Full wwPDB X-ray Structure Validation Report (i)

Aug 25, 2026 – 02:08 am BST

PDB ID	:	6S2Y / pdb_00006s2y
Title	:	Water-soluble Chlorophyll Protein (WSCP) from Lepidium virginicum with Chlorophyll-b
Authors	:	Agostini, A.; Meneghin, E.; Gewehr, L.; Pedron, D.; Palm, D.M.; Carbonera, D.; Paulsen, H.; Jaenicke, E.; Collini, E.
Deposited on	:	2019-06-23
Resolution	:	2.30 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 (i) 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 (i)) were used in the production of this report:

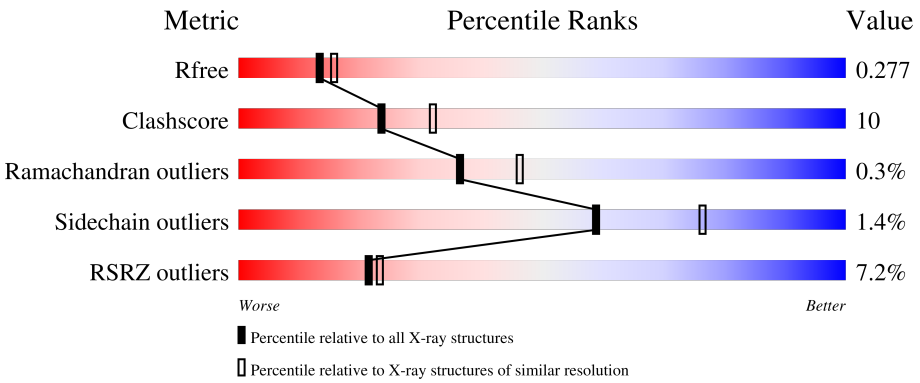
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 <=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	2%, 74%, 13%, 13%
1	B	180	11%, 73%, 14%, •, 12%
1	C	180	6%, 78%, 11%, •, 11%
1	D	180	7%, 75%, 15%, 10%

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CHL	B	1001	-	-	X	-

2 Entry composition (i)

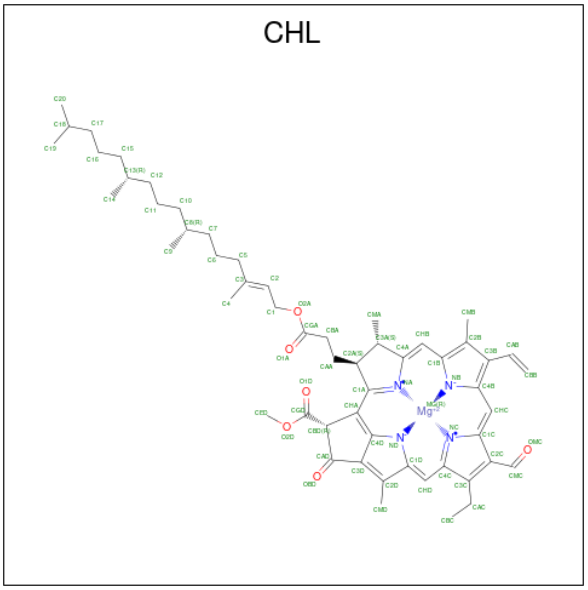
There are 3 unique types of molecules in this entry. The entry contains 5308 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			Total	C	N	O	S			
1	A	157	1207	772	200	233	2	0	0	0
1	B	159	1218	777	199	240	2	0	0	0
1	C	161	1240	788	204	246	2	0	0	0
1	D	162	1249	794	205	248	2	0	0	0

- Molecule 2 is CHLOROPHYLL B (CCD ID: CHL) (formula: $C_{55}H_{70}MgN_4O_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Mg	N	O		
2	A	1	66	55	1	4	6	0	0
2	B	1	66	55	1	4	6	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Mg	N	O		
2	C	1	66	55	1	4	6	0	0
			Total	C	Mg	N	O		
2	D	1	66	55	1	4	6	0	0

- Molecule 3 is water.

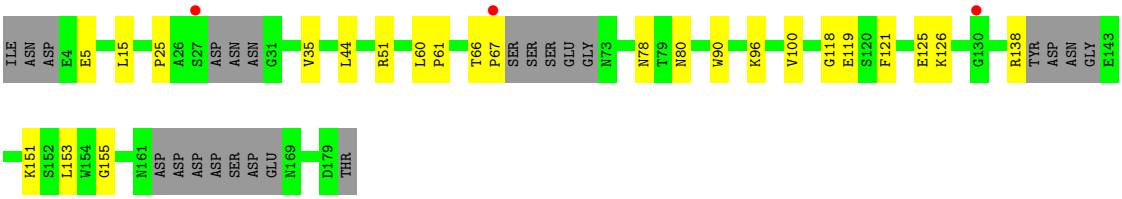
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	36	36	36	0	0
			Total	O		
3	B	40	40	40	0	0
			Total	O		
3	C	30	30	30	0	0
			Total	O		
3	D	24	24	24	0	0

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.

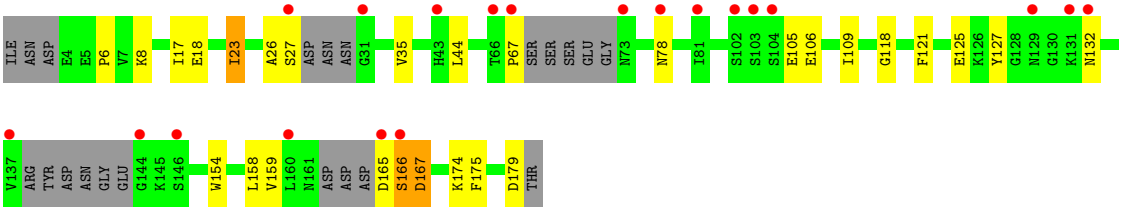
• Molecule 1: Water-soluble chlorophyll protein

Chain A:



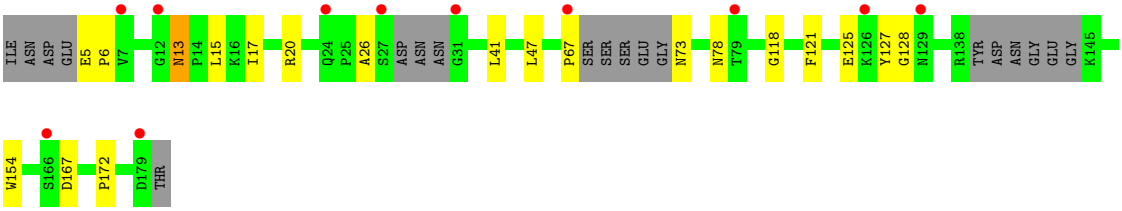
• Molecule 1: Water-soluble chlorophyll protein

Chain B:



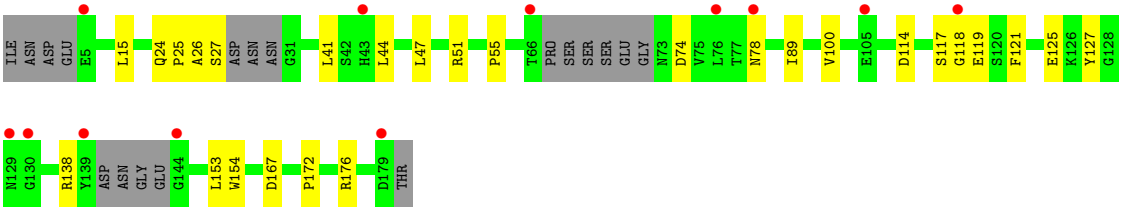
• Molecule 1: Water-soluble chlorophyll protein

Chain C:



• Molecule 1: Water-soluble chlorophyll protein

Chain D:


ILE
ASN
ASP
GLU
E5
L15
Q24
P25
A26
S27
ASP
ASN
ASN
G31
L41
S42
H43
L44
L47
R51
P55
T66
PRO
SER
SER
SER
GLU
GLY
N73
D74
V75
L76
T77
N78
I89
V100
E105
D114
S117
G118
E119
S120
F121
E125
K126
Y127
G128

N129
G130
R138
Y139
ASP
ASN
GLY
GLU
G144
L153
W154
D167
P172
R176
D179
THR

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	73.31Å 82.90Å 122.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.63 – 2.30 19.63 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.7 (19.63-2.30) 98.6 (19.63-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.243 , 0.277 0.243 , 0.277	Depositor DCC
R_{free} test set	1667 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	40.0	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 39.8	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	0.92	EDS
Total number of atoms	5308	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CHL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.54	0/1234	0.96	0/1677
1	B	0.51	0/1245	0.97	2/1693 (0.1%)
1	C	0.55	1/1268 (0.1%)	0.95	0/1726
1	D	0.54	0/1277	0.95	2/1737 (0.1%)
All	All	0.54	1/5024 (0.0%)	0.96	4/6833 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	20	ARG	CZ-NH2	6.67	1.42	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	179	ASP	CB-CA-C	5.90	121.32	110.10
1	B	167	ASP	CB-CA-C	5.32	119.30	111.17
1	D	55	PRO	CA-C-N	-5.02	114.77	122.60
1	D	55	PRO	C-N-CA	-5.02	114.77	122.60

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	1207	0	1199	20	0
1	B	1218	0	1199	24	0
1	C	1240	0	1216	13	0
1	D	1249	0	1221	27	0
2	A	66	0	70	5	0
2	B	66	0	70	21	0
2	C	66	0	70	10	0
2	D	66	0	70	20	0
3	A	36	0	0	0	0
3	B	40	0	0	4	0
3	C	30	0	0	0	0
3	D	24	0	0	0	0
All	All	5308	0	5115	105	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 10.

All (105) 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)
2:B:1001:CHL:H192	2:D:1001:CHL:C20	1.72	1.19
2:B:1001:CHL:H192	2:D:1001:CHL:H201	1.15	1.12
2:B:1001:CHL:H203	2:D:1001:CHL:H202	1.32	1.07
1:B:78:ASN:ND2	1:B:125:GLU:HG2	1.83	0.93
2:B:1001:CHL:H201	1:D:154:TRP:HZ2	1.35	0.92
2:B:1001:CHL:H201	1:D:154:TRP:CZ2	2.10	0.86
2:B:1001:CHL:C20	2:D:1001:CHL:H202	2.07	0.84
2:B:1001:CHL:C20	1:D:154:TRP:HZ2	1.90	0.83
1:D:47:LEU:HD21	2:D:1001:CHL:HBB1	1.64	0.78
2:B:1001:CHL:H192	2:D:1001:CHL:H202	1.69	0.75
2:B:1001:CHL:C19	2:D:1001:CHL:C20	2.61	0.73
1:B:6:PRO:HB3	3:B:1128:HOH:O	1.89	0.73
1:C:17:ILE:HG12	1:C:73:ASN:HA	1.70	0.72
1:B:78:ASN:HD21	1:B:125:GLU:HG2	1.58	0.68
1:A:67:PRO:CD	1:A:80:ASN:O	2.42	0.68
2:A:1001:CHL:HBB1	2:A:1001:CHL:HMB1	1.74	0.67
1:D:47:LEU:HD21	2:D:1001:CHL:CBB	2.23	0.67
1:B:78:ASN:HD22	1:B:125:GLU:HG2	1.60	0.67
2:B:1001:CHL:H193	1:D:41:LEU:HD21	1.77	0.67
1:A:44:LEU:HD21	2:C:1001:CHL:H172	1.77	0.67
2:C:1001:CHL:HBB1	2:C:1001:CHL:HHC	1.78	0.63
2:B:1001:CHL:C19	2:D:1001:CHL:H201	2.09	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:25:PRO:HG2	1:D:51:ARG:HE	1.64	0.62
1:C:13:ASN:HD22	1:C:13:ASN:N	1.97	0.62
2:B:1001:CHL:H193	1:D:41:LEU:CD2	2.32	0.60
1:B:17:ILE:HD12	1:B:18:GLU:HG2	1.82	0.60
1:C:67:PRO:HG3	1:C:121:PHE:CE1	2.36	0.60
2:A:1001:CHL:HBB1	2:A:1001:CHL:CMB	2.32	0.59
1:B:23:ILE:HD13	1:B:175:PHE:CE2	2.39	0.58
1:A:138:ARG:HH11	1:A:138:ARG:HG3	1.69	0.57
1:B:67:PRO:HG3	1:B:121:PHE:CE1	2.39	0.57
2:A:1001:CHL:H162	2:D:1001:CHL:H142	1.87	0.57
1:C:127:TYR:CE2	1:C:167:ASP:HB3	2.41	0.56
1:A:100:VAL:HG21	1:A:138:ARG:HD2	1.88	0.56
1:D:25:PRO:HG2	1:D:51:ARG:NE	2.21	0.56
1:A:67:PRO:HD3	1:A:80:ASN:O	2.06	0.55
1:B:8:LYS:HE3	3:B:1134:HOH:O	2.05	0.55
1:A:138:ARG:HG3	1:A:138:ARG:NH1	2.21	0.55
1:D:100:VAL:HG21	1:D:138:ARG:CD	2.38	0.53
2:B:1001:CHL:H171	2:D:1001:CHL:H18	1.91	0.53
1:D:100:VAL:HG21	1:D:138:ARG:HD2	1.90	0.52
1:A:60:LEU:HD12	1:A:61:PRO:HD2	1.91	0.52
2:C:1001:CHL:H112	2:C:1001:CHL:H62	1.90	0.52
1:B:127:TYR:CE2	1:B:167:ASP:HB2	2.46	0.51
1:D:119:GLU:O	1:D:138:ARG:NH2	2.43	0.51
1:B:127:TYR:CD2	1:B:167:ASP:HB2	2.45	0.51
1:C:154:TRP:HH2	2:C:1001:CHL:H202	1.76	0.51
2:C:1001:CHL:H43	1:D:89:ILE:HG21	1.93	0.51
2:A:1001:CHL:H151	2:D:1001:CHL:H141	1.93	0.51
1:D:78:ASN:OD1	1:D:125:GLU:HG2	2.11	0.51
2:B:1001:CHL:C19	2:D:1001:CHL:H202	2.33	0.50
1:D:119:GLU:C	1:D:138:ARG:HH22	2.20	0.50
1:A:5:GLU:OE2	1:A:126:LYS:HE3	2.12	0.49
1:C:78:ASN:OD1	1:C:125:GLU:HG2	2.10	0.49
1:C:47:LEU:HD21	2:C:1001:CHL:CBB	2.43	0.49
1:D:127:TYR:CE2	1:D:167:ASP:HB3	2.48	0.49
1:C:26:ALA:HB3	1:C:172:PRO:HB2	1.94	0.49
2:C:1001:CHL:H8	2:D:1001:CHL:NB	2.28	0.48
2:B:1001:CHL:H191	1:D:153:LEU:HD21	1.96	0.48
1:C:67:PRO:HG3	1:C:121:PHE:CZ	2.49	0.48
1:A:78:ASN:OD1	1:A:125:GLU:HG2	2.12	0.48
1:B:67:PRO:HG3	1:B:121:PHE:CZ	2.50	0.47
1:A:153:LEU:CD1	1:C:41:LEU:HD11	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1001:CHL:H203	2:D:1001:CHL:C20	2.22	0.47
2:D:1001:CHL:H141	2:D:1001:CHL:H161	1.57	0.47
1:A:67:PRO:HD2	1:A:80:ASN:O	2.14	0.46
2:D:1001:CHL:HBB1	2:D:1001:CHL:HHC	1.97	0.46
1:A:90:TRP:HB2	1:A:96:LYS:HE2	1.97	0.46
1:B:154:TRP:HB3	2:B:1001:CHL:HBA2	1.98	0.46
1:A:66:THR:HA	1:A:67:PRO:HD3	1.68	0.45
1:D:114:ASP:HB3	1:D:117:SER:HB3	1.98	0.45
1:B:44:LEU:HD21	3:B:1139:HOH:O	2.16	0.45
2:B:1001:CHL:C20	1:D:154:TRP:CZ2	2.80	0.44
1:B:26:ALA:HB2	1:B:174:LYS:HG3	1.98	0.44
2:C:1001:CHL:H13	2:C:1001:CHL:H171	1.29	0.44
1:B:44:LEU:CD2	3:B:1139:HOH:O	2.65	0.44
1:B:8:LYS:HE2	1:B:132:ASN:ND2	2.32	0.44
1:C:154:TRP:HH2	2:C:1001:CHL:C20	2.31	0.44
1:B:109:ILE:HD13	1:B:158:LEU:HB3	2.00	0.43
1:B:165:ASP:O	1:B:166:SER:C	2.61	0.43
1:D:100:VAL:CG2	1:D:138:ARG:HD2	2.48	0.43
1:A:25:PRO:HG2	1:A:51:ARG:HG3	2.00	0.43
1:B:35:VAL:HG11	2:B:1001:CHL:CAD	2.49	0.43
1:A:119:GLU:HA	1:A:138:ARG:HH22	1.83	0.43
1:A:151:LYS:HZ2	1:A:155:GLY:HA2	1.83	0.43
2:B:1001:CHL:C18	2:D:1001:CHL:H202	2.49	0.43
1:B:78:ASN:ND2	1:B:125:GLU:CG	2.71	0.42
1:D:26:ALA:HB3	1:D:172:PRO:HB2	2.00	0.42
2:D:1001:CHL:H151	2:D:1001:CHL:H111	1.48	0.42
1:A:118:GLY:HA2	1:A:121:PHE:CD2	2.55	0.42
1:D:138:ARG:HG3	1:D:138:ARG:HH11	1.84	0.42
1:D:27:SER:HB2	1:D:172:PRO:HG2	2.02	0.41
1:A:44:LEU:HD13	1:D:44:LEU:HD13	2.02	0.41
1:A:35:VAL:HG11	2:A:1001:CHL:CAD	2.51	0.41
1:B:118:GLY:HA2	1:B:121:PHE:CD2	2.55	0.41
1:A:151:LYS:NZ	1:A:155:GLY:HA2	2.36	0.41
2:B:1001:CHL:H161	1:D:44:LEU:HD21	2.03	0.41
1:D:24:GLN:OE1	1:D:176:ARG:NH1	2.52	0.41
1:B:78:ASN:HD21	1:B:125:GLU:CG	2.31	0.41
1:C:118:GLY:HA2	1:C:121:PHE:CD2	2.56	0.41
1:B:106:GLU:O	1:B:159:VAL:HB	2.22	0.40
1:B:44:LEU:HD21	2:D:1001:CHL:H172	2.03	0.40
1:C:5:GLU:HA	1:C:6:PRO:HD3	1.90	0.40
1:D:118:GLY:HA2	1:D:121:PHE:CD2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1001:CHL:H62	2:C:1001:CHL:C11	2.51	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	147/180 (82%)	145 (99%)	2 (1%)	0	100	100
1	B	149/180 (83%)	144 (97%)	4 (3%)	1 (1%)	18	23
1	C	153/180 (85%)	152 (99%)	0	1 (1%)	18	23
1	D	154/180 (86%)	152 (99%)	2 (1%)	0	100	100
All	All	603/720 (84%)	593 (98%)	8 (1%)	2 (0%)	36	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	128	GLY
1	B	166	SER

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	137/158 (87%)	136 (99%)	1 (1%)	76	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	139/158 (88%)	136 (98%)	3 (2%)	45	65
1	C	142/158 (90%)	140 (99%)	2 (1%)	59	76
1	D	142/158 (90%)	140 (99%)	2 (1%)	59	76
All	All	560/632 (89%)	552 (99%)	8 (1%)	59	76

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	B	23	ILE
1	B	27	SER
1	B	105	GLU
1	C	13	ASN
1	C	15	LEU
1	D	15	LEU
1	D	74	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	ASN
1	A	169	ASN
1	B	57	GLN
1	B	78	ASN
1	B	129	ASN
1	B	132	ASN
1	C	11	ASN
1	C	13	ASN
1	D	73	ASN
1	D	132	ASN
1	D	169	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 oligosaccharides 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	CHL	B	1001	1	70,74,74	1.97	17 (24%)	80,114,114	2.78	34 (42%)
2	CHL	C	1001	1	70,74,74	1.96	19 (27%)	80,114,114	2.94	30 (37%)
2	CHL	D	1001	1	70,74,74	1.89	18 (25%)	80,114,114	2.56	24 (30%)
2	CHL	A	1001	1	70,74,74	1.99	20 (28%)	80,114,114	2.79	26 (32%)

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	CHL	B	1001	1	-	10/41/117/117	-
2	CHL	C	1001	1	-	12/41/117/117	-
2	CHL	D	1001	1	-	15/41/117/117	-
2	CHL	A	1001	1	-	15/41/117/117	-

All (74) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1001	CHL	C3D-C4D	-6.25	1.30	1.44
2	A	1001	CHL	C3D-C4D	-6.19	1.30	1.44
2	B	1001	CHL	C3D-C4D	-6.00	1.30	1.44
2	D	1001	CHL	C3D-C4D	-5.94	1.30	1.44
2	A	1001	CHL	C4B-NB	-5.45	1.31	1.37
2	A	1001	CHL	C1D-ND	-5.36	1.31	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	CHL	C1D-ND	-5.36	1.31	1.37
2	B	1001	CHL	C4B-NB	-5.23	1.31	1.37
2	C	1001	CHL	C1D-ND	-5.04	1.31	1.37
2	D	1001	CHL	C1B-NB	-4.54	1.32	1.37
2	B	1001	CHL	C1B-NB	-4.53	1.32	1.37
2	A	1001	CHL	C1B-NB	-4.49	1.32	1.37
2	D	1001	CHL	C4B-NB	-4.48	1.32	1.37
2	C	1001	CHL	C1B-NB	-4.32	1.32	1.37
2	D	1001	CHL	C1D-ND	-4.13	1.32	1.37
2	C	1001	CHL	C1C-NC	-4.13	1.31	1.37
2	C	1001	CHL	CHC-C1C	3.92	1.46	1.38
2	A	1001	CHL	O2D-CGD	3.85	1.42	1.33
2	C	1001	CHL	C4B-NB	-3.84	1.33	1.37
2	B	1001	CHL	O2D-CGD	3.75	1.42	1.33
2	A	1001	CHL	C4D-ND	-3.51	1.32	1.37
2	A	1001	CHL	C1C-NC	-3.50	1.32	1.37
2	A	1001	CHL	CHD-C1D	3.45	1.45	1.38
2	C	1001	CHL	CHC-C4B	3.44	1.47	1.39
2	A	1001	CHL	CHC-C1C	3.38	1.45	1.38
2	D	1001	CHL	C2C-C3C	3.36	1.44	1.36
2	D	1001	CHL	CHD-C1D	3.34	1.44	1.38
2	D	1001	CHL	CHC-C4B	3.32	1.46	1.39
2	B	1001	CHL	C1C-NC	-3.23	1.33	1.37
2	B	1001	CHL	CHB-C1B	3.22	1.46	1.39
2	B	1001	CHL	C4D-ND	-3.21	1.33	1.37
2	C	1001	CHL	C4D-ND	-3.20	1.33	1.37
2	C	1001	CHL	CHB-C4A	-3.20	1.30	1.37
2	B	1001	CHL	CHC-C1C	3.17	1.45	1.38
2	D	1001	CHL	CHC-C1C	3.10	1.44	1.38
2	C	1001	CHL	O2D-CGD	3.08	1.40	1.33
2	B	1001	CHL	CHC-C4B	3.04	1.46	1.39
2	B	1001	CHL	CHD-C1D	3.03	1.44	1.38
2	C	1001	CHL	O2A-CGA	3.03	1.42	1.33
2	C	1001	CHL	OMC-CMC	-2.99	1.15	1.22
2	B	1001	CHL	CHD-C4C	2.99	1.46	1.39
2	D	1001	CHL	CHB-C1B	2.96	1.46	1.39
2	D	1001	CHL	CHB-C4A	-2.95	1.30	1.37
2	C	1001	CHL	CHD-C1D	2.94	1.44	1.38
2	D	1001	CHL	C1C-NC	-2.91	1.33	1.37
2	D	1001	CHL	O2A-CGA	2.91	1.41	1.33
2	A	1001	CHL	CHC-C4B	2.87	1.45	1.39
2	C	1001	CHL	CHD-C4C	2.85	1.45	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1001	CHL	CHD-C4C	2.75	1.45	1.39
2	B	1001	CHL	O2D-CED	-2.75	1.38	1.45
2	D	1001	CHL	O2D-CED	-2.74	1.38	1.45
2	A	1001	CHL	CHB-C1B	2.66	1.45	1.39
2	A	1001	CHL	CHD-C4C	2.65	1.45	1.39
2	A	1001	CHL	O2A-CGA	2.64	1.41	1.33
2	C	1001	CHL	O2D-CED	-2.58	1.39	1.45
2	D	1001	CHL	O2D-CGD	2.53	1.39	1.33
2	B	1001	CHL	O2A-CGA	2.49	1.40	1.33
2	B	1001	CHL	CHB-C4A	-2.48	1.31	1.37
2	A	1001	CHL	C2C-C3C	2.38	1.41	1.36
2	D	1001	CHL	C4D-ND	-2.38	1.34	1.37
2	C	1001	CHL	CHB-C1B	2.38	1.44	1.39
2	C	1001	CHL	O1A-CGA	-2.35	1.15	1.22
2	B	1001	CHL	C2C-C3C	2.34	1.41	1.36
2	A	1001	CHL	C3A-C2A	-2.25	1.48	1.54
2	A	1001	CHL	CHB-C4A	-2.23	1.32	1.37
2	D	1001	CHL	C3D-C2D	2.18	1.45	1.39
2	A	1001	CHL	O2D-CED	-2.13	1.40	1.45
2	A	1001	CHL	OMC-CMC	-2.12	1.17	1.22
2	A	1001	CHL	O2A-C1	-2.10	1.40	1.46
2	C	1001	CHL	O2A-C1	-2.10	1.40	1.46
2	C	1001	CHL	C2C-C3C	2.09	1.41	1.36
2	B	1001	CHL	OMC-CMC	-2.06	1.17	1.22
2	D	1001	CHL	C3A-C2A	-2.05	1.48	1.54
2	A	1001	CHL	C3D-C2D	2.00	1.44	1.39

All (114) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	1001	CHL	C2C-C3C-C4C	-10.58	98.95	106.49
2	B	1001	CHL	C2B-C1B-NB	9.28	116.45	110.23
2	C	1001	CHL	C2B-C1B-NB	8.88	116.19	110.23
2	A	1001	CHL	C2B-C1B-NB	8.51	115.94	110.23
2	D	1001	CHL	C2B-C1B-NB	8.49	115.92	110.23
2	A	1001	CHL	C2C-C3C-C4C	-7.98	100.80	106.49
2	C	1001	CHL	CMD-C2D-C1D	7.93	138.70	124.71
2	B	1001	CHL	CMD-C2D-C1D	7.23	137.45	124.71
2	D	1001	CHL	C2C-C3C-C4C	-6.94	101.54	106.49
2	B	1001	CHL	C2C-C3C-C4C	-6.82	101.63	106.49
2	C	1001	CHL	C3C-C4C-NC	6.77	118.16	110.57
2	D	1001	CHL	CMD-C2D-C1D	6.73	136.58	124.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1001	CHL	O2D-CGD-CBD	6.60	123.00	111.27
2	A	1001	CHL	C3C-C4C-NC	6.47	117.83	110.57
2	A	1001	CHL	CMD-C2D-C1D	6.39	135.98	124.71
2	A	1001	CHL	C3B-C2B-C1B	-6.18	99.71	107.16
2	B	1001	CHL	C3B-C2B-C1B	-6.12	99.77	107.16
2	B	1001	CHL	O2D-CGD-CBD	5.89	121.73	111.27
2	C	1001	CHL	CHD-C4C-C3C	-5.89	116.18	124.84
2	D	1001	CHL	C3C-C4C-NC	5.72	116.98	110.57
2	D	1001	CHL	O2D-CGD-CBD	5.59	121.20	111.27
2	D	1001	CHL	C3B-C2B-C1B	-5.50	100.52	107.16
2	B	1001	CHL	C3C-C4C-NC	5.45	116.68	110.57
2	C	1001	CHL	O2D-CGD-CBD	5.39	120.85	111.27
2	C	1001	CHL	C3B-C2B-C1B	-5.37	100.68	107.16
2	C	1001	CHL	CAC-C3C-C4C	5.36	131.77	124.81
2	A	1001	CHL	CHD-C4C-C3C	-5.32	117.02	124.84
2	C	1001	CHL	C3D-C2D-C1D	-5.23	98.69	105.83
2	D	1001	CHL	CHD-C1D-ND	-5.08	119.78	124.45
2	C	1001	CHL	C2D-C1D-ND	5.07	113.84	110.10
2	A	1001	CHL	C2D-C1D-ND	5.05	113.82	110.10
2	B	1001	CHL	CAC-C3C-C4C	5.03	131.34	124.81
2	A	1001	CHL	C3D-C2D-C1D	-5.00	99.01	105.83
2	D	1001	CHL	C3D-C2D-C1D	-4.91	99.13	105.83
2	B	1001	CHL	C3D-C2D-C1D	-4.79	99.29	105.83
2	B	1001	CHL	C2D-C1D-ND	4.76	113.61	110.10
2	A	1001	CHL	CAC-C3C-C4C	4.67	130.87	124.81
2	D	1001	CHL	CHD-C4C-C3C	-4.67	117.98	124.84
2	A	1001	CHL	CHD-C1D-ND	-4.64	120.19	124.45
2	D	1001	CHL	C2D-C1D-ND	4.50	113.42	110.10
2	A	1001	CHL	CHB-C1B-NB	-4.49	119.50	124.26
2	C	1001	CHL	CHD-C1D-ND	-4.42	120.39	124.45
2	B	1001	CHL	CHD-C1D-ND	-4.35	120.46	124.45
2	B	1001	CHL	CHD-C4C-C3C	-4.11	118.80	124.84
2	B	1001	CHL	C3B-C4B-NB	4.10	114.31	110.52
2	C	1001	CHL	C1D-ND-C4D	-4.03	103.47	106.33
2	A	1001	CHL	C1D-ND-C4D	-4.01	103.48	106.33
2	A	1001	CHL	O2D-CGD-O1D	-3.97	116.08	123.84
2	D	1001	CHL	C1C-C2C-C3C	-3.86	104.05	107.11
2	B	1001	CHL	CHB-C1B-NB	-3.83	120.20	124.26
2	A	1001	CHL	C3D-C4D-ND	3.78	116.35	110.24
2	D	1001	CHL	CMB-C2B-C1B	3.77	131.11	125.37
2	A	1001	CHL	CMB-C2B-C1B	3.66	130.95	125.37
2	B	1001	CHL	C1D-ND-C4D	-3.54	103.82	106.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	1001	CHL	CMB-C2B-C1B	3.52	130.73	125.37
2	D	1001	CHL	O2A-CGA-CBA	3.51	122.92	111.91
2	D	1001	CHL	O2D-CGD-O1D	-3.46	117.08	123.84
2	C	1001	CHL	CED-O2D-CGD	3.45	123.74	115.94
2	C	1001	CHL	OMC-CMC-C2C	-3.45	117.89	125.69
2	A	1001	CHL	C3B-C4B-NB	3.34	113.62	110.52
2	D	1001	CHL	O2A-CGA-O1A	-3.34	115.16	123.59
2	C	1001	CHL	C1-O2A-CGA	3.32	125.16	116.44
2	B	1001	CHL	O2A-C1-C2	3.31	117.34	108.64
2	B	1001	CHL	C1C-C2C-C3C	-3.27	104.52	107.11
2	C	1001	CHL	C3D-C4D-ND	3.24	115.48	110.24
2	B	1001	CHL	O2A-CGA-CBA	3.22	122.00	111.91
2	C	1001	CHL	O2A-CGA-CBA	3.19	121.92	111.91
2	B	1001	CHL	C3D-C4D-ND	3.17	115.36	110.24
2	B	1001	CHL	CMB-C2B-C1B	3.15	130.16	125.37
2	A	1001	CHL	CBC-CAC-C3C	-3.12	103.82	112.43
2	B	1001	CHL	O2D-CGD-O1D	-3.08	117.81	123.84
2	C	1001	CHL	C7-C6-C5	-3.05	105.06	113.36
2	D	1001	CHL	C1D-ND-C4D	-3.02	104.19	106.33
2	D	1001	CHL	CHB-C1B-NB	-3.01	121.07	124.26
2	D	1001	CHL	C3B-C4B-NB	2.94	113.24	110.52
2	A	1001	CHL	C1-C2-C3	-2.88	121.06	126.04
2	D	1001	CHL	C3D-C4D-ND	2.82	114.80	110.24
2	A	1001	CHL	O2A-CGA-CBA	2.76	120.57	111.91
2	D	1001	CHL	CAC-C3C-C4C	2.70	128.31	124.81
2	D	1001	CHL	CHC-C1C-NC	-2.69	120.12	124.20
2	A	1001	CHL	C1C-C2C-C3C	-2.68	104.99	107.11
2	B	1001	CHL	CBC-CAC-C3C	-2.64	105.15	112.43
2	A	1001	CHL	O2A-CGA-O1A	-2.64	116.93	123.59
2	A	1001	CHL	C2A-C1A-CHA	-2.63	119.26	123.86
2	C	1001	CHL	CHC-C4B-NB	-2.63	121.48	124.26
2	B	1001	CHL	O2A-CGA-O1A	-2.62	116.97	123.59
2	C	1001	CHL	O2A-CGA-O1A	-2.60	117.04	123.59
2	C	1001	CHL	C6-C5-C3	-2.57	106.72	113.45
2	C	1001	CHL	O1D-CGD-CBD	-2.55	119.27	124.48
2	B	1001	CHL	C2A-C1A-CHA	-2.51	119.46	123.86
2	B	1001	CHL	C4-C3-C5	2.51	119.49	115.27
2	C	1001	CHL	CHC-C1C-NC	-2.43	120.52	124.20
2	D	1001	CHL	C11-C10-C8	-2.39	108.20	115.92
2	A	1001	CHL	CHC-C1C-NC	-2.37	120.61	124.20
2	B	1001	CHL	C16-C15-C13	-2.37	108.27	115.92
2	D	1001	CHL	CHB-C4A-NA	2.35	127.77	124.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	1001	CHL	C2A-C1A-CHA	-2.35	119.75	123.86
2	A	1001	CHL	C16-C15-C13	-2.33	108.38	115.92
2	B	1001	CHL	C11-C10-C8	-2.33	108.38	115.92
2	B	1001	CHL	C7-C6-C5	-2.33	107.04	113.36
2	B	1001	CHL	CED-O2D-CGD	2.32	121.18	115.94
2	B	1001	CHL	C11-C12-C13	-2.31	108.47	115.92
2	C	1001	CHL	C4D-C3D-CAD	2.29	110.79	108.10
2	D	1001	CHL	C2A-C1A-CHA	-2.28	119.88	123.86
2	B	1001	CHL	CHB-C4A-NA	2.28	127.66	124.51
2	C	1001	CHL	CMD-C2D-C3D	-2.17	122.62	127.61
2	B	1001	CHL	C1-C2-C3	-2.14	122.35	126.04
2	A	1001	CHL	C4-C3-C5	2.09	118.78	115.27
2	B	1001	CHL	CHC-C1C-NC	-2.06	121.08	124.20
2	C	1001	CHL	CHB-C1B-C2B	-2.04	121.47	127.24
2	B	1001	CHL	C6-C5-C3	-2.04	108.12	113.45
2	C	1001	CHL	O2D-CGD-O1D	-2.03	119.86	123.84
2	C	1001	CHL	CHB-C4A-NA	2.01	127.29	124.51
2	B	1001	CHL	O1D-CGD-CBD	-2.01	120.37	124.48

There are no chirality outliers.

All (52) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1001	CHL	O2A-C1-C2-C3
2	D	1001	CHL	CBD-CGD-O2D-CED
2	C	1001	CHL	C13-C15-C16-C17
2	B	1001	CHL	C13-C15-C16-C17
2	D	1001	CHL	C14-C13-C15-C16
2	A	1001	CHL	C11-C10-C8-C7
2	D	1001	CHL	C11-C12-C13-C15
2	B	1001	CHL	C10-C11-C12-C13
2	A	1001	CHL	C10-C11-C12-C13
2	C	1001	CHL	C16-C17-C18-C20
2	C	1001	CHL	C16-C17-C18-C19
2	D	1001	CHL	C16-C17-C18-C19
2	C	1001	CHL	CBD-CGD-O2D-CED
2	D	1001	CHL	C8-C10-C11-C12
2	D	1001	CHL	O1D-CGD-O2D-CED
2	D	1001	CHL	C13-C15-C16-C17
2	C	1001	CHL	C12-C13-C15-C16
2	D	1001	CHL	C6-C7-C8-C10
2	D	1001	CHL	C16-C17-C18-C20

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Mol	Chain	Res	Type	Atoms
2	A	1001	CHL	C3-C5-C6-C7
2	C	1001	CHL	C14-C13-C15-C16
2	D	1001	CHL	C11-C12-C13-C14
2	D	1001	CHL	C10-C11-C12-C13
2	C	1001	CHL	C10-C11-C12-C13
2	A	1001	CHL	C12-C13-C15-C16
2	B	1001	CHL	C11-C10-C8-C7
2	B	1001	CHL	C12-C13-C15-C16
2	A	1001	CHL	C11-C10-C8-C9
2	A	1001	CHL	C14-C13-C15-C16
2	A	1001	CHL	C5-C6-C7-C8
2	D	1001	CHL	C12-C13-C15-C16
2	A	1001	CHL	C16-C17-C18-C20
2	A	1001	CHL	CAD-CBD-CGD-O2D
2	C	1001	CHL	O1D-CGD-O2D-CED
2	B	1001	CHL	C16-C17-C18-C19
2	B	1001	CHL	C11-C10-C8-C9
2	B	1001	CHL	C14-C13-C15-C16
2	B	1001	CHL	C16-C17-C18-C20
2	A	1001	CHL	C4-C3-C5-C6
2	C	1001	CHL	C2-C1-O2A-CGA
2	A	1001	CHL	C16-C17-C18-C19
2	A	1001	CHL	C2-C1-O2A-CGA
2	A	1001	CHL	C2-C3-C5-C6
2	D	1001	CHL	C6-C7-C8-C9
2	C	1001	CHL	CHA-CBD-CGD-O2D
2	D	1001	CHL	CHA-CBD-CGD-O2D
2	A	1001	CHL	CAA-CBA-CGA-O2A
2	C	1001	CHL	CAA-CBA-CGA-O2A
2	C	1001	CHL	CAA-CBA-CGA-O1A
2	A	1001	CHL	CAA-CBA-CGA-O1A
2	D	1001	CHL	CAA-CBA-CGA-O2A
2	B	1001	CHL	CAA-CBA-CGA-O2A

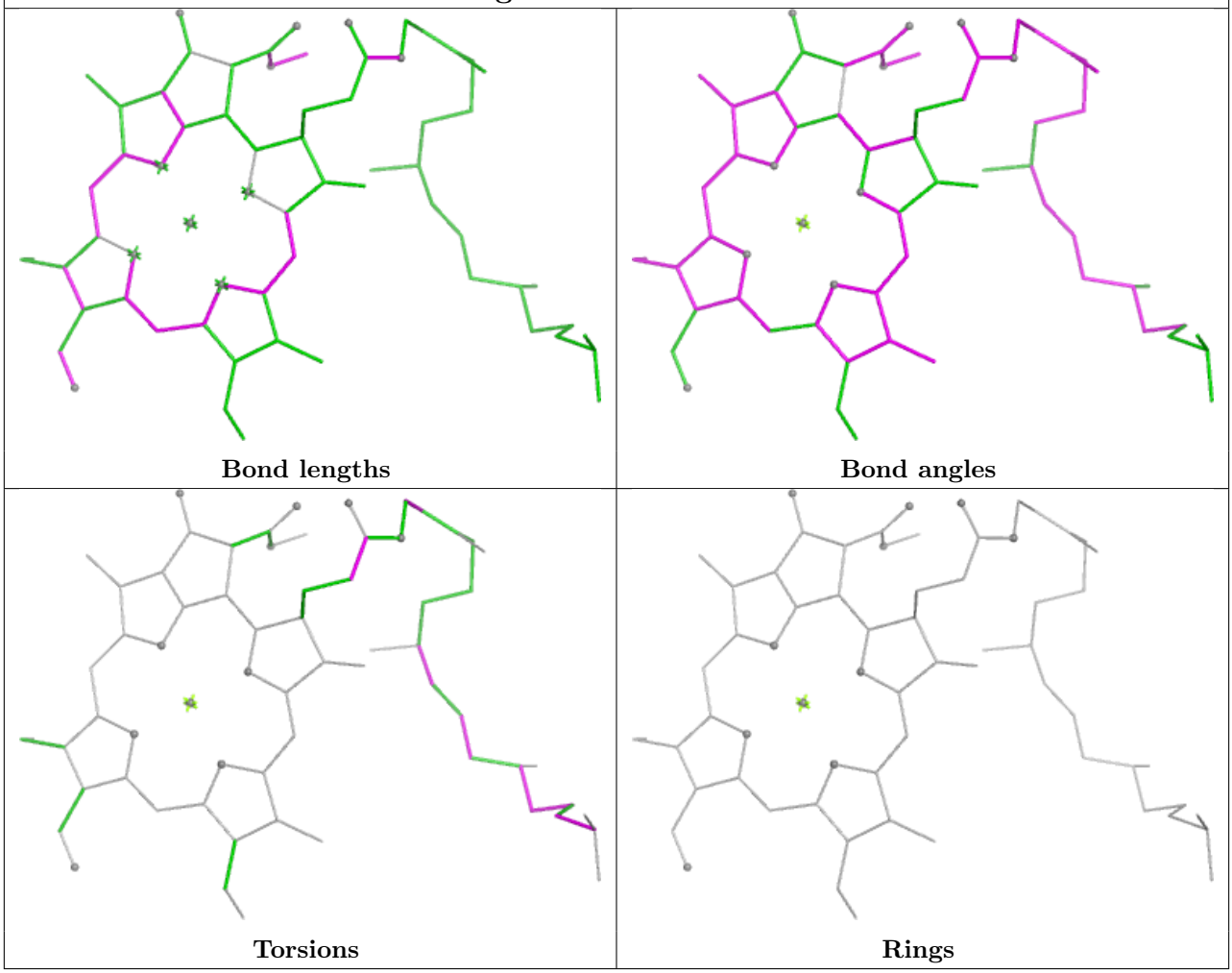
There are no ring outliers.

4 monomers are involved in 42 short contacts:

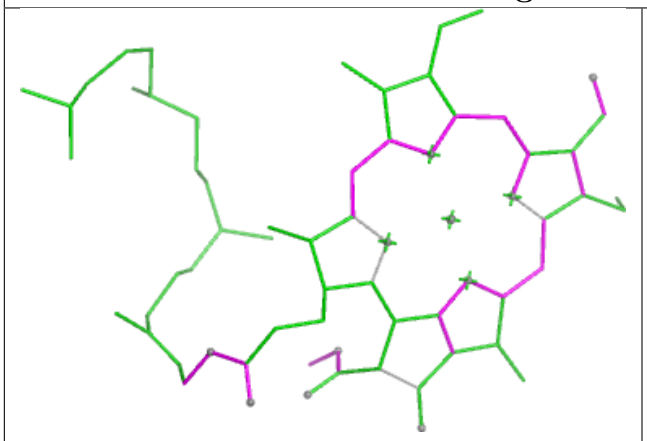
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1001	CHL	21	0
2	C	1001	CHL	10	0
2	D	1001	CHL	20	0
2	A	1001	CHL	5	0

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.

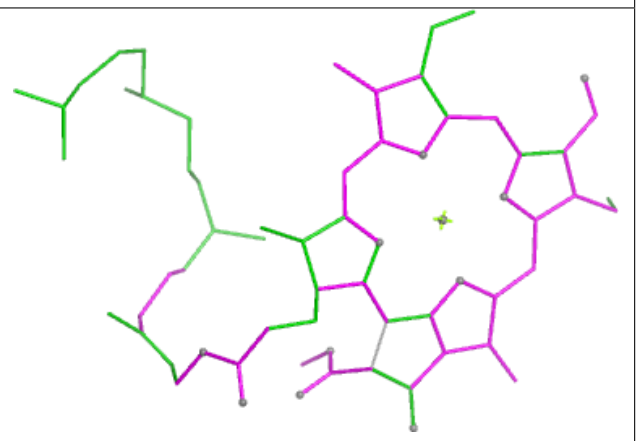
Ligand CHL B 1001



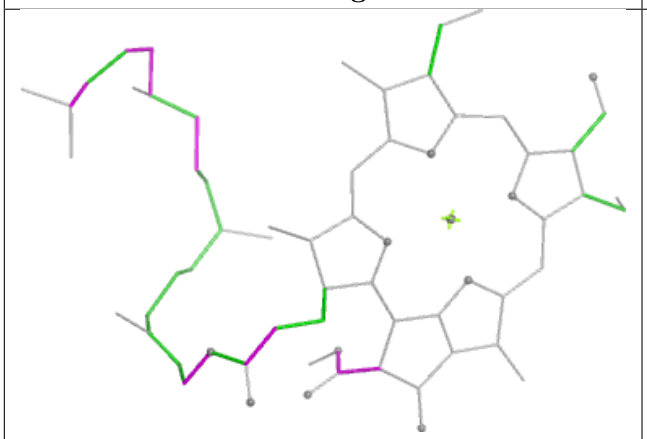
Ligand CHL C 1001



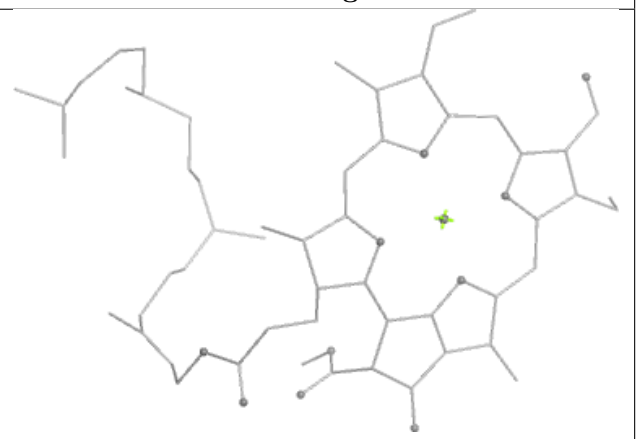
Bond lengths



Bond angles

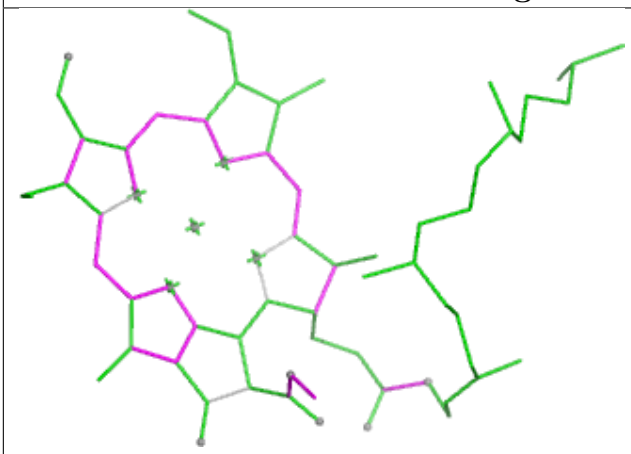


Torsions

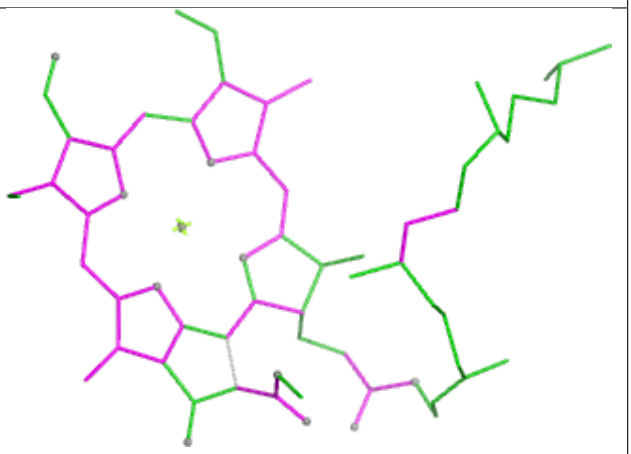


Rings

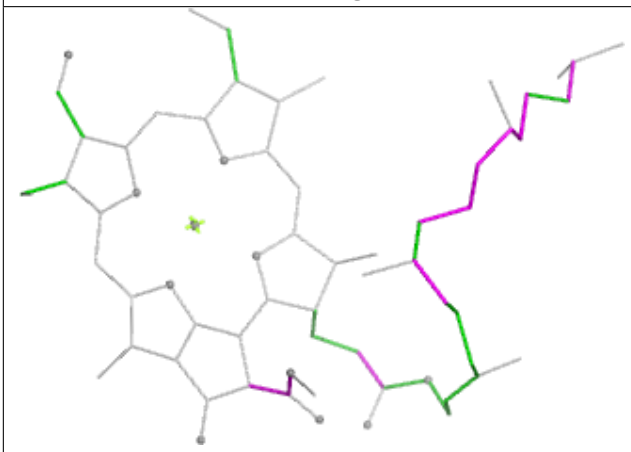
Ligand CHL D 1001



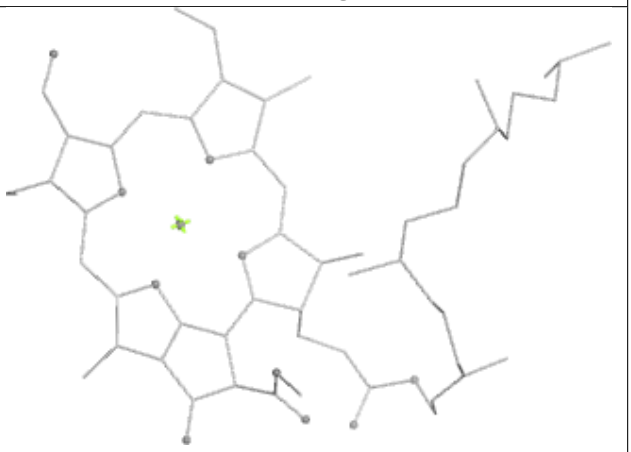
Bond lengths



Bond angles

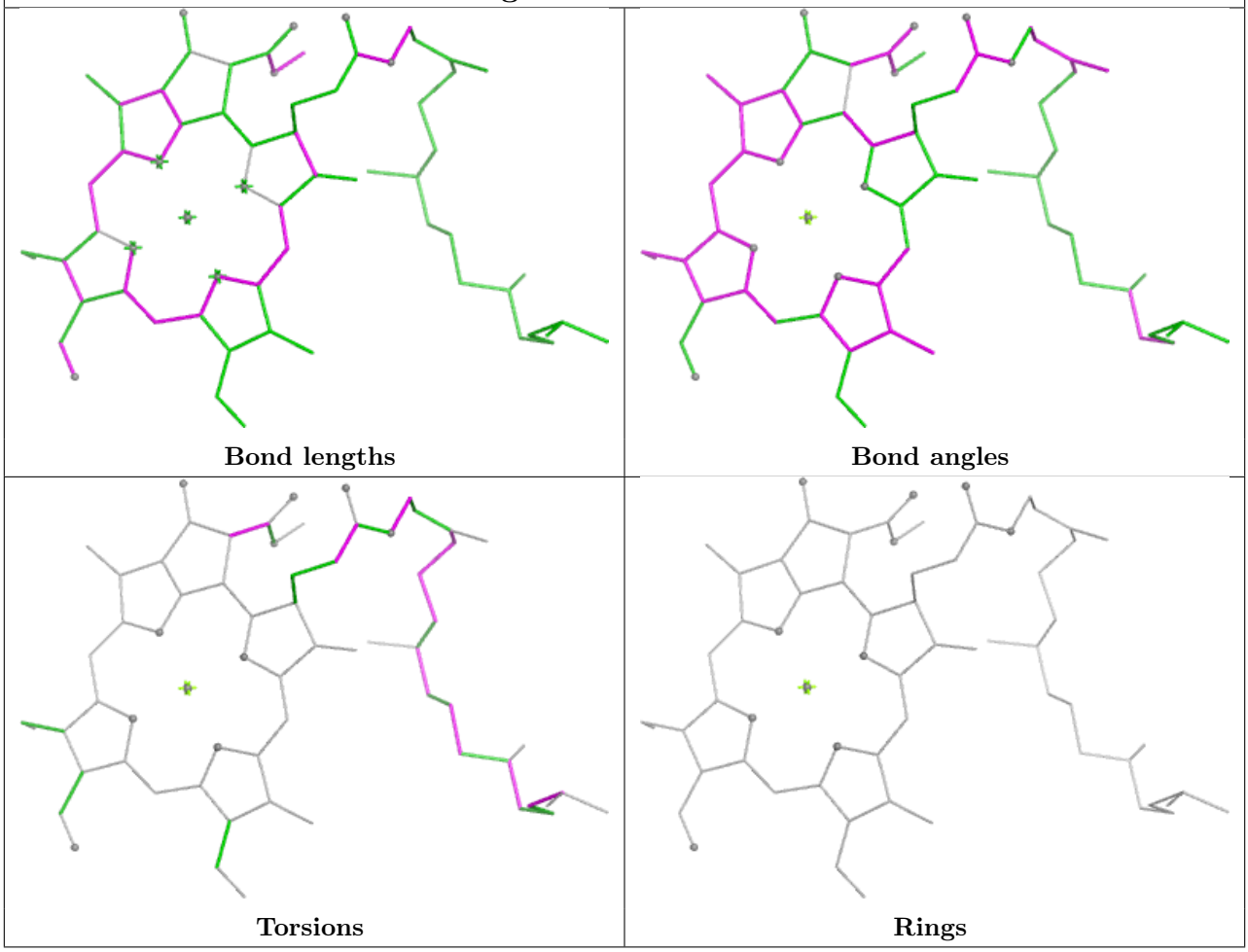


Torsions



Rings

Ligand CHL A 1001



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 (i)

6.1 Protein, DNA and RNA chains (i)

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	157/180 (87%)	0.22	3 (1%)	66	68	20, 34, 66, 100	0
1	B	159/180 (88%)	0.74	20 (12%)	8	9	22, 43, 82, 96	0
1	C	161/180 (89%)	0.46	11 (6%)	23	25	18, 40, 73, 84	0
1	D	162/180 (90%)	0.59	12 (7%)	20	22	22, 43, 79, 108	0
All	All	639/720 (88%)	0.50	46 (7%)	21	23	18, 40, 77, 108	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	67	PRO	5.0
1	A	67	PRO	5.0
1	B	27	SER	4.5
1	B	144	GLY	4.4
1	D	66	THR	4.1
1	B	73	ASN	3.9
1	D	129	ASN	3.8
1	B	103	SER	3.7
1	D	139	TYR	3.4
1	D	130	GLY	3.4
1	B	165	ASP	3.3
1	B	67	PRO	3.3
1	B	131	LYS	3.2
1	A	27	SER	3.2
1	B	102	SER	3.1
1	D	144	GLY	3.1
1	D	179	ASP	3.0
1	D	76	LEU	2.9
1	C	166	SER	2.9
1	B	43	HIS	2.9
1	B	104	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	105	GLU	2.8
1	B	160	LEU	2.6
1	B	31	GLY	2.6
1	B	166	SER	2.6
1	D	5	GLU	2.5
1	B	146	SER	2.4
1	B	137	VAL	2.4
1	C	31	GLY	2.3
1	D	118	GLY	2.3
1	B	66	THR	2.3
1	C	12	GLY	2.3
1	C	79	THR	2.3
1	C	27	SER	2.3
1	C	179	ASP	2.3
1	B	81	ILE	2.3
1	A	130	GLY	2.2
1	D	43	HIS	2.2
1	D	78	ASN	2.2
1	C	129	ASN	2.2
1	B	129	ASN	2.1
1	C	24	GLN	2.1
1	B	132	ASN	2.1
1	C	7	VAL	2.1
1	B	78	ASN	2.0
1	C	126	LYS	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 oligosaccharides in this entry.

6.4 Ligands (i)

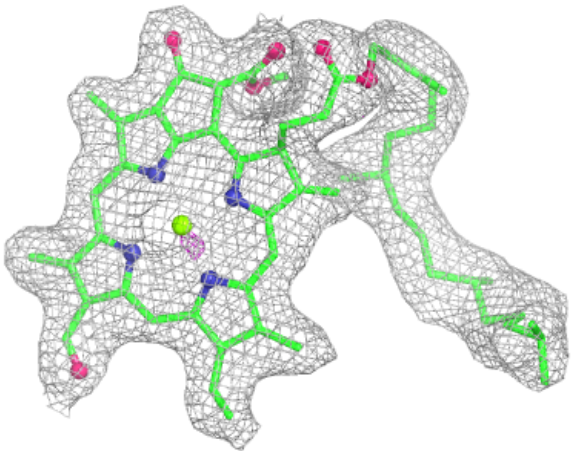
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

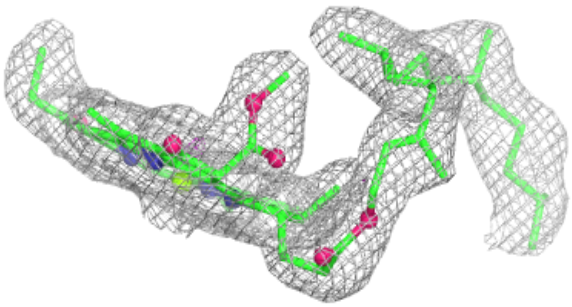
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CHL	B	1001	66/66	0.94	0.07	23,27,51,58	0
2	CHL	C	1001	66/66	0.94	0.08	17,21,60,77	0
2	CHL	A	1001	66/66	0.95	0.07	22,24,67,72	0
2	CHL	D	1001	66/66	0.95	0.07	19,22,57,69	0

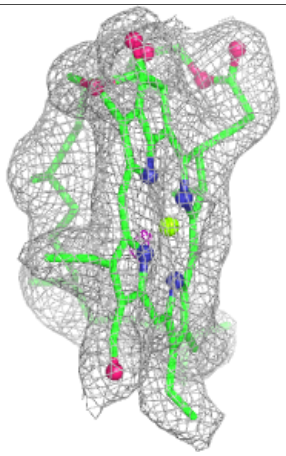
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around CHL B 1001:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

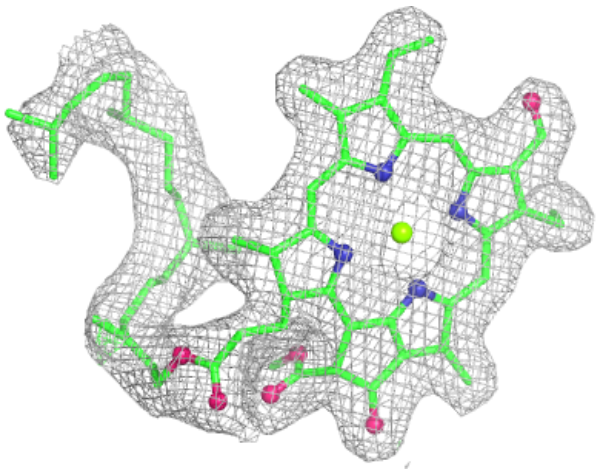


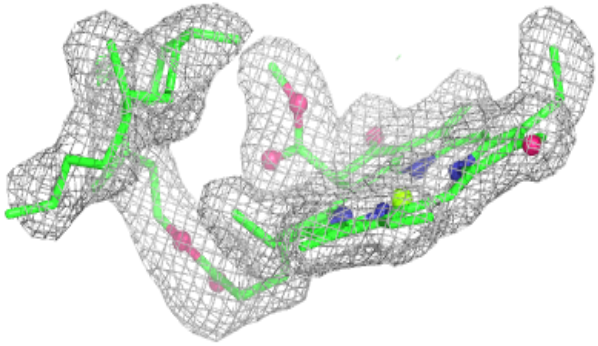


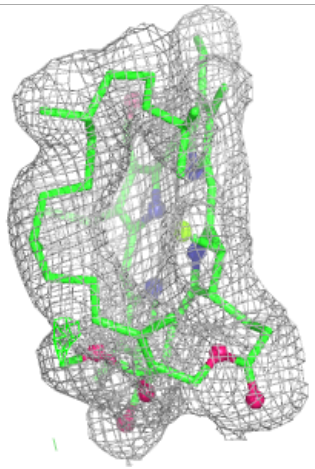


Electron density around CHL C 1001:

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

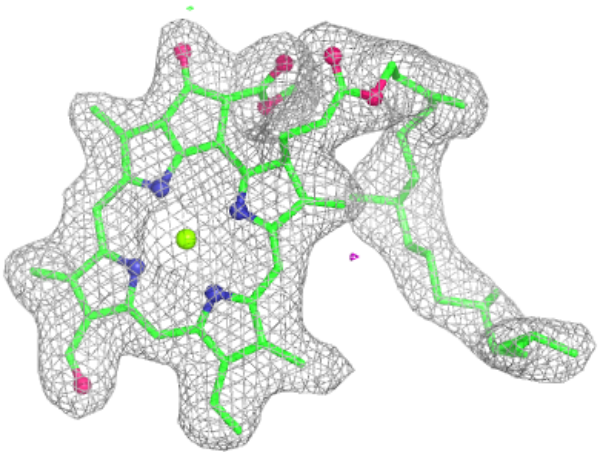


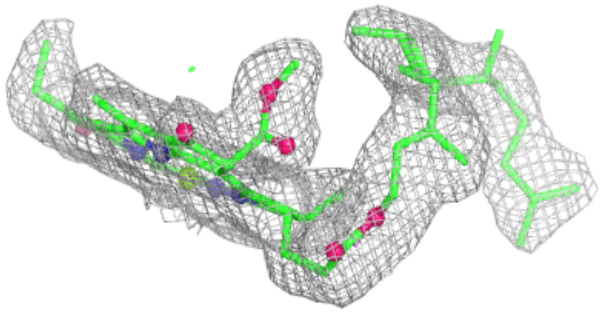


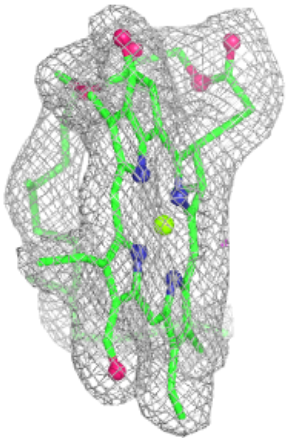


Electron density around CHL A 1001:

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

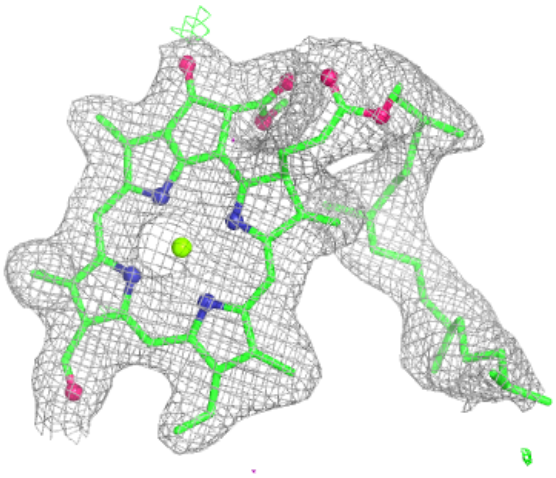


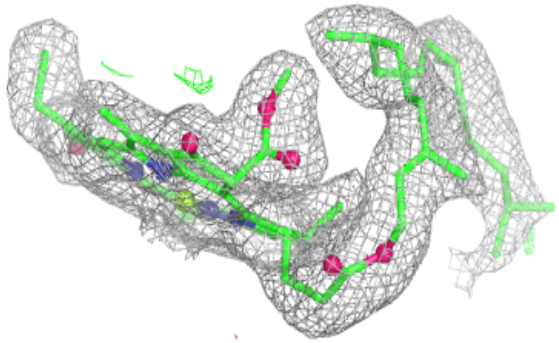


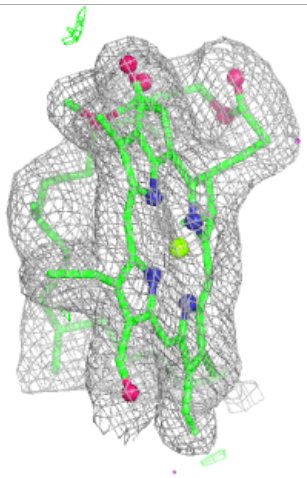


Electron density around CHL D 1001:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.