



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2024 – 09:55 PM EDT

PDB ID : 6RCX
Title : Mycobacterial 4'-phosphopantetheinyl transferase PptAb in complex with the ACP domain of PpsC.
Authors : Nguyen, M.C.; Mourey, L.; Pedelacq, J.D.
Deposited on : 2019-04-12
Resolution : 2.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

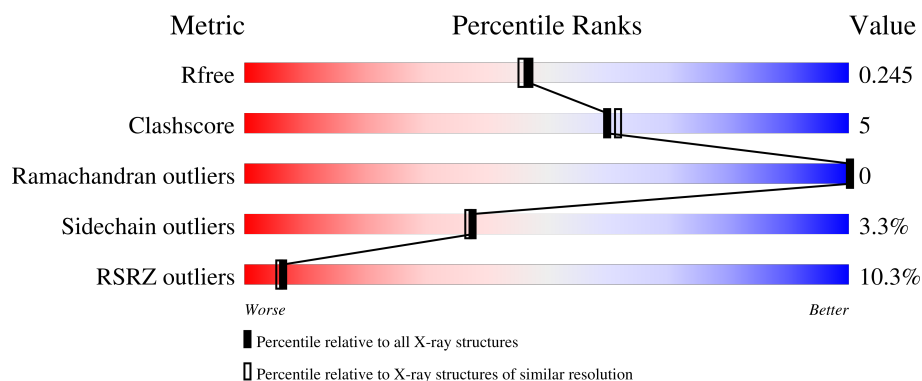
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	232	<div> <div>3%</div> <div>86%</div> <div>6% • 6%</div> </div>
2	B	157	<div> <div>15%</div> <div>39%</div> <div>7% • 52%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 2439 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 Possible 4'-phosphopantetheinyl transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1672	1072	284	313	3			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	220	LYS	-	expression tag	UNP B1MD73
A	221	LEU	-	expression tag	UNP B1MD73
A	222	ALA	-	expression tag	UNP B1MD73
A	223	ALA	-	expression tag	UNP B1MD73
A	224	ALA	-	expression tag	UNP B1MD73
A	225	LEU	-	expression tag	UNP B1MD73
A	226	GLU	-	expression tag	UNP B1MD73
A	227	HIS	-	expression tag	UNP B1MD73
A	228	HIS	-	expression tag	UNP B1MD73
A	229	HIS	-	expression tag	UNP B1MD73
A	230	HIS	-	expression tag	UNP B1MD73
A	231	HIS	-	expression tag	UNP B1MD73
A	232	HIS	-	expression tag	UNP B1MD73

- Molecule 2 is a protein called Phthiocerol synthesis polyketide synthase type I PpsC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	75	Total	C	N	O	S	0	0	0
			567	358	101	105	3			

There are 26 discrepancies between the modelled and reference sequences:

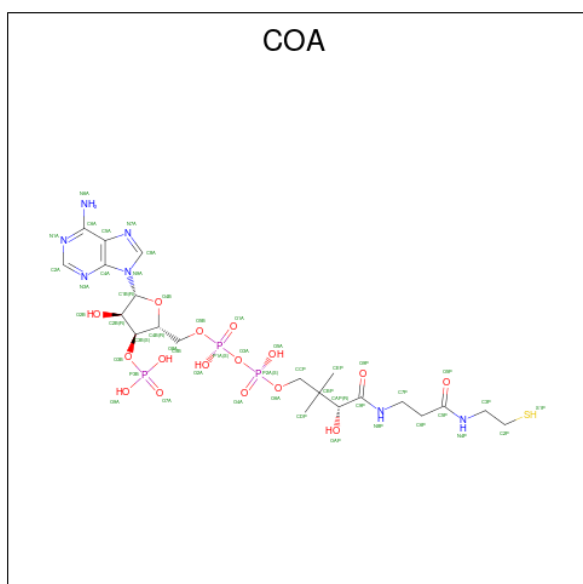
Chain	Residue	Modelled	Actual	Comment	Reference
B	2036	MET	-	initiating methionine	UNP P96202
B	2037	GLY	-	expression tag	UNP P96202
B	2038	SER	-	expression tag	UNP P96202

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2039	SER	-	expression tag	UNP P96202
B	2040	HIS	-	expression tag	UNP P96202
B	2041	HIS	-	expression tag	UNP P96202
B	2042	HIS	-	expression tag	UNP P96202
B	2043	HIS	-	expression tag	UNP P96202
B	2044	HIS	-	expression tag	UNP P96202
B	2045	HIS	-	expression tag	UNP P96202
B	2046	SER	-	expression tag	UNP P96202
B	2047	SER	-	expression tag	UNP P96202
B	2048	GLY	-	expression tag	UNP P96202
B	2049	LEU	-	expression tag	UNP P96202
B	2050	VAL	-	expression tag	UNP P96202
B	2051	PRO	-	expression tag	UNP P96202
B	2052	ARG	-	expression tag	UNP P96202
B	2053	GLY	-	expression tag	UNP P96202
B	2054	SER	-	expression tag	UNP P96202
B	2055	HIS	-	expression tag	UNP P96202
B	2056	MET	-	expression tag	UNP P96202
B	2105	ALA	SER	engineered mutation	UNP P96202
B	2189	THR	-	expression tag	UNP P96202
B	2190	SER	-	expression tag	UNP P96202
B	2191	GLY	-	expression tag	UNP P96202
B	2192	SER	-	expression tag	UNP P96202

- Molecule 3 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$) (labeled as "Ligand of Interest" by depositor).

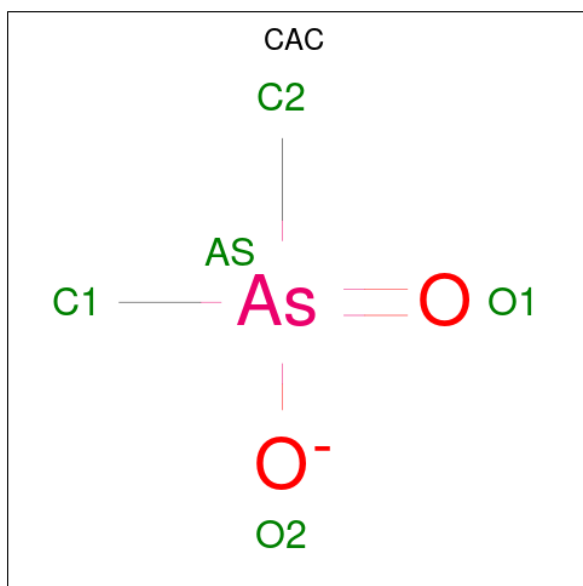


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	
			48	21	7	16	3	1	
									0
									0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Mn		
			3	3	0	0

- Molecule 5 is CACODYLATE ION (three-letter code: CAC) (formula: C₂H₆AsO₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	As	C	O		
			5	1	2	2	0	0

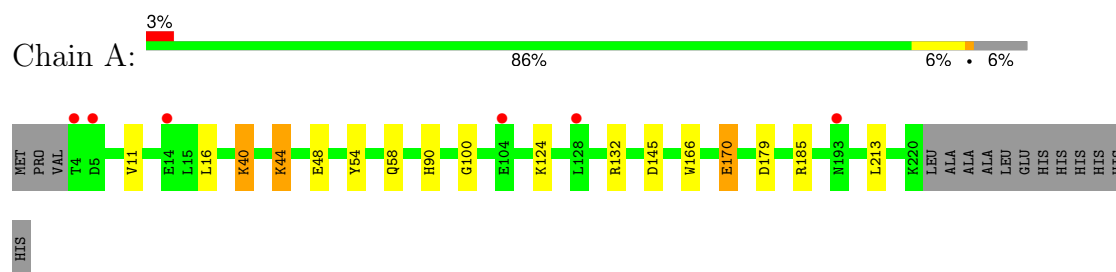
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	126	Total	O		
			126	126	0	0
6	B	18	Total	O		
			18	18	0	0

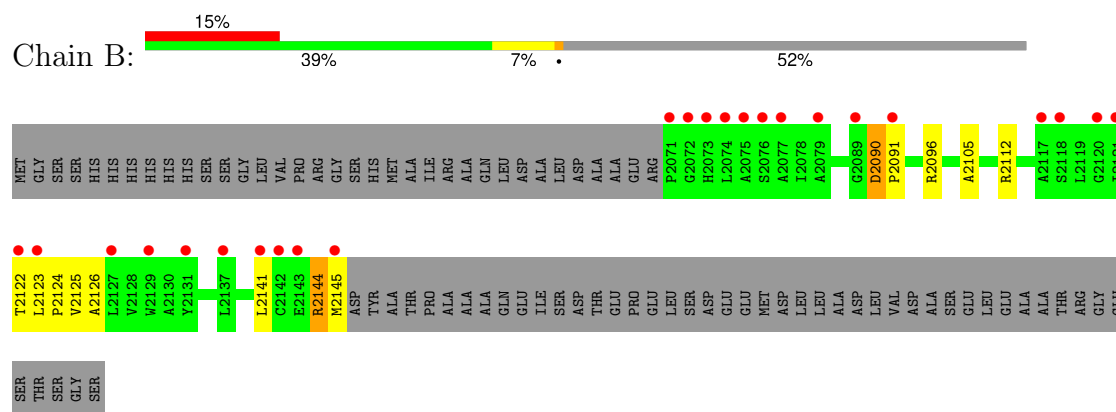
3 Residue-property plots [i](#)

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: Possible 4'-phosphopantetheinyl transferase



- Molecule 2: Phthiocerol synthesis polyketide synthase type I PpsC



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.14Å 63.17Å 108.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.15 – 2.00 45.51 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.2 (41.15-2.00) 86.8 (45.51-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.52 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.206 , 0.244 0.208 , 0.245	Depositor DCC
R_{free} test set	1993 reflections (7.18%)	wwPDB-VP
Wilson B-factor (Å ²)	30.8	Xtriage
Anisotropy	0.775	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2439	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.04% 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: MN, COA, CAC

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	0.35	0/1713	0.48	0/2340
2	B	0.47	0/577	0.49	0/786
All	All	0.38	0/2290	0.48	0/3126

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1672	0	1681	12	0
2	B	567	0	581	11	0
3	A	48	0	32	1	0
4	A	3	0	0	0	0
5	B	5	0	0	0	0
6	A	126	0	0	2	0
6	B	18	0	0	1	0
All	All	2439	0	2294	21	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 5.

All (21) 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)
2:B:2090:ASP:N	2:B:2090:ASP:OD2	2.26	0.69
1:A:40:LYS:O	2:B:2096:ARG:NH2	2.35	0.57
2:B:2112:ARG:HD2	2:B:2125:VAL:HG13	1.88	0.56
2:B:2141:LEU:O	2:B:2145:MET:HB3	2.05	0.56
1:A:16:LEU:HD22	1:A:100:GLY:HA3	1.90	0.54
1:A:58:GLN:NE2	6:A:406:HOH:O	2.41	0.53
1:A:124:LYS:HG3	1:A:132:ARG:NH1	2.25	0.51
1:A:58:GLN:NE2	6:A:402:HOH:O	2.27	0.50
3:A:301:COA:H10	2:B:2105:ALA:HB2	1.92	0.50
2:B:2112:ARG:HG3	2:B:2125:VAL:HA	1.96	0.48
1:A:166:TRP:CZ2	2:B:2126:ALA:HB2	2.51	0.46
2:B:2124:PRO:HD3	2:B:2144:ARG:HH22	1.81	0.46
1:A:44:LYS:C	1:A:44:LYS:HD3	2.37	0.45
2:B:2122:THR:O	2:B:2123:LEU:HD13	2.15	0.45
2:B:2112:ARG:CZ	2:B:2125:VAL:HG22	2.47	0.45
1:A:54:TYR:O	1:A:58:GLN:HG2	2.17	0.44
1:A:170:GLU:H	1:A:170:GLU:CD	2.21	0.44
1:A:44:LYS:HE2	1:A:48:GLU:OE1	2.17	0.43
1:A:11:VAL:HG21	1:A:213:LEU:HD23	2.03	0.41
1:A:145:ASP:OD1	1:A:145:ASP:N	2.53	0.41
2:B:2091:PRO:O	6:B:2301:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	215/232 (93%)	212 (99%)	3 (1%)	0	100	100
2	B	73/157 (46%)	70 (96%)	3 (4%)	0	100	100
All	All	288/389 (74%)	282 (98%)	6 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	180/192 (94%)	174 (97%)	6 (3%)	38	37
2	B	60/124 (48%)	58 (97%)	2 (3%)	38	37
All	All	240/316 (76%)	232 (97%)	8 (3%)	38	37

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	LYS
1	A	44	LYS
1	A	90	HIS
1	A	170	GLU
1	A	179	ASP
1	A	185	ARG
2	B	2090	ASP
2	B	2144	ARG

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

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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
5	CAC	B	2201	-	2,4,4	0.79	0	2,6,6	0.01	0
3	COA	A	301	4	43,50,50	3.74	17 (39%)	56,75,75	2.88	7 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	COA	A	301	4	-	13/44/64/64	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	COA	O4B-C1B	13.47	1.58	1.40
3	A	301	COA	C2B-C3B	-8.38	1.34	1.53
3	A	301	COA	C1B-N9A	-6.94	1.32	1.49
3	A	301	COA	P2A-O3A	6.52	1.66	1.59
3	A	301	COA	P1A-O3A	6.27	1.66	1.59
3	A	301	COA	O4B-C4B	-6.19	1.31	1.45
3	A	301	COA	C5P-N4P	6.04	1.47	1.33
3	A	301	COA	C9P-N8P	5.33	1.46	1.33
3	A	301	COA	C6A-N6A	4.17	1.49	1.34
3	A	301	COA	C3B-C4B	3.91	1.63	1.52
3	A	301	COA	C2A-N3A	3.47	1.37	1.32
3	A	301	COA	CCP-CBP	3.03	1.57	1.52
3	A	301	COA	OAP-CAP	-2.82	1.37	1.42
3	A	301	COA	P1A-O5B	2.67	1.69	1.59
3	A	301	COA	O5P-C5P	-2.54	1.18	1.23
3	A	301	COA	CDP-CBP	2.39	1.58	1.53
3	A	301	COA	P3B-O3B	2.27	1.63	1.59

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	301	COA	C5A-C6A-N6A	13.81	141.35	120.31
3	A	301	COA	N6A-C6A-N1A	-9.52	98.00	118.33
3	A	301	COA	C1B-N9A-C4A	-8.45	111.79	126.64
3	A	301	COA	N3A-C2A-N1A	-6.38	120.02	128.67
3	A	301	COA	C4B-O4B-C1B	-5.50	104.88	109.92
3	A	301	COA	C3B-C2B-C1B	2.34	105.03	99.89
3	A	301	COA	C6P-C5P-N4P	2.01	120.00	116.34

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	COA	CCP-O6A-P2A-O3A
3	A	301	COA	CDP-CBP-CCP-O6A
3	A	301	COA	CEP-CBP-CCP-O6A
3	A	301	COA	CAP-CBP-CCP-O6A
3	A	301	COA	S1P-C2P-C3P-N4P
3	A	301	COA	C2B-C3B-O3B-P3B
3	A	301	COA	C4B-C3B-O3B-P3B
3	A	301	COA	C5B-O5B-P1A-O2A
3	A	301	COA	CCP-O6A-P2A-O4A
3	A	301	COA	C3B-O3B-P3B-O9A
3	A	301	COA	N8P-C9P-CAP-OAP
3	A	301	COA	P1A-O3A-P2A-O4A
3	A	301	COA	P1A-O3A-P2A-O5A

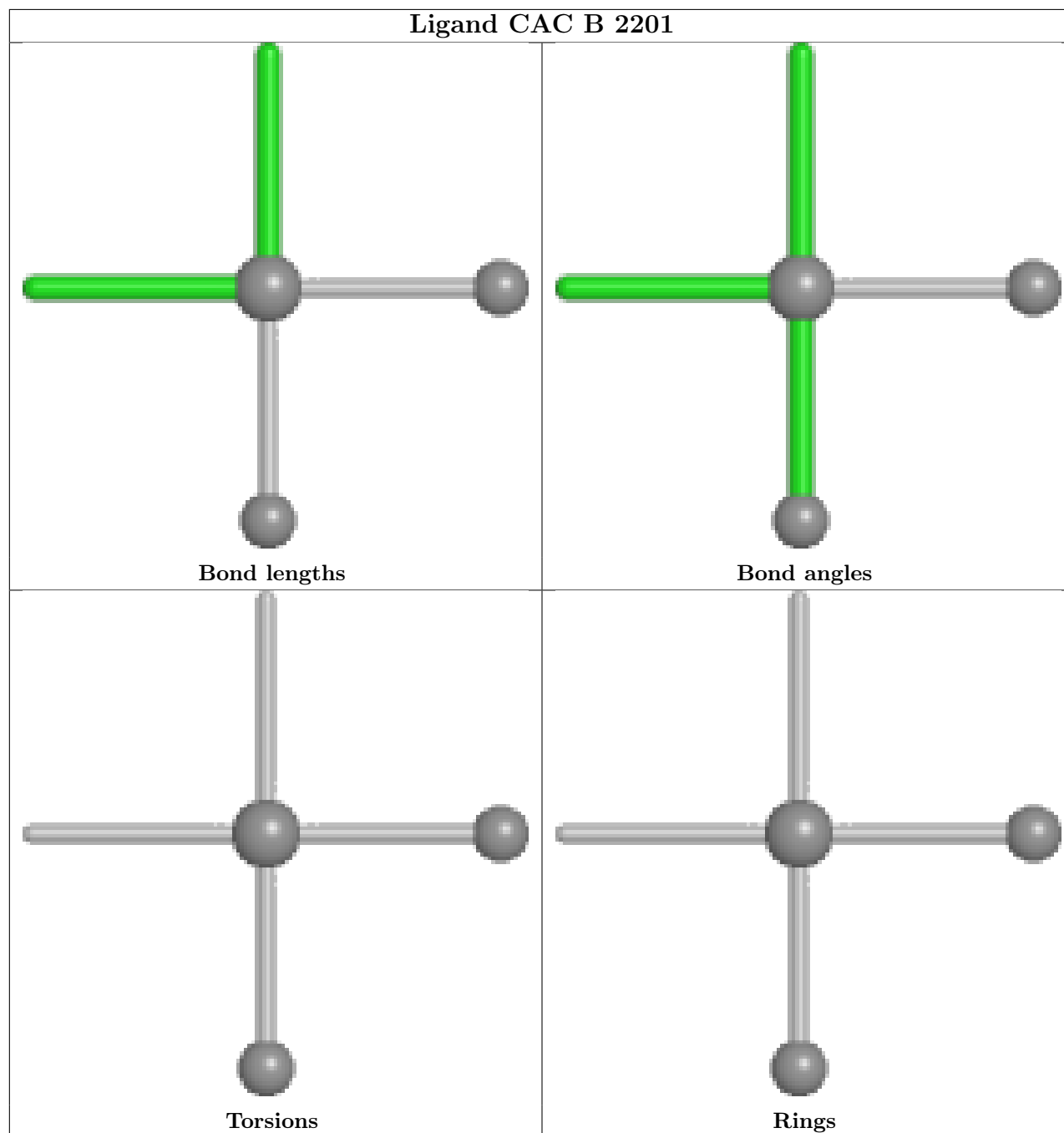
There are no ring outliers.

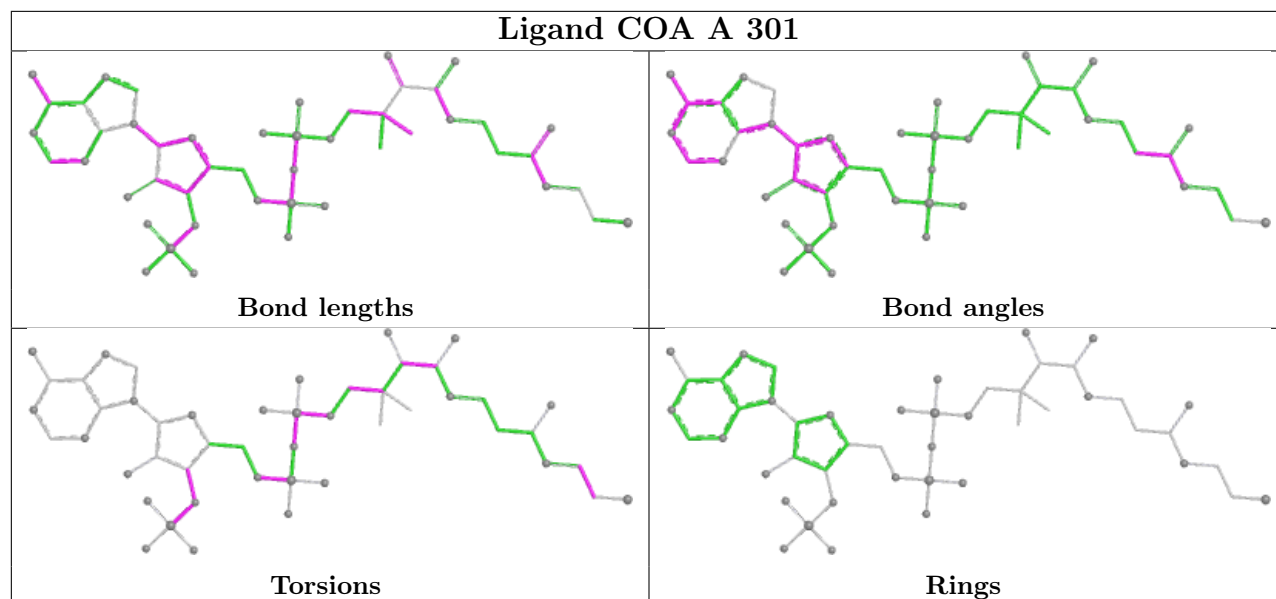
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	COA	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	217/232 (93%)	0.37	6 (2%) 53 51	26, 41, 64, 118	0
2	B	75/157 (47%)	1.62	24 (32%) 0 0	36, 65, 103, 124	0
All	All	292/389 (75%)	0.69	30 (10%) 6 6	26, 44, 92, 124	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	4	THR	7.6
2	B	2120	GLY	6.7
2	B	2123	LEU	6.6
2	B	2075	ALA	5.7
2	B	2073	HIS	5.6
2	B	2117	ALA	4.8
2	B	2121	ILE	4.4
2	B	2145	MET	4.4
2	B	2076	SER	4.3
2	B	2122	THR	4.1
2	B	2141	LEU	3.8
2	B	2127	LEU	3.8
2	B	2118	SER	3.7
2	B	2129	TRP	3.5
1	A	14	GLU	3.1
2	B	2074	LEU	3.1
2	B	2072	GLY	3.1
2	B	2071	PRO	3.1
1	A	5	ASP	3.0
2	B	2131	TYR	2.9
2	B	2137	LEU	2.8
2	B	2089	GLY	2.8
2	B	2077	ALA	2.8
2	B	2091	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	104	GLU	2.7
2	B	2079	ALA	2.6
1	A	128	LEU	2.6
2	B	2142	CYS	2.5
1	A	193	ASN	2.4
2	B	2143	GLU	2.1

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](#)

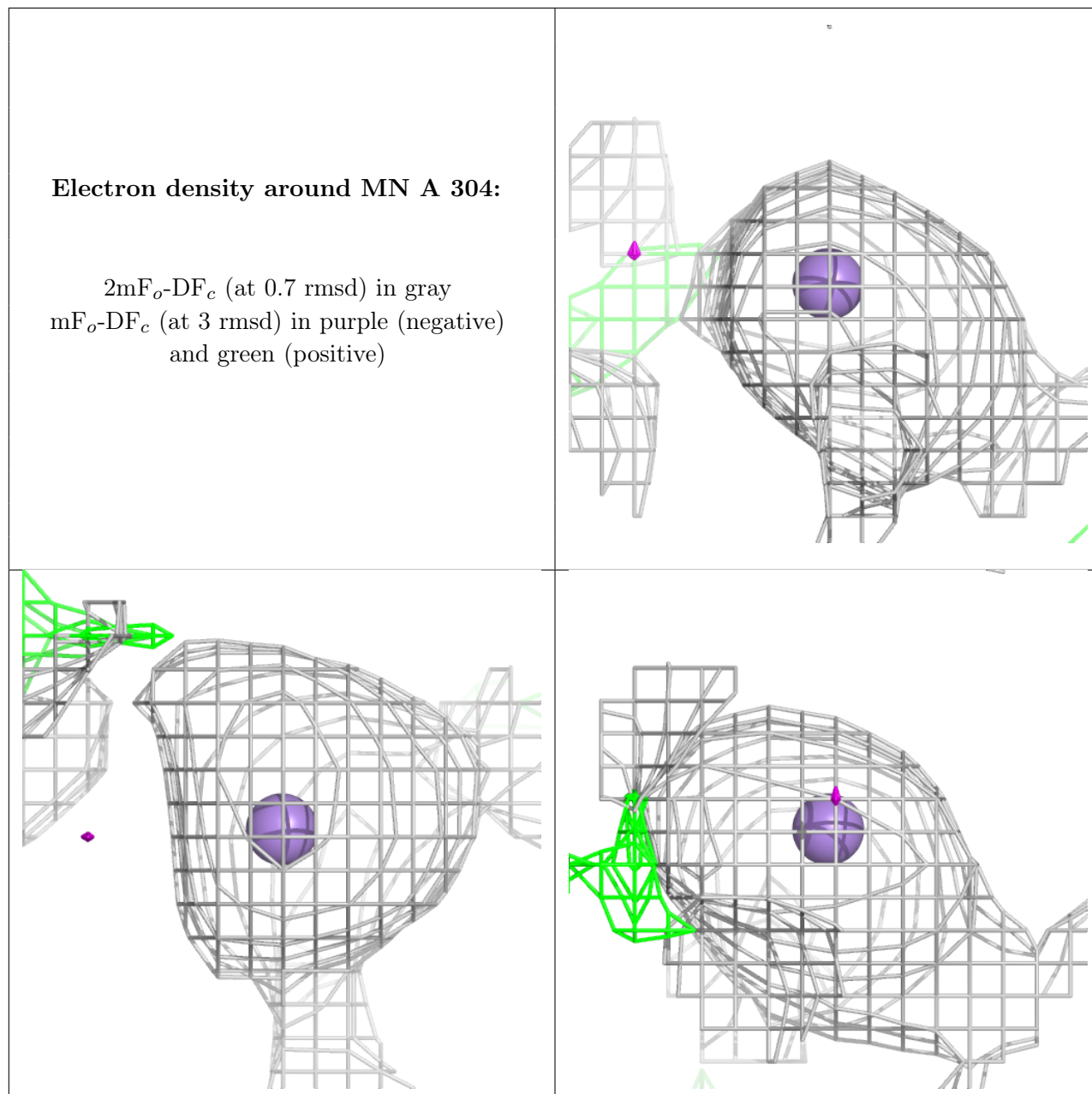
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	MN	A	304	1/1	0.86	0.16	110,110,110,110	0
3	COA	A	301	48/48	0.93	0.17	25,36,62,66	0
5	CAC	B	2201	5/5	0.94	0.18	119,119,120,121	0
4	MN	A	302	1/1	0.98	0.06	31,31,31,31	1
4	MN	A	303	1/1	1.00	0.14	24,24,24,24	1

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.

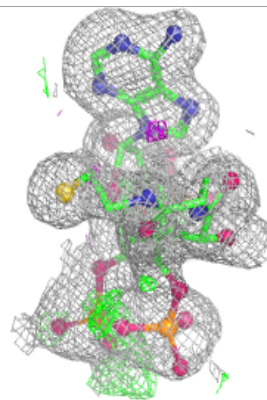
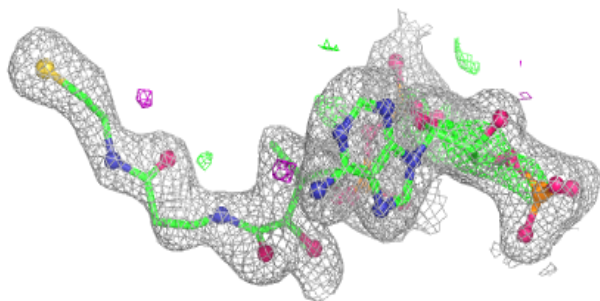
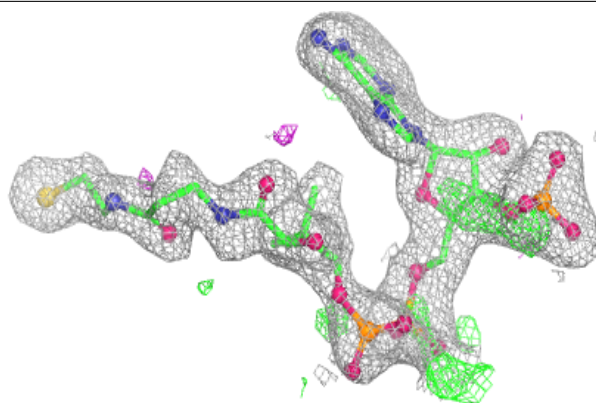
Electron density around MN A 304:

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



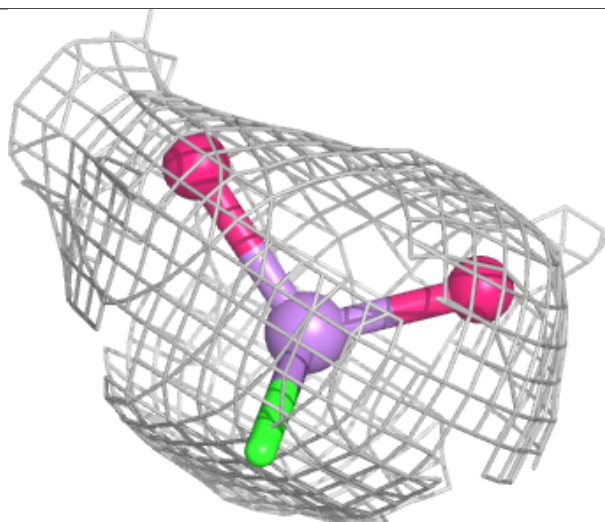
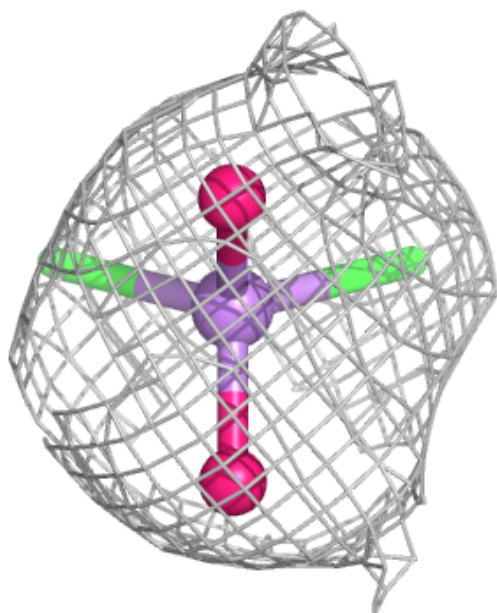
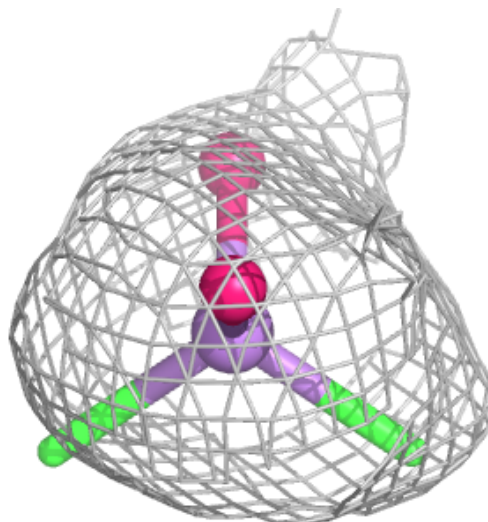
Electron density around COA A 301:

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



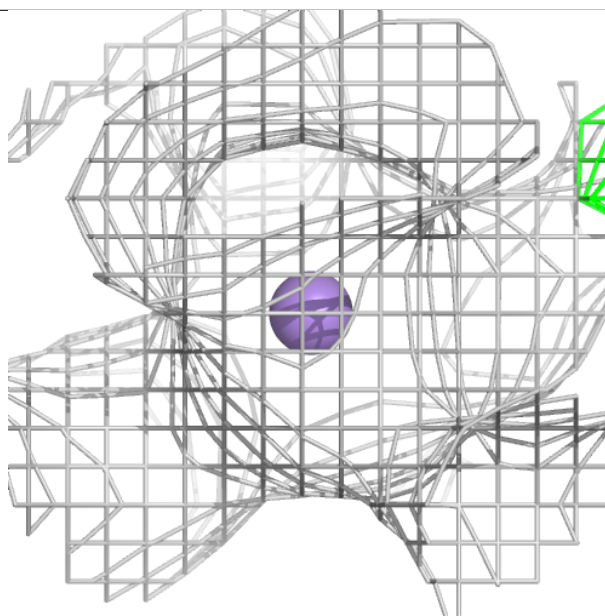
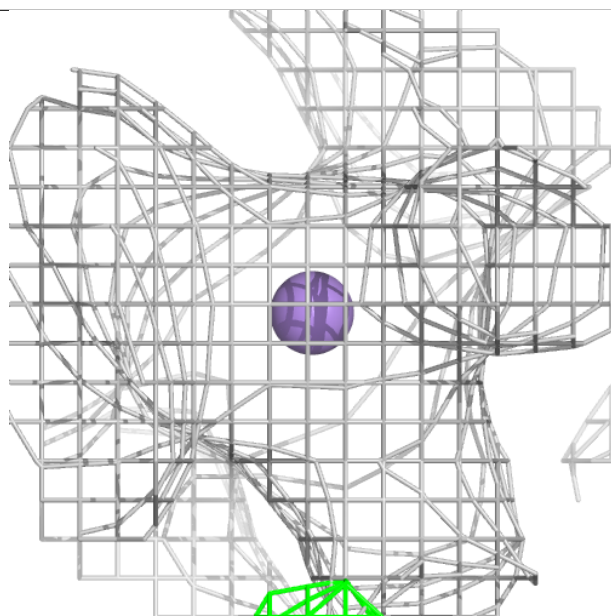
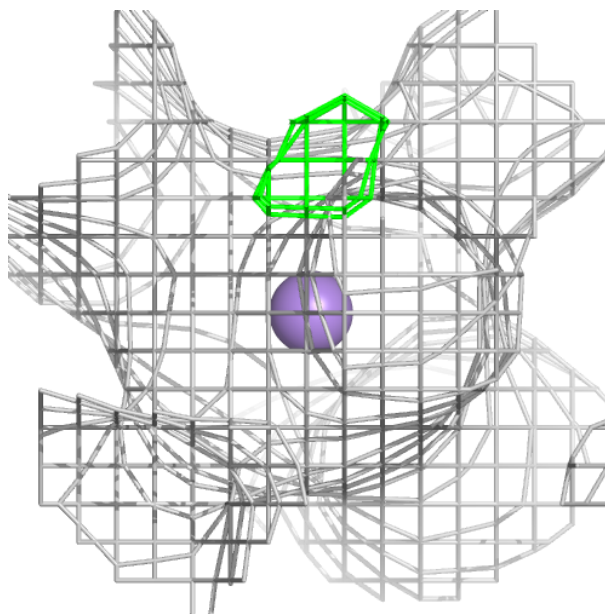
Electron density around CAC B 2201:

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



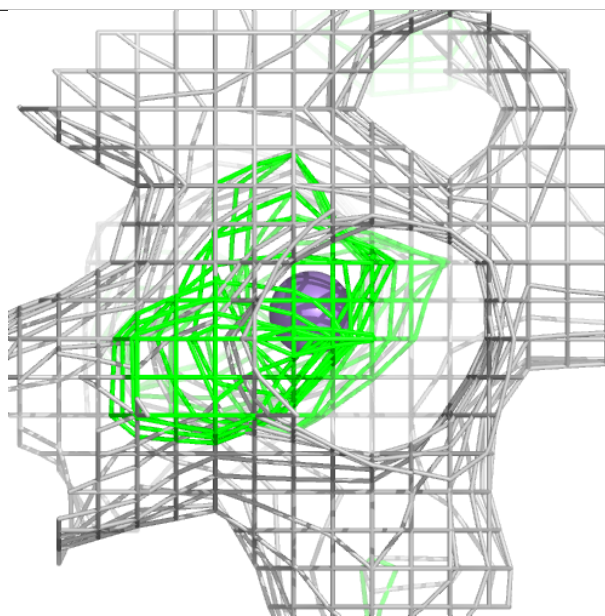
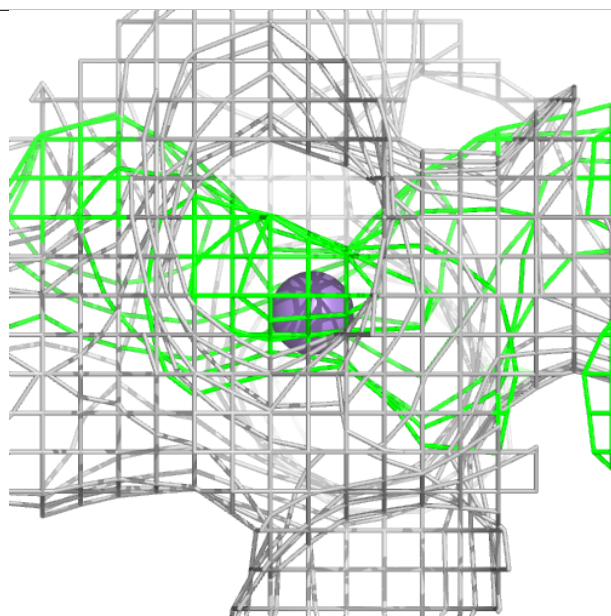
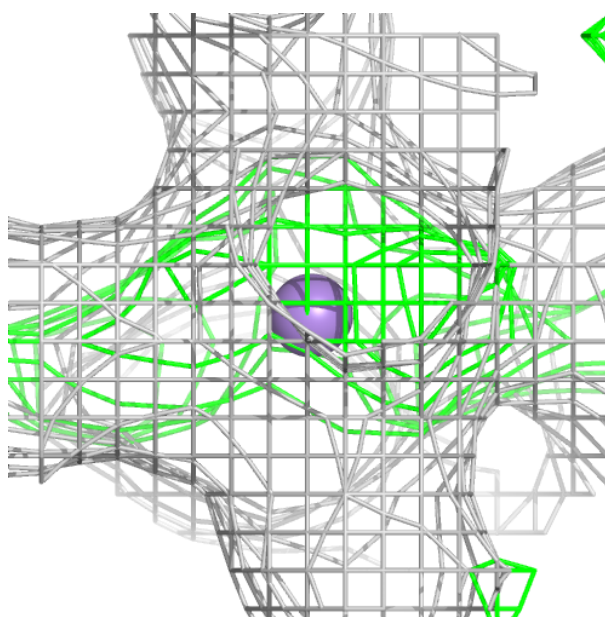
Electron density around MN A 302:

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



Electron density around MN A 303:

$2mF_o-DF_c$ (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.