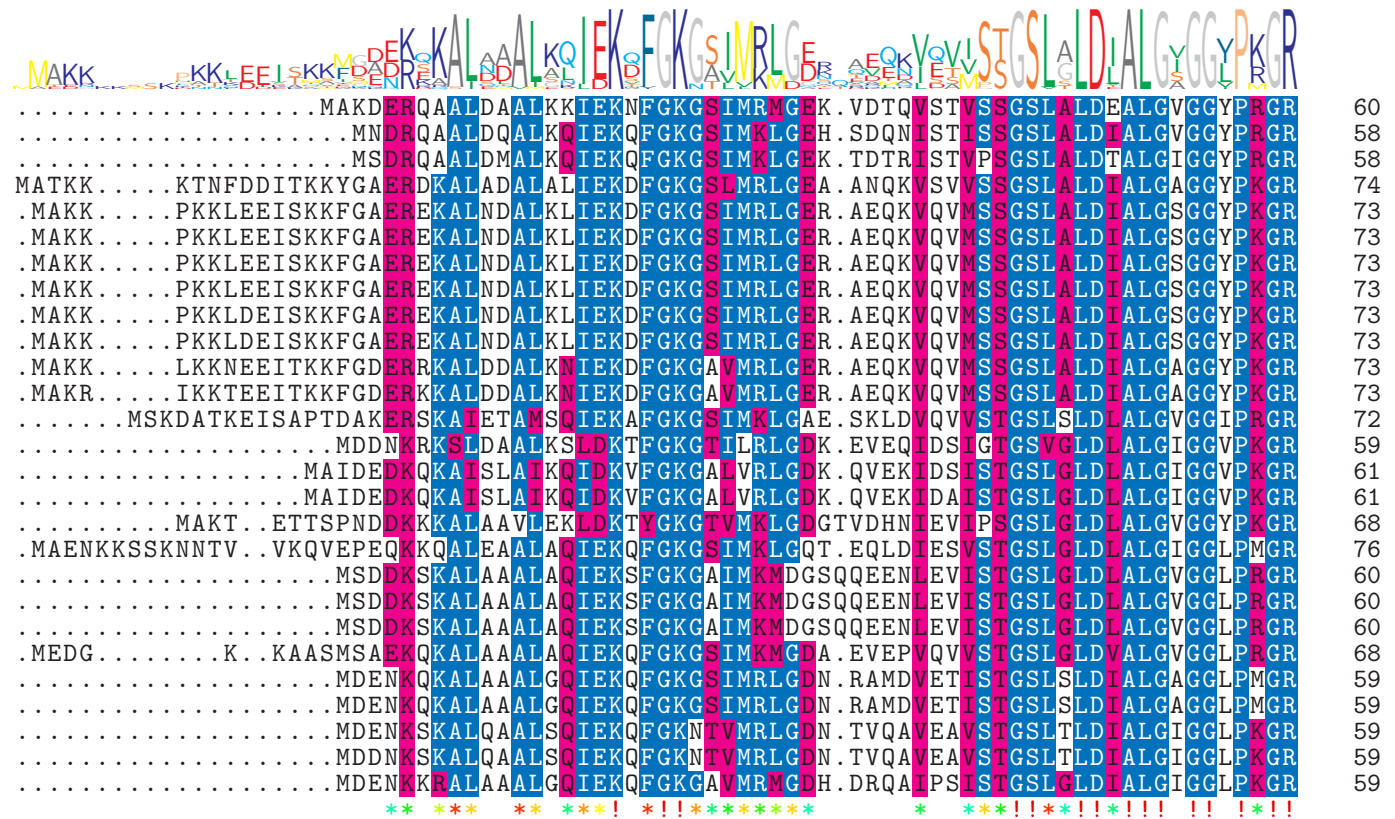


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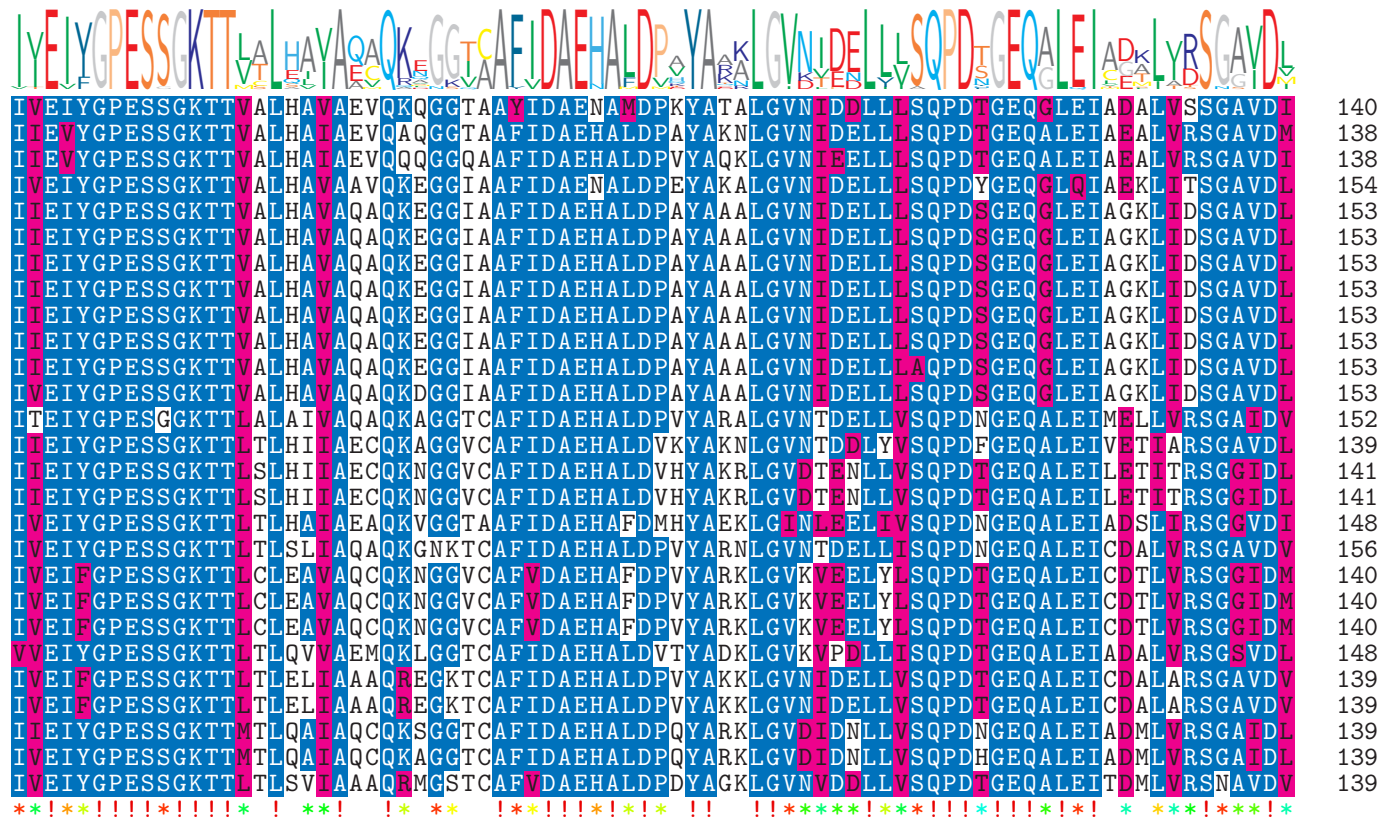
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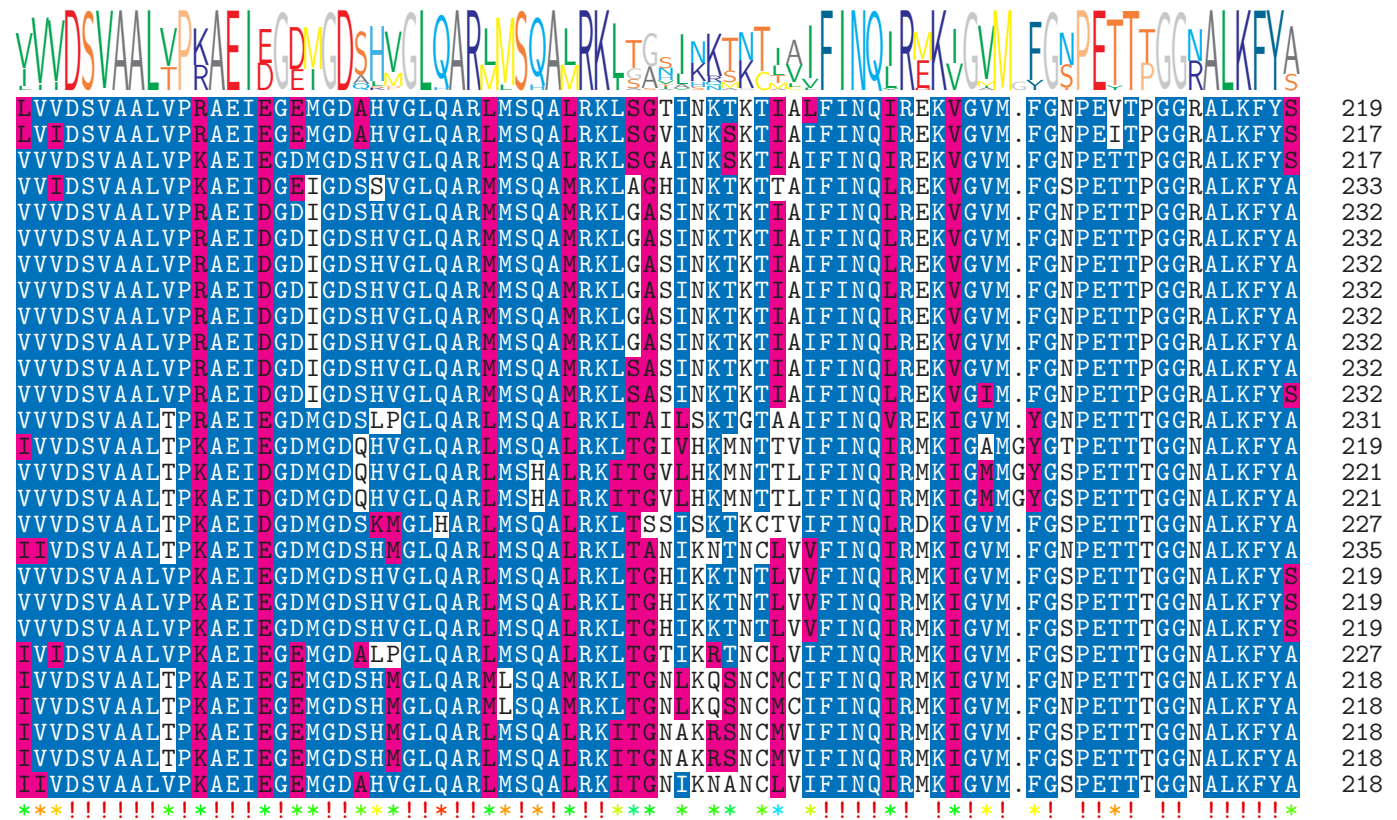
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consensus

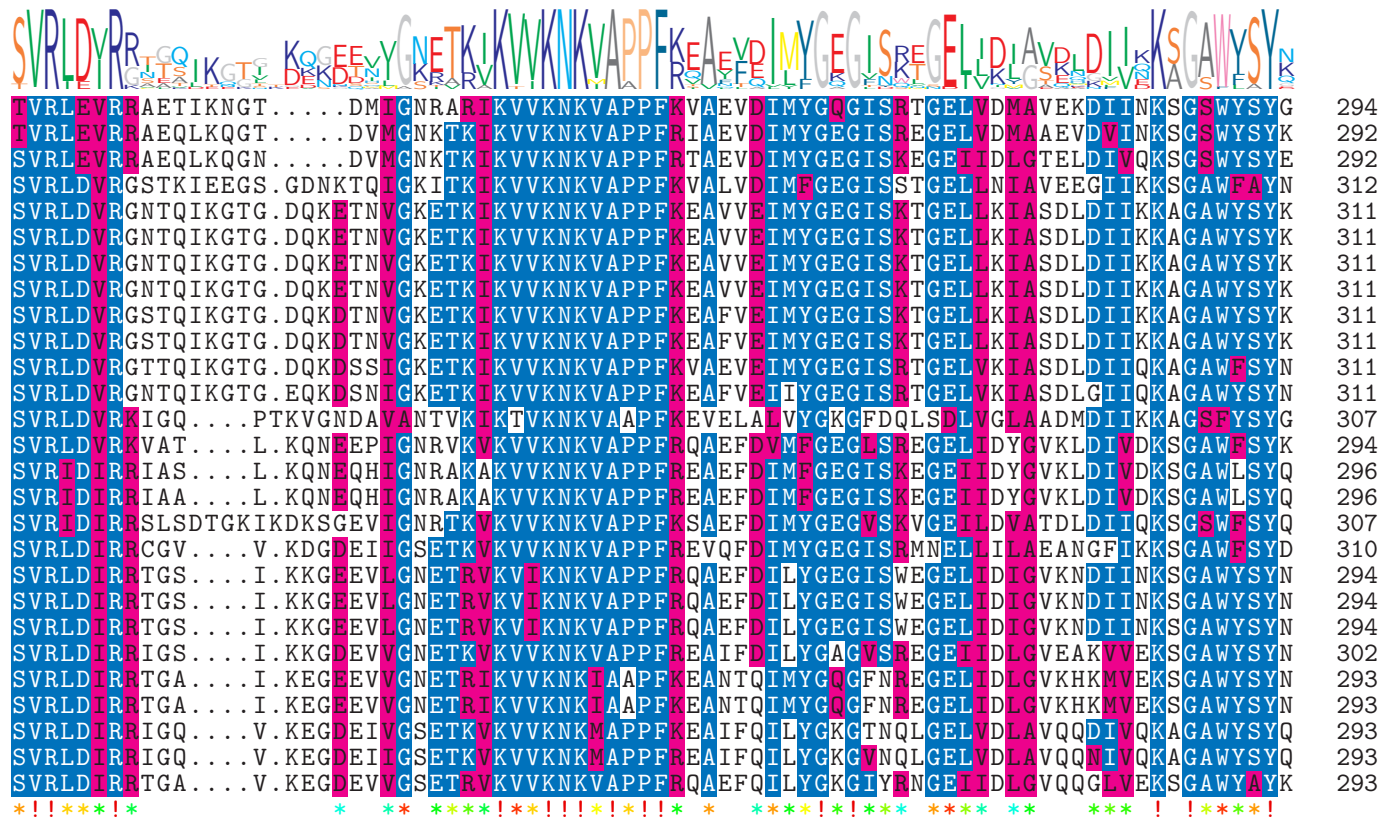
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consensus

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consensus

Sequence	Score
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EERIGGGRENAKQFLKENKDIMLMIQEIREHYGLDNNGVVQQAAEETQEELEFEE.....	348
DEKIGGGAEKAKNYLKEHQDVFEIDHKKVRAAHGLDDSEVAETEEETTASKTAKAKKEEKAVETEEIELELED....	387
DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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GEKIGGGSSENAKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
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DKKLGGRRENAKALLKEDKALADEITLKKIKESIGSNEEI.....MPLPDEP..LEEME.....	347
DKKLGGRRENAKALLKEDKALADEITLKKIKESIGSNEEI.....MPLPDEP..LEEME.....	347
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDET.....GE..RPEE.....	348
GERIGGGRDNCREFLRENAELARLEIENKVRHGLVTPMG.....AV.TLAEVEED.....	352
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GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNEM.....QLIAETSSAADDVEFGA..VPEEF.....	354
GNKIGGQKKNVIRYFEENNQIAEEIERNIREQLLTGTN.....GAVQ.I.EDEEEDPD..L..LLES.....	349
GNKIGGQKKNVIRYLEENQISTEIEAVIREQLLTQASD.....QTAA.HDETEEEDPD..L..LES.....	349
GSKIGGQKANAAYLEENPEIQEIEEQIRAKLLVTSAN.....TKATPVAEDLADAD..I.....	347

logo

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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved