



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:37 AM UTC

PDB ID : 4L2C / pdb_00004l2c
Title : X-ray structure of the C57R mutant of the iron superoxide dismutase from Pseudoalteromonas haloplanktis (crystal form I)
Authors : Russo Krauss, I.; Merlino, A.; Sica, F.
Deposited on : 2013-06-04
Resolution : 1.66 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:

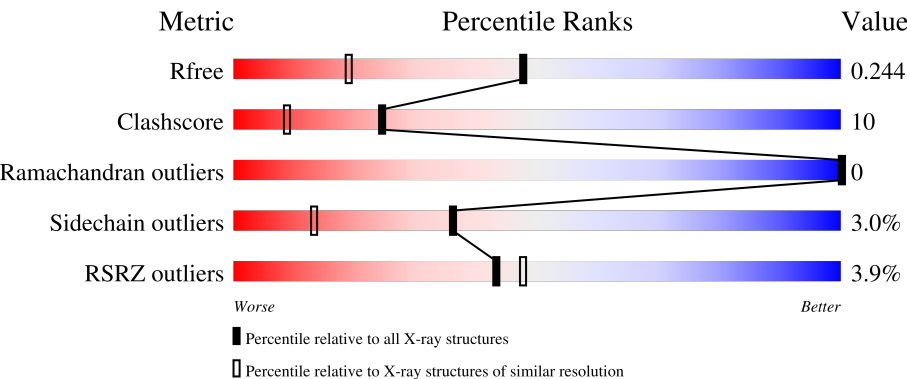
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 1.66 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.



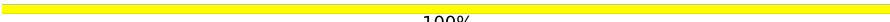
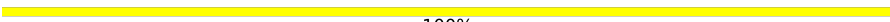
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	192	7% 82% 16% .
1	B	192	80% 19% .
1	C	192	7% 71% 24% ..
1	D	192	7% 78% 16% 6%
2	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	F	2	 100%
2	G	2	 100%
2	H	2	 50% 50%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7155 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.

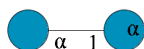
- Molecule 1 is a protein called Superoxide dismutase [Fe].

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	192	Total	C	N	O	0	7	0
			1541	996	252	293			
1	B	192	Total	C	N	O	0	3	0
			1526	984	252	290			
1	C	192	Total	C	N	O	0	6	0
			1540	997	255	288			
1	D	192	Total	C	N	O	0	8	0
			1547	1000	256	291			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	57	ARG	CYS	engineered mutation	UNP P84612
B	57	ARG	CYS	engineered mutation	UNP P84612
C	57	ARG	CYS	engineered mutation	UNP P84612
D	57	ARG	CYS	engineered mutation	UNP P84612

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			23	12	11			
2	F	2	Total	C	O	0	0	0
			23	12	11			
2	G	2	Total	C	O	0	0	0
			23	12	11			
2	H	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Fe 1	0	0
3	B	1	Total 1	Fe 1	0	0
3	C	1	Total 1	Fe 1	0	0
3	D	1	Total 1	Fe 1	0	0

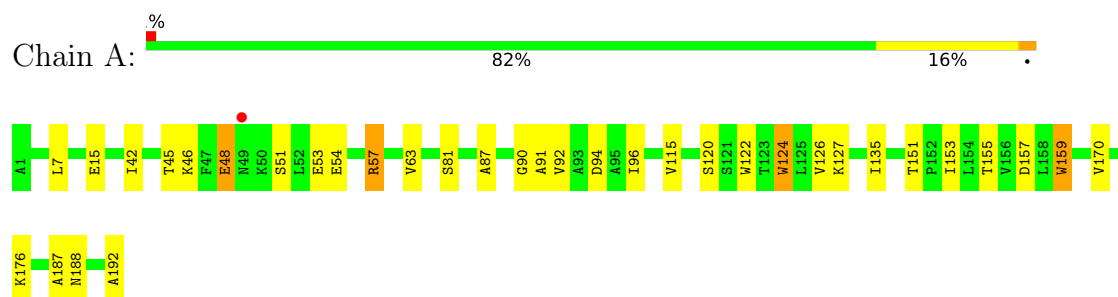
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	258	Total 259	O 259	0	1
4	B	248	Total 251	O 251	0	3
4	C	194	Total 196	O 196	0	2
4	D	197	Total 199	O 199	0	2

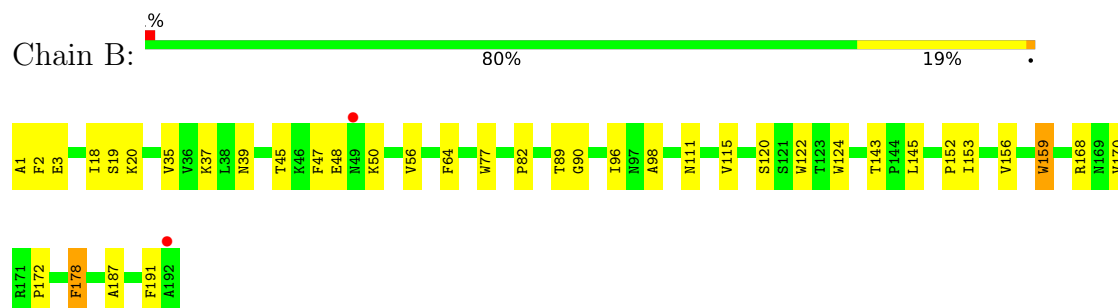
3 Residue-property plots

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.

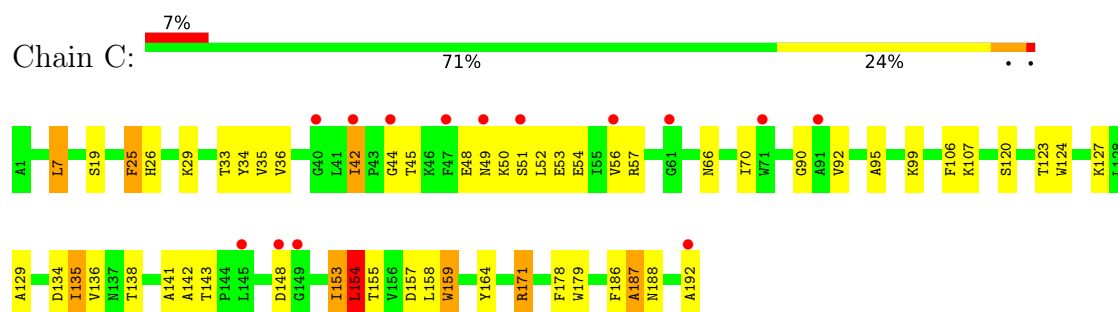
- Molecule 1: Superoxide dismutase [Fe]



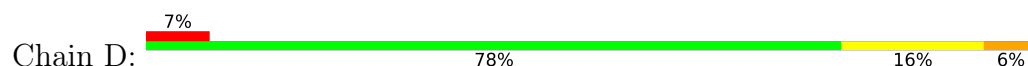
- Molecule 1: Superoxide dismutase [Fe]

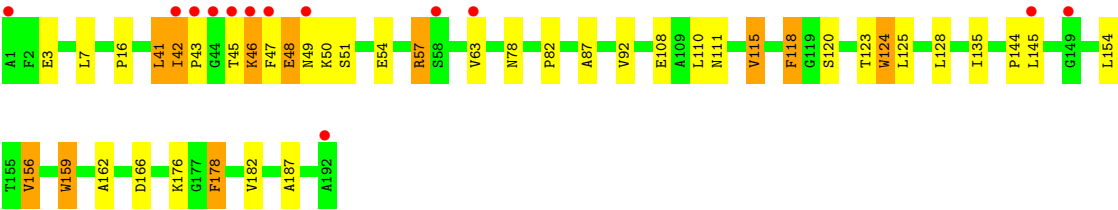


- Molecule 1: Superoxide dismutase [Fe]



- Molecule 1: Superoxide dismutase [Fe]

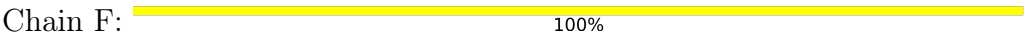




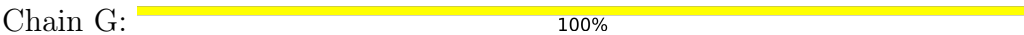
● Molecule 2: alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose



● Molecule 2: alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose



● Molecule 2: alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose



● Molecule 2: alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.49Å 103.77Å 89.83Å 90.00° 103.63° 90.00°	Depositor
Resolution (Å)	30.27 – 1.66 30.27 – 1.66	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.27-1.66) 85.7 (30.27-1.66)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 1.66Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.200 , 0.245 0.201 , 0.244	Depositor DCC
R_{free} test set	4786 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	13.8	Xtriage
Anisotropy	0.737	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 51.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7155	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 79.61 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.3722e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	1.63	6/1618 (0.4%)	1.41	9/2215 (0.4%)
1	B	1.64	13/1587 (0.8%)	1.39	16/2170 (0.7%)
1	C	1.57	12/1613 (0.7%)	1.41	10/2205 (0.5%)
1	D	1.52	9/1628 (0.6%)	1.47	13/2225 (0.6%)
All	All	1.59	40/6446 (0.6%)	1.42	48/8815 (0.5%)

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	152	PRO	C-O	7.92	1.32	1.23
1	C	95	ALA	CA-CB	6.93	1.64	1.53
1	B	187	ALA	CA-CB	6.93	1.64	1.53
1	B	56	VAL	CA-CB	6.79	1.62	1.54
1	D	187	ALA	N-CA	6.79	1.54	1.46
1	C	153	ILE	N-CA	6.63	1.52	1.46
1	B	168	ARG	C-O	6.52	1.30	1.24
1	C	129	ALA	CA-CB	6.22	1.63	1.53
1	C	25	PHE	C-O	6.13	1.31	1.24
1	A	96	ILE	CA-C	6.06	1.60	1.52
1	B	178	PHE	CA-C	5.98	1.60	1.52
1	A	170	VAL	CA-CB	5.96	1.60	1.53
1	D	7	LEU	C-O	5.88	1.31	1.23
1	C	136	VAL	C-O	-5.82	1.18	1.24
1	C	178	PHE	C-O	5.77	1.30	1.24
1	D	178	PHE	C-O	5.76	1.30	1.24
1	C	187	ALA	CA-CB	5.76	1.62	1.53
1	A	81	SER	C-O	-5.61	1.18	1.24
1	B	153	ILE	N-CA	5.47	1.51	1.46
1	B	64	PHE	C-O	-5.45	1.17	1.24
1	D	187	ALA	CA-C	5.41	1.59	1.52
1	A	42	ILE	CA-C	5.36	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	159	TRP	CA-C	5.33	1.59	1.52
1	B	191	PHE	C-O	-5.33	1.17	1.24
1	D	162	ALA	CA-CB	5.30	1.62	1.53
1	B	89	THR	CA-CB	5.24	1.63	1.53
1	C	123	THR	CA-CB	5.20	1.61	1.53
1	B	77	TRP	N-CA	5.18	1.52	1.46
1	D	92	VAL	CA-CB	5.15	1.61	1.54
1	A	91	ALA	CA-CB	5.12	1.61	1.53
1	B	98	ALA	N-CA	-5.11	1.40	1.46
1	C	164	TYR	C-O	5.09	1.30	1.24
1	D	154	LEU	N-CA	5.07	1.52	1.45
1	D	156	VAL	N-CA	5.05	1.52	1.46
1	C	141	ALA	CA-CB	5.03	1.61	1.53
1	B	122	TRP	C-O	-5.03	1.18	1.23
1	B	82	PRO	C-O	5.03	1.31	1.24
1	C	154[A]	LEU	N-CA	5.02	1.52	1.45
1	C	154[B]	LEU	N-CA	5.02	1.52	1.45
1	A	87	ALA	CA-CB	5.01	1.61	1.53

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	19	SER	N-CA-C	8.25	121.42	110.53
1	C	186	PHE	N-CA-C	-8.08	102.55	111.36
1	D	42	ILE	CA-C-N	-7.70	111.83	119.76
1	D	42	ILE	C-N-CA	-7.70	111.83	119.76
1	C	49	ASN	N-CA-C	7.61	122.28	113.38
1	B	153	ILE	N-CA-C	-7.58	105.75	112.12
1	C	42	ILE	N-CA-C	7.55	125.18	108.88
1	A	159	TRP	N-CA-C	-7.13	100.65	110.35
1	A	42	ILE	N-CA-C	7.08	120.84	112.35
1	A	48	GLU	N-CA-C	6.96	119.71	111.71
1	C	7	LEU	N-CA-C	-6.88	101.41	109.93
1	C	99	LYS	N-CA-C	6.72	119.60	111.40
1	D	87	ALA	CA-C-N	6.67	126.64	120.03
1	D	87	ALA	C-N-CA	6.67	126.64	120.03
1	A	48	GLU	CA-C-N	-6.67	108.81	121.54
1	A	48	GLU	C-N-CA	-6.67	108.81	121.54
1	D	118	PHE	N-CA-C	6.52	119.73	109.96
1	D	125	LEU	N-CA-C	-6.49	98.66	109.24
1	C	159	TRP	N-CA-C	-6.36	101.01	110.23
1	B	159	TRP	N-CA-C	-6.08	101.42	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	18	ILE	N-CA-C	-5.98	99.51	108.12
1	B	48	GLU	N-CA-C	5.93	118.50	111.33
1	D	82	PRO	N-CA-C	-5.76	106.94	114.03
1	D	159	TRP	N-CA-C	-5.50	102.88	110.35
1	B	152	PRO	CA-C-N	-5.46	117.04	122.77
1	B	152	PRO	C-N-CA	-5.46	117.04	122.77
1	A	187	ALA	N-CA-C	-5.45	105.24	111.07
1	B	48	GLU	CA-C-N	-5.45	114.53	122.86
1	B	48	GLU	C-N-CA	-5.45	114.53	122.86
1	D	48	GLU	CA-C-N	-5.44	114.02	122.67
1	D	48	GLU	C-N-CA	-5.44	114.02	122.67
1	D	166	ASP	N-CA-C	5.42	120.00	112.90
1	C	171	ARG	NE-CZ-NH2	5.38	124.04	119.20
1	B	90	GLY	N-CA-C	5.37	122.00	112.02
1	B	145	LEU	N-CA-C	-5.36	105.55	111.71
1	B	20	LYS	N-CA-C	-5.33	105.47	111.28
1	A	63	VAL	N-CA-C	-5.32	105.53	110.53
1	B	35	VAL	N-CA-C	-5.23	105.40	110.42
1	C	19	SER	N-CA-C	5.21	117.40	110.53
1	B	124	TRP	N-CA-C	5.20	117.88	109.40
1	A	124	TRP	N-CA-C	5.15	117.85	109.24
1	B	170	VAL	N-CA-CB	-5.14	107.07	112.06
1	D	124	TRP	N-CA-C	5.08	118.03	109.95
1	C	127	LYS	N-CA-C	-5.07	100.25	108.52
1	B	96	ILE	N-CA-C	-5.04	105.63	110.72
1	C	90	GLY	N-CA-C	5.03	120.43	111.73
1	A	90	GLY	N-CA-C	5.03	120.95	111.80
1	D	176	LYS	N-CA-C	-5.01	105.90	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1541	0	1452	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1526	0	1435	11	0
1	C	1540	0	1463	43	0
1	D	1547	0	1466	30	0
2	E	23	0	21	0	0
2	F	23	0	21	0	0
2	G	23	0	21	0	0
2	H	23	0	21	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	259	0	0	9	0
4	B	251	0	0	4	0
4	C	196	0	0	4	0
4	D	199	0	0	5	0
All	All	7155	0	5900	121	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 (121) 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:135:ILE:HD12	4:A:552:HOH:O	1.51	1.10
1:A:127:LYS:HB3	1:A:151[A]:THR:HG22	1.46	0.96
1:A:127:LYS:N	1:A:153[A]:ILE:HD11	1.84	0.93
1:D:42:ILE:O	1:D:45[A]:THR:HG22	1.76	0.86
1:D:43:PRO:HG2	4:D:321:HOH:O	1.76	0.84
1:A:127:LYS:HB3	1:A:151[A]:THR:CG2	2.09	0.82
1:D:111:ASN:O	1:D:115[A]:VAL:HG12	1.78	0.82
1:A:176:LYS:NZ	1:A:176:LYS:HB3	1.96	0.81
1:A:126:VAL:HA	1:A:153[A]:ILE:CD1	2.13	0.79
1:C:192:ALA:HB2	4:C:488:HOH:O	1.83	0.77
1:C:53:GLU:O	1:C:57[A]:ARG:HG3	1.85	0.76
1:A:94:ASP:HB3	4:A:327:HOH:O	1.84	0.75
1:A:176:LYS:HB3	1:A:176:LYS:HZ1	1.51	0.74
1:D:51:SER:OG	1:D:54:GLU:HB2	1.88	0.74
1:D:63:VAL:HG23	4:D:304:HOH:O	1.87	0.73
1:C:134:ASP:C	1:C:135[A]:ILE:HD13	2.15	0.72
1:C:153:ILE:O	1:C:154[B]:LEU:CD1	2.38	0.71
1:C:44:GLY:N	1:C:48:GLU:OE2	2.22	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:VAL:C	1:A:153[A]:ILE:CD1	2.66	0.69
1:D:45[A]:THR:HG23	1:D:47:PHE:H	1.58	0.68
1:A:126:VAL:CA	1:A:153[A]:ILE:CD1	2.72	0.68
1:C:35:VAL:N	1:C:70[A]:ILE:HD11	2.07	0.68
1:A:192:ALA:HB2	4:A:551:HOH:O	1.95	0.66
1:A:126:VAL:HA	1:A:153[A]:ILE:HD12	1.76	0.66
1:C:153:ILE:O	1:C:154[B]:LEU:HD12	1.94	0.66
1:B:156:VAL:HG22	1:B:178:PHE:CE1	2.30	0.65
1:D:45[A]:THR:HG23	1:D:47:PHE:N	2.12	0.65
1:C:35:VAL:HG22	1:C:70[A]:ILE:HD12	1.79	0.64
1:A:57:ARG:HG2	1:A:57:ARG:HH11	1.62	0.64
1:D:57[A]:ARG:HG2	1:D:57[A]:ARG:HH11	1.62	0.64
1:C:52:LEU:O	1:C:56:VAL:HG23	1.98	0.64
1:B:1:ALA:HB3	1:B:39:ASN:OD1	1.97	0.64
1:D:57[A]:ARG:HH11	1:D:57[A]:ARG:CG	2.09	0.64
1:A:176:LYS:HD2	4:A:549:HOH:O	1.98	0.63
1:C:34:TYR:C	1:C:70[A]:ILE:HD11	2.24	0.62
1:C:45:THR:O	1:C:48:GLU:HG3	1.99	0.62
1:D:57[A]:ARG:HG2	1:D:57[A]:ARG:NH1	2.15	0.62
1:C:53:GLU:HB3	1:C:57[B]:ARG:HH11	1.65	0.62
1:C:33:THR:HA	1:C:36[B]:VAL:HG22	1.81	0.61
1:A:126:VAL:C	1:A:153[A]:ILE:HD11	2.24	0.61
1:D:78:ASN:HA	4:D:420[B]:HOH:O	1.99	0.61
1:D:46[A]:LYS:HD3	1:D:47:PHE:CE2	2.36	0.60
1:B:50:LYS:HE3	4:B:5106:HOH:O	2.01	0.60
1:A:176:LYS:CD	4:A:549:HOH:O	2.48	0.60
1:D:46[A]:LYS:HD2	4:D:443:HOH:O	2.02	0.59
1:A:92[B]:VAL:HG13	1:A:188:ASN:OD1	2.02	0.59
1:C:35:VAL:CG2	1:C:70[A]:ILE:HD12	2.32	0.59
1:C:53:GLU:HG3	4:C:366:HOH:O	2.03	0.58
1:C:138:THR:HB	1:C:142:ALA:HB3	1.85	0.58
1:D:47:PHE:HA	1:D:50:LYS:HG2	1.86	0.58
1:A:126:VAL:CA	1:A:153[A]:ILE:HD13	2.33	0.58
1:C:120:SER:HB3	1:C:159:TRP:CD2	2.39	0.57
1:C:134:ASP:C	1:C:135[A]:ILE:CD1	2.77	0.57
1:C:153:ILE:O	1:C:154[B]:LEU:HD13	2.03	0.56
1:A:127:LYS:N	1:A:153[A]:ILE:CD1	2.64	0.56
1:C:57[A]:ARG:NH2	1:C:148:ASP:OD1	2.40	0.55
1:A:57:ARG:HG2	1:A:57:ARG:NH1	2.22	0.55
1:C:154[A]:LEU:HD21	1:C:187:ALA:HB2	1.88	0.55
1:B:47:PHE:HA	1:B:50:LYS:HD2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:66:ASN:O	1:C:70[B]:ILE:HG13	2.06	0.55
1:D:46[A]:LYS:CE	4:D:443:HOH:O	2.55	0.54
1:D:178:PHE:CZ	1:D:182[B]:VAL:HG22	2.44	0.53
1:C:51[A]:SER:OG	1:C:54:GLU:HG3	2.08	0.53
1:B:1:ALA:HB1	4:B:5329:HOH:O	2.09	0.53
1:D:120:SER:HB3	1:D:159:TRP:CD2	2.44	0.52
1:A:176:LYS:NZ	1:A:176:LYS:CB	2.68	0.52
1:D:41[A]:LEU:HD23	1:D:63:VAL:HG22	1.92	0.52
1:B:120:SER:HB3	1:B:159:TRP:CE2	2.46	0.51
1:D:178:PHE:O	1:D:182[B]:VAL:HG23	2.11	0.50
1:C:92:VAL:HG22	1:C:188:ASN:OD1	2.12	0.49
1:C:33:THR:HA	1:C:36[B]:VAL:CG2	2.43	0.49
1:A:126:VAL:C	1:A:153[A]:ILE:HD13	2.38	0.49
1:D:124:TRP:CE2	1:D:144:PRO:HD3	2.49	0.48
1:C:134:ASP:O	1:C:135[A]:ILE:HD12	2.13	0.48
1:A:192:ALA:CB	4:A:551:HOH:O	2.58	0.48
1:B:111:ASN:O	1:B:115[B]:VAL:HG13	2.12	0.48
1:B:120:SER:HB3	1:B:159:TRP:CD2	2.49	0.47
1:A:45:THR:O	1:A:48:GLU:HG3	2.15	0.47
1:D:42:ILE:O	1:D:45[A]:THR:CG2	2.54	0.47
1:A:120:SER:HB3	1:A:159:TRP:CD2	2.50	0.46
1:A:122:TRP:CZ3	1:A:157:ASP:HB2	2.50	0.45
1:C:26:HIS:CE1	1:C:157:ASP:OD2	2.70	0.45
1:A:53:GLU:HG3	4:A:371:HOH:O	2.15	0.45
1:A:120:SER:HB3	1:A:159:TRP:CE2	2.52	0.45
1:D:110:LEU:HA	1:D:135:ILE:HD13	1.98	0.45
1:C:50:LYS:HE3	4:C:349:HOH:O	2.17	0.44
1:D:123:THR:HB	1:D:156:VAL:HG12	1.99	0.44
1:C:42:ILE:O	1:C:45:THR:HG23	2.18	0.43
1:C:107:LYS:HE3	1:C:179:TRP:CG	2.53	0.43
1:C:154[B]:LEU:HD11	1:C:187:ALA:HB2	2.00	0.43
1:C:66:ASN:O	1:C:70[A]:ILE:HG12	2.17	0.43
1:D:118:PHE:HB3	2:H:2:GLC:O6	2.19	0.43
1:D:123:THR:HB	1:D:156:VAL:CG1	2.48	0.43
1:B:2:PHE:C	1:B:3:GLU:HG2	2.44	0.43
1:A:57:ARG:HH11	1:A:57:ARG:CG	2.27	0.42
1:D:156:VAL:O	1:D:156:VAL:HG13	2.17	0.42
1:C:120:SER:HB3	1:C:159:TRP:CE2	2.54	0.42
1:B:45:THR:HA	4:B:5124:HOH:O	2.19	0.42
1:C:45:THR:HB	4:C:357:HOH:O	2.19	0.42
1:B:37:LYS:HE3	4:B:5336:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15[A]:GLU:CD	4:A:521:HOH:O	2.63	0.42
1:A:51:SER:OG	1:A:54:GLU:HG3	2.20	0.42
1:A:126:VAL:HA	1:A:153[A]:ILE:HD13	1.94	0.41
1:C:7:LEU:HD12	1:C:7:LEU:HA	1.93	0.41
1:C:106:PHE:HE1	1:C:135[A]:ILE:HD11	1.85	0.41
1:C:153:ILE:C	1:C:154[B]:LEU:HD13	2.44	0.41
1:C:158:LEU:HD22	1:C:171:ARG:HD3	2.03	0.41
1:D:41[A]:LEU:HD23	1:D:63:VAL:CG2	2.51	0.41
1:A:124:TRP:CE3	1:A:155:THR:HB	2.56	0.41
1:C:25:PHE:O	1:C:29:LYS:HB2	2.21	0.41
1:A:46:LYS:HG2	4:A:304:HOH:O	2.21	0.40
1:C:124:TRP:CE3	1:C:155:THR:HB	2.56	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	197/192 (103%)	192 (98%)	5 (2%)	0	100	100
1	B	193/192 (100%)	187 (97%)	6 (3%)	0	100	100
1	C	196/192 (102%)	189 (96%)	7 (4%)	0	100	100
1	D	198/192 (103%)	195 (98%)	3 (2%)	0	100	100
All	All	784/768 (102%)	763 (97%)	21 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	165/158 (104%)	161 (98%)	4 (2%)	43	20
1	B	161/158 (102%)	159 (99%)	2 (1%)	63	45
1	C	164/158 (104%)	159 (97%)	5 (3%)	36	13
1	D	166/158 (105%)	151 (91%)	15 (9%)	9	1
All	All	656/632 (104%)	630 (96%)	26 (4%)	36	7

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	57	ARG
1	A	115[A]	VAL
1	A	115[B]	VAL
1	B	143	THR
1	B	172	PRO
1	C	135[A]	ILE
1	C	135[B]	ILE
1	C	143	THR
1	C	154[A]	LEU
1	C	154[B]	LEU
1	D	3	GLU
1	D	16	PRO
1	D	41[A]	LEU
1	D	41[B]	LEU
1	D	46[A]	LYS
1	D	46[B]	LYS
1	D	48	GLU
1	D	49	ASN
1	D	57[A]	ARG
1	D	57[B]	ARG
1	D	108	GLU
1	D	115[A]	VAL
1	D	115[B]	VAL
1	D	128	LEU
1	D	145	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	ASN
1	A	116	ASN
1	B	65	ASN
1	C	17	HIS
1	C	78	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

8 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	GLC	E	1	2	11,11,12	0.33	0	15,15,17	0.90	0
2	GLC	E	2	2	12,12,12	0.56	0	17,17,17	0.88	1 (5%)
2	GLC	F	1	2	11,11,12	0.33	0	15,15,17	1.15	2 (13%)
2	GLC	F	2	2	12,12,12	0.59	0	17,17,17	0.79	1 (5%)
2	GLC	G	1	2	11,11,12	0.33	0	15,15,17	1.10	1 (6%)
2	GLC	G	2	2	12,12,12	0.50	0	17,17,17	0.98	1 (5%)
2	GLC	H	1	2	11,11,12	0.30	0	15,15,17	0.92	0
2	GLC	H	2	2	12,12,12	0.54	0	17,17,17	0.59	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	E	1	2	-	0/2/19/22	0/1/1/1
2	GLC	E	2	2	-	0/2/22/22	0/1/1/1
2	GLC	F	1	2	-	0/2/19/22	0/1/1/1
2	GLC	F	2	2	-	0/2/22/22	0/1/1/1
2	GLC	G	1	2	-	0/2/19/22	0/1/1/1
2	GLC	G	2	2	-	0/2/22/22	0/1/1/1
2	GLC	H	1	2	-	0/2/19/22	0/1/1/1
2	GLC	H	2	2	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1	GLC	O5-C5-C6	2.74	112.99	107.66
2	G	2	GLC	C6-C5-C4	-2.42	107.07	113.02
2	F	1	GLC	O5-C5-C6	2.40	112.33	107.66
2	E	2	GLC	O5-C5-C6	2.12	111.69	106.44
2	F	2	GLC	O5-C5-C6	2.08	111.60	106.44
2	F	1	GLC	C1-O5-C5	-2.04	109.45	112.19

There are no chirality outliers.

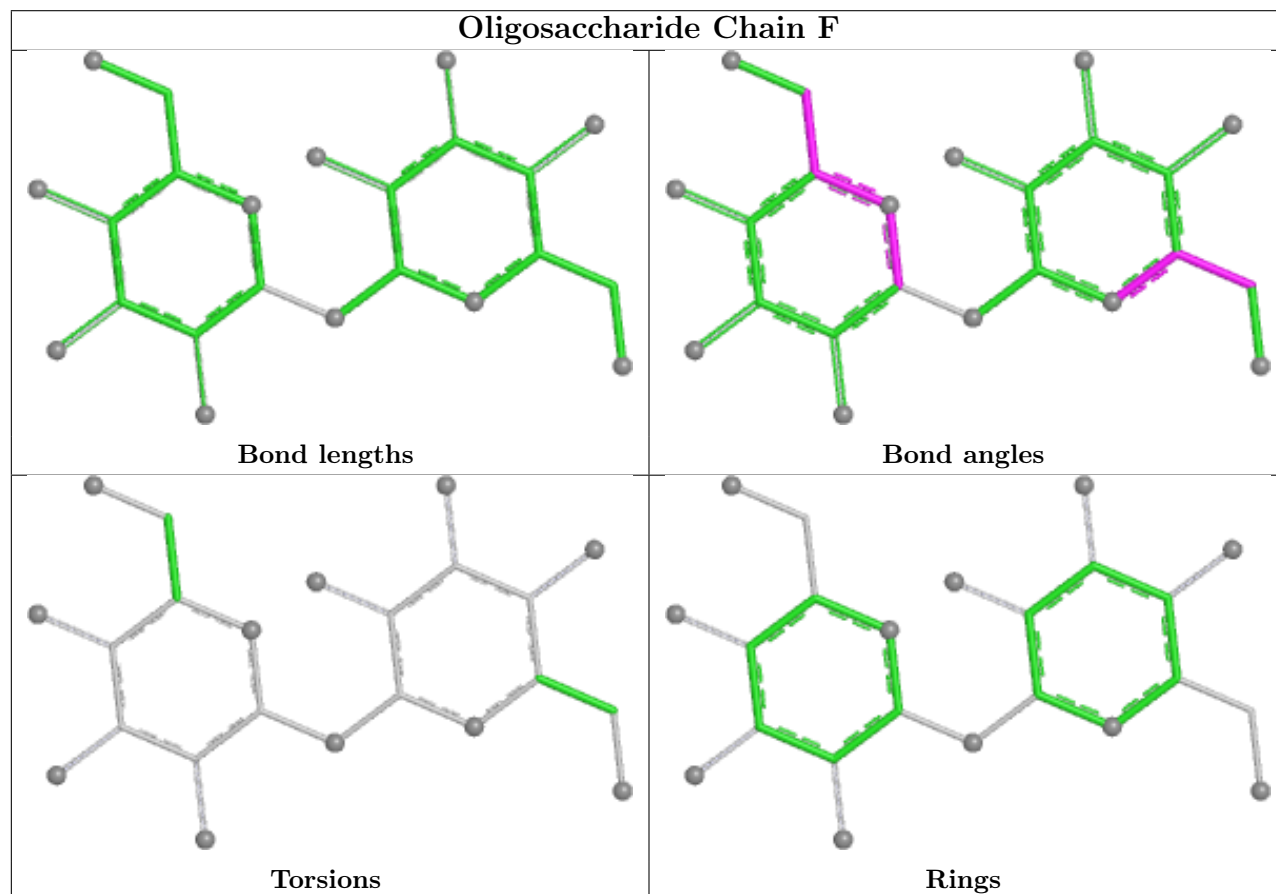
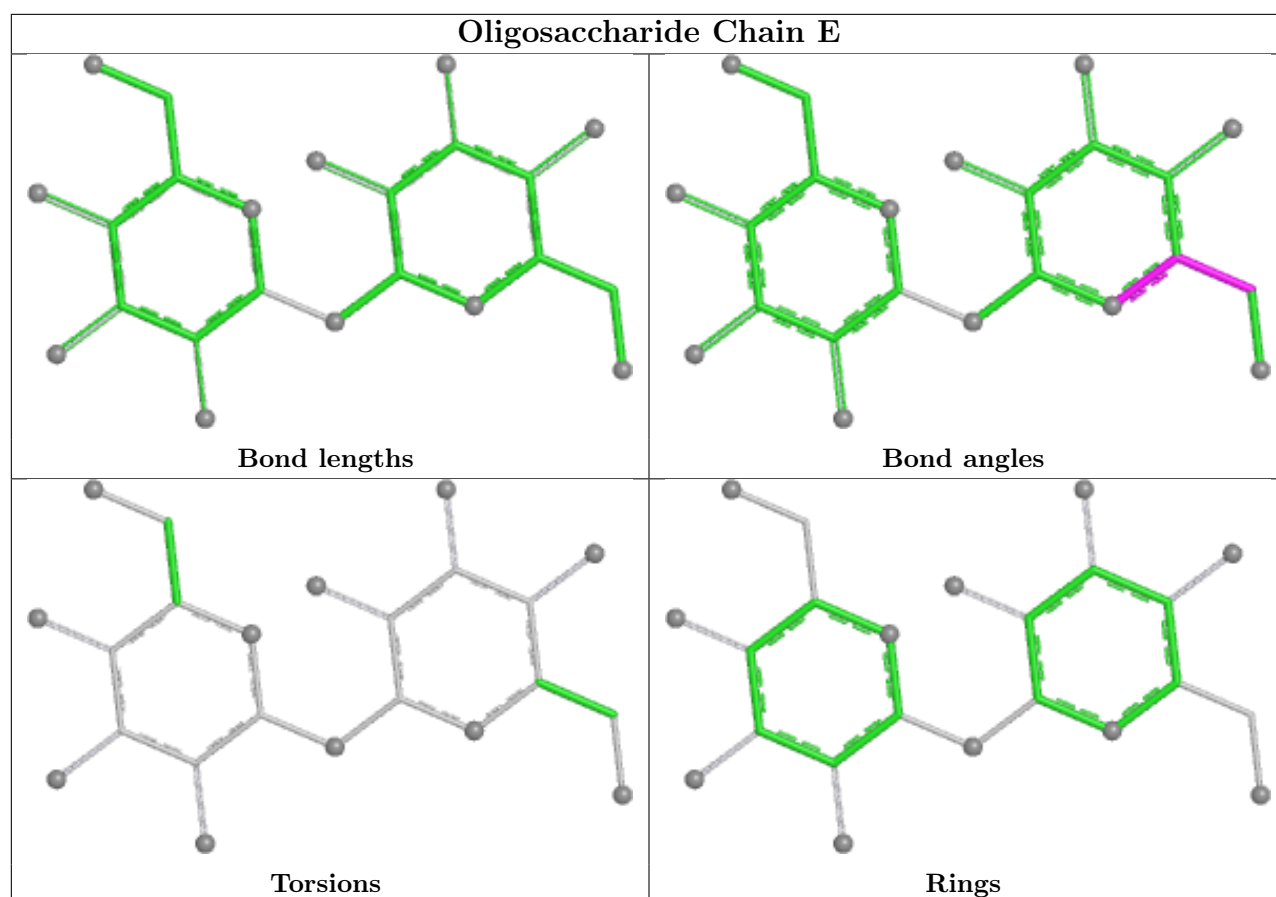
There are no torsion outliers.

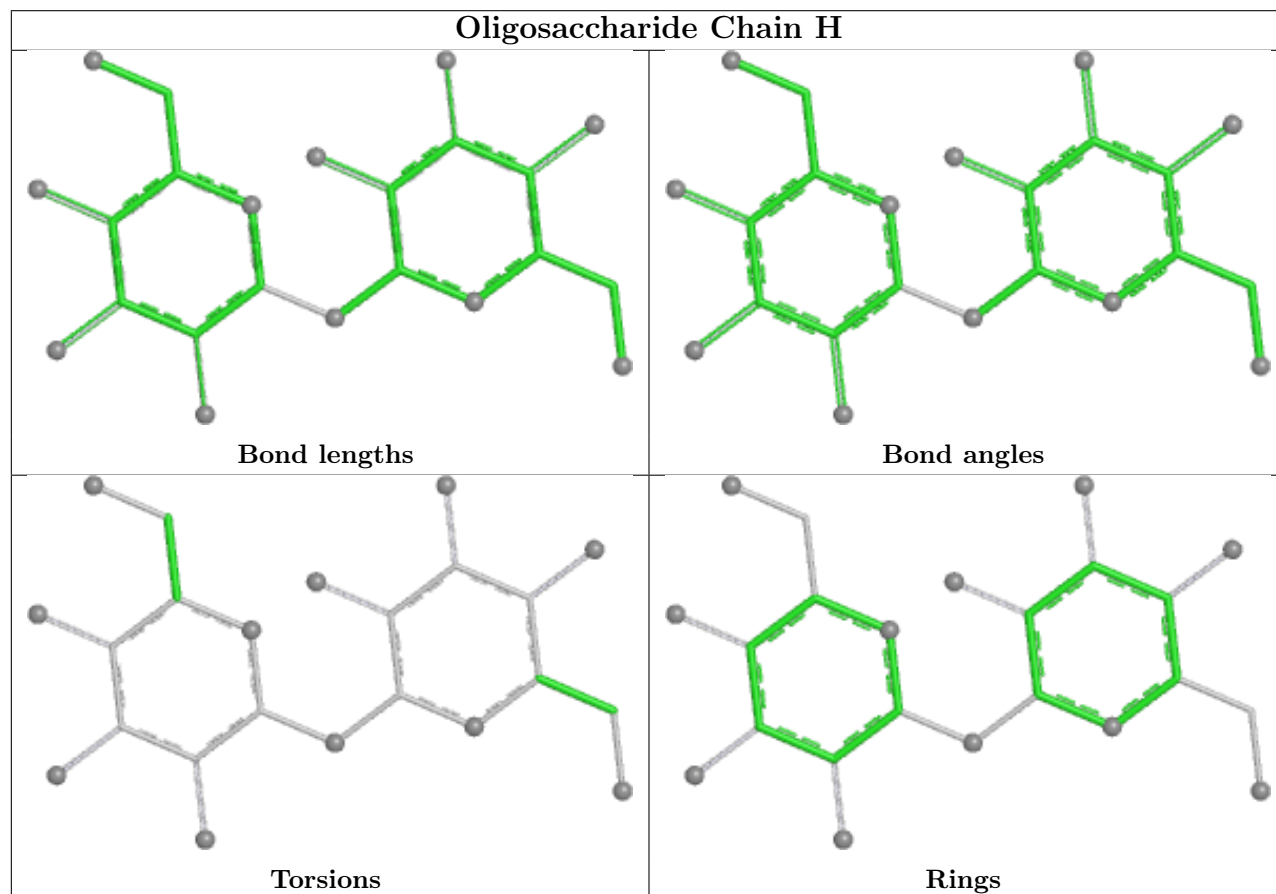
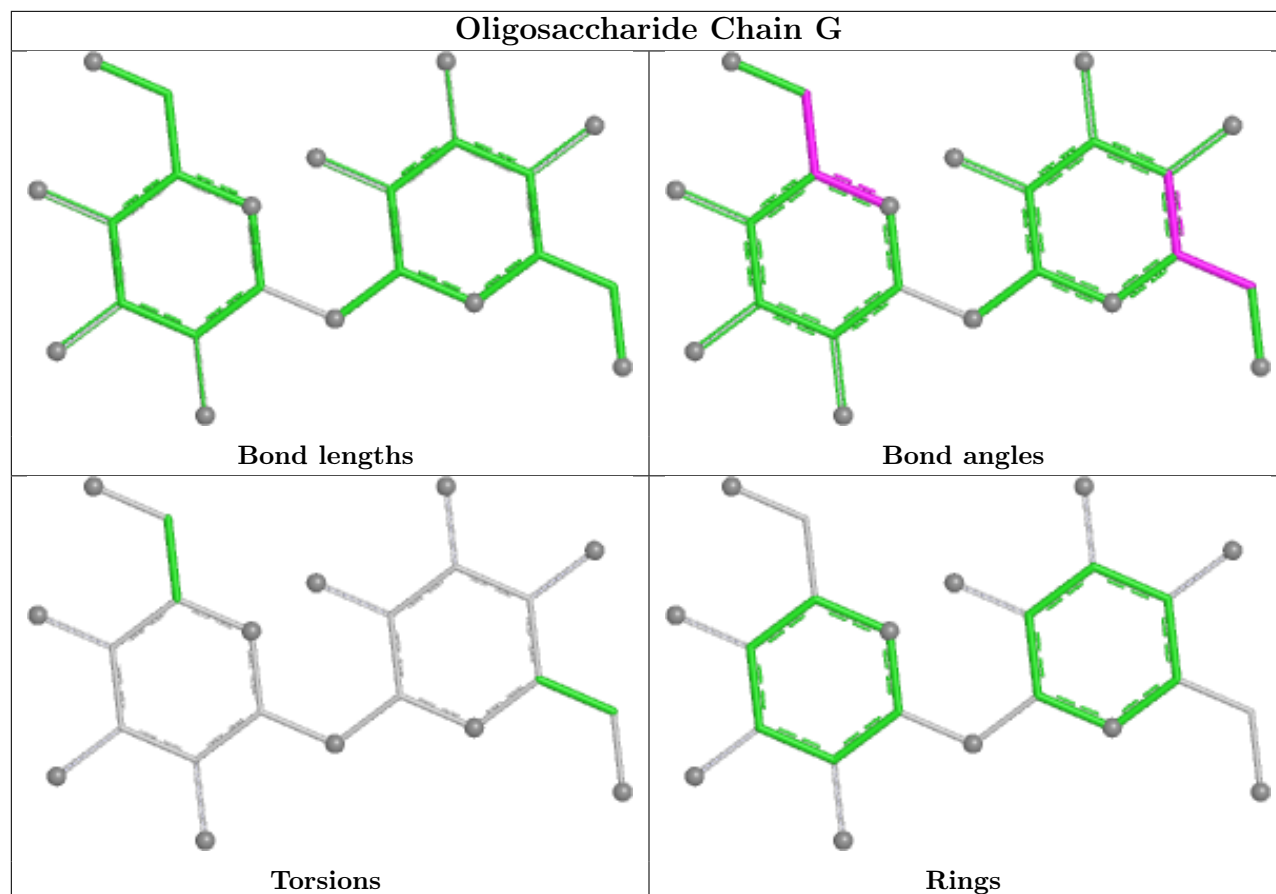
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	2	GLC	1	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.





5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	192/192 (100%)	-0.13	1 (0%) 87 91	6, 12, 23, 30	7 (3%)
1	B	192/192 (100%)	-0.21	2 (1%) 79 84	7, 12, 20, 30	3 (1%)
1	C	192/192 (100%)	0.61	14 (7%) 21 24	9, 17, 29, 41	6 (3%)
1	D	192/192 (100%)	0.54	13 (6%) 23 26	10, 16, 29, 43	8 (4%)
All	All	768/768 (100%)	0.21	30 (3%) 43 48	6, 15, 26, 43	24 (3%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	42	ILE	4.6
1	D	49	ASN	4.1
1	D	44	GLY	4.0
1	D	45[A]	THR	3.9
1	A	49	ASN	3.8
1	C	49	ASN	3.7
1	C	42	ILE	3.2
1	C	192	ALA	3.2
1	D	47	PHE	3.1
1	C	40	GLY	3.0
1	D	145	LEU	3.0
1	D	149	GLY	2.9
1	C	148	ASP	2.9
1	C	47	PHE	2.8
1	B	49	ASN	2.8
1	C	51[A]	SER	2.6
1	D	192	ALA	2.6
1	C	61	GLY	2.5
1	C	91	ALA	2.5
1	C	56	VAL	2.5
1	C	71	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	43	PRO	2.4
1	D	63	VAL	2.4
1	D	46[A]	LYS	2.3
1	B	192	ALA	2.3
1	C	145	LEU	2.2
1	C	44	GLY	2.1
1	D	58	SER	2.1
1	C	149	GLY	2.0
1	D	1	ALA	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](#)

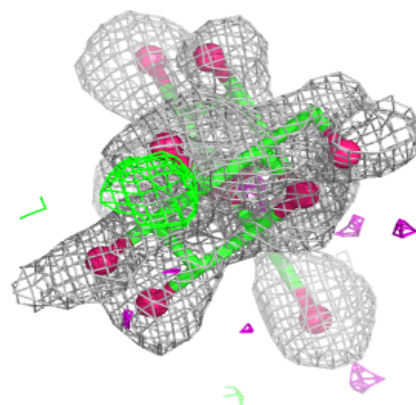
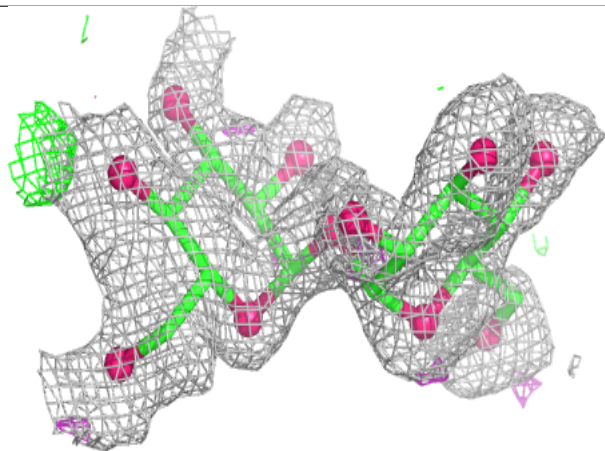
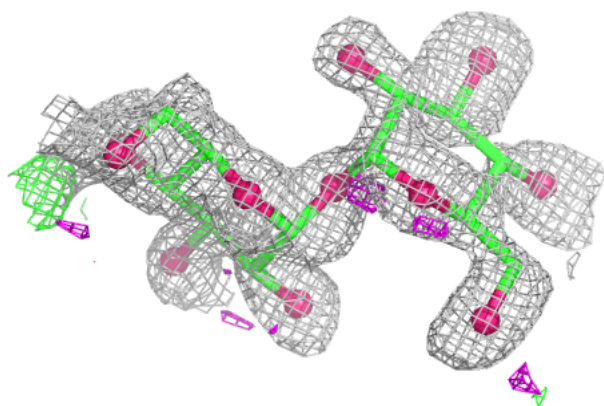
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	GLC	G	1	11/12	0.82	0.12	33,35,37,39	0
2	GLC	E	1	11/12	0.83	0.12	25,27,30,31	0
2	GLC	H	1	11/12	0.86	0.11	36,37,39,40	0
2	GLC	G	2	12/12	0.89	0.10	21,23,27,30	0
2	GLC	H	2	12/12	0.89	0.11	28,30,33,34	0
2	GLC	F	1	11/12	0.90	0.09	25,29,31,32	0
2	GLC	E	2	12/12	0.93	0.09	16,21,24,24	0
2	GLC	F	2	12/12	0.93	0.10	17,20,23,23	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.

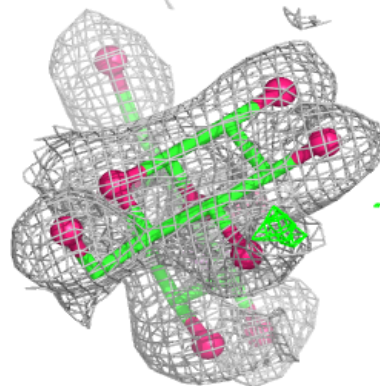
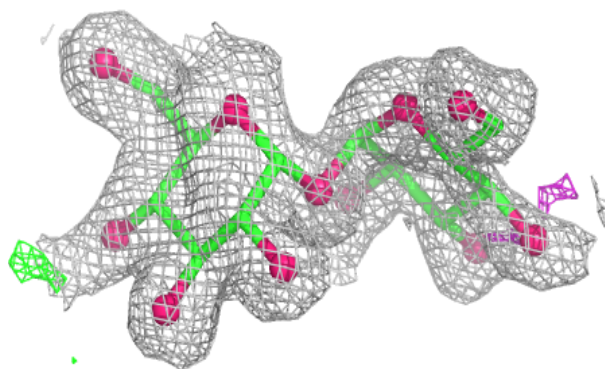
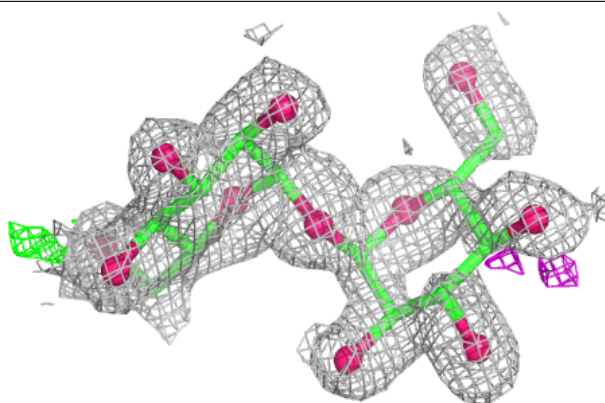
Electron density around Chain E:

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

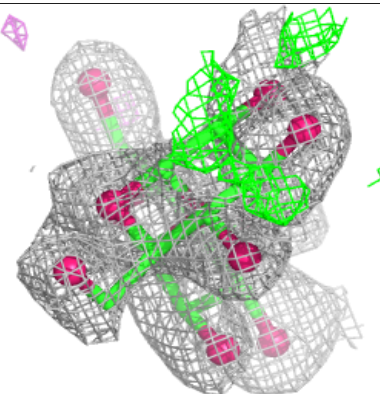
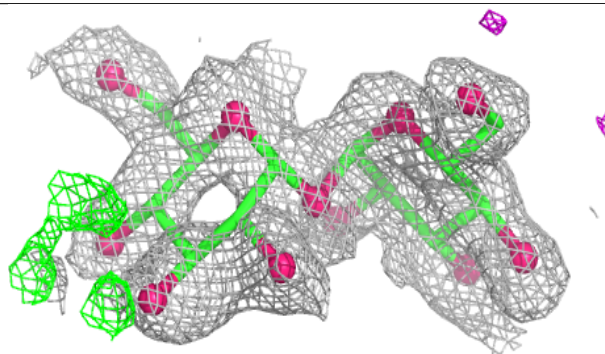
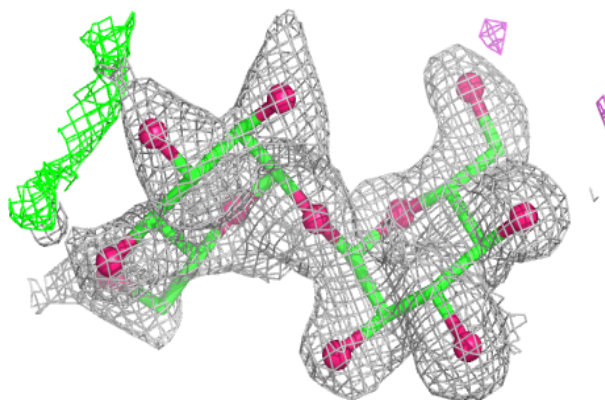


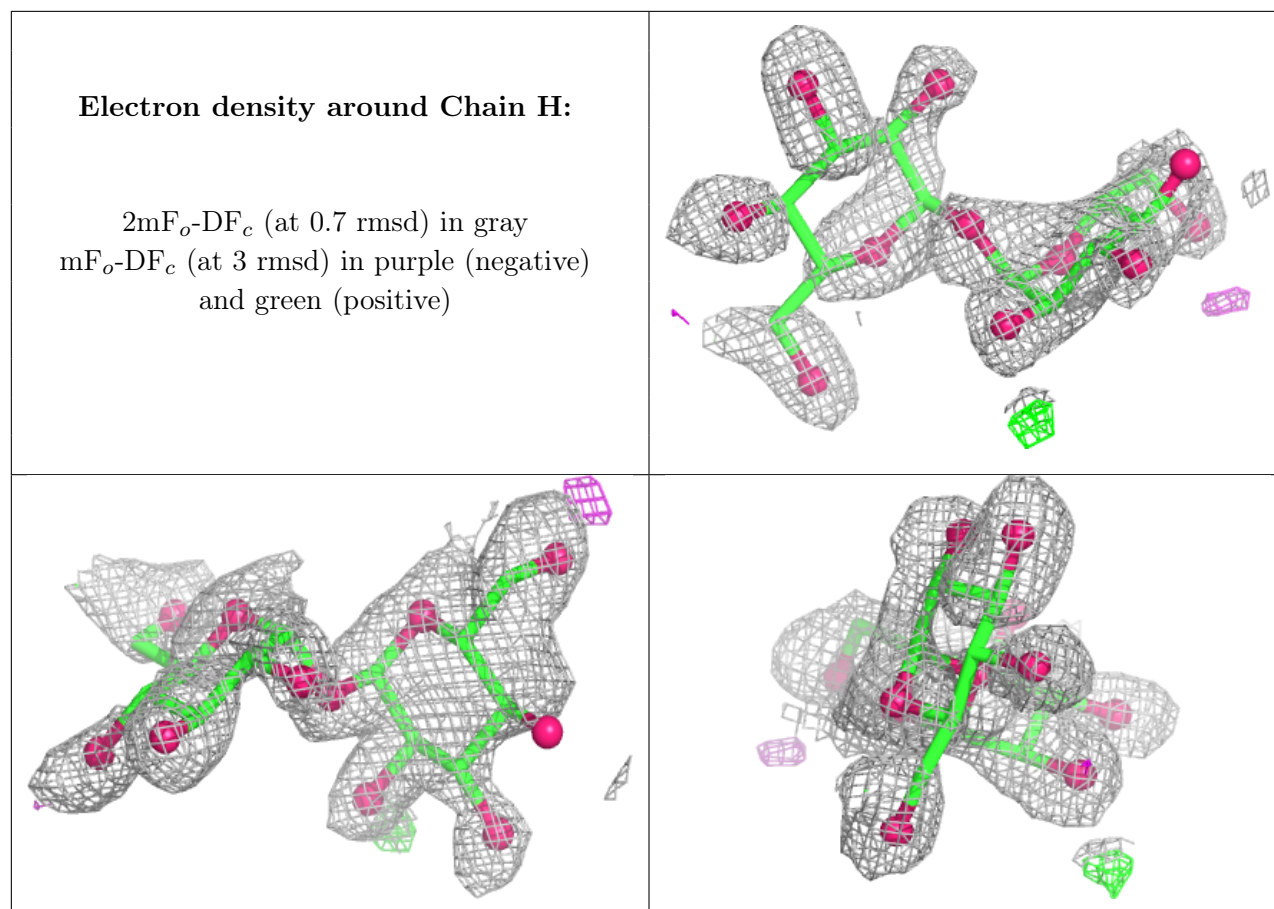
Electron density around Chain F:

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

**Electron density around Chain G:**

$2mF_o - DF_c$ (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($\text{\AA}^2$)	Q<0.9
3	FE	C	201	1/1	0.99	0.03	15,15,15,15	0
3	FE	D	201	1/1	0.99	0.05	13,13,13,13	0
3	FE	A	201	1/1	1.00	0.03	9,9,9,9	0
3	FE	B	5001	1/1	1.00	0.04	9,9,9,9	0

6.5 Other polymers [i](#)

There are no such residues in this entry.