



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 02:27 AM GMT

PDB ID : 2F4B  
Title : Crystal structure of the ligand binding domain of human PPAR-gamma in complex with an agonist  
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Deposited on : 2005-11-23  
Resolution : 2.07 Å(reported)

This is a wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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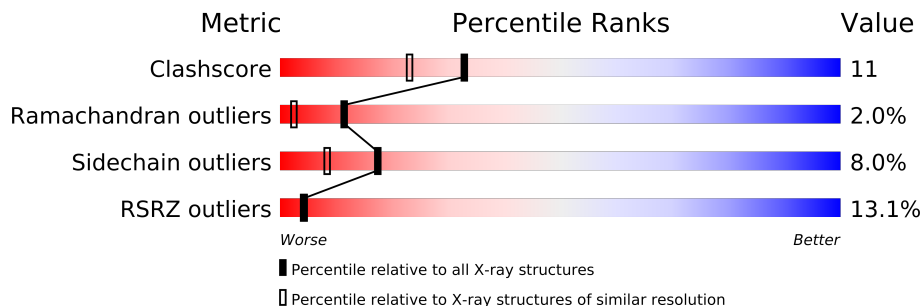
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.07 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))
Clashscore	79885	1390 (2.08-2.04)
Ramachandran outliers	78287	1381 (2.08-2.04)
Sidechain outliers	78261	1381 (2.08-2.04)
RSRZ outliers	66119	1225 (2.08-2.04)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	271	
1	B	271	

## 2 Entry composition i

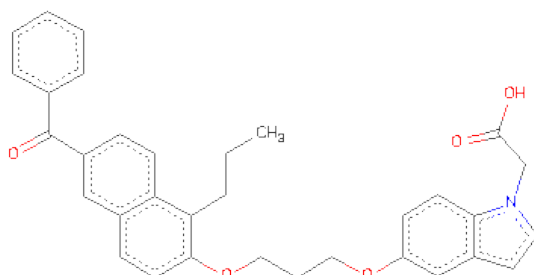
There are 3 unique types of molecules in this entry. The entry contains 4535 atoms, of which 0 are hydrogen and 0 are deuterium.

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
1	A	271	Total	C	N	O	S	0	0	0
			2178	1406	355	407	10			
1	B	271	Total	C	N	O	S	0	0	0
			2178	1406	355	407	10			

- Molecule 2 is (5-{3-[(6-BENZOYL-1-PROPYL-2-NAPHTHYL)OXY]PROPOXY}-1H-INDOL-1-YL)ACETICACID (three-letter code: EHA) (formula: C<sub>33</sub>H<sub>31</sub>NO<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			39	33	1	5		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	59	Total	O	0	0
			59	59		

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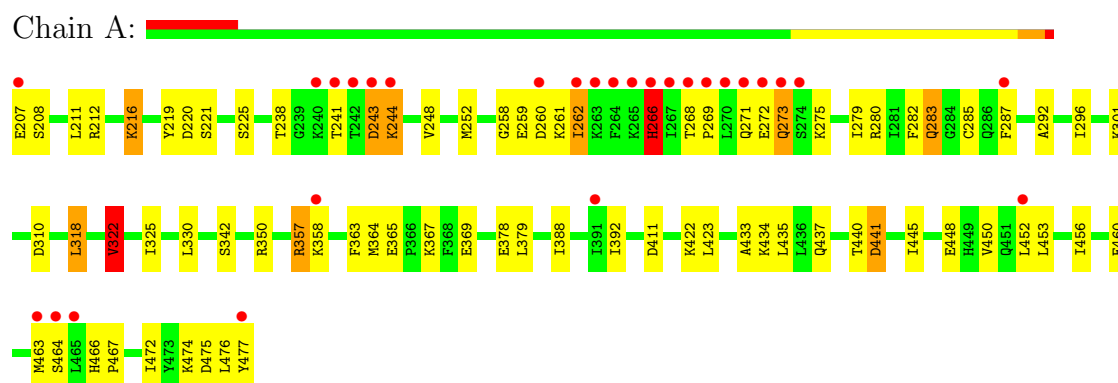
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	81	Total	O	0	0
			81	81		

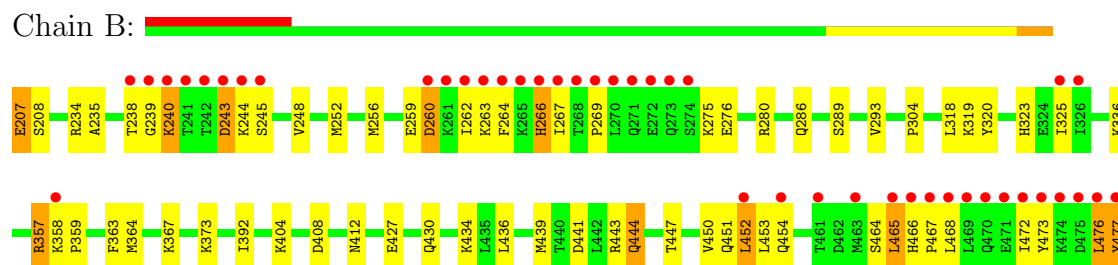
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Peroxisome proliferator-activatedreceptor gamma



- Molecule 1: Peroxisome proliferator-activatedreceptor gamma



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.97Å 88.64Å 57.88Å 90.00° 90.01° 90.00°	Depositor
Resolution (Å)	30.00 – 2.07 26.69 – 2.07	Depositor EDS
% Data completeness (in resolution range)	97.2 (30.00-2.07) 93.3 (26.69-2.07)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.56 (at 2.06Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, $R_{free}$	0.219 , 0.288 0.221 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	29.0	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 39.8	EDS
Estimated twinning fraction	0.000 for l,k,-h 0.031 for h,-k,-l 0.022 for l,-k,h	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 33485 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4535	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.22% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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

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	0.97	1/2216 (0.0%)	0.90	3/2985 (0.1%)
1	B	1.00	2/2216 (0.1%)	0.94	3/2985 (0.1%)
All	All	0.98	3/4432 (0.1%)	0.92	6/5970 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	238	THR	C-O	6.08	1.34	1.23
1	B	207	GLU	CD-OE1	5.87	1.32	1.25
1	A	369	GLU	CG-CD	5.07	1.59	1.51

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	266	HIS	O-C-N	-7.47	110.75	122.70
1	A	266	HIS	CA-C-O	-6.29	106.89	120.10
1	B	234	ARG	NE-CZ-NH1	-5.96	117.32	120.30
1	A	322	VAL	CG1-CB-CG2	5.84	120.24	110.90
1	B	452	LEU	CA-CB-CG	5.17	127.20	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	266	HIS	Mainchain
1	A	357	ARG	Peptide
1	B	245	SER	Mainchain

## 5.2 Close contacts

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2178	0	2241	56	0
1	B	2178	0	2241	45	0
2	A	39	0	30	5	0
3	A	59	0	0	3	0
3	B	81	0	0	11	0
All	All	4535	0	4512	100	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 11.

The worst 5 of 100 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:444:GLN:HB3	3:B:98:HOH:O	1.47	1.11
1:B:412:ASN:HB3	3:B:3:HOH:O	1.60	1.01
1:A:275:LYS:HD3	1:A:279:ILE:HG21	1.52	0.90
1:A:216:LYS:NZ	1:A:219:TYR:CD2	2.44	0.85
1:A:243:ASP:HB2	1:A:244:LYS:HG2	1.58	0.84

There are no symmetry-related clashes.



## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	269/271 (99%)	249 (93%)	13 (5%)	7 (3%)	8	1
1	B	269/271 (99%)	254 (94%)	11 (4%)	4 (2%)	15	4
All	All	538/542 (99%)	503 (94%)	24 (4%)	11 (2%)	11	2

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	262	ILE
1	B	266	HIS
1	A	260	ASP
1	B	473	TYR
1	A	271	GLN

### 5.3.2 Protein sidechains ⓘ

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	244/244 (100%)	225 (92%)	19 (8%)	18	9
1	B	244/244 (100%)	224 (92%)	20 (8%)	17	8
All	All	488/488 (100%)	449 (92%)	39 (8%)	17	8

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	441	ASP
1	B	240	LYS
1	B	465	LEU
1	A	477	TYR

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Mol	Chain	Res	Type
1	B	207	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	273	GLN
1	B	470	GLN
1	B	286	GLN
1	A	437	GLN
1	B	283	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

1 ligand is 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	EHA	A	201	-	43,43,43	1.62	6 (13%)	59,59,59	1.12	5 (8%)

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	EHA	A	201	-	-	2/23/23/23	0/1/5/5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	201	EHA	CAV-N	-5.62	1.34	1.39
2	A	201	EHA	CAL-CAK	3.90	1.56	1.49
2	A	201	EHA	CAH-CAK	3.13	1.55	1.49
2	A	201	EHA	CAZ-N	-3.05	1.34	1.38
2	A	201	EHA	CAF-CAE	2.54	1.41	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	EHA	CAW-CAV-N	-3.48	105.50	108.61
2	A	201	EHA	CAU-CAV-N	2.50	134.85	130.29
2	A	201	EHA	CBA-CAW-CAV	2.31	108.17	106.20
2	A	201	EHA	CAJ-CAD-CAE	-2.22	119.86	122.77
2	A	201	EHA	OBf-CBG-CBH	2.19	117.04	108.42

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	EHA	OXT-C-CA-N
2	A	201	EHA	O-C-CA-N

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	271/271 (100%)	0.67	28 (10%) 7 7	17, 33, 69, 99	0
1	B	271/271 (100%)	1.03	43 (15%) 3 2	15, 31, 99, 130	0
All	All	542/542 (100%)	0.85	71 (13%) 4 4	15, 32, 94, 130	0

The worst 5 of 71 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	477	TYR	13.9
1	B	476	LEU	13.8
1	B	465	LEU	12.0
1	A	269	PRO	11.7
1	A	264	PHE	11.5

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	EHA	A	201	39/39	0.24	0.59	58,62,64,64	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.