



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 28, 2026 – 05:40 PM UTC

PDB ID : 6V9L / pdb_00006v9l
Title : Expanding the Chemical Landscape of SOS1 Activators Using Fragment Based Methods
Authors : Phan, J.; Fesik, S.W.
Deposited on : 2019-12-13
Resolution : 1.70 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

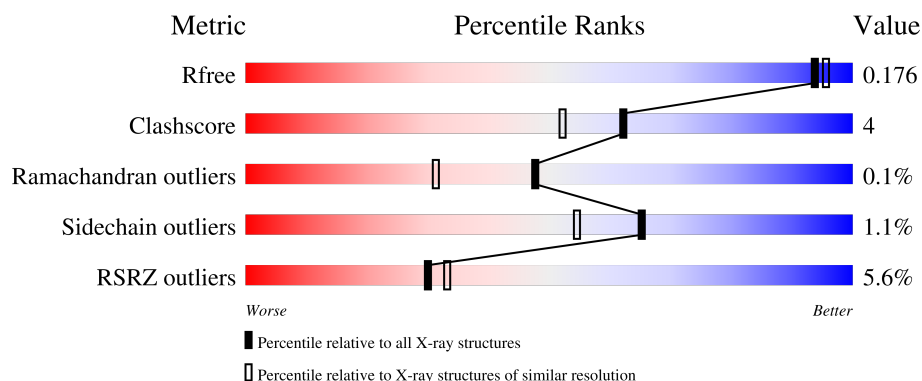
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 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	167	5% 92% 7% ..
2	B	482	4% 90% 7% .
3	C	167	11% 87% 11% .

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 7980 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 GTPase HRas.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	166	Total	C	N	O	S	0	9	0
			1383	858	239	278	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P01112
A	64	ALA	TYR	conflict	UNP P01112

- Molecule 2 is a protein called Son of sevenless homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	469	Total	C	N	O	S	0	24	0
			4050	2597	694	743	16			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	565	GLY	-	expression tag	UNP Q07889

- Molecule 3 is a protein called GTPase HRas.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	167	Total	C	N	O	S	0	5	0
			1363	849	234	273	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	GLY	-	expression tag	UNP P01112

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID:

The chemical structure of GNP (Guanosine Nucleotide Phosphate) is shown. It consists of a guanine base (a purine ring system with an amino group at position 6) attached to a ribose sugar (a five-membered ring with hydroxyl groups at positions 2' and 3'). The ribose sugar is linked to a triphosphate chain (three phosphate groups) via a phosphodiester bond. The triphosphate chain is shown with various atoms labeled, including phosphorus (P), oxygen (O), and nitrogen (N). The structure is color-coded: blue for the guanine base, red for the ribose sugar, and green for the triphosphate chain.

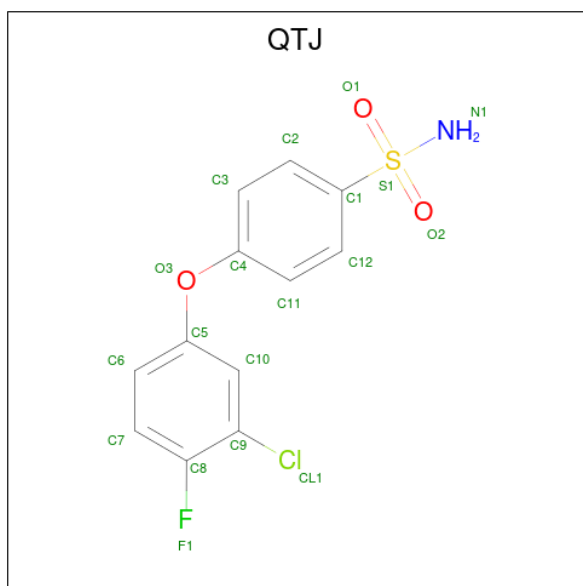
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 5 | A | 1 | Total Mg
1 1 | 0 | 0 |

- 
- ACT
- CH₃
- C
- O⁻
- O

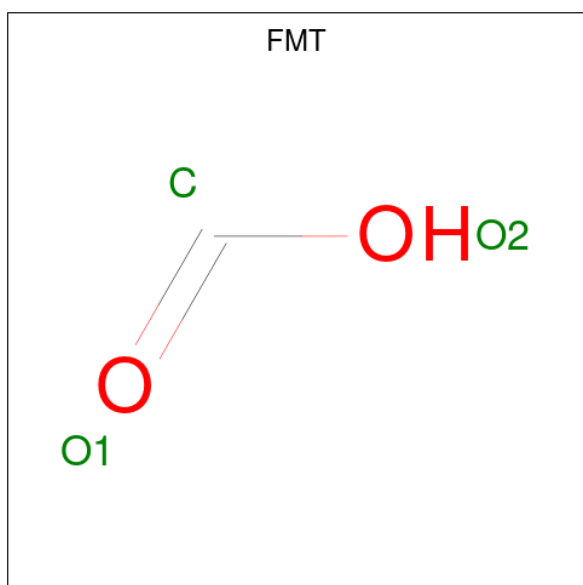
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is 4-(3-chloro-4-fluorophenoxy)benzene-1-sulfonamide (CCD ID: QTJ) (formula: $C_{12}H_9ClFNO_3S$) (labeled as "Ligand of Interest" by depositor).



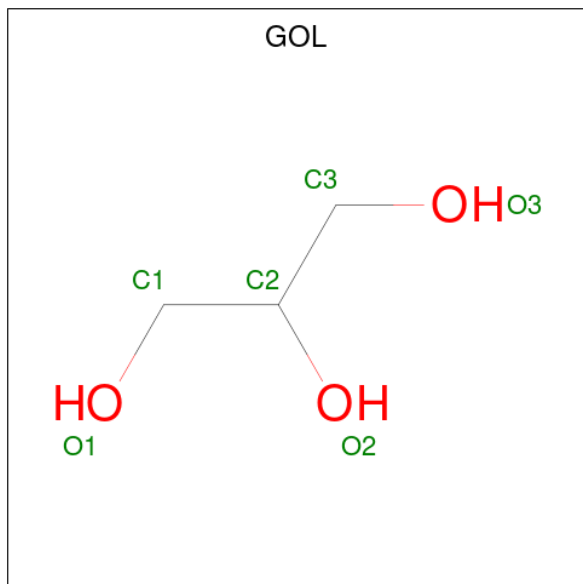
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
7	B	1	Total	C	Cl	F	N	O	S	0	0
			19	12	1	1	1	3	1		

- Molecule 8 is FORMIC ACID (CCD ID: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			3	1	2		
8	B	1	Total	C	O	0	0
			3	1	2		
8	B	1	Total	C	O	0	0
			3	1	2		
8	B	1	Total	C	O	0	0
			3	1	2		
8	C	1	Total	C	O	0	0
			3	1	2		

- Molecule 9 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			6	3	3		
9	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 10 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	C	1	Total	Na	0	0
			1	1		

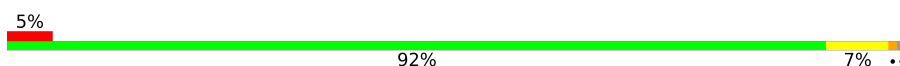
- Molecule 11 is water.

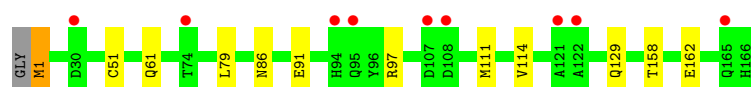
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	175	Total 175	O 175	0	0
11	B	702	Total 702	O 702	0	0
11	C	220	Total 220	O 220	0	0

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.

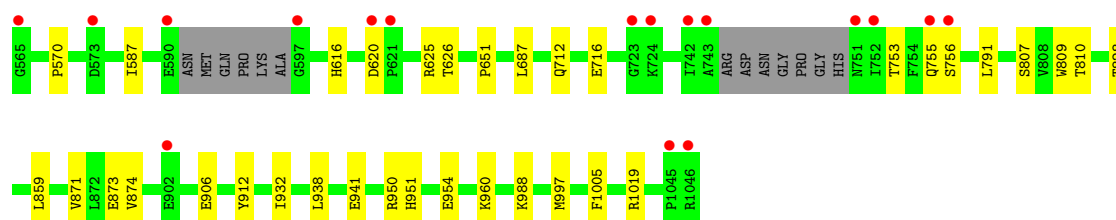
- Molecule 1: GTPase HRas

Chain A: 



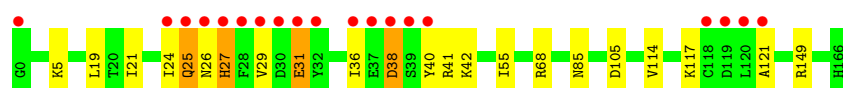
- Molecule 2: Son of sevenless homolog 1

Chain B: 



- Molecule 3: GTPase HRas

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	183.38Å 183.38Å 178.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.58 – 1.70 42.58 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.58-1.70) 99.9 (42.58-1.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.158 , 0.175 0.161 , 0.176	Depositor DCC
R_{free} test set	2015 reflections (1.22%)	wwPDB-VP
Wilson B-factor (Å ²)	19.6	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.004 for l,-k,h 0.004 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7980	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% 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: MG, QTJ, GOL, FMT, CSO, NA, GNP, ACT

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	0/1402	0.49	0/1888
2	B	0.28	0/4176	0.48	0/5642
3	C	0.28	0/1385	0.52	0/1867
All	All	0.28	0/6963	0.49	0/9397

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
3	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	25	GLN	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	1383	0	1355	9	0
2	B	4050	0	4092	25	0
3	C	1363	0	1337	19	0
4	A	32	0	13	0	0
5	A	1	0	0	0	0
6	A	4	0	3	1	0
7	B	19	0	0	0	0
8	B	15	0	5	1	0
8	C	3	0	1	1	0
9	B	12	0	16	1	0
10	C	1	0	0	0	0
11	A	175	0	0	5	0
11	B	702	0	0	12	1
11	C	220	0	0	10	1
All	All	7980	0	6822	56	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 4.

All (56) 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)
2:B:951:HIS:ND1	11:B:2101:HOH:O	1.96	0.96
3:C:105:ASP:OD2	11:C:301:HOH:O	1.84	0.96
3:C:41:ARG:NH1	11:C:302:HOH:O	2.05	0.90
1:A:129:GLN:OE1	11:A:301:HOH:O	2.00	0.78
2:B:755:GLN:NE2	11:B:2107:HOH:O	2.19	0.75
2:B:954:GLU:OE2	11:B:2102:HOH:O	2.04	0.75
3:C:68:ARG:NH2	11:C:304:HOH:O	2.18	0.75
1:A:91:GLU:OE1	11:A:302:HOH:O	2.07	0.72
8:C:201:FMT:O2	11:C:303:HOH:O	2.09	0.70
1:A:86[B]:ASN:ND2	11:A:304:HOH:O	2.23	0.69
3:C:68:ARG:NH1	11:C:307:HOH:O	2.27	0.66
3:C:85:ASN:HD22	3:C:121:ALA:HB3	1.61	0.65
3:C:27:HIS:N	11:C:311:HOH:O	2.30	0.65
2:B:620:ASP:OD1	11:B:2103:HOH:O	2.15	0.63
2:B:988[B]:LYS:NZ	11:B:2113:HOH:O	2.31	0.62
2:B:755:GLN:HG2	11:B:2105:HOH:O	2.01	0.60
3:C:41:ARG:HD2	11:C:302:HOH:O	2.03	0.58
2:B:997[B]:MET:HG2	2:B:1005:PHE:CD2	2.40	0.56
2:B:755:GLN:OE1	11:B:2105:HOH:O	2.18	0.55
3:C:117[A]:LYS:NZ	11:C:312:HOH:O	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:616:HIS:ND1	8:B:2005:FMT:O2	2.37	0.54
2:B:791[A]:LEU:HD12	11:B:2490:HOH:O	2.06	0.54
2:B:587:ILE:HD11	2:B:950:ARG:HG3	1.91	0.53
3:C:21:ILE:O	3:C:25:GLN:HB2	2.09	0.53
2:B:906:GLU:OE1	11:B:2106:HOH:O	2.19	0.52
1:A:158:THR:O	1:A:162[B]:GLU:HG3	2.10	0.51
3:C:24:ILE:HD11	3:C:55:ILE:HD12	1.92	0.50
2:B:912:TYR:CG	2:B:932:ILE:HD11	2.47	0.50
3:C:24:ILE:HD13	3:C:42:LYS:HB2	1.95	0.49
2:B:859[B]:LEU:HD23	2:B:874:VAL:HB	1.96	0.48
2:B:1019[B]:ARG:NH1	11:B:2127:HOH:O	2.47	0.47
1:A:1:MET:HG2	1:A:51:CSO:HA	1.96	0.46
3:C:38:ASP:N	3:C:38:ASP:OD1	2.46	0.46
2:B:712:GLN:O	2:B:716[B]:GLU:HG2	2.17	0.45
2:B:859[A]:LEU:HD11	2:B:871:VAL:HG13	1.99	0.45
2:B:828:THR:HG23	2:B:873:GLU:HG2	1.99	0.45
1:A:79[B]:LEU:HG	1:A:114:VAL:HG21	1.99	0.45
9:B:2008:GOL:O2	11:B:2104:HOH:O	2.17	0.44
3:C:5:LYS:HD3	11:C:417:HOH:O	2.16	0.44
2:B:807:SER:HA	2:B:809:TRP:CZ3	2.53	0.44
2:B:810:THR:HG21	2:B:938[B]:LEU:HD12	2.00	0.43
1:A:111[B]:MET:HE3	1:A:111[B]:MET:HB3	1.74	0.43
2:B:941[A]:GLU:HA	2:B:960:LYS:HE3	2.02	0.42
3:C:19[A]:LEU:HD11	3:C:114:VAL:HG11	2.01	0.42
1:A:61:GLN:HG2	11:A:369:HOH:O	2.19	0.42
1:A:97:ARG:HD2	1:A:111[A]:MET:HE1	2.01	0.41
2:B:587:ILE:CD1	2:B:950:ARG:HG3	2.50	0.41
3:C:27:HIS:ND1	3:C:27:HIS:C	2.78	0.41
2:B:570:PRO:HB3	2:B:651:PRO:HG2	2.02	0.41
2:B:625:ARG:NH2	11:B:2138:HOH:O	2.53	0.41
3:C:29:VAL:HG12	3:C:31:GLU:HB2	2.01	0.41
3:C:40:TYR:HB3	11:C:427:HOH:O	2.20	0.41
6:A:203:ACT:H3	11:A:472:HOH:O	2.21	0.40
3:C:27:HIS:CE1	3:C:149:ARG:HD3	2.56	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)
11:B:2368:HOH:O	11:C:324:HOH:O[3_555]	2.00	0.20

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	172/167 (103%)	169 (98%)	3 (2%)	0	100	100
2	B	487/482 (101%)	482 (99%)	5 (1%)	0	100	100
3	C	170/167 (102%)	162 (95%)	7 (4%)	1 (1%)	21	9
All	All	829/816 (102%)	813 (98%)	15 (2%)	1 (0%)	48	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	26	ASN

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	151/142 (106%)	150 (99%)	1 (1%)	76	69
2	B	461/447 (103%)	458 (99%)	3 (1%)	76	69
3	C	149/144 (104%)	145 (97%)	4 (3%)	39	23
All	All	761/733 (104%)	753 (99%)	8 (1%)	65	54

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
2	B	687	LEU

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Mol	Chain	Res	Type
2	B	753	THR
2	B	756	SER
3	C	27	HIS
3	C	31	GLU
3	C	36	ILE
3	C	38	ASP

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	129	GLN
2	B	755	GLN
2	B	866	ASN
3	C	61	GLN
3	C	85	ASN
3	C	95	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	CSO	A	51	1	3,6,7	1.08	0	1,6,8	1.12	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
1	CSO	A	51	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	51	CSO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 2 are monoatomic - leaving 11 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	$\# Z > 2$
4	GNP	A	201	5	34,34,34	1.18	5 (14%)	47,54,54	0.80	1 (2%)
6	ACT	A	203	-	3,3,3	1.52	1 (33%)	3,3,3	1.57	0
8	FMT	C	201	-	2,2,2	0.62	0	1,1,1	0.04	0
8	FMT	B	2004	-	2,2,2	0.72	0	1,1,1	0.21	0
8	FMT	B	2006	-	2,2,2	0.72	0	1,1,1	0.22	0
8	FMT	B	2003	-	2,2,2	0.73	0	1,1,1	0.21	0
9	GOL	B	2008	-	5,5,5	1.01	0	5,5,5	1.10	1 (20%)
7	QTJ	B	2001	-	20,20,20	0.34	0	29,29,29	0.48	0
8	FMT	B	2002	-	2,2,2	0.73	0	1,1,1	0.22	0
9	GOL	B	2007	-	5,5,5	0.84	0	5,5,5	0.90	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	FMT	B	2005	-	2,2,2	0.55	0	1,1,1	0.38	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
9	GOL	B	2008	-	-	3/4/4/4	-
7	QTJ	B	2001	-	-	0/10/10/10	0/2/2/2
4	GNP	A	201	5	-	4/18/38/38	0/3/3/3
9	GOL	B	2007	-	-	0/4/4/4	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	201	GNP	PG-O1G	3.58	1.51	1.46
4	A	201	GNP	PB-O1B	3.18	1.51	1.46
4	A	201	GNP	PG-N3B	2.47	1.69	1.63
6	A	203	ACT	CH3-C	2.24	1.57	1.49
4	A	201	GNP	PB-O2B	-2.18	1.51	1.56
4	A	201	GNP	PB-O3A	2.03	1.61	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	201	GNP	O1G-PG-N3B	-4.30	105.44	111.77
9	B	2008	GOL	C3-C2-C1	-2.13	103.97	111.80

There are no chirality outliers.

All (7) torsion outliers are listed below:

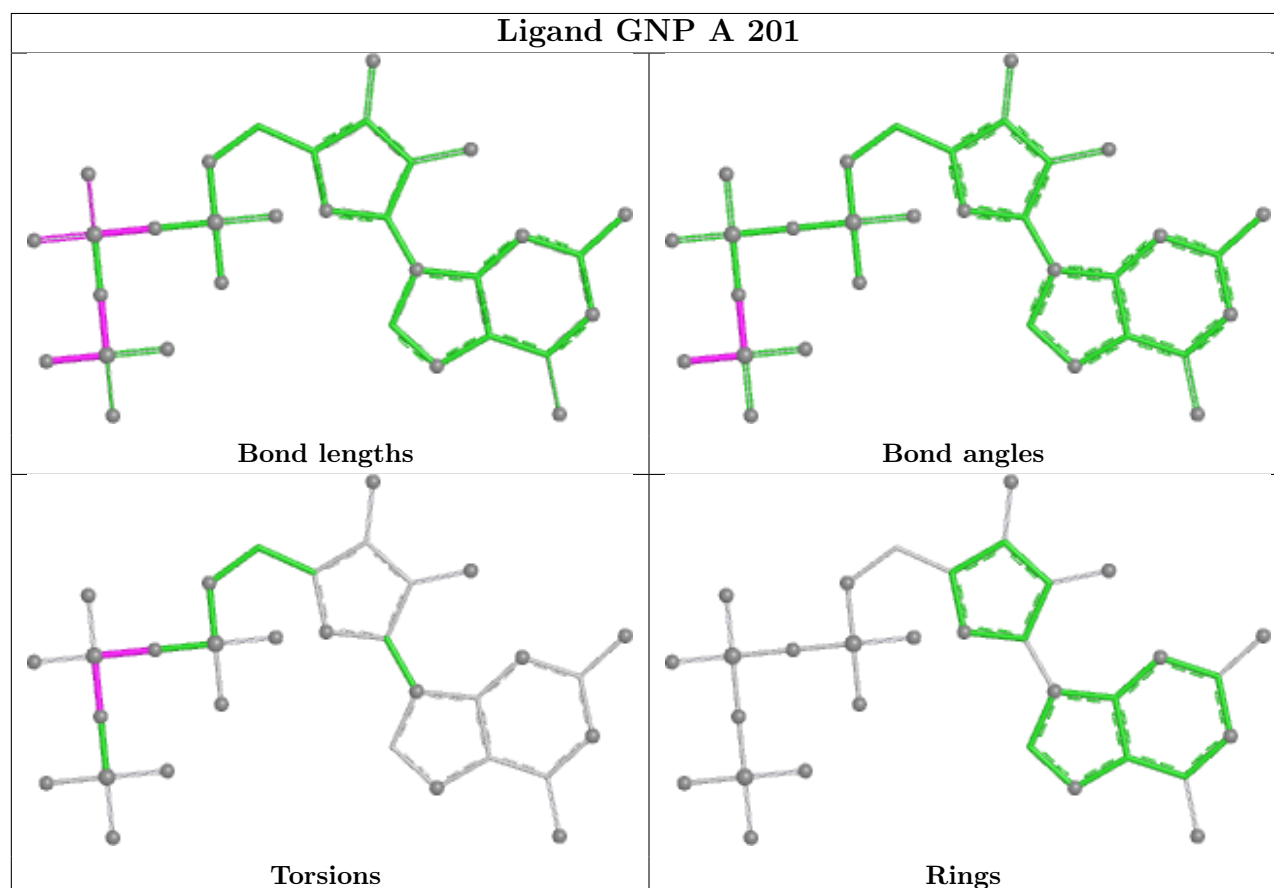
Mol	Chain	Res	Type	Atoms
4	A	201	GNP	PG-N3B-PB-O1B
9	B	2008	GOL	C1-C2-C3-O3
9	B	2008	GOL	O2-C2-C3-O3
9	B	2008	GOL	O1-C1-C2-O2
4	A	201	GNP	PA-O3A-PB-O2B
4	A	201	GNP	PA-O3A-PB-O1B
4	A	201	GNP	PG-N3B-PB-O3A

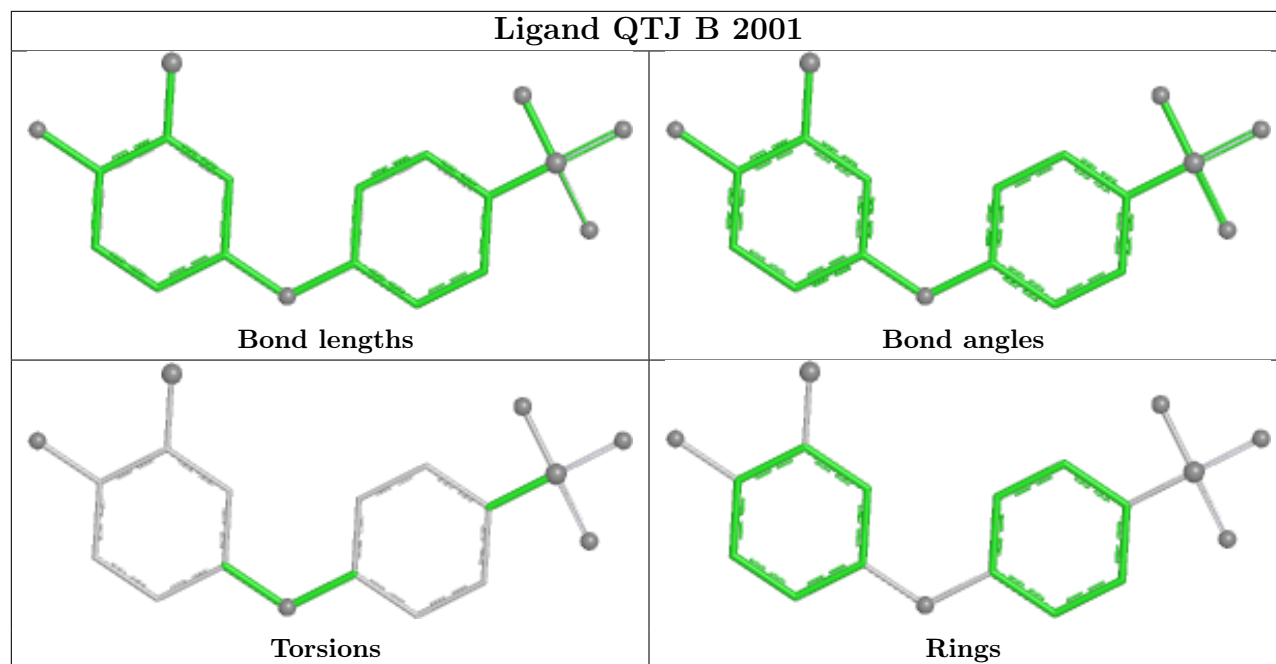
There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	203	ACT	1	0
8	C	201	FMT	1	0
9	B	2008	GOL	1	0
8	B	2005	FMT	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, 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	165/167 (98%)	-0.16	9 (5%) 30 34	7, 20, 41, 57	9 (5%)
2	B	469/482 (97%)	-0.24	17 (3%) 46 50	7, 18, 40, 64	24 (5%)
3	C	167/167 (100%)	0.20	19 (11%) 10 9	9, 20, 56, 83	5 (2%)
All	All	801/816 (98%)	-0.13	45 (5%) 30 33	7, 19, 44, 83	38 (4%)

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	27	HIS	9.3
3	C	29	VAL	8.2
3	C	26	ASN	5.9
2	B	743	ALA	5.9
2	B	751	ASN	4.7
3	C	38	ASP	4.6
3	C	31	GLU	4.5
2	B	597	GLY	4.3
3	C	120	LEU	4.3
3	C	30	ASP	4.1
3	C	28	PHE	4.0
3	C	24	ILE	3.9
3	C	0	GLY	3.9
2	B	1045	PRO	3.8
3	C	25	GLN	3.7
3	C	39[A]	SER	3.6
3	C	37	GLU	3.5
3	C	36	ILE	3.4
2	B	590	GLU	3.1
1	A	165	GLN	2.9
2	B	724	LYS	2.9
2	B	755	GLN	2.8
1	A	121	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	565	GLY	2.7
2	B	573	ASP	2.6
3	C	121	ALA	2.5
2	B	1046	ARG	2.5
3	C	40	TYR	2.5
2	B	723	GLY	2.4
2	B	742	ILE	2.4
2	B	752	ILE	2.4
2	B	756	SER	2.4
3	C	32	TYR	2.4
1	A	122	ALA	2.3
1	A	95[A]	GLN	2.3
1	A	108	ASP	2.2
2	B	902	GLU	2.2
3	C	118	CYS	2.1
1	A	30	ASP	2.1
1	A	107	ASP	2.1
2	B	620	ASP	2.1
1	A	74	THR	2.1
2	B	621	PRO	2.0
3	C	119	ASP	2.0
1	A	94	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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($\text{\AA}^2$)	Q<0.9
1	CSO	A	51	7/8	0.95	0.11	18,19,29,34	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

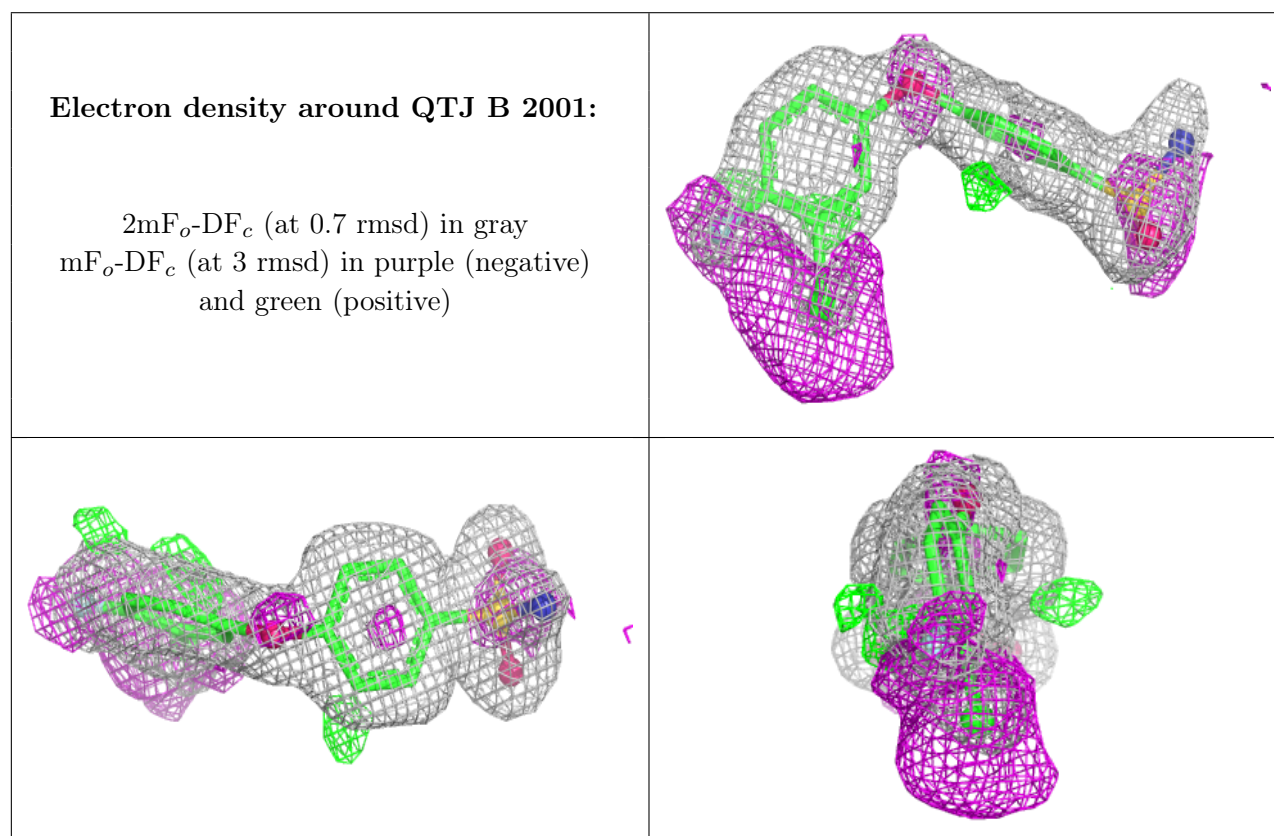
6.4 Ligands [i](#)

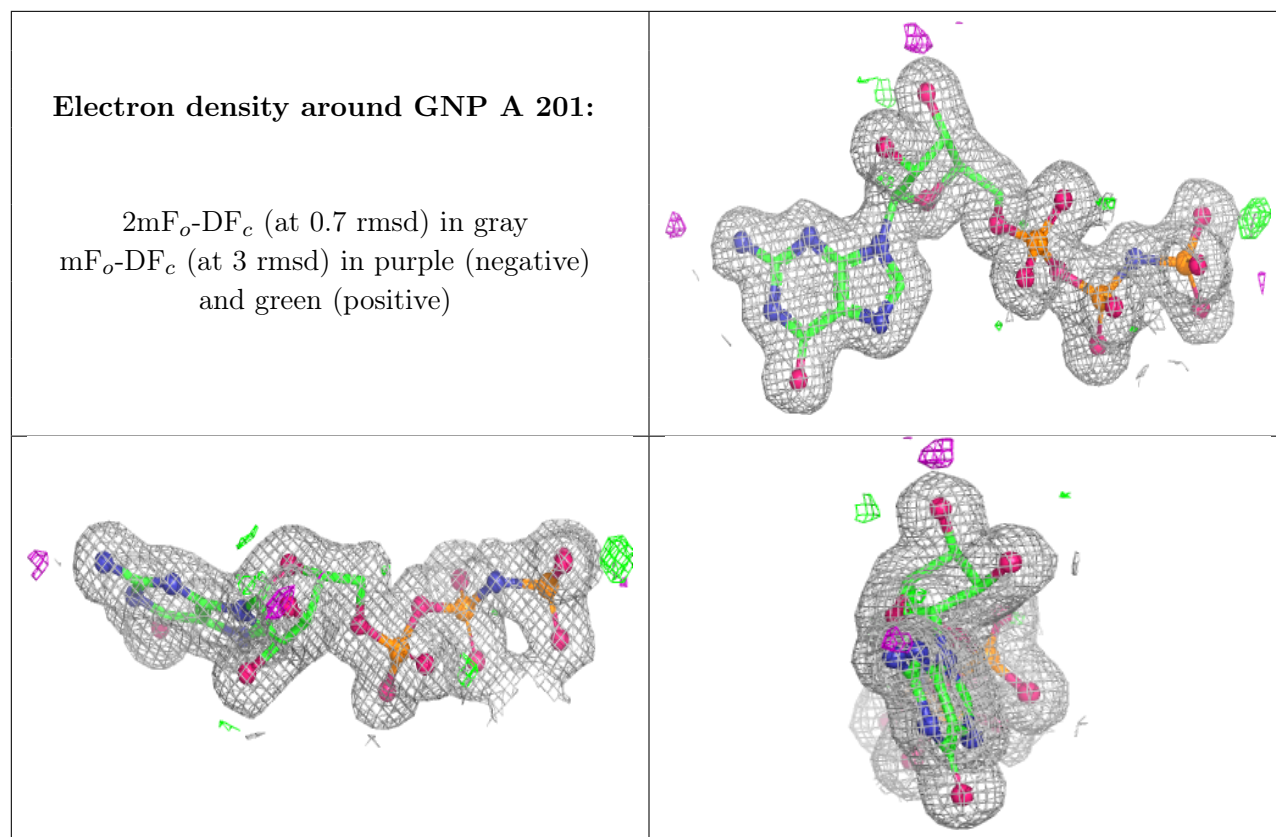
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

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
6	ACT	A	203	4/4	0.74	0.25	49,53,54,55	0
8	FMT	C	201	3/3	0.82	0.19	28,28,33,35	0
8	FMT	B	2003	3/3	0.87	0.14	49,49,51,55	0
8	FMT	B	2006	3/3	0.88	0.16	64,64,64,64	0
9	GOL	B	2007	6/6	0.88	0.14	22,38,44,50	0
9	GOL	B	2008	6/6	0.88	0.14	25,43,47,51	0
7	QTJ	B	2001	19/19	0.90	0.12	19,26,43,56	0
8	FMT	B	2002	3/3	0.91	0.14	48,48,51,55	0
8	FMT	B	2004	3/3	0.93	0.21	32,32,33,42	0
8	FMT	B	2005	3/3	0.95	0.12	21,21,21,28	0
10	NA	C	202	1/1	0.97	0.07	32,32,32,32	0
5	MG	A	202	1/1	0.99	0.02	13,13,13,13	0
4	GNP	A	201	32/32	0.99	0.04	13,15,19,22	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.