



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2023 – 02:30 AM JST

PDB ID : 6KRH
Title : Structural basis for domain rotation during adenylation of active site K123 and fragment library screening against NAD⁺ -dependent DNA ligase from *Mycobacterium tuberculosis*
Authors : Ramachandran, R.; Shukla, A.; Afsar, M.
Deposited on : 2019-08-21
Resolution : 2.60 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

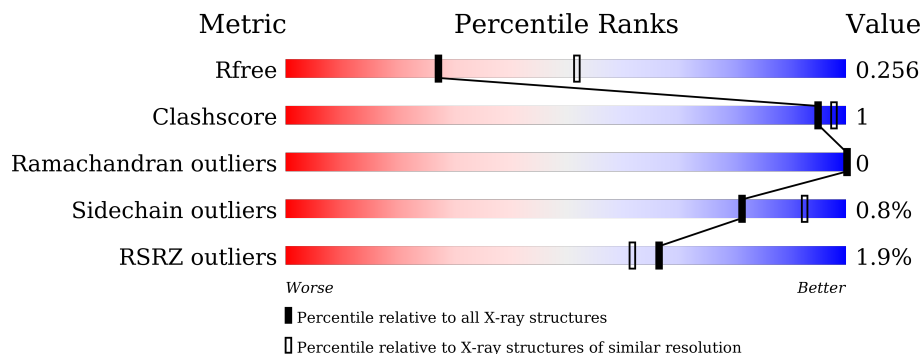
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	327	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5039 atoms, of which 2425 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.

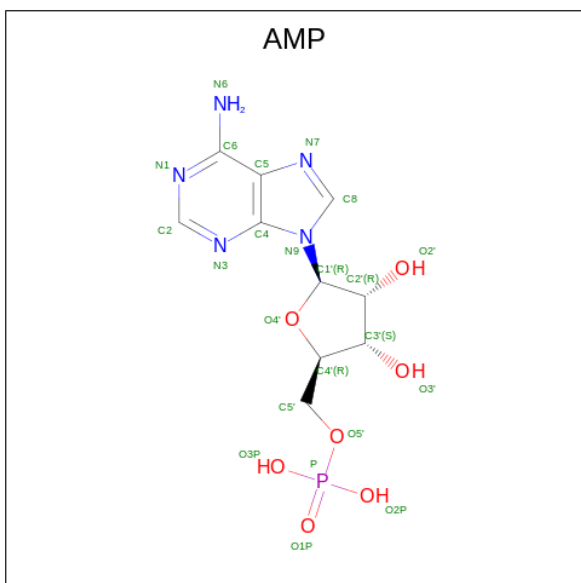
- Molecule 1 is a protein called DNA ligase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	321	4905	1571	2399	453	478	4	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

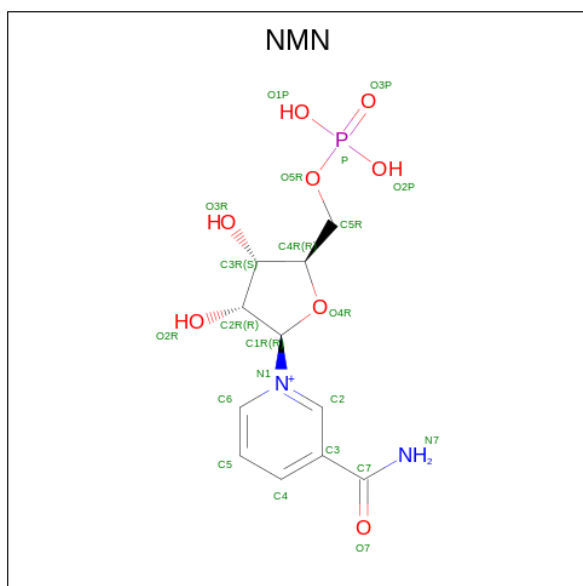
Chain	Residue	Modelled	Actual	Comment	Reference
A	236	TYR	HIS	engineered mutation	UNP P9WNV1
A	329	HIS	-	expression tag	UNP P9WNV1
A	330	HIS	-	expression tag	UNP P9WNV1
A	331	HIS	-	expression tag	UNP P9WNV1
A	332	HIS	-	expression tag	UNP P9WNV1
A	333	HIS	-	expression tag	UNP P9WNV1
A	334	HIS	-	expression tag	UNP P9WNV1

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$) (labeled as "Ligand of Interest" by depositor).



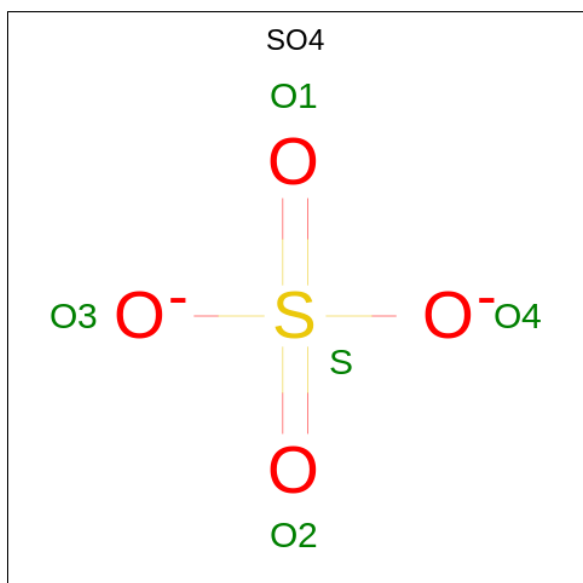
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			P
2	A	1	35	10	12	5	7	1	0	0

- Molecule 3 is BETA-NICOTINAMIDE RIBOSE MONOPHOSPHATE (three-letter code: NMN) (formula: $C_{11}H_{16}N_2O_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			P
3	A	1	36	11	14	2	8	1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S) (labeled as "Ligand of Interest" by depositor).



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

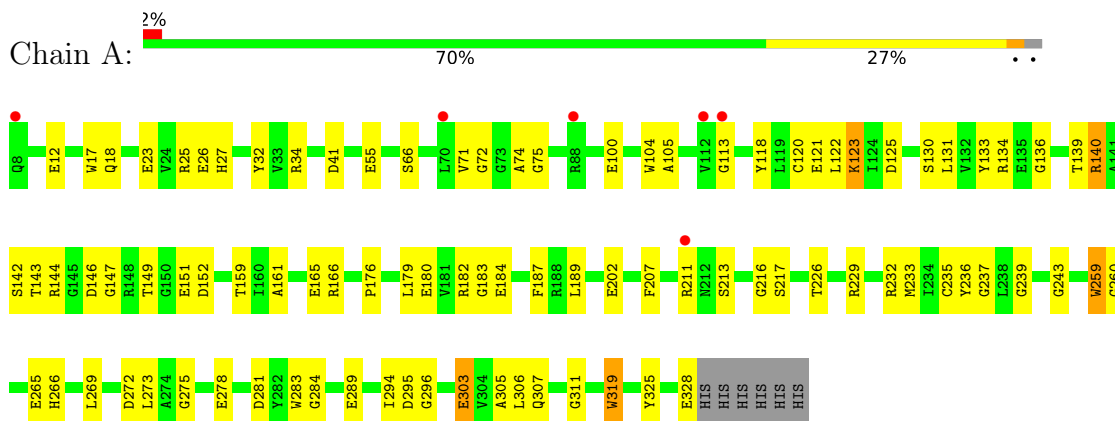
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	43	Total	O	0	0
			43	43		

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: DNA ligase A



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	95.55Å 95.55Å 200.59Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.13 – 2.60 47.77 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.13-2.60) 100.0 (47.77-2.60)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 2.61Å)	Xtrriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.224 , 0.264 0.243 , 0.256	Depositor DCC
R_{free} test set	880 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	41.1	Xtrriage
Anisotropy	0.239	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5039	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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: NMN, SO4, AMP

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	2.57	99/2564 (3.9%)	1.22	15/3493 (0.4%)

All (99) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	236	TYR	CE1-CZ	-13.53	1.21	1.38
1	A	184	GLU	CD-OE1	-11.62	1.12	1.25
1	A	180	GLU	CD-OE2	-9.69	1.15	1.25
1	A	180	GLU	CD-OE1	-8.92	1.15	1.25
1	A	202	GLU	CD-OE2	-8.38	1.16	1.25
1	A	217	SER	CB-OG	-8.02	1.31	1.42
1	A	325	TYR	CE1-CZ	-7.71	1.28	1.38
1	A	144	ARG	CZ-NH2	-7.66	1.23	1.33
1	A	236	TYR	CD1-CE1	-7.45	1.28	1.39
1	A	151	GLU	CD-OE1	-7.37	1.17	1.25
1	A	12	GLU	CD-OE1	-7.37	1.17	1.25
1	A	184	GLU	CD-OE2	-7.22	1.17	1.25
1	A	283	TRP	C-O	-7.00	1.10	1.23
1	A	144	ARG	CZ-NH1	-6.90	1.24	1.33
1	A	303	GLU	CA-CB	-6.84	1.38	1.53
1	A	118	TYR	CE1-CZ	-6.62	1.29	1.38
1	A	121	GLU	CD-OE2	-6.40	1.18	1.25
1	A	134	ARG	CZ-NH1	-6.40	1.24	1.33
1	A	105	ALA	CA-CB	-6.39	1.39	1.52
1	A	26	GLU	CD-OE1	-6.37	1.18	1.25
1	A	34	ARG	CZ-NH1	-6.32	1.24	1.33
1	A	289	GLU	CD-OE2	-6.29	1.18	1.25
1	A	143	THR	C-O	-6.18	1.11	1.23
1	A	23	GLU	CD-OE1	-6.18	1.18	1.25
1	A	130	SER	CB-OG	-6.15	1.34	1.42
1	A	140	ARG	CZ-NH1	-6.14	1.25	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	278	GLU	CD-OE2	-6.14	1.18	1.25
1	A	23	GLU	CD-OE2	-6.12	1.19	1.25
1	A	182	ARG	CZ-NH2	-6.08	1.25	1.33
1	A	26	GLU	CD-OE2	-6.07	1.19	1.25
1	A	216	GLY	C-O	-6.05	1.14	1.23
1	A	136	GLY	C-O	-6.05	1.14	1.23
1	A	296	GLY	C-O	-6.04	1.14	1.23
1	A	66	SER	C-O	-6.03	1.11	1.23
1	A	142	SER	CB-OG	-5.95	1.34	1.42
1	A	235	CYS	C-O	-5.85	1.12	1.23
1	A	161	ALA	C-O	-5.84	1.12	1.23
1	A	283	TRP	CG-CD1	-5.83	1.28	1.36
1	A	211	ARG	C-O	-5.81	1.12	1.23
1	A	147	GLY	C-O	-5.81	1.14	1.23
1	A	75	GLY	C-O	-5.76	1.14	1.23
1	A	121	GLU	C-O	-5.75	1.12	1.23
1	A	319	TRP	CE3-CZ3	-5.75	1.28	1.38
1	A	259	TRP	CD2-CE2	-5.74	1.34	1.41
1	A	123	LYS	N-CA	-5.73	1.34	1.46
1	A	165	GLU	CD-OE2	-5.71	1.19	1.25
1	A	104	TRP	CG-CD1	-5.65	1.28	1.36
1	A	303	GLU	CD-OE2	-5.62	1.19	1.25
1	A	303	GLU	CD-OE1	-5.60	1.19	1.25
1	A	123	LYS	CA-CB	-5.57	1.41	1.53
1	A	237	GLY	C-O	-5.56	1.14	1.23
1	A	275	GLY	C-O	-5.56	1.14	1.23
1	A	260	GLY	C-O	-5.55	1.14	1.23
1	A	229	ARG	CZ-NH2	-5.54	1.25	1.33
1	A	41	ASP	C-O	-5.52	1.12	1.23
1	A	239	GLY	C-O	-5.52	1.14	1.23
1	A	265	GLU	C-O	-5.51	1.12	1.23
1	A	226	THR	CB-CG2	-5.45	1.34	1.52
1	A	226	THR	C-O	-5.42	1.13	1.23
1	A	207	PHE	C-O	-5.42	1.13	1.23
1	A	133	TYR	CE1-CZ	-5.35	1.31	1.38
1	A	183	GLY	C-O	-5.35	1.15	1.23
1	A	100	GLU	CD-OE2	-5.34	1.19	1.25
1	A	232	ARG	C-O	-5.33	1.13	1.23
1	A	142	SER	C-O	-5.33	1.13	1.23
1	A	32	TYR	CG-CD2	-5.33	1.32	1.39
1	A	18	GLN	C-O	-5.33	1.13	1.23
1	A	266	HIS	C-O	-5.30	1.13	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243	GLY	C-O	-5.29	1.15	1.23
1	A	284	GLY	C-O	-5.27	1.15	1.23
1	A	187	PHE	C-O	-5.27	1.13	1.23
1	A	166	ARG	CZ-NH1	-5.26	1.26	1.33
1	A	27	HIS	C-O	-5.25	1.13	1.23
1	A	104	TRP	CD2-CE2	-5.25	1.35	1.41
1	A	189	LEU	C-O	-5.25	1.13	1.23
1	A	269	LEU	C-O	-5.23	1.13	1.23
1	A	104	TRP	CE3-CZ3	-5.22	1.29	1.38
1	A	272	ASP	CB-CG	-5.21	1.40	1.51
1	A	139	THR	C-O	-5.21	1.13	1.23
1	A	134	ARG	CZ-NH2	-5.19	1.26	1.33
1	A	131	LEU	C-O	-5.17	1.13	1.23
1	A	213	SER	CB-OG	-5.17	1.35	1.42
1	A	159	THR	C-O	-5.17	1.13	1.23
1	A	34	ARG	CZ-NH2	-5.16	1.26	1.33
1	A	149	THR	C-O	-5.14	1.13	1.23
1	A	182	ARG	CZ-NH1	-5.12	1.26	1.33
1	A	140	ARG	CZ-NH2	-5.09	1.26	1.33
1	A	259	TRP	CG-CD1	-5.08	1.29	1.36
1	A	295	ASP	C-O	-5.08	1.13	1.23
1	A	130	SER	C-O	-5.08	1.13	1.23
1	A	311	GLY	C-O	-5.07	1.15	1.23
1	A	152	ASP	CB-CG	-5.06	1.41	1.51
1	A	151	GLU	C-O	-5.06	1.13	1.23
1	A	179	LEU	C-O	-5.05	1.13	1.23
1	A	17	TRP	CD2-CE2	-5.04	1.35	1.41
1	A	182	ARG	C-O	-5.04	1.13	1.23
1	A	233	MET	C-O	-5.03	1.13	1.23
1	A	72	GLY	C-O	-5.01	1.15	1.23
1	A	305	ALA	C-O	-5.01	1.13	1.23

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	GLY	N-CA-C	11.17	141.03	113.10
1	A	71	VAL	CB-CA-C	9.15	128.78	111.40
1	A	123	LYS	CD-CE-NZ	-8.93	91.17	111.70
1	A	55	GLU	OE1-CD-OE2	-6.99	114.91	123.30
1	A	281	ASP	CB-CG-OD1	6.39	124.05	118.30
1	A	144	ARG	CA-CB-CG	6.27	127.20	113.40
1	A	146	ASP	CB-CG-OD1	6.22	123.90	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	120	CYS	CA-CB-SG	6.22	125.20	114.00
1	A	125	ASP	CB-CG-OD2	5.83	123.55	118.30
1	A	236	TYR	CE1-CZ-OH	-5.41	105.49	120.10
1	A	71	VAL	N-CA-C	-5.35	96.56	111.00
1	A	328	GLU	N-CA-CB	5.23	120.02	110.60
1	A	151	GLU	OE1-CD-OE2	-5.12	117.16	123.30
1	A	273	LEU	CB-CG-CD1	5.09	119.65	111.00
1	A	74	ALA	N-CA-CB	-5.05	103.03	110.10

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	2506	2399	2394	5	0
2	A	23	12	11	2	0
3	A	22	14	14	0	0
4	A	20	0	0	0	0
5	A	43	0	0	0	0
All	All	2614	2425	2419	6	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (6) 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:307:GLN:HG2	1:A:319:TRP:CD2	2.36	0.60
1:A:303:GLU:HB2	1:A:306:LEU:HD13	1.85	0.58
2:A:401:AMP:H2'	2:A:401:AMP:N3	2.20	0.57
1:A:123:LYS:HZ1	2:A:401:AMP:P	2.33	0.51
1:A:176:PRO:HD3	1:A:259:TRP:CZ2	2.47	0.49
1:A:122:LEU:HB3	1:A:294:ILE:HD12	1.97	0.46

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	319/327 (98%)	313 (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	252/267 (94%)	250 (99%)	2 (1%)	81	92

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

Mol	Chain	Res	Type
1	A	25	ARG
1	A	140	ARG

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

Mol	Chain	Res	Type
1	A	109	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](#)

6 ligands are modelled in this entry.

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
4	SO4	A	403	-	4,4,4	0.32	0	6,6,6	0.05	0
4	SO4	A	404	-	4,4,4	0.29	0	6,6,6	0.32	0
2	AMP	A	401	-	22,25,25	2.52	14 (63%)	25,38,38	1.73	8 (32%)
4	SO4	A	406	-	4,4,4	0.10	0	6,6,6	0.45	0
3	NMN	A	402	-	22,23,23	2.19	8 (36%)	30,34,34	2.57	9 (30%)
4	SO4	A	405	-	4,4,4	0.16	0	6,6,6	0.17	0

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	NMN	A	402	-	-	6/14/30/30	0/2/2/2
2	AMP	A	401	-	-	5/6/26/26	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	AMP	C4-N3	-5.26	1.28	1.35
3	A	402	NMN	O7-C7	-4.80	1.15	1.24
2	A	401	AMP	C2'-C1'	-3.92	1.47	1.53
3	A	402	NMN	C2-N1	-3.33	1.30	1.35
2	A	401	AMP	C2-N3	-3.31	1.26	1.32
2	A	401	AMP	P-O2P	-3.16	1.42	1.54
3	A	402	NMN	C7-N7	-3.05	1.27	1.33
2	A	401	AMP	C5-N7	-2.98	1.28	1.39
2	A	401	AMP	C8-N7	-2.95	1.29	1.34
2	A	401	AMP	P-O3P	-2.86	1.43	1.54
3	A	402	NMN	C5-C4	-2.81	1.33	1.38
2	A	401	AMP	C3'-C4'	-2.76	1.45	1.53
2	A	401	AMP	O3'-C3'	-2.73	1.36	1.43
3	A	402	NMN	C4-C3	-2.68	1.34	1.39
3	A	402	NMN	O4R-C4R	-2.63	1.39	1.45
3	A	402	NMN	C6-N1	-2.60	1.29	1.35
3	A	402	NMN	C2R-C1R	-2.60	1.49	1.53
2	A	401	AMP	O2'-C2'	-2.41	1.37	1.43
2	A	401	AMP	C2-N1	-2.35	1.29	1.33
2	A	401	AMP	C2'-C3'	-2.34	1.46	1.53
2	A	401	AMP	O4'-C4'	-2.17	1.40	1.45
2	A	401	AMP	O5'-C5'	-2.07	1.36	1.44

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	NMN	O4R-C1R-C2R	-5.94	98.24	106.93
3	A	402	NMN	O2P-P-O5R	-5.57	91.90	106.73
3	A	402	NMN	C3-C7-N7	5.55	124.41	117.75
3	A	402	NMN	O7-C7-N7	-5.52	114.73	122.58
3	A	402	NMN	P-O5R-C5R	4.37	130.33	118.30
2	A	401	AMP	O4'-C4'-C3'	-3.47	98.26	105.11
2	A	401	AMP	N3-C2-N1	-3.38	123.40	128.68
3	A	402	NMN	O1P-P-O5R	3.11	115.00	106.73
2	A	401	AMP	O2P-P-O1P	3.08	122.75	110.68
2	A	401	AMP	C1'-N9-C4	2.80	131.56	126.64
3	A	402	NMN	C4-C3-C7	-2.63	113.99	121.04
2	A	401	AMP	C4-C5-N7	-2.56	106.73	109.40
2	A	401	AMP	O4'-C4'-C5'	2.45	117.44	109.37
3	A	402	NMN	O2P-P-O1P	2.45	117.00	107.64
2	A	401	AMP	C2-N1-C6	2.42	122.90	118.75
3	A	402	NMN	C2-C3-C7	2.37	126.35	119.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	AMP	C5-C6-N1	-2.01	115.80	120.35

There are no chirality outliers.

All (11) torsion outliers are listed below:

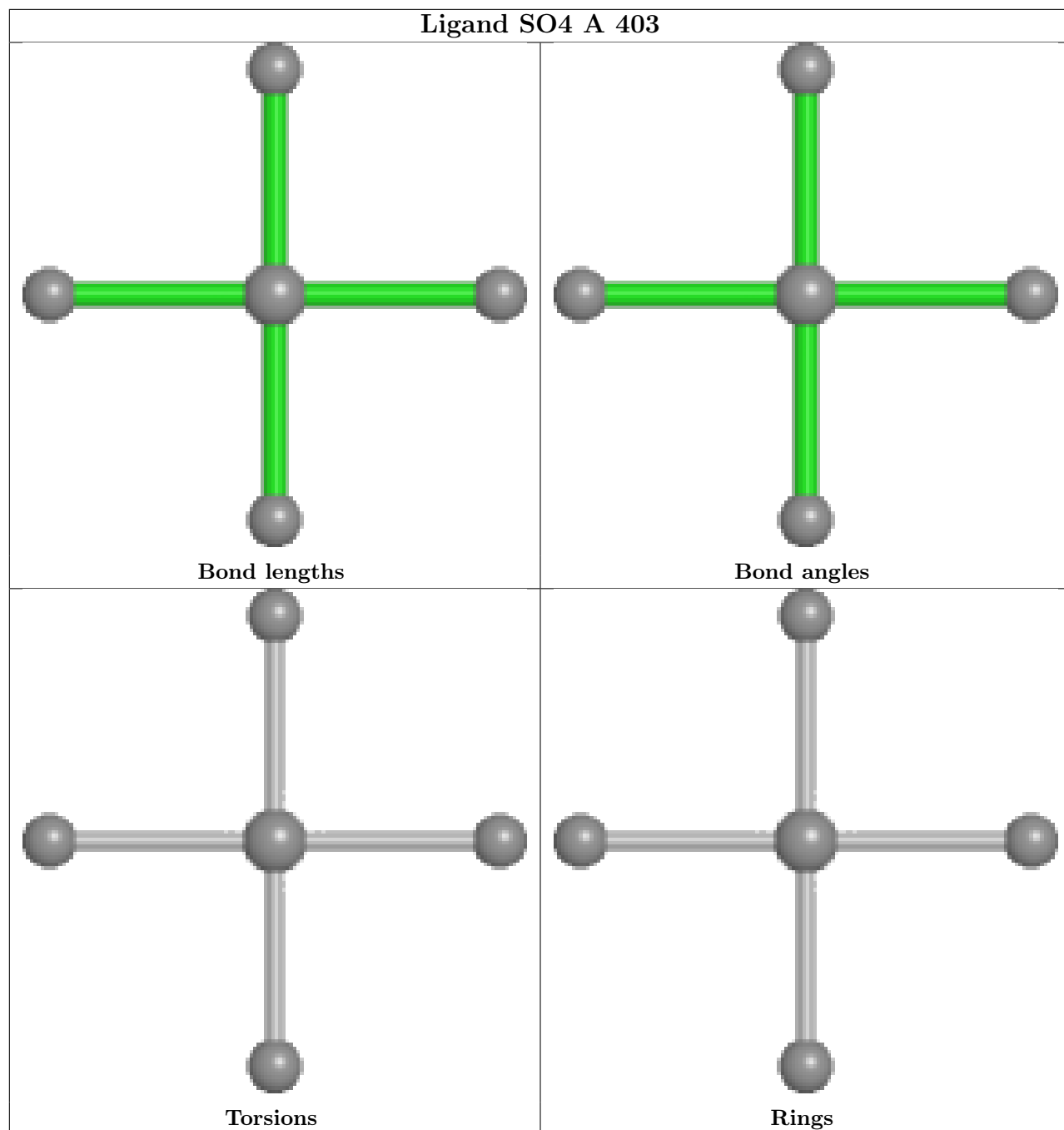
Mol	Chain	Res	Type	Atoms
2	A	401	AMP	C5'-O5'-P-O1P
2	A	401	AMP	C5'-O5'-P-O2P
2	A	401	AMP	C5'-O5'-P-O3P
2	A	401	AMP	O4'-C4'-C5'-O5'
3	A	402	NMN	C5R-O5R-P-O3P
3	A	402	NMN	C5R-O5R-P-O1P
3	A	402	NMN	C5R-O5R-P-O2P
3	A	402	NMN	O4R-C4R-C5R-O5R
3	A	402	NMN	C3R-C4R-C5R-O5R
2	A	401	AMP	C3'-C4'-C5'-O5'
3	A	402	NMN	C4R-C5R-O5R-P

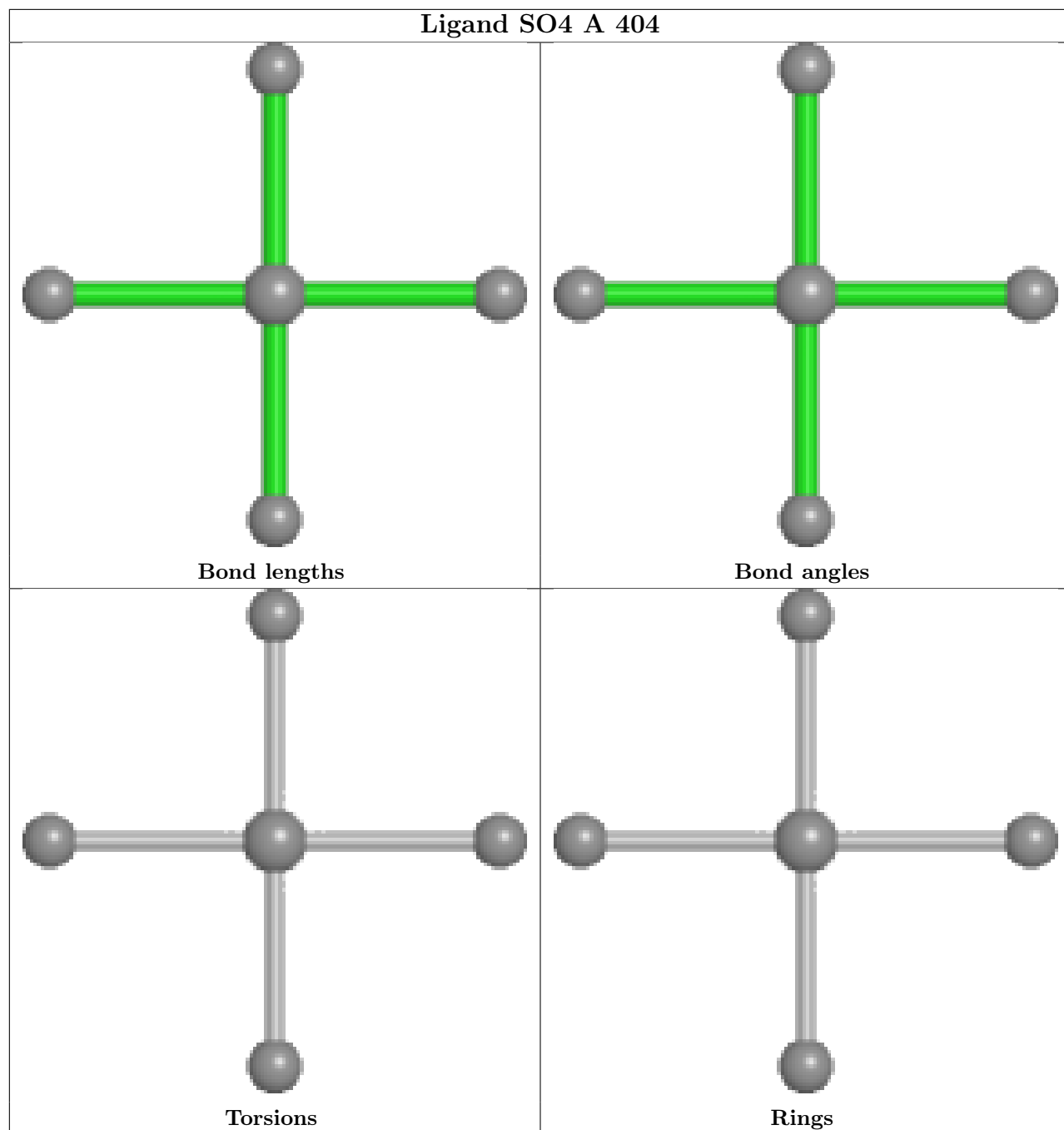
There are no ring outliers.

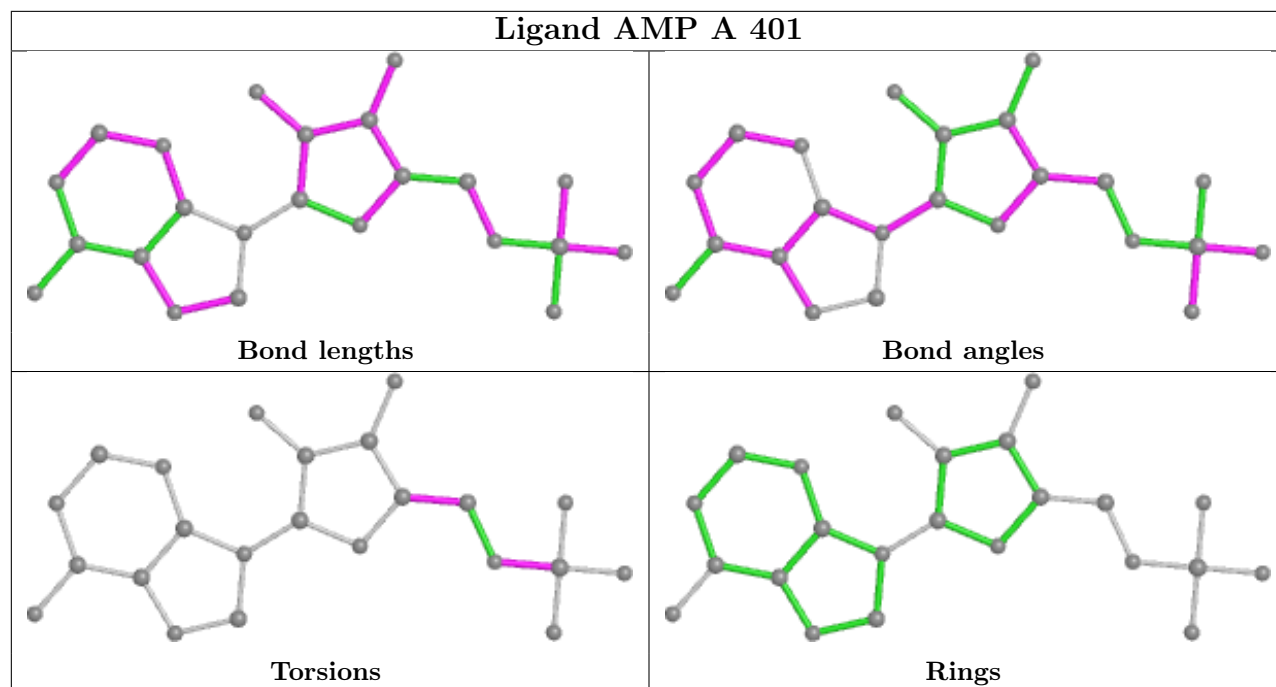
1 monomer is involved in 2 short contacts:

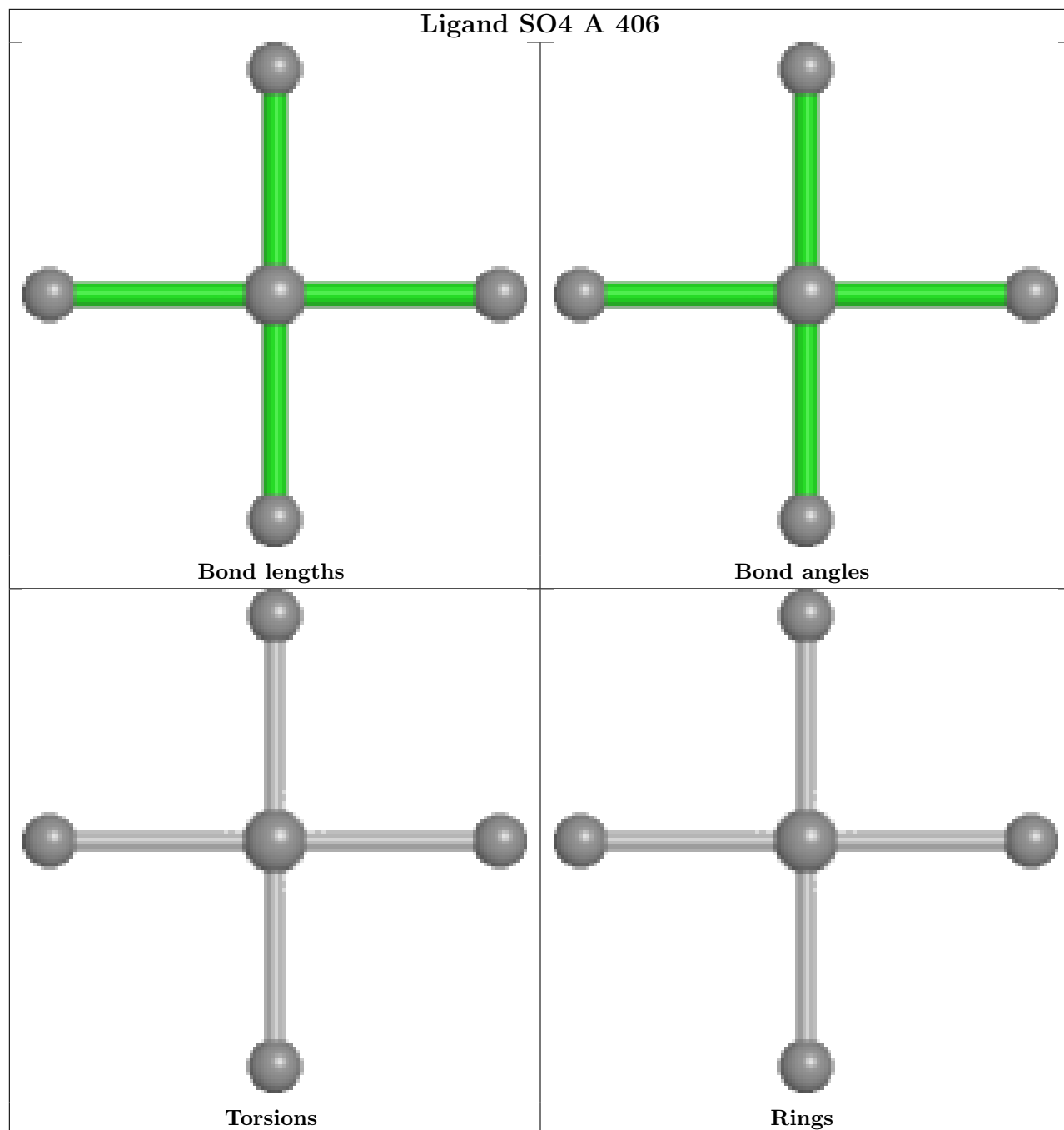
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	AMP	2	0

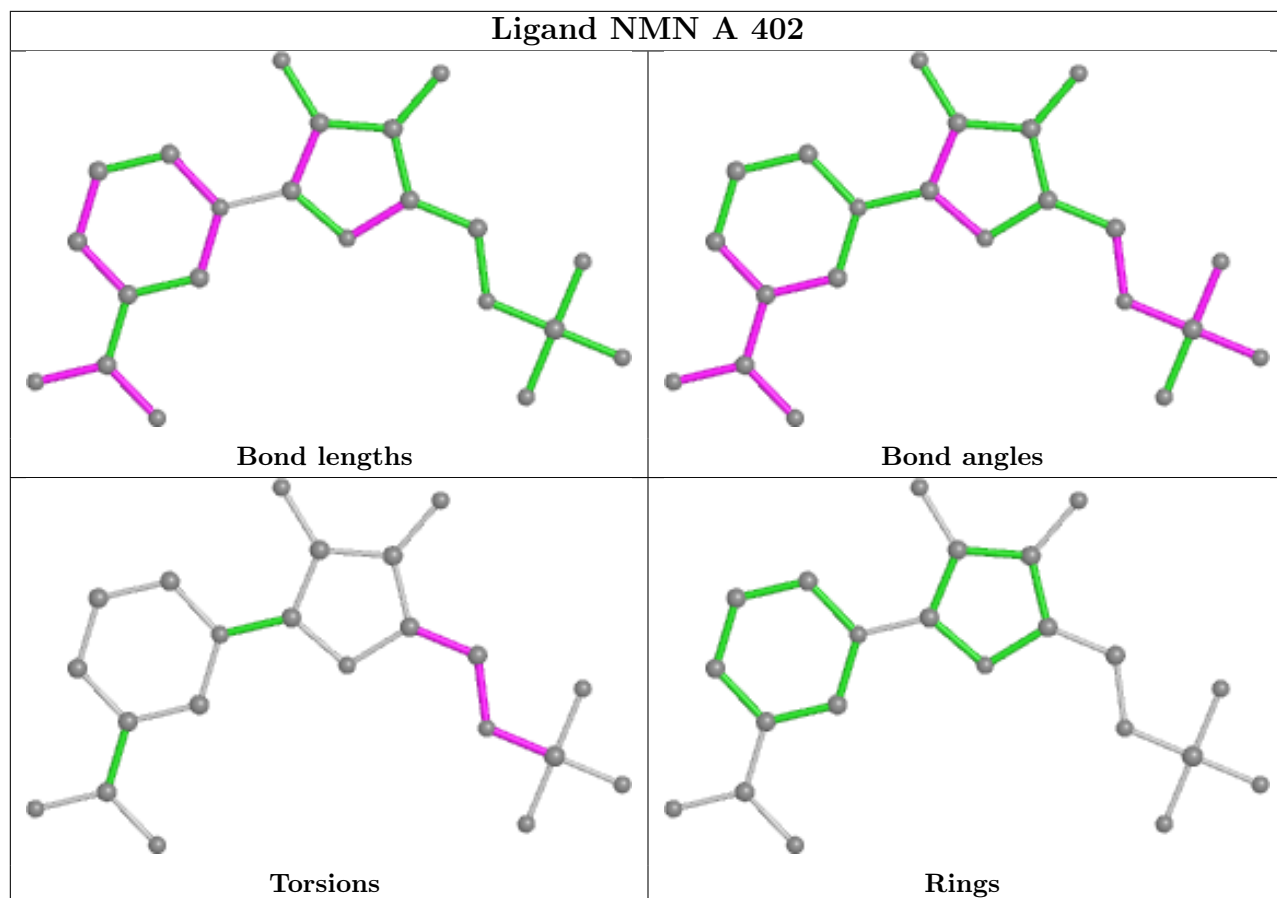
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

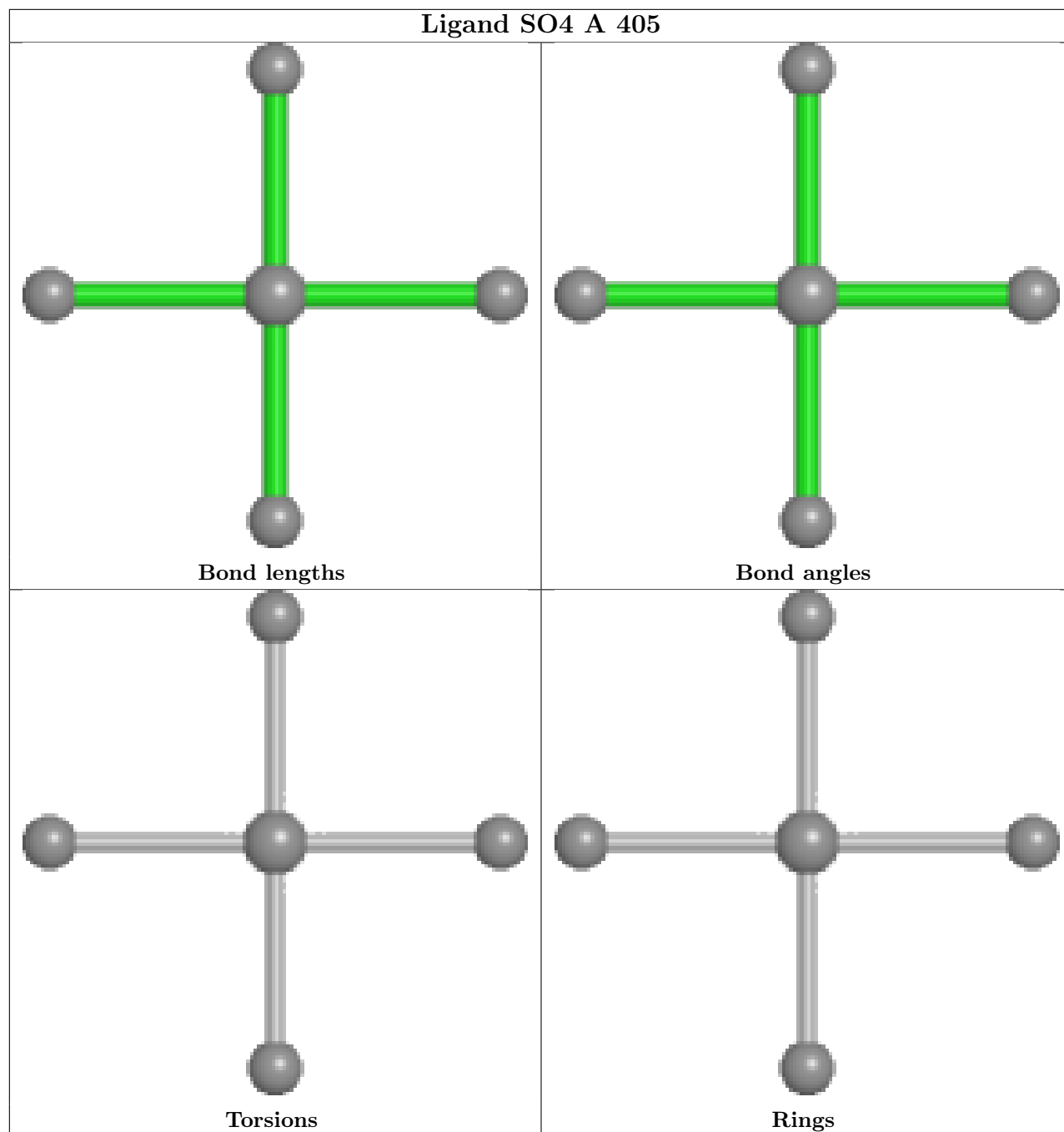












5.7 Other polymers [i](#)

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	321/327 (98%)	-0.03	6 (1%) 66 62	27, 43, 70, 175	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	70	LEU	7.6
1	A	113	GLY	6.6
1	A	112	VAL	3.7
1	A	211	ARG	2.5
1	A	88	ARG	2.2
1	A	8	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.

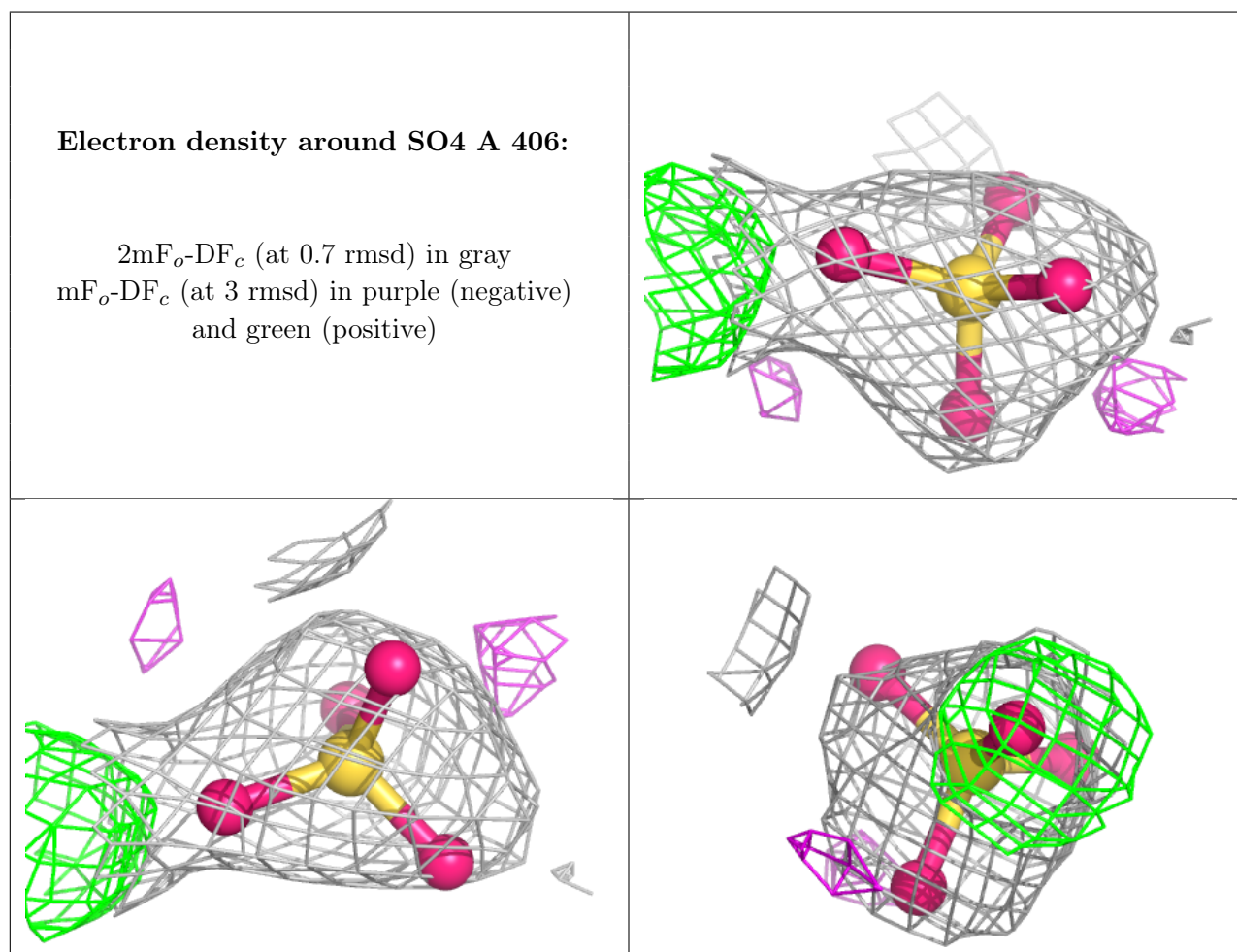
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	A	406	5/5	0.78	0.33	82,89,89,91	0

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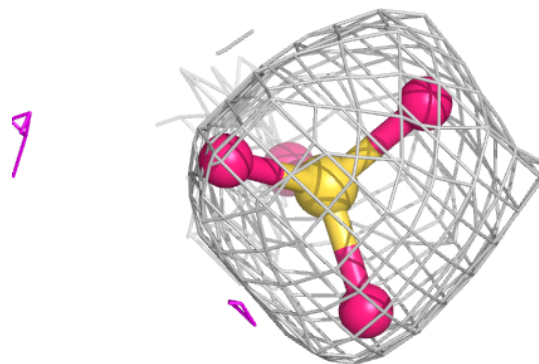
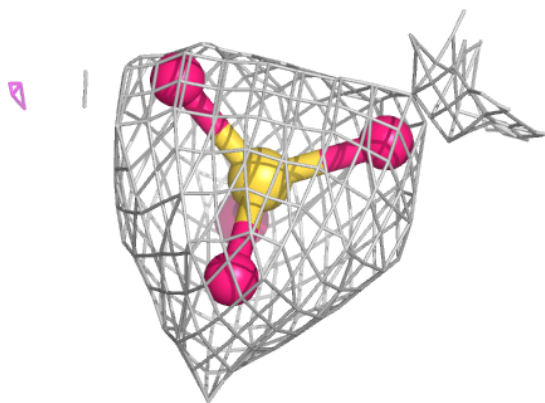
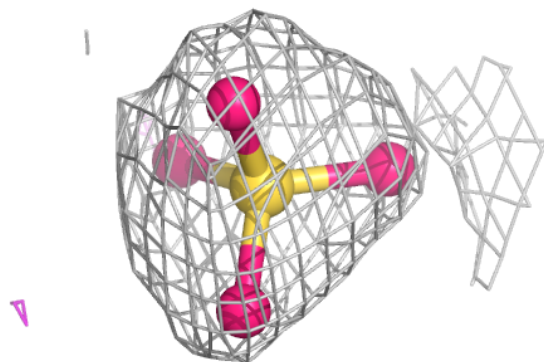
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	A	405	5/5	0.85	0.21	89,90,98,98	0
3	NMN	A	402	22/22	0.85	0.21	50,76,105,107	0
2	AMP	A	401	23/23	0.93	0.16	35,60,84,96	0
4	SO4	A	404	5/5	0.98	0.22	38,39,41,56	0
4	SO4	A	403	5/5	0.99	0.15	43,48,48,52	0

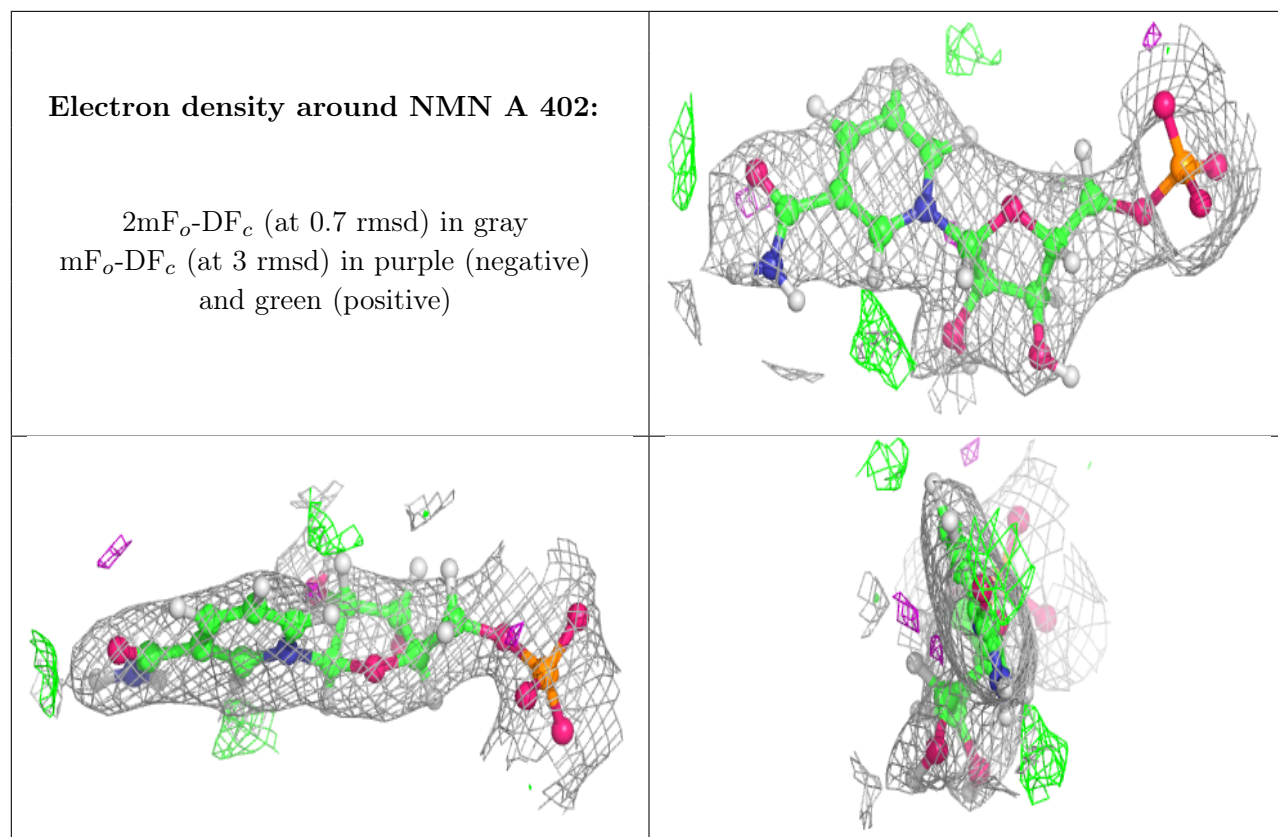
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around SO4 A 405:

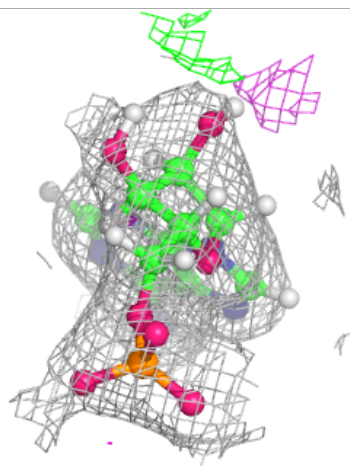
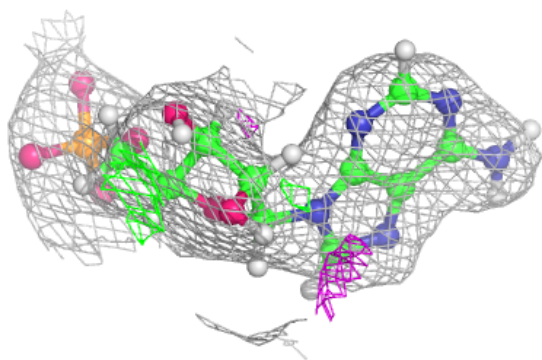
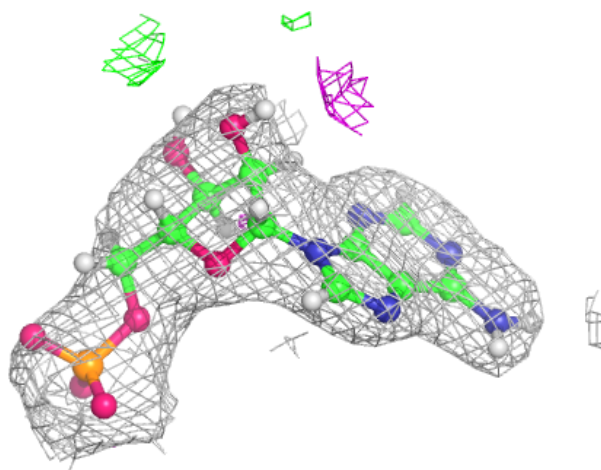
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





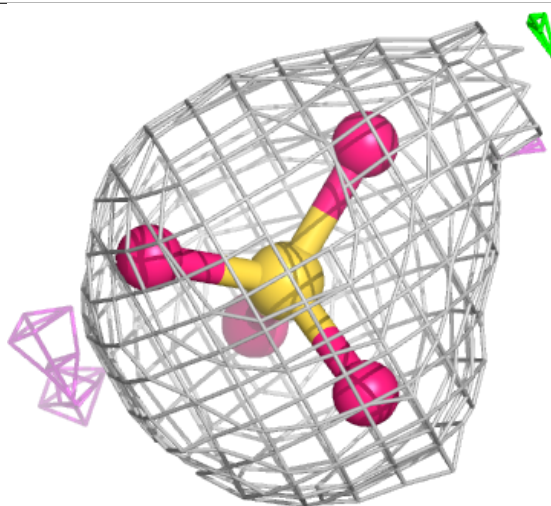
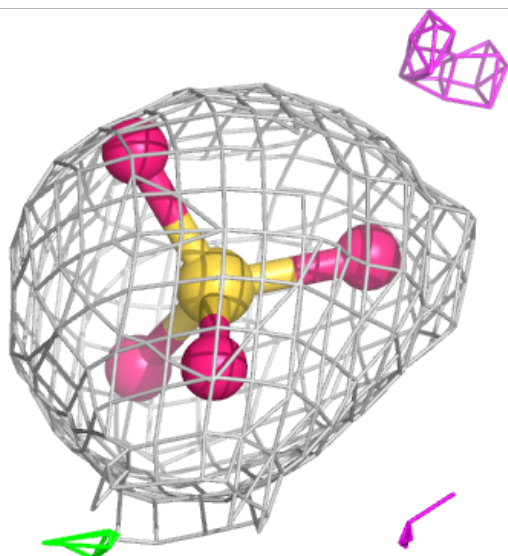
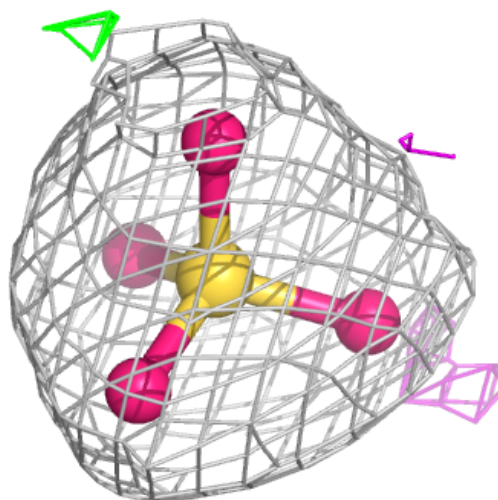
Electron density around AMP A 401:

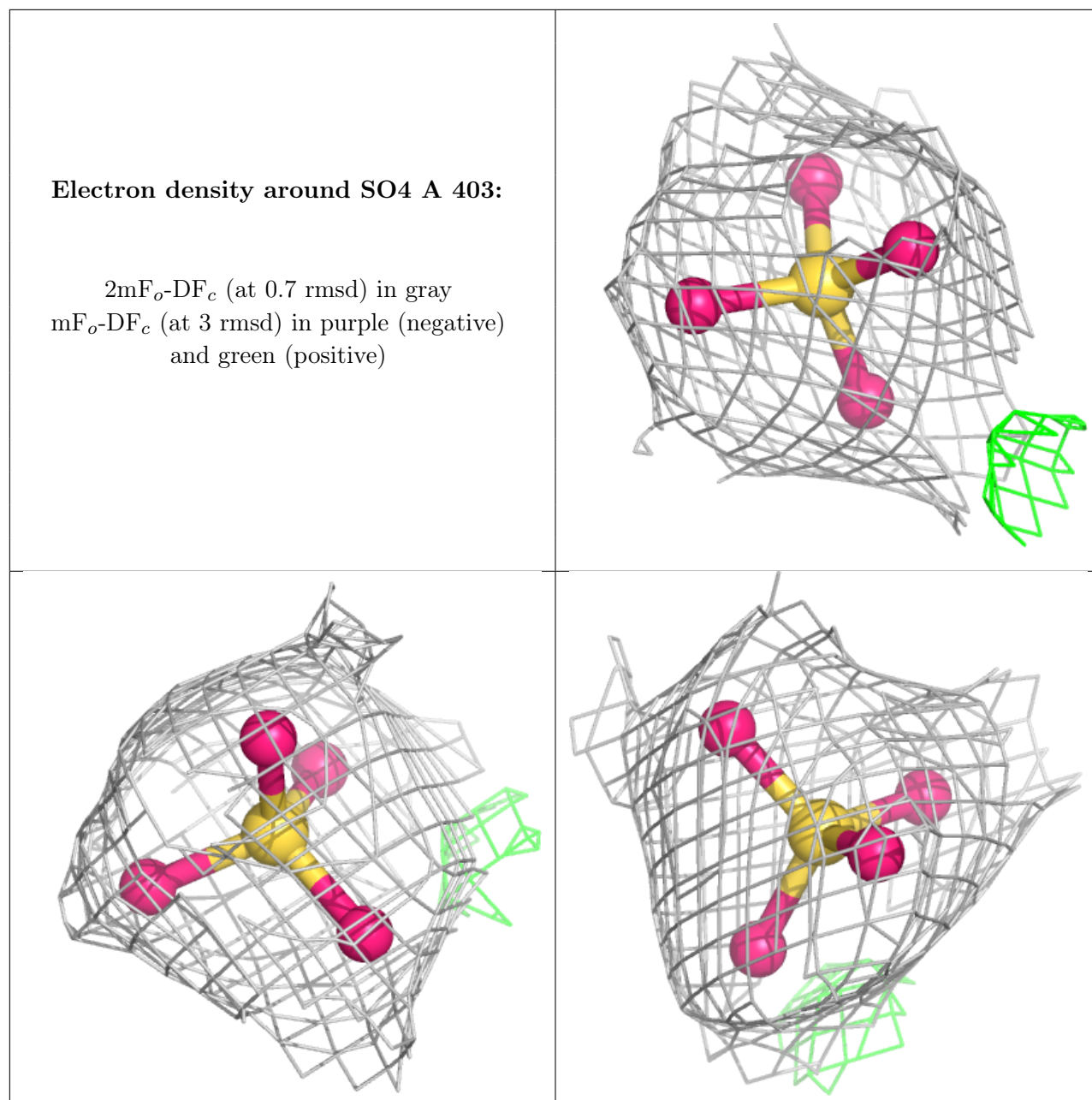
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around SO4 A 404:

$2mF_o-DF_c$ (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.