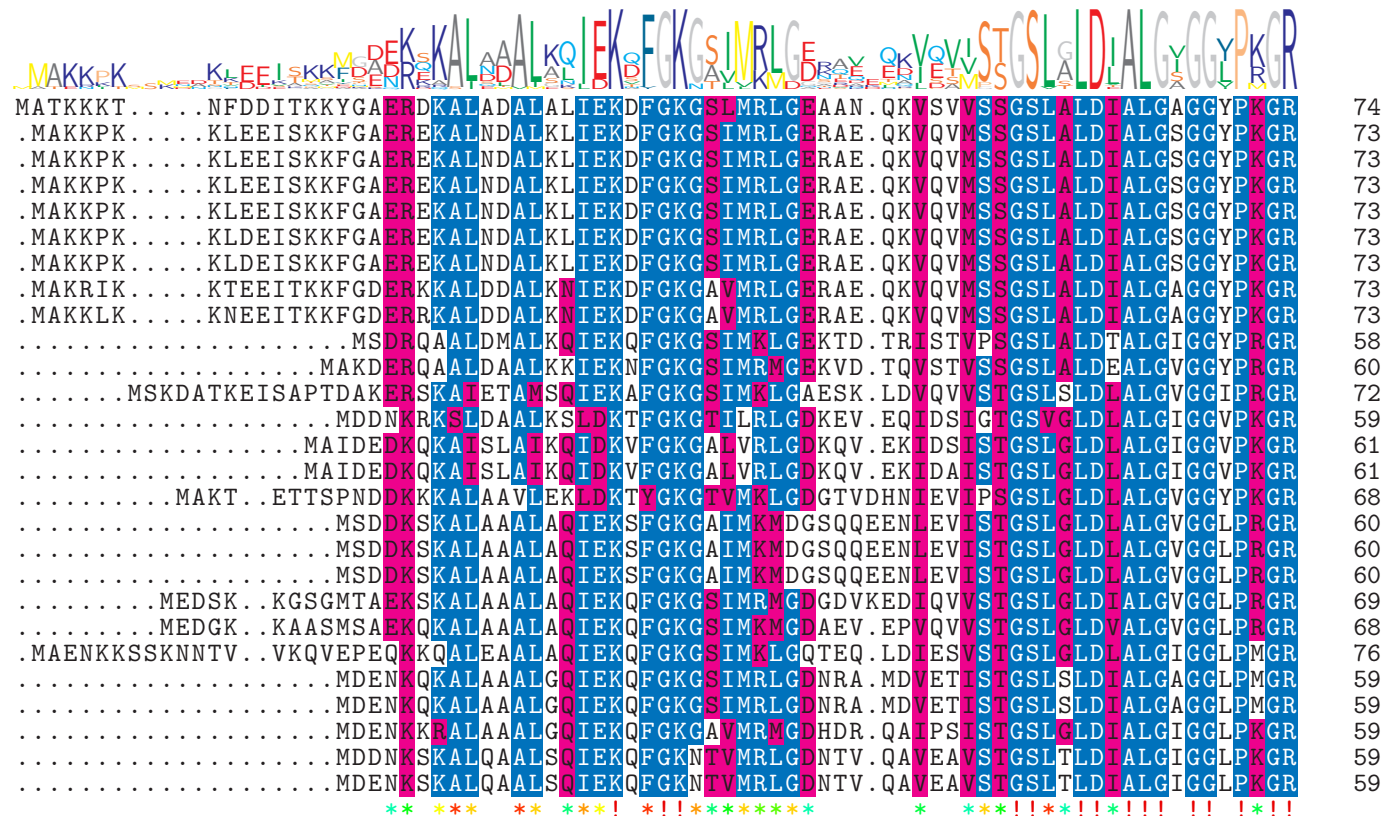


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consensus

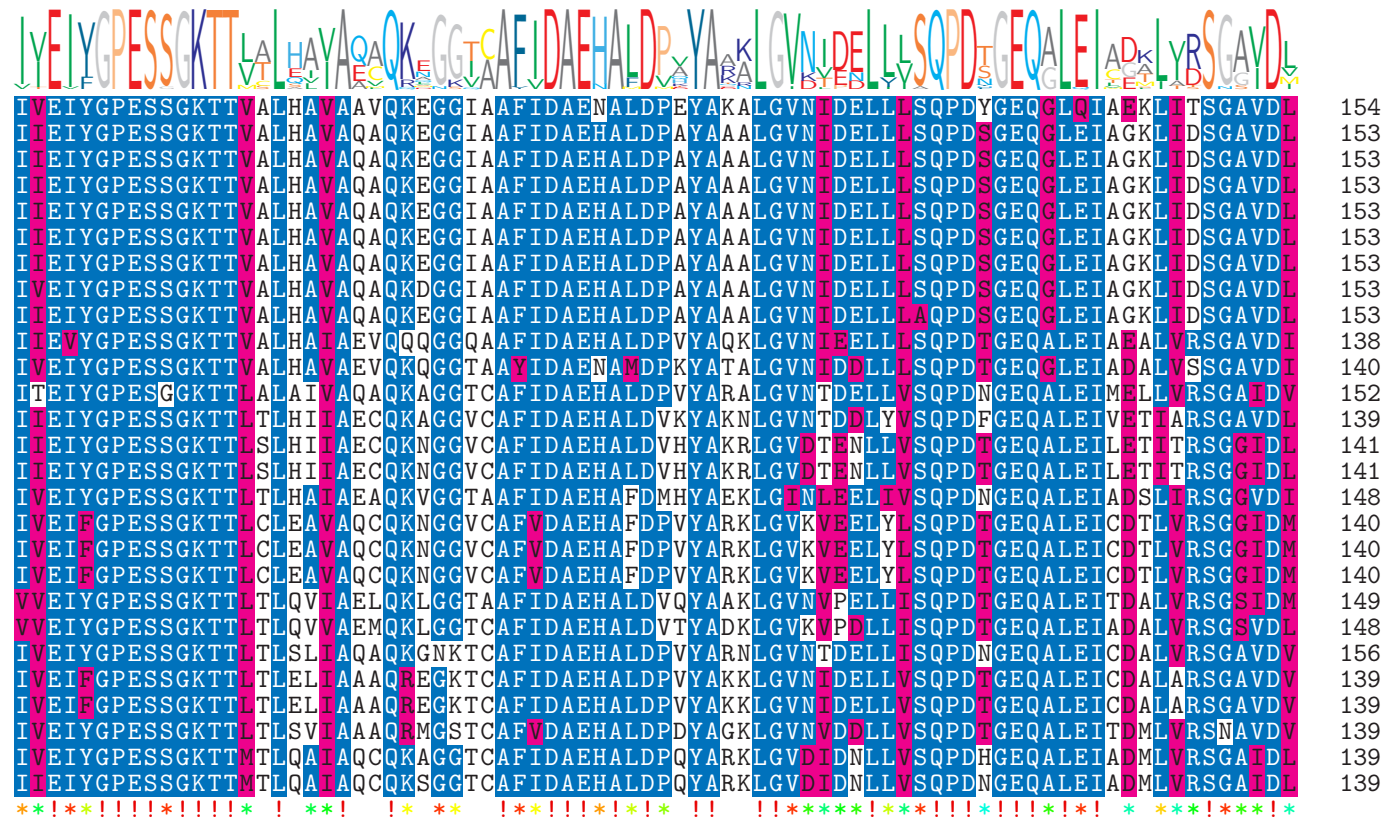
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consensus

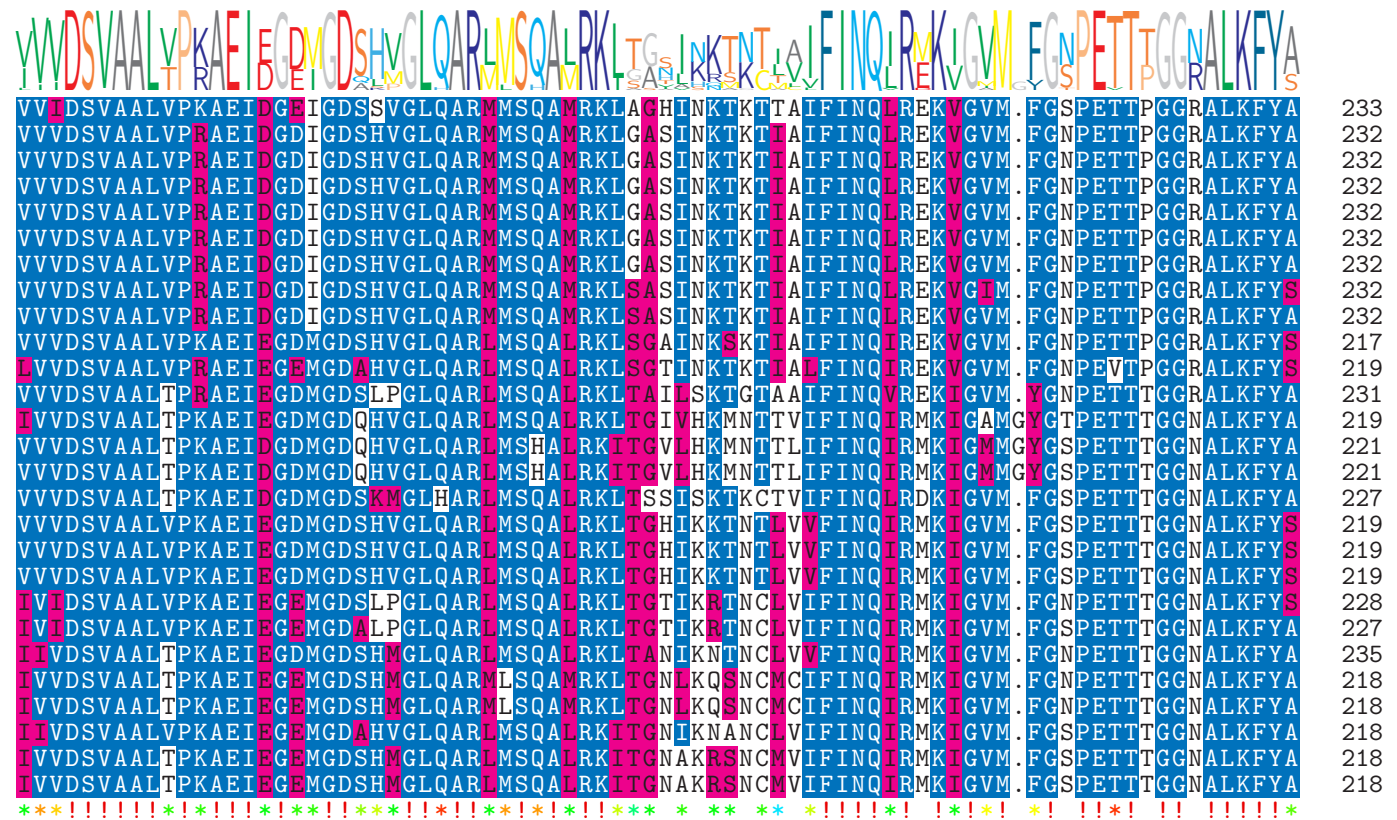
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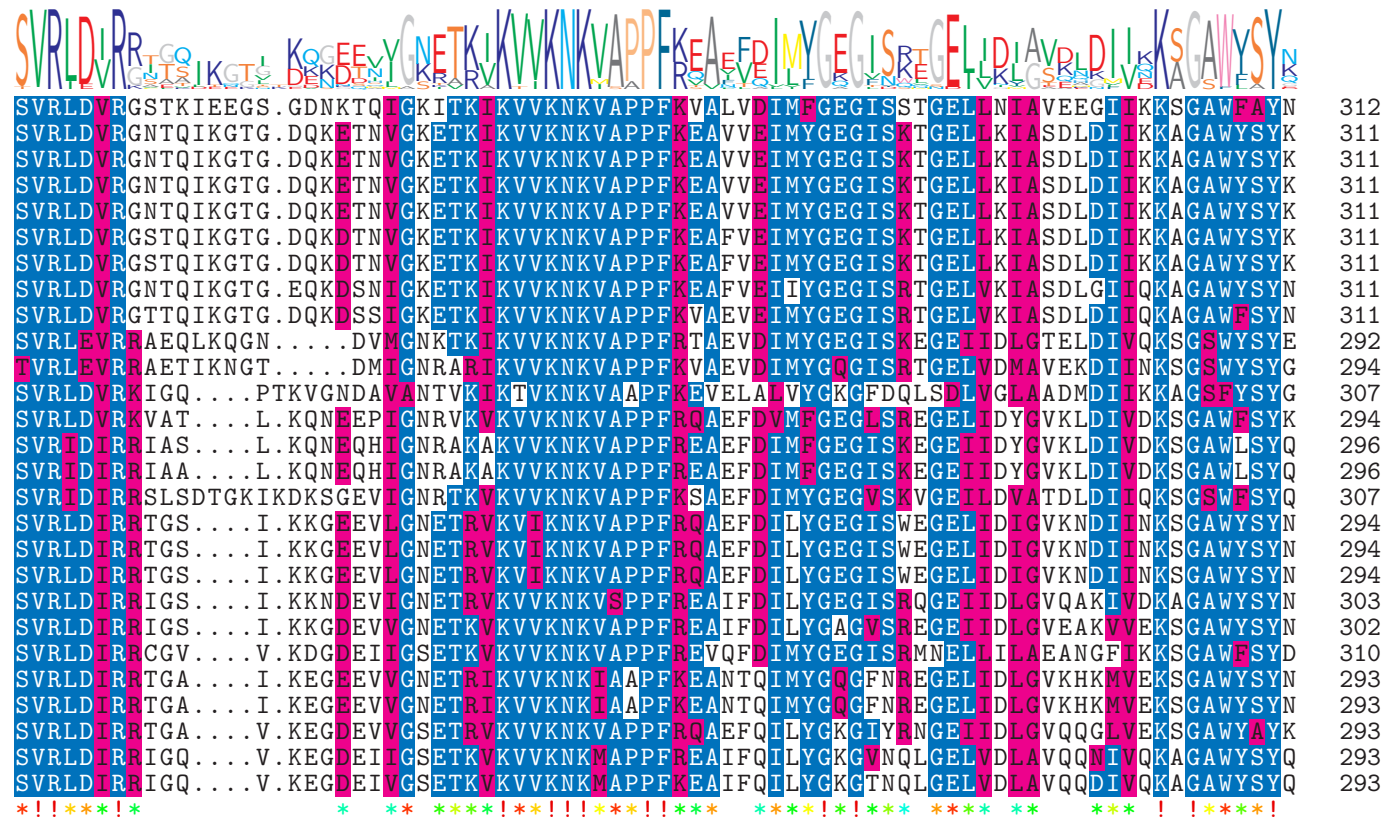
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
DEKIGQGA ¹ AKAKNYL ² KEHQ ³ DV ⁴ F ⁵ DEIDHKV ⁶ RAAH ⁷ GL ⁸ LDSEVAETEEETTAS ⁹ KT ¹⁰ KAKAKKEEK ¹¹ AVETEEIELE ¹² D.....	387
DEKIGQGS ¹ ENAKKYLA ² EHPEIF ³ DEIDKQV ⁴ RSKF ⁵ GL ⁶ IDGEEVSEQDTENKK ⁷ DE...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ ENAKKYLA ² EHPEIF ³ DEIDKQV ⁴ RSKF ⁵ GL ⁶ IDGEEVSEQDTENKK ⁷ DE...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ ENAKKYLA ² EHPEIF ³ DEIDKQV ⁴ RSKF ⁵ GL ⁶ IDGEEVSEQDTENKK ⁷ DE...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ ENAKKYLA ² DNPEIF ³ DEIDHQV ⁴ RVQF ⁵ GL ⁶ IDGEEIAES...KKDE...AAQVDS...VNEEVTLDLGDLEIE	381
DEKIGQGS ¹ ENAKKYLA ² DNPEVFA ³ EIDHQV ⁴ RVQF ⁵ GL ⁶ IDGEEAAES...KKDE...VAQVDS...VNEEVTLDLGDLEIE	381
GEKIGQGS ¹ ENAKKFLAD ² NPEIF ³ DDIDHKV ⁴ RVQY ⁵ GL ⁶ IEEDNTEEKQSSK ⁷ KE.....ETDEK...ADKNLVLELDDTIELE	382
GEKIGQGS ¹ ENAKRYLA ² DHPQLF ³ DEIDRKV ⁴ RVKF ⁵ GL ⁶ LEESEESAMAVASE.....E.....TDDLALDLNGLIEIE	377
EE ¹ RLGQGR ² ENAKQFL ³ KENK ⁴ DI ⁵ MLMIQE ⁶ QIREHY ⁷ GL ⁸ DNNGVVQQAEETQE ⁹ EL ¹⁰ .EFE.E.....	348
SERIGQGR ¹ ENAKNYLA ² DHEDVE ³ DEVRLK ⁴ VRAAY ⁵ GIS ⁶ SDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGQG ¹ KEKTIA ² YIAERP ³ EMEQE ⁴ IRDRVMAAIRAGNAGEAPALAPAPA.AP.....E...AAEA.....	363
DKKLGGGR ¹ ENSKAF ² LKENPEIA ³ DEITKAIQNSM ⁴ GIEGMISGSEDDEGEE.....	343
DKKLGGGR ¹ ENAKALLKEDKALADEITLKI ² ESIG ³ SNEEIMPLPDEPLEEME.....	347
DKKLGGGR ¹ ENAKALLKEDKALADEITLKI ² ESIG ³ SNEEIMPLPDEPLEEME.....	347
DTKLGGGR ¹ DTVKEL ² IKDNPELA ³ EEL ⁴ EAKI ⁵ REKLQAK.....	343
GAKIGQGK ¹ DNVRVWLKENPEIS ² DEIDAKI ³ RALNGVEMHITEGTQDET ⁴ DGERP.....E..E.....	348
GAKIGQGK ¹ DNVRVWLKENPEIS ² DEIDAKI ³ RALNGVEMHITEGTQDET ⁴ DGERP.....E..E.....	348
GAKIGQGK ¹ DNVRVWLKENPEIS ² DEIDAKI ³ RALNGVEMHITEGTQDET ⁴ DGERP.....E..E.....	348
GEKIGQGK ¹ DNAREFLRENPEIAREIENR ² IRESLGV ³ VAMP.DGVVDEAEAM ⁴ DE.....E..E.....	356
GERIGQGR ¹ DNCREFLRENAELAREIENK ² VREHLGV ³ TPMG.AVTLA...EEVEE.....D.....	352
GDKIGQGK ¹ NNAVKWLKENPEIAD ² KLQE ³ IRNTLASNPNSVLKATASDSN ⁴ DES.....D...VEEFSEEL.....	372
GDKIGQGGKANACKYLKENPEIAKT ² LDKKLREMLLNPENMQLIAETSSAADDV.....E..FGAVPEEF.....	354
GDKIGQGGKANACKYLKENPEIAKT ² LDKKLREMLLNPENMQLIAETSSAADDV.....E..FGAVPEEF.....	354
GSKIGQGGKANAAKYLEENPEIGQ ² EIEQQI ³ IRAKLLV ⁴ TSANTKATPVAEDLADA.....D..I.....	347
GNKIGQGK ¹ NNVIRYLEENPQISTEIEAV ² IREQLLTKASDQTAA.HDETEEEP.....D..LL..ES.....	349
GNKIGQGK ¹ NNVIRYFEENNQIAEIEERN ² IREQLLTGTNGAVQ.I.EDEEEP.....D..LL..LES.....	349

logo

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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...		349
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved