Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

Supplemental Information

Recognition between CD147 and cyclophilin A deciphered by accelerated molecular dynamics simulations

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Table S1. The detailed information on the CD147-CypA systems.

system	Docking site				P180A-G181A mutation	P211A mutation	R201A mutation
	CypA active site	CD147 P180-G181	CD147 P211	CD147 groove			
Model-0	√	×	×	√	×	×	×
Model-0-P180A-G181A	√	×	×	√	√	×	×
Model-0-P211A	√	×	×	√	×	√	×
Model-0-R201A	√	×	×	√	×	×	√
Model-1	√	√	×	×	×	×	×
Model-1-P180A-G181A	√	√	×	×	√	×	×
Model-1-P211A	√	√	×	×	×	√	×
Model-2	√	×	√	×	×	×	×
Model-2-P180A-G181A	√	×	√	×	√	×	×
Model-2-P211A	√	×	√	×	×	√	×

Table S2. The binding free energy between CD147 and CypA in different mutant models.

	ΔE_{vdw} [a]	ΔE_{ele} [b]	ΔE_{GB} [c]	ΔE_{surf} [d]	ΔG_{bind}
model-0-P180A-G181A	−57.50±1.50	−437.07±7.52	478.40±7.83	−8.62±0.21	−24.80±1.18
model-0-P211A	−86.55±1.11	−554.94±5.73	618.68±5.61	−12.68±0.15	−35.49±1.06
model-0-R201A	−53.15±1.82	−400.45±6.12	438.30±6.27	−7.49±0.23	−22.77±0.65
model-1-P180A-G181A	−70.54±0.68	−578.16±5.12	637.35±4.74	−10.72±0.10	−22.07±1.04
model-1-P211A	−66.01±1.06	−474.61±5.98	523.50±5.43	−9.63±0.13	−26.74±0.77
model-2-P180A-G181A	−69.95±0.81	−399.23±3.36	455.24±3.34	−9.92±0.10	−23.87±0.71
model-2-P211A	−53.55±1.97	−411.50±6.99	451.97±5.93	−7.37±0.20	−20.46±1.54

[a]van der Waals connection, [b]Electrostatic connection, [c]Polar contribution of the solvation effect, [d]Non-polar contribution of solvation effect. (units in kcal mol^{-1})

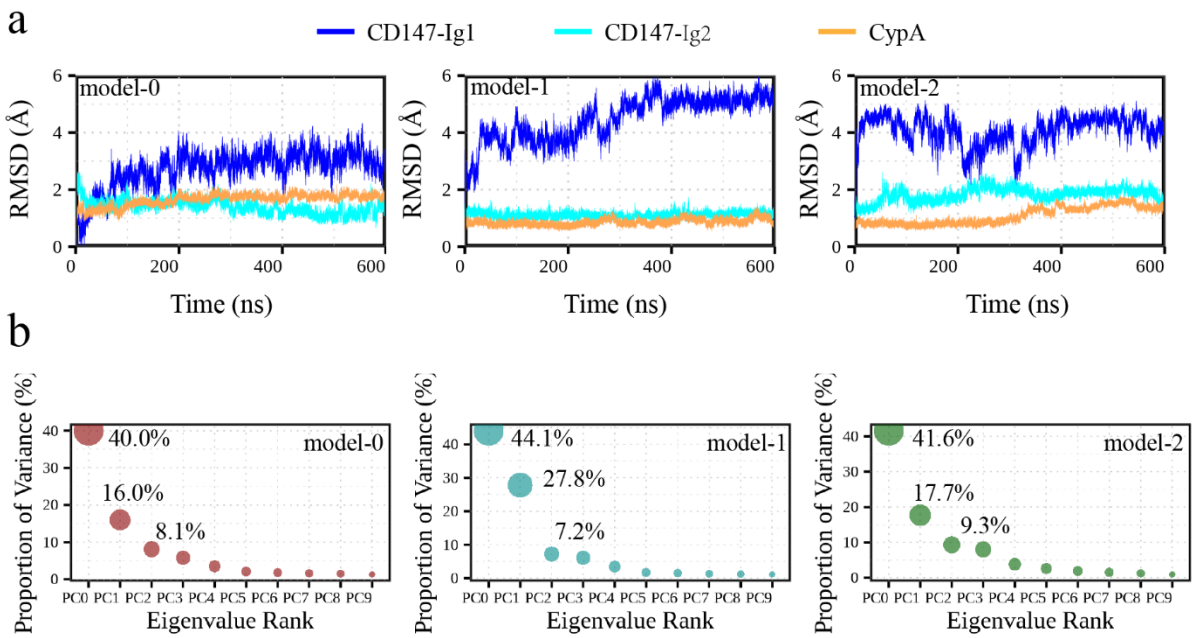

Fig. S1 (a) The root-mean-square deviation (RMSD) of Ig1 domain (blue), Ig2 domain (cyan) and CypA (orange) in model-0, modle-1 and model-3 simulations. (b) Percentage of top ten PCs in the three CD147-CypA complex models.

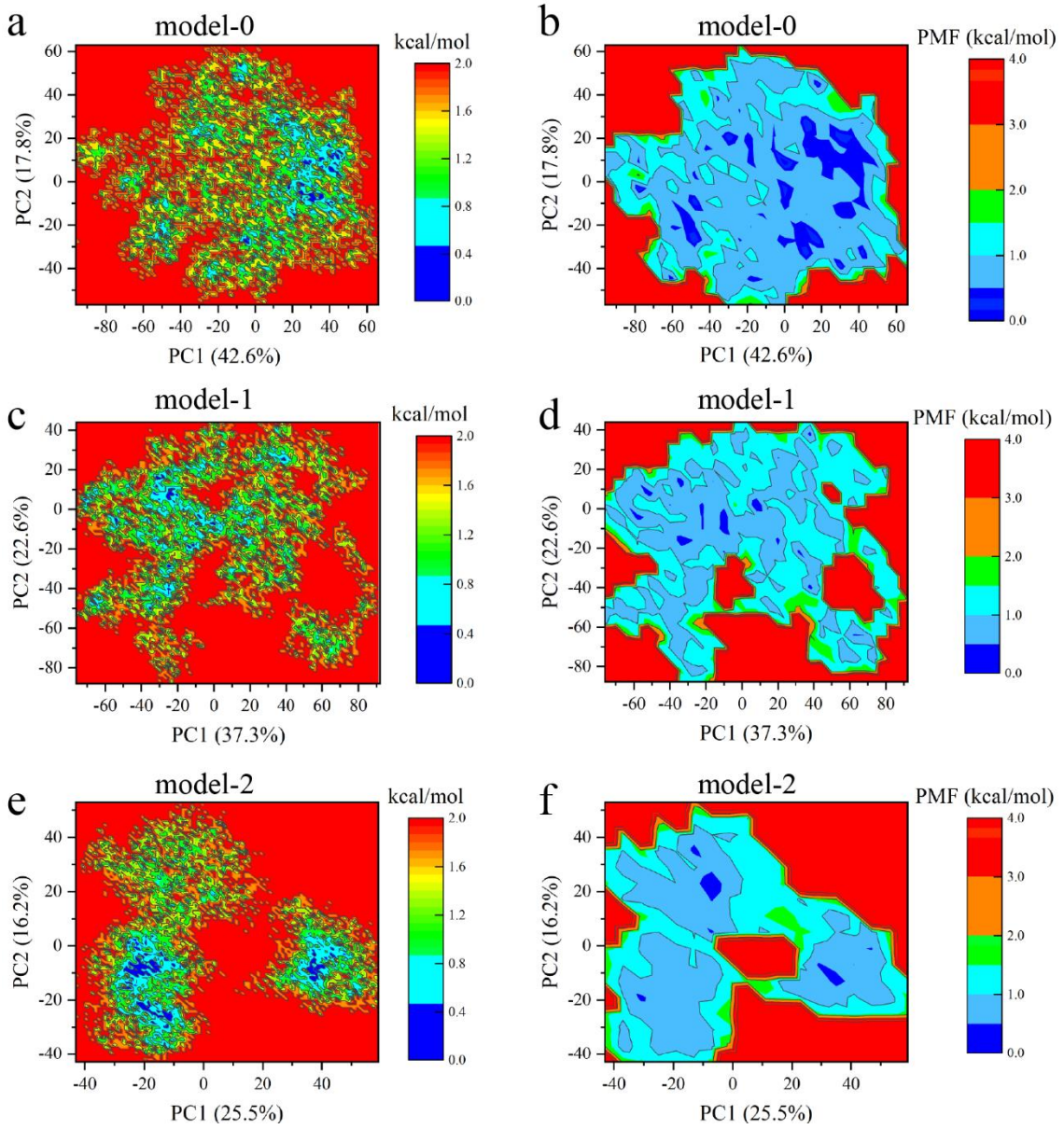

Fig. S2 The free-energy surfaces of CD147-CypA complexes generated using PC1 and PC2 in (a) model-0, (c) model-1 and (e) model-2 simulations. The aMD simulations were reweighted using the PyReweighting toolkit to calculate the 2D PMF profiles of PC1 and PC2 in (b) model-0, (d) model-1 and (f) model-2 simulations. The results were constructed using the last 100 ns of aMD simulation trajectories.

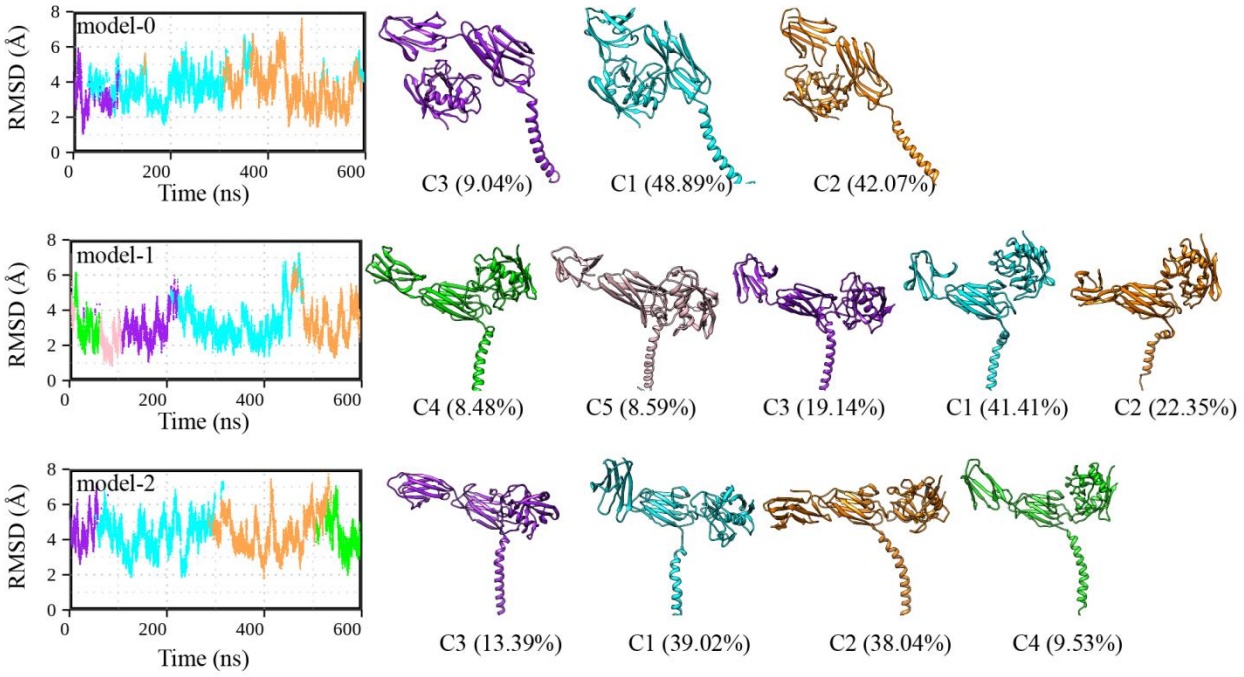

Fig. S3 RMSD of CD147-CypA complex aligning to the centroidal structure of each cluster in the model-0, model-1, and model-2 simulations. Purple, cyan, orange, green, and pink colors correspond to the clusters. The representative conformations and percentages of each cluster are given.

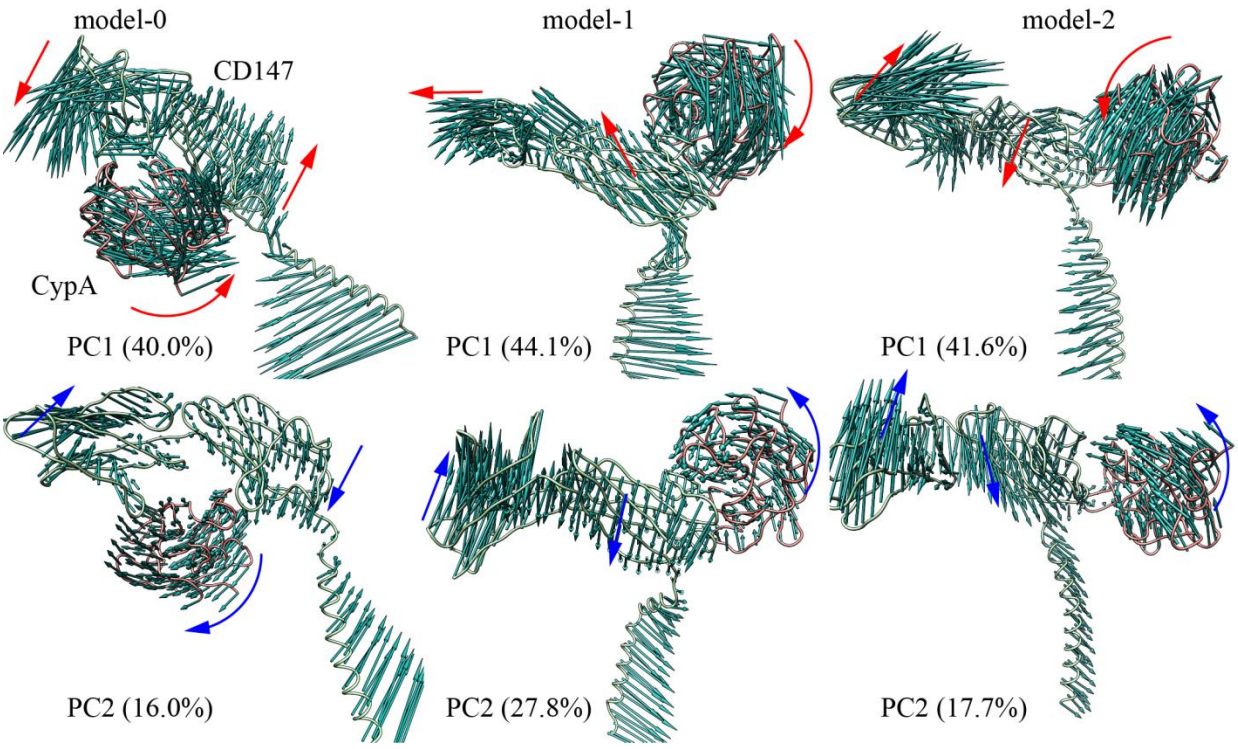

Fig. S4 Vector field representations of the first two principal component (PC1 and PC2) obtained for CD147-CypA complex in the model-0, model-1 and model-2 simulations. The red and blue arrows representation of the first and second motion modes of CD147-CypA complex.

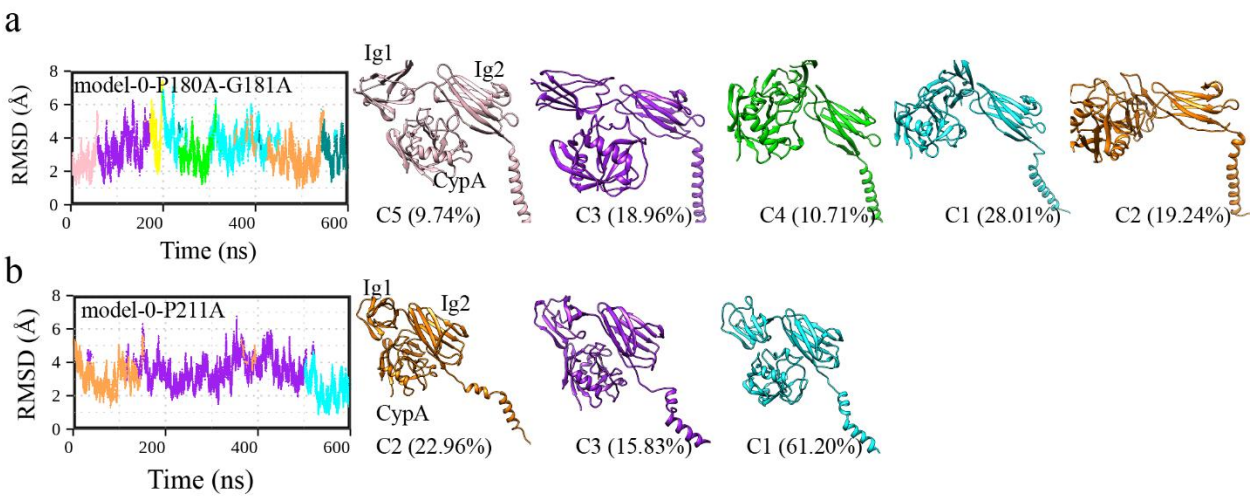

Fig. S5 RMSD of CD147-CypA complex aligning to the centroidal conformation of each cluster in P180A-G181A and P211 mutant model-0 simulations. Purple, cyan, orange, green, pink, yellow, and light tea green colors correspond to the clusters. The representative conformations and percentages of the first five clusters are given.

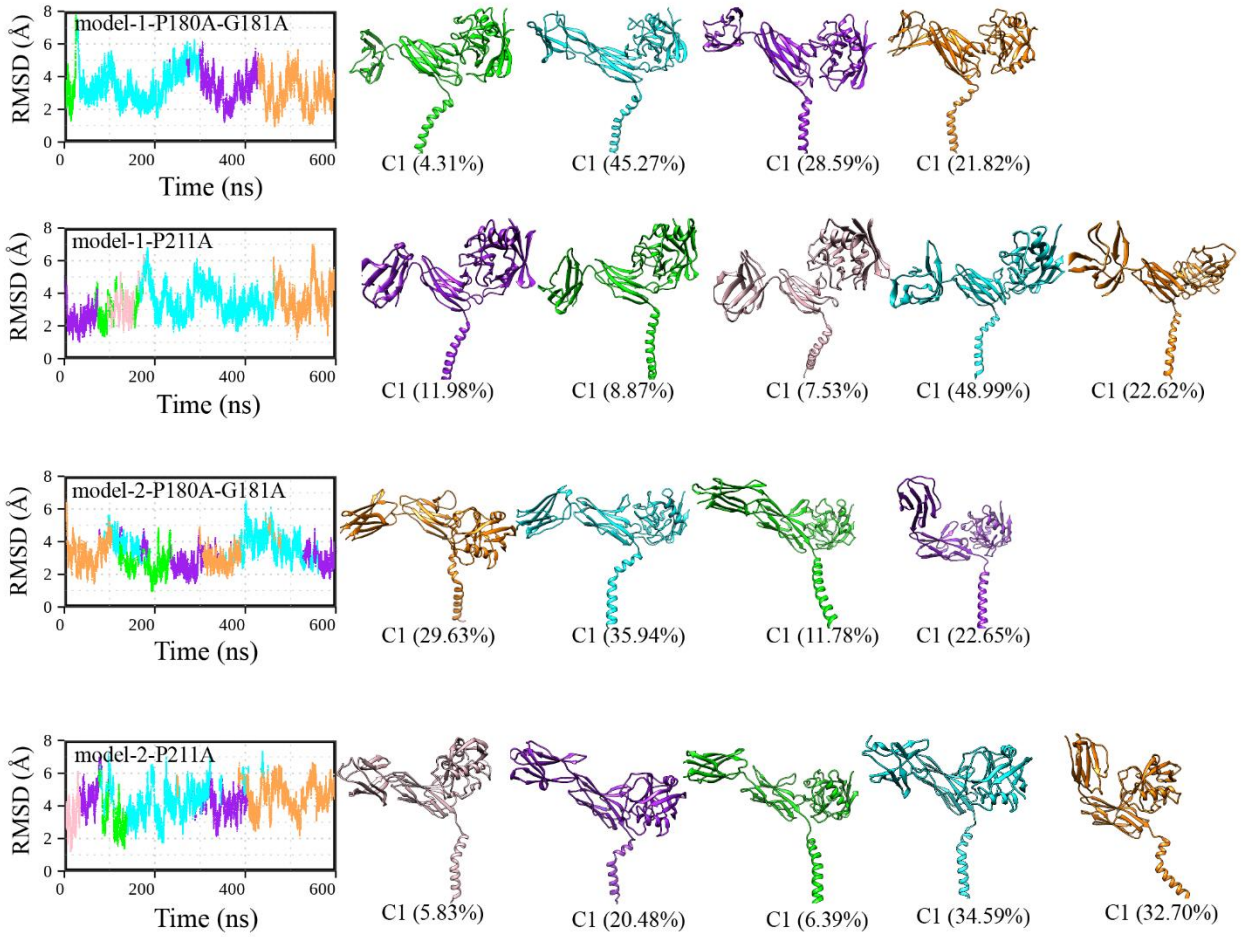

Fig. S6 RMSD of CD147-CypA complex aligning to the centroidal conformation of each cluster in mutant model-1 and model-2 simulations. Purple, cyan, orange, green, pink, yellow, and light tea green colors correspond to the clusters. The representative conformations and percentages of the first five clusters are given.

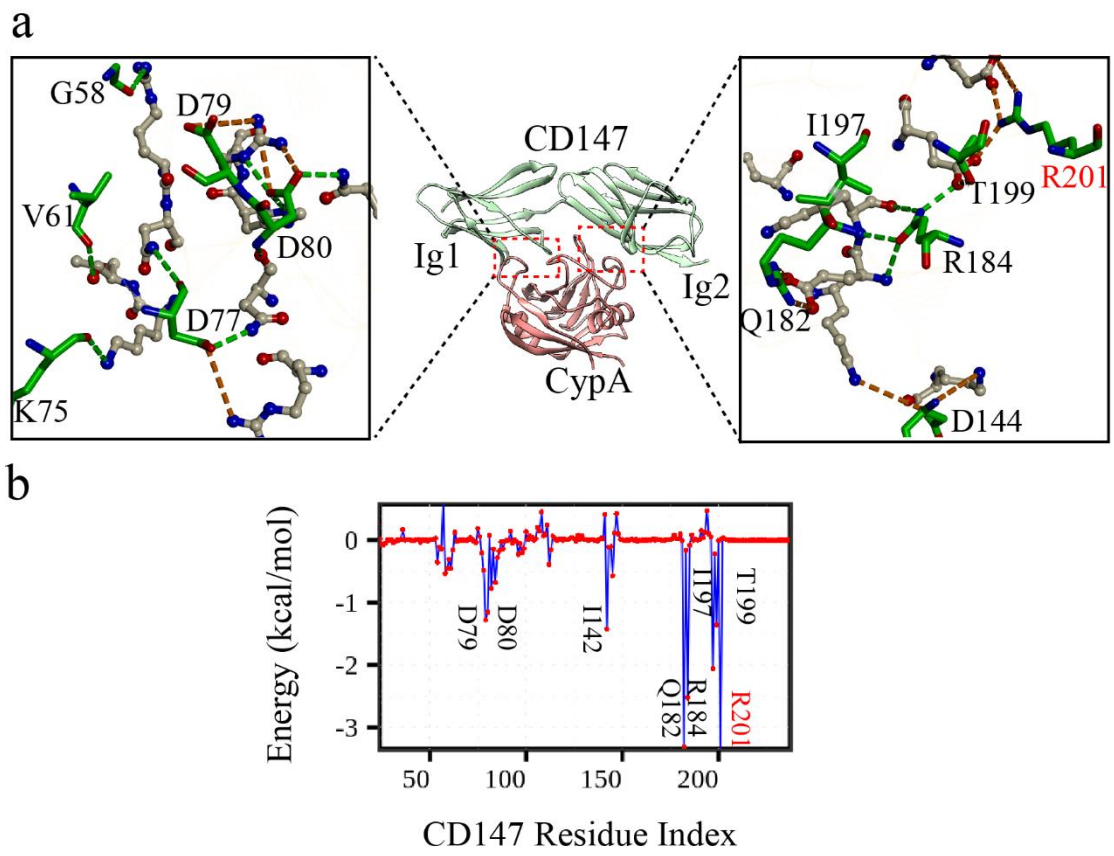

Fig. S7 Key residues in the interaction interface between CD147 and CypA in model-0. (a) Interaction networks between CD147 and CypA. The residues of CD147 and CypA are highlighted using the stick, and ball and stick models, respectively. The important H-bonding interactions are highlighted by the green dotted lines, the salt bridge and electrostatic interactions are in orange dotted lines. (b) Per-residue of CD147 decomposition of the binding free energy of CD147 with CypA.

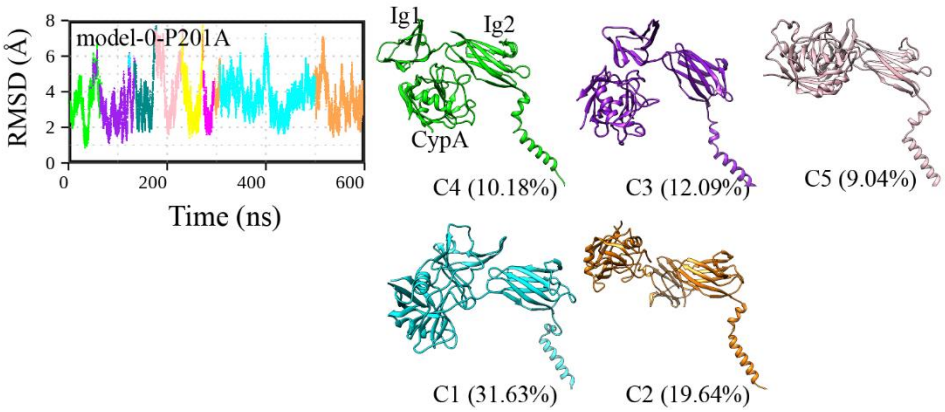

Fig. S8 RMSD of CD147-CypA complex aligning to the centroidal conformation of each cluster in model-0-R201A simulation. Purple, cyan, orange, green, pink, tan1, yellow, and light tea green colors correspond to the clusters. The representative conformations and percentages of the first five clusters are given.