

Table S2: Secondary structure prediction and comparison of Omicron (BA.1, B.A.1.1, BA.2, BA.3) variant and sub-variants with reference to wild type (Wuhan-Hu-1)

	Wuhan-Hu-1-whole Spike	Omicron-Spike (BA.1)	Omicron Spike (BA.1.1)	Omicron Whole Spike (BA.2)	Omicron Whole Spike (BA.3)	Wuhan-Hu-1- RDB	Omicron-RDB (BA.1)	Omicron-RDB (BA.1.1)	Omicron-RBD (BA.2)	Omicron-RBD (BA.3)
Alpha helix (Hh)	21.52%	23.46%	22.91%	23.31%	23.68%	6.55%	8.30%	5.61%	8.73%	8.30%
Extended strand (Ee)	22.07%	20.55%	20.87%	20.87%	20.92%	22.71%	18.34%	23.36%	18.34%	20.09%
Random coil (Cc)	56.40%	55.98%	56.22%	55.83%	55.41%	70.74%	73.36%	71.03%	72.93%	71.62%

Table S3: Intrinsically disordered prediction using PONDR®VLXT tool.

	No.of residues disordered	Overall percent disordered	Predicted disorder segment	Number Disordered Regions
Wuhan-HU-1	98	7.70	[17]-[20] [468]-[475] [601]-[608] [672]-[709] [869]-[871] [945]-[950] [982]-[986] [992]-[994] [1023]-[1023] [1174]-[1194] [1264]-[1264]	11
Wuhan-RBD	18	7.86	[317]-[322] [468]-[473]	2
Omicron (BA.1)	85	6.69	[17]-[20] [208]-[221] [598]-[607] [675]-[706] [867]-[868] [1020]-[1020] [1171]-[1191] [1261]-[1261]	8
Omicron-RBD (BA.1)	6	2.62	[317]-[322]	1
Omicron (BA.1.1)	85	6.69		8
Omicron RBD (BA1.1)	6	2.62	[317]-[322]	1
Omicron (BA.2)	78	6.14	[406]-[407] [598]-[607] [675]-[706] [866]-[868] [979]-[983] [989]-[991] [1020]-[1020] [1171]-[1191] [1261]-[1261]	9
Omicron RBD (BA.2)	8	3.49	[317]-[322] [408]-[409]	2
Omicron (BA.3)	80	6.31	[17]-[20] [595]-[604] [672]-[703]	9

			[863]-[865] [976]-[980] [986]-[988] [1017]-[1017] [1168]-[1188] [1258]-[1258]	
Omicron RBD (BA.3)	6	2.62	[317]-[322]	1