



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 08:16 pm BST

PDB ID : 5JNL
Title : Structure of Plasmodium falciparum DXR in complex with a beta-substituted fosmidomycin analogue, LC54 and manganese
Authors : Sooriyaarachchi, S.; Bergfors, T.; Jones, T.A.; Mowbray, S.L.
Deposited on : 2016-04-30
Resolution : 1.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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

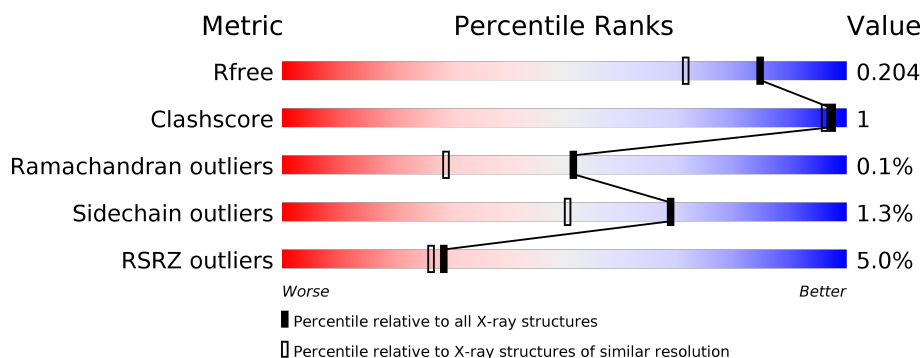
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	422	
1	B	422	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7269 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.

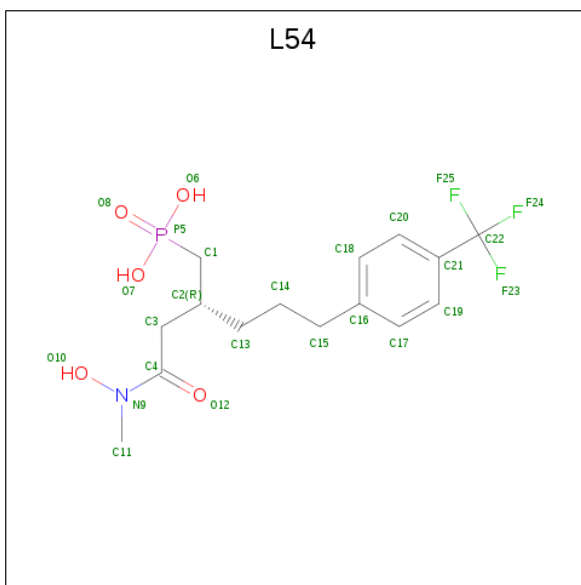
- Molecule 1 is a protein called 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	410	Total	C	N	O	S	0	8	0
			3328	2132	545	630	21			
1	B	410	Total	C	N	O	S	0	8	0
			3321	2129	543	629	20			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	MET	-	initiating methionine	UNP Q8IKG4
A	68	ALA	-	expression tag	UNP Q8IKG4
A	69	HIS	-	expression tag	UNP Q8IKG4
A	70	HIS	-	expression tag	UNP Q8IKG4
A	71	HIS	-	expression tag	UNP Q8IKG4
A	72	HIS	-	expression tag	UNP Q8IKG4
A	73	HIS	-	expression tag	UNP Q8IKG4
A	74	HIS	-	expression tag	UNP Q8IKG4
B	67	MET	-	initiating methionine	UNP Q8IKG4
B	68	ALA	-	expression tag	UNP Q8IKG4
B	69	HIS	-	expression tag	UNP Q8IKG4
B	70	HIS	-	expression tag	UNP Q8IKG4
B	71	HIS	-	expression tag	UNP Q8IKG4
B	72	HIS	-	expression tag	UNP Q8IKG4
B	73	HIS	-	expression tag	UNP Q8IKG4
B	74	HIS	-	expression tag	UNP Q8IKG4

- Molecule 2 is {(2R)-2-{2-[hydroxy(methyl)amino]-2-oxoethyl}-5-[4-(trifluoromethyl)phenyl]pentyl}phosphonic acid (three-letter code: L54) (formula: C₁₅H₂₁F₃NO₅P).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	P	0	0
			25	15	3	1	5	1		
2	B	1	Total	C	F	N	O	P	0	0
			25	15	3	1	5	1		

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

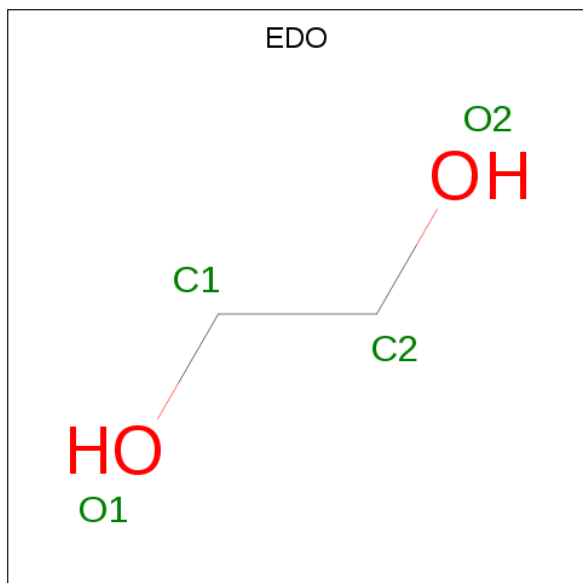
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mn	0	0
			1	1		
3	A	1	Total	Mn	0	0
			1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

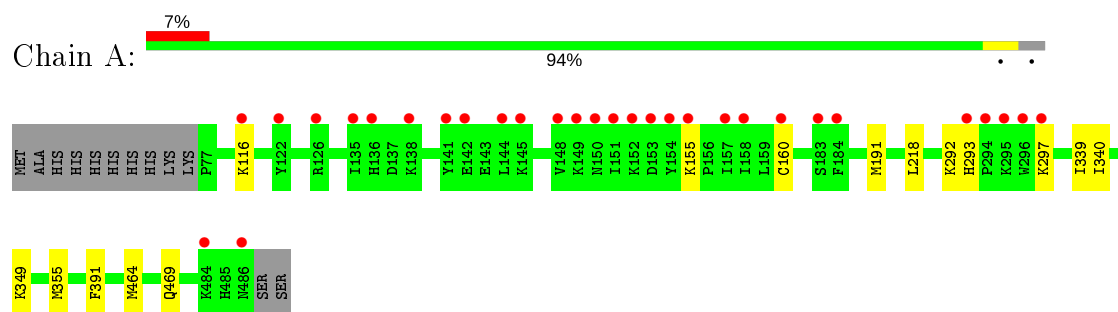
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	234	Total O 234 234	0	0
6	B	274	Total O 274 274	0	0

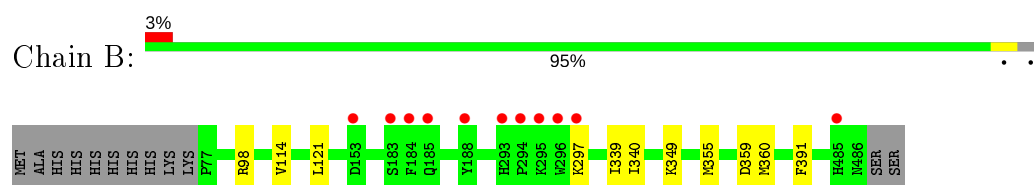
3 Residue-property plots [i](#)

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: 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplactic



- Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplactic



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.47Å 56.03Å 86.04Å 103.10° 102.89° 100.90°	Depositor
Resolution (Å)	30.00 – 1.60 47.88 – 1.60	Depositor EDS
% Data completeness (in resolution range)	94.3 (30.00-1.60) 94.3 (47.88-1.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.178 , 0.199 0.187 , 0.204	Depositor DCC
R_{free} test set	5527 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	18.6	Xtriage
Anisotropy	0.250	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.008 for -h,-k,h+k+l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7269	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.57% 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: GOL, MN, L54, EDO

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	0.37	0/3394	0.58	0/4583
1	B	0.37	0/3393	0.59	1/4583 (0.0%)
All	All	0.37	0/6787	0.58	1/9166 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	98	ARG	NE-CZ-NH1	5.14	122.87	120.30

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	3328	0	3363	5	0
1	B	3321	0	3363	4	0
2	A	25	0	0	0	0
2	B	25	0	0	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	12	0	16	2	0
4	B	12	0	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	12	0	18	0	0
5	B	24	0	36	0	0
6	A	234	0	0	1	0
6	B	274	0	0	1	0
All	All	7269	0	6812	11	0

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

All (11) 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:464[A]:MET:HE3	1:A:464[A]:MET:O	1.89	0.72
4:A:504:GOL:O2	6:A:601:HOH:O	2.09	0.60
1:B:339:ILE:HG22	1:B:355:MET:HG2	1.94	0.50
1:B:359:ASP:N	2:B:501:L54:F25	2.36	0.48
1:B:114:VAL:HG22	1:B:121:LEU:HD22	1.98	0.46
1:A:340:ILE:HD12	1:A:391:PHE:HZ	1.80	0.46
1:A:191:MET:HG3	1:A:218:LEU:HD11	1.99	0.45
1:A:339:ILE:HG22	1:A:355:MET:HG2	2.01	0.42
4:A:504:GOL:H11	6:B:602:HOH:O	2.20	0.42
1:B:340:ILE:HD12	1:B:391:PHE:HZ	1.85	0.41
1:A:340:ILE:HG12	1:A:355:MET:HG3	2.03	0.41

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	416/422 (99%)	404 (97%)	11 (3%)	1 (0%)	47 26
1	B	416/422 (99%)	405 (97%)	11 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	832/844 (99%)	809 (97%)	22 (3%)	1 (0%)	51 29

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	293	HIS

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	385/388 (99%)	378 (98%)	7 (2%)	59 36
1	B	385/388 (99%)	382 (99%)	3 (1%)	81 70
All	All	770/776 (99%)	760 (99%)	10 (1%)	69 50

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116	LYS
1	A	155	LYS
1	A	160	CYS
1	A	292	LYS
1	A	297	LYS
1	A	349	LYS
1	A	469	GLN
1	B	297	LYS
1	B	349	LYS
1	B	360	MET

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

Mol	Chain	Res	Type
1	A	459	ASN
1	B	197	ASN

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 17 ligands modelled in this entry, 2 are monoatomic - leaving 15 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	$\# Z > 2$
4	GOL	A	503	-	5,5,5	0.31	0	5,5,5	0.60	0
5	EDO	B	510	-	3,3,3	0.47	0	2,2,2	0.26	0
5	EDO	B	507	-	3,3,3	0.48	0	2,2,2	0.16	0
5	EDO	A	505	-	3,3,3	0.49	0	2,2,2	0.16	0
4	GOL	A	504	-	5,5,5	0.31	0	5,5,5	0.60	0
2	L54	A	501	3	23,25,25	0.96	3 (13%)	30,36,36	1.23	3 (10%)
5	EDO	A	506	-	3,3,3	0.56	0	2,2,2	0.20	0
5	EDO	B	506	-	3,3,3	0.43	0	2,2,2	0.21	0
5	EDO	A	507	-	3,3,3	0.44	0	2,2,2	0.24	0
5	EDO	B	509	-	3,3,3	0.44	0	2,2,2	0.32	0
5	EDO	B	508	-	3,3,3	0.55	0	2,2,2	0.15	0
5	EDO	B	505	-	3,3,3	0.42	0	2,2,2	0.32	0
2	L54	B	501	3	23,25,25	1.05	3 (13%)	30,36,36	1.24	3 (10%)
4	GOL	B	503	-	5,5,5	0.30	0	5,5,5	0.33	0
4	GOL	B	504	-	5,5,5	0.29	0	5,5,5	0.34	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	503	-	-	0/4/4/4	-
5	EDO	B	510	-	-	1/1/1/1	-
5	EDO	B	507	-	-	0/1/1/1	-
5	EDO	A	505	-	-	0/1/1/1	-
4	GOL	A	504	-	-	1/4/4/4	-
2	L54	A	501	3	-	7/25/25/25	0/1/1/1
5	EDO	A	506	-	-	1/1/1/1	-
5	EDO	B	506	-	-	0/1/1/1	-
5	EDO	A	507	-	-	1/1/1/1	-
5	EDO	B	509	-	-	1/1/1/1	-
5	EDO	B	508	-	-	1/1/1/1	-
5	EDO	B	505	-	-	1/1/1/1	-
2	L54	B	501	3	-	8/25/25/25	0/1/1/1
4	GOL	B	503	-	-	0/4/4/4	-
4	GOL	B	504	-	-	0/4/4/4	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	L54	P5-C1	2.70	1.81	1.78
2	B	501	L54	P5-O6	-2.66	1.48	1.54
2	B	501	L54	P5-C1	2.63	1.81	1.78
2	B	501	L54	P5-O7	-2.23	1.49	1.54
2	A	501	L54	P5-O6	-2.22	1.49	1.54
2	A	501	L54	P5-O7	-2.03	1.50	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	L54	C2-C3-C4	-3.18	108.65	113.02
2	A	501	L54	C2-C3-C4	-2.97	108.94	113.02
2	A	501	L54	C3-C4-N9	2.80	121.05	117.63
2	B	501	L54	C3-C4-N9	2.60	120.81	117.63
2	A	501	L54	O12-C4-C3	-2.18	118.26	122.20
2	B	501	L54	O12-C4-C3	-2.17	118.28	122.20

There are no chirality outliers.

All (22) torsion outliers are listed below:

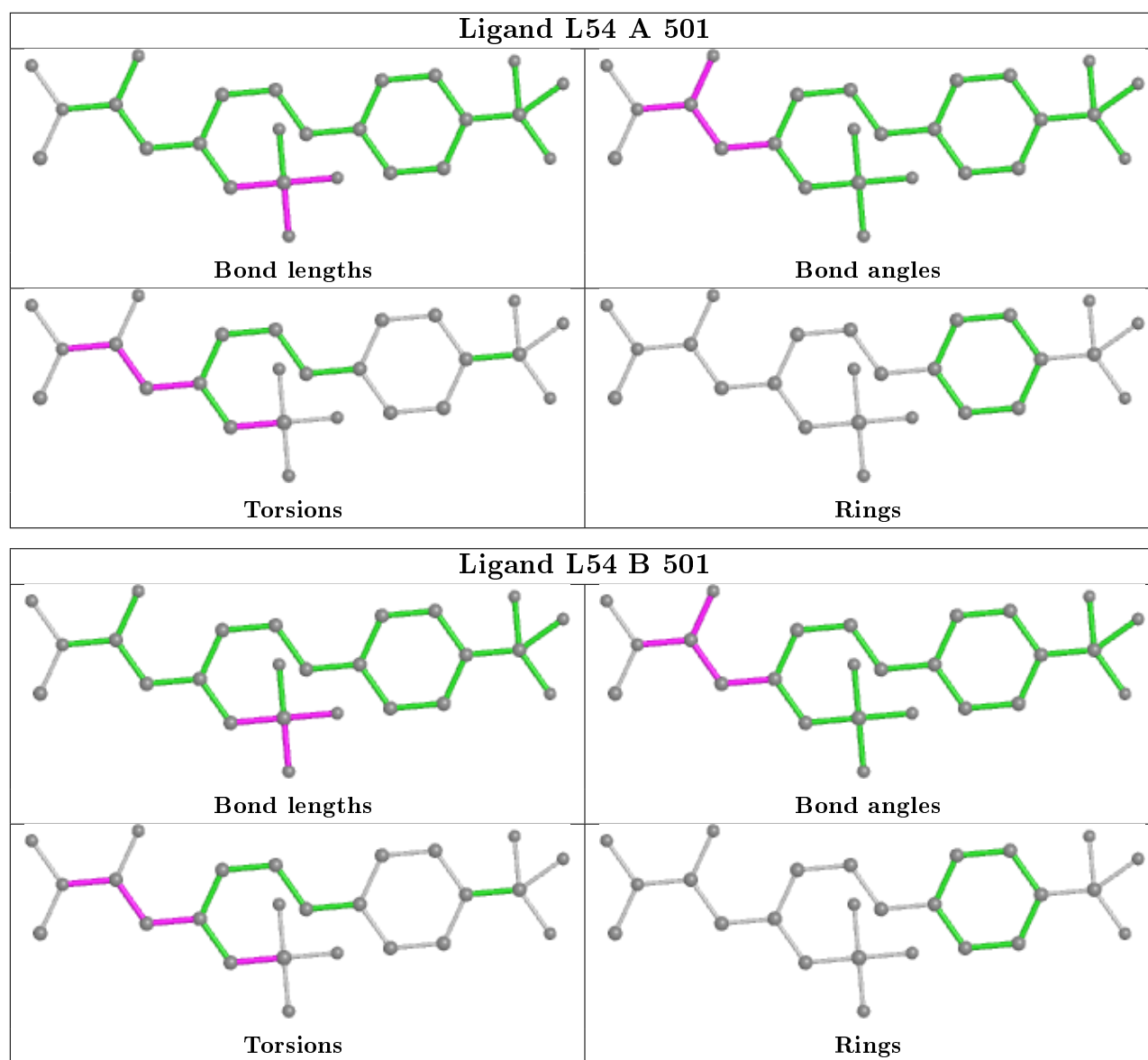
Mol	Chain	Res	Type	Atoms
2	A	501	L54	C1-C2-C3-C4
2	A	501	L54	C13-C2-C3-C4
2	B	501	L54	C1-C2-C3-C4
2	B	501	L54	C13-C2-C3-C4
2	B	501	L54	C2-C1-P5-O6
2	A	501	L54	C2-C1-P5-O6
2	B	501	L54	C2-C1-P5-O7
5	A	506	EDO	O1-C1-C2-O2
5	B	508	EDO	O1-C1-C2-O2
5	B	505	EDO	O1-C1-C2-O2
2	B	501	L54	C2-C3-C4-N9
5	B	509	EDO	O1-C1-C2-O2
2	A	501	L54	C2-C3-C4-O12
2	B	501	L54	C2-C3-C4-O12
2	A	501	L54	C2-C1-P5-O7
2	A	501	L54	C2-C3-C4-N9
5	A	507	EDO	O1-C1-C2-O2
4	A	504	GOL	O1-C1-C2-C3
2	B	501	L54	C2-C1-P5-O8
5	B	510	EDO	O1-C1-C2-O2
2	A	501	L54	O12-C4-N9-O10
2	B	501	L54	O12-C4-N9-O10

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	504	GOL	2	0
2	B	501	L54	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 [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	410/422 (97%)	0.27	30 (7%) 15 13	11, 21, 46, 100	0
1	B	410/422 (97%)	0.00	11 (2%) 54 52	10, 18, 35, 96	0
All	All	820/844 (97%)	0.13	41 (5%) 28 26	10, 19, 44, 100	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	296	TRP	16.1
1	B	296	TRP	15.3
1	B	184	PHE	8.2
1	A	293	HIS	7.5
1	A	295	LYS	7.4
1	B	183	SER	6.8
1	B	297	LYS	6.3
1	B	294	PRO	5.9
1	A	294	PRO	5.6
1	B	293	HIS	5.3
1	A	183	SER	5.1
1	B	295	LYS	5.0
1	A	141	TYR	4.6
1	A	153	ASP	4.4
1	A	116	LYS	4.3
1	A	160	CYS	4.2
1	A	150	ASN	3.9
1	A	122	TYR	3.7
1	A	126	ARG	3.7
1	A	148	VAL	3.4
1	A	297	LYS	3.3
1	A	154	TYR	3.3
1	A	157	ILE	3.1
1	A	138	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	149	LYS	2.9
1	A	184	PHE	2.8
1	B	185	GLN	2.8
1	A	144	LEU	2.8
1	A	155	LYS	2.8
1	A	142	GLU	2.7
1	A	152	LYS	2.7
1	A	484	LYS	2.7
1	B	153	ASP	2.7
1	B	485	HIS	2.6
1	A	158	ILE	2.5
1	A	145	LYS	2.5
1	A	486	ASN	2.2
1	B	188	TYR	2.2
1	A	135	ILE	2.2
1	A	151	ILE	2.1
1	A	136	HIS	2.1

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(Å ²)	Q<0.9
5	EDO	A	505	4/4	0.75	0.11	50,51,51,51	0
4	GOL	B	504	6/6	0.76	0.16	30,33,35,37	0
5	EDO	B	508	4/4	0.79	0.16	26,31,33,36	0
5	EDO	A	507	4/4	0.81	0.17	36,37,38,40	0
5	EDO	B	507	4/4	0.82	0.14	46,46,46,47	0
5	EDO	B	509	4/4	0.86	0.11	34,35,36,37	0

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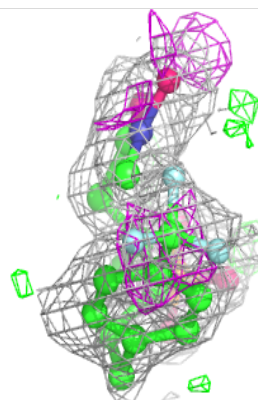
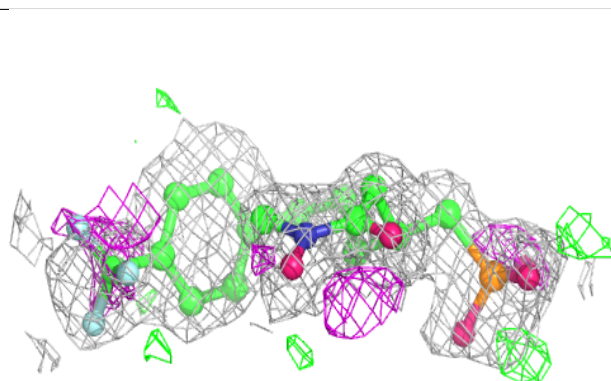
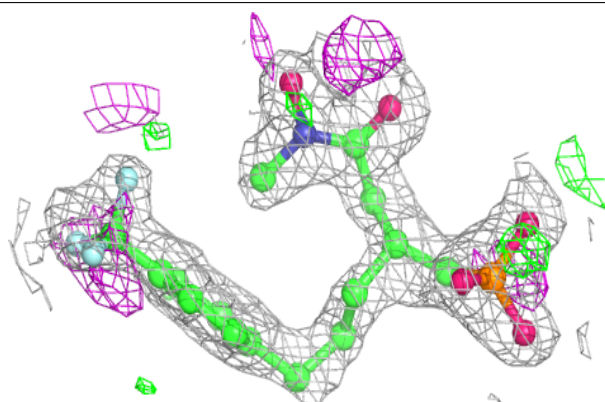
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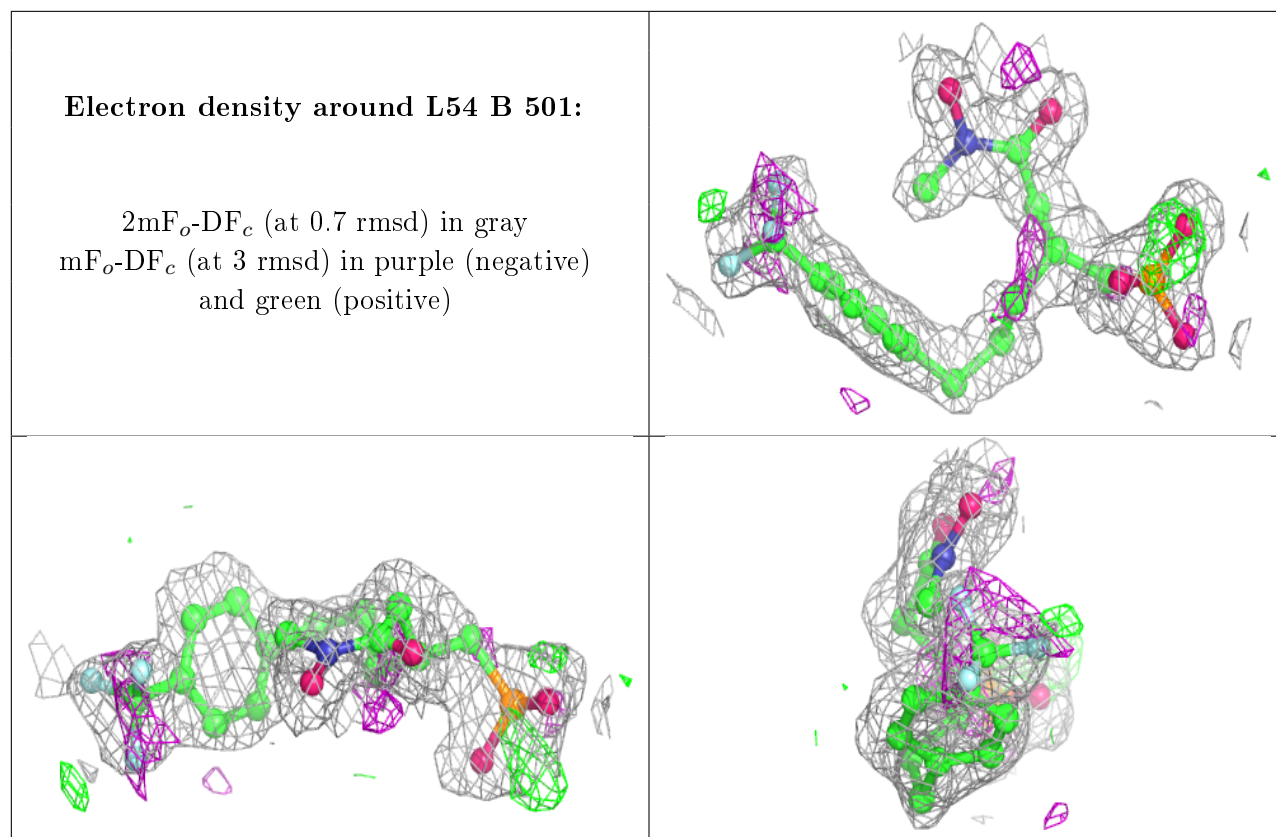
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GOL	A	503	6/6	0.88	0.11	27,29,29,30	0
4	GOL	A	504	6/6	0.89	0.14	24,28,30,30	0
5	EDO	A	506	4/4	0.89	0.11	28,29,29,30	0
5	EDO	B	506	4/4	0.91	0.12	24,24,24,26	0
5	EDO	B	505	4/4	0.92	0.09	25,27,27,27	0
5	EDO	B	510	4/4	0.93	0.15	42,42,42,43	0
2	L54	A	501	25/25	0.93	0.14	22,31,54,55	0
4	GOL	B	503	6/6	0.93	0.09	21,22,23,23	0
2	L54	B	501	25/25	0.93	0.14	16,28,42,44	0
3	MN	A	502	1/1	1.00	0.02	17,17,17,17	0
3	MN	B	502	1/1	1.00	0.05	13,13,13,13	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 L54 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.