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NTDB id 1028 TT RS08215 WP 011173991.1	MSXLSIGDRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306 DR RS10060 WP 027479822.1	.MALSIGDRLGAILLDQGYLGDNLDLRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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		

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NTDB id 1028 TT RS08215 WP 011173991.1	RLTPEERKELRPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEYPSPGK	158
NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGA	157
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consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQKGTGDLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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NTDB id 1028 TT RS08215 WP 011173991.1	LRLSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYLAALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
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NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPPYVDPEE	397
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NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAILRQAEILSATQEQAIVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSR	66
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSTILRQKGLTFSQEESSLIEQVKASGISMPEALLSSGFFTSSSELAEHLSSIFGLSQPELSQ	66
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEESSLIEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQ	66
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQAQNFQVPMLDINC	74
NTDB id 349091 EZZ79 RS03950 WP 024664613.1	MTDAVLTGLAKQLVLAELLTETVAQQAYQHARRDKVSLVSYLVQSKLVKSLTLAEMASEQFGVPFMDIAS	70
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAATMQTALDAAKRAKQDTVAYLIEEVHLSPSLLAETISAEFAEPYFDLDV	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDIVPYLIDNFSISPLTIAEIIISLEFGEPLLDLGV	74
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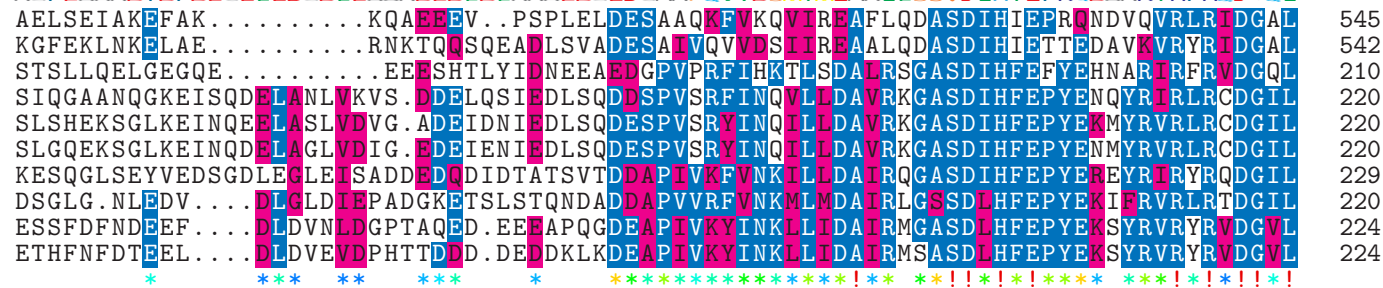
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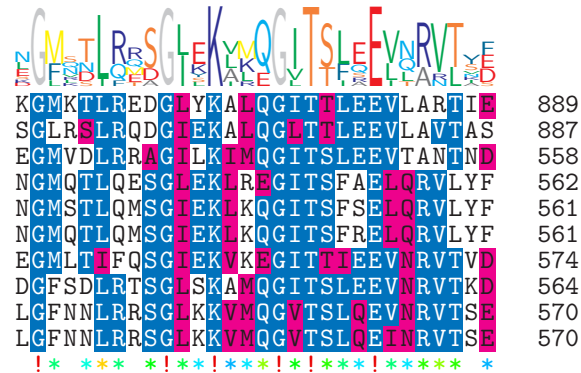
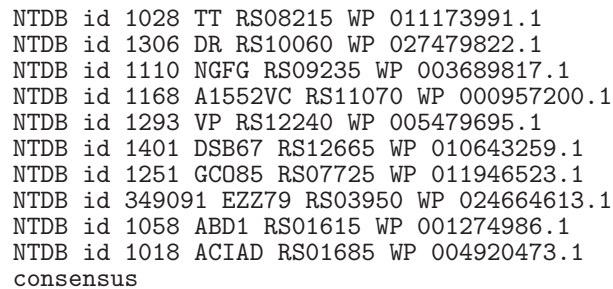
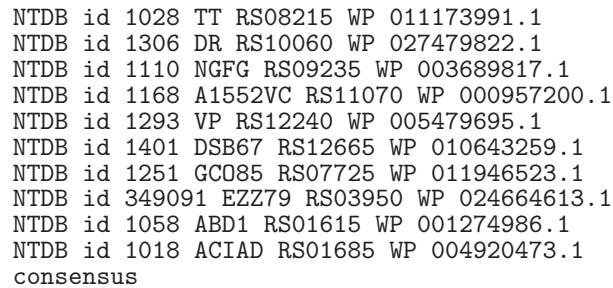
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consensus

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-  non conserved
-  similar
-  > 50% conserved