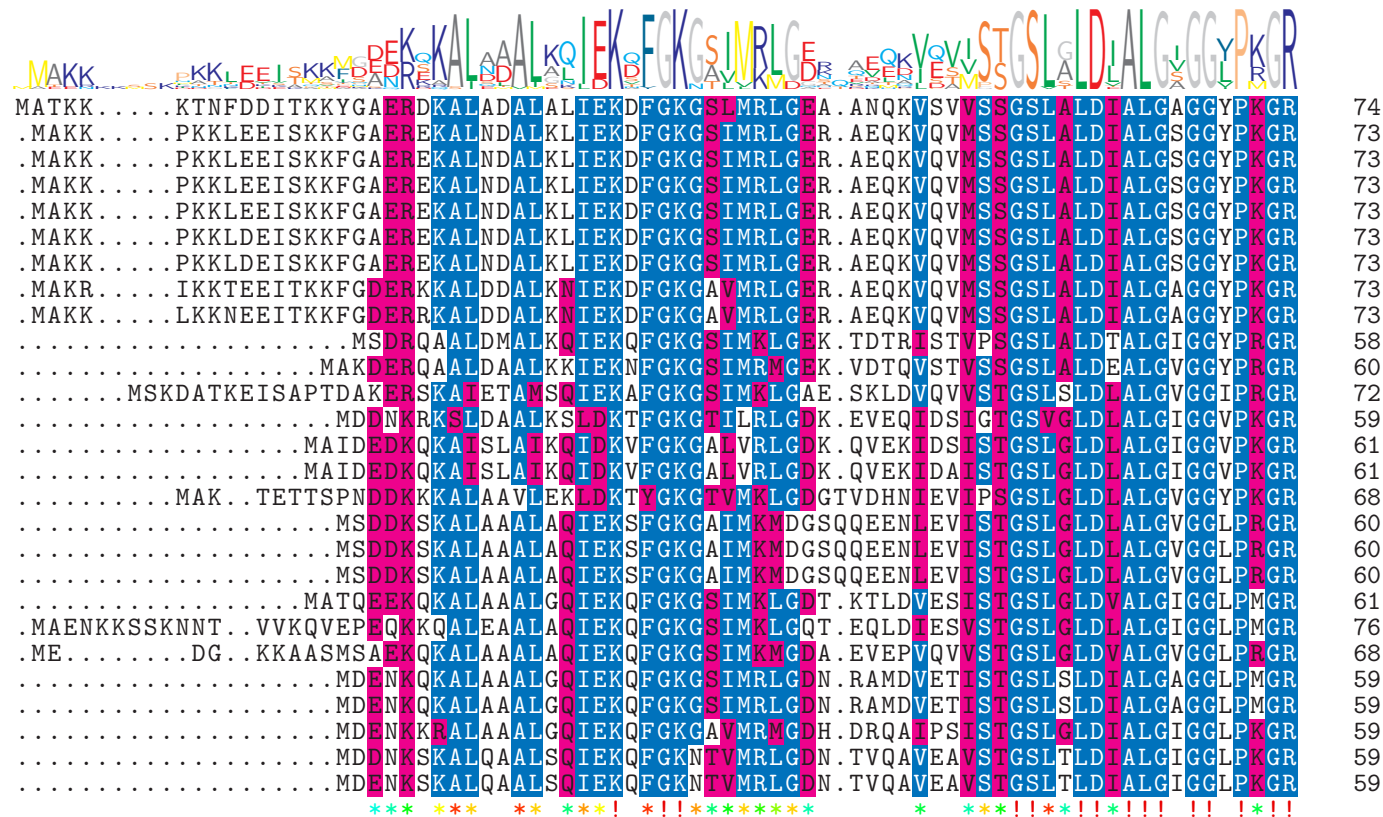


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NTDB id 625 LCA RS02525 WP 011374196.1
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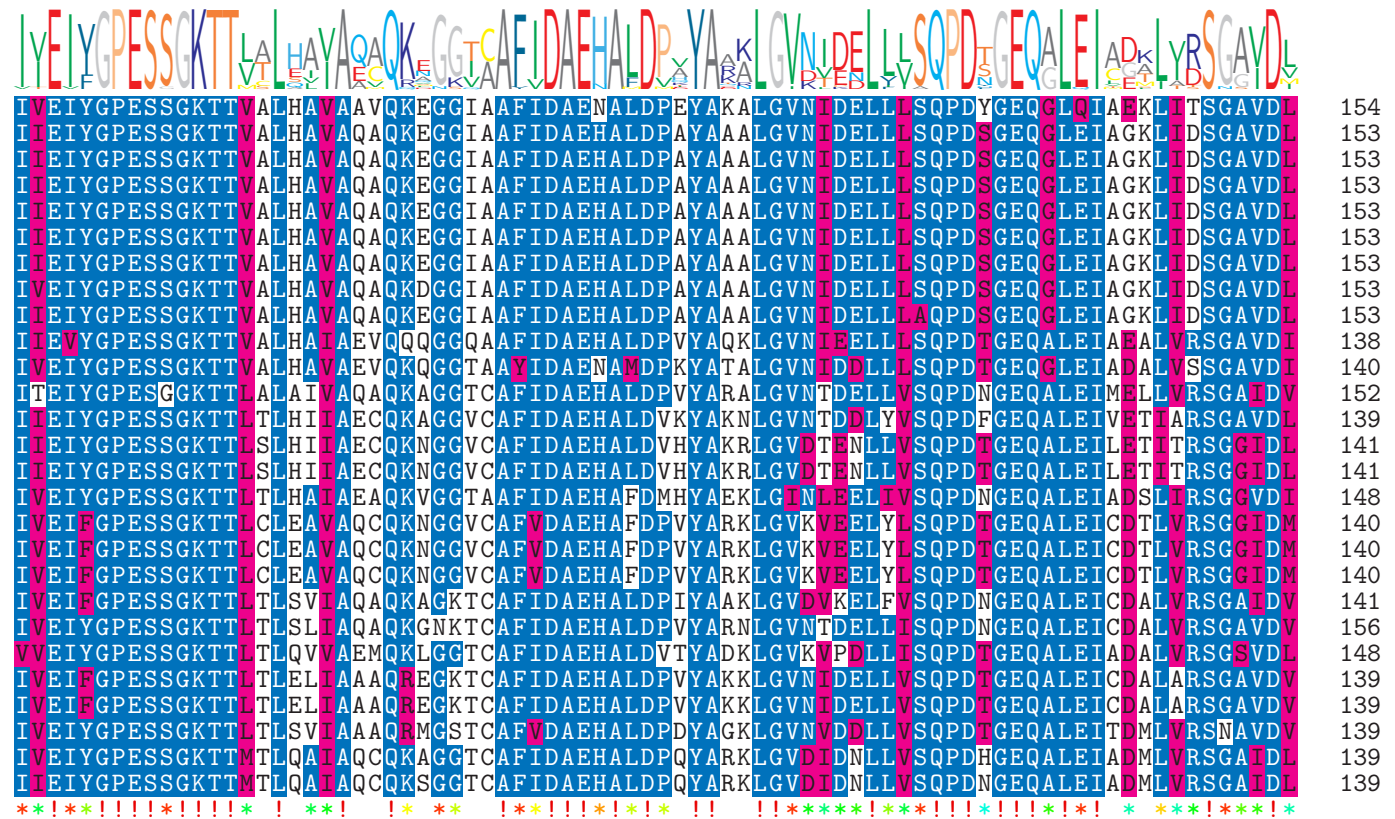
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consensus

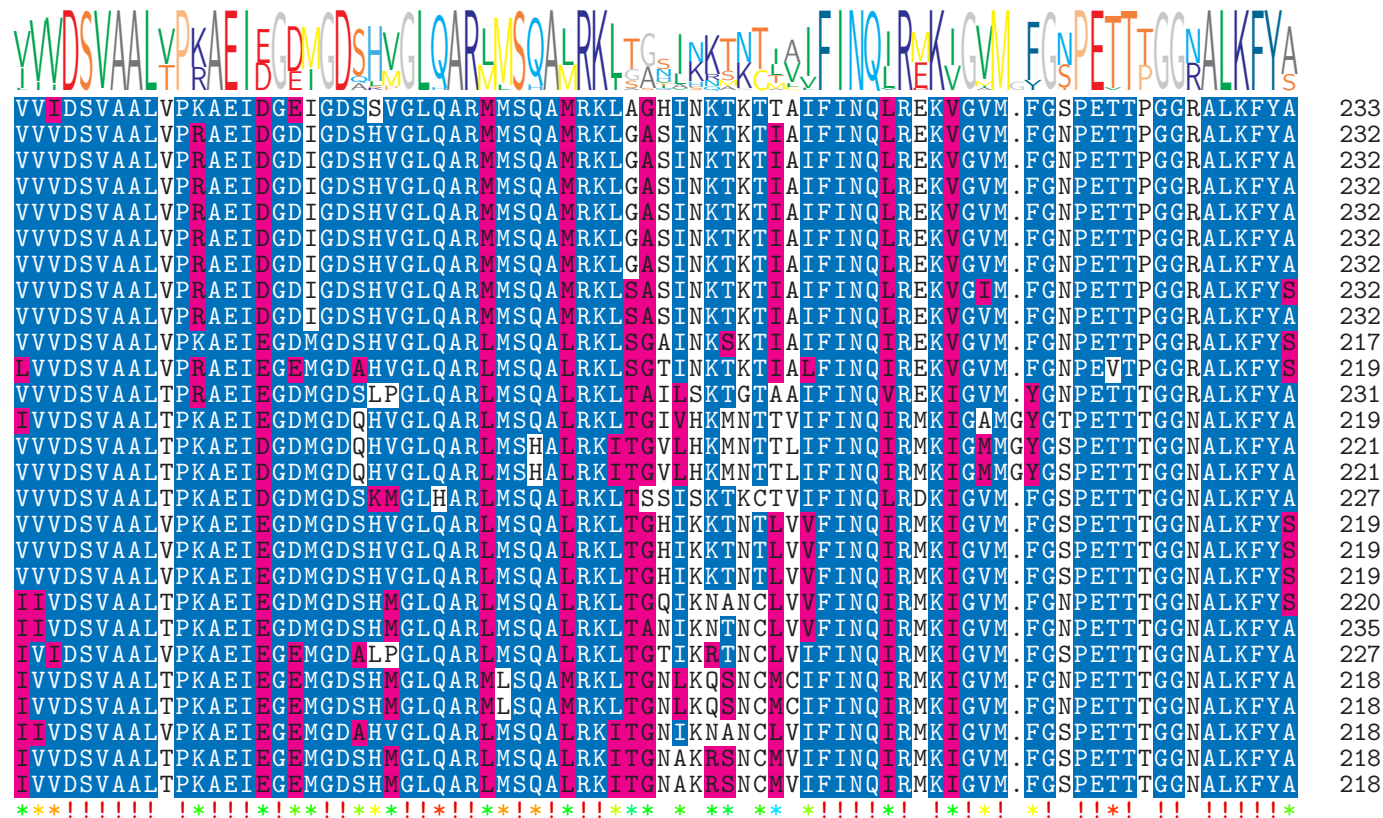
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NTDB id 1205 PSJM300 05545 AFN77183.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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logo

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NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTNVGKETKIKVVKNKVAPPFKEAFVEIMYEGEGISKTGELLKIASDLDI IKKAGAWYSYK	311
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NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN.....DVMGNKTKIKVVKNKVAPPFRTAEVDIMYEGEGISKEGEIIDLGTEL DIVQKSGSWYSYE	292
NTDB id 625 LCA RS02525 WP 011374196.1	TVRLEVRRAETIKNGT.....DMIGNRARIKVVKNKVAPPFKVAEVDIMYGGISRTGELVDMAVEKDI INKSGSWYSYG	294
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	SVRLDIRRTGA....I.KEGEVLGNETRIKVVKNKIAAPFKEANTQIMYGGGFNREGELIDLGVKHKMVEKSGAWYSYN	293
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEVVGSETRVKVVKNKVAPPFRQAEFIQILYKGKGIYRNGEIIDLGVQQGLVEKSGAWYAYK	293
NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEGDEIIGSETKVVKNKMAPPFRQAEFIQILYGKGVNQLGELVDLAVQQNIVQKAGAWYSYQ	293
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consensus	*!!**!* * * ** *****!!*!!*!!*!!* * * *****!!*!!** * * * * *	

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consensus

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Sequence	Score
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GEKIGGGSSENAKKFLADNPEIFDDIDHKVVRVQGLIEEDNTEEEKQ.SSKEK.....ETDEK..ADKNLVLELDDDTIEL	381
GEKIGGGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAS.AVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQQA.EETQEEL.EFE.E.....	348
SERIGGGSRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPT.TEDE.QI.NILPDDST.....EE.....	355
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DKKLGQGRESNAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGQGRESNAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
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GTKIGGQKKNNAVKWLKENPEIADKLEQEIRNTLASNPNSVLK..ATASDSNDESDVE.EFSE.....EEL.....	372
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GSKIGGQKANAACKYLEENPEIGQEIEQQIRAKLLVTSANTKA..TPVAEDLADADI.....	347
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logo

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NTDB id 1130	NGFG	RS03960	WP	003688695.1		348
NTDB id 1124	NGFG	RS03960	WP	003688695.1		348
NTDB id 1123	OK783	RS03845	WP	003688695.1		348
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NTDB id 1427	RS	RS02760	WP	011000510.1		352
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consensus						

-  non conserved
-  similar
-  ≥ 50% conserved