Full wwPDB X-ray Structure Validation Report (i)

Jun 24, 2024 – 07:51 AM EDT

PDB ID	:	6ZSI
Title	:	The mechanism of activation of the actin binding protein EHBP1 by Rab8 family members.
Authors	:	Rai, A.; Bleimling, N.; Vetter, I.R.; Goody, R.S.
Deposited on	:	2020-07-15
Resolution	:	1.91 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:

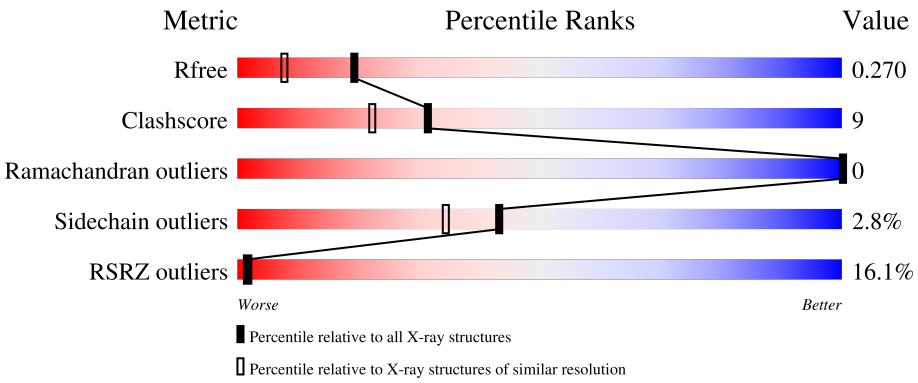
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.91 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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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% 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	178	15% 75% 21% • •
1	B	178	% 89% 8% •
2	C	156	28% 60% 20% • 17%
2	D	156	17% 67% 16% • 15%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5111 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 Ras-related protein Rab-8A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	171	1392	887	236	262	7	0	2	0
1	B	173	1408	896	243	262	7	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P61006
A	0	HIS	-	expression tag	UNP P61006
B	-1	GLY	-	expression tag	UNP P61006
B	0	HIS	-	expression tag	UNP P61006

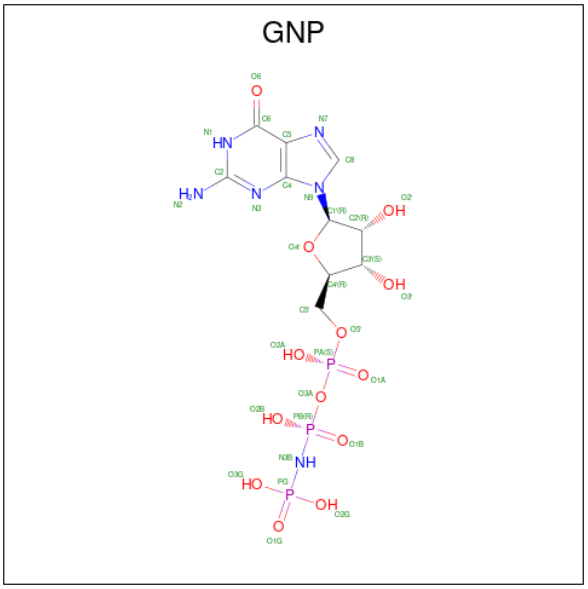
- Molecule 2 is a protein called EH domain-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	130	1081	668	201	207	5	0	0	0
2	D	133	1108	683	204	216	5	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

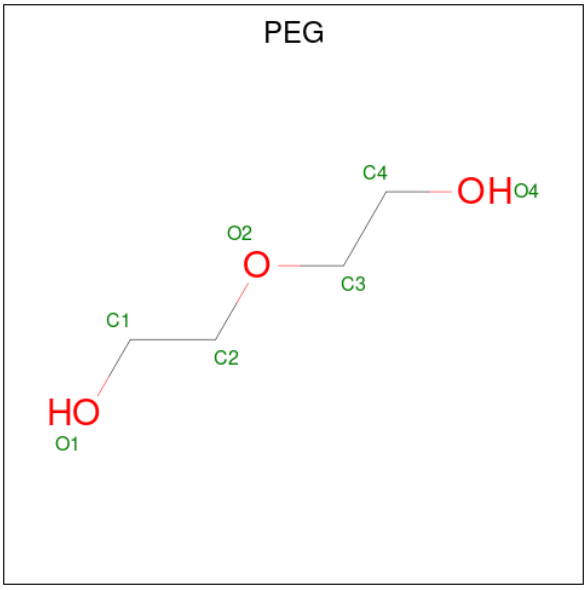
Chain	Residue	Modelled	Actual	Comment	Reference
C	1057	GLY	-	expression tag	UNP Q8NDI1
C	1058	HIS	-	expression tag	UNP Q8NDI1
C	1059	MET	-	expression tag	UNP Q8NDI1
C	1116	ALA	MET	engineered mutation	UNP Q8NDI1
D	1057	GLY	-	expression tag	UNP Q8NDI1
D	1058	HIS	-	expression tag	UNP Q8NDI1
D	1059	MET	-	expression tag	UNP Q8NDI1
D	1116	ALA	MET	engineered mutation	UNP Q8NDI1

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	7	4	3	0	0
			Total	C	O		
4	B	1	7	4	3	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 6 is water.

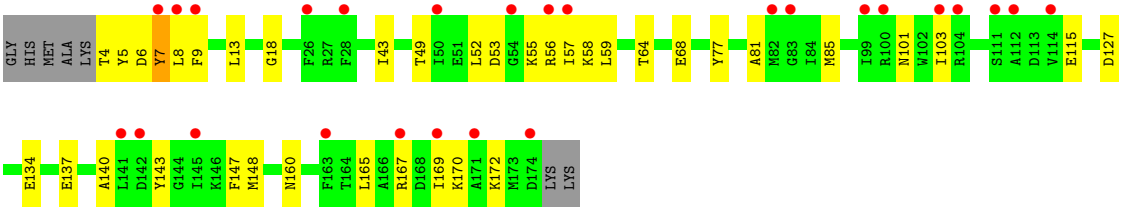
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	18	18	18	0	0
			Total	O		
6	B	22	22	22	0	0
			Total	O		
6	D	2	2	2	0	0

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: Ras-related protein Rab-8A

Chain A:

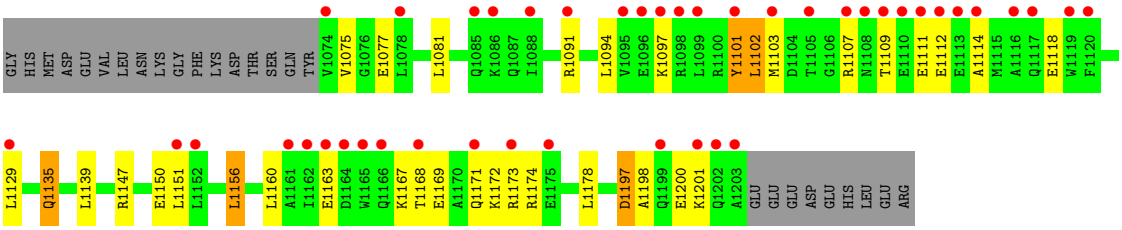


• Molecule 1: Ras-related protein Rab-8A

Chain B:

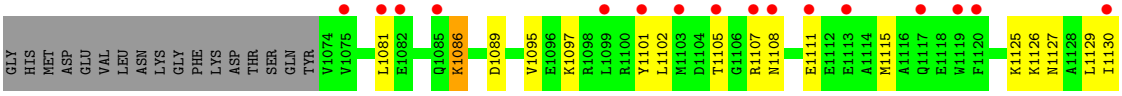
• Molecule 2: EH domain-binding protein 1

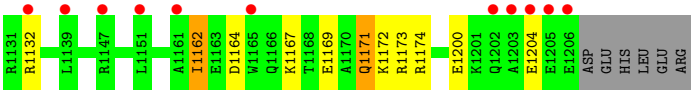
Chain C:



• Molecule 2: EH domain-binding protein 1

Chain D:




R1131
R1132
L1139
R1147
L1151
A1161
I1162
E1163
D1164
W1165
Q1166
K1167
T1168
E1169
A1170
Q1171
K1172
R1173
R1174
E1200
K1201
Q1202
A1203
E1204
E1205
E1206
ASP
GLU
HIS
LEU
GLU
ARG

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	116.36Å 35.38Å 165.67Å 90.00° 93.76° 90.00°	Depositor
Resolution (Å)	46.11 – 1.91 49.04 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.5 (46.11-1.91) 99.5 (49.04-1.91)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.99 (at 1.91Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.223 , 0.267 0.230 , 0.270	Depositor DCC
R_{free} test set	2630 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	41.5	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 55.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5111	wwPDB-VP
Average B, all atoms (Å^2)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.34% 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: MG, PEG, GNP

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	0.54	0/1419	0.67	0/1904
1	B	0.50	0/1432	0.60	1/1918 (0.1%)
2	C	0.41	0/1088	0.63	0/1457
2	D	0.34	0/1115	0.52	0/1493
All	All	0.46	0/5054	0.61	1/6772 (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
2	D	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	89	ASP	CB-CG-OD1	5.73	123.46	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	1204	GLU	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	1392	0	1401	38	0
1	B	1408	0	1425	9	0
2	C	1081	0	1104	25	0
2	D	1108	0	1122	22	0
3	A	32	0	13	1	0
3	B	32	0	13	0	0
4	A	7	0	10	1	0
4	B	7	0	10	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	18	0	0	1	0
6	B	22	0	0	1	0
6	D	2	0	0	0	0
All	All	5111	0	5098	91	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 9.

All (91) 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:C:1169:GLU:HA	2:C:1172:LYS:HD2	1.44	0.95
1:A:7:TYR:CE2	1:A:55:LYS:HE3	2.10	0.86
2:C:1091:ARG:NH2	2:C:1118:GLU:OE2	2.09	0.85
2:D:1101:TYR:OH	2:D:1107:ARG:NH1	2.11	0.82
1:A:4:THR:HG23	1:A:56:ARG:NH1	1.99	0.78
1:A:81:ALA:O	6:A:301:HOH:O	2.04	0.75
1:A:68:GLU:N	1:A:68:GLU:OE1	2.19	0.75
1:B:67:GLN:HG3	6:B:318:HOH:O	1.87	0.73
1:A:7:TYR:HD2	1:A:57[A]:ILE:HG13	1.54	0.72
2:D:1169:GLU:OE1	2:D:1173:ARG:NH1	2.22	0.72
1:A:115:GLU:OE1	1:A:172:LYS:NZ	2.22	0.72
2:C:1103:MET:HE1	2:C:1112:GLU:HG3	1.76	0.68
1:A:53:ASP:OD1	1:A:167:ARG:NH2	2.29	0.66
1:A:169:ILE:HA	1:A:172:LYS:HZ1	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:THR:HG23	1:A:56:ARG:HH12	1.61	0.65
2:D:1162:ILE:HD11	2:D:1167:LYS:HG2	1.76	0.65
2:D:1102:LEU:HD22	2:D:1108:ASN:HB2	1.80	0.64
1:A:5:TYR:OH	2:C:1197:ASP:HB2	1.98	0.63
1:A:169:ILE:HA	1:A:172:LYS:NZ	2.14	0.62
2:D:1095:VAL:HA	2:D:1115:MET:HE1	1.83	0.61
2:C:1198:ALA:O	2:C:1201:LYS:HD2	2.00	0.61
1:A:7:TYR:CD2	1:A:57[A]:ILE:HG13	2.36	0.60
1:A:13:LEU:HD23	1:A:85:MET:HB2	1.83	0.60
2:C:1169:GLU:OE2	2:C:1173:ARG:HB2	2.01	0.60
2:D:1169:GLU:HA	2:D:1172:LYS:HE2	1.86	0.58
1:A:52:LEU:HB3	1:A:57[A]:ILE:HD13	1.86	0.57
2:D:1108:ASN:HB3	2:D:1111:GLU:OE1	2.04	0.57
1:A:6:ASP:HB3	1:A:7:TYR:CZ	2.40	0.57
1:A:8:LEU:HD23	1:A:58:LYS:HE2	1.87	0.56
2:D:1111:GLU:H	2:D:1111:GLU:CD	2.08	0.55
1:A:165:LEU:O	1:A:169:ILE:HG12	2.06	0.55
2:C:1198:ALA:HA	2:C:1201:LYS:HE3	1.89	0.54
2:D:1164:ASP:O	2:D:1172:LYS:NZ	2.41	0.54
1:B:71:ARG:O	1:B:75:THR:HG23	2.07	0.54
1:A:140:ALA:CB	1:A:147:PHE:HB2	2.38	0.54
2:C:1077:GLU:O	2:C:1081:LEU:HD13	2.08	0.53
1:A:5:TYR:HA	1:A:56:ARG:NE	2.24	0.52
2:D:1171:GLN:HG3	2:D:1174:ARG:HH12	1.74	0.52
2:D:1127:ASN:O	2:D:1130:ILE:HG13	2.10	0.52
2:C:1102:LEU:HD23	2:C:1112:GLU:HB2	1.92	0.51
1:A:7:TYR:HE2	1:A:55:LYS:HG3	1.75	0.51
2:C:1094:LEU:HA	2:C:1097:LYS:HE3	1.91	0.51
2:C:1101:TYR:OH	2:C:1107:ARG:NH1	2.44	0.50
1:A:43:ILE:HD13	1:A:77:TYR:CD2	2.47	0.49
2:C:1168:THR:OG1	2:C:1171:GLN:HG3	2.13	0.49
1:B:4:THR:OG1	2:D:1200:GLU:OE2	2.22	0.49
1:A:9:PHE:HB2	1:A:59:LEU:HD23	1.94	0.49
1:B:13:LEU:HD23	1:B:85:MET:HB2	1.94	0.49
1:A:101:ASN:HB3	4:A:202:PEG:H22	1.93	0.49
1:B:75:THR:HA	1:B:78:TYR:CE1	2.48	0.49
1:A:6:ASP:HB2	1:A:56:ARG:O	2.13	0.48
1:A:55:LYS:HE2	1:A:170:LYS:CE	2.43	0.48
1:B:75:THR:HA	1:B:78:TYR:CD1	2.49	0.48
2:D:1089:ASP:HB3	2:D:1126:LYS:HE3	1.96	0.48
2:D:1107:ARG:O	2:D:1108:ASN:ND2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:TYR:CZ	1:A:55:LYS:HE3	2.49	0.46
2:D:1167:LYS:O	2:D:1172:LYS:NZ	2.37	0.46
2:D:1171:GLN:HG3	2:D:1174:ARG:NH1	2.30	0.46
1:B:140:ALA:CB	1:B:147:PHE:HB2	2.46	0.45
2:C:1156:LEU:HD22	2:C:1160:LEU:HG	1.98	0.45
1:A:5:TYR:HA	1:A:56:ARG:CD	2.46	0.45
1:A:43:ILE:HD12	1:A:64:THR:HG22	1.98	0.45
1:A:127:ASP:OD1	1:A:127:ASP:N	2.50	0.45
2:C:1168:THR:HG23	2:C:1171:GLN:NE2	2.32	0.45
2:C:1135:GLN:O	2:C:1139:LEU:HD23	2.17	0.44
1:A:4:THR:HA	2:C:1200:GLU:OE2	2.18	0.44
1:B:79:ARG:NH1	1:B:111:SER:OG	2.51	0.43
1:A:49:THR:HA	1:A:58:LYS:HA	2.00	0.43
1:A:148:MET:HE1	1:A:160:ASN:HB3	2.01	0.43
2:C:1156:LEU:CD2	2:C:1160:LEU:HG	2.49	0.43
2:D:1086:LYS:HA	2:D:1089:ASP:OD1	2.19	0.43
2:D:1125:LYS:O	2:D:1129:LEU:HB2	2.18	0.42
2:D:1089:ASP:OD1	2:D:1089:ASP:N	2.50	0.42
2:D:1105:THR:C	2:D:1107:ARG:H	2.22	0.42
2:C:1198:ALA:HA	2:C:1201:LYS:CE	2.49	0.42
2:C:1147:ARG:O	2:C:1151:LEU:HG	2.19	0.42
2:C:1109:THR:HA	2:C:1112:GLU:HB3	2.02	0.42
2:C:1102:LEU:HD21	2:C:1111:GLU:HG2	2.01	0.42
1:A:52:LEU:HD11	1:A:167:ARG:CG	2.49	0.42
2:C:1111:GLU:O	2:C:1114:ALA:HB3	2.20	0.41
2:C:1081:LEU:HB3	2:C:1129:LEU:HD11	2.01	0.41
2:C:1150:GLU:HG2	2:C:1151:LEU:HD23	2.03	0.41
1:A:6:ASP:CB	1:A:7:TYR:CE2	3.03	0.41
2:D:1081:LEU:HD13	2:D:1132:ARG:HG2	2.02	0.41
2:C:1174:ARG:O	2:C:1178:LEU:HG	2.21	0.41
1:B:3:LYS:HD2	1:B:3:LYS:HA	1.73	0.40
2:D:1097:LYS:HA	2:D:1097:LYS:HD2	1.95	0.40
1:A:103:ILE:HD13	1:A:143:TYR:CZ	2.56	0.40
1:A:6:ASP:HB3	1:A:7:TYR:CE2	2.56	0.40
1:A:18:GLY:H	3:A:201:GNP:HNB3	1.68	0.40
1:A:137:GLU:HG3	1:A:147:PHE:CD2	2.57	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	171/178 (96%)	167 (98%)	4 (2%)	0	100	100
1	B	172/178 (97%)	170 (99%)	2 (1%)	0	100	100
2	C	128/156 (82%)	124 (97%)	4 (3%)	0	100	100
2	D	131/156 (84%)	128 (98%)	3 (2%)	0	100	100
All	All	602/668 (90%)	589 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	150/153 (98%)	148 (99%)	2 (1%)	69	66
1	B	151/153 (99%)	148 (98%)	3 (2%)	55	49
2	C	114/138 (83%)	106 (93%)	8 (7%)	15	6
2	D	117/138 (85%)	114 (97%)	3 (3%)	46	37
All	All	532/582 (91%)	516 (97%)	16 (3%)	43	31

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	TYR
1	A	134	GLU

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Mol	Chain	Res	Type
1	B	37	PHE
1	B	69[A]	ARG
1	B	69[B]	ARG
2	C	1075	VAL
2	C	1101	TYR
2	C	1102	LEU
2	C	1135	GLN
2	C	1156	LEU
2	C	1163	GLU
2	C	1167	LYS
2	C	1197	ASP
2	D	1086	LYS
2	D	1162	ILE
2	D	1171	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	67	GLN
2	D	1108	ASN

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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	GNP	A	201	5	29,34,34	1.89	7 (24%)	33,54,54	2.58	10 (30%)
4	PEG	B	202	-	6,6,6	0.52	0	5,5,5	0.32	0
3	GNP	B	201	5	29,34,34	1.79	4 (13%)	33,54,54	2.46	7 (21%)
4	PEG	A	202	-	6,6,6	0.49	0	5,5,5	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
3	GNP	A	201	5	-	3/14/38/38	0/3/3/3
4	PEG	B	202	-	-	2/4/4/4	-
3	GNP	B	201	5	-	3/14/38/38	0/3/3/3
4	PEG	A	202	-	-	3/4/4/4	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	201	GNP	C6-N1	4.93	1.41	1.33
3	A	201	GNP	C6-N1	4.91	1.41	1.33
3	A	201	GNP	PG-O1G	4.67	1.53	1.46
3	B	201	GNP	PG-O1G	4.20	1.52	1.46
3	A	201	GNP	PB-O2B	-3.93	1.46	1.56
3	B	201	GNP	PB-O3A	-3.46	1.54	1.59
3	B	201	GNP	PB-O2B	-2.84	1.49	1.56
3	A	201	GNP	C8-N7	-2.67	1.29	1.34
3	A	201	GNP	PG-O2G	-2.47	1.50	1.56
3	A	201	GNP	PA-O3A	-2.22	1.57	1.59
3	A	201	GNP	PB-O1B	2.12	1.49	1.46

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	201	GNP	C5-C6-N1	-9.47	110.76	123.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	201	GNP	C5-C6-N1	-9.29	111.00	123.42
3	B	201	GNP	C2-N1-C6	6.01	124.32	115.96
3	A	201	GNP	C2-N1-C6	5.51	123.62	115.96
3	A	201	GNP	O1G-PG-N3B	-4.95	104.48	111.77
3	A	201	GNP	C2-N3-C4	-4.33	110.81	115.48
3	B	201	GNP	C2-N3-C4	-3.71	111.49	115.48
3	B	201	GNP	O2B-PB-O1B	3.42	117.19	109.87
3	A	201	GNP	O2B-PB-O1B	3.31	116.97	109.87
3	A	201	GNP	O1B-PB-N3B	-3.24	107.00	111.77
3	B	201	GNP	O1G-PG-N3B	-3.11	107.19	111.77
3	A	201	GNP	O2G-PG-O3G	2.70	114.85	107.59
3	B	201	GNP	O3G-PG-O1G	-2.68	106.73	113.45
3	B	201	GNP	O2B-PB-O3A	2.60	113.33	104.64
3	A	201	GNP	O4'-C1'-N9	2.55	112.12	108.75
3	A	201	GNP	O3G-PG-O1G	-2.43	107.37	113.45
3	A	201	GNP	O2B-PB-O3A	2.39	112.62	104.64

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	201	GNP	PG-N3B-PB-O1B
3	A	201	GNP	PA-O3A-PB-O2B
3	B	201	GNP	PG-N3B-PB-O1B
3	B	201	GNP	PA-O3A-PB-O2B
4	B	202	PEG	O1-C1-C2-O2
4	A	202	PEG	O1-C1-C2-O2
4	A	202	PEG	C1-C2-O2-C3
4	A	202	PEG	O2-C3-C4-O4
4	B	202	PEG	O2-C3-C4-O4
3	A	201	GNP	PA-O3A-PB-O1B
3	B	201	GNP	PA-O3A-PB-O1B

There are no ring outliers.

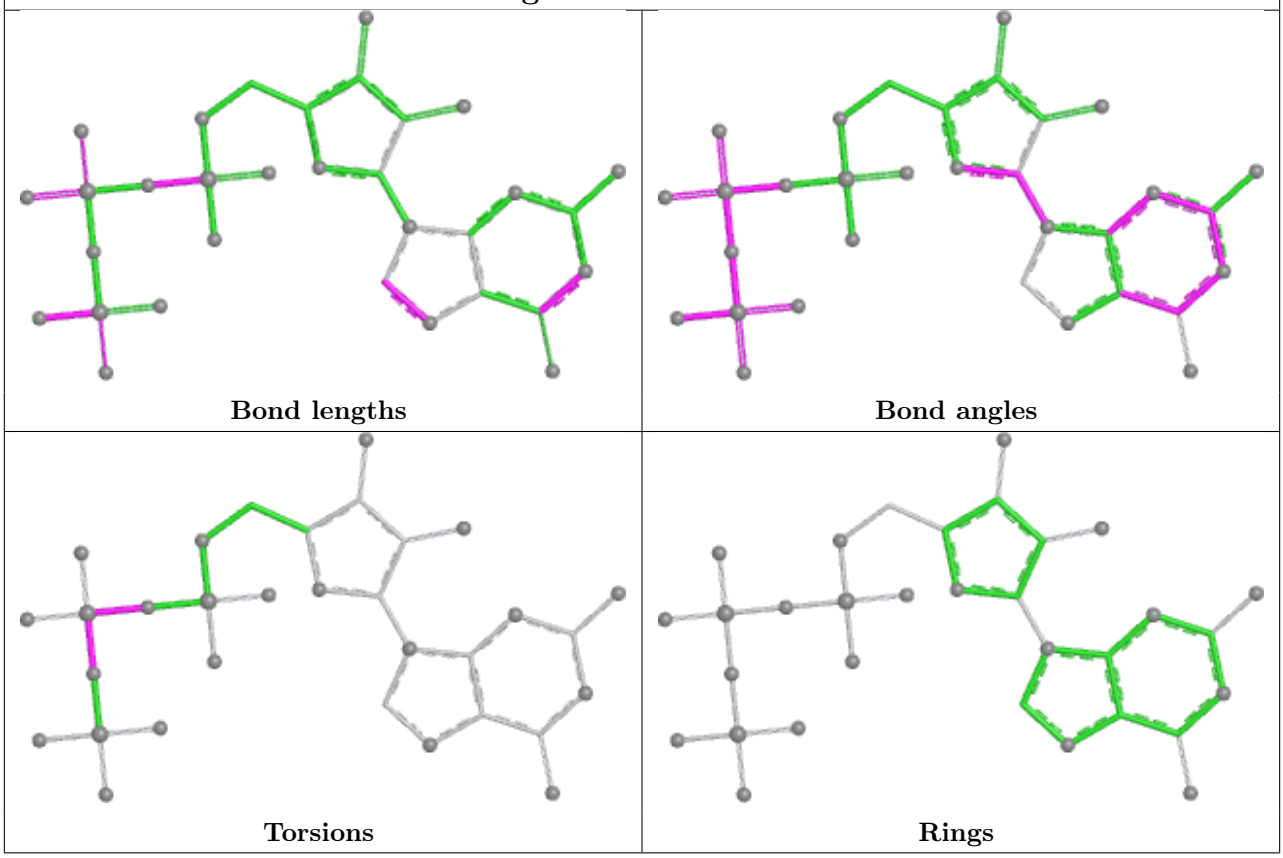
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	201	GNP	1	0
4	A	202	PEG	1	0

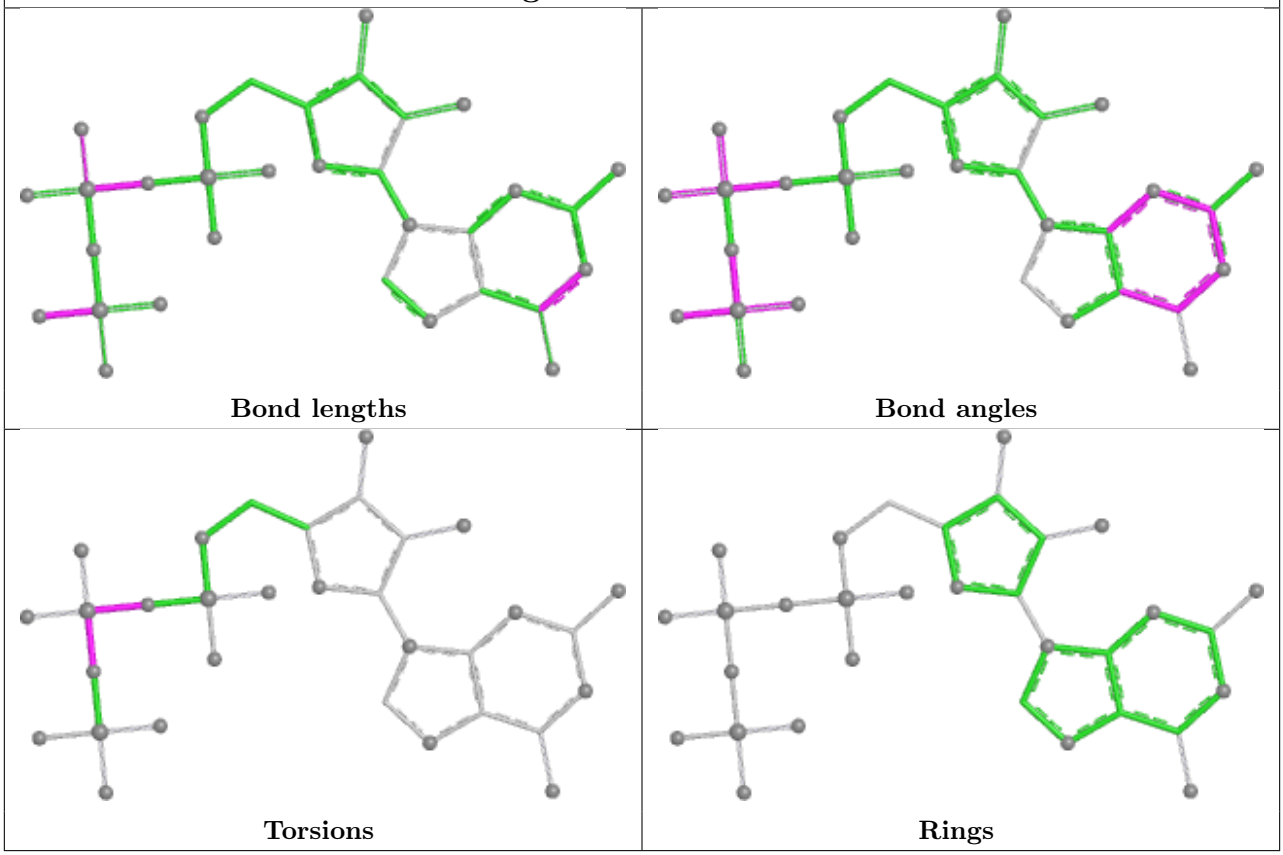
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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 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 GNP A 201



Ligand GNP B 201



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	171/178 (96%)	1.14	26 (15%)	2	2	31, 61, 124, 162	0
1	B	173/178 (97%)	0.54	2 (1%)	79	81	29, 46, 69, 94	0
2	C	130/156 (83%)	1.81	43 (33%)	0	0	47, 88, 139, 151	0
2	D	133/156 (85%)	1.19	27 (20%)	1	1	43, 79, 123, 142	0
All	All	607/668 (90%)	1.13	98 (16%)	1	2	29, 66, 126, 162	0

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	54	GLY	14.2
2	C	1103	MET	9.4
2	C	1099	LEU	8.9
2	C	1108	ASN	7.5
2	C	1109	THR	7.0
1	A	7	TYR	6.3
2	D	1108	ASN	6.2
2	D	1206	GLU	5.9
2	C	1107	ARG	5.2
2	D	1099	LEU	5.0
1	A	174	ASP	4.9
2	C	1165	TRP	4.8
2	D	1205	GLU	4.8
1	A	167	ARG	4.7
2	C	1117	GLN	4.7
1	A	83	GLY	4.6
1	A	112	ALA	4.4
2	C	1120	PHE	4.1
2	C	1203	ALA	4.1
2	C	1110	GLU	4.0
1	A	145	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
2	C	1078	LEU	3.8
2	C	1113	GLU	3.8
1	B	26	PHE	3.7
2	C	1101	TYR	3.7
2	C	1168	THR	3.7
2	C	1074	VAL	3.7
2	C	1119	TRP	3.7
2	D	1101	TYR	3.7
2	D	1203	ALA	3.6
2	C	1129	LEU	3.6
2	C	1105	THR	3.5
2	D	1120	PHE	3.5
2	C	1164	ASP	3.5
2	C	1161	ALA	3.5
2	C	1151	LEU	3.5
2	D	1204	GLU	3.5
1	A	100	ARG	3.4
1	A	56	ARG	3.3
1	A	26	PHE	3.2
1	A	103	ILE	3.2
1	A	9	PHE	3.1
1	A	169	ILE	3.1
1	A	8	LEU	3.0
2	D	1147	ARG	3.0
2	C	1201	LYS	3.0
1	A	50	ILE	3.0
2	C	1086	LYS	3.0
2	C	1112	GLU	3.0
2	C	1166	GLN	3.0
1	A	28	PHE	2.9
2	D	1085	GLN	2.9
2	D	1132	ARG	2.8
2	D	1119	TRP	2.8
2	C	1085	GLN	2.8
2	C	1088	ILE	2.8
2	D	1165	TRP	2.8
1	A	57[A]	ILE	2.7
2	C	1163	GLU	2.7
2	C	1111	GLU	2.6
1	A	141	LEU	2.6
1	A	82	MET	2.6
2	C	1202	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
2	C	1096	GLU	2.6
1	A	171	ALA	2.5
2	C	1199	GLN	2.5
2	C	1173	ARG	2.5
2	D	1117	GLN	2.4
2	C	1175	GLU	2.4
2	D	1151	LEU	2.4
2	C	1095	VAL	2.4
1	A	163	PHE	2.4
2	D	1202	GLN	2.4
2	D	1111	GLU	2.4
2	C	1098	ARG	2.4
2	D	1105	THR	2.4
2	D	1082	GLU	2.4
1	A	104	ARG	2.3
2	D	1139	LEU	2.3
2	D	1161	ALA	2.3
2	D	1075	VAL	2.3
2	C	1116	ALA	2.3
2	D	1113	GLU	2.3
2	C	1171	GLN	2.3
2	C	1114	ALA	2.3
2	D	1130	ILE	2.2
2	D	1103	MET	2.2
1	A	99	ILE	2.2
1	A	111	SER	2.2
2	C	1097	LYS	2.2
1	B	163	PHE	2.2
2	D	1081	LEU	2.1
2	C	1162	ILE	2.1
2	D	1107	ARG	2.0
1	A	114	VAL	2.0
2	C	1152	LEU	2.0
1	A	142[A]	ASP	2.0
2	C	1091	ARG	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)

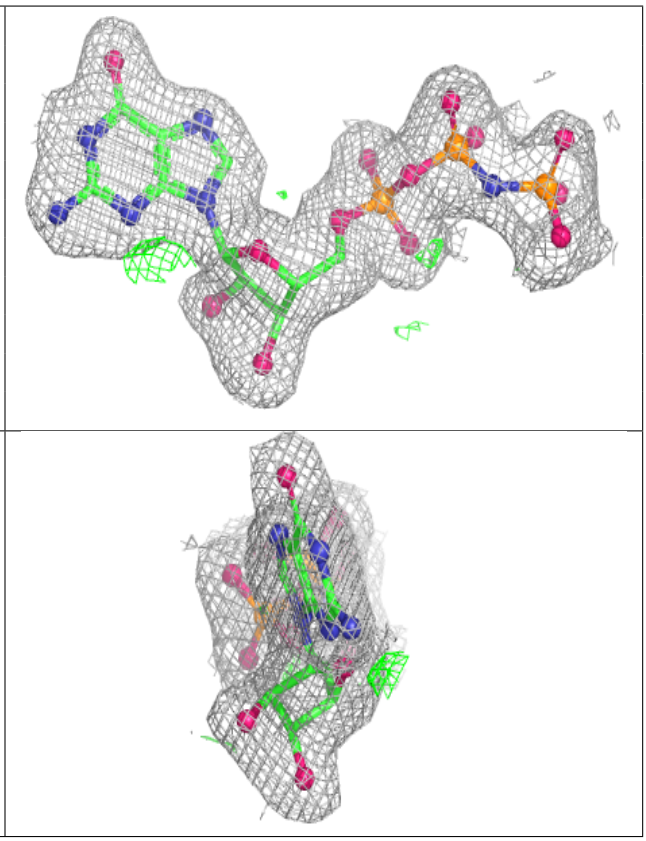
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	PEG	A	202	7/7	0.85	0.15	51,67,70,76	0
4	PEG	B	202	7/7	0.94	0.15	44,47,51,56	0
5	MG	B	203	1/1	0.96	0.15	35,35,35,35	0
5	MG	A	203	1/1	0.97	0.09	37,37,37,37	0
3	GNP	A	201	32/32	0.97	0.14	30,34,45,46	0
3	GNP	B	201	32/32	0.98	0.13	28,33,40,44	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.

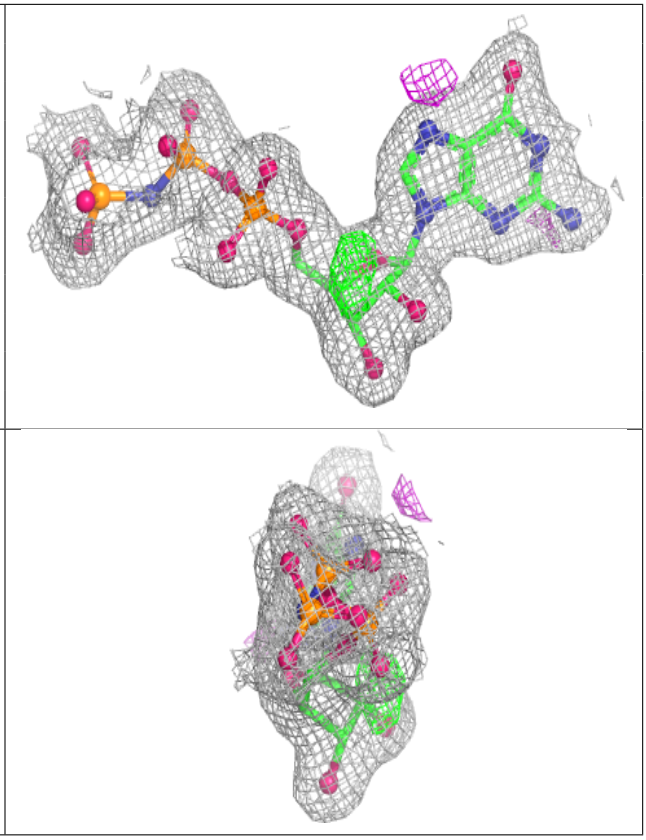
Electron density around GNP A 201:

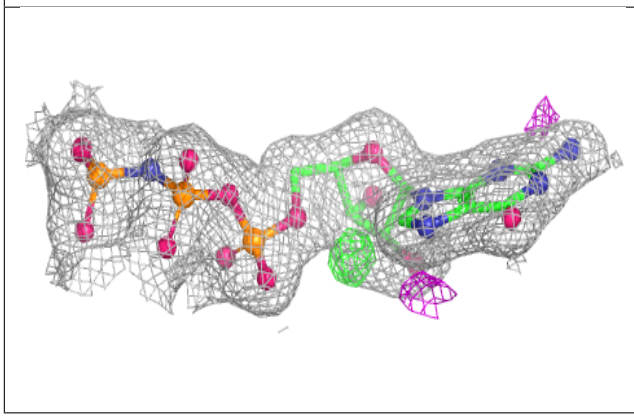
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



Electron density around GNP B 201:

$2mF_o$-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)

There are no such residues in this entry.