



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 5, 2024 – 08:10 PM JST

PDB ID : 8WKR
Title : Crystal structure of O-acetylhomoserine sulfhydrylase from *Lactobacillus plantarum* in the open form
Authors : Oda, K.; Matoba, Y.
Deposited on : 2023-09-28
Resolution : 2.05 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

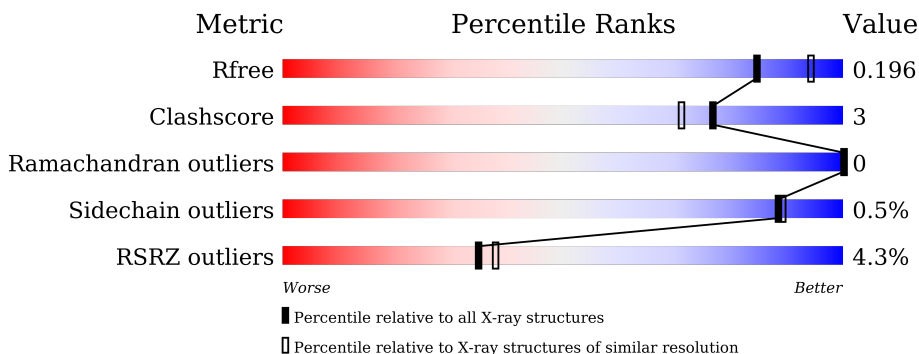
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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	448	 3% 84% 6% 10%
1	B	448	 2% 87% 10%
1	C	448	 5% 82% 8% 10%
1	D	448	 4% 85% 5% 10%

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 13526 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
			Total	C	N	O	S			
1	A	404	3071	1959	516	595	1	0	1	0
1	B	404	3079	1964	519	595	1	0	2	0
1	C	404	3089	1971	521	596	1	0	4	0
1	D	404	3079	1964	519	595	1	0	2	0

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A0G9F7S9
A	-18	GLY	-	expression tag	UNP A0A0G9F7S9
A	-17	SER	-	expression tag	UNP A0A0G9F7S9
A	-16	SER	-	expression tag	UNP A0A0G9F7S9
A	-15	HIS	-	expression tag	UNP A0A0G9F7S9
A	-14	HIS	-	expression tag	UNP A0A0G9F7S9
A	-13	HIS	-	expression tag	UNP A0A0G9F7S9
A	-12	HIS	-	expression tag	UNP A0A0G9F7S9
A	-11	HIS	-	expression tag	UNP A0A0G9F7S9
A	-10	HIS	-	expression tag	UNP A0A0G9F7S9
A	-9	SER	-	expression tag	UNP A0A0G9F7S9
A	-8	SER	-	expression tag	UNP A0A0G9F7S9
A	-7	GLY	-	expression tag	UNP A0A0G9F7S9
A	-6	LEU	-	expression tag	UNP A0A0G9F7S9
A	-5	VAL	-	expression tag	UNP A0A0G9F7S9
A	-4	PRO	-	expression tag	UNP A0A0G9F7S9
A	-3	ARG	-	expression tag	UNP A0A0G9F7S9
A	-2	GLY	-	expression tag	UNP A0A0G9F7S9
A	-1	SER	-	expression tag	UNP A0A0G9F7S9
A	0	HIS	-	expression tag	UNP A0A0G9F7S9
B	-19	MET	-	initiating methionine	UNP A0A0G9F7S9

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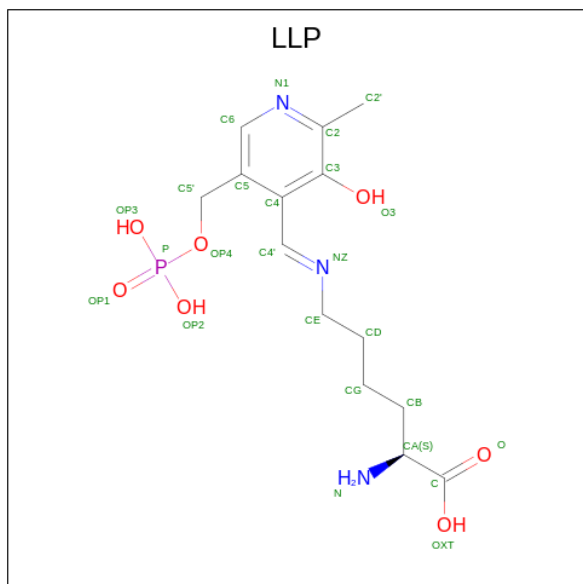
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP A0A0G9F7S9
B	-17	SER	-	expression tag	UNP A0A0G9F7S9
B	-16	SER	-	expression tag	UNP A0A0G9F7S9
B	-15	HIS	-	expression tag	UNP A0A0G9F7S9
B	-14	HIS	-	expression tag	UNP A0A0G9F7S9
B	-13	HIS	-	expression tag	UNP A0A0G9F7S9
B	-12	HIS	-	expression tag	UNP A0A0G9F7S9
B	-11	HIS	-	expression tag	UNP A0A0G9F7S9
B	-10	HIS	-	expression tag	UNP A0A0G9F7S9
B	-9	SER	-	expression tag	UNP A0A0G9F7S9
B	-8	SER	-	expression tag	UNP A0A0G9F7S9
B	-7	GLY	-	expression tag	UNP A0A0G9F7S9
B	-6	LEU	-	expression tag	UNP A0A0G9F7S9
B	-5	VAL	-	expression tag	UNP A0A0G9F7S9
B	-4	PRO	-	expression tag	UNP A0A0G9F7S9
B	-3	ARG	-	expression tag	UNP A0A0G9F7S9
B	-2	GLY	-	expression tag	UNP A0A0G9F7S9
B	-1	SER	-	expression tag	UNP A0A0G9F7S9
B	0	HIS	-	expression tag	UNP A0A0G9F7S9
C	-19	MET	-	initiating methionine	UNP A0A0G9F7S9
C	-18	GLY	-	expression tag	UNP A0A0G9F7S9
C	-17	SER	-	expression tag	UNP A0A0G9F7S9
C	-16	SER	-	expression tag	UNP A0A0G9F7S9
C	-15	HIS	-	expression tag	UNP A0A0G9F7S9
C	-14	HIS	-	expression tag	UNP A0A0G9F7S9
C	-13	HIS	-	expression tag	UNP A0A0G9F7S9
C	-12	HIS	-	expression tag	UNP A0A0G9F7S9
C	-11	HIS	-	expression tag	UNP A0A0G9F7S9
C	-10	HIS	-	expression tag	UNP A0A0G9F7S9
C	-9	SER	-	expression tag	UNP A0A0G9F7S9
C	-8	SER	-	expression tag	UNP A0A0G9F7S9
C	-7	GLY	-	expression tag	UNP A0A0G9F7S9
C	-6	LEU	-	expression tag	UNP A0A0G9F7S9
C	-5	VAL	-	expression tag	UNP A0A0G9F7S9
C	-4	PRO	-	expression tag	UNP A0A0G9F7S9
C	-3	ARG	-	expression tag	UNP A0A0G9F7S9
C	-2	GLY	-	expression tag	UNP A0A0G9F7S9
C	-1	SER	-	expression tag	UNP A0A0G9F7S9
C	0	HIS	-	expression tag	UNP A0A0G9F7S9
D	-19	MET	-	initiating methionine	UNP A0A0G9F7S9
D	-18	GLY	-	expression tag	UNP A0A0G9F7S9
D	-17	SER	-	expression tag	UNP A0A0G9F7S9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP A0A0G9F7S9
D	-15	HIS	-	expression tag	UNP A0A0G9F7S9
D	-14	HIS	-	expression tag	UNP A0A0G9F7S9
D	-13	HIS	-	expression tag	UNP A0A0G9F7S9
D	-12	HIS	-	expression tag	UNP A0A0G9F7S9
D	-11	HIS	-	expression tag	UNP A0A0G9F7S9
D	-10	HIS	-	expression tag	UNP A0A0G9F7S9
D	-9	SER	-	expression tag	UNP A0A0G9F7S9
D	-8	SER	-	expression tag	UNP A0A0G9F7S9
D	-7	GLY	-	expression tag	UNP A0A0G9F7S9
D	-6	LEU	-	expression tag	UNP A0A0G9F7S9
D	-5	VAL	-	expression tag	UNP A0A0G9F7S9
D	-4	PRO	-	expression tag	UNP A0A0G9F7S9
D	-3	ARG	-	expression tag	UNP A0A0G9F7S9
D	-2	GLY	-	expression tag	UNP A0A0G9F7S9
D	-1	SER	-	expression tag	UNP A0A0G9F7S9
D	0	HIS	-	expression tag	UNP A0A0G9F7S9

- Molecule 2 is (2S)-2-amino-6-[[3-hydroxy-2-methyl-5-(phosphonooxymethyl)pyridin-4-yl]methylideneamino]hexanoic acid (three-letter code: LLP) (formula: C₁₄H₂₂N₃O₇P).



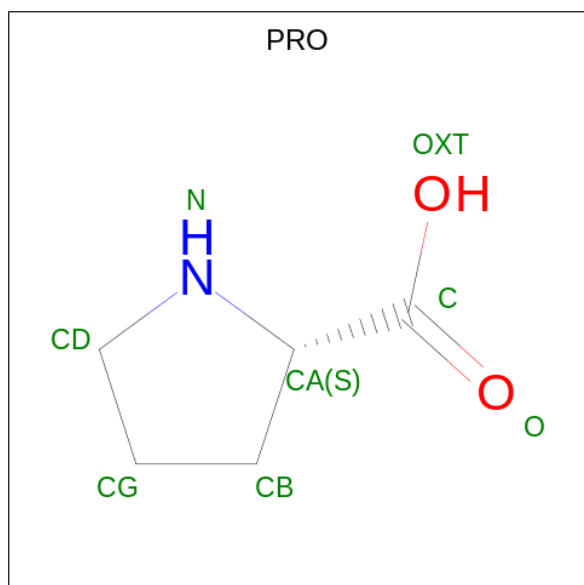
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	A	1	Total	C	N	O	P	0	0
			24	14	3	6	1		
2	B	1	Total	C	N	O	P	0	0
			24	14	3	6	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	C	1	Total	C	N	O	P	0	0
			24	14	3	6	1		
2	D	1	Total	C	N	O	P	0	0
			24	14	3	6	1		

- Molecule 3 is PROLINE (three-letter code: PRO) (formula: C₅H₉NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			8	5	1	2		
3	D	1	Total	C	N	O	0	0
			8	5	1	2		

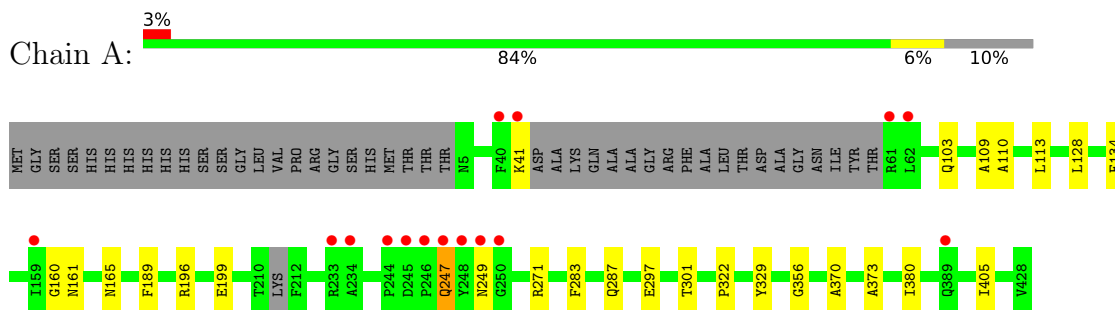
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	312	Total	O	0	0
			312	312		
4	B	267	Total	O	0	0
			267	267		
4	C	256	Total	O	0	0
			256	256		
4	D	261	Total	O	0	0
			261	261		

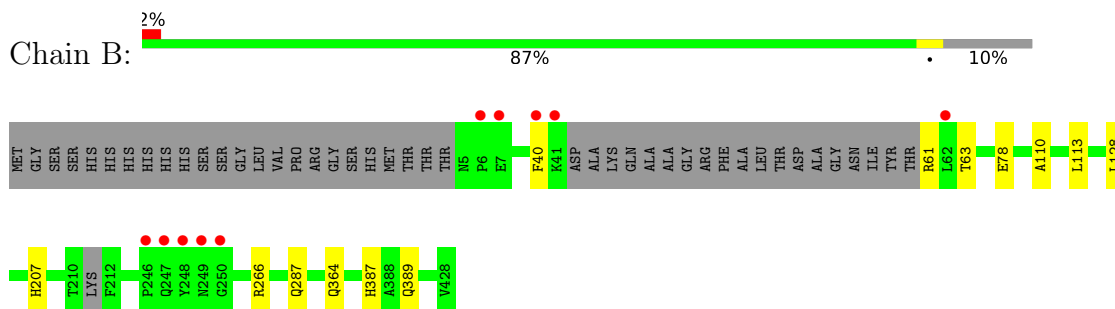
3 Residue-property plots [i](#)

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.

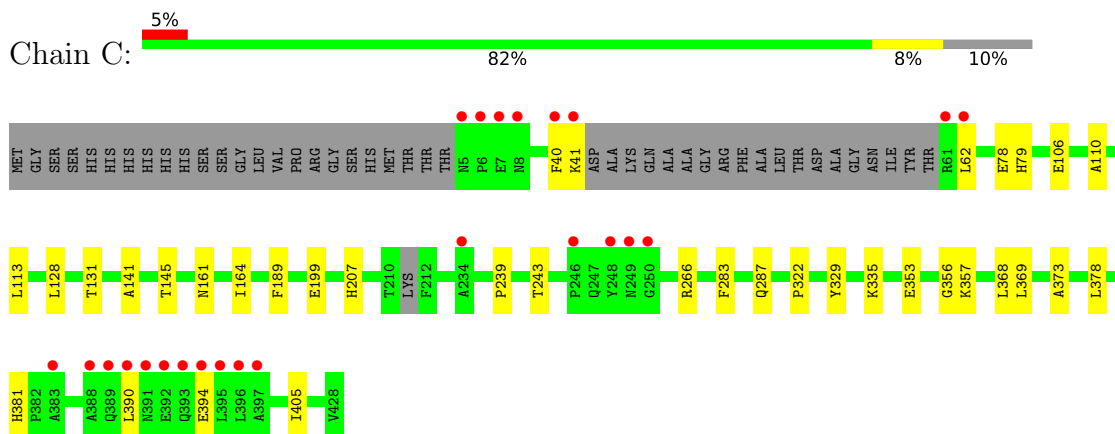
- Molecule 1: L-methionine gamma-lyase



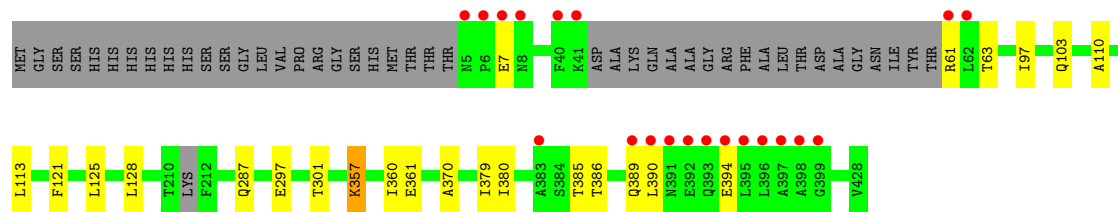
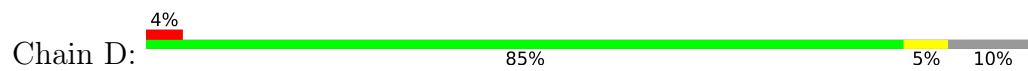
- Molecule 1: L-methionine gamma-lyase



- Molecule 1: L-methionine gamma-lyase



- Molecule 1: L-methionine gamma-lyase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.28Å 114.93Å 98.91Å 90.00° 110.28° 90.00°	Depositor
Resolution (Å)	39.53 – 2.05 39.53 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.5 (39.53-2.05) 99.5 (39.53-2.05)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.05Å)	Xtrriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.153 , 0.196 0.152 , 0.196	Depositor DCC
R_{free} test set	5702 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å ²)	23.7	Xtrriage
Anisotropy	0.403	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13526	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: LLP

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	0.40	0/3141	0.53	0/4287
1	B	0.37	0/3152	0.52	0/4301
1	C	0.38	0/3169	0.53	0/4324
1	D	0.37	0/3152	0.52	0/4301
All	All	0.38	0/12614	0.52	0/17213

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	3071	0	3015	21	0
1	B	3079	0	3028	10	0
1	C	3089	0	3040	25	0
1	D	3079	0	3028	20	0
2	A	24	0	17	3	0
2	B	24	0	16	1	0
2	C	24	0	18	1	0
2	D	24	0	17	0	0
3	B	8	0	7	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	8	0	7	3	0
4	A	312	0	0	1	0
4	B	267	0	0	1	0
4	C	256	0	0	1	0
4	D	261	0	0	1	0
All	All	13526	0	12193	73	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 (73) 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:247:GLN:HE22	1:A:271:ARG:NH1	1.55	1.04
1:A:247:GLN:NE2	1:A:271:ARG:HH12	1.64	0.95
1:A:247:GLN:NE2	1:A:271:ARG:NH1	2.21	0.84
1:D:390:LEU:HD13	1:D:394:GLU:HB3	1.76	0.68
1:C:390:LEU:HB3	1:C:394:GLU:HB3	1.75	0.67
1:A:287:GLN:HB3	3:B:501:PRO:HD2	1.80	0.63
2:A:501:LLP:OP4	2:A:501:LLP:H4'1	2.00	0.61
1:A:196:ARG:O	1:A:199:GLU:HG2	2.05	0.57
1:D:287:GLN:HB2	3:D:501:PRO:HG2	1.87	0.57
1:C:239:PRO:O	1:C:243:THR:HG23	2.05	0.56
1:C:79[A]:HIS:ND1	1:C:199:GLU:OE2	2.36	0.55
1:A:113:LEU:O	4:A:601:HOH:O	2.18	0.55
1:D:61:ARG:NH1	1:D:63:THR:O	2.40	0.54
1:A:128:LEU:HD13	1:D:128:LEU:HD13	1.90	0.54
2:B:502:LLP:H4'1	2:B:502:LLP:OP4	2.07	0.53
1:A:322:PRO:HB3	1:A:329:TYR:HB2	1.91	0.53
1:B:389:GLN:H	1:B:389:GLN:CD	2.13	0.51
1:D:287:GLN:HB3	3:D:501:PRO:HD2	1.92	0.51
1:D:357:LYS:HE3	1:D:361:GLU:OE1	2.10	0.51
1:C:353:GLU:HG3	1:C:381:HIS:CE1	2.45	0.51
1:C:106:GLU:HG2	1:C:131:THR:HB	1.93	0.50
1:D:97:ILE:HG13	1:D:121:PHE:HE1	1.77	0.49
1:D:360:ILE:HD13	1:D:379:ILE:HG23	1.92	0.49
1:B:387:HIS:HA	1:B:389:GLN:HE22	1.77	0.49
1:D:385:THR:OG1	1:D:386:THR:N	2.45	0.49
1:D:360:ILE:HD11	1:D:379:ILE:HG12	1.95	0.48
1:B:110:ALA:O	1:B:113:LEU:HG	2.13	0.48
1:D:121:PHE:HD1	1:D:125:LEU:HD12	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:356:GLY:HA2	1:C:405:ILE:HD11	1.94	0.48
1:A:287:GLN:HB2	3:B:501:PRO:HG2	1.95	0.48
1:D:61:ARG:NH2	4:D:607:HOH:O	2.46	0.48
1:C:62:LEU:HD13	1:C:62:LEU:O	2.14	0.48
1:B:387:HIS:HA	1:B:389:GLN:NE2	2.29	0.47
1:C:78:GLU:OE2	1:C:207:HIS:NE2	2.39	0.47
1:A:103:GLN:HG3	1:D:103:GLN:NE2	2.29	0.47
2:A:501:LLP:O3	2:A:501:LLP:HE3	2.14	0.47
1:D:360:ILE:HD13	1:D:379:ILE:CG2	2.44	0.47
1:B:364:GLN:OE1	4:B:601:HOH:O	2.20	0.47
1:C:369:LEU:HD11	1:C:378:LEU:HD13	1.97	0.47
1:C:62:LEU:HD12	1:C:266:ARG:HG2	1.97	0.47
1:C:141:ALA:O	1:C:145:THR:HG23	2.15	0.47
1:D:110:ALA:O	1:D:113:LEU:HG	2.15	0.46
1:B:78:GLU:OE2	1:B:207:HIS:NE2	2.43	0.46
1:A:110:ALA:O	1:A:113:LEU:HG	2.16	0.45
1:C:40:PHE:O	1:C:41:LYS:HB3	2.16	0.45
1:A:160:GLY:HA3	1:A:165:ASN:OD1	2.16	0.45
1:A:370:ALA:HA	1:A:380:ILE:HD12	1.99	0.44
1:A:128:LEU:HB3	1:D:128:LEU:HB3	2.00	0.44
1:A:249:ASN:ND2	1:D:389:GLN:OE1	2.51	0.43
1:C:283:PHE:O	1:C:287:GLN:HG2	2.18	0.43
1:A:161:ASN:HB2	1:A:189:PHE:CE2	2.53	0.43
1:C:161:ASN:HB2	1:C:189:PHE:CE2	2.54	0.43
1:B:128:LEU:HD13	1:C:128:LEU:HD13	2.00	0.43
1:B:287:GLN:HB3	3:B:501:PRO:HG3	2.01	0.43
1:C:373:ALA:HB3	2:C:501:LLP:HB2	2.00	0.43
1:C:110:ALA:O	1:C:113:LEU:HG	2.19	0.43
1:D:297:GLU:O	1:D:301:THR:HG23	2.19	0.43
1:C:164:ILE:O	1:C:322:PRO:HG3	2.19	0.42
1:C:287:GLN:HB3	3:D:501:PRO:HG3	2.02	0.42
1:C:353:GLU:HG3	1:C:381:HIS:HE1	1.83	0.42
1:A:356:GLY:HA2	1:A:405:ILE:HD11	2.02	0.42
1:A:373:ALA:HB3	2:A:501:LLP:HB2	2.01	0.41
1:C:335:LYS:NZ	4:C:615:HOH:O	2.50	0.41
1:D:370:ALA:HA	1:D:380:ILE:HD12	2.02	0.41
1:C:322:PRO:HB3	1:C:329:TYR:HB2	2.03	0.41
1:D:360:ILE:CD1	1:D:379:ILE:HG12	2.51	0.41
1:A:297:GLU:O	1:A:301:THR:HG23	2.20	0.40
1:B:63:THR:HG22	1:B:266[A]:ARG:HD3	2.03	0.40
1:C:41:LYS:HA	1:C:41:LYS:HE2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ALA:O	1:A:134:PHE:HA	2.21	0.40
1:B:40:PHE:HB2	1:C:368:LEU:HG	2.01	0.40
1:C:390:LEU:HD12	1:C:394:GLU:CD	2.41	0.40
1:A:283:PHE:O	1:A:287:GLN:HG2	2.22	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	399/448 (89%)	392 (98%)	7 (2%)	0	100	100
1	B	400/448 (89%)	391 (98%)	9 (2%)	0	100	100
1	C	402/448 (90%)	392 (98%)	10 (2%)	0	100	100
1	D	400/448 (89%)	388 (97%)	12 (3%)	0	100	100
All	All	1601/1792 (89%)	1563 (98%)	38 (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	324/357 (91%)	322 (99%)	2 (1%)	86	87
1	B	325/357 (91%)	324 (100%)	1 (0%)	92	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	327/357 (92%)	326 (100%)	1 (0%)	92	93
1	D	325/357 (91%)	323 (99%)	2 (1%)	86	87
All	All	1301/1428 (91%)	1295 (100%)	6 (0%)	88	89

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LYS
1	A	247	GLN
1	B	61	ARG
1	C	357	LYS
1	D	7	GLU
1	D	357	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	229	GLN
1	A	247	GLN
1	B	249	ASN
1	B	389	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no 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
3	PRO	D	501	-	8,8,8	1.19	1 (12%)	10,10,10	1.78	4 (40%)
2	LLP	A	501	1	23,24,25	0.86	1 (4%)	25,32,34	1.97	6 (24%)
3	PRO	B	501	-	8,8,8	1.18	0	10,10,10	1.88	4 (40%)
2	LLP	D	502	1	23,24,25	0.84	1 (4%)	25,32,34	1.06	2 (8%)
2	LLP	C	501	1	23,24,25	0.89	1 (4%)	25,32,34	1.03	1 (4%)
2	LLP	B	502	1	23,24,25	0.83	1 (4%)	25,32,34	1.09	2 (8%)

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	PRO	D	501	-	-	2/4/11/11	0/1/1/1
2	LLP	A	501	1	-	6/16/17/19	0/1/1/1
3	PRO	B	501	-	-	3/4/11/11	0/1/1/1
2	LLP	D	502	1	-	7/16/17/19	0/1/1/1
2	LLP	C	501	1	-	5/16/17/19	0/1/1/1
2	LLP	B	502	1	-	8/16/17/19	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	LLP	C4-C4'	2.53	1.51	1.46
2	C	501	LLP	C4-C4'	2.40	1.51	1.46
2	B	502	LLP	C4-C4'	2.11	1.50	1.46
3	D	501	PRO	OXT-C	-2.09	1.23	1.30
2	D	502	LLP	C4-C4'	2.00	1.50	1.46

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	LLP	CE-NZ-C4'	4.55	132.88	118.90
2	A	501	LLP	C5-C4-C4'	-3.83	115.26	121.56
2	A	501	LLP	C4-C4'-NZ	3.81	141.79	124.31
2	A	501	LLP	C3-C4-C4'	3.78	127.46	120.41
3	B	501	PRO	OXT-C-O	-3.59	115.94	124.09
2	A	501	LLP	CD-CE-NZ	-3.10	103.32	110.93
3	D	501	PRO	OXT-C-CA	3.02	123.43	113.40
3	B	501	PRO	OXT-C-CA	2.80	122.71	113.40
2	B	502	LLP	OP4-C5'-C5	2.69	114.47	109.35
3	D	501	PRO	OXT-C-O	-2.64	118.09	124.09
2	B	502	LLP	C5'-C5-C6	-2.63	115.06	119.37
3	D	501	PRO	C-CA-N	2.63	117.08	106.73
3	B	501	PRO	C-CA-N	2.55	116.79	106.73
2	D	502	LLP	C5'-C5-C6	-2.34	115.52	119.37
3	B	501	PRO	CD-N-CA	2.31	113.45	107.08
3	D	501	PRO	CD-N-CA	2.23	113.22	107.08
2	D	502	LLP	CD-CE-NZ	-2.17	105.62	110.93
2	A	501	LLP	C5-C6-N1	-2.15	120.24	123.82
2	C	501	LLP	C5'-C5-C6	-2.11	115.90	119.37

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	LLP	C4-C4'-NZ-CE
2	A	501	LLP	O-C-CA-CB
2	B	502	LLP	C4-C5-C5'-OP4
2	B	502	LLP	C6-C5-C5'-OP4
2	B	502	LLP	C5'-OP4-P-OP1
2	B	502	LLP	C5'-OP4-P-OP2
2	B	502	LLP	C5'-OP4-P-OP3
2	B	502	LLP	O-C-CA-CB
2	C	501	LLP	O-C-CA-CB
2	D	502	LLP	C4-C5-C5'-OP4
2	D	502	LLP	C6-C5-C5'-OP4
2	D	502	LLP	C5'-OP4-P-OP1
2	D	502	LLP	C5'-OP4-P-OP2
2	D	502	LLP	O-C-CA-CB
2	B	502	LLP	CG-CD-CE-NZ
2	D	502	LLP	CG-CD-CE-NZ
2	C	501	LLP	CG-CD-CE-NZ
2	A	501	LLP	CG-CD-CE-NZ
2	B	502	LLP	CA-CB-CG-CD

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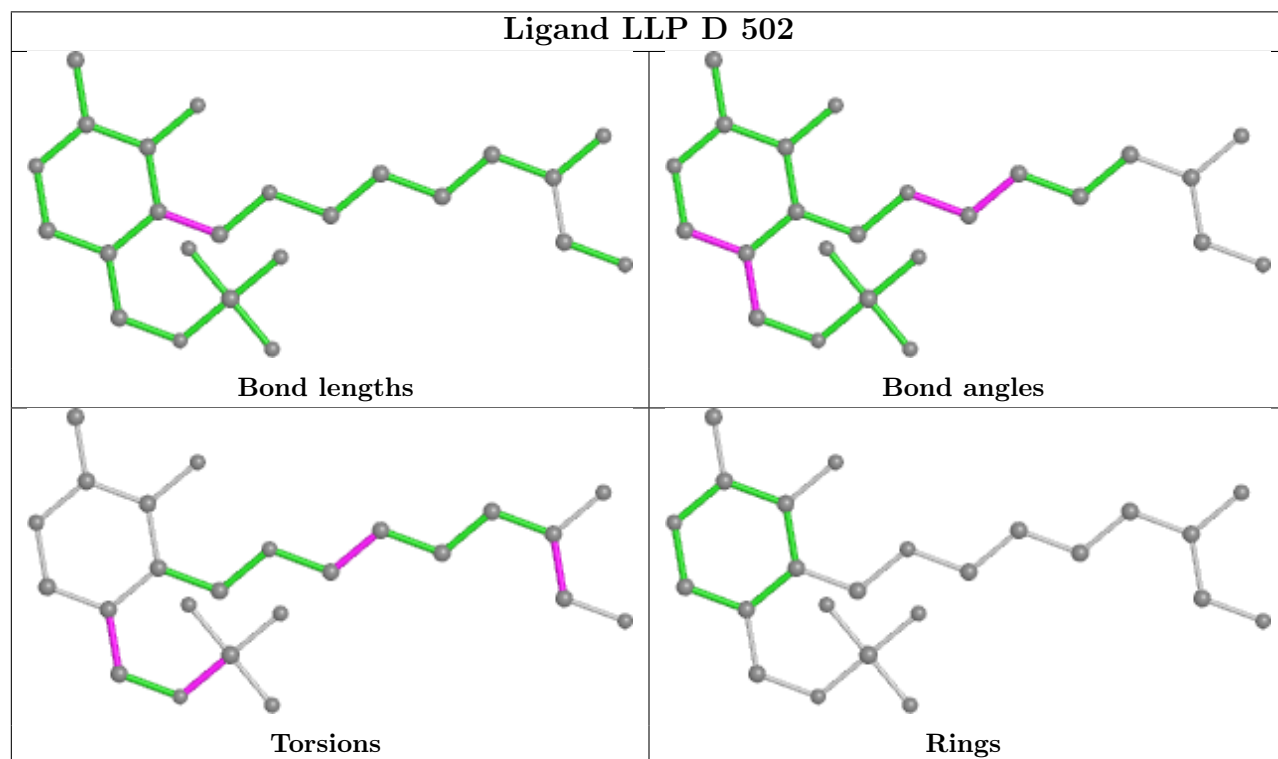
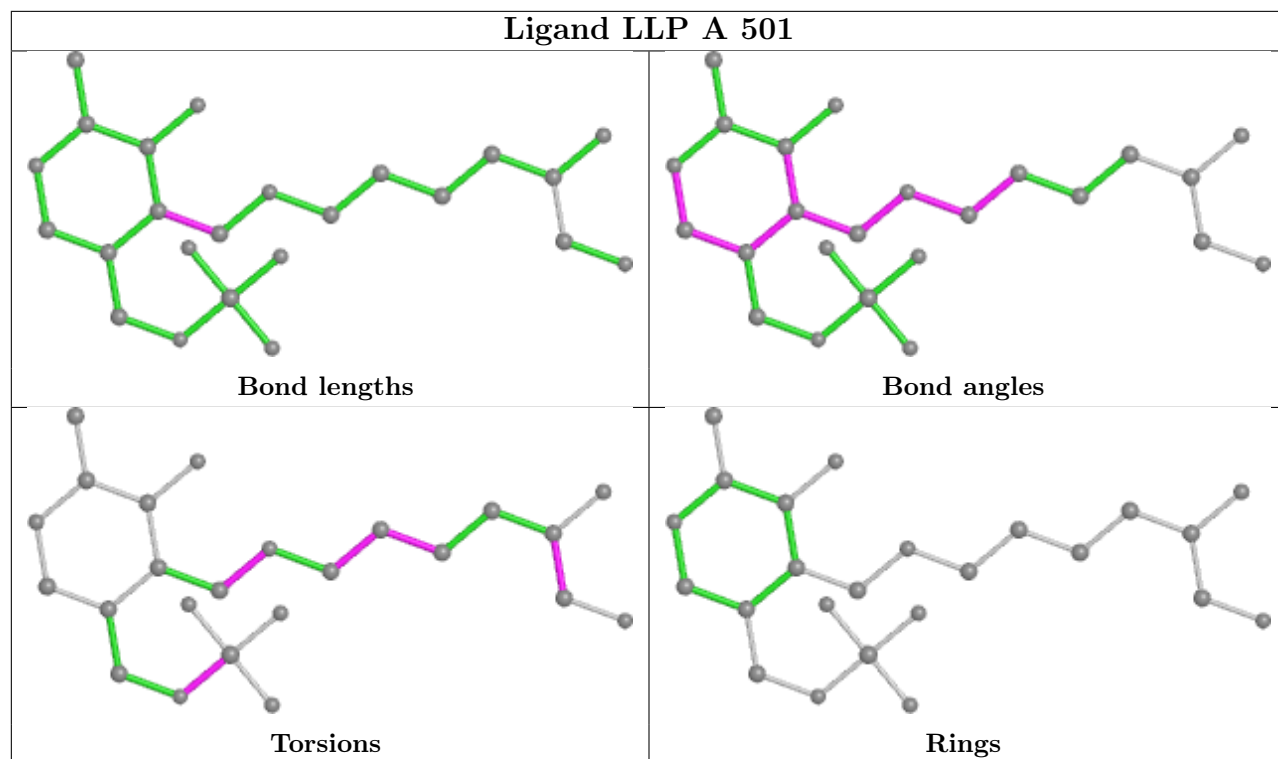
Mol	Chain	Res	Type	Atoms
2	A	501	LLP	C5'-OP4-P-OP1
2	C	501	LLP	C5'-OP4-P-OP1
2	A	501	LLP	C5'-OP4-P-OP2
2	A	501	LLP	CE-CD-CG-CB
2	C	501	LLP	C4-C5-C5'-OP4
3	B	501	PRO	O-C-CA-CB
3	B	501	PRO	OXT-C-CA-CB
3	D	501	PRO	O-C-CA-CB
3	D	501	PRO	OXT-C-CA-CB
2	C	501	LLP	C5'-OP4-P-OP2
2	D	502	LLP	C5'-OP4-P-OP3
3	B	501	PRO	OXT-C-CA-N

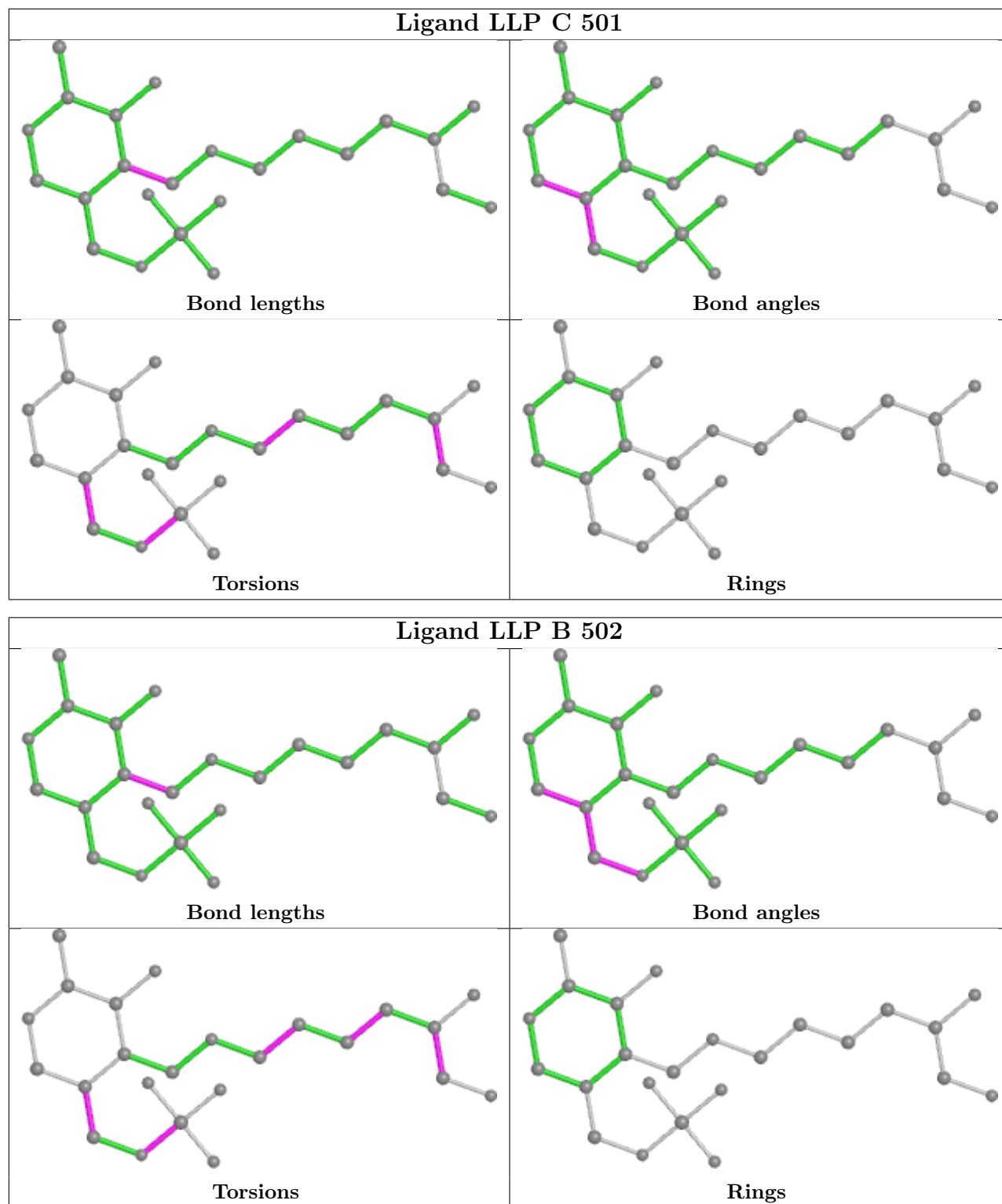
There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	501	PRO	3	0
2	A	501	LLP	3	0
3	B	501	PRO	3	0
2	C	501	LLP	1	0
2	B	502	LLP	1	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

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	404/448 (90%)	-0.15	15 (3%) 41 45	14, 22, 40, 69	0
1	B	404/448 (90%)	-0.18	10 (2%) 57 61	14, 26, 44, 64	0
1	C	404/448 (90%)	-0.04	24 (5%) 22 24	15, 26, 57, 80	0
1	D	404/448 (90%)	-0.05	20 (4%) 28 31	14, 24, 52, 80	0
All	All	1616/1792 (90%)	-0.10	69 (4%) 35 38	14, 24, 49, 80	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	6	PRO	5.8
1	C	389	GLN	5.4
1	C	390	LEU	5.4
1	B	62	LEU	5.2
1	D	389	GLN	5.1
1	D	393	GLN	5.1
1	D	41	LYS	4.8
1	C	391	ASN	4.4
1	A	62	LEU	4.4
1	C	393	GLN	4.3
1	D	392	GLU	4.2
1	D	396	LEU	4.1
1	D	62	LEU	4.0
1	C	6	PRO	3.9
1	B	41	LYS	3.9
1	C	62	LEU	3.8
1	D	391	ASN	3.8
1	C	392	GLU	3.7
1	A	41	LYS	3.6
1	B	250	GLY	3.6
1	D	7	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	398	ALA	3.4
1	A	245	ASP	3.4
1	D	397	ALA	3.4
1	B	249	ASN	3.3
1	D	390	LEU	3.3
1	A	234	ALA	3.3
1	A	249	ASN	3.1
1	D	395	LEU	3.1
1	A	61	ARG	3.1
1	B	246	PRO	3.1
1	C	40	PHE	3.1
1	C	7	GLU	3.1
1	C	41	LYS	3.1
1	C	246	PRO	3.0
1	C	250	GLY	3.0
1	A	246	PRO	3.0
1	B	7	GLU	3.0
1	C	397	ALA	3.0
1	D	394	GLU	2.9
1	C	395	LEU	2.9
1	C	396	LEU	2.9
1	A	248	TYR	2.8
1	A	247	GLN	2.8
1	C	61	ARG	2.7
1	D	61	ARG	2.6
1	C	383	ALA	2.6
1	B	40	PHE	2.6
1	C	388	ALA	2.6
1	C	394	GLU	2.6
1	C	249	ASN	2.5
1	C	8	ASN	2.4
1	C	248	TYR	2.4
1	A	389	GLN	2.4
1	B	247	GLN	2.4
1	A	244	PRO	2.3
1	B	248	TYR	2.3
1	A	250	GLY	2.3
1	D	8	ASN	2.2
1	D	383	ALA	2.2
1	D	399	GLY	2.2
1	A	159	ILE	2.1
1	A	233	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	40	PHE	2.1
1	B	6	PRO	2.1
1	D	5	ASN	2.0
1	C	234	ALA	2.0
1	D	40	PHE	2.0
1	C	5	ASN	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](#)

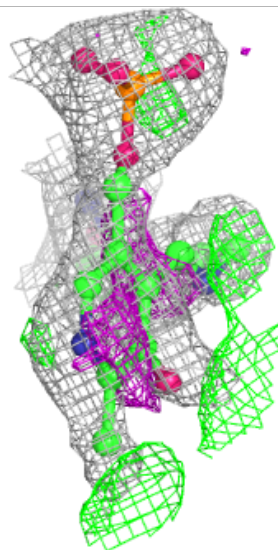
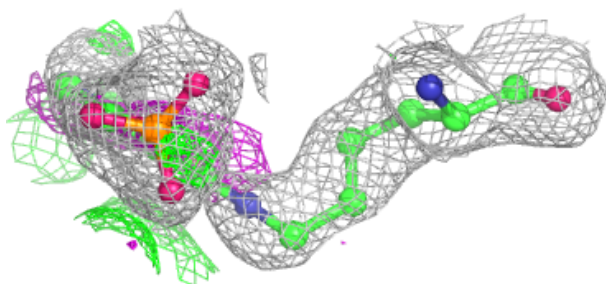
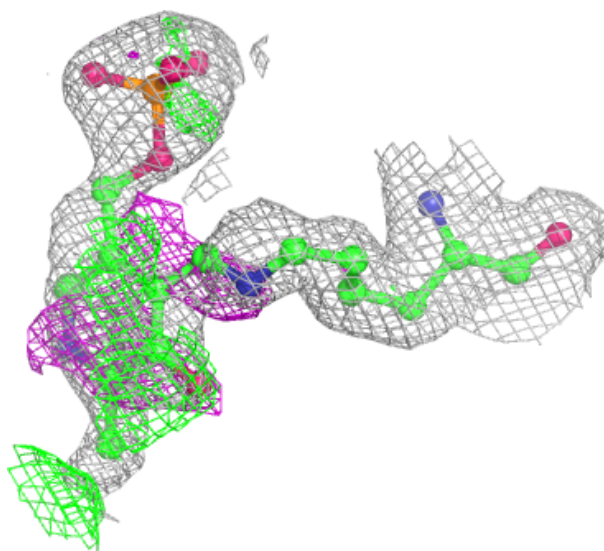
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PRO	B	501	8/8	0.91	0.15	15,19,20,21	0
2	LLP	B	502	24/25	0.93	0.21	16,39,48,51	0
2	LLP	C	501	24/25	0.94	0.16	16,30,39,42	0
2	LLP	A	501	24/25	0.94	0.20	13,33,40,44	0
3	PRO	D	501	8/8	0.94	0.17	14,18,22,23	0
2	LLP	D	502	24/25	0.95	0.17	12,29,39,40	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.

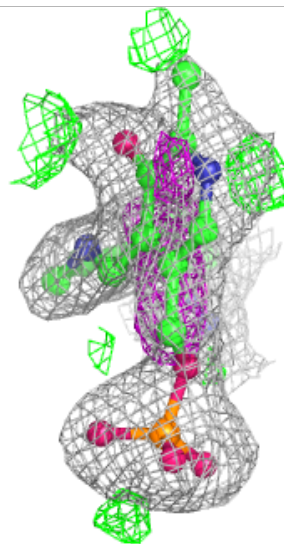
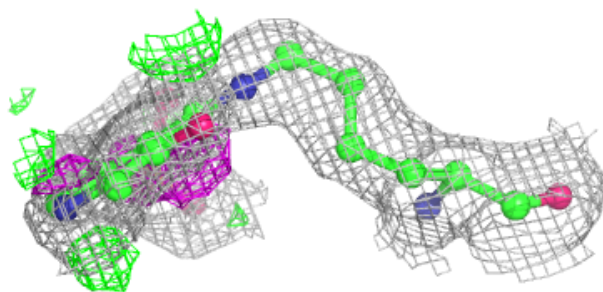
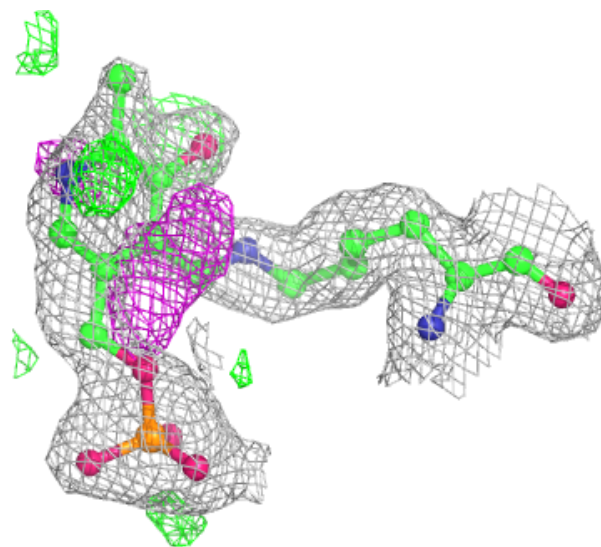
Electron density around LLP B 502:

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



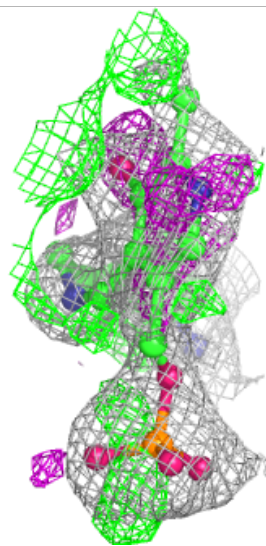
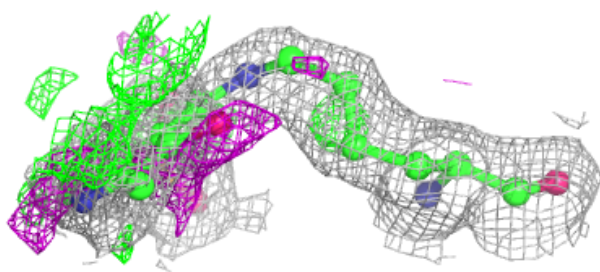
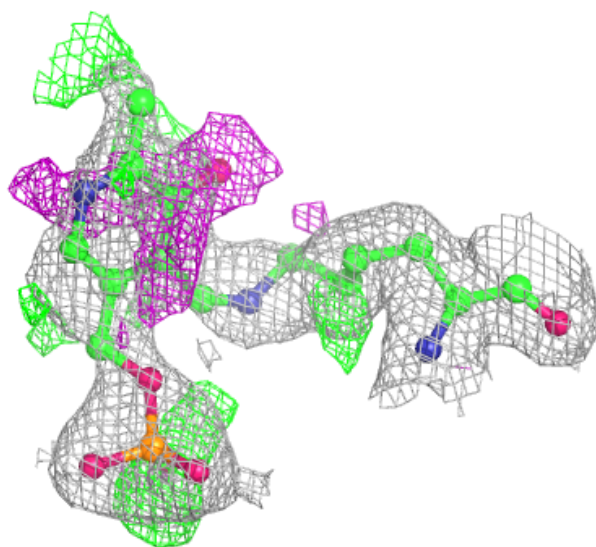
Electron density around LLP C 501:

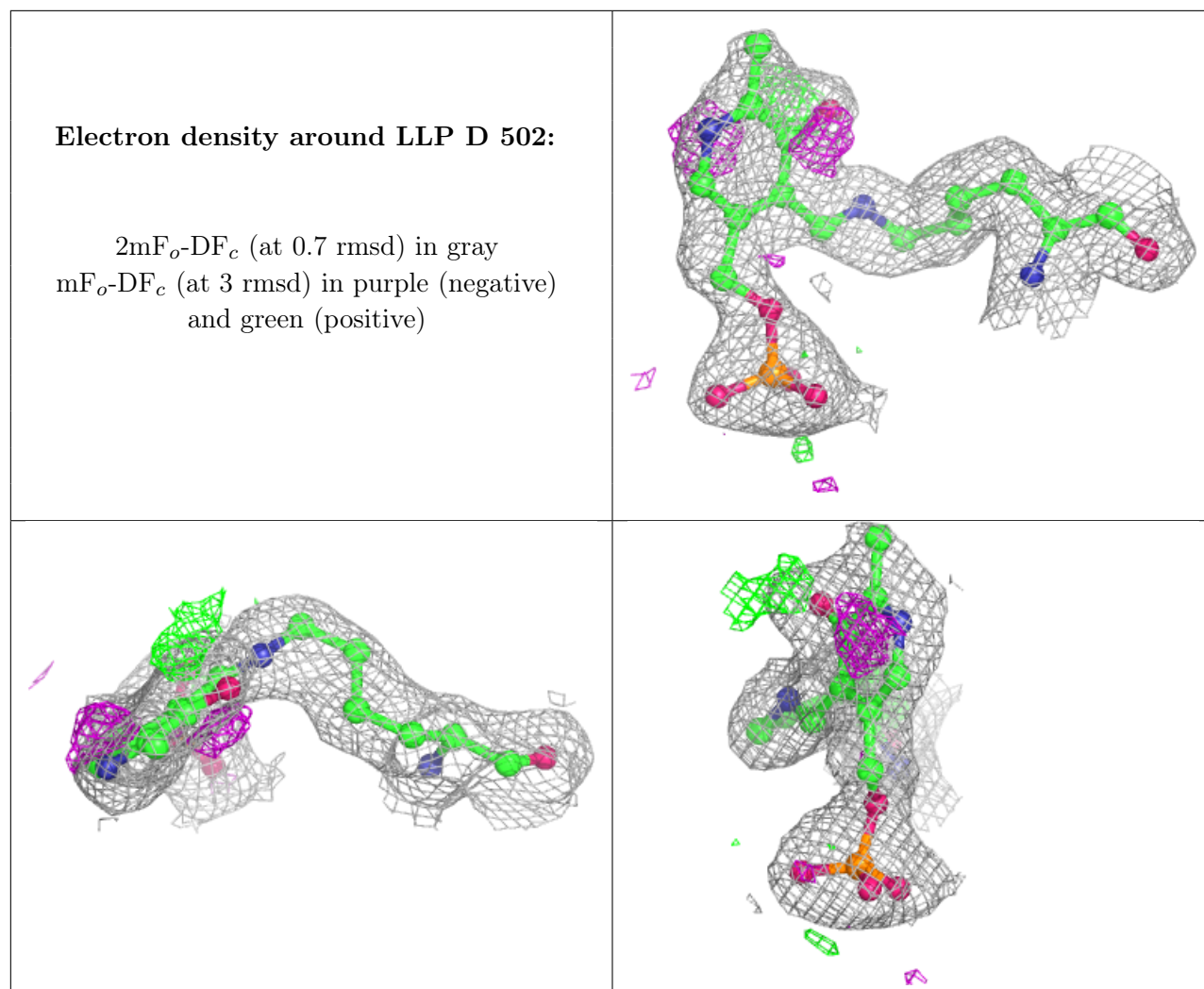
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around LLP A 501:

$2mF_o-DF_c$ (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.