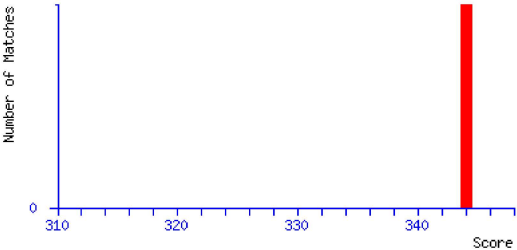


User : Lily-mascot
E-mail : l.r.adair@pgr.reading.ac.uk
Search title : C_albicans_6903
MS data file : C_albicans_6903_Da_merged.txt
Databases : 1: contaminants 20160129 (247 sequences; 128,130 residues)
2: Swissprot_22_05_2024 22_05_2024_02 (571,282 sequences; 206,678,396 residues)
Timestamp : 27 May 2025 at 07:46:51 GMT

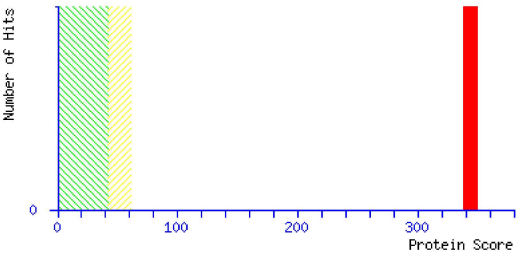
▼Search parameters

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 **> 42** (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	SSGTSYDPVLK	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	1.129
FHR2_HUMAN	1330		0.859	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

Max. number of families

AUTO

Target FDR (overrides sig. threshold)

(not set) ▾

FDR type

Sequence ▾

Display non-sig. matches

☐

Min. number of sig. unique sequences

1 ▾

Dendrograms cut at

0

Preferred taxonomy

All entries ▾

▼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 ▾ above <div>homology ▾</div>	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 page 1

▼1 2::WHS11_CANAW 344 White colony protein WHS11 OS=Candida albicans (strain WO-1) OX=294748 G...

		Score	Mass	Matches	Sequences
1.1	2::WHS11 CANAW	344	6991	1 (1)	1 (1)
White colony protein WHS11 OS=Candida albicans (strain WO-1) OX=294748 GN=WHS11 PE=2 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		6903.4326	6902.4253	6902.4221	0.47	0	344	3.9e-32	1	U	M.SDLGRKDIGDKIESKLTPDSQKSTPEQFKDKVTDSLDSAAGKAI + Acetyl (Protein N-term)

10 ▾ per page 1

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

Protein View: WHS11_CANAW

White colony protein WHS11 OS=Candida albicans (strain WO-1) OX=294748 GN=WHS11 PE=2 SV=1

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

Database: Swissprot_22_05_2024
Score: 344
Monoisotopic mass (M_r): 6991
Calculated pI: 4.92
Taxonomy: Candida albicans WO-1

Sequence similarity is available as [an NCBI BLAST search of WHS11_CANAW against nr](#).

Search parameters

MS data file: C_albicans_6903_Da_merged.txt
Enzyme: No enzyme cleavage specificity.
Variable modifications: Acetyl (Protein N-term)

Protein sequence coverage: 98%

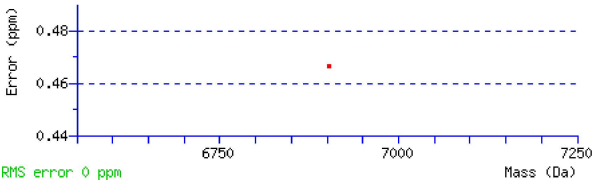
Matched peptides shown in **bold red**.

1 **MSDLGRKDIG DKIESKLTDP SQKSTPEQFK DKVTDSLDSA AGKATSENDK**
51 **SFVQKASDAI FGDSK**

Unformatted sequence string: **65 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
1	2 - 65	6903.4326	6902.4253	6902.4221	0.47	0	344	3.9e-32	1	U	M_SDLGRKDIGDKIESKLTDPDSQKSTPEQFKDKVTDSLDSAAQ + Acetyl (Protein N-term)



ID WHS11_CANAW Reviewed; 65 AA.
AC P43074; C4YIJ4;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 24-JAN-2024, entry version 83.
DE RecName: Full=White colony protein WHS11;
GN Name=WHS11; Synonyms=WH11; ORFNames=CAWG_04270;
OS Candida albicans (strain WO-1) (Yeast).
OC Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Debaryomycetaceae; Candida/Lodderomyces clade; Candida.
OX NCBI_TaxID=294748;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=WO-1;
RX PubMed=7916716; DOI=10.1016/0378-1119(93)90668-s;
RA Srikantha T., Soll D.R.;
RT "A white-specific gene in the white-opaque switching system of Candida
RT albicans.";
RL Gene 131:53-60(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=WO-1;
RX PubMed=19465905; DOI=10.1038/nature08064;
RA Butler G., Rasmussen M.D., Lin M.F., Santos M.A.S., Sakthikumar S.,
RA Munro C.A., Rheinbay E., Grabherr M., Forche A., Reedy J.L., Agrafioti I.,
RA Arnaud M.B., Bates S., Brown A.J.P., Brunke S., Costanzo M.C.,
RA Fitzpatrick D.A., de Groot P.W.J., Harris D., Hoyer L.L., Hube B.,
RA Klis F.M., Kodira C., Lennard N., Logue M.E., Martin R., Neiman A.M.,
RA Nikolaou E., Quail M.A., Quinn J., Santos M.C., Schmitzberger F.F.,
RA Sherlock G., Shah P., Silverstein K.A.T., Skrzypek M.S., Soll D.,
RA Staggs R., Stansfield I., Stumpf M.P.H., Sudbery P.E., Srikantha T.,
RA Zeng Q., Berman J., Berriman M., Heitman J., Gow N.A.R., Lorenz M.C.,
RA Birren B.W., Kellis M., Cuomo C.A.;
RT "Evolution of pathogenicity and sexual reproduction in eight Candida
RT genomes.";
RL Nature 459:657-662(2009).
CC **!- INDUCTION:** By temperature-induced mass conversion from opaque to white
CC colonies. WH11 is abruptly activated at the second cell doubling.
CC **!- SIMILARITY:** To yeast HSP12/GLP1 and S.pombe hsp9. {ECO:0000305}.
CC -----

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 CC -----
 DR EMBL; S65451; AAB28155.1; -; mRNA.
 DR EMBL; CH672350; EEQ45929.1; -; Genomic_DNA.
 DR PIR; JN0802; JN0802.
 DR AlphaFoldDB; P43074; -.
 DR SMR; P43074; -.
 DR PaxDb; 5476-P43074; -.
 DR VEuPathDB; FungiDB:CAWG_04270; -.
 DR HOGENOM; CLU_102617_3_1_1; -.
 DR OMA; DNQKSYS; -.
 DR Proteomes; UP000001429; Chromosome 2, Supercontig 1.5.
 DR Gene3D; 6.10.280.100; -; 1.
 DR InterPro; IPR007250; HSP9_HSP12.
 DR Pfam; PF04119; HSP9_HSP12; 1.
 DR PIRSF; PIRSF002590; HSP9/HSP12_fun; 1.
 PE 2: Evidence at transcript level;
 KW Stress response.
 FT CHAIN 1..65
 FT /note="White colony protein WHS11"
 FT /id="PRO_0000065971"
 FT REGION 1..32
 FT /note="Disordered"
 FT /evidence="ECO:0000256|SAM:MobiDB-lite"
 FT COMPIAS 1..18
 FT /note="Basic and acidic residues"
 FT /evidence="ECO:0000256|SAM:MobiDB-lite"
 SQ SEQUENCE 65 AA; 6996 MW; C0E734525A083E24 CRC64;
 MSDLGKRDIG DKIESKLTPD SQKSTPEQFK DKVTDSLDSA AGKATSENDK SFVQKASDAI
 FGDSK

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

Peptide View

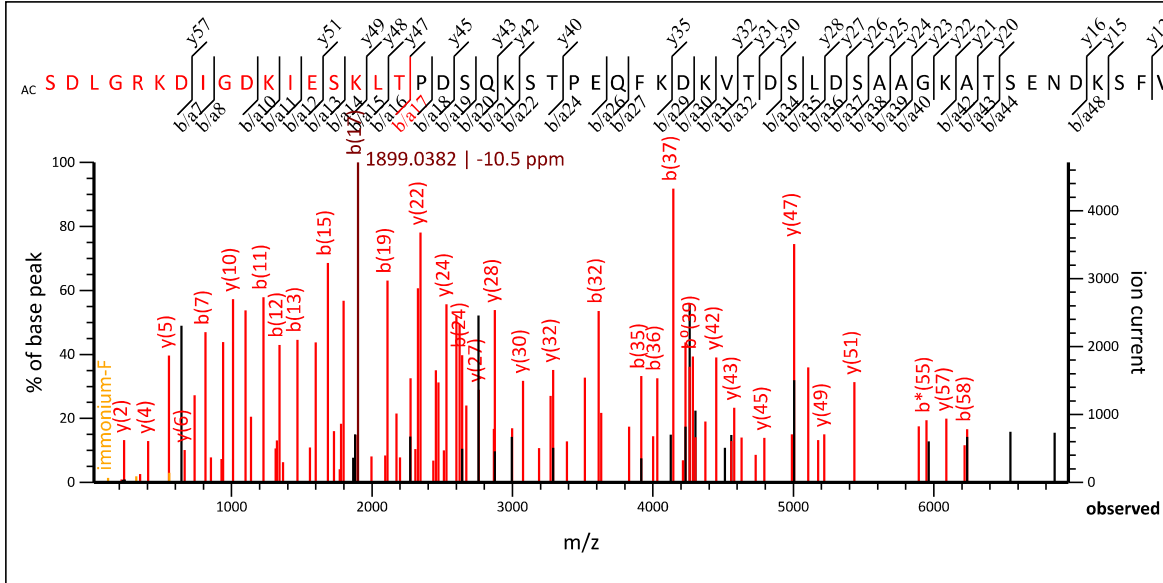
MS/MS Fragmentation of **SDLGRKDIGDKIESKLTTPDSQKSTPEQFKDKVTDLSAAGKATSENDKSFVQKASDAIFGDSK**

Found in **WHS11_CANAW** in **Swissprot_22_05_2024**, White colony protein WHS11 OS=Candida albicans (strain WO-1) OX=294748 GN=WHS11 PE=2 SV=1

Match to Query 1: 6902.425324 from(6903.432600,1+) intensity(159009.5544) index(0)

Title: Reading Top-Down experiment

Data file C_albicans_6903_Da_merged.txt



20.08 to 6959.51

Monoisotopic mass of neutral peptide Mr(calc): 6902.4221

Variable modifications:

N-term : Acetyl (Protein N-term)

Ions Score: 344 Expect: 3.9e-32

Peak matches: 100/1230 fragment ions using 105 most intense peaks

Annotated fragments: 104/1230 ([help](#))

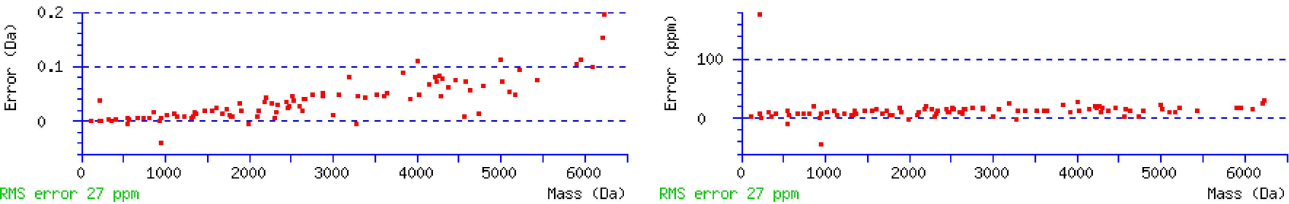
#	Immon.	a	a*	a ⁰	b	b*	b ⁰	Seq.	y	y*	y ⁰	#
1	60.0444	102.0550		84.0444	130.0499		112.0393	S				64
2	88.0393	217.0819		199.0713	245.0768		227.0662	D	6774.3868	6757.3603	6756.3763	63
3	86.0964	330.1660		312.1554	358.1609		340.1503	L	6659.3599	6642.3333	6641.3493	62
4	30.0338	387.1874		369.1769	415.1823		397.1718	G	6546.2758	6529.2493	6528.2653	61
5	129.1135	543.2885	526.2620	525.2780	571.2835	554.2569	553.2729	R	6489.2544	6472.2278	6471.2438	60
6	101.1073	671.3835	654.3570	653.3729	699.3784	682.3519	681.3678	K	6333.1532	6316.1267	6315.1427	59
7	88.0393	786.4104	769.3839	768.3999	814.4054	797.3788	796.3948	D	6205.0583	6188.0317	6187.0477	58
8	86.0964	899.4945	882.4680	881.4839	927.4894	910.4629	909.4789	I	6090.0313	6073.0048	6072.0208	57
9	30.0338	956.5160	939.4894	938.5054	984.5109	967.4843	966.5003	G	5976.9473	5959.9207	5958.9367	56
10	88.0393	1071.5429	1054.5164	1053.5323	1099.5378	1082.5113	1081.5273	D	5919.9258	5902.8993	5901.9152	55
11	101.1073	1199.6379	1182.6113	1181.6273	1227.6328	1210.6062	1209.6222	K	5804.8989	5787.8723	5786.8883	54
12	86.0964	1312.7219	1295.6954	1294.7114	1340.7169	1323.6903	1322.7063	I	5676.8039	5659.7774	5658.7933	53
13	102.0550	1441.7645	1424.7380	1423.7540	1469.7594	1452.7329	1451.7489	E	5563.7198	5546.6933	5545.7093	52
14	60.0444	1528.7966	1511.7700	1510.7860	1556.7915	1539.7649	1538.7809	S	5434.6772	5417.6507	5416.6667	51
15	101.1073	1656.8915	1639.8650	1638.8810	1684.8864	1667.8599	1666.8759	K	5347.6452	5330.6187	5329.6347	50
16	86.0964	1769.9756	1752.9490	1751.9650	1797.9705	1780.9440	1779.9599	L	5219.5503	5202.5237	5201.5397	49
17	74.0600	1871.0233	1853.9967	1853.0127	1899.0182	1881.9916	1881.0076	T	5106.4662	5089.4396	5088.4556	48
18	70.0651	1968.0760	1951.0495	1950.0655	1996.0709	1979.0444	1978.0604	P	5005.4185	4988.3920	4987.4080	47
19	88.0393	2083.1030	2066.0764	2065.0924	2111.0979	2094.0713	2093.0873	D	4908.3658	4891.3392	4890.3552	46
20	60.0444	2170.1350	2153.1085	2152.1244	2198.1299	2181.1034	2180.1194	S	4793.3388	4776.3123	4775.3282	45

21	101.0709	2298.1936	2281.1670	2280.1830	2326.1885	2309.1619	2308.1779	Q	4706.3068	4689.2802	4688.2962	44
22	101.1073	2426.2885	2409.2620	2408.2780	2454.2835	2437.2569	2436.2729	K	4578.2482	4561.2217	4560.2376	43
23	60.0444	2513.3206	2496.2940	2495.3100	2541.3155	2524.2889	2523.3049	S	4450.1532	4433.1267	4432.1427	42
24	74.0600	2614.3683	2597.3417	2596.3577	2642.3632	2625.3366	2624.3526	T	4363.1212	4346.0947	4345.1106	41
25	70.0651	2711.4210	2694.3945	2693.4104	2739.4159	2722.3894	2721.4054	P	4262.0735	4245.0470	4244.0630	40
26	102.0550	2840.4636	2823.4371	2822.4530	2868.4585	2851.4320	2850.4480	E	4165.0208	4147.9942	4147.0102	39
27	101.0709	2968.5222	2951.4956	2950.5116	2996.5171	2979.4906	2978.5065	Q	4035.9782	4018.9516	4017.9676	38
28	120.0808	3115.5906	3098.5641	3097.5800	3143.5855	3126.5590	3125.5749	F	3907.9196	3890.8930	3889.9090	37
29	101.1073	3243.6856	3226.6590	3225.6750	3271.6805	3254.6539	3253.6699	K	3760.8512	3743.8246	3742.8406	36
30	88.0393	3358.7125	3341.6860	3340.7019	3386.7074	3369.6809	3368.6969	D	3632.7562	3615.7297	3614.7457	35
31	101.1073	3486.8075	3469.7809	3468.7969	3514.8024	3497.7758	3496.7918	K	3517.7293	3500.7027	3499.7187	34
32	72.0808	3585.8759	3568.8493	3567.8653	3613.8708	3596.8442	3595.8602	V	3389.6343	3372.6078	3371.6237	33
33	74.0600	3686.9236	3669.8970	3668.9130	3714.9185	3697.8919	3696.9079	T	3290.5659	3273.5394	3272.5553	32
34	88.0393	3801.9505	3784.9240	3783.9399	3829.9454	3812.9189	3811.9349	D	3189.5182	3172.4917	3171.5077	31
35	60.0444	3888.9825	3871.9560	3870.9720	3916.9774	3899.9509	3898.9669	S	3074.4913	3057.4647	3056.4807	30
36	86.0964	4002.0666	3985.0400	3984.0560	4030.0615	4013.0350	4012.0509	L	2987.4592	2970.4327	2969.4487	29
37	88.0393	4117.0935	4100.0670	4099.0830	4145.0885	4128.0619	4127.0779	D	2874.3752	2857.3486	2856.3646	28
38	60.0444	4204.1256	4187.0990	4186.1150	4232.1205	4215.0939	4214.1099	S	2759.3482	2742.3217	2741.3377	27
39	44.0495	4275.1627	4258.1361	4257.1521	4303.1576	4286.1310	4285.1470	A	2672.3162	2655.2897	2654.3057	26
40	44.0495	4346.1998	4329.1732	4328.1892	4374.1947	4357.1682	4356.1841	A	2601.2791	2584.2526	2583.2685	25
41	30.0338	4403.2213	4386.1947	4385.2107	4431.2162	4414.1896	4413.2056	G	2530.2420	2513.2154	2512.2314	24
42	101.1073	4531.3162	4514.2897	4513.3057	4559.3111	4542.2846	4541.3006	K	2473.2205	2456.1940	2455.2100	23
43	44.0495	4602.3533	4585.3268	4584.3428	4630.3483	4613.3217	4612.3377	A	2345.1256	2328.0990	2327.1150	22
44	74.0600	4703.4010	4686.3745	4685.3905	4731.3959	4714.3694	4713.3854	T	2274.0884	2257.0619	2256.0779	21
45	60.0444	4790.4330	4773.4065	4772.4225	4818.4280	4801.4014	4800.4174	S	2173.0408	2156.0142	2155.0302	20
46	102.0550	4919.4756	4902.4491	4901.4651	4947.4706	4930.4440	4929.4600	E	2086.0087	2068.9822	2067.9982	19
47	87.0553	5033.5186	5016.4920	5015.5080	5061.5135	5044.4869	5043.5029	N	1956.9661	1939.9396	1938.9556	18
48	88.0393	5148.5455	5131.5190	5130.5349	5176.5404	5159.5139	5158.5299	D	1842.9232	1825.8967	1824.9127	17
49	101.1073	5276.6405	5259.6139	5258.6299	5304.6354	5287.6088	5286.6248	K	1727.8963	1710.8697	1709.8857	16
50	60.0444	5363.6725	5346.6459	5345.6619	5391.6674	5374.6409	5373.6568	S	1599.8013	1582.7748	1581.7907	15
51	120.0808	5510.7409	5493.7144	5492.7303	5538.7358	5521.7093	5520.7253	F	1512.7693	1495.7427	1494.7587	14
52	72.0808	5609.8093	5592.7828	5591.7988	5637.8042	5620.7777	5619.7937	V	1365.7009	1348.6743	1347.6903	13
53	101.0709	5737.8679	5720.8414	5719.8573	5765.8628	5748.8363	5747.8523	Q	1266.6325	1249.6059	1248.6219	12
54	101.1073	5865.9629	5848.9363	5847.9523	5893.9578	5876.9312	5875.9472	K	1138.5739	1121.5473	1120.5633	11
55	44.0495	5937.0000	5919.9734	5918.9894	5964.9949	5947.9683	5946.9843	A	1010.4789	993.4524	992.4684	10
56	60.0444	6024.0320	6007.0055	6006.0214	6052.0269	6035.0004	6034.0164	S	939.4418	922.4153	921.4312	9
57	88.0393	6139.0590	6122.0324	6121.0484	6167.0539	6150.0273	6149.0433	D	852.4098	835.3832	834.3992	8
58	44.0495	6210.0961	6193.0695	6192.0855	6238.0910	6221.0644	6220.0804	A	737.3828	720.3563	719.3723	7
59	86.0964	6323.1801	6306.1536	6305.1696	6351.1750	6334.1485	6333.1645	I	666.3457	649.3192	648.3352	6
60	120.0808	6470.2485	6453.2220	6452.2380	6498.2435	6481.2169	6480.2329	F	553.2617	536.2351	535.2511	5
61	30.0338	6527.2700	6510.2435	6509.2594	6555.2649	6538.2384	6537.2544	G	406.1932	389.1667	388.1827	4
62	88.0393	6642.2970	6625.2704	6624.2864	6670.2919	6653.2653	6652.2813	D	349.1718	332.1452	331.1612	3
63	60.0444	6729.3290	6712.3024	6711.3184	6757.3239	6740.2973	6739.3133	S	234.1448	217.1183	216.1343	2
64	101.1073							K	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DL	201.1234	229.1183	DLG	258.1448	286.1397	DLGR	414.2459	442.2409
DLGRK	542.3409	570.3358	DLGRKD	657.3678	685.3628	LG	143.1179	171.1128
LGR	299.2190	327.2139	LGRK	427.3140	455.3089	LGRKD	542.3409	570.3358
LGRKDI	655.4250	683.4199	GR	186.1349	214.1299	GRK	314.2299	342.2248
GRKD	429.2568	457.2518	GRKDI	542.3409	570.3358	GRKDIG	599.3624	627.3573
RK	257.2084	285.2034	RKD	372.2354	400.2303	RKDI	485.3194	513.3144
RKDIG	542.3409	570.3358	RKDIGD	657.3678	685.3628	KD	216.1343	244.1292
KDI	329.2183	357.2132	KDIG	386.2398	414.2347	KDIGD	501.2667	529.2617
KDIGDK	629.3617	657.3566	DI	201.1234	229.1183	DIG	258.1448	286.1397
DIGD	373.1718	401.1667	DIGDK	501.2667	529.2617	DIGDKI	614.3508	642.3457

IG	143.1179	171.1128	IGD	258.1448	286.1397	IGDK	386.2398	414.2347
IGDKI	499.3239	527.3188	IGDKIE	628.3665	656.3614	GD	145.0608	173.0557
GDK	273.1557	301.1506	GDKI	386.2398	414.2347	GDKIE	515.2824	543.2773
GDKIES	602.3144	630.3093	DK	216.1343	244.1292	DKI	329.2183	357.2132
DKIE	458.2609	486.2558	DKIES	545.2930	573.2879	DKIESK	673.3879	
KI	214.1914	242.1863	KIE	343.2340	371.2289	KIES	430.2660	458.2609
KIESK	558.3610	586.3559	KIESKL	671.4450	699.4400	IE	215.1390	243.1339
IES	302.1710	330.1660	IESK	430.2660	458.2609	IESKL	543.3501	571.3450
IESKLT	644.3978	672.3927	ES	189.0870	217.0819	ESK	317.1819	345.1769
ESKL	430.2660	458.2609	ESKLT	531.3137	559.3086	ESKLTP	628.3665	656.3614
SK	188.1394	216.1343	SKL	301.2234	329.2183	SKLT	402.2711	430.2660
SKLTP	499.3239	527.3188	SKLTPD	614.3508	642.3457	KL	214.1914	242.1863
KLT	315.2391	343.2340	KLTP	412.2918	440.2867	KLTPD	527.3188	555.3137
KLTPDS	614.3508	642.3457	LT	187.1441	215.1390	LTP	284.1969	312.1918
LTPD	399.2238	427.2187	LTPDS	486.2558	514.2508	LTPDSQ	614.3144	642.3093
TP	171.1128	199.1077	TPD	286.1397	314.1347	TPDS	373.1718	401.1667
TPDSQ	501.2304	529.2253	TPDSQK	629.3253	657.3202	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	DSQKST	619.3046	647.2995
SQ	188.1030	216.0979	SQK	316.1979	344.1928	SQKS	403.2300	431.2249
SQKST	504.2776	532.2726	SQKSTP	601.3304	629.3253	QK	229.1659	257.1608
QKS	316.1979	344.1928	QKST	417.2456	445.2405	QKSTP	514.2984	542.2933
QKSTPE	643.3410	671.3359	KS	188.1394	216.1343	KST	289.1870	317.1819
KSTP	386.2398	414.2347	KSTPE	515.2824	543.2773	KSTPEQ	643.3410	671.3359
ST	161.0921	189.0870	STP	258.1448	286.1397	STPE	387.1874	415.1823
STPEQ	515.2460	543.2409	STPEQF	662.3144	690.3093	TPE	300.1554	328.1503
TPEQ	428.2140	456.2089	TPEQF	575.2824	603.2773	PE	199.1077	227.1026
PEQ	327.1663	355.1612	PEQF	474.2347	502.2296	PEQFK	602.3297	630.3246
EQ	230.1135	258.1084	EQF	377.1819	405.1769	EQFK	505.2769	533.2718
EQFKD	620.3039	648.2988	QF	248.1394	276.1343	QFK	376.2343	404.2292
QFKD	491.2613	519.2562	QFKDK	619.3562	647.3511	FK	248.1757	276.1707
FKD	363.2027	391.1976	FKDK	491.2976	519.2926	FKDKV	590.3661	618.3610
FKDKVT	691.4137		KDK	344.2292	372.2241	KDKV	443.2976	471.2926
KDKVT	544.3453	572.3402	KDKVTD	659.3723	687.3672	DKV	315.2027	343.1976
DKVT	416.2504	444.2453	DKVTD	531.2773	559.2722	DKVTDs	618.3093	646.3042
KV	200.1757	228.1707	KVT	301.2234	329.2183	KVTD	416.2504	444.2453
KVTDs	503.2824	531.2773	KVTDsL	616.3665	644.3614	VT	173.1285	201.1234
VTD	288.1554	316.1503	VTDS	375.1874	403.1823	VTDSL	488.2715	516.2664
VTDSLd	603.2984	631.2933	VTDSLDS	690.3305		TD	189.0870	217.0819
TDS	276.1190	304.1139	TDSL	389.2031	417.1980	TDSLd	504.2300	532.2249
TDSLDS	591.2620	619.2570	TDSLDSA	662.2992	690.2941	DSL	288.1554	316.1503
DSLd	403.1823	431.1773	DSLDS	490.2144	518.2093	DSLDSA	561.2515	589.2464
DSLDSAA	632.2886	660.2835	DSLDSAAg	689.3101		SL	173.1285	201.1234
SLD	288.1554	316.1503	SLDS	375.1874	403.1823	SLDSA	446.2245	474.2195
SLDSAA	517.2617	545.2566	SLDSAAg	574.2831	602.2780	LD	201.1234	229.1183
LDS	288.1554	316.1503	LDSA	359.1925	387.1874	LDSAA	430.2296	458.2245
LDSAAg	487.2511	515.2460	LDSAAgK	615.3461	643.3410	LDSAAgKA	686.3832	
DSA	246.1084	274.1034	DSAA	317.1456	345.1405	DSAAg	374.1670	402.1619
DSAAgK	502.2620	530.2569	DSAAgKA	573.2991	601.2940	DSAAgKAT	674.3468	
SA	131.0815	159.0764	SAA	202.1186	230.1135	SAAG	259.1401	287.1350
SAAGK	387.2350	415.2300	SAAGKA	458.2722	486.2671	SAAGKAT	559.3198	587.3148
SAAGKATS	646.3519	674.3468	AA	115.0866	143.0815	AAG	172.1081	200.1030
AAGK	300.2030	328.1979	AAGKA	371.2401	399.2350	AAGKAT	472.2878	500.2827
AAGKATS	559.3198	587.3148	AAGKATSE	688.3624		AG	101.0709	129.0659
AGK	229.1659	257.1608	AGKA	300.2030	328.1979	AGKAT	401.2507	429.2456

AGKATS	488.2827	516.2776	AGKATSE	617.3253	645.3202	GK	158.1288	186.1237
GKA	229.1659	257.1608	GKAT	330.2136	358.2085	GKATS	417.2456	445.2405
GKATSE	546.2882	574.2831	GKATSEN	660.3311	688.3260	KA	172.1444	200.1394
KAT	273.1921	301.1870	KATS	360.2241	388.2191	KATSE	489.2667	517.2617
KATSEN	603.3097	631.3046	AT	145.0972	173.0921	ATS	232.1292	260.1241
ATSE	361.1718	389.1667	ATSEN	475.2147	503.2096	ATSEND	590.2416	618.2366
TS	161.0921	189.0870	TSE	290.1347	318.1296	TSEN	404.1776	432.1725
TSEND	519.2045	547.1994	TSENDK	647.2995	675.2944	SE	189.0870	217.0819
SEN	303.1299	331.1248	SEND	418.1569	446.1518	SENDK	546.2518	574.2467
SENDKS	633.2838	661.2788	EN	216.0979	244.0928	END	331.1248	359.1197
ENDK	459.2198	487.2147	ENDKS	546.2518	574.2467	ENDKSF	693.3202	
ND	202.0822	230.0771	NDK	330.1772	358.1721	NDKS	417.2092	445.2041
NDKSF	564.2776	592.2726	NDKSFV	663.3461	691.3410	DKS	303.1663	331.1612
DKSF	450.2347	478.2296	DKSFV	549.3031	577.2980	DKSFVQ	677.3617	
KSF	335.2078	363.2027	KSFV	434.2762	462.2711	KSFVQ	562.3348	590.3297
KSFVQK	690.4297		SF	207.1128	235.1077	SFV	306.1812	334.1761
SFVQ	434.2398	462.2347	SFVQK	562.3348	590.3297	SFVQKA	633.3719	661.3668
FV	219.1492	247.1441	FVQ	347.2078	375.2027	FVQK	475.3027	503.2976
FVQKA	546.3398	574.3348	FVQKAS	633.3719	661.3668	VQ	200.1394	228.1343
VQK	328.2343	356.2292	VQKA	399.2714	427.2663	VQKAS	486.3035	514.2984
VQKASD	601.3304	629.3253	VQKASDA	672.3675		QKA	300.2030	328.1979
QKAS	387.2350	415.2300	QKASD	502.2620	530.2569	QKASDA	573.2991	601.2940
QKASDAI	686.3832		KAS	259.1765	287.1714	KASD	374.2034	402.1983
KASDA	445.2405	473.2354	KASDAI	558.3246	586.3195	AS	131.0815	159.0764
ASD	246.1084	274.1034	ASDA	317.1456	345.1405	ASDAI	430.2296	458.2245
ASDAIF	577.2980	605.2930	ASDAIFG	634.3195	662.3144	SD	175.0713	203.0662
SDA	246.1084	274.1034	SDAI	359.1925	387.1874	SDAIF	506.2609	534.2558
SDAIFG	563.2824	591.2773	SDAIFGD	678.3093		DA	159.0764	187.0713
DAI	272.1605	300.1554	DAIF	419.2289	447.2238	DAIFG	476.2504	504.2453
DAIFGD	591.2773	619.2722	DAIFGDS	678.3093		AI	157.1335	185.1285
AIF	304.2020	332.1969	AIFG	361.2234	389.2183	AIFGD	476.2504	504.2453
AIFGDS	563.2824	591.2773	IF	233.1648	261.1598	IFG	290.1863	318.1812
IFGD	405.2132	433.2082	IFGDS	492.2453	520.2402	FG	177.1022	205.0972
FGD	292.1292	320.1241	FGDS	379.1612	407.1561	GDS	232.0928	260.0877



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
344.0	6902.4221	0.0032	SDLGRKDIGDKIESKLTGPSQKSTPEQFKDKVTDLSAAGKATSENDKSFVQKASDAIFGDSK
8.5	6902.3863	0.0390	GKKKQRAPATPKSSSGGAGASTGSGTSSAAVTSGPGSGSTKVSVAASSAQSGLOGATGAGGGSSTPGTQPGSGAGGAI
7.8	6902.5215	-0.0962	EIQESYAVLKDAKGRLPNPGYORSALVKVKEGDDHHHGILGIGRDGTINYWNGNVNLNGFKOM
6.8	6902.3985	0.0268	DRGGDMILRELQGVGSLDFVARAPMGECVEDLSRRTVDSALRNKTPASAAAPIATTQSETAATDGSA
6.4	6902.4615	-0.0362	SPDAKAMLFMNFENGEAADSISKYQEVAHQFKGEGHILLGDVEASQGAFOYFGLKEDQVPLI
5.0	6902.6386	-0.2133	STYKDVKYKNKPFIRIKDGLPQLNEVIGTNYTDIGFVYNETTGVLTISSVIDNLKGAAGQAIQ
4.9	6902.4511	-0.0258	GNDAVIYPAPALVEGEQEKTKLYPKFVDDYMKLYVGLKFQAKEPRFEAMKAMESTNLNM
4.1	6902.4305	-0.0052	WGPQRHANGEIATRAISMLAILTGNVGINGGNSGAREGSYSLPFVRMPTLENPIQTSISMFMWT
4.0	6902.6214	-0.1961	DAYYRKAQVRRLLRDELLAALGQCDALLAPVSPVTARDLGGNTADPLQIYLMDAYTLNLAG

3.8	6902.3392	0.0861	GTGDVLTIFYDGDDLTARVLGQYSGPRGHFKLFTSMADVTIQFQSDPGASVLGYQQGFVIHFFE
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