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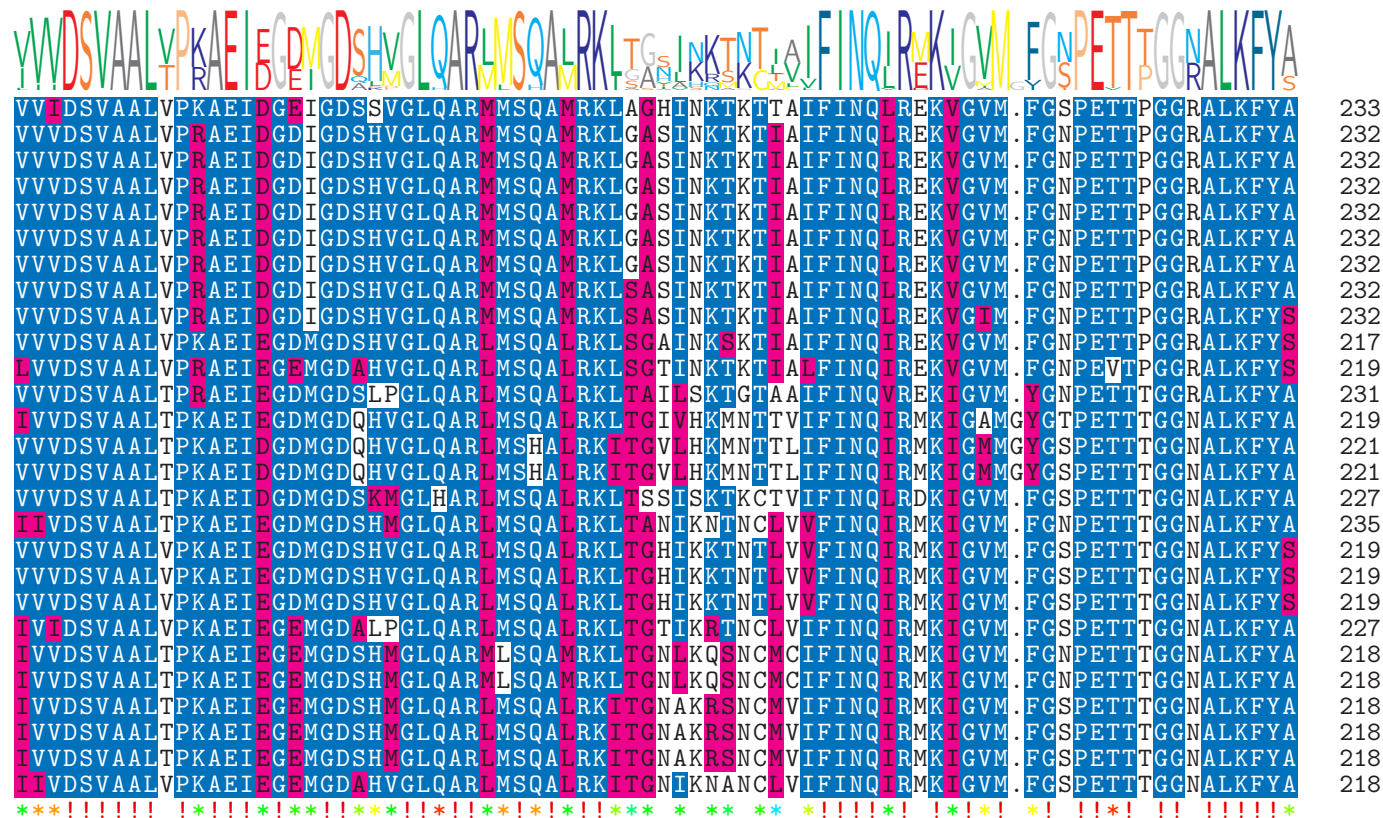
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Sequence	Score
DEKIGQGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ FD ⁹ EID ¹⁰ HK ¹¹ VRAAH ¹² GL ¹³ LDSEVAETEEE ¹⁴ .TTASKTK ¹⁵ ..AKAKKEEKAVETEEIELELED ¹⁶ ..	387
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTE ¹³ .NKKD ¹⁴ E ¹⁵PKKEEA ¹⁶ ..VNEEVPLDLGDEL ¹⁷	382
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTE ¹³ .NKKD ¹⁴ E ¹⁵PKKEEA ¹⁶ ..VNEEVPLDLGDEL ¹⁷	382
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTE ¹³ .NKKD ¹⁴ E ¹⁵PKKEEA ¹⁶ ..VNEEVPLDLGDEL ¹⁷	382
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ VFA ⁷ EID ⁸ HQ ⁹ VR ¹⁰ VQF ¹¹ GL ¹² IDGEEAAE ¹³SKKD ¹⁴ E ¹⁵VAQVDS ¹⁶ ..VNEEVTLDLGDEL ¹⁷	378
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ IF ⁷ DEID ⁸ HQ ⁹ VR ¹⁰ VQF ¹¹ GL ¹² IDGEEIAE ¹³SKKD ¹⁴ E ¹⁵AAQVDS ¹⁶ ..VNEEVTLDLGDEL ¹⁷	378
GEKIGQGS ¹ EN ² AK ³ RYLA ⁴ DHP ⁵ QL ⁶ FD ⁷ EID ⁸ RK ⁹ VR ¹⁰ VKF ¹¹ GL ¹² LEEESEESAMAV ¹³ .ASE ¹⁴E ¹⁵TDDLALDLNGI ¹⁶	374
GEKIGQGS ¹ EN ² AK ³ KFLA ⁴ DN ⁵ PE ⁶ IF ⁷ DD ⁸ ID ⁹ HK ¹⁰ VR ¹¹ VQY ¹² GL ¹³ IEEDNTEEKQSS ¹⁴ .KEK ¹⁵ETDEK ¹⁶ ..ADKNLVLELDDTI ¹⁷	379
EE ¹ RL ² GG ³ RE ⁴ NA ⁵ KQ ⁶ FL ⁷ KN ⁸ KD ⁹ IM ¹⁰ LI ¹¹ QE ¹² QI ¹³ RE ¹⁴ HY ¹⁵ GL ¹⁶ DNNGVVQQQAEE ¹⁷ .TQEEL ¹⁸ .E ¹⁹ .FE ²⁰ .E ²¹	348
SERIGQGS ¹ RE ² NA ³ KNYLA ⁴ DH ⁵ ED ⁶ VE ⁷ DE ⁸ VR ⁹ LK ¹⁰ VRAAY ¹¹ GIS ¹² DVPEEDLPTTE ¹³ .DE ¹⁴ .QI ¹⁵ .N ¹⁶ ..ILPDDST ¹⁷EE ¹⁸	355
DERIGQG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ER ⁶ PE ⁷ ME ⁸ QE ⁹ IR ¹⁰ DRV ¹¹ MAA ¹² IRAGNAGEAPALAPAPAAPEAAEA ¹³	363
DKKLGGGREN ¹ SKA ² FL ³ KN ⁴ PEIA ⁵ DEIT ⁶ KA ⁷ IQNSM ⁸ GI ⁹ EGMISGS ¹⁰ ..EDDEGE ¹¹ .E ¹²	343
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKES ⁸ IG ⁹ SNEEIMPL ¹⁰ ..PDEPLE ¹¹ ..EME ¹²	347
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKES ⁸ IG ⁹ SNEEIMPL ¹⁰ ..PDEPLE ¹¹ ..EME ¹²	347
DTKLGGGRD ¹ TV ² KEL ³ IK ⁴ DN ⁵ PELA ⁶ E ⁷ LE ⁸ AK ⁹ IREKLQAK ¹⁰	343
GTKIGQG ¹ KNN ² AVK ³ WL ⁴ KN ⁵ PEIA ⁶ DK ⁷ LE ⁸ QE ⁹ IR ¹⁰ NTL ¹¹ ASN ¹² PNSVLK ¹³ ..ATASDSND ¹⁴ ESDVEEFSE ¹⁵EEL ¹⁶	372
GAKIGGQKDN ¹ VR ² VL ³ KN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALN ⁸ GVEMHITEG ⁹ ..TQDET ¹⁰GERPE ¹¹E ¹²	348
GAKIGGQKDN ¹ VR ² VL ³ KN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALN ⁸ GVEMHITEG ⁹ ..TQDET ¹⁰GERPE ¹¹E ¹²	348
GAKIGGQKDN ¹ VR ² VL ³ KN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALN ⁸ GVEMHITEG ⁹ ..TQDET ¹⁰GERPE ¹¹E ¹²	348
GERIGGGRD ¹ NC ² REFL ³ RENA ⁴ E ⁵ LAR ⁶ EI ⁷ EN ⁸ KV ⁹ REHL ¹⁰ GV ¹¹ TPMGAV ¹² ..TLAEEVEED ¹³	352
GDKIGQG ¹ KAN ² ACKYL ³ KN ⁴ PEIA ⁵ AK ⁶ LD ⁷ KKL ⁸ REMLLN ⁹ PENMQLI ¹⁰ ..AETSSAAD ¹¹ VEFGAVPE ¹²EF ¹³	354
GDKIGGQKAN ¹ ACKYL ² KN ³ PEIA ⁴ AK ⁵ LD ⁶ KKL ⁷ REMLLN ⁸ PENMQLI ⁹ ..AETSSAAD ¹⁰ VEFGAVPE ¹¹EF ¹²	354
GNKIGQG ¹ KNN ² VIRY ³ FEENT ⁴ QIA ⁵ E ⁶ EI ⁷ ERN ⁸ IREQLLT ⁹ TGTNGAV ¹⁰ ..Q ¹¹ .I ¹² .EDEE ¹³ EPD ¹⁴ ..LLE ¹⁵S ¹⁶	349
GNKIGQG ¹ KNN ² VIRY ³ FEENN ⁴ QIA ⁵ E ⁶ EI ⁷ ERN ⁸ IREQLLT ⁹ TGTNGAV ¹⁰ ..Q ¹¹ .I ¹² .EDEE ¹³ EPD ¹⁴ ..LLE ¹⁵S ¹⁶	349
GNKIGQG ¹ KNN ² VIRY ³ LEEN ⁴ PQIST ⁵ EI ⁶ EAV ⁷ IREQLLT ⁸ KASDQTA ⁹ ..A ¹⁰ .HDETEE ¹¹ EPD ¹² ..LLES ¹³	349

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved