



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 17, 2021 – 08:12 PM EST

PDB ID : 7RSV
Title : Structure of the VPS34 kinase domain with compound 5
Authors : Hu, D.X.; Patel, S.; Chen, H.; Wang, S.; Staben, S.; Dimitrova, Y.N.; Wallweber, H.A.; Lee, J.Y.; Chan, G.K.Y.; Sneeringer, C.J.; Prangley, M.S.; Moffat, J.G.; Wu, C.; Schutt, L.K.; Salphati, L.; Pang, J.; McNamara, E.; Huang, H.; Chen, Y.; Wang, Y.; Zhao, W.; Lim, J.; Murthy, A.; Siu, M.
Deposited on : 2021-08-11
Resolution : 1.78 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

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 : 2.23.2
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) : 2.23.2

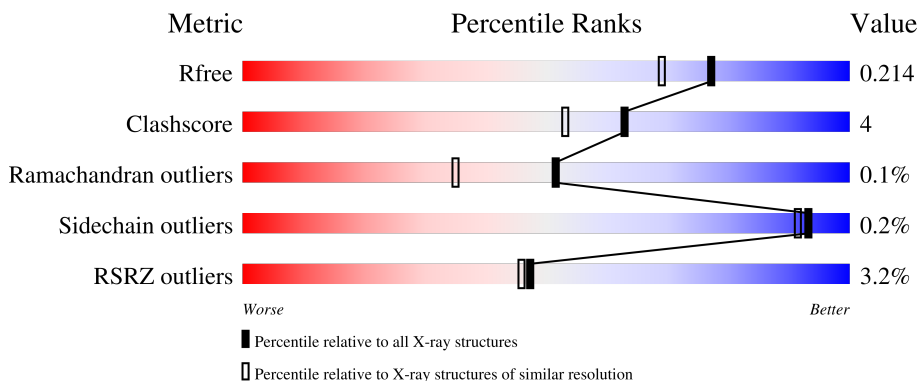
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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 ≥ 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	612	 3% 81% 6% 14%
1	B	612	 3% 78% 9% 13%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 9565 atoms, of which 8 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 Phosphatidylinositol 3-kinase catalytic subunit type 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	529	4277	2733	722	798	24	0	5	0
1	B	534	4373	2785	740	822	26	0	13	0

There are 28 discrepancies between the modelled and reference sequences:

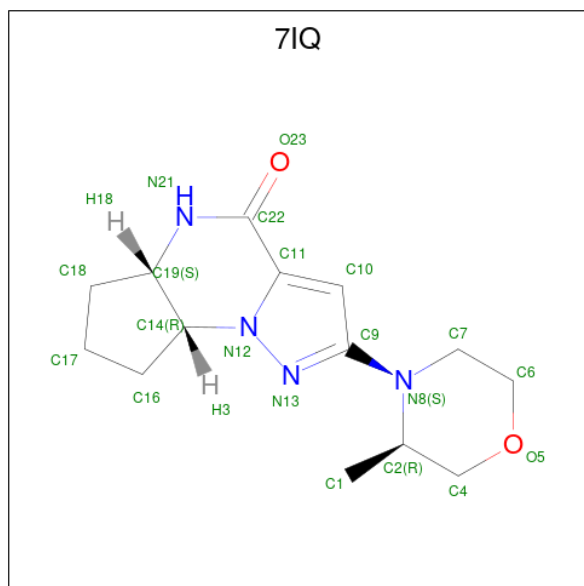
Chain	Residue	Modelled	Actual	Comment	Reference
A	268	HIS	-	expression tag	UNP Q8NEB9
A	269	HIS	-	expression tag	UNP Q8NEB9
A	270	HIS	-	expression tag	UNP Q8NEB9
A	271	HIS	-	expression tag	UNP Q8NEB9
A	272	HIS	-	expression tag	UNP Q8NEB9
A	273	HIS	-	expression tag	UNP Q8NEB9
A	274	GLY	-	expression tag	UNP Q8NEB9
A	275	GLU	-	expression tag	UNP Q8NEB9
A	276	ASN	-	expression tag	UNP Q8NEB9
A	277	LEU	-	expression tag	UNP Q8NEB9
A	278	TYR	-	expression tag	UNP Q8NEB9
A	279	PHE	-	expression tag	UNP Q8NEB9
A	280	GLN	-	expression tag	UNP Q8NEB9
A	281	GLY	-	expression tag	UNP Q8NEB9
B	268	HIS	-	expression tag	UNP Q8NEB9
B	269	HIS	-	expression tag	UNP Q8NEB9
B	270	HIS	-	expression tag	UNP Q8NEB9
B	271	HIS	-	expression tag	UNP Q8NEB9
B	272	HIS	-	expression tag	UNP Q8NEB9
B	273	HIS	-	expression tag	UNP Q8NEB9
B	274	GLY	-	expression tag	UNP Q8NEB9
B	275	GLU	-	expression tag	UNP Q8NEB9
B	276	ASN	-	expression tag	UNP Q8NEB9
B	277	LEU	-	expression tag	UNP Q8NEB9
B	278	TYR	-	expression tag	UNP Q8NEB9

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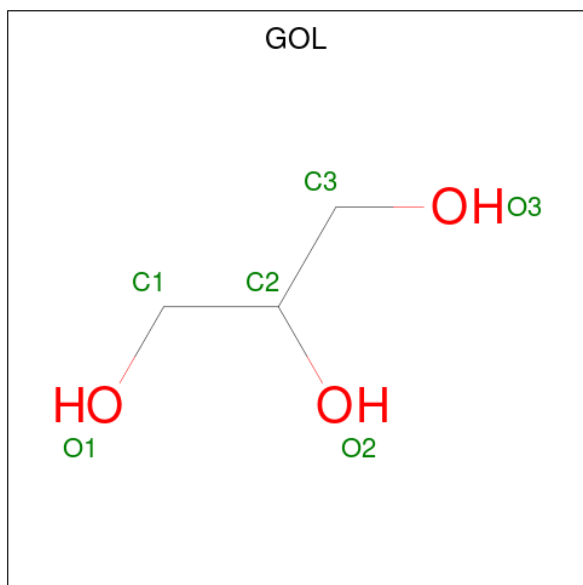
Chain	Residue	Modelled	Actual	Comment	Reference
B	279	PHE	-	expression tag	UNP Q8NEB9
B	280	GLN	-	expression tag	UNP Q8NEB9
B	281	GLY	-	expression tag	UNP Q8NEB9

- Molecule 2 is (5a*S*,8a*R*,9*S*)-2-[(3*R*)-3-methylmorpholin-4-yl]-5,5a,6,7,8,8a-hexahydro-4*H*-cyclopenta[*e*]pyrazolo[1,5-*a*]pyrazin-4-one (three-letter code: 7IQ) (formula: C₁₄H₂₀N₄O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
2	A	1	Total	C	N	O	0	0
			20	14	4	2		
2	B	1	Total	C	N	O	0	0
			20	14	4	2		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C H O 14 3 8 3	0	0
3	B	1	Total C O 6 3 3	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	4	Total Na 4 4	0	0
4	B	1	Total Na 1 1	0	0

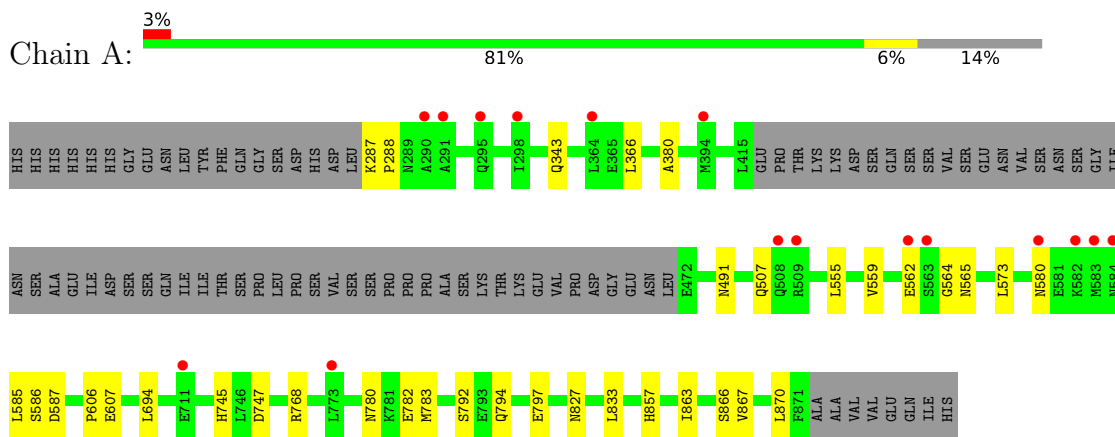
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	426	Total O 431 431	0	5
5	B	410	Total O 413 413	0	3

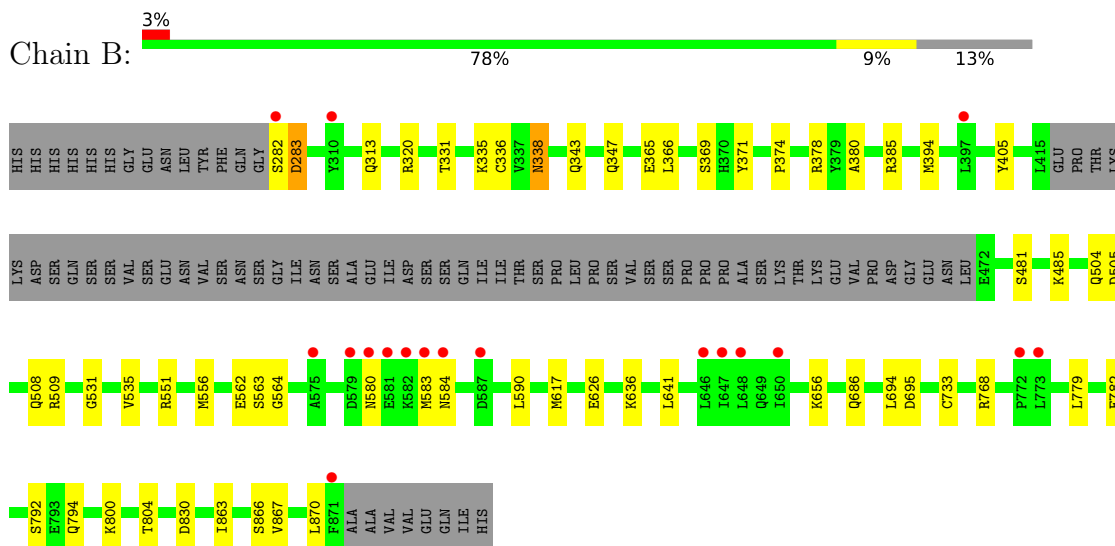
3 Residue-property plots [i](#)

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: Phosphatidylinositol 3-kinase catalytic subunit type 3



- Molecule 1: Phosphatidylinositol 3-kinase catalytic subunit type 3



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.71Å 119.03Å 91.29Å 90.00° 108.95° 90.00°	Depositor
Resolution (Å)	34.50 – 1.78 36.05 – 1.34	Depositor EDS
% Data completeness (in resolution range)	96.7 (34.50-1.78) 54.0 (36.05-1.34)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.06 (at 1.34Å)	Xtrriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.179 , 0.214 0.179 , 0.214	Depositor DCC
R_{free} test set	1853 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å ²)	16.8	Xtrriage
Anisotropy	0.335	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 50.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.022 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9565	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% 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: 7IQ, NA, GOL

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	0.26	0/4361	0.42	0/5902
1	B	0.26	0/4460	0.43	0/6041
All	All	0.26	0/8821	0.43	0/11943

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 [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	4277	0	4274	27	0
1	B	4373	0	4321	48	0
2	A	20	0	0	0	0
2	B	20	0	0	0	0
3	A	12	8	15	0	0
3	B	6	0	8	0	0
4	A	4	0	0	0	0
4	B	1	0	0	0	0
5	A	431	0	0	5	0
5	B	413	0	0	8	0
All	All	9557	8	8618	74	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 4.

All (74) 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:694:LEU:HD11	1:B:782:GLU:HG2	1.53	0.90
1:B:686:GLN:NE2	5:B:1002:HOH:O	2.16	0.78
1:A:792[B]:SER:OG	1:A:794:GLN:NE2	2.19	0.75
1:B:580:ASN:ND2	1:B:584:ASN:HA	2.04	0.73
1:A:287:LYS:HB3	1:A:288:PRO:HD3	1.74	0.69
1:A:694:LEU:HD11	1:A:782:GLU:HG2	1.77	0.66
1:B:792[B]:SER:OG	1:B:794:GLN:NE2	2.29	0.64
1:B:800:LYS:HE2	5:B:1106:HOH:O	1.99	0.63
1:B:509:ARG:HH11	1:B:509:ARG:HG3	1.64	0.62
1:A:562:GLU:HG3	1:A:564:GLY:H	1.65	0.61
1:B:481:SER:O	1:B:485:LYS:HD2	2.00	0.60
1:B:863:ILE:O	1:B:867:VAL:HG23	2.02	0.60
1:A:606:PRO:HD2	1:A:607:GLU:OE2	2.04	0.58
1:B:509:ARG:HG3	1:B:509:ARG:NH1	2.20	0.57
1:B:636:LYS:HB2	1:B:641:LEU:HD11	1.86	0.57
1:A:366:LEU:HB2	1:A:380:ALA:HB2	1.87	0.56
1:A:797:GLU:HG2	5:A:1358:HOH:O	2.05	0.55
1:A:780:ASN:H	1:A:783:MET:HE3	1.71	0.55
1:B:320:ARG:HH21	1:B:347:GLN:HE22	1.55	0.54
1:A:580:ASN:ND2	1:A:587:ASP:H	2.06	0.54
1:A:287:LYS:HB3	1:A:288:PRO:CD	2.37	0.53
1:B:617:MET:SD	5:B:1014:HOH:O	2.59	0.53
1:A:827[A]:ASN:ND2	5:A:1010:HOH:O	2.42	0.52
1:B:335:LYS:HE3	1:B:365:GLU:OE2	2.09	0.52
1:B:590:LEU:HD11	1:B:626:GLU:HG3	1.90	0.52
1:A:863:ILE:O	1:A:867:VAL:HG23	2.10	0.52
1:B:800:LYS:O	1:B:804[B]:THR:HG23	2.10	0.52
1:A:565:ASN:HB2	1:B:695:ASP:O	2.09	0.51
1:B:366:LEU:HB2	1:B:380:ALA:HB2	1.92	0.51
1:B:505:ASP:CB	1:B:509:ARG:HH12	2.24	0.51
1:A:555:LEU:HD13	1:A:585:LEU:HD12	1.93	0.51
1:B:374:PRO:O	1:B:378:ARG:HG2	2.11	0.51
1:B:335:LYS:HE2	5:B:1146:HOH:O	2.11	0.51
1:A:580:ASN:HB2	1:A:586:SER:OG	2.11	0.50
1:A:694:LEU:CD1	1:A:782:GLU:HG2	2.42	0.50
1:B:481:SER:HA	5:B:1026:HOH:O	2.12	0.49
1:A:866[A]:SER:O	1:A:870:LEU:HG	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:505:ASP:HB3	1:B:509:ARG:HH12	1.78	0.49
1:A:857:HIS:HD2	5:A:1354:HOH:O	1.94	0.48
1:B:505:ASP:HB3	1:B:509:ARG:NH1	2.29	0.47
1:B:378:ARG:NH2	5:B:1017:HOH:O	2.47	0.46
1:B:505:ASP:HB3	1:B:509:ARG:HH22	1.81	0.46
1:B:580:ASN:HD22	1:B:584:ASN:HA	1.79	0.46
1:A:745:HIS:CE1	1:A:747:ASP:HB2	2.51	0.46
1:B:505:ASP:HB3	1:B:509:ARG:NH2	2.31	0.46
1:B:866[A]:SER:O	1:B:870:LEU:HG	2.16	0.46
1:A:555:LEU:HD21	1:A:573:LEU:HD12	1.97	0.45
1:A:559:VAL:O	1:A:562:GLU:HB3	2.17	0.45
1:B:369:SER:HB3	1:B:405:TYR:CE1	2.52	0.45
1:A:866[B]:SER:O	1:A:870:LEU:HG	2.17	0.45
1:B:335:LYS:HG3	1:B:371:TYR:OH	2.17	0.45
1:A:507:GLN:NE2	5:A:1019:HOH:O	2.50	0.45
1:A:768:ARG:HD2	1:A:833:LEU:HD12	1.99	0.45
1:B:385:ARG:HG3	5:B:1229:HOH:O	2.16	0.45
1:B:394[B]:MET:HE3	1:B:656:LYS:HE3	1.99	0.44
1:A:768:ARG:HD2	1:A:833:LEU:CD1	2.48	0.44
1:B:733[B]:CYS:SG	1:B:779:LEU:HD22	2.59	0.43
1:B:338:ASN:C	1:B:338:ASN:HD22	2.20	0.43
1:B:768:ARG:NE	1:B:830:ASP:OD1	2.51	0.43
1:B:320:ARG:NH2	1:B:347:GLN:HE22	2.17	0.43
1:B:531:GLY:HA3	1:B:535:VAL:HG21	2.00	0.43
1:B:282:SER:O	1:B:283:ASP:OD1	2.37	0.42
1:B:562:GLU:HG3	1:B:563:SER:N	2.34	0.42
1:B:485:LYS:NZ	5:B:1026:HOH:O	2.52	0.42
1:B:580:ASN:ND2	1:B:584:ASN:HD22	2.17	0.42
1:B:866[B]:SER:O	1:B:870:LEU:HG	2.20	0.42
1:B:331:THR:O	1:B:335:LYS:HD2	2.20	0.42
1:A:491:ASN:ND2	5:A:1001:HOH:O	2.02	0.42
1:B:551:ARG:HD2	1:B:583:MET:O	2.20	0.42
1:B:313:GLN:HA	1:B:336[A]:CYS:SG	2.61	0.41
1:A:343:GLN:H	1:A:343:GLN:CD	2.23	0.41
1:B:504:GLN:O	1:B:508:GLN:HG3	2.21	0.41
1:B:556:MET:HB3	1:B:556:MET:HE2	1.82	0.41
1:B:562:GLU:HG3	1:B:564:GLY:H	1.87	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	530/612 (87%)	526 (99%)	4 (1%)	0	100	100
1	B	543/612 (89%)	539 (99%)	3 (1%)	1 (0%)	47	32
All	All	1073/1224 (88%)	1065 (99%)	7 (1%)	1 (0%)	51	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	283	ASP

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	471/553 (85%)	471 (100%)	0	100	100
1	B	482/553 (87%)	480 (100%)	2 (0%)	91	88
All	All	953/1106 (86%)	951 (100%)	2 (0%)	93	91

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

Mol	Chain	Res	Type
1	B	338	ASN
1	B	343	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	507	GLN
1	A	580	ASN
1	A	584	ASN
1	A	794	GLN
1	B	338	ASN
1	B	347	GLN
1	B	580	ASN
1	B	584	ASN
1	B	794	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 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	7IQ	B	901	-	18,23,23	0.74	0	18,34,34	2.49	4 (22%)
3	GOL	A	903	-	5,5,5	1.22	1 (20%)	5,5,5	1.21	0
3	GOL	A	902	-	5,5,5	0.84	0	5,5,5	1.01	0
2	7IQ	A	901	-	18,23,23	0.77	0	18,34,34	2.46	5 (27%)
3	GOL	B	902	-	5,5,5	0.90	0	5,5,5	0.96	0

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	7IQ	B	901	-	-	0/0/37/37	0/3/4/4
3	GOL	A	903	-	-	4/4/4/4	-
3	GOL	A	902	-	-	0/4/4/4	-
2	7IQ	A	901	-	-	0/0/37/37	0/3/4/4
3	GOL	B	902	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	903	GOL	O2-C2	-2.21	1.36	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	7IQ	C9-N13-N12	6.51	109.08	104.33
2	A	901	7IQ	C9-N13-N12	6.16	108.83	104.33
2	B	901	7IQ	C11-N12-N13	-5.99	107.34	111.86
2	A	901	7IQ	C11-N12-N13	-5.68	107.58	111.86
2	A	901	7IQ	C7-N8-C9	-3.46	112.39	120.40
2	B	901	7IQ	C7-N8-C9	-3.45	112.41	120.40
2	A	901	7IQ	C6-O5-C4	3.24	114.47	109.97
2	B	901	7IQ	C6-O5-C4	2.14	112.93	109.97
2	A	901	7IQ	C11-C10-C9	2.13	106.93	103.72

There are no chirality outliers.

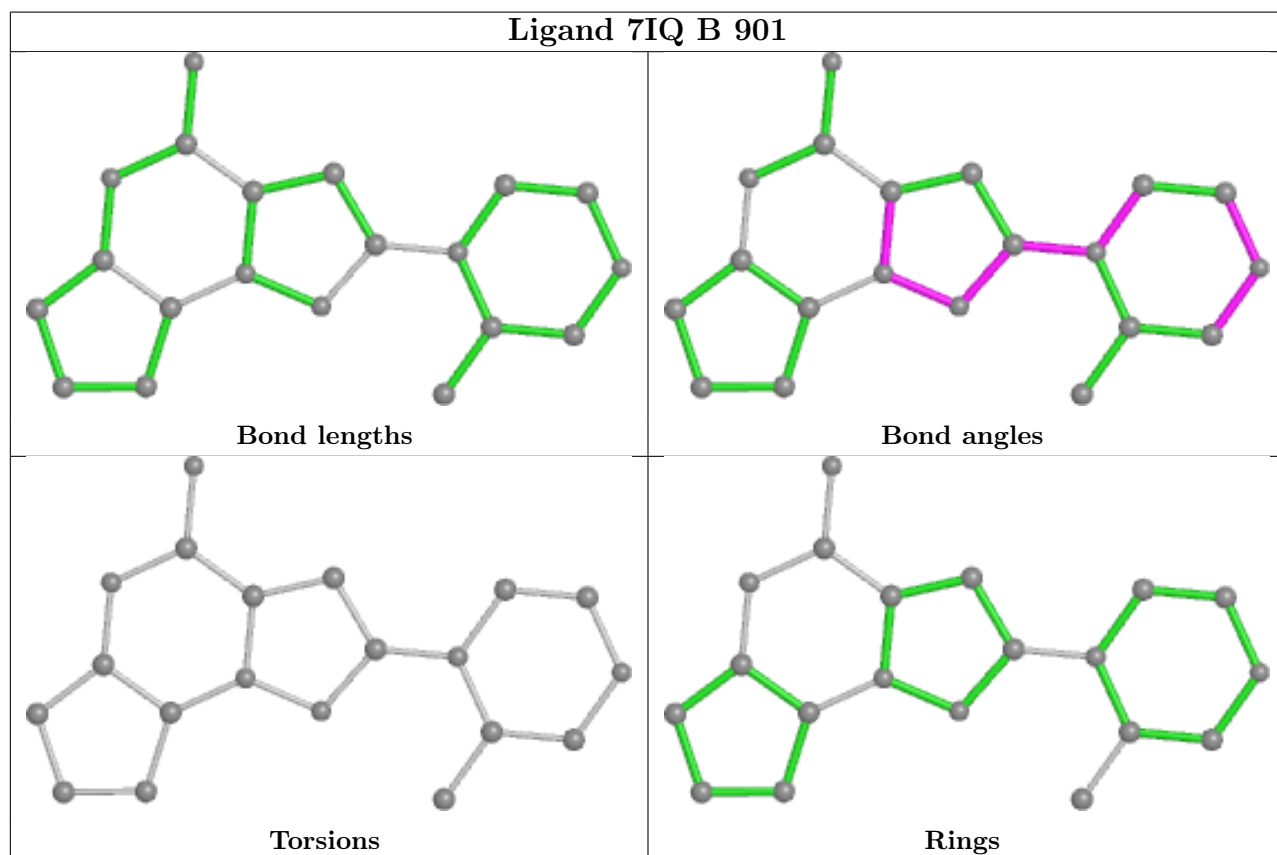
All (6) torsion outliers are listed below:

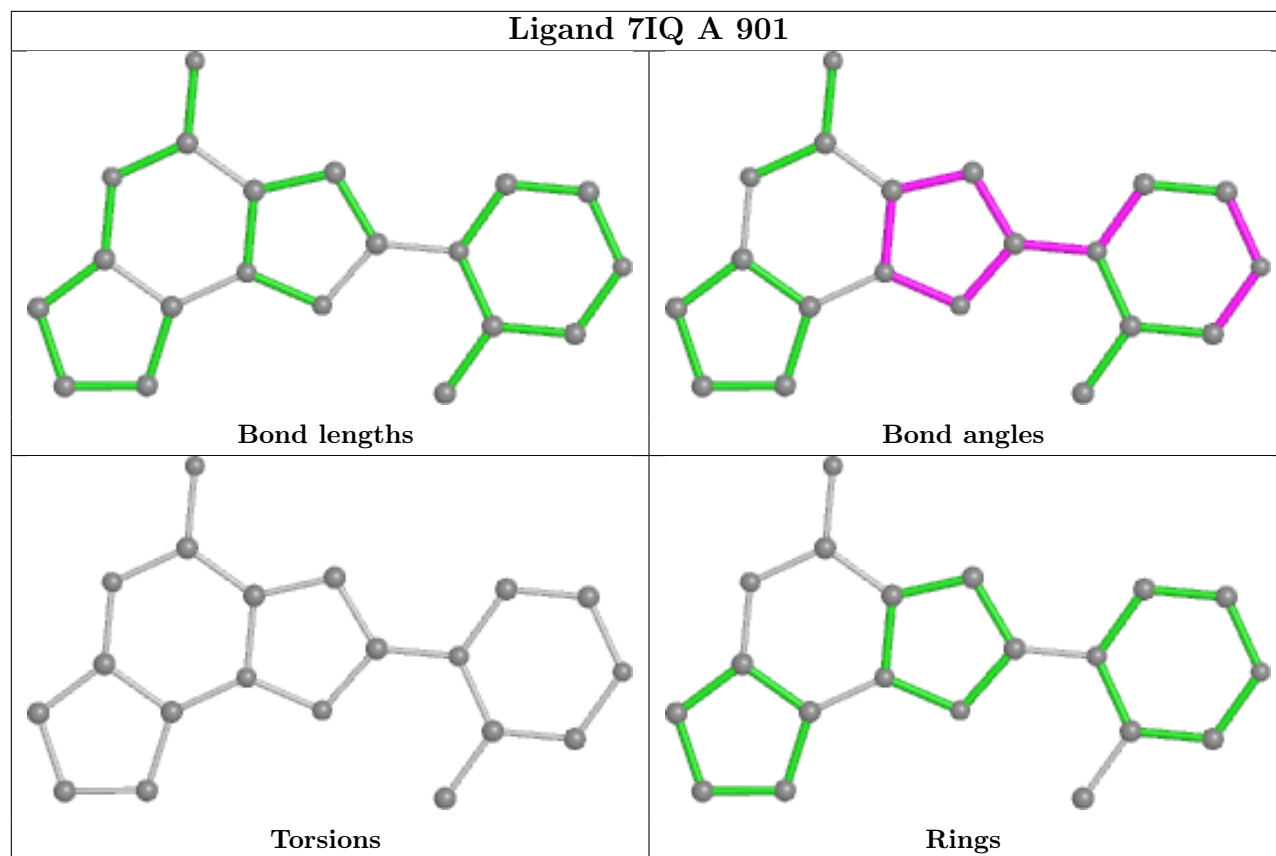
Mol	Chain	Res	Type	Atoms
3	A	903	GOL	O1-C1-C2-C3
3	A	903	GOL	C1-C2-C3-O3
3	B	902	GOL	O1-C1-C2-C3
3	A	903	GOL	O2-C2-C3-O3
3	B	902	GOL	O1-C1-C2-O2
3	A	903	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	529/612 (86%)	-0.27	16 (3%) 50 48	21, 31, 53, 86	0
1	B	534/612 (87%)	-0.19	18 (3%) 45 44	22, 30, 55, 91	0
All	All	1063/1224 (86%)	-0.23	34 (3%) 47 46	21, 30, 54, 91	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	773	LEU	4.8
1	A	394	MET	3.8
1	B	583	MET	3.7
1	B	580	ASN	3.6
1	A	711	GLU	3.4
1	B	587	ASP	3.3
1	B	310	TYR	3.3
1	B	650	ILE	3.1
1	B	648	LEU	3.0
1	B	581	GLU	2.9
1	B	773	LEU	2.9
1	B	584	ASN	2.9
1	A	509	ARG	2.8
1	A	290	ALA	2.8
1	B	582	LYS	2.7
1	A	580	ASN	2.6
1	B	282	SER	2.6
1	A	583	MET	2.6
1	A	563	SER	2.5
1	B	397[A]	LEU	2.5
1	B	579	ASP	2.5
1	B	646	LEU	2.4
1	A	295	GLN	2.3
1	A	582	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	584	ASN	2.3
1	B	647	ILE	2.2
1	A	298	ILE	2.2
1	B	772	PRO	2.2
1	A	291	ALA	2.2
1	B	575	ALA	2.1
1	A	562	GLU	2.1
1	A	364	LEU	2.0
1	A	508	GLN	2.0
1	B	871	PHE	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.

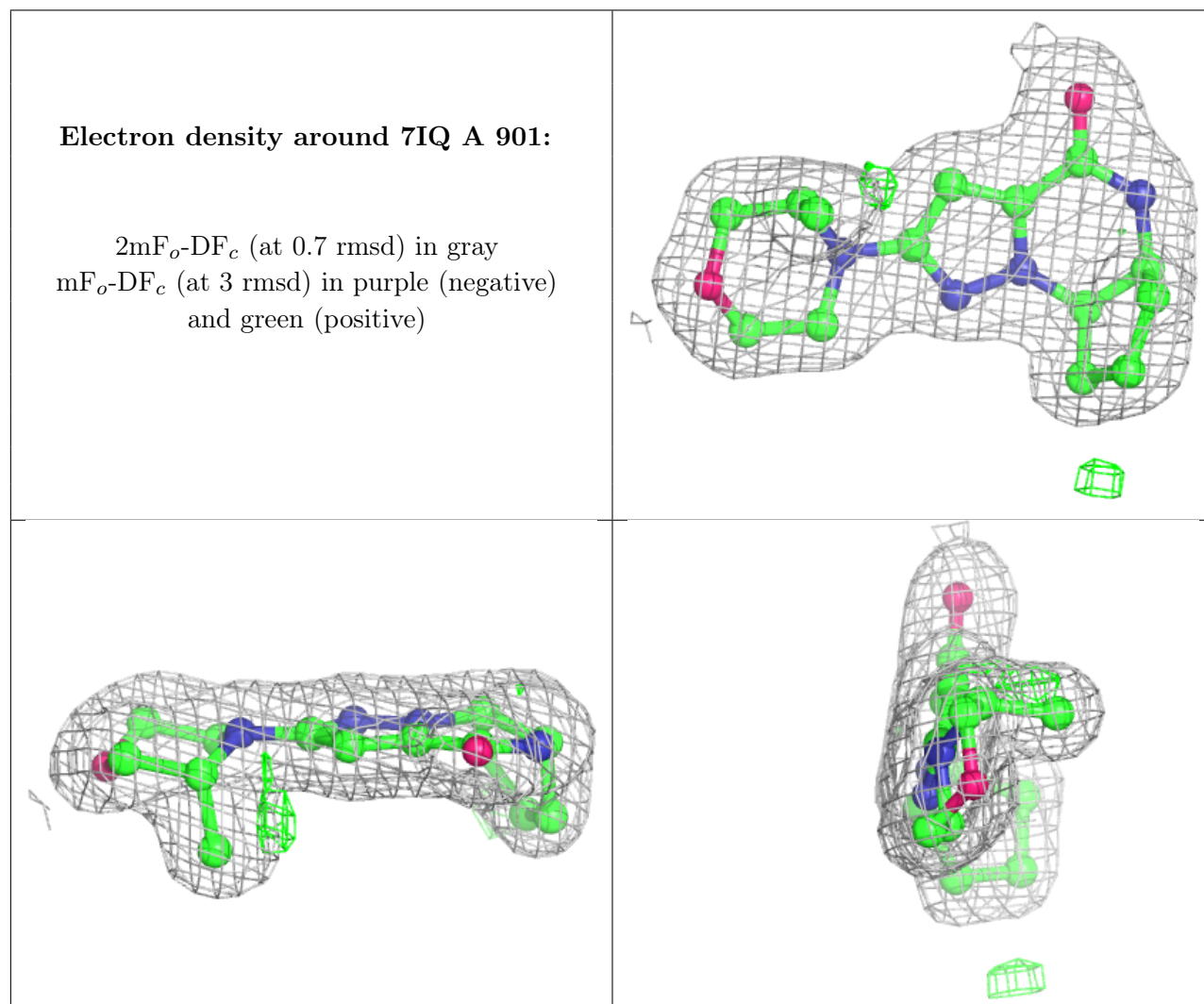
6.4 Ligands [i](#)

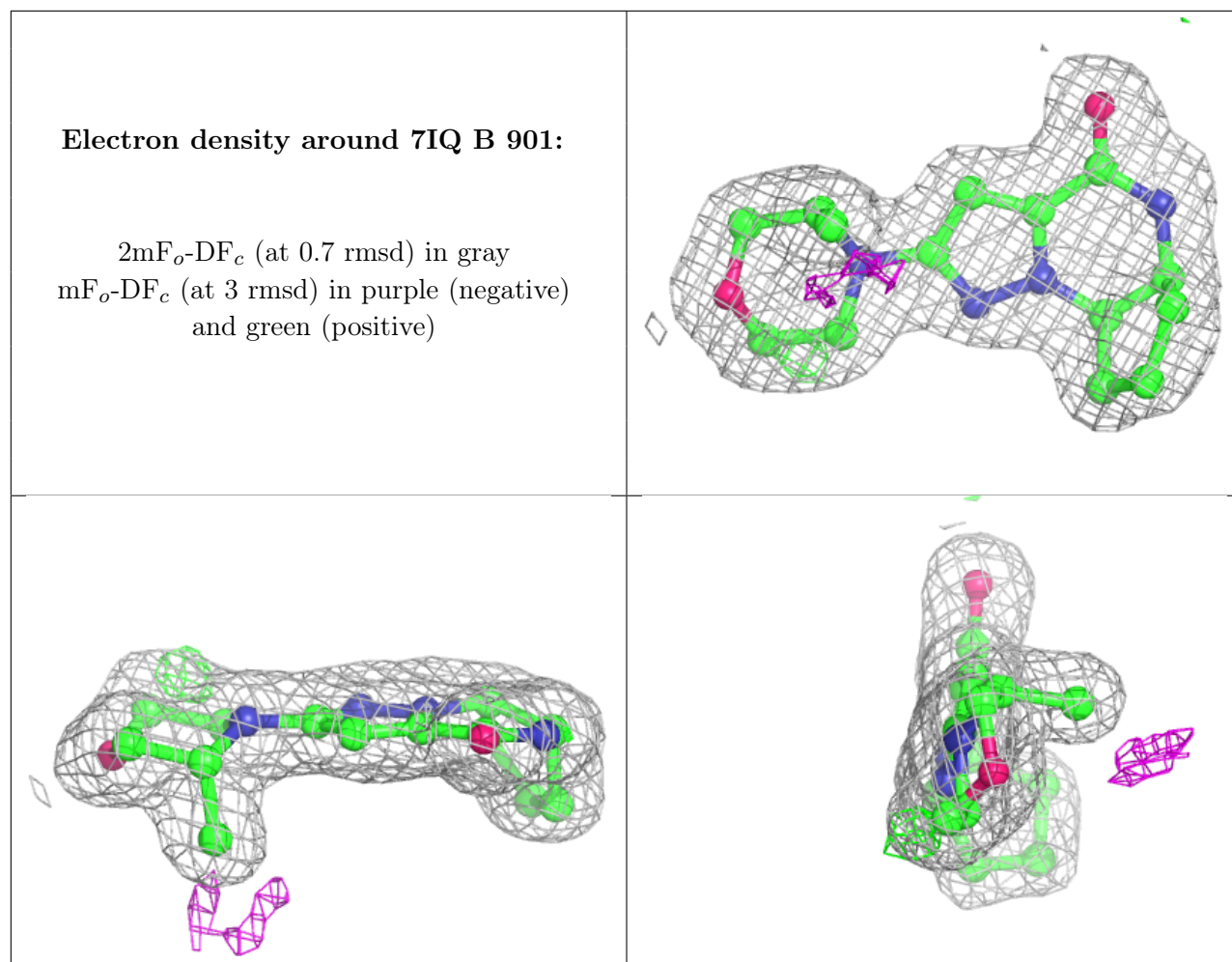
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NA	A	905	1/1	0.72	0.15	60,60,60,60	0
4	NA	A	906	1/1	0.79	0.31	70,70,70,70	0
4	NA	A	904	1/1	0.81	0.09	62,62,62,62	0
4	NA	B	903	1/1	0.82	0.53	62,62,62,62	0
3	GOL	A	903	6/6	0.84	0.16	26,44,63,65	0
3	GOL	B	902	6/6	0.84	0.12	44,54,56,56	0
4	NA	A	907	1/1	0.87	0.24	58,58,58,58	0
3	GOL	A	902	6/6	0.88	0.10	42,47,48,49	0
2	7IQ	A	901	20/20	0.96	0.08	22,25,34,35	0
2	7IQ	B	901	20/20	0.96	0.06	22,23,33,33	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.