



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 29, 2024 – 01:36 pm BST

PDB ID : 5O2S  
Title : Human KRAS in complex with darpin K27  
Authors : Debreczeni, J.E.; Guillard, S.; Kolasinska-Zwierz, P.; Breed, J.; Zhang, J.; Bery, N.; Marwood, R.; Tart, J.; Stocki, P.; Mistry, B.; Phillips, C.; Rabbitts, T.; Jackson, R.; Minter, R.  
Deposited on : 2017-05-22  
Resolution : 3.22 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

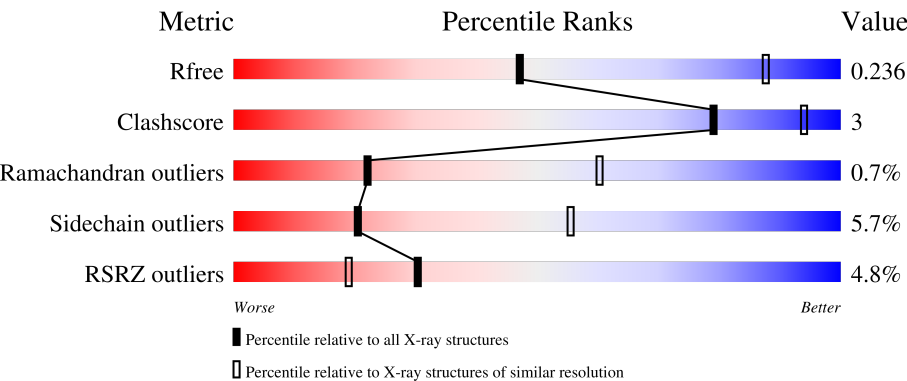
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

# 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 3.22 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 <sub>free</sub>	130704	1335 (3.24-3.20)
Clashscore	141614	1460 (3.24-3.20)
Ramachandran outliers	138981	1437 (3.24-3.20)
Sidechain outliers	138945	1436 (3.24-3.20)
RSRZ outliers	127900	1291 (3.24-3.20)

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  $\geq 3$ , 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	169	<div><div></div><div>82%14%..</div></div>
1	C	169	<div><div></div><div>83%13%..</div></div>
1	E	169	<div><div></div><div>80%16%...</div></div>
1	G	169	<div><div>20%</div><div>83%12%...</div></div>

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Mol	Chain	Length	Quality of chain
2	B	178	<div><div></div><div>79%</div><div>8% • 12%</div></div>
2	D	178	<div><div></div><div>76%</div><div>10% • 12%</div></div>
2	F	178	<div><div>%</div><div></div><div>79%</div><div>7% • 12%</div></div>
2	H	178	<div><div>15%</div><div></div><div>79%</div><div>7% • 12%</div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9902 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	165	Total	C	N	O	S	0	0	0
			1282	806	219	250	7			
1	C	165	Total	C	N	O	S	0	1	0
			1294	812	223	252	7			
1	E	165	Total	C	N	O	S	0	1	0
			1284	805	219	253	7			
1	G	164	Total	C	N	O	S	0	0	0
			1241	781	204	249	7			

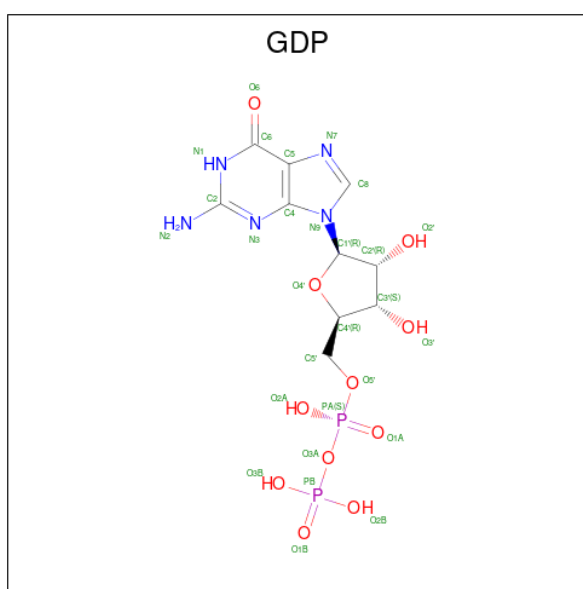
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P01116
A	-1	SER	-	expression tag	UNP P01116
A	0	HIS	-	expression tag	UNP P01116
A	12	VAL	GLY	variant	UNP P01116
C	-2	GLY	-	expression tag	UNP P01116
C	-1	SER	-	expression tag	UNP P01116
C	0	HIS	-	expression tag	UNP P01116
C	12	VAL	GLY	variant	UNP P01116
E	-2	GLY	-	expression tag	UNP P01116
E	-1	SER	-	expression tag	UNP P01116
E	0	HIS	-	expression tag	UNP P01116
E	12	VAL	GLY	variant	UNP P01116
G	-2	GLY	-	expression tag	UNP P01116
G	-1	SER	-	expression tag	UNP P01116
G	0	HIS	-	expression tag	UNP P01116
G	12	VAL	GLY	variant	UNP P01116

- Molecule 2 is a protein called darpin K27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	156	Total	C	N	O	S	0	0	0
			1156	723	205	226	2			
2	D	156	Total	C	N	O	S	0	0	0
			1163	727	205	228	3			
2	F	156	Total	C	N	O	S	0	0	0
			1155	722	205	226	2			
2	H	156	Total	C	N	O	S	0	0	0
			1152	721	201	227	3			

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	C	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	E	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	G	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

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

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

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total 1	Mg 1	0	0
4	E	1	Total 1	Mg 1	0	0
4	G	1	Total 1	Mg 1	0	0


- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	14	Total 14	O 14	0	0
5	B	6	Total 6	O 6	0	0
5	C	20	Total 20	O 20	0	0
5	D	2	Total 2	O 2	0	0
5	E	12	Total 12	O 12	0	0
5	F	1	Total 1	O 1	0	0
5	G	4	Total 4	O 4	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 KRas

Chain A: 




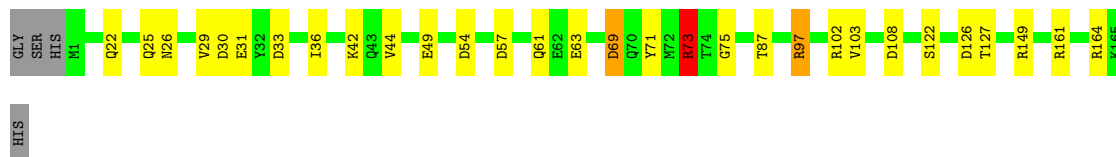
- Molecule 1: GTPase KRas

Chain C: 




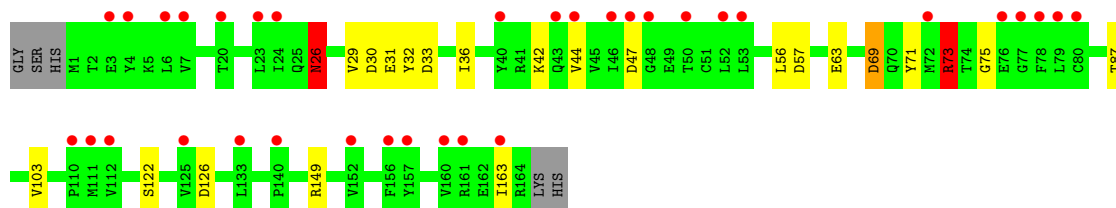
- Molecule 1: GTPase KRas

Chain E: 




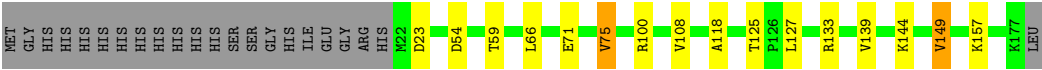
- Molecule 1: GTPase KRas

Chain G: 

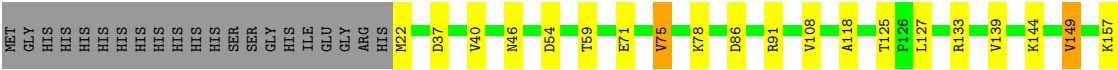


- Molecule 2: darpin K27

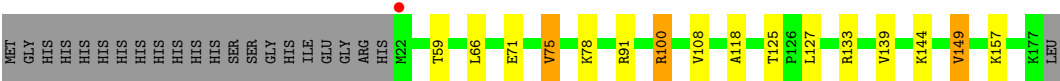
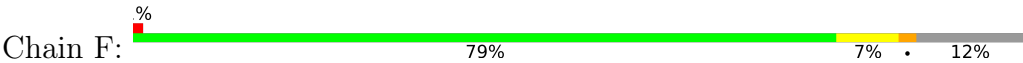
Chain B: 



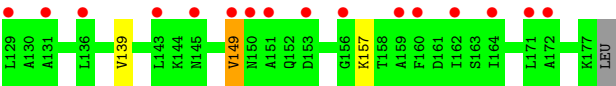
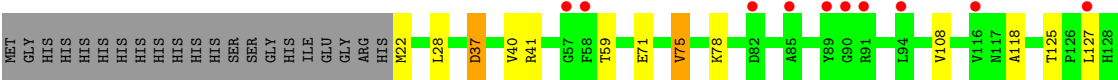
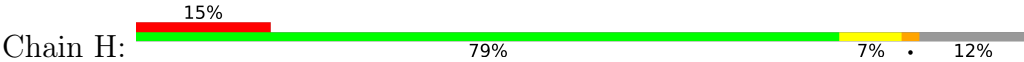
• Molecule 2: darpin K27



• Molecule 2: darpin K27



• Molecule 2: darpin K27





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	197.14Å 197.14Å 84.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	98.57 – 3.22 98.57 – 3.22	Depositor EDS
% Data completeness (in resolution range)	100.0 (98.57-3.22) 100.0 (98.57-3.22)	Depositor EDS
$R_{merge}$	0.36	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.76 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.201 , 0.235 0.203 , 0.236	Depositor DCC
$R_{free}$ test set	1471 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	75.3	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 69.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.054 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9902	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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: MG, GDP

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	0.87	1/1302 (0.1%)	1.12	5/1764 (0.3%)
1	C	0.86	0/1315	1.11	4/1782 (0.2%)
1	E	0.83	0/1305	1.10	9/1772 (0.5%)
1	G	0.75	1/1260 (0.1%)	1.10	7/1715 (0.4%)
2	B	0.66	0/1172	0.89	3/1592 (0.2%)
2	D	0.68	0/1179	0.86	2/1600 (0.1%)
2	F	0.66	0/1171	0.86	3/1591 (0.2%)
2	H	0.61	0/1168	0.85	2/1587 (0.1%)
All	All	0.75	2/9872 (0.0%)	1.00	35/13403 (0.3%)

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
1	A	0	1
1	C	0	1
1	E	0	3
1	G	0	2
All	All	0	7

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	94	HIS	CA-CB	7.82	1.71	1.53
1	G	56	LEU	C-O	-5.12	1.13	1.23

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	47	ASP	CB-CG-OD1	8.79	126.22	118.30
2	B	100	ARG	NE-CZ-NH1	7.30	123.95	120.30
1	G	47	ASP	CB-CG-OD2	-6.85	112.14	118.30
1	E	73	ARG	NE-CZ-NH2	6.48	123.54	120.30
1	E	126	ASP	N-CA-CB	-6.08	99.65	110.60
2	F	133	ARG	NE-CZ-NH2	6.08	123.34	120.30
1	C	108	ASP	CB-CG-OD2	-6.00	112.91	118.30
2	D	133	ARG	NE-CZ-NH2	5.99	123.30	120.30
2	D	91	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	G	73	ARG	NE-CZ-NH2	5.82	123.21	120.30
1	E	69	ASP	CB-CG-OD2	-5.81	113.07	118.30
1	E	108	ASP	CB-CG-OD2	-5.73	113.14	118.30
1	G	126	ASP	CB-CA-C	5.64	121.68	110.40
1	G	26	ASN	N-CA-CB	5.58	120.64	110.60
1	C	69	ASP	N-CA-CB	-5.57	100.58	110.60
1	G	69	ASP	CB-CG-OD2	-5.51	113.34	118.30
1	C	135	ARG	NE-CZ-NH1	5.46	123.03	120.30
2	F	100	ARG	NE-CZ-NH1	5.37	122.98	120.30
2	H	37	ASP	CB-CG-OD1	5.33	123.10	118.30
1	A	129	GLN	CA-CB-CG	5.32	125.10	113.40
2	B	100	ARG	NE-CZ-NH2	-5.31	117.65	120.30
2	F	91	ARG	NE-CZ-NH1	5.26	122.93	120.30
2	B	133	ARG	NE-CZ-NH2	5.25	122.93	120.30
1	E	69	ASP	CB-CA-C	-5.21	99.98	110.40
1	E	97	ARG	NE-CZ-NH2	5.17	122.89	120.30
1	E	161	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	G	73	ARG	NE-CZ-NH1	-5.07	117.76	120.30
1	E	102	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	A	108	ASP	CB-CG-OD2	-5.07	113.74	118.30
1	A	69	ASP	CB-CA-C	-5.04	100.32	110.40
1	A	135	ARG	NE-CZ-NH2	5.04	122.82	120.30
1	E	73	ARG	NE-CZ-NH1	-5.03	117.78	120.30
2	H	41	ARG	NE-CZ-NH1	5.00	122.80	120.30
1	C	103	VAL	N-CA-CB	5.00	122.51	111.50
1	A	103	VAL	N-CA-CB	5.00	122.50	111.50

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	29	VAL	Peptide
1	C	29	VAL	Peptide
1	E	29	VAL	Peptide

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Mol	Chain	Res	Type	Group
1	E	54	ASP	Mainchain
1	E	73	ARG	Mainchain
1	G	29	VAL	Peptide
1	G	73	ARG	Mainchain

## 5.2 Too-close contacts ⓘ

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	1282	0	1247	11	0
1	C	1294	0	1251	10	0
1	E	1284	0	1224	9	0
1	G	1241	0	1169	9	0
2	B	1156	0	1113	5	0
2	D	1163	0	1124	6	0
2	F	1155	0	1111	4	0
2	H	1152	0	1105	4	0
3	A	28	0	12	1	0
3	C	28	0	12	1	0
3	E	28	0	12	1	0
3	G	28	0	12	1	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
5	A	14	0	0	0	0
5	B	6	0	0	0	0
5	C	20	0	0	0	0
5	D	2	0	0	0	0
5	E	12	0	0	0	0
5	F	1	0	0	0	0
5	G	4	0	0	0	0
All	All	9902	0	9392	54	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 3.

All (54) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ARG:NH2	1:E:25:GLN:O	2.28	0.67
1:C:84:ILE:HD12	1:C:123:ARG:HG2	1.77	0.66
1:A:30:ASP:HA	3:A:201:GDP:O2'	2.01	0.61
1:G:26:ASN:O	1:G:26:ASN:ND2	2.32	0.60
1:C:22:GLN:O	1:C:149:ARG:NH2	2.36	0.59
1:A:22:GLN:O	1:A:149:ARG:NH2	2.36	0.58
1:A:31:GLU:OE2	2:B:54:ASP:HB2	2.04	0.57
1:C:84:ILE:CD1	1:C:123:ARG:HG2	2.34	0.57
1:E:22:GLN:O	1:E:149:ARG:NH2	2.38	0.57
1:C:31:GLU:OE1	2:D:54:ASP:HB2	2.04	0.56
1:E:30:ASP:HA	3:E:201:GDP:O2'	2.06	0.56
1:E:33:ASP:HB3	1:E:36:ILE:HD11	1.89	0.55
2:H:71:GLU:O	2:H:75:VAL:HG13	2.07	0.55
1:G:33:ASP:HB3	1:G:36:ILE:HD11	1.90	0.54
1:E:97:ARG:HG2	1:E:97:ARG:HH21	1.73	0.54
2:F:71:GLU:O	2:F:75:VAL:HG13	2.08	0.54
2:D:71:GLU:O	2:D:75:VAL:HG13	2.08	0.53
2:B:127:LEU:HD11	2:B:139:VAL:HG13	1.91	0.53
2:B:71:GLU:O	2:B:75:VAL:HG13	2.08	0.52
1:C:33:ASP:HB3	1:C:36:ILE:HD11	1.92	0.52
2:D:127:LEU:HD11	2:D:139:VAL:HG13	1.93	0.51
1:A:33:ASP:HB3	1:A:36:ILE:HD11	1.92	0.50
1:A:71:TYR:O	1:A:75:GLY:N	2.43	0.49
2:F:127:LEU:HD11	2:F:139:VAL:HG13	1.93	0.49
2:H:127:LEU:HD11	2:H:139:VAL:HG13	1.93	0.49
1:G:30:ASP:HA	3:G:201:GDP:O2'	2.11	0.48
1:E:69:ASP:HB3	1:E:73:ARG:NH1	2.28	0.48
1:C:71:TYR:O	1:C:75:GLY:N	2.43	0.47
1:G:71:TYR:O	1:G:75:GLY:N	2.43	0.47
1:G:69:ASP:HB3	1:G:73:ARG:NH1	2.29	0.47
1:C:118:CYS:HB2	1:C:123:ARG:NH2	2.30	0.47
1:G:42:LYS:HG3	1:G:44:VAL:HG13	1.99	0.45
1:E:71:TYR:O	1:E:75:GLY:N	2.41	0.44
1:A:69:ASP:HB3	1:A:73:ARG:NH1	2.33	0.44
2:B:118:ALA:O	2:B:125:THR:HA	2.19	0.43
1:C:30:ASP:O	1:C:31:GLU:C	2.57	0.43
1:A:97:ARG:HD3	1:A:137:TYR:CZ	2.54	0.43
1:A:97:ARG:HD3	1:A:137:TYR:CE1	2.54	0.42
1:E:42:LYS:HG3	1:E:44:VAL:HG13	2.01	0.42
1:A:42:LYS:HG3	1:A:44:VAL:HG13	2.00	0.42
2:D:118:ALA:O	2:D:125:THR:HA	2.19	0.42
2:H:118:ALA:O	2:H:125:THR:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:32:TYR:CE2	1:G:36:ILE:HD12	2.54	0.42
2:F:118:ALA:O	2:F:125:THR:HA	2.19	0.42
1:A:36:ILE:HG12	2:B:66:LEU:HD11	2.02	0.41
2:F:66:LEU:HD21	2:F:100:ARG:NH2	2.35	0.41
1:C:42:LYS:HG3	1:C:44:VAL:HG13	2.02	0.41
1:C:146:ALA:N	3:C:201:GDP:O6	2.53	0.41
1:E:49:GLU:OE2	1:E:164:ARG:NH2	2.53	0.41
2:D:37:ASP:HA	2:D:40:VAL:HG12	2.03	0.41
2:D:86:ASP:OD1	2:D:86:ASP:N	2.53	0.41
1:G:30:ASP:OD1	1:G:30:ASP:N	2.53	0.41
2:H:28:LEU:HD11	2:H:40:VAL:HG23	2.03	0.40
1:G:26:ASN:OD1	1:G:149:ARG:CZ	2.70	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	163/169 (96%)	159 (98%)	3 (2%)	1 (1%)	25	63
1	C	164/169 (97%)	160 (98%)	3 (2%)	1 (1%)	25	63
1	E	164/169 (97%)	160 (98%)	3 (2%)	1 (1%)	25	63
1	G	162/169 (96%)	157 (97%)	3 (2%)	2 (1%)	13	48
2	B	154/178 (86%)	146 (95%)	7 (4%)	1 (1%)	25	63
2	D	154/178 (86%)	146 (95%)	7 (4%)	1 (1%)	25	63
2	F	154/178 (86%)	147 (96%)	6 (4%)	1 (1%)	25	63
2	H	154/178 (86%)	145 (94%)	8 (5%)	1 (1%)	25	63
All	All	1269/1388 (91%)	1220 (96%)	40 (3%)	9 (1%)	22	60

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	31	GLU
2	B	149	VAL
1	C	31	GLU
2	D	149	VAL
2	F	149	VAL
1	G	31	GLU
2	H	149	VAL
1	E	31	GLU
1	G	163	ILE

### 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	138/149 (93%)	132 (96%)	6 (4%)	29	63
1	C	139/149 (93%)	133 (96%)	6 (4%)	29	63
1	E	137/149 (92%)	129 (94%)	8 (6%)	20	54
1	G	130/149 (87%)	124 (95%)	6 (5%)	27	62
2	B	113/140 (81%)	106 (94%)	7 (6%)	18	52
2	D	115/140 (82%)	106 (92%)	9 (8%)	12	42
2	F	113/140 (81%)	106 (94%)	7 (6%)	18	52
2	H	113/140 (81%)	105 (93%)	8 (7%)	14	46
All	All	998/1156 (86%)	941 (94%)	57 (6%)	20	55

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	26	ASN
1	A	57	ASP
1	A	87	THR
1	A	103	VAL
1	A	122	SER
2	B	23	ASP

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Mol	Chain	Res	Type
2	B	59	THR
2	B	75	VAL
2	B	108	VAL
2	B	144	LYS
2	B	149	VAL
2	B	157	LYS
1	C	5	LYS
1	C	26	ASN
1	C	57	ASP
1	C	87	THR
1	C	103	VAL
1	C	122	SER
2	D	22	MET
2	D	46	ASN
2	D	59	THR
2	D	75	VAL
2	D	78	LYS
2	D	108	VAL
2	D	144	LYS
2	D	149	VAL
2	D	157	LYS
1	E	26	ASN
1	E	57	ASP
1	E	61	GLN
1	E	63	GLU
1	E	87	THR
1	E	103	VAL
1	E	122	SER
1	E	127	THR
2	F	59	THR
2	F	75	VAL
2	F	78	LYS
2	F	108	VAL
2	F	144	LYS
2	F	149	VAL
2	F	157	LYS
1	G	26	ASN
1	G	57	ASP
1	G	63	GLU
1	G	87	THR
1	G	103	VAL
1	G	122	SER

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Mol	Chain	Res	Type
2	H	22	MET
2	H	37	ASP
2	H	59	THR
2	H	75	VAL
2	H	78	LYS
2	H	108	VAL
2	H	149	VAL
2	H	157	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 8 ligands modelled in this entry, 4 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	GDP	A	201	4	24,30,30	0.88	0	30,47,47	1.43	6 (20%)
3	GDP	G	201	4	24,30,30	1.01	1 (4%)	30,47,47	1.43	3 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GDP	E	201	4	24,30,30	0.99	1 (4%)	30,47,47	1.32	5 (16%)
3	GDP	C	201	4	24,30,30	1.18	2 (8%)	30,47,47	1.27	2 (6%)

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	GDP	A	201	4	-	0/12/32/32	0/3/3/3
3	GDP	G	201	4	-	2/12/32/32	0/3/3/3
3	GDP	E	201	4	-	0/12/32/32	0/3/3/3
3	GDP	C	201	4	-	0/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	201	GDP	C6-N1	-2.89	1.33	1.37
3	G	201	GDP	C6-N1	-2.68	1.33	1.37
3	C	201	GDP	C2'-C1'	-2.45	1.50	1.53
3	E	201	GDP	C6-N1	-2.35	1.34	1.37

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	201	GDP	PA-O3A-PB	-3.43	121.06	132.83
3	A	201	GDP	PA-O3A-PB	-2.75	123.39	132.83
3	E	201	GDP	C8-N7-C5	2.69	108.11	102.99
3	G	201	GDP	C3'-C2'-C1'	2.68	105.01	100.98
3	A	201	GDP	O2A-PA-O1A	2.62	125.20	112.24
3	E	201	GDP	O2B-PB-O1B	2.61	120.90	110.68
3	E	201	GDP	PA-O3A-PB	-2.55	124.08	132.83
3	G	201	GDP	C8-N7-C5	2.44	107.64	102.99
3	A	201	GDP	C8-N7-C5	2.36	107.48	102.99
3	A	201	GDP	O6-C6-C5	-2.34	119.80	124.37
3	C	201	GDP	C8-N7-C5	2.33	107.43	102.99
3	E	201	GDP	C5-C6-N1	2.18	117.81	113.95
3	A	201	GDP	C5-C6-N1	2.13	117.70	113.95
3	A	201	GDP	O3B-PB-O1B	2.08	118.82	110.68
3	C	201	GDP	O3A-PB-O1B	-2.01	100.06	111.19
3	E	201	GDP	O3A-PB-O1B	-2.01	100.06	111.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

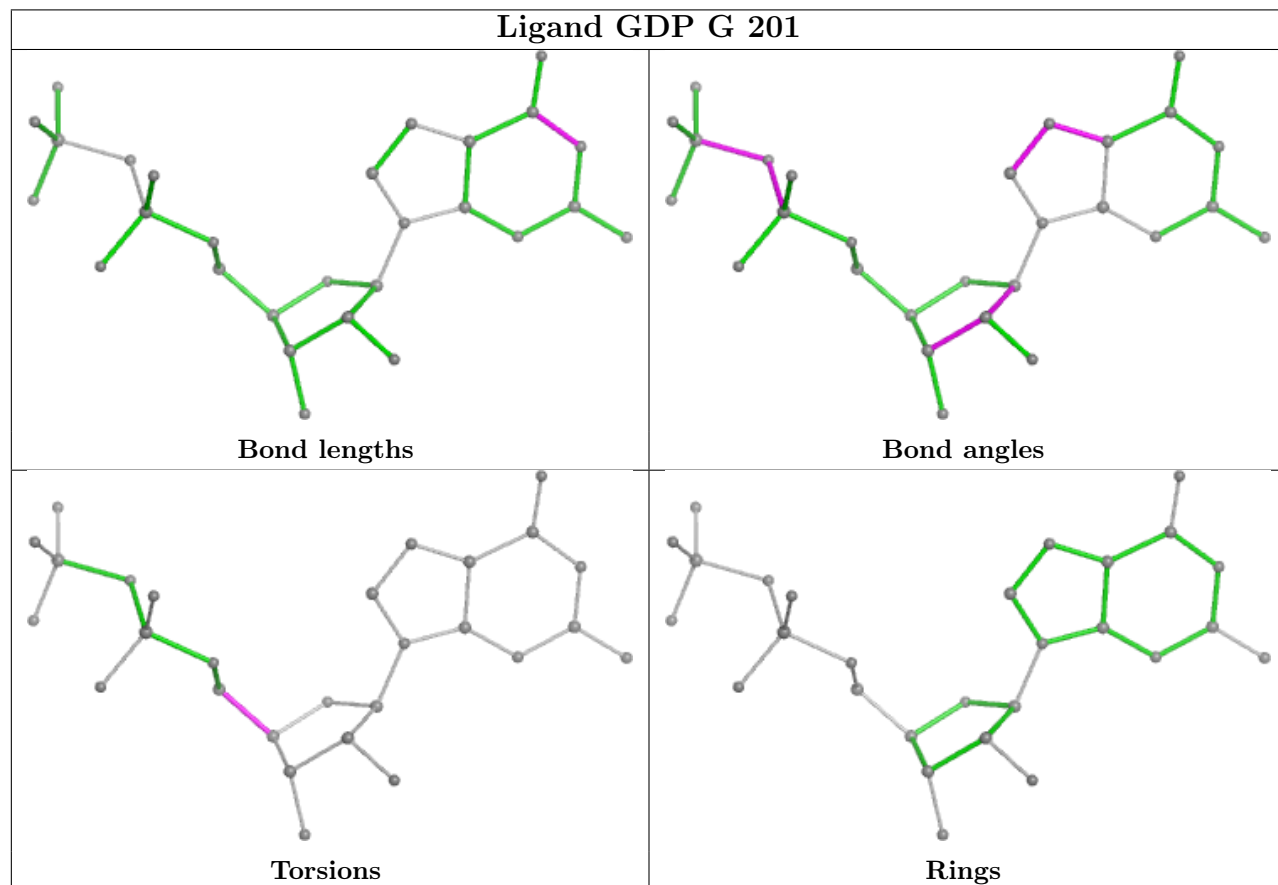
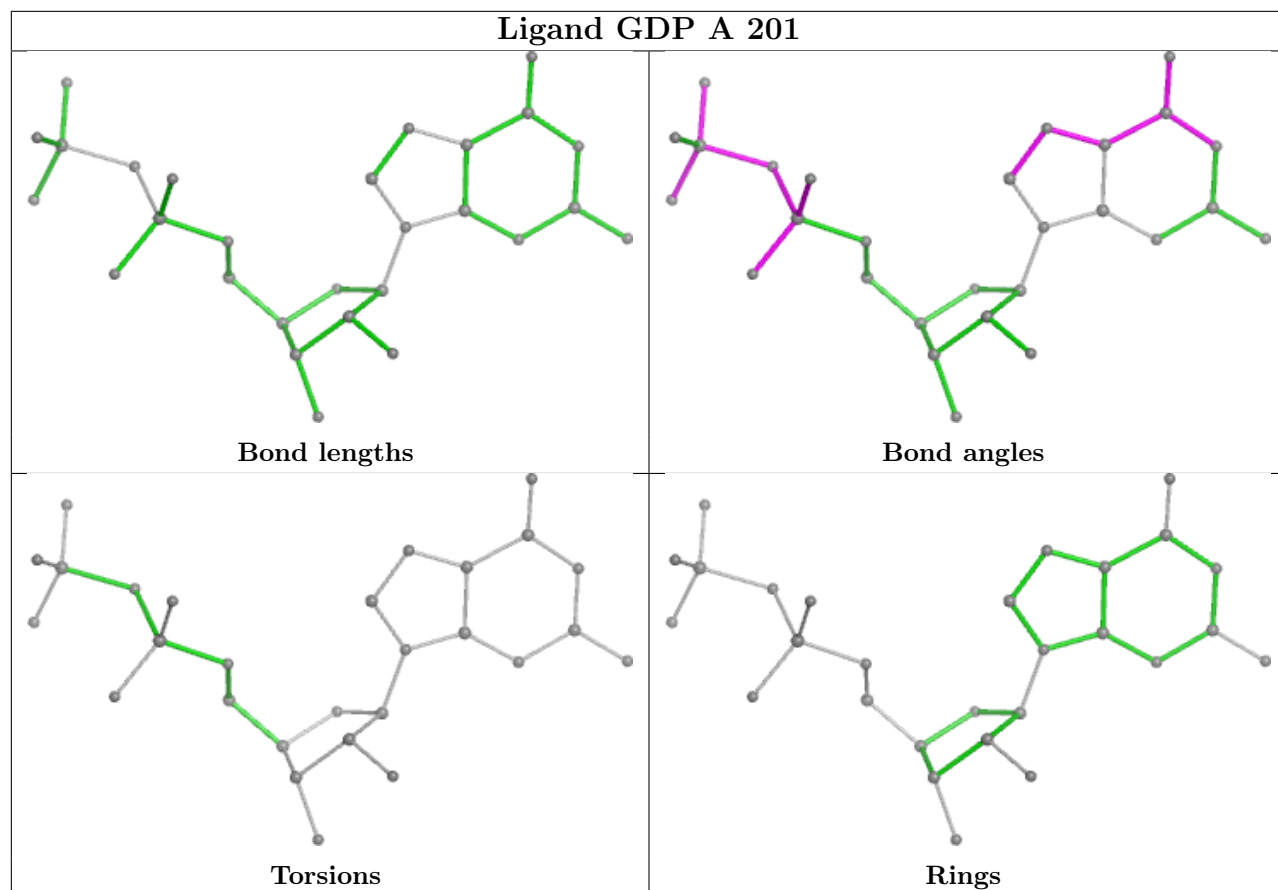
Mol	Chain	Res	Type	Atoms
3	G	201	GDP	O4'-C4'-C5'-O5'
3	G	201	GDP	C3'-C4'-C5'-O5'

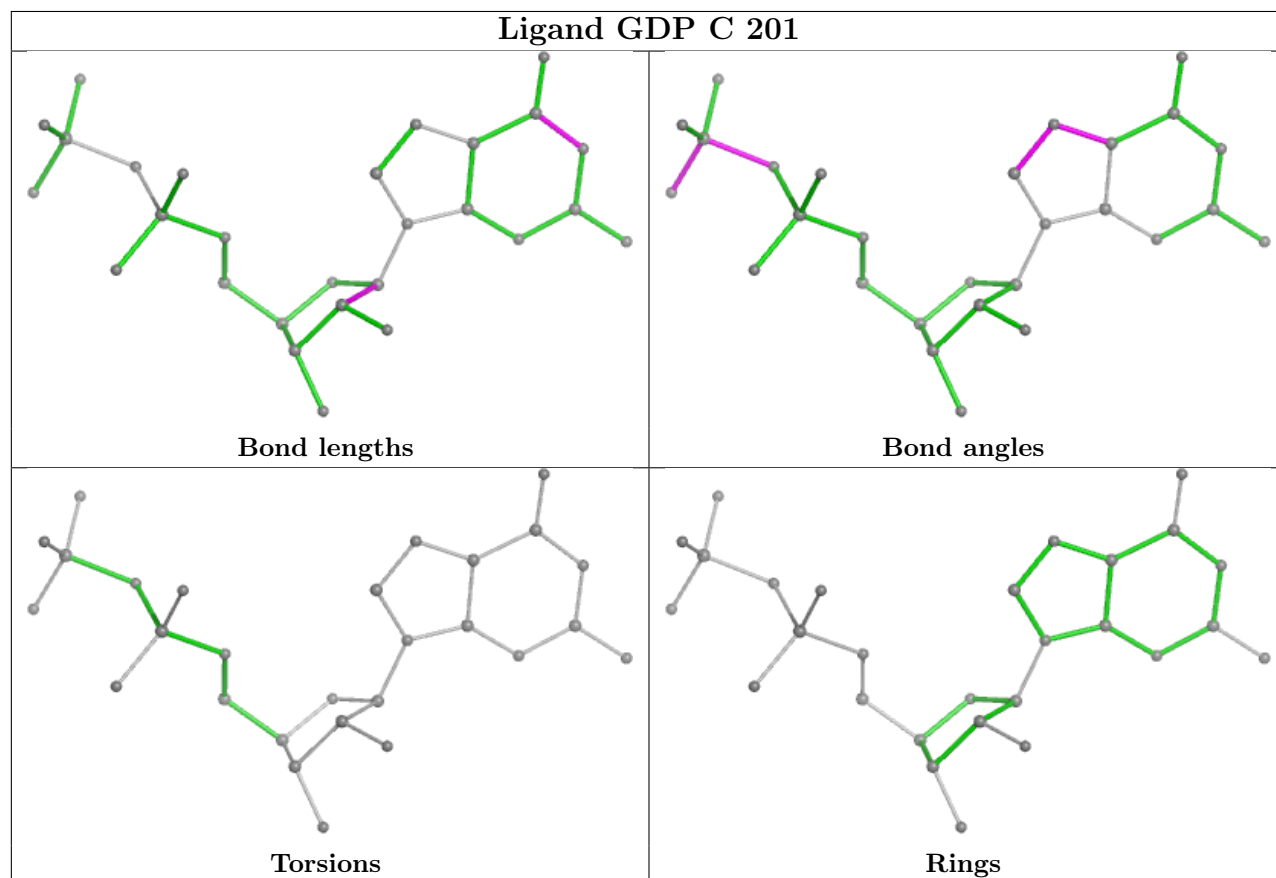
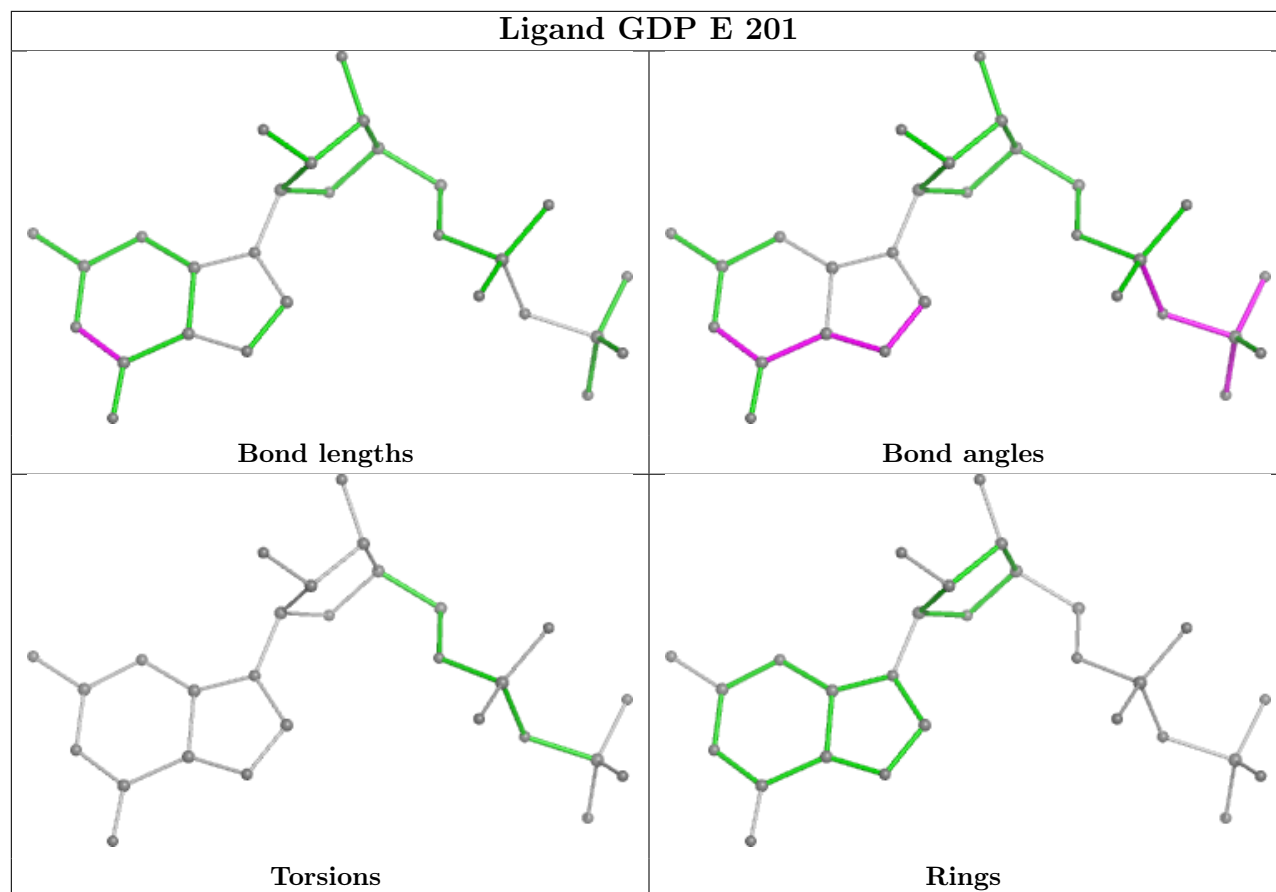
There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	201	GDP	1	0
3	G	201	GDP	1	0
3	E	201	GDP	1	0
3	C	201	GDP	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, 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	165/169 (97%)	0.06	0  100  100	42, 61, 83, 98	0
1	C	165/169 (97%)	0.03	0  100  100	40, 60, 80, 91	0
1	E	165/169 (97%)	-0.00	0  100  100	45, 69, 104, 125	0
1	G	164/169 (97%)	1.25	34 (20%)  1  0	84, 128, 153, 167	0
2	B	156/178 (87%)	-0.11	0  100  100	48, 66, 94, 109	0
2	D	156/178 (87%)	-0.05	0  100  100	55, 73, 97, 112	0
2	F	156/178 (87%)	0.14	1 (0%)  89  84	60, 86, 120, 134	0
2	H	156/178 (87%)	0.97	26 (16%)  1  1	78, 116, 154, 168	0
All	All	1283/1388 (92%)	0.29	61 (4%)  30  19	40, 76, 142, 168	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	48	GLY	5.2
1	G	77	GLY	5.0
1	G	152	VAL	4.9
1	G	156	PHE	4.8
1	G	47	ASP	4.8
1	G	111	MET	4.7
1	G	76	GLU	4.7
1	G	110	PRO	4.5
2	H	159	ALA	4.4
2	H	149	VAL	4.3
1	G	46	ILE	4.2
2	H	160	PHE	4.1
1	G	7	VAL	3.8
1	G	80	CYS	3.7
1	G	4	TYR	3.6
1	G	163	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
2	H	162	ILE	3.3
2	H	91	ARG	3.3
1	G	112	VAL	3.3
1	G	40	TYR	3.2
2	F	22	MET	3.1
1	G	72	MET	3.0
1	G	24	ILE	3.0
1	G	78	PHE	3.0
2	H	131	ALA	2.9
2	H	171	LEU	2.9
1	G	79	LEU	2.9
2	H	85	ALA	2.8
1	G	6	LEU	2.8
2	H	89	TYR	2.8
2	H	151	ALA	2.7
2	H	127	LEU	2.6
2	H	150	ASN	2.6
1	G	44	VAL	2.6
1	G	50	THR	2.6
2	H	143	LEU	2.6
2	H	57	GLY	2.5
2	H	172	ALA	2.5
2	H	153	ASP	2.5
1	G	133	LEU	2.4
1	G	53	LEU	2.4
2	H	82	ASP	2.4
1	G	160	VAL	2.4
2	H	136	LEU	2.4
1	G	140	PRO	2.4
1	G	23	LEU	2.3
2	H	58	PHE	2.3
2	H	145	ASN	2.2
1	G	161	ARG	2.2
2	H	129	LEU	2.2
2	H	164	ILE	2.2
2	H	94	LEU	2.2
2	H	90	GLY	2.2
1	G	52	LEU	2.2
2	H	116	VAL	2.2
1	G	3	GLU	2.1
1	G	20	THR	2.1
2	H	156	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	43	GLN	2.1
1	G	157	TYR	2.0
1	G	125	VAL	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](#)

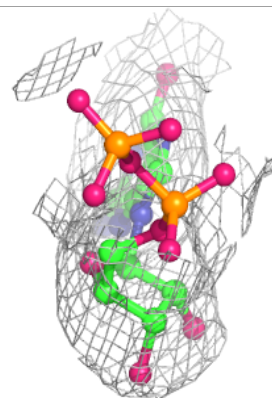
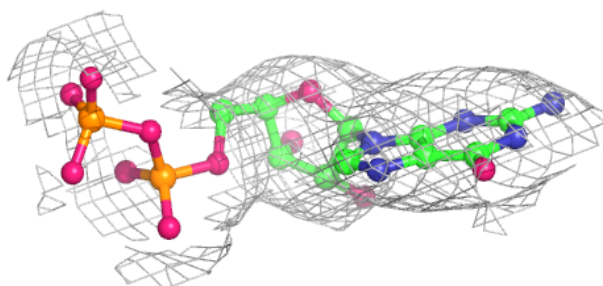
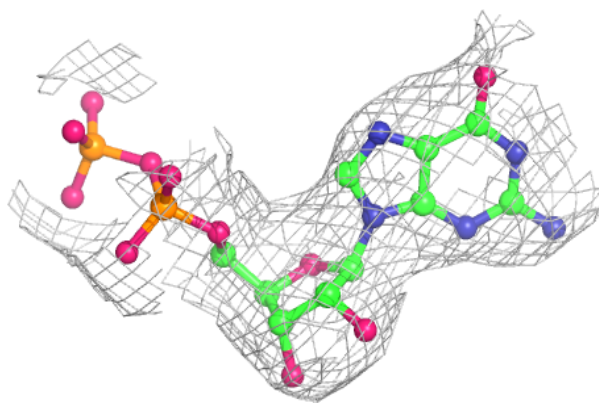
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	GDP	G	201	28/28	0.95	0.16	74,87,91,92	0
3	GDP	E	201	28/28	0.98	0.20	38,55,59,64	0
3	GDP	A	201	28/28	0.98	0.19	36,44,51,53	0
3	GDP	C	201	28/28	0.99	0.16	39,44,50,51	0
4	MG	A	202	1/1	0.99	0.12	33,33,33,33	0
4	MG	C	202	1/1	0.99	0.10	41,41,41,41	0
4	MG	E	202	1/1	0.99	0.14	50,50,50,50	0
4	MG	G	202	1/1	0.99	0.07	53,53,53,53	0

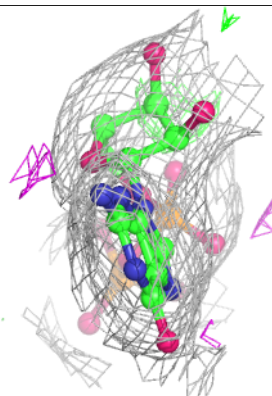
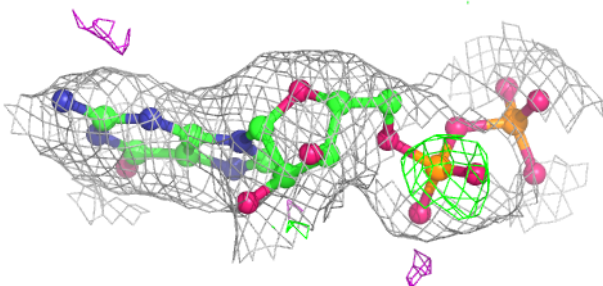
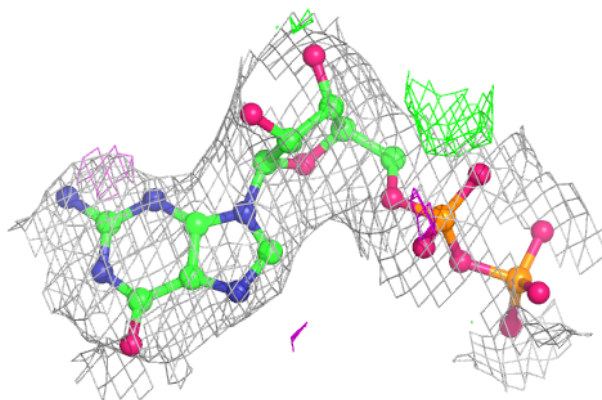
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around GDP G 201:**

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

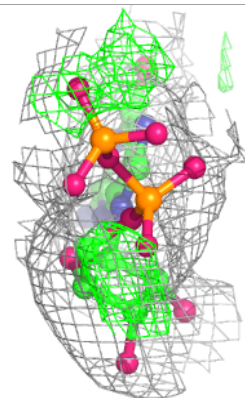
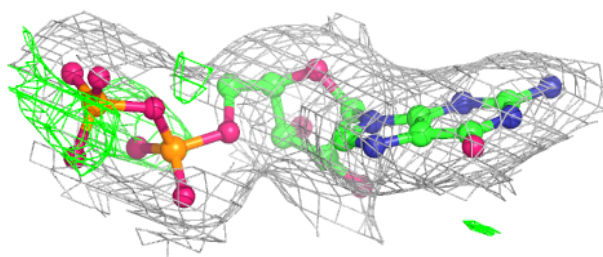
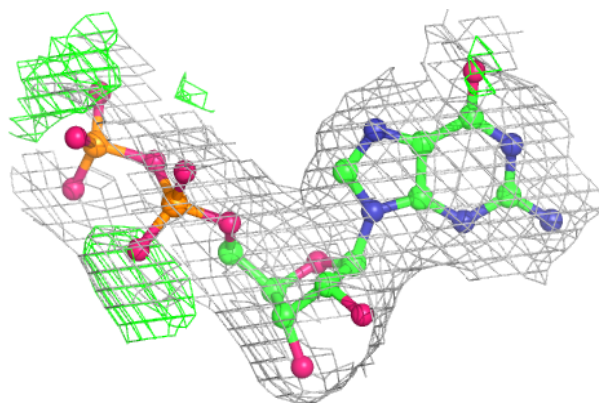
**Electron density around GDP E 201:**

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

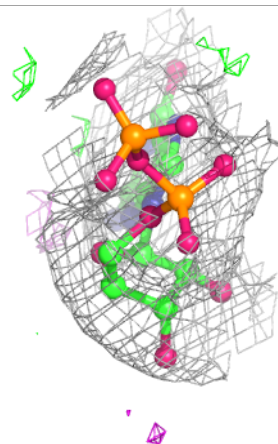
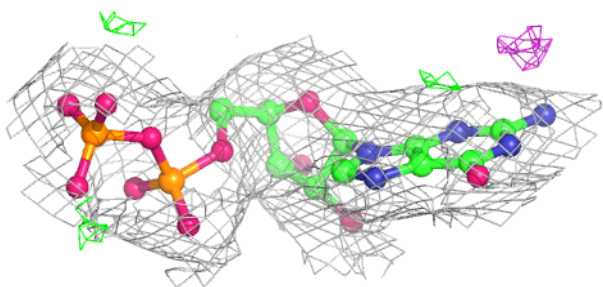
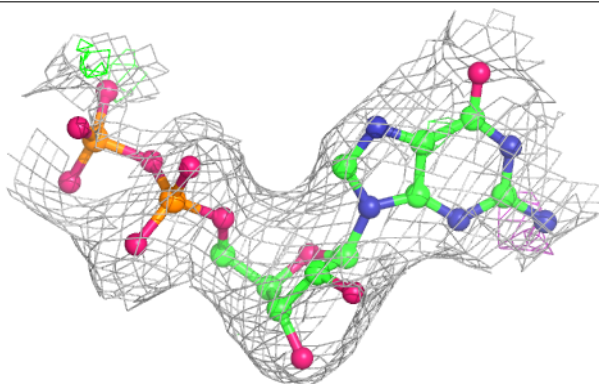


**Electron density around GDP A 201:**

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

**Electron density around GDP 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)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.