

ES	RBD Residue (Range)	Amino Acid Sequences	Structural feature	ASA (Å ²)	Ab (H chain) (%)	Nb (%)
1	339-341	GEV	α -helix	155	0.78	0.16
2	343-349	NATRFAS	loop	455	4.07	2.83
3	351-357	YAWNRRKR	3,10 \rightarrow β -strand	410	2.60	3.76
4	368-374	LYNSASF	α -helix \rightarrow loop	469	3.17	7.03
5	375-380	STFKCY	β -strand	287	2.90	6.97
6	381-386	GVSPTK	Loop \rightarrow 3,10	381	2.49	5.50
7	403-409	RGDEVQR	3,10	321	2.76	4.68
8	411-417	APGQTGK	loop	342	4.91	2.78
9	420-428	DYNYKLPDD	α -helix \rightarrow loop	371	3.24	1.69
10	437-443	NSNNLDS	β -strand \rightarrow α -helix	378	3.59	1.47
11	444-449	KVGGNY	loop/strand	457	7.10	8.39
12	450-454	NYLYR	β -strand	194	4.57	5.72
13	455-460	LFRKSN	loop	448	9.98	4.25
14	462-467	KPFERD	loop	470	1.28	1.31
15	468-472	ISTEI	loop	384	2.44	4.47
16	473-479	YQAGSTP	β -strand \rightarrow loop	466	9.34	0.71
17	481-484	NGVE	loop	404	4.36	5.28
18	485-487	GFN	loop	275	7.06	3.65
19	488-491	CYFP	β -strand \rightarrow loop	181	5.98	5.88
20	492-496	LQSYG	β -strand	126	7.15	9.69
21	497-502	FQPTNG	loop	307	3.38	2.94
22	503-509	VGYQPYP	3,10 \rightarrow β -strand	253	2.42	4.14
23	516-520	ELLHA	loop	548	0.44	1.20