromatine organization
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	EILPTTPISEQKGGKPEPPAMPQPVPTA	Donor E	Purified	28	C	Gene expression /chromatine organization
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	PVKKLVVKGGKKKKQVLKFTLD	Donor E	Purified	22	C	Gene expression /chromatine organization
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	APVKKLVVKGGKKKKQVLKFTLD	Donor E	Purified	23	C	Gene expression /chromatine organization
P49591	Seryl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN]	VLDLDLFRVDKGGD	Donor E	Purified	14	C	Gene expression /chromatine organization
P53999	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3 - [TCP4_HUMAN]	DIREYWMDPEGEMKPG	Donor E	Purified	16	N	Gene expression /chromatine organization
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	GYEPPVQESV	Donor E	Purified	10	C	Gene expression /chromatine organization
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	LVREIAQDFKTDLRF	Donor E	Purified	15	N	Gene expression /chromatine organization
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	VREIAQDFKTDLRFQ	Donor E	Purified	15	N	Gene expression /chromatine organization
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	LVREIAQDFKTDLRFQ	Donor E	Purified	16	N	Gene expression /chromatine organization
O00602	Ficolin-1 OS=Homo sapiens GN=FCN1 PE=1 SV=2 - [FCN1_HUMAN]	NHQFAKYKSFKVADE	Donor E	Purified	15	EM/S	Immune response
O00626	C-C motif chemokine 22 OS=Homo sapiens GN=CCL22 PE=1 SV=2 - [CCL22_HUMAN]	PRVPWVKMILNKLSQ	Donor E	Purified	15	EM/S	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	KSWITFDLKNKEVS	Donor E	Purified	14	M	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	KSWITFDLKNKEVSVK	Donor E	Purified	16	M	Immune response
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]	SKSWITFDLKNKEVSVK	Donor E	Purified	17	M	Immune response

P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	LEEFGRFASFEAQG	Donor E	Purified	14	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	RLEEFGRFASFEAQG	Donor E	Purified	15	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	LEEFGRFASFEAQGAL	Donor E	Purified	16	M	Immune response
P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	RLEEFGRFASFEAQGAL	Donor E	Purified	17	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	VGEFRAVTELGRPD	Donor E	Purified	14	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	DVGEFRAVTELGRPD	Donor E	Purified	15	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	DVGEFRAVTELGRPDA	Donor E	Purified	16	M	Immune response
P01911	HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens GN=HLA-DRB1 PE=1 SV=2 - [2B1F_HUMAN]	SDVGEFRAVTELGRPDA	Donor E	Purified	17	M	Immune response
P04440	HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens GN=HLA-DPB1 PE=1 SV=1 - [DPB1_HUMAN]	DVGEFRAVTELGRPA	Donor E	Purified	15	M	Immune response
P04440	HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens GN=HLA-DPB1 PE=1 SV=1 - [DPB1_HUMAN]	SDVGEFRAVTELGRPA	Donor E	Purified	16	M	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	LPRIICDNTGITT	Donor E	Purified	13	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	SLPRIICDNTGITT	Donor E	Purified	14	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	QNQIAVDEIRERLFE	Donor E	Purified	15	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	RQNQIAVDEIRERLFE	Donor E	Purified	16	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	VSNEIVRFPTDQLTPD	Donor E	Purified	16	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	RQNQIAVDEIRERLFEQ	Donor E	Purified	17	Lys/End	Immune response
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	VSNEIVRFPTDQLTPDQ	Donor E	Purified	17	Lys/End	Immune response
P08575	Receptor-type tyrosine-protein phosphatase C OS=Homo sapiens GN=PTPRC PE=1 SV=2 - [PTPRC_HUMAN]	VDIFQVVKALRKARPG	Donor E	Purified	16	M	Immune response
P08575	Receptor-type tyrosine-protein phosphatase C OS=Homo sapiens GN=PTPRC PE=1 SV=2 - [PTPRC_HUMAN]	VVDIFQVVKALRKARPG	Donor E	Purified	17	M	Immune response
P0C0L4	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1 - [CO4A_HUMAN]	HPQYLLDSNSWIEE	Donor E	Purified	14	EM/S	Immune response
P0C0L4	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1 - [CO4A_HUMAN]	GHPQYLLDSNSWIEEMPS	Donor E	Purified	18	EM/S	Immune response
P10145	Interleukin-8 OS=Homo sapiens GN=IL8 PE=1 SV=1 - [IL8_HUMAN]	DGRELCLDPKENWVQ	Donor E	Purified	15	EM/S	Immune response
P10145	Interleukin-8 OS=Homo sapiens GN=IL8 PE=1 SV=1 - [IL8_HUMAN]	PKENWVQRVVEKFLKRAENS	Donor E	Purified	20	EM/S	Immune response
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	DDIIVNWVNETLRE	Donor E	Purified	14	C	Immune response
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	NDDIIVNWVNETLR	Donor E	Purified	14	C	Immune response
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	NDDIIVNWVNETLRE	Donor E	Purified	15	C	Immune response
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	VNDDIIVNWVNETLREAK	Donor E	Purified	18	C	Immune response
P15260	Interferon gamma receptor 1 OS=Homo sapiens GN=IFNGR1 PE=1 SV=1 - [INGR1_HUMAN]	GPPKLDIRKEEKQIMIDIFHP	Donor E	Purified	21	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	FYVDLDKKETVWH	Donor E	Purified	13	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	MFYVDLDKKETVWH	Donor E	Purified	14	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	EMFYVDLDKKETVWH	Donor E	Purified	15	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	MFYVDLDKKETVWHLE	Donor E	Purified	16	M	Immune response
P20036	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 - [DPA1_HUMAN]	EMFYVDLDKKETVWHLE	Donor E	Purified	17	M	Immune response

P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	WDVLKCDEKAKFV	Donor E	Purified	13	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	EKNIMLYKGSGLWS	Donor E	Purified	14	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	QEKNIMLYKGSGLWS	Donor E	Purified	15	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	QEKNIMLYKGSGLWSR	Donor E	Purified	16	M	Immune response
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]	RQEKNIMLYKGSGLWSRW	Donor E	Purified	18	M	Immune response
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 - [PSA5_HUMAN]	GPQLFHMDPSGTFVQ	Donor E	Purified	15	C	Immune response
P28068	HLA class II histocompatibility antigen, DM beta chain OS=Homo sapiens GN=HLA-DMB PE=1 SV=1 - [DMB_HUMAN]	TPKDFTYCISFNK	Donor E	Purified	13	Lys/End	Immune response
P31994	Low affinity immunoglobulin gamma Fc region receptor II-b OS=Homo sapiens GN=FCGR2B PE=1 SV=2 - [FCG2B_HUMAN]	SPESDSIQWFHNGNLIPT	Donor E	Purified	18	M	Immune response
P38484	Interferon gamma receptor 2 OS=Homo sapiens GN=IFNGR2 PE=1 SV=2 - [INGR2_HUMAN]	IEEYLKDPTQPILE	Donor E	Purified	14	M	Immune response
P79483	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 - [DRB3_HUMAN]	DRYFHNQEEFLRFDS	Donor E	Purified	15	M	Immune response
P79483	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 - [DRB3_HUMAN]	DVGEYRAVTELGRPV	Donor E	Purified	15	M	Immune response
P79483	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 - [DRB3_HUMAN]	DRYFHNQEEFLRFDSD	Donor E	Purified	16	M	Immune response
P79483	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 - [DRB3_HUMAN]	FQTLVMLETVPRSGEVY	Donor E	Purified	17	M	Immune response
P80075	C-C motif chemokine 8 OS=Homo sapiens GN=CCL8 PE=1 SV=2 - [CCL8_HUMAN]	PKERWVRDSMKHLDQIFQNLKP	Donor E	Purified	22	EM/S	Immune response
Q9NPH3	Interleukin-1 receptor accessory protein OS=Homo sapiens GN=IL1RAP PE=1 SV=2 - [IL1AP_HUMAN]	LPGGIVTDETLSFIQK	Donor E	Purified	16	M	Immune response
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	LGEYLFERLTLKHD	Donor E	Purified	14	C	Ion homeostasis
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	VSHFFRELAEEKREG	Donor E	Purified	15	C	Ion homeostasis
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	AGLGEYLFERLTLKHD	Donor E	Purified	16	C	Ion homeostasis
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	GVSHFFRELAEEKREG	Donor E	Purified	16	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTGKF	Donor E	Purified	17	C	Ion homeostasis
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	YGKDLIADLKYELTGKFE	Donor E	Purified	18	C	Ion homeostasis
Q13557	Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D PE=1 SV=3 - [KCC2D_HUMAN]	PGYLSPEVLRKDPYGKPVDMWACGVILYIL	Donor E	Purified	30	M	Ion homeostasis
Q93050	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3 - [VPP1_HUMAN]	RRKHLGTLNFGGIR	Donor E	Purified	14	M	Ion homeostasis
A6NMY6	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2 - [AXA2L_HUMAN]	DLEKDIISDTSGDFRK	Donor E	Purified	16	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	SSKFQVDNNNRLL	Donor E	Purified	13	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	FSSKFQVDNNNRLL	Donor E	Purified	14	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	GNRIAQWQSFQLEG	Donor E	Purified	14	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	GNRIAQWQSFQLEGG	Donor E	Purified	15	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	GNRIAQWQSFQLEGGL	Donor E	Purified	16	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	DPKGNRIAQWQSFQLEG	Donor E	Purified	17	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	DPKGNRIAQWQSFQLEGG	Donor E	Purified	18	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	DPKGNRIAQWQSFQLEGGL	Donor E	Purified	19	EM/S	Others
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	IQDPKGNRIAQWQSFQLEGGL	Donor E	Purified	21	EM/S	Others

P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	IQDPKGNRIAQWQSFQLEGGLK	Donor E	Purified	22	EM/S	Others
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]	TPNGLAIDHRAEKLYF	Donor E	Purified	16	M	Others
Q68CQ7	Glycosyltransferase 8 domain-containing protein 1 OS=Homo sapiens GN=GLT8D1 PE=1 SV=2 - [GL8D1_HUMAN]	WEKWYIPDPTGKFN	Donor E	Purified	14	M	Others
Q9BZQ8	Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1 - [NIBAN_HUMAN]	ILHQILLDETLKVIKE	Donor E	Purified	16	C	Others
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]	VISALLADPTRRF	Donor E	Purified	13	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GAFSVYSDFLLYK	Donor E	Purified	13	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GAFSVYSDFLLYKS	Donor E	Purified	14	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GAFSVYSDFLLYKSG	Donor E	Purified	15	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GPVEGAFSVYSDFLLYK	Donor E	Purified	17	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GPVEGAFSVYSDFLLYKS	Donor E	Purified	18	Lys/End	Proteolysis
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]	GPVEGAFSVYSDFLLYKSG	Donor E	Purified	19	Lys/End	Proteolysis
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	RGLFIIDPNGVIK	Donor E	Purified	13	Mit	Redox homeostasis
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN]	FPTIYFSPANKKLNPK	Donor E	Purified	16	ER/G	Redox homeostasis
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN]	GFPTIYFSPANKKLNPK	Donor E	Purified	17	ER/G	Redox homeostasis
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	PAGKLKYFDKLN	Donor E	Purified	12	C	Redox homeostasis
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	RGLFIIDDKGILRQ	Donor E	Purified	14	C	Redox homeostasis
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	KIMQYFSHFIR	Donor E	Purified	11	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LKIMQYFSHFIR	Donor E	Purified	12	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	PIIDMASAWAKR	Donor E	Purified	12	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	KIMQYFSHFIRSG	Donor E	Purified	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LKIMQYFSHFIRS	Donor E	Purified	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIR	Donor E	Purified	13	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LKIMQYFSHFIRSG	Donor E	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSLKIMQYFSHFIR	Donor E	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFD	Donor E	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	MIFDLVHSYNRFPD	Donor E	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIRS	Donor E	Purified	14	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSLKIMQYFSHFIRS	Donor E	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDV	Donor E	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	MMIFDLVHSYNRFPD	Donor E	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIRSG	Donor E	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLSLKIMQYFSHFIR	Donor E	Purified	15	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	VPESKVIFDANAPVA	Donor E	Purified	15	EM/S	Thyroid

P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDV	Donor E	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	KIMQYFSHFIRSGNPN	Donor E	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSLKIMQYFSHFIRSG	Donor E	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSSVVVDPSIRHFDVA	Donor E	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	MMIFDLVHSYNRFPDA	Donor E	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIRSGN	Donor E	Purified	16	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	ALSSVVVDPSIRHFDVA	Donor E	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	DMMIFDLVHSYNRFPDA	Donor E	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	EKSLSLKIMQYFSHFIR	Donor E	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LKIMQYFSHFIRSGNPN	Donor E	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LSLKIMQYFSHFIRSGN	Donor E	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	TDMMIFDLVHSYNRFPD	Donor E	Purified	17	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVA	Donor E	Purified	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLKIMQYFSHFIRSGNPN	Donor E	Purified	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	TDMMIFDLVHSYNRFPDA	Donor E	Purified	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	TTDMMIFDLVHSYNRFPD	Donor E	Purified	18	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LALSSVVVDPSIRHFDVAH	Donor E	Purified	19	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLALSSVVVDPSIRHFDVAH	Donor E	Purified	20	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	SLSLKIMQYFSHFIRSGNPN	Donor E	Purified	20	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	EKSLSLKIMQYFSHFIRSGNPN	Donor E	Purified	22	EM/S	Thyroid
P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5 - [THYG_HUMAN]	LDSWQSLALSSVVVDPSIRHFDVAH	Donor E	Purified	25	EM/S	Thyroid
O14579	Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3 - [COPE_HUMAN]	RDVFLYRAYLAQR	Donor E	Purified	13	C	Transport
O14579	Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3 - [COPE_HUMAN]	VERDVFLYRAYLAQR	Donor E	Purified	15	C	Transport
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2 - [RAB5C_HUMAN]	SPNIVIALAGNKADL	Donor E	Purified	15	M	Transport
P62491	Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RB11A_HUMAN]	ATRSIQVDGKTIKAQIWD	Donor E	Purified	18	M	Transport
Q14108	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	IHVFRPDISPYFG	Donor E	Purified	13	Lys/End	Transport
Q86Y82	Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1 - [STX12_HUMAN]	KDLAMMIHDQGDLIDSI	Donor E	Purified	17	ER/G	Transport

ANNEX 3. LIST OF THYROGLOBULIN PEPTIDES ASSOCIATED TO HLA-DR AND ISOLATED FROM MONOCYTE-DERIVED DENDRITIC CELLS AFTER PULSING WITH PURIFIED THYROGLOBULIN OR THYROID EXTRACT

				Thyroglobulin							Thyroid extracts			
				Donor A	Donor B	Donor C	Donor D	Donor E	Donor F	Donor G	Donor C	Donor D	Donor E	Donor H
Binding core/s	Allele/s	Affinity	Peptide sequence	*0301	*0301 *1301	*0301 *0901	*0301 *1101	*0301 *1501	*0701 *1501	*1101 *1501	*0301 *0901	*0301 *1101	*0301 *1501	*0101 *0701
VVVDPSIRH	DR3	HB	ALSSVVVDPSIRHFD	X										
VVVDPSIRH	DR3	HB	ALSSVVVDPSIRHFDV	X	X			X				X	X	
VVVDPSIRH	DR3	HB	ALSSVVVDPSIRHFDVA	X	X	X	X	X			X	X	X	
VVVDPSIRH	DR3	HB	ALSSVVVDPSIRHFDVAH			X							X	
VVVDPSIRH	DR3	HB	DSWQSLALSSVVVDPSIRHFDVAH				X							
VVVDPSIRH	DR3	HB	LALSSVVVDPSIRHFDV	X	X	X	X				X			
VVVDPSIRH	DR3	HB	LALSSVVVDPSIRHFDVA	X		X	X	X			X	X	X	
VVVDPSIRH	DR3	HB	LALSSVVVDPSIRHFDVAH	X	X	X	X	X			X	X		
VVVDPSIRH	DR3	HB	LDSWQSLALSSVVVDPSIRHFDVAH			X	X	X						
VVVDPSIRH	DR3	HB	LSSVVVDPSIRHFD	X	X	X		X				X	X	
VVVDPSIRH	DR3	HB	LSSVVVDPSIRHFDV	X	X	X	X	X				X	X	
VVVDPSIRH	DR3	HB	LSSVVVDPSIRHFDVA	X	X	X		X			X	X	X	
VVVDPSIRH	DR3	HB	LSSVVVDPSIRHFDVAH	X	X									
VVVDPSIRH	DR3	HB	SLALSSVVVDPSIRHFDV	X	X						X			
VVVDPSIRH	DR3	HB	SLALSSVVVDPSIRHFDVA	X		X	X				X	X		
VVVDPSIRH	DR3	HB	SLALSSVVVDPSIRHFDVAH	X	X	X	X	X				X	X	
VVVDPSIRH	DR3	HB	SSVVVDPSIRHFD	X										
VVVDPSIRH	DR3	HB	SVVVDPSIRHFDV	X										

VVVDPSIRH	DR3	HB	SWQSLALSSVVVDPSIRHFDVAH			X									
VIFDANAPV	DR3	HB	EKVPESKVIFDANAPVA	X											
VIFDANAPV	DR3	HB	KVPESKVIFDANAPVA	X	X										
VIFDANAPV	DR15	IB	KVPESKVIFDANAPVAVRSKVPDSEFPV							X					
VIFDANAPV	DR3	HB	KVPESKVIFDANAPVAVRSKVPDSEFPVM				X								
VIFDANAPV	DR3	HB	VPESKVIFDANAPV	X	X										
VIFDANAPV	DR3	HB	VPESKVIFDANAPVA	X	X	X	X	X				X		X	
IMQYFSHFI	DR15	HB	EKSLSLKIMQYFSHFIR					X	X	X					
IMQYFSHFI	DR15	HB	EKSLSLKIMQYFSHFIRSGNPN					X	X	X				X	
IMQYFSHFI	DR15	HB	KIMQYFSHFIR					X	X					X	
IMQYFSHFI	DR15	HB	KIMQYFSHFIRS						X						
IMQYFSHFI	DR15	HB	KIMQYFSHFIRSG					X	X						
IMQYFSHFI/FSHFIRSGN	DR15/DR13	HB	KIMQYFSHFIRSGN						X						
IMQYFSHFI/FSHFIRSGN	DR15/DR13	HB	KIMQYFSHFIRSGNPN		X			X	X					X	
IMQYFSHFI	DR15	HB	KSLSLKIMQYFSHFIR							X					
IMQYFSHFI	DR15	HB	KSLSLKIMQYFSHFIRSGNPN							X					
IMQYFSHFI	DR15	HB	LKIMQYFSHFIR					X	X	X				X	
IMQYFSHFI	DR15	HB	LKIMQYFSHFIRS					X	X						
IMQYFSHFI	DR15	HB	LKIMQYFSHFIRSG					X	X	X				X	
IMQYFSHFI	DR15	HB	LKIMQYFSHFIRSGN						X						
IMQYFSHFI/FSHFIRSGN	DR15/DR13	HB	LKIMQYFSHFIRSGNPN		X			X	X	X				X	
IMQYFSHFI	DR15	HB	LSLKIMQYFSHFIR					X	X	X				X	
IMQYFSHFI	DR15	HB	LSLKIMQYFSHFIRS					X	X	X				X	
IMQYFSHFI	DR15	HB	LSLKIMQYFSHFIRSG					X	X	X				X	
IMQYFSHFI	DR15	HB	LSLKIMQYFSHFIRSGN					X	X					X	
IMQYFSHFI	DR15	HB	SLKIMQYFSHFIRS					X	X	X				X	
IMQYFSHFI	DR15	HB	SLKIMQYFSHFIRSGN					X	X					X	

IMQYFSHFI/FSHFIRSGN	DR15/DR13	HB	SLKIMQYFSHFIRSGNPN		X			X	X	X				X	
IMQYFSHFI	DR15	HB	SLSLKIMQYFSHFIR					X	X						
IMQYFSHFI	DR15	HB	SLSLKIMQYFSHFIRSGNPN					X	X	X				X	
IHLLTARAT	DR1	HB	ADVASIHLLTARATNSQ												X
FLVAKGIRL	DR1/DR7/DR15	HB	ESFLVAKGIRL						X						X
FLVAKGIRL	DR1/DR7/DR15	HB	ESFLVAKGIRLR						X						X
FLVAKGIRL	DR7/DR15	HB	ESFLVAKGIRLRN						X						
FLVAKGIRL	DR15	HB	ESFLVAKGIRLRNED											X	
LVAKGIRLR/VAKGIRLRN	DR3/DR15	IB	ESFLVAKGIRLRNEDL											X	
FLVAKGIRL	DR7/DR15	HB	ESFLVAKGIRLRNEDLG						X						
FLVAKGIRL	DR7/DR15	HB	GESFLVAKGIRL						X						
FLVAKGIRL	DR1/DR7	HB	GESFLVAKGIRLR												X
FLVAKGIRL	DR1/DR7	HB	GESFLVAKGIRLRNED						X						X
FLVAKGIRL	DR1/DR7	HB	LGESFLVAKGIRLR												X
FLVAKGIRL	DR1/DR7/DR15	HB	LGESFLVAKGIRLRN						X						X
FLVAKGIRL	DR7/DR15	HB	LGESFLVAKGIRLRNED						X						
FLVAKGIRL	DR7/DR15	HB	FPLGESFLVAKGIRLR						X						
FLVAKGIRL	DR7/DR15	HB	FPLGESFLVAKGIRLRN						X						
FLVAKGIRL	DR7/DR15	HB	FPLGESFLVAKGIRLRNED						X						
IVVTASYRV	DR1/DR7/DR15	HB	GNLIVVTASYRVG						X						X
IVVTASYRV	DR7/DR15	HB	VGNLIVVTASYRV						X						
IVVTASYRV	DR7/DR15	HB	VGNLIVVTASYRVG						X						
IVVTASYRV	DR7/DR15	HB	VGNLIVVTASYRVGVF						X						
FLREPPARA	DR1	HB	IDGHFLREPPARALKR												X
WQILNGQLS	DR1	HB	LFWQILNGQLSQYPG												X
FLAVQSVIS	DR7	HB	ETTLYRILQRRFLAVQSVISGRF						X						
FLAVQSVIS(VQSVISGRF)	DR7/DR9	HB (IB)	ILQRRFLAVQSVISGRF			X			X		X				X

VQSVISGRF	DR9	IB	LQRRFLAVQSVISGRF			X									
VQSVISGRF	DR9	IB	RFLAVQSVISGRF			X									
FLAVQSVIS(VQSVISGRF)	DR7/DR9	HB (IB)	RRFLAVQSVISGRF			X			X		X				X
FLAVQSVIS	DR7	HB	QRRFLAVQSVISGR						X						
VQSVISGRF	DR9	IB	QRRFLAVQSVISGRF			X					X				
VQSVISGRF	DR9	IB	QRRFLAVQSVISGRFR			X					X				
FLAAVGNLI	DR9/DR7	IB (HB)	GSFLAAVGNLI						X		X				
FLAAVGNLI	DR9/DR7	IB (HB)	IDGSFLAAVGNLI			X			X		X				
FLAAVGNLI	DR9	IB	IDGSFLAAVGNLIV			X									
FLAAVGNLI	DR9	IB	IDGSFLAAVGNLIVVT			X									
FQKLMGISI	DR1/DR7	HB	LPFQKLMGISIR												X
FQKLMGISI	DR1/DR7	HB	LPFQKLMGISIRN												X
FQKLMGISI	DR1/DR7	HB	LPFQKLMGISIRNK												X
FQKLMGISI	DR1/DR7	HB	RLPFQKLMGISIR												X
FQKLMGISI	DR1/DR7	HB	RLPFQKLMGISIRN												X
FQKLMGISI	DR1/DR7	HB	RLPFQKLMGISIRNK												X
FQKLMGISI	DR1/DR7	HB	TRLPFQKLMGISIR												X
FQKLMGISI	DR1/DR7	HB	TRLPFQKLMGISIRN												X
FQKLMGISI	DR1/DR7	HB	TRLPFQKLMGISIRNK												X
FQKLMGISI	DR1/DR7	HB	YTRLPFQKLMGISIRNK												X
FYQALQNSL	DR9	IB	KTAFYQALQNSLG			X									
FYQALQNSL	DR9	IB	KTAFYQALQNSLGG			X									
FYQALQNSL	DR9	IB	SKTAFYQALQNSLG			X					X				
FYQALQNSL	DR9	IB	SKTAFYQALQNSLGG								X				
FYQALQNSL	DR9	IB	SKTAFYQALQNSLGGE			X					X				
FYQALQNSL	DR9	IB	SKTAFYQALQNSLGGED			X					X				
FYQALQNSL	DR9	IB	SSKTAFYQALQNSLGGED			X					X				

FTETTLYRI	DR7	HB	LPSTFTETTLYRI						X						X
FTETTLYRI	DR7	HB	LPSTFTETTLYRILQ												X
FTETTLYRI	DR7	HB	LPSTFTETTLYRILQR						X						X
FTETTLYRI	DR7	HB	LPSTFTETTLYRILQRR						X						
LIQSGSFQL	DR7/DR15	HB	RFTDLIQSGSFQLHLDS						X						X
LIQSGSFQL	DR7/DR15	HB	RFTDLIQSGSFQLHLDSK						X						
LIQSGSFQL	DR7/DR15	HB	RFTDLIQSGSFQLHLDSKT						X						
FTTNPKRLQ	DR11	HB	ALQFTTNPKRLQQNL							X					
FTTNPKRLQ	DR11	HB	LALQFTTNPKRLQQ							X					
FTTNPKRLQ	DR11	HB	LALQFTTNPKRLQQNL							X					
FTTNPKRLQ	DR11	HB	LALQFTTNPKRLQQNLFG							X					
VGKDLLGRF	DR3	HB	DIERALVGKDLLGRFTDL		X										
MIFDLVHSY/VHSYNRFPD	DR3/DR15	HB	DMMIFDLVHSYNRFPDA					X	X	X			X		
MIFDLVHSY/VHSYNRFPD	DR3/DR15	HB	MIFDLVHSYNRFPD					X	X				X		
VHSYNRFPD	DR15	HB	MIFDLVHSYNRFPDA						X						
MIFDLVHSY/VHSYNRFPD	DR3/DR15	HB	MMIFDLVHSYNRFPD					X	X	X			X		
MIFDLVHSY/VHSYNRFPD	DR3/DR15	HB	MMIFDLVHSYNRFPDA					X	X				X		
MIFDLVHSY/VHSYNRFPD	DR3/DR15	HB	TDMMIFDLVHSYNRFPD					X	X	X			X		
MIFDLVHSY/VHSYNRFPD	DR3/DR15	HB	TDMMIFDLVHSYNRFPDA					X	X	X					
MIFDLVHSY/VHSYNRFPD	DR3/DR15	HB	TTDMMIFDLVHSYNRFPD					X	X	X			X		
VHSYNRFPD	DR15	HB	TTDMMIFDLVHSYNRFPDA						X						
FCVDGEGRR	DR3	HB	DRGSGKAFCVDGEGRRLPWWE	X											
ETTLYRILQ	DR11	HB	ETTLYRILQRR							X					
VDPASGEEL	DR13	IB	GAGTWCVDPASGEELRPG		X										
ILEDKVKNF	DR3	HB	KKVILEDKVKNFYTR	X											
ILEDKVKNF	DR3	HB	RKKVILEDKVKNFYTR	X											

FIKSLTPLE	DR3/DR9	IB	GDQEFIKSLTPLE			X									
FIKSLTPLE	DR3/DR9	IB	LGDQEFIKSLTPLE			X									
FYPAYEGQF	DR9	IB	LPFYPAYEGQFS			X									
FYPAYEGQF	DR9	IB	LPFYPAYEGQFSL			X					X				
FYPAYEGQF	DR9	IB	LPFYPAYEGQFSLE			X									
FYPAYEGQF	DR9	IB	LPFYPAYEGQFSLEE								X				
LTWVQTHIR	DR3	IB	DQVAALTWVQTHIRG		X										
LTWVQTHIR	DR3	IB	QVAALTWVQTHIRG		X										
LTWVQTHIR	DR3	IB	VAALTWVQTHIRG		X										
LTWVQTHIR	DR3	IB	VAALTWVQTHIRGFG		X										
IDMASAWAK/IIDMASAWA	DR3 (DR15)	IB (IB)	PIIDMASAWAKR					X	X	X				X	
LRCQVKVRS/FGSLRCQVK	DR3/DR11	IB	SFGSLRCQVKVRSHGQD									X			

ANNEX 4. THYROGLOBULIN PEPTIDES IDENTIFIED IN CELL-FREE SYSTEM SAMPLES

Intact thyroglobulin in DC-like condition

Sequence	# PSMs	Sample	Cathepsins	Length	Binding core (HLA-DR3)	Theoretical Affinity
GSQPAGSTLFVPA	1	Intact+DC	BHS	13	AGSTLFVPA	IB
GSQPAGSTLFVPA	1	Intact+DC	BHS	13	AGSTLFVPA	IB
ASGAGTWCVDPASGEELRPG	1	Intact+DC	BHS	20	AGTWCVDPA	IB
ASGAGTWCVDPASGEELRPG	1	Intact+DC	BHS	20	AGTWCVDPA	IB
STGTPEAAKKDGTMNKPT	2	Intact+DC	BHS	18	AKKDGTMNK	IB
STGTPEAAKKDGTMNKPT	2	Intact+DC	BHS	18	AKKDGTMNK	IB
GSALSPAAVISHERA	1	Intact+DC	BHS	15	ALSPAAVIS	IB
GSALSPAAVISHERA	1	Intact+DC	BHS	15	ALSPAAVIS	IB
MGGSALSPAAVISH	1	Intact+DC	BHS	14	ALSPAAVIS	IB
MGGSALSPAAVISH	1	Intact+DC	BHS	14	ALSPAAVIS	IB
MGGSALSPAAVISHERA	1	Intact+DC	BHS	17	ALSPAAVIS	IB
MGGSALSPAAVISHERA	1	Intact+DC	BHS	17	ALSPAAVIS	IB
ARATNSQLFRR	1	Intact+DC	BHS	11	ARATNSQLF	IB
ARATNSQLFRR	1	Intact+DC	BHS	11	ARATNSQLF	IB
ARSLQIPQCPT	1	Intact+DC	BHS	11	ARSLQIPQC	LB
ARSLQIPQCPT	1	Intact+DC	BHS	11	ARSLQIPQC	LB
ARSLQIPQCPTTCEKSR	1	Intact+DC	BHS	17	ARSLQIPQC	LB
ARSLQIPQCPTTCEKSR	1	Intact+DC	BHS	17	ARSLQIPQC	LB
QARSQENPSPKDLFVPA	1	Intact+DC	BHS	17	ARSQENPSP	IB
QARSQENPSPKDLFVPA	1	Intact+DC	BHS	17	ARSQENPSP	IB
SSWKQARSQENPSPK	1	Intact+DC	BHS	15	ARSQENPSP	IB
SSWKQARSQENPSPK	1	Intact+DC	BHS	15	ARSQENPSP	IB
SSWKQARSQENPSPKD	1	Intact+DC	BHS	16	ARSQENPSP	IB
SSWKQARSQENPSPKD	1	Intact+DC	BHS	16	ARSQENPSP	IB
SWKQARSQENPSPKD	1	Intact+DC	BHS	15	ARSQENPSP	IB
SWKQARSQENPSPKD	1	Intact+DC	BHS	15	ARSQENPSP	IB
REEATHIYRKPG	1	Intact+DC	BHS	12	ATHIYRKPG	LB
REEATHIYRKPG	1	Intact+DC	BHS	12	ATHIYRKPG	LB
GSALSPAAVISHERAQQ	1	Intact+DC	BHS	17	AVISHERAQ	IB
GSALSPAAVISHERAQQ	1	Intact+DC	BHS	17	AVISHERAQ	IB
GSALSPAAVISHERAQQQA	1	Intact+DC	BHS	19	AVISHERAQ	IB
GSALSPAAVISHERAQQQA	1	Intact+DC	BHS	19	AVISHERAQ	IB
SHGQDSPAVYLKKGQGSTTTLQ	1	Intact+DC	BHS	22	AVYLKKGQG	IB
SHGQDSPAVYLKKGQGSTTTLQ	1	Intact+DC	BHS	22	AVYLKKGQG	IB
CGSPDIEVH	1	Intact+DC	BHS	9	CGSPDIEVH	LB
CGSPDIEVH	1	Intact+DC	BHS	9	CGSPDIEVH	LB
GGQPRCPTDCEKQR	1	Intact+DC	BHS	14	CPTDCEKQR	LB

GGQPRCPTDCEKQR	1	Intact+DC	BHS	14	CPTDCEKQR	LB
GGQPRCPTDCEKQRAR	1	Intact+DC	BHS	16	CPTDCEKQR	LB
GGQPRCPTDCEKQRAR	1	Intact+DC	BHS	16	CPTDCEKQR	LB
LGDQEFIKSLTPLE	1	Intact+DC	BHS	14	FIKSLTPLE	IB
LGDQEFIKSLTPLE	1	Intact+DC	BHS	14	FIKSLTPLE	IB
EFSELLPNRQG	1	Intact+DC	BHS	11	FSELLPNRQ	IB
EFSELLPNRQG	1	Intact+DC	BHS	11	FSELLPNRQ	IB
FSELLPNRQGLKK	2	Intact+DC	BHS	13	FSELLPNRQ	IB
FSELLPNRQGLKK	2	Intact+DC	BHS	13	FSELLPNRQ	IB
TSGYFSQHDLFSSPEKR	1	Intact+DC	BHS	17	FSQHDLFSS	LB
TSGYFSQHDLFSSPEKR	1	Intact+DC	BHS	17	FSQHDLFSS	LB
GQSQQFSVSENLLK	2	Intact+DC	BHS	14	FSVSENLLK	HB
GQSQQFSVSENLLK	2	Intact+DC	BHS	14	FSVSENLLK	HB
RFTDLIQSGSFQ	1	Intact+DC	BHS	12	FTDLIQSGS	LB
RFTDLIQSGSFQ	1	Intact+DC	BHS	12	FTDLIQSGS	LB
FVDSGLLRPM	1	Intact+DC	BHS	10	FVDSGLLRP	IB
FVDSGLLRPM	1	Intact+DC	BHS	10	FVDSGLLRP	IB
DSGEEVPGTRVT	1	Intact+DC	BHS	12	GEEVPGTRV	LB
DSGEEVPGTRVT	1	Intact+DC	BHS	12	GEEVPGTRV	LB
SHGQDSPAVYLKK	2	Intact+DC	BHS	13	HGQDSPAVY	LB
SHGQDSPAVYLKK	2	Intact+DC	BHS	13	HGQDSPAVY	LB
AIGKPKKCPTPCQ	1	Intact+DC	BHS	13	IGKPKKCPT	IB
AIGKPKKCPTPCQ	1	Intact+DC	BHS	13	IGKPKKCPT	IB
QAIPGTRSAIGKPKKCPTPCQ	1	Intact+DC	BHS	21	IGKPKKCPT	IB
QAIPGTRSAIGKPKKCPTPCQ	1	Intact+DC	BHS	21	IGKPKKCPT	IB
SAIGKPKKCPTPCQ	1	Intact+DC	BHS	14	IGKPKKCPT	IB
SAIGKPKKCPTPCQ	1	Intact+DC	BHS	14	IGKPKKCPT	IB
IPQCPTTCEKSR	1	Intact+DC	BHS	12	IPQCPTTCE	LB
IPQCPTTCEKSR	1	Intact+DC	BHS	12	IPQCPTTCE	LB
DTYIPQCSTDGQWRQ	1	Intact+DC	BHS	15	IPQCSTDGQ	LB
DTYIPQCSTDGQWRQ	1	Intact+DC	BHS	15	IPQCSTDGQ	LB
ISAGAFSQTHC	1	Intact+DC	BHS	11	ISAGAFSQT	LB
ISAGAFSQTHC	1	Intact+DC	BHS	11	ISAGAFSQT	LB
ISAGAFSQTHCVT	1	Intact+DC	BHS	13	ISAGAFSQT	LB
ISAGAFSQTHCVT	1	Intact+DC	BHS	13	ISAGAFSQT	LB
LAADRGGADVASIHL	1	Intact+DC	BHS	15	LAADRGGAD	IB
LAADRGGADVASIHL	1	Intact+DC	BHS	15	LAADRGGAD	IB
ELFVDSGLLR	1	Intact+DC	BHS	10	LFVDSGLLR	HB
ELFVDSGLLR	1	Intact+DC	BHS	10	LFVDSGLLR	HB
ELFVDSGLLRPM	1	Intact+DC	BHS	12	LFVDSGLLR	HB
ELFVDSGLLRPM	1	Intact+DC	BHS	12	LFVDSGLLR	HB
LHLDSKTFPAETIR	2	Intact+DC	BHS	14	LHLDSKTFP	HB
LHLDSKTFPAETIR	2	Intact+DC	BHS	14	LHLDSKTFP	HB
DCQRNEAGLQCDQNGQYRASQK	1	Intact+DC	BHS	22	LQCDQNGQY	HB
DCQRNEAGLQCDQNGQYRASQK	1	Intact+DC	BHS	22	LQCDQNGQY	HB
LALQFTTNPKR	2	Intact+DC	BHS	11	LQFTTNPKR	HB
LALQFTTNPKR	2	Intact+DC	BHS	11	LQFTTNPKR	HB

KGQGSTTTLQKRFEPTG	1	Intact+DC	BHS	17	LQKRFEPTG	LB
KGQGSTTTLQKRFEPTG	1	Intact+DC	BHS	17	LQKRFEPTG	LB
LQSEQAFLRT	1	Intact+DC	BHS	10	LQSEQAFLR	HB
LQSEQAFLRT	1	Intact+DC	BHS	10	LQSEQAFLR	HB
LREEATHIYR	1	Intact+DC	BHS	10	LREEATHIY	IB
LREEATHIYR	1	Intact+DC	BHS	10	LREEATHIY	IB
LREEATHIYRKPG	1	Intact+DC	BHS	13	LREEATHIY	IB
LREEATHIYRKPG	1	Intact+DC	BHS	13	LREEATHIY	IB
GVLSRRVSPGYVPACR	1	Intact+DC	BHS	16	LSRRVSPGY	IB
GVLSRRVSPGYVPACR	1	Intact+DC	BHS	16	LSRRVSPGY	IB
LSSVVVDPSIR	1	Intact+DC	BHS	11	LSSVVVDPS	LB
LSSVVVDPSIR	1	Intact+DC	BHS	11	LSSVVVDPS	LB
QVYLWKDSDMGSRPE	1	Intact+DC	BHS	15	LWKDSDMGS	IB
QVYLWKDSDMGSRPE	1	Intact+DC	BHS	15	LWKDSDMGS	IB
QVYLWKDSDMGSRPES	2	Intact+DC	BHS	16	LWKDSDMGS	IB
QVYLWKDSDMGSRPES	2	Intact+DC	BHS	16	LWKDSDMGS	IB
QVYLWKDSDMGSRPESMG	1	Intact+DC	BHS	18	LWKDSDMGS	IB
QVYLWKDSDMGSRPESMG	1	Intact+DC	BHS	18	LWKDSDMGS	IB
QVYLWKDSDMGSRPESMG	1	Intact+DC	BHS	18	LWKDSDMGS	IB
QVYLWKDSDMGSRPESMG	1	Intact+DC	BHS	18	LWKDSDMGS	IB
EKSRTSGLLSSWKQARSQEN	1	Intact+DC	BHS	20	LLSSWKQAR	HB
EKSRTSGLLSSWKQARSQEN	1	Intact+DC	BHS	20	LLSSWKQAR	HB
EKSRTSGLLSSWKQARSQENPSPKD	1	Intact+DC	BHS	25	LLSSWKQAR	HB
EKSRTSGLLSSWKQARSQENPSPKD	1	Intact+DC	BHS	25	LLSSWKQAR	HB
SMGCRKNTVPRPA	1	Intact+DC	BHS	13	MGCRKNTVP	LB
SDNVACMTSDQKRDALGNSK	1	Intact+DC	BHS	20	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSK	1	Intact+DC	BHS	20	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSK	1	Intact+DC	BHS	20	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSK	1	Intact+DC	BHS	20	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSKA	1	Intact+DC	BHS	21	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSKA	1	Intact+DC	BHS	21	MTSDQKRDA	HB
TSGYFSQHDL	1	Intact+DC	BHS	10	SGYFSQHDL	LB
TSGYFSQHDL	1	Intact+DC	BHS	10	SGYFSQHDL	LB
SSQEVVSCLR	1	Intact+DC	BHS	10	SQEVVSCLR	LB
SSQEVVSCLR	1	Intact+DC	BHS	10	SQEVVSCLR	LB
GQGSTTTLQKRFEPTG	1	Intact+DC	BHS	16	STTTLQKRF	LB
GQGSTTTLQKRFEPTG	1	Intact+DC	BHS	16	STTTLQKRF	LB
QTIQTQGHFQ	2	Intact+DC	BHS	10	TIQTQGHFQ	LB
QTIQTQGHFQ	2	Intact+DC	BHS	10	TIQTQGHFQ	LB
TPWPDFVPR	1	Intact+DC	BHS	9	TPWPDFVPR	LB
TPWPDFVPR	1	Intact+DC	BHS	9	TPWPDFVPR	LB
VDAEGQAIPGTRSAIGKPKK	1	Intact+DC	BHS	20	VDAEGQAIP	LB
VDAEGQAIPGTRSAIGKPKK	1	Intact+DC	BHS	20	VDAEGQAIP	LB
VDAQPLRPC	1	Intact+DC	BHS	9	VDAQPLRPC	LB
VDAQPLRPC	1	Intact+DC	BHS	9	VDAQPLRPC	LB
VDPASGEELRPGSSS	1	Intact+DC	BHS	15	VDPASGEEL	LB
VDPASGEELRPGSSS	1	Intact+DC	BHS	15	VDPASGEEL	LB

KVPESKVIFDANAPVA	2	Intact+DC	BHS	16	VIFDANAPV	HB
KVPESKVIFDANAPVA	2	Intact+DC	BHS	16	VIFDANAPV	HB
KVPESKVIFDANAPVAVR	3	Intact+DC	BHS	18	VIFDANAPV	HB
KVPESKVIFDANAPVAVR	3	Intact+DC	BHS	18	VIFDANAPV	HB
KVPESKVIFDANAPVAVRS	1	Intact+DC	BHS	19	VIFDANAPV	HB
KVPESKVIFDANAPVAVRS	1	Intact+DC	BHS	19	VIFDANAPV	HB
KVPESKVIFDANAPVAVRSK	4	Intact+DC	BHS	20	VIFDANAPV	HB
KVPESKVIFDANAPVAVRSK	4	Intact+DC	BHS	20	VIFDANAPV	HB
KVPESKVIFDANAPVAVRSKVPDS	1	Intact+DC	BHS	24	VIFDANAPV	HB
KVPESKVIFDANAPVAVRSKVPDS	1	Intact+DC	BHS	24	VIFDANAPV	HB
KVPESKVIFDANAPVAVRSKVPDSE	1	Intact+DC	BHS	25	VIFDANAPV	HB
KVPESKVIFDANAPVAVRSKVPDSE	1	Intact+DC	BHS	25	VIFDANAPV	HB
MQKFEKVPESKVIFDANAPVA	1	Intact+DC	BHS	21	VIFDANAPV	HB
MQKFEKVPESKVIFDANAPVA	1	Intact+DC	BHS	21	VIFDANAPV	HB
QKFEKVPESKVIFDANAPVAVR	2	Intact+DC	BHS	22	VIFDANAPV	HB
QKFEKVPESKVIFDANAPVAVR	2	Intact+DC	BHS	22	VIFDANAPV	HB
QKFEKVPESKVIFDANAPVAVRSK	1	Intact+DC	BHS	24	VIFDANAPV	HB
QKFEKVPESKVIFDANAPVAVRSK	1	Intact+DC	BHS	24	VIFDANAPV	HB
VPESKVIFDANAPVA	1	Intact+DC	BHS	15	VIFDANAPV	HB
VPESKVIFDANAPVA	1	Intact+DC	BHS	15	VIFDANAPV	HB
VPESKVIFDANAPVAVRSK	1	Intact+DC	BHS	19	VIFDANAPV	HB
VPESKVIFDANAPVAVRSK	1	Intact+DC	BHS	19	VIFDANAPV	HB
KKVILEDKVKN	2	Intact+DC	BHS	11	VILEDKVKN	IB
KKVILEDKVKN	2	Intact+DC	BHS	11	VILEDKVKN	IB
QKPANVLNDAQTKL	1	Intact+DC	BHS	14	VLNDAQTKL	IB
QKPANVLNDAQTKL	1	Intact+DC	BHS	14	VLNDAQTKL	IB
SKVPDSEFPVM	2	Intact+DC	BHS	11	VPDSEFPVM	IB
SKVPDSEFPVM	2	Intact+DC	BHS	11	VPDSEFPVM	IB
SMGCRKDTVPRPASPTE	1	Intact+DC	BHS	17	VPRPASPTE	LB
SMGCRKNTVPRPASPTE	1	Intact+DC	BHS	17	VPRPASPTE	LB
ASVPSVPISTHGRL	1	Intact+DC	BHS	14	VPSVPISTH	LB
ASVPSVPISTHGRL	1	Intact+DC	BHS	14	VPSVPISTH	LB
VPYAAPPLAERRFQ	1	Intact+DC	BHS	14	VPYAAPPLA	IB
VPYAAPPLAERRFQ	1	Intact+DC	BHS	14	VPYAAPPLA	IB
RRVSPGYVPACR	2	Intact+DC	BHS	12	VSPGYVPAC	LB
RRVSPGYVPACR	2	Intact+DC	BHS	12	VSPGYVPAC	LB
SGVLSRRVSPGYVPACR	1	Intact+DC	BHS	17	VSPGYVPAC	LB
SGVLSRRVSPGYVPACR	1	Intact+DC	BHS	17	VSPGYVPAC	LB
SRRVSPGYVPACR	1	Intact+DC	BHS	13	VSPGYVPAC	LB
SRRVSPGYVPACR	1	Intact+DC	BHS	13	VSPGYVPAC	LB
ATCPGVTYDQESHQVILR	1	Intact+DC	BHS	18	VTYDQESHQ	IB
ATCPGVTYDQESHQVILR	1	Intact+DC	BHS	18	VTYDQESHQ	IB
SSQEVVSCLRQKPAN	1	Intact+DC	BHS	15	VVSCLRQKP	IB
SSQEVVSCLRQKPAN	1	Intact+DC	BHS	15	VVSCLRQKP	IB
LSSVVVDPSIRH	2	Intact+DC	BHS	12	VVVDPSIRH	HB
LSSVVVDPSIRH	2	Intact+DC	BHS	12	VVVDPSIRH	HB
LSSVVVDPSIRHFDVAH	1	Intact+DC	BHS	17	VVVDPSIRH	HB

LSSVVVDPSIRHFDVAH	1	Intact+DC	BHS	17	VVVDPSIRH	HB
LSSVVVDPSIRHFDVAHVS	1	Intact+DC	BHS	19	VVVDPSIRH	HB
LSSVVVDPSIRHFDVAHVS	1	Intact+DC	BHS	19	VVVDPSIRH	HB
SLALSSVVVDPSIRHFDVAH	1	Intact+DC	BHS	20	VVVDPSIRH	HB
SLALSSVVVDPSIRHFDVAH	1	Intact+DC	BHS	20	VVVDPSIRH	HB
SSVVVDPSIRHFDVAH	1	Intact+DC	BHS	16	VVVDPSIRH	HB
SSVVVDPSIRHFDVAH	1	Intact+DC	BHS	16	VVVDPSIRH	HB
SVVVDPSIRH	1	Intact+DC	BHS	10	VVVDPSIRH	HB
SVVVDPSIRH	1	Intact+DC	BHS	10	VVVDPSIRH	HB
SVVVDPSIRHFDV	1	Intact+DC	BHS	13	VVVDPSIRH	HB
SVVVDPSIRHFDV	1	Intact+DC	BHS	13	VVVDPSIRH	HB
SVVVDPSIRHFDVAH	1	Intact+DC	BHS	15	VVVDPSIRH	HB
SVVVDPSIRHFDVAH	1	Intact+DC	BHS	15	VVVDPSIRH	HB
SGRWESQLPQPR	1	Intact+DC	BHS	12	WESQLPQPR	LB
SGRWESQLPQPR	1	Intact+DC	BHS	12	WESQLPQPR	LB
YDQESHQVILR	1	Intact+DC	BHS	11	YDQESHQVI	LB
YDQESHQVILR	1	Intact+DC	BHS	11	YDQESHQVI	LB
LSYEASVPSVPISTHG	1	Intact+DC	BHS	16	YEASVPSVP	IB
LSYEASVPSVPISTHG	1	Intact+DC	BHS	16	YEASVPSVP	IB
LSYEASVPSVPISTHGR	1	Intact+DC	BHS	17	YEASVPSVP	IB
LSYEASVPSVPISTHGR	1	Intact+DC	BHS	17	YEASVPSVP	IB
LSYEASVPSVPISTHGRL	1	Intact+DC	BHS	18	YEASVPSVP	IB
LSYEASVPSVPISTHGRL	1	Intact+DC	BHS	18	YEASVPSVP	IB
SYEASVPSVPISTHGRL	1	Intact+DC	BHS	17	YEASVPSVP	IB
SYEASVPSVPISTHGRL	1	Intact+DC	BHS	17	YEASVPSVP	IB
YEASVPSVPISTHG	1	Intact+DC	BHS	14	YEASVPSVP	IB
YEASVPSVPISTHG	1	Intact+DC	BHS	14	YEASVPSVP	IB
YEASVPSVPISTHGRL	1	Intact+DC	BHS	16	YEASVPSVP	IB
YEASVPSVPISTHGRL	1	Intact+DC	BHS	16	YEASVPSVP	IB
SYNRFPDAFVT	1	Intact+DC	BHS	11	YNRFPDAFV	LB
SYNRFPDAFVT	1	Intact+DC	BHS	11	YNRFPDAFV	LB
QYPGSYSDFSTPLAH	1	Intact+DC	BHS	15	YPGSYSDFS	IB
QYPGSYSDFSTPLAH	1	Intact+DC	BHS	15	YPGSYSDFS	IB
IFEYQVDAQPLRPCE	1	Intact+DC	BHS	15	YQVDAQPLR	HB
IFEYQVDAQPLRPCE	1	Intact+DC	BHS	15	YQVDAQPLR	HB

Predigested thyroglobulin in DC-like condition

Sequence	# PSMs	Sample	Cathepsins	Length	Binding core (HLA-DR3)	Theoretical Affinity
AEGQAIPGTRSAIGKPKK	1	Pre+DCs	BLS_BHS	18	AEGQAIPGT	LB
AEGQAIPGTRSAIGKPKKCPTPCQ	1	Pre+DCs	BLS_BHS	24	AEGQAIPGT	LB
QRWEAQNKGQDLTPAK	1	Pre+DCs	BLS_BHS	16	AQNKGQDLT	LB
RWEAQNKGQDLTPAK	2	Pre+DCs	BLS_BHS	15	AQNKGQDLT	LB
ARSLQIPQCPTTCEK	1	Pre+DCs	BLS_BHS	15	ARSLQIPQC	LB
ARSLQIPQCPTTCEKS	1	Pre+DCs	BLS_BHS	16	ARSLQIPQC	LB
ARSLQIPQCPTTCEKSR	1	Pre+DCs	BLS_BHS	17	ARSLQIPQC	LB
SSWKQARSQENPSPKDLFVPA	1	Pre+DCs	BLS_BHS	21	ARSQENPSP	IB
REEATHIYRKPG	1	Pre+DCs	BLS_BHS	12	ATHIYRKPG	LB
GSALSPAAVISHERAQ	1	Pre+DCs	BLS_BHS	16	AVISHERAQ	IB
GSALSPAAVISHERAQQQA	1	Pre+DCs	BLS_BHS	19	AVISHERAQ	IB
SPAAVISHERAQ	1	Pre+DCs	BLS_BHS	12	AVISHERAQ	IB
GGQPRCPTDCEKQR	2	Pre+DCs	BLS_BHS	14	CPTDCEKQR	LB
ASQKDRGSGKAFCVDGEGRR	1	Pre+DCs	BLS_BHS	20	FCVDGEGRR	HB
SQKDRGSGKAFCVDGEGRR	1	Pre+DCs	BLS_BHS	19	FCVDGEGRR	HB
LGDQEFIKSLTPLE	1	Pre+DCs	BLS_BHS	14	FIKSLTPLE	IB
EFSELLPNRQG	1	Pre+DCs	BLS_BHS	11	FSELLPNRQ	IB
EFSELLPNRQGLKK	1	Pre+DCs	BLS_BHS	14	FSELLPNRQ	IB
FSELLPNRQGLKK	2	Pre+DCs	BLS_BHS	13	FSELLPNRQ	IB
GQSQQFSVSENLLK	2	Pre+DCs	BLS_BHS	14	FSVSENLLK	HB
RFTDLIQSGSFQ	1	Pre+DCs	BLS_BHS	12	FTDLIQSGS	LB
TPWPDFVPRAGGENYK	1	Pre+DCs	BLS_BHS	16	FVPRAGGEN	LB
CMFYADTQSCTHS	2	Pre+DCs	BLS_BHS	13	FYADTQSCT	IB
CMFYADTQSCTHSLQ	1	Pre+DCs	BLS_BHS	15	FYADTQSCT	IB
CMFYADTQSCTHSLQG	1	Pre+DCs	BLS_BHS	16	FYADTQSCT	IB
WTGSWDASKPR	1	Pre+DCs	BLS_BHS	11	GSWDASKPR	LB
AIFPSRGLARLA	1	Pre+DCs	BLS_BHS	12	IFPSRGLAR	IB
AIGKPKKCPTPCQ	2	Pre+DCs	BLS_BHS	13	IGKPKKCPT	IB
IGKPKKCPTPCQ	1	Pre+DCs	BLS_BHS	12	IGKPKKCPT	IB
SAIGKPKKCPTPCQ	2	Pre+DCs	BLS_BHS	14	IGKPKKCPT	IB
IPQCPTTCEKS	1	Pre+DCs	BLS_BHS	11	IPQCPTTCE	LB

IPQCPTTCEKSR	2	Pre+DCs	BLS_BHS	12	IPQCPTTCE	LB
DTYIPQCSTDGQWRQ	1	Pre+DCs	BLS_BHS	15	IPQCSTDGQ	LB
ISAGAFSQTHC	1	Pre+DCs	BLS_BHS	11	ISAGAFSQT	LB
ETISGPTGSAMQ	1	Pre+DCs	BLS_BHS	12	ISGPTGSAM	IB
ETISGPTGSAMQQ	1	Pre+DCs	BLS_BHS	13	ISGPTGSAM	IB
LAADRGGADVASIHL	2	Pre+DCs	BLS_BHS	15	LAADRGGAD	IB
LAKEVSCPMS	1	Pre+DCs	BLS_BHS	10	LAKEVSCPM	IB
LAKEVSCPMS	1	Pre+DCs	BLS_BHS	10	LAKEVSCPM	IB
ELFVDSGLLR	1	Pre+DCs	BLS_BHS	10	LFVDSGLLR	HB
ELFVDSGLLRPMVE	2	Pre+DCs	BLS_BHS	14	LFVDSGLLR	HB
NSLGGEDSDARVE	1	Pre+DCs	BLS_BHS	13	LGGEDSDAR	IB
SDQKRDALGNSKATSFGSLR	1	Pre+DCs	BLS_BHS	20	LGNSKATSF	HB
LHLDSKTFPAETIR	2	Pre+DCs	BLS_BHS	14	LHLDSKTFP	HB
SEPSKLPTCPGSCEEAKLR	1	Pre+DCs	BLS_BHS	19	LPTCPGSCE	LB
AGLQCDQNGQYR	1	Pre+DCs	BLS_BHS	12	LQCDQNGQY	HB
DCQRNEAGLQCDQNGQYR	1	Pre+DCs	BLS_BHS	18	LQCDQNGQY	HB
DCQRNEAGLQCDQNGQYRA	1	Pre+DCs	BLS_BHS	19	LQCDQNGQY	HB
DCQRNEAGLQCDQNGQYRASQK	1	Pre+DCs	BLS_BHS	22	LQCDQNGQY	HB
DCQRNEAGLQCDQNGQYRASQKDR	2	Pre+DCs	BLS_BHS	24	LQCDQNGQY	HB
DCQRNEAGLQCDQNGQYRASQKDRG	1	Pre+DCs	BLS_BHS	25	LQCDQNGQY	HB
LALQFTTNPKR	1	Pre+DCs	BLS_BHS	11	LQFTTNPKR	HB
LALQFTTNPKRLQ	2	Pre+DCs	BLS_BHS	13	LQFTTNPKR	HB
LALQFTTNPKRLQQ	1	Pre+DCs	BLS_BHS	14	LQFTTNPKR	HB
LQFTTNPKR	1	Pre+DCs	BLS_BHS	9	LQFTTNPKR	HB
LQFTTNPKRLQ	1	Pre+DCs	BLS_BHS	11	LQFTTNPKR	HB
LQFTTNPKRLQQ	1	Pre+DCs	BLS_BHS	12	LQFTTNPKR	HB
RLALQFTTNPKRLQ	1	Pre+DCs	BLS_BHS	14	LQFTTNPKR	HB
LQSEQAFLRT	1	Pre+DCs	BLS_BHS	10	LQSEQAFLR	HB
LREEATHIYR	1	Pre+DCs	BLS_BHS	10	LREEATHIY	IB
LREEATHIYRKPGISL	1	Pre+DCs	BLS_BHS	16	LREEATHIY	IB
LSSVVVDPSIR	1	Pre+DCs	BLS_BHS	11	LSSVVVDPS	LB
QVYLWKDSDMGSRPE	1	Pre+DCs	BLS_BHS	15	LWKDSDMGS	IB
QVYLWKDSDMGSRPES	1	Pre+DCs	BLS_BHS	16	LWKDSDMGS	IB
QVYLWKDSDMGSRPESMG	1	Pre+DCs	BLS_BHS	18	LWKDSDMGS	IB
ELLPNRQGLKK	1	Pre+DCs	BLS_BHS	11	LLPNRQGLK	IB
SDNVACMTSDQKRDALG	1	Pre+DCs	BLS_BHS	17	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSK	1	Pre+DCs	BLS_BHS	20	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSKA	1	Pre+DCs	BLS_BHS	21	MTSDQKRDA	HB
QNLFGGKFL	1	Pre+DCs	BLS_BHS	9	QNLFGGKFL	LB
TSGYFSQHDL	1	Pre+DCs	BLS_BHS	10	SGYFSQHDL	LB
SSQEVVSCLR	1	Pre+DCs	BLS_BHS	10	SQEVVSCLR	LB
SYNRFPDAF	1	Pre+DCs	BLS_BHS	9	SYNRFPDAF	LB
QTIQTQGHFQ	1	Pre+DCs	BLS_BHS	10	TIQTQGHFQ	LB
TPWPDFVPR	1	Pre+DCs	BLS_BHS	9	TPWPDFVPR	LB
VPEDVARDLGDVME	1	Pre+DCs	BLS_BHS	14	VARDLGDVM	HB
CVDAEGQAIPGTRSAIGKPKK	1	Pre+DCs	BLS_BHS	21	VDAEGQAIP	LB
VDAEGQAIPGTR	1	Pre+DCs	BLS_BHS	12	VDAEGQAIP	LB

VDAEGQAIPGTRSAIGKPK	1	Pre+DCs	BLS_BHS	19	VDAEGQAIP	LB
VDAEGQAIPGTRSAIGKPKK	1	Pre+DCs	BLS_BHS	20	VDAEGQAIP	LB
VDEKGGFIPGSLT	1	Pre+DCs	BLS_BHS	13	VDEKGGFIP	LB
VDPASGEELRPGSSS	1	Pre+DCs	BLS_BHS	15	VDPASGEEL	LB
EKVPESKVIFDANAPVA	1	Pre+DCs	BLS_BHS	17	VIFDANAPV	HB
KVPESKVIFDANAPVA	6	Pre+DCs	BLS_BHS	16	VIFDANAPV	HB
KVPESKVIFDANAPVAVR	1	Pre+DCs	BLS_BHS	18	VIFDANAPV	HB
MQKFEKVPESKVIFDANAPVA	1	Pre+DCs	BLS_BHS	21	VIFDANAPV	HB
MQKFEKVPESKVIFDANAPVA	1	Pre+DCs	BLS_BHS	21	VIFDANAPV	HB
QKFEKVPESKVIFDANAPVA	1	Pre+DCs	BLS_BHS	20	VIFDANAPV	HB
QKFEKVPESKVIFDANAPVAVR	1	Pre+DCs	BLS_BHS	22	VIFDANAPV	HB
SKVIFDANAPVA	1	Pre+DCs	BLS_BHS	12	VIFDANAPV	HB
VPESKVIFDANAPVA	2	Pre+DCs	BLS_BHS	15	VIFDANAPV	HB
KKVILEDKVKN	2	Pre+DCs	BLS_BHS	11	VILEDKVKN	IB
KKVILEDKVKNFYTR	1	Pre+DCs	BLS_BHS	15	VILEDKVKN	IB
KVPDSEFPVM	1	Pre+DCs	BLS_BHS	10	VPDSEFPVM	IB
SKVPDSEFPVM	2	Pre+DCs	BLS_BHS	11	VPDSEFPVM	IB
SKVPDSEFPVMQ	2	Pre+DCs	BLS_BHS	12	VPDSEFPVM	IB
SKVPDSEFPVMQ	1	Pre+DCs	BLS_BHS	12	VPDSEFPVM	IB
ASVPSVPISTHGRL	1	Pre+DCs	BLS_BHS	14	VPSVPISTH	LB
ASVPSVPISTHGRLL	2	Pre+DCs	BLS_BHS	15	VPSVPISTH	LB
RRVSPGYVPACR	1	Pre+DCs	BLS_BHS	12	VSPGYVPAC	LB
SGVLSRRVSPGYVPACR	1	Pre+DCs	BLS_BHS	17	VSPGYVPAC	LB
SRRVSPGYVPACR	1	Pre+DCs	BLS_BHS	13	VSPGYVPAC	LB
ATCPGVTYDQESHQVILR	1	Pre+DCs	BLS_BHS	18	VTYDQESHQ	IB
CPGVTYDQESHQVILR	2	Pre+DCs	BLS_BHS	16	VTYDQESHQ	IB
LSSVVVDPSIRH	1	Pre+DCs	BLS_BHS	12	VVVDPSIRH	HB
LSSVVVDPSIRHF	1	Pre+DCs	BLS_BHS	13	VVVDPSIRH	HB
LSSVVVDPSIRHFDV	1	Pre+DCs	BLS_BHS	15	VVVDPSIRH	HB
LSSVVVDPSIRHFDVAH	2	Pre+DCs	BLS_BHS	17	VVVDPSIRH	HB
LSSVVVDPSIRHFDVAHVS	1	Pre+DCs	BLS_BHS	19	VVVDPSIRH	HB
SSVVVDPSIRHF	1	Pre+DCs	BLS_BHS	12	VVVDPSIRH	HB
SSVVVDPSIRHFDVAH	3	Pre+DCs	BLS_BHS	16	VVVDPSIRH	HB
SVVVDPSIRHFDV	1	Pre+DCs	BLS_BHS	13	VVVDPSIRH	HB
SVVVDPSIRHFDVAH	3	Pre+DCs	BLS_BHS	15	VVVDPSIRH	HB
SVVVDPSIRHFDVAHVS	1	Pre+DCs	BLS_BHS	17	VVVDPSIRH	HB
YDQESHQVILR	2	Pre+DCs	BLS_BHS	11	YDQESHQVI	LB
LSYEASVPSVPISTHGR	2	Pre+DCs	BLS_BHS	17	YEASVPSVP	IB
YEASVPSVPISTHGR	1	Pre+DCs	BLS_BHS	15	YEASVPSVP	IB
YEASVPSVPISTHGRL	1	Pre+DCs	BLS_BHS	16	YEASVPSVP	IB
QYPGSYSDFSTPLA	1	Pre+DCs	BLS_BHS	14	YPGSYSDFS	IB
QYPGSYSDFSTPLAH	2	Pre+DCs	BLS_BHS	15	YPGSYSDFS	IB
YPGSYSDFSTPLAH	1	Pre+DCs	BLS_BHS	14	YPGSYSDFS	IB
LYQRWEAQNKGQDLTPAK	1	Pre+DCs	BLS_BHS	18	YQRWEAQNK	IB
YQRWEAQNKGQDLTPAK	1	Pre+DCs	BLS_BHS	17	YQRWEAQNK	IB
IFEYQVDAQPLRPCE	1	Pre+DCs	BLS_BHS	15	YQVDAQPLR	HB
NIFEYQVDAQPLRPCE	1	Pre+DCs	BLS_BHS	16	YQVDAQPLR	HB

YQVDAQPLRPCE	1	Pre+DCs	BLS_BHS	12	YQVDAQPLR	HB

Intact thyroglobulin in mTEC-like condition

Sequence	# PSMs	Sample	Cathepsins	Length	Binding core (HLA-DR3)	Theoretical Affinity
VPACLETGEYAR	1	mTEC	BHL	12	ACLETGEYA	IB
VPACLETGEYAR	1	mTEC	BHL	12	ACLETGEYA	IB
VPACTSEGHFLPVQ	1	mTEC	BHL	14	ACTSEGHFL	IB
VPACTSEGHFLPVQ	1	mTEC	BHL	14	ACTSEGHFL	IB
ADRGGADVASIHL	2	mTEC	BHL	13	ADRGGADVA	IB
ADRGGADVASIHL	2	mTEC	BHL	13	ADRGGADVA	IB
DKSPPQCSAEGEFMPVQ	2	mTEC	BHL	17	AEGEFMPVQ	LB
DKSPPQCSAEGEFMPVQ	2	mTEC	BHL	17	AEGEFMPVQ	LB
GSQPAGSTLFVPA	2	mTEC	BHL	13	AGSTLFVPA	IB
GSQPAGSTLFVPA	2	mTEC	BHL	13	AGSTLFVPA	IB
SQPAGSTLFVPA	1	mTEC	BHL	12	AGSTLFVPA	IB
SQPAGSTLFVPA	1	mTEC	BHL	12	AGSTLFVPA	IB
GGQPRCPTDCEKQR	2	mTEC	BHL	14	CPTDCEKQR	LB
GGQPRCPTDCEKQR	2	mTEC	BHL	14	CPTDCEKQR	LB
GGQPRCPTDCEKQRA	1	mTEC	BHL	15	CPTDCEKQR	LB
GGQPRCPTDCEKQRA	1	mTEC	BHL	15	CPTDCEKQR	LB
SQENPSPKDLFVPAC	1	mTEC	BHL	15	ENPSPKDLF	LB
SQENPSPKDLFVPAC	1	mTEC	BHL	15	ENPSPKDLF	LB
IPQCPTTCEK	1	mTEC	BHL	10	IPQCPTTCE	LB
IPQCPTTCEK	1	mTEC	BHL	10	IPQCPTTCE	LB
IPQCPTTCEKS	1	mTEC	BHL	11	IPQCPTTCE	LB

IPQCPTTCEKS	1	mTEC	BHL	11	IPQCPTTCE	LB
IPQCPTTCEKSR	1	mTEC	BHL	12	IPQCPTTCE	LB
IPQCPTTCEKSR	1	mTEC	BHL	12	IPQCPTTCE	LB
IPQCPTTCEKSRT	1	mTEC	BHL	13	IPQCPTTCE	LB
IPQCPTTCEKSRT	1	mTEC	BHL	13	IPQCPTTCE	LB
DTYIPQCSTDGQWRQ	1	mTEC	BHL	15	IPQCSTDGQ	LB
DTYIPQCSTDGQWRQ	1	mTEC	BHL	15	IPQCSTDGQ	LB
SLTPLEGTQDTFTN	1	mTEC	BHL	14	LEGTQDTFT	LB
SLTPLEGTQDTFTN	1	mTEC	BHL	14	LEGTQDTFT	LB
DPASGEELRPGSSSSAQCPS	1	mTEC	BHL	20	LRPGSSSSA	IB
DPASGEELRPGSSSSAQCPS	1	mTEC	BHL	20	LRPGSSSSA	IB
SDNVACMTSDQKRDALGNSK	1	mTEC	BHL	20	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSK	1	mTEC	BHL	20	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSK	1	mTEC	BHL	20	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSK	1	mTEC	BHL	20	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSKA	1	mTEC	BHL	21	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSKA	1	mTEC	BHL	21	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSKA	1	mTEC	BHL	21	MTSDQKRDA	HB
SDNVACMTSDQKRDALGNSKA	1	mTEC	BHL	21	MTSDQKRDA	HB
LPPLFPPR	1	mTEC	BHL	8	NA	NA
LPPLFPPR	1	mTEC	BHL	8	NA	NA
KSLTPLEGTQDTFTN	1	mTEC	BHL	15	PLEGTQDTF	LB
KSLTPLEGTQDTFTN	1	mTEC	BHL	15	PLEGTQDTF	LB
GPVIDGHFLR	1	mTEC	BHL	10	PVIDGHFLR	LB
GPVIDGHFLR	1	mTEC	BHL	10	PVIDGHFLR	LB
PSPKDLFVPAC	1	mTEC	BHL	11	SPKDLFVPA	LB
PSPKDLFVPAC	1	mTEC	BHL	11	SPKDLFVPA	LB
VDAEGQAIPGTRSAIGKPK	1	mTEC	BHL	19	VDAEGQAIP	LB
VDAEGQAIPGTRSAIGKPK	1	mTEC	BHL	19	VDAEGQAIP	LB
VDAEGQAIPGTRSAIGKPKK	1	mTEC	BHL	20	VDAEGQAIP	LB
VDAEGQAIPGTRSAIGKPKK	1	mTEC	BHL	20	VDAEGQAIP	LB
VDEKGGFIPGSLT	1	mTEC	BHL	13	VDEKGGFIP	LB
VDEKGGFIPGSLT	1	mTEC	BHL	13	VDEKGGFIP	LB
VDPASGEELRPGSSSSAQCPS	2	mTEC	BHL	21	VDPASGEEL	LB
VDPASGEELRPGSSSSAQCPS	2	mTEC	BHL	21	VDPASGEEL	LB
KVPESKVIFDANAPVA	2	mTEC	BHL	16	VIFDANAPV	HB
KVPESKVIFDANAPVA	2	mTEC	BHL	16	VIFDANAPV	HB
VPESKVIFDANAPVA	1	mTEC	BHL	15	VIFDANAPV	HB
VPESKVIFDANAPVA	1	mTEC	BHL	15	VIFDANAPV	HB
KKVILEDKVKN	1	mTEC	BHL	11	VILEDKVKN	IB
KKVILEDKVKN	1	mTEC	BHL	11	VILEDKVKN	IB
KVPDSEFPVM	1	mTEC	BHL	10	VPDSEFPVM	IB
KVPDSEFPVM	1	mTEC	BHL	10	VPDSEFPVM	IB
SKVPDSEFPVM	4	mTEC	BHL	11	VPDSEFPVM	IB
SKVPDSEFPVM	4	mTEC	BHL	11	VPDSEFPVM	IB
SKVPDSEFPVMQ	2	mTEC	BHL	12	VPDSEFPVM	IB
SKVPDSEFPVMQ	2	mTEC	BHL	12	VPDSEFPVM	IB

KDTVPRPASPTE	2	mTEC	BHL	12	VPRPASPTE	LB
KNTVPRPASPTE	1	mTEC	BHL	12	VPRPASPTE	LB
ASVPSVPISTHG	1	mTEC	BHL	12	VPSVPISTH	LB
ASVPSVPISTHG	1	mTEC	BHL	12	VPSVPISTH	LB
ASVPSVPISTHGRL	1	mTEC	BHL	14	VPSVPISTH	LB
ASVPSVPISTHGRL	1	mTEC	BHL	14	VPSVPISTH	LB
VPSVPISTHG	1	mTEC	BHL	10	VPSVPISTH	LB
VPSVPISTHG	1	mTEC	BHL	10	VPSVPISTH	LB
RRVSPGYVPACR	1	mTEC	BHL	12	VSPGYVPAC	LB
RRVSPGYVPACR	1	mTEC	BHL	12	VSPGYVPAC	LB
LSSVVVDPSIRH	1	mTEC	BHL	12	VVVDPSIRH	HB
LSSVVVDPSIRH	1	mTEC	BHL	12	VVVDPSIRH	HB
SSVVVDPSIRH	2	mTEC	BHL	11	VVVDPSIRH	HB
SSVVVDPSIRH	2	mTEC	BHL	11	VVVDPSIRH	HB
SVVVDPSIRH	2	mTEC	BHL	10	VVVDPSIRH	HB
SVVVDPSIRH	2	mTEC	BHL	10	VVVDPSIRH	HB
SVVVDPSIRHF	1	mTEC	BHL	11	VVVDPSIRH	HB
SVVVDPSIRHF	1	mTEC	BHL	11	VVVDPSIRH	HB
YQVDAQPLRPCE	2	mTEC	BHL	12	YQVDAQPLR	HB
YQVDAQPLRPCE	2	mTEC	BHL	12	YQVDAQPLR	HB
KQADYVPQCAEDGSFQ	1	mTEC	BHL	16	YVPQCAEDG	IB
KQADYVPQCAEDGSFQ	1	mTEC	BHL	16	YVPQCAEDG	IB

Only pre-digestion of thyroglobulin

Sequence	# PSMs	Sample	Cathepsins	Length	Binding core (HLA-DR3)	Theoretical Affinity
TSADGAKGGQSAESEEEELTAGS	1	Pre only	BLS	23	AESEEEELT	NB
DEAGQELEGMR	1	Pre only	BLS	11	AGQELEGMR	NB
QQAIALAKEVS	1	Pre only	BLS	11	AIALAKEVS	NB
SSTGTPEAAKKDGTMNKPTVG	1	Pre only	BLS	21	AKKDGTMNK	NB
QNNAPSFCPLVV	1	Pre only	BLS	12	APSFCPLVV	NB
AAATWYYSLEHS	1	Pre only	BLS	12	ATWYYSLEH	NB
SQTCEQTPERLF	1	Pre only	BLS	12	CEQTPERLF	NB
SSQTCEQTPERLF	1	Pre only	BLS	13	CEQTPERLF	NB
CNGPPEQVFELY	1	Pre only	BLS	12	CNGPPEQVF	NB
EAFAEQFLR	1	Pre only	BLS	9	EAFAEQFLR	NB
GENYKEFSELLPNR	1	Pre only	BLS	14	EFSELLPNR	NB
GEPPSCAEGQSCASERQQ	1	Pre only	BLS	18	EGQSCASER	NB
ASQKDRGSGKAFCVDGEGRR	1	Pre only	BLS	20	FCVDGEGRR	HB
MQKFEKVPESKVIFD	2	Pre only	BLS	15	FEKVPESKV	LB
QKFEKVPESKVIFD	1	Pre only	BLS	14	FEKVPESKV	LB
FGCSEGFYQVLT	1	Pre only	BLS	12	FGCSEGFYQ	IB
TYPFGWYQKPIAQ	1	Pre only	BLS	13	FGWYQKPIA	IB
DQEFIKSLTPLE	2	Pre only	BLS	12	FIKSLTPLE	LB
GDQEFIKSLTPLE	1	Pre only	BLS	13	FIKSLTPLE	LB
LGDQEFIKSLTPLE	7	Pre only	BLS	14	FIKSLTPLE	LB
EFSELLPNRQGLK	1	Pre only	BLS	13	FSELLPNRQ	IB

EFSELLPNRQGLKK	1	Pre only	BLS	14	FSELLPNRQ	IB
GENYKEFSELLPNRQGLK	1	Pre only	BLS	18	FSELLPNRQ	IB
EFSELLPNRQG	1	Pre only	BLS	11	FSELLPNRQ	IB
FSPDDSAGASALL	1	Pre only	BLS	13	FSPDDSAGA	IB
FSPDDSAGASALLR	2	Pre only	BLS	14	FSPDDSAGA	IB
FYQRRRFSPDDSAGASALLR	2	Pre only	BLS	20	FSPDDSAGA	IB
RFSPDDSAGASAL	1	Pre only	BLS	13	FSPDDSAGA	IB
RFSPDDSAGASALLR	1	Pre only	BLS	15	FSPDDSAGA	IB
RRFSPDDSAGASALLR	2	Pre only	BLS	16	FSPDDSAGA	IB
RRRFSPDDSAGASALLR	2	Pre only	BLS	17	FSPDDSAGA	IB
SFYQRRRFSPDDSAGASALLR	1	Pre only	BLS	21	FSPDDSAGA	IB
AEDGGFSPVQCDQAQG	1	Pre only	BLS	16	FSPVQCDQA	LB
GQSQQFSVSENLLK	3	Pre only	BLS	14	FSVSENLLK	IB
GQSQQFSVSENLLKEAIR	1	Pre only	BLS	18	FSVSENLLK	IB
RPMVEGQSQQFSVSENLLK	1	Pre only	BLS	19	FSVSENLLK	IB
VEGQSQQFSVSENLLK	1	Pre only	BLS	16	FSVSENLLK	IB
ATPWPDFVPRAGGENY	1	Pre only	BLS	16	FVPRAGGEN	LB
ATPWPDFVPRAGGENYK	3	Pre only	BLS	17	FVPRAGGEN	LB
TPWPDFVPRAGGENY	1	Pre only	BLS	15	FVPRAGGEN	LB
TPWPDFVPRAGGENYK	2	Pre only	BLS	16	FVPRAGGEN	LB
TPWPDFVPRAGGENYKEFSELLPNR	2	Pre only	BLS	25	FVPRAGGEN	LB
FWQILNGQLS	1	Pre only	BLS	10	FWQILNGQL	IB
LEPYLFWQILNGQLS	1	Pre only	BLS	15	FWQILNGQL	IB
ADCSFWSKYISSLK	6	Pre only	BLS	14	FWSKYISSL	LB
ADCSFWSKYISSLKT	1	Pre only	BLS	15	FWSKYISSL	LB
DCSFWSKYISSLK	1	Pre only	BLS	13	FWSKYISSL	LB
FWSKYISSLK	1	Pre only	BLS	10	FWSKYISSL	LB
KADCSFWSKYISSLK	8	Pre only	BLS	15	FWSKYISSL	LB
LKKADCSFWSKYISSLK	1	Pre only	BLS	17	FWSKYISSL	LB
FYADTQSCTHSLQ	1	Pre only	BLS	13	FYADTQSCT	HB
LPFYPAYEGQFS	1	Pre only	BLS	12	FYPAYEGQF	IB
LPFYPAYEGQFSLE	1	Pre only	BLS	14	FYPAYEGQF	IB
LPFYPAYEGQFSLEEKSLS	1	Pre only	BLS	19	FYPAYEGQF	IB
LPFYPAYEGQFSLEEKSLSLK	1	Pre only	BLS	21	FYPAYEGQF	IB
LPFYPAYEGQFSLEEKSLSLKIMQ	1	Pre only	BLS	24	FYPAYEGQF	IB
AADRGGADVASIHL	1	Pre only	BLS	14	GGADVASIH	NB
TSADGAKGGQSAESEEEELT	1	Pre only	BLS	20	GQSAESEEE	NB
WTGSWDASKPR	1	Pre only	BLS	11	GSWDASKPR	NB
WTGSWDASKPRA	1	Pre only	BLS	12	GSWDASKPR	NB
TSPGVSEDCLYL	1	Pre only	BLS	12	GVSEDCLYL	NB
SHGQDSPAVYLKK	1	Pre only	BLS	13	HGQDSPAVY	NB
DCGSPDIEVHTYPFGWYQ	1	Pre only	BLS	18	IEVHTYPFG	LB
AEGQAIPGTRSAIGKPKKCPTPCQ	1	Pre only	BLS	24	IGKPKKCPT	LB
KKVILEDKVKNFYTR	2	Pre only	BLS	15	ILEDKVKNF	HB
SSQDDGLINRAKAVKQFE	1	Pre only	BLS	18	INRAKAVKQ	IB
AEGQAIPGTRSAIGKPK	1	Pre only	BLS	17	IPGTRSAIG	LB
ARSLQIPQCPTTCEKSRTSGLL	1	Pre only	BLS	22	IPQCPTTCE	LB

IPQCPTTCEKSRTSG	1	Pre only	BLS	15	IPQCPTTCE	LB
IPQCPTTCEKSRTSGLL	1	Pre only	BLS	17	IPQCPTTCE	LB
IPQCPTTCEKSRTSGLLS	1	Pre only	BLS	18	IPQCPTTCE	LB
DTYIPQCSTDGQWRQ	1	Pre only	BLS	15	IPQCSTDGQ	IB
DTYIPQCSTDGQWRQVQ	2	Pre only	BLS	17	IPQCSTDGQ	IB
DTYIPQCSTDGQWRQVQC	1	Pre only	BLS	18	IPQCSTDGQ	IB
RTTISAGAFSQTHCVT	1	Pre only	BLS	16	ISAGAFSQT	LB
TTEPEISCDFYAWT	1	Pre only	BLS	14	ISCDFYAWT	IB
ETISGPTGSAMQ	1	Pre only	BLS	12	ISGPTGSAM	IB
ETISGPTGSAMQQCQ	1	Pre only	BLS	15	ISGPTGSAM	IB
HAISVPEDVARD	1	Pre only	BLS	12	ISVPEDVAR	HB
QRWEAQNKGQDLTPAK	3	Pre only	BLS	16	KGQDLTPAK	NB
QRWEAQNKGQDLTPAKL	1	Pre only	BLS	17	KGQDLTPAK	NB
QRWEAQNKGQDLTPAKLL	1	Pre only	BLS	18	KGQDLTPAK	NB
QRWEAQNKGQDLTPAKLLVK	2	Pre only	BLS	20	KGQDLTPAK	NB
RWEAQNKGQDLTPAK	1	Pre only	BLS	15	KGQDLTPAK	NB
RWEAQNKGQDLTPAKL	1	Pre only	BLS	16	KGQDLTPAK	NB
RWEAQNKGQDLTPAKLL	1	Pre only	BLS	17	KGQDLTPAK	NB
RWEAQNKGQDLTPAKLLVK	3	Pre only	BLS	19	KGQDLTPAK	NB
LAADRGGADVASIHLL	1	Pre only	BLS	16	LAADRGGAD	IB
LAADRGGADVASIHLLT	1	Pre only	BLS	17	LAADRGGAD	IB
LAKEVSCPMS	2	Pre only	BLS	10	LAKEVSCPM	IB
LAKEVSCPMSSSQEVV	1	Pre only	BLS	16	LAKEVSCPM	IB
LAKEVSCPMSSSQEVVS	1	Pre only	BLS	17	LAKEVSCPM	IB
LAKEVSCPMSSSQEVVSCLR	1	Pre only	BLS	20	LAKEVSCPM	IB
LDSKTFPAETIR	1	Pre only	BLS	12	LDSKTFPAE	LB
TEAPLEDSQCLMM	1	Pre only	BLS	13	LEDSQCLMM	IB
LPPLFPPREAFA	6	Pre only	BLS	12	LFPPREAFA	LB
LPPLFPPREAFAE	2	Pre only	BLS	13	LFPPREAFA	LB
LPPLFPPREAFAEQFLR	12	Pre only	BLS	17	LFPPREAFA	LB
NEDLGLPPLFPPREAFA	3	Pre only	BLS	17	LFPPREAFA	LB
ELFVDSGLLRPMV	1	Pre only	BLS	13	LFVDSGLLR	HB
ELFVDSGLLRPMVE	1	Pre only	BLS	14	LFVDSGLLR	HB
LGDQEFIKSL	1	Pre only	BLS	10	LGDQEFIKS	LB
ALQNSLGGEDSDARVE	1	Pre only	BLS	16	LGGEDSDAR	IB
NSLGGEDSDARVE	1	Pre only	BLS	13	LGGEDSDAR	IB
QALQNSLGGEDSDARVE	1	Pre only	BLS	17	LGGEDSDAR	IB
SDQKRDALGNSKATSFGSLR	2	Pre only	BLS	20	LGNSKATSF	IB
TSDQKRDALGNSKATSFGSLR	1	Pre only	BLS	21	LGNSKATSF	IB
LHLDSKTFPAETIR	5	Pre only	BLS	14	LHLDSKTFP	HB
LHLDSKTFPAETIRF	2	Pre only	BLS	15	LHLDSKTFP	HB
LHLDSKTFPAETIRFL	8	Pre only	BLS	16	LHLDSKTFP	HB
LHLDSKTFPAETIRFLQ	2	Pre only	BLS	17	LHLDSKTFP	HB
SGSFQLHLDSKTFPAETIRFL	6	Pre only	BLS	21	LHLDSKTFP	HB
SSQDDGLINRAKAVK	1	Pre only	BLS	15	LINRAKAVK	IB
LPDLHDIERALVG	5	Pre only	BLS	13	LPDLHDIER	HB
SLPDLHDIERA	1	Pre only	BLS	11	LPDLHDIER	HB

SLPDLHDIERAL	1	Pre only	BLS	12	LPDLHDIER	HB
SLPDLHDIERALVG	2	Pre only	BLS	14	LPDLHDIER	HB
LILPQMPKALFR	1	Pre only	BLS	12	LPQMPKALF	HB
LPQMPKALFR	2	Pre only	BLS	10	LPQMPKALF	HB
SEPSKLPTCPGSCEEAKLR	1	Pre only	BLS	19	LPTCPGSCE	LB
SEPSKLPTCPGSCEEAKLRV	1	Pre only	BLS	20	LPTCPGSCE	LB
SEPSKLPTCPGSCEEAKLRVL	1	Pre only	BLS	21	LPTCPGSCE	LB
SEPSKLPTCPGSCEEAKLRVLQ	1	Pre only	BLS	22	LPTCPGSCE	LB
LPWWETEAPLE	3	Pre only	BLS	11	LPWWETEAP	LB
VDGEGRRLPWWETEAPLE	1	Pre only	BLS	18	LPWWETEAP	LB
VDGEGRRLPWWETEAPLEDSQCLM	1	Pre only	BLS	24	LPWWETEAP	LB
VDGEGRRLPWWETEAPLEDSQCLMM	1	Pre only	BLS	25	LPWWETEAP	LB
FEINLQENQNALK	1	Pre only	BLS	13	LQENQNALK	IB
FEINLQENQNALKFL	2	Pre only	BLS	15	LQENQNALK	IB
GFEINLQENQNALK	1	Pre only	BLS	14	LQENQNALK	IB
INLQENQNALK	1	Pre only	BLS	11	LQENQNALK	IB
SFGFEINLQENQNALK	1	Pre only	BLS	16	LQENQNALK	IB
SFGFEINLQENQNALKF	1	Pre only	BLS	17	LQENQNALK	IB
KGQGSTTTLQKRFEPTGFQ	1	Pre only	BLS	19	LQKRFEPTG	LB
LKKGQGSTTTLQKRFEPTGFQ	1	Pre only	BLS	21	LQKRFEPTG	LB
LQSEQAFLRT	1	Pre only	BLS	10	LQSEQAFLR	HB
LQSEQAFLRTVQ	1	Pre only	BLS	12	LQSEQAFLR	HB
LREEATHIYR	1	Pre only	BLS	10	LREEATHIY	IB
LREEATHIYRKPGIS	1	Pre only	BLS	15	LREEATHIY	IB
LREEATHIYRKPGISL	1	Pre only	BLS	16	LREEATHIY	IB
EAFAEQFLRGSDYAIRLA	1	Pre only	BLS	18	LRGSDYAIR	IB
GGSALSPAAVISHERAQ	1	Pre only	BLS	17	LSPAAVISH	IB
GSALSPAAVISHERAQ	1	Pre only	BLS	16	LSPAAVISH	IB
AQNKGQDLTPAKLLVK	1	Pre only	BLS	16	LTPAKLLVK	LB
LWKDSDMGSRPESMG	1	Pre only	BLS	15	LWKDSDMGS	HB
LWKDSDMGSRPESMG	1	Pre only	BLS	15	LWKDSDMGS	HB
QVYLWKDSDMGSRPESMG	1	Pre only	BLS	18	LWKDSDMGS	HB
QVYLWKDSDMGSRPESMG	3	Pre only	BLS	18	LWKDSDMGS	HB
LYPEAQVCDDIME	1	Pre only	BLS	13	LYPEAQVCD	IB
IQMCSEENGGAWRIL	1	Pre only	BLS	15	MCSEENGGA	IB
IQMCSEENGGAWRILD	1	Pre only	BLS	16	MCSEENGGA	IB
SDNVACMTSDQKRDALG	1	Pre only	BLS	17	MTSDQKRDA	HB
DVPLAALE	1	Pre only	BLS	8	NA	NA
LGDQEFIK	1	Pre only	BLS	8	NA	NA
LPQMPKAL	1	Pre only	BLS	8	NA	NA
VFPPGPLI	1	Pre only	BLS	8	NA	NA
DKSPPQCSAEGEFMPVQ	2	Pre only	BLS	17	PQCSAEGEF	NB
DKSPPQCSAEGEFMPVQ	1	Pre only	BLS	17	PQCSAEGEF	NB
GVGDKSPPQCSAEGEFMPVQ	1	Pre only	BLS	20	PQCSAEGEF	NB
GVGDKSPPQCSAEGEFMPVQ	1	Pre only	BLS	20	PQCSAEGEF	NB
HGVGDKSPPQCSAEGEFMPVQ	2	Pre only	BLS	21	PQCSAEGEF	NB
CPTKCEVERFT	1	Pre only	BLS	11	PTKCEVERF	NB

AVSGPFHYWGPVIDGHFLR	1	Pre only	BLS	19	PVIDGHFLR	NB
GPFHYWGPVIDGHFLR	2	Pre only	BLS	16	PVIDGHFLR	NB
VSGPFHYWGPVIDGHFLR	4	Pre only	BLS	18	PVIDGHFLR	NB
YWGPVIDGHFLR	2	Pre only	BLS	12	PVIDGHFLR	NB
GQSQQFSVSENLL	1	Pre only	BLS	13	QQFSVSENL	NB
REEATHIYRKPGISL	1	Pre only	BLS	15	REEATHIYR	NB
SPDDSAGASALLR	1	Pre only	BLS	13	SAGASALLR	NB
KADCSFWSKYISS	1	Pre only	BLS	13	SFWSKYISS	NB
CVMDSGEEVPGTRVT	1	Pre only	BLS	15	SGEEVPGTR	NB
DSGEEVPGTRVTGGQPACE	1	Pre only	BLS	19	SGEEVPGTR	NB
MDSGEEVPGTRVT	1	Pre only	BLS	13	SGEEVPGTR	NB
ARSQENPSPKDLFVPACL	1	Pre only	BLS	18	SPKDLFVPA	NB
ENPSPKDLFVPACLE	1	Pre only	BLS	15	SPKDLFVPA	NB
QARSQENPSPKDLFVPACL	1	Pre only	BLS	19	SPKDLFVPA	NB
QARSQENPSPKDLFVPACLE	1	Pre only	BLS	20	SPKDLFVPA	NB
SSWKQARSQENPSPKDLFVPACLE	1	Pre only	BLS	24	SPKDLFVPA	NB
SWKQARSQENPSPKDLFVPACL	1	Pre only	BLS	22	SPKDLFVPA	NB
SSQDDGLINRAKA	1	Pre only	BLS	13	SQDDGLINR	NB
CPMSSSQEVVSCLR	1	Pre only	BLS	14	SQEVVSCLR	NB
KEVSCPMSSSQEVVSCLR	2	Pre only	BLS	18	SQEVVSCLR	NB
SSQEVVSCLR	1	Pre only	BLS	10	SQEVVSCLR	NB
SSSQEVVSCLR	1	Pre only	BLS	11	SQEVVSCLR	NB
GSQPAGSTLFVPACT	2	Pre only	BLS	15	SQPAGSTLF	NB
TTDMMIFDLVH	4	Pre only	BLS	11	TDMMIFDLV	NB
TDMMIFDLVH	1	Pre only	BLS	10	TDMXIFDLV	NB
TTDMMIFDLVH	2	Pre only	BLS	11	TDMXIFDLV	NB
TTDMMIFDLVH	3	Pre only	BLS	11	TDXXIFDLV	NB
LDSKTFPAETIRFL	3	Pre only	BLS	14	TFPAETIRF	NB
SKTFPAETIRFL	1	Pre only	BLS	12	TFPAETIRF	NB
QTIQTQGHFQL	1	Pre only	BLS	11	TIQTQGHFQ	NB
RTTISAGAFSQ	1	Pre only	BLS	11	TISAGAFSQ	NB
TPLAHFDLR	1	Pre only	BLS	9	TPLAHFDLR	NB
AISVPEDVARDLGDVM	1	Pre only	BLS	16	VARDLGDVM	HB
AISVPEDVARDLGDVME	1	Pre only	BLS	17	VARDLGDVM	HB
HAISVPEDVARDLGDVM	1	Pre only	BLS	17	VARDLGDVM	HB
HAISVPEDVARDLGDVME	2	Pre only	BLS	18	VARDLGDVM	HB
HAISVPEDVARDLGDVMET	1	Pre only	BLS	19	VARDLGDVM	HB
ISVPEDVARDLGDVME	1	Pre only	BLS	16	VARDLGDVM	HB
ISVPEDVARDLGDVMET	1	Pre only	BLS	17	VARDLGDVM	HB
LQHAISVPEDVARDLGDVME	2	Pre only	BLS	20	VARDLGDVM	HB
QHAISVPEDVARDLGDVME	1	Pre only	BLS	19	VARDLGDVM	HB
VPEDVARDLGDVM	1	Pre only	BLS	13	VARDLGDVM	HB
VPEDVARDLGDVME	1	Pre only	BLS	14	VARDLGDVM	HB
VPEDVARDLGDVMET	1	Pre only	BLS	15	VARDLGDVM	HB
VPEDVARDLGDVMETV	1	Pre only	BLS	16	VARDLGDVM	HB
SECYCVDAEGQAIPGTRSAIGKPKK	1	Pre only	BLS	25	VDAEGQAIP	IB
VDAEGQAIPGTR	1	Pre only	BLS	12	VDAEGQAIP	IB

VDAEGQAIPGTRSA	1	Pre only	BLS	14	VDAEGQAIP	IB
VDAEGQAIPGTRSAIGKPK	1	Pre only	BLS	19	VDAEGQAIP	IB
VDAEGMEVYGTRQLG	1	Pre only	BLS	15	VDAEGXEVY	IB
CVDAQGKEMHGTRQQ	1	Pre only	BLS	15	VDAQGKEMH	HB
TEGPCWCVDAQGKEMHGTRQQ	1	Pre only	BLS	21	VDAQGKEMH	HB
CVDEAGQELEGMR	1	Pre only	BLS	13	VDEAGQELE	IB
NCWCVDEAGQELEG	1	Pre only	BLS	14	VDEAGQELE	IB
NCWCVDEAGQELEGMR	5	Pre only	BLS	16	VDEAGQELE	IB
NCWCVDEAGQELEGMR	1	Pre only	BLS	16	VDEAGQELE	IB
VDEAGQELEGMR	1	Pre only	BLS	12	VDEAGQELE	IB
WCVDEAGQELEGMR	1	Pre only	BLS	14	VDEAGQELE	IB
CVDEKGGFIPGSLT	2	Pre only	BLS	14	VDEKGGFIP	LB
WCVDEKGGFIPGSLT	2	Pre only	BLS	15	VDEKGGFIP	LB
ASGAGTWCVDPASGEELRPG	2	Pre only	BLS	20	VDPASGEEL	IB
ASGAGTWCVDPASGEELRPGS	1	Pre only	BLS	21	VDPASGEEL	IB
ASGAGTWCVDPASGEELRPGSS	1	Pre only	BLS	22	VDPASGEEL	IB
ASGAGTWCVDPASGEELRPGSSS	1	Pre only	BLS	23	VDPASGEEL	IB
ASGAGTWCVDPASGEELRPGSSSS	1	Pre only	BLS	24	VDPASGEEL	IB
GAGTWCVDPASGEELRPGSS	1	Pre only	BLS	20	VDPASGEEL	IB
GAGTWCVDPASGEELRPGSSS	1	Pre only	BLS	21	VDPASGEEL	IB
VDPASGEELRPG	1	Pre only	BLS	12	VDPASGEEL	IB
VDPASGEELRPGSS	1	Pre only	BLS	14	VDPASGEEL	IB
VDPASGEELRPGSSS	1	Pre only	BLS	15	VDPASGEEL	IB
VDPASGEELRPGSSSSA	1	Pre only	BLS	17	VDPASGEEL	IB
VDPASGEELRPGSSSSAQ	1	Pre only	BLS	18	VDPASGEEL	IB
VDPASGEELRPGSSSSAQCPS	1	Pre only	BLS	21	VDPASGEEL	IB
VDPASGEELRPGSSSSAQCPSLC	1	Pre only	BLS	23	VDPASGEEL	IB
VFFHNTMDREESEGWPAIDGSFL	1	Pre only	BLS	23	VFFHNTMDR	IB
RQGSWSVFPPGPLIC	2	Pre only	BLS	15	VFPPGPLIC	LB
RQGSWSVFPPGPLICS	5	Pre only	BLS	16	VFPPGPLIC	LB
VFPPGPLICSLE	1	Pre only	BLS	12	VFPPGPLIC	LB
VGTSWKQVDQFL	1	Pre only	BLS	12	VGTSWKQVD	IB
EKVPESKVIFDANAPVA	1	Pre only	BLS	17	VIFDANAPV	HB
KVPESKVIFDANAPVA	4	Pre only	BLS	16	VIFDANAPV	HB
KVPESKVIFDANAPVAVR	8	Pre only	BLS	18	VIFDANAPV	HB
MQKFEKVPESKVIFDANAPVAVR	1	Pre only	BLS	23	VIFDANAPV	HB
QKFEKVPESKVIFDANAPVA	2	Pre only	BLS	20	VIFDANAPV	HB
QKFEKVPESKVIFDANAPVAVR	6	Pre only	BLS	22	VIFDANAPV	HB
VPESKVIFDANAPVAVR	1	Pre only	BLS	17	VIFDANAPV	HB
GGSALSPAAVISHERAQQ	1	Pre only	BLS	18	VISHERAQQ	HB
GGSALSPAAVISHERAQQQ	1	Pre only	BLS	19	VISHERAQQ	HB
GGSALSPAAVISHERAQQQAIA	1	Pre only	BLS	22	VISHERAQQ	HB
GGSALSPAAVISHERAQQQAIALA	1	Pre only	BLS	24	VISHERAQQ	HB
GSALSPAAVISHERAQQ	1	Pre only	BLS	17	VISHERAQQ	HB
GSALSPAAVISHERAQQQ	2	Pre only	BLS	18	VISHERAQQ	HB
GSALSPAAVISHERAQQQA	1	Pre only	BLS	19	VISHERAQQ	HB
GSALSPAAVISHERAQQQAIA	2	Pre only	BLS	21	VISHERAQQ	HB

GSALSPAAVISHERAQQQAIALA	1	Pre only	BLS	23	VISHERAQQ	HB
MGGSALSPAAVISHERAQQQAIA	1	Pre only	BLS	23	VISHERAQQ	HB
SPAAVISHERAQQQA	1	Pre only	BLS	15	VISHERAQQ	HB
SPAAVISHERAQQQAIA	1	Pre only	BLS	17	VISHERAQQ	HB
DKVKNFYTRLPFQ	1	Pre only	BLS	13	VKNFYTRLP	LB
QKPANVLNDAQTKL	1	Pre only	BLS	14	VLNDAQTKL	HB
QKPANVLNDAQTKLL	1	Pre only	BLS	15	VLNDAQTKL	HB
TVLSSQTCEQTPERLF	1	Pre only	BLS	16	VLSSQTCEQ	IB
SKVPDSEFPVM	1	Pre only	BLS	11	VPDSEFPVM	IB
SKVPDSEFPVMQ	4	Pre only	BLS	12	VPDSEFPVM	IB
SKVPDSEFPVMQCLT	2	Pre only	BLS	15	VPDSEFPVM	IB
SRPESMGCRKDTVPRPASPTE	1	Pre only	BLS	21	VPRPASPTE	LB
TVPRPASPTEAGLT	1	Pre only	BLS	14	VPRPASPTE	LB
TVPRPASPTEAGLTTELF	1	Pre only	BLS	18	VPRPASPTE	LB
ASVPSVPISTHGRLL	1	Pre only	BLS	15	VPSVPISTH	IB
LSYEASVPSVPISTHGRLL	5	Pre only	BLS	19	VPSVPISTH	IB
SYEASVPSVPISTHGRLL	3	Pre only	BLS	18	VPSVPISTH	IB
YEASVPSVPISTHGRLL	4	Pre only	BLS	17	VPSVPISTH	IB
DSGDYAPVQCDVQQVQ	1	Pre only	BLS	16	VQCDVQQVQ	HB
KEVSCPMSSSQEVV	1	Pre only	BLS	14	VSCPMSSSQ	IB
KEVSCPMSSSQEVVS	1	Pre only	BLS	15	VSCPMSSSQ	IB
EKVSLDSWQSLA	2	Pre only	BLS	12	VSLDSWQSL	IB
RRVSPGYVPACR	1	Pre only	BLS	12	VSPGYVPAC	LB
SRRVSPGYVPACR	1	Pre only	BLS	13	VSPGYVPAC	LB
AGAFSQTHCVTDCQRNEAGLQ	1	Pre only	BLS	21	VTDCQRNEA	LB
QTHCVTDCQRNEAGLQ	1	Pre only	BLS	16	VTDCQRNEA	LB
CPGVTYDQESHQVILR	2	Pre only	BLS	16	VTYDQESHQ	HB
VTYDQESHQVILR	2	Pre only	BLS	13	VTYDQESHQ	HB
LSSVVVDPSIRHFDVAH	2	Pre only	BLS	17	VVVDPSIRH	HB
LSSVVVDPSIRHFDVAHVS	1	Pre only	BLS	19	VVVDPSIRH	HB
SSVVVDPSIRHFDVAHVS	2	Pre only	BLS	18	VVVDPSIRH	HB
SVVVDPSIRHFDVAH	1	Pre only	BLS	15	VVVDPSIRH	HB
SVVVDPSIRHFDVAHVS	4	Pre only	BLS	17	VVVDPSIRH	HB
SHGQDSPAVYLKKGQGSTTTLQ	1	Pre only	BLS	22	VYLKKGQGS	LB
LESGRWESQLPQPRAC	1	Pre only	BLS	16	WESQLPQPR	NB
SWGKELPGSRVR	1	Pre only	BLS	12	WGKELPGSR	NB
WGPVIDGHF	1	Pre only	BLS	9	WGPVIDGHF	NB
WKDSDMGSRPESMG	1	Pre only	BLS	14	WKDSDMGSR	NB
WKDSDMGSRPESMG	1	Pre only	BLS	14	WKDSDMGSR	NB
SSWKQARSQENPSPKD	1	Pre only	BLS	16	WKQARSQEN	NB
SSWKQARSQENPSPKDLF	1	Pre only	BLS	18	WKQARSQEN	NB
NTMDREESEGWPAIDGSFL	1	Pre only	BLS	19	WPAIDGSFL	NB
WQILNGQLS	1	Pre only	BLS	9	WQILNGQLS	NB
RQGSWSVFPPGPLI	5	Pre only	BLS	14	WSVFPPGPL	NB
YDQESHQVILR	4	Pre only	BLS	11	YDQESHQVI	IB
SLYEAGQQDVFPVL	1	Pre only	BLS	14	YEAGQQDVF	HB
SLYEAGQQDVFPVLS	1	Pre only	BLS	15	YEAGQQDVF	HB

MYHAPENYGHGSLE	1	Pre only	BLS	14	YHAPENYGH	HB
YHAPENYGHGSLE	1	Pre only	BLS	13	YHAPENYGH	HB
YHAPENYGHGSLELL	1	Pre only	BLS	15	YHAPENYGH	HB
QVYLWKDSDMG	1	Pre only	BLS	11	YLWKDSDMG	LB
HSYNRFPDAFVT	2	Pre only	BLS	12	YNRFPDAFV	IB
SYNRFPDAFVT	1	Pre only	BLS	11	YNRFPDAFV	IB
QYPGSYSDFSTPLA	2	Pre only	BLS	14	YPGSYSDFS	LB
QYPGSYSDFSTPLAHFD	1	Pre only	BLS	17	YPGSYSDFS	LB
QYPGSYSDFSTPLAHFDLR	2	Pre only	BLS	19	YPGSYSDFS	LB
ELYQRWEAQNKGQDLTPAKLLVK	1	Pre only	BLS	23	YQRWEAQNK	LB
LYQRWEAQNKGQDLTPAKLL	1	Pre only	BLS	20	YQRWEAQNK	LB
LYQRWEAQNKGQDLTPAKLLVK	2	Pre only	BLS	22	YQRWEAQNK	LB
NIFEYQVDAQPLRPCE	1	Pre only	BLS	16	YQVDAQPLR	HB
NIFEYQVDAQPLRPCELQ	1	Pre only	BLS	18	YQVDAQPLR	HB
YQVDAQPLRPCE	1	Pre only	BLS	12	YQVDAQPLR	HB
YQVDAQPLRPCELQ	1	Pre only	BLS	14	YQVDAQPLR	HB
KQADYVPQCAEDGSFQTVQ	1	Pre only	BLS	19	YVPQCAEDG	LB
QADYVPQCAEDGSFQTVQ	1	Pre only	BLS	18	YVPQCAEDG	LB
YWGPVIDGHFL	1	Pre only	BLS	11	YWGPVIDGH	IB

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