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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGFA RS09215 WP 003689811.1
NTDB id 1113 AAG85695.1 219..1451( )
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 214254 BHL62 RS16585 WP 011408067.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
consensus

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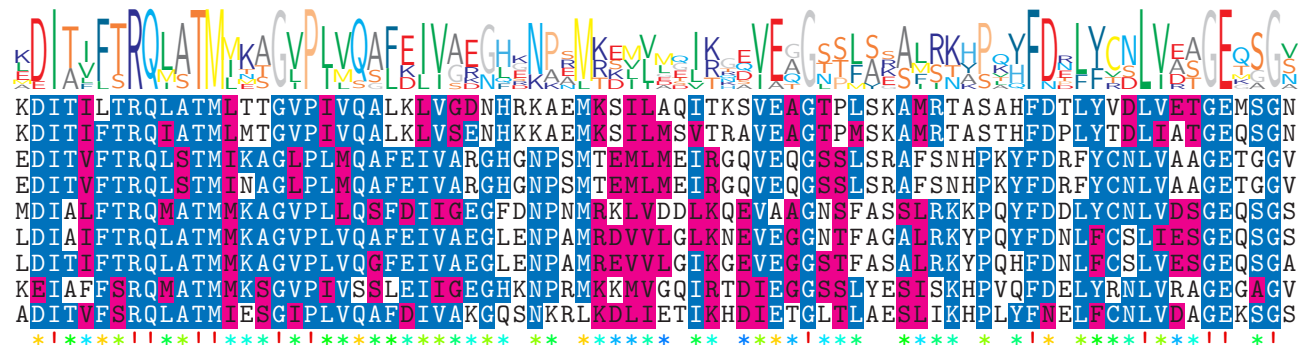


67
66
69
69
65
68
68
78
66

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NTDB id 1169 A1552VC RS11075 WP 000648511.1
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NTDB id 1112 NGFG RS09215 WP 003689811.1
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NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 214254 BHL62 RS16585 WP 011408067.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
consensus

```

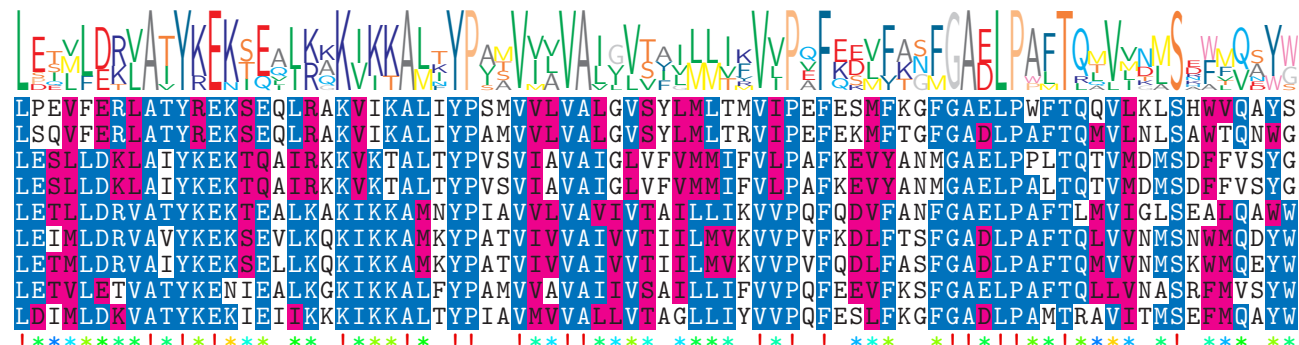


147
146
149
149
145
148
148
158
146

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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1198 PSJM300 03950 AFN76868.1
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NTDB id 214254 BHL62 RS16585 WP 011408067.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
consensus

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227
226
229
229
225
228
228
238
226

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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGGF RS09215 WP 003689811.1
NTDB id 1113 AAG85695.1 219..1451( )
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NTDB id 214254 BHL62 RS16585 WP 011408067.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
consensus

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307
306
309
309
305
308
308
318
306

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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
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NTDB id 214254 BHL62 RS16585 WP 011408067.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
consensus

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logo

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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
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NTDB id 214254 BHL62 RS16585 WP 011408067.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
consensus

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QLAIEEVYRDTAAGMPMYIAMRHCHVPFELVLQVMVIGEESGLDMLNKIAIYEFVDNTVDNLGKILEPLTIIVFLGV	386
EEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSIGEESGLDMLNKAAEFYEEVDNAVGRLSAMMEPTIIVILGL	389
EEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSIGEESGLDMLNKAAEFYEEVDNAVGRLSAMMEPTIILILGL	389
RSATNKKIKSDVSSGQQLNFSMRTTGTFFPMAVQMTAIGESGALDEMLSKVATFYEEVDNMVDGLTALMEPMIMAVILG	385
EQAVLKIREDDVSTGQQLNFAAMRVSNRFPTMAIQMVAIGESGALDEMLDKVANYEYSEVDHVAVDGLTSMMEPLIMAILGI	388
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EEAVFRMRDDVSVGYPVNMAAMKQVNLFPHMVIQMTAIGEEAGALDAMLFKVAEYFEEEVNNAVDALSSILEPLIMVFIGT	398
AKATDKIREEDVATGQQMFIAMENTHLLFPNMVIQMVAIGESGALDKMLSKVADFYEEEVNNAVDALSSILEPTIMSLIGI	386

Position	Sequence	Score
1	VVGGGLVYAMLP	408
2	VVGGGLVTAMYP	407
3	VIGTLLVAMYP	410
4	VIGTLLVAMYP	410
5	LVGGLIIAMYP	405
6	LVGGLVIAMYP	408
7	LVGGLVIAMYP	408
8	IVGGMVIGMYLP	419
9	LVGGLVYAMYP	406

- ☐ non conserved
- ☒ similar
- ☒ $\geq 50\%$ conserved