Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 04:38 am BST

PDB ID	:	5O3N
Title	:	Crystal structure of E. cloacae 3,4-dihydroxybenzoic acid decarboxylase (AroY) reconstituted with prFMN
Authors	:	Marshall, S.A.; Leys, D.
Deposited on	:	2017-05-24
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 following versions of software and data (see references ⓘ) were used in the production of this report:

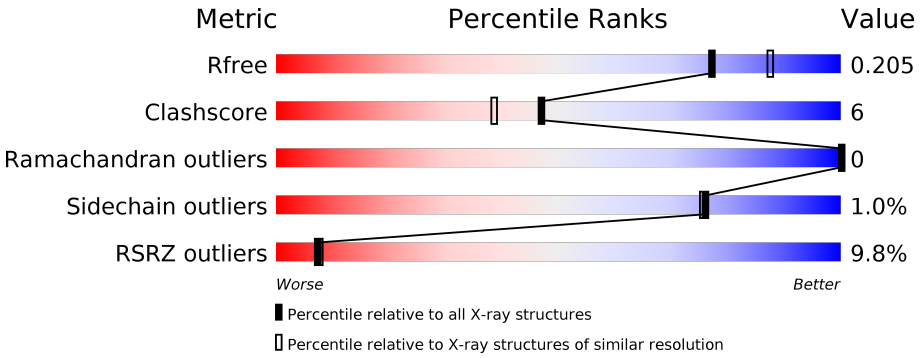
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.05 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 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 <=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	515	7% 81% 13% 5%
1	B	515	11% 80% 14% 5%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7934 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 3,4-dihydroxybenzoate decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	488	Total	C	N	O	S	0	5	0
			3746	2371	658	698	19			
1	B	488	Total	C	N	O	S	0	2	0
			3723	2356	654	693	20			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP B2DCZ6
A	-18	GLY	-	expression tag	UNP B2DCZ6
A	-17	SER	-	expression tag	UNP B2DCZ6
A	-16	SER	-	expression tag	UNP B2DCZ6
A	-15	HIS	-	expression tag	UNP B2DCZ6
A	-14	HIS	-	expression tag	UNP B2DCZ6
A	-13	HIS	-	expression tag	UNP B2DCZ6
A	-12	HIS	-	expression tag	UNP B2DCZ6
A	-11	HIS	-	expression tag	UNP B2DCZ6
A	-10	HIS	-	expression tag	UNP B2DCZ6
A	-9	SER	-	expression tag	UNP B2DCZ6
A	-8	SER	-	expression tag	UNP B2DCZ6
A	-7	GLY	-	expression tag	UNP B2DCZ6
A	-6	LEU	-	expression tag	UNP B2DCZ6
A	-5	VAL	-	expression tag	UNP B2DCZ6
A	-4	PRO	-	expression tag	UNP B2DCZ6
A	-3	ARG	-	expression tag	UNP B2DCZ6
A	-2	GLY	-	expression tag	UNP B2DCZ6
A	-1	SER	-	expression tag	UNP B2DCZ6
A	0	HIS	-	expression tag	UNP B2DCZ6
B	-19	MET	-	initiating methionine	UNP B2DCZ6
B	-18	GLY	-	expression tag	UNP B2DCZ6
B	-17	SER	-	expression tag	UNP B2DCZ6
B	-16	SER	-	expression tag	UNP B2DCZ6
B	-15	HIS	-	expression tag	UNP B2DCZ6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP B2DCZ6
B	-13	HIS	-	expression tag	UNP B2DCZ6
B	-12	HIS	-	expression tag	UNP B2DCZ6
B	-11	HIS	-	expression tag	UNP B2DCZ6
B	-10	HIS	-	expression tag	UNP B2DCZ6
B	-9	SER	-	expression tag	UNP B2DCZ6
B	-8	SER	-	expression tag	UNP B2DCZ6
B	-7	GLY	-	expression tag	UNP B2DCZ6
B	-6	LEU	-	expression tag	UNP B2DCZ6
B	-5	VAL	-	expression tag	UNP B2DCZ6
B	-4	PRO	-	expression tag	UNP B2DCZ6
B	-3	ARG	-	expression tag	UNP B2DCZ6
B	-2	GLY	-	expression tag	UNP B2DCZ6
B	-1	SER	-	expression tag	UNP B2DCZ6
B	0	HIS	-	expression tag	UNP B2DCZ6

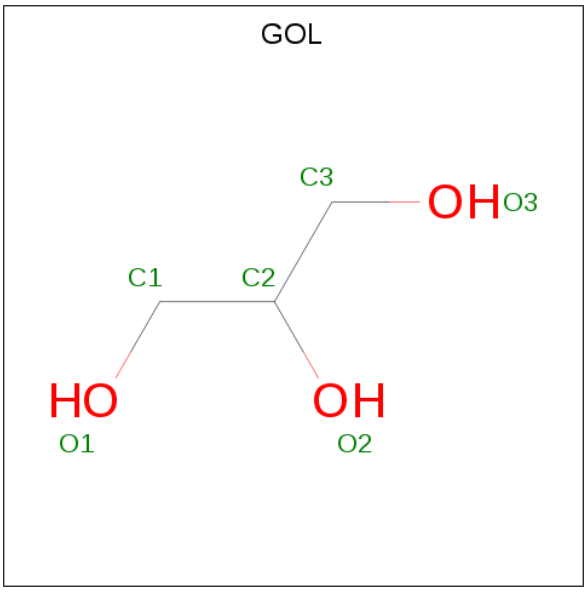
- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

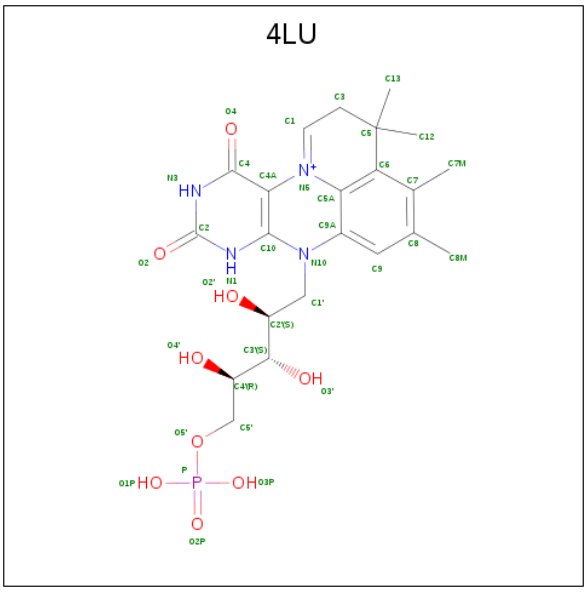
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Na 1 1	0	0
3	A	1	Total Na 1 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is 1-deoxy-5-O-phosphono-1-(3,3,4,5-tetramethyl-9,11-dioxo-2,3,8,9,10,11-hexahydro-7H-quinolino[1,8-fg]pteridin-12-ium-7-yl)-D-ribitol (three-letter code: 4LU) (formula: $C_{22}H_{30}N_4O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			36	22	4	9	1		
5	B	1	Total	C	N	O	P	0	0
			36	22	4	9	1		

- Molecule 6 is water.

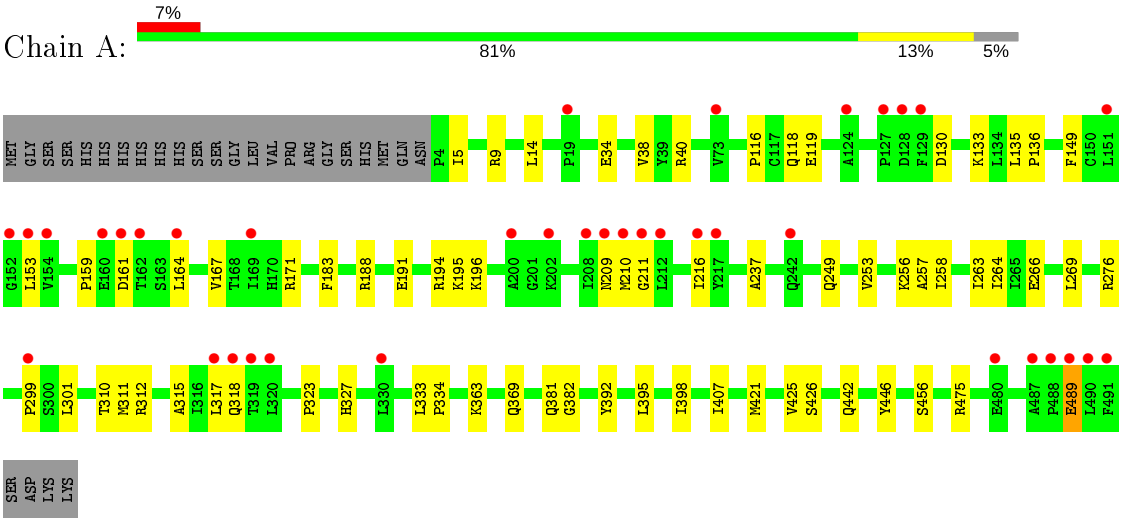
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	196	Total	O	0	0
			196	196		
6	B	157	Total	O	0	0
			157	157		

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.

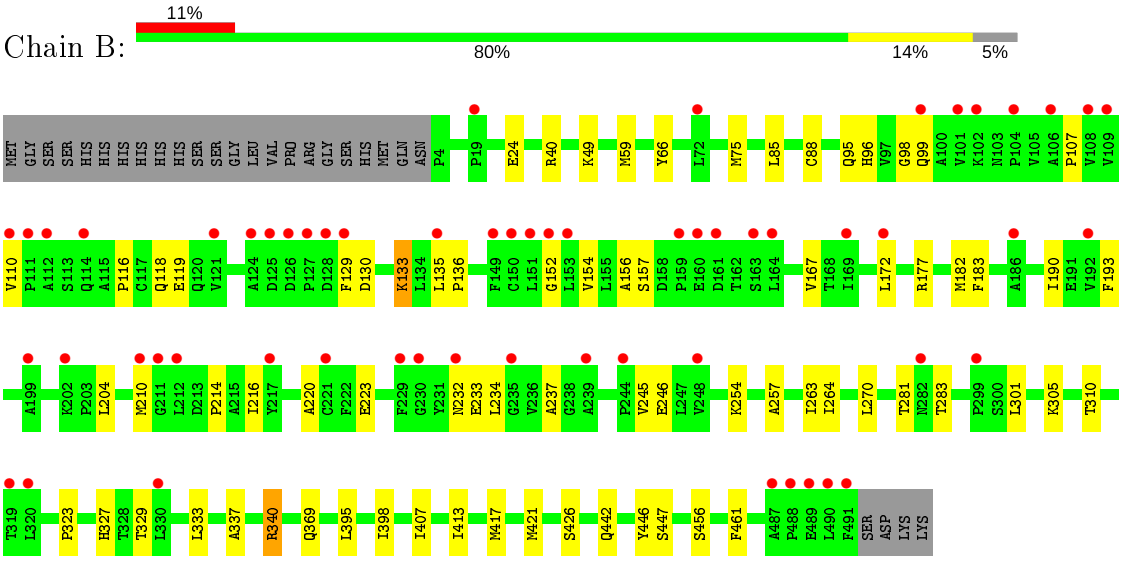
- Molecule 1: 3,4-dihydroxybenzoate decarboxylase

Chain A:



- Molecule 1: 3,4-dihydroxybenzoate decarboxylase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	208.31Å 208.31Å 157.91Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.07 – 2.05 30.07 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.4 (30.07-2.05) 99.4 (30.07-2.05)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.51 (at 2.05Å)	Xtriage
Refinement program	PHENIX (dev_2689: ???)	Depositor
R, R_{free}	0.184 , 0.205 0.184 , 0.205	Depositor DCC
R_{free} test set	4126 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	41.9	Xtriage
Anisotropy	0.246	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 51.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	7934	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 3.11% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MN, 4LU, 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	0.27	0/3840	0.48	0/5230
1	B	0.30	0/3813	0.50	0/5195
All	All	0.28	0/7653	0.49	0/10425

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

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	3746	0	3745	42	0
1	B	3723	0	3722	47	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	30	0	40	0	0
4	B	6	0	8	0	0
5	A	36	0	28	6	0
5	B	36	0	28	4	0
6	A	196	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	157	0	0	0	0
All	All	7934	0	7571	94	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 6.

All (94) 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)
5:A:508:4LU:H13	5:A:508:4LU:H14	1.30	1.12
5:B:504:4LU:H13	5:B:504:4LU:H14	1.30	1.12
1:B:234:LEU:HD12	1:B:245:VAL:HG21	1.38	1.04
1:B:130:ASP:HB3	1:B:133:LYS:HG3	1.50	0.94
5:B:504:4LU:C12	5:B:504:4LU:H14	2.08	0.81
1:A:9:ARG:HH21	1:A:312:ARG:HD2	1.48	0.78
1:B:234:LEU:CD1	1:B:245:VAL:HG21	2.16	0.73
5:A:508:4LU:C7M	5:A:508:4LU:H13	2.15	0.73
1:B:281:THR:HB	1:B:283:THR:HG23	1.72	0.71
1:A:257:ALA:HB1	1:A:264:ILE:HD13	1.75	0.68
1:A:211:GLY:HA2	1:A:318:GLN:HE21	1.60	0.67
1:A:159:PRO:HD2	1:A:196:LYS:HE3	1.79	0.64
1:B:234:LEU:HD12	1:B:245:VAL:CG2	2.23	0.64
1:A:209:ASN:ND2	1:A:258:ILE:H	1.96	0.63
1:A:171:ARG:HB3	5:A:508:4LU:H10	1.79	0.63
1:B:118:GLN:HA	1:B:310:THR:HG23	1.81	0.62
1:B:167:VAL:HG21	1:B:234:LEU:CD2	2.30	0.62
1:B:129:PHE:O	1:B:177:ARG:NH1	2.32	0.62
1:B:154:VAL:HG21	1:B:182:MET:HE2	1.83	0.59
1:B:135:LEU:HD22	1:B:263:ILE:HD13	1.84	0.59
1:B:167:VAL:HG21	1:B:234:LEU:HD23	1.85	0.59
1:A:196:LYS:HZ2	1:A:196:LYS:HB3	1.68	0.59
1:A:475:ARG:HD3	1:B:49:LYS:HD3	1.86	0.57
1:A:118:GLN:HG2	1:A:310:THR:HG21	1.87	0.57
5:A:508:4LU:C12	5:A:508:4LU:H14	2.13	0.56
1:B:323:PRO:HB2	1:B:327:HIS:HB2	1.86	0.55
1:B:110:VAL:HG21	1:B:246:GLU:HB3	1.88	0.55
1:A:118:GLN:HA	1:A:310:THR:HG23	1.89	0.55
1:A:323:PRO:HB2	1:A:327:HIS:HB2	1.89	0.54
1:A:149:PHE:CD1	1:A:210:MET:HE1	2.43	0.54
1:B:257:ALA:HB1	1:B:264:ILE:HD12	1.89	0.54
1:A:311:MET:HE3	1:A:315:ALA:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:GLY:HA2	1:B:337:ALA:HB1	1.91	0.53
1:B:369:GLN:HB2	1:B:407:ILE:HG21	1.90	0.53
1:B:223:GLU:OE2	5:B:504:4LU:O3'	2.27	0.53
1:A:161:ASP:HB3	1:A:164:LEU:HD12	1.90	0.53
1:B:118:GLN:HG2	1:B:310:THR:HG21	1.91	0.52
1:B:172:LEU:HD21	1:B:182:MET:HE3	1.92	0.51
1:A:116:PRO:O	1:A:312:ARG:HG2	2.12	0.50
1:B:183:PHE:HA	1:B:301:LEU:HD22	1.93	0.50
1:B:216:ILE:HA	1:B:237:ALA:HB2	1.93	0.50
1:A:5:ILE:HD11	1:A:14:LEU:HD13	1.94	0.50
1:B:24:GLU:HG2	1:B:59:MET:HB3	1.93	0.50
1:A:116:PRO:HB2	1:A:312:ARG:NE	2.27	0.49
1:B:156:ALA:HB1	1:B:204:LEU:HD21	1.94	0.49
1:A:249:GLN:HG2	1:A:256:LYS:HZ3	1.77	0.49
1:A:363[B]:LYS:NZ	1:A:392:TYR:OH	2.39	0.49
1:A:135:LEU:HD22	1:A:263:ILE:HD13	1.95	0.48
1:A:489:GLU:CD	1:A:489:GLU:H	2.17	0.48
1:A:253:VAL:HG22	1:A:266:GLU:HB3	1.96	0.48
1:A:183:PHE:HA	1:A:301:LEU:HD22	1.95	0.48
1:B:421:MET:HG3	1:B:426:SER:HB2	1.96	0.48
1:B:442:GLN:CD	1:B:456:SER:HB2	2.34	0.48
1:B:190:ILE:HA	1:B:193:PHE:CD1	2.48	0.47
1:B:116:PRO:O	1:B:119:GLU:HG3	2.15	0.47
1:A:421:MET:HG2	1:A:426:SER:HB2	1.95	0.47
1:B:220:ALA:HA	1:B:233:GLU:HB3	1.97	0.47
1:A:381:GLN:HG2	1:A:382:GLY:N	2.30	0.47
1:A:188:ARG:HE	5:A:508:4LU:H7	1.64	0.46
1:A:194:ARG:HG3	1:A:269:LEU:HD13	1.98	0.46
1:A:257:ALA:HB1	1:A:264:ILE:CD1	2.42	0.46
1:B:329:THR:O	1:B:333:LEU:HG	2.15	0.45
1:B:395:LEU:HD13	1:B:398:ILE:HD11	1.98	0.45
1:B:270:LEU:HD11	1:B:305:LYS:HB2	1.99	0.45
1:B:85:LEU:HD13	1:B:214:PRO:HG2	1.98	0.45
5:B:504:4LU:C12	5:B:504:4LU:C7M	2.85	0.44
1:A:196:LYS:NZ	1:A:196:LYS:HB3	2.28	0.44
1:B:75:MET:HB2	1:B:75:MET:HE2	1.83	0.44
1:A:395:LEU:HD13	1:A:398:ILE:HD11	1.98	0.44
1:A:153:LEU:HG	1:A:167:VAL:HG22	1.98	0.44
1:A:369:GLN:HB2	1:A:407:ILE:HG21	1.99	0.44
1:A:34:GLU:O	1:A:38:VAL:HG23	2.18	0.44
1:B:66:TYR:CD1	1:B:136:PRO:HB3	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:PRO:HB3	1:B:245:VAL:HG22	2.01	0.43
1:A:333:LEU:HB2	1:A:334:PRO:HD3	2.01	0.43
1:A:442:GLN:CD	1:A:456:SER:HB2	2.39	0.43
1:B:152:GLY:HA2	1:B:210:MET:HG2	2.01	0.43
1:B:88[C]:CYS:HG	1:B:96:HIS:CG	2.33	0.43
1:B:270:LEU:HD21	1:B:305:LYS:HB2	1.99	0.43
5:A:508:4LU:C7M	5:A:508:4LU:C12	2.85	0.42
1:B:254:LYS:HA	1:B:254:LYS:HD3	1.84	0.42
1:B:95:GLN:HA	1:B:340[A]:ARG:HD3	2.01	0.42
1:A:136:PRO:O	1:A:317:LEU:HD22	2.20	0.42
1:A:276:ARG:HG3	1:A:299:PRO:HA	2.01	0.42
1:B:421:MET:HE1	1:B:461:PHE:HD1	1.85	0.42
1:B:99:GLN:HE22	1:B:340[A]:ARG:NH1	2.18	0.42
1:A:216:ILE:HA	1:A:237:ALA:HB2	2.02	0.42
1:B:154:VAL:HG11	1:B:182:MET:HE1	2.01	0.41
1:A:116:PRO:O	1:A:119:GLU:HG3	2.21	0.41
1:A:130:ASP:HB3	1:A:133:LYS:HG3	2.02	0.41
1:B:413:ILE:O	1:B:417:MET:HG3	2.21	0.41
1:A:191:GLU:O	1:A:195:LYS:HG3	2.21	0.41
1:B:232:ASN:OD1	1:B:234:LEU:HB2	2.21	0.40
1:A:425:VAL:HG21	1:B:447:SER:HB2	2.04	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	491/515 (95%)	478 (97%)	13 (3%)	0	100	100
1	B	489/515 (95%)	475 (97%)	14 (3%)	0	100	100
All	All	980/1030 (95%)	953 (97%)	27 (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	401/420 (96%)	398 (99%)	3 (1%)	84	84
1	B	398/420 (95%)	392 (98%)	6 (2%)	65	63
All	All	799/840 (95%)	790 (99%)	9 (1%)	76	73

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

Mol	Chain	Res	Type
1	A	40	ARG
1	A	446	TYR
1	A	489	GLU
1	B	40	ARG
1	B	133	LYS
1	B	157	SER
1	B	340[A]	ARG
1	B	340[B]	ARG
1	B	446	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	GLN
1	A	209	ASN
1	A	249	GLN
1	A	318	GLN
1	A	453	ASN
1	B	16	GLN
1	B	383	GLN
1	B	453	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 12 ligands modelled in this entry, 4 are 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	$\#\|Z\| > 2$
4	GOL	A	506	-	5,5,5	0.97	0	5,5,5	1.02	0
4	GOL	B	503	-	5,5,5	0.82	0	5,5,5	0.97	0
4	GOL	A	503	-	5,5,5	0.92	0	5,5,5	1.00	0
4	GOL	A	507	-	5,5,5	0.87	0	5,5,5	1.12	0
4	GOL	A	504	-	5,5,5	0.93	0	5,5,5	0.92	0
5	4LU	B	504	3,2	32,39,39	1.46	6 (18%)	41,62,62	1.97	10 (24%)
5	4LU	A	508	3,2	32,39,39	1.70	7 (21%)	41,62,62	1.89	9 (21%)
4	GOL	A	505	-	5,5,5	0.89	0	5,5,5	1.03	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	506	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	B	503	-	-	1/4/4/4	-
4	GOL	A	503	-	-	0/4/4/4	-
4	GOL	A	507	-	-	2/4/4/4	-
4	GOL	A	504	-	-	0/4/4/4	-
5	4LU	B	504	3,2	-	0/18/30/30	0/3/4/4
5	4LU	A	508	3,2	-	0/18/30/30	0/3/4/4
4	GOL	A	505	-	-	2/4/4/4	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	508	4LU	C2-N3	-3.93	1.30	1.38
5	A	508	4LU	C1'-N10	-3.90	1.44	1.48
5	B	504	4LU	C2-N3	-3.41	1.31	1.38
5	B	504	4LU	C2-N1	-3.27	1.31	1.38
5	B	504	4LU	C1'-N10	-3.14	1.45	1.48
5	B	504	4LU	C6-C5A	-3.07	1.38	1.43
5	A	508	4LU	C6-C5A	-3.04	1.38	1.43
5	A	508	4LU	C2-N1	-3.00	1.32	1.38
5	A	508	4LU	O4-C4	-2.76	1.17	1.24
5	B	504	4LU	O4-C4	-2.40	1.18	1.24
5	A	508	4LU	P-O2P	-2.31	1.43	1.50
5	B	504	4LU	C9-C9A	-2.26	1.36	1.40
5	A	508	4LU	C9-C9A	-2.11	1.36	1.40

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	504	4LU	C4-N3-C2	7.01	121.06	115.14
5	A	508	4LU	C4-N3-C2	5.62	119.89	115.14
5	A	508	4LU	C13-C5-C6	4.40	116.02	111.72
5	A	508	4LU	C4-C4A-C10	-3.87	117.39	119.95
5	B	504	4LU	C1'-N10-C9A	3.82	121.30	118.29
5	A	508	4LU	C12-C5-C3	-3.74	103.12	109.60
5	B	504	4LU	C12-C5-C6	3.73	115.37	111.72
5	B	504	4LU	C4-C4A-C10	-3.33	117.75	119.95
5	B	504	4LU	C12-C5-C3	-3.27	103.94	109.60
5	A	508	4LU	C1'-N10-C9A	3.26	120.86	118.29
5	A	508	4LU	C13-C5-C3	-2.98	104.44	109.60
5	B	504	4LU	C9A-N10-C10	-2.85	118.17	121.91
5	B	504	4LU	C4A-N5-C5A	-2.80	118.96	120.99
5	A	508	4LU	P-O5'-C5'	2.80	126.00	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	504	4LU	C4A-C4-N3	-2.67	119.78	123.43
5	B	504	4LU	P-O5'-C5'	2.56	125.36	118.30
5	B	504	4LU	O5'-P-O2P	2.13	112.45	106.47
5	A	508	4LU	C3-C5-C6	2.03	112.03	107.38
5	A	508	4LU	O3P-P-O5'	2.02	112.11	106.73

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	506	GOL	O1-C1-C2-C3
4	A	507	GOL	C1-C2-C3-O3
4	A	505	GOL	C1-C2-C3-O3
4	A	505	GOL	O2-C2-C3-O3
4	A	506	GOL	O1-C1-C2-O2
4	B	503	GOL	O1-C1-C2-C3
4	A	507	GOL	O2-C2-C3-O3

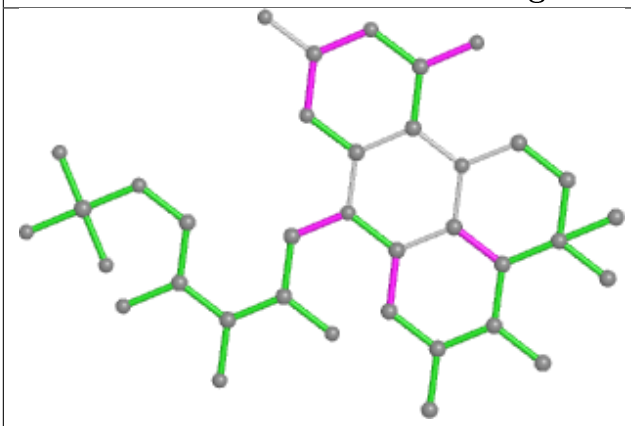
There are no ring outliers.

2 monomers are involved in 10 short contacts:

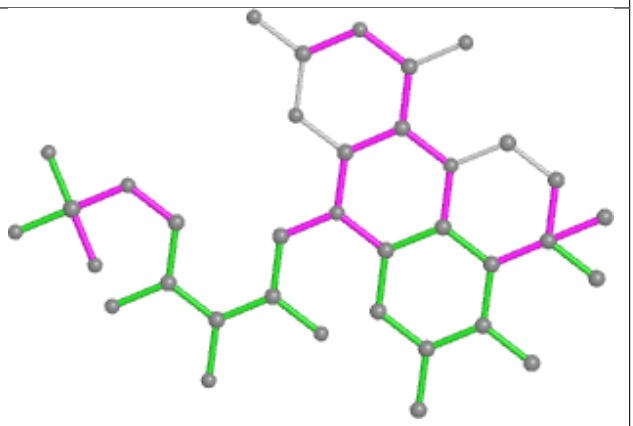
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	504	4LU	4	0
5	A	508	4LU	6	0

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 then 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.

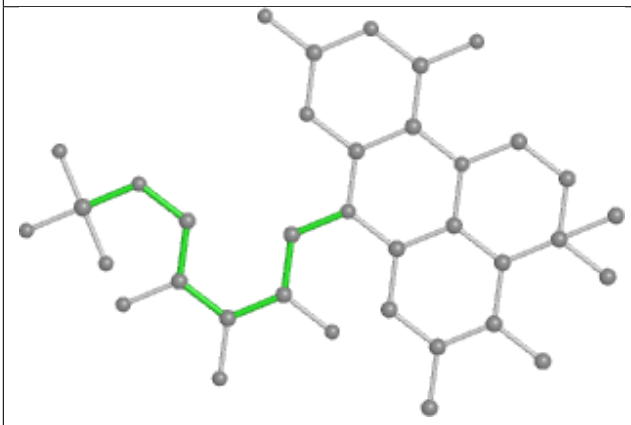
Ligand 4LU B 504



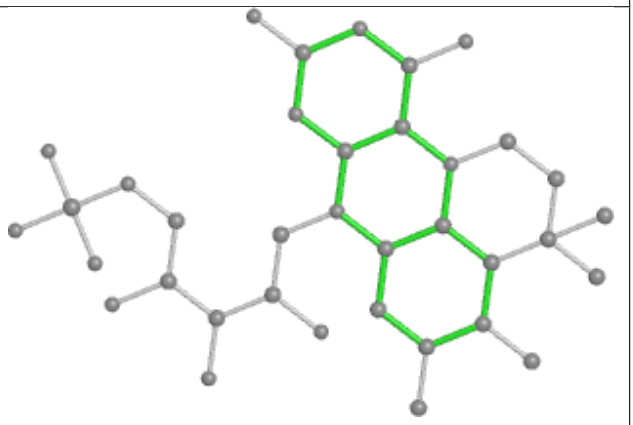
Bond lengths



Bond angles

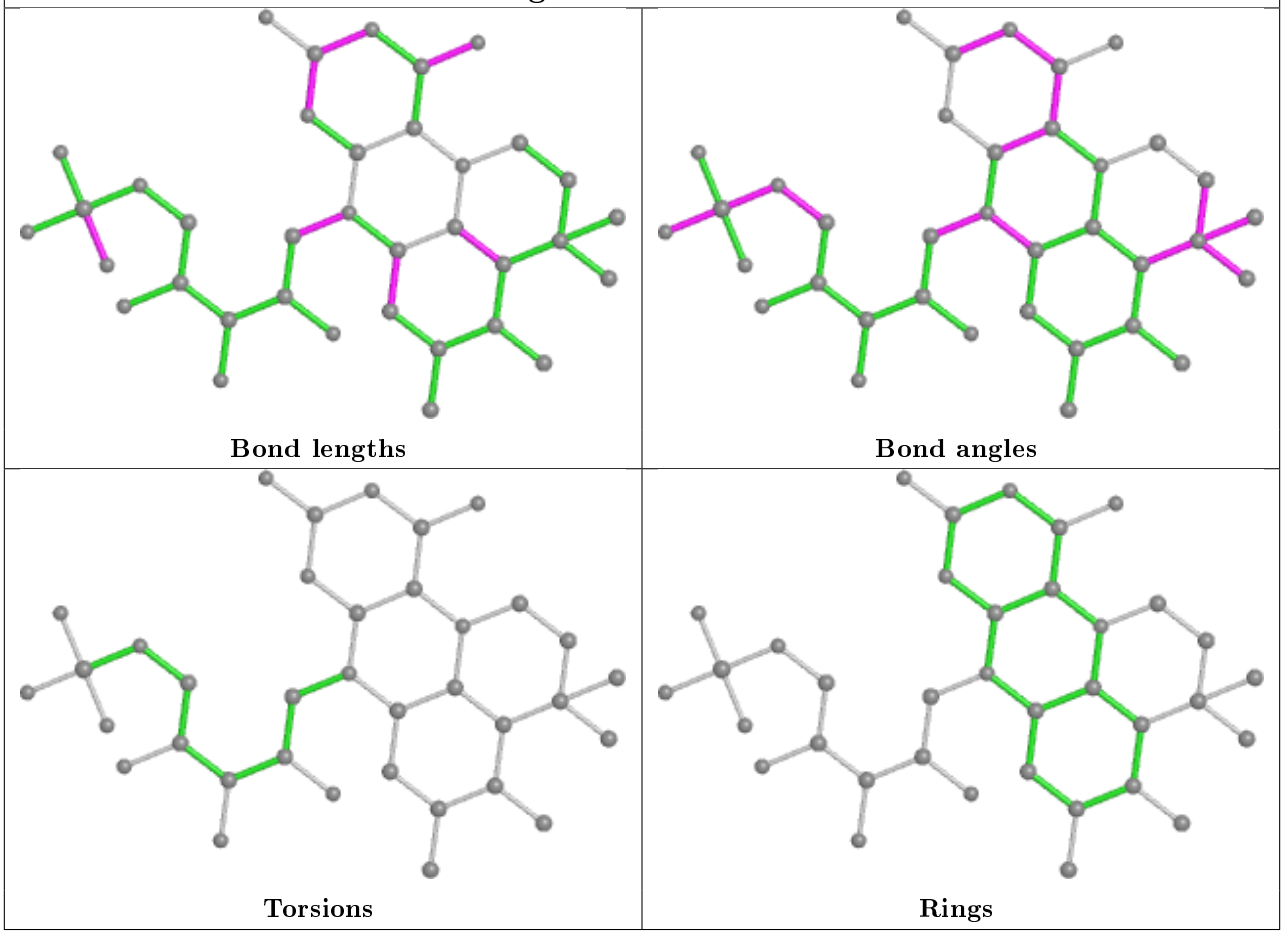


Torsions



Rings

Ligand 4LU A 508



5.7 Other polymers

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, 95^{th} 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	488/515 (94%)	0.24	37 (7%) 13 14	27, 54, 79, 108	0
1	B	488/515 (94%)	0.53	59 (12%) 4 4	28, 60, 98, 132	0
All	All	976/1030 (94%)	0.38	96 (9%) 7 8	27, 56, 94, 132	0

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	164	LEU	6.6
1	B	230	GLY	5.1
1	A	151	LEU	4.9
1	B	229	PHE	4.7
1	B	491	PHE	4.6
1	B	127	PRO	4.5
1	A	153	LEU	4.5
1	B	490	LEU	4.4
1	A	491	PHE	4.3
1	B	320	LEU	4.3
1	B	101	VAL	4.3
1	B	111	PRO	4.3
1	A	212	LEU	4.2
1	B	109	VAL	4.1
1	B	163	SER	4.1
1	A	490	LEU	4.0
1	B	239	ALA	3.9
1	A	127	PRO	3.9
1	A	169	ILE	3.8
1	B	169	ILE	3.7
1	B	160	GLU	3.7
1	B	151	LEU	3.7
1	A	154	VAL	3.7
1	B	488	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	153	LEU	3.4
1	B	235	GLY	3.4
1	B	202	LYS	3.3
1	B	161	ASP	3.3
1	B	199	ALA	3.3
1	A	320	LEU	3.2
1	A	217	TYR	3.1
1	B	19	PRO	3.1
1	B	102	LYS	3.0
1	B	110	VAL	3.0
1	B	124	ALA	3.0
1	A	208	ILE	2.9
1	A	19	PRO	2.9
1	B	106	ALA	2.9
1	A	330	LEU	2.9
1	B	212	LEU	2.9
1	A	319	THR	2.8
1	B	282	ASN	2.8
1	B	192	VAL	2.8
1	B	150	CYS	2.8
1	B	114	GLN	2.7
1	B	112	ALA	2.7
1	A	73	VAL	2.7
1	A	216	ILE	2.7
1	B	319	THR	2.7
1	B	149	PHE	2.7
1	A	488	PRO	2.7
1	B	487	ALA	2.7
1	A	152	GLY	2.6
1	B	121	VAL	2.6
1	A	489	GLU	2.6
1	A	318	GLN	2.6
1	B	210	MET	2.5
1	A	124	ALA	2.5
1	B	104	PRO	2.5
1	A	128	ASP	2.5
1	A	211	GLY	2.5
1	A	164	LEU	2.4
1	B	126	ASP	2.4
1	A	129	PHE	2.4
1	A	160	GLU	2.4
1	B	489	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	186	ALA	2.4
1	A	317	LEU	2.4
1	B	330	LEU	2.4
1	B	248	VAL	2.4
1	A	162	THR	2.4
1	A	161	ASP	2.4
1	B	159	PRO	2.3
1	B	217	TYR	2.3
1	A	202	LYS	2.3
1	B	232	ASN	2.3
1	A	480	GLU	2.3
1	B	125	ASP	2.2
1	A	299	PRO	2.2
1	B	299	PRO	2.2
1	B	99	GLN	2.2
1	B	172	LEU	2.2
1	B	108	VAL	2.2
1	A	210	MET	2.2
1	A	200	ALA	2.2
1	B	128	ASP	2.2
1	B	135	LEU	2.1
1	A	242	GLN	2.1
1	B	244	PRO	2.1
1	B	72	LEU	2.1
1	A	209	ASN	2.1
1	A	487	ALA	2.1
1	B	129	PHE	2.1
1	B	152	GLY	2.1
1	B	211	GLY	2.0
1	B	221	CYS	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 carbohydrates in this entry.

6.4 Ligands (i)

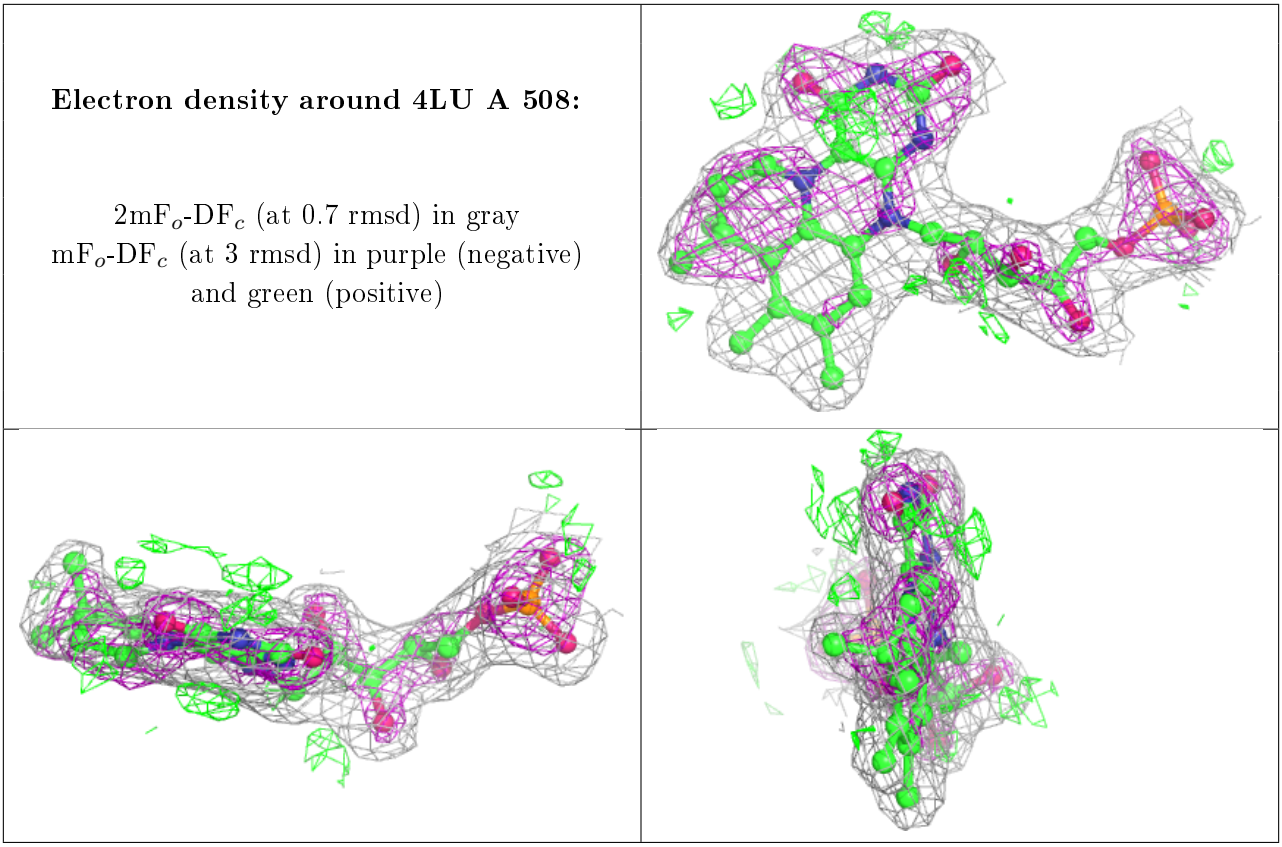
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	NA	B	502	1/1	0.50	0.10	66,66,66,66	0
4	GOL	A	507	6/6	0.75	0.24	67,70,72,73	0
4	GOL	A	503	6/6	0.87	0.21	58,61,62,62	0
4	GOL	B	503	6/6	0.87	0.20	51,61,65,76	0
4	GOL	A	506	6/6	0.89	0.26	54,61,65,69	0
4	GOL	A	505	6/6	0.90	0.18	62,71,74,77	0
2	MN	B	501	1/1	0.91	0.11	81,81,81,81	0
5	4LU	A	508	36/36	0.94	0.12	30,30,30,30	0
5	4LU	B	504	36/36	0.94	0.37	20,20,20,20	0
4	GOL	A	504	6/6	0.95	0.14	55,57,58,60	0
3	NA	A	502	1/1	0.96	0.13	46,46,46,46	0
2	MN	A	501	1/1	0.97	0.04	61,61,61,61	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.

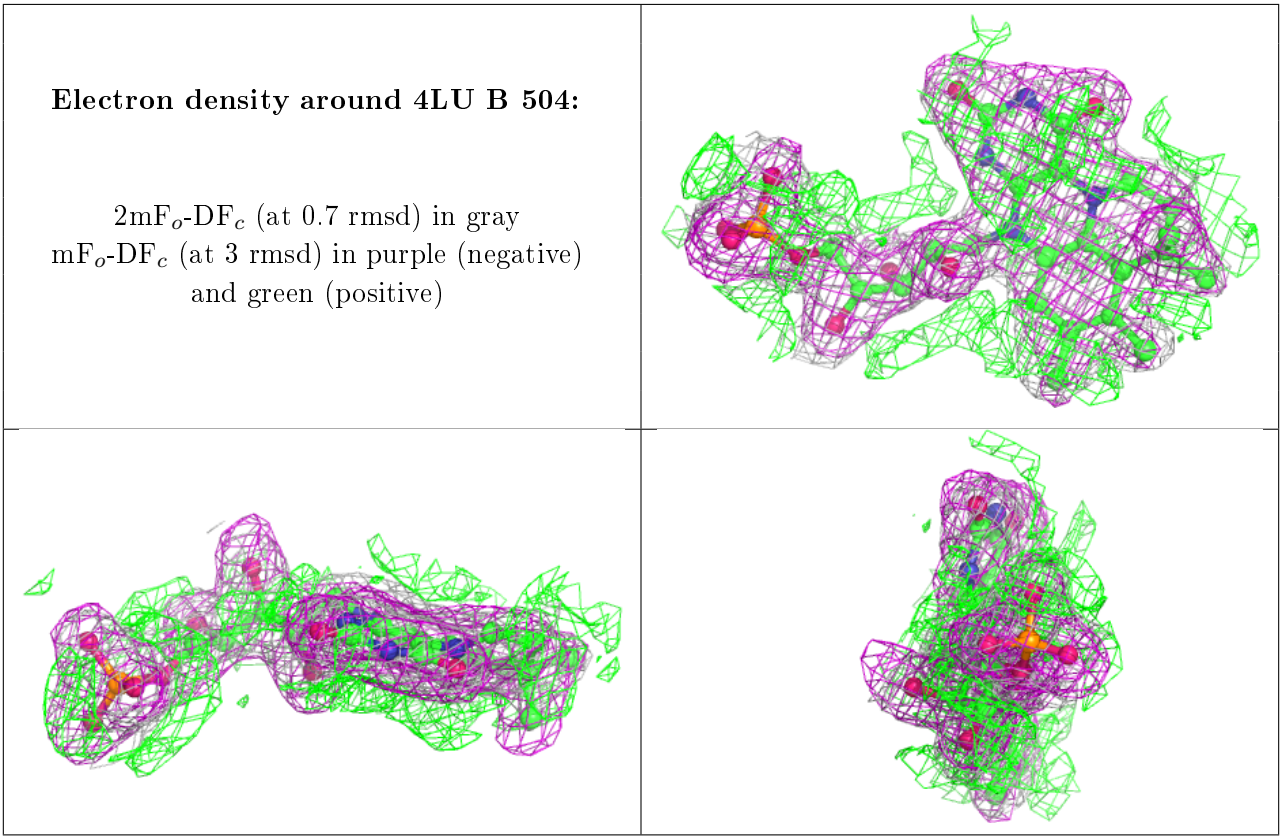
Electron density around 4LU A 508:

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



Electron density around 4LU B 504:

$2mF_o$-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.