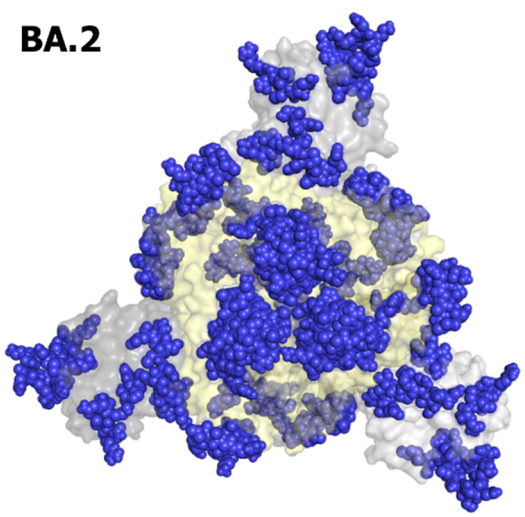
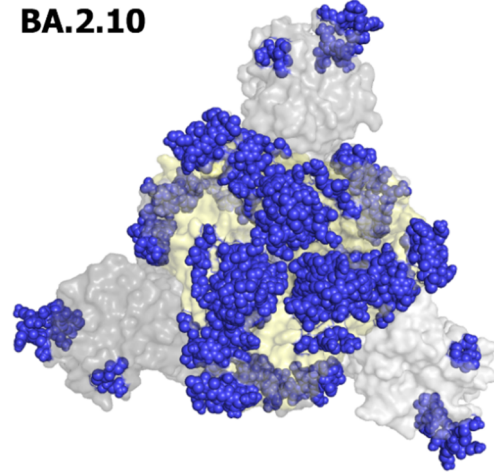
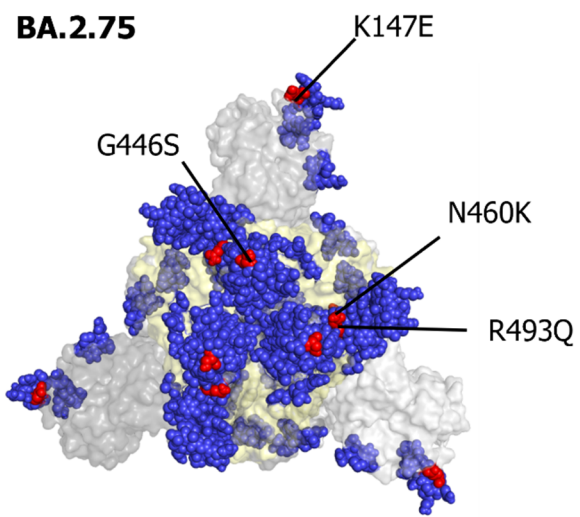
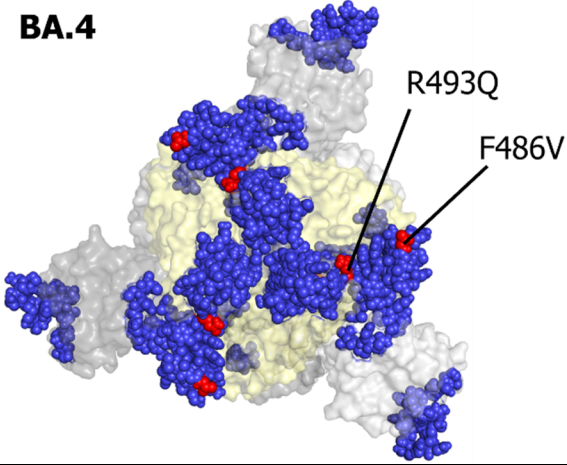
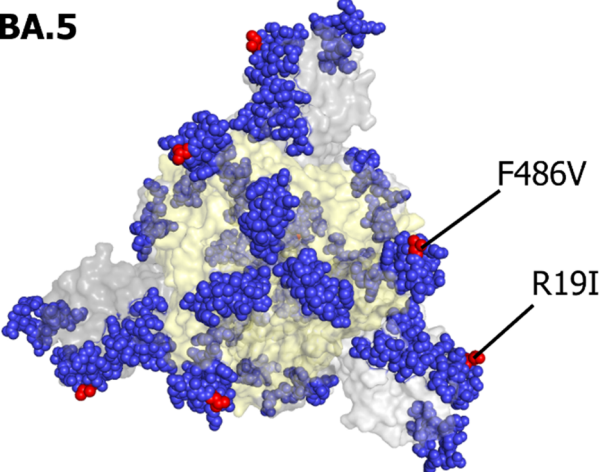
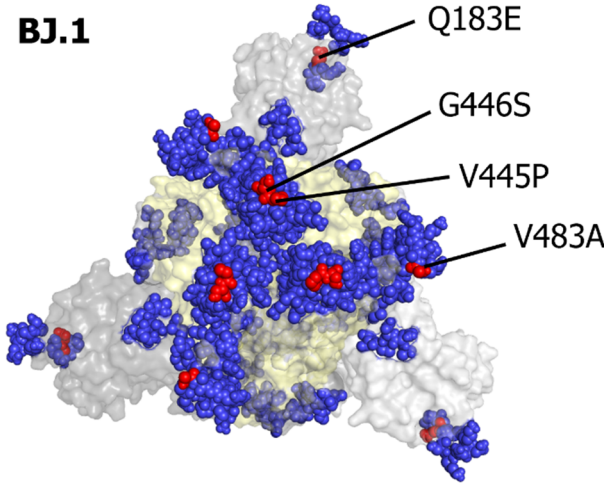
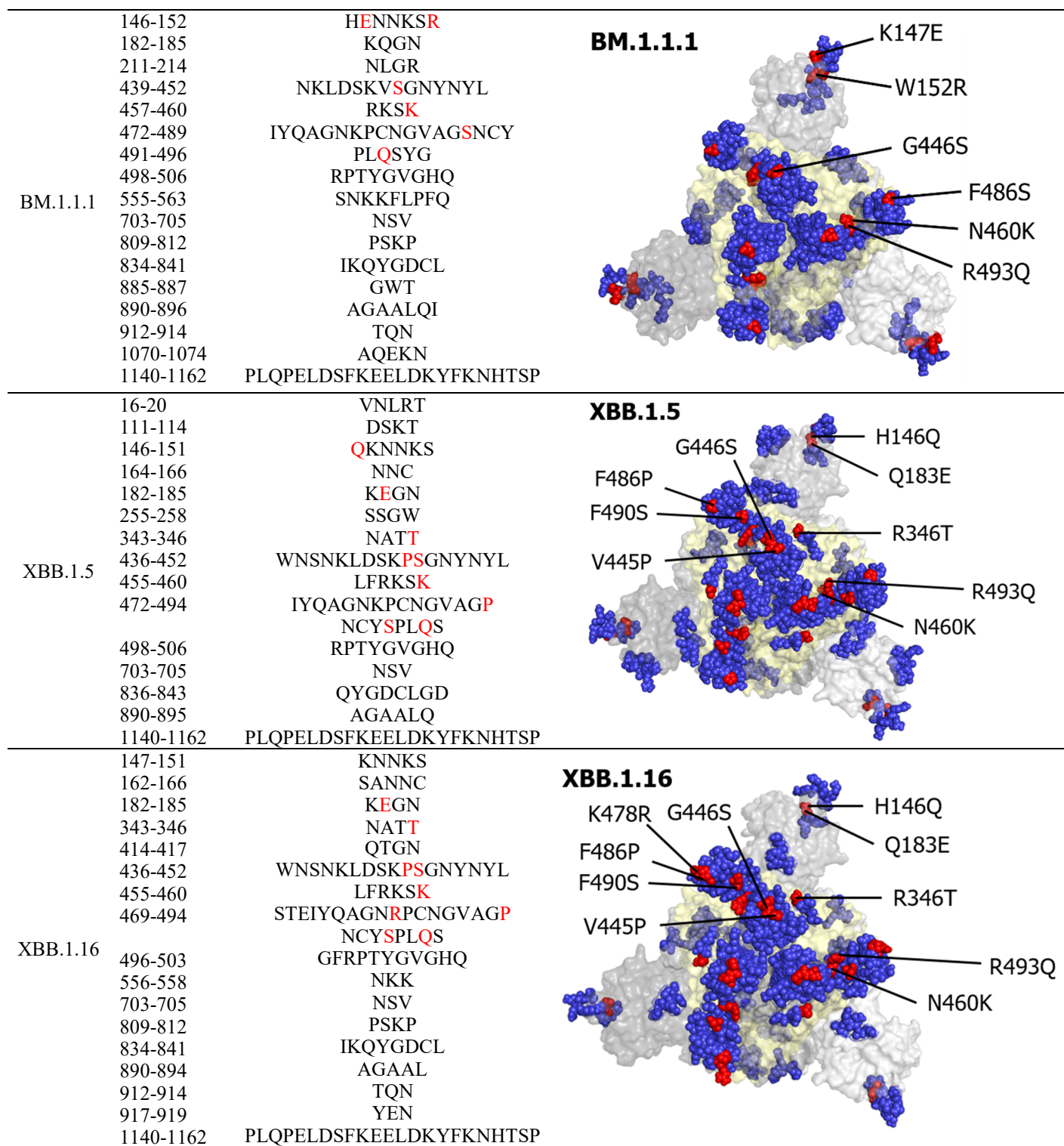


	Protein	Predicted epitopes	
BA.2	14-19	QCVNLR	<b>BA.2</b> 
	109114	TLDSKT	
	144-154	YYHKNNKSWME	
	160-169	YSSANNCTFE	
	177-185	MDLEGKQGN	
	436-452	WNSNKLDISKVGGNYNYL	
	458-460	KSN	
	474-488	QAGNKPCNGVAGFNC	
	493-496	RSYG	
	498-506	RPTYGVGHQ	
	553-563	TESNKKFLPFQ	
	582-584	LEI	
	703-705	NSV	
	809-812	PSKP	
	834-842	IKQYGDCLG	
	890-897	AGAALQIP	
	912-914	TQN	
	917-919	YEN	
	1140-1162	PLQPELDSFKEELDKYFKNHTSP	
BA.2.10	15-17	CVN	<b>BA.2.10</b> 
	146-151	HKNNKS	
	180-185	EGKQGN	
	343-346	NATR	
	415-417	TGN	
	436-452	WNSNKLDISKVGGNYNYL	
	455-460	LFRKSN	
	468-472	ISTEI	
	474-488	QAGNKPCNGVAGFNC	
	490-496	FPLRSYG	
	498-506	RPTYGVGHQ	
	553-563	TESNKKFLPFQ	
	703-705	NSV	
	809-812	PSKP	
	834-843	IKQYGDCLGD	
	890-895	AGAALQ	
	1140-1162	PLQPELDSFKEELDKYFKNHTSP	
BA.2.75	146-151	HENNKS	<b>BA.2.75</b> 
	172-175	SQPE	
	180-185	EGKQGN	
	343-346	NATR	
	415-417	YGN	
	436-452	WNSNKLDISKVSGNYNYL	
	455-460	LFRKSK	
	468-506	ISTEIQAGNKPCNGVAGFN	
		CYFPLQSYGFRPTYGVGHQ	
	555-561	SNKKFLP	
	703-705	NSV	
	808-813	DPSKPS	
	836-842	QYGDCLG	
	890-895	AGAALQ	
	912-914	TQN	
	917-919	YEN	
	1070-1074	AQEKNN	
	1140-1162	PLQPELDSFKEELDKYFKNHTSP	

BA.4	108-114	TTLDSKT	<b>BA.4</b>	
	142-152	DVYYHKNNKSW		
	164-167	NNCT		
	182-185	KQGN		
	254-256	SSS		
	415-417	TGN		
	437-450	NSNKLDSKVGGNYN		
	455-460	LFRKSN		
	468-494	ISTEIQAGNKPCNGVAGV		
		NCYFPLQS		
	497-506	FRPTYGVGHQ		
	703-705	NSV		
	836-841	QYGDCL		
	890-895	AGAALQ		
	1140-1162	PLQPELDSFKEELDKYFKNHTSP		
BA.5	14-17	QCVN	<b>BA.5</b>	
	19-21	ITR		
	109-114	TLDSKT		
	134-137	QFCN		
	145-152	YHKNNKSW		
	160-167	YSSANNCT		
	182-185	KQGN		
	254-259	SSSGWT		
	443-450	SKVGGNYN		
	457-460	RKSN		
	472-489	IYQAGNKPCNGVAGVNCY		
	496-506	GFRPTYGVGHQ		
	554-561	ESNKKFLP		
	703-705	NSV		
	809-812	PSKP		
	836-841	QYGDCL		
	890-897	AGAALQIP		
	912-914	TQN		
	917-919	YEN		
	1070-1074	AQEKD		
	1140-1162	PLQPELDSFKEELDKYFKNHTSL		
BJ.1	147-151	KNNKS	<b>BJ.1</b>	
	163-167	ANNCT		
	182-185	KEGN		
	415-417	TGN		
	437-452	NSNKLDSKPSGNYNYL		
	455-460	LFRKSN		
	468-472	ISTEI		
	474-489	QAGNKPCNGAAGFNCY		
	491-506	PLRSYGFRPTYGVGHQ		
	703-705	NSV		
	809-812	PSKP		
	836-842	QYGDCLG		
	890-896	AGAALQI		
	1140-1162	PLQPELDSFKEELDKYFKNHTSP		



**Figure S1.** Conformational epitopes and mutation mapped on three-dimensional structure models of the SARS-CoV-2 variants in the S protein. The results of the conformational epitope analysis of the SARS-CoV-2 mutant and the mapping of the predicted conformational epitopes and mutation sites on the conformational model of the SARS-CoV-2 S protein are shown. Amino acids mutated from BA.2 on the predicted epitope are indicated in red letters. The chains of the trimeric structure are color-coded in dark gray (chain A), gray (chain B), and light gray (chain C). Conformational epitopes, mutations on conformational epitopes, and RBDs are shown in blue, red, and light yellow, respectively.