Supporting Information S1 Table. Available X-ray structures of $hA_{2A}R$. X-ray resolution, mutations and missing regions are reported. Underlined structures are the templates used for constructing the model corresponding to the 1-329 residues of $hA_{2A}R$ target sequence. For the 4 used templates, bound ligand and all-atom RMSD of the binding cavity with respect 3RFM are also shown. 20 residues within 6.5 Å of CFF in 3RFM were considered for calculation of binding cavity RMSD.

PDB ID	X-ray resolution [Å]	Organism	Mutations	Sequence length	Missing residues	Bound ligand	binding cavity RMSD [Å]
2YDO[1]	3.00	Homo sapiens	L48A; A54L; T65A; Q89A; N154A	1-325	1-5; 214-223; 325		
3REY[2]	3.31	Homo sapiens	A54L; T88A; R107A; K122A; L202A; L235A; V239A; S277A	1-329	1-6; 150-157; 306-329		
3PWH[2]	3.30	Homo sapiens	A54L; T88A; K122A; V239A; R107A; L202A; L235A; S277A	1-329	1-6; 150-157; 306-329		
2YDV[1]	2.60	Homo sapiens	L48A; A54L; T65A Q89A; N154A	1-325	1-2; 215-222	NEC agonist	1.448
3VGA[3]	3.10	Homo sapiens	N154Q	1-326	1-5; 149-155; 309-326		
3VG9[3]	2.70	Homo sapiens	N154G	1-326	1-5; 149-155; 310-326	zm241385 antagonist	1.328
3EML[4]	2.60	Homo sapiens	No mutation	1-488	-14-2; 149-155; 311-326	zm241385 antagonist	1.113
3UZC[5]	3.34	Homo sapiens	A54L; T88A; R107A; K122A; L202A; L235A; V239A; S277A	1-329	1-6; 150-157; 306-329		
3UZA[5]	3.27	Homo sapiens	A54L; T88A; R107A; K122A; L202A; L235A; V239A; S277A	1-329	1-6; 150-157; 306-329		
3QAK[6]	2.71	Homo sapiens; Expressed in Enterobacteria phageT4	C54T; C97A	1-488	-14-2; 149-157; 309-326		
4EIY[7]	1.80	Homo sapiens; Expressed in Escherichia coli	M29W; H124I; R128L	1-447	-24--2; 308-326	zm241385 antagonist	1.139
3RFM[2]	3.60	Homo sapiens	A54L; T88A; R107A; K122A L202A; L235A; V239A; S277A	1-329	1-6; 150-157; 306-329	CFF antagonist	

Supporting References

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