

logo

NTDB id 413 AAK55817.1 141..845()	MTSDPNPAQAFENWFEEEEGDDAFTSLIAGEETNSGIEELDFGDLFEGEPTVIQGEFGSPSSGEEDPPVRMTLDFNSPE	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1419 SGL RS12550 WP 010873252.1	MTSDPNPAQAFENWFEEEEGDDAFTSLIAGEETNSGIEELDFGDLFEGEPTVIQGEFGSPSSGEEDPPVRMTLDFNSPE	80
NTDB id 227965 B6N60 RS07285 WP 190607035.1		0
NTDB id 1417 SGL RS04200 WP 014407071.1		0
NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 413 AAK55817.1 141..845()	AELDALFTDEDAPTTAIDPFESSWLEIDQMMEADPLASIPETNAPAYQTAGGLDDNDLAEQLDLLGVGDVEPAITNPGL	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1419 SGL RS12550 WP 010873252.1	AELDALFTDEDAPTTAIDPFESSWLEIDQMMEADPLASIPETNAPAYQTAGGLDDNDLAEQLDLLGVGDVEPAITNPGL	160
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NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 413 AAK55817.1 141..845()	HSFAGADRVTPLTNEVLLFAAIDDL DGLINAPVLDEEFSFTELETIDTPAPKSFATISHPFRLPVAMEEDEDEFKDLEA	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1419 SGL RS12550 WP 010873252.1	HSFAGADRVTPLTNEVLLFAAIDDL DGLINAPVLDEEFSFTELETIDTPAPKSFATISHPFRLPVAMEEDEDEFKDLEA	240
NTDB id 227965 B6N60 RS07285 WP 190607035.1		0
NTDB id 1417 SGL RS04200 WP 014407071.1		0
NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 413 AAK55817.1 141..845()	LLEQADSSLGGGIAGMGGARLPARPRQVKSRSFEQTMRVPIKQLDNLSNLIGELVVKRNRLEQDQERLRQFLDNLLNQAQ	0
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NTDB id 227965 B6N60 RS07285 WP 190607035.1		0
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NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 413 AAK55817.1 141..845()	NLSDVGGRMQDLYERTLLEGALLASRSTNSRHHSSKTTYPDARITASSSSTMNDQPLDALEMDRFTGFHLLSQEMI ELIV	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
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consensus		

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NTDB id 413 AAK55817.1 141..845()	RVRESASDIQYLVDETDQVARTLRQVTTQLQEGMTKSRMVPFTQTADRLPRAIREVSMKLNKKVNLEVEGGDVLIDKMIL	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1419 SGL RS12550 WP 010873252.1	RVRESASDIQYLVDETDQVARTLRQVTTQLQEGMTKSRMVPFTQTADRLPRAIREVSMKLNKKVNLEVEGGDVLIDKMIL	480
NTDB id 227965 B6N60 RS07285 WP 190607035.1		0
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NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 413 AAK55817.1 141..845()	EHLYNPMTHLVNNAITHG IETPAERQKL GKSP EGH LAVRAFLQGNQTLITVSDDGAGINTEMVKQKAVEKGLISRMEAQS	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1419 SGL RS12550 WP 010873252.1	EHLYNPMTHLVNNAITHG IETPAERQKL GKSP EGH LAVRAFLQGNQTLITVSDDGAGINTEMVKQKAVEKGLISRMEAQS	560
NTDB id 227965 B6N60 RS07285 WP 190607035.1		0
NTDB id 1417 SGL RS04200 WP 014407071.1		0
NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 413 AAK55817.1 141..845()	LSQSEVYDLLFHAGFSTKDTADDFAGRGVGLDVVRTSLIDIRGAINIESTVGKGTTFITIRLPLTLSICKALCCLSDRARI	0
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NTDB id 1419 SGL RS12550 WP 010873252.1	LSQSEVYDLLFHAGFSTKDTADDFAGRGVGLDVVRTSLIDIRGAINIESTVGKGTTFITIRLPLTLSICKALCCLSDRARI	640
NTDB id 227965 B6N60 RS07285 WP 190607035.1		0
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consensus		

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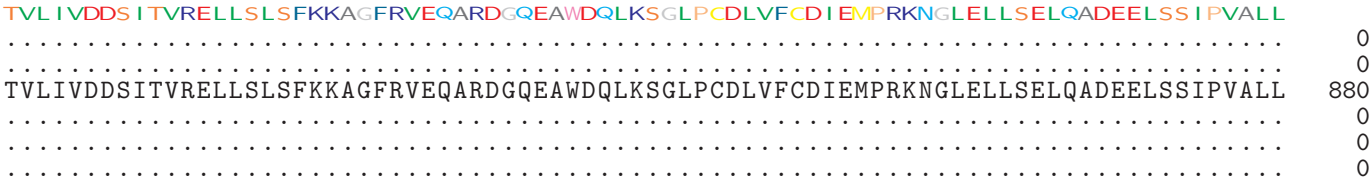
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NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1419 SGL RS12550 WP 010873252.1	AFPM DGVEDTRDYLPKD I VTD E D G Q K C V K Y G K E A L L L P L Y P L K D L L N Y N R Q L S R G S V Y G G K Q E E D V V R V I I A R G S S G N L L	720
NTDB id 227965 B6N60 RS07285 WP 190607035.1		0
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consensus		

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NTDB id 413 AAK55817.1 141..845()	ALQIDQVLGEEEEIVIKQIEGPIPKPPGIAGATVRGDGSI MP IADVLELIEIAQGRLRTDSSGGLWRKTLTPTVNEVHMDP	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1419 SGL RS12550 WP 010873252.1	ALQIDQVLGEEEEIVIKQIEGPIPKPPGIAGATVRGDGSI MP IADVLELIEIAQGRLRTDSSGGLWRKTLTPTVNEVHMDP	800
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NTDB id 1417 SGL RS04200 WP 014407071.1		0
NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 413 AAK55817.1 141..845()
NTDB id 374 SMU RS06885 WP 002262930.1
NTDB id 1419 SGL RS12550 WP 010873252.1
NTDB id 227965 B6N60 RS07285 WP 190607035.1
NTDB id 1417 SGL RS04200 WP 014407071.1
NTDB id 1047 HON27 RS03110 WP 000389061.1
consensus



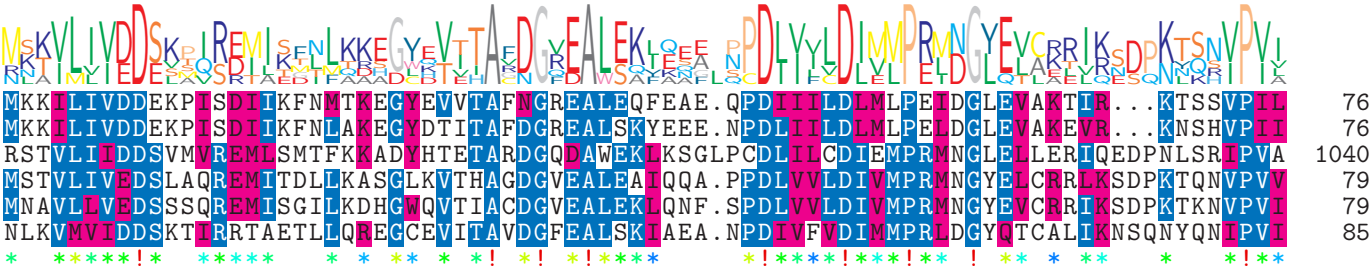
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NTDB id 413 AAK55817.1 141..845()
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consensus



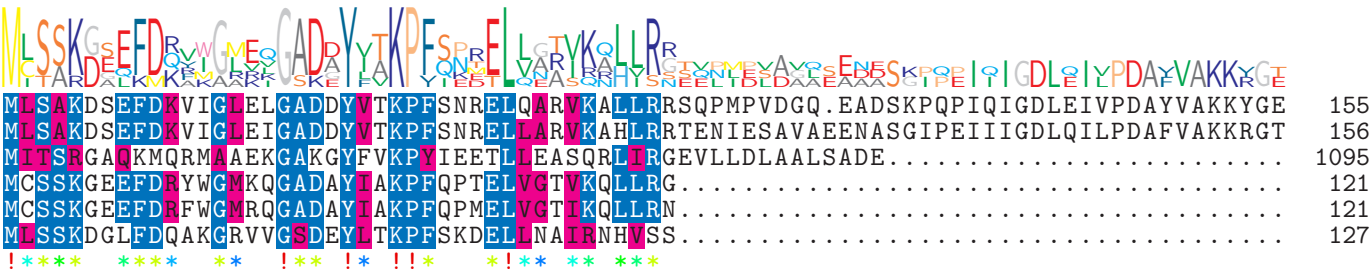
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consensus



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NTDB id 413 AAK55817.1 141..845()
NTDB id 374 SMU RS06885 WP 002262930.1
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NTDB id 1417 SGL RS04200 WP 014407071.1
NTDB id 1047 HON27 RS03110 WP 000389061.1
consensus



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NTDB id 413 AAK55817.1 141..845()	EYELTHREFELLYHLASHTGQVMTREHLLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYMRSYD	234
NTDB id 374 SMU RS06885 WP 002262930.1	ELDLTHREFELLYHLASHTGQVITREHLLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYMRNNA*	235
NTDB id 1419 SGL RS12550 WP 010873252.1	EVELTHREFELLHHLATHTGQVMTREHLLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYMKSVD.	1095
NTDB id 227965 B6N60 RS07285 WP 190607035.1		121
NTDB id 1417 SGL RS04200 WP 014407071.1		121
NTDB id 1047 HON27 RS03110 WP 000389061.1		127
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved