



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 06:46 pm BST

PDB ID : 6OB2  
Title : Crystal structure of wild-type KRAS (GMPPNP-bound) in complex with  
GAP-related domain (GRD) of neurofibromin (NF1)  
Authors : Tran, T.H.; Dharmaiah, S.; Simanshu, D.K.  
Deposited on : 2019-03-19  
Resolution : 2.85 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

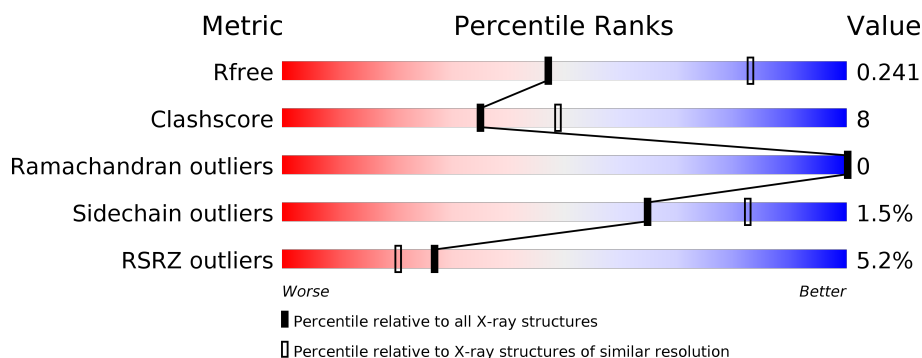
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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	1031 (2.86-2.82)
Clashscore	141614	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)
RSRZ outliers	127900	1019 (2.86-2.82)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	170	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 88%, yellow 11%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>88%</span> <span>11% ..</span> </div> </div>
1	C	170	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 22%, green 79%, yellow 17%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>22%</span> <span>79%</span> <span>17% ..</span> </div> </div>
2	B	256	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 74%, yellow 20%, grey 6%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>74%</span> <span>20% 6%</span> </div> </div>
2	D	256	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 79%, yellow 16%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span></span> <span>79%</span> <span>16% .</span> </div> </div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6413 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 KRas.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	169	Total	C	N	O	S	0	0	0
			1332	834	229	262	7			
1	C	165	Total	C	N	O	S	0	0	0
			1118	699	189	224	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P01116
C	0	GLY	-	expression tag	UNP P01116

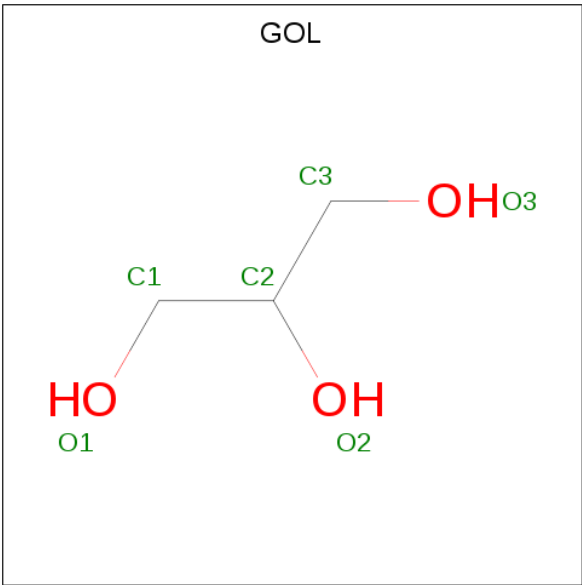
- Molecule 2 is a protein called Neurofibromin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	241	Total	C	N	O	S	0	0	0
			1907	1236	322	337	12			
2	D	245	Total	C	N	O	S	0	0	0
			1930	1248	326	344	12			

There are 2 discrepancies between the modelled and reference sequences:

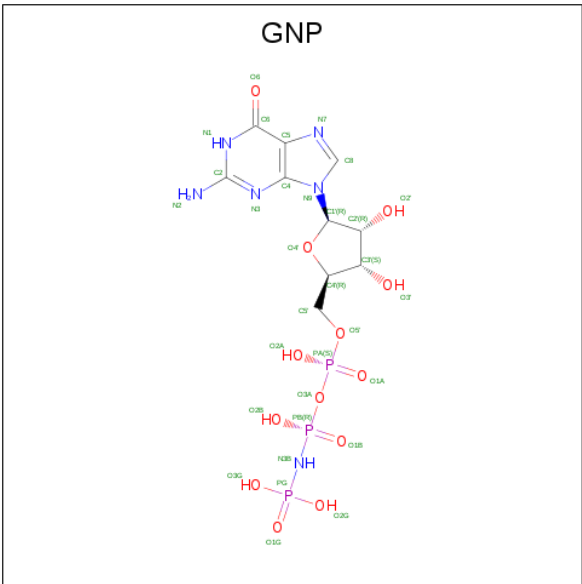
Chain	Residue	Modelled	Actual	Comment	Reference
B	1208	GLY	-	expression tag	UNP P21359
D	1208	GLY	-	expression tag	UNP P21359

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>13</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by author).



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

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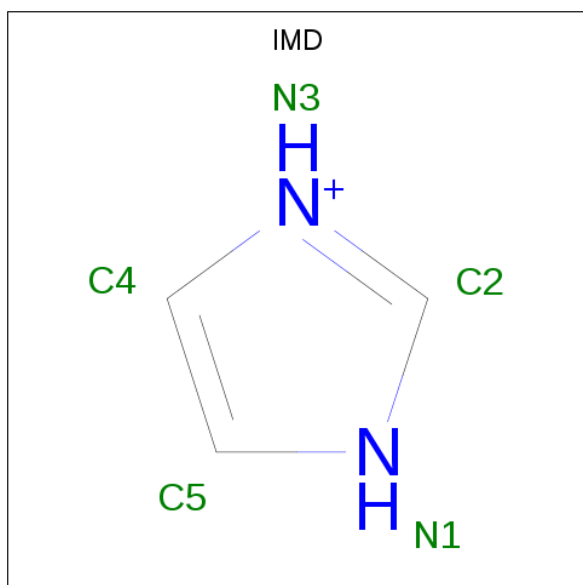
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by author).

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

- Molecule 6 is IMIDAZOLE (three-letter code: IMD) (formula: C<sub>3</sub>H<sub>5</sub>N<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	N	0	0
			5	3	2		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Cl	0	0
			1	1		

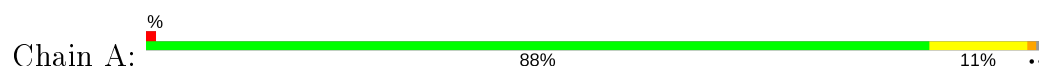
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	16	Total 16	O 16	0	0
8	B	13	Total 13	O 13	0	0
8	C	3	Total 3	O 3	0	0
8	D	10	Total 10	O 10	0	0

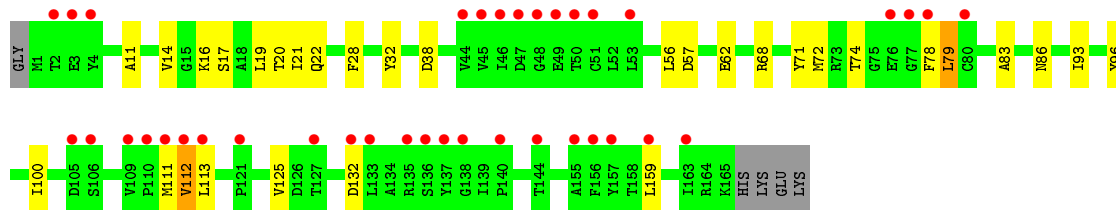
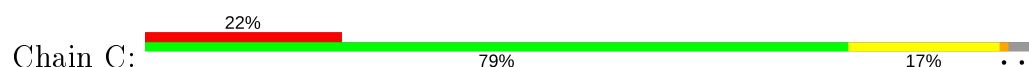
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

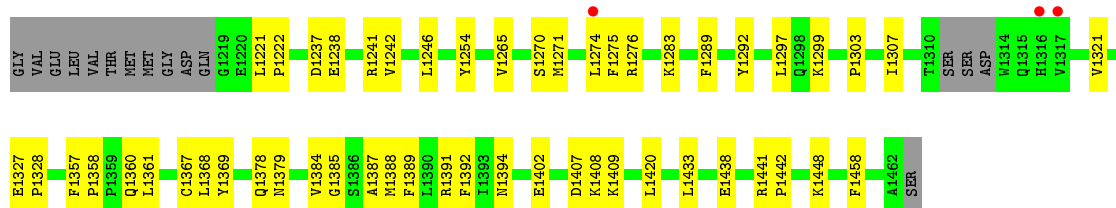
#### • Molecule 1: GTPase KRas



#### • Molecule 1: GTPase KRas



#### • Molecule 2: Neurofibromin



#### • Molecule 2: Neurofibromin



G1382	A1383	V1384	G1385	M1388	F1389	L1390	R1391	F1392	P1410	E1415	L1420	Q1426	N1430	R1441	P1442	F1458	S1463
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.73 Å 99.74 Å 155.51 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.00 – 2.85 46.00 – 2.85	Depositor EDS
% Data completeness (in resolution range)	98.1 (46.00-2.85) 92.1 (46.00-2.85)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.36 (at 2.86 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.199 , 0.247 0.201 , 0.241	Depositor DCC
$R_{free}$ test set	2000 reflections (6.51%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	68.2	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 45.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6413	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, MG, IMD, GNP, CL

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	0.47	0/1353	0.63	0/1828
1	C	0.36	0/1134	0.58	0/1553
2	B	0.48	0/1951	0.58	0/2643
2	D	0.44	0/1977	0.59	0/2683
All	All	0.45	0/6415	0.59	0/8707

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	1332	0	1295	16	0
1	C	1118	0	938	23	0
2	B	1907	0	1911	37	0
2	D	1930	0	1907	28	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
4	A	32	0	13	0	0
4	C	32	0	13	0	0
5	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	1	0	0	0	0
6	B	5	0	5	0	0
7	B	1	0	0	0	0
8	A	16	0	0	0	0
8	B	13	0	0	0	0
8	C	3	0	0	0	0
8	D	10	0	0	0	0
All	All	6413	0	6098	102	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 8.

All (102) 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:D:1368:LEU:HD23	2:D:1384:VAL:HG22	1.68	0.75
2:B:1265:VAL:HG22	2:B:1274:LEU:HD11	1.73	0.70
1:C:79:LEU:HD12	1:C:79:LEU:C	2.12	0.70
1:A:68:ARG:HB3	1:A:72:MET:HE1	1.73	0.69
2:B:1271:MET:SD	2:B:1274:LEU:HD22	2.31	0.69
2:B:1271:MET:CE	2:B:1274:LEU:HD22	2.25	0.67
1:C:93:ILE:HD13	1:C:113:LEU:CD1	2.26	0.66
1:C:79:LEU:HD12	1:C:79:LEU:O	1.96	0.65
2:B:1275:PHE:CE2	2:B:1368:LEU:HD11	2.34	0.62
2:D:1265:VAL:HG22	2:D:1375:ARG:HD2	1.83	0.60
2:D:1375:ARG:HD3	2:D:1376:PHE:CE2	2.39	0.58
2:D:1375:ARG:O	2:D:1375:ARG:HG2	2.03	0.57
1:C:17:SER:O	1:C:21:ILE:HG12	2.04	0.57
2:B:1327:GLU:HG3	2:B:1328:PRO:CD	2.34	0.56
2:B:1368:LEU:HD23	2:B:1384:VAL:HG22	1.89	0.55
1:C:14:VAL:HA	1:C:83:ALA:HB2	1.89	0.54
2:B:1327:GLU:HG3	2:B:1328:PRO:HD2	1.89	0.54
1:C:22:GLN:HE21	1:C:28:PHE:HB2	1.74	0.53
1:C:62:GLU:H	2:D:1278:ASN:HD21	1.56	0.52
1:C:68:ARG:HA	1:C:71:TYR:CE2	2.44	0.52
2:D:1390:LEU:HG	2:D:1390:LEU:O	2.08	0.51
2:D:1292:TYR:CD1	2:D:1360:GLN:HG2	2.46	0.51
2:D:1271:MET:O	2:D:1272:GLN:C	2.47	0.50
1:A:72:MET:O	1:A:104:LYS:HE2	2.11	0.50
2:B:1275:PHE:O	2:B:1391:ARG:NH2	2.45	0.50
2:D:1388:MET:O	2:D:1392:PHE:HB3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:PHE:HB3	1:A:93:ILE:HD11	1.93	0.50
2:D:1381:ILE:O	2:D:1384:VAL:N	2.44	0.50
2:D:1368:LEU:O	2:D:1372:VAL:HG23	2.11	0.49
2:B:1389:PHE:O	2:B:1394:ASN:HB2	2.13	0.49
1:C:19:LEU:HD12	1:C:20:THR:N	2.27	0.49
2:B:1438:GLU:OE1	2:B:1441:ARG:NE	2.46	0.49
2:B:1385:GLY:HA3	2:B:1458:PHE:CE2	2.47	0.49
2:B:1433:LEU:HD11	2:B:1448:LYS:HE3	1.94	0.49
2:D:1309:ILE:HD11	2:D:1410:PRO:HB3	1.95	0.48
1:A:68:ARG:O	1:A:72:MET:HE2	2.13	0.48
2:B:1238:GLU:HG3	2:B:1241:ARG:HH12	1.78	0.48
2:B:1299:LYS:HE3	2:B:1299:LYS:HB3	1.68	0.48
2:D:1300:LEU:O	2:D:1304:LEU:HD13	2.14	0.48
1:C:112:VAL:HG11	1:C:159:LEU:HA	1.96	0.48
2:B:1292:TYR:CD1	2:B:1360:GLN:HG2	2.49	0.47
2:B:1242:VAL:O	2:B:1246:LEU:HB2	2.15	0.47
2:B:1388:MET:O	2:B:1392:PHE:HB3	2.14	0.47
2:D:1381:ILE:O	2:D:1382:GLY:C	2.52	0.46
1:A:32:TYR:CZ	2:B:1276:ARG:HB3	2.50	0.46
2:D:1410:PRO:HG2	2:D:1415:GLU:HG2	1.98	0.46
1:A:68:ARG:HB3	1:A:72:MET:CE	2.45	0.46
1:C:68:ARG:HG2	1:C:71:TYR:OH	2.15	0.46
2:D:1378:GLN:O	2:D:1379:ASN:CB	2.63	0.45
2:B:1369:TYR:HB2	2:B:1384:VAL:HG21	1.98	0.45
1:C:71:TYR:HA	1:C:74:THR:HG22	1.99	0.45
1:C:93:ILE:CD1	1:C:113:LEU:HD11	2.47	0.45
2:D:1321:VAL:HG22	2:D:1420:LEU:HD13	1.99	0.45
2:D:1376:PHE:O	2:D:1380:SER:HB3	2.17	0.44
1:A:83:ALA:CB	1:A:117:LYS:HD2	2.47	0.44
2:D:1275:PHE:O	2:D:1391:ARG:NH1	2.45	0.44
2:D:1358:PRO:HG2	2:D:1361:LEU:HB2	2.00	0.44
1:A:93:ILE:HD13	1:A:113:LEU:HD11	1.99	0.44
1:A:101:LYS:HD2	1:A:107:GLU:HA	1.98	0.44
1:C:38:ASP:HB2	1:C:57:ASP:HB3	1.99	0.44
2:B:1303:PRO:O	2:B:1307:ILE:HG12	2.17	0.43
2:D:1441:ARG:N	2:D:1442:PRO:HD2	2.32	0.43
1:C:93:ILE:HD13	1:C:113:LEU:HD11	1.98	0.43
2:B:1289:PHE:HA	2:B:1361:LEU:HD21	2.01	0.43
2:B:1297:LEU:HD22	2:B:1392:PHE:CE1	2.54	0.43
2:D:1340:LEU:HD23	2:D:1340:LEU:HA	1.80	0.43
2:B:1321:VAL:HG22	2:B:1420:LEU:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:125:VAL:O	1:C:125:VAL:HG23	2.18	0.43
2:B:1237:ASP:OD1	2:B:1283:LYS:HD3	2.18	0.43
2:B:1246:LEU:HD12	2:B:1246:LEU:HA	1.93	0.42
2:B:1361:LEU:HD23	2:B:1361:LEU:HA	1.87	0.42
2:B:1387:ALA:O	2:B:1391:ARG:HG3	2.18	0.42
1:A:71:TYR:HA	1:A:74:THR:HG22	2.02	0.42
2:B:1378:GLN:HG2	2:B:1379:ASN:OD1	2.19	0.42
1:C:11:ALA:O	1:C:16:LYS:NZ	2.52	0.42
2:B:1441:ARG:N	2:B:1442:PRO:HD2	2.34	0.42
1:A:141:PHE:CZ	1:A:143:GLU:HG2	2.55	0.42
1:C:78:PHE:O	1:C:111:MET:HA	2.20	0.42
2:B:1358:PRO:HG2	2:B:1361:LEU:HB2	2.02	0.41
1:A:83:ALA:HB1	1:A:117:LYS:HD2	2.01	0.41
2:B:1221:LEU:N	2:B:1222:PRO:HD2	2.35	0.41
2:B:1270:SER:OG	2:B:1271:MET:N	2.52	0.41
2:D:1317:VAL:HG13	2:D:1338:ASN:ND2	2.35	0.41
1:A:84:ILE:HD11	1:A:117:LYS:O	2.20	0.41
1:A:149:ARG:HG3	1:A:152:VAL:HG22	2.03	0.41
1:A:68:ARG:C	1:A:72:MET:HE2	2.41	0.41
2:B:1409:LYS:HB3	2:B:1409:LYS:HE3	1.79	0.41
2:D:1225:MET:HE1	2:D:1259:ASN:HB3	2.02	0.41
1:A:88:LYS:HD3	1:A:92:ASP:OD2	2.20	0.41
2:D:1426:GLN:NE2	2:D:1430:ASN:OD1	2.50	0.41
1:C:56:LEU:HD23	1:C:71:TYR:HB2	2.02	0.41
2:D:1385:GLY:HA3	2:D:1458:PHE:CE2	2.56	0.41
1:C:96:TYR:O	1:C:100:ILE:HG13	2.20	0.41
2:B:1254:TYR:CE2	2:B:1367:CYS:HB2	2.56	0.41
2:B:1408:LYS:HE2	2:B:1408:LYS:HB3	1.88	0.41
1:C:72:MET:HA	1:C:78:PHE:CE2	2.55	0.41
2:B:1402:GLU:OE1	2:B:1402:GLU:N	2.53	0.40
1:C:56:LEU:HD12	1:C:56:LEU:HA	1.86	0.40
2:B:1441:ARG:HH11	2:B:1441:ARG:HD2	1.74	0.40
2:D:1265:VAL:CG2	2:D:1375:ARG:HD2	2.49	0.40
1:C:112:VAL:O	1:C:112:VAL:CG2	2.70	0.40
2:D:1271:MET:O	2:D:1273:THR:N	2.53	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	167/170 (98%)	165 (99%)	2 (1%)	0	100	100
1	C	163/170 (96%)	158 (97%)	5 (3%)	0	100	100
2	B	237/256 (93%)	233 (98%)	4 (2%)	0	100	100
2	D	243/256 (95%)	237 (98%)	6 (2%)	0	100	100
All	All	810/852 (95%)	793 (98%)	17 (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	144/149 (97%)	143 (99%)	1 (1%)	84	91
1	C	94/149 (63%)	89 (95%)	5 (5%)	22	43
2	B	209/231 (90%)	207 (99%)	2 (1%)	76	88
2	D	210/231 (91%)	208 (99%)	2 (1%)	76	88
All	All	657/760 (86%)	647 (98%)	10 (2%)	65	82

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	TYR
2	B	1357	PHE

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Mol	Chain	Res	Type
2	B	1407	ASP
1	C	32	TYR
1	C	79	LEU
1	C	86	ASN
1	C	112	VAL
1	C	132	ASP
2	D	1357	PHE
2	D	1381	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	C	22	GLN
1	C	61	GLN
1	C	116	ASN
2	D	1259	ASN
2	D	1278	ASN
2	D	1379	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 3 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
4	GNP	A	202	5	28,34,34	2.23	10 (35%)	30,54,54	1.94	5 (16%)
3	GOL	B	1501	-	5,5,5	1.09	0	5,5,5	0.84	0
6	IMD	B	1502	-	3,5,5	0.39	0	4,5,5	0.66	0
4	GNP	C	201	5	28,34,34	2.36	10 (35%)	30,54,54	1.94	7 (23%)
3	GOL	A	201	-	5,5,5	0.96	0	5,5,5	1.16	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
4	GNP	A	202	5	-	5/17/38/38	0/3/3/3
3	GOL	B	1501	-	-	2/4/4/4	-
4	GNP	C	201	5	-	8/17/38/38	0/3/3/3
6	IMD	B	1502	-	-	-	0/1/1/1
3	GOL	A	201	-	-	0/4/4/4	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	201	GNP	C4-N9	-7.42	1.37	1.47
4	A	202	GNP	C4-N9	-7.35	1.37	1.47
4	A	202	GNP	C5-C6	-4.70	1.44	1.52
4	C	201	GNP	C5-C6	-4.61	1.44	1.52
4	C	201	GNP	PB-O3A	3.85	1.63	1.59
4	C	201	GNP	PG-N3B	3.60	1.72	1.63
4	C	201	GNP	PB-O1B	3.22	1.51	1.46
4	C	201	GNP	C6-N1	3.20	1.38	1.33
4	A	202	GNP	C6-N1	2.93	1.38	1.33
4	A	202	GNP	PB-O1B	2.73	1.50	1.46
4	A	202	GNP	PB-O2B	-2.72	1.49	1.56
4	C	201	GNP	PG-O1G	2.59	1.50	1.46
4	A	202	GNP	PB-O3A	2.59	1.62	1.59
4	A	202	GNP	C5-C4	-2.56	1.37	1.53
4	A	202	GNP	C8-N9	-2.47	1.37	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	201	GNP	C5-C4	-2.44	1.38	1.53
4	A	202	GNP	PG-O1G	2.39	1.49	1.46
4	C	201	GNP	C8-N9	-2.36	1.37	1.45
4	A	202	GNP	PG-N3B	2.30	1.69	1.63
4	C	201	GNP	PB-O2B	-2.17	1.50	1.56

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	202	GNP	C4-C5-N7	6.19	110.66	102.46
4	C	201	GNP	C4-C5-N7	6.09	110.54	102.46
4	A	202	GNP	C5-C6-N1	-5.10	111.90	118.19
4	C	201	GNP	C5-C6-N1	-5.04	111.97	118.19
4	A	202	GNP	O6-C6-C5	3.60	127.21	119.86
4	C	201	GNP	O6-C6-C5	3.57	127.14	119.86
4	A	202	GNP	PA-O3A-PB	-3.56	120.08	132.62
4	C	201	GNP	PA-O3A-PB	-3.55	120.10	132.62
4	A	202	GNP	O2B-PB-O1B	2.70	115.59	109.92
4	C	201	GNP	O3A-PB-N3B	2.50	113.53	106.59
4	C	201	GNP	O2G-PG-O1G	-2.21	107.90	113.45
4	C	201	GNP	O1G-PG-N3B	-2.04	108.77	111.77

There are no chirality outliers.

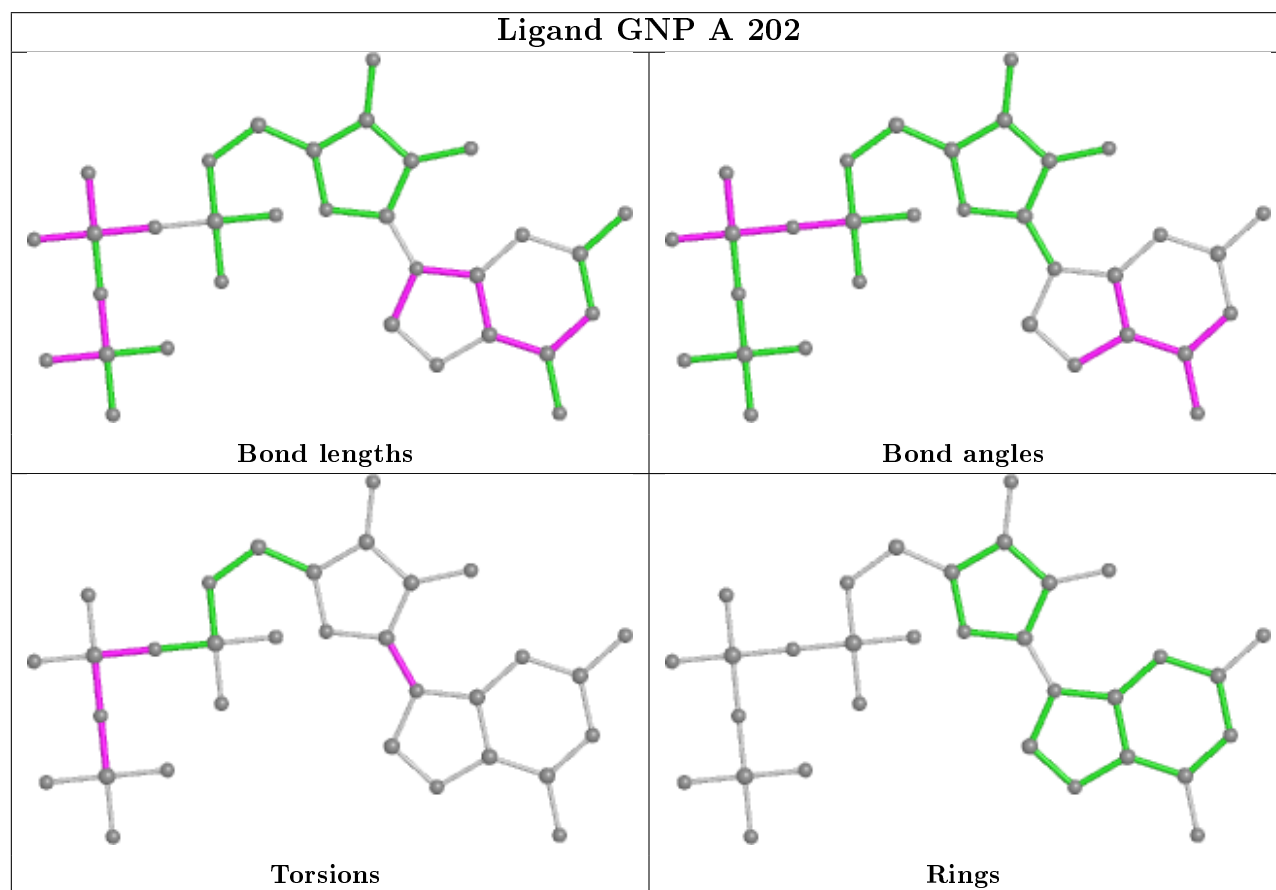
All (15) torsion outliers are listed below:

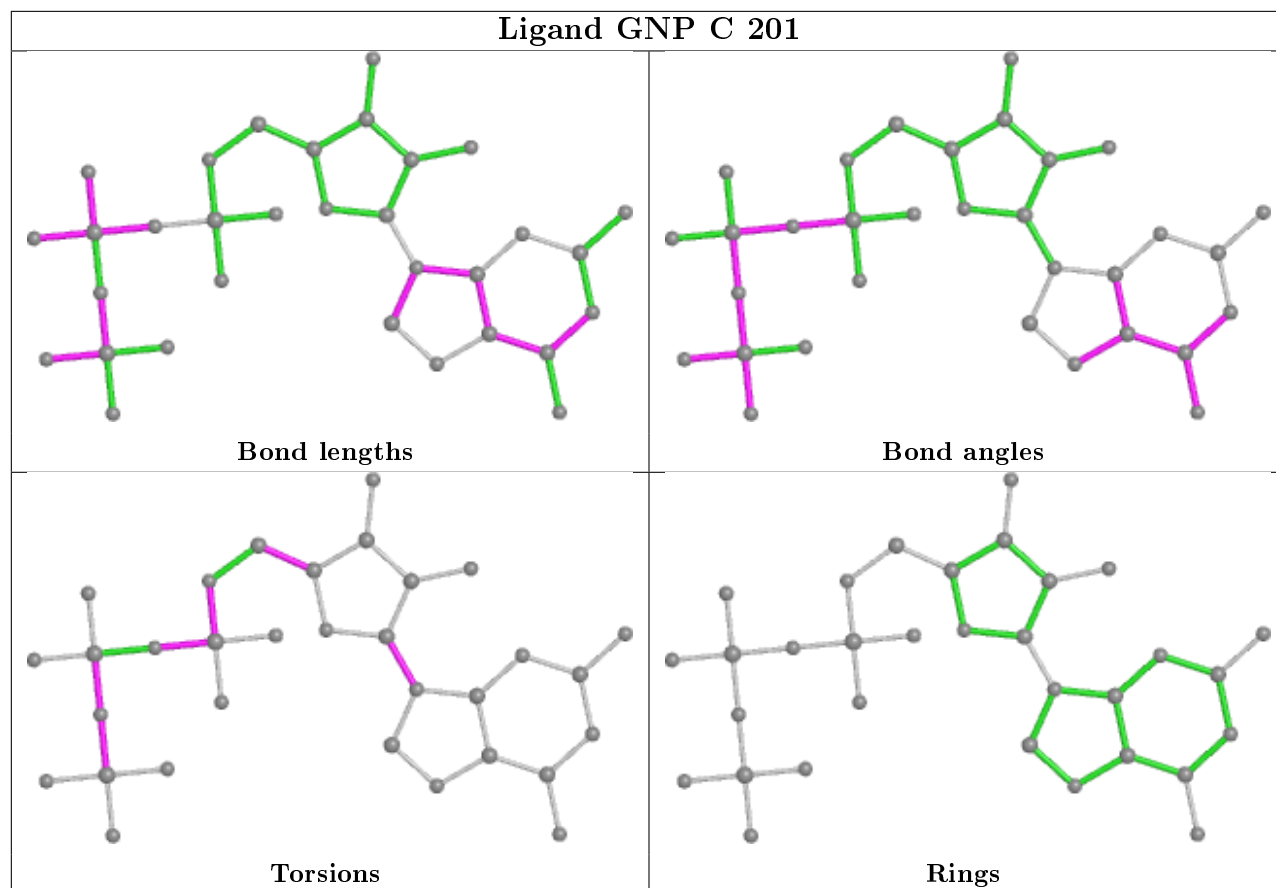
Mol	Chain	Res	Type	Atoms
4	A	202	GNP	PB-N3B-PG-O1G
4	A	202	GNP	PG-N3B-PB-O1B
4	A	202	GNP	PG-N3B-PB-O3A
4	A	202	GNP	PA-O3A-PB-O1B
4	A	202	GNP	C2'-C1'-N9-C4
4	C	201	GNP	PB-N3B-PG-O1G
4	C	201	GNP	PG-N3B-PB-O1B
4	C	201	GNP	C5'-O5'-PA-O3A
4	C	201	GNP	C5'-O5'-PA-O1A
4	C	201	GNP	C2'-C1'-N9-C4
4	C	201	GNP	O4'-C4'-C5'-O5'
3	B	1501	GOL	O1-C1-C2-C3
4	C	201	GNP	C3'-C4'-C5'-O5'
3	B	1501	GOL	O1-C1-C2-O2
4	C	201	GNP	PB-O3A-PA-O2A

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 ⓘ

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	169/170 (99%)	-0.26	1 (0%) 89 88	42, 61, 91, 104	0
1	C	165/170 (97%)	0.88	38 (23%) 0 0	78, 124, 151, 159	4 (2%)
2	B	241/256 (94%)	-0.10	3 (1%) 79 76	49, 67, 93, 138	3 (1%)
2	D	245/256 (95%)	-0.15	1 (0%) 92 91	53, 79, 111, 131	2 (0%)
All	All	820/852 (96%)	0.05	43 (5%) 27 20	42, 76, 134, 159	9 (1%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	51	CYS	5.2
1	C	106	SER	4.8
1	C	111	MET	4.2
1	C	156	PHE	4.2
1	C	110	PRO	4.2
1	C	137	TYR	4.0
2	B	1316	HIS	3.9
1	C	140	PRO	3.8
1	C	2	THR	3.8
1	C	109	VAL	3.8
1	C	44	VAL	3.5
1	C	138	GLY	3.5
2	B	1317	VAL	3.5
1	C	157	TYR	3.4
2	B	1274	LEU	3.4
1	C	121	PRO	3.2
1	C	155	ALA	3.1
1	C	46	ILE	3.1
1	C	50	THR	3.1
1	C	105	ASP	3.0
1	C	53	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	169	LYS	2.8
1	C	133	LEU	2.8
1	C	132	ASP	2.8
1	C	49	GLU	2.8
1	C	113	LEU	2.7
1	C	77	GLY	2.7
1	C	112	VAL	2.6
1	C	127	THR	2.6
1	C	144	THR	2.5
1	C	163	ILE	2.5
1	C	45	VAL	2.5
1	C	135	ARG	2.5
1	C	48	GLY	2.5
1	C	136	SER	2.4
1	C	78	PHE	2.3
1	C	47	ASP	2.3
1	C	4	TYR	2.2
1	C	80	CYS	2.2
1	C	76	GLU	2.1
2	D	1377	PRO	2.1
1	C	3	GLU	2.1
1	C	159	LEU	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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
5	MG	C	202	1/1	0.88	0.20	80,80,80,80	0

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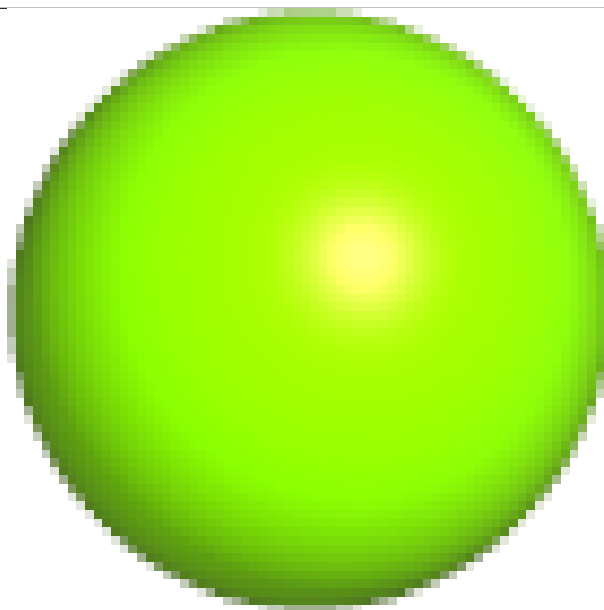
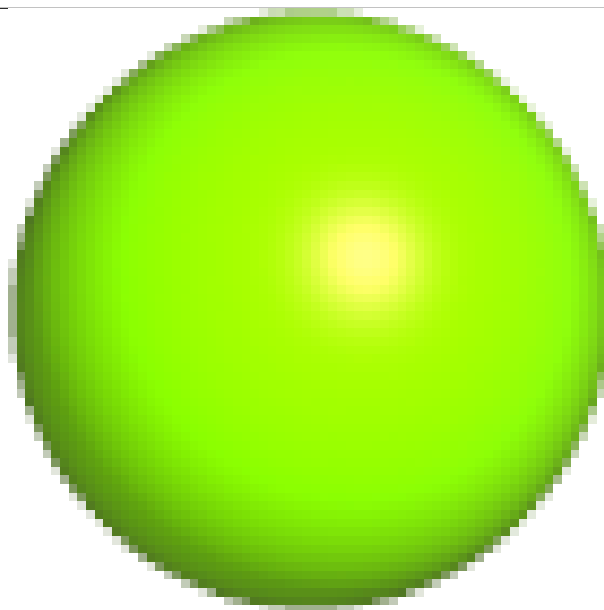
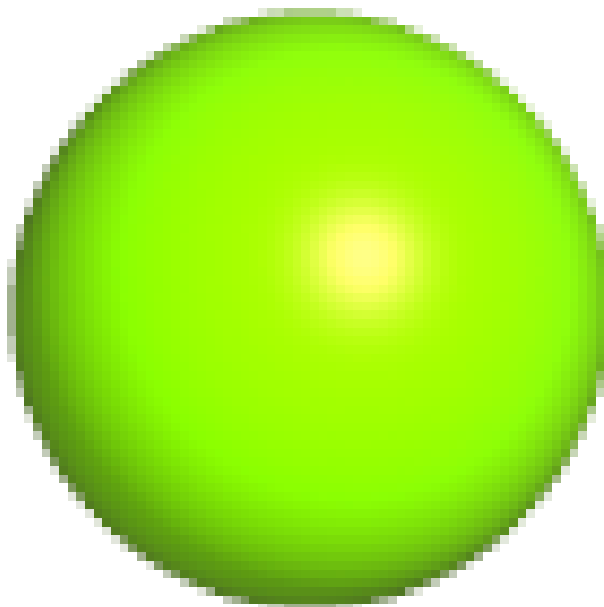
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	GOL	A	201	6/6	0.89	0.28	64,71,73,73	0
6	IMD	B	1502	5/5	0.90	0.14	103,103,104,105	0
7	CL	B	1503	1/1	0.92	0.18	85,85,85,85	0
3	GOL	B	1501	6/6	0.94	0.16	76,79,81,82	0
4	GNP	C	201	32/32	0.95	0.17	87,97,122,125	0
4	GNP	A	202	32/32	0.97	0.18	38,50,57,59	0
5	MG	A	203	1/1	0.98	0.25	55,55,55,55	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.

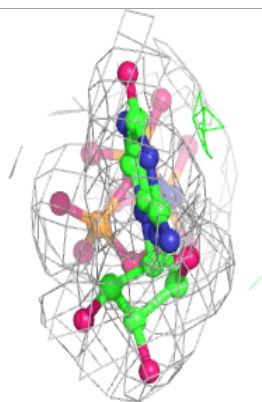
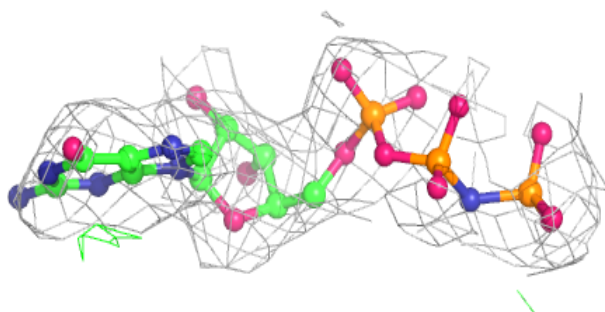
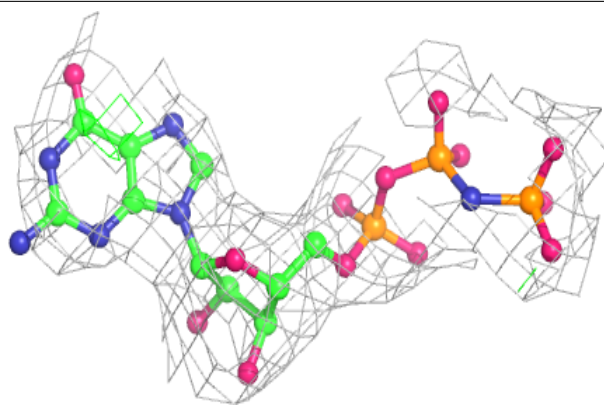
**Electron density around MG C 202:**

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

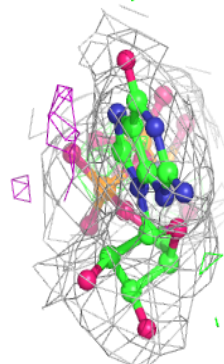
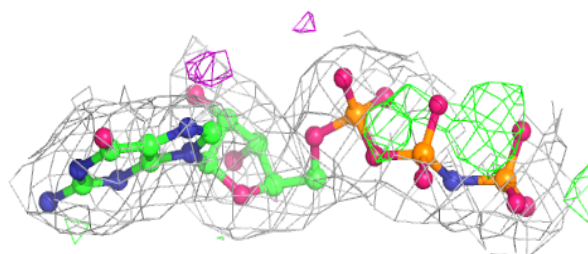
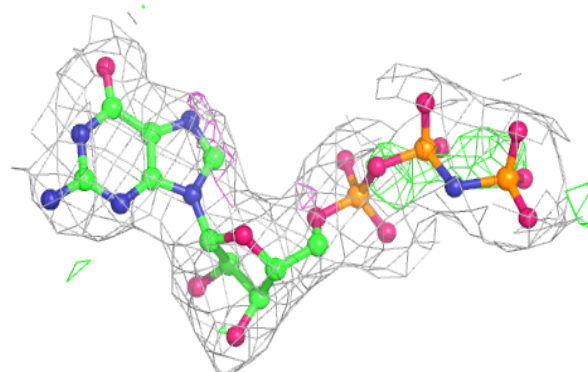


**Electron density around GNP C 201:**

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

**Electron density around GNP A 202:**

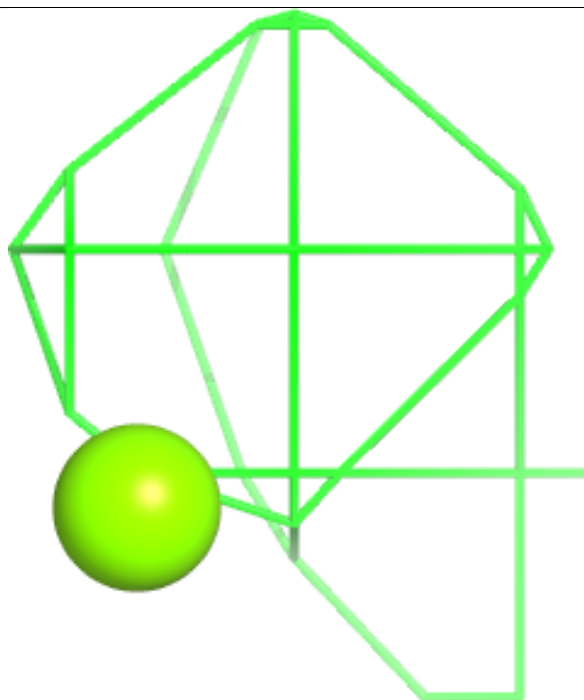
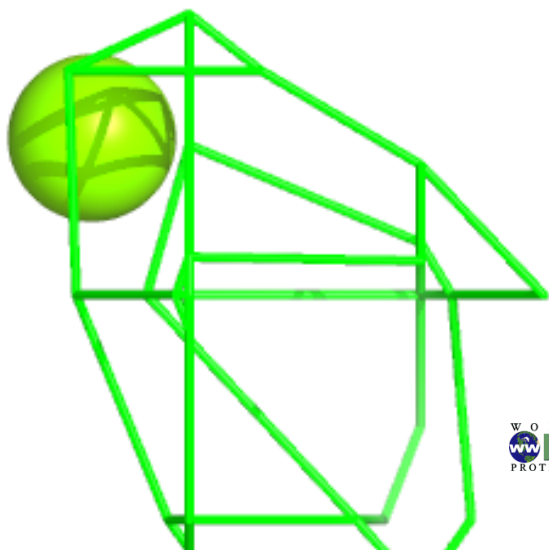
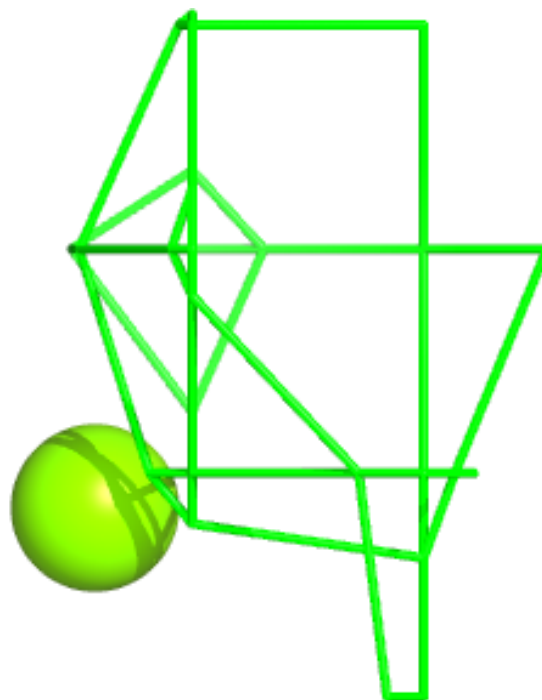
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around MG A 203:**

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



## 6.5 Other polymers

There are no such residues in this entry.