

```

NTDB id 619 LCA RS06470 WP 011374999.1
NTDB id 32 MW RS07995 WP 000472256.1
NTDB id 16 SA RS07765 WP 000472256.1
NTDB id 588 KW2 RS10845 WP 051303741.1
NTDB id 460 GPW51 RS00790 WP 011921720.1
NTDB id 502 SM12261 RS00955 WP 000738641.1
NTDB id 530 SMSK321 RS09230 WP 000738643.1
NTDB id 206170 BOC71 RS10295 WP 000738650.1
NTDB id 272 KZH43 RS09255 WP 000738626.1
NTDB id 231 SPD RS09885 WP 000738626.1
NTDB id 197 SPR RS09420 WP 000738626.1
NTDB id 162 SP RS10370 WP 000738627.1
NTDB id 431 SGO RS09410 WP 012130940.1
NTDB id 396 FSA28 RS09395 WP 002263437.1
NTDB id 387 SMU RS09025 WP 002263437.1
consensus

```

Position	Sequence	Accession
1	M	65
2	S	68
3	K	68
4	A	68
5	L	68
6	S	68
7	L	68
8	V	68
9	K	68
10	I	68
11	H	68
12	R	68
13	G	68
14	L	68
15	C	68
16	Q	68
17	K	68
18	Q	68
19	K	68
20	A	68
21	F	68
22	T	68
23	L	68
24	I	68
25	E	68
26	M	68
27	L	68
28	V	68
29	L	68
30	I	68
31	I	68
32	S	68
33	I	68
34	L	68
35	L	68
36	F	68
37	V	68
38	F	68
39	N	68
40	L	68
41	T	68
42	Q	68
43	K	68
44	E	68
45	A	68
46	V	68
47	N	68
48	D	68
49	K	68
50	G	68
51	K	68
52	A	68
53	A	68
54	V	68
55	K	68
56	K	68
57	V	68
58	V	68
59	S	68
60	E	68
61	S	68
62	Q	68
63	A	68
64	E	68
65	L	68
66	S	68
67	L	68
68	D	68
69	K	68
70	N	68
71	E	68
72	E	68
73	E	68
74	D	68
75	N	68
76	E	68
77	E	68
78	D	68
79	K	68
80	N	68
81	E	68
82	E	68
83	D	68
84	K	68
85	N	68
86	E	68
87	E	68
88	D	68
89	K	68
90	N	68
91	E	68
92	E	68
93	D	68
94	K	68
95	N	68
96	E	68
97	E	68
98	D	68
99	K	68
100	N	68

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NTDB id 231 SPD RS09885 WP 000738626.1
NTDB id 197 SPR RS09420 WP 000738626.1
NTDB id 162 SP RS10370 WP 000738627.1
NTDB id 431 SGD RS09410 WP 012130940.1
NTDB id 396 FSA28 RS09395 WP 002263437.1
NTDB id 387 SMU RS09025 WP 002263437.1
```

ASLSKLQADGRITEEQAKAYKEYHAKNGGANRKVND	99
SSIEDLIADGFIKEAQTCKSGETITIS.NGEAVAN	103
SSIEDLIADGFIKEAQTCKSGETITIS.NGEAVAN	103
PNLSSELLSAGMITCKQVTAAYDDYDQNKNEQRNFDD	116
ATVADLQAKGYITEKQAKQYATAKK.....	93
ASLSKLQADGRITEEQAKAYKEYHAKNGNTSQTIVAD.	107
ASLSKLQADGRITEEQAKAYNEYAKNGGANRKVND	108
ASLSKLQADGRITEEQAKAYKEYHDKNGVANRKVND	108
ASLRKLQADGRITEEQAKAYKEYHDKNGGANRKVND	108
ASLRKLQADGRITEEQAKAYKEYHDKNGGANRKVND	108
ASLRKLQADGRITEEQAKAYKEYHDKNGGANRKVND	108
ASLRKLQADGRITEEQAKAYKEYNDKNGGANRKVND	108
ATLSKLVAAGNISQKQADSYPKAYYGKNNSETQAVAN	105
ATLSKLVASGDITQEANSYKDDYAKHPSKTRHVN	104
ATLSKLVASGDITQEANSYKDDYAKHPSKTRHVN	104

- X non conserved
- X similar
- X > 50% conserved