SUPPLEMENTARY TABLE S1. Basic information of COVID-19 convalescent patients in this study.

ID	Gender	Age (years)	Sample collection time[†] (day)	HLA-A	HLA-B
1	Male	29	176	A*0207, A*1101	B*2704, B*4601
2	Male	48	165	A*1101, A*2402	B*3505, B*5101
8	Female	62	184	A*0207, A*2420	B*4001, B*6701
9	Male	36	168	A*1101, A*2407	B*3505, B*4006
11	Female	68	174	A*1101, A*3101	B*4001, B*5102

Abbreviations: COVID-19=coronavirus disease 2019; HLA=human leukocyte antigen.
[†] Days post disease onset.

SUPPLEMENTARY TABLE S2. X-ray data processing and refinement statistics.

Parameter	HLA-A*1101/N25
Data processing	
Space group	P22121
Cell parameters	
a (Å)	43.98
b (Å)	81.90
c (Å)	116.84
α (°)	90.00
β (°)	90.00
γ (°)	90.00
Wavelength (Å)	0.97853
Resolution (Å)	50.0–1.5 (1.55–1.5)*
Total reflections	939401
Unique reflections	68099
Completeness (%)	99.70 (97.10)
Redundancy	13.80 (9.00)
R_{merge} (%)[†]	7.40 (115.60)
I/σ	1.70 (33.42)
Refinement	
R_{work} (%)[§]	21.9
R_{free} (%)	22.0
RMSD	
Bond length (Å)	0.007
Bond Angle (°)	1.31
Average B factor (Å^2)	12.81
Ramachandran plot quality (%)	
Favored (%)	98.14
Allowed (%)	1.86
Outliers (%)	0

Abbreviations: HLA=human leukocyte antigen; RMSD=root mean squared deviation.
* Numbers in parentheses represent the highest-resolution shell.
[†] $R_{merge} = \sum_{hkl}\sum_i|I_i-<I>| / \sum hkl\sum_i I_i$, where I_i refers to the observed intensity and $<I>$ is the average intensity of multiple observations of symmetry related reflections.
[§] $R = \sum_{hkl}||F_{obs}|-k|F_{call}|| / \sum_{hkl}|F_{obs}|$, where R_{free} is calculated for a randomly chosen 5% of reflections and R_{work} is calculated for the remaining 95% of reflections used for structure refinement.