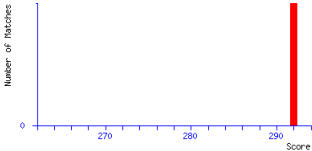


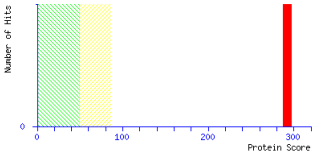
User : Lily-mascot  
E-mail : l.r.adair@pgr.reading.ac.uk  
Search title : K\_pneumoniae\_VIM1\_7700\_Da  
MS data file : K\_pneumoniae\_VIM1\_7700\_Da.mgf  
Databases : 1: contaminants 20160129 (247 sequences; 128,130 residues)  
2: Trembl\_22\_05\_2024 22\_05\_2024\_2024\_02 (248,234,451 sequences; 87,367,689,973 residues)  
Taxonomy : 1: (none)  
2: Bacteria (Eubacteria) (158,221,737 sequences)  
Timestamp : 21 Jul 2025 at 15:58:12 GMT

▼Search parameters  
Type of search : MS/MS Ion Search  
Enzyme : None  
Variable modifications : Oxidation (M)  
Mass values : Monoisotopic  
Protein mass : Unrestricted  
Peptide mass tolerance : ± 20 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 > 49 (beyond yellow shading) indicate **significant homology**, while individual ions scores > 86 (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.

▼Legend

Peptide columns and rows

Dupes	...	Expect	Rank	U	1	2	Peptide	
		0.037	▶	2			GAYLSLR	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			VCNYSYWIW	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			LNTLETEWFFK	peptide has two duplicates
		0.18	▶	1			LNTLETEWFFK	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. IPPL), 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<  Max. number of families   
Target FDR (overrides sig. threshold)  FDR type   
Display non-sig. matches ☐ Min. number of sig. unique sequences   
Dendrograms cut at   
Preferred taxonomy

▼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 homology	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::A0A087FU90_KLEVA	Score	Mass	Matches	Sequences
1.1	2::A0A087FU90_KLEV	292	9527	1 (1)	1 (1)
	DUF1471 domain-containing protein OS=Klebsiella varicola OX=244366 GN=AN2335V1_2139 PE=4 SV=1				
	▼18 same sets of 2::A0A087FU90_KLEVA				
	2::A0A0E1CHX1_KLEF	292	9527	1 (1)	1 (1)
	YdgH/BhsA/McbA-like domain-containing protein OS=Klebsiella pneumoniae 30660/NIST258_1 OX=1420012 GN=KPN01_04116 PE=4 SV=1				
	2::A0A0H3GT82_KLEF	292	9527	1 (1)	1 (1)
	YdgH/BhsA/McbA-like domain-containing protein OS=Klebsiella pneumoniae subsp. pneumoniae (strain HS11286) OX=1125630 GN=KPHS_13060 PE=4 SV=1				
	2::A0A1F2M9U2_9EN	292	9527	1 (1)	1 (1)
	YdgH/BhsA/McbA-like domain-containing protein OS=Klebsiella sp. HMSC16C06 OX=1581110 GN=HMPREF3142_06415 PE=4 SV=1				
	2::A0A1Y0Q3K0_KLEF	292	9527	1 (1)	1 (1)
	DUF1471 domain-containing protein OS=Klebsiella pneumoniae subsp. pneumoniae OX=72407 GN=E9161_10165 PE=4 SV=1				
	2::A0A2N4VZ74_9EN	292	9527	1 (1)	1 (1)
	DUF1471 domain-containing protein OS=Klebsiella quasipneumoniae OX=1463165 GN=C2767_20750 PE=4 SV=1				
	2::A0A377Z7M3_KLEF	292	9527	1 (1)	1 (1)
	Exported protein OS=Klebsiella pneumoniae subsp. ozaenae OX=574 GN=NCTC10313_01963 PE=4 SV=1				
	2::A0A486D4T2_KLEF	292	9555	1 (1)	1 (1)
	Exported protein OS=Klebsiella pneumoniae OX=573 GN=SAMEA4873652_01610 PE=4 SV=1				
	2::A0A486DJG0_KLEF	292	9587	1 (1)	1 (1)
	Exported protein OS=Klebsiella pneumoniae OX=573 GN=SAMEA4873656_01500 PE=4 SV=1				
	2::A0A5ESTMA4_9EN	292	9527	1 (1)	1 (1)
	Exported protein OS=Klebsiella quasivaricola OX=2026240 GN=SAMEA3538780_02069 PE=4 SV=1				
	2::A0A7S9HEW6_KLE	292	9771	1 (1)	1 (1)
	DUF1471 domain-containing protein OS=Klebsiella pneumoniae subsp. pneumoniae OX=72407 GN=IU134_06265 PE=4 SV=1				
	2::A0A7U3F2R1_9EN	292	9527	1 (1)	1 (1)
	YdgH/BhsA/McbA-like domain-containing protein OS=Klebsiella africana OX=2489010 GN=SB5857_01022 PE=4 SV=1				



Protein View: A0A087FU90\_KLEVA

DUF1471 domain-containing protein OS=Klebsiella variicola OX=244366 GN=AN2335V1\_2139 PE=4 SV=1

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

Database: Trembl\_22\_05\_2024  
Score: 292  
Monoisotopic mass (M<sub>r</sub>): 9527  
Calculated pI: 7.98  
Taxonomy: Klebsiella variicola

Sequence similarity is available as an NCBI BLAST search of A0A087FU90\_KLEVA against nr.

Search parameters

MS data file: K\_pneumoniae\_YIM1\_7700\_Da.mgf  
Enzyme: No enzyme cleavage specificity.  
Variable modifications: Oxidation (M)

Protein sequence coverage: 78%

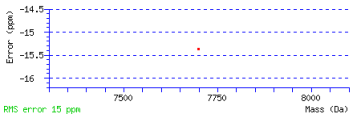
Matched peptides shown in bold red.

1 MKKVIVALAL SAVAFGASAA QLITKEEVKH FKLTKVGPI SVGPSGEFSS  
51 PSDLHDQLSK LADEKGGKYY VITAARENGF NFEATAEVYK

Unformatted sequence string: 90 residues (or 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 20 - 90 7699.8528 7698.8455 7698.9638 -15.4 0 292 2.9e-26 1 U A.QLITKEEVKHFKLTKVGPI SVGPSGEFSSPSDLHDQLSKLADEKGGKYYVITAARENGFNFEATAEVYK.-



ID A0A087FU90\_KLEVA Unreviewed; 90 AA.  
AC A0A087FU90  
DT 29-OCT-2014, integrated into UniProtKB/TrEMBL.  
DT 29-OCT-2014, sequence version 1.  
DT 18-JUN-2025, entry version 73  
DE SubName: Full=DUF1471 domain-containing protein (ECO:0000313|EMBL:PLP46680.1);  
DE SubName: Full=Exported protein (ECO:0000313|EMBL:SKF93190.1);  
GN ORFNames=AN2335V1\_2139 (ECO:0000313|EMBL:CAH6063631.1), CWM98\_09130  
GN (ECO:0000313|EMBL:PLP46680.1), CWM47\_12400  
GN (ECO:0000313|EMBL:FLM94979.1), LAP99\_19885  
GN (ECO:0000313|EMBL:QNP23645.1), NUKP37\_00130  
GN (ECO:0000313|EMBL:GKJ84586.1), QAB22\_020555  
GN (ECO:0000313|EMBL:MCC6058903.1), SAMBA3729809\_01907  
GN (ECO:0000313|EMBL:SKF93190.1);  
OS Klebsiella variicola.  
OC Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria;  
OC Enterobacterales; Enterobacteriaceae; Klebsiella/Raoultella group;  
OC Klebsiella; Klebsiella pneumoniae complex.  
OX NCBI\_TaxID=244366 (ECO:0000313|EMBL:PLP46680.1, ECO:0000313|Proteomes:UP000234473);  
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RA Han C.G.;  
RL Submitted (NOV-2017) to the EMBL/GenBank/DBJ databases.  
RN [2] (ECO:0000313|Proteomes:UP000234412, ECO:0000313|Proteomes:UP000234473)  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
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RC ECO:0000313|Proteomes:UP000234473), and A8  
RC (ECO:0000313|EMBL:FLM94979.1, ECO:0000313|Proteomes:UP000234412);  
RA Yang Y., Bicalho R.;  
RT "Genomic study of Klebsiella pneumoniae.";  
RL Submitted (JAN-2018) to the EMBL/GenBank/DBJ databases.  
RN [3] (ECO:0000313|EMBL:SKF93190.1, ECO:0000313|Proteomes:UP000258928)  
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RC STRAIN=EucSPE\_TK218 (ECO:0000313|EMBL:SKF93190.1,  
RC ECO:0000313|Proteomes:UP000258928);  
RG Pathogen Informatics;  
RL Submitted (AUG-2018) to the EMBL/GenBank/DBJ databases.  
RN [4] (ECO:0000313|EMBL:QNP23645.1, ECO:0000313|Proteomes:UP000516181)  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=KP2757 (ECO:0000313|EMBL:QNP23645.1,  
RC ECO:0000313|Proteomes:UP000516181);  
RA Zhang X.;  
RT "Complete genome sequence of Klebsiella pneumoniae KP2757.";  
RL Submitted (AUG-2020) to the EMBL/GenBank/DBJ databases.  
RN [5] (ECO:0000313|EMBL:GKJ84586.1)  
RP NUCLEOTIDE SEQUENCE  
RC STRAIN=NUKP-37 (ECO:0000313|EMBL:GKJ84586.1);  
RX PubMed=35797348; DOI=10.1111/jam.15701;  
RA Nonogaki R., Iijima A., Kawamura K., Kayama S., Sugai M., Yagi T.,  
RA Arakawa Y., Doi Y., Suzuki M.,  
RT "PCR-based ORF typing of Klebsiella pneumoniae for rapid identification of  
RT global clones and transmission events.";  
RL J. Appl. Microbiol. 133:2050-2062 (2022).  
RN [6] (ECO:0000313|EMBL:CAH6063631.1)  
RP NUCLEOTIDE SEQUENCE  
RC STRAIN=0 (ECO:0000313|EMBL:CAH6063631.1);  
RA Alioto T., Alioto T., Gomez Garrido J.;  
RL Submitted (MAY-2022) to the EMBL/GenBank/DBJ databases.  
RN [7] (ECO:0000313|EMBL:MCC6058903.1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CP0071 (ECO:0000313|EMBL:MCC6058903.1);  
RX PubMed=3753339;  
RA Macesic N., Hawkey J., Vezina B., Wisniewski J.A., Cottingham H.,  
RA Blakeway L.V., Harshaghi T., Pragastia K., Badoordeen G.Z., Dennison A.,  
RA Spelman D.W., Denney A.W.J., Feig A.Y.;  
RT "Genomic dissection of emic carbapenem resistance reveals metallo-beta-  
RT lactamase dissemination through clonal, plasmid and integron transfer.";  
RL Nat. Commun. 14:0-0 (2023).  
RN [8] (ECO:0000313|EMBL:MCC6058903.1)  
RP NUCLEOTIDE SEQUENCE  
RC STRAIN=CP0071 (ECO:0000313|EMBL:MCC6058903.1);  
RA Macesic N.;  
RL Submitted (JAN-2024) to the EMBL/GenBank/DBJ databases.  
CC -----  
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CC Distributed under the Creative Commons Attribution (CC BY 4.0) License  
CC -----  
DR EMBL: CAJ0X8020000001; CAH6063631.1; -; Genomic DNA.  
DR EMBL: BQTA01000001; GKJ84586.1; -; Genomic DNA.  
DR EMBL: JARTN0200000001; MCC6058903.1; -; Genomic DNA.  
DR EMBL: FIDF01000349; PLM94979.1; -; Genomic DNA.  
DR EMBL: PICB01000353; PLP46680.1; -; Genomic DNA.  
DR EMBL: CP060807; QNP23645.1; -; Genomic DNA.  
DR EMBL: UKAS01000004; SKF93190.1; -; Genomic DNA.  
DR RefSeq: WP\_026892402.1; NZ\_LXNM01000001.1.  
DR KEGG: kpe:RPK\_4095; -.  
DR KEGG: kpk:A593\_16885; -.  
DR KEGG: kvd:KR75\_14320; -.  
DR KEGG: kvq:SP68\_20975; -.  
DR OMA: KDAHUP; -.  
DR Proteomes: UP000234412; Unassembled WGS sequence.  
DR Proteomes: UP000234473; Unassembled WGS sequence.  
DR Proteomes: UP000258928; Unassembled WGS sequence.  
DR Proteomes: UP000516181; Chromosome.  
DR Proteomes: UP000789617; Unassembled WGS sequence.  
DR Proteomes: UP001060507; Unassembled WGS sequence.  
DR Proteomes: UP001176846; Unassembled WGS sequence.  
DR Gene3D: 3.30.1460.10; Flavin-binding protein dodecin; 1.  
DR InterPro: IPR051096; BhaA/McbA\_stress\_biofilm\_assoc.  
DR InterPro: IPR025543; Dodecin-like.  
DR InterPro: IPR036275; YdgH-like\_sf.  
DR InterPro: IPR010854; YdgH/BhaA/McbA-like\_dom.  
DR PANTHER: PTHR34156; OUTER MEMBRANE PROTEIN-RELATED-RELATED; 1.  
DR PANTHER: PTHR34156:SF9; SECRETED PROTEIN; 1.  
DR Pfam: PF07338; YdgH\_BhaA-like; 1.  
DR SUPFAM: SPS159871; YdgH-like; 1.  
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KW Signal (ECO:0000256|ARBA:ARBA00022729, ECO:0000256|SAM:SignalP).  
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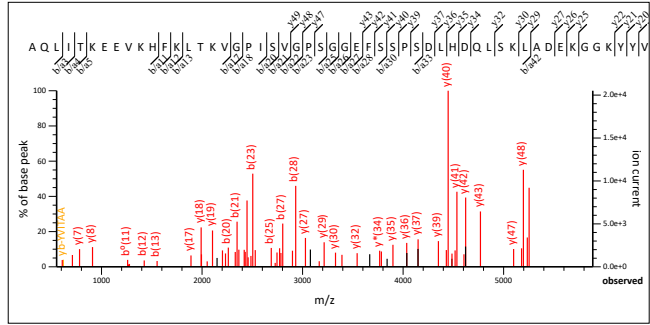
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LADERGGRIY VITAAREHGPF NFEATAEVYK  
//

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

Peptide View

MS/MS Fragmentation of AQLITKEEVKHFKLTKVGVSPISVGPSSDLHDQLSLADEKGGKYVITAAREHGNPFEATAEYVK  
Found in A0A087FU90\_KLEVA in Trembl\_22\_05\_2024, DUF1471 domain-containing protein OS=Klebsiella varicola OX=244366 GN=AN2335V1\_2139 PE=4 SV=1

Match to Query 1: 7698.845524 from(7699.852800,1+) intensity(174388.6127) index(0)  
Title: Reading Top-Down experiment  
Data file K\_pneumoniae\_VIM1\_7700\_Da.mgf



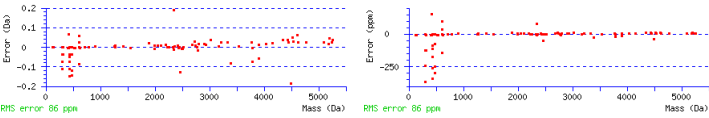
Monoisotopic mass of neutral peptide Mr(calc): 7698.9638  
Ions Score: 292 Expect: 2.9e-26  
Peak matches: 181/1371 fragment ions using 76 most intense peaks  
Annotated Fragments: 183/1371 (help)

#	Immon.	a	a <sup>+</sup>	a <sup>0</sup>	b	b <sup>+</sup>	b <sup>0</sup>	Seq.	y	y <sup>+</sup>	y <sup>0</sup>	#
1	44.0495	44.0495			72.0444			A				71
2	101.0709	172.1081	155.0815		200.1030	183.0764		Q	7628.9340	7611.9075	7610.9235	70
3	86.0964	285.1921	268.1656		313.1870	296.1605		L	7500.8754	7483.8489	7482.8649	69
4	86.0964	398.2762	381.2496		426.2711	409.2445		I	7387.7914	7370.7648	7369.7808	68
5	74.0600	499.3239	482.2973	481.3133	527.3188	510.2922	509.3082	T	7274.7073	7257.6808	7256.6968	67
6	101.1073	627.4188	610.3923	609.4083	655.4137	638.3872	637.4032	K	7173.6596	7156.6331	7155.6491	66
7	102.0550	756.4614	739.4349	738.4509	784.4563	767.4298	766.4458	E	7045.5647	7028.5381	7027.5541	65
8	102.0550	885.5040	868.4775	867.4934	913.4989	896.4724	895.4884	E	6916.5221	6899.4955	6898.5115	64
9	72.0808	984.5724	967.5459	966.5619	1012.5673	995.5408	994.5568	V	6787.4795	6770.4529	6769.4689	63
10	101.1073	1112.6674	1095.6408	1094.6568	1140.6623	1123.6358	1122.6517	K	6688.4111	6671.3845	6670.4005	62
11	110.0713	1249.7263	1232.6997	1231.7157	1277.7212	1260.6947	1259.7106	H	6560.3161	6543.2896	6542.3055	61
12	120.0808	1396.7947	1379.7682	1378.7841	1424.7896	1407.7631	1406.7791	F	6423.2572	6406.2307	6405.2466	60
13	101.1073	1524.8897	1507.8631	1506.8791	1552.8846	1535.8580	1534.8740	K	6276.1888	6259.1622	6258.1782	59
14	86.0964	1637.9737	1620.9472	1619.9632	1665.9687	1648.9421	1647.9581	L	6148.0938	6131.0673	6130.0833	58
15	74.0600	1739.0214	1721.9949	1721.0109	1767.0163	1749.9898	1749.0058	T	6035.0098	6017.9832	6016.9992	57
16	101.1073	1867.1164	1850.0898	1849.1058	1895.1113	1878.0847	1877.1007	K	5933.9621	5916.9355	5915.9515	56
17	72.0808	1966.1848	1949.1582	1948.1742	1994.1797	1977.1532	1976.1691	V	5805.8671	5788.8406	5787.8566	55
18	30.0338	2023.2063	2006.1797	2005.1957	2051.2012	2034.1746	2033.1906	G	5706.7987	5689.7722	5688.7881	54
19	70.0651	2120.2590	2103.2325	2102.2485	2148.2539	2131.2274	2130.2434	P	5649.7772	5632.7507	5631.7667	53
20	86.0964	2233.3431	2216.3165	2215.3325	2261.3380	2244.3115	2243.3274	I	5552.7245	5535.6979	5534.7139	52
21	60.0444	2320.3751	2303.3486	2302.3646	2348.3700	2331.3435	2330.3595	S	5439.6404	5422.6139	5421.6298	51
22	72.0808	2419.4435	2402.4170	2401.4330	2447.4384	2430.4119	2429.4279	V	5352.6084	5335.5818	5334.5978	50
23	30.0338	2476.4650	2459.4384	2458.4544	2504.4599	2487.4334	2486.4493	G	5253.5400	5236.5134	5235.5294	49
24	70.0651	2573.5178	2556.4912	2555.5072	2601.5127	2584.4861	2583.5021	P	5196.5185	5179.4920	5178.5079	48
25	60.0444	2660.5498	2643.5232	2642.5392	2688.5447	2671.5182	2670.5341	S	5099.4657	5082.4392	5081.4552	47
26	30.0338	2717.5712	2700.5447	2699.5607	2745.5662	2728.5396	2727.5556	G	5012.4337	4995.4072	4994.4231	46
27	30.0338	2774.5927	2757.5662	2756.5821	2802.5876	2785.5611	2784.5771	G	4955.4122	4938.3857	4937.4017	45
28	102.0550	2903.6353	2886.6088	2885.6247	2931.6302	2914.6037	2913.6197	E	4898.3908	4881.3642	4880.3802	44
29	120.0808	3050.7037	3033.6772	3032.6932	3078.6986	3061.6721	3060.6881	F	4769.3482	4752.3216	4751.3376	43
30	60.0444	3137.7357	3120.7092	3119.7252	3165.7307	3148.7041	3147.7201	S	4622.2798	4605.2532	4604.2692	42
31	60.0444	3224.7678	3207.7412	3206.7572	3252.7627	3235.7361	3234.7521	S	4535.2478	4518.2212	4517.2372	41
32	70.0651	3321.8205	3304.7940	3303.8100	3349.8155	3332.7889	3331.8049	P	4448.2157	4431.1892	4430.2052	40
33	60.0444	3408.8526	3391.8260	3390.8420	3436.8475	3419.8209	3418.8369	S	4351.1630	4334.1364	4333.1524	39
34	88.0393	3523.8795	3506.8530	3505.8689	3551.8744	3534.8479	3533.8639	D	4264.1309	4247.1044	4246.1204	38
35	86.0964	3636.9636	3619.9370	3618.9530	3664.9585	3647.9319	3646.9479	L	4149.1040	4132.0774	4131.0934	37
36	110.0713	3774.0225	3756.9959	3756.0119	3802.0174	3784.9909	3784.0068	H	4036.0199	4018.9934	4018.0094	36
37	88.0393	3889.0494	3872.0229	3871.0389	3917.0443	3900.0178	3899.0338	D	3898.9610	3881.9345	3880.9504	35
38	101.0709	4017.1080	4000.0815	3999.0974	4045.1029	4028.0764	4027.0924	Q	3783.9341	3766.9075	3765.9235	34
39	86.0964	4130.1921	4113.1655	4112.1815	4158.1870	4141.1604	4140.1764	L	3655.8755	3638.8489	3637.8649	33
40	60.0444	4217.2241	4200.1976	4199.2135	4245.2190	4228.1925	4227.2085	S	3542.7914	3525.7649	3524.7809	32
41	101.1073	4345.3191	4328.2925	4327.3085	4373.3140	4356.2874	4355.3034	K	3455.7594	3438.7328	3437.7488	31
42	86.0964	4458.4031	4441.3766	4440.3926	4486.3980	4469.3715	4468.3875	L	3327.6644	3310.6379	3309.6539	30
43	44.0495	4529.4402	4512.4137	4511.4297	4557.4352	4540.4086	4539.4246	A	3214.5804	3197.5538	3196.5698	29
44	88.0393	4644.4672	4627.4406	4626.4566	4672.4621	4655.4355	4654.4515	D	3143.5433	3126.5167	3125.5327	28
45	102.0550	4773.5098	4756.4832	4755.4992	4801.5047	4784.4781	4783.4941	E	3028.5163	3011.4898	3010.5058	27
46	101.1073	4901.6047	4884.5782	4883.5942	4929.5997	4912.5731	4911.5891	K	2899.4737	2882.4472	2881.4632	26
47	30.0338	4958.6262	4941.5997	4940.6156	4986.6211	4969.5946	4968.6106	G	2771.3788	2754.3522	2753.3682	25
48	30.0338	5015.6477	4998.6211	4997.6371	5043.6426	5026.6160	5025.6320	G	2714.3573	2697.3307	2696.3467	24
49	101.1073	5143.7426	5126.7161	5125.7321	5171.7375	5154.7110	5153.7270	K	2657.3358	2640.3093	2639.3253	23
50	136.0757	5306.8060	5289.7794	5288.7954	5334.8009	5317.7743	5316.7903	Y	2529.2409	2512.2143	2511.2303	22
51	136.0757	5469.8693	5452.8427	5451.8587	5497.8642	5480.8377	5479.8536	Y	2366.1775	2349.1510	2348.1670	21
52	72.0808	5568.9377	5551.9112	5550.9271	5596.9326	5579.9061	5578.9221	V	2203.1142	2186.0877	2185.1036	20
53	86.0964	5682.0218	5664.9952	5664.0112	5710.0167	5692.9901	5692.0061	I	2104.0458	2087.0192	2086.0352	19
54	74.0600	5783.0694	5766.0429	5765.0589	5811.0644	5794.0378	5793.0538	T	1990.9617	1973.9352	1972.9512	18
55	44.0495	5854.1066	5837.0800	5836.0960	5882.1015	5865.0749	5864.0909	A	1889.9141	1872.8875	1871.9035	17
56	44.0495	5925.1437	5908.1171	5907.1331	5953.1386	5936.1120	5935.1280	A	1818.8769	1801.8504	1800.8664	16
57	129.1135	6081.2448	6064.2182	6063.2342	6109.2397	6092.2132	6091.2291	R	1747.8398	1730.8133	1729.8293	15
58	102.0550	6210.2874	6193.2608	6192.2768	6238.2823	6221.2557	6220.2717	E	1591.7387	1574.7122	1573.7281	14
59	110.0713	6347.3463	6330.3197	6329.3357	6375.3412	6358.3147	6357.3306	H	1462.6961	1445.6696	1444.6856	13
60	30.0338	6404.3678	6387.3412	6386.3572	6432.3627	6415.3361	6414.3521	G	1325.6372	1308.6107	1307.6266	12
61	70.0651	6501.4205	6484.3940	6483.4100	6529.4154	6512.3889	6511.4049	P	1268.6157	1251.5892	1250.6052	11
62	87.0553	6615.4634	6598.4369	6597.4529	6643.4584	6626.4318	6625.4478	N	1171.5630	1154.5364	1153.5524	10
63	120.0808	6762.5319	6745.5053	6744.5213	6790.5268	6773.5002	6772.5162	F	1057.5201	1040.4935	1039.5095	9
64	102.0550	6891.5745	6874.5479	6873.5639	6919.5694	6902.5428	6901.5588	E	910.4516	893.4251	892.4411	8
65	44.0495	6962.6116	6945.5850	6944.6010	6990.6065	6973.5799	6972.5959	A	781.4090	764.3825	763.3985	7
66	74.0600	7063.6592	7046.6327	7045.6487	7091.6542	7074.6276	7073.6436	T	710.3719	693.3454	692.3614	6
67	44.0495	7134.6964	7117.6698	7116.6858	7162.6913	7145.6647	7144.6807	A	609.3243	592.2977	591.3137	5
68	102.0550	7263.7390	7246.7124	7245.7284	7291.7339	7274.7073	7273.7233	E	538.2871	521.2606	520.2766	4
69	72.0808	7362.8074	7345.7808	7344.7968	7390.8023	7373.7757	7372.7917	F	409.2445	392.2180	391.2340	3
70	136.0757	7525.8707	7508.8441	7507.8601	7553.8656	7536.8391	7535.8550	Y	310.1761	293.1496		2
71	101.1073							K	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QL	214.1550	242.1499	QLI	327.2391	355.2340	QLIT	428.2867	456.2817
QLITK	556.3817	584.3766	QLITKE	685.4243		LI	199.1805	227.1754

LIT	300.2282	328.2231	LITK	428.3231	456.3180	LITKE	557.3657	585.3606
LITKEE	686.4083		IT	187.1441	215.1390	ITK	315.2391	343.2340
ITKE	444.2817	472.2766	ITKEE	573.3243	601.3192	ITKEEV	672.3927	
TK	202.1550	230.1499	TKE	331.1976	359.1925	TKEE	460.2402	488.2351
TKEEV	559.3086	587.3035	TKEEVK	687.4036		KE	230.1499	258.1448
KEE	359.1925	387.1874	KEEV	458.2609	486.2558	KEEVK	586.3559	614.3508
EE	231.0975	259.0925	EEV	330.1660	358.1609	EEVK	458.2609	486.2558
EEVKH	595.3198	623.3148	EV	201.1234	229.1183	EVK	329.2183	357.2132
EVKH	466.2772	494.2722	EVKHF	613.3457	641.3406	VK	200.1757	228.1707
VKH	337.2347	365.2296	VKHF	484.3031	512.2980	VKHFK	612.3980	640.3929
KH	238.1662	266.1612	KHF	385.2347	413.2296	KHFK	513.3296	541.3245
KHFKL	626.4137	654.4086	HF	257.1397	285.1346	HFK	385.2347	413.2296
HFKL	498.3187	526.3136	HFKLT	599.3664	627.3613	FK	248.1757	276.1707
FKL	361.2598	389.2547	FKLT	462.3075	490.3024	FKLTK	590.4024	618.3974
FKLTKV	689.4709		KL	214.1914	242.1863	KLTK	315.2391	343.2340
KLTK	443.3340	471.3289	KLTKV	542.4024	570.3974	KLTKVG	599.4239	627.4188
KLTKVGP	696.4767		LT	187.1441	215.1390	LTK	315.2391	343.2340
LTKV	414.3075	442.3024	LTKVG	471.3289	499.3239	LTKVGP	568.3817	596.3766
LTKVGPI	681.4658		TKV	301.2234	329.2183	TKVG	358.2449	386.2398
TKVGP	455.2976	483.2926	TKVGPI	568.3817	596.3766	TKVGPIB	655.4137	683.4087
KV	200.1757	228.1707	KVG	257.1972	285.1921	KVGP	354.2500	382.2449
KVGP	467.3340	495.3289	KVGPIB	554.3661	582.3610	KVGPIBIV	653.4345	681.4294
VG	129.1022	157.0972	VGP	226.1550	254.1499	VGPI	339.2391	367.2340
VGPIS	426.2711	454.2660	VGPISV	525.3395	553.3344	VGPISVG	582.3610	610.3559
VGPISVGP	679.4137		GP	127.0866	155.0815	GPI	240.1707	268.1656
GPIB	327.2027	355.1976	GPIBIV	426.2711	454.2660	GPIBIVG	483.2926	511.2875
GPIBIVGP	580.3453	608.3402	GPIBIVGPIB	667.3774	695.3723	PI	183.1492	211.1441
PIS	270.1812	298.1761	PISV	369.2496	397.2445	PISVG	426.2711	454.2660
PISVGP	523.3239	551.3188	PISVGPB	610.3559	638.3508	PISVGPBIV	667.3774	695.3723
IS	173.1285	201.1234	ISV	272.1969	300.1918	ISVG	329.2183	357.2132
ISVGP	426.2711	454.2660	ISVGPIB	513.3031	541.2980	ISVGPIBIV	570.3246	598.3195
ISVGPIBIV	627.3461	655.3410	SV	159.1128	187.1077	SVG	216.1343	244.1292
SVGP	313.1870	341.1819	SVGPIB	400.2191	428.2140	SVGPIBIV	457.2405	485.2354
SVGPIBIV	514.2620	542.2569	SVGPIBIVG	643.3046	671.2995	VGPS	313.1870	341.1819
SVGPS	370.2085	398.2034	SVGPSG	427.2300	455.2249	SVGPSGIV	556.2726	584.2675
GPIB	214.1186	242.1135	GPIBIV	271.1401	299.1350	GPIBIVG	328.1615	356.1565
GPIBIVG	457.2041	485.1991	GPIBIVGPIB	604.2726	632.2675	GPIBIVGPIBIV	691.3046	
PS	157.0972	185.0921	PSG	214.1186	242.1135	PSGIV	271.1401	299.1350
PSGIV	400.1827	428.1776	PSGIVG	547.2511	575.2460	PSGIVGPIB	634.2831	662.2780
SG	117.0659	145.0608	SGG	174.0873	202.0822	SGGIV	303.1299	331.1248
SGGIV	450.1983	478.1932	SGGIVG	537.2304	565.2253	SGGIVGPIB	624.2624	652.2573
GG	87.0553	115.0502	GGE	216.0979	244.0928	GGEIV	363.1663	391.1612
GGEIV	450.1983	478.1932	GGEIVG	537.2304	565.2253	GGEIVGPIB	634.2831	662.2780
GE	159.0764	187.0713	GEF	306.1448	334.1397	GEFIV	393.1769	421.1718
GEFIV	480.2089	508.2038	GEFIVG	577.2617	605.2566	GEFIVGPIB	664.2937	692.2886
EF	249.1234	277.1183	EFB	336.1554	364.1503	EFBIV	423.1874	451.1823
EFBIV	520.2402	548.2351	EFBIVG	607.2722	635.2671	FB	207.1128	235.1077
FBB	294.1448	322.1397	FBBIV	391.1976	419.1925	FBBIVG	478.2296	506.2245
FBBIVG	593.2566	621.2515	SS	147.0764	175.0713	SSIV	244.1292	272.1241
SSIV	331.1612	359.1561	SSIVG	446.1882	474.1831	SSIVGPIB	559.2722	587.2671
SSIVGPIB	696.3311		SP	157.0972	185.0921	SPB	244.1292	272.1241
SPBIV	359.1561	387.1510	SPBIVG	472.2402	500.2351	SPBIVGPIB	609.2991	637.2940
PSD	272.1241	300.1190	PSDIV	385.2082	413.2031	PSDIVG	522.2671	550.2620
PSDIVG	637.2940	665.2889	SD	175.0713	203.0662	SDIV	288.1554	316.1503
SDIV	425.2143	453.2092	SDIVG	540.2413	568.2362	SDIVGPIB	668.2998	696.2947
DL	201.1234	229.1183	DLB	338.1823	366.1772	DLBIV	453.2092	481.2041
DLBIV	581.2678	609.2627	DLBIVG	694.3519		LH	223.1553	251.1503
LHB	338.1823	366.1772	LHBIV	466.2409	494.2358	LHBIVG	579.3249	607.3198
LHBIVG	666.3570	694.3519	HD	225.0982	253.0931	HDIV	353.1568	381.1517
HDIV	466.2409	494.2358	HDIVG	553.2729	581.2678	HDIVGPIB	681.3678	
DQ	216.0979	244.0928	DQIV	329.1819	357.1769	DQIVG	416.2140	444.2089
DQIVG	544.3089	572.3039	DQIVGPIB	657.3930	685.3879	QIS	301.1870	329.1819
QISIV	429.2820	457.2769	QISIVG	542.3661	570.3610	QISIVGPIB	613.4032	641.3981
LS	173.1285	201.1234	LSK	301.2234	329.2183	LSKIV	414.3075	442.3024
LSKIV	485.3446	513.3395	LSKIVG	600.3715	628.3665	SK	188.1394	216.1343
SKIV	301.2234	329.2183	SKIVG	372.2605	400.2554	SKIVGPIB	487.2875	515.2824
SKIVGPIB	616.3301	644.3250	KLA	285.2285	313.2234	KLAD	400.2554	428.2504
KLADIV	529.2980	557.2930	KLADIVG	657.3930	685.3879	LA	157.1335	185.1285
LAD	272.1605	300.1554	LADIV	401.2031	429.1980	LADIVG	529.2980	557.2930
LADIVG	586.3195	614.3144	LADIVGPIB	643.3410	671.3359	AD	159.0764	187.0713
ADE	288.1190	316.1139	ADEIV	416.2140	444.2089	ADEIVG	473.2354	501.2304
ADEIVG	530.2569	558.2518	ADEIVGPIB	658.3519	686.3468	DE	217.0819	245.0768
DEK	345.1769	373.1718	DEKIV	402.1983	430.1932	DEKIVG	459.2198	487.2147
DEKIVG	587.3148	615.3097	EK	230.1499	258.1448	EKIV	287.1714	315.1663
EKIV	344.1928	372.1878	EKIVG	472.2878	500.2827	EKIVGPIB	635.3511	663.3461
KG	158.1288	186.1237	KGG	215.1503	243.1452	KGGIV	343.2452	371.2401
KGGIV	506.3085	534.3035	KGGIVG	669.3719	697.3668	GKG	215.1503	243.1452
GKGIV	378.2136	406.2085	GKGIVG	541.2769	569.2718	GKGIVGPIB	640.3453	668.3402
GK	158.1288	186.1237	GKY	321.1921	349.1870	GKYIV	484.2554	512.2504
GKYIV	583.3239	611.3188	GKYIVG	696.4079		KY	264.1707	292.1656
KYIV	427.2340	455.2289	KYIVG	526.3024	554.2973	KYIVGPIB	639.3865	667.3814
YY	299.1390	327.1339	YYIV	398.2074	426.2023	YYIVG	511.2915	539.2864
YYIVG	612.3392	640.3341	YYIVGPIB	683.3763		YV	235.1441	263.1390
YVIV	348.2282	376.2231	YVIVG	449.2758	477.2708	YVIVGPIB	520.3130	548.3079
YVIVGPIB	591.3501	619.3450	VI	185.1648	213.1598	VIT	286.2125	314.2074
VITIV	357.2496	385.2445	VITIVG	428.2867	456.2817	VITIVGPIB	584.3879	612.3828
ITA	258.1812	286.1761	ITAA	329.2183	357.2132	ITAAIV	485.3194	513.3144
ITAAIV	614.3620	642.3570	TA	145.0972	173.0921	TAA	216.1343	244.1292
TAAIV	372.2354	400.2303	TAAIVG	501.2780	529.2729	TAAIVGPIB	638.3369	666.3318
TAAIVGPIB	695.3583		AA	115.0866	143.0815	AAR	271.1877	299.1826
AARIV	400.2303	428.2252	AARIVG	537.2892	565.2841	AARIVGPIB	594.3107	622.3056
AARIVGPIB	691.3634		AR	200.1506	228.1455	ARE	329.1932	357.1881
AREIV	466.2521	494.2470	AREIVG	523.2736	551.2685	AREIVGPIB	620.3263	648.3212
RE	258.1561	286.1510	REH	395.2150	423.2099	REHIV	452.2364	480.2314
REHIV	549.2892	577.2841	REHIVG	663.3321	691.3270	EH	239.1139	267.1088
EHIV	296.1353	324.1302	EHIVG	393.1881	421.1830	EHIVGPIB	507.2310	535.2259
EHIVGPIB	654.2994	682.2944	HG	167.0927	195.0877	HGP	264.1455	292.1404
HGPIV	378.1884	406.1833	HGPIVG	525.2568	553.2518	HGPIVGPIB	654.2994	682.2944
GPN	241.1295	269.1244	GPNIV	388.1979	416.1928	GPNIVG	517.2405	545.2354
GPNIVG	588.2776	616.2726	GPNIVGPIB	689.3253		PN	184.1081	212.1030
PNIV	331.1765	359.1714	PNIVG	460.2191	488.2140	PNIVGPIB	531.2562	559.2511
PNIVGPIB	632.3039	660.2988	NF	234.1237	262.1186	NFE	363.1663	391.1612
NFEIV	434.2034	462.1983	NFEIVG	535.2511	563.2460	NFEIVGPIB	606.2882	634.2831
FE	249.1234	277.1183	FEA	320.1605	348.1554	FEAT	421.2082	449.2031
FEATIV	492.2453	520.2402	FEATIVG	621.2879	649.2828	EA	173.0921	201.0870
EATIV	274.1397	302.1347	EATIVG	345.1769	373.1718	EATIVGPIB	474.2195	502.2144
EATIVGPIB	573.2879	601.2828	AT	145.0972	173.0921	ATA	216.1343	244.1292
ATAIV	345.1769	373.1718	ATAIVG	444.2453	472.2402	ATAIVGPIB	607.3086	635.3035
TAE	274.1397	302.1347	TAEIV	373.2082	401.2031	TAEIVG	536.2715	564.2664

AE	173.0921	201.0870	AEV	272.1605	300.1554	AEVY	435.2238	463.2187
EVY	364.1867	392.1816	VY	235.1441	263.1390			



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
292.3	7698.9638	-0.1183	<a href="#">AQLITKEEVKHKFLTKVGPISVGPSSGGFSSPSDLHDOLSKLADEKGGKYYVITAAREHGPNFEATAEVYK</a>
19.5	7698.9220	-0.0765	<a href="#">FTYFKFIPMGRALVMSAODVRPYLGNTWVGTANYSEILGSESFRSALKNTVVLAIGOTFGSMLLGFCLAL</a>
19.5	7698.9220	-0.0765	<a href="#">FTYFKFIPMGRALVMSAODVRPYLGNTWVGTANYSEILGSESFRSALKNTVVLAIGOTFGSMLLGFCLAL</a>
19.4	7698.8185	0.0271	<a href="#">ARLDERTIIKOKGYEQAMLDAGLVPYSVMVEOSSSYSSGIELIROARREYPOLNGVFCTNDDLAVGAAE</a>
19.1	7698.7893	0.0562	<a href="#">NHKVVTAFESKTYEIWTLDDLONLPEADLNGKYLMADIDASETRNWNNDGLGFAPIGKNSSTGILDGOG</a>
18.6	7698.9335	-0.0880	<a href="#">LASGKOLWLYRPGTHAGEWGFSENPVLFKDMVIVDGDGSGDSFLIALNREDGKTRWRISRTHOGISYSA</a>
17.7	7698.8832	-0.0377	<a href="#">DOALEANKVYAMLGDKORKQAEVARTPGEGAIAFOGSSGRTTGLPVSEMSSDOKEALOKTLOKLVEMYRO</a>
17.6	7698.9202	-0.0747	<a href="#">LPDPSMPOGLWLHEISKAGGPVLAGVINELAVODLPLPASEADMAAADPNADRSAIOLRPATEAERAFAROLI</a>
17.2	7698.7921	0.0534	<a href="#">DWACARSIDALCTPVAIPPPKRLDEFGELSLDAIHLELNMAQAPPEIOALAEANPDVYLLEVGEDTMVAID</a>
17.2	7698.8138	0.0317	<a href="#">ODPDVAVPPATAIOEIGOELGLVGGYOARFVSDOPMNPANAPKDTFEOKALELMKNGAKSVSEIETINGVPT</a>

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