



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 04:50 am BST

PDB ID : 5X2X
Title : Crystal structure of Pseudomonas putida methionine gamma-lyase wild type with L-homocysteine intermediates
Authors : Shiba, T.; Sato, D.; Harada, S.
Deposited on : 2017-02-02
Resolution : 2.00 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 : 2.11
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) : 2.11

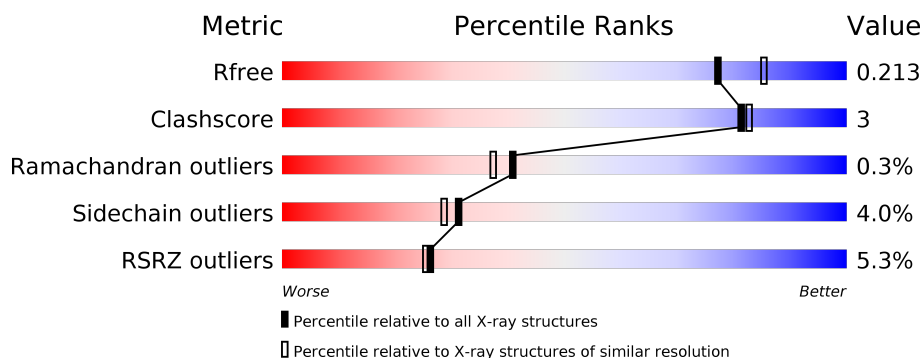
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 on 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	398	<div> <div>7%</div> <div> <div></div> <div>91%</div> <div>7%</div> <div>••</div> </div> </div>
1	B	398	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>••</div> </div> </div>
1	C	398	<div> <div>6%</div> <div> <div></div> <div>91%</div> <div>7%</div> <div>••</div> </div> </div>
1	D	398	<div> <div>6%</div> <div> <div></div> <div>93%</div> <div>7%</div> <div>•</div> </div> </div>

2 Entry composition [i](#)

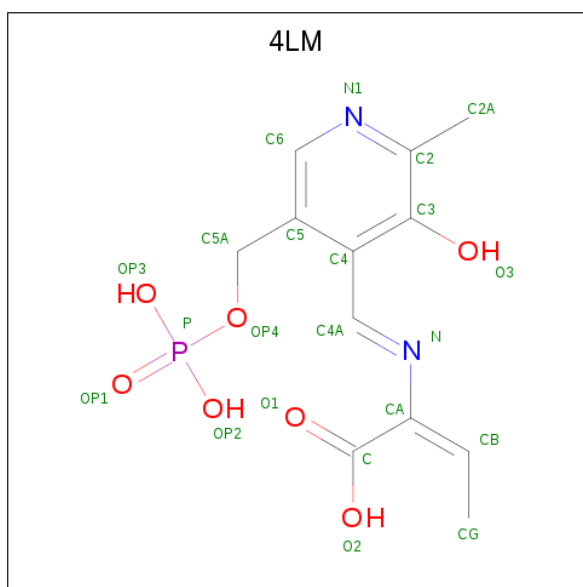
There are 4 unique types of molecules in this entry. The entry contains 12365 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 L-methionine gamma-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	0	0
			2951	1863	522	549	17			
1	B	392	Total	C	N	O	S	0	0	0
			2951	1863	522	549	17			
1	C	392	Total	C	N	O	S	0	1	0
			2960	1868	524	551	17			
1	D	398	Total	C	N	O	S	0	1	0
			3006	1895	535	558	18			

- Molecule 2 is (2E)-2-[(1E)-{3-hydroxy-2-methyl-5-[(phosphonoxy)methyl]pyridin-4-yl}methylidene]amino}but-2-enoic acid (three-letter code: 4LM) (formula: C₁₂H₁₅N₂O₇P).



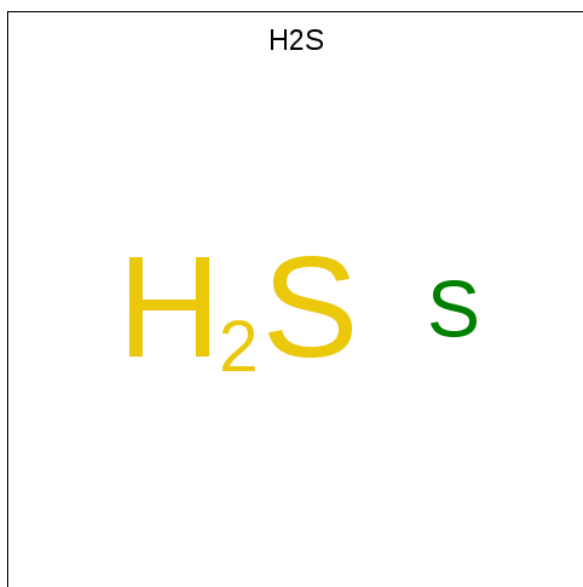
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	12	2	7	1		
2	B	1	Total	C	N	O	P	0	0
			22	12	2	7	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			22	12	2	7	1		
2	D	1	Total	C	N	O	P	0	0
			22	12	2	7	1		

- Molecule 3 is HYDROSULFURIC ACID (three-letter code: H2S) (formula: H₂S).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	71	Total	O	0	0
			71	71		
4	B	126	Total	O	0	0
			126	126		
4	C	95	Total	O	0	0
			95	95		

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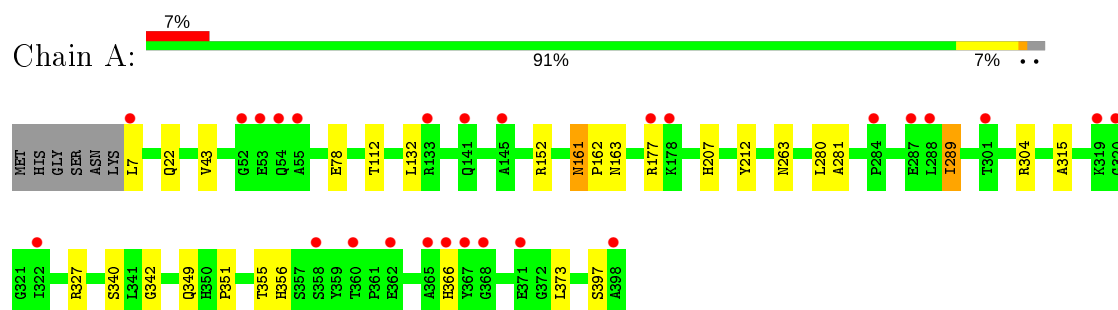
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	113	Total	O	0	0
			113	113		

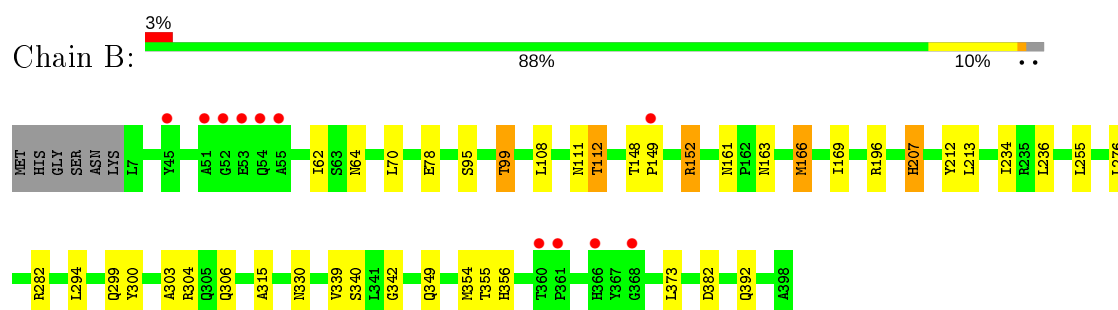
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

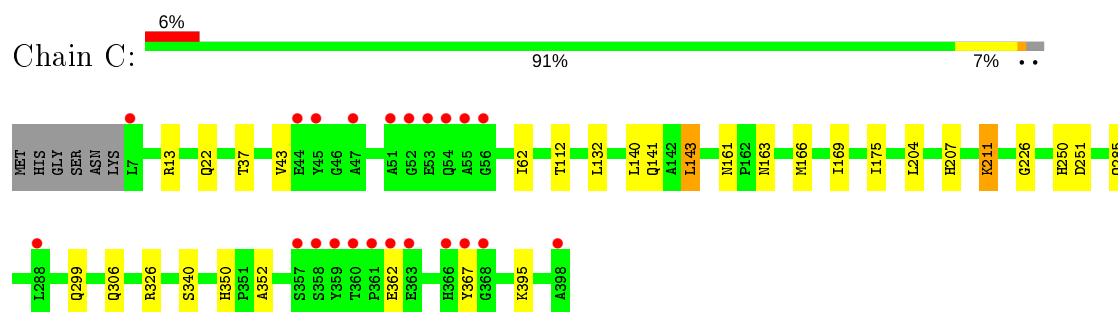
• Molecule 1: L-methionine gamma-lyase



• Molecule 1: L-methionine gamma-lyase

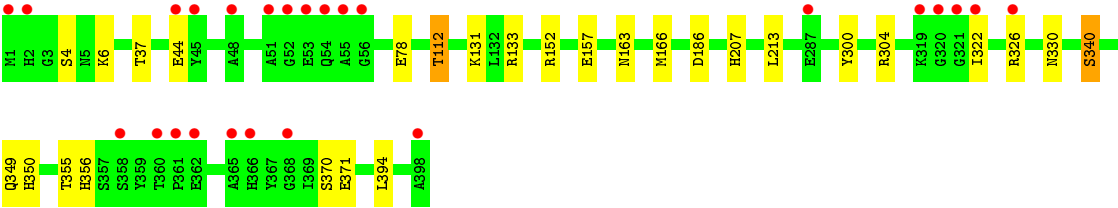


• Molecule 1: L-methionine gamma-lyase



• Molecule 1: L-methionine gamma-lyase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	154.41Å 152.88Å 80.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 19.98 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.7 (20.00-2.00) 96.8 (19.98-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.34 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.179 , 0.206 0.188 , 0.213	Depositor DCC
R_{free} test set	6310 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	24.1	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.013 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12365	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.56% 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: H2S, 4LM

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	0.54	0/3015	0.74	0/4093
1	B	0.60	0/3015	0.79	4/4093 (0.1%)
1	C	0.60	0/3024	0.76	1/4105 (0.0%)
1	D	0.61	0/3072	0.77	0/4168
All	All	0.59	0/12126	0.77	5/16459 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	196	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	B	382	ASP	CB-CG-OD2	5.43	123.19	118.30
1	C	13	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	B	152	ARG	NE-CZ-NH2	5.07	122.84	120.30
1	B	282	ARG	NE-CZ-NH2	5.05	122.83	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	207	HIS	Peptide
1	C	207	HIS	Peptide

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	2951	0	2921	13	0
1	B	2951	0	2921	24	0
1	C	2960	0	2928	14	0
1	D	3006	0	2973	13	0
2	A	22	0	11	1	0
2	B	22	0	12	0	0
2	C	22	0	12	3	0
2	D	22	0	11	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	71	0	0	1	0
4	B	126	0	0	3	0
4	C	95	0	0	2	0
4	D	113	0	0	1	0
All	All	12365	0	11789	62	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 3.

All (62) 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:112:THR:HG21	1:B:163:ASN:HD21	1.49	0.76
1:A:281:ALA:HA	1:A:289:ILE:HD11	1.68	0.74
1:C:112:THR:HG22	1:C:367:TYR:O	1.89	0.72
1:C:169:ILE:H	1:C:306:GLN:HE22	1.38	0.71
1:B:349:GLN:HE22	1:B:355:THR:CG2	2.05	0.69
1:B:99:THR:HG21	1:B:234:ILE:HA	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:112:THR:HG21	1:D:163:ASN:HD21	1.58	0.68
1:B:349:GLN:HE22	1:B:355:THR:HG21	1.60	0.66
1:B:166:MET:H	1:B:299:GLN:HE22	1.45	0.64
1:C:43:VAL:H	1:D:330:ASN:HD21	1.46	0.64
1:C:211:LYS:HZ1	2:C:401:4LM:C4A	2.17	0.58
1:C:62:ILE:HA	4:C:529:HOH:O	2.04	0.58
1:B:95:SER:O	1:B:99:THR:CG2	2.53	0.57
1:A:349:GLN:HE22	1:A:355:THR:CG2	2.18	0.56
1:A:349:GLN:HE22	1:A:355:THR:HG21	1.71	0.54
1:B:355:THR:HG23	1:B:356:HIS:ND1	2.24	0.53
1:A:43:VAL:H	1:B:330:ASN:HD21	1.55	0.53
1:C:211:LYS:NZ	2:C:401:4LM:C4A	2.73	0.52
1:B:354:MET:HE1	4:B:616:HOH:O	2.09	0.52
1:D:349:GLN:HE22	1:D:355:THR:CG2	2.23	0.51
1:B:62:ILE:HA	4:B:597:HOH:O	2.10	0.51
1:D:300:TYR:CZ	1:D:304:ARG:HD2	2.45	0.50
1:D:349:GLN:HE22	1:D:355:THR:HG22	1.77	0.50
1:C:350:HIS:CE1	1:C:352:ALA:HB3	2.48	0.49
1:B:78:GLU:OE2	1:B:207:HIS:CE1	2.66	0.48
1:B:78:GLU:OE2	1:B:207:HIS:HE1	1.96	0.48
4:A:533:HOH:O	1:B:339:VAL:HG22	2.14	0.48
1:D:78:GLU:OE1	1:D:207:HIS:HE1	1.97	0.47
1:B:148:THR:HB	1:B:149:PRO:HD2	1.97	0.47
1:B:349:GLN:HE22	1:B:355:THR:HG22	1.79	0.47
1:B:95:SER:O	1:B:99:THR:HG23	2.14	0.46
1:C:211:LYS:HZ1	2:C:401:4LM:CA	2.28	0.46
1:B:315:ALA:HB1	1:B:373:LEU:HD11	1.96	0.46
1:B:300:TYR:CZ	1:B:304:ARG:HD2	2.51	0.46
1:A:315:ALA:HB1	1:A:373:LEU:HD11	1.98	0.45
1:A:78:GLU:OE2	1:A:207:HIS:CE1	2.70	0.45
1:A:327:ARG:NH2	1:A:397:SER:O	2.50	0.45
1:D:78:GLU:OE1	1:D:207:HIS:CE1	2.70	0.45
1:A:355:THR:HG23	1:A:356:HIS:ND1	2.32	0.45
1:B:166:MET:CE	1:B:303:ALA:HA	2.48	0.44
4:C:510:HOH:O	1:D:37:THR:HG22	2.17	0.44
1:C:326:ARG:HD3	1:D:44:GLU:OE2	2.17	0.44
1:B:349:GLN:NE2	1:B:355:THR:HG21	2.31	0.44
1:C:166:MET:H	1:C:299:GLN:HE22	1.64	0.44
1:B:70:LEU:HD21	1:B:255:LEU:HD23	2.00	0.44
1:C:204:LEU:HD23	1:C:226:GLY:HA3	1.99	0.44
1:B:95:SER:O	1:B:99:THR:HG22	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:250:HIS:HD2	1:C:251:ASP:OD2	2.02	0.43
1:A:161:ASN:HA	1:A:162:PRO:HA	1.90	0.42
1:A:212:TYR:CE1	1:A:342:GLY:HA2	2.54	0.42
1:A:327:ARG:HB3	1:A:397:SER:HA	2.01	0.42
1:D:152:ARG:HA	1:D:152:ARG:NE	2.35	0.42
1:A:43:VAL:HG12	4:B:616:HOH:O	2.20	0.42
1:D:157:GLU:HG2	1:D:186:ASP:HB3	2.02	0.41
1:D:355:THR:HG23	1:D:356:HIS:ND1	2.35	0.41
1:C:37:THR:HG22	4:D:519:HOH:O	2.21	0.41
1:B:212:TYR:CE1	1:B:342:GLY:HA2	2.56	0.41
2:A:401:4LM:O3	2:A:401:4LM:N	2.54	0.41
1:D:350:HIS:HE1	1:D:371:GLU:O	2.04	0.41
1:A:351:PRO:HA	1:A:355:THR:HG22	2.03	0.40
1:B:169:ILE:H	1:B:306:GLN:HE22	1.69	0.40
1:C:143:LEU:HD13	1:C:175:ILE:HG21	2.03	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	390/398 (98%)	377 (97%)	12 (3%)	1 (0%)	41	37
1	B	390/398 (98%)	379 (97%)	10 (3%)	1 (0%)	41	37
1	C	391/398 (98%)	381 (97%)	8 (2%)	2 (0%)	29	23
1	D	397/398 (100%)	384 (97%)	12 (3%)	1 (0%)	41	37
All	All	1568/1592 (98%)	1521 (97%)	42 (3%)	5 (0%)	41	37

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	340	SER
1	C	340	SER
1	D	340	SER
1	B	340	SER
1	C	211	LYS

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	302/307 (98%)	289 (96%)	13 (4%)	29	26
1	B	302/307 (98%)	289 (96%)	13 (4%)	29	26
1	C	303/307 (99%)	293 (97%)	10 (3%)	38	37
1	D	308/307 (100%)	296 (96%)	12 (4%)	32	30
All	All	1215/1228 (99%)	1167 (96%)	48 (4%)	31	29

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	22	GLN
1	A	112	THR
1	A	132	LEU
1	A	152	ARG
1	A	161	ASN
1	A	163	ASN
1	A	177	ARG
1	A	263	ASN
1	A	280	LEU
1	A	289	ILE
1	A	304	ARG
1	A	366	HIS
1	B	64	ASN
1	B	99	THR
1	B	108	LEU
1	B	111	ASN

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Mol	Chain	Res	Type
1	B	112	THR
1	B	152	ARG
1	B	161	ASN
1	B	166	MET
1	B	213	LEU
1	B	236	LEU
1	B	276	LEU
1	B	294	LEU
1	B	392	GLN
1	C	22	GLN
1	C	132	LEU
1	C	140	LEU
1	C	141	GLN
1	C	143	LEU
1	C	161	ASN
1	C	163	ASN
1	C	285	GLN
1	C	362	GLU
1	C	395	LYS
1	D	4	SER
1	D	6	LYS
1	D	112	THR
1	D	131	LYS
1	D	133	ARG
1	D	166	MET
1	D	213	LEU
1	D	322	ILE
1	D	326	ARG
1	D	340	SER
1	D	370	SER
1	D	394	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	ASN
1	A	134	HIS
1	A	161	ASN
1	A	163	ASN
1	A	207	HIS
1	A	250	HIS
1	A	263	ASN

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Mol	Chain	Res	Type
1	A	349	GLN
1	A	350	HIS
1	B	24	HIS
1	B	57	HIS
1	B	64	ASN
1	B	68	ASN
1	B	111	ASN
1	B	161	ASN
1	B	207	HIS
1	B	274	GLN
1	B	299	GLN
1	B	306	GLN
1	B	330	ASN
1	B	349	GLN
1	B	350	HIS
1	B	392	GLN
1	C	34	GLN
1	C	57	HIS
1	C	141	GLN
1	C	161	ASN
1	C	187	ASN
1	C	250	HIS
1	C	285	GLN
1	C	299	GLN
1	C	306	GLN
1	C	309	GLN
1	C	350	HIS
1	D	34	GLN
1	D	187	ASN
1	D	195	GLN
1	D	207	HIS
1	D	237	GLN
1	D	274	GLN
1	D	330	ASN
1	D	350	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 are modelled with single atom - leaving 4 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	4LM	B	401	-	19,22,22	1.57	4 (21%)	21,31,31	1.30	3 (14%)
2	4LM	A	401	-	19,22,22	1.61	4 (21%)	21,31,31	1.37	4 (19%)
2	4LM	D	401	-	19,22,22	1.30	2 (10%)	21,31,31	1.62	4 (19%)
2	4LM	C	401	-	19,22,22	1.63	3 (15%)	21,31,31	1.30	4 (19%)

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
2	4LM	B	401	-	-	0/11/17/17	0/1/1/1
2	4LM	A	401	-	-	0/11/17/17	0/1/1/1
2	4LM	D	401	-	-	0/11/17/17	0/1/1/1
2	4LM	C	401	-	-	0/11/17/17	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	4LM	C5A-C5	-3.28	1.42	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	4LM	C2-N1	3.21	1.39	1.33
2	C	401	4LM	C5A-C5	-3.14	1.42	1.50
2	B	401	4LM	C3-C2	-3.10	1.37	1.40
2	C	401	4LM	C2-N1	2.96	1.39	1.33
2	A	401	4LM	C5A-C5	-2.95	1.42	1.50
2	D	401	4LM	P-OP2	-2.65	1.44	1.54
2	D	401	4LM	C5A-C5	-2.55	1.44	1.50
2	C	401	4LM	C2A-C2	2.37	1.54	1.50
2	B	401	4LM	P-OP2	-2.29	1.46	1.54
2	A	401	4LM	P-OP2	-2.27	1.46	1.54
2	B	401	4LM	C2-N1	2.17	1.38	1.33
2	A	401	4LM	C-CA	2.16	1.55	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	4LM	C4-C3-C2	4.56	123.01	120.19
2	D	401	4LM	C3-C2-N1	-3.60	116.12	120.77
2	A	401	4LM	C4-C3-C2	3.54	122.38	120.19
2	C	401	4LM	C3-C2-N1	-3.00	116.89	120.77
2	A	401	4LM	C3-C2-N1	-2.91	117.00	120.77
2	B	401	4LM	C3-C2-N1	-2.84	117.10	120.77
2	C	401	4LM	C4-C3-C2	2.70	121.86	120.19
2	D	401	4LM	C2A-C2-C3	2.67	124.19	120.89
2	A	401	4LM	C4-C4A-N	-2.57	116.95	123.19
2	B	401	4LM	C4-C3-C2	2.35	121.64	120.19
2	C	401	4LM	C4-C4A-N	-2.17	117.92	123.19
2	B	401	4LM	C6-N1-C2	2.17	123.18	119.17
2	C	401	4LM	C2A-C2-N1	2.12	121.81	117.67
2	D	401	4LM	C4-C4A-N	-2.10	118.10	123.19
2	A	401	4LM	C2A-C2-C3	2.07	123.44	120.89

There are no chirality outliers.

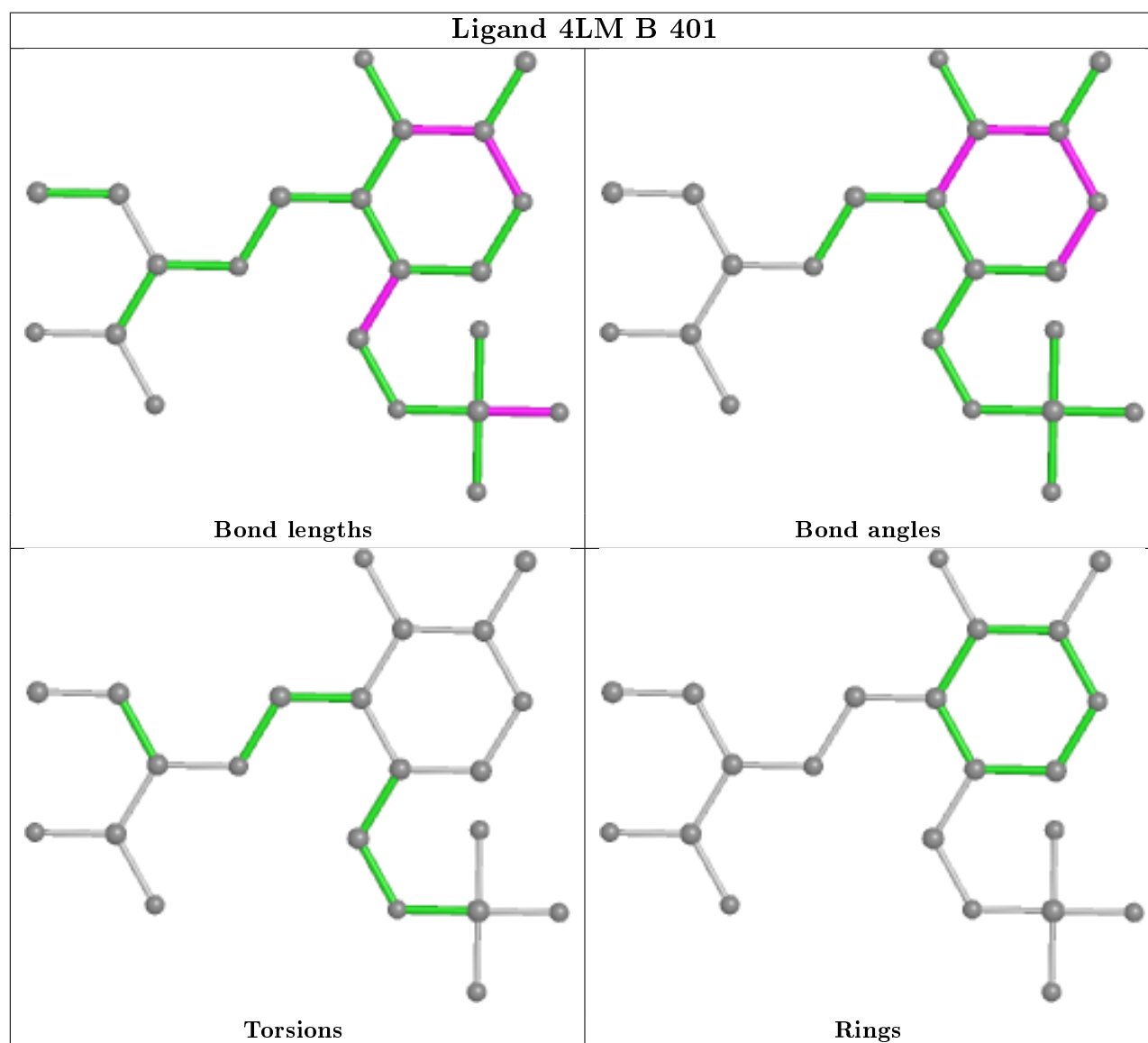
There are no torsion outliers.

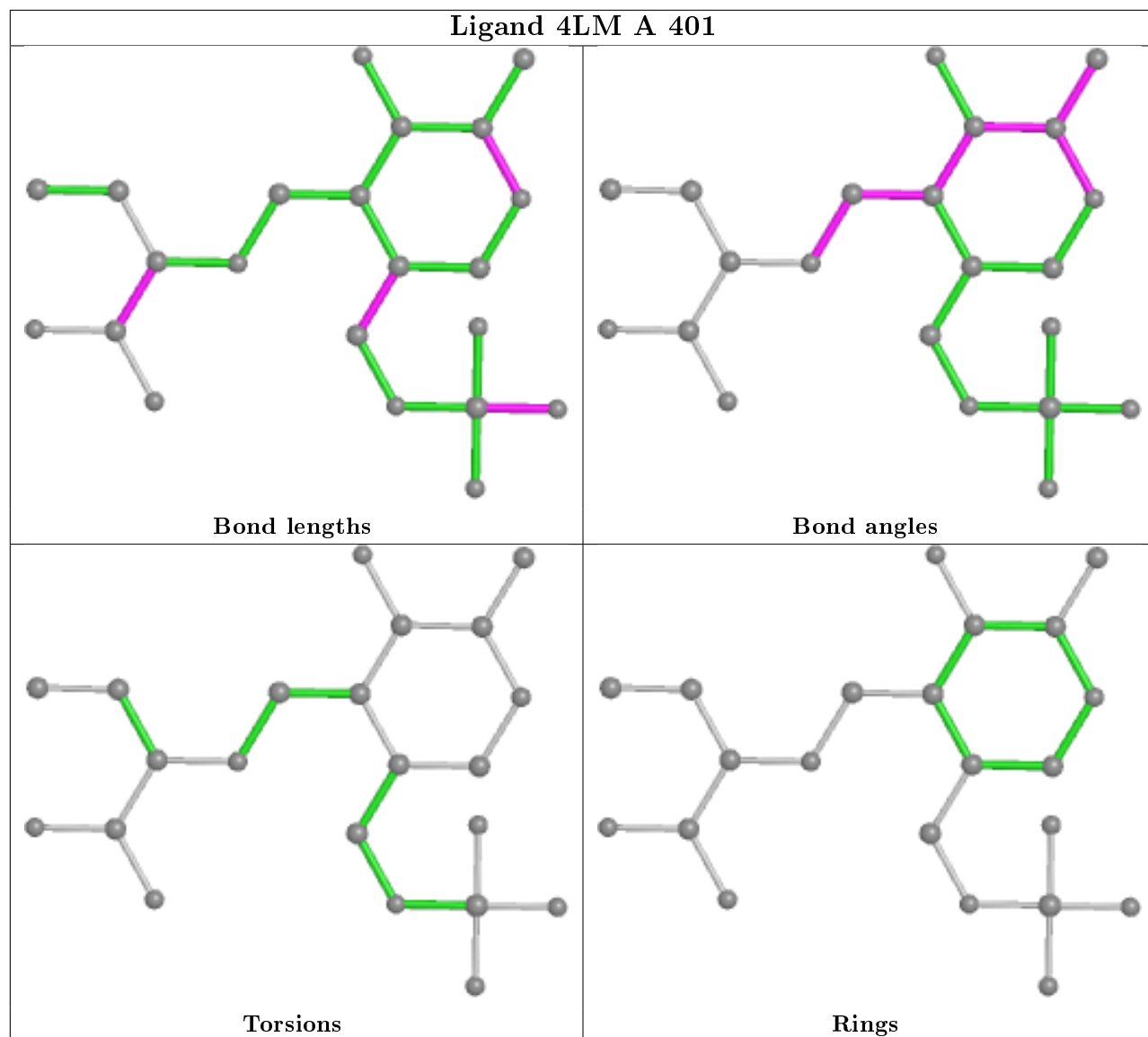
There are no ring outliers.

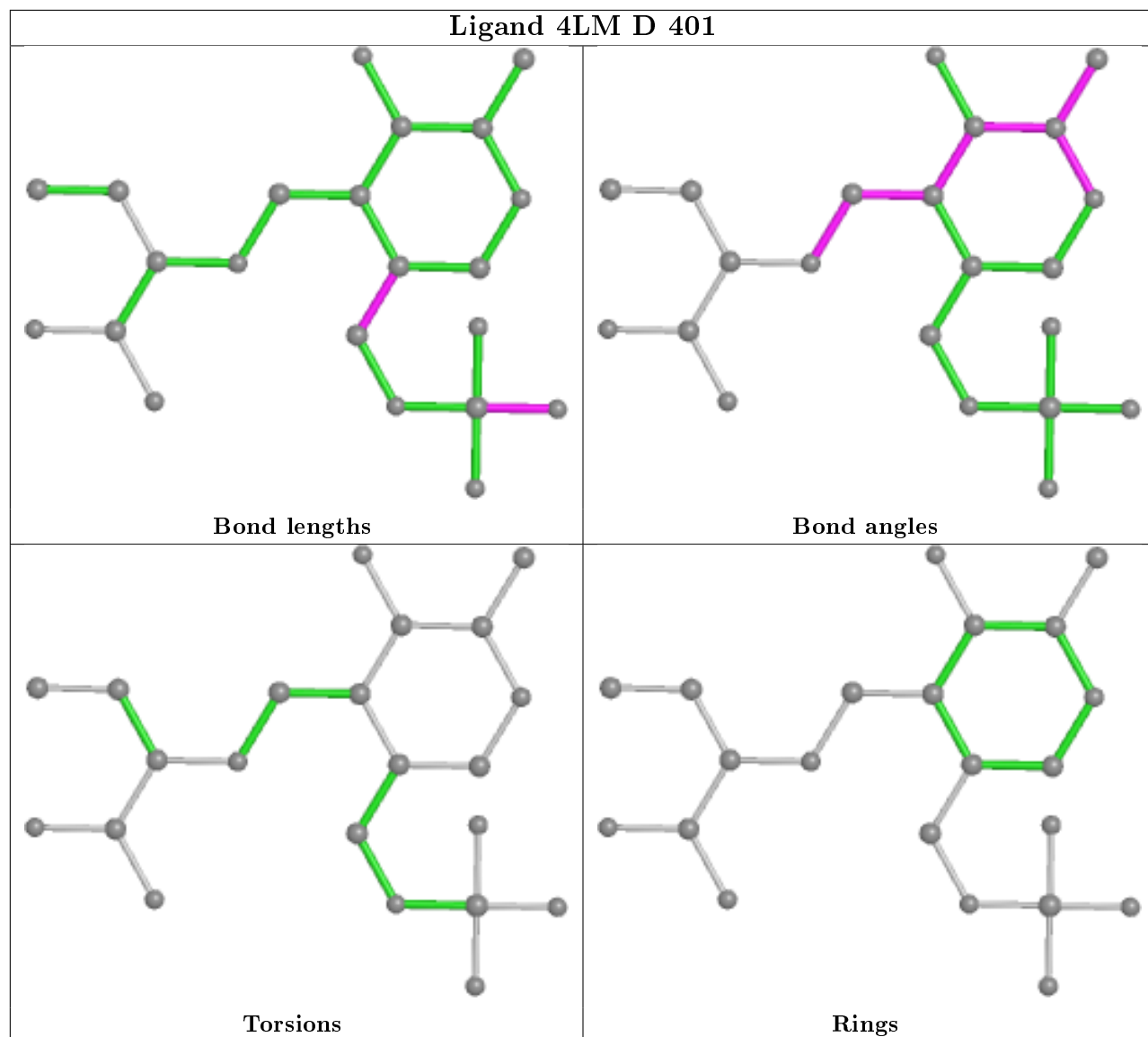
2 monomers are involved in 4 short contacts:

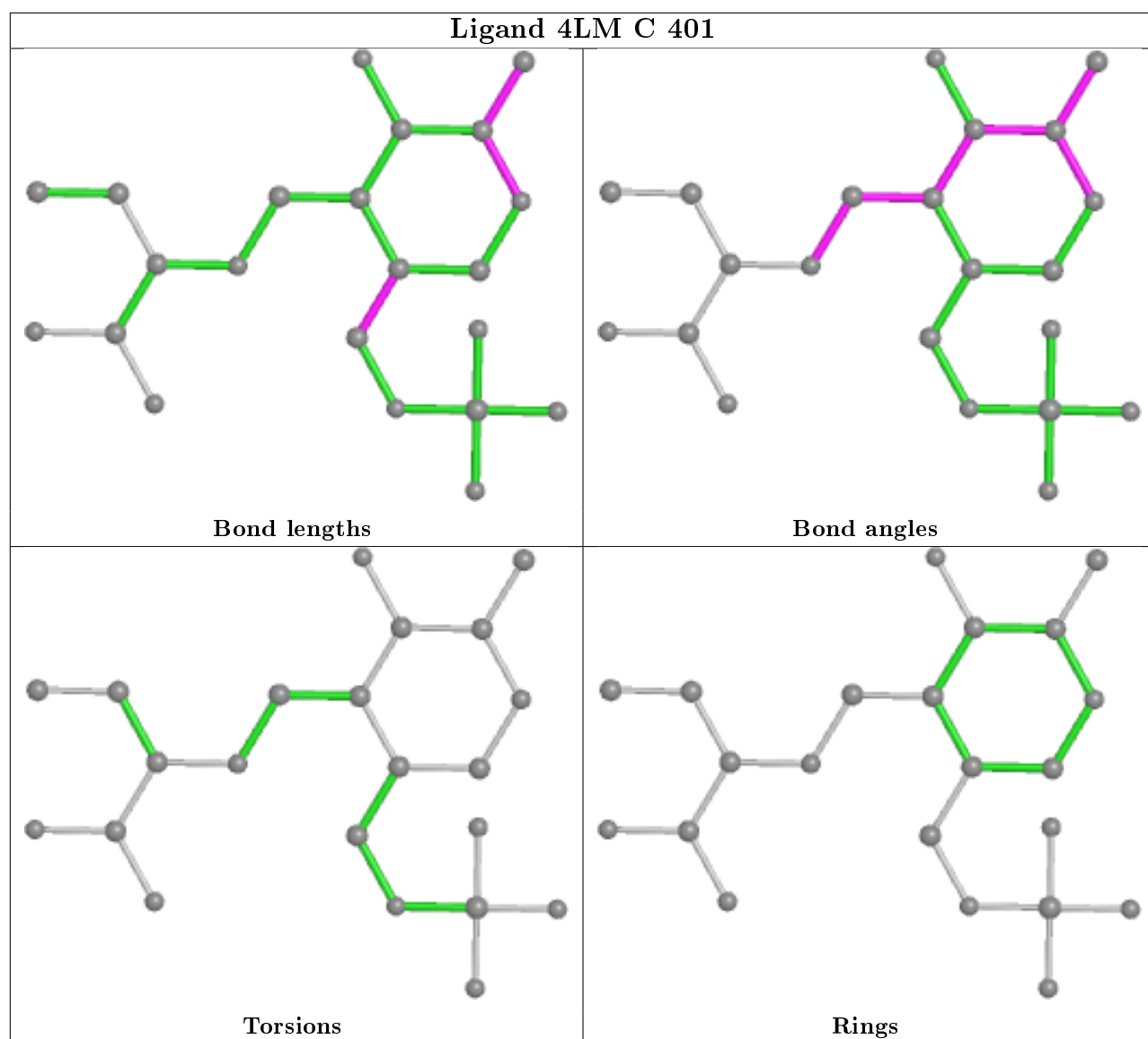
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	4LM	1	0
2	C	401	4LM	3	0

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 ⓘ

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	392/398 (98%)	0.21	26 (6%)	18 17	15, 32, 62, 86	0
1	B	392/398 (98%)	-0.15	11 (2%)	53 51	15, 24, 47, 73	0
1	C	392/398 (98%)	-0.03	22 (5%)	24 23	15, 27, 52, 82	0
1	D	398/398 (100%)	0.06	25 (6%)	20 19	13, 24, 57, 90	0
All	All	1574/1592 (98%)	0.02	84 (5%)	26 25	13, 27, 56, 90	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	55	ALA	7.3
1	A	398	ALA	7.2
1	D	55	ALA	6.5
1	D	52	GLY	6.5
1	C	55	ALA	6.4
1	D	1	MET	6.3
1	D	398	ALA	6.2
1	A	366	HIS	6.2
1	D	362	GLU	5.8
1	D	2	HIS	5.6
1	B	55	ALA	5.5
1	A	54	GLN	5.4
1	B	52	GLY	5.1
1	A	52	GLY	5.1
1	D	361	PRO	5.1
1	A	53	GLU	5.0
1	D	53	GLU	4.5
1	D	358	SER	4.4
1	A	178	LYS	4.3
1	A	367	TYR	4.3
1	C	366	HIS	4.2

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Mol	Chain	Res	Type	RSRZ
1	D	322	ILE	4.2
1	C	53	GLU	4.1
1	C	7	LEU	4.1
1	A	7	LEU	4.1
1	C	398	ALA	4.0
1	C	360	THR	3.9
1	A	365	ALA	3.9
1	D	366	HIS	3.8
1	B	53	GLU	3.8
1	C	52	GLY	3.8
1	A	368	GLY	3.7
1	B	51	ALA	3.7
1	D	54	GLN	3.7
1	A	322	ILE	3.6
1	D	365	ALA	3.6
1	C	367	TYR	3.5
1	B	360	THR	3.5
1	D	51	ALA	3.4
1	A	362	GLU	3.2
1	C	368	GLY	3.1
1	C	47	ALA	3.1
1	B	366	HIS	3.1
1	A	360	THR	3.0
1	D	360	THR	3.0
1	A	284	PRO	3.0
1	A	141	GLN	3.0
1	D	319	LYS	2.9
1	A	287	GLU	2.8
1	C	54	GLN	2.8
1	A	133	ARG	2.8
1	B	45	TYR	2.8
1	D	320	GLY	2.8
1	C	44	GLU	2.8
1	C	45	TYR	2.8
1	A	319	LYS	2.7
1	D	56	GLY	2.7
1	D	326	ARG	2.7
1	A	177	ARG	2.6
1	A	358	SER	2.6
1	C	362	GLU	2.5
1	C	51	ALA	2.5
1	B	368	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	45	TYR	2.5
1	D	368	GLY	2.5
1	D	321	GLY	2.4
1	A	145	ALA	2.4
1	C	361	PRO	2.4
1	C	357	SER	2.4
1	C	358	SER	2.4
1	D	287	GLU	2.4
1	C	288	LEU	2.4
1	B	149	PRO	2.3
1	B	54	GLN	2.3
1	C	363	GLU	2.3
1	A	288	LEU	2.2
1	B	361	PRO	2.2
1	A	371	GLU	2.2
1	A	320	GLY	2.1
1	D	48	ALA	2.1
1	C	359	TYR	2.1
1	D	44	GLU	2.0
1	A	301	THR	2.0
1	C	56	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	H2S	D	402	1/1	0.79	0.12	62,62,62,62	0
3	H2S	B	402	1/1	0.82	0.14	63,63,63,63	0

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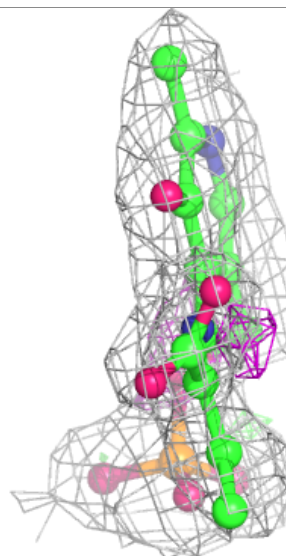
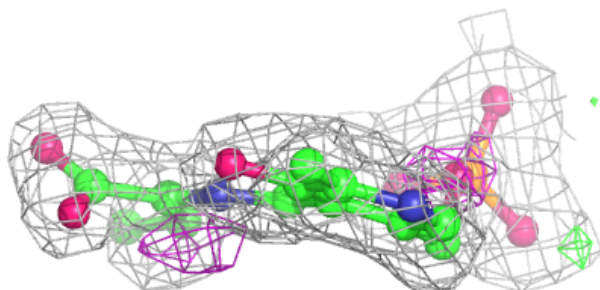
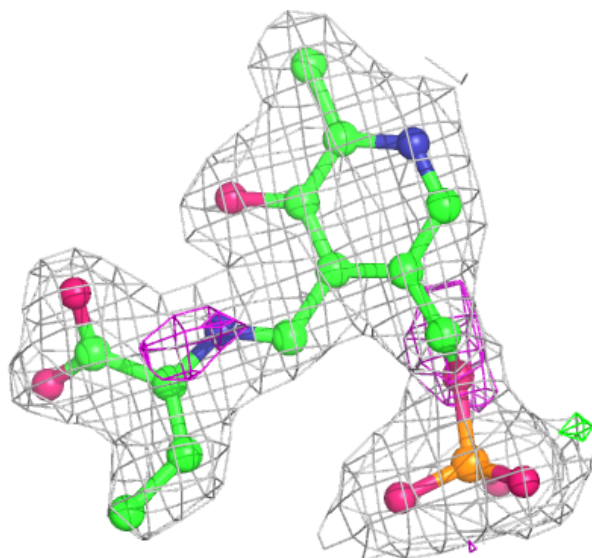
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	H2S	C	402	1/1	0.83	0.12	71,71,71,71	0
3	H2S	A	402	1/1	0.84	0.26	69,69,69,69	0
2	4LM	A	401	22/22	0.95	0.13	21,34,46,46	0
2	4LM	C	401	22/22	0.96	0.13	17,32,47,50	0
2	4LM	D	401	22/22	0.97	0.09	16,26,40,43	0
2	4LM	B	401	22/22	0.97	0.11	19,29,46,51	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.

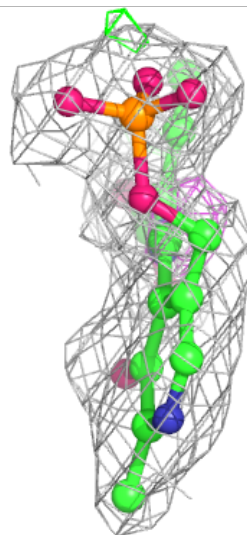
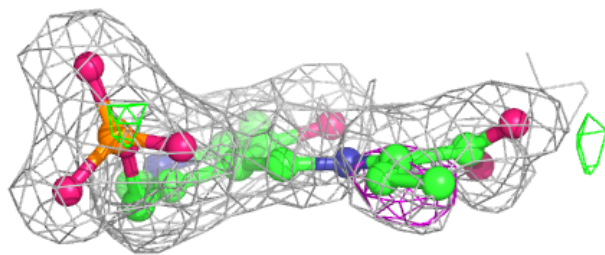
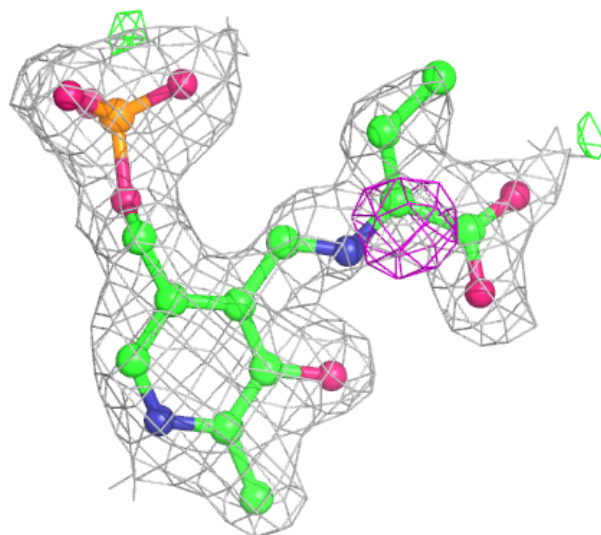
Electron density around 4LM A 401:

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



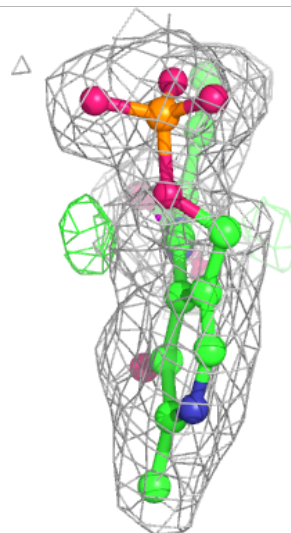
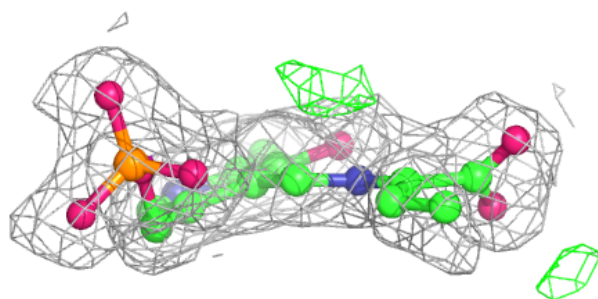
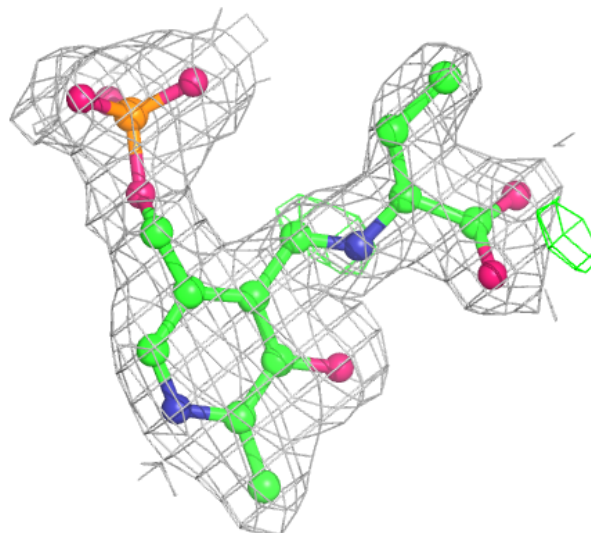
Electron density around 4LM C 401:

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



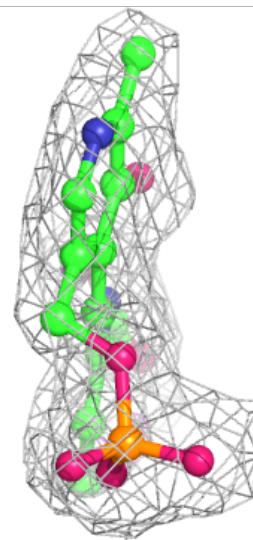
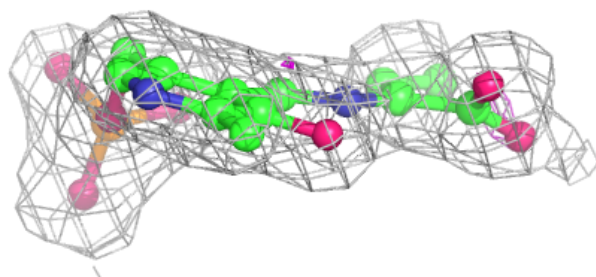
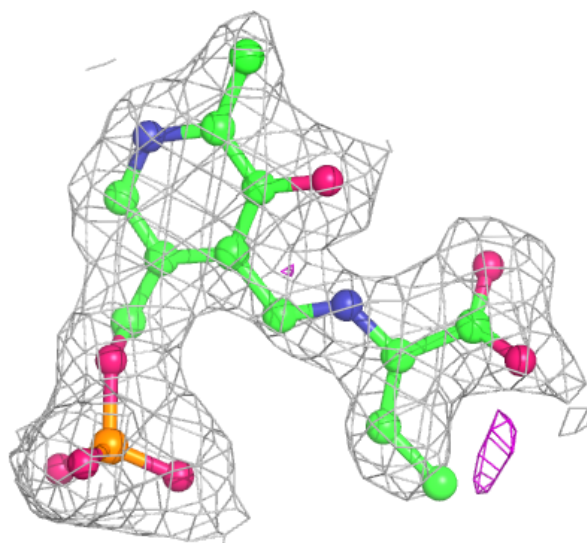
Electron density around 4LM D 401:

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



Electron density around 4LM 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)



6.5 Other polymers ⓘ

There are no such residues in this entry.