



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 3, 2021 – 05:03 pm GMT

PDB ID : 7BDW
Title : Crystal structure of mycobacterial PptAb in complex with ACP and compound 8918
Authors : Carivenc, C.; Nguyen, M.C.; Mourey, L.; Pedelacq, J.D.
Deposited on : 2020-12-22
Resolution : 2.55 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4 (270009), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.23.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

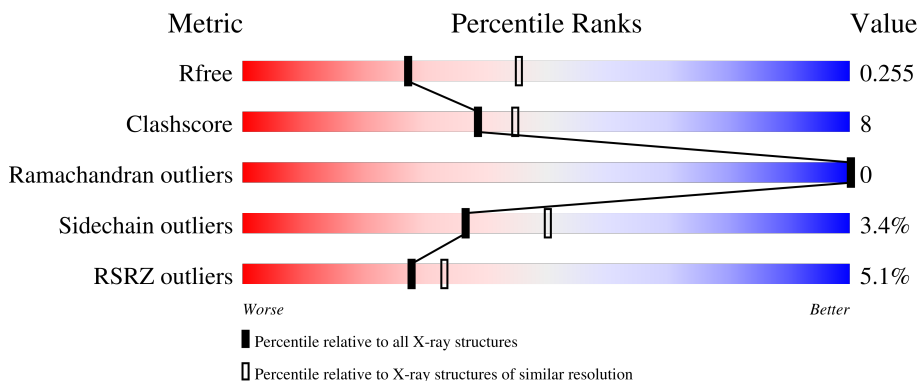
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	
2	B	157	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2290 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
			Total	C	N	O	S			
1	A	218	1673	1072	284	314	3	0	0	0

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
			Total	C	N	O	S			
2	B	75	561	355	98	105	3	0	0	0

There are 29 discrepancies between the modelled and reference sequences:

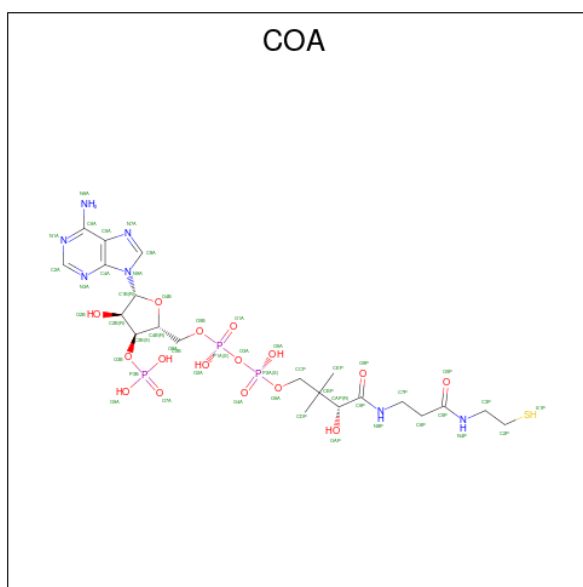
Chain	Residue	Modelled	Actual	Comment	Reference
B	2036	MET	-	initiating methionine	UNP A0A2I7WB16
B	2037	GLY	-	expression tag	UNP A0A2I7WB16
B	2038	SER	-	expression tag	UNP A0A2I7WB16

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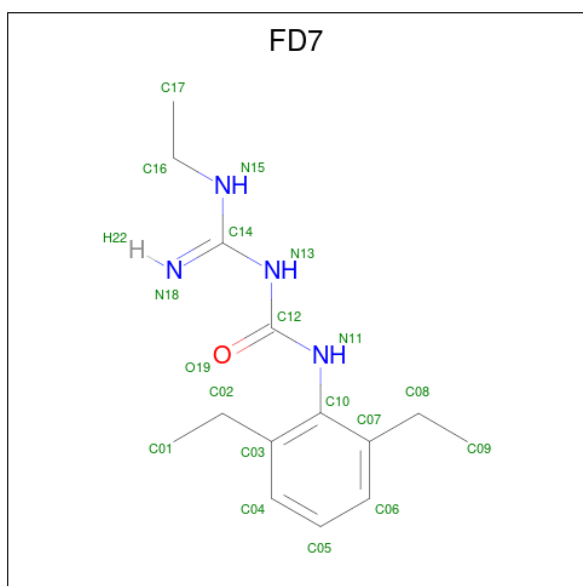
Chain	Residue	Modelled	Actual	Comment	Reference
B	2039	SER	-	expression tag	UNP A0A2I7WB16
B	2040	HIS	-	expression tag	UNP A0A2I7WB16
B	2041	HIS	-	expression tag	UNP A0A2I7WB16
B	2042	HIS	-	expression tag	UNP A0A2I7WB16
B	2043	HIS	-	expression tag	UNP A0A2I7WB16
B	2044	HIS	-	expression tag	UNP A0A2I7WB16
B	2045	HIS	-	expression tag	UNP A0A2I7WB16
B	2046	SER	-	expression tag	UNP A0A2I7WB16
B	2047	SER	-	expression tag	UNP A0A2I7WB16
B	2048	GLY	-	expression tag	UNP A0A2I7WB16
B	2049	LEU	-	expression tag	UNP A0A2I7WB16
B	2050	VAL	-	expression tag	UNP A0A2I7WB16
B	2051	PRO	-	expression tag	UNP A0A2I7WB16
B	2052	ARG	-	expression tag	UNP A0A2I7WB16
B	2053	GLY	-	expression tag	UNP A0A2I7WB16
B	2054	SER	-	expression tag	UNP A0A2I7WB16
B	2055	HIS	-	expression tag	UNP A0A2I7WB16
B	2056	MET	-	expression tag	UNP A0A2I7WB16
B	2057	ALA	-	expression tag	UNP A0A2I7WB16
B	2058	ILE	-	expression tag	UNP A0A2I7WB16
B	2059	ARG	-	expression tag	UNP A0A2I7WB16
B	2105	ALA	SER	engineered mutation	UNP A0A2I7WB16
B	2189	THR	-	expression tag	UNP A0A2I7WB16
B	2190	SER	-	expression tag	UNP A0A2I7WB16
B	2191	GLY	-	expression tag	UNP A0A2I7WB16
B	2192	SER	-	expression tag	UNP A0A2I7WB16

- Molecule 3 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	27	10	5	10	2	0	0

- Molecule 4 is N-(2,6-diethylphenyl)-N'-(N-ethylcarbamimidoyl)urea (three-letter code: FD7) (formula: $C_{14}H_{22}N_4O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	19	14	4	1	0	0

- Molecule 5 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mn	0	0
			2	2		


- Molecule 6 is water.

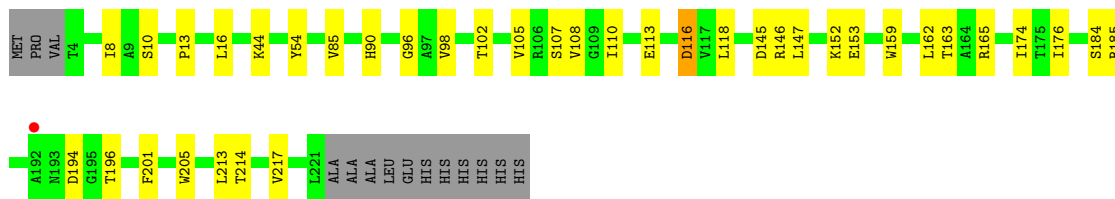
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	8	Total	O	0	0
			8	8		

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.

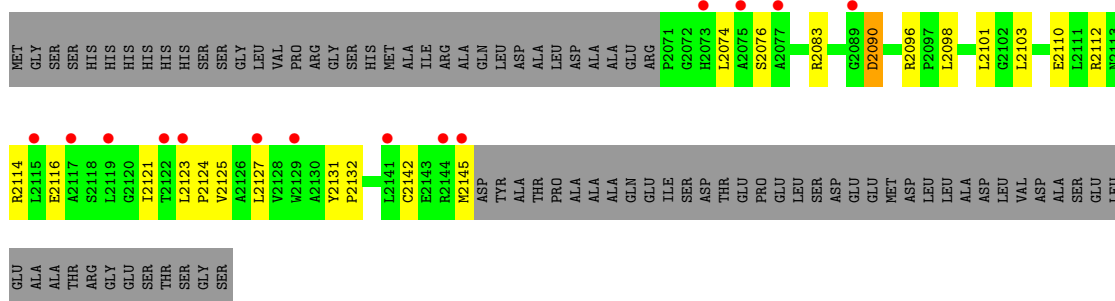
- Molecule 1: Possible 4'-phosphopantetheinyl transferase

Chain A:  78% 16% 6%



- Molecule 2: Phthiocerol synthesis polyketide synthase type I PpsC

Chain B:  9% 34% 13% 52%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.84Å 63.04Å 108.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.13 – 2.55 46.04 – 2.56	Depositor EDS
% Data completeness (in resolution range)	98.9 (41.13-2.55) 91.3 (46.04-2.56)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.19 (at 2.54Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.212 , 0.255 0.211 , 0.255	Depositor DCC
R_{free} test set	1175 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å ²)	58.9	Xtriage
Anisotropy	0.591	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2290	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.32% 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, FD7

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	0.25	0/1714	0.43	0/2343
2	B	0.22	0/571	0.40	0/779
All	All	0.24	0/2285	0.42	0/3122

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	1673	0	1672	21	1
2	B	561	0	570	13	0
3	A	27	0	11	0	0
4	A	19	0	0	1	0
5	A	2	0	0	0	0
6	A	8	0	0	0	0
All	All	2290	0	2253	34	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (34) 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:2098:LEU:HD22	2:B:2132:PRO:O	1.66	0.95
1:A:85:VAL:HG21	1:A:107:SER:HA	1.63	0.79
2:B:2142:CYS:HA	2:B:2145:MET:HG2	1.75	0.68
2:B:2124:PRO:HG2	2:B:2127:LEU:HD13	1.79	0.64
1:A:102:THR:HA	1:A:105:VAL:O	1.99	0.62
1:A:153:GLU:OE2	4:A:302:FD7:N13	2.33	0.61
2:B:2098:LEU:CD2	2:B:2132:PRO:O	2.44	0.60
1:A:194:ASP:OD2	1:A:196:THR:HG23	2.03	0.59
1:A:108:VAL:HG23	1:A:217:VAL:HG22	1.87	0.57
2:B:2096:ARG:HH11	2:B:2101:LEU:HG	1.69	0.56
1:A:147:LEU:HG	1:A:176:ILE:HD13	1.88	0.55
1:A:184:SER:HB2	1:A:201:PHE:HB2	1.87	0.55
1:A:107:SER:HB2	1:A:162:LEU:HD21	1.89	0.54
1:A:152:LYS:HG3	1:A:174:ILE:HD13	1.90	0.54
1:A:185:ARG:HG3	1:A:185:ARG:HH11	1.72	0.52
2:B:2110:GLU:O	2:B:2114:ARG:HG3	2.12	0.48
2:B:2112:ARG:NH1	2:B:2116:GLU:OE2	2.47	0.48
1:A:98:VAL:HG12	1:A:110:ILE:HD13	1.97	0.47
1:A:163:THR:HG22	1:A:165:ARG:H	1.80	0.46
2:B:2074:LEU:HD12	2:B:2074:LEU:O	2.16	0.45
2:B:2083:ARG:HD3	2:B:2090:ASP:O	2.17	0.45
1:A:118:LEU:HD12	1:A:145:ASP:HB2	1.97	0.45
2:B:2112:ARG:HD2	2:B:2125:VAL:HG12	1.98	0.45
2:B:2123:LEU:HD12	2:B:2124:PRO:HD2	1.98	0.45
1:A:159:TRP:CE2	1:A:163:THR:HG21	2.52	0.44
1:A:113:GLU:HB3	1:A:146:ARG:HD3	1.99	0.43
2:B:2127:LEU:HG	2:B:2131:TYR:HE2	1.83	0.43
2:B:2121:ILE:HD12	2:B:2121:ILE:O	2.18	0.43
1:A:205:TRP:HB3	1:A:214:THR:HG22	2.01	0.42
1:A:159:TRP:CZ2	1:A:163:THR:HG21	2.54	0.42
1:A:13:PRO:HG2	1:A:16:LEU:HD13	2.02	0.41
1:A:185:ARG:HG3	1:A:185:ARG:NH1	2.35	0.41
1:A:8:ILE:HD11	1:A:96:GLY:HA3	2.03	0.40
1:A:16:LEU:HD11	1:A:105:VAL:HG11	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:TYR:OH	1:A:116:ASP:OD1[3_554]	2.05	0.15

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	216/232 (93%)	208 (96%)	8 (4%)	0	100	100
2	B	73/157 (46%)	72 (99%)	1 (1%)	0	100	100
All	All	289/389 (74%)	280 (97%)	9 (3%)	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	179/192 (93%)	174 (97%)	5 (3%)	43	58
2	B	59/124 (48%)	56 (95%)	3 (5%)	24	32
All	All	238/316 (75%)	230 (97%)	8 (3%)	37	50

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

Mol	Chain	Res	Type
1	A	10	SER
1	A	44	LYS
1	A	90	HIS
1	A	116	ASP
1	A	213	LEU
2	B	2076	SER
2	B	2090	ASP
2	B	2103	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	2094	HIS

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

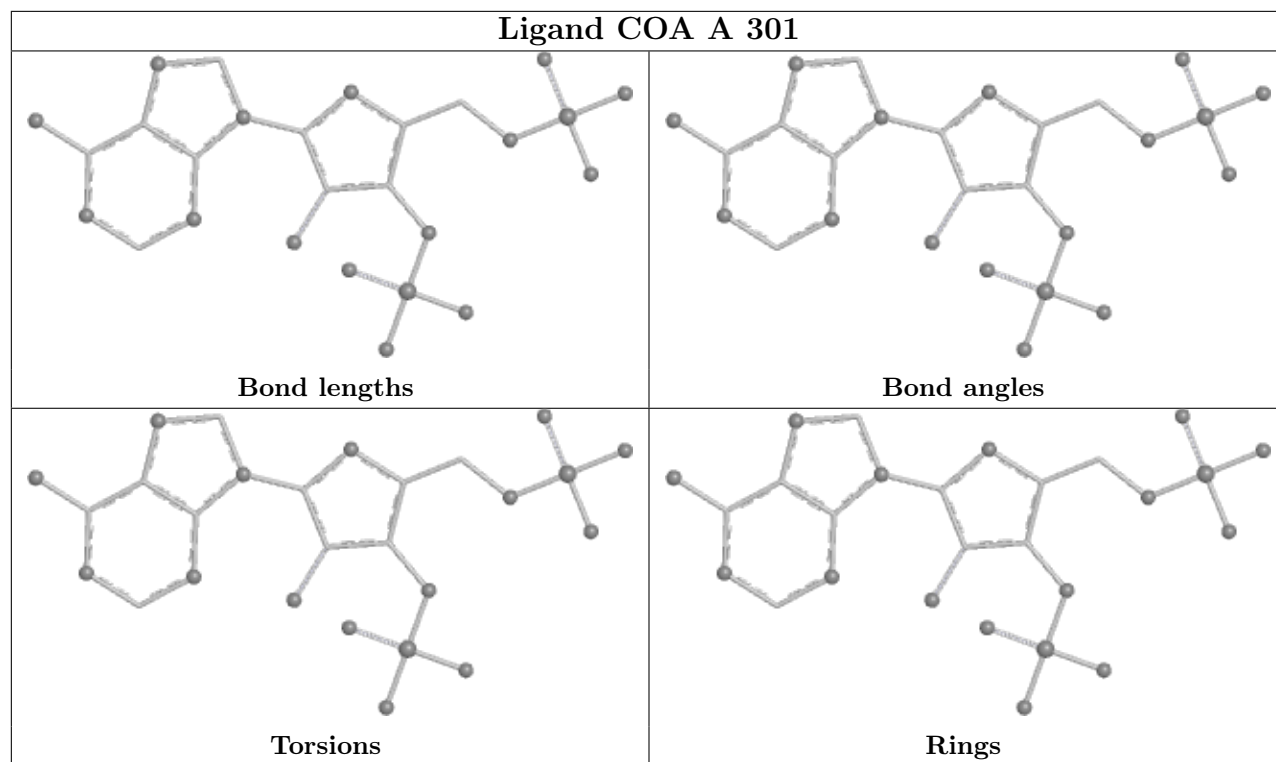
There are no chirality outliers.

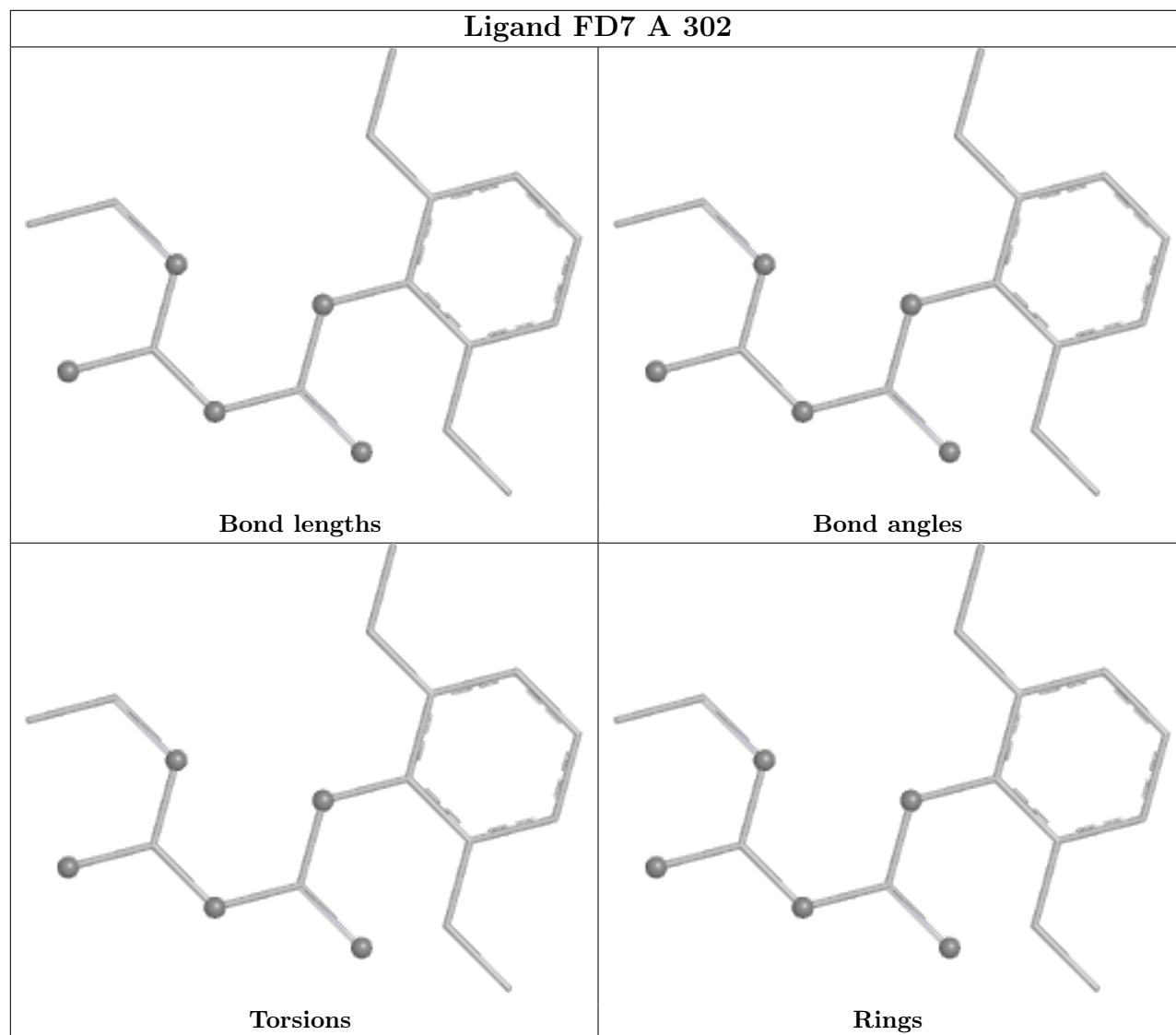
There are no torsion outliers.

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	A	218/232 (93%)	0.01	1 (0%) 91 94	50, 71, 108, 139	0
2	B	75/157 (47%)	0.83	14 (18%) 1 1	55, 100, 137, 164	0
All	All	293/389 (75%)	0.22	15 (5%) 28 33	50, 74, 129, 164	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	2127	LEU	4.8
2	B	2073	HIS	4.6
2	B	2075	ALA	4.3
2	B	2089	GLY	3.4
2	B	2119	LEU	3.2
2	B	2141	LEU	2.8
2	B	2117	ALA	2.6
2	B	2129	TRP	2.6
2	B	2115	LEU	2.6
2	B	2123	LEU	2.5
2	B	2145	MET	2.4
2	B	2122	THR	2.4
2	B	2144	ARG	2.4
1	A	192	ALA	2.1
2	B	2077	ALA	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 monosaccharides in this entry.

6.4 Ligands

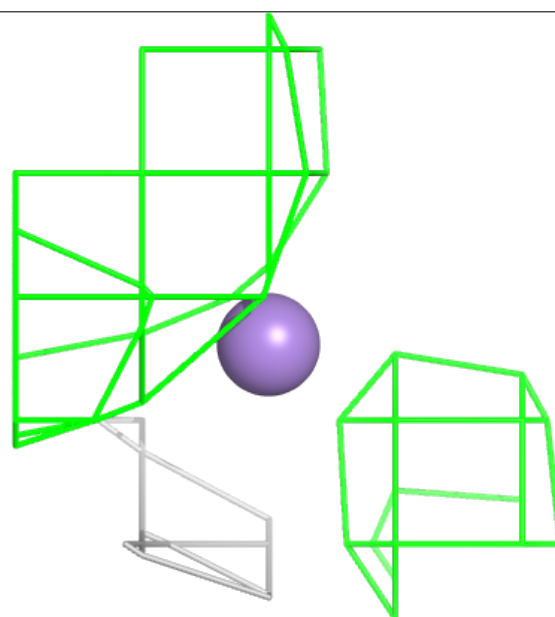
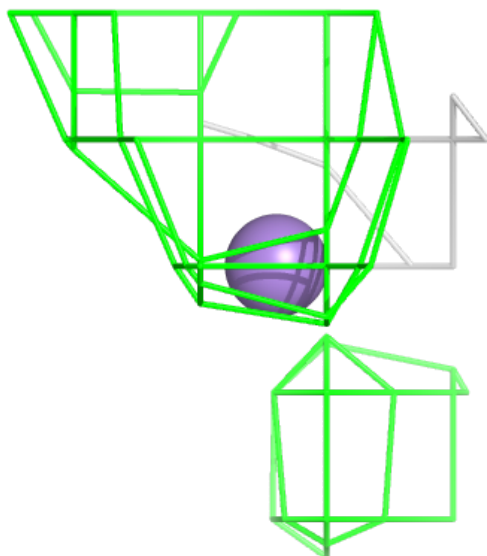
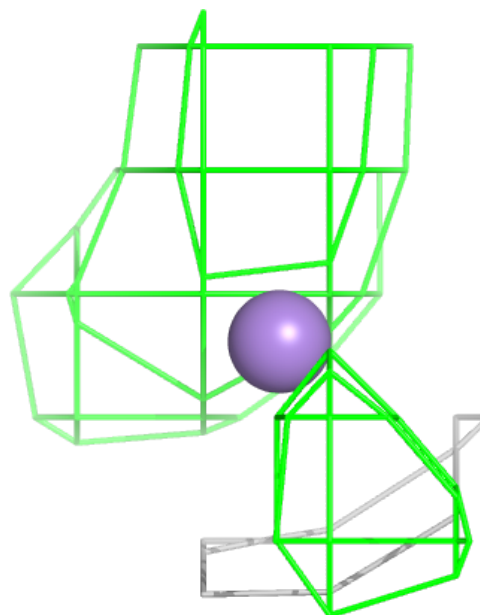
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MN	A	303	1/1	0.89	0.21	96,96,96,96	0
4	FD7	A	302	19/19	0.92	0.21	64,75,83,85	0
3	COA	A	301	27/48	0.94	0.16	42,70,85,87	0
5	MN	A	304	1/1	0.94	0.13	56,56,56,56	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.

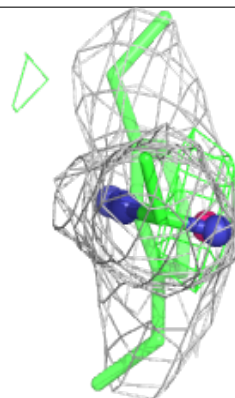
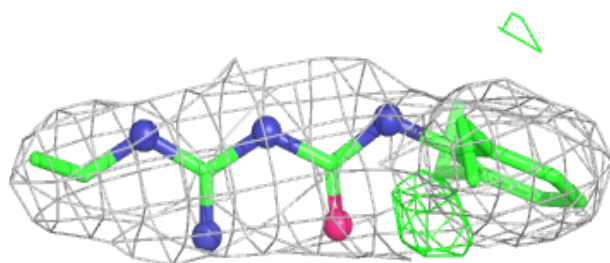
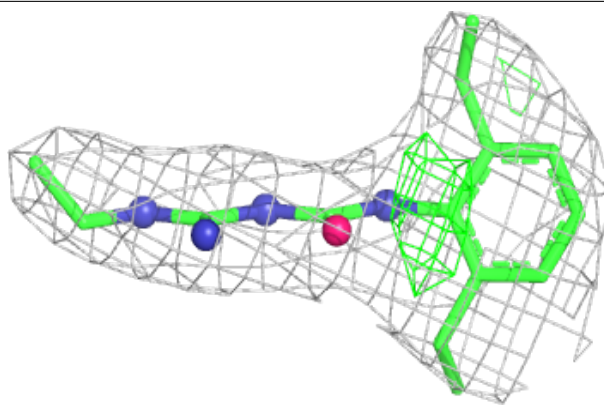
Electron density around MN A 303:

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



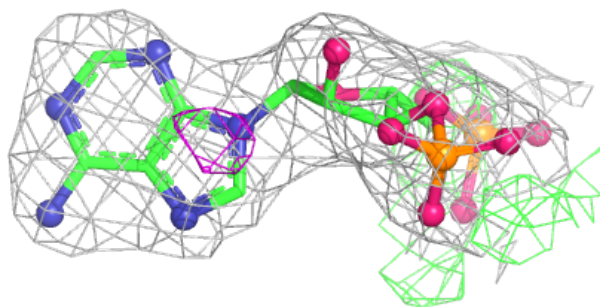
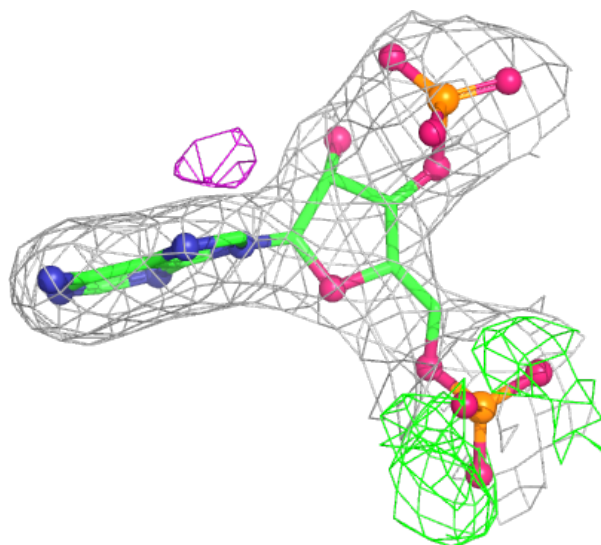
Electron density around FD7 A 302:

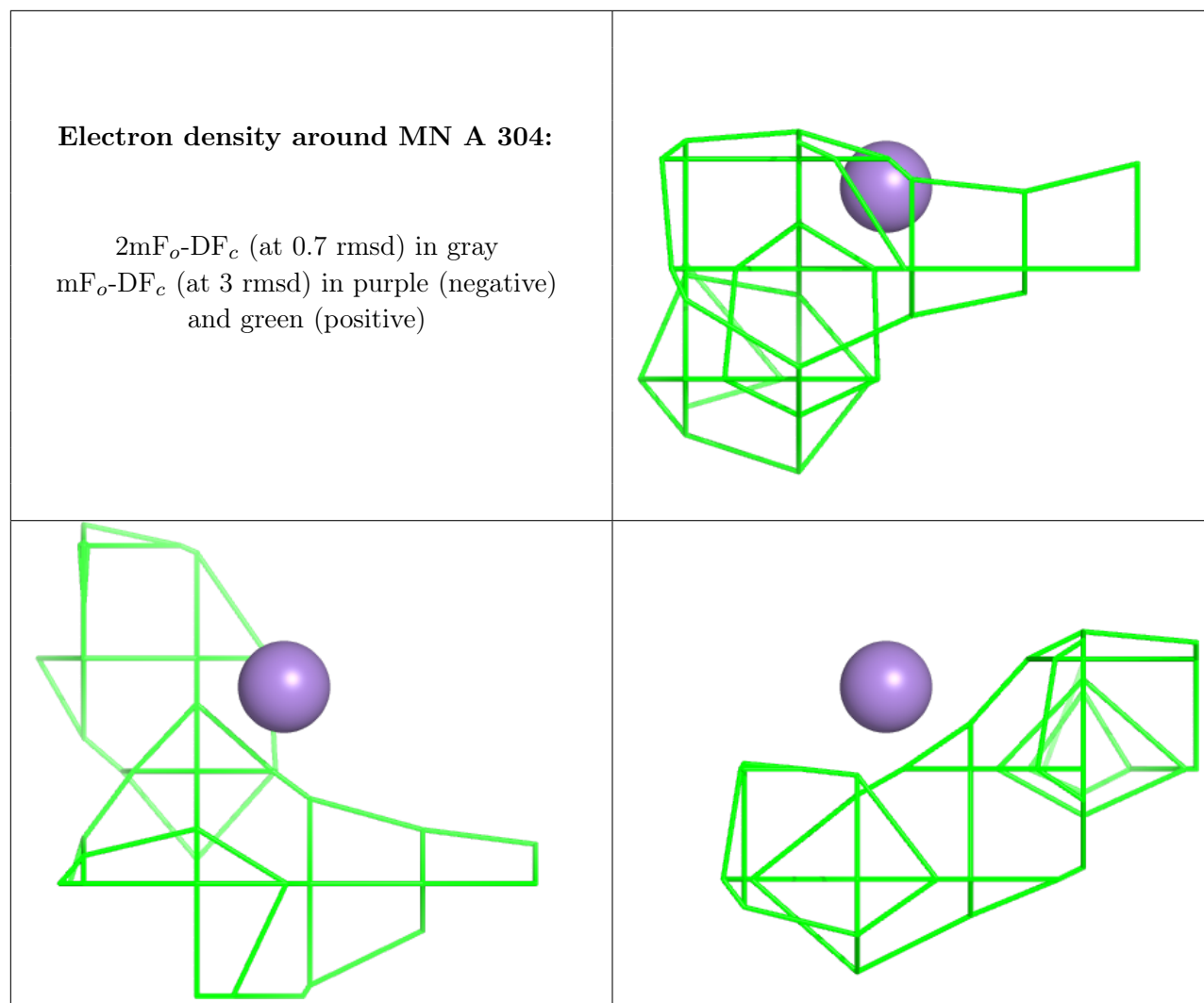
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.