



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:08 PM UTC

PDB ID : 6KVO / pdb_00006kvo
Title : Crystal structure of chloroplast resolvase in complex with Holliday junction
Authors : Yan, J.J.; Hong, S.X.; Guan, Z.Y.; Yin, P.
Deposited on : 2019-09-05
Resolution : 2.50 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

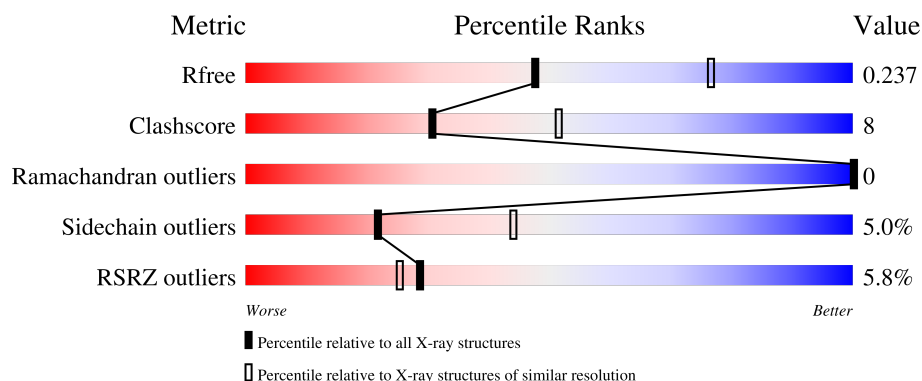
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	171	5% 80% 16% ..
1	B	171	9% 75% 15% .. 7%
2	C	18	83% 17%
3	D	18	83% 17%
4	E	18	61% 39%

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Mol	Chain	Length	Quality of chain
5	F	18	 78% 22%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 4007 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 NtMOC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	165	Total	C	N	O	S	0	0	0
			1272	822	220	228	2			
1	B	159	Total	C	N	O	S	0	0	0
			1208	781	207	219	1			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	ALA	-	expression tag	UNP A0A1S4CVP6
A	106	HIS	-	expression tag	UNP A0A1S4CVP6
A	107	MET	-	expression tag	UNP A0A1S4CVP6
A	162	LYS	GLN	engineered mutation	UNP A0A1S4CVP6
A	235	GLN	GLU	engineered mutation	UNP A0A1S4CVP6
A	239	GLN	GLU	engineered mutation	UNP A0A1S4CVP6
B	105	ALA	-	expression tag	UNP A0A1S4CVP6
B	106	HIS	-	expression tag	UNP A0A1S4CVP6
B	107	MET	-	expression tag	UNP A0A1S4CVP6
B	162	LYS	GLN	engineered mutation	UNP A0A1S4CVP6
B	235	GLN	GLU	engineered mutation	UNP A0A1S4CVP6
B	239	GLN	GLU	engineered mutation	UNP A0A1S4CVP6

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*CP*AP*AP*CP*AP*GP*AP*TP*GP*AP*TP*GP*GP*AP*GP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	18	Total	C	N	O	P	0	0	0
			370	177	75	101	17			

- Molecule 3 is a DNA chain called DNA (5'-D(*GP*CP*CP*TP*TP*GP*CP*TP*TP*GP*GP*AP*CP*AP*TP*CP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	18	Total	C	N	O	P	0	0	0
			361	175	59	110	17			

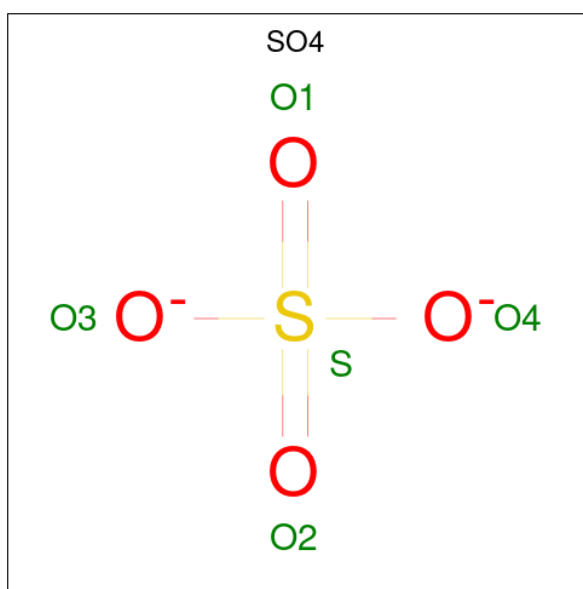
- Molecule 4 is a DNA chain called DNA (5'-D(P*AP*GP*CP*TP*CP*CP*AP*TP*CP*AP*AP*GP*CP*AP*AP*GP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	18	Total	C	N	O	P	0	0	0
			368	174	72	104	18			

- Molecule 5 is a DNA chain called DNA (5'-D(P*AP*AP*GP*AP*TP*GP*TP*CP*CP*AP*TP*CP*TP*GP*TP*TP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	18	Total	C	N	O	P	0	0	0
			369	177	63	111	18			

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of

Interest" by depositor).

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

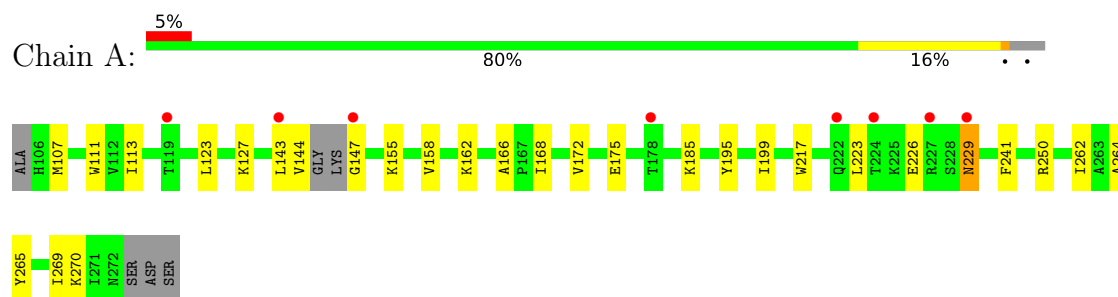
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	16	Total 16	O 16	0	0
8	B	15	Total 15	O 15	0	0
8	C	4	Total 4	O 4	0	0
8	D	5	Total 5	O 5	0	0
8	E	4	Total 4	O 4	0	0
8	F	3	Total 3	O 3	0	0

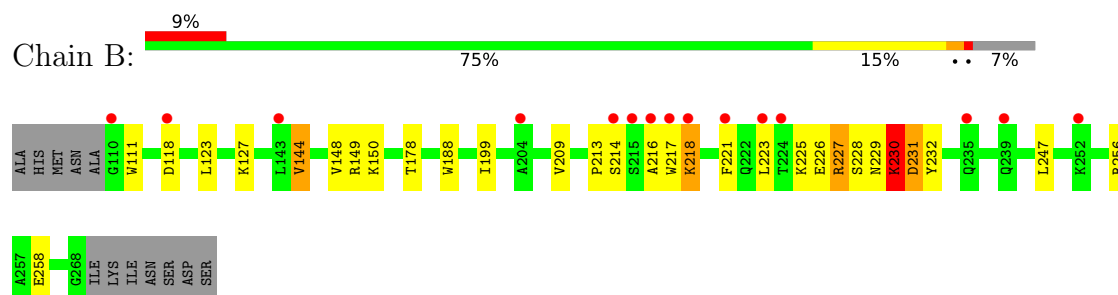
3 Residue-property plots [i](#)

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.

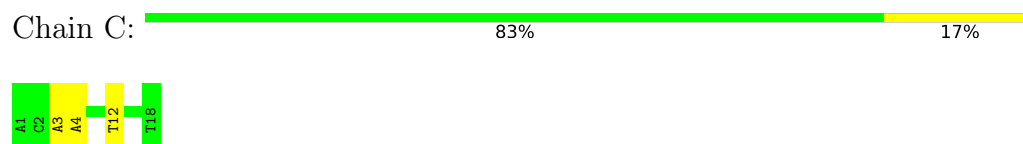
- Molecule 1: NtMOC1



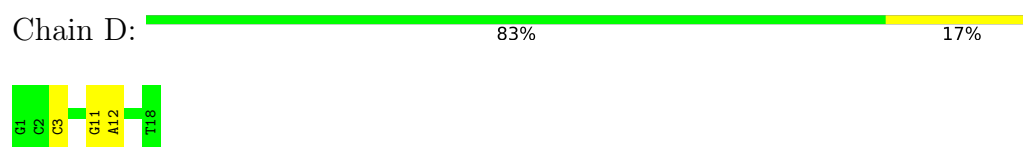
- Molecule 1: NtMOC1



- Molecule 2: DNA (5'-D(*AP*CP*AP*AP*CP*AP*GP*AP*TP*GP*AP*TP*GP*GP*AP*GP*CP*T)-3')



- Molecule 3: DNA (5'-D(*GP*CP*CP*TP*TP*GP*CP*TP*TP*GP*GP*AP*CP*AP*TP*CP*TP*T)-3')



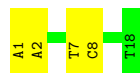
- Molecule 4: DNA (5'-D(P*AP*GP*CP*TP*CP*CP*AP*TP*CP*AP*AP*GP*CP*AP*AP*GP*GP*C)-3')

Chain E:  61% 39%



- Molecule 5: DNA (5'-D(P*AP*AP*GP*AP*TP*GP*TP*CP*CP*AP*TP*CP*TP*GP*TP*TP*GP*T)-3')

Chain F:  78% 22%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	121.32Å 92.16Å 65.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.02 – 2.50 31.02 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (31.02-2.50) 99.8 (31.02-2.50)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.14rc3_3206	Depositor
R, R_{free}	0.202 , 0.234 0.206 , 0.237	Depositor DCC
R_{free} test set	1306 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	70.2	Xtriage
Anisotropy	0.198	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 78.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4007	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SO4

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	0.52	0/1305	0.73	0/1769
1	B	0.60	0/1240	0.82	3/1683 (0.2%)
2	C	0.18	0/417	0.35	0/643
3	D	0.19	0/402	0.39	0/619
4	E	0.19	0/413	0.33	0/634
5	F	0.20	0/412	0.40	0/634
All	All	0.45	0/4189	0.63	3/5982 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	230	LYS	N-CA-C	-5.49	105.21	111.14
1	B	221	PHE	CA-C-N	5.03	128.25	121.05
1	B	221	PHE	C-N-CA	5.03	128.25	121.05

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1272	0	1286	18	0
1	B	1208	0	1217	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	370	0	200	5	0
3	D	361	0	204	3	0
4	E	368	0	201	5	0
5	F	369	0	206	2	0
6	A	5	0	0	0	0
6	D	5	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	16	0	0	1	0
8	B	15	0	0	0	0
8	C	4	0	0	0	0
8	D	5	0	0	0	0
8	E	4	0	0	0	0
8	F	3	0	0	0	0
All	All	4007	0	3314	57	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 8.

All (57) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:LYS:HD3	1:B:223:LEU:HD22	1.52	0.89
1:B:217:TRP:CH2	1:B:258:GLU:OE2	2.28	0.86
1:B:218:LYS:HG2	1:B:223:LEU:HB3	1.61	0.83
1:B:199:ILE:HD13	1:B:209:VAL:HG11	1.66	0.78
4:E:15:DA:H2''	4:E:16:DG:H5''	1.67	0.77
1:B:227:ARG:HH11	1:B:227:ARG:HG2	1.55	0.70
1:B:218:LYS:HD3	1:B:223:LEU:CD2	2.24	0.67
1:B:230:LYS:NZ	1:B:230:LYS:H	1.95	0.65
1:B:144:VAL:CG1	1:B:149:ARG:HB2	2.28	0.64
1:B:217:TRP:CZ2	1:B:258:GLU:OE2	2.50	0.64
1:B:227:ARG:HG2	1:B:227:ARG:NH1	2.13	0.64
1:B:213:PRO:HD2	1:B:216:ALA:HB2	1.84	0.60
1:A:223:LEU:HD22	1:A:229:ASN:HA	1.86	0.57
1:B:218:LYS:CG	1:B:223:LEU:HB3	2.33	0.57
1:A:195:TYR:CZ	1:A:199:ILE:HD11	2.40	0.57
1:A:217:TRP:HH2	1:A:229:ASN:ND2	2.03	0.56
1:A:107:MET:HE2	1:A:270:LYS:NZ	2.21	0.55
1:B:230:LYS:H	1:B:230:LYS:HZ2	1.55	0.55
2:C:3:DA:H2''	2:C:4:DA:O5'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:230:LYS:HZ3	1:B:231:ASP:H	1.56	0.53
1:A:217:TRP:CH2	1:A:229:ASN:ND2	2.77	0.52
3:D:3:DC:H42	4:E:16:DG:H1	1.58	0.51
1:B:118:ASP:HB2	4:E:11:DA:OP1	2.11	0.50
3:D:11:DG:H2''	3:D:12:DA:H5'	1.94	0.49
1:A:185:LYS:HB2	1:B:188:TRP:CD2	2.48	0.49
1:B:111:TRP:CH2	1:B:127:LYS:HE3	2.48	0.48
1:B:217:TRP:CH2	1:B:258:GLU:CD	2.92	0.47
2:C:3:DA:H2'	2:C:4:DA:C8	2.49	0.47
1:B:218:LYS:CD	1:B:223:LEU:HB3	2.45	0.47
1:B:214:SER:HA	1:B:217:TRP:CZ3	2.50	0.47
5:F:7:DT:H2''	5:F:8:DC:O5'	2.15	0.47
1:A:113:ILE:HB	1:A:172:VAL:HG22	1.98	0.46
1:A:111:TRP:CZ3	1:A:166:ALA:HA	2.51	0.46
1:A:250:ARG:NH2	2:C:3:DA:OP1	2.50	0.45
2:C:3:DA:H4'	2:C:4:DA:OP1	2.17	0.44
1:B:230:LYS:HZ3	1:B:230:LYS:N	2.15	0.44
1:B:230:LYS:NZ	1:B:230:LYS:N	2.65	0.43
1:B:149:ARG:NH2	3:D:12:DA:OP1	2.48	0.43
1:A:168:ILE:HD12	1:A:168:ILE:O	2.18	0.43
1:B:247:LEU:HB3	1:B:256:ARG:NH1	2.33	0.43
1:A:127:LYS:NZ	8:A:402:HOH:O	2.52	0.43
4:E:6:DC:H2''	4:E:7:DA:C8	2.54	0.43
5:F:1:DA:H2''	5:F:2:DA:H5''	2.01	0.43
1:B:230:LYS:H	1:B:230:LYS:HZ3	1.67	0.43
4:E:13:DC:H2''	4:E:14:DA:C8	2.55	0.42
1:A:175:GLU:HB2	1:A:262:ILE:CD1	2.50	0.42
1:B:218:LYS:CB	1:B:218:LYS:NZ	2.83	0.42
1:A:241:PHE:HZ	1:A:264:ALA:HB2	1.85	0.42
1:A:123:LEU:C	1:A:123:LEU:HD23	2.44	0.41
1:A:175:GLU:HB2	1:A:262:ILE:HD13	2.01	0.41
1:A:155:LYS:O	1:A:158:VAL:HG22	2.20	0.41
1:B:229:ASN:HA	1:B:232:TYR:CB	2.50	0.41
1:B:123:LEU:C	1:B:123:LEU:HD23	2.45	0.41
1:A:143:LEU:HA	1:A:147:GLY:O	2.21	0.41
1:A:265:TYR:CZ	1:A:269:ILE:HD11	2.56	0.41
1:B:150:LYS:O	1:B:150:LYS:HG3	2.20	0.41
1:B:178:THR:HG23	2:C:12:DT:H4'	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	161/171 (94%)	160 (99%)	1 (1%)	0	100	100
1	B	157/171 (92%)	156 (99%)	1 (1%)	0	100	100
All	All	318/342 (93%)	316 (99%)	2 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	135/140 (96%)	131 (97%)	4 (3%)	36	64
1	B	127/140 (91%)	118 (93%)	9 (7%)	13	29
All	All	262/280 (94%)	249 (95%)	13 (5%)	22	44

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	VAL
1	A	162	LYS
1	A	226	GLU
1	A	229	ASN
1	B	144	VAL
1	B	148	VAL
1	B	218	LYS
1	B	225	LYS

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Mol	Chain	Res	Type
1	B	226	GLU
1	B	227	ARG
1	B	228	SER
1	B	230	LYS
1	B	231	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	176	GLN
1	B	186	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 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	$\# Z > 2$
6	SO4	A	301	-	4,4,4	0.39	0	6,6,6	0.09	0
6	SO4	D	301	-	4,4,4	0.37	0	6,6,6	0.07	0

There are no bond length outliers.

There are no bond angle outliers.

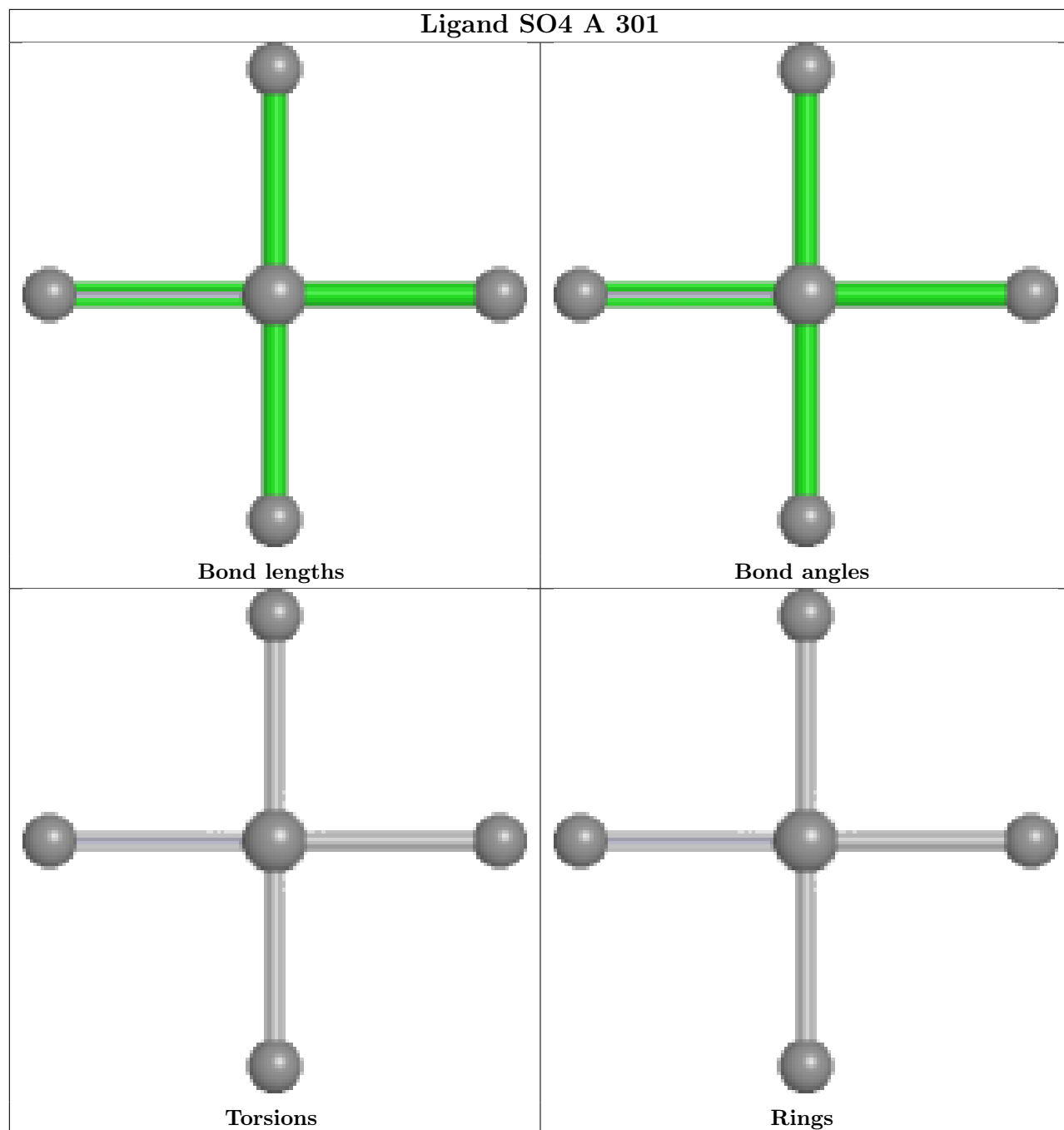
There are no chirality outliers.

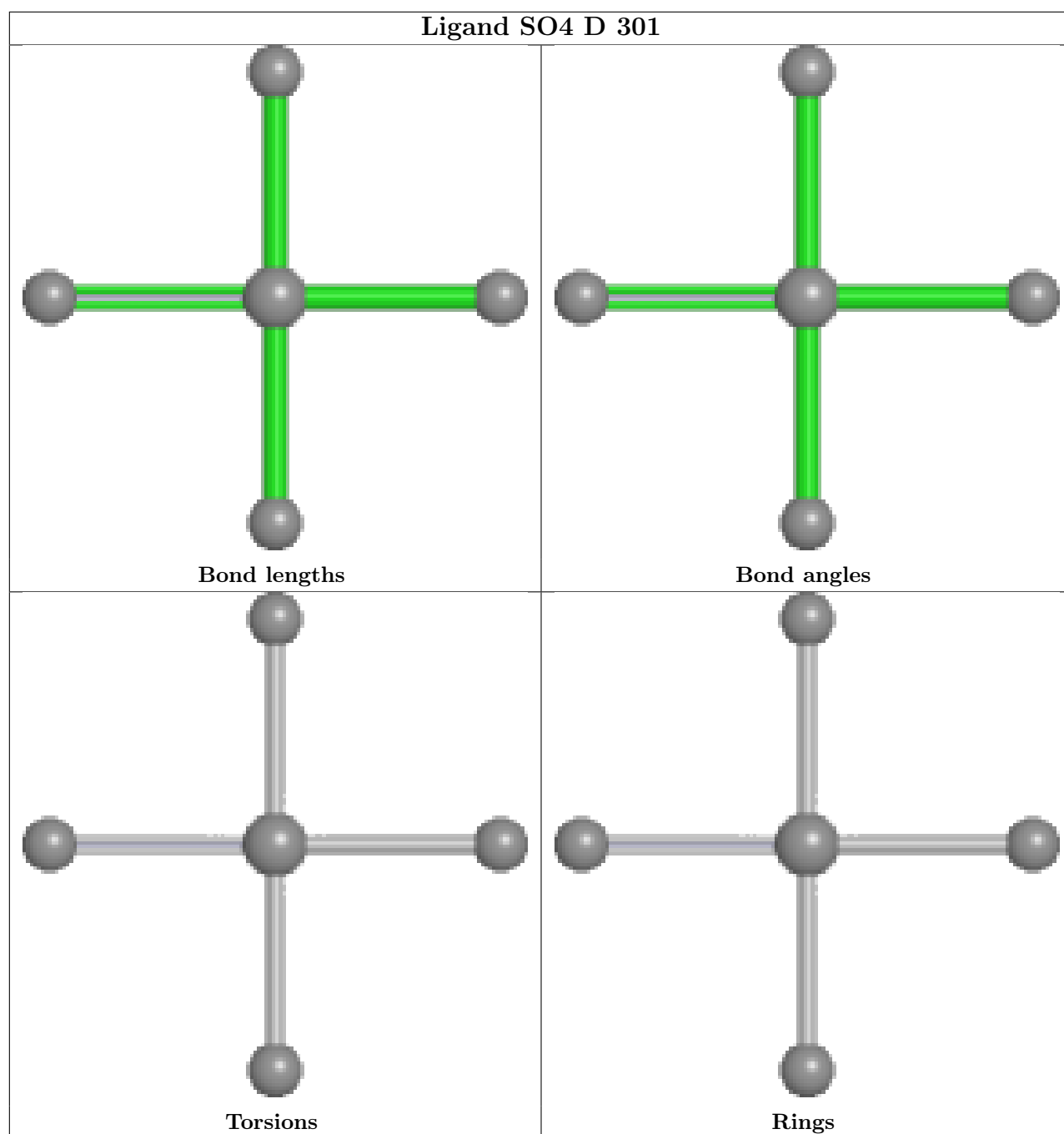
There are no torsion outliers.

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	165/171 (96%)	0.33	8 (4%) 35 31	48, 80, 124, 193	0
1	B	159/171 (92%)	0.55	15 (9%) 14 12	48, 77, 163, 195	0
2	C	18/18 (100%)	0.24	0 100 100	61, 96, 135, 137	0
3	D	18/18 (100%)	0.20	0 100 100	60, 94, 126, 128	0
4	E	18/18 (100%)	0.59	0 100 100	66, 112, 140, 140	0
5	F	18/18 (100%)	0.75	0 100 100	67, 109, 139, 149	0
All	All	396/414 (95%)	0.44	23 (5%) 29 25	48, 82, 138, 195	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	223	LEU	5.5
1	B	221	PHE	3.6
1	A	222	GLN	3.5
1	B	214	SER	3.5
1	B	235	GLN	3.3
1	B	217	TRP	2.9
1	A	147	GLY	2.8
1	A	227	ARG	2.8
1	B	218	LYS	2.8
1	A	229	ASN	2.7
1	B	239	GLN	2.6
1	B	224	THR	2.6
1	B	118	ASP	2.5
1	A	224	THR	2.5
1	B	215	SER	2.5
1	B	216	ALA	2.5
1	B	204	ALA	2.3
1	A	178	THR	2.3
1	B	252	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	143	LEU	2.0
1	B	143	LEU	2.0
1	B	110	GLY	2.0
1	A	119	THR	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

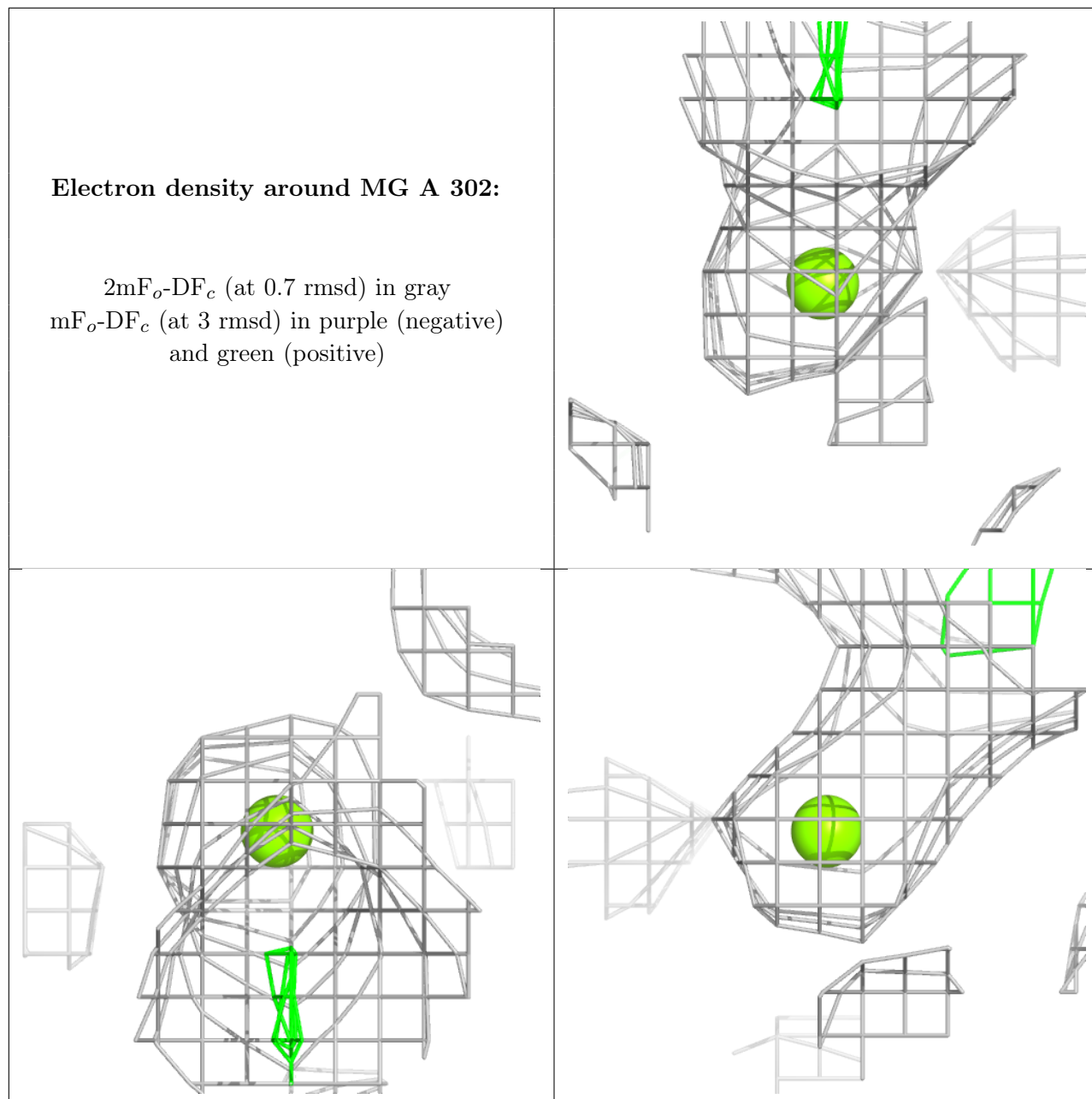
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	MG	A	302	1/1	0.84	0.13	89,89,89,89	0
7	MG	B	301	1/1	0.85	0.22	147,147,147,147	0
6	SO4	A	301	5/5	0.92	0.25	182,190,194,195	0
6	SO4	D	301	5/5	0.93	0.21	172,175,175,183	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.

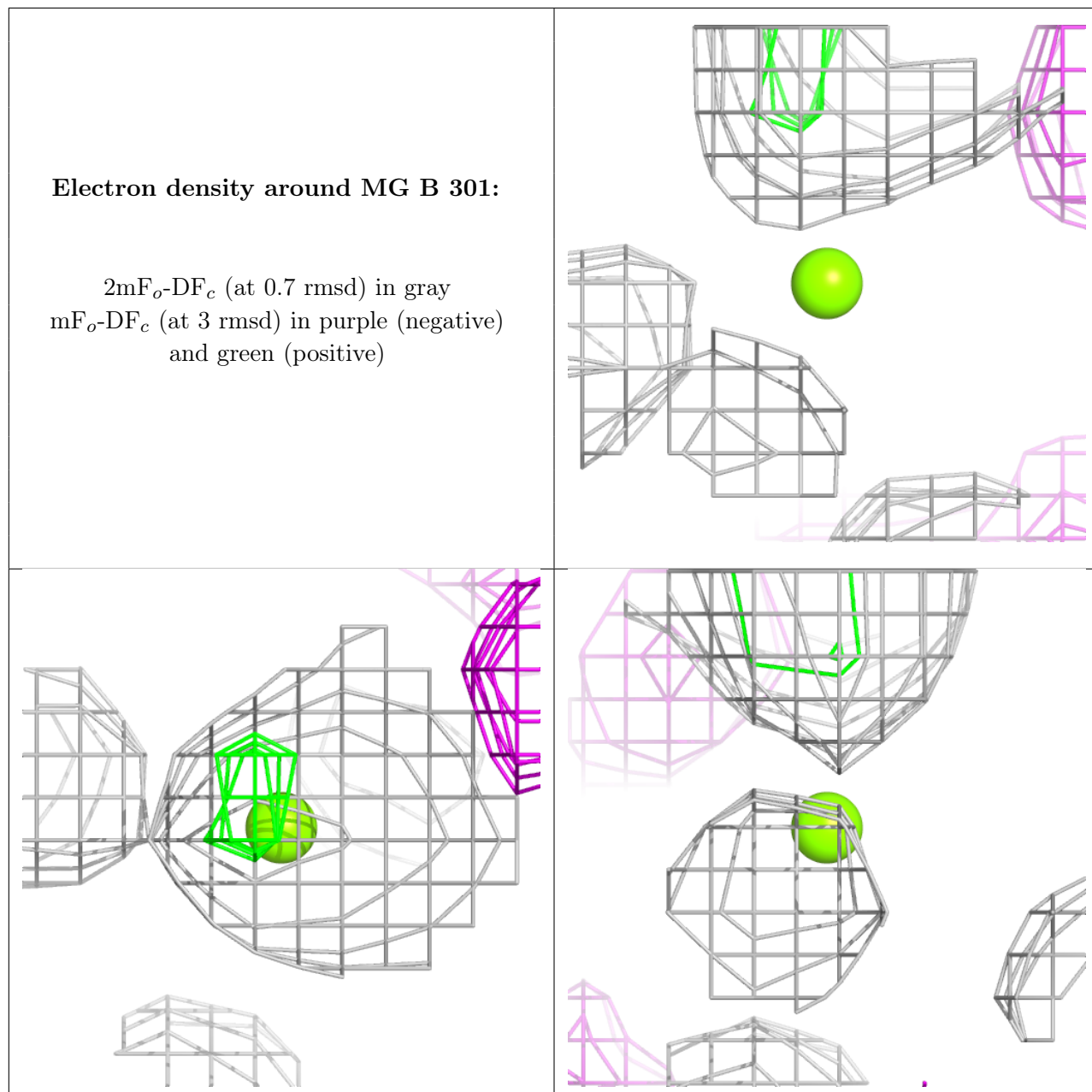
Electron density around MG A 302:

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



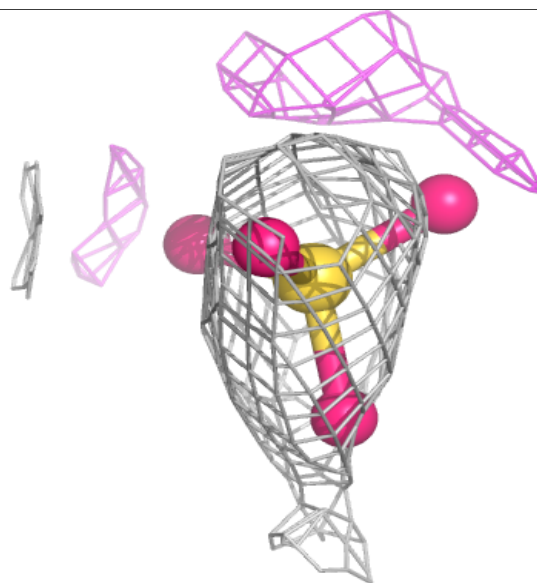
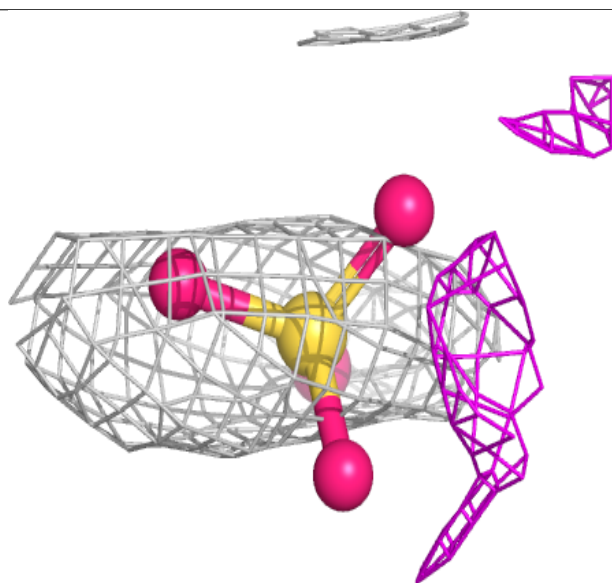
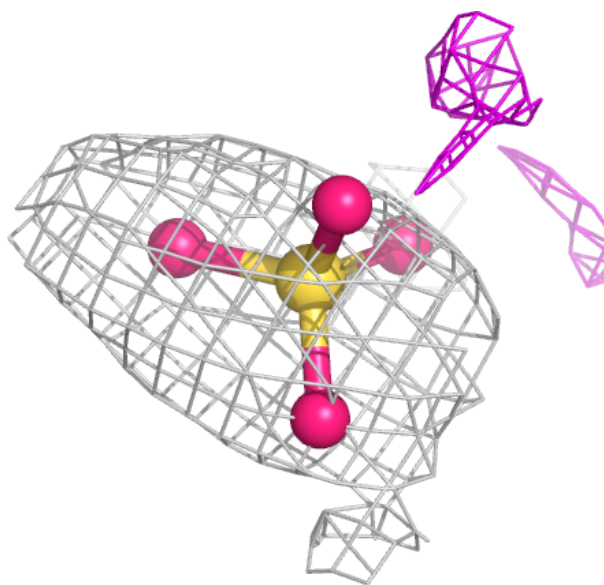
Electron density around MG B 301:

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



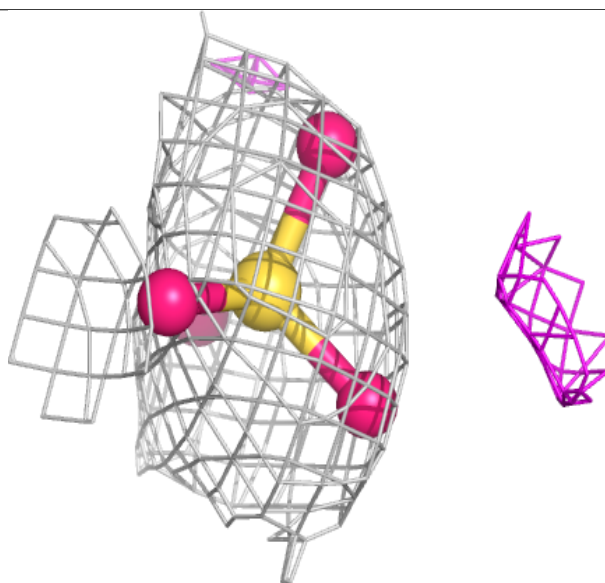
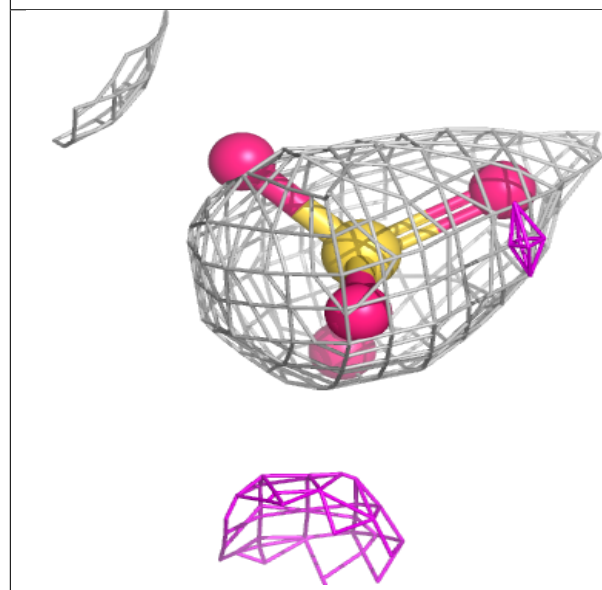
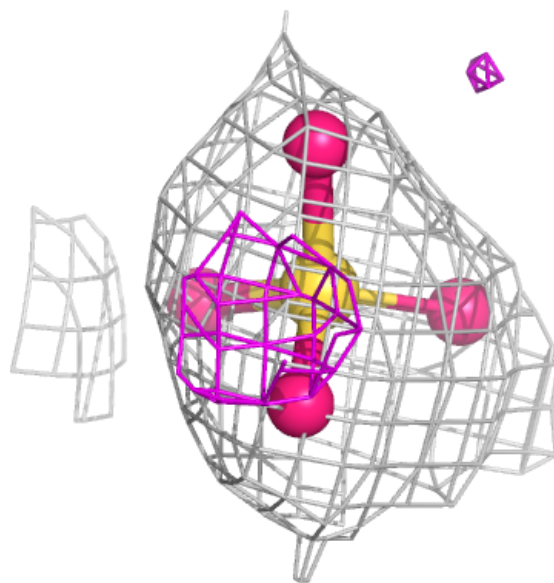
Electron density around SO4 A 301:

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



Electron density around SO4 D 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.