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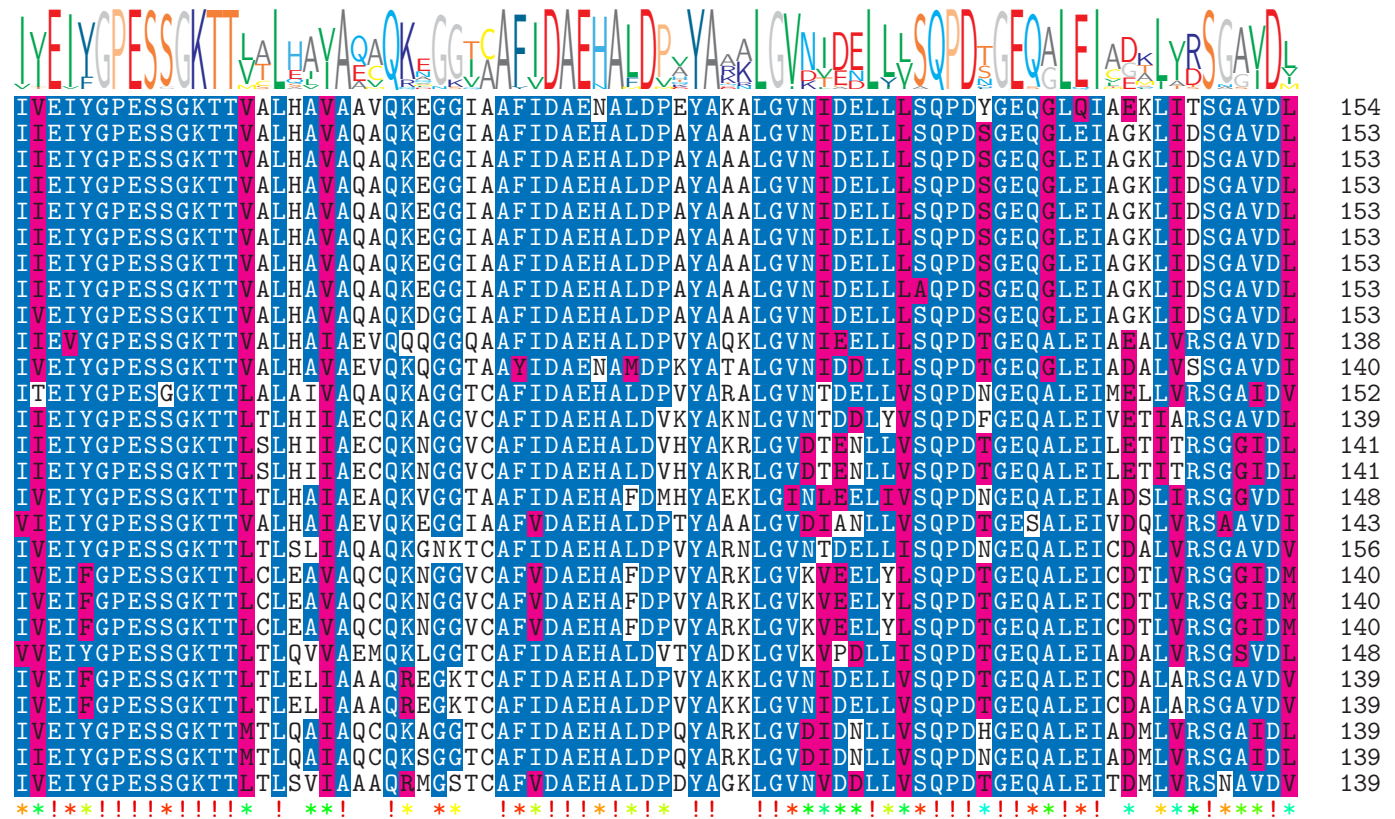
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consensus

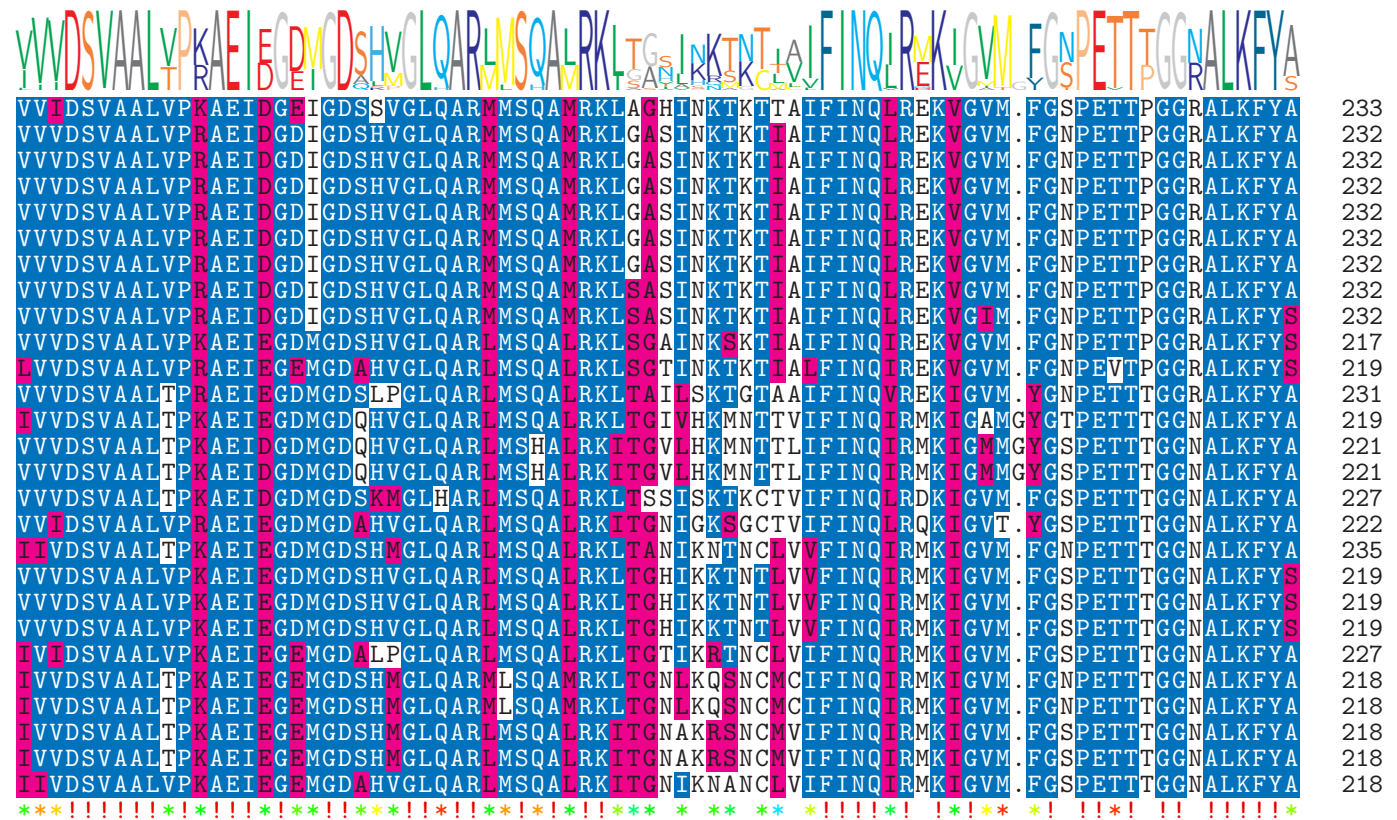
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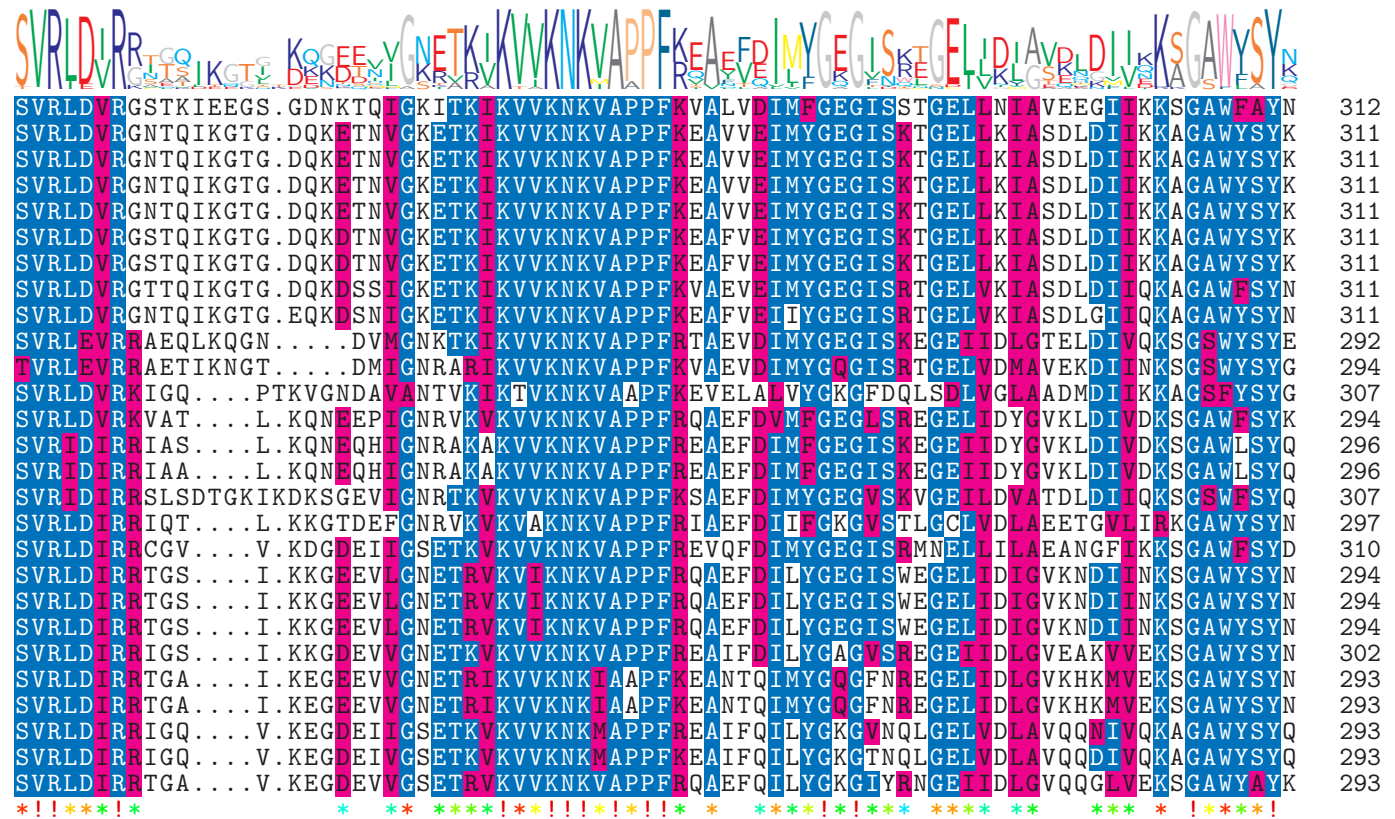
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NTDB id 1205 PSJM300 Q5545 AEN77183.1

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consensus

Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE.....PKKEEA..VNEEVPLDLGDELE	383
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE.....PKKEEA..VNEEVPLDLGDELE	383
DEKIGQGSSENAKKYLAHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE.....PKKEEA..VNEEVPLDLGDELE	383
DEKIGQGSSENAKKYLADNPEIFDEIDHQVRVQFLIDGEEIAES....KKDE.....AAQVDS..VNEEVTLDLGDLE	379
DEKIGQGSSENAKKYLADNPEVFAEIDHQVRVQFLIDGEEIAES....KKDE.....VAQVDS..VNEEVTLDLGDLE	379
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIE	375
GEKIGQGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIE	380
EERLGGGRENAAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL...EFE.E.....	348
SERIGGGRENAAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTTEDE.QI...NILPDDST....EE.....	355
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DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEEIMPL.....PDEPLEEME.....	347
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GTKIGQGGKNNAVKWLKENPEIADKLEQEIRNTLASNPNSVL...KATASDSNDESDVEEFS.....EEEL.....	372
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHITE...GTQDETGDGER.....P.....EE.....	348
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHITE...GTQDETGDGER.....P.....EE.....	348
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHITE...GTQDETGDGER.....P.....EE.....	348
GERIGQGRDNCREFLRNAELARIEIENKREHLGVTPMGAV...TLA.EEVEED.....	352
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GDKIGQGGKANACKYLKENPEIAKTLDDKLREMLLNPNENMQL...IAETSSAADDVEFGAVP.....EEF.....	354
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQT...AA.HDETEEEPDLL..E.....S.....	349
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GSKIGQGGKANAAYLEENPEIQEIEEQIRAKLLVTSANTK...ATPVAEDLADADI.....	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1		387
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consensus

 non conserved
 similar
 ≥ 50% conserved