Table S1. Omicron spike trimer interface analysis by PDBePISA

a Overall interface comparison between Omicron and G614 S trimer

	Protomer1			Protomer2			interface	ΔiG	ΔiG	#HB	#SB
	iNat	iNres	Surface Å^2	iNat	iNres	Surface Å^2	area, Å^2	kcal/mol	P-value		
Omicron	660	188	59124	714	191	58896	6397.6	-60.4	0.092	56	14
G614	623	176	56231	670	181	56824	6017.4	-59.6	0.056	46	10

Note:
iNat: the number of interfacing atoms.
iNres: the number of interfacing residues.
ΔiG: Solvation energy effect, kcal/mol
HB: Hydrogen bond
SB: Salt bridge

b Unique hydrophilic interaction contributed by Omicron mutations

Hydrogen bonds

Protomer 1	Dist. [Å]	Protomer 2
A:ASN 317[OD1]	3.79	B:LYS 764[NZ]
A:ASP 568[OD2]	2.80	B:LYS 856[NZ]
A:THR 572[OG1]	2.79	B:LYS 856[NZ]

Salt bridges

Protomer 1	Dist. [Å]	Protomer 2
A:ASP 568[OD2	2.80	B:LYS 856[NZ]

c Individual interface contact contributed by Omicron mutations

	HSDC	ASA	BSA	ΔiG
A:ASN 417		55.99	8.14 ||	-0.12
A:LYS 547		117.56	65.99 ||||||	0.31
A:GLY 614	H	75.10	57.25 ||||||||	0.04
A:LYS 969	H	95.26	26.12 |||	0.29
B:LYS 764	H	77.78	11.22 ||	-0.41
B:TYR 796	H	192.06	50.52 |||	0.24
B:PHE 981		124.99	44.63 ||||	0.41

ASA: Accessible Surface Area, Å^2
BSA: Buried Surface Area, Å^2
ΔiG: Solvation energy effect, kcal/mol
||||: Buried area percentage, one bar per 10%

Supplementary Table 1