



Full wwPDB X-ray Structure Validation Report ⓘ

May 20, 2021 – 04:17 PM EDT

PDB ID : 7JW9
Title : Ternary cocrystal structure of alkanesulfonate monooxygenase Msd from *Pseudomonas fluorescens*
Authors : Liew, J.J.M.; Dowling, D.P.
Deposited on : 2020-08-25
Resolution : 2.39 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.18
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) : 2.18

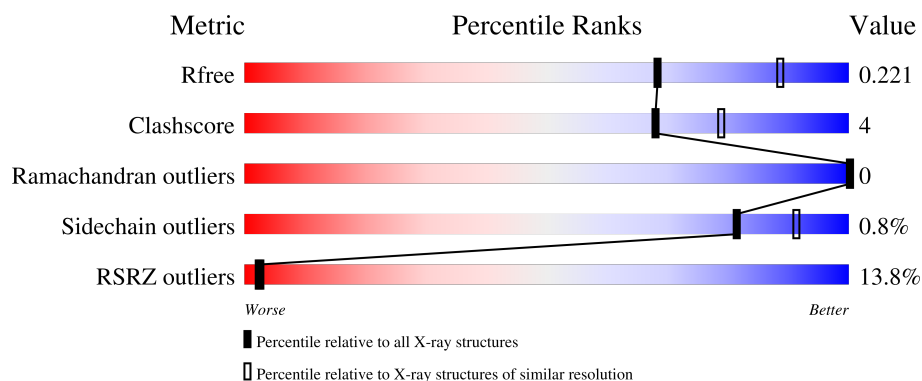
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	404	<div> <div>11%</div> <div> <div></div> <div>82%</div> <div>12%</div> <div>6%</div> </div> </div>
1	B	404	<div> <div>15%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>6%</div> </div> </div>
1	C	404	<div> <div>12%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>6%</div> </div> </div>
1	D	404	<div> <div>14%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>6%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12019 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 Alkanesulfonate monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	378	Total	C	N	O	S	0	1	0
			2922	1854	517	546	5			
1	B	378	Total	C	N	O	S	0	1	0
			2940	1866	523	546	5			
1	C	378	Total	C	N	O	S	0	0	0
			2928	1859	520	544	5			
1	D	378	Total	C	N	O	S	0	2	0
			2946	1870	523	548	5			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	initiating methionine	UNP Q3K9A1
A	-21	GLY	-	expression tag	UNP Q3K9A1
A	-20	SER	-	expression tag	UNP Q3K9A1
A	-19	SER	-	expression tag	UNP Q3K9A1
A	-18	HIS	-	expression tag	UNP Q3K9A1
A	-17	HIS	-	expression tag	UNP Q3K9A1
A	-16	HIS	-	expression tag	UNP Q3K9A1
A	-15	HIS	-	expression tag	UNP Q3K9A1
A	-14	HIS	-	expression tag	UNP Q3K9A1
A	-13	HIS	-	expression tag	UNP Q3K9A1
A	-12	SER	-	expression tag	UNP Q3K9A1
A	-11	SER	-	expression tag	UNP Q3K9A1
A	-10	GLY	-	expression tag	UNP Q3K9A1
A	-9	LEU	-	expression tag	UNP Q3K9A1
A	-8	VAL	-	expression tag	UNP Q3K9A1
A	-7	PRO	-	expression tag	UNP Q3K9A1
A	-6	ARG	-	expression tag	UNP Q3K9A1
A	-5	GLY	-	expression tag	UNP Q3K9A1
A	-4	SER	-	expression tag	UNP Q3K9A1
A	-3	HIS	-	expression tag	UNP Q3K9A1
A	-2	MET	-	expression tag	UNP Q3K9A1

Continued on next page...

Continued from previous page...

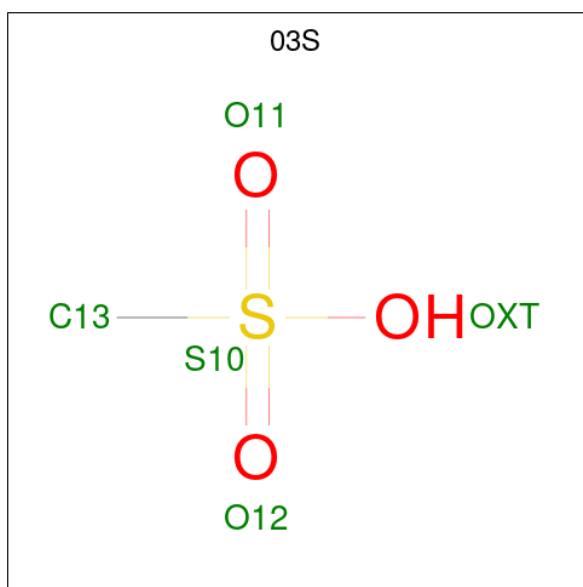
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ALA	-	expression tag	UNP Q3K9A1
A	0	SER	-	expression tag	UNP Q3K9A1
B	-22	MET	-	initiating methionine	UNP Q3K9A1
B	-21	GLY	-	expression tag	UNP Q3K9A1
B	-20	SER	-	expression tag	UNP Q3K9A1
B	-19	SER	-	expression tag	UNP Q3K9A1
B	-18	HIS	-	expression tag	UNP Q3K9A1
B	-17	HIS	-	expression tag	UNP Q3K9A1
B	-16	HIS	-	expression tag	UNP Q3K9A1
B	-15	HIS	-	expression tag	UNP Q3K9A1
B	-14	HIS	-	expression tag	UNP Q3K9A1
B	-13	HIS	-	expression tag	UNP Q3K9A1
B	-12	SER	-	expression tag	UNP Q3K9A1
B	-11	SER	-	expression tag	UNP Q3K9A1
B	-10	GLY	-	expression tag	UNP Q3K9A1
B	-9	LEU	-	expression tag	UNP Q3K9A1
B	-8	VAL	-	expression tag	UNP Q3K9A1
B	-7	PRO	-	expression tag	UNP Q3K9A1
B	-6	ARG	-	expression tag	UNP Q3K9A1
B	-5	GLY	-	expression tag	UNP Q3K9A1
B	-4	SER	-	expression tag	UNP Q3K9A1
B	-3	HIS	-	expression tag	UNP Q3K9A1
B	-2	MET	-	expression tag	UNP Q3K9A1
B	-1	ALA	-	expression tag	UNP Q3K9A1
B	0	SER	-	expression tag	UNP Q3K9A1
C	-22	MET	-	initiating methionine	UNP Q3K9A1
C	-21	GLY	-	expression tag	UNP Q3K9A1
C	-20	SER	-	expression tag	UNP Q3K9A1
C	-19	SER	-	expression tag	UNP Q3K9A1
C	-18	HIS	-	expression tag	UNP Q3K9A1
C	-17	HIS	-	expression tag	UNP Q3K9A1
C	-16	HIS	-	expression tag	UNP Q3K9A1
C	-15	HIS	-	expression tag	UNP Q3K9A1
C	-14	HIS	-	expression tag	UNP Q3K9A1
C	-13	HIS	-	expression tag	UNP Q3K9A1
C	-12	SER	-	expression tag	UNP Q3K9A1
C	-11	SER	-	expression tag	UNP Q3K9A1
C	-10	GLY	-	expression tag	UNP Q3K9A1
C	-9	LEU	-	expression tag	UNP Q3K9A1
C	-8	VAL	-	expression tag	UNP Q3K9A1
C	-7	PRO	-	expression tag	UNP Q3K9A1
C	-6	ARG	-	expression tag	UNP Q3K9A1

Continued on next page...

Continued from previous page...

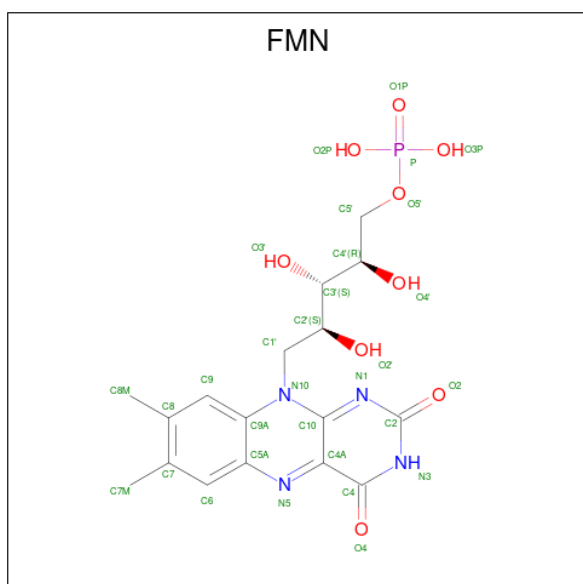
Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	GLY	-	expression tag	UNP Q3K9A1
C	-4	SER	-	expression tag	UNP Q3K9A1
C	-3	HIS	-	expression tag	UNP Q3K9A1
C	-2	MET	-	expression tag	UNP Q3K9A1
C	-1	ALA	-	expression tag	UNP Q3K9A1
C	0	SER	-	expression tag	UNP Q3K9A1
D	-22	MET	-	initiating methionine	UNP Q3K9A1
D	-21	GLY	-	expression tag	UNP Q3K9A1
D	-20	SER	-	expression tag	UNP Q3K9A1
D	-19	SER	-	expression tag	UNP Q3K9A1
D	-18	HIS	-	expression tag	UNP Q3K9A1
D	-17	HIS	-	expression tag	UNP Q3K9A1
D	-16	HIS	-	expression tag	UNP Q3K9A1
D	-15	HIS	-	expression tag	UNP Q3K9A1
D	-14	HIS	-	expression tag	UNP Q3K9A1
D	-13	HIS	-	expression tag	UNP Q3K9A1
D	-12	SER	-	expression tag	UNP Q3K9A1
D	-11	SER	-	expression tag	UNP Q3K9A1
D	-10	GLY	-	expression tag	UNP Q3K9A1
D	-9	LEU	-	expression tag	UNP Q3K9A1
D	-8	VAL	-	expression tag	UNP Q3K9A1
D	-7	PRO	-	expression tag	UNP Q3K9A1
D	-6	ARG	-	expression tag	UNP Q3K9A1
D	-5	GLY	-	expression tag	UNP Q3K9A1
D	-4	SER	-	expression tag	UNP Q3K9A1
D	-3	HIS	-	expression tag	UNP Q3K9A1
D	-2	MET	-	expression tag	UNP Q3K9A1
D	-1	ALA	-	expression tag	UNP Q3K9A1
D	0	SER	-	expression tag	UNP Q3K9A1

- Molecule 2 is methanesulfonic acid (three-letter code: 03S) (formula: CH₄O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			5	1	3	1		
2	B	1	Total	C	O	S	0	0
			5	1	3	1		
2	C	1	Total	C	O	S	0	0
			5	1	3	1		
2	D	1	Total	C	O	S	0	0
			5	1	3	1		

- Molecule 3 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
3	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
3	C	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
3	D	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		

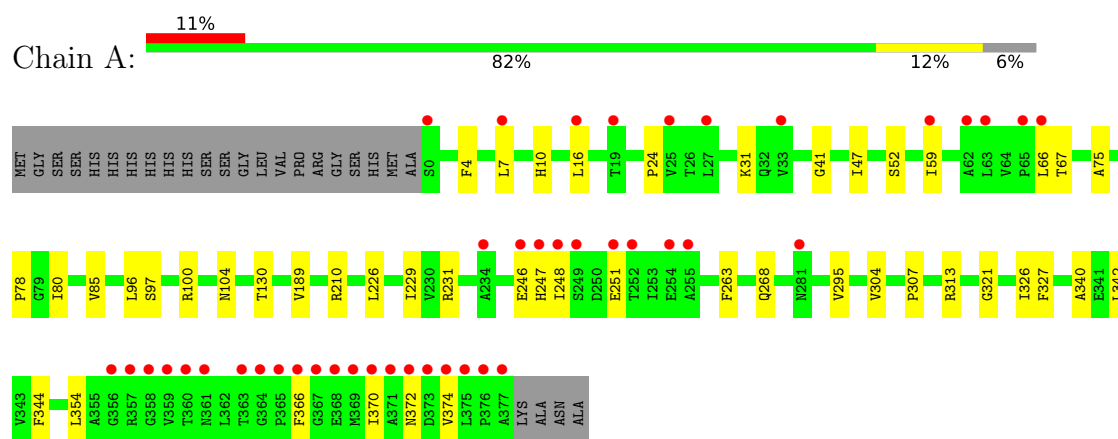
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	34	Total	O	0	0
			34	34		
5	B	27	Total	O	0	0
			27	27		
5	C	39	Total	O	0	0
			39	39		
5	D	38	Total	O	0	0
			38	38		

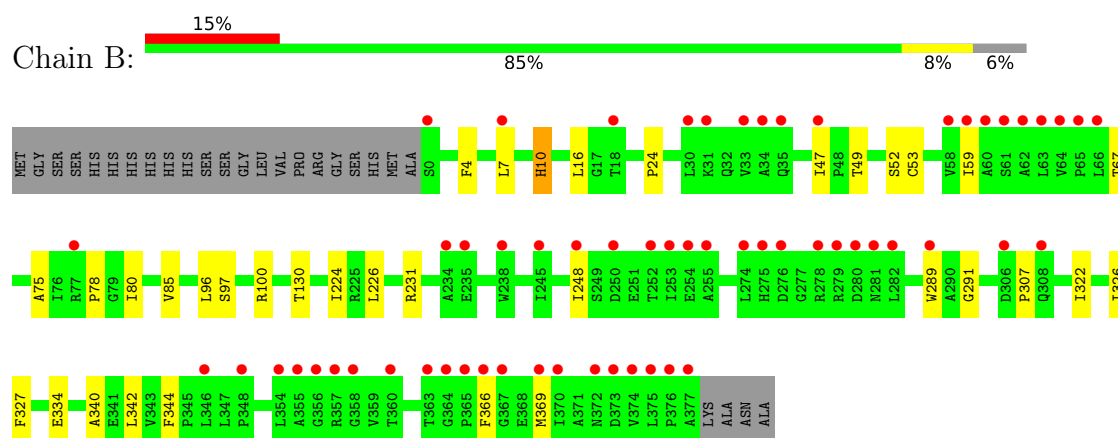
3 Residue-property plots [i](#)

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.

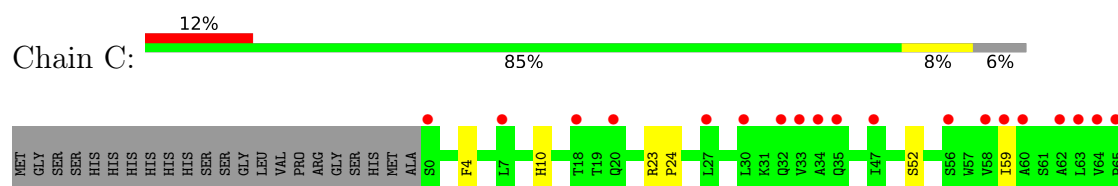
• Molecule 1: Alkanesulfonate monooxygenase

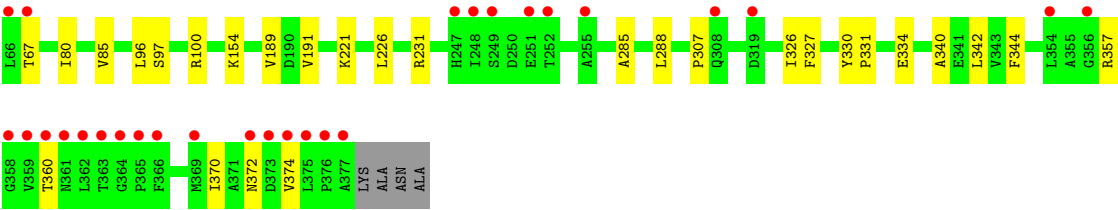


• Molecule 1: Alkanesulfonate monooxygenase

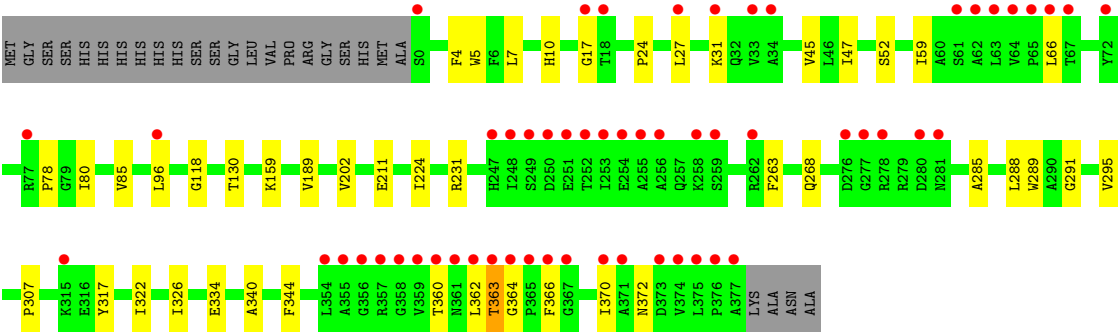
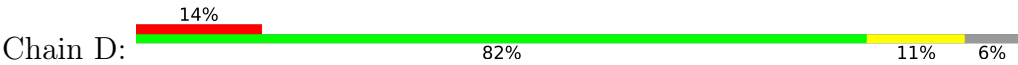


• Molecule 1: Alkanesulfonate monooxygenase





● Molecule 1: Alkanesulfonate monooxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	92.47 Å 92.47 Å 320.54 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.24 – 2.39 46.24 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.6 (46.24-2.39) 99.6 (46.24-2.39)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.39 Å)	Xtriage
Refinement program	PHENIX 1.18.2	Depositor
R, R_{free}	0.184 , 0.221 0.184 , 0.221	Depositor DCC
R_{free} test set	3032 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.340	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 45.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.047 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12019	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% 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: 03S, FMN, NA

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	0.24	0/2996	0.41	0/4078
1	B	0.24	0/3014	0.41	0/4097
1	C	0.24	0/2999	0.41	0/4077
1	D	0.24	0/3023	0.41	0/4109
All	All	0.24	0/12032	0.41	0/16361

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 [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	2922	0	2858	32	0
1	B	2940	0	2902	24	0
1	C	2928	0	2885	25	0
1	D	2946	0	2908	31	0
2	A	5	0	3	0	0
2	B	5	0	3	0	0
2	C	5	0	3	0	0
2	D	5	0	3	0	0
3	A	31	0	19	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	31	0	19	0	0
3	C	31	0	19	0	0
3	D	31	0	19	0	0
4	A	1	0	0	0	0
5	A	34	0	0	0	0
5	B	27	0	0	0	0
5	C	39	0	0	0	0
5	D	38	0	0	1	0
All	All	12019	0	11641	90	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 (90) 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:85:VAL:HG21	1:B:80:ILE:HD12	1.72	0.72
1:A:80:ILE:HD13	1:B:85:VAL:HG21	1.77	0.65
1:A:210:ARG:HH22	1:A:321:GLY:HA3	1.62	0.65
1:A:372:ASN:HA	1:D:52:SER:HB3	1.78	0.64
1:C:59:ILE:HD13	1:D:96:LEU:HD11	1.80	0.64
1:D:360:THR:HG22	1:D:362:LEU:H	1.64	0.62
1:A:31:LYS:HD3	1:A:66:LEU:HD13	1.81	0.62
1:A:59:ILE:HD13	1:B:96:LEU:HD11	1.81	0.62
1:C:85:VAL:HG21	1:D:80:ILE:HD13	1.84	0.60
1:D:263:PHE:HD2	1:D:268:GLN:HG2	1.69	0.58
1:A:370:ILE:HD11	1:D:17:GLY:HA2	1.86	0.58
1:A:96:LEU:HD11	1:B:59:ILE:HD13	1.86	0.57
1:B:78:PRO:HG2	1:B:130:THR:HG23	1.88	0.55
1:A:370:ILE:HD12	1:D:295:VAL:HB	1.89	0.55
1:D:317:TYR:HB3	1:D:322:ILE:HD12	1.88	0.55
1:D:159:LYS:NZ	5:D:502:HOH:O	2.40	0.54
1:C:96:LEU:HD22	1:D:27:LEU:HB2	1.89	0.54
1:C:96:LEU:HD11	1:D:59:ILE:HD13	1.90	0.53
1:C:4:PHE:HB2	1:C:326:ILE:HA	1.91	0.53
1:A:78:PRO:HG2	1:A:130:THR:HG23	1.91	0.53
1:D:340:ALA:O	1:D:344:PHE:HB2	2.09	0.52
1:C:370:ILE:HB	1:C:374:VAL:HB	1.92	0.52
1:B:231:ARG:O	1:B:307:PRO:HD3	2.10	0.51
1:C:357:ARG:NH2	1:C:360:THR:O	2.43	0.51
1:A:16:LEU:HB2	1:A:248:ILE:HD11	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:PHE:HD2	1:A:268:GLN:HG2	1.76	0.51
1:B:97:SER:O	1:B:100:ARG:HD3	2.11	0.51
1:C:80:ILE:HD13	1:D:85:VAL:HG21	1.92	0.51
1:C:285:ALA:HB3	1:C:288:LEU:HB3	1.92	0.51
1:B:340:ALA:O	1:B:344:PHE:HB2	2.11	0.50
1:B:369:MET:HG3	1:C:52:SER:HB2	1.94	0.50
1:A:251:GLU:OE1	1:A:251:GLU:N	2.39	0.50
1:C:340:ALA:O	1:C:344:PHE:HB2	2.12	0.49
1:B:4:PHE:HB2	1:B:326:ILE:HA	1.94	0.49
1:A:340:ALA:O	1:A:344:PHE:HB2	2.12	0.49
1:A:52:SER:HB3	1:D:372:ASN:HA	1.94	0.49
1:D:202:VAL:HG11	1:D:322:ILE:HD11	1.94	0.49
1:D:363:THR:OG1	1:D:364:GLY:N	2.45	0.48
1:D:78:PRO:HG2	1:D:130:THR:HG23	1.95	0.48
1:A:41:GLY:HA3	1:A:354:LEU:HD13	1.96	0.48
1:A:97:SER:O	1:A:100:ARG:HD3	2.14	0.48
1:C:231:ARG:O	1:C:307:PRO:HD3	2.13	0.48
1:A:231:ARG:O	1:A:307:PRO:HD3	2.14	0.48
1:A:307:PRO:HG3	1:A:342:LEU:HB3	1.95	0.48
1:B:16:LEU:HB2	1:B:248:ILE:HD11	1.96	0.48
1:C:334:GLU:N	1:C:334:GLU:OE1	2.46	0.47
1:A:295:VAL:HG13	1:D:370:ILE:HG23	1.97	0.47
1:D:285:ALA:HB3	1:D:288:LEU:HB3	1.96	0.47
1:D:289:TRP:CZ2	1:D:291:GLY:HA3	2.49	0.47
1:A:4:PHE:HB2	1:A:326:ILE:HA	1.96	0.47
1:B:7:LEU:HD12	1:B:47:ILE:HG12	1.97	0.47
1:B:224:ILE:HB	1:B:322:ILE:HD13	1.97	0.47
1:A:246:GLU:HG3	1:A:247:HIS:CD2	2.51	0.46
1:B:226:LEU:O	1:B:327:PHE:HA	2.16	0.46
1:D:231:ARG:O	1:D:307:PRO:HD3	2.16	0.45
1:D:4:PHE:HB2	1:D:326:ILE:HA	1.98	0.45
1:C:307:PRO:HG3	1:C:342:LEU:HB3	1.99	0.45
1:A:7:LEU:HD12	1:A:47:ILE:HG12	1.98	0.45
1:D:224:ILE:HB	1:D:322:ILE:HD13	1.97	0.45
1:A:366:PHE:HE1	1:D:24:PRO:HD3	1.81	0.45
1:B:67:THR:OG1	1:B:100:ARG:NH2	2.50	0.45
1:C:97:SER:O	1:C:100:ARG:HD3	2.17	0.45
1:C:191:VAL:HG22	1:C:221:LYS:HB2	1.99	0.44
1:B:10:HIS:HB3	1:B:53:CYS:SG	2.57	0.44
1:B:334:GLU:N	1:B:334:GLU:OE1	2.47	0.44
1:B:24:PRO:HG3	1:C:357:ARG:HA	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:7:LEU:HD12	1:D:47:ILE:HG12	1.99	0.43
1:B:289:TRP:CZ2	1:B:291:GLY:HA3	2.54	0.43
1:D:5:TRP:HB3	1:D:45:VAL:HG12	2.00	0.43
1:B:307:PRO:HG3	1:B:342:LEU:HB3	2.01	0.43
1:C:67:THR:OG1	1:C:100:ARG:NH2	2.51	0.43
1:A:67:THR:OG1	1:A:100:ARG:NH2	2.52	0.43
1:A:229:ILE:HB	1:A:304:VAL:HG22	2.01	0.42
1:C:23:ARG:NH2	1:C:334:GLU:OE2	2.27	0.42
1:B:52:SER:HB3	1:C:372:ASN:HA	2.01	0.42
1:B:334:GLU:HG3	1:C:334:GLU:HG3	2.01	0.42
1:A:370:ILE:HB	1:A:374:VAL:HB	2.00	0.42
1:C:226:LEU:O	1:C:327:PHE:HA	2.19	0.42
1:D:31:LYS:HD3	1:D:66:LEU:HD13	2.01	0.42
1:D:334:GLU:OE1	1:D:334:GLU:N	2.51	0.41
1:B:49:THR:HB	1:B:75:ALA:HB3	2.02	0.41
1:D:263:PHE:CD2	1:D:268:GLN:HG2	2.51	0.41
1:A:75:ALA:HA	1:A:104:ASN:O	2.21	0.41
1:B:366:PHE:HE1	1:C:24:PRO:HD3	1.86	0.41
1:A:24:PRO:HD3	1:D:366:PHE:HE1	1.86	0.40
1:C:330:TYR:HA	1:C:331:PRO:HA	1.95	0.40
1:A:226:LEU:O	1:A:327:PHE:HA	2.20	0.40
1:A:248:ILE:HD13	1:A:295:VAL:HG21	2.02	0.40
1:C:154:LYS:O	1:D:118:GLY:HA2	2.22	0.40
1:A:313:ARG:HA	1:A:313:ARG:HD3	1.93	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	377/404 (93%)	364 (97%)	13 (3%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	377/404 (93%)	367 (97%)	10 (3%)	0	100	100
1	C	376/404 (93%)	363 (96%)	13 (4%)	0	100	100
1	D	378/404 (94%)	367 (97%)	11 (3%)	0	100	100
All	All	1508/1616 (93%)	1461 (97%)	47 (3%)	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	298/321 (93%)	296 (99%)	2 (1%)	84	92
1	B	302/321 (94%)	301 (100%)	1 (0%)	92	97
1	C	300/321 (94%)	298 (99%)	2 (1%)	84	92
1	D	303/321 (94%)	299 (99%)	4 (1%)	69	84
All	All	1203/1284 (94%)	1194 (99%)	9 (1%)	81	92

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	HIS
1	A	189	VAL
1	B	10	HIS
1	C	10	HIS
1	C	189	VAL
1	D	10	HIS
1	D	189	VAL
1	D	211	GLU
1	D	363	THR

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 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 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	$\# Z > 2$
2	03S	A	401	-	4,4,4	0.46	0	5,6,6	1.12	1 (20%)
2	03S	D	401	-	4,4,4	0.46	0	5,6,6	1.10	1 (20%)
3	FMN	C	402	-	31,33,33	1.99	3 (9%)	40,50,50	2.05	10 (25%)
3	FMN	D	402	-	31,33,33	1.99	3 (9%)	40,50,50	2.03	10 (25%)
2	03S	B	401	-	4,4,4	0.46	0	5,6,6	1.10	1 (20%)
3	FMN	B	402	-	31,33,33	1.99	3 (9%)	40,50,50	2.05	9 (22%)
3	FMN	A	402	-	31,33,33	1.99	3 (9%)	40,50,50	2.08	10 (25%)
2	03S	C	401	-	4,4,4	0.46	0	5,6,6	1.11	1 (20%)

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	FMN	D	402	-	-	3/18/18/18	0/3/3/3
3	FMN	B	402	-	-	5/18/18/18	0/3/3/3
3	FMN	C	402	-	-	3/18/18/18	0/3/3/3
3	FMN	A	402	-	-	3/18/18/18	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	402	FMN	C4A-C10	8.98	1.47	1.38
3	D	402	FMN	C4A-C10	8.98	1.47	1.38
3	B	402	FMN	C4A-C10	8.97	1.47	1.38
3	A	402	FMN	C4A-C10	8.96	1.47	1.38
3	A	402	FMN	C4-C4A	4.06	1.48	1.41
3	C	402	FMN	C4-C4A	4.03	1.48	1.41
3	D	402	FMN	C4-C4A	4.01	1.48	1.41
3	B	402	FMN	C4-C4A	4.00	1.48	1.41
3	A	402	FMN	C2-N1	-2.35	1.33	1.38
3	D	402	FMN	C2-N1	-2.30	1.33	1.38
3	C	402	FMN	C2-N1	-2.29	1.33	1.38
3	B	402	FMN	C2-N1	-2.29	1.33	1.38

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	FMN	C4-N3-C2	7.26	121.28	115.14
3	D	402	FMN	C4-N3-C2	7.12	121.16	115.14
3	C	402	FMN	C4-N3-C2	7.10	121.14	115.14
3	B	402	FMN	C4-N3-C2	7.06	121.11	115.14
3	A	402	FMN	C4A-C4-N3	-4.60	117.14	123.43
3	B	402	FMN	C4A-C4-N3	-4.60	117.14	123.43
3	D	402	FMN	C4A-C4-N3	-4.59	117.15	123.43
3	B	402	FMN	C1'-N10-C9A	4.59	121.91	118.29
3	C	402	FMN	C4A-C4-N3	-4.56	117.19	123.43
3	C	402	FMN	C1'-N10-C9A	4.18	121.58	118.29
3	D	402	FMN	C1'-N10-C9A	4.17	121.58	118.29
3	A	402	FMN	C4-C4A-C10	-4.01	117.30	119.95
3	A	402	FMN	C1'-N10-C9A	3.95	121.40	118.29
3	A	402	FMN	C4A-N5-C5A	3.89	120.66	116.77
3	B	402	FMN	C4A-N5-C5A	3.83	120.60	116.77
3	C	402	FMN	C4A-N5-C5A	3.81	120.57	116.77
3	D	402	FMN	C4A-N5-C5A	3.78	120.55	116.77
3	C	402	FMN	C4-C4A-C10	-3.74	117.47	119.95

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	402	FMN	C4-C4A-C10	-3.71	117.50	119.95
3	C	402	FMN	C5A-C9A-N10	3.52	120.26	117.72
3	B	402	FMN	C4-C4A-C10	-3.51	117.62	119.95
3	A	402	FMN	C5A-C9A-N10	3.51	120.26	117.72
3	B	402	FMN	C5A-C9A-N10	3.46	120.23	117.72
3	D	402	FMN	C5A-C9A-N10	3.41	120.19	117.72
3	A	402	FMN	C4-C4A-N5	3.11	122.16	118.60
3	B	402	FMN	C9A-N10-C10	-3.04	117.92	121.91
3	C	402	FMN	C9A-N10-C10	-2.92	118.08	121.91
3	C	402	FMN	C4-C4A-N5	2.91	121.92	118.60
3	D	402	FMN	C9A-N10-C10	-2.88	118.13	121.91
3	D	402	FMN	C4-C4A-N5	2.84	121.84	118.60
3	A	402	FMN	C9A-N10-C10	-2.79	118.25	121.91
3	B	402	FMN	C4-C4A-N5	2.74	121.73	118.60
3	A	402	FMN	P-O5'-C5'	2.41	124.94	118.30
3	B	402	FMN	P-O5'-C5'	2.30	124.63	118.30
2	A	401	03S	O12-S10-O11	-2.29	111.83	118.02
2	C	401	03S	O12-S10-O11	-2.27	111.90	118.02
3	C	402	FMN	P-O5'-C5'	2.27	124.54	118.30
2	D	401	03S	O12-S10-O11	-2.26	111.93	118.02
2	B	401	03S	O12-S10-O11	-2.25	111.94	118.02
3	D	402	FMN	P-O5'-C5'	2.19	124.32	118.30
3	A	402	FMN	C1'-N10-C10	2.14	120.33	118.41
3	C	402	FMN	C1'-N10-C10	2.13	120.31	118.41
3	D	402	FMN	C1'-N10-C10	2.09	120.28	118.41

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	FMN	N10-C1'-C2'-O2'
3	A	402	FMN	N10-C1'-C2'-C3'
3	B	402	FMN	N10-C1'-C2'-O2'
3	B	402	FMN	N10-C1'-C2'-C3'
3	B	402	FMN	C1'-C2'-C3'-C4'
3	C	402	FMN	N10-C1'-C2'-O2'
3	C	402	FMN	N10-C1'-C2'-C3'
3	D	402	FMN	N10-C1'-C2'-O2'
3	D	402	FMN	N10-C1'-C2'-C3'
3	B	402	FMN	O2'-C2'-C3'-C4'
3	D	402	FMN	O2'-C2'-C3'-C4'
3	B	402	FMN	O2'-C2'-C3'-O3'

Continued on next page...

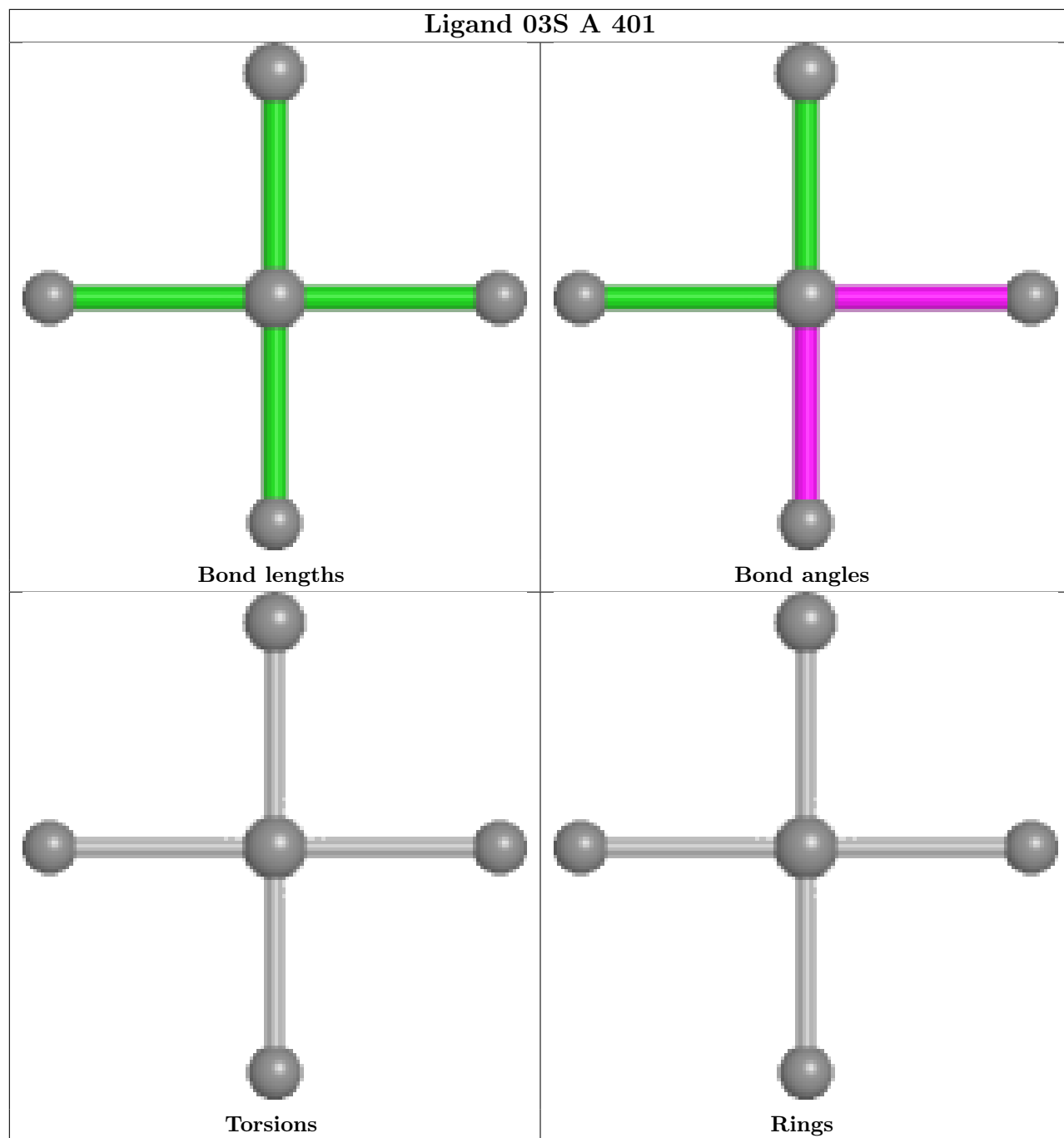
Continued from previous page...

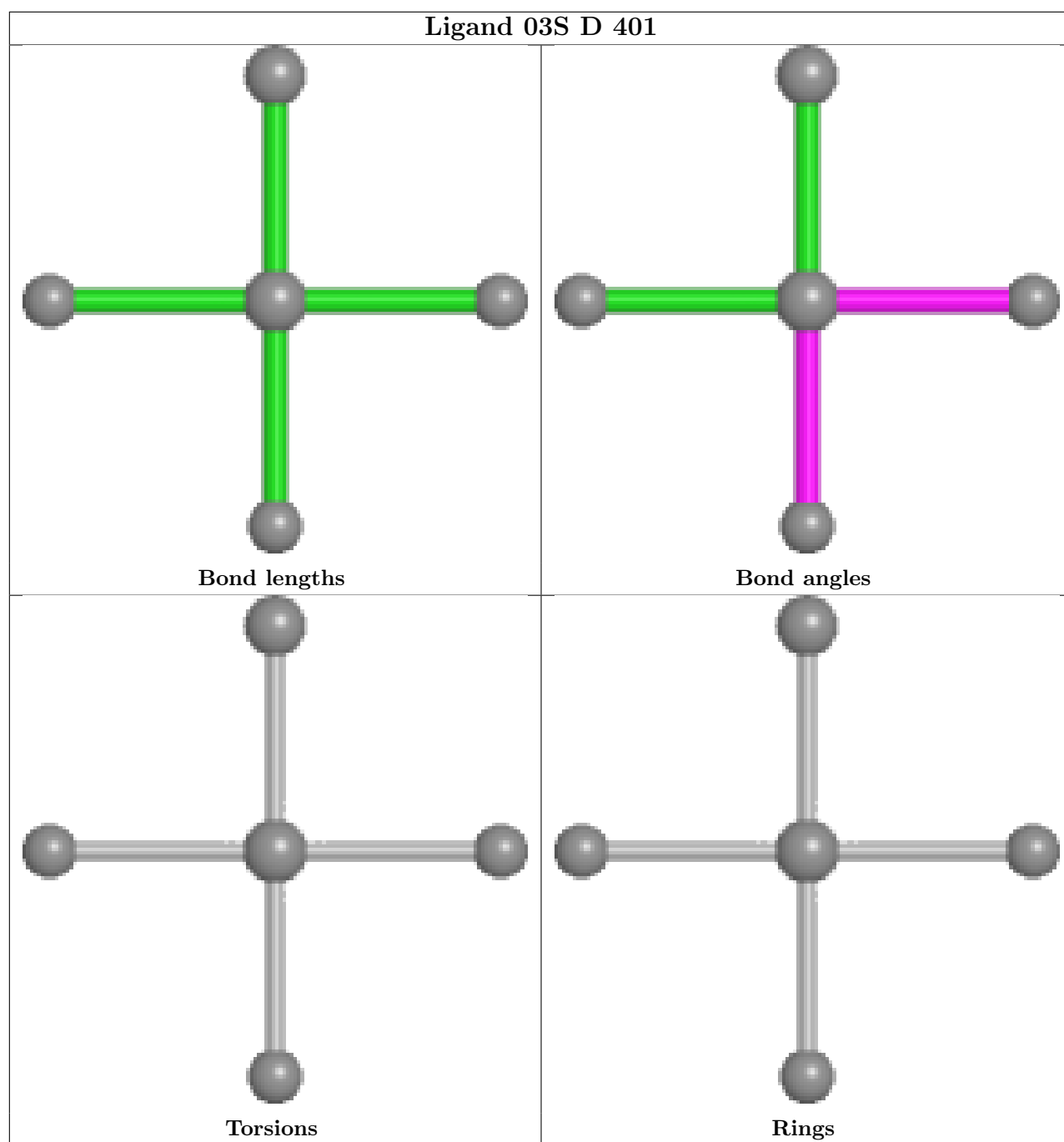
Mol	Chain	Res	Type	Atoms
3	A	402	FMN	O2'-C2'-C3'-C4'
3	C	402	FMN	O2'-C2'-C3'-C4'

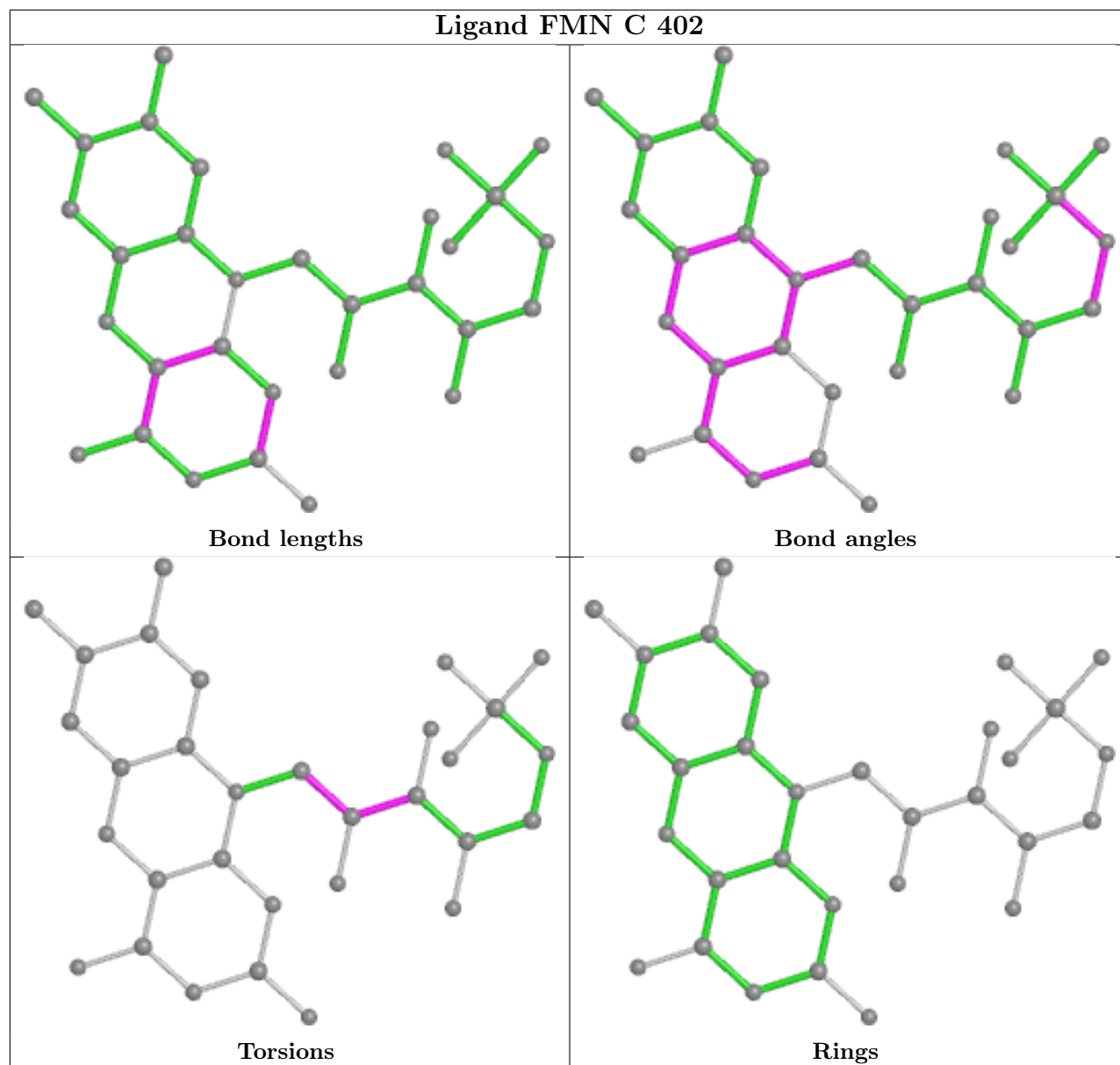
There are no ring outliers.

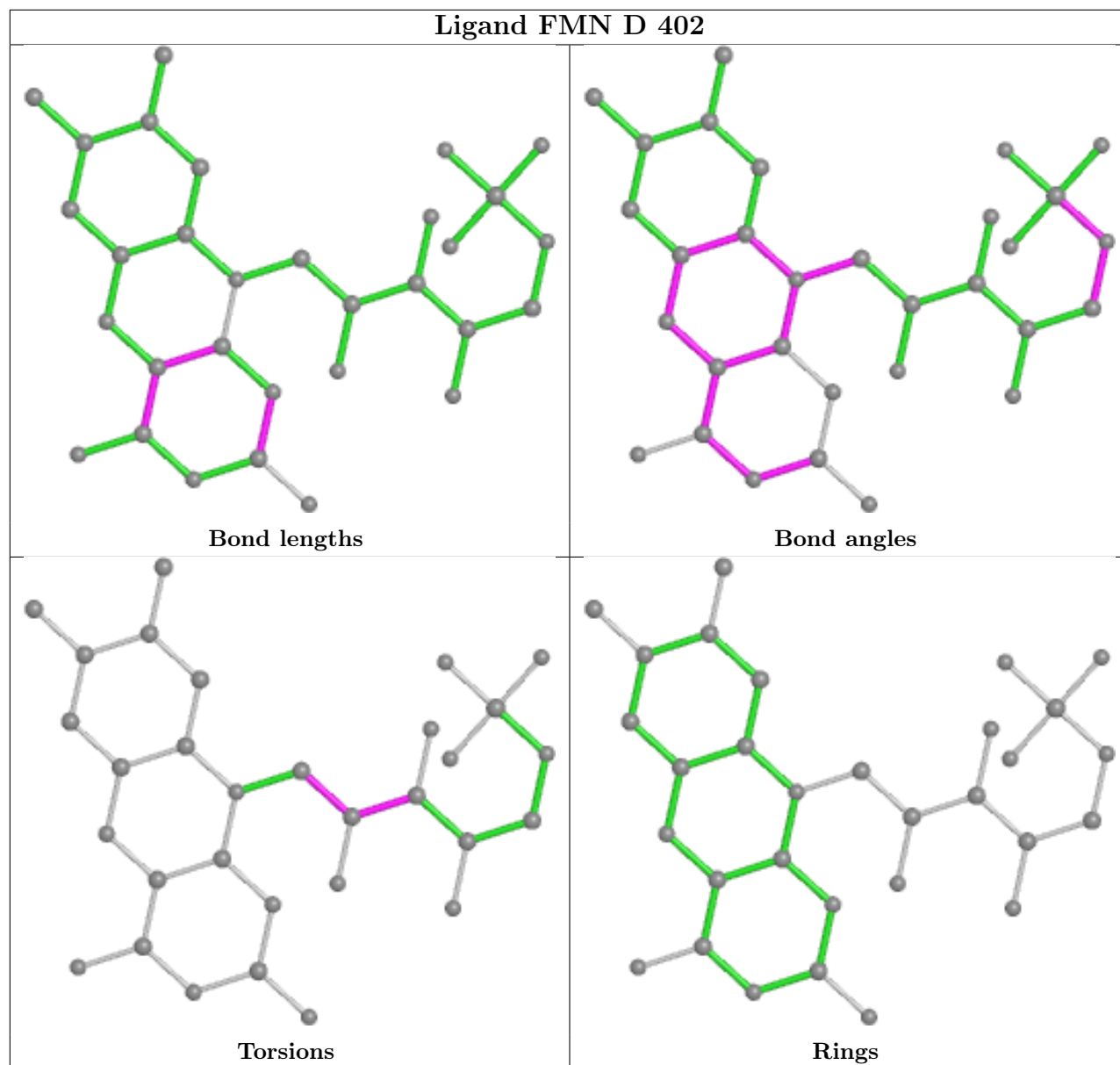
No monomer is involved in short contacts.

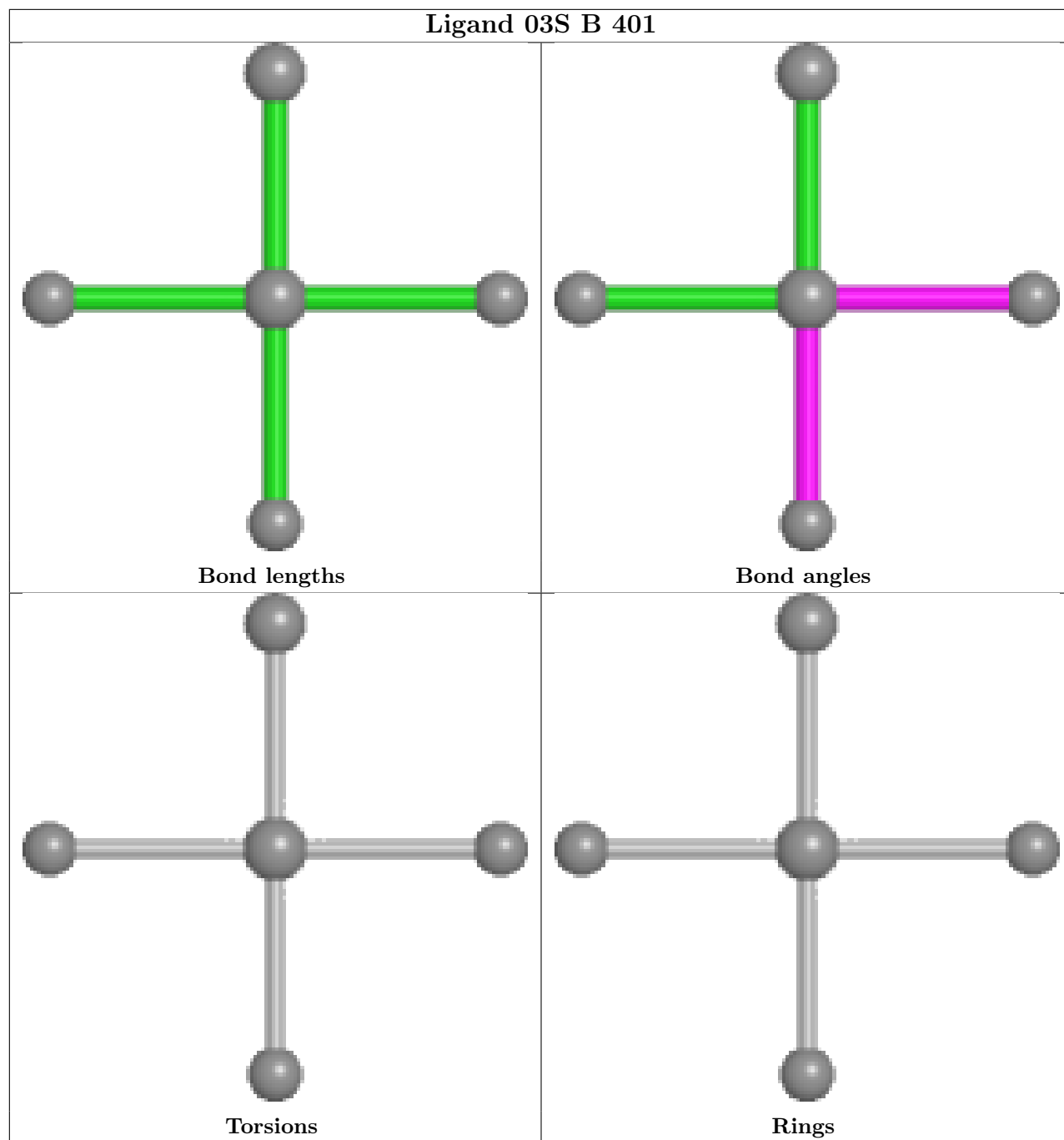
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

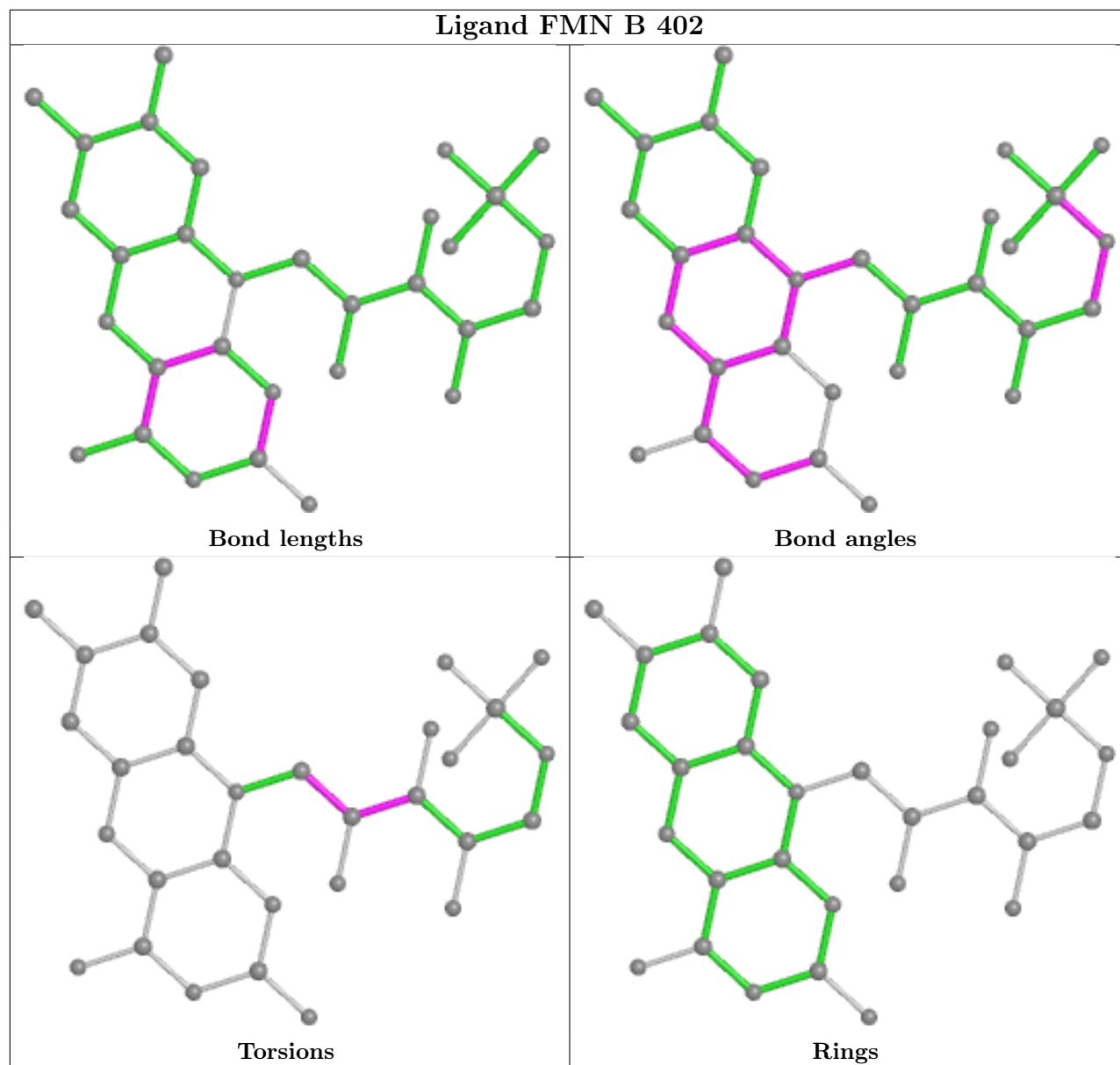


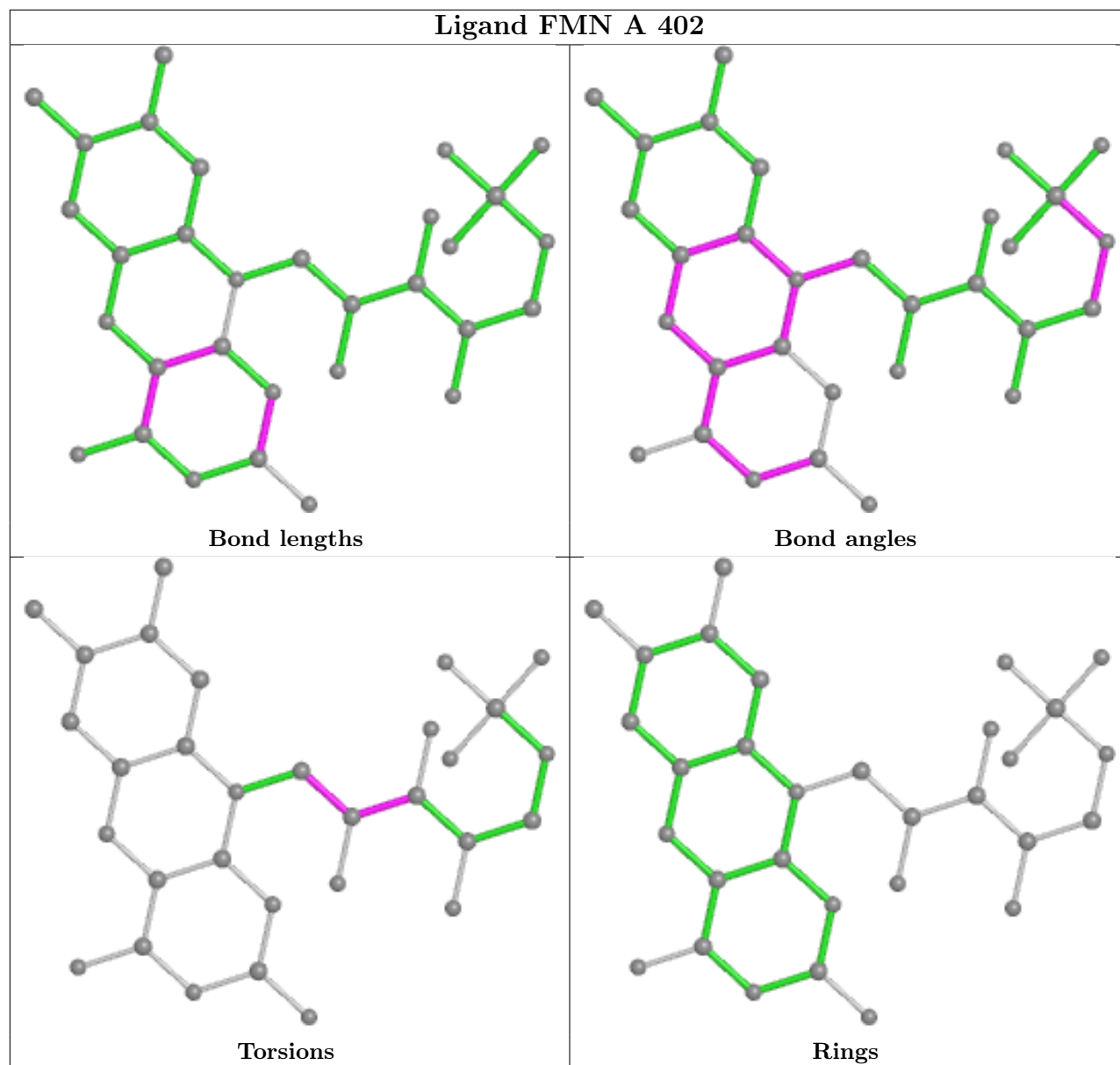


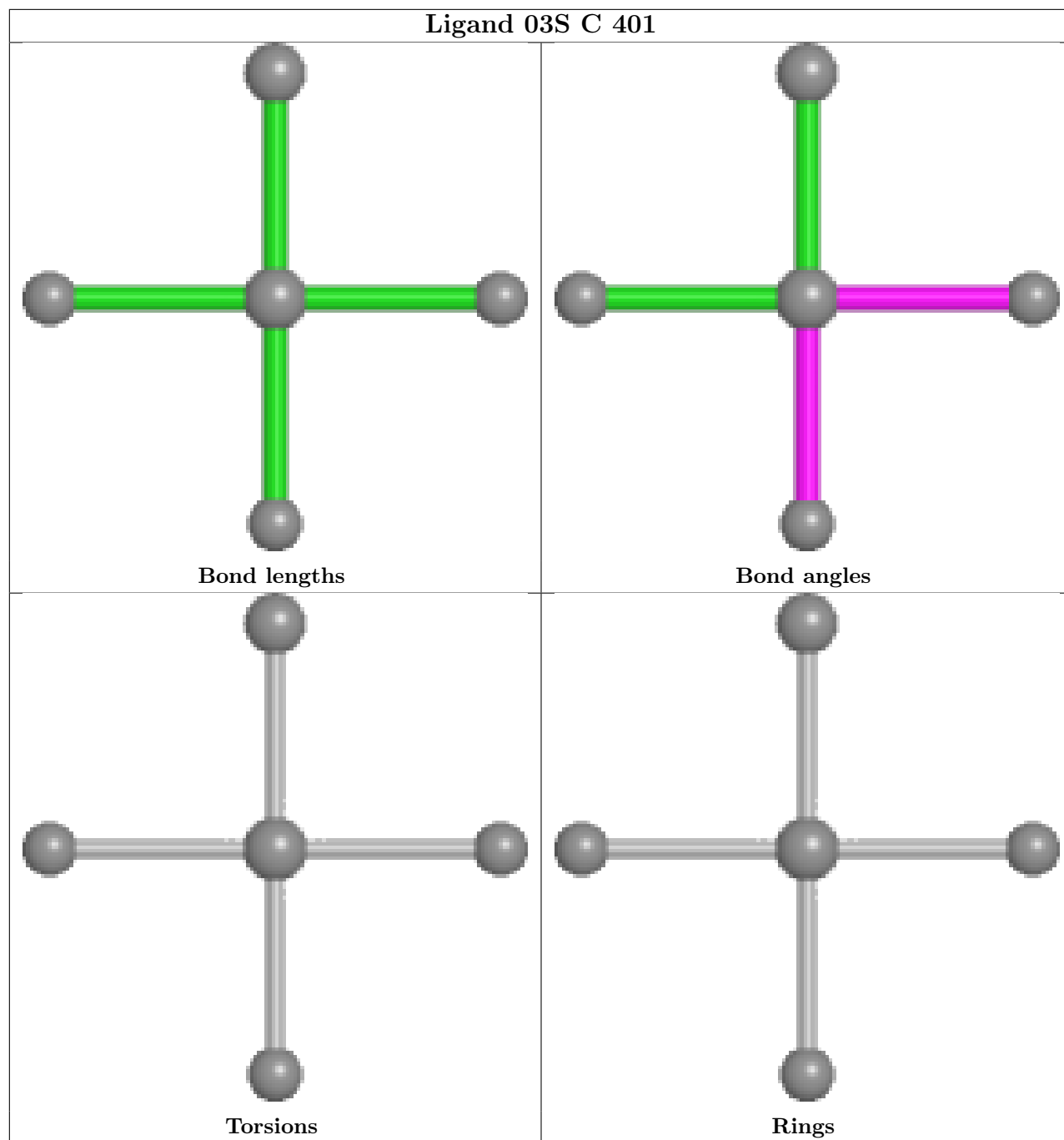












5.7 Other polymers [i](#)

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	378/404 (93%)	0.59	43 (11%) 5 4	39, 52, 89, 103	0
1	B	378/404 (93%)	0.82	61 (16%) 1 1	39, 54, 90, 104	0
1	C	378/404 (93%)	0.69	47 (12%) 4 3	37, 54, 90, 107	0
1	D	378/404 (93%)	0.74	57 (15%) 2 1	37, 51, 95, 113	0
All	All	1512/1616 (93%)	0.71	208 (13%) 2 2	37, 53, 91, 113	0

All (208) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	373	ASP	8.2
1	A	374	VAL	7.1
1	A	366	PHE	7.1
1	B	375	LEU	6.9
1	B	356	GLY	6.6
1	C	361	ASN	6.3
1	C	363	THR	6.0
1	A	370	ILE	5.9
1	A	377	ALA	5.9
1	C	366	PHE	5.8
1	D	366	PHE	5.7
1	C	360	THR	5.7
1	C	364	GLY	5.7
1	D	374	VAL	5.6
1	D	364	GLY	5.6
1	A	375	LEU	5.5
1	D	255	ALA	5.5
1	B	366	PHE	5.4
1	C	374	VAL	5.3
1	A	363	THR	5.3
1	A	0	SER	5.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	377	ALA	5.2
1	D	375	LEU	5.2
1	C	365	PRO	5.0
1	A	372	ASN	5.0
1	D	254	GLU	5.0
1	D	359	VAL	4.9
1	D	17	GLY	4.9
1	C	377	ALA	4.9
1	B	281	ASN	4.9
1	B	248	ILE	4.9
1	D	258	LYS	4.9
1	D	360	THR	4.9
1	D	371	ALA	4.8
1	C	249	SER	4.8
1	C	373	ASP	4.8
1	B	252	THR	4.8
1	D	365	PRO	4.8
1	A	361	ASN	4.8
1	D	362	LEU	4.7
1	B	376	PRO	4.6
1	C	356	GLY	4.6
1	A	365	PRO	4.6
1	B	276	ASP	4.5
1	D	277	GLY	4.4
1	B	280	ASP	4.3
1	A	247	HIS	4.3
1	B	346	LEU	4.3
1	B	279	ARG	4.2
1	D	356	GLY	4.2
1	B	363	THR	4.2
1	C	375	LEU	4.2
1	A	19	THR	4.1
1	A	371	ALA	4.1
1	A	358	GLY	4.1
1	A	252	THR	4.0
1	C	359	VAL	4.0
1	C	66	LEU	4.0
1	A	66	LEU	4.0
1	B	365	PRO	3.9
1	B	253	ILE	3.9
1	A	251	GLU	3.9
1	D	66	LEU	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	356	GLY	3.9
1	B	63	LEU	3.9
1	D	363	THR	3.9
1	B	367	GLY	3.9
1	B	355	ALA	3.9
1	C	63	LEU	3.9
1	B	278	ARG	3.8
1	B	377	ALA	3.8
1	D	281	ASN	3.8
1	C	251	GLU	3.8
1	C	252	THR	3.8
1	C	47	ILE	3.7
1	B	374	VAL	3.7
1	D	355	ALA	3.6
1	D	367	GLY	3.6
1	C	65	PRO	3.6
1	B	358	GLY	3.6
1	A	367	GLY	3.5
1	D	373	ASP	3.5
1	C	354	LEU	3.5
1	C	30	LEU	3.5
1	D	358	GLY	3.5
1	D	251	GLU	3.4
1	C	0	SER	3.4
1	D	62	ALA	3.4
1	D	63	LEU	3.4
1	D	247	HIS	3.3
1	A	65	PRO	3.3
1	B	360	THR	3.3
1	C	248	ILE	3.3
1	D	376	PRO	3.3
1	B	77[A]	ARG	3.3
1	B	62	ALA	3.2
1	C	255	ALA	3.2
1	D	276	ASP	3.2
1	D	370	ILE	3.2
1	B	282	LEU	3.2
1	D	278	ARG	3.2
1	D	250	ASP	3.2
1	B	66	LEU	3.2
1	D	27	LEU	3.2
1	D	361	ASN	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	274	LEU	3.1
1	A	63	LEU	3.1
1	A	62	ALA	3.1
1	C	64	VAL	3.0
1	B	357	ARG	3.0
1	C	376	PRO	3.0
1	D	253	ILE	3.0
1	D	64	VAL	3.0
1	A	376	PRO	2.9
1	D	252	THR	2.9
1	D	0	SER	2.9
1	B	373	ASP	2.9
1	D	249	SER	2.9
1	C	62	ALA	2.9
1	A	368	GLU	2.9
1	B	370	ILE	2.9
1	B	31	LYS	2.9
1	D	259	SER	2.8
1	C	27	LEU	2.8
1	B	255	ALA	2.8
1	B	250	ASP	2.8
1	B	61	SER	2.8
1	B	275	HIS	2.8
1	B	34	ALA	2.7
1	C	34	ALA	2.7
1	D	357	ARG	2.7
1	A	249	SER	2.7
1	A	357	ARG	2.7
1	B	64	VAL	2.7
1	B	289	TRP	2.7
1	B	0	SER	2.7
1	B	372	ASN	2.7
1	B	7	LEU	2.7
1	B	254	GLU	2.7
1	C	369	MET	2.7
1	B	238	TRP	2.7
1	C	60	ALA	2.7
1	D	31	LYS	2.6
1	C	18	THR	2.6
1	B	47	ILE	2.6
1	A	364	GLY	2.6
1	A	360	THR	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	354	LEU	2.6
1	D	65	PRO	2.6
1	B	306	ASP	2.6
1	C	358	GLY	2.6
1	B	308	GLN	2.5
1	B	30	LEU	2.5
1	A	369	MET	2.5
1	D	280	ASP	2.5
1	C	7	LEU	2.5
1	D	61	SER	2.5
1	C	319	ASP	2.5
1	A	7	LEU	2.5
1	A	33	VAL	2.5
1	D	248	ILE	2.5
1	D	72	TYR	2.4
1	A	16	LEU	2.4
1	B	33	VAL	2.4
1	B	348	PRO	2.4
1	C	33	VAL	2.4
1	D	33	VAL	2.4
1	B	364	GLY	2.4
1	B	58	VAL	2.4
1	A	234	ALA	2.4
1	D	67	THR	2.4
1	B	369	MET	2.4
1	A	248	ILE	2.3
1	C	247	HIS	2.3
1	B	35	GLN	2.3
1	B	234	ALA	2.3
1	B	235	GLU	2.3
1	B	65	PRO	2.3
1	D	354	LEU	2.2
1	B	245	ILE	2.2
1	C	308	GLN	2.2
1	D	256	ALA	2.2
1	A	254	GLU	2.2
1	C	58	VAL	2.2
1	B	60	ALA	2.2
1	A	281	ASN	2.2
1	C	20	GLN	2.2
1	C	362	LEU	2.2
1	C	56	SER	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	59	ILE	2.1
1	C	59	ILE	2.1
1	A	27	LEU	2.1
1	A	255	ALA	2.1
1	B	59	ILE	2.1
1	D	96	LEU	2.1
1	C	35	GLN	2.1
1	B	18	THR	2.1
1	C	67	THR	2.1
1	C	372	ASN	2.1
1	D	34	ALA	2.1
1	D	315	LYS	2.1
1	A	25	VAL	2.0
1	D	262	ARG	2.0
1	D	77[A]	ARG	2.0
1	A	359	VAL	2.0
1	A	246	GLU	2.0
1	C	32	GLN	2.0
1	D	18	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 monosaccharides in this entry.

6.4 Ligands [i](#)

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

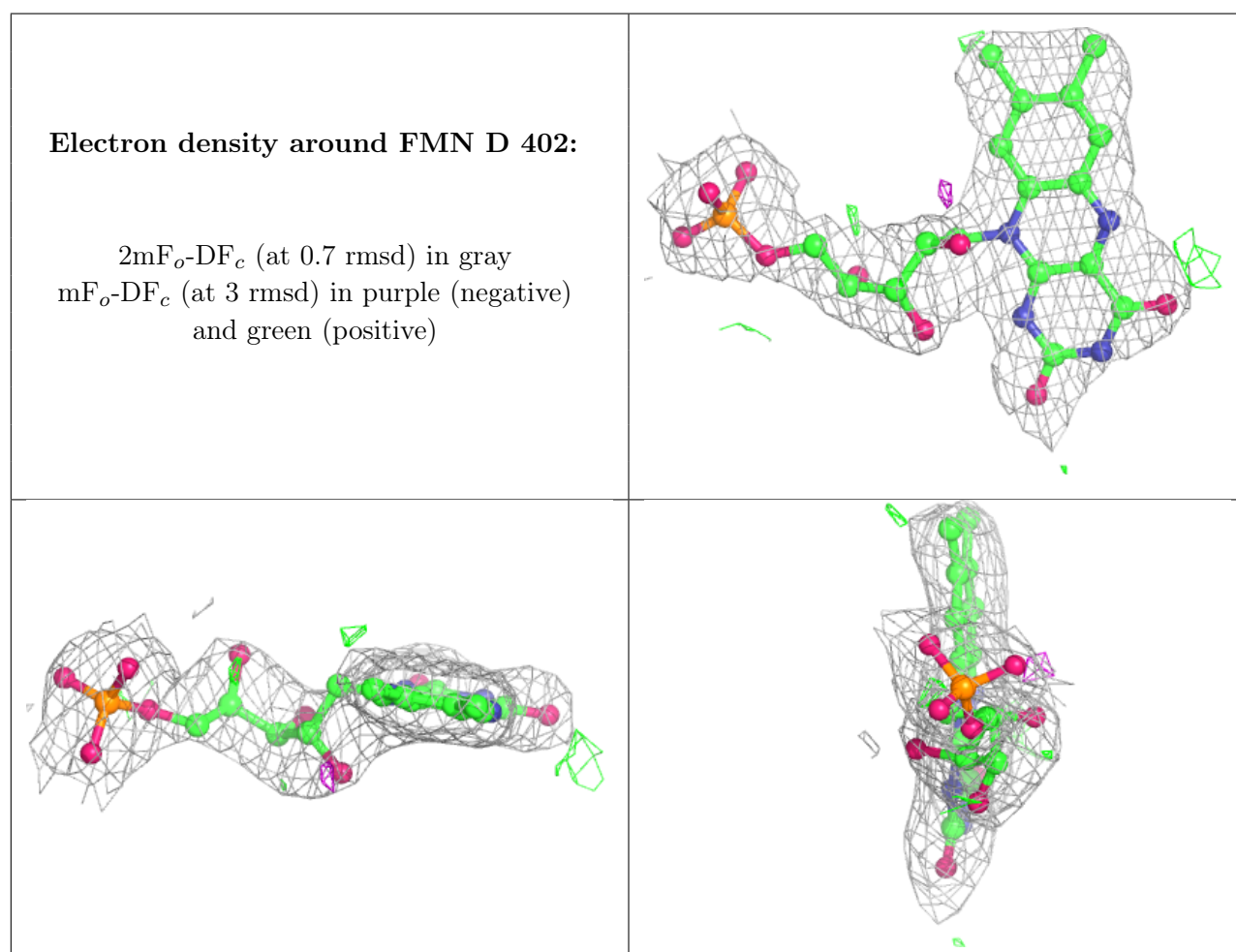
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NA	A	403	1/1	0.93	0.21	68,68,68,68	0
3	FMN	D	402	31/31	0.94	0.15	46,57,65,67	0
3	FMN	B	402	31/31	0.94	0.14	49,61,66,69	0
3	FMN	A	402	31/31	0.96	0.13	43,51,57,59	0

Continued on next page...

Continued from previous page...

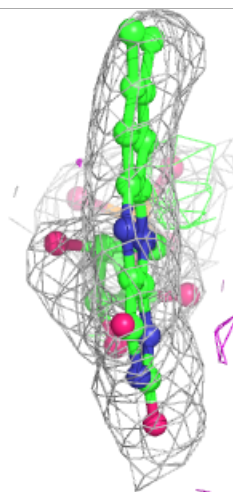
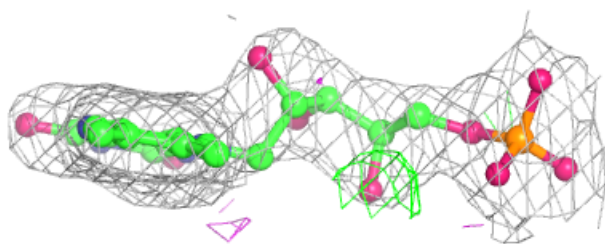
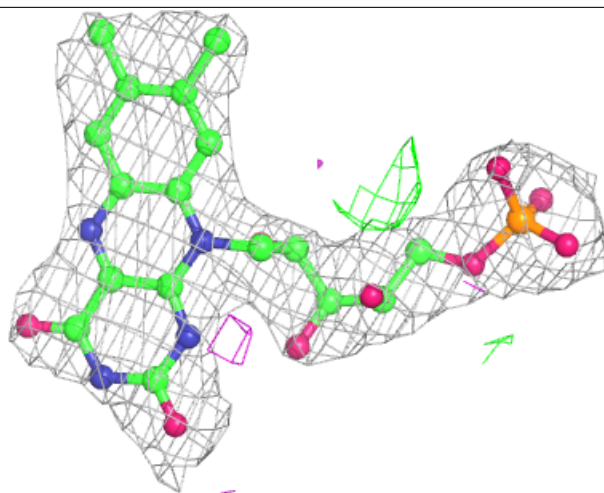
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	03S	B	401	5/5	0.97	0.13	44,56,62,67	0
3	FMN	C	402	31/31	0.97	0.14	42,50,58,60	0
2	03S	D	401	5/5	0.99	0.12	59,59,62,62	0
2	03S	A	401	5/5	0.99	0.16	36,47,54,57	0
2	03S	C	401	5/5	0.99	0.16	38,45,51,52	0

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.



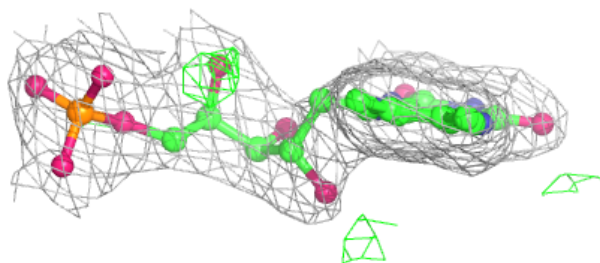
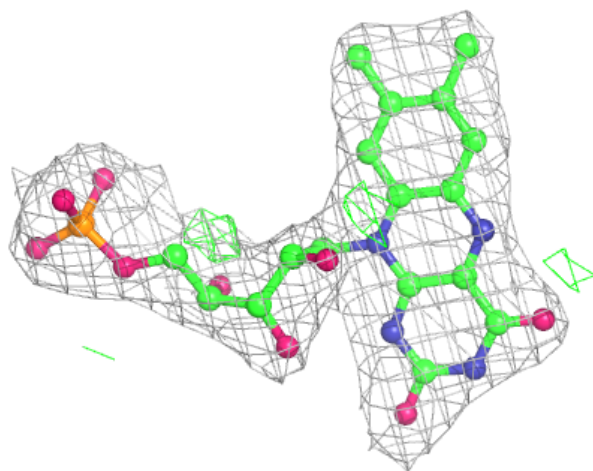
Electron density around FMN B 402:

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



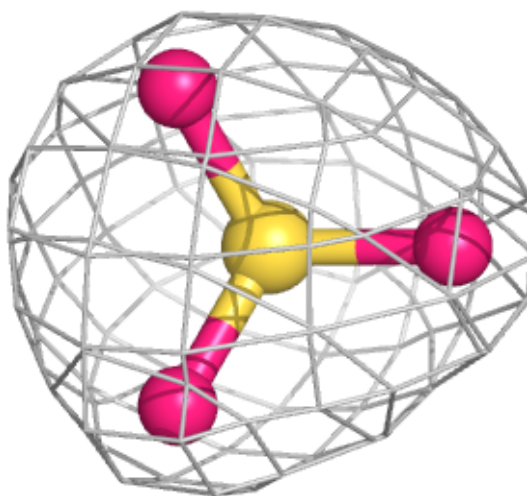
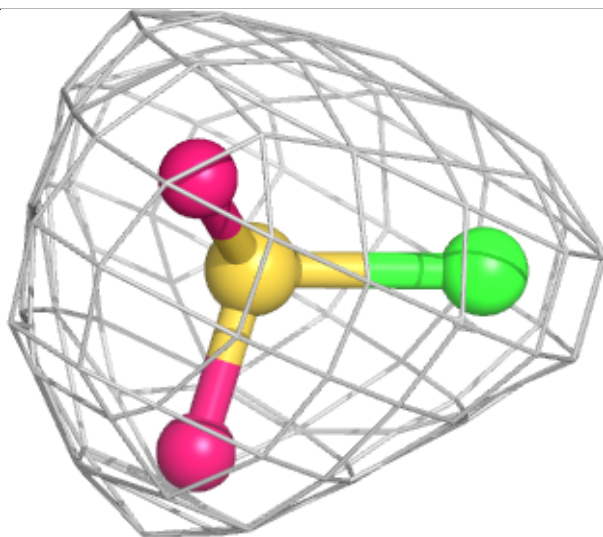
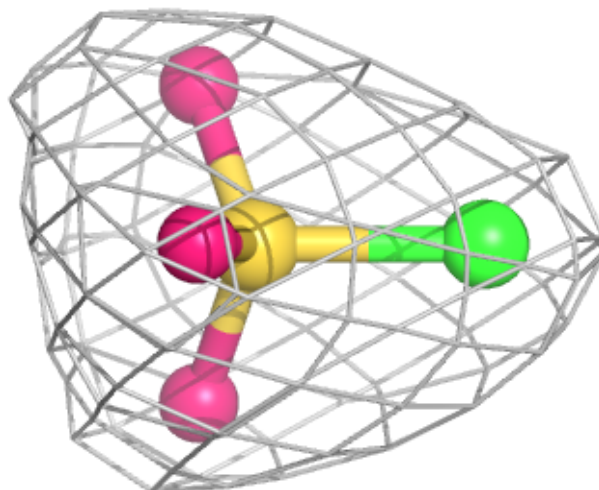
Electron density around FMN A 402:

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



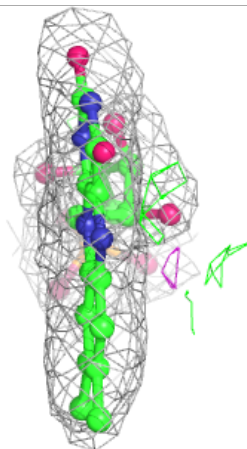
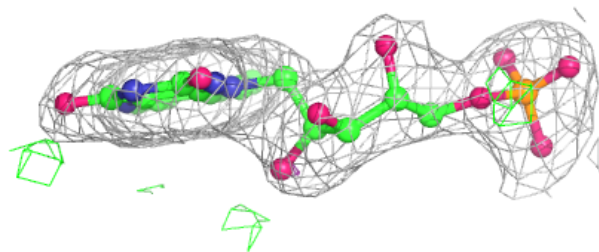
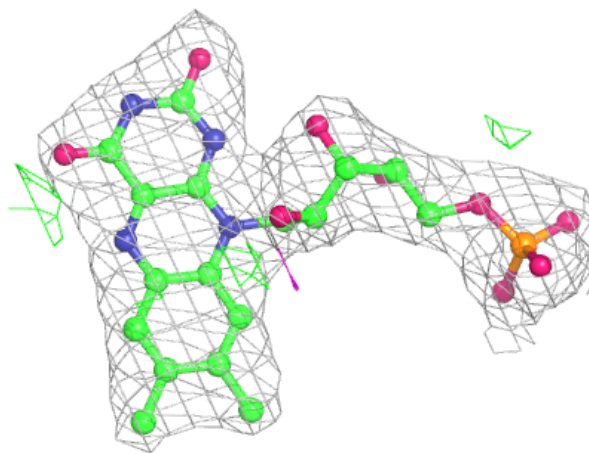
Electron density around 03S B 401:

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



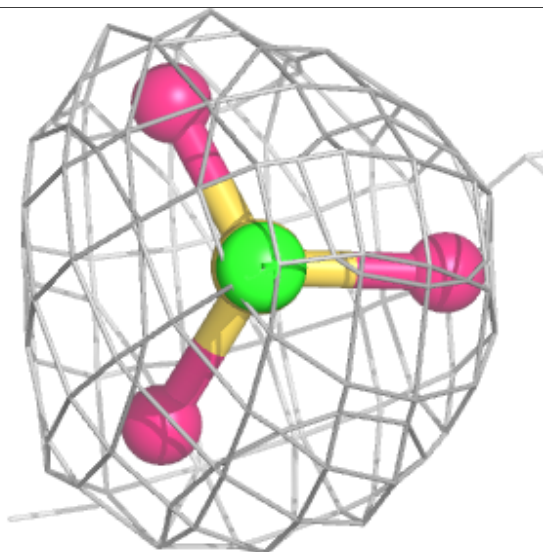
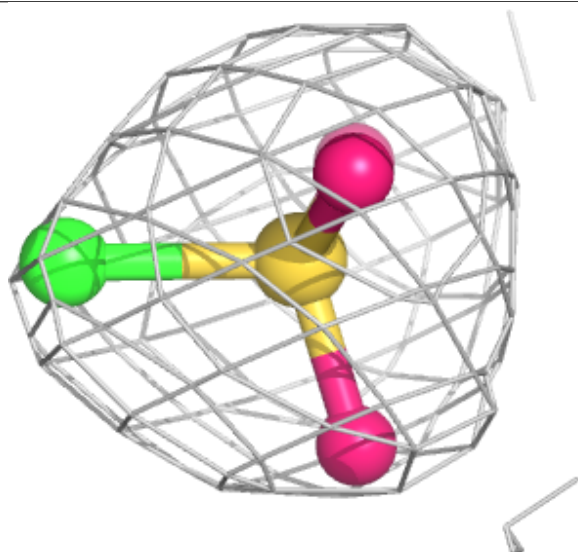
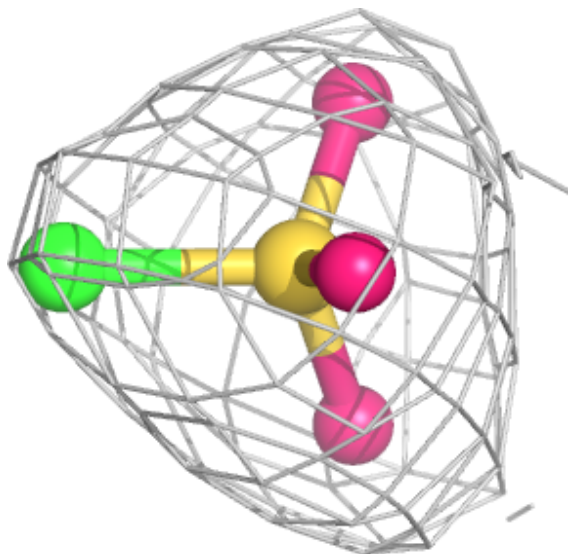
Electron density around FMN C 402:

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



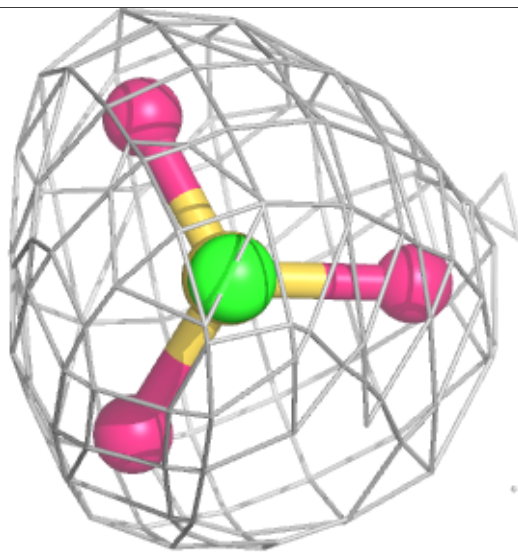
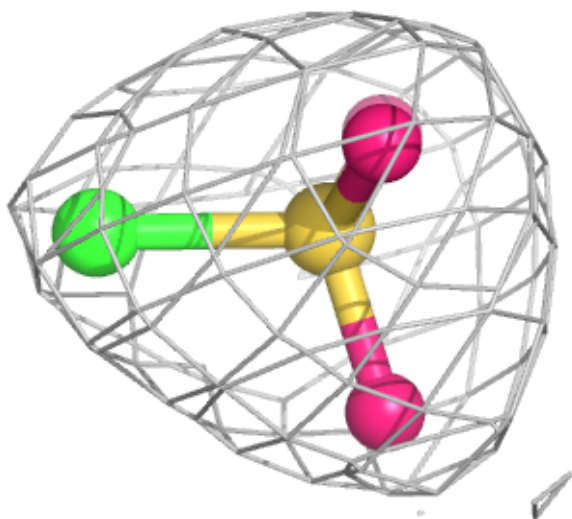
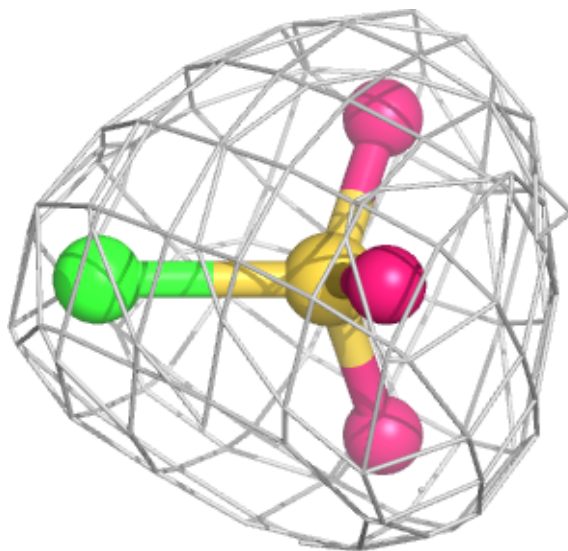
Electron density around 03S D 401:

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



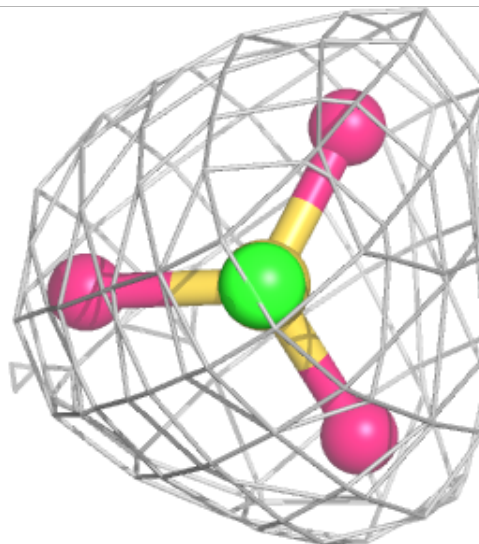
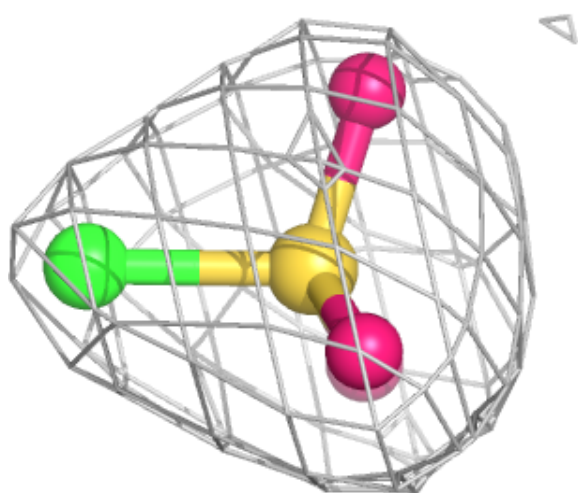
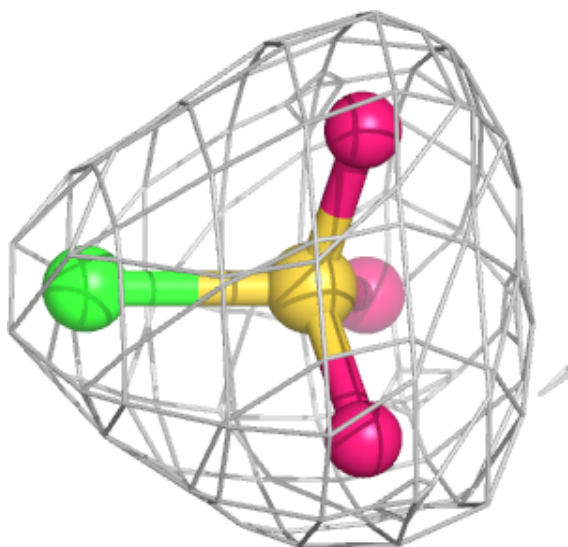
Electron density around 03S A 401:

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



Electron density around 03S C 401:

$2mF_o-DF_c$ (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.