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NTDB id 527 SMSK321 RS11065 WP 001085454.1
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NTDB id 1389 A4U84 RS07560 WP 021112712.1
NTDB id 1130 NGFG RS03960 WP 003688695.1
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NTDB id 1123 OK783 RS03845 WP 003688695.1
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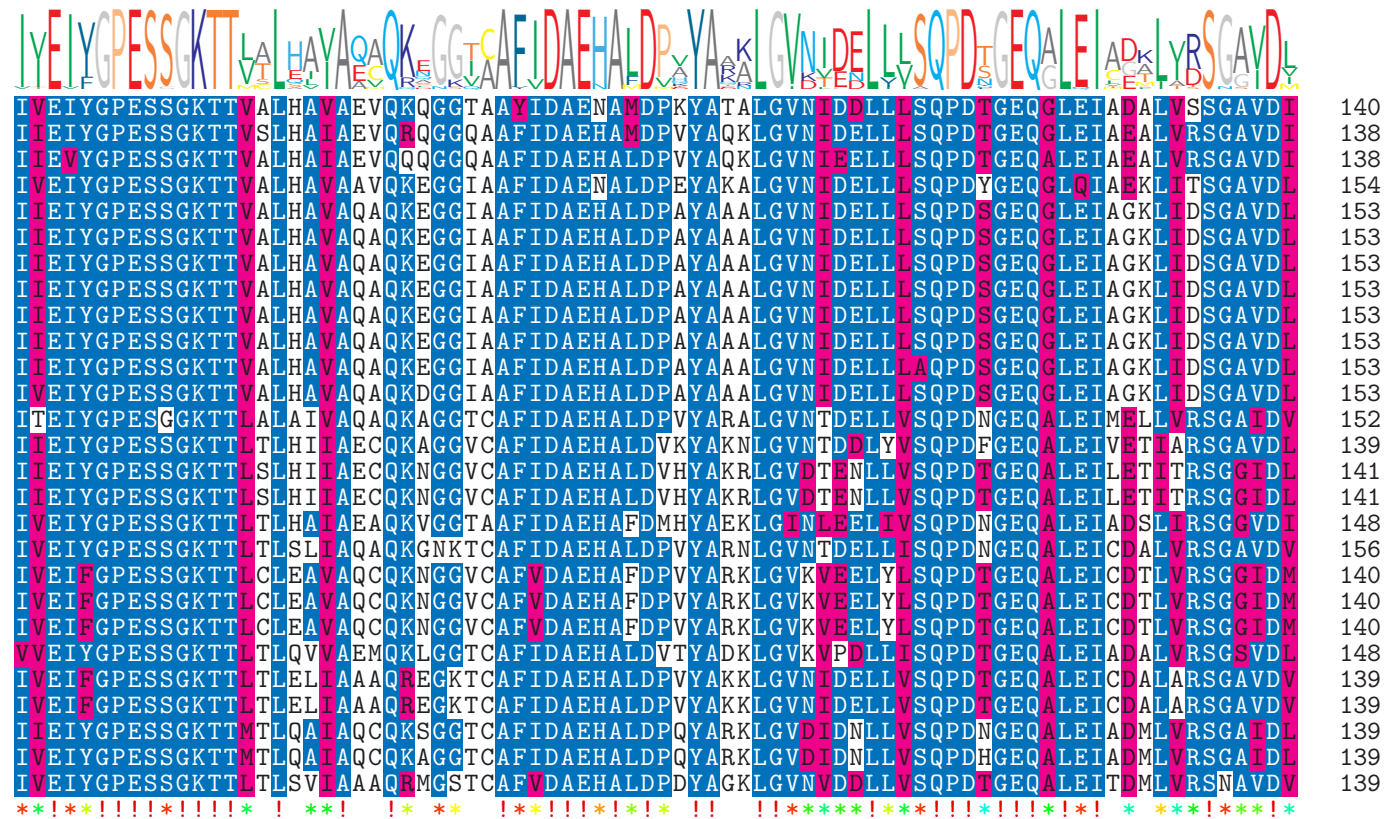
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consensus

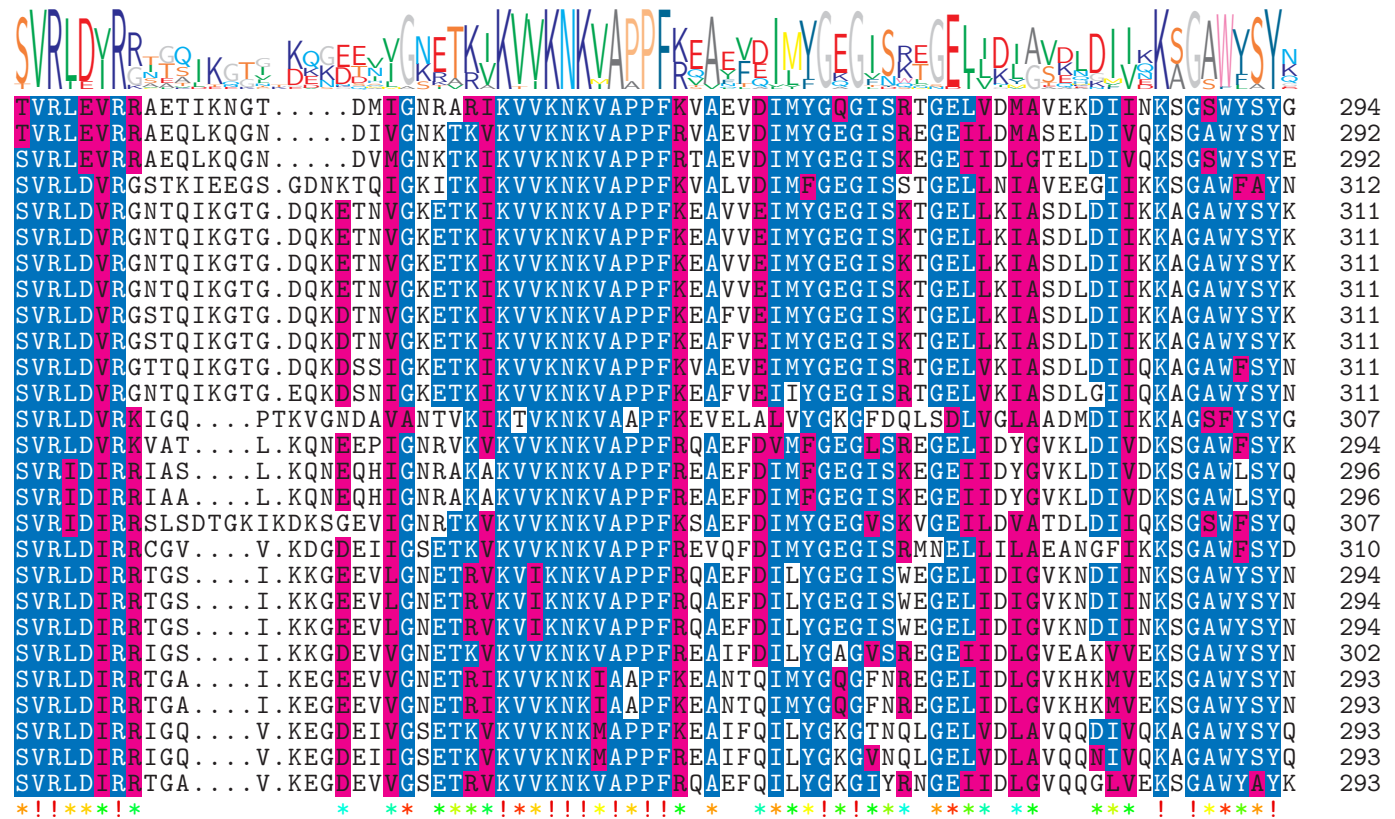
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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EERLGGGRENASKQFLKENTLREETIAFFVRDHHGIGEDSGVEDTE..DATLQD	348
DEKIGQGAEKAKNYLKEHQDVFEIDHKKVRAAHGLDDSEVAETEETETASKTKAKAKKEEKAVETEEIELELED	387
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAADNPEIFDEIDHQRVVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAADNPEVFAEIDHQRVVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKRVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
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DERIGGKKEKTIAIYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA	363
DKKLGGGRENASKAFLKENPEIAD EITKAIQNSMGI EGMI.....SGSEDDE..GEE.....	343
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GERIGQGRDNCREFLRNAAELAR E IENKVRHGLVTPMG.....AV.TLAEVEED	352
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GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM.....QLIAETSSAADDVEFGAV..PEEF	354
GNKIGQGGKNNVIRYFEENNQIAEEIERNIREQLLTGTN.....GAVQ.I.EDEEEDPD..LL..LES	349
GNKIGQGGKNNVIRYFEENNQIAEEIERNIREQLLTGTN.....GAVQ.I.EDEEEDPD..LL..LES	349
GSKIGQGGKANAAKYLENPEIQEIEQQIRAKLLVTSAN.....TKATPVAEDLADAD..I.....	347

logo

		IEE	
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NTDB id 128781 AS86 RS06280 WP 001283853.1	...	343	
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consensus			

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