

logo

NTDB id 1028 TT RS08215 WP 011173991.1	MSXLSIGDRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306 DR RS10060 WP 027479822.1	.MALSIGDRLGAILLDQGYLGDNLDLRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
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NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
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NTDB id 384393 FYK34 RS13930 WP 149297374.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		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
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
NTDB id 384393 FYK34 RS13930 WP 149297374.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
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consensus

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[illegible]

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EALKEAL¹EVQKGLPRAK²LG³ET⁴LV⁵EL⁶GL⁷AR⁸PEDV⁹EAL¹⁰LQK¹¹QR¹²RG¹³CG¹⁴RL¹⁵ED¹⁶TL¹⁷VQ¹⁸SG¹⁹KLR²⁰PEAL²¹LA²²QAV²³AT²⁴QL²⁵GY²⁶PY²⁷VD²⁸P²⁹EE
 DQLREAL³⁰LQVQAREG³¹KV³²KPL³³GEV³⁴IT³⁵EL³⁶GF³⁷ASP³⁸DEV³⁹DSAL⁴⁰LQK⁴¹QNV⁴²GG⁴³RL⁴⁴ED⁴⁵TL⁴⁶VQ⁴⁷SG⁴⁸KLSPE⁴⁹ML⁵⁰ARS⁵¹LA⁵²Q⁵³LY⁵⁴GF⁵⁵LD⁵⁶PI⁵⁷Q
ML⁵⁸TN⁵⁹LV⁶⁰AIL⁶¹RQ⁶²AE⁶³LIS⁶⁴AT⁶⁵REQ⁶⁶AV⁶⁷TQ⁶⁸VS⁶⁹AS⁷⁰GT⁷¹SV⁷²PEAL⁷³LE⁷⁴LS⁷⁵IF⁷⁶HA⁷⁷QEL⁷⁸TE⁷⁹QL⁸⁰SH⁸¹IF⁸²GL⁸³PET⁸⁴DL⁸⁵SR
M⁸⁶HS⁸⁷NL⁸⁸ST⁸⁹IL⁹⁰RQ⁹¹KGL⁹²L⁹³TF⁹⁴SQ⁹⁵EES⁹⁶LIE⁹⁷QV⁹⁸KAS⁹⁹GIS¹⁰⁰MEAL¹⁰¹LS¹⁰²GFF¹⁰³TS¹⁰⁴SE¹⁰⁵LA¹⁰⁶EH¹⁰⁷SS¹⁰⁸IF¹⁰⁹GL¹¹⁰SQ¹¹¹PE¹¹²LS¹¹³Q
ML¹¹⁴TN¹¹⁵LV¹¹⁶RL¹¹⁷QAG¹¹⁸IL¹¹⁹TF¹²⁰SQ¹²¹EES¹²²LIE¹²³QV¹²⁴KAS¹²⁵GIS¹²⁶MEAL¹²⁷LS¹²⁸GFF¹²⁹TS¹³⁰SE¹³¹LA¹³²EH¹³³SS¹³⁴IF¹³⁵GL¹³⁶SCT¹³⁷SL¹³⁸NQ
MAL¹³⁹ATEEY¹⁴⁰RL¹⁴¹QIG¹⁴²QGL¹⁴³VLE¹⁴⁴KL¹⁴⁵DK¹⁴⁶TKA¹⁴⁷IEL¹⁴⁸HKL¹⁴⁹AA¹⁵⁰EKI¹⁵¹SL¹⁵²LQ¹⁵³YIV¹⁵⁴KN¹⁵⁵KIL¹⁵⁶SAEQ¹⁵⁷IAL¹⁵⁸TA¹⁵⁹QNF¹⁶⁰GV¹⁶¹PML¹⁶²DI¹⁶³NC
MSA¹⁶⁴LHTSP¹⁶⁵KFT¹⁶⁶GF¹⁶⁷FRRL¹⁶⁸VEE¹⁶⁹KH¹⁷⁰VS¹⁷¹AAT¹⁷²MQT¹⁷³AL¹⁷⁴DAAK¹⁷⁵RAK¹⁷⁶QDT¹⁷⁷VAY¹⁷⁸LIE¹⁷⁹VHL¹⁸⁰SP¹⁸¹SL¹⁸²LAET¹⁸³IS¹⁸⁴AE¹⁸⁵FA¹⁸⁶EPY¹⁸⁷F¹⁸⁸LD¹⁸⁹LV
MSA¹⁹⁰FTTP¹⁹¹PK¹⁹²FG¹⁹³SF¹⁹⁴IRRL¹⁹⁵VEE¹⁹⁶GY¹⁹⁷VNA¹⁹⁸QNM¹⁹⁹QQA²⁰⁰LEK²⁰¹AK²⁰²KFK²⁰³QDI²⁰⁴VPY²⁰⁵LID²⁰⁶NFS²⁰⁷IS²⁰⁸PL²⁰⁹TH²¹⁰AE²¹¹II²¹²SL²¹³EF²¹⁴GE²¹⁵PL²¹⁶LD²¹⁷LV
MEATAG²¹⁸IS²¹⁹GL²²⁰GRAL²²¹VQH²²²NML²²³LQ²²⁴QDAD²²⁵AI²²⁶QK²²⁷HAA²²⁸ASH²²⁹IS²³⁰FVE²³¹QL²³²IL²³³SK²³⁴MS²³⁵ARE²³⁶VAV²³⁷FAS²³⁸RI²³⁹FGY²⁴⁰PL²⁴¹LD²⁴²MSA
MSV²⁴³GL²⁴⁴LRIL²⁴⁵VQN²⁴⁶QVV²⁴⁷TV²⁴⁸EQ²⁴⁹AHHY²⁵⁰YNES²⁵¹QA²⁵²GKE²⁵³VL²⁵⁴PL²⁵⁵MF²⁵⁶SD²⁵⁷GV²⁵⁸IS²⁵⁹PKS²⁶⁰LAAL²⁶¹LAR²⁶²VFSY²⁶³SIL²⁶⁴DL²⁶⁵RH

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DPPDPGAPLLLPEDLCRRYGVFPHRLEGRLVLMLLKDPNRNIALDDVRLALKRKGLNYEVAPAVATEAAITKLTIERFYCK 477

NPPDPKVALMPEIATARRVVVPVRLLQGNSLVAMKDPRNVFALDDLKLITG.....KEILPAVMAEKDIIRLIERYFGE 472

YDYANLCQQQLGLRELITRYDALPIAKQGNLLLLVADPTNLLQAEEFFRFATG.....LQVELALADHRAHQAAIRRRLYGR 141

YEYASLCQQQLGLRELITRHNAPLHRTPSTLLLAVADPTNQQAEDDFRFATG.....LQVELVLADFRELSTAIRRRLYGR 141

YEYASLCQTLGLRLDLITRHNAFLPNRTSSTLILAVADPTNLQAEDDFRFATG.....LQVELVLADFRELSTAIRRRLYGR 141

IDVCTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDPSKQASLKEIKYFHTG.....LNTHAIVETDKLSALIDNLTA 149

YDTSQIPKDLVDQKLLIKHRIPLPIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVIQGHFAE 149

FDPALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDARFNSK.....LKVEPTIVEHDKLERLLSEHFVE 149

LDIEQLPKGLVDEELIASRRLLPILLKRGNKLYICTSDPTQTSAHYHAITFKTG.....LTVEIVVEDDKLSKLVGRYQDS 146

YPRHRVLMGLVLEEQMVEFHCVFVRFGDKVFFAVSDPTQMPQIQKTVSAG.....TAVELVIVEDDQLAGLLDWGSR 140

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consensus
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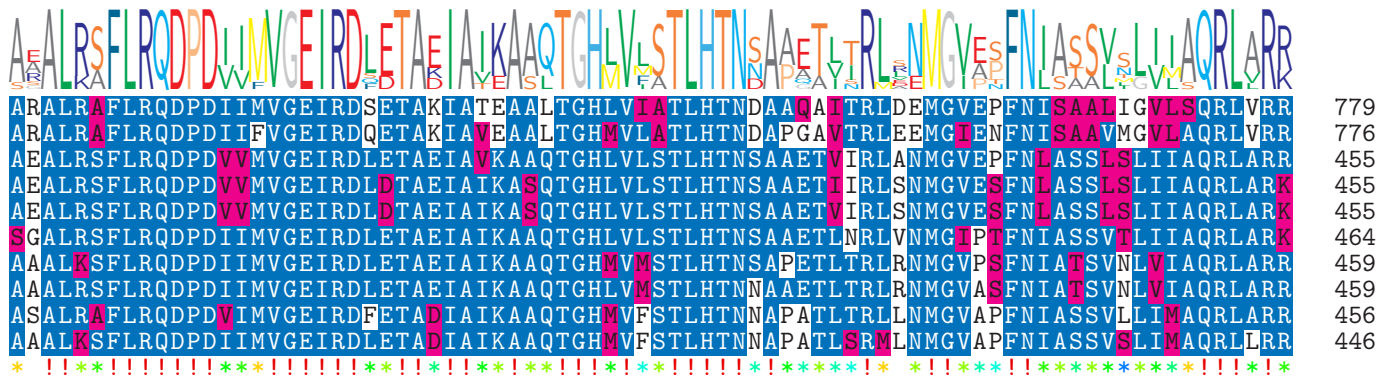
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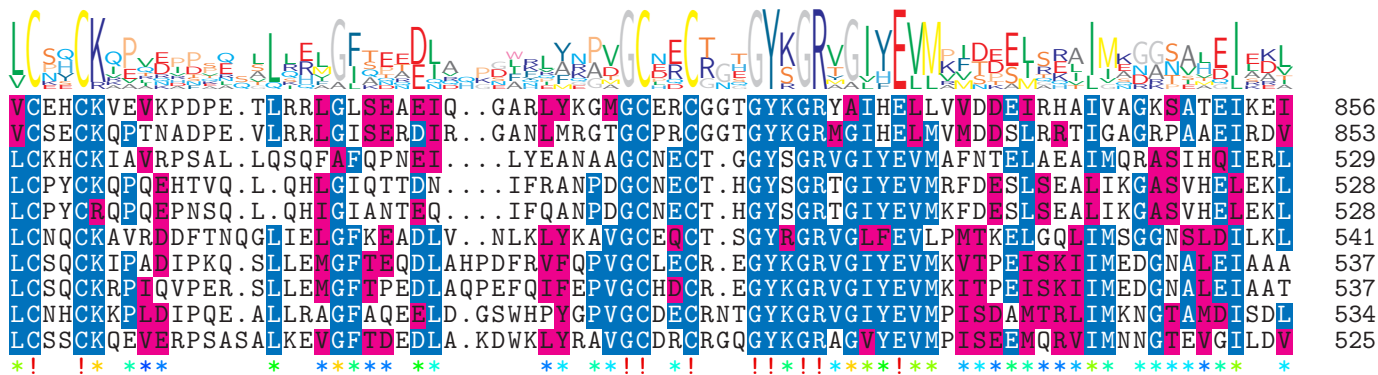
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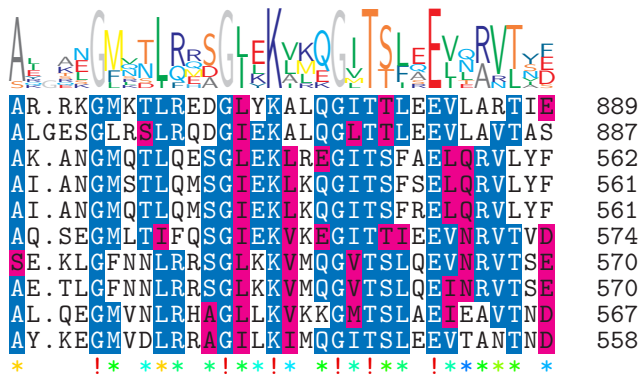
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consensus
```



- X non conserved
- X similar
- X ≥ 50% conserved