

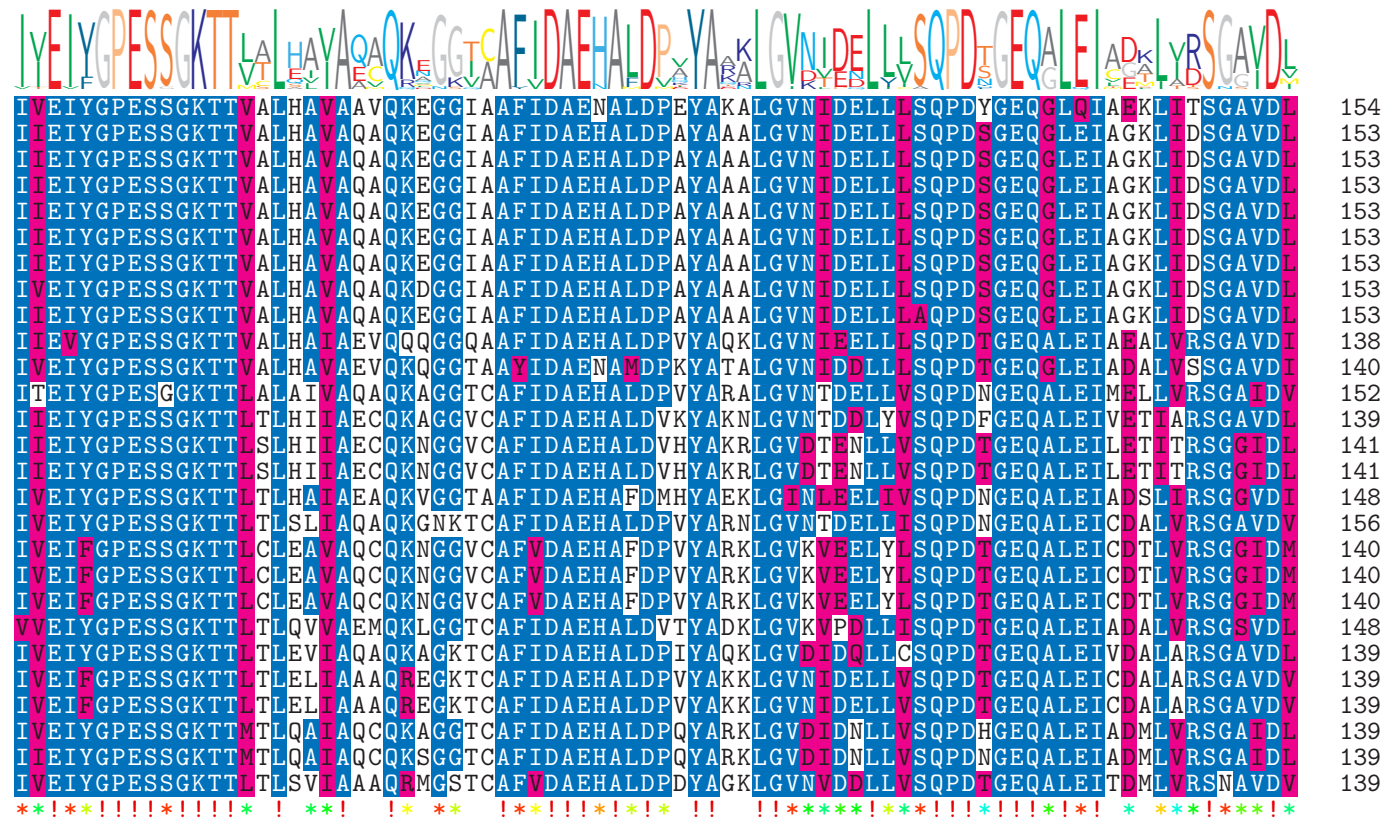
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NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALKQIEKQFGKGSIMKLGEK.TDTRISTVPSGSLALDTALGIGGYPRGR	58
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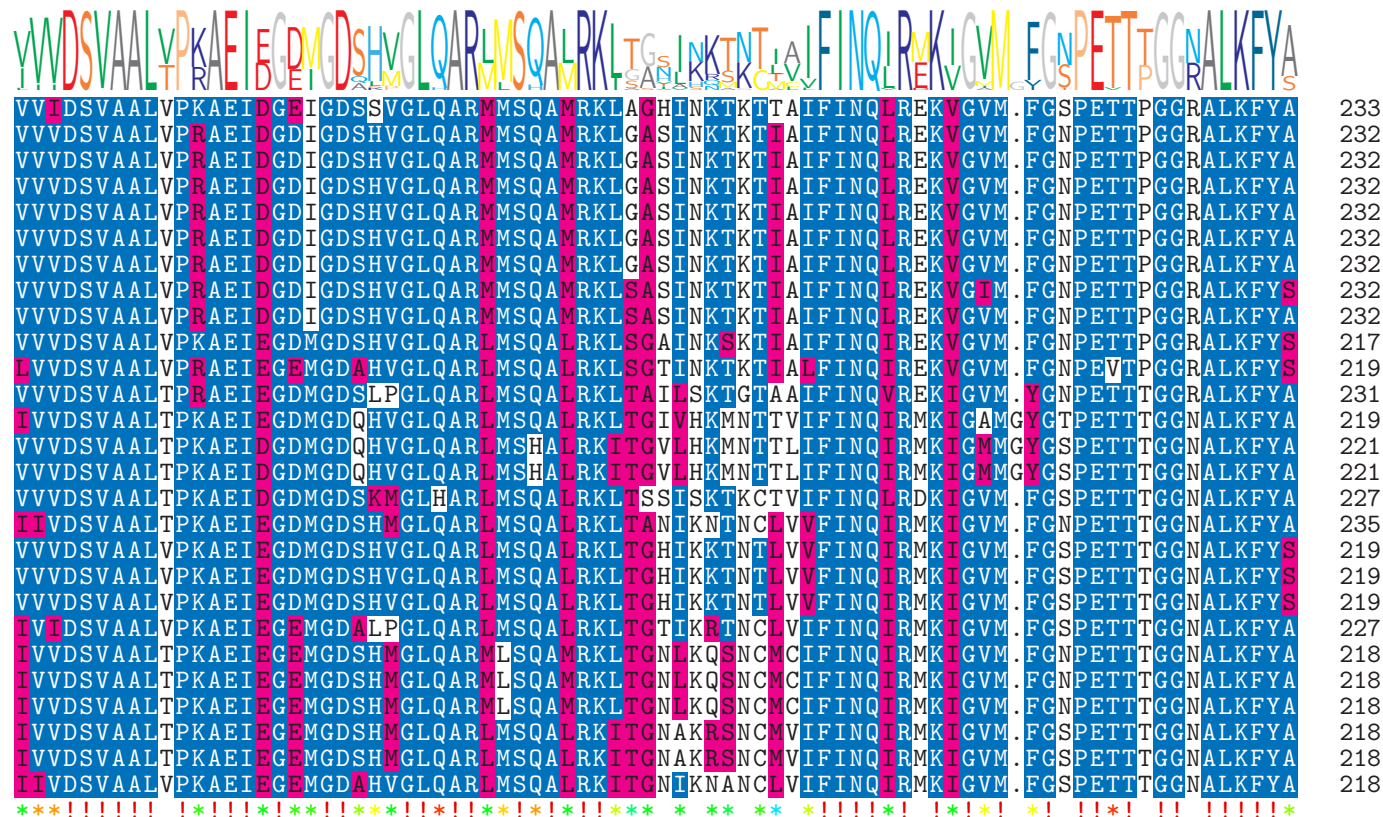
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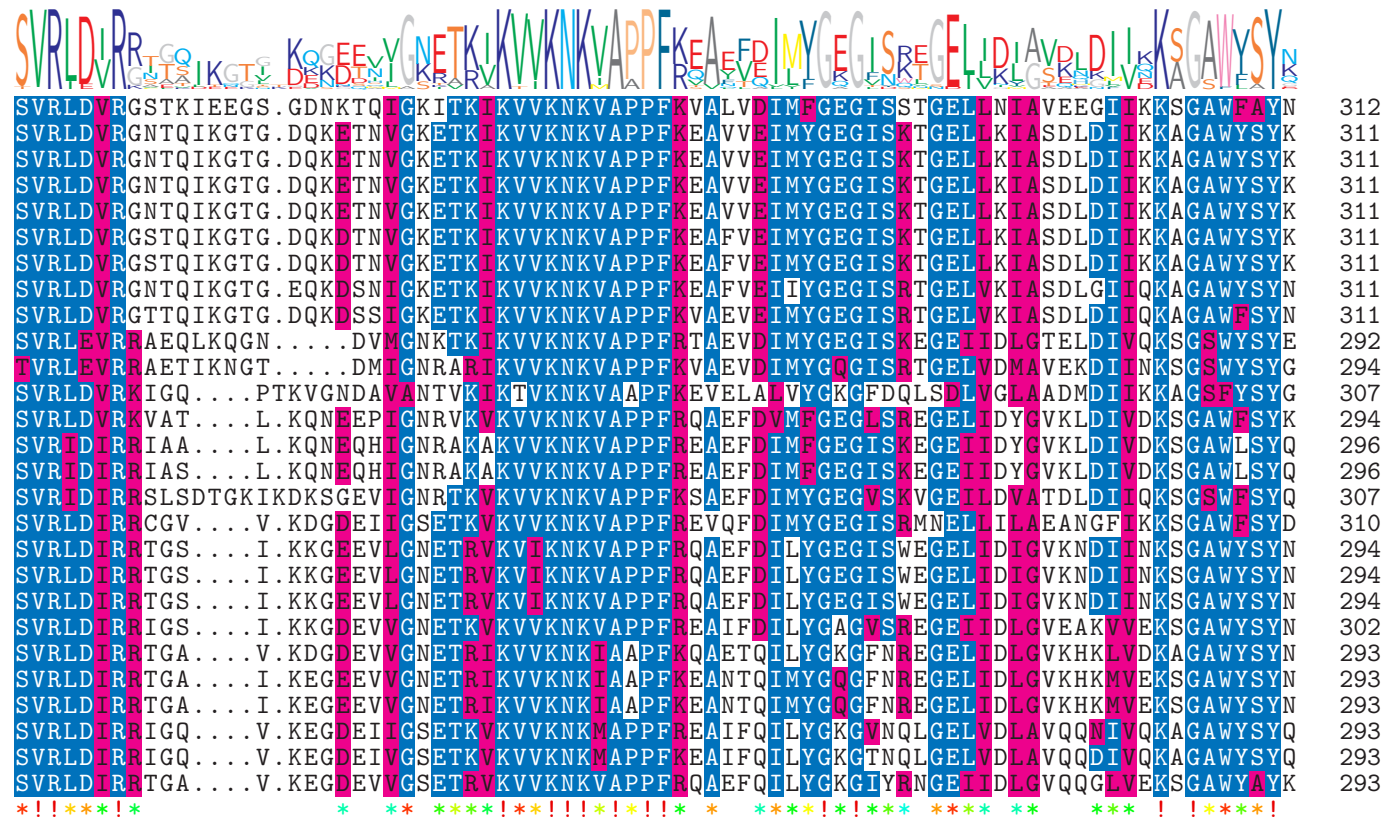
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consensus

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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FLIDGEEVSEQDTENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FLIDGEEVSEQDTENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FLIDGEEVSEQDTENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FLIDGEEVSEQDTENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ VFAE ⁷ ID ⁸ HQ ⁹ VR ¹⁰ VQ ¹¹ FLIDGEEAAE . . . SKKDE . . . VAQVDS . . VNEEVTLDLGDLEIE	381
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ HQ ¹⁰ VR ¹¹ VQ ¹² FLIDGEEIAE . . . SKKDE . . . AAQVDS . . VNEEVTLDLGDLEIE	381
GEKIGQGS ¹ EN ² AK ³ FLAD ⁴ NPE ⁵ IF ⁶ DD ⁷ ID ⁸ HK ⁹ VR ¹⁰ VQ ¹¹ GLIEEDNTEEEKSSKEK ETDEK . . ADKNLVLELDDTTIELE	382
GEKIGQGS ¹ EN ² AK ³ RYLA ⁴ DHP ⁵ QL ⁶ F ⁷ DE ⁸ ID ⁹ RV ¹⁰ VK ¹¹ FLLEESEEEESAMAVASE E TDDLALDLNNGIEIE	377
EERLGGGREN ¹ AK ² QFL ³ KEN ⁴ KDIM ⁵ LI ⁶ QEQ ⁷ IRE ⁸ HY ⁹ GLD ¹⁰ NG ¹¹ VV ¹² QQ ¹³ AE ¹⁴ ET ¹⁵ QE ¹⁶ EL ¹⁷ .EFE.E	348
SERIGGGREN ¹ AK ² NYLA ³ DH ⁴ ED ⁵ VE ⁶ DEV ⁷ RL ⁸ KV ⁹ RA ¹⁰ AY ¹¹ GIS ¹² DV ¹³ PEED ¹⁴ LPT ¹⁵ TE ¹⁶ DE ¹⁷ .QI.NILPDDST EE	355
DERIGGGKE ¹ KTI ² AY ³ IA ⁴ ERP ⁵ ME ⁶ QE ⁷ IR ⁸ DRV ⁹ MA ¹⁰ AIR ¹¹ AG ¹² NAGE ¹³ AP ¹⁴ AL ¹⁵ AP ¹⁶ AA ¹⁷ PE ¹⁸ AA ¹⁹ .EA	363
DKKLGGGREN ¹ SKA ² FL ³ KN ⁴ PE ⁵ IDE ⁶ IT ⁷ KA ⁸ IQ ⁹ NS ¹⁰ MG ¹¹ IE ¹² GMI SGSEDDGEEE	343
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DE ⁶ IT ⁷ LK ⁸ IK ⁹ ES ¹⁰ IG ¹¹ SNEEI MPLPDEPLEEME	347
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DE ⁶ IT ⁷ LK ⁸ IK ⁹ ES ¹⁰ IG ¹¹ SNEEI MPLPDEPLEEME	347
DTKLGGGRD ¹ TV ² KEL ³ IK ⁴ DN ⁵ PE ⁶ LAE ⁷ ELE ⁸ AK ⁹ IRE ¹⁰ KL ¹¹ QAK	343
GTKIGQGK ¹ NN ² AV ³ WL ⁴ KN ⁵ PE ⁶ IA ⁷ DK ⁸ LE ⁹ QIR ¹⁰ T ¹¹ LA ¹² SN ¹³ PS VLKATASDSNDES ¹⁴ DVEE . . FSEEE ¹⁵ L	372
GAKIGGQK ¹ DN ² VR ³ VL ⁴ KN ⁵ PE ⁶ IS ⁷ DE ⁸ IA ⁹ KIR ¹⁰ AL ¹¹ NG ¹² VEM ¹³ HI TEGTQDET DGE . . RPEE	348
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GAKIGGQK ¹ DN ² VR ³ VL ⁴ KN ⁵ PE ⁶ IS ⁷ DE ⁸ IA ⁹ KIR ¹⁰ AL ¹¹ NG ¹² VEM ¹³ HI TEGTQDET DGE . . RPEE	348
GERIGGGRD ¹ NC ² REF ³ LREN ⁴ AE ⁵ LA ⁶ RE ⁷ IE ⁸ NK ⁹ VRE ¹⁰ HL ¹¹ GV ¹² TPMG AVTLAEEVEED	352
GDKIGGQKAN ¹ ASK ² FM ³ RN ⁴ PE ⁵ IGA ⁶ EL ⁷ DK ⁸ LRE ⁹ ML ¹⁰ LTP ¹¹ ED KPEVVEKIEEENE ¹² EF	347
GDKIGGQKAN ¹ ACK ² YL ³ KN ⁴ PE ⁵ IA ⁶ KT ⁷ LD ⁸ KK ⁹ LRE ¹⁰ ML ¹¹ LN ¹² PN ¹³ EM QLIAETSSAADDVEFGA . . VPEEF	354
GDKIGGQKAN ¹ ACK ² YL ³ KN ⁴ PE ⁵ IA ⁶ KT ⁷ LD ⁸ KK ⁹ LRE ¹⁰ ML ¹¹ LN ¹² PN ¹³ EM QLIAETSSAADDVEFGA . . VPEEF	354
GNKIGGQK ¹ NN ² VIR ³ YLE ⁴ EN ⁵ PQ ⁶ ISTE ⁷ IE ⁸ AV ⁹ IRE ¹⁰ QL ¹¹ LTK ¹² ASD QTAA.HDETEEE ¹³ PDL . . . LES	349
GNKIGGQK ¹ NN ² VIR ³ YFE ⁴ EN ⁵ NQ ⁶ IA ⁷ EIE ⁸ IE ⁹ RN ¹⁰ IRE ¹¹ QL ¹² LTT ¹³ GTN GAVQ.I.EDEEE ¹⁴ PDL . . . LLES	349

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved