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NTDB id 1186 GTF74 RS01320 WP 000788426.1
NTDB id 1175 A1552VC RS12105 WP 000788426.1
NTDB id 1408 DSB67 RS13980 WP 010643500.1
NTDB id 1381 A4U84 RS02010 WP 021113424.1
NTDB id 70725 K6J65 RS03395 WP 011272046.1
NTDB id 1373 NTHI RS02645 WP 011272046.1
NTDB id 1347 HI 0435 AAC22094.1
consensus

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ELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPSTQLVVTVDGEFQHDYTLTKGKYLEVVISK.LKADEKPKPKSVLEKE 155
ELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPSTQLVVTVDGEFQHDYTLTKGKYLEVVISK.LKADEKPKPKSVLEKE 155
DLNNTSVKDDQLYLLDVKDFSTTVESVEVFRDTSSTRLVAYIDEDYSHDYRLTGRLYEIVKVGK.LKANEKAPDKSILDKE 156
.....MRYLFLLF FAF.....PVLA 16
.....MKKYFLKCGYFLVCFCLPLIVFAN.....PKTD 28
.....MKKYFLKCGYFLVCFCLPLIVFAN.....PKTD 28
.....MKKYFLKCGYFLVCFCLPLIVFAN.....PKTD 28

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consensus
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[illegible]

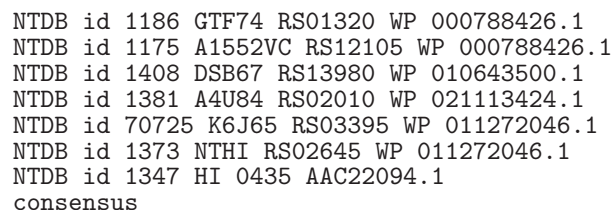
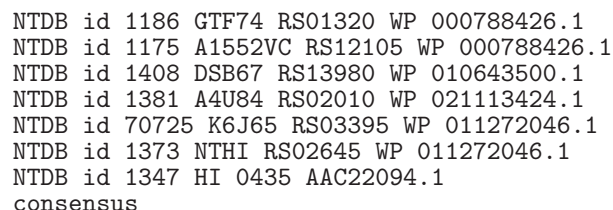
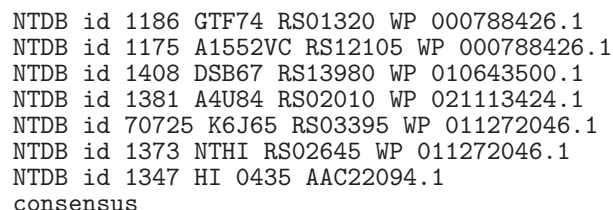
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Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83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

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consensus



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