Full wwPDB X-ray Structure Validation Report (i)

Nov 13, 2023 – 02:57 PM JST

PDB ID	:	5XG3
Title	:	Crystal structure of the ATPgS-engaged Smc head domain with an extended coiled coil bound to the C-terminal domain of ScpA derived from Bacillus subtilis
Authors	:	Shin, H.-C.; Lee, H.; Oh, B.-H.
Deposited on	:	2017-04-11
Resolution	:	3.50 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 (i) 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 (i)) were used in the production of this report:

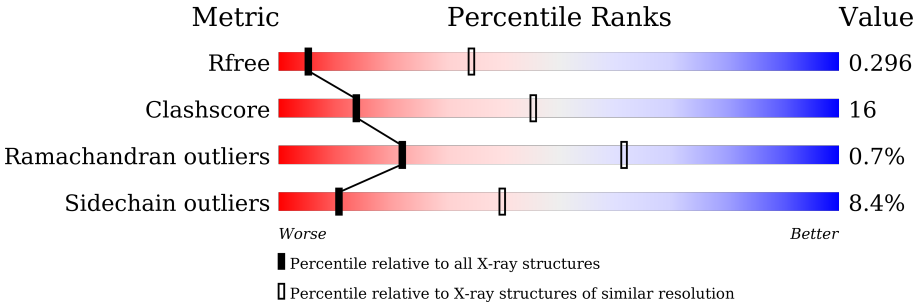
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	435	61% 23% • 15%
1	B	435	63% 20% • 14%
2	C	89	60% 17% 24%
2	D	89	52% 7% • 40%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5698 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 Chromosome partition protein Smc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	371	2400	1492	429	475	4	0	0	0
1	B	374	2459	1546	426	482	5	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	971	SER	-	linker	UNP P51834
A	972	GLY	-	linker	UNP P51834
A	973	GLY	-	linker	UNP P51834
A	974	SER	-	linker	UNP P51834
A	1118	GLN	GLU	engineered mutation	UNP P51834
B	971	SER	-	linker	UNP P51834
B	972	GLY	-	linker	UNP P51834
B	973	GLY	-	linker	UNP P51834
B	974	SER	-	linker	UNP P51834
B	1118	GLN	GLU	engineered mutation	UNP P51834

- Molecule 2 is a protein called Segregation and condensation protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	68	453	282	80	89	2	0	0	0
2	D	53	318	195	60	62	1	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	252	VAL	-	expression tag	UNP A0A1N6WAJ8
C	253	ASP	-	expression tag	UNP A0A1N6WAJ8

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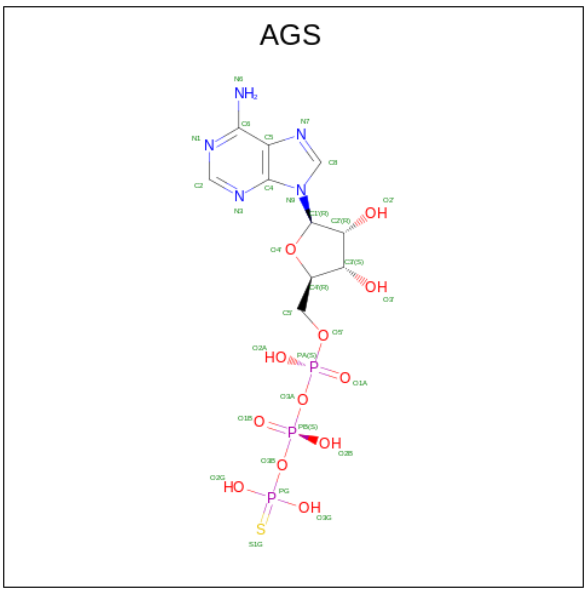
Chain	Residue	Modelled	Actual	Comment	Reference
C	254	LYS	-	expression tag	UNP A0A1N6WAJ8
C	255	LEU	-	expression tag	UNP A0A1N6WAJ8
D	252	VAL	-	expression tag	UNP A0A1N6WAJ8
D	253	ASP	-	expression tag	UNP A0A1N6WAJ8
D	254	LYS	-	expression tag	UNP A0A1N6WAJ8
D	255	LEU	-	expression tag	UNP A0A1N6WAJ8

- Molecule 3 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
3	A	1	31	10	5	12	3	1	0	0
3	B	1	31	10	5	12	3	1	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 5 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Co		
5	A	1	1	1	0	0

- Molecule 6 is water.

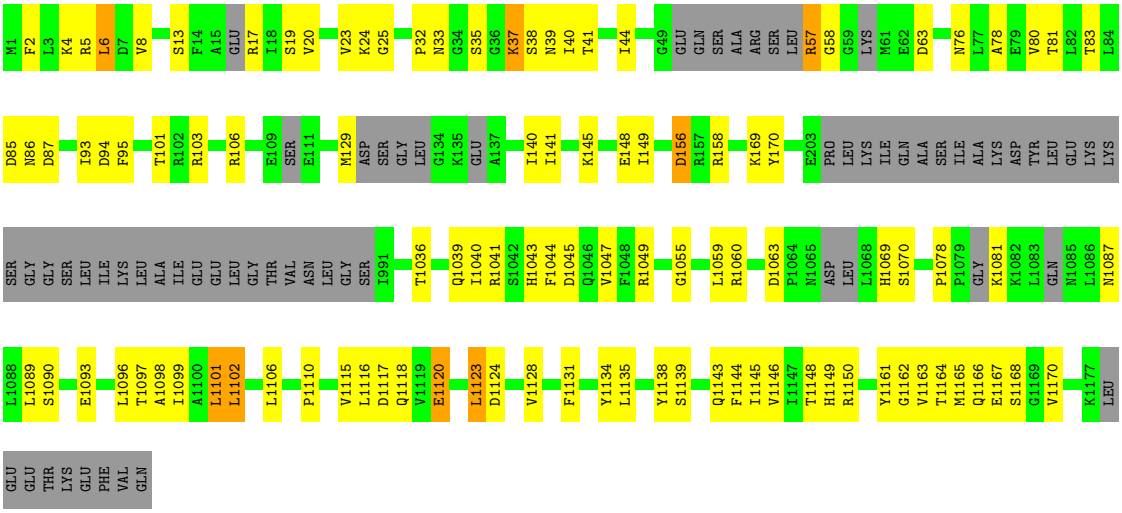
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	B	3	3	3	0	0

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. 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. 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.

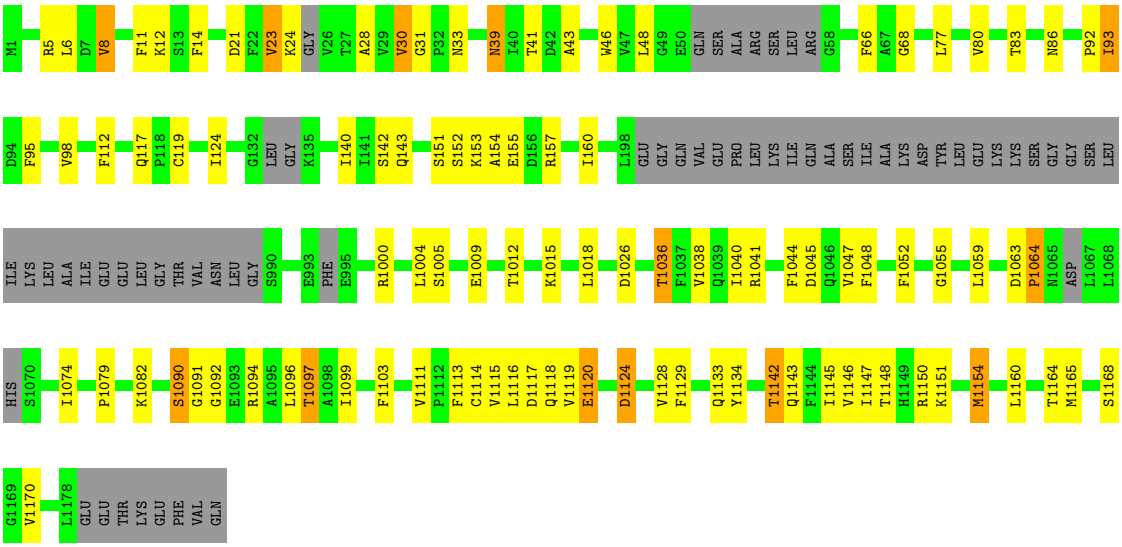
- Molecule 1: Chromosome partition protein Smc

Chain A: 61% 23% • 15%



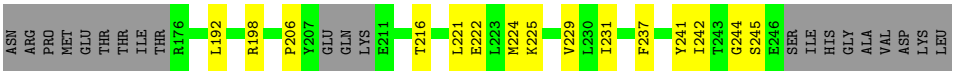
- Molecule 1: Chromosome partition protein Smc

Chain B: 63% 20% • 14%



• Molecule 2: Segregation and condensation protein A

Chain C:



• Molecule 2: Segregation and condensation protein A

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	88.10Å 104.78Å 185.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.99 – 3.50 40.99 – 3.01	Depositor EDS
% Data completeness (in resolution range)	84.1 (40.99-3.50) 71.0 (40.99-3.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.36 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.261 , 0.296 0.261 , 0.296	Depositor DCC
R_{free} test set	1686 reflections (6.81%)	wwPDB-VP
Wilson B-factor (Å^2)	34.5	Xtriage
Anisotropy	0.640	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.12 , -0.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.30$, $< L^2 > = 0.14$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.78	EDS
Total number of atoms	5698	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.77% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: CO, AGS, MG

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	0.49	0/2417	0.72	3/3296 (0.1%)
1	B	0.54	0/2486	0.73	1/3398 (0.0%)
2	C	0.41	0/458	0.63	0/627
2	D	0.47	0/317	0.63	0/435
All	All	0.51	0/5678	0.71	4/7756 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1064	PRO	N-CA-CB	7.46	112.25	103.30
1	A	6	LEU	CA-CB-CG	5.54	128.04	115.30
1	A	1131	PHE	O-C-N	5.11	130.87	122.70
1	A	57	ARG	C-N-CA	-5.11	111.58	122.30

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	2400	0	1954	85	0
1	B	2459	0	2006	71	0
2	C	453	0	366	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	318	0	221	5	0
3	A	31	0	12	5	0
3	B	31	0	12	3	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	1	0	0	0	0
6	B	3	0	0	2	0
All	All	5698	0	4571	162	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 16.

All (162) 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)
3:B:1201:AGS:S1G	6:B:1302:HOH:O	2.22	0.96
1:B:12:LYS:HD2	1:B:39:ASN:HD21	1.36	0.87
1:B:30:VAL:HG12	1:B:31:GLY:H	1.42	0.83
1:B:28:ALA:HB3	1:B:1160:LEU:HD22	1.63	0.80
1:B:1116:LEU:HB2	1:B:1146:VAL:HA	1.65	0.79
2:C:206:PRO:HG3	2:C:216:THR:HG21	1.66	0.77
1:A:1115:VAL:HG22	1:A:1145:ILE:HB	1.67	0.76
1:B:92:PRO:O	1:B:93:ILE:HD12	1.89	0.73
3:A:1201:AGS:H8	3:A:1201:AGS:O5'	1.89	0.72
1:A:57:ARG:NH1	3:A:1201:AGS:O2A	2.21	0.72
1:A:1123:LEU:HA	1:B:33:ASN:HD21	1.53	0.72
1:A:8:VAL:O	1:A:17:ARG:HA	1.90	0.71
1:B:152:SER:O	1:B:157:ARG:NH2	2.26	0.68
1:A:1041:ARG:HA	1:A:1044:PHE:HD2	1.59	0.67
1:A:33:ASN:ND2	1:B:1092:GLY:HA3	2.10	0.66
1:A:1106:LEU:O	1:A:1110:PRO:HB3	1.96	0.65
1:A:1164:THR:HG21	2:C:224:MET:HG3	1.78	0.65
1:A:41:THR:HG22	1:A:1115:VAL:HG11	1.80	0.64
1:A:1123:LEU:O	1:A:1150:ARG:NH1	2.30	0.64
1:A:5:ARG:HA	1:A:20:VAL:O	1.96	0.64
1:B:30:VAL:HG11	2:D:218:LEU:HD22	1.79	0.62
1:B:66:PHE:CZ	1:B:68:GLY:HA2	2.34	0.62
1:A:1096:LEU:HD23	1:A:1099:ILE:HD12	1.82	0.61
1:B:1116:LEU:HD22	1:B:1119:VAL:HG21	1.82	0.61
1:A:1138:TYR:HB2	1:A:1144:PHE:HE2	1.65	0.61
2:D:222:GLU:O	2:D:225:LYS:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:ILE:HG23	1:B:95:PHE:H	1.66	0.60
1:A:32:PRO:C	2:C:225:LYS:HZ1	2.04	0.60
1:A:33:ASN:O	2:C:225:LYS:NZ	2.30	0.60
1:B:1090:SER:OG	1:B:1091:GLY:N	2.35	0.59
1:A:145:LYS:O	1:A:148:GLU:CB	2.50	0.59
1:B:112:PHE:HB3	1:B:124:ILE:HD11	1.84	0.59
1:B:112:PHE:HB2	1:B:119:CYS:HB2	1.84	0.58
1:B:12:LYS:HD2	1:B:39:ASN:ND2	2.15	0.58
1:A:33:ASN:HD21	1:B:1092:GLY:HA3	1.67	0.58
1:A:149:ILE:HG21	1:A:1101:LEU:HD21	1.84	0.58
1:B:1165:MET:HG2	1:B:1168:SER:O	2.03	0.57
1:A:1165:MET:HG3	1:A:1170:VAL:O	2.04	0.57
2:C:231:ILE:HG12	2:C:242:ILE:HA	1.86	0.57
1:A:1041:ARG:HA	1:A:1044:PHE:CD2	2.40	0.57
1:B:140:ILE:HG23	1:B:1115:VAL:HB	1.87	0.57
1:A:1049:ARG:HG2	1:A:1055:GLY:O	2.05	0.57
1:A:1089:LEU:HD22	1:A:1093:GLU:HB3	1.87	0.56
1:A:140:ILE:HG23	1:A:1115:VAL:HB	1.87	0.56
1:B:1036:THR:O	1:B:1040:ILE:HG13	2.06	0.56
1:A:86:ASN:HB3	1:A:95:PHE:O	2.05	0.56
1:B:1151:LYS:HA	1:B:1154:MET:HG3	1.88	0.56
1:A:156:ASP:OD1	1:A:156:ASP:N	2.39	0.56
1:B:1103:PHE:CZ	1:B:1134:TYR:HB3	2.42	0.55
1:A:149:ILE:HD12	1:A:1098:ALA:HB1	1.89	0.55
1:B:143:GLN:HB2	1:B:1117:ASP:HB3	1.88	0.55
1:A:1036:THR:O	1:A:1040:ILE:HG13	2.07	0.54
1:A:1146:VAL:HG12	1:A:1148:THR:HG23	1.90	0.54
1:A:1047:VAL:HG13	1:A:1134:TYR:CZ	2.42	0.54
1:A:58:GLY:HA2	1:A:63:ASP:HB2	1.89	0.54
1:B:86:ASN:HB3	1:B:95:PHE:O	2.06	0.54
1:A:1118:GLN:HA	1:A:1148:THR:HG22	1.89	0.54
1:A:4:LYS:CB	1:A:83:THR:O	2.55	0.54
1:A:20:VAL:HG13	1:A:1161:TYR:CE2	2.43	0.54
1:A:1123:LEU:HD13	1:A:1128:VAL:HG22	1.89	0.53
1:A:76:ASN:O	1:A:106:ARG:N	2.40	0.53
1:B:1045:ASP:N	1:B:1045:ASP:OD1	2.41	0.53
1:A:13:SER:OG	1:A:39:ASN:ND2	2.42	0.53
1:B:1059:LEU:HD11	1:B:1074:ILE:HG12	1.91	0.53
1:B:1120:GLU:OE2	1:B:1148:THR:HG23	2.08	0.53
1:A:35:SER:HB3	1:A:1163:VAL:HG12	1.90	0.53
1:A:1098:ALA:HA	1:A:1101:LEU:HD23	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1081:LYS:NZ	3:B:1201:AGS:O3'	2.42	0.52
1:A:1165:MET:O	2:C:225:LYS:HA	2.09	0.52
1:B:1118:GLN:NE2	6:B:1301:HOH:O	2.11	0.52
1:A:141:ILE:O	1:A:1117:ASP:N	2.34	0.52
2:C:229:VAL:HA	2:C:244:GLY:HA2	1.91	0.51
1:A:57:ARG:NH2	3:A:1201:AGS:O1A	2.43	0.51
1:B:23:VAL:HG12	1:B:24:LYS:H	1.75	0.51
1:B:1059:LEU:HD21	1:B:1074:ILE:HG23	1.92	0.51
2:D:215:VAL:HA	2:D:218:LEU:HG	1.93	0.51
1:A:1078:PRO:HG2	1:A:1081:LYS:NZ	2.25	0.51
1:B:1012:THR:O	1:B:1015:LYS:N	2.42	0.51
1:A:1165:MET:H	2:C:225:LYS:HG2	1.76	0.50
1:B:1099:ILE:HD11	1:B:1119:VAL:HG12	1.94	0.50
1:A:2:PHE:HB3	1:A:85:ASP:HB2	1.93	0.50
1:B:11:PHE:CE2	1:B:43:ALA:HB2	2.47	0.50
1:B:1048:PHE:CE1	1:B:1052:PHE:HD2	2.29	0.50
2:C:192:LEU:HD21	2:C:198:ARG:HA	1.93	0.50
1:A:1164:THR:HG22	2:C:221:LEU:O	2.10	0.50
1:B:66:PHE:CE2	1:B:68:GLY:HA2	2.46	0.49
1:A:39:ASN:OD1	1:A:57:ARG:NH1	2.46	0.49
1:B:1000:ARG:O	1:B:1004:LEU:N	2.45	0.49
1:A:1166:GLN:O	1:A:1167:GLU:C	2.51	0.49
1:B:1038:VAL:O	1:B:1041:ARG:HB2	2.11	0.49
1:A:23:VAL:HG12	1:A:24:LYS:H	1.78	0.49
1:B:1124:ASP:N	1:B:1124:ASP:OD1	2.46	0.48
1:A:1081:LYS:NZ	3:B:1201:AGS:O2'	2.29	0.48
1:B:153:LYS:HE2	1:B:155:GLU:HB2	1.95	0.48
1:A:25:GLY:HA2	1:A:1139:SER:HB2	1.95	0.48
1:B:1165:MET:HG3	1:B:1170:VAL:O	2.13	0.48
1:B:1103:PHE:CE1	1:B:1134:TYR:HB3	2.48	0.48
1:B:1048:PHE:HE2	1:B:1097:THR:HG22	1.79	0.48
1:A:37:LYS:HG3	3:A:1201:AGS:O3G	2.14	0.47
1:A:1090:SER:N	1:A:1093:GLU:HB2	2.28	0.47
1:A:1059:LEU:HD22	1:A:1060:ARG:N	2.30	0.47
1:A:1123:LEU:CD1	1:A:1128:VAL:HG22	2.45	0.47
1:A:1165:MET:HG2	1:A:1168:SER:O	2.14	0.47
1:B:1113:PHE:HA	1:B:1143:GLN:O	2.15	0.47
1:A:35:SER:OG	2:C:225:LYS:NZ	2.43	0.47
1:A:6:LEU:O	1:A:19:SER:HA	2.15	0.47
1:A:40:ILE:O	1:A:44:ILE:HG13	2.15	0.47
1:A:1162:GLY:HA3	2:C:221:LEU:HD13	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1124:ASP:O	1:A:1128:VAL:HG23	2.15	0.46
1:B:1055:GLY:HA2	1:B:1079:PRO:HD3	1.97	0.46
1:B:1048:PHE:CZ	1:B:1052:PHE:CD2	3.03	0.46
2:C:244:GLY:O	2:C:245:SER:HB2	2.14	0.46
2:D:233:GLN:HG3	2:D:240:ILE:HA	1.98	0.46
1:A:1039:GLN:O	1:A:1043:HIS:ND1	2.49	0.46
1:B:1048:PHE:HE2	1:B:1097:THR:CG2	2.29	0.46
1:A:129:MET:HG2	1:A:169:LYS:HG2	1.98	0.46
1:A:1120:GLU:H	1:A:1120:GLU:HG3	1.62	0.46
1:A:78:ALA:O	1:A:103:ARG:HA	2.17	0.45
1:B:1047:VAL:HG13	1:B:1134:TYR:HE2	1.81	0.45
1:A:1047:VAL:HA	1:A:1134:TYR:OH	2.16	0.45
1:A:1165:MET:HG3	1:A:1170:VAL:C	2.38	0.44
1:A:1116:LEU:HB2	1:A:1146:VAL:HG13	1.98	0.44
1:B:1117:ASP:OD1	1:B:1147:ILE:HD12	2.16	0.44
1:B:1154:MET:H	1:B:1154:MET:HG2	1.55	0.44
1:B:1128:VAL:HG21	1:B:1150:ARG:HH11	1.83	0.44
1:A:32:PRO:HG2	2:C:222:GLU:HA	1.99	0.43
1:A:33:ASN:OD1	1:B:1090:SER:OG	2.33	0.43
1:B:8:VAL:HG13	1:B:80:VAL:HG13	2.01	0.43
1:A:158:ARG:NH1	1:A:1070:SER:H	2.17	0.43
1:B:151:SER:HB3	1:B:1094:ARG:NH1	2.33	0.43
1:B:1148:THR:HG22	1:B:1150:ARG:H	1.83	0.43
1:A:58:GLY:CA	1:A:63:ASP:HB2	2.49	0.42
1:B:1111:VAL:O	1:B:1142:THR:HB	2.19	0.42
1:A:93:ILE:HG22	1:A:94:ASP:H	1.83	0.42
1:A:1102:LEU:HA	1:A:1102:LEU:HD23	1.68	0.42
1:B:83:THR:HA	1:B:98:VAL:O	2.19	0.42
1:A:1059:LEU:C	1:A:1059:LEU:HD13	2.40	0.42
1:A:8:VAL:HG12	1:A:80:VAL:HG22	2.00	0.42
1:B:1059:LEU:HA	1:B:1059:LEU:HD13	1.83	0.42
1:A:1047:VAL:HG13	1:A:1134:TYR:CE1	2.55	0.42
1:A:1069:HIS:ND1	1:A:1069:HIS:N	2.68	0.42
1:B:5:ARG:O	1:B:6:LEU:HD23	2.19	0.42
1:A:81:THR:HB	1:A:101:THR:HG22	2.02	0.42
1:A:32:PRO:HD2	2:C:225:LYS:HE3	2.00	0.41
1:B:41:THR:HB	1:B:1115:VAL:HG11	2.01	0.41
1:B:11:PHE:O	1:B:14:PHE:N	2.48	0.41
1:A:33:ASN:ND2	1:B:1124:ASP:OD1	2.46	0.41
1:B:1005:SER:O	1:B:1009:GLU:N	2.51	0.41
1:B:1048:PHE:CZ	1:B:1052:PHE:HD2	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1129:PHE:O	1:B:1133:GLN:HG2	2.20	0.41
1:B:1048:PHE:CD1	1:B:1055:GLY:HA3	2.56	0.41
1:A:1115:VAL:HA	1:A:1145:ILE:O	2.20	0.41
1:A:38:SER:HB3	1:A:57:ARG:HH22	1.85	0.41
1:B:154:ALA:HA	1:B:157:ARG:HG2	2.03	0.41
1:B:157:ARG:O	1:B:160:ILE:HG22	2.21	0.41
1:B:1164:THR:HG22	2:D:221:LEU:HA	2.02	0.41
1:B:140:ILE:HG21	1:B:140:ILE:HD13	1.71	0.40
1:B:1116:LEU:N	1:B:1145:ILE:O	2.55	0.40
1:B:1118:GLN:OE1	1:B:1148:THR:HA	2.21	0.40
1:A:1135:LEU:HD23	1:A:1135:LEU:HA	1.93	0.40
1:A:57:ARG:CZ	3:A:1201:AGS:O1A	2.69	0.40
2:C:231:ILE:HG23	2:C:241:TYR:O	2.22	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	349/435 (80%)	326 (93%)	23 (7%)	0	100 100
1	B	358/435 (82%)	322 (90%)	30 (8%)	6 (2%)	9 42
2	C	64/89 (72%)	59 (92%)	5 (8%)	0	100 100
2	D	45/89 (51%)	41 (91%)	4 (9%)	0	100 100
All	All	816/1048 (78%)	748 (92%)	62 (8%)	6 (1%)	22 61

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1063	ASP
1	B	1064	PRO

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Mol	Chain	Res	Type
1	B	1082	LYS
1	B	117	GLN
1	B	1044	PHE
1	B	30	VAL

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	182/381 (48%)	168 (92%)	14 (8%)	13	42
1	B	192/381 (50%)	172 (90%)	20 (10%)	7	31
2	C	38/83 (46%)	37 (97%)	1 (3%)	46	74
2	D	19/83 (23%)	18 (95%)	1 (5%)	22	55
All	All	431/928 (46%)	395 (92%)	36 (8%)	11	40

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	LYS
1	A	87	ASP
1	A	156	ASP
1	A	170	TYR
1	A	1045	ASP
1	A	1063	ASP
1	A	1087	ASN
1	A	1097	THR
1	A	1101	LEU
1	A	1102	LEU
1	A	1120	GLU
1	A	1123	LEU
1	A	1143	GLN
1	A	1149	HIS
1	B	8	VAL
1	B	21	ASP
1	B	23	VAL

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Mol	Chain	Res	Type
1	B	39	ASN
1	B	46	TRP
1	B	48	LEU
1	B	77	LEU
1	B	93	ILE
1	B	142	SER
1	B	1018	LEU
1	B	1026	ASP
1	B	1036	THR
1	B	1090	SER
1	B	1096	LEU
1	B	1097	THR
1	B	1114	CYS
1	B	1120	GLU
1	B	1124	ASP
1	B	1142	THR
1	B	1154	MET
2	C	237	PHE
2	D	233	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	33	ASN
1	B	39	ASN
1	B	1084	GLN
2	D	233	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 5 ligands modelled in this entry, 3 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	$\#\|Z\| > 2$
3	AGS	A	1201	4	26,33,33	0.83	0	26,52,52	1.28	3 (11%)
3	AGS	B	1201	4	26,33,33	0.75	1 (3%)	26,52,52	1.59	5 (19%)

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
3	AGS	A	1201	4	-	2/17/38/38	0/3/3/3
3	AGS	B	1201	4	-	2/17/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1201	AGS	C4-N3	-2.06	1.32	1.35

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1201	AGS	O5'-PA-O1A	3.55	122.92	109.07
3	B	1201	AGS	PA-O3A-PB	-3.51	120.78	132.83
3	A	1201	AGS	PA-O3A-PB	-3.27	121.61	132.83
3	A	1201	AGS	O2G-PG-O3B	2.96	114.53	104.64
3	B	1201	AGS	O2G-PG-O3B	2.88	114.25	104.64
3	A	1201	AGS	C5-C6-N6	2.85	124.68	120.35
3	B	1201	AGS	C3'-C2'-C1'	2.57	104.85	100.98
3	B	1201	AGS	C5-C6-N6	2.49	124.13	120.35

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1201	AGS	O4'-C4'-C5'-O5'
3	A	1201	AGS	C3'-C4'-C5'-O5'
3	B	1201	AGS	O4'-C4'-C5'-O5'
3	B	1201	AGS	C3'-C4'-C5'-O5'

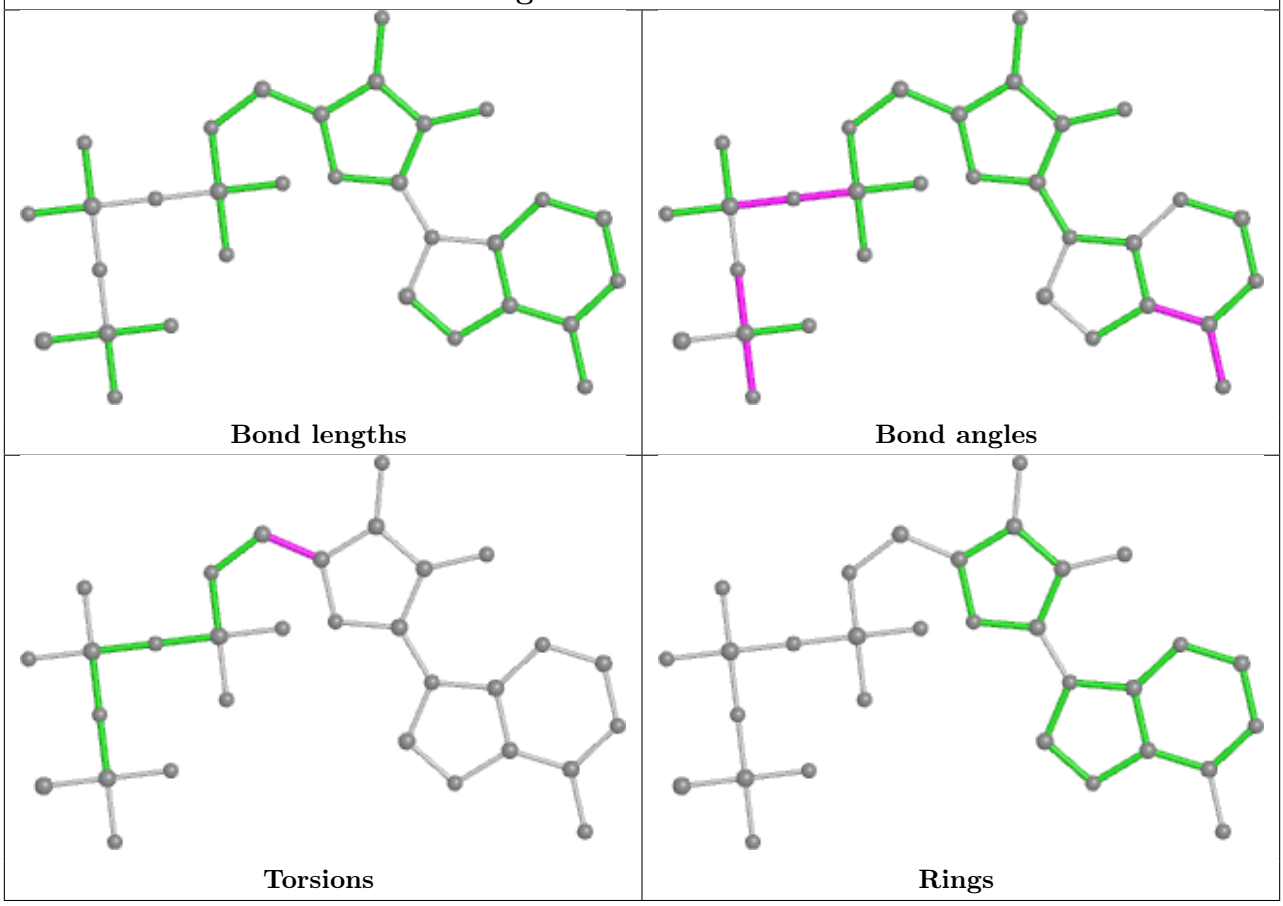
There are no ring outliers.

2 monomers are involved in 8 short contacts:

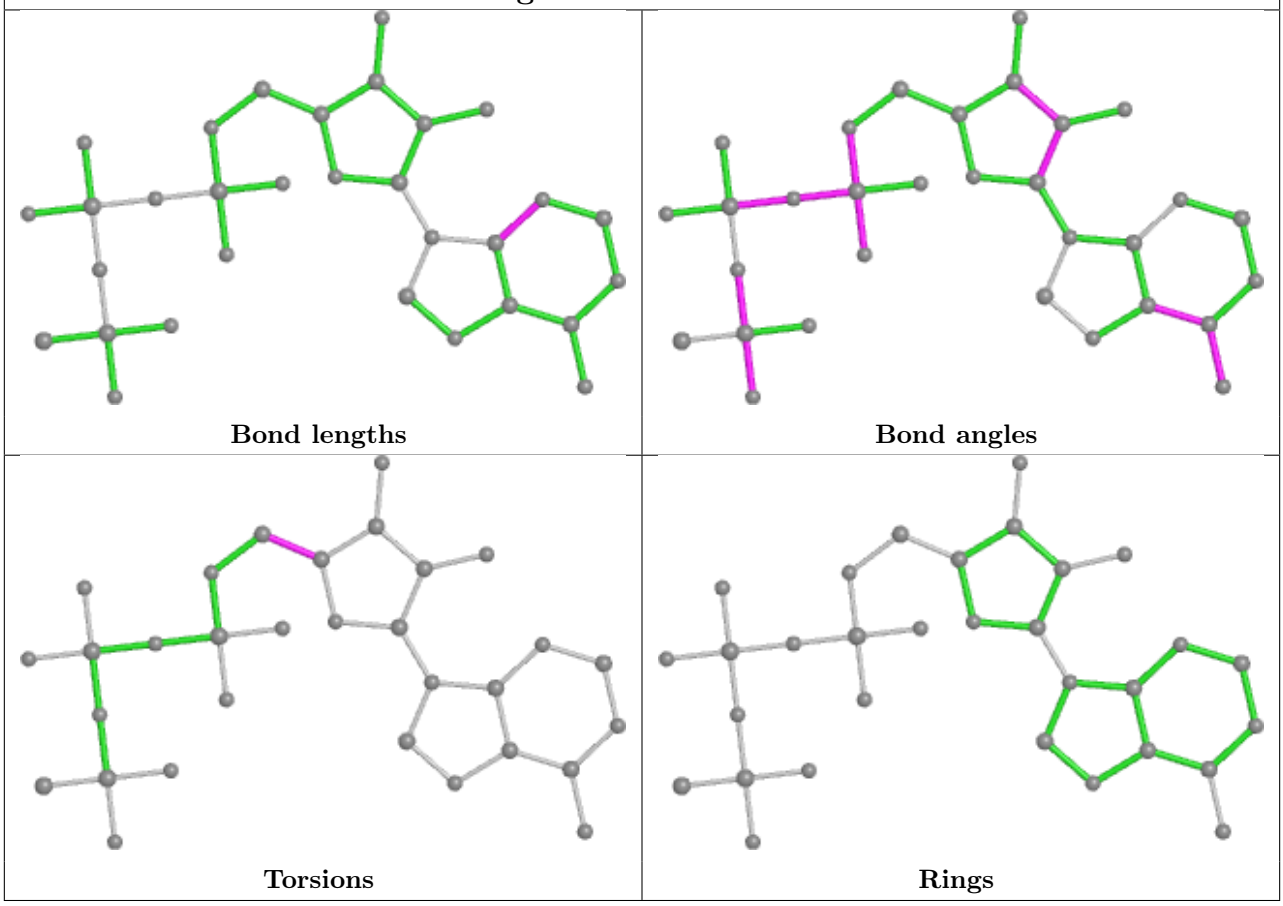
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1201	AGS	5	0
3	B	1201	AGS	3	0

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 then 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.

Ligand AGS A 1201



Ligand AGS B 1201



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)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

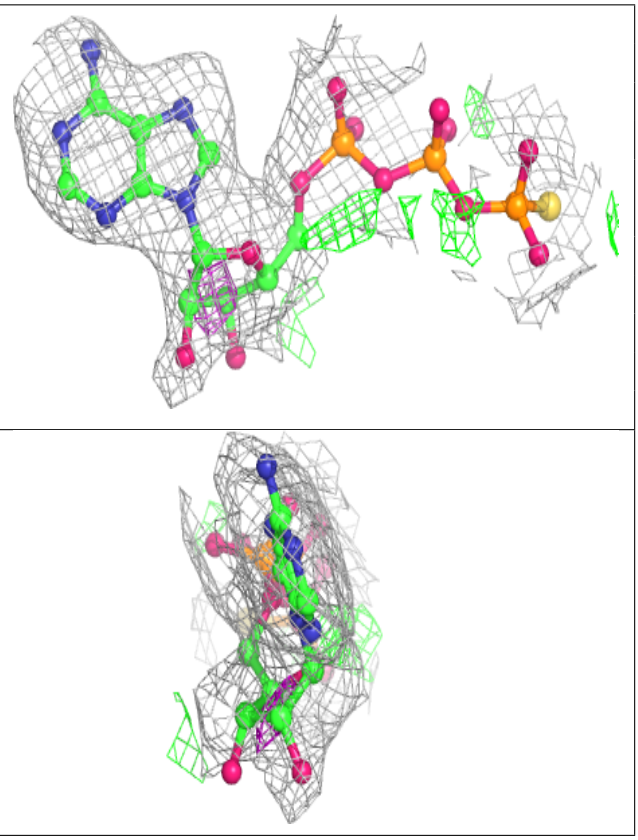
6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

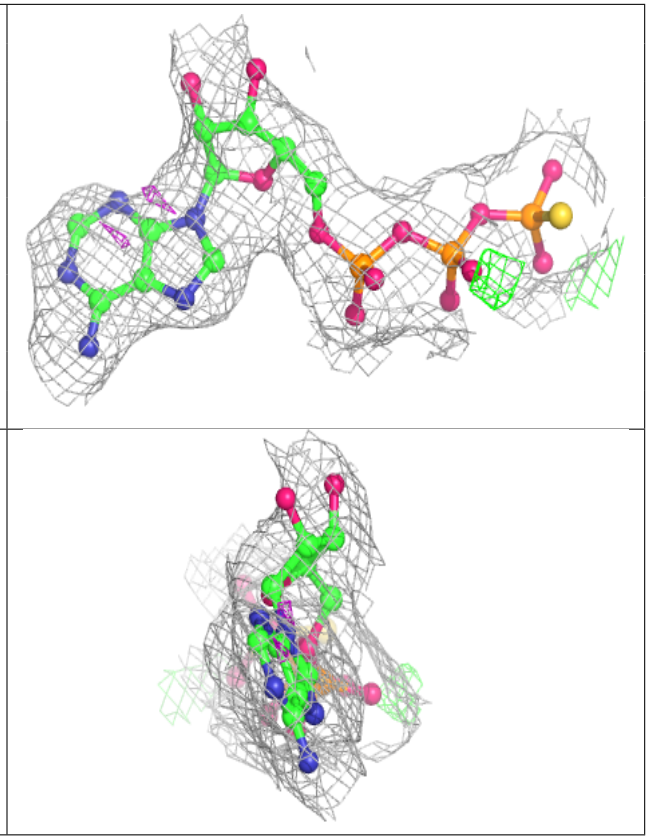
Electron density around AGS A 1201:

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



Electron density around AGS B 1201:

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



6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.