



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 05:27 am BST

PDB ID : 6GIW
Title : Water-soluble Chlorophyll Protein (WSCP) from *Lepidium virginicum* (Mutation L91P) with Chlorophyll-a
Authors : Palm, D.M.; Agostini, A.; Aversch, V.; Girr, P.; Werwie, M.; Takahashi, S.; Satoh, H.; Jaenicke, E.; Paulsen, H.
Deposited on : 2018-05-15
Resolution : 2.80 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

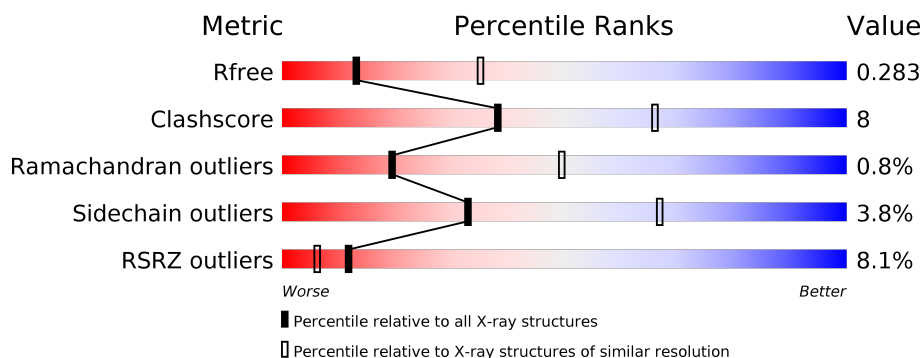
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	180	<div> <div>6%</div> <div> <div></div> <div>74%</div> <div>12%</div> <div>•</div> <div>13%</div> </div> </div>
1	B	180	<div> <div>8%</div> <div> <div></div> <div>70%</div> <div>16%</div> <div></div> <div>14%</div> </div> </div>
1	C	180	<div> <div>8%</div> <div> <div></div> <div>72%</div> <div>14%</div> <div>•</div> <div>13%</div> </div> </div>
1	D	180	<div> <div>6%</div> <div> <div></div> <div>72%</div> <div>17%</div> <div>••</div> <div>9%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CLA	A	1001	X	-	-	-
2	CLA	B	1001	X	-	-	-
2	CLA	C	1001	X	-	-	-
2	CLA	D	1001	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5147 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.

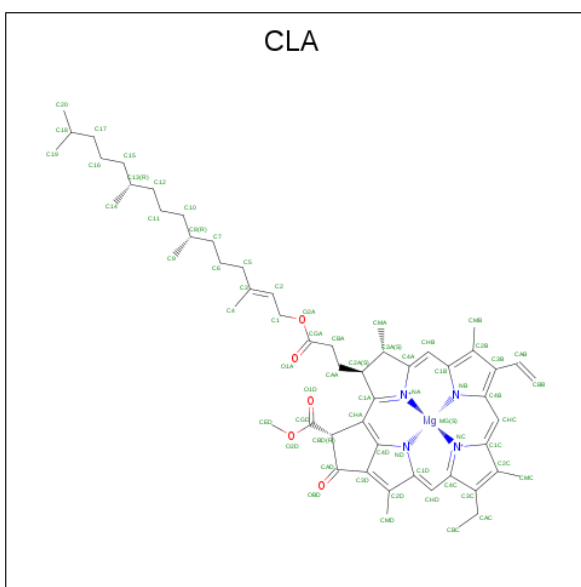
- Molecule 1 is a protein called Water-soluble chlorophyll protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	156	Total	C	N	O	S	0	0	0
			1200	770	198	230	2			
1	B	155	Total	C	N	O	S	0	0	0
			1186	760	194	230	2			
1	C	157	Total	C	N	O	S	0	0	0
			1208	774	200	232	2			
1	D	163	Total	C	N	O	S	0	0	0
			1255	798	206	249	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	91	PRO	LEU	engineered mutation	UNP O04797
B	91	PRO	LEU	engineered mutation	UNP O04797
C	91	PRO	LEU	engineered mutation	UNP O04797
D	91	PRO	LEU	engineered mutation	UNP O04797

- Molecule 2 is CHLOROPHYLL A (three-letter code: CLA) (formula: C₅₅H₇₂MgN₄O₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
2	B	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
2	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
2	D	1	Total 65	C 55	Mg 1	N 4	O 5	0	0

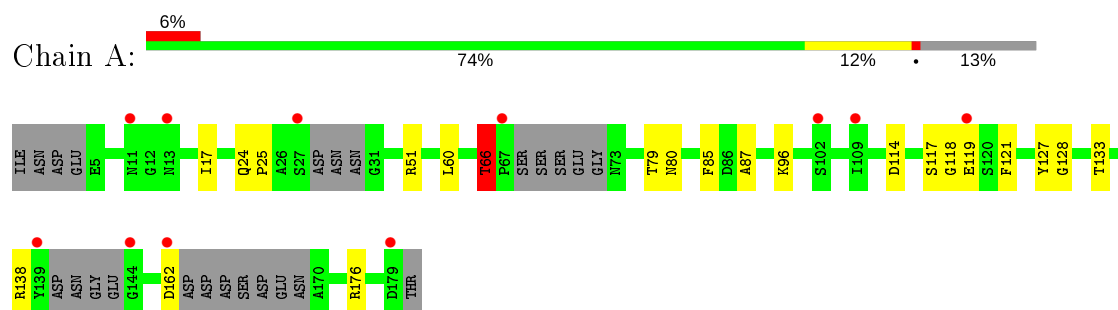
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	12	Total O 12 12	0	0
3	B	7	Total O 7 7	0	0
3	C	9	Total O 9 9	0	0
3	D	10	Total O 10 10	0	0

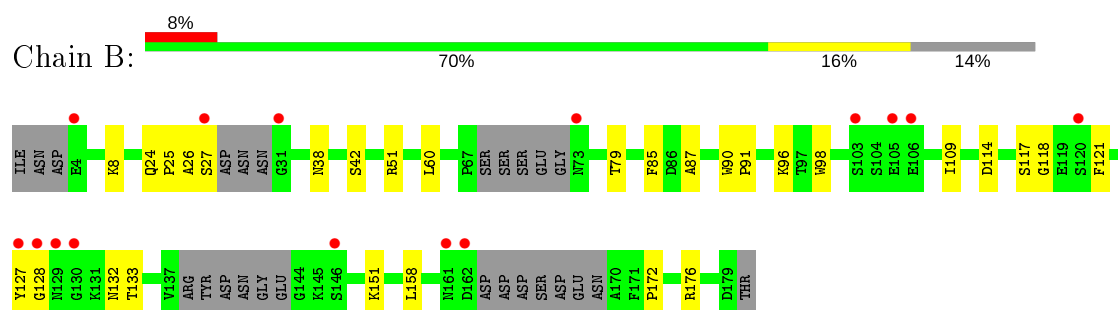
3 Residue-property plots [i](#)

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.

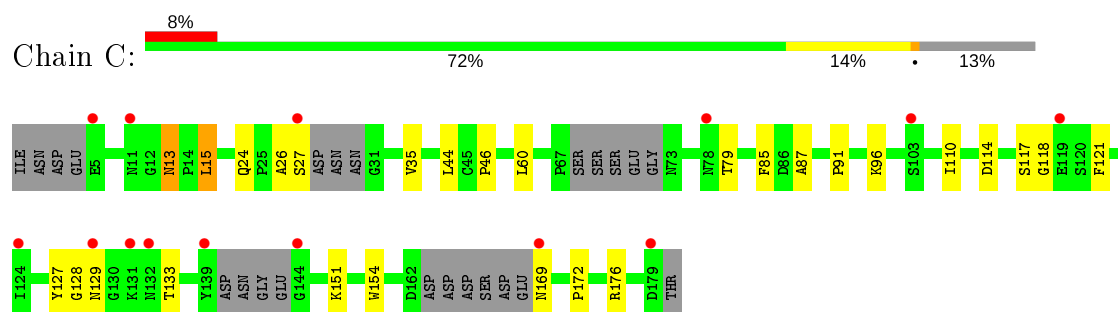
• Molecule 1: Water-soluble chlorophyll protein



• Molecule 1: Water-soluble chlorophyll protein

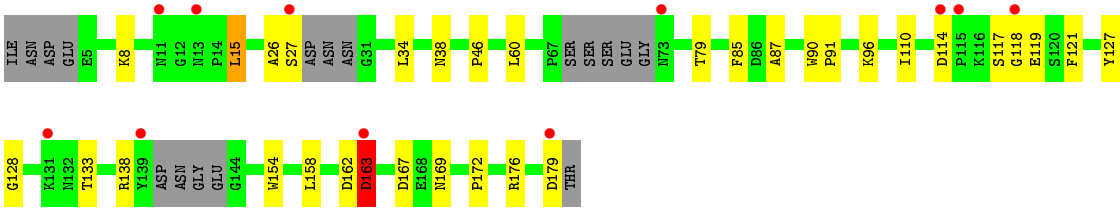


• Molecule 1: Water-soluble chlorophyll protein



• Molecule 1: Water-soluble chlorophyll protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.72Å 81.71Å 121.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.73 – 2.80 19.73 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.1 (19.73-2.80) 99.5 (19.73-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.234 , 0.277 0.243 , 0.283	Depositor DCC
R_{free} test set	917 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	5147	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% 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: CLA

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	0.49	0/1229	0.72	1/1672 (0.1%)
1	B	0.48	0/1214	0.67	0/1652
1	C	0.48	0/1237	0.72	1/1683 (0.1%)
1	D	0.50	0/1285	0.74	1/1750 (0.1%)
All	All	0.49	0/4965	0.71	3/6757 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	15	LEU	CA-CB-CG	6.35	129.91	115.30
1	C	15	LEU	CA-CB-CG	6.08	129.27	115.30
1	A	66	THR	CA-CB-CG2	5.48	120.08	112.40

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	1200	0	1190	10	0
1	B	1186	0	1174	25	0
1	C	1208	0	1196	15	0
1	D	1255	0	1224	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	65	0	72	9	0
2	B	65	0	72	8	0
2	C	65	0	72	7	0
2	D	65	0	72	6	0
3	A	12	0	0	0	0
3	B	7	0	0	0	0
3	C	9	0	0	0	0
3	D	10	0	0	0	0
All	All	5147	0	5072	77	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 8.

All (77) 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:109:ILE:CG2	1:B:158:LEU:HB2	1.95	0.96
2:B:1001:CLA:HBB1	2:B:1001:CLA:HMB1	1.52	0.89
2:C:1001:CLA:H202	2:C:1001:CLA:H143	1.61	0.82
1:B:109:ILE:CG2	1:B:158:LEU:CB	2.65	0.73
1:B:109:ILE:HG21	1:B:158:LEU:HB2	1.72	0.71
1:A:80:ASN:HD22	1:A:121:PHE:HB3	1.56	0.71
2:B:1001:CLA:H202	2:B:1001:CLA:H141	1.72	0.69
1:B:109:ILE:HG21	1:B:158:LEU:CB	2.24	0.68
1:B:109:ILE:HG22	1:B:158:LEU:HB2	1.74	0.68
1:C:154:TRP:HH2	2:C:1001:CLA:H101	1.64	0.63
2:C:1001:CLA:H193	2:D:1001:CLA:H72	1.81	0.63
1:B:8:LYS:HB2	1:B:132:ASN:HD22	1.64	0.63
1:D:119:GLU:HA	1:D:138:ARG:HH22	1.66	0.60
1:A:119:GLU:HA	1:A:138:ARG:HH22	1.66	0.60
2:A:1001:CLA:HBB1	2:A:1001:CLA:HMB1	1.83	0.60
1:A:17:ILE:HG21	1:A:66:THR:HG22	1.87	0.56
1:B:109:ILE:HG22	1:B:158:LEU:CB	2.32	0.56
1:B:98:TRP:CE3	1:B:109:ILE:HD11	2.42	0.55
2:A:1001:CLA:H141	2:C:1001:CLA:HMB1	1.88	0.55
2:A:1001:CLA:H111	1:C:44:LEU:HD21	1.89	0.55
1:B:8:LYS:HB2	1:B:132:ASN:ND2	2.23	0.54
1:C:13:ASN:HD22	1:C:13:ASN:N	2.05	0.54
2:D:1001:CLA:HMB1	2:D:1001:CLA:HBB1	1.90	0.53
1:D:127:TYR:CE2	1:D:167:ASP:HB3	2.42	0.53
2:A:1001:CLA:H61	2:B:1001:CLA:C19	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:SER:O	1:C:91:PRO:HA	2.10	0.51
1:B:98:TRP:CE3	1:B:109:ILE:CD1	2.93	0.51
1:B:109:ILE:HG22	1:B:158:LEU:O	2.10	0.51
2:A:1001:CLA:H93	2:B:1001:CLA:H193	1.91	0.50
1:D:38:ASN:OD1	2:D:1001:CLA:HMB2	2.12	0.50
2:C:1001:CLA:H191	2:D:1001:CLA:H41	1.94	0.50
1:B:98:TRP:HE3	1:B:109:ILE:HD11	1.76	0.50
1:A:118:GLY:HA2	1:A:121:PHE:CD2	2.48	0.49
2:A:1001:CLA:H91	1:C:44:LEU:HD11	1.94	0.49
1:B:98:TRP:HB3	1:B:109:ILE:HD11	1.95	0.48
1:B:118:GLY:HA2	1:B:121:PHE:CD2	2.48	0.48
1:C:118:GLY:HA2	1:C:121:PHE:CD2	2.47	0.48
1:D:118:GLY:HA2	1:D:121:PHE:CD2	2.48	0.48
1:C:114:ASP:HB3	1:C:117:SER:HB3	1.96	0.48
1:D:60:LEU:HD21	1:D:87:ALA:HB2	1.96	0.48
1:A:114:ASP:HB3	1:A:117:SER:HB3	1.96	0.47
1:D:114:ASP:HB3	1:D:117:SER:HB3	1.96	0.47
2:A:1001:CLA:H112	2:B:1001:CLA:H193	1.95	0.47
1:C:85:PHE:HB2	1:C:96:LYS:HB3	1.97	0.47
1:B:114:ASP:HB3	1:B:117:SER:HB3	1.97	0.46
1:C:35:VAL:HG11	2:C:1001:CLA:CAD	2.46	0.46
1:A:85:PHE:HB2	1:A:96:LYS:HB3	1.98	0.45
1:B:109:ILE:HG21	1:B:158:LEU:HB3	1.98	0.45
1:B:85:PHE:HB2	1:B:96:LYS:HB3	1.98	0.45
1:D:85:PHE:HB2	1:D:96:LYS:HB3	1.97	0.45
1:A:25:PRO:HG2	1:A:51:ARG:HG3	1.99	0.44
2:A:1001:CLA:H61	2:B:1001:CLA:H191	1.98	0.44
1:B:25:PRO:HG2	1:B:51:ARG:HG3	2.00	0.43
1:C:24:GLN:HE22	1:C:176:ARG:HD2	1.84	0.43
1:D:127:TYR:HB3	1:D:133:THR:HG22	2.00	0.43
1:A:127:TYR:HB3	1:A:133:THR:HG22	2.01	0.43
1:A:24:GLN:HE22	1:A:176:ARG:HD2	1.84	0.43
1:C:127:TYR:HB3	1:C:133:THR:HG22	2.01	0.43
1:B:60:LEU:HD21	1:B:87:ALA:HB2	2.00	0.42
1:D:154:TRP:HH2	2:D:1001:CLA:H111	1.83	0.42
1:C:46:PRO:HG2	1:C:110:ILE:HD12	2.01	0.42
1:D:162:ASP:O	1:D:163:ASP:O	2.38	0.42
1:B:24:GLN:HE22	1:B:176:ARG:HD2	1.84	0.42
1:B:26:ALA:HB3	1:B:172:PRO:HB2	2.01	0.42
1:C:26:ALA:HB3	1:C:172:PRO:HB2	2.01	0.42
1:D:26:ALA:HB3	1:D:172:PRO:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:LEU:HD21	1:A:87:ALA:HB2	2.02	0.41
1:B:127:TYR:HB3	1:B:133:THR:HG22	2.01	0.41
2:D:1001:CLA:HMB1	2:D:1001:CLA:CBB	2.51	0.41
1:C:60:LEU:HD21	1:C:87:ALA:HB2	2.03	0.41
1:D:46:PRO:HG2	1:D:110:ILE:HD12	2.01	0.41
1:C:154:TRP:CH2	2:C:1001:CLA:H101	2.49	0.41
1:D:90:TRP:HA	1:D:91:PRO:HD3	1.96	0.41
1:B:38:ASN:OD1	2:B:1001:CLA:HMB2	2.21	0.41
2:A:1001:CLA:H93	2:B:1001:CLA:C19	2.50	0.40
1:D:34:LEU:HD13	1:D:158:LEU:HD11	2.04	0.40
1:B:90:TRP:HA	1:B:91:PRO:HD3	1.95	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	146/180 (81%)	144 (99%)	1 (1%)	1 (1%)	22	53
1	B	145/180 (81%)	142 (98%)	2 (1%)	1 (1%)	22	53
1	C	147/180 (82%)	144 (98%)	2 (1%)	1 (1%)	22	53
1	D	155/180 (86%)	151 (97%)	2 (1%)	2 (1%)	12	36
All	All	593/720 (82%)	581 (98%)	7 (1%)	5 (1%)	19	49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	128	GLY
1	D	163	ASP
1	A	128	GLY
1	B	128	GLY

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Mol	Chain	Res	Type
1	D	128	GLY

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	136/158 (86%)	133 (98%)	3 (2%)	52	83
1	B	135/158 (85%)	132 (98%)	3 (2%)	52	83
1	C	137/158 (87%)	130 (95%)	7 (5%)	24	55
1	D	143/158 (90%)	135 (94%)	8 (6%)	21	51
All	All	551/632 (87%)	530 (96%)	21 (4%)	33	67

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	THR
1	A	79	THR
1	A	162	ASP
1	B	27	SER
1	B	79	THR
1	B	151	LYS
1	C	13	ASN
1	C	15	LEU
1	C	27	SER
1	C	79	THR
1	C	129	ASN
1	C	151	LYS
1	C	169	ASN
1	D	8	LYS
1	D	15	LEU
1	D	27	SER
1	D	79	THR
1	D	163	ASP
1	D	169	ASN
1	D	176	ARG

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Mol	Chain	Res	Type
1	D	179	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS
1	A	80	ASN
1	B	43	HIS
1	B	73	ASN
1	B	132	ASN
1	C	11	ASN
1	C	13	ASN
1	C	43	HIS
1	D	43	HIS
1	D	73	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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
2	CLA	C	1001	1	59,73,73	1.65	10 (16%)	67,113,113	1.97	17 (25%)
2	CLA	D	1001	1	59,73,73	1.56	10 (16%)	67,113,113	1.64	15 (22%)
2	CLA	A	1001	1	59,73,73	1.57	10 (16%)	67,113,113	1.71	14 (20%)
2	CLA	B	1001	1	59,73,73	1.65	10 (16%)	67,113,113	1.65	18 (26%)

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	CLA	C	1001	1	2/2/20/25	19/37/135/135	-
2	CLA	D	1001	1	2/2/20/25	9/37/135/135	-
2	CLA	A	1001	1	2/2/20/25	12/37/135/135	-
2	CLA	B	1001	1	2/2/20/25	18/37/135/135	-

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1001	CLA	O2D-CGD	5.55	1.46	1.33
2	C	1001	CLA	CHC-C1C	5.42	1.48	1.35
2	D	1001	CLA	O2D-CGD	5.24	1.46	1.33
2	B	1001	CLA	O2D-CGD	4.95	1.45	1.33
2	D	1001	CLA	CHC-C1C	4.90	1.47	1.35
2	B	1001	CLA	CHC-C1C	4.90	1.47	1.35
2	A	1001	CLA	CHC-C1C	4.86	1.47	1.35
2	A	1001	CLA	O2D-CGD	4.77	1.44	1.33
2	B	1001	CLA	OBD-CAD	4.71	1.28	1.22
2	B	1001	CLA	O2A-CGA	4.56	1.46	1.33
2	A	1001	CLA	OBD-CAD	4.52	1.28	1.22
2	A	1001	CLA	O2A-CGA	4.45	1.46	1.33
2	C	1001	CLA	O2A-CGA	4.41	1.46	1.33
2	D	1001	CLA	OBD-CAD	4.23	1.28	1.22
2	C	1001	CLA	OBD-CAD	4.21	1.28	1.22
2	B	1001	CLA	C4C-C3C	-3.70	1.38	1.45
2	D	1001	CLA	O2A-CGA	3.65	1.44	1.33
2	B	1001	CLA	C1C-NC	-3.24	1.33	1.37
2	C	1001	CLA	C4C-C3C	-3.22	1.39	1.45
2	D	1001	CLA	C4C-C3C	-3.07	1.39	1.45
2	C	1001	CLA	C1C-NC	-2.92	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	CLA	C1C-NC	-2.86	1.33	1.37
2	A	1001	CLA	CHD-C4C	2.85	1.49	1.41
2	D	1001	CLA	C1C-C2C	-2.72	1.39	1.44
2	D	1001	CLA	C4B-CHC	2.64	1.48	1.41
2	B	1001	CLA	CHD-C4C	2.61	1.48	1.41
2	C	1001	CLA	C4B-CHC	2.58	1.48	1.41
2	A	1001	CLA	C4C-C3C	-2.56	1.40	1.45
2	D	1001	CLA	C1C-NC	-2.56	1.34	1.37
2	D	1001	CLA	CHD-C4C	2.49	1.48	1.41
2	A	1001	CLA	C1B-CHB	2.48	1.47	1.41
2	B	1001	CLA	C1C-C2C	-2.46	1.39	1.44
2	A	1001	CLA	C1C-C2C	-2.46	1.39	1.44
2	D	1001	CLA	C1B-CHB	2.41	1.47	1.41
2	C	1001	CLA	C1C-C2C	-2.38	1.40	1.44
2	C	1001	CLA	CHD-C4C	2.36	1.47	1.41
2	A	1001	CLA	C4B-CHC	2.27	1.47	1.41
2	B	1001	CLA	C4B-CHC	2.22	1.47	1.41
2	B	1001	CLA	C1B-CHB	2.18	1.47	1.41
2	C	1001	CLA	C1B-CHB	2.03	1.46	1.41

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1001	CLA	O2D-CGD-CBD	5.87	121.70	111.27
2	A	1001	CLA	C2C-C1C-NC	5.76	115.37	109.97
2	D	1001	CLA	O2D-CGD-CBD	5.54	121.11	111.27
2	D	1001	CLA	C2C-C1C-NC	4.76	114.43	109.97
2	B	1001	CLA	O2D-CGD-CBD	4.57	119.39	111.27
2	B	1001	CLA	C2C-C1C-NC	4.56	114.25	109.97
2	A	1001	CLA	O2D-CGD-CBD	4.47	119.21	111.27
2	C	1001	CLA	C2C-C1C-NC	4.24	113.94	109.97
2	A	1001	CLA	CAC-C3C-C4C	4.11	130.14	124.81
2	C	1001	CLA	C4-C3-C2	-4.05	113.28	123.68
2	C	1001	CLA	C1-O2A-CGA	3.85	126.55	116.44
2	B	1001	CLA	C3C-C4C-NC	3.83	114.87	110.57
2	C	1001	CLA	CAC-C3C-C4C	3.73	129.66	124.81
2	C	1001	CLA	C3C-C4C-NC	3.71	114.73	110.57
2	C	1001	CLA	C4-C3-C5	3.56	121.26	115.27
2	C	1001	CLA	O2A-CGA-CBA	3.43	122.67	111.91
2	A	1001	CLA	C3B-C4B-NB	3.39	113.60	109.21
2	D	1001	CLA	C3C-C4C-NC	3.24	114.20	110.57
2	A	1001	CLA	C3C-C4C-NC	3.16	114.12	110.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1001	CLA	O1D-CGD-CBD	-3.16	118.03	124.48
2	C	1001	CLA	CMB-C2B-C3B	3.14	130.56	124.68
2	B	1001	CLA	C11-C10-C8	-3.04	106.08	115.92
2	A	1001	CLA	CMB-C2B-C3B	3.04	130.36	124.68
2	B	1001	CLA	CED-O2D-CGD	3.03	122.79	115.94
2	C	1001	CLA	O1D-CGD-CBD	-3.02	118.31	124.48
2	A	1001	CLA	CMC-C2C-C1C	2.99	129.59	125.04
2	B	1001	CLA	C3B-C4B-NB	2.97	113.05	109.21
2	B	1001	CLA	C1-O2A-CGA	2.95	124.19	116.44
2	D	1001	CLA	CAC-C3C-C4C	2.87	128.53	124.81
2	B	1001	CLA	CMB-C2B-C3B	2.86	130.04	124.68
2	C	1001	CLA	O2A-CGA-O1A	-2.75	116.66	123.59
2	D	1001	CLA	C6-C7-C8	-2.68	107.26	115.92
2	C	1001	CLA	C1B-CHB-C4A	-2.66	124.84	130.12
2	D	1001	CLA	C3B-C4B-NB	2.60	112.57	109.21
2	C	1001	CLA	C3B-C4B-NB	2.57	112.54	109.21
2	D	1001	CLA	CMB-C2B-C3B	2.51	129.38	124.68
2	C	1001	CLA	CHB-C4A-NA	2.41	127.84	124.51
2	B	1001	CLA	O1D-CGD-CBD	-2.40	119.58	124.48
2	D	1001	CLA	C4A-NA-C1A	-2.39	105.63	106.71
2	B	1001	CLA	C6-C7-C8	-2.39	108.21	115.92
2	A	1001	CLA	C1-O2A-CGA	2.37	122.67	116.44
2	A	1001	CLA	CED-O2D-CGD	2.37	121.30	115.94
2	B	1001	CLA	CHD-C4C-C3C	-2.35	121.39	124.84
2	A	1001	CLA	C1D-CHD-C4C	2.33	125.63	122.56
2	A	1001	CLA	CHC-C1C-NC	-2.31	120.70	124.20
2	B	1001	CLA	C6-C5-C3	-2.30	107.42	113.45
2	B	1001	CLA	CHB-C4A-NA	2.28	127.66	124.51
2	D	1001	CLA	O2A-CGA-CBA	2.26	119.01	111.91
2	B	1001	CLA	CAC-C3C-C4C	2.26	127.74	124.81
2	C	1001	CLA	C4C-C3C-C2C	-2.22	103.66	106.90
2	A	1001	CLA	C1C-C2C-C3C	-2.22	104.62	106.96
2	B	1001	CLA	O2A-CGA-CBA	2.20	118.80	111.91
2	B	1001	CLA	CHC-C1C-NC	-2.18	120.89	124.20
2	A	1001	CLA	CMD-C2D-C3D	-2.18	120.60	124.68
2	D	1001	CLA	C1B-CHB-C4A	-2.17	125.82	130.12
2	C	1001	CLA	C5-C3-C2	2.15	125.46	121.12
2	B	1001	CLA	C4C-C3C-C2C	-2.14	103.78	106.90
2	A	1001	CLA	C4-C3-C5	2.08	118.77	115.27
2	D	1001	CLA	C11-C10-C8	-2.06	109.26	115.92
2	C	1001	CLA	C7-C6-C5	-2.05	107.78	113.36
2	B	1001	CLA	CMC-C2C-C1C	2.04	128.14	125.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1001	CLA	CHB-C4A-NA	2.03	127.32	124.51
2	D	1001	CLA	C4C-C3C-C2C	-2.02	103.96	106.90
2	D	1001	CLA	CHC-C1C-NC	-2.00	121.17	124.20

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	1001	CLA	NC
2	C	1001	CLA	NA
2	D	1001	CLA	NC
2	D	1001	CLA	NA
2	A	1001	CLA	NC
2	A	1001	CLA	NA
2	B	1001	CLA	NC
2	B	1001	CLA	NA

All (58) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1001	CLA	CBA-CGA-O2A-C1
2	C	1001	CLA	O1A-CGA-O2A-C1
2	D	1001	CLA	O1D-CGD-O2D-CED
2	D	1001	CLA	CBD-CGD-O2D-CED
2	B	1001	CLA	CBD-CGD-O2D-CED
2	D	1001	CLA	C3-C5-C6-C7
2	C	1001	CLA	CBD-CGD-O2D-CED
2	A	1001	CLA	CBD-CGD-O2D-CED
2	B	1001	CLA	O1D-CGD-O2D-CED
2	C	1001	CLA	C6-C7-C8-C9
2	C	1001	CLA	C14-C13-C15-C16
2	A	1001	CLA	C11-C10-C8-C9
2	A	1001	CLA	C5-C6-C7-C8
2	C	1001	CLA	C8-C10-C11-C12
2	C	1001	CLA	C15-C16-C17-C18
2	B	1001	CLA	C13-C15-C16-C17
2	C	1001	CLA	C6-C7-C8-C10
2	C	1001	CLA	C3-C5-C6-C7
2	B	1001	CLA	C15-C16-C17-C18
2	C	1001	CLA	C16-C17-C18-C19
2	C	1001	CLA	O1D-CGD-O2D-CED
2	C	1001	CLA	C13-C15-C16-C17
2	B	1001	CLA	C5-C6-C7-C8

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Mol	Chain	Res	Type	Atoms
2	A	1001	CLA	O1D-CGD-O2D-CED
2	C	1001	CLA	C10-C11-C12-C13
2	C	1001	CLA	C16-C17-C18-C20
2	C	1001	CLA	C11-C12-C13-C15
2	B	1001	CLA	C6-C7-C8-C10
2	B	1001	CLA	C11-C10-C8-C7
2	B	1001	CLA	C6-C7-C8-C9
2	B	1001	CLA	C11-C10-C8-C9
2	D	1001	CLA	C8-C10-C11-C12
2	C	1001	CLA	C12-C13-C15-C16
2	D	1001	CLA	C6-C7-C8-C10
2	A	1001	CLA	C11-C10-C8-C7
2	B	1001	CLA	C12-C13-C15-C16
2	C	1001	CLA	C11-C12-C13-C14
2	B	1001	CLA	C16-C17-C18-C19
2	D	1001	CLA	C6-C7-C8-C9
2	B	1001	CLA	C14-C13-C15-C16
2	A	1001	CLA	C3-C5-C6-C7
2	B	1001	CLA	C16-C17-C18-C20
2	A	1001	CLA	C10-C11-C12-C13
2	B	1001	CLA	C4-C3-C5-C6
2	C	1001	CLA	C2A-CAA-CBA-CGA
2	A	1001	CLA	CAA-CBA-CGA-O2A
2	A	1001	CLA	C15-C16-C17-C18
2	B	1001	CLA	C2-C3-C5-C6
2	D	1001	CLA	CAA-CBA-CGA-O2A
2	B	1001	CLA	CAA-CBA-CGA-O2A
2	A	1001	CLA	CAA-CBA-CGA-O1A
2	D	1001	CLA	CAA-CBA-CGA-O1A
2	C	1001	CLA	CAD-CBD-CGD-O1D
2	D	1001	CLA	CAD-CBD-CGD-O1D
2	A	1001	CLA	CAD-CBD-CGD-O1D
2	B	1001	CLA	CAD-CBD-CGD-O1D
2	B	1001	CLA	CAA-CBA-CGA-O1A
2	A	1001	CLA	C16-C17-C18-C20

There are no ring outliers.

4 monomers are involved in 22 short contacts:

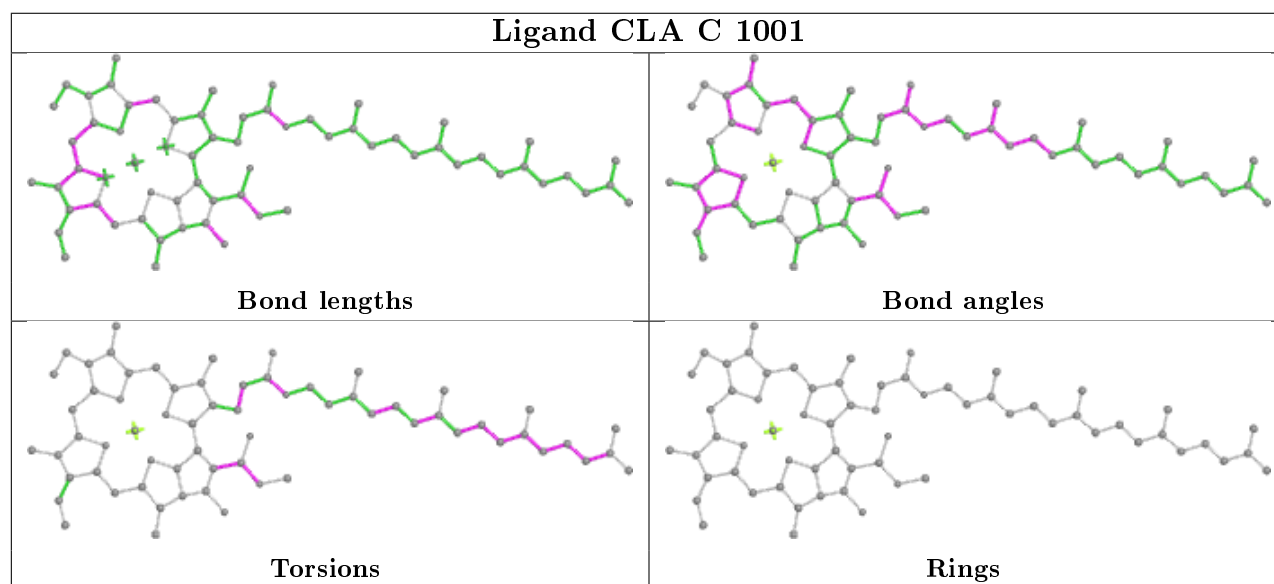
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1001	CLA	7	0
2	D	1001	CLA	6	0

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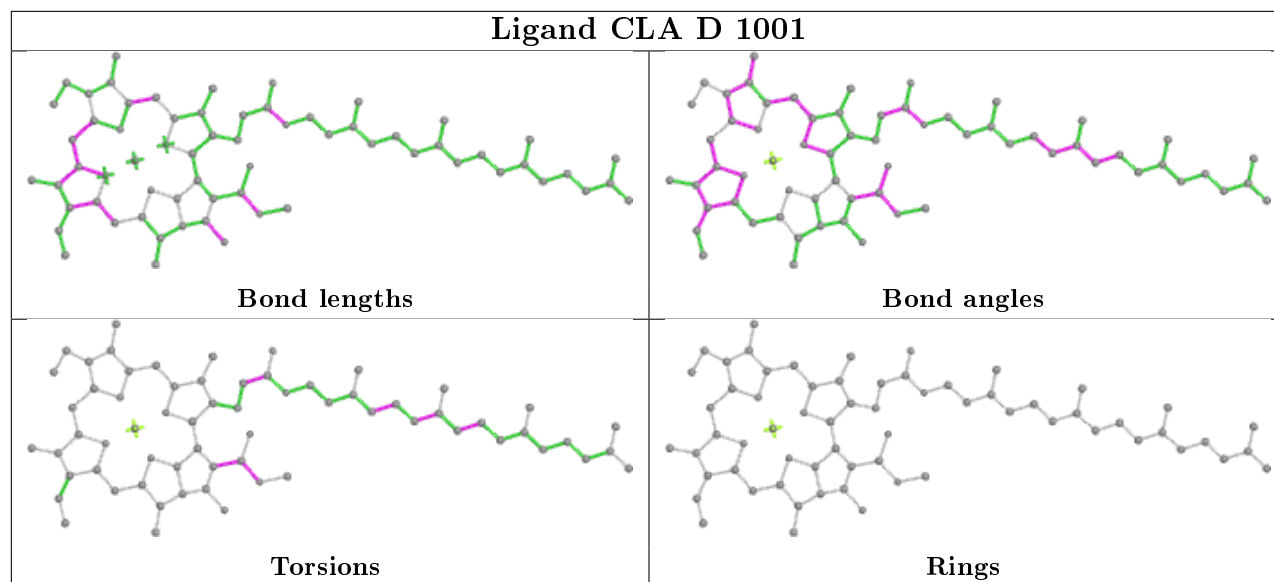
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	CLA	9	0
2	B	1001	CLA	8	0

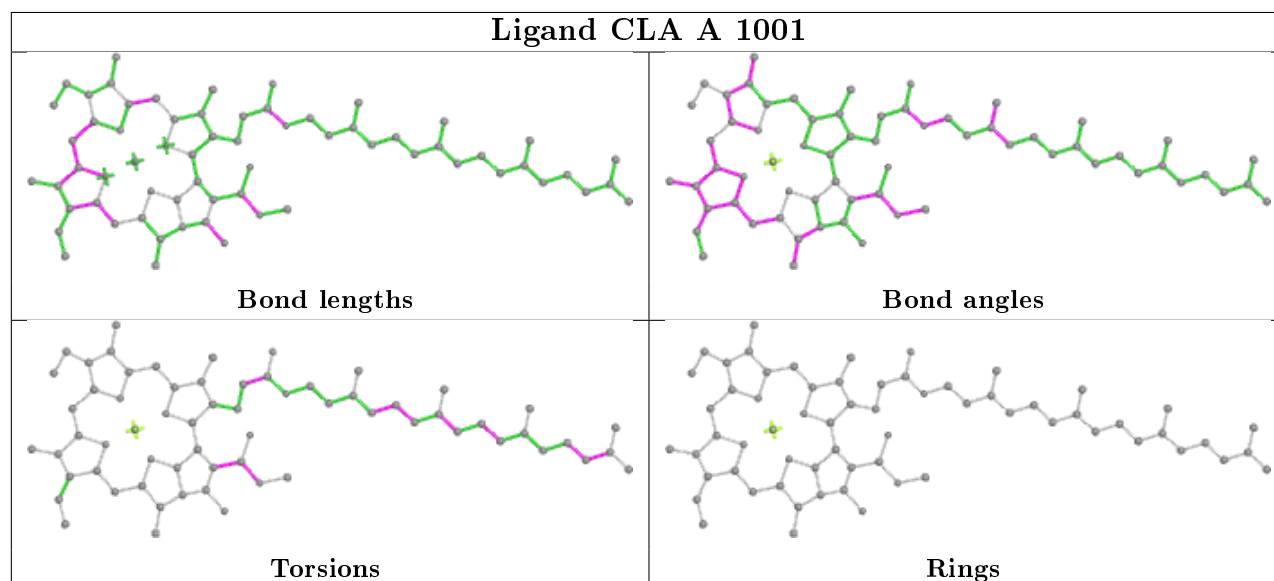
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



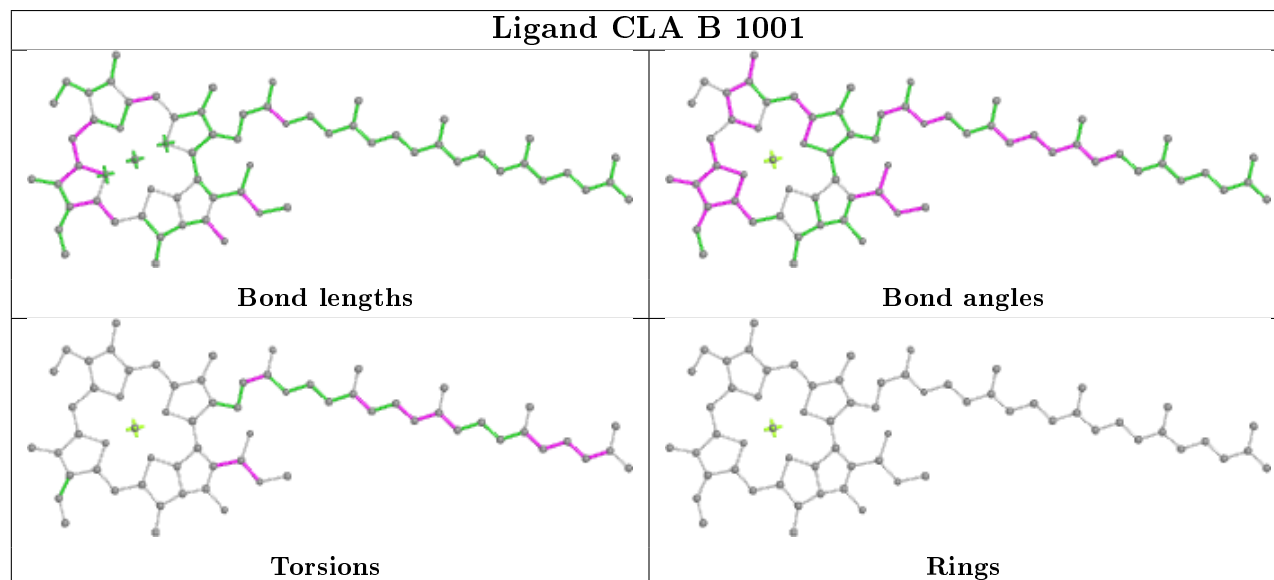
Ligand CLA D 1001



Ligand CLA A 1001



Ligand CLA B 1001



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, 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	156/180 (86%)	0.40	11 (7%) 16 9	25, 38, 68, 83	0
1	B	155/180 (86%)	0.58	15 (9%) 7 4	25, 45, 90, 104	0
1	C	157/180 (87%)	0.39	14 (8%) 9 5	24, 40, 71, 95	0
1	D	163/180 (90%)	0.37	11 (6%) 17 10	22, 42, 72, 91	0
All	All	631/720 (87%)	0.43	51 (8%) 12 6	22, 41, 75, 104	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	129	ASN	6.3
1	B	105	GLU	4.5
1	C	144	GLY	4.4
1	C	169	ASN	4.3
1	A	144	GLY	4.1
1	D	179	ASP	3.9
1	B	146	SER	3.7
1	D	27	SER	3.7
1	B	103	SER	3.7
1	C	179	ASP	3.6
1	D	73	ASN	3.6
1	A	139	TYR	3.3
1	C	27	SER	3.2
1	B	128	GLY	3.1
1	B	27	SER	3.0
1	A	179	ASP	3.0
1	B	4	GLU	3.0
1	D	131	LYS	2.8
1	C	132	ASN	2.7
1	D	115	PRO	2.7
1	C	11	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	129	ASN	2.7
1	D	118	GLY	2.7
1	C	78	ASN	2.6
1	A	11	ASN	2.6
1	D	114	ASP	2.6
1	A	27	SER	2.5
1	C	139	TYR	2.5
1	A	119	GLU	2.5
1	B	161	ASN	2.5
1	D	11	ASN	2.5
1	B	130	GLY	2.5
1	A	102	SER	2.5
1	A	67	PRO	2.4
1	C	103	SER	2.4
1	B	31	GLY	2.3
1	B	120	SER	2.3
1	A	162	ASP	2.3
1	B	162	ASP	2.2
1	D	13	ASN	2.2
1	D	163	ASP	2.2
1	B	127	TYR	2.2
1	A	13	ASN	2.2
1	C	119	GLU	2.2
1	C	124	ILE	2.1
1	D	139	TYR	2.1
1	A	109	ILE	2.1
1	B	106	GLU	2.1
1	C	5	GLU	2.1
1	C	131	LYS	2.0
1	B	73	ASN	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 ⓘ

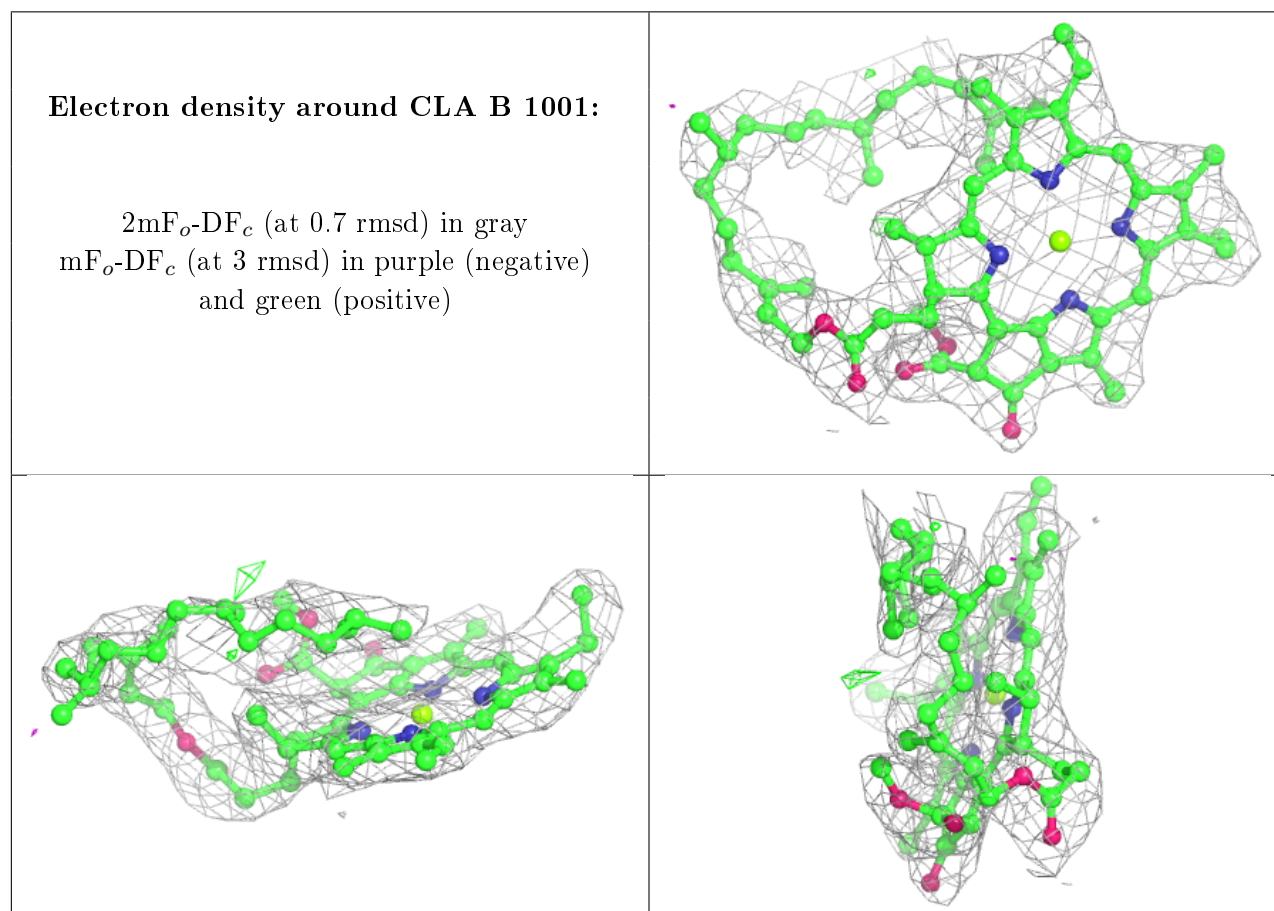
There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

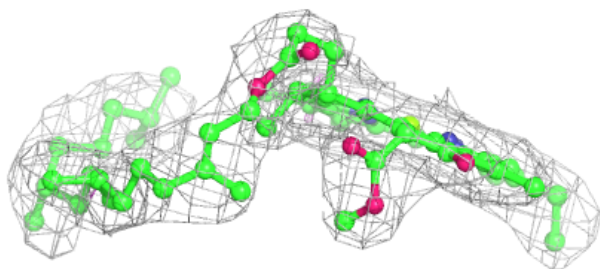
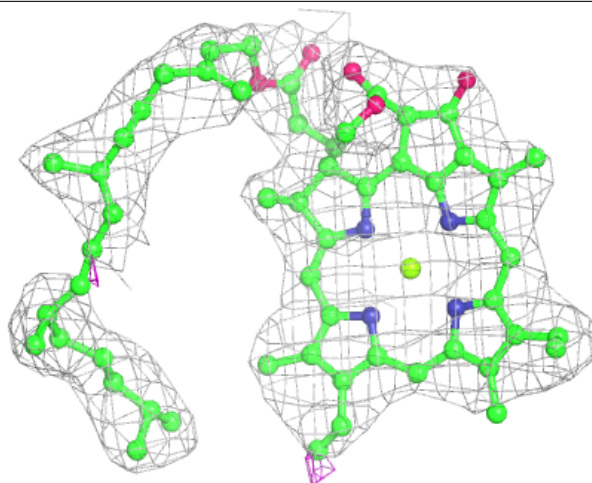
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CLA	B	1001	65/65	0.92	0.23	24,28,74,77	0
2	CLA	D	1001	65/65	0.94	0.18	17,18,49,52	0
2	CLA	A	1001	65/65	0.94	0.22	25,29,66,67	0
2	CLA	C	1001	65/65	0.94	0.21	20,24,67,73	0

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.



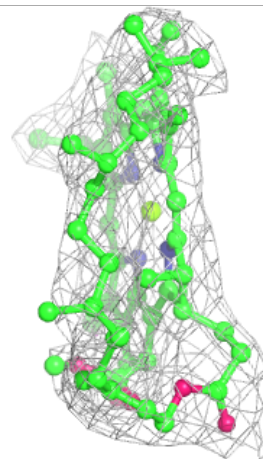
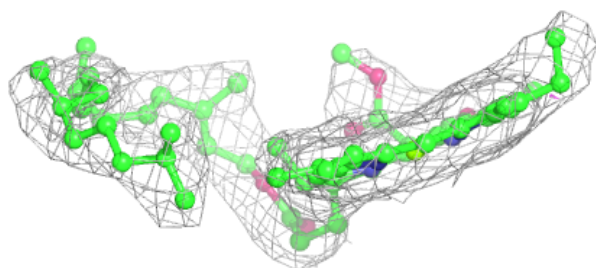
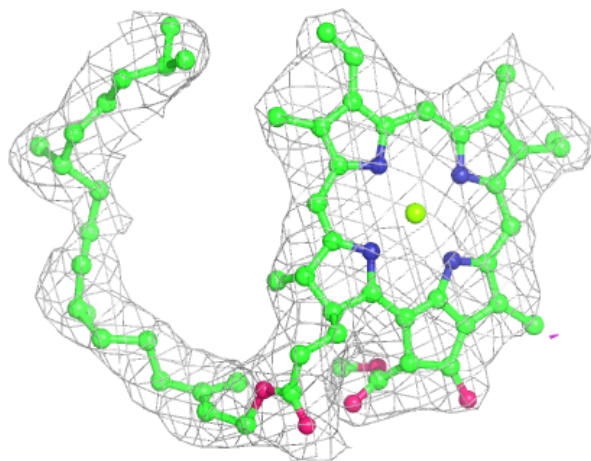
Electron density around CLA D 1001:

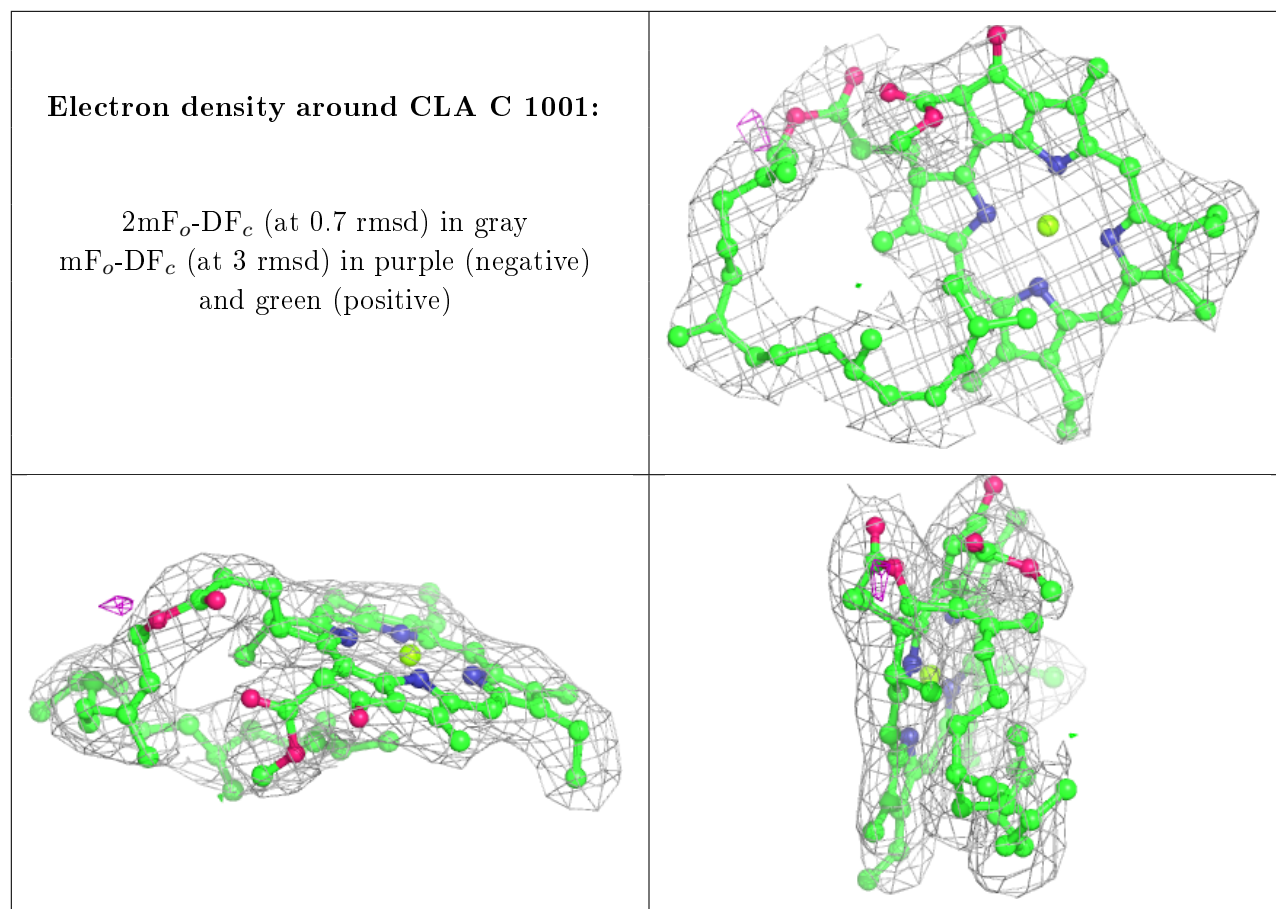
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CLA A 1001:

$2mF_o-DF_c$ (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.