



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 11:29 AM EDT

PDB ID : 3FNL / pdb_00003fnl
Title : Crystal Structure of the Complex of Buffalo Lactoperoxidase with Salicylhydroxamic Acid at 2.48 Å Resolution
Authors : Sheikh, I.A.; Vikram, G.; Singh, N.; Sinha, M.; Bhushan, A.; Sharma, S.; Kaur, P.; Singh, T.P.
Deposited on : 2008-12-25
Resolution : 2.48 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
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

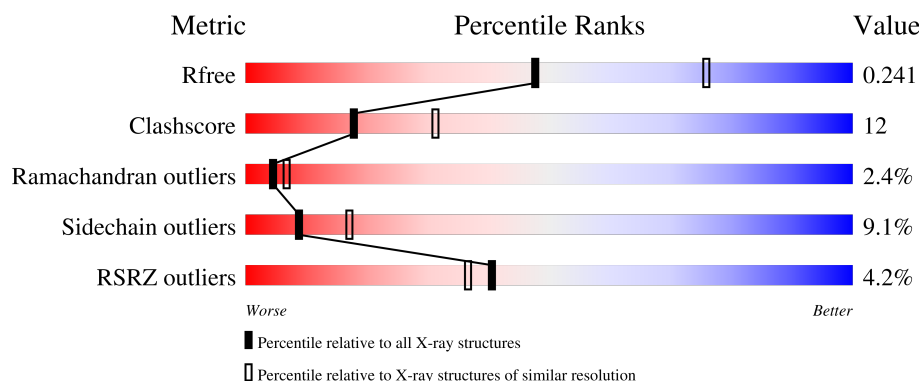
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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.



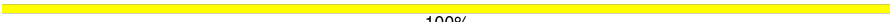
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	595	4% 72% 21% 6%
2	B	3	33% 67%
2	D	3	100%
3	C	2	100%

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Mol	Chain	Length	Quality of chain
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
5	IOD	A	609	-	-	X	-

2 Entry composition [i](#)

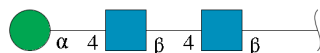
There are 9 unique types of molecules in this entry. The entry contains 5286 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	595	Total	C	N	O	P	S	0	0	0
			4770	3032	845	865	1	27			

- 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
2	B	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	D	3	Total	C	N	O	0	0	0
			39	22	2	15			

- 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
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

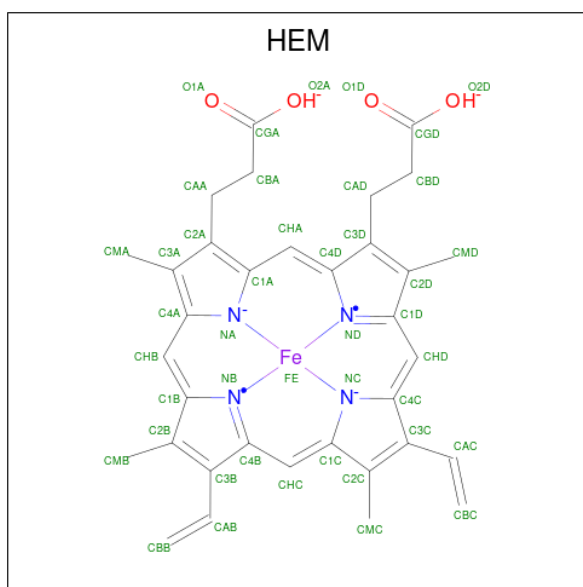
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

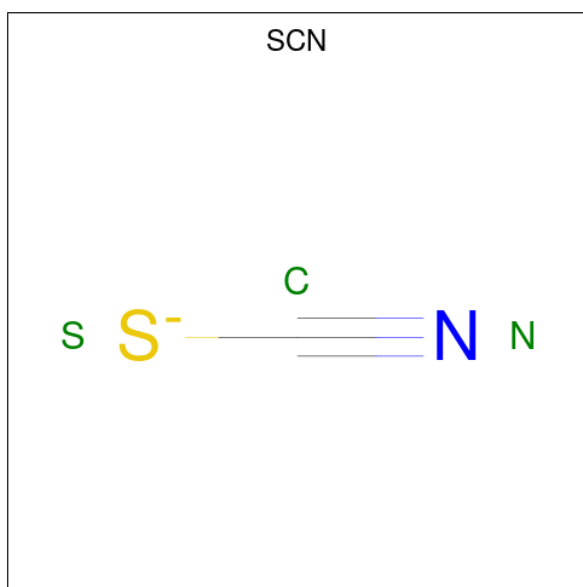
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Ca 1 1	0	0

- Molecule 5 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	8	Total I 8 8	0	0

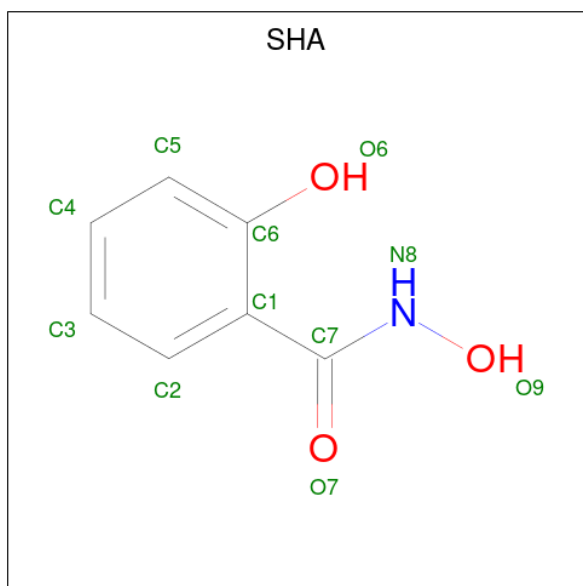
- Molecule 6 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 8 is SALICYLHYDROXAMIC ACID (CCD ID: SHA) (formula: $C_7H_7NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			11	7	1	3		

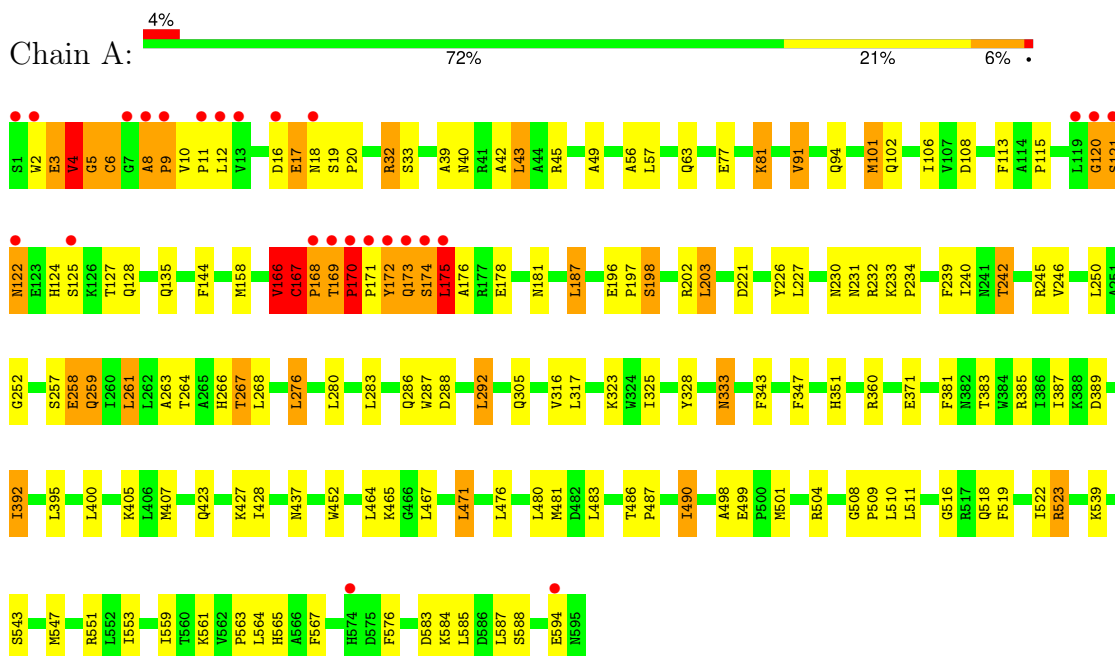
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	316	Total 316	O 316	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.

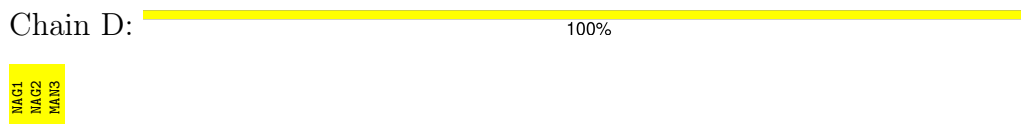
- Molecule 1: Lactoperoxidase



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



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



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

Chain C:  100%

MAG1
MAG2

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

Chain E:  100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.48Å 80.63Å 78.12Å 90.00° 102.75° 90.00°	Depositor
Resolution (Å)	20.00 – 2.48 20.00 – 2.48	Depositor EDS
% Data completeness (in resolution range)	99.2 (20.00-2.48) 99.0 (20.00-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.49Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.200 , 0.240 0.198 , 0.241	Depositor DCC
R_{free} test set	1191 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	38.1	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5286	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.95% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SHA, IOD, HEM, CA, MAN, NAG, SEP, SCN

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	0.68	4/4886 (0.1%)	1.02	22/6627 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	486	THR	C-N	-7.11	1.25	1.33
1	A	135	GLN	C-N	-6.11	1.24	1.33
1	A	483	LEU	C-N	-5.38	1.26	1.33
1	A	39	ALA	C-N	5.21	1.41	1.33

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	486	THR	O-C-N	-15.11	110.05	121.84
1	A	486	THR	CA-C-N	11.54	131.33	119.56
1	A	486	THR	C-N-CA	11.54	131.33	119.56
1	A	5	GLY	N-CA-C	9.39	124.79	112.77
1	A	121	SER	N-CA-C	-8.78	102.49	113.02
1	A	3	GLU	N-CA-C	-8.12	101.38	113.72
1	A	175	LEU	CA-C-N	-7.94	108.47	120.94
1	A	175	LEU	C-N-CA	-7.94	108.47	120.94
1	A	167	CYS	CA-C-N	7.82	129.62	119.84
1	A	167	CYS	C-N-CA	7.82	129.62	119.84
1	A	258	GLU	N-CA-CB	7.56	121.41	110.06
1	A	170	PRO	N-CA-C	6.97	119.20	110.70
1	A	108	ASP	CA-CB-CG	6.12	118.72	112.60
1	A	173	GLN	N-CA-C	5.73	123.01	110.80
1	A	423	GLN	CA-C-N	5.58	125.25	119.56
1	A	423	GLN	C-N-CA	5.58	125.25	119.56
1	A	33	SER	CA-C-N	5.38	125.20	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	33	SER	C-N-CA	5.38	125.20	119.28
1	A	508	GLY	CA-C-N	5.29	124.47	118.97
1	A	508	GLY	C-N-CA	5.29	124.47	118.97
1	A	175	LEU	O-C-N	5.25	128.82	122.68
1	A	316	VAL	N-CA-C	-5.09	106.83	111.67

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	4770	0	4675	116	0
2	B	39	0	34	0	0
2	D	39	0	34	0	0
3	C	28	0	25	0	0
3	E	28	0	25	0	0
4	A	1	0	0	0	0
5	A	8	0	0	2	0
6	A	43	0	30	5	0
7	A	3	0	0	0	0
8	A	11	0	6	1	0
9	A	316	0	0	7	0
All	All	5286	0	4829	120	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 12.

All (120) 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:167:CYS:HB3	1:A:168:PRO:CD	1.69	1.21
1:A:32:ARG:CB	1:A:32:ARG:HH21	1.54	1.19
1:A:167:CYS:HB3	1:A:168:PRO:HD2	1.20	1.17
1:A:2:TRP:CB	1:A:4:VAL:HG22	1.76	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:ARG:HH21	1:A:32:ARG:HB3	1.07	1.15
1:A:8:ALA:HB1	1:A:9:PRO:HD2	1.28	1.09
1:A:167:CYS:CB	1:A:168:PRO:HD2	1.81	1.09
1:A:2:TRP:HB2	1:A:4:VAL:HG22	1.13	1.09
1:A:32:ARG:HB3	1:A:32:ARG:NH2	1.79	0.97
1:A:196:GLU:HB3	1:A:198:SEP:O2P	1.68	0.94
1:A:2:TRP:HB2	1:A:4:VAL:CG2	1.97	0.94
1:A:101:MET:HE2	1:A:102:GLN:HA	1.46	0.94
1:A:487:PRO:HA	1:A:490:ILE:HD13	1.51	0.93
1:A:8:ALA:CB	1:A:9:PRO:HD2	2.02	0.89
1:A:169:THR:HB	1:A:170:PRO:HD2	1.54	0.89
1:A:169:THR:HB	1:A:170:PRO:CD	2.05	0.86
1:A:8:ALA:HB1	1:A:9:PRO:CD	2.07	0.83
1:A:202:ARG:HD3	9:A:656:HOH:O	1.78	0.83
1:A:173:GLN:HG3	1:A:174:SER:H	1.43	0.83
1:A:32:ARG:CB	1:A:32:ARG:NH2	2.39	0.83
6:A:615:HEM:HMC2	6:A:615:HEM:HBC2	1.59	0.83
1:A:167:CYS:HB3	1:A:168:PRO:HD3	1.61	0.81
1:A:263:ALA:O	1:A:267:THR:HG22	1.84	0.77
1:A:333:ASN:C	1:A:333:ASN:HD22	1.93	0.76
1:A:32:ARG:HH21	1:A:32:ARG:HB2	1.49	0.74
1:A:231:ASN:HA	9:A:817:HOH:O	1.86	0.74
1:A:101:MET:HE2	1:A:102:GLN:CA	2.16	0.73
1:A:246:VAL:HG11	1:A:387:ILE:HD13	1.70	0.71
1:A:43:LEU:HD13	1:A:181:ASN:HB2	1.73	0.71
1:A:351:HIS:HD1	1:A:437:ASN:HD21	1.37	0.70
1:A:264:THR:HG23	1:A:392:ILE:HD12	1.75	0.69
1:A:2:TRP:C	1:A:4:VAL:H	2.01	0.69
1:A:487:PRO:HA	1:A:490:ILE:CD1	2.23	0.68
1:A:567:PHE:HB2	5:A:609:IOD:I	2.64	0.67
1:A:328:TYR:HD1	1:A:523:ARG:HD3	1.60	0.66
1:A:2:TRP:HB3	1:A:4:VAL:HG22	1.76	0.65
1:A:63:GLN:HG2	9:A:911:HOH:O	1.98	0.64
1:A:168:PRO:HG2	1:A:172:TYR:CZ	2.33	0.63
1:A:551:ARG:HD3	1:A:584:LYS:HA	1.78	0.63
1:A:259:GLN:HE22	1:A:261:LEU:HB2	1.62	0.62
1:A:167:CYS:HB2	1:A:168:PRO:HD2	1.77	0.62
1:A:407:MET:HB3	1:A:501:MET:HE3	1.79	0.62
1:A:8:ALA:O	1:A:10:VAL:HG22	1.99	0.61
1:A:169:THR:O	1:A:170:PRO:O	2.19	0.61
1:A:2:TRP:C	1:A:4:VAL:N	2.60	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:TYR:CD1	1:A:523:ARG:HD3	2.36	0.59
1:A:42:ALA:HB2	1:A:166:VAL:HG21	1.86	0.57
1:A:8:ALA:CB	1:A:9:PRO:CD	2.75	0.57
1:A:168:PRO:HG2	1:A:172:TYR:CE1	2.40	0.57
1:A:120:GLY:C	1:A:122:ASN:H	2.14	0.56
1:A:333:ASN:C	1:A:333:ASN:ND2	2.65	0.54
1:A:121:SER:O	1:A:122:ASN:HB2	2.06	0.54
1:A:101:MET:CE	1:A:102:GLN:HA	2.31	0.54
6:A:615:HEM:HBC2	6:A:615:HEM:CMC	2.35	0.53
1:A:169:THR:CB	1:A:170:PRO:CD	2.85	0.52
1:A:467:LEU:HD22	1:A:481:MET:CE	2.40	0.52
1:A:547:MET:HE2	1:A:585:LEU:HD22	1.92	0.51
1:A:173:GLN:HG3	1:A:174:SER:N	2.20	0.51
1:A:8:ALA:O	1:A:9:PRO:C	2.53	0.51
1:A:588:SER:HB3	9:A:755:HOH:O	2.11	0.51
1:A:383:THR:O	1:A:387:ILE:HD12	2.11	0.51
1:A:187:LEU:HD13	1:A:305:GLN:HA	1.92	0.51
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.45	0.50
1:A:232:ARG:O	1:A:232:ARG:HG3	2.11	0.50
1:A:11:PRO:HA	9:A:739:HOH:O	2.10	0.50
1:A:476:LEU:HD21	1:A:498:ALA:HB1	1.94	0.50
1:A:173:GLN:CG	1:A:174:SER:H	2.09	0.49
1:A:242:THR:O	1:A:245:ARG:CZ	2.59	0.49
1:A:481:MET:HE1	1:A:487:PRO:HG3	1.94	0.49
1:A:276:LEU:O	1:A:280:LEU:HB2	2.13	0.49
6:A:615:HEM:HMB2	6:A:615:HEM:HBB2	1.95	0.49
1:A:8:ALA:O	1:A:10:VAL:N	2.47	0.48
6:A:615:HEM:HBB2	6:A:615:HEM:CMB	2.44	0.47
1:A:230:ASN:CG	1:A:232:ARG:HG2	2.38	0.47
1:A:3:GLU:O	1:A:5:GLY:N	2.48	0.47
1:A:347:PHE:HB3	6:A:615:HEM:HMD2	1.97	0.47
1:A:197:PRO:HD2	1:A:198:SEP:O2P	2.16	0.46
1:A:467:LEU:HG	1:A:471:LEU:HD22	1.97	0.45
1:A:487:PRO:CA	1:A:490:ILE:HD13	2.35	0.45
1:A:258:GLU:HG3	8:A:617:SHA:H2	1.97	0.45
1:A:19:SER:HA	1:A:20:PRO:HD3	1.83	0.45
1:A:257:SER:O	1:A:381:PHE:HA	2.17	0.45
1:A:16:ASP:HB3	1:A:19:SER:HB2	1.98	0.45
1:A:125:SER:C	1:A:127:THR:H	2.24	0.44
1:A:563:PRO:HD3	1:A:576:PHE:CE2	2.52	0.44
1:A:325:ILE:HD11	1:A:516:GLY:HA2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:LEU:HD11	1:A:553:ILE:HD13	2.00	0.44
1:A:287:TRP:HB3	1:A:292:LEU:HD22	1.99	0.44
1:A:10:VAL:HG12	1:A:40:ASN:O	2.17	0.44
1:A:203:LEU:HD21	1:A:252:GLY:HA2	1.99	0.44
1:A:259:GLN:HE21	1:A:259:GLN:HB2	1.50	0.44
1:A:227:LEU:HD11	1:A:266:HIS:HB3	2.01	0.43
1:A:276:LEU:HD12	1:A:587:LEU:HD11	1.99	0.43
1:A:360:ARG:NH2	1:A:371:GLU:O	2.48	0.43
1:A:239:PHE:CZ	1:A:427:LYS:HG2	2.54	0.43
1:A:565:HIS:HB3	5:A:609:IOD:I	2.88	0.43
1:A:175:LEU:HD23	1:A:176:ALA:H	1.83	0.43
1:A:519:PHE:HA	1:A:522:ILE:HG12	2.01	0.43
1:A:91:VAL:HG13	1:A:405:LYS:HG3	2.00	0.42
1:A:360:ARG:HD2	9:A:803:HOH:O	2.19	0.42
1:A:385:ARG:O	1:A:389:ASP:HB3	2.20	0.42
1:A:233:LYS:HA	1:A:234:PRO:C	2.44	0.42
1:A:56:ALA:HB3	9:A:740:HOH:O	2.19	0.42
1:A:5:GLY:O	1:A:6:CYS:C	2.63	0.41
1:A:113:PHE:O	1:A:115:PRO:HD3	2.20	0.41
1:A:280:LEU:HB3	1:A:292:LEU:HD12	2.02	0.41
1:A:387:ILE:HD12	1:A:387:ILE:H	1.85	0.41
1:A:499:GLU:OE1	1:A:509:PRO:HD2	2.20	0.41
1:A:124:HIS:O	1:A:128:GLN:HB2	2.21	0.41
1:A:288:ASP:O	1:A:292:LEU:CD2	2.69	0.41
1:A:325:ILE:O	1:A:325:ILE:HG22	2.20	0.41
1:A:77:GLU:HG2	1:A:81:LYS:HD3	2.02	0.41
1:A:292:LEU:HD13	1:A:292:LEU:HA	1.92	0.41
1:A:452:TRP:HB3	1:A:510:LEU:HD11	2.03	0.41
1:A:202:ARG:HD2	1:A:250:LEU:HD21	2.03	0.41
1:A:144:PHE:HE2	1:A:158:MET:HE2	1.86	0.40
1:A:45:ARG:CZ	1:A:49:ALA:HB2	2.52	0.40
1:A:343:PHE:CD1	1:A:518:GLN:HG2	2.56	0.40
1:A:166:VAL:HG22	1:A:178:GLU:O	2.22	0.40
1:A:170:PRO:HB3	1:A:171:PRO:CD	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	554 (94%)	24 (4%)	14 (2%)	4 7

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	8	ALA
1	A	9	PRO
1	A	122	ASN
1	A	168	PRO
1	A	169	THR
1	A	170	PRO
1	A	174	SER
1	A	6	CYS
1	A	17	GLU
1	A	167	CYS
1	A	594	GLU
1	A	166	VAL
1	A	120	GLY

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	516/516 (100%)	469 (91%)	47 (9%)	9 17

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	12	LEU
1	A	17	GLU
1	A	18	ASN
1	A	32	ARG
1	A	43	LEU
1	A	57	LEU
1	A	81	LYS
1	A	91	VAL
1	A	94	GLN
1	A	101	MET
1	A	106	ILE
1	A	166	VAL
1	A	172	TYR
1	A	175	LEU
1	A	187	LEU
1	A	203	LEU
1	A	240	ILE
1	A	242	THR
1	A	259	GLN
1	A	261	LEU
1	A	267	THR
1	A	268	LEU
1	A	276	LEU
1	A	283	LEU
1	A	286	GLN
1	A	292	LEU
1	A	317	LEU
1	A	323	LYS
1	A	333	ASN
1	A	392	ILE
1	A	395	LEU
1	A	428	ILE
1	A	464	LEU
1	A	465	LYS
1	A	471	LEU
1	A	480	LEU
1	A	490	ILE
1	A	504	ARG
1	A	511	LEU
1	A	523	ARG
1	A	539	LYS
1	A	543	SER

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Mol	Chain	Res	Type
1	A	559	ILE
1	A	561	LYS
1	A	564	LEU
1	A	583	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	68	ASN
1	A	138	ASN
1	A	217	GLN
1	A	259	GLN
1	A	333	ASN
1	A	364	ASN
1	A	460	GLN
1	A	497	ASN
1	A	545	GLN
1	A	570	ASN
1	A	574	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	1.60	1 (12%)	7,12,14	1.38	2 (28%)

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	-	4/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	P-O1P	3.26	1.60	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	SEP	OG-CB-CA	2.66	110.73	108.14
1	A	198	SEP	OG-P-O1P	2.10	112.11	106.44

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	198	SEP	CB-OG-P-O2P
1	A	198	SEP	CB-OG-P-O3P
1	A	198	SEP	CB-OG-P-O1P
1	A	198	SEP	CA-CB-OG-P

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

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	0.58	0	17,19,21	1.70	4 (23%)
2	NAG	B	2	2	14,14,15	0.76	0	17,19,21	0.91	0
2	MAN	B	3	2	11,11,12	0.62	0	15,15,17	1.48	1 (6%)
3	NAG	C	1	1,3	14,14,15	0.58	0	17,19,21	0.84	1 (5%)
3	NAG	C	2	3	14,14,15	0.69	0	17,19,21	1.30	3 (17%)
2	NAG	D	1	1,2	14,14,15	0.57	0	17,19,21	1.20	1 (5%)
2	NAG	D	2	2	14,14,15	0.45	0	17,19,21	1.92	4 (23%)
2	MAN	D	3	2	11,11,12	0.62	0	15,15,17	1.49	1 (6%)
3	NAG	E	1	1,3	14,14,15	0.66	0	17,19,21	1.51	1 (5%)
3	NAG	E	2	3	14,14,15	0.65	0	17,19,21	1.31	3 (17%)

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	-	4/6/23/26	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	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	1/6/23/26	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	1/1/1/1
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	C1-O5-C5	6.30	120.64	112.19
2	D	3	MAN	C1-O5-C5	5.13	119.06	112.19
2	B	3	MAN	C1-O5-C5	5.08	118.99	112.19
3	E	1	NAG	C4-C3-C2	5.04	118.41	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAG	O5-C1-C2	-3.58	105.75	111.29
3	E	2	NAG	C1-O5-C5	-3.30	107.76	112.19
3	C	2	NAG	C1-O5-C5	3.29	116.59	112.19
2	D	1	NAG	O5-C1-C2	-2.92	106.78	111.29
2	B	1	NAG	C1-O5-C5	2.66	115.75	112.19
2	B	1	NAG	O4-C4-C5	2.48	115.43	109.32
2	D	2	NAG	C4-C3-C2	-2.42	107.47	111.02
3	E	2	NAG	C2-N2-C7	-2.36	119.74	122.90
3	C	2	NAG	C6-C5-C4	-2.30	107.37	113.02
3	E	2	NAG	O5-C1-C2	-2.29	107.74	111.29
2	D	2	NAG	C1-C2-N2	2.26	114.00	110.43
2	B	1	NAG	C6-C5-C4	2.17	118.36	113.02
2	D	2	NAG	O5-C5-C6	2.16	111.87	107.66
3	C	2	NAG	C3-C4-C5	2.15	114.13	110.23
3	C	1	NAG	C4-C3-C2	2.10	114.10	111.02

There are no chirality outliers.

All (15) torsion outliers are listed below:

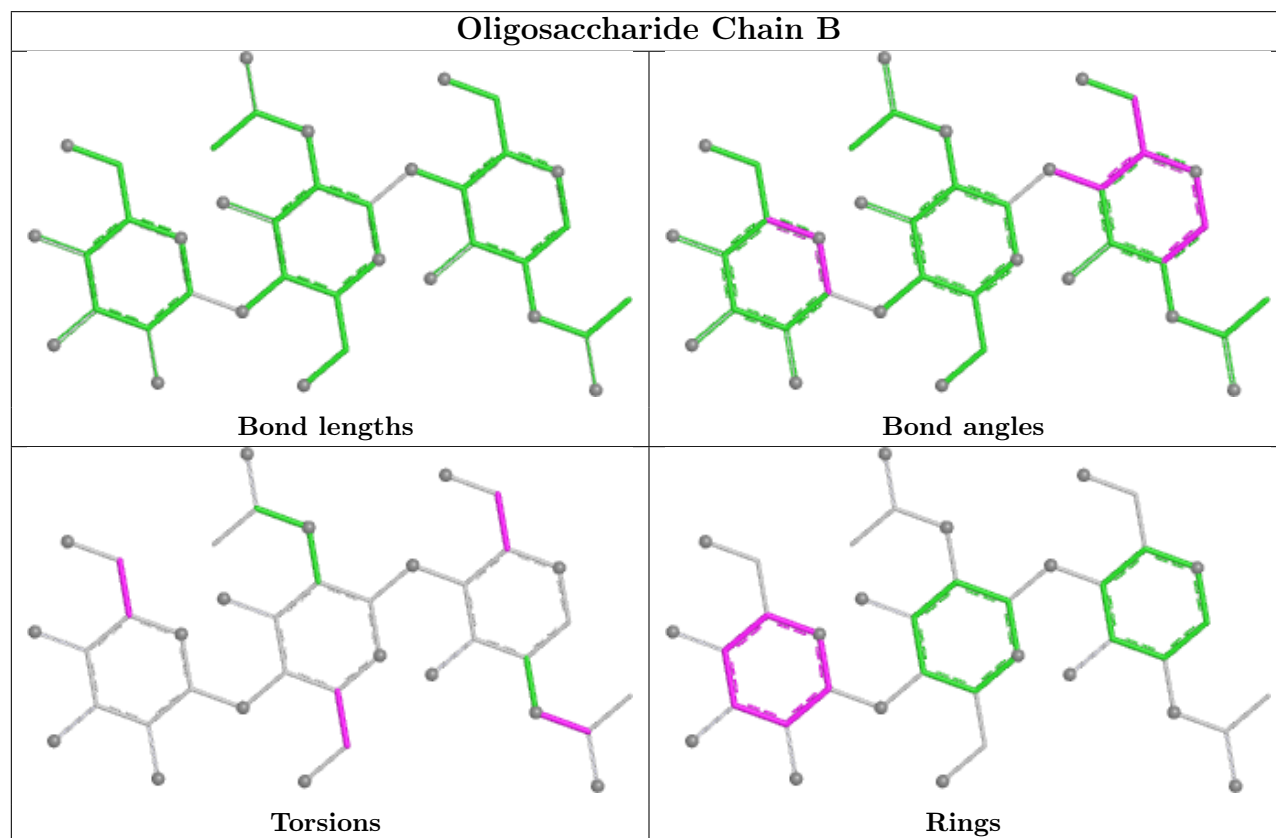
Mol	Chain	Res	Type	Atoms
3	E	2	NAG	O7-C7-N2-C2
3	E	2	NAG	C8-C7-N2-C2
2	B	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6
2	B	3	MAN	C4-C5-C6-O6
2	D	3	MAN	C4-C5-C6-O6
3	E	1	NAG	C8-C7-N2-C2
2	B	2	NAG	O5-C5-C6-O6
2	B	1	NAG	C8-C7-N2-C2
2	B	1	NAG	O7-C7-N2-C2
3	E	1	NAG	O7-C7-N2-C2
2	B	3	MAN	O5-C5-C6-O6
2	D	3	MAN	O5-C5-C6-O6
2	B	2	NAG	C4-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6

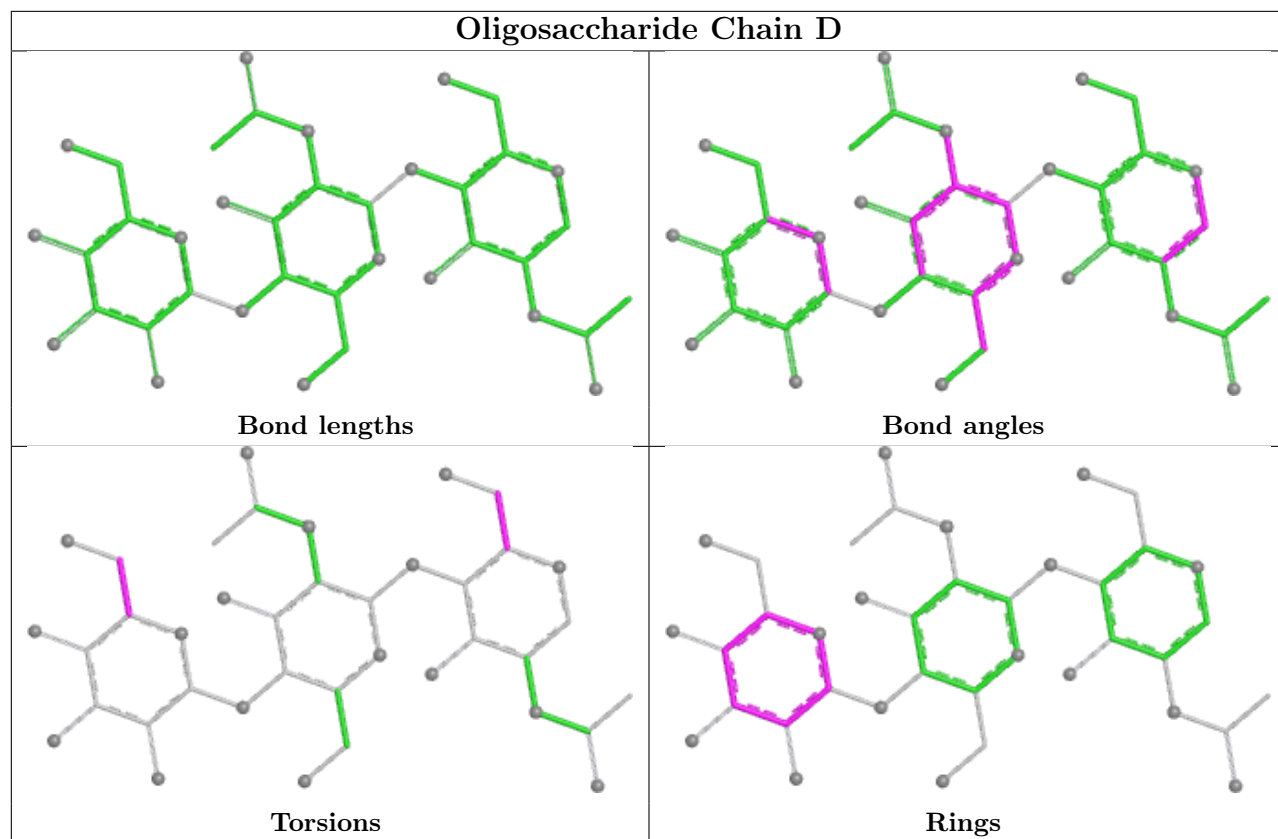
All (2) ring outliers are listed below:

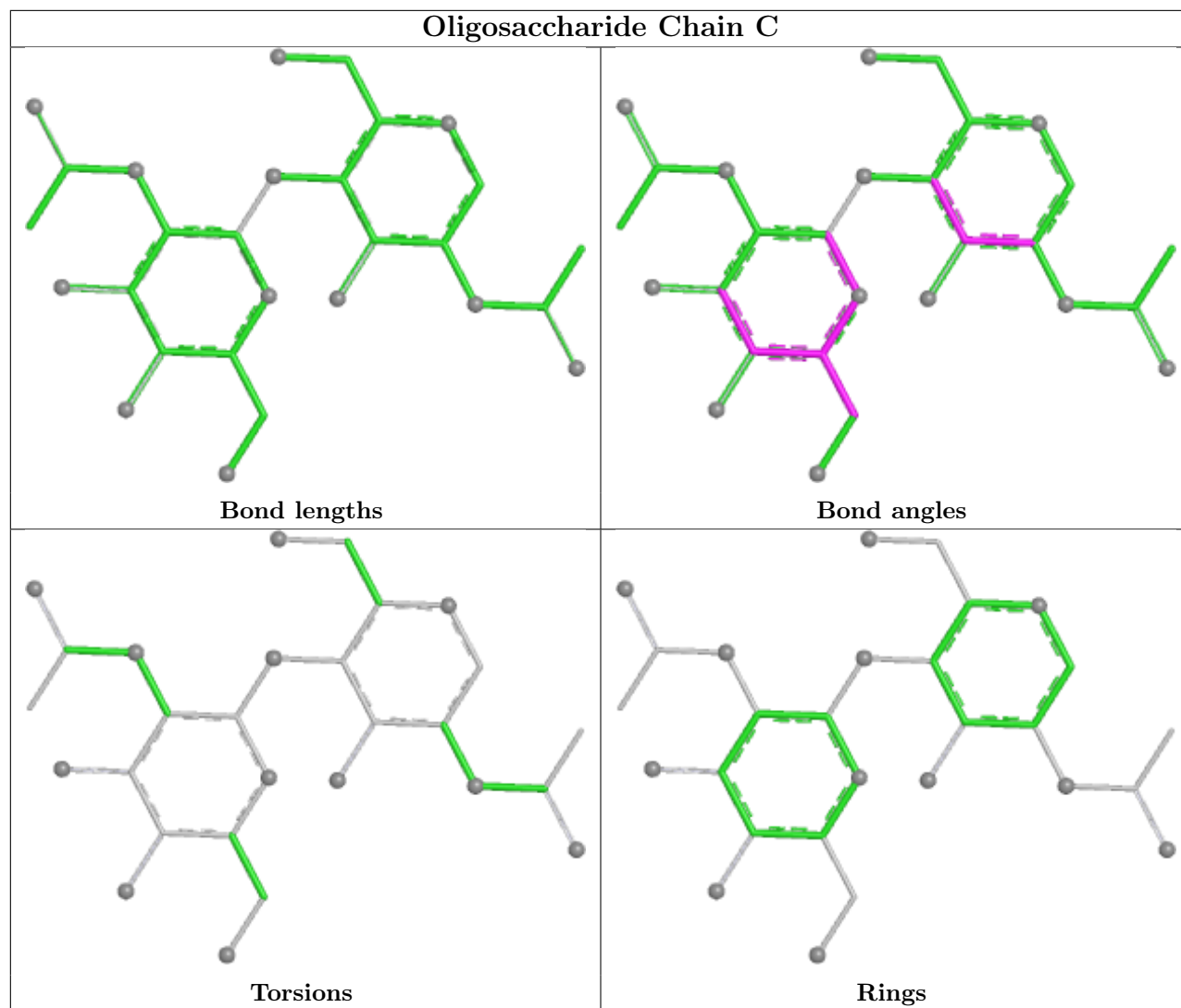
Mol	Chain	Res	Type	Atoms
2	B	3	MAN	C1-C2-C3-C4-C5-O5
2	D	3	MAN	C1-C2-C3-C4-C5-O5

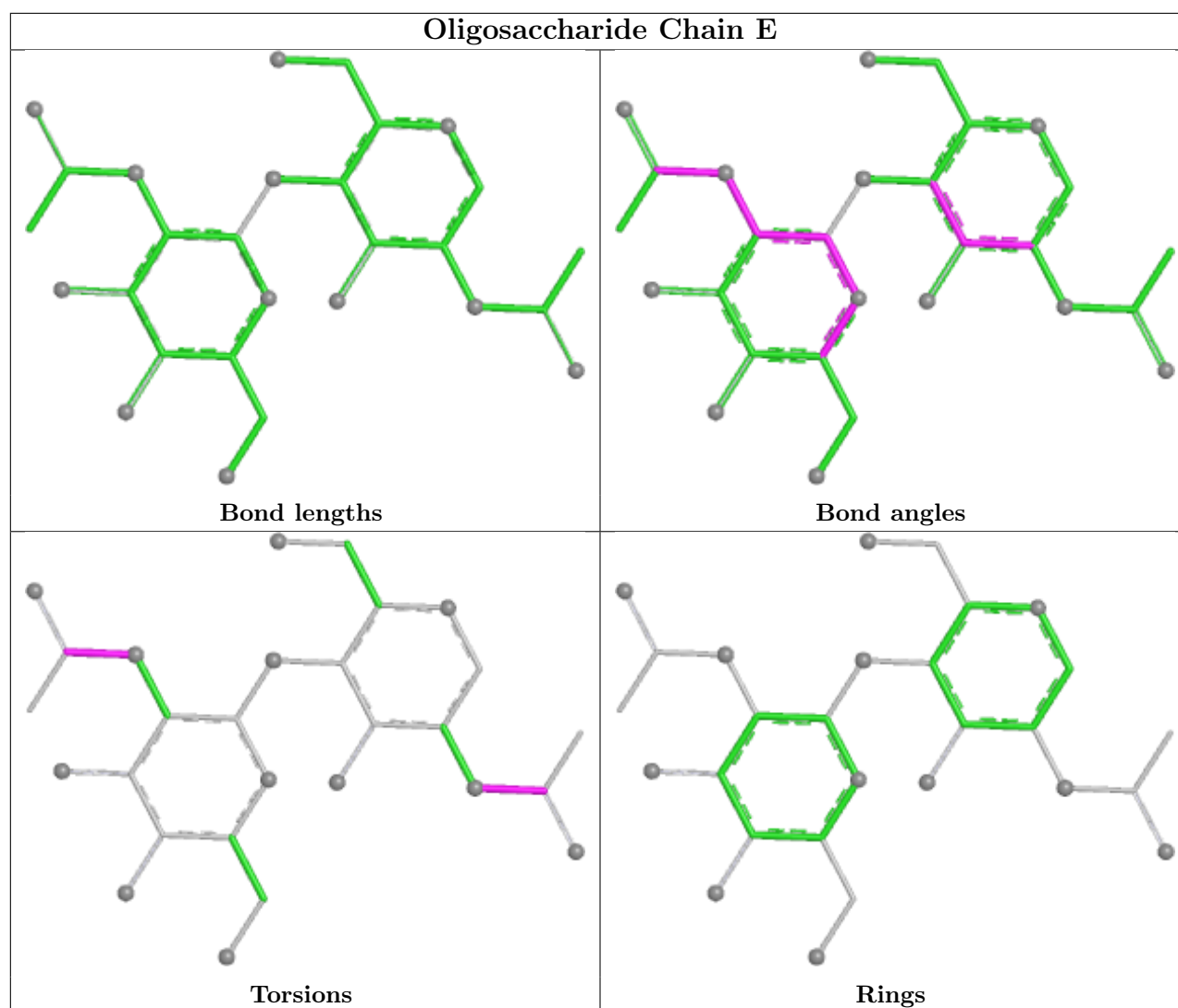
No monomer is involved in short contacts.

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









5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 9 are monoatomic - leaving 3 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	$\# Z > 2$
7	SCN	A	616	-	1,2,2	0.95	0	0,1,1	-	-
8	SHA	A	617	6	11,11,11	1.84	1 (9%)	13,14,14	0.72	0
6	HEM	A	615	8,1	50,50,50	1.97	8 (16%)	67,82,82	1.39	8 (11%)

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
8	SHA	A	617	6	-	0/6/6/6	0/1/1/1
6	HEM	A	615	8,1	-	4/14/54/54	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	615	HEM	C3D-C2D	7.65	1.53	1.36
6	A	615	HEM	FE-NC	6.26	2.15	1.95
8	A	617	SHA	C1-C6	5.45	1.49	1.40
6	A	615	HEM	FE-NB	4.35	2.08	1.94
6	A	615	HEM	CAB-C3B	3.22	1.56	1.47
6	A	615	HEM	CAC-C3C	3.17	1.55	1.47
6	A	615	HEM	FE-ND	2.83	2.03	1.94
6	A	615	HEM	FE-NA	2.44	2.03	1.95
6	A	615	HEM	CMA-C3A	2.18	1.55	1.50

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	615	HEM	C4D-ND-C1D	5.27	111.45	105.21
6	A	615	HEM	CHD-C1D-ND	3.59	128.29	124.42
6	A	615	HEM	C3B-C2B-C1B	3.37	108.94	106.41
6	A	615	HEM	CHC-C4B-NB	2.49	127.11	124.42
6	A	615	HEM	C2B-C1B-NB	-2.45	107.03	109.84
6	A	615	HEM	C1B-NB-C4B	2.35	108.00	105.21
6	A	615	HEM	CBD-CAD-C3D	-2.23	106.37	112.53
6	A	615	HEM	C2A-C1A-NA	-2.22	107.69	110.15

There are no chirality outliers.

All (4) torsion outliers are listed below:

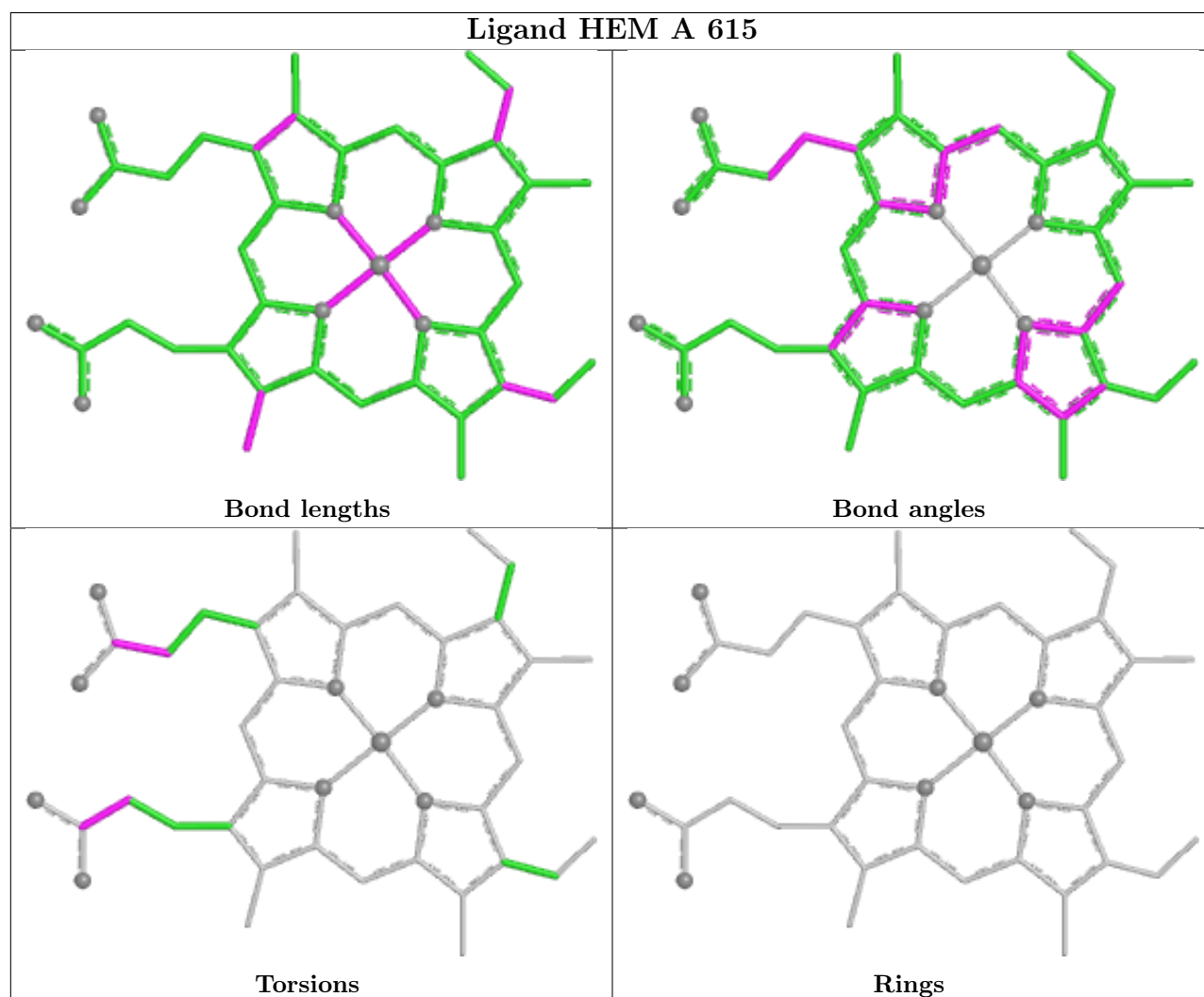
Mol	Chain	Res	Type	Atoms
6	A	615	HEM	CAD-CBD-CGD-O2D
6	A	615	HEM	CAD-CBD-CGD-O1D
6	A	615	HEM	CAA-CBA-CGA-O2A
6	A	615	HEM	CAA-CBA-CGA-O1A

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	617	SHA	1	0
6	A	615	HEM	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	594/595 (99%)	-0.15	25 (4%)	40 36	21, 35, 68, 86	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	7	GLY	4.6
1	A	1	SER	4.0
1	A	172	TYR	3.8
1	A	175	LEU	3.8
1	A	8	ALA	3.4
1	A	125	SER	3.4
1	A	2	TRP	3.3
1	A	12	LEU	3.2
1	A	119	LEU	3.0
1	A	11	PRO	2.9
1	A	121	SER	2.8
1	A	169	THR	2.7
1	A	170	PRO	2.7
1	A	9	PRO	2.5
1	A	574	HIS	2.5
1	A	594	GLU	2.4
1	A	168	PRO	2.3
1	A	18	ASN	2.3
1	A	171	PRO	2.3
1	A	122	ASN	2.2
1	A	16	ASP	2.2
1	A	120	GLY	2.2
1	A	173	GLN	2.1
1	A	174	SER	2.0
1	A	13	VAL	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	0.85	0.15	35,36,41,42	0

6.3 Carbohydrates [i](#)

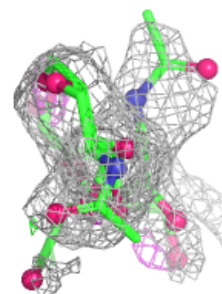
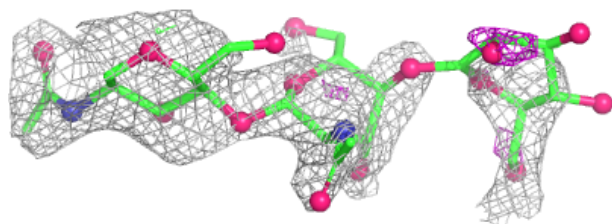
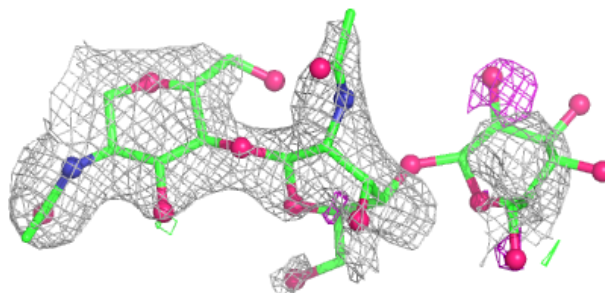
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MAN	B	3	11/12	0.22	0.17	76,78,78,78	0
2	NAG	D	2	14/15	0.58	0.15	66,69,72,74	0
3	NAG	E	2	14/15	0.58	0.13	78,81,84,84	0
2	MAN	D	3	11/12	0.62	0.11	76,78,78,78	0
2	NAG	B	2	14/15	0.63	0.14	78,82,84,88	0
3	NAG	E	1	14/15	0.67	0.12	58,66,69,74	0
3	NAG	C	2	14/15	0.69	0.14	67,70,72,74	0
2	NAG	B	1	14/15	0.82	0.10	59,65,68,73	0
3	NAG	C	1	14/15	0.87	0.10	54,56,61,63	0
2	NAG	D	1	14/15	0.91	0.10	51,54,56,61	0

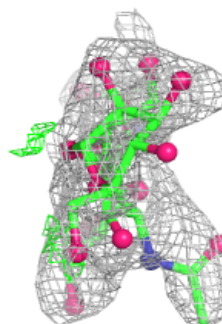
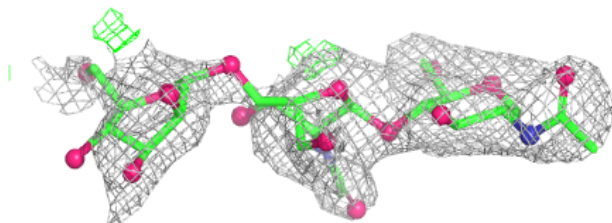
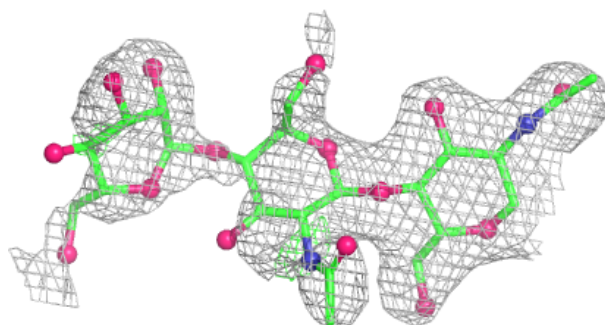
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

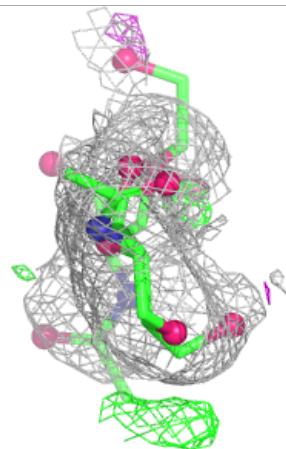
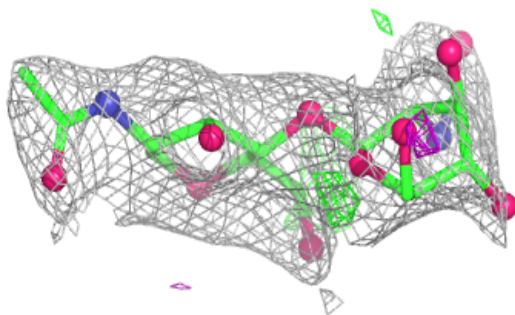
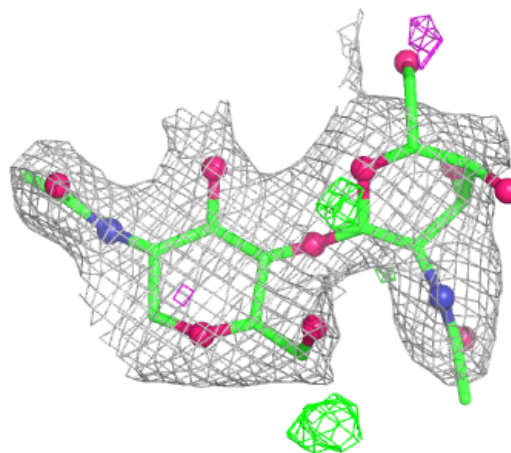
**Electron density around Chain D:**

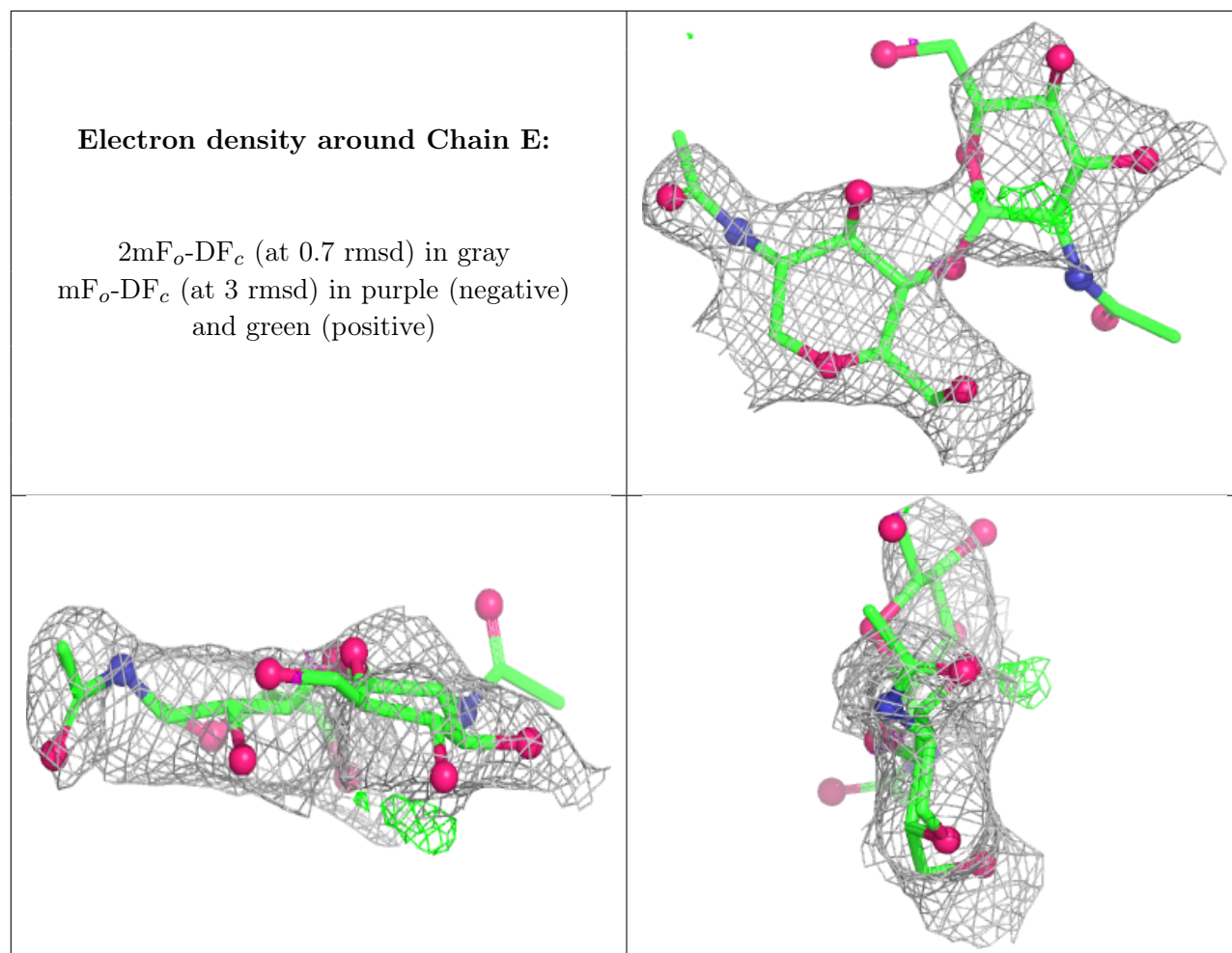
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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.

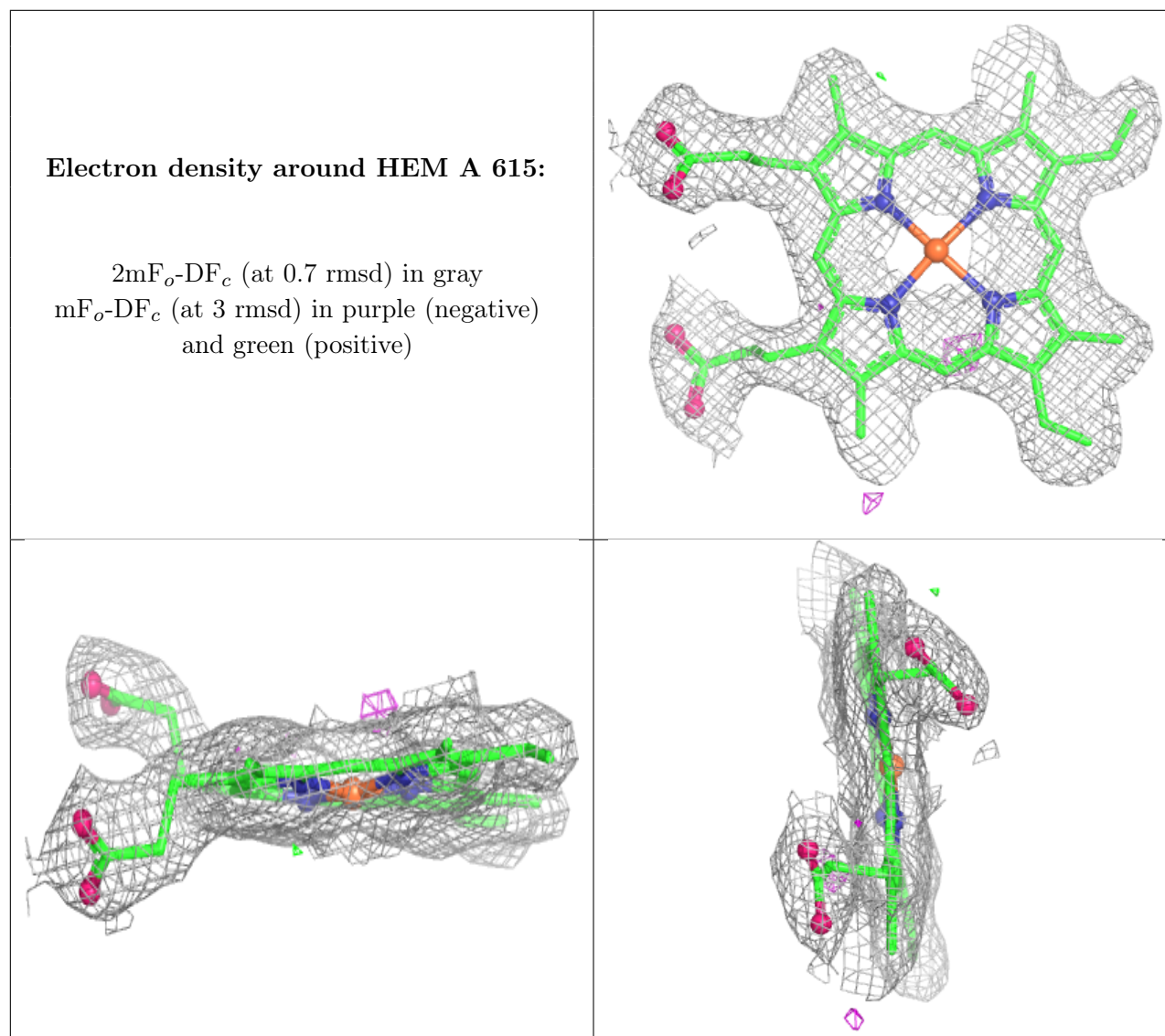
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	SCN	A	616	3/3	0.87	0.13	33,33,33,35	0
8	SHA	A	617	11/11	0.89	0.11	26,27,29,30	0
5	IOD	A	614	1/1	0.92	0.06	67,67,67,67	1
5	IOD	A	609	1/1	0.93	0.11	85,85,85,85	1
5	IOD	A	610	1/1	0.94	0.13	72,72,72,72	0
5	IOD	A	607	1/1	0.94	0.13	93,93,93,93	0
6	HEM	A	615	43/43	0.96	0.07	22,26,29,31	0
5	IOD	A	608	1/1	0.97	0.11	86,86,86,86	0
4	CA	A	606	1/1	0.98	0.02	29,29,29,29	0
5	IOD	A	612	1/1	0.98	0.11	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	IOD	A	613	1/1	0.99	0.09	72,72,72,72	0
5	IOD	A	611	1/1	1.00	0.03	30,30,30,30	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.



6.5 Other polymers ⓘ

There are no such residues in this entry.