



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:21 AM UTC

PDB ID : 9MR6 / pdb_00009mr6
Title : X-ray crystal structure of SAMHD1 from Rhizophagus irregularis
Authors : Lachowicz, J.C.; Zizola, C.; Grove, T.G.
Deposited on : 2025-01-07
Resolution : 2.27 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

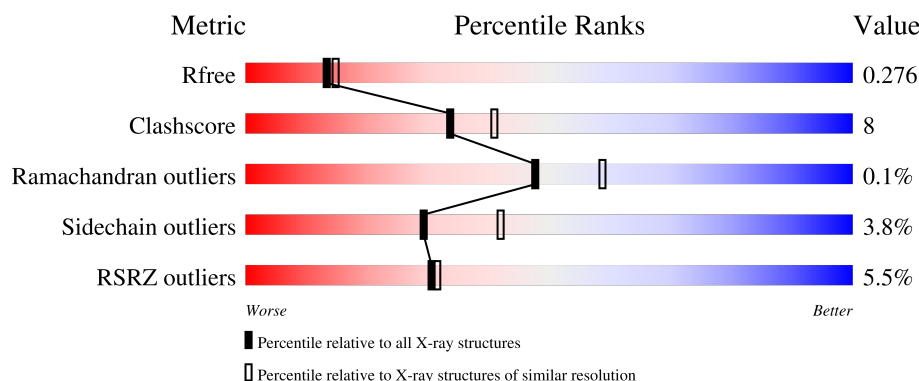
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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}	180053	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	483	4% 73% 17% 9%
1	B	483	7% 68% 22% 9%
1	C	483	5% 72% 18% 9%
1	D	483	4% 71% 19% 9%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15052 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 HD domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	440	Total	C	N	O	S	0	0	0
			3685	2367	624	680	14			
1	B	440	Total	C	N	O	S	0	0	0
			3686	2369	624	679	14			
1	C	440	Total	C	N	O	S	0	0	0
			3682	2366	623	679	14			
1	D	441	Total	C	N	O	S	0	0	0
			3690	2371	626	679	14			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A015K8Z8
A	-18	GLY	-	expression tag	UNP A0A015K8Z8
A	-17	SER	-	expression tag	UNP A0A015K8Z8
A	-16	SER	-	expression tag	UNP A0A015K8Z8
A	-15	HIS	-	expression tag	UNP A0A015K8Z8
A	-14	HIS	-	expression tag	UNP A0A015K8Z8
A	-13	HIS	-	expression tag	UNP A0A015K8Z8
A	-12	HIS	-	expression tag	UNP A0A015K8Z8
A	-11	HIS	-	expression tag	UNP A0A015K8Z8
A	-10	HIS	-	expression tag	UNP A0A015K8Z8
A	-9	SER	-	expression tag	UNP A0A015K8Z8
A	-8	SER	-	expression tag	UNP A0A015K8Z8
A	-7	GLY	-	expression tag	UNP A0A015K8Z8
A	-6	LEU	-	expression tag	UNP A0A015K8Z8
A	-5	VAL	-	expression tag	UNP A0A015K8Z8
A	-4	PRO	-	expression tag	UNP A0A015K8Z8
A	-3	ARG	-	expression tag	UNP A0A015K8Z8
A	-2	GLY	-	expression tag	UNP A0A015K8Z8
A	-1	SER	-	expression tag	UNP A0A015K8Z8
A	0	HIS	-	expression tag	UNP A0A015K8Z8
B	-19	MET	-	initiating methionine	UNP A0A015K8Z8

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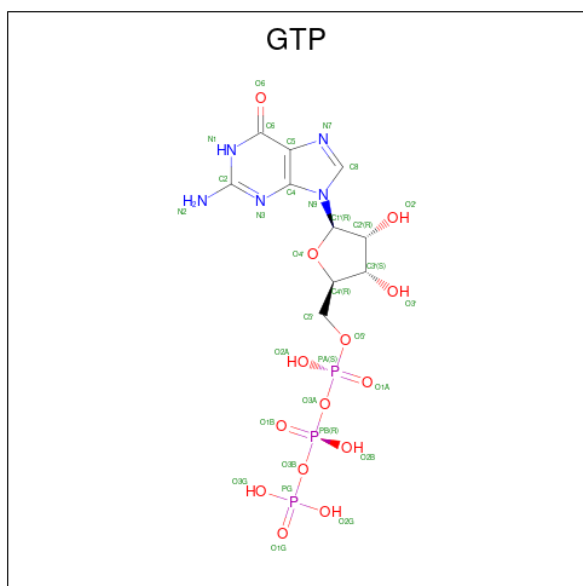
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP A0A015K8Z8
B	-17	SER	-	expression tag	UNP A0A015K8Z8
B	-16	SER	-	expression tag	UNP A0A015K8Z8
B	-15	HIS	-	expression tag	UNP A0A015K8Z8
B	-14	HIS	-	expression tag	UNP A0A015K8Z8
B	-13	HIS	-	expression tag	UNP A0A015K8Z8
B	-12	HIS	-	expression tag	UNP A0A015K8Z8
B	-11	HIS	-	expression tag	UNP A0A015K8Z8
B	-10	HIS	-	expression tag	UNP A0A015K8Z8
B	-9	SER	-	expression tag	UNP A0A015K8Z8
B	-8	SER	-	expression tag	UNP A0A015K8Z8
B	-7	GLY	-	expression tag	UNP A0A015K8Z8
B	-6	LEU	-	expression tag	UNP A0A015K8Z8
B	-5	VAL	-	expression tag	UNP A0A015K8Z8
B	-4	PRO	-	expression tag	UNP A0A015K8Z8
B	-3	ARG	-	expression tag	UNP A0A015K8Z8
B	-2	GLY	-	expression tag	UNP A0A015K8Z8
B	-1	SER	-	expression tag	UNP A0A015K8Z8
B	0	HIS	-	expression tag	UNP A0A015K8Z8
C	-19	MET	-	initiating methionine	UNP A0A015K8Z8
C	-18	GLY	-	expression tag	UNP A0A015K8Z8
C	-17	SER	-	expression tag	UNP A0A015K8Z8
C	-16	SER	-	expression tag	UNP A0A015K8Z8
C	-15	HIS	-	expression tag	UNP A0A015K8Z8
C	-14	HIS	-	expression tag	UNP A0A015K8Z8
C	-13	HIS	-	expression tag	UNP A0A015K8Z8
C	-12	HIS	-	expression tag	UNP A0A015K8Z8
C	-11	HIS	-	expression tag	UNP A0A015K8Z8
C	-10	HIS	-	expression tag	UNP A0A015K8Z8
C	-9	SER	-	expression tag	UNP A0A015K8Z8
C	-8	SER	-	expression tag	UNP A0A015K8Z8
C	-7	GLY	-	expression tag	UNP A0A015K8Z8
C	-6	LEU	-	expression tag	UNP A0A015K8Z8
C	-5	VAL	-	expression tag	UNP A0A015K8Z8
C	-4	PRO	-	expression tag	UNP A0A015K8Z8
C	-3	ARG	-	expression tag	UNP A0A015K8Z8
C	-2	GLY	-	expression tag	UNP A0A015K8Z8
C	-1	SER	-	expression tag	UNP A0A015K8Z8
C	0	HIS	-	expression tag	UNP A0A015K8Z8
D	-19	MET	-	initiating methionine	UNP A0A015K8Z8
D	-18	GLY	-	expression tag	UNP A0A015K8Z8
D	-17	SER	-	expression tag	UNP A0A015K8Z8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP A0A015K8Z8
D	-15	HIS	-	expression tag	UNP A0A015K8Z8
D	-14	HIS	-	expression tag	UNP A0A015K8Z8
D	-13	HIS	-	expression tag	UNP A0A015K8Z8
D	-12	HIS	-	expression tag	UNP A0A015K8Z8
D	-11	HIS	-	expression tag	UNP A0A015K8Z8
D	-10	HIS	-	expression tag	UNP A0A015K8Z8
D	-9	SER	-	expression tag	UNP A0A015K8Z8
D	-8	SER	-	expression tag	UNP A0A015K8Z8
D	-7	GLY	-	expression tag	UNP A0A015K8Z8
D	-6	LEU	-	expression tag	UNP A0A015K8Z8
D	-5	VAL	-	expression tag	UNP A0A015K8Z8
D	-4	PRO	-	expression tag	UNP A0A015K8Z8
D	-3	ARG	-	expression tag	UNP A0A015K8Z8
D	-2	GLY	-	expression tag	UNP A0A015K8Z8
D	-1	SER	-	expression tag	UNP A0A015K8Z8
D	0	HIS	-	expression tag	UNP A0A015K8Z8

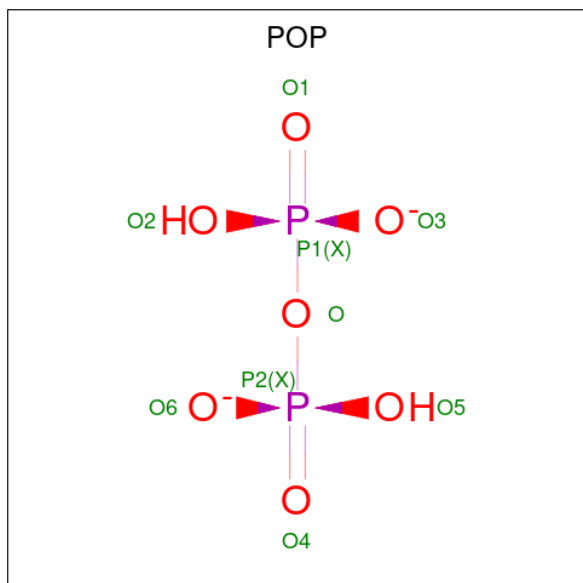
- Molecule 2 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
2	D	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 3 is PYROPHOSPHATE 2- (CCD ID: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			9	7	2		
3	B	1	Total	O	P	0	0
			9	7	2		
3	C	1	Total	O	P	0	0
			9	7	2		
3	D	1	Total	O	P	0	0
			9	7	2		

- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

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

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total 1	Mn 1	0	0
4	D	1	Total 1	Mn 1	0	0

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

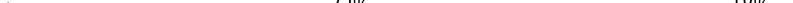
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	Ca 1	0	0
5	B	1	Total 1	Ca 1	0	0
5	C	1	Total 1	Ca 1	0	0
5	D	1	Total 1	Ca 1	0	0

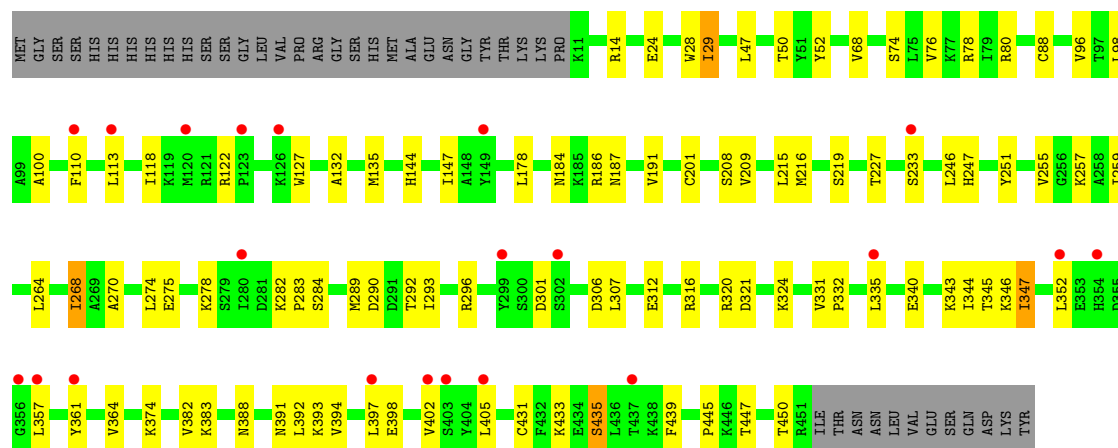
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	38	Total 38	O 38	0	0
6	B	24	Total 24	O 24	0	0
6	C	42	Total 42	O 42	0	0
6	D	33	Total 33	O 33	0	0

- Molecule 1: HD domain-containing protein



- Chain C:  5% 72% 18% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	84.36Å 85.42Å 87.03Å 104.58° 111.65° 99.51°	Depositor
Resolution (Å)	41.50 – 2.27 41.50 – 2.27	Depositor EDS
% Data completeness (in resolution range)	93.0 (41.50-2.27) 93.0 (41.50-2.27)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 2.27Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.220 , 0.280 0.218 , 0.276	Depositor DCC
R_{free} test set	4459 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å ²)	46.4	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 56.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15052	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.84% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, MN, POP, GTP

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	0.12	0/3767	0.27	0/5064
1	B	0.23	0/3768	0.36	0/5064
1	C	0.15	0/3764	0.29	0/5060
1	D	0.22	0/3773	0.36	0/5073
All	All	0.19	0/15072	0.33	0/20261

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	3685	0	3683	51	0
1	B	3686	0	3690	70	0
1	C	3682	0	3679	57	0
1	D	3690	0	3693	60	0
2	A	64	0	24	1	0
2	D	64	0	24	4	0
3	A	9	0	0	0	0
3	B	9	0	0	0	0
3	C	9	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	9	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	38	0	0	0	0
6	B	24	0	0	0	0
6	C	42	0	0	1	0
6	D	33	0	0	1	0
All	All	15052	0	14793	230	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 (230) 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:B:387:LYS:C	1:B:389:GLN:N	2.31	0.88
1:C:390:PRO:C	1:C:392:LEU:N	2.32	0.87
1:D:289:MET:HE1	1:D:293:ILE:HD12	1.65	0.77
1:B:426:LYS:HE3	1:B:427:GLN:HE22	1.50	0.75
1:A:405:LEU:HG	1:D:405:LEU:HD12	1.69	0.75
1:B:398:GLU:HG3	1:B:401:GLN:HB2	1.69	0.74
1:D:433:LYS:HG2	1:D:445:PRO:HG2	1.71	0.73
1:D:118:ILE:HG21	1:D:127:TRP:HB3	1.71	0.72
1:C:340:GLU:HB3	1:C:343:LYS:HB2	1.74	0.69
1:B:397:LEU:HD13	1:B:402:VAL:HG11	1.75	0.69
1:B:14:ARG:HB3	1:B:22:LEU:HD22	1.73	0.69
1:A:80:ARG:NH2	1:A:90:ASP:OD1	2.28	0.66
1:D:340:GLU:HB2	1:D:343:LYS:HE3	1.78	0.66
1:A:351:GLN:HE22	1:A:434:GLU:HB3	1.62	0.65
1:B:293:ILE:HA	1:B:296:ARG:HG3	1.78	0.64
1:B:347:ILE:HD13	1:B:439:PHE:HB2	1.78	0.64
1:B:247:HIS:HA	1:B:251:TYR:HB2	1.77	0.64
1:C:68:VAL:HG12	1:C:100:ALA:HB1	1.79	0.64
1:C:331:VAL:HG22	1:C:413:LEU:HB3	1.80	0.63
1:B:406:VAL:HG22	1:B:407:PRO:HD2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:398:GLU:N	1:D:398:GLU:OE1	2.31	0.62
1:A:130:GLU:OE1	1:A:130:GLU:N	2.24	0.62
1:C:61:ARG:NH1	1:C:104:ASP:OD2	2.33	0.61
1:A:68:VAL:HG12	1:A:100:ALA:HB1	1.81	0.61
1:B:447:THR:O	1:C:401:GLN:NE2	2.33	0.61
1:D:290:ASP:OD1	1:D:292:THR:OG1	2.18	0.61
1:A:379:ILE:HD11	1:A:384:PHE:HZ	1.66	0.61
1:A:372:GLY:O	1:A:374:LYS:N	2.33	0.61
1:D:431:CYS:O	1:D:435:SER:OG	2.19	0.61
1:B:27:ASN:HA	1:B:30:VAL:HB	1.83	0.60
1:A:302:SER:HB3	1:A:307:LEU:HD12	1.82	0.60
1:C:76:VAL:HG21	1:C:96:VAL:HG11	1.83	0.60
1:B:448:TYR:OH	1:C:231:LYS:NZ	2.29	0.59
1:C:255:VAL:HG11	2:D:601:GTP:H5''	1.83	0.59
1:C:371:TYR:HE2	1:C:378:PRO:HG3	1.68	0.58
1:D:187:ASN:ND2	6:D:704:HOH:O	2.35	0.58
2:A:603:GTP:H5''	1:B:255:VAL:HG21	1.85	0.58
1:A:345:THR:O	1:A:349:THR:OG1	2.19	0.58
1:D:301:ASP:OD1	1:D:301:ASP:N	2.36	0.58
1:D:14:ARG:HG2	1:D:24:GLU:HG2	1.86	0.57
1:C:347:ILE:HD13	1:C:439:PHE:HB2	1.85	0.57
1:D:80:ARG:HG2	1:D:88:CYS:HB3	1.87	0.57
1:C:78:ARG:NH2	1:C:219:SER:OG	2.38	0.56
1:A:351:GLN:NE2	1:A:434:GLU:HB3	2.20	0.56
1:C:357:LEU:HD23	1:C:361:TYR:HE2	1.69	0.56
1:A:148:ALA:HB1	1:A:151:LEU:HD23	1.87	0.56
1:B:430:LYS:O	1:B:434:GLU:HG2	2.06	0.55
1:B:136:MET:HE2	1:B:286:TYR:HB3	1.87	0.55
1:C:262:MET:HE2	1:C:317:ILE:HG12	1.88	0.55
1:D:264:LEU:O	1:D:268:ILE:HD12	2.07	0.55
1:A:169:GLU:OE1	1:A:169:GLU:N	2.40	0.54
1:C:320:ARG:HH21	2:D:601:GTP:H5'	1.72	0.54
1:B:68:VAL:HG12	1:B:100:ALA:HB1	1.90	0.54
1:A:247:HIS:HA	1:A:251:TYR:HB2	1.90	0.54
1:B:170:ASP:N	1:B:170:ASP:OD1	2.41	0.54
1:C:390:PRO:O	1:C:392:LEU:N	2.40	0.54
1:A:379:ILE:HD11	1:A:384:PHE:CZ	2.43	0.54
1:B:45:LYS:HA	1:B:60:ASN:HD22	1.72	0.53
1:D:52:TYR:O	1:D:320:ARG:NH2	2.41	0.53
1:B:76:VAL:HG21	1:B:96:VAL:HG11	1.90	0.53
1:C:247:HIS:HA	1:C:251:TYR:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:220:ARG:NH1	1:C:220:ARG:HB3	2.23	0.53
1:D:357:LEU:HB3	1:D:361:TYR:HE2	1.73	0.53
1:A:293:ILE:HA	1:A:296:ARG:HG3	1.91	0.53
1:B:328:GLU:HG2	1:B:448:TYR:HB2	1.91	0.52
1:D:122:ARG:CZ	1:D:122:ARG:HA	2.39	0.52
1:B:326:VAL:HG12	1:B:429:ARG:HG3	1.90	0.52
1:A:428:ILE:H	1:A:428:ILE:HD12	1.75	0.52
1:B:282:LYS:HD3	1:B:284:SER:H	1.75	0.52
1:D:127:TRP:HE1	1:D:132:ALA:HB2	1.75	0.52
1:D:76:VAL:HG21	1:D:96:VAL:HG11	1.92	0.51
1:A:392:LEU:H	1:A:393:LYS:HZ2	1.57	0.51
1:A:329:PHE:CE2	1:A:331:VAL:HG12	2.46	0.51
1:B:171:THR:HB	1:B:176:PRO:HB3	1.93	0.51
1:B:186:ARG:HG2	1:B:187:ASN:OD1	2.12	0.50
1:A:76:VAL:HG13	1:A:93:LEU:HD12	1.93	0.50
1:B:400:SER:HB2	1:C:330:LEU:HD22	1.94	0.50
1:C:254:ARG:HG2	1:C:325:PHE:HE2	1.76	0.50
1:B:426:LYS:HE3	1:B:427:GLN:NE2	2.24	0.50
1:D:282:LYS:HD2	1:D:284:SER:OG	2.11	0.50
1:A:348:ILE:O	1:A:352:LEU:HD23	2.12	0.50
1:B:227:THR:HG21	1:B:394:VAL:HG11	1.94	0.50
1:A:80:ARG:HG2	1:A:88:CYS:HB3	1.94	0.50
1:B:326:VAL:O	1:B:429:ARG:NH1	2.45	0.49
1:A:262:MET:HE2	1:A:317:ILE:HG13	1.93	0.49
1:C:367:LEU:HB3	1:C:414:ASN:HB2	1.95	0.49
1:A:340:GLU:HG3	1:A:343:LYS:H	1.76	0.49
1:C:146:GLU:CD	1:C:146:GLU:H	2.20	0.49
1:C:325:PHE:HE1	1:C:327:ASP:C	2.20	0.49
1:C:392:LEU:HD23	1:C:392:LEU:HA	1.68	0.49
1:B:210:PHE:CZ	1:B:239:LEU:HD12	2.47	0.48
1:B:340:GLU:HB3	1:B:343:LYS:HB2	1.95	0.48
1:B:419:THR:HG21	1:B:428:ILE:HD12	1.95	0.48
1:D:282:LYS:HD3	1:D:283:PRO:HD2	1.95	0.48
1:A:347:ILE:HD11	1:A:438:LYS:HB3	1.96	0.48
1:A:351:GLN:HE21	1:A:431:CYS:HA	1.78	0.48
1:B:370:ASN:HB3	1:B:372:GLY:O	2.14	0.48
1:C:237:TYR:CE1	1:C:379:ILE:HG13	2.49	0.48
1:C:371:TYR:CE2	1:C:378:PRO:HG3	2.48	0.48
1:D:343:LYS:HD2	1:D:439:PHE:CE2	2.49	0.48
1:A:207:LYS:HA	1:A:207:LYS:HD3	1.65	0.48
1:D:28:TRP:CE2	1:D:29:ILE:HG12	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:ASN:OD1	1:A:379:ILE:HG22	2.13	0.47
1:B:125:ARG:NH1	1:B:131:GLU:OE2	2.32	0.47
1:B:23:MET:HE3	1:B:25:PHE:HE2	1.78	0.47
1:B:47:LEU:HB3	1:B:50:THR:HB	1.96	0.47
1:D:135:MET:SD	1:D:283:PRO:HG3	2.54	0.47
1:D:312:GLU:O	1:D:316:ARG:HG3	2.15	0.47
1:D:255:VAL:HG21	2:D:602:GTP:H5'	1.96	0.47
1:A:61:ARG:NH1	1:A:104:ASP:OD2	2.39	0.47
1:A:451:ARG:HE	1:A:451:ARG:HA	1.78	0.47
1:B:28:TRP:NE1	1:B:29:ILE:HG23	2.29	0.47
1:A:209:VAL:HG23	1:D:209:VAL:HG23	1.96	0.47
1:C:220:ARG:HB3	1:C:220:ARG:HH11	1.79	0.47
1:D:347:ILE:HG22	1:D:435:SER:HB3	1.96	0.47
1:D:255:VAL:O	1:D:259:ILE:HG13	2.15	0.47
1:B:305:PRO:O	1:B:309:LYS:NZ	2.48	0.47
1:A:238:GLU:HA	1:A:241:HIS:HB2	1.98	0.46
1:B:434:GLU:HA	1:B:437:THR:HG22	1.98	0.46
1:D:270:ALA:HB1	1:D:274:LEU:HD23	1.96	0.46
1:A:118:ILE:HD13	1:A:280:ILE:HD13	1.97	0.46
1:B:352:LEU:HD11	1:B:428:ILE:HG23	1.98	0.46
1:B:347:ILE:HG13	1:B:348:ILE:N	2.31	0.46
1:C:335:LEU:HD11	1:C:442:ILE:HD11	1.98	0.46
1:A:433:LYS:HB3	1:A:445:PRO:HG3	1.96	0.46
1:C:270:ALA:HB1	1:C:274:LEU:HD12	1.98	0.46
1:C:304:ASP:OD2	1:C:306:ASP:HB2	2.16	0.46
1:A:32:PHE:CZ	1:A:148:ALA:HB2	2.51	0.46
1:C:155:ASP:O	1:C:159:ILE:HG13	2.16	0.45
1:C:296:ARG:HD3	1:D:296:ARG:HD3	1.99	0.45
1:B:355:ASP:OD1	1:B:355:ASP:N	2.48	0.45
1:D:216:MET:HE3	1:D:216:MET:HB3	1.86	0.45
1:A:64:HIS:O	1:A:68:VAL:HG23	2.16	0.45
1:B:326:VAL:HG21	1:B:419:THR:HG23	1.99	0.45
1:B:413:LEU:HD12	1:B:413:LEU:HA	1.84	0.45
1:D:374:LYS:HA	1:D:374:LYS:HD3	1.82	0.45
1:B:257:LYS:HA	1:B:260:ASP:HB2	1.98	0.45
1:D:247:HIS:HA	1:D:251:TYR:HB2	1.97	0.45
1:A:44:ILE:HA	1:A:291:ASP:OD1	2.15	0.45
1:D:47:LEU:HB3	1:D:50:THR:HB	1.97	0.45
1:A:216:MET:HA	1:A:216:MET:HE2	1.99	0.45
1:B:357:LEU:HG	1:B:424:LYS:HZ3	1.82	0.45
1:A:91:LYS:HE3	1:A:91:LYS:HB2	1.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:LYS:HD2	1:B:387:LYS:HA	1.79	0.44
1:C:127:TRP:NE1	6:C:601:HOH:O	2.28	0.44
1:A:72:ALA:O	1:A:76:VAL:HG12	2.17	0.44
1:D:346:LYS:HE3	1:D:347:ILE:HG12	1.99	0.44
1:C:387:LYS:HB2	1:C:387:LYS:HE2	1.56	0.44
1:D:307:LEU:HD23	1:D:307:LEU:HA	1.80	0.44
1:A:379:ILE:HD12	1:A:379:ILE:HA	1.80	0.44
1:D:68:VAL:HG12	1:D:100:ALA:HB1	1.98	0.44
1:A:109:PRO:HD2	1:A:114:PHE:CD1	2.53	0.44
1:A:341:LYS:HD2	1:A:366:ILE:HG12	1.99	0.44
1:D:227:THR:HG21	1:D:394:VAL:HG11	2.00	0.44
1:B:243:ARG:HH22	1:B:372:GLY:HA2	1.82	0.43
1:C:358:LYS:NZ	1:C:361:TYR:OH	2.48	0.43
1:D:447:THR:HG22	1:D:450:THR:OG1	2.18	0.43
1:A:257:LYS:HA	1:A:260:ASP:HB2	2.00	0.43
1:D:257:LYS:HA	1:D:257:LYS:HD3	1.75	0.43
1:D:392:LEU:HD13	1:D:393:LYS:O	2.18	0.43
1:B:263:ILE:O	1:B:267:LEU:HG	2.19	0.43
1:C:28:TRP:CE2	1:C:94:LYS:HD3	2.54	0.43
1:C:64:HIS:CE1	1:C:196:TYR:HB3	2.54	0.43
1:C:327:ASP:HB3	1:C:432:PHE:HD2	1.83	0.43
1:D:78:ARG:NH2	1:D:219:SER:OG	2.50	0.43
1:B:13:LYS:HG3	1:B:30:VAL:HG21	2.01	0.43
1:B:150:ASP:OD1	1:B:150:ASP:N	2.41	0.43
1:B:309:LYS:H	1:B:309:LYS:HG2	1.58	0.43
1:B:447:THR:HG22	1:B:450:THR:HG23	1.99	0.43
1:B:80:ARG:HG2	1:B:88:CYS:HB3	2.00	0.43
1:D:397:LEU:HD22	1:D:402:VAL:HG22	2.01	0.43
1:C:238:GLU:OE2	1:C:404:TYR:OH	2.35	0.43
1:B:25:PHE:HB3	1:B:29:ILE:HD11	2.01	0.42
1:D:110:PHE:HB2	1:D:113:LEU:HB3	2.01	0.42
1:C:144:HIS:O	1:C:147:ILE:HG12	2.19	0.42
1:D:144:HIS:O	1:D:147:ILE:HG12	2.18	0.42
1:D:343:LYS:HD2	1:D:439:PHE:HE2	1.84	0.42
1:B:86:LEU:HD11	1:B:221:VAL:HB	2.01	0.42
1:B:269:ALA:HB1	1:B:309:LYS:HG3	2.00	0.42
1:C:247:HIS:HB3	1:C:369:LEU:HD21	2.01	0.42
1:B:144:HIS:O	1:B:147:ILE:HG12	2.18	0.42
1:A:171:THR:HB	1:A:176:PRO:HB3	2.00	0.42
1:A:326:VAL:HB	1:A:417:ILE:HG22	2.02	0.42
1:A:351:GLN:HG2	1:A:431:CYS:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:ARG:HG3	1:C:88:CYS:HB3	2.00	0.42
1:C:343:LYS:O	1:C:347:ILE:HG22	2.19	0.42
1:C:421:ASN:OD1	1:C:423:ASP:HB2	2.19	0.42
1:C:367:LEU:HD22	1:C:416:ARG:CZ	2.49	0.42
1:D:324:LYS:HD2	1:D:324:LYS:HA	1.84	0.42
1:D:332:PRO:HD2	1:D:335:LEU:HB2	2.02	0.42
1:B:37:HIS:HB2	1:B:140:LEU:HD12	2.01	0.42
1:C:366:ILE:HD12	1:C:366:ILE:O	2.19	0.42
1:D:275:GLU:HB3	1:D:278:LYS:HD3	2.01	0.42
1:D:346:LYS:HE2	1:D:346:LYS:HB3	1.78	0.42
1:B:64:HIS:CE1	1:B:196:TYR:HB3	2.54	0.42
1:C:269:ALA:O	1:C:306:ASP:HB3	2.20	0.41
1:D:397:LEU:HB3	1:D:402:VAL:HG21	2.01	0.41
1:C:31:LYS:HD2	1:C:31:LYS:HA	1.71	0.41
1:D:340:GLU:O	1:D:344:ILE:HG22	2.20	0.41
2:D:602:GTP:O1A	2:D:602:GTP:N2	2.54	0.41
1:B:379:ILE:H	1:B:379:ILE:HD12	1.86	0.41
1:D:68:VAL:HG13	1:D:191:VAL:HG23	2.01	0.41
1:D:98:LEU:HD23	1:D:98:LEU:HA	1.94	0.41
1:A:332:PRO:HD2	1:A:335:LEU:HD12	2.02	0.41
1:B:377:ASN:HB3	1:B:380:ASP:OD2	2.20	0.41
1:B:28:TRP:CD1	1:B:29:ILE:HG23	2.56	0.41
1:B:238:GLU:HA	1:B:241:HIS:HB3	2.03	0.41
1:B:338:LYS:HE2	1:B:440:PHE:HB3	2.03	0.41
1:D:316:ARG:HB3	1:D:321:ASP:HB3	2.02	0.41
1:A:128:THR:HG23	1:A:131:GLU:H	1.86	0.41
1:A:332:PRO:HB2	1:A:334:ASP:OD1	2.20	0.41
1:C:98:LEU:HD12	1:C:98:LEU:HA	1.89	0.41
1:C:186:ARG:HG3	1:C:381:ASN:HD22	1.84	0.41
1:B:392:LEU:HD23	1:C:451:ARG:HH12	1.86	0.41
1:C:34:ASP:CG	1:D:320:ARG:HG3	2.46	0.41
1:C:246:LEU:HD23	1:C:246:LEU:HA	1.90	0.41
1:D:201:CYS:SG	1:D:246:LEU:HD21	2.61	0.41
1:C:137:PHE:HZ	1:C:159:ILE:HD12	1.86	0.40
1:C:238:GLU:HA	1:C:241:HIS:HB2	2.02	0.40
1:A:135:MET:HE1	1:A:280:ILE:O	2.21	0.40
1:B:257:LYS:HA	1:B:257:LYS:HD2	1.82	0.40
1:C:187:ASN:HD22	1:C:187:ASN:HA	1.64	0.40
1:B:35:THR:HG21	1:B:140:LEU:HD21	2.03	0.40
1:C:254:ARG:HG2	1:C:325:PHE:CE2	2.56	0.40
1:D:184:ASN:OD1	1:D:186:ARG:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:293:ILE:HA	1:D:296:ARG:HG3	2.03	0.40
1:A:63:GLU:HB3	1:B:55:PRO:HB2	2.04	0.40
1:B:146:GLU:HA	1:B:149:TYR:CZ	2.57	0.40
1:B:434:GLU:O	1:B:438:LYS:HB2	2.21	0.40
1:D:345:THR:HG23	1:D:364:VAL:HG21	2.04	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	436/483 (90%)	421 (97%)	15 (3%)	0	100	100
1	B	436/483 (90%)	418 (96%)	17 (4%)	1 (0%)	43	53
1	C	436/483 (90%)	420 (96%)	16 (4%)	0	100	100
1	D	439/483 (91%)	420 (96%)	19 (4%)	0	100	100
All	All	1747/1932 (90%)	1679 (96%)	67 (4%)	1 (0%)	48	59

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	390	PRO

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	411/449 (92%)	399 (97%)	12 (3%)	37	52
1	B	411/449 (92%)	397 (97%)	14 (3%)	32	46
1	C	410/449 (91%)	390 (95%)	20 (5%)	22	31
1	D	411/449 (92%)	395 (96%)	16 (4%)	28	41
All	All	1643/1796 (92%)	1581 (96%)	62 (4%)	29	42

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LYS
1	A	142	LYS
1	A	152	ASP
1	A	217	ASN
1	A	248	LYS
1	A	319	LYS
1	A	374	LYS
1	A	382	VAL
1	A	392	LEU
1	A	406	VAL
1	A	446	LYS
1	A	447	THR
1	B	27	ASN
1	B	53	VAL
1	B	85	ASP
1	B	157	LEU
1	B	170	ASP
1	B	209	VAL
1	B	213	SER
1	B	282	LYS
1	B	334	ASP
1	B	338	LYS
1	B	346	LYS
1	B	350	ASP
1	B	358	LYS
1	B	450	THR
1	C	12	SER
1	C	19	ILE
1	C	53	VAL
1	C	170	ASP
1	C	185	LYS
1	C	279	SER
1	C	288	LYS

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Mol	Chain	Res	Type
1	C	291	ASP
1	C	302	SER
1	C	326	VAL
1	C	330	LEU
1	C	369	LEU
1	C	380	ASP
1	C	387	LYS
1	C	392	LEU
1	C	399	SER
1	C	402	VAL
1	C	413	LEU
1	C	422	ARG
1	C	431	CYS
1	D	29	ILE
1	D	74	SER
1	D	178	LEU
1	D	208	SER
1	D	215	LEU
1	D	233	SER
1	D	268	ILE
1	D	306	ASP
1	D	331	VAL
1	D	347	ILE
1	D	352	LEU
1	D	382	VAL
1	D	383	LYS
1	D	388	ASN
1	D	391	ASN
1	D	435	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	225	GLN
1	A	351	GLN
1	A	427	GLN
1	B	60	ASN
1	B	187	ASN
1	B	414	ASN
1	B	427	GLN
1	C	46	GLN

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Mol	Chain	Res	Type
1	C	187	ASN
1	C	217	ASN
1	C	381	ASN
1	C	388	ASN
1	C	414	ASN
1	C	427	GLN
1	D	129	HIS
1	D	217	ASN
1	D	427	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	$\# Z > 2$
2	GTP	A	603	5	33,34,34	0.98	2 (6%)	50,54,54	1.58	8 (16%)
2	GTP	A	601	5	33,34,34	0.96	2 (6%)	50,54,54	1.58	10 (20%)
3	POP	B	501	4	6,8,8	0.79	0	12,13,13	0.79	0
3	POP	C	501	4	6,8,8	0.80	0	12,13,13	0.78	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GTP	D	601	5	33,34,34	0.96	0	50,54,54	1.58	9 (18%)
3	POP	A	602	4	6,8,8	0.80	0	12,13,13	0.79	0
2	GTP	D	602	5	33,34,34	1.03	4 (12%)	50,54,54	1.63	9 (18%)
3	POP	D	603	4	6,8,8	0.85	0	12,13,13	0.73	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
2	GTP	A	603	5	-	2/22/38/38	0/3/3/3
2	GTP	A	601	5	-	1/22/38/38	0/3/3/3
3	POP	B	501	4	-	0/6/6/6	-
3	POP	C	501	4	-	0/6/6/6	-
2	GTP	D	601	5	-	5/22/38/38	0/3/3/3
3	POP	A	602	4	-	0/6/6/6	-
2	GTP	D	602	5	-	4/22/38/38	0/3/3/3
3	POP	D	603	4	-	0/6/6/6	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	602	GTP	PB-O3B	2.32	1.62	1.59
2	D	602	GTP	PA-O3A	2.26	1.61	1.59
2	D	602	GTP	C2-N3	2.26	1.38	1.33
2	A	601	GTP	PB-O3B	2.25	1.61	1.59
2	A	601	GTP	C2-N3	2.20	1.38	1.33
2	A	603	GTP	C2-N3	2.17	1.38	1.33
2	D	602	GTP	PB-O3A	2.17	1.61	1.59
2	A	603	GTP	PA-O3A	2.04	1.61	1.59

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	602	GTP	C5-C4-N3	-5.30	119.96	128.39
2	D	601	GTP	C5-C4-N3	-5.28	119.99	128.39
2	A	601	GTP	C5-C4-N3	-5.24	120.06	128.39
2	A	603	GTP	C5-C4-N3	-5.17	120.16	128.39
2	D	601	GTP	C2-N3-C4	4.89	120.73	112.30
2	D	602	GTP	C2-N3-C4	4.73	120.45	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	603	GTP	C2-N3-C4	4.73	120.45	112.30
2	A	601	GTP	C2-N3-C4	4.72	120.43	112.30
2	D	602	GTP	N9-C4-N3	3.61	133.17	125.95
2	A	603	GTP	N9-C4-N3	3.49	132.92	125.95
2	A	601	GTP	N9-C4-N3	3.41	132.77	125.95
2	D	601	GTP	N9-C4-N3	3.36	132.68	125.95
2	D	602	GTP	C2-N1-C6	-3.00	119.68	125.11
2	A	601	GTP	C2-N1-C6	-2.92	119.82	125.11
2	A	603	GTP	C2-N1-C6	-2.89	119.88	125.11
2	D	601	GTP	C2-N1-C6	-2.83	119.97	125.11
2	D	602	GTP	O6-C6-C5	-2.56	119.79	126.53
2	A	603	GTP	O6-C6-C5	-2.55	119.80	126.53
2	D	602	GTP	C5-C6-N1	2.54	119.71	113.25
2	A	601	GTP	N9-C8-N7	-2.53	108.70	113.40
2	A	601	GTP	C5-C6-N1	2.51	119.65	113.25
2	A	601	GTP	C8-N7-C5	2.50	108.72	104.26
2	A	603	GTP	N9-C8-N7	-2.50	108.77	113.40
2	D	601	GTP	C5-C6-N1	2.49	119.58	113.25
2	A	603	GTP	C5-C6-N1	2.46	119.50	113.25
2	D	602	GTP	N9-C8-N7	-2.45	108.86	113.40
2	A	603	GTP	C8-N7-C5	2.43	108.59	104.26
2	D	602	GTP	C8-N7-C5	2.40	108.53	104.26
2	D	601	GTP	O6-C6-C5	-2.29	120.50	126.53
2	A	601	GTP	O6-C6-C5	-2.26	120.55	126.53
2	D	601	GTP	C8-N7-C5	2.26	108.28	104.26
2	D	601	GTP	N9-C8-N7	-2.25	109.23	113.40
2	D	602	GTP	C3'-C2'-C1'	2.24	105.69	101.46
2	A	601	GTP	O3G-PG-O3B	2.18	111.94	104.64
2	D	601	GTP	C3'-C2'-C1'	2.07	105.38	101.46
2	A	601	GTP	C3'-C2'-C1'	2.06	105.35	101.46

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	601	GTP	C5'-O5'-PA-O1A
2	A	603	GTP	O4'-C4'-C5'-O5'
2	A	603	GTP	C3'-C4'-C5'-O5'
2	D	602	GTP	PB-O3A-PA-O1A
2	D	601	GTP	C5'-O5'-PA-O3A
2	D	601	GTP	C5'-O5'-PA-O2A
2	D	602	GTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
2	D	602	GTP	C5'-O5'-PA-O1A
2	A	601	GTP	PB-O3B-PG-O1G
2	D	601	GTP	PB-O3A-PA-O2A
2	D	602	GTP	C4'-C5'-O5'-PA
2	D	601	GTP	PB-O3A-PA-O1A

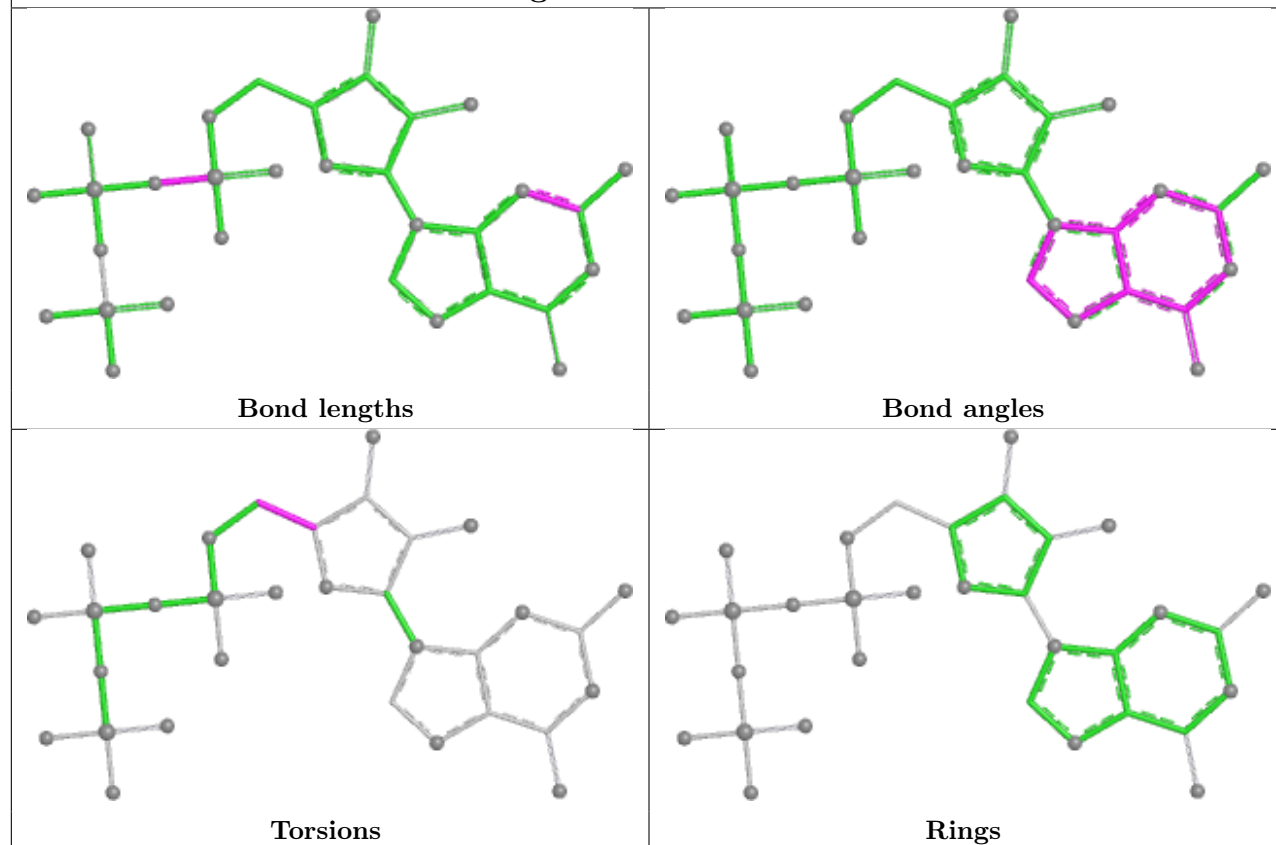
There are no ring outliers.

3 monomers are involved in 5 short contacts:

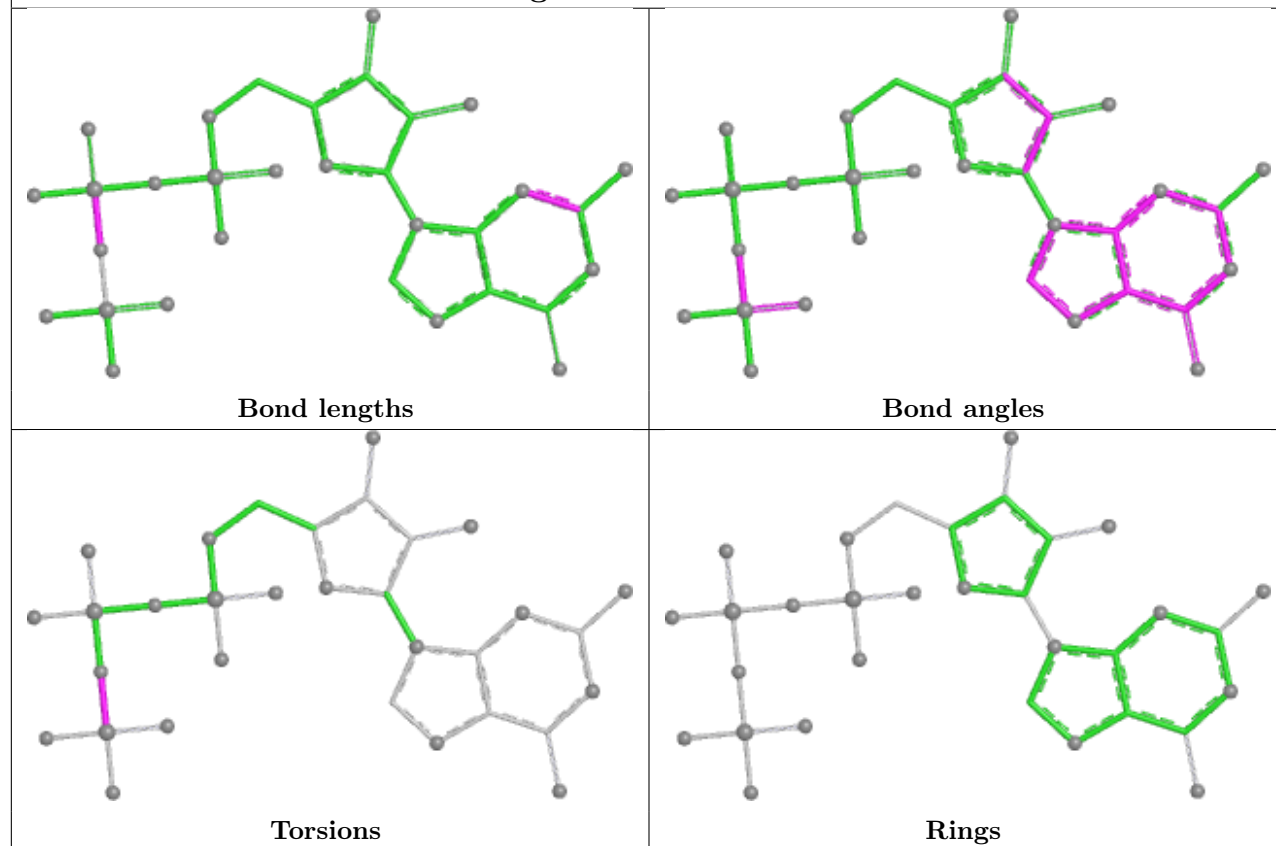
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	603	GTP	1	0
2	D	601	GTP	2	0
2	D	602	GTP	2	0

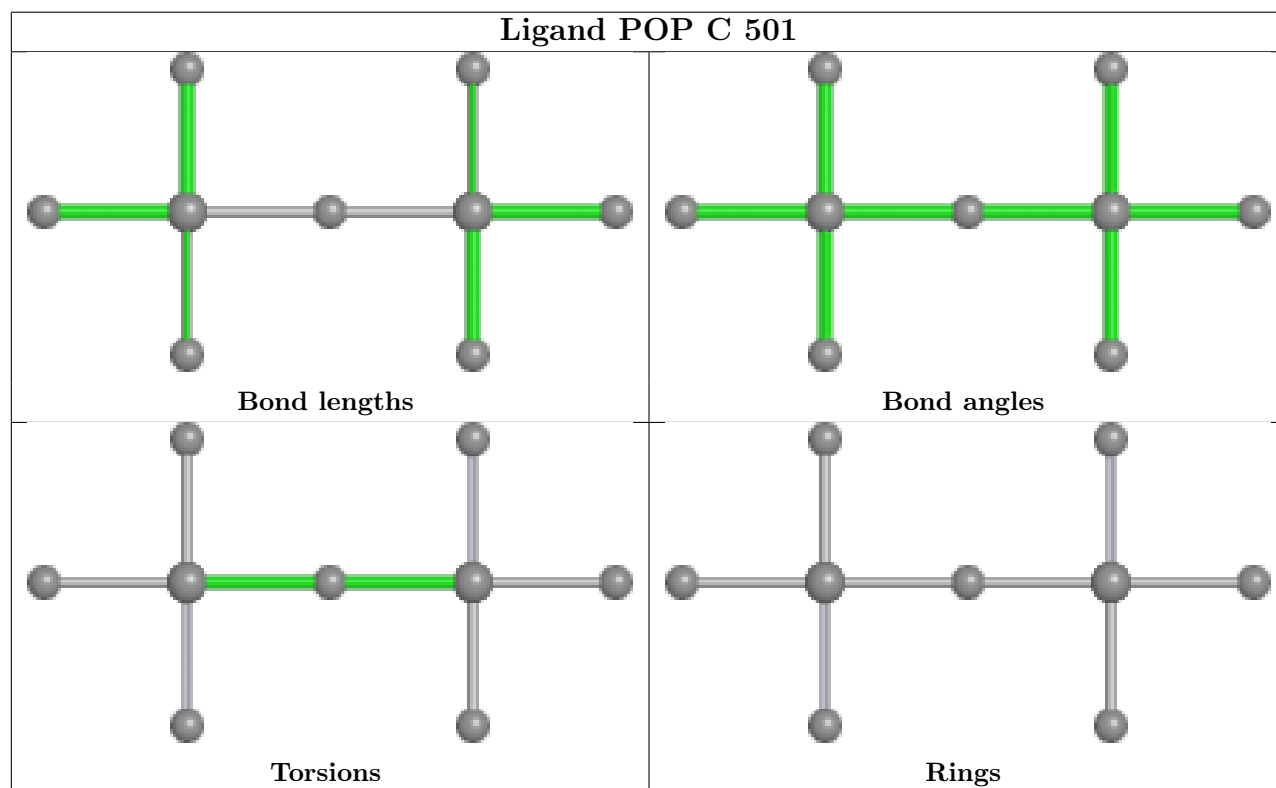
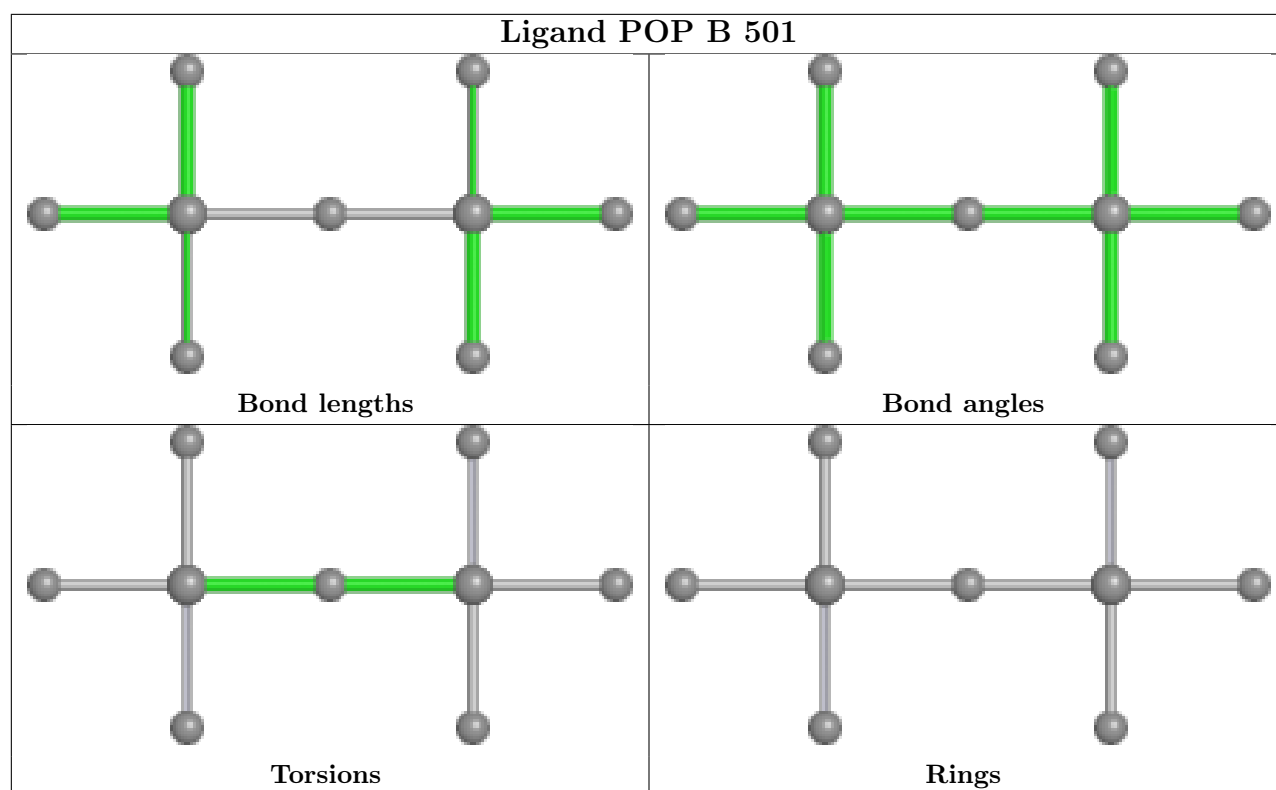
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

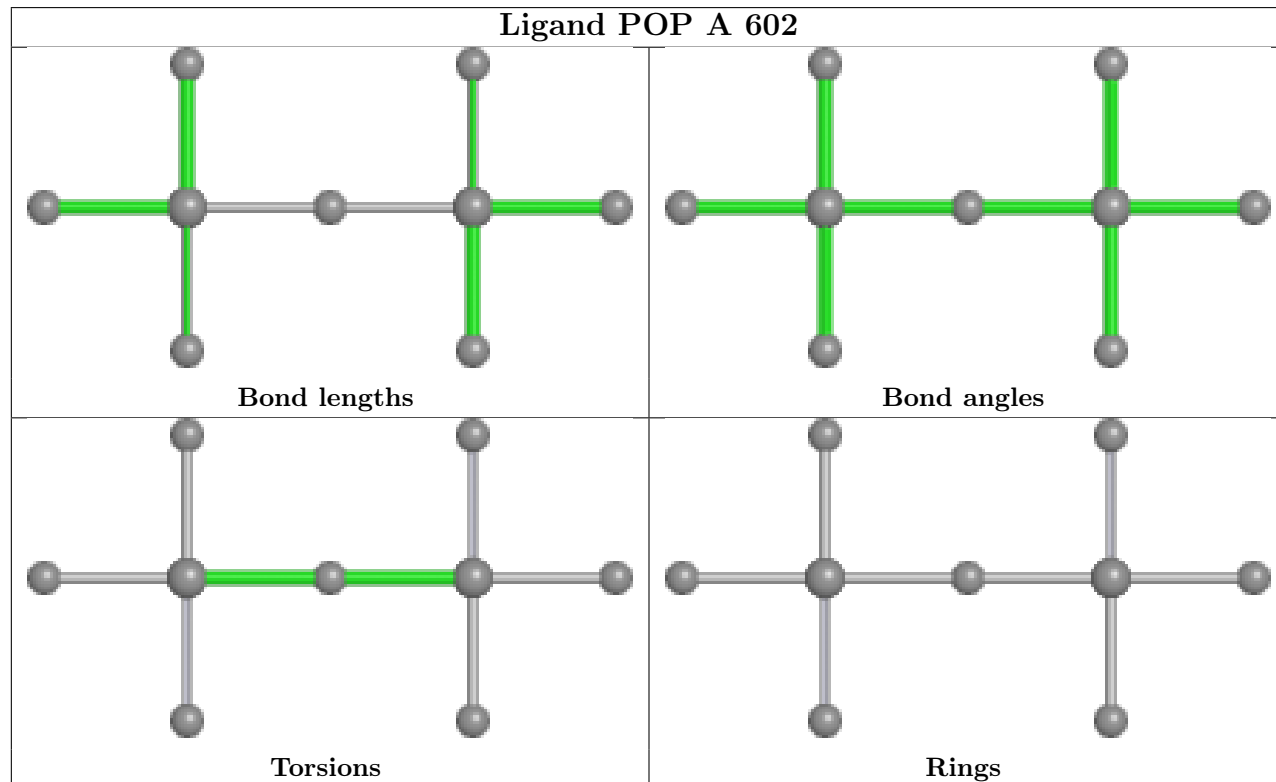
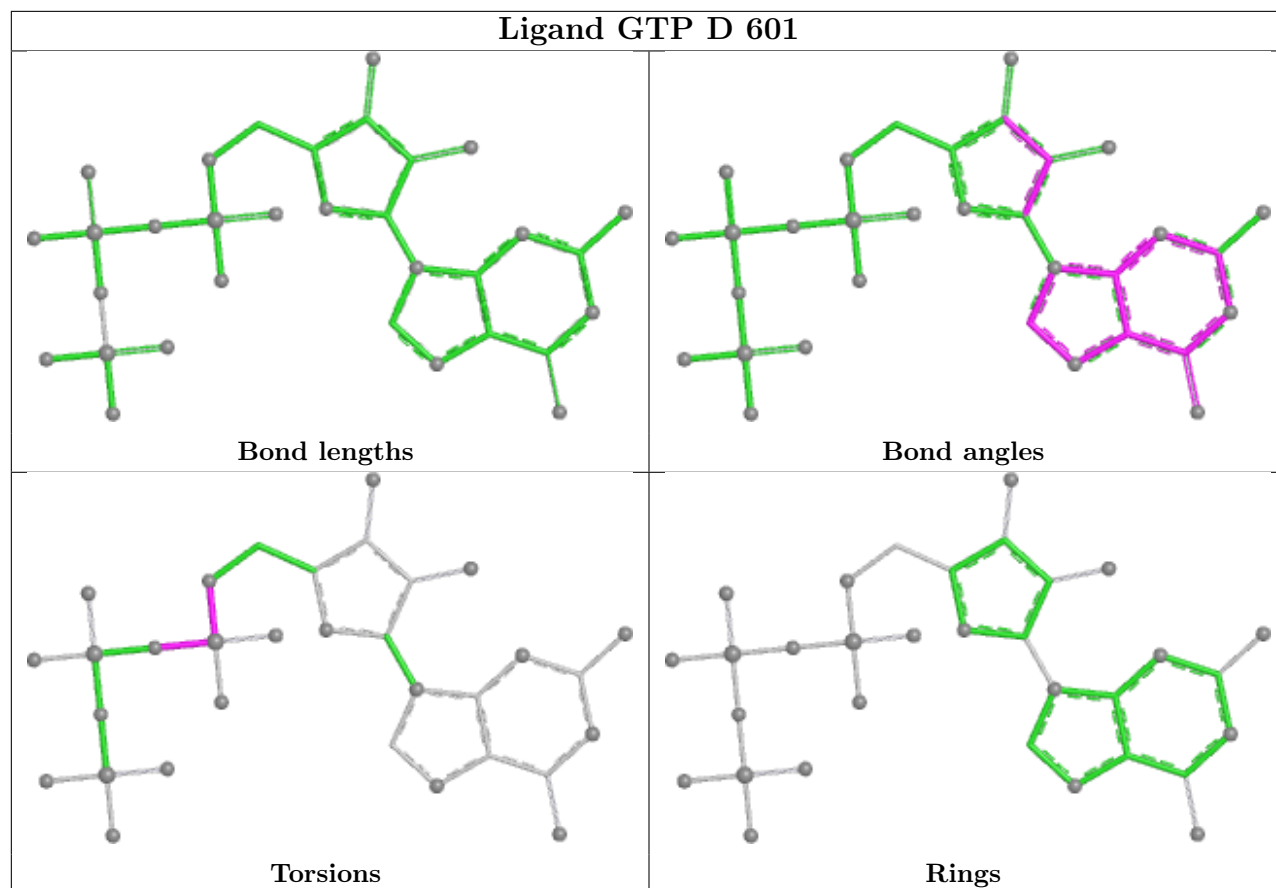
Ligand GTP A 603

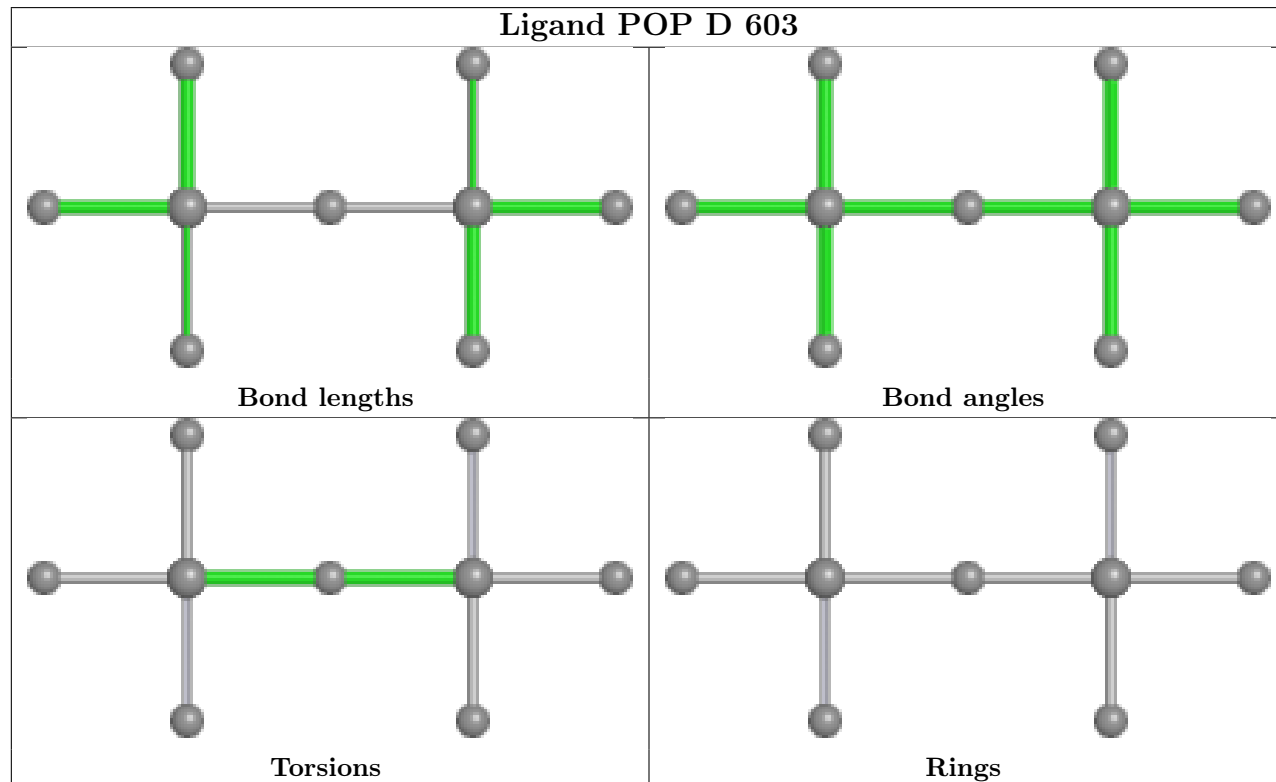
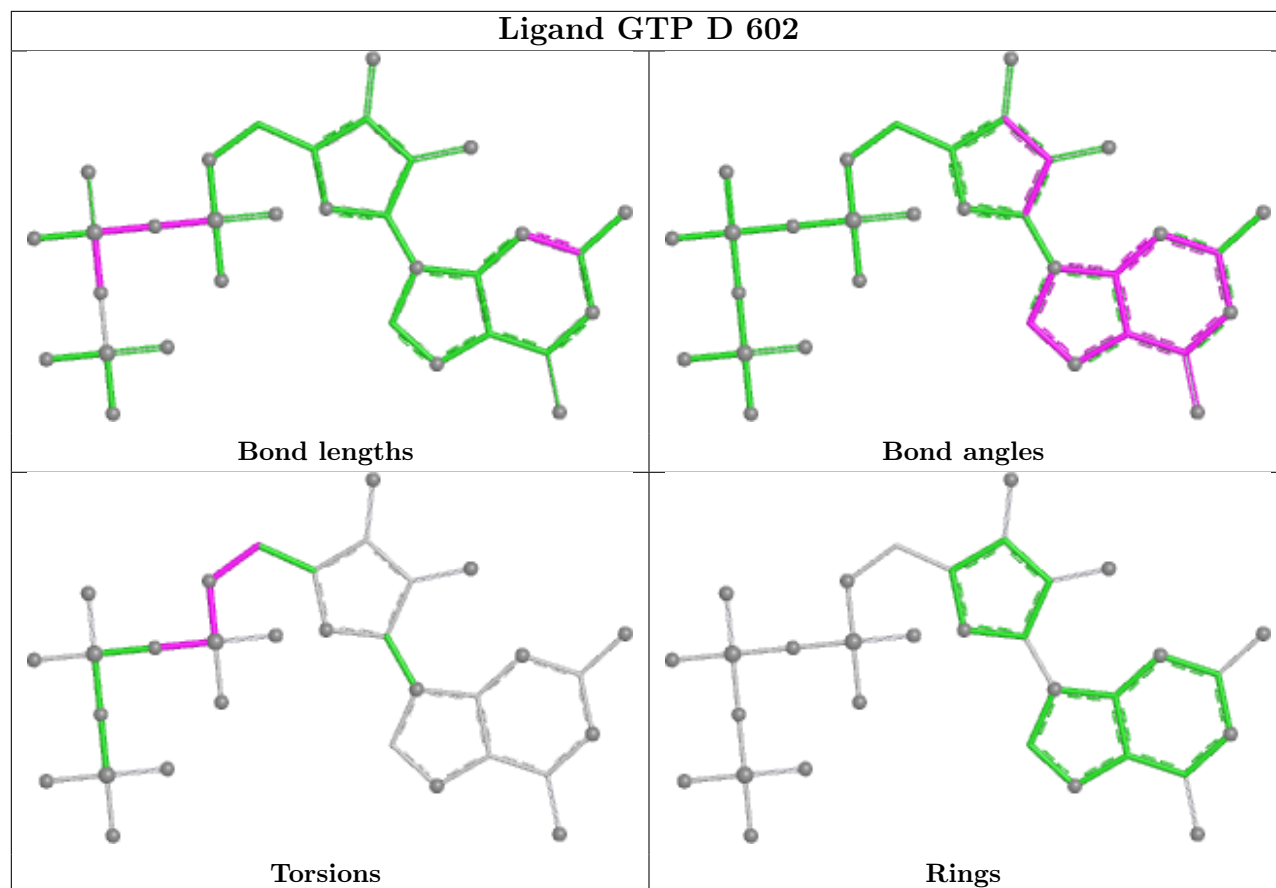


Ligand GTP A 601









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, 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	440/483 (91%)	0.51	18 (4%) 41 43	28, 57, 106, 137	0
1	B	440/483 (91%)	0.74	33 (7%) 20 21	34, 65, 109, 131	0
1	C	440/483 (91%)	0.63	24 (5%) 30 31	33, 63, 103, 132	0
1	D	441/483 (91%)	0.52	21 (4%) 35 36	30, 57, 106, 135	0
All	All	1761/1932 (91%)	0.60	96 (5%) 30 31	28, 61, 106, 137	0

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	405	LEU	5.0
1	D	357	LEU	4.3
1	A	388	ASN	4.2
1	D	280	ILE	3.9
1	D	299	TYR	3.8
1	A	427	GLN	3.8
1	B	28	TRP	3.5
1	B	348	ILE	3.5
1	B	445	PRO	3.3
1	B	366	ILE	3.2
1	A	448	TYR	3.2
1	A	386	ASP	3.1
1	B	397	LEU	3.1
1	C	366	ILE	3.0
1	D	113	LEU	3.0
1	C	379	ILE	3.0
1	A	445	PRO	3.0
1	B	406	VAL	3.0
1	B	428	ILE	3.0
1	A	392	LEU	2.9
1	C	361	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	302	SER	2.8
1	D	361	TYR	2.8
1	D	397	LEU	2.8
1	D	302	SER	2.8
1	A	150	ASP	2.7
1	C	357	LEU	2.7
1	D	402	VAL	2.7
1	B	425	ILE	2.7
1	B	439	PHE	2.6
1	C	95	CYS	2.6
1	B	272	PRO	2.6
1	B	299	TYR	2.6
1	B	357	LEU	2.5
1	A	390	PRO	2.5
1	C	28	TRP	2.5
1	B	364	VAL	2.5
1	B	273	VAL	2.4
1	A	449	TYR	2.4
1	D	120	MET	2.4
1	D	403	SER	2.4
1	B	402	VAL	2.4
1	C	390	PRO	2.4
1	D	356	GLY	2.4
1	D	437	THR	2.4
1	A	379	ILE	2.4
1	B	440	PHE	2.4
1	C	29	ILE	2.4
1	B	151	LEU	2.4
1	B	112	HIS	2.4
1	C	388	ASN	2.3
1	C	445	PRO	2.3
1	B	379	ILE	2.3
1	C	432	PHE	2.3
1	B	405	LEU	2.3
1	B	390	PRO	2.3
1	C	325	PHE	2.3
1	C	448	TYR	2.3
1	D	149	TYR	2.3
1	B	392	LEU	2.3
1	C	392	LEU	2.3
1	D	352	LEU	2.3
1	A	355	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	345	THR	2.3
1	A	424	LYS	2.3
1	A	428	ILE	2.3
1	D	335	LEU	2.2
1	B	350	ASP	2.2
1	B	269	ALA	2.2
1	C	378	PRO	2.2
1	A	442	ILE	2.2
1	A	366	ILE	2.2
1	B	314	ILE	2.2
1	C	124	ASP	2.2
1	C	326	VAL	2.2
1	D	110	PHE	2.2
1	B	55	PRO	2.2
1	D	126	LYS	2.2
1	A	357	LEU	2.1
1	A	374	LYS	2.1
1	C	354	HIS	2.1
1	B	280	ILE	2.1
1	B	352	LEU	2.1
1	C	449	TYR	2.1
1	D	354	HIS	2.1
1	A	447	THR	2.1
1	D	233	SER	2.1
1	B	307	LEU	2.1
1	C	15	ILE	2.1
1	C	187	ASN	2.1
1	C	442	ILE	2.1
1	B	113	LEU	2.0
1	C	347	ILE	2.0
1	D	123	PRO	2.0
1	B	361	TYR	2.0
1	C	362	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 oligosaccharides in this entry.

6.4 Ligands

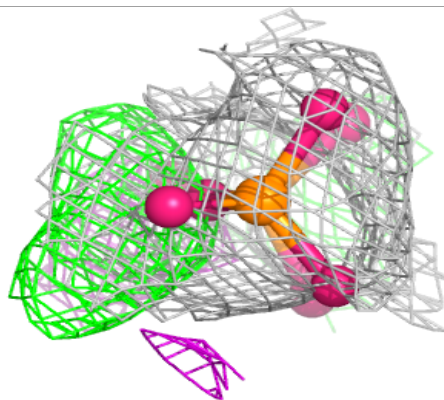
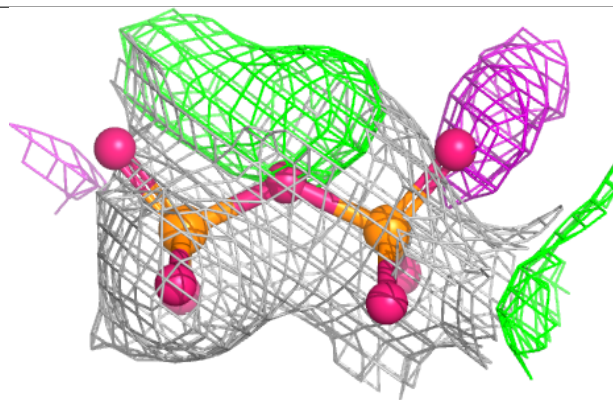
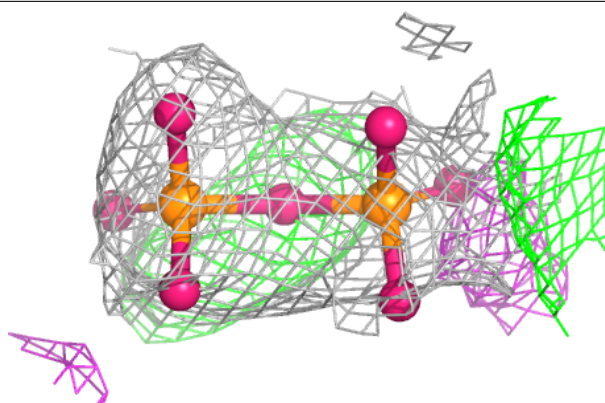
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	POP	C	501	9/9	0.76	0.19	74,74,74,74	9
5	CA	A	605	1/1	0.76	0.12	76,76,76,76	0
3	POP	A	602	9/9	0.82	0.16	69,69,69,69	9
3	POP	B	501	9/9	0.84	0.19	66,66,66,66	9
3	POP	D	603	9/9	0.85	0.20	62,62,62,62	9
5	CA	B	503	1/1	0.87	0.10	82,82,82,82	0
5	CA	C	503	1/1	0.91	0.09	81,81,81,81	0
2	GTP	D	602	32/32	0.92	0.10	39,63,84,94	0
2	GTP	A	603	32/32	0.94	0.09	46,56,79,81	0
2	GTP	D	601	32/32	0.94	0.08	28,45,74,81	0
2	GTP	A	601	32/32	0.95	0.09	41,54,82,90	0
5	CA	D	605	1/1	0.96	0.08	80,80,80,80	0
4	MN	B	502	1/1	0.99	0.03	42,42,42,42	0
4	MN	C	502	1/1	0.99	0.06	44,44,44,44	0
4	MN	A	604	1/1	0.99	0.05	40,40,40,40	0
4	MN	D	604	1/1	1.00	0.05	36,36,36,36	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.

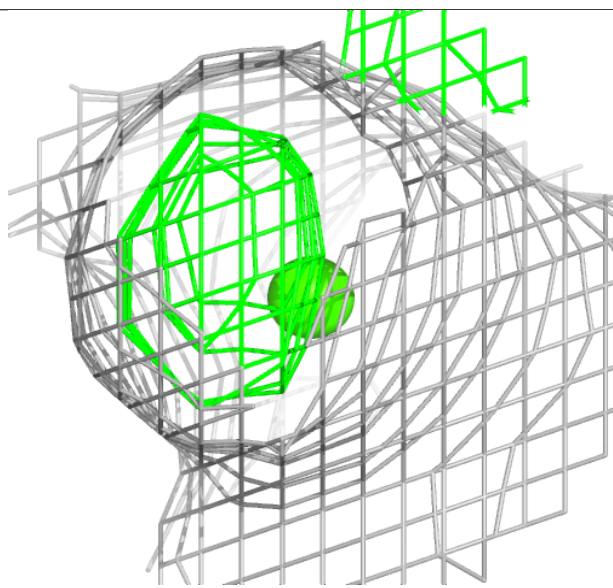
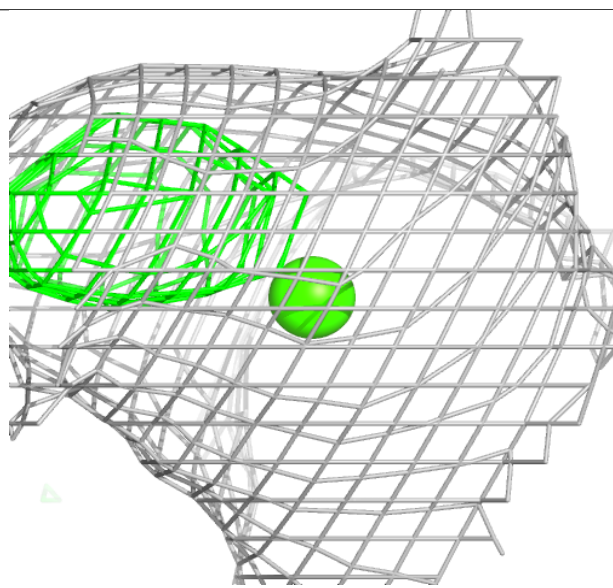
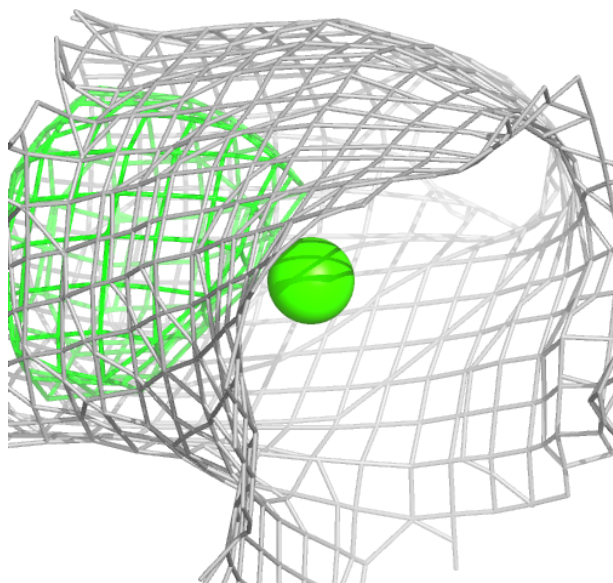
Electron density around POP C 501:

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



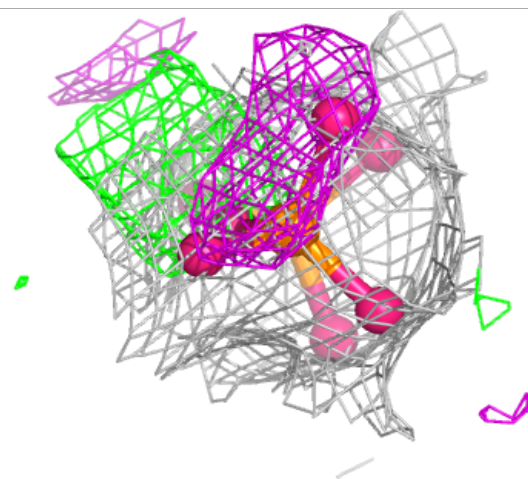
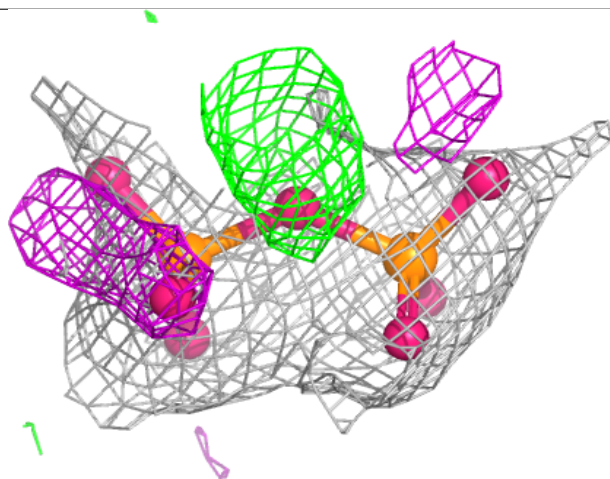
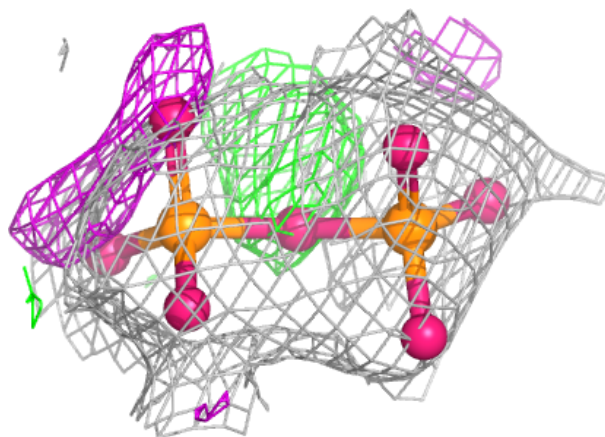
Electron density around CA A 605:

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



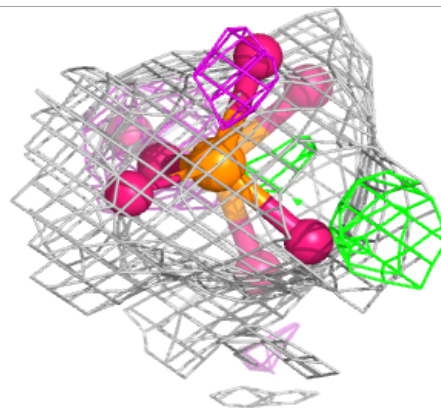
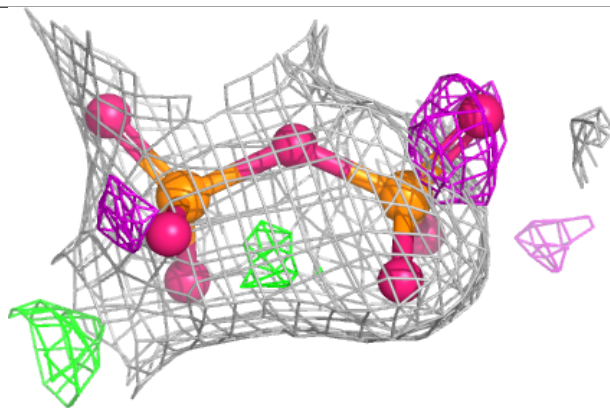
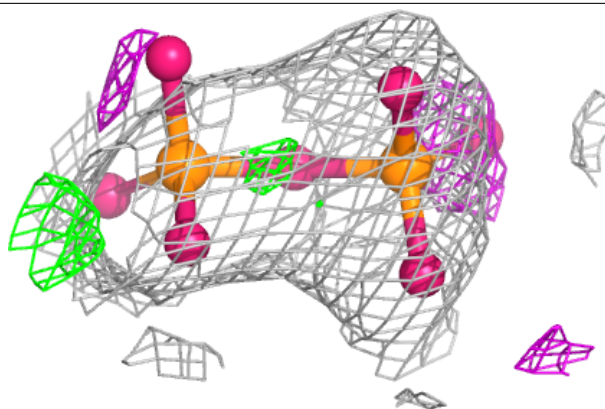
Electron density around POP A 602:

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

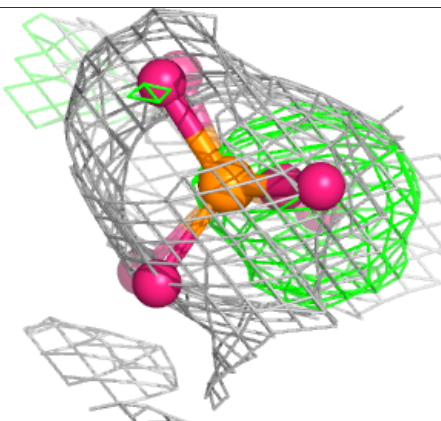
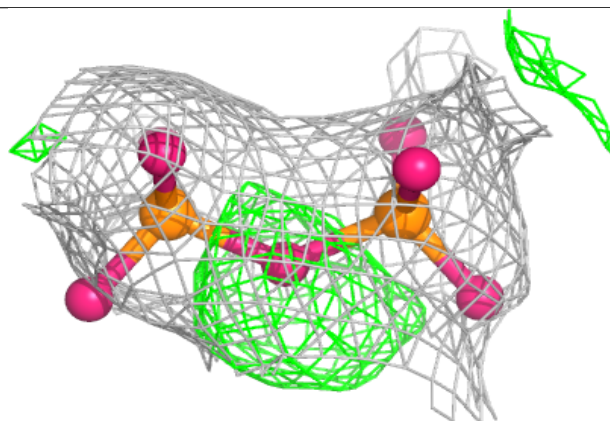
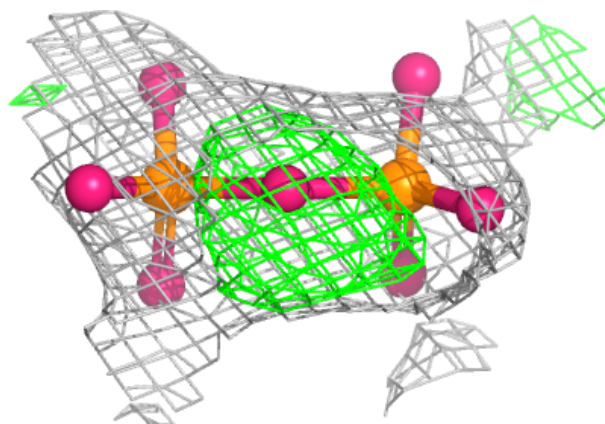


Electron density around POP B 501:

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

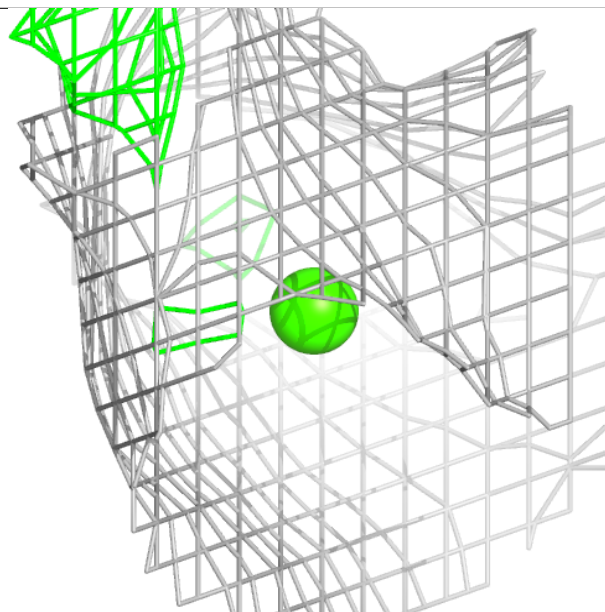
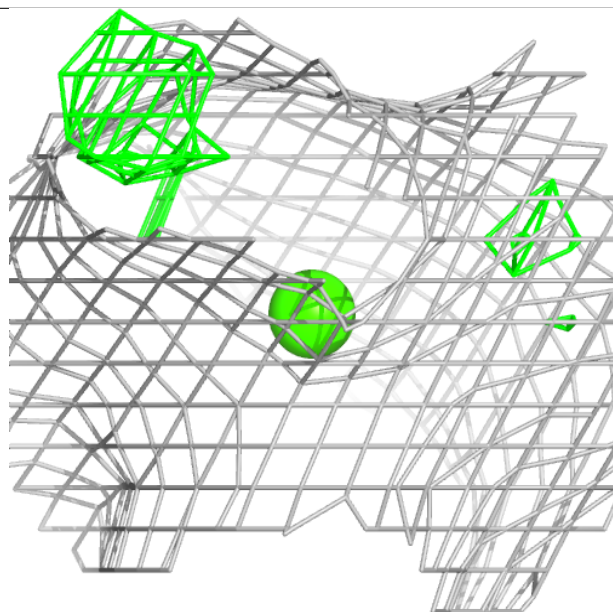
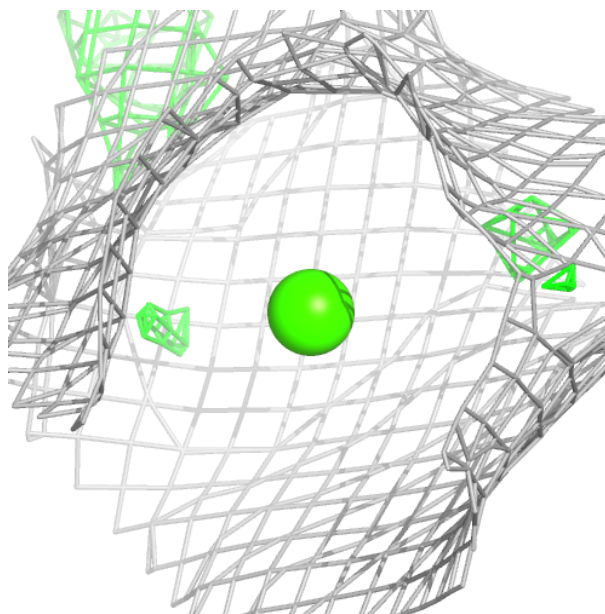
**Electron density around POP D 603:**

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



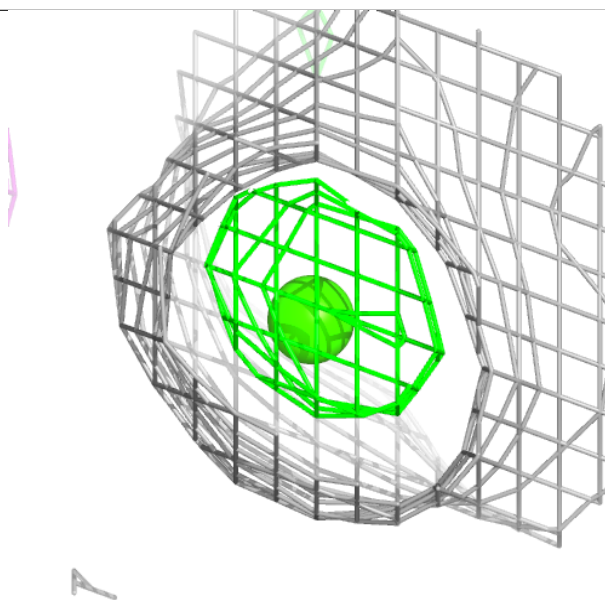
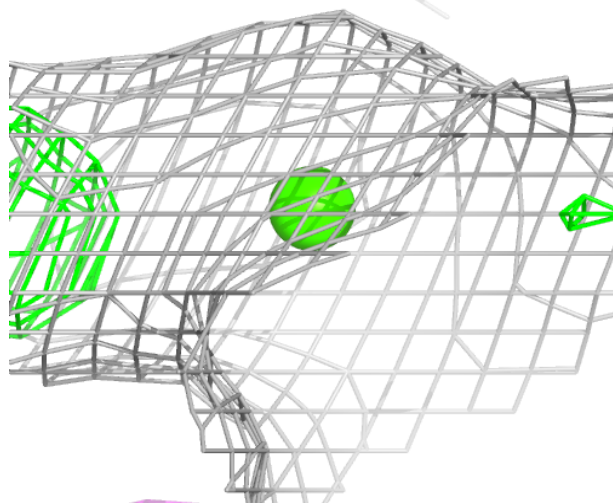
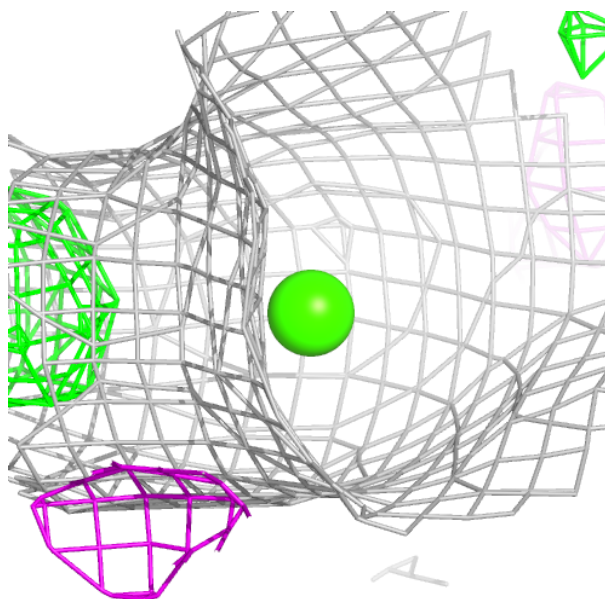
Electron density around CA B 503:

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



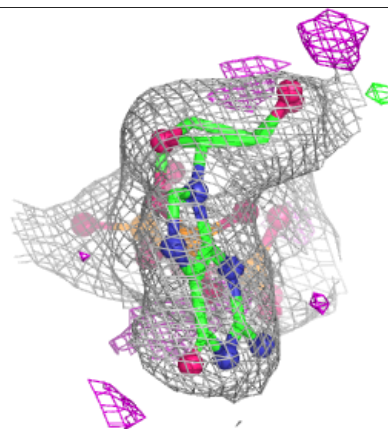
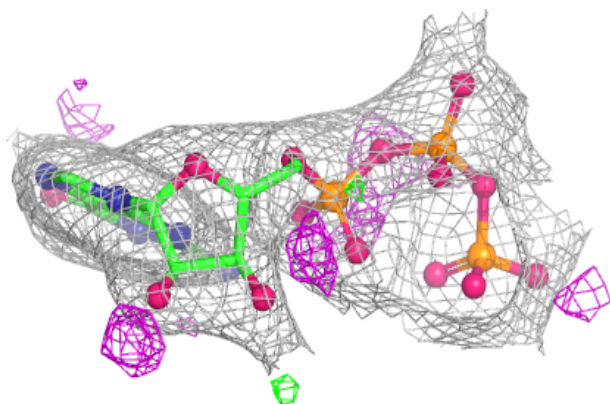
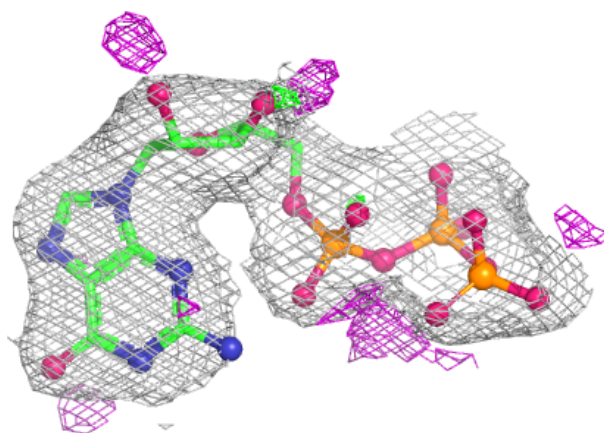
Electron density around CA C 503:

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

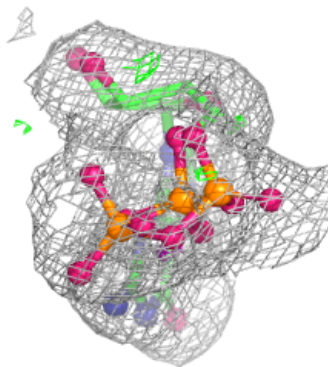
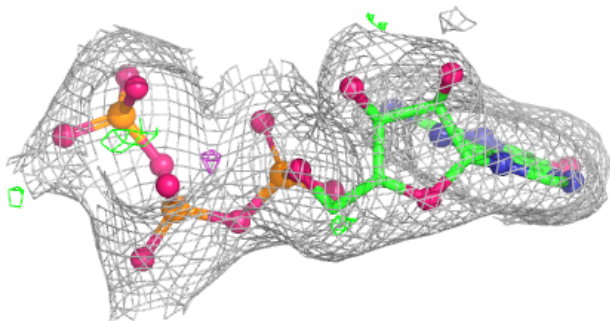
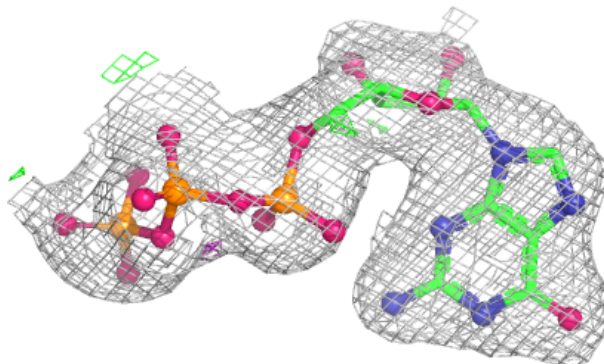


Electron density around GTP D 602:

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

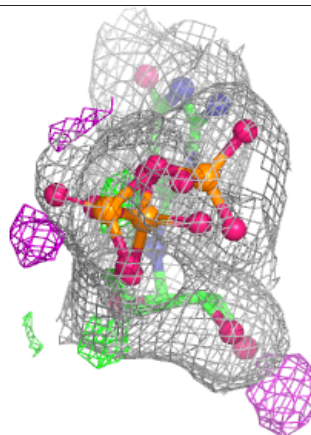
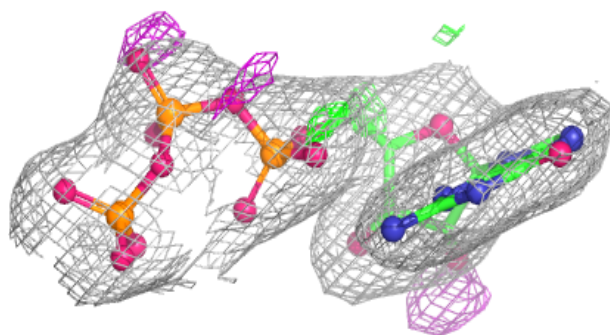
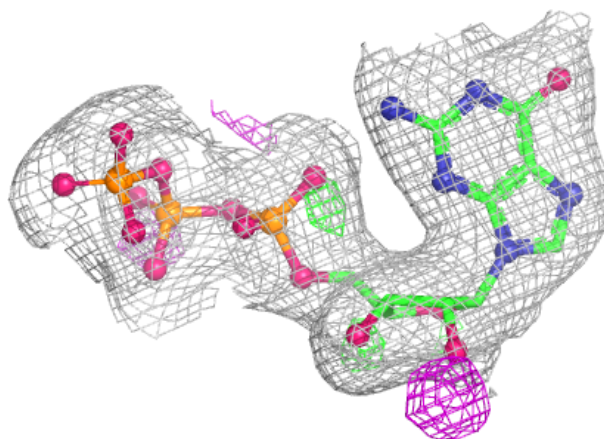
**Electron density around GTP A 603:**

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



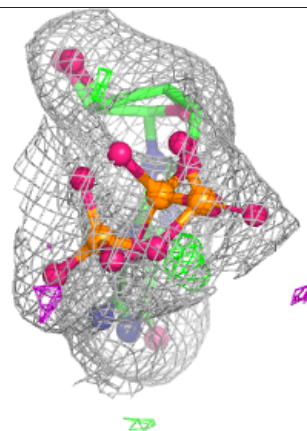
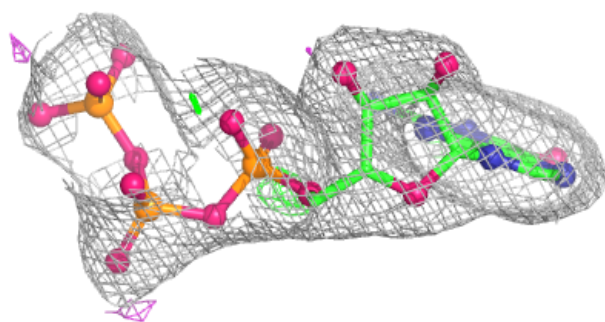
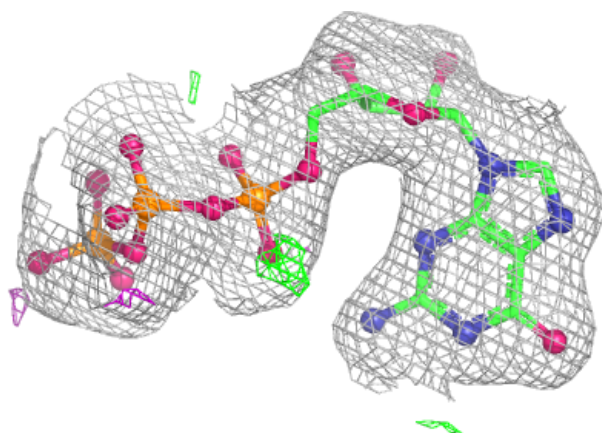
Electron density around GTP D 601:

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



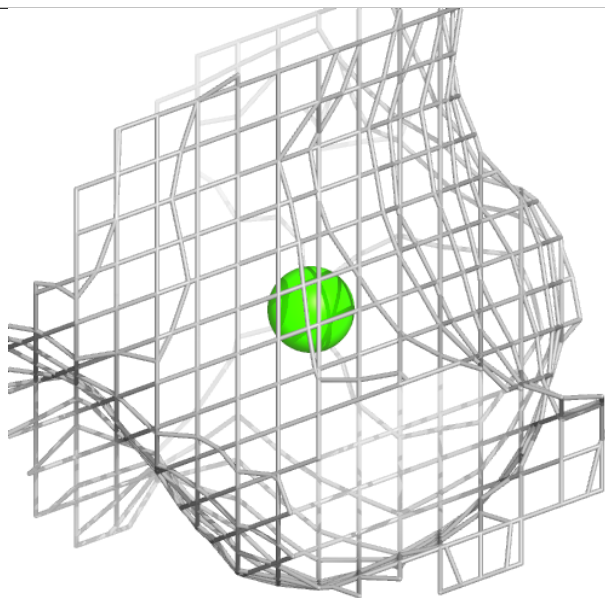
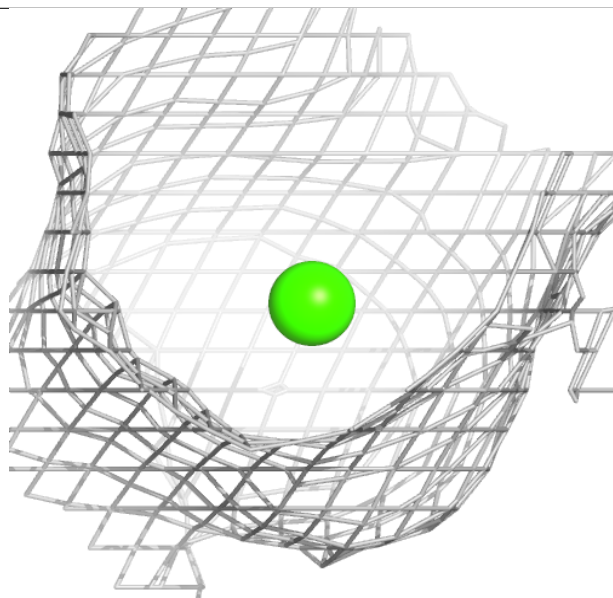
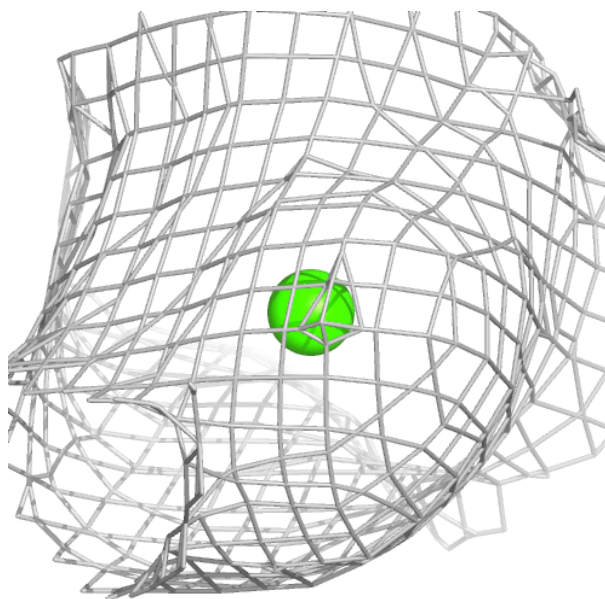
Electron density around GTP A 601:

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



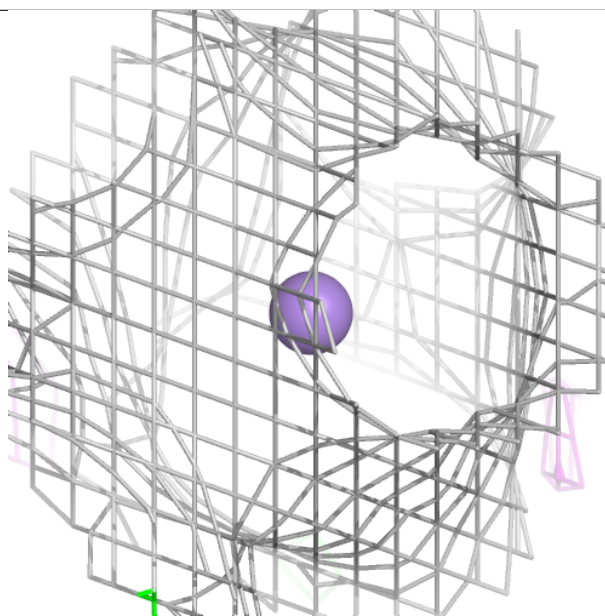
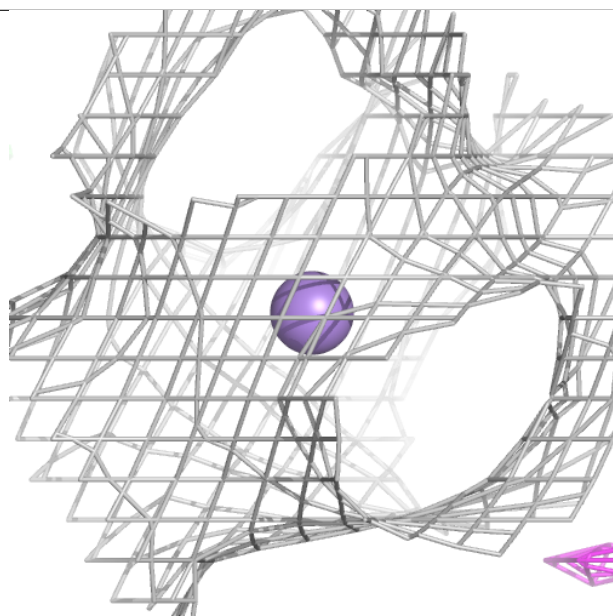
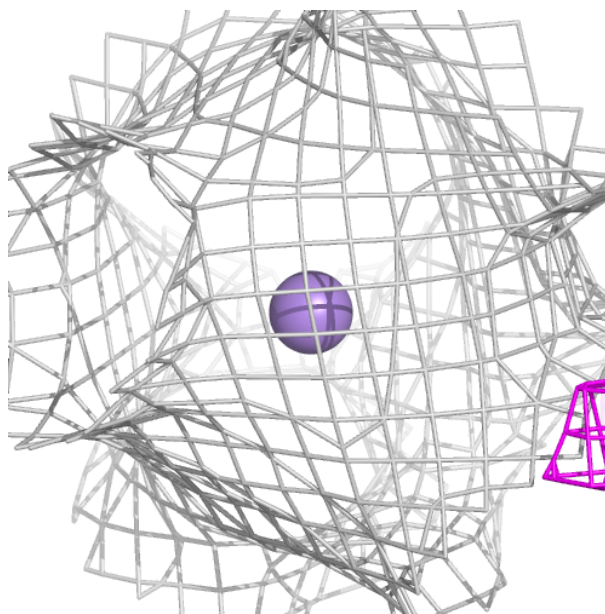
Electron density around CA D 605:

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



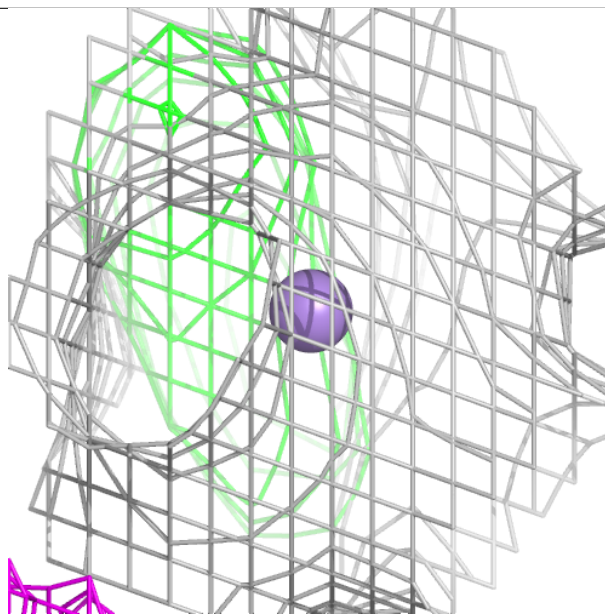
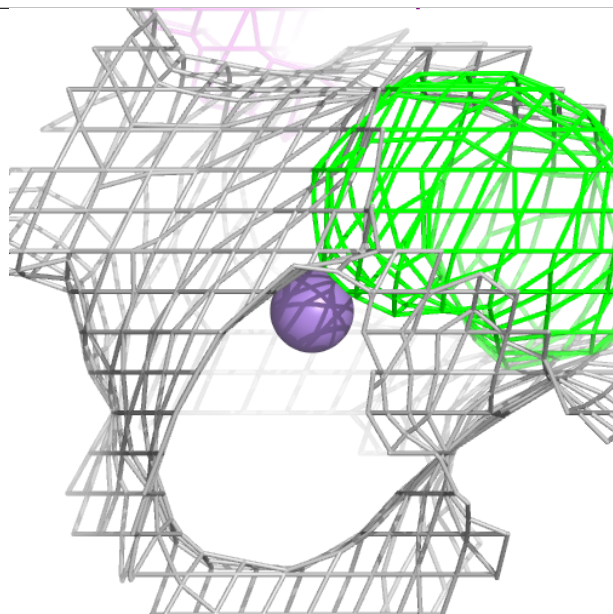
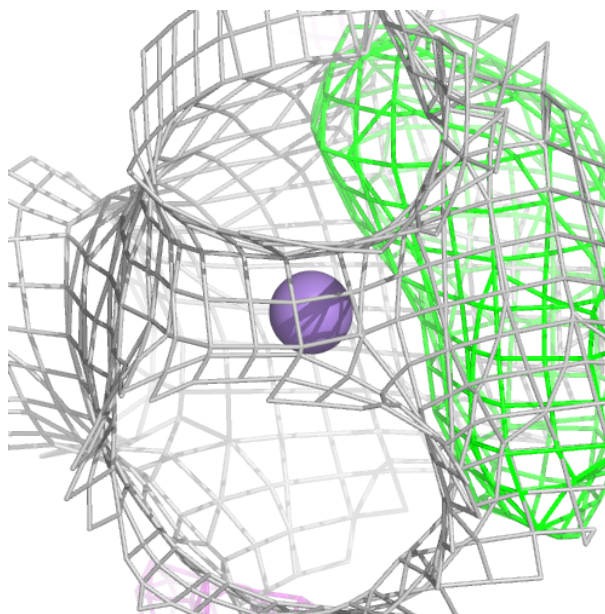
Electron density around MN B 502:

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



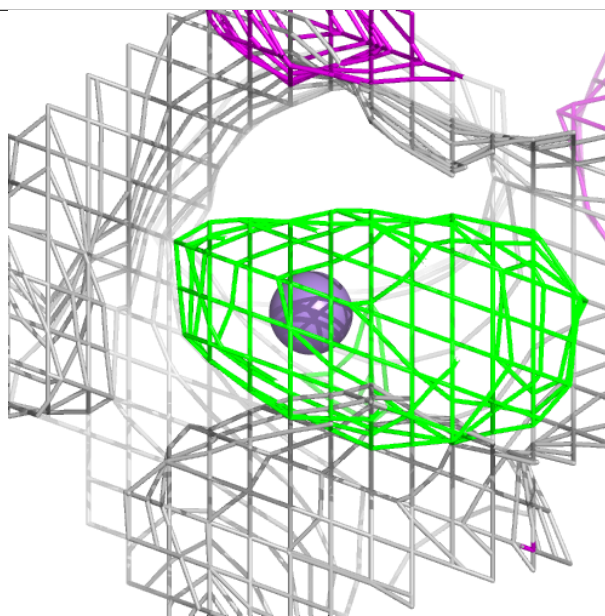
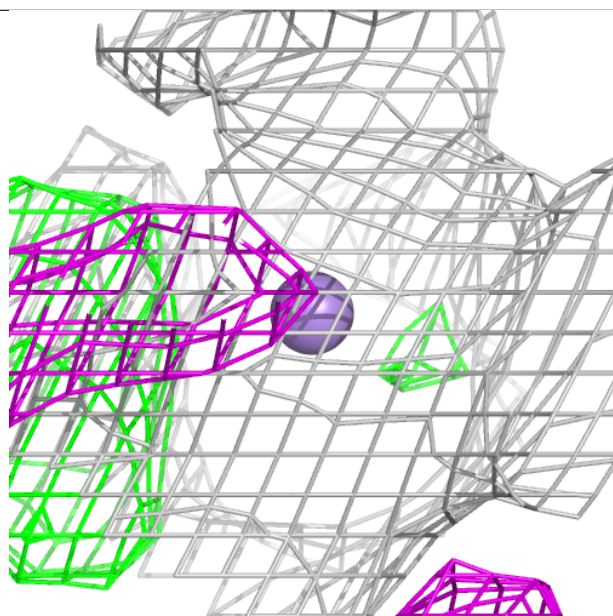
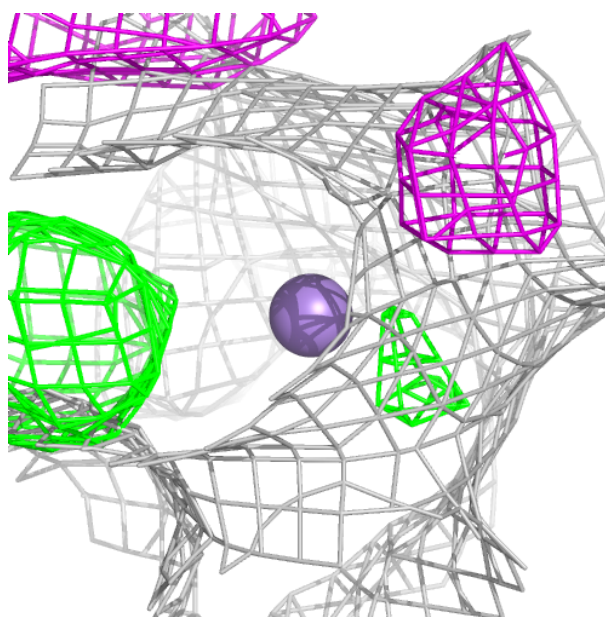
Electron density around MN C 502:

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



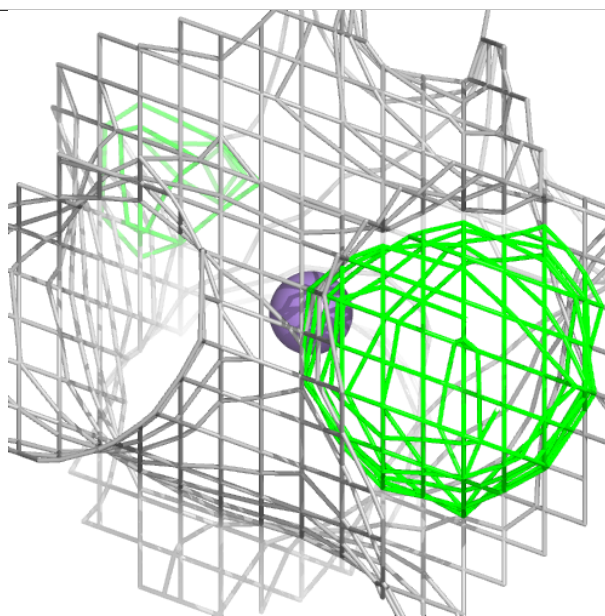
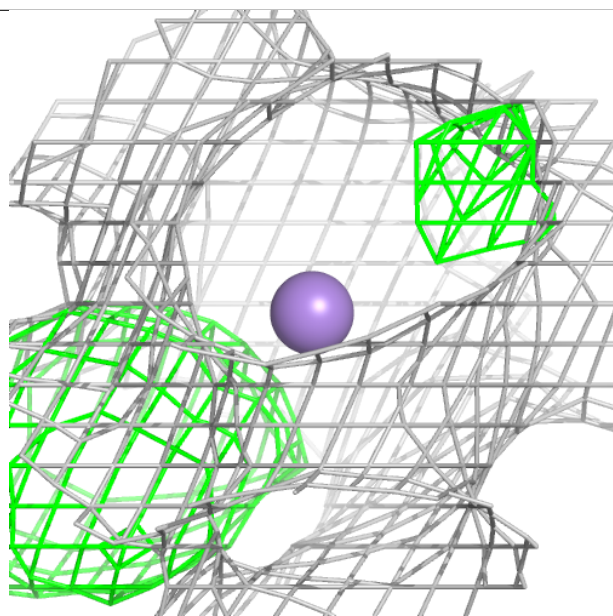
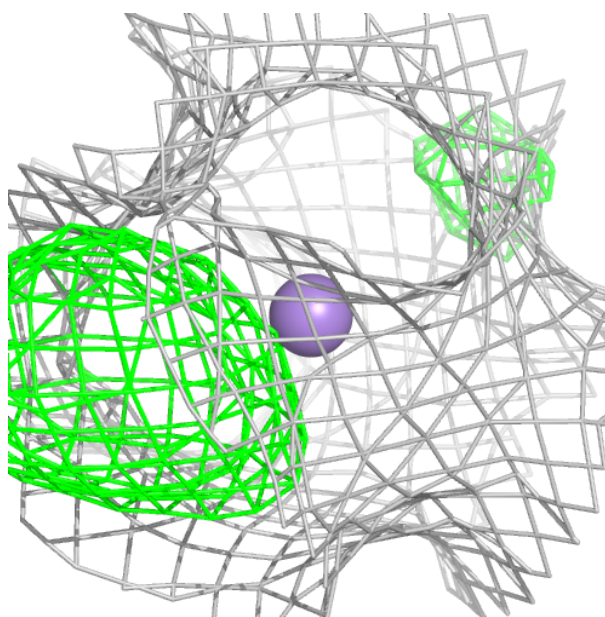
Electron density around MN A 604:

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



Electron density around MN D 604:

$2mF_o-DF_c$ (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.