

logo

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NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306	DR RS10060 WP 027479822.1	.MALSIGDRLGAILLDQGYLGDNLDLRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
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NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 183711	A9F03 RS07780 WP 010947251.1		0
NTDB id 1251	GCO85 RS07725 WP 011946523.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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		RLTPEERKELRPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEVPSPGK	
NTDB id 1028	TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEVPSPGK	158
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consensus			

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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	
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NTDB id 1306	DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
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NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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consensus

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[illegible]

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consensus

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[illegible]

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consensus

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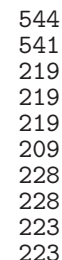
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NPPDPKVALLMPEATARRYVVPLRLQGNSLVAMKDPRNVFAADDLKLTG.....KEILPAVMAEKDIIRLIERFYGE 472
YDYANCCQQLGLRELITRYDALPIAQKNLLLLVASDPTLLQAEERFRATG.....LQVELLAADHRAQLAIRRLYGR 141
YEYASICQQQLGLRELITRHNAIPLHRTPSTLLLVAADPTNQQAEDDFRFATG.....LQVELVIADFRELSTAIRRLYGR 141
YEYASICQTLLGLRDLITHRIHALPLNRSTSLLIVAADPTNQAEDDFRFATG.....LQVELVIADFRELTAAIRRLYGR 141
YPRHRVLMTGVLTIEQMVEFHCVPLVFRGDKVFFAVSDPTQMPQIQKTVSAAAG.....IAVELVIVEDDQLAGLDLVGSR 140
IDVGTIPANLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQHTG.....LNTHAIVVETDKLSALIDNLTA 149
IDVGTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQHTG.....LNTHAIVVETDKLSALIDNLTA 149
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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

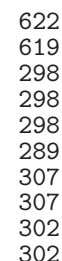
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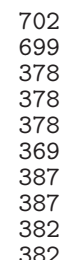
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consensus



782
779
458
458
458
449
467
467
462
462

logo

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consensus



858
856
531
530
530
527
543
543
539
539

logo

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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus



889
887
562
561
561
558
574
574
570
570

☒ non conserved
☒ similar
☒ ≥ 50% conserved