

NTDB id	Accession	Sequence	Score
NTDB id 1410	SGL RS13950 WP 010873519.1	MSVLTITGDKRLGAAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0
NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
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 1251	GC085 RS07725 WP 011946523.1		0
NTDB id 1039126	ABQZ61 RS17065 WP 316687911.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

NTDB id	Accession	Sequence	Score
NTDB id 1410	SGL RS13950 WP 010873519.1		0
NTDB id 1028	TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLD	160
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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 1251	GC085 RS07725 WP 011946523.1		0
NTDB id 1039126	ABQZ61 RS17065 WP 316687911.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

NTDB id	Accession	Sequence	Score
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NTDB id 1028	TT RS08215 WP 011173991.1	EGQKDLKLGE LLLQKGWISREALEEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	240
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NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GC085 RS07725 WP 011946523.1		0
NTDB id 1039126	ABQZ61 RS17065 WP 316687911.1		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 1018 ACIAD RS01685 WP 004920473.1
consensus
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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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MSA: M T G L V Q C L Y A E Q E A L E Q K A S G S L P E X L S S G L S P A E E L A E L A E F G P
K K E R S . A V A L R N Y F S P F G N K L V A G G H V D A E Q L R Q A L V Q V K K T G R S L P E E L K A V T G R E L S P E I L R Y K K N Q L F E L K V L Y G V D 86
K E A L E V Q K G L P R A K P L G E I L V E L G I A R P E D V E E A L Q K Q R G G R L E D T L V Q . S G K L R P E A L A Q A V A T Q L G Y P 391
. M L T N L V A I L R Q A E L I S A T Q E Q A V V T Q V S A S G T S V P E A L L E . . L S I F H A Q E L T E Q L S H I F G L P 60
. M H S N L S T I L R Q K G L L T F S Q E E S L I E Q V K A S G I S M P E A L L S . . S G F F T S S E L A E H L S S I F G L S 60
. M L T N L S T V L R Q A G I L T F S Q E E S L E Q V K A S G I S M P E A L L S . . S G F F Q S H E L T E H L S S V F G L S 60
. M S V G L L R I L V Q N Q V V T V E Q A E H Y Y N E S Q . A G K E V L P M L F S . D G V I S P K S L A A L . . I A R V F S Y S 59
. . M A L A T E E Y R L Q G I G Q L L V L E K L L D K T K A I E L H K L A A A E K I S L L Q Y I V K . N K I L S A E Q I A L T A A Q N F G V P 68
. M N A V V S A N L V G I T G I A R R L V Q D G A L D E A A A R T A M E Q A A S A R V P L P Q W F A E . K K L V T A A Q L A A A . N A V E F G M P 70
. M S A L . . H T S P K F T G F F R R L V E E K H V S A A T M Q T A L D A A K R A K Q D T V A Y L I E . E V H L S P S L L A E T I S A E F A E P 68
. M S A F . . T T P P K F S G F I R R L V E E G Y V N A Q N M M Q A L E K A K K F K Q D I V P Y L I D . . N F S I S P L T I A E I I S L E F G E P 68

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NTDB id 1410 SGL RS13950 WP 010873519.1
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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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Sequence	Position
SVDPEVAPIATQMAELIGRFFPLDTCRRFKFLPLAAQEGDPPSVLAVMVDPTNLAAQDENRILRVKG..FEFRRRLVVT	164
YVDPEEDPPDP.....GAPLLLPEDLCRRYGVFPHRL....GNRLVLLMKDPRNIIATDDVRLALKRKGGLNYEVAPAVAT	463
ETDLSRYDYAN.....LCQQLGLRELITRYDALPTAKQ....GNLLLLAVSDPTLLQAEERFRFATG.....LQVELALAD	127
QPELSQY EYAS.....LCQQLGLRELITRHNALPLHRT...PSTLLLAVADPTNQQAEDIFRFATG.....LQVELVLAD	127
CTSLNQY EYAS.....LCQTGLRLDITRHNALPLNRT...SSTLLLAVADPTNLQAEDIFRFATG.....LQVELVLAD	127
ILDRLHYPRHR.....VLMGVLT EEQMV EHCVPVFR...GDKVFFAVSDPTQMPQIQKT VSAAG.....LAVELVIVE	126
MLDINCIDVGT.....IPVNLVNEKLIKRRHAMVPLFSR...GTNLVYLATDDPSKQASLKEIQFHTG.....LNTHAIVE	135
LMDVSVF DNASQ.....NAVKL VSEELLKQYQVLP LFKR...GNRLVFGVSNPTQTRALDDIKFHTN.....LVVEPILVD	137
YFDLDVYDTSQ.....IPKDLVDQKLLKHLRILPLIQR...GQILYVATSNPSNTEADDAIFRNSK.....LLVEPVIVE	135
LLDLGVFDPSAL.....FLKDKID EKKLIQKYRIMPLVHR...GHVLYVATSNPTNTEADDAIFRNSK.....LKVEPILIVE	135

logo

NTDB id 1410	SGL RS13950 WP 010873519.1	QDDFNQLLEQYVAIREEWAAAEKRDQERALDKLNDLTDIVGSLDMNLGEDKEDVDNALDSNDANQA	PVILNVLNKILLAK	243
NTDB id 1028	TT RS08215 WP 011173991.1	EAAITTKLIERFYGAELSEIAKEFAKK.....	QAEVEVPSPLELDESAAQKFVKQVIRE	517
NTDB id 1168	A1552VC RS11070 WP 000957200.1	HRAIQAAIRRLYGRSIIQAANQGKEISQDELA.....	NLVKVSDD...ELQSIEDLSQDPSVSRFINQVLLD	192
NTDB id 1293	VP RS12240 WP 005479695.1	FRELSTAIRRLYGRSLSHEKSGLKEINQEELA.....	SLVDVGAD...EIDNIEDLSQDPSVRYINQILLD	192
NTDB id 1401	DSB67 RS12665 WP 010643259.1	FRELTAAIRRLYGRSLGQEKSGLKEINQDELA.....	GLVDIGED...EIENIEDLSQDPSVRYINQILLD	192
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NTDB id 1039126	ABQZ61 RS17065 WP 316687911.1	EDQIRRALQWQASNASLGSSSLGNDDD.EMGD.....	LDVSSGDEDMGAGGDSGVDAKGDDTPVVVKFVNKVLLD	205
NTDB id 1058	ABD1 RS01615 WP 001274986.1	HHKLEKVLGGHF AEESSFDF....ND.EEFD.....	L DVNL..DGPTAQEDEEEAPQGDEAPIVKYINKLLID	196
NTDB id 1018	ACIAD RS01685 WP 004920473.1	HDKLERLLSEHFVEETHFNF....DT.EELD.....	LDVEVL..DPHTTDDDDEDDKLKDEAPIVKYINKLLID	196
consensus		* * ** * **** * *	**** * **	*** **

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NTDB id 1410 SGL RS13950 WP 010873519.1
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NTDB id 1168 A1552VC RS11070 WP 000957200.1
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NTDB id 1018 ACIAD RS01685 WP 004920473.1

consensus

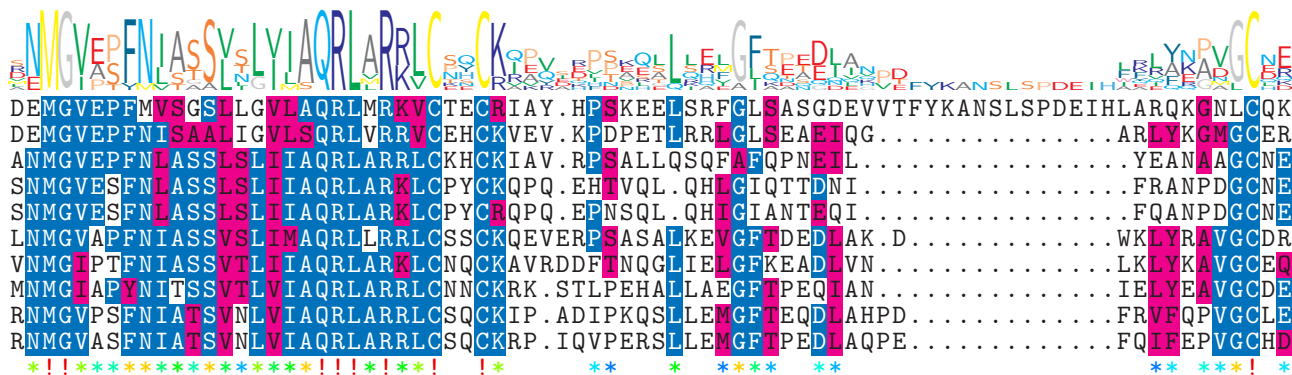


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434

logo

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NTDB id 1018 ACIAD RS01685 WP 004920473.1

consensus

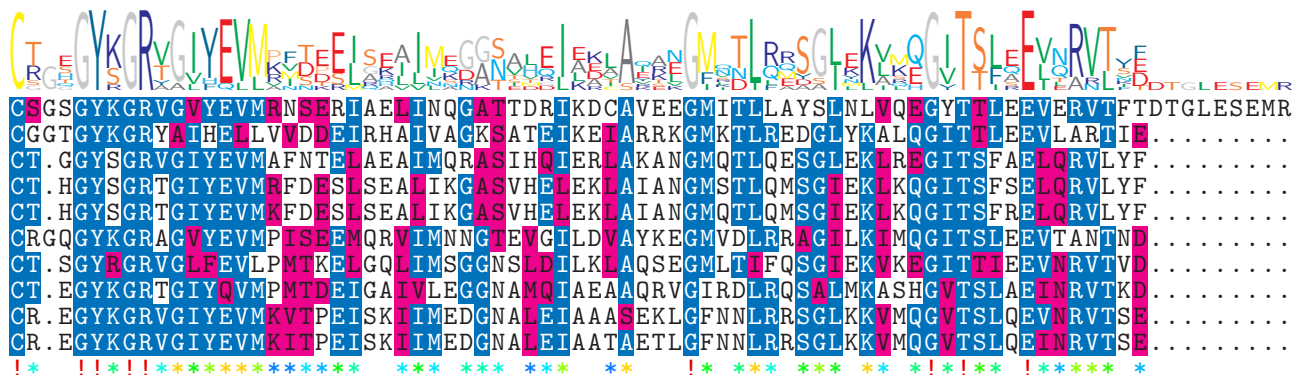


560
818
492
491
491
487
504
507
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logo

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NTDB id 1168 A1552VC RS11070 WP 000957200.1
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NTDB id 1401 DSB67 RS12665 WP 010643259.1
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NTDB id 1039126 ABQZ61 RS17065 WP 316687911.1
NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1

consensus



640
889
562
561
561
558
574
577
570
570

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	AKRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
NTDB id 1028 TT RS08215 WP 011173991.1		889
NTDB id 1168 A1552VC RS11070 WP 000957200.1		562
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NTDB id 1401 DSB67 RS12665 WP 010643259.1		561
NTDB id 1110 NGFG RS09235 WP 003689817.1		558
NTDB id 1251 GC085 RS07725 WP 011946523.1		574
NTDB id 1039126 ABQZ61 RS17065 WP 316687911.1		577
NTDB id 1058 ABD1 RS01615 WP 001274986.1		570
NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved