

Supplementary information, Table. S1

	NTSR1-Arr2-Fab30 (EMDB-20505; PDB 6PWC)
Data collection and processing	
Magnification	48,497
Voltage (kV)	300
Electron exposure (e ⁻ /Å ²)	68
Defocus range (μm)	-2.0 ~ -3.5
Pixel size (Å)	1.031
Symmetry imposed	C1
Initial particle images (no.)	4,960,230
Final particle images (no.)	220,464
Map resolution (Å)	4.8
FSC threshold	0.143
Map resolution range (Å)	4.5~7.5
Refinement	
Initial model used (PDB code)	4GRV, 4JQI
Model resolution (Å)	4.8
FSC threshold	0.143
Model resolution range (Å)	50-4.8
Map sharpening <i>B</i> factor (Å ²)	-250
Model composition	
Non-hydrogen atoms	5879
Protein residues	1060
<i>B</i> factors (Å ²)	
Protein	302
R.M.S. deviations	
Bond lengths (Å)	0.005
Bond angles (°)	1.14
Validation	
MolProbity score	0.98
Clash score	2.08
Poor rotamers (%)	0.00
Ramachandran plot	
Favored (%)	98.8
Allowed (%)	1.2
Disallowed (%)	0.00

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