



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 22, 2021 – 09:04 am GMT

PDB ID : 7OYH
Title : Crystal structure of depupylase Dop in complex with Pup and ADP/tetrafluoromagnesate
Authors : Cui, H.
Deposited on : 2021-06-24
Resolution : 1.75 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)
Xtriage (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

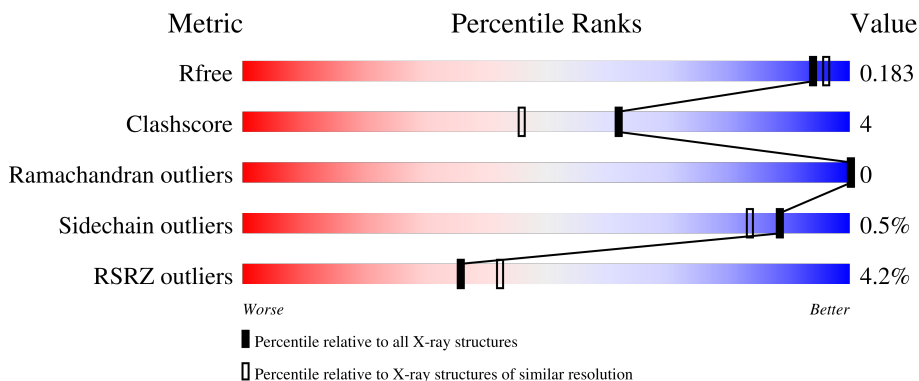
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	508	 4% 85% 8% 7%
2	B	28	 7% 89% 11%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	ACT	A	621	-	-	X	-
7	ACT	A	622	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 4638 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 Depupylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	471	3862	2419	711	712	20	0	18	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	503	GLU	-	expression tag	UNP A0LU48
A	504	ASN	-	expression tag	UNP A0LU48
A	505	LEU	-	expression tag	UNP A0LU48
A	506	TYR	-	expression tag	UNP A0LU48
A	507	PHE	-	expression tag	UNP A0LU48
A	508	GLN	-	expression tag	UNP A0LU48

- Molecule 2 is a protein called Prokaryotic ubiquitin-like protein Pup.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	28	225	138	34	53	0	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	Mg	0	0
			4	4		
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



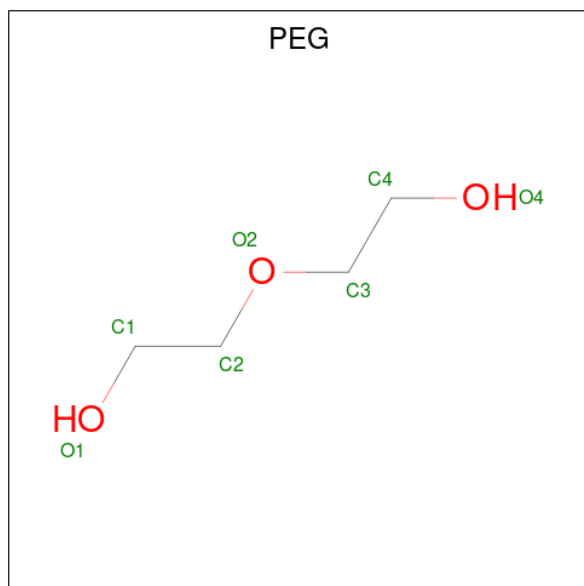
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	C O		
5	A	1	8	4 4	0	1
5	A	1	4	2 2	0	0
5	A	1	4	2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 8 4 4	0	1

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



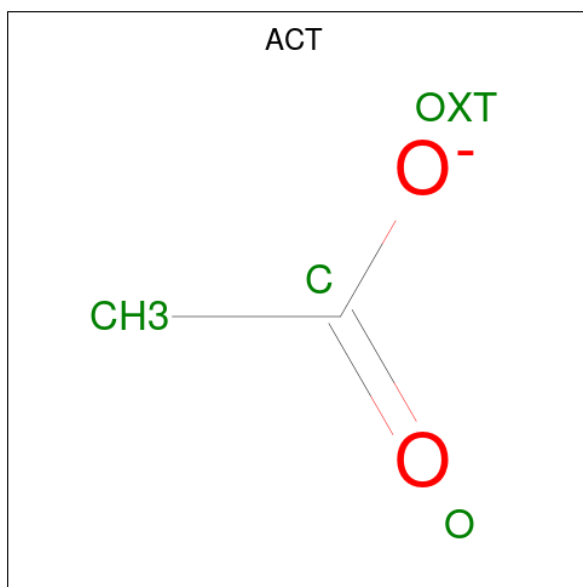
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 7 4 3	0	0
6	A	1	Total C O 7 4 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	1
			14	8	6		
6	A	1	Total	C	O	0	1
			14	8	6		

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



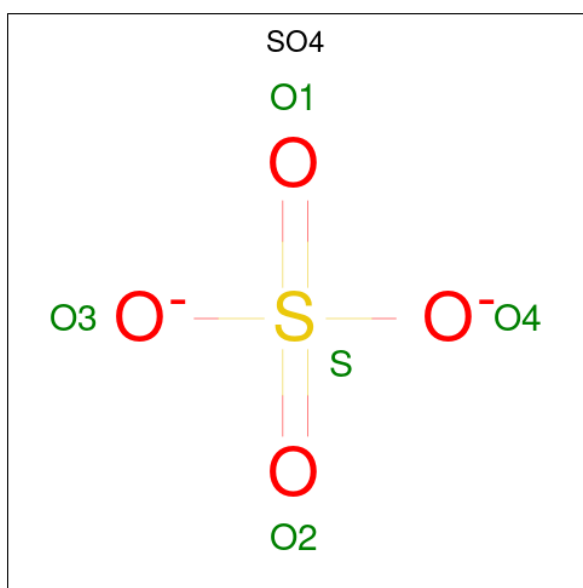
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



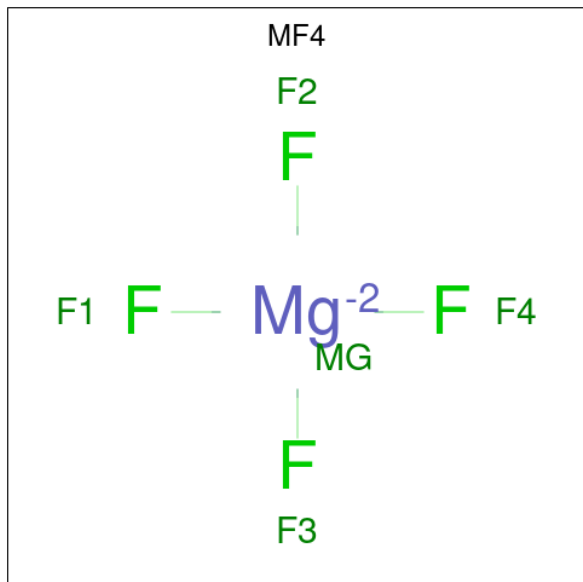
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 10 6 4	0	0
8	A	1	Total C O 10 6 4	0	0

- Molecule 9 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total O S 5 4 1	0	0
9	A	1	Total O S 5 4 1	0	0

- Molecule 10 is TETRAFLUOROMAGNESATE(2-) (three-letter code: MF4) (formula: F_4Mg) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	F	Mg		
10	A	1	5	4	1	0	0

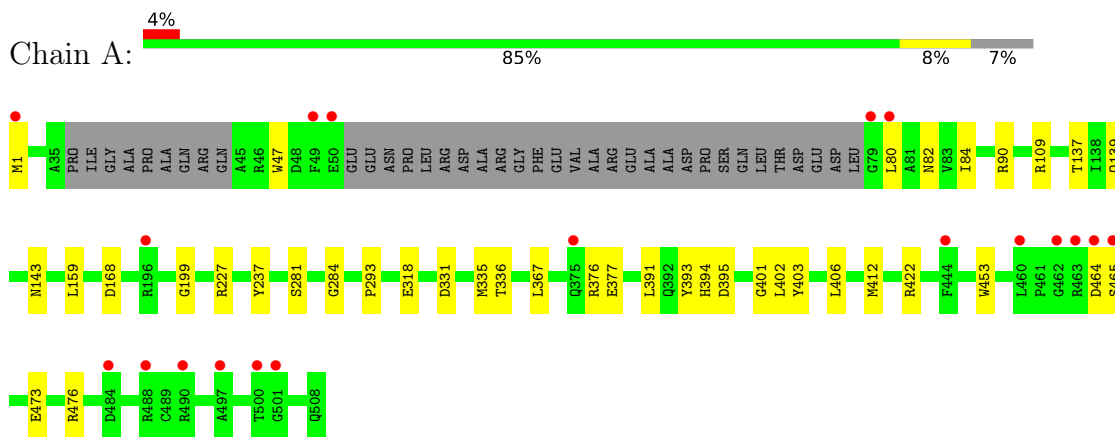
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
11	A	338	338	338	0	0
11	B	36	36	36	0	0

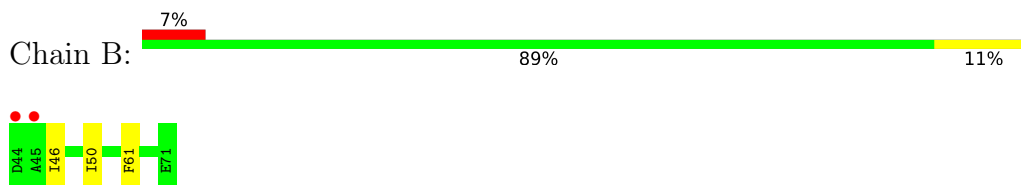
3 Residue-property plots [i](#)

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: Depupylase



- Molecule 2: Prokaryotic ubiquitin-like protein Pup



4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	106.83Å 106.83Å 107.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.87 – 1.75 47.87 – 1.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.87-1.75) 100.0 (47.87-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 1.75Å)	Xtrriage
Refinement program	PHENIX 1.19_4092	Depositor
R, R_{free}	0.162 , 0.184 0.161 , 0.183	Depositor DCC
R_{free} test set	3622 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	23.4	Xtrriage
Anisotropy	0.117	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.013 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4638	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% 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: PEG, EDO, MG, PGE, ACT, SO4, ADP, MF4

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	0.37	0/3984	0.64	0/5396
2	B	0.34	0/226	0.55	0/302
All	All	0.37	0/4210	0.64	0/5698

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	3862	0	3818	34	0
2	B	225	0	203	2	0
3	A	4	0	0	0	0
3	B	1	0	0	0	0
4	A	27	0	12	0	0
5	A	44	0	66	2	0
5	B	12	0	18	0	0
6	A	42	0	60	1	0
7	A	12	0	9	5	0
8	A	20	0	28	4	0
9	A	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	A	5	0	0	1	0
11	A	338	0	0	5	0
11	B	36	0	0	0	0
All	All	4638	0	4214	37	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 4.

All (37) 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:A:82:ASN:HD21	1:A:90:ARG:HH21	1.29	0.80
1:A:293:PRO:HG2	8:A:623:PGE:H22	1.74	0.69
1:A:168:ASP:OD2	5:A:610:EDO:H21	1.96	0.66
1:A:47:TRP:CE3	1:A:84:ILE:HD11	2.33	0.64
9:A:625:SO4:O3	11:A:701:HOH:O	2.15	0.62
1:A:393:TYR:HA	1:A:402:LEU:HB2	1.88	0.55
1:A:376[B]:ARG:NH2	1:A:377:GLU:OE2	2.34	0.55
1:A:391[B]:LEU:HD23	2:B:61:PHE:HE1	1.72	0.55
1:A:47:TRP:CZ3	1:A:84:ILE:HD11	2.44	0.52
1:A:464:ASP:HB2	7:A:622:ACT:H1	1.91	0.51
1:A:137:THR:HG22	1:A:139[B]:GLN:OE1	2.09	0.51
1:A:473[A]:GLU:HG2	1:A:476:ARG:HG3	1.93	0.51
1:A:47:TRP:HH2	1:A:453:TRP:CD1	2.29	0.50
1:A:281:SER:HB3	7:A:621:ACT:H1	1.92	0.50
1:A:82:ASN:HD21	1:A:90:ARG:NH2	2.05	0.49
2:B:46:ILE:O	2:B:50:ILE:HG12	2.12	0.48
1:A:82:ASN:ND2	1:A:90:ARG:HH21	2.06	0.47
1:A:284:GLY:H	7:A:621:ACT:H1	1.80	0.47
1:A:159:LEU:HD11	1:A:237:TYR:HB3	1.96	0.47
1:A:465:SER:HB2	7:A:622:ACT:H2	1.97	0.46
1:A:473[A]:GLU:HG2	5:A:609:EDO:H21	1.97	0.46
1:A:80:LEU:HB2	11:A:863:HOH:O	2.15	0.46
1:A:284:GLY:H	7:A:621:ACT:CH3	2.30	0.45
1:A:335:MET:HA	6:A:616:PEG:H22	1.99	0.44
1:A:47:TRP:HE3	1:A:84:ILE:HD11	1.79	0.44
1:A:199:GLY:HA3	8:A:623:PGE:H52	1.98	0.44
1:A:367:LEU:HD21	8:A:623:PGE:H1	1.99	0.44
1:A:139[A]:GLN:HG3	11:A:907:HOH:O	2.18	0.43
1:A:109[A]:ARG:HD3	11:A:853:HOH:O	2.18	0.43
1:A:395:ASP:HB3	1:A:401:GLY:HA2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:TYR:CE1	1:A:412[A]:MET:HG2	2.54	0.42
1:A:1[B]:MET:HG2	1:A:336:THR:OG1	2.19	0.42
1:A:227:ARG:NH1	10:A:627:MF4:F2	2.30	0.41
1:A:406:LEU:HB3	1:A:412[B]:MET:HG2	2.03	0.41
8:A:624:PGE:H3	11:A:740:HOH:O	2.21	0.40
1:A:143:ASN:HB3	1:A:394:HIS:CG	2.57	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	482/508 (95%)	474 (98%)	8 (2%)	0	100	100
2	B	26/28 (93%)	26 (100%)	0	0	100	100
All	All	508/536 (95%)	500 (98%)	8 (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	409/420 (97%)	407 (100%)	2 (0%)	88	83
2	B	24/24 (100%)	24 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	433/444 (98%)	431 (100%)	2 (0%)	88	83

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	331	ASP
1	A	422	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 [i](#)

Of 34 ligands modelled in this entry, 5 are monoatomic - leaving 29 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

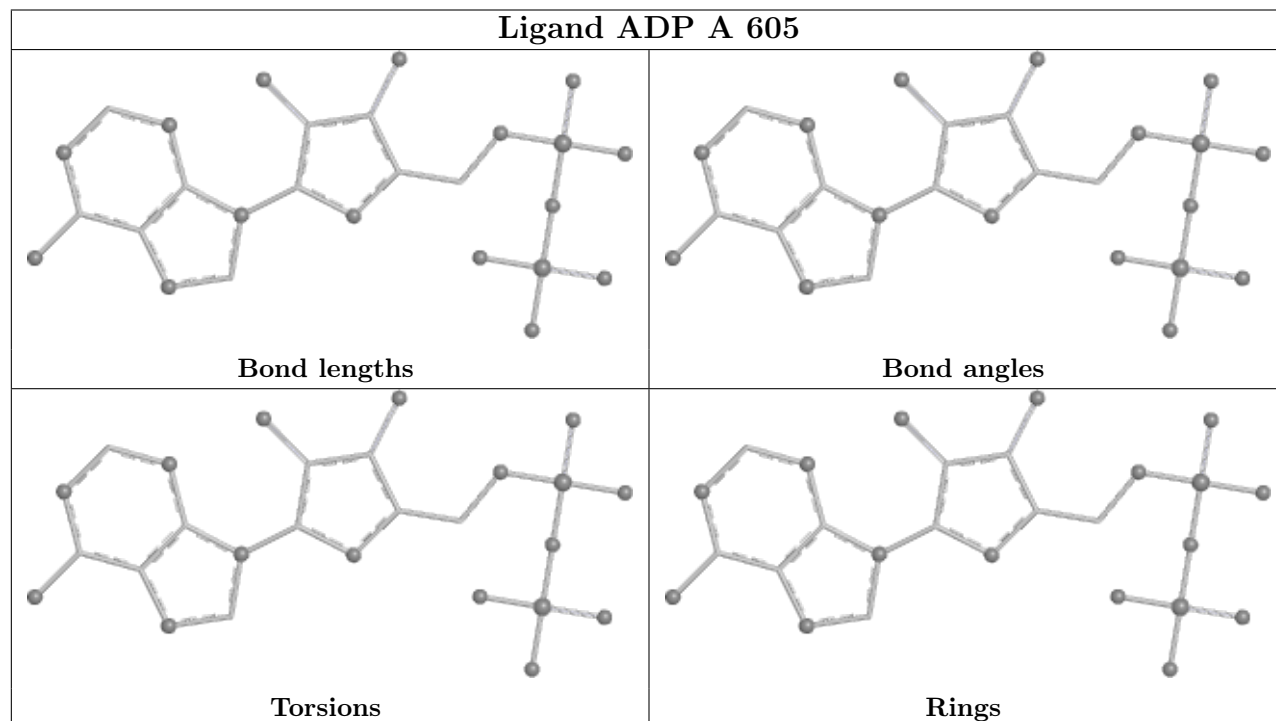
There are no torsion outliers.

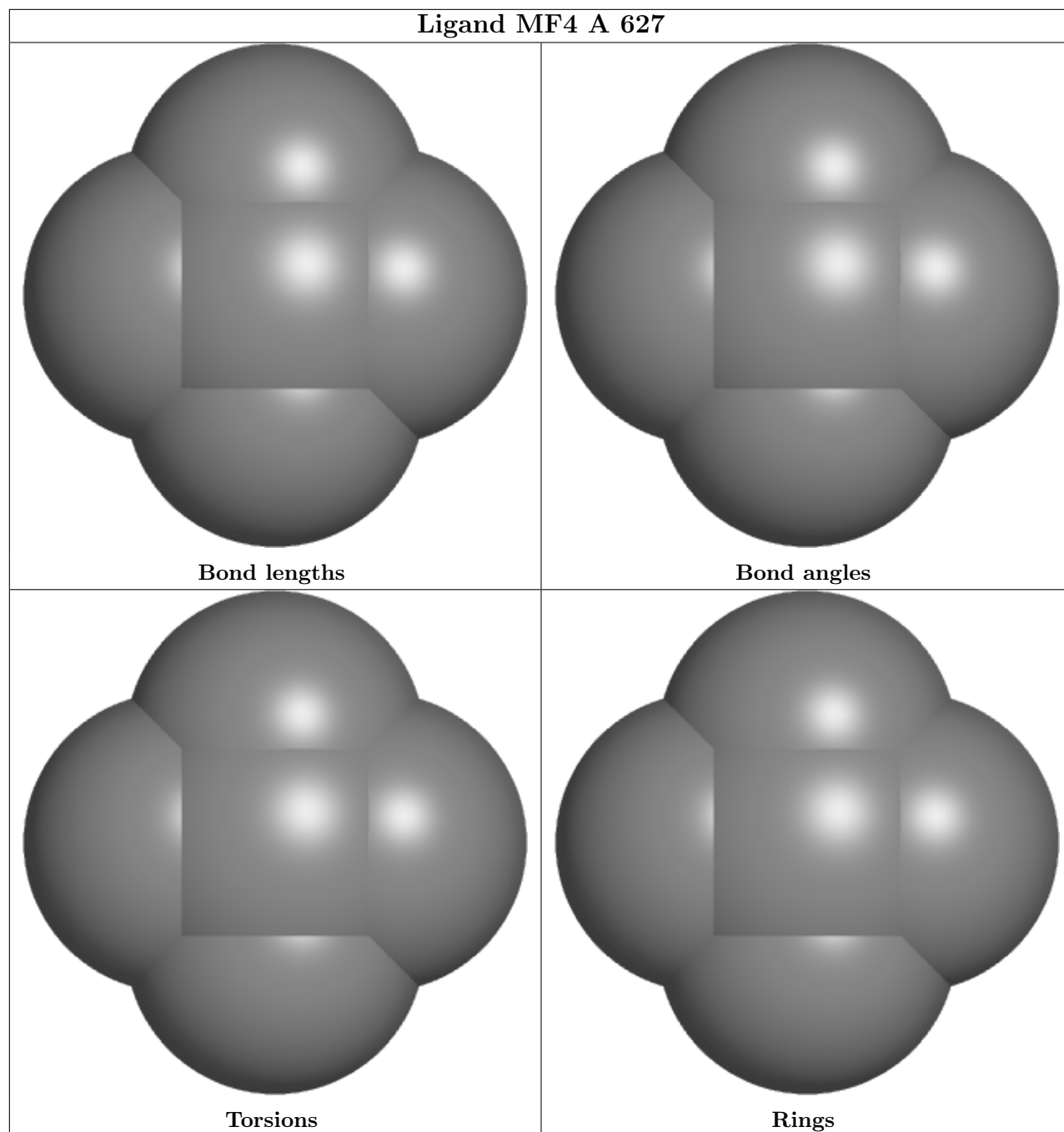
There are no ring outliers.

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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	471/508 (92%)	-0.04	19 (4%) 38 45	15, 23, 45, 82	5 (1%)
2	B	28/28 (100%)	0.01	2 (7%) 16 21	20, 29, 46, 61	0
All	All	499/536 (93%)	-0.03	21 (4%) 36 42	15, 24, 45, 82	5 (1%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1[A]	MET	5.2
1	A	49	PHE	4.6
1	A	490	ARG	3.5
1	A	464	ASP	3.3
2	B	44	ASP	3.0
1	A	462	GLY	2.9
1	A	497	ALA	2.9
1	A	465	SER	2.8
1	A	488	ARG	2.8
1	A	196	ARG	2.7
1	A	500	THR	2.6
1	A	50	GLU	2.4
1	A	79	GLY	2.3
1	A	463	ARG	2.3
2	B	45	ALA	2.3
1	A	501	GLY	2.3
1	A	80	LEU	2.2
1	A	444	PHE	2.2
1	A	460	LEU	2.2
1	A	484	ASP	2.2
1	A	375	GLN	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(Å ²)	Q<0.9
5	EDO	A	609	4/4	0.56	0.20	45,46,52,59	0
5	EDO	A	610	4/4	0.61	0.16	46,52,52,54	0
7	ACT	A	620	4/4	0.61	0.16	44,53,54,60	0
6	PEG	A	618[B]	7/7	0.65	0.20	40,49,51,52	7
6	PEG	A	618[A]	7/7	0.65	0.20	46,50,53,54	7
5	EDO	B	102	4/4	0.68	0.26	56,59,61,61	0
6	PEG	A	617	7/7	0.71	0.21	50,52,58,58	0
8	PGE	A	624	10/10	0.77	0.18	45,59,72,75	0
6	PEG	A	619[B]	7/7	0.78	0.15	40,43,46,48	7
5	EDO	A	608	4/4	0.78	0.31	55,63,63,69	0
6	PEG	A	619[A]	7/7	0.78	0.15	34,44,47,48	7
8	PGE	A	623	10/10	0.81	0.47	39,47,55,57	0
6	PEG	A	616	7/7	0.84	0.23	36,43,51,54	0
5	EDO	A	613	4/4	0.85	0.16	37,39,47,49	0
5	EDO	A	606[A]	4/4	0.87	0.19	33,43,43,43	4
5	EDO	A	606[B]	4/4	0.87	0.19	40,42,42,45	4
5	EDO	B	103[B]	4/4	0.88	0.17	28,37,38,40	4
5	EDO	B	103[A]	4/4	0.88	0.17	27,36,39,40	4
5	EDO	A	611	4/4	0.89	0.14	32,38,43,46	0
7	ACT	A	621	4/4	0.90	0.19	33,35,35,48	0
5	EDO	A	614	4/4	0.91	0.15	40,49,50,51	0
5	EDO	A	612	4/4	0.91	0.24	45,45,51,55	0
5	EDO	A	607	4/4	0.92	0.16	30,31,41,47	0
7	ACT	A	622	4/4	0.92	0.09	51,53,56,61	0
3	MG	A	604	1/1	0.93	0.19	49,49,49,49	0
5	EDO	A	615	4/4	0.93	0.21	49,55,55,59	0
9	SO4	A	626	5/5	0.95	0.25	52,63,77,82	0

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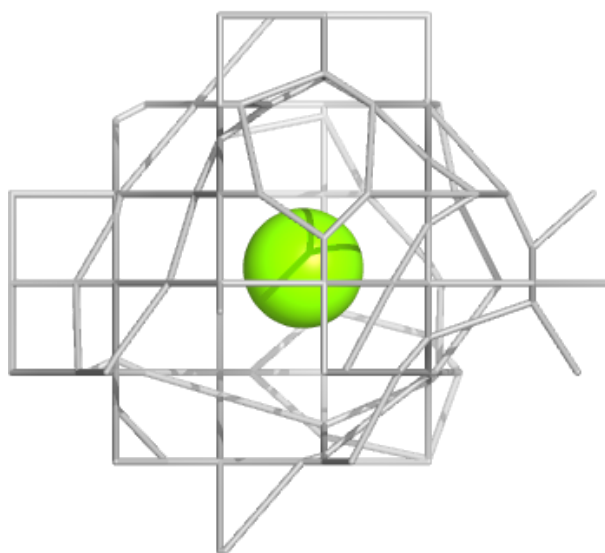
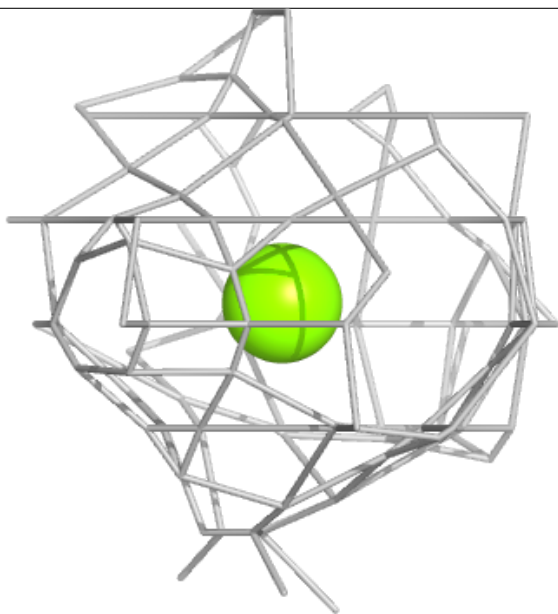
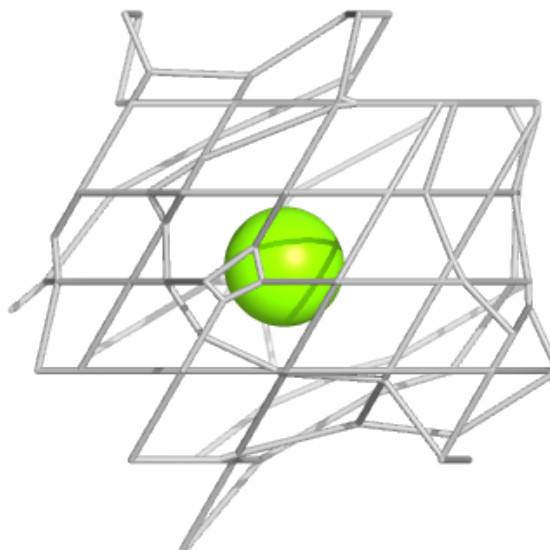
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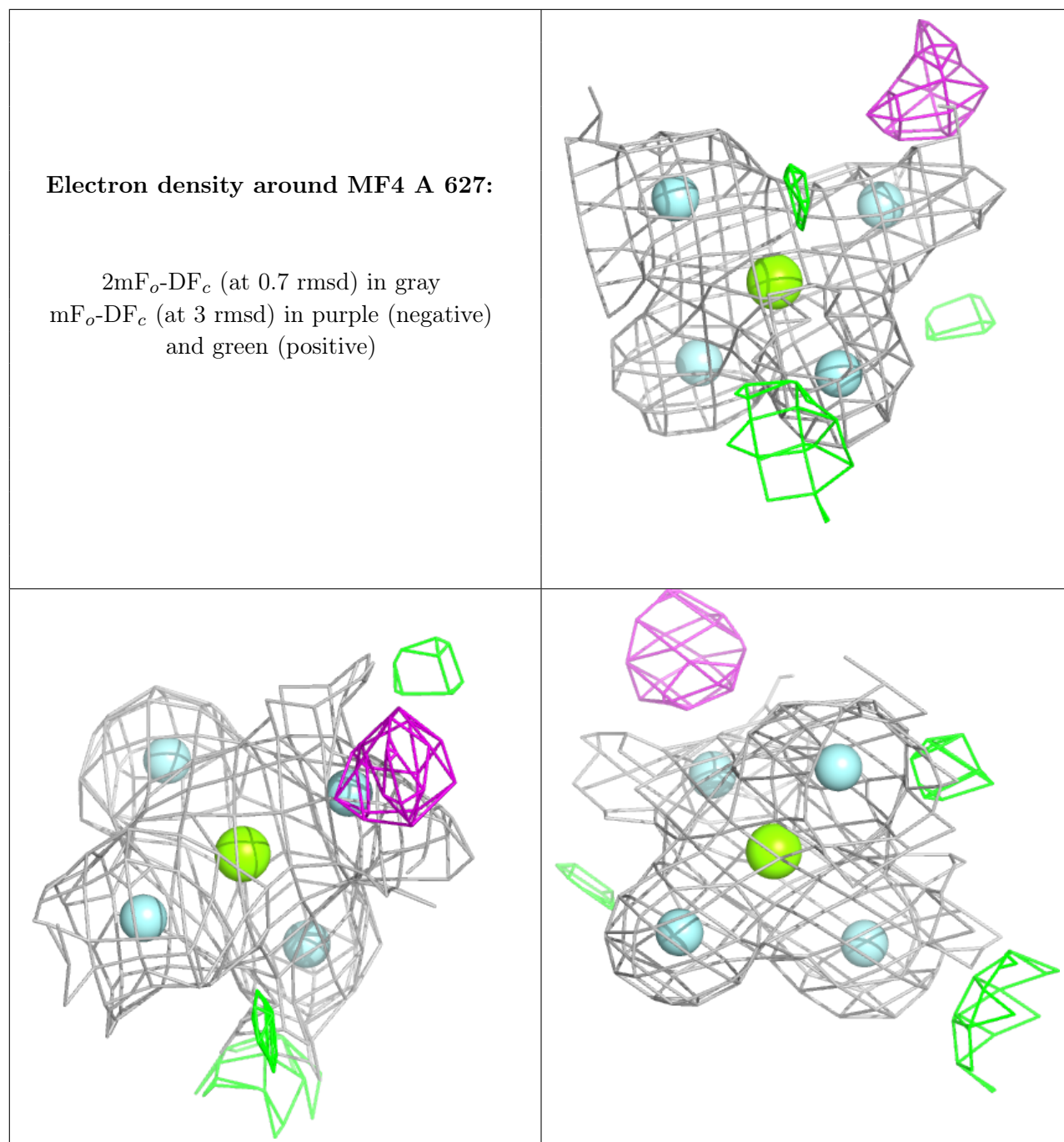
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
9	SO4	A	625	5/5	0.96	0.08	19,24,31,33	5
10	MF4	A	627	5/5	0.97	0.10	23,24,27,37	5
4	ADP	A	605	27/27	0.98	0.07	18,22,27,29	0
3	MG	A	603	1/1	0.99	0.21	31,31,31,31	0
3	MG	A	601	1/1	0.99	0.04	20,20,20,20	0
3	MG	B	101	1/1	0.99	0.04	22,22,22,22	0
3	MG	A	602	1/1	0.99	0.06	19,19,19,19	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 MG A 604:

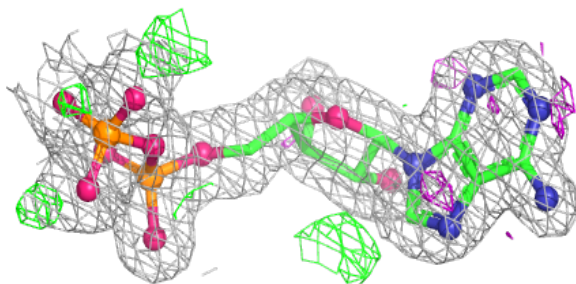
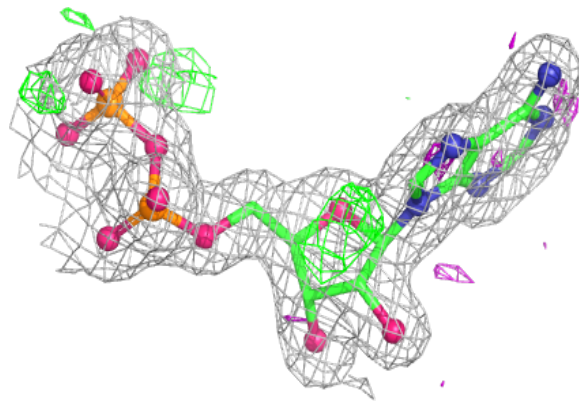
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





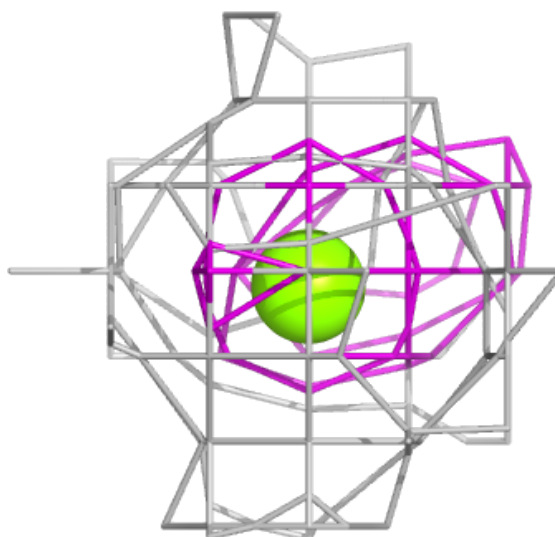
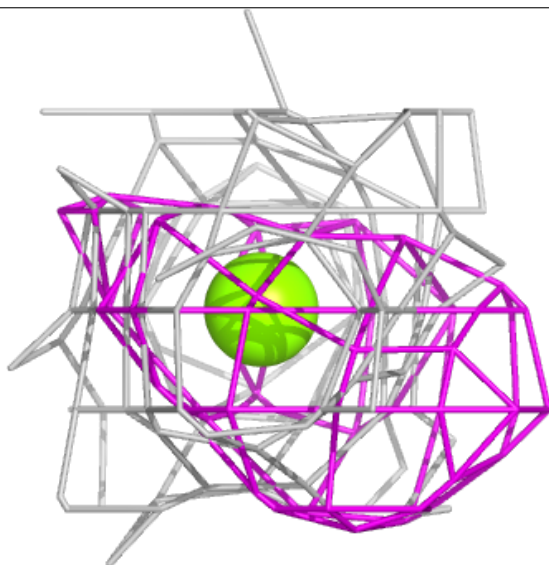
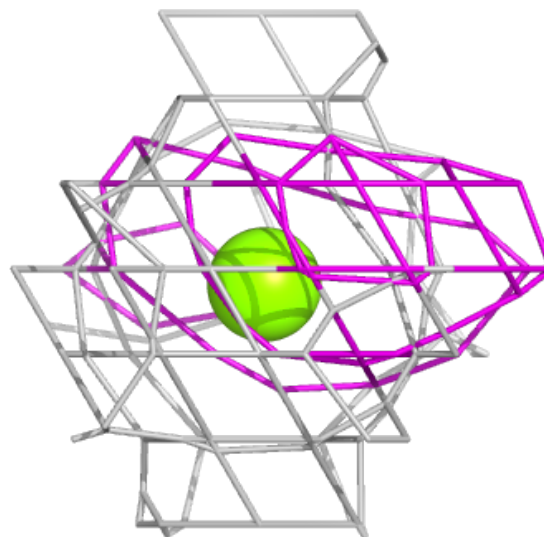
Electron density around ADP A 605:

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



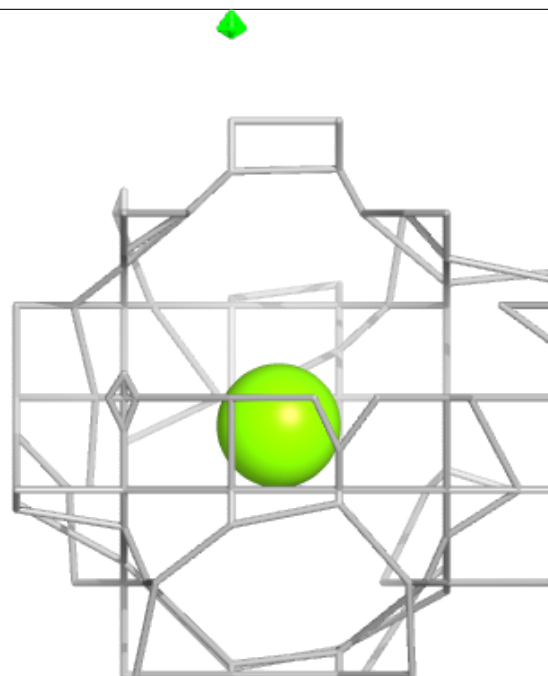
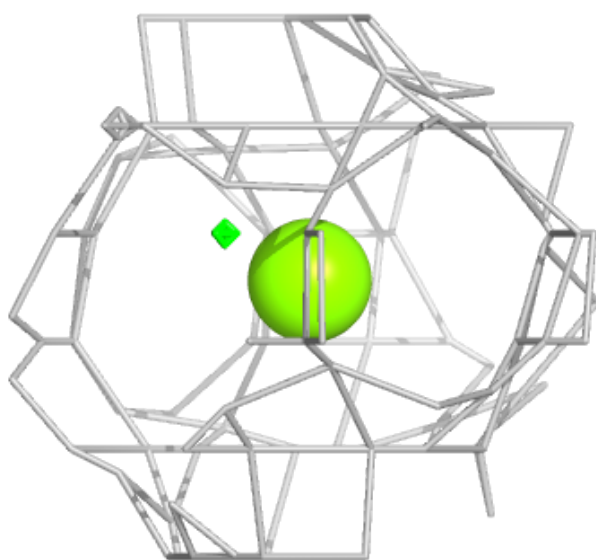
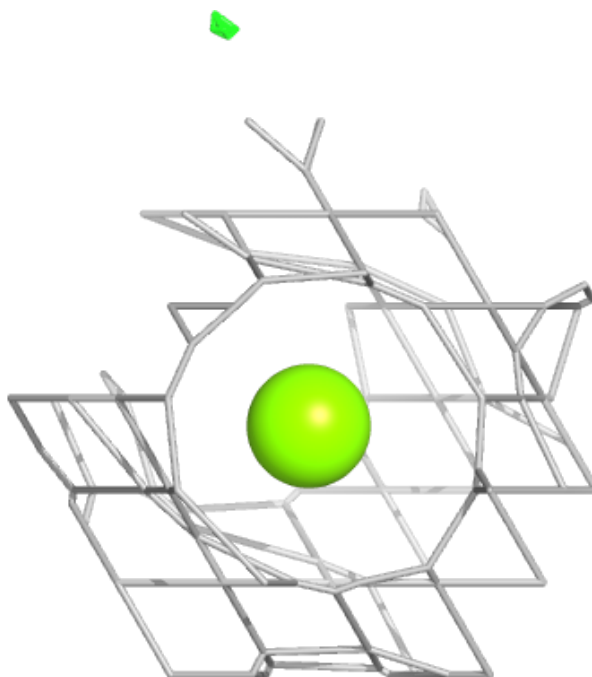
Electron density around MG A 603:

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



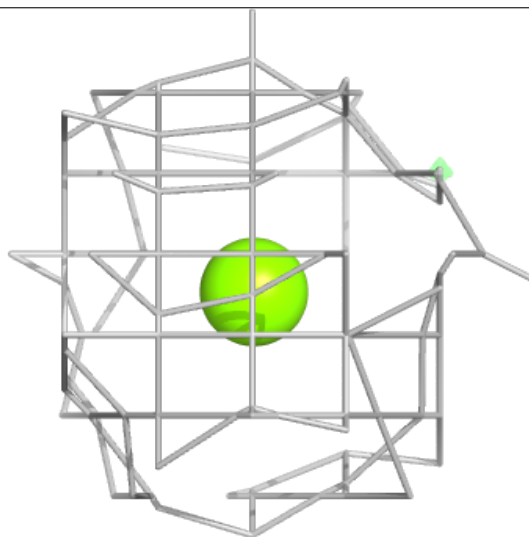
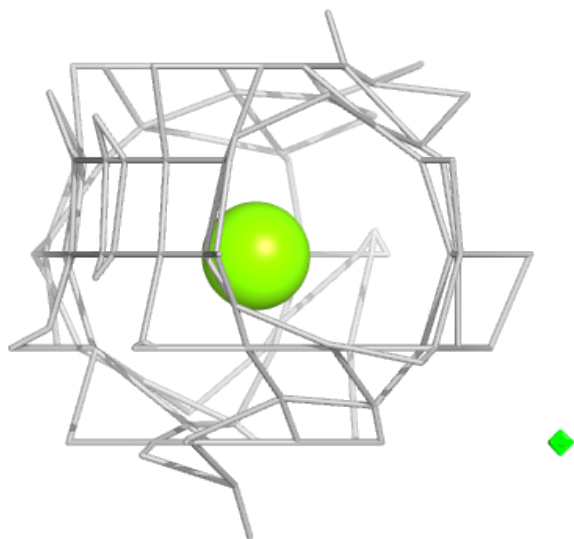
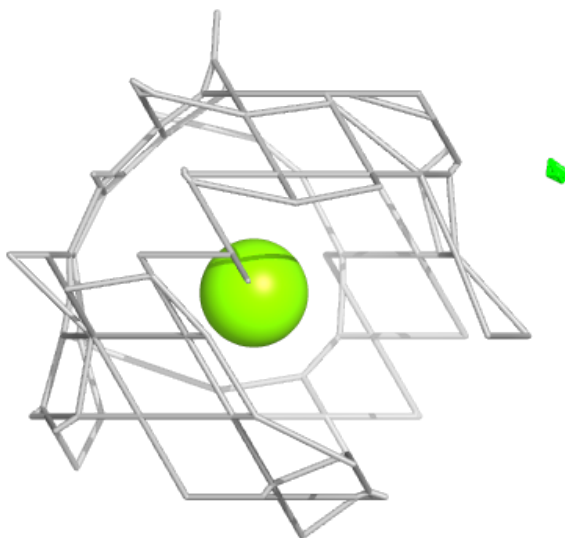
Electron density around MG A 601:

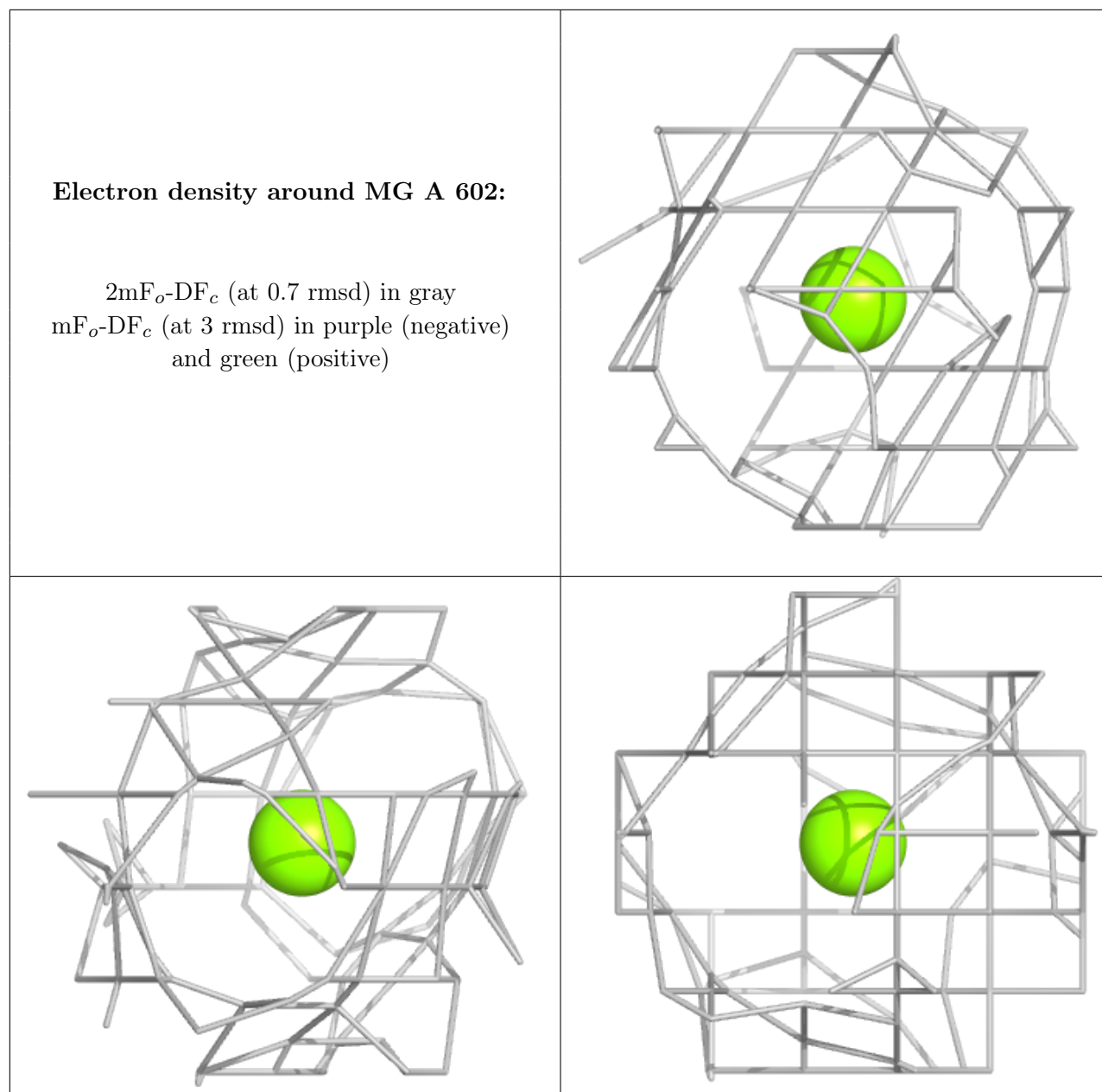
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG B 101:

$2mF_o-DF_c$ (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.