



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 10:53 AM UTC

PDB ID : 3ADV / pdb_00003adv
Title : Human PPARgamma ligand-binding domain in complex with serotonin
Authors : Waku, T.; Shiraki, T.; Oyama, T.; Morikawa, K.
Deposited on : 2010-01-29
Resolution : 2.27 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

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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

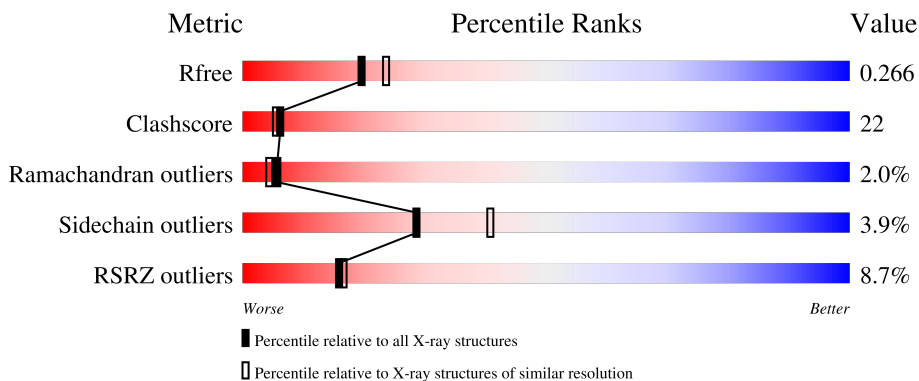
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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}	180053	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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 ≥ 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	287	
1	B	287	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SRO	A	3	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4294 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.

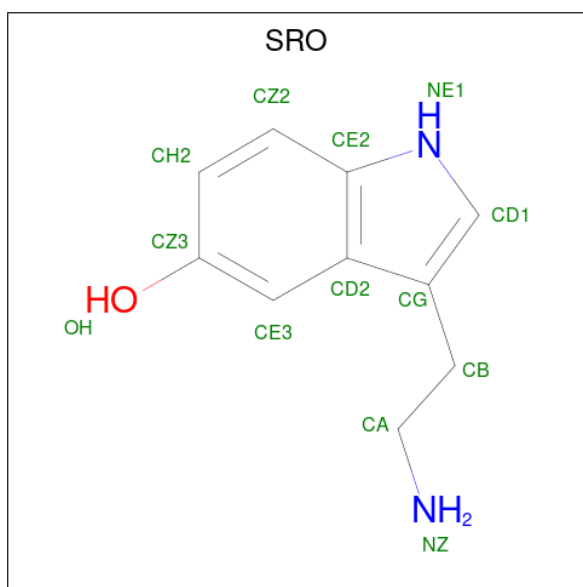
- Molecule 1 is a protein called Peroxisome proliferator-activated receptor gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	262	2083	1343	340	390	10	0	0	0
1	B	257	2063	1336	338	380	9	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	191	GLY	-	expression tag	UNP P37231
A	192	SER	-	expression tag	UNP P37231
A	193	HIS	-	expression tag	UNP P37231
A	194	MET	-	expression tag	UNP P37231
B	191	GLY	-	expression tag	UNP P37231
B	192	SER	-	expression tag	UNP P37231
B	193	HIS	-	expression tag	UNP P37231
B	194	MET	-	expression tag	UNP P37231

- Molecule 2 is SEROTONIN (CCD ID: SRO) (formula: C₁₀H₁₂N₂O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
2	A	1	13	10	2	1	0	0
2	A	1	13	10	2	1	0	0
2	B	1	13	10	2	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	60	60	60	0	0
3	B	49	49	49	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	93.06Å 61.46Å 118.47Å 90.00° 102.89° 90.00°	Depositor
Resolution (Å)	44.60 – 2.27 44.60 – 2.27	Depositor EDS
% Data completeness (in resolution range)	92.1 (44.60-2.27) 93.2 (44.60-2.27)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.80 (at 2.27Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.224 , 0.267 0.221 , 0.266	Depositor DCC
R_{free} test set	1431 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	39.2	Xtrriage
Anisotropy	0.608	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4294	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SRO

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	0.42	0/2116	0.92	8/2851 (0.3%)
1	B	0.40	0/2097	0.88	4/2822 (0.1%)
All	All	0.41	0/4213	0.90	12/5673 (0.2%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	241	THR	N-CA-C	8.05	119.25	108.38
1	B	264	PHE	N-CA-C	-6.98	103.70	113.20
1	B	266	HIS	N-CA-C	-6.95	105.34	113.88
1	A	322	VAL	N-CA-C	6.65	117.34	110.36
1	A	335	ASN	N-CA-C	-6.49	99.47	109.14

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	2083	0	2133	95	0
1	B	2063	0	2126	100	0
2	A	26	0	22	6	0
2	B	13	0	11	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	60	0	0	3	0
3	B	49	0	0	1	0
All	All	4294	0	4292	190	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 22.

The worst 5 of 190 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)
1:B:358:LYS:HB3	1:B:359:PRO:HD2	1.19	1.09
1:A:358:LYS:HB2	1:A:359:PRO:HD3	1.39	1.01
1:B:358:LYS:HB3	1:B:359:PRO:CD	1.94	0.96
1:A:325:ILE:HG23	1:A:388:ILE:HD12	1.54	0.89
1:A:329:MET:HB3	2:A:3:SRO:HA2	1.55	0.89

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	258/287 (90%)	243 (94%)	9 (4%)	6 (2%)	5	3
1	B	249/287 (87%)	234 (94%)	11 (4%)	4 (2%)	7	6
All	All	507/574 (88%)	477 (94%)	20 (4%)	10 (2%)	6	4

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	358	LYS
1	B	270	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	358	LYS
1	A	357	ARG
1	A	240	LYS

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	231/258 (90%)	223 (96%)	8 (4%)	32	45
1	B	230/258 (89%)	220 (96%)	10 (4%)	26	36
All	All	461/516 (89%)	443 (96%)	18 (4%)	28	41

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	333	LEU
1	B	362	ASP
1	B	340	LEU
1	B	211	LEU
1	B	319	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	449	HIS
1	B	454	GLN
1	B	253	ASN
1	B	271	GLN
1	B	283	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SRO	A	1	-	14,14,14	1.39	3 (21%)	19,19,19	0.93	1 (5%)
2	SRO	A	3	-	14,14,14	1.43	3 (21%)	19,19,19	0.92	1 (5%)
2	SRO	B	4	-	14,14,14	1.36	2 (14%)	19,19,19	0.95	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SRO	A	1	-	-	3/3/3/3	0/2/2/2
2	SRO	A	3	-	-	1/3/3/3	0/2/2/2
2	SRO	B	4	-	-	1/3/3/3	0/2/2/2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3	SRO	CE3-CD2	2.26	1.43	1.39
2	B	4	SRO	CD2-CG	2.23	1.47	1.44
2	A	1	SRO	CE3-CD2	2.20	1.43	1.39
2	A	1	SRO	CD2-CG	2.18	1.47	1.44

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	4	SRO	CE3-CD2	2.17	1.43	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3	SRO	CZ2-CE2-CD2	-2.82	119.46	122.19
2	A	1	SRO	CZ2-CE2-CD2	-2.74	119.53	122.19
2	B	4	SRO	CZ2-CE2-CD2	-2.65	119.62	122.19

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	SRO	NZ-CA-CB-CG
2	A	3	SRO	NZ-CA-CB-CG
2	B	4	SRO	NZ-CA-CB-CG
2	A	1	SRO	CA-CB-CG-CD2
2	A	1	SRO	CA-CB-CG-CD1

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3	SRO	6	0

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, 95th 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 ²)	Q<0.9
1	A	262/287 (91%)	0.44	21 (8%) 18 19	29, 45, 75, 99	0
1	B	257/287 (89%)	0.54	24 (9%) 14 15	29, 47, 100, 111	0
All	All	519/574 (90%)	0.49	45 (8%) 16 16	29, 46, 88, 111	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	363	PHE	6.4
1	B	264	PHE	5.2
1	B	267	ILE	4.4
1	A	241	THR	3.8
1	A	262	ILE	3.6

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SRO	A	3	13/13	0.67	0.25	79,84,85,85	0
2	SRO	B	4	13/13	0.77	0.25	91,93,94,94	0
2	SRO	A	1	13/13	0.82	0.23	83,85,86,86	0

6.5 Other polymers [i](#)

There are no such residues in this entry.