

logo

NTDB id 146 SP RS08570 WP 000614538.1
NTDB id 216 SPD RS08205 WP 000614552.1
NTDB id 182 SPR RS07820 WP 000614552.1
NTDB id 257 KZH43 RS07655 WP 220041236.1
NTDB id 467 HSISS4 RS06915 WP 021143821.1
NTDB id 1136629 DQL59 RS05450 WP 111681221.1
NTDB id 384 SMU RS02325 WP 002263039.1
consensus



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logo

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logo

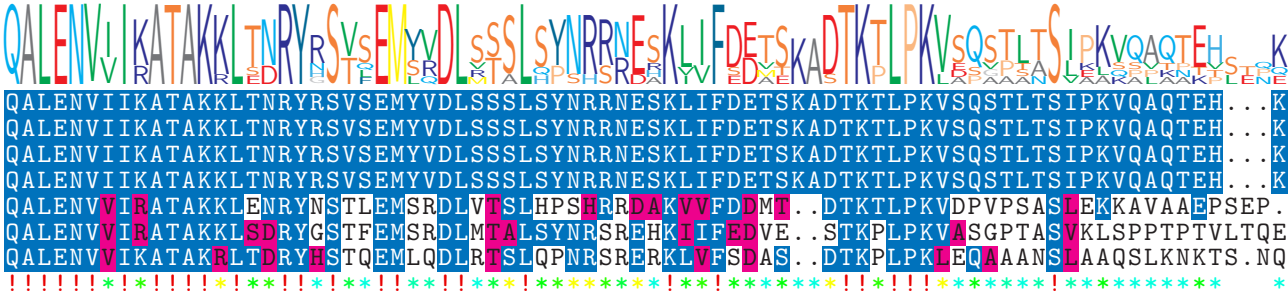
NTDB id 146 SP RS08570 WP 000614538.1
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consensus
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[illegible]

Sequence	Position
EAGTVLKQSLPEGTTTDL	1-10
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	11-40
EAGTVLKQSLPEGTTTDL	41-50
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	51-80
EAGTVLKQSLPEGTTTDL	81-90
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	91-120
EAGTVLKQSLPEGTTTDL	121-130
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	131-160
EAGTVLKQSLPEGTTTDL	161-170
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	171-200
EAGTVLKQSLPEGTTTDL	201-210
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	211-240
EAGTVLKQSLPEGTTTDL	241-250
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	251-280
EAGTVLKQSLPEGTTTDL	281-290
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	291-320
EAGTVLKQSLPEGTTTDL	321-330
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	331-360
EAGTVLKQSLPEGTTTDL	361-370
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	371-400
EAGTVLKQSLPEGTTTDL	401-410
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	411-440
EAGTVLKQSLPEGTTTDL	441-450
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EAGTVLKQSLPEGTTTDL	481-490
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	491-520
EAGTVLKQSLPEGTTTDL	521-530
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	531-560
EAGTVLKQSLPEGTTTDL	561-570
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	571-600
EAGTVLKQSLPEGTTTDL	601-610
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	611-640
EAGTVLKQSLPEGTTTDL	641-650
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	651-680
EAGTVLKQSLPEGTTTDL	681-690
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	691-720
EAGTVLKQSLPEGTTTDL	721-730
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	731-760
EAGTVLKQSLPEGTTTDL	761-770
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	771-800
EAGTVLKQSLPEGTTTDL	801-810
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	811-840
EAGTVLKQSLPEGTTTDL	841-850
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	851-880
EAGTVLKQSLPEGTTTDL	881-890
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EAGTVLKQSLPEGTTTDL	921-930
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	931-960
EAGTVLKQSLPEGTTTDL	961-970
TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	971-1000

logo

NTDB id 146 SP RS08570 WP 000614538.1	GMVVEQSPRAGEKVDLNKTRVKISIIYKPKTTSATP	659
NTDB id 216 SPD RS08205 WP 000614552.1	GMVVEQSPRAGEKVDLNKTRVKISIIYKPKTTSATP	659
NTDB id 182 SPR RS07820 WP 000614552.1	GMVVEQSPRAGEKVDLNKTRVKISIIYKPKTTSATP	659
NTDB id 257 KZH43 RS07655 WP 220041236.1	GMVVEQSPRAGEKVDLNKTRVKISIIYKPKTTSATP	659
NTDB id 467 HSISS4 RS06915 WP 021143821.1	..STETSTE.....THIELQ	624
NTDB id 1136629 DQL59 RS05450 WP 111681221.1	..NTELSPE.....TTAQTP	632
NTDB id 384 SMU RS02325 WP 002263039.1	..STSSSA.....TTTSH.	616
consensus	*****!*****!*****	

- non conserved
- similar
- ≥ 50% conserved