

logo

NTDB id 1306 DR RS10060 WP 027479822.1	MSXLSIGDRRLGAILLDQGYLGDNLDLQRALERHSEVGGRLADVLDIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	80
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 103322 A1D13 RS07675 WP 014843847.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIYVPPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 103322 A1D13 RS07675 WP 014843847.1		0
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	LSMLRSDALRLRLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQGRGLGEQLVQEGTLSR	317
NTDB id 1028 TT RS08215 WP 011173991.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
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NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 103322 A1D13 RS07675 WP 014843847.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
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NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGEVITELGFASPDDEVDSALQKQNVGGGRLEDTLVQSGKLSPEMLARSLAAQLGYEFLDPIQ	397
NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEITLVELGLARPEDVEALQKQRRGGGRLEDTLVQSGKLRPEALAAVATQLGYPYVDPEE	397
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAILRQAEELISATQEQAVVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSR	66
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSITLRQKGLLTFSQEEELIEQVKASGISMPEALLSSGFFTSSELAEHLSSIFGLSQPELSQ	66
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEEELIEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQ	66
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAHHY.NESQAGKEVLPMLFSDGVISPKSLAALIARVFSYSILDLRH	65
NTDB id 103322 A1D13 RS07675 WP 014843847.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAAQNFQVPMLDINC	74
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAAQNFQVPMLDINC	74
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQDVTAVYLIEEVHLSPSLAETISAEFAEPYFDLDV	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDTPYPLIDNFSISPLTIAEIIISLEFGEPLLDLGV	74
consensus	* ***** *** **** ** * * * ** * **** ** * *** *** * ***** ***	

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NTDB id 1306 DR RS10060 WP 027479822.1	NPPDPKVALMIPAEATARRYVVVPVRLQGNLSLVAMKDPNRNVFALDDLKLITG.....KEILPAVMAEKDIIRLIERYFGE	472
NTDB id 1028 TT RS08215 WP 011173991.1	DPPDPGAPLILPEDLCRRYGVFPHRLEGNRLVILMKDPRNIALDDVRLALKRKGLNVEVAPAVATEAAITKLIERYFGK	477
NTDB id 1168 A1552VC RS11070 WP 000957200.1	YDYANLCQQGLGLRELITRYDALPIAKQGNLLLLAVSDPTLLQAEFEFRFATG.....LQVELALADHRALQAAIRRLYGR	141
NTDB id 1293 VP RS12240 WP 005479695.1	YEYASLCQQGLGLRELITRHNAIPLHRTPTSTLLLAVADPTNQQAEDDFRFATG.....LQVELVLADFRELSTAIRRLYGR	141
NTDB id 1401 DSB67 RS12665 WP 010643259.1	YEYASLCQTLGLRLDLITRHNAIPLNRTSSTLILAVADPTNLQAEDDFRFATG.....LQVELVLADFRELTAAIRRLYGR	141
NTDB id 1110 NGFG RS09235 WP 003689817.1	YPRHRVLMGVLTEEQMVFEHCVPVFRRGDKVFFAVSDPTQMPQIQKTVSAAG.....IAVELVIVEDDQLAGLLDWVGSR	140
NTDB id 103322 A1D13 RS07675 WP 014843847.1	IDVGTIPANLVNEKLIKRRHAMVPLFSRGTNLVYLATDDPSKQASLKEIQFHTG.....LNTHAIVVETDKLSALIDNLLTA	149
NTDB id 1251 GC085 RS07725 WP 011946523.1	IDVGTIPVNLVNEKLIKRRHAMVPLFSRGTNLVYLATDDPSKQASLKEIQFHTG.....LNTHAIVVETDKLSALIDNLLTA	149
NTDB id 1058 ABD1 RS01615 WP 001274986.1	YDTSQIPKDLVDQKLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAE	149
NTDB id 1018 ACIAD RS01685 WP 004920473.1	FDPALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDAIRFNSK.....LKVEPIIVEHDKLERLLSEHFVE	149
consensus	** * * ** ***** ** *! * ** * ***** *! *** ***** ***** ***** ***** ***** *****	

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consensus

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Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Sequence 1	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 2	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 3	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 4	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 5	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 6	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 7	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 8	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 9	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 10	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M																																																		

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consensus



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logo

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consensus



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consensus



887
889
562
561
561
558
574
574
570
570

ⓧ non conserved
ⓧ similar
ⓧ ≥ 50% conserved