Cell, Volume *178*

Supplemental Information

Structural Basis for Allosteric Ligand Recognition in the Human CC Chemokine Receptor 7

Kathrin Jaeger, Steffen Bruenle, Tobias Weinert, Wolfgang Guba, Jonas Muehle, Takuya Miyazaki, Martin Weber, Antonia Furrer, Noemi Haenggi, Tim Tetaz, Chia-Ying Huang, Daniel Mattle, Jean-Marie Vonach, Alain Gast, Andreas Kuglstatter, Markus G. Rudolph, Przemyslaw Nogly, Joerg Benz, Roger J.P. Dawson, and Joerg Standfuss

Data Statistics	**CCR7**	**CCR7$_{6keV}$**
Crystals merged	11	726
Space group	$P2_12_12$	$P2_12_12$
Unit cell (a; b; c; α=β=γ)	79.1; 128.8; 100.6; 90.0	79.1; 129.0; 100.0; 90.0
Wavelength (Å)	1.0	2.066
Resolution (Å)	79.3 – 2.1 (2.4 – 2.1)	50.0 – 3.0 (3.1-3.0)
R_{pim}	10.0 (92.3)	7.6 (163.4)
I/σI	8.1 (1.6)	12.64 (1.6)
Spherical completeness (%)	53.3 (8.7)	100.0 (100.0)
Ellipsoidal completeness (%)	93.7 (83.0)	
Ellipsoidal truncation resolution limits along a*/b*/c*(Å)	2.66 / 2.12 / 3.06	no truncation applied
Multiplicity	27.4 (33.8)	134.5 (103.6)
$CC_{1/2}$	98.6 (63.9)	99.7 (82.9)
Refinement Statistics		
Resolution	54.2 – 2.1	
No. Reflections	31344	
R_{work} / R_{free}	19.6 / 24.4	
Ramachandran favored	92.3	
Ramachandran outliers	0.53	
R.m.s.d. Bond length (Å)	0.003	
R.m.s.d. Bond angles (°)	0.589	
PDB Code	6QZH	

Table S1: Related to Figure 1. X-ray crystallographic data

Helix Loop	allosteric							orthosteric			
		CCR2 CCR2-RA-[*R*]	CCR7 Cmp2105	CCR9 Vercirnon	β2AR G_s	rhodopsin G_i	rhodopsin arrestin		CCR2 BMS-681	CXCR4 IT1t	CCR5 Maraviroc
TM1	1.53		Val79	Val69				1.26		Glu32	
	1.56		Thr82	Val72				1.27	Va37		
	1.57		Tyr83	Tyr73				1.31	Gly41		
	1.60		Phe86					1.35	Leu45		
								1.39	***Tyr49**		
ICL1				Arg78							
			Leu89								
TM2	2.37		***Thr91**	***Thr81**			Thr70	2.60	Trp98	Trp94	Trp86
	2.39	Thr77	***Thr93**	Thr83			Leu72	2.63		***Asp97**	Tyr89
	2.40		****Asp94**	Asp84							
	2.43	Leu81		Leu87							
ELC1										Trp102	
TM3	3.50		Arg154	Arg144	Arg131	Arg135	Arg135	3.29	Thr117		
	3.53				Ala134			3.32	Tyr120	Tyr116	Tyr108
	3.54				Ile135		Val139	3.33			Phe109
	3.55				Thr136		Cys140	3.36			Phe112
	3.56						Lys141				
ICL2					Pro138		Pro142				
					Phe139		Met143				
					Tyr141		Asn145				
					Gln142		Phe146				
					Ser143	Arg147	Arg147				
ELC2										Arg183	
										Ile185	
									Cys190	Cys186	
										Asp187	
										Arg188	
TM5	5.61				Val222		Leu226	5.39			Gln194
	5.64				Glu225		Thr229	5.40			Thr195
	5.65				Ala226			5.43			Ile198
	5.68				Gln229		Ala233				
	5.69				Leu230						
	5.71				Lys232		Gln236				
	5.72				Ile233	Gln237	Gln237				
	5.74					Glu239	Glu239				
	5.78				Arg239						
TM6	6.23					Ser240					
	6.24					Ala241					
	6.25					Thr242	Thr242				
	6.28					Lys245					
	6.29	Arg237				Ala246	Ala246	6.48			Trp248
	6.32					Glu249	Glu249	6.51			***Tyr251**
	6.33	Ala241			Ala271		Val250	6.55			Leu255
	6.36	Val244		Ala255	Thr274	Met253					
	6.37		Ile265	Thr256	Leu275						
	6.40			Va259							
TM7	7.53	Tyr305	Tyr326	Tyr317				7.34			Met279
								7.35	***Gln288**		
								7.38	Glu291	***Glu288**	Glu283
								7.39	***Thr292**		Thr284
	7.56					Met309		7.42	Met295		
H8	8.47	Gly309	Gly330	Gly321		Asn310	Asn310				
	8.48	Glu310	Val331	Glu322		Lys311	Lys311				
	8.49	Lys311	****Lys332**	***Arg323**			Gln312				
	8.50	***Phe312**	***Phe333**	***Phe324**							
	8.53			Asp327							

Table S2: Related to Figure 3. Contact regions between small molecule ligands in chemokine receptors and between receptor-effector complexes. Interactions in the allosteric (left) and orthosteric (right) binding pockets in CCR2 (pdb code: 5t1a), CXCR4 (pdb code: 3odu), CCR5 (pdb code: 4mbs), CCR7 (pdb code: 6qzh) and CCR9 (pdb code: 5lwe) are listed according to the Ballesteros-Weinstein numbering system for GPCRs. Residues involved into hydrogen bonding with a small molecule ligand shown in bold and are marked based on selection using LigPlot+(Laskowski and Swindells, 2011). A selection of the Gs protein (pdb code: 3sn6), Gi protein (pdb code: 3cmo) and arrestin (pdb code: 4zwj) complexes are included as comparison in which residues were included when they had a minimum distance of 4Å between their closest atoms.