

logo

NTDB id 114 BSU 16110 NP 389493.1
NTDB id 599 KW2 RS05940 WP 021037268.1
NTDB id 525 SMSK321 RS06295 WP 000705298.1
NTDB id 267 KZH43 RS05590 WP 000705306.1
NTDB id 226 SPD RS05990 WP 000705306.1
NTDB id 192 SPR RS05715 WP 000705306.1
NTDB id 157 SP RS06205 WP 000705306.1
NTDB id 497 SM12261 RS05565 WP 000705318.1
NTDB id 33525 SEQ RS05940 WP 012679593.1
NTDB id 407 SMU RS04605 WP 002262865.1
consensus

[illegible]

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Sequence	Residue 1	Residue 2	Residue 3	Residue 4	Residue 5	Residue 6	Residue 7	Residue 8	Residue 9	Residue 10	Residue 11	Residue 12	Residue 13	Residue 14	Residue 15	Residue 16	Residue 17	Residue 18	Residue 19	Residue 20	Residue 21	Residue 22	Residue 23	Residue 24	Residue 25	Residue 26	Residue 27	Residue 28	Residue 29	Residue 30	Residue 31	Residue 32	Residue 33	Residue 34	Residue 35	Residue 36	Residue 37	Residue 38	Residue 39	Residue 40	Residue 41	Residue 42	Residue 43	Residue 44	Residue 45	Residue 46	Residue 47	Residue 48	Residue 49	Residue 50	Residue 51	Residue 52	Residue 53	Residue 54	Residue 55	Residue 56	Residue 57	Residue 58	Residue 59	Residue 60	Residue 61	Residue 62	Residue 63	Residue 64	Residue 65	Residue 66	Residue 67	Residue 68	Residue 69	Residue 70	Residue 71	Residue 72	Residue 73	Residue 74	Residue 75	Residue 76	Residue 77	Residue 78	Residue 79	Residue 80	Residue 81	Residue 82	Residue 83	Residue 84	Residue 85	Residue 86	Residue 87	Residue 88	Residue 89	Residue 90	Residue 91	Residue 92	Residue 93	Residue 94	Residue 95	Residue 96	Residue 97	Residue 98	Residue 99	Residue 100	Accession
YPKLPRVLAAYRE	Q	G	I	N	T	I	P	I	S	S	K	Q	Y	P	F	W	L	K	S	I	Y	D	P	P	A	V	L	F	A	K	G	D	M	T	L	L	S	K	G	R	K	I	G	I	V	C	T	P	N	P	I	A	Y	C	K	Q	V	V	N	H	L	T	K	E	I	C	R	K	G	W	V	I	144																												
...	Y	K	K	F	S	S	F	S	I	L	D	D	C	Y	P	W	L	S	I	Y	D	P	P	A	V	L	F	A	K	G	D	M	T	L	L	S	K	G	R	K	I	G	I	V	C	T	P	N	P	I	A	Y	C	K	Q	V	V	N	H	L	T	K	E	I	C	R	K	G	W	V	I	147																													
...	F	K	K	I	P	S	F	S	I	L	D	D	C	Y	P	W	L	S	I	Y	D	P	P	A	V	L	F	A	K	G	D	M	T	L	L	S	K	G	R	K	I	G	I	V	C	T	P	N	P	I	A	Y	C	K	Q	V	V	N	H	L	T	K	E	I	C	R	K	G	W	V	I	148																													
...	F	Q	K	F	S	F	S	I	L	D	D	C	Y	P	W	L	S	I	Y	D	P	P	A	V	L	F	A	K	G	D	M	T	L	L	S	K	G	R	K	I	G	I	V	C	T	P	N	P	I	A	Y	C	K	Q	V	V	N	H	L	T	K	E	I	C	R	K	G	W	V	I	149																														
...	F	Q	K	F	S	F	S	I	L	D	D	C	Y	P	W	L	S	I	Y	D	P	P	A	V	L	F	A	K	G	D	M	T	L	L	S	K	G	R	K	I	G	I	V	C	T	P	N	P	I	A	Y	C	K	Q	V	V	N	H	L	T	K	E	I	C	R	K	G	W	V	I	150																														
...	F	Q	K	F	S	F	S	I	L	D	D	C	Y	P	W	L	S	I	Y	D	P	P	A	V	L	F	A	K	G	D	M	T	L	L	S	K	G	R	K	I	G	I	V	C	T	P	N	P	I	A	Y	C	K	Q	V	V	N	H	L	T	K	E	I	C	R	K	G	W	V	I	151																														
...	F	Q	K	F	S	F	S	I</																																																																																													

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VSGLAKGIDTAAHMAALQNGGKTI	AVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRI	IAGLCRGVIVAE	229
VSGLAKGIDTAHSLAIKTKPT	IAVIGTGLDIFYPLENKKIQEYLAQYLVSEYSLGKPLKVFHFPARNRI	IAGLCRGVIVAE	222
VSGLAKGIDTAAHMAALQNGGKTI	AVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRI	IAGLCRGVIVAE	223
VSGLAKGIDTAAHMAALQNGGKTI	AVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRI	IAGLCRGVIVAE	223
VSGLAKGIDTAAHMAALQNGGKTI	AVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRI	IAGLCRGVIVAE	223
VSGLAKGIDTAAHMAALQNGGKTI	AVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRI	IAGLCRGVIVAE	223
VSGLAKGIDTAAHMAALQNGGKTI	AVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRI	IAGLCRGVIVAE	223
VSGLAKGIDTAHSLAHLACLKAGGQT	IAVIGTGLDRYYPKENHQLQEFLSQRHLVLSEYGAEEALS	YHFPERNRIIAGLSRGVLVVE	221
ISGLARGIDTAHSLKSGGAT	IAVIGTGLDVHYPKENRRLQDYIAKNHL	LLSEYEAQSQPLKYHFPERNRIIAGLSQGVMAAE	221

logo



 non conserved
 similar
 ≥ 50% conserved