

wwPDB X-ray Structure Validation Summary Report (i)

Nov 22, 2023 – 10:32 PM JST

:	7XQE
:	Crystal Structure of human RORgamma (C455E) LBD in complex with com-
	pound XY039
:	Wu, X.; Li, C.; Zhang, Y.; Xu, Y.
:	2022-05-07
:	2.57 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 (i) 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 (1)) were used in the production of this report:

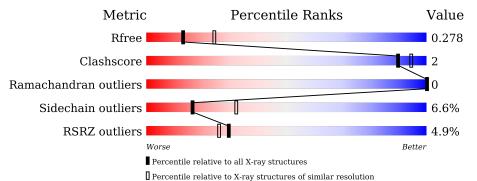
MolProbity Mogul Xtriage (Phenix) EDS	:	4.02b-467 1.8.5 (274361), CSD as541be (2020) 1.13 2.36
buster-report Percentile statistics Refmac	: : :	1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.57 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	$\begin{array}{l} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	3676 (2.60-2.56)
Clashscore	141614	4049(2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614 (2.60-2.56)

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 <=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	267	6%	7%	25%
1	В	267	^{2%} 69%	9%	22%



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3455 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Δ	201	Total	С	Ν	0	\mathbf{S}	0	0	0
	A	201	1640	1039	290	299	12	0	0	0
1	Р	209	Total	С	Ν	0	S	0	0	0
	D	209	1709	1082	307	308	12	0	0	0

• Molecule 1 is a protein called Nuclear receptor ROR-gamma.

Chain	Residue	Modelled	Actual	Comment	Reference
А	241	GLU	-	expression tag	UNP P51449
А	242	GLY	-	expression tag	UNP P51449
А	243	ASP	-	expression tag	UNP P51449
А	244	ILE	-	expression tag	UNP P51449
А	245	HIS	-	expression tag	UNP P51449
А	246	MET	-	expression tag	UNP P51449
А	247	LYS	-	expression tag	UNP P51449
А	248	LYS	-	expression tag	UNP P51449
А	249	GLY	-	expression tag	UNP P51449
А	250	TYR	-	expression tag	UNP P51449
А	251	HIS	-	expression tag	UNP P51449
А	252	HIS	-	expression tag	UNP P51449
А	253	HIS	-	expression tag	UNP P51449
А	254	HIS	-	expression tag	UNP P51449
А	255	HIS	-	expression tag	UNP P51449
А	256	LEU	-	expression tag	UNP P51449
А	257	VAL	-	expression tag	UNP P51449
А	258	PRO	-	expression tag	UNP P51449
А	259	ARG	-	expression tag	UNP P51449
А	260	GLY	-	expression tag	UNP P51449
А	261	SER	-	expression tag	UNP P51449
А	455	GLU	CYS	engineered mutation	UNP P51449
В	241	GLU	-	expression tag	UNP P51449
В	242	GLY	-	expression tag	UNP P51449
В	243	ASP	-	expression tag	UNP P51449

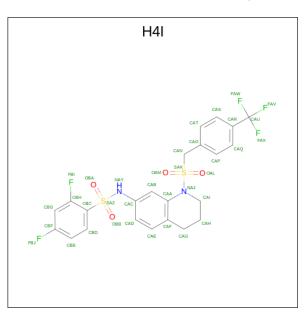
There are 44 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
В	244	ILE	-	expression tag	UNP P51449
В	245	HIS	-	expression tag	UNP P51449
В	246	MET	-	expression tag	UNP P51449
В	247	LYS	-	expression tag	UNP P51449
В	248	LYS	-	expression tag	UNP P51449
В	249	GLY	-	expression tag	UNP P51449
В	250	TYR	-	expression tag	UNP P51449
В	251	HIS	-	expression tag	UNP P51449
В	252	HIS	-	expression tag	UNP P51449
В	253	HIS	-	expression tag	UNP P51449
В	254	HIS	-	expression tag	UNP P51449
В	255	HIS	-	expression tag	UNP P51449
В	256	LEU	-	expression tag	UNP P51449
В	257	VAL	-	expression tag	UNP P51449
В	258	PRO	-	expression tag	UNP P51449
В	259	ARG	-	expression tag	UNP P51449
В	260	GLY	-	expression tag	UNP P51449
В	261	SER	-	expression tag	UNP P51449
В	455	GLU	CYS	engineered mutation	UNP P51449

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• Molecule 2 is 2,4-difluoro-N-(1-((4-(trifluoromethyl)benzyl)sulfonyl)-1,2,3,4-tetrahydroquin olin-7-yl)benzenesulfonamide (three-letter code: H4I) (formula: C₂₃H₁₉F₅N₂O₄S₂) (labeled as "Ligand of Interest" by depositor).



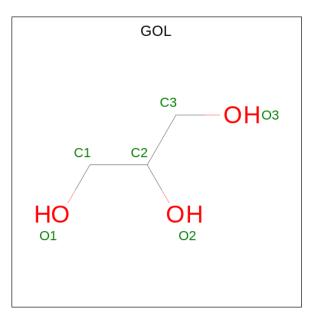
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
2	А	1	Total 36	C 23				$\frac{S}{2}$	0	0



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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
2	В	1	Total 36	C 23	F 5	N 2	0 4	${ m S} { m 2}$	0	0

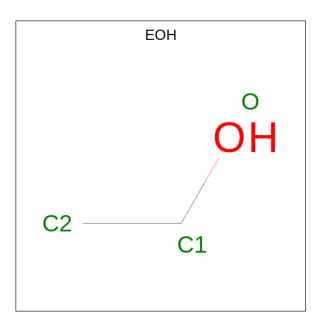
• Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0

• Molecule 4 is ETHANOL (three-letter code: EOH) (formula: C_2H_6O).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	А	1	Total 3	$\begin{array}{c} \mathrm{C} \\ \mathrm{2} \end{array}$	0 1	0	0

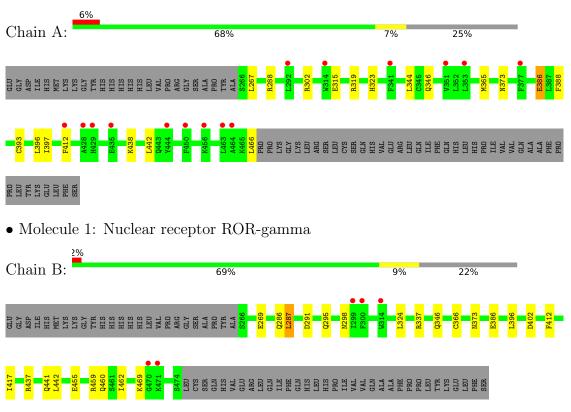
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	8	Total O 8 8	0	0
5	В	5	Total O 5 5	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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	I 41 2 2	Depositor
Cell constants	83.47Å 83.47Å 317.32Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 - 2.57	Depositor
Resolution (A)	80.72 - 2.57	EDS
% Data completeness	99.5 (20.00-2.57)	Depositor
(in resolution range)	$99.8 \ (80.72 - 2.57)$	EDS
R _{merge}	0.08	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.16 (at 2.58 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
D D.	0.227 , 0.277	Depositor
R, R_{free}	0.232 , 0.278	DCC
R_{free} test set	919 reflections (4.98%)	wwPDB-VP
Wilson B-factor $(Å^2)$	63.6	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34 , 44.9	EDS
L-test for twinning ²	$ \langle L \rangle = 0.47, \langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3455	wwPDB-VP
Average B, all atoms $(Å^2)$	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.20% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities 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: GOL, EOH, H4I

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		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.45	0/1671	0.71	1/2248~(0.0%)	
1	В	0.47	0/1742	0.71	1/2341~(0.0%)	
All	All	0.46	0/3413	0.71	2/4589~(0.0%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	В	291	ASP	CB-CG-OD1	5.32	123.09	118.30
1	А	412	PHE	CB-CG-CD1	5.29	124.50	120.80

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	1640	0	1619	6	0
1	В	1709	0	1709	8	0
2	А	36	0	0	1	0
2	В	36	0	0	0	0
3	А	12	0	16	0	0
3	В	6	0	8	0	0
4	А	3	0	6	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	А	8	0	0	0	0
5	В	5	0	0	2	0
All	All	3455	0	3358	12	0

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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 2.

The worst 5 of 12 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:A:344:LEU:HD23	1:A:438:LYS:HE3	1.88	0.56
1:B:462:ILE:HG21	5:B:701:HOH:O	2.08	0.52
1:A:373:ASN:HA	1:B:373:ASN:HA	1.92	0.51
1:A:386:GLU:HG2	1:B:402:ASP:OD1	2.13	0.49
1:A:388:PHE:HB2	1:A:397:ILE:HD13	1.97	0.46

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	ntiles
1	А	199/267~(74%)	192 (96%)	7 (4%)	0	100	100
1	В	207/267~(78%)	202~(98%)	5(2%)	0	100	100
All	All	406/534~(76%)	394~(97%)	12 (3%)	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	177/237~(75%)	167~(94%)	10 (6%)	21 40
1	В	186/237~(78%)	172 (92%)	14 (8%)	13 26
All	All	363/474 (77%)	339~(93%)	24 (7%)	16 32

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	346	GLN
1	В	396	LEU
1	В	386	GLU
1	В	437	ARG
1	А	365	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	309	GLN
1	В	295	GLN
1	В	309	GLN
1	В	460	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

6 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	e Chain Res		no Chain	Dec	Link	B	ond leng	gths	Bond angles		
INIOI	туре	Unaim	nes	nes Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2		
3	GOL	А	603	-	$5,\!5,\!5$	0.58	0	$5,\!5,\!5$	0.53	0		
2	H4I	В	601	-	38,39,39	3.48	13 (34%)	55,60,60	2.18	12 (21%)		
3	GOL	А	602	-	$5,\!5,\!5$	0.48	0	$5,\!5,\!5$	0.58	0		
2	H4I	А	601	-	38, 39, 39	3.53	11 (28%)	55,60,60	2.53	14 (25%)		
4	EOH	А	604	-	2,2,2	0.41	0	1,1,1	0.20	0		
3	GOL	В	602	-	$5,\!5,\!5$	0.53	0	$5,\!5,\!5$	0.43	0		

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
3	GOL	А	603	-	-	0/4/4/4	-
2	H4I	В	601	-	-	3/27/38/38	0/4/4/4
3	GOL	А	602	-	-	2/4/4/4	-
2	H4I	А	601	-	-	4/27/38/38	0/4/4/4
3	GOL	В	602	-	-	2/4/4/4	-

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
2	А	601	H4I	OBA-SAZ	9.37	1.54	1.43
2	В	601	H4I	OBA-SAZ	9.05	1.53	1.43
2	В	601	H4I	OAL-SAK	8.59	1.53	1.43



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Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	А	601	H4I	OAL-SAK	8.29	1.52	1.43
2	А	601	H4I	OBB-SAZ	7.61	1.52	1.43

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	601	H4I	OAM-SAK-OAL	-11.19	107.50	118.98
2	В	601	H4I	OAM-SAK-OAL	-8.62	110.13	118.98
2	В	601	H4I	OBB-SAZ-OBA	-8.42	109.20	119.55
2	А	601	H4I	OBB-SAZ-OBA	-8.37	109.27	119.55
2	А	601	H4I	CBG-CBH-CBC	-4.50	120.49	123.10

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	601	H4I	CAI-NAJ-SAK-OAL
2	В	601	H4I	CAI-NAJ-SAK-OAL
3	А	602	GOL	O1-C1-C2-C3
3	А	602	GOL	O1-C1-C2-O2
2	А	601	H4I	CAI-NAJ-SAK-OAM

There are no ring outliers.

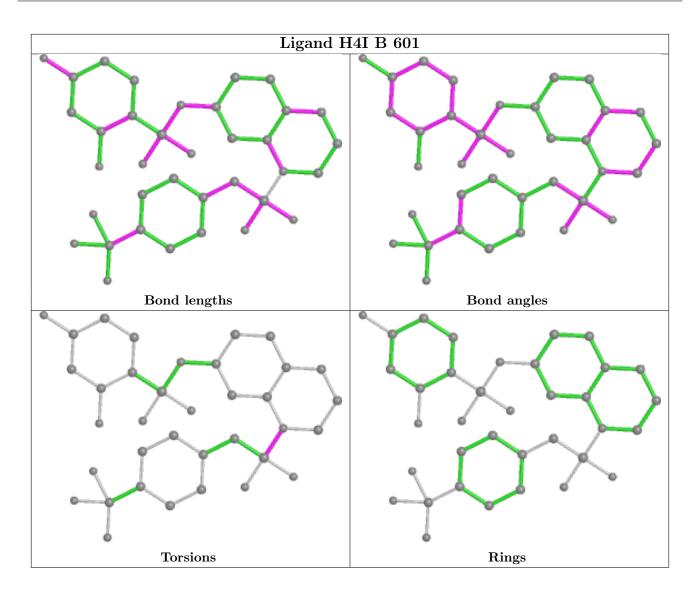
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	601	H4I	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and sufficient the outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

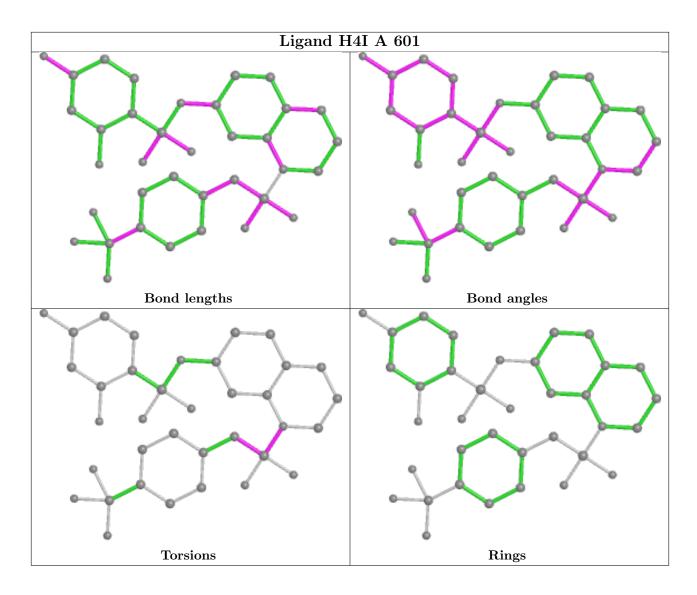












5.7 Other polymers (i)

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^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	201/267~(75%)	0.57	15 (7%) 14 11	42, 68, 106, 117	0
1	В	209/267~(78%)	0.49	5 (2%) 59 55	39, 64, 97, 118	0
All	All	410/534~(76%)	0.53	20 (4%) 29 26	39, 66, 104, 118	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	428	ALA	4.7
1	А	353	LEU	3.4
1	А	464	ALA	3.0
1	А	450	PHE	2.9
1	А	429	HIS	2.9

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.

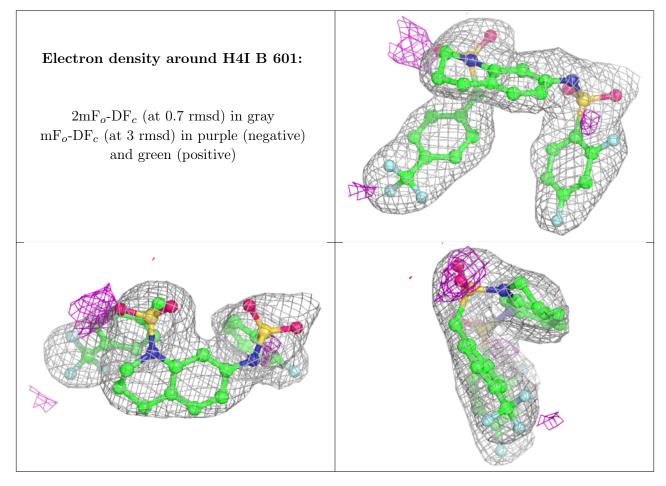
6.4 Ligands (i)

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.

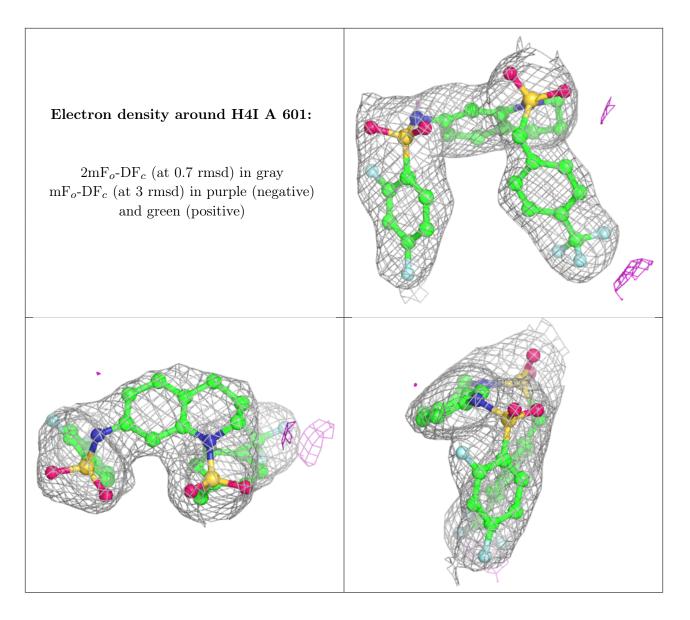


Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GOL	А	603	6/6	0.67	0.30	64,73,76,78	0
3	GOL	А	602	6/6	0.78	0.19	67,77,84,86	0
4	EOH	А	604	3/3	0.83	0.25	61,61,65,66	0
3	GOL	В	602	6/6	0.86	0.32	$63,\!66,\!69,\!75$	0
2	H4I	В	601	36/36	0.94	0.20	58,65,73,79	0
2	H4I	А	601	36/36	0.96	0.20	$61,\!69,\!77,\!82$	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.







6.5 Other polymers (i)

There are no such residues in this entry.

