



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 01:28 am BST

PDB ID : 5APK  
Title : Ligand complex of RORg LBD  
Authors : Xue, Y.; Aagaard, A.; Narjes, F.  
Deposited on : 2015-09-16  
Resolution : 2.10 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.

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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 : 2.11  
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)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

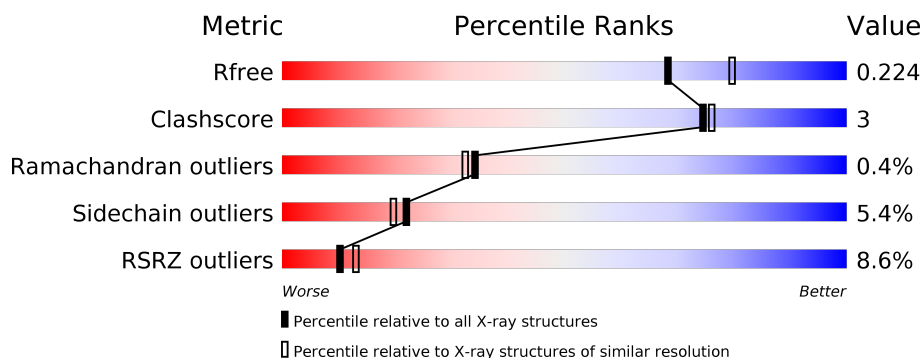
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 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	265	<div> <div>8%</div> <div> <div></div> <div>75%</div> <div>10%</div> <div>•</div> <div>14%</div> </div> </div>
1	B	265	<div> <div>6%</div> <div> <div></div> <div>80%</div> <div>8%</div> <div>•</div> <div>11%</div> </div> </div>
2	D	13	<div> <div>38%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>8%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4285 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	A	229	Total	C	N	O	S	0	0	0
			1874	1188	336	336	14			
1	B	236	Total	C	N	O	S	0	0	0
			1923	1222	347	340	14			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	243	MET	-	expression tag	UNP P51449
A	244	HIS	-	expression tag	UNP P51449
A	245	ASN	-	expression tag	UNP P51449
A	246	HIS	-	expression tag	UNP P51449
A	247	ASN	-	expression tag	UNP P51449
A	248	HIS	-	expression tag	UNP P51449
A	249	ASN	-	expression tag	UNP P51449
A	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
A	254	HIS	-	expression tag	UNP P51449
A	255	ASN	-	expression tag	UNP P51449
A	256	GLY	-	expression tag	UNP P51449
A	257	GLY	-	expression tag	UNP P51449
A	258	GLU	-	expression tag	UNP P51449
A	259	ASN	-	expression tag	UNP P51449
A	260	LEU	-	expression tag	UNP P51449
A	261	TYR	-	expression tag	UNP P51449
A	262	PHE	-	expression tag	UNP P51449
A	263	GLN	-	expression tag	UNP P51449
A	264	GLY	-	expression tag	UNP P51449
B	243	MET	-	expression tag	UNP P51449
B	244	HIS	-	expression tag	UNP P51449
B	245	ASN	-	expression tag	UNP P51449

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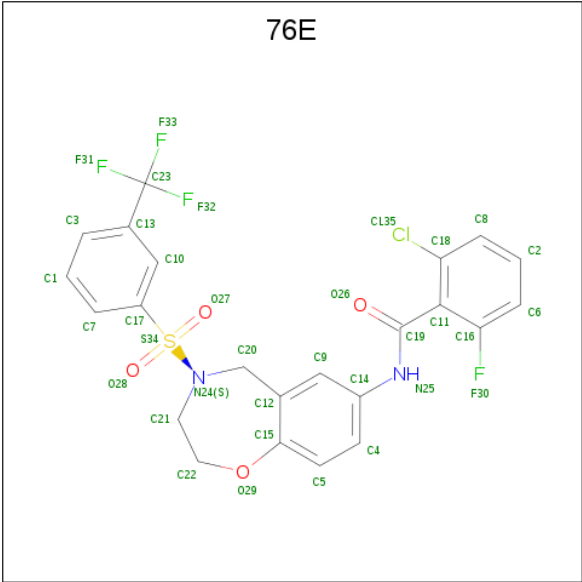
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Chain	Residue	Modelled	Actual	Comment	Reference
B	246	HIS	-	expression tag	UNP P51449
B	247	ASN	-	expression tag	UNP P51449
B	248	HIS	-	expression tag	UNP P51449
B	249	ASN	-	expression tag	UNP P51449
B	250	HIS	-	expression tag	UNP P51449
B	251	ASN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

- Molecule 2 is a protein called NUCLEAR RECEPTOR ROR-GAMMA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	13	Total	C	N	O	0	0	0
			115	76	22	17			

- Molecule 3 is 2-CHLORO-6-FLUORO-N-[4-[3-(TRIFLUOROMETHYL)PHENYL]SULFONYL-3,5-DIHYDRO-2H-1,4-BENZOXAZEPIN-7-YL]BENZAMIDE (three-letter code: 76E) (formula: C<sub>23</sub>H<sub>17</sub>ClF<sub>4</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	A	1	Total	C	Cl	F	N	O	S	0	0
			35	23	1	4	2	4	1		
3	B	1	Total	C	Cl	F	N	O	S	0	0
			35	23	1	4	2	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	147	Total	O	0	0
			147	147		
4	B	151	Total	O	0	0
			151	151		
4	D	5	Total	O	0	0
			5	5		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.75Å 99.75Å 129.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.54 – 2.10 43.19 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.54-2.10) 99.9 (43.19-2.10)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.59 (at 2.10Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, $R_{free}$	0.196 , 0.224 0.197 , 0.224	Depositor DCC
$R_{free}$ test set	2227 reflections (5.24%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.9	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 58.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.069 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4285	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% 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: 76E

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	0.50	0/1911	0.64	0/2569
1	B	0.49	0/1964	0.65	0/2646
2	D	0.81	0/118	0.80	0/159
All	All	0.51	0/3993	0.65	0/5374

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

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	1874	0	1868	15	0
1	B	1923	0	1926	12	0
2	D	115	0	117	1	0
3	A	35	0	17	2	0
3	B	35	0	17	1	0
4	A	147	0	0	1	0
4	B	151	0	0	2	0
4	D	5	0	0	0	0
All	All	4285	0	3945	25	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 (25) 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:499:PRO:HB2	1:B:500:PRO:HD2	1.59	0.82
1:B:359:GLU:HB3	1:B:472:LEU:HD13	1.72	0.72
1:A:333:GLU:HG3	1:B:493:VAL:HG22	1.81	0.62
1:A:468:PRO:HD2	1:A:471:LYS:HD3	1.85	0.58
1:A:359:GLU:HB3	1:A:472:LEU:HD13	1.87	0.56
1:A:332:VAL:HG21	2:D:488:HIS:HB3	1.88	0.55
1:B:342:MET:HB2	4:B:2048:HOH:O	2.07	0.55
1:A:317:TRP:CD2	1:A:486:PHE:HB3	2.44	0.52
1:B:499:PRO:HB2	1:B:500:PRO:CD	2.36	0.50
1:A:293:LEU:HA	1:A:296:ARG:HD2	1.94	0.48
1:A:329:GLN:HG3	1:B:493:VAL:HG13	1.96	0.48
1:A:287:LEU:HD13	1:A:292:LEU:HD21	1.97	0.47
1:B:469:LYS:O	1:B:473:ARG:HD3	2.14	0.47
1:A:270:ILE:HG21	1:A:448:LEU:HD23	1.97	0.47
1:A:317:TRP:HZ3	1:A:483:LEU:HG	1.80	0.47
1:B:396:LEU:HD23	3:B:1501:76E:H6	1.99	0.45
1:B:287:LEU:HD13	1:B:292:LEU:HD21	1.98	0.44
1:A:262:PHE:HE1	1:A:442:LEU:HD22	1.82	0.44
1:A:376:VAL:HG21	3:A:1487:76E:H1	2.00	0.43
1:A:482:ARG:HA	1:A:485:ILE:HD12	2.00	0.43
1:B:497:ALA:O	1:B:498:PHE:HB2	2.18	0.43
1:A:412:PHE:HB2	4:A:2101:HOH:O	2.18	0.42
1:B:412:PHE:HB2	4:B:2101:HOH:O	2.18	0.42
1:B:317:TRP:CD2	1:B:486:PHE:HB3	2.55	0.41
1:A:320:CYS:HB3	3:A:1487:76E:CL35	2.59	0.40

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	227/265 (86%)	224 (99%)	3 (1%)	0	100	100
1	B	234/265 (88%)	228 (97%)	5 (2%)	1 (0%)	34	32
2	D	11/13 (85%)	10 (91%)	0	1 (9%)	1	0
All	All	472/543 (87%)	462 (98%)	8 (2%)	2 (0%)	34	32

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	498	PHE
2	D	481	GLU

### 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	204/236 (86%)	194 (95%)	10 (5%)	25	23
1	B	210/236 (89%)	198 (94%)	12 (6%)	20	18
2	D	13/13 (100%)	12 (92%)	1 (8%)	13	9
All	All	427/485 (88%)	404 (95%)	23 (5%)	22	20

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	263	GLN
1	A	290	GLU
1	A	398	SER
1	A	412	PHE
1	A	437	ARG
1	A	442	LEU
1	A	473	ARG
1	A	475	LEU
1	A	481	GLU
1	A	483	LEU
1	B	297	SER

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Mol	Chain	Res	Type
1	B	315	GLU
1	B	342	MET
1	B	398	SER
1	B	412	PHE
1	B	437	ARG
1	B	471	LYS
1	B	472	LEU
1	B	483	LEU
1	B	489	LEU
1	B	494	VAL
1	B	495	GLN
2	D	481	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	346	GLN
1	A	441	GLN
1	A	453	HIS
1	B	329	GLN
1	B	405	HIS
2	D	484	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](#)

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	76E	B	1501	-	37,38,38	1.55	3 (8%)	53,57,57	1.75	10 (18%)
3	76E	A	1487	-	37,38,38	1.62	4 (10%)	53,57,57	1.70	10 (18%)

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	76E	B	1501	-	-	2/26/36/36	0/3/4/4
3	76E	A	1487	-	-	4/26/36/36	0/3/4/4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1487	76E	S34-N24	8.14	1.75	1.63
3	B	1501	76E	S34-N24	7.51	1.74	1.63
3	B	1501	76E	C17-S34	2.33	1.79	1.76
3	A	1487	76E	C17-S34	2.13	1.79	1.76
3	A	1487	76E	O27-S34	2.11	1.45	1.43
3	B	1501	76E	O27-S34	2.10	1.45	1.43
3	A	1487	76E	C21-N24	2.04	1.50	1.48

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1501	76E	C22-O29-C15	-6.56	106.93	116.03
3	B	1501	76E	O27-S34-N24	5.72	111.91	106.69
3	A	1487	76E	C22-O29-C15	-5.50	108.40	116.03
3	A	1487	76E	O27-S34-N24	4.54	110.83	106.69
3	A	1487	76E	C20-N24-C21	-3.91	108.80	116.07
3	B	1501	76E	C20-N24-C21	-3.65	109.29	116.07
3	A	1487	76E	O27-S34-C17	-3.54	103.56	108.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1501	76E	C20-N24-S34	-2.87	111.86	118.13
3	A	1487	76E	C20-N24-S34	-2.81	111.99	118.13
3	B	1501	76E	C7-C17-S34	-2.79	116.82	119.76
3	B	1501	76E	O28-S34-C17	-2.55	104.82	108.05
3	A	1487	76E	C17-S34-N24	2.45	110.22	107.30
3	B	1501	76E	C10-C13-C23	2.40	122.82	119.58
3	B	1501	76E	O27-S34-C17	-2.33	105.10	108.05
3	A	1487	76E	C21-N24-S34	2.30	123.59	117.41
3	A	1487	76E	O28-S34-C17	-2.14	105.34	108.05
3	B	1501	76E	C10-C17-S34	2.12	121.70	119.34
3	A	1487	76E	F30-C16-C11	2.10	121.28	118.01
3	B	1501	76E	O28-S34-N24	-2.04	104.83	106.69
3	A	1487	76E	C6-C16-C11	-2.03	119.96	123.58

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1487	76E	C21-N24-S34-O28
3	A	1487	76E	C21-N24-S34-C17
3	B	1501	76E	C21-N24-S34-C17
3	B	1501	76E	C21-N24-S34-O28
3	A	1487	76E	C9-C14-N25-C19
3	A	1487	76E	C4-C14-N25-C19

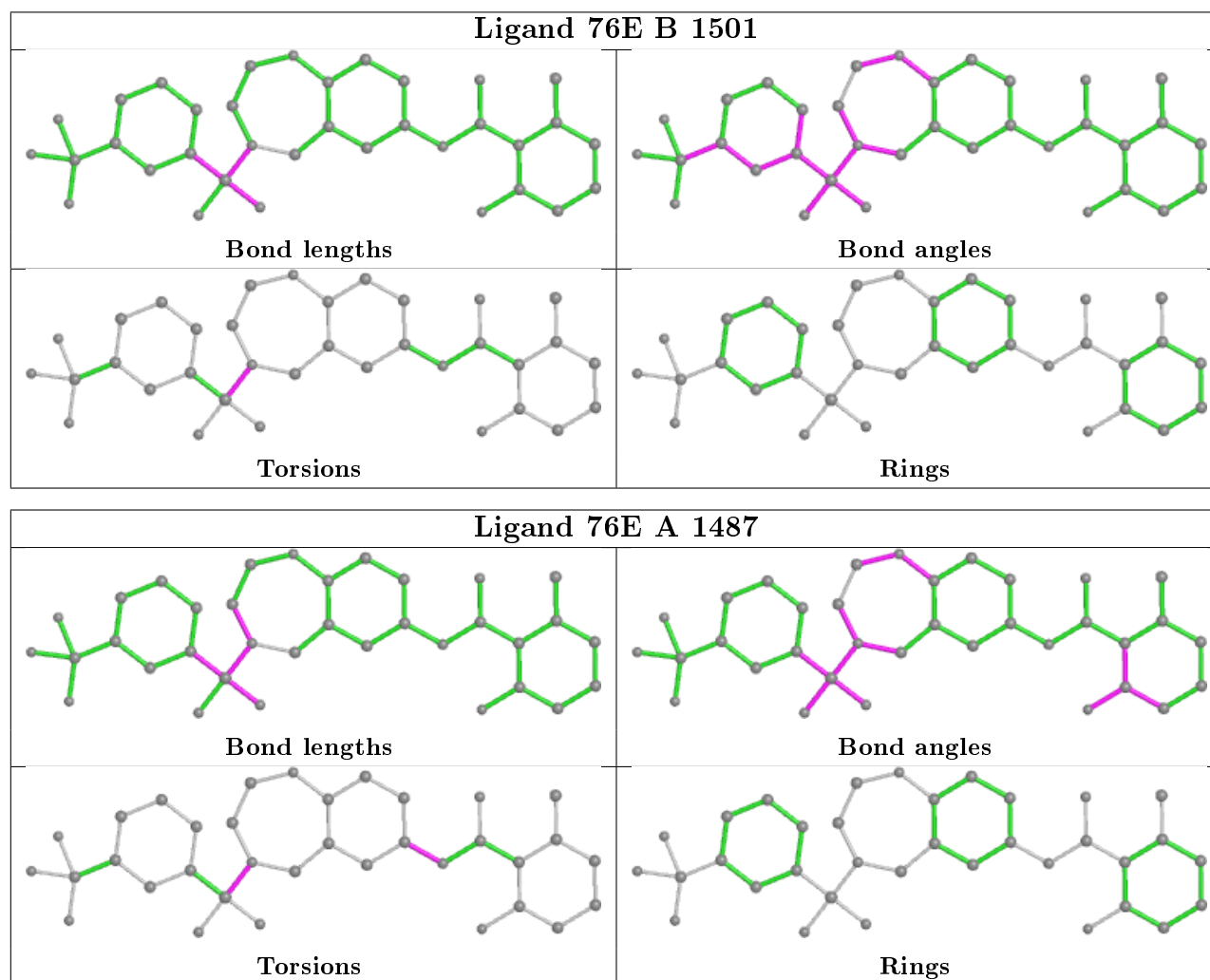
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1501	76E	1	0
3	A	1487	76E	2	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.



## 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

### 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	229/265 (86%)	0.55	20 (8%) 10 13	25, 41, 86, 109	0
1	B	236/265 (89%)	0.42	16 (6%) 17 21	29, 45, 98, 140	0
2	D	13/13 (100%)	1.72	5 (38%) 0 0	38, 48, 73, 77	0
All	All	478/543 (88%)	0.51	41 (8%) 10 13	25, 43, 88, 140	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	258	GLU	6.6
1	A	479	HIS	4.8
1	B	485	ILE	4.6
1	A	477	SER	4.3
2	D	480	VAL	4.2
1	B	488	HIS	4.1
1	B	492	ILE	3.9
1	A	481	GLU	3.8
1	A	480	VAL	3.5
1	B	500	PRO	3.5
1	B	499	PRO	3.4
1	A	262	PHE	3.4
2	D	481	GLU	3.3
1	A	486	PHE	3.2
1	B	494	VAL	3.2
2	D	485	ILE	3.1
1	A	297	SER	3.1
1	A	294	ARG	3.0
1	B	267	LEU	3.0
1	B	297	SER	2.9
1	A	260	LEU	2.9
1	B	484	GLN	2.9
1	A	259	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	317	TRP	2.9
1	A	473	ARG	2.8
1	B	495	GLN	2.8
1	A	470	GLY	2.8
1	A	478	GLN	2.6
1	A	484	GLN	2.5
2	D	482	ARG	2.4
1	B	463	LEU	2.4
1	B	487	GLN	2.3
1	B	498	PHE	2.3
1	B	483	LEU	2.2
1	A	437	ARG	2.2
2	D	492	ILE	2.2
1	B	481	GLU	2.2
1	A	299	ILE	2.1
1	A	469	LYS	2.1
1	B	317	TRP	2.1
1	A	476	CYS	2.0

## 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<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	76E	B	1501	35/35	0.95	0.15	44,49,57,63	0
3	76E	A	1487	35/35	0.95	0.14	43,51,69,74	0

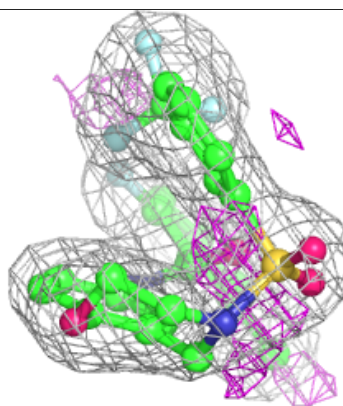
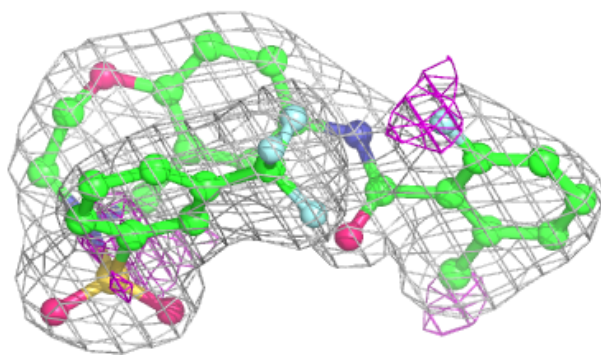
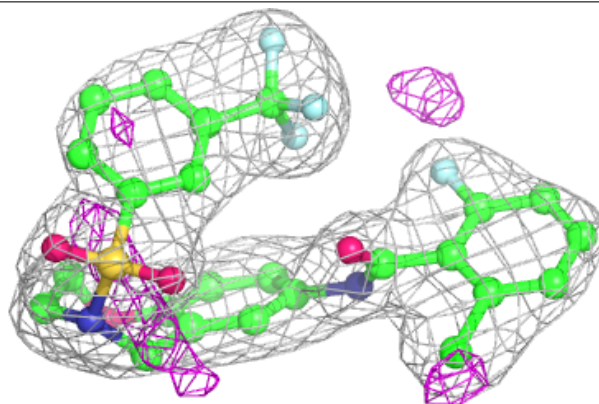
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers



as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

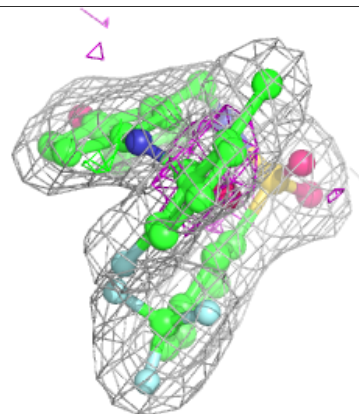
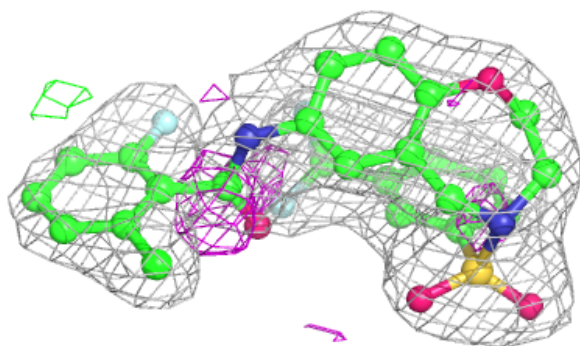
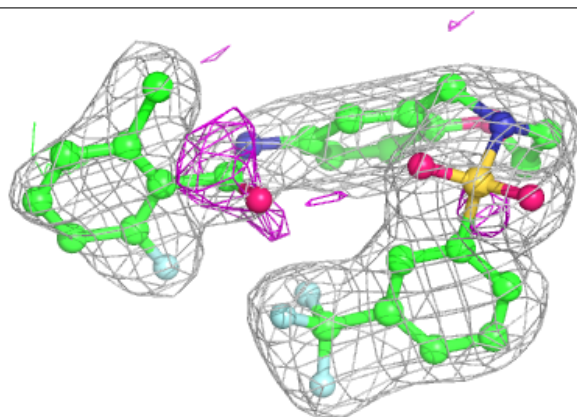
**Electron density around 76E B 1501:**

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



**Electron density around 76E A 1487:**

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



## 6.5 Other polymers

There are no such residues in this entry.