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NTDB id 161832 ASZ87 RS10995 WP 000648511.1
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 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

```

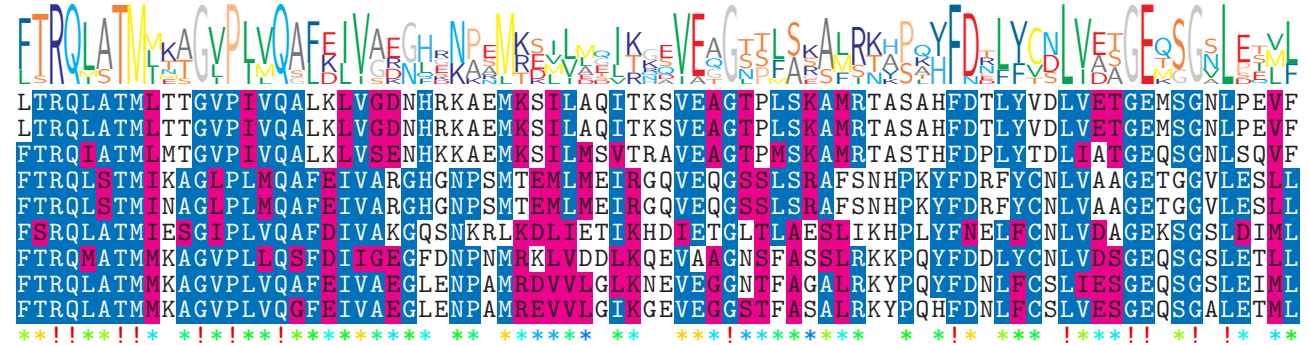


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73

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NTDB id 161832 ASZ87 RS10995 WP 000648511.1
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NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NFGF RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

```

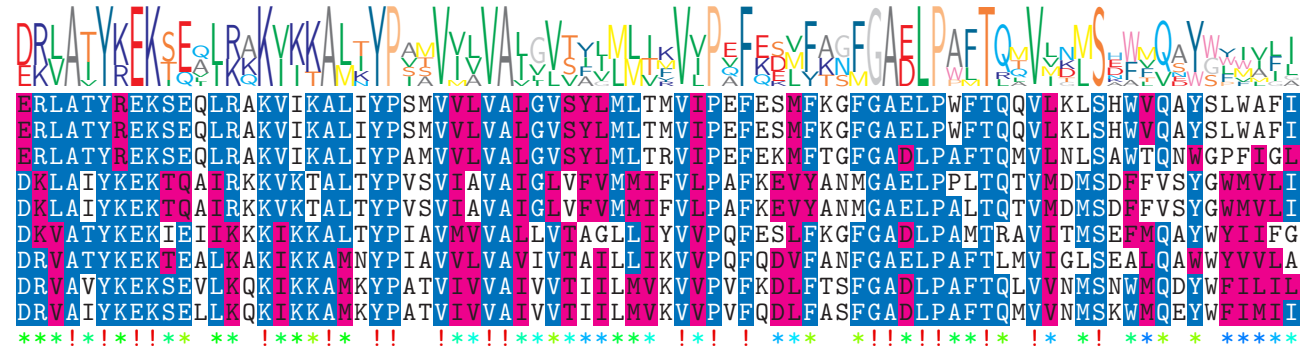


152
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NTDB id 161832 ASZ87 RS10995 WP 000648511.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
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NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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232
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NTDB id 161832 ASZ87 RS10995 WP 000648511.1
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NTDB id 1402 DSB67 RS12670 WP 010643257.1
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NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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312
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NTDB id 161832 ASZ87 RS10995 WP 000648511.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
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NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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logo

Sequence	Position
EYRDTAAGMPMYIAMRNTTEAFPEMVLQMVMIGEESQLDDMLNKVATIYEFYEDVNTVDNLGKILEPLIIIVFLGTIVVGG	392
EYRDTAAGMPMYIAMRNTTEAFPEMVLQMVMIGEESQLDDMLNKVATIYEFYEDVNTVDNLGKILEPLIIIVFLGTIVVGG	392
EYRDTAAGMPMYIAMRHCHVPELVLQMVMIGEESGRDDMLNLKTAATYEFYEDVNTVDNLGKILEPLIIIVFLGTIVVGG	391
EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGLDDMLNKAAEFYEDVDNAVGRLSAMMEPTIIIVILGLVIGTL	394
EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGLDDMLNKAAEFYEDVDNAVGRLSAMMEPTIIIVILGLVIGTL	394
KIREEVATGQQMFIAENTHLPNMVIMQVAIGEESGALDKMLSKVADFYEEVNNAVDALSSILEPIIMSILGILVGG	391
KIKSDVSSGQMLNFSMRTNGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDVDNMVDGLTALMEPMIMAVLGVLVGG	390
KIREVDSTGQQLNFAAMRVSGTFFPSMAITQMTAIGEESGALDEMLDKVANFYEEVDHVDGLTSMMEPLIMAILGILVGG	393
KIREVDVATGQQLQFAMRISNRFPSPMAITQMTAIGEESGALDSMLDKVATYYENYEDVDNAVGLTSMMEPLIMAILGVLVGG	393

[illegible]

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