

## Extended Data Table 1 | Data collection and refinement statistics for C5aR1 StaR

Data collection Number of crystals	11
Space group Cell dimensions	P1211
a, b, c (Å) α, β, γ (*)  Number of reflections measured  Number of unique reflections  Resolution (Å)  R <sub>merge</sub> CC <sub>1/2</sub> Mean I/sd(I)  Completeness (%)  Redundancy	83.1, 51.1, 119.0 90.0, 106.7, 90.0 131919 26541 34.60 – 2.70 (2.83 – 2.70) 0.195 (0.923) 0.987 (0.631) 7.0 (1.7) 99.3 (99.6) 5.0 (5.1)
Refinement	
Resolution (Å)	19.89 – 2.70
Number of reflections (test set)	26440 (1352)
R <sub>work</sub> /R <sub>free</sub>	0.2079 / 0.2385
Number of atoms All	5349
Protein	4662
Ligand (NDT9513727)	86
Others (Lipids, ions, waters)	601
Average B factors (Å <sup>2</sup> )	001
All	46.24
C5aR	45.02
Ligand	28.41
Others (Lipid, ion, water)	58.19
RMSD	
Bond lengths (Å)	0.004
Bond angles (°)	1.035
Ramachandran statistics	
Favored regions (%)	98.62
Allowed regions (%)	1.38
Outliers (%)	0.0
MolProbity overall score (percentile)	1.33 (98 <sup>th</sup> )

Values in parentheses indicate highest resolution shell.