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NTDB id 1214 NCTC11637 00359 SQJ03206.1
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

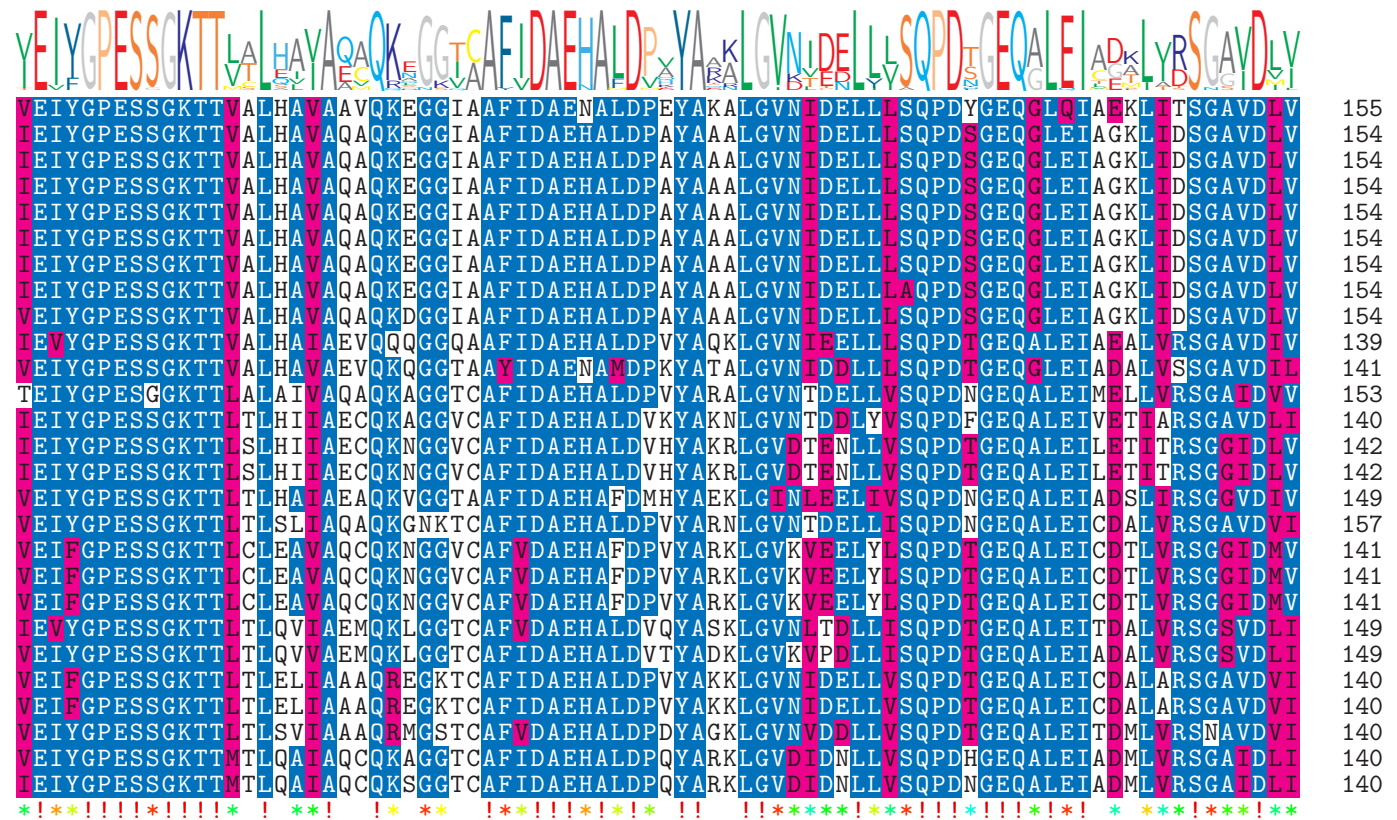
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consensus

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logo

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NTDB id 1427 RS RS02760 WP 011000510.1	VR	L	D	I	R	R	I	G	S	.	.	.	.	.	.	.	.	.	.	I	.	K	K	G	.	D	E	V	V	G	N	E	T	K	V	K	V	V	K	N	K	V	A	P	P	F	R	E	A	I	F	D	I	L	Y	G	A	G	V	S	R	E	G	E	I	I	D	L	G	V	E	A	K	V	V	E	K	S	G	A	W	Y	S	Y	N	G	303
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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EKIGQGSENAKKYLA EHP E I FDEIDKQVRSKFG LIDGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
EKIGQGSENAKKYLA EHP E I FDEIDKQVRSKFG LIDGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
EKIGQGSENAKKYLA EHP E I FDEIDKQVRSKFG LIDGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
EKIGQGSENAKKYLA DNPEVFAEIDHQVRVQFGLIDGEEAAE.....SKKDE...VAQVDS..VNEEVPLDLGDELEI	380
EKIGQGSENAKKYLA DNPEI FDEIDHQVRVQFGLIDGEEIAE.....SKKDE...AAQVDS..VNEEVPLDLGDELEI	380
EKIGQGSENAKRYLA DHPQLFDEIDRKVRVKFGLLEESEES..AMAVASE.....ETD...TDDLALDLNGIEI	376
EKIGQGSENAKKFLADNPEI FDDIDHKVRVQYGLIEEDNTEE..KQSSKEK.....ETDEK..ADKNLVLELDDTIEL	381
ERLGGGR ENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQ..QAETQEEL.EFE.E.....	348
ERIGGGRENAKNYLADHEDVEDEVRLKVRAAYGISDVPEEDL..PTTEDE.QI.NILPDDST.....EE.....	355
ERIGGGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAA.EA.....	363
KKLGGGRENKAF LKENPEIADEITKAIQNSMGIEGMIS..GSE...DDEGE.E.....	343
KKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIM..PLP...DEPLE.EME.....	347
KKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIM..PLP...DEPLE.EME.....	347
TKLGGGRD TVKELIKDNPELAEELEAKIREKLQAK.....	343
TKIGQGKNNAVKWLKENPEIADKLEQEI RNTLASNPNSV..LKATASDSND ESDVEEF.....SEEL.....	372
AKIGQKDNVRVWLKENPEISDEIDAKIRALNGVMHIT..E.....GTQDE.TDGER.....PEE.....	348
AKIGQKDNVRVWLKENPEISDEIDAKIRALNGVMHIT..E.....GTQDE.TDGER.....PEE.....	348
AKIGQKDNVRVWLKENPEISDEIDAKIRALNGVMHIT..E.....GTQDE.TDGER.....PEE.....	348
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ERIGGGRDNCREFLR ENAELARIENKVRHGLVTPMGA..V.TLAEVEED.....	352
DKIGQK KANACKYLKENPEIAKTLDDKKLREMLLNPNMQ..LIAETSSAADV.EFGAV.....PEEF.....	354
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NKIGQKKNVIRYLEENPQISTEIEAVIREQLLTKASDQ..TAA.HDETEEEP.DLL.....ES.....	349
NKIGQKKNVIRYFEENNQIAEIERNI REQLLTGTNG..AVQ.I.EDEEEP.DLL.....LES.....	349

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consensus						

-  non conserved
-  similar
-  ≥ 50% conserved