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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 93340 DE8555 RS09910 WP 002216405.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus

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Position	MAKN	AKKK	LR	F	Y	R	N	S	G	K	LYN	G	E	V	A	E	S	E	F	A	R	K	R	K	Q	G	L	P	L	K	T	K	S	K	S	F	K	T	S	K	K	K	I	T	D	I	T	Y																											
1	M	A	K	T	G	G	F	S	L	F	A	K	K	E	K	R	F	I	F	E	G	R	H	S	A	S	D	K	L	V	N	G	E	V	S	A	F	T	E	B	E	A	R	K	K	L	A	K	R	G	I	R	P	L	Q	I	T	R	V	...	K	T	S	S	K	R	K	I	T	Q	E	D	I	T	V
2	M	A	K	T	G	G	F	S	L	F	A	K	K	E	K	R	F	I	F	E	G	R	H	S	A	S	D	K	L	V	N	G	E	V	S	A	F	T	E	B	E	A	R	K	K	L	A	K	R	G	I	R	P	L	Q	I	T	R	V	...	K	T	S	S	K	R	K	I	T	Q	E	D	I	T	V
3	M	A	K	T	G	G	F	S	L	F	A	K	K	E	K	R	F	I	F	E	G	R	H	S	A	S	D	K	L	V	N	G	E	V	S	A	F	T	E	B	E	A	R	K	K	L	A	K	R	G	I	R	P	L	Q	I	T	R	V	...	K	T	S	S	K	R	K	I	T	Q	E	D	I	T	V
4	M	A	K	T	G	G	F	S	L	F	A	K	K	E	K	R	F	I	F	E	G	R	H	S	A	S	D	K	L	V	N	G	E	V	S	A	F	T	E	B	E	A	R	K	K	L	A	K	R	G	I	R	P	L	Q	I	T	R	V	...	K	T	S	S	K	R	K	I	T	Q	E	D	I	T	V
5	M	A	K	T	G	G	F	S	L	F	A	K	K	E	K	R	F	I	F	E	G	R	H	S	A	S	D	K	L	V	N	G	E	V	S	A	F	T	E	B	E	A	R	K	K	L	A	K	R	G	I	R	P	L	Q	I	T	R	V	...	K	T	S	S	K	R	K	I	T	Q	E	D	I	T	V
6	M	A	K	T	G	G	F	S	L	F	A	K	K	E	K	R	F	I	F	E	G	R	H	S	A	S	D	K	L	V	N	G	E	V	S	A	F	T	E	B	E	A	R	K	K	L	A	K	R	G	I	R	P	L	Q	I	T	R	V	...	K	T	S	S	K	R	K	I	T	Q	E	D	I	T	V
7	M	A	K	T	G	G	F	S	L	F	A	K	K	E	K	R	F	I	F	E	G	R	H	S	A	S	D	K	L	V	N	G	E	V	S	A	F	T	E	B	E	A	R	K	K	L	A	K	R	G	I	R	P	L	Q	I	T	R	V	...	K	T	S	S	K	R	K	I	T	Q	E	D	I	T	V
8	M	A	K	T	G	G	F	S	L	F	A	K	K	E	K	R	F	I	F	E	G	R	H	S	A	S	D	K	L	V	N	G	E	V	S	A	F	T	E	B	E	A	R	K	K	L	A	K	R	G	I	R	P	L	Q	I	T	R	V	...	K														

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LTRQLATMIMKAGVPLVQAFELVAGHNPMTMELMEIRGEVEGSSLSARLKHPPYFDLYCNLVAAEESGGLVLESL
 152
 FTRQIATMLMTGVPVIVQALKLVSENHKKAEKMSILMSVTRAVEACTPMSKAMRTASTHFDPLYTDLIAITGEQSGNLSQVF
 151
 FTRQLSTMINAGLPLMQAFEIVARGHGNSMTEMLMEIRGQVEQCSSLRAFSNHPKYFDRFYCNLVAAAGETGGVLESLL
 154
 FTRQLSTMIKAGLPLMQAFEIVARGHGNSMTEMLMEIRGEVEQCSSLRAFSNHPKYFDRFYCNLVAAAGETGGVLESLL
 154
 FTRQLSTMIKAGLPLMQAFEIVARGHGNSMTEMLMEIRGQVEQCSSLRAFSNHPKYFDRFYCNLVAAAGETGGVLESLL
 154
 FSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETCLTAESELIKHPLYFNELEFCNLVDAGEKSGSLDIML
 151
 FTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAACNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL
 150
 FTRQLATMMKAGVPLVQGEFIVAEGLENPAMRREVLGIKGEVEGCSTFASALRKYPQHFDNLFCSLVESGEQSGALETML
 153
 FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGCNIFAGALRKYPQYFDNLFCSLVESGEQSGSLEIML
 153


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DRLATYKEKTEALKKAKIKKALYTPVSVIAVAIGLVFVMMIFVLPFAFKEVYANMGAELPALTQTQVMDMSDFVSYGWMVLI	232
ERLATYREKSEQLRAKVIKALYIPSMVVLVALGVSYLMLTVLPFEFSEKFGGAELPWFQTQVILKLSHWVQAYSLWAFI	231
DKLATYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPFAFKEVYANMGAELPALTQTQVMDMSDFVSYGWMVLI	234
DKLATYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPFAFKEVYANMGAELPALTQTQVMDMSDFVSYGWMVLI	234
DKLATYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPFAFKEVYANMGAELPPLTQTQVMDMSDFVSYGWMVLI	234
DKVATYKEKIEIKKKIKKALTYPVAVMVALLVTAGLLIVVVPQFESLFGFGADLPAMTRAVITMSEFMQAYWYIIFG	231
DRVATYKEKTEALKKAKIKKAMNYPVAVVLVAIVTATILLIKVVPVQFQDVANFGAELPAFTLMVIGLSEALQAWWYVVLIA	230
DRVATYKEKSELLKKKIKKAMKYPATVIVVAIVVTIILLVVKVVPVVFQDIFASFGADLPFTQVLVNVNMSKWMQYWFIMII	233
DRVAVYKEKSEVLKKIKKAMKYPATVIVVAIVVTIILLVVKVVPVVFKLFTSFGADLPFAFTQLVNVNMSNWMQDYWFILII	233

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Position	1	2	3	4	5	6	7	8	9	10	11	12	
Sequence	AIAAAIFGLKAL	LRKNS	QFQIRL	KTSRL	GLK	FPIT	ICNV	LAKA	SAIK	AFS	RTLAT	FAAGVPLVDAL	STAGAGNLIYEATR
Score	312	311	314	314	314	314	311	310	313	313	313	313	

The sequence logo displays the conservation of amino acids at each position. The y-axis represents the information content in bits, ranging from 0 to 1.5. The x-axis shows the 12 positions. The most conserved positions are 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, and 12, with position 12 being the most conserved (approx. 1.4 bits). The logo shows a high degree of conservation across all positions, with the most common amino acids being Lysine (K), Arginine (R), and Glutamine (Q) at position 12.

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logo

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consensus

```

Protein	Sequence	Position
392	EYRDTAAGMPMYIAMRNTTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFYEVNDNTVDNLGKILEPLIIVFLGTVVGGGL	392
391	EYRDTAAGMPMYIAMRHCHVFPELVLMQMVMIGEESGRLDDMLNKTAAIYEFYEVNDNTVDNLSKILEPLIIVFLGTVVGGGL	391
394	EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDVDNAVGRLSAMMEPIIILVLGLVIGTL	394
394	EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDVDNAVGRLSAMMEPIIIVILGLVIGTL	394
391	KIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALDEKMLSKVADFYEVEVNNAVDALSSLLEPIIMSILGILVGGGL	391
390	KIKSDVSSGMQLNFSMRTTGTFFPSMAVQMTAIGEESGALDEMLSKVATFYEDVDNMVDGLTALMEPMIMAVLGVLVGGGL	390
393	KIREDVSTGQQLQFAMRISNRRFSPMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVVDGLTSMMEPLIMAILGLVLVGGGL	393
393	KIREDVSTGQQLNFAAMRVSNRRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDNAVVDGLTSMMEPLIMAILGLVLVGGGL	393

[illegible]

- non conserved
- similar
- $\geq 50\%$ conserved