

A

Per Sample Scores Summary

Sort: Class Masked mAb Escape ▾

Sample ID	Pango-Lineage	Bloom ACE2 (Wuhan)	Bloom ACE2 (BA.1)	Bloom ACE2 (BA.2)	Vibrational Difference Score	Serum Escape	mAb Escape	Class Masked mAb Escape	mAb Escape Class 1	mAb Escape Class 2	mAb Escape Class 3	mAb Escape Class 4	BEC Escape Factor	Quality Warnings
BQ.1		-0.48	-0.11	-0.04	0.02	0.83	1.34	2.14	1.39	1.74	0.78	0.23	0.63	
KP.3.1		-0.45	-0.19	-0.11	-0.05	0.85	2.03	3.1	2.11	2.77	0.96	0.23	0.79	
JN.1		-0.42	-0.13	-0.02	-0.01	0.78	1.89	2.93	1.97	2.51	0.95	0.23	0.77	
HK.3		-0.45	-0.15	-0.13	-0.08	0.93	1.75	2.75	1.63	2.24	1.39	0.23	0.73	
EG.5		-0.45	-0.16	-0.1	-0.04	0.9	1.66	2.62	1.56	2.05	1.39	0.23	0.73	
BA.2.86		-0.42	-0.13	-0.02	0.01	0.71	1.7	2.6	1.54	2.28	0.95	0.23	0.75	
XBB.1.5		-0.45	-0.08	-0.01	0.01	0.87	1.57	2.51	1.55	1.85	1.39	0.23	0.7	
BQ.1		-0.48	-0.11	-0.04	0.02	0.83	1.34	2.14	1.39	1.74	0.78	0.23	0.63	
BA.5		-0.51	-0.13	-0.05	0.02	0.79	1.2	1.77	1.2	1.73	0.42	0.23	0.54	
BA.2		-0.51	-0.08	0.0	-0.01	0.66	0.98	1.31	0.96	1.42	0.26	0.23	0.36	
BA.1		-0.61	0.0	-0.02	-0.01	0.77	0.94	1.25	0.9	1.43	0.4	0.02	0.4	
B.1.617.2		-0.02	-0.04	-0.02	0.04	0.13	0.2	0.28		0.39	0.17		0.14	
B.1.1.7		1.07	0.0	0.0	0.25	0.01	0.05	0.09	0.16	0.01			0.02	

Summarised scores per sample (sum across sample), cells with values higher than selected baseline are highlighted. Selected baseline is always shown in the top row, table is sorted by the cm mAb escape all classes sum column by default, the drop down can be used to sort on other scores. For a description of these scores see [Table 4](#) in the SPEAR README. For a full screen view of this table see [here](#). Source data used to produce this table can be found in the file [spear_score_summary.tsv](#)

Quality warnings: ! - Spike N contig (default 150nt) ; ^ - Spike RBD N content (default 12nt) ; * - Global N percentage (default > half N percentage cutoff) ; # - Spike N percentage (default > 5%)

B

Residue Score Heatmap

Class Masked mAb Escape ▾

Class Masked mAb Escape



Summary heatmap of all residue positions for which there is at least one mutation across all samples. Individual sample IDs and mutations are plotted on datapoint, for large samples sets these become visible at higher zoom levels. Residues are labelled in the following format: sample_id(pango_lineage):mutation. Hover text will show z: selected score for sample-residue and sample ID and mutation. For a description of these scores see [Table 3](#) in the SPEAR README. For a full screen view of the current plot see [here](#), and for a fullscreen heatmap across all residues (easier comparison between reports), see [here](#).