



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 1, 2022 – 04:17 PM EDT

PDB ID : 7TLG
Title : Crystal Structure of small molecule beta-lactone 5 covalently bound to K-Ras(G12S)
Authors : Ziyang, Z.; Guiley, K.Z.; Shokat, K.M.
Deposited on : 2022-01-18
Resolution : 1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at <http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.29
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) : 2.29

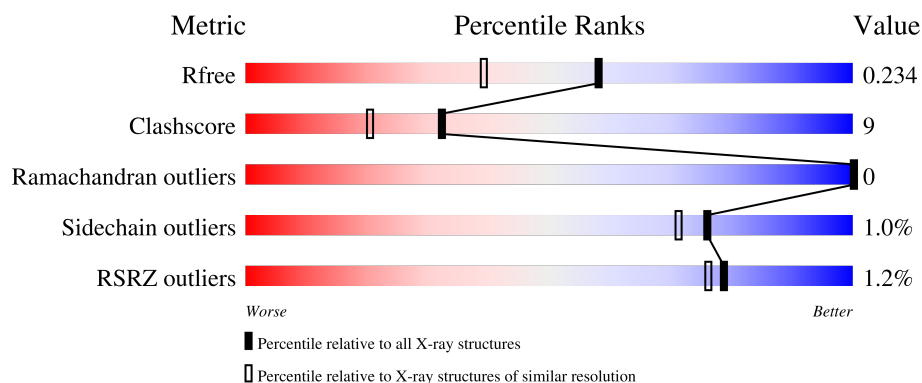
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	170	 88% 12%
1	B	170	 2% 79% 21%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3262 atoms, of which 56 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.

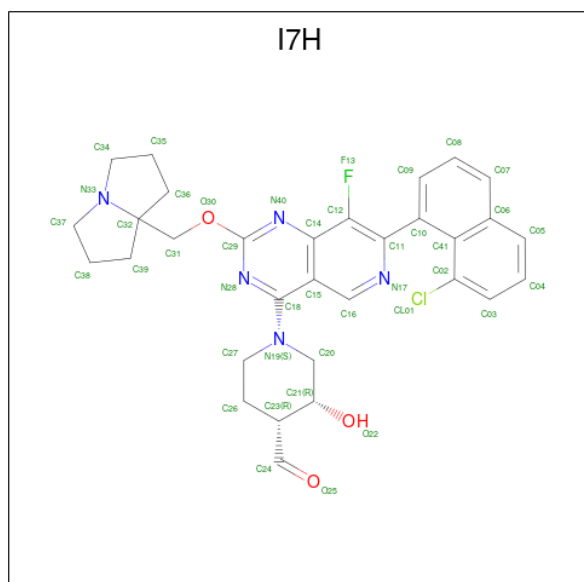
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	170	Total	C	N	O	S	0	1	0
			1365	854	234	273	4			
1	B	170	Total	C	N	O	S	0	0	0
			1359	851	233	271	4			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P01116
A	12	SER	GLY	engineered mutation	UNP P01116
A	51	SER	CYS	conflict	UNP P01116
A	80	LEU	CYS	conflict	UNP P01116
A	118	SER	CYS	conflict	UNP P01116
A	151	GLY	ARG	conflict	UNP P01116
A	153	ASP	GLU	conflict	UNP P01116
A	165	LYS	-	expression tag	UNP P01116
A	166	HIS	-	expression tag	UNP P01116
A	167	LYS	-	expression tag	UNP P01116
A	168	GLU	-	expression tag	UNP P01116
A	169	LYS	-	expression tag	UNP P01116
B	0	GLY	-	expression tag	UNP P01116
B	12	SER	GLY	engineered mutation	UNP P01116
B	51	SER	CYS	conflict	UNP P01116
B	80	LEU	CYS	conflict	UNP P01116
B	118	SER	CYS	conflict	UNP P01116
B	151	GLY	ARG	conflict	UNP P01116
B	153	ASP	GLU	conflict	UNP P01116
B	165	LYS	-	expression tag	UNP P01116
B	166	HIS	-	expression tag	UNP P01116
B	167	LYS	-	expression tag	UNP P01116
B	168	GLU	-	expression tag	UNP P01116
B	169	LYS	-	expression tag	UNP P01116

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- The image displays the chemical structure of GDP (Guanosine Diphosphate). It consists of a guanine base (a purine ring system with an amino group at C2 and a carbonyl group at C6) linked to a ribose sugar via a glycosidic bond at the N9 position. The ribose sugar is further linked to a diphosphate group at the C5' position. The diphosphate group is composed of two phosphate groups, labeled PA(S) and PB, connected by an oxygen atom. The terminal phosphate group (PB) is shown with its constituent atoms (P, O, H) and is labeled with 'OB' and 'OH'.

- Molecule 3 is (3R,4R)-1-[7-(8-chloronaphthalen-1-yl)-8-fluoro-2-{[(4S,7as)-tetrahydro-1H-pyrrolizin-7a(5H)-yl]methoxy}pyrido[4,3-d]pyrimidin-4-yl]-3-hydroxypiperidine-4-carbaldehyde (three-letter code: I7H) (formula: C₃₁H₃₁ClFN₅O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	A	1	Total	C	Cl	F	H	N	O	0	0
			69	31	1	1	28	5	3		
3	B	1	Total	C	Cl	F	H	N	O	0	0
			69	31	1	1	28	5	3		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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


- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	189	Total	O	0	0
			189	189		
5	B	153	Total	O	0	0
			153	153		

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:  88% 12%



- Molecule 1: GTPase KRas

Chain B:  2% 79% 21%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	41.55Å 66.53Å 60.80Å 90.00° 101.89° 90.00°	Depositor
Resolution (Å)	44.35 – 1.80 44.35 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.2 (44.35-1.80) 99.2 (44.35-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.40 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.10.1-2155	Depositor
R, R_{free}	0.179 , 0.233 0.179 , 0.234	Depositor DCC
R_{free} test set	1464 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3262	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, I7H, 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	0.43	0/1386	0.61	0/1867
1	B	0.41	0/1380	0.62	0/1859
All	All	0.42	0/2766	0.61	0/3726

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

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	1365	0	1347	16	0
1	B	1359	0	1343	31	1
2	A	28	0	12	0	0
2	B	28	0	12	1	0
3	A	41	28	0	1	0
3	B	41	28	0	3	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	189	0	0	4	1
5	B	153	0	0	6	2
All	All	3206	56	2714	49	3

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 (49) 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:1:MET:HE1	1:A:52:LEU:HB2	1.59	0.85
1:A:126:ASP:OD1	1:A:128:LYS:HG2	1.80	0.81
1:A:105:ASP:HB2	5:A:447:HOH:O	1.83	0.79
1:B:31:GLU:OE1	5:B:301:HOH:O	2.09	0.70
1:A:168:GLU:OE1	5:A:301:HOH:O	2.09	0.68
1:B:72:MET:HE2	3:B:203:I7H:C03	2.25	0.67
1:B:99:GLN:NE2	5:B:302:HOH:O	2.15	0.64
1:A:63:GLU:OE1	5:A:302:HOH:O	2.15	0.63
1:B:24:ILE:HD13	1:B:42:LYS:HB2	1.81	0.62
1:B:31:GLU:HG2	1:B:31:GLU:O	2.02	0.59
1:B:119:ASP:OD1	2:B:201:GDP:N1	2.26	0.59
1:B:23:LEU:HD21	1:B:53:LEU:HD12	1.86	0.58
1:B:142:ILE:HD13	1:B:155:ALA:HA	1.85	0.58
1:B:23:LEU:CD2	1:B:55:ILE:HD11	2.34	0.57
1:A:23:LEU:HD23	1:A:55:ILE:CD1	2.35	0.56
1:A:32:TYR:OH	1:A:40:TYR:OH	2.20	0.56
1:B:84:ILE:HD13	1:B:118:SER:HA	1.88	0.56
1:B:122:SER:HB2	5:B:371:HOH:O	2.07	0.55
1:B:5:LYS:HD3	1:B:74:THR:O	2.07	0.54
1:B:70:GLN:HG2	5:B:422:HOH:O	2.07	0.54
1:B:84:ILE:CD1	1:B:118:SER:HA	2.39	0.53
1:A:23:LEU:CD2	1:A:55:ILE:HD11	2.39	0.52
1:A:21:ILE:HD11	1:A:32:TYR:CD2	2.45	0.52
1:B:24:ILE:CD1	1:B:42:LYS:HB2	2.42	0.49
1:B:28:PHE:CE2	1:B:30:ASP:HB3	2.48	0.49
1:B:72:MET:HE2	3:B:203:I7H:C04	2.43	0.49
1:A:23:LEU:CD2	1:A:55:ILE:CD1	2.92	0.47
3:A:202:I7H:C11	3:A:202:I7H:CL01	3.00	0.46
1:A:41:ARG:HG2	1:A:52:LEU:HD11	1.98	0.46
1:A:108:ASP:OD2	5:A:304:HOH:O	2.21	0.45
1:B:17:SER:O	1:B:21:ILE:HG12	2.17	0.44
1:B:112:VAL:HG11	1:B:142:ILE:HD12	1.99	0.44
1:B:70:GLN:O	1:B:74:THR:HG23	2.18	0.44
1:A:28:PHE:CE2	1:A:30:ASP:HB3	2.53	0.44
1:B:24:ILE:HD13	1:B:42:LYS:CB	2.47	0.44
1:B:23:LEU:CD2	1:B:55:ILE:CD1	2.96	0.43
1:B:112:VAL:CG1	1:B:142:ILE:HD12	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:GLN:O	1:A:74:THR:HG23	2.20	0.42
1:A:126:ASP:O	1:A:129:GLN:HB3	2.18	0.42
1:B:28:PHE:CG	1:B:147:LYS:HA	2.54	0.42
3:B:203:I7H:CL01	3:B:203:I7H:C11	3.04	0.42
1:B:23:LEU:HD22	1:B:55:ILE:HD11	2.00	0.42
1:B:111:MET:HE2	5:B:414:HOH:O	2.20	0.42
1:B:16:LYS:HE2	1:B:58:THR:O	2.20	0.41
1:A:68:ARG:NH2	1:A:72:MET:HE1	2.35	0.41
1:B:128:LYS:O	1:B:128:LYS:HD3	2.21	0.41
1:B:141:PHE:CZ	1:B:143:GLU:HG2	2.55	0.41
1:B:63:GLU:HG2	1:B:64:TYR:N	2.36	0.41
1:B:97:ARG:NE	5:B:303:HOH:O	2.21	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:THR:OG1	1:B:126:ASP:OD1[2_556]	1.75	0.45
5:B:367:HOH:O	5:B:418:HOH:O[2_656]	2.13	0.07
5:A:481:HOH:O	5:B:431:HOH:O[1_554]	2.16	0.04

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	169/170 (99%)	164 (97%)	5 (3%)	0	100	100
1	B	168/170 (99%)	164 (98%)	4 (2%)	0	100	100
All	All	337/340 (99%)	328 (97%)	9 (3%)	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	151/150 (101%)	150 (99%)	1 (1%)	84	81
1	B	150/150 (100%)	148 (99%)	2 (1%)	69	62
All	All	301/300 (100%)	298 (99%)	3 (1%)	76	71

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	B	1	MET
1	B	150	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	25	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

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	I7H	B	203	1	44,47,47	4.78	14 (31%)	48,70,70	3.45	13 (27%)
2	GDP	B	201	4	24,30,30	0.95	1 (4%)	30,47,47	1.39	6 (20%)
2	GDP	A	201	4	24,30,30	0.95	1 (4%)	30,47,47	1.19	3 (10%)
3	I7H	A	202	1	44,47,47	4.70	15 (34%)	48,70,70	3.42	14 (29%)

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	I7H	B	203	1	-	3/16/49/49	0/7/7/7
2	GDP	B	201	4	-	0/12/32/32	0/3/3/3
2	GDP	A	201	4	-	0/12/32/32	0/3/3/3
3	I7H	A	202	1	-	1/16/49/49	0/7/7/7

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	203	I7H	C36-C32	-20.62	1.33	1.54
3	A	202	I7H	C36-C32	-20.11	1.34	1.54
3	B	203	I7H	C23-C24	9.53	1.65	1.50
3	A	202	I7H	C39-C32	9.51	1.63	1.54
3	A	202	I7H	C32-N33	9.07	1.60	1.49
3	A	202	I7H	C34-N33	-8.98	1.34	1.47
3	B	203	I7H	C39-C32	8.88	1.63	1.54
3	A	202	I7H	C23-C24	8.46	1.63	1.50
3	B	203	I7H	C32-N33	8.34	1.59	1.49
3	B	203	I7H	C34-N33	-8.08	1.36	1.47
3	B	203	I7H	C37-N33	7.55	1.57	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	202	I7H	C37-N33	7.24	1.57	1.47
3	B	203	I7H	C31-C32	6.03	1.62	1.52
3	B	203	I7H	C38-C37	6.00	1.72	1.51
3	A	202	I7H	C31-C32	5.91	1.62	1.52
3	A	202	I7H	C38-C37	5.85	1.72	1.51
3	B	203	I7H	C27-N19	5.43	1.55	1.46
3	A	202	I7H	O30-C29	5.32	1.40	1.34
3	B	203	I7H	O30-C29	5.27	1.40	1.34
3	A	202	I7H	C27-N19	3.87	1.52	1.46
3	B	203	I7H	C26-C23	-3.75	1.47	1.53
3	B	203	I7H	C16-C15	3.70	1.46	1.42
3	A	202	I7H	C16-C15	3.63	1.46	1.42
3	B	203	I7H	C20-N19	3.59	1.53	1.46
3	B	203	I7H	C18-N19	3.59	1.47	1.37
3	A	202	I7H	C20-N19	3.36	1.53	1.46
3	A	202	I7H	C26-C23	-3.36	1.47	1.53
3	A	202	I7H	C18-N19	3.00	1.46	1.37
3	A	202	I7H	C15-C14	-2.64	1.35	1.42
2	B	201	GDP	C6-N1	-2.49	1.34	1.37
2	A	201	GDP	C6-N1	-2.28	1.34	1.37

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	203	I7H	C37-N33-C34	18.63	141.43	115.25
3	A	202	I7H	C37-N33-C34	18.20	140.83	115.25
3	A	202	I7H	C02-C41-C06	9.27	119.18	114.93
3	B	203	I7H	C02-C41-C06	9.06	119.08	114.93
3	B	203	I7H	C10-C11-N17	4.85	125.05	115.52
3	A	202	I7H	C10-C11-N17	4.67	124.70	115.52
3	B	203	I7H	C10-C11-C12	-4.51	112.53	123.26
3	A	202	I7H	C10-C11-C12	-4.40	112.79	123.26
3	A	202	I7H	N40-C29-N28	-3.45	120.99	127.64
2	B	201	GDP	O3B-PB-O3A	3.39	116.00	104.64
3	B	203	I7H	N40-C29-N28	-3.35	121.19	127.64
3	A	202	I7H	O25-C24-C23	-3.16	117.78	125.16
2	B	201	GDP	PA-O3A-PB	-2.92	122.81	132.83
3	B	203	I7H	C07-C06-C05	-2.84	116.55	123.19
3	B	203	I7H	C15-C18-N19	2.84	126.50	120.97
3	A	202	I7H	C09-C10-C41	2.80	122.44	118.73
2	B	201	GDP	C8-N7-C5	2.73	108.19	102.99
3	A	202	I7H	C36-C32-N33	2.59	107.97	102.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	203	I7H	C03-C02-C41	-2.53	118.63	122.58
2	B	201	GDP	O5'-PA-O1A	2.48	118.77	109.07
3	B	203	I7H	O25-C24-C23	-2.42	119.52	125.16
3	B	203	I7H	C36-C32-N33	2.38	107.54	102.49
2	A	201	GDP	O6-C6-C5	-2.31	119.86	124.37
3	A	202	I7H	C27-N19-C18	2.25	125.16	118.73
3	A	202	I7H	C07-C06-C05	-2.22	118.01	123.19
2	A	201	GDP	C5-C6-N1	2.21	117.85	113.95
2	B	201	GDP	O4'-C1'-C2'	-2.17	103.75	106.93
3	A	202	I7H	C38-C37-N33	2.17	107.09	103.95
3	B	203	I7H	C39-C32-N33	2.16	107.05	102.49
2	B	201	GDP	C5-C6-N1	2.15	117.75	113.95
3	A	202	I7H	C39-C32-N33	2.15	107.04	102.49
3	A	202	I7H	C03-C02-C41	-2.14	119.23	122.58
3	B	203	I7H	C36-C35-C34	-2.08	100.27	104.26
2	A	201	GDP	C8-N7-C5	2.06	106.92	102.99
3	B	203	I7H	C27-N19-C18	2.06	124.60	118.73
3	A	202	I7H	C26-C27-N19	-2.04	106.91	111.10

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	203	I7H	N28-C29-O30-C31
3	B	203	I7H	N40-C29-O30-C31
3	A	202	I7H	C26-C23-C24-O25
3	B	203	I7H	C15-C18-N19-C20

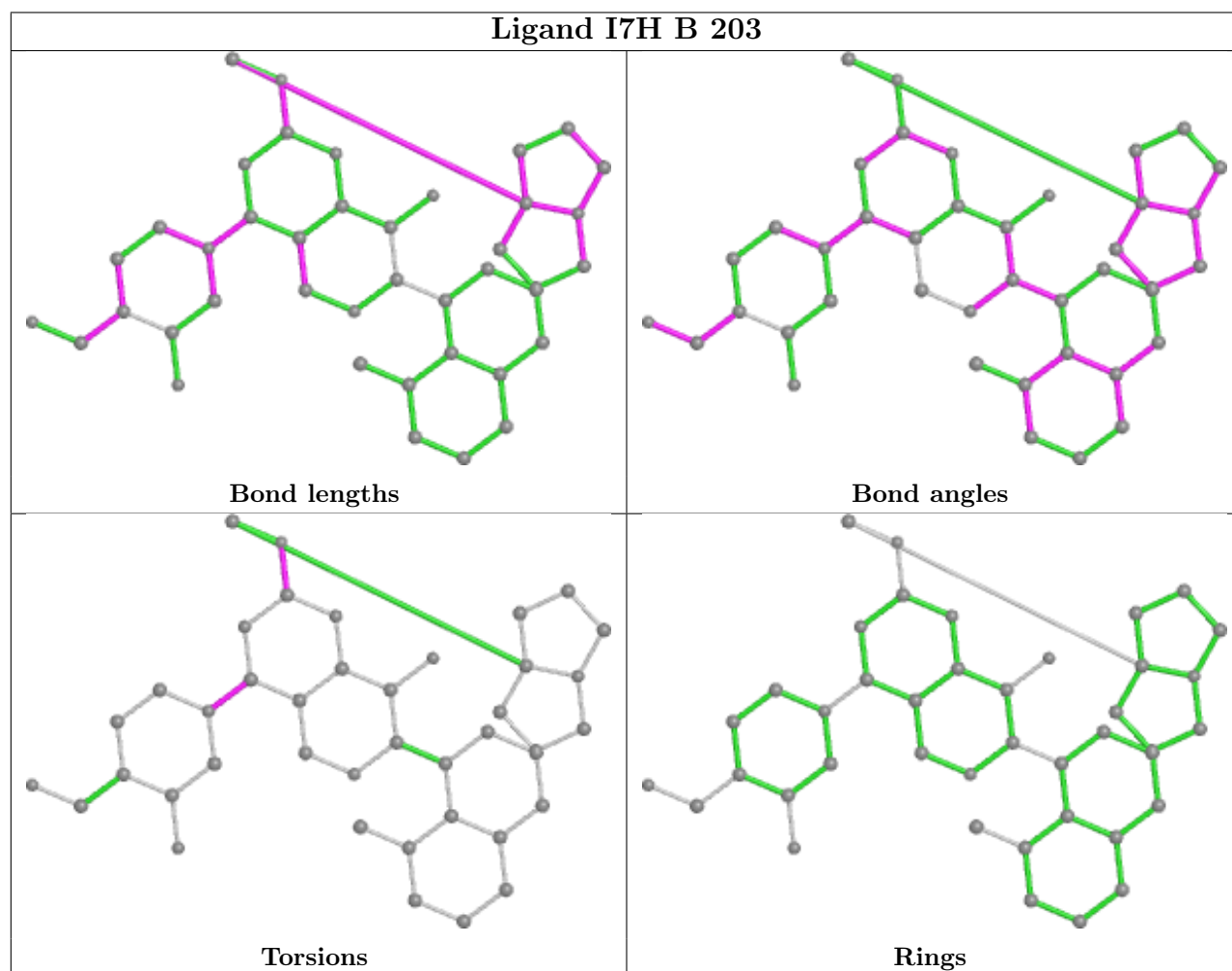
There are no ring outliers.

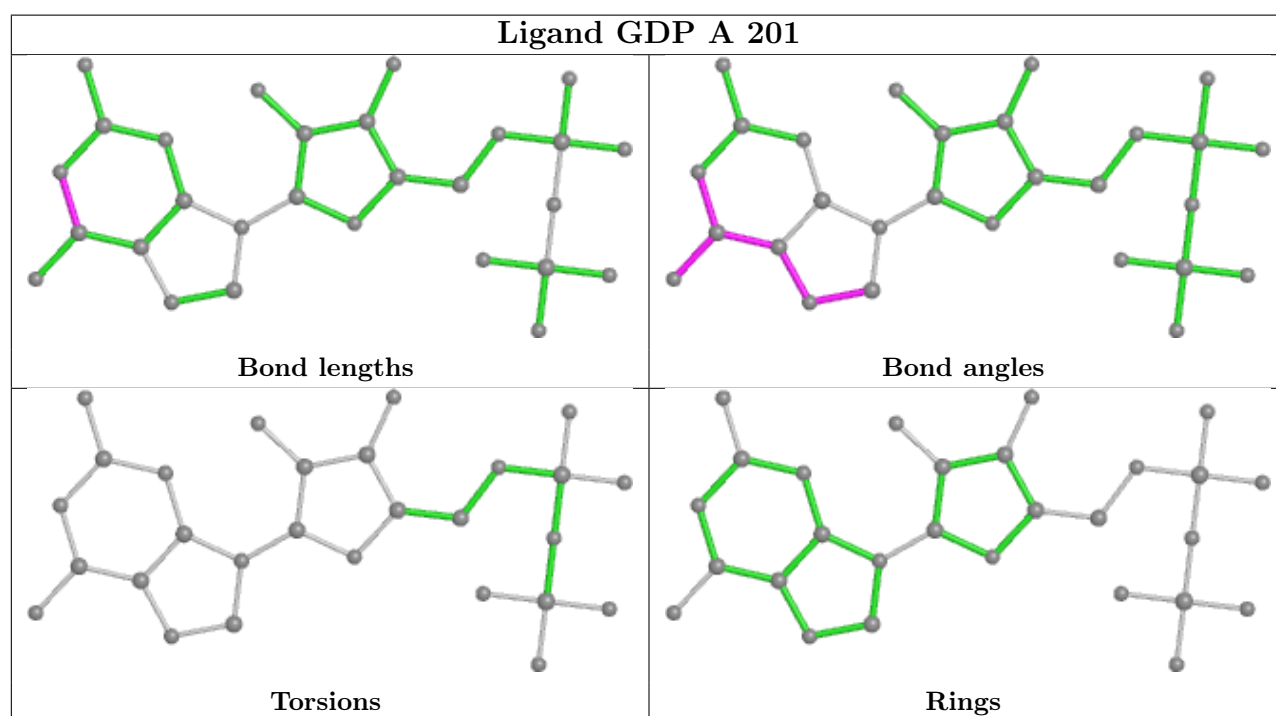
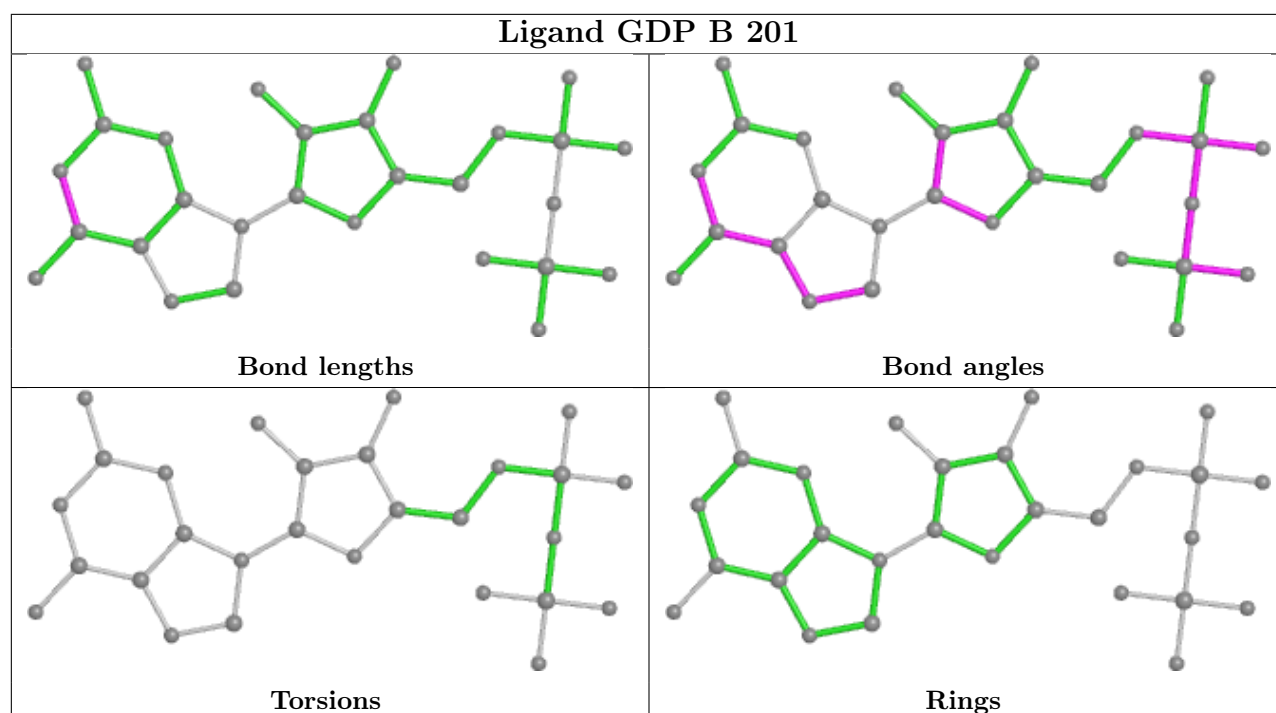
3 monomers are involved in 5 short contacts:

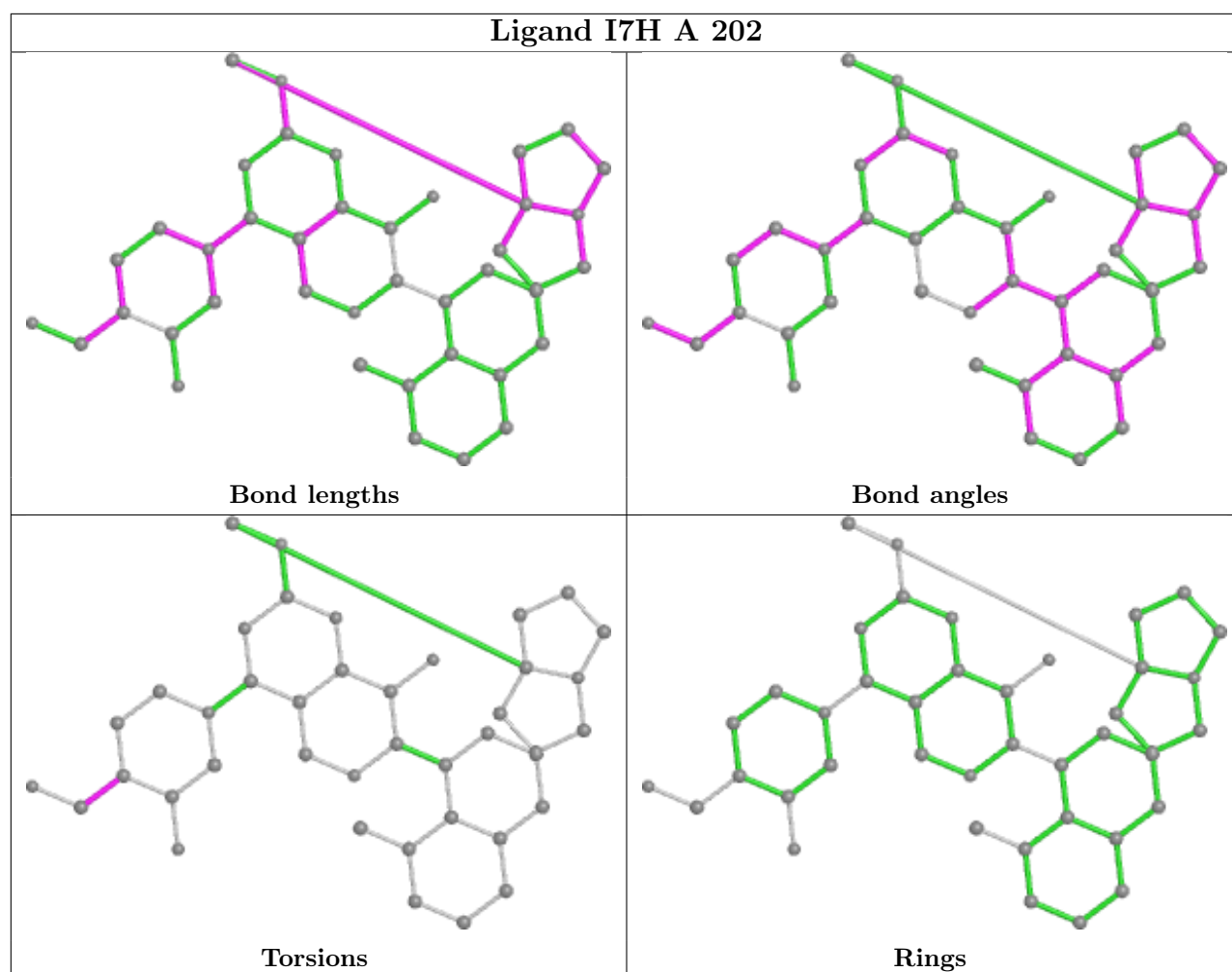
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	203	I7H	3	0
2	B	201	GDP	1	0
3	A	202	I7H	1	0

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 [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	170/170 (100%)	-0.35	0 100 100	8, 16, 28, 35	0
1	B	170/170 (100%)	-0.04	4 (2%) 59 54	11, 21, 36, 48	0
All	All	340/340 (100%)	-0.20	4 (1%) 79 76	8, 19, 33, 48	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	107	GLU	2.7
1	B	36	ILE	2.6
1	B	31	GLU	2.2
1	B	33	ASP	2.2

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
3	I7H	B	203	41/41	0.92	0.10	16,25,34,39	0

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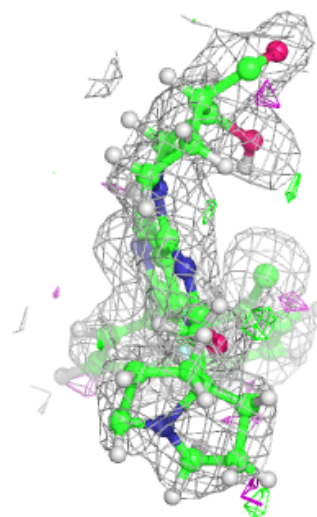
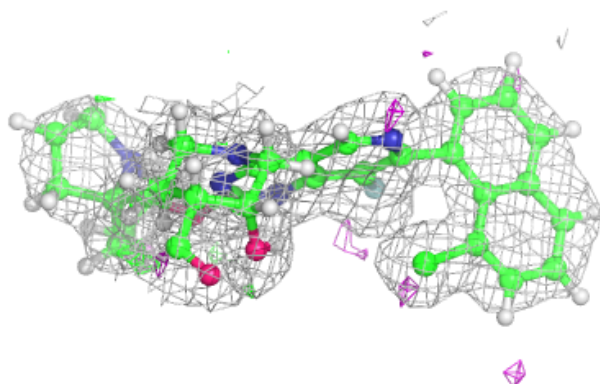
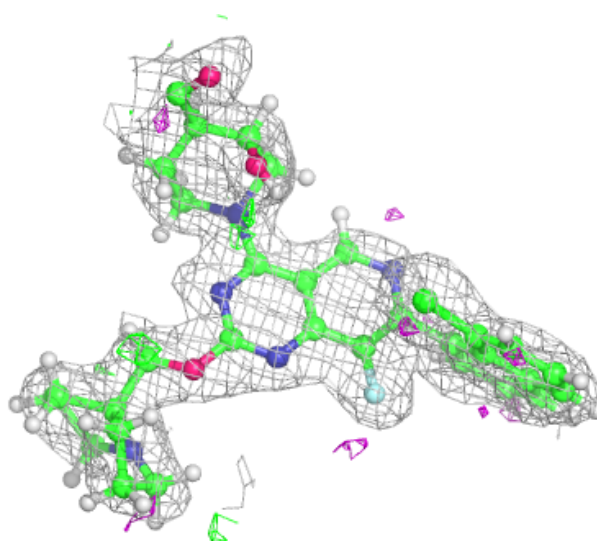
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	I7H	A	202	41/41	0.94	0.10	11,15,23,27	0
2	GDP	B	201	28/28	0.94	0.10	13,22,30,35	0
4	MG	B	202	1/1	0.96	0.05	21,21,21,21	0
4	MG	A	203	1/1	0.99	0.05	9,9,9,9	0
2	GDP	A	201	28/28	0.99	0.07	8,11,15,16	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.

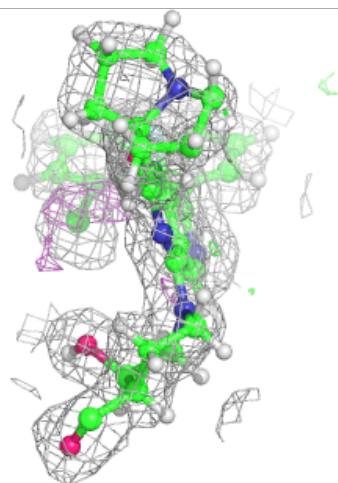
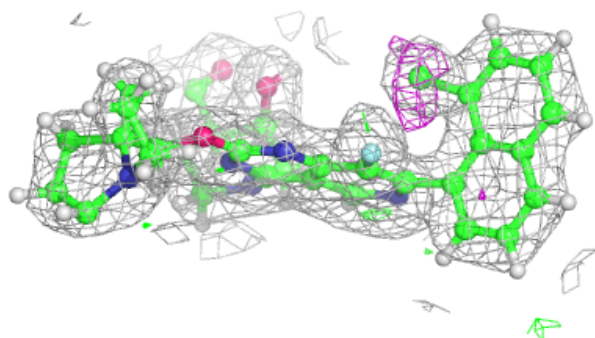
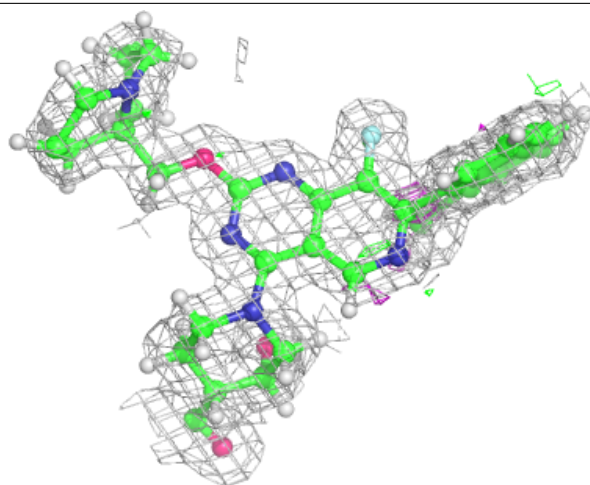
Electron density around I7H B 203:

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



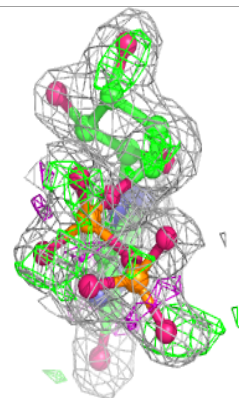
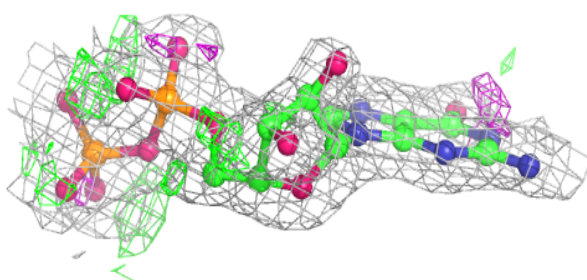
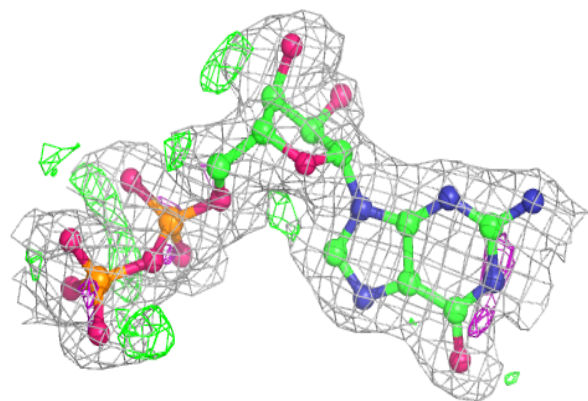
Electron density around I7H A 202:

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



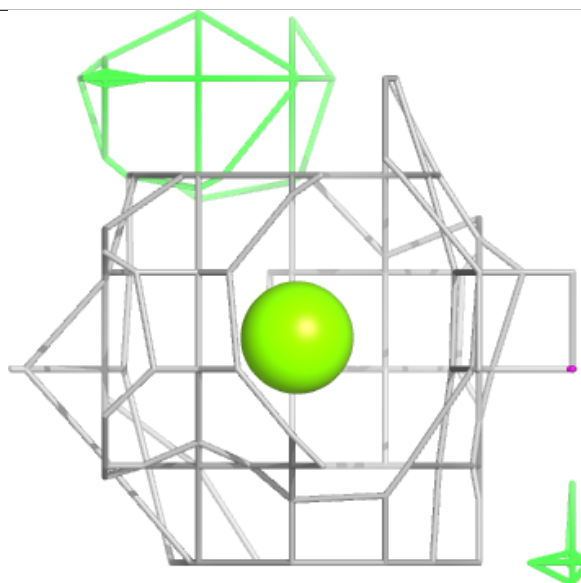
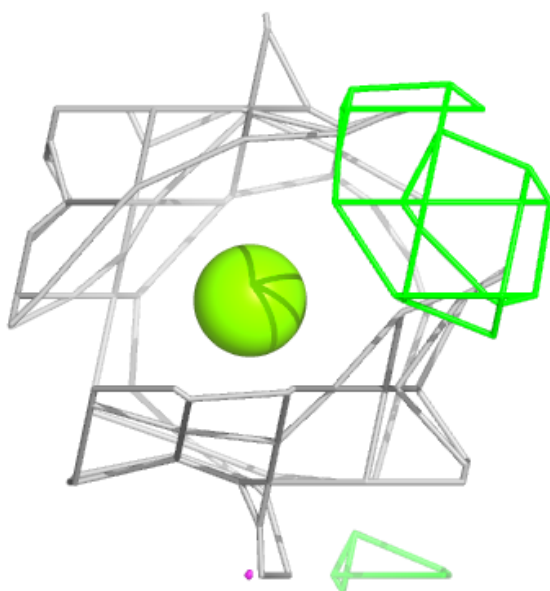
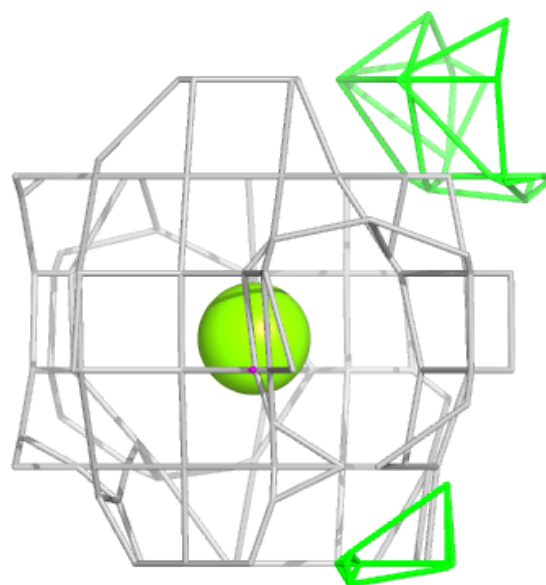
Electron density around GDP B 201:

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



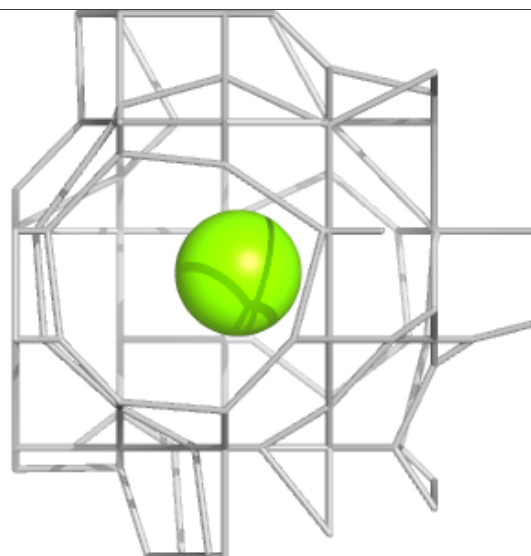
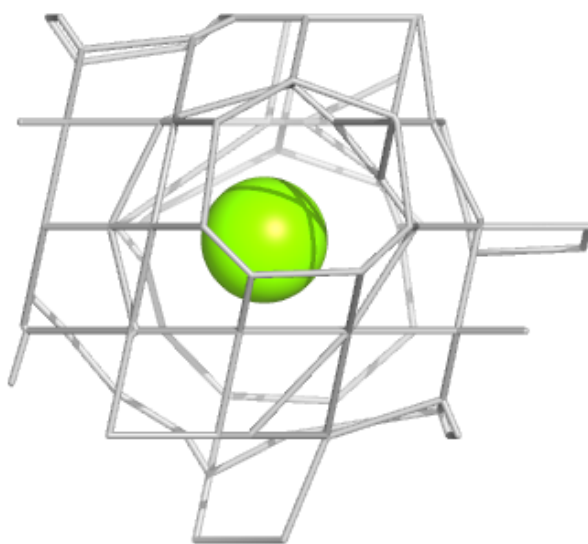
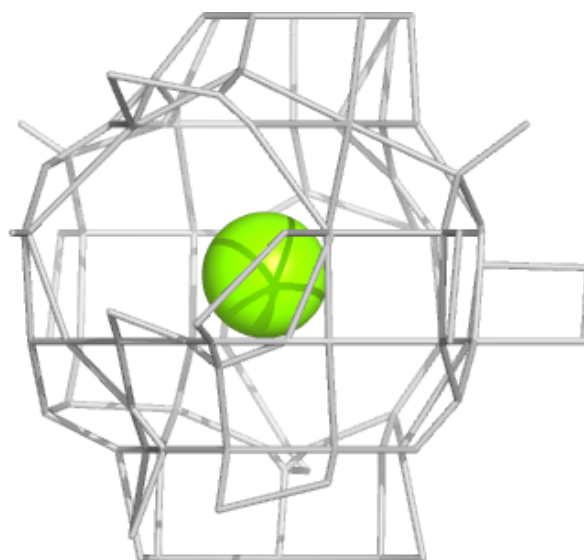
Electron density around MG B 202:

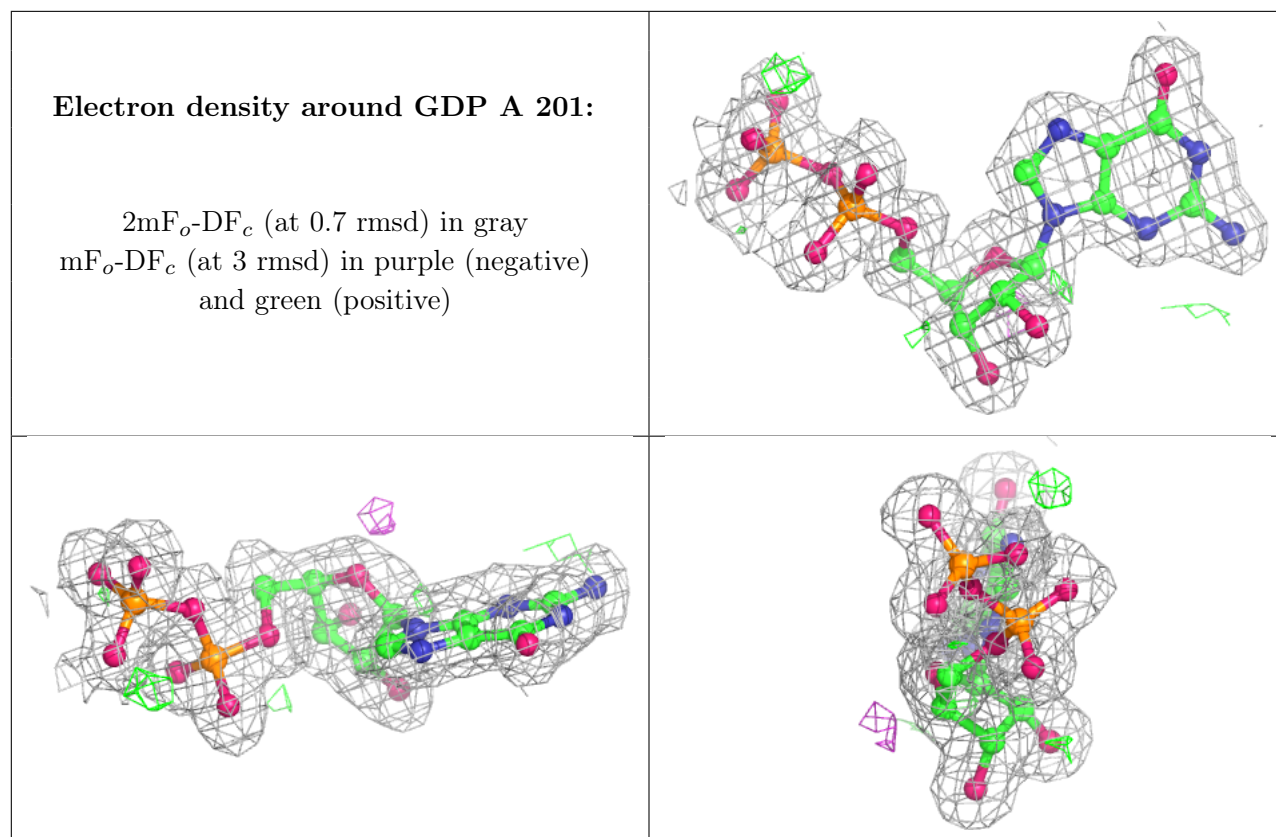
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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.