



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 10:32 AM UTC

PDB ID : 7CJ2 / pdb_00007cj2
Title : Crystal structure of the Fab antibody complexed with human YKL-40
Authors : Choi, S.; Na, J.H.; Lee, S.J.; Woo, J.R.; Kim, D.Y.; Hong, J.T.; Lee, W.K.
Deposited on : 2020-07-09
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

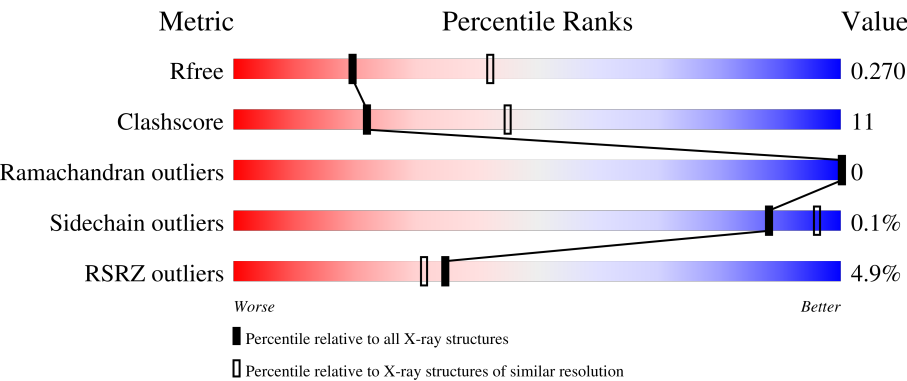
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C	222	5% 71% 21% 8%
1	K	222	5% 66% 18% 15%
2	D	215	5% 77% 21%
2	L	215	17% 72% 25%
3	A	362	% 82% 18%

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Mol	Chain	Length	Quality of chain
3	B	362	% 81% 18%
4	E	3	67% 33%
5	F	2	50% 50%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11717 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 Fab(Heavy chain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	204	Total	C	N	O	S	0	0	0
			1456	916	243	291	6			
1	K	188	Total	C	N	O	S	0	0	0
			1335	845	222	263	5			

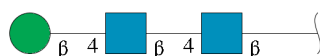
- Molecule 2 is a protein called Fab(Light chain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	211	Total	C	N	O	S	0	0	0
			1539	963	254	317	5			
2	L	208	Total	C	N	O	S	0	0	0
			1517	952	250	310	5			

- Molecule 3 is a protein called Chitinase 3-like 1 (Cartilage glycoprotein-39), isoform CRA_a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	361	Total	C	N	O	S	0	0	0
			2785	1781	472	521	11			
3	B	361	Total	C	N	O	S	0	0	0
			2809	1800	474	524	11			

- Molecule 4 is an oligosaccharide called 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
4	E	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

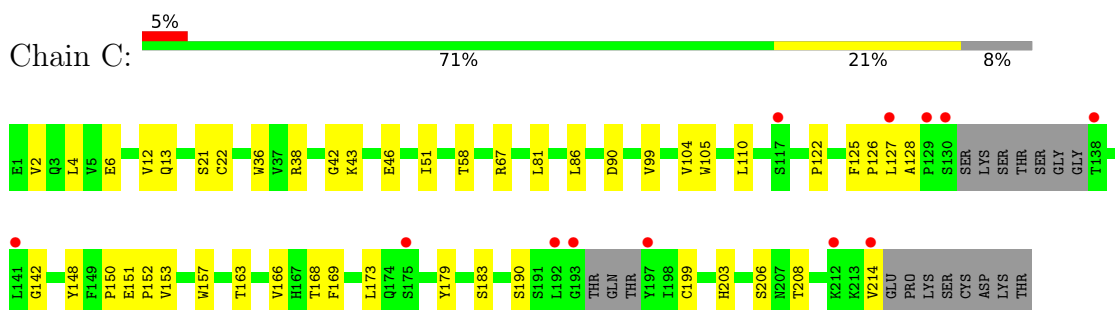
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	32	Total	O	0	0
			32	32		
6	D	24	Total	O	0	0
			24	24		
6	A	48	Total	O	0	0
			48	48		
6	B	46	Total	O	0	0
			46	46		
6	K	27	Total	O	0	0
			27	27		
6	L	32	Total	O	0	0
			32	32		

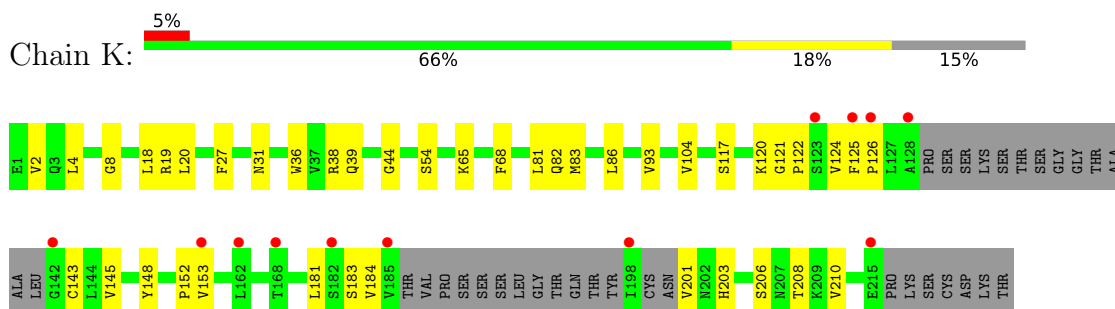
3 Residue-property plots [i](#)

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.

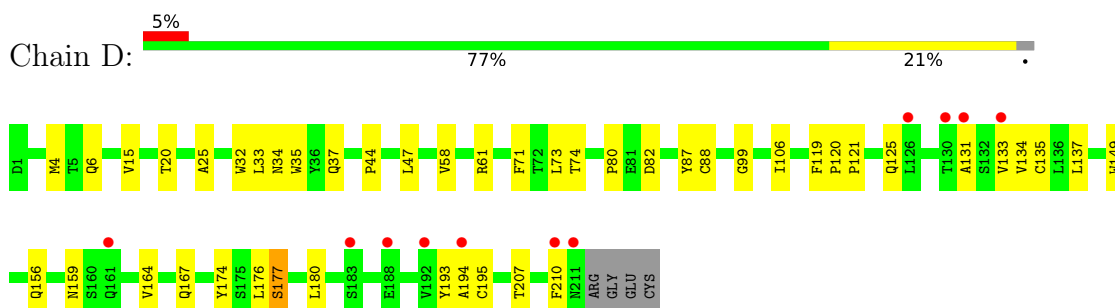
- Molecule 1: Fab(Heavy chain)



- Molecule 1: Fab(Heavy chain)

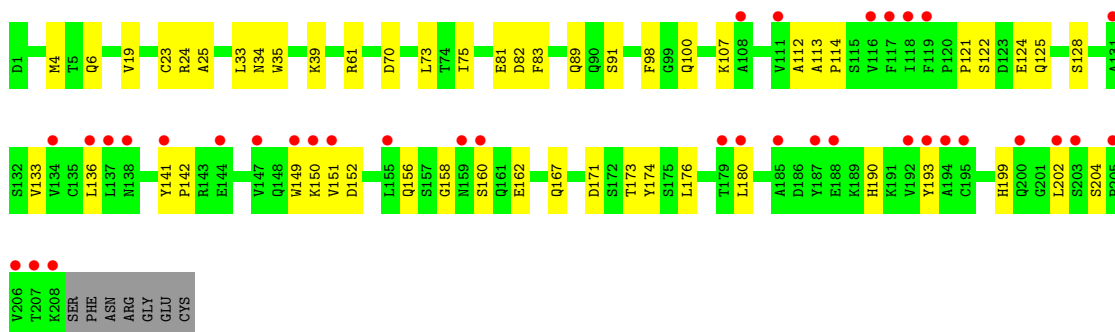


- Molecule 2: Fab(Light chain)

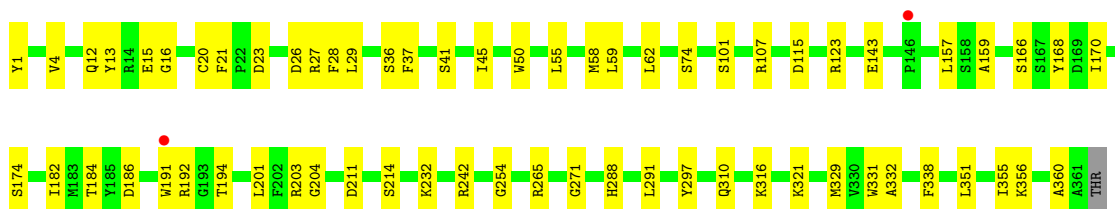
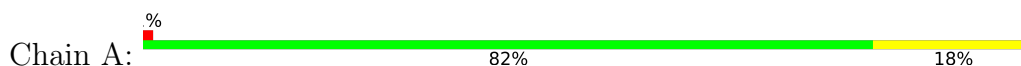


- Molecule 2: Fab(Light chain)

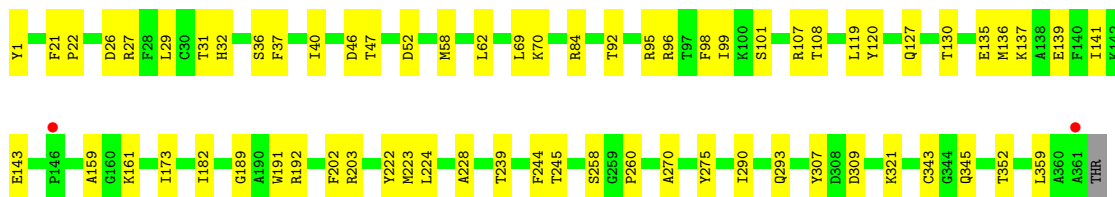
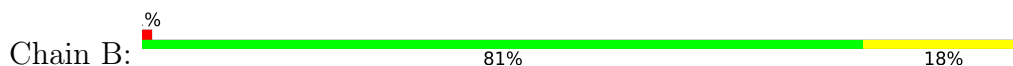




- Molecule 3: Chitinase 3-like 1 (Cartilage glycoprotein-39), isoform CRA_a



- Molecule 3: Chitinase 3-like 1 (Cartilage glycoprotein-39), isoform CRA_a



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



- Molecule 5: 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, α , β , γ	89.58Å 132.53Å 160.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.83 – 2.70 45.83 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.83-2.70) 99.9 (45.83-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.45Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.212 , 0.269 0.217 , 0.270	Depositor DCC
R_{free} test set	2640 reflections (3.72%)	wwPDB-VP
Wilson B-factor (Å ²)	59.0	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11717	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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: BMA, NAG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	C	0.36	0/1488	0.57	0/2035
1	K	0.39	0/1364	0.61	0/1860
2	D	0.36	0/1574	0.57	0/2156
2	L	0.42	0/1551	0.68	0/2121
3	A	0.41	0/2858	0.61	0/3881
3	B	0.40	0/2885	0.59	0/3918
All	All	0.39	0/11720	0.60	0/15971

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	C	1456	0	1366	32	1
1	K	1335	0	1230	35	1
2	D	1539	0	1411	38	0
2	L	1517	0	1404	50	0
3	A	2785	0	2653	49	1
3	B	2809	0	2681	50	1
4	E	39	0	34	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	28	0	25	2	0
6	A	48	0	0	2	0
6	B	46	0	0	0	0
6	C	32	0	0	0	0
6	D	24	0	0	0	0
6	K	27	0	0	0	0
6	L	32	0	0	1	0
All	All	11717	0	10804	238	2

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 11.

All (238) 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:L:150:LYS:HG2	2:L:151:VAL:H	1.41	0.85
2:L:149:TRP:CH2	2:L:180:LEU:HB3	2.12	0.85
3:A:203:ARG:HH21	3:B:203:ARG:NH2	1.73	0.85
1:C:126:PRO:HB3	1:C:214:VAL:HG22	1.58	0.83
3:B:21:PHE:HB3	3:B:58:MET:HE1	1.59	0.83
3:A:203:ARG:NH2	3:B:203:ARG:NH2	2.27	0.83
2:D:20:THR:HG22	2:D:74:THR:HG23	1.63	0.80
1:K:18:LEU:HD12	1:K:19:ARG:H	1.47	0.80
2:D:37:GLN:HB2	2:D:47:LEU:HD11	1.64	0.79
3:A:203:ARG:HH21	3:B:203:ARG:HH21	1.27	0.79
1:C:206:SER:OG	1:C:208:THR:OG1	2.02	0.77
1:C:110:LEU:HD23	1:C:152:PRO:HD3	1.69	0.73
2:L:61:ARG:NH2	2:L:82:ASP:OD1	2.22	0.72
2:D:156:GLN:HB3	2:D:159:ASN:HD21	1.55	0.71
2:L:150:LYS:HD3	2:L:156:GLN:OE1	1.89	0.71
2:D:61:ARG:NH1	2:D:82:ASP:OD1	2.25	0.70
2:D:4:MET:HE1	2:D:25:ALA:HB2	1.73	0.69
2:D:133:VAL:HG13	2:D:180:LEU:HB3	1.76	0.68
1:K:124:VAL:HG21	1:K:201:VAL:HG21	1.76	0.67
2:L:61:ARG:HH21	2:L:82:ASP:CG	2.02	0.66
2:L:171:ASP:HB3	2:L:173:THR:HG22	1.77	0.66
3:A:203:ARG:NH2	3:B:203:ARG:CZ	2.58	0.65
3:B:99:ILE:HG12	3:B:136:MET:HE2	1.78	0.65
2:D:193:TYR:HB2	2:D:210:PHE:CE1	2.32	0.63
2:L:150:LYS:HD2	2:L:152:ASP:O	1.99	0.63
1:K:4:LEU:HD11	1:K:104:VAL:HG23	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:112:ALA:O	2:L:199:HIS:NE2	2.32	0.63
1:C:13:GLN:CD	1:C:13:GLN:H	2.06	0.63
3:B:191:TRP:CD1	3:B:192:ARG:HD3	2.34	0.63
2:L:202:LEU:HD12	2:L:202:LEU:O	1.99	0.62
2:D:167:GLN:HG3	2:D:174:TYR:CE1	2.34	0.62
1:K:18:LEU:HD12	1:K:19:ARG:N	2.14	0.62
2:L:125:GLN:O	2:L:128:SER:OG	2.13	0.62
1:K:203:HIS:ND1	1:K:206:SER:HB3	2.15	0.61
2:L:149:TRP:HH2	2:L:180:LEU:HB3	1.66	0.60
3:B:107:ARG:NH1	3:B:143:GLU:OE1	2.34	0.60
2:D:120:PRO:HB3	2:D:210:PHE:CE2	2.37	0.60
1:C:67:ARG:NH2	1:C:90:ASP:OD2	2.34	0.60
3:A:41:SER:HB2	4:E:1:NAG:H61	1.84	0.59
2:D:106:ILE:H	2:D:167:GLN:HE22	1.48	0.59
2:D:193:TYR:HB2	2:D:210:PHE:HE1	1.67	0.58
3:A:310:GLN:HG3	6:A:423:HOH:O	2.04	0.58
3:A:186:ASP:OD1	3:A:242:ARG:NH1	2.31	0.58
2:L:39:LYS:HE2	2:L:81:GLU:O	2.04	0.58
2:L:141:TYR:CD1	2:L:142:PRO:HA	2.39	0.57
2:D:137:LEU:HB2	2:D:176:LEU:HB3	1.86	0.57
2:D:6:GLN:HE22	2:D:87:TYR:HA	1.68	0.57
2:D:164:VAL:HG22	2:D:176:LEU:HD23	1.87	0.57
1:C:203:HIS:ND1	1:C:206:SER:HB3	2.21	0.56
3:A:123:ARG:HG2	3:A:166:SER:HB3	1.88	0.56
2:D:164:VAL:HG22	2:D:176:LEU:CD2	2.35	0.56
1:K:120:LYS:HD3	1:K:121:GLY:O	2.06	0.55
2:L:89:GLN:HB2	2:L:98:PHE:CD1	2.41	0.55
1:K:122:PRO:HB3	1:K:148:TYR:HB3	1.89	0.55
3:A:27:ARG:NH1	6:A:401:HOH:O	2.35	0.55
3:A:36:SER:HB2	3:A:37:PHE:CD1	2.42	0.55
2:L:19:VAL:HG12	2:L:75:ILE:HB	1.88	0.55
1:C:2:VAL:HG11	1:C:104:VAL:HG11	1.89	0.55
2:L:124:GLU:CD	2:L:124:GLU:H	2.15	0.55
2:D:195:CYS:O	2:D:207:THR:HA	2.06	0.55
3:B:239:THR:O	3:B:275:TYR:HB2	2.07	0.55
2:D:119:PHE:HB2	2:D:134:VAL:HG23	1.89	0.54
2:L:107:LYS:HA	2:L:141:TYR:OH	2.07	0.54
1:C:128:ALA:HB3	2:D:120:PRO:HG2	1.88	0.54
1:C:42:GLY:O	1:C:43:LYS:HD3	2.08	0.54
1:C:122:PRO:HB3	1:C:148:TYR:HB3	1.90	0.54
3:B:139:GLU:O	3:B:139:GLU:HG3	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:150:LYS:HG2	2:L:151:VAL:N	2.19	0.53
2:L:151:VAL:HG21	2:L:193:TYR:CD2	2.43	0.53
1:C:51:ILE:HG13	1:C:58:THR:HG22	1.89	0.53
2:L:81:GLU:OE1	2:L:81:GLU:N	2.30	0.53
5:F:1:NAG:H83	5:F:1:NAG:H3	1.90	0.53
1:C:36:TRP:CD1	1:C:81:LEU:HD13	2.43	0.53
2:L:113:ALA:HA	2:L:199:HIS:CD2	2.44	0.53
2:L:158:GLY:O	2:L:180:LEU:HD11	2.09	0.53
2:L:35:TRP:CE2	2:L:73:LEU:HB2	2.44	0.52
2:D:35:TRP:CE2	2:D:73:LEU:HB2	2.43	0.52
3:B:95:ARG:NH1	3:B:135:GLU:OE2	2.36	0.52
2:L:151:VAL:HG22	2:L:193:TYR:HA	1.91	0.52
3:A:41:SER:HB2	4:E:1:NAG:C6	2.40	0.51
3:B:159:ALA:HA	3:B:182:ILE:HD11	1.91	0.51
3:A:288:HIS:HB2	3:A:297:TYR:CE2	2.46	0.51
3:B:137:LYS:O	3:B:141:ILE:HG13	2.10	0.51
1:C:173:LEU:HD13	1:C:179:TYR:CE1	2.45	0.51
3:B:47:THR:HB	3:B:52:ASP:HB2	1.93	0.51
1:C:168:THR:HA	1:C:183:SER:HB2	1.92	0.51
1:K:124:VAL:HG22	1:K:145:VAL:HG13	1.92	0.51
1:K:125:PHE:CE2	2:L:125:GLN:HG3	2.46	0.50
1:K:2:VAL:HG13	1:K:27:PHE:CD1	2.47	0.50
2:L:162:GLU:OE1	2:L:176:LEU:HD11	2.11	0.50
3:B:260:PRO:HB2	3:B:270:ALA:HB1	1.93	0.50
3:B:31:THR:OG1	3:B:32:HIS:ND1	2.43	0.50
3:B:36:SER:HB2	3:B:37:PHE:CD2	2.47	0.50
1:K:2:VAL:HG13	1:K:27:PHE:HD1	1.77	0.50
2:D:106:ILE:N	2:D:167:GLN:HE22	2.10	0.49
3:A:1:TYR:CZ	3:A:321:LYS:HG2	2.47	0.49
2:L:6:GLN:O	2:L:100:GLN:NE2	2.45	0.49
2:L:114:PRO:HD3	2:L:199:HIS:CD2	2.46	0.49
3:A:15:GLU:OE2	3:A:265:ARG:NH1	2.45	0.49
3:B:98:PHE:O	3:B:101:SER:OG	2.29	0.49
3:A:28:PHE:O	3:A:356:LYS:NZ	2.44	0.49
2:L:142:PRO:HD2	2:L:199:HIS:CE1	2.47	0.49
2:L:151:VAL:CG2	2:L:193:TYR:HA	2.43	0.49
3:B:40:ILE:O	3:B:84:ARG:NH2	2.46	0.49
2:D:194:ALA:HB1	2:D:207:THR:CG2	2.42	0.49
3:A:211:ASP:OD2	3:A:214:SER:OG	2.31	0.49
1:C:153:VAL:CG2	1:C:203:HIS:HD2	2.25	0.48
2:L:190:HIS:HB3	6:L:301:HOH:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:32:HIS:HA	3:B:70:LYS:O	2.13	0.48
2:D:32:TRP:HE1	3:A:12:GLN:HG3	1.77	0.48
2:L:202:LEU:HB2	2:L:204:SER:O	2.13	0.48
3:A:174:SER:O	3:A:232:LYS:NZ	2.44	0.48
3:B:130:THR:HG22	3:B:173:ILE:HG23	1.96	0.48
3:A:203:ARG:CZ	3:B:203:ARG:NH2	2.77	0.48
1:K:39:GLN:HG3	1:K:44:GLY:O	2.14	0.48
1:K:153:VAL:CG2	1:K:181:LEU:HD21	2.44	0.48
2:L:33:LEU:HG	2:L:34:ASN:N	2.28	0.48
2:D:133:VAL:CG1	2:D:180:LEU:HB3	2.43	0.47
3:B:36:SER:HA	3:B:37:PHE:HA	1.65	0.47
2:L:114:PRO:HD3	2:L:199:HIS:CG	2.50	0.47
2:L:149:TRP:O	2:L:156:GLN:NE2	2.48	0.47
2:D:6:GLN:HE21	2:D:99:GLY:HA3	1.79	0.47
3:A:26:ASP:HB3	3:A:29:LEU:HB2	1.96	0.47
3:A:74:SER:HA	3:A:115:ASP:O	2.15	0.47
3:B:36:SER:HB2	3:B:37:PHE:CG	2.49	0.47
2:L:4:MET:HE1	2:L:25:ALA:HB2	1.95	0.47
3:B:84:ARG:NH2	5:F:1:NAG:H62	2.30	0.47
1:K:153:VAL:HG23	1:K:181:LEU:HD21	1.96	0.47
3:A:20:CYS:HB2	3:A:338:PHE:CZ	2.49	0.47
3:A:23:ASP:HB3	3:A:58:MET:HE2	1.96	0.47
3:A:182:ILE:HG13	3:A:184:THR:HG23	1.96	0.47
3:B:29:LEU:HD21	3:B:352:THR:HB	1.96	0.47
3:B:189:GLY:C	3:B:244:PHE:HE1	2.22	0.47
3:B:224:LEU:HD23	3:B:228:ALA:O	2.15	0.47
2:D:6:GLN:NE2	2:D:88:CYS:H	2.12	0.47
3:A:15:GLU:HG2	3:A:16:GLY:N	2.28	0.47
1:K:8:GLY:O	1:K:18:LEU:HD11	2.15	0.47
2:L:24:ARG:HG3	2:L:70:ASP:OD1	2.15	0.47
1:K:68:PHE:CE2	1:K:83:MET:HG2	2.50	0.47
1:C:150:PRO:C	1:C:152:PRO:HD2	2.40	0.47
3:A:45:ILE:HG22	3:A:101:SER:OG	2.16	0.46
3:B:92:THR:O	3:B:96:ARG:HG3	2.14	0.46
3:B:95:ARG:O	3:B:99:ILE:HG13	2.14	0.46
1:K:83:MET:HB3	1:K:86:LEU:HD21	1.98	0.46
3:A:1:TYR:OH	3:A:321:LYS:HG2	2.15	0.46
1:K:83:MET:HE2	1:K:86:LEU:HD21	1.98	0.46
3:B:27:ARG:HB3	3:B:62:LEU:HB3	1.97	0.46
1:C:142:GLY:HA2	1:C:157:TRP:CH2	2.50	0.46
1:C:157:TRP:CZ3	1:C:199:CYS:HB3	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:157:LEU:HB3	3:A:168:TYR:CE2	2.52	0.45
2:D:119:PHE:HB2	2:D:134:VAL:CG2	2.47	0.45
3:B:202:PHE:O	3:B:293:GLN:HG2	2.17	0.45
3:A:203:ARG:NH1	3:A:204:GLY:O	2.40	0.45
3:B:22:PRO:HD2	3:B:58:MET:HE2	1.98	0.45
3:B:26:ASP:OD2	3:B:29:LEU:HB2	2.17	0.45
1:K:20:LEU:N	1:K:81:LEU:O	2.46	0.45
1:K:36:TRP:CE2	1:K:81:LEU:HB2	2.52	0.45
2:L:160:SER:OG	2:L:180:LEU:HD13	2.17	0.45
1:C:153:VAL:HG22	1:C:203:HIS:HD2	1.82	0.45
2:L:167:GLN:HG3	2:L:174:TYR:CZ	2.51	0.45
3:B:108:THR:OG1	1:K:31:ASN:OD1	2.29	0.45
1:K:203:HIS:O	1:K:206:SER:OG	2.31	0.45
1:K:65:LYS:HD3	1:K:65:LYS:C	2.42	0.44
3:A:159:ALA:HA	3:A:182:ILE:HD11	1.99	0.44
2:L:202:LEU:HD12	2:L:202:LEU:C	2.42	0.44
3:A:59:LEU:HD12	3:A:62:LEU:HD12	1.98	0.44
3:B:119:LEU:HA	3:B:120:TYR:CD1	2.53	0.44
3:A:211:ASP:CG	3:A:214:SER:HG	2.26	0.44
2:L:4:MET:HA	2:L:4:MET:HE3	1.98	0.44
1:C:169:PHE:CZ	2:D:177:SER:HB3	2.53	0.44
3:A:194:THR:HG23	3:A:254:GLY:HA2	1.99	0.44
3:B:107:ARG:HH12	3:B:143:GLU:CD	2.25	0.44
1:K:203:HIS:HB3	1:K:206:SER:OG	2.17	0.44
2:L:4:MET:HE2	2:L:23:CYS:SG	2.57	0.44
3:B:343:CYS:O	3:B:345:GLN:NE2	2.50	0.44
1:C:4:LEU:HD22	1:C:22:CYS:SG	2.58	0.43
3:A:36:SER:HA	3:A:37:PHE:HA	1.59	0.43
2:D:47:LEU:HA	2:D:58:VAL:HG21	1.99	0.43
3:A:36:SER:HB2	3:A:37:PHE:CE1	2.52	0.43
1:K:208:THR:HG22	1:K:210:VAL:HG23	1.99	0.43
2:L:124:GLU:OE2	2:L:124:GLU:N	2.46	0.43
2:L:149:TRP:O	2:L:150:LYS:HB2	2.19	0.43
2:D:121:PRO:HG2	2:D:131:ALA:HB1	2.01	0.43
2:D:149:TRP:CD2	2:D:180:LEU:HD22	2.54	0.43
2:D:32:TRP:CE3	2:D:32:TRP:HA	2.53	0.43
1:K:143:CYS:N	1:K:183:SER:O	2.51	0.43
1:C:36:TRP:CE2	1:C:81:LEU:HB2	2.54	0.43
1:C:86:LEU:HD23	1:C:86:LEU:HA	1.84	0.42
2:D:135:CYS:HB2	2:D:149:TRP:CH2	2.53	0.42
3:A:21:PHE:HB3	3:A:58:MET:HE1	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:152:PRO:O	1:K:203:HIS:HD2	2.02	0.42
1:C:12:VAL:HG11	1:C:86:LEU:HD13	2.00	0.42
3:A:12:GLN:HG2	3:A:13:TYR:CD2	2.55	0.42
3:B:46:ASP:OD2	1:K:54:SER:OG	2.34	0.42
2:L:121:PRO:HG3	2:L:133:VAL:HG23	2.01	0.42
1:C:163:THR:O	1:C:166:VAL:HG23	2.19	0.42
2:L:19:VAL:CG1	2:L:75:ILE:HB	2.50	0.42
1:C:127:LEU:N	1:C:142:GLY:O	2.53	0.42
2:D:15:VAL:HG22	2:D:80:PRO:HD3	2.02	0.42
1:K:83:MET:HE2	1:K:86:LEU:CD2	2.50	0.42
2:L:39:LYS:NZ	2:L:83:PHE:O	2.45	0.42
1:C:6:GLU:HA	1:C:21:SER:O	2.20	0.42
2:D:167:GLN:HG3	2:D:174:TYR:CZ	2.55	0.42
3:A:170:ILE:HD13	3:A:170:ILE:HA	1.86	0.42
1:K:184:VAL:HG21	2:L:136:LEU:HD22	2.02	0.41
3:B:290:ILE:HG21	3:B:293:GLN:OE1	2.20	0.41
1:K:126:PRO:HD2	2:L:122:SER:OG	2.20	0.41
3:A:191:TRP:CE3	3:A:192:ARG:HG2	2.55	0.41
3:A:201:LEU:HD13	3:A:316:LYS:HG2	2.02	0.41
1:K:81:LEU:HD12	1:K:81:LEU:HA	1.90	0.41
3:B:69:LEU:HD12	3:B:70:LYS:N	2.34	0.41
1:K:19:ARG:HG2	1:K:82:GLN:HG3	2.02	0.41
3:A:203:ARG:NH2	3:B:203:ARG:NE	2.68	0.41
3:B:127:GLN:HA	3:B:130:THR:OG1	2.20	0.41
3:B:307:TYR:HE2	3:B:309:ASP:HB3	1.85	0.41
1:K:122:PRO:HB2	1:K:145:VAL:HG12	2.01	0.41
3:A:4:VAL:O	3:A:329:MET:HA	2.20	0.41
3:A:331:TRP:HA	3:A:332:ALA:HA	1.86	0.41
3:A:351:LEU:O	3:A:355:ILE:HG13	2.21	0.41
3:B:182:ILE:HD13	3:B:223:MET:SD	2.61	0.41
3:B:245:THR:O	3:B:258:SER:N	2.52	0.41
1:C:125:PHE:CG	2:D:125:GLN:HB2	2.56	0.41
2:D:33:LEU:HG	2:D:34:ASN:N	2.33	0.41
3:A:12:GLN:NE2	3:A:55:LEU:HD22	2.36	0.41
3:B:130:THR:HG22	3:B:173:ILE:CG2	2.51	0.41
3:B:359:LEU:HD23	3:B:359:LEU:HA	1.92	0.41
3:A:107:ARG:HH21	3:A:143:GLU:CD	2.29	0.41
1:C:105:TRP:CE3	2:D:44:PRO:HD2	2.57	0.40
2:D:33:LEU:HD22	2:D:71:PHE:CB	2.51	0.40
3:B:1:TYR:CZ	3:B:321:LYS:HG2	2.55	0.40
3:B:161:LYS:HE2	3:B:222:TYR:CZ	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:38:ARG:HA	1:K:93:VAL:O	2.21	0.40
1:C:38:ARG:HG2	1:C:46:GLU:HB2	2.03	0.40
1:C:99:VAL:HG23	3:A:50:TRP:NE1	2.36	0.40
3:A:242:ARG:HA	3:A:271:GLY:O	2.21	0.40
1:C:151:GLU:N	1:C:152:PRO:HD2	2.37	0.40
3:A:291:LEU:HD12	3:A:291:LEU:HA	1.83	0.40
2:L:34:ASN:HD21	2:L:91:SER:HB3	1.86	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:190:SER:OG	3:A:360:ALA:O[3_655]	1.85	0.35
3:B:192:ARG:NH2	1:K:117:SER:O[3_755]	2.11	0.09

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	C	198/222 (89%)	193 (98%)	5 (2%)	0	100	100
1	K	181/222 (82%)	173 (96%)	8 (4%)	0	100	100
2	D	209/215 (97%)	201 (96%)	8 (4%)	0	100	100
2	L	206/215 (96%)	194 (94%)	12 (6%)	0	100	100
3	A	359/362 (99%)	351 (98%)	8 (2%)	0	100	100
3	B	359/362 (99%)	349 (97%)	10 (3%)	0	100	100
All	All	1512/1598 (95%)	1461 (97%)	51 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	C	154/182 (85%)	154 (100%)	0	100	100
1	K	134/182 (74%)	134 (100%)	0	100	100
2	D	165/189 (87%)	164 (99%)	1 (1%)	78	91
2	L	161/189 (85%)	161 (100%)	0	100	100
3	A	284/302 (94%)	284 (100%)	0	100	100
3	B	289/302 (96%)	289 (100%)	0	100	100
All	All	1187/1346 (88%)	1186 (100%)	1 (0%)	88	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	177	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	6	GLN
2	D	79	GLN
2	D	125	GLN
2	D	148	GLN
3	A	176	HIS
1	K	84	ASN
1	K	202	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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$
4	NAG	E	1	3,4	14,14,15	0.56	0	17,19,21	1.23	2 (11%)
4	NAG	E	2	4	14,14,15	0.73	1 (7%)	17,19,21	1.60	2 (11%)
4	BMA	E	3	4	11,11,12	0.44	0	15,15,17	1.20	1 (6%)
5	NAG	F	1	3,5	14,14,15	0.33	0	17,19,21	1.61	2 (11%)
5	NAG	F	2	5	14,14,15	1.30	1 (7%)	17,19,21	0.82	1 (5%)

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

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	2	NAG	O5-C1	-4.46	1.36	1.43
4	E	2	NAG	O4-C4	-2.09	1.37	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	2	NAG	O4-C4-C5	5.73	123.43	109.32
5	F	1	NAG	C2-N2-C7	4.69	129.18	122.90
5	F	1	NAG	C1-C2-N2	3.33	115.68	110.43
4	E	1	NAG	C1-O5-C5	3.07	116.30	112.19
4	E	3	BMA	C1-O5-C5	2.60	115.67	112.19
5	F	2	NAG	C1-O5-C5	2.18	115.11	112.19
4	E	2	NAG	C1-O5-C5	2.15	115.07	112.19
4	E	1	NAG	O3-C3-C2	-2.01	105.23	109.40

There are no chirality outliers.

All (12) torsion outliers are listed below:

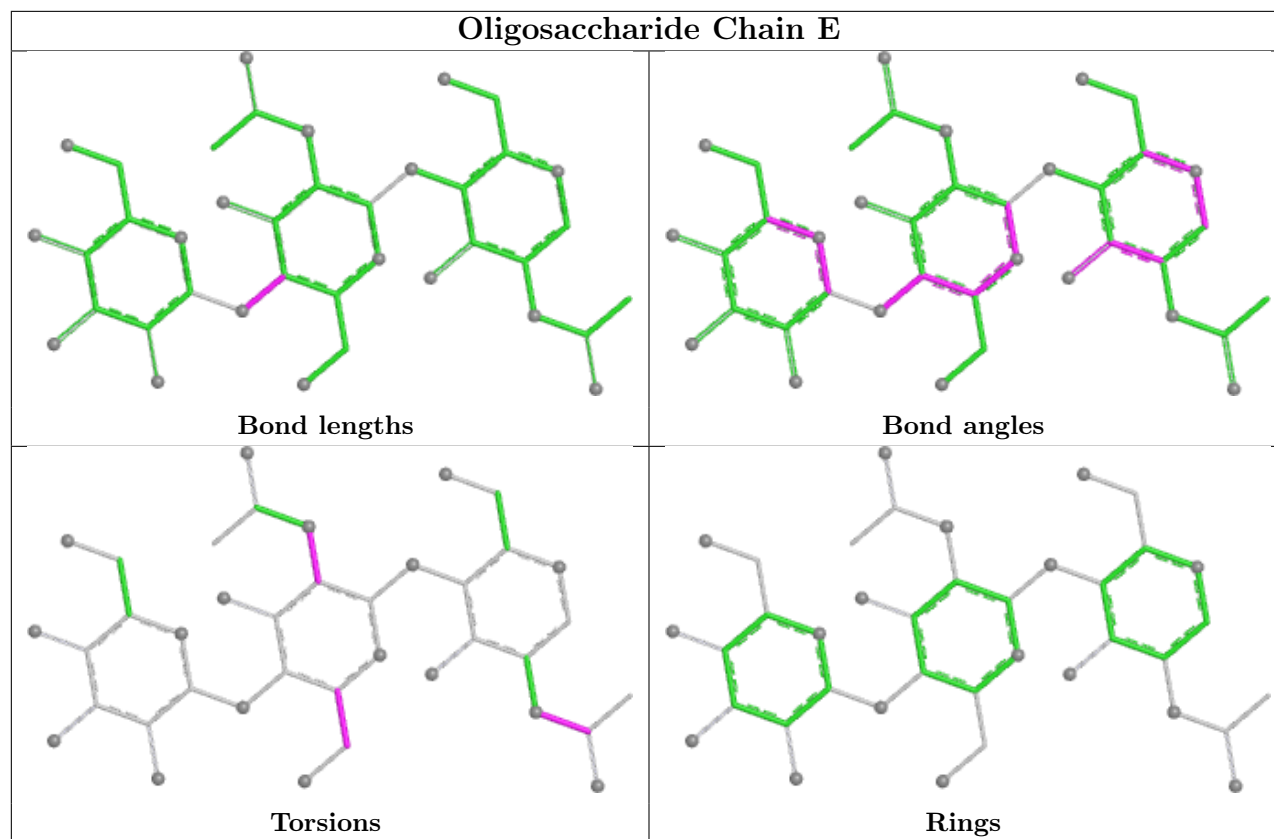
Mol	Chain	Res	Type	Atoms
4	E	2	NAG	O5-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6
4	E	1	NAG	C8-C7-N2-C2
4	E	1	NAG	O7-C7-N2-C2
5	F	1	NAG	C8-C7-N2-C2
5	F	1	NAG	O7-C7-N2-C2
5	F	2	NAG	O5-C5-C6-O6
4	E	2	NAG	C3-C2-N2-C7
5	F	1	NAG	C3-C2-N2-C7
5	F	2	NAG	C3-C2-N2-C7
5	F	2	NAG	C4-C5-C6-O6
5	F	2	NAG	C1-C2-N2-C7

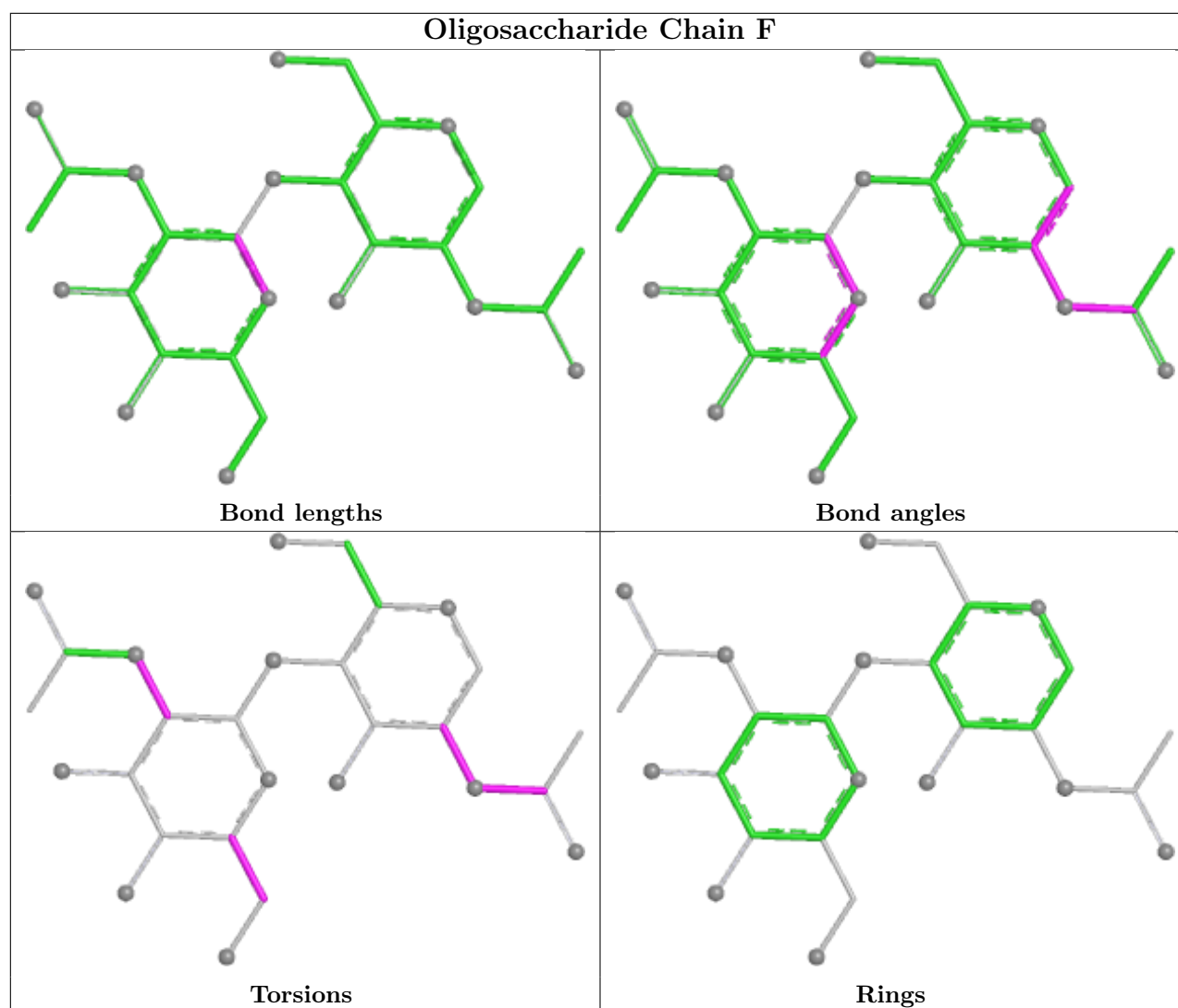
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1	NAG	2	0
5	F	1	NAG	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, 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	C	204/222 (91%)	0.31	12 (5%)	28 25	44, 63, 119, 163	0
1	K	188/222 (84%)	0.31	12 (6%)	25 22	43, 61, 109, 144	0
2	D	211/215 (98%)	0.25	11 (5%)	33 29	43, 61, 115, 125	0
2	L	208/215 (96%)	0.74	36 (17%)	4 3	42, 71, 123, 143	0
3	A	361/362 (99%)	-0.22	2 (0%)	85 85	37, 52, 76, 109	0
3	B	361/362 (99%)	-0.07	2 (0%)	85 85	41, 56, 79, 161	0
All	All	1533/1598 (95%)	0.15	75 (4%)	35 31	37, 57, 114, 163	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	195	CYS	5.0
1	K	198	ILE	4.5
1	K	128	ALA	4.3
2	L	147	VAL	4.2
1	C	193	GLY	4.1
2	L	206	VAL	3.9
2	L	136	LEU	3.9
2	L	202	LEU	3.9
2	L	159	ASN	3.9
3	A	191	TRP	3.8
1	C	130	SER	3.8
2	L	208	LYS	3.8
2	L	192	VAL	3.6
1	K	215	GLU	3.5
1	C	192	LEU	3.4
2	L	116	VAL	3.3
1	C	197	TYR	3.2
2	L	149	TRP	3.1
2	D	183	SER	3.1

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Mol	Chain	Res	Type	RSRZ
2	L	200	GLN	3.1
2	L	137	LEU	3.0
2	L	151	VAL	3.0
2	L	150	LYS	2.9
2	L	141	TYR	2.9
2	L	205	PRO	2.8
2	L	207	THR	2.8
2	D	211	ASN	2.7
1	K	125	PHE	2.7
1	K	123	SER	2.7
2	L	131	ALA	2.7
1	C	117	SER	2.7
2	L	134	VAL	2.7
2	L	185	ALA	2.7
1	K	168	THR	2.7
2	L	187	TYR	2.6
1	K	142	GLY	2.6
2	D	131	ALA	2.6
2	L	111	VAL	2.6
2	L	188	GLU	2.6
2	L	108	ALA	2.6
2	L	194	ALA	2.5
2	L	160	SER	2.5
2	D	194	ALA	2.5
1	K	182	SER	2.4
2	D	192	VAL	2.4
1	C	127	LEU	2.4
2	D	133	VAL	2.4
1	C	141	LEU	2.3
2	D	130	THR	2.3
1	C	129	PRO	2.3
3	B	146	PRO	2.3
1	C	138	THR	2.3
2	L	138	ASN	2.3
2	L	119	PHE	2.3
2	L	179	THR	2.2
2	L	118	ILE	2.2
2	D	161	GLN	2.2
2	L	203	SER	2.2
2	D	188	GLU	2.2
2	L	117	PHE	2.2
2	L	193	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	175	SER	2.2
1	K	126	PRO	2.1
3	B	361	ALA	2.1
2	D	126	LEU	2.1
1	K	153	VAL	2.1
2	L	144	GLU	2.1
3	A	146	PRO	2.1
1	K	162	LEU	2.1
1	K	185	VAL	2.1
1	C	212	LYS	2.1
1	C	214	VAL	2.1
2	L	155	LEU	2.0
2	D	210	PHE	2.0
2	L	180	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

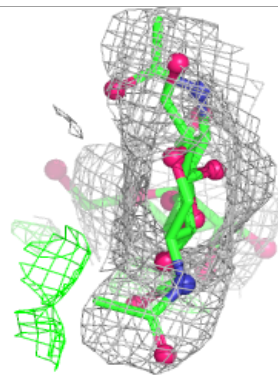
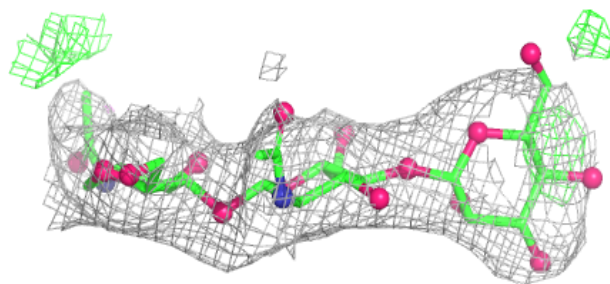
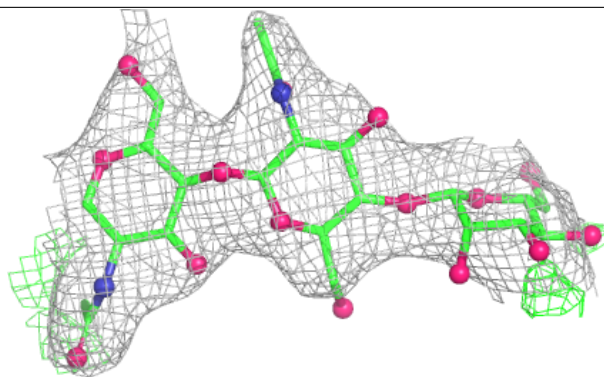
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

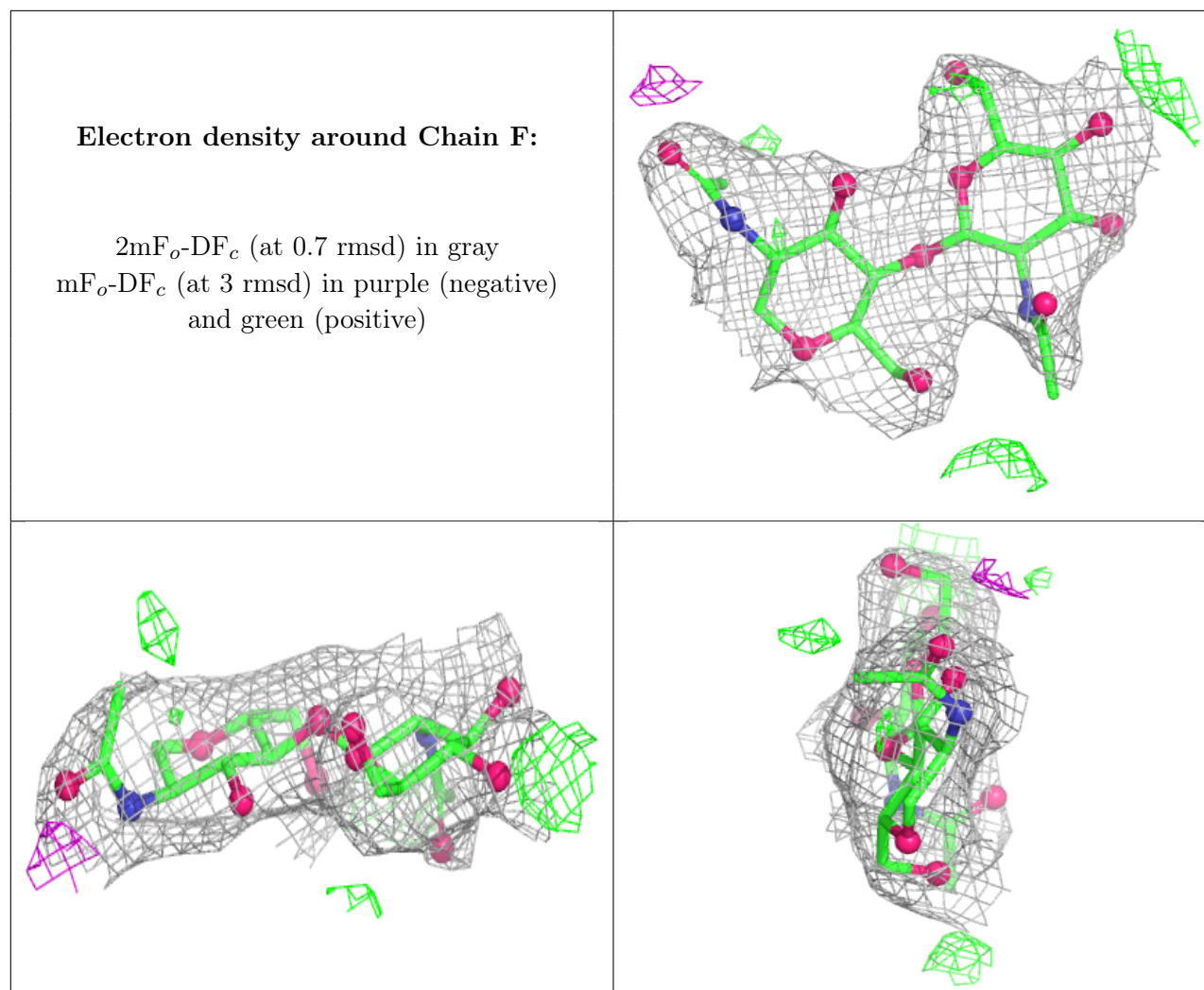
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	E	1	14/15	-	-	51,57,64,65	0
4	NAG	E	2	14/15	-	-	67,82,85,88	0
4	BMA	E	3	11/12	-	-	91,101,109,114	0
5	NAG	F	1	14/15	-	-	56,64,69,69	0
5	NAG	F	2	14/15	-	-	68,77,84,84	0

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)





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.