

AbRSA: Improving Antibody Numbering by Region-specific Alignment

Antibody sequences in Figure 1.

>QueryH

EVQVVESGGGVVQPGRSLRLSCTASGFTFSNFAMGWVRQAPGKGLEWVAFISSDGSNKNYGDSVKGRFT
ISRDNSKNTVFLQMNSLRVEDTALYYCAKDVGDYKSDEWGTEYYDISISYPIQDPRAMVGAFDLWGQGT
MVTVSPAS

>QueryL

SYDLTQPPSVSVSPGQTASISCSGDKLDDKYVSWYYQRPGQSPVLLMYQDFKRPSGIPERLSGSKSGKTAT
LTISGTQSLDEGDYYCQAWDASTGVSGGGTKLTVLFGDGTRTLTVLGQPK

Table S1. The consensus sequence of heavy chain. Residues in a row are the most frequent residues at that position. The numbers highlighting in yellow at the first column indicates CDRs while the other indicate FRs. The numbers in red at the first column indicates the conserved positions (CPs). And the numbers in blue at the first column indicates the insertion positions (IPs).

Number	Amino acids of consensus sequence (Heavy chain)				
1	Q	E	D		
2	V	Q			
3	Q	K	H	S	T
4	L	V			
5	V	Q	L	E	K T
6	E	Q	A		
7	S	P	W		
8	G	E			
9	G	A	P	S	
10	G	E	D	V	
11	L	V			
12	V	K	L		
13	K	Q	R		
14	P	A			
15	G	S	T		
16	G	A	E	Q	R S D
17	S	T			
18	L	V			
19	R	K	S	T	
20	L	I	V	M	
21	S	T			
22	C				
23	A	K	T	V	S
24	A	V	T	G	I
25	S	T	Y		
26	G	E			
27	F	Y	G	D	S
28	T	S	I	N	D A
29	F	I	L	S	V
30	S	T	D	G	N R
31	S	D	N	G	T R

32	Y A F H N S V
33	A G W Y D L S T V F
34	M I W V L
35	A G H N S T Y
36	W
37	V I F
38	R K
39	Q
40	A P R S T M V
41	P A H
42	G E S
43	K Q R N
44	G A R S
45	L
46	E Q
47	W Y
48	I V K M
49	A G S
50	A Y D E F G W I V L T N S R
51	I V T M
52	S N Y D K I H G W R T
53	A D Y W G H I T S N R
54	A D F G K N T S
55	A D E G S T W Y
56	A D D G N S T W Y
57	T A I K N P S
58	Y N K D E F G H R S T
59	Y F
60	A N S P T V G
61	D E Q A S P
62	S K A W
63	F V L A
64	K Q R E
65	G S D N
66	R K Q
67	F V A L I
68	T S I
69	I L M V F
70	S T N
71	R V A K L P T
72	D N E
73	N T K D E S R
74	S A P D N
75	K S T A E I R Q N L
76	N S D K T
77	T Q S I M
78	L A V F
79	Y S F H T V
80	L M
81	Q E K D T
82	L M I V W
83	R T K
84	A S T V P
85	E A D G S V
86	D

87	T S
88	A G
89	V T I L M
90	Y
91	Y F
92	C
93	A T V
94	R K S T A G
95	A D E G H I L N P Q R S T V W Y
96	A D E F G H I K L N P Q R S T V W Y
97	A C D E F G I L N P R S T V W Y
98	A C D E F G I L N P R S T V W Y
99	A C D E F G I L N P Q R S T V W Y
100	A D E G L R S Y H I N P V W T
101	D A G E N
102	Y V I L F P H S
103	W
104	G
105	Q P R K A T
106	G
107	T V A I
108	L T M S Q P
109	V L I
110	T I V
111	V
112	S T
113	S A
114	S

Table S2. The consensus sequence of light chain. Residues in a row are the most frequent residues at that position. The numbers highlighting in yellow at the first column indicates CDRs while the other indicate FRs. The numbers in red at the first column indicates the conserved positions (CPs). And the numbers in blue at the first column indicates the insertion positions (IPs).

Numbering	Amino acids of consensus sequence (Light chain)							
1	D	Q	E	S	A	N		
2	I	S	A	V	Y	L	Q	P
3	V	Q	E	A	L	M	S	T
4	L	M	V					
5	T	S	A					
6	Q	S	T					
7	S	P	T	D	E			
8	P	A	S	H	T			
9	S	A	L	G	D	K		
10	S	T	I	F	P			
11	L	V	M	A				
12	S	A	P	T				
13	A	V	G	L	T	E		
14	S	A	T	N				
15	P	L	V	A	I			
16	G							
17	E	Q	D	K	A	G		
18	R	T	S	K	P	Q		
19	V	A	I					

20	T	S	R	K								
21	I	L	M									
22	S	T	N									
23	C											
24	R	S	T	K	Q	G						
25	A	G	S	L	T							
26	S	D	T	N	G							
27	Q	S	T	E	K	N	G	A				
28	S	G	D	N	L	I	A	T				
29	I	V	L	N	D	G	A	S	R			
30	S	V	I	L	N	Y	D	G	R	K	T	
31	N	S	T	Y	K	D	G	H	R			
32	Y	N	W	S	F	D	A	G	H	L	R	T
33	L	V	A	M	I							
34	A	N	S	H	Y	G	D	E	Q	C	T	
35	W											
36	Y	F	L	V	H							
37	Q	L	R									
38	Q	H	E									
39	K	R	H	L	I	V						
40	P	S										
41	G	D										
42	Q	K	T	S	E	G	H	R				
43	A	S	P	T	G	L	V					
44	P	F										
45	K	R	V	Q	T							
46	L	R	T	V	Y	F	G					
47	L	V	W	M	I							
48	I	V	M	L								
49	Y	S	F	K	G	H						
50	G	A	D	E	K	L	S	R	Y	W	N	Q
51	A	T	V	N	D	G	K	S				
52	S	N	T	D								
53	N	T	S	K	D	Q	R	Y	E			
54	R	L	G	S								
55	A	P	Q	E	F	G	H	D	Y			
56	S	T	P	D								
57	G											
58	V	I	T									
59	P	S										
60	D	S	A	E	N							
61	R											
62	F											
63	S	T	K									
64	G	A										
65	S											
66	G	K	N	R	S	I	L					
67	S	I										
68	G	A	S									
69	T	N	S	A	D							
70	D	T	S	E	K	Q	A					
71	F	A	Y									
72	T	S	A									
73	L	F										
74	T	K	A	G	S	N						

