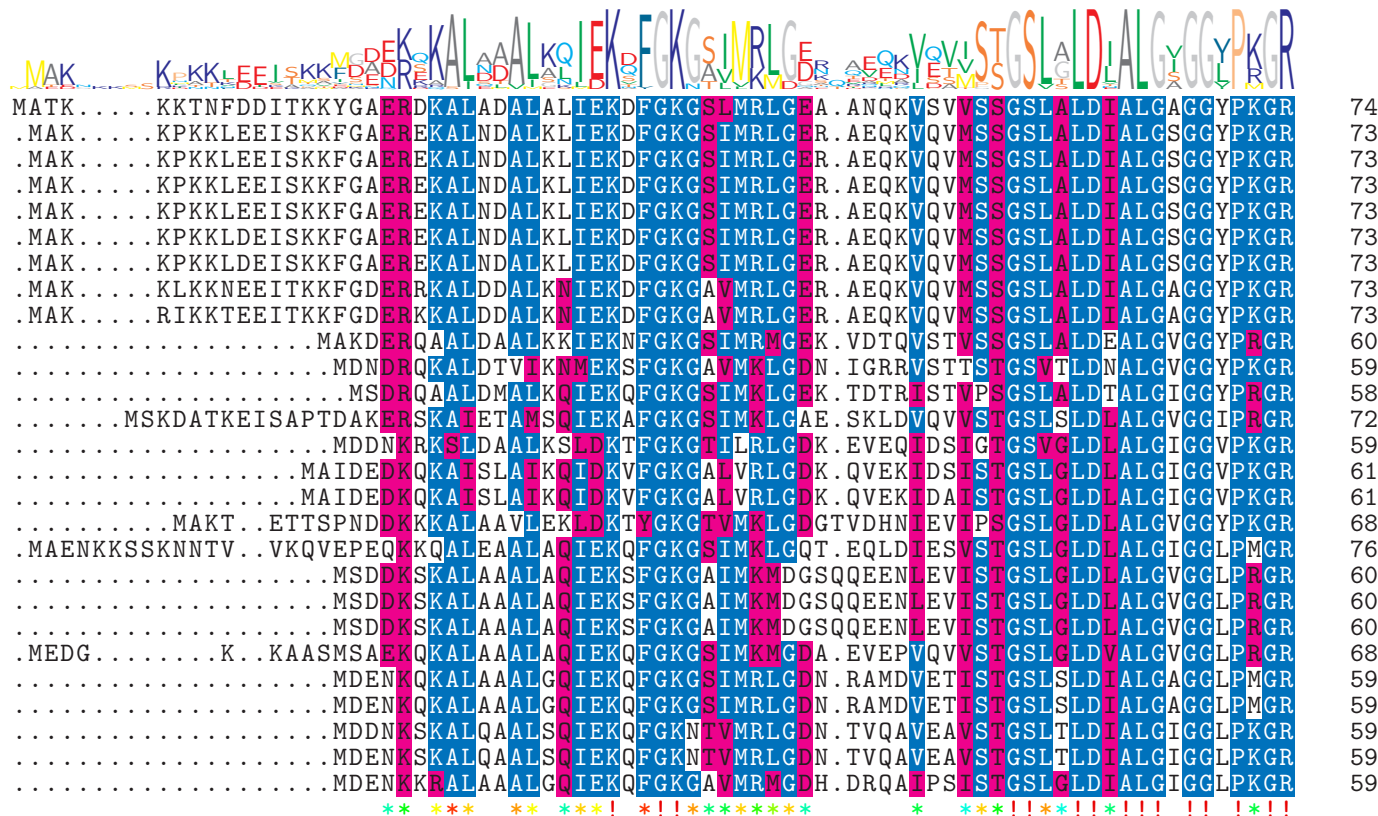


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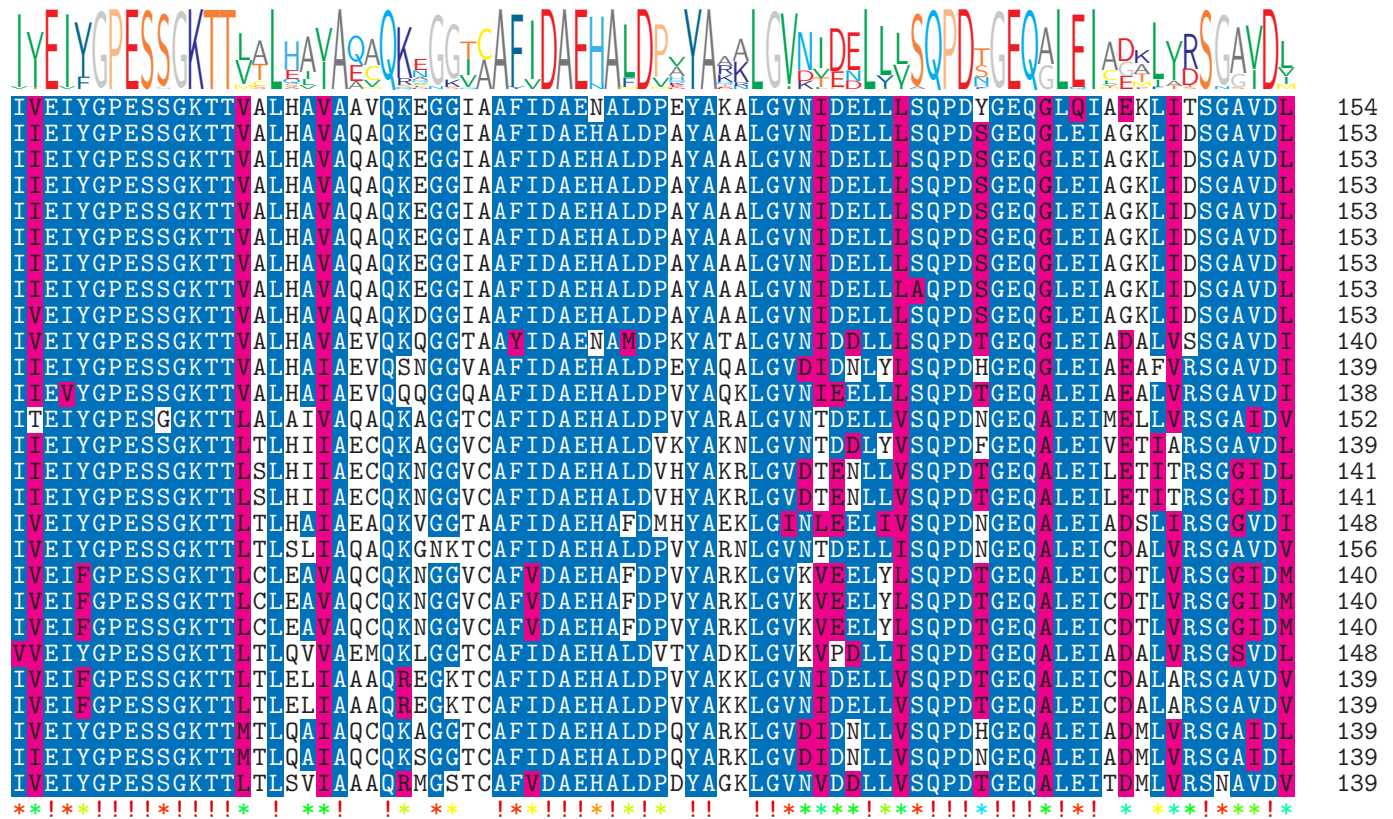
consensus



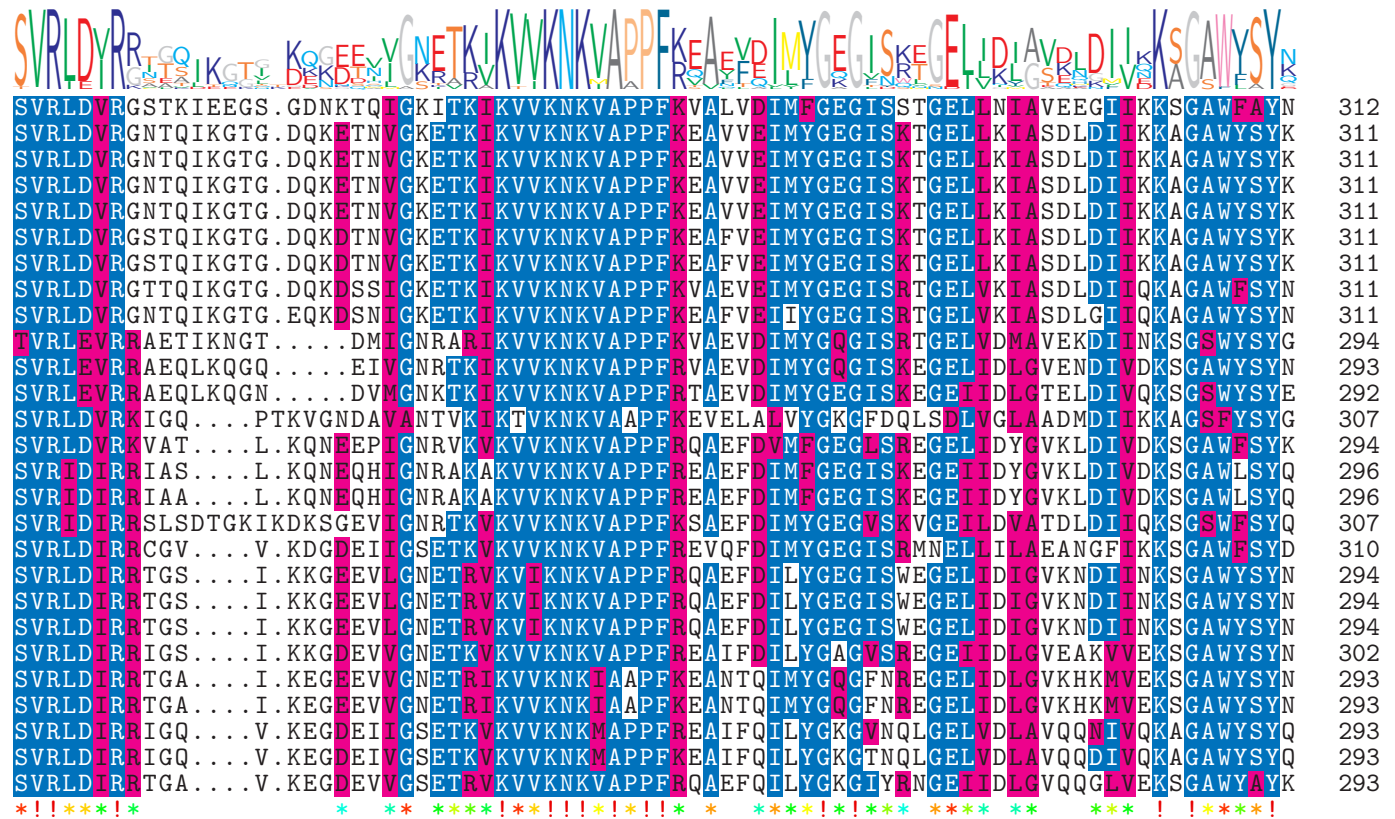
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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIF DEID KQVRSKF LIDGEEVSEQDTEN KKDE ...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIF DEID KQVRSKF LIDGEEVSEQDTEN KKDE ...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIF DEID KQVRSKF LIDGEEVSEQDTEN KKDE ...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAADNPEIF FEID HQVRVQF LIDGEEIAES...KKDE...AAQVDS...VNEEVTLDLGDLEIE	381
DEKIGQGS ENAKKYLAADNPEIF FEID HQVRVQF LIDGEEIAES...KKDE...AAQVDS...VNEEVTLDLGDLEIE	381
GEKIGQGS ENAKRYLADHPQLF FEID RKVRVKF GLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ENAKKFLADNPEIF DDID HKVRVQY GLIEEDNTEEKQSSKEK.....ETDEK...ADKNLVLELDDTIELE	382
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DERIGQG EKTIAYIAERPEMEQ EIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
DKKLGGG RENSKAF LKENPEIAD EITKAIQNSM GIEGMI....SGSEDD..EGEE.....	343
DKKLGGG RENAKALLKEDKAL AD EITLKIKESIG SNEEI....MPLPDE..PLEEME.....	347
DKKLGGG RENAKALLKEDKAL AD EITLKIKESIG SNEEI....MPLPDE..PLEEME.....	347
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GAKIGQGK DNVRVWLKENPEIS DEIDAK IRALNGVEMHITEGTQDET DGER ...PEE.....	348
GAKIGQGK DNVRVWLKENPEIS DEIDAK IRALNGVEMHITEGTQDET DGER ...PEE.....	348
GAKIGQGK DNVRVWLKENPEIS DEIDAK IRALNGVEMHITEGTQDET DGER ...PEE.....	348
GERIGQGRD NCREFLRENAELAR EIENK VREHL GVT PMGAVTLA.EEEVE.....	352
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GDKIGQGK ANACKYLKENPEIAKT LDKKL REMLLNPENMQLIAETSSAADDVE..FGAVPEEF.....	354
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GNKIGQGK NNVIRYFEENNQIAE EIERN IREQLLTTGTNGAVQ.I.EDEEEP D ..LL..LES.....	349
GSKIGQGA NAAKYILENPEI GQIEEQ IRAKLLVTSANTKATPVAEDLADAD..I.....	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	... 387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE 388
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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved