



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:16 AM UTC

PDB ID : 1JS8 / pdb_00001js8
Title : Structure of a Functional Unit from Octopus Hemocyanin
Authors : Cuff, M.E.; Miller, K.I.; van Holde, K.E.; Hendrickson, W.A.
Deposited on : 2001-08-16
Resolution : 2.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ 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

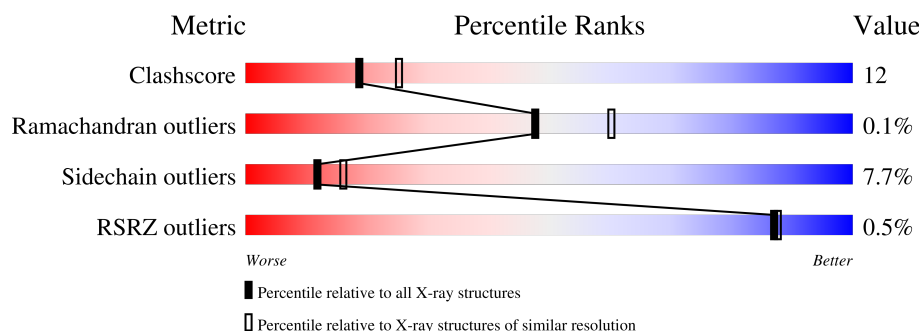
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	394	% 72% 22% ...
1	B	394	% 71% 20% 5% ...
2	C	7	29% 71%
3	D	2	50% 50%
4	E	3	33% 33% 33%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MAN	A	992	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6593 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.

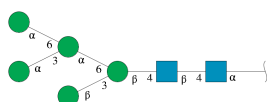
- Molecule 1 is a protein called Hemocyanin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	382	Total	C	N	O	S	0	0	0
			3067	1959	521	573	14			
1	B	382	Total	C	N	O	S	0	0	0
			3067	1959	521	573	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2843	LEU	PRO	see remark 999	? O61363
B	2843	LEU	PRO	see remark 999	? O61363

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[beta-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose.



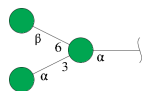
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			83	46	2	35			

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



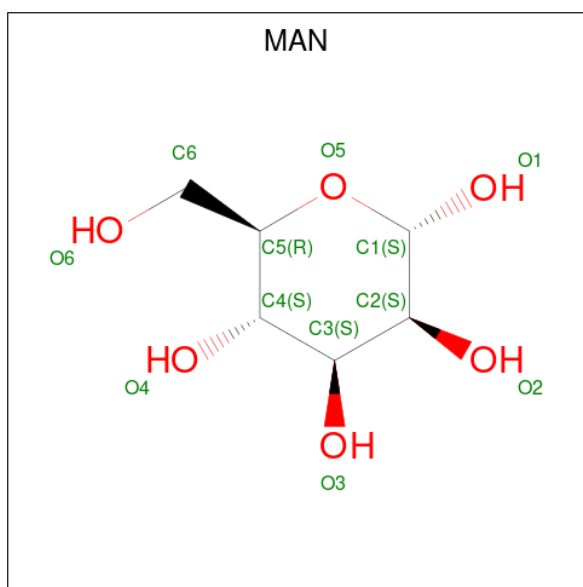
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-6)]alpha-D-mannopyranose.



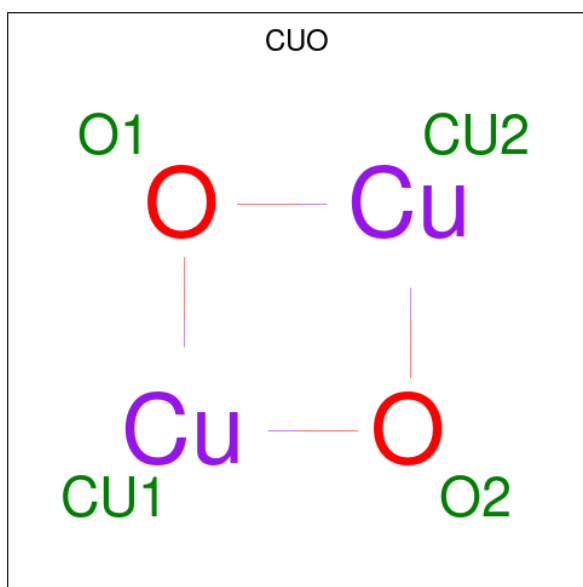
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	E	3	Total	C	O	0	0	0
			33	18	15			

- Molecule 5 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 6 is CU2-O2 CLUSTER (CCD ID: CUO) (formula: Cu₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	Cu	O	0	0
			4	2	2		
6	B	1	Total	Cu	O	0	0
			4	2	2		

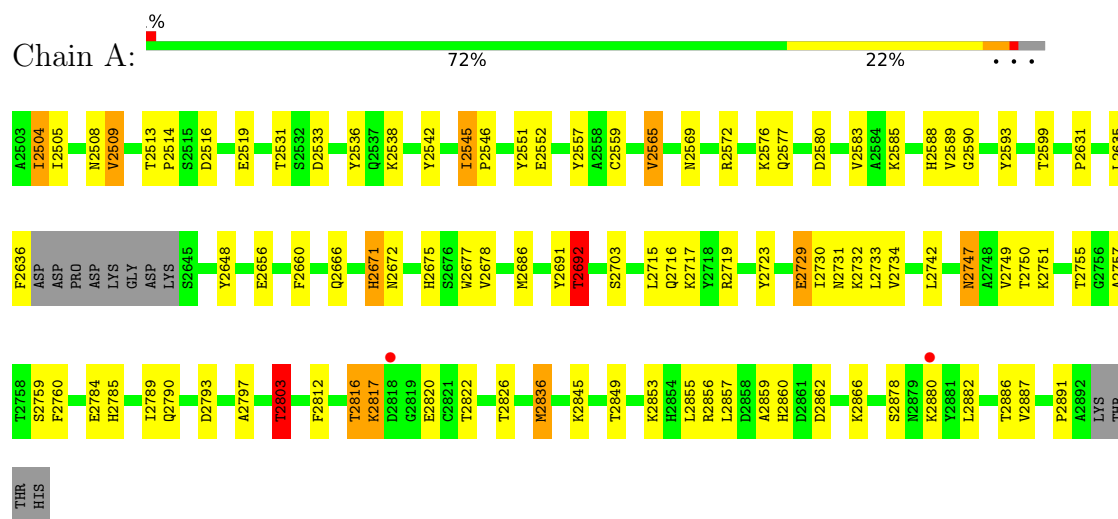
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	175	Total	O	0	0
			175	175		
7	B	121	Total	O	0	0
			121	121		

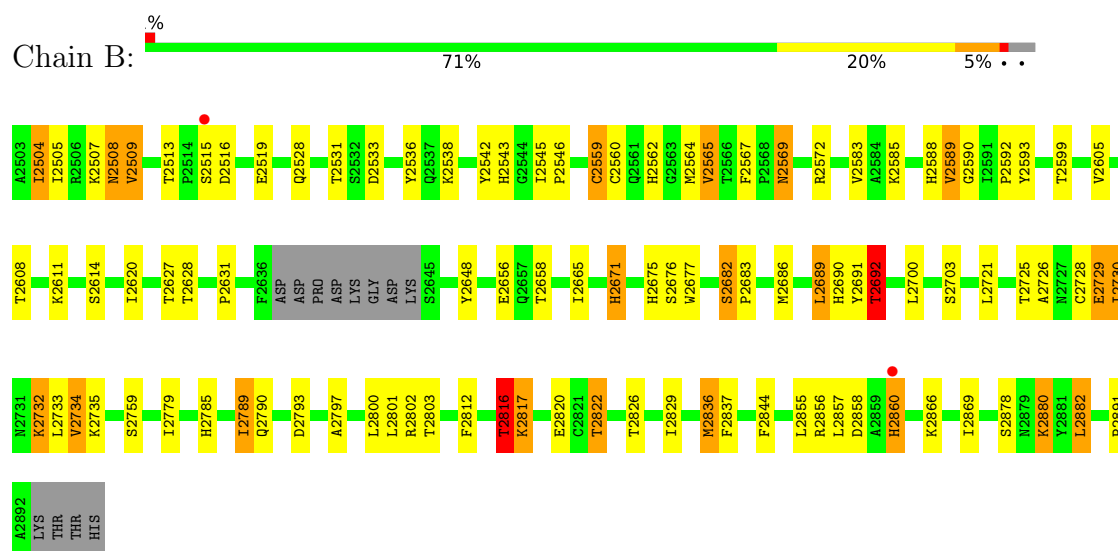
3 Residue-property plots

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.

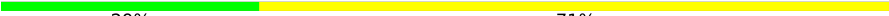
• Molecule 1: Hemocyanin



• Molecule 1: Hemocyanin



• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[beta-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose

Chain C:  29% 71%



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

Chain D:  50% 50%



- Molecule 4: alpha-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-6)]alpha-D-mannopyranose

Chain E:  33% 33% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.86Å 168.39Å 58.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.30 10.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.30) 93.2 (10.00-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.03 (at 2.30Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.202 , 0.262 0.190 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	24.5	Xtriage
Anisotropy	0.475	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 61.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6593	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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: BMA, MAN, CUO, NDG, NAG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.81	1/3157 (0.0%)	1.09	9/4293 (0.2%)
1	B	0.75	1/3157 (0.0%)	1.10	18/4293 (0.4%)
All	All	0.78	2/6314 (0.0%)	1.09	27/8586 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2836	MET	SD-CE	-8.69	1.57	1.79
1	B	2836	MET	SD-CE	-5.82	1.65	1.79

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2505	ILE	N-CA-C	7.40	119.23	108.58
1	A	2692	THR	CB-CA-C	-7.25	99.21	110.81
1	B	2797	ALA	N-CA-C	-7.12	98.12	109.59
1	B	2572	ARG	N-CA-C	-7.09	103.63	111.36
1	B	2692	THR	CB-CA-C	-7.08	99.76	110.88
1	A	2797	ALA	N-CA-C	-7.02	98.16	109.96
1	A	2816	THR	N-CA-C	-6.61	101.81	110.53
1	B	2690	HIS	N-CA-C	6.53	118.39	111.28
1	B	2703	SER	N-CA-C	-6.51	104.26	111.36
1	B	2611	LYS	N-CA-C	6.17	118.69	109.25
1	B	2559	CYS	N-CA-C	6.15	118.95	111.82
1	A	2703	SER	N-CA-C	-5.84	104.50	111.69
1	A	2505	ILE	N-CA-C	5.82	116.97	108.58
1	B	2543	HIS	N-CA-C	5.75	118.66	111.24
1	B	2682	SER	CA-C-N	5.59	125.20	119.56
1	B	2682	SER	C-N-CA	5.59	125.20	119.56
1	B	2816	THR	N-CA-C	-5.49	103.28	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2665	ILE	N-CA-C	5.49	116.26	110.72
1	A	2678	VAL	N-CA-C	-5.49	106.35	111.45
1	A	2803	THR	CB-CA-C	-5.45	100.93	109.70
1	B	2844	PHE	N-CA-C	-5.39	100.39	108.96
1	B	2689	LEU	N-CA-C	-5.36	105.60	111.82
1	B	2683	PRO	N-CA-C	5.25	120.42	113.86
1	A	2536	TYR	N-CA-C	5.25	116.69	110.97
1	B	2515	SER	N-CA-C	-5.19	105.53	111.14
1	B	2676	SER	N-CA-C	5.18	116.61	111.07
1	A	2755	THR	N-CA-C	-5.14	101.56	109.52

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	3067	0	2906	71	0
1	B	3067	0	2906	71	0
2	C	83	0	69	0	0
3	D	28	0	25	5	0
4	E	33	0	28	1	0
5	A	11	0	10	6	0
6	A	4	0	0	0	0
6	B	4	0	0	0	0
7	A	175	0	0	6	0
7	B	121	0	0	7	0
All	All	6593	0	5944	143	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 (143) 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:2880:LYS:HB3	1:B:2880:LYS:NZ	1.72	1.01
1:B:2880:LYS:HB3	1:B:2880:LYS:HZ2	1.28	0.94
1:A:2666:GLN:HE22	1:A:2845:LYS:H	1.28	0.80
1:B:2878:SER:OG	1:B:2880:LYS:HB2	1.84	0.76
1:A:2880:LYS:HG2	5:A:992:MAN:O2	1.86	0.74
1:B:2675:HIS:HD1	1:B:2692:THR:HG21	1.53	0.73
1:A:2519:GLU:HG3	1:A:2588:HIS:CE1	2.24	0.73
1:A:2675:HIS:ND1	1:A:2692:THR:HG21	2.03	0.72
1:A:2675:HIS:HD1	1:A:2692:THR:HG21	1.54	0.72
1:B:2533:ASP:HA	1:B:2538:LYS:HG2	1.72	0.72
1:B:2675:HIS:ND1	1:B:2692:THR:HG21	2.06	0.71
1:A:2675:HIS:CE1	1:A:2692:THR:HG21	2.25	0.71
1:B:2686:MET:HA	1:B:2692:THR:HG23	1.74	0.69
1:B:2519:GLU:HG3	1:B:2588:HIS:CE1	2.28	0.69
1:B:2565:VAL:HG11	1:B:2729:GLU:HG3	1.74	0.68
5:A:992:MAN:C5	3:D:2:NAG:H61	2.24	0.68
1:B:2565:VAL:CG1	1:B:2729:GLU:HG3	2.25	0.67
1:B:2816:THR:HG22	1:B:2857:LEU:HD21	1.77	0.67
1:B:2675:HIS:CE1	1:B:2692:THR:HG21	2.30	0.67
1:A:2686:MET:HA	1:A:2692:THR:HG23	1.76	0.66
1:B:2569:ASN:H	1:B:2569:ASN:HD22	1.42	0.66
1:A:2886:THR:HG21	7:B:537:HOH:O	1.95	0.65
1:A:2716:GLN:HE21	1:A:2719:ARG:HH11	1.45	0.65
1:A:2533:ASP:HA	1:A:2538:LYS:HG2	1.77	0.65
1:A:2729:GLU:HG3	7:A:580:HOH:O	1.97	0.64
1:A:2716:GLN:NE2	1:A:2719:ARG:HH11	1.96	0.64
1:A:2859:ALA:HB1	1:B:2730:ILE:HD12	1.80	0.64
1:B:2686:MET:HA	1:B:2692:THR:CG2	2.30	0.61
1:A:2504:ILE:HD11	1:A:2590:GLY:HA2	1.83	0.61
5:A:992:MAN:H5	3:D:2:NAG:H61	1.81	0.60
1:A:2793:ASP:OD1	1:A:2891:PRO:HA	2.03	0.59
1:A:2545:ILE:HD11	1:A:2691:TYR:HE1	1.66	0.59
1:A:2803:THR:HG21	7:A:564:HOH:O	2.02	0.57
1:A:2504:ILE:HD12	1:A:2583:VAL:HG21	1.85	0.57
1:B:2592:PRO:HG2	1:B:2700:LEU:HD22	1.87	0.57
1:A:2878:SER:OG	1:A:2880:LYS:HB2	2.06	0.56
1:B:2880:LYS:HB3	1:B:2880:LYS:HZ3	1.70	0.56
1:A:2542:TYR:O	1:A:2559:CYS:HB2	2.05	0.56
1:A:2545:ILE:HD11	1:A:2691:TYR:CE1	2.40	0.55
1:A:2686:MET:HA	1:A:2692:THR:CG2	2.37	0.55
1:A:2817:LYS:HE2	1:A:2817:LYS:HA	1.88	0.54
1:B:2513:THR:O	1:B:2516:ASP:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2817:LYS:HE3	1:B:2817:LYS:HA	1.88	0.54
1:B:2562:HIS:CE1	1:B:2689:LEU:HD11	2.43	0.54
1:B:2569:ASN:H	1:B:2569:ASN:ND2	2.03	0.54
1:B:2812:PHE:HA	1:B:2866:LYS:O	2.07	0.54
1:B:2656:GLU:HG3	1:B:2790:GLN:NE2	2.24	0.53
1:B:2793:ASP:OD1	1:B:2891:PRO:HA	2.08	0.53
1:B:2732:LYS:HB3	7:B:664:HOH:O	2.08	0.53
1:A:2557:TYR:CE2	1:A:2836:MET:HE2	2.44	0.52
1:A:2565:VAL:HG23	1:A:2660:PHE:CE2	2.44	0.52
5:A:992:MAN:O5	3:D:2:NAG:H61	2.10	0.52
1:B:2789:ILE:HG22	1:B:2790:GLN:HG3	1.92	0.51
1:A:2557:TYR:HE2	1:A:2836:MET:CE	2.24	0.51
1:B:2565:VAL:HG11	1:B:2728:CYS:SG	2.52	0.50
1:B:2631:PRO:HA	1:B:2677:TRP:O	2.11	0.50
1:B:2508:ASN:HD22	1:B:2509:VAL:N	2.10	0.50
1:A:2671:HIS:CE1	1:A:2672:ASN:OD1	2.65	0.49
1:A:2816:THR:HG22	1:A:2857:LEU:HD21	1.94	0.49
1:B:2560:CYS:SG	1:B:2689:LEU:HD11	2.52	0.49
1:B:2605:VAL:HA	1:B:2608:THR:OG1	2.12	0.49
1:A:2648:TYR:OH	1:A:2785:HIS:CE1	2.66	0.49
1:A:2715:LEU:O	1:A:2719:ARG:HG3	2.12	0.49
1:B:2545:ILE:HD11	1:B:2691:TYR:CE1	2.47	0.49
1:B:2878:SER:C	1:B:2880:LYS:H	2.21	0.49
1:A:2747:ASN:HD22	1:A:2747:ASN:C	2.20	0.49
1:B:2648:TYR:OH	1:B:2785:HIS:NE2	2.45	0.49
1:B:2802:ARG:NH1	7:B:512:HOH:O	2.45	0.49
1:B:2822:THR:HG21	1:B:2855:LEU:HG	1.95	0.48
1:A:2812:PHE:HA	1:A:2866:LYS:O	2.12	0.48
1:A:2545:ILE:HA	1:A:2546:PRO:C	2.38	0.48
1:A:2734:VAL:HG11	1:B:2860:HIS:O	2.13	0.48
1:A:2565:VAL:HG23	1:A:2660:PHE:HE2	1.79	0.48
1:A:2656:GLU:HG3	1:A:2790:GLN:NE2	2.28	0.48
1:B:2620:ILE:HD11	1:B:2627:THR:HG22	1.96	0.48
1:A:2729:GLU:OE2	1:A:2732:LYS:HE3	2.14	0.48
5:A:992:MAN:C5	3:D:2:NAG:C6	2.90	0.48
1:B:2542:TYR:O	1:B:2559:CYS:HB2	2.14	0.48
1:B:2509:VAL:HG22	1:B:2593:TYR:O	2.13	0.47
1:B:2816:THR:OG1	1:B:2820:GLU:HB3	2.15	0.47
1:B:2822:THR:CG2	1:B:2855:LEU:HG	2.45	0.47
5:A:992:MAN:C6	3:D:2:NAG:O6	2.63	0.47
1:A:2717:LYS:HD2	1:A:2723:TYR:CZ	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2628:THR:HB	1:B:2682:SER:HB2	1.97	0.47
1:A:2513:THR:O	1:A:2516:ASP:HB2	2.16	0.46
1:A:2557:TYR:CE2	1:A:2836:MET:CE	2.99	0.46
1:B:2822:THR:HG22	1:B:2855:LEU:HD11	1.96	0.46
1:B:2789:ILE:HD13	7:B:552:HOH:O	2.14	0.46
1:A:2880:LYS:NZ	1:A:2880:LYS:HB3	2.31	0.46
1:B:2858:ASP:OD1	1:B:2860:HIS:CE1	2.69	0.46
1:B:2779:ILE:HD13	7:B:501:HOH:O	2.14	0.46
1:B:2507:LYS:HE3	1:B:2589:VAL:HG21	1.97	0.45
1:B:2658:THR:HB	1:B:2721:LEU:HD13	1.98	0.45
1:A:2747:ASN:ND2	1:A:2750:THR:H	2.15	0.45
1:B:2504:ILE:HD12	1:B:2583:VAL:HG21	1.97	0.45
1:B:2802:ARG:HD2	7:B:529:HOH:O	2.16	0.45
1:A:2551:TYR:HE2	7:A:657:HOH:O	1.99	0.45
1:A:2569:ASN:HD22	1:A:2569:ASN:H	1.64	0.45
1:A:2576:LYS:HZ2	1:A:2580:ASP:CG	2.24	0.45
1:B:2545:ILE:HA	1:B:2546:PRO:C	2.40	0.45
1:A:2509:VAL:HG22	1:A:2593:TYR:O	2.17	0.44
1:B:2817:LYS:HA	1:B:2817:LYS:CE	2.48	0.44
1:B:2726:ALA:HB3	1:B:2733:LEU:HD11	1.99	0.44
1:A:2822:THR:HG22	1:A:2855:LEU:HD11	1.99	0.44
1:A:2569:ASN:H	1:A:2569:ASN:ND2	2.15	0.44
1:B:2545:ILE:HD11	1:B:2691:TYR:HE1	1.82	0.44
1:B:2567:PHE:CZ	1:B:2671:HIS:CE1	3.06	0.44
1:B:2686:MET:CA	1:B:2692:THR:HG23	2.47	0.43
1:A:2849:THR:O	1:A:2853:LYS:HG2	2.19	0.43
1:A:2577:GLN:HE21	1:A:2750:THR:HG21	1.83	0.43
1:A:2731:ASN:O	1:A:2734:VAL:HG22	2.18	0.43
1:A:2717:LYS:HA	7:A:682:HOH:O	2.19	0.43
1:B:2729:GLU:O	1:B:2732:LYS:HB2	2.19	0.42
1:A:2742:LEU:O	1:A:2751:LYS:HE3	2.19	0.42
1:A:2860:HIS:O	1:B:2734:VAL:HG21	2.19	0.42
1:B:2508:ASN:HD22	1:B:2508:ASN:C	2.26	0.42
1:A:2686:MET:O	1:A:2692:THR:HG23	2.19	0.42
1:B:2801:LEU:HD22	1:B:2829:ILE:HD11	2.00	0.42
1:A:2572:ARG:NH1	1:A:2760:PHE:O	2.52	0.42
1:B:2837:PHE:HD1	4:E:2:MAN:HO6	1.63	0.42
1:A:2733:LEU:O	1:A:2757:ALA:N	2.52	0.42
1:B:2528:GLN:HA	1:B:2536:TYR:HB2	2.00	0.42
1:A:2631:PRO:HA	1:A:2677:TRP:O	2.20	0.42
1:B:2585:LYS:HD3	1:B:2585:LYS:HA	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2635:LEU:HD23	1:A:2636:PHE:CZ	2.55	0.42
1:A:2747:ASN:ND2	1:A:2749:VAL:H	2.18	0.42
1:A:2816:THR:OG1	1:A:2820:GLU:HB3	2.19	0.42
1:B:2504:ILE:HD11	1:B:2590:GLY:HA2	2.02	0.41
1:B:2656:GLU:HG3	1:B:2790:GLN:HE21	1.85	0.41
1:A:2886:THR:HG22	1:A:2887:VAL:N	2.35	0.41
1:B:2869:ILE:HD11	1:B:2882:LEU:HB2	2.02	0.41
1:A:2836:MET:HE1	7:A:459:HOH:O	2.19	0.41
1:A:2565:VAL:HG12	7:A:593:HOH:O	2.21	0.41
1:A:2675:HIS:HD1	1:A:2692:THR:CG2	2.28	0.41
1:A:2504:ILE:HD12	1:A:2583:VAL:CG2	2.50	0.41
1:A:2585:LYS:HA	1:A:2585:LYS:HD3	1.92	0.41
1:A:2862:ASP:OD1	1:B:2735:LYS:HE3	2.21	0.41
1:B:2565:VAL:HG13	1:B:2729:GLU:HG3	2.02	0.41
1:B:2628:THR:CB	1:B:2682:SER:HB2	2.51	0.41
1:B:2803:THR:HG21	7:B:548:HOH:O	2.20	0.40
1:A:2577:GLN:NE2	1:A:2750:THR:OG1	2.49	0.40
1:A:2878:SER:C	1:A:2880:LYS:H	2.28	0.40
1:A:2880:LYS:HB3	1:A:2880:LYS:HE3	1.90	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	378/394 (96%)	368 (97%)	9 (2%)	1 (0%)	36	46
1	B	378/394 (96%)	364 (96%)	14 (4%)	0	100	100
All	All	756/788 (96%)	732 (97%)	23 (3%)	1 (0%)	48	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2730	ILE

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	332/343 (97%)	310 (93%)	22 (7%)	15	21
1	B	332/343 (97%)	303 (91%)	29 (9%)	9	12
All	All	664/686 (97%)	613 (92%)	51 (8%)	12	16

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2504	ILE
1	A	2508	ASN
1	A	2509	VAL
1	A	2514	PRO
1	A	2531	THR
1	A	2545	ILE
1	A	2552	GLU
1	A	2565	VAL
1	A	2589	VAL
1	A	2599	THR
1	A	2671	HIS
1	A	2692	THR
1	A	2729	GLU
1	A	2747	ASN
1	A	2759	SER
1	A	2784	GLU
1	A	2789	ILE
1	A	2803	THR
1	A	2817	LYS
1	A	2826	THR
1	A	2856	ARG
1	A	2882	LEU
1	B	2504	ILE

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Mol	Chain	Res	Type
1	B	2508	ASN
1	B	2509	VAL
1	B	2531	THR
1	B	2564	MET
1	B	2565	VAL
1	B	2569	ASN
1	B	2589	VAL
1	B	2599	THR
1	B	2614	SER
1	B	2671	HIS
1	B	2692	THR
1	B	2725	THR
1	B	2729	GLU
1	B	2730	ILE
1	B	2732	LYS
1	B	2734	VAL
1	B	2759	SER
1	B	2789	ILE
1	B	2800	LEU
1	B	2816	THR
1	B	2817	LYS
1	B	2822	THR
1	B	2826	THR
1	B	2836	MET
1	B	2856	ARG
1	B	2860	HIS
1	B	2880	LYS
1	B	2882	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2508	ASN
1	A	2534	ASN
1	A	2569	ASN
1	A	2577	GLN
1	A	2657	GLN
1	A	2666	GLN
1	A	2704	ASN
1	A	2713	GLN
1	A	2716	GLN
1	A	2724	ASN

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Mol	Chain	Res	Type
1	A	2747	ASN
1	A	2773	ASN
1	A	2775	HIS
1	A	2785	HIS
1	A	2790	GLN
1	A	2806	GLN
1	A	2834	HIS
1	B	2508	ASN
1	B	2534	ASN
1	B	2537	GLN
1	B	2569	ASN
1	B	2577	GLN
1	B	2704	ASN
1	B	2713	GLN
1	B	2773	ASN
1	B	2775	HIS
1	B	2790	GLN

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 ⓘ

12 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	NDG	C	1	2	14,14,15	1.46	3 (21%)	17,19,21	0.91	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	2	2	14,14,15	0.69	0	17,19,21	0.96	1 (5%)
2	BMA	C	3	2	11,11,12	1.17	1 (9%)	15,15,17	1.70	2 (13%)
2	MAN	C	4	2	11,11,12	0.70	0	15,15,17	0.84	0
2	MAN	C	5	2	11,11,12	0.64	0	15,15,17	0.96	1 (6%)
2	MAN	C	6	2	11,11,12	0.62	0	15,15,17	0.72	0
2	BMA	C	7	2	11,11,12	1.32	2 (18%)	15,15,17	1.30	3 (20%)
3	NAG	D	1	3,1	14,14,15	1.12	2 (14%)	17,19,21	1.57	4 (23%)
3	NAG	D	2	3	14,14,15	1.37	2 (14%)	17,19,21	1.39	3 (17%)
4	MAN	E	1	4	11,11,12	0.43	0	15,15,17	0.96	0
4	MAN	E	2	4	11,11,12	0.93	1 (9%)	15,15,17	0.84	1 (6%)
4	BMA	E	3	4	11,11,12	1.01	0	15,15,17	1.68	3 (20%)

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	NDG	C	1	2	-	1/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
2	MAN	C	5	2	-	2/2/19/22	0/1/1/1
2	MAN	C	6	2	-	2/2/19/22	0/1/1/1
2	BMA	C	7	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
4	MAN	E	1	4	-	1/2/19/22	0/1/1/1
4	MAN	E	2	4	-	2/2/19/22	0/1/1/1
4	BMA	E	3	4	-	2/2/19/22	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	NDG	C1-C2	-3.35	1.47	1.52
2	C	7	BMA	O5-C5	2.68	1.48	1.43
3	D	1	NAG	C4-C5	2.68	1.58	1.53
3	D	2	NAG	C3-C2	2.63	1.58	1.52
3	D	2	NAG	C8-C7	2.43	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	NDG	C2-N2	-2.40	1.42	1.46
4	E	2	MAN	O5-C5	2.34	1.48	1.43
3	D	1	NAG	O5-C5	2.32	1.48	1.43
2	C	7	BMA	C2-C3	2.17	1.55	1.52
2	C	3	BMA	O3-C3	2.04	1.48	1.43
2	C	1	NDG	O5-C5	2.00	1.47	1.43

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3	BMA	O3-C3-C2	4.45	119.14	110.05
4	E	3	BMA	C1-C2-C3	-3.70	104.25	109.64
4	E	3	BMA	O5-C1-C2	3.38	118.86	110.79
2	C	3	BMA	C1-C2-C3	-3.37	104.73	109.64
2	C	7	BMA	C1-C2-C3	3.33	114.50	109.64
4	E	3	BMA	C3-C4-C5	3.23	116.08	110.23
3	D	1	NAG	O4-C4-C3	-3.21	102.82	110.38
3	D	1	NAG	C4-C3-C2	3.13	115.60	111.02
3	D	2	NAG	C6-C5-C4	2.92	120.19	113.02
2	C	5	MAN	C1-O5-C5	2.91	116.08	112.19
3	D	2	NAG	C1-O5-C5	-2.68	108.59	112.19
3	D	2	NAG	C4-C3-C2	-2.62	107.19	111.02
2	C	1	NDG	C1-O5-C5	-2.59	108.71	112.19
3	D	1	NAG	C8-C7-N2	-2.57	111.86	116.12
3	D	1	NAG	O5-C1-C2	-2.21	107.88	111.29
4	E	2	MAN	C1-O5-C5	2.20	115.14	112.19
2	C	7	BMA	C3-C4-C5	-2.17	106.30	110.23
2	C	2	NAG	C4-C3-C2	-2.11	107.93	111.02
2	C	7	BMA	C1-O5-C5	2.02	114.89	112.19

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	2	MAN	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
2	C	6	MAN	O5-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6
2	C	6	MAN	C4-C5-C6-O6
4	E	3	BMA	O5-C5-C6-O6
4	E	2	MAN	C4-C5-C6-O6
2	C	5	MAN	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	D	2	NAG	C4-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6
4	E	3	BMA	C4-C5-C6-O6
2	C	1	NDG	O5-C5-C6-O6
2	C	5	MAN	C4-C5-C6-O6
4	E	1	MAN	C4-C5-C6-O6

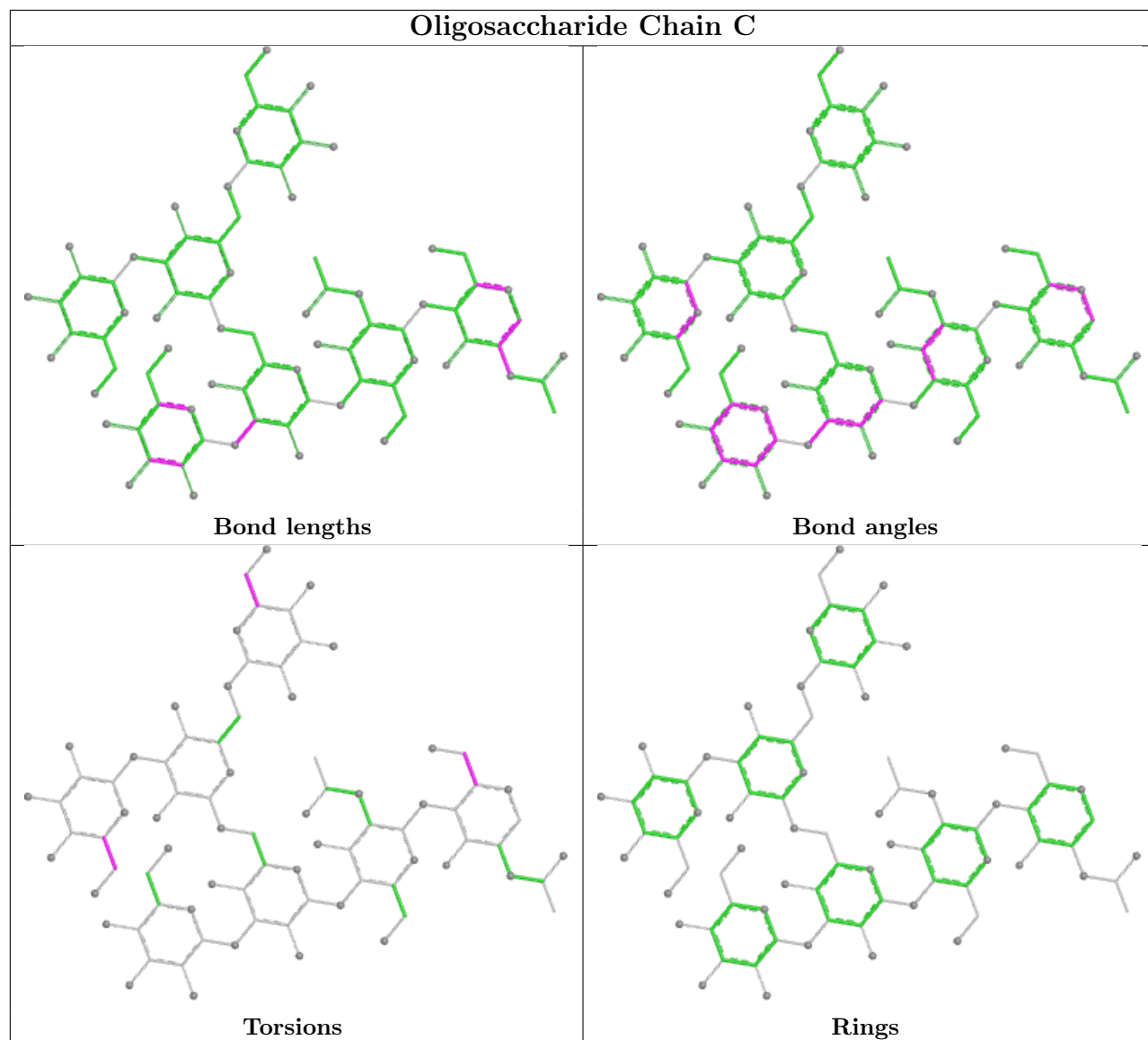
There are no ring outliers.

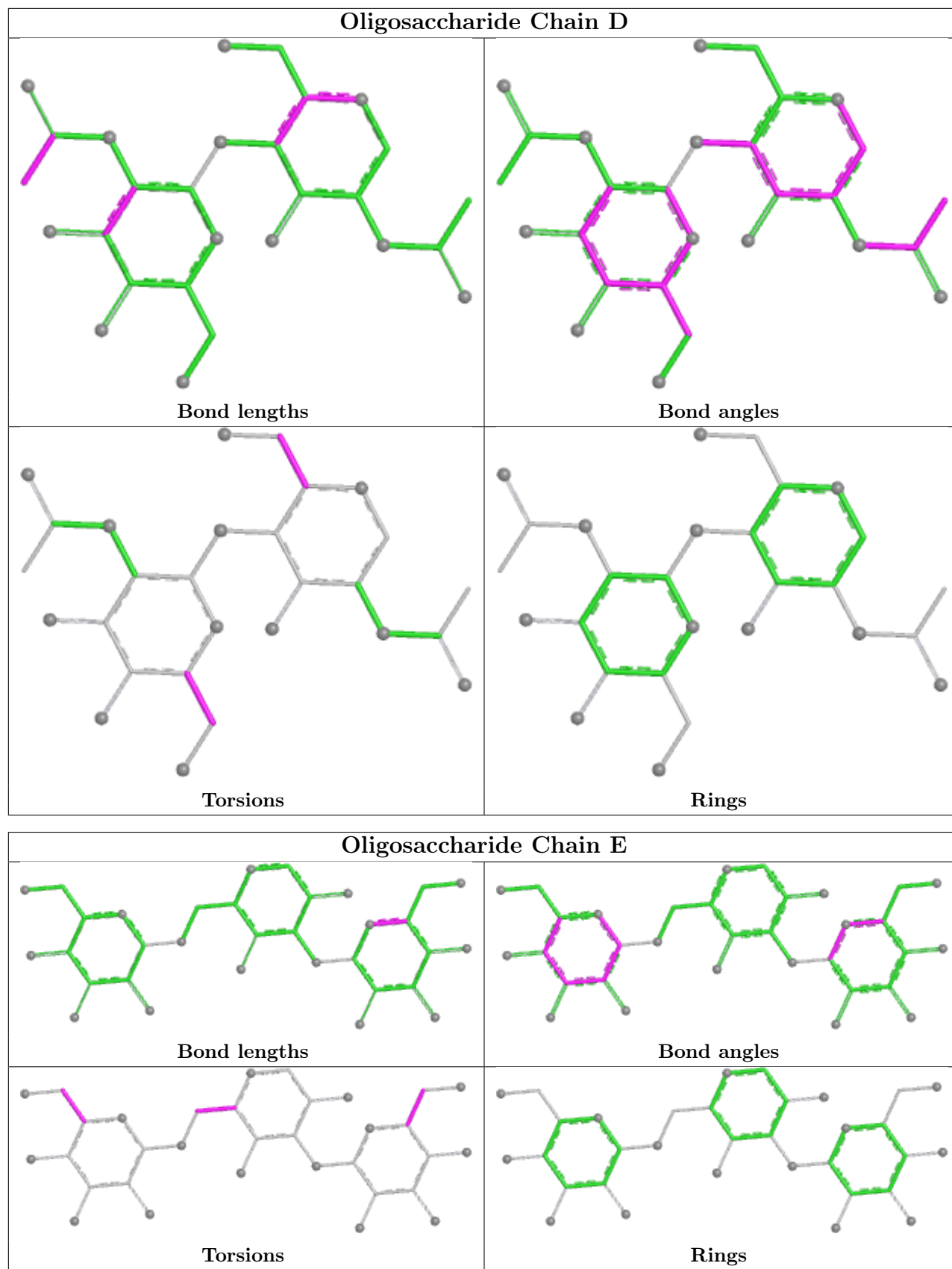
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2	NAG	5	0
4	E	2	MAN	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.

Oligosaccharide Chain C





5.6 Ligand geometry

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CUO	B	999	1	0,4,4	-	-	-		
5	MAN	A	992	-	11,11,12	1.55	3 (27%)	15,15,17	1.27	2 (13%)
6	CUO	A	888	1	0,4,4	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	CUO	B	999	1	-	-	0/1/1/1
5	MAN	A	992	-	-	2/2/19/22	0/1/1/1
6	CUO	A	888	1	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	992	MAN	O5-C5	2.74	1.48	1.43
5	A	992	MAN	C2-C3	2.71	1.56	1.52
5	A	992	MAN	O5-C1	2.14	1.47	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	992	MAN	C2-C3-C4	-3.23	105.19	110.86
5	A	992	MAN	C3-C4-C5	-2.34	105.98	110.23

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	992	MAN	O5-C5-C6-O6
5	A	992	MAN	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	992	MAN	6	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	382/394 (96%)	-0.35	2 (0%) 87 87	4, 17, 38, 51	0
1	B	382/394 (96%)	-0.27	2 (0%) 87 87	5, 19, 40, 53	0
All	All	764/788 (96%)	-0.31	4 (0%) 87 87	4, 18, 39, 53	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2860	HIS	3.4
1	A	2818	ASP	3.1
1	B	2515	SER	2.3
1	A	2880	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

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.

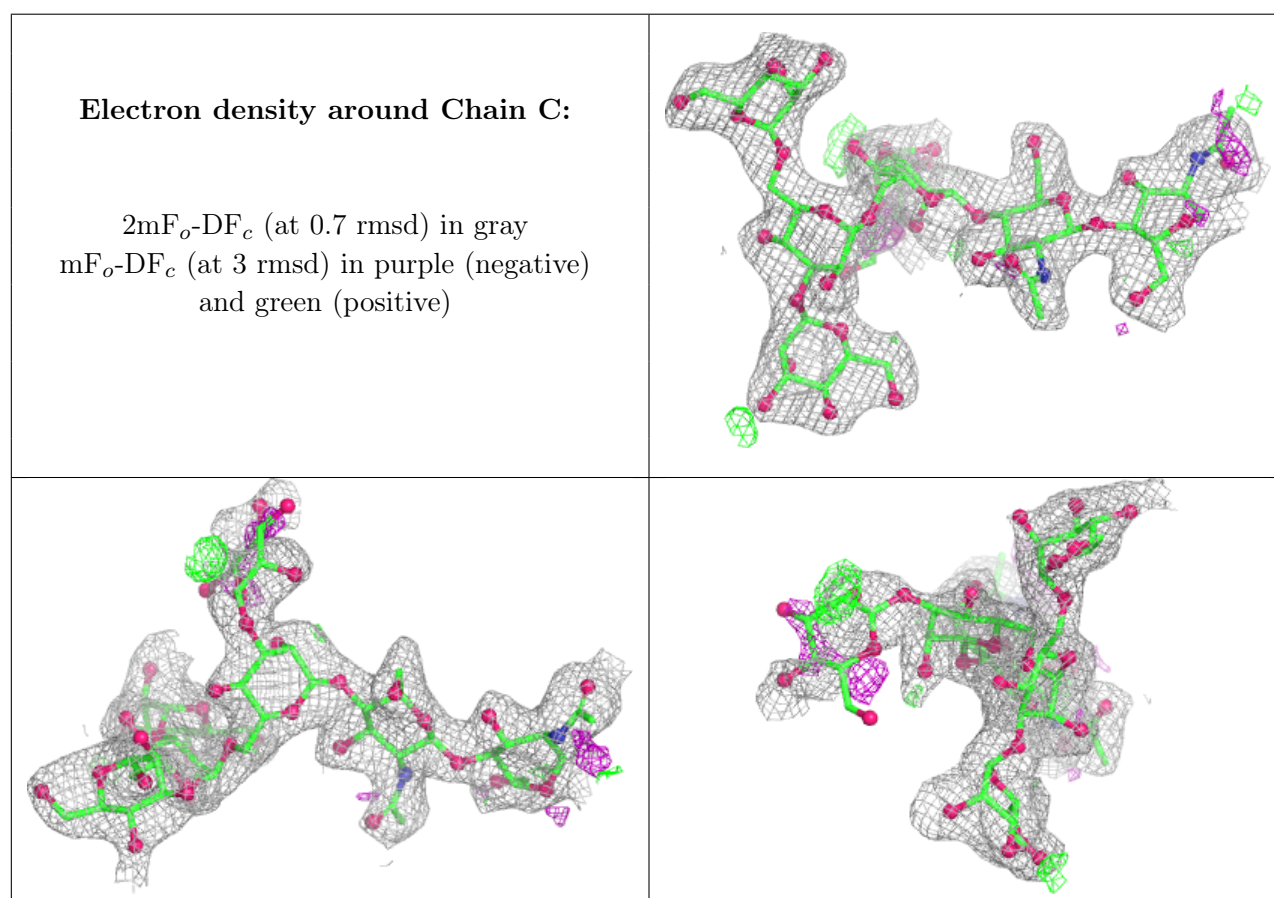
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	D	2	14/15	0.56	0.15	45,52,54,58	0
4	BMA	E	3	11/12	0.59	0.12	62,65,68,72	0
2	BMA	C	7	11/12	0.60	0.20	37,39,44,45	0
4	MAN	E	1	11/12	0.79	0.09	32,37,46,56	0
3	NAG	D	1	14/15	0.79	0.09	41,47,52,52	0

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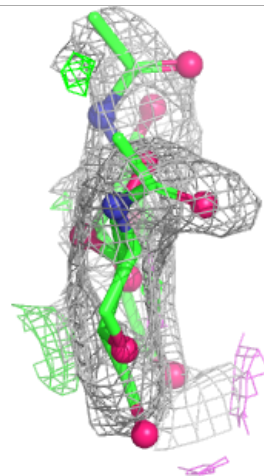
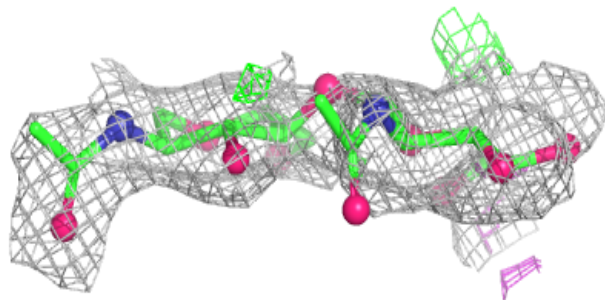
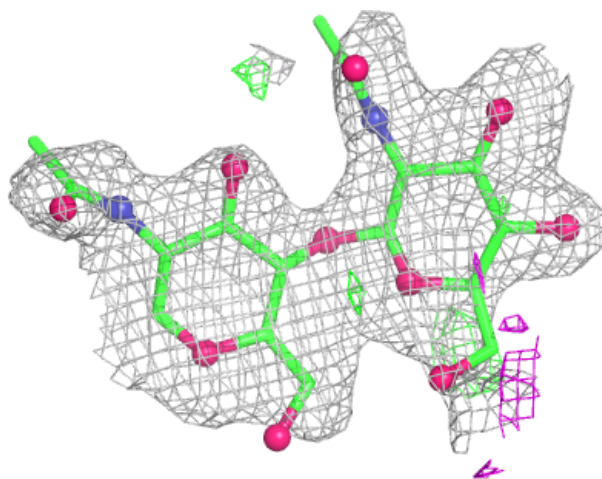
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MAN	E	2	11/12	0.80	0.10	39,43,48,60	0
2	BMA	C	3	11/12	0.84	0.09	31,33,39,41	0
2	NAG	C	2	14/15	0.85	0.09	26,30,33,36	0
2	MAN	C	6	11/12	0.85	0.09	40,44,49,50	0
2	NDG	C	1	14/15	0.86	0.10	18,21,27,31	0
2	MAN	C	5	11/12	0.88	0.08	19,27,35,39	0
2	MAN	C	4	11/12	0.91	0.09	16,21,28,35	0

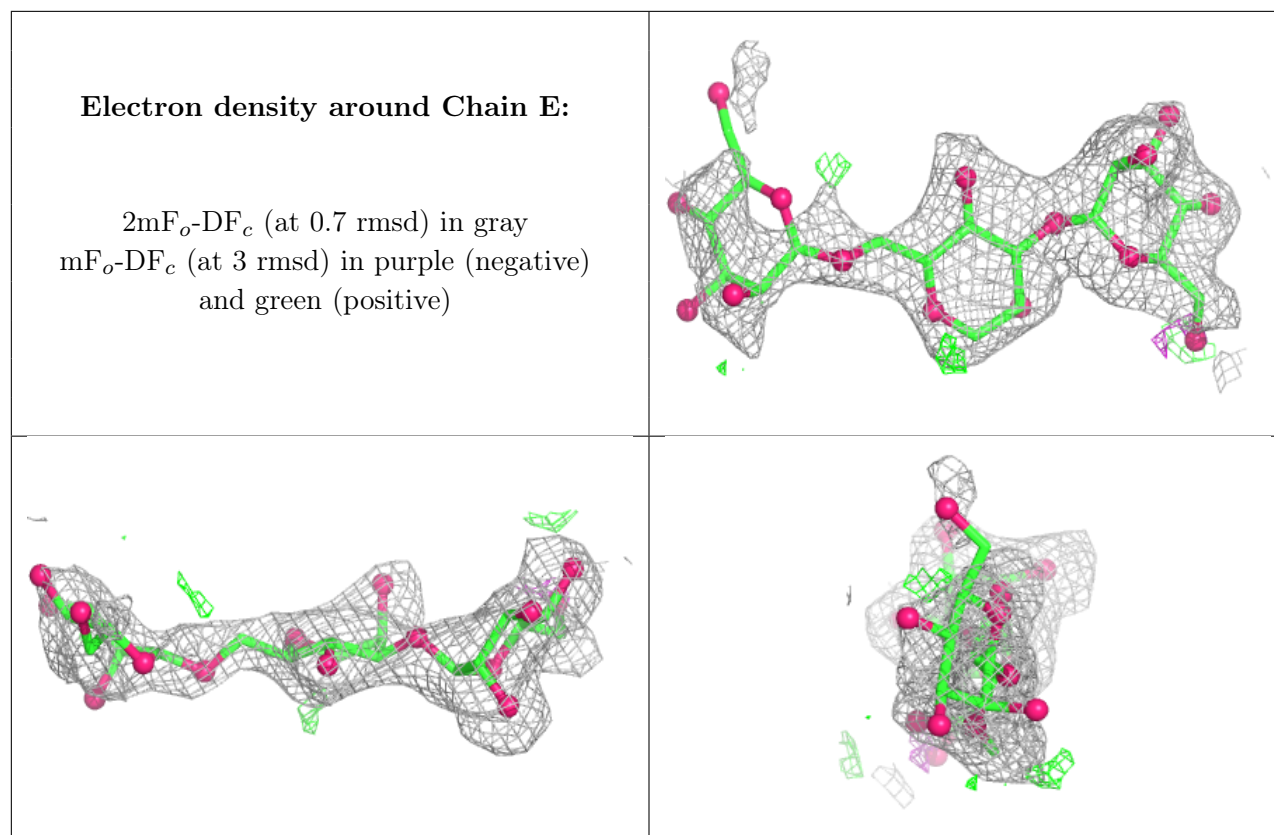
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around Chain D:

$2mF_o-DF_c$ (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
5	MAN	A	992	11/12	0.53	0.28	34,36,39,40	0
6	CUO	B	999	4/4	0.95	0.16	11,15,17,22	0
6	CUO	A	888	4/4	0.98	0.16	9,10,11,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.