



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2024 – 07:07 AM EST

PDB ID : 3HMX  
Title : Crystal structure of ustekinumab FAB/IL-12 complex  
Authors : Luo, J.  
Deposited on : 2009-05-29  
Resolution : 3.00 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 : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

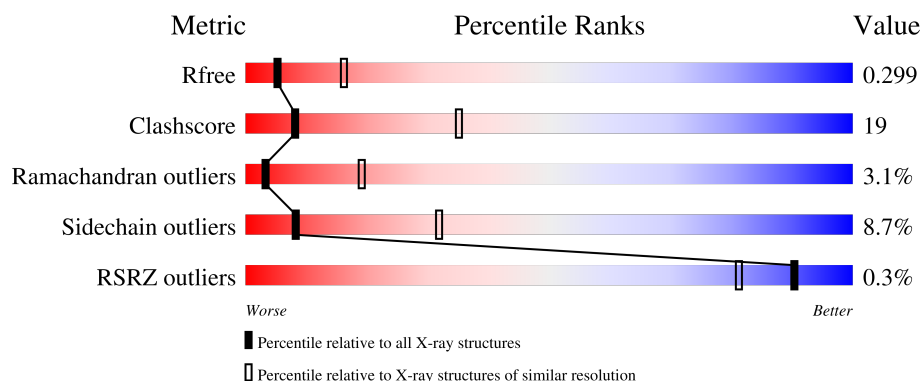
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 3.00 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	2511 (3.00-3.00)
Clashscore	180529	2866 (3.00-3.00)
Ramachandran outliers	177936	2778 (3.00-3.00)
Sidechain outliers	177891	2781 (3.00-3.00)
RSRZ outliers	164620	2523 (3.00-3.00)

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	306	
2	B	197	
3	L	214	
4	H	226	
5	C	5	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7078 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 Interleukin-12 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2331	1475	380	464	12			

- Molecule 2 is a protein called Interleukin-12 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	176	Total	C	N	O	S	0	0	0
			1351	852	229	254	16			

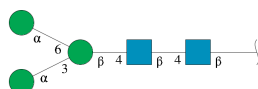
- Molecule 3 is a protein called USTEKINUMAB FAB LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	214	Total	C	N	O	S	0	0	0
			1649	1034	274	336	5			

- Molecule 4 is a protein called USTEKINUMAB FAB HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	217	Total	C	N	O	S	0	0	0
			1642	1045	273	316	8			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-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
5	C	5	Total	C	N	O	0	0	0
			61	34	2	25			

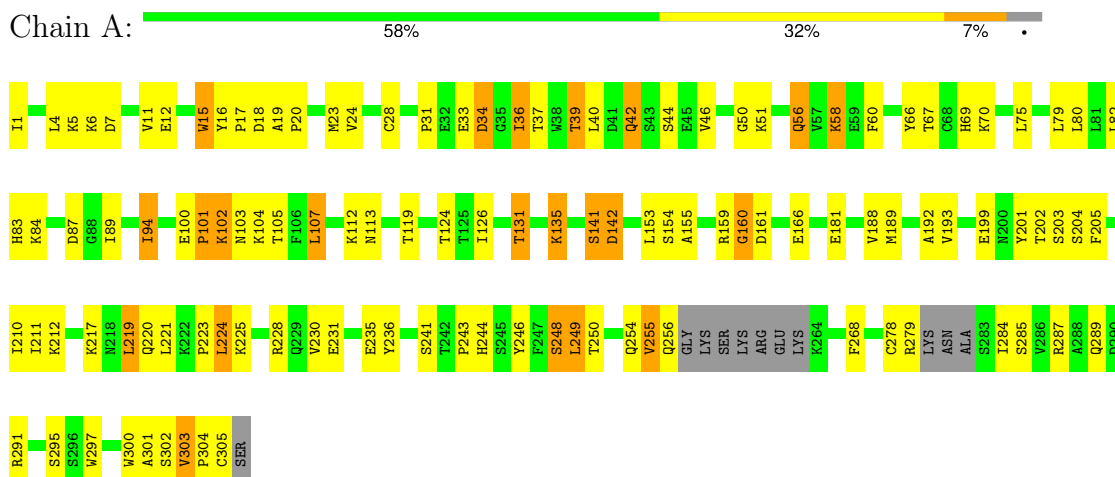
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	15	Total 15	O 15	0	0
6	B	2	Total 2	O 2	0	0
6	L	11	Total 11	O 11	0	0
6	H	16	Total 16	O 16	0	0

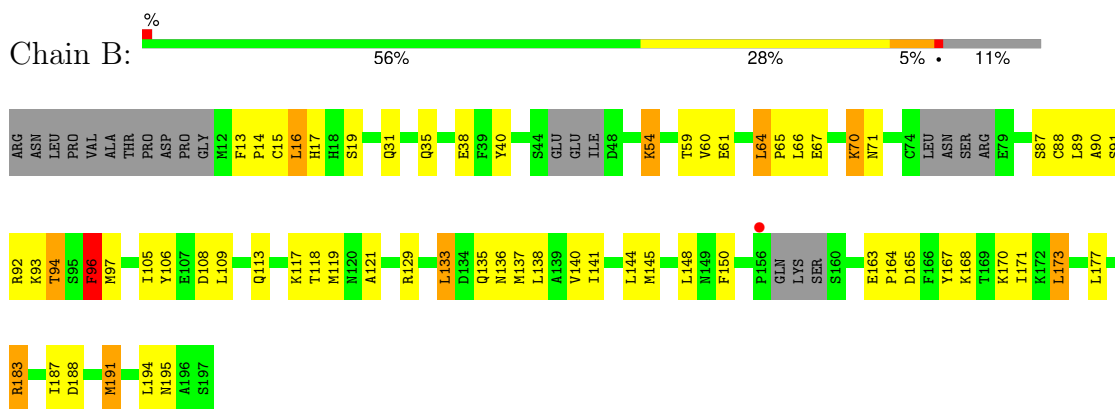
### 3 Residue-property plots

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

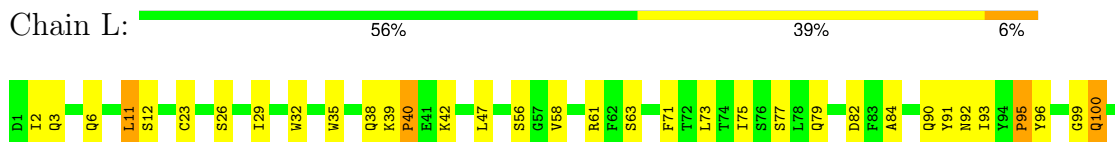
#### • Molecule 1: Interleukin-12 subunit beta

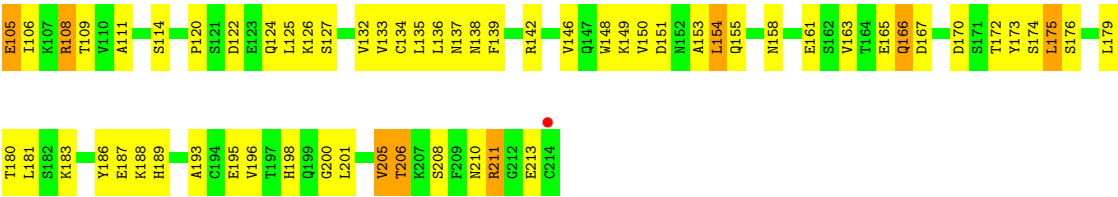


#### • Molecule 2: Interleukin-12 subunit alpha

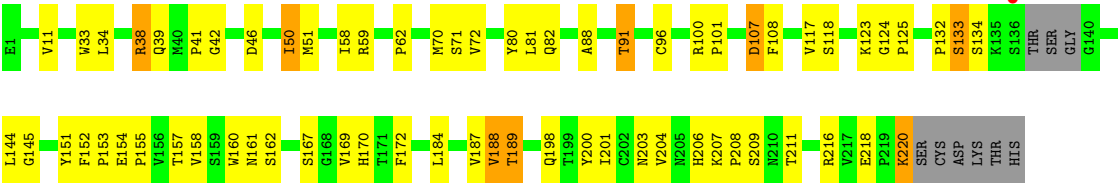


#### • Molecule 3: USTEKINUMAB FAB LIGHT CHAIN

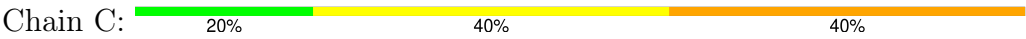




● Molecule 4: USTEKINUMAB FAB HEAVY CHAIN



● Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.09Å 116.44Å 182.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.66 – 3.00 26.66 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (26.66-3.00) 99.5 (26.66-3.00)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.73 (at 3.00Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.211 , 0.303 0.206 , 0.299	Depositor DCC
$R_{free}$ test set	1169 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	87.0	Xtriage
Anisotropy	0.521	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 89.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7078	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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: NAG, BMA, 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	0.27	0/2388	0.47	0/3249
2	B	0.26	0/1369	0.44	0/1845
3	L	0.29	0/1686	0.49	0/2290
4	H	0.30	0/1685	0.49	0/2294
All	All	0.28	0/7128	0.47	0/9678

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	2331	0	2216	97	0
2	B	1351	0	1312	48	0
3	L	1649	0	1593	73	0
4	H	1642	0	1607	56	0
5	C	61	0	52	3	0
6	A	15	0	0	1	0
6	B	2	0	0	0	0
6	H	16	0	0	1	0
6	L	11	0	0	0	0
All	All	7078	0	6780	264	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 19.

All (264) 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)
3:L:187:GLU:HA	3:L:211:ARG:HH22	1.22	1.02
2:B:91:SER:HA	2:B:94:THR:HG23	1.46	0.96
1:A:33:GLU:HG2	1:A:51:LYS:HD2	1.46	0.96
3:L:29:ILE:HA	3:L:92:ASN:HD22	1.31	0.95
4:H:88:ALA:O	4:H:91:THR:HG23	1.65	0.95
2:B:94:THR:HG22	2:B:194:LEU:HD22	1.56	0.87
1:A:15:TRP:HA	1:A:15:TRP:CE3	2.13	0.83
1:A:15:TRP:HA	1:A:15:TRP:HE3	1.46	0.80
3:L:38:GLN:HE22	4:H:39:GLN:HE22	1.30	0.80
1:A:303:VAL:HG22	1:A:304:PRO:HD2	1.64	0.79
1:A:284:ILE:HB	1:A:303:VAL:HG12	1.65	0.78
1:A:1:ILE:HG13	1:A:11:VAL:HG12	1.65	0.78
1:A:255:VAL:HG22	1:A:256:GLN:H	1.48	0.77
1:A:36:ILE:HD11	1:A:50:GLY:C	2.05	0.76
4:H:91:THR:HG22	4:H:117:VAL:HB	1.68	0.75
3:L:193:ALA:HB2	3:L:208:SER:HB3	1.68	0.74
3:L:95:PRO:HG3	4:H:62:PRO:HD2	1.72	0.71
3:L:198:HIS:CD2	3:L:200:GLY:H	2.09	0.70
4:H:153:PRO:O	4:H:206:HIS:HE1	1.73	0.70
3:L:175:LEU:HD12	3:L:176:SER:N	2.07	0.70
3:L:90:GLN:HE21	3:L:93:ILE:H	1.40	0.69
1:A:15:TRP:CD1	1:A:84:LYS:HD3	2.26	0.69
3:L:120:PRO:HB2	3:L:125:LEU:HD11	1.75	0.68
3:L:166:GLN:HG3	3:L:173:TYR:CZ	2.28	0.67
2:B:91:SER:C	2:B:93:LYS:H	1.97	0.67
1:A:248:SER:HB2	1:A:291:ARG:HD2	1.76	0.67
2:B:70:LYS:HD2	2:B:71:ASN:N	2.09	0.67
1:A:36:ILE:HD13	1:A:36:ILE:H	1.59	0.66
2:B:59:THR:HG21	2:B:108:ASP:OD2	1.95	0.66
3:L:91:TYR:HA	3:L:96:TYR:CD2	2.30	0.66
3:L:132:VAL:HG13	3:L:179:LEU:HB3	1.77	0.65
2:B:13:PHE:HE2	2:B:90:ALA:H	1.45	0.64
3:L:139:PHE:CE2	3:L:174:SER:HA	2.33	0.64
3:L:90:GLN:NE2	3:L:93:ILE:H	1.96	0.64
3:L:139:PHE:HE2	3:L:174:SER:HA	1.62	0.64
3:L:108:ARG:HG2	3:L:109:THR:N	2.13	0.63
1:A:100:GLU:HB2	1:A:101:PRO:HD3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:ARG:HA	1:A:228:ARG:HH11	1.63	0.62
2:B:109:LEU:O	2:B:113:GLN:HB2	1.99	0.62
2:B:106:TYR:HE1	2:B:145:MET:HB3	1.64	0.62
4:H:11:VAL:HG11	4:H:153:PRO:HG3	1.82	0.62
2:B:167:TYR:HA	2:B:170:LYS:HE3	1.81	0.62
3:L:183:LYS:O	3:L:187:GLU:HG2	2.00	0.62
3:L:158:ASN:HD21	3:L:181:LEU:HD21	1.65	0.62
2:B:106:TYR:CE1	2:B:145:MET:HB3	2.35	0.61
5:C:5:MAN:H62	5:C:5:MAN:O3	2.00	0.61
4:H:220:LYS:N	4:H:220:LYS:HE3	2.16	0.61
3:L:125:LEU:HD21	3:L:186:TYR:CE2	2.35	0.61
3:L:187:GLU:HA	3:L:211:ARG:NH2	2.05	0.61
1:A:155:ALA:HB3	1:A:166:GLU:HB3	1.83	0.60
2:B:64:LEU:HD12	2:B:64:LEU:H	1.66	0.60
4:H:161:ASN:ND2	4:H:201:ILE:H	1.99	0.60
3:L:61:ARG:HG3	3:L:75:ILE:HG23	1.82	0.60
2:B:137:MET:O	2:B:141:ILE:HG13	2.02	0.59
2:B:109:LEU:HD21	2:B:187:ILE:HD11	1.84	0.59
1:A:36:ILE:HD11	1:A:50:GLY:CA	2.32	0.59
3:L:29:ILE:HA	3:L:92:ASN:ND2	2.12	0.59
4:H:144:LEU:HG	4:H:188:VAL:HG23	1.84	0.58
1:A:107:LEU:HD21	1:A:203:SER:HB2	1.84	0.58
4:H:123:LYS:HG2	4:H:124:GLY:O	2.03	0.58
1:A:284:ILE:O	1:A:302:SER:HA	2.03	0.58
2:B:105:ILE:O	2:B:109:LEU:HD23	2.03	0.58
1:A:248:SER:CB	1:A:291:ARG:HD2	2.33	0.57
2:B:165:ASP:OD1	2:B:168:LYS:HB2	2.05	0.57
3:L:38:GLN:O	3:L:84:ALA:HB1	2.04	0.57
3:L:210:ASN:O	3:L:211:ARG:HG3	2.03	0.57
4:H:91:THR:HG22	4:H:117:VAL:H	1.69	0.57
4:H:132:PRO:HG3	4:H:144:LEU:HB3	1.87	0.57
1:A:223:PRO:HB3	1:A:228:ARG:NH1	2.20	0.57
3:L:124:GLN:O	3:L:127:SER:HB3	2.05	0.57
4:H:33:TRP:HE3	4:H:50:ILE:HG23	1.70	0.56
2:B:144:LEU:O	2:B:148:LEU:HG	2.04	0.56
4:H:162:SER:HA	4:H:203:ASN:ND2	2.21	0.56
1:A:131:THR:HG23	1:A:193:VAL:HB	1.87	0.55
3:L:108:ARG:HH21	3:L:111:ALA:HB2	1.72	0.55
1:A:16:TYR:CE2	1:A:19:ALA:HB2	2.41	0.55
1:A:285:SER:HB2	1:A:300:TRP:CE3	2.42	0.54
2:B:119:MET:HE3	2:B:173:LEU:HG	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:GLN:HG2	1:A:255:VAL:H	1.72	0.54
3:L:167:ASP:HB3	3:L:170:ASP:OD2	2.07	0.54
4:H:145:GLY:HA2	4:H:160:TRP:CH2	2.43	0.54
1:A:5:LYS:NZ	6:A:307:HOH:O	2.40	0.53
3:L:136:LEU:N	3:L:136:LEU:HD12	2.23	0.53
4:H:91:THR:CG2	4:H:117:VAL:H	2.21	0.53
2:B:91:SER:C	2:B:93:LYS:N	2.62	0.53
1:A:219:LEU:H	1:A:219:LEU:HD12	1.74	0.53
4:H:125:PRO:HB3	4:H:151:TYR:HB3	1.90	0.53
1:A:135:LYS:HG2	1:A:189:MET:HB2	1.90	0.53
1:A:79:LEU:O	1:A:80:LEU:HD23	2.08	0.53
2:B:141:ILE:O	2:B:145:MET:HG3	2.08	0.53
4:H:220:LYS:HE3	4:H:220:LYS:H	1.73	0.53
1:A:34:ASP:HB2	1:A:70:LYS:NZ	2.24	0.52
1:A:36:ILE:H	1:A:36:ILE:CD1	2.22	0.52
1:A:20:PRO:O	1:A:58:LYS:HE3	2.10	0.52
4:H:51:MET:SD	4:H:70:MET:HB3	2.49	0.52
1:A:15:TRP:NE1	1:A:84:LYS:HD3	2.24	0.52
1:A:284:ILE:HD11	1:A:305:CYS:HA	1.92	0.52
3:L:146:VAL:HG22	3:L:196:VAL:HG22	1.92	0.52
4:H:161:ASN:HD21	4:H:201:ILE:H	1.56	0.52
1:A:219:LEU:HD12	1:A:219:LEU:N	2.24	0.52
3:L:63:SER:O	3:L:73:LEU:HD12	2.10	0.52
2:B:16:LEU:HD23	2:B:191:MET:HB3	1.92	0.51
1:A:220:GLN:O	1:A:221:LEU:HD12	2.10	0.51
4:H:91:THR:HG22	4:H:117:VAL:CB	2.38	0.51
1:A:83:HIS:HD2	5:C:1:NAG:O6	1.93	0.51
3:L:174:SER:O	4:H:172:PHE:HE2	1.92	0.51
4:H:107:ASP:HB3	4:H:108:PHE:HD2	1.76	0.51
4:H:118:SER:HB3	4:H:152:PHE:CZ	2.46	0.51
1:A:16:TYR:CZ	1:A:19:ALA:HB2	2.46	0.51
1:A:303:VAL:CG2	1:A:304:PRO:HD2	2.36	0.51
1:A:284:ILE:HD12	1:A:284:ILE:N	2.25	0.50
4:H:58:ILE:HG22	4:H:59:ARG:N	2.26	0.50
1:A:39:THR:CG2	1:A:69:HIS:HE1	2.24	0.50
4:H:162:SER:H	4:H:203:ASN:HD21	1.58	0.50
1:A:94:ILE:HG12	1:A:199:GLU:OE1	2.11	0.50
1:A:285:SER:HB2	1:A:300:TRP:HE3	1.76	0.50
3:L:12:SER:HB3	3:L:105:GLU:OE2	2.11	0.49
1:A:36:ILE:HD13	1:A:36:ILE:N	2.28	0.49
1:A:112:LYS:HA	1:A:212:LYS:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:193:ALA:CB	3:L:208:SER:HB3	2.41	0.49
3:L:165:GLU:O	3:L:166:GLN:C	2.50	0.49
2:B:19:SER:OG	2:B:188:ASP:HA	2.13	0.49
3:L:122:ASP:O	3:L:126:LYS:HG2	2.12	0.49
1:A:224:LEU:HG	1:A:225:LYS:H	1.77	0.49
1:A:23:MET:O	1:A:23:MET:HG2	2.12	0.49
4:H:153:PRO:O	4:H:206:HIS:CE1	2.61	0.48
4:H:201:ILE:HG22	4:H:216:ARG:HB2	1.95	0.48
4:H:161:ASN:HA	4:H:201:ILE:HD11	1.94	0.48
1:A:40:LEU:HD13	1:A:66:TYR:CZ	2.49	0.48
1:A:153:LEU:HD13	1:A:154:SER:N	2.29	0.48
1:A:236:TYR:CD1	1:A:244:HIS:CG	3.02	0.48
1:A:230:VAL:HG23	1:A:278:CYS:HB2	1.96	0.48
1:A:101:PRO:HG2	1:A:105:THR:HG21	1.96	0.47
3:L:39:LYS:HB3	3:L:40:PRO:HD2	1.96	0.47
3:L:137:ASN:ND2	4:H:189:THR:HG21	2.29	0.47
4:H:201:ILE:HG22	4:H:216:ARG:HA	1.95	0.47
3:L:29:ILE:HD11	3:L:71:PHE:CE1	2.49	0.47
3:L:195:GLU:HG3	3:L:206:THR:HB	1.97	0.47
3:L:210:ASN:N	3:L:210:ASN:HD22	2.12	0.47
2:B:173:LEU:HD22	2:B:177:LEU:HG	1.97	0.47
4:H:154:GLU:CB	4:H:155:PRO:HA	2.45	0.47
2:B:15:CYS:HB3	2:B:191:MET:HG3	1.97	0.47
3:L:6:GLN:OE1	3:L:99:GLY:HA3	2.15	0.47
4:H:33:TRP:CE3	4:H:50:ILE:HG23	2.50	0.47
1:A:101:PRO:HB2	1:A:102:LYS:H	1.58	0.47
3:L:23:CYS:HB2	3:L:35:TRP:CH2	2.50	0.47
1:A:221:LEU:HA	1:A:231:GLU:O	2.13	0.46
1:A:181:GLU:OE1	2:B:183:ARG:NH1	2.48	0.46
3:L:100:GLN:H	3:L:100:GLN:CD	2.16	0.46
4:H:154:GLU:HB3	4:H:155:PRO:HA	1.97	0.46
1:A:255:VAL:HG22	1:A:256:GLN:N	2.26	0.46
3:L:166:GLN:HG3	3:L:173:TYR:CE2	2.50	0.46
4:H:216:ARG:HD2	4:H:218:GLU:OE2	2.15	0.46
4:H:71:SER:OG	4:H:80:TYR:HB2	2.15	0.46
1:A:94:ILE:HD12	1:A:192:ALA:HB1	1.98	0.46
1:A:141:SER:O	1:A:142:ASP:C	2.53	0.46
3:L:108:ARG:HG2	3:L:109:THR:H	1.80	0.46
1:A:254:GLN:CG	1:A:255:VAL:H	2.26	0.46
3:L:125:LEU:O	3:L:183:LYS:HD2	2.15	0.46
1:A:56:GLN:HB2	3:L:32:TRP:CZ2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:ARG:HD2	1:A:297:TRP:HB3	1.97	0.46
3:L:154:LEU:HD13	3:L:155:GLN:H	1.81	0.46
3:L:188:LYS:O	3:L:189:HIS:CG	2.69	0.46
4:H:133:SER:OG	4:H:134:SER:N	2.49	0.46
1:A:6:LYS:O	1:A:7:ASP:HB2	2.16	0.45
1:A:107:LEU:CD2	1:A:107:LEU:H	2.28	0.45
1:A:255:VAL:HG13	1:A:256:GLN:N	2.31	0.45
3:L:149:LYS:HA	3:L:153:ALA:O	2.15	0.45
4:H:100:ARG:HA	4:H:101:PRO:HD3	1.71	0.45
5:C:1:NAG:H83	5:C:1:NAG:O3	2.15	0.45
1:A:103:ASN:CG	1:A:104:LYS:H	2.19	0.45
2:B:105:ILE:O	2:B:108:ASP:HB2	2.14	0.45
2:B:173:LEU:CD2	2:B:177:LEU:HG	2.46	0.45
4:H:158:VAL:HG22	4:H:204:VAL:HG22	1.98	0.45
3:L:3:GLN:HB2	3:L:26:SER:HB3	1.97	0.45
1:A:1:ILE:HG23	1:A:1:ILE:O	2.17	0.45
3:L:2:ILE:HD11	3:L:93:ILE:HD12	1.97	0.45
1:A:100:GLU:CB	1:A:101:PRO:HD3	2.44	0.45
2:B:96:PHE:HD2	2:B:97:MET:H	1.64	0.45
3:L:125:LEU:C	3:L:127:SER:H	2.20	0.45
1:A:107:LEU:CD2	1:A:203:SER:HB2	2.46	0.45
2:B:109:LEU:HD12	2:B:141:ILE:HG23	1.99	0.45
3:L:11:LEU:HD12	3:L:11:LEU:C	2.38	0.45
3:L:136:LEU:N	3:L:136:LEU:CD1	2.80	0.45
1:A:28:CYS:SG	1:A:75:LEU:HD23	2.57	0.44
2:B:163:GLU:HA	2:B:164:PRO:HD3	1.71	0.44
1:A:39:THR:HG22	1:A:67:THR:HB	1.98	0.44
1:A:250:THR:HG22	1:A:289:GLN:O	2.18	0.44
4:H:38:ARG:HG2	4:H:46:ASP:HB2	2.00	0.44
2:B:31:GLN:O	2:B:35:GLN:HB2	2.18	0.44
3:L:151:ASP:C	3:L:153:ALA:H	2.21	0.44
1:A:287:ARG:HG3	1:A:300:TRP:CZ3	2.52	0.44
4:H:34:LEU:O	4:H:50:ILE:HD13	2.18	0.44
1:A:201:TYR:N	1:A:201:TYR:CD1	2.84	0.44
2:B:113:GLN:O	2:B:117:LYS:HB2	2.18	0.43
3:L:114:SER:HB2	3:L:137:ASN:HB3	2.00	0.43
1:A:135:LYS:HD3	1:A:189:MET:HB3	2.00	0.43
3:L:201:LEU:HD13	3:L:205:VAL:CG1	2.48	0.43
3:L:210:ASN:O	3:L:211:ARG:CG	2.65	0.43
4:H:42:GLY:HA2	6:H:238:HOH:O	2.19	0.43
4:H:161:ASN:HD21	4:H:200:TYR:HA	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:THR:HB	1:A:46:VAL:HG22	1.99	0.43
1:A:284:ILE:HG22	1:A:285:SER:N	2.33	0.43
2:B:137:MET:O	2:B:137:MET:HG2	2.18	0.43
4:H:184:LEU:HD12	4:H:184:LEU:C	2.38	0.43
1:A:220:GLN:C	1:A:221:LEU:HD12	2.39	0.43
1:A:246:TYR:CZ	2:B:65:PRO:HD3	2.54	0.43
4:H:161:ASN:ND2	4:H:201:ILE:HG13	2.33	0.43
3:L:135:LEU:HD22	4:H:187:VAL:HG21	2.00	0.43
1:A:16:TYR:HA	1:A:17:PRO:HD3	1.89	0.43
2:B:183:ARG:HA	2:B:183:ARG:HD3	1.73	0.43
3:L:174:SER:HB2	4:H:170:HIS:HD2	1.84	0.43
1:A:79:LEU:C	1:A:80:LEU:HD23	2.39	0.43
1:A:243:PRO:HG3	2:B:67:GLU:OE1	2.18	0.43
1:A:268:PHE:HE2	1:A:297:TRP:CZ2	2.36	0.43
1:A:285:SER:HA	1:A:301:ALA:O	2.19	0.43
3:L:134:CYS:HB2	3:L:148:TRP:CH2	2.54	0.43
2:B:14:PRO:O	2:B:17:HIS:HB3	2.19	0.42
3:L:149:LYS:HG2	3:L:154:LEU:HD22	2.01	0.42
1:A:205:PHE:CD2	1:A:210:ILE:HG12	2.54	0.42
2:B:38:GLU:H	2:B:38:GLU:HG2	1.61	0.42
3:L:106:ILE:HD12	3:L:166:GLN:OE1	2.20	0.42
2:B:70:LYS:HD2	2:B:71:ASN:H	1.84	0.42
4:H:209:SER:C	4:H:211:THR:H	2.23	0.42
4:H:81:LEU:HD12	4:H:82:GLN:H	1.84	0.42
1:A:112:LYS:O	1:A:113:ASN:HB3	2.20	0.42
4:H:152:PHE:HA	4:H:153:PRO:HA	1.79	0.42
1:A:16:TYR:CD2	1:A:19:ALA:HB2	2.55	0.41
1:A:60:PHE:CE2	1:A:82:LEU:HB2	2.55	0.41
2:B:91:SER:CA	2:B:94:THR:HG23	2.34	0.41
3:L:12:SER:HA	3:L:105:GLU:O	2.19	0.41
4:H:100:ARG:HB2	4:H:107:ASP:OD1	2.20	0.41
2:B:137:MET:HA	2:B:140:VAL:HG22	2.03	0.41
3:L:61:ARG:NH1	3:L:82:ASP:OD2	2.54	0.41
3:L:142:ARG:HB3	3:L:173:TYR:CG	2.54	0.41
1:A:107:LEU:H	1:A:107:LEU:HD23	1.85	0.41
1:A:188:VAL:O	1:A:202:THR:HA	2.20	0.41
2:B:133:LEU:HD12	2:B:138:LEU:HG	2.01	0.41
1:A:142:ASP:OD1	1:A:142:ASP:O	2.38	0.41
2:B:66:LEU:N	2:B:66:LEU:HD12	2.35	0.41
3:L:132:VAL:CG1	3:L:179:LEU:HB3	2.45	0.41
4:H:161:ASN:HD22	4:H:201:ILE:HG13	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:207:LYS:O	4:H:209:SER:N	2.53	0.41
1:A:159:ARG:CG	1:A:160:GLY:N	2.83	0.41
2:B:16:LEU:HD23	2:B:16:LEU:HA	1.74	0.41
3:L:135:LEU:CD2	4:H:187:VAL:HG21	2.50	0.41
3:L:174:SER:CB	4:H:170:HIS:HD2	2.34	0.41
1:A:4:LEU:HB3	1:A:5:LYS:H	1.72	0.41
1:A:236:TYR:HD1	1:A:244:HIS:ND1	2.19	0.41
2:B:60:VAL:HG13	2:B:61:GLU:N	2.35	0.41
2:B:118:THR:O	2:B:121:ALA:HB3	2.20	0.41
3:L:79:GLN:O	3:L:82:ASP:HB2	2.21	0.41
1:A:236:TYR:CZ	1:A:249:LEU:HB2	2.56	0.41
1:A:103:ASN:O	1:A:104:LYS:C	2.60	0.40
1:A:126:ILE:H	1:A:126:ILE:HD12	1.86	0.40
2:B:87:SER:OG	2:B:88:CYS:N	2.53	0.40
2:B:88:CYS:O	2:B:89:LEU:HD23	2.21	0.40
1:A:42:GLN:H	1:A:42:GLN:HG3	1.73	0.40
1:A:255:VAL:HG13	1:A:256:GLN:O	2.21	0.40
3:L:47:LEU:HA	3:L:58:VAL:HG11	2.02	0.40
4:H:169:VAL:HG22	4:H:188:VAL:CG1	2.50	0.40
1:A:254:GLN:HB2	1:A:300:TRP:CH2	2.56	0.40
2:B:40:TYR:HD1	2:B:171:ILE:CD1	2.34	0.40
3:L:108:ARG:NE	3:L:109:THR:O	2.53	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	289/306 (94%)	240 (83%)	36 (12%)	13 (4%)	2	12
2	B	168/197 (85%)	134 (80%)	29 (17%)	5 (3%)	3	20
3	L	212/214 (99%)	181 (85%)	27 (13%)	4 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	H	213/226 (94%)	190 (89%)	18 (8%)	5 (2%)	5	26
All	All	882/943 (94%)	745 (84%)	110 (12%)	27 (3%)	3	19

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	PRO
1	A	217	LYS
1	A	255	VAL
2	B	54	LYS
3	L	138	ASN
3	L	211	ARG
2	B	96	PHE
1	A	87	ASP
1	A	102	LYS
1	A	161	ASP
1	A	295	SER
2	B	92	ARG
2	B	129	ARG
2	B	150	PHE
3	L	40	PRO
4	H	41	PRO
4	H	133	SER
4	H	167	SER
1	A	34	ASP
1	A	141	SER
3	L	166	GLN
4	H	208	PRO
1	A	142	ASP
1	A	224	LEU
4	H	72	VAL
1	A	160	GLY
1	A	31	PRO

### 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	262/277 (95%)	236 (90%)	26 (10%)	6	26
2	B	147/183 (80%)	134 (91%)	13 (9%)	8	31
3	L	187/188 (100%)	168 (90%)	19 (10%)	6	24
4	H	184/195 (94%)	174 (95%)	10 (5%)	18	50
All	All	780/843 (92%)	712 (91%)	68 (9%)	8	32

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLU
1	A	15	TRP
1	A	18	ASP
1	A	24	VAL
1	A	36	ILE
1	A	39	THR
1	A	42	GLN
1	A	44	SER
1	A	56	GLN
1	A	58	LYS
1	A	89	ILE
1	A	94	ILE
1	A	107	LEU
1	A	119	THR
1	A	124	THR
1	A	131	THR
1	A	135	LYS
1	A	204	SER
1	A	211	ILE
1	A	219	LEU
1	A	235	GLU
1	A	241	SER
1	A	248	SER
1	A	249	LEU
1	A	279	ARG
1	A	303	VAL
2	B	16	LEU
2	B	54	LYS
2	B	64	LEU
2	B	70	LYS
2	B	94	THR
2	B	96	PHE
2	B	133	LEU

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Mol	Chain	Res	Type
2	B	135	GLN
2	B	136	ASN
2	B	173	LEU
2	B	183	ARG
2	B	191	MET
2	B	195	ASN
3	L	11	LEU
3	L	42	LYS
3	L	56	SER
3	L	77	SER
3	L	95	PRO
3	L	100	GLN
3	L	105	GLU
3	L	108	ARG
3	L	133	VAL
3	L	150	VAL
3	L	154	LEU
3	L	161	GLU
3	L	163	VAL
3	L	172	THR
3	L	175	LEU
3	L	180	THR
3	L	205	VAL
3	L	206	THR
3	L	213	GLU
4	H	38	ARG
4	H	50	ILE
4	H	91	THR
4	H	96	CYS
4	H	107	ASP
4	H	157	THR
4	H	188	VAL
4	H	189	THR
4	H	198	GLN
4	H	220	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	A	56	GLN
1	A	69	HIS

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Mol	Chain	Res	Type
1	A	83	HIS
1	A	98	GLN
1	A	220	GLN
1	A	226	ASN
1	A	256	GLN
2	B	28	ASN
2	B	35	GLN
2	B	71	ASN
2	B	113	GLN
2	B	120	ASN
2	B	130	GLN
2	B	135	GLN
2	B	136	ASN
2	B	146	GLN
3	L	3	GLN
3	L	27	GLN
3	L	90	GLN
3	L	92	ASN
3	L	155	GLN
3	L	158	ASN
3	L	198	HIS
3	L	210	ASN
4	H	39	GLN
4	H	103	GLN
4	H	161	ASN
4	H	198	GLN
4	H	206	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](#)

5 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
5	NAG	C	1	5,1	14,14,15	0.39	0	17,19,21	1.44	1 (5%)
5	NAG	C	2	5	14,14,15	0.55	0	17,19,21	1.85	3 (17%)
5	BMA	C	3	5	11,11,12	1.34	1 (9%)	15,15,17	2.43	6 (40%)
5	MAN	C	4	5	11,11,12	0.57	0	15,15,17	0.72	0
5	MAN	C	5	5	11,11,12	1.46	2 (18%)	15,15,17	2.48	5 (33%)

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	3	BMA	O5-C1	-3.52	1.37	1.43
5	C	5	MAN	C6-C5	2.21	1.59	1.51
5	C	5	MAN	C4-C3	2.06	1.57	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	3	BMA	C1-O5-C5	-6.58	103.37	112.19
5	C	2	NAG	C1-O5-C5	5.57	119.66	112.19
5	C	5	MAN	C1-O5-C5	5.54	119.61	112.19
5	C	1	NAG	C1-O5-C5	4.89	118.74	112.19
5	C	5	MAN	O5-C5-C6	3.78	115.03	107.66
5	C	5	MAN	O4-C4-C3	3.50	118.64	110.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	5	MAN	O2-C2-C3	3.19	116.75	110.15
5	C	3	BMA	O2-C2-C3	3.18	116.75	110.15
5	C	5	MAN	O6-C6-C5	3.05	121.73	111.33
5	C	3	BMA	C2-C3-C4	-2.81	105.91	110.86
5	C	2	NAG	C2-N2-C7	-2.74	119.23	122.90
5	C	3	BMA	O4-C4-C5	2.66	115.88	109.32
5	C	3	BMA	O6-C6-C5	2.49	119.82	111.33
5	C	3	BMA	O5-C5-C6	2.27	112.08	107.66
5	C	2	NAG	C6-C5-C4	-2.02	108.05	113.02

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	1	NAG	C8-C7-N2-C2
5	C	1	NAG	O7-C7-N2-C2
5	C	4	MAN	O5-C5-C6-O6
5	C	5	MAN	O5-C5-C6-O6
5	C	5	MAN	C4-C5-C6-O6
5	C	3	BMA	O5-C5-C6-O6
5	C	3	BMA	C4-C5-C6-O6
5	C	4	MAN	C4-C5-C6-O6
5	C	2	NAG	C8-C7-N2-C2
5	C	2	NAG	O5-C5-C6-O6
5	C	2	NAG	O7-C7-N2-C2

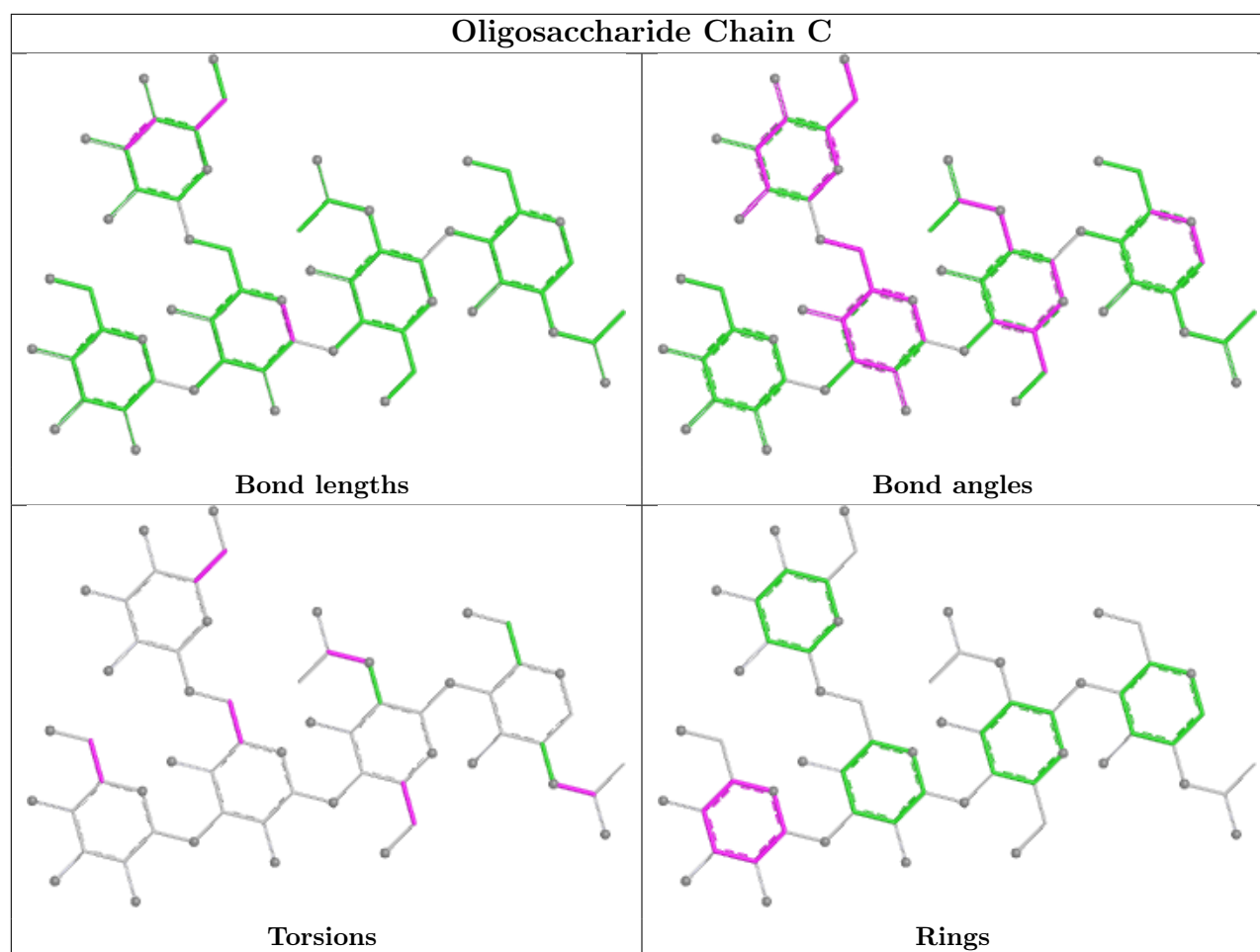
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	4	MAN	C1-C2-C3-C4-C5-O5

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1	NAG	2	0
5	C	5	MAN	1	0

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



## 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 [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, 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	295/306 (96%)	-0.32	0 <a href="#">100</a> <a href="#">100</a>	60, 97, 200, 255	0
2	B	176/197 (89%)	-0.27	1 (0%) <a href="#">85</a> <a href="#">71</a>	70, 106, 181, 238	0
3	L	214/214 (100%)	-0.42	1 (0%) <a href="#">87</a> <a href="#">75</a>	52, 90, 121, 164	0
4	H	217/226 (96%)	-0.55	1 (0%) <a href="#">87</a> <a href="#">75</a>	45, 81, 134, 178	0
All	All	902/943 (95%)	-0.39	3 (0%) <a href="#">90</a> <a href="#">81</a>	45, 92, 175, 255	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	214	CYS	2.3
4	H	136	SER	2.2
2	B	156	PRO	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](#)

SUGAR-RSR INFOmissingINFO

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.