

Extended Data Table 2: Cryo-EM data collection, 3D reconstruction and model statistics

	Nlrp1-DPP9	NLRP1-FIIND(S969A)-DPP9
PDB ID	7CRW	NA
EMDB ID	EMD-30458	EMD-30459
Data collection		
Cryo electron microscope	FEI Titan Krios	FEI Titan Krios
Voltage (kV)	300	300
Detector	Gatan K2 Summit with Gatan GIF Quantum (20eV slit)	Gatan K2 Summit with Gatan GIF Quantum (20eV slit) and Cs corrector
Magnification	130,000	105,000
Pixel size (Å)	1.061	1.091
Total electron dose (e-/Å ²)	49.784	49.969
Exposure rate (e-/pixel/sec)	10.008	10.621
Defocus range (µm)	-1.0 ~ -2.0	-1.0 ~ -2.0
Micrographs collected	7,157	4,971
Micrographs used	7,033	4,667
3D reconstruction		
Software	RELION 3.1	RELION 3.1
Total extracted particles	2,700,586	1,725,380
Number of particles used for 3D reconstruction	182,116	252,425
Symmetry imposed	C1	C1
Resolution range (Å)	3.06-4.65	3.60-6.14
Resolution (Å) after refinement	3.64 (FSC=0.143)	4.29(FSC=0.143)
Resolution (Å) after post-processing	3.18 (FSC=0.143)	3.69(FSC=0.143)
Map sharpening B-factor (Å ²)	-50	-100
Refinement and validation		
Software	Phenix.real_space_refine	NA
Model resolution (Å)	3.3 (FSC=0.5)	NA
Model composition		
Non-hydrogen atoms	16,614	NA
Protein residues	2057	NA
Map-model CC (overall/local)	0.85/0.85	NA
Rwork/Rfree (%)	33.41/33.41	NA
B factors	80.08	NA
R.M.S deviations		
Bonds lengths (Å)	0.005	NA
Bonds angles (°)	0.723	NA
MolProbity score	1.90	NA
Clash score	9.23	NA
Rotamer outliers (%)	0.60	NA
EMRinger score	3.00	NA
Ramachandran plot statistics		
Preferred (%)	93.91	NA
Allowed (%)	5.94	NA
Outlier (%)	0.15	NA