


```
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 1116153 SP119 RS07050 WP 010922538.1
NTDB id 384 SMU RS02325 WP 002263039.1
consensus
```

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NTDB id 146 SP RS08570 WP 000614538.1
NTDB id 216 SPD RS08205 WP 000614552.1
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consensus

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NTDB id 1116153 SP119 RS07050 WP 010922538.1
NTDB id 384 SMU RS02325 WP 002263039.1
consensus

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[illegible]

Sequence	Position 1	Position 2	Position 3	Position 4	Position 5	Position 6	Position 7	Position 8	Position 9	Position 10	Position 11	Position 12	Position 13	Position 14	Position 15	Position 16	Position 17	Position 18	Position 19	Position 20	Position 21	Position 22	Position 23	Position 24	Position 25	Position 26	Position 27	Position 28	Position 29	Position 30	Position 31	Position 32	Position 33	Position 34	Position 35	Position 36	Position 37	Position 38	Position 39	Position 40	Position 41	Position 42	Position 43	Position 44	Position 45	Position 46	Position 47	Position 48	Position 49	Position 50	Position 51	Position 52	Position 53	Position 54	Position 55	Position 56	Position 57	Position 58	Position 59	Position 60	Position 61	Position 62	Position 63	Position 64	Position 65	Position 66	Position 67	Position 68	Position 69	Position 70	Position 71	Position 72	Position 73	Position 74	Position 75	Position 76	Position 77	Position 78	Position 79	Position 80	Position 81	Position 82	Position 83	Position 84	Position 85	Position 86	Position 87	Position 88	Position 89	Position 90	Position 91	Position 92	Position 93	Position 94	Position 95	Position 96	Position 97	Position 98	Position 99	Position 100
EAGTVLKQSLPEGTTYDLSKA	TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	544																																																																																																		
EAGTVLKQSLPEGTTYDLSKA	TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	544																																																																																																		
EAGTVLKQSLPEGTTYDLSKA	TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	544																																																																																																		
EAGTVLKQSLPEGTTYDLSKA	TQIVLTVAKKATTIQLGNYIGRNSTEVISELKQKKVPENLIKIEE	544																																																																																																		
EEGEILSQQSPGKNSFNPDKSKAKIKFRVATP.KIVTMPDVTGLTVSTAVQTNRKNISSSSTEYHDYNTGAK.LDKAK	553																																																																																																			
PENTVISIQSSPSACGDKFNPNG.KSKITLSVAVS.DTITMPMVTEYSYADAVNTITALGIDASRIKAYVPSSSSSATGFVPIH	556																																																																																																			
SCGTVIGSSPKPKGKTYHPSS.DKKITLKVVV...KVTMPNLKNSTYEAESTITAMGISSRIKAYKADSDYS...SEIS	546																																																																																																			

SESEP GTIMKQSPGAGTT YDVS KPTQLVLTVAKKVT SVAMP SYIGSSSLEFTKNNL IQIVGIKEANI EWVEVTTAPAGSV E
IPSSSTEI.LYQDPQAG...TSVDGT VILYVSVATASSSLQSSSSSTT...HSS.....STSSSTDTSTSS.. 624

SESEP GTIMKQSPGAGTT YDVS KPTQLVLTVAKKVT SVAMP SYIGSSSLEFTKNNL IQIVGIKEANIEVVETTTAPAGSV E 624

SESEP GTIMKQSPGAGTT YDVS KPTQLVLTVAKKVT SVAMP SYIGSSSLEFTKNNL IQIVGIKEANIEVVETTTAPAGSV E 624

SESEP GTIMKQSPGAGTT YDVS KPTQLVLTVAKKVT SVAMP SYIGSSSLEFTKNNL IQIVGIKEANIEVVETTTAPAGSV E 624

IPSSSTEI.LYQDPQAG...TSVDGT VILYVSVATASSSLQSSSSSTT...HSS.....STSSSTDTSTSS.. 611

SPSSSKAIVSG QSPYYG TSLSLSDKG EISLYLYPEETHSSSSSSSTSS...SNS.....SSIND STAPGCSN.. 619

SPSSSSLVVGQSPYYGNTVSLNSND DIILYVSTSGGSHSGSSSSESN...SEG.....TTSSE....AS.. 604

!!*****!*!*!*!*!*****!*!*!*!*!*****!*!*!*!*!*****!*!*!*!*!*****!*!*!*!*!*****!*!*!*!*!*****!

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	...TETSTEAE.....THIELQ	624
NTDB id 1116153 SP119 RS07050 WP 010922538.1	...TELSPSE.....TTSQTP	632
NTDB id 384 SMU RS02325 WP 002263039.1	...TSSSSA.....TTSSH.	616
consensus	*****!*****!*****	

- non conserved
- similar
- ≥ 50% conserved