



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 27, 2023 – 05:04 AM EDT

PDB ID : 3I02  
Title : Crystal structure of S54-10 antibody in complex with antigen Kdo(2.4)Kdo(2.4)Kdo  
Authors : Brooks, C.L.; Muller-Loennies, S.; Borisova, S.N.; Brade, L.; Kosma, P.; Hirama, T.; MacKenzie, C.R.; Brade, H.; Evans, S.V.  
Deposited on : 2009-06-24  
Resolution : 2.60 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](mailto: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>.

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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 : 2.35  
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) : 2.35

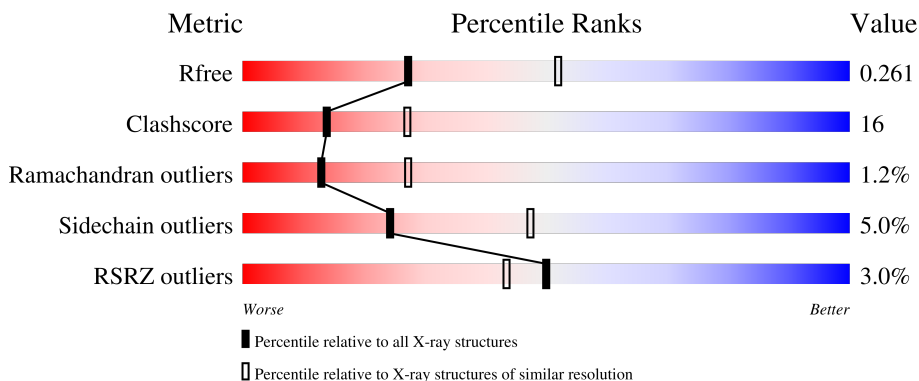
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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.



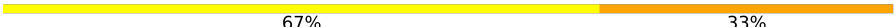
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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  $\geq 3$ , 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	219	
1	C	219	
2	B	224	
2	D	224	
3	E	3	

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Mol	Chain	Length	Quality of chain
3	F	3	 67% 33%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6864 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 Immunoglobulin light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	219	Total 1707	C 1060	N 293	O 346	S 8	0	0	0
1	C	196	Total 1504	C 936	N 256	O 305	S 7	0	0	0

- Molecule 2 is a protein called Immunoglobulin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	220	Total 1681	C 1064	N 280	O 327	S 10	0	0	0
2	D	212	Total 1617	C 1028	N 267	O 313	S 9	0	0	0

- Molecule 3 is an oligosaccharide called 3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid-(2-4)-3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid-(2-4)-prop-2-en-1-yl 3-deoxy-alpha-D-manno-oct-2-ulopyranosidonic acid.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
3	E	3	Total 49	C 27	O 22	0	0	0
3	F	3	Total 49	C 27	O 22	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	78	Total 78	O 78	0	0
4	B	74	Total 74	O 74	0	0
4	C	62	Total 62	O 62	0	0

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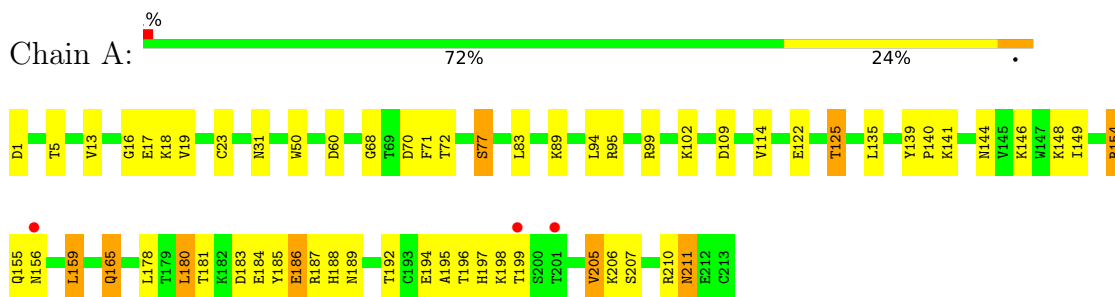
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	D	43	Total	O	0	0
			43	43		

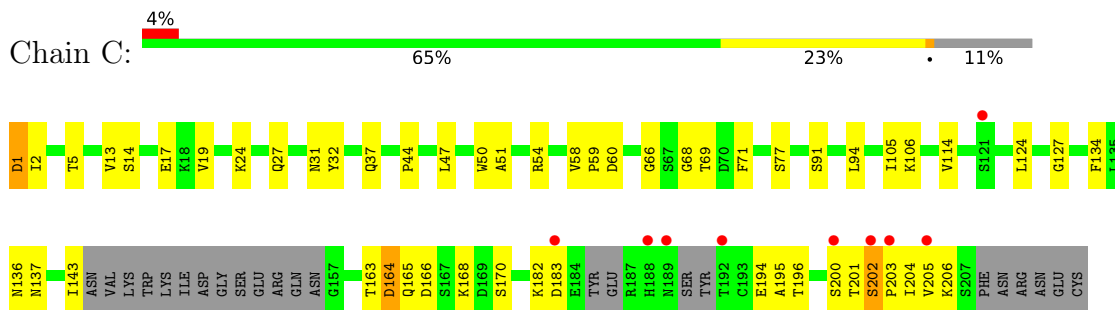
### 3 Residue-property plots

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.

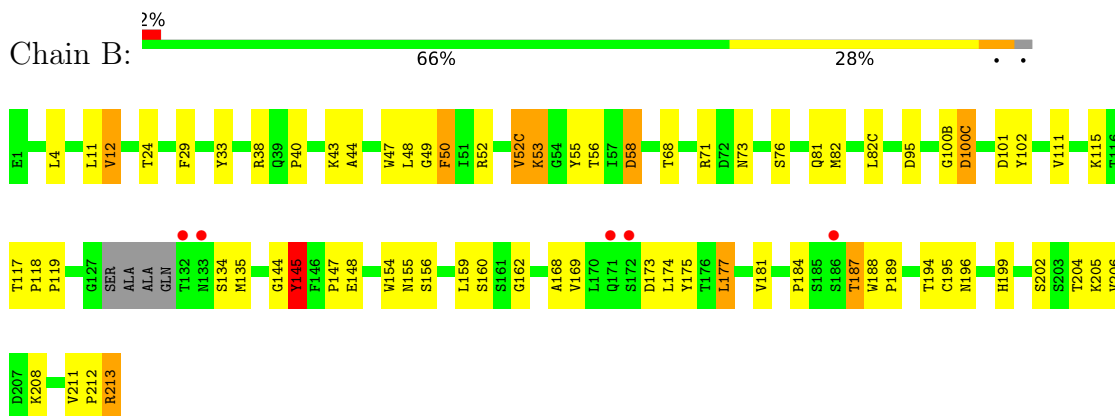
- Molecule 1: Immunoglobulin light chain



- Molecule 1: Immunoglobulin light chain

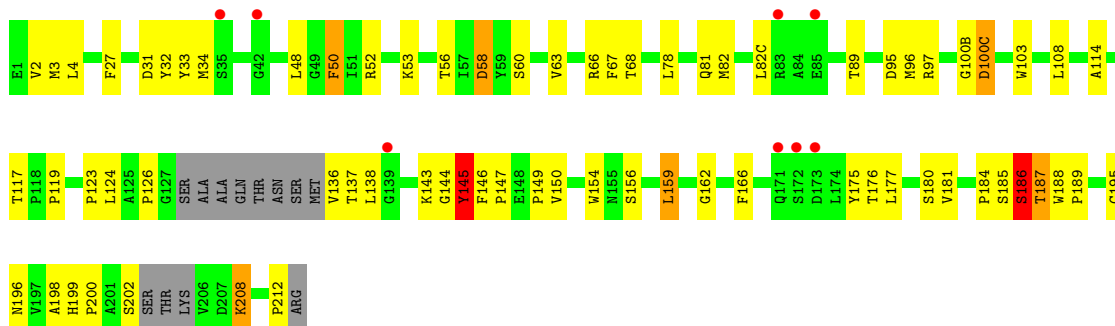


- Molecule 2: Immunoglobulin heavy chain



- Molecule 2: Immunoglobulin heavy chain





- Molecule 3: 3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid-(2-4)-3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid-(2-4)-prop-2-en-1-yl 3-deoxy-alpha-D-manno-oct-2-ulopyranosidonic acid

- Molecule 3: 3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid-(2-4)-3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid-(2-4)-prop-2-en-1-yl 3-deoxy-alpha-D-manno-oct-2-ulopyranosidonic acid

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.98Å 53.36Å 142.23Å 90.00° 102.13° 90.00°	Depositor
Resolution (Å)	19.99 – 2.60 19.99 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.2 (19.99-2.60) 97.3 (19.99-2.60)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.25 (at 2.59Å)	Xtrriage
Refinement program	PHENIX 1.4_4	Depositor
R, $R_{free}$	0.211 , 0.268 0.206 , 0.261	Depositor DCC
$R_{free}$ test set	1463 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.2	Xtrriage
Anisotropy	0.205	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 48.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6864	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.96% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: KDO, KDA

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	0.26	0/1742	0.46	0/2358
1	C	0.26	0/1531	0.47	0/2071
2	B	0.26	0/1723	0.50	0/2348
2	D	0.25	0/1658	0.48	0/2261
All	All	0.26	0/6654	0.48	0/9038

There are no bond length outliers.

There are no bond angle outliers.

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	1707	0	1659	51	0
1	C	1504	0	1475	32	0
2	B	1681	0	1645	65	0
2	D	1617	0	1575	63	0
3	E	49	0	39	2	0
3	F	49	0	39	1	0
4	A	78	0	0	5	0
4	B	74	0	0	1	0
4	C	62	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	43	0	0	1	0
All	All	6864	0	6432	206	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 16.

All (206) 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)
2:B:100(B):GLY:HA2	2:B:100(C):ASP:HB2	1.32	1.12
2:D:100(B):GLY:HA2	2:D:100(C):ASP:HB2	1.27	1.09
1:A:154:ARG:HG3	1:A:156:ASN:H	1.30	0.96
2:D:100(B):GLY:CA	2:D:100(C):ASP:HB2	1.97	0.94
2:B:156:SER:H	2:B:196:ASN:HD21	1.11	0.90
3:E:1:KDA:H10	3:E:1:KDA:O1A	1.72	0.90
1:C:202:SER:HB3	1:C:203:PRO:HA	1.57	0.85
2:B:71:ARG:HE	2:B:73:ASN:HD21	1.26	0.83
2:D:144:GLY:HA2	2:D:145:TYR:CB	2.08	0.83
2:D:156:SER:H	2:D:196:ASN:HD21	1.28	0.82
1:A:149:ILE:HD11	1:A:178:LEU:HD21	1.63	0.81
1:A:189:ASN:HD21	1:A:211:ASN:H	1.30	0.80
2:B:100(B):GLY:CA	2:B:100(C):ASP:HB2	2.12	0.79
2:B:100(B):GLY:HA2	2:B:100(C):ASP:CB	2.12	0.78
2:B:144:GLY:HA2	2:B:145:TYR:CB	2.13	0.77
2:B:33:TYR:HB2	2:B:95:ASP:HB3	1.68	0.75
2:D:34:MET:HB3	2:D:78:LEU:HD22	1.71	0.73
2:B:144:GLY:HA2	2:B:145:TYR:HB3	1.71	0.73
2:D:108:LEU:HD22	2:D:149:PRO:HD3	1.71	0.72
2:D:50:PHE:HE1	2:D:58:ASP:HB2	1.53	0.72
2:B:52(C):VAL:HG12	2:B:53:LYS:HD2	1.72	0.72
2:D:144:GLY:HA2	2:D:145:TYR:HB3	1.71	0.71
2:D:100(B):GLY:CA	2:D:100(C):ASP:CB	2.69	0.71
1:C:13:VAL:HG21	1:C:19:VAL:HG22	1.73	0.70
1:A:31:ASN:HD21	1:A:68:GLY:H	1.39	0.70
2:B:159:LEU:HD13	2:B:181:VAL:HG21	1.72	0.70
2:D:159:LEU:HD13	2:D:181:VAL:HG21	1.73	0.70
2:B:100(B):GLY:CA	2:B:100(C):ASP:CB	2.70	0.69
2:B:156:SER:H	2:B:196:ASN:ND2	1.87	0.69
1:C:54:ARG:NH2	1:C:60:ASP:HB2	2.06	0.69
2:B:71:ARG:NE	2:B:73:ASN:HD21	1.90	0.69
2:D:108:LEU:HD13	2:D:149:PRO:HG3	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:127:GLY:HA2	1:C:182:LYS:HE3	1.75	0.68
1:A:109:ASP:HB3	1:A:199:THR:HG22	1.75	0.67
1:C:1:ASP:CG	1:C:1:ASP:O	2.33	0.67
2:D:82:MET:HB3	2:D:82(C):LEU:HD21	1.76	0.67
2:B:33:TYR:CB	2:B:95:ASP:HB3	2.24	0.66
1:A:148:LYS:HE2	1:A:194:GLU:CD	2.16	0.66
1:C:194:GLU:HG2	1:C:205:VAL:HG22	1.77	0.66
2:D:123:PRO:HD3	2:D:208:LYS:HD3	1.78	0.65
1:A:135:LEU:HD21	1:A:195:ALA:HB2	1.79	0.65
1:A:192:THR:HA	1:A:207:SER:HB3	1.79	0.65
2:D:117:THR:O	2:D:145:TYR:HA	1.97	0.64
1:C:202:SER:CB	1:C:203:PRO:HA	2.27	0.64
2:D:144:GLY:HA2	2:D:145:TYR:CG	2.32	0.63
1:C:14:SER:HB2	1:C:17:GLU:OE1	1.99	0.63
2:D:144:GLY:HA2	2:D:145:TYR:CD1	2.34	0.62
2:D:33:TYR:HB2	2:D:95:ASP:HB3	1.82	0.62
2:B:155:ASN:ND2	2:B:194:THR:H	1.98	0.62
2:B:155:ASN:HD21	2:B:194:THR:H	1.48	0.62
1:A:139:TYR:O	1:A:197:HIS:HE1	1.83	0.61
2:B:71:ARG:HE	2:B:73:ASN:ND2	1.97	0.61
1:C:37:GLN:HB2	1:C:47:LEU:HD11	1.83	0.61
2:B:11:LEU:HB2	2:B:147:PRO:HG3	1.83	0.60
1:A:31:ASN:ND2	1:A:68:GLY:H	1.98	0.60
2:B:147:PRO:O	2:B:199:HIS:HE1	1.85	0.59
2:D:108:LEU:HD23	4:D:224:HOH:O	2.04	0.58
2:B:82:MET:HB3	2:B:82(C):LEU:HD21	1.86	0.58
2:D:33:TYR:CB	2:D:95:ASP:HB3	2.35	0.57
2:B:134:SER:O	2:B:135:MET:HE2	2.05	0.56
1:A:192:THR:HG23	1:A:205:VAL:HG23	1.88	0.56
2:B:117:THR:O	2:B:145:TYR:HA	2.05	0.56
2:B:33:TYR:CE2	2:B:52:ARG:HG2	2.40	0.56
2:D:156:SER:N	2:D:196:ASN:HD21	1.98	0.56
1:A:122:GLU:O	1:A:125:THR:HG22	2.05	0.55
1:A:189:ASN:ND2	1:A:211:ASN:H	2.01	0.55
2:D:199:HIS:HD2	2:D:202:SER:OG	1.89	0.54
1:A:146:LYS:NZ	1:A:146:LYS:HB2	2.23	0.54
2:B:144:GLY:CA	2:B:175:TYR:O	2.54	0.54
2:B:177:LEU:C	2:B:177:LEU:HD12	2.28	0.54
2:D:186:SER:O	2:D:188:TRP:N	2.41	0.54
2:B:199:HIS:HD2	2:B:202:SER:OG	1.90	0.54
2:B:50:PHE:HE1	2:B:58:ASP:HB2	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:29:PHE:CD2	2:B:76:SER:HA	2.43	0.53
2:D:50:PHE:CE1	2:D:58:ASP:HB2	2.41	0.53
1:A:1:ASP:O	1:A:1:ASP:CG	2.47	0.53
1:A:109:ASP:OD1	1:A:198:LYS:HE2	2.09	0.53
2:D:33:TYR:CE2	2:D:52:ARG:HG2	2.44	0.53
2:B:184:PRO:O	2:B:187:THR:HB	2.07	0.53
2:D:154:TRP:CZ3	2:D:195:CYS:HB3	2.44	0.53
1:A:13:VAL:HG21	1:A:19:VAL:HG22	1.91	0.53
2:B:144:GLY:CA	2:B:145:TYR:HB3	2.36	0.52
2:B:213:ARG:HB2	2:B:213:ARG:NH1	2.23	0.52
1:C:105:ILE:H	1:C:165:GLN:HE22	1.57	0.52
1:A:186:GLU:HG2	4:A:229:HOH:O	2.09	0.52
2:B:68:THR:HB	2:B:81:GLN:HB3	1.92	0.52
2:B:204:THR:O	2:B:205:LYS:HD2	2.10	0.51
2:D:66:ARG:C	2:D:67:PHE:HD1	2.14	0.51
2:B:4:LEU:HD23	2:B:24:THR:HG22	1.93	0.51
2:D:52:ARG:HD2	2:D:56:THR:OG1	2.11	0.50
1:A:99:ARG:HD2	2:B:44:ALA:HB3	1.93	0.50
1:A:102:LYS:HE2	4:A:272:HOH:O	2.10	0.50
1:A:180:LEU:HG	1:A:184:GLU:HG2	1.92	0.50
1:C:166:ASP:O	1:C:170:SER:HA	2.12	0.50
1:C:114:VAL:O	1:C:206:LYS:HE3	2.11	0.50
1:C:164:ASP:OD1	1:C:164:ASP:N	2.38	0.50
2:D:184:PRO:O	2:D:187:THR:HB	2.12	0.50
1:A:139:TYR:CG	1:A:140:PRO:HA	2.47	0.49
1:A:154:ARG:HD3	1:A:156:ASN:HB2	1.93	0.49
2:B:204:THR:HG22	2:B:206:VAL:HG23	1.93	0.49
2:B:40:PRO:HB2	2:B:43:LYS:HE3	1.94	0.49
2:D:177:LEU:C	2:D:177:LEU:HD12	2.33	0.49
1:C:66:GLY:HA3	1:C:71:PHE:HA	1.94	0.49
1:C:202:SER:HB3	1:C:203:PRO:CA	2.36	0.48
2:B:12:VAL:O	2:B:111:VAL:HA	2.13	0.48
2:B:144:GLY:HA2	2:B:145:TYR:CG	2.49	0.48
1:C:124:LEU:O	1:C:182:LYS:HD3	2.13	0.48
2:B:212:PRO:O	2:B:213:ARG:HB3	2.14	0.48
2:B:12:VAL:HG21	2:B:82(C):LEU:HD12	1.95	0.48
2:B:188:TRP:CD1	2:B:189:PRO:HA	2.49	0.47
2:B:188:TRP:CG	2:B:189:PRO:HA	2.49	0.47
2:D:136:VAL:HG12	2:D:185:SER:HA	1.96	0.47
2:B:38:ARG:HD3	2:B:48:LEU:HD11	1.96	0.47
2:B:47:TRP:CZ2	2:B:49:GLY:HA2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:31:ASN:ND2	1:C:68:GLY:H	2.12	0.47
1:C:136:ASN:HB3	1:C:137:ASN:ND2	2.30	0.47
1:C:32:TYR:HD1	2:D:100(C):ASP:OD2	1.97	0.47
1:A:146:LYS:HB2	1:A:146:LYS:HZ2	1.79	0.46
2:B:52:ARG:HD2	2:B:56:THR:OG1	2.14	0.46
2:B:154:TRP:CZ3	2:B:195:CYS:HB3	2.49	0.46
1:A:181:THR:O	1:A:184:GLU:HB3	2.15	0.46
1:A:114:VAL:HG12	1:A:206:LYS:HG3	1.98	0.46
2:D:137:THR:O	2:D:138:LEU:HD23	2.16	0.46
2:D:159:LEU:CD1	2:D:181:VAL:HG21	2.44	0.46
2:D:188:TRP:CD1	2:D:189:PRO:HA	2.51	0.46
2:D:150:VAL:HG22	2:D:177:LEU:HD21	1.97	0.46
2:B:145:TYR:CD2	2:B:145:TYR:C	2.89	0.46
1:C:44:PRO:HG2	2:D:103:TRP:CZ3	2.51	0.46
1:A:144:ASN:HB3	1:A:196:THR:OG1	2.15	0.45
1:A:211:ASN:N	1:A:211:ASN:HD22	2.15	0.45
2:B:159:LEU:HD23	2:B:159:LEU:HA	1.86	0.45
1:C:91:SER:HA	1:C:94:LEU:O	2.15	0.45
1:C:202:SER:CB	1:C:203:PRO:CA	2.90	0.45
2:D:108:LEU:HD22	2:D:149:PRO:CD	2.43	0.45
2:B:211:VAL:HG12	4:B:241:HOH:O	2.17	0.45
2:B:38:ARG:NE	2:B:48:LEU:HD21	2.31	0.45
1:A:1:ASP:HA	4:A:275:HOH:O	2.16	0.45
2:D:144:GLY:CA	2:D:145:TYR:HB3	2.43	0.45
2:B:50:PHE:HD1	2:B:50:PHE:O	2.00	0.44
2:D:162:GLY:O	2:D:181:VAL:HA	2.16	0.44
1:A:94:LEU:C	1:A:95:ARG:HD2	2.37	0.44
1:C:203:PRO:O	1:C:205:VAL:HG23	2.16	0.44
2:D:2:VAL:HG13	2:D:27:PHE:CD1	2.52	0.44
2:D:150:VAL:HG12	2:D:199:HIS:ND1	2.33	0.44
3:E:1:KDA:O1A	3:E:1:KDA:C10	2.56	0.44
2:B:55:TYR:CD1	2:B:71:ARG:HD3	2.52	0.44
1:A:188:HIS:O	1:A:210:ARG:NH1	2.51	0.44
1:A:94:LEU:HB3	2:B:47:TRP:CZ3	2.53	0.44
1:A:109:ASP:HB3	1:A:199:THR:CG2	2.46	0.44
2:B:47:TRP:CH2	2:B:49:GLY:HA2	2.53	0.44
2:D:186:SER:HB2	2:D:187:THR:H	1.40	0.44
1:A:16:GLY:O	1:A:77:SER:HA	2.17	0.44
2:B:101:ASP:HB3	2:B:102:TYR:HD2	1.83	0.44
3:F:1:KDA:C1	3:F:1:KDA:H10	2.47	0.44
2:B:173:ASP:O	2:B:174:LEU:HD23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:54:ARG:HD3	1:C:60:ASP:HA	2.00	0.43
2:D:114:ALA:HB3	2:D:146:PHE:CE2	2.53	0.43
1:A:23:CYS:HB3	1:A:71:PHE:HB2	2.00	0.43
2:D:3:MET:O	2:D:4:LEU:HD23	2.17	0.43
1:C:195:ALA:HB3	1:C:204:ILE:HB	2.01	0.43
2:D:31:ASP:HB3	2:D:97:ARG:HG3	2.01	0.43
1:A:18:LYS:HG2	1:A:19:VAL:N	2.33	0.43
1:A:148:LYS:HE2	1:A:194:GLU:OE2	2.17	0.43
1:A:13:VAL:HG13	1:A:17:GLU:HB2	2.01	0.43
1:A:154:ARG:HG3	1:A:155:GLN:N	2.33	0.43
1:A:183:ASP:O	1:A:187:ARG:HG3	2.18	0.43
1:C:24:LYS:HA	1:C:69:THR:O	2.19	0.43
2:D:48:LEU:HD22	2:D:63:VAL:HG11	2.01	0.43
1:A:83:LEU:CD2	1:A:165:GLN:HB3	2.49	0.43
1:C:143:ILE:HG13	1:C:196:THR:O	2.19	0.43
2:D:144:GLY:CA	2:D:175:TYR:O	2.67	0.43
2:D:147:PRO:O	2:D:199:HIS:HE1	2.02	0.43
2:B:50:PHE:C	2:B:50:PHE:CD1	2.93	0.42
2:B:162:GLY:O	2:B:181:VAL:HA	2.19	0.42
2:D:32:TYR:CE1	2:D:97:ARG:HB2	2.54	0.42
1:A:72:THR:HG22	4:A:289:HOH:O	2.18	0.42
1:A:185:TYR:CZ	1:A:210:ARG:HG3	2.54	0.42
2:D:144:GLY:HA3	2:D:175:TYR:O	2.19	0.42
1:C:2:ILE:HG12	1:C:27:GLN:HB2	2.01	0.42
1:A:89:LYS:HB3	1:A:89:LYS:HE2	1.79	0.42
2:D:95:ASP:OD2	2:D:96:MET:N	2.50	0.42
1:A:148:LYS:HB2	1:A:192:THR:HB	2.02	0.42
2:D:60:SER:OG	2:D:63:VAL:HG22	2.19	0.42
2:D:89:THR:OG1	2:D:108:LEU:HD12	2.20	0.42
1:C:50:TRP:O	1:C:51:ALA:HB3	2.20	0.42
1:C:163:THR:HG23	2:D:166:PHE:CD1	2.54	0.42
2:B:148:GLU:OE2	2:B:168:ALA:HB3	2.19	0.42
1:A:141:LYS:NZ	4:A:227:HOH:O	2.52	0.42
2:D:198:ALA:O	2:D:200:PRO:HD3	2.20	0.42
2:D:123:PRO:O	2:D:124:LEU:HD23	2.19	0.42
2:D:143:LYS:HA	2:D:176:THR:HG23	2.01	0.42
1:A:189:ASN:ND2	1:A:210:ARG:N	2.68	0.41
2:B:177:LEU:C	2:B:177:LEU:CD1	2.88	0.41
1:A:31:ASN:O	1:A:50:TRP:HA	2.20	0.41
1:A:210:ARG:NH1	1:A:210:ARG:HB3	2.35	0.41
1:C:58:VAL:HA	1:C:59:PRO:HD2	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ARG:HD2	2:B:44:ALA:CB	2.50	0.41
1:A:159:LEU:HD13	2:B:169:VAL:HB	2.03	0.41
2:D:119:PRO:HG3	2:D:145:TYR:HB2	2.02	0.41
2:D:188:TRP:CH2	2:D:212:PRO:HG3	2.56	0.41
1:C:134:PHE:CE2	2:D:180:SER:HB3	2.56	0.41
2:D:68:THR:HB	2:D:81:GLN:HB3	2.02	0.41
2:D:145:TYR:CD2	2:D:145:TYR:C	2.94	0.40
2:B:115:LYS:HD3	2:B:115:LYS:HA	1.90	0.40
2:B:118:PRO:HA	2:B:119:PRO:HD3	1.89	0.40
2:D:156:SER:HA	2:D:196:ASN:ND2	2.37	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	217/219 (99%)	205 (94%)	11 (5%)	1 (0%)	29	52
1	C	188/219 (86%)	176 (94%)	10 (5%)	2 (1%)	14	30
2	B	216/224 (96%)	203 (94%)	11 (5%)	2 (1%)	17	35
2	D	206/224 (92%)	195 (95%)	6 (3%)	5 (2%)	6	10
All	All	827/886 (93%)	779 (94%)	38 (5%)	10 (1%)	13	27

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	187	THR
1	A	77	SER
2	B	100(C)	ASP
1	C	202	SER
2	D	100(C)	ASP

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Mol	Chain	Res	Type
2	D	186	SER
1	C	77	SER
2	B	145	TYR
2	D	145	TYR
2	D	126	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	196/196 (100%)	185 (94%)	11 (6%)	21	42
1	C	174/196 (89%)	166 (95%)	8 (5%)	27	51
2	B	189/191 (99%)	178 (94%)	11 (6%)	20	40
2	D	180/191 (94%)	173 (96%)	7 (4%)	32	58
All	All	739/774 (96%)	702 (95%)	37 (5%)	24	47

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	60	ASP
1	A	70	ASP
1	A	125	THR
1	A	154	ARG
1	A	159	LEU
1	A	165	GLN
1	A	180	LEU
1	A	186	GLU
1	A	205	VAL
1	A	211	ASN
2	B	12	VAL
2	B	50	PHE
2	B	52(C)	VAL
2	B	53	LYS
2	B	58	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	145	TYR
2	B	160	SER
2	B	177	LEU
2	B	187	THR
2	B	208	LYS
2	B	213	ARG
1	C	1	ASP
1	C	5	THR
1	C	106	LYS
1	C	164	ASP
1	C	168	LYS
1	C	183	ASP
1	C	200	SER
1	C	201	THR
2	D	50	PHE
2	D	53	LYS
2	D	58	ASP
2	D	145	TYR
2	D	159	LEU
2	D	186	SER
2	D	208	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	31	ASN
1	A	42	GLN
1	A	79	GLN
1	A	93	ASN
1	A	136	ASN
1	A	137	ASN
1	A	165	GLN
1	A	188	HIS
1	A	189	ASN
1	A	197	HIS
1	A	211	ASN
2	B	73	ASN
2	B	155	ASN
2	B	171	GLN
2	B	196	ASN
2	B	199	HIS
1	C	31	ASN

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Mol	Chain	Res	Type
1	C	42	GLN
1	C	79	GLN
1	C	93	ASN
1	C	165	GLN
1	C	189	ASN
2	D	73	ASN
2	D	155	ASN
2	D	196	ASN
2	D	199	HIS

### 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](#)

6 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	$\# Z  > 2$
3	KDA	E	1	3	18,19,19	1.25	1 (5%)	22,27,27	1.84	4 (18%)
3	KDO	E	2	3	15,15,16	0.83	0	19,21,24	1.28	4 (21%)
3	KDO	E	3	3	15,15,16	0.93	1 (6%)	19,21,24	1.10	2 (10%)
3	KDA	F	1	3	18,19,19	1.38	2 (11%)	22,27,27	1.85	3 (13%)
3	KDO	F	2	3	15,15,16	0.89	0	19,21,24	1.33	3 (15%)
3	KDO	F	3	3	15,15,16	0.89	0	19,21,24	1.08	2 (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
3	KDA	E	1	3	-	8/17/35/35	0/1/1/1
3	KDO	E	2	3	-	0/10/26/30	0/1/1/1
3	KDO	E	3	3	-	0/10/26/30	0/1/1/1
3	KDA	F	1	3	-	5/17/35/35	0/1/1/1
3	KDO	F	2	3	-	0/10/26/30	0/1/1/1
3	KDO	F	3	3	-	0/10/26/30	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	1	KDA	O2-C9	-3.23	1.36	1.43
3	F	1	KDA	O2-C9	-3.10	1.36	1.43
3	F	1	KDA	C3-C4	-2.64	1.49	1.53
3	E	3	KDO	C2-C1	2.25	1.54	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1	KDA	C3-C4-C5	-6.46	104.52	110.84
3	E	1	KDA	C7-C6-C5	5.08	122.46	114.03
3	E	1	KDA	O2-C2-O6	-3.32	100.84	110.07
3	E	2	KDO	O4-C4-C5	3.03	116.20	110.14
3	F	1	KDA	C3-C2-C1	-2.95	104.41	111.19
3	F	2	KDO	C7-C6-C5	-2.93	109.17	114.03
3	E	1	KDA	C3-C2-C1	-2.83	104.68	111.19
3	E	1	KDA	O4-C4-C5	2.54	115.23	110.14
3	E	2	KDO	C7-C6-C5	-2.52	109.85	114.03
3	F	2	KDO	C3-C4-C5	-2.48	107.08	110.69
3	F	3	KDO	C3-C4-C5	-2.32	107.32	110.69
3	F	2	KDO	O1A-C1-C2	-2.26	117.23	122.57
3	F	3	KDO	O1A-C1-C2	-2.25	117.26	122.57
3	E	3	KDO	O1A-C1-C2	-2.23	117.30	122.57
3	E	3	KDO	C3-C4-C5	-2.19	107.50	110.69
3	E	2	KDO	O6-C2-C3	2.18	113.46	110.46
3	F	1	KDA	O1A-C1-C2	-2.12	116.88	123.70
3	E	2	KDO	O1A-C1-C2	-2.07	117.69	122.57

There are no chirality outliers.

All (13) torsion outliers are listed below:

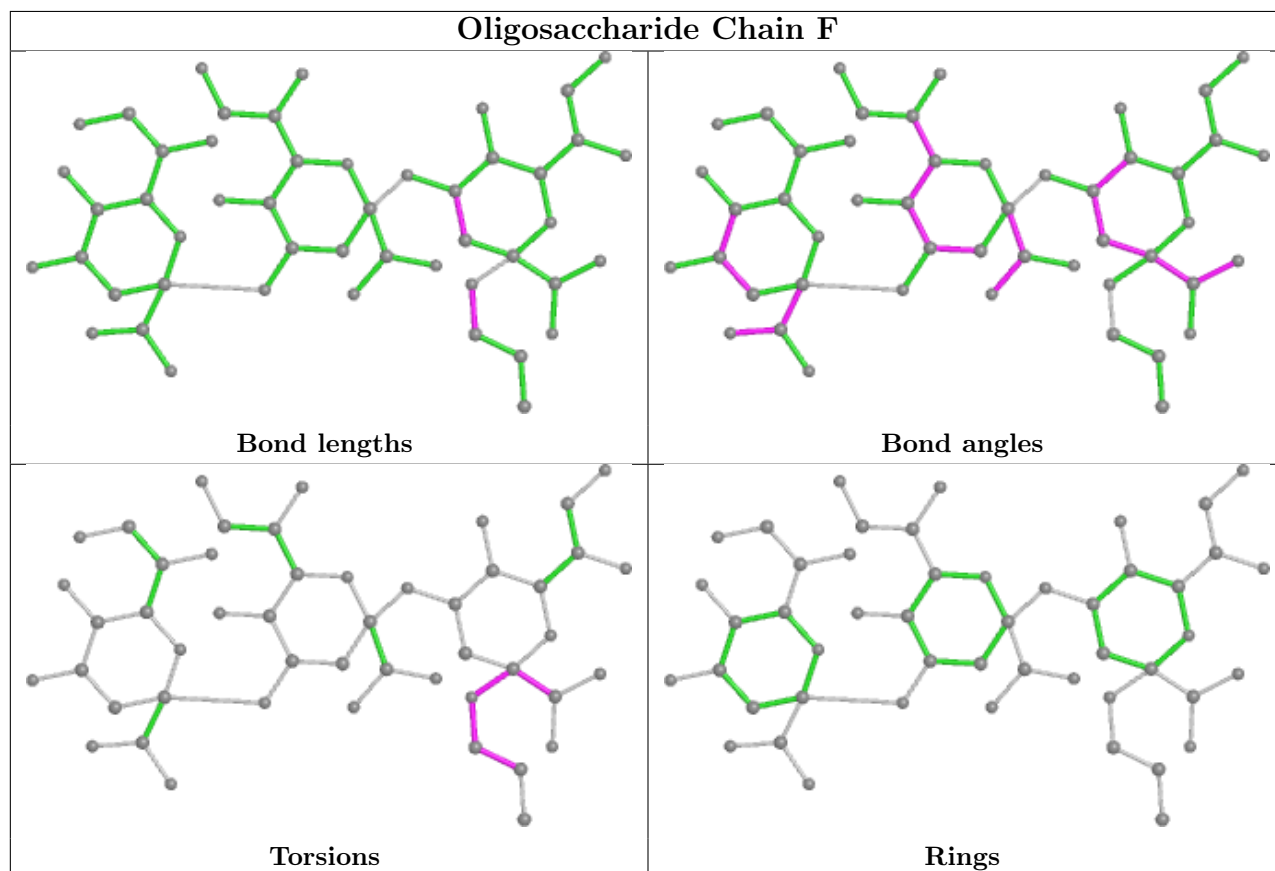
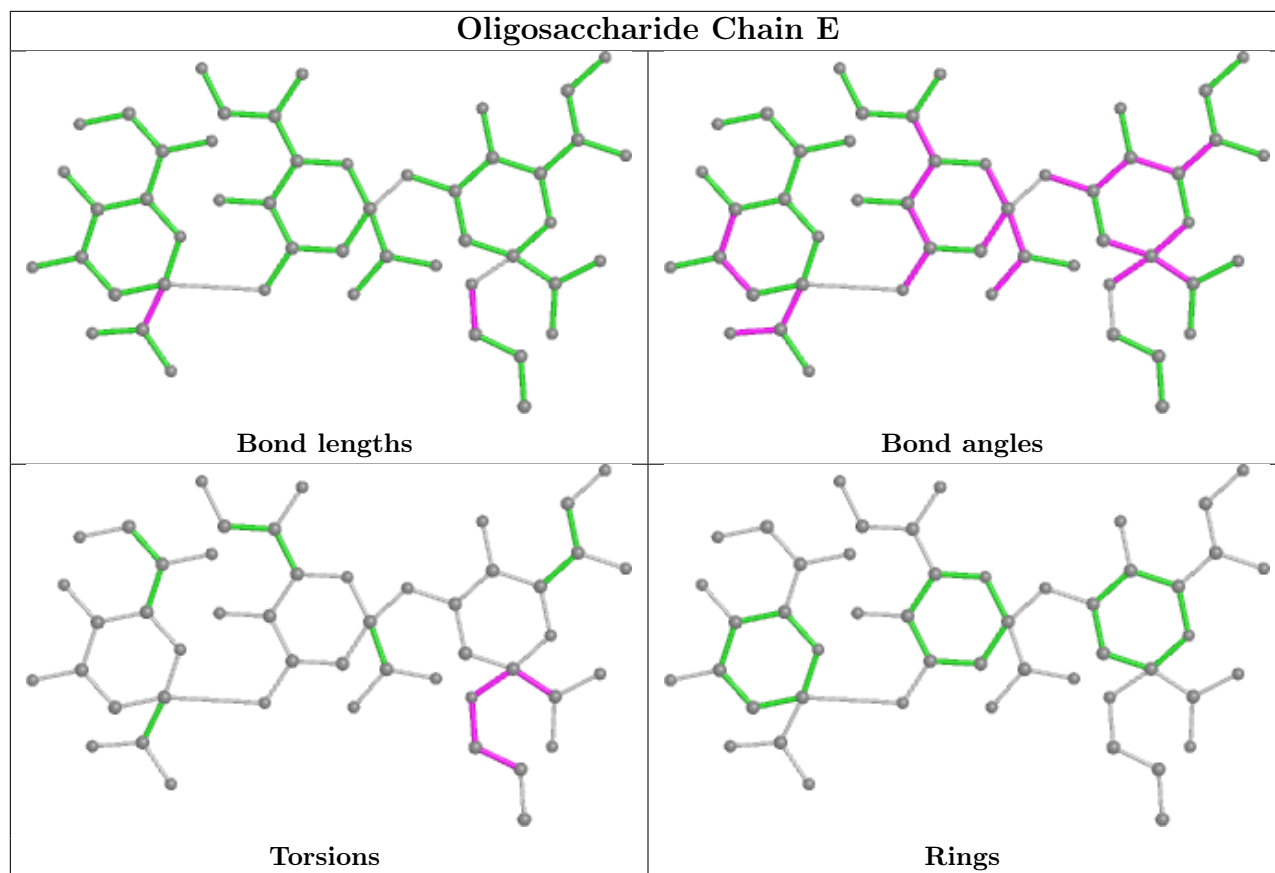
Mol	Chain	Res	Type	Atoms
3	E	1	KDA	O1B-C1-C2-O2
3	E	1	KDA	C1-C2-O2-C9
3	E	1	KDA	O6-C2-O2-C9
3	E	1	KDA	C10-C9-O2-C2
3	F	1	KDA	C3-C2-O2-C9
3	F	1	KDA	C10-C9-O2-C2
3	E	1	KDA	C11-C10-C9-O2
3	F	1	KDA	C11-C10-C9-O2
3	F	1	KDA	O1A-C1-C2-C3
3	E	1	KDA	C3-C2-O2-C9
3	E	1	KDA	O1A-C1-C2-O2
3	F	1	KDA	O1A-C1-C2-O6
3	E	1	KDA	O1B-C1-C2-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1	KDA	1	0
3	E	1	KDA	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](#)

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 [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	219/219 (100%)	-0.14	3 (1%) 75 71	17, 28, 51, 67	0
1	C	196/219 (89%)	0.06	9 (4%) 32 26	19, 35, 70, 84	0
2	B	220/224 (98%)	-0.16	5 (2%) 60 54	17, 28, 46, 71	0
2	D	212/224 (94%)	0.17	8 (3%) 40 33	22, 41, 60, 76	0
All	All	847/886 (95%)	-0.02	25 (2%) 50 43	17, 32, 60, 84	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	188	HIS	5.4
2	B	132	THR	4.3
1	A	156	ASN	3.1
1	C	192	THR	3.1
1	A	201	THR	3.0
1	C	200	SER	2.8
1	C	202	SER	2.7
2	D	172	SER	2.7
2	D	139	GLY	2.6
2	D	42	GLY	2.6
1	C	189	ASN	2.5
2	B	171	GLN	2.4
2	D	173	ASP	2.3
2	B	186	SER	2.3
1	C	203	PRO	2.3
2	D	171	GLN	2.2
2	B	172	SER	2.2
1	C	183	ASP	2.2
2	B	133	ASN	2.1
1	C	121	SER	2.1
2	D	83	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	205	VAL	2.1
2	D	85	GLU	2.1
1	A	199	THR	2.1
2	D	35	SER	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, 95<sup>th</sup> 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.

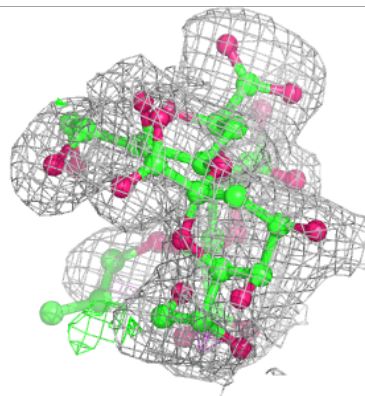
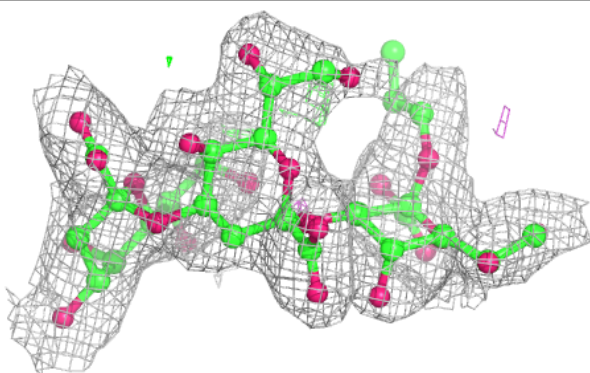
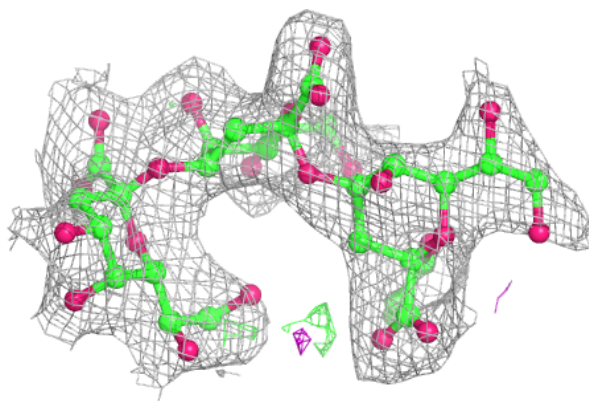
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q < 0.9
3	KDA	F	1	19/19	0.83	0.26	47,59,71,71	0
3	KDA	E	1	19/19	0.88	0.26	32,41,51,67	0
3	KDO	E	3	15/16	0.91	0.16	22,26,37,45	0
3	KDO	F	2	15/16	0.91	0.20	33,40,56,65	0
3	KDO	E	2	15/16	0.92	0.17	25,31,39,46	0
3	KDO	F	3	15/16	0.95	0.12	29,34,41,42	0

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

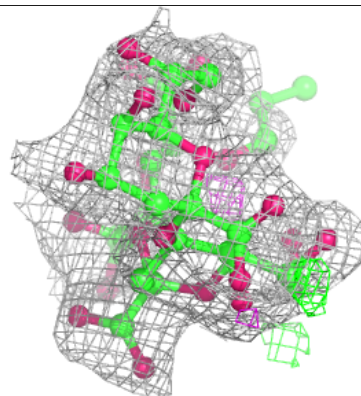
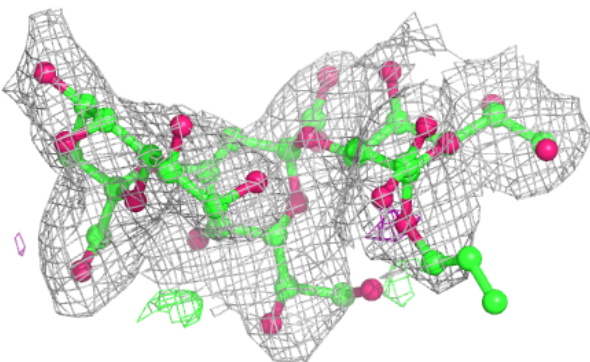
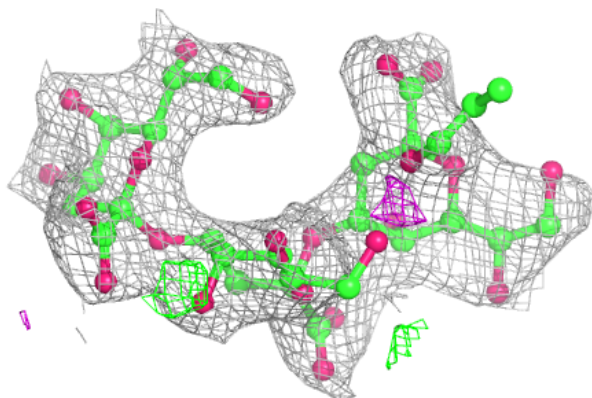


**Electron density around Chain E:**

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

**Electron density around Chain F:**

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



## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.