



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 20, 2022 – 01:21 PM EDT

PDB ID : 7TRB

Title : CRYSTAL STRUCTURE OF FARNESOID X-ACTIVATED RECEPTOR COMPLEXED WITH COMPOUND-32 AKA (1S,3S)-N-({4-[5-(2-FLUOROPROPAN-2-YL)-1,2,4-OXADIAZOL-3-YL]BICYCLO[2.2.2]OCTAN-1-YL}METHYL)-3-HYDROXY-N-[4'-(2-HYDROXYPROPAN-2-YL)-[1,1'-BIPHENYL]-3-YL]-3-(TRIFLUOROMETHYL)CYCLOBUTANE-1-CARBOXYAMIDE

Authors : Khan, J.A.; Ruzanov, M.

Deposited on : 2022-01-28

Resolution : 2.15 Å(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](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
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
buster-report	:	1.1.7 (2018)
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)

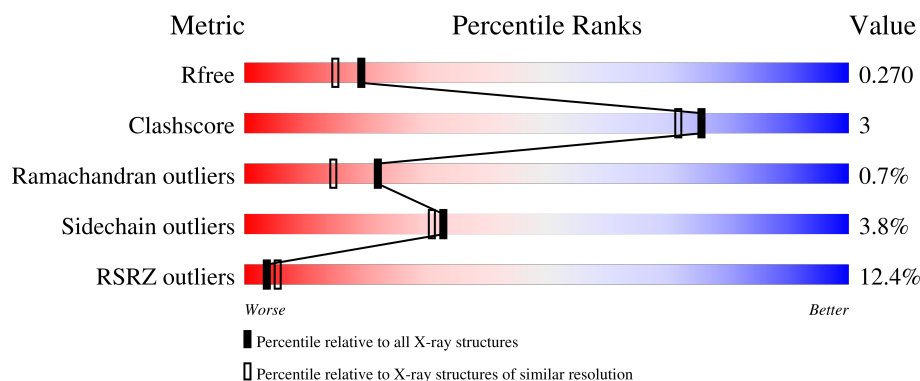
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)


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	251	<div> <div>12%</div> <div>85%</div> <div>5%</div> <div>10%</div> </div>
1	B	251	<div> <div>11%</div> <div>75%</div> <div>12%</div> <div>12%</div> </div>
2	C	14	<div> <div>71%</div> <div>7%</div> <div>21%</div> </div>

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.29

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Mol	Chain	Length	Quality of chain
2	D	14	 79% 21%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3809 atoms, of which 82 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 Bile acid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	1	0
			1717	1101	288	318	10			
1	B	221	Total	C	N	O	S	0	2	0
			1728	1107	285	326	10			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	226	MET	-	expression tag	UNP Q96RI1
A	227	GLY	-	expression tag	UNP Q96RI1
A	228	SER	-	expression tag	UNP Q96RI1
A	229	SER	-	expression tag	UNP Q96RI1
A	230	HIS	-	expression tag	UNP Q96RI1
A	231	HIS	-	expression tag	UNP Q96RI1
A	232	HIS	-	expression tag	UNP Q96RI1
A	233	HIS	-	expression tag	UNP Q96RI1
A	234	HIS	-	expression tag	UNP Q96RI1
A	235	HIS	-	expression tag	UNP Q96RI1
A	236	SER	-	expression tag	UNP Q96RI1
A	237	SER	-	expression tag	UNP Q96RI1
A	238	GLY	-	expression tag	UNP Q96RI1
A	239	GLU	-	expression tag	UNP Q96RI1
A	240	THR	-	expression tag	UNP Q96RI1
A	241	VAL	-	expression tag	UNP Q96RI1
A	242	ARG	-	expression tag	UNP Q96RI1
A	243	PHE	-	expression tag	UNP Q96RI1
A	244	GLN	-	expression tag	UNP Q96RI1
A	245	GLY	-	expression tag	UNP Q96RI1
A	246	HIS	-	expression tag	UNP Q96RI1
A	247	MET	-	expression tag	UNP Q96RI1
A	281	ALA	GLU	conflict	UNP Q96RI1
A	354	ALA	GLU	conflict	UNP Q96RI1
B	226	MET	-	expression tag	UNP Q96RI1

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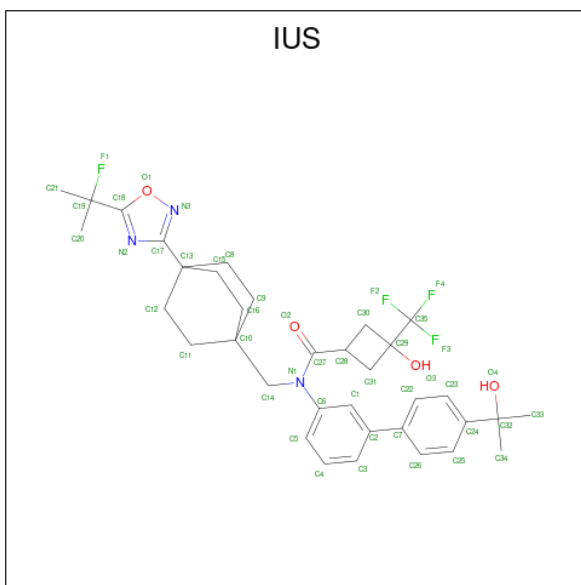
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Chain	Residue	Modelled	Actual	Comment	Reference
B	227	GLY	-	expression tag	UNP Q96RI1
B	228	SER	-	expression tag	UNP Q96RI1
B	229	SER	-	expression tag	UNP Q96RI1
B	230	HIS	-	expression tag	UNP Q96RI1
B	231	HIS	-	expression tag	UNP Q96RI1
B	232	HIS	-	expression tag	UNP Q96RI1
B	233	HIS	-	expression tag	UNP Q96RI1
B	234	HIS	-	expression tag	UNP Q96RI1
B	235	HIS	-	expression tag	UNP Q96RI1
B	236	SER	-	expression tag	UNP Q96RI1
B	237	SER	-	expression tag	UNP Q96RI1
B	238	GLY	-	expression tag	UNP Q96RI1
B	239	GLU	-	expression tag	UNP Q96RI1
B	240	THR	-	expression tag	UNP Q96RI1
B	241	VAL	-	expression tag	UNP Q96RI1
B	242	ARG	-	expression tag	UNP Q96RI1
B	243	PHE	-	expression tag	UNP Q96RI1
B	244	GLN	-	expression tag	UNP Q96RI1
B	245	GLY	-	expression tag	UNP Q96RI1
B	246	HIS	-	expression tag	UNP Q96RI1
B	247	MET	-	expression tag	UNP Q96RI1
B	281	ALA	GLU	conflict	UNP Q96RI1
B	354	ALA	GLU	conflict	UNP Q96RI1

- Molecule 2 is a protein called co-activator.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	11	Total	C	N	O	0	0	0
			87	58	15	14			
2	D	11	Total	C	N	O	0	0	0
			90	59	14	17			

- Molecule 3 is (1s,3s)-N-( {4-[5-(2-fluoropropan-2-yl)-1,2,4-oxadiazol-3-yl]bicyclo[2.2.2]octan-1-yl}methyl)-3-hydroxy-N-[4'-(2-hydroxypropan-2-yl)[1,1'-biphenyl]-3-yl]-3-(trifluoromethyl)cyclobutane-1-carboxamide (three-letter code: IUS) (formula: C<sub>35</sub>H<sub>41</sub>F<sub>4</sub>N<sub>3</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 87	C 35	F 4	H 41	N 3	O 4	41	0
3	B	1	Total 87	C 35	F 4	H 41	N 3	O 4	41	0

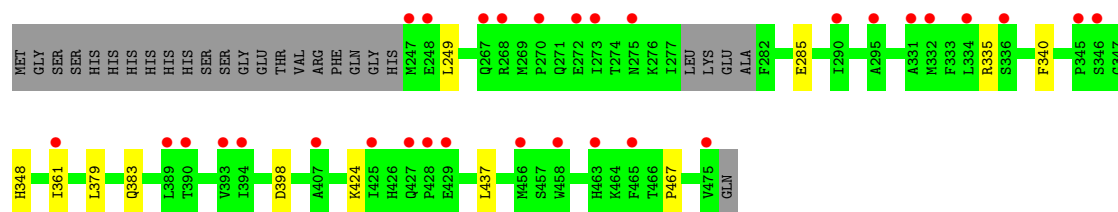
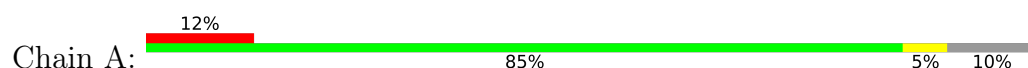
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	8	Total O 8 8	0	0
4	B	5	Total O 5 5	0	0

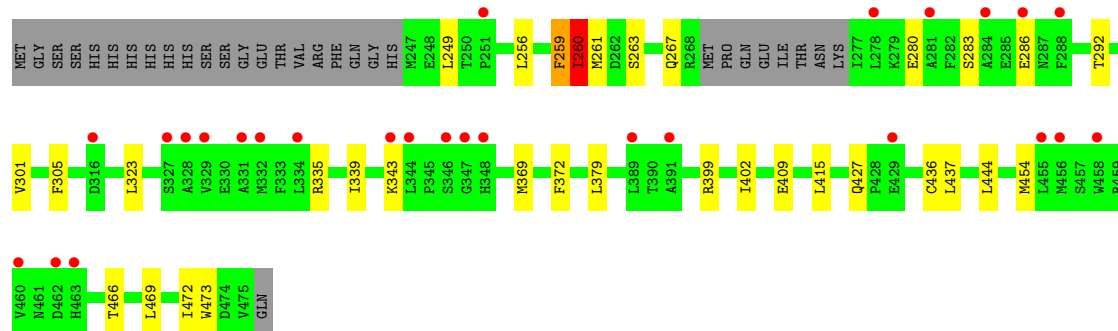
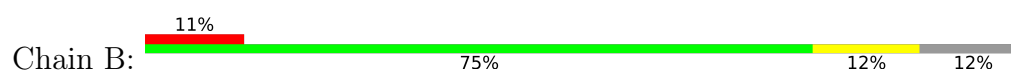
### 3 Residue-property plots [i](#)

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: Bile acid receptor



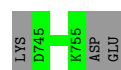
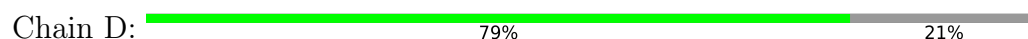
#### • Molecule 1: Bile acid receptor



#### • Molecule 2: co-activator



#### • Molecule 2: co-activator



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.71Å 119.26Å 36.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.97 – 2.15 26.97 – 2.16	Depositor EDS
% Data completeness (in resolution range)	68.4 (26.97-2.15) 68.5 (26.97-2.16)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 2.15Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, $R_{free}$	0.214 , 0.256 0.227 , 0.270	Depositor DCC
$R_{free}$ test set	854 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.8	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 56.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3809	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.43% 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

### 5.1 Standard geometry

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

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	0.54	0/1753	0.66	0/2386
1	B	0.81	2/1768 (0.1%)	0.76	5/2403 (0.2%)
2	C	0.45	0/87	0.74	0/116
2	D	0.50	0/91	0.67	0/123
All	All	0.68	2/3699 (0.1%)	0.71	5/5028 (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	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	259	PHE	C-N	-17.82	0.93	1.34
1	B	260	ILE	C-N	-17.63	0.93	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	260	ILE	O-C-N	-10.36	106.12	122.70
1	B	259	PHE	C-N-CA	10.09	146.91	121.70
1	B	259	PHE	O-C-N	-7.42	110.83	122.70
1	B	260	ILE	CA-C-N	6.47	131.44	117.20
1	B	259	PHE	CA-C-N	5.28	128.81	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	260	ILE	Mainchain

## 5.2 Too-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 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	1717	0	1608	4	0
1	B	1728	0	1632	20	0
2	C	87	0	88	1	0
2	D	90	0	81	0	0
3	A	46	41	0	0	0
3	B	46	41	0	3	0
4	A	8	0	0	0	0
4	B	5	0	0	0	0
All	All	3727	82	3409	22	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 3.

All (22) 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:369:MET:HE3	3:B:501:IUS:C5	1.95	0.96
1:B:399:ARG:HB2	1:B:402:ILE:HD12	1.70	0.74
1:B:369:MET:CE	3:B:501:IUS:C5	2.68	0.72
1:B:399:ARG:HB2	1:B:402:ILE:CD1	2.30	0.62
1:B:469:LEU:HD22	1:B:473:TRP:CZ3	2.36	0.61
1:A:379:LEU:HD13	1:A:437:LEU:HD12	1.90	0.54
1:B:369:MET:CE	3:B:501:IUS:C4	2.86	0.54
1:B:339:ILE:HA	1:B:343:LYS:HB2	1.91	0.53
1:A:424:LYS:HE2	1:B:409:GLU:OE1	2.11	0.51
1:B:260:ILE:O	1:B:261:MET:C	2.44	0.50
1:A:467:PRO:HB2	2:C:748:LEU:HD11	1.93	0.50
1:B:267:GLN:HB3	1:B:301:VAL:HG13	1.96	0.47
1:B:323:LEU:HD23	1:B:402:ILE:HD11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:LYS:HE2	1:B:409:GLU:CD	2.36	0.45
1:B:469:LEU:HA	1:B:472:ILE:HG22	1.97	0.45
1:B:267:GLN:HG3	1:B:305:PHE:HB2	1.98	0.45
1:B:379:LEU:HD13	1:B:437:LEU:HD12	1.99	0.45
1:B:379:LEU:HD21	1:B:436:CYS:HB3	1.97	0.45
1:B:256:LEU:HD21	1:B:415:LEU:HD23	1.99	0.44
1:B:263:SER:O	1:B:267:GLN:HG2	2.19	0.42
1:B:372:PHE:CZ	1:B:444:LEU:HD13	2.55	0.42
1:B:292:THR:HG22	1:B:466:THR:HG23	2.01	0.42

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	222/251 (88%)	215 (97%)	5 (2%)	2 (1%)	17	11
1	B	219/251 (87%)	211 (96%)	7 (3%)	1 (0%)	29	22
2	C	9/14 (64%)	9 (100%)	0	0	100	100
2	D	9/14 (64%)	9 (100%)	0	0	100	100
All	All	459/530 (87%)	444 (97%)	12 (3%)	3 (1%)	22	15

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	348	HIS
1	B	260	ILE
1	A	361	ILE

### 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	172/229 (75%)	166 (96%)	6 (4%)	36	34
1	B	180/229 (79%)	172 (96%)	8 (4%)	28	25
2	C	8/14 (57%)	8 (100%)	0	100	100
2	D	9/14 (64%)	9 (100%)	0	100	100
All	All	369/486 (76%)	355 (96%)	14 (4%)	33	31

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	249	LEU
1	A	285	GLU
1	A	335	ARG
1	A	340	PHE
1	A	383	GLN
1	A	398	ASP
1	B	249	LEU
1	B	259	PHE
1	B	280	GLU
1	B	283	SER
1	B	286	GLU
1	B	335	ARG
1	B	427	GLN
1	B	454	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	267	GLN
1	B	300	GLN
1	B	427	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

2 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	$\# Z  > 2$
3	IUS	A	501	-	41,51,51	0.37	0	58,83,83	0.82	2 (3%)
3	IUS	B	501	-	41,51,51	0.36	0	58,83,83	0.65	1 (1%)

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	IUS	A	501	-	-	6/39/79/79	0/7/6/6
3	IUS	B	501	-	-	5/39/79/79	0/7/6/6

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	IUS	C31-C29-C35	3.56	117.87	112.99
3	A	501	IUS	C30-C29-C35	3.01	117.12	112.99
3	B	501	IUS	C31-C29-C35	2.65	116.63	112.99

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	501	IUS	C16-C10-C14-N1
3	B	501	IUS	C9-C10-C14-N1
3	B	501	IUS	C11-C10-C14-N1
3	A	501	IUS	C23-C24-C32-C33
3	A	501	IUS	C30-C29-C35-F2
3	A	501	IUS	C30-C29-C35-F3
3	A	501	IUS	C30-C29-C35-F4
3	B	501	IUS	C23-C24-C32-C33
3	B	501	IUS	C25-C24-C32-C33
3	A	501	IUS	C15-C13-C17-N3
3	A	501	IUS	C12-C13-C17-N3

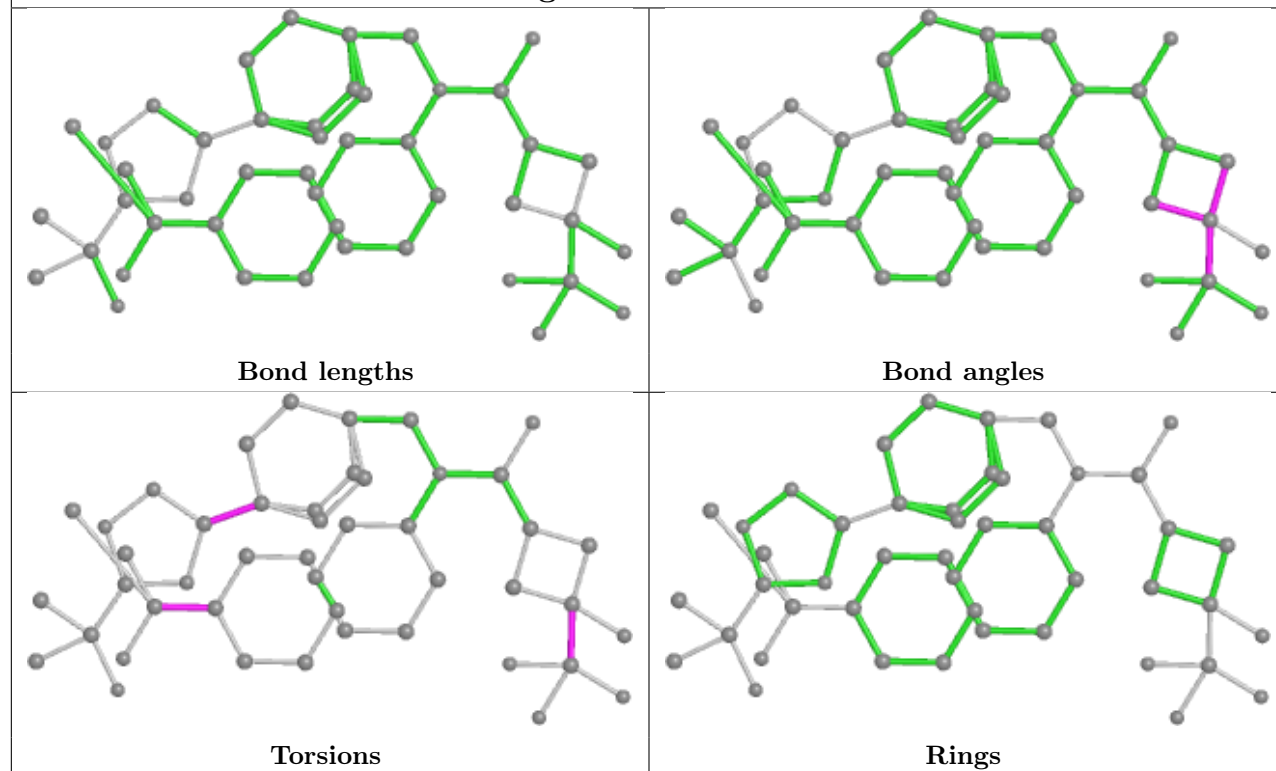
There are no ring outliers.

1 monomer is involved in 3 short contacts:

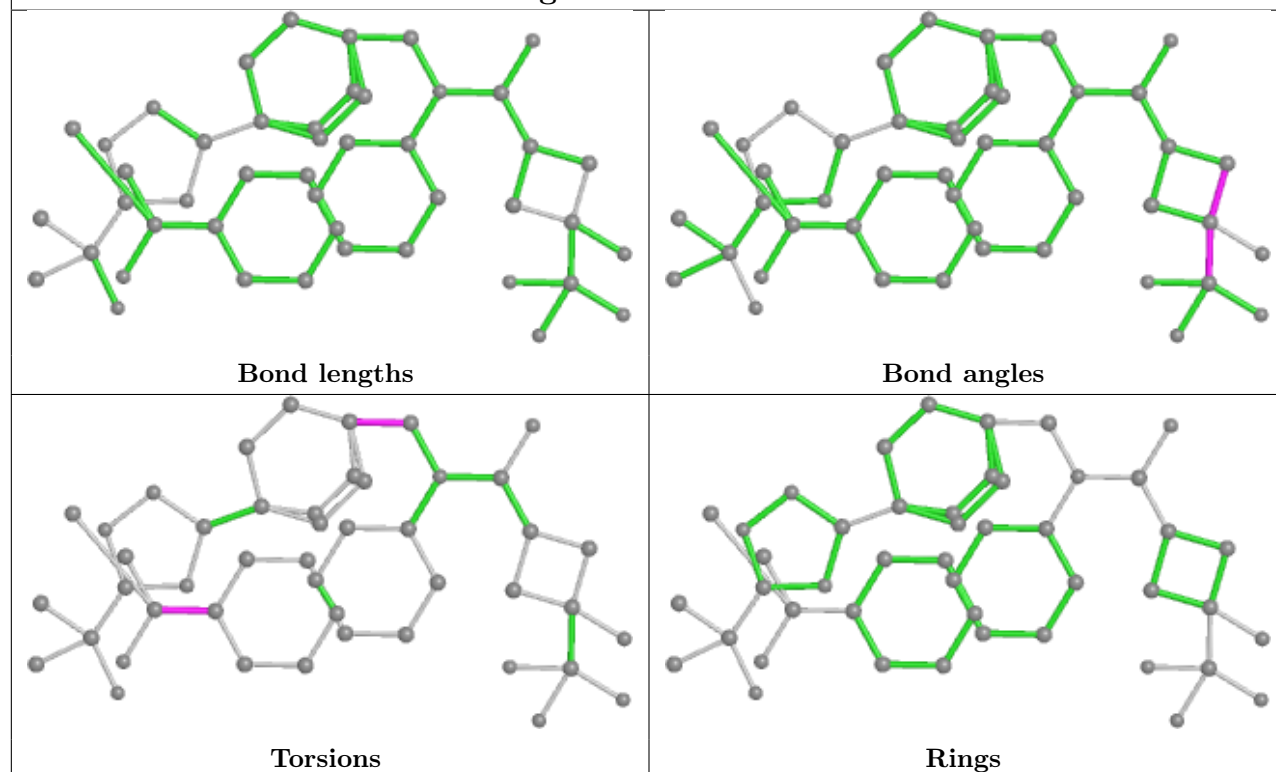
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	IUS	3	0

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 than 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 any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

## Ligand IUS A 501



## Ligand IUS B 501



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	259:PHE	C	260:ILE	N	0.93
1	B	260:ILE	C	261:MET	N	0.93



## 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	225/251 (89%)	0.56	31 (13%) <span>2</span> <span>3</span>	38, 62, 103, 134	0
1	B	221/251 (88%)	0.52	27 (12%) <span>4</span> <span>6</span>	34, 60, 96, 122	0
2	C	11/14 (78%)	0.01	0 <span>100</span> <span>100</span>	53, 60, 75, 87	0
2	D	11/14 (78%)	-0.06	0 <span>100</span> <span>100</span>	55, 59, 82, 97	0
All	All	468/530 (88%)	0.52	58 (12%) <span>4</span> <span>5</span>	34, 61, 102, 134	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	460	VAL	7.4
1	A	275	ASN	6.3
1	A	458	TRP	5.7
1	A	428	PRO	4.9
1	B	348	HIS	4.8
1	B	278	LEU	4.3
1	A	267	GLN	3.9
1	B	281	ALA	3.9
1	B	455	LEU	3.6
1	B	429	GLU	3.6
1	B	347	GLY	3.6
1	A	425	ILE	3.5
1	A	465	PHE	3.4
1	B	456	MET	3.2
1	A	247	MET	3.2
1	A	393	VAL	3.2
1	A	389	LEU	3.0
1	B	251	PRO	3.0
1	A	334	LEU	3.0
1	A	248	GLU	2.9
1	A	463	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	273	ILE	2.7
1	B	329	VAL	2.6
1	B	389	LEU	2.6
1	B	327[A]	SER	2.5
1	A	268	ARG	2.5
1	B	346	SER	2.5
1	A	429	GLU	2.5
1	B	331	ALA	2.5
1	B	344	LEU	2.5
1	A	345	PRO	2.4
1	B	328	ALA	2.4
1	A	270	PRO	2.4
1	B	316	ASP	2.4
1	A	346	SER	2.3
1	B	288	PHE	2.3
1	A	361	ILE	2.3
1	A	336	SER	2.3
1	A	331	ALA	2.2
1	A	427	GLN	2.2
1	B	284	ALA	2.2
1	B	334	LEU	2.2
1	B	286	GLU	2.2
1	A	272	GLU	2.1
1	B	462	ASP	2.1
1	A	332	MET	2.1
1	A	407	ALA	2.1
1	A	290	ILE	2.1
1	B	391	ALA	2.1
1	A	456	MET	2.1
1	A	475	VAL	2.1
1	A	295	ALA	2.1
1	A	390	THR	2.1
1	B	463	HIS	2.1
1	B	332	MET	2.0
1	B	458	TRP	2.0
1	A	394	ILE	2.0
1	B	343	LYS	2.0

## 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 [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

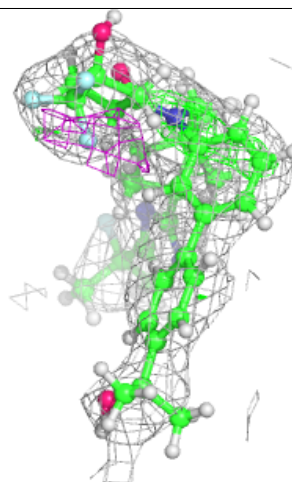
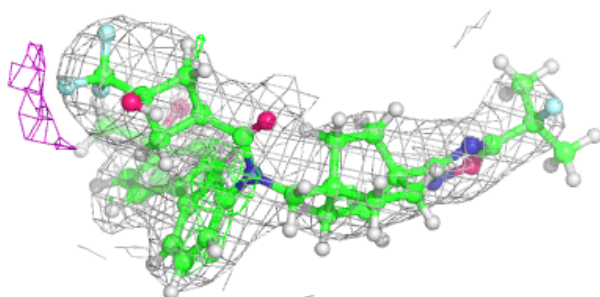
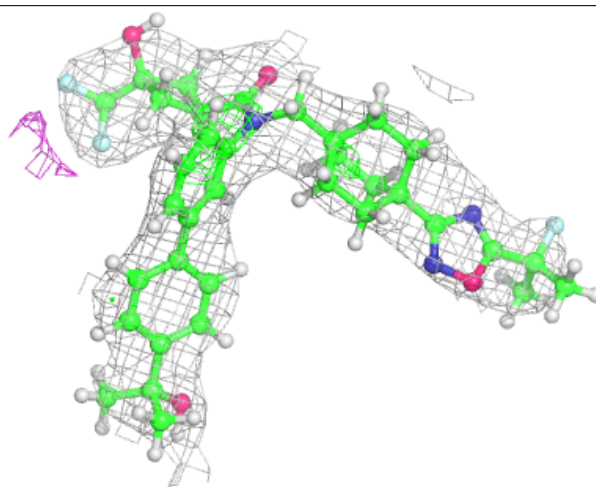
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	IUS	A	501	46/46	0.76	0.29	88,95,95,95	41
3	IUS	B	501	46/46	0.80	0.24	91,95,96,100	41

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.

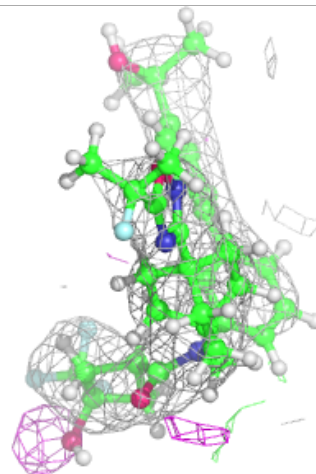
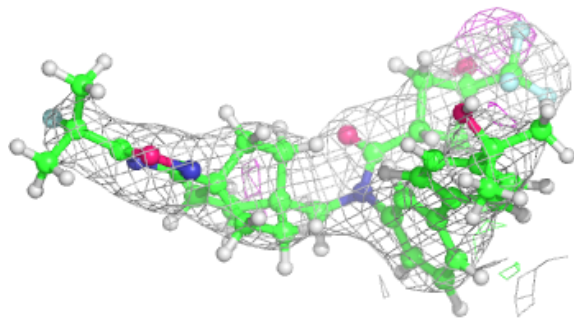
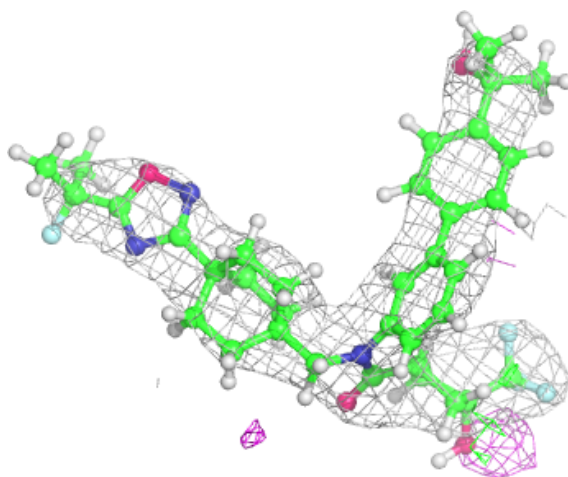
### Electron density around IUS A 501:

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around IUS B 501:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.