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**Structural basis of a novel PD-L1 nanobody for immune
checkpoint blockade**

Supplementary Materials

Supplementary methods

Table S1-S2

Figure S1-S7

1 **Supplementary Methods**

2 **Competitive binding of KN035 and PD-1 on PD-L1 assessed by ELISA**

3 ELISA plates were coated with PD-L1-Fc at 2 μ g/ml in 50mM Na₂CO₃/NaHCO₃, pH 9.6⁴⁷.
4 After the plates were washed three times with PBST containing 0.05% Tween-20 and
5 blocked with 3% BSA in PBS for 1 hour, serially diluted KN035 were applied to the
6 ELISA plate containing PD-1-hIgG-biotin (10 μ g/ml) and incubated for 2 hours at 37 °C.
7 Binding was detected with the horseradish peroxidase (HRP)-conjugated goat anti-human
8 IgG, which was developed using tetramethylbenzidine (TMB) substrate and stopped by
9 H₂SO₄. The concentration was determined by absorbance at 450 nm.

10 **Displacement of PD-1 from PD-1/ PD-L1 complex**

11 ELISA plates were coated with PD-L1-Fc at 5 μ g/ml in 50mM Na₂CO₃/NaHCO₃, pH 9.6⁴⁷.
12 After the plates were washed three times with PBST containing 0.05% Tween-20 and
13 blocked with 1% BSA in PBS for 1 hour, PD1-muFc (1 μ g/mL) was added and incubated
14 for 2 hours at room temperature. Then serially diluted KN035-Fc/Durvalumab were
15 applied to ELISA plate, incubated for 2 hours at 37 °C. Binding was assessed by the
16 horseradish peroxidase (HRP)-conjugated goat anti-mouse IgG1 secondary antibody,
17 which was developed using tetramethylbenzidine (TMB) substrate and stopped by H₂SO₄.
18 The concentration was determined by absorbance at 450 nm.

19 **Flow cytometry analysis**

20 Binding property of KN035-Fc with other B7/CD28 superfamily proteins were evaluated
21 by flow cytometry analysis. HEK293T cells were transfected with 2 μ g plasmids DNA of
22 hPD-L1-EGFP, hPD-L2-EGFP, hB7H4-EGFP, hCD28-EGFP, hB7H3-EGFP,
23 hICOS-EGFP and mouse PD-L1-EGFP respectively. After 48 hours incubation, the
24 transfected HEK293T cells were suspended and 1 \times 10⁶ cells of each sample were stained
25 in 1% BSA/PBS buffer containing 5 μ g/ml KN035-Fc or mouse anti-ICOS antibody or
26 mouse anti-PD-L2 antibody on ice for 30 mins. After washing, the cells were incubated
27 with secondary antibodyallophycocyanin (APC) conjugated secondary antibody
28 (Biolegend) for 30 mins. The cells were then washed and fixed in 2% formaldehyde/PBS
29 and acquired on GUAVA easy Cyte flowcytometry. Data were analyzed with the GUAVA
30 5.3.1 program.

1 **Pharmacokinetics of KN035-Fc in Sprague Dawley (SD) rats**

2 In a single-dose pharmacokinetic (PK) study⁴⁷, Sprague Dawley rats (5 males and 5
3 females) received intraperitoneal injection of KN035-Fc at 10 mg/kg dosage. The optical
4 densities (OD) of a set of KN035-Fc concentration standards were determined to plot an
5 OD versus concentration standard curve. KN035-Fc serum concentrations were
6 determined from the standard curve using SoftMax pro software and the data was
7 analyzed by four-parameter curve fitting⁴⁷.

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1 **Supplementary Tables**

2 **Supplementary Table S1. PD-L1 mutants and binding affinities with KN035-Fc**

PD-L1 mutation	K_d (M)	$K_{d,mutant}/K_{d,WT}$	mPD-L1 mutation Wang et al. ⁴¹	#Binding to mPD-1 by ELISA ⁴¹ , %
WT	3.0E-09	1	WT	100
I54A	2.42E-07	80.7	-	-
Y56A	1.24E-06	413.3	Y56S	100
E58A	1.49E-07	49.7	E58S	300
D61A	1.99E-08	6.6	-	-
N63A	2.30E-08	7.7	-	-
Q66A	4.88E-07	162.7	-	-
V68A	2.76E-08	9.2	-	-
R113A	5.34E-07	178	C113Y	300
M115A	5.51E-08	18.4	I115A	3
S117A	1.26E-08	4.2	S117Y	100
Y123A	4.24E-08	14.1	-	-
R125A	2.97E-08	9.9	-	-

3 #Binding of mPD-L1 variants to mPD-1 was assessed by performing an ELISA in Wang *et al.*⁴¹.

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Supplementary Table S2. Polar interactions between KN035 and PD-L1 (distance \leq 3.5 Å)

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Hydrogen bonds and salt bridges			
KN035 contact residue	KN035 residue location	PD-L1 contact residue	PD-L1 residue location
S30	CDR1	D61	CC' loop
S35	CDR1	D61	CC' loop
R37	CDR1	D61	CC' loop
D107	CDR3	R113	F strand
S108	CDR3	E58	C strand
E110	CDR3	Y56	C strand
D111	CDR3	Q66	C' strand
T111.2	CDR3	Q66	C' strand
Q116	CDR3	R125	G strand
Water-mediated hydrogen bonds			
S108	CDR3	D61	CC' loop
T112.2	CDR3	S117	F strand
S112.1	CDR3	A121	G strand
G113	CDR3	A121, D122	G strand

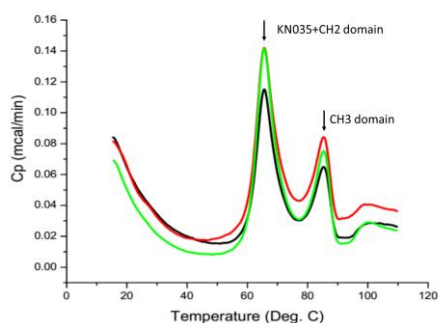
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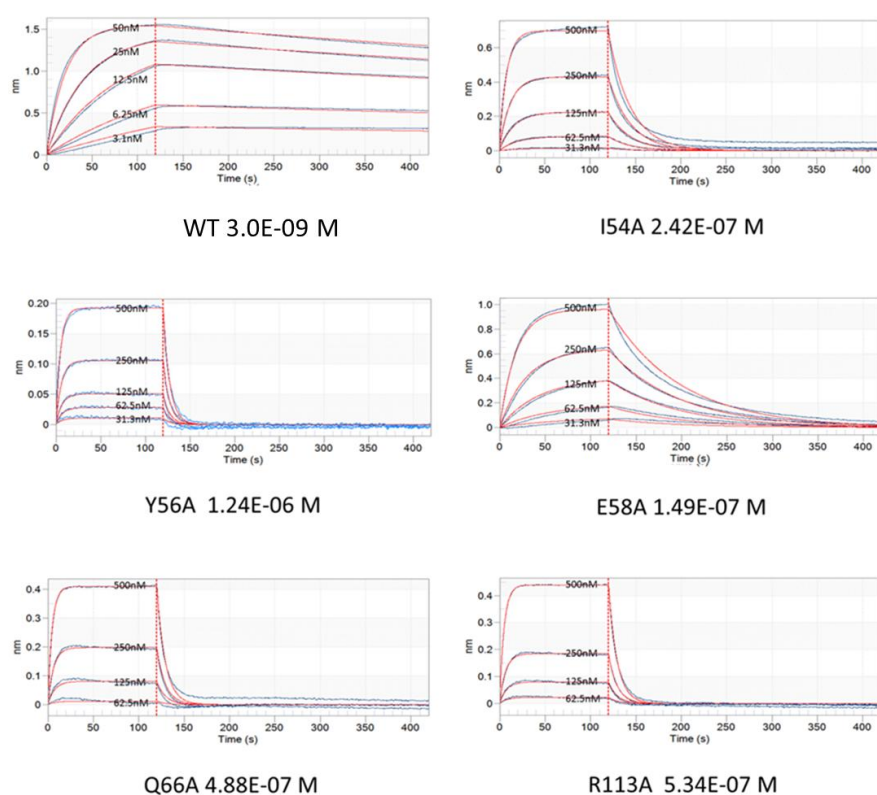
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1 Supplementary Figures

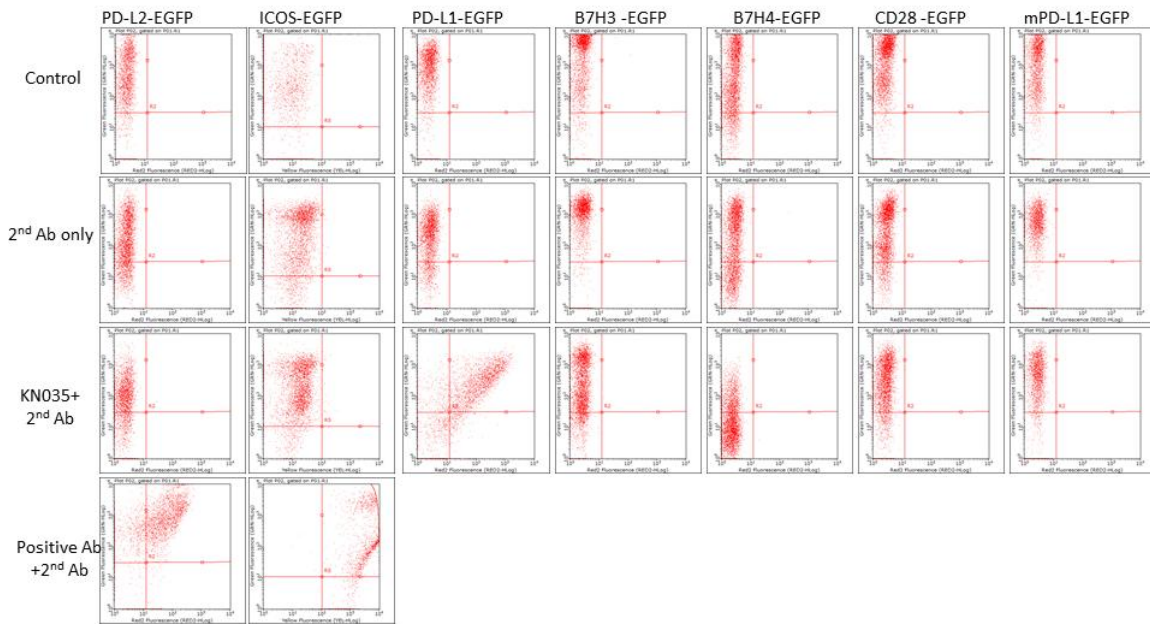
2 A



4 B



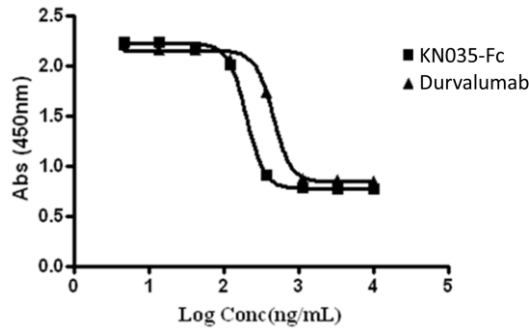
6 **Figure S1.** A. The thermal stability of KN035-Fc. The thermal stability of three
7 preparations of KN035-Fc in PBS was measured by differential scanning calorimetry
8 (DSC) on a MicroCal VP-Capillary DSC (GE Healthcare). The proteins were heated from
9 10 °C to 110 °C at a rate of 110 °C/hour. The thermogram was fitted using the Cp value
10 versus temperature after subtracting the buffer reference scan, with the first transition of
11 the CH2+KN035 domain unfolding ($T_m \approx 66$ °C) and the second transition of the CH3
12 domain unfolding ($T_m \approx 85$ °C). B. Binding affinities of KN035-Fc with PD-L1 mutants.
13 Serial dilutions of the PD-L1 mutants were applied to KN035-Fc immobilized on an Fc
14 sensor chip. The blue lines represent the measured data, and the red lines show the fitted
15 curves.



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2 **Figure S2.** Binding specificity of KN035-Fc to various members of the B7/CD28 superfamily.
 3 HEK293T cells were transfected with PD-L1-EGFP, PD-L2-EGFP, mPD-L1-EGFP, B7H4-EGFP,
 4 B7H3-EGFP, and ICOS-EGFP and then incubated with KN035 or positive antibodies (anti-PD-L2
 5 and anti-ICOS). The cells were stained with a secondary antibody and were detected by flow
 6 cytometry. The red fluorescence from allophycocyanin (APC)-labeled secondary antibody is shown
 7 on the abscissa, and the green fluorescence from the EGFP fusion protein is shown on the ordinate.
 8 The results showed that KN035-Fc could specifically bind PD-L1. The positive antibody recognized
 9 the corresponding ligands PD-L2 and ICOS.

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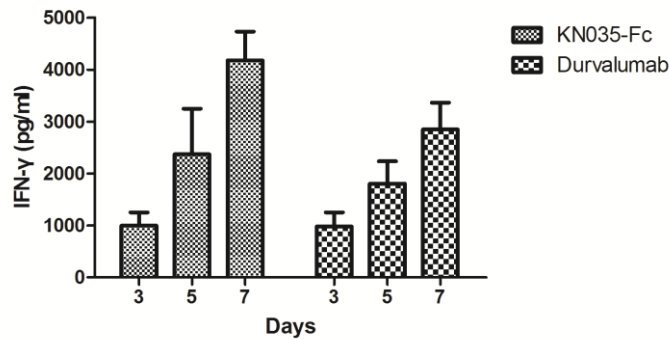


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3 **Figure S3.** Displacement of PD-1 from the PD-1/PD-L1 complex by KN035-Fc and Durvalumab.
4 Plates coated with human PD-L1 were incubated with PD1-muFc (1 μ g/mL) for 2 hours at RT.
5 Serially diluted KN035-Fc/Durvalumab antibodies were applied to the ELISA plate and incubated
6 for 2 hours at 37 $^{\circ}$ C. Binding was detected with a horseradish peroxidase (HRP)-conjugated goat
7 anti-mouse IgG1 secondary antibody. The EC_{50} for KN035-Fc and Durvalumab to displace PD-1 is
8 198.3 ng/mL (2.5 nM) and 452.7 ng/ml (3.1 nM), respectively.

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12 **Figure S4.** The time course of IFN- γ secretion by CD4+ cells after incubation with KN035-Fc and
13 Durvalumab. IFN- γ levels were determined on day 3, 5, and 7 after the incubation with the
14 antibodies KN035-Fc and Durvalumab (2.51 nM).

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<----- FR1(1-26) -----> CDR1(27-38) <--- FR2(39-55) ----->
 ----- 27 28 29 30 35 36 37 38 -----
 QVQLQESGGGLVQPGGSLRLSCAAS G K M S S R R C MAWFRQAPGKERERVAK

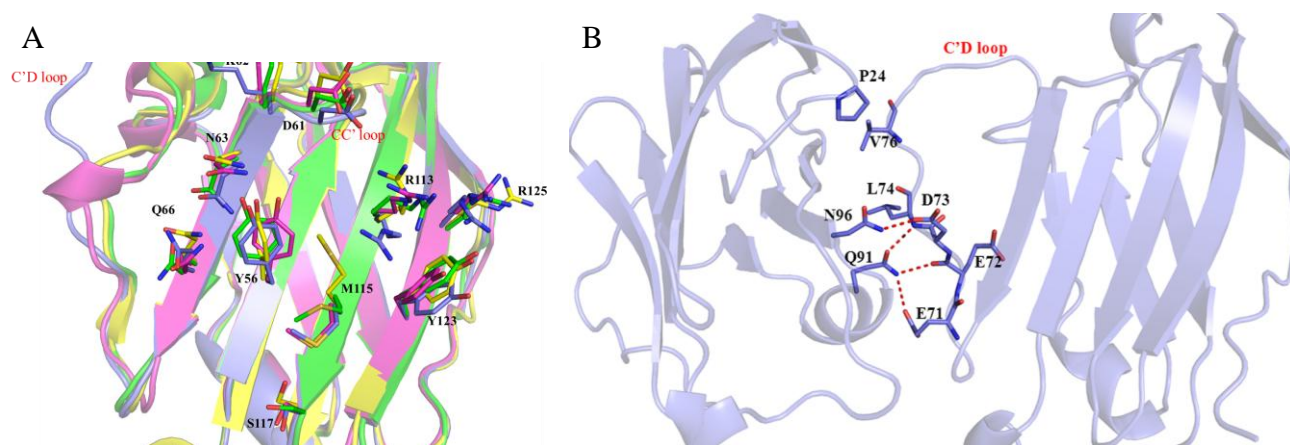
 CDR2(56-65) <----- FR3(66-104) ----->
 ----- 56 57 58 59 62 63 64 65 -----
L L T T S G S T YLADSVKGRFTISQNNAKSTVYLMNSLKPEDTAMYYC

 CDR3(105-117) <· FR4(118-127) ·->
 ----- 105 106 107 108 109 110 111 111.1 111.2 111.3 111.4 112.3 112.2 112.1 112 113 114 115 116 117 -----
A A D S F E D P T C T L V T S S G A F Q Y WGQGTQVTVS

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Figure S5. Amino acid sequence of KN035, numbered according to the IMGT numbering²⁹.

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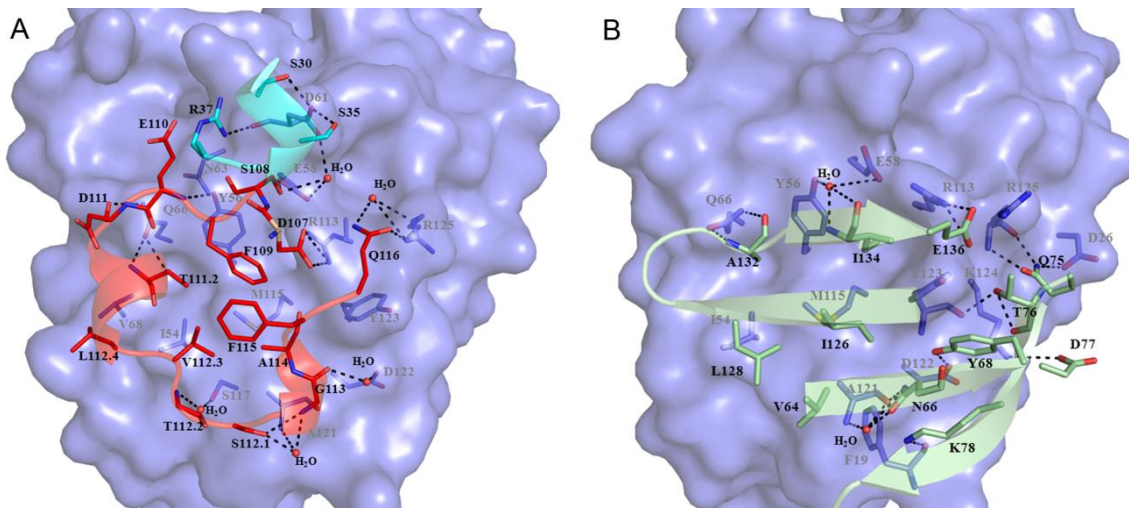


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3 **Figure S6. Conformational changes of PD-L1.** (A) Overlaid structures of the IgV domains of
 4 PD-L1. The structures of the PD-L1 IgV domains from the PD-1/PD-L1 complex (PDB: 4ZQK,
 5 magenta), the KN035/PD-L1 complex (slate), the free PD-L1 structure obtained here (green) and the
 6 previously reported free PD-L1 structure (PDB: 5C3T, yellow) are superimposed in this cartoon. The
 7 C'D loop of PD-L1 shifts approximately 7.5 Å in the PD-L1/KN035 complex, which is likely
 8 induced by crystal packing (B). The other minor conformational changes of the mainchain amongst
 9 the PD-L1 molecules, especially the changes between the two free PD-L1 structures (green and
 10 yellow), likely reflect the thermal dynamics of the PD-L1 molecule. The conformations of the key
 11 residues shown as sticks indicate the flexibility of these sidechains in the structures of the free form
 12 of PD-L1 (green and yellow), as they adopt slightly altered conformations following PD-1 or KN035
 13 binding. This result is consistent with previous NMR studies of PD-1/PD-L1 interactions that show
 14 movements in the surface residues during binding⁴⁰. (B) The movement of the C'D loop of PD-L1
 15 following KN035 binding shown in A is induced by crystal packing. Residues 71-74 and 76 from one
 16 PD-L1 molecule form hydrogen bonds or hydrophobic interactions with other residues, including 24,
 17 91, and 96, from a neighboring PD-L1 molecule. The residues at the interface are shown as slate
 18 sticks. Dashed lines represent polar interactions.

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2 **Figure S7.** The detailed binding interactions at the interfaces of KN035/PD-L1 (A) and PD-1/PD-L1
 3 (B). Residues of KN035 in the binding interface are shown as red or cyan sticks and, those of PD-1
 4 are shown as green sticks. Hydrogen bonds are depicted as black dashed lines, and water molecules
 5 are depicted as red spheres.

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