

logo

NTDB id 1306 DR RS10060 WP 027479822.1	MSXLGI GDRRLGAALLDQGYLGDNDLQRALERHSEVGGRLAEVLVDMSGMLLSERRIAQTIEDRFGIPLVELHRVEIPPVK	79
NTDB id 1028 TT RS08215 WP 011173991.1	.MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL	80
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGMLLSERRIAQTIEDRFGIPLVELHRVEIPPVK	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 1093978 ACMG4L RS08050 WP 035249308.1		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 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
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NTDB id 1306 DR RS10060 WP 027479822.1	LSMLRSDALRYLAVPYGSEVVEVYSDPRHREYRLYLRPXSHMLTSPBYEELFBSYPQRRLGELVQEGELSR	317
NTDB id 1028 TT RS08215 WP 011173991.1	GSMLRADALRLLAVPVDETEQQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRLGEQLVQEGTLSR	317
NTDB id 1110 NGFG RS09235 WP 003689817.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	0
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NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPYVDPEE	397
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVITVEQAEHYNE.SQAGKEVLPMLFSDGVISPKSLAALIARVFSYSILDLRH	65
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAILRQAEILISATQEAVVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLR	66
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLTSTILRQKGLTFSQEESLIEQVKASGISMPEALLSSGFFTISSELAEHLSSIFGLSQPELSQ	66
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEESLIEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQ	66
NTDB id 1251 GCO85 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQNFGVPMLDINC	74
NTDB id 1093978 ACMG4L RS08050 WP 035249308.1	MTSQTLSFSGLPQRLIKQELLTAEDAQAQQQARQERVSLVHQLVSSGKLSARVVANAVAEFFGDPILDLSA	72
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTIGFFRRLVEEKHVSAAATMQTALDAAKRAKQDTVAYLIEEVHLSPSLSLAETISAEFAEPYFDLDV	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRVEECYVNAQNMQQALEKAKKFKQDIVPYLIDNFSISPLTIAEILSLEFGEPLLDLGV	74
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NTDB id 1306 DR RS10060 WP 027479822.1	NPPDPKVALMIPAEATARRYVVPVRLQGNLSLVAMKDPRNVFALDDLKLITG.....KEILPAVMAEKDIIRLIERYFGE	472
NTDB id 1028 TT RS08215 WP 011173991.1	DPPDPGAPLLIPEDLCRRYGVFPHRLEGNRLVLLMKDPRNILALDDVRLALKRKGLNYEVAPAVATEAAITKLIERFYGK	477
NTDB id 1110 NGFG RS09235 WP 003689817.1	YPRHRVLMGVLTEEQMVFEHCVPVFRRGDKVFFAVSDPTQMPQIQKTVSAAG.....IAVELVIVEDDQLAGLLDWVGSR	140
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NTDB id 1093978 ACMG4L RS08050 WP 035249308.1	FQRDSL IKDLVDPKLITKHHVLPFLFRGSRFLFVAVSDPTNIPALEEIRFNTG.....LNVETIIVEEDKLTHWIDHLESE	147
NTDB id 1058 ABD1 RS01615 WP 001274986.1	YDTSQIPKDLVDQKLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAE	149
NTDB id 1018 ACIAD RS01685 WP 004920473.1	FDPALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDAIRFNSK.....LKVEPIIVEHDKLERLLSEHFVE	149
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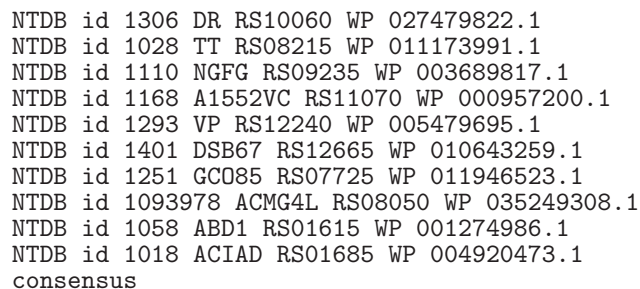
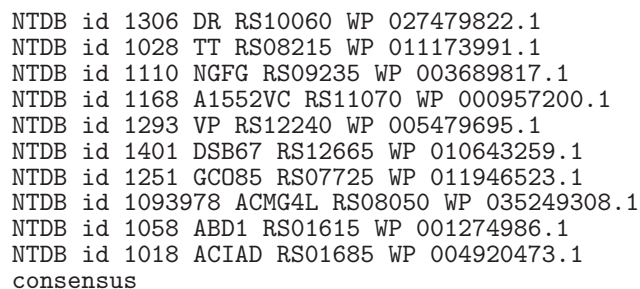
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consensus

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- X non conserved
- X similar
- X > 50% conserved