



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 09:42 PM BST

PDB ID : 5ZM8  
Title : Crystal structure of ORP2-ORD in complex with PI(4,5)P2  
Authors : Wang, H.; Dong, J.Q.; Wang, J.; Wu, J.W.  
Deposited on : 2018-04-01  
Resolution : 2.70 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

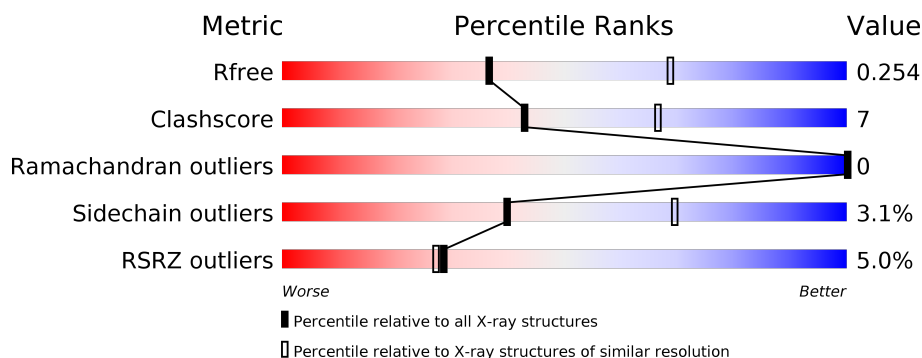
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	455	<div> <div>5%</div> <div> <div></div> <div>70%</div> <div>14%</div> <div>15%</div> </div> </div>
1	B	455	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>13%</div> <div>9%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6836 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 Oxysterol-binding protein-related protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	386	Total	C	N	O	S	0	0	0
			3159	2024	547	570	18			
1	B	413	Total	C	N	O	S	0	0	0
			3384	2162	591	613	18			

There are 46 discrepancies between the modelled and reference sequences:

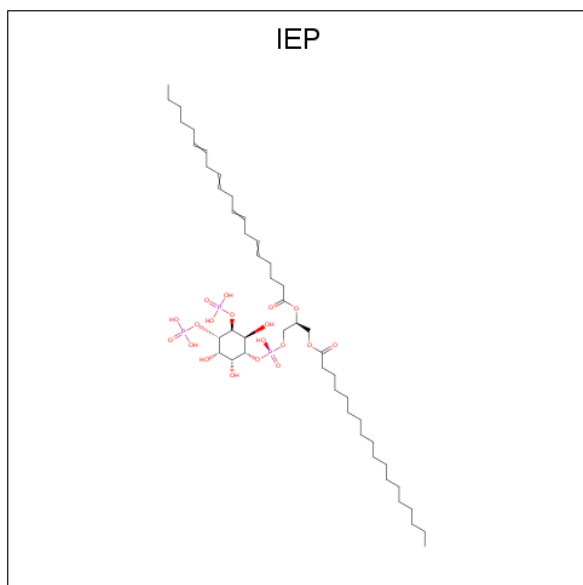
Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MET	-	initiating methionine	UNP Q9H1P3
A	27	GLY	-	expression tag	UNP Q9H1P3
A	28	SER	-	expression tag	UNP Q9H1P3
A	29	SER	-	expression tag	UNP Q9H1P3
A	30	HIS	-	expression tag	UNP Q9H1P3
A	31	HIS	-	expression tag	UNP Q9H1P3
A	32	HIS	-	expression tag	UNP Q9H1P3
A	33	HIS	-	expression tag	UNP Q9H1P3
A	34	HIS	-	expression tag	UNP Q9H1P3
A	35	HIS	-	expression tag	UNP Q9H1P3
A	36	SER	-	expression tag	UNP Q9H1P3
A	37	GLN	-	expression tag	UNP Q9H1P3
A	38	ASP	-	expression tag	UNP Q9H1P3
A	39	LEU	-	expression tag	UNP Q9H1P3
A	40	GLU	-	expression tag	UNP Q9H1P3
A	41	VAL	-	expression tag	UNP Q9H1P3
A	42	LEU	-	expression tag	UNP Q9H1P3
A	43	PHE	-	expression tag	UNP Q9H1P3
A	44	GLN	-	expression tag	UNP Q9H1P3
A	45	GLY	-	expression tag	UNP Q9H1P3
A	46	PRO	-	expression tag	UNP Q9H1P3
A	47	HIS	-	expression tag	UNP Q9H1P3
A	48	MET	-	expression tag	UNP Q9H1P3
B	26	MET	-	initiating methionine	UNP Q9H1P3
B	27	GLY	-	expression tag	UNP Q9H1P3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	28	SER	-	expression tag	UNP Q9H1P3
B	29	SER	-	expression tag	UNP Q9H1P3
B	30	HIS	-	expression tag	UNP Q9H1P3
B	31	HIS	-	expression tag	UNP Q9H1P3
B	32	HIS	-	expression tag	UNP Q9H1P3
B	33	HIS	-	expression tag	UNP Q9H1P3
B	34	HIS	-	expression tag	UNP Q9H1P3
B	35	HIS	-	expression tag	UNP Q9H1P3
B	36	SER	-	expression tag	UNP Q9H1P3
B	37	GLN	-	expression tag	UNP Q9H1P3
B	38	ASP	-	expression tag	UNP Q9H1P3
B	39	LEU	-	expression tag	UNP Q9H1P3
B	40	GLU	-	expression tag	UNP Q9H1P3
B	41	VAL	-	expression tag	UNP Q9H1P3
B	42	LEU	-	expression tag	UNP Q9H1P3
B	43	PHE	-	expression tag	UNP Q9H1P3
B	44	GLN	-	expression tag	UNP Q9H1P3
B	45	GLY	-	expression tag	UNP Q9H1P3
B	46	PRO	-	expression tag	UNP Q9H1P3
B	47	HIS	-	expression tag	UNP Q9H1P3
B	48	MET	-	expression tag	UNP Q9H1P3

- Molecule 2 is [(2 {S})-1-octadecanoyloxy-3-[oxidanyl-[(1 {R},2 {R},3 {S},4 {S},5 {S},6 {S})-2,3,6-tris(oxidanyl)-4,5-diphosphonoxy-cyclohexyl]oxy-phosphoryl]oxy-propan-2-yl] icosadecanoate (three-letter code: IEP) (formula: C<sub>47</sub>H<sub>85</sub>O<sub>19</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			69	47	19	3		
2	B	1	Total	C	O	P	0	0
			69	47	19	3		

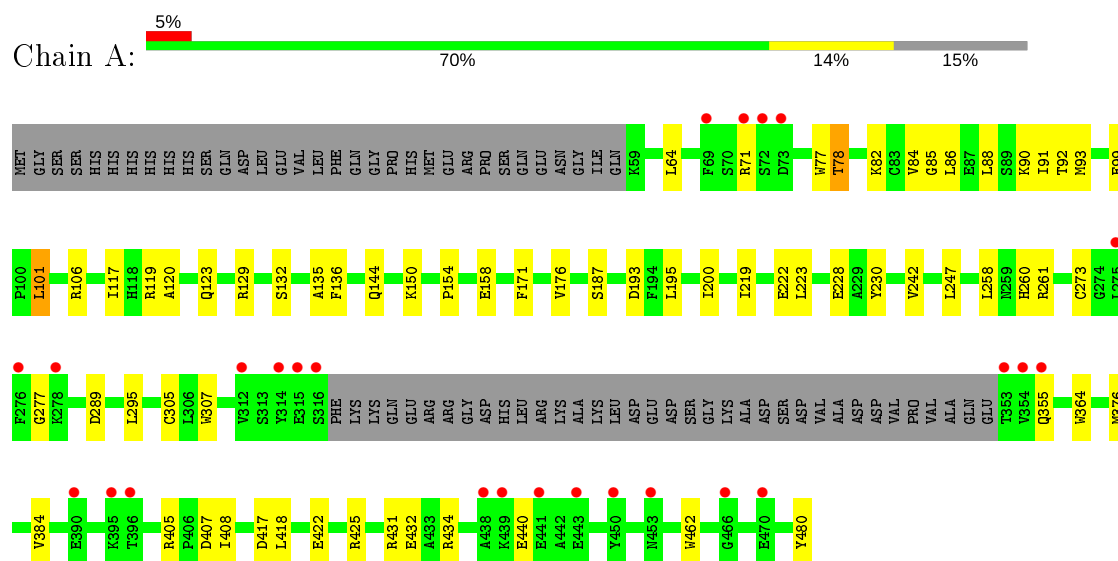
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	42	Total	O	0	0
			42	42		
3	B	113	Total	O	0	0
			113	113		

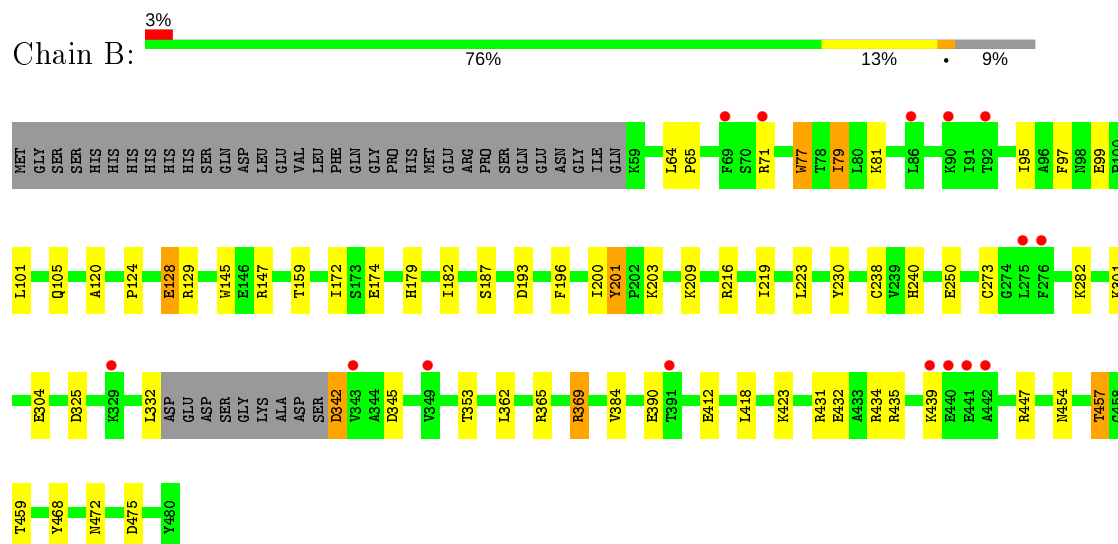
### 3 Residue-property plots [i](#)

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: Oxysterol-binding protein-related protein 2



- Molecule 1: Oxysterol-binding protein-related protein 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	156.16 Å   156.16 Å   199.22 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	42.32 – 2.70 42.32 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.2 (42.32-2.70) 97.2 (42.32-2.70)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.39 (at 2.69 Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, $R_{free}$	0.216   ,   0.254 0.216   ,   0.254	Depositor DCC
$R_{free}$ test set	1686 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.6	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 44.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6836	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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: IEP

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	0.28	0/3253	0.44	0/4409
1	B	0.35	0/3481	0.47	0/4713
All	All	0.32	0/6734	0.45	0/9122

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	3159	0	3078	51	0
1	B	3384	0	3307	38	0
2	A	69	0	0	2	0
2	B	69	0	0	1	0
3	A	42	0	0	0	0
3	B	113	0	0	2	0
All	All	6836	0	6385	89	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 7.

All (89) 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:128:GLU:HG3	3:B:674:HOH:O	1.67	0.95
1:A:84:VAL:HG12	1:A:86:LEU:HD12	1.56	0.86
1:A:90:LYS:HE3	1:A:92:THR:CG2	2.06	0.85
1:A:84:VAL:HG11	1:A:86:LEU:CD1	2.11	0.81
1:A:176:VAL:HG21	1:A:462:TRP:CE3	2.18	0.78
1:A:90:LYS:HE3	1:A:92:THR:HG21	1.65	0.77
1:A:84:VAL:CG1	1:A:86:LEU:CD1	2.61	0.77
1:A:84:VAL:HG12	1:A:85:GLY:N	2.00	0.77
1:A:84:VAL:HG11	1:A:86:LEU:HD13	1.68	0.75
1:B:124:PRO:HD2	3:B:674:HOH:O	1.86	0.75
1:A:84:VAL:CG1	1:A:86:LEU:HD12	2.16	0.75
1:A:84:VAL:HG12	1:A:85:GLY:H	1.54	0.72
1:B:145:TRP:O	1:B:369:ARG:NH2	2.22	0.71
1:A:431:ARG:HD3	2:A:501:IEP:O44	1.93	0.69
1:A:417:ASP:OD1	1:A:418:LEU:N	2.26	0.69
1:A:176:VAL:HG21	1:A:462:TRP:CZ3	2.32	0.65
1:B:179:HIS:NE2	2:B:501:IEP:O44	2.28	0.64
1:A:106:ARG:HH21	1:A:144:GLN:HG2	1.64	0.63
1:A:154:PRO:HA	1:A:405:ARG:HH12	1.64	0.62
1:A:84:VAL:CG1	1:A:85:GLY:H	2.13	0.61
1:B:454:ASN:HB3	1:B:457:THR:HG22	1.82	0.61
1:B:182:ILE:HG12	1:B:201:TYR:HB3	1.83	0.61
1:A:425:ARG:NH1	1:A:480:TYR:O	2.34	0.61
1:B:172:ILE:HD13	1:B:468:TYR:CE2	2.36	0.60
1:A:84:VAL:CG1	1:A:85:GLY:N	2.65	0.58
1:B:79:ILE:HG22	1:B:97:PHE:HE2	1.71	0.56
1:B:457:THR:HG23	1:B:459:THR:H	1.71	0.56
1:B:342:ASP:N	1:B:342:ASP:OD1	2.39	0.56
1:A:123:GLN:HB2	1:A:129:ARG:HG2	1.89	0.55
1:A:193:ASP:N	1:A:193:ASP:OD1	2.39	0.54
1:A:176:VAL:CG2	1:A:462:TRP:CZ3	2.90	0.54
1:A:376:MET:SD	1:A:384:VAL:HG11	2.47	0.54
1:B:200:ILE:HD11	1:B:219:ILE:HD11	1.90	0.52
1:B:159:THR:HG22	1:B:174:GLU:HG3	1.91	0.52
1:B:304:GLU:OE2	1:B:353:THR:OG1	2.28	0.52
1:A:71:ARG:HG3	1:A:71:ARG:O	2.09	0.51
1:A:158:GLU:OE2	1:A:405:ARG:NH1	2.43	0.51
1:A:273:CYS:HB2	1:A:277:GLY:HA2	1.92	0.50
1:A:258:LEU:HD23	1:A:260:HIS:CE1	2.47	0.50
1:A:91:ILE:HG22	2:A:501:IEP:O50	2.12	0.50
1:A:305:CYS:HG	1:A:307:TRP:HE1	1.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:GLU:O	1:A:101:LEU:N	2.45	0.49
1:B:193:ASP:N	1:B:193:ASP:OD1	2.46	0.49
1:B:99:GLU:O	1:B:101:LEU:N	2.44	0.49
1:B:172:ILE:HD13	1:B:468:TYR:CZ	2.47	0.48
1:A:195:LEU:HB2	1:A:222:GLU:HB2	1.96	0.48
1:A:223:LEU:HD12	1:A:230:TYR:HE1	1.79	0.48
1:B:362:LEU:HD21	1:B:365:ARG:HD2	1.96	0.48
1:A:407:ASP:OD1	1:A:408:ILE:N	2.48	0.47
1:B:282:LYS:HA	1:B:301:LYS:HG2	1.96	0.47
1:A:84:VAL:CG1	1:A:86:LEU:HD13	2.38	0.46
1:B:238:CYS:HG	1:B:240:HIS:CE1	2.34	0.46
1:A:135:ALA:HB1	1:A:364:TRP:HB2	1.96	0.46
1:A:289:ASP:HB3	1:A:295:LEU:HD11	1.96	0.46
1:B:447:ARG:NH1	1:B:475:ASP:O	2.48	0.46
1:A:171:PHE:HD1	1:A:187:SER:HB2	1.81	0.46
1:B:101:LEU:CD2	1:B:147:ARG:NH2	2.78	0.46
1:A:106:ARG:NH2	1:A:144:GLN:HG2	2.30	0.46
1:A:93:MET:HG2	1:A:150:LYS:HE2	1.98	0.46
1:A:90:LYS:HE3	1:A:92:THR:HG23	1.93	0.46
1:B:65:PRO:HD2	1:B:412:GLU:HG2	1.97	0.45
1:A:200:ILE:HD11	1:A:219:ILE:HD11	1.97	0.45
1:B:439:LYS:HE3	1:B:439:LYS:HB2	1.74	0.45
1:B:101:LEU:CD1	1:B:105:GLN:HB2	2.46	0.45
1:B:240:HIS:NE2	1:B:250:GLU:OE1	2.47	0.45
1:B:223:LEU:HD12	1:B:230:TYR:HE1	1.82	0.44
1:B:172:ILE:CD1	1:B:468:TYR:CZ	3.00	0.44
1:B:79:ILE:HG22	1:B:97:PHE:CE2	2.51	0.44
1:A:78:THR:O	1:A:82:LYS:HG2	2.18	0.43
1:B:431:ARG:O	1:B:435:ARG:HG3	2.18	0.43
1:B:77:TRP:CZ3	1:B:81:LYS:HD2	2.53	0.43
1:B:432:GLU:OE1	1:B:435:ARG:NH1	2.46	0.43
1:B:95:ILE:HD13	1:B:423:LYS:HD2	1.99	0.42
1:B:64:LEU:HD22	1:B:412:GLU:HG3	2.02	0.42
1:A:228:GLU:HB3	1:A:261:ARG:HG2	2.02	0.42
1:B:203:LYS:HB2	1:B:216:ARG:HD2	2.02	0.42
1:A:120:ALA:HB2	1:A:132:SER:HB2	2.02	0.42
1:A:422:GLU:OE1	1:A:425:ARG:NH2	2.53	0.42
1:A:154:PRO:HA	1:A:405:ARG:NH1	2.34	0.41
1:B:250:GLU:OE2	1:B:273:CYS:N	2.53	0.41
1:A:242:VAL:HA	1:A:247:LEU:CD2	2.49	0.41
1:A:77:TRP:NE1	1:A:88:LEU:O	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:ARG:HG2	1:A:407:ASP:OD1	2.21	0.41
1:A:90:LYS:NZ	1:A:431:ARG:NH1	2.69	0.41
1:A:117:ILE:HD11	1:A:136:PHE:CZ	2.56	0.40
1:B:120:ALA:O	1:B:129:ARG:HG2	2.20	0.40
1:B:209:LYS:HB3	1:B:345:ASP:HB2	2.03	0.40
1:B:187:SER:OG	1:B:196:PHE:HB3	2.21	0.40
1:A:119:ARG:O	1:A:123:GLN:HG2	2.21	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	382/455 (84%)	368 (96%)	14 (4%)	0	100	100
1	B	409/455 (90%)	391 (96%)	18 (4%)	0	100	100
All	All	791/910 (87%)	759 (96%)	32 (4%)	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	A	345/406 (85%)	338 (98%)	7 (2%)	55	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	369/406 (91%)	354 (96%)	15 (4%)	30	59
All	All	714/812 (88%)	692 (97%)	22 (3%)	40	69

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	LEU
1	A	78	THR
1	A	101	LEU
1	A	355	GLN
1	A	432	GLU
1	A	434	ARG
1	A	440	GLU
1	B	71	ARG
1	B	77	TRP
1	B	79	ILE
1	B	128	GLU
1	B	201	TYR
1	B	325	ASP
1	B	332	LEU
1	B	342	ASP
1	B	369	ARG
1	B	384	VAL
1	B	390	GLU
1	B	418	LEU
1	B	434	ARG
1	B	457	THR
1	B	472	ASN

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 [i](#)

There are no monosaccharides 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
2	IEP	A	501	-	69,69,69	1.76	18 (26%)	83,87,87	2.68	19 (22%)
2	IEP	B	501	-	69,69,69	1.85	17 (24%)	83,87,87	1.91	15 (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
2	IEP	A	501	-	-	34/66/90/90	0/1/1/1
2	IEP	B	501	-	-	39/66/90/90	0/1/1/1

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	IEP	P42-O41	-5.30	1.49	1.59
2	B	501	IEP	O50-C49	5.08	1.37	1.22
2	B	501	IEP	O35-C34	-3.95	1.33	1.43
2	B	501	IEP	C23-C22	3.91	1.62	1.50
2	A	501	IEP	O20-C21	-3.81	1.36	1.45
2	A	501	IEP	O50-C49	3.80	1.33	1.22
2	A	501	IEP	C61-C60	3.73	1.53	1.31
2	B	501	IEP	C64-C63	3.73	1.53	1.31
2	A	501	IEP	C58-C57	3.72	1.53	1.31
2	B	501	IEP	C61-C60	3.72	1.53	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	IEP	C55-C54	3.70	1.53	1.31
2	A	501	IEP	C55-C54	3.66	1.53	1.31
2	B	501	IEP	C58-C57	3.66	1.53	1.31
2	A	501	IEP	P25-O28	-3.65	1.50	1.60
2	A	501	IEP	C64-C63	3.64	1.52	1.31
2	A	501	IEP	O35-C34	-3.39	1.35	1.43
2	A	501	IEP	C21-C22	3.20	1.60	1.50
2	A	501	IEP	C23-C22	3.11	1.60	1.50
2	A	501	IEP	P42-O41	-3.00	1.53	1.59
2	B	501	IEP	O20-C21	-2.95	1.38	1.45
2	B	501	IEP	P37-O36	-2.94	1.53	1.59
2	B	501	IEP	C21-C22	2.85	1.59	1.50
2	B	501	IEP	P42-O44	-2.84	1.43	1.54
2	A	501	IEP	P37-O36	-2.76	1.54	1.59
2	B	501	IEP	O20-C18	2.74	1.41	1.33
2	B	501	IEP	O46-C31	-2.73	1.36	1.43
2	A	501	IEP	P42-O43	-2.68	1.44	1.54
2	B	501	IEP	O48-C49	2.40	1.41	1.34
2	B	501	IEP	P42-O43	-2.33	1.45	1.54
2	A	501	IEP	O24-C23	-2.30	1.35	1.44
2	A	501	IEP	P25-O24	-2.29	1.50	1.59
2	A	501	IEP	C34-C29	2.24	1.58	1.52
2	A	501	IEP	C51-C49	2.20	1.57	1.50
2	B	501	IEP	P25-O28	2.19	1.66	1.60
2	A	501	IEP	C30-C29	2.14	1.58	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	IEP	O48-C49-O50	-14.85	87.81	123.70
2	B	501	IEP	O41-C32-C31	8.63	128.73	108.66
2	A	501	IEP	C34-C29-C30	7.96	122.33	110.85
2	A	501	IEP	O28-C29-C34	6.86	124.63	108.66
2	A	501	IEP	O41-C32-C31	-5.65	95.53	108.66
2	A	501	IEP	O48-C49-C51	5.31	122.94	111.50
2	B	501	IEP	C23-C22-C21	5.07	123.78	111.79
2	A	501	IEP	O41-C32-C33	4.97	120.40	108.69
2	B	501	IEP	O36-C33-C32	4.78	119.95	108.69
2	A	501	IEP	O28-C29-C30	-4.77	97.57	108.66
2	B	501	IEP	O48-C49-O50	-4.48	112.87	123.70
2	A	501	IEP	C22-O48-C49	4.24	128.22	117.79
2	A	501	IEP	O43-P42-O45	-4.17	94.36	110.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	IEP	O48-C22-C21	4.05	123.08	108.40
2	B	501	IEP	C34-C29-C30	3.70	116.18	110.85
2	B	501	IEP	O35-C34-C33	3.26	118.59	109.94
2	B	501	IEP	C34-C33-C32	3.19	118.94	111.66
2	B	501	IEP	O36-C33-C34	3.09	115.84	108.66
2	A	501	IEP	C30-C31-C32	3.03	116.61	109.68
2	A	501	IEP	O46-C31-C32	2.92	117.69	109.94
2	B	501	IEP	C31-C32-C33	2.84	118.15	111.66
2	B	501	IEP	O50-C49-C51	-2.84	112.66	123.73
2	B	501	IEP	O35-C34-C29	2.80	117.37	109.94
2	A	501	IEP	C34-C33-C32	2.62	117.65	111.66
2	B	501	IEP	O28-C29-C34	2.42	114.30	108.66
2	A	501	IEP	O48-C22-C21	2.37	116.98	108.40
2	A	501	IEP	O28-P25-O26	2.32	118.18	109.47
2	A	501	IEP	O27-P25-O28	2.27	115.74	106.78
2	A	501	IEP	O48-C22-C23	2.24	116.50	108.40
2	A	501	IEP	O43-P42-O41	2.19	115.81	105.99
2	A	501	IEP	O46-C31-C30	-2.18	105.31	110.35
2	B	501	IEP	O38-P37-O36	2.16	115.67	105.99
2	A	501	IEP	O41-P42-O45	2.12	117.57	109.39
2	B	501	IEP	O20-C18-C17	2.04	118.30	111.91

There are no chirality outliers.

All (73) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	IEP	O50-C49-O48-C22
2	A	501	IEP	C33-O36-P37-O40
2	B	501	IEP	C30-C29-O28-P25
2	B	501	IEP	C31-C32-O41-P42
2	B	501	IEP	C51-C49-O48-C22
2	B	501	IEP	C23-O24-P25-O26
2	B	501	IEP	C23-O24-P25-O27
2	B	501	IEP	C23-O24-P25-O28
2	B	501	IEP	C29-O28-P25-O27
2	A	501	IEP	O19-C18-O20-C21
2	A	501	IEP	C17-C18-O20-C21
2	A	501	IEP	C08-C09-C10-C11
2	B	501	IEP	O19-C18-O20-C21
2	A	501	IEP	C51-C49-O48-C22
2	B	501	IEP	C17-C18-O20-C21
2	A	501	IEP	C56-C57-C58-C59

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Mol	Chain	Res	Type	Atoms
2	B	501	IEP	C56-C57-C58-C59
2	B	501	IEP	C03-C04-C05-C06
2	B	501	IEP	C14-C15-C16-C17
2	A	501	IEP	C07-C08-C09-C10
2	B	501	IEP	C12-C13-C14-C15
2	B	501	IEP	C13-C14-C15-C16
2	B	501	IEP	C02-C03-C04-C05
2	B	501	IEP	C04-C05-C06-C07
2	A	501	IEP	C53-C54-C55-C56
2	B	501	IEP	C59-C60-C61-C62
2	A	501	IEP	C05-C06-C07-C08
2	A	501	IEP	C11-C12-C13-C14
2	B	501	IEP	C10-C11-C12-C13
2	A	501	IEP	C09-C10-C11-C12
2	B	501	IEP	C62-C63-C64-C1
2	A	501	IEP	C12-C13-C14-C15
2	B	501	IEP	C29-O28-P25-O24
2	A	501	IEP	C64-C1-C2-C3
2	A	501	IEP	C23-C22-O48-C49
2	B	501	IEP	O48-C22-C23-O24
2	B	501	IEP	C01-C02-C03-C04
2	A	501	IEP	C49-C51-C52-C53
2	A	501	IEP	C03-C04-C05-C06
2	A	501	IEP	O20-C21-C22-C23
2	B	501	IEP	C29-O28-P25-O26
2	A	501	IEP	C14-C15-C16-C17
2	B	501	IEP	C11-C12-C13-C14
2	A	501	IEP	C29-O28-P25-O24
2	B	501	IEP	O20-C21-C22-C23
2	A	501	IEP	C34-C33-O36-P37
2	A	501	IEP	C04-C05-C06-C07
2	A	501	IEP	C21-C22-C23-O24
2	B	501	IEP	C21-C22-C23-O24
2	A	501	IEP	C02-C03-C04-C05
2	B	501	IEP	C52-C53-C54-C55
2	A	501	IEP	C2-C3-C4-C5
2	B	501	IEP	C23-C22-O48-C49
2	B	501	IEP	C32-C33-O36-P37
2	B	501	IEP	C34-C33-O36-P37
2	A	501	IEP	C55-C56-C57-C58
2	A	501	IEP	C57-C58-C59-C60
2	A	501	IEP	C60-C61-C62-C63

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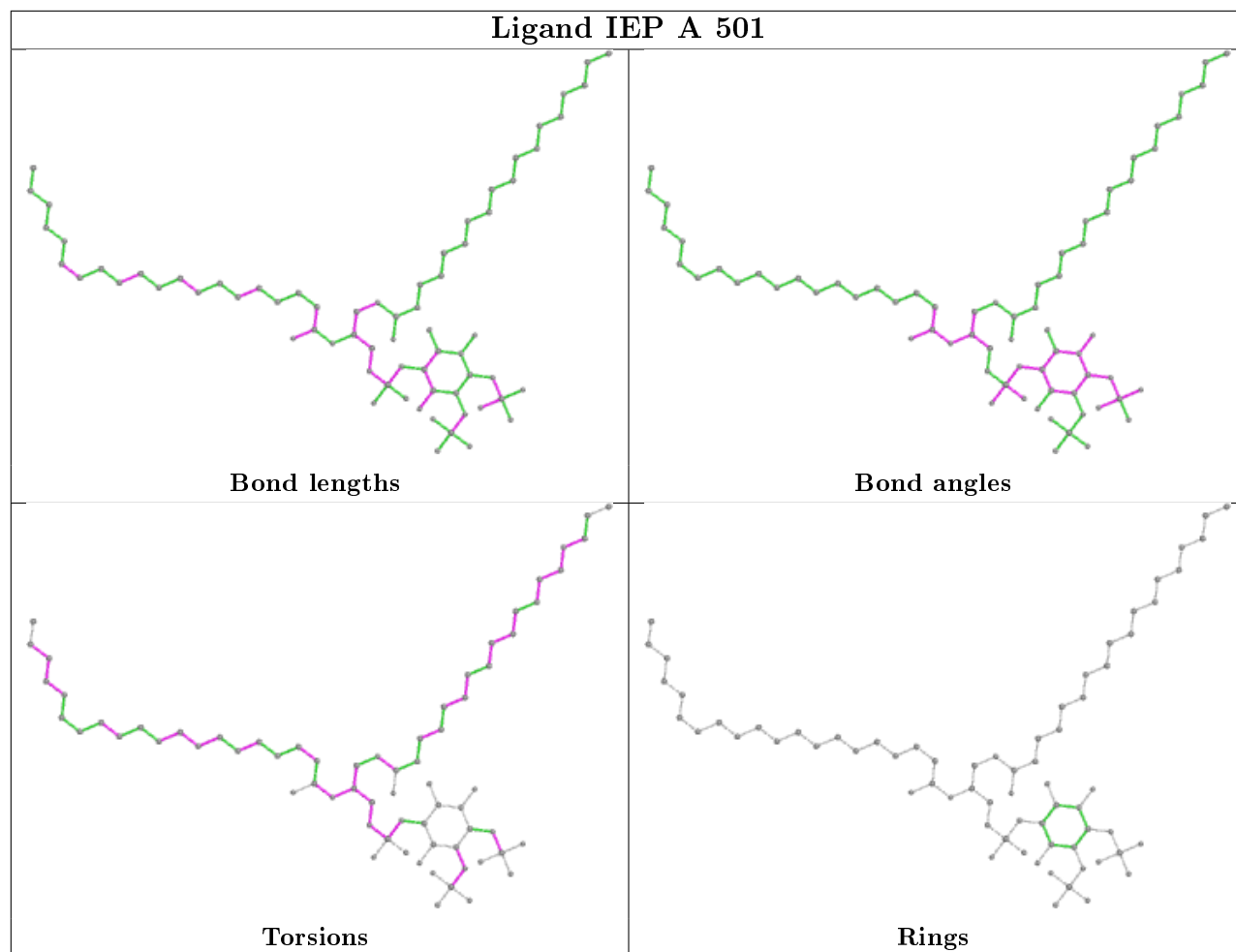
Mol	Chain	Res	Type	Atoms
2	B	501	IEP	C55-C56-C57-C58
2	B	501	IEP	C60-C61-C62-C63
2	B	501	IEP	C08-C09-C10-C11
2	B	501	IEP	C53-C54-C55-C56
2	B	501	IEP	C09-C10-C11-C12
2	B	501	IEP	O48-C49-C51-C52
2	A	501	IEP	C1-C2-C3-C4
2	A	501	IEP	C22-C23-O24-P25
2	A	501	IEP	C32-O41-P42-O45
2	B	501	IEP	C32-O41-P42-O45
2	A	501	IEP	C21-C22-O48-C49
2	A	501	IEP	C33-O36-P37-O38
2	B	501	IEP	C34-C29-O28-P25
2	B	501	IEP	C32-O41-P42-O44
2	A	501	IEP	C23-O24-P25-O26

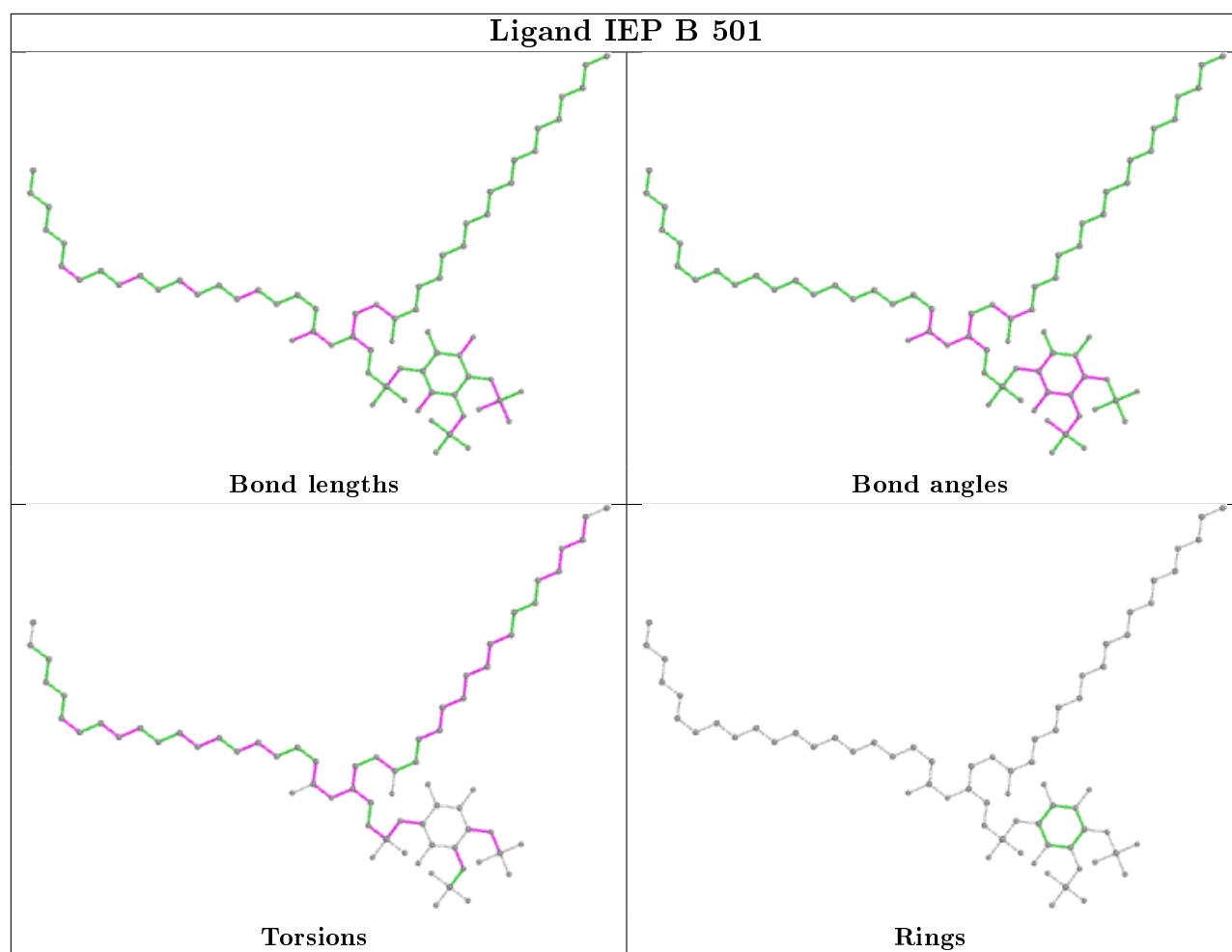
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	IEP	2	0
2	B	501	IEP	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	386/455 (84%)	0.20	25 (6%) 18 17	26, 44, 74, 99	0
1	B	413/455 (90%)	-0.06	15 (3%) 42 42	10, 24, 63, 87	0
All	All	799/910 (87%)	0.07	40 (5%) 28 27	10, 36, 68, 99	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	276	PHE	5.4
1	A	275	LEU	5.2
1	A	71	ARG	4.3
1	B	92	THR	3.8
1	A	276	PHE	3.8
1	A	441	GLU	3.5
1	A	439	LYS	3.3
1	A	353	THR	3.3
1	A	450	TYR	3.2
1	A	314	TYR	3.2
1	A	73	ASP	3.2
1	A	312	VAL	2.8
1	B	441	GLU	2.8
1	A	355	GLN	2.7
1	A	354	VAL	2.7
1	B	439	LYS	2.7
1	B	275	LEU	2.7
1	B	90	LYS	2.7
1	A	395	LYS	2.6
1	B	440	GLU	2.6
1	A	278	LYS	2.6
1	B	329	LYS	2.6
1	B	391	THR	2.5
1	B	442	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	72	SER	2.4
1	B	69	PHE	2.4
1	B	71	ARG	2.4
1	B	349	VAL	2.3
1	A	466	GLY	2.3
1	A	396	THR	2.3
1	A	316	SER	2.2
1	A	470	GLU	2.2
1	A	69	PHE	2.2
1	A	453	ASN	2.1
1	B	86	LEU	2.1
1	A	390	GLU	2.1
1	A	438	ALA	2.1
1	A	315	GLU	2.0
1	A	443	GLU	2.0
1	B	343	VAL	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](#)

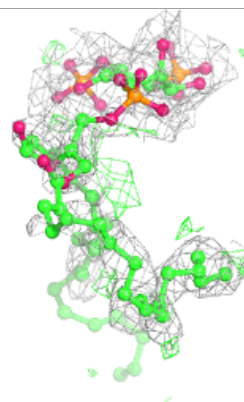
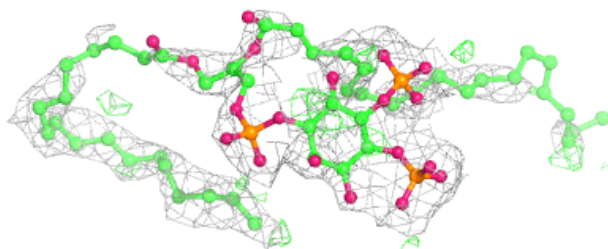
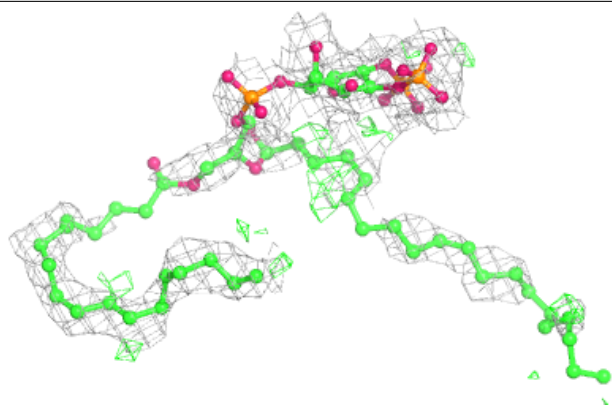
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
2	IEP	B	501	69/69	0.81	0.28	22,66,100,110	0
2	IEP	A	501	69/69	0.88	0.25	37,66,84,88	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.

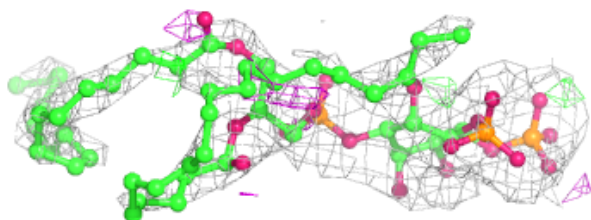
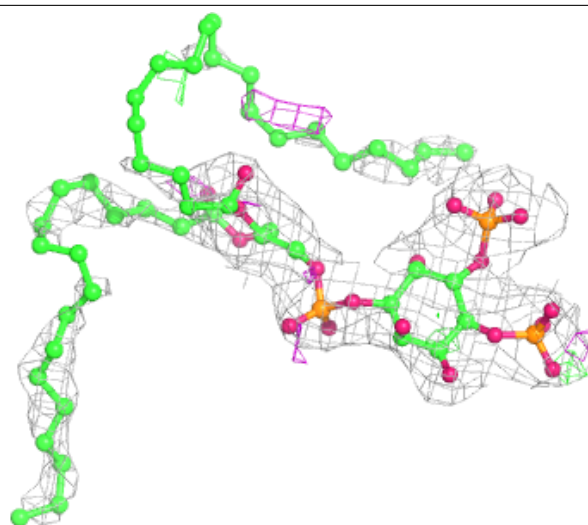
**Electron density around IEP B 501:**

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



**Electron density around IEP 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.