

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 142127 VU14 RS02355 WP 045525681.1		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 1410 SGL RS13950 WP 010873519.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	0
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	160
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 142127 VU14 RS02355 WP 045525681.1		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 1410 SGL RS13950 WP 010873519.1	EGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	0
NTDB id 1028 TT RS08215 WP 011173991.1	EGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	240
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 142127 VU14 RS02355 WP 045525681.1		0
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consensus		

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[illegible]

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consensus

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Sequence	Position
SKKSRAVALRNYPSPFGNKL	1-10
LVAGCHVDAEQLRQAL	11-20
LQVKKTRSLPEEL	21-30
KAVTGRLEL	31-40
SPELLRQYKKNQLFEL	41-50
KVLYGVD	51-55
KEALEVQKGLPRAKPL	56-65
GEILVELGLARPEDEAL	66-75
QKQRRGGRL	76-85
EDTLVQSGKLRPEALACA	86-95
.....	96-100
VATQLGYP	101-105
.....	106-110
MSVGLLRLLVQNQVVTVEQAEHYYN	111-120
ESQACGEVLPMLFS	121-130
.....	131-135
DGVTPSKSLAAL	136-145
.....	146-150
IARVFSYS	151-155
.....	156-160
MLTNLVAILRQAE	161-170
LSATQEQAVTQVSASGTSVPEAL	171-180
LELSIFHAQELTEQ	181-190
.....	191-195
LSHIFGLP	196-200
.....	201-205
MHSNLS	206-210
TLTQKGLTFSQEESL	211-220
LEQVKASGISMP	221-230
EAALSSGFFQSH	231-240
ELTEH	241-245
.....	246-250
LSISVFGLS	251-255
.....	256-260
MLTNLSTVLRQAGILTFSQEESL	261-270
LEQVKASGISMP	271-280
EAALSSGFFQSH	281-290
ELTEH	291-295
.....	296-300
LSISVFGLS	301-305
.....	306-310
MALATEEYRLQGI	311-320
LGQLVLEKILDKTKAIELHKLAA	321-330
EKISLQYIVK	331-340
.....	341-345
NKILSAEQIALT	346-355
.....	356-360
AAQNFGVP	361-365
.....	366-370
MTSSPNSGLALS	371-380
LAASSLLSESDSQRY	381-390
LSQAKAQRKPFVTF	391-400
LIENEILDSKALAF	401-410
.....	411-415
CELEYGVP	416-420
.....	421-425
MSALHTSPKFTGFFRRL	426-435
VEEKHVS	436-440
AATMQTALDAAKRAKQD	441-450
TVAYLIE	451-455
.....	456-460
EVHLSPLSLAET	461-470
.....	471-475
ISAEFAEP	476-480
.....	481-485
MSAFTTPPKFS	486-495
SGFIRRLVEEGYVNAQNM	496-505
MQQALEKAKFKFKQD	506-515
IVPYLID	516-520
.....	521-525
NFSLPLTIAEI	526-535
.....	536-540
ISLEFGEP	541-545

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consensus

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Sequence	Position
SVDPEVAPITATQQMAELIGRFFPLDTCRRFKFLPLAQEGDPSSVLVAVDPDPNLAQDEINRILRVKGF..EIRRLVVT	164
YVDPEEDPPD....PGAPLIPEDLCRRYGFPHRLEG...NRVLVLMKDPNRNILADDDVLALAKRKGLNVEVAPAVAT	463
ILDRLHYPRH....RVLMGVITEEGYVEFHCVPLVFRRG...DKYFFAVSDPTQMPQIQKTVSAAG....LAVELVIVE	126
ETDLTRYDYA....NLCCQLGLRELITRYDALPIAKQG...NLLLAVSDPTLLQAEFFRFATG....LQVELALAD	127
QPELSQYEYA....SCCQLGLRELITRHNALPLHRT...STLLAVADPTNQQAEDDFRFATG....LQVELVLAD	127
MTSLNQYEYA....SLCQTLGLRDLITRHNALPLNRTP...STLILAVADPTNQAEDDFRFATG....LQVELVLAD	127
CMDINCIDVGC....TIPVNLVNEKLIKRRHAMVPLFSRG...TNLYLATDDPSKQASKEIQFHTG....LNTHAIVVE	135
LLDLAAFDLA....EIPQKYNQKLIKHHVLPITYTQG...HTLYIAMSPTNTVSALEDFGFSFG....LHTEALLVE	131
YFDLDVYDTS....QIPKDLVDQKLILKHRILPLIQRG...QILYVATSNPSNIEADAIRFNSK....LLVEPVIVE	135
LLDLGVFDPA....LFLKDKLDEKLIQKYRIMPLVHRG...HVLVATSNPTNIEAMDARFNSK....LKVEPIIVE	135

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



logo

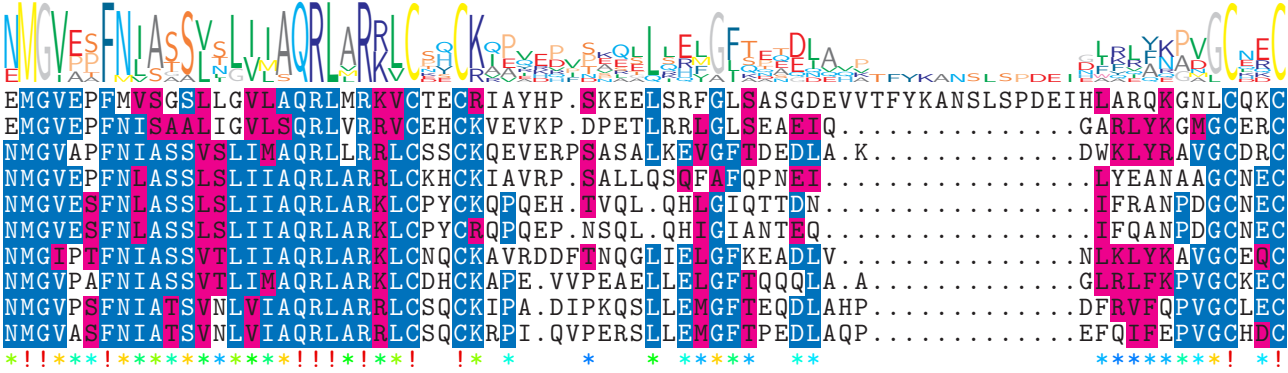
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NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus



482
755
422
431
431
440
434
435
435

logo

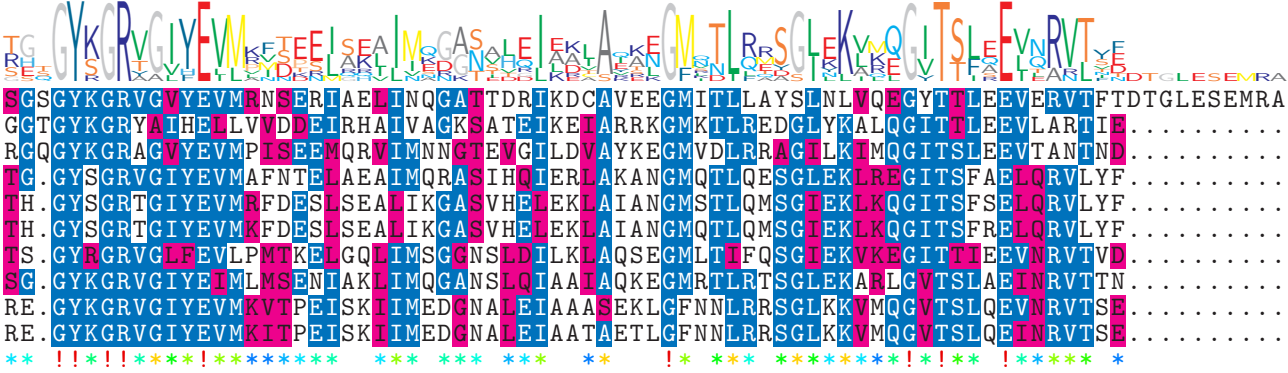
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NTDB id 1028 TT RS08215 WP 011173991.1
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consensus



561
819
488
493
492
492
505
499
501
501

logo

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NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1110 NGFG RS09235 WP 003689817.1
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consensus



641
889
558
562
561
561
574
568
570
570

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	KRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
NTDB id 1028 TT RS08215 WP 011173991.1		889
NTDB id 1110 NGFG RS09235 WP 003689817.1		558
NTDB id 1168 A1552VC RS11070 WP 000957200.1		562
NTDB id 1293 VP RS12240 WP 005479695.1		561
NTDB id 1401 DSB67 RS12665 WP 010643259.1		561
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NTDB id 142127 VU14 RS02355 WP 045525681.1		568
NTDB id 1058 ABD1 RS01615 WP 001274986.1		570
NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved