

```

NTDB id 1193 PAKAF RS26665 WP 003161249.1
NTDB id 1009 ACIAD RS15175 WP 004923730.1
NTDB id 88490 OCUAc17 RS01595 WP 002116833.1
NTDB id 1052 ABD1 RS15850 WP 001017033.1
NTDB id 1039 HON27 RS01460 WP 031993779.1
consensus

```

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
1	M	N	H	V	R	Q	F	S	M	G	A	V	A	I	A	I	M	Q	V	A	S	A	Q	V	S	M	T	N	I	V	P	M	Q	I	A	G	G	T	E	I	R	V	M	F	N	G	L	P	P	Q	P	Q	A	Y	Q	L	E	N	P	S	R	L	I	L	D	F	D	K	A	Q	Q	G	K	L	K	Q	S	K	I																					
2	K	Q	G	T	S	R	L	G	I	A	L	L	A	A	M	F	A	P	I	L	L	A	A	A	T	E	K	L	D	V	A	A	L	P	G	D	R	V	E	L	K	L	Q	F	D	E	P	V	A	A	P	R	G	T	T	E	I	Q	A	I	A	L	L	N	G	V	G	N	L	A	K	K	L	R																										
3	M	N	S	G	L	S	R	L	G	I	A	L	L	A	A	M	F	A	P	A	L	L	A	A	D	L	E	K	L	D	V	A	A	L	P	G	D	R	V	E	L	K	L	Q	F	D	E	P	V	A	A	P	R	G	T	T	E	I	Q	P	A	R	I	A	L	D	L	P	G	V	Q	N	K	L	G	T	K	N	R																					
4	M	K	Q	I	I	R	Q	F	S	I	G	T	V	A	Y	A	I	M	Q	V	A	S	A	Q	V	A	I	T	N	V	P	M	Q	I	P	G	Q	G	T	E	I	R	V	M	F	N	G	L	P	P	Q	P	Q	A	Y	Q	L	E	Q	P	A	R	L	I	L	D	F	D	K	A	Q	G	K	L	A	K	S	L	I																					
5	M	N	H	V	R	Q	F	S	M	G	A	V	A	I	A	I	M	Q	V	A	S	A	Q	V	S	M	T	N	I	V	P	M	Q	I	A	G	G	T	E	I	R	V	M	F	N	G	L	P	P	Q	P	Q	A	Y	Q	L	E	N	P	S	R	L	I	L	D	F	N	K	A	Q	Q	N	L	I	Q	S	K	V																						
6	M	N	H	V	R	Q	F	S	M	G	A	V	A	I	A	I	M	Q	V	A	S	A	Q	V	S	M	T	N	I	V	P	M	Q	I	A	G	G	T	E	I	R	V	M	F	N	G	L	P	P	Q	P	Q	A	Y	Q	L	E																																											

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consensus

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Position	Sequence	Score
1	ELISVGNT	159
2	SVT	141
3	SVT	140
4	SVT	140
5	SVT	140
6	SVT	140
7	SVT	140
8	SVT	140
9	SVT	140
10	SVT	140
11	SVT	140
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13	SVT	140
14	SVT	140
15	SVT	140
16	SVT	140
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18	SVT	140
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20	SVT	140
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118	SVT	140
119	SVT	140
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121	SVT	140
122	SVT	140
123	SVT	140
124	SVT	140
125		

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[illegible]

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logo

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consensus



453
451
459
459
459

logo

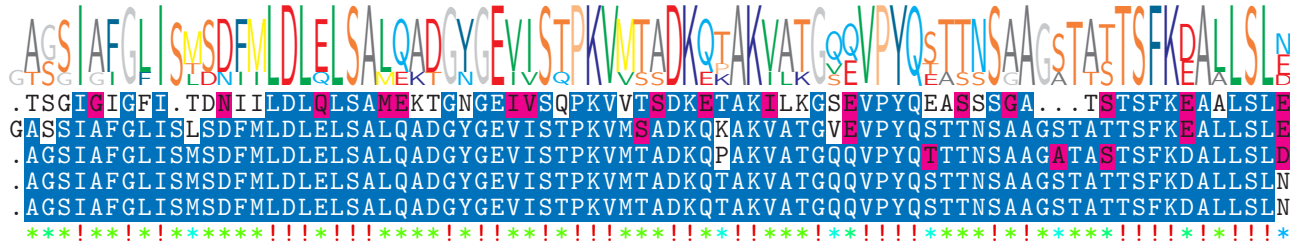
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consensus



528
520
533
533
533

logo

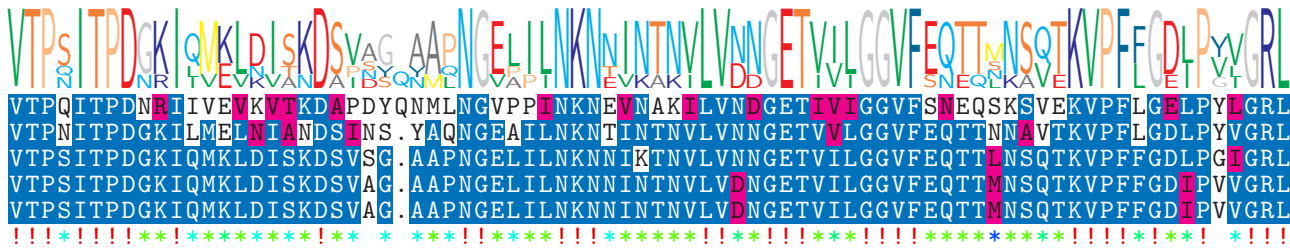
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consensus



603
600
612
612
612

logo

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consensus



683
679
691
691
691

logo

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consensus



714
709
721
721
721

 non conserved
 similar
 $\geq 50\%$ conserved