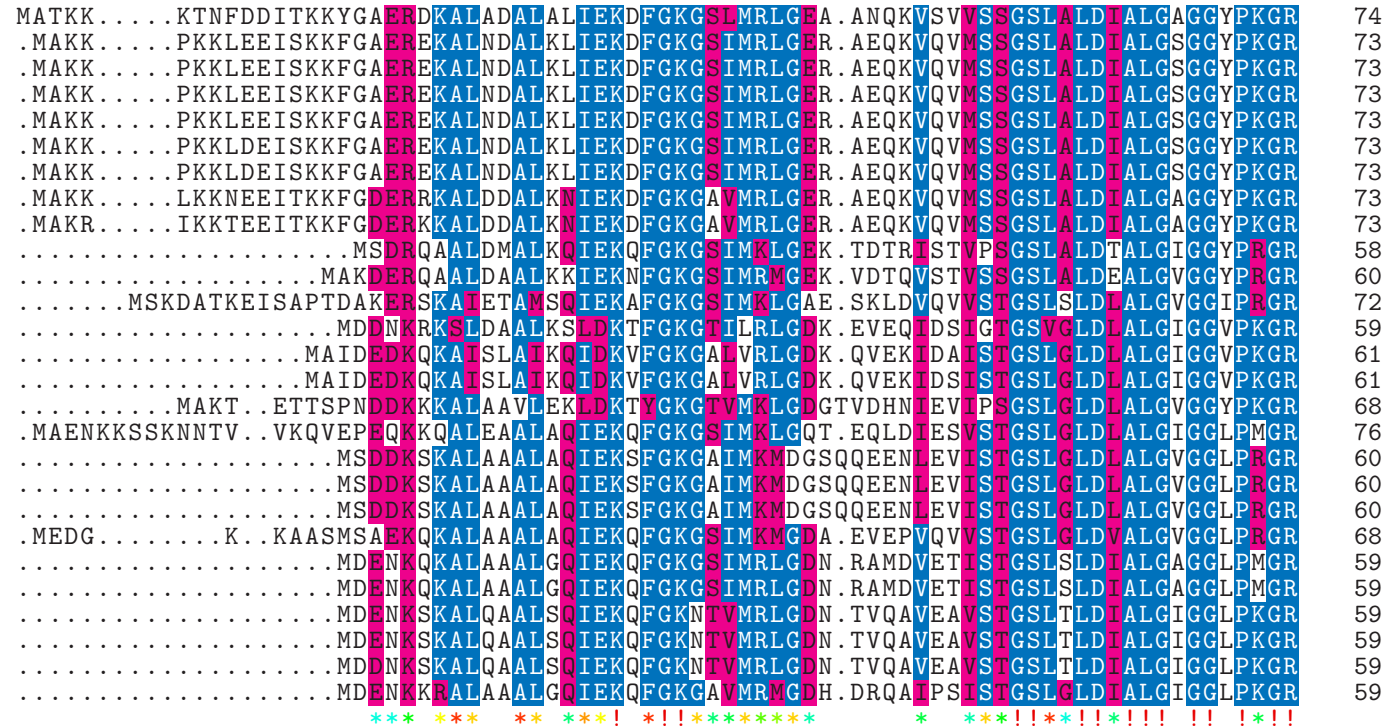


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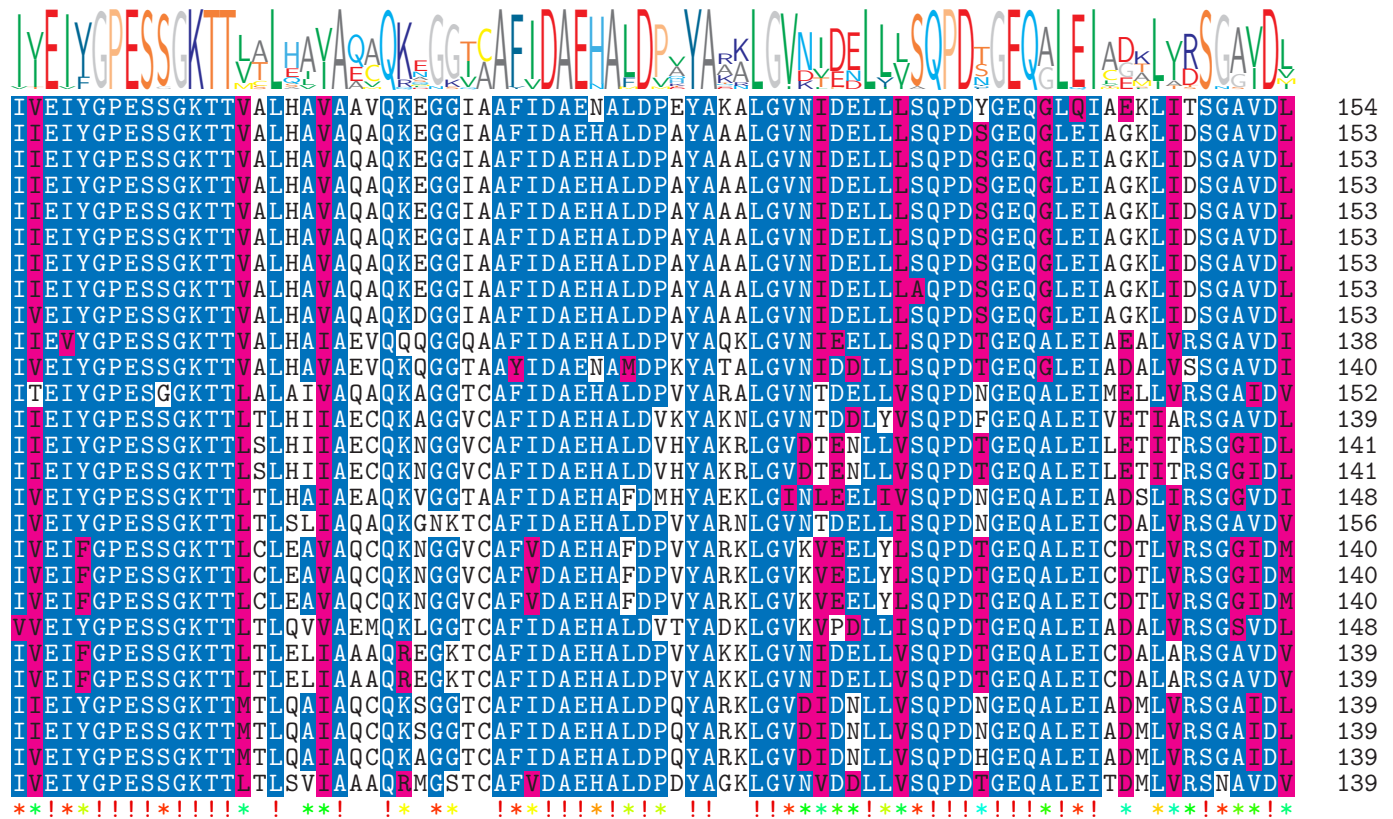
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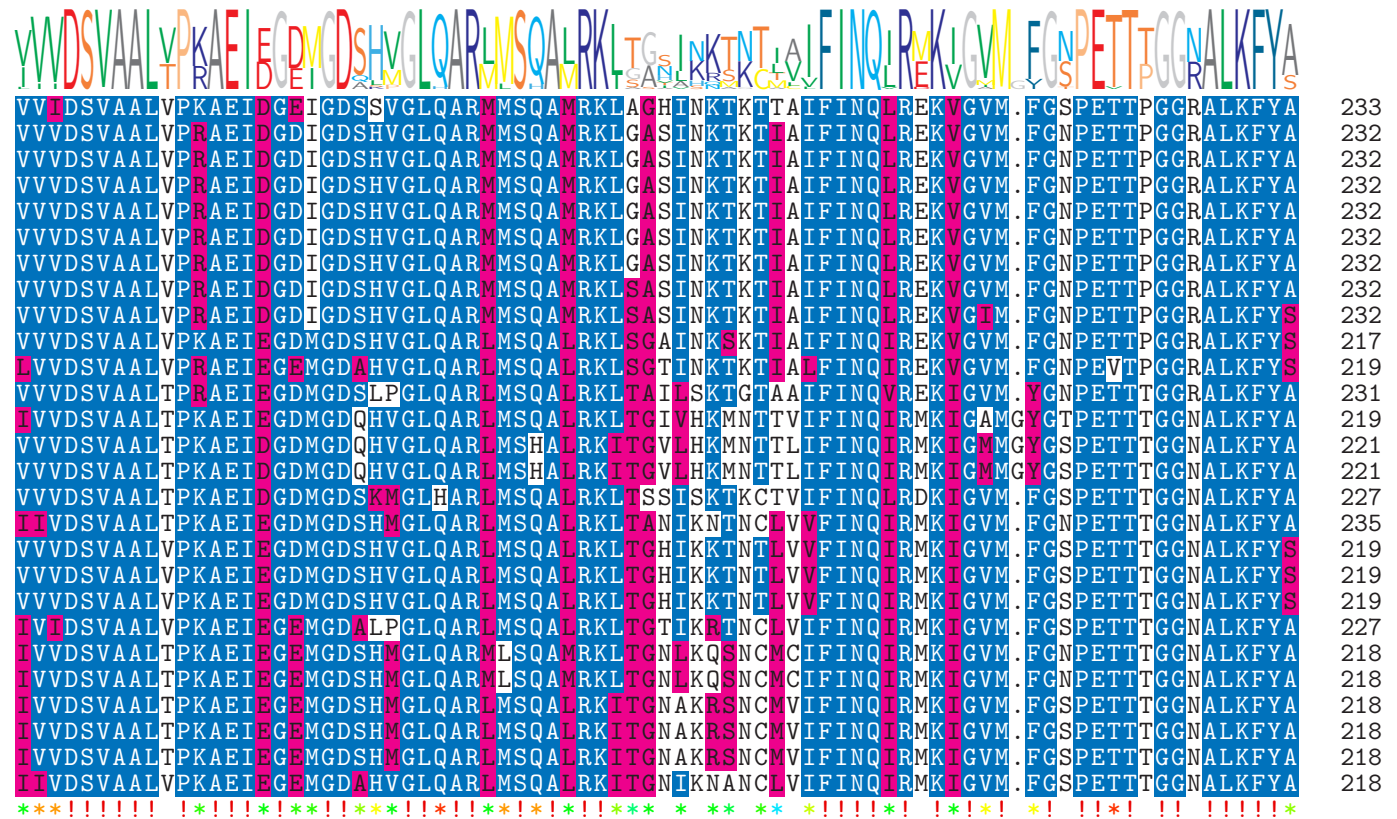
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Sequence	Score
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ ID ⁺ KQ ⁺ V ⁺ RS ⁺ KF ⁺ GL ⁺ ID ⁺ GEE ⁺ V ⁺ SEQ ⁺ DTE ⁺ .NKK ⁺ D ⁺PK ⁺ KEEA ⁺ ..VN ⁺ EE ⁺ V ⁺ PL ⁺ DL ⁺ GD ⁺ EL ⁺	382
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ ID ⁺ KQ ⁺ V ⁺ RS ⁺ KF ⁺ GL ⁺ ID ⁺ GEE ⁺ V ⁺ SEQ ⁺ DTE ⁺ .NKK ⁺ D ⁺PK ⁺ KEEA ⁺ ..VN ⁺ EE ⁺ V ⁺ PL ⁺ DL ⁺ GD ⁺ EL ⁺	382
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GEKIGQGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NP ⁺ EI ⁺ FD ⁺ ID ⁺ HK ⁺ VR ⁺ VQ ⁺ YL ⁺ IE ⁺ ED ⁺ NT ⁺ EEK ⁺ QSS ⁺ .KEK.....ET ⁺ DEK ⁺ ..AD ⁺ KN ⁺ LV ⁺ LE ⁺ LD ⁺ DT ⁺ I	379
EER ⁺ LG ⁺ QG ⁺ REN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KDIM ⁺ LI ⁺ QE ⁺ Q ⁺ IRE ⁺ HY ⁺ GL ⁺ DN ⁺ NG ⁺ VV ⁺ QQ ⁺ AA ⁺ EE ⁺ .TQE ⁺ EL ⁺ .E..FE ⁺ .E.....	348
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DER ⁺ IG ⁺ QG ⁺ KE ⁺ KT ⁺ IA ⁺ Y ⁺ IA ⁺ ERP ⁺ ME ⁺ QE ⁺ IR ⁺ DR ⁺ V ⁺ MA ⁺ AIR ⁺ AG ⁺ NAGE ⁺ AP ⁺ AL ⁺ AP ⁺ AP ⁺ AA ⁺ PE ⁺ AA ⁺ EE.....	363
DKKL ⁺ GG ⁺ REN ⁺ SK ⁺ AF ⁺ LKEN ⁺ PE ⁺ IS ⁺ DE ⁺ IT ⁺ KA ⁺ IQ ⁺ NS ⁺ MG ⁺ IE ⁺ GM ⁺ IS ⁺ GS ⁺ ..ED ⁺ DEGE ⁺ .E.....	343
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GDK ⁺ IG ⁺ QG ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE	

logo

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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved