



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2R4S  
Title : Crystal structure of the human beta2 adrenoceptor  
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Deposited on : 2007-08-31  
Resolution : 3.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35

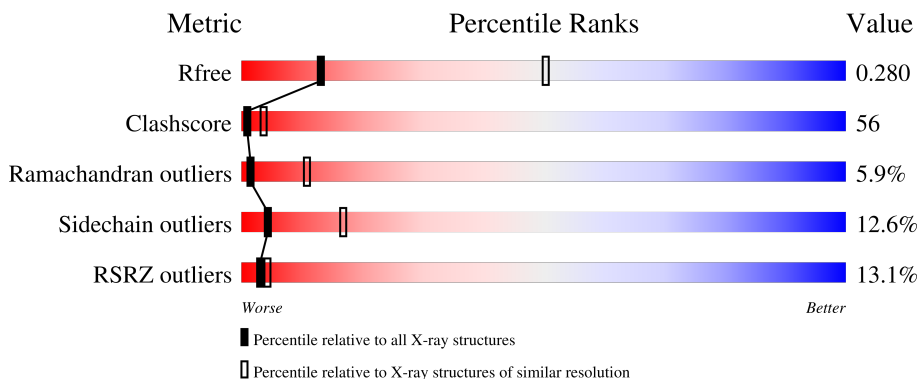
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	342	
2	L	214	
3	H	217	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4925 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Beta-2 adrenergic receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	216	1612	1052	271	279	10	0	0	0

- Molecule 2 is a protein called antibody for beta2 adrenoceptor, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	214	1678	1050	278	341	9	0	0	0

- Molecule 3 is a protein called antibody for beta2 adrenoceptor, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	217	1635	1031	269	328	7	0	0	0



V206  
K207  
S208  
F209  
N210  
R211  
M212  
E213  
C214

- Molecule 3: antibody for beta2 adrenoceptor, heavy chain



E1 V2 Q3 L4 O5 O6 S7 L11 A12 A16 S17 V18 K19 L20 C22 C23 K24 A24 S25 G26 Y27 Y27 L28 F29 T30 D31 Y32 Y33 I34 N35 K36 Y37 R38 Q39 R40 T41 T41 G42 Q43 Q44 F45 E46 W47 I48 I51 Y52 P53 G54 S55 G56 R57 L58 A129 D59 Y60 Q61 N61 F64 K67

A68 T69 L70 T71 A72 D73 K74 S77 T78 A79 M81 Q82 L83 L86 T87 T87 D90 S91 A92 C96 V97 R98 G99 F100 Y102 Y102 W103 T107 T108 L109 T110 T110 V111 A114 K115 T116 T117 P118 P119 S120 V121 L124 A125 P126 G127 S128 A129 A130 Q131 Y132 T132 M133 S134 A135 V136

T137 L138 G139 C140 L141 V142 K143 G144 Y145 F146 P147 E148 P149 V150 T151 V152 T153 W154 M155 S158 L159 S160 V163 F166 P167 A168 V169 L170 Q171 S172 D173 L174 L177 S178 S179 S180 V181 T182 V183 P184 S185 S186 T187 W188 P189 S190 E191 C195 N196 V197 A198 H199 P200 A201 S202

V206 I210 P211 R213 D214 C215 G216 C217

## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	338.38Å 48.48Å 89.35Å 90.00° 104.60° 90.00°	Depositor
Resolution (Å)	19.99 – 3.40 44.67 – 3.38	Depositor EDS
% Data completeness (in resolution range)	97.7 (19.99-3.40) 96.1 (44.67-3.38)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.49 (at 3.40Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.226 , 0.280 0.230 , 0.280	Depositor DCC
$R_{free}$ test set	1904 reflections (9.77%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	97.9	Xtrriage
Anisotropy	0.231	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 121.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.018 for -h-2*1,-k,l	Xtrriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	4925	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	123.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.35	0/1636	0.56	0/2216
2	L	0.43	0/1716	0.75	1/2324 (0.0%)
3	H	0.44	0/1677	0.75	0/2290
All	All	0.41	0/5029	0.70	1/6830 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	L	104	LEU	CA-CB-CG	5.54	128.03	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1612	0	1610	184	0
2	L	1678	0	1610	199	0
3	H	1635	0	1578	183	0
All	All	4925	0	4798	549	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 56.

The worst 5 of 549 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:193:THR:HG23	2:L:208:SER:HB2	1.29	1.10
2:L:169:LYS:H	2:L:169:LYS:HD2	1.20	1.03
2:L:108:ARG:HG2	2:L:109:ALA:H	1.25	0.99
2:L:38:GLN:NE2	3:H:39:GLN:HE22	1.60	0.98
2:L:38:GLN:HE21	3:H:39:GLN:HE22	0.98	0.94

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	204/342 (60%)	155 (76%)	36 (18%)	13 (6%)	1	9
2	L	212/214 (99%)	174 (82%)	27 (13%)	11 (5%)	2	13
3	H	215/217 (99%)	157 (73%)	45 (21%)	13 (6%)	1	10
All	All	631/773 (82%)	486 (77%)	108 (17%)	37 (6%)	1	11

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	140	LYS
1	A	142	GLN
1	A	143	SER
1	A	241	HIS
1	A	343	ARG

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was



analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	167/300 (56%)	153 (92%)	14 (8%)	11	36
2	L	191/191 (100%)	165 (86%)	26 (14%)	3	14
3	H	183/183 (100%)	155 (85%)	28 (15%)	2	11
All	All	541/674 (80%)	473 (87%)	68 (13%)	4	17

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	146	PHE
3	H	153	THR
3	H	195	CYS
2	L	87	TYR
2	L	75	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	137	ASN
3	H	35	ASN
2	L	161	ASN
3	H	133	ASN
2	L	212	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	216/342 (63%)	1.41	74 (34%) <b>0</b> <b>0</b>	58, 192, 250, 290	0
2	L	214/214 (100%)	0.10	4 (1%) 66 65	44, 86, 138, 179	0
3	H	217/217 (100%)	0.18	7 (3%) 47 46	44, 88, 154, 232	0
All	All	647/773 (83%)	0.56	85 (13%) <b>3</b> <b>4</b>	44, 104, 228, 290	0

The worst 5 of 85 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	279	MET	8.0
1	A	89	PHE	6.6
1	A	281	THR	6.4
1	A	218	VAL	5.8
1	A	146	THR	5.5

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.