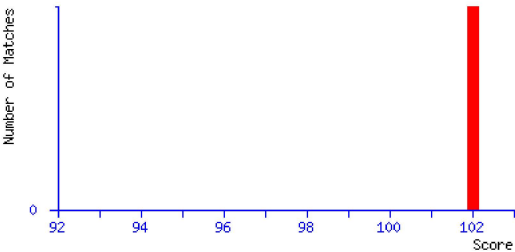


User : Lily-mascot  
E-mail : l.r.adair@pgr.reading.ac.uk  
Search title : S\_cerevisiae\_11600  
MS data file : S\_cerevisiae\_11600\_Da\_merged.txt  
Databases : 1: contaminants 20160129 (247 sequences; 128,130 residues)  
2: Swissprot\_22\_05\_2024 22\_05\_2024\_02 (571,282 sequences; 206,678,396 residues)  
Timestamp : 27 May 2025 at 07:53:27 GMT

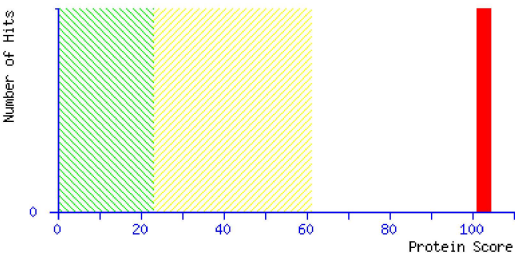
▼Search parameters

Type of search : MS/MS Ion Search  
Enzyme : None  
Variable modifications : **Acetyl (Protein N-term)**  
Mass values : Monoisotopic  
Protein mass : Unrestricted  
Peptide mass tolerance : ± 50 ppm  
Fragment mass tolerance : ± 0.2 Da  
Max missed cleavages : 0  
Instrument type : MALDI-QIT-TOF  
Number of queries : 1

▼Score distribution



**Peptide score distribution.** Ions score is  $-10 \log(P)$ , where  $P$  is the probability that the observed match is a random event. There is **1** peptide match above identity threshold and **1** match above homology threshold for **1** queries. On average, individual ions scores **> 23** (beyond yellow shading) indicate **significant homology**, while individual ions scores **> 61** (beyond green shading) indicate **identity or extensive homology** ( $p < 0.05$ ).



**[Deprecated]** Protein score distribution. Score distribution for family members in the first 50 proteins. Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein families.

▼Modification statistics for all protein families

Modification	Delta	Type	Site	Total matches
Acetyl	42.010565	variable	Protein N-term	1

▼Legend

Peptide columns and rows

Dupes	...	Expect	Rank	U	1	2	Peptide	
		0.037	▶	2			GAYSLSLR	significant
		9	▶	1			GFFLFVEGGR	top ranking
		6.4e-05	▶	1			GSSIFGLAPGK	significant and top ranking
		1.3e-06	▶	1	■		SSGTSYPDVLK	peptide is found in all proteins in family member 1
		6.2e-07	▶	1	■		VCNYVSWIK	peptide is found in some but not all proteins in family member 2
		6.4e-05	▶	1	U		GSSIFGLAPGK	unique
▶ 2		5.7e-05	▶	1			LNTLETEEWFFK	peptide has two duplicates
		0.18	▶	1			LNTLETEEWFFK	duplicate peptide

Right-facing triangle (▶) in the Dupes or Rank column indicates content that can be expanded by clicking on it. Down-facing triangle (▼) indicates the content is expanded and can be collapsed. For more details about particular columns, see [results format help](#).

Protein quantitation ratios				
	Score	...	114/113	115/113
CFAH_HUMAN	37559		0.962	<b>1.129</b>
FHR2_HUMAN	1330		<b>0.859</b>	1.128

When quantitation method is Reporter (e.g. iTRAQ) or Multiplex (e.g. IPTL), protein ratios are displayed when a family is expanded. Ratios in *italic* indicate that the peptide log-ratios do not appear to come from a normal distribution. **Bold** indicates that if you can assume peptide ratios are normally distributed, the protein ratio is significantly different from 1.0 (at significance level 0.05).

Note that lack of bold or italic can also mean that significance or normality testing has not been performed (for example, if protein ratio type does not support it).

Protein Family Summary

Significance threshold p<0.05

Target FDR (overrides sig. threshold)(not set)

Display non-sig. matches☐

Preferred taxonomyAll entries

Max. number of familiesAUTO

FDR typeSequence

Min. number of sig. unique sequences1

Dendrograms cut at0

Sensitivity and FDR (random protein sequences)

	Target	Decoy	FDR	
Protein family members	1	0	0.00%	Not enough decoy protein hits for a meaningful FDR calculation.
Sequences abovehomology	1	0	0.00%	Not enough decoy matches above significance threshold for a meaningful FDR calculation.

Decoy results are available in the decoy report.

Protein family 1 (out of 1)

10 per page1

12::HSP12\_YEAST10312 kDa heat shock protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / ...

	Score	Mass	Matches	Sequences
1.12::HSP12_YEAST	103	11686	1 (1)	1 (1)
12 kDa heat shock protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP12 PE=1 SV=1				

1 peptide matches (1 non-duplicate, 0 duplicate)

Query	Dupes	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
1		11598.1492	11597.1419	11596.6289	44.2	0	103	6.5e-10	1	U	M.SDAGRKGFGKEKASEALKPDSQKSYAEGQKEYITDKADKVAGKV + Acetyl (Protein N-term)

10 per page1

Mascot: http://www.matrixscience.com/

Protein View: HSP12\_YEAST

12 kDa heat shock protein OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=HSP12 PE=1 SV=1

Detailed information about this protein hit is shown below. ([help](#)).

Database: Swissprot\_22\_05\_2024  
Score: 103  
Monoisotopic mass (M<sub>r</sub>): 11686  
Calculated pI: 5.22  
Taxonomy: [Saccharomyces cerevisiae S288C](#)

Sequence similarity is available as [an NCBI BLAST search of HSP12\\_YEAST against nr](#).

Search parameters

MS data file: S\_cerevisiae\_11600\_Da\_merged.txt  
Enzyme: No enzyme cleavage specificity.  
Variable modifications: [Acetyl \(Protein N-term\)](#)

Protein sequence coverage: 99%

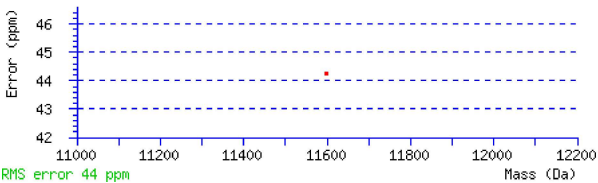
Matched peptides shown in **bold red**.

1 **MSDAGRKGFG EKASEALKPD SQKSYAEQ GK EYITDKADKV AGKVQPEDNK**  
51 **GVFQGVHDSA EKGKDNAEGQ GESLADQARD YMGAAKSKLN DAVEYVSGRV**  
101 **HGEEDPTTK**

Unformatted sequence string: [109 residues](#) (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass

Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
<a href="#">1</a>	2 - 109	11598.1492	11597.1419	11596.6289	44.2	0	103	6.5e-10	1	U	<b>M.SDAGRKGFG EKASEALKPD SQKSYAEQ GK EYITDKADKV A</b> + Acetyl (Protein N-term)



ID HSP12\_YEAST Reviewed; 109 AA.  
AC P22943; D6VTL5; Q8X145;  
DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.  
DT 01-AUG-1991, sequence version 1.  
DT 27-MAR-2024, entry version 194.  
DE RecName: Full=12 kDa heat shock protein;  
DE AltName: Full=Glucose and lipid-regulated protein;  
GN Name=HSP12; Synonyms=GLP1, HOR5; OrderedLocusNames=YFL014W;  
OS *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) (Baker's yeast).  
OC Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=559292;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND PARTIAL PROTEIN SEQUENCE.  
RC STRAIN=ATCC 204508 / S288c;  
RX PubMed=2129531; DOI=10.1016/0378-1119(90)90249-q;  
RA Stone R.L., Matarese V., Magee B.B., Magee P.T., Bernlohr D.A.;  
RT "Cloning, sequencing and chromosomal assignment of a gene from  
RT *Saccharomyces cerevisiae* which is negatively regulated by glucose and  
RT positively by lipids.";  
RL Gene 96:171-176(1990).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 204508 / S288c;  
RX PubMed=2175390; DOI=10.1007/bf00315801;  
RA Praekelt U.M., Meacock P.A.;  
RT "HSP12, a new small heat shock gene of *Saccharomyces cerevisiae*: analysis  
RT of structure, regulation and function.";  
RL Mol. Gen. Genet. 223:97-106(1990).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 204511 / S288c / AB972;  
RA Barrell B.G., Churcher C., Rajandream M.A.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 204508 / S288c;  
RX PubMed=7670463; DOI=10.1038/ng0795-261;  
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.,

RA Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K., Yamazaki M., Tashiro H.,  
 RA Eki T.;  
 RT "Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces*  
 RT *cerevisiae*.";  
 RL Nat. Genet. 10:261-268(1995).  
 RN [5]  
 RP GENOME REANNOTATION.  
 RC STRAIN=ATCC 204508 / S288c;  
 RX PubMed=24374639; DOI=10.1534/g3.113.008995;  
 RA Engel S.R., Dietrich F.S., Fisk D.G., Binkley G., Balakrishnan R.,  
 RA Costanzo M.C., Dwight S.S., Hitz B.C., Karra K., Nash R.S., Weng S.,  
 RA Wong E.D., Lloyd P., Skrzypek M.S., Miyasato S.R., Simison M., Cherry J.M.;  
 RT "The reference genome sequence of *Saccharomyces cerevisiae*: Then and now.";  
 RL G3 (Bethesda) 4:389-398(2014).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=KBY001;  
 RA Sone H., Tomizuka K., Suda H., Iwamatsu A., Kondo K., Inouye M., Tanaka J.;  
 RT "Transcriptional regulation of bottom-fermenting yeast specific HSP12  
 RT gene.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=Ar5-H12 / Arvisionadu wine isolate;  
 RX PubMed=11816034; DOI=10.1002/yea.831.abs;  
 RA Zara S., Farris G.A., Budroni M., Bakalinsky A.T.;  
 RT "HSP12 is essential for biofilm formation by a Sardinian wine strain of  
 RT *Saccharomyces cerevisiae*.";  
 RL Yeast 19:269-276(2002).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=ATCC 204508 / S288c;  
 RX PubMed=17322287; DOI=10.1101/gr.6037607;  
 RA Hu Y., Rolfs A., Bhullar B., Murthy T.V.S., Zhu C., Berger M.F.,  
 RA Camargo A.A., Kelley F., McCarron S., Jepson D., Richardson A., Raphael J.,  
 RA Moreira D., Taycher E., Zuo D., Mohr S., Kane M.F., Williamson J.,  
 RA Simpson A.J.G., Bullyk M.L., Harlow E., Marsischky G., Kolodner R.D.,  
 RA LaBaer J.;  
 RT "Approaching a complete repository of sequence-verified protein-encoding  
 RT clones for *Saccharomyces cerevisiae*.";  
 RL Genome Res. 17:536-543(2007).  
 RN [9]  
 RP LEVEL OF PROTEIN EXPRESSION [LARGE SCALE ANALYSIS].  
 RX PubMed=14562106; DOI=10.1038/nature02046;  
 RA Ghaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A., Dephoure N.,  
 RA O'Shea E.K., Weissman J.S.;  
 RT "Global analysis of protein expression in yeast.";  
 RL Nature 425:737-741(2003).  
 RN [10]  
 RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-21, AND IDENTIFICATION BY  
 RP MASS SPECTROMETRY [LARGE SCALE ANALYSIS].  
 RX PubMed=17287358; DOI=10.1073/pnas.0607084104;  
 RA Chi A., Huttenhower C., Geer L.Y., Coon J.J., Syka J.E.P., Bai D.L.,  
 RA Shabanowitz J., Burke D.J., Troyanskaya O.G., Hunt D.F.;  
 RT "Analysis of phosphorylation sites on proteins from *Saccharomyces*  
 RT *cerevisiae* by electron transfer dissociation (ETD) mass spectrometry.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 104:2193-2198(2007).  
 RN [11]  
 RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-21; SER-59; SER-73 AND  
 RP SER-97, AND IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].  
 RX PubMed=18407956; DOI=10.1074/mcp.m700468-mcp200;  
 RA Albuquerque C.P., Smolka M.B., Payne S.H., Bafna V., Eng J., Zhou H.;  
 RT "A multidimensional chromatography technology for in-depth phosphoproteome  
 RT analysis.";  
 RL Mol. Cell. Proteomics 7:1389-1396(2008).  
 RN [12]  
 RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-21; SER-24; SER-59; SER-73  
 RP AND SER-97, AND IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].  
 RX PubMed=19779198; DOI=10.1126/science.1172867;  
 RA Holt L.J., Tuch B.B., Villen J., Johnson A.D., Gygi S.P., Morgan D.O.;  
 RT "Global analysis of Cdk1 substrate phosphorylation sites provides insights  
 RT into evolution.";  
 RL Science 325:1682-1686(2009).  
 CC !- FUNCTION: May play a role in a switch from carbohydrate utilizing  
 CC metabolism to fatty acid utilizing metabolism.  
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 CC phase, and by cAMP, probably via the activity of a cAMP-dependent  
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 CC !- SIMILARITY: To *S.pombe* hsp9 and *C.albicans* WH11. {ECO:0000305}.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <https://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution (CC BY 4.0) license  
 CC -----  
 DR EMBL; M60827; AAA34647.1; -; Genomic\_DNA.  
 DR EMBL; X55785; CAA39306.1; -; mRNA.  
 DR EMBL; Z46255; CAA86349.1; -; Genomic\_DNA.  
 DR EMBL; D50617; BAA09224.1; -; Genomic\_DNA.  
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 DR PDB; 2L9Q; NMR; -; A=1-109.  
 DR PDB; 2LJL; NMR; -; A=1-109.  
 DR PDB; 4AXP; NMR; -; A=1-109.

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 DR PDBsum; 2LJL; -.  
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 DR SMR; P22943; -.  
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 DR IntAct; P22943; 5.  
 DR MINT; P22943; -.  
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 DR iPTMnet; P22943; -.  
 DR MaxQB; P22943; -.  
 DR PaxDb; 4932-YFL014W; -.  
 DR PeptideAtlas; P22943; -.  
 DR TopDownProteomics; P22943; -.  
 DR EnsemblFungi; YFL014W\_mRNA; YFL014W; YFL014W.  
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 DR KEGG; sce:YFL014W; -.  
 DR AGR; SGD:S000001880; -.  
 DR SGD; S000001880; HSP12.  
 DR VEuPathDB; FungiDB:YFL014W; -.  
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 DR HOGENOM; CLU\_102617\_1\_1\_1; -.  
 DR InParanoid; P22943; -.  
 DR OMA; NKGVFQG; -.  
 DR OrthoDB; 1699855at2759; -.  
 DR BioCyc; YEAST:G30-30442-MONOMER; -.  
 DR BioGRID-ORCS; 850532; 8 hits in 10 CRISPR screens.  
 DR PRO; PR:P22943; -.  
 DR Proteomes; UP000002311; Chromosome VI.  
 DR RNAct; P22943; Protein.  
 DR GO; GO:0005737; C:cytoplasm; HDA:SGD.  
 DR GO; GO:0005829; C:cytosol; IDA:SGD.  
 DR GO; GO:0005768; C:endosome; IDA:SGD.  
 DR GO; GO:0005634; C:nucleus; HDA:SGD.  
 DR GO; GO:0005886; C:plasma membrane; IDA:SGD.  
 DR GO; GO:0008289; F:lipid binding; IDA:SGD.  
 DR GO; GO:0044183; F:protein folding chaperone; EXP:DisProt.  
 DR GO; GO:0007155; P:cell adhesion; IDA:SGD.  
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 DR GO; GO:0071470; P:cellular response to osmotic stress; IMP:SGD.  
 DR GO; GO:0034599; P:cellular response to oxidative stress; IMP:SGD.  
 DR GO; GO:0007009; P:plasma membrane organization; IMP:SGD.  
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 DR PIRSF; PIRSF002590; HSP9/HSP12\_fun; 1.  
 PE 1: Evidence at protein level;  
 KW 3D-structure; Direct protein sequencing; Phosphoprotein;  
 KW Reference proteome; Stress response.  
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 FT /note="12 kDa heat shock protein"  
 FT /id="PRO\_0000084081"  
 FT REGION 1..82  
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 FT COMPBIAS 54..69  
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 FT ECO:0007744|PubMed:19779198"  
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 FT HELIX 25..42  
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 FT HELIX 53..56  
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 FT HELIX 58..61  
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 FT STRAND 71..73

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FT HELIX 74..100  
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SQ SEQUENCE 109 AA; 11693 MW; 7C73862689759B4A CRC64;  
MSDAGRKGFG EKASEALKPD SQKSYAEQ GK EYITDKADKV AGKVQPEDNK GVFQGVHDSA  
EKGKDNAEGQ GESLADQARD YMGAAKSKLN DAVEYVSGRV HGEEDPTKK

Mascot: <http://www.matrixscience.com/>

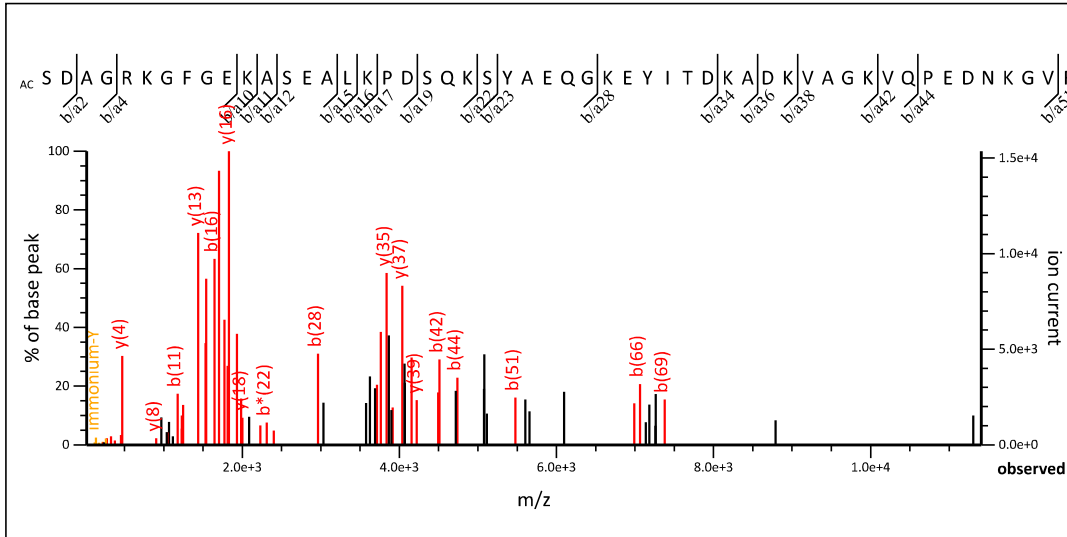
Peptide View

MS/MS Fragmentation of

**SDAGRKGFGKEASEALKPDSQKSYAEQGKEYITDKADKVAGKVQPEDNKGVFQGVHDSAEEKGKDNAEGQGESLADQARDYMGAAKSKLNDAVEYVSG**  
Found in **HSP12\_YEAST** in **Swissprot\_22\_05\_2024**, 12 kDa heat shock protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP12  
PE=1 SV=1

Match to Query 1: 11597.141924 from(11598.149200,1+) intensity(188193.9713) index(0)

Data file S\_cerevisiae\_11600\_Da\_merged.txt



20.08 to 11409.03



Monoisotopic mass of neutral peptide Mr(calc): 11596.6289

Variable modifications:

N-term : Acetyl (Protein N-term)

Ions Score: 103 Expect: 6.5e-10

Peak matches: 60/2126 fragment ions using 69 most intense peaks

Annotated fragments: 62/2126 ([help](#))

#	Immon.	a	a*	a <sup>0</sup>	b	b*	b <sup>0</sup>	Seq.	y	y*	y <sup>0</sup>	#
1	60.0444	102.0550		84.0444	130.0499		112.0393	S				108
2	88.0393	217.0819		199.0713	245.0768		227.0662	D	11468.5937	11451.5672	11450.5832	107
3	44.0495	288.1190		270.1084	316.1139		298.1034	A	11353.5668	11336.5402	11335.5562	106
4	30.0338	345.1405		327.1299	373.1354		355.1248	G	11282.5297	11265.5031	11264.5191	105
5	129.1135	501.2416	484.2150	483.2310	529.2365	512.2100	511.2259	R	11225.5082	11208.4817	11207.4976	104
6	101.1073	629.3365	612.3100	611.3260	657.3315	640.3049	639.3209	K	11069.4071	11052.3805	11051.3965	103
7	30.0338	686.3580	669.3315	668.3474	714.3529	697.3264	696.3424	G	10941.3121	10924.2856	10923.3016	102
8	120.0808	833.4264	816.3999	815.4159	861.4213	844.3948	843.4108	F	10884.2907	10867.2641	10866.2801	101
9	30.0338	890.4479	873.4213	872.4373	918.4428	901.4163	900.4322	G	10737.2223	10720.1957	10719.2117	100
10	102.0550	1019.4905	1002.4639	1001.4799	1047.4854	1030.4588	1029.4748	E	10680.2008	10663.1742	10662.1902	99
11	101.1073	1147.5854	1130.5589	1129.5749	1175.5804	1158.5538	1157.5698	K	10551.1582	10534.1317	10533.1476	98
12	44.0495	1218.6226	1201.5960	1200.6120	1246.6175	1229.5909	1228.6069	A	10423.0632	10406.0367	10405.0527	97
13	60.0444	1305.6546	1288.6280	1287.6440	1333.6495	1316.6230	1315.6389	S	10352.0261	10334.9996	10334.0156	96
14	102.0550	1434.6972	1417.6706	1416.6866	1462.6921	1445.6655	1444.6815	E	10264.9941	10247.9675	10246.9835	95
15	44.0495	1505.7343	1488.7077	1487.7237	1533.7292	1516.7027	1515.7186	A	10135.9515	10118.9250	10117.9409	94
16	86.0964	1618.8184	1601.7918	1600.8078	1646.8133	1629.7867	1628.8027	L	10064.9144	10047.8878	10046.9038	93
17	101.1073	1746.9133	1729.8868	1728.9028	1774.9082	1757.8817	1756.8977	K	9951.8303	9934.8038	9933.8198	92
18	70.0651	1843.9661	1826.9395	1825.9555	1871.9610	1854.9345	1853.9504	P	9823.7354	9806.7088	9805.7248	91
19	88.0393	1958.9930	1941.9665	1940.9825	1986.9879	1969.9614	1968.9774	D	9726.6826	9709.6560	9708.6720	90
20	60.0444	2046.0251	2028.9985	2028.0145	2074.0200	2056.9934	2056.0094	S	9611.6557	9594.6291	9593.6451	89
21	101.0709	2174.0836	2157.0571	2156.0731	2202.0786	2185.0520	2184.0680	Q	9524.6236	9507.5971	9506.6131	88
22	101.1073	2302.1786	2285.1521	2284.1680	2330.1735	2313.1470	2312.1629	K	9396.5650	9379.5385	9378.5545	87
23	60.0444	2389.2106	2372.1841	2371.2001	2417.2055	2400.1790	2399.1950	S	9268.4701	9251.4435	9250.4595	86
24	136.0757	2552.2740	2535.2474	2534.2634	2580.2689	2563.2423	2562.2583	Y	9181.4381	9164.4115	9163.4275	85
25	44.0495	2623.3111	2606.2845	2605.3005	2651.3060	2634.2794	2633.2954	A	9018.3747	9001.3482	9000.3642	84

26	102.0550	2752.3537	2735.3271	2734.3431	2780.3486	2763.3220	2762.3380	E	8947.3376	8930.3111	8929.3271	83
27	101.0709	2880.4122	2863.3857	2862.4017	2908.4072	2891.3806	2890.3966	Q	8818.2950	8801.2685	8800.2845	82
28	30.0338	2937.4337	2920.4072	2919.4231	2965.4286	2948.4021	2947.4181	G	8690.2364	8673.2099	8672.2259	81
29	101.1073	3065.5287	3048.5021	3047.5181	3093.5236	3076.4970	3075.5130	K	8633.2150	8616.1884	8615.2044	80
30	102.0550	3194.5713	3177.5447	3176.5607	3222.5662	3205.5396	3204.5556	E	8505.1200	8488.0935	8487.1095	79
31	136.0757	3357.6346	3340.6080	3339.6240	3385.6295	3368.6030	3367.6189	Y	8376.0774	8359.0509	8358.0669	78
32	86.0964	3470.7187	3453.6921	3452.7081	3498.7136	3481.6870	3480.7030	I	8213.0141	8195.9875	8195.0035	77
33	74.0600	3571.7663	3554.7398	3553.7558	3599.7612	3582.7347	3581.7507	T	8099.9300	8082.9035	8081.9195	76
34	88.0393	3686.7933	3669.7667	3668.7827	3714.7882	3697.7616	3696.7776	D	7998.8824	7981.8558	7980.8718	75
35	101.1073	3814.8882	3797.8617	3796.8777	3842.8832	3825.8566	3824.8726	K	7883.8554	7866.8289	7865.8448	74
36	44.0495	3885.9254	3868.8988	3867.9148	3913.9203	3896.8937	3895.9097	A	7755.7604	7738.7339	7737.7499	73
37	88.0393	4000.9523	3983.9257	3982.9417	4028.9472	4011.9207	4010.9366	D	7684.7233	7667.6968	7666.7128	72
38	101.1073	4129.0473	4112.0207	4111.0367	4157.0422	4140.0156	4139.0316	K	7569.6964	7552.6698	7551.6858	71
39	72.0808	4228.1157	4211.0891	4210.1051	4256.1106	4239.0840	4238.1000	V	7441.6014	7424.5749	7423.5909	70
40	44.0495	4299.1528	4282.1262	4281.1422	4327.1477	4310.1212	4309.1371	A	7342.5330	7325.5065	7324.5224	69
41	30.0338	4356.1743	4339.1477	4338.1637	4384.1692	4367.1426	4366.1586	G	7271.4959	7254.4693	7253.4853	68
42	101.1073	4484.2692	4467.2427	4466.2586	4512.2641	4495.2376	4494.2536	K	7214.4744	7197.4479	7196.4639	67
43	72.0808	4583.3376	4566.3111	4565.3271	4611.3325	4594.3060	4593.3220	V	7086.3795	7069.3529	7068.3689	66
44	101.0709	4711.3962	4694.3697	4693.3856	4739.3911	4722.3646	4721.3806	Q	6987.3111	6970.2845	6969.3005	65
45	70.0651	4808.4490	4791.4224	4790.4384	4836.4439	4819.4173	4818.4333	P	6859.2525	6842.2259	6841.2419	64
46	102.0550	4937.4916	4920.4650	4919.4810	4965.4865	4948.4599	4947.4759	E	6762.1997	6745.1732	6744.1892	63
47	88.0393	5052.5185	5035.4920	5034.5079	5080.5134	5063.4869	5062.5029	D	6633.1571	6616.1306	6615.1466	62
48	87.0553	5166.5614	5149.5349	5148.5509	5194.5563	5177.5298	5176.5458	N	6518.1302	6501.1036	6500.1196	61
49	101.1073	5294.6564	5277.6298	5276.6458	5322.6513	5305.6248	5304.6407	K	6404.0873	6387.0607	6386.0767	60
50	30.0338	5351.6779	5334.6513	5333.6673	5379.6728	5362.6462	5361.6622	G	6275.9923	6258.9657	6257.9817	59
51	72.0808	5450.7463	5433.7197	5432.7357	5478.7412	5461.7146	5460.7306	V	6218.9708	6201.9443	6200.9603	58
52	120.0808	5597.8147	5580.7881	5579.8041	5625.8096	5608.7831	5607.7990	F	6119.9024	6102.8759	6101.8918	57
53	101.0709	5725.8733	5708.8467	5707.8627	5753.8682	5736.8416	5735.8576	Q	5972.8340	5955.8074	5954.8234	56
54	30.0338	5782.8947	5765.8682	5764.8842	5810.8896	5793.8631	5792.8791	G	5844.7754	5827.7489	5826.7649	55
55	72.0808	5881.9631	5864.9366	5863.9526	5909.9581	5892.9315	5891.9475	V	5787.7540	5770.7274	5769.7434	54
56	110.0713	6019.0221	6001.9955	6001.0115	6047.0170	6029.9904	6029.0064	H	5688.6855	5671.6590	5670.6750	53
57	88.0393	6134.0490	6117.0225	6116.0384	6162.0439	6145.0174	6144.0333	D	5551.6266	5534.6001	5533.6161	52
58	60.0444	6221.0810	6204.0545	6203.0705	6249.0759	6232.0494	6231.0654	S	5436.5997	5419.5731	5418.5891	51
59	44.0495	6292.1181	6275.0916	6274.1076	6320.1131	6303.0865	6302.1025	A	5349.5677	5332.5411	5331.5571	50
60	102.0550	6421.1607	6404.1342	6403.1502	6449.1556	6432.1291	6431.1451	E	5278.5305	5261.5040	5260.5200	49
61	101.1073	6549.2557	6532.2291	6531.2451	6577.2506	6560.2241	6559.2400	K	5149.4880	5132.4614	5131.4774	48
62	30.0338	6606.2772	6589.2506	6588.2666	6634.2721	6617.2455	6616.2615	G	5021.3930	5004.3664	5003.3824	47
63	101.1073	6734.3721	6717.3456	6716.3616	6762.3670	6745.3405	6744.3565	K	4964.3715	4947.3450	4946.3610	46
64	88.0393	6849.3991	6832.3725	6831.3885	6877.3940	6860.3674	6859.3834	D	4836.2766	4819.2500	4818.2660	45
65	87.0553	6963.4420	6946.4154	6945.4314	6991.4369	6974.4104	6973.4263	N	4721.2496	4704.2231	4703.2391	44
66	44.0495	7034.4791	7017.4526	7016.4685	7062.4740	7045.4475	7044.4635	A	4607.2067	4590.1801	4589.1961	43
67	102.0550	7163.5217	7146.4952	7145.5111	7191.5166	7174.4901	7173.5061	E	4536.1696	4519.1430	4518.1590	42
68	30.0338	7220.5432	7203.5166	7202.5326	7248.5381	7231.5115	7230.5275	G	4407.1270	4390.1004	4389.1164	41
69	101.0709	7348.6017	7331.5752	7330.5912	7376.5967	7359.5701	7358.5861	Q	4350.1055	4333.0790	4332.0950	40
70	30.0338	7405.6232	7388.5967	7387.6126	7433.6181	7416.5916	7415.6076	G	4222.0469	4205.0204	4204.0364	39
71	102.0550	7534.6658	7517.6393	7516.6552	7562.6607	7545.6342	7544.6502	E	4165.0255	4147.9989	4147.0149	38
72	60.0444	7621.6978	7604.6713	7603.6873	7649.6927	7632.6662	7631.6822	S	4035.9829	4018.9563	4017.9723	37
73	86.0964	7734.7819	7717.7553	7716.7713	7762.7768	7745.7503	7744.7662	L	3948.9509	3931.9243	3930.9403	36
74	44.0495	7805.8190	7788.7925	7787.8084	7833.8139	7816.7874	7815.8034	A	3835.8668	3818.8402	3817.8562	35
75	88.0393	7920.8459	7903.8194	7902.8354	7948.8409	7931.8143	7930.8303	D	3764.8297	3747.8031	3746.8191	34
76	101.0709	8048.9045	8031.8780	8030.8940	8076.8994	8059.8729	8058.8889	Q	3649.8027	3632.7762	3631.7922	33
77	44.0495	8119.9416	8102.9151	8101.9311	8147.9366	8130.9100	8129.9260	A	3521.7442	3504.7176	3503.7336	32
78	129.1135	8276.0428	8259.0162	8258.0322	8304.0377	8287.0111	8286.0271	R	3450.7070	3433.6805	3432.6965	31
79	88.0393	8391.0697	8374.0431	8373.0591	8419.0646	8402.0381	8401.0540	D	3294.6059	3277.5794	3276.5954	30
80	136.0757	8554.1330	8537.1065	8536.1225	8582.1279	8565.1014	8564.1174	Y	3179.5790	3162.5524	3161.5684	29
81	104.0528	8685.1735	8668.1470	8667.1629	8713.1684	8696.1419	8695.1579	M	3016.5157	2999.4891	2998.5051	28
82	30.0338	8742.1950	8725.1684	8724.1844	8770.1899	8753.1633	8752.1793	G	2885.4752	2868.4486	2867.4646	27
83	44.0495	8813.2321	8796.2055	8795.2215	8841.2270	8824.2005	8823.2164	A	2828.4537	2811.4272	2810.4431	26
84	44.0495	8884.2692	8867.2427	8866.2586	8912.2641	8895.2376	8894.2536	A	2757.4166	2740.3900	2739.4060	25
85	101.1073	9012.3642	8995.3376	8994.3536	9040.3591	9023.3325	9022.3485	K	2686.3795	2669.3529	2668.3689	24
86	60.0444	9099.3962	9082.3696	9081.3856	9127.3911	9110.3646	9109.3805	S	2558.2845	2541.2580	2540.2740	23



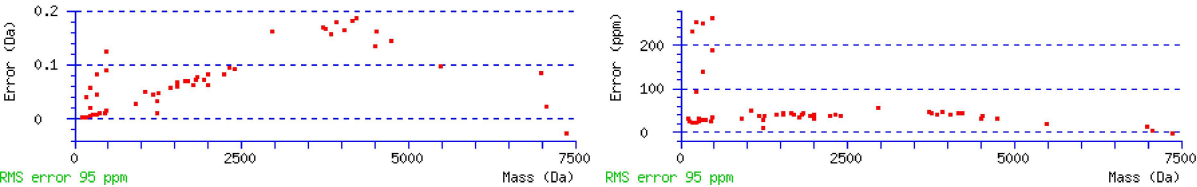
87	101.1073	9227.4912	9210.4646	9209.4806	9255.4861	9238.4595	9237.4755	K	2471.2525	2454.2259	2453.2419	22
88	86.0964	9340.5752	9323.5487	9322.5647	9368.5701	9351.5436	9350.5596	L	2343.1575	2326.1310	2325.1470	21
89	87.0553	9454.6181	9437.5916	9436.6076	9482.6131	9465.5865	9464.6025	N	2230.0735	2213.0469	2212.0629	20
90	88.0393	9569.6451	9552.6185	9551.6345	9597.6400	9580.6135	9579.6294	D	2116.0305	2099.0040	2098.0200	19
91	44.0495	9640.6822	9623.6557	9622.6716	9668.6771	9651.6506	9650.6666	A	2001.0036	1983.9770	1982.9930	18
92	72.0808	9739.7506	9722.7241	9721.7401	9767.7455	9750.7190	9749.7350	V	1929.9665	1912.9399	1911.9559	17
93	102.0550	9868.7932	9851.7667	9850.7826	9896.7881	9879.7616	9878.7776	E	1830.8981	1813.8715	1812.8875	16
94	136.0757	10031.8565	10014.8300	10013.8460	10059.8515	10042.8249	10041.8409	Y	1701.8555	1684.8289	1683.8449	15
95	72.0808	10130.9250	10113.8984	10112.9144	10158.9199	10141.8933	10140.9093	V	1538.7921	1521.7656	1520.7816	14
96	60.0444	10217.9570	10200.9304	10199.9464	10245.9519	10228.9253	10227.9413	S	1439.7237	1422.6972	1421.7132	13
97	30.0338	10274.9784	10257.9519	10256.9679	10302.9734	10285.9468	10284.9628	G	1352.6917	1335.6652	1334.6811	12
98	129.1135	10431.0796	10414.0530	10413.0690	10459.0745	10442.0479	10441.0639	R	1295.6702	1278.6437	1277.6597	11
99	72.0808	10530.1480	10513.1214	10512.1374	10558.1429	10541.1163	10540.1323	V	1139.5691	1122.5426	1121.5586	10
100	110.0713	10667.2069	10650.1803	10649.1963	10695.2018	10678.1752	10677.1912	H	1040.5007	1023.4742	1022.4902	9
101	30.0338	10724.2283	10707.2018	10706.2178	10752.2233	10735.1967	10734.2127	G	903.4418	886.4153	885.4312	8
102	102.0550	10853.2709	10836.2444	10835.2604	10881.2659	10864.2393	10863.2553	E	846.4203	829.3938	828.4098	7
103	102.0550	10982.3135	10965.2870	10964.3030	11010.3084	10993.2819	10992.2979	E	717.3777	700.3512	699.3672	6
104	88.0393	11097.3405	11080.3139	11079.3299	11125.3354	11108.3088	11107.3248	D	588.3352	571.3086	570.3246	5
105	70.0651	11194.3932	11177.3667	11176.3827	11222.3882	11205.3616	11204.3776	P	473.3082	456.2817	455.2976	4
106	74.0600	11295.4409	11278.4144	11277.4304	11323.4358	11306.4093	11305.4253	T	376.2554	359.2289	358.2449	3
107	101.1073	11423.5359	11406.5093	11405.5253	11451.5308	11434.5042	11433.5202	K	275.2078	258.1812		2
108	101.1073							K	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DA	159.0764	187.0713	DAG	216.0979	244.0928	DAGR	372.1990	400.1939
DAGRK	500.2940	528.2889	DAGRKG	557.3154	585.3103	AG	101.0709	129.0659
AGR	257.1721	285.1670	AGRK	385.2670	413.2619	AGRKG	442.2885	470.2834
AGRKGF	589.3569	617.3518	AGRKGFG	646.3784	674.3733	GR	186.1349	214.1299
GRK	314.2299	342.2248	GRKG	371.2514	399.2463	GRKGF	518.3198	546.3147
GRKGFG	575.3412	603.3362	RK	257.2084	285.2034	RKG	314.2299	342.2248
RKGF	461.2983	489.2932	RKGFGE	518.3198	546.3147	RKGFGE	647.3624	675.3573
KG	158.1288	186.1237	KGF	305.1972	333.1921	KGFG	362.2187	390.2136
KGFGE	491.2613	519.2562	KGFGEK	619.3562	647.3511	KGFGEKA	690.3933	
GF	177.1022	205.0972	GFG	234.1237	262.1186	GFGE	363.1663	391.1612
GFGEK	491.2613	519.2562	GFGEKA	562.2984	590.2933	GFGEKAS	649.3304	677.3253
FG	177.1022	205.0972	FGE	306.1448	334.1397	FGEK	434.2398	462.2347
FGEKA	505.2769	533.2718	FGEKAS	592.3089	620.3039	GE	159.0764	187.0713
GEK	287.1714	315.1663	GEKA	358.2085	386.2034	GEKAS	445.2405	473.2354
GEKASE	574.2831	602.2780	GEKASEA	645.3202	673.3151	EK	230.1499	258.1448
EKA	301.1870	329.1819	EKAS	388.2191	416.2140	EKASE	517.2617	545.2566
EKASEA	588.2988	616.2937	KA	172.1444	200.1394	KAS	259.1765	287.1714
KASE	388.2191	416.2140	KASEA	459.2562	487.2511	KASEAL	572.3402	600.3352
AS	131.0815	159.0764	ASE	260.1241	288.1190	ASEA	331.1612	359.1561
ASEAL	444.2453	472.2402	ASEALK	572.3402	600.3352	ASEALKP	669.3930	697.3879
SE	189.0870	217.0819	SEA	260.1241	288.1190	SEAL	373.2082	401.2031
SEALK	501.3031	529.2980	SEALKP	598.3559	626.3508	EA	173.0921	201.0870
EAL	286.1761	314.1710	EALK	414.2711	442.2660	EALKP	511.3239	539.3188
EALKPD	626.3508	654.3457	AL	157.1335	185.1285	ALK	285.2285	313.2234
ALKP	382.2813	410.2762	ALKPD	497.3082	525.3031	ALKPDS	584.3402	612.3352
LK	214.1914	242.1863	LKP	311.2442	339.2391	LKPD	426.2711	454.2660
LKPDS	513.3031	541.2980	LKPDSQ	641.3617	669.3566	KP	198.1601	226.1550
KPD	313.1870	341.1819	KPDS	400.2191	428.2140	KPDSQ	528.2776	556.2726
KPDSQK	656.3726	684.3675	PD	185.0921	213.0870	PDS	272.1241	300.1190
PDSQ	400.1827	428.1776	PDSQK	528.2776	556.2726	PDSQKS	615.3097	643.3046
DS	175.0713	203.0662	DSQ	303.1299	331.1248	DSQK	431.2249	459.2198
DSQKS	518.2569	546.2518	DSQKSY	681.3202		SQ	188.1030	216.0979
SQK	316.1979	344.1928	SQKS	403.2300	431.2249	SQKSY	566.2933	594.2882
SQKSYA	637.3304	665.3253	QK	229.1659	257.1608	QKS	316.1979	344.1928
QKSY	479.2613	507.2562	QKSYA	550.2984	578.2933	QKSYAE	679.3410	
KS	188.1394	216.1343	KSY	351.2027	379.1976	KSYA	422.2398	450.2347
KSYAE	551.2824	579.2773	KSYAEQ	679.3410		SY	223.1077	251.1026

SYA	294.1448	322.1397	SYAE	423.1874	451.1823	SYAEQ	551.2460	579.2409
SYAEQG	608.2675	636.2624	YA	207.1128	235.1077	YAE	336.1554	364.1503
YAEQ	464.2140	492.2089	YAEQG	521.2354	549.2304	YAEQ GK	649.3304	677.3253
AE	173.0921	201.0870	AEQ	301.1506	329.1456	AEQG	358.1721	386.1670
AEQGK	486.2671	514.2620	AEQGKE	615.3097	643.3046	EQ	230.1135	258.1084
EQG	287.1350	315.1299	EQGK	415.2300	443.2249	EQGKE	544.2726	572.2675
QG	158.0924	186.0873	QGK	286.1874	314.1823	QGKE	415.2300	443.2249
QGKEY	578.2933	606.2882	QGKEYI	691.3774		GK	158.1288	186.1237
GKE	287.1714	315.1663	GKEY	450.2347	478.2296	GKEYI	563.3188	591.3137
GKEYIT	664.3665	692.3614	KE	230.1499	258.1448	KEY	393.2132	421.2082
KEYI	506.2973	534.2922	KEYIT	607.3450	635.3399	EY	265.1183	293.1132
EYI	378.2023	406.1973	EYIT	479.2500	507.2449	EYITD	594.2770	622.2719
YI	249.1598	277.1547	YIT	350.2074	378.2023	YITD	465.2344	493.2293
YITDK	593.3293	621.3243	YITDKA	664.3665	692.3614	IT	187.1441	215.1390
ITD	302.1710	330.1660	ITDK	430.2660	458.2609	ITDKA	501.3031	529.2980
ITDKAD	616.3301	644.3250	TD	189.0870	217.0819	TDK	317.1819	345.1769
TDKA	388.2191	416.2140	TDKAD	503.2460	531.2409	TDKADK	631.3410	659.3359
DK	216.1343	244.1292	DKA	287.1714	315.1663	DKAD	402.1983	430.1932
DKADK	530.2933	558.2882	DKADKV	629.3617	657.3566	KAD	287.1714	315.1663
KADK	415.2663	443.2613	KADKV	514.3348	542.3297	KADKVA	585.3719	613.3668
KADKVAG	642.3933	670.3883	AD	159.0764	187.0713	ADK	287.1714	315.1663
ADKV	386.2398	414.2347	ADKVA	457.2769	485.2718	ADKVAG	514.2984	542.2933
ADKVAGK	642.3933	670.3883	DKV	315.2027	343.1976	DKVA	386.2398	414.2347
DKVAG	443.2613	471.2562	DKVAGK	571.3562	599.3511	DKVAGKV	670.4246	698.4196
KV	200.1757	228.1707	KVA	271.2129	299.2078	KVAG	328.2343	356.2292
KVAGK	456.3293	484.3242	KVAGKV	555.3977	583.3926	KVAGKVQ	683.4563	
VA	143.1179	171.1128	VAG	200.1394	228.1343	VAGK	328.2343	356.2292
VAGKV	427.3027	455.2976	VAGKVQ	555.3613	583.3562	VAGKVQP	652.4141	680.4090
AGK	229.1659	257.1608	AGKV	328.2343	356.2292	AGKVQ	456.2929	484.2878
AGKVQP	553.3457	581.3406	AGKVQPE	682.3883		GKV	257.1972	285.1921
GKVQ	385.2558	413.2507	GKVQP	482.3085	510.3035	GKVQPE	611.3511	639.3461
KVQ	328.2343	356.2292	KVQP	425.2871	453.2820	KVQPE	554.3297	582.3246
KVQPED	669.3566	697.3515	VQ	200.1394	228.1343	VQP	297.1921	325.1870
VQPE	426.2347	454.2296	VQPED	541.2617	569.2566	VQPEDN	655.3046	683.2995
QP	198.1237	226.1186	QPE	327.1663	355.1612	QPED	442.1932	470.1882
QPEDN	556.2362	584.2311	QPEDNK	684.3311		PE	199.1077	227.1026
PED	314.1347	342.1296	PEDN	428.1776	456.1725	PEDNK	556.2726	584.2675
PEDNKG	613.2940	641.2889	ED	217.0819	245.0768	EDN	331.1248	359.1197
EDNK	459.2198	487.2147	EDNKG	516.2413	544.2362	EDNKG V	615.3097	643.3046
DN	202.0822	230.0771	DNK	330.1772	358.1721	DNKG	387.1987	415.1936
DNKG V	486.2671	514.2620	DNKGVF	633.3355	661.3304	NK	215.1503	243.1452
NKG	272.1717	300.1666	NKGV	371.2401	399.2350	NKGVF	518.3085	546.3035
NKGVFQ	646.3671	674.3620	KGV	257.1972	285.1921	KGVF	404.2656	432.2605
KGVFQ	532.3242	560.3191	KGVFQG	589.3457	617.3406	KGVFQGV	688.4141	
GV	129.1022	157.0972	GVF	276.1707	304.1656	GVFQ	404.2292	432.2241
GVFQG	461.2507	489.2456	GVFQGV	560.3191	588.3140	GVFQGVH	697.3780	
VF	219.1492	247.1441	VFQ	347.2078	375.2027	VFQG	404.2292	432.2241
VFQGV	503.2976	531.2926	VFQGVH	640.3566	668.3515	FQ	248.1394	276.1343
FQG	305.1608	333.1557	FQGV	404.2292	432.2241	FQGVH	541.2881	569.2831
FQGVHD	656.3151	684.3100	QGV	257.1608	285.1557	QGVH	394.2197	422.2146
QGVHD	509.2467	537.2416	QGVHDS	596.2787	624.2736	QGVHDSA	667.3158	695.3107
GVH	266.1612	294.1561	GVHD	381.1881	409.1830	GVHDS	468.2201	496.2150
GVHDSA	539.2572	567.2522	GVHDSAE	668.2998	696.2947	VH	209.1397	237.1346
VHD	324.1666	352.1615	VHDS	411.1987	439.1936	VHDSA	482.2358	510.2307
VHDSAE	611.2784	639.2733	HD	225.0982	253.0931	HDS	312.1302	340.1252
HDSA	383.1674	411.1623	HDSAE	512.2100	540.2049	HDSAEK	640.3049	668.2998
HDSAEKG	697.3264		DSA	246.1084	274.1034	DSAE	375.1510	403.1460
DSAEK	503.2460	531.2409	DSAEKG	560.2675	588.2624	DSAEKGK	688.3624	
SA	131.0815	159.0764	SAE	260.1241	288.1190	SAEK	388.2191	416.2140
SAEKG	445.2405	473.2354	SAEKGK	573.3355	601.3304	SAEKGKD	688.3624	
AEK	301.1870	329.1819	AEKG	358.2085	386.2034	AEKGK	486.3035	514.2984

AEKGKD	601.3304	629.3253	EKG	287.1714	315.1663	EKGK	415.2663	443.2613
EKGKD	530.2933	558.2882	EKGKDN	644.3362	672.3311	KGK	286.2238	314.2187
KGKD	401.2507	429.2456	KGKDN	515.2936	543.2885	KGKDNA	586.3307	614.3257
GKD	273.1557	301.1506	GKDN	387.1987	415.1936	GKDNA	458.2358	486.2307
GKDNAE	587.2784	615.2733	GKDNAEG	644.2998	672.2947	KD	216.1343	244.1292
KDN	330.1772	358.1721	KDNA	401.2143	429.2092	KDNAE	530.2569	558.2518
KDNAEG	587.2784	615.2733	DNA	273.1193	301.1143	DNAE	402.1619	430.1569
DNAEG	459.1834	487.1783	DNAEGQ	587.2420	615.2369	DNAEGQG	644.2634	672.2584
NA	158.0924	186.0873	NAE	287.1350	315.1299	NAEG	344.1565	372.1514
NAEGQ	472.2150	500.2100	NAEGQG	529.2365	557.2314	NAEGQGE	658.2791	686.2740
AEG	230.1135	258.1084	AEGQ	358.1721	386.1670	AEGQG	415.1936	443.1885
AEGQGE	544.2362	572.2311	AEGQGES	631.2682	659.2631	EG	159.0764	187.0713
EGQ	287.1350	315.1299	EGQG	344.1565	372.1514	EGQGE	473.1991	501.1940
EGQGES	560.2311	588.2260	EGQGESL	673.3151		GQ	158.0924	186.0873
GQG	215.1139	243.1088	GQGE	344.1565	372.1514	GQGES	431.1885	459.1834
GQGESL	544.2726	572.2675	GQGESLA	615.3097	643.3046	QGE	287.1350	315.1299
QGES	374.1670	402.1619	QGESL	487.2511	515.2460	QGESLA	558.2882	586.2831
QGESLAD	673.3151		GES	246.1084	274.1034	GESL	359.1925	387.1874
GESLA	430.2296	458.2245	GESLAD	545.2566	573.2515	GESLADQ	673.3151	
ES	189.0870	217.0819	ESL	302.1710	330.1660	ESLA	373.2082	401.2031
ESLAD	488.2351	516.2300	ESLADQ	616.2937	644.2886	ESLADQA	687.3308	
SL	173.1285	201.1234	SLA	244.1656	272.1605	SLAD	359.1925	387.1874
SLADQ	487.2511	515.2460	SLADQA	558.2882	586.2831	LA	157.1335	185.1285
LAD	272.1605	300.1554	LADQ	400.2191	428.2140	LADQA	471.2562	499.2511
LADQAR	627.3573	655.3522	ADQ	287.1350	315.1299	ADQA	358.1721	386.1670
ADQAR	514.2732	542.2681	ADQARD	629.3002	657.2951	DQ	216.0979	244.0928
DQA	287.1350	315.1299	DQAR	443.2361	471.2310	DQARD	558.2631	586.2580
QA	172.1081	200.1030	QAR	328.2092	356.2041	QARD	443.2361	471.2310
QARDY	606.2994	634.2944	AR	200.1506	228.1455	ARD	315.1775	343.1724
ARDY	478.2409	506.2358	ARDYM	609.2813	637.2763	ARDYMG	666.3028	694.2977
RD	244.1404	272.1353	RDY	407.2037	435.1987	RDYM	538.2442	566.2391
RDYMG	595.2657	623.2606	RDYMGAA	666.3028	694.2977	DY	251.1026	279.0975
DYM	382.1431	410.1380	DYMG	439.1646	467.1595	DYMGAA	510.2017	538.1966
DYMGAA	581.2388	609.2337	YM	267.1162	295.1111	YMG	324.1376	352.1326
YMGAA	395.1748	423.1697	YMGAA	466.2119	494.2068	YMGAAK	594.3068	622.3017
YMGAAKS	681.3389		MG	161.0743	189.0692	MGA	232.1114	260.1063
MGAA	303.1485	331.1435	MGAAK	431.2435	459.2384	MGAAKS	518.2755	546.2704
MGAAKSK	646.3705	674.3654	GA	101.0709	129.0659	GAA	172.1081	200.1030
GAAK	300.2030	328.1979	GAAKS	387.2350	415.2300	GAAKSK	515.3300	543.3249
GAAKSKL	628.4141	656.4090	AA	115.0866	143.0815	AAK	243.1816	271.1765
AAKS	330.2136	358.2085	AAKSK	458.3085	486.3035	AAKSKL	571.3926	599.3875
AAKSKLN	685.4355		AK	172.1444	200.1394	AKS	259.1765	287.1714
AKSK	387.2714	415.2663	AKSKL	500.3555	528.3504	AKSKLN	614.3984	642.3933
KSK	316.2343	344.2292	KSKL	429.3184	457.3133	KSKLN	543.3613	571.3562
KSKLND	658.3882	686.3832	SK	188.1394	216.1343	SKL	301.2234	329.2183
SKLN	415.2663	443.2613	SKLND	530.2933	558.2882	SKLNDA	601.3304	629.3253
KL	214.1914	242.1863	KLN	328.2343	356.2292	KLND	443.2613	471.2562
KLNDA	514.2984	542.2933	KLNDAY	613.3668	641.3617	LN	200.1394	228.1343
LND	315.1663	343.1612	LNDA	386.2034	414.1983	LNDAY	485.2718	513.2667
LNDAY	614.3144	642.3093	ND	202.0822	230.0771	NDA	273.1193	301.1143
NDAY	372.1878	400.1827	NDAY	501.2304	529.2253	NDAYEY	664.2937	692.2886
DAY	258.1448	286.1397	DAVE	387.1874	415.1823	DAVEY	550.2508	578.2457
DAVEYV	649.3192	677.3141	AV	143.1179	171.1128	AVE	272.1605	300.1554
AVEY	435.2238	463.2187	AVEYV	534.2922	562.2871	AVEYVS	621.3243	649.3192
AVEYVSG	678.3457		VE	201.1234	229.1183	VEY	364.1867	392.1816
VEYV	463.2551	491.2500	VEYVS	550.2871	578.2821	VEYVSG	607.3086	635.3035
EYV	364.1867	392.1816	EYVS	451.2187	479.2136	EYVSG	508.2402	536.2351
EYVSGR	664.3413	692.3362	YV	235.1441	263.1390	YVS	322.1761	350.1710
YVSG	379.1976	407.1925	YVSGR	535.2987	563.2936	YVSGRV	634.3671	662.3620
VS	159.1128	187.1077	VSG	216.1343	244.1292	VSGR	372.2354	400.2303
VSGRV	471.3038	499.2987	VSGRVH	608.3627	636.3576	VSGRVHG	665.3842	693.3791

SG	117.0659	145.0608	SGR	273.1670	301.1619	SGRV	372.2354	400.2303
SGRVH	509.2943	537.2892	SGRVHG	566.3158	594.3107	SGRVHGE	695.3583	
GRV	285.2034	313.1983	GRVH	422.2623	450.2572	GRVHG	479.2837	507.2786
GRVHGE	608.3263	636.3212	RV	228.1819	256.1768	RVH	365.2408	393.2357
RVHG	422.2623	450.2572	RVHGE	551.3049	579.2998	RVHGEE	680.3474	
VHG	266.1612	294.1561	VHGE	395.2037	423.1987	VHGEE	524.2463	552.2413
VHGEE	639.2733	667.2682	HG	167.0927	195.0877	HGE	296.1353	324.1302
HGEE	425.1779	453.1728	HGEED	540.2049	568.1998	HGEEDP	637.2576	665.2525
GEE	288.1190	316.1139	GEED	403.1460	431.1409	GEEDP	500.1987	528.1936
GEEDPT	601.2464	629.2413	EE	231.0975	259.0925	EED	346.1245	374.1194
EEDP	443.1773	471.1722	EEDPT	544.2249	572.2198	EEDPTK	672.3199	
EDP	314.1347	342.1296	EDPT	415.1823	443.1773	EDPTK	543.2773	571.2722
DP	185.0921	213.0870	DPT	286.1397	314.1347	DPTK	414.2347	442.2296
PT	171.1128	199.1077	PTK	299.2078	327.2027	TK	202.1550	230.1499



NCBI BLAST search of [SDAGRKGGEKASEALKPDSQKS](#)YAEQKEYITDKADKVAGKVQPEDNKGVFQGVHDSAEEKGKDNAEGQGESLADQARDYMGAASKLNDAVEYVSGRVHGI  
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)  
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
102.8	11596.6289	0.5130	<a href="#">SDAGRKGGEKASEALKPDSQKS</a> YAEQKEYITDKADKVAGKVQPEDNKGVFQGVHDSAEEKGKDNAEGQGESLADQARDYMGAAS
4.6	11597.7109	-0.5690	<a href="#">ALFDQSGLWEGPEDERVKGKRVAVTAASGAVGMWILQFARIAGF</a> DAVIGTCGDGNEDFVKSMTATDAVNYKTTSLTAWAAEKQGRKA
3.8	11596.9540	0.1879	<a href="#">GGAANQTTLNNGVLQVYGAANDTTIKGGRLIVEKDGGA</a> VFVAIEKGGLLEVKEGGFAFAVDQKAGGAIKTTTRAMEVFGTNRLGQFI
3.6	11596.9388	0.2032	<a href="#">YEPTHEYTSARQVYMIAAGIIGCLYLCLISVFLGVKERDDPYALVAGKVIPFFKGFRET</a> MQFGPYLNLISSFLLSAAVQIQSNFVLFCT
3.4	11596.8824	0.2596	<a href="#">TGGLWLSDEAHHHLAIAVLFLIAGHQYRTNWGIGHSMKEILEAHKGPFTGEGHKGLYEIL</a> TTSWHAQLAINLAMLGSLSIIVAHHMYAN
3.3	11596.5920	0.5499	<a href="#">GTFTADFPNLQARDNEGPSIYHATGMSASLASNRLSWFYNL</a> RGPSLTVDACSSSLTAFLACQSIRTGEAEMSVVGGANLMFGPDMSI
3.3	11597.0230	0.1189	<a href="#">RAVAGSHRVLSKAHQCRRIHMLKPLKEFENTTCSTLAIRQ</a> NLDLFLPDKTAGGLNKSQILEMNQKKSDTSMLSPLNAAHYQDEKAH
3.0	11596.9737	0.1682	<a href="#">ARGDAEAVSLPLYGRIAAGLPIEALRDTTASIDVPTGLIAS</a> GEHYALEVAGDSMVDAGILDGDTVIIQRCETAENGTVIVALVDDNEVTLI
2.8	11596.8329	0.3091	<a href="#">ASVAGVTLPAGAA</a> NFVTDSEVTKLWKAAPCRFCGTGCGVTVAVKDNKVAVATQGDPAEVNKGKLCVKGKYFLSKIMYQDRLRPL
2.6	11597.6437	-0.5018	<a href="#">SLKRTKRKAPPPSKTPLAQTDERNSAMAHGLPLEDGIAPDS</a> MLELSSPEGMSTPEGSLGPGFLSQEQCAVPKPPDEISEGPGTPETAVAS

Mascot: <http://www.matrixscience.com/>