



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 25, 2024 – 03:01 PM EST

PDB ID : 1GQH
Title : Quercetin 2,3-dioxygenase in complex with the inhibitor kojic acid
Authors : Steiner, R.A.; Dijkstra, B.W.
Deposited on : 2001-11-23
Resolution : 2.15 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

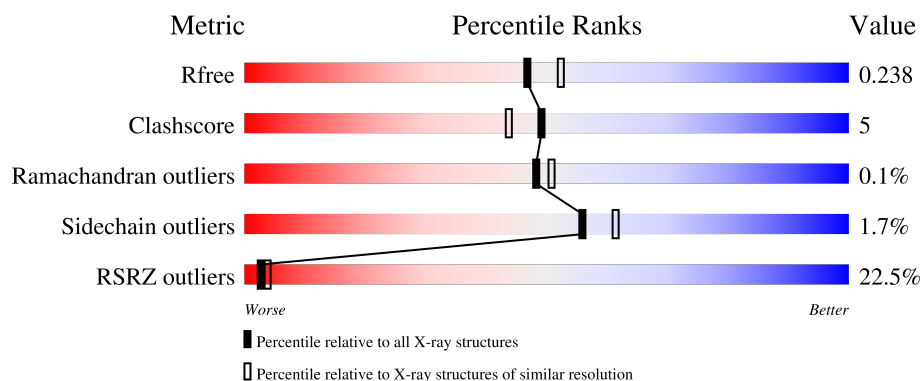
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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.



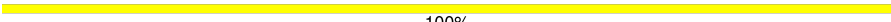
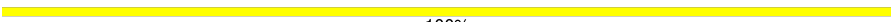
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1881 (2.16-2.16)
Clashscore	180529	2047 (2.16-2.16)
Ramachandran outliers	177936	2027 (2.16-2.16)
Sidechain outliers	177891	2026 (2.16-2.16)
RSRZ outliers	164620	1882 (2.16-2.16)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	350	 83% 14% • •
1	B	350	 84% 10% • 5%
1	C	350	 85% 10% 5%
1	D	350	 83% 12% 5%
2	E	3	 33% 67%
3	F	4	 25% 50% 25%

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Mol	Chain	Length	Quality of chain
3	G	4	 100%
4	H	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MAN	E	3	X	-	-	-
3	MAN	F	3	X	-	-	-
3	MAN	G	3	X	-	-	-

2 Entry composition [i](#)

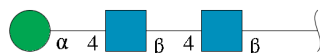
There are 8 unique types of molecules in this entry. The entry contains 11746 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 QUERCETIN 2,3-DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	3	0
			2633	1671	428	529	5			
1	B	334	Total	C	N	O	S	0	0	0
			2581	1644	420	512	5			
1	C	333	Total	C	N	O	S	0	2	0
			2573	1636	419	513	5			
1	D	331	Total	C	N	O	S	0	0	0
			2561	1631	417	508	5			

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



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

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	4	Total	C	N	O	0	0	0
			50	28	2	20			

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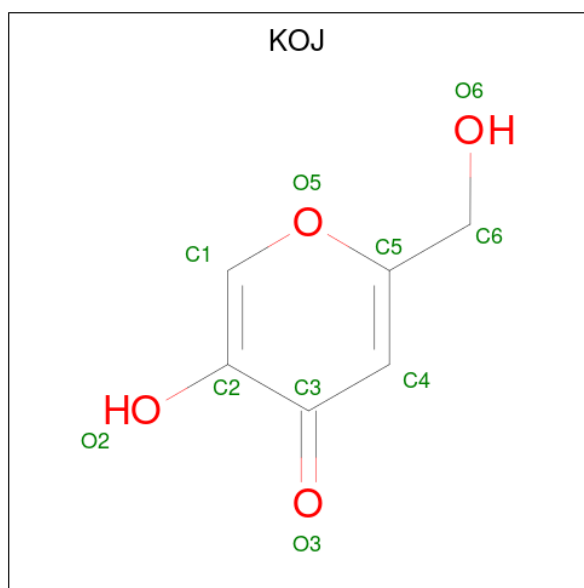
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 4 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
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is 5-HYDROXY-2-(HYDROXYMETHYL)-4H-PYRAN-4-ONE (three-letter code: KOJ) (formula: C₆H₆O₄).

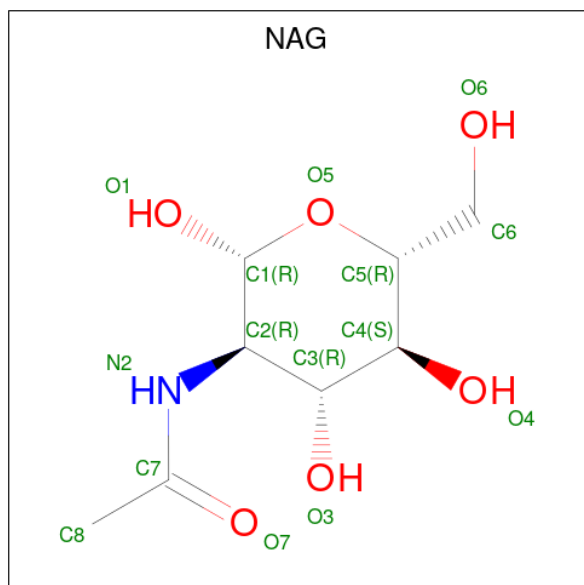


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		
5	B	1	Total	C	O	0	0
			10	6	4		
5	C	1	Total	C	O	0	0
			10	6	4		
5	D	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cu	0	0
			1	1		
6	B	1	Total	Cu	0	0
			1	1		
6	C	1	Total	Cu	0	0
			1	1		
6	D	1	Total	Cu	0	0
			1	1		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	B	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		

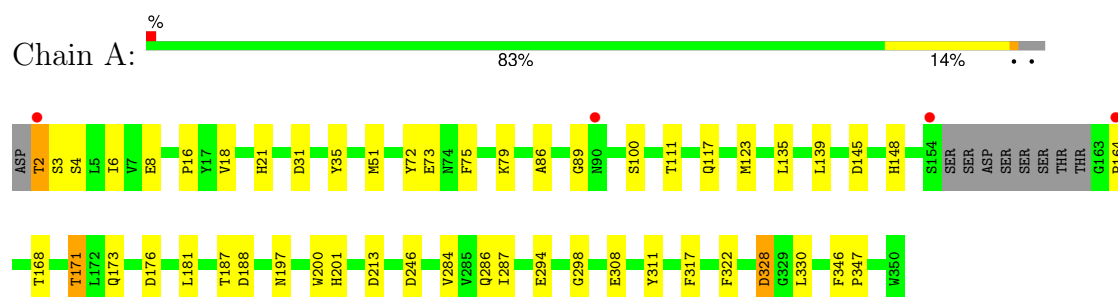
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	294	Total	O	0	0
			294	294		
8	B	251	Total	O	0	0
			251	251		
8	C	251	Total	O	0	0
			251	251		
8	D	223	Total	O	0	0
			223	223		

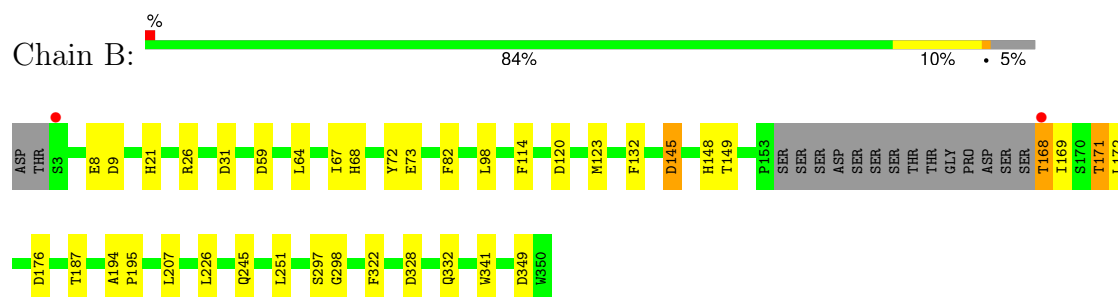
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

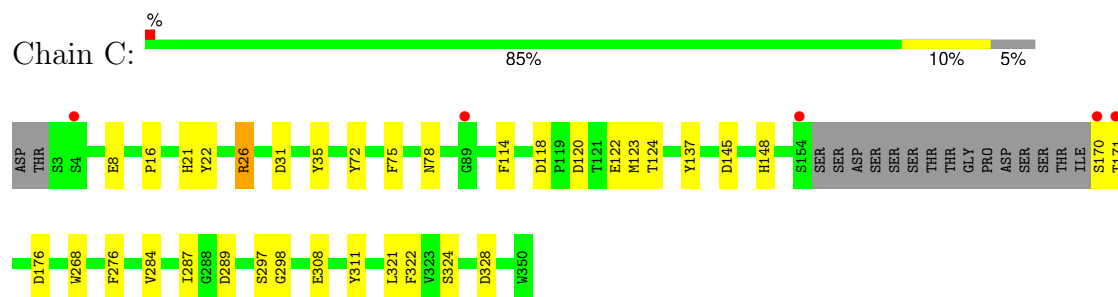
- Molecule 1: QUERCETIN 2,3-DIOXYGENASE



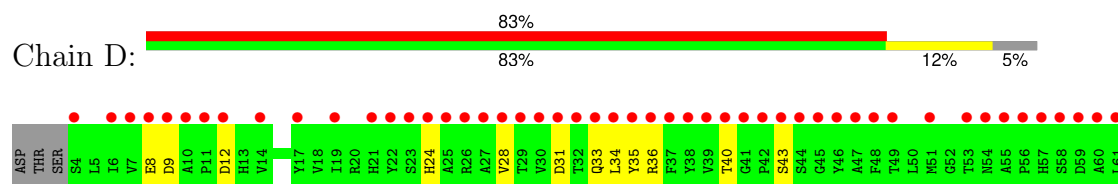
- Molecule 1: QUERCETIN 2,3-DIOXYGENASE

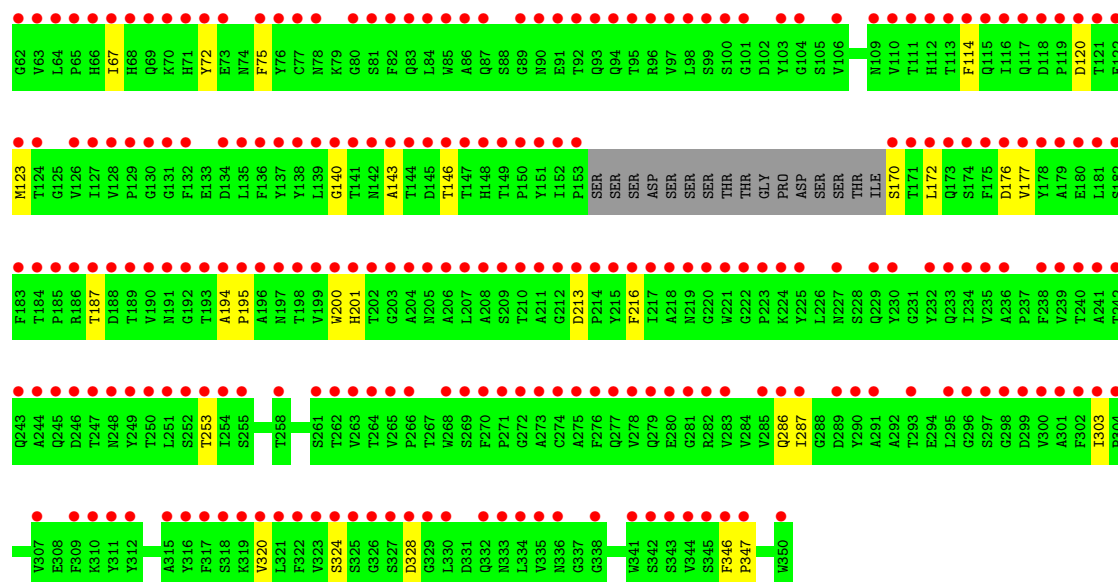


- Molecule 1: QUERCETIN 2,3-DIOXYGENASE



- Molecule 1: QUERCETIN 2,3-DIOXYGENASE





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

Chain E: 33% 67%



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

Chain F: 25% 50% 25%



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

Chain G: 100%



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

Chain H: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	108.64Å 55.40Å 124.42Å 90.00° 98.26° 90.00°	Depositor
Resolution (Å)	49.39 – 2.15 49.39 – 2.15	Depositor EDS
% Data completeness (in resolution range)	89.2 (49.39-2.15) 89.2 (49.39-2.15)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.74 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.178 , 0.228 0.195 , 0.238	Depositor DCC
R_{free} test set	3587 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	20.8	Xtriage
Anisotropy	0.629	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	11746	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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: KOJ, NAG, CU, MAN

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	0.51	0/2728	0.79	6/3740 (0.2%)
1	B	0.49	0/2660	0.82	8/3647 (0.2%)
1	C	0.46	0/2662	0.79	7/3648 (0.2%)
1	D	0.48	0/2640	0.80	6/3619 (0.2%)
All	All	0.49	0/10690	0.80	27/14654 (0.2%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	176	ASP	CB-CG-OD2	7.39	124.96	118.30
1	D	31	ASP	CB-CG-OD2	7.23	124.81	118.30
1	D	120	ASP	CB-CG-OD2	7.01	124.61	118.30
1	C	176	ASP	CB-CG-OD2	6.80	124.42	118.30
1	B	145	ASP	CB-CG-OD2	6.38	124.04	118.30
1	A	176	ASP	CB-CG-OD2	6.29	123.96	118.30
1	C	31	ASP	CB-CG-OD2	6.12	123.80	118.30
1	C	120	ASP	CB-CG-OD2	5.91	123.62	118.30
1	D	328	ASP	CB-CG-OD2	5.89	123.60	118.30
1	B	31	ASP	CB-CG-OD2	5.89	123.60	118.30
1	C	145	ASP	CB-CG-OD2	5.81	123.53	118.30
1	A	31	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	213	ASP	CB-CG-OD2	5.54	123.29	118.30
1	C	289	ASP	CB-CG-OD2	5.50	123.25	118.30
1	B	349	ASP	CB-CG-OD2	5.34	123.11	118.30
1	A	188	ASP	CB-CG-OD2	5.31	123.08	118.30
1	B	59	ASP	CB-CG-OD2	5.30	123.07	118.30
1	D	213	ASP	CB-CG-OD2	5.18	122.97	118.30
1	A	246	ASP	CB-CG-OD2	5.18	122.96	118.30
1	C	118	ASP	CB-CG-OD2	5.11	122.90	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	120	ASP	CB-CG-OD2	5.08	122.88	118.30
1	B	328	ASP	CB-CG-OD2	5.08	122.87	118.30
1	B	9	ASP	CB-CG-OD2	5.06	122.86	118.30
1	D	12	ASP	CB-CG-OD2	5.04	122.84	118.30
1	A	145	ASP	CB-CG-OD2	5.03	122.83	118.30
1	B	176	ASP	CB-CG-OD2	5.01	122.81	118.30
1	C	328	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2633	0	2432	39	0
1	B	2581	0	2392	25	0
1	C	2573	0	2380	20	0
1	D	2561	0	2373	27	0
2	E	39	0	34	0	0
3	F	50	0	43	2	0
3	G	50	0	43	0	0
4	H	28	0	25	0	0
5	A	10	0	4	2	0
5	B	10	0	4	3	0
5	C	10	0	4	3	0
5	D	10	0	4	1	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	56	0	52	0	0
7	B	42	0	39	0	0
7	C	42	0	39	0	0
7	D	28	0	26	0	0
8	A	294	0	0	10	0
8	B	251	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	C	251	0	0	3	0
8	D	223	0	0	4	0
All	All	11746	0	9894	110	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 5.

All (110) 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:8[A]:GLU:OE2	1:A:148:HIS:HE1	1.44	0.99
1:A:8[A]:GLU:OE2	1:A:148:HIS:CE1	2.31	0.82
1:C:114:PHE:CE1	5:C:1351:KOJ:H4	2.15	0.81
1:B:245:GLN:HG2	8:B:2172:HOH:O	1.80	0.81
1:A:139:LEU:HD13	1:A:164:PRO:HG3	1.66	0.76
1:C:8:GLU:OE2	1:C:148:HIS:HE1	1.67	0.76
1:B:8:GLU:OE2	1:B:148:HIS:HE1	1.72	0.72
1:B:168:THR:O	1:B:172:LEU:HG	1.92	0.69
1:A:173:GLN:HG3	8:A:2143:HOH:O	1.92	0.69
1:A:8[B]:GLU:OE2	8:A:2006:HOH:O	2.10	0.68
1:B:332:GLN:NE2	8:B:2231:HOH:O	2.28	0.65
1:A:197:ASN:O	1:A:197:ASN:OD1	2.14	0.65
1:A:171:THR:HG23	8:A:2141:HOH:O	1.96	0.65
1:D:75:PHE:CD2	1:D:123:MET:HE1	2.32	0.64
1:A:171:THR:O	1:A:171:THR:CG2	2.47	0.63
1:D:33:GLN:NE2	1:D:35:TYR:OH	2.34	0.61
1:A:308:GLU:HB2	8:A:2248:HOH:O	2.00	0.61
8:B:2013:HOH:O	1:C:171:THR:HG23	2.00	0.60
1:A:117:GLN:HG3	8:C:2156:HOH:O	2.02	0.60
1:B:168:THR:HA	1:B:171:THR:HG23	1.84	0.59
1:B:114:PHE:CE1	5:B:1351:KOJ:H4	2.37	0.59
1:D:28:VAL:HG21	1:D:140:GLY:HA3	1.84	0.59
1:D:75:PHE:HD2	1:D:123:MET:HE1	1.69	0.58
1:D:28:VAL:CG2	1:D:140:GLY:HA3	2.32	0.58
1:A:86:ALA:HA	1:A:111:THR:O	2.05	0.56
1:C:26:ARG:NH1	8:C:2025:HOH:O	2.38	0.56
1:D:24:HIS:HE1	1:D:143:ALA:O	1.89	0.55
1:D:287:ILE:HD13	1:D:303:ILE:HG13	1.88	0.55
1:D:75:PHE:HD2	1:D:123:MET:CE	2.21	0.53
8:B:2013:HOH:O	1:C:171:THR:CG2	2.55	0.53
1:A:294:GLU:HG2	8:A:2240:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:35:TYR:HE2	5:C:1351:KOJ:H6C2	1.74	0.53
1:D:40:THR:H	1:D:43:SER:HB3	1.75	0.52
1:B:8:GLU:HG2	8:B:2002:HOH:O	2.08	0.52
1:A:73:GLU:OE2	5:A:1351:KOJ:O2	2.28	0.51
1:D:8:GLU:HG2	8:D:2005:HOH:O	2.10	0.51
1:A:16:PRO:HB3	1:A:287:ILE:HG21	1.92	0.51
1:D:146:THR:HG22	8:D:2112:HOH:O	2.10	0.51
1:B:82:PHE:CE2	1:B:123:MET:HG2	2.45	0.51
1:A:197:ASN:OD1	1:A:197:ASN:C	2.49	0.50
1:A:2:THR:OG1	1:A:3:SER:N	2.40	0.50
1:B:73:GLU:OE2	5:B:1351:KOJ:C1	2.60	0.50
1:C:114:PHE:HE1	5:C:1351:KOJ:H4	1.75	0.50
1:A:21:HIS:CG	1:A:298:GLY:HA3	2.47	0.49
1:C:26:ARG:HD2	8:C:2025:HOH:O	2.12	0.49
1:A:328:ASP:HB2	8:A:2264:HOH:O	2.11	0.49
1:A:4:SER:HB3	8:A:2003:HOH:O	2.12	0.49
1:C:26:ARG:HD3	1:C:137:TYR:OH	2.13	0.49
1:B:73:GLU:OE2	5:B:1351:KOJ:C2	2.60	0.49
1:D:67:ILE:HD11	8:D:2084:HOH:O	2.12	0.48
1:C:78[A]:ASN:ND2	1:C:124:THR:OG1	2.45	0.48
1:C:8:GLU:OE2	1:C:148:HIS:CE1	2.58	0.48
1:D:9:ASP:OD1	1:D:24:HIS:HD2	1.96	0.48
1:A:35:TYR:HD2	1:A:51:MET:CE	2.27	0.47
1:D:114:PHE:CE2	5:D:1351:KOJ:H4	2.50	0.47
1:A:171:THR:HG23	1:A:171:THR:O	2.14	0.46
1:D:172:LEU:HB2	1:D:177:VAL:HB	1.97	0.46
1:B:251:LEU:HD12	1:B:322:PHE:O	2.16	0.46
1:B:297:SER:HB2	8:B:2199:HOH:O	2.16	0.46
1:B:297:SER:HB3	8:B:2200:HOH:O	2.15	0.45
1:C:21:HIS:CG	1:C:298:GLY:HA3	2.51	0.45
1:C:78[A]:ASN:HB2	1:C:122:GLU:HB3	1.99	0.45
1:A:284:VAL:O	1:A:311:TYR:HA	2.16	0.45
1:D:216:PHE:CD1	1:D:216:PHE:N	2.85	0.45
1:B:21:HIS:CG	1:B:298:GLY:HA3	2.52	0.45
1:A:73:GLU:CD	5:A:1351:KOJ:O2	2.55	0.44
1:B:8:GLU:OE2	1:B:148:HIS:CE1	2.62	0.44
1:B:82:PHE:CD2	1:B:123:MET:HG2	2.53	0.44
1:D:253:THR:HA	1:D:320:VAL:O	2.17	0.44
1:D:346:PHE:HB2	1:D:347:PRO:HD2	1.99	0.44
1:D:187:THR:OG1	3:F:3:MAN:H62	2.18	0.44
1:A:317:PHE:HB3	1:C:22:TYR:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:268:TRP:O	1:C:308:GLU:HA	2.19	0.43
1:A:346:PHE:HB2	1:A:347:PRO:CD	2.48	0.43
1:B:98:LEU:HD12	1:B:98:LEU:N	2.33	0.43
1:D:75:PHE:CE2	1:D:123:MET:HE1	2.54	0.43
1:A:187:THR:HG23	8:A:2154:HOH:O	2.18	0.43
1:D:200:TRP:O	1:D:201:HIS:HB2	2.18	0.43
1:D:346:PHE:HB2	1:D:347:PRO:CD	2.49	0.42
1:A:75:PHE:HD2	1:A:123:MET:HE2	1.83	0.42
1:B:132:PHE:CB	8:B:2098:HOH:O	2.67	0.42
1:C:322:PHE:CZ	1:C:324:SER:HB2	2.54	0.42
1:A:8[A]:GLU:HG2	8:A:2007:HOH:O	2.18	0.42
1:C:16:PRO:HB3	1:C:287:ILE:HG21	2.02	0.42
1:B:145:ASP:OD2	1:B:149:THR:O	2.37	0.42
1:A:168:THR:O	1:A:171:THR:HB	2.19	0.42
1:B:67:ILE:CG2	1:B:68:HIS:N	2.82	0.42
1:B:226:LEU:HB2	1:B:341:TRP:CG	2.54	0.42
1:D:40:THR:OG1	1:D:43:SER:HB2	2.20	0.42
1:C:75:PHE:HD2	1:C:123:MET:CE	2.33	0.42
1:A:322:PHE:CZ	1:A:330:LEU:HB3	2.55	0.42
1:C:284:VAL:O	1:C:311:TYR:HA	2.20	0.42
1:D:286:GLN:HA	8:D:2178:HOH:O	2.19	0.42
1:A:75:PHE:CD2	1:A:123:MET:HE2	2.54	0.41
1:A:79:LYS:HA	1:A:100[B]:SER:OG	2.20	0.41
1:D:34:LEU:HD22	1:D:36:ARG:NH1	2.36	0.41
1:A:171:THR:O	1:A:171:THR:HG22	2.20	0.41
1:A:346:PHE:HB2	1:A:347:PRO:HD2	2.01	0.41
1:D:187:THR:HG21	3:F:3:MAN:H62	2.02	0.41
1:D:194:ALA:HA	1:D:195:PRO:C	2.40	0.41
1:B:132:PHE:HB3	8:B:2098:HOH:O	2.20	0.41
1:B:187:THR:HG22	8:B:2131:HOH:O	2.21	0.41
1:B:207:LEU:N	1:B:207:LEU:HD12	2.36	0.41
1:A:200:TRP:O	1:A:201:HIS:HB2	2.20	0.41
1:A:286:GLN:NE2	8:A:2233:HOH:O	2.54	0.41
1:C:276:PHE:HA	1:C:321:LEU:O	2.21	0.40
1:A:6:ILE:HA	1:A:18:VAL:O	2.21	0.40
1:A:75:PHE:HD2	1:A:123:MET:CE	2.34	0.40
1:B:194:ALA:HA	1:B:195:PRO:C	2.41	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	340/350 (97%)	329 (97%)	10 (3%)	1 (0%)	37	34
1	B	330/350 (94%)	319 (97%)	11 (3%)	0	100	100
1	C	331/350 (95%)	318 (96%)	13 (4%)	0	100	100
1	D	327/350 (93%)	320 (98%)	7 (2%)	0	100	100
All	All	1328/1400 (95%)	1286 (97%)	41 (3%)	1 (0%)	48	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	GLY

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	287/294 (98%)	281 (98%)	6 (2%)	48	53
1	B	278/294 (95%)	272 (98%)	6 (2%)	47	51
1	C	279/294 (95%)	275 (99%)	4 (1%)	62	68
1	D	276/294 (94%)	273 (99%)	3 (1%)	70	75
All	All	1120/1176 (95%)	1101 (98%)	19 (2%)	56	61

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	72	TYR
1	A	135	LEU
1	A	171	THR
1	A	181	LEU
1	A	328	ASP
1	B	26	ARG
1	B	64	LEU
1	B	72	TYR
1	B	168	THR
1	B	169	ILE
1	B	171	THR
1	C	26	ARG
1	C	72	TYR
1	C	170	SER
1	C	297	SER
1	D	72	TYR
1	D	170	SER
1	D	324	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	117	GLN
1	A	148	HIS
1	A	173	GLN
1	A	332	GLN
1	A	336	ASN
1	B	83	GLN
1	B	148	HIS
1	B	286	GLN
1	B	332	GLN
1	C	83	GLN
1	C	148	HIS
1	D	24	HIS
1	D	33	GLN
1	D	83	GLN
1	D	332	GLN
1	D	336	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 ⓘ

13 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	E	1	2,1	14,14,15	0.56	0	17,19,21	1.34	4 (23%)
2	NAG	E	2	2	14,14,15	0.62	0	17,19,21	1.04	1 (5%)
2	MAN	E	3	2	11,11,12	0.77	0	15,15,17	0.79	0
3	NAG	F	1	1,3	14,14,15	0.74	0	17,19,21	1.04	0
3	NAG	F	2	3	14,14,15	0.76	0	17,19,21	1.00	1 (5%)
3	MAN	F	3	3	11,11,12	0.60	0	15,15,17	1.05	1 (6%)
3	MAN	F	4	3	11,11,12	0.53	0	15,15,17	1.07	1 (6%)
3	NAG	G	1	1,3	14,14,15	0.69	0	17,19,21	1.04	1 (5%)
3	NAG	G	2	3	14,14,15	0.53	0	17,19,21	1.07	1 (5%)
3	MAN	G	3	3	11,11,12	0.73	0	15,15,17	1.13	2 (13%)
3	MAN	G	4	3	11,11,12	0.65	0	15,15,17	1.17	1 (6%)
4	NAG	H	1	4,1	14,14,15	0.55	0	17,19,21	1.04	1 (5%)
4	NAG	H	2	4	14,14,15	0.59	0	17,19,21	1.34	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	MAN	E	3	2	1/1/4/5	0/2/19/22	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	MAN	F	3	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	F	4	3	-	2/2/19/22	0/1/1/1
3	NAG	G	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	MAN	G	3	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	G	4	3	-	2/2/19/22	0/1/1/1
4	NAG	H	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	2	NAG	C1-O5-C5	4.29	117.93	112.19
4	H	1	NAG	O5-C1-C2	-3.16	106.40	111.29
2	E	2	NAG	O5-C1-C2	-2.97	106.70	111.29
3	G	4	MAN	O5-C5-C6	2.91	113.33	107.66
3	F	2	NAG	O5-C1-C2	-2.81	106.95	111.29
2	E	1	NAG	O5-C1-C2	-2.56	107.33	111.29
2	E	1	NAG	C1-O5-C5	2.31	115.28	112.19
3	F	3	MAN	O5-C5-C6	2.21	111.96	107.66
3	F	4	MAN	C3-C4-C5	-2.19	106.27	110.23
3	G	1	NAG	O5-C1-C2	-2.16	107.94	111.29
3	G	2	NAG	O5-C1-C2	-2.13	108.00	111.29
2	E	1	NAG	C1-C2-N2	2.12	113.78	110.43
3	G	3	MAN	C3-C4-C5	2.09	114.03	110.23
2	E	1	NAG	C2-N2-C7	-2.09	120.10	122.90
3	G	3	MAN	C1-C2-C3	2.03	112.60	109.64

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	E	3	MAN	C1
3	F	3	MAN	C1
3	G	3	MAN	C1

All (6) torsion outliers are listed below:

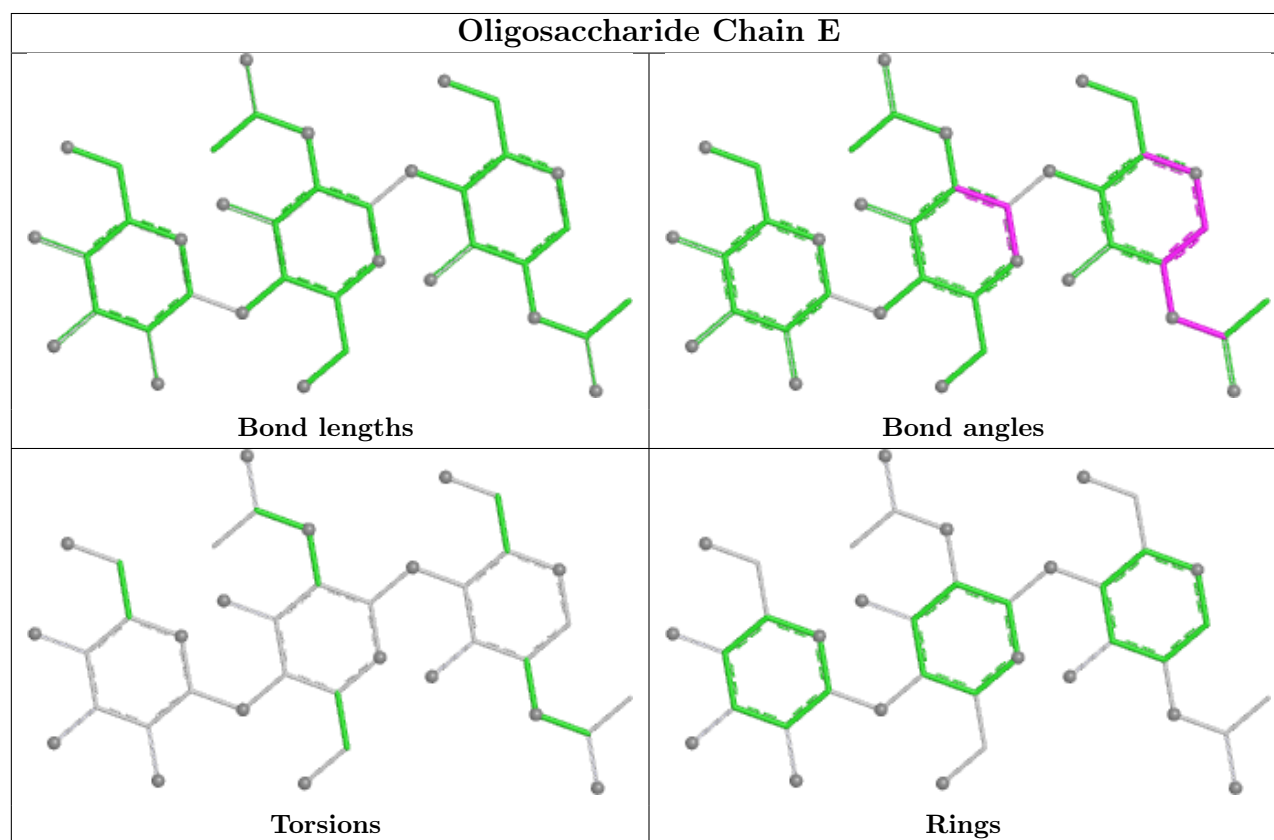
Mol	Chain	Res	Type	Atoms
3	G	4	MAN	O5-C5-C6-O6
3	G	4	MAN	C4-C5-C6-O6
3	F	4	MAN	O5-C5-C6-O6
3	F	4	MAN	C4-C5-C6-O6
3	G	1	NAG	C8-C7-N2-C2
3	G	1	NAG	O7-C7-N2-C2

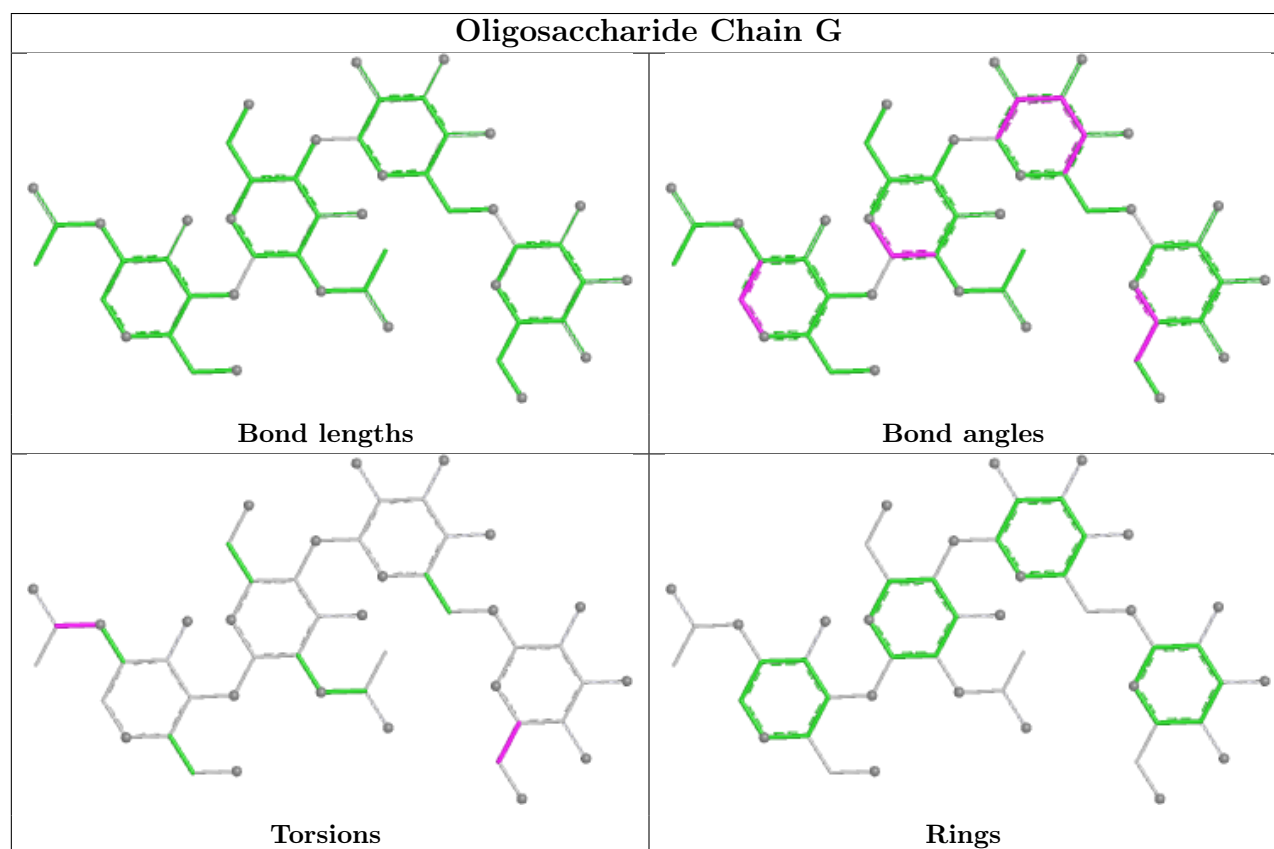
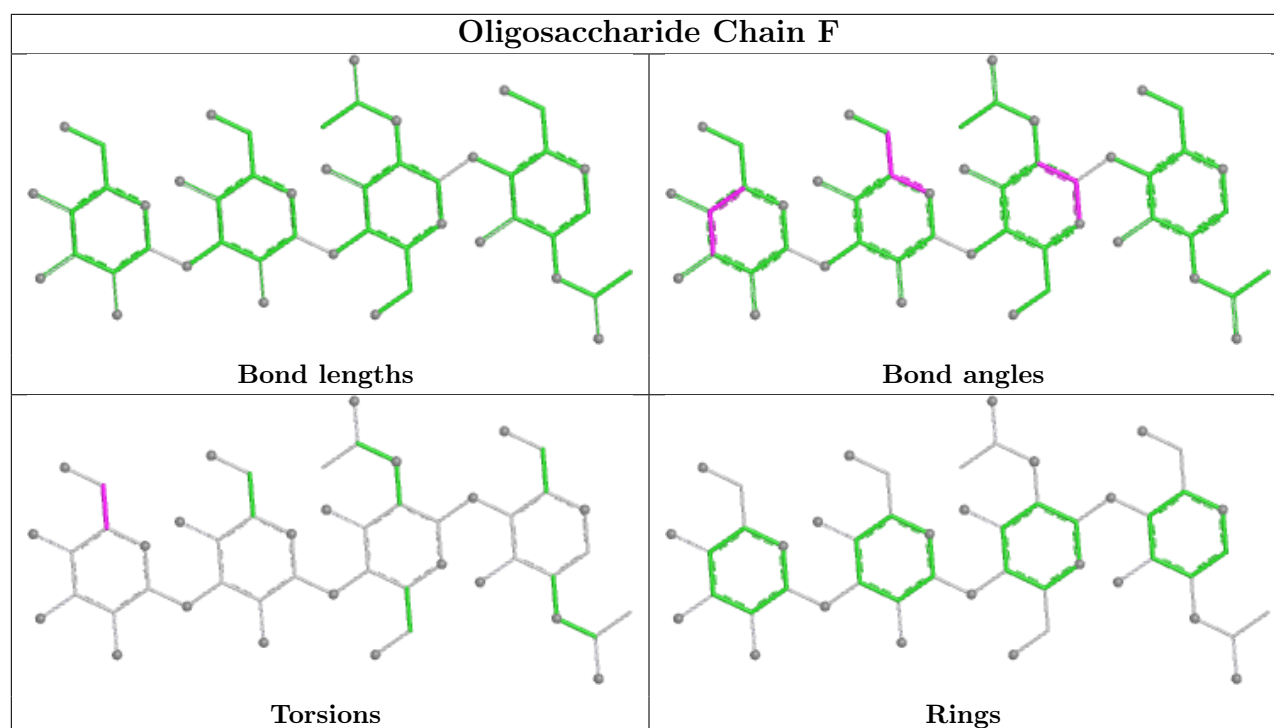
There are no ring outliers.

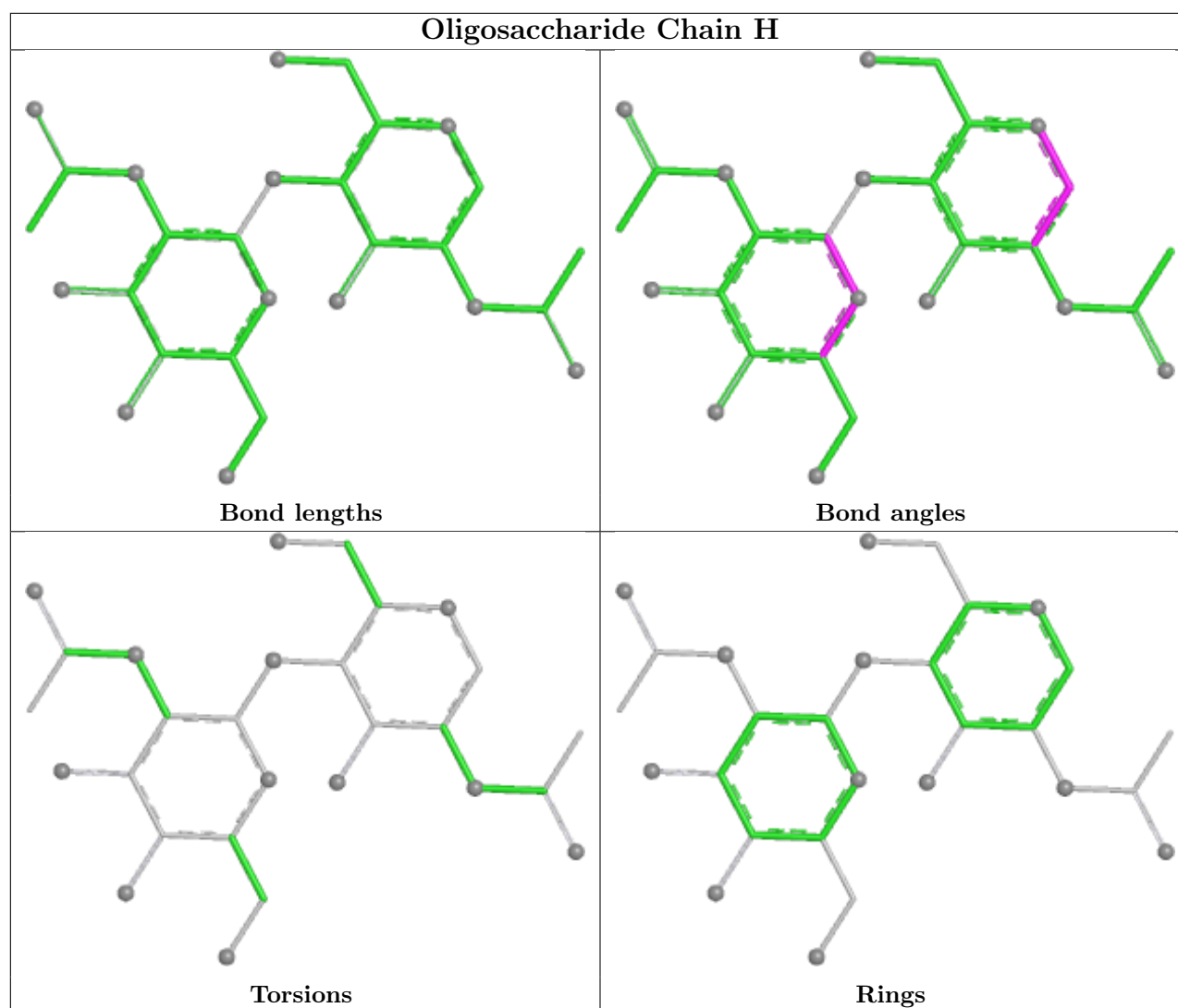
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	3	MAN	2	0

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







5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 4 are monoatomic - leaving 16 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	NAG	A	1358	1	14,14,15	0.49	0	17,19,21	1.31	2 (11%)
7	NAG	B	1357	1	14,14,15	0.64	0	17,19,21	1.01	0
7	NAG	C	1358	1	14,14,15	0.63	0	17,19,21	1.95	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	D	1356	1	14,14,15	0.62	0	17,19,21	1.16	3 (17%)
7	NAG	B	1356	1	14,14,15	0.68	0	17,19,21	1.64	5 (29%)
7	NAG	C	1357	1	14,14,15	0.75	0	17,19,21	1.22	2 (11%)
7	NAG	B	1353	1	14,14,15	0.63	0	17,19,21	0.99	1 (5%)
7	NAG	A	1357	1	14,14,15	0.63	0	17,19,21	1.51	3 (17%)
7	NAG	A	1353	1	14,14,15	0.73	0	17,19,21	1.18	1 (5%)
7	NAG	D	1353	1	14,14,15	0.51	0	17,19,21	1.26	2 (11%)
7	NAG	A	1356	1	14,14,15	0.64	0	17,19,21	1.31	2 (11%)
5	KOJ	D	1351	6	8,10,10	3.49	3 (37%)	6,13,13	1.03	1 (16%)
5	KOJ	C	1351	6	8,10,10	3.24	3 (37%)	6,13,13	1.48	1 (16%)
5	KOJ	B	1351	6	8,10,10	3.08	2 (25%)	6,13,13	1.91	1 (16%)
5	KOJ	A	1351	6	8,10,10	3.29	3 (37%)	6,13,13	1.45	1 (16%)
7	NAG	C	1354	1	14,14,15	0.64	0	17,19,21	1.31	3 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	A	1358	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1357	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1358	1	-	2/6/23/26	0/1/1/1
7	NAG	D	1356	1	-	0/6/23/26	0/1/1/1
7	NAG	B	1356	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1357	1	-	0/6/23/26	0/1/1/1
7	NAG	B	1353	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1357	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1353	1	-	2/6/23/26	0/1/1/1
7	NAG	D	1353	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1356	1	-	0/6/23/26	0/1/1/1
5	KOJ	D	1351	6	-	0/1/2/2	0/1/1/1
5	KOJ	C	1351	6	-	0/1/2/2	0/1/1/1
5	KOJ	B	1351	6	-	0/1/2/2	0/1/1/1
5	KOJ	A	1351	6	-	1/1/2/2	0/1/1/1
7	NAG	C	1354	1	-	0/6/23/26	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	1351	KOJ	O5-C5	-7.18	1.24	1.35
5	A	1351	KOJ	O5-C5	-6.83	1.25	1.35
5	B	1351	KOJ	O5-C5	-6.29	1.25	1.35
5	C	1351	KOJ	O5-C5	-6.11	1.26	1.35
5	D	1351	KOJ	O3-C3	5.72	1.33	1.23
5	C	1351	KOJ	O3-C3	5.72	1.33	1.23
5	B	1351	KOJ	O3-C3	5.22	1.32	1.23
5	A	1351	KOJ	O3-C3	5.18	1.32	1.23
5	C	1351	KOJ	C6-C5	-2.36	1.48	1.50
5	A	1351	KOJ	C6-C5	-2.32	1.48	1.50
5	D	1351	KOJ	C6-C5	-2.17	1.48	1.50

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	1358	NAG	C2-N2-C7	-4.34	117.08	122.90
5	B	1351	KOJ	O6-C6-C5	4.28	121.57	112.03
7	C	1358	NAG	C1-O5-C5	-3.89	106.98	112.19
7	B	1356	NAG	O5-C1-C2	-3.68	105.59	111.29
7	A	1353	NAG	C2-N2-C7	-3.26	118.53	122.90
5	C	1351	KOJ	O6-C6-C5	3.19	119.13	112.03
7	A	1357	NAG	C1-O5-C5	3.18	116.45	112.19
7	A	1356	NAG	C1-O5-C5	3.14	116.40	112.19
7	C	1358	NAG	O5-C1-C2	-3.12	106.47	111.29
7	C	1358	NAG	C4-C3-C2	3.12	115.59	111.02
5	A	1351	KOJ	O6-C6-C5	2.99	118.69	112.03
7	B	1356	NAG	C1-O5-C5	2.95	116.13	112.19
7	C	1357	NAG	O5-C1-C2	-2.89	106.82	111.29
7	B	1356	NAG	C2-N2-C7	-2.85	119.08	122.90
7	C	1354	NAG	O5-C5-C6	2.74	113.00	107.66
7	C	1358	NAG	O5-C5-C6	2.62	112.76	107.66
7	A	1357	NAG	C3-C4-C5	2.53	114.83	110.23
7	A	1358	NAG	C2-N2-C7	2.52	126.28	122.90
7	D	1353	NAG	C1-O5-C5	2.49	115.53	112.19
7	B	1353	NAG	O5-C1-C2	-2.47	107.47	111.29
7	C	1354	NAG	C3-C4-C5	-2.46	105.78	110.23
7	D	1356	NAG	O5-C1-C2	-2.45	107.51	111.29
7	A	1356	NAG	C2-N2-C7	-2.42	119.65	122.90
7	D	1356	NAG	C2-N2-C7	-2.39	119.70	122.90
7	B	1356	NAG	C1-C2-N2	2.28	114.02	110.43
7	D	1356	NAG	C1-O5-C5	2.25	115.20	112.19
7	A	1357	NAG	O5-C1-C2	-2.24	107.83	111.29
7	A	1358	NAG	O7-C7-C8	-2.24	118.07	122.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	1357	NAG	C2-N2-C7	-2.08	120.11	122.90
7	D	1353	NAG	O5-C1-C2	-2.07	108.09	111.29
7	C	1354	NAG	O5-C5-C4	-2.06	105.82	110.83
7	B	1356	NAG	C4-C3-C2	-2.04	108.03	111.02
5	D	1351	KOJ	O6-C6-C5	2.00	116.49	112.03

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	1358	NAG	O5-C5-C6-O6
7	C	1358	NAG	C4-C5-C6-O6
7	A	1353	NAG	O5-C5-C6-O6
7	B	1353	NAG	C4-C5-C6-O6
7	D	1353	NAG	O5-C5-C6-O6
7	A	1353	NAG	C4-C5-C6-O6
7	D	1353	NAG	C4-C5-C6-O6
7	A	1358	NAG	O5-C5-C6-O6
7	B	1357	NAG	O5-C5-C6-O6
7	B	1357	NAG	C4-C5-C6-O6
7	B	1353	NAG	O5-C5-C6-O6
7	A	1358	NAG	C4-C5-C6-O6
7	B	1356	NAG	C4-C5-C6-O6
7	B	1356	NAG	O5-C5-C6-O6
5	A	1351	KOJ	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	1351	KOJ	1	0
5	C	1351	KOJ	3	0
5	B	1351	KOJ	3	0
5	A	1351	KOJ	2	0

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 ⓘ

Warning: The R factor obtained from EDS is 0.2525, which does not match the depositor's R factor of 0.178. Please interpret the results in this section carefully.

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	341/350 (97%)	-0.13	4 (1%) 76 79	6, 11, 17, 25	3 (0%)
1	B	334/350 (95%)	-0.08	2 (0%) 85 87	6, 11, 16, 26	0
1	C	333/350 (95%)	-0.03	5 (1%) 71 75	7, 11, 16, 24	2 (0%)
1	D	331/350 (94%)	3.36	290 (87%) 0 0	7, 11, 16, 24	0
All	All	1339/1400 (95%)	0.77	301 (22%) 3 4	6, 11, 16, 26	5 (0%)

All (301) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	171	THR	8.5
1	D	78	ASN	8.2
1	D	181	LEU	7.2
1	D	217	ILE	7.2
1	D	28	VAL	7.2
1	D	194	ALA	7.2
1	D	262	THR	7.0
1	D	170	SER	6.9
1	D	183	PHE	6.8
1	D	207	LEU	6.6
1	D	214	PRO	6.5
1	D	4	SER	6.4
1	D	208	ALA	6.3
1	D	138	TYR	6.1
1	D	153	PRO	6.0
1	D	216	PHE	5.9
1	D	321	LEU	5.8
1	D	190	VAL	5.8
1	D	55	ALA	5.7

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Mol	Chain	Res	Type	RSRZ
1	D	172	LEU	5.6
1	D	261	SER	5.6
1	D	218	ALA	5.6
1	D	90	ASN	5.6
1	D	350	TRP	5.6
1	D	152	ILE	5.5
1	D	84	LEU	5.5
1	D	116	ILE	5.4
1	D	198	THR	5.4
1	D	189	THR	5.4
1	D	177	VAL	5.3
1	D	230	TYR	5.3
1	D	184	THR	5.2
1	D	252	SER	5.1
1	D	25	ALA	5.1
1	D	80	GLY	5.0
1	D	175	PHE	5.0
1	D	213	ASP	5.0
1	D	193	THR	4.9
1	D	215	TYR	4.9
1	D	51	MET	4.8
1	D	182	SER	4.8
1	D	34	LEU	4.8
1	D	137	TYR	4.8
1	D	109	ASN	4.7
1	D	44	SER	4.7
1	D	178	TYR	4.7
1	D	143	ALA	4.7
1	D	328	ASP	4.7
1	D	245	GLN	4.6
1	D	174	SER	4.6
1	D	239	VAL	4.5
1	D	219	ASN	4.5
1	D	209	SER	4.5
1	D	149	THR	4.5
1	D	199	VAL	4.5
1	D	58	SER	4.4
1	D	249	TYR	4.4
1	D	176	ASP	4.4
1	D	14	VAL	4.4
1	D	211	ALA	4.4
1	D	225	TYR	4.3

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Mol	Chain	Res	Type	RSRZ
1	D	82	PHE	4.3
1	D	289	ASP	4.3
1	D	192	GLY	4.3
1	D	244	ALA	4.3
1	D	196	ALA	4.2
1	D	43	SER	4.2
1	D	29	THR	4.2
1	D	75	PHE	4.2
1	D	188	ASP	4.2
1	D	300	VAL	4.2
1	D	31	ASP	4.1
1	D	141	THR	4.1
1	D	238	PHE	4.1
1	D	85	TRP	4.1
1	D	62	GLY	4.1
1	D	142	ASN	4.1
1	D	185	PRO	4.0
1	C	89	GLY	4.0
1	D	298	GLY	4.0
1	D	151	TYR	4.0
1	D	37	PHE	4.0
1	D	136	PHE	4.0
1	D	139	LEU	4.0
1	D	200	TRP	4.0
1	D	72	TYR	4.0
1	D	247	THR	3.9
1	D	32	THR	3.9
1	D	123	MET	3.9
1	D	297	SER	3.9
1	D	204	ALA	3.9
1	D	76	TYR	3.9
1	D	54	ASN	3.8
1	D	241	ALA	3.8
1	D	320	VAL	3.8
1	D	124	THR	3.8
1	D	144	THR	3.8
1	D	120	ASP	3.8
1	D	295	LEU	3.8
1	D	64	LEU	3.8
1	D	333	ASN	3.8
1	D	266	PRO	3.8
1	D	35	TYR	3.8

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Mol	Chain	Res	Type	RSRZ
1	D	111	THR	3.7
1	D	117	GLN	3.7
1	D	173	GLN	3.7
1	D	327	SER	3.7
1	D	250	THR	3.7
1	D	338	GLY	3.7
1	D	278	VAL	3.7
1	D	277	GLN	3.7
1	D	27	ALA	3.7
1	D	251	LEU	3.7
1	D	40	THR	3.7
1	D	210	THR	3.7
1	D	114	PHE	3.7
1	D	263	VAL	3.6
1	D	19	ILE	3.6
1	D	145	ASP	3.6
1	D	179	ALA	3.6
1	D	135	LEU	3.6
1	D	201	HIS	3.6
1	D	77	CYS	3.6
1	D	17	TYR	3.6
1	D	344	VAL	3.6
1	D	246	ASP	3.5
1	D	269	SER	3.5
1	D	38	TYR	3.5
1	D	322	PHE	3.5
1	D	53	THR	3.5
1	D	57	HIS	3.5
1	D	98	LEU	3.5
1	D	97	VAL	3.4
1	D	293	THR	3.4
1	D	342	SER	3.4
1	D	326	GLY	3.4
1	D	86	ALA	3.4
1	D	195	PRO	3.4
1	D	236	ALA	3.4
1	D	99	SER	3.4
1	D	70	LYS	3.4
1	D	7	VAL	3.4
1	D	330	LEU	3.4
1	D	270	PHE	3.3
1	D	335	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	D	254	ILE	3.3
1	D	334	LEU	3.3
1	D	224	LYS	3.3
1	A	90	ASN	3.3
1	D	291	ALA	3.3
1	D	286	GLN	3.3
1	D	67	ILE	3.3
1	D	299	ASP	3.3
1	D	227	ASN	3.3
1	D	132	PHE	3.3
1	D	146	THR	3.3
1	D	329	GLY	3.2
1	D	323	VAL	3.2
1	D	113	THR	3.2
1	D	274	CYS	3.2
1	D	191	ASN	3.2
1	D	197	ASN	3.2
1	D	319	LYS	3.2
1	D	73	GLU	3.2
1	D	180	GLU	3.2
1	D	24	HIS	3.2
1	D	83	GLN	3.1
1	D	221	TRP	3.1
1	D	341	TRP	3.1
1	D	65	PRO	3.1
1	D	104	GLY	3.1
1	D	301	ALA	3.1
1	D	248	ASN	3.1
1	D	187	THR	3.1
1	D	242	THR	3.1
1	D	272	GLY	3.1
1	D	6	ILE	3.1
1	D	332	GLN	3.1
1	D	324	SER	3.1
1	D	304	PRO	3.1
1	D	235	VAL	3.1
1	D	148	HIS	3.0
1	D	268	TRP	3.0
1	D	56	PRO	3.0
1	D	112	HIS	3.0
1	D	220	GLY	3.0
1	D	275	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	186	ARG	3.0
1	B	3	SER	3.0
1	D	39	VAL	3.0
1	D	36	ARG	3.0
1	D	46	TYR	2.9
1	D	60	ALA	2.9
1	D	134	ASP	2.9
1	D	95	THR	2.9
1	D	150	PRO	2.9
1	D	8	GLU	2.9
1	D	312	TYR	2.9
1	D	281	GLY	2.9
1	D	223	PRO	2.9
1	D	127	ILE	2.9
1	D	118	ASP	2.8
1	D	276	PHE	2.8
1	D	280	GLU	2.8
1	D	229	GLN	2.8
1	D	205	ASN	2.8
1	D	234	ILE	2.8
1	D	140	GLY	2.8
1	D	147	THR	2.8
1	D	22	TYR	2.8
1	D	119	PRO	2.8
1	D	91	GLU	2.8
1	D	310	LYS	2.8
1	D	264	THR	2.8
1	D	110	VAL	2.8
1	D	343	SER	2.8
1	D	346	PHE	2.7
1	D	222	GLY	2.7
1	D	336	ASN	2.7
1	D	10	ALA	2.7
1	D	41	GLY	2.7
1	D	59	ASP	2.7
1	D	103	TYR	2.7
1	D	30	VAL	2.7
1	D	106	VAL	2.7
1	D	317	PHE	2.7
1	D	93	GLN	2.7
1	D	253	THR	2.7
1	D	47	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	63	VAL	2.7
1	D	94	GLN	2.7
1	D	92	THR	2.6
1	D	122	GLU	2.6
1	D	240	THR	2.6
1	D	33	GLN	2.6
1	D	232	TYR	2.6
1	D	71	HIS	2.6
1	D	12	ASP	2.6
1	D	23	SER	2.6
1	D	26	ARG	2.6
1	D	69	GLN	2.6
1	D	203	GLY	2.6
1	D	315	ALA	2.6
1	D	347	PRO	2.6
1	D	283	VAL	2.5
1	D	287	ILE	2.5
1	D	45	GLY	2.5
1	D	285	VAL	2.5
1	D	307	VAL	2.5
1	D	258	THR	2.5
1	C	170	SER	2.5
1	D	273	ALA	2.5
1	D	311	TYR	2.5
1	C	154	SER	2.5
1	D	131	GLY	2.5
1	D	212	GLY	2.5
1	D	202	THR	2.5
1	D	290	TYR	2.4
1	C	4	SER	2.4
1	D	66	HIS	2.4
1	D	126	VAL	2.4
1	D	130	GLY	2.4
1	D	61	LEU	2.4
1	D	87	GLN	2.4
1	D	279	GLN	2.4
1	D	81	SER	2.3
1	D	100	SER	2.3
1	D	255	SER	2.3
1	D	265	VAL	2.3
1	D	309	PHE	2.3
1	D	49	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	128	VAL	2.3
1	D	243	GLN	2.3
1	D	21	HIS	2.3
1	D	316	TYR	2.3
1	C	171	THR	2.3
1	D	121	THR	2.3
1	D	206	ALA	2.3
1	D	42	PRO	2.2
1	D	9	ASP	2.2
1	D	296	GLY	2.2
1	D	115	GLN	2.2
1	D	345	SER	2.2
1	D	271	PRO	2.2
1	D	302	PHE	2.2
1	D	233	GLN	2.2
1	D	101	GLY	2.2
1	D	303	ILE	2.2
1	B	168	THR	2.2
1	D	318	SER	2.2
1	D	325	SER	2.2
1	D	48	PHE	2.1
1	D	11	PRO	2.1
1	D	89	GLY	2.1
1	D	129	PRO	2.1
1	A	154	SER	2.1
1	D	68	HIS	2.1
1	D	282	ARG	2.0
1	A	2	THR	2.0
1	A	164	PRO	2.0
1	D	96	ARG	2.0

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

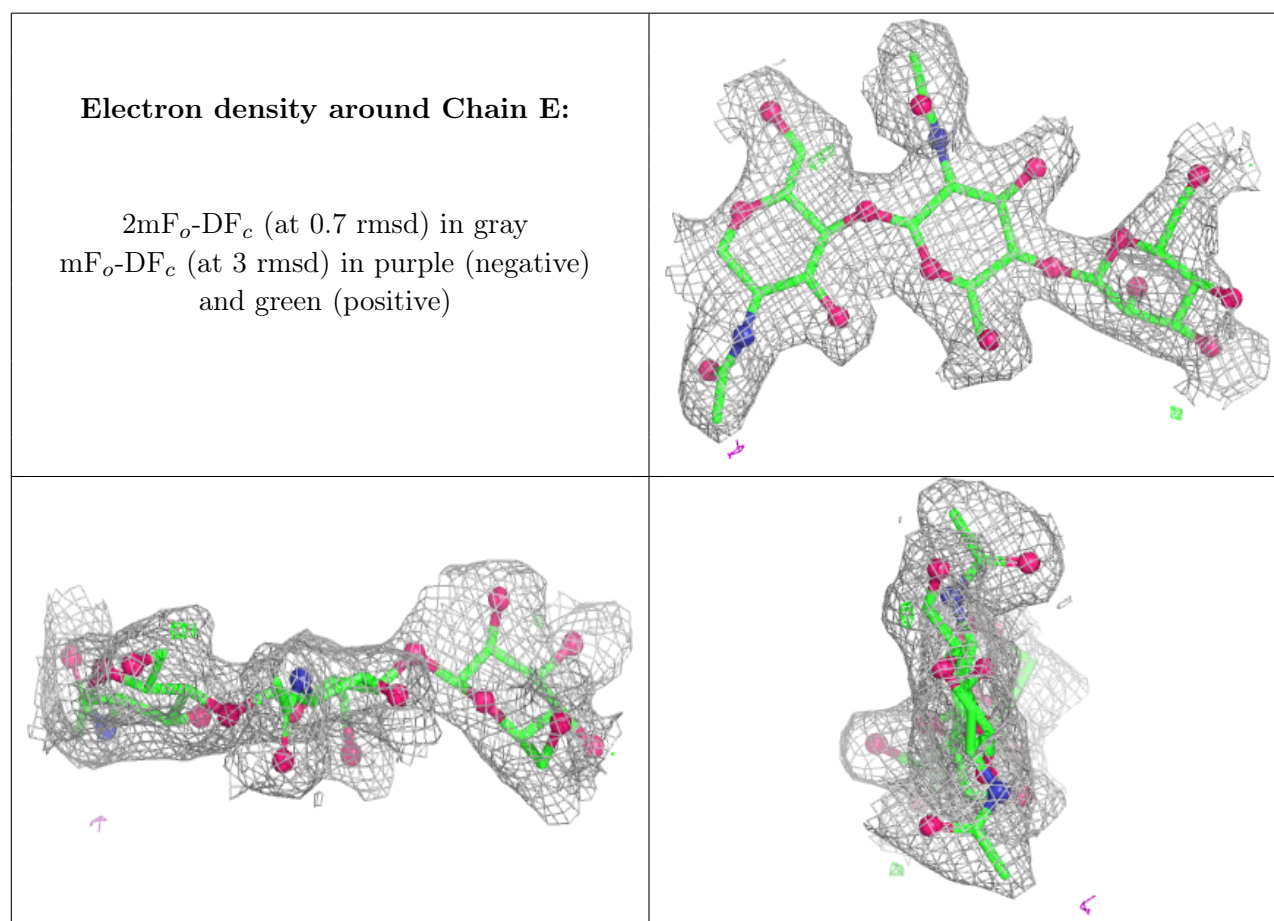
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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.

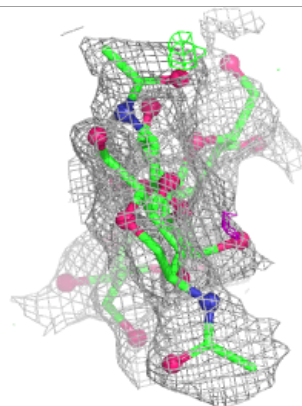
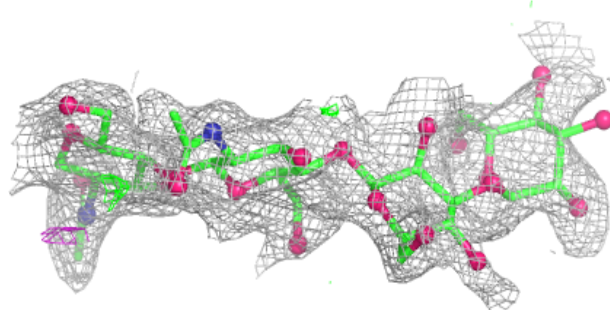
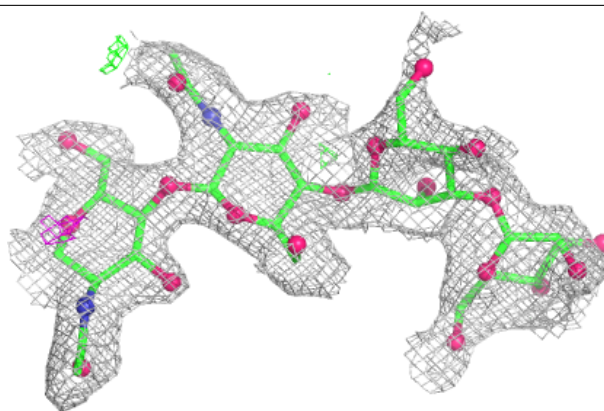
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MAN	F	4	11/12	0.64	0.17	46,48,50,50	0
3	MAN	G	4	11/12	0.64	0.17	41,42,44,44	0
2	MAN	E	3	11/12	0.72	0.14	37,40,41,43	0
3	MAN	F	3	11/12	0.77	0.13	43,45,47,50	0
4	NAG	H	2	14/15	0.79	0.12	24,30,34,35	0
3	MAN	G	3	11/12	0.81	0.13	37,40,42,43	0
3	NAG	F	2	14/15	0.84	0.11	27,35,38,41	0
2	NAG	E	1	14/15	0.84	0.10	22,26,27,29	0
2	NAG	E	2	14/15	0.86	0.10	26,30,35,35	0
3	NAG	F	1	14/15	0.90	0.09	24,29,31,31	0
3	NAG	G	2	14/15	0.91	0.08	25,30,34,34	0
4	NAG	H	1	14/15	0.91	0.08	22,26,29,30	0
3	NAG	G	1	14/15	0.91	0.08	23,26,32,33	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.

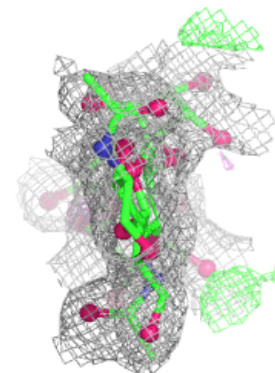
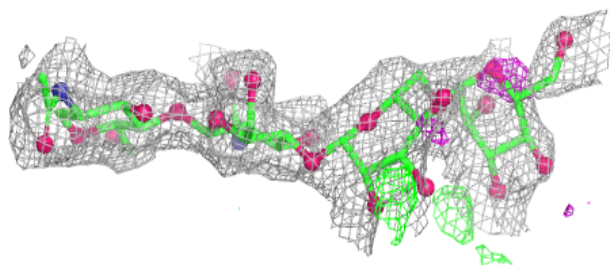
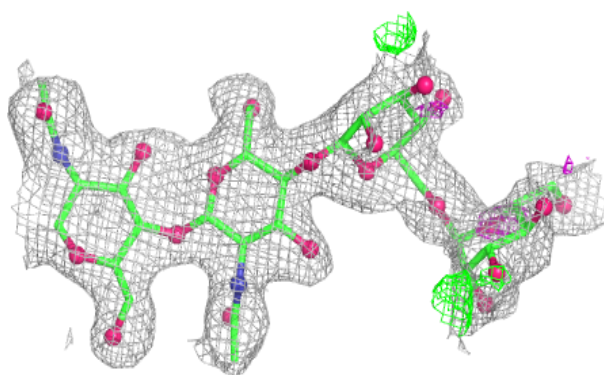


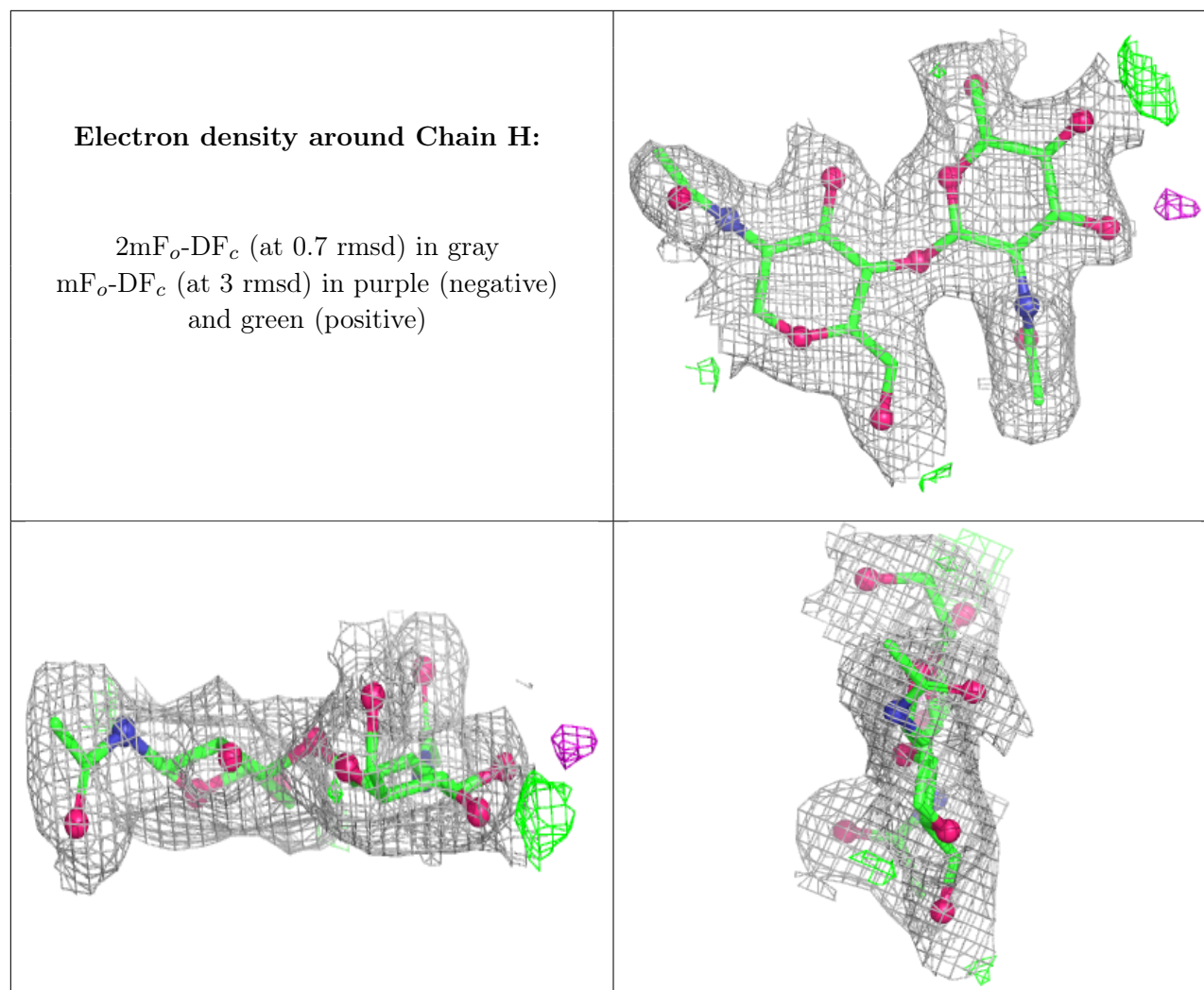
Electron density around Chain F:

$2mF_o-DF_c$ (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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	NAG	C	1358	14/15	0.65	0.20	36,43,45,46	0
5	KOJ	D	1351	10/10	0.69	0.23	25,28,32,34	0
7	NAG	B	1356	14/15	0.71	0.14	29,35,40,41	0
7	NAG	A	1358	14/15	0.72	0.16	31,37,40,40	0
7	NAG	A	1357	14/15	0.75	0.13	30,34,37,38	0
7	NAG	B	1357	14/15	0.78	0.13	33,39,41,41	0
7	NAG	D	1356	14/15	0.78	0.12	30,34,41,42	0
5	KOJ	C	1351	10/10	0.81	0.12	30,30,32,32	0
7	NAG	D	1353	14/15	0.82	0.11	31,36,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	NAG	A	1356	14/15	0.82	0.11	25,31,37,38	0
7	NAG	C	1357	14/15	0.84	0.09	31,35,41,41	0
7	NAG	C	1354	14/15	0.84	0.11	30,35,40,40	0
7	NAG	B	1353	14/15	0.87	0.09	25,29,32,34	0
5	KOJ	A	1351	10/10	0.89	0.10	21,24,26,27	0
7	NAG	A	1353	14/15	0.90	0.08	24,27,30,34	0
5	KOJ	B	1351	10/10	0.91	0.12	29,30,31,32	0
6	CU	D	1352	1/1	0.91	0.28	12,12,12,12	0
6	CU	B	1352	1/1	0.99	0.02	14,14,14,14	0
6	CU	A	1352	1/1	0.99	0.04	12,12,12,12	0
6	CU	C	1352	1/1	1.00	0.05	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.