



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 08:00 PM UTC

PDB ID : 5OLK / pdb_00005olk
Title : Crystal structure of the ATP-cone-containing NrdB from *Leeuwenhoekiella blandensis*
Authors : Hasan, M.; Grinberg, A.R.; Sjoberg, B.M.; Logan, D.T.
Deposited on : 2017-07-28
Resolution : 2.45 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

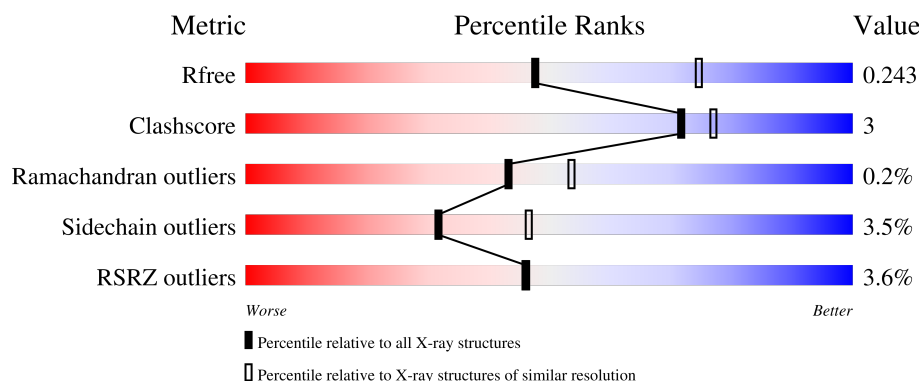
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

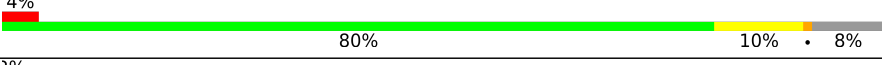
The reported resolution of this entry is 2.45 Å.

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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	430	
1	B	430	
1	C	430	
1	D	430	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13380 atoms, of which 48 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.

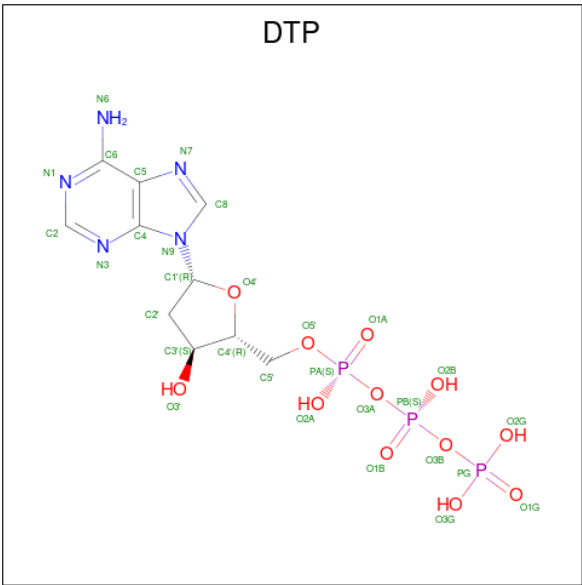
- Molecule 1 is a protein called Ribonucleoside-diphosphate reductase, beta subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			3240	2081	533	616	10			
1	B	392	Total	C	N	O	S	0	0	0
			3218	2065	531	612	10			
1	C	394	Total	C	N	O	S	0	0	0
			3235	2076	533	616	10			
1	D	393	Total	C	N	O	S	0	0	0
			3226	2071	532	613	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP A3XHF9
A	-1	SER	-	expression tag	UNP A3XHF9
A	0	HIS	-	expression tag	UNP A3XHF9
B	-2	GLY	-	expression tag	UNP A3XHF9
B	-1	SER	-	expression tag	UNP A3XHF9
B	0	HIS	-	expression tag	UNP A3XHF9
C	-2	GLY	-	expression tag	UNP A3XHF9
C	-1	SER	-	expression tag	UNP A3XHF9
C	0	HIS	-	expression tag	UNP A3XHF9
D	-2	GLY	-	expression tag	UNP A3XHF9
D	-1	SER	-	expression tag	UNP A3XHF9
D	0	HIS	-	expression tag	UNP A3XHF9

- Molecule 2 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: $C_{10}H_{16}N_5O_{12}P_3$) (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	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	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	D	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
2	D	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

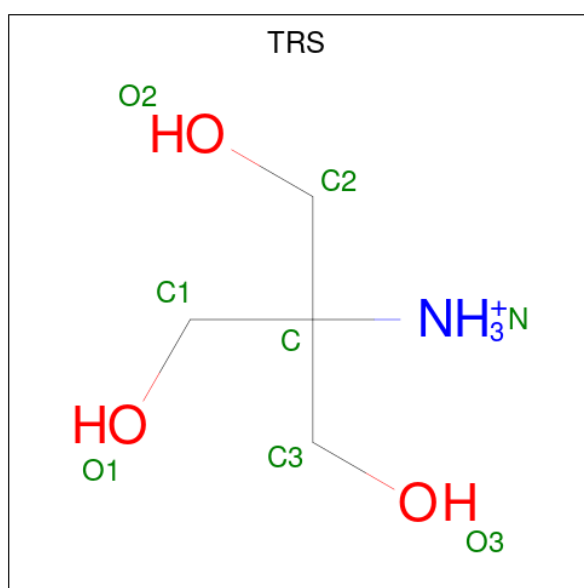
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

- 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	2	Total	Mn	0	0
			2	2		
4	B	2	Total	Mn	0	0
			2	2		
4	C	2	Total	Mn	0	0
			2	2		
4	D	2	Total	Mn	0	0
			2	2		

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0	0
			20	4	12	1	3		
5	B	1	Total	C	H	N	O	0	0
			20	4	12	1	3		
5	C	1	Total	C	H	N	O	0	0
			20	4	12	1	3		
5	D	1	Total	C	H	N	O	0	0
			20	4	12	1	3		

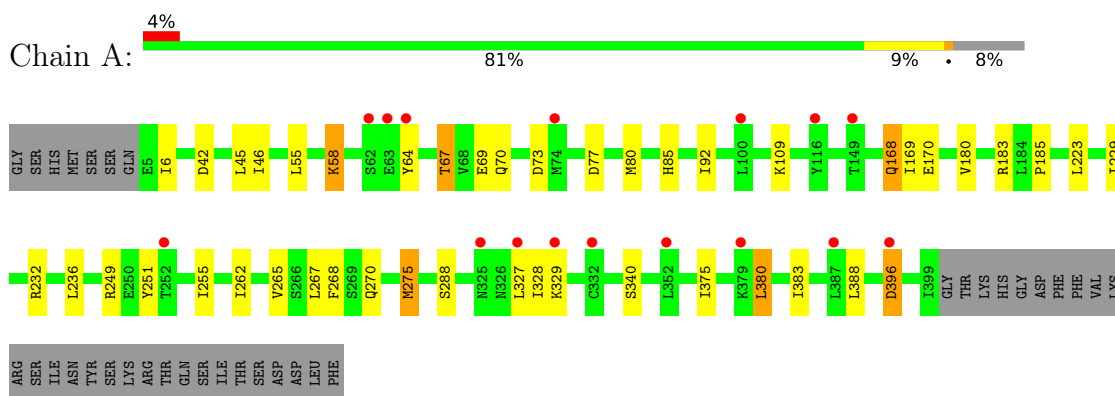
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	33	Total 33	O 33	0	0
6	B	31	Total 31	O 31	0	0
6	C	33	Total 33	O 33	0	0
6	D	32	Total 32	O 32	0	0

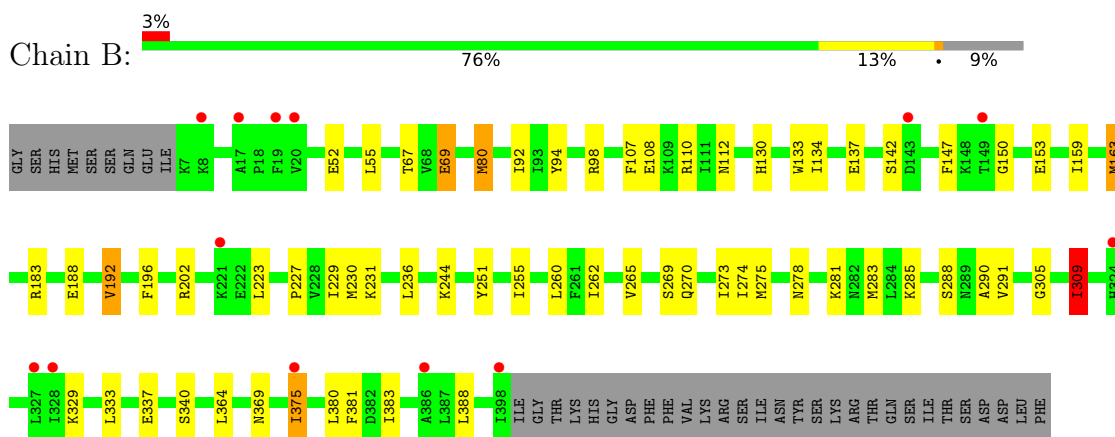
3 Residue-property plots [i](#)

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

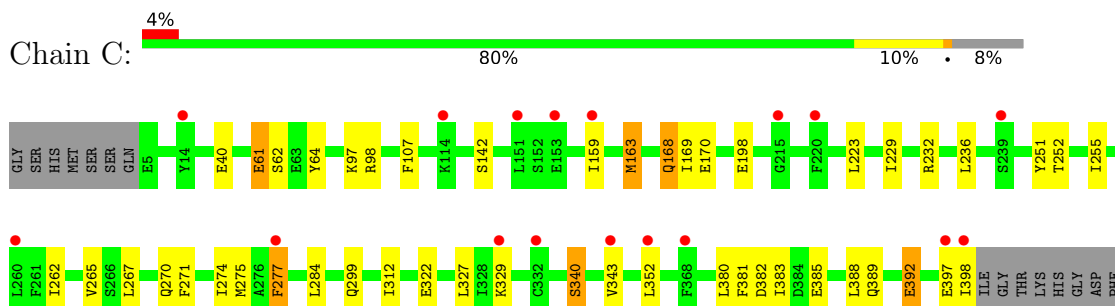
- Molecule 1: Ribonucleoside-diphosphate reductase, beta subunit 1



- Molecule 1: Ribonucleoside-diphosphate reductase, beta subunit 1

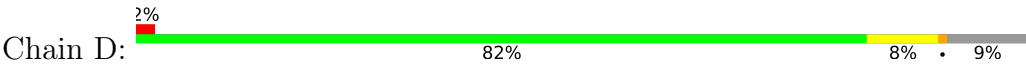


- Molecule 1: Ribonucleoside-diphosphate reductase, beta subunit 1



PHE
VAL
LYS
ARG
SER
ILE
ASN
TYR
SER
LYS
ARG
THR
GLN
SER
ILE
THR
SER
ASP
ASP
LEU
PHE

● Molecule 1: Ribonucleoside-diphosphate reductase, beta subunit 1



GLY
SER
HIS
MET
SER
SER
GLN
GLU
I6
T16
S63
K58
Y64
T67
V66
E69
M74
M80
S81
F84
V87
A88
I92
I111
A126
W133
E153
M163
Q168
I169
E170
E198
R202
L223
I229
R232
L236

Y251
I255
I262
V265
S266
L267
F268
S269
Q270
F271
I274
M275
K281
H324
I328
K329
C332
K341
K349
I383
L388
E397
I398
ILE
GLY
THR
LYS
HIS
GLY
ASP
PHE
PHE
VAL
LYS
ARG
SER
ILE
ASN
TYR
SER
LYS
ARG
THR
GLN
SER
ILE
THR

SER
ASP
ASP
LEU
PHE

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	74.00Å 90.54Å 90.95Å 110.78° 98.99° 114.11°	Depositor
Resolution (Å)	44.70 – 2.45 44.70 – 2.45	Depositor EDS
% Data completeness (in resolution range)	97.8 (44.70-2.45) 97.8 (44.70-2.45)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.45Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.205 , 0.238 0.212 , 0.243	Depositor DCC
R_{free} test set	3353 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	52.6	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13380	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.57% 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: MN, MG, DTP, TRS

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.87	0/3308	1.44	8/4460 (0.2%)
1	B	0.88	4/3286 (0.1%)	1.45	12/4430 (0.3%)
1	C	0.83	1/3303 (0.0%)	1.45	11/4453 (0.2%)
1	D	0.89	2/3294 (0.1%)	1.44	8/4441 (0.2%)
All	All	0.87	7/13191 (0.1%)	1.44	39/17784 (0.2%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	163	MET	SD-CE	-9.10	1.56	1.79
1	D	80	MET	SD-CE	-8.13	1.59	1.79
1	B	80	MET	SD-CE	-7.13	1.61	1.79
1	B	309	ILE	CG1-CD1	-6.38	1.26	1.51
1	B	163	MET	SD-CE	-6.23	1.64	1.79

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	381	PHE	CA-C-N	7.15	132.64	121.99
1	C	381	PHE	C-N-CA	7.15	132.64	121.99
1	C	322	GLU	CB-CG-CD	6.39	123.46	112.60
1	A	396	ASP	CA-CB-CG	5.98	118.58	112.60
1	B	285	LYS	CA-C-N	5.67	126.23	119.94

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	3240	0	3205	15	0
1	B	3218	0	3181	33	0
1	C	3235	0	3198	22	0
1	D	3226	0	3192	20	0
2	A	60	0	24	0	0
2	B	60	0	24	0	0
2	C	60	0	24	0	0
2	D	60	0	24	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	8	12	12	0	0
5	B	8	12	12	3	0
5	C	8	12	12	1	0
5	D	8	12	12	0	0
6	A	33	0	0	0	0
6	B	31	0	0	1	0
6	C	33	0	0	0	0
6	D	32	0	0	0	0
All	All	13332	48	12920	86	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.

The worst 5 of 86 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:107:PHE:O	5:B:1006:TRS:H21	1.63	0.97
1:D:53:SER:HB2	1:D:74:MET:HE1	1.53	0.91
1:D:84:PHE:HB3	1:D:87:VAL:HG13	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:PHE:O	5:B:1006:TRS:C2	2.31	0.78
1:D:271:PHE:O	1:D:275:MET:HG2	1.83	0.77

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	393/430 (91%)	385 (98%)	7 (2%)	1 (0%)	36	45
1	B	390/430 (91%)	383 (98%)	6 (2%)	1 (0%)	36	45
1	C	392/430 (91%)	380 (97%)	11 (3%)	1 (0%)	36	45
1	D	391/430 (91%)	382 (98%)	9 (2%)	0	100	100
All	All	1566/1720 (91%)	1530 (98%)	33 (2%)	3 (0%)	43	54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	58	LYS
1	C	62	SER
1	B	150	GLY

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	354/387 (92%)	338 (96%)	16 (4%)	24	37
1	B	352/387 (91%)	344 (98%)	8 (2%)	44	59
1	C	354/387 (92%)	341 (96%)	13 (4%)	30	44
1	D	353/387 (91%)	341 (97%)	12 (3%)	32	47
All	All	1413/1548 (91%)	1364 (96%)	49 (4%)	32	46

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	270	GLN
1	C	385	GLU
1	C	277	PHE
1	C	340	SER
1	D	16	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	366	ASN
1	D	135	HIS
1	C	49	GLN
1	D	30	ASN
1	C	30	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 24 ligands modelled in this entry, 12 are monoatomic - leaving 12 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	B	1001	3	31,32,32	1.56	6 (19%)	46,50,50	0.93	1 (2%)
5	TRS	A	1006	-	7,7,7	0.33	0	9,9,9	0.34	0
2	DTP	D	1001	3	31,32,32	1.65	7 (22%)	46,50,50	0.81	0
5	TRS	B	1006	-	7,7,7	0.29	0	9,9,9	0.38	0
2	DTP	A	1001	3	31,32,32	1.56	6 (19%)	46,50,50	0.80	1 (2%)
2	DTP	C	1001	3	31,32,32	1.96	8 (25%)	46,50,50	0.83	0
2	DTP	C	1002	3	31,32,32	1.89	8 (25%)	46,50,50	0.91	1 (2%)
5	TRS	D	1006	-	7,7,7	0.28	0	9,9,9	0.35	0
2	DTP	A	1002	3	31,32,32	1.92	8 (25%)	46,50,50	0.94	2 (4%)
2	DTP	D	1002	3	31,32,32	1.80	8 (25%)	46,50,50	0.94	2 (4%)
2	DTP	B	1002	3	31,32,32	1.85	9 (29%)	46,50,50	0.79	0
5	TRS	C	1006	-	7,7,7	0.32	0	9,9,9	0.30	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	B	1001	3	-	3/22/34/34	0/3/3/3
5	TRS	A	1006	-	-	4/9/9/9	-
2	DTP	D	1001	3	-	3/22/34/34	0/3/3/3
5	TRS	B	1006	-	-	5/9/9/9	-
2	DTP	A	1001	3	-	3/22/34/34	0/3/3/3
2	DTP	C	1001	3	-	3/22/34/34	0/3/3/3
2	DTP	C	1002	3	-	5/22/34/34	0/3/3/3
5	TRS	D	1006	-	-	3/9/9/9	-
2	DTP	A	1002	3	-	4/22/34/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DTP	D	1002	3	-	4/22/34/34	0/3/3/3
2	DTP	B	1002	3	-	3/22/34/34	0/3/3/3
5	TRS	C	1006	-	-	4/9/9/9	-

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1001	DTP	PB-O3B	-5.29	1.53	1.59
2	C	1001	DTP	C8-N9	4.53	1.45	1.37
2	D	1001	DTP	PB-O3B	-4.24	1.54	1.59
2	B	1002	DTP	PB-O3B	-3.84	1.55	1.59
2	C	1002	DTP	PB-O3B	-3.75	1.55	1.59

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1002	DTP	O3G-PG-O3B	3.32	115.76	104.64
2	A	1002	DTP	O2A-PA-O3A	2.86	115.01	107.27
2	B	1001	DTP	O2B-PB-O3B	2.61	114.32	107.27
2	A	1002	DTP	O2B-PB-O3A	2.35	113.61	107.27
2	C	1002	DTP	O2A-PA-O3A	2.34	113.60	107.27

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1006	TRS	C2-C-C1-O1
5	B	1006	TRS	C3-C-C1-O1
5	B	1006	TRS	N-C-C1-O1
5	D	1006	TRS	C2-C-C1-O1
2	C	1001	DTP	PB-O3B-PG-O1G

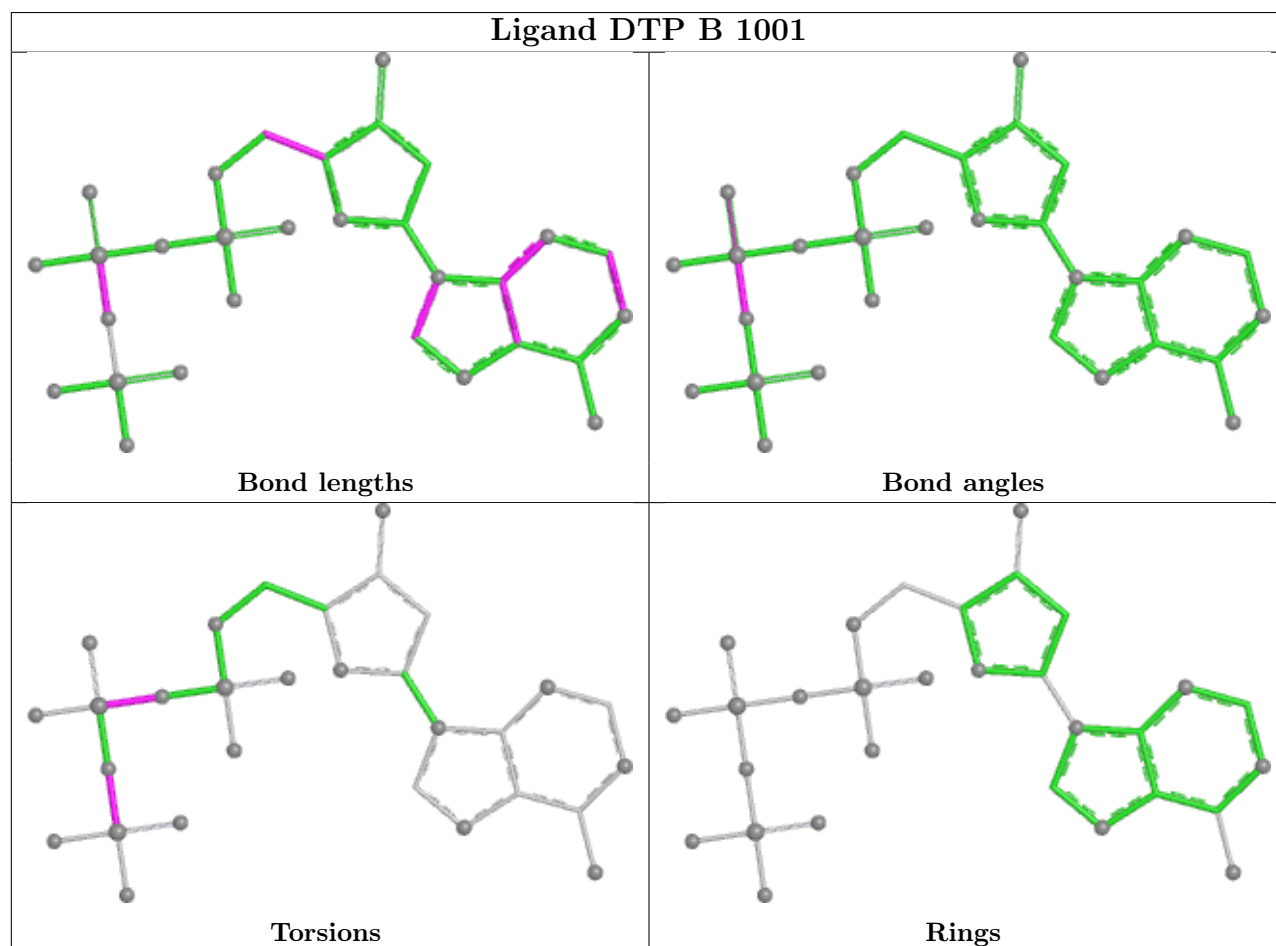
There are no ring outliers.

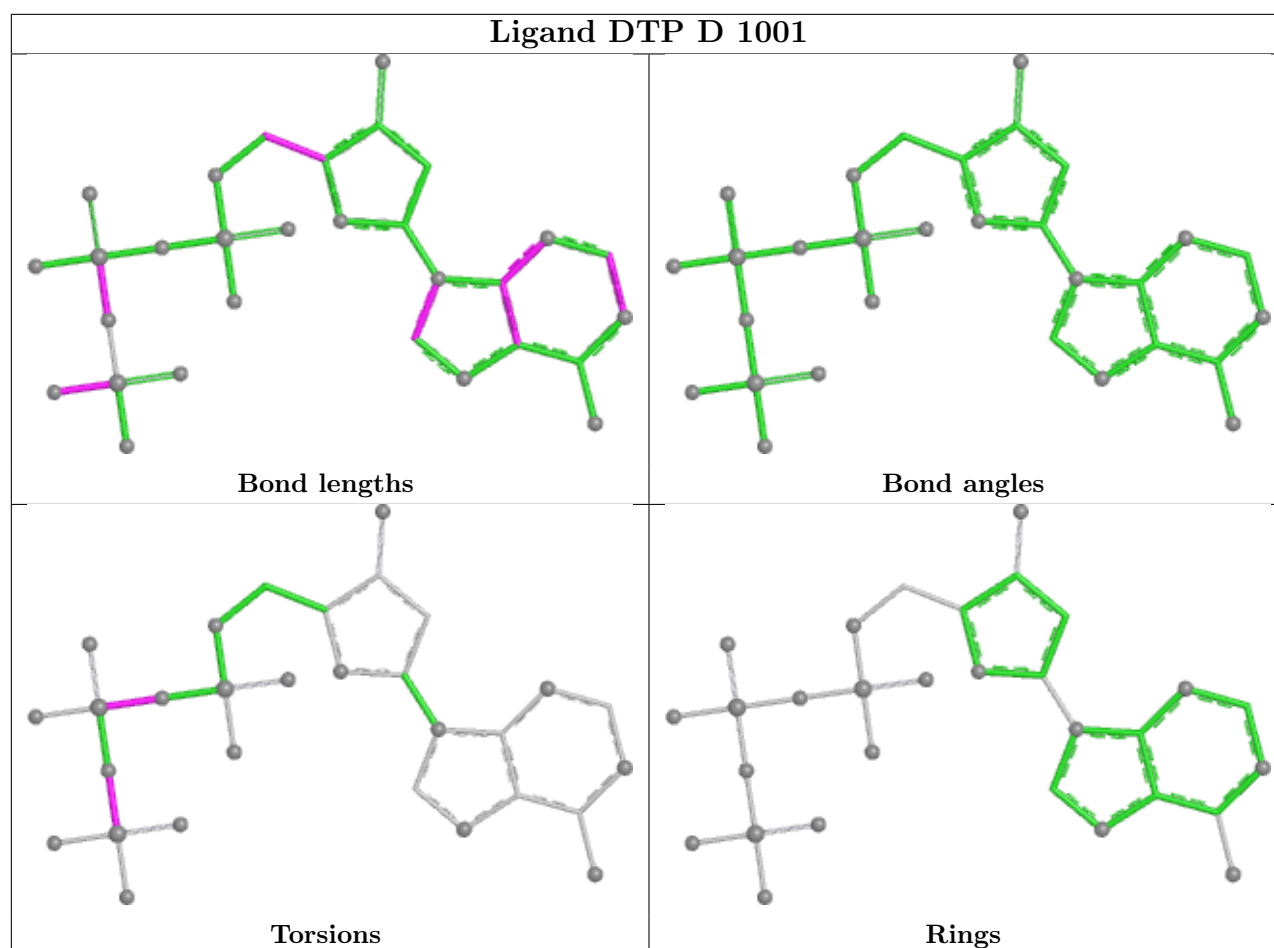
2 monomers are involved in 4 short contacts:

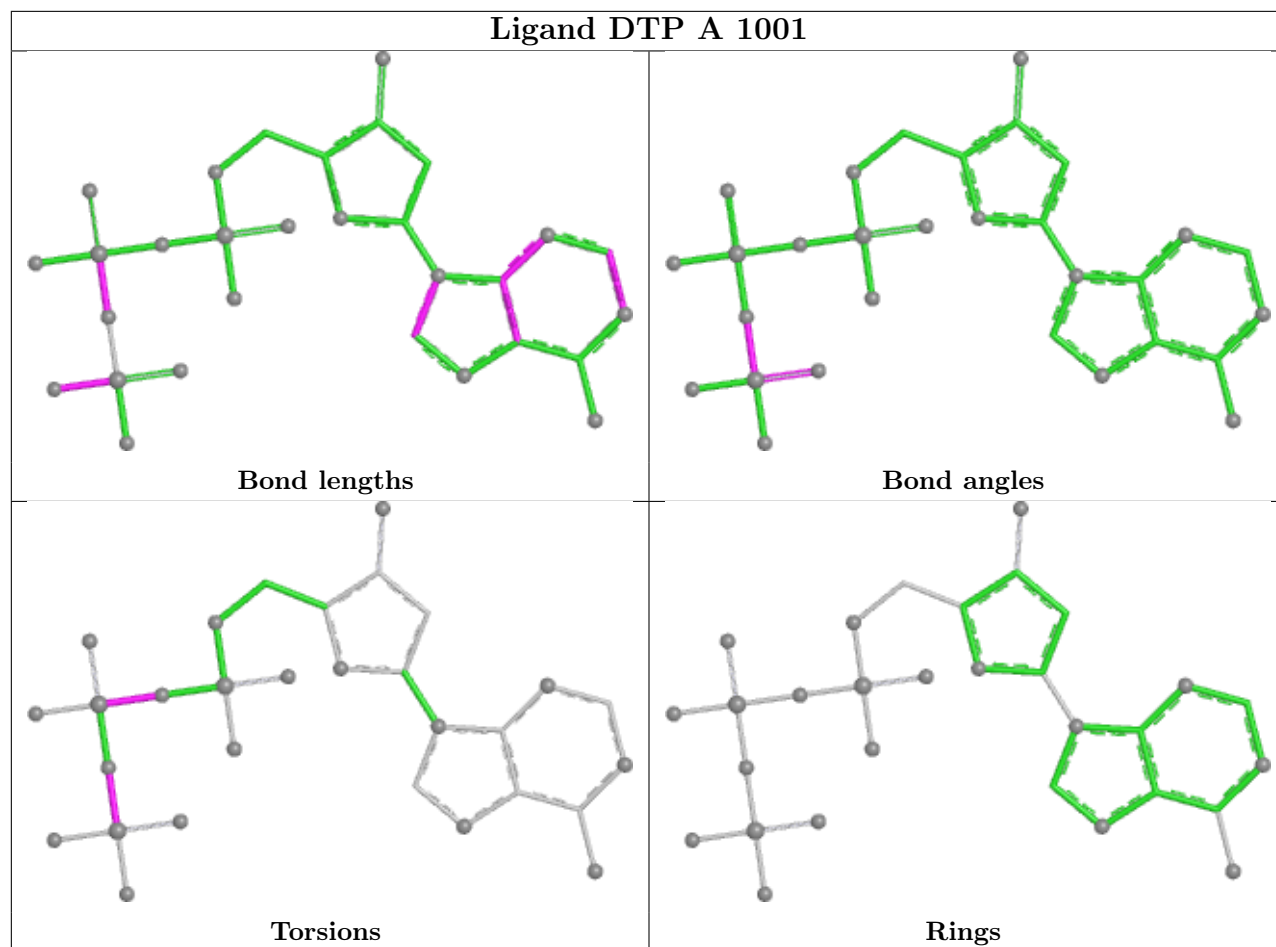
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1006	TRS	3	0
5	C	1006	TRS	1	0

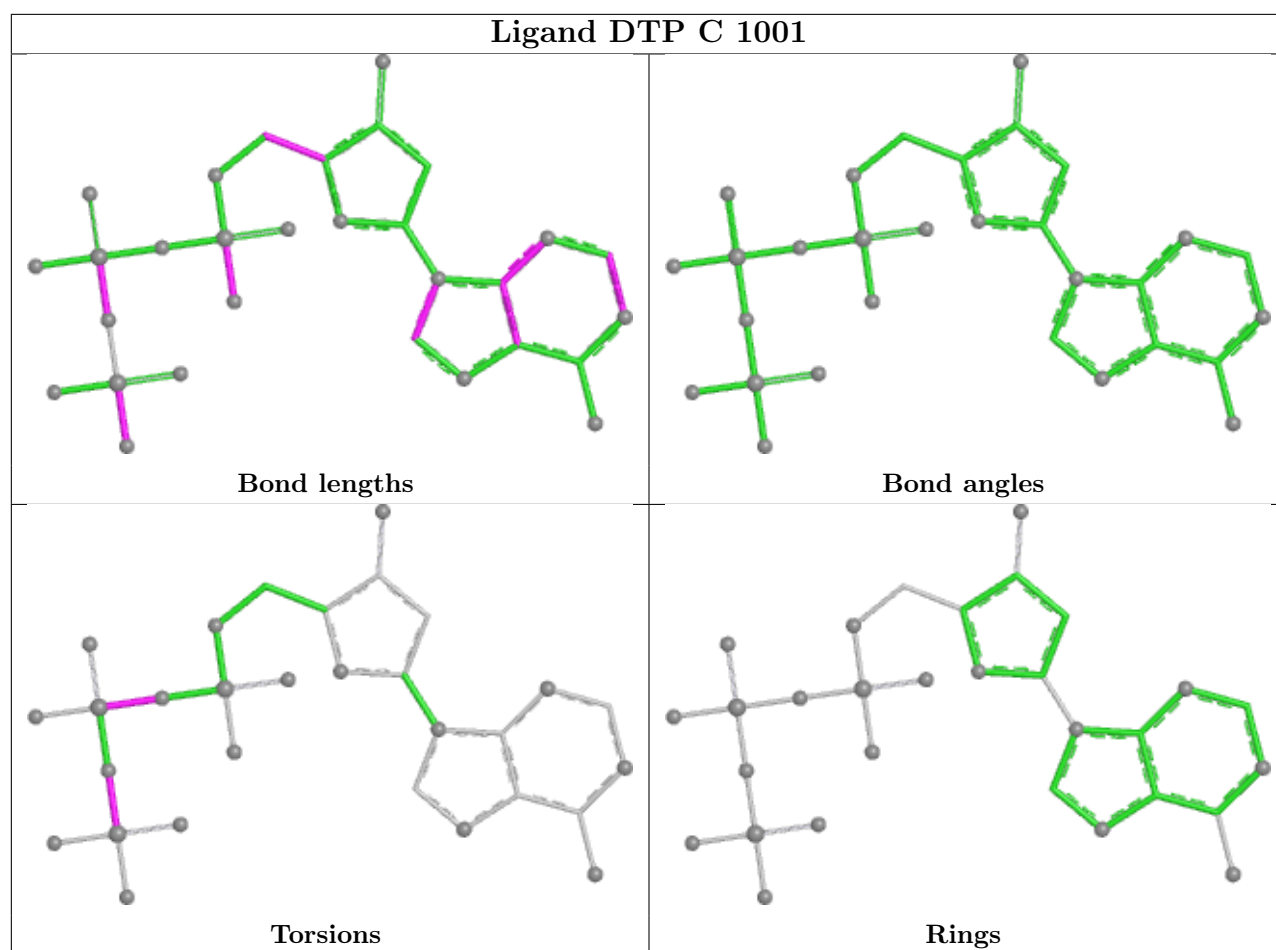
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

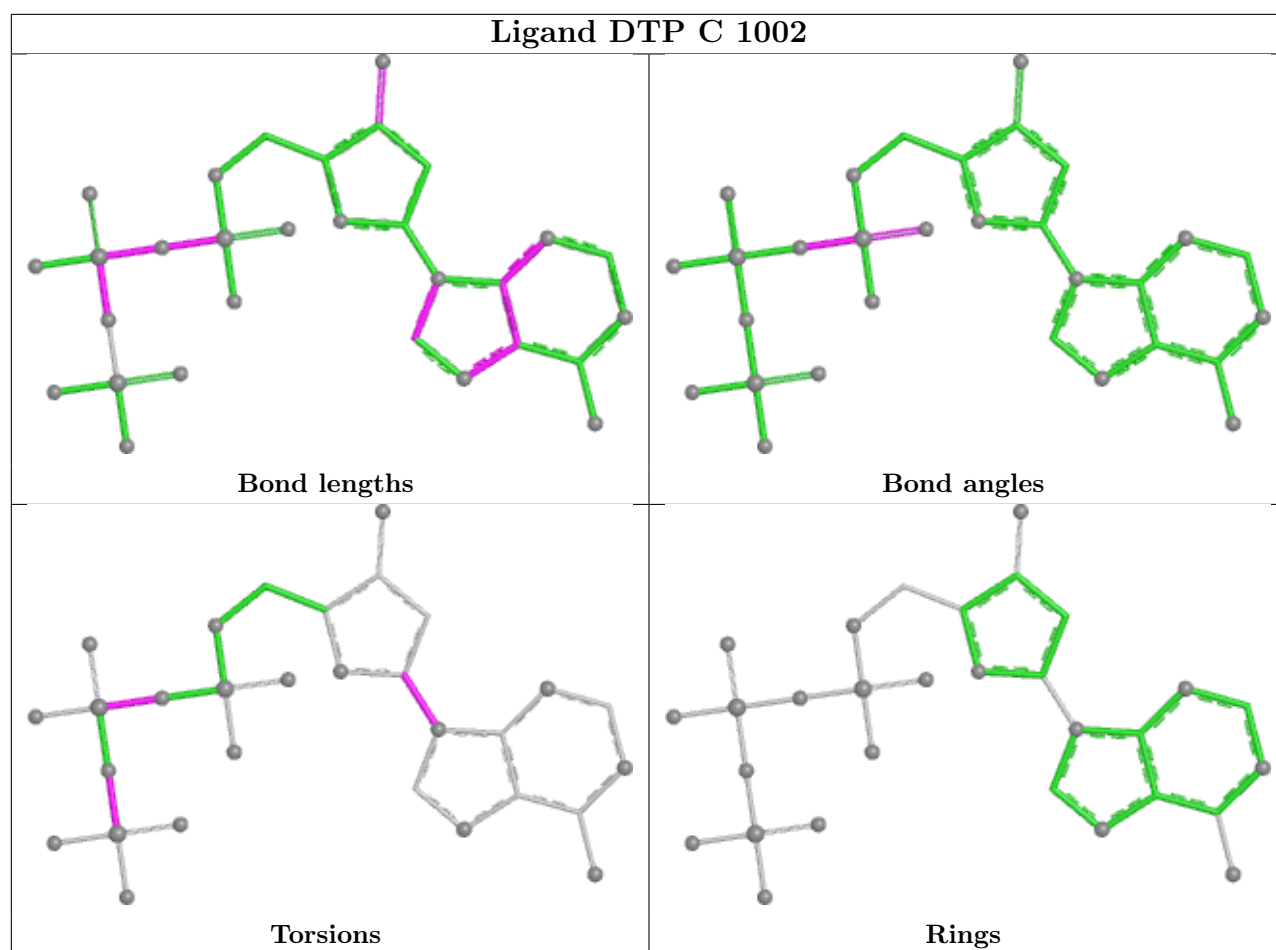
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.

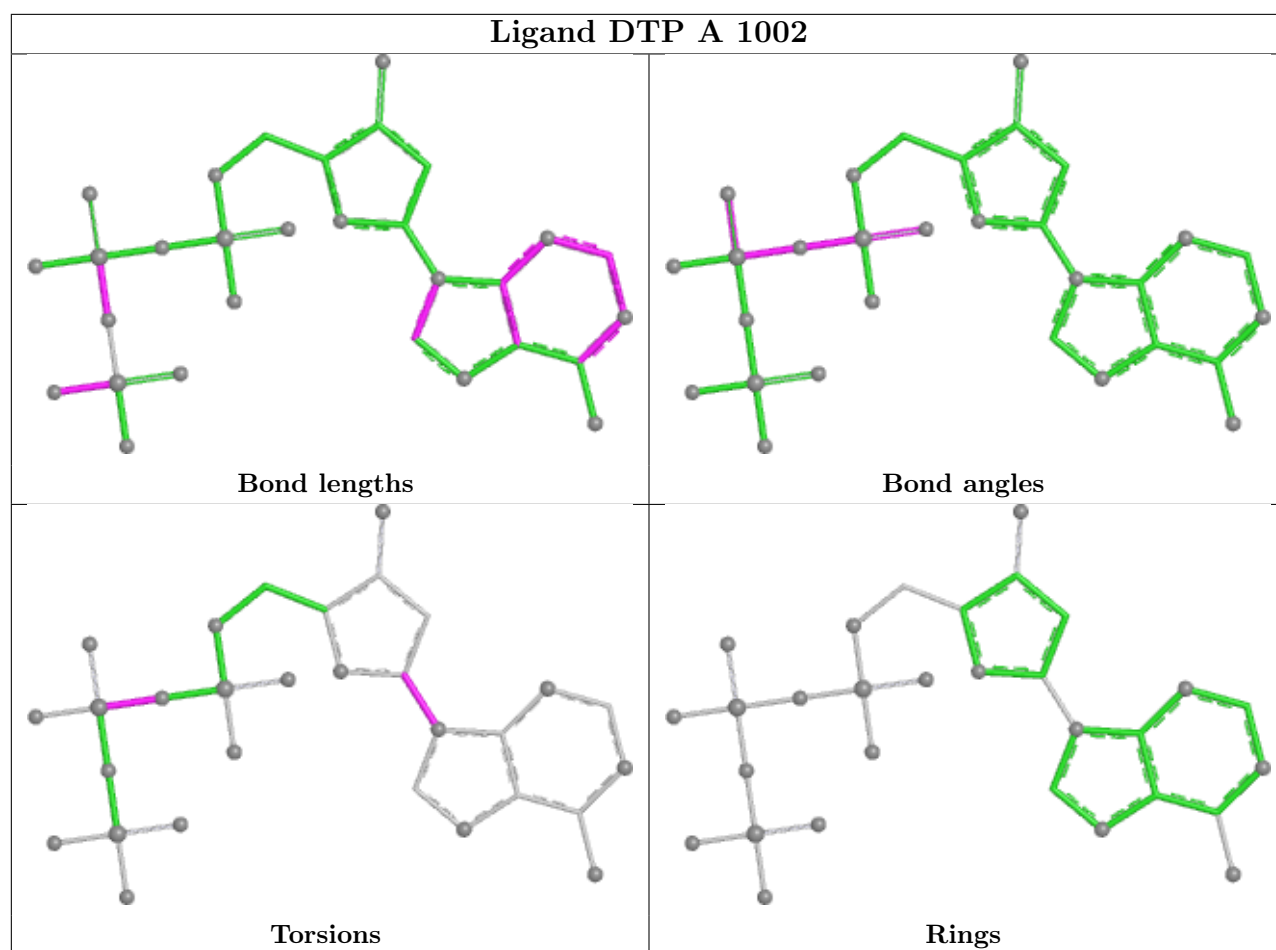


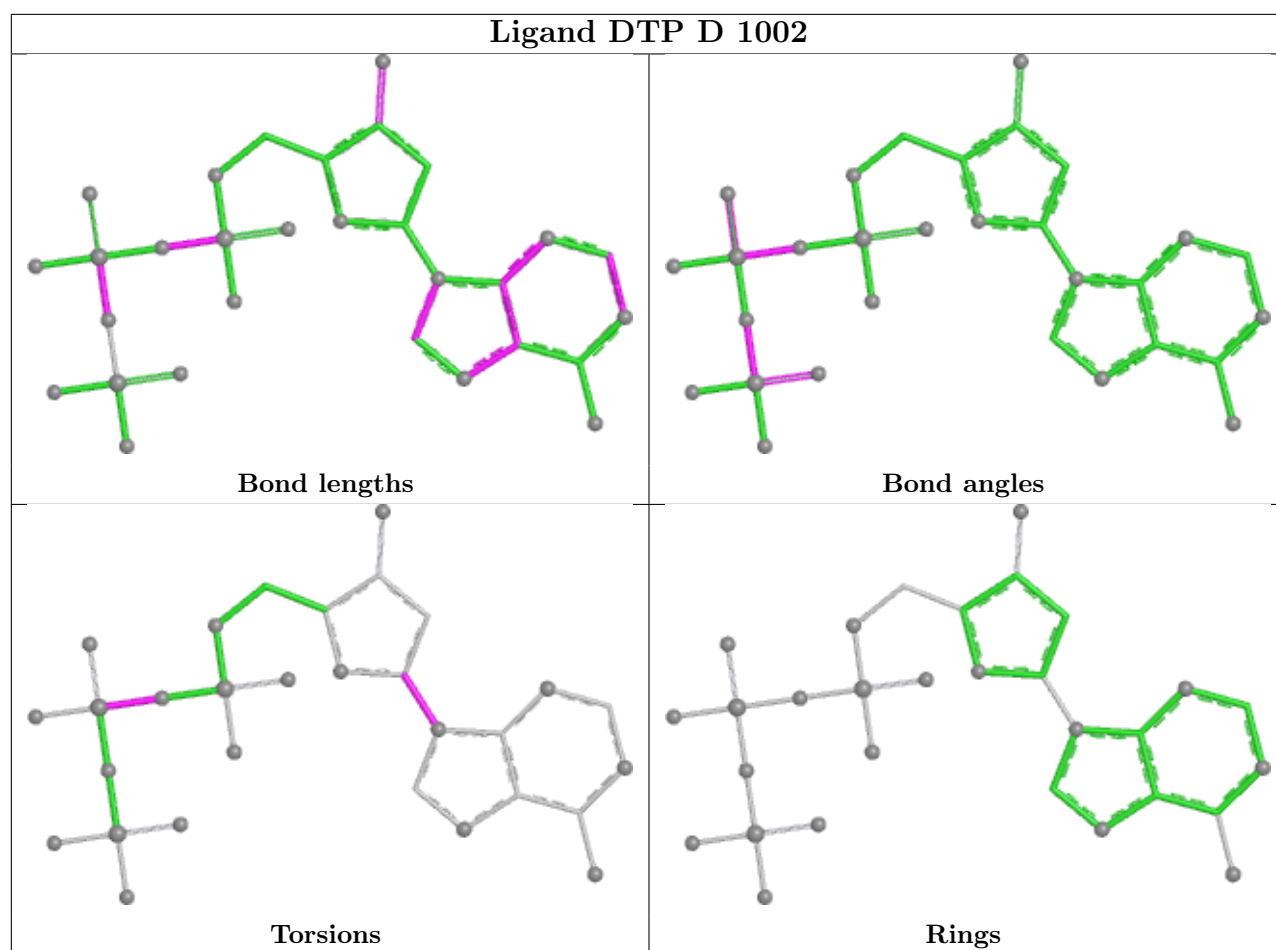


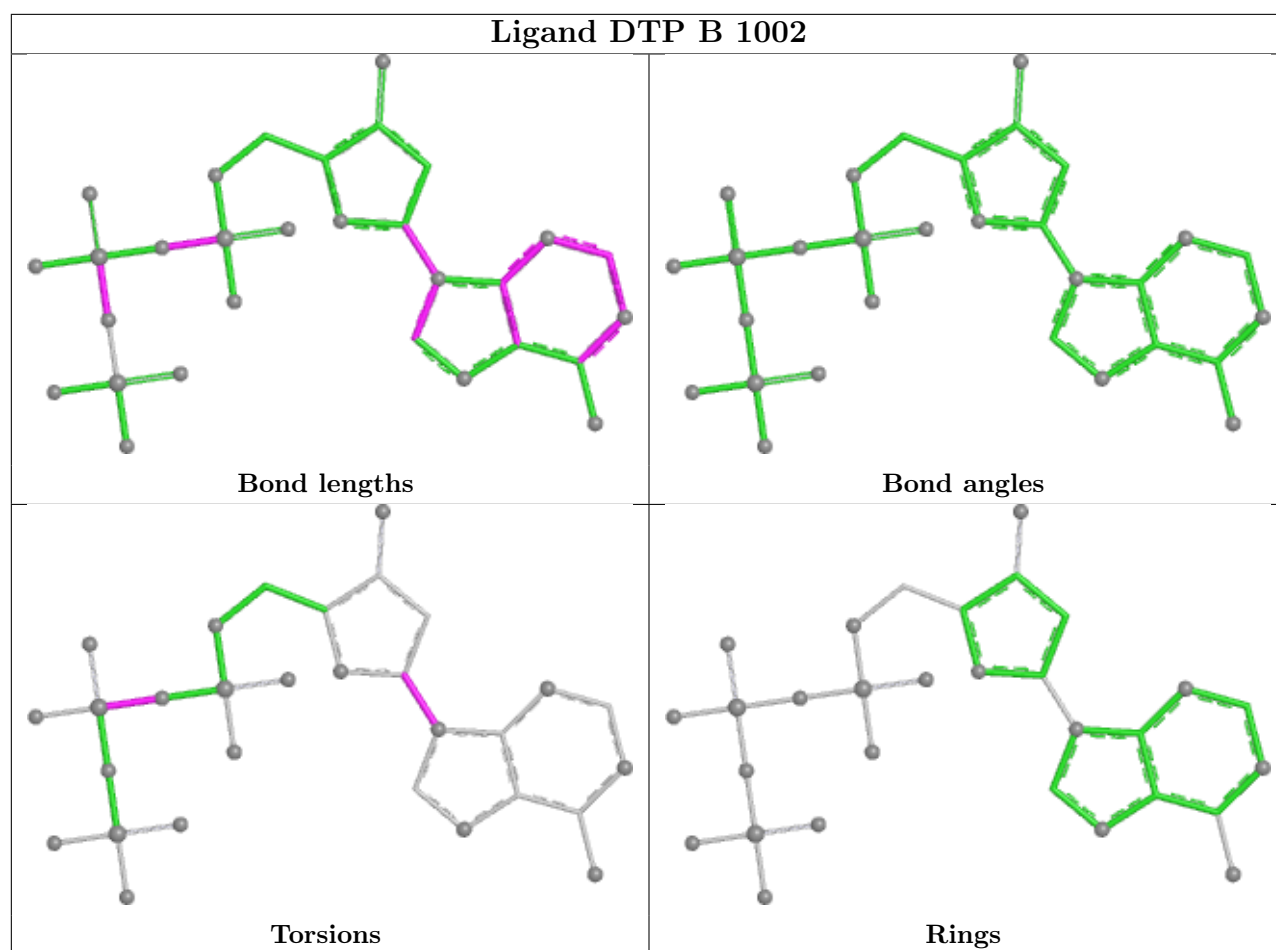












5.7 Other polymers [i](#)

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	395/430 (91%)	0.47	16 (4%) 41 41	40, 61, 87, 118	0
1	B	392/430 (91%)	0.48	13 (3%) 49 50	40, 65, 98, 115	0
1	C	394/430 (91%)	0.55	17 (4%) 40 39	40, 66, 95, 114	0
1	D	393/430 (91%)	0.45	10 (2%) 58 61	40, 63, 90, 127	0
All	All	1574/1720 (91%)	0.49	56 (3%) 46 46	40, 64, 93, 127	0

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	398	ILE	3.4
1	C	220	PHE	3.3
1	D	324	HIS	3.1
1	B	328	ILE	3.1
1	C	397	GLU	3.0

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](#)

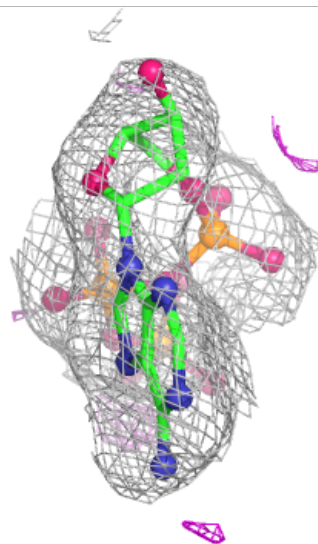
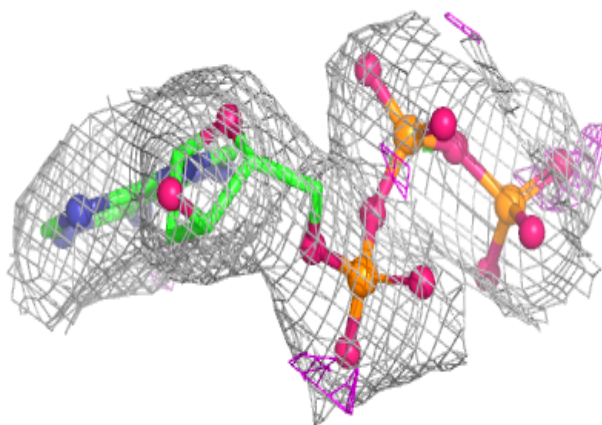
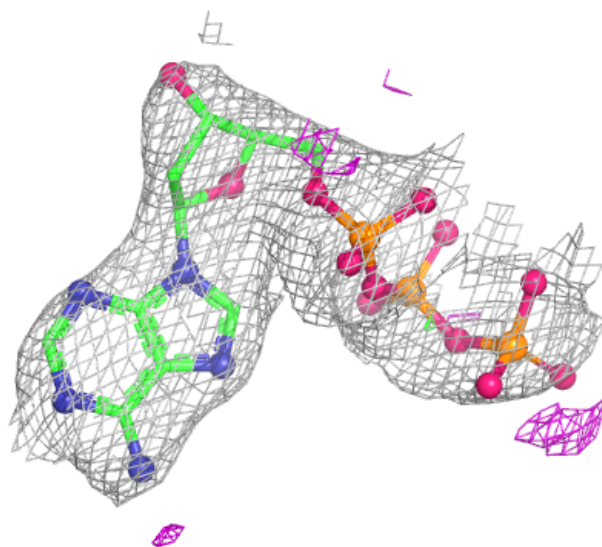
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	TRS	D	1006	8/8	0.75	0.13	88,92,94,94	0
5	TRS	B	1006	8/8	0.76	0.13	67,74,77,77	0
5	TRS	A	1006	8/8	0.77	0.16	66,79,83,83	0
5	TRS	C	1006	8/8	0.86	0.11	56,64,71,71	0
2	DTP	D	1001	30/30	0.87	0.12	77,83,115,116	0
2	DTP	B	1001	30/30	0.88	0.10	80,88,108,109	0
2	DTP	D	1002	30/30	0.91	0.09	53,62,95,97	0
2	DTP	A	1002	30/30	0.94	0.08	52,59,84,85	0
2	DTP	B	1002	30/30	0.94	0.08	61,66,81,85	0
2	DTP	A	1001	30/30	0.96	0.07	46,50,86,88	0
2	DTP	C	1001	30/30	0.96	0.07	34,48,81,85	0
2	DTP	C	1002	30/30	0.96	0.07	40,49,61,65	0
4	MN	A	1004	1/1	0.99	0.03	71,71,71,71	0
4	MN	B	1004	1/1	0.99	0.03	63,63,63,63	0
4	MN	C	1004	1/1	0.99	0.03	69,69,69,69	0
4	MN	C	1005	1/1	0.99	0.03	76,76,76,76	0
4	MN	D	1004	1/1	0.99	0.03	66,66,66,66	0
4	MN	D	1005	1/1	0.99	0.02	71,71,71,71	0
3	MG	A	1003	1/1	0.99	0.06	48,48,48,48	0
3	MG	B	1003	1/1	0.99	0.07	62,62,62,62	0
3	MG	C	1003	1/1	0.99	0.03	28,28,28,28	0
3	MG	D	1003	1/1	0.99	0.07	52,52,52,52	0
4	MN	A	1005	1/1	1.00	0.02	54,54,54,54	0
4	MN	B	1005	1/1	1.00	0.02	67,67,67,67	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.

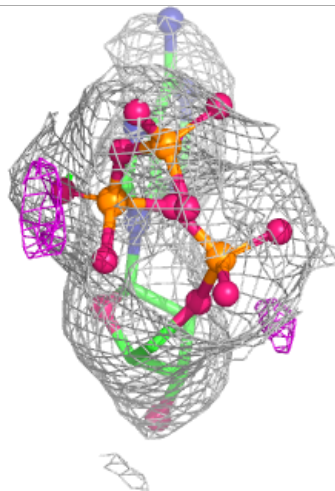
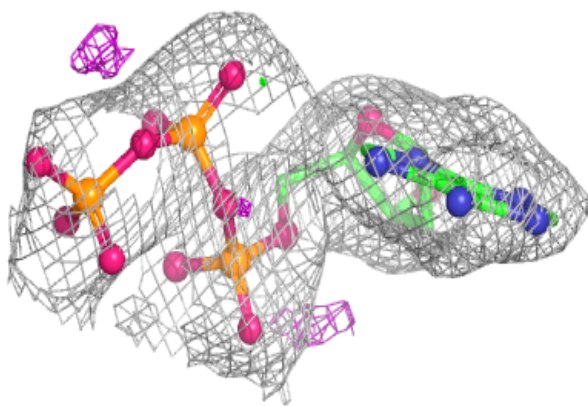
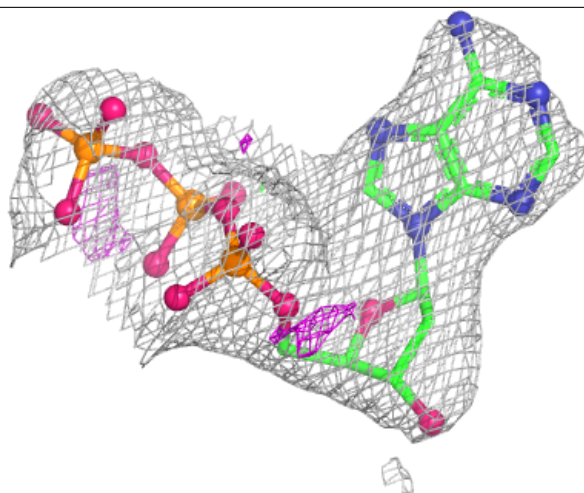
Electron density around DTP D 1001:

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



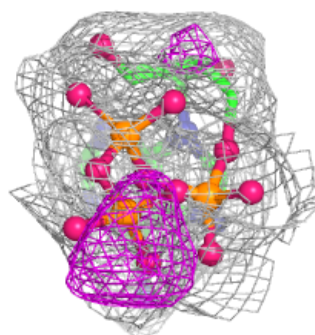
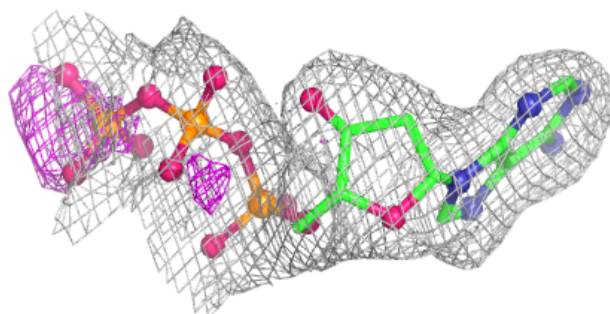
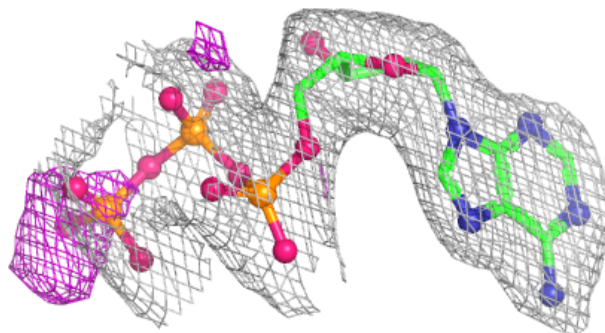
Electron density around DTP B 1001:

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

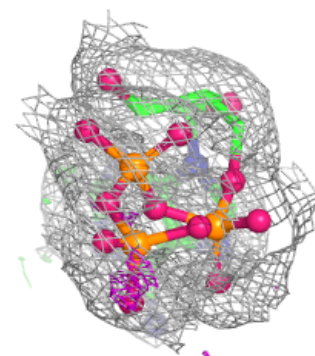
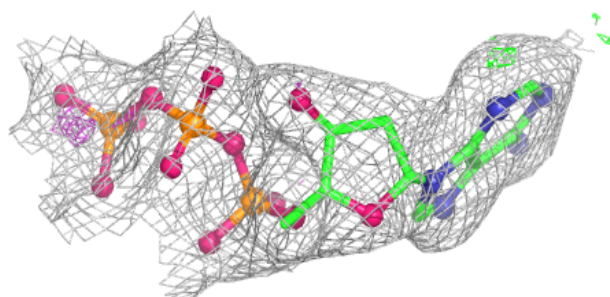
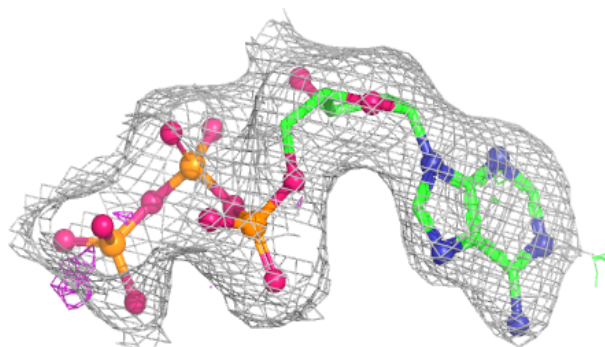


Electron density around DTP D 1002:

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

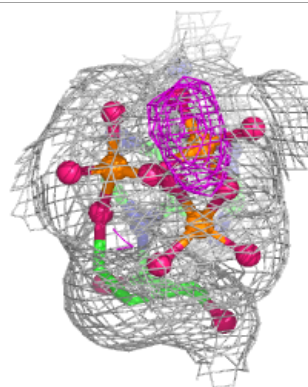
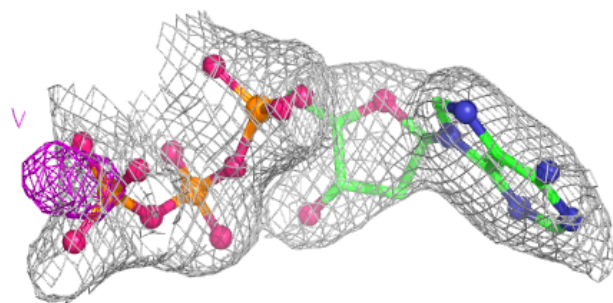
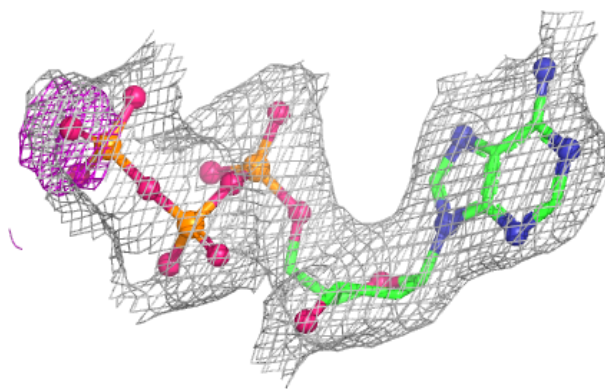
**Electron density around DTP A 1002:**

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



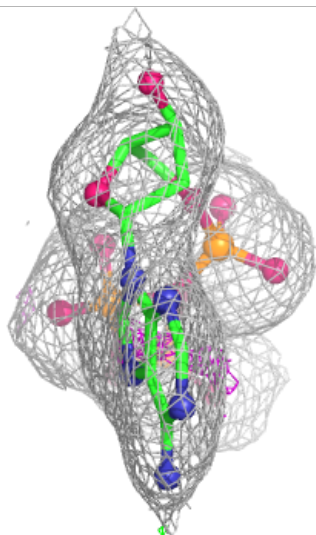
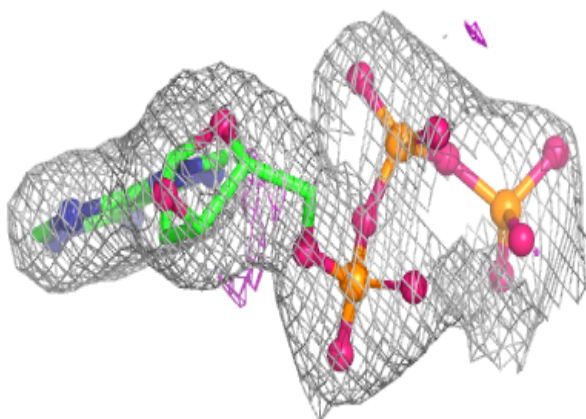
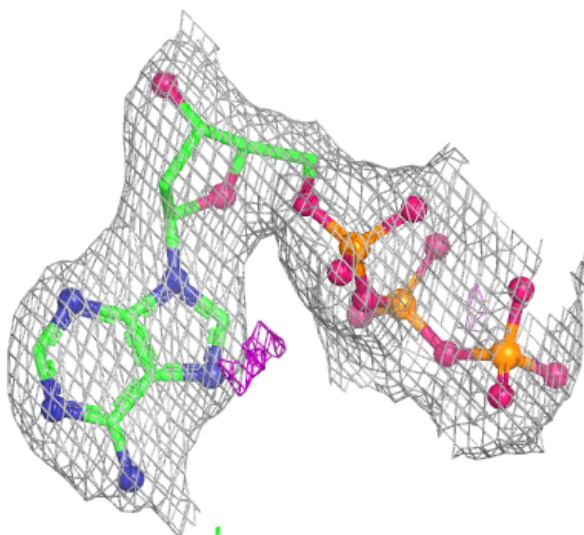
Electron density around DTP B 1002:

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



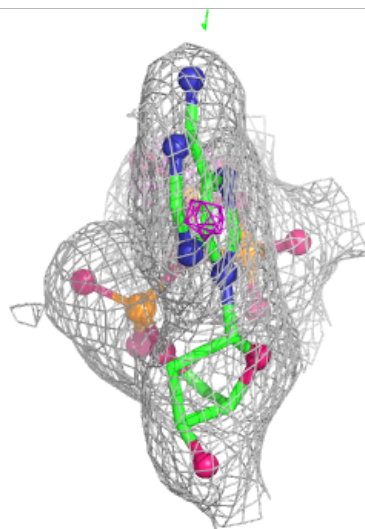
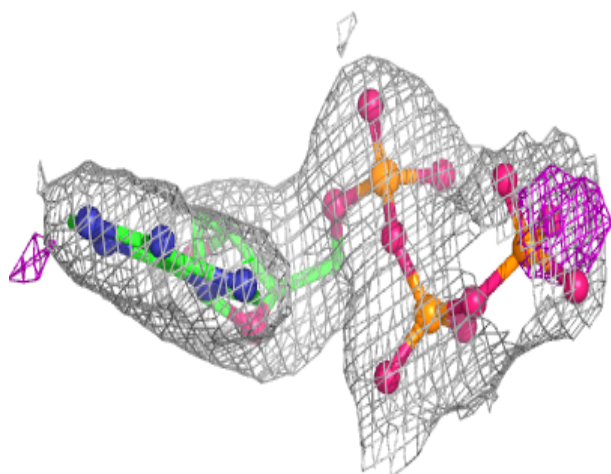
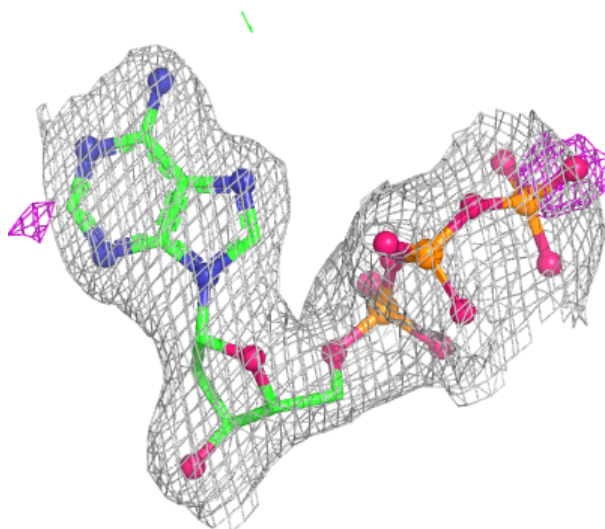
Electron density around DTP A 1001:

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



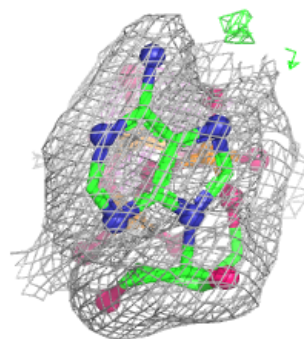
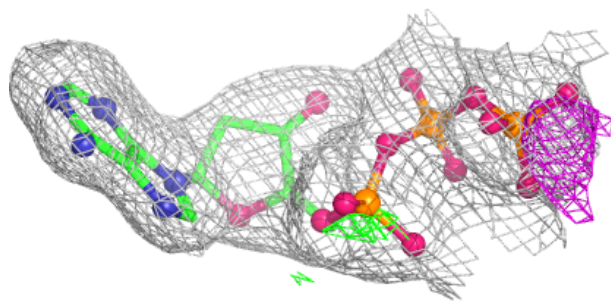
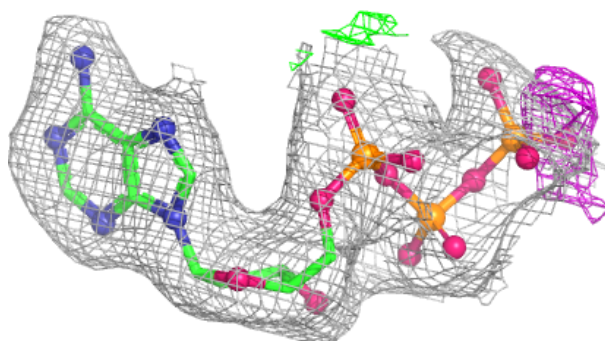
Electron density around DTP C 1001:

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



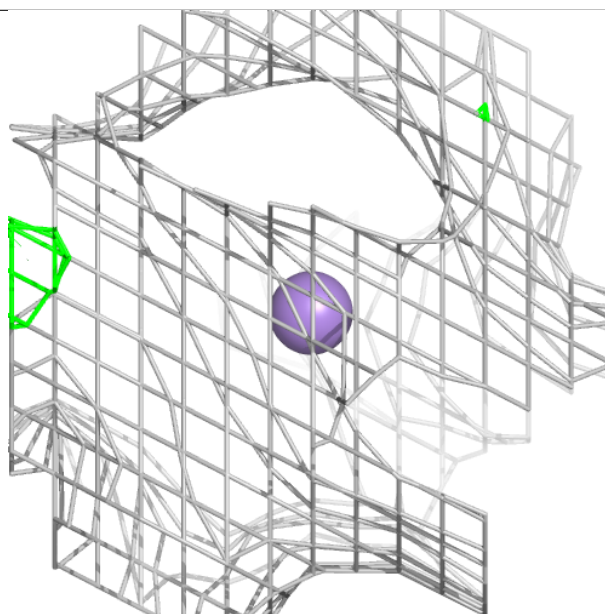
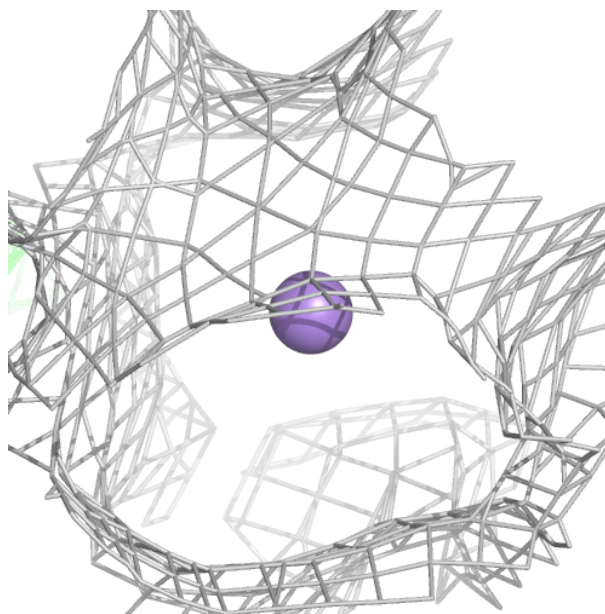
Electron density around DTP C 1002:

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



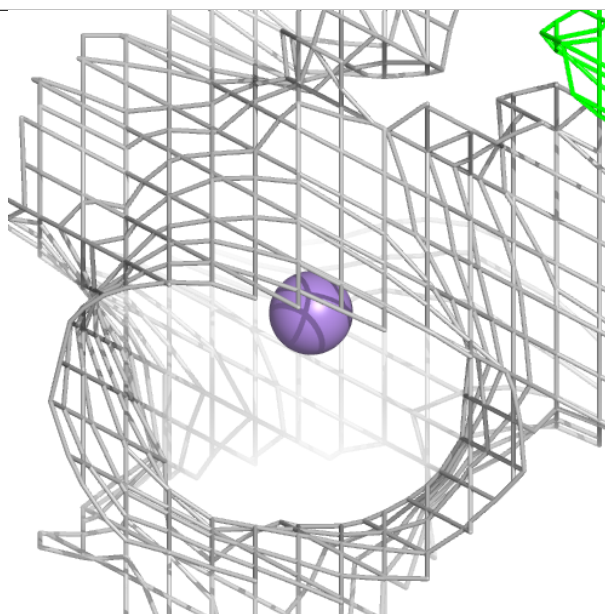
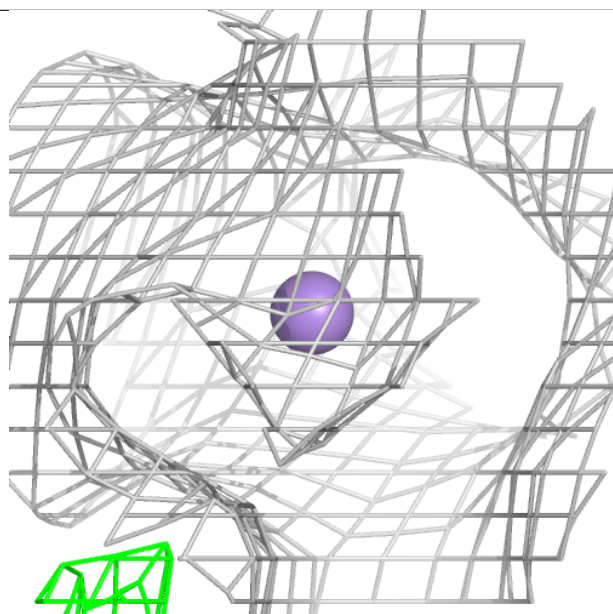
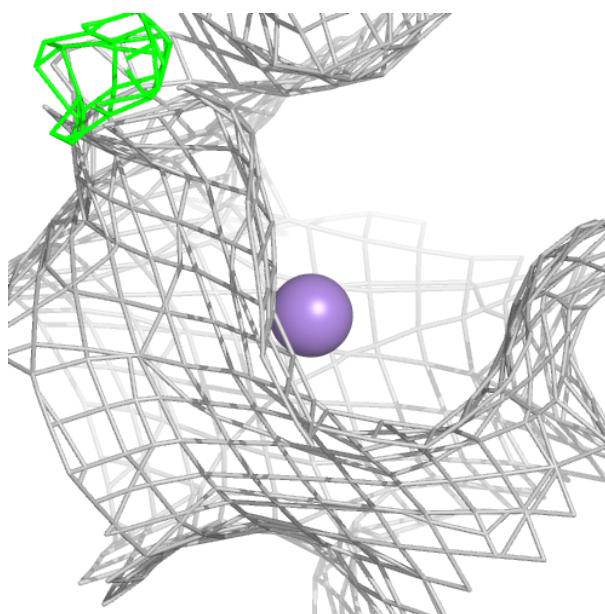
Electron density around MN A 1004:

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



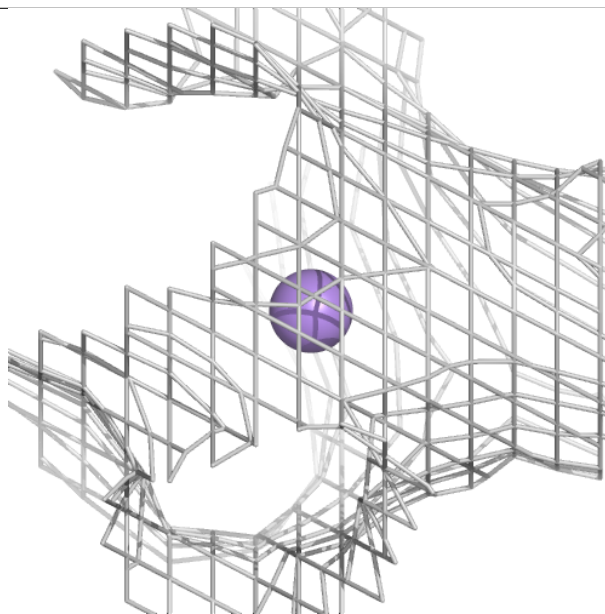
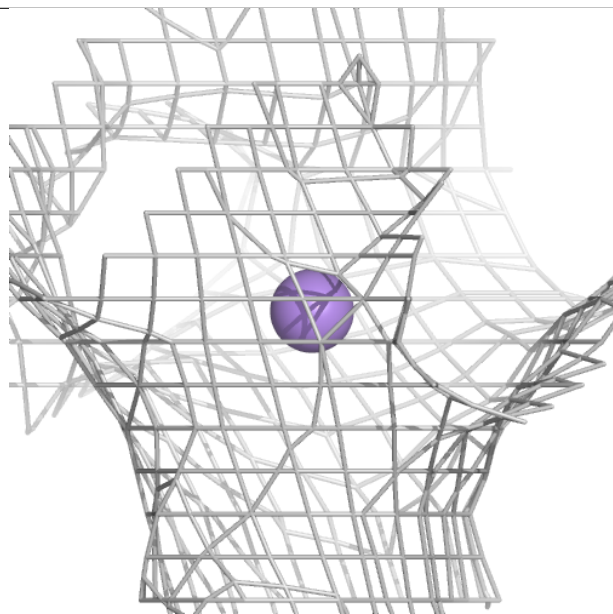
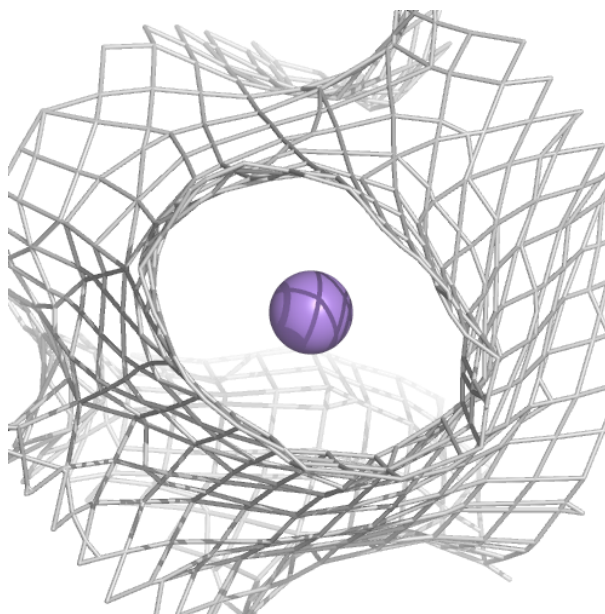
Electron density around MN B 1004:

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



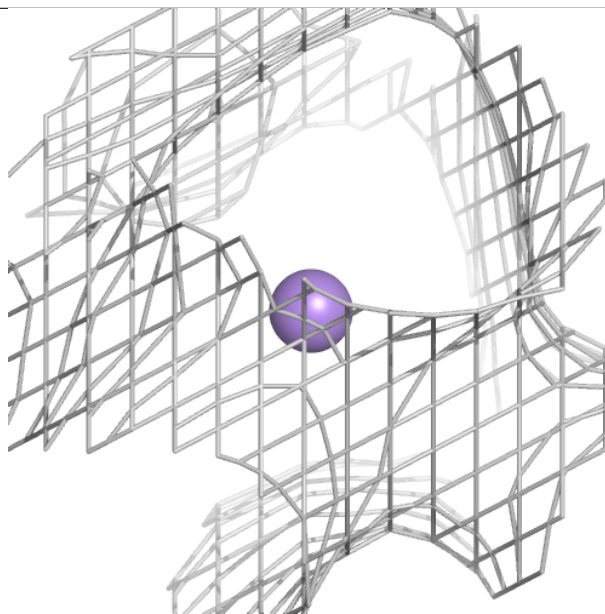
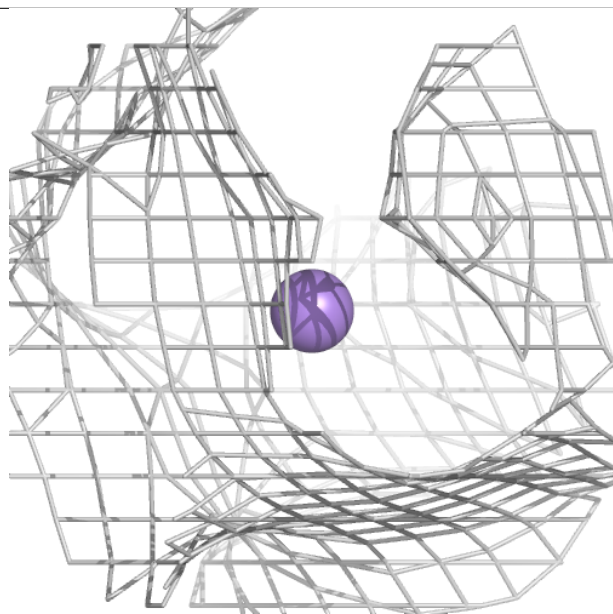
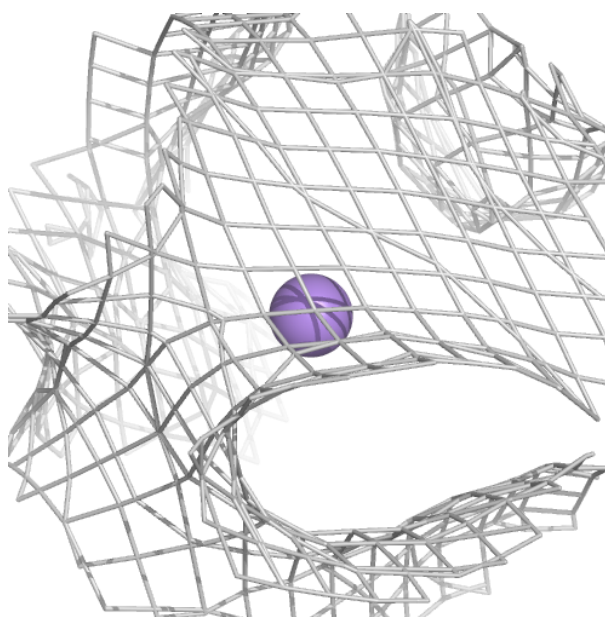
Electron density around MN C 1004:

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



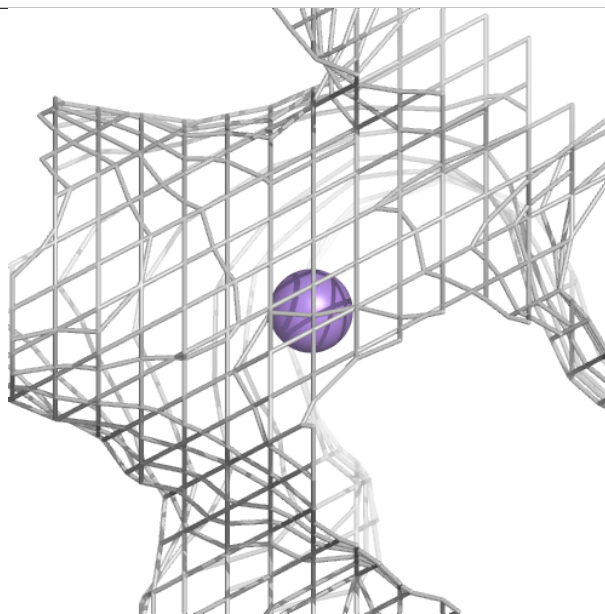
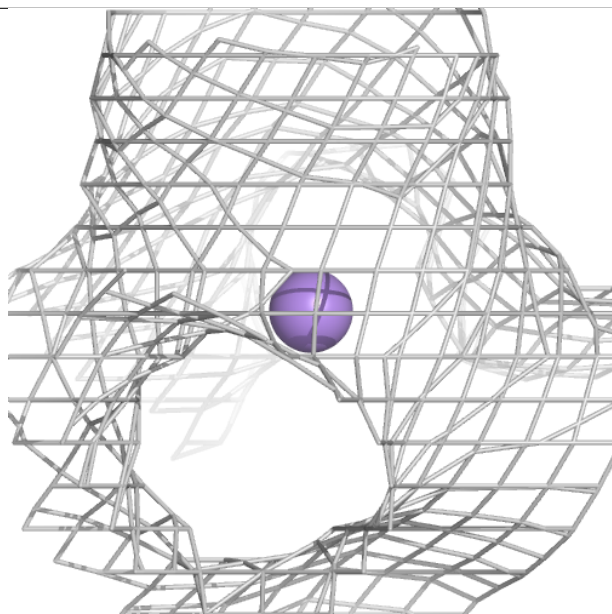
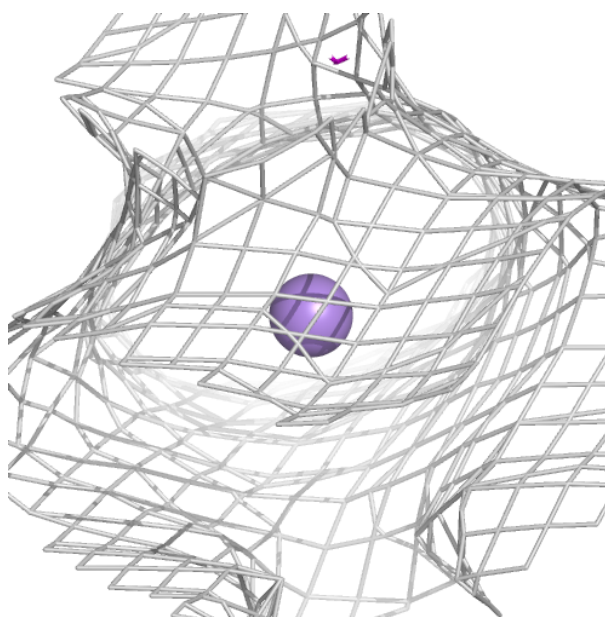
Electron density around MN C 1005:

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



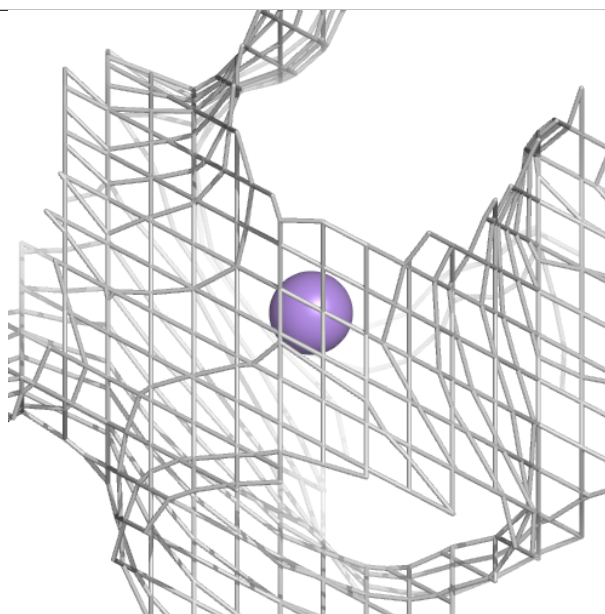
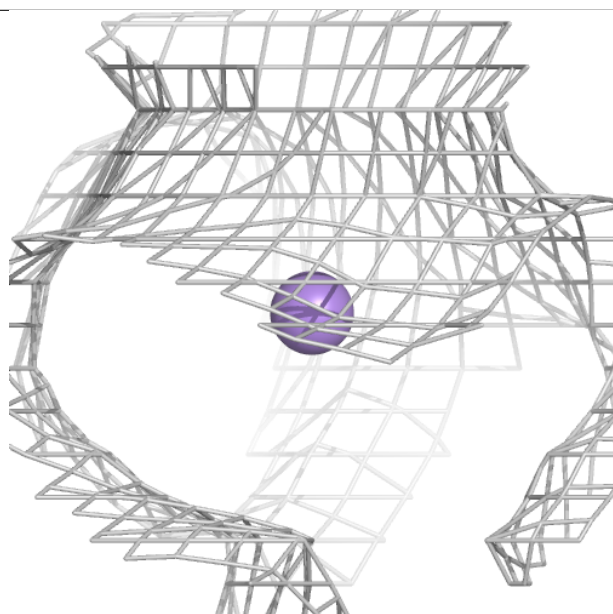
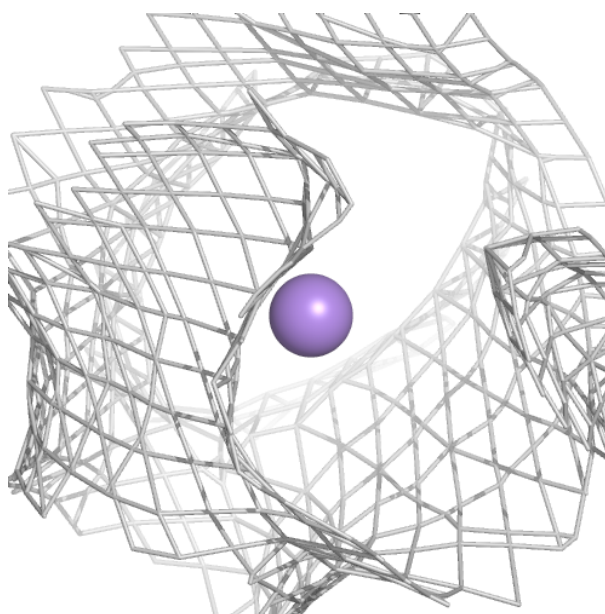
Electron density around MN D 1004:

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and green (positive)



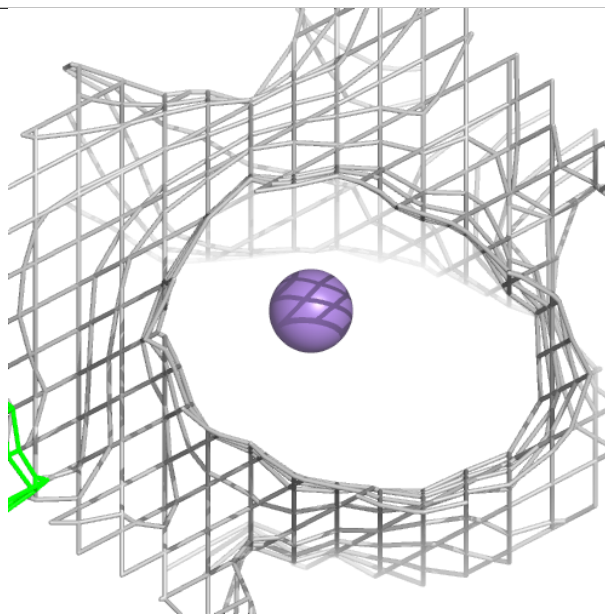
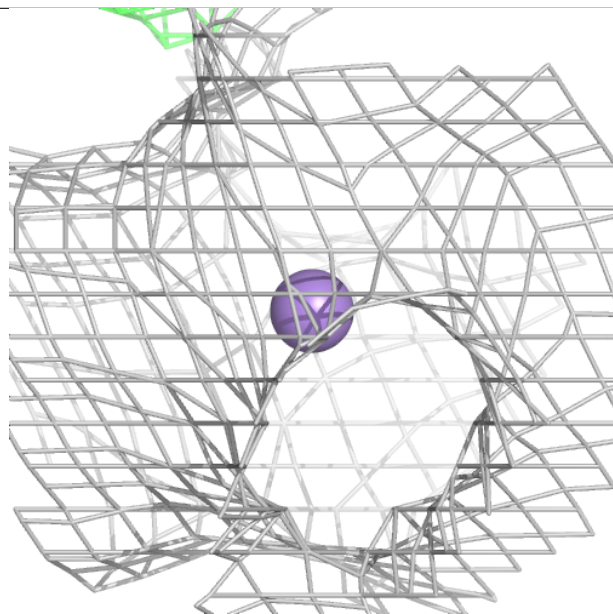
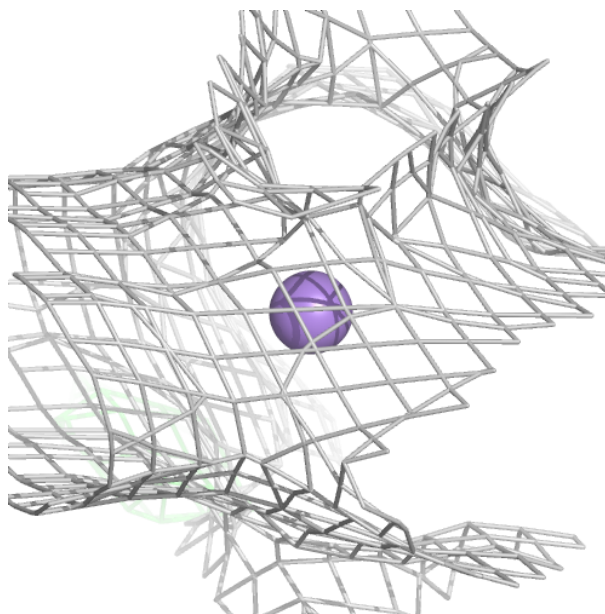
Electron density around MN D 1005:

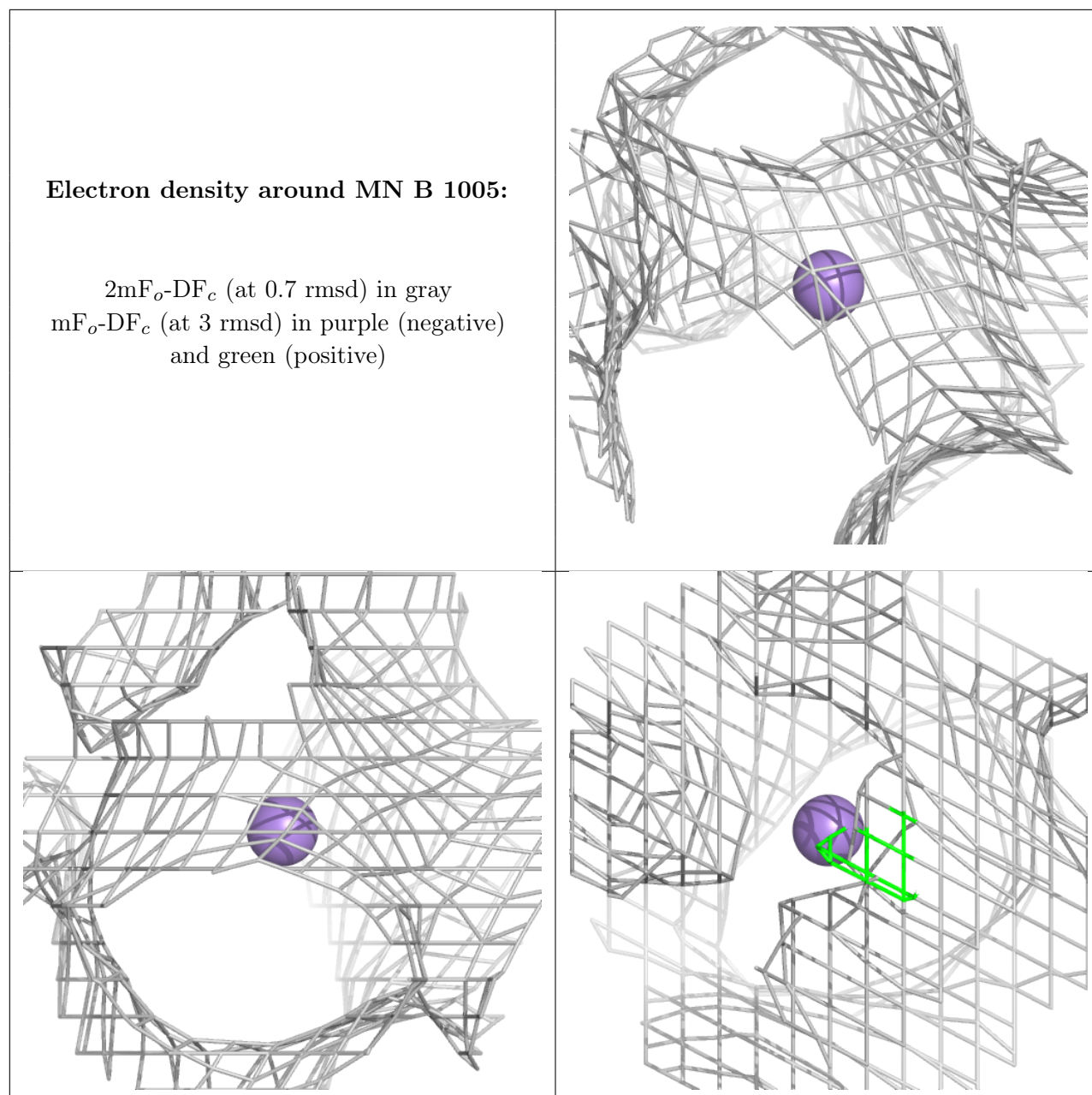
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MN A 1005:

$2mF_o-DF_c$ (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.