

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
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NTDB id 1251 GC085 RS07725 WP 011946523.1		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 1410 SGL RS13950 WP 010873519.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	0
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	160
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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 1410 SGL RS13950 WP 010873519.1	EGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	0
NTDB id 1028 TT RS08215 WP 011173991.1	EGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	240
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NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 129918 LX00 RS01725 WP 001274984.1		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

[illegible]

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NTDB id 129918 LX00 RS01725 WP 001274984.1
NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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MSA of the protein sequences of the 1000 randomly selected sequences. The sequences are aligned using the ClustalW algorithm. The alignment is shown in the figure, with the sequences numbered 1 to 1000. The sequences are color-coded by domain: blue for the NBD, red for the CSD, green for the CTD, and yellow for the CTD. The alignment shows that the NBD is highly conserved across all sequences, while the CSD and CTD are more variable. The CSD is particularly conserved in the sequences that are involved in the formation of the CTD. The CTD is highly conserved in the sequences that are involved in the formation of the CTD. The alignment also shows that the sequences are highly similar to each other, with many identical residues. This suggests that the sequences are likely to be involved in the same biological process.

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NTDB id 1110 NGFG RS09235 WP 003689817.1
NTDB id 1251 GC085 RS07725 WP 011946523.1
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consensus

Position	Sequence	Score
1	SVDPEVAP	164
2	YVDPEEDPPDP	463
3	ETDLSRYDYAN	127
4	QPELSQY EYAS	127
5	CTSLNQY EYAS	127
6	ILDRLHYPRHR	126
7	MDINCIDVGT	135
8	YFDLDVYDTSQ	135
9	YFDLDVYDTSQ	135
10	LDLGVFDPAL	135

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consensus

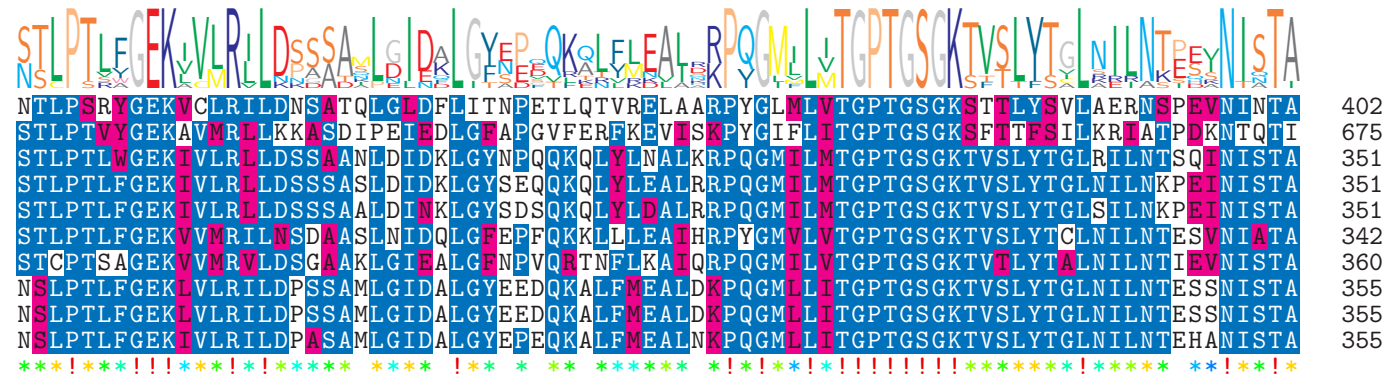
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NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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logo

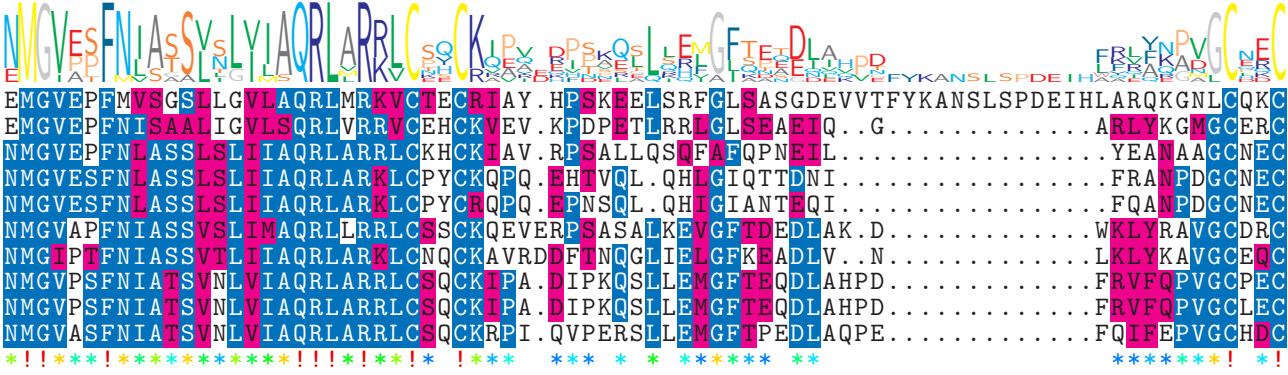
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NTDB id	1058	ABD1 RS01615 WP 001274986.1
NTDB id	1018	ACIAD RS01685 WP 004920473.1
consensus		



482
755
431
431
431
422
440
435
435
435

logo

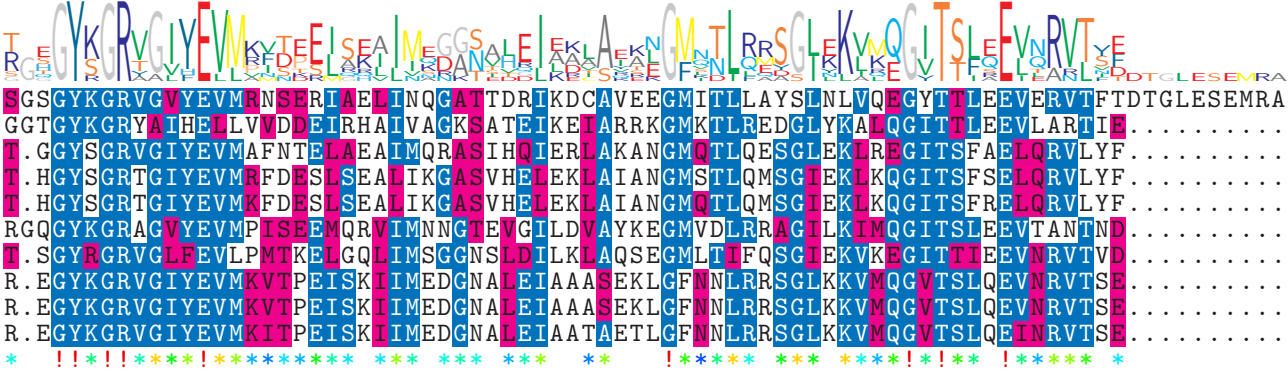
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NTDB id	1028	TT RS08215 WP 011173991.1
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NTDB id	1058	ABD1 RS01615 WP 001274986.1
NTDB id	1018	ACIAD RS01685 WP 004920473.1
consensus		



561
819
493
492
492
488
505
501
501
501

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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		



641
889
562
561
561
558
574
570
570
570

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	KRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
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NTDB id 1168 A1552VC RS11070 WP 000957200.1		562
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NTDB id 1251 GC085 RS07725 WP 011946523.1		574
NTDB id 129918 LX00 RS01725 WP 001274984.1		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