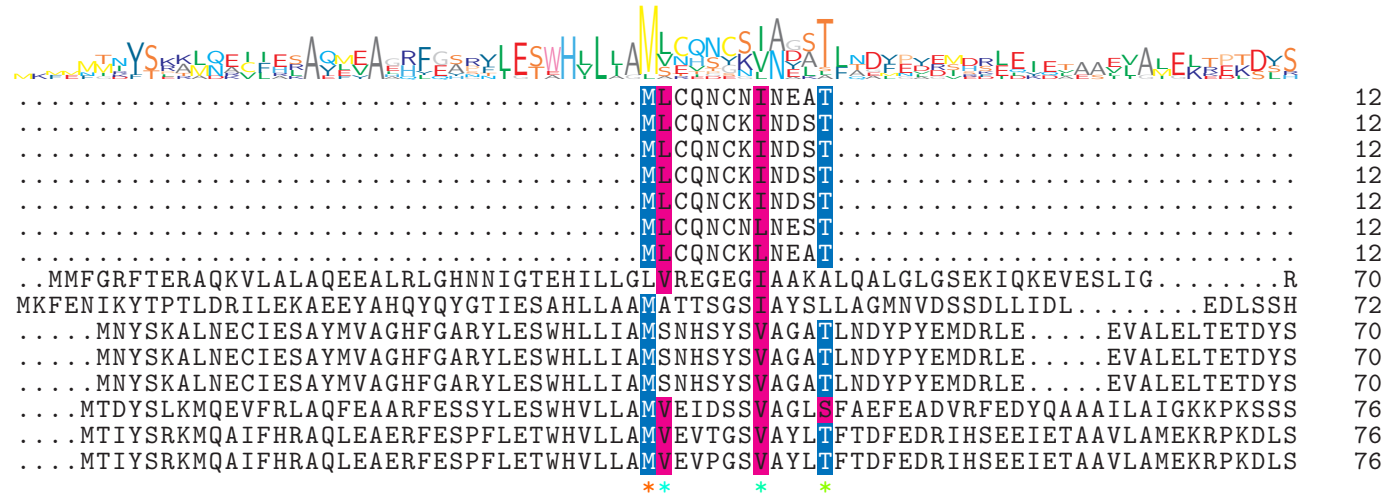


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NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 281 KZH43 RS03550 WP 000882517.1
NTDB id 245 SPD RS03860 WP 000882517.1
NTDB id 243 SPR RS03635 WP 000882517.1
NTDB id 241 SP RS04015 WP 000882523.1
NTDB id 1038032 ACB339 RS06185 WP 011054709.1
NTDB id 378 SMU RS02690 WP 002263569.1
NTDB id 85 BSU 00860 NP 387967.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 290 KZH43 RS10025 WP 001109677.1
NTDB id 289 SPD RS10700 WP 001109677.1
NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 377 SMU RS09275 WP 002262344.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

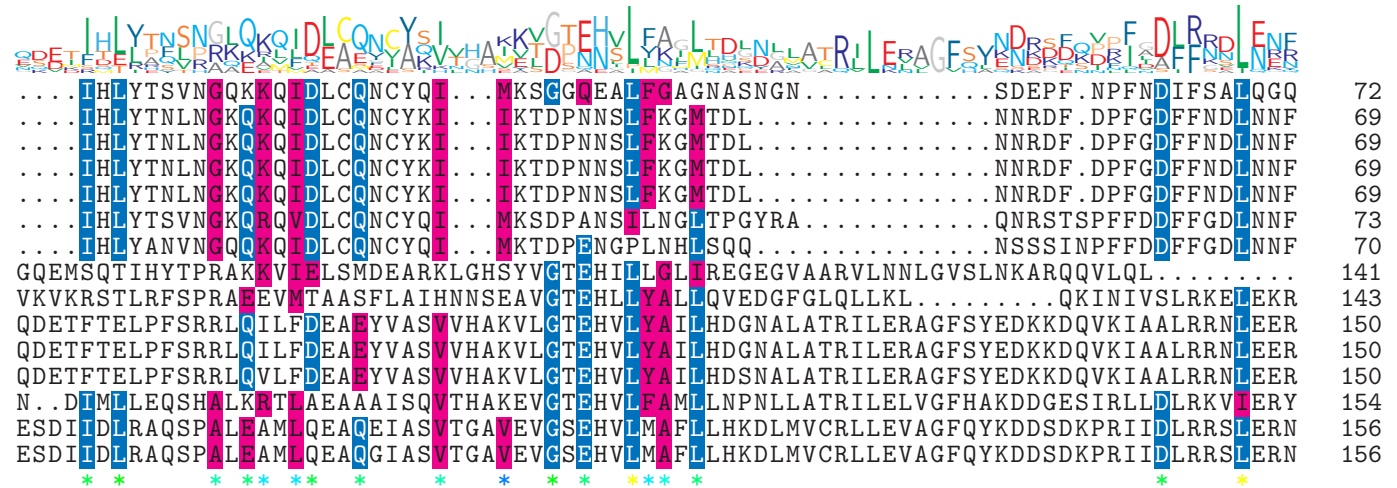
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NTDB id 601 KW2 RS02615 WP 021036805.1
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NTDB id 85 BSU 00860 NP 387967.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 290 KZH43 RS10025 WP 001109677.1
NTDB id 289 SPD RS10700 WP 001109677.1
NTDB id 287 SP RS11210 WP 001109712.1
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NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

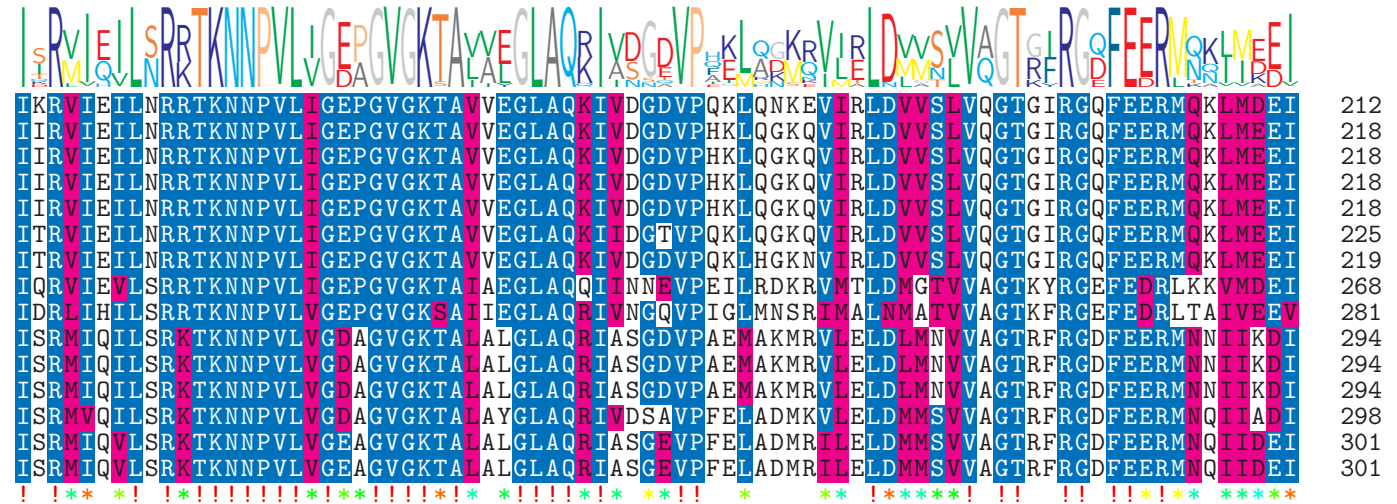
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NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 281 KZH43 RS03550 WP 000882517.1
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NTDB id 243 SPR RS03635 WP 000882517.1
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NTDB id 290 KZH43 RS10025 WP 001109677.1
NTDB id 289 SPD RS10700 WP 001109677.1
NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 377 SMU RS09275 WP 002262344.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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NTDB id 601 KW2 RS02615 WP 021036805.1
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NTDB id 243 SPR RS03635 WP 000882517.1
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NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 377 SMU RS09275 WP 002262344.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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NTDB id	601	KW2	RS02615	WP	021036805.1	GAPPGYVGYDEAGQLTEKVRNKPYSYLILLDEVEKAHPDVFNMLLQVLDDGRLTDSQGRTVDFKNTIIIMTSNLGATKLR	601
NTDB id	281	KZH43	RS03550	WP	000882517.1	GAPPGYVGYDEAGQLTEKVRHN	607
NTDB id	245	SPD	RS03860	WP	000882517.1	GAPPGYVGYDEAGQLTEKVRHN	607
NTDB id	243	SPR	RS03635	WP	000882517.1	GAPPGYVGYDEAGQLTEKVRHN	607
NTDB id	241	SP	RS04015	WP	000882523.1	GAPPGYVGYDEAGQLTEKVRHN	607
NTDB id	1038032	ACB339	RS06185	WP	011054709.1	GAPPGYVGYDEAGQLTEQVRRN	614
NTDB id	378	SMU	RS02690	WP	002263569.1	GAPPGYVGYDEAGQLTEKVRN	608
NTDB id	85	BSU	00860	NP	387967.1	GSPPGYVGYDEGGQLTEKVRNK	667
NTDB id	610	V4T04	RS10165	WP	012897346.1	GAPPGYVGYDEGGQLTEKVRNK	676
NTDB id	290	KZH43	RS10025	WP	001109677.1	GAPPGYVGYDEGGELTEKVRNK	671
NTDB id	289	SPD	RS10700	WP	001109677.1	GAPPGYVGYDEGGELTEKVRNK	671
NTDB id	287	SP	RS11210	WP	001109712.1	GAPPGYVGYDEGGELTEKVRNK	671
NTDB id	377	SMU	RS09275	WP	002262344.1	GAPPGYVGYDEGGELTEKVRNK	674
NTDB id	297	STER	RS00545	WP	011680614.1	GAPPGYVGYDEGGELTEKVRNK	677
NTDB id	329	STU	RS10020	WP	011225298.1	GAPPGYVGYDEGGELTEKVRNK	677
consensus						!*!!!!!!!!*!*!*!!!!*!! !!!**!*!*!*!!!!!!* * !*!*?! *!! !! ! !* ***!!!!!! !	

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NTDB id	601	KW2	RS02615	WP	021036805.1	EASVGFGAAREG....RTKSVLGQLGDFFSPEFMNRFDGIEFSALESKENLLKIVDLMIDEVNEQIGRNDIHLSTQAA	676
NTDB id	281	KZH43	RS03550	WP	000882517.1	EASVGFGAAREG....RTNSVLGELGNFFSPEFMNRFDGIEFKALS	682
NTDB id	245	SPD	RS03860	WP	000882517.1	EASVGFGAAREG....RTNSVLGELGNFFSPEFMNRFDGIEFKALS	682
NTDB id	243	SPR	RS03635	WP	000882517.1	EASVGFGAAREG....RTNSVLGELGNFFSPEFMNRFDGIEFKALS	682
NTDB id	241	SP	RS04015	WP	000882523.1	EASVGFGAAREG....RTNSVLGELGNFFSPEFMNRFDGIEFKALS	682
NTDB id	1038032	ACB339	RS06185	WP	011054709.1	EASVGFGAAREG....RTSSVLGELSNFFSPEFMNRFDGIEFKALS	689
NTDB id	378	SMU	RS02690	WP	002263569.1	EANVGFGASREG....RTNSVLGELGNFFSPEFMNRFDGIEFQALS	683
NTDB id	85	BSU	00860	NP	387967.1	NKYVGFNVQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIVFHS	747
NTDB id	610	V4T04	RS10165	WP	012897346.1	DKTVGFGAKNITADYSAMKSRILEELKRHYRPEFLNRIDENIVFHS	756
NTDB id	290	KZH43	RS10025	WP	001109677.1	DKTVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHS	751
NTDB id	289	SPD	RS10700	WP	001109677.1	DKTVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHS	751
NTDB id	287	SP	RS11210	WP	001109712.1	DKTVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHS	751
NTDB id	377	SMU	RS09275	WP	002262344.1	DKTVGFGAKSFSQDYKAMESRIILEELKKVYRPEFINRIDEKVVFH	754
NTDB id	297	STER	RS00545	WP	011680614.1	DKTVGFGAQTISHNHQAMQARIMEELKKSYPPEFINRIDEKVVFHS	757
NTDB id	329	STU	RS10020	WP	011225298.1	DKTVGFGAQTISHNHQAMQARIMEELKKSYPPEFINRIDEKVVFHS	757
consensus						* * !!!!!* ** *! * !!!!! ! * ! !* * * *! *!* * ** * * *	

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X non conserved
X similar
X ≥ 50% conserved