

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	MSVLTITCDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0
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 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GCO85 RS07725 WP 011946523.1		0
NTDB id 1145133 B5474 RS01675 WP 001274987.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	0
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	160
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	0
NTDB id 1028 TT RS08215 WP 011173991.1	EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	240
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
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NTDB id 1251 GCO85 RS07725 WP 011946523.1		0
NTDB id 1145133 B5474 RS01675 WP 001274987.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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consensus

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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus
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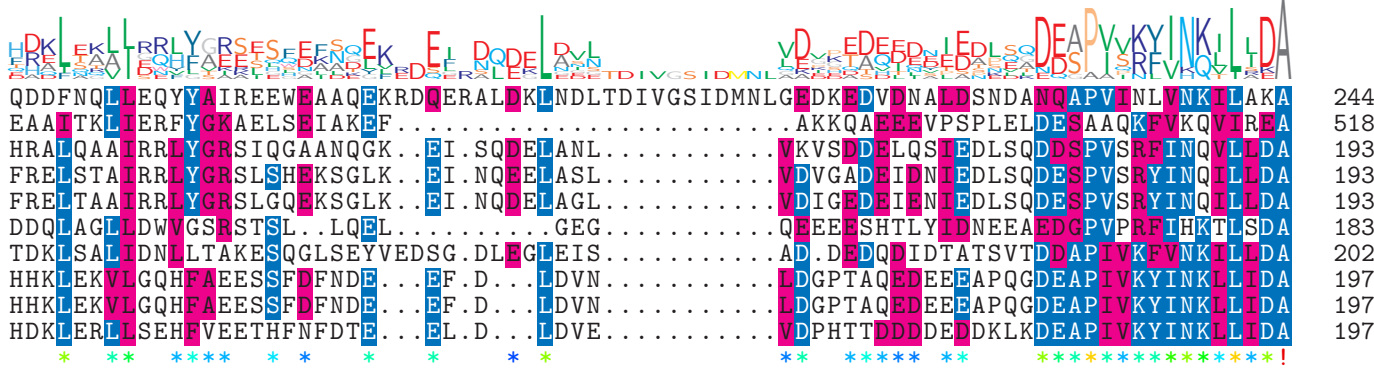
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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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Position	Sequence	Conservation Score (approx.)
1	SVDPEVAPIATQQMAELIGRFFFLDTCRRFKFLPAAQQEGDPPSVLAVVDPDNLAAQDELNRILRVKGF.E	164
2	YVDPEEDPPDP...GAPLLLPEDLCRRYGVFPHRLE...GNRLVLLMKDPRNIALATD	463
3	ETDLSRYDYAN...LCQQGLGLRELITRYDALPTAKQ...GNLLLVASDPTLLQAE	127
4	QPELSQYFYAS...LCQQGLGLRELITRHNALPLHRT...PSTLLLAVADPTNQQA	127
5	CTSLNQYFYAS...LCQTLGLRLITRHNALPLNRT...SSTLLLAVADPTNQQA	127
6	IDLRLHYPRHR...VLMGVLTTEEQMVFEHCVFVFR...GDKVFFAVSDPTQMPQ	126
7	MLDINCIIVGT...IPVNLVNEKLIKRHAMVPLFSR...GTNLVATDPSKQASLKE	135
8	YFDLDVYDTSQ...IPKDLVDQKLLIKHRILPLIQR...GQILYVATSNPSNTEA	135
9	YFDLDVYDTSQ...IPKDLVDQKLLIKHRILPLIQR...GQILYVATSNPSNTEA	135
10	LLDLGVFDPAL...FLDKDIDEXLIQKYRIMPLVHR...GHVLYVATSNPTNTEA	135

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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus



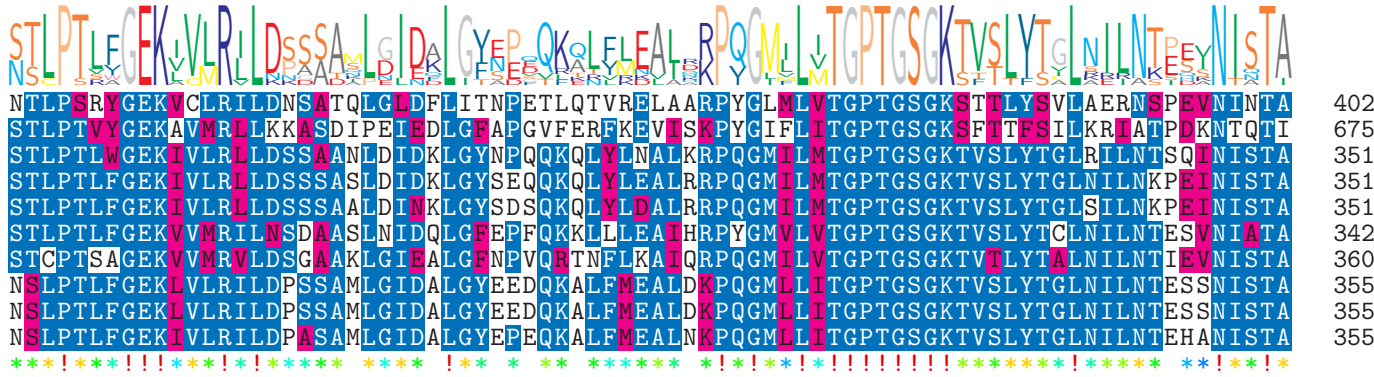
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NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus



logo

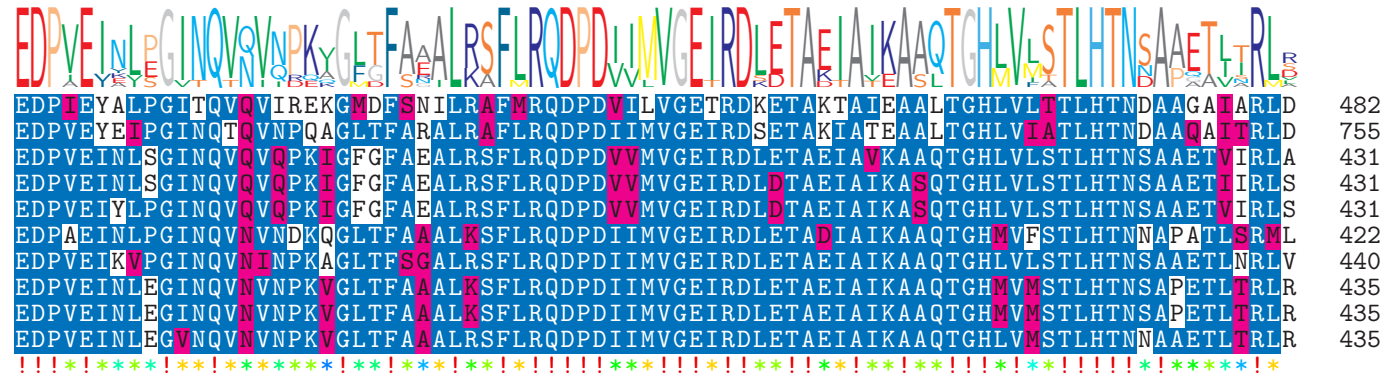
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NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1168 A1552VC RS11070 WP 000957200.1
NTDB id 1293 VP RS12240 WP 005479695.1
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NTDB id 1293 VP RS12240 WP 005479695.1
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NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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NTDB id 1410 SGL RS13950 WP 010873519.1	KRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
NTDB id 1028 TT RS08215 WP 011173991.1		889
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
NTDB id 1110 NGFG RS09235 WP 003689817.1		558
NTDB id 1251 GC085 RS07725 WP 011946523.1		574
NTDB id 1145133 B5474 RS01675 WP 001274987.1		570
NTDB id 1058 ABD1 RS01615 WP 001274986.1		570
NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved