



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 20, 2023 – 12:06 AM EDT

PDB ID : 5IXC  
Title : Human GIVD cytosolic phospholipase A2 in complex with Methyl gamma-Linolenyl Fluorophosphate  
Authors : Wang, H.; Klein, M.G.  
Deposited on : 2016-03-23  
Resolution : 2.65 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)  
Xtrriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

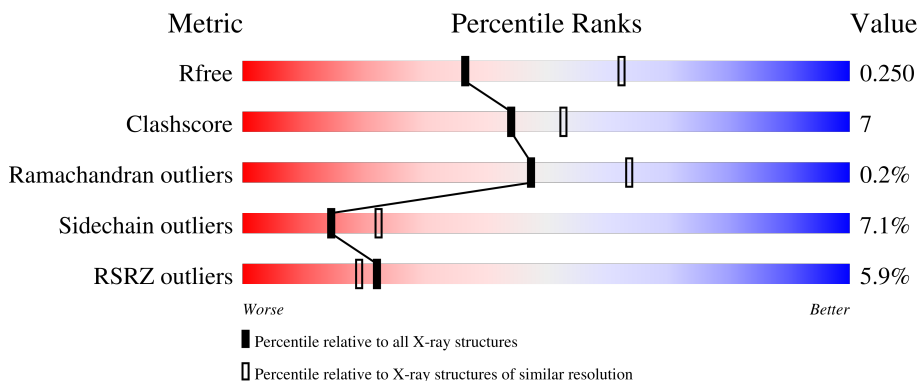
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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	814	 6% (poor fit), 70% (0 outliers), 12% (1 outlier), 16% (2+ outliers)
1	B	814	 4% (poor fit), 69% (0 outliers), 13% (1 outlier), 16% (2+ outliers)

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10961 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.

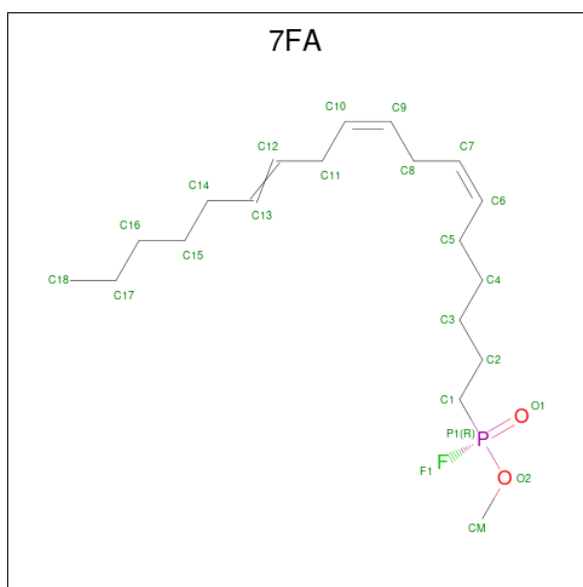
- Molecule 1 is a protein called Cytosolic phospholipase A2 delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	684	Total	C	N	O	S	0	0	0
			5436	3470	925	1016	25			
1	B	680	Total	C	N	O	S	0	0	0
			5404	3447	920	1012	25			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q86XP0
A	-2	ALA	-	expression tag	UNP Q86XP0
A	-1	MET	-	expression tag	UNP Q86XP0
A	0	GLY	-	expression tag	UNP Q86XP0
A	1	SER	-	expression tag	UNP Q86XP0
B	-3	GLY	-	expression tag	UNP Q86XP0
B	-2	ALA	-	expression tag	UNP Q86XP0
B	-1	MET	-	expression tag	UNP Q86XP0
B	0	GLY	-	expression tag	UNP Q86XP0
B	1	SER	-	expression tag	UNP Q86XP0

- Molecule 2 is methyl (R)-(6Z,9Z,12Z)-octadeca-6,9,12-trien-1-ylphosphonofluoridate (three-letter code: 7FA) (formula: C<sub>19</sub>H<sub>34</sub>FO<sub>2</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
2	A	1	Total	C	O	P	0	0
			22	19	2	1		
2	B	1	Total	C	O	P	0	0
			22	19	2	1		

- Molecule 3 is BARIUM ION (three-letter code: BA) (formula: Ba).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Ba	0	0
			3	3		
3	B	3	Total	Ba	0	0
			3	3		

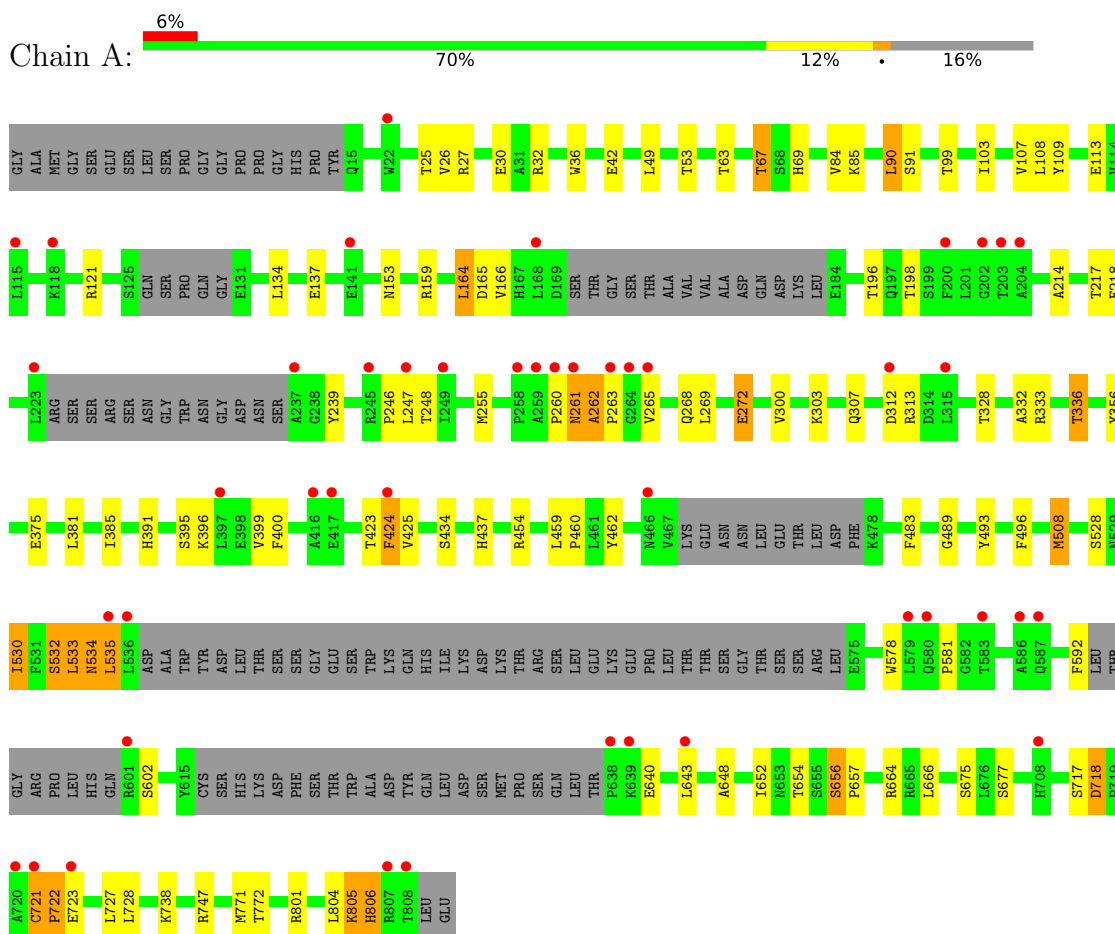
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	22	Total	O	0	0
			22	22		
4	B	49	Total	O	0	0
			49	49		

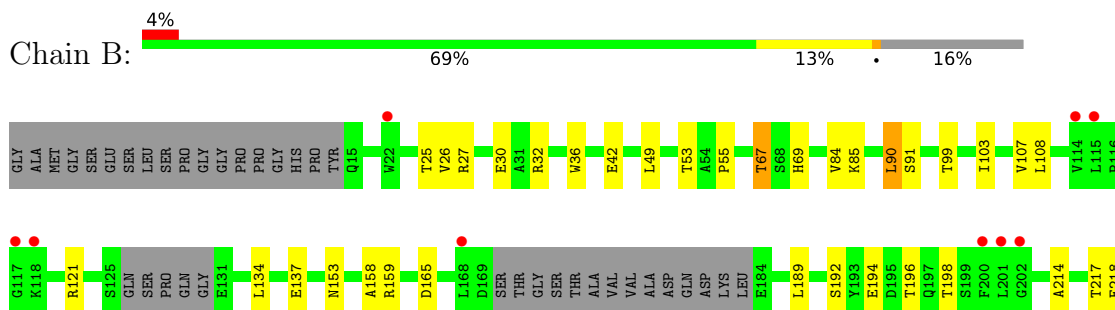
### 3 Residue-property plots

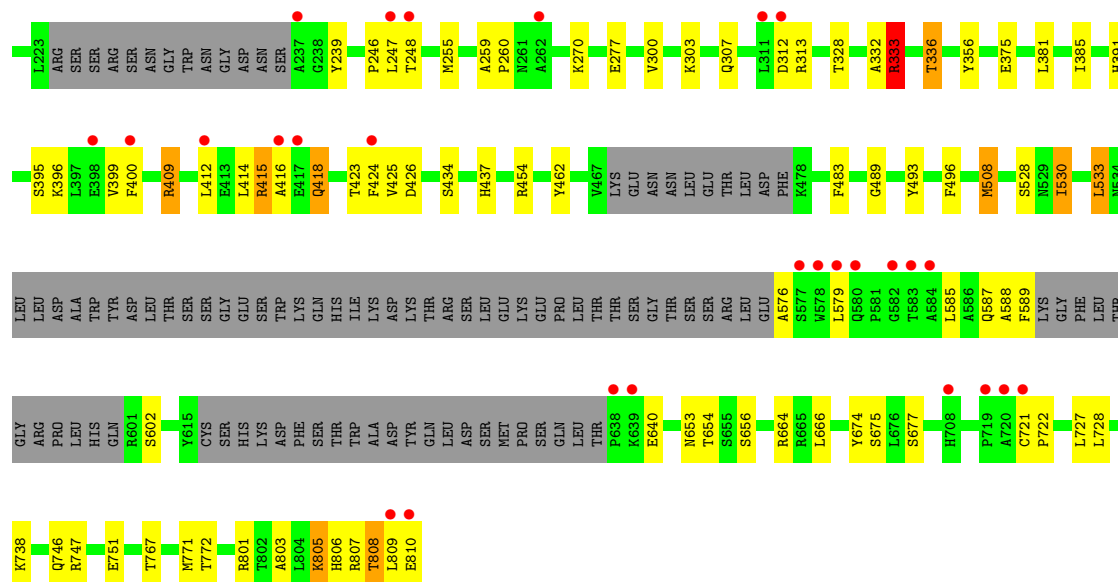
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Cytosolic phospholipase A2 delta



- Molecule 1: Cytosolic phospholipase A2 delta





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.57Å 111.38Å 157.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.97 – 2.65 48.72 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.9 (90.97-2.65) 99.9 (48.72-2.65)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.21 (at 2.65Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.237 , 0.251 0.238 , 0.250	Depositor DCC
$R_{free}$ test set	2647 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.7	Xtrriage
Anisotropy	0.390	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 36.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10961	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.74 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0959e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: BA, 7FA

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	0.43	0/5558	0.66	2/7534 (0.0%)
1	B	0.45	1/5525 (0.0%)	0.66	2/7491 (0.0%)
All	All	0.44	1/11083 (0.0%)	0.66	4/15025 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	810	GLU	CD-OE1	5.61	1.31	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	333	ARG	NE-CZ-NH1	5.33	122.97	120.30
1	B	508	MET	CG-SD-CE	-5.19	91.90	100.20
1	A	508	MET	CG-SD-CE	-5.13	91.99	100.20
1	B	333	ARG	NE-CZ-NH1	5.06	122.83	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	5436	0	5379	65	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5404	0	5343	78	1
2	A	22	0	34	1	0
2	B	22	0	34	8	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	22	0	0	0	0
4	B	49	0	0	5	0
All	All	10961	0	10790	143	1

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 (143) 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:375:GLU:OE2	1:B:454:ARG:NH2	1.75	1.20
1:B:375:GLU:CD	1:B:454:ARG:NH2	2.10	1.03
1:B:375:GLU:CD	1:B:454:ARG:HH22	1.63	1.01
1:A:109:TYR:OH	1:A:113:GLU:OE2	1.78	1.01
1:B:159:ARG:N	1:B:508:MET:HE1	1.83	0.94
1:B:533:LEU:HD12	1:B:533:LEU:H	1.31	0.93
1:A:532:SER:OG	1:A:643:LEU:O	1.89	0.91
1:B:576:ALA:CB	1:B:579:LEU:HD12	2.01	0.91
1:A:159:ARG:N	1:A:508:MET:HE1	1.86	0.90
1:B:375:GLU:OE1	1:B:454:ARG:NH2	2.08	0.84
1:B:805:LYS:O	1:B:808:THR:OG1	1.96	0.84
1:B:767:THR:HG22	4:B:1014:HOH:O	1.77	0.83
1:A:532:SER:OG	1:A:643:LEU:C	2.18	0.81
1:A:534:ASN:O	1:A:534:ASN:ND2	2.10	0.81
1:B:159:ARG:CZ	4:B:1004:HOH:O	2.30	0.80
1:A:675:SER:OG	1:A:677:SER:O	1.98	0.80
1:A:805:LYS:HD2	1:A:805:LYS:H	1.47	0.79
1:B:675:SER:OG	1:B:677:SER:O	2.00	0.78
1:A:718:ASP:HB3	1:A:721:CYS:HB2	1.66	0.77
1:A:303:LYS:O	1:A:307:GLN:OE1	2.06	0.73
1:B:303:LYS:O	1:B:307:GLN:OE1	2.06	0.73
1:B:533:LEU:H	1:B:533:LEU:CD1	2.01	0.72
1:B:576:ALA:HB1	1:B:579:LEU:HD12	1.70	0.72
1:B:530:ILE:HD13	2:B:901:7FA:H3	1.72	0.71
1:A:262:ALA:HB1	1:A:263:PRO:CD	2.22	0.70
1:B:332:ALA:O	1:B:336:THR:HG23	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:648:ALA:O	1:A:652:ILE:HG12	1.95	0.67
1:A:262:ALA:HB1	1:A:263:PRO:HD2	1.77	0.67
1:A:375:GLU:OE2	1:A:454:ARG:NH2	2.28	0.66
1:B:415:ARG:NH1	1:B:426:ASP:OD2	2.28	0.66
1:A:332:ALA:O	1:A:336:THR:HG23	1.95	0.66
1:B:400:PHE:HE1	1:B:585:LEU:HD11	1.60	0.66
1:B:530:ILE:CD1	2:B:901:7FA:H2A	2.28	0.64
1:B:576:ALA:HB2	1:B:579:LEU:HD12	1.80	0.63
1:B:530:ILE:HD11	2:B:901:7FA:H2A	1.80	0.63
1:A:381:LEU:O	1:A:385:ILE:HG12	2.00	0.62
1:B:381:LEU:O	1:B:385:ILE:HG12	2.00	0.62
1:B:530:ILE:HD13	2:B:901:7FA:C3	2.31	0.61
1:B:640:GLU:O	1:B:640:GLU:HG2	2.01	0.60
1:A:640:GLU:O	1:A:640:GLU:HG2	2.02	0.60
1:A:424:PHE:CD1	1:A:535:LEU:HG	2.38	0.59
1:A:307:GLN:OE1	1:A:307:GLN:N	2.36	0.58
1:B:307:GLN:OE1	1:B:307:GLN:N	2.36	0.58
1:B:530:ILE:CD1	2:B:901:7FA:C2	2.82	0.57
1:B:530:ILE:CD1	2:B:901:7FA:H3	2.36	0.55
1:B:259:ALA:HB1	1:B:260:PRO:HD2	1.88	0.55
1:A:36:TRP:CZ2	1:A:42:GLU:HG3	2.43	0.53
1:A:328:THR:HG22	1:A:654:THR:HB	1.90	0.53
1:B:576:ALA:CB	1:B:579:LEU:CD1	2.82	0.52
1:B:721:CYS:N	1:B:722:PRO:HD3	2.24	0.52
1:B:36:TRP:CZ2	1:B:42:GLU:HG3	2.44	0.52
1:B:328:THR:HG22	1:B:654:THR:HB	1.91	0.52
1:A:217:THR:OG1	1:A:218:GLU:N	2.43	0.51
1:A:262:ALA:CB	1:A:263:PRO:HD2	2.40	0.51
1:B:489:GLY:HA3	1:B:496:PHE:CD1	2.45	0.51
1:A:489:GLY:HA3	1:A:496:PHE:CD1	2.46	0.51
1:A:721:CYS:SG	1:A:722:PRO:HD3	2.51	0.51
1:B:399:VAL:HG13	1:B:400:PHE:CD2	2.46	0.51
1:A:399:VAL:HG13	1:A:400:PHE:CD2	2.46	0.51
1:A:262:ALA:CB	1:A:263:PRO:CD	2.89	0.50
1:A:806:HIS:CD2	1:A:806:HIS:C	2.84	0.50
1:A:533:LEU:O	1:A:533:LEU:HD23	2.11	0.50
1:B:414:LEU:O	1:B:418:GLN:HB2	2.11	0.49
1:B:576:ALA:HB1	1:B:579:LEU:CD1	2.41	0.49
1:B:462:TYR:HB2	1:B:483:PHE:HB2	1.95	0.48
1:A:36:TRP:CE2	1:A:42:GLU:HG3	2.48	0.48
1:B:217:THR:OG1	1:B:218:GLU:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:391:HIS:O	1:B:396:LYS:NZ	2.46	0.48
1:B:747:ARG:NH1	1:B:751:GLU:O	2.39	0.48
1:B:55:PRO:HD2	4:B:1006:HOH:O	2.14	0.47
1:B:653:ASN:ND2	4:B:1002:HOH:O	2.39	0.47
1:A:356:TYR:CZ	1:A:664:ARG:HD3	2.49	0.47
1:B:576:ALA:HB2	1:B:579:LEU:CD1	2.45	0.47
1:A:462:TYR:HB2	1:A:483:PHE:HB2	1.96	0.47
1:A:391:HIS:O	1:A:396:LYS:NZ	2.47	0.47
1:B:159:ARG:H	1:B:508:MET:HE1	1.69	0.47
1:B:192:SER:OG	1:B:194:GLU:O	2.22	0.46
1:B:530:ILE:HD12	2:B:901:7FA:H1	1.98	0.46
1:A:90:LEU:HD12	1:A:107:VAL:HG12	1.97	0.46
1:B:803:ALA:HA	1:B:806:HIS:HB3	1.98	0.46
1:A:261:ASN:HD22	1:A:261:ASN:N	2.14	0.46
1:B:90:LEU:HD12	1:B:107:VAL:HG12	1.97	0.46
1:B:738:LYS:O	1:B:747:ARG:HD2	2.16	0.46
1:B:36:TRP:CE2	1:B:42:GLU:HG3	2.50	0.46
1:B:259:ALA:HB1	1:B:260:PRO:CD	2.46	0.45
1:B:801:ARG:O	1:B:805:LYS:HD2	2.16	0.45
1:A:424:PHE:HD1	1:A:535:LEU:HG	1.81	0.45
1:B:356:TYR:CZ	1:B:664:ARG:HD3	2.52	0.45
1:A:434:SER:O	1:A:437:HIS:O	2.34	0.44
1:B:530:ILE:CD1	2:B:901:7FA:C3	2.94	0.44
1:B:434:SER:O	1:B:437:HIS:O	2.35	0.44
1:A:53:THR:HG21	1:A:84:VAL:CG1	2.47	0.44
1:B:67:THR:HG22	1:B:69:HIS:H	1.83	0.44
1:A:423:THR:OG1	1:A:425:VAL:HG12	2.18	0.44
1:A:578:TRP:HA	1:A:581:PRO:HD2	2.00	0.43
1:A:67:THR:HG22	1:A:69:HIS:H	1.83	0.43
1:A:396:LYS:HE2	1:A:772:THR:HG22	2.00	0.43
1:A:738:LYS:O	1:A:747:ARG:HD2	2.18	0.43
1:B:158:ALA:C	1:B:508:MET:HE1	2.37	0.43
1:A:164:LEU:HD13	1:A:166:VAL:HG23	2.00	0.43
1:A:214:ALA:HA	1:A:247:LEU:CD2	2.48	0.43
1:B:53:THR:HG21	1:B:84:VAL:CG1	2.48	0.43
1:B:396:LYS:HE2	1:B:772:THR:HG22	2.00	0.43
1:B:423:THR:OG1	1:B:425:VAL:HG12	2.19	0.43
1:B:159:ARG:NH1	4:B:1004:HOH:O	2.48	0.43
1:B:214:ALA:HA	1:B:247:LEU:CD2	2.48	0.43
1:A:261:ASN:HD22	1:A:261:ASN:H	1.66	0.43
1:B:412:LEU:O	1:B:416:ALA:N	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:ARG:HG2	1:A:69:HIS:CD2	2.54	0.43
1:A:535:LEU:CD2	1:A:535:LEU:N	2.81	0.42
1:A:722:PRO:HB2	1:A:723:GLU:OE1	2.19	0.42
1:A:91:SER:HB2	1:A:103:ILE:HD11	2.01	0.42
1:B:32:ARG:HG2	1:B:69:HIS:CD2	2.54	0.42
1:B:91:SER:HB2	1:B:103:ILE:HD11	2.01	0.42
1:B:333:ARG:NH1	1:B:674:TYR:O	2.40	0.42
1:A:268:GLN:C	1:A:269:LEU:HD12	2.39	0.42
1:A:805:LYS:HD2	1:A:805:LYS:N	2.24	0.42
1:A:90:LEU:HD13	1:A:134:LEU:CD2	2.50	0.42
1:A:49:LEU:HD23	1:A:90:LEU:HB3	2.01	0.42
1:A:806:HIS:O	1:A:806:HIS:HD2	2.02	0.41
1:B:49:LEU:HD23	1:B:90:LEU:HB3	2.01	0.41
1:B:90:LEU:HD13	1:B:134:LEU:CD2	2.50	0.41
1:B:153:ASN:ND2	1:B:493:TYR:O	2.53	0.41
1:A:424:PHE:HE1	1:A:535:LEU:CD1	2.33	0.41
1:B:409:ARG:CZ	1:B:589:PHE:HD1	2.33	0.41
1:B:396:LYS:HG2	1:B:772:THR:HG22	2.03	0.41
1:A:159:ARG:H	1:A:508:MET:HE1	1.73	0.41
1:B:121:ARG:NH2	1:B:137:GLU:OE2	2.54	0.41
1:B:409:ARG:CZ	1:B:589:PHE:CD1	3.04	0.41
1:A:459:LEU:HD12	1:A:460:PRO:HD2	2.02	0.41
1:A:656:SER:N	1:A:657:PRO:CD	2.84	0.41
1:B:396:LYS:HG2	1:B:772:THR:CG2	2.50	0.41
1:A:121:ARG:NH2	1:A:137:GLU:OE2	2.54	0.40
1:A:396:LYS:HG2	1:A:772:THR:HG22	2.04	0.40
1:A:246:PRO:O	1:A:248:THR:HG23	2.21	0.40
1:A:801:ARG:O	1:A:805:LYS:HD2	2.21	0.40
1:B:189:LEU:O	1:B:192:SER:OG	2.39	0.40
1:A:153:ASN:ND2	1:A:493:TYR:O	2.55	0.40
1:A:396:LYS:HG2	1:A:772:THR:CG2	2.50	0.40
1:A:530:ILE:HG13	2:A:901:7FA:H3	2.02	0.40
1:B:246:PRO:O	1:B:248:THR:HG23	2.22	0.40
1:B:585:LEU:HA	1:B:585:LEU:HD23	1.81	0.40
1:B:588:ALA:O	1:B:589:PHE:C	2.59	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:GLU:OE2	1:B:270:LYS:NZ[3_547]	2.14	0.06

## 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	668/814 (82%)	638 (96%)	27 (4%)	3 (0%)	34	48
1	B	664/814 (82%)	636 (96%)	28 (4%)	0	100	100
All	All	1332/1628 (82%)	1274 (96%)	55 (4%)	3 (0%)	47	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	722	PRO
1	A	260	PRO
1	A	262	ALA

### 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	592/705 (84%)	548 (93%)	44 (7%)	13	21
1	B	589/705 (84%)	549 (93%)	40 (7%)	16	24
All	All	1181/1410 (84%)	1097 (93%)	84 (7%)	14	22

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	THR
1	A	26	VAL
1	A	27	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	30	GLU
1	A	63	THR
1	A	67	THR
1	A	85	LYS
1	A	90	LEU
1	A	99	THR
1	A	108	LEU
1	A	164	LEU
1	A	165	ASP
1	A	196	THR
1	A	198	THR
1	A	239	TYR
1	A	255	MET
1	A	261	ASN
1	A	265	VAL
1	A	272	GLU
1	A	300	VAL
1	A	312	ASP
1	A	313	ARG
1	A	336	THR
1	A	395	SER
1	A	424	PHE
1	A	528	SER
1	A	530	ILE
1	A	532	SER
1	A	533	LEU
1	A	534	ASN
1	A	535	LEU
1	A	592	PHE
1	A	602	SER
1	A	656	SER
1	A	666	LEU
1	A	717	SER
1	A	718	ASP
1	A	721	CYS
1	A	727	LEU
1	A	728	LEU
1	A	771	MET
1	A	804	LEU
1	A	805	LYS
1	A	806	HIS
1	B	25	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	26	VAL
1	B	27	ARG
1	B	30	GLU
1	B	67	THR
1	B	85	LYS
1	B	90	LEU
1	B	99	THR
1	B	108	LEU
1	B	165	ASP
1	B	196	THR
1	B	198	THR
1	B	239	TYR
1	B	255	MET
1	B	277	GLU
1	B	300	VAL
1	B	312	ASP
1	B	313	ARG
1	B	333	ARG
1	B	336	THR
1	B	395	SER
1	B	409	ARG
1	B	415	ARG
1	B	418	GLN
1	B	424	PHE
1	B	528	SER
1	B	530	ILE
1	B	533	LEU
1	B	587	GLN
1	B	602	SER
1	B	656	SER
1	B	666	LEU
1	B	727	LEU
1	B	728	LEU
1	B	746	GLN
1	B	771	MET
1	B	805	LYS
1	B	807	ARG
1	B	808	THR
1	B	809	LEU

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

Mol	Chain	Res	Type
1	A	261	ASN
1	A	798	GLN
1	A	806	HIS
1	B	746	GLN
1	B	798	GLN
1	B	806	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

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	7FA	B	901	1	18,21,22	0.36	0	16,21,24	1.04	1 (6%)
2	7FA	A	901	1	18,21,22	0.30	0	16,21,24	1.05	1 (6%)

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	7FA	B	901	1	-	2/16/20/22	-
2	7FA	A	901	1	-	2/16/20/22	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	7FA	C3-C2-C1	-3.11	106.14	113.85
2	B	901	7FA	C3-C2-C1	-2.99	106.44	113.85

There are no chirality outliers.

All (4) torsion outliers are listed below:

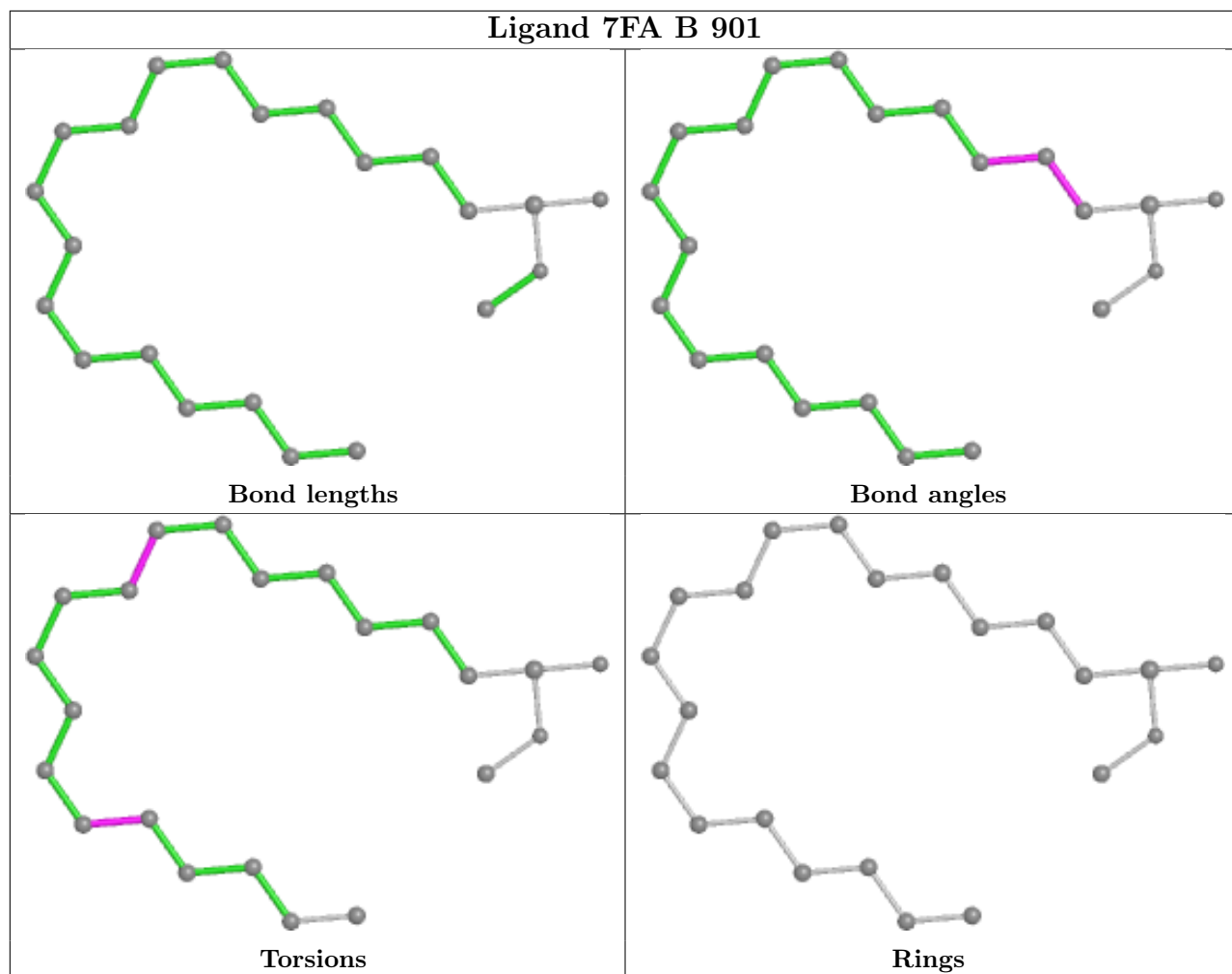
Mol	Chain	Res	Type	Atoms
2	A	901	7FA	C6-C7-C8-C9
2	B	901	7FA	C6-C7-C8-C9
2	A	901	7FA	C12-C13-C14-C15
2	B	901	7FA	C12-C13-C14-C15

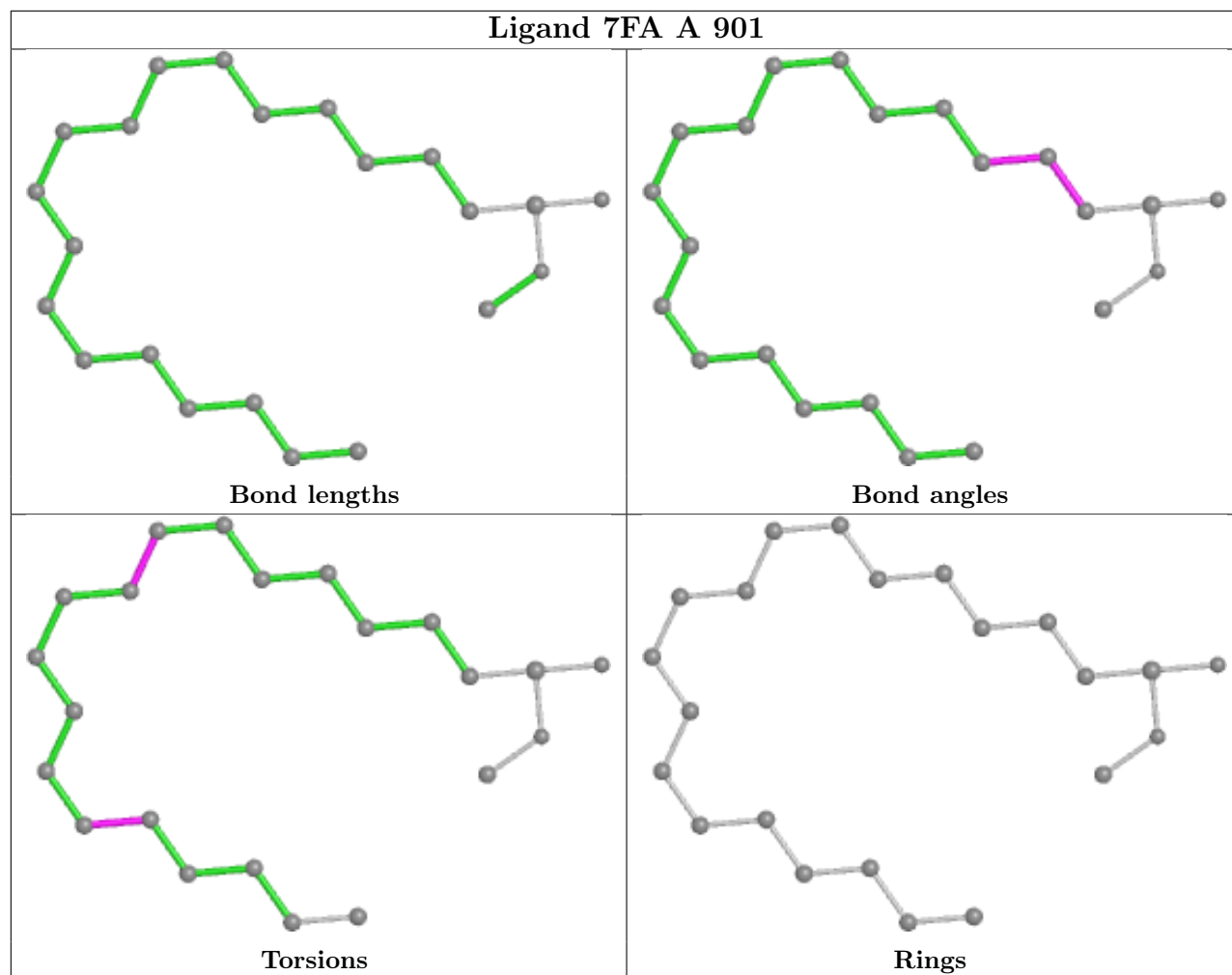
There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	7FA	8	0
2	A	901	7FA	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	684/814 (84%)	0.28	45 (6%) 18 15	39, 61, 113, 159	0
1	B	680/814 (83%)	0.21	36 (5%) 26 23	35, 57, 109, 161	0
All	All	1364/1628 (83%)	0.25	81 (5%) 22 19	35, 60, 109, 161	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	638	PRO	11.8
1	A	639	LYS	8.6
1	B	638	PRO	7.9
1	B	639	LYS	5.4
1	A	416	ALA	5.3
1	A	417	GLU	5.3
1	A	587	GLN	5.2
1	A	579	LEU	5.1
1	A	601	ARG	5.0
1	B	584	ALA	4.7
1	B	262	ALA	4.3
1	A	721	CYS	4.3
1	B	580	GLN	4.3
1	B	424	PHE	4.3
1	B	577	SER	4.3
1	A	203	THR	4.2
1	A	259	ALA	4.1
1	B	400	PHE	4.1
1	A	260	PRO	4.1
1	A	583	THR	4.0
1	B	579	LEU	3.9
1	B	417	GLU	3.8
1	A	808	THR	3.8
1	B	398	GLU	3.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	643	LEU	3.7
1	B	201	LEU	3.6
1	B	810	GLU	3.5
1	B	416	ALA	3.5
1	A	263	PRO	3.5
1	A	535	LEU	3.5
1	A	807	ARG	3.5
1	B	583	THR	3.3
1	A	118	LYS	3.2
1	B	118	LYS	3.2
1	A	312	ASP	3.1
1	B	200	PHE	3.1
1	B	117	GLY	3.0
1	A	200	PHE	3.0
1	B	809	LEU	3.0
1	A	202	GLY	3.0
1	B	720	ALA	2.9
1	A	168	LEU	2.8
1	A	22	TRP	2.8
1	A	261	ASN	2.8
1	B	578	TRP	2.7
1	A	247	LEU	2.7
1	B	719	PRO	2.7
1	A	397	LEU	2.7
1	B	115	LEU	2.7
1	B	311	LEU	2.7
1	B	22	TRP	2.7
1	A	586	ALA	2.6
1	B	168	LEU	2.6
1	A	580	GLN	2.6
1	A	245	ARG	2.5
1	B	721	CYS	2.5
1	A	223	LEU	2.5
1	B	248	THR	2.4
1	B	412	LEU	2.4
1	A	424	PHE	2.4
1	A	258	PRO	2.4
1	A	536	LEU	2.4
1	A	720	ALA	2.4
1	B	247	LEU	2.4
1	A	237	ALA	2.3
1	B	237	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	115	LEU	2.3
1	A	204	ALA	2.3
1	A	315	LEU	2.3
1	B	582	GLY	2.3
1	A	264	GLY	2.3
1	B	708	HIS	2.3
1	A	466	ASN	2.3
1	B	114	VAL	2.3
1	A	249	ILE	2.2
1	B	312	ASP	2.2
1	A	265	VAL	2.1
1	B	202	GLY	2.1
1	A	708	HIS	2.0
1	A	141	GLU	2.0
1	A	723	GLU	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](#)

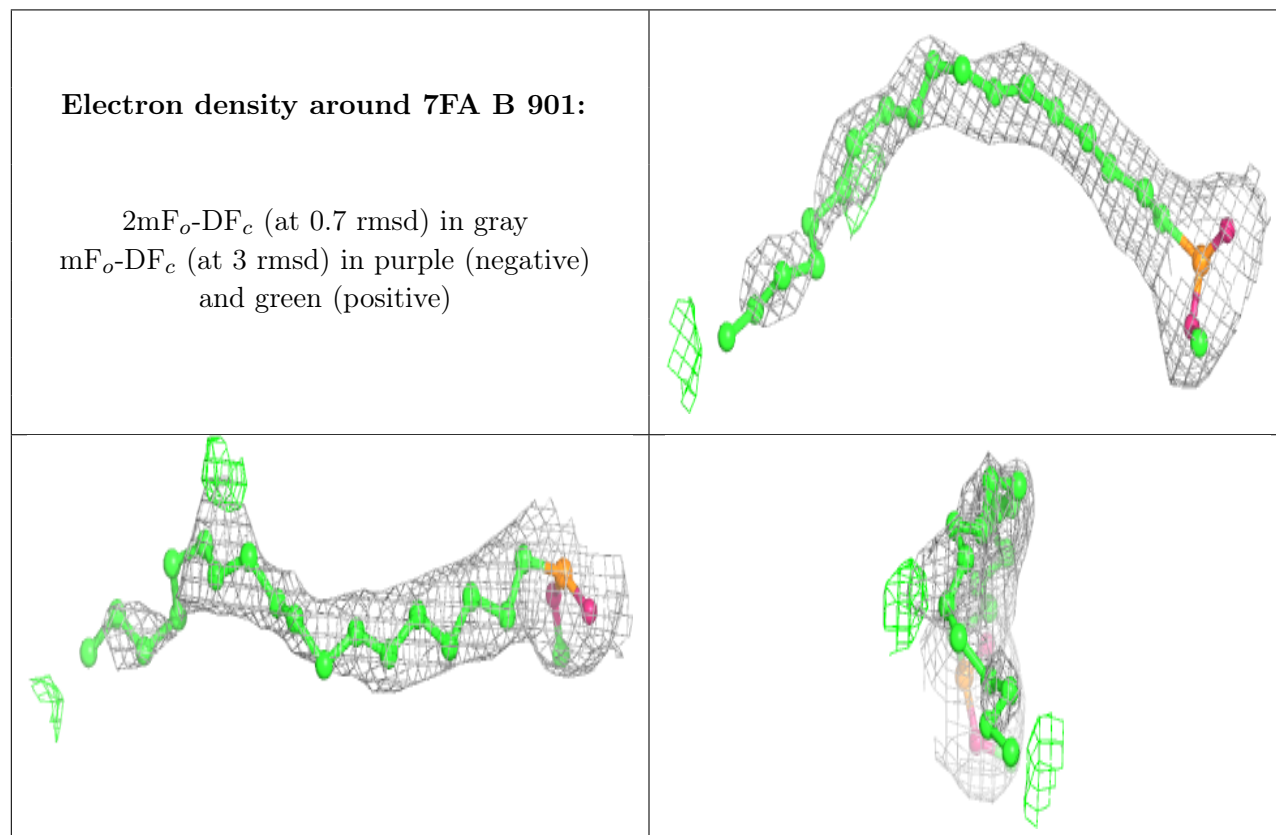
There are no monosaccharides in this entry.

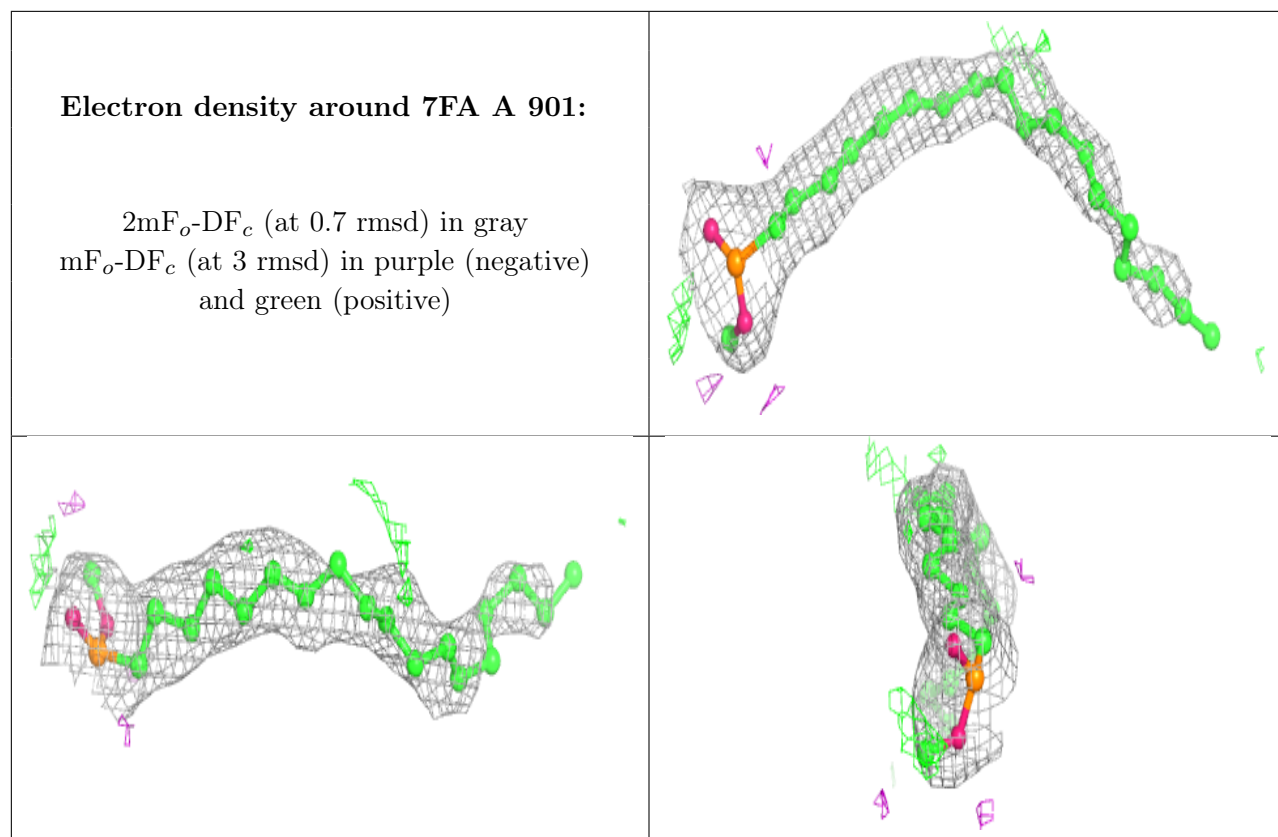
## 6.4 Ligands [i](#)

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(Å <sup>2</sup> )	Q<0.9
3	BA	B	904	1/1	0.92	0.07	152,152,152,152	0
3	BA	A	904	1/1	0.93	0.10	158,158,158,158	0
3	BA	B	902	1/1	0.93	0.04	103,103,103,103	1
2	7FA	B	901	22/23	0.93	0.32	42,75,98,103	0
2	7FA	A	901	22/23	0.94	0.29	43,71,98,106	0
3	BA	A	902	1/1	0.97	0.06	125,125,125,125	1
3	BA	B	903	1/1	0.99	0.07	85,85,85,85	0
3	BA	A	903	1/1	0.99	0.09	80,80,80,80	0

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.