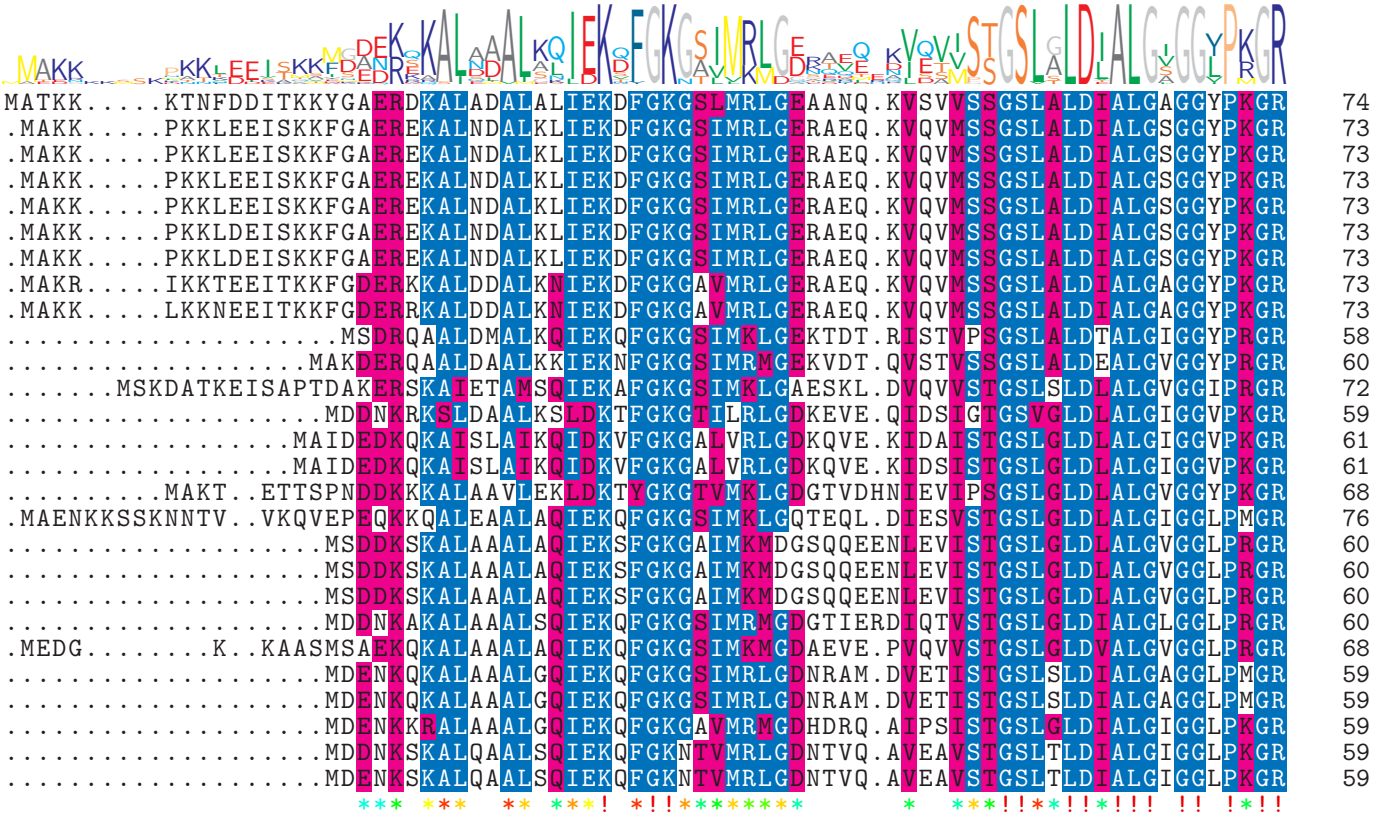


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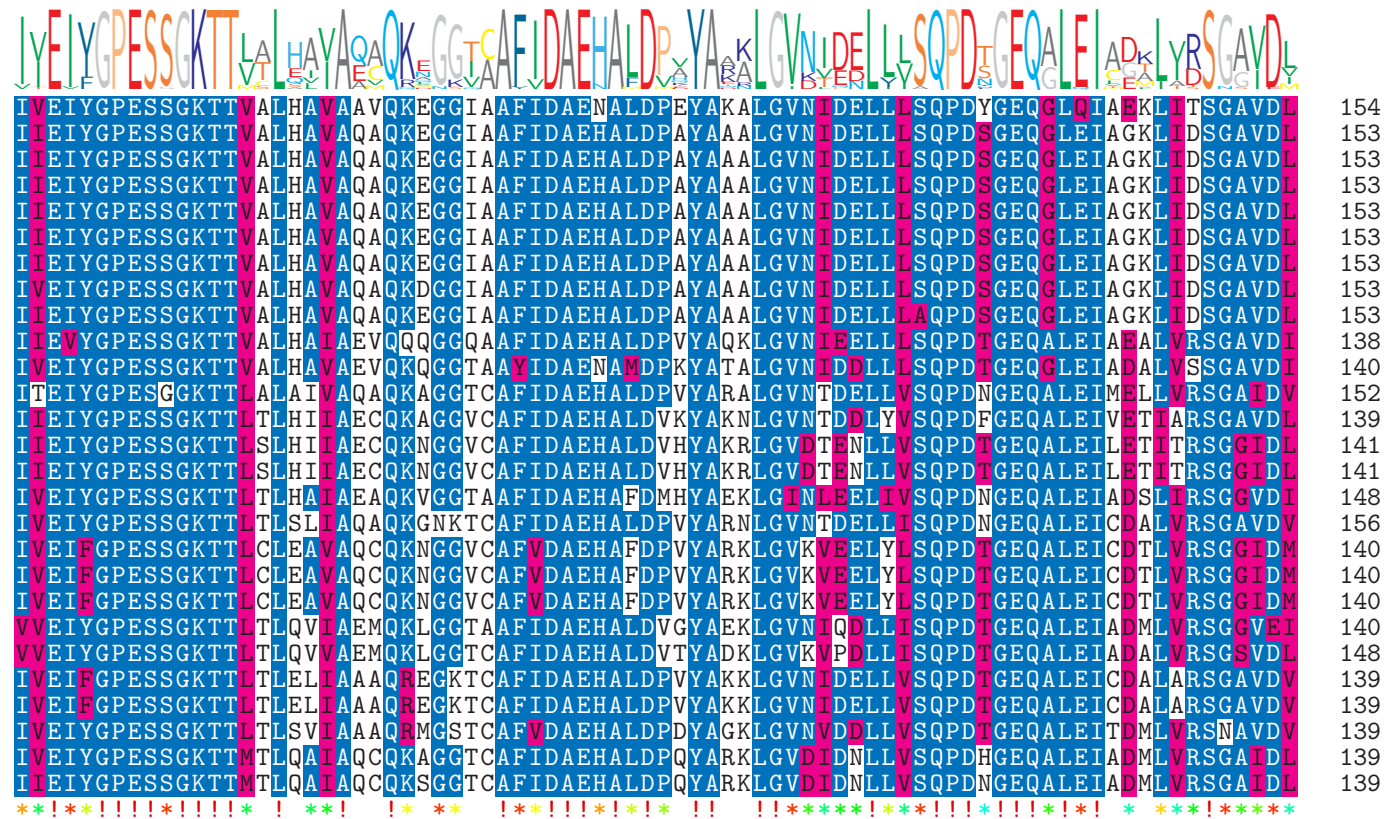
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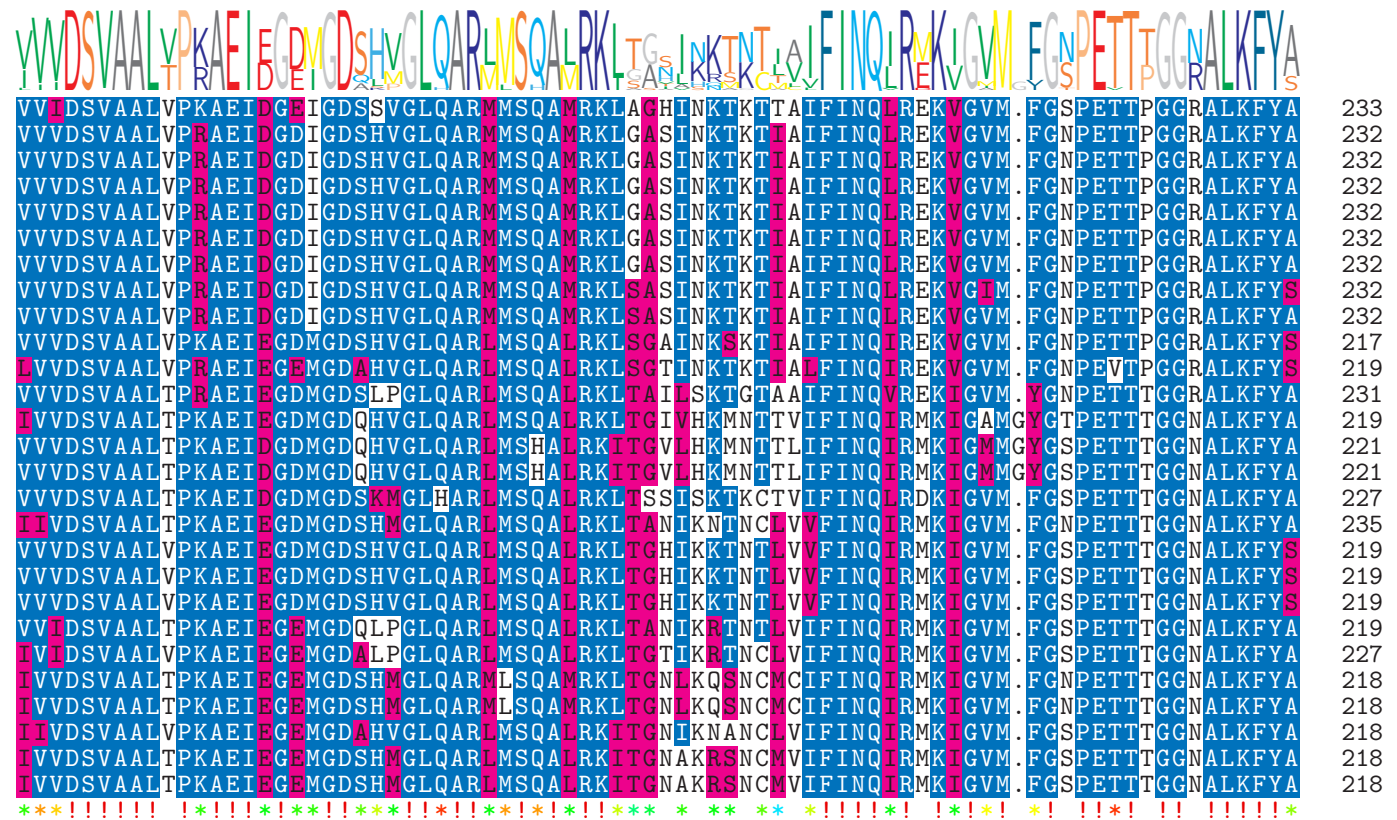
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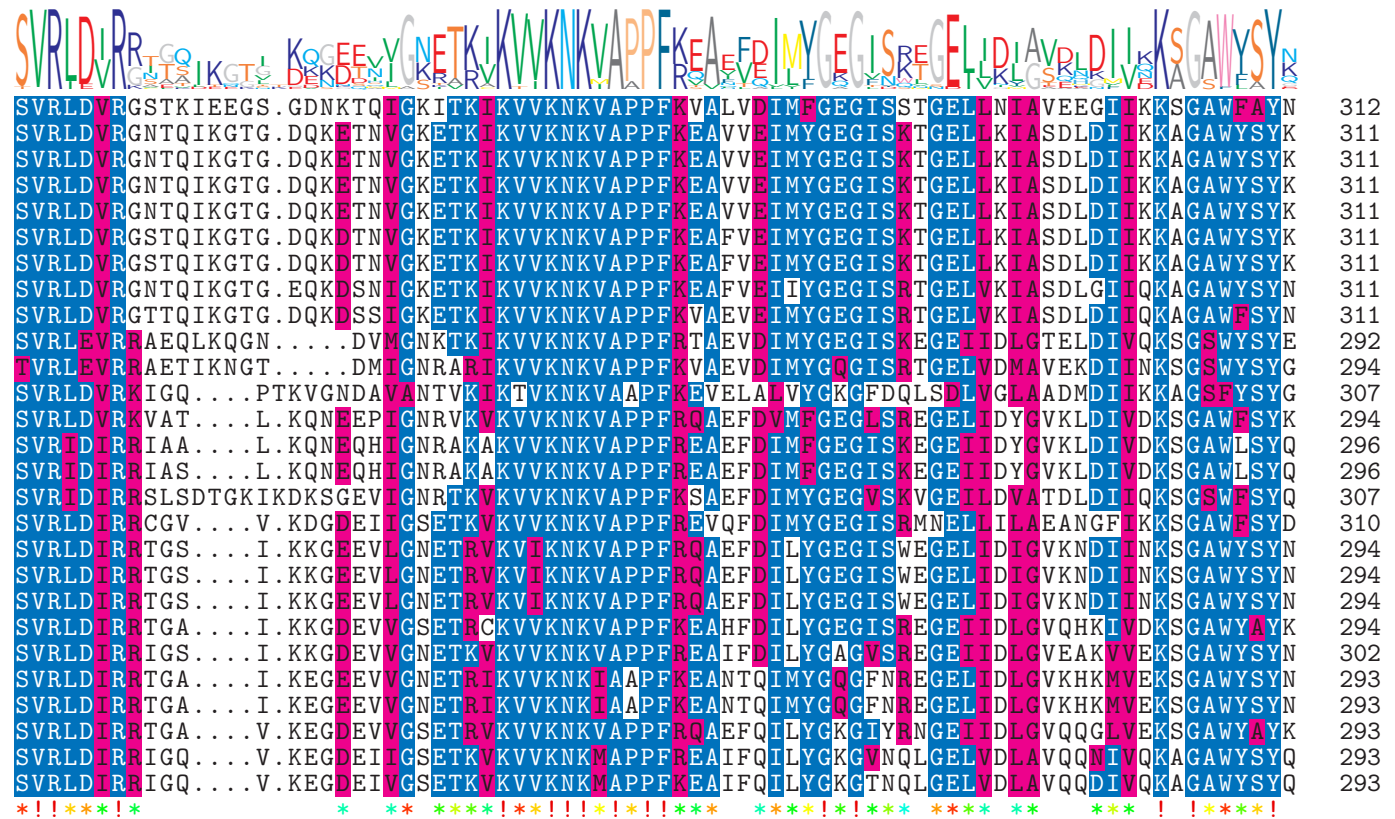
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consensus

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Sequence	Score
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DEKIGQGS ⁺ ENAKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTENK.KDE...PKKEEA..VNEEVPLDLGDELEI	384
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GEKIGQGS ⁺ ENAKKFLADNPEIF ⁺ DDID ⁺ HKVRVQYGLIEEDNTEEEKSSKE.K.....ETDEK..ADKNLVLELDGTIEL	381
GEKIGQGS ⁺ ENAKRYLADHPQLF ⁺ DEID ⁺ RKVRVKFGLLEESEESAMAVAS.E.....E.....TDDLALDLNGIEI	376
EERLGGGREN ⁺ AQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQ.EEL.EFE.E.....	348
SERIGGGREN ⁺ AKNYLADHEDVEDEVRLKVR ⁺ AAYGISDVPEEDLPTTEDE..QI.NILPDDST....EE	355
DERIGGQKEKTIA ⁺ YIAERP ⁺ MEQEIT ⁺ DRVMAAIRAGNAGEAPALAPAPAAPAAEA	363
DKKLGQGR ⁺ ENSAFLKENPEIADEITKATIQNSMGIEGMIS..GSEDDEGEE.....	343
DKKLGQGR ⁺ ENAKALLKEDKALADEITLKIKESIGSNEEIM..PLPDEPLEEME.....	347
DKKLGQGR ⁺ ENAKALLKEDKALADEITLKIKESIGSNEEIM..PLPDEPLEEME.....	347
DTKLGQGRD ⁺ TVKELIKDNPELAELEAKIREKLQAK.....	343
GTKIGQGK ⁺ NNAVKWLKENPEIADKLEQEIRNTLASNPNSV..LKATASDSNDES ⁺ DVEE.....FSEEL	372
GAKIGQGD ⁺ KNVRVWLKENPEISDEIDAKIRALNGVEMHIT..EGTQDET ⁺ DGER.....PEE	348
GAKIGQGD ⁺ KNVRVWLKENPEISDEIDAKIRALNGVEMHIT..EGTQDET ⁺ DGER.....PEE	348
GAKIGQGD ⁺ KNVRVWLKENPEISDEIDAKIRALNGVEMHIT..EGTQDET ⁺ DGER.....PEE	348
GEKIGQGD ⁺ KNRREFLRANPALAREIENKVR ⁺ AQVGLNAMAV..EAAPAGVAPVEP.....	346
GERIGQGRD ⁺ NCREFLR ⁺ ENAE ⁺ LARIENKVR ⁺ REHLGVTPMGA..VTLAEVEED.....	352
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNMQ..LIAETSSAAD ⁺ DVEFGA.....VPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNMQ..LIAETSSAAD ⁺ DVEFGA.....VPEEF	354
GSKIGGQKANAACKYLENPEIGQ ⁺ EIEQQIRAKLLVTSANT..KATPVAEDLADADI.....	347
GNKIGQGGK ⁺ NNVIRYLEENPQISTEIEAVIREQLLTKASDQ..TAA.HDETEEPDLL.....ES	349
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logo

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consensus

 non conserved
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