

Sequencing coverage for mutant-ABTLA light chain

Contig	After homology matching to true protein sequence (for validation purposes only)																			
	D	I	E	M	S	Q	S	P	S	S	L	A	V	S	A	G	E	K	V	T
13	D	I	E	M	S	Q	S	P	S	S	L	A	V	S	A	G	E	K	V	T
13	D	I	E	M	S	Q	S	P	S	S	L	A	V	S	A	G	E	K	V	T
13	N	S	R	T	R	K	N	Y	L	A	W	Y	Q	Q	K	P	G	Q	S	P
13	N	S	R	T	R	K	N	Y	L	A	W	Y	Q	Q	K	P	G	Q	S	P
13	E	S	G	V	P	D	R	F	T	G	S	G	S	G	T	D	F	T	L	T
13	E	S	G	V	P	D	R	F	T	G	S	G	S	G	T	D	F	T	L	T
13	V	Y	Y	C	K	Q	S	Y	N	L	P	T	F	G	S	G	T	K	V	E
13	V	Y	Y	C	K	Q	S	Y	N	L	P	T	F	G	S	G	T	K	V	E
13	S	I	F	P	P	S	S	S	E	Q	L	T	S	G	G	A	S	V	C	F
13	S	I	F	P	P	S	S	S	E	Q	L	T	S	G	G	A	S	V	C	F
13	V	K	W	K	I	D	G	S	E	R	Q	N	G	V	L	N	S	W	T	D
13	V	K	W	K	I	D	G	S	E	R	Q	N	G	V	L	N	S	W	T	D
13	S	S	T	L	T	L	T	K	D	E	Y	E	R	H	N	S	Y	T	C	E
13	S	S	T	L	T	L	T	K	D	E	Y	E	R	H	N	S	Y	T	C	E
13	V	K	S	F	N	R	N	E	C											
13	V	K	S	F	N	R	N	E	C											

With no knowledge of the true protein sequence

13	D	I	V	M	S	Q	S	P	S	S	L	A	V	S	A	G	E	K	V	T	M	S	C	K	S	C	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
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Confirmed modifications / mutations

Unconfirmed modifications / mutations

Amino acid groups (jumps)

Sequencing error

Non-covered regions



	S	S	I	F	P	P	S	S	E	Q	L	T	S	G	G	A	S	V	V	C	F	L	N	N	F	Y	P	K	D	I	N	
24		S		I		F		P		P		P		S		S		S		V		C		F								
14		S		I		F		P		P		P		S		S		S		V		C		F								
15		S		I		F		P		P		P		S		S		S		V		C		F								
162		S		I		F		P		P		P		S		S		S		V		C		F								
92		S		I		F		P		P		P		S		S		S		V		C		F								
81		S		I		F		P		P		P		S		S		S		V		C		F								
116		S		I		F		P		P		P		S		S		S		V		C		F								
5		S		I		F		P		P		P		S		S		S		V		C		F								
96		S		I		F		P		P		P		S		S		S		V		C		F								
145		S		I		F		P		P		P		S		S		S		V		C		F								
125		S		I		F		P		P		P		S		S		S		V		C		F								
166		S		I		F		P		P		P		S		S		S		V		C		F								
127		S		I		F		P		P		P		S		S		S		V		C		F								

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