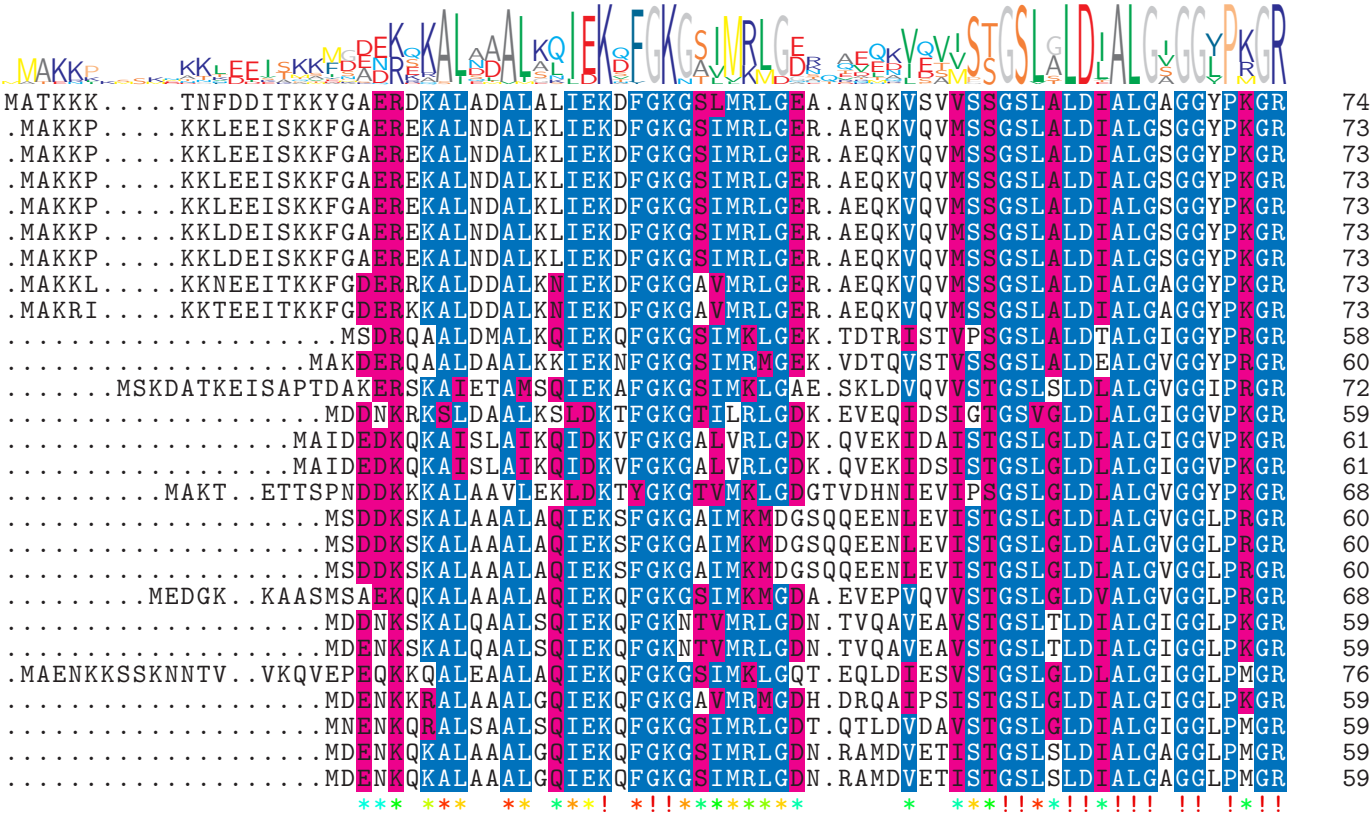


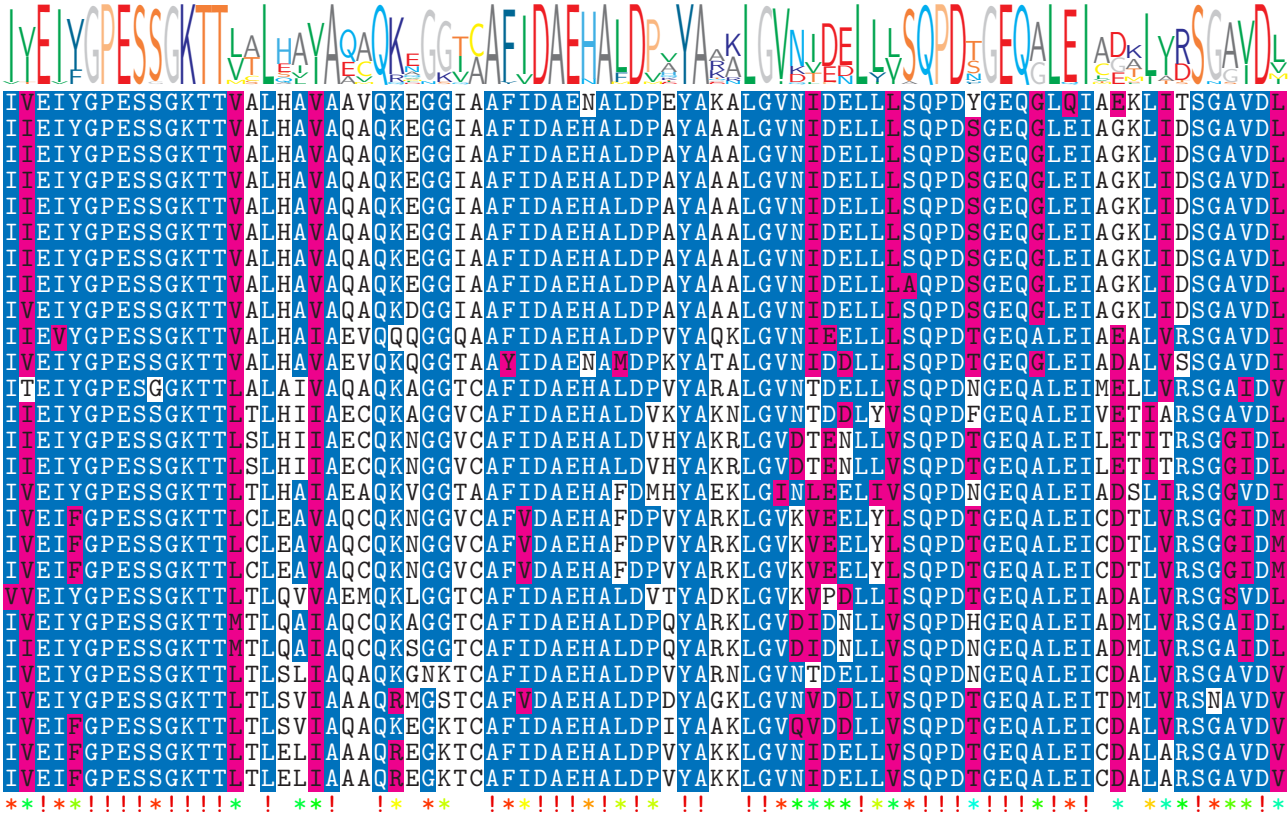
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consensus



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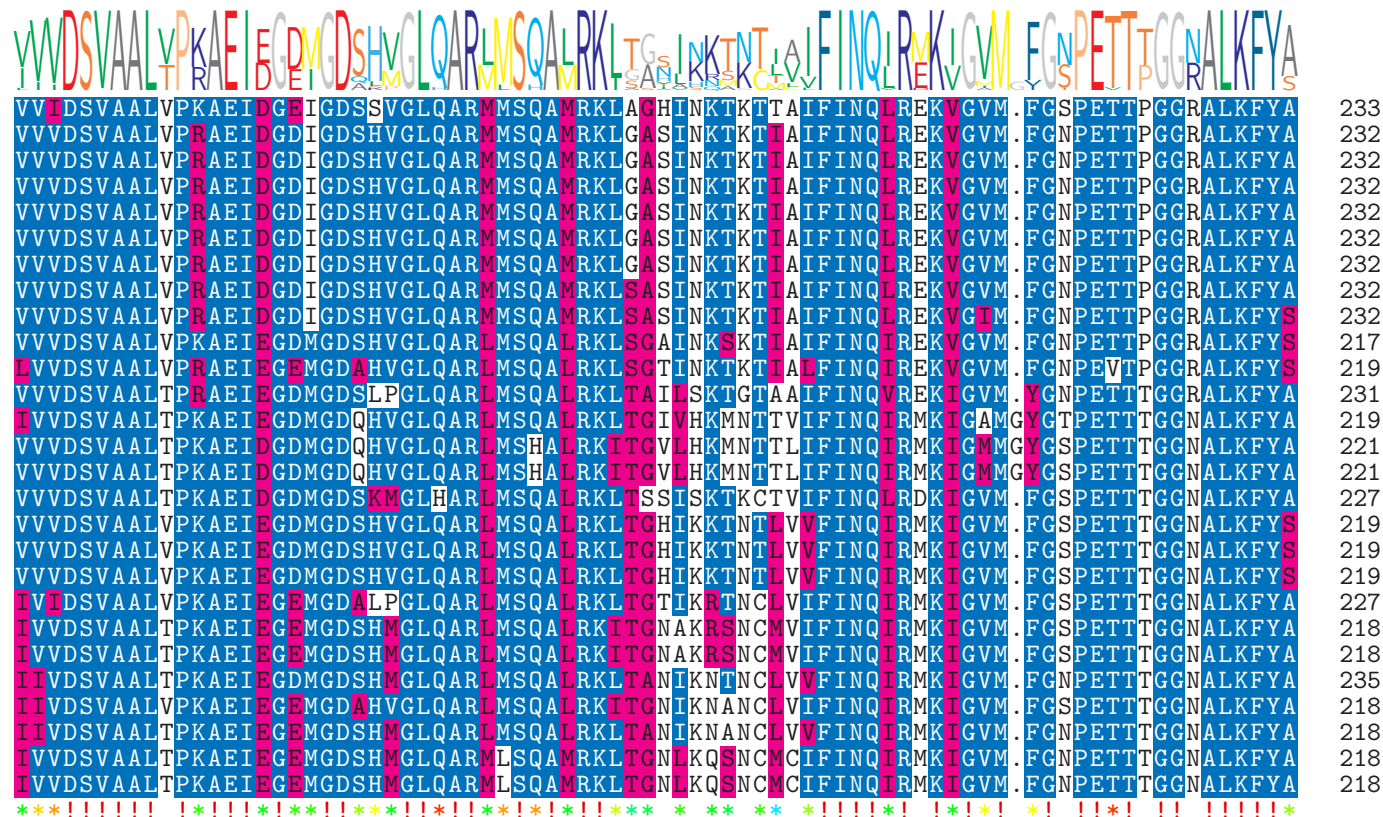


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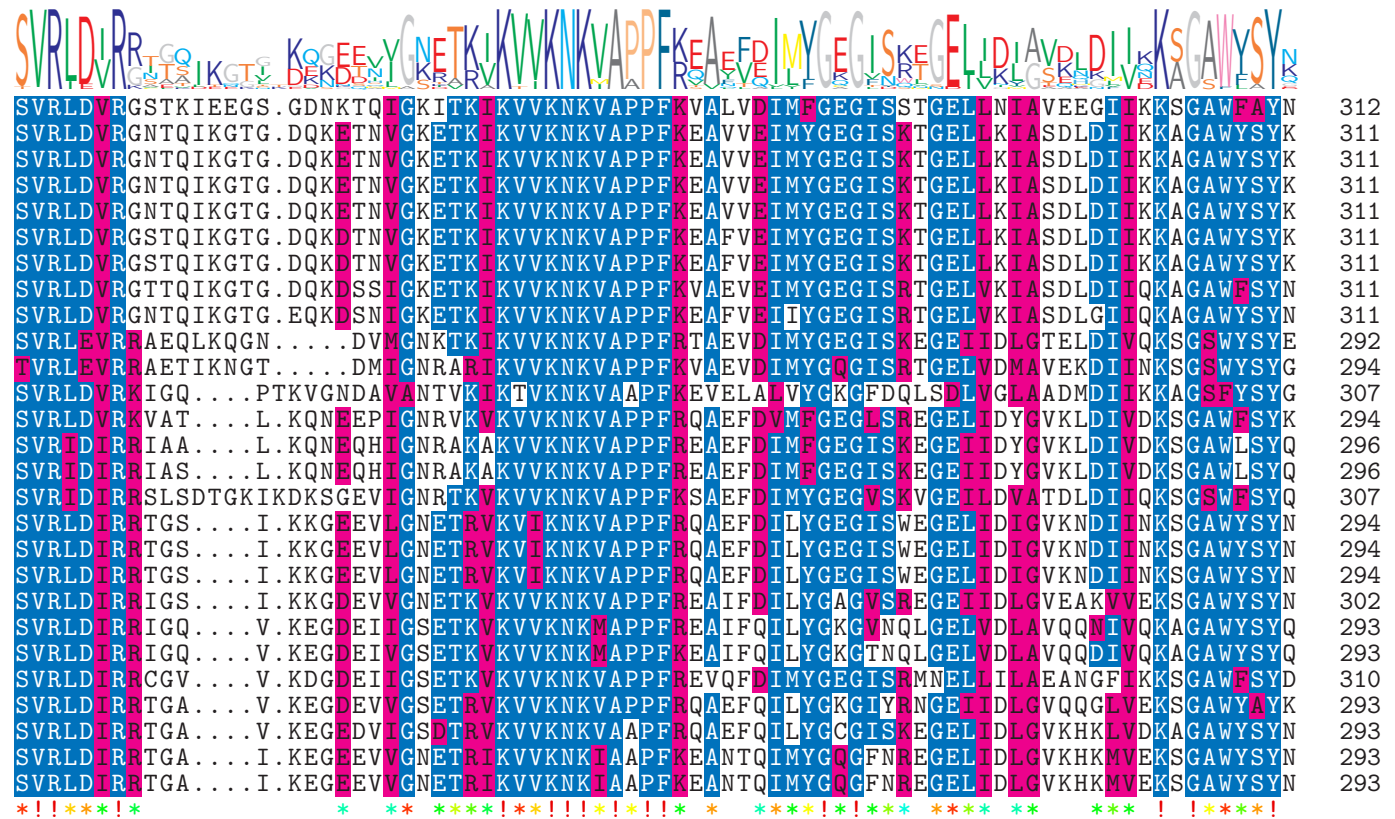
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NTDB id 1165 A1552VC RS01565 WP 000344154.1
NTDB id 1142 GTF74 RS11550 WP 000344154.1
consensus

Sequence	Score
DEKIGQGA ¹ EKA ² KNY ³ LKEHQ ⁴ DV ⁵ FDEID ⁶ HKV ⁷ RAAH ⁸ G ⁹ LDDSEVAETEEEE...TTASKTKAKAKKKEEKAVETEEIELELED.	387
DEKIGQGSEN ¹ AKKYLA ² EHPEIF ³ DEID ⁴ KQVRSKF ⁵ GLIDGEEVSEQDTE...NKKDE...PKKEEA...VNEEVPLDLGDE	381
DEKIGQGS ¹ ENAKKYLA ² EHPEIF ³ DEID ⁴ KQVRSKF ⁵ GLIDGEEVSEQDTE...NKKDE...PKKEEA...VNEEVPLDLGDE	381
DEKIGQGS ¹ ENAKKYLA ² EHPEIF ³ DEID ⁴ KQVRSKF ⁵ GLIDGEEVSEQDTE...NKKDE...PKKEEA...VNEEVPLDLGDE	381
DEKIGQGS ¹ ENAKKYLA ² ADNPEIF ³ DEID ⁴ HQVRVQF ⁵ GLIDGEEIAES...KKDE...AAQVDS...VNEEVTLDLGDE	377
DEKIGQGS ¹ ENAKKYLA ² ADNPEVFA ³ EID ⁴ HQVRVQF ⁵ GLIDGEEAAES...KKDE...VAQVDS...VNEEVTLDLGDE	377
GEKIGQGS ¹ ENAKRYLA ² DHPQL ³ FDEID ⁴ RKVRVKF ⁵ GLLEESEEAESAMAV...ASE...E...TDDLALDLNG	373
GEKIGQGS ¹ ENAKKFLADN ² PEIF ³ DDID ⁴ HKVRVQY ⁵ GLIEEDNTEEKQSS...KEK...ETDEK...ADKNLVLELDDT	378
EER ¹ LGQGR ² ENAKQFL ³ KENK ⁴ DIMLM ⁵ IQEQ ⁶ IREHY ⁷ GLDNGGVVQQAAEE...TQEEL.EFE.E...	348
SERIGQGR ¹ ENAKNYLA ² DHED ³ VEDEV ⁴ RLK ⁵ VRAAY ⁶ GISDVPEEDLPTTE...DE.QI.NILPDDST...EE...	355
DERIGQG ¹ KEKTIAY ² IAER ³ PEMEQ ⁴ EITDRV ⁵ MAAIRAGNAGEAPALAPAPAAPEA.AEA...	363
DKKL ¹ GQGR ² ENSKAFL ³ KENPEIA ⁴ DEITKAI ⁵ QNSMG ⁶ IEGMI...SGSEDDGEE...	343
DKKL ¹ GQGR ² ENAKALL ³ KEDKALA ⁴ DEITLK ⁵ IKESIG ⁶ SNEEI...MPLPDEPLEEME...	347
DKKL ¹ GQGR ² ENAKALL ³ KEDKALA ⁴ DEITLK ⁵ IKESIG ⁶ SNEEI...MPLPDEPLEEME...	347
DTKL ¹ GQGR ² DTVKEL ³ IKDN ⁴ PELAE ⁵ LEAK ⁶ IREKLQAK...	343
GA ¹ KIGQG ² KDNVRV ³ WLKEN ⁴ PEIS ⁵ DEIDAK ⁶ IRALN ⁷ G ⁸ VMHI...TEGTQDET...GERPE...E...	348
GA ¹ KIGQG ² KDNVRV ³ WLKEN ⁴ PEIS ⁵ DEIDAK ⁶ IRALN ⁷ G ⁸ VMHI...TEGTQDET...GERPE...E...	348
GA ¹ KIGQG ² KDNVRV ³ WLKEN ⁴ PEIS ⁵ DEIDAK ⁶ IRALN ⁷ G ⁸ VMHI...TEGTQDET...GERPE...E...	348
GER ¹ IGQGR ² DNCREFL ³ RENAEL ⁴ AREI ⁵ ENK ⁶ VREHL ⁷ G ⁸ VTMPG...AVTLAAEEVEED...	352
GN ¹ KIGQG ² KNNVIR ³ YLEEN ⁴ PQISTE ⁵ IEAV ⁶ IREQLLT ⁷ KASD...QTAAHDETEE.EPDLLES...	349
GN ¹ KIGQG ² KNNVIR ³ YFENN ⁴ QIAE ⁵ IEIERN ⁶ IREQLLT ⁷ TG ⁸ TN...GAVQI.EDEE.EPDLLES...	349
GT ¹ KIGQG ² KNNAVK ³ WLKEN ⁴ PEIAD ⁵ KLEQE ⁶ IRNTL ⁷ ASNPN ⁸ S...VLKATASDNSDESVEEFSE...EEL...	372
GS ¹ KIGQG ² KANA ³ AKYLEEN ⁴ PEIG ⁵ QIE ⁶ EQ ⁷ IRAKLL ⁸ VT ⁹ SA ¹⁰ N...TKATPVAEDLADADI...	347
GE ¹ KVGG ² KANS ³ IKFL ⁴ QEH ⁵ PEVAN ⁶ E ⁷ LEAK ⁸ LRDLL ⁹ NSPAV...FSADDQETITEEESF...	347
GD ¹ KIGQG ² KANACKYL ³ KEN ⁴ PEIA ⁵ KTLD ⁶ KKL ⁷ REMLLN ⁸ PNEM...QLIAETSSAADDVEFGAVPE...EF...	354
GD ¹ KIGQG ² KANACKYL ³ KEN ⁴ PEIA ⁵ KTLD ⁶ KKL ⁷ REMLLN ⁸ PNEM...QLIAETSSAADDVEFGAVPE...EF...	354

logo

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NTDB id 1142 GTF74 RS11550 WP 000344154.1		354
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved