

# Full wwPDB X-ray Structure Validation Report (i)

#### May 26, 2020 – 07:30 pm BST

PDB ID	:	5G45
$\operatorname{Title}$	:	Ligand complex of RORg LBD
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Deposited on	:	2016-05-04
Resolution	:	$2.07 \ { m \AA(reported)}$

This is a Full wwPDB X-ray Structure Validation 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

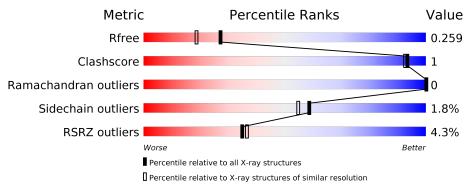
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
$\operatorname{CCP4}$	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (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 >=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 <=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	А	266	86%	5% 8%					
2	С	10	50% 80%	20%					



## 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2306 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 NUCLEAR RECEPTOR ROR-GAMMA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	244	Total 1990	C 1268	N 356	O 352	S 14	0	0	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	244	HIS	-	expression tag	UNP P51449
A	245	ASN	-	expression tag	UNP P51449
А	246	HIS	-	expression tag	UNP P51449
А	247	ASN	-	expression tag	UNP P51449
A	248	HIS	-	expression tag	UNP P51449
A	249	ASN	-	expression tag	UNP P51449
А	250	HIS	-	expression tag	UNP P51449
A	251	ASN	-	expression tag	UNP P51449
A	252	HIS	-	expression tag	UNP P51449
A	253	ASN	-	expression tag	UNP P51449
А	254	HIS	-	expression tag	UNP P51449
A	255	ASN	-	expression tag	UNP P51449
A	256	GLY	-	expression tag	UNP P51449
А	257	GLY	-	expression tag	UNP P51449
A	258	GLU	-	expression tag	UNP P51449
A	259	ASN	-	expression tag	UNP P51449
А	260	LEU	-	expression tag	UNP P51449
А	261	TYR	-	expression tag	UNP P51449
А	262	PHE	-	expression tag	UNP P51449
А	263	GLN	-	expression tag	UNP P51449
А	264	GLY	-	expression tag	UNP P51449
А	508	GLY	-	expression tag	UNP P51449
A	509	GLY	-	expression tag	UNP P51449

There are 23 discrepancies between the modelled and reference sequences:

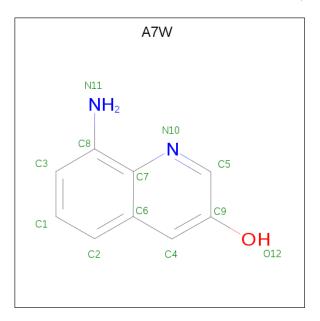
• Molecule 2 is a protein called RORG.



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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	С	10	Total 85	$\begin{array}{c} \mathrm{C} \\ 54 \end{array}$	N 17	O 14	0	0	0

• Molecule 3 is 8-AMINO-3-QUINOLINOL (three-letter code: A7W) (formula: C<sub>9</sub>H<sub>8</sub>N<sub>2</sub>O).



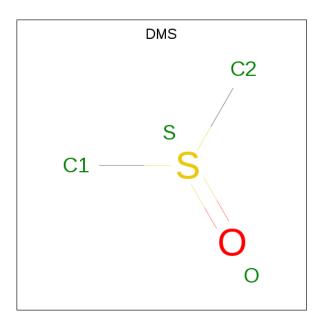
ľ	Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
	3	А	1	Total 12	С 9	N 2	O 1	0	0

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Na 1 1	0	0

• Molecule 5 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C<sub>2</sub>H<sub>6</sub>OS).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	А	1	Total 4	$\begin{array}{c} \mathrm{C} \\ \mathrm{2} \end{array}$	0 1	${ m S}$ 1	0	0

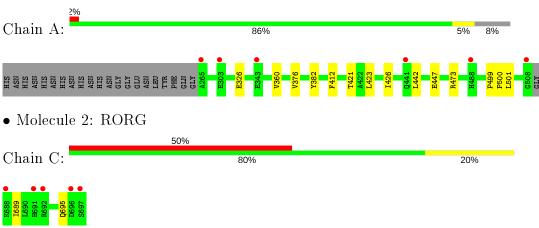
• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	209	Total O 209 209	0	0
6	С	5	Total O 5 5	0	0



## 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: NUCLEAR RECEPTOR ROR-GAMMA



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	62.22Å 62.22Å 154.06Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	21.00 - 2.07	Depositor
Resolution (A)	20.75 - 2.07	EDS
% Data completeness	99.9 (21.00-2.07)	Depositor
(in resolution range)	99.9(20.75 - 2.07)	EDS
R <sub>merge</sub>	0.26	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.76 (at 2.07 \text{\AA})$	Xtriage
Refinement program	BUSTER 2.11.1	Depositor
D D.	0.208 , $0.256$	Depositor
$R, R_{free}$	0.211 , $0.259$	DCC
$R_{free}$ test set	987 reflections $(5.14\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	30.4	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35 , $53.3$	EDS
L-test for $twinning^2$	$ \langle L  \rangle = 0.48, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2306	wwPDB-VP
Average B, all atoms $(Å^2)$	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.59% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



 $<sup>^1 {\</sup>rm Intensities}$  estimated from amplitudes.

## 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: A7W, NA, DMS

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
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.51	0/2033	0.62	0/2738
2	С	0.47	0/85	0.57	0/112
All	All	0.51	0/2118	0.62	0/2850

There are no bond length outliers.

There are no bond angle outliers.

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	А	1990	0	1992	6	0
2	С	85	0	93	1	0
3	А	12	0	0	0	0
4	А	1	0	0	0	0
5	А	4	0	6	0	0
6	А	209	0	0	0	0
6	С	5	0	0	0	0
All	All	2306	0	2091	6	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 1.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:ILE:HG21	1:A:442:LEU:HG	1.92	0.49
1:A:423:LEU:HD11	1:A:447:GLU:HA	1.96	0.48
1:A:499:PRO:HA	1:A:500:PRO:HD3	1.92	0.44
1:A:376:VAL:O	1:A:382:TYR:HA	2.19	0.43
1:A:360:VAL:HG13	1:A:421:THR:HB	2.00	0.42
1:A:501:LEU:HB2	2:C:689:ILE:HG21	2.01	0.42

All (6) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	Perce	$\mathbf{n}$ tiles
1	А	242/266~(91%)	239~(99%)	3~(1%)	0	100	100
2	С	8/10~(80%)	8 (100%)	0	0	100	100
All	All	250/276~(91%)	247 (99%)	3 (1%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	А	217/235~(92%)	214~(99%)	3~(1%)	67 64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	С	10/10~(100%)	9~(90%)	1 (10%)	7 2
All	All	227/245~(93%)	223~(98%)	4 (2%)	59 55

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	326	GLU
1	А	412	PHE
1	А	473	ARG
2	С	695	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	405	HIS
1	А	487	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 carbohydrates in this entry.

#### 5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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



Γ	Mol	Type	Chain	Res	Link	Bo	ond leng	$\mathbf{ths}$	В	ond ang	les
	10101	туре	Unam	ries	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
	3	A7W	A	1509	-	12, 13, 13	1.14	0	$18,\!18,\!18$	1.12	1 (5%)
	5	DMS	А	1511	-	3, 3, 3	0.92	0	$3,\!3,\!3$	0.60	0

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).

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.

Mo	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	A7W	А	1509	-	-	-	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	1509	A7W	C9-C4-C6	-3.44	116.72	120.45

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

#### 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 $>$	$\# RSRZ {>}2$	$OWAB(Å^2)$	Q<0.9
1	А	244/266~(91%)	0.03	6 (2%) 57 60	20, 29, 49, 66	0
2	С	10/10~(100%)	1.92	5 (50%) 0 0	35, 48, 68, 95	0
All	All	254/276~(92%)	0.10	11 (4%) 35 36	20, 30, 53, 95	0

All (11) RSRZ outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	RSRZ
2	С	697	SER	4.2
1	А	265	ALA	4.0
2	С	691	HIS	3.7
2	С	696	ASP	2.9
1	А	488	HIS	2.8
1	А	303	GLU	2.7
2	С	688	LYS	2.5
1	А	343	GLU	2.3
1	А	441	GLN	2.3
1	А	508	GLY	2.2
2	С	692	ARG	2.2

### 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 carbohydrates 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,  $95^{th}$  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	$\mathbf{RSR}$	$\mathbf{B} extsf{-factors}(\mathrm{\AA}^2)$	Q<0.9
3	A7W	А	1509	12/12	0.90	0.14	22,26,29,30	0
4	NA	А	1510	1/1	0.92	0.20	$30,\!30,\!30,\!30$	0
5	DMS	А	1511	4/4	0.98	0.09	25,44,45,49	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

