

Supplemental information

Antibody escape of SARS-CoV-2

Omicron BA.4 and BA.5

from vaccine and BA.1 serum

Aekkachai Tuekprakhon, Rungtiwa Nutalai, Aiste Dijokaite-Guraliuc, Daming Zhou, Helen M. Ginn, Muneeswaran Selvaraj, Chang Liu, Alexander J. Mentzer, Piyada Supasa, Helen M.E. Duyvesteyn, Raksha Das, Donal Skelly, Thomas G. Ritter, Ali Amini, Sagida Bibi, Sandra Adele, Sile Ann Johnson, Bede Constantinides, Hermione Webster, Nigel Temperton, Paul Klenerman, Eleanor Barnes, Susanna J. Dunachie, Derrick Crook, Andrew J. Pollard, Teresa Lambe, Philip Goulder, Neil G. Paterson, Mark A. Williams, David R. Hall, OPTIC Consortium, ISARIC4C Consortium, Elizabeth E. Fry, Jiandong Huo, Juthathip Mongkolsapaya, Jingshan Ren, David I. Stuart, and Gavin R. Screaton

Table S1: Structure determination and refinement. Related to Methods.

Structure	BA.4/5 RBD/Beta-27/NbC1, PDB: 7ZXU
Data collection	
Space group	P2 ₁ 2 ₁ 2 ₁
Cell dimensions	
a, b, c (Å)	84.1, 100.4, 105.4
α , β , γ (°)	90, 90, 90
Resolution (Å)	66–1.89 (1.92–1.89) ^a
R _{merge}	0.313 (---)
R _{pim}	0.061 (0.848)
I/s(I)	7.7 (0.5)
CC _{1/2}	0.996 (0.418)
Completeness (%)	100 (99.4)
Redundancy	27.4 (28.2)
Refinement	
Resolution (Å)	66–1.89
No. reflections	68286/3756
R _{work} / R _{free}	0.183/0.210
No. atoms	
Protein	5805
Ligand/ion/water	672
B factors (Å ²)	
Protein	39
Ligand/ion/water	47
r.m.s. deviations	
Bond lengths (Å)	0.002
Bond angles (Å)	0.5

Table S1