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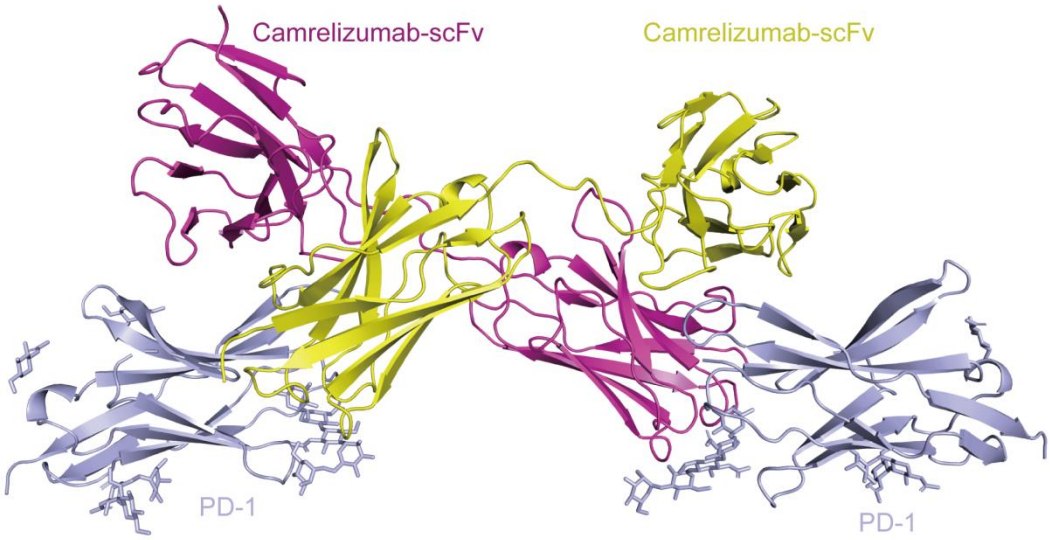
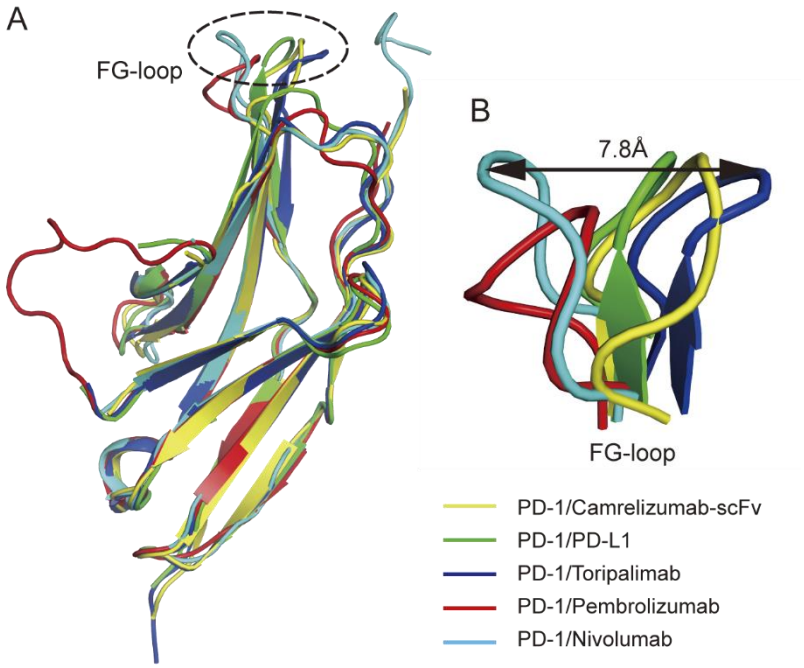
Appendix Figure S1



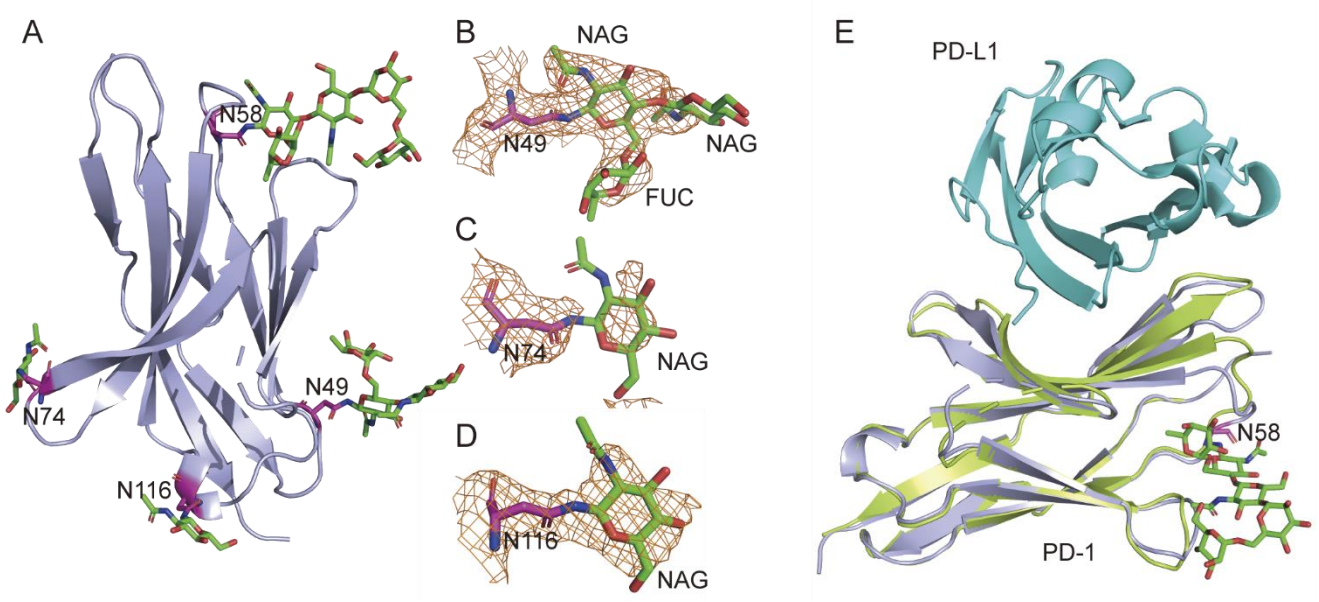
Appendix Figure S1. Overall complex structure of camrelizumab-scFv/PD-1. Camrelizumab-scFv is constructed as VH-GGGGS-VL and refolded as dimer. The complex structure of camrelizumab-scFv/PD-1 includes two camrelizumab-scFvs and two PD-1 molecules.

Appendix Figure S2



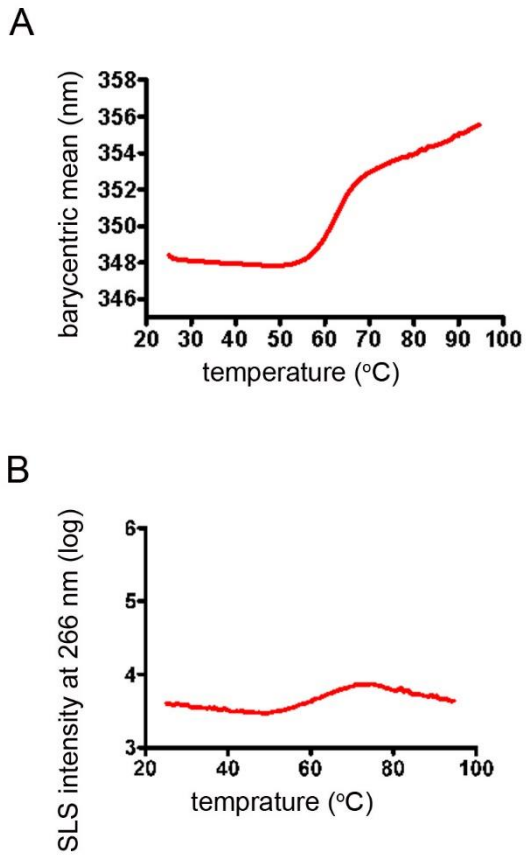
Appendix Figure S2. Comparison of PD-1 structures complexed with different MAbs. (A) Superimposition of PD-1s extracted from complex structure of PD-1/camrelizumab (yellow), PD-1/PD-L1 (green), PD-1/toripalimab (marine blue), PD-1/pembrolizumab (red) and PD-1/nivolumab (cyan). The FG loops of PD-1 targeted by nivolumab or pembrolizumab are colored differently as follows, N-loop, red; BC loop, green; FG loop, blue; C'D loop, magenta. **(B)** The variation of FG loop of PD-1 is highlighted and substantially shift of the FG loop upon binding to nivolumab and toripalimab is indicated.

Appendix Figure S3



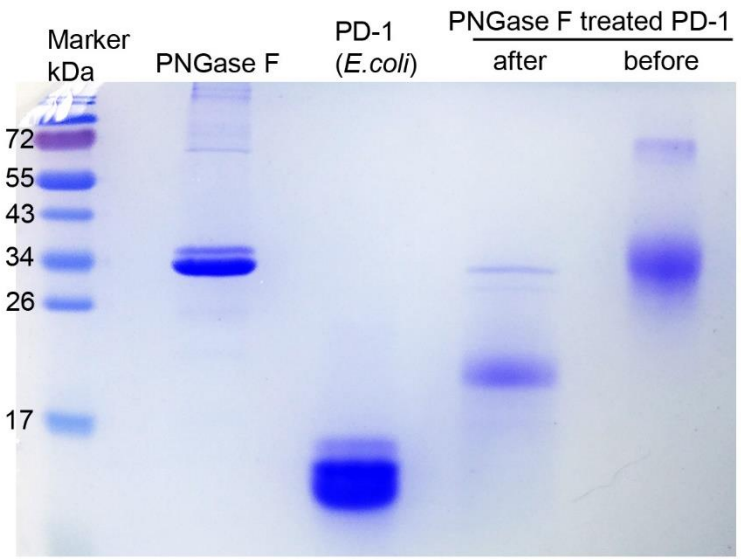
Appendix Figure S3. Glycosylations observed in the PD-1 structure. (A) The four N-linked glycosylation sites (N49, N58, N74, and N116) are shown in sticks and colored in purple. The observed glycans are highlighted in sticks and colored in lemon. **(B-D)** The 2 Fo-Fc electron density map of the N49, N74, N116 N-linked glycans contoured at 1.0 sigma is represented in orange. **(E)** Modeling of the location the N58 glycosylation in the complex of PD-1 and PD-L1.

Appendix Figure S4



Appendix Figure S4. Thermal stability of N58A mutated PD-1 protein. Accelerated thermal stability of N58A mutated PD-1 proteins obtained from 293T cells (red line) was characterized in all-in-one UNcle platform. Protein unfolding was observed as an increase in barycentric mean **(A)** while small particle formation of the samples was observed as an increase in SLS intensity at 266 nm **(B)**.

Appendix Figure S5



Appendix Figure S5. SDS-PAGE analysis of PNGase F treated PD-1 proteins. The protein samples before and after PNGase F treatment were analyzed by SDS-PAGE, with PNGase F and PD-1 proteins obtained from *E.coli* cells analyzed in parallel as control.

Appendix Table S1. SPR analysis of the binding between MAbs and PD-1

	Ka (Ms)	Kd (1/s)	KD (nM)
Camrelizumab vs PD-1-293T	1.91×10^{5}	1.13×10^{-3}	5.92
Camrelizumab vs PD-1-insect cell	2.29×10^{5}	1.54×10^{-3}	6.73
Camrelizumab vs PD-1-E.coli	7.51×10^{4}	1.17×10^{-1}	1 555
Camrelizumab vs PD-1-N58A	9.00×10^{4}	1.02×10^{-2}	113
Camrelizumab vs PD-1-WT	1.47×10^{4}	1.54×10^{-3}	4.74
Camrelizumab vs PD-1-PNGase-treated	3.07×10^{5}	1.45×10^{-3}	105
Nivolumab vs PD-1-WT	6.09×10^{5}	6.93×10^{-3}	11.4
Nivolumab vs PD-1-N58A	7.23×10^{5}	7.60×10^{-3}	10.5
Pembrolizumab vs PD-1-WT	8.33×10^{5}	6.23×10^{-3}	7.48
Pembrolizumab vs PD-1- N58A	9.37×10^{5}	5.29×10^{-3}	5.65

Appendix Table S2. Crystallographic data collection and refinement statistics.

	camrelizumab/PD-1
Data collection	
Space group	P1
Wavelength (Å)	0.97918
Unit cell dimensions	
a, b, c (Å)	43.11, 77.62, 96.05
α, β, γ(°)	69.38, 78.44, 88.57
Resolution (Å)	50.00-2.80 (2.90-2.80)

Unique. reflections	27286 (2726)
R_{merge}	0.079/0.692
I/σ	11.58(1.29)
Completeness (%)	98.4 (98.4)
Redundancy	3.4 (3.6)
Refinement	
Resolution (Å)	29.68-2.81
R_{work} / R_{free}	0.212/0.252
No. atoms	5486
Protein	5248
Ligands	0
Water	0
R.m.s. deviations	
Bond lengths (Å)	0.005
Bond angles (°)	0.678
Ramachandran plot	
Favored (%)	93.13
Allowed (%)	6.87
Outliers (%)	0.00

*Values in parentheses are for highest-resolution shell.

Appendix Table S3. Residues contributed interaction between camrelizumab and PD-1

	Antibody	Contacts	hPD-L1	Total Contacts
H Chain(V_H)	S30	3[1]	FUC303	142
	S31	5, 10 (1)[2]	P83, FUC303	
	Y32	12, 4	P83, E84	
	M33	3, 6	S62, L128	
	S52	8 (1), 1	E61, S62	
	G53	2, 4 (1)	E61, FUC303	
	G54	11, 2, 5	E61, NAG302, FUC303	
	G55	3	E61	
	A56	9 (1), 1	E61, NAG302	
	N57	4, 7 (1), 4	S60, E61, S62	
	Y59	4 (2), 1, 7	S62, A129, P130	
	L100	1, 8	V64, L128	
	Y101	2, 1, 6, 7	V64, K78, I126, L128	
L Chain(V_L)	W32	2, 18, 3, 5	I126, A132, 133Q, 134I	74
	V91	3	A132	
	Y92	3, 8, 13 (1)	P130, K131, A132	

S93	5, 4	P130, Q131
I94	8 (1)	P130
W96	2	L128

[1] Numbers represent the number of atom-to-atom contacts between camrelizumab and PD-1 residues, which were analyzed by the Contact program in CCP4 suite (the distance cutoff is 4.5Å).

[2] Numbers in the parentheses represent the number of hydrogen bonds between camrelizumab and PD-1 residues which were analyzed by the Contact program in CCP4 suite (the distance cutoff is 3.5 Å).