Electronic Supplementary Material (ESI) for Analyst.

Supplementary Table 1 Tryptic peptide mass biomarkers for spike and nucleocapsid proteins for detection by high resolution MALDI-MS [36]

***m/z* (mono) theoretical**	**viral protein code**	**residues***	**sequence****	**domain*****
749.3536	N	178-185	GGSQASSR	RNA-binding domain
831.4570	N	227-233	LNQLESK	dimerization domain
843.4247	S	1206-1211	YEQYIK	S2 subunit heptad repeat 2 (HR2) domain
899.4945	S	409-417	QIAPGQTGK	S1 subunit C-terminal domain (CTD)
1085.5374	S	311-319	GIYQTSNFR	undefined
1126.5640	N	267-276	*AYNVTQAFGR*	dimerization domain
1224.6259	S	103-113	GWIFGTTLDSK	S1 subunit N-terminal domain (NTD)
1267.6946	S	558-567 (1)	KFLPFQQFGR	undefined
1281.5892	S	836-847	QYGDCLGDIAAR	S2 subunit fusion peptide (FP)
1455.7550	S	404-417 (1)	GDEVRQIAPGQTGK	S1 subunit C-terminal domain (CTD)
1670.8894	N	210-226	MAGNGGDAALALLLLDR	undefined
1788.8511	N	278-293	GPEQTQGNFGDQELIR	dimerization domain
1989.9738	S	387-403	LNDLCFTNVYADSFVIR	S1 subunit receptor binding domain (RBD)
2040.0007	S	329-346	FPNITNLCPFGEVFNATR	S1 subunit receptor binding domain (RBD)
2181.0207	N	69-88	GQGVPINTNSSPDDQIGYYR	RNA-binding domain
2267.0807	N	108-127	*WYFYYLGTGPEAGLPYGANK*	N-terminal domain (NTD)
2324.1894	N	41-61	*RPQGLPNNTASWFTALTQHGK*	RNA-binding domain
2742.2425	S	159-182	VYSSANNCTFEYVSQPFLMDLEGK	S1 subunit N-terminal domain (NTD)

*residues denoted with a (1) are associated with one missed cleavage site; all others contain no missed cleavage sites
** nucleocapsid (N) segments detected in separate study (Yoshinari et al. [41]) are shown in italics
***as defined on UniPro knowledge base (uniprokb) at https://covid-19.uniprot.org/uniprotkb/

Supplementary Table 2 Spike protein tryptic peptides with masses unique to a specific omicron lineage [38]*

lineage	mutation	residues**	subunit	sequence	tryptic peptide mass [M+H]+ monoisotopic
BA.1	Δ143-145	130-147 (-143-145)	S1	VCEFQFCNDPFLDHK	1841.7986
BA.1	+EPE214	214-239	S1	EPEDLPQGFSALEPLVDLPIGINITR	2833.4982
BA.1	G339D	329-346	S1	FPNITNLCPFDEVFNATR	2098.0063
BA.1	S371L	358-378	S1	ISNCVADYSVLYNLAPFFTFK	2412.1945
BA.1	G496S	494-498	S1	SYSFR ***	659.3148
BA.1	T547K	538-547	S1	CVNFNFNGLK	1155.5616
BA.1	L981F	970-983	S2	FGAISSVLNDIFSR	1525.8010
BA.1.1	R346K	341-346	S1	GDEVK ***	547.2723
BA.2.12.1	L452Q	452-454	S1	QFR ***	450.2460
BA.2.12.1	S704L	686-733	S2	SVASQSIIAYTMSLGAENLVAYSNNSIAIPTNFTISVTTEILPVSMTK	5047.5894
BA.2.75	K147E	130-150	S1	VCEFQFCNDPFLDVYYHENNK	2624.1221
BA.2.75	F157L	152-158	S1	MESELR	764.3608
BA.2.75	I210V	207-214	S1	HTPVNLGR	893.4952
BA.2.75	G339H	336-346	S1	FPNITNLCPFHEVFNATR	2120.0383
BA.4 / BA.5	L452R	445-452	S1	VGGNYNYR	942.4429
BA.4 / BA.5	F486V	479-498	S1	PCNGVAGVNCYFPLQSYGFR	2192.0052
BA.5	G3V	1-21	S1	MFVFLVLLPLVSSQCVNLITR	2392.3495
BA.5	T71I	42-72	S1	SSVLHSTQDLFLPFFSNVTWFHAISGTNGIK	3450.7481

*or unique to the closely related BA.4 / BA.5 lineages
**residue numbering is associated with the protein sequence for particular sub-variant which vary from one to the next due to deletions and insertions
***shares its sequence with a known protein of the human proteome based on a BLASTp search.