



wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 03:26 am BST

PDB ID : 5GUG
Title : Crystal structure of inositol 1,4,5-trisphosphate receptor large cytosolic domain with inositol 1,4,5-trisphosphate
Authors : Hamada, K.; Miyatake, H.; Terauchi, A.; Mikoshiba, K.
Deposited on : 2016-08-29
Resolution : 7.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at 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 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

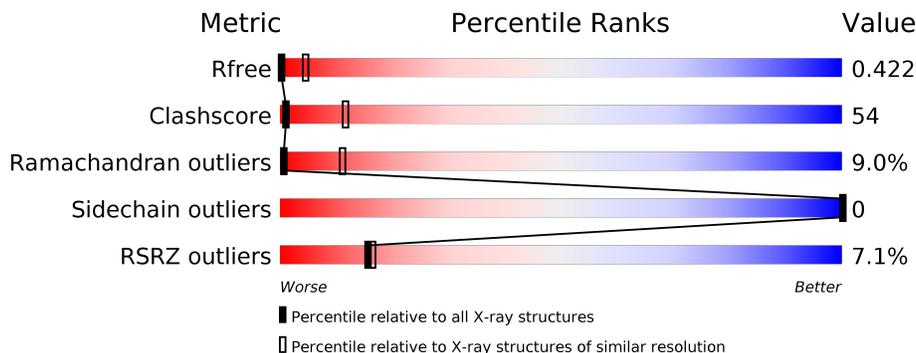
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 7.40 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	1004 (10.00-3.90)
Clashscore	141614	1069 (10.00-3.90)
Ramachandran outliers	138981	1002 (10.00-3.90)
Sidechain outliers	138945	1002 (10.00-3.86)
RSRZ outliers	127900	1004 (9.50-3.80)

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 ≥ 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	2217	 6% 43% 30% 22%
1	B	2217	 5% 43% 30% 5% 22%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	I3P	B	3000	-	-	-	X

2 Entry composition [i](#)

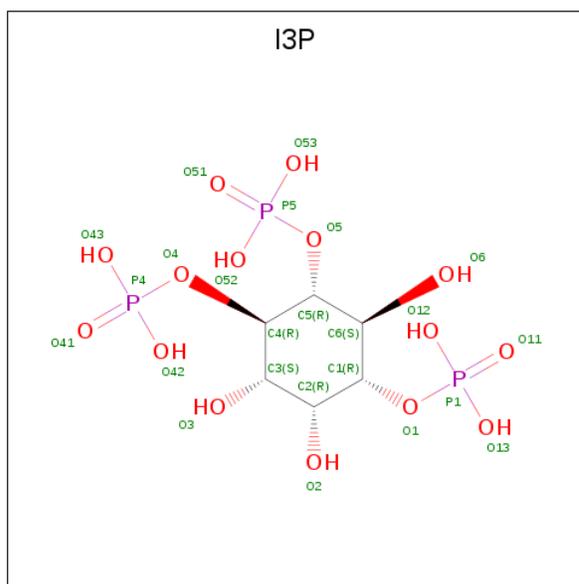
There are 2 unique types of molecules in this entry. The entry contains 25117 atoms, of which 7810 are hydrogens and 0 are deuteriums.

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 Inositol 1,4,5-trisphosphate receptor type 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	1721	Total 12529	C 5147	H 3897	N 1746	O 1738	S 1	0	0	0
1	B	1720	Total 12522	C 5144	H 3895	N 1745	O 1737	S 1	0	0	0

- Molecule 2 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (three-letter code: I3P) (formula: $C_6H_{15}O_{15}P_3$).

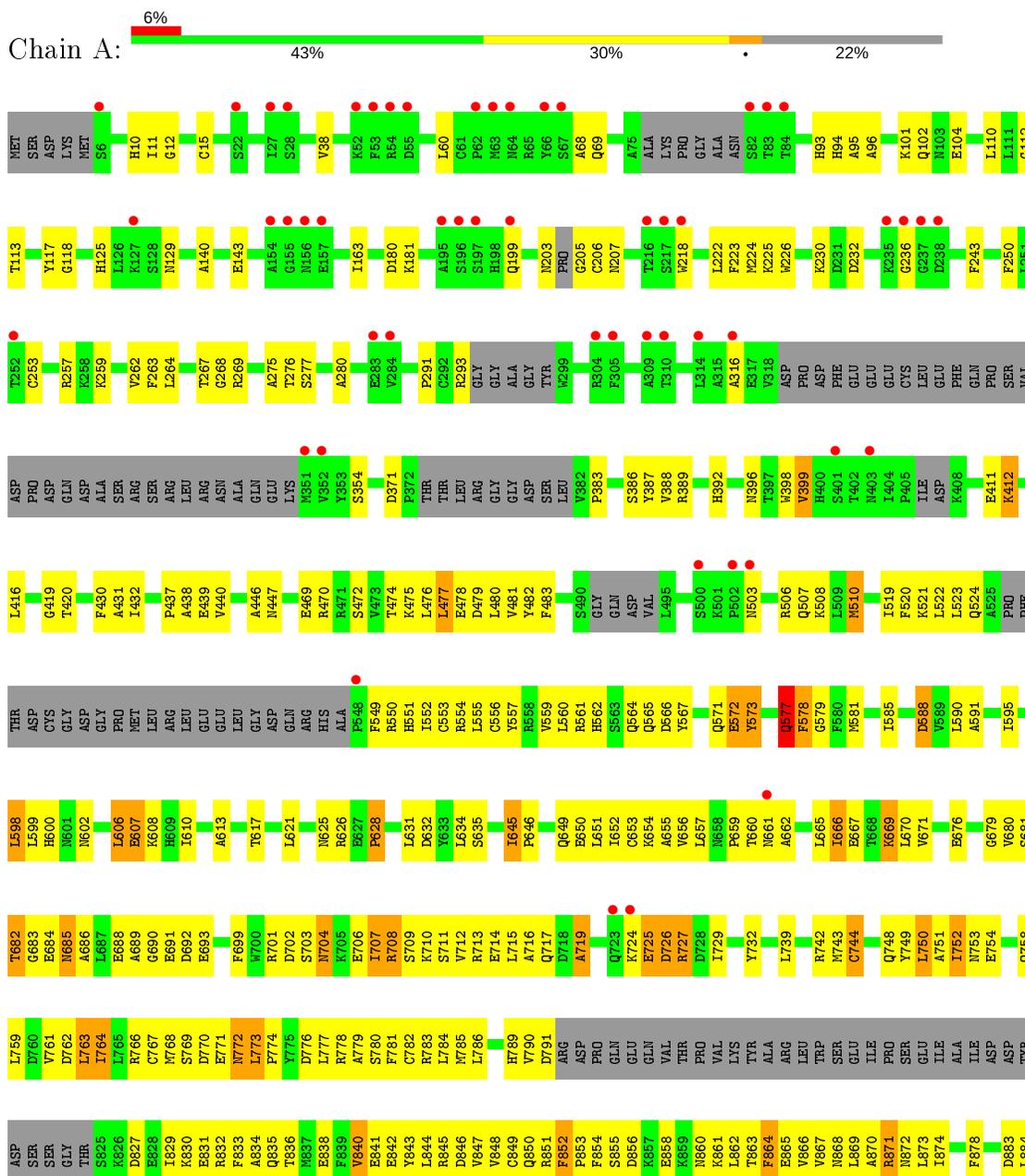


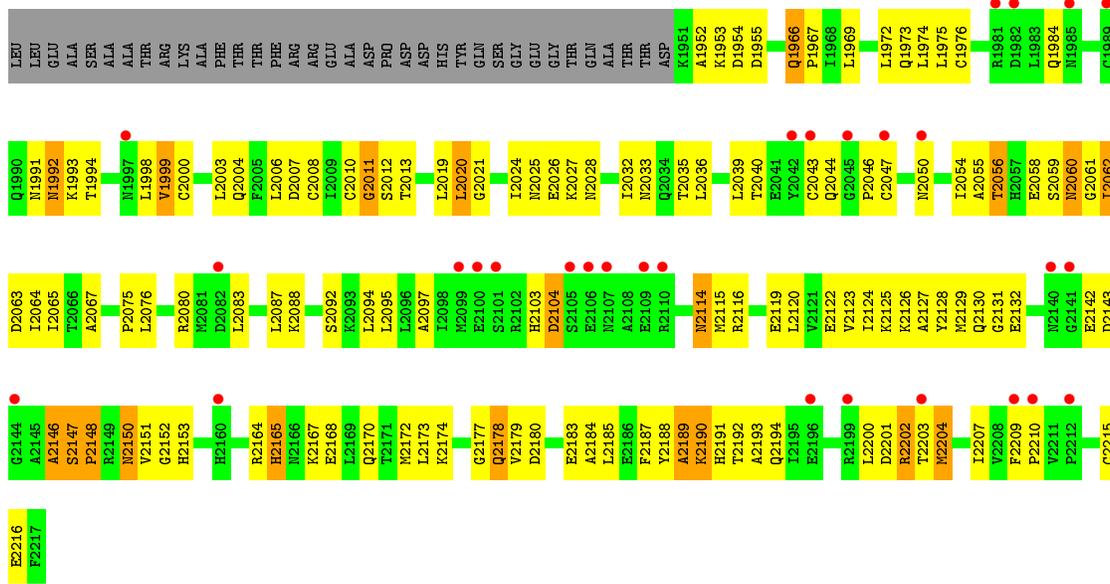
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	O	P		
2	A	1	Total 33	C 6	H 9	O 15	P 3	0	0
2	B	1	Total 33	C 6	H 9	O 15	P 3	0	0

3 Residue-property plots

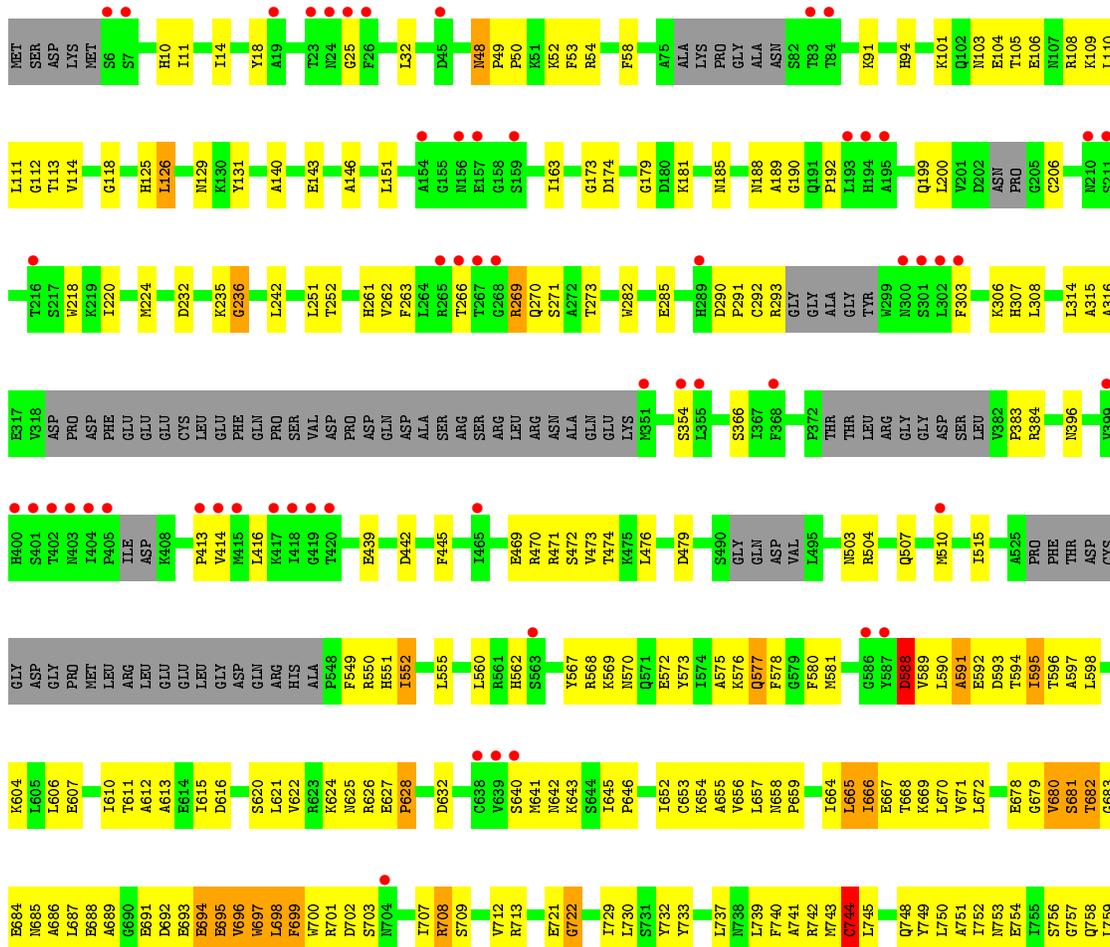
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Inositol 1,4,5-trisphosphate receptor type 1





• Molecule 1: Inositol 1,4,5-trisphosphate receptor type 1



PRO	G1650	GLN	E1436	C1245	ASN	V1104	SER	ALA	1890	ASP	D760
GLY	F1651	GLY	M1345	A1246	TYR	F1105	GLN	PRO	L891	SER	V761
PRO	I1652	VAL	K1437	M1247	ARG	S1106	GLU	GLU	L892	SER	D762
TRP	C1653	PHE	R1348	M1248	VAL	Q1107	GLY	GLY	A893	GLY	L763
LEU	K1654	ARG	E1439	M1251	V1117	D1108	PRO	ASN	I894	THR	I764
ARG	L1655	VAL	T1442	M1257	K1177	I1115	SER	VAL	L895	THR	L765
LEU	K1656	THR	S1443	K1257	E1178	I1116	ASN	LYS	D896	THR	R766
GLN	L1657	HIS	M1444	H1258	I1179	Q1117	VAL	GLN	C897	THR	C767
LEU	K1658	CYS	H1445	L1268	R1182	D1118	PRO	ALA	I898	THR	M768
ASP	M1660	ASN	M1446	E1269	L1183	L1119	GLU	ALA	H899	THR	S769
HIS	L1661	TRP	M1449	V1271	E1190	D1122	G1026	PRO	H900	THR	D770
ARG	M1662	MET	F1483	T1272	S1191	L1122	G1040	GLU	E961	THR	E771
ARG	E1667	PRO	F1483	T1272	A1192	V1126	G1042	PRO	K962	THR	M772
ASP	E1668	SER	D1456	H1275	E1127	E1127	G1043	PHE	I965	THR	L773
LEU	C1671	GLN	R1459	I1276	K1128	S1129	E1046	PRO	M966	THR	F774
LEU	L1677	ALA	A1460	F1277	S1129	E1130	L1051	ILE	V967	THR	Y775
GLN	L1678	SER	C1461	M1278	R1188	L1131	L1052	SER	M968	THR	D776
ILE	L1679	VAL	M1462	M1279	K1199	W1132	L1053	LYS	E841	THR	R777
LEU	R1679	GLU	H1376	M1280	R1199	W1133	D1054	THR	E842	THR	A778
VAL	E1680	SER	L1377	M1281	K1199	Y1133	H1055	THR	E844	THR	S780
ASN	M1681	CYS	E1379	F1281	Q1201	Y1134	H1055	LYS	L844	THR	F781
ARG	M1682	ILE	L1380	Q1282	Q1202	LYS	G1056	GLY	V848	THR	C782
ARG	T1683	ARG	L1381	L1283	R1203	GLY	G1057	GLU	G849	THR	R783
VAL	S1472	VAL	A1382	C1284	K1203	GLN	R1058	ASN	Q850	THR	L784
LEU	K1476	LEU	V1383	E1285	A1210	PRO	T1059	ARG	P853	THR	M785
SER	K1476	SER	E1286	H1211	H1211	GLY	F1060	LYS	R853	THR	L786
ASP	E1480	ASP	I1287	A1212	A1212	PRO	L1061	GLY	F854	THR	H787
VAL	E1480	VAL	M1288	V1213	V1213	ASP	R1062	SER	S855	THR	M788
ALA	M1483	ALA	K1388	E1289	V1214	GLU	R1062	ASN	S855	THR	H789
LYS	S1484	LYS	M1389	R1290	L1215	PRO	V1063	VAL	D856	THR	V790
SER	I1485	SER	M1397	V1292	L1216	MET	L1064	ARG	K857	THR	D791
ALA	V1486	ALA	I1400	Q1293	L1217	ASP	T1068	ASP	E858	THR	ARG
ILE	T1487	ILE	L1400	H1294	L1218	GLY	L1072	PRO	K859	THR	PRO
ILE	F1488	ILE	D1403	F1295	Q1219	ALA	Y1072	GLN	R860	THR	GLN
LEU	F1489	LEU	D1404	E1300	I1220	SER	L1075	GLY	R861	THR	GLN
PRO	S1492	PRO	D1404	E1301	Y1222	ASN	L1080	VAL	F864	THR	VAL
ASP	P1493	ASP	I1405	T1301	E1223	GLU	Q1081	GLU	E865	THR	THR
SER	PHE	SER	V1406	R1304	K1224	HIS	L1082	LEU	V866	THR	PRO
ASP	ASP	ASP	G1414	K1304	A1225	LYS	L1083	MET	V867	THR	VAL
GLN	GLN	GLN	P1416	F1311	E1226	LYS	F1084	THR	M868	THR	VAL
VAL	THR	THR	E1417	L1312	D1227	THR	R1085	GLN	L869	THR	LYS
ASN	THR	THR	A1421	T1314	T1228	GLU	F1086	VAL	A870	THR	ALA
LEU	THR	THR	Y1422	I1315	K1229	GLU	F1087	VAL	R871	THR	ARG
THR	THR	THR	L1426	V1316	Q1231	THR	S1088	LEU	M872	THR	LEU
LYS	THR	THR	M1427	K1317	M1234	LYS	V1093	GLY	K873	THR	TRP
GLN	GLN	GLN	M1428	A1318	A1235	PRO	L1094	GLY	L874	THR	SER
PRO	PRO	PRO	C1429	G1326	L1236	LEU	Q1095	PHE	F875	THR	ILE
VAL	VAL	VAL	V1430	Q1327	L1236	LYS	A1096	LEU	S882	THR	GLU
PHE	PHE	PHE	V1431	V1330	H1238	HIS	F1097	PRO	D883	THR	GLU
THR	THR	THR	D1432	V1330	E1239	GLU	K1098	THR	L884	THR	ILE
GLN	GLN	GLN	T1433	V1341	F1240	SER	Q1099	SER	L885	THR	ILE
LEU	LEU	LEU	E1434	V1341	L1241	THR	V1100	PRO	R886	THR	ILE
LEU	LEU	LEU	V1435	V1341	Q1242	SER	Q1101	ASP	L887	THR	ASP
THR	THR	THR	V1435	V1341	M1243	SER	L1102	ALA	T888	THR	ASP
					F1244	TYR	L1103	SER	K889	THR	TYR

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	211.99Å 223.49Å 319.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.49 – 7.40 49.49 – 7.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.49-7.40) 85.7 (49.49-7.40)	Depositor EDS
R_{merge}	0.29	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 7.37Å)	Xtrriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.356 , 0.416 0.359 , 0.422	Depositor DCC
R_{free} test set	526 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	159.4	Xtrriage
Anisotropy	0.177	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 212.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.23$, $\langle L^2 \rangle = 0.08$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.62	EDS
Total number of atoms	25117	wwPDB-VP
Average B, all atoms (Å ²)	166.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: I3P

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	0.72	9/8617 (0.1%)	0.84	6/11978 (0.1%)
1	B	0.71	6/8612 (0.1%)	0.83	5/11971 (0.0%)
All	All	0.71	15/17229 (0.1%)	0.83	11/23949 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	8
1	B	0	9
All	All	0	17

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	270	GLN	CD-NE2	-9.15	1.09	1.32
1	B	270	GLN	CD-OE1	-7.90	1.06	1.24
1	A	577	GLN	C-O	7.33	1.37	1.23
1	B	1026	GLY	C-O	-6.82	1.12	1.23
1	A	579	GLY	N-CA	-6.53	1.36	1.46

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	577	GLN	C-N-CA	9.25	144.83	121.70
1	A	578	PHE	N-CA-CB	8.28	125.51	110.60
1	B	588	ASP	N-CA-C	6.75	129.24	111.00
1	B	588	ASP	N-CA-CB	-6.54	98.82	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	510	MET	CB-CG-SD	-5.91	94.68	112.40

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1034	GLU	Peptide
1	A	1375	ILE	Peptide
1	A	1380	LEU	Peptide
1	A	577	GLN	Peptide
1	A	588	ASP	Peptide

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	8632	3897	3899	667	0
1	B	8627	3895	3898	687	0
2	A	24	9	9	6	0
2	B	24	9	9	1	0
All	All	17307	7810	7815	1353	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 54.

The worst 5 of 1353 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:A:2020:LEU:O	1:A:2024:ILE:N	1.57	1.38
1:B:863:THR:O	1:B:867:VAL:N	1.72	1.21
1:A:1210:ALA:O	1:A:1214:VAL:CB	1.89	1.20
1:A:1125:ILE:O	1:A:1129:SER:CB	1.91	1.19
1:B:1682:MET:O	1:B:1686:ARG:N	1.78	1.16

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	1689/2217 (76%)	1219 (72%)	330 (20%)	140 (8%)	1	12
1	B	1688/2217 (76%)	1173 (70%)	350 (21%)	165 (10%)	0	9
All	All	3377/4434 (76%)	2392 (71%)	680 (20%)	305 (9%)	1	11

5 of 305 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	598	LEU
1	A	628	PRO
1	A	659	PRO
1	A	666	ILE
1	A	669	LYS

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	26/1980 (1%)	26 (100%)	0	100	100
1	B	26/1980 (1%)	26 (100%)	0	100	100
All	All	52/3960 (1%)	52 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	270	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
2	I3P	A	3000	-	24,24,24	1.13	1 (4%)	36,39,39	1.08	3 (8%)
2	I3P	B	3000	-	24,24,24	1.15	2 (8%)	36,39,39	1.09	4 (11%)

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	I3P	A	3000	-	-	0/15/39/39	0/1/1/1
2	I3P	B	3000	-	-	0/15/39/39	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3000	I3P	P5-O53	-2.23	1.46	1.54
2	A	3000	I3P	P4-O42	-2.15	1.46	1.54
2	B	3000	I3P	P1-O13	-2.12	1.46	1.54

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3000	I3P	O13-P1-O12	2.51	117.24	107.64
2	B	3000	I3P	O43-P4-O42	2.38	116.74	107.64
2	A	3000	I3P	O53-P5-O52	2.27	116.32	107.64
2	A	3000	I3P	O1-P1-O11	-2.26	100.67	109.39
2	B	3000	I3P	O1-C1-C2	2.12	113.60	108.66

There are no chirality outliers.

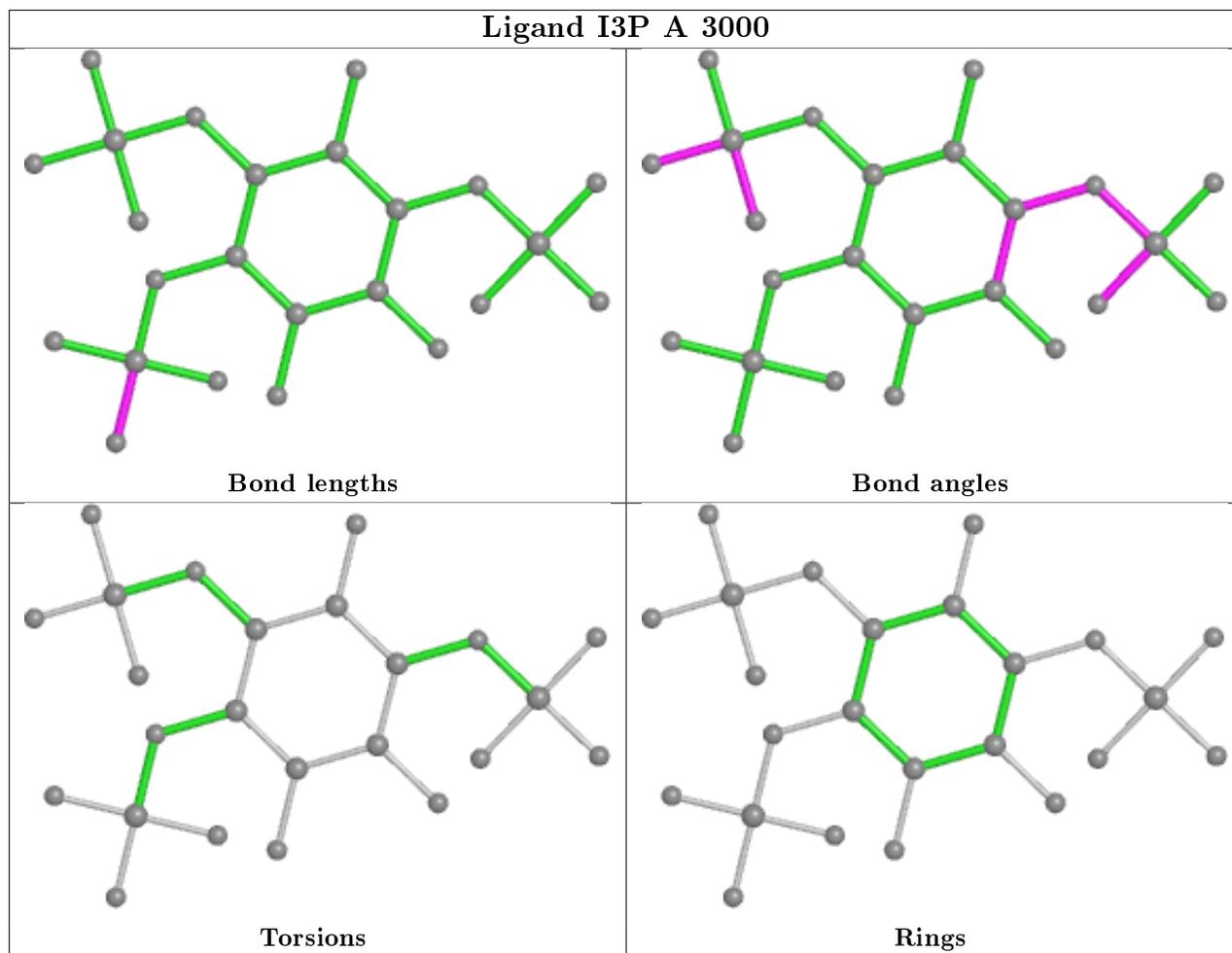
There are no torsion outliers.

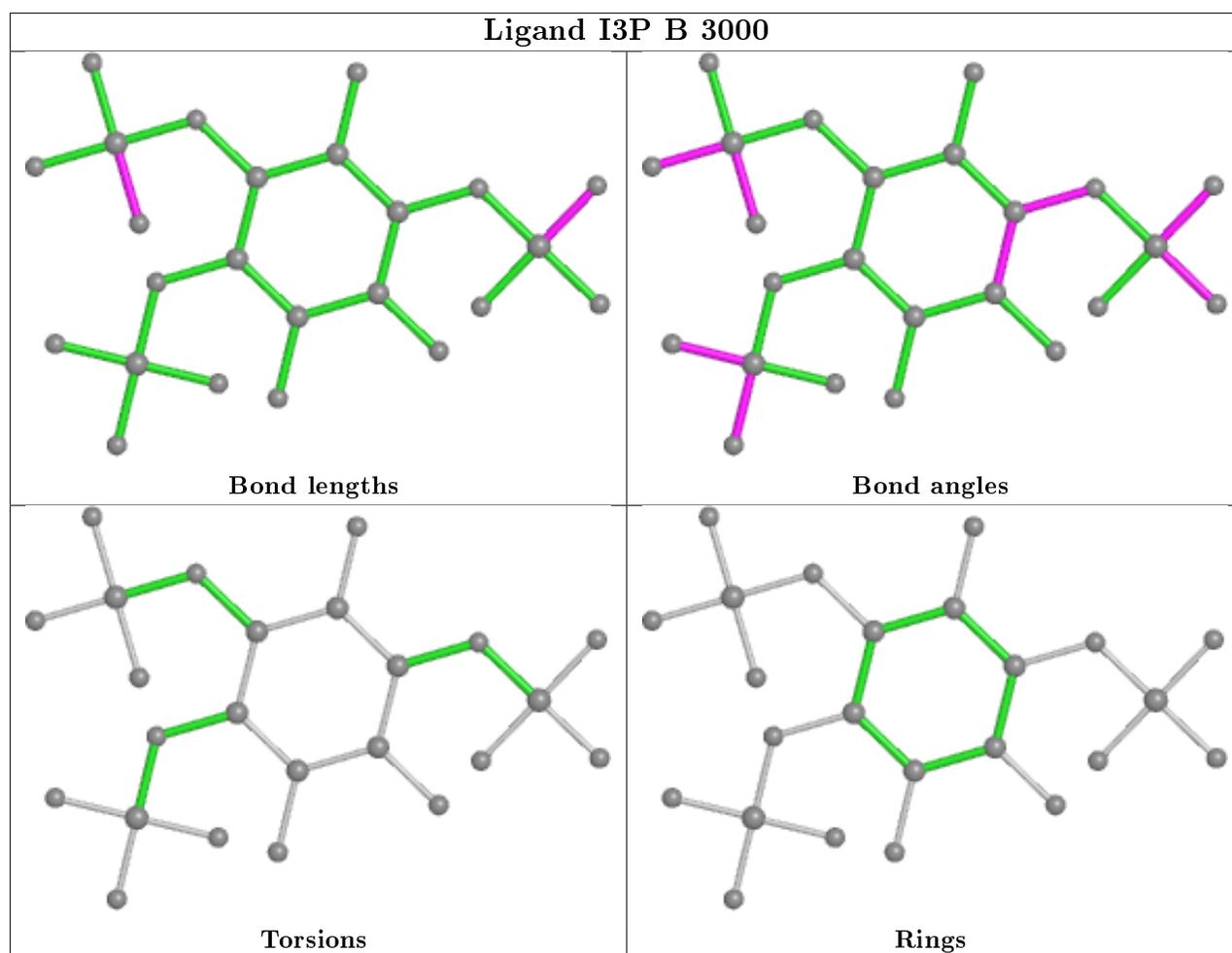
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3000	I3P	6	0
2	B	3000	I3P	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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 ²)	Q<0.9
1	A	1721/2217 (77%)	0.15	126 (7%) 15 16	135, 166, 176, 187	0
1	B	1720/2217 (77%)	0.10	117 (6%) 17 18	145, 165, 178, 192	0
All	All	3441/4434 (77%)	0.12	243 (7%) 16 16	135, 166, 177, 192	0

The worst 5 of 243 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1436	GLU	7.8
1	B	401	SER	7.8
1	A	1468	LYS	7.3
1	B	1437	MET	6.8
1	A	1368	ASN	6.3

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](#)

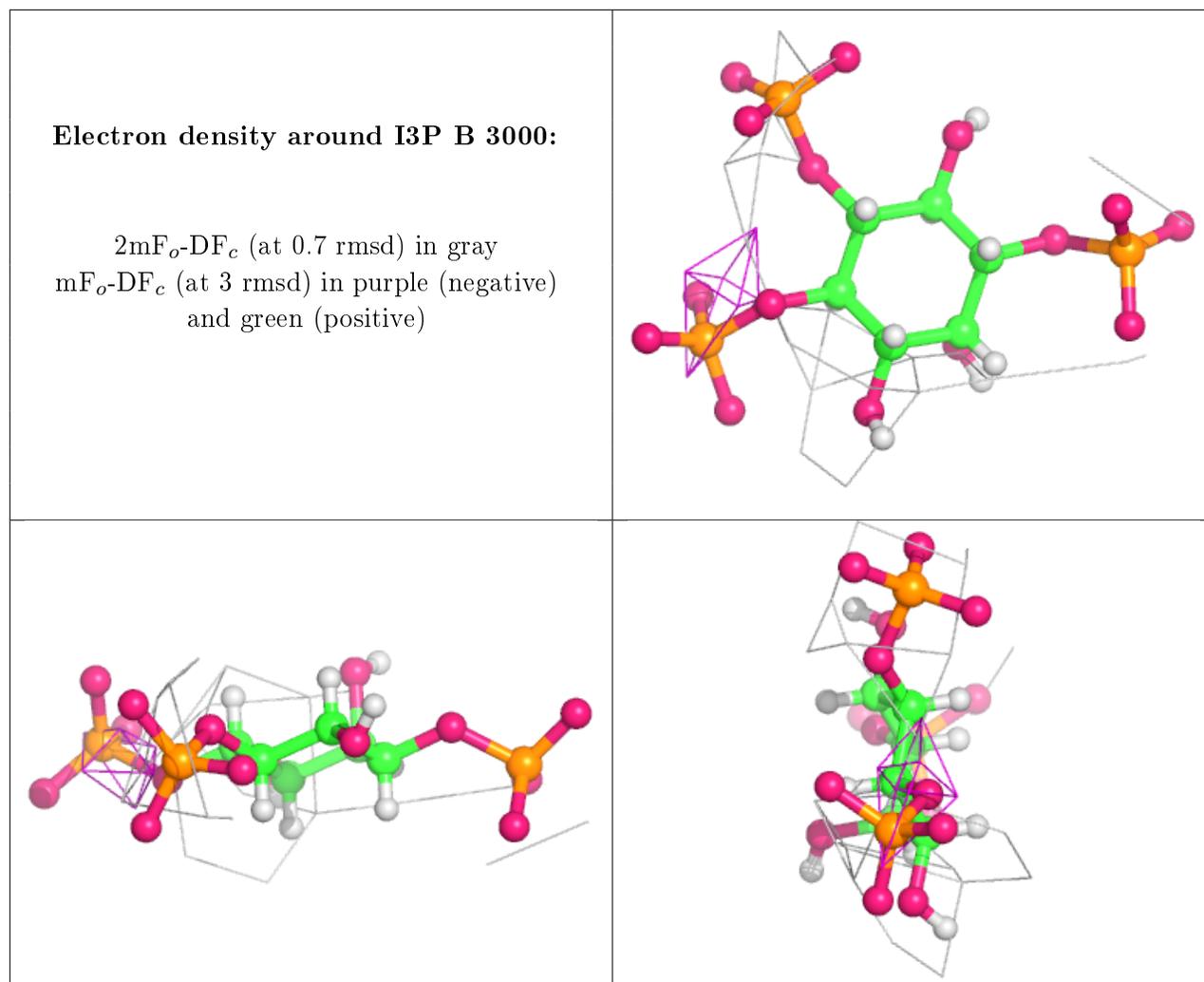
There are no carbohydrates in this entry.

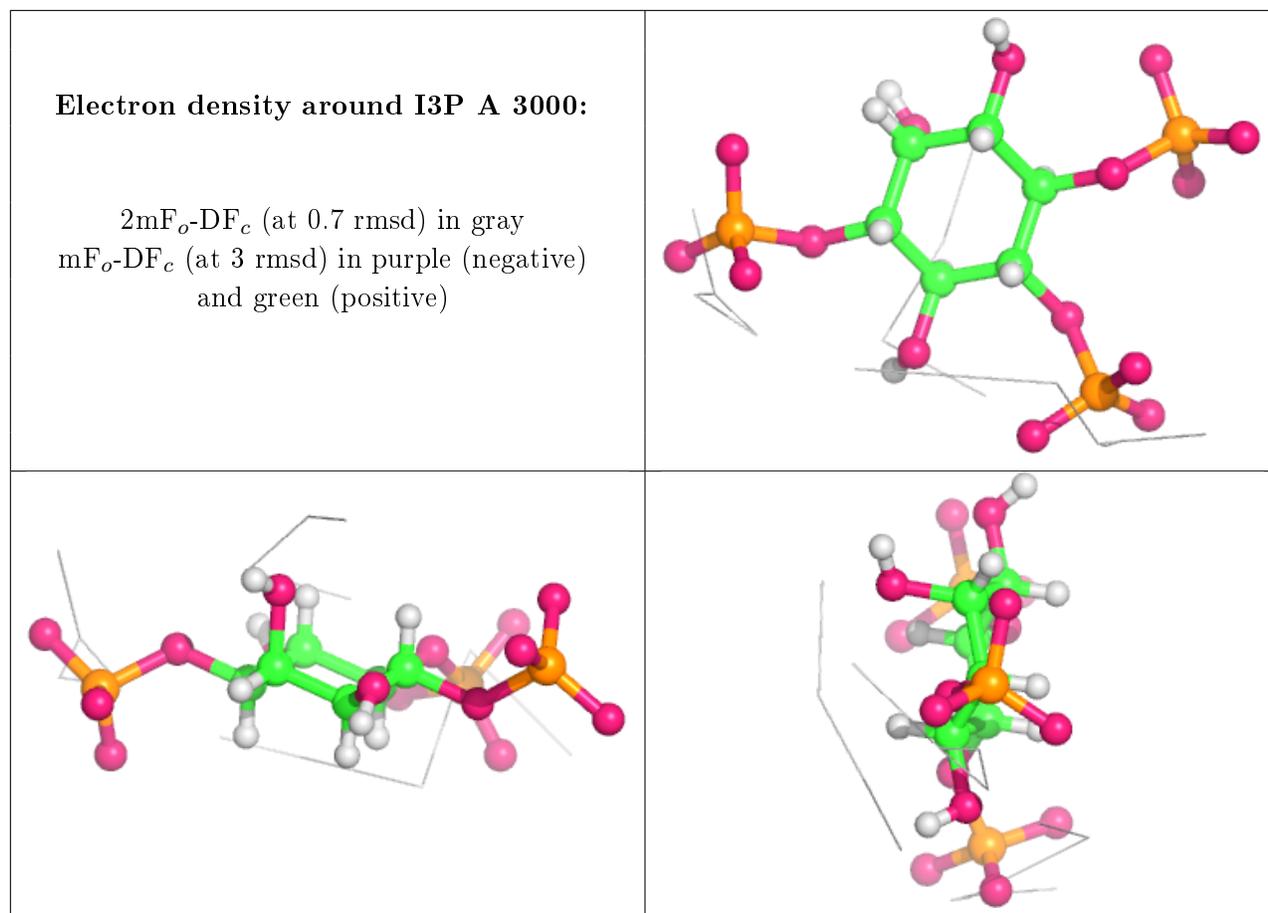
6.4 Ligands [i](#)

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, 95th 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(\AA^2)	Q<0.9
2	I3P	B	3000	24/24	0.57	0.70	199,199,203,203	0
2	I3P	A	3000	24/24	0.59	0.35	169,172,172,172	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.