



wwPDB X-ray Structure Validation Summary Report ⓘ

May 19, 2024 – 12:40 pm BST

PDB ID : 8OVS
Title : Crystal structure of YeGT glycosyltransferase with bound UDP
Authors : Wirth, C.; Hunte, C.
Deposited on : 2023-04-26
Resolution : 1.12 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

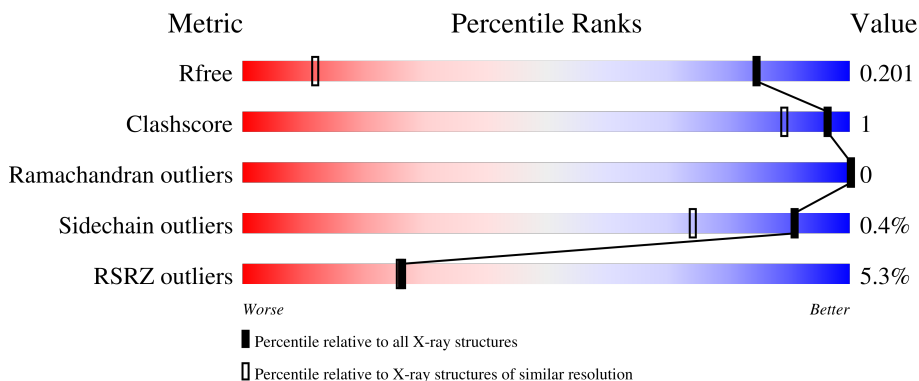
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

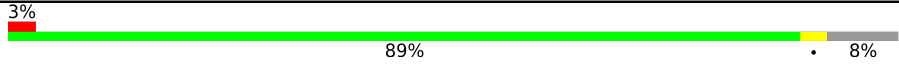
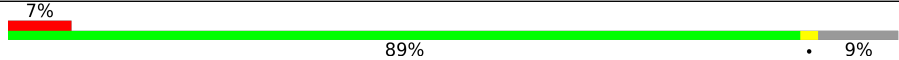
The reported resolution of this entry is 1.12 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1168 (1.14-1.10)
Clashscore	141614	1205 (1.14-1.10)
Ramachandran outliers	138981	1168 (1.14-1.10)
Sidechain outliers	138945	1165 (1.14-1.10)
RSRZ outliers	127900	1146 (1.14-1.10)

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	AAA	299	
1	BBB	299	

2 Entry composition [i](#)

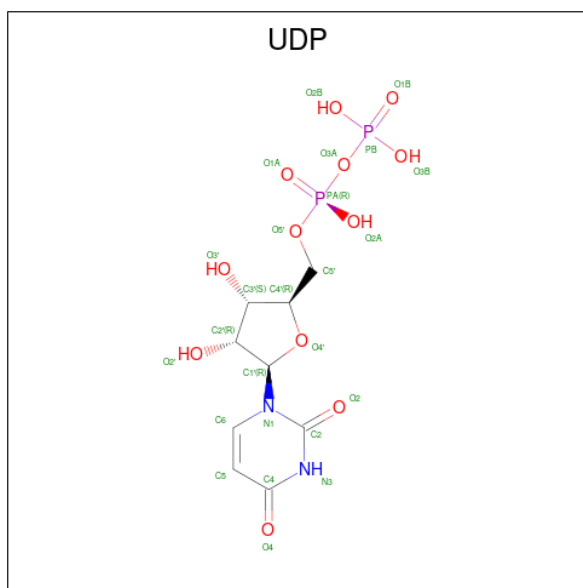
There are 8 unique types of molecules in this entry. The entry contains 5565 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 YeGT glycosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	276	Total 2306	C 1472	N 399	O 428	S 7	24	13	0
1	BBB	271	Total 2252	C 1445	N 386	O 414	S 7	21	12	0

- Molecule 2 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C₉H₁₄N₂O₁₂P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	AAA	1	Total 25	C 9	N 2	O 12	P 2	0	0
2	BBB	1	Total 25	C 9	N 2	O 12	P 2	0	0

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AAA	1	Total C O 4 2 2	0	0
3	AAA	1	Total C O 4 2 2	0	0
3	AAA	1	Total C O 4 2 2	0	0
3	BBB	1	Total C O 4 2 2	0	0
3	BBB	1	Total C O 4 2 2	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	1	Total C O 4 2 2	0	0
4	AAA	1	Total C O 4 2 2	0	0
4	AAA	1	Total C O 4 2 2	0	0
4	BBB	1	Total C O 8 4 4	0	1
4	BBB	1	Total C O 4 2 2	0	0
4	BBB	1	Total C O 4 2 2	0	0
4	BBB	1	Total C O 4 2 2	0	0
4	BBB	1	Total C O 4 2 2	0	0
4	BBB	1	Total C O 4 2 2	0	0
4	BBB	1	Total C O 4 2 2	0	0

- Molecule 5 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	AAA	10	Total Cd 10 10	0	0
5	BBB	7	Total Cd 7 7	0	0

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	AAA	1	Total Mn 1 1	0	0
6	BBB	1	Total Mn 1 1	0	0

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	AAA	2	Total Na 2 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	BBB	1	Total	Na	0	0
			1	1		

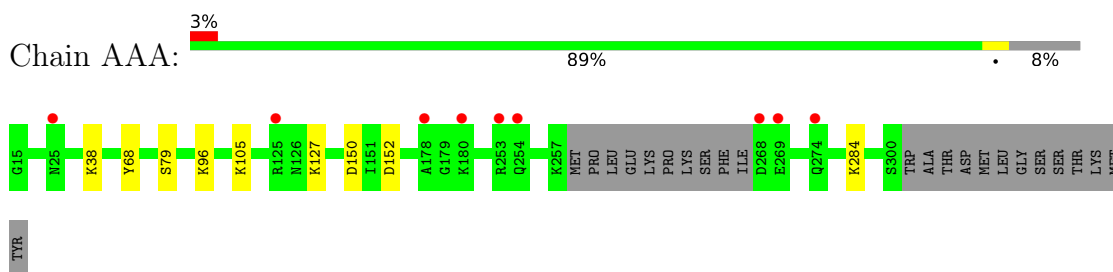
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	AAA	428	Total	O	0	0
			428	428		
8	BBB	443	Total	O	0	0
			443	443		

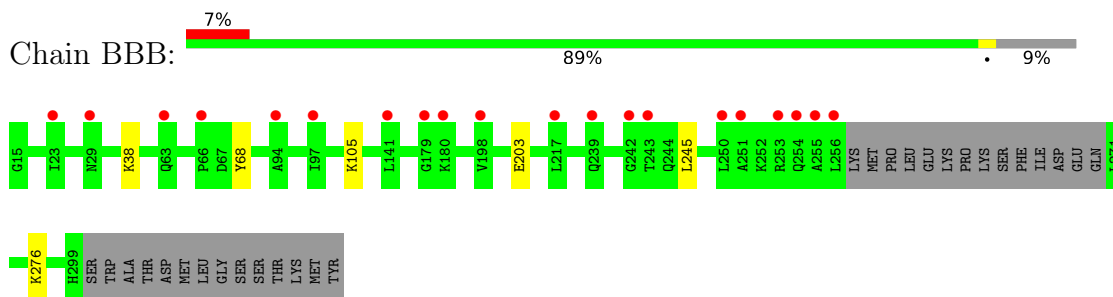
3 Residue-property plots [i](#)

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: YeGT glycosyltransferase



- Molecule 1: YeGT glycosyltransferase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	47.13Å 114.55Å 69.38Å 90.00° 89.99° 90.00°	Depositor
Resolution (Å)	47.13 – 1.12 47.13 – 1.12	Depositor EDS
% Data completeness (in resolution range)	76.6 (47.13-1.12) 80.1 (47.13-1.12)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 1.12Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.153 , 0.169 0.179 , 0.201	Depositor DCC
R_{free} test set	11268 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	11.9	Xtriage
Anisotropy	0.763	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.108 for h,-k,-l	Xtriage
Reported twinning fraction	0.534 for H, K, L 0.466 for -h,-k,l	Depositor
Outliers	0 of 223599 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5565	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, NA, MN, UDP, CD, ACT

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	AAA	0.62	0/2361	0.66	0/3176
1	BBB	0.63	0/2319	0.66	0/3122
All	All	0.63	0/4680	0.66	0/6298

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AAA	2306	0	2332	5	0
1	BBB	2252	0	2294	4	0
2	AAA	25	0	11	0	0
2	BBB	25	0	11	0	0
3	AAA	12	0	9	0	0
3	BBB	8	0	6	0	0
4	AAA	12	0	18	0	0
4	BBB	32	0	46	0	0
5	AAA	10	0	0	0	0
5	BBB	7	0	0	0	0
6	AAA	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	BBB	1	0	0	0	0
7	AAA	2	0	0	0	0
7	BBB	1	0	0	0	0
8	AAA	428	0	0	2	0
8	BBB	443	0	0	2	0
All	All	5565	0	4727	9	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 1.

The worst 5 of 9 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:AAA:152:ASP:OD2	8:AAA:501:HOH:O	2.08	0.70
1:AAA:105:LYS:NZ	8:AAA:502:HOH:O	2.25	0.70
1:BBB:105:LYS:NZ	8:BBB:503:HOH:O	2.38	0.56
1:BBB:245:LEU:HD22	1:BBB:276:LYS:HD2	1.92	0.51
1:BBB:203:GLU:HG3	8:BBB:608:HOH:O	2.12	0.49

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	AAA	285/299 (95%)	284 (100%)	1 (0%)	0	100	100
1	BBB	280/299 (94%)	277 (99%)	3 (1%)	0	100	100
All	All	565/598 (94%)	561 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AAA	250/258 (97%)	247 (99%)	3 (1%)	71	35
1	BBB	245/258 (95%)	245 (100%)	0	100	100
All	All	495/516 (96%)	492 (99%)	3 (1%)	91	61

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

Mol	Chain	Res	Type
1	AAA	96	LYS
1	AAA	284[A]	LYS
1	AAA	284[B]	LYS

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 40 ligands modelled in this entry, 22 are monoatomic - leaving 18 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ACT	AAA	406	-	3,3,3	0.93	0	3,3,3	0.84	0
4	EDO	BBB	408	-	3,3,3	0.06	0	2,2,2	0.19	0
4	EDO	BBB	410	-	3,3,3	0.09	0	2,2,2	0.33	0
3	ACT	AAA	402	-	3,3,3	0.95	0	3,3,3	0.84	0
4	EDO	BBB	405	-	3,3,3	0.05	0	2,2,2	0.16	0
3	ACT	AAA	403	5	3,3,3	1.05	0	3,3,3	0.70	0
3	ACT	BBB	401	5	3,3,3	1.09	0	3,3,3	0.71	0
4	EDO	AAA	407	-	3,3,3	0.06	0	2,2,2	0.16	0
4	EDO	AAA	405	-	3,3,3	0.06	0	2,2,2	0.23	0
4	EDO	BBB	404[B]	5	3,3,3	0.07	0	2,2,2	0.24	0
4	EDO	BBB	407	-	3,3,3	0.06	0	2,2,2	0.27	0
4	EDO	BBB	409	-	3,3,3	0.05	0	2,2,2	0.22	0
3	ACT	BBB	402	-	3,3,3	0.97	0	3,3,3	0.78	0
4	EDO	BBB	404[A]	5	3,3,3	0.06	0	2,2,2	0.09	0
4	EDO	AAA	404	-	3,3,3	0.07	0	2,2,2	0.15	0
2	UDP	BBB	403	5,6	24,26,26	0.41	0	37,40,40	0.66	0
4	EDO	BBB	406	-	3,3,3	0.06	0	2,2,2	0.20	0
2	UDP	AAA	401	5,6	24,26,26	0.41	0	37,40,40	0.81	1 (2%)

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
4	EDO	BBB	408	-	-	0/1/1/1	-
4	EDO	BBB	410	-	-	1/1/1/1	-
4	EDO	AAA	407	-	-	0/1/1/1	-
4	EDO	AAA	405	-	-	0/1/1/1	-
4	EDO	BBB	404[B]	5	-	0/1/1/1	-
4	EDO	BBB	407	-	-	1/1/1/1	-
4	EDO	BBB	409	-	-	1/1/1/1	-
4	EDO	BBB	405	-	-	0/1/1/1	-
4	EDO	BBB	404[A]	5	-	1/1/1/1	-
4	EDO	AAA	404	-	-	0/1/1/1	-
2	UDP	BBB	403	5,6	-	1/16/32/32	0/2/2/2
4	EDO	BBB	406	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UDP	AAA	401	5,6	-	2/16/32/32	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AAA	401	UDP	O5'-PA-O1A	-2.06	101.01	109.07

There are no chirality outliers.

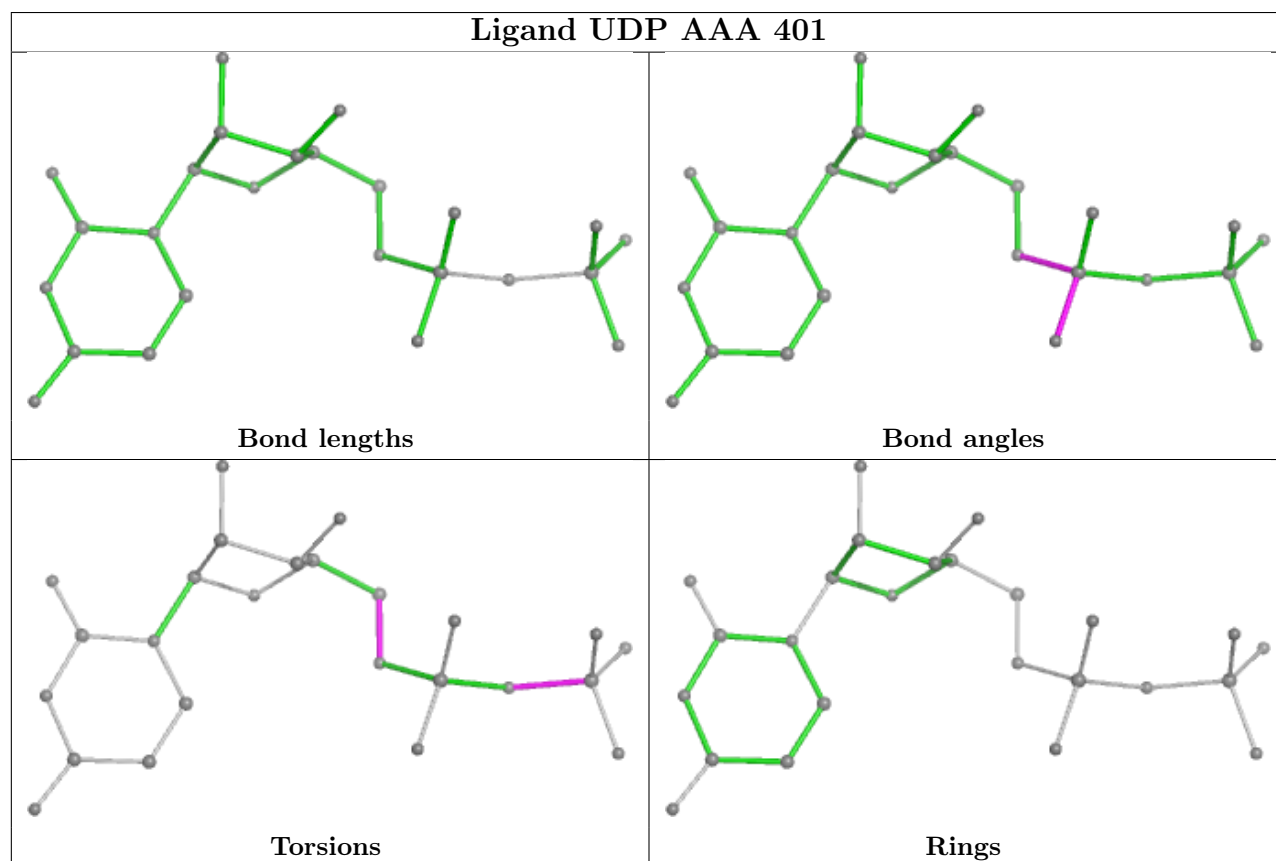
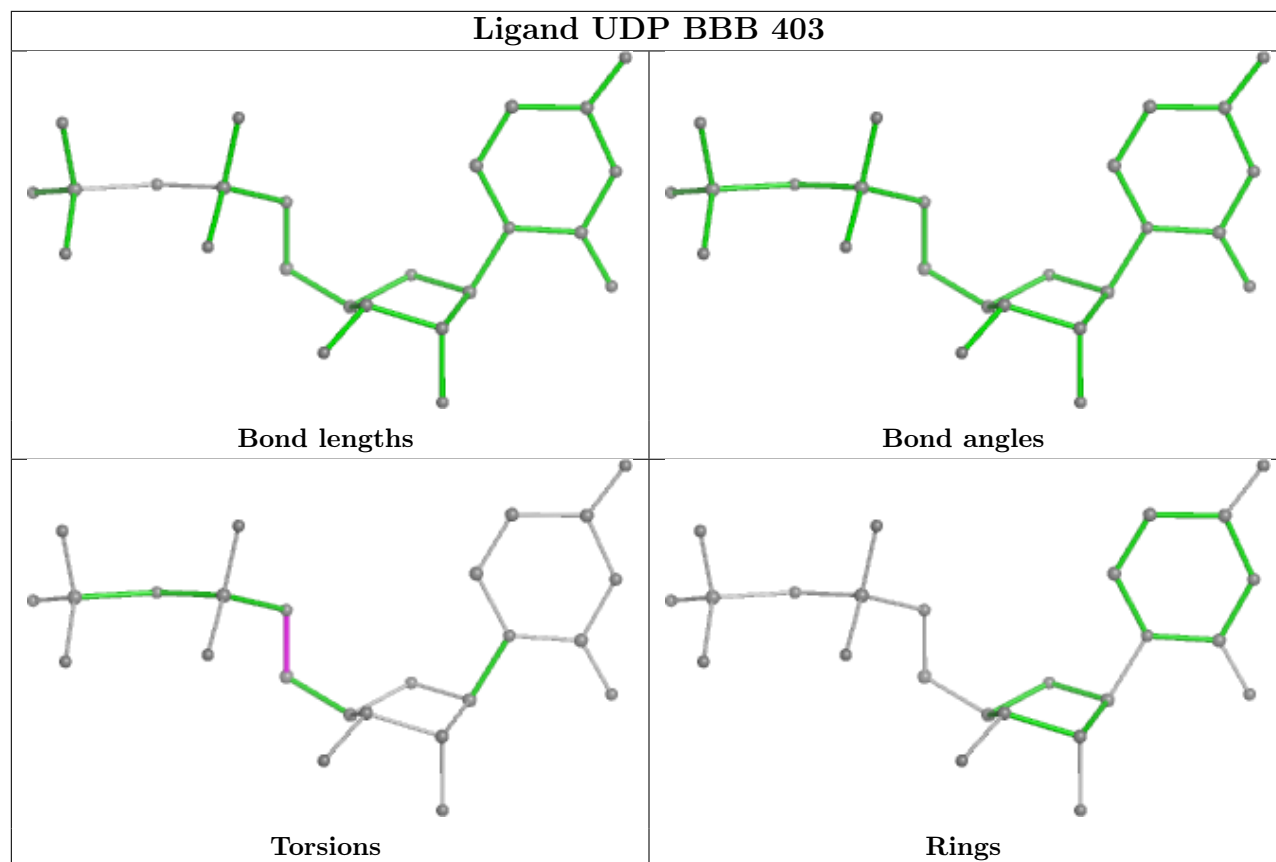
5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	BBB	410	EDO	O1-C1-C2-O2
2	AAA	401	UDP	PA-O3A-PB-O1B
4	BBB	406	EDO	O1-C1-C2-O2
4	BBB	404[A]	EDO	O1-C1-C2-O2
4	BBB	407	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	AAA	276/299 (92%)	0.64	9 (3%) 46 45	9, 16, 25, 35	7 (2%)
1	BBB	271/299 (90%)	0.81	20 (7%) 14 15	10, 17, 31, 40	6 (2%)
All	All	547/598 (91%)	0.73	29 (5%) 26 26	9, 16, 28, 40	13 (2%)

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	254	GLN	5.0
1	BBB	256	LEU	4.1
1	BBB	94	ALA	3.3
1	AAA	254	GLN	3.2
1	BBB	250	LEU	2.9

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

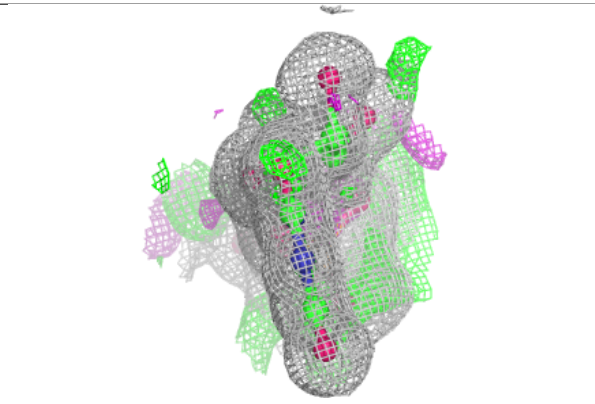
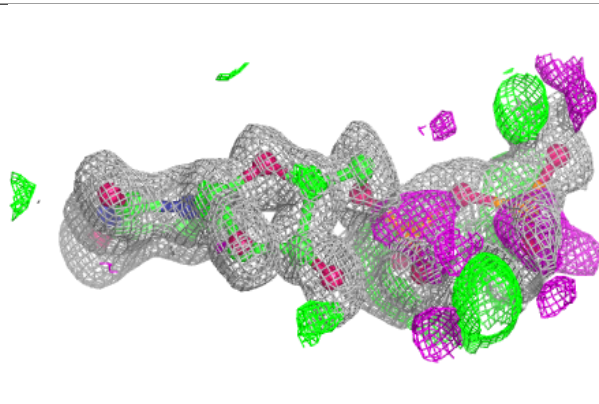
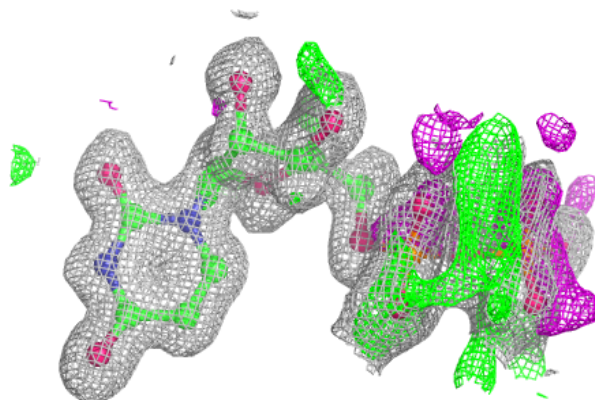
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	AAA	405	4/4	0.55	0.21	35,36,37,39	0
4	EDO	BBB	407	4/4	0.72	0.17	30,30,30,31	0
4	EDO	BBB	410	4/4	0.77	0.18	26,26,27,30	0
4	EDO	BBB	408	4/4	0.78	0.18	28,30,31,33	0
7	NA	AAA	420	1/1	0.81	0.08	41,41,41,41	0
4	EDO	BBB	406	4/4	0.82	0.18	33,34,34,36	0
4	EDO	BBB	409	4/4	0.82	0.10	32,32,33,34	0
3	ACT	AAA	406	4/4	0.83	0.19	30,30,31,32	0
5	CD	BBB	412	1/1	0.86	0.10	29,29,29,29	0
5	CD	AAA	409	1/1	0.88	0.09	26,26,26,26	0
4	EDO	BBB	405	4/4	0.88	0.11	28,30,30,31	0
4	EDO	AAA	407	4/4	0.88	0.13	23,24,26,26	0
3	ACT	AAA	403	4/4	0.90	0.10	16,17,17,19	0
4	EDO	BBB	404[A]	4/4	0.90	0.16	17,17,18,18	4
4	EDO	BBB	404[B]	4/4	0.90	0.16	12,14,15,16	4
4	EDO	AAA	404	4/4	0.91	0.14	27,27,27,28	0
2	UDP	BBB	403	25/25	0.92	0.11	10,12,19,23	0
5	CD	BBB	414	1/1	0.93	0.17	42,42,42,42	0
3	ACT	BBB	402	4/4	0.95	0.10	15,15,16,16	0
2	UDP	AAA	401	25/25	0.95	0.09	10,12,18,21	0
3	ACT	AAA	402	4/4	0.95	0.10	17,17,17,18	0
3	ACT	BBB	401	4/4	0.95	0.11	16,16,17,18	0
5	CD	BBB	413	1/1	0.96	0.10	36,36,36,36	1
5	CD	AAA	414	1/1	0.97	0.05	28,28,28,28	0
5	CD	AAA	416	1/1	0.98	0.19	36,36,36,36	1
5	CD	AAA	412	1/1	0.99	0.04	31,31,31,31	0
5	CD	AAA	415	1/1	0.99	0.05	13,13,13,13	1
5	CD	AAA	413	1/1	0.99	0.09	24,24,24,24	1
5	CD	BBB	415	1/1	0.99	0.15	24,24,24,24	1
5	CD	BBB	416	1/1	0.99	0.04	14,14,14,14	1
5	CD	BBB	417	1/1	0.99	0.03	22,22,22,22	1
5	CD	AAA	417	1/1	0.99	0.08	20,20,20,20	1
7	NA	BBB	419	1/1	0.99	0.10	13,13,13,13	0
5	CD	AAA	408	1/1	1.00	0.07	12,12,12,12	0
5	CD	AAA	410	1/1	1.00	0.06	13,13,13,13	0
6	MN	AAA	418	1/1	1.00	0.14	10,10,10,10	0
6	MN	BBB	418	1/1	1.00	0.15	11,11,11,11	0
7	NA	AAA	419	1/1	1.00	0.07	14,14,14,14	0
5	CD	AAA	411	1/1	1.00	0.05	15,15,15,15	0
5	CD	BBB	411	1/1	1.00	0.07	13,13,13,13	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.

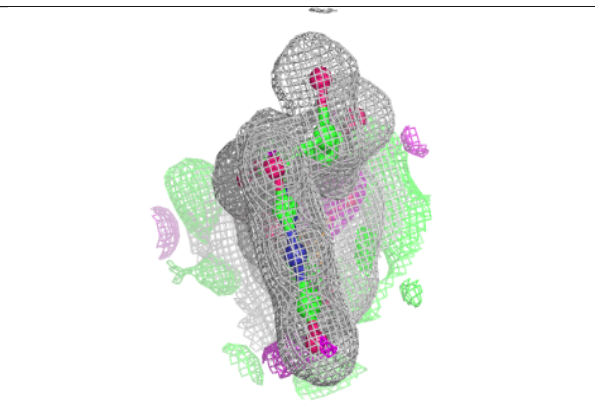
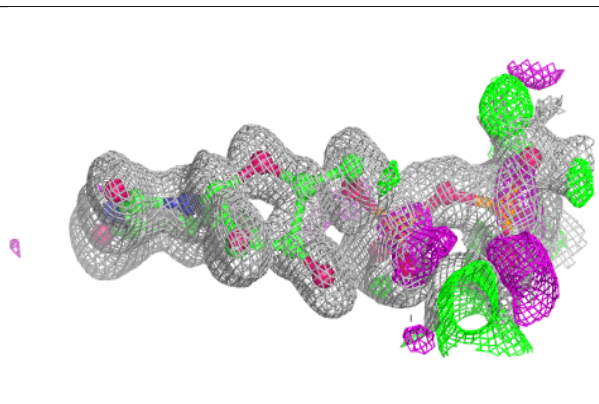
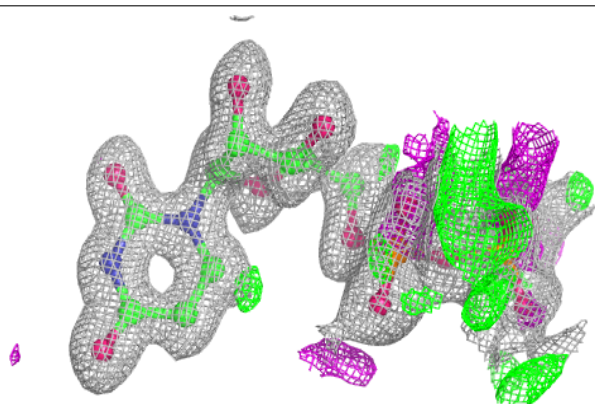
Electron density around UDP BBB 403:

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



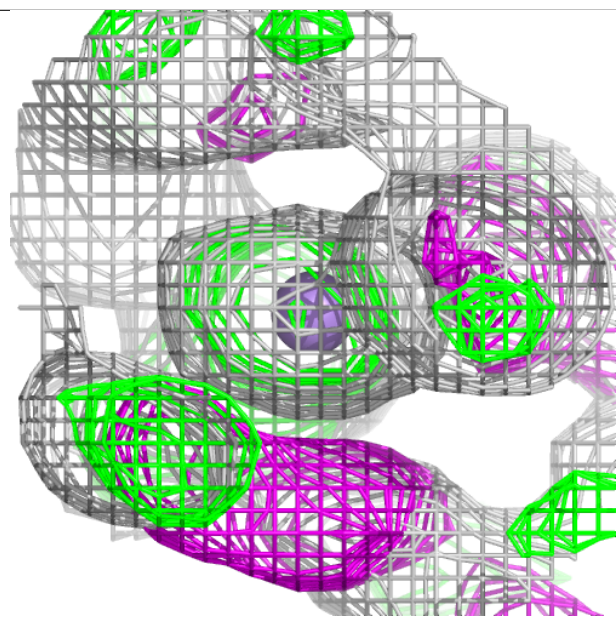
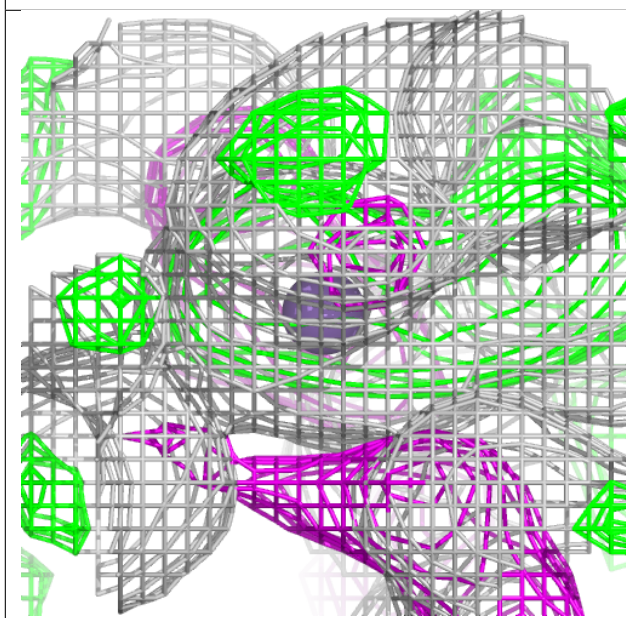
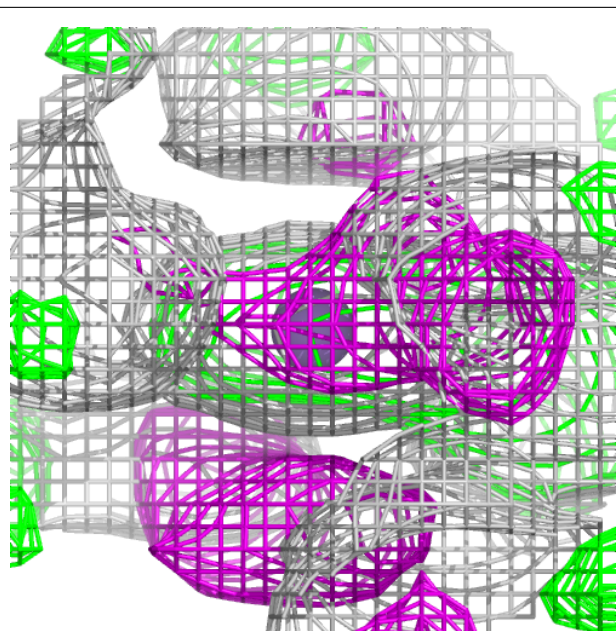
Electron density around UDP AAA 401:

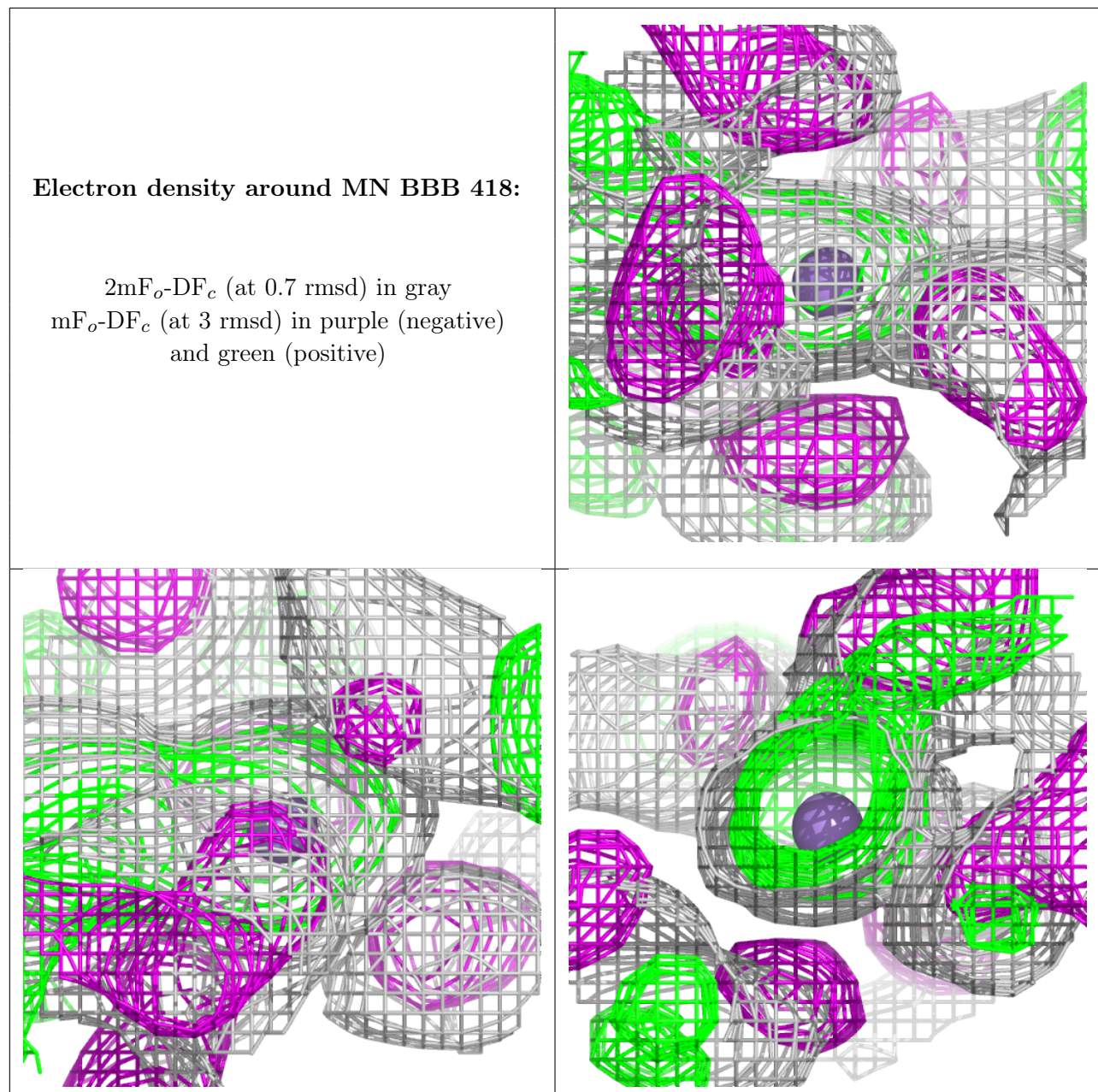
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MN AAA 418:

$2mF_o-DF_c$ (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.