



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:01 AM UTC

PDB ID : 4L2D / pdb_00004l2d
Title : X-ray structure of the Fe(II) form of the iron superoxide dismutase from *Pseudomonas haloplanktis*
Authors : Russo Krauss, I.; Merlino, A.; Sica, F.
Deposited on : 2013-06-04
Resolution : 2.07 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:

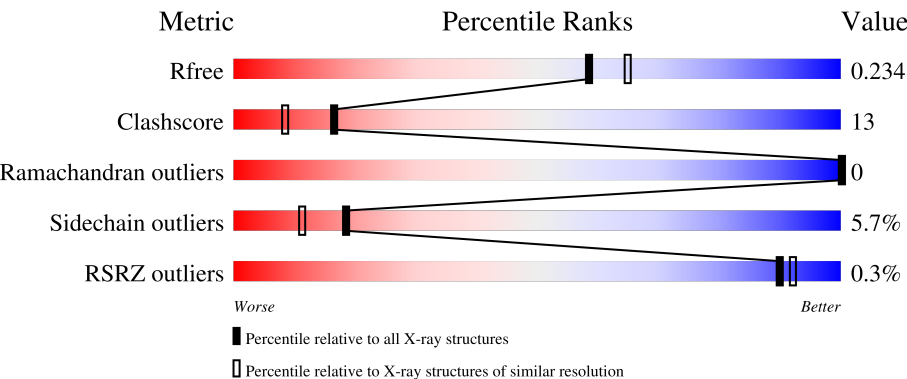
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 2.07 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	67%28% . .
1	B	192	% 72%26% ..
1	C	192	% 70%26% . .
1	D	192	72%22%5% .
2	E	2	100%

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

2 Entry composition

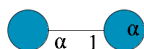
There are 4 unique types of molecules in this entry. The entry contains 6765 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	S	0	0	0
			1511	974	249	287	1			
1	C	192	Total	C	N	O	S	0	0	0
			1511	974	249	287	1			
1	B	192	Total	C	N	O	S	0	1	0
			1513	975	249	288	1			
1	D	192	Total	C	N	O	S	0	0	0
			1511	974	249	287	1			

- 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 (II) ION (CCD ID: FE2) (formula: Fe).

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

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

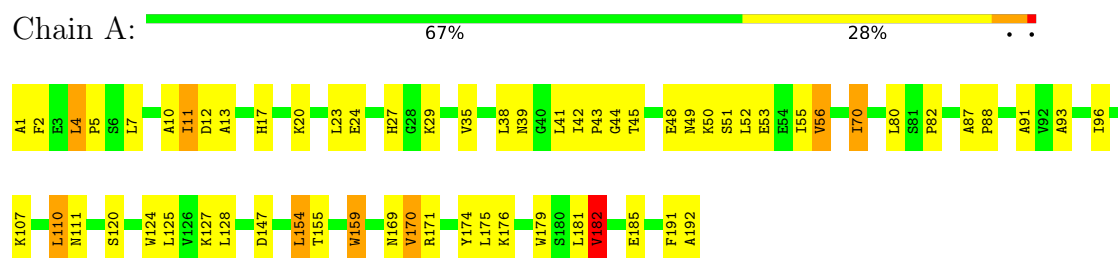
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	150	Total 150	O 150	0	0
4	C	168	Total 168	O 168	0	0
4	B	149	Total 149	O 149	0	0
4	D	156	Total 156	O 156	0	0

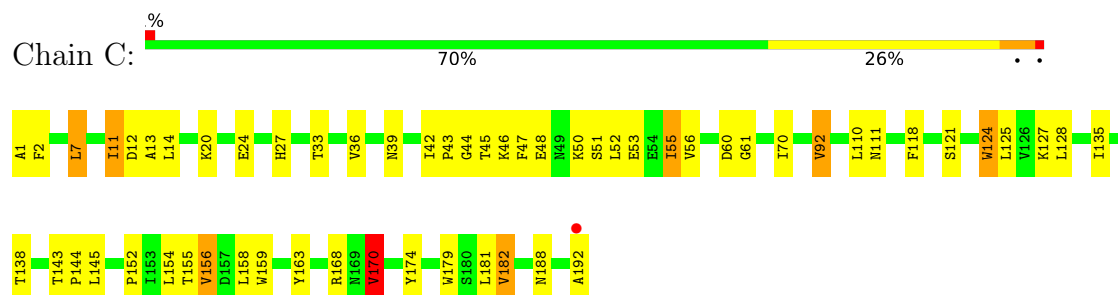
3 Residue-property plots

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.

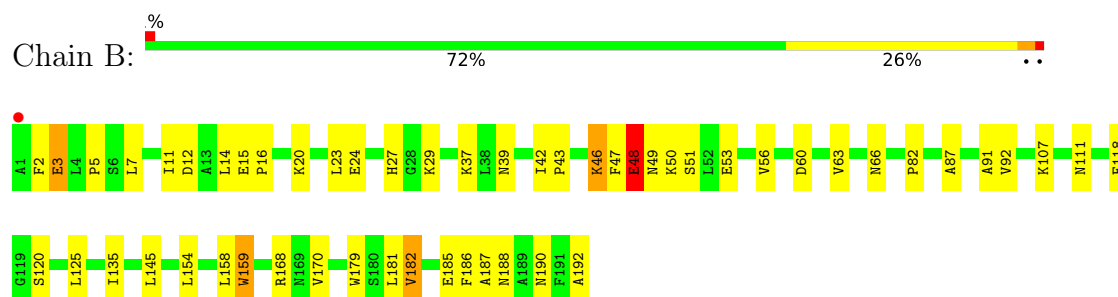
• Molecule 1: Superoxide dismutase [Fe]



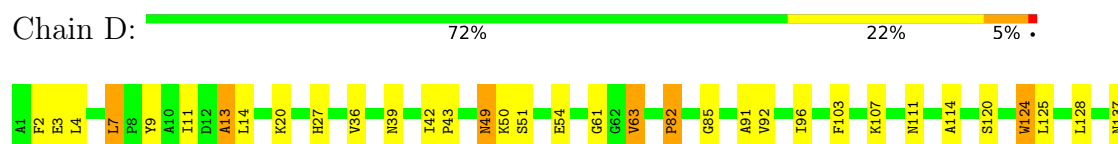
• Molecule 1: Superoxide dismutase [Fe]

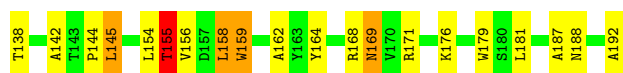


• Molecule 1: Superoxide dismutase [Fe]



• Molecule 1: Superoxide dismutase [Fe]





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

Chain E:  100%



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

Chain F:  50% 50%



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

Chain G:  50% 50%



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

Chain H:  50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.30Å 103.62Å 89.34Å 90.00° 103.68° 90.00°	Depositor
Resolution (Å)	29.20 – 2.07 29.20 – 2.07	Depositor EDS
% Data completeness (in resolution range)	(Not available) (29.20-2.07) 98.2 (29.20-2.07)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.64 (at 2.06Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.200 , 0.220 0.191 , 0.234	Depositor DCC
R_{free} test set	2663 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtriage
Anisotropy	0.735	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.078 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6765	wwPDB-VP
Average B, all atoms (Å ²)	20.0	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 64.50 % 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 8.2069e-06. 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, FE2

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	1.36	7/1560 (0.4%)	1.34	16/2134 (0.7%)
1	B	1.39	5/1566 (0.3%)	1.38	12/2142 (0.6%)
1	C	1.39	4/1560 (0.3%)	1.38	19/2134 (0.9%)
1	D	1.43	11/1560 (0.7%)	1.39	12/2134 (0.6%)
All	All	1.39	27/6246 (0.4%)	1.38	59/8544 (0.7%)

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	170	VAL	CA-CB	8.09	1.64	1.53
1	C	156	VAL	CA-CB	7.41	1.64	1.54
1	D	96	ILE	CA-CB	7.38	1.63	1.54
1	A	96	ILE	CA-CB	7.32	1.62	1.54
1	B	29	LYS	CA-C	7.23	1.57	1.52
1	B	7	LEU	CA-C	6.88	1.60	1.53
1	D	156	VAL	CA-CB	6.80	1.62	1.54
1	C	124	TRP	C-O	-6.11	1.16	1.23
1	D	171	ARG	C-O	-5.83	1.19	1.24
1	C	12	ASP	CB-CG	-5.63	1.38	1.52
1	D	13	ALA	CA-CB	5.59	1.63	1.53
1	A	93	ALA	CA-CB	5.54	1.62	1.53
1	D	164	TYR	C-O	-5.51	1.17	1.24
1	B	182	VAL	CA-CB	-5.50	1.47	1.54
1	A	182	VAL	N-CA	5.32	1.52	1.46
1	D	91	ALA	CA-CB	5.31	1.61	1.53
1	D	137	ASN	C-O	5.29	1.30	1.24
1	D	9	TYR	C-O	-5.26	1.17	1.23
1	D	187	ALA	CA-CB	5.20	1.61	1.53
1	D	63	VAL	CA-CB	5.13	1.60	1.54
1	A	80	LEU	N-CA	5.11	1.52	1.45
1	B	186	PHE	CA-C	5.11	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	91	ALA	CA-CB	5.03	1.61	1.53
1	B	135	ILE	CA-CB	5.02	1.60	1.54
1	D	162	ALA	CA-CB	5.02	1.61	1.53
1	A	88	PRO	CA-C	5.01	1.58	1.52
1	C	138	THR	CA-C	5.00	1.58	1.52

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	87	ALA	N-CA-C	9.05	121.33	109.83
1	D	4	LEU	CA-C-N	-8.74	111.38	120.03
1	D	4	LEU	C-N-CA	-8.74	111.38	120.03
1	D	50	LYS	N-CA-C	8.44	123.00	110.52
1	D	7	LEU	N-CA-C	-7.31	100.54	109.83
1	D	155	THR	CB-CA-C	-7.27	93.42	109.56
1	B	182	VAL	CB-CA-C	-7.24	100.27	111.71
1	A	170	VAL	N-CA-C	7.23	117.96	106.32
1	B	82	PRO	N-CA-C	-7.20	104.86	113.86
1	D	125	LEU	N-CA-C	-7.16	97.57	109.24
1	C	125	LEU	N-CA-C	-7.04	97.76	109.24
1	C	170	VAL	N-CA-C	7.04	117.65	106.32
1	A	169	ASN	CA-C-N	-6.69	115.23	122.59
1	A	169	ASN	C-N-CA	-6.69	115.23	122.59
1	A	125	LEU	N-CA-C	-6.67	97.85	108.73
1	C	121	SER	N-CA-C	6.57	117.14	107.88
1	B	125	LEU	N-CA-C	-6.55	98.58	109.46
1	A	182	VAL	CB-CA-C	-6.55	100.55	111.29
1	D	63	VAL	N-CA-C	-6.47	104.21	110.42
1	D	159	TRP	N-CA-C	-6.46	101.57	110.35
1	A	159	TRP	N-CA-C	-6.21	101.23	110.23
1	C	7	LEU	CA-C-N	-6.13	114.58	120.83
1	C	7	LEU	C-N-CA	-6.13	114.58	120.83
1	A	87	ALA	N-CA-C	6.04	117.31	109.64
1	A	41	LEU	N-CA-C	6.01	119.80	112.23
1	C	182	VAL	N-CA-CB	5.84	117.75	110.05
1	A	170	VAL	CB-CA-C	5.77	119.61	112.45
1	D	82	PRO	N-CA-C	-5.77	106.93	114.03
1	C	168	ARG	CB-CA-C	-5.77	109.91	116.54
1	C	70	ILE	CB-CA-C	-5.76	104.27	112.22
1	A	154	LEU	CA-CB-CG	5.74	136.37	116.30
1	C	118	PHE	N-CA-C	5.71	118.61	110.10
1	B	159	TRP	N-CA-C	-5.68	101.99	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	LEU	CA-C-N	-5.65	113.87	119.92
1	A	4	LEU	C-N-CA	-5.65	113.87	119.92
1	A	82	PRO	N-CA-C	-5.61	107.13	114.03
1	C	13	ALA	N-CA-C	5.61	119.22	112.38
1	A	70	ILE	CB-CA-C	-5.59	104.70	112.02
1	C	182	VAL	CB-CA-C	-5.57	102.91	111.71
1	A	13	ALA	N-CA-C	5.53	119.28	112.54
1	D	155	THR	N-CA-CB	5.49	121.73	111.53
1	B	63	VAL	N-CA-C	-5.48	105.16	110.42
1	C	7	LEU	N-CA-C	-5.43	102.59	110.08
1	C	55	ILE	N-CA-C	-5.39	105.24	110.42
1	A	49	ASN	N-CA-C	5.38	119.82	112.88
1	B	51	SER	N-CA-C	-5.38	103.59	110.53
1	B	135	ILE	N-CA-C	-5.38	100.58	108.11
1	D	124	TRP	N-CA-C	5.36	118.22	109.59
1	B	118	PHE	N-CA-C	5.27	117.87	109.96
1	C	11	ILE	CA-C-N	5.19	131.07	121.52
1	C	11	ILE	C-N-CA	5.19	131.07	121.52
1	C	60	ASP	N-CA-C	-5.14	101.56	108.19
1	C	12	ASP	N-CA-CB	-5.13	102.63	110.33
1	C	92	VAL	N-CA-C	5.13	115.85	110.62
1	C	159	TRP	N-CA-C	-5.12	102.81	110.23
1	B	7	LEU	N-CA-C	-5.08	103.39	109.83
1	B	168	ARG	CB-CA-C	-5.08	110.70	116.54
1	B	48	GLU	N-CA-C	5.04	117.43	111.33
1	D	168	ARG	CB-CA-C	-5.00	110.78	116.54

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	1511	0	1419	44	0
1	B	1513	0	1420	35	0
1	C	1511	0	1419	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1511	0	1419	36	0
2	E	23	0	21	0	0
2	F	23	0	21	1	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	150	0	0	10	0
4	B	149	0	0	9	0
4	C	168	0	0	10	0
4	D	156	0	0	5	0
All	All	6765	0	5761	153	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 13.

All (153) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:ALA:HB2	4:B:415:HOH:O	1.28	1.26
1:D:192:ALA:HB2	4:D:455:HOH:O	1.42	1.17
1:C:192:ALA:HB2	4:C:421:HOH:O	1.50	1.12
1:A:185:GLU:HG2	4:A:429:HOH:O	1.52	1.08
1:A:42:ILE:HD11	4:A:376:HOH:O	1.56	1.05
1:C:92:VAL:H	1:C:188:ASN:HD21	1.08	0.99
1:D:124:TRP:CE3	1:D:155:THR:HG23	1.98	0.98
1:A:192:ALA:HB2	4:A:407:HOH:O	1.61	0.98
1:A:111:ASN:HD21	1:A:179:TRP:HE1	1.06	0.96
1:B:2:PHE:H	1:B:39:ASN:HD21	1.12	0.95
1:D:2:PHE:H	1:D:39:ASN:HD21	1.13	0.91
1:C:44:GLY:N	1:C:48:GLU:OE2	2.03	0.91
1:C:111:ASN:HD21	1:C:179:TRP:HE1	1.13	0.90
1:B:111:ASN:HD21	1:B:179:TRP:HE1	1.16	0.89
1:A:2:PHE:H	1:A:39:ASN:HD21	1.21	0.87
1:D:111:ASN:HD21	1:D:179:TRP:HE1	1.16	0.87
1:A:53:GLU:HG3	4:A:388:HOH:O	1.74	0.86
1:C:42:ILE:HD11	4:C:384:HOH:O	1.75	0.85
1:C:45:THR:HG21	4:C:439:HOH:O	1.78	0.83
1:C:20:LYS:O	1:C:24:GLU:HG3	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:27:HIS:HD2	4:C:418:HOH:O	1.66	0.78
1:B:92:VAL:H	1:B:188:ASN:HD21	1.32	0.77
1:A:111:ASN:ND2	1:A:179:TRP:HE1	1.83	0.76
1:B:2:PHE:H	1:B:39:ASN:ND2	1.84	0.75
1:A:27:HIS:HD2	4:A:410:HOH:O	1.68	0.75
1:A:29:LYS:HE2	4:B:370:HOH:O	1.85	0.75
1:C:45:THR:O	1:C:48:GLU:HG3	1.88	0.74
1:A:50:LYS:HE3	4:A:418:HOH:O	1.87	0.73
1:A:44:GLY:N	1:A:48:GLU:OE1	2.22	0.72
1:B:46:LYS:HD3	1:B:50:LYS:HE3	1.72	0.72
1:C:2:PHE:H	1:C:39:ASN:HD21	1.37	0.72
1:B:20:LYS:HE2	1:B:24:GLU:OE2	1.91	0.71
1:C:92:VAL:H	1:C:188:ASN:ND2	1.84	0.71
1:A:45:THR:O	1:A:48:GLU:HG3	1.91	0.70
1:A:42:ILE:CD1	4:A:376:HOH:O	2.28	0.70
1:D:92:VAL:HG22	1:D:188:ASN:OD1	1.93	0.69
1:B:2:PHE:N	1:B:39:ASN:HD21	1.90	0.68
1:C:127:LYS:NZ	4:C:434:HOH:O	2.27	0.68
1:C:111:ASN:ND2	1:C:179:TRP:HE1	1.91	0.67
1:D:124:TRP:CD2	1:D:155:THR:HG23	2.30	0.66
1:A:11:ILE:HD12	1:A:12:ASP:N	2.11	0.64
1:D:63:VAL:HG23	4:D:398:HOH:O	1.98	0.63
1:D:27:HIS:HD2	4:D:416:HOH:O	1.80	0.63
1:C:1:ALA:HA	4:C:384:HOH:O	1.99	0.62
1:A:1:ALA:HA	4:A:376:HOH:O	2.00	0.61
1:D:124:TRP:CZ3	1:D:155:THR:HG23	2.34	0.61
1:B:53:GLU:HA	1:B:56:VAL:HG12	1.81	0.61
1:D:169:ASN:HD22	1:D:169:ASN:H	1.47	0.61
1:A:120:SER:HB3	1:A:159:TRP:CD2	2.36	0.61
1:D:49:ASN:CB	4:D:343:HOH:O	2.49	0.60
1:C:53:GLU:HG3	4:C:397:HOH:O	1.99	0.60
1:C:144:PRO:HG2	1:C:152:PRO:HG3	1.83	0.60
1:A:147:ASP:OD2	4:A:450:HOH:O	2.17	0.60
1:B:91:ALA:HA	4:B:410:HOH:O	2.01	0.59
1:B:92:VAL:H	1:B:188:ASN:ND2	1.99	0.59
1:C:124:TRP:CE3	1:C:155:THR:HB	2.39	0.58
1:C:42:ILE:HG13	1:C:43:PRO:HD3	1.85	0.57
1:C:46:LYS:HE3	1:C:47:PHE:CZ	2.39	0.57
1:D:107:LYS:HE3	1:D:179:TRP:CG	2.40	0.56
1:B:42:ILE:N	1:B:43:PRO:HD3	2.22	0.54
1:B:47:PHE:HA	1:B:50:LYS:HD2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:ILE:CG1	1:A:43:PRO:HD3	2.37	0.54
1:B:185:GLU:OE2	1:B:185:GLU:HA	2.09	0.53
1:D:42:ILE:O	1:D:43:PRO:C	2.51	0.52
1:A:27:HIS:CD2	4:A:410:HOH:O	2.51	0.52
1:D:49:ASN:HB3	4:D:343:HOH:O	2.10	0.52
1:D:145:LEU:HD22	1:D:145:LEU:O	2.09	0.52
1:A:20:LYS:O	1:A:24:GLU:HG3	2.10	0.51
1:C:92:VAL:HG23	1:C:188:ASN:ND2	2.25	0.51
1:C:110:LEU:HA	1:C:135:ILE:HD13	1.91	0.51
1:C:33:THR:HA	1:C:36:VAL:HG22	1.92	0.51
1:C:52:LEU:O	1:C:56:VAL:HG23	2.10	0.51
1:B:120:SER:HB3	1:B:159:TRP:CD2	2.46	0.51
1:D:120:SER:HB3	1:D:159:TRP:CE2	2.45	0.51
1:C:110:LEU:C	1:C:110:LEU:HD23	2.35	0.51
1:B:5:PRO:O	1:B:27:HIS:HE1	1.94	0.51
1:D:92:VAL:HG22	1:D:188:ASN:CG	2.35	0.51
1:D:2:PHE:N	1:D:39:ASN:HD21	1.95	0.50
1:D:111:ASN:ND2	1:D:179:TRP:HE1	1.97	0.50
1:C:170:VAL:HG13	4:C:365:HOH:O	2.13	0.49
1:B:42:ILE:N	1:B:43:PRO:CD	2.76	0.49
1:B:11:ILE:O	1:B:23:LEU:HD12	2.11	0.49
1:C:50:LYS:HE2	4:C:383:HOH:O	2.12	0.49
1:C:55:ILE:O	1:C:56:VAL:C	2.56	0.49
1:B:3:GLU:HG3	4:B:400:HOH:O	2.12	0.49
1:B:37:LYS:HD2	1:B:66:ASN:HD21	1.77	0.49
1:A:127:LYS:HD3	1:A:191:PHE:CD1	2.48	0.48
1:A:107:LYS:HE3	1:A:179:TRP:CD1	2.49	0.48
1:B:48:GLU:O	1:B:48:GLU:HG3	2.13	0.48
1:D:51:SER:OG	1:D:54:GLU:HB2	2.14	0.48
1:D:13:ALA:HB1	1:D:82:PRO:HB3	1.96	0.47
1:D:120:SER:HB3	1:D:159:TRP:CD2	2.49	0.47
1:D:124:TRP:CE2	1:D:144:PRO:HD3	2.50	0.47
1:B:107:LYS:CE	4:B:325:HOH:O	2.63	0.46
1:A:42:ILE:HG12	1:A:43:PRO:HD3	1.98	0.46
1:C:124:TRP:CZ3	1:C:155:THR:HB	2.51	0.46
1:D:61:GLY:HA2	2:F:1:GLC:O3	2.16	0.46
1:A:120:SER:HB3	1:A:159:TRP:CE2	2.51	0.46
1:C:42:ILE:CG1	1:C:43:PRO:HD3	2.45	0.46
1:C:43:PRO:O	1:C:45:THR:HG23	2.15	0.46
1:C:7:LEU:HD12	1:C:7:LEU:HA	1.87	0.45
1:D:11:ILE:HG23	1:D:20:LYS:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:37:LYS:HD2	4:B:421:HOH:O	2.15	0.45
1:A:53:GLU:HA	1:A:56:VAL:HG13	1.98	0.45
1:B:46:LYS:HB3	1:B:46:LYS:NZ	2.31	0.45
1:B:53:GLU:HG3	4:B:346:HOH:O	2.17	0.45
1:A:2:PHE:N	1:A:39:ASN:HD21	2.02	0.44
1:B:46:LYS:HD3	1:B:50:LYS:CE	2.45	0.44
1:C:110:LEU:HD23	1:C:110:LEU:O	2.18	0.44
1:C:61:GLY:HA2	2:H:1:GLC:O3	2.16	0.44
1:D:103:PHE:CZ	1:D:107:LYS:HD2	2.53	0.44
1:A:17:HIS:HB2	1:A:181:LEU:HD11	1.98	0.44
1:D:124:TRP:CD2	1:D:155:THR:CG2	2.98	0.43
1:A:42:ILE:HG13	1:A:43:PRO:HD3	2.00	0.43
1:C:11:ILE:HG23	1:C:20:LYS:HG3	2.01	0.43
1:C:27:HIS:CD2	4:C:418:HOH:O	2.53	0.43
1:C:163:TYR:HB3	1:C:174:TYR:CD1	2.54	0.43
1:A:175:LEU:HD23	1:A:175:LEU:HA	1.91	0.43
1:A:181:LEU:O	1:A:182:VAL:C	2.61	0.43
1:A:11:ILE:HD12	1:A:11:ILE:C	2.43	0.43
1:D:42:ILE:N	1:D:43:PRO:CD	2.82	0.43
1:A:51:SER:O	1:A:52:LEU:C	2.61	0.43
1:B:14:LEU:HD22	1:B:181:LEU:HD22	2.01	0.42
1:A:7:LEU:HD21	1:A:23:LEU:HD13	2.01	0.42
1:A:110:LEU:HD12	1:A:110:LEU:C	2.45	0.42
1:A:35:VAL:HA	1:A:70:ILE:HD11	2.02	0.42
1:A:171:ARG:O	1:A:174:TYR:HB3	2.19	0.42
1:A:11:ILE:O	1:A:20:LYS:HA	2.20	0.42
1:B:43:PRO:HA	1:B:48:GLU:OE2	2.20	0.42
1:D:7:LEU:HD13	1:D:27:HIS:CG	2.55	0.42
1:B:12:ASP:O	1:B:15:GLU:HG3	2.20	0.42
1:D:85:GLY:HA2	1:D:179:TRP:O	2.20	0.42
1:B:154:LEU:HG	1:B:187:ALA:HB2	2.02	0.42
1:A:4:LEU:HD12	1:A:5:PRO:HD2	2.02	0.41
1:A:39:ASN:HD22	1:A:39:ASN:HA	1.67	0.41
1:A:10:ALA:C	1:A:12:ASP:H	2.27	0.41
1:D:138:THR:HB	1:D:142:ALA:HB3	2.01	0.41
1:B:190:ASN:ND2	4:B:381:HOH:O	2.53	0.41
1:B:46:LYS:O	1:B:46:LYS:HG2	2.21	0.41
1:B:53:GLU:HA	1:B:56:VAL:CG1	2.47	0.41
1:D:39:ASN:HD22	1:D:39:ASN:HA	1.71	0.41
1:A:55:ILE:O	1:A:56:VAL:C	2.63	0.41
1:A:124:TRP:CZ3	1:A:155:THR:HB	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:42:ILE:N	1:D:43:PRO:HD3	2.36	0.41
1:A:11:ILE:HD13	1:A:20:LYS:HD2	2.04	0.40
1:D:14:LEU:HD22	1:D:181:LEU:HD22	2.02	0.40
1:B:37:LYS:HE3	4:B:435:HOH:O	2.20	0.40
1:B:39:ASN:O	1:B:43:PRO:HD3	2.20	0.40
1:D:7:LEU:HD12	1:D:7:LEU:HA	1.85	0.40
1:D:114:ALA:HB1	1:D:158:LEU:HD21	2.04	0.40
1:A:38:LEU:HD22	1:A:70:ILE:HD12	2.04	0.40
1:C:14:LEU:HD22	1:C:181:LEU:HD22	2.03	0.40
1:C:51:SER:O	1:C:52:LEU:C	2.64	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	190/192 (99%)	185 (97%)	5 (3%)	0	100	100
1	B	191/192 (100%)	184 (96%)	7 (4%)	0	100	100
1	C	190/192 (99%)	183 (96%)	7 (4%)	0	100	100
1	D	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
All	All	761/768 (99%)	739 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	158/158 (100%)	150 (95%)	8 (5%)	21	14
1	B	159/158 (101%)	149 (94%)	10 (6%)	16	9
1	C	158/158 (100%)	150 (95%)	8 (5%)	21	14
1	D	158/158 (100%)	148 (94%)	10 (6%)	16	9
All	All	633/632 (100%)	597 (94%)	36 (6%)	18	11

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ILE
1	A	56	VAL
1	A	110	LEU
1	A	128	LEU
1	A	154	LEU
1	A	170	VAL
1	A	176	LYS
1	A	182	VAL
1	C	128	LEU
1	C	143	THR
1	C	145	LEU
1	C	154	LEU
1	C	156	VAL
1	C	158	LEU
1	C	170	VAL
1	C	182	VAL
1	B	3	GLU
1	B	16	PRO
1	B	46	LYS
1	B	48	GLU
1	B	49	ASN
1	B	60	ASP
1	B	145	LEU
1	B	158	LEU
1	B	170	VAL
1	B	182	VAL
1	D	3	GLU
1	D	36	VAL
1	D	49	ASN
1	D	128	LEU

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Mol	Chain	Res	Type
1	D	145	LEU
1	D	154	LEU
1	D	155	THR
1	D	158	LEU
1	D	169	ASN
1	D	176	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	HIS
1	A	27	HIS
1	A	32	ASN
1	A	39	ASN
1	A	111	ASN
1	A	190	ASN
1	C	27	HIS
1	C	39	ASN
1	C	97	ASN
1	C	111	ASN
1	C	140	ASN
1	C	188	ASN
1	C	190	ASN
1	B	27	HIS
1	B	32	ASN
1	B	39	ASN
1	B	66	ASN
1	B	97	ASN
1	B	111	ASN
1	B	116	ASN
1	B	140	ASN
1	B	188	ASN
1	B	190	ASN
1	D	27	HIS
1	D	39	ASN
1	D	49	ASN
1	D	97	ASN
1	D	111	ASN
1	D	140	ASN
1	D	169	ASN
1	D	190	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	0.35	0	15,15,17	0.94	0
2	GLC	E	2	2	12,12,12	0.56	0	17,17,17	0.73	0
2	GLC	F	1	2	11,11,12	0.33	0	15,15,17	0.98	1 (6%)
2	GLC	F	2	2	12,12,12	0.53	0	17,17,17	0.66	0
2	GLC	G	1	2	11,11,12	0.31	0	15,15,17	0.86	0
2	GLC	G	2	2	12,12,12	0.53	0	17,17,17	0.91	1 (5%)
2	GLC	H	1	2	11,11,12	0.26	0	15,15,17	0.93	0
2	GLC	H	2	2	12,12,12	0.56	0	17,17,17	0.69	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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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 (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	GLC	O5-C5-C6	2.22	111.97	107.66
2	G	2	GLC	C6-C5-C4	-2.02	108.06	113.02

There are no chirality outliers.

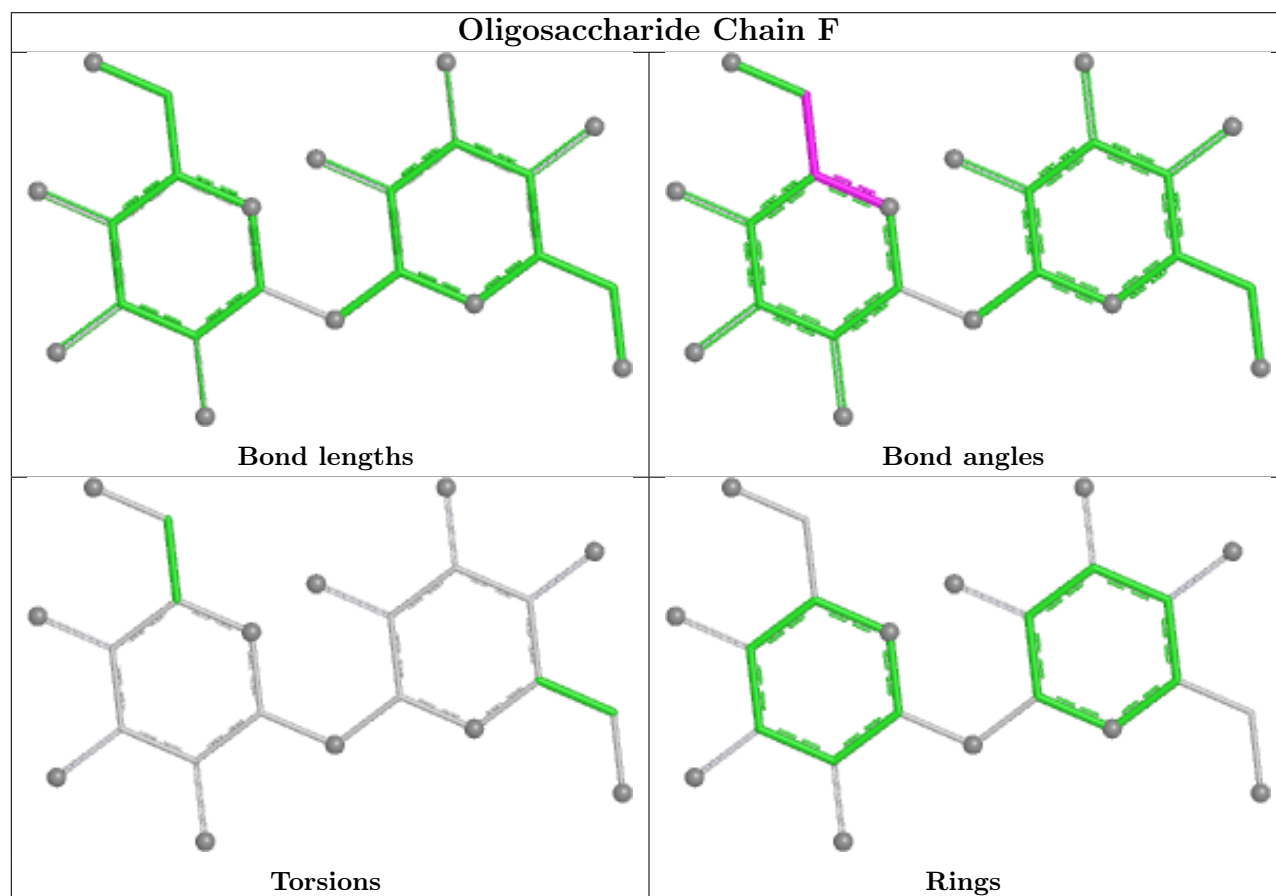
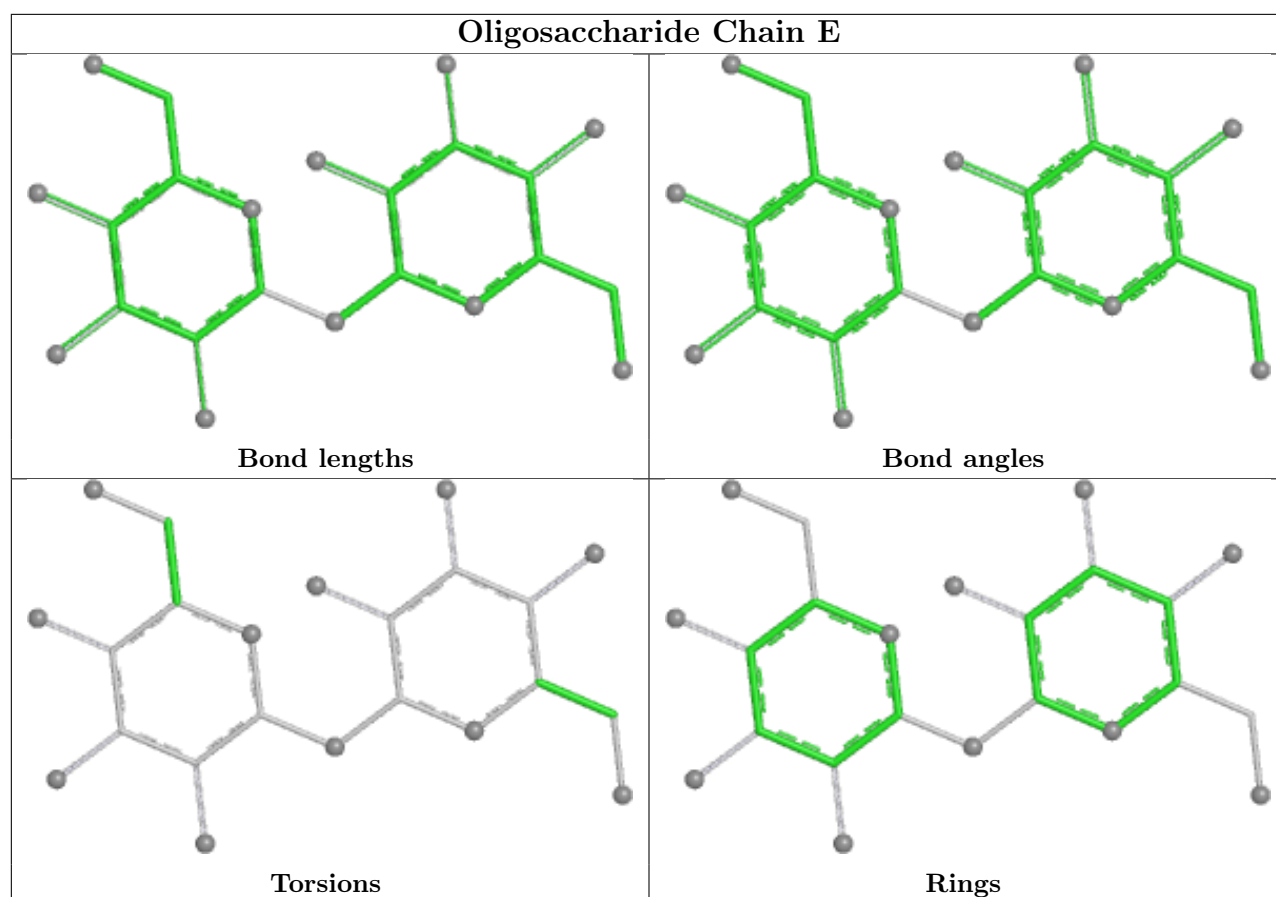
There are no torsion outliers.

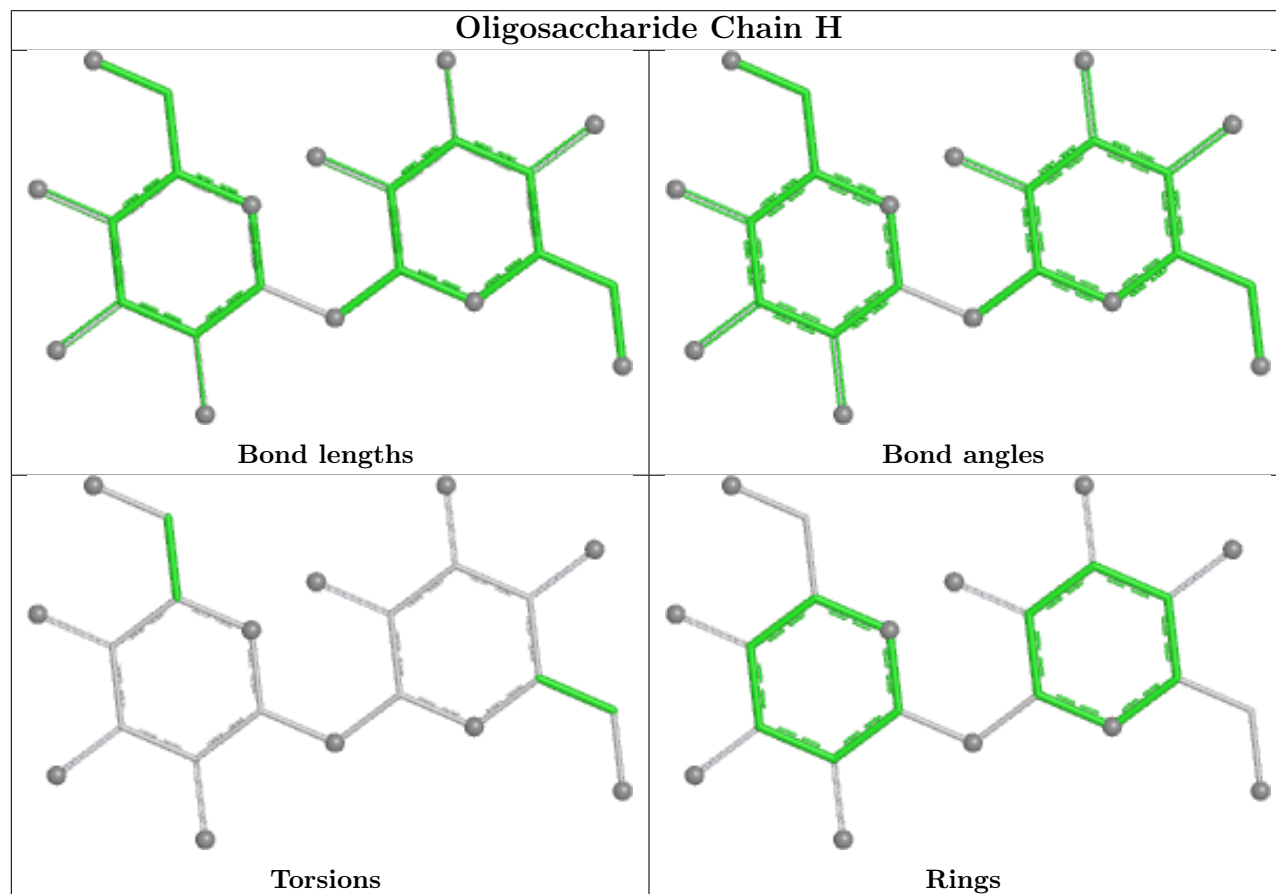
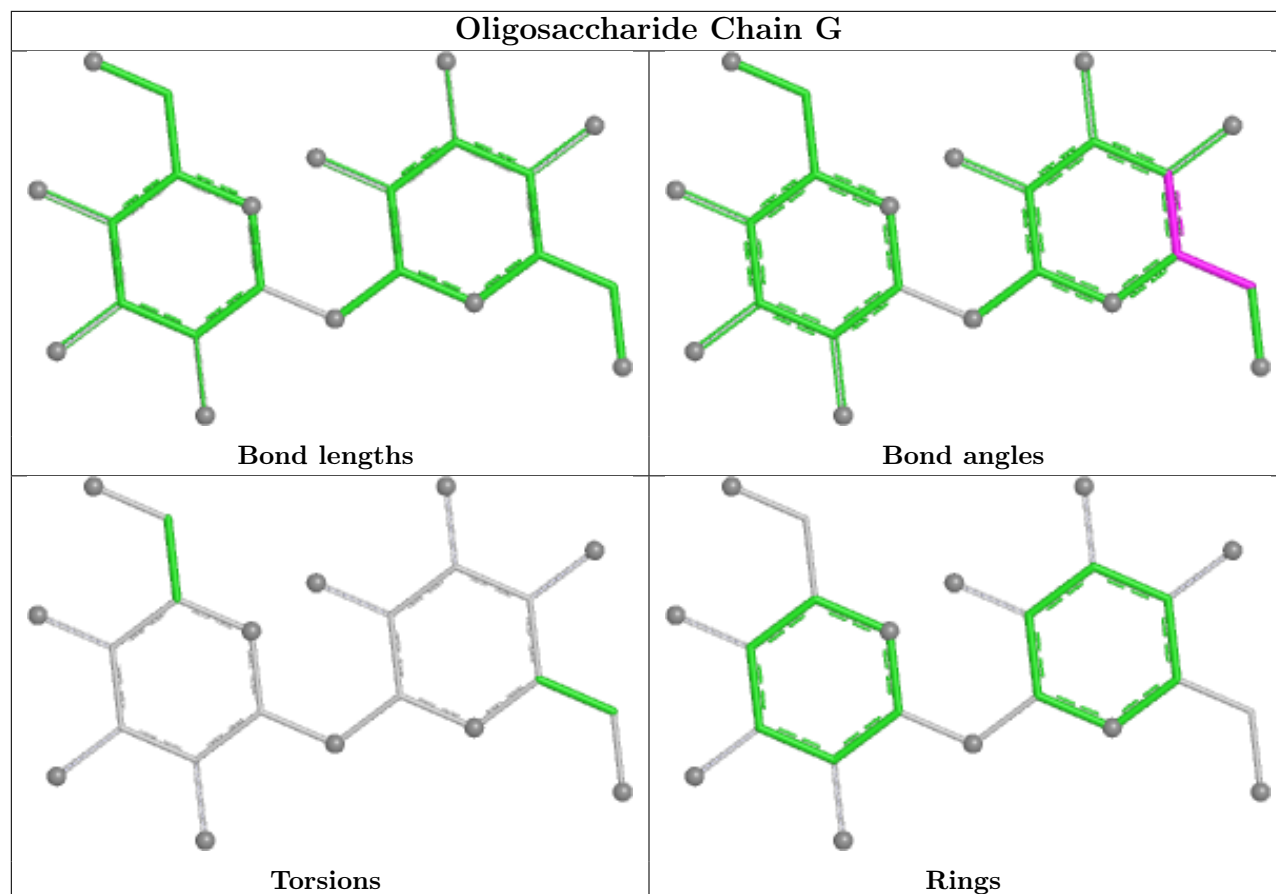
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1	GLC	1	0
2	H	1	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 [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	192/192 (100%)	-0.37	0 100 100	12, 19, 33, 51	0
1	B	192/192 (100%)	-0.40	1 (0%) 87 89	12, 19, 30, 41	1 (0%)
1	C	192/192 (100%)	-0.34	1 (0%) 87 89	12, 18, 34, 55	0
1	D	192/192 (100%)	-0.33	0 100 100	10, 18, 34, 51	0
All	All	768/768 (100%)	-0.36	2 (0%) 90 92	10, 18, 34, 55	1 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	ALA	2.6
1	C	192	ALA	2.3

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.

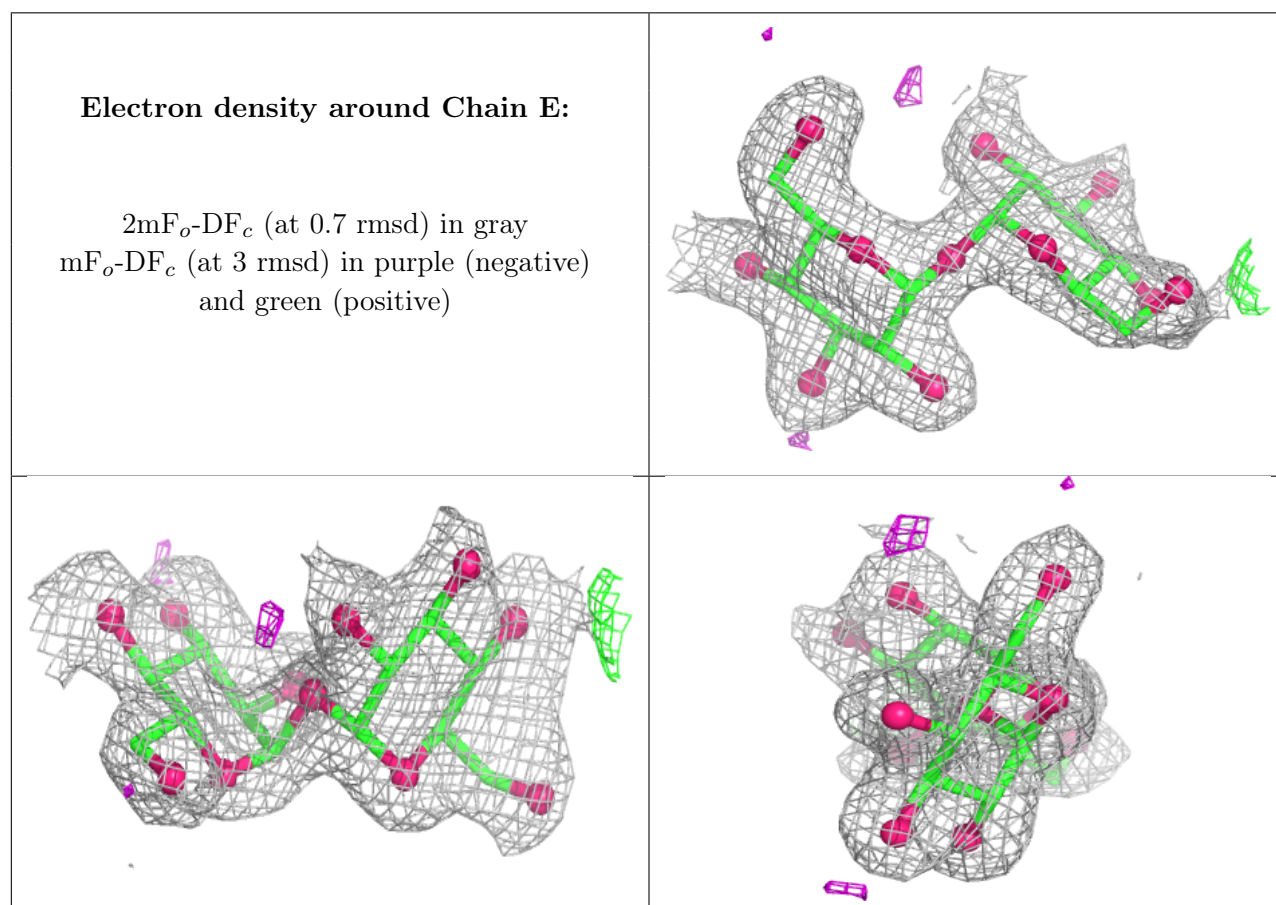
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GLC	E	1	11/12	0.89	0.09	25,33,40,42	0
2	GLC	F	1	11/12	0.89	0.10	28,33,43,44	0
2	GLC	H	1	11/12	0.91	0.09	33,37,43,43	0
2	GLC	G	1	11/12	0.92	0.08	26,31,35,37	0
2	GLC	H	2	12/12	0.92	0.08	23,26,27,27	0

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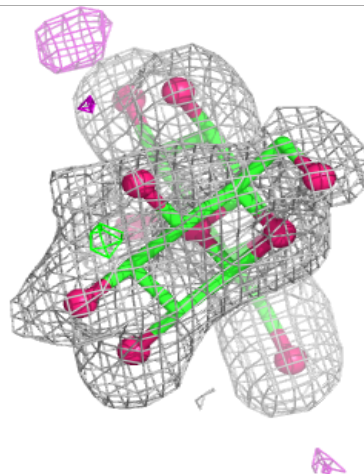
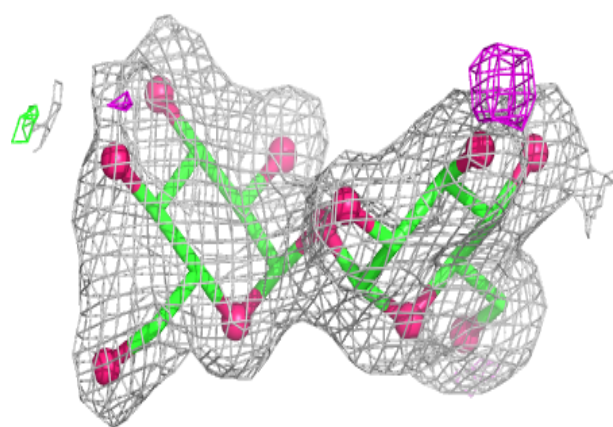
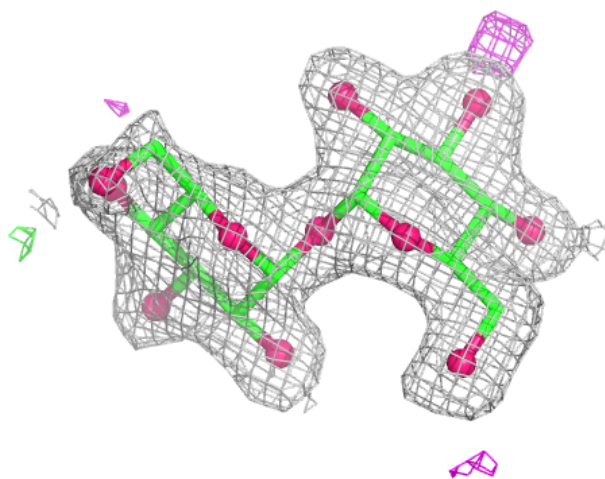
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GLC	F	2	12/12	0.93	0.07	18,22,25,26	0
2	GLC	G	2	12/12	0.93	0.08	21,24,25,26	0
2	GLC	E	2	12/12	0.94	0.07	19,21,25,27	0

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.



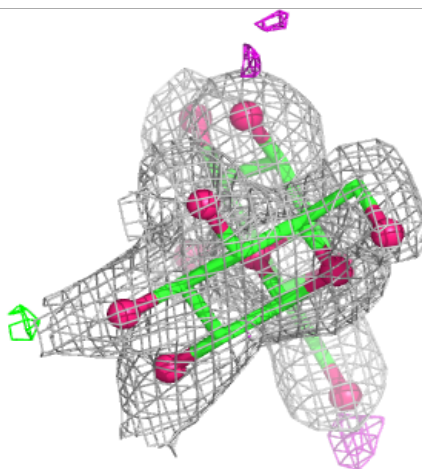
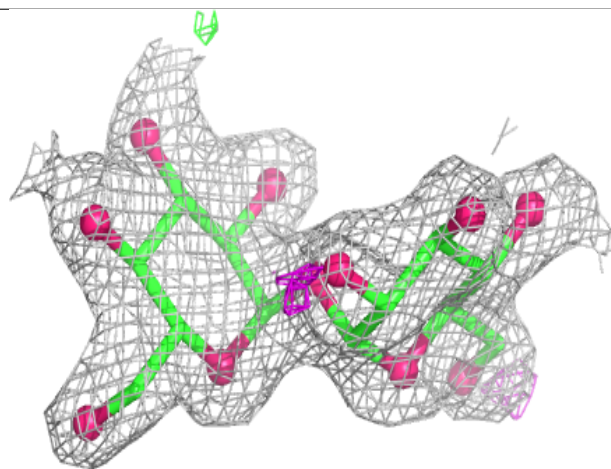
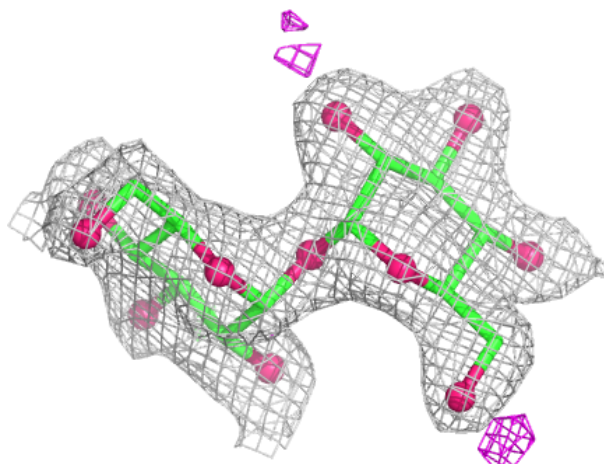
Electron density around Chain F:

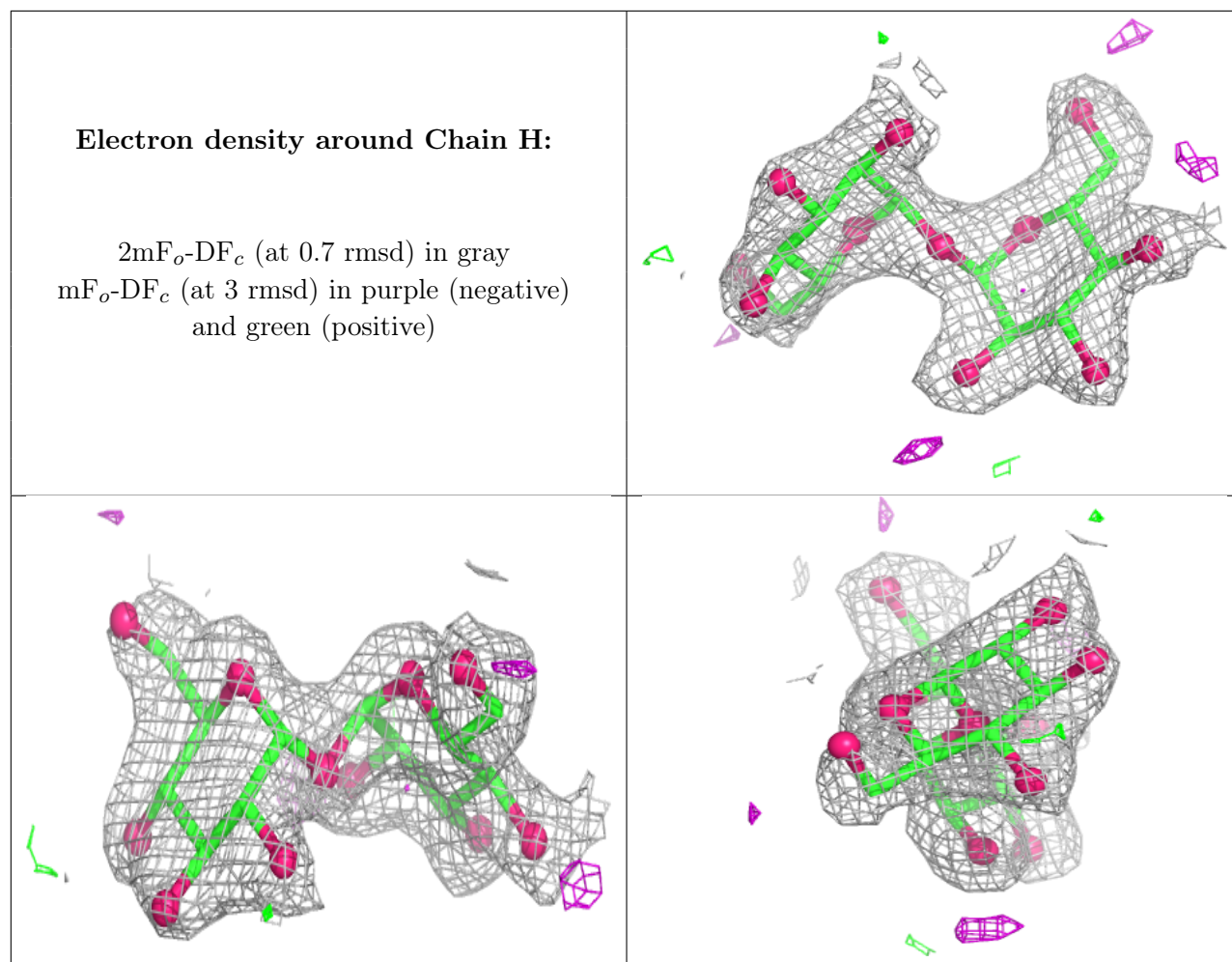
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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	FE2	A	201	1/1	1.00	0.03	17,17,17,17	0
3	FE2	C	201	1/1	1.00	0.04	15,15,15,15	0
3	FE2	B	201	1/1	1.00	0.03	13,13,13,13	0
3	FE2	D	201	1/1	1.00	0.05	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.