

logo

NTDB id 1306 DR RS10060 WP 027479822.1	MSXLSIGDRRLGAALLDQGYLGNDLQRALERHSEVGGRLADVLDIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	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 231650 CCD85 RS08640 WP 002228974.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSEEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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NTDB id 1293 VP RS12240 WP 005479695.1		0
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		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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consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	LSMRLSDALRYLAVPYGEVVEVYSDPRKREXYRLYRPXSMLEPBYEELFESYYPQRRLGELVQEGELSR	317
NTDB id 1028 TT RS08215 WP 011173991.1	GSMLRADALRLLAVPVDETEQQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRLLGEQLVQEGTLSR	317
NTDB id 1168 A1552VC RS11070 WP 000957200.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	0
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGEVITELGFASPDVDSALQKQNVGGGRLEDTLVQSGKLSPEMLARSLAAQLGYEFLDPIQ	397
NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPPVDPPEE	397
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAAILRQAEILSATQEQAQVVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSR	66
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSTILRQKGLLTFSQEESLIEQVKASGISMPEALLSSGFFTSSSELAEHLSSIFGLSQPELSQ	66
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEESSLIEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQ	66
NTDB id 231650 CCD85 RS08640 WP 002228974.1	MSVGLLRILVQNQVVTVEQAHEHY.KESQAGKEVLPILFSDGVIISPKSLAALIARVFSYSILDLRH	65
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAHEHY.NESQAGKEVLPMLFSDGVIISPKSLAALIARVFSYSILDLRH	65
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAAQNFQGVPMLDINC	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDIVPYLIDNFSISPLTIAEIIISLEFGEPLLDLGV	74
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMTALDAAKRAKQDVTAYLIEEVHLSPSLLAETISAEFAEYPFDLDV	74
consensus	* * * * *	

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NTDB id 1306 DR RS10060 WP 027479822.1	NPPDPKVALMPEATARRVVVPVRLQGNLSLVAMKDPNRNVFALDDLKLITG.....KEILPAVMAEKDIIRLIERYFGE	472
NTDB id 1028 TT RS08215 WP 011173991.1	DPPDPGAPLLIPEDLCRRYGVPFHRLEGNRLVLLMKDPRNIALDDVRLALKRKGLNVEVAPAVATEAAITKLIERYFGK	477
NTDB id 1168 A1552VC RS11070 WP 000957200.1	YDYANLCQQLGLRELITRYDALPIAKQGNLLLLAVSDPTLLQAEFEFRFATG.....LQVELALADHRALQAAIRRLYGR	141
NTDB id 1293 VP RS12240 WP 005479695.1	YEYASLCQQLGLRELITRHNAIPLHRTPTSTLLLAVADPTNQQAEDDFRFATG.....LQVELVLADFRELSTAIRRLYGR	141
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NTDB id 231650 CCD85 RS08640 WP 002228974.1	YPRHRVLMGVLTTEEQMVEFHCVPVFRRGDKVFFAVSDPTQMPQIQKTVSAAG.....IEVELVIVEDDQLAGLLDWVGSR	140
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NTDB id 1251 GC085 RS07725 WP 011946523.1	IDVGTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTG.....LNTHAIVVETDKLSALIDNLLTA	149
NTDB id 1018 ACIAD RS01685 WP 004920473.1	FDPALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDAIRFNSK.....LKVEPIIVEHDKLERLLSEHFVE	149
NTDB id 1058 ABD1 RS01615 WP 001274986.1	YDTSQIPKDLVDQKLLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAE	149
consensus	* * * * *	

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consensus

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AELSEIAKEL	A	E	L	S	E	I	A	K	E	L	...	A	K	.	K	Q	A	E	E	V	.	P	S	P	L	E	D	.	...	D	E	S	A	A	Q	K	F	V	K	Q	V	I	R	E	A	F	L	Q	D	A	S	D	I	H	I	E	P	R	N	D	V	Q	V	R	L	R	I	D	G	A	.																													
SISGAANQGG	S	I	S	G	A	N	Q	G	G	.	...	E	I	S	Q	D	E	L	A	N	L	V	K	V	S	.	...	D	D	E	L	S	Q	.	...	D	S	P	V	S	R	F	I	N	Q	I	L	D	A	V	R	K	G	A	S	D	I	H	F	E	P	Y	E	K	M	Y	R	V	R	L	R	C	D	G	I	.																								
SLSHEKSGLK	S	L	S	H	E	K	S	G	L	K	...	E	I	N	Q	E	E	L	A	S	L	V	D	V	G	A	D	E	I	D	N	I	E	D	L	S	Q	.	...	D	E	S	P	V	S	R	Y	I	N	Q	I	L	D	A	V	R	K	G	A	S	D	I	H	F	E	P	Y	E	K	M	Y	R	V	R	L	R	C	D	G	I	.																			
SLGQEKSGLK	S	L	G	Q	E	K	S	G	L	K	...	E	I	N	Q	D	E	L	A	G	L	V	D	I	G	E	.	...	D	E	S	P	V	S	R	Y	I	N	Q	I	L	D	A	V	R	K	G	A	S	D	I	H	F	E	P	Y	E	K	M	Y	R	V	R	L	R	C	D	G	I	.																														
STSL.LQEL	S	T	S	L	.	L	Q	E	L	...	G	E	G	.	E	E	E	.	...	E	S	H	T	L	I	D	N	E	E	A	.	...	D	E	G	P	V	P	R	.	...	F	I	H	K	T	L	S	D	A	L	R	S	G	A	S	D	I	H	F	E	F	Y	E	H	N	A	R	I	R	F	V	D	G	.																									
STSL.LQEL	S	T	S	L	.	L	Q	E	L	...	G	E	G	.	E	E	E	.	...	E	S	H	T	L	I	D	N	E	E	A	.	...	D	E	G	P	V	P	R	.	...	F	I	H	K	T	L	S	D	A	L	R	S	G	A	S	D	I	H	F	E	F	Y	E	H	N	A	R	I	R	F	V	D	G	.																									
KE.SQGLSEYVEDSGDLEG	K	E	.	S	Q	G	L	S	E	Y	V	E	D	S	G	D	L	E	G	...	L	E	I	S	A	D	.	...	D	E	.	...	D	E	Q	D	I	D	T	A	T	S	V	T	.	...	D	D	A	P	I	V	.	...	K	F	V	N	K	I	L	D	A	I	R	Q	G	A	S	D	I	H	F	E	P	Y	E	R	E	Y	R	I	R	Y	R	Q	D	G	I											

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consensus

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NTDB id 1018 ACIAD RS01685 WP 004920473.1
NTDB id 1058 ABD1 RS01615 WP 001274986.1
consensus
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logo

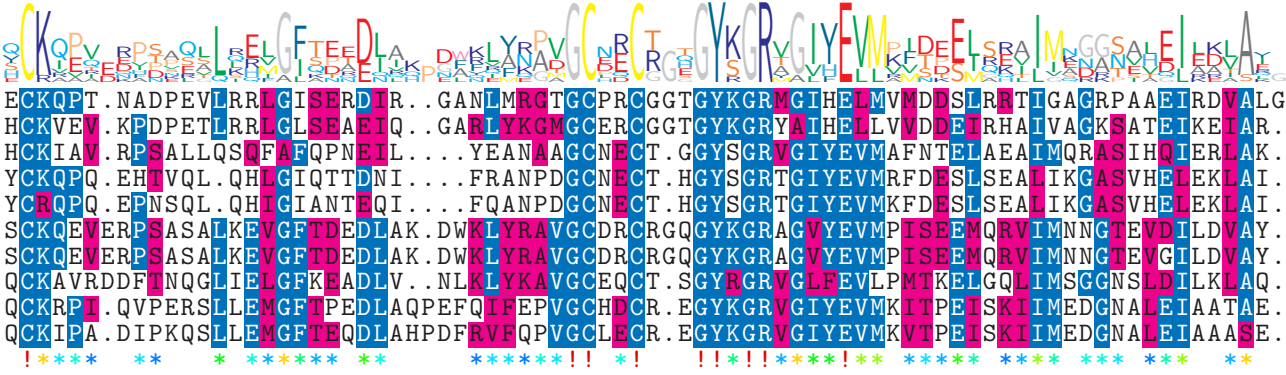
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consensus



779
782
458
458
458
449
449
467
462
462

logo

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NTDB id 1058 ABD1 RS01615 WP 001274986.1
consensus



856
858
531
530
530
527
527
543
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539

logo

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NTDB id 1058 ABD1 RS01615 WP 001274986.1
consensus



887
889
562
561
561
558
558
574
570
570

☒ non conserved
☒ similar
☒ ≥ 50% conserved