



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:37 AM UTC

PDB ID : 9DRF / pdb_00009drf
Title : Crystal structure of ADP-ribose diphosphatase from *Klebsiella pneumoniae* (DTP bound, P21 form)
Authors : Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2024-09-25
Resolution : 1.78 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

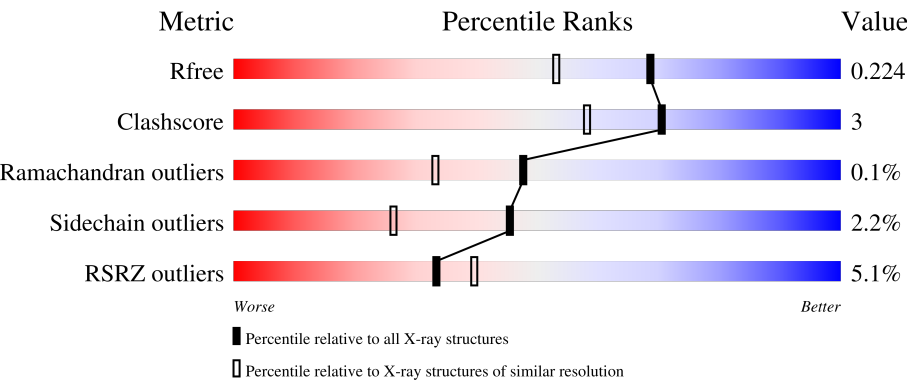
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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	218	6% 81% 10% 10%
1	B	218	6% 78% 12% 10%
1	C	218	3% 85% 6% 9%
1	D	218	3% 82% 8% 11%

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Mol	Chain	Length	Quality of chain
1	E	218	
1	F	218	
1	G	218	
1	H	218	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13581 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 ADP-ribose pyrophosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	197	Total	C	N	O	S	0	5	0
			1597	1014	283	297	3			
1	B	197	Total	C	N	O	S	0	2	0
			1571	994	275	299	3			
1	C	199	Total	C	N	O	S	0	2	0
			1585	1004	277	301	3			
1	D	195	Total	C	N	O	S	0	1	0
			1559	985	275	296	3			
1	E	202	Total	C	N	O	S	0	3	0
			1626	1031	290	301	4			
1	F	194	Total	C	N	O	S	0	3	0
			1545	981	267	294	3			
1	G	198	Total	C	N	O	S	0	2	0
			1577	1001	276	297	3			
1	H	200	Total	C	N	O	S	0	4	0
			1596	1012	279	302	3			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP A0A0H3GVQ7
A	-6	ALA	-	expression tag	UNP A0A0H3GVQ7
A	-5	HIS	-	expression tag	UNP A0A0H3GVQ7
A	-4	HIS	-	expression tag	UNP A0A0H3GVQ7
A	-3	HIS	-	expression tag	UNP A0A0H3GVQ7
A	-2	HIS	-	expression tag	UNP A0A0H3GVQ7
A	-1	HIS	-	expression tag	UNP A0A0H3GVQ7
A	0	HIS	-	expression tag	UNP A0A0H3GVQ7
B	-7	MET	-	expression tag	UNP A0A0H3GVQ7
B	-6	ALA	-	expression tag	UNP A0A0H3GVQ7
B	-5	HIS	-	expression tag	UNP A0A0H3GVQ7
B	-4	HIS	-	expression tag	UNP A0A0H3GVQ7
B	-3	HIS	-	expression tag	UNP A0A0H3GVQ7

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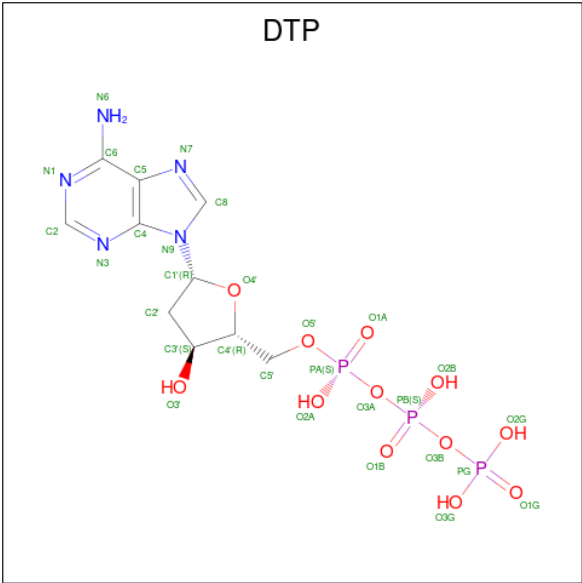
Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	expression tag	UNP A0A0H3GVQ7
B	-1	HIS	-	expression tag	UNP A0A0H3GVQ7
B	0	HIS	-	expression tag	UNP A0A0H3GVQ7
C	-7	MET	-	expression tag	UNP A0A0H3GVQ7
C	-6	ALA	-	expression tag	UNP A0A0H3GVQ7
C	-5	HIS	-	expression tag	UNP A0A0H3GVQ7
C	-4	HIS	-	expression tag	UNP A0A0H3GVQ7
C	-3	HIS	-	expression tag	UNP A0A0H3GVQ7
C	-2	HIS	-	expression tag	UNP A0A0H3GVQ7
C	-1	HIS	-	expression tag	UNP A0A0H3GVQ7
C	0	HIS	-	expression tag	UNP A0A0H3GVQ7
D	-7	MET	-	expression tag	UNP A0A0H3GVQ7
D	-6	ALA	-	expression tag	UNP A0A0H3GVQ7
D	-5	HIS	-	expression tag	UNP A0A0H3GVQ7
D	-4	HIS	-	expression tag	UNP A0A0H3GVQ7
D	-3	HIS	-	expression tag	UNP A0A0H3GVQ7
D	-2	HIS	-	expression tag	UNP A0A0H3GVQ7
D	-1	HIS	-	expression tag	UNP A0A0H3GVQ7
D	0	HIS	-	expression tag	UNP A0A0H3GVQ7
E	-7	MET	-	expression tag	UNP A0A0H3GVQ7
E	-6	ALA	-	expression tag	UNP A0A0H3GVQ7
E	-5	HIS	-	expression tag	UNP A0A0H3GVQ7
E	-4	HIS	-	expression tag	UNP A0A0H3GVQ7
E	-3	HIS	-	expression tag	UNP A0A0H3GVQ7
E	-2	HIS	-	expression tag	UNP A0A0H3GVQ7
E	-1	HIS	-	expression tag	UNP A0A0H3GVQ7
E	0	HIS	-	expression tag	UNP A0A0H3GVQ7
F	-7	MET	-	expression tag	UNP A0A0H3GVQ7
F	-6	ALA	-	expression tag	UNP A0A0H3GVQ7
F	-5	HIS	-	expression tag	UNP A0A0H3GVQ7
F	-4	HIS	-	expression tag	UNP A0A0H3GVQ7
F	-3	HIS	-	expression tag	UNP A0A0H3GVQ7
F	-2	HIS	-	expression tag	UNP A0A0H3GVQ7
F	-1	HIS	-	expression tag	UNP A0A0H3GVQ7
F	0	HIS	-	expression tag	UNP A0A0H3GVQ7
G	-7	MET	-	expression tag	UNP A0A0H3GVQ7
G	-6	ALA	-	expression tag	UNP A0A0H3GVQ7
G	-5	HIS	-	expression tag	UNP A0A0H3GVQ7
G	-4	HIS	-	expression tag	UNP A0A0H3GVQ7
G	-3	HIS	-	expression tag	UNP A0A0H3GVQ7
G	-2	HIS	-	expression tag	UNP A0A0H3GVQ7
G	-1	HIS	-	expression tag	UNP A0A0H3GVQ7

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Chain	Residue	Modelled	Actual	Comment	Reference
G	0	HIS	-	expression tag	UNP A0A0H3GVQ7
H	-7	MET	-	expression tag	UNP A0A0H3GVQ7
H	-6	ALA	-	expression tag	UNP A0A0H3GVQ7
H	-5	HIS	-	expression tag	UNP A0A0H3GVQ7
H	-4	HIS	-	expression tag	UNP A0A0H3GVQ7
H	-3	HIS	-	expression tag	UNP A0A0H3GVQ7
H	-2	HIS	-	expression tag	UNP A0A0H3GVQ7
H	-1	HIS	-	expression tag	UNP A0A0H3GVQ7
H	0	HIS	-	expression tag	UNP A0A0H3GVQ7

- Molecule 2 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: C₁₀H₁₆N₅O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
2	B	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
2	C	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
2	C	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
2	E	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
2	E	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	G	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
2	G	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

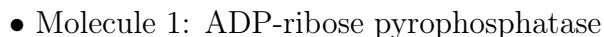
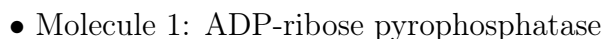
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

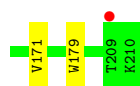
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		
3	F	2	Total	Mg	0	0
			2	2		
3	G	1	Total	Mg	0	0
			1	1		
3	H	1	Total	Mg	0	0
			1	1		

- Molecule 4 is water.

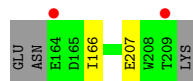
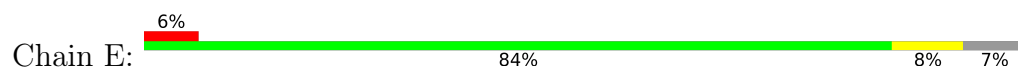
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	91	Total	O	0	0
			91	91		
4	B	85	Total	O	0	1
			85	85		
4	C	103	Total	O	0	1
			104	104		
4	D	63	Total	O	0	0
			63	63		
4	E	78	Total	O	0	0
			78	78		
4	F	83	Total	O	0	0
			83	83		
4	G	95	Total	O	0	0
			95	95		
4	H	79	Total	O	0	0
			79	79		

- Molecule 1: ADP-ribose pyrophosphatase

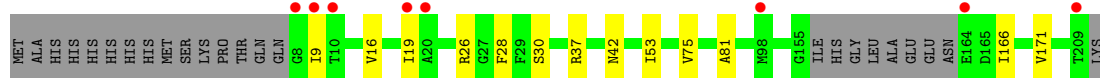
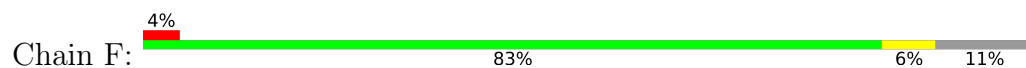




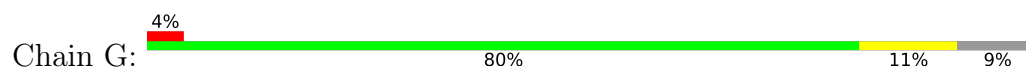
- Molecule 1: ADP-ribose pyrophosphatase



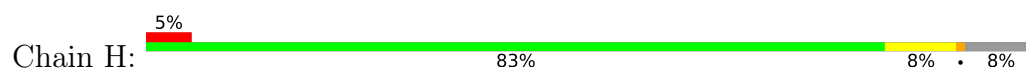
- Molecule 1: ADP-ribose pyrophosphatase



- Molecule 1: ADP-ribose pyrophosphatase



- Molecule 1: ADP-ribose pyrophosphatase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.03Å 80.13Å 116.19Å 90.00° 90.13° 90.00°	Depositor
Resolution (Å)	49.23 – 1.78 49.23 – 1.78	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.23-1.78) 99.9 (49.23-1.78)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 1.78Å)	Xtriage
Refinement program	PHENIX (dev_5295: ???)	Depositor
R, R_{free}	0.179 , 0.217 0.186 , 0.224	Depositor DCC
R_{free} test set	8046 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.676	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.040 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13581	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.51 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.1293e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MG, DTP

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	0.45	0/1642	0.60	0/2226
1	B	0.44	0/1606	0.61	0/2174
1	C	0.47	0/1621	0.64	0/2194
1	D	0.42	0/1591	0.59	0/2155
1	E	0.43	0/1669	0.59	0/2259
1	F	0.43	0/1583	0.59	0/2145
1	G	0.47	0/1613	0.64	0/2184
1	H	0.45	0/1638	0.61	0/2220
All	All	0.44	0/12963	0.61	0/17557

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	1597	0	1561	13	0
1	B	1571	0	1535	17	0
1	C	1585	0	1552	8	0
1	D	1559	0	1525	10	0
1	E	1626	0	1592	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1545	0	1517	9	0
1	G	1577	0	1547	17	0
1	H	1596	0	1553	14	0
2	A	30	0	12	1	0
2	B	30	0	12	0	0
2	C	60	0	24	1	0
2	E	60	0	24	2	0
2	G	60	0	24	1	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	F	2	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	91	0	0	0	0
4	B	85	0	0	1	0
4	C	104	0	0	1	0
4	D	63	0	0	0	0
4	E	78	0	0	0	0
4	F	83	0	0	0	0
4	G	95	0	0	0	0
4	H	79	0	0	1	0
All	All	13581	0	12478	87	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 (87) 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:75:VAL:HG13	1:B:166:ILE:HG23	1.50	0.94
1:F:75:VAL:HG13	1:F:166:ILE:HG23	1.60	0.84
1:E:75[B]:VAL:HG23	1:E:166:ILE:HG23	1.62	0.80
1:H:75:VAL:HG13	1:H:166:ILE:HG23	1.63	0.79
1:G:81:ALA:HB2	1:H:53:ILE:HD12	1.65	0.78
1:A:57:GLY:HA3	1:A:98:MET:HE3	1.66	0.78
1:A:75[A]:VAL:HG13	1:A:166:ILE:HG23	1.65	0.77
1:E:125:LYS:NZ	1:E:207:GLU:OE2	2.21	0.74
1:E:75[A]:VAL:HG13	1:E:166:ILE:HG23	1.70	0.73
1:E:35:ARG:NH1	1:E:48:GLU:OE2	2.23	0.71
1:A:81:ALA:HB2	1:B:53:ILE:HD12	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:119:LEU:HD21	1:G:153:ALA:HB2	1.77	0.65
1:B:75:VAL:HG13	1:B:166:ILE:CG2	2.26	0.65
1:D:75:VAL:HG13	1:D:166:ILE:CG2	2.27	0.64
1:A:35:ARG:NH1	1:A:48[A]:GLU:OE2	2.28	0.64
1:D:75:VAL:HG13	1:D:166:ILE:HG23	1.78	0.64
1:B:19:ILE:HD11	1:B:37:ARG:HG3	1.81	0.63
1:G:182:GLU:OE1	1:G:184:LYS:NZ	2.24	0.63
1:E:0:HIS:HB2	1:F:171:VAL:HG12	1.79	0.62
1:C:81:ALA:HB2	1:D:53:ILE:HD12	1.82	0.61
1:H:19:ILE:HD11	1:H:37:ARG:HG3	1.85	0.59
1:G:53:ILE:HD12	1:H:81:ALA:HB2	1.85	0.58
1:A:23:THR:HG23	1:A:26:ARG:NH1	2.19	0.58
1:D:19:ILE:HD11	1:D:37:ARG:HG3	1.85	0.57
1:C:19:ILE:HD11	1:C:37:ARG:HG3	1.86	0.57
1:C:209:THR:O	1:C:210:LYS:CB	2.54	0.55
1:G:26:ARG:NH2	1:G:32:ASP:OD1	2.40	0.54
1:E:53:ILE:HD12	1:F:81:ALA:HB2	1.91	0.53
1:A:23:THR:OG1	1:A:26:ARG:NH2	2.41	0.53
1:B:184:LYS:HG3	4:B:427:HOH:O	2.08	0.53
1:C:37:ARG:NH2	4:C:401:HOH:O	2.40	0.53
2:A:301:DTP:H2'1	1:B:28:PHE:CD1	2.45	0.52
1:H:75:VAL:HG13	1:H:166:ILE:CG2	2.37	0.52
1:H:156:ILE:HA	1:H:166:ILE:O	2.10	0.52
1:A:10:THR:OG1	1:A:11:PHE:N	2.34	0.51
1:G:112:GLU:HA	1:G:115:GLU:HG2	1.92	0.51
1:B:22[A]:GLU:OE2	1:B:35:ARG:NH1	2.40	0.51
1:A:53:ILE:HD12	1:B:81:ALA:HB2	1.92	0.51
1:D:26:ARG:HD2	1:D:30:SER:OG	2.11	0.50
1:G:154:LYS:O	1:G:157:HIS:NE2	2.30	0.50
1:A:75[A]:VAL:HG13	1:A:166:ILE:CG2	2.38	0.50
1:F:75:VAL:HG13	1:F:166:ILE:CG2	2.35	0.49
1:E:75[B]:VAL:HG23	1:E:166:ILE:CG2	2.37	0.49
1:G:179:TRP:CD1	1:G:184:LYS:HD2	2.49	0.48
1:B:52:GLU:O	1:B:53:ILE:HD13	2.13	0.48
1:H:19:ILE:HD11	1:H:37:ARG:CG	2.43	0.48
1:H:203:ASN:ND2	4:H:403:HOH:O	2.47	0.48
1:G:23:THR:HG23	1:G:26:ARG:NH1	2.30	0.47
1:B:75:VAL:CG1	1:B:166:ILE:HG23	2.32	0.47
1:G:119:LEU:HD13	1:G:148:VAL:HG11	1.96	0.47
1:C:53:ILE:HD12	1:D:81:ALA:HB2	1.96	0.47
1:B:103:GLU:OE2	1:B:111:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:ARG:O	1:B:209:THR:HG23	2.14	0.46
1:F:42:ASN:OD1	1:F:42:ASN:C	2.59	0.46
2:E:302:DTP:H2'1	1:F:28:PHE:CD1	2.50	0.46
2:G:302:DTP:H5'1	2:G:302:DTP:O1B	2.16	0.45
1:F:26:ARG:NE	1:F:30[A]:SER:OG	2.49	0.45
1:D:171:VAL:HG11	1:D:179:TRP:CZ3	2.52	0.44
1:B:57:GLY:HA3	1:B:98:MET:HE2	1.99	0.44
1:H:114:LEU:O	1:H:118:GLY:HA2	2.17	0.44
1:D:52:GLU:O	1:D:53:ILE:HD13	2.17	0.44
1:G:35:ARG:NE	1:G:48:GLU:OE2	2.47	0.44
1:H:35:ARG:HB2	1:H:35:ARG:CZ	2.47	0.43
1:H:119:LEU:HD21	1:H:153:ALA:HB2	1.99	0.43
1:E:23:THR:HG23	1:E:26:ARG:HH11	1.82	0.43
1:C:128[B]:LEU:HD21	1:C:192:ILE:CG2	2.48	0.43
1:A:-1:HIS:CE1	1:G:23:THR:HG21	2.53	0.43
1:G:10:THR:CB	1:H:167:ARG:HH22	2.32	0.43
1:B:26[A]:ARG:CZ	1:B:30:SER:OG	2.67	0.43
2:E:302:DTP:H8	2:E:302:DTP:H2'2	1.87	0.43
1:E:119:LEU:HD21	1:E:153:ALA:HB2	2.00	0.43
1:E:62:LEU:HD11	1:E:146:GLY:HA3	2.01	0.42
1:E:81:ALA:HB2	1:F:53:ILE:HD12	2.01	0.42
2:C:302:DTP:H2'1	1:D:28:PHE:CD1	2.54	0.42
1:A:34:TYR:O	1:A:50:THR:HA	2.19	0.42
1:G:22:GLU:OE2	1:G:35:ARG:HD2	2.20	0.42
1:F:19:ILE:HD11	1:F:37:ARG:HG3	2.02	0.41
1:E:45:MET:O	1:H:6:GLN:CB	2.68	0.41
1:A:25:TYR:CE2	1:B:31:LEU:CD2	3.03	0.41
1:B:34:TYR:O	1:B:50:THR:HA	2.20	0.41
1:D:24:LEU:HD11	1:D:33:LEU:HB2	2.02	0.41
1:G:25:TYR:CE1	1:H:31:LEU:CD2	3.04	0.41
1:G:9:ILE:CG2	1:G:10:THR:N	2.84	0.41
1:A:10:THR:HG22	1:B:167:ARG:HH21	1.86	0.41
1:C:34:TYR:O	1:C:50:THR:HA	2.22	0.40

There are no symmetry-related clashes.

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	196/218 (90%)	186 (95%)	10 (5%)	0	100	100
1	B	195/218 (89%)	186 (95%)	9 (5%)	0	100	100
1	C	197/218 (90%)	191 (97%)	6 (3%)	0	100	100
1	D	192/218 (88%)	182 (95%)	10 (5%)	0	100	100
1	E	199/218 (91%)	194 (98%)	5 (2%)	0	100	100
1	F	193/218 (88%)	185 (96%)	7 (4%)	1 (0%)	24	11
1	G	196/218 (90%)	191 (97%)	5 (3%)	0	100	100
1	H	200/218 (92%)	190 (95%)	10 (5%)	0	100	100
All	All	1568/1744 (90%)	1505 (96%)	62 (4%)	1 (0%)	48	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	9	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	168/183 (92%)	162 (96%)	6 (4%)	31	10
1	B	163/183 (89%)	158 (97%)	5 (3%)	35	14
1	C	165/183 (90%)	161 (98%)	4 (2%)	43	24
1	D	163/183 (89%)	160 (98%)	3 (2%)	51	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	171/183 (93%)	166 (97%)	5 (3%)	37	16
1	F	162/183 (88%)	161 (99%)	1 (1%)	78	70
1	G	164/183 (90%)	163 (99%)	1 (1%)	78	70
1	H	165/183 (90%)	159 (96%)	6 (4%)	31	10
All	All	1321/1464 (90%)	1290 (98%)	31 (2%)	45	25

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	16[A]	VAL
1	A	16[B]	VAL
1	A	62	LEU
1	A	114	LEU
1	A	174	GLU
1	B	10	THR
1	B	42	ASN
1	B	95	VAL
1	B	98	MET
1	B	164	GLU
1	C	16	VAL
1	C	100	GLU
1	C	115[A]	GLU
1	C	115[B]	GLU
1	D	9	ILE
1	D	16	VAL
1	D	22	GLU
1	E	16[A]	VAL
1	E	16[B]	VAL
1	E	26	ARG
1	E	114	LEU
1	E	144	LEU
1	F	16	VAL
1	G	16	VAL
1	H	9	ILE
1	H	26	ARG
1	H	34	TYR
1	H	98	MET
1	H	156	ILE
1	H	167	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	42	ASN
1	C	157	HIS
1	C	175	GLN
1	D	187	ASN
1	E	-2	HIS
1	E	187	ASN
1	F	187	ASN
1	G	202	HIS
1	H	195	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 15 ligands modelled in this entry, 7 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	DTP	C	301	-	31,32,32	0.54	1 (3%)	46,50,50	0.50	0
2	DTP	E	302	-	31,32,32	1.03	2 (6%)	46,50,50	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DTP	A	301	-	31,32,32	0.74	2 (6%)	46,50,50	0.60	0
2	DTP	E	301	-	31,32,32	0.86	2 (6%)	46,50,50	0.56	0
2	DTP	G	302	-	31,32,32	1.12	2 (6%)	46,50,50	0.58	0
2	DTP	B	301	-	31,32,32	0.53	1 (3%)	46,50,50	0.50	0
2	DTP	C	302	-	31,32,32	0.40	0	46,50,50	0.51	0
2	DTP	G	301	-	31,32,32	0.85	2 (6%)	46,50,50	0.54	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	DTP	C	301	-	-	11/22/34/34	0/3/3/3
2	DTP	E	302	-	-	8/22/34/34	0/3/3/3
2	DTP	A	301	-	-	6/22/34/34	0/3/3/3
2	DTP	E	301	-	-	6/22/34/34	0/3/3/3
2	DTP	G	302	-	-	3/22/34/34	0/3/3/3
2	DTP	B	301	-	-	6/22/34/34	0/3/3/3
2	DTP	C	302	-	-	7/22/34/34	0/3/3/3
2	DTP	G	301	-	-	4/22/34/34	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	302	DTP	PA-O3A	5.56	1.65	1.59
2	E	302	DTP	PA-O3A	4.27	1.64	1.59
2	E	301	DTP	PA-O3A	3.97	1.63	1.59
2	G	301	DTP	PA-O3A	3.84	1.63	1.59
2	E	302	DTP	PB-O3B	3.58	1.63	1.59
2	A	301	DTP	PA-O3A	2.93	1.62	1.59
2	A	301	DTP	PB-O3B	2.64	1.62	1.59
2	G	302	DTP	PB-O3B	2.43	1.62	1.59
2	G	301	DTP	PB-O3B	2.42	1.62	1.59
2	B	301	DTP	PA-O3A	2.39	1.62	1.59
2	E	301	DTP	PB-O3B	2.21	1.61	1.59
2	C	301	DTP	PB-O3B	2.17	1.61	1.59

There are no bond angle outliers.

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	DTP	C4'-C5'-O5'-PA
2	B	301	DTP	PB-O3B-PG-O2G
2	C	301	DTP	C5'-O5'-PA-O1A
2	C	301	DTP	C5'-O5'-PA-O2A
2	C	301	DTP	C5'-O5'-PA-O3A
2	E	301	DTP	C5'-O5'-PA-O1A
2	E	301	DTP	C5'-O5'-PA-O2A
2	E	301	DTP	C5'-O5'-PA-O3A
2	E	302	DTP	PB-O3B-PG-O2G
2	E	302	DTP	C5'-O5'-PA-O1A
2	G	301	DTP	C5'-O5'-PA-O2A
2	G	302	DTP	PB-O3B-PG-O2G
2	G	302	DTP	C5'-O5'-PA-O1A
2	C	302	DTP	C4'-C5'-O5'-PA
2	C	301	DTP	O4'-C4'-C5'-O5'
2	C	301	DTP	C3'-C4'-C5'-O5'
2	C	301	DTP	C4'-C5'-O5'-PA
2	B	301	DTP	C3'-C4'-C5'-O5'
2	A	301	DTP	C3'-C4'-C5'-O5'
2	B	301	DTP	O4'-C4'-C5'-O5'
2	E	301	DTP	PB-O3A-PA-O1A
2	E	302	DTP	C4'-C5'-O5'-PA
2	A	301	DTP	PB-O3A-PA-O5'
2	B	301	DTP	PB-O3A-PA-O5'
2	C	301	DTP	PB-O3A-PA-O5'
2	E	301	DTP	PB-O3A-PA-O5'
2	C	302	DTP	PG-O3B-PB-O3A
2	E	302	DTP	PA-O3A-PB-O3B
2	C	302	DTP	C5'-O5'-PA-O1A
2	C	302	DTP	C5'-O5'-PA-O2A
2	C	302	DTP	C5'-O5'-PA-O3A
2	G	301	DTP	C5'-O5'-PA-O3A
2	B	301	DTP	PB-O3B-PG-O1G
2	A	301	DTP	O4'-C4'-C5'-O5'
2	A	301	DTP	PA-O3A-PB-O2B
2	E	302	DTP	PG-O3B-PB-O2B
2	G	302	DTP	C4'-C5'-O5'-PA
2	G	301	DTP	PB-O3A-PA-O2A
2	E	302	DTP	PB-O3B-PG-O1G
2	C	301	DTP	PB-O3B-PG-O3G

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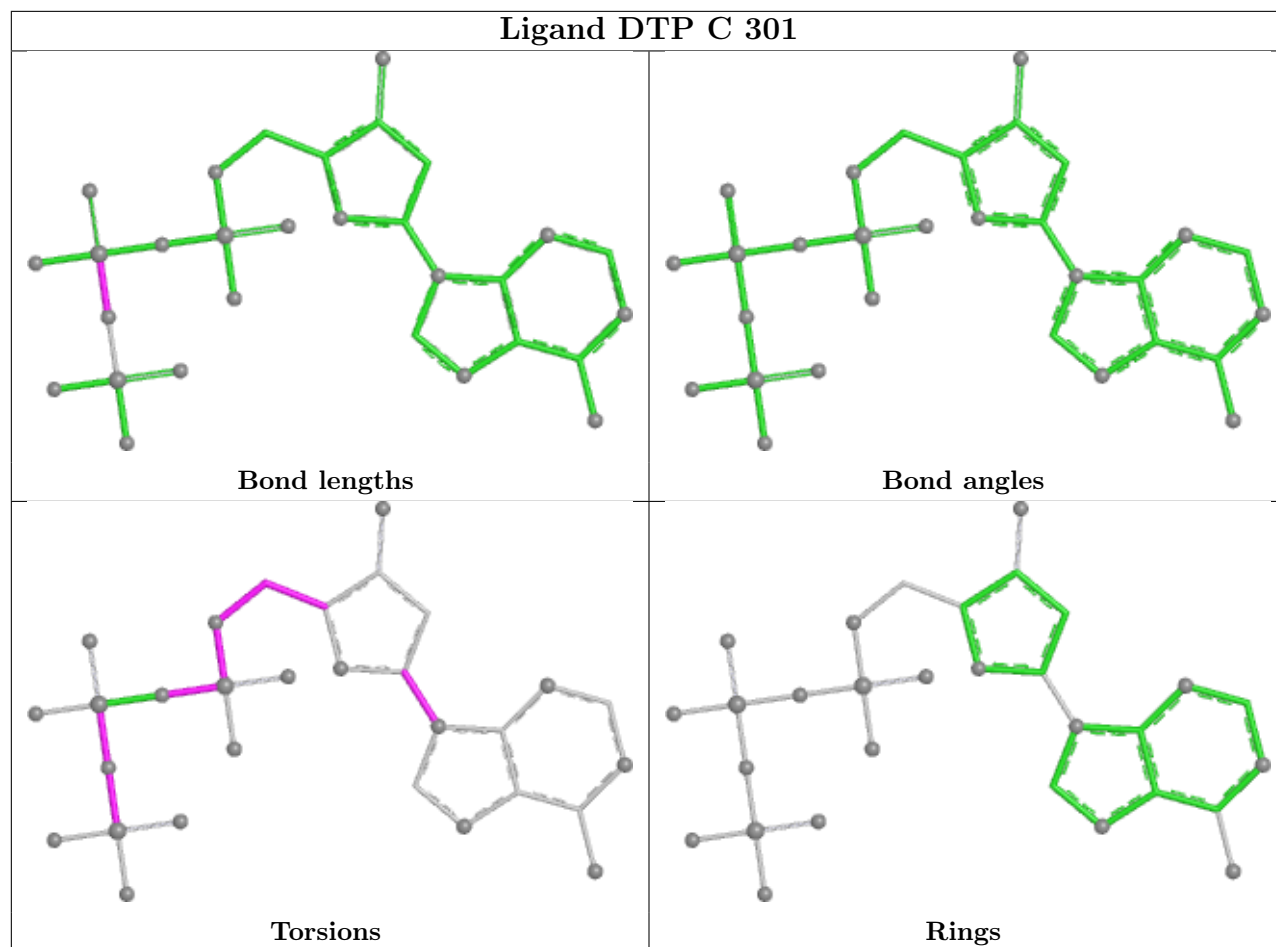
Mol	Chain	Res	Type	Atoms
2	E	302	DTP	PB-O3B-PG-O3G
2	A	301	DTP	PA-O3A-PB-O1B
2	C	302	DTP	PG-O3B-PB-O1B
2	C	302	DTP	PG-O3B-PB-O2B
2	E	302	DTP	PA-O3A-PB-O1B
2	B	301	DTP	C2'-C1'-N9-C4
2	C	301	DTP	C2'-C1'-N9-C4
2	G	301	DTP	C2'-C1'-N9-C4
2	E	301	DTP	C3'-C4'-C5'-O5'
2	C	301	DTP	PG-O3B-PB-O2B
2	C	301	DTP	PB-O3A-PA-O2A

There are no ring outliers.

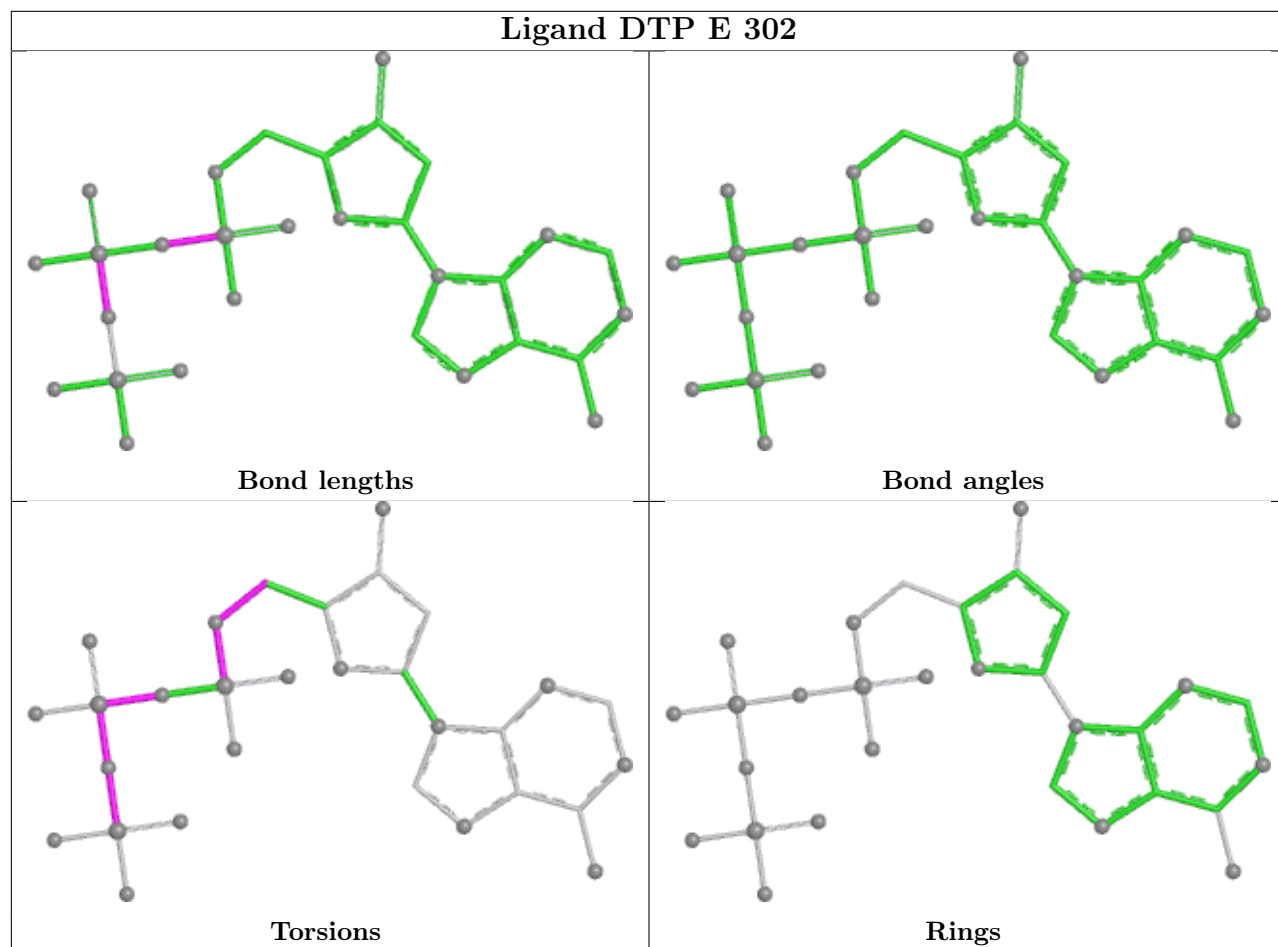
4 monomers are involved in 5 short contacts:

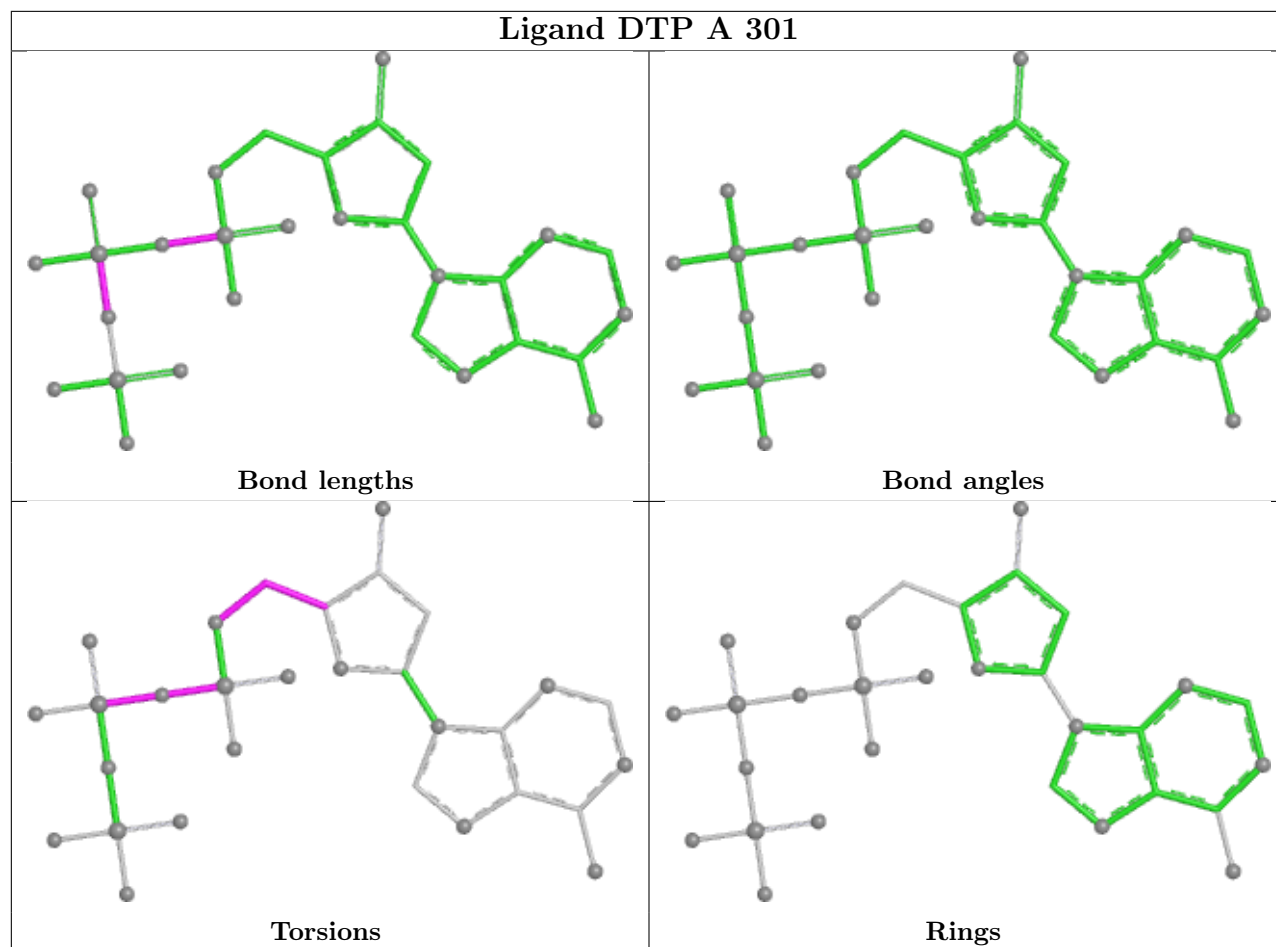
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	302	DTP	2	0
2	A	301	DTP	1	0
2	G	302	DTP	1	0
2	C	302	DTP	1	0

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.

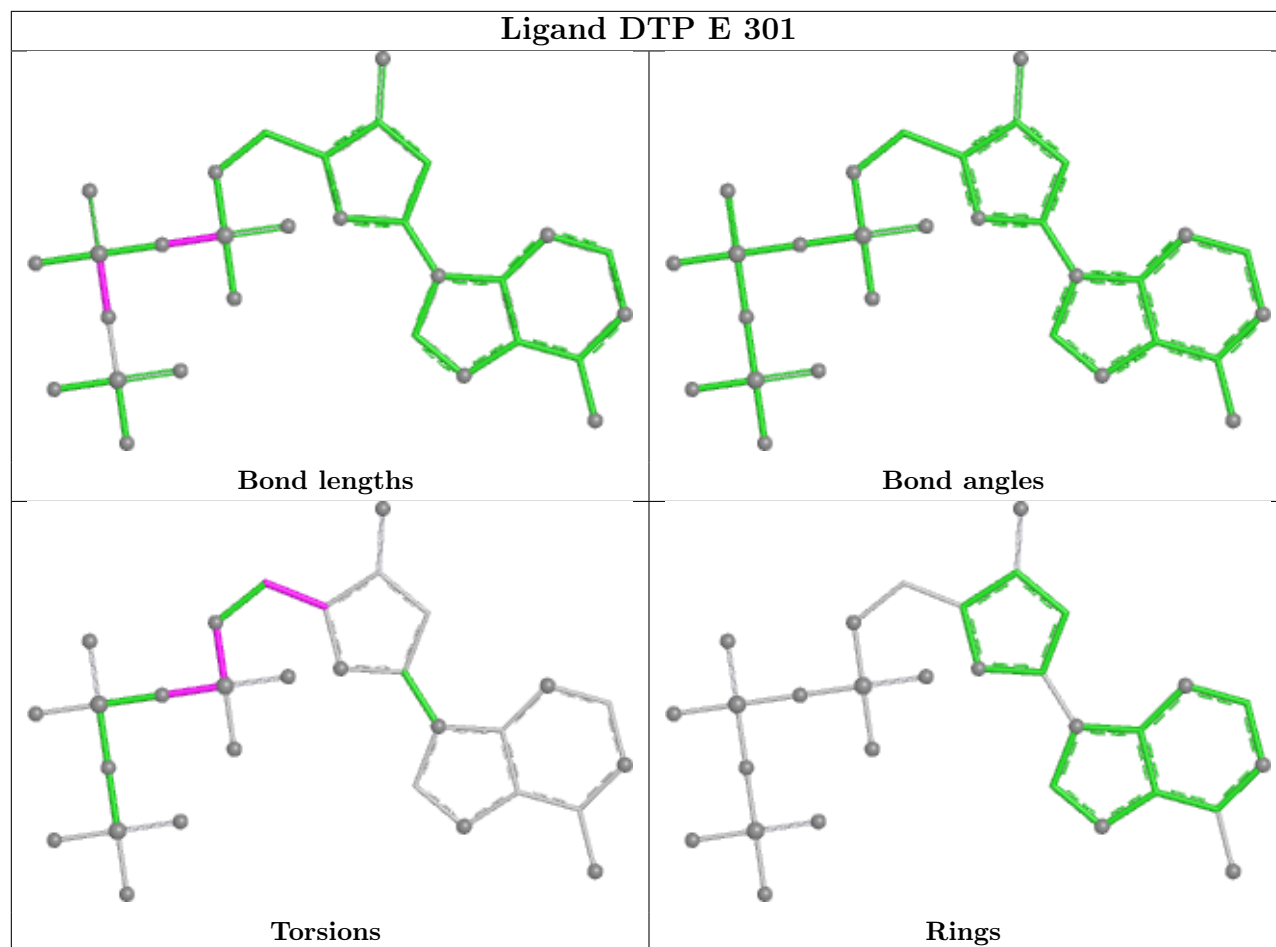


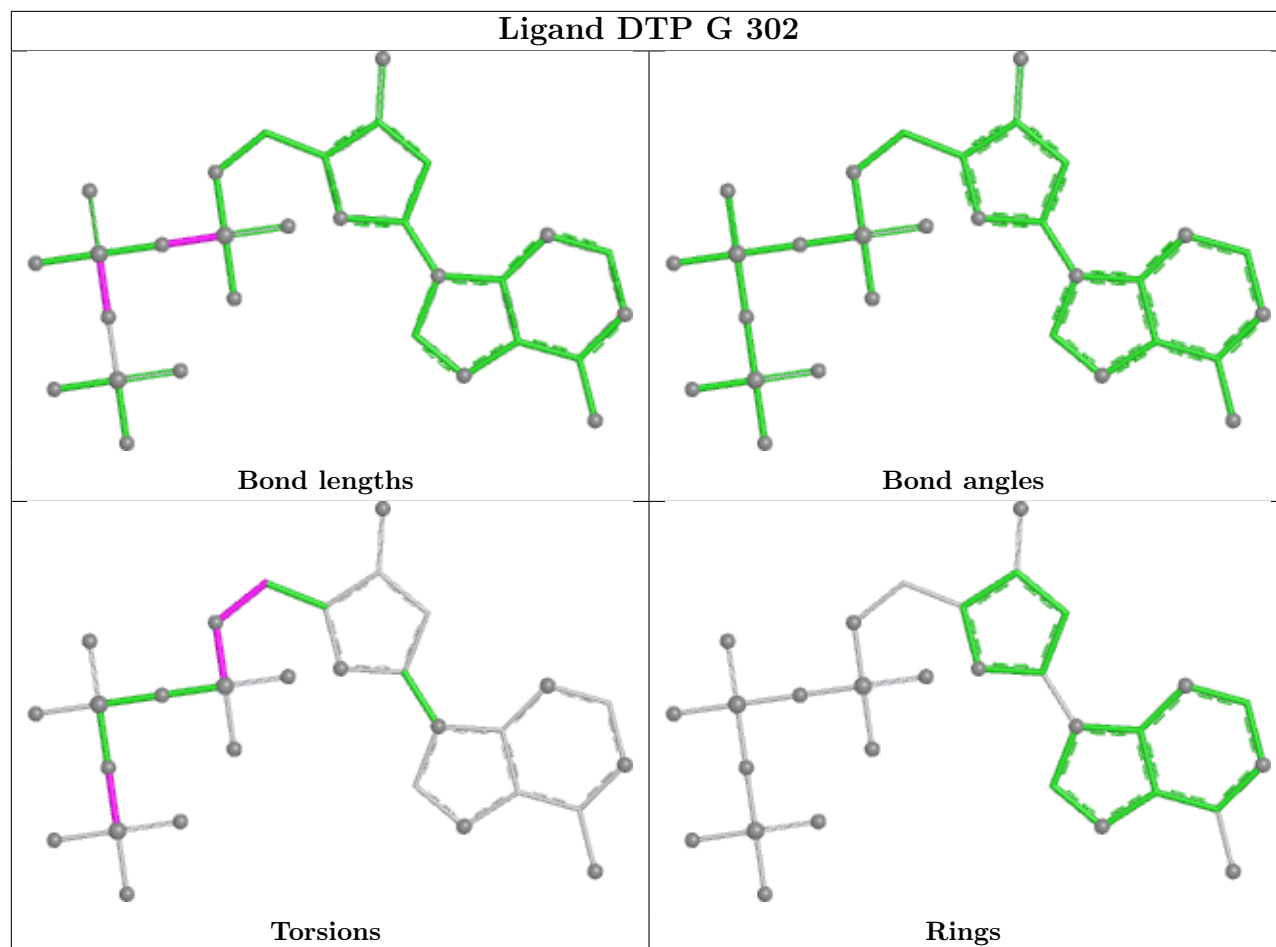
Ligand DTP E 302

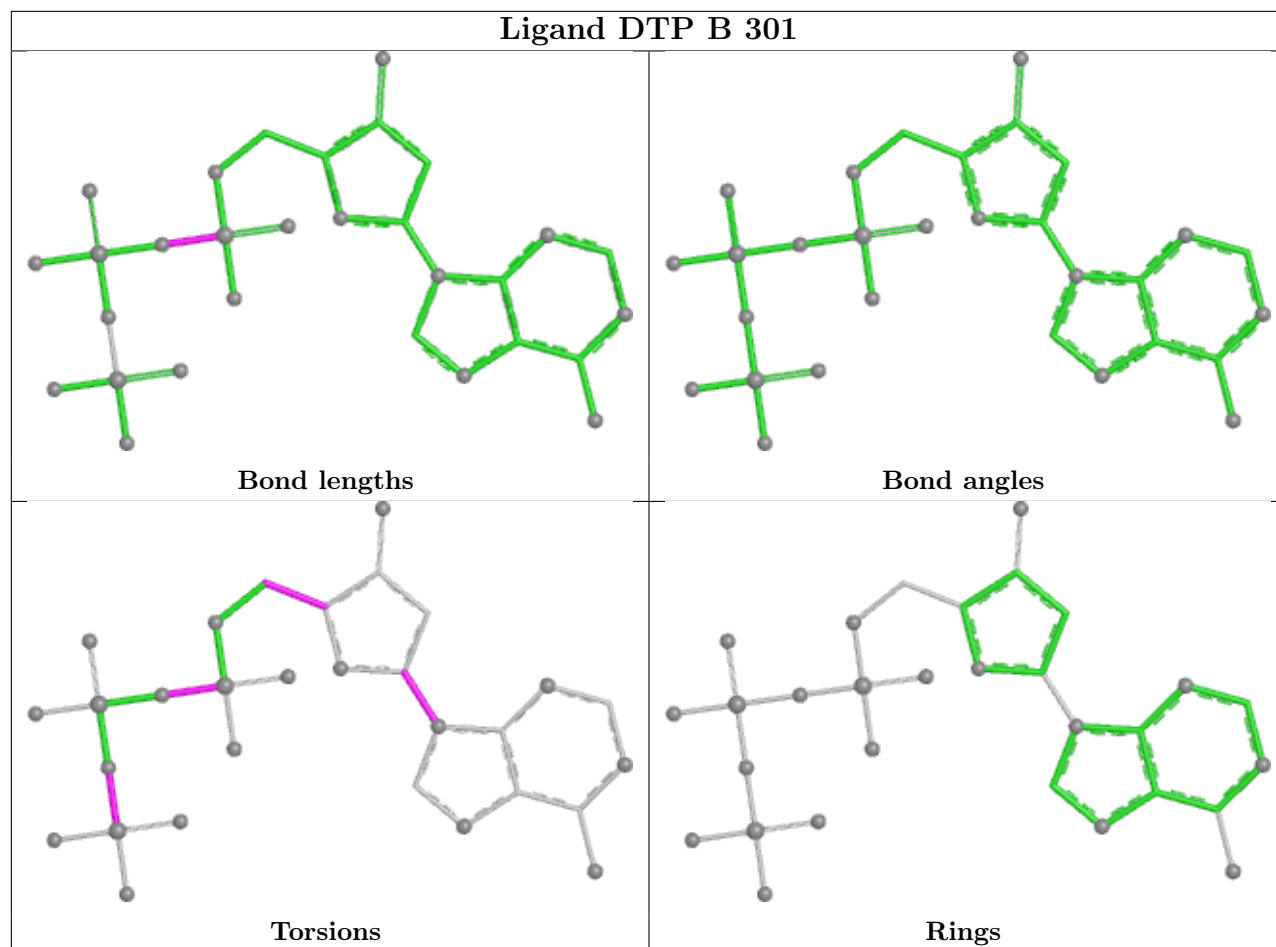


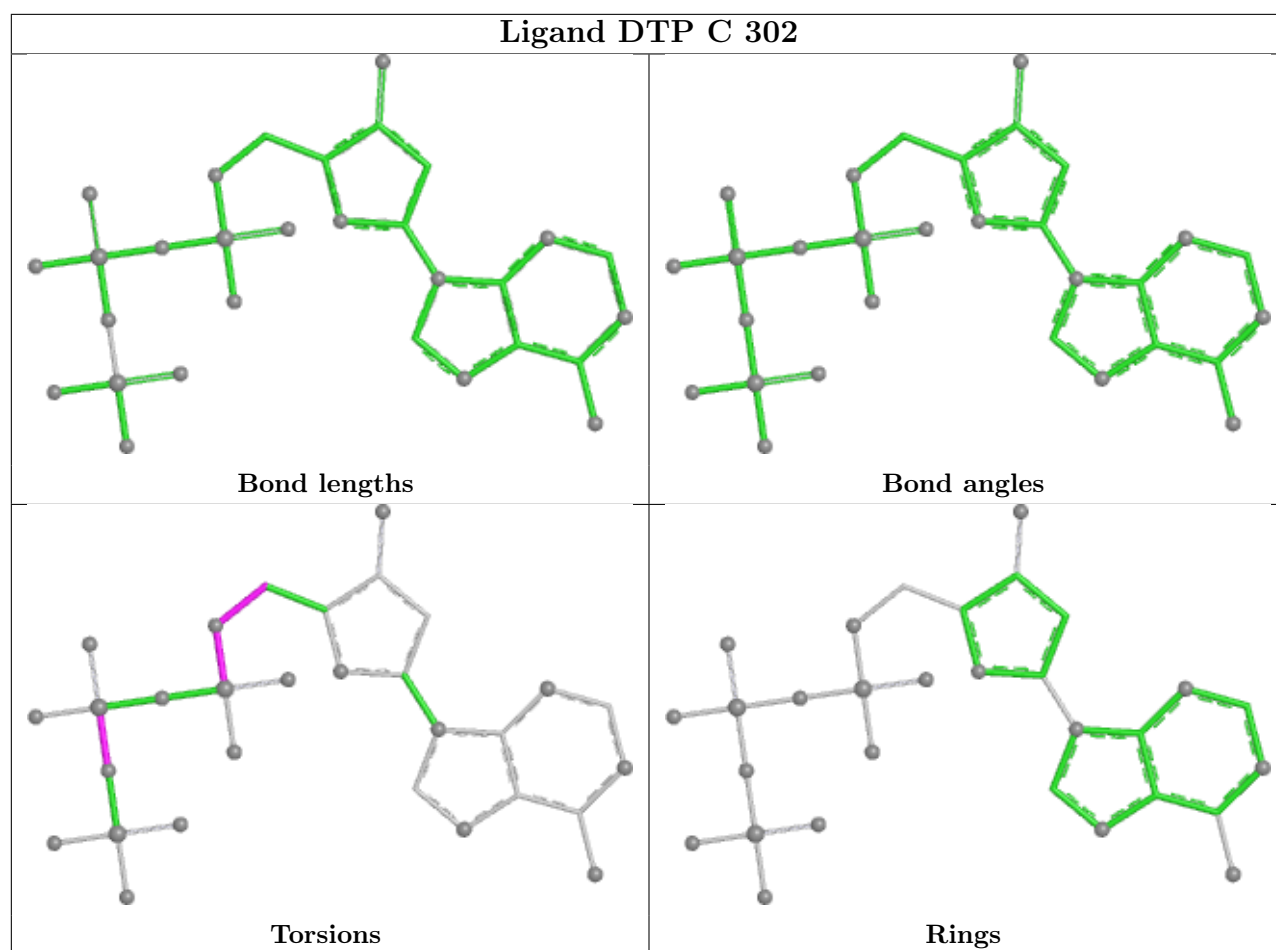


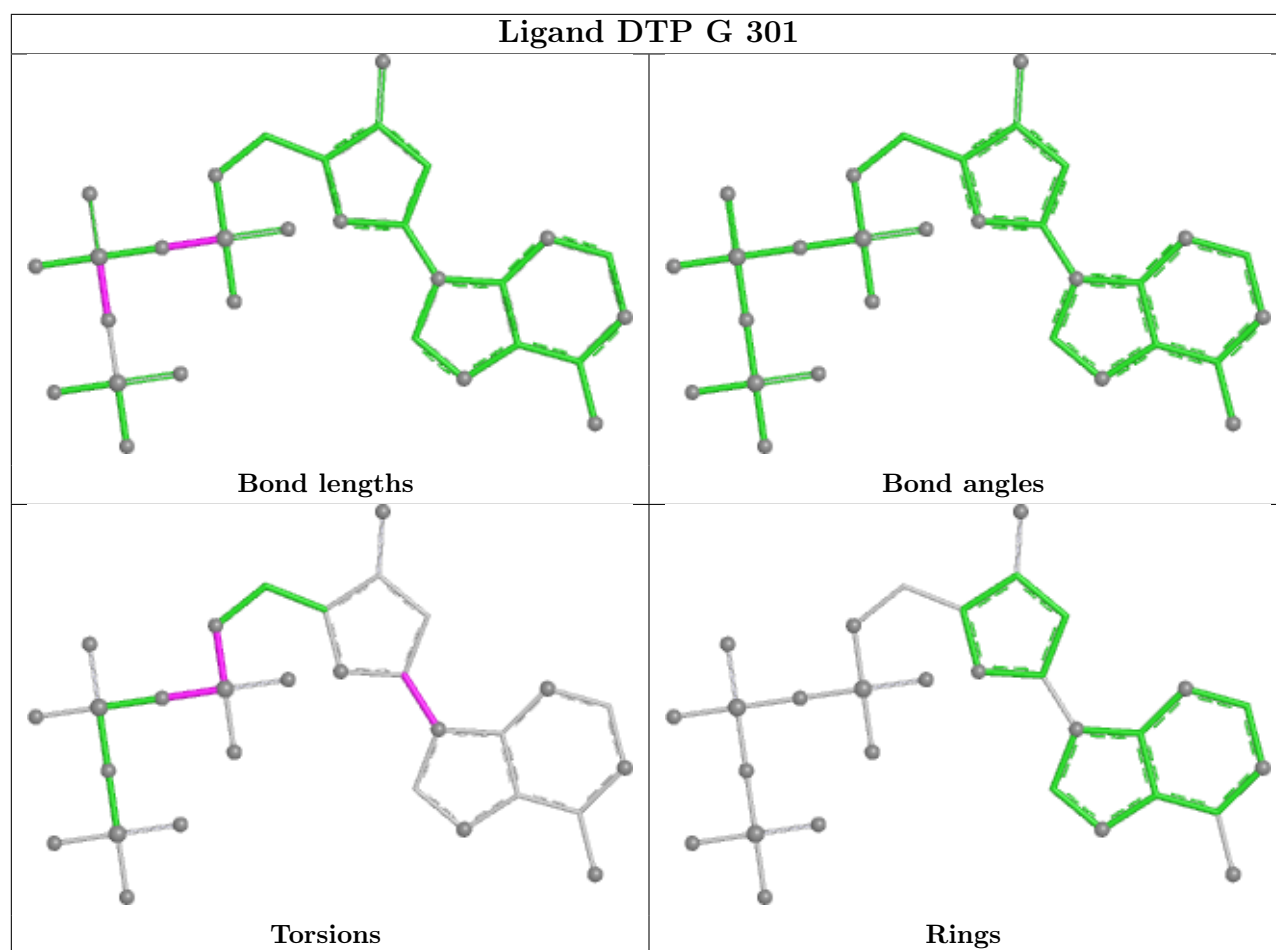
Ligand DTP E 301











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	197/218 (90%)	0.39	13 (6%) 24 29	21, 42, 78, 105	5 (2%)
1	B	197/218 (90%)	0.42	14 (7%) 22 26	25, 44, 86, 102	2 (1%)
1	C	199/218 (91%)	0.17	7 (3%) 47 53	20, 40, 62, 89	2 (1%)
1	D	195/218 (89%)	0.42	6 (3%) 51 59	28, 50, 84, 97	1 (0%)
1	E	202/218 (92%)	0.59	14 (6%) 23 27	21, 51, 76, 88	3 (1%)
1	F	194/218 (88%)	0.40	8 (4%) 41 48	26, 44, 82, 106	3 (1%)
1	G	198/218 (90%)	0.31	8 (4%) 42 48	20, 40, 69, 88	2 (1%)
1	H	200/218 (91%)	0.48	11 (5%) 30 36	21, 44, 81, 104	4 (2%)
All	All	1582/1744 (90%)	0.40	81 (5%) 33 39	20, 44, 80, 106	22 (1%)

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	-3	HIS	5.5
1	A	0	HIS	5.3
1	B	156	ILE	5.2
1	A	10	THR	4.5
1	F	209	THR	4.5
1	G	8	GLY	4.5
1	H	156	ILE	4.3
1	A	-2	HIS	4.1
1	G	9	ILE	3.8
1	E	10	THR	3.8
1	H	6	GLN	3.7
1	F	9	ILE	3.6
1	G	10	THR	3.5
1	E	-2	HIS	3.5
1	G	153	ALA	3.5
1	E	0	HIS	3.5

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Mol	Chain	Res	Type	RSRZ
1	E	-4	HIS	3.4
1	A	155	GLY	3.4
1	H	209	THR	3.3
1	B	155	GLY	3.2
1	A	114	LEU	3.1
1	E	2	SER	3.1
1	B	7	GLN	3.0
1	G	156	ILE	3.0
1	B	118	GLY	3.0
1	H	157	HIS	2.9
1	E	209	THR	2.9
1	F	8	GLY	2.9
1	E	158	GLY	2.8
1	D	119	LEU	2.7
1	B	101	ALA	2.7
1	A	-1	HIS	2.7
1	C	7	GLN	2.7
1	A	209	THR	2.7
1	D	209	THR	2.7
1	G	163	ASN	2.7
1	B	209	THR	2.6
1	D	101	ALA	2.6
1	B	44	GLY	2.6
1	E	-3	HIS	2.6
1	C	10	THR	2.5
1	B	6	GLN	2.5
1	E	156	ILE	2.5
1	H	152	THR	2.5
1	G	26	ARG	2.5
1	E	68	VAL	2.5
1	D	102	GLY	2.4
1	A	164	GLU	2.4
1	C	31	LEU	2.4
1	B	20	ALA	2.4
1	F	20	ALA	2.4
1	B	10	THR	2.4
1	B	116	GLU	2.4
1	H	9	ILE	2.4
1	E	-1	HIS	2.4
1	C	164	GLU	2.3
1	C	158	GLY	2.3
1	A	154	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	H	153	ALA	2.3
1	H	44	GLY	2.3
1	F	10	THR	2.3
1	G	25	TYR	2.3
1	D	19	ILE	2.3
1	A	101	ALA	2.2
1	H	163	ASN	2.2
1	H	117	ALA	2.2
1	B	12	SER	2.2
1	B	102	GLY	2.2
1	C	102	GLY	2.2
1	E	155	GLY	2.2
1	H	8	GLY	2.2
1	F	19	ILE	2.2
1	A	-4	HIS	2.1
1	F	164	GLU	2.1
1	E	1	MET	2.1
1	E	164	GLU	2.1
1	D	154	LYS	2.1
1	B	19	ILE	2.1
1	F	98	MET	2.0
1	A	151	SER	2.0
1	C	9	ILE	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 [i](#)

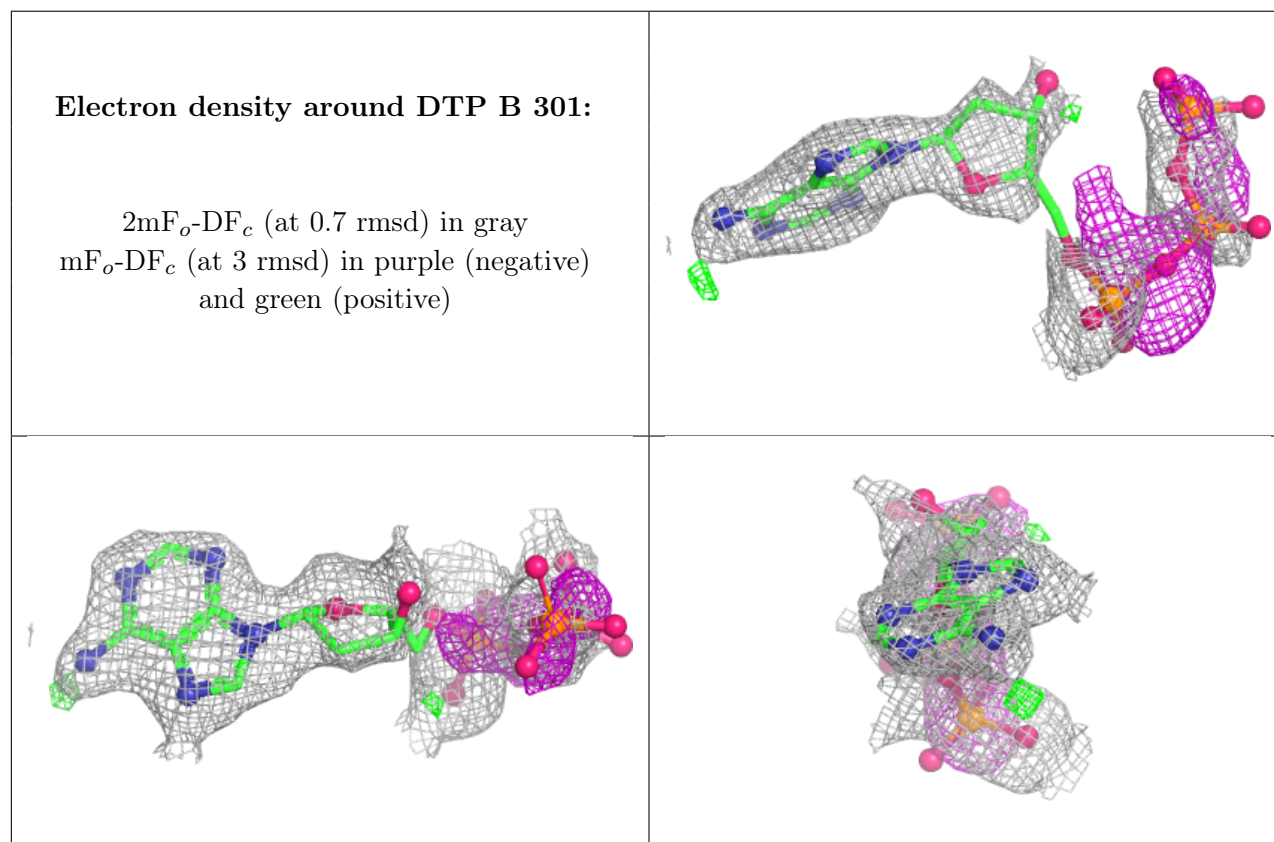
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

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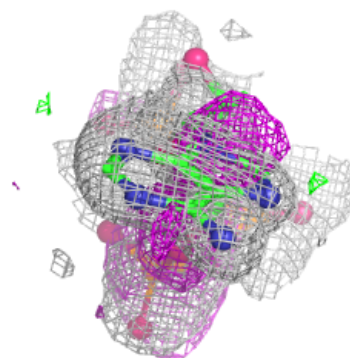
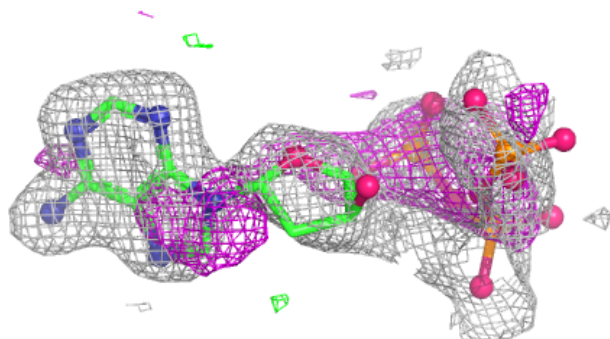
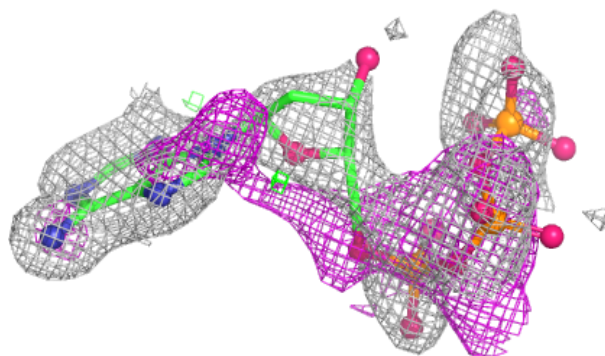
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	DTP	B	301	30/30	0.60	0.12	55,92,128,133	0
2	DTP	E	302	30/30	0.60	0.14	40,86,125,129	0
2	DTP	C	302	30/30	0.65	0.13	40,81,121,122	0
2	DTP	E	301	30/30	0.66	0.13	56,83,116,121	0
2	DTP	C	301	30/30	0.66	0.12	47,83,125,132	0
2	DTP	G	301	30/30	0.66	0.12	48,82,120,126	0
3	MG	E	303	1/1	0.69	0.16	64,64,64,64	0
2	DTP	A	301	30/30	0.70	0.13	33,67,119,130	0
2	DTP	G	302	30/30	0.71	0.13	30,72,118,129	0
3	MG	C	303	1/1	0.74	0.14	56,56,56,56	0
3	MG	G	303	1/1	0.77	0.14	62,62,62,62	0
3	MG	F	302	1/1	0.78	0.14	61,61,61,61	0
3	MG	B	302	1/1	0.80	0.20	72,72,72,72	0
3	MG	H	301	1/1	0.88	0.14	59,59,59,59	0
3	MG	F	301	1/1	0.93	0.14	52,52,52,52	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.

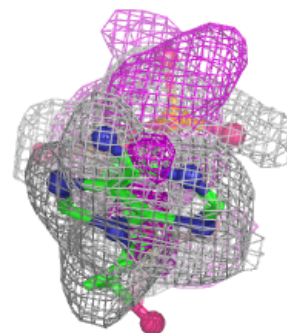
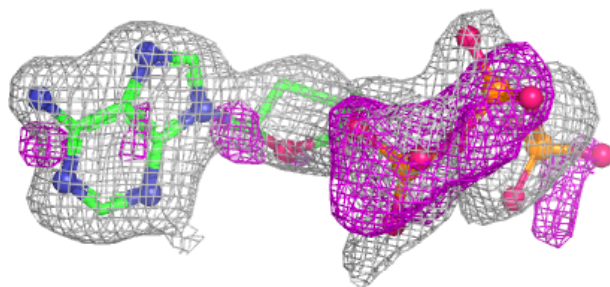
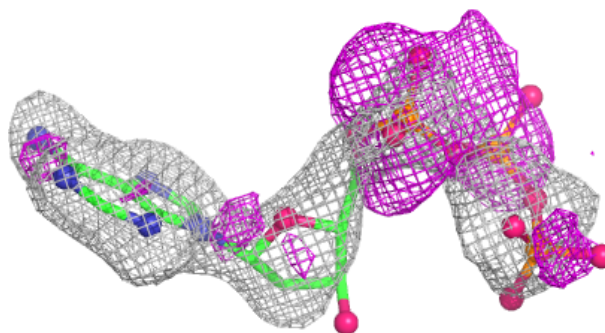


Electron density around DTP E 302:

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

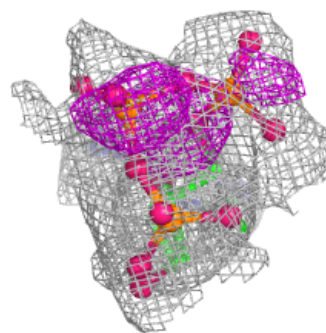
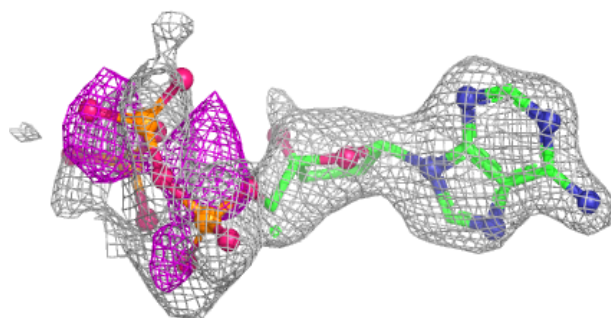
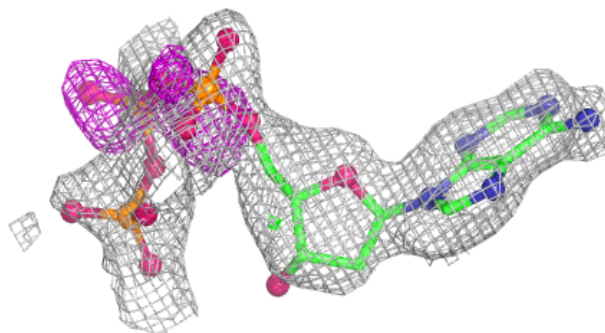
**Electron density around DTP C 302:**

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

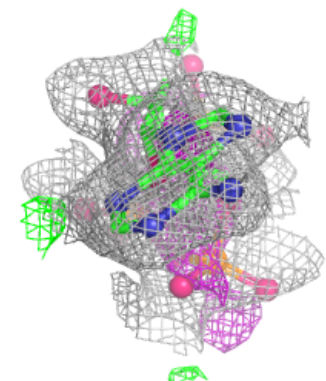
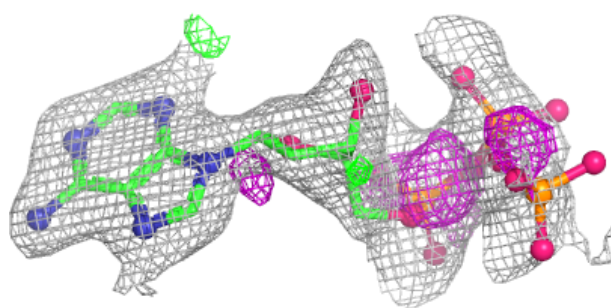
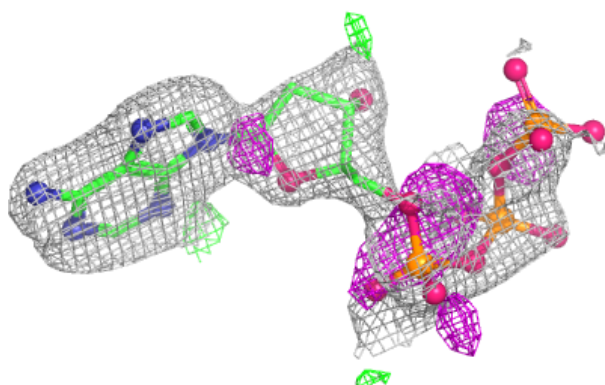


Electron density around DTP E 301:

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

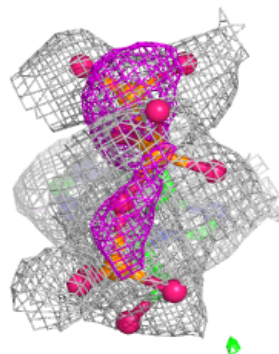
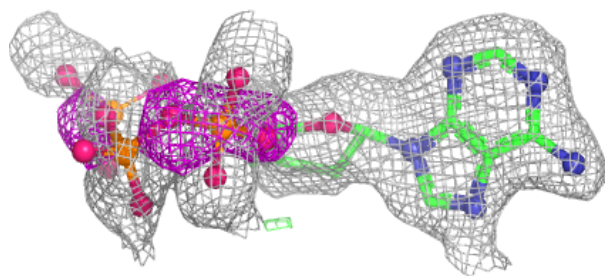
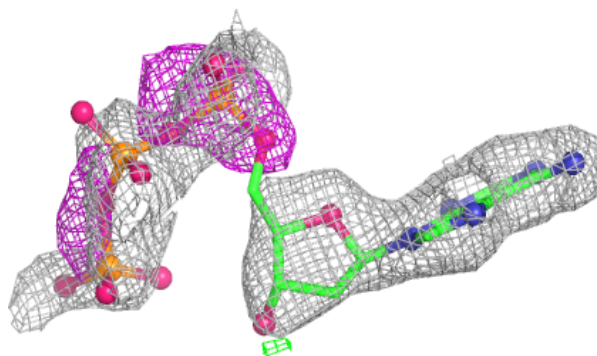
**Electron density around DTP C 301:**

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



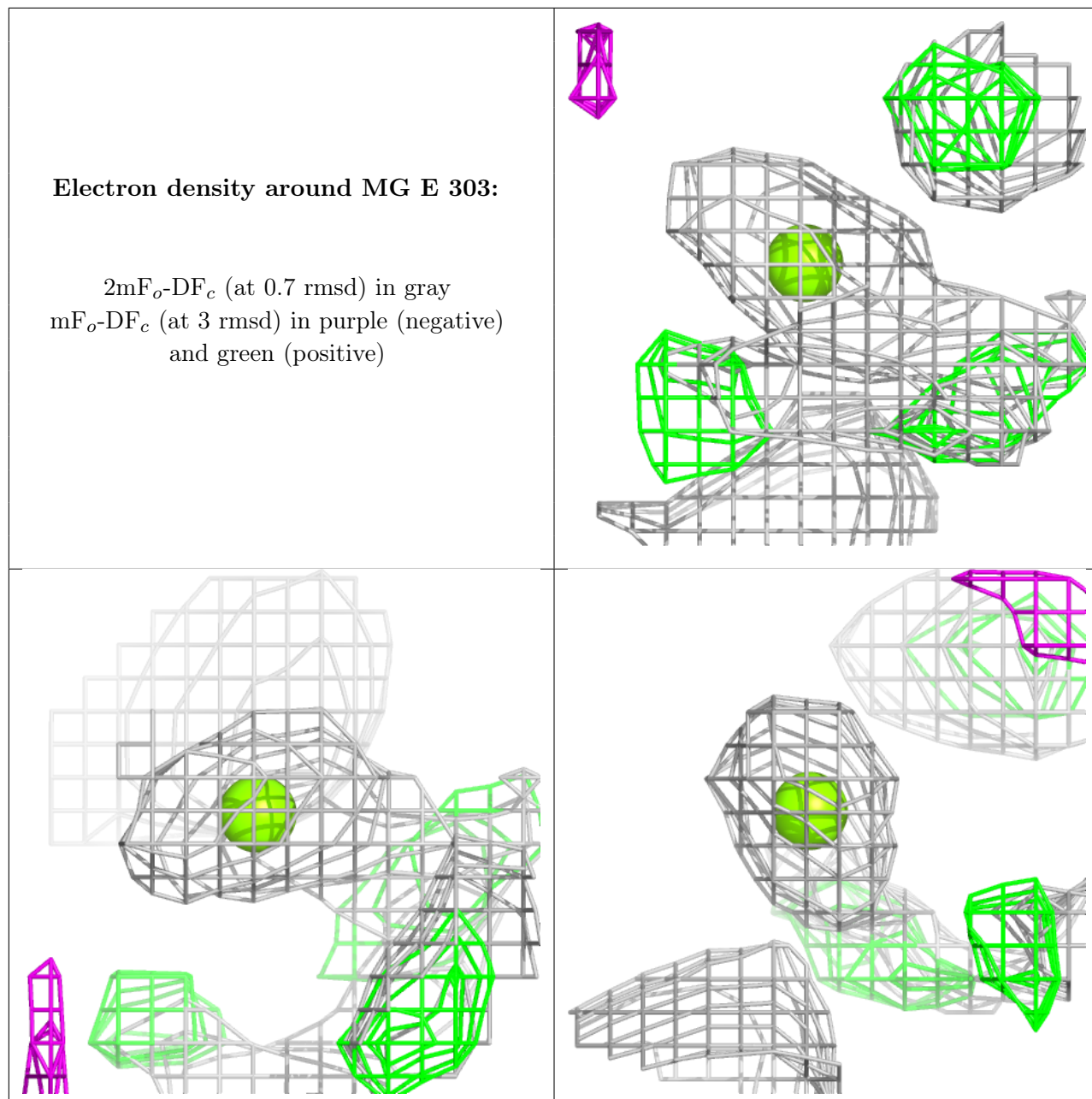
Electron density around DTP G 301:

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



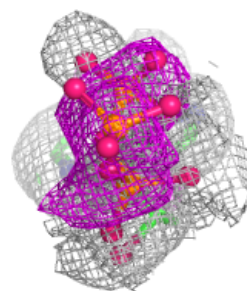
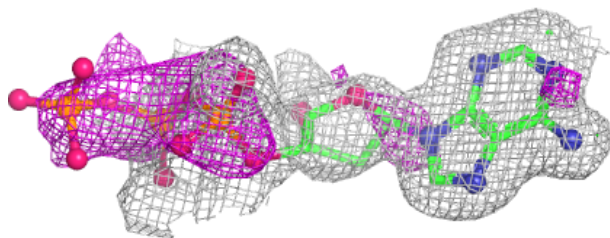
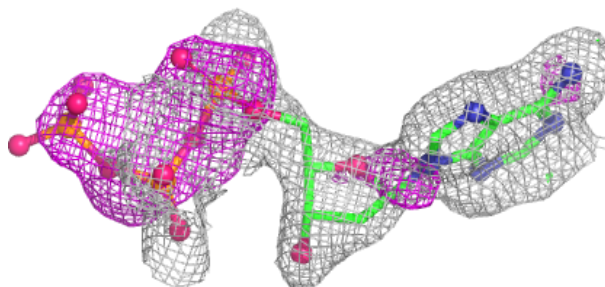
Electron density around MG E 303:

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

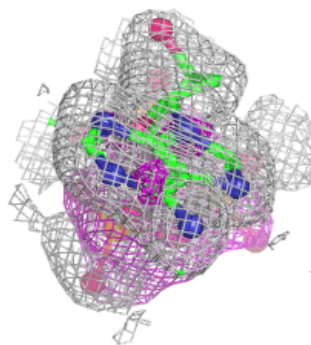
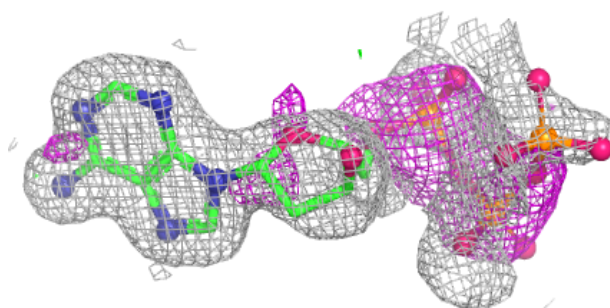
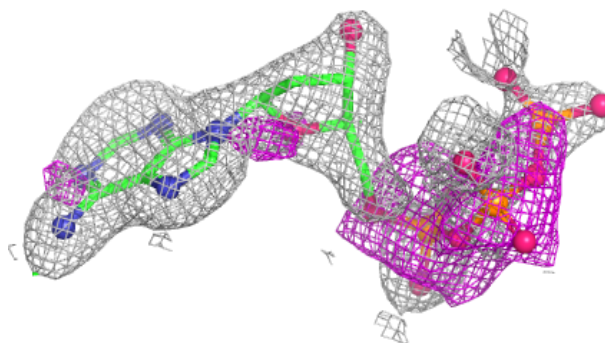


Electron density around DTP A 301:

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

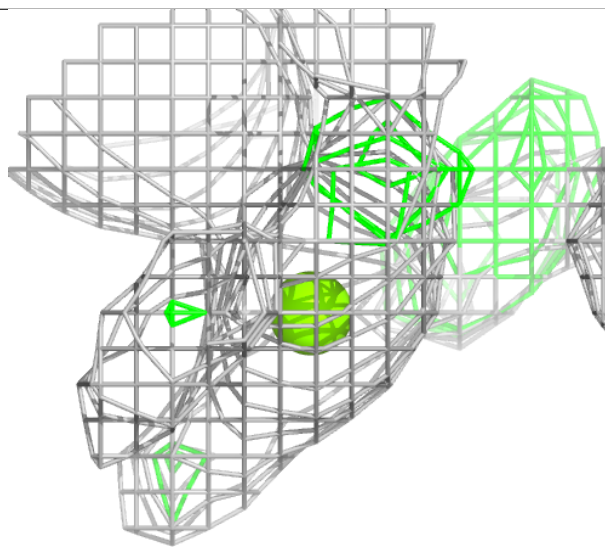
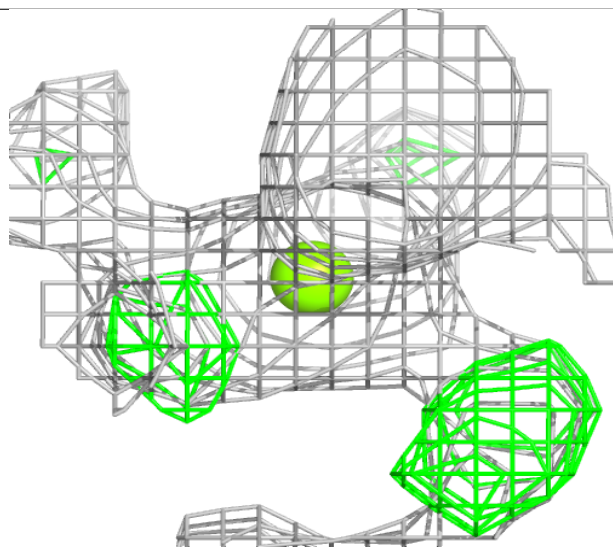
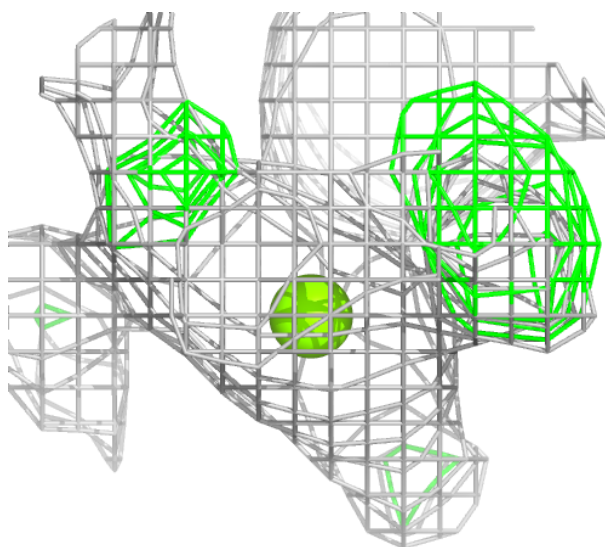
**Electron density around DTP G 302:**

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



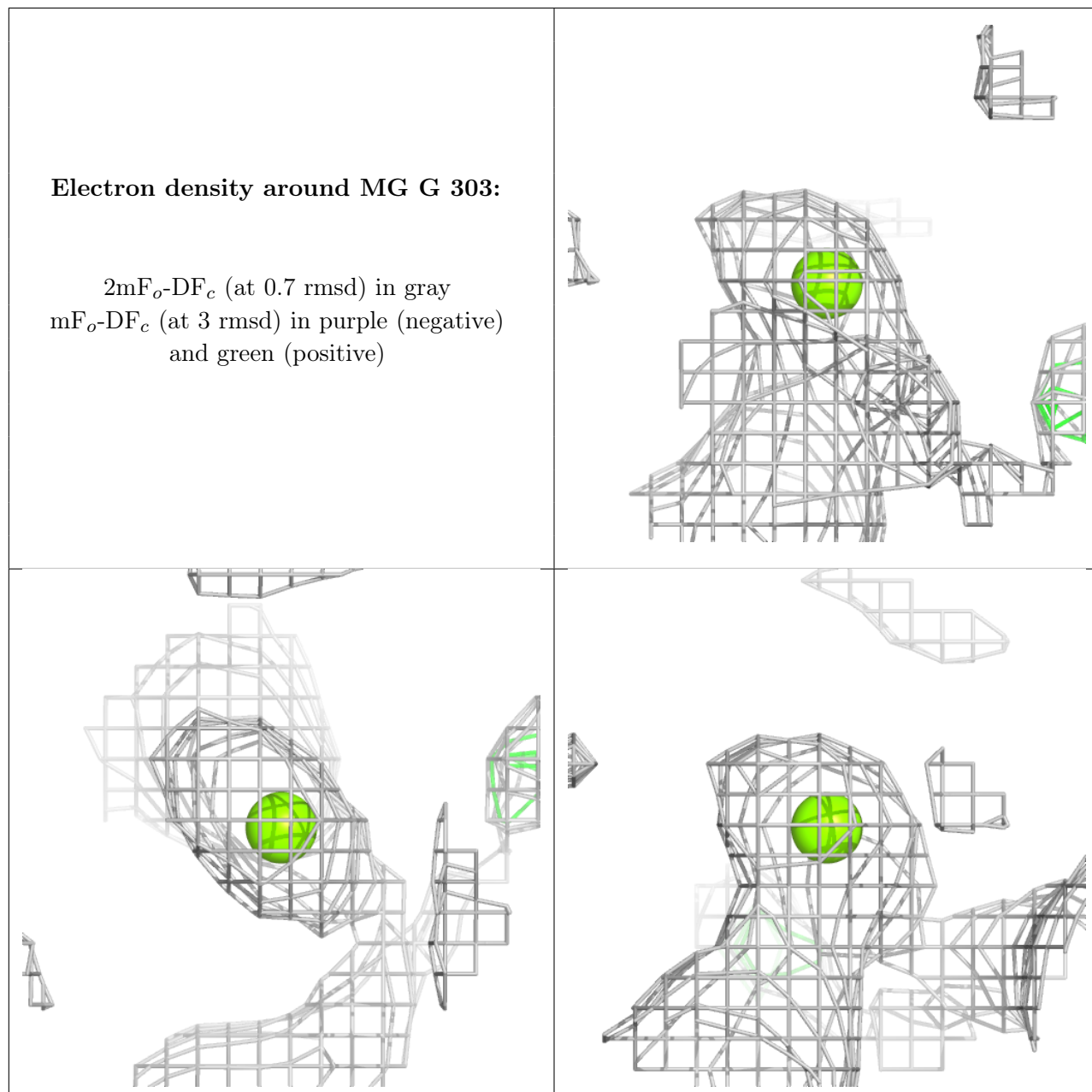
Electron density around MG C 303:

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



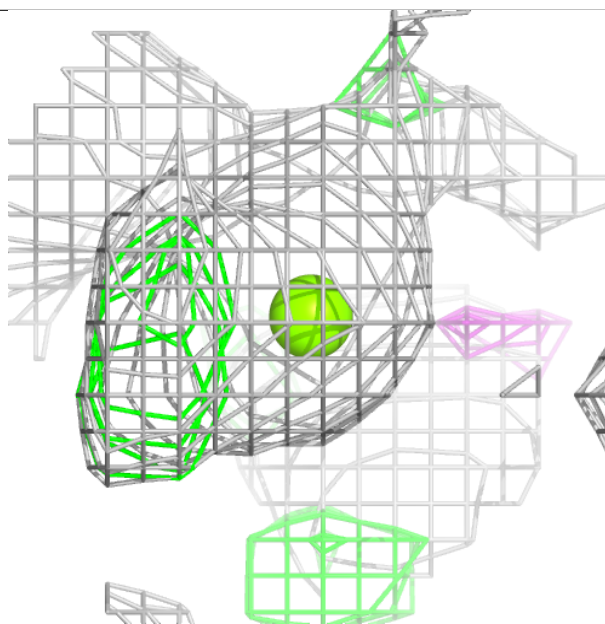
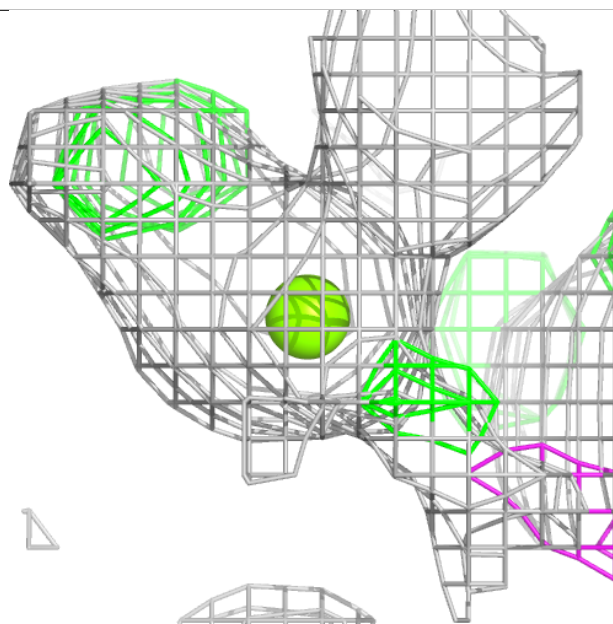
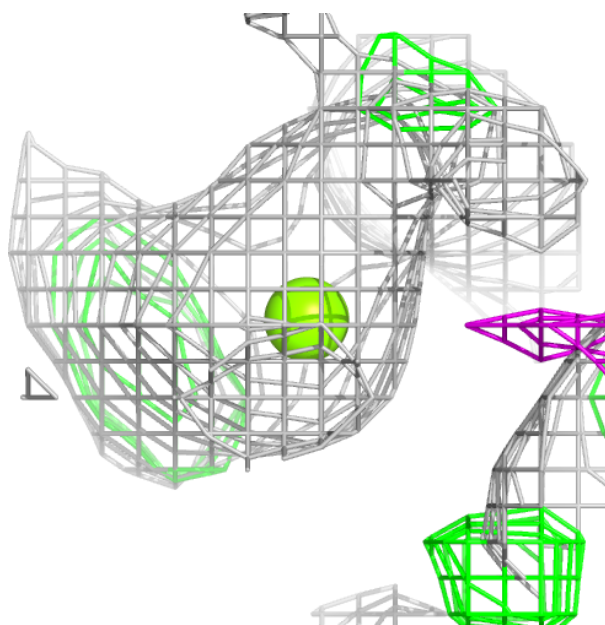
Electron density around MG G 303:

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



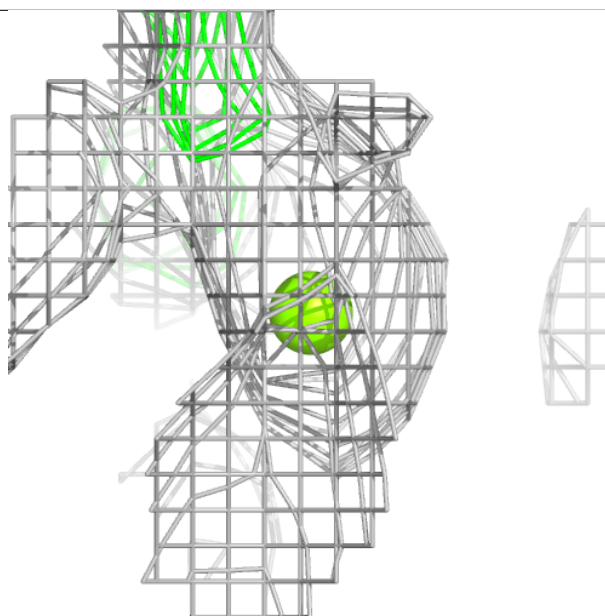
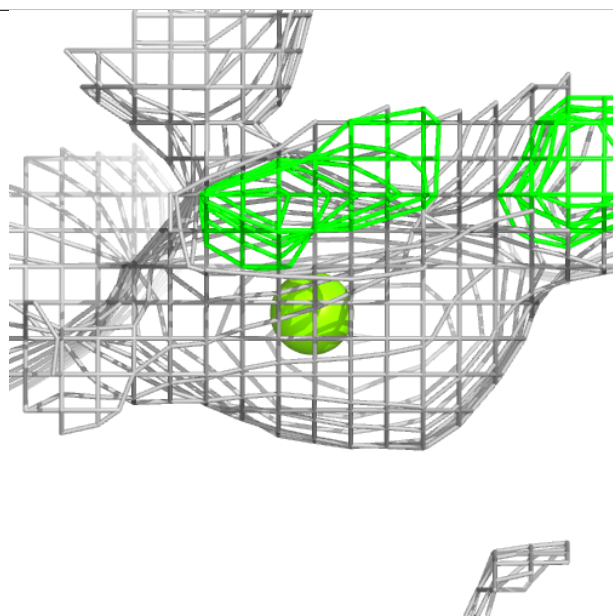
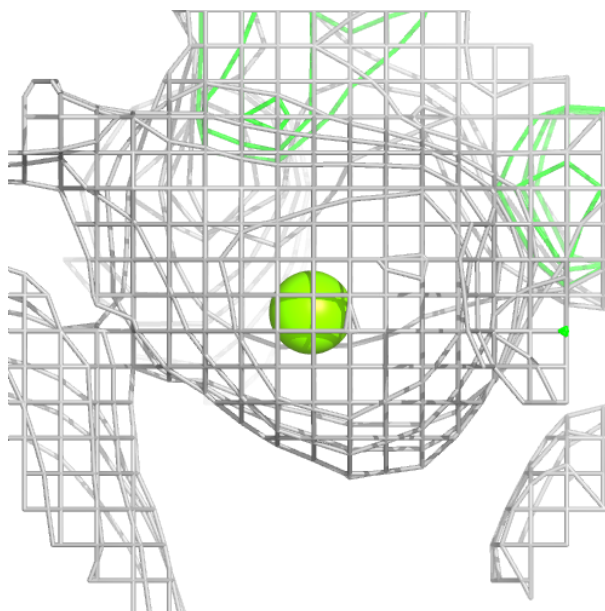
Electron density around MG F 302:

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



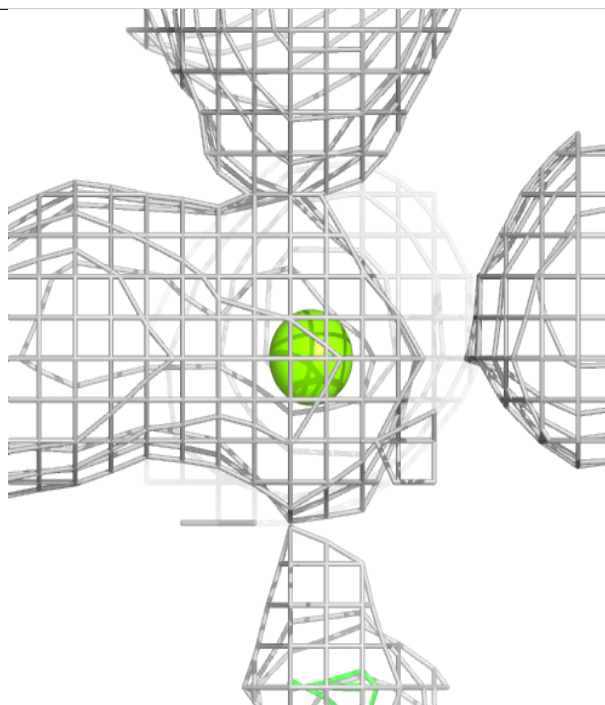
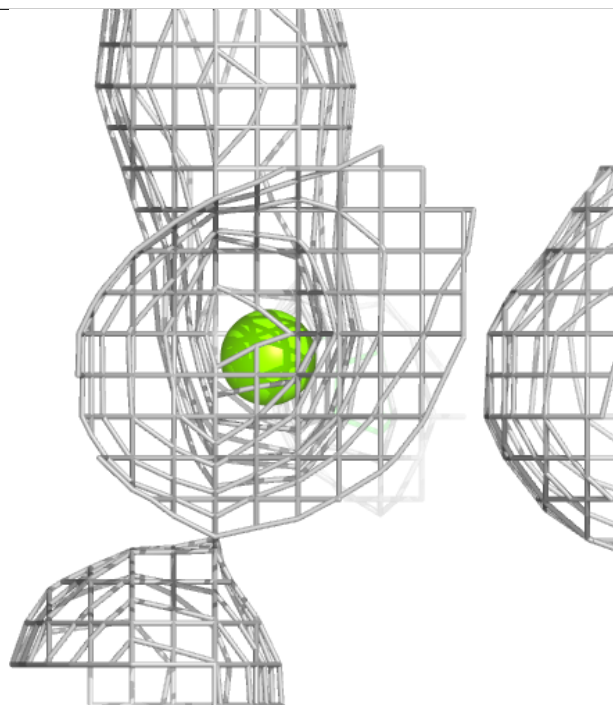
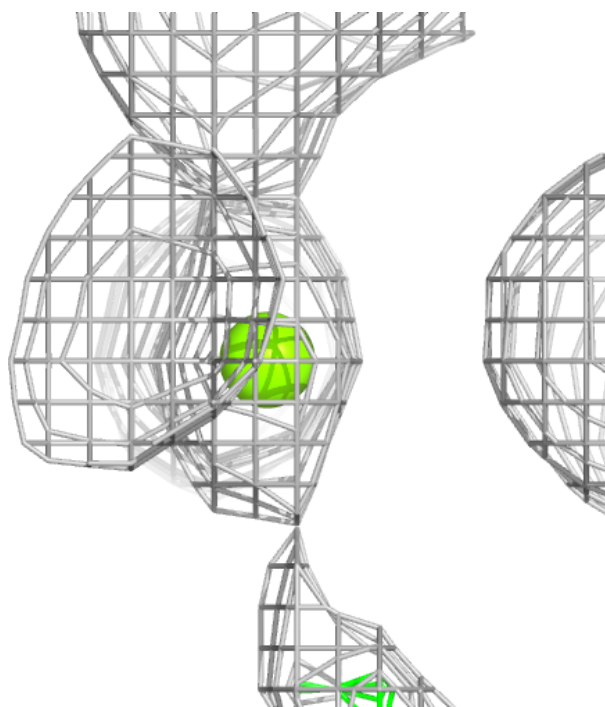
Electron density around MG B 302:

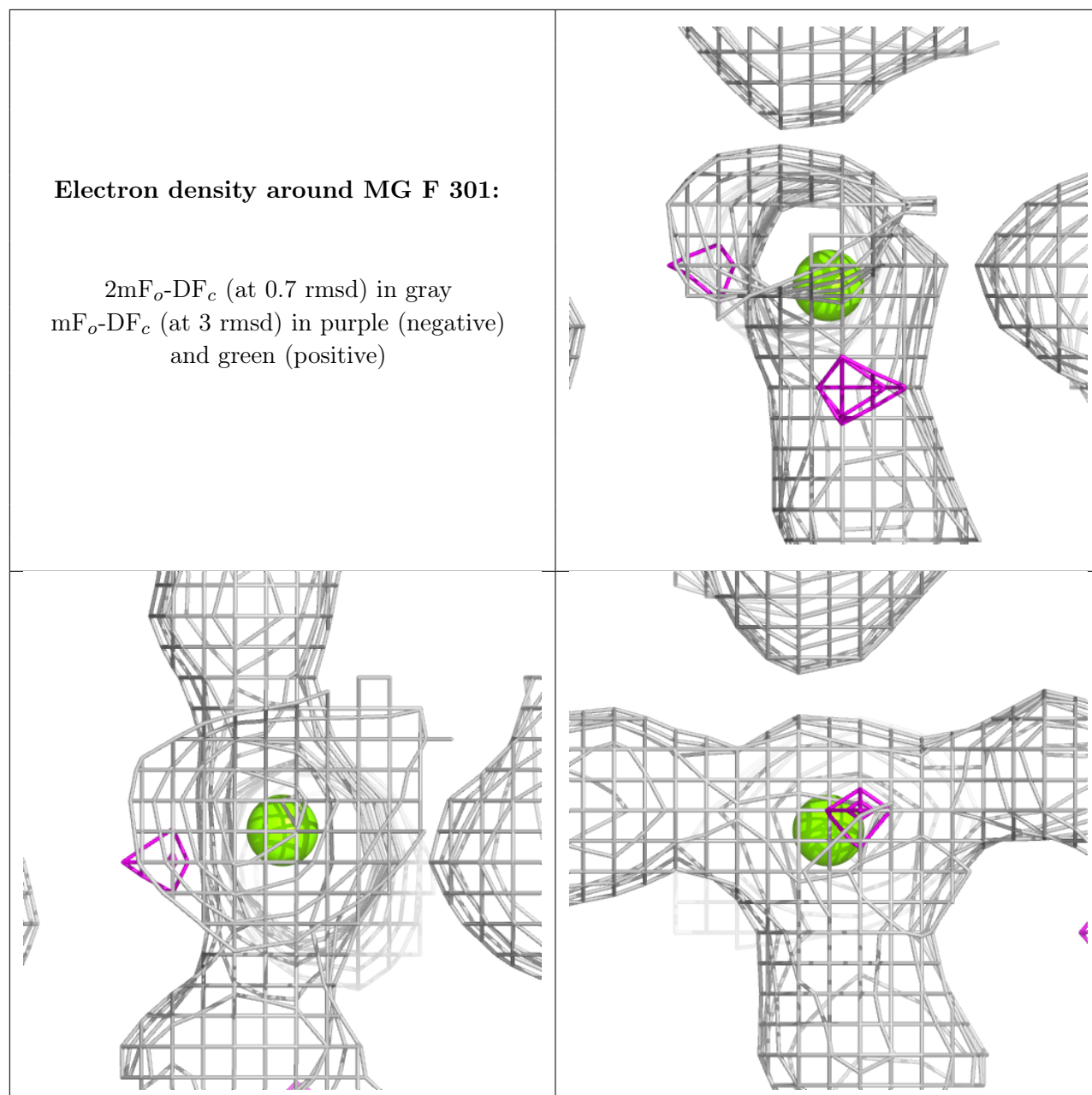
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG H 301:

$2mF_o-DF_c$ (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.