

H. APÈNDIX

Nº d'accés i alineament de les seqüències de glicogen sintases eucariotes

En la següent taula es resumeixen els codis de referència de les seqüències de proteïna de les glicogen sintases eucariotes utilitzades en aquest projecte. Només es mostren les seqüències completes. Les referències en negre indiquen que la seqüència estava anotada i identificada prèviament. En vermell es destaquen les seqüències que tot i estar anotades i disponibles en les bases de dades, no s'han identificat explícitament com a glicogen sintases. Les seqüències marcades amb # s'han identificat amb el treball desenvolupat en aquesta tesi a partir de fragments de seqüència en brut disponibles en els projectes genoma de cada organisme o per seqüenciació dels corresponents clons d'EST.

Organsime	Nº d'accés	Organsime	Nº d'accés
<i>GYS Giardia lamblia</i>	XP_779057	<i>GYS2 Tetraodon nigroviridis</i>	#
<i>GYS Dictyostelium discoideum</i>	XP_647210	<i>GYS2 Takifugu rubripes</i>	#
<i>GYS Cryptococcus neoformans</i>	AAW45795	<i>GYS2 Xenopus laevis</i>	AAH70667
<i>GYS Ustilago maydis</i>	XP_757156	<i>GYS2 Gallus gallus</i>	#
<i>GYS Yarrowia lipolytica</i>	XP_505581	<i>GYS2 Monodelphis domestica</i>	#
<i>GYS Debaryomyces hansenii</i>	XP_457217	<i>GYS2 Rattus norvegicus</i>	NP_037221
<i>GYS Candida albicans</i>	XP_717968	<i>GYS2 Mus musculus</i>	NP_663547
<i>GYS Candida glabrata</i>	XP_448679	<i>GYS2 Oryctolagus cuniculus</i>	#
<i>GYS Ashbya gossypii</i>	AAS50373	<i>GYS2 Bos taurus</i>	#
<i>GSY1 Saccharomyces cerevisiae</i>	NP_116670	<i>GYS2 Canis familiaris</i>	XP_534869
<i>GYS Saccharomyces paradoxus</i>	#	<i>GYS2 Macaca mulatta</i>	XP_001098578
<i>GSY2 Saccharomyces cerevisiae</i>	NP_013359	<i>GYS2 Pan troglodytes</i>	#
<i>GYS Kluyveromyces lactis</i>	XP_456111	<i>GYS2 Homo sapiens</i>	NP_068776
<i>GYS Aspergillus fumigatus</i>	EAL86056	<i>GYS1 Tetraodon nigroviridis</i>	#
<i>GYS Aspergillus nidulans</i>	XP_681279	<i>GYS1 Takifugu rubripes</i>	#
<i>GYS Gibberella zeae</i>	XP_386998	<i>GYS1 Danio rerio</i>	NP_957474
<i>GYS Magnaporthe grisea</i>	XP_367364	<i>GYS1 Pimephales promelas</i>	#
<i>GYS Neurospora crassa</i>	AAL08574	<i>GYS1 Xenopus tropicalis</i>	#
<i>GYS Steinernema feltiae</i>	AAK28335	<i>GYS1 Monodelphis domestica</i>	#
<i>GYS Caenorhabditis briggsae</i>	CAE71482	<i>GYS1 Rattus norvegicus</i>	#
<i>GYS Caenorhabditis elegans</i>	NP_496736	<i>GYS1 Mus musculus</i>	NP_109603
<i>GYS Crassostrea gigas</i>	AAS93900	<i>GYS1 Oryctolagus cuniculus</i>	P13834
<i>GYS Drosophila melanogaster</i>	NP_731968	<i>GYS1 Canis familiaris</i>	#
<i>GYS Drosophila pseudoobscura</i>	EAL28473	<i>GYS1 Macaca mulatta</i>	NP_001028058
<i>GYS Apis mellifera</i>	XP_624707	<i>GYS1 Pongo pygmaeus</i>	CAH91590
<i>GYS Anopheles gambiae</i>	EAA08045	<i>GYS1 Homo sapiens</i>	NP_002094
<i>GYS Ciona intestinalis</i>	#		
<i>GYS Ciona savignyi</i>	#		

GS_Giardia_lamblia	1MEEEQMYDVEGGPGPG	DVLCMEFCYEVIHKVGGIET
GS_Dictyostelium_discoideum	1MNELNIQQPTS	HTVLFDLSEVAKKVGGIYT
GS_Cryptococcus_neoformans	1MPSRVH	NPFLEAAWEVANKVGGIYT
GS_Aspergillus_fumigatus	1MDSEDTGPDPPKRDVR	NHLLFEIATEVANRVGGIYS
GS_Aspergillus_nidulans	1MADDQDPPRRDVR	NHMLFEIATEVANRVGGIYS
GS_Gibberella_zeae	1MSSGG.EQTRDIK	NHLLFEIATEVAHRVGGIYS
GS_Magnaporthe_grisea	1MAEGGEREPREVK	NHLLFEIATEVAHRVGGIYS
GS_Neurospora_crassa	1MAHDN.REPREVK	NHLLFEVATEVAHRVGGIYS
GS_Ustilago_maydis	1MASSSPKRDVH	NPLLEAAWEVANKVGGIYT
GS_Deбaryomyces_hansenii	1MTRDIK	NHLLFEVATEVAHKVGGIYS
GS_Kluyveromyces_lactis	1MTRDIV	NHLLFEVATEVANKVGGIYS
GS_Yarrowia_lipolytica	1MTRDTR	NHLLFEVATEVANRVGGIYS
GS_Candida_albicans	1MARDID	NHLLFEVATEVAHKVGGIYS
GS_Candida_glabrata	1MPRDLO	NHLLFEVATEVANKVGGIYS
GS_Ashbya_gossypii	1MTRDIQ	NHLLFETATEVANKVGGIYS
GS_Saccharomyces_paradoxus	1MSRDLO	NHLLFETATEVANRVGGIYS
GSY1_Saccharomyces_cerevisiae	1MARDLO	NHLLFEVATEVTNRVGGIYS
GSY2_Saccharomyces_cerevisiae	1MSRDLO	NHLLFETATEVANRVGGIYS
GS_Caenorhabditis_briggsae	1MPDHGRMPRNLSNKI	AKTIAGEDLDEEEVLEMDAGRSAREEGRFVFEC
GS_Caenorhabditis_elegans	1MPDHARMPRNLSNKI	AKTIAGEDLDEEEVLEMDAGQSAREEGRFVFEC
GS_Steinernema_feltiae	1	MTTDETVMGATTPKVTRKFSSKIVRQLSGLNISDQG.SVTD	DRGENARTEGRYVFECSWEVANKVGGIYT
GS_Crassostrea_gigas	1MRRRNSFYRSFKDACPEFEEMLMDRGATAAAQ	NKWVFEIAWEVANKVGGIYT
GS_Drosophila_pseudoobscura	1MNRRFSRVESGVLDKDYFDRGDIASREN	NRWNFEVAWEVANKVGGIYT
GS_Drosophila_melanogaster	1MNRRFSRVESGADLKDYFDRGDIASREN	NRWNFEVAWEVANKVGGIYT
GS_Apis_mellifera	1MSRERVSRRFYRMDSSNDLLEFMDRGYSAQHEN	NRWYFEVAWEAANKVGGIYT
GS_Anopheles_Gambiae	1MSRRYSRVESSDLMQFLDRGHSANTEN	NRWTFEIAWEVANKVGGIYT
GS_Ciona_intestinalis	1MAEEAP	ALFTFEVAWEVANKVGGIYT
GS_Ciona_savignyi	1MADEAP	ALFTFEVAWEVANKVGGIYT
GYS1_Fugu_rubirpes	1MPLARSLSVTSLSG.LEEWDEE...FDLEDAV	LFEIAWEVANKVGGIYT
GYS1_Tetraodon_nigrovidiris	1MPLARSLSVTSLSG.LEEWDEE...FDLEDAV	LFEIAWEVANKVGGIYT
GYS1_Danio_erio	1MPLARSLSVTSLSG.LDDWDEE...FDREDAV	LFEIAWEVANKVGGIYT
GYS1_Pimephales_promelas	1MPLARSLSVTSLSG.LEDWDEE...FDREDAV	LFEIAWEVSNKVGGIYT
GYS1_Xenopus_tropicalis	1MPLARSLSVTSLTG.LEDWDD...LDLENSIL	FEVAWEVANKVGGIYT
GYS1_Rattus_norvegicus	1MPLSRSLSMSSLPG.LEDWEDE...FDPENAV	LFEVAWEVANKVGGIYT
GYS1_Mus_musculus	1MPLSRSLSVSSLPG.LEDWEDE...FDPENAV	LFEVAWEVANKVGGIYT
GYS1_Oryctolagus_cuniculus	1MPLSRTL SVSSLPG.LEDWEDE...FDLENSV	LFEVAWEVANKVGGIYT
GYS1_Canis_familiaris	1MPLSRTL SMSSLPG.LEDWEDE...FDLENTV	LFEVAWEVANKVGGIYT
GYS1_Macaca_mulatta	1MPLNRTL SMSSLPG.LEDWEDE...FDLENTV	LFEVAWEVANKVGGIYT
GYS1_Pongo_pygmaeus	1MPLNRTL SMSSLPG.LEDWEDE...FDLENAV	LFEVAWEVANKVGGIYT
GYS1_Homo_sapiens	1MPLNRTL SMSSLPG.LEDWEDE...FDLENAV	LFEVAWEVANKVGGIYT
GYS2_Fugu_rubirpes	1MPLPRSVSMTSLSGLLPAWEEDP...LPVEE	LLLFVAWEVTNKVGGIYT
GYS2_Tetraodont_nigrovidiris	1MPLSRSLSMTSLSGLLPAWEEDQ...LPVEE	LLLFVAWEVTNKVGGIYT
GYS2_Danio_erio	1MRLSRSLSITSLSG.LPLFEES...LPVEE	LLLFVAWEVTNKVGGIYT
GYS2_Xenopus_laevis	1MPLSRSLSVSSLNG.LPLWQDED...LPLQD	LLLFVAWEVTNKVGGIYT
GYS2_Xenopus_tropicalis	1MPLSRSLSVSSLNG.LPQWQDED...LPLQD	LLLFVAWEVTNKVGGIYT
GYS2_Gallus_gallus	1MPLARSLSMTSLNG.LPQWEDED...LPVEE	LLLFVSWEVTNKVGGIYT
GYS2_Monodelphis_domestica	1MLRGRSLSVTSLSG.LPLWDVQE...LPVEE	LLLFVAWEVTNKVGGIYT
GYS2_Mus_musculus	1MLRGRSLSVTSLGG.LPVWEAER...LPVEE	LLLFVSWEVTNKVGGICT
GYS2_Rattus_norvegicus	1MLRGRSLSVTSLGG.LPAWEAER...LPVEE	LLLFVSWEVTNKVGGICT
GYS2_Bos_taurus	1MLRGRSLSVTSLGG.LPRWEAG...LPVEN	LLLFVSWEVTNKVGGIYT
GYS2_Canis_familiaris	1MLRGRSLSVTSLSG.LPQWEVEE...LPVEE	LLLFVAWEVTNKVGGIYT
GYS2_Macaca_mulatta	1MLRGRSLSVTSLSG.LPRWEVKE...LPVEE	LLLFVAWEVTNKVGGIYT
GYS2_Homo_sapiens	1MLRGRSLSVTSLGG.LPQWEVEE...LPVEE	LLLFVAWEVTNKVGGIYT

Alineament total de les seqüències de proteïna de les glicogen sintases eucariotes

GS_Giardia_lamblia	37	VVRTKA	PAMVNV	EYGD	NYF	MVGP	LSWDDKFAT	NFE	EAE	ERNEESE	ILYKLIDS	F	EARY	G	IGIKGV	Y					
GS_Dictyostelium_discoideum	32	VLKTKA	PVTV	EYKS	RYAL	LIGPY	N..ASTAPT	EFE	PLI	PGPLS	S.PIENNM	M	KKY	G	..IHVH	F					
GS_Cryptococcus_neoformans	27	VIKTKV	PVTV	EYGD	RCL	CLIGPLS	..YKSAPV	EVE	AEL	PGPGP	FGDALRS	M	QER	G	..VKLL	Y					
GS_Aspergillus_fumigatus	37	VLKSKA	PVTTA	EYGD	RYT	LI	GPLN..RASA	AVE	ELT	PSNPR	MVETMNS	M	KER	G	..IGMV	Y					
GS_Aspergillus_nidulans	34	VLKSKA	PVTTA	EYGE	RYT	LI	GPLN..RNSAAV	EVE	ELT	PSSPA	MKETMQS	M	KER	G	..IEMV	Y					
GS_Gibberella_zeae	33	VIKSKA	PVTTA	EYGD	RYT	LI	GPLN..HQSAAV	EVE	ELT	PTNPE	IAATIQS	M	RDR	G	..VHIV	Y					
GS_Magnaporthe_grisea	34	VIKSKA	PVTTA	EYGD	RYT	LI	GPLN..HTSAAV	EVE	ELT	PKDPA	LTATIQS	M	KDR	G	..IGIL	Y					
GS_Neurospora_crassa	33	VLKSKA	PVTTA	EYGD	RYT	LI	GPLN..HQSAAV	EVE	ELT	PSNPE	LKATIQA	M	RDR	G	..IGIL	Y					
GS_Ustilago_maydis	32	VIKTKA	PVTHQ	EYGE	RYT	LI	GPLS..YKTAPM	EVE	ALP	EDPI	LKETLDS	M	RDA	G	..VKFL	Y					
GS_Debaryomyces_hansenii	27	VLKSKA	PITVA	EYRE	RYT	LI	GPLN..YNSAQI	EVE	ELP	VKDPLIK	ALDS	M	SER	G	..IRWL	Y					
GS_Kluyveromyces_lactis	27	VLKSKA	PITCK	QYGP	KYL	LL	GPLN..PQSVQV	EVE	PVD	WEDES	NFH..	IKEVQWS	L	RS	M	HNR	G	..VRFT	Y			
GS_Yarrowia_lipolytica	27	VIKSKA	PVTVY	EYGD	RYH	LI	GPLN..RKSADI	EVE	EIT	DESQI	PEA... ..	INKTLKS	M	ER	G	..IQVY	Y					
GS_Candida_albicans	27	VLKSKA	PVTTVA	EYRE	RYT	LL	GPLH..YDSAQI	EVE	ELP	VTDPHIK	TLDS	M	SSK	G	..IRWL	Y					
GS_Candida_glabrata	27	VLKSKA	PVTTVA	QYQD	NYT	LI	GPLN..KGTYQI	EVE	ELD	WEDPS	IFSEEL	QPVQQA	L	KY	M	REK	G	..VYFV	Y			
GS_Ashbya_gossypii	27	VLKSNP	PITVA	QYKD	HYH	LI	GPLN..PDSVQI	EVE	ALD	WEDDS	VWSREML	PVKRSLQ	H	M	ER	G	..VNFV	Y				
GS_Saccharomyces_paradoxus	27	VLKSKA	PITVA	QYKD	HYH	LI	GPLN..KATYQN	EVD	ILD	WKKPE	AFSDEM	KPVQHA	L	Q	T	M	ESR	G	..VHFI	Y		
GYS1_Saccharomyces_cerevisiae	27	VLKSKA	PVTTVA	QYQD	NYT	LL	GPLN..KATYES	EVE	KLD	WEDDES	IFPEELL	PIQTL	M	S	M	REK	G	..VNFV	Y			
GYS2_Saccharomyces_cerevisiae	27	VLKSKA	PITVA	QYKD	HYH	LI	GPLN..KATYQN	EVD	ILD	WKKPE	AFSDEM	RPVQHA	L	Q	T	M	ESR	G	..VHFI	Y		
GS_Caenorhabditis_briggsae	63	VLRSKA	QISTE	ELGD	QYCM	F	GP	MK..DGKWRL	EVD	PIE	P.ENR	TIRAAMK	R	F	QAD	G	..FRCM	Y			
GS_Caenorhabditis_elegans	63	VLRSKA	QISTE	ELGD	QYCM	F	GP	MK..DGKWRL	EVD	PIE	P.ENR	TIRAAMK	R	F	QAD	G	..FRCM	Y			
GS_Steinernema_feltiae	70	VIRSKA	PVSTD	ELGD	QYCM	L	GP	YN..EERVKL	EVE	ILP	.SHY	VYRQTLQ	T	M	RDA	G	..IKVH	F			
GS_Crassostrea_gigas	53	VIKSKA	PVSVA	ELGE	QYCL	L	GP	YN..EACVRT	EVE	ILP	.SHY	VYRQTLQ	T	M	RDA	G	..IKVH	F			
GS_Drosophila_pseudoobscura	48	VIRSKA	YVSTE	EMGE	QLCM	M	GP	YK..EVCART	EME	EMF	PRGN	PLLDVNS	L	R	SR	G	..YKIH	T			
GS_Drosophila_melanogaster	48	VIRSKA	YVSTE	EMGE	QLCM	M	GP	YK..EHCART	EME	EMF	PRGN	PLLDVNS	L	R	SR	G	..YKIH	T			
GS_Apis_mellifera	53	VIRSKA	YVSTE	EMGD	QYCL	L	GP	YK..ETSART	EVE	EAD	FPHNN	PLHIAVQ	V	L	R	DQ	G	..FKVV	T		
GS_Anopheles_Gambiae	48	VIRSKA	FVSTE	ELGD	QYCL	L	GP	YK..EASART	EVE	ACE	FPNG	PFYRAVT	A	M	R	NQ	G	..FKVH	C		
GS_Ciona_intestinalis	27	VLRSKA	ESTVE	ELGED	YCM	I	GCN..ERFVAM	EVE	KME	P.SLP	QMKRAVD	L	M	R	EK	H	..IGVV	T			
GS_Ciona_savignyi	27	VLRSKA	ESTVE	ELGED	YCM	I	GCN..ERYVAM	EVE	KME	P.VLP	QMKRTVD	L	M	R	EQ	N	..IKVV	T			
GYS1_Fugu_rubripes	46	VIQTKA	RLTAE	EWGEN	YF	LV	GP	YM..ESNVRT	QVE	LIE	P.PTP	ILRRTID	K	M	N	S	R	G	..CKIY	F	
GYS1_Tetraodon_nigrovidiris	46	VIQTKA	RLTAE	EWGEN	YF	LV	GP	YV..ESNVRT	QVE	LIE	P.PTP	VLRRTID	K	M	N	S	R	G	..CKIY	F	
GYS1_Danio_rerio	46	VIQTKA	RLTCE	EWGEN	YF	LV	GP	YM..ESNVRT	QVE	LIE	P.CNA	ALRRTID	K	M	N	S	S	R	G	..CKVY	F
GYS1_Pimephales_promelas	46	VIQTKA	RLTCE	EWGEN	YF	LV	GP	YM..ESNVRT	QVE	LIE	P.CNA	ALRRTID	K	M	N	S	S	R	G	..CKVY	F
GYS1_Xenopus_tropicalis	46	VIQTKA	KVTTD	EWGEN	YF	LI	GP	YF..ENNVRT	QVE	LIE	P.THP	AIKRALD	S	M	N	A	K	G	..CKVY	F	
GYS1_Rattus_norvegicus	46	VLQTKA	KVTGD	EWGD	NYF	LV	GP	YT..EQGVRT	QVE	LLE	P.PTP	ELKRTL	D	S	M	N	S	K	G	..CKVY	F
GYS1_Mus_musculus	46	VLQTKA	KVTGD	EWGD	NYF	LV	GP	YT..VQGVRT	QVE	LLE	P.PTP	ELKRTL	D	S	M	N	S	K	G	..CKVY	F
GYS1_Oryctolagus_cuniculus	46	VLQTKA	KVTGD	EWGD	NYF	LV	GP	YT..EQGVRT	QVE	LLE	P.PTP	ALKRTL	D	S	M	N	S	K	G	..CKVY	F
GYS1_Canis_familiaris	46	VLQTKA	KVTGD	EWGD	NYF	LV	GP	YT..EQGVRT	QVE	LLE	P.PTP	ALKRTL	D	S	M	N	S	K	G	..CKVY	F
GYS1_Macaca_mulatta	46	VLQTKA	KVTGD	EWGD	NYF	LV	GP	YT..EQGVRT	QVE	LLE	P.PTP	ALKRTL	D	S	M	N	S	K	G	..CKVY	F
GYS1_Pongo_pygmaeus	46	VLQTKA	KVTGD	EWGAN	YF	LV	GP	YT..EQGVRT	QVE	LLE	P.PTP	ALKRTL	D	S	M	N	S	K	G	..CKVY	F
GYS1_Homo_sapiens	46	VLQTKA	KVTGD	EWGD	NYF	LV	GP	YT..EQGVRT	QVE	LLE	P.PTP	ALKRTL	D	S	M	N	S	K	G	..CKVY	F
GYS2_Fugu_rubripes	48	VIQTKA	KVTVD	EWGEN	YF	MM	GP	YF..EHNFKT	QVE	ACE	P.PNQ	AIRKAMD	A	L	H	N	G	..CQVY	F		
GYS2_Tetraodont_nigrovidiris	48	VIQTKA	KVTVD	EWGEN	YF	MM	GP	YF..EHNFKT	QVE	ACE	P.PNP	AIRKAMD	A	L	L	H	N	G	..CQVH	F	
GYS2_Danio_rerio	47	VIQTKA	KIITVD	EWGEN	YF	MM	GP	YY..EHNFKT	QVE	KCE	P.PNQ	AIRAAMD	S	L	I	N	N	G	..CQVH	F	
GYS2_Xenopus_laevis	47	VIQTKA	KVTAD	EWGD	NYF	LM	GP	YF..EHNVRT	QVE	ICD	P.PNG	HIRKAID	V	L	Q	S	G	..CQVY	F		
GYS2_Xenopus_tropicalis	47	VIQTKA	KVTAD	EWGD	NYF	LM	GP	YM..EQNVRT	QVE	ICD	P.PSP	QIRKAID	L	L	Q	S	G	..CQVY	F		
GYS2_Gallus_gallus	47	VIQTKA	KIITAD	EWGEN	YF	LI	GP	YF..EHNVRT	QVE	VCE	P.PNP	AIKKAMD	T	M	K	S	Q	G	..CQVF	F	
GYS2_Monodelphis_domestica	47	VIQTKA	KTTAD	EWGEN	YF	LI	GP	YF..EHNMKT	QVE	CE	P.PSP	AIKKAVE	A	M	N	L	H	G	..CQVF	F	
GYS2_Mus_musculus	47	VIQTKA	KTTAD	EWGEN	YF	LI	GP	YF..EHNMKT	QVE	CE	P.TND	AVRKAVD	A	M	N	K	H	G	..CQVF	F	
GYS2_Rattus_norvegicus	47	VIQSKA	KTTAN	EWGEN	YF	LI	GP	YF..EHNVRT	QVE	PC	R.AND	AVRKAVD	A	M	N	K	H	G	..CQVF	F	
GYS2_Bos_taurus	46	VIQTKA	KTTAD	EWGD	NYF	LI	GP	YF..EHNMKT	QVE	CE	P.VND	AVRRAMD	T	M	N	K	H	G	..CQVF	F	
GYS2_Canis_familiaris	47	VIQTKA	KTTAD	EWGD	NYF	LI	GP	YF..EHNMKT	QVE	QC	E.P.IND	AVRRAVD	T	M	N	K	H	G	..CQVF	F	
GYS2_Macaca_mulatta	47	VIQTKA	KTTAD	EWGD	NYF	LI	GP	YF..EHNMKT	QVE	QC	E.P.VND	AVRRAVD	T	M	N	K	H	G	..CQVF	F	
GYS2_Homo_sapiens	47	VIQTKA	KTTAD	EWGEN	YF	LI	GP	YF..EHNMKT	QVE	QC	E.P.VND	AVRRAVD	T	M	N	K	H	G	..CQVF	F	

GS_Giardia_lamblia	101	GRWLTAGN	PQVFLFP	MIYNSGTHFE	HKIDHARN	ILRTACN	LEIP	PNPGFGER	EPIYI	WNA	FLFG	VV	GWCFVS	
GS_Dictyostelium_discoideum	90	GKWLVEGY	PKVFLID	LHSSM	HKLGWRW	DLMSGFE	QAG			DNETNE	TIVFG	YS	ALLLK	
GS_Cryptococcus_neoformans	85	GRWLIIEG	APRVLLFD	TGSCY	DRMDEWK	GDLWNLAG	IPSP			PNDHETNE	TIVFGY	LV	AWFLG	
GS_Aspergillus_fumigatus	95	GRWLIIEG	APRVLLID	TGTGY	KYLDEWK	GDLWNLAG	IPSP			ASDHE	TNEA	IVFGY	LV	AWFLG
GS_Aspergillus_nidulans	92	GRWLIIEG	APRVLLID	TGTGY	KYLDEWK	GDLWNTAG	IPSP			ASDHE	TNEA	IVFGY	LV	AWFLG
GS_Gibberella_zeae	91	GRWLIIEG	APRVLLFD	TKTAY	GRMDEWK	ADLWNEAS	IPSP			PGDDE	TNEA	IVFGY	LV	AWFLG
GS_Magnaporthe_grisea	92	GRWLIIEG	APRVLLID	TKTAY	KHLDEWK	TDLWNVAS	IPSP			PGDDE	TNEA	IVFGY	LV	AWFLG
GS_Neurospora_crassa	91	GRWLIIEG	APRVLLFD	TKTAY	GYMNEWK	TDLWNVAS	IPSP			DNDEE	TNEA	IVFGY	LV	AWFLG
GS_Ustilago_maydis	90	GRWLIIEG	APRVLLFD	TSSMY	HRMDEWK	GDLWNLAG	IPTP			PNDHETNE	TIVFGY	LV	AWFLG	
GS_Debaryomyces_hansenii	85	GRWLIIEG	APRVLLFD	IHSAG	HHLNEWK	ADLWNLAG	IPTP			EHDQE	SSEA	ILLGY	LV	AWFLG
GS_Kluyveromyces_lactis	91	GRWLIDG	APMVLFD	LNSVR	NYLNEWK	ADLWEIAG	IPSP			DGDFE	TNDA	ILLGY	TV	AWFLG
GS_Yarrowia_lipolytica	88	GRWLIIEG	APRVLLFD	LVSVA	CYLP	EWKSDLWTVAG	IPAP			EGDKE	SND	AVVLG	LV	AWFLG
GS_Candida_albicans	85	GRWLIIEG	APRVLLFD	IWSAG	HYLNEWK	ADLWNVAG	IPTP			DHDLE	TNDA	ILLGY	LV	AWFLG
GS_Candida_glabrata	93	ARWLIIEG	APRVLLFD	LDSVR	YKLN	EWKADLWSLVG	IPSP			ENDWE	TNDA	ILLGY	TV	VWFLG
GS_Ashbya_gossypii	93	GRWLVEG	APRVLLFD	LVSVT	HHLNEWK	ADLWNEAS	IPSP			QDDQE	TNNS	ILLGY	TV	AWFLG
GS_Saccharomyces_paradoxus	93	GRWLIIEG	APKVLFD	LDSVR	GYSNEWK	GDLWSLVG	IPSP			ENDFE	TNDA	ILLGY	TV	AWFLG
GSY1_Saccharomyces_cerevisiae	93	GNWLIIEG	APRVLLFD	LDSVR	HFLNEWK	ADLWSLVG	IPSP			EHDHE	TNDA	ILLGY	VV	VWFLG
GSY2_Saccharomyces_cerevisiae	93	GRWLIIEG	APKVLFD	LDSVR	GYSNEWK	GDLWSLVG	IPSP			ENDFE	TNDA	ILLGY	TV	AWFLG
GS_Caenorhabditis_briggsae	121	GRWLIIEG	YPKVLFD	LGSGA	VKMNEWK	HELFEKCK	IGIP			HEDIE	SND	AVILG	FM	VAILFK
GS_Caenorhabditis_elegans	121	GRWLIIEG	YPKVLFD	LGSGA	VKMNEWK	HELFEKCK	IGIP			HEDIE	SND	AVILG	FM	VAILFK
GS_Steinernema_feltiae	128	GRWLIIEG	YPKVVLF	IGSAA	WKLD	TWKHEIWEKCH	IGVP			YHDQE	SND	AVILG	FM	VAILFK
GS_Crassostrea_gigas	111	GRWLIDG	YPKVLFD	IGSAA	WKLDE	FKHELWEKAS	IGIP			WHDRE	SND	AVIFG	AL	VAWFIG
GS_Drosophila_pseudoobscura	107	GRWLVDGN	PQLILFD	IGSAA	WKLLD	QFKSEMWEKCH	IGIP			HLDIE	TNDA	ILGFM	IA	AEFLE
GS_Drosophila_melanogaster	107	GRWLVDGN	PQLILFD	IGSAA	WKLLD	QFKSEMWEKCH	IGIP			HLDIE	TNDA	ILGFM	IA	AEFLE
GS_Apis_mellifera	112	GTWLVDGN	PQIILFD	IGSAA	WKLDE	EYQELWNTCN	LGIP			HLDIE	SND	AVILG	YL	VCQFIS
GS_Anopheles_Gambiae	107	GRWLVDGN	PQIILFD	IGSAA	WKMD	GYQELWNTCN	VGIP			HLDIE	CNDA	ILGY	TV	ATFID
GS_Ciona_intestinalis	85	GRWLIIEG	YPKVVLF	LDTAW	DMYNT	WSWEMFDKT	GVGIP			EHDTE	AKRC	CVLFG	FL	TAWFLG
GS_Ciona_savignyi	85	GRWLIIEG	YPKVVLF	LDSAW	DKYNS	WSWELFDKT	GVGIP			DHDNE	TKR	CVLFG	FL	TAWFLG
GYS1_Fugu_rubripes	104	GRWLIIEG	SPYVILFD	VGFTA	WSLDT	WKSELWDISG	IGVP			WFDRE	AND	AVLFG	FL	TAWLLG
GYS1_Tetraodon_nigrovidiris	104	GRWLIIEG	SPYVILFD	VGFTA	WSLDT	WKSELWDISG	IGVP			WFDRE	AND	SVLFG	FL	TAWLLG
GYS1_Danio_rerio	104	GRWLIIEG	SPYVLLD	VGFTA	WSLDR	WKSELWEKCN	IGVP			WFDRE	AND	AVLFG	FL	TAWLLG
GYS1_Pimephales_promelas	104	GRWLIIEG	SPYVILFD	VGFTA	WSLDR	WKSELWEKCG	IGVP			WFDRE	AND	AVLFG	FL	TAWLLG
GYS1_Xenopus_tropicalis	104	GRWLIIEG	SPYVILFD	IAATA	WNLDR	WKTELWDS	CDIGIP			WYDRE	AND	AVLFG	FL	TAWFLG
GYS1_Rattus_norvegicus	104	GRWLIIEG	GPLVLLD	VGASA	WALER	WKGELWDT	CNIGVP			WYDRE	AND	AVLFG	FL	TWFLG
GYS1_Mus_musculus	104	GRWLIIEG	GPLVLLD	VAASA	WALER	WKGELWDT	CNIGVP			WYDRE	AND	AVLFG	FL	TWFLG
GYS1_Oryctolagus_cuniculus	104	GRWLIIEG	GPLVLLD	VGASA	WALER	WKGELWDT	CNIGVP			WYDRE	AND	AVLFG	FL	TWFLG
GYS1_Canis_familiaris	104	GRWLIIEG	GPLVLLD	VGASA	WALER	WKGELWDT	CNIGVP			WYDRE	AND	AVLFG	FL	TWFLG
GYS1_Macaca_mulatta	104	GRWLIIEG	GPLVLLD	VGASA	WALER	WKGELWDT	CNIGVP			WYDRE	AND	AVLFG	FL	TWFLG
GYS1_Pongo_pygmaeus	104	GRWLIIEG	GPLVLLD	VGASA	WALER	WKGELWDT	CNIGVP			WYDRE	AND	AVLFG	FL	TWFLG
GYS1_Homo_sapiens	104	GRWLIIEG	GPLVLLD	VGASA	WALER	WKGELWDT	CNIGVP			WYDRE	AND	AVLFG	FL	TWFLG
GYS2_Fugu_rubripes	106	GRWLIIEG	SPYVILFD	IGSAA	WNLDR	WKGDWLQ	TCISGLP			YHDRE	AND	ALILG	SL	IAWFFK
GYS2_Tetraodon_nigrovidiris	106	GRWLIIEG	SPYVILFD	IGSAA	WNLDR	WKGDWLQ	TCISGLP			YHDRE	AND	ALILG	SL	IAWFFK
GYS2_Danio_rerio	105	GRWLIIEG	SPYVILFD	IGAAA	WNLDR	WKGDWLS	ACGIGLP			YHDRE	AND	SLILG	SL	VAWFFK
GYS2_Xenopus_laevis	105	GRWLIIEG	NPYVLLD	IGSAA	WNLDR	WKGEFWD	CVGIP			YNDRE	AND	ALIFG	SL	TAWFLK
GYS2_Xenopus_tropicalis	105	GRWLIIEG	NPYVLLD	IGSAA	WNLDR	WKGEFWE	CVGIP			YNDRE	AND	ALIFG	SL	TAWFLK
GYS2_Gallus_gallus	105	GRWLIIEG	SPYVLLD	IGSAA	WNLDR	WKGEFWD	ATNIGIP			FHDRE	AND	AVIFG	SL	TAWFLK
GYS2_Monodelphis_domestica	105	GRWLIIEG	SPYVLLD	IGYSA	WNLDR	WKGDLE	EACNIGIP			YHDQE	AND	MILIFG	SL	TAWFLK
GYS2_Mus_musculus	105	GRWLIIEG	SPYVLLD	ISSSA	WNLDR	WKGEFWE	ACGVGIP			HHDRE	AND	MILIFG	SL	TAWFLK
GYS2_Rattus_norvegicus	105	GRWLIIEG	SPYVLLD	ISSSV	WNLDR	WKGEFWE	ACGVGIP			HHDRE	AND	MILIFG	SL	TAWFLK
GYS2_Bos_taurus	104	GRWLIIEG	SPYVLLD	IGYSA	WNLDR	WKGDLE	EACNIGIP			YHDQE	AND	MILIFG	SL	TAWFLK
GYS2_Canis_familiaris	105	GRWLIIEG	SPYVLLD	IGYSA	WNLDR	WKGDLE	EACNIGIP			YHDRE	AND	MILIFG	SL	TAWFLK
GYS2_Macaca_mulatta	105	GRWLIIEG	SPYVLLD	IGYSA	WNLDR	WKGDLE	EACNIGIP			YHDRE	AND	MILIFG	SL	TAWFLK
GYS2_Homo_sapiens	105	GRWLIIEG	SPYVLLD	IGYSA	WNLDR	WKGDLE	EACNIGIP			YHDRE	AND	MILIFG	SL	TAWFLK

GS Giardia lamblia	171	HAMS.....FLFTDVN	VIMHSEWIGCV	AQVLYS	RNGNCETGQ	RENHLH	FLFTTHAT	TLGRHLSAG
GS Dictyostelium discoideum	147	EFAEAN.....PNDK	YIAHFHEWQAS	VGLIL	LLKK.....	WKVPVST	TIFTTTHAT	TLGRYLAAG
GS Cryptococcus neoformans	145	EFAARE.....TDNA	IVAHFHEWQAG	LAIPL	LCRK.....	RHIDVT	TIFTTTHAT	TLGRYLCAG
GS Aspergillus fumigatus	155	EFIAHE.....RRRA	VVAHFHEWLAG	VALPL	TKK.....	RHMDLT	TIFTTTHAT	TLGRYLCAG
GS Aspergillus nidulans	152	EYIAHE.....RRRA	VVAHFHEWLAG	VALPL	TKK.....	RHMDLT	TIFTTTHAT	TLGRYLCAG
GS Gibberella zeae	151	EFVCHE.....KKKA	VIAHFHEWLAG	VALPL	LCRK.....	RRIDVT	TIFTTTHAT	TLGRYLCAG
GS Magnaporthe grisea	152	EYVCHE.....KKKA	VIAHFHEWLAG	VGLPL	LCRK.....	RRIDVT	TIFTTTHAT	TLGRYLCAG
GS Neurospora crassa	151	EFVCHE.....KRKA	VIAHFHEWLAG	VALPL	TKK.....	ROIDVT	TIFTTTHAT	TLGPYLCAG
GS Ustilago maydis	150	EFSSRD.....KRKA	IIAHFHEWQAG	LAIPL	LCRK.....	RHIDVT	TIFTTTHAT	TLGRYLCAG
GS Debaryomyces hansenii	145	ELVYHD.....RERA	VICHHEWLAG	IALPL	LCRK.....	RRIDVT	TVFTTHAT	TLGRYLCAG
GS Kluyveromyces lactis	151	ELAHMN.....QTNA	IVAHFHEWLAG	VAIPL	LCRK.....	RRIDVT	TIFTTTHAT	TLGRYLCAG
GS Yarrowia lipolytica	148	ELTTHE.....TERA	VIAHFHEWLSG	IALPL	LCRK.....	RRIDVT	TIFTTTHAT	TLGRYLCAG
GS Candida albicans	145	ELVYND.....RDRA	VICQCHEWLAG	IALPL	LCRK.....	RRIDVT	TIFTTTHAT	TLGRYLCAG
GS Candida glabrata	153	ELTQLD.....HKHA	IIGHFHEWLAG	VALPL	LCRK.....	KRIDVT	TIFTTTHAT	TLGRYLCAG
GS Ashbya gossypii	153	ELTAQD.....QQHA	IVAHFHEWLAG	VALPL	LCRK.....	RRIDVT	TIFTTTHAT	TLGRYLCAG
GS Saccharomyces paradoxus	153	ELAHLN.....SQHA	IVAHFHEWLAG	VALPL	LCRK.....	RRIDVT	TIFTTTHAT	TLGRYLCAG
GSY1 Saccharomyces cerevisiae	153	EVSKLD.....SSHA	IIGHFHEWLAG	VALPL	LCRK.....	KRIDVT	TIFTTTHAT	TLGRYLCAG
GSY2 Saccharomyces cerevisiae	153	EVAHLD.....SQHA	IVAHFHEWLAG	VALPL	LCRK.....	RRIDVT	TIFTTTHAT	TLGRYLCAG
GS Caenorhabditis briggsae	181	HFR.....ESVTSYQPL	VVAHFHEWQAG	VGLLM	TRL.....	WKLDIA	TVFTTHAT	TLGRHLCAG
GS Caenorhabditis elegans	181	HFR.....ESVTSYTP	VVAHFHEWQAG	VGLLM	TRL.....	WKLDIA	TVFTTHAT	TLGRHLCAG
GS Steinernema feltiae	188	TFT.....NSVEGFDP	VVAHFHEWQAG	VGLIL	LCRL.....	WKLNV	STVFTTHAT	TLGRHLCAG
GS Crassostrea gigas	171	EFR.....KNLTDQPI	VVTHFHEWLAG	AGLMD	DLRT.....	RKVDC	ITIFTTTHAT	TLGRYLCAG
GS Drosophila pseudoobscura	167	EFRNFVAVTYSQNHDLNPPR	VVAHFHEWQAG	VALIV	LRTR.....	ROVEIA	TVFTTHAT	TLGRYLCAG
GS Drosophila melanogaster	167	EFRNFVAVTYSQNNELSA	IVAHFHEWQAG	VGLIV	LRTR.....	RLVEIA	TVFTTHAT	TLGRYLCAG
GS Apis mellifera	172	EFRLLAAEGYIDV...PPR	IVVHCHWQAG	VGLIAL	RLTR.....	RHVDA	TVFTTHAT	TLGRYLCAG
GS Anopheles Gambiae	167	EFKRCAEVYSHENEYGP	IVAHFHEWQAG	VGLIAL	RLTR.....	ROVDA	TVFTTHAT	TLGRYLCAG
GS Ciona intestinalis	145	EFR.....YQCGKKS	VIVAQFHEWLSG	IGLM	LCRM.....	ROIDIS	TIFFTHAT	TLGRYLCAG
GS Ciona savignyi	145	EFR.....YQCGKKS	VIVAQFHEWLSG	IGLM	LCRM.....	REIDIS	TIFFTHAT	TLGRYLCAG
GYS1 Fugu rubripes	164	EYAA.....QSEEP	HIVAHFHEWLAG	LGLV	LCRQ.....	RQLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Tetraodon nigrovidiris	164	EYAA.....QSEDP	HIVAHFHEWLAG	LGLV	LCRQ.....	RQLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Danio rerio	164	EYAA.....QCDEPP	HIVAHFHEWLAG	LGLV	LCRQ.....	RQLPVS	TIFFTHAT	TLGRYLCAG
GYS1 Pimephales promelas	164	EYAA.....QCDDPP	HIVAHFHEWLAG	LGLV	LCRQ.....	RHLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Xenopus tropicalis	164	EYAA.....QCEEK	FIIAHFHEWLAG	VGLIC	LCRI.....	RKLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Rattus norvegicus	164	EFLA.....QNEEK	YVVAHFHEWLAG	VGLIC	LCRA.....	RRLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Mus musculus	164	EFLA.....QNEEK	YVVAHFHEWLAG	VGLIC	LCRA.....	RRLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Oryctolagus cuniculus	164	EFLA.....QNEEK	HVVAHFHEWLAG	IGLIC	LCRA.....	RRLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Canis familiaris	164	EFLA.....QNEEK	HVVAHFHEWLAG	IGLIC	LCRA.....	RRLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Macaca mulatta	164	EFLA.....QSEEK	HVVAHFHEWLAG	IGLIC	LCRA.....	RRLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Pongo pygmaeus	164	EFLA.....QSEEK	HVVAHFHEWLAG	IGLIC	LCRA.....	RRLPVA	TIFFTHAT	TLGRYLCAG
GYS1 Homo sapiens	164	EFLA.....QSEEK	HVVAHFHEWLAG	VGLIC	LCRA.....	RRLPVA	TIFFTHAT	TLGRYLCAG
GSY2 Fugu rubripes	166	EYAA.....YQLGDKPN	VIGHFHEWQAG	PGLIL	LSRS.....	RKIPVA	TVFTTHAT	TLGRYLCAG
GYS2 Tetraodon nigrovidiris	166	EYAA.....HQLGDKPN	VIGHFHEWQAG	PGLIL	LSRS.....	RKIPVA	TVFTTHAT	TLGRYLCAG
GYS2 Danio rerio	165	ELT.....DQLQDKLN	VVAHFHEWQAG	TGLV	LSRS.....	RNLPVA	TIFFTHAT	TLGRYLCAG
GYS2 Xenopus laevis	165	ELT.....DQFQDKPG	VIAHFHEWQAG	AGLVL	LCRN.....	QKLPVA	TIFFTHAT	TLGRYLCAG
GYS2 Xenopus tropicalis	165	ELT.....DQFQDKPN	LIAHFHEWQAG	AGLVL	LCRN.....	QKLPVA	TIFFTHAT	TLGRYLCAG
GYS2 Gallus gallus	165	ELS.....CQFDDKPN	VVAHFHEWQAG	VGLIL	LSRS.....	QKLPVA	TIFFTHAT	TLGRYLCAG
GYS2 Monodelphis domestica	165	EVT.....DHVDGK	HVIAQFHEWQAG	TGLIL	LSRA.....	RRLPVA	TIFFTHAT	TLGRYLCAG
GYS2 Mus musculus	165	EVT.....DHADGK	HVIAQFHEWQAG	TGLIL	LSRA.....	RKLPVA	TVFTTHAT	TLGRYLCAG
GYS2 Rattus norvegicus	165	EVT.....DHADGK	HVIAQFHEWQAG	TGLIL	LSRA.....	RKLPVA	TIFFTHAT	TLGRYLCAG
GYS2 Bos taurus	164	EVT.....DHADGR	HVIVQFHEWQAG	IGLIL	LSRA.....	RKLPVA	TVFTTHAT	TLGRYLCAG
GYS2 Canis familiaris	165	EVT.....DHADGK	HVIAQFHEWQAG	TGLIL	LSRA.....	RKLPVA	TIFFTHAT	TLGRYLCAG
GYS2 Macaca mulatta	165	EVT.....DHADDK	HVVAQFHEWQAG	IGLIL	LSRA.....	RKLPVA	TIFFTHAT	TLGRYLCAG
GYS2 Homo sapiens	165	EVT.....DHADGK	YVVAQFHEWQAG	IGLIL	LSRA.....	RKLPVA	TIFFTHAT	TLGRYLCAG

GS_Giardia_lamblia	232	NI	CLMDCL	QV	L	KEKSADQCASH	WDM	EAS	RR	K	I	A	V	E	H	R	I	E	R	A	A	H	T	A	D	V	F	T	T	V	S	E	I	T	G	R	E	A	E	C	F	L	G	K	T	P	.	D					
GS_Dictyostelium_discoideum	199	GV	DLYNQM	QV	LN	MDF	EAS	KR	G	I	Y	H	R	H	W	I	E	K	K	S	A	A	D	S	H	V	F	T	T	V	S	E	I	T	G	Y	E	S	E	H	L	L	M	R	K	P	.	D				
GS_Cryptococcus_neoformans	197	SV	DFYNNL	QY	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	S	S	A	H	C	A	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	H	L	L	K	R	K	P	.	D				
GS_Aspergillus_fumigatus	207	SV	DFYNNL	QH	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	S	A	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	H	L	L	K	R	K	P	.	D					
GS_Aspergillus_nidulans	204	SV	DFYNNL	QY	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	S	A	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	H	L	L	K	R	K	P	.	D					
GS_Gibberella_zeae	203	SV	DFYNNL	QW	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	A	C	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	H	L	L	K	R	K	P	.	D					
GS_Magnaporthe_grisea	204	SV	DFYNNL	QW	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	S	C	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	H	L	L	K	R	K	P	.	D					
GS_Neurospora_crassa	203	SV	DFYNNL	QW	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	S	C	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	H	L	L	K	R	K	P	.	D					
GS_Ustilago_maydis	202	SV	DFYNNL	QY	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	C	A	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	H	L	L	K	R	K	P	.	D					
GS_Debaryomyces_hansenii	197	ST	DFYNNL	AN	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	S	A	T	H	S	A	D	V	F	T	T	V	S	E	I	T	A	F	E	A	E	H	L	L	K	R	K	P	.	D				
GS_Kluyveromyces_lactis	203	NV	DFYNNL	DK	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	S	A	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	Y	L	L	K	R	K	P	.	D					
GS_Yarrowia_lipolytica	200	SV	DFYNNL	QG	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	S	H	S	A	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	H	L	L	K	R	K	P	.	D				
GS_Candida_albicans	197	ST	DFYNNL	DK	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	S	A	T	H	S	A	D	V	F	T	T	V	S	E	I	T	A	F	E	A	E	H	L	L	K	R	K	P	.	D				
GS_Candida_glabrata	206	DV	DFYNNL	QY	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	T	A	D	V	F	T	T	V	S	E	I	T	A	L	E	A	E	H	L	L	K	R	K	P	.	D					
GS_Ashbya_gossypii	205	NAD	DFYNNL	QW	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	T	A	D	V	F	T	T	V	S	E	I	T	A	F	E	S	E	H	L	L	K	R	K	P	.	D					
GS_Saccharomyces_paradoxus	206	SF	DFYNNL	ES	VD	VD	EAG	R	F	G	I	Y	H	R	Y	C	I	E	R	A	A	H	S	A	D	V	F	T	T	V	S	E	I	T	A	F	E	A	E	H	L	L	K	R	K	P	.	D				
GYS1_Saccharomyces_cerevisiae	206	DV	DFYNNL	QY	FD	VD	EAG	KR	G	I	Y	H	R	Y	C	I	E	R	A	A	H	T	A	D	V	F	T	T	V	S	E	I	T	A	L	E	A	E	H	L	L	K	R	K	P	.	D					
GYS2_Saccharomyces_cerevisiae	206	SF	DFYNNL	ES	VD	VD	EAG	R	F	G	I	Y	H	R	Y	C	I	E	R	A	A	H	S	A	D	V	F	T	T	V	S	E	I	T	A	F	E	A	E	H	L	L	K	R	K	P	.	D				
GS_Caenorhabditis_briggsae	235	GAD	LYNNL	DA	FD	LD	EAG	KR	K	I	Y	H	Q	Y	C	L	E	R	A	A	C	Q	T	A	H	I	F	T	T	V	S	E	I	T	G	L	E	A	E	H	F	L	C	R	K	P	.	D				
GS_Caenorhabditis_elegans	235	GAD	LYNNL	DS	FD	LD	EAG	KR	K	I	Y	H	Q	Y	C	L	E	R	A	A	C	Q	T	A	H	I	F	T	T	V	S	E	I	T	G	L	E	A	E	H	F	L	C	R	K	P	.	D				
GS_Steinernema_feltiae	242	GAD	LYNNL	DK	FS	VD	N	E	A	G	K	K	N	I	Y	H	R	Y	C	I	E	R	A	A	S	H	A	H	T	F	T	T	V	S	E	I	T	G	L	E	A	E	H	L	L	K	R	K	P	.	D	
GS_Crassostrea_gigas	224	SS	DFYNNL	DK	YN	LV	K	E	A	G	D	R	Q	I	Y	H	C	Y	C	M	E	R	T	A	V	H	S	S	Q	V	F	I	S	V	S	E	I	T	E	V	E	A	E	H	L	L	K	R	K	P	.	NM
GS_Drosophila_pseudoobscura	228	NT	DFYNNM	DK	FA	VD	EAG	KR	Q	I	Y	H	R	Y	C	L	E	R	G	A	T	H	L	A	H	V	F	T	T	V	S	E	I	T	G	Y	E	A	E	H	L	L	K	R	K	P	.	D				
GS_Drosophila_melanogaster	228	NT	DFYNNL	DK	FA	VD	EAG	KR	Q	I	Y	H	R	Y	C	L	E	R	G	A	T	H	L	A	H	V	F	T	T	V	S	E	I	T	G	Y	E	A	E	H	L	L	K	R	K	P	.	D				
GS_Apis_mellifera	229	KT	DFYNNL	DL	FN	VD	EAG	KR	Q	I	Y	H	R	Y	C	M	E	R	A	A	T	H	L	A	H	I	F	T	T	V	S	E	I	T	G	F	E	A	E	H	L	L	K	R	K	P	.	D				
GS_Anopheles_Gambiae	228	NT	DFYNNL	DK	FP	VD	EAG	KR	Q	I	Y	H	R	Y	C	L	E	R	A	A	T	H	L	S	H	V	F	T	T	V	S	E	I	T	G	Y	E	A	E	H	L	L	K	R	K	P	.	D				
GS_Ciona_intestinalis	198	NV	DFYNNL	SN	FQ	VD	I	E	A	G	N	R	Q	I	Y	H	R	Y	C	M	E	R	A	A	H	S	A	H	V	F	A	T	V	S	D	I	T	S	L	E	A	E	H	L	L	K	R	K	P	.	D	
GS_Ciona_savignyi	198	NV	DFYNNL	DK	FK	VD	I	E	A	G	N	R	Q	I	Y	H	R	Y	C	M	E	R	A	A	T	H	S	A	H	V	F	T	T	V	S	D	I	T	A	L	E	A	Q	H	L	L	K	R	K	P	.	D
GYS1_Fugu_rubripes	216	NV	DFYNNL	SE	FN	VD	K	E	A	G	D	R	Q	I	Y	H	R	Y	C	I	E	R	A	A	H	C	A	H	V	F	S	T	V	S	K	I	T	A	I	E	A	E	H	L	L	K	R	K	P	.	D	
GYS1_Tetraodon_nigrovidiris	217	NV	DFYNNL	SE	FN	VD	K	E	A	G	D	R	Q	I	Y	H	R	Y	C	I	E	R	A	A	H	C	A	H	V	F	T	T	V	S	K	I	T	A	I	E	A	E	H	L	L	K	R	K	P	.	D	
GYS1_Danio_rerio	217	NV	DFYNNL	AE	FN	VD	K	E	A	G	D	R	Q	I	Y	H	R	Y	C	L	E	R	A	A	C	R	C	A	H	V	F	T	T	V	S	Q	I	T	A	I	E	A	E	H	L	L	K	R	K	P	.	D
GYS1_Pimephales_promelas	217	SV	DFYNNL	AD	FN	VD	K	E	A	G	D	R	Q	I	Y	H	R	Y	C	L	E	R	A	A	R	C	T	H	V	F	T	T	V	S	Q	I	T	A	I	E	A	E	H	L	L	K	R	K	P	.	D	
GYS1_Xenopus_tropicalis	217	NV	DFYNNL	QS	FN	VD	K	E	A	G	D	R	Q	I	Y	H	R	Y	C	M	E	R	A	A	V	C	S	H	V	F	T	T	V	S	Q	I	T	A	I	E	A	E	H	L	L	K	R	K	P	.	D	
GYS1_Rattus_norvegicus	217	AV	DFYNNL	EN	FN	VD	K	E	A	G	E	R	Q	I	Y	H	R	Y	C	M	E	R	A	A	H	C	A	H	V	F	T	T	V	S	Q	I	T	A	I	E	A	Q	H	L	L	K	R	K	P	.	D	
GYS1_Mus_musculus	217	AV	DFYNNL	EN	FI	VD	K	E	A	G	E	R	Q	I	Y	H	R	Y	C	M	E	R	A	A	H	C	A	H	V	F	T	T	V	S	Q	I	T	A	I	E	A	Q	H	L	L	K	R	K	P	.	D	
GYS1_Oryctolagus_cuniculus	217	AV	DFYNNL	EN	FN	VD	K	E	A	G	E	R	Q	I	Y	H	R	Y	C	M	E	R	A	A	H	C	A	H	V	F	T	T	V	S	Q	I	T	A	I	E	A	Q	H	L	L	K	R	K	P	.	D	
GYS1_Canis_familiaris	217	AV	DFYNNL	EN	FK	GD	K	E	A	G	E	R	Q	I	Y	H	R	Y	C	M	E	G	A	A	H	G	A	Q	V	C	T	T	V	S	Q	I	T	F	F	E	A	Q	H	L	L	K	R	K	P	.	D	
GYS1_Macaca_mulatta	217	AV	DFYNNL	EN	FN	VD	K	E	A	G	E	R	Q	I	Y	H	R	Y	C	M	E	R	A	A	H	C	A	H	V	F	T	T	V	S	Q	I	T	A	I	E	A	Q	H	L	L	K	R	K	P	.	D	
GYS1_Pongo_pygmaeus	217	AV	DFYNNL	EN	FN	VD	K	E	A	G	E	R	Q	I	Y	H	R	Y	C	M	E	R	A	A	H	C	A	H	V	F	T	T	V	S	Q	I	T	A	I	E	A	Q	Y	L	L	K	R	K	P	.	D	
GYS1_Homo_sapiens	217	AV	DFYNNL	EN	FN	VD	K	E	A	G	E	R	Q	I	Y	H	R	Y	C	M	E	R	A	A	H	C	A	H	V	F	T	T	V	S	Q	I	T	A	I	E	A	Q	H	L	L	K	R	K	P	.	D	
GYS2_Fugu_rubripes	220	NAD	DFYNNL	DK	FD	ID	R	E	A	G	D	R	Q	I	Y	H	R	Y	C	L	E	R	A	A	V	H	C	A	H	V	F	T	T	V	S	Q	I	T	A	V	E	A	N	H	M	L	H	R	K	P	.	D
GYS2_Tetraodon_nigrovidiris	220	NAD	DFYNNL	DK	FN	ID	R	E	A	G	E	R	Q	I	Y	H	R	Y	C	L	E	R	A	A	V	H	C	A	H	V	F	T	T	V	S	Q	I	T	A	V	E	A	N	H	M	L	H	R	K	P	.	D
GYS2_Danio_rerio	218	NAD	DFYNNL	DK	FD	ID	R	E	A	G	E	R	Q	I	Y	H	R	Y	C	L	E	R	A	A	V	H	C	A	H	V	F	T	T	V	S	Q	I	T	A	V	E	A	D	H	M	L	H	R	N	P	.	D
GYS2_Xenopus_laevis	218	NV	DFYNNL	DQ	FD	ID	R	E	A	G	D	R	E																																							

GS_Giardia_lamblia	301	VIT	Y	N	G	M	D	V	S	A	R	S	V	G	S	D	I	G	A	S	H	S	Y	H	G	K	I	L	D	F	C	R	G	H	F	Y	G	T	F	N	P	.	E	K	T	I	I	F	S	A	G	R	L	E	Y	K	N	K	G	Y						
GS_Dictyostelium_discoideum	258	V	I	L	P	N	G	L	K	L	D	K	F	T	A	L	H	.	E	F	Q	N	L	H	A	K	Y	K	G	V	L	N	E	F	V	R	G	H	F	Y	G	H	S	D	F	L	D	N	T	L	Y	F	T	A	G	R	H	E	F	F	N	K	G	V		
GS_Cryptococcus_neoformans	256	G	V	L	P	N	G	L	N	V	K	F	A	A	M	H	.	E	F	Q	N	L	H	V	Q	S	K	E	K	I	N	E	F	V	R	G	H	F	Y	G	H	S	D	F	L	D	N	T	I	Y	M	F	T	A	G	R	Y	E	F	R	N	K	G	V		
GS_Aspergillus_fumigatus	266	G	V	L	P	N	G	L	N	V	K	K	F	A	V	H	.	E	F	Q	N	L	H	S	Q	S	K	E	K	I	N	D	F	V	R	G	H	F	Y	G	H	N	D	F	L	D	N	T	L	Y	V	F	T	A	G	R	Y	E	F	R	N	K	G	V		
GS_Aspergillus_nidulans	263	G	V	L	P	N	G	L	N	V	K	K	F	S	A	V	H	.	E	F	Q	N	L	H	S	Q	S	K	E	K	I	N	E	F	V	R	G	H	F	Y	G	H	N	D	F	D	D	T	L	Y	V	F	T	S	G	R	Y	E	F	R	N	K	G	V		
GS_Gibberella_zeae	262	G	V	L	P	N	G	L	N	V	T	K	F	S	A	V	H	.	E	F	Q	N	L	H	Q	Q	A	K	E	K	I	H	D	F	V	R	G	H	F	Y	G	H	Y	D	F	D	V	N	T	L	Y	L	F	T	A	G	R	Y	E	F	R	N	K	G	V	
GS_Magnaporthe_grisea	263	G	V	L	P	N	G	L	N	V	T	K	F	A	A	M	H	.	E	F	Q	N	L	H	A	Q	S	K	E	K	I	H	D	F	V	R	G	H	F	Y	G	H	Y	D	F	E	P	E	N	T	L	Y	F	F	T	A	G	R	Y	E	F	R	N	K	G	C
GS_Neurospora_crassa	262	G	V	L	P	N	G	L	N	V	T	K	F	S	A	M	H	.	E	F	Q	N	L	H	Q	Q	N	K	E	K	I	H	D	F	V	R	G	H	F	Y	G	H	Y	D	F	E	P	E	N	T	L	Y	F	F	T	A	G	R	Y	E	F	R	N	K	G	V
GS_Ustilago_maydis	261	G	V	L	P	N	G	L	N	V	T	K	F	S	A	M	H	.	E	F	Q	N	L	H	A	V	S	K	A	K	I	N	E	F	V	K	G	H	F	Y	G	H	Y	D	F	L	D	N	T	L	Y	F	F	T	A	G	R	Y	E	F	R	N	K	G	V	
GS_Debaryomyces_hansenii	256	G	V	L	P	N	G	L	N	V	K	F	Q	A	V	H	.	E	F	Q	N	L	H	A	L	K	K	E	K	I	N	E	F	V	K	G	H	F	Y	G	N	Y	D	F	D	L	D	N	T	L	Y	F	F	I	A	G	R	Y	E	F	R	N	K	G	C	
GS_Kluyveromyces_lactis	262	G	I	L	P	N	G	L	N	V	I	K	F	Q	A	V	H	.	E	F	Q	N	L	H	A	L	K	K	E	K	I	N	D	F	I	R	G	H	F	H	G	Q	F	D	F	L	E	K	T	L	Y	F	F	I	A	G	R	Y	E	F	R	N	K	G	A	
GS_Yarrowia_lipolytica	259	G	V	V	P	N	G	L	N	V	K	F	S	A	M	H	.	E	F	Q	N	L	H	A	L	M	K	D	K	I	N	Q	F	V	K	G	H	F	Y	G	H	L	D	F	D	L	D	D	T	L	Y	T	F	T	A	G	R	Y	E	F	R	N	K	G	V	
GS_Candida_albicans	256	G	V	L	P	N	G	L	N	V	K	F	Q	A	V	H	.	E	F	Q	N	L	H	A	I	K	K	A	K	I	N	E	F	V	K	G	H	F	Y	G	N	Y	D	F	D	L	D	N	T	L	Y	F	F	I	A	G	R	Y	E	F	R	N	K	G	C	
GS_Candida_glabrata	265	G	I	L	P	N	G	L	N	V	I	K	F	Q	A	V	H	.	E	F	Q	N	L	H	A	L	K	K	E	K	I	N	D	F	V	R	A	H	F	H	G	N	F	D	F	L	D	N	T	L	Y	F	F	I	A	G	R	Y	E	F	R	N	K	G	A	
GS_Ashbya_gossypii	264	G	I	L	P	N	G	L	N	V	I	K	F	Q	T	V	H	.	E	F	Q	N	L	H	A	L	K	K	E	K	I	H	D	F	V	R	G	H	F	H	W	N	Y	D	F	D	L	D	K	T	L	Y	F	F	I	A	G	R	Y	E	F	R	N	K	G	A
GS_Saccharomyces_paradoxus	265	G	I	L	P	N	G	L	N	V	I	K	F	Q	A	F	H	.	E	F	Q	N	L	H	A	L	K	K	E	K	I	N	D	F	V	R	G	H	F	H	G	C	F	D	F	L	D	N	T	L	Y	F	F	I	A	G	R	Y	E	F	R	N	K	G	A	
GSY1_Saccharomyces_cerevisiae	265	G	I	L	P	N	G	L	N	V	I	K	F	Q	A	V	H	.	E	F	Q	N	L	H	A	L	K	K	D	K	I	N	D	F	V	R	G	H	F	H	G	C	F	D	F	L	D	N	T	V	Y	F	F	I	A	G	R	Y	E	F	R	N	K	G	A	
GSY2_Saccharomyces_cerevisiae	265	G	I	L	P	N	G	L	N	V	I	K	F	Q	A	F	H	.	E	F	Q	N	L	H	A	L	K	K	E	K	I	N	D	F	V	R	G	H	F	H	G	C	F	D	F	L	D	N	T	L	Y	F	F	I	A	G	R	Y	E	F	R	N	K	G	A	
GS_Caenorhabditis_briggsae	294	I	L	T	P	N	G	L	N	V	I	K	F	A	A	L	H	.	E	F	Q	N	L	H	A	Q	N	K	E	K	I	N	Q	F	I	R	G	H	F	H	G	H	L	D	F	D	L	D	K	T	L	Y	F	F	T	A	G	R	Y	E	F	S	N	K	G	D
GS_Caenorhabditis_elegans	294	V	L	T	P	N	G	L	N	V	I	K	F	A	A	L	H	.	E	F	Q	N	L	H	A	Q	N	K	E	K	I	N	Q	F	I	R	G	H	F	H	G	H	L	D	F	D	L	D	K	T	L	Y	F	F	T	A	G	R	Y	E	F	S	N	K	G	D
GS_Steinernema_feltiae	301	I	I	T	P	N	G	L	N	V	I	K	F	A	A	L	H	.	E	F	Q	N	L	H	A	M	A	K	E	K	V	H	D	F	V	R	G	H	F	Y	G	H	L	N	D	L	D	K	T	L	Y	M	F	T	A	G	R	Y	E	F	R	N	K	G	D	
GS_Crassostrea_gigas	284	I	V	P	P	N	G	L	N	V	K	F	S	T	I	H	.	E	F	Q	N	M	H	A	I	C	K	E	K	I	H	D	I	V	R	G	H	F	Y	G	H	Y	D	F	D	L	D	K	T	L	Y	F	F	T	A	G	R	Y	E	F	S	N	K	G	A	
GS_Drosophila_pseudoobscura	287	I	I	T	P	N	G	L	N	V	K	K	F	S	A	I	H	.	E	F	Q	N	M	H	A	V	A	K	E	K	I	N	E	F	V	R	G	H	F	Y	G	H	M	D	F	D	L	D	K	T	L	Y	F	F	I	A	G	R	Y	E	F	G	N	K	G	A
GS_Drosophila_melanogaster	287	I	I	T	P	N	G	L	N	V	K	K	F	S	A	I	H	.	E	F	Q	N	L	H	A	V	A	K	E	K	I	N	E	F	V	R	G	H	F	Y	G	H	I	D	F	D	L	D	K	T	L	Y	F	F	I	A	G	R	Y	E	F	R	N	K	G	A
GS_Apis_mellifera	288	I	I	T	P	N	G	L	N	V	K	K	F	A	A	L	H	.	E	F	Q	N	L	H	A	V	S	K	E	K	I	H	E	F	V	R	G	H	F	Y	G	H	Y	D	F	D	L	D	K	T	L	Y	F	F	I	A	G	R	Y	E	F	G	N	K	G	A
GS_Anopheles_Gambiae	287	I	I	T	P	N	G	L	N	V	K	K	F	A	A	I	H	.	E	F	Q	N	M	H	A	M	A	K	E	K	I	H	E	F	T	R	G	H	F	Y	G	H	F	N	F	N	I	E	K	T	L	Y	M	F	I	A	G	R	Y	E	F	S	N	K	G	A
GS_Ciona_intestinalis	257	L	I	L	P	N	G	L	S	I	K	N	A	C	M	H	.	E	F	Q	N	L	H	A	I	A	K	E	K	I	H	H	F	V	R	G	H	F	Y	G	H	F	D	L	N	L	D	K	T	L	Y	M	F	I	A	G	R	Y	E	F	S	N	K	G	A	
GS_Ciona_savignyi	257	L	I	L	P	N	G	L	S	I	K	N	T	Q	C	M	H	.	E	F	Q	N	L	H	A	I	A	K	E	K	I	H	N	F	V	R	G	H	F	Y	G	H	F	D	L	N	L	D	K	T	L	Y	M	F	I	A	G	R	Y	E	F	S	N	K	G	A
GYS1_Fugu_rubripes	275	I	I	T	P	N	G	L	N	V	K	K	F	S	A	M	H	.	E	F	Q	N	L	H	A	Q	S	K	N	R	I	Q	E	F	V	R	G	H	F	Y	G	H	L	D	F	N	L	D	K	C	L	F	L	F	I	A	G	R	Y	E	F	S	N	K	G	A
GYS1_Tetraodon_nigrovidiris	276	I	V	T	P	N	G	L	N	V	K	K	F	S	A	M	H	.	E	F	Q	N	L	H	A	Q	S	K	N	R	I	Q	E	F	I	R	G	H	F	Y	G	H	L	D	F	N	L	D	K	C	L	F	L	F	I	A	G	R	Y	E	F	S	N	K	G	A
GYS1_Danio_rerio	276	I	V	T	P	N	G	L	N	V	K	K	F	S	A	M	H	.	E	F	Q	N	L	H	A	Q	S	K	A	R	I	Q	E	F	V	R	G	H	F	Y	G	H	L	D	F	N	L	D	K	T	V	F	L	F	I	A	G	R	Y	E	F	S	N	K	G	A
GYS1_Pimephales_promelas	276	I	V	T	P	N	X	L	N	V	K	K	F	S	A	M	H	.	E	F	Q	N	L	H	A	Q	S	K	A	R	I	Q	E	F	V	R	G	H	F	Y	G	H	L	D	F	N	L	D	K	T	V	F	L	F	I	A	G	R	Y	E	F	S	N	K	G	A
GYS1_Xenopus_tropicalis	276	I	V	T	P	N	G	L	N	V	K	K	F	S	A	M	H	.	E	F	Q	N	L	H	A	Q	S	K	G	R	I	Q	E	F	I	R	G	H	F	Y	G	H	L	D	F	N	L	D	K	T	L	F	F	F	I	A	G	R	Y	E	F	S	N	K	G	A
GYS1_Rattus_norvegicus	276	I	V	T	P	N	G	L	N	V	K	K	F	S	A	M	H	.	E	F	Q	N	L	H	A	Q	S	K	A	R	I	Q	E	F	V	R	G																													

GS_Giardia_lamblia	366	MFLDALHSLNERFFRDP	LLEDYKDI	TVVGI	IAPS	QVSQYQVD	TLKGISLMQETK	DC	TRL	LANKI	STNLV																																		
GS_Dictyostelium_discoideum	324	MFLDSLGLNKLLOQSGSKM	TVVAF	IMPAA	TNNFNVE	SLKGHSYLKDMRRT	CNT	IVEAM	GERLF																																			
GS_Cryptococcus_neoformans	321	MFIESLARLNHR	LKKMGSKT	TVVAF	IMPAA	TNSYTI	EAL	KGQAV	TSQ	LKDC	VEQ	TNRI	SKRIF																															
GS_Aspergillus_fumigatus	331	MFIEGLARLNHR	LKASGSKT	TVVAF	IMPAA	TSSLTVE	AL	KGQAV	VKSL	RDT	IEM	IEKSI	GKRMV																															
GS_Aspergillus_nidulans	328	MFIEGLARLNHR	LKSSGSKT	TVVAF	IMPAA	TSSLTVE	SL	KGQAV	VKSL	RDT	IHM	IEQGI	GKRMV																															
GS_Gibberella_zeae	327	MFIESLARLNHR	LKASGSKT	TVVAF	IMPAA	TSSLTVE	AL	KGQAV	VKSL	RDT	THV	IEQSI	GRRLF																															
GS_Magnaporthe_grisea	328	MFIESLARLNHR	LKASGSKT	TVVAF	IMPAA	TSSLTVE	AL	RGQAV	VKSL	RDT	VDV	IEKSI	GRRIF																															
GS_Neurospora_crassa	327	MFIESLARLNHR	LKTAGSKT	TVVAF	IMPAA	TSSLTVE	AL	KGQAV	VKSL	RDT	VDV	I	ERGI	GRRIF																														
GS_Ustilago_maydis	326	MFIESLARLNHR	LKQSGSKT	TVVAF	IMPAA	TNSYTI	EAL	KGQAV	TQ	L	RDT	VEQ	I	QARV	GERLF																													
GS_Debaryomyces_hansenii	321	FFVESLARLNHR	LKEAGSKM	TLVAF	IMP	GKTNSY	TVE	TL	KGQAV	I	KQ	E	GT	EEV	Q	KKV	GERLF																											
GS_Kluyveromyces_lactis	327	MFIESLARLNHR	LKASGSKM	TVVAF	IMPAA	KNSY	TVE	EL	RGQAV	V	RQ	L	ENS	V	KD	V	TQ	L	I	G	K	R	I	F																				
GS_Yarrowia_lipolytica	324	MFIESLARLNHR	LKSEKSTK	TIVAF	IMPAA	TSSY	TVE	T	L	KGQAV	M	K	A	L	E	D	T	V	N	E	I	Q	Q	I	G	R	R	M	L															
GS_Candida_albicans	321	FFIESLARLNHR	LKEAGSKT	TVVAF	IMP	GKTQ	S	T	V	E	T	L	KGQAV	V	K	Q	E	S	T	I	G	E	V	Q	K	K	V	GERLF																
GS_Candida_glabrata	330	MFVEALARLNHR	LKMAGSKK	TVVAF	IMPAA	QNS	F	T	V	E	A	L	R	S	Q	A	V	V	K	S	L	E	N	T	V	N	E	V	T	S	L	I	G	K	R	I	F							
GS_Ashbya_gossypii	329	MFIEALARLNHR	LKAAGSKM	TVIAF	IMPAA	KNSY	TVE	EAL	KGQAV	V	K	A	L	E	S	T	V	K	D	V	N	E	I	Q	Q	I	G	R	R	L	F													
GS_Saccharomyces_paradoxus	330	MFIEALARLNHR	LKVSGSKK	TVVAF	IMPAA	KNS	F	T	V	E	A	L	R	S	Q	A	V	V	K	S	L	E	N	T	V	N	E	V	T	S	I	G	K	R	I	F								
GSY1_Saccharomyces_cerevisiae	330	MFIEALARLNHR	LKVSGSKK	TVVAF	IMPAA	KNS	F	T	V	E	A	L	R	S	Q	A	V	V	K	S	L	E	N	T	V	N	E	V	T	S	I	G	K	R	I	F								
GSY2_Saccharomyces_cerevisiae	330	MFIEALARLNHR	LKVSGSKK	TVVAF	IMPAA	KNS	F	T	V	E	A	L	R	S	Q	A	V	V	K	S	L	E	N	T	V	N	E	V	T	S	I	G	K	R	I	F								
GS_Caenorhabditis_briggsae	359	MFIESLARLNHR	LKTTND	PR	HM	GV	TVVAF	L	I	P	A	P	A	N	S	F	N	V	E	S	L	K	G	Q	A	V	T	K	Q	L	K	E	A	V	D	R	I	K	E	K	V	Q	R	I	F
GS_Caenorhabditis_elegans	359	MFIESLARLNHR	LKTTSD	PR	HM	GV	TVVAF	L	I	P	A	P	A	N	S	F	N	V	E	S	L	K	G	Q	A	V	T	K	Q	L	K	E	A	V	D	R	I	K	E	K	V	Q	R	I	F
GS_Steinernema_feltiae	366	FFIESLARLNHR	LKTTSD	PR	CK	DV	TVIAF	L	I	P	A	A	N	S	F	N	V	E	S	L	K	G	Q	A	V	C	K	Q	L	K	D	T	I	S	K	I	Q	E	N	V	A	S	R	M	L
GS_Crassostrea_gigas	349	MFIESLARLNHR	LKQANSEA	TVVAF	L	I	F	P	T	K	T	N	N	F	N	V	E	S	L	R	G	H	A	V	I	K	Q	L	K	E	T	V	H	H	V	Q	T	I	G	K	R	I	F	
GS_Drosophila_pseudoobscura	352	IFIEALARLNHR	LKHERPDT	TVVAF	L	I	F	P	T	K	T	N	N	F	N	V	E	S	L	R	G	H	A	V	I	K	Q	L	R	D	T	I	N	N	V	Q	Q	A	V	G	K	R	M	F
GS_Drosophila_melanogaster	352	IFIEALARLNHR	LKHERPDT	TVVAF	L	I	F	P	T	K	T	N	N	F	N	V	E	S	L	R	G	H	A	V	I	K	Q	L	R	D	T	I	N	N	V	Q	Q	A	V	G	K	R	M	F
GS_Apis_mellifera	353	IFIEALARLNHR	LKTSRPDI	TIVAF	L	I	F	P	A	T	T	N	N	F	N	V	E	S	L	R	G	H	A	V	T	K	S	L	R	D	T	I	N	D	I	Q	Q	K	I	G	K	R	M	V
GS_Anopheles_Gambiae	352	IFIEALARLNHR	LKSSNSDV	TVVAF	L	I	F	P	A	T	T	N	N	F	N	V	E	S	L	R	G	H	A	V	T	K	S	L	R	D	T	I	N	S	I	Q	Q	D	I	G	K	R	M	V
GS_Ciona_intestinalis	322	LYIEAMSRLNHR	LKMINNSDV	TVIAF	L	I	F	P	A	S	T	N	N	F	N	V	E	S	L	K	G	Q	A	V	V	K	Q	L	K	E	T	V	D	V	I	K	D	D	I	G	N	K	L	F
GS_Ciona_savignyi	322	LYIEAMSRLNHR	LKMINNSEV	TVVAF	L	I	F	P	A	S	T	N	N	F	N	V	E	S	L	K	G	Q	A	V	V	K	Q	L	K	E	T	V	D	V	I	K	D	D	I	G	H	K	L	F
GYS1_Fugu_rubripes	340	LFLIESLARLNHR	LRVSHSDL	TVIAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	Q	T	V	K	E	R	F	G	K	K	L	V			
GYS1_Tetraodon_nigrovidiris	341	LFLIEALARLNHR	LRVSHSDV	TVIAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	Q	T	V	K	E	R	F	G	K	K	L	V			
GYS1_Danio_riero	341	IFLEALARLNHR	LRRVNSEV	TVIAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	Q	T	V	K	E	R	F	G	K	K	L	V			
GYS1_Pimephales_promelas	341	IFLEALARLNHR	LRRVNSEV	TVIAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	Q	T	V	K	E	R	F	G	K	K	L	V			
GYS1_Xenopus_tropicalis	341	VFLEALARLNHR	LRRVNSET	TLVAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	N	T	V	K	E	K	F	G	R	K	L	V			
GYS1_Rattus_norvegicus	341	IFLEALARLNHR	LRRVNSEQ	TVVAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	N	T	V	K	E	K	F	G	R	K	L	V			
GYS1_Mus_musculus	341	VFLEALARLNHR	LRRVNSEQ	TVVAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	N	T	V	K	E	K	F	G	R	K	L	V			
GYS1_Oryctolagus_cuniculus	341	VFLEALARLNHR	LRRVNSEQ	TVVAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	N	T	V	K	E	K	F	G	R	K	L	V			
GYS1_Canis_familiaris	341	VFLEALARLNHR	LRRVNSEQ	TVVAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	N	T	V	K	E	K	F	G	R	K	L	V			
GYS1_Macaca_mulatta	341	VFLEALARLNHR	LRRVNSEQ	TVVAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	N	T	V	K	E	K	F	G	R	K	L	V			
GYS1_Pongo_pygmaeus	341	VFLEALARLNHR	LRRVNSEQ	TVVAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	N	T	V	K	E	K	F	G	R	K	L	V			
GYS1_Homo_sapiens	341	VFLEALARLNHR	LRRVNSEQ	TVVAF	F	IMP	A	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	N	T	V	K	E	K	F	G	R	K	L	V			
GYS2_Fugu_rubripes	348	LFLIESLARLNHR	LRRVHRNDV	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	S	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	H	T	V	K	E	K	F	G	K	K	L	V		
GYS2_Tetraodon_nigrovidiris	345	LFLIESLARLNHR	LRRVHRNDM	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	S	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	H	T	V	K	E	K	F	G	K	K	L	V		
GYS2_Danio_riero	342	LFLIESLARLNHR	LRRVHKSDV	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	S	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	Q	S	V	K	E	K	F	G	K	K	L	V		
GYS2_Xenopus_laevis	342	IFLEALSRLNHR	LRRVHRSDV	TVVVF	F	IMP	T	K	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	H	S	V	K	E	K	F	G	K	K	L	V		
GYS2_Xenopus_tropicalis	342	IFLEALSRLNHR	LRRVHRSDV	TVVVF	F	IMP	T	K	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	H	S	V	K	E	K	F	G	K	K	L	V		
GYS2_Gallus_gallus	342	MFLIEALSRLNHR	LRRVHKSDV	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	Q	S	V	K	E	K	F	G	K	K	L	V		
GYS2_Monodelphis_domestica	341	IFLEALSRLNHR	LRRVHKNDV	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	N	S	V	K	E	K	F	G	K	K	L	V		
GYS2_Mus_musculus	341	IFLEALSRLNHR	LRRMHKSNV	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	A	H	S	V	K	E	K	F	G	K	K	L	V		
GYS2_Rattus_norvegicus	341	IFLEALSRLNHR	LRRMHKSNV	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	T	V	H	C	M	K	E	K	F	G	K	K	L	V		
GYS2_Bos_taurus	340	IFLEALSRLNHR	LRRMHKSDV	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	T	L	K	G	P	G	S	A	Q	T	R	D	T	A	H	S	V	K	E	K	F	G	K	K	L	V			
GYS2_Canis_familiaris	341	IFLEALSRLNHR	LRRMHKSDV	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	I	A	H	S	V	K	E	K	F	G	K	K	L	V		
GYS2_Macaca_mulatta	341	IFLEALSRLNHR	LRRMHKSDV	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	I	A	H	S	V	K	E	K	F	G	K	K	L	V		
GYS2_Homo_sapiens	341	IFLEALSRLNHR	LRRMHKSDI	TVVVF	F	IMP	A	K	T	N	N	F	N	V	E	T	L	K	G	Q	A	V	R	K	Q	L	W	D	V	A	H	S	V	K	E	K	F	G	K	K	L	V		

GS_Giardia_lamblia	436	DLLTNTALSON.....LASLTLGD	LLSKNDIVL	MKRCQSSYASRNN	LPSTMTHTLRDP	PSLQDAT	EPI		
GS_Dictyostelium_discoideum	389	EATSRGKMIS.....PEE	LLSQEDLVM	LKRRIFALKQKSS	GPPVV	TNMIN	DNDEI		
GS_Cryptococcus_neoformans	386	EHACRYSGEHG.....TEVNPED	LLSNE	DRVLLKRRVFAL	KRNS	LPPIV	TNMIN	ANDEI	
GS_Aspergillus_fumigatus	396	ERCLAWKEGD.....NMPDEKD	LITSQDRVL	LRRRLFAM	KRHG	LPPIV	TNMIN	HEDEI	
GS_Aspergillus_nidulans	393	ERCLAWKEGD.....NMPDEKD	LITSQDRVL	LRRRLFAM	KRHT	LPPIV	TNMIN	SEDEI	
GS_Gibberella_zeae	392	ERSLKWHEGE.....PLPDEKE	LISAQDRVL	LRRRLFAM	KRHG	LPPIV	TNMIN	HEDEI	
GS_Magnaporthe_grisea	393	ERSLKWHHDGD.....PLPDEKE	LITSQDRVL	LRRRLFAM	KRHG	LPPIV	TNMIN	SEDEI	
GS_Neurospora_crassa	392	ERSVKWHEGD.....PLPEEKE	LITSQDRVL	LRRRLFAM	KRHT	LPPIV	TNMIN	HEDEI	
GS_Ustilago_maydis	391	EKMARYQGETG.....SDVIDPAT	LLSDADKIA	LKRRIFAL	KRNS	LPPIV	TNMIN	DNDEI	
GS_Debaryomyces_hansenii	386	EHCARFPNNHSTTTA	NGNEVPSIDD	LKPADRVL	LKRRIFAL	KRDG	LPPIV	TNMTDD	STDPV
GS_Kluyveromyces_lactis	392	EHAMRYPHNG.....TKTEIPTSIDE	LFKPSDKVV	LKRRVFAL	RRPEGT	LPPIV	TNMTDD	ANDEI	
GS_Yarrowia_lipolytica	389	DHACARHNSHDG.....KEIPGLDQ	LLSPS	DRVLLKRRVFAL	KRET	FPPIV	TNMTDD	STDPV	
GS_Candida_albicans	386	EYCARYPN..TDHH	GNDEVPTIDE	LKPADRVL	LKRRIFAL	KRDG	LPPIV	TNMTDD	STDPV
GS_Candida_glabrata	395	EHAMKFPHNG.....ITNEIPNNLEE	LLKPSDKVL	LKRRVLA	RRPYGEL	LPPIV	TNMTDD	ANDEI	
GS_Ashbya_gossypii	394	EHAMRYPRSG.....KSEIPTDLGE	LLKPSDKVM	LKRRVFAL	RRPESS	LPPIV	TNMTDD	ANDEI	
GS_Saccharomyces_paradoxus	395	DHAIRFPHNG.....LTTELPTDLSE	LLKSSDKVM	LKRRILA	RRPEGQL	LPPIV	TNMTDD	ANDEI	
GYS1_Saccharomyces_cerevisiae	395	EHTMRYPHNG.....LESELPTNLDE	LLKSSDKVL	LKRRVLA	RRPYGEL	FPPIV	TNMTDD	ANDEI	
GYS2_Saccharomyces_cerevisiae	395	DHAIRYPHNG.....LTTELPTDLGE	LLKSSDKVM	LKRRILA	RRPEGQL	LPPIV	TNMTDD	ANDEI	
GS_Caenorhabditis_briggsae	428	DICLQGHLP.....PEELM	SPADNILL	LKRCIMSL	HNSS	LPPIV	TNMTDD	ADDPV	
GS_Caenorhabditis_elegans	428	DICLQGHLP.....PEELM	SPADNILL	LKRCIMSL	HNSS	LPPIV	TNMTDD	ADDPV	
GS_Steinernema_feltiae	435	ESCVRGQIPE.....RDD	LLHPAEMVQ	LKRCILA	ARRDG	LPPIV	TNMTDD	ADDPV	
GS_Crassostrea_gigas	414	EQSLKGGKILT.....GDE	ILEQEDIVK	LKRCIYSA	QRNS	LPPIV	TNMTDD	ANDEI	
GS_Drosophila_pseudoobscura	417	DTCVKGRLE.....VGD	LLKDDMVK	IKRCMYAM	QRNS	MPPIV	TNMTDD	WNPV	
GS_Drosophila_melanogaster	417	DTCLQGNIPN.....ADD	LLQKDDLVK	IKRCMFAM	QRNS	MPPIV	TNMTDD	WNPV	
GS_Apis_mellifera	418	EMCLSGRMPD.....VQD	LLQKEDTIK	IKRCLYAL	QRNG	LPPIV	TNMTDD	WNPV	
GS_Anopheles_Gambiae	417	ETCLQGLPE.....GAE	ILTKEDIVK	IKRCLYAL	QRNG	NPPIV	TNMTDD	WNPV	
GS_Ciona_intestinalis	387	DLCIRGKLPN.....EEQ	LLDRDHVIK	LKRCMYAN	QCST	LPPIV	TNMTDD	ANDEI	
GS_Ciona_savignyi	387	DLCIRGKLPN.....EEQ	LLDRDHVIK	LKRCMYAN	QCST	LPPIV	TNMTDD	ANDEI	
GYS1_Fugu_rubripes	405	ESLLVGQLPD.....VSK	MLDKE	DFTIMKRA	IFAT	QRQS	QPPV	TNMTDD	ANDEI
GYS1_Tetraodon_nigrovidiris	406	ESLLVGQLPD.....VSK	MLDKE	DFTIMKRA	IFAT	QRQS	QPPV	TNMTDD	ANDEI
GYS1_Danio_rerio	406	ESLLVGQLPD.....VSK	MLDKE	DFTIMKRA	IFAT	QRQS	QPPV	TNMTDD	ANDEI
GYS1_Pimephales_promelas	406	ESLLVGQLPD.....VSK	MLDKE	DFTIMKRA	IFAT	QRQS	LPPIV	TNMTDD	ANDEI
GYS1_Xenopus_tropicalis	406	ESLLVGNLPD.....MNK	MLDKE	DFTIMKRA	IFAT	QRHS	FPPIV	TNMTDD	ANDEI
GYS1_Rattus_norvegicus	406	ESLLVGSPLD.....MNK	MLDKE	DFTIMKRA	IFAT	QRQS	FPPIV	TNMTDD	ANDEI
GYS1_Mus_musculus	406	ESLLVGSPLD.....MNK	MLDKE	DFTIMKRA	IFAT	QRQS	FPPIV	TNMTDD	ANDEI
GYS1_Oryctolagus_cuniculus	406	ESLLVGSPLD.....MNK	MLDKE	DFTIMKRA	IFAT	QRQS	FPPIV	TNMTDD	ANDEI
GYS1_Canis_familiaris	406	ESLLVGSPLD.....MNK	KVGEVFTL	LRRALYGT	QRQS	FPPIV	TNMTDD	ANDEI	
GYS1_Macaca_mulatta	406	ESLLVGSPLD.....MNK	MLDKE	DFTIMKRA	IFAT	QRQS	FPPIV	TNMTDD	ANDEI
GYS1_Pongo_pygmaeus	406	ESLLVGSPLD.....MNK	MLDKE	DFTIMKRA	IFAT	QRQS	FPPIV	TNMTDD	ANDEI
GYS1_Homo_sapiens	406	ESLLVGSPLD.....MNK	MLDKE	DFTIMKRA	IFAT	QRQS	FPPIV	TNMTDD	ANDEI
GYS2_Fugu_rubripes	413	DALLKGEIPD.....MNS	ILDRD	DFTIMKRA	IYAT	QRHS	LPPIV	TNMTDD	ANDEI
GYS2_Tetraodon_nigrovidiris	410	DALLKGEIPD.....MNA	ILDRD	DFTIMKRA	IYAT	QRHS	LPPIV	TNMTDD	ANDEI
GYS2_Danio_rerio	407	ESLLRGEIPD.....MSK	ILDRD	DFTIMKRA	IYAT	QRHS	LPPIV	TNMTDD	ANDEI
GYS2_Xenopus_laevis	407	EALLKGEIPD.....LNK	ILDRD	DFTIMKRA	IFAT	QRQS	LPPIV	TNMTDD	ANDEI
GYS2_Xenopus_tropicalis	407	DALLKGEIPD.....LNK	ILDRD	DFTIMKRA	IFAT	QRQS	LPPIV	TNMTDD	ANDEI
GYS2_Gallus_gallus	407	NALLKGEIPD.....LSK	ILDRD	DFTIMKRA	IFST	QRHS	LPPIV	TNMTDD	ANDEI
GYS2_Monodelphis_domestica	406	DALLKGEIPD.....LNK	ILDRD	DFTIMKRA	IFST	QRQS	LPPIV	TNMTDD	ANDEI
GYS2_Mus_musculus	406	DGLLRGEIPD.....MNS	ILDRD	DFTIMKRA	IFST	QRQS	LPPIV	TNMTDD	ANDEI
GYS2_Rattus_norvegicus	406	DGLLRGEIPD.....MNS	ILDRD	DFTIMKRA	IFST	QRHS	LPPIV	TNMTDD	ANDEI
GYS2_Bos_taurus	405	DALLRGEIPD.....MNN	ILDRD	DFTIMKRA	IFST	QRQS	LPPIV	TNMTDD	ANDEI
GYS2_Canis_familiaris	406	DALLRGEIPD.....MNN	ILDRD	DFTIMKRA	IFST	QRQS	LPPIV	TNMTDD	ANDEI
GYS2_Macaca_mulatta	406	DALLRGEIPD.....MNN	ILDRD	DFTIMKRA	IFST	QRQS	LPPIV	TNMTDD	ANDEI
GYS2_Homo_sapiens	406	DALLRGEIPD.....LND	ILDRD	DFTIMKRA	IFST	QRQS	LPPIV	TNMTDD	ANDEI

GS_Giardia_lamblia	498	LVRMRELG	LVNQKE	SRVKVWVI	PEFVSKT	SPVGL	LDYNEFTL	GGSLGV	FCSLYEPW	GYTSP	ECCAGT	PS
GS_Dictyostelium_discoideum	440	LQHIRRIK	LFNSQE	DRVKVIYH	PEFLTST	NPILP	LDYEEFVR	GCHLGI	FPSYIEPF	GMTPAE	CASGCP	PS
GS_Cryptococcus_neoformans	443	LNQLRRVQ	LFNRPE	DRVKVI FH	PEFLNS	NPVLP	LDYDDFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	N
GS_Aspergillus_fumigatus	451	LNQIRRV	LFNYPT	DRVKVI FH	PEFLNS	NPVLP	LDYDDFVR	GTHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Aspergillus_nidulans	448	LNQIRRV	LFNQSS	DRKIVFH	PEFLNS	NPVLP	LDYDDFVR	GTHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Gibberella_zeae	447	LNQIRRV	LFNHPT	DRVKVI FH	PEFLNS	NPVLP	LDYDDFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Magnaporthe_grisea	448	LNQIRRV	LFNHPT	DRKIVFH	PEFLNS	NPVLP	LDYDDFVR	GTHLGV	FASVIEPF	GYTPAE	CTVMGVP	S
GS_Neurospora_crassa	447	LNQIRRV	LFNHPS	DRKIVFH	PEFLNS	NPVLP	LDYDDFVR	GTHLGV	FASVIEPF	GYTPAE	CTVMGVP	S
GS_Ustilago_maydis	448	LNQIRRV	LFNRST	DRVKVI FH	PEFLNS	NPVLP	LDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Debaryomyces_hansenii	449	LNHIRRV	LFNKPD	DRVKIIFH	PEFLNAN	NPILS	LDYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Kluyveromyces_lactis	453	LNQIRRV	LFNNSY	DRVKIIFH	PEFLNAN	NPILS	LDYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GS_Yarrowia_lipolytica	446	LNQIRRV	LFNRPE	DRVKIIFH	PEFLNS	NPVLP	LDYDDFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Candida_albicans	446	LNHIRRV	LFNKPE	DRVKIIFH	PEFLNAN	NPILS	LDYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GS_Candida_glabrata	456	LNQIRRV	LFNNSH	DRKVI FH	PEFLNAN	NPILS	LDYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Ashbya_gossypii	454	LNQIRRV	LFNNSP	DRVKIIFH	PEFLNAN	NPILS	LDYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Saccharomyces_paradoxus	456	LNKIRRV	LFNNSP	DRVKMI FH	PEFLNAN	NPILG	LDYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GSY1_Saccharomyces_cerevisiae	456	LNQIRRV	LFNNSP	DRKVI FH	PEFLNAN	NPILG	LDYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GSY2_Saccharomyces_cerevisiae	456	LNKIRRV	LFNNSP	DRVKMI FH	PEFLNAN	NPILG	LDYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Caenorhabditis_briggsae	478	LEALRR	TALFNKPE	DRVKVVFH	PEFLSSV	SPILG	LDYEDFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GS_Caenorhabditis_elegans	478	LESRR	TSLFNKPE	DRVKVVFH	PEFLSSV	SPILG	LDYEDFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GS_Steinernema_feltiae	486	LNAFRK	TNLINQHF	DRVKVI FH	PEFLSSV	SPILG	LDYEDFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGVP	S
GS_Crassostrea_gigas	465	LNALRR	CQLFNKPE	DRVKVVFH	PEFLNST	NPLFG	LDYEDFVR	GCHLGV	FASVIEPF	GYSPA	ECTVYG	IPS
GS_Drosophila_pseudoobscura	468	LASIRRV	CHLFNSVD	DRKVMVFH	PEFLNS	NPVLP	IDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GS_Drosophila_melanogaster	468	LSSIRRV	CHLFNSRH	DRKVMVFH	PEFLNST	NPLFG	IDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GS_Apis_mellifera	469	LNAIRRV	CNLFNTVH	DRKVI FH	PEFLS	STNPLFG	LDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GS_Anopheles_Gambiae	468	LESIRRV	CHLFNTKY	DRKVMVFH	PEFLNST	NPLFG	LDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GS_Ciona_intestinalis	438	LKQIRE	CKLFNARS	DRVKLI FH	PEFLS	QTSPLISM	DMYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CAIKGIP	S
GS_Ciona_savignyi	438	LKQIRE	CNLFNARS	DRVKLI FH	PEFLS	QTSPLISM	DMYDEFVR	GCHLGV	FPSYIEPF	GYTPAE	CAIKGIP	S
GYS1_Fugu_rubripes	456	LNSVRR	IGLFNSSD	DRVKIIFH	PEFLS	STSPLLP	MDYEDFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Tetraodon_nigrovidiris	457	LNCVRR	IGLFNSSA	DRVKIIFH	PEFLS	STSPLLP	MDYEDFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Danio_erio	457	LNCIRRV	IGLFNSSA	DRKVI FH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Pimephales_promelas	457	LHCIRRV	IGLFNSSD	DRKVI FH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Xenopus_tropicalis	457	LNTIRRV	IGLFNSSS	DRKVI FH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Rattus_norvegicus	457	LTTIRRV	IGLFNSSA	DRKVI FH	PEFLS	STSPLLP	VDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Mus_musculus	457	LTTIRRV	IGLFNSSA	DRKVI FH	PEFLS	STSPLLP	VDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Oryctolagus_cuniculus	457	LTTIRRV	IGLFNSSA	DRKVI FH	PEFLS	STSPLLP	VDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Canis_familiaris	457	LTTIRRV	IGLFNSSA	DRKVI FH	PEFLS	STSPLLP	VDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Macaca_mulatta	457	LTTIRRV	IGLFNSSA	DRKVI FH	PEFLS	STSPLLP	VDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Pongo_pygmaeus	457	LTTIRRV	IGLFNSSA	DRKVI FH	PEFLS	STSPLLP	VDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS1_Homo_sapiens	457	LTTIRRV	IGLFNSSA	DRKVI FH	PEFLS	STSPLLP	VDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Fugu_rubripes	464	LNSIRRV	ISLFNSRD	DRVKIIFH	PEFLS	STSPLLP	MDYEDFVR	GNLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Tetraodon_nigrovidiris	461	LNSIRRV	ISLFNSRN	DRVKIIFH	PEFLS	STSPLLP	MDYEDFVR	GNLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Danio_erio	458	LGNIRRV	IGLFNGRN	DRKVI FH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPGE	CTVMGIP	S
GYS2_Xenopus_laevis	458	LNTVRR	IGLFNSTR	DRVKIIFH	PEFLS	STSPLLP	LDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Xenopus_tropicalis	458	LNTIRRV	IGLFNSTR	DRKVI FH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Gallus_gallus	458	LNTIRRV	IGLFNSTR	DRKVI FH	PEFLS	STSPLLP	LDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Monodelphis_domestica	457	LSTIRRV	IGLFNSTR	DRKVI LH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Mus_musculus	457	LSTIRRV	IGLFNSTR	DRKVI LH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Rattus_norvegicus	457	LSTIRRV	IGLFNSTR	DRKVI LH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Bos_taurus	456	LSTIRRV	IGLFNSTR	DRKVI LH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Canis_familiaris	457	LSTIRRV	IGLFNSTR	DRKVI LH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Macaca_mulatta	457	LSTIRRV	IGLFNSTR	DRKVI LH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S
GYS2_Homo_sapiens	457	LSTIRRV	IGLFNSTR	DRKVI LH	PEFLS	STSPLLP	MDYEEFVR	GCHLGV	FPSYIEPF	GYTPAE	CTVMGIP	S

GS_Giardia_lamblia	567	I V S N L C G F G S F I E S M V S R D	TFKNRSKSVIEQSERLHHVASLTSISNLNSKRYPHSGSVSDYGASPRDSDT
GS_Dictyostelium_discoideum	510	I T S N L T G F A N Y M S R A L Q D T
GS_Cryptococcus_neoformans	513	I T T N L S G F G C F M E D L L E S P
GS_Aspergillus_fumigatus	521	I T T N L S G F G C Y M E E L I E N S
GS_Aspergillus_nidulans	518	I T T N L S G F G C Y M E E L I E N S
GS_Gibberella_zeae	517	I T T N L S G F G C Y M E E L I E N S
GS_Magnaporthe_grisea	518	I T T N L S G F G C Y M E E L I E N S
GS_Neurospora_crassa	517	I T T N L S G F G C Y M E E L I E N S
GS_Ustilago_maydis	518	I T T N L S G F G C F M E D T I E R G
GS_Debaryomyces_hansenii	519	I T T N L S G F G C Y M E D L I E N T
GS_Kluyveromyces_lactis	523	I T T N L S G F G A Y M E D L I E K D Q A
GS_Yarrowia_lipolytica	516	I T T N L S G F G C Y M E D L I E N . A
GS_Candida_albicans	516	I T T N L S G F G C Y M N D L V E N P
GS_Candida_glabrata	526	I T T N L S G F G A Y M E D L I E T N Q A
GS_Ashbya_gossypii	524	I T T N L S G F G A Y M E D L I E R D Q A
GS_Saccharomyces_paradoxus	526	I T T N V S G F G A Y M E D L I E T N Q A
GSY1_Saccharomyces_cerevisiae	526	I T T N V S G F G A Y M E D L I E T D Q A
GSY2_Saccharomyces_cerevisiae	526	I T T N V S G F G A Y M E D L I E T N Q A
GS_Caenorhabditis_briggsae	548	V S T N L S G F G C F M Q E H V E D H
GS_Caenorhabditis_elegans	548	V S T N L S G F G C F M Q E H V E D H
GS_Steinernema_feltiae	556	V T T N L S G F G C F I Q D S V H E P
GS_Crassostrea_gigas	535	I S T N L S G F G C F M Q E H I N D P
GS_Drosophila_pseudoobscura	538	V T T N L S G F G C F M Q E H I S D P
GS_Drosophila_melanogaster	538	V T T N L S G F G C F M E E H I S D P
GS_Apis_mellifera	539	I T T N L S G F G C F M Q E H I A D P
GS_Anopheles_Gambiae	538	I T T N L S G F G C F M H E H V A D P
GS_Ciona_intestinalis	508	V T S N L S G F G C F M Q S H L S D P
GS_Ciona_savignyi	508	V T S N L S C F G C F M Q S H L S D P
GYS1_Fugu_rubripes	526	I S T N L S G F G C F M E E H I A D P
GYS1_Tetraodon_nigrovidiris	527	V S T N L S G F G C F M E E H I A D P
GYS1_Danio_rerio	527	I S T N L S C F G C F M E E H I A D P
GYS1_Pimephales_promelas	527	I S T N L S G F G C F M E E H I A D P
GYS1_Xenopus_tropicalis	527	V S T N L S G F G C F M E E H I A D P
GYS1_Rattus_norvegicus	527	I S T N L S G F G C F M E E H I A D P
GYS1_Mus_musculus	527	I S T N L S G F G C F M E E H I A D P
GYS1_Oryctolagus_cuniculus	527	I S T N L S G F G C F M E E H I A D P
GYS1_Canis_familiaris	527	I S T N L S G F G C F M E E H I A D P
GYS1_Macaca_mulatta	527	I S T N L S G F G C F M E E H I A D P
GYS1_Pongo_pygmaeus	527	I S T N L S G F G C F M E E H I A D P
GYS1_Homo_sapiens	527	I S T N L S G F G C F M E E H I A D P
GYS2_Fugu_rubripes	534	V T T N L S G F G C F M E E H V S D P
GYS2_Tetraodont_nigrovidiris	531	V T T N L S G F G C F M E E H V S D P
GYS2_Danio_rerio	528	V T T N L S G F G C F M E E H V S D P
GYS2_Xenopus_laevis	528	V T T N L S G F G C F M Q E H V A D P
GYS2_Xenopus_tropicalis	528	V T T N L S G F G C F M Q E H V A D P
GYS2_Gallus_gallus	528	V T T N L S G F G C F M Q E H V A D P
GYS2_Monodelphis_domestica	527	V T T N L S G F G C F M Q E H V T D P
GYS2_Mus_musculus	527	V T T N L S G F G C F V Q E H V A D P
GYS2_Rattus_norvegicus	527	V T T N L S G F G C F M Q E H V A D P
GYS2_Bos_taurus	526	V T T N L S G F G C F M Q E H V A D P
GYS2_Canis_familiaris	527	V T T N L S G F G C F M Q E H V A D P
GYS2_Macaca_mulatta	527	V T T N L S G F G C F M Q E H V A D P
GYS2_Homo_sapiens	527	V T T N L S G F G C F M Q E H V A D P

GS_Giardia_lamblia	637	PSSPSGTTTPELRSKAVSNRILHQKSI EYI ISEHDKNSWNMSK	F	G	V	Q	V	D	R	V	I	D	Y	H	E	S	V	D	R	L	A	N	M	L	V	D	F		
GS_Dictyostelium_discoideum	529DS	K	G	I	F	I	V	D	R	R	F	K	S	S	R	E	T	V	D	Q	M	T	Q	Y	L	W	K	F
GS_Cryptococcus_neoformans	532ED	Y	G	C	Y	I	V	D	R	R	G	Q	Q	I	E	E	S	V	D	Q	L	T	Q	Y	L	L	S	F
GS_Aspergillus_fumigatus	540SD	Y	G	I	Y	I	V	D	R	R	M	K	G	V	D	E	S	V	N	Q	L	T	D	F	M	F	N	F
GS_Aspergillus_nidulans	537SD	Y	G	I	Y	I	V	D	R	R	M	K	G	V	D	D	S	V	N	Q	L	T	D	F	M	Y	N	F
GS_Gibberella_zeae	536SD	Y	G	I	Y	I	V	D	R	R	T	K	G	V	D	D	S	V	N	Q	L	T	S	F	M	F	D	F
GS_Magnaporthe_grisea	537SD	Y	G	I	Y	I	V	D	R	R	T	K	G	V	D	D	S	V	N	Q	L	T	N	C	M	L	E	F
GS_Neurospora_crassa	536SD	Y	G	I	Y	I	V	D	R	R	S	K	G	V	D	D	S	V	N	Q	L	T	Q	Y	M	F	E	F
GS_Ustilago_maydis	537ED	Y	G	I	Y	I	V	D	R	R	M	K	S	V	E	D	S	V	N	Q	L	T	D	Q	M	F	S	F
GS_Deбaryomyces_hansenii	538SD	Y	G	I	Y	I	V	D	R	R	M	K	A	V	D	E	S	I	N	Q	L	T	D	Y	M	F	D	F
GS_Kluyveromyces_lactis	544KD	Y	G	I	Y	I	V	D	R	R	F	K	N	P	N	E	S	V	E	Q	L	V	D	Y	M	E	D	F
GS_Yarrowia_lipolytica	535SD	Y	G	I	Y	I	V	D	R	R	L	K	S	I	D	E	S	V	D	Q	L	T	D	Y	M	F	E	F
GS_Candida_albicans	535TD	Y	G	I	Y	I	V	D	R	R	M	K	S	V	D	E	S	I	N	Q	L	T	D	Y	M	F	D	F
GS_Candida_glabrata	547KD	Y	G	I	Y	I	V	D	R	R	Y	K	A	P	D	E	S	V	E	Q	L	V	D	Y	M	E	F	F
GS_Ashbya_gossypii	545KD	Y	G	I	Y	I	V	D	R	R	F	K	N	P	D	E	S	V	E	Q	L	V	D	Y	L	D	D	F
GS_Saccharomyces_paradoxus	547KD	Y	G	I	Y	I	V	D	R	R	F	K	A	P	D	E	S	V	E	Q	L	V	D	Y	M	E	F	F
GYS1_Saccharomyces_cerevisiae	547KD	Y	G	I	Y	I	V	D	R	R	F	K	S	P	D	E	S	V	E	Q	L	A	D	Y	M	E	F	F
GYS2_Saccharomyces_cerevisiae	547KD	Y	G	I	Y	I	V	D	R	R	F	K	A	P	D	E	S	V	E	Q	L	V	D	Y	M	E	F	F
GS_Caenorhabditis_briggsae	567EQ	K	G	I	Y	V	I	D	R	R	H	K	A	A	E	E	S	V	Q	E	L	A	N	V	M	Y	D	F
GS_Caenorhabditis_elegans	567EQ	K	G	I	Y	V	I	D	R	R	H	K	A	A	E	E	S	V	Q	E	L	A	Q	V	M	Y	D	F
GS_Steinernema_feltiae	575QT	Y	G	I	F	V	V	D	R	R	F	K	A	H	S	E	S	I	D	Q	L	A	Q	F	L	Y	D	Y
GS_Crassostrea_gigas	554KS	Y	G	L	Y	I	V	D	R	R	Y	K	S	P	D	E	S	I	H	Q	L	T	Q	Y	M	Y	D	F
GS_Drosophila_pseudoobscura	557KS	Y	G	I	Y	I	V	D	R	R	Y	I	G	L	E	D	S	I	Q	L	S	F	M	M	D	F	F	
GS_Drosophila_melanogaster	557KS	Y	G	I	Y	I	V	D	R	R	Y	I	G	L	E	N	S	V	Q	L	S	F	M	M	E	F	F	
GS_Apis_mellifera	558MS	Y	G	I	Y	I	V	D	R	R	F	I	S	L	E	S	S	V	Q	L	A	Q	Y	M	F	D	F	
GS_Anopheles_Gambiae	557KS	Y	G	I	Y	I	V	D	R	R	H	V	A	V	E	E	S	V	Q	L	S	K	Y	M	F	E	F	F
GS_Ciona_intestinalis	527EAY	G	I	Y	I	V	D	R	R	F	K	N	V	D	E	T	C	N	Q	L	T	D	Y	L	Y	H	F	F
GS_Ciona_savignyi	527EAY	G	I	Y	I	I	D	R	R	F	K	S	V	D	E	T	C	N	Q	L	T	D	Y	L	Y	H	F	F
GYS1_Fugu_rubripes	545SAY	G	I	Y	I	L	D	R	R	F	R	G	V	D	E	S	C	N	Q	L	T	S	F	L	F	Q	F	F
GYS1_Tetraodon_nigrovidiris	546SAY	G	I	Y	I	L	D	R	R	F	R	G	V	D	E	S	C	N	Q	L	T	S	F	L	F	Q	F	F
GYS1_Danio_rerio	546SAY	G	I	Y	I	L	D	R	R	Y	R	S	V	D	E	S	C	N	Q	L	T	S	F	L	F	Q	F	F
GYS1_Pimephales_promelas	546SAY	G	I	Y	I	L	D	R	R	Y	R	G	V	D	E	S	C	N	Q	L	T	S	F	L	F	Q	F	F
GYS1_Xenopus_tropicalis	546TAY	G	I	Y	I	Q	D	R	R	F	R	S	V	D	E	S	C	T	Q	L	T	S	F	L	Y	S	F	F
GYS1_Rattus_norvegicus	546SAY	G	I	Y	I	L	D	R	R	F	R	S	L	D	D	S	C	S	Q	L	T	S	F	L	Y	S	F	F
GYS1_Mus_musculus	546SAY	G	I	Y	I	L	D	R	R	F	R	S	L	D	D	S	C	S	Q	L	T	S	F	L	Y	S	F	F
GYS1_Oryctolagus_cuniculus	546SAY	G	I	Y	I	L	D	R	R	F	R	S	L	D	D	S	C	S	Q	L	T	S	F	L	Y	S	F	F
GYS1_Canis_familiaris	546SAY	G	I	Y	I	L	D	R	R	F	R	S	L	D	D	S	C	S	Q	L	T	S	F	L	Y	S	F	F
GYS1_Macaca_mulatta	546SAY	G	I	Y	I	L	D	R	R	F	R	S	L	D	D	S	C	S	Q	L	T	S	F	L	Y	S	F	F
GYS1_Pongo_pygmaeus	546SAY	G	I	Y	I	L	D	R	R	F	R	S	L	D	D	S	C	S	Q	L	T	S	F	L	Y	S	F	F
GYS1_Homo_sapiens	546SAY	G	I	Y	I	L	D	R	R	F	R	S	L	D	D	S	C	S	Q	L	T	S	F	L	Y	S	F	F
GYS2_Fugu_rubripes	553AA	Y	G	I	Y	I	V	D	R	R	F	R	S	A	E	E	S	C	N	Q	L	T	Q	F	M	F	T	F
GYS2_Tetraodont_nigrovidiris	550TAY	G	I	Y	I	V	D	R	R	F	R	S	A	E	E	S	C	N	Q	L	T	Q	F	M	F	S	F	F
GYS2_Danio_rerio	547SE	Y	G	I	Y	I	V	D	R	R	F	R	S	A	E	E	S	C	N	Q	L	T	Q	F	M	F	S	F
GYS2_Xenopus_laеvis	547TAY	G	V	Y	I	T	D	R	R	F	R	S	P	D	E	S	C	N	Q	L	T	Q	L	L	Y	G	F	F
GYS2_Xenopus_tropicalis	547AA	Y	G	V	Y	I	T	D	R	R	F	R	S	P	D	E	S	C	N	Q	L	T	Q	F	L	Y	G	F
GYS2_Gallus_gallus	547AA	Y	G	I	Y	I	V	D	R	R	F	R	S	P	D	E	S	C	N	Q	L	T	Q	F	L	Y	G	F
GYS2_Monodelphis_domestica	546AA	Y	G	I	Y	I	V	D	R	R	F	C	S	P	D	E	S	C	N	Q	L	T	Q	F	L	Y	G	F
GYS2_Mus_musculus	546TAY	G	I	Y	I	V	D	R	R	F	R	S	P	D	D	S	C	N	Q	L	T	Q	F	L	Y	G	F	F
GYS2_Rattus_norvegicus	546TAY	G	I	Y	I	V	D	S	.	V	R	S	P	D	D	S	C	N	Q	L	T	Q	F	L	Y	G	F	F
GYS2_Bos_taurus	545TAY	G	I	Y	I	V	D	R	R	F	C	S	P	D	D	S	C	N	Q	L	T	Q	F	L	Y	G	F	F
GYS2_Canis_familiaris	546TAY	G	I	Y	I	V	D	R	R	F	R	S	P	D	D	S	C	N	Q	L	T	Q	F	L	Y	G	F	F
GYS2_Macaca_mulatta	546TAY	G	I	Y	I	V	D	R	R	F	R	S	P	D	D	S	C	N	Q	L	T	Q	F	L	Y	G	F	F
GYS2_Homo_sapiens	546TAY	G	I	Y	I	V	D	R	R	F	R	S	P	D	D	S	C	N	Q	L	T	K	F	L	Y	G	F	F

GS_Giardia_lamblia	707	VRLSPIERTINLRHKTERASVLCDSAMISRYNEAHKLAITRRRKHFN
GS_Dictyostelium_discoideum	558	TQLDRRQRIELRNATEKLSSELLDWRTLGKFYKTAARALALERAFPP	..
GS_Cryptococcus_neoformans	561	TTKRRRQRIINQRNTERLSSELLDWRSLGLEYSKARQLALRRAYPDS	FNDDEP.....DFTGVQ
GS_Aspergillus_fumigatus	569	TQKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLALRRAYPS	FDGPEYF.....DVIGGTEQ
GS_Aspergillus_nidulans	566	TLKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLALRRAYPS	FDNQEDYF.....DVIGGTEQ
GS_Gibberella_zeae	565	CGKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLALRRAYPNS	FVGDEEEE.....DFIPGVEQ
GS_Magnaporthe_grisea	566	CQKRRRQRIINQRNTERLSSELLDWRKMGLEYIKARQLALRRAYPNS	FDGDDTA.....DFMNSSDL
GS_Neurospora_crassa	565	TQKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLALRRAYPTS	FNGEEEE.....DFIPGVEQ
GS_Ustilago_maydis	566	SQKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLALRRAYPDS	FDEDDTIESYFD.....DIHHDG
GS_Debaryomyces_hansenii	567	AEKRRRQRIINQRNTERLSSELLDWRKMGLEYIKARQLSLKRAYPKF	KNGAN.....PFNNTSNL
GS_Kluyveromyces_lactis	573	VNKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLALRRAYPDE	FKELTGGTDLDDSNMDSLGNPKV
GS_Yarrowia_lipolytica	564	SKKRRRQRIINQRNTERLSSELLDWRKMGLEYIKARQLALRRAYPDQ	FDHENP.....FEDEEPL
GS_Candida_albicans	564	CAKRRRQRIINQRNTERLSVLLDWRSVHSEYSKARLLALRRAYPDYV	G.....EKVVESKM
GS_Candida_glabrata	576	VNKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLGLRRAYPDQ	FKEIVG.EDVNDSSMEALAGGKKL
GS_Ashbya_gossypii	574	CKKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLALRRAYPEE	FRALVG.EDLDDHDMDSLGGQKF
GS_Saccharomyces_paradoxus	576	VKKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLALRRAYPDQ	FKELVG.EELNDSNMDTLAGGKKL
GYS1_Saccharomyces_cerevisiae	576	VNKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLGLRRAYPEQ	FKQLVG.ETISDANMNTLAGGKKF
GYS2_Saccharomyces_cerevisiae	576	VKKRRRQRIINQRNTERLSSELLDWRKMGLEYVVKARQLALRRAYPDQ	FRELVG.EELNDSNMDALAGGKKL
GS_Caenorhabditis_briggsae	596	CGQRRRQRIILRNANEGLSALLDWNLGVFYRDCCRLLALERLHPDGV	VDKIIRENE.....
GS_Caenorhabditis_elegans	596	CGQRRRQRIILRNSNEGLSALLDWNLGVFYRDCCRLLALERLHPD.	VDKIMRDNE.....
GS_Steinernema_feltiae	604	SCLRRRQRIILRNRSERLSSELLDWRNLGCFYREARRMALKKTHPDLE	MKISETIKR.....
GS_Crassostrea_gigas	583	TCLRQRRIINQRNTERLSSELLDWRNLGVIYRQARQIAVARGYPDLA	AKEEEIILQ.....EKRF
GS_Drosophila_pseudoobscura	586	SRLNRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDELSLYGS.....RSNL
GS_Drosophila_melanogaster	586	SRLNRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDELSLYGS.....KNNL
GS_Apis_mellifera	587	ARLRRRQRIINQRNTERLSSELLDWRNLGVIYRQARIKALTTVYPELA	SEFAEGG.....VGRF
GS_Anopheles_Gambiae	586	SKLNRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....ATDF
GS_Ciona_intestinalis	556	CRMTRRERIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TGSV
GS_Ciona_savignyi	556	CRMTRRERIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TGSV
GYS1_Fugu_rubripes	574	CKQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TGSF
GYS1_Tetraodon_nigrovidiris	575	CKQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TGSF
GYS1_Danio_riero	575	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....AAGF
GYS1_Pimephales_promelas	575	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....ATGF
GYS1_Xenopus_tropicalis	575	SQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....AQGF
GYS1_Rattus_norvegicus	575	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TQGY
GYS1_Mus_musculus	575	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TQGY
GYS1_Oryctolagus_cuniculus	575	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TQGY
GYS1_Canis_familiaris	575	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TQGY
GYS1_Macaca_mulatta	575	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....AQGY
GYS1_Pongo_pygmaeus	575	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....AQGY
GYS1_Homo_sapiens	575	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....AQGY
GYS2_Fugu_rubripes	582	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TEGF
GYS2_Tetraodont_nigrovidiris	579	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TEGF
GYS2_Danio_riero	576	CQKRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TQGF
GYS2_Xenopus_laevis	576	CQKRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TEGF
GYS2_Xenopus_tropicalis	576	CQKRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TEGF
GYS2_Gallus_gallus	576	CQQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TEGF
GYS2_Monodelphis_domestica	575	CKQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TQGF
GYS2_Mus_musculus	575	CKQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TQGF
GYS2_Rattus_norvegicus	574	CKQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TQGF
GYS2_Bos_taurus	574	CKQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TEGF
GYS2_Canis_familiaris	575	CKQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TEGF
GYS2_Macaca_mulatta	575	CKQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TEGF
GYS2_Homo_sapiens	575	CKQRRRQRIINQRNTERLSSELLDWRNLGVIYRQARVKKLQAVYPDY	VDESTEYLK.R.....TEGF

GS_Giardia_lamblia 603 ... KPI SRSP SPSS
GS_Dictyostelium_discoideum 619 KVGAPLSAPASPR..... MRTGMTPGDYATLTHEEMEHLSTQDYMG... AKSWKGINDDDENHYFPFP
GS_Cryptococcus_neoformans 631 KLSRPLSVPGSPR..... DRSGVMTPGDFATIQEVKEGLDTEDEYIA... WRLPNSEEEEPPDDHYFPPLT
GS_Aspergillus_fumigatus 628 KISRPLSVPGSPR..... DRSGMTPGDFAFSLQEVKEGLSTEDYVA... WRLPTSEEDDAEDHFYPLT
GS_Aspergillus_nidulans 627 KISRPLSVPGSPR..... DRTGMTPGDFAFSLQEGREGLNTEDEYVA... WKLP... EEEEDPEEYPFPPLT
GS_Gibberella_zeae 627 KISRPLSVPGSPR..... DRAGMTPGDFAFSLQEGREGLSTEDYVS... WKLP... EEEEDPDEYTFPPLT
GS_Magnaporthe_grisea 626 KISRPLSVPGSPR..... DRTGMTPGDFAFSLQESHEGLSTEDYVA... WKLP... EEEEDPEEYPFPPLT
GS_Neurospora_crassa 630 KMPPLSLMPGSPR..... FGSGARTPGFEGTLTEELQSLSTSDYRHHQQFWKTMSQHGSDEEENRYRP
GS_Ustilago_maydis 627 KLTRPLSVPGSPRSK..... VGLMTPGDLGSLQEAHQSLNTEDEYIG... FKLGENEDDDATEDANVYP
GS_Debaryomyces_hansenii 643 KVARPLSVPGSPRDRSASSVAVMMTPGDLGTLQDANNADD... Y... FHLSMGDNEDEDEDQFN
GS_Kluyveromyces_lactis 624 KLTRPLSVPGSPR..... DRAGLMTGDLGSLGELGELDTDDYVG... FRLP.QDDDDEEETSYPAT
GS_Yarrowia_lipolytica 620 KITRPM SVPGSPRS..... LLTPGDLGSLQDANQDIS... Y... FELG... EEEET.....
GS_Candida_albicans 645 KIARPLSVPGSPRDAAKSPS.TVFMTPGDLGTIQDANNVDD... Y... FHLSVN.DNEEE.....
GS_Candida_glabrata 643 KVARPLSVPGSPRDR.SSSMSAILMTPGDLGTLQDANNAND... Y... FHLSMQTDDDEEGEDGRED
GS_Ashbya_gossypii 645 KVARPLSVPGSPR.DLRSNS.TVYMTGDLGTLQEVNNADD... Y... FSLGVNPAADDDDDGYPAD
GS_Saccharomyces_paradoxus 645 KIARPLSVPGSPR.KVRSNS.TVYMTGDLGTLQDANNADD... Y... FNLSTNGAINDDDDDNDTS
GSY1_Saccharomyces_cerevisiae 645 KVARPLSVPGSPR.DLRSNS.TVYMTGDLGTLQEVNNADD... Y... FSLGVNPAADDDDDGYPAD
GS_Caenorhabditis_briggsae 651 GKVP SAATSRRP..... SIHSS..... DGEDEE.....
GS_Caenorhabditis_elegans 650 GKVP SAATSRRP..... SIHSS..... DGEDDE.....
GS_Steinernema_feltiae 660 VPRA.TSAPSTSPSTPG..... SPHSS..... DAEDSDTA..... EQVEHENKAWQE.
GS_Crassostrea_gigas 642 MYPRPASEPSPSASRS..... STPAPSEHG..... DEDDDID..... EDEENAEMSSNPE
GS_Drosophila_pseudoobscura 645 VFSRPHSEPPSPSTSSRH..... TTPAPSVHG..... SEDESDV..... EETELKELGIK..
GS_Drosophila_melanogaster 645 IFSRPHSEPPSPSTSSRH..... TTPAPSVHG..... SEDESDV..... EETELKELGIK..
GS_Apis_mellifera 645 SYPRPISEPPSPSSSRH..... TTPAASVHG..... SDEEDEV..... DEKELLELRQTS
GS_Anopheles_Gambiae 646 TYPRPI SAPPSPSSSRH..... TTPAPSLHGS..... DDEQSDV..... SEELQELNSH.
GS_Ciona_intestinalis 615 RLP RPY SAPPSPFGSRI..... ASPYQSD.EEDNKVFDDDDGDSGLH..... TSNLIVSTDTESVL
GS_Ciona_savignyi 615 RLP RPY SAPPSPFGSRI..... ASPCPSDAEEDNKVFDEDDGDSGLH..... TSNLIVSTDTESMM
GYS1_Fugu_rubirpes 634 RYPRP ASVPPSPALSRH..... SSPHHSEADN..... DEDESVD..... EDLEAEKDRVNIR
GYS1_Tetraodon_nigrovidiris 634 RYPRP ASVPPSPALSRH..... SSPHHSEADN..... DEEEDYD..... EDLEAEKDRVNIR
GYS1_Danio_riero 635 RYPRP ASVPPSPAHSLH..... SSPHHSEAE..... DEEEDYD..... EDLEAEKDRVNIR
GYS1_Pimephales_promelas 635 HYPRP ASVPPSPAHSLH..... SSPHHSEGE..... DEDEPYD..... EDLEAEKDRVNIR
GYS1_Xenopus_tropicalis 635 RYPRP ASVPPSPSLSRH..... SSPHHSETEDD..... ER... YD..... EEEEA AKDRQNIK
GYS1_Rattus_norvegicus 635 RYPRP ASVPPSPSLSRH..... SSPHQSEDEEPRDGLPREDSEYD..... EEEEA AKDRRNIR
GYS1_Mus_musculus 635 RYPRP ASVPPSPSLSRH..... SSPHQSEDEEPRDGLPREDSEYD..... EEEEA AKDRRNIR
GYS1_Oryctolagus_cuniculus 635 RYPRP ASVPPSPSLSRH..... SSPHQSEDEEPRDGLPEEDGERYD..... EDEEA AKDRRNIR
GYS1_Canis_familiaris 635 RYPRP ASVPPSPSLSRH..... SSPHQSEDEEPRDGLPPEEDGERYD..... EDEEA AKDRRNIR
GYS1_Macaca_mulatta 635 RYPRP ASVPPSPSLSRH..... SSPHQSEDEEPRNGPLEEDSEYD..... EDEEA AKDRRNIR
GYS1_Pongo_pygmaeus 635 RYPRP ASVPPSPSLSRH..... SSPHQSEDEEPRNGPLEEDGERYD..... EDEEA AKDRRNIR
GYS1_Homo_sapiens 635 RYPRP ASVPPSPSLSRH..... SSPHQSEDEEPRNGPLEEDGERYD..... EDEEA AKDRRNIR
GYS2_Fugu_rubirpes 642 RYPRP YSVPPSPSASLH..... STPHHSVDVDD... DDDDDGEPYN..... EEEEA ERDRLNIK
GYS2_Tetraodont_nigrovidiris 639 RYPRP YSVPPSPSASLH..... STPHHSVDEDD... DDDNDGEPYN..... EEEEA ERDRLNIK
GYS2_Danio_riero 636 RYPRP YSVPPSPSASIH..... STPHHSDEEDD... DTYDE..... EE EAERDRLNIK
GYS2_Xenopus_laevis 636 RYPRP YSVPPSPAVSQP..... SSPHDSE.E... EDDEERYD..... EDE EAERDRQNIK
GYS2_Xenopus_tropicalis 636 RYPRP YSVPPSPAVSQP..... SSPHDSE.EE... DEDEERYD..... EDE EAERDRQNIK
GYS2_Gallus_gallus 636 RYPRP YSVPPSPSVSQH..... SSPHQSEGED... EDEDERYD..... EDE EAERDRQNIK
GYS2_Monodelphis_domestica 633 KFPRP YSVPPSPSSSQH..... SSPQASDVED... EDERYD..... EEE EAERDRLNIK
GYS2_Mus_musculus 635 KYPRP YSVPPSPSGSQA..... SSPQSSDAEDE... EDEDERYD..... EEE EAERDRLNIK
GYS2_Rattus_norvegicus 634 KYPRP YSVPPSPSGSQT..... SSPQSSDVENE... GDEDERYD..... EEE EAERDRLNIK
GYS2_Bos_taurus 634 KYPRP YSVPPSPSGSQG..... SSPQSSDAED... DDEDERYD..... EEE EAERDRLNIK
GYS2_Canis_familiaris 635 KYPRP YSVPPSPSGSQV..... SSPQSSDVED... EEDERYN..... EEE EAERDRLNIK
GYS2_Macaca_mulatta 635 KYPRP YSVPPSPSGSQA..... SSPQSSDVED... EVEDERYD..... EEK EAERDRLNIK
GYS2_Homo_sapiens 635 KYPRP YSVPPSPSGSQA..... SSPQSSDVED... EVEDERYD..... EEE EAERDRLNIK

GS_Giardia_lamblia	
GS_Dictyostelium_discoideum	
GS_Cryptococcus_neoformans	679	LVMKPKRRSDSLASAI SGNATPSSGGRKLS ENDLARADAALS NVEGVHADGINGHH...
GS_Aspergillus_fumigatus	691	LRTKKSSDRPSSPLDSIPVNGGR.....
GS_Aspergillus_nidulans	688	LRTKKS.DRPSSPLDRISINGGQSS.....
GS_Gibberella_zeae	685	LRKQ..P.APPSPSETVPVNGTQ.....
GS_Magnaporthe_grisea	685	LGAKQRPSGPASPLDGVHLNNGN.....
GS_Neurospora_crassa	684	LKQRTGPGSPLDSIQGLQLNGTR.....
GS_Ustilago_maydis	694	LVIKSRARGTSVGSMSGASTPGLGGGKFLSSADLDRADAALS NHSGAPNGHGY.....
GS_Deব্যomyces_hansenii	687	LTLRGN SVPPTDDAT.....
GS_Kluyveromyces_lactis	
GS_Yarrowia_lipolytica	683	LTLAGSRK.....
GS_Candida_albicans	
GS_Candida_glabrata	
GS_Ashbya_gossypii	703	D.....
GS_Saccharomyces_paradoxus	704	DS.....
GYS1_Saccharomyces_cerevisiae	703	AYYEDN.....
GYS2_Saccharomyces_cerevisiae	704	DS.....
GS_Caenorhabditis_briggsae	
GS_Caenorhabditis_elegans	
GS_Steinernema_feltiae	
GS_Crassostrea_gigas	689	SDMPMFK.....
GS_Drosophila_pseudoobscura	
GS_Drosophila_melanogaster	
GS_Apis_mellifera	692	R.....
GS_Anopheles_Gambiae	
GS_Ciona_intestinalis	669 STATTPNGTGNDVISSTASDL
GS_Ciona_savignyi	670 SSATTTNDVISNASSDA
GYS1_Fugu_rubripes	682	QP..... FVVPFKNKSSLFV TNGDGE GDATEKN
GYS1_Tetraodon_nigrovidiris	682	QP..... YSVPFKNKSSLSVANGSGDGVAAEKN
GYS1_Danio_rerio	681	QP..... YNLPNRNKNQTVGLP.EKN
GYS1_Pimephales_promelas	681	QP..... IIVPSRNKNHTVGLP.EKN
GYS1_Xenopus_tropicalis	680	QPSITSMASAPEWRRRSKKSID.ATNSSNASNASTPTNPSSPSDLSSPTSSLIERN
GYS1_Rattus_norvegicus	690	AP..... EWPRRASCSSTGGSKRSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
GYS1_Mus_musculus	690	AP..... EWPRRASCSSTGGSKRSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
GYS1_Oryctolagus_cuniculus	690	AP..... EWPRRASCTSSSGSKRSNSVDT...SSLSTPSEPLSPASSLGEERN
GYS1_Canis_familiaris	690	AP..... EWPRRASCTSSSTGGSKRS.SVDTAPSSSLSTPSEPLSPASSLGEERN
GYS1_Macaca_mulatta	690	AP..... EWPRRASCTSSSTSGSKR.NSVDTATSSSLSTPSEPLSPTSSLGEERN
GYS1_Pongo_pygmaeus	690	AP..... EWPRRASCTSSSTSGSKR.NSVDTATSSSLSTPSEPLSPTSSLGEERN
GYS1_Homo_sapiens	690	AP..... EWPRRASCTSSSTSGSKR.NSVDTATSSSLSTPSEPLSPTSSLGEERN
GYS2_Fugu_rubripes	693	AP..... FVLGAVPEGKKKQPGESGN
GYS2_Tetraodont_nigrovidiris	690	AP..... FVLGAVPEGKKKQPGESGN
GYS2_Danio_rerio	681	AP..... FSVGADTDGKRTQPVENG
GYS2_Xenopus_laevis	682	ST..... FSFGPVS RGKKKHGENRN
GYS2_Xenopus_tropicalis	683	SD..... FSLGPVSRGKKKHGEFRN
GYS2_Gallus_gallus	684	SP..... FSLGVLPQGGKKKHGEFRN
GYS2_Monodelphis_domestica	679	SP..... FILGQVPHEKKKHGEHKN
GYS2_Mus_musculus	684	SP..... FSLNHFPKGKKKLHGEYKN
GYS2_Rattus_norvegicus	683	SP..... FSLNHI PKGKKKLHGEYKN
GYS2_Bos_taurus	682	SP..... FSLSHVSRGKKKHGEYKN
GYS2_Canis_familiaris	683	SP..... FSLGRVPRGKKKLHGEYKN
GYS2_Macaca_mulatta	683	SP..... FALSHVPRGKKKLHGEYKN
GYS2_Homo_sapiens	683	SP..... FSLSHVPHGKKKLHGEYKN