Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2023 – 02:30 AM EDT

PDB ID	:	2PT3
Title	:	Crystal structure of bovine lactoperoxidase at 2.34 A resolution reveals multiple anion binding sites
Authors	:	Singh, A.K.; Singh, N.; Sharma, S.; Kaur, P.; Betzel, C.; Singh, T.P.
Deposited on	:	2007-05-08
Resolution	:	2.34 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:

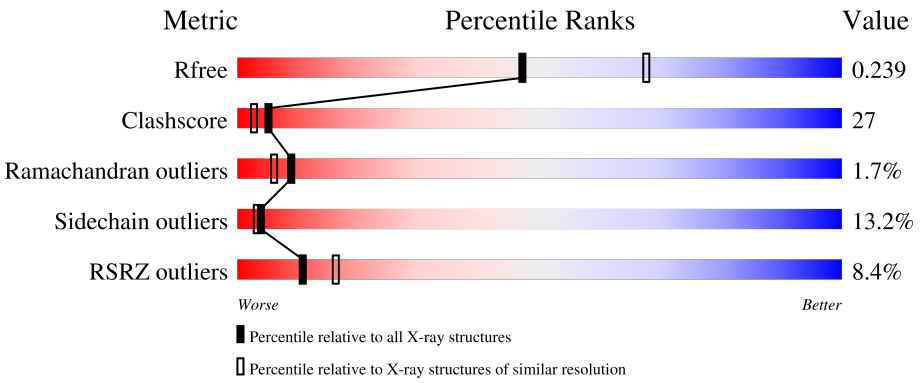
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.34 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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	595	8%; 54%; 37%; 8%; •
2	B	3	33%; 67%
2	D	3	67%; 33%
3	C	2	50%; 50%
3	E	2	100%

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	NAG	B	1	X	-	-	-
2	NAG	B	2	-	-	-	X
2	MAN	B	3	-	-	-	X
5	PO4	A	607	-	-	X	-
5	PO4	A	608	-	X	X	-
5	PO4	A	609	-	X	-	-
5	PO4	A	610	-	X	X	-
5	PO4	A	611	-	X	-	-
5	PO4	A	612	-	X	-	-
5	PO4	A	614	-	X	-	-
5	PO4	A	615	-	X	-	-
5	PO4	A	616	-	-	X	-
5	PO4	A	618	-	X	-	-
5	PO4	A	621	-	X	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5281 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.

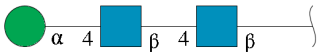
- Molecule 1 is a protein called Lactoperoxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	595	4774	3037	847	863	1	26	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	198	SEP	SER	modified residue	UNP P80025

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	3	39	22	2	15	0	0	0
2	D	3	39	22	2	15	0	0	0

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	2	28	16	2	10	0	0	0

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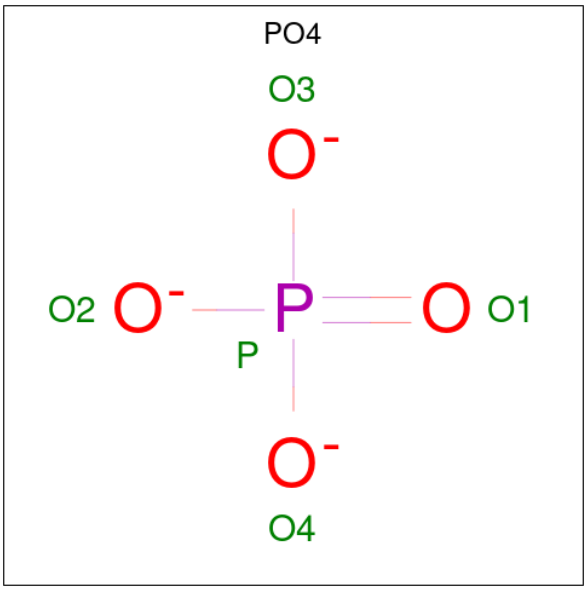
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	2	28	16	2	10	0	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
4	A	1	1	1	0	0

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
5	A	1	5	4	1	0	0
			Total	O	P		
5	A	1	5	4	1	0	0
			Total	O	P		
5	A	1	5	4	1	0	0
			Total	O	P		
5	A	1	5	4	1	0	0
			Total	O	P		
5	A	1	5	4	1	0	0
			Total	O	P		
5	A	1	5	4	1	0	0
			Total	O	P		
5	A	1	5	4	1	0	0

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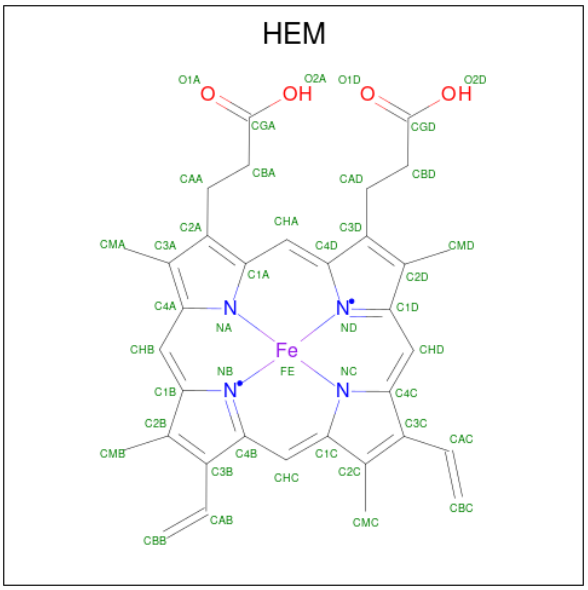
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	P			
5	A	1	5	4	1		0	0
			Total	O	P			
5	A	1	5	4	1		0	0
			Total	O	P			
5	A	1	5	4	1		0	0
			Total	O	P			
5	A	1	5	4	1		0	0
			Total	O	P			
5	A	1	5	4	1		0	0
			Total	O	P			
5	A	1	5	4	1		0	0
			Total	O	P			
5	A	1	5	4	1		0	0
			Total	O	P			
5	A	1	5	4	1		0	0
			Total	O	P			
5	A	1	5	4	1		0	0

- Molecule 6 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
6	A	1	43	34	1	4	4	0	0

- Molecule 7 is water.

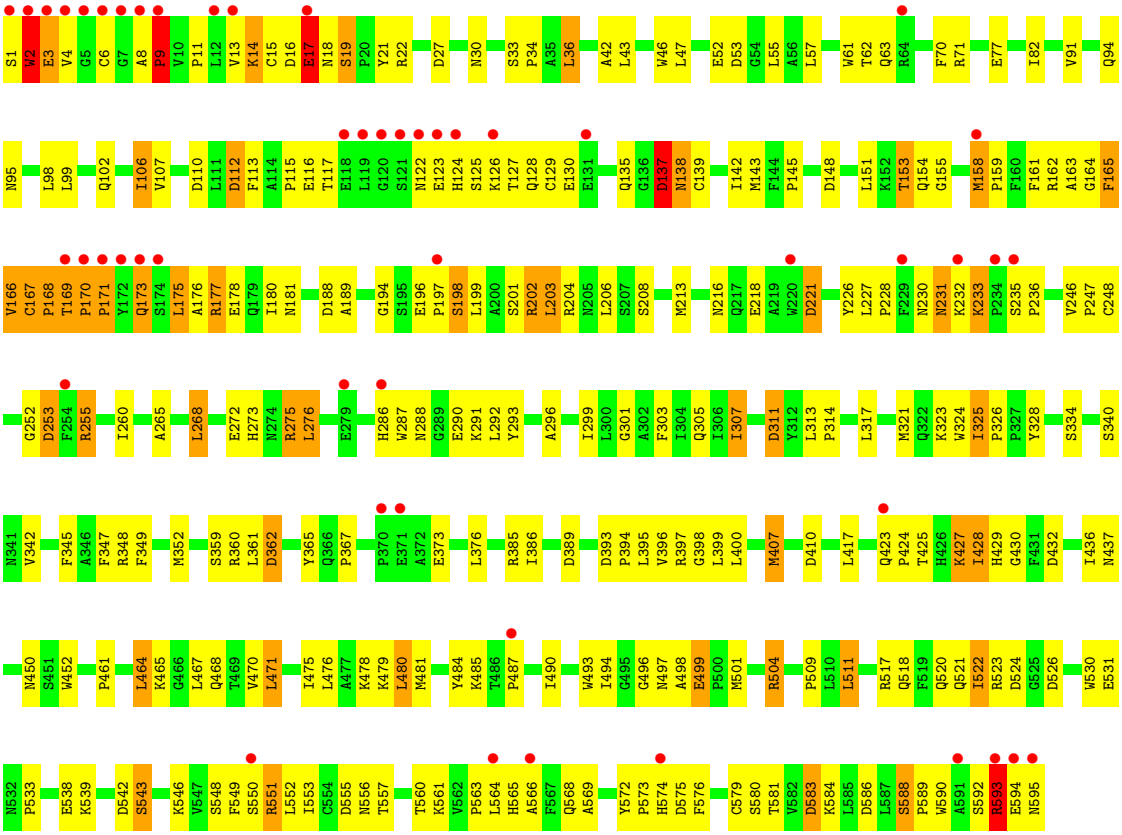
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	249	249	249	0	0

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: Lactoperoxidase

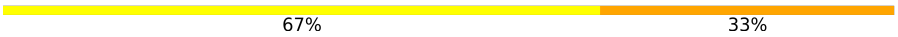
Chain A: 8% 54% 37% 8%



• Molecule 2: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 33% 67%

• Molecule 2: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D: 

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	53.91Å 80.05Å 75.67Å 90.00° 103.23° 90.00°	Depositor
Resolution (Å)	19.38 – 2.34 19.38 – 2.31	Depositor EDS
% Data completeness (in resolution range)	96.8 (19.38-2.34) 94.8 (19.38-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	1.08 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.231 , 0.247 0.236 , 0.239	Depositor DCC
R_{free} test set	834 reflections (3.20%)	wwPDB-VP
Wilson B-factor (Å^2)	49.6	Xtriage
Anisotropy	0.690	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 60.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5281	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% 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: MAN, SEP, HEM, CA, PO4, NAG

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	0.78	1/4891 (0.0%)	1.02	17/6634 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	158	MET	SD-CE	5.25	2.07	1.77

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	17	GLU	N-CA-C	-6.40	93.73	111.00
1	A	221	ASP	CB-CG-OD2	6.17	123.85	118.30
1	A	110	ASP	CB-CG-OD2	5.89	123.60	118.30
1	A	27	ASP	CB-CG-OD2	5.85	123.56	118.30
1	A	410	ASP	CB-CG-OD2	5.79	123.52	118.30
1	A	555	ASP	CB-CG-OD2	5.78	123.50	118.30
1	A	137	ASP	CB-CG-OD2	5.73	123.46	118.30
1	A	232	LYS	N-CA-CB	-5.67	100.39	110.60
1	A	253	ASP	CB-CG-OD2	5.51	123.26	118.30
1	A	575	ASP	CB-CG-OD2	5.44	123.20	118.30
1	A	311	ASP	CB-CG-OD2	5.34	123.11	118.30
1	A	542	ASP	CB-CG-OD2	5.32	123.09	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	15	CYS	CA-C-N	-5.31	105.51	117.20
1	A	362	ASP	CB-CG-OD2	5.19	122.97	118.30
1	A	53	ASP	CB-CG-OD2	5.14	122.93	118.30
1	A	14	LYS	CA-C-N	-5.07	106.05	117.20
1	A	169	THR	N-CA-C	-5.05	97.37	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	135	GLN	Peptide
1	A	231	ASN	Peptide
1	A	233	LYS	Peptide

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	4774	0	4687	257	0
2	B	39	0	34	6	0
2	D	39	0	34	1	0
3	C	28	0	25	0	0
3	E	28	0	25	2	0
4	A	1	0	0	0	0
5	A	80	0	0	17	0
6	A	43	0	30	7	0
7	A	249	0	0	19	0
All	All	5281	0	4835	265	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 27.

All (265) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:MET:CE	1:A:158:MET:SD	2.07	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:LYS:HB3	7:A:701:HOH:O	1.36	1.20
1:A:169:THR:HG22	1:A:170:PRO:HD3	1.34	1.06
1:A:561:LYS:HG3	7:A:638:HOH:O	1.57	1.04
1:A:504:ARG:HG2	1:A:504:ARG:HH11	1.19	1.03
1:A:504:ARG:HH11	1:A:504:ARG:CG	1.72	0.99
1:A:538:GLU:HB3	7:A:688:HOH:O	1.65	0.96
1:A:504:ARG:HH21	2:B:1:NAG:H2	1.30	0.95
1:A:196:GLU:HB3	1:A:198:SEP:O3P	1.67	0.94
1:A:311:ASP:HB3	5:A:621:PO4:O2	1.66	0.94
1:A:424:PRO:C	1:A:425:THR:HG23	1.89	0.92
2:D:2:NAG:H2	2:D:2:NAG:H61	1.52	0.91
1:A:42:ALA:HB2	1:A:166:VAL:HG21	1.52	0.91
1:A:359:SER:HB3	5:A:616:PO4:O4	1.72	0.90
1:A:167:CYS:HB3	1:A:168:PRO:HD2	1.53	0.90
1:A:14:LYS:HE3	1:A:14:LYS:HA	1.55	0.89
1:A:82:ILE:CD1	1:A:480:LEU:HD13	2.03	0.87
1:A:424:PRO:O	1:A:425:THR:HG23	1.74	0.87
1:A:125:SER:HA	1:A:128:GLN:HB3	1.57	0.86
1:A:153:THR:HG22	1:A:154:GLN:HG3	1.55	0.86
1:A:504:ARG:NH2	2:B:1:NAG:H2	1.89	0.86
1:A:8:ALA:HB3	1:A:9:PRO:HD3	1.58	0.84
1:A:504:ARG:HG2	1:A:504:ARG:NH1	1.82	0.84
1:A:117:THR:CG2	1:A:164:GLY:HA2	2.07	0.84
1:A:481:MET:SD	1:A:487:PRO:HD3	2.18	0.83
1:A:352:MET:SD	1:A:407:MET:SD	2.77	0.82
1:A:16:ASP:HB3	1:A:19:SER:HB2	1.61	0.82
1:A:504:ARG:CZ	5:A:610:PO4:O4	2.29	0.80
1:A:117:THR:HG22	1:A:164:GLY:HA2	1.62	0.79
1:A:113:PHE:O	1:A:115:PRO:HD3	1.82	0.79
1:A:549:PHE:HD2	1:A:549:PHE:O	1.67	0.78
1:A:342:VAL:HB	5:A:608:PO4:O2	1.84	0.77
5:A:607:PO4:O1	6:A:623:HEM:C4A	2.38	0.77
1:A:548:SER:OG	1:A:551:ARG:HB2	1.85	0.76
1:A:14:LYS:CD	7:A:698:HOH:O	2.33	0.76
1:A:467:LEU:HG	1:A:471:LEU:HD22	1.67	0.75
1:A:407:MET:HB3	1:A:501:MET:CE	2.17	0.75
1:A:373:GLU:HB2	5:A:616:PO4:O3	1.86	0.74
1:A:106:ILE:HD11	1:A:265:ALA:CB	2.17	0.74
1:A:530:TRP:CE2	1:A:531:GLU:HG3	2.22	0.74
1:A:169:THR:HG22	1:A:170:PRO:CD	2.14	0.73
1:A:167:CYS:HB3	1:A:168:PRO:CD	2.18	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:ARG:HH11	1:A:275:ARG:HB3	1.55	0.71
1:A:202:ARG:HH12	1:A:231:ASN:HB2	1.55	0.71
1:A:423:GLN:HE21	1:A:423:GLN:HA	1.56	0.71
1:A:14:LYS:HD3	7:A:698:HOH:O	1.90	0.70
1:A:175:LEU:HD22	1:A:176:ALA:H	1.56	0.70
1:A:427:LYS:O	1:A:428:ILE:HG23	1.91	0.70
1:A:428:ILE:O	1:A:430:GLY:N	2.25	0.70
1:A:158:MET:CE	1:A:432:ASP:H	2.05	0.70
1:A:530:TRP:CZ2	1:A:531:GLU:HG3	2.27	0.69
1:A:303:PHE:CE1	1:A:307:ILE:HD13	2.26	0.69
1:A:400:LEU:HD22	1:A:563:PRO:HG2	1.74	0.69
1:A:549:PHE:O	1:A:549:PHE:CD2	2.47	0.68
1:A:166:VAL:HG13	1:A:180:ILE:HG12	1.75	0.68
1:A:504:ARG:HD2	2:B:2:NAG:H62	1.76	0.68
1:A:8:ALA:HB3	1:A:9:PRO:CD	2.24	0.68
1:A:572:TYR:CG	1:A:573:PRO:HA	2.29	0.67
1:A:176:ALA:HB3	7:A:651:HOH:O	1.93	0.67
1:A:14:LYS:HD2	7:A:698:HOH:O	1.94	0.67
1:A:2:TRP:CE3	1:A:2:TRP:HA	2.30	0.67
1:A:106:ILE:HD11	1:A:265:ALA:HB1	1.76	0.67
1:A:199:LEU:O	1:A:203:LEU:HD22	1.94	0.67
1:A:325:ILE:N	1:A:325:ILE:HD12	2.11	0.66
1:A:2:TRP:HA	1:A:2:TRP:HE3	1.61	0.66
1:A:423:GLN:HA	1:A:423:GLN:NE2	2.10	0.66
1:A:531:GLU:O	1:A:533:PRO:HD3	1.96	0.65
1:A:16:ASP:CB	1:A:19:SER:HB2	2.27	0.65
1:A:77:GLU:HB2	1:A:145:PRO:HG3	1.79	0.64
1:A:493:TRP:O	1:A:497:ASN:ND2	2.28	0.64
1:A:117:THR:HG23	1:A:164:GLY:HA2	1.79	0.63
1:A:539:LYS:HB3	1:A:589:PRO:HB3	1.79	0.63
1:A:594:GLU:O	1:A:594:GLU:HG3	1.98	0.63
1:A:130:GLU:HA	1:A:159:PRO:HG3	1.82	0.62
1:A:324:TRP:C	1:A:325:ILE:HD12	2.20	0.62
1:A:123:GLU:O	1:A:126:LYS:HB3	1.99	0.62
1:A:484:TYR:O	1:A:485:LYS:HB2	1.99	0.61
1:A:288:ASN:O	1:A:292:LEU:HD23	2.00	0.61
1:A:360:ARG:NH1	1:A:389:ASP:OD2	2.26	0.61
1:A:167:CYS:CB	1:A:168:PRO:HD2	2.30	0.61
1:A:424:PRO:C	1:A:425:THR:CG2	2.62	0.61
1:A:253:ASP:OD1	1:A:255:ARG:NH1	2.34	0.61
1:A:14:LYS:HA	1:A:14:LYS:CE	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:MET:CB	1:A:501:MET:CE	2.79	0.60
3:E:1:NAG:H61	3:E:2:NAG:O7	2.02	0.59
1:A:113:PHE:C	1:A:115:PRO:HD3	2.23	0.59
1:A:95:ASN:ND2	2:B:1:NAG:C7	2.64	0.59
1:A:145:PRO:HG2	5:A:609:PO4:O2	2.02	0.59
1:A:499:GLU:OE1	1:A:509:PRO:HD2	2.02	0.59
1:A:275:ARG:HB3	1:A:275:ARG:NH1	2.18	0.59
1:A:194:GLY:HA2	1:A:252:GLY:O	2.03	0.58
1:A:504:ARG:HH21	2:B:1:NAG:C2	2.11	0.58
1:A:432:ASP:O	1:A:436:ILE:HG13	2.03	0.58
1:A:204:ARG:HG2	1:A:213:MET:CE	2.33	0.58
1:A:137:ASP:C	1:A:139:CYS:H	2.07	0.58
1:A:169:THR:HB	1:A:170:PRO:HD2	1.84	0.58
1:A:70:PHE:CD2	1:A:485:LYS:HG3	2.39	0.57
6:A:623:HEM:HBC2	6:A:623:HEM:CMC	2.35	0.57
1:A:393:ASP:OD1	1:A:557:THR:HB	2.04	0.57
1:A:46:TRP:HB2	5:A:608:PO4:O4	2.05	0.57
1:A:151:LEU:HD23	1:A:155:GLY:O	2.05	0.57
1:A:169:THR:CG2	1:A:170:PRO:HD3	2.22	0.57
1:A:204:ARG:HG2	1:A:213:MET:HE2	1.86	0.57
1:A:165:PHE:HB3	1:A:177:ARG:HD2	1.85	0.56
1:A:359:SER:CB	5:A:616:PO4:O4	2.49	0.56
1:A:461:PRO:HG3	1:A:470:VAL:HG21	1.87	0.56
1:A:572:TYR:CD1	1:A:573:PRO:HA	2.40	0.56
1:A:188:ASP:O	1:A:189:ALA:HB3	2.05	0.56
1:A:407:MET:HB3	1:A:501:MET:HE2	1.87	0.56
1:A:496:GLY:O	1:A:511:LEU:HD22	2.06	0.56
1:A:560:THR:HA	1:A:579:CYS:SG	2.46	0.56
3:E:1:NAG:H61	3:E:2:NAG:C7	2.36	0.56
1:A:348:ARG:NH2	6:A:623:HEM:HAD1	2.21	0.55
1:A:475:ILE:HG22	1:A:479:LYS:HE3	1.89	0.55
1:A:287:TRP:CZ2	1:A:592:SER:HB2	2.41	0.55
1:A:588:SER:N	1:A:589:PRO:CD	2.69	0.55
1:A:167:CYS:CB	1:A:168:PRO:CD	2.84	0.54
1:A:367:PRO:HG3	5:A:616:PO4:O1	2.07	0.54
1:A:106:ILE:HD11	1:A:265:ALA:HB3	1.88	0.53
1:A:268:LEU:HB3	1:A:552:LEU:HD21	1.89	0.53
6:A:623:HEM:HBC2	6:A:623:HEM:HMC1	1.90	0.53
1:A:158:MET:HE1	1:A:432:ASP:H	1.73	0.53
1:A:165:PHE:CB	1:A:177:ARG:HD2	2.39	0.53
1:A:565:HIS:O	1:A:568:GLN:HG2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:ARG:NH1	1:A:231:ASN:HB2	2.23	0.53
1:A:407:MET:HB3	1:A:501:MET:HE3	1.90	0.53
1:A:165:PHE:CG	1:A:177:ARG:HD2	2.44	0.53
1:A:248:CYS:HB2	7:A:628:HOH:O	2.08	0.53
1:A:253:ASP:OD2	1:A:255:ARG:HD3	2.09	0.53
1:A:325:ILE:HG22	7:A:647:HOH:O	2.08	0.53
1:A:321:MET:HB3	7:A:694:HOH:O	2.08	0.53
1:A:324:TRP:C	1:A:326:PRO:HD3	2.30	0.52
1:A:106:ILE:HG22	1:A:107:VAL:N	2.24	0.52
1:A:169:THR:CB	1:A:170:PRO:CD	2.88	0.52
1:A:345:PHE:O	1:A:348:ARG:HB2	2.09	0.52
1:A:504:ARG:HH11	1:A:504:ARG:HG3	1.70	0.52
1:A:299:ILE:HD11	1:A:590:TRP:CE2	2.44	0.52
1:A:170:PRO:HB3	1:A:171:PRO:HD2	1.91	0.52
2:B:2:NAG:O7	2:B:2:NAG:H3	2.09	0.52
1:A:303:PHE:CZ	1:A:307:ILE:HD13	2.44	0.51
1:A:82:ILE:CD1	1:A:480:LEU:CD1	2.84	0.51
1:A:286:HIS:CE1	1:A:592:SER:HB3	2.46	0.51
1:A:361:LEU:O	1:A:397:ARG:HD2	2.11	0.50
1:A:82:ILE:HD13	1:A:480:LEU:HD13	1.93	0.50
1:A:450:ASN:HD21	1:A:487:PRO:HB2	1.75	0.50
1:A:17:GLU:HG2	1:A:18:ASN:N	2.26	0.50
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.46	0.50
1:A:362:ASP:C	1:A:362:ASP:OD1	2.50	0.50
1:A:518:GLN:O	1:A:522:ILE:HG23	2.12	0.50
1:A:142:ILE:HG23	7:A:803:HOH:O	2.11	0.50
1:A:365:TYR:CE1	1:A:576:PHE:CE2	3.00	0.50
1:A:407:MET:HG2	7:A:675:HOH:O	2.11	0.50
1:A:584:LYS:HE3	5:A:620:PO4:O4	2.12	0.49
1:A:106:ILE:CD1	1:A:265:ALA:HB1	2.41	0.49
1:A:158:MET:HE3	1:A:432:ASP:H	1.77	0.49
1:A:476:LEU:HD21	1:A:498:ALA:HB1	1.95	0.49
1:A:125:SER:HA	1:A:128:GLN:CB	2.35	0.49
1:A:16:ASP:CG	1:A:19:SER:HB2	2.32	0.49
1:A:400:LEU:HD11	1:A:553:ILE:HD13	1.95	0.49
1:A:169:THR:CG2	1:A:170:PRO:CD	2.85	0.49
1:A:286:HIS:HE1	1:A:592:SER:HB3	1.78	0.48
1:A:396:VAL:O	1:A:396:VAL:HG12	2.12	0.48
1:A:272:GLU:HG3	1:A:276:LEU:HD22	1.95	0.48
1:A:539:LYS:CB	1:A:589:PRO:HB3	2.43	0.48
1:A:393:ASP:HB2	1:A:394:PRO:HD3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:ILE:N	1:A:325:ILE:CD1	2.76	0.48
1:A:574:HIS:C	1:A:574:HIS:CD2	2.85	0.48
1:A:424:PRO:O	1:A:425:THR:CG2	2.52	0.48
1:A:70:PHE:CD2	1:A:485:LYS:HB3	2.49	0.48
1:A:129:CYS:CB	1:A:161:PHE:HE2	2.26	0.48
1:A:188:ASP:HA	7:A:676:HOH:O	2.14	0.48
1:A:230:ASN:OD1	1:A:231:ASN:N	2.37	0.48
1:A:572:TYR:HD1	1:A:576:PHE:CG	2.32	0.48
1:A:102:GLN:HE21	1:A:106:ILE:HD12	1.79	0.48
1:A:99:LEU:HD21	1:A:549:PHE:CE2	2.49	0.47
1:A:199:LEU:HD11	1:A:203:LEU:HD21	1.95	0.47
1:A:360:ARG:HG2	1:A:395:LEU:HD23	1.95	0.47
1:A:552:LEU:O	1:A:556:ASN:HB2	2.13	0.47
1:A:272:GLU:O	1:A:276:LEU:HB2	2.14	0.47
1:A:543:SER:OG	1:A:586:ASP:O	2.26	0.47
1:A:213:MET:CE	1:A:293:TYR:HE1	2.28	0.46
1:A:464:LEU:C	1:A:464:LEU:CD2	2.84	0.46
1:A:137:ASP:HB3	1:A:138:ASN:H	1.50	0.46
1:A:563:PRO:HD3	1:A:576:PHE:CE2	2.50	0.46
1:A:43:LEU:HG	1:A:181:ASN:HB2	1.97	0.46
1:A:197:PRO:O	1:A:198:SEP:C	2.64	0.45
1:A:8:ALA:CB	1:A:9:PRO:CD	2.91	0.45
1:A:169:THR:CB	1:A:170:PRO:HD2	2.43	0.45
1:A:303:PHE:CE1	1:A:307:ILE:CD1	2.99	0.45
1:A:417:LEU:HD21	6:A:623:HEM:HMB3	1.98	0.45
1:A:57:LEU:HD12	1:A:57:LEU:HA	1.84	0.45
1:A:112:ASP:O	1:A:255:ARG:NH2	2.43	0.45
1:A:17:GLU:HA	7:A:857:HOH:O	2.17	0.45
1:A:175:LEU:HD22	1:A:176:ALA:N	2.29	0.45
1:A:348:ARG:HH11	1:A:437:ASN:HD22	1.63	0.45
1:A:417:LEU:CD2	6:A:623:HEM:HMB3	2.46	0.45
1:A:481:MET:SD	1:A:487:PRO:CD	3.01	0.45
5:A:607:PO4:O1	6:A:623:HEM:CHB	2.65	0.45
1:A:476:LEU:O	1:A:480:LEU:HB2	2.17	0.45
1:A:504:ARG:NE	5:A:610:PO4:O4	2.49	0.45
1:A:452:TRP:HH2	5:A:608:PO4:O4	1.98	0.45
1:A:313:LEU:N	1:A:314:PRO:CD	2.80	0.44
1:A:227:LEU:HD23	7:A:806:HOH:O	2.18	0.44
1:A:566:ALA:N	5:A:621:PO4:O4	2.50	0.44
1:A:129:CYS:CB	1:A:161:PHE:CE2	3.00	0.44
1:A:236:PRO:HD2	1:A:248:CYS:SG	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:LEU:HD12	1:A:480:LEU:HA	1.50	0.44
1:A:82:ILE:HD11	1:A:480:LEU:HD13	1.94	0.44
1:A:166:VAL:O	1:A:167:CYS:HB2	2.17	0.44
1:A:162:ARG:CZ	1:A:177:ARG:NH2	2.80	0.44
1:A:230:ASN:HB3	7:A:628:HOH:O	2.17	0.44
1:A:484:TYR:CD1	1:A:490:ILE:HA	2.53	0.44
1:A:325:ILE:O	7:A:647:HOH:O	2.21	0.43
1:A:546:LYS:HE3	1:A:583:ASP:HB3	2.00	0.43
1:A:564:LEU:HD12	1:A:564:LEU:HA	1.87	0.43
1:A:574:HIS:HD2	1:A:574:HIS:O	2.02	0.43
1:A:173:GLN:HG2	1:A:173:GLN:O	2.19	0.43
1:A:349:PHE:CD1	1:A:349:PHE:C	2.92	0.43
1:A:398:GLY:HA3	7:A:631:HOH:O	2.19	0.43
1:A:52:GLU:OE1	1:A:62:THR:OG1	2.28	0.43
1:A:70:PHE:CE2	1:A:485:LYS:HB3	2.54	0.43
1:A:82:ILE:HD12	1:A:480:LEU:CD1	2.49	0.42
1:A:273:HIS:CE1	1:A:296:ALA:HB3	2.54	0.42
1:A:129:CYS:SG	1:A:161:PHE:CE2	3.12	0.42
1:A:235:SER:HA	1:A:236:PRO:HD3	1.83	0.42
1:A:46:TRP:CE2	1:A:340:SER:HB3	2.54	0.42
1:A:22:ARG:NH2	1:A:526:ASP:OD2	2.34	0.42
1:A:94:GLN:O	1:A:569:ALA:CB	2.67	0.42
1:A:137:ASP:C	1:A:139:CYS:N	2.70	0.42
1:A:57:LEU:HG	1:A:61:TRP:CD1	2.54	0.42
1:A:246:VAL:HA	1:A:247:PRO:HD3	1.91	0.42
1:A:522:ILE:HD12	7:A:684:HOH:O	2.20	0.42
1:A:70:PHE:CD2	1:A:485:LYS:CB	3.03	0.42
1:A:517:ARG:O	1:A:521:GLN:HG3	2.20	0.42
1:A:572:TYR:CD1	1:A:576:PHE:HB2	2.54	0.42
1:A:202:ARG:NH2	5:A:611:PO4:O1	2.50	0.42
1:A:99:LEU:HD21	1:A:549:PHE:CD2	2.55	0.42
1:A:216:ASN:HB2	1:A:228:PRO:HA	2.01	0.41
1:A:287:TRP:CG	1:A:291:LYS:HG2	2.55	0.41
1:A:301:GLY:O	1:A:305:GLN:HG3	2.20	0.41
1:A:593:ARG:NE	5:A:622:PO4:O3	2.53	0.41
1:A:328:TYR:CD1	1:A:523:ARG:HD3	2.54	0.41
1:A:348:ARG:HH11	1:A:437:ASN:ND2	2.18	0.41
1:A:464:LEU:O	1:A:468:GLN:HG3	2.20	0.41
1:A:385:ARG:O	1:A:389:ASP:HB3	2.20	0.41
1:A:396:VAL:HA	1:A:399:LEU:HD12	2.02	0.41
1:A:124:HIS:O	1:A:128:GLN:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:ILE:HD11	1:A:386:ILE:HG13	2.02	0.41
1:A:393:ASP:CB	1:A:394:PRO:HD3	2.50	0.41
1:A:213:MET:CE	1:A:293:TYR:CE1	3.04	0.41
1:A:436:ILE:HG21	1:A:436:ILE:HD13	1.78	0.41
1:A:33:SER:HB3	1:A:36:LEU:HD22	2.02	0.41
1:A:360:ARG:HG2	1:A:395:LEU:CD2	2.51	0.41
1:A:213:MET:HE1	1:A:293:TYR:HE1	1.85	0.41
1:A:292:LEU:HD13	1:A:292:LEU:HA	1.89	0.41
1:A:520:GLN:NE2	1:A:524:ASP:OD2	2.44	0.41
1:A:137:ASP:O	1:A:139:CYS:N	2.53	0.41
1:A:148:ASP:O	1:A:151:LEU:HB2	2.20	0.41
1:A:581:THR:O	1:A:581:THR:HG22	2.21	0.41
1:A:30:ASN:O	1:A:34:PRO:HA	2.22	0.40
1:A:348:ARG:HD3	1:A:437:ASN:ND2	2.36	0.40
1:A:19:SER:HB3	1:A:21:TYR:O	2.22	0.40
1:A:116:GLU:HA	1:A:163:ALA:HA	2.02	0.40
1:A:178:GLU:HA	1:A:178:GLU:OE1	2.22	0.40
1:A:501:MET:H	1:A:501:MET:HG3	1.78	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	592/595 (100%)	539 (91%)	43 (7%)	10 (2%)	9 6

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	CYS
1	A	593	ARG
1	A	2	TRP

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Mol	Chain	Res	Type
1	A	3	GLU
1	A	138	ASN
1	A	429	HIS
1	A	170	PRO
1	A	427	LYS
1	A	428	ILE
1	A	9	PRO

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	517/517 (100%)	449 (87%)	68 (13%)	4 3

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	SER
1	A	2	TRP
1	A	3	GLU
1	A	4	VAL
1	A	6	CYS
1	A	9	PRO
1	A	11	PRO
1	A	13	VAL
1	A	17	GLU
1	A	19	SER
1	A	36	LEU
1	A	47	LEU
1	A	55	LEU
1	A	63	GLN
1	A	71	ARG
1	A	91	VAL
1	A	98	LEU
1	A	106	ILE
1	A	112	ASP

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Mol	Chain	Res	Type
1	A	122	ASN
1	A	127	THR
1	A	137	ASP
1	A	143	MET
1	A	153	THR
1	A	165	PHE
1	A	166	VAL
1	A	168	PRO
1	A	171	PRO
1	A	173	GLN
1	A	175	LEU
1	A	177	ARG
1	A	201	SER
1	A	202	ARG
1	A	203	LEU
1	A	206	LEU
1	A	208	SER
1	A	218	GLU
1	A	233	LYS
1	A	255	ARG
1	A	268	LEU
1	A	275	ARG
1	A	276	LEU
1	A	290	GLU
1	A	307	ILE
1	A	317	LEU
1	A	323	LYS
1	A	325	ILE
1	A	334	SER
1	A	347	PHE
1	A	376	LEU
1	A	407	MET
1	A	464	LEU
1	A	465	LYS
1	A	471	LEU
1	A	480	LEU
1	A	494	ILE
1	A	499	GLU
1	A	504	ARG
1	A	511	LEU
1	A	522	ILE
1	A	543	SER

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Mol	Chain	Res	Type
1	A	550	SER
1	A	551	ARG
1	A	580	SER
1	A	583	ASP
1	A	588	SER
1	A	593	ARG
1	A	595	ASN

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	173	GLN
1	A	288	ASN
1	A	333	ASN
1	A	364	ASN
1	A	366	GLN
1	A	423	GLN
1	A	429	HIS
1	A	437	ASN
1	A	468	GLN
1	A	521	GLN
1	A	574	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
1	SEP	A	198	1	8,9,10	1.46	1 (12%)	8,12,14	3.32	5 (62%)

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
1	SEP	A	198	1	-	1/5/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	CA-N	-2.69	1.40	1.48

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	198	SEP	OG-P-O1P	6.02	123.37	106.47
1	A	198	SEP	O2P-P-OG	4.04	117.47	106.73
1	A	198	SEP	OG-CB-CA	-3.51	104.73	108.14
1	A	198	SEP	O3P-P-O1P	-3.29	97.81	110.68
1	A	198	SEP	P-OG-CB	2.68	125.69	118.30

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	198	SEP	N-CA-CB-OG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	198	SEP	2	0

5.5 Carbohydrates (i)

10 monosaccharides 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	NAG	B	1	1,2	14,14,15	0.74	0	17,19,21	2.13	6 (35%)
2	NAG	B	2	2	14,14,15	0.74	1 (7%)	17,19,21	1.70	5 (29%)
2	MAN	B	3	2	11,11,12	0.80	0	15,15,17	1.52	4 (26%)
3	NAG	C	1	3,1	14,14,15	0.57	0	17,19,21	2.30	3 (17%)
3	NAG	C	2	3	14,14,15	0.64	0	17,19,21	0.97	0
2	NAG	D	1	1,2	14,14,15	0.74	0	17,19,21	1.62	2 (11%)
2	NAG	D	2	2	14,14,15	0.76	1 (7%)	17,19,21	1.23	1 (5%)
2	MAN	D	3	2	11,11,12	0.63	0	15,15,17	1.96	3 (20%)
3	NAG	E	1	3,1	14,14,15	0.72	1 (7%)	17,19,21	1.24	1 (5%)
3	NAG	E	2	3	14,14,15	0.60	0	17,19,21	1.10	1 (5%)

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	NAG	B	1	1,2	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
2	MAN	B	3	2	-	2/2/19/22	1/1/1/1
3	NAG	C	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	MAN	D	3	2	-	2/2/19/22	0/1/1/1
3	NAG	E	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	NAG	O5-C1	-2.38	1.39	1.43
2	B	2	NAG	O5-C1	-2.18	1.40	1.43
3	E	1	NAG	O5-C1	-2.16	1.40	1.43

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	1	NAG	C1-O5-C5	7.72	122.65	112.19
2	B	1	NAG	C1-O5-C5	5.53	119.68	112.19
2	D	3	MAN	C1-C2-C3	5.20	116.06	109.67
2	D	1	NAG	O5-C1-C2	-4.17	104.71	111.29
2	D	1	NAG	C2-N2-C7	-3.75	117.56	122.90
2	D	3	MAN	O5-C1-C2	3.61	116.34	110.77
2	D	3	MAN	C1-O5-C5	3.58	117.05	112.19
2	B	1	NAG	O5-C5-C6	3.42	112.56	107.20
2	B	3	MAN	O3-C3-C2	3.37	116.45	109.99
2	D	2	NAG	C1-O5-C5	3.36	116.75	112.19
3	E	1	NAG	O5-C1-C2	-3.29	106.10	111.29
2	B	2	NAG	C3-C4-C5	3.26	116.06	110.24
3	C	1	NAG	C6-C5-C4	-3.21	105.50	113.00
2	B	2	NAG	C2-N2-C7	3.10	127.32	122.90
2	B	2	NAG	C4-C3-C2	3.00	115.41	111.02
3	C	1	NAG	O5-C5-C4	2.97	118.06	110.83
2	B	3	MAN	O5-C5-C6	2.83	111.64	107.20
2	B	1	NAG	O5-C5-C4	2.66	117.30	110.83
2	B	1	NAG	O5-C1-C2	2.59	115.37	111.29
3	E	2	NAG	C4-C3-C2	2.52	114.72	111.02
2	B	2	NAG	O7-C7-C8	-2.22	117.94	122.06
2	B	2	NAG	O7-C7-N2	2.15	125.90	121.95
2	B	1	NAG	O4-C4-C5	-2.13	104.00	109.30
2	B	3	MAN	C2-C3-C4	-2.12	107.23	110.89
2	B	1	NAG	O3-C3-C4	2.09	115.19	110.35
2	B	3	MAN	O2-C2-C3	2.07	114.29	110.14

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	1	NAG	C1

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C3-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
3	E	1	NAG	O5-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
2	D	3	MAN	O5-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
2	B	3	MAN	O5-C5-C6-O6
2	B	1	NAG	C4-C5-C6-O6
2	D	3	MAN	C4-C5-C6-O6
2	B	3	MAN	C4-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
2	B	2	NAG	C1-C2-N2-C7

All (1) ring outliers are listed below:

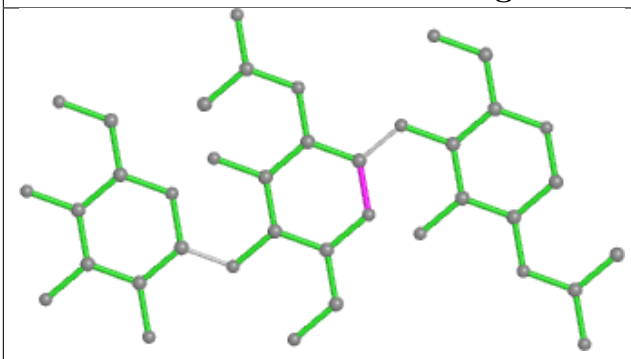
Mol	Chain	Res	Type	Atoms
2	B	3	MAN	C1-C2-C3-C4-C5-O5

5 monomers are involved in 9 short contacts:

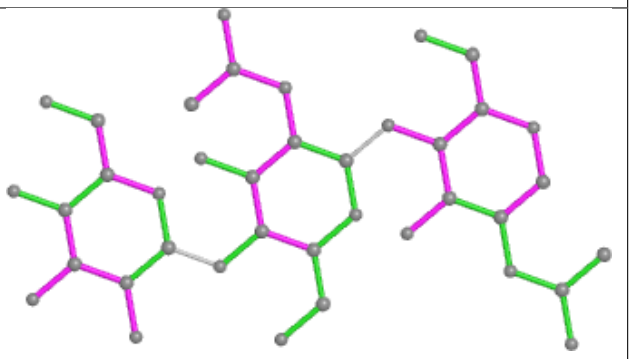
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2	NAG	1	0
3	E	2	NAG	2	0
3	E	1	NAG	2	0
2	B	2	NAG	2	0
2	B	1	NAG	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

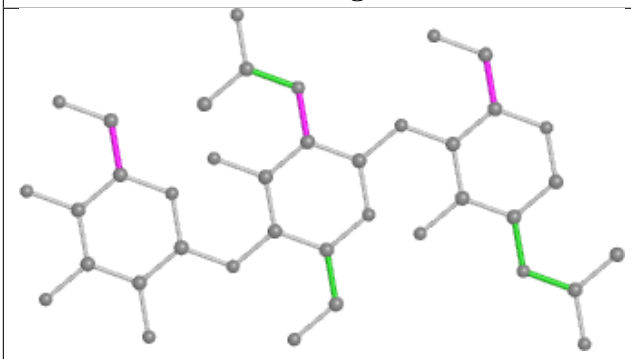
Oligosaccharide Chain B



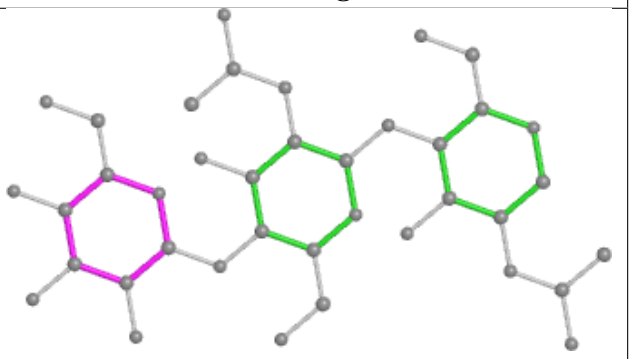
Bond lengths



Bond angles

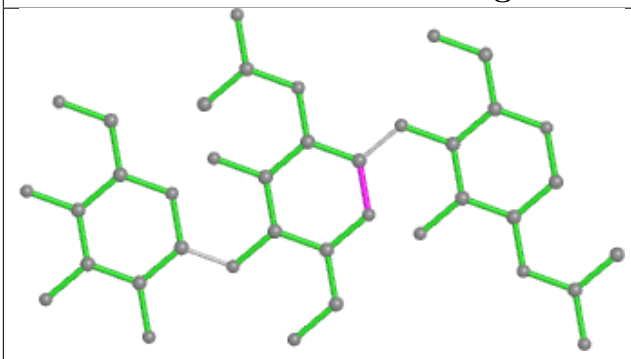


Torsions

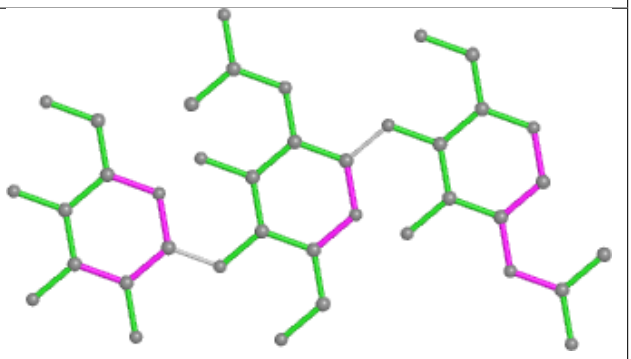


Rings

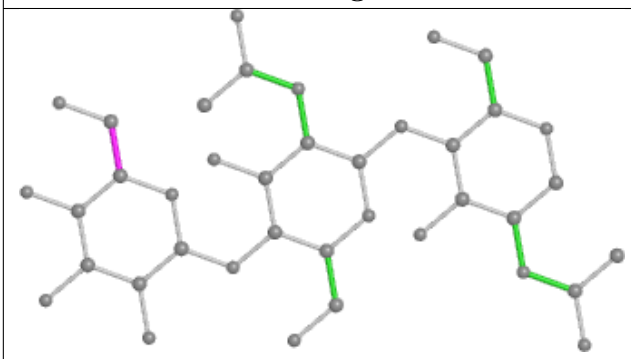
Oligosaccharide Chain D



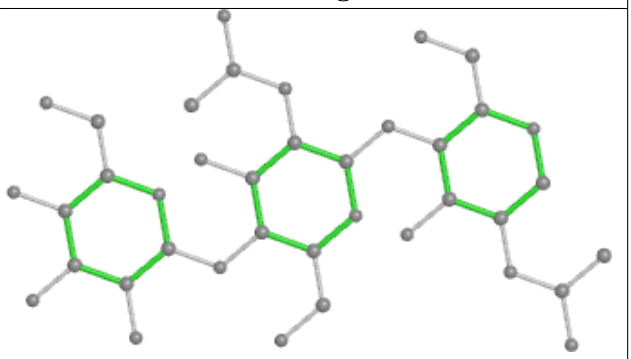
Bond lengths



Bond angles

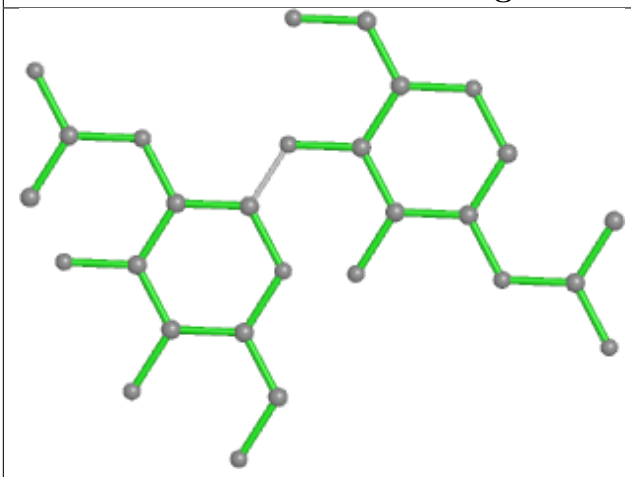


Torsions

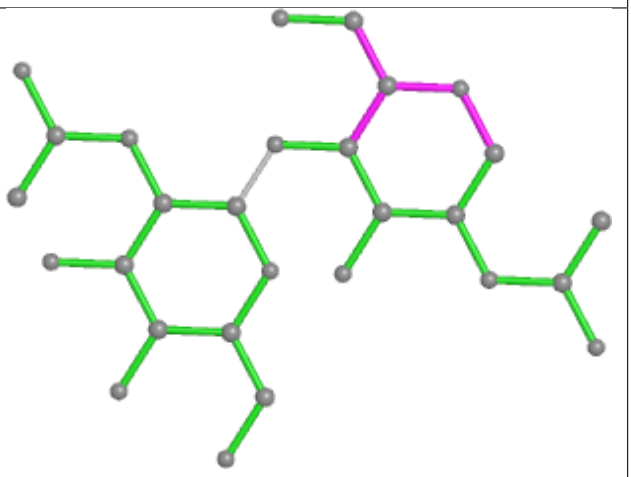


Rings

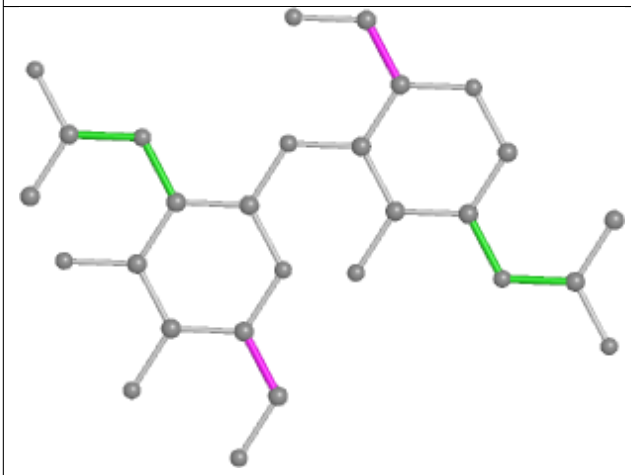
Oligosaccharide Chain C



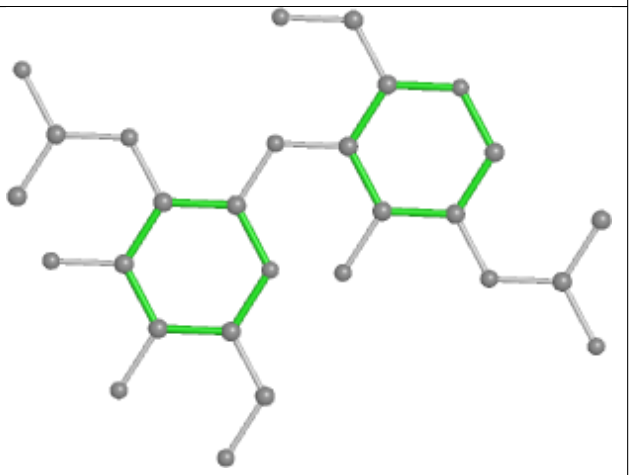
Bond lengths



Bond angles

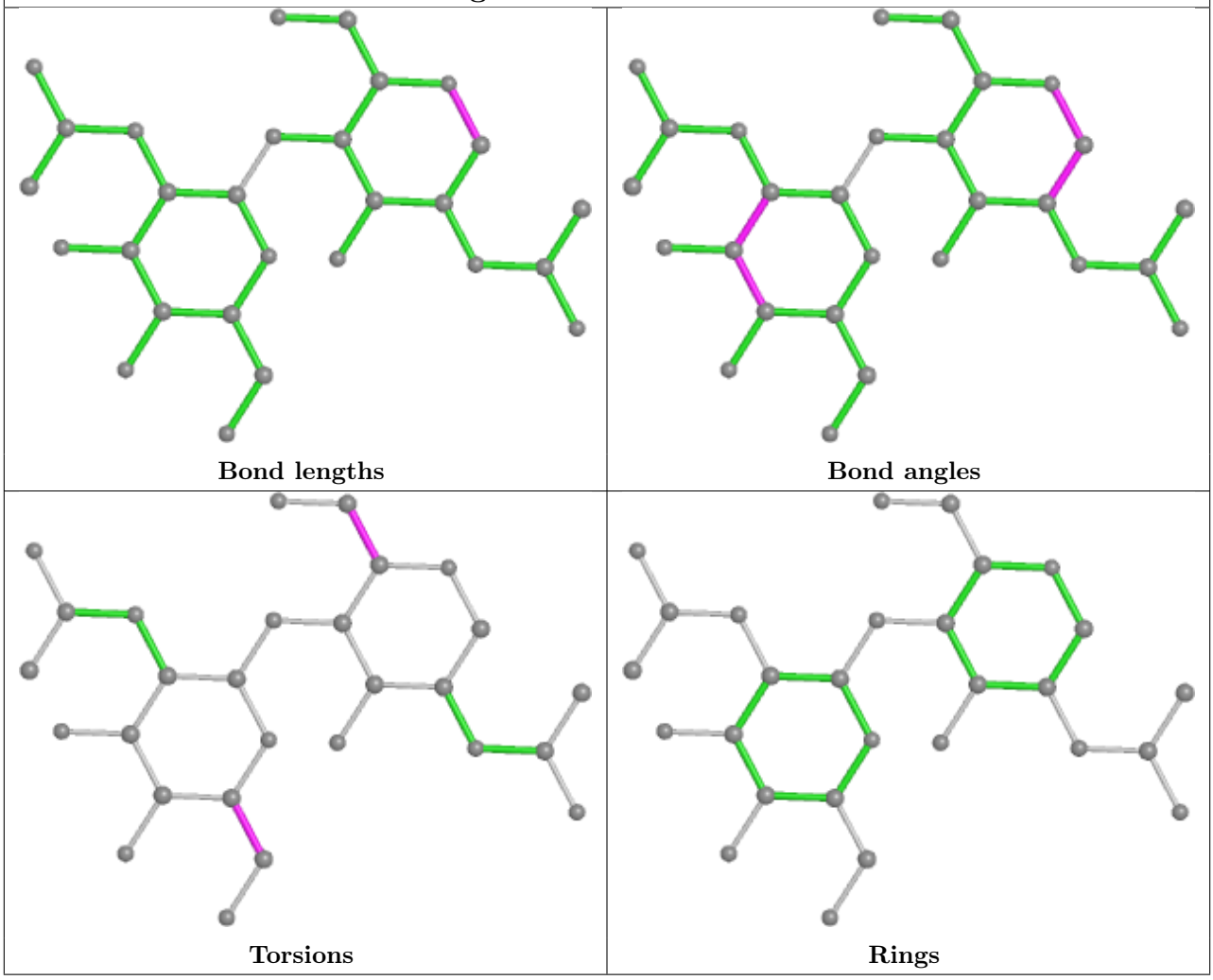


Torsions



Rings

Oligosaccharide Chain E



5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 1 is monoatomic - leaving 17 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	$\#\|Z\| > 2$
5	PO4	A	611	-	4,4,4	2.48	2 (50%)	6,6,6	1.63	3 (50%)
5	PO4	A	609	-	4,4,4	2.66	3 (75%)	6,6,6	1.40	2 (33%)
5	PO4	A	610	-	4,4,4	1.87	2 (50%)	6,6,6	3.55	4 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	PO4	A	613	-	4,4,4	0.87	0	6,6,6	0.88	0
5	PO4	A	612	-	4,4,4	1.87	2 (50%)	6,6,6	2.22	3 (50%)
5	PO4	A	618	-	4,4,4	2.34	2 (50%)	6,6,6	2.06	3 (50%)
5	PO4	A	621	-	4,4,4	2.29	2 (50%)	6,6,6	3.14	4 (66%)
5	PO4	A	608	-	4,4,4	2.96	4 (100%)	6,6,6	0.43	0
5	PO4	A	614	-	4,4,4	2.07	2 (50%)	6,6,6	2.95	4 (66%)
5	PO4	A	616	-	4,4,4	1.63	1 (25%)	6,6,6	1.61	1 (16%)
5	PO4	A	617	-	4,4,4	1.37	1 (25%)	6,6,6	1.06	0
5	PO4	A	619	-	4,4,4	1.63	1 (25%)	6,6,6	1.67	2 (33%)
5	PO4	A	622	-	4,4,4	0.74	0	6,6,6	0.36	0
5	PO4	A	620	-	4,4,4	1.07	0	6,6,6	0.45	0
6	HEM	A	623	1,7	41,50,50	1.85	6 (14%)	45,82,82	1.89	14 (31%)
5	PO4	A	615	-	4,4,4	4.65	4 (100%)	6,6,6	3.17	4 (66%)
5	PO4	A	607	-	4,4,4	1.21	0	6,6,6	1.17	1 (16%)

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
6	HEM	A	623	1,7	-	4/12/54/54	-

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	615	PO4	P-O1	-7.02	1.34	1.50
6	A	623	HEM	C3D-C2D	6.03	1.49	1.36
6	A	623	HEM	C3C-C2C	-4.91	1.33	1.40
5	A	608	PO4	P-O1	4.52	1.61	1.50
5	A	615	PO4	P-O4	-3.77	1.43	1.54
5	A	615	PO4	P-O2	-3.52	1.44	1.54
5	A	611	PO4	P-O4	-3.49	1.44	1.54
6	A	623	HEM	CAB-C3B	3.47	1.56	1.47
5	A	611	PO4	P-O3	-3.39	1.44	1.54
5	A	609	PO4	P-O3	-3.37	1.44	1.54
5	A	615	PO4	P-O3	-3.27	1.44	1.54
5	A	618	PO4	P-O3	-3.17	1.45	1.54
5	A	614	PO4	P-O3	-3.03	1.45	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	621	PO4	P-O2	-2.94	1.45	1.54
5	A	618	PO4	P-O2	-2.94	1.45	1.54
6	A	623	HEM	C3C-CAC	2.92	1.53	1.47
5	A	610	PO4	P-O3	-2.92	1.45	1.54
5	A	609	PO4	P-O4	-2.77	1.46	1.54
5	A	609	PO4	P-O1	-2.56	1.44	1.50
5	A	621	PO4	P-O4	-2.48	1.47	1.54
5	A	614	PO4	P-O2	-2.41	1.47	1.54
5	A	617	PO4	P-O3	-2.38	1.47	1.54
5	A	608	PO4	P-O2	2.29	1.61	1.54
5	A	608	PO4	P-O3	2.29	1.61	1.54
5	A	612	PO4	P-O3	-2.20	1.48	1.54
5	A	619	PO4	P-O3	-2.20	1.48	1.54
5	A	612	PO4	P-O2	-2.19	1.48	1.54
5	A	616	PO4	P-O4	-2.15	1.48	1.54
6	A	623	HEM	CMD-C2D	2.13	1.55	1.50
5	A	610	PO4	P-O4	-2.07	1.48	1.54
5	A	608	PO4	P-O4	-2.03	1.48	1.54
6	A	623	HEM	C1A-CHA	-2.00	1.35	1.41

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	610	PO4	O4-P-O3	-7.02	85.43	107.97
5	A	621	PO4	O3-P-O2	6.20	127.88	107.97
6	A	623	HEM	CBA-CAA-C2A	-5.12	103.88	112.62
5	A	615	PO4	O4-P-O1	-5.07	92.33	110.89
5	A	614	PO4	O3-P-O1	4.52	127.43	110.89
5	A	614	PO4	O3-P-O2	-4.23	94.38	107.97
6	A	623	HEM	CMD-C2D-C1D	3.98	131.10	125.04
6	A	623	HEM	CAD-C3D-C4D	3.67	131.07	124.66
5	A	616	PO4	O4-P-O1	-3.55	97.92	110.89
5	A	615	PO4	O3-P-O1	3.52	123.78	110.89
5	A	612	PO4	O4-P-O2	3.44	119.03	107.97
5	A	615	PO4	O2-P-O1	3.33	123.09	110.89
6	A	623	HEM	C4C-CHD-C1D	3.30	126.92	122.56
5	A	610	PO4	O3-P-O2	3.30	118.58	107.97
6	A	623	HEM	C3B-C2B-C1B	3.21	108.87	106.49
5	A	619	PO4	O3-P-O2	-3.11	98.00	107.97
5	A	618	PO4	O3-P-O1	-3.09	99.59	110.89
5	A	612	PO4	O4-P-O1	-2.99	99.94	110.89
5	A	615	PO4	O4-P-O2	-2.87	98.77	107.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	623	HEM	CBD-CAD-C3D	-2.87	104.66	112.63
5	A	618	PO4	O3-P-O2	2.70	116.64	107.97
5	A	610	PO4	O4-P-O2	2.70	116.64	107.97
5	A	621	PO4	O4-P-O2	-2.66	99.45	107.97
5	A	614	PO4	O4-P-O2	2.64	116.45	107.97
5	A	621	PO4	O3-P-O1	-2.58	101.47	110.89
6	A	623	HEM	CMC-C2C-C3C	2.48	129.32	124.68
6	A	623	HEM	C4D-ND-C1D	2.45	107.60	105.07
6	A	623	HEM	CHD-C1D-ND	2.37	127.01	124.43
5	A	610	PO4	O3-P-O1	2.34	119.47	110.89
5	A	614	PO4	O2-P-O1	-2.32	102.42	110.89
6	A	623	HEM	C4B-CHC-C1C	2.28	125.56	122.56
5	A	611	PO4	O2-P-O1	-2.26	102.64	110.89
6	A	623	HEM	O1D-CGD-CBD	-2.24	115.88	123.08
6	A	623	HEM	O2D-CGD-CBD	2.19	121.08	114.03
5	A	621	PO4	O2-P-O1	-2.17	102.97	110.89
5	A	619	PO4	O3-P-O1	2.16	118.79	110.89
5	A	607	PO4	O4-P-O2	2.14	114.84	107.97
5	A	609	PO4	O4-P-O2	-2.13	101.15	107.97
5	A	618	PO4	O4-P-O3	2.11	114.73	107.97
5	A	612	PO4	O4-P-O3	2.10	114.70	107.97
5	A	611	PO4	O4-P-O1	2.07	118.45	110.89
5	A	609	PO4	O4-P-O1	2.04	118.36	110.89
6	A	623	HEM	CAD-C3D-C2D	-2.04	124.08	127.88
6	A	623	HEM	CAD-CBD-CGD	-2.04	109.22	113.60
5	A	611	PO4	O4-P-O3	-2.00	101.54	107.97

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	623	HEM	CAD-CBD-CGD-O1D
6	A	623	HEM	CAA-CBA-CGA-O2A
6	A	623	HEM	CAD-CBD-CGD-O2D
6	A	623	HEM	CAA-CBA-CGA-O1A

There are no ring outliers.

10 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	611	PO4	1	0

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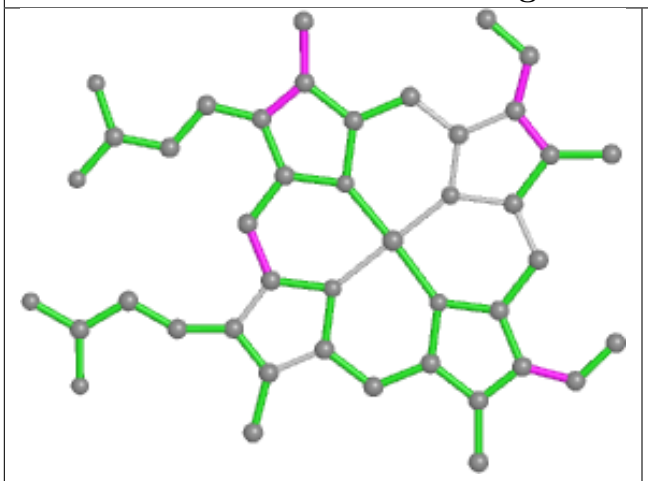
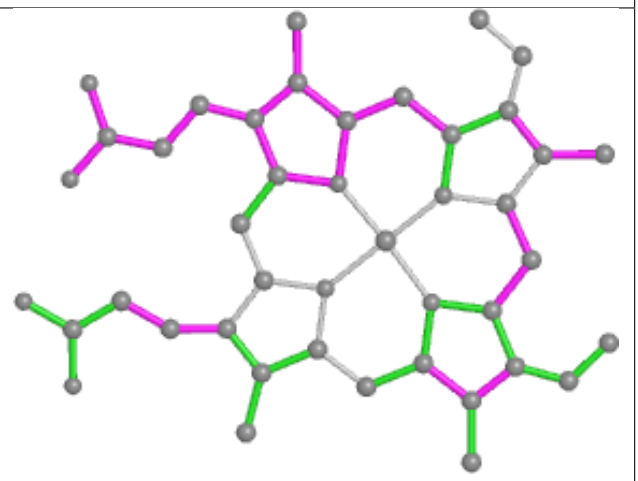
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	609	PO4	1	0
5	A	610	PO4	2	0
5	A	621	PO4	2	0
5	A	608	PO4	3	0
5	A	616	PO4	4	0
5	A	622	PO4	1	0
5	A	620	PO4	1	0
6	A	623	HEM	7	0
5	A	607	PO4	2	0

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.

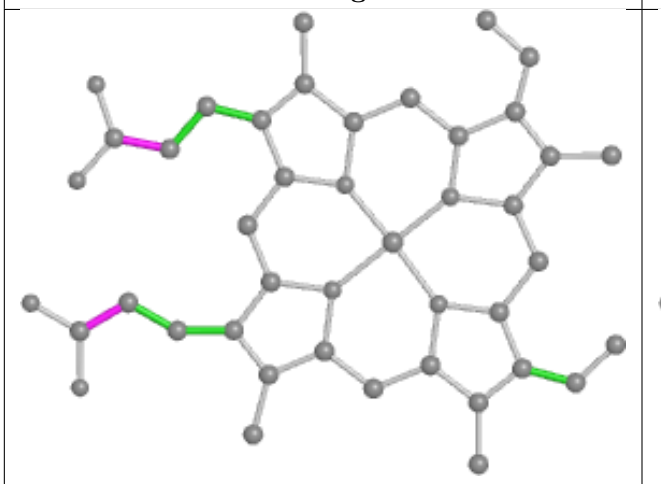
Ligand HEM A 623



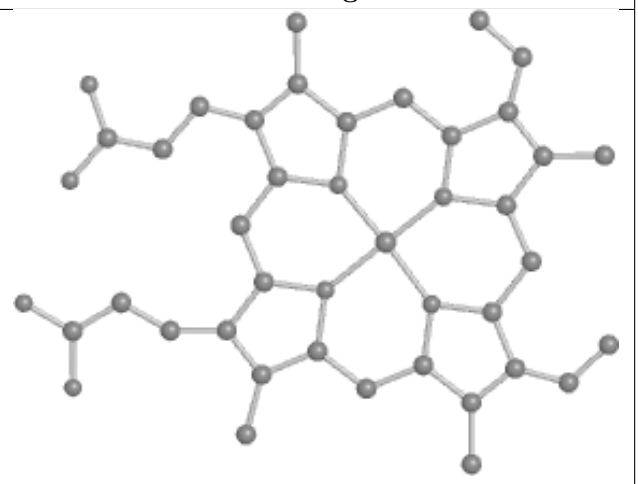
Bond lengths



Bond angles



Torsions



Rings

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	594/595 (99%)	0.57	50 (8%) 11 16	36, 58, 92, 100	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	TRP	9.8
1	A	1	SER	9.3
1	A	121	SER	8.1
1	A	4	VAL	7.8
1	A	120	GLY	7.3
1	A	595	ASN	7.3
1	A	7	GLY	7.2
1	A	174	SER	7.2
1	A	122	ASN	6.6
1	A	172	TYR	6.2
1	A	173	GLN	5.6
1	A	119	LEU	5.4
1	A	171	PRO	5.4
1	A	8	ALA	5.3
1	A	6	CYS	4.0
1	A	13	VAL	3.7
1	A	234	PRO	3.5
1	A	593	ARG	3.4
1	A	3	GLU	3.1
1	A	169	THR	3.1
1	A	131	GLU	3.0
1	A	254	PHE	2.9
1	A	124	HIS	2.9
1	A	170	PRO	2.9
1	A	64	ARG	2.9
1	A	594	GLU	2.8
1	A	9	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	229	PHE	2.8
1	A	279	GLU	2.8
1	A	370	PRO	2.7
1	A	550	SER	2.6
1	A	17	GLU	2.6
1	A	232	LYS	2.6
1	A	123	GLU	2.6
1	A	158	MET	2.5
1	A	371	GLU	2.5
1	A	235	SER	2.5
1	A	118	GLU	2.5
1	A	126	LYS	2.4
1	A	423	GLN	2.4
1	A	574	HIS	2.4
1	A	12	LEU	2.2
1	A	566	ALA	2.2
1	A	487	PRO	2.2
1	A	564	LEU	2.1
1	A	220	TRP	2.1
1	A	5	GLY	2.1
1	A	591	ALA	2.1
1	A	197	PRO	2.0
1	A	286	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	SEP	A	198	10/11	0.94	0.14	43,55,57,61	0

6.3 Carbohydrates (i)

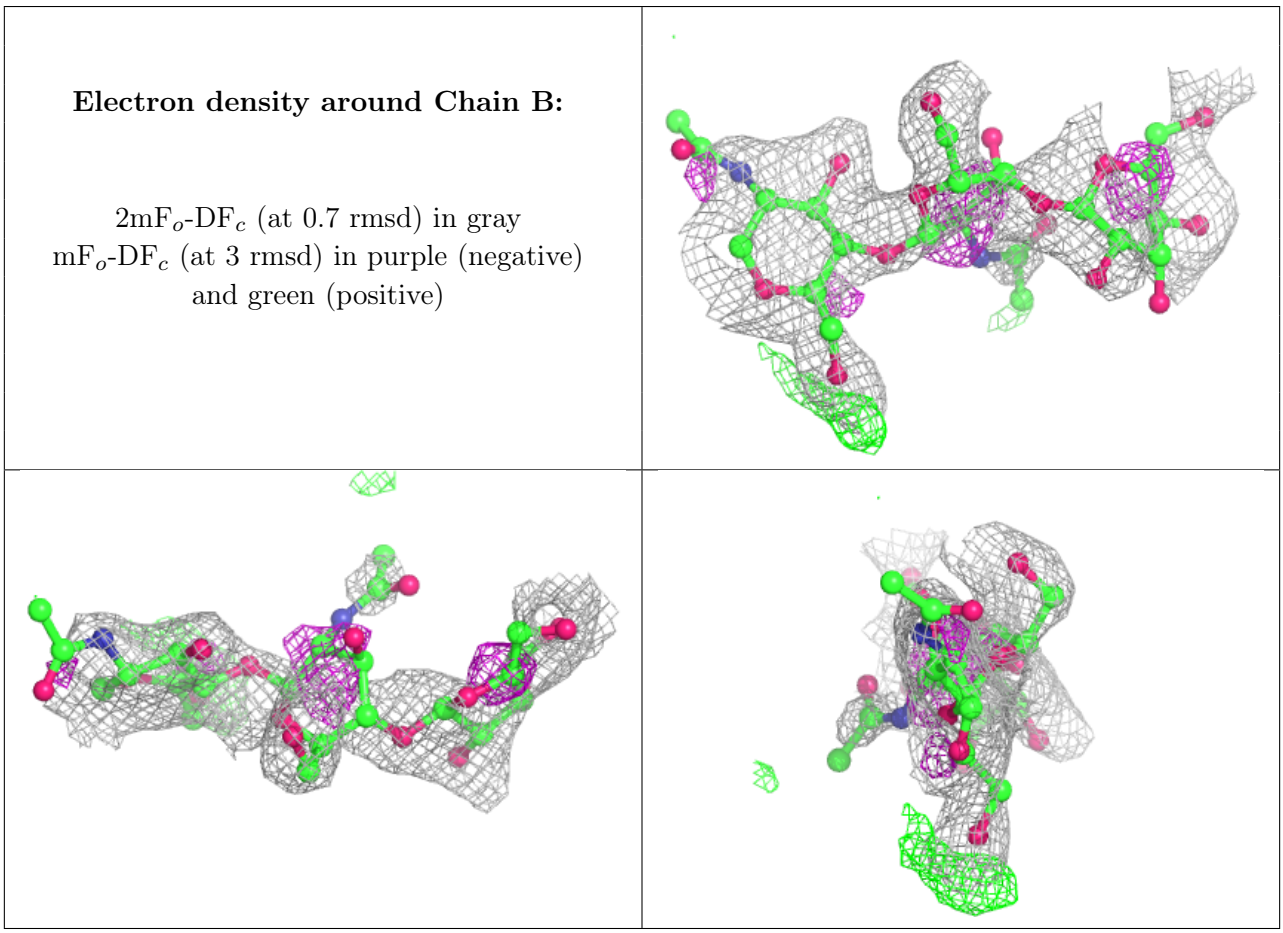
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	NAG	B	2	14/15	0.41	0.51	91,94,97,97	0
2	MAN	B	3	11/12	0.51	0.51	90,94,95,95	0
2	NAG	B	1	14/15	0.65	0.33	73,80,84,86	0
3	NAG	E	1	14/15	0.75	0.28	82,90,92,96	0
3	NAG	C	2	14/15	0.78	0.38	95,96,98,100	0
2	MAN	D	3	11/12	0.81	0.26	93,94,97,99	0
3	NAG	C	1	14/15	0.84	0.13	78,83,87,91	0
3	NAG	E	2	14/15	0.86	0.36	98,100,102,103	0
2	NAG	D	2	14/15	0.87	0.25	81,85,90,91	0
2	NAG	D	1	14/15	0.93	0.12	64,67,72,76	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

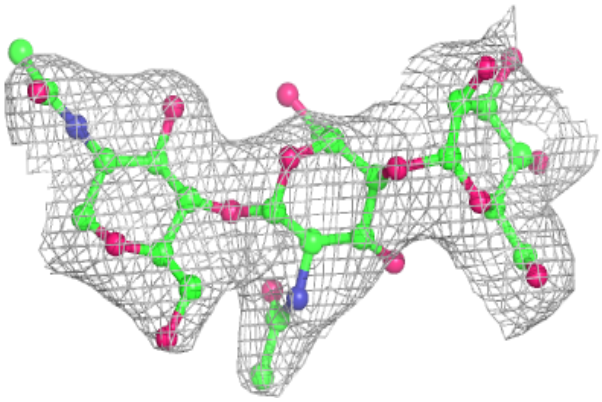
Electron density around Chain B:

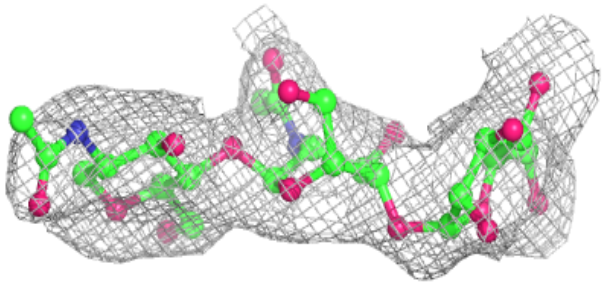
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

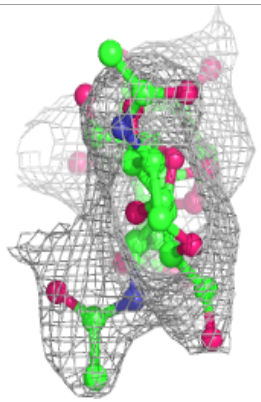


Electron density around Chain D:

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

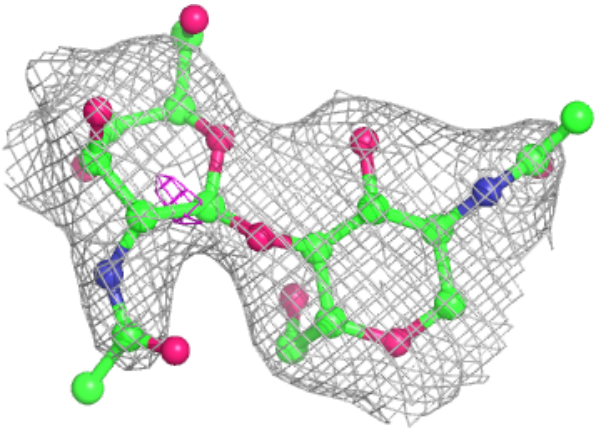


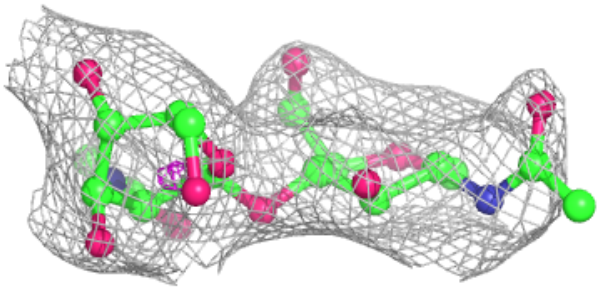


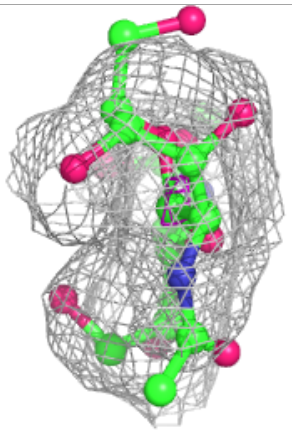


Electron density around Chain C:

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

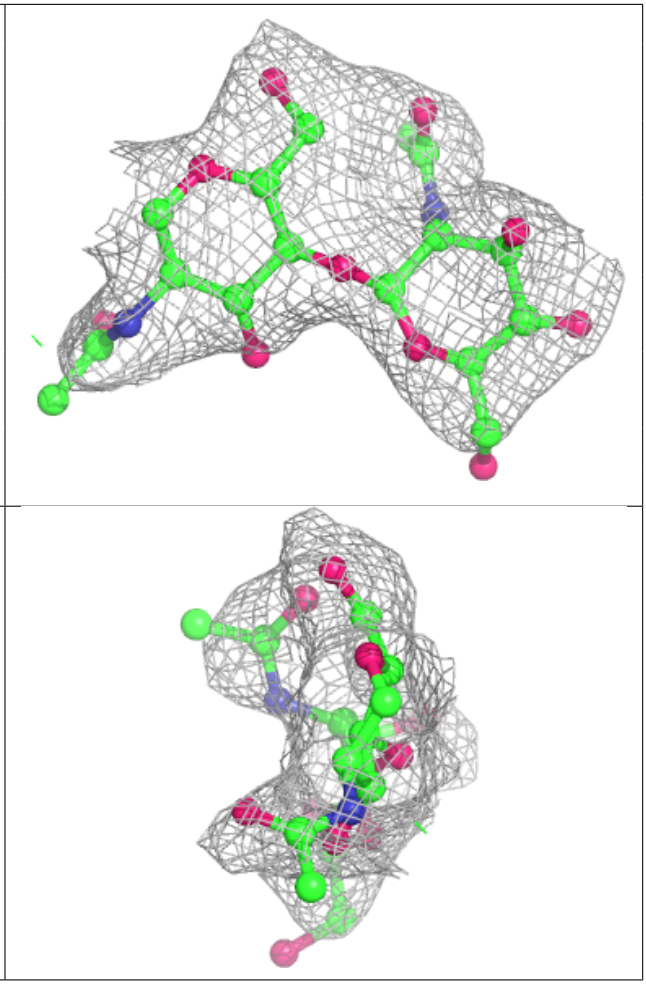






Electron density around Chain E:

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



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
5	PO4	A	622	5/5	0.75	0.33	97,98,99,100	0
5	PO4	A	620	5/5	0.84	0.26	95,95,97,97	0
5	PO4	A	621	5/5	0.91	0.15	45,49,60,63	0
5	PO4	A	616	5/5	0.93	0.20	54,60,61,65	0
5	PO4	A	617	5/5	0.93	0.11	55,58,63,67	0
5	PO4	A	619	5/5	0.93	0.23	49,54,61,64	0
5	PO4	A	608	5/5	0.94	0.28	14,23,33,40	0
5	PO4	A	613	5/5	0.94	0.29	69,70,71,72	0
5	PO4	A	610	5/5	0.95	0.21	52,54,58,62	0
5	PO4	A	607	5/5	0.96	0.22	47,49,53,55	0
5	PO4	A	609	5/5	0.97	0.12	31,43,47,51	0

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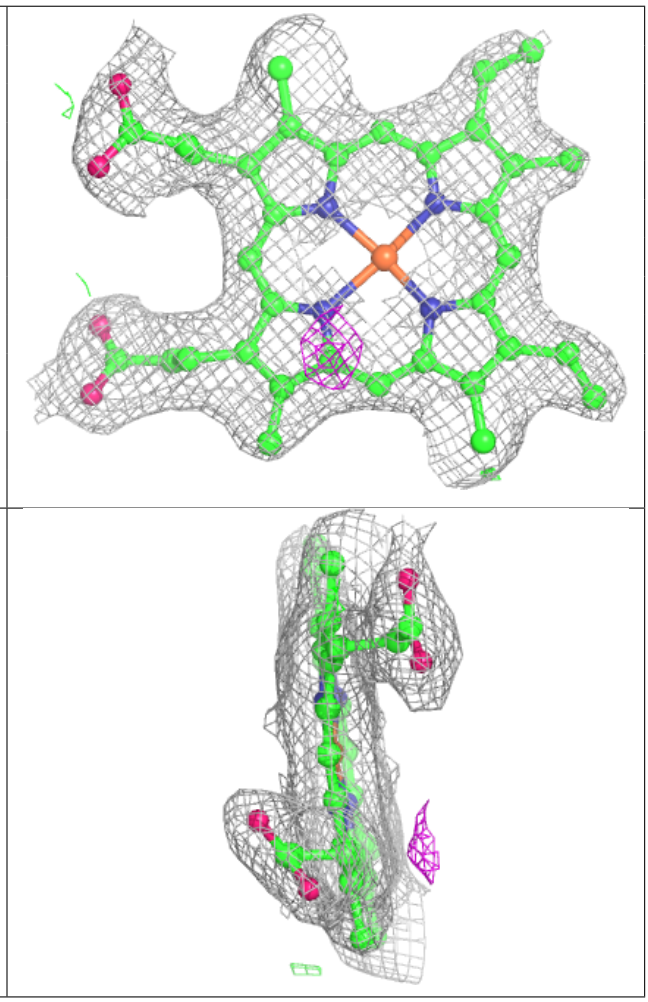
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PO4	A	618	5/5	0.97	0.16	35,40,50,57	0
5	PO4	A	612	5/5	0.97	0.11	40,45,51,56	0
6	HEM	A	623	43/43	0.97	0.11	29,36,47,50	0
4	CA	A	606	1/1	0.98	0.07	44,44,44,44	0
5	PO4	A	611	5/5	0.98	0.09	33,33,48,49	0
5	PO4	A	614	5/5	0.98	0.14	27,40,54,54	0
5	PO4	A	615	5/5	0.98	0.19	29,31,45,53	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 HEM A 623:

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.