



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 08:01 AM BST

PDB ID : 5GQE
Title : Crystal structure of michaelis complex of xylanase mutant (T82A, N127S, and E128H) from *Streptomyces olivaceoviridis* E-86
Authors : Suzuki, R.; Fujimoto, Z.; Kaneko, S.; Kuno, A.
Deposited on : 2016-08-07
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

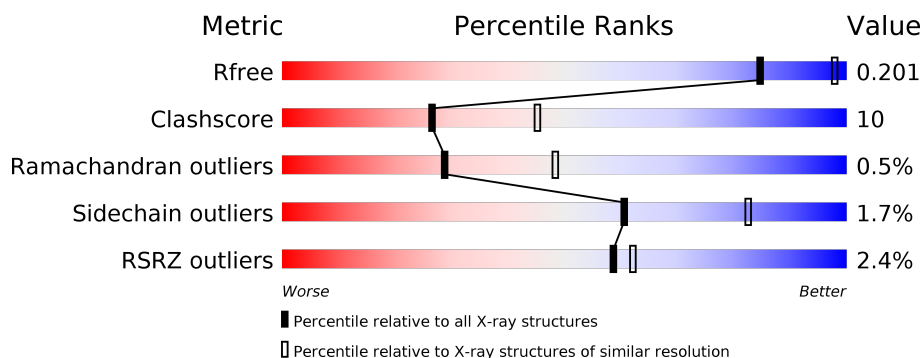
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 on 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	436	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> <div style="width: 78%; height: 10px; background-color: green;"></div> <div style="width: 20%; height: 10px; background-color: yellow;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; align-items: center;"> 78% 20% .. </div> </div>
1	B	436	<div> <div style="width: 4%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> <div style="width: 77%; height: 10px; background-color: green;"></div> <div style="width: 20%; height: 10px; background-color: yellow;"></div> <div style="width: 3%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; align-items: center;"> 77% 20% .. </div> </div>
2	C	5	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="width: 40%; height: 10px; background-color: green;"></div> <div style="width: 60%; height: 10px; background-color: yellow;"></div> </div> <div style="display: flex; justify-content: space-between; align-items: center;"> 40% 60% </div>
2	F	5	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="width: 20%; height: 10px; background-color: green;"></div> <div style="width: 80%; height: 10px; background-color: yellow;"></div> </div> <div style="display: flex; justify-content: space-between; align-items: center;"> 20% 80% </div>
3	D	4	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="width: 50%; height: 10px; background-color: green;"></div> <div style="width: 50%; height: 10px; background-color: yellow;"></div> </div> <div style="display: flex; justify-content: space-between; align-items: center;"> 50% 50% </div>
4	E	2	<div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="text-align: center;">100%</div>

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Mol	Chain	Length	Quality of chain
4	G	2	 50% 50%
5	H	3	 67% 33%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7400 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.

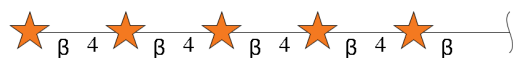
- Molecule 1 is a protein called Beta-xylanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	429	Total	C	N	O	S	0	0	0
			3239	1991	590	642	16			
1	B	429	Total	C	N	O	S	0	0	0
			3239	1991	590	642	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	ALA	THR	engineered mutation	UNP Q7SI98
A	127	SER	ASN	engineered mutation	UNP Q7SI98
A	128	HIS	GLU	engineered mutation	UNP Q7SI98
B	582	ALA	THR	engineered mutation	UNP Q7SI98
B	627	SER	ASN	engineered mutation	UNP Q7SI98
B	628	HIS	GLU	engineered mutation	UNP Q7SI98

- Molecule 2 is an oligosaccharide called beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	5	Total	C	O	0	0	0
			46	25	21			
2	F	5	Total	C	O	0	0	0
			46	25	21			

- Molecule 3 is an oligosaccharide called beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose.



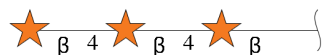
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	D	4	Total	C	O	0	0	0
			37	20	17			

- Molecule 4 is an oligosaccharide called beta-D-xylopyranose-(1-4)-beta-D-xylopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	E	2	Total	C	O	0	0	0
			19	10	9			
4	G	2	Total	C	O	0	0	0
			19	10	9			

- Molecule 5 is an oligosaccharide called beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
5	H	3	Total	C	O	0	0	0
			28	15	13			

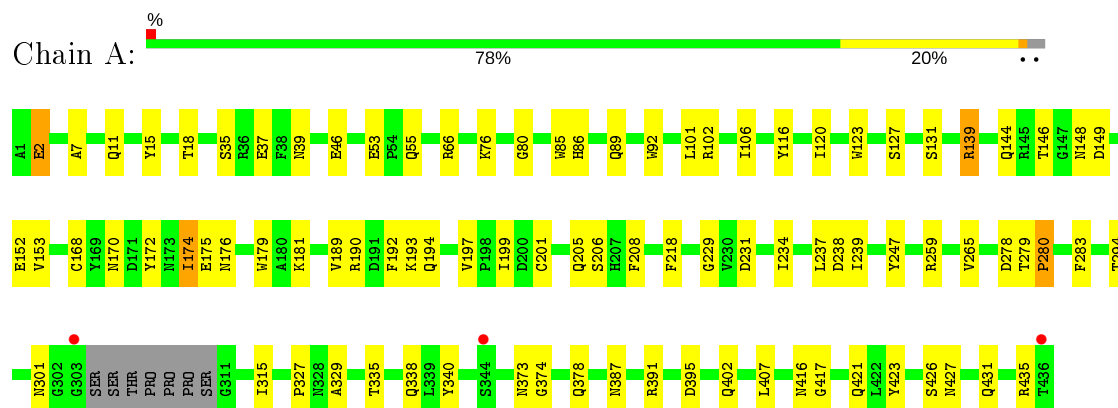
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	342	Total	O	0	0
			342	342		
6	B	385	Total	O	0	0
			385	385		

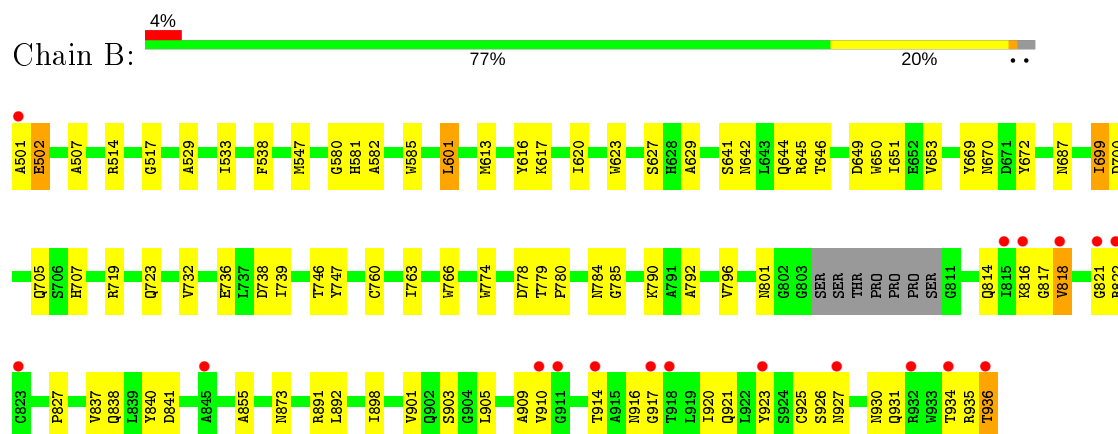
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

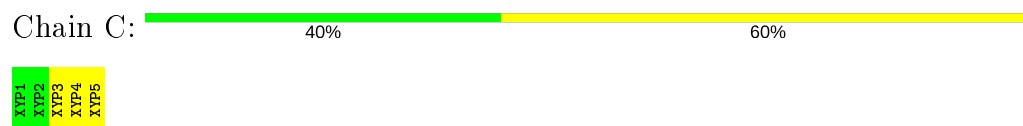
• Molecule 1: Beta-xylanase



• Molecule 1: Beta-xylanase



• Molecule 2: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose



• Molecule 2: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

Chain F:  20% 80%



- Molecule 3: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

Chain D:  50% 50%



- Molecule 4: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

Chain E:  100%



- Molecule 4: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

Chain G:  50% 50%



- Molecule 5: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

Chain H:  67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.13Å 94.01Å 137.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.16 – 2.50 39.16 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.2 (39.16-2.50) 96.3 (39.16-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.23 (at 2.51Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.179 , 0.249 0.198 , 0.201	Depositor DCC
R_{free} test set	1671 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7400	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.32	0/3304	0.61	0/4480
1	B	0.32	0/3304	0.60	0/4480
All	All	0.32	0/6608	0.60	0/8960

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	669	TYR	Sidechain

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	3239	0	3047	65	0
1	B	3239	0	3044	66	0
2	C	46	0	0	0	0
2	F	46	0	0	0	0
3	D	37	0	0	0	0
4	E	19	0	0	1	0
4	G	19	0	0	0	0
5	H	28	0	0	0	0
6	A	342	0	0	4	0
6	B	385	0	0	2	0
All	All	7400	0	6091	132	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (132) 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:616:TYR:HB3	1:B:620:ILE:HD13	1.58	0.83
1:B:892:LEU:HD22	1:B:898:ILE:HD12	1.61	0.82
1:B:910:VAL:HA	1:B:921:GLN:HE21	1.48	0.79
1:B:816:LYS:HE2	1:B:934:THR:HG22	1.71	0.72
1:B:719:ARG:O	1:B:723:GLN:HG3	1.89	0.72
1:A:174:ILE:H	1:A:174:ILE:HD13	1.58	0.69
1:B:910:VAL:HA	1:B:921:GLN:NE2	2.07	0.68
1:B:501:ALA:N	1:B:507:ALA:HB1	2.10	0.66
1:B:502:GLU:HG3	1:B:801:ASN:OD1	1.95	0.66
1:A:86:HIS:HA	1:A:89:GLN:HE21	1.61	0.65
1:B:838:GLN:OE1	1:B:917:GLY:HA2	1.96	0.65
1:B:814:GLN:HB2	1:B:936:THR:HG23	1.79	0.65
4:E:1:XYP:C5	4:E:2:XYP:O2	2.46	0.64
1:A:149:ASP:O	1:A:153:VAL:HG23	1.98	0.64
1:B:816:LYS:HD2	1:B:817:GLY:N	2.13	0.63
1:B:925:CYS:HA	1:B:931:GLN:OE1	1.99	0.62
1:A:176:ASN:HB3	1:A:179:TRP:CD2	2.35	0.62
1:A:11:GLN:HE22	1:A:301:ASN:HA	1.64	0.61
1:A:373:ASN:OD1	1:A:423:TYR:HA	2.00	0.61
1:B:627:SER:HA	1:B:670:ASN:O	2.01	0.61
1:B:909:ALA:HB3	1:B:930:ASN:HB2	1.82	0.61
1:B:514:ARG:HG3	1:B:514:ARG:HH11	1.66	0.60
1:B:816:LYS:HD3	1:B:821:GLY:HA2	1.83	0.60
1:A:192:PHE:HB3	1:A:197:VAL:HB	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:GLN:HE22	1:A:148:ASN:HA	1.68	0.58
1:B:649:ASP:O	1:B:653:VAL:HG23	2.04	0.58
1:A:238:ASP:HB2	1:A:280:PRO:HB2	1.86	0.57
1:B:855:ALA:HA	6:B:1144:HOH:O	2.05	0.57
1:B:873:ASN:OD1	1:B:923:TYR:HA	2.06	0.55
1:A:190:ARG:O	1:A:194:GLN:HG3	2.06	0.55
1:B:840:TYR:CE1	1:B:916:ASN:HB3	2.41	0.55
1:B:672:TYR:HB3	1:B:705:GLN:NE2	2.21	0.55
1:A:66:ARG:HH11	1:A:66:ARG:HG2	1.72	0.54
1:B:779:THR:N	1:B:780:PRO:HD3	2.23	0.53
1:B:792:ALA:O	1:B:796:VAL:HG23	2.07	0.53
1:B:601:LEU:HD11	1:B:642:ASN:ND2	2.23	0.53
1:A:229:GLY:HA2	1:A:259:ARG:HH21	1.74	0.52
1:A:101:LEU:HD23	1:A:146:THR:CG2	2.39	0.52
1:A:106:ILE:HD11	1:A:153:VAL:CG1	2.40	0.52
1:B:580:GLY:HA3	1:B:623:TRP:CE3	2.45	0.52
1:B:732:VAL:O	1:B:760:CYS:HA	2.10	0.52
1:B:816:LYS:HE2	1:B:934:THR:CG2	2.40	0.51
1:A:340:TYR:HA	1:A:416:ASN:OD1	2.09	0.51
1:A:37:GLU:HG3	1:A:283:PHE:CZ	2.46	0.51
1:B:816:LYS:HE3	1:B:818:VAL:HA	1.91	0.51
1:B:903:SER:HB2	1:B:905:LEU:HD13	1.93	0.51
1:A:86:HIS:HA	1:A:89:GLN:NE2	2.25	0.51
1:B:822:ARG:NH1	1:B:841:ASP:OD1	2.43	0.50
1:B:827:PRO:HG3	1:B:838:GLN:NE2	2.27	0.50
1:A:80:GLY:HA3	1:A:123:TRP:CE3	2.46	0.50
1:B:739:ILE:HD13	1:B:746:THR:HG22	1.94	0.50
1:B:763:ILE:HD12	1:B:763:ILE:N	2.26	0.50
1:A:278:ASP:O	1:A:279:THR:C	2.51	0.49
1:A:46:GLU:CD	1:A:46:GLU:H	2.15	0.49
1:A:37:GLU:HG3	1:A:283:PHE:HZ	1.77	0.49
1:B:529:ALA:O	1:B:533:ILE:HG12	2.12	0.49
1:A:102:ARG:O	1:A:106:ILE:HG12	2.13	0.49
1:A:2:GLU:HB3	1:A:11:GLN:OE1	2.12	0.49
1:B:926:SER:O	1:B:927:ASN:HB2	2.13	0.48
1:B:892:LEU:CD2	1:B:898:ILE:HD12	2.39	0.48
1:A:426:SER:O	1:A:427:ASN:HB2	2.12	0.48
1:A:106:ILE:HD11	1:A:153:VAL:HG12	1.94	0.48
1:A:234:ILE:N	1:A:234:ILE:HD12	2.29	0.48
1:B:837:VAL:HG23	1:B:920:ILE:CG1	2.44	0.48
1:A:395:ASP:HB3	6:A:689:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:GLY:HA3	1:A:123:TRP:CZ3	2.49	0.48
1:A:101:LEU:HD23	1:A:146:THR:HG21	1.96	0.47
1:A:294:THR:OG1	1:A:391:ARG:HD2	2.15	0.47
1:A:15:TYR:CD1	1:A:15:TYR:C	2.88	0.47
1:B:514:ARG:HG3	1:B:514:ARG:NH1	2.28	0.47
1:B:517:GLY:HA2	1:B:538:PHE:HB3	1.96	0.47
1:A:175:GLU:HB3	1:A:218:PHE:CD1	2.49	0.47
1:A:174:ILE:HG22	1:A:181:LYS:HG2	1.96	0.47
1:B:784:ASN:HD22	1:B:790:LYS:HG2	1.81	0.46
1:B:827:PRO:HA	1:B:838:GLN:HE21	1.79	0.46
1:B:736:GLU:HG2	1:B:766:TRP:CZ3	2.51	0.46
1:A:338:GLN:OE1	1:A:417:GLY:HA2	2.16	0.46
1:A:116:TYR:HB3	1:A:120:ILE:HG12	1.97	0.45
1:B:822:ARG:NE	1:B:914:THR:O	2.47	0.45
1:B:644:GLN:HA	1:B:650:TRP:CD1	2.51	0.45
1:A:127:SER:HA	1:A:170:ASN:O	2.17	0.45
1:B:738:ASP:HB2	1:B:780:PRO:HB2	1.99	0.45
1:B:613:MET:O	1:B:617:LYS:N	2.50	0.45
1:A:152:GLU:HG3	1:A:197:VAL:HG22	1.99	0.45
1:A:131:SER:HB2	1:A:139:ARG:HA	1.99	0.45
1:B:778:ASP:C	1:B:780:PRO:HD3	2.38	0.44
1:A:234:ILE:CG2	1:A:237:LEU:HB2	2.47	0.44
1:A:174:ILE:N	1:A:174:ILE:HD13	2.26	0.44
1:B:581:HIS:HA	1:B:582:ALA:HA	1.87	0.44
1:B:641:SER:O	1:B:645:ARG:HG3	2.17	0.44
1:B:629:ALA:HB1	1:B:651:ILE:HD11	1.99	0.44
1:A:374:GLY:HA2	1:A:421:GLN:OE1	2.17	0.43
1:A:39:ASN:HA	1:A:76:LYS:HG3	2.00	0.43
1:A:53:GLU:HG2	1:A:92:TRP:HZ2	1.83	0.43
1:B:774:TRP:H	1:B:774:TRP:HD1	1.65	0.43
1:A:35:SER:HA	1:A:76:LYS:CE	2.49	0.43
1:A:329:ALA:HB1	6:A:617:HOH:O	2.18	0.43
1:A:335:THR:O	1:A:378:GLN:HB2	2.18	0.43
1:A:231:ASP:OD1	1:A:259:ARG:HD2	2.19	0.43
1:B:705:GLN:HE21	1:B:707:HIS:HD2	1.66	0.42
1:A:239:ILE:O	1:A:280:PRO:HA	2.18	0.42
1:B:778:ASP:O	1:B:779:THR:C	2.57	0.42
1:A:172:TYR:HB3	1:A:205:GLN:NE2	2.35	0.42
1:B:502:GLU:HG2	1:B:502:GLU:O	2.20	0.42
1:A:199:ILE:O	1:A:199:ILE:HG23	2.19	0.42
1:B:642:ASN:HA	1:B:645:ARG:NH1	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:ILE:HD13	1:A:435:ARG:HB3	2.01	0.42
1:B:779:THR:N	1:B:780:PRO:CD	2.83	0.42
1:A:2:GLU:HB2	1:A:301:ASN:OD1	2.20	0.42
1:B:642:ASN:HA	1:B:645:ARG:HH11	1.85	0.42
1:A:435:ARG:NH1	6:A:621:HOH:O	2.53	0.41
1:B:935:ARG:HH11	1:B:935:ARG:HG3	1.85	0.41
1:A:327:PRO:HG3	1:A:338:GLN:HG2	2.02	0.41
1:A:189:VAL:O	1:A:193:LYS:HG2	2.20	0.41
1:A:168:CYS:HA	1:A:201:CYS:O	2.20	0.41
1:A:7:ALA:HB2	6:A:798:HOH:O	2.21	0.41
1:B:705:GLN:HE21	1:B:707:HIS:CD2	2.38	0.41
1:B:699:ILE:HD13	1:B:700:ASP:N	2.36	0.41
1:B:502:GLU:CG	1:B:801:ASN:OD1	2.66	0.41
1:A:206:SER:HB3	1:A:208:PHE:CE2	2.56	0.41
1:A:18:THR:HA	1:A:265:VAL:O	2.21	0.41
1:B:687:ASN:ND2	6:B:1115:HOH:O	2.54	0.41
1:B:935:ARG:NH1	1:B:935:ARG:HG3	2.36	0.41
1:A:407:LEU:O	1:A:431:GLN:HG2	2.21	0.41
1:B:547:MET:CE	1:B:623:TRP:CH2	3.04	0.41
1:B:642:ASN:O	1:B:646:THR:HG23	2.21	0.40
1:B:891:ARG:HG3	1:B:901:VAL:HG22	2.03	0.40
1:A:174:ILE:CD1	1:A:174:ILE:N	2.84	0.40
1:A:279:THR:N	1:A:280:PRO:HD3	2.36	0.40
1:A:387:ASN:HB3	1:A:402:GLN:OE1	2.21	0.40
1:A:139:ARG:HG3	1:A:139:ARG:O	2.21	0.40
1:A:192:PHE:CB	1:A:197:VAL:HB	2.50	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	425/436 (98%)	406 (96%)	18 (4%)	1 (0%)	47	68
1	B	425/436 (98%)	399 (94%)	23 (5%)	3 (1%)	22	39
All	All	850/872 (98%)	805 (95%)	41 (5%)	4 (0%)	29	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	B	502	GLU
1	B	818	VAL
1	B	785	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	333/340 (98%)	327 (98%)	6 (2%)	59	81
1	B	333/340 (98%)	328 (98%)	5 (2%)	65	85
All	All	666/680 (98%)	655 (98%)	11 (2%)	60	82

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	85	TRP
1	A	139	ARG
1	A	174	ILE
1	A	247	TYR
1	A	280	PRO
1	B	585	TRP
1	B	601	LEU
1	B	699	ILE
1	B	747	TYR
1	B	936	THR

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

Mol	Chain	Res	Type
1	A	11	GLN
1	A	108	HIS
1	A	173	ASN
1	A	284	ASN
1	A	314	GLN
1	A	349	GLN
1	B	511	GLN
1	B	558	GLN
1	B	577	GLN
1	B	628	HIS
1	B	670	ASN
1	B	673	ASN
1	B	694	GLN
1	B	705	GLN
1	B	828	ASN
1	B	838	GLN
1	B	921	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

21 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	XYP	C	1	2	10,10,10	0.63	0	14,14,14	0.57	0
2	XYP	C	2	2	9,9,10	0.52	0	10,12,14	0.88	0
2	XYP	C	3	2	9,9,10	0.79	0	10,12,14	1.02	1 (10%)
2	XYP	C	4	2	9,9,10	0.64	0	10,12,14	0.91	1 (10%)
2	XYP	C	5	2	9,9,10	0.68	0	10,12,14	0.89	1 (10%)
3	XYP	D	1	3	10,10,10	0.67	0	14,14,14	0.59	0
3	XYP	D	2	3	9,9,10	0.64	0	10,12,14	0.84	1 (10%)
3	XYP	D	3	3	9,9,10	0.66	0	10,12,14	0.83	0
3	XYP	D	4	3	9,9,10	0.69	0	10,12,14	0.85	1 (10%)
4	XYP	E	1	4	10,10,10	0.58	0	14,14,14	0.83	0
4	XYP	E	2	4	9,9,10	0.68	0	10,12,14	0.81	0
2	XYP	F	1	2	10,10,10	0.55	0	14,14,14	0.59	0
2	XYP	F	2	2	9,9,10	0.66	0	10,12,14	0.99	1 (10%)
2	XYP	F	3	2	9,9,10	0.87	0	10,12,14	1.08	1 (10%)
2	XYP	F	4	2	9,9,10	1.76	3 (33%)	10,12,14	1.81	3 (30%)
2	XYP	F	5	2	9,9,10	0.79	0	10,12,14	0.81	1 (10%)
4	XYP	G	1	4	10,10,10	0.63	0	14,14,14	0.57	0
4	XYP	G	2	4	9,9,10	0.67	0	10,12,14	0.88	1 (10%)
5	XYP	H	1	5	10,10,10	0.63	0	14,14,14	0.58	0
5	XYP	H	2	5	9,9,10	0.68	0	10,12,14	0.78	0
5	XYP	H	3	5	9,9,10	0.71	0	10,12,14	0.87	1 (10%)

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	XYP	C	1	2	-	-	0/1/1/1
2	XYP	C	2	2	-	-	0/1/1/1
2	XYP	C	3	2	-	-	0/1/1/1
2	XYP	C	4	2	-	-	0/1/1/1
2	XYP	C	5	2	-	-	0/1/1/1
3	XYP	D	1	3	-	-	0/1/1/1
3	XYP	D	2	3	-	-	0/1/1/1
3	XYP	D	3	3	-	-	0/1/1/1
3	XYP	D	4	3	-	-	0/1/1/1
4	XYP	E	1	4	-	-	0/1/1/1
4	XYP	E	2	4	-	-	0/1/1/1
2	XYP	F	1	2	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	XYP	F	2	2	-	-	0/1/1/1
2	XYP	F	3	2	-	-	0/1/1/1
2	XYP	F	4	2	-	-	1/1/1/1
2	XYP	F	5	2	-	-	0/1/1/1
4	XYP	G	1	4	-	-	0/1/1/1
4	XYP	G	2	4	-	-	0/1/1/1
5	XYP	H	1	5	-	-	0/1/1/1
5	XYP	H	2	5	-	-	0/1/1/1
5	XYP	H	3	5	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	4	XYP	C2-C3	3.11	1.57	1.52
2	F	4	XYP	O5-C5	2.59	1.47	1.42
2	F	4	XYP	C5-C4	2.09	1.57	1.52

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	4	XYP	C5-C4-C3	-3.97	104.78	109.67
2	F	4	XYP	C4-C3-C2	-3.26	107.05	110.92
2	C	4	XYP	C4-C3-C2	-2.58	107.86	110.92
4	G	2	XYP	C4-C3-C2	-2.37	108.10	110.92
2	F	3	XYP	C4-C3-C2	-2.35	108.13	110.92
5	H	3	XYP	C4-C3-C2	-2.35	108.13	110.92
2	C	5	XYP	C4-C3-C2	-2.30	108.19	110.92
3	D	2	XYP	C4-C3-C2	-2.26	108.23	110.92
2	F	4	XYP	C1-C2-C3	2.18	112.34	109.67
3	D	4	XYP	C4-C3-C2	-2.16	108.36	110.92
2	C	3	XYP	C4-C3-C2	-2.12	108.41	110.92
2	F	5	XYP	C4-C3-C2	-2.09	108.44	110.92
2	F	2	XYP	C4-C3-C2	-2.07	108.46	110.92

There are no chirality outliers.

There are no torsion outliers.

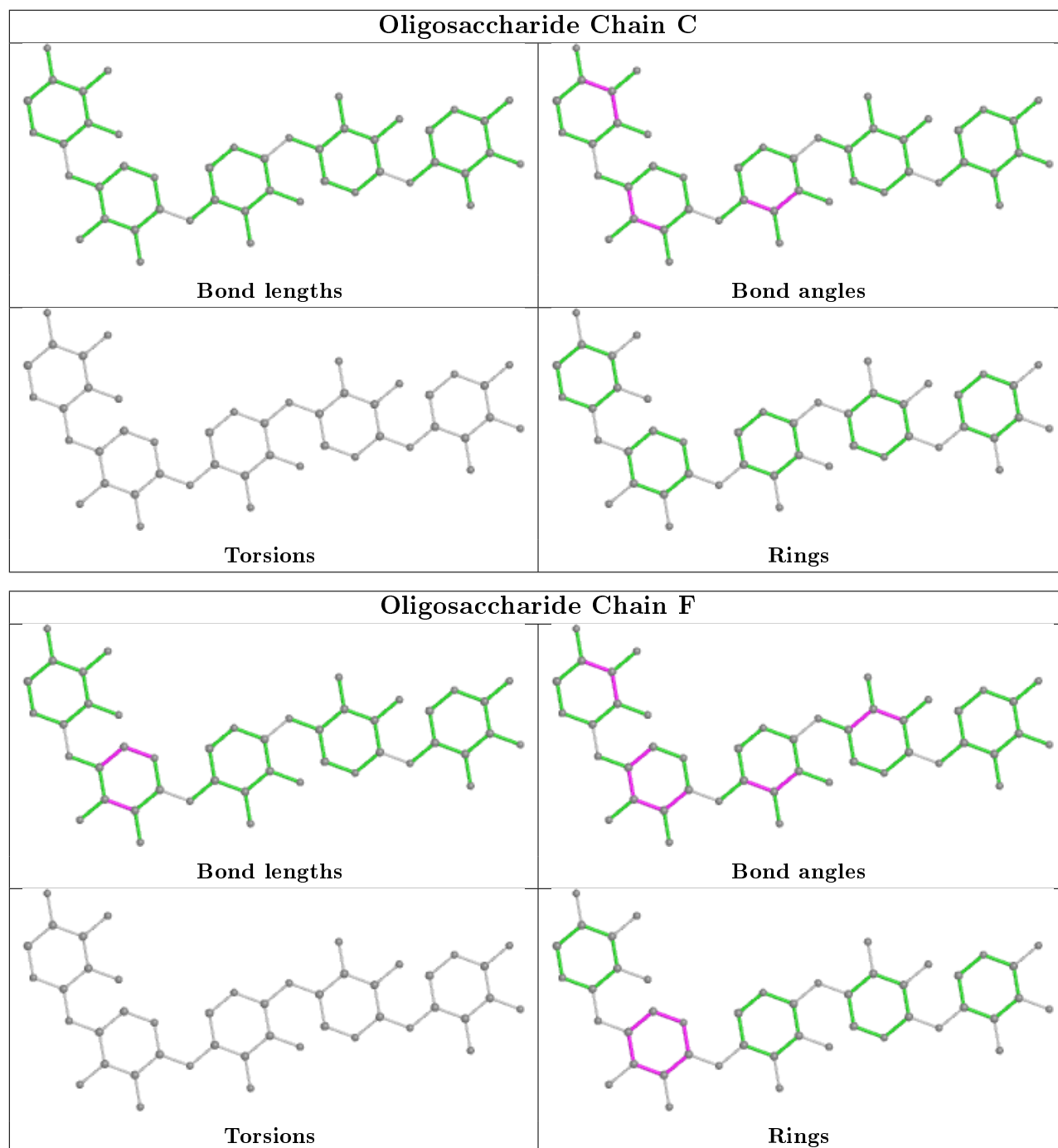
All (1) ring outliers are listed below:

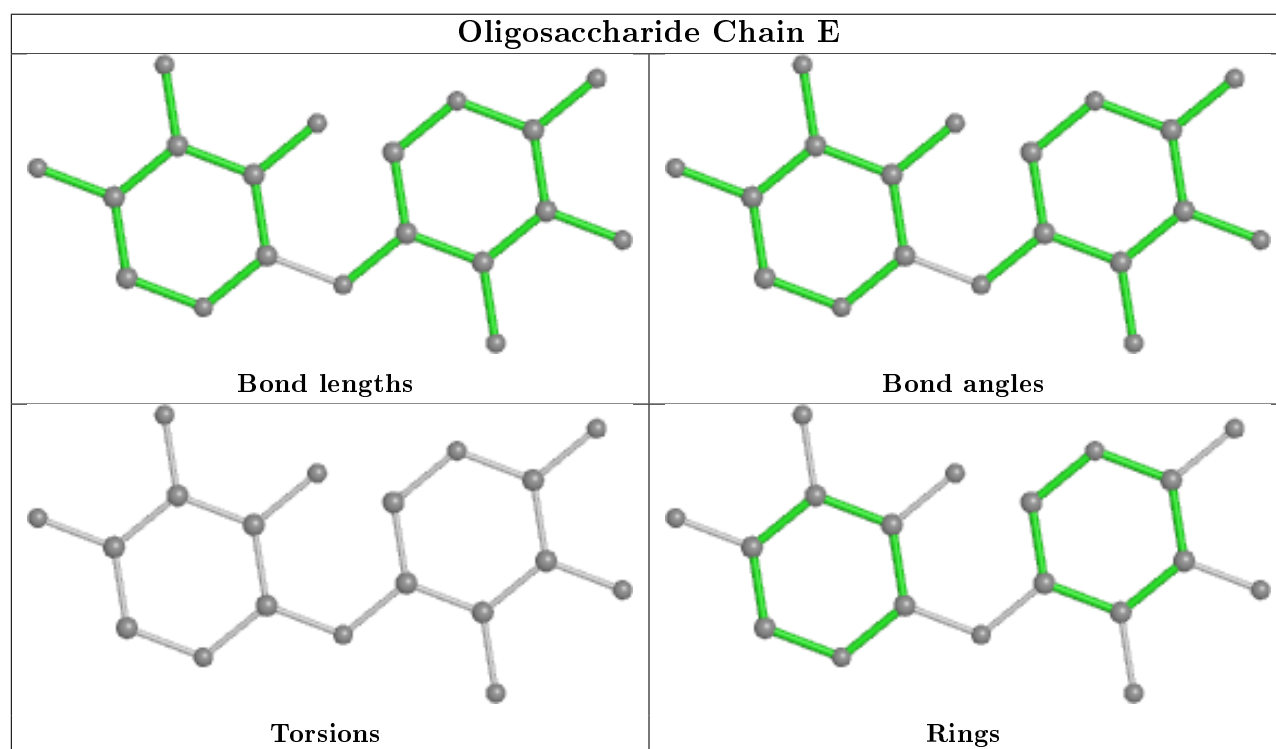
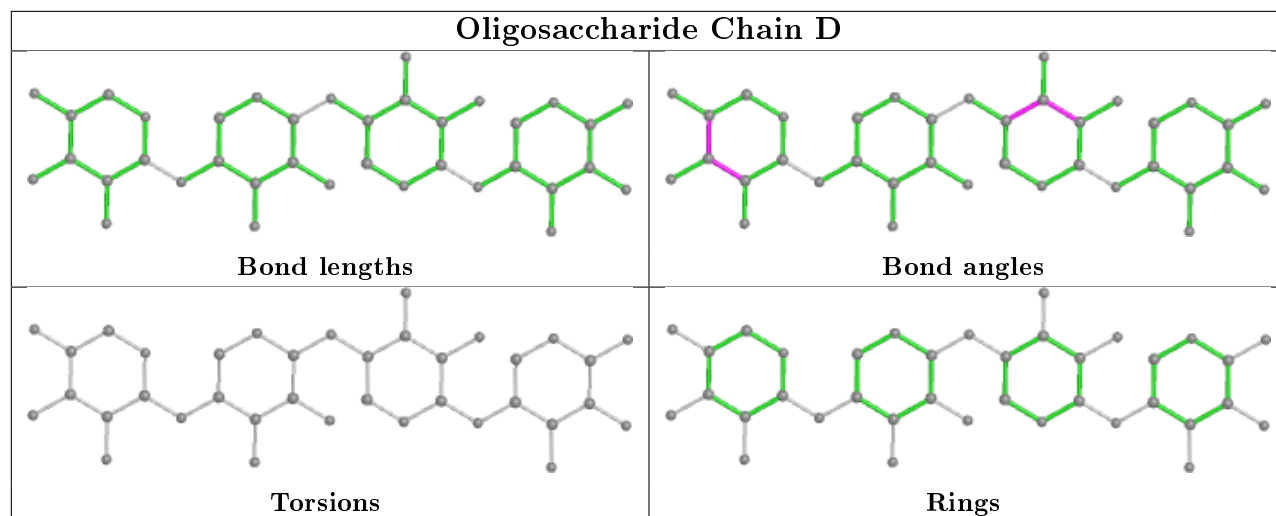
Mol	Chain	Res	Type	Atoms
2	F	4	XYP	C1-C2-C3-C4-C5-O5

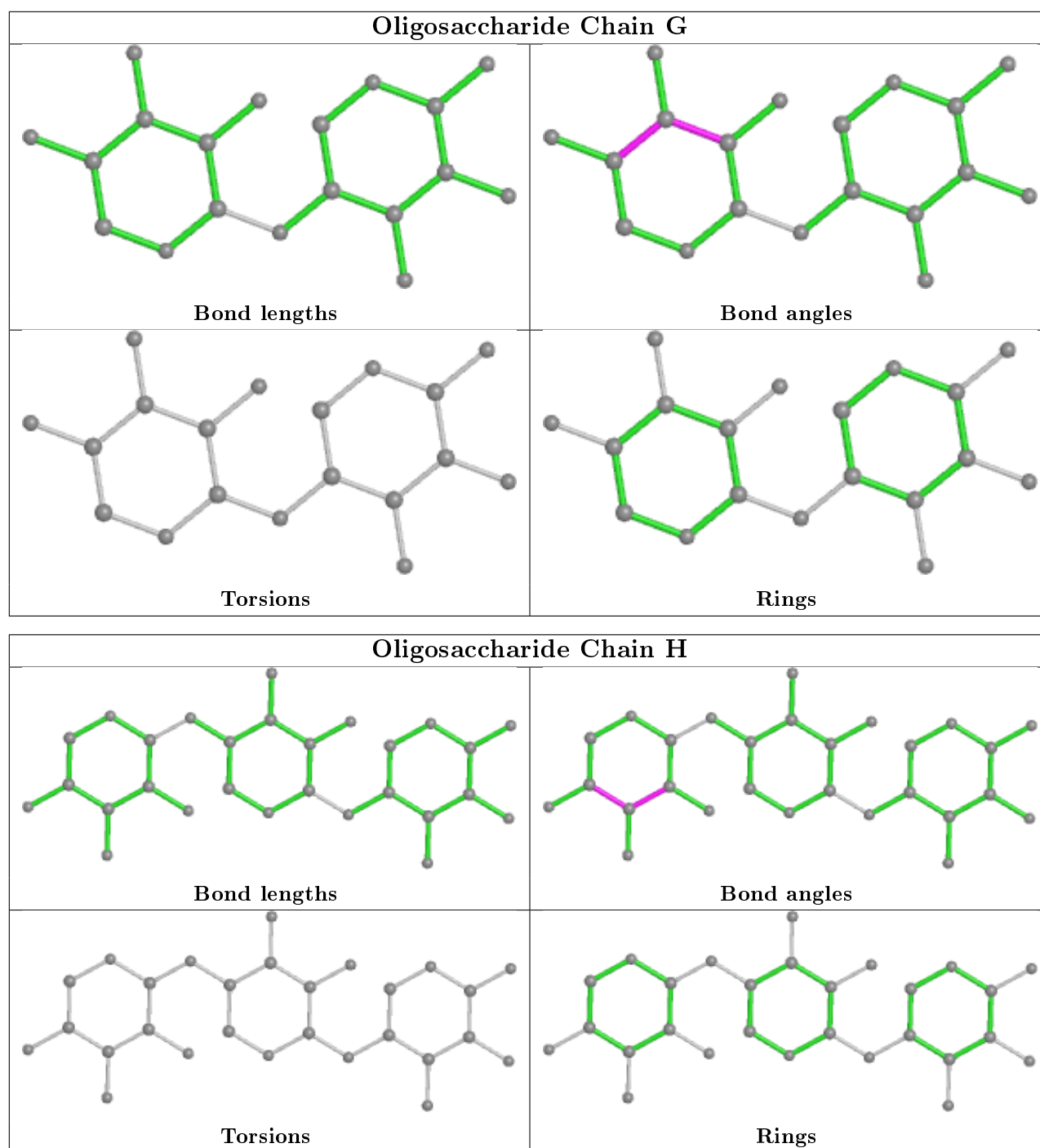
2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	2	XYP	1	0
4	E	1	XYP	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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

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	429/436 (98%)	-0.29	3 (0%) 87 89	14, 26, 44, 60	0
1	B	429/436 (98%)	-0.23	18 (4%) 36 39	15, 25, 62, 75	0
All	All	858/872 (98%)	-0.26	21 (2%) 59 62	14, 25, 53, 75	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	936	THR	5.4
1	B	818	VAL	4.2
1	B	845	ALA	3.6
1	A	303	GLY	3.4
1	B	917	GLY	3.3
1	B	911	GLY	3.3
1	B	816	LYS	3.2
1	B	822	ARG	3.1
1	B	815	ILE	2.6
1	A	436	THR	2.5
1	B	934	THR	2.5
1	B	914	THR	2.5
1	A	344	SER	2.4
1	B	821	GLY	2.4
1	B	823	CYS	2.4
1	B	910	VAL	2.3
1	B	923	TYR	2.3
1	B	927	ASN	2.3
1	B	932	ARG	2.2
1	B	918	THR	2.2
1	B	501	ALA	2.1

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 ⓘ

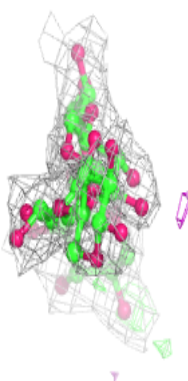
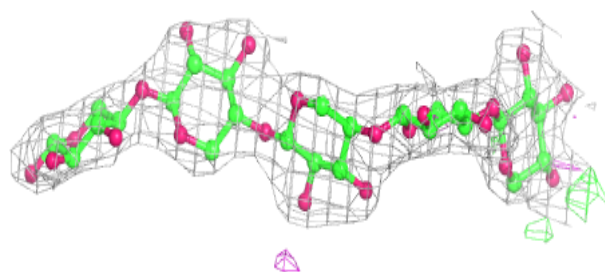
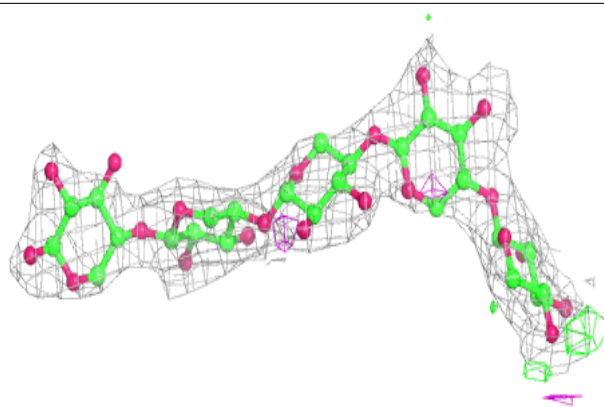
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	XYP	E	2	9/10	0.83	0.24	51,53,55,57	0
4	XYP	G	1	10/10	0.83	0.33	68,70,71,71	0
5	XYP	H	1	10/10	0.85	0.16	67,68,69,69	0
3	XYP	D	1	10/10	0.85	0.26	42,50,52,54	0
5	XYP	H	3	9/10	0.85	0.38	76,77,77,77	0
5	XYP	H	2	9/10	0.87	0.27	70,71,72,74	0
4	XYP	G	2	9/10	0.88	0.25	71,73,74,74	0
2	XYP	C	1	10/10	0.89	0.29	47,55,56,57	0
3	XYP	D	4	9/10	0.90	0.17	44,45,47,47	0
4	XYP	E	1	10/10	0.92	0.16	43,44,45,48	0
2	XYP	F	1	10/10	0.93	0.16	36,44,47,48	0
2	XYP	C	4	9/10	0.93	0.16	32,34,37,38	0
2	XYP	C	3	9/10	0.93	0.17	35,36,37,37	0
2	XYP	F	5	9/10	0.94	0.14	20,22,24,25	0
3	XYP	D	3	9/10	0.94	0.12	42,43,46,47	0
2	XYP	C	5	9/10	0.94	0.15	32,33,34,35	0
3	XYP	D	2	9/10	0.95	0.12	35,37,38,40	0
2	XYP	C	2	9/10	0.95	0.14	39,40,42,42	0
2	XYP	F	4	9/10	0.96	0.14	20,23,25,29	0
2	XYP	F	3	9/10	0.97	0.14	29,31,34,34	0
2	XYP	F	2	9/10	0.98	0.13	29,32,32,33	0

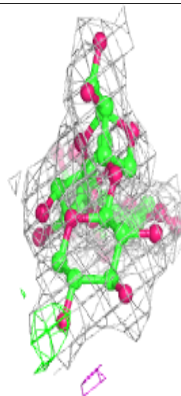
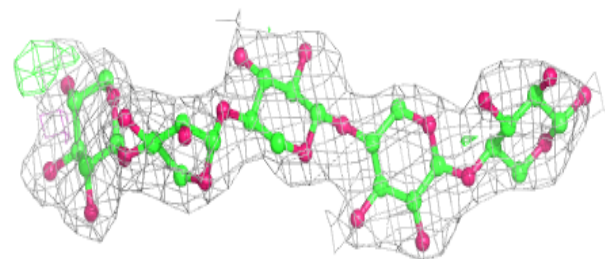
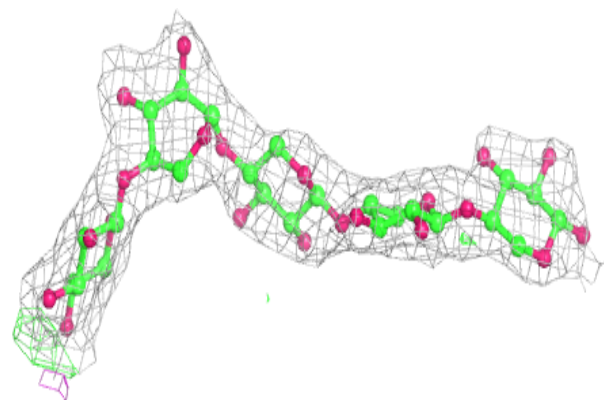
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

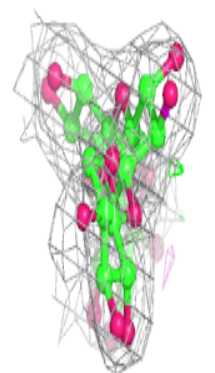
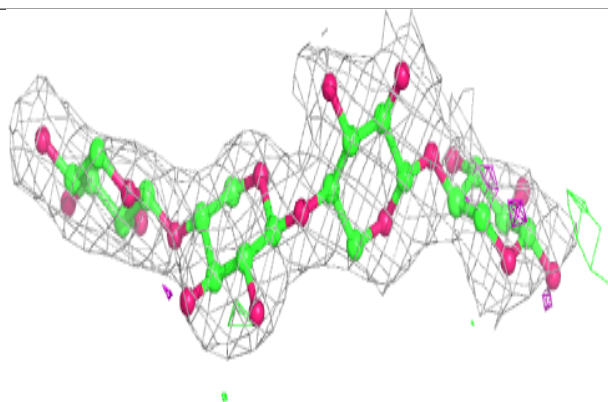
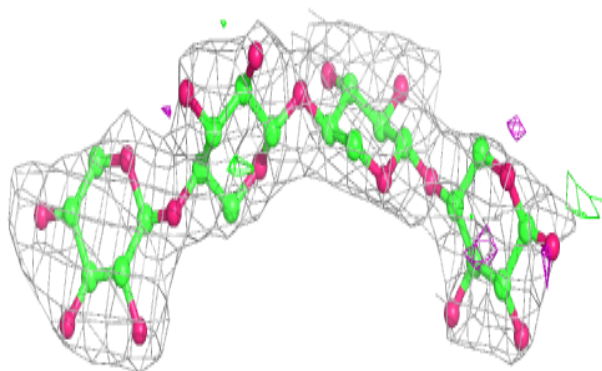
**Electron density around Chain F:**

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

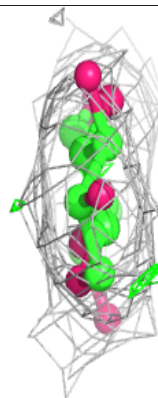
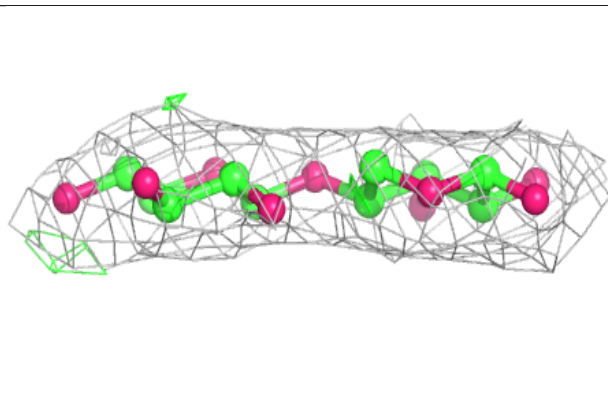
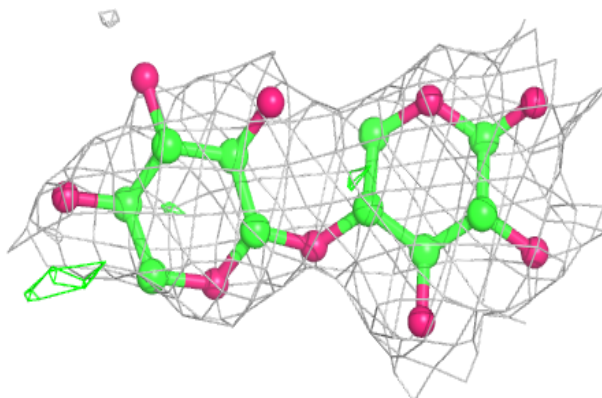


Electron density around Chain D:

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

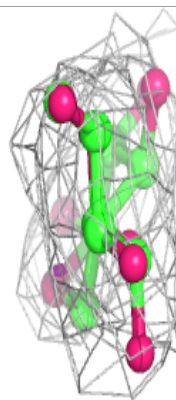
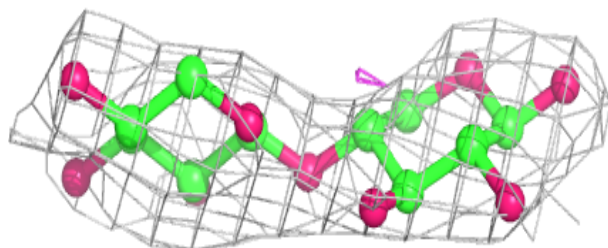
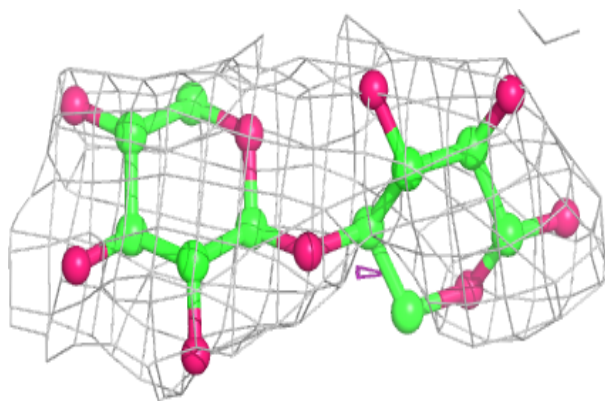
**Electron density around Chain E:**

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

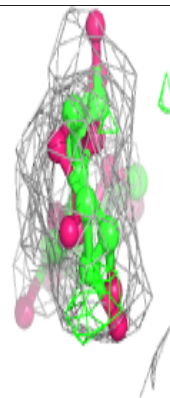
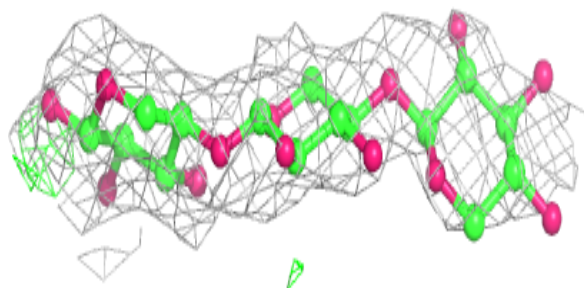
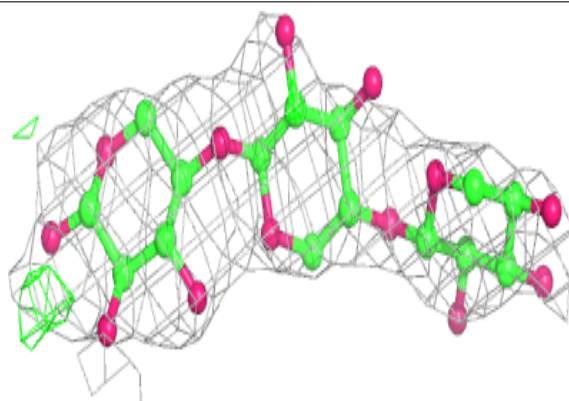


Electron density around Chain G:

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

**Electron density around Chain H:**

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



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.