



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 08:13 AM BST

PDB ID : 6A6P  
Title : Crystal Structure of Peroxisome Proliferator-Activated Receptor Delta (PPAR $\delta$ )LBD in Complex with DN003316  
Authors : Chin, J.W.; Cho, S.J.; Song, J.Y.; Ha, J.H.  
Deposited on : 2018-06-29  
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	:	2.13.1
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)	:	2.13.1

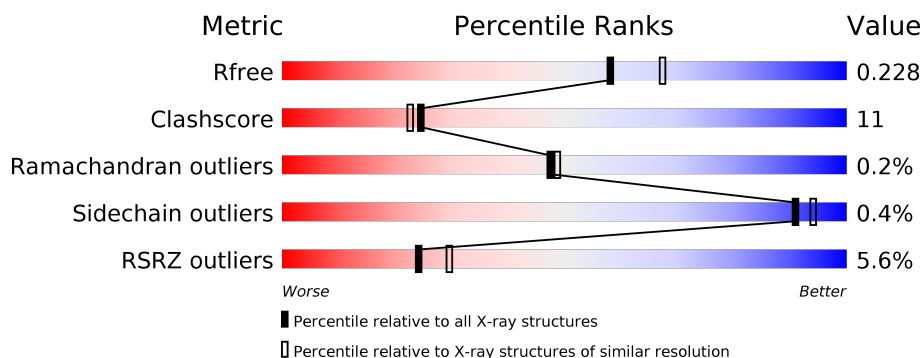
# 1 Overall quality at a glance

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	270	<div> <div>5%</div> <div> <div></div> <div>78%</div> <div>20%</div> <div>..</div> </div> </div>
1	B	270	<div> <div>6%</div> <div> <div></div> <div>83%</div> <div>16%</div> <div>.</div> </div> </div>

## 2 Entry composition [i](#)

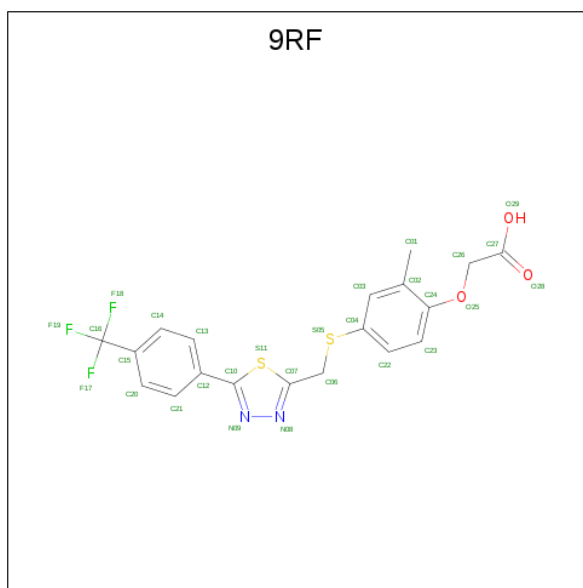
There are 5 unique types of molecules in this entry. The entry contains 4898 atoms, of which 196 are hydrogens and 0 are deuteriums.

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 Peroxisome proliferator-activated receptor delta.

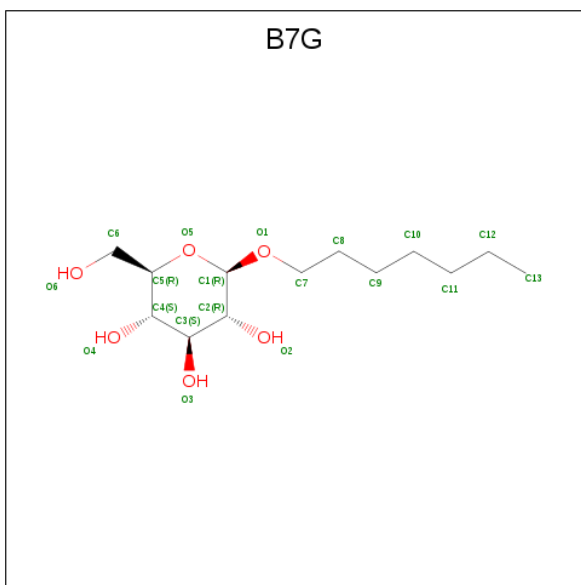
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	1	0
			2147	1388	362	387	10			
1	B	267	Total	C	N	O	S	0	1	0
			2150	1391	363	385	11			

- Molecule 2 is {2-methyl-4-[(5-[4-(trifluoromethyl)phenyl]-1,3,4-thiadiazol-2-yl)methyl]sulfanylphenoxy}acetic acid (three-letter code: 9RF) (formula: C<sub>19</sub>H<sub>15</sub>F<sub>3</sub>N<sub>2</sub>O<sub>3</sub>S<sub>2</sub>).



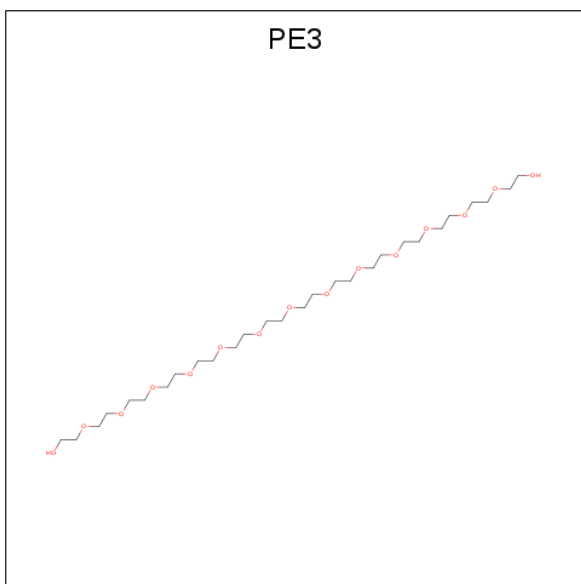
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	A	1	Total	C	F	H	N	O	S	0	0
			43	19	3	14	2	3	2		
2	B	1	Total	C	F	H	N	O	S	0	0
			43	19	3	14	2	3	2		

- Molecule 3 is heptyl beta-D-glucopyranoside (three-letter code: B7G) (formula: C<sub>13</sub>H<sub>26</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 45	C 13	H 26	O 6	0	0
3	B	1	Total 45	C 13	H 26	O 6	0	0

- Molecule 4 is 3,6,9,12,15,18,21,24,27,30,33,36,39-TRIDCAOXAHENTETRACONTANE-1,41-DIOL (three-letter code: PE3) (formula:  $C_{28}H_{58}O_{15}$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			101	28	58	15		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	0	0
			101	28	58	15		

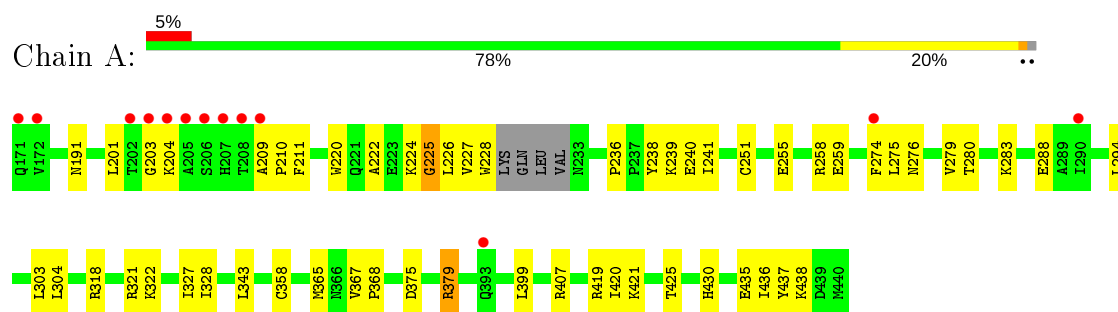
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	125	Total	O	0	0
			125	125		
5	B	98	Total	O	0	0
			98	98		

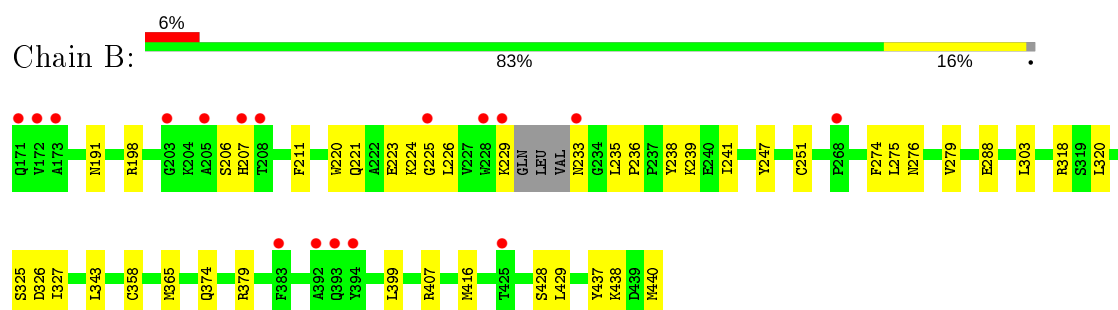
### 3 Residue-property plots [i](#)

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: Peroxisome proliferator-activated receptor delta



- Molecule 1: Peroxisome proliferator-activated receptor delta



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	39.60Å 95.75Å 96.94Å 90.00° 97.91° 90.00°	Depositor
Resolution (Å)	38.20 – 2.10 38.20 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.4 (38.20-2.10) 98.4 (38.20-2.10)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.48 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.13_2998)	Depositor
R, $R_{free}$	0.194 , 0.228 0.194 , 0.228	Depositor DCC
$R_{free}$ test set	2025 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.9	Xtriage
Anisotropy	0.601	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 48.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4898	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.89% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: B7G, 9RF, PE3

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	0.45	0/2193	0.61	2/2964 (0.1%)
1	B	0.39	0/2199	0.57	0/2971
All	All	0.42	0/4392	0.59	2/5935 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	379	ARG	NE-CZ-NH1	6.79	123.70	120.30
1	A	379	ARG	NE-CZ-NH2	-5.37	117.61	120.30

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	A	2147	0	2181	60	0
1	B	2150	0	2193	40	0
2	A	29	14	0	1	0
2	B	29	14	0	0	0
3	A	19	26	26	3	0
3	B	19	26	26	5	0
4	A	43	58	58	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	43	58	56	3	0
5	A	125	0	0	6	0
5	B	98	0	0	7	0
All	All	4702	196	4540	98	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 11.

All (98) 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:438:LYS:O	3:B:502:B7G:O3	1.81	0.96
1:B:358:CYS:SG	5:B:641:HOH:O	2.27	0.91
1:B:429:LEU:HB3	3:B:502:B7G:H132	1.53	0.88
1:A:318:ARG:NH2	5:A:601:HOH:O	2.05	0.87
1:A:220:TRP:CZ2	1:A:224:LYS:HD2	2.15	0.82
1:B:236:PRO:HG2	1:B:247:TYR:CE2	2.17	0.79
1:A:294:LEU:HD11	1:A:303:LEU:HD11	1.64	0.79
1:A:225:GLY:HA2	1:A:228:TRP:O	1.85	0.76
1:A:358:CYS:SG	5:A:604:HOH:O	2.45	0.73
1:B:238:TYR:OH	1:B:241:ILE:HD13	1.89	0.73
1:A:255[B]:GLU:OE1	1:A:258:ARG:NH1	2.24	0.70
1:B:429:LEU:HB3	3:B:502:B7G:C13	2.21	0.69
1:A:435:GLU:OE1	1:A:438:LYS:HE3	1.93	0.68
1:A:288:GLU:OE2	1:A:407:ARG:HG2	1.93	0.68
1:A:280:THR:OG1	5:A:602:HOH:O	2.10	0.68
1:A:283:LYS:HD2	4:A:503:PE3:H21	1.76	0.67
1:A:201:LEU:HD21	1:A:304:LEU:HG	1.78	0.66
1:B:379:ARG:NH1	5:B:601:HOH:O	2.07	0.66
1:A:203:GLY:O	1:A:204:LYS:HD2	1.95	0.66
1:B:236:PRO:HG2	1:B:247:TYR:CD2	2.30	0.65
1:A:279:VAL:HG22	1:B:275:LEU:HD23	1.79	0.64
1:A:227:VAL:HG23	1:A:228:TRP:CE3	2.34	0.63
1:A:435:GLU:HG3	4:A:503:PE3:C3	2.30	0.62
1:A:209:ALA:HB1	1:A:210:PRO:HD2	1.82	0.62
1:A:251:CYS:SG	4:A:503:PE3:H412	2.39	0.61
1:B:211:PHE:CE1	1:B:226:LEU:HD21	2.35	0.61
1:A:294:LEU:HD11	1:A:303:LEU:CD1	2.30	0.61
1:A:240:GLU:OE2	1:A:321:ARG:NH1	2.34	0.60
1:B:428:SER:O	1:B:429:LEU:HD23	2.02	0.60
1:A:222:ALA:HB1	1:A:227:VAL:CG2	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:LYS:HZ1	1:B:233:ASN:N	1.99	0.60
1:A:435:GLU:HG3	4:A:503:PE3:H32	1.85	0.59
1:A:279:VAL:CG2	1:B:275:LEU:HD23	2.35	0.57
1:B:221:GLN:O	1:B:226:LEU:HB3	2.05	0.55
1:B:288:GLU:OE2	1:B:407:ARG:HG2	2.07	0.55
1:A:238:TYR:OH	1:A:241:ILE:HD13	2.06	0.55
1:B:235:LEU:HB3	1:B:236:PRO:HD2	1.88	0.55
1:A:251:CYS:SG	4:A:503:PE3:C41	2.95	0.55
1:A:222:ALA:HB1	1:A:227:VAL:HG22	1.89	0.54
1:A:236:PRO:HG2	4:A:503:PE3:H361	1.90	0.54
1:A:236:PRO:CG	4:A:503:PE3:H361	2.39	0.53
1:A:211:PHE:CD1	1:A:226:LEU:HD21	2.43	0.53
1:B:320:LEU:O	1:B:325:SER:HB3	2.09	0.53
1:B:251[B]:CYS:HA	4:B:503:PE3:H381	1.91	0.53
1:B:326:ASP:HB3	1:B:416:MET:HE3	1.90	0.52
1:B:251[A]:CYS:HA	4:B:503:PE3:H381	1.91	0.52
1:A:375:ASP:OD2	1:A:379:ARG:NH1	2.41	0.52
1:B:318:ARG:NH1	5:B:605:HOH:O	2.43	0.51
1:A:437:TYR:O	3:A:502:B7G:H41	2.11	0.51
1:B:223:GLU:O	5:B:603:HOH:O	2.19	0.51
1:A:367:VAL:HB	1:A:368:PRO:HD3	1.93	0.51
1:B:429:LEU:CB	3:B:502:B7G:H132	2.32	0.51
1:B:238:TYR:OH	1:B:241:ILE:CD1	2.58	0.50
1:A:251:CYS:HG	4:A:503:PE3:C41	2.25	0.49
1:B:274:PHE:CG	1:B:365:MET:HE2	2.48	0.49
1:A:275:LEU:HD23	1:B:279:VAL:HG22	1.94	0.48
1:B:220:TRP:CZ2	1:B:224:LYS:HD2	2.48	0.48
1:A:211:PHE:CE1	1:A:226:LEU:HD21	2.48	0.48
1:B:251[B]:CYS:HB2	4:B:503:PE3:C36	2.43	0.48
1:B:274:PHE:HB3	1:B:276:ASN:OD1	2.13	0.48
1:A:321:ARG:HG2	1:A:322:LYS:O	2.12	0.48
1:A:274:PHE:CG	1:A:365:MET:HE2	2.49	0.47
1:B:225:GLY:HA2	1:B:229:LYS:C	2.35	0.47
1:A:236:PRO:HD3	4:A:503:PE3:H381	1.97	0.47
1:A:421:LYS:HD2	3:A:502:B7G:H72	1.96	0.46
1:A:222:ALA:HB1	1:A:227:VAL:HG21	1.96	0.46
1:A:328:ILE:HD13	2:A:501:9RF:S11	2.56	0.46
1:A:327:ILE:HD11	1:A:420:ILE:HD11	1.98	0.45
1:A:239:LYS:HA	1:A:239:LYS:HD3	1.70	0.45
1:A:224:LYS:O	1:A:226:LEU:N	2.50	0.45
1:A:191:ASN:HB2	1:A:259:GLU:OE2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:ARG:HA	1:A:419:ARG:HD2	1.81	0.44
1:A:328:ILE:HG13	5:A:642:HOH:O	2.17	0.44
1:A:425:THR:OG1	5:A:603:HOH:O	2.21	0.44
1:B:239:LYS:HD3	1:B:239:LYS:HA	1.79	0.43
1:A:209:ALA:HB1	1:A:210:PRO:CD	2.45	0.43
1:B:206:SER:O	1:B:207:HIS:CG	2.72	0.43
1:A:258:ARG:NE	5:A:606:HOH:O	2.35	0.43
4:A:503:PE3:H201	1:B:274:PHE:CZ	2.54	0.43
1:A:222:ALA:O	1:A:227:VAL:HG22	2.19	0.43
1:A:430:HIS:HA	4:A:503:PE3:H352	2.01	0.43
1:A:227:VAL:CG2	1:A:228:TRP:CE3	3.01	0.42
4:A:503:PE3:C33	4:A:503:PE3:H291	2.48	0.42
1:B:440:MET:HE3	5:B:685:HOH:O	2.19	0.42
1:A:435:GLU:HG3	4:A:503:PE3:H31	2.00	0.42
1:A:220:TRP:CH2	1:A:224:LYS:HD2	2.54	0.42
1:A:343:LEU:HD11	1:A:399:LEU:HD21	2.02	0.42
1:B:437:TYR:O	3:B:502:B7G:H41	2.19	0.42
1:A:274:PHE:CD2	1:A:365:MET:HE2	2.55	0.42
1:B:327:ILE:HD13	1:B:416:MET:HE1	2.01	0.42
1:A:274:PHE:HB3	1:A:276:ASN:OD1	2.19	0.41
1:B:374:GLN:NE2	5:B:608:HOH:O	2.53	0.41
1:B:198:ARG:HD3	5:B:606:HOH:O	2.20	0.41
1:A:436:ILE:HG12	4:A:503:PE3:H61	2.02	0.41
1:A:251:CYS:O	1:A:255[A]:GLU:HG3	2.20	0.41
1:A:421:LYS:CD	3:A:502:B7G:H72	2.51	0.40
4:A:503:PE3:H201	1:B:274:PHE:CE1	2.57	0.40
1:B:343:LEU:HD11	1:B:399:LEU:HD21	2.03	0.40

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	263/270 (97%)	259 (98%)	3 (1%)	1 (0%)	34	32
1	B	264/270 (98%)	258 (98%)	6 (2%)	0	100	100
All	All	527/540 (98%)	517 (98%)	9 (2%)	1 (0%)	47	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	GLY

### 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	235/238 (99%)	235 (100%)	0	100	100
1	B	236/238 (99%)	234 (99%)	2 (1%)	81	86
All	All	471/476 (99%)	469 (100%)	2 (0%)	91	94

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	191	ASN
1	B	303	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

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	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	B7G	B	502	-	19,19,19	1.33	1 (5%)	24,24,24	1.02	1 (4%)
4	PE3	B	503	-	42,42,42	0.55	0	41,41,41	0.44	0
4	PE3	A	503	-	42,42,42	0.57	0	41,41,41	0.58	0
3	B7G	A	502	-	19,19,19	1.35	1 (5%)	24,24,24	1.43	5 (20%)
2	9RF	A	501	-	25,31,31	0.91	2 (8%)	31,44,44	1.44	3 (9%)
2	9RF	B	501	-	25,31,31	0.94	2 (8%)	31,44,44	1.53	4 (12%)

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	B7G	B	502	-	-	7/10/30/30	0/1/1/1
4	PE3	B	503	-	-	18/40/40/40	-
4	PE3	A	503	-	-	26/40/40/40	-
3	B7G	A	502	-	-	6/10/30/30	0/1/1/1
2	9RF	A	501	-	-	2/16/20/20	0/3/3/3
2	9RF	B	501	-	-	2/16/20/20	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	B7G	O5-C1	4.23	1.52	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	B7G	O5-C1	4.09	1.52	1.41
2	B	501	9RF	C04-S05	2.40	1.81	1.76
2	A	501	9RF	C06-C07	2.20	1.52	1.50
2	B	501	9RF	C06-C07	2.12	1.52	1.50
2	A	501	9RF	C04-S05	2.09	1.81	1.76

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	9RF	C10-N09-N08	5.29	116.19	105.29
2	A	501	9RF	C10-N09-N08	5.10	115.80	105.29
3	A	502	B7G	O5-C1-C2	3.01	116.72	110.35
2	B	501	9RF	F17-C16-C15	-2.92	106.51	112.93
3	A	502	B7G	O1-C1-C2	2.79	112.66	108.30
3	A	502	B7G	C3-C4-C5	2.61	114.90	110.24
2	B	501	9RF	O25-C24-C02	2.58	119.99	115.10
2	B	501	9RF	C26-O25-C24	-2.52	112.80	117.76
3	B	502	B7G	O1-C1-C2	2.31	111.91	108.30
3	A	502	B7G	O2-C2-C1	-2.21	104.69	110.05
3	A	502	B7G	O4-C4-C5	-2.20	103.83	109.30
2	A	501	9RF	C26-O25-C24	-2.08	113.67	117.76
2	A	501	9RF	F18-C16-C15	-2.05	108.43	112.93

There are no chirality outliers.

All (61) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	B7G	C2-C1-O1-C7
4	A	503	PE3	C29-C30-O31-C32
4	A	503	PE3	O31-C32-C33-O34
4	A	503	PE3	O4-C5-C6-O7
4	A	503	PE3	O19-C20-C21-O22
4	A	503	PE3	O16-C17-C18-O19
3	B	502	B7G	C4-C5-C6-O6
4	A	503	PE3	O13-C14-C15-O16
4	A	503	PE3	O7-C8-C9-O10
4	B	503	PE3	O4-C5-C6-O7
4	A	503	PE3	O28-C29-C30-O31
4	B	503	PE3	O7-C8-C9-O10
3	A	502	B7G	O5-C1-O1-C7
4	B	503	PE3	O10-C11-C12-O13
4	A	503	PE3	C15-C14-O13-C12

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Mol	Chain	Res	Type	Atoms
4	B	503	PE3	O34-C35-C36-O37
4	A	503	PE3	O37-C38-C39-O40
3	B	502	B7G	O5-C5-C6-O6
4	B	503	PE3	O28-C29-C30-O31
4	B	503	PE3	O25-C26-C27-O28
4	A	503	PE3	O40-C41-C42-O43
4	A	503	PE3	O10-C11-C12-O13
3	B	502	B7G	C10-C11-C12-C13
3	A	502	B7G	C7-C8-C9-C10
3	B	502	B7G	C7-C8-C9-C10
3	B	502	B7G	O1-C7-C8-C9
4	A	503	PE3	O22-C23-C24-O25
3	A	502	B7G	C9-C10-C11-C12
4	A	503	PE3	O1-C2-C3-O4
4	A	503	PE3	C18-C17-O16-C15
4	B	503	PE3	O16-C17-C18-O19
4	A	503	PE3	C26-C27-O28-C29
4	B	503	PE3	O40-C41-C42-O43
4	B	503	PE3	O1-C2-C3-O4
4	B	503	PE3	C21-C20-O19-C18
4	A	503	PE3	C21-C20-O19-C18
4	A	503	PE3	C11-C12-O13-C14
3	A	502	B7G	C11-C10-C9-C8
4	B	503	PE3	C29-C30-O31-C32
4	B	503	PE3	O37-C38-C39-O40
4	A	503	PE3	C35-C36-O37-C38
4	B	503	PE3	C8-C9-O10-C11
4	A	503	PE3	C33-C32-O31-C30
4	B	503	PE3	C14-C15-O16-C17
4	A	503	PE3	C32-C33-O34-C35
4	A	503	PE3	C38-C39-O40-C41
2	B	501	9RF	C03-C04-S05-C06
2	A	501	9RF	C22-C04-S05-C06
2	A	501	9RF	C03-C04-S05-C06
2	B	501	9RF	C22-C04-S05-C06
4	A	503	PE3	C27-C26-O25-C24
4	B	503	PE3	O19-C20-C21-O22
4	B	503	PE3	O13-C14-C15-O16
4	B	503	PE3	C35-C36-O37-C38
4	A	503	PE3	C39-C38-O37-C36
3	B	502	B7G	C11-C10-C9-C8
4	B	503	PE3	C9-C8-O7-C6

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Mol	Chain	Res	Type	Atoms
4	A	503	PE3	C23-C24-O25-C26
3	A	502	B7G	O1-C7-C8-C9
4	A	503	PE3	C6-C5-O4-C3
3	B	502	B7G	C8-C7-O1-C1

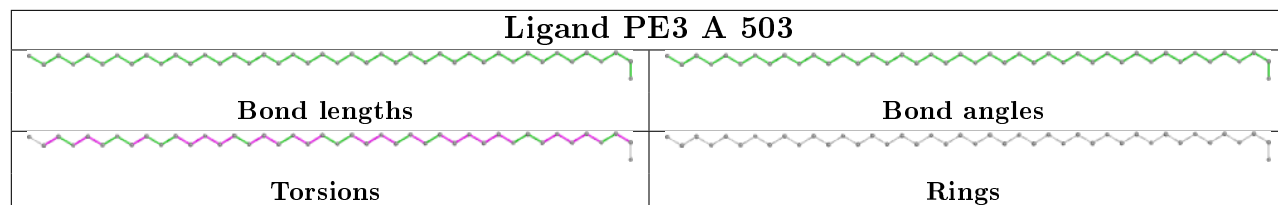
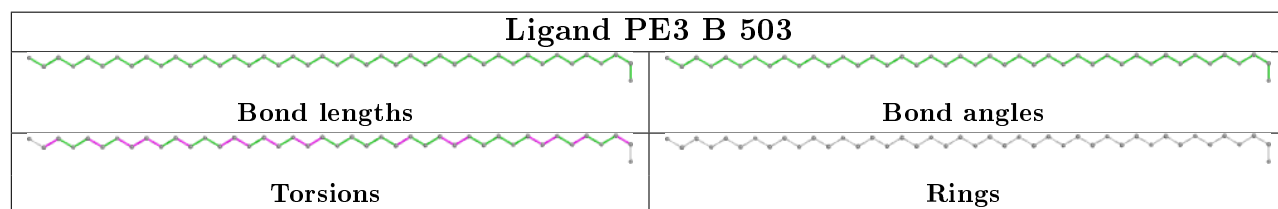
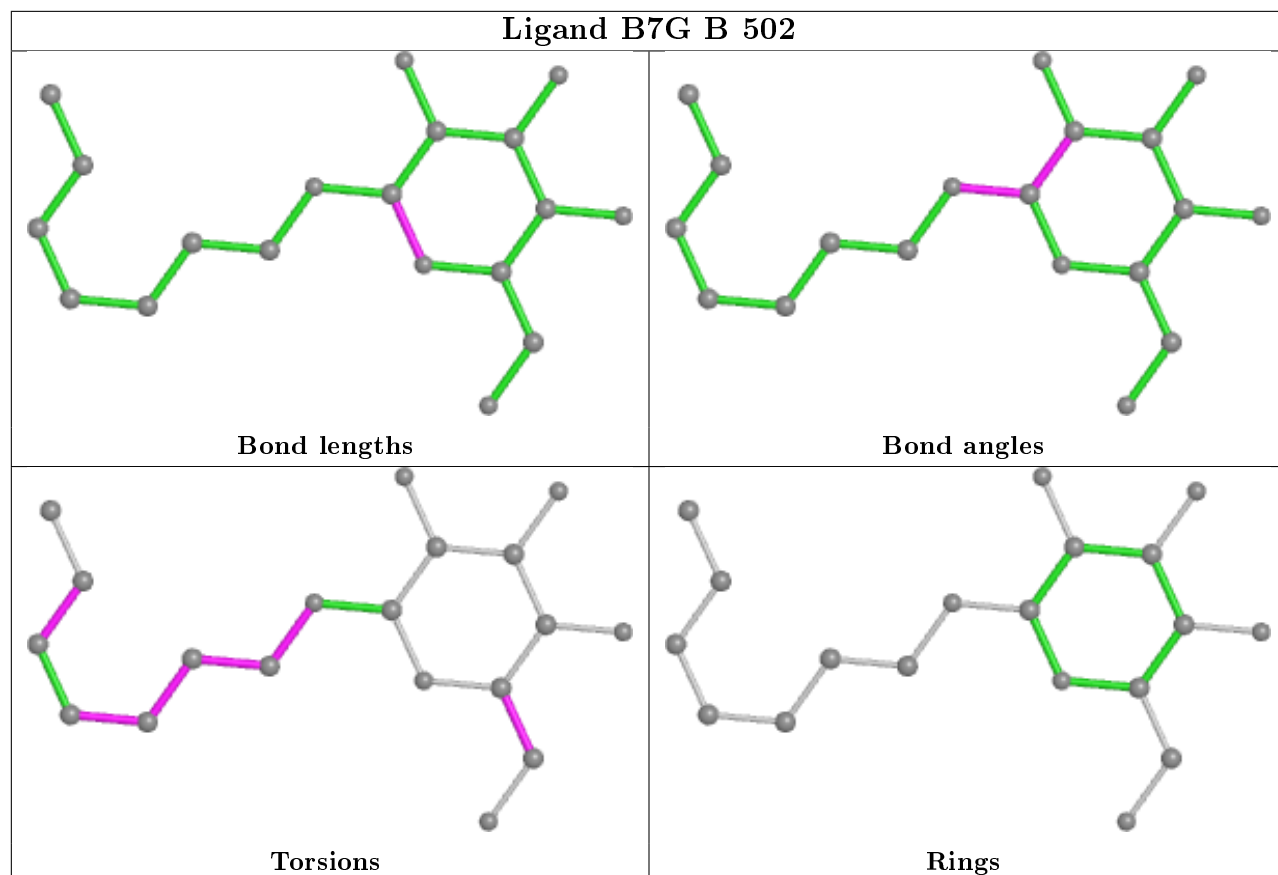
There are no ring outliers.

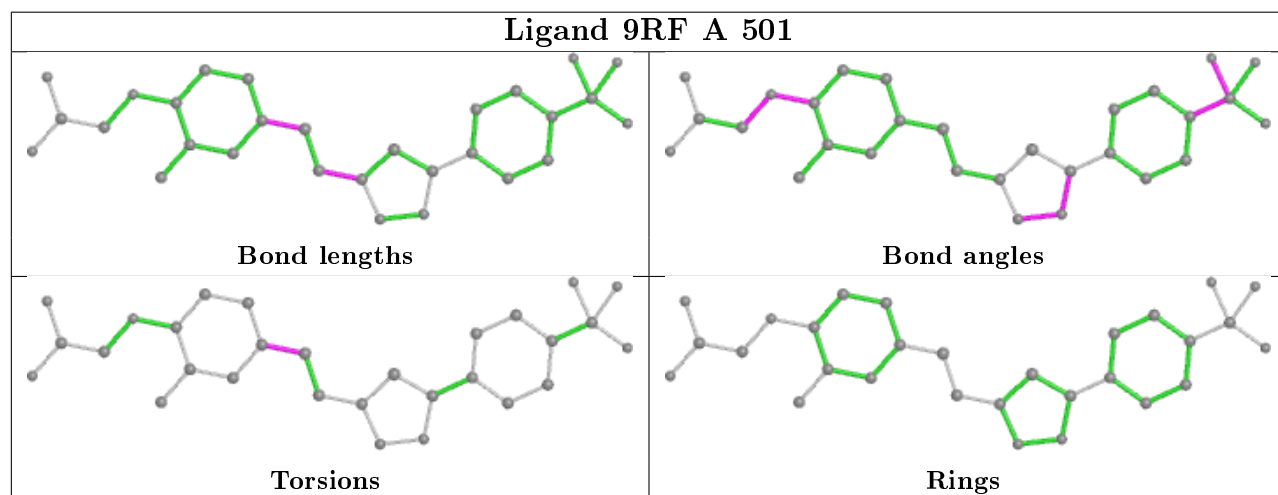
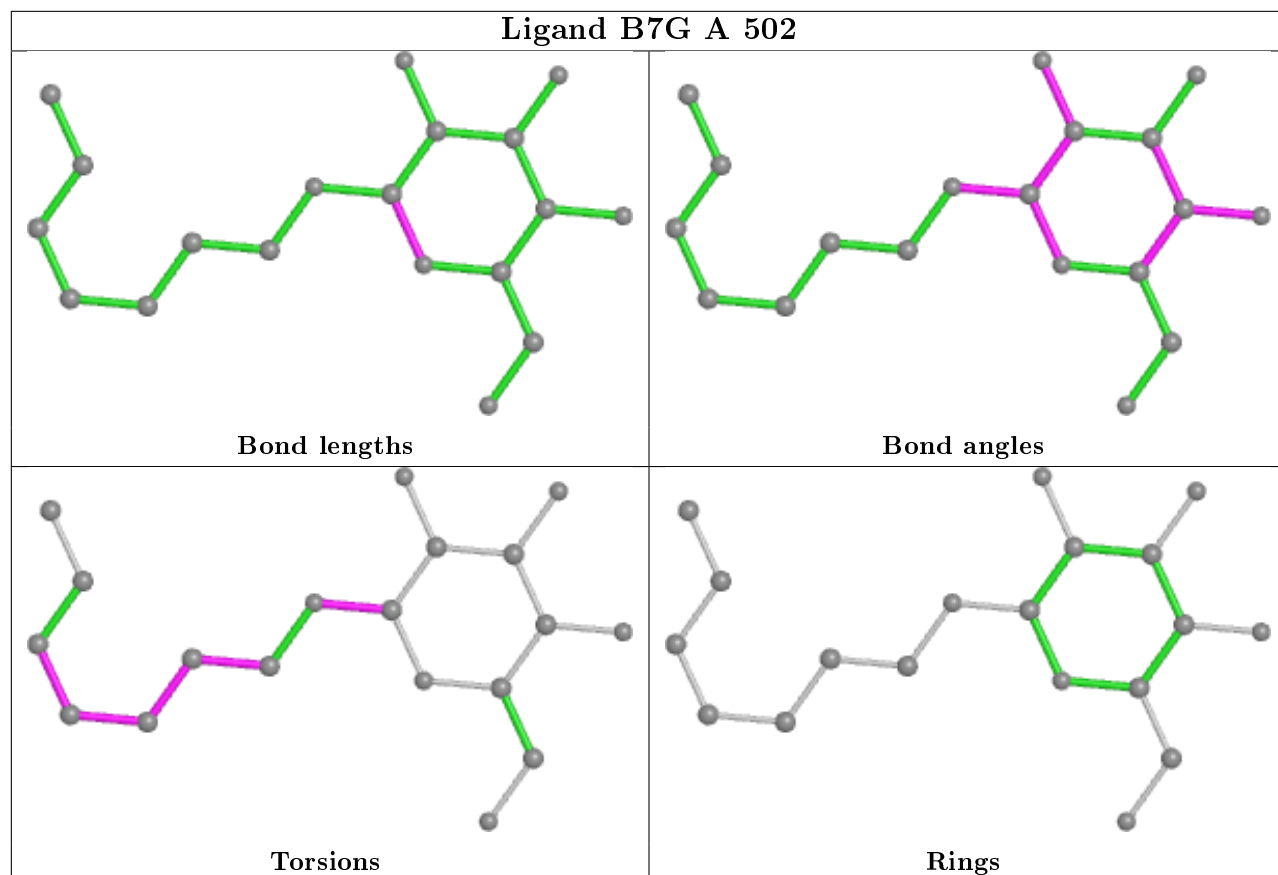
5 monomers are involved in 27 short contacts:

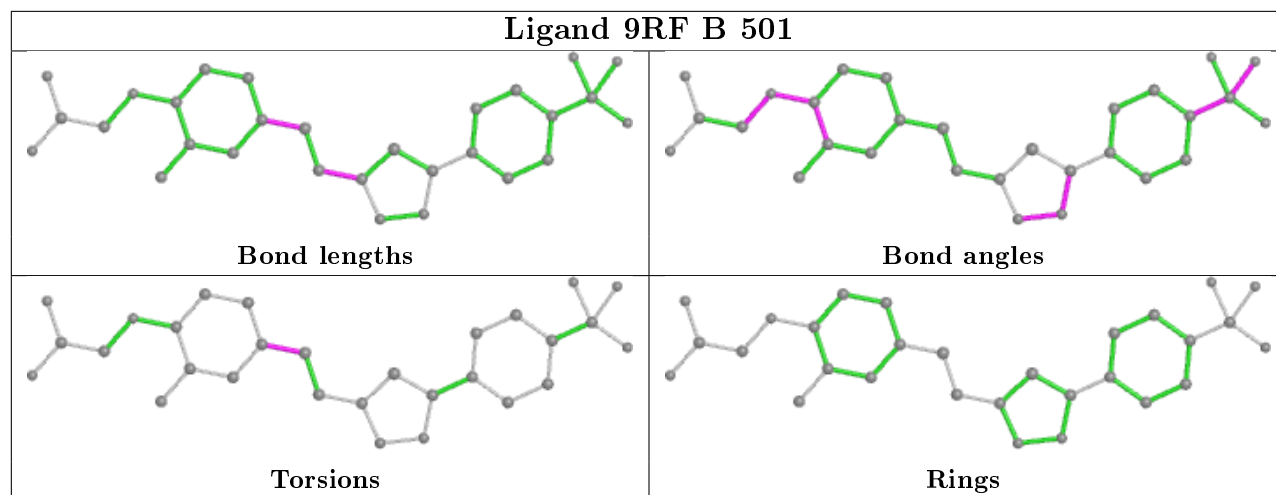
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502	B7G	5	0
4	B	503	PE3	3	0
4	A	503	PE3	15	0
3	A	502	B7G	3	0
2	A	501	9RF	1	0

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 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	266/270 (98%)	0.08	13 (4%) 29 35	23, 37, 72, 134	0
1	B	267/270 (98%)	0.19	17 (6%) 19 24	25, 42, 84, 130	0
All	All	533/540 (98%)	0.14	30 (5%) 24 29	23, 40, 81, 134	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	172	VAL	10.1
1	A	172	VAL	9.3
1	B	173	ALA	6.4
1	A	204	LYS	5.8
1	A	203	GLY	5.4
1	A	205	ALA	5.0
1	A	207	HIS	4.8
1	B	171	GLN	4.8
1	B	207	HIS	4.5
1	A	208	THR	4.3
1	B	229	LYS	3.6
1	B	383	PHE	3.4
1	B	233	ASN	3.4
1	B	425	THR	3.3
1	B	225	GLY	3.3
1	B	203	GLY	3.2
1	B	393	GLN	2.6
1	B	268	PRO	2.6
1	B	228	TRP	2.5
1	A	209	ALA	2.4
1	B	205	ALA	2.4
1	A	274	PHE	2.3
1	A	206	SER	2.2
1	A	171	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	208	THR	2.2
1	A	290	ILE	2.1
1	B	392	ALA	2.1
1	B	394	TYR	2.1
1	A	393	GLN	2.0
1	A	202	THR	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

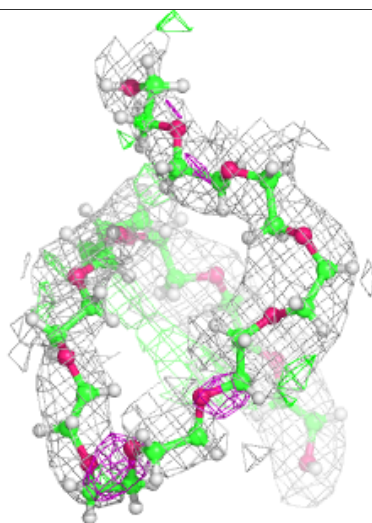
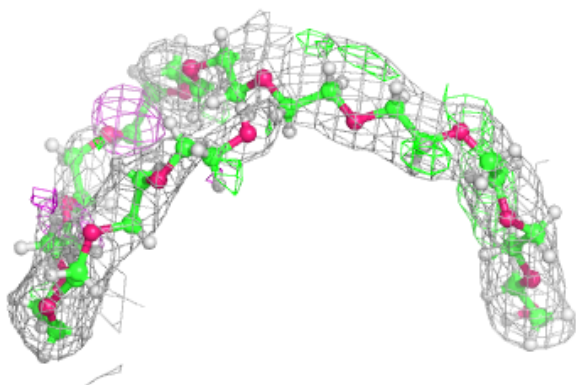
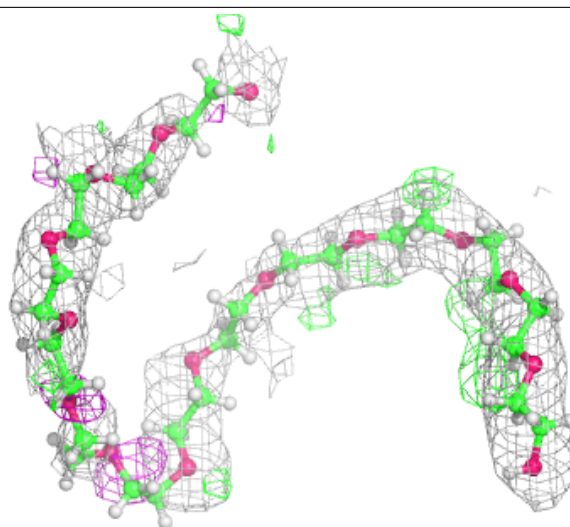
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
4	PE3	B	503	43/43	0.59	0.26	51,70,83,95	0
4	PE3	A	503	43/43	0.71	0.22	50,67,83,88	0
3	B7G	B	502	19/19	0.80	0.27	60,81,91,96	0
3	B7G	A	502	19/19	0.86	0.24	50,65,77,83	0
2	9RF	B	501	29/29	0.93	0.14	36,47,58,60	0
2	9RF	A	501	29/29	0.94	0.13	34,42,50,60	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.

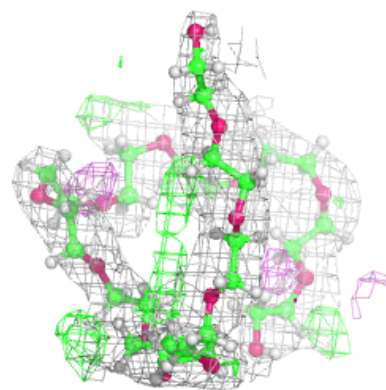
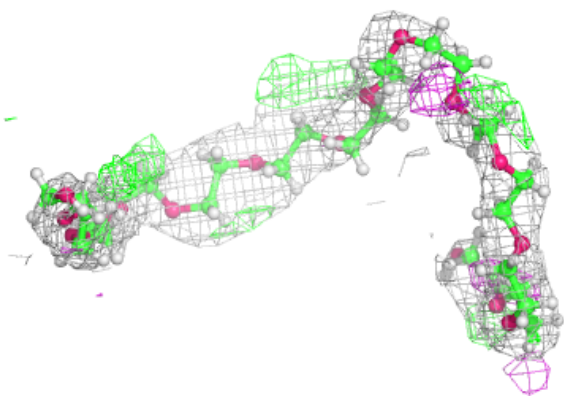
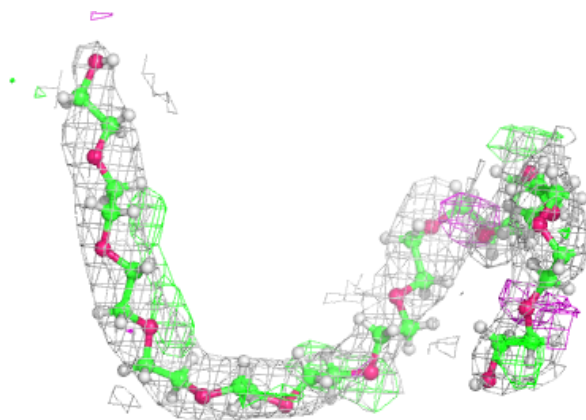
**Electron density around PE3 B 503:**

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



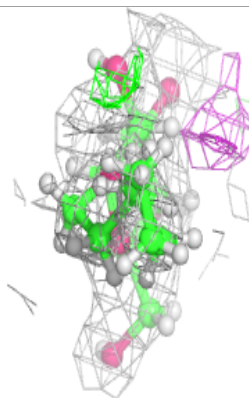
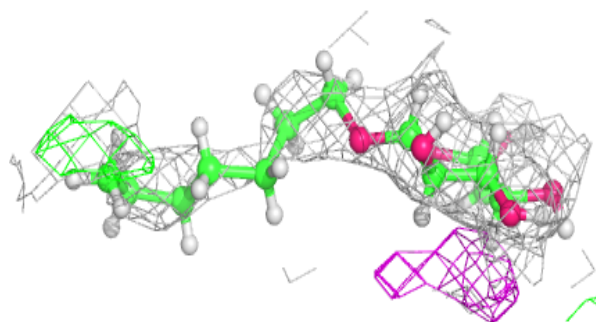
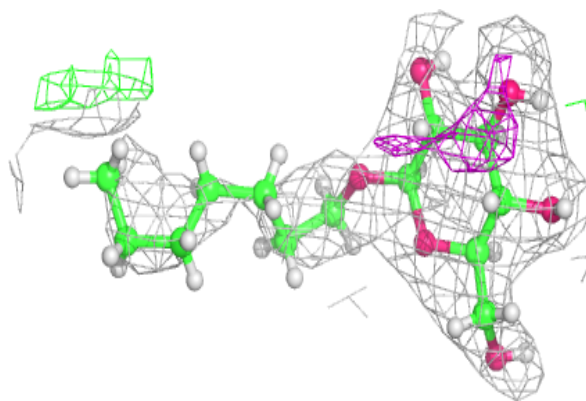
**Electron density around PE3 A 503:**

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

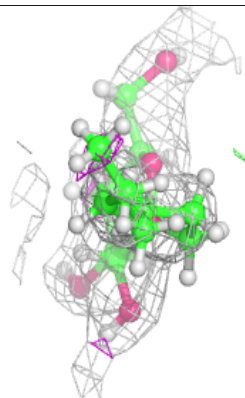
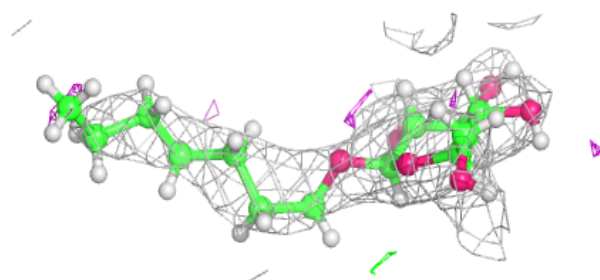
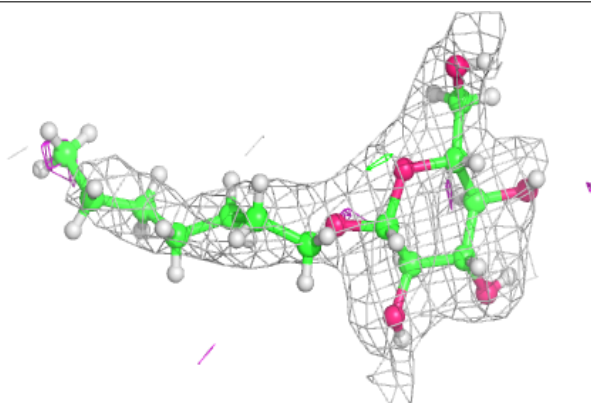


**Electron density around B7G B 502:**

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

**Electron density around B7G A 502:**

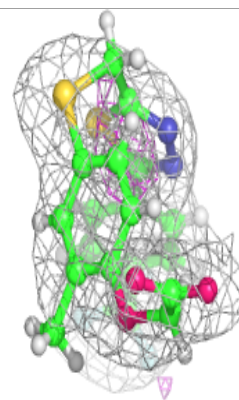
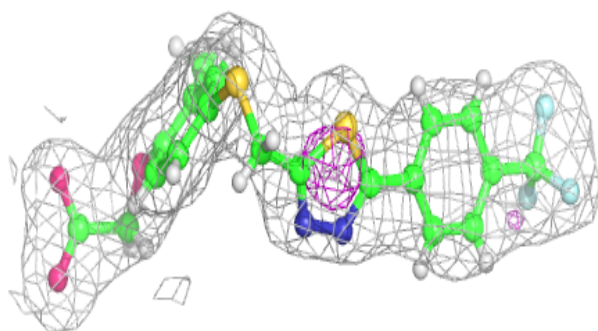
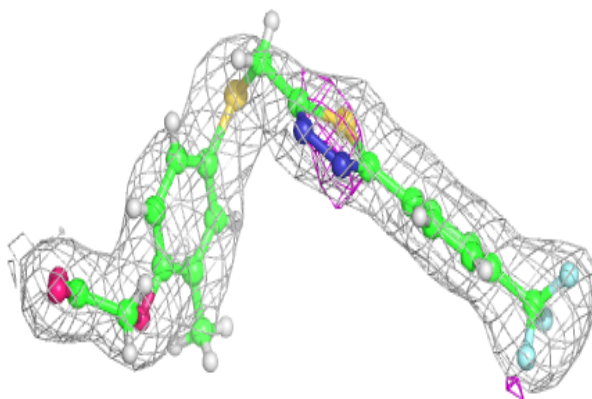
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



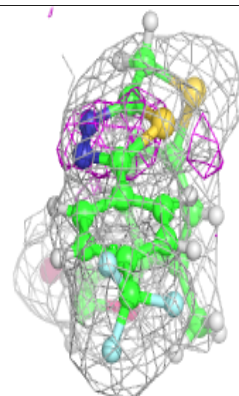
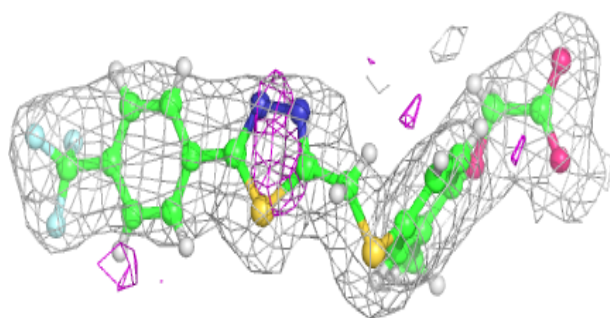
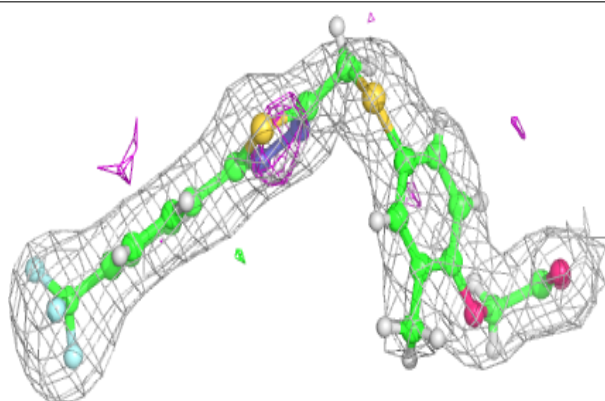


**Electron density around 9RF B 501:**

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

**Electron density around 9RF A 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.