



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 03:04 AM UTC

PDB ID : 1FUJ / pdb_00001fuj
Title : PR3 (MYELOBLASTIN)
Authors : Fujinaga, M.; Chernaia, M.M.; Halenbeck, R.; Koths, K.; James, M.N.G.
Deposited on : 1996-01-25
Resolution : 2.20 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

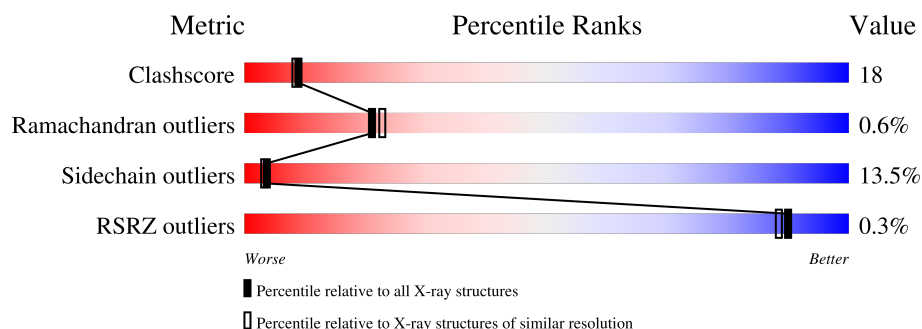
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	A	221	
1	B	221	
1	C	221	
1	D	221	
2	E	2	
2	F	2	
2	G	2	

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Mol	Chain	Length	Quality of chain
2	H	2	 50%50%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7174 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 PR3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1708	1083	311	303	11			
1	B	221	Total	C	N	O	S	0	0	0
			1708	1083	311	303	11			
1	C	221	Total	C	N	O	S	0	0	0
			1708	1083	311	303	11			
1	D	221	Total	C	N	O	S	0	0	0
			1708	1083	311	303	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	ILE	VAL	conflict	UNP P24158
B	103	ILE	VAL	conflict	UNP P24158
C	103	ILE	VAL	conflict	UNP P24158
D	103	ILE	VAL	conflict	UNP P24158

- Molecule 2 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			24	14	1	9			
2	F	2	Total	C	N	O	0	0	0
			24	14	1	9			
2	G	2	Total	C	N	O	0	0	0
			24	14	1	9			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	H	2	Total	C	N	O	0	0	0
			24	14	1	9			

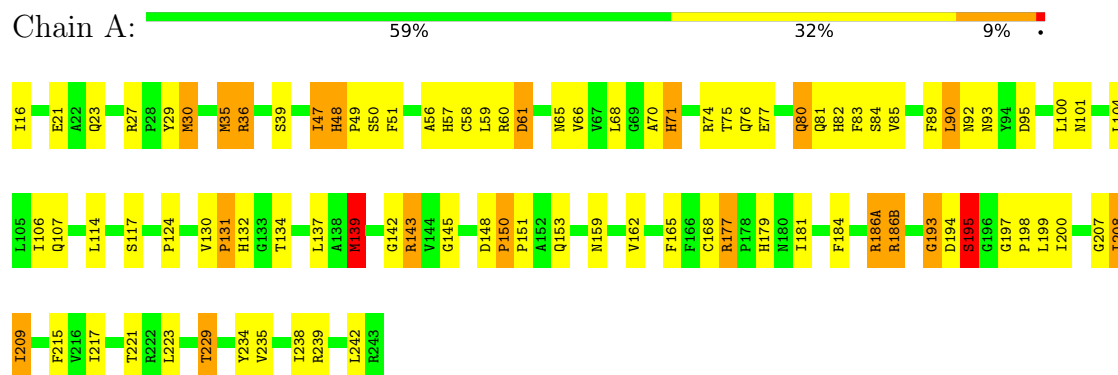
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	74	Total	O	0	0
			74	74		
3	B	48	Total	O	0	0
			48	48		
3	C	67	Total	O	0	0
			67	67		
3	D	57	Total	O	0	0
			57	57		

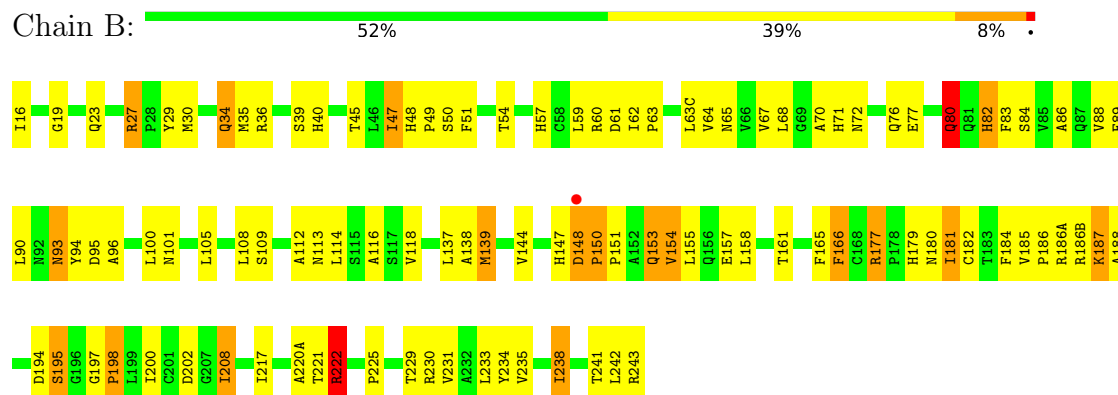
3 Residue-property plots

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.

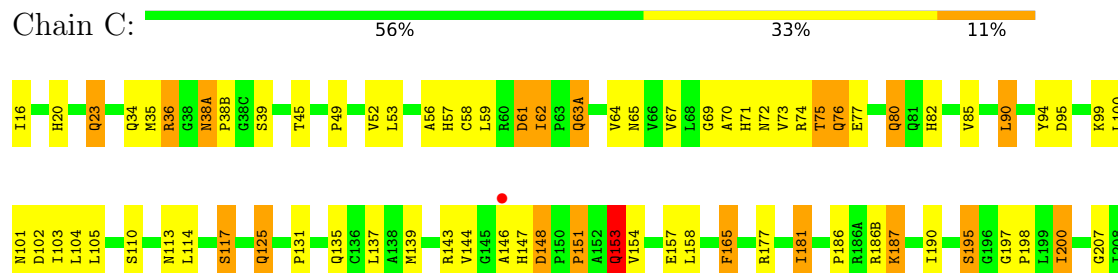
• Molecule 1: PR3



• Molecule 1: PR3



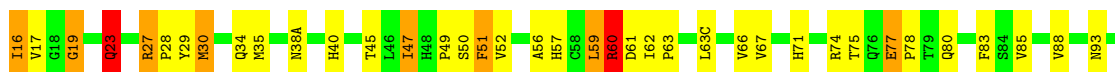
• Molecule 1: PR3





- Molecule 1: PR3

Chain D: 55% 35% 9%



- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 50% 50%



- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 50% 50%



- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 50% 50%



- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H: 50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.60Å 54.07Å 113.51Å 90.00° 90.69° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20 10.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	93.4 (10.00-2.20) 93.4 (10.00-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 1.98Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	(Not available) , (Not available) 0.179 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.716	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 99.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.043 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7174	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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: FUC, 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	A	1.30	9/1754 (0.5%)	1.40	18/2393 (0.8%)
1	B	1.22	4/1754 (0.2%)	1.43	19/2393 (0.8%)
1	C	1.21	4/1754 (0.2%)	1.36	20/2393 (0.8%)
1	D	1.23	5/1754 (0.3%)	1.41	22/2393 (0.9%)
All	All	1.24	22/7016 (0.3%)	1.40	79/9572 (0.8%)

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	139	MET	SD-CE	-9.82	1.54	1.79
1	B	238	ILE	CA-CB	-8.53	1.44	1.54
1	D	30	MET	SD-CE	-8.44	1.58	1.79
1	A	200	ILE	CA-CB	8.04	1.63	1.54
1	D	238	ILE	CA-CB	-8.01	1.44	1.54
1	A	209	ILE	CA-CB	7.11	1.62	1.54
1	A	130	VAL	CA-CB	6.61	1.62	1.54
1	B	54	THR	CA-CB	6.52	1.64	1.53
1	D	110	SER	CA-C	6.36	1.58	1.52
1	C	209	ILE	CA-CB	6.16	1.60	1.53
1	A	184	PHE	CA-C	-6.03	1.44	1.52
1	B	154	VAL	CA-CB	-5.96	1.47	1.54
1	A	66	VAL	CA-CB	-5.74	1.47	1.53
1	A	71	HIS	CA-CB	-5.62	1.44	1.53
1	C	139	MET	SD-CE	-5.56	1.65	1.79
1	A	162	VAL	CA-CB	-5.37	1.47	1.54
1	B	82	HIS	CA-C	-5.32	1.46	1.52
1	C	131	PRO	CA-C	-5.27	1.46	1.52
1	D	136	CYS	CA-C	-5.25	1.46	1.52
1	C	226	ASP	CA-C	-5.20	1.46	1.52
1	A	195	SER	CA-CB	5.10	1.61	1.53
1	D	38(A)	ASN	CA-C	-5.05	1.47	1.52

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	148	ASP	N-CA-C	-9.37	98.22	110.39
1	B	23	GLN	N-CA-C	-8.59	99.28	109.93
1	A	181	ILE	N-CA-C	-8.38	96.39	108.11
1	D	23	GLN	N-CA-C	-8.18	99.44	109.83
1	C	231	VAL	N-CA-C	8.10	119.85	110.62
1	C	226	ASP	N-CA-C	-8.08	97.16	110.17
1	D	226	ASP	N-CA-C	-7.99	97.25	109.95
1	B	186(A)	ARG	N-CA-C	7.57	123.47	111.81
1	C	181	ILE	N-CA-C	-7.41	97.74	108.11
1	B	165	PHE	N-CA-C	7.35	120.98	109.96
1	B	235	VAL	N-CA-C	7.23	117.36	110.42
1	C	63(A)	GLN	N-CA-C	7.14	121.09	112.38
1	A	153	GLN	N-CA-C	-7.11	102.73	111.40
1	A	80	GLN	N-CA-C	7.03	119.80	110.53
1	A	150	PRO	N-CA-C	6.95	119.18	110.70
1	B	47	ILE	N-CA-C	-6.93	106.38	113.10
1	D	215	PHE	N-CA-C	6.90	119.04	108.42
1	A	186(B)	ARG	N-CA-C	6.88	119.86	109.95
1	D	148	ASP	O-C-N	6.87	127.50	121.39
1	B	138	ALA	N-CA-C	-6.87	98.73	109.72
1	A	186(A)	ARG	N-CA-C	6.83	120.06	111.24
1	A	70	ALA	N-CA-C	6.82	120.61	110.52
1	B	150	PRO	CA-C-N	6.76	128.29	119.84
1	B	150	PRO	C-N-CA	6.76	128.29	119.84
1	B	198	PRO	CB-CA-C	-6.75	100.42	111.56
1	D	85	VAL	N-CA-C	6.67	118.43	108.23
1	C	125	GLN	N-CA-C	-6.58	100.78	110.52
1	B	80	GLN	N-CA-C	6.55	119.98	110.28
1	C	23	GLN	N-CA-C	-6.55	101.52	109.83
1	D	159	ASN	OD1-CG-ND2	6.39	128.99	122.60
1	A	215	PHE	N-CA-C	6.23	118.33	108.79
1	A	23	GLN	N-CA-C	-6.14	101.91	109.65
1	D	229	THR	N-CA-C	-6.07	101.29	110.28
1	D	231	VAL	N-CA-C	6.07	117.54	110.62
1	C	70	ALA	N-CA-C	6.07	119.50	110.52
1	C	80	GLN	N-CA-C	6.04	119.03	109.96
1	A	84	SER	N-CA-C	-5.96	101.37	109.95
1	D	154	VAL	N-CA-C	5.81	118.30	109.12
1	D	67	VAL	CB-CA-C	-5.79	103.13	111.19
1	C	67	VAL	N-CA-C	5.79	117.09	108.23
1	D	181	ILE	N-CA-C	-5.76	100.04	108.11
1	D	186(B)	ARG	N-CA-C	5.75	117.70	109.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	221	THR	N-CA-C	-5.63	105.29	111.82
1	D	60	ARG	N-CA-C	-5.56	102.23	110.46
1	B	181	ILE	N-CA-C	-5.56	100.33	108.11
1	B	222	ARG	N-CA-C	-5.52	105.88	113.56
1	A	132	HIS	N-CA-C	-5.50	102.26	110.23
1	A	235	VAL	N-CA-C	5.49	116.12	110.36
1	D	77	GLU	CA-C-N	5.49	125.31	119.28
1	D	77	GLU	C-N-CA	5.49	125.31	119.28
1	C	229	THR	N-CA-C	-5.48	102.17	110.28
1	B	116	ALA	N-CA-C	-5.44	105.51	111.82
1	B	34	GLN	N-CA-C	5.42	116.88	109.18
1	D	145	GLY	N-CA-C	-5.40	100.38	113.18
1	B	231	VAL	N-CA-C	5.39	116.77	110.62
1	A	229	THR	N-CA-C	-5.39	102.30	110.28
1	D	200	ILE	N-CA-C	5.37	115.83	107.99
1	C	153	GLN	N-CA-C	-5.37	103.35	111.56
1	C	151	PRO	N-CA-C	-5.35	103.44	111.57
1	C	72	ASN	N-CA-C	-5.33	100.04	108.73
1	D	177	ARG	N-CA-C	-5.32	101.95	110.10
1	B	148	ASP	N-CA-C	-5.31	102.81	110.40
1	C	187	LYS	N-CA-C	-5.24	100.55	108.67
1	D	19	GLY	N-CA-C	-5.21	103.38	112.55
1	D	50	SER	N-CA-C	5.20	119.72	113.17
1	A	199	LEU	N-CA-C	-5.17	98.83	107.99
1	B	153	GLN	N-CA-C	-5.16	103.67	111.56
1	B	177	ARG	CA-C-N	5.15	124.76	119.56
1	B	177	ARG	C-N-CA	5.15	124.76	119.56
1	C	113	ASN	N-CA-C	-5.14	100.13	108.41
1	C	62	ILE	N-CA-C	5.14	119.98	108.88
1	C	215	PHE	N-CA-C	5.12	116.59	108.96
1	A	61	ASP	N-CA-C	5.10	118.38	112.97
1	C	186	PRO	N-CA-C	5.10	122.04	113.78
1	D	51	PHE	N-CA-C	5.08	117.34	108.76
1	A	131	PRO	N-CA-C	5.05	118.99	111.41
1	D	146	ALA	N-CA-C	5.05	118.90	112.34
1	A	193	GLY	N-CA-C	-5.01	107.92	113.79
1	A	48	HIS	N-CA-C	-5.00	101.66	108.11

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	1708	0	1672	57	0
1	B	1708	0	1672	69	0
1	C	1708	0	1672	59	0
1	D	1708	0	1672	71	0
2	E	24	0	22	1	0
2	F	24	0	22	2	0
2	G	24	0	22	1	0
2	H	24	0	22	1	0
3	A	74	0	0	3	0
3	B	48	0	0	3	0
3	C	67	0	0	2	0
3	D	57	0	0	2	0
All	All	7174	0	6776	253	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 18.

All (253) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:49:PRO:HG3	1:D:114:LEU:HD11	1.46	0.98
1:C:59:LEU:HD22	1:C:62:ILE:HD11	1.51	0.92
1:D:63:PRO:HD2	1:D:63(C):LEU:HD12	1.53	0.91
1:B:230:ARG:HG2	1:B:233:LEU:HD13	1.56	0.86
1:D:123:LEU:HD23	1:D:209:ILE:HD11	1.60	0.83
1:B:77:GLU:HB2	1:B:80:GLN:HG3	1.63	0.81
1:C:95:ASP:HB3	1:C:100:LEU:HB2	1.62	0.81
1:A:143:ARG:HA	1:A:151:PRO:HA	1.63	0.79
1:A:30:MET:HG2	1:A:139:MET:HE3	1.70	0.74
1:A:90:LEU:HD22	1:A:104:LEU:HG	1.69	0.74
1:C:49:PRO:HG3	1:C:114:LEU:HD11	1.69	0.74
1:B:63:PRO:HB2	1:B:63(C):LEU:HD13	1.69	0.73
1:C:90:LEU:HG	1:C:104:LEU:HD12	1.70	0.72
1:D:77:GLU:HB2	1:D:80:GLN:NE2	2.05	0.71
1:D:105:LEU:HD23	1:D:241:THR:HG21	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:57:HIS:CE1	1:C:195:SER:HB3	2.26	0.70
1:B:166:PHE:HD2	1:C:165:PHE:HE1	1.39	0.70
1:D:101:ASN:H	1:D:179:HIS:HE1	1.40	0.70
1:B:222:ARG:HH11	1:B:222:ARG:HG2	1.57	0.69
1:A:198:PRO:HB3	1:A:209:ILE:HD12	1.73	0.69
1:A:29:TYR:CE1	1:A:139:MET:HE1	2.28	0.68
1:A:29:TYR:HE1	1:A:139:MET:HE1	1.58	0.67
1:C:65:ASN:HD21	1:C:82:HIS:HB3	1.58	0.67
1:D:49:PRO:HG3	1:D:114:LEU:CD1	2.23	0.67
1:B:86:ALA:HB2	1:B:109:SER:HA	1.76	0.66
1:B:184:PHE:CE2	1:B:186:PRO:HA	2.31	0.65
1:D:77:GLU:HB2	1:D:80:GLN:HE21	1.57	0.65
1:D:123:LEU:CD2	1:D:209:ILE:HD11	2.26	0.65
1:C:190:ILE:HD12	1:C:213:ASP:HB3	1.78	0.65
1:C:59:LEU:CD2	1:C:62:ILE:HD11	2.27	0.64
1:C:187:LYS:HG2	1:C:220(A):ALA:HB1	1.79	0.63
1:A:101:ASN:H	1:A:179:HIS:HE1	1.46	0.62
1:D:51:PHE:CE2	1:D:107:GLN:HG3	2.34	0.62
1:B:62:ILE:HD13	1:B:64:VAL:HG22	1.82	0.62
1:D:105:LEU:HD23	1:D:241:THR:CG2	2.29	0.62
1:B:49:PRO:HG3	1:B:114:LEU:HD11	1.81	0.62
1:D:77:GLU:HB2	1:D:80:GLN:HG3	1.82	0.62
1:A:137:LEU:HD12	1:A:159:ASN:HA	1.82	0.62
1:A:101:ASN:H	1:A:179:HIS:CE1	2.18	0.61
1:C:74:ARG:HD2	1:C:153:GLN:NE2	2.16	0.60
1:D:23:GLN:NE2	1:D:23:GLN:HA	2.16	0.60
1:B:65:ASN:HD21	1:B:82:HIS:HB3	1.65	0.60
1:D:144:VAL:HG13	1:D:152:ALA:HB2	1.82	0.60
1:D:101:ASN:H	1:D:179:HIS:CE1	2.19	0.60
1:C:53:LEU:HD23	1:C:209:ILE:HD13	1.84	0.59
1:B:230:ARG:CG	1:B:233:LEU:HD13	2.31	0.59
1:A:239:ARG:HD3	3:A:301:HOH:O	2.03	0.59
1:C:143:ARG:HA	1:C:151:PRO:HA	1.84	0.59
1:C:239:ARG:O	1:C:243:ARG:HD2	2.03	0.59
1:A:186(A):ARG:HG3	1:A:186(B):ARG:HD3	1.85	0.58
1:D:59:LEU:HD22	1:D:104:LEU:HD21	1.86	0.58
1:D:135:GLN:HE21	1:D:135:GLN:HA	1.67	0.58
1:A:48:HIS:HB3	1:A:51:PHE:HB2	1.84	0.58
1:D:52:VAL:HG21	1:D:66:VAL:HG11	1.84	0.58
1:D:238:ILE:O	1:D:242:LEU:HD13	2.04	0.58
1:D:144:VAL:CG1	1:D:152:ALA:HB2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ILE:N	1:A:194:ASP:OD2	2.37	0.58
1:C:62:ILE:HD13	1:C:64:VAL:CG2	2.34	0.57
1:C:63(A):GLN:NE2	1:C:85:VAL:HG12	2.19	0.57
1:C:95:ASP:CB	1:C:100:LEU:HB2	2.35	0.57
1:A:186(A):ARG:CG	1:A:186(B):ARG:HD3	2.34	0.57
1:D:23:GLN:HA	1:D:23:GLN:HE21	1.69	0.57
1:A:58:CYS:C	1:A:59:LEU:HD12	2.30	0.57
1:D:45:THR:OG1	1:D:198:PRO:HB3	2.04	0.57
1:C:75:THR:HG22	1:C:76:GLN:H	1.70	0.56
1:B:200:ILE:HD13	2:F:2:FUC:H62	1.87	0.56
1:C:77:GLU:HB2	1:C:80:GLN:HG3	1.88	0.56
1:C:59:LEU:HD22	1:C:62:ILE:CD1	2.31	0.56
1:D:19:GLY:HA2	1:D:158:LEU:HD13	1.86	0.56
1:B:63:PRO:HB2	1:B:63(C):LEU:CD1	2.36	0.56
1:D:47:ILE:HG12	1:D:123:LEU:HD21	1.87	0.56
1:A:51:PHE:CD2	1:A:242:LEU:HD22	2.42	0.55
1:B:16:ILE:N	1:B:194:ASP:OD2	2.40	0.55
1:D:71:HIS:CD2	1:D:154:VAL:HG22	2.41	0.55
1:A:234:TYR:O	1:A:238:ILE:HG13	2.05	0.55
1:D:28:PRO:HG2	1:D:119:ALA:HB3	1.89	0.55
1:B:93:ASN:OD1	1:B:93:ASN:N	2.40	0.55
1:C:207:GLY:H	2:G:2:FUC:HO4	1.54	0.54
1:C:187:LYS:HE3	1:C:220(A):ALA:O	2.06	0.54
1:B:197:GLY:HA3	3:B:247:HOH:O	2.08	0.54
1:C:232:ALA:HA	1:C:235:VAL:HG23	1.90	0.54
1:D:57:HIS:NE2	1:D:195:SER:HB3	2.22	0.54
1:A:124:PRO:HD3	1:A:209:ILE:O	2.07	0.54
1:B:27:ARG:HG2	1:B:139:MET:SD	2.48	0.54
1:C:58:CYS:C	1:C:59:LEU:HD23	2.33	0.54
1:A:197:GLY:HA3	3:A:248:HOH:O	2.09	0.53
1:B:95:ASP:HB3	1:B:100:LEU:HB2	1.88	0.53
1:D:77:GLU:CB	1:D:80:GLN:HG3	2.38	0.53
1:A:229:THR:HG23	3:A:258:HOH:O	2.09	0.53
1:C:38(A):ASN:HB3	1:C:39:SER:HB3	1.90	0.53
1:D:34:GLN:HG2	1:D:40:HIS:HA	1.89	0.53
1:A:57:HIS:CE1	1:A:195:SER:HB3	2.43	0.53
1:C:73:VAL:HG22	1:C:153:GLN:O	2.08	0.53
1:A:168:CYS:SG	1:A:177:ARG:N	2.81	0.53
1:D:187:LYS:HA	1:D:222:ARG:HD2	1.90	0.53
1:C:137:LEU:HD12	1:C:158:LEU:O	2.09	0.52
1:A:35:MET:HB2	1:A:39:SER:OG	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:TYR:CE2	1:B:96:ALA:HB2	2.44	0.52
1:D:60:ARG:O	1:D:62:ILE:HD12	2.09	0.52
1:C:36:ARG:HB3	1:C:36:ARG:HH11	1.73	0.52
1:C:210:GLN:NE2	3:C:306:HOH:O	2.40	0.52
1:A:47:ILE:HD12	1:A:242:LEU:HD11	1.92	0.52
1:D:16:ILE:HD13	1:D:194:ASP:OD2	2.09	0.52
1:D:19:GLY:CA	1:D:158:LEU:HD13	2.40	0.51
1:B:27:ARG:HD3	1:B:157:GLU:OE1	2.11	0.51
1:B:34:GLN:HG2	1:B:40:HIS:HA	1.93	0.51
1:B:200:ILE:HD12	1:B:200:ILE:O	2.11	0.51
1:D:59:LEU:HD22	1:D:104:LEU:CD2	2.41	0.51
1:A:85:VAL:HG13	1:A:106:ILE:HG23	1.91	0.51
1:D:234:TYR:O	1:D:238:ILE:HG13	2.11	0.51
1:A:186(A):ARG:HG3	1:A:186(B):ARG:N	2.25	0.51
1:B:45:THR:OG1	1:B:198:PRO:HG3	2.11	0.50
1:B:180:ASN:O	1:B:230:ARG:NH1	2.45	0.50
1:D:104:LEU:HD23	1:D:106:ILE:HG13	1.92	0.50
1:A:49:PRO:HG3	1:A:114:LEU:HD11	1.93	0.50
1:C:71:HIS:O	1:C:154:VAL:HA	2.12	0.50
1:C:186(B):ARG:HG2	1:C:186(B):ARG:HH11	1.77	0.50
1:D:59:LEU:CD2	1:D:88:VAL:HG11	2.41	0.50
1:D:57:HIS:CE1	1:D:195:SER:HB3	2.47	0.49
1:C:103:ILE:HD13	1:C:234:TYR:CD2	2.47	0.49
1:A:65:ASN:HD21	1:A:82:HIS:HB3	1.77	0.49
1:C:213:ASP:OD1	1:C:213:ASP:N	2.44	0.49
1:D:16:ILE:N	1:D:194:ASP:OD2	2.45	0.49
1:C:105:LEU:HD11	1:C:238:ILE:HG23	1.93	0.49
1:A:131:PRO:O	1:A:134:THR:HG23	2.13	0.49
1:B:144:VAL:CG2	1:B:148:ASP:HB3	2.42	0.49
1:A:36:ARG:HG2	1:A:65:ASN:HB2	1.94	0.49
1:B:182:CYS:HB3	1:B:225:PRO:HB2	1.94	0.49
1:B:200:ILE:CD1	2:F:2:FUC:H62	2.43	0.49
1:C:197:GLY:HA3	3:C:264:HOH:O	2.12	0.49
1:D:59:LEU:HD23	1:D:88:VAL:HG11	1.95	0.48
1:A:90:LEU:HD22	1:A:104:LEU:CG	2.40	0.48
1:B:36:ARG:NH1	1:B:84:SER:HB3	2.28	0.48
1:B:67:VAL:HG22	1:B:82:HIS:ND1	2.29	0.48
1:B:51:PHE:CD2	1:B:242:LEU:HD22	2.48	0.48
1:C:38(A):ASN:HB3	1:C:39:SER:CB	2.43	0.48
1:D:200:ILE:O	2:H:2:FUC:H4	2.13	0.48
1:B:48:HIS:HB3	1:B:51:PHE:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:ALA:HA	1:B:77:GLU:OE1	2.14	0.47
1:B:71:HIS:O	1:B:154:VAL:HA	2.14	0.47
1:B:89:PHE:HB2	1:B:105:LEU:HB2	1.96	0.47
1:D:56:ALA:HA	1:D:104:LEU:HD13	1.97	0.47
1:A:68:LEU:HD12	1:A:83:PHE:CE1	2.49	0.47
1:B:222:ARG:HG2	1:B:222:ARG:NH1	2.27	0.47
1:C:211:GLY:HA2	1:C:229:THR:O	2.14	0.47
1:D:19:GLY:HA2	1:D:158:LEU:CD1	2.44	0.47
1:A:21:GLU:OE2	1:A:71:HIS:NE2	2.40	0.47
1:B:83:PHE:CZ	1:B:112:ALA:HA	2.49	0.47
1:B:230:ARG:O	1:B:233:LEU:HB2	2.15	0.47
1:C:69:GLY:HA2	1:C:117:SER:O	2.14	0.47
1:B:59:LEU:HG	1:B:62:ILE:HD11	1.97	0.47
1:D:212:ILE:HD12	1:D:231:VAL:HG22	1.97	0.47
1:A:165:PHE:CZ	1:D:165:PHE:HB2	2.51	0.46
1:D:197:GLY:HA3	3:D:248:HOH:O	2.16	0.46
1:A:27:ARG:O	1:A:30:MET:HB2	2.14	0.46
1:A:51:PHE:CE1	1:A:107:GLN:HB2	2.50	0.46
1:A:57:HIS:NE2	1:A:195:SER:HB3	2.31	0.46
1:D:45:THR:HG22	1:D:47:ILE:CD1	2.46	0.46
1:A:77:GLU:HB2	1:A:80:GLN:HG3	1.97	0.46
1:B:27:ARG:HG2	1:B:139:MET:CE	2.45	0.46
1:B:68:LEU:O	1:B:80:GLN:HA	2.15	0.46
1:A:186(B):ARG:H	1:A:186(B):ARG:HG2	1.45	0.46
1:B:187:LYS:HD2	1:B:220(A):ALA:O	2.15	0.46
1:C:45:THR:OG1	1:C:198:PRO:HB3	2.15	0.46
1:C:57:HIS:NE2	1:C:195:SER:HB3	2.30	0.46
1:D:182:CYS:HB3	1:D:225:PRO:HB2	1.97	0.46
1:D:17:VAL:HG23	1:D:191:CYS:HB2	1.97	0.46
1:D:83:PHE:CZ	1:D:112:ALA:HA	2.51	0.46
1:C:59:LEU:HD23	1:C:59:LEU:N	2.31	0.45
1:B:184:PHE:HE2	1:B:186:PRO:HA	1.81	0.45
1:C:187:LYS:CG	1:C:220(A):ALA:HB1	2.44	0.45
1:D:208:ILE:HD13	3:D:295:HOH:O	2.16	0.45
1:A:56:ALA:HA	1:A:104:LEU:HB2	1.99	0.45
1:C:212:ILE:HB	1:C:229:THR:HB	1.99	0.45
1:A:101:ASN:ND2	1:A:234:TYR:OH	2.44	0.45
1:B:202:ASP:O	1:B:208:ILE:HD12	2.17	0.45
1:C:61:ASP:OD1	1:C:61:ASP:N	2.50	0.45
1:C:186(B):ARG:HG2	1:C:186(B):ARG:NH1	2.32	0.45
1:B:72:ASN:HA	1:B:153:GLN:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:PHE:CB	1:B:108:LEU:HD22	2.46	0.45
1:B:101:ASN:HA	1:B:234:TYR:OH	2.17	0.45
1:C:74:ARG:HD2	1:C:153:GLN:HE21	1.82	0.45
1:A:95:ASP:HB3	1:A:100:LEU:HB2	1.99	0.44
1:A:198:PRO:CB	1:A:209:ILE:HD12	2.45	0.44
1:C:56:ALA:N	1:C:102:ASP:OD1	2.50	0.44
1:D:51:PHE:CZ	1:D:107:GLN:HG3	2.52	0.44
1:B:19:GLY:HA2	1:B:158:LEU:HD13	2.00	0.44
1:B:57:HIS:NE2	1:B:195:SER:HB3	2.33	0.44
1:B:83:PHE:HB2	1:B:108:LEU:HD22	2.00	0.44
1:B:100:LEU:HA	1:B:100:LEU:HD23	1.76	0.44
1:D:61:ASP:O	1:D:62:ILE:HG13	2.17	0.44
1:D:105:LEU:HD12	1:D:105:LEU:HA	1.68	0.44
1:B:77:GLU:HB2	1:B:80:GLN:CG	2.41	0.44
1:B:234:TYR:O	1:B:238:ILE:HG13	2.18	0.44
1:C:223:LEU:HD13	1:C:224:PHE:CZ	2.53	0.44
1:D:230:ARG:HD2	1:D:233:LEU:HD21	1.99	0.44
1:A:186(A):ARG:HE	1:A:186(A):ARG:HB2	1.57	0.43
1:B:185:VAL:HG11	1:B:188:ALA:HB3	1.99	0.43
1:B:137:LEU:HB3	1:B:200:ILE:HD11	2.00	0.43
1:C:95:ASP:O	1:C:99:LYS:N	2.52	0.43
1:A:238:ILE:HG21	1:A:238:ILE:HD13	1.67	0.43
1:C:20:HIS:O	1:C:157:GLU:N	2.40	0.43
1:D:77:GLU:CD	1:D:80:GLN:HE21	2.27	0.43
1:D:142:GLY:HA2	1:D:193:GLY:HA3	2.00	0.43
1:D:235:VAL:O	1:D:239:ARG:HG3	2.18	0.43
1:B:63:PRO:CB	1:B:63(C):LEU:HD13	2.45	0.43
1:B:137:LEU:HD12	1:B:137:LEU:HA	1.85	0.43
1:A:142:GLY:HA2	1:A:193:GLY:HA3	2.01	0.43
1:D:77:GLU:HA	1:D:78:PRO:HD3	1.82	0.43
1:A:75:THR:HG22	1:A:76:GLN:N	2.34	0.43
1:C:197:GLY:O	1:C:212:ILE:HA	2.19	0.43
1:D:143:ARG:HB3	1:D:191:CYS:SG	2.59	0.43
1:A:89:PHE:C	1:A:90:LEU:HD23	2.44	0.42
1:B:113:ASN:HD22	1:B:113:ASN:HA	1.76	0.42
1:C:198:PRO:HB2	1:C:200:ILE:HD13	2.00	0.42
1:D:27:ARG:HE	1:D:27:ARG:HB3	1.70	0.42
1:D:62:ILE:HA	1:D:63:PRO:HD3	1.89	0.42
1:A:208:ILE:HD13	1:A:208:ILE:HG23	1.55	0.42
1:B:242:LEU:N	1:B:242:LEU:HD23	2.34	0.42
1:D:59:LEU:HA	1:D:59:LEU:HD12	1.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:LEU:HA	1:A:179:HIS:CE1	2.54	0.42
1:B:241:THR:C	1:B:243:ARG:H	2.28	0.42
1:C:198:PRO:HB2	1:C:200:ILE:CD1	2.50	0.42
1:C:75:THR:HG22	1:C:76:GLN:N	2.34	0.42
1:D:182:CYS:HB3	1:D:225:PRO:CB	2.50	0.42
1:B:48:HIS:CG	1:B:49:PRO:HD2	2.55	0.41
1:C:223:LEU:HD23	1:C:223:LEU:HA	1.49	0.41
1:A:35:MET:HE3	1:A:35:MET:HB3	1.31	0.41
1:B:186(B):ARG:HE	1:B:186(B):ARG:HB2	1.68	0.41
1:C:36:ARG:HA	1:C:65:ASN:HB2	2.02	0.41
1:D:45:THR:HG21	1:D:209:ILE:HG21	2.01	0.41
1:C:94:TYR:HA	1:C:101:ASN:HB2	2.03	0.41
1:D:60:ARG:HA	1:D:60:ARG:HD2	1.65	0.41
1:D:217:ILE:HD11	1:D:227:PHE:CE1	2.56	0.41
1:B:179:HIS:HB2	3:B:273:HOH:O	2.19	0.41
1:A:143:ARG:C	1:A:145:GLY:H	2.29	0.41
1:D:83:PHE:HZ	1:D:112:ALA:HA	1.85	0.41
1:B:88:VAL:HA	1:B:105:LEU:O	2.20	0.41
1:D:217:ILE:O	1:D:219:GLY:N	2.45	0.41
1:A:68:LEU:O	1:A:80:GLN:HA	2.21	0.41
1:B:83:PHE:HZ	1:B:112:ALA:HA	1.85	0.41
1:A:30:MET:CG	1:A:139:MET:HE3	2.45	0.41
1:C:16:ILE:O	1:C:144:VAL:HG12	2.20	0.41
1:A:142:GLY:N	1:A:194:ASP:OD1	2.51	0.41
1:A:208:ILE:HG21	1:A:208:ILE:HD12	1.74	0.40
1:B:114:LEU:HA	1:B:118:VAL:O	2.20	0.40
1:B:155:LEU:HA	1:B:155:LEU:HD12	1.84	0.40
1:D:52:VAL:HG21	1:D:66:VAL:CG1	2.49	0.40
1:A:207:GLY:N	2:E:2:FUC:O4	2.43	0.40
1:B:166:PHE:HD2	1:C:165:PHE:CE1	2.29	0.40
1:B:27:ARG:HG3	1:B:29:TYR:OH	2.21	0.40
1:D:29:TYR:HA	1:D:119:ALA:O	2.22	0.40
1:B:229:THR:HG23	3:B:291:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	219/221 (99%)	204 (93%)	14 (6%)	1 (0%)	24	27
1	B	219/221 (99%)	197 (90%)	20 (9%)	2 (1%)	14	14
1	C	219/221 (99%)	201 (92%)	17 (8%)	1 (0%)	24	27
1	D	219/221 (99%)	205 (94%)	13 (6%)	1 (0%)	24	27
All	All	876/884 (99%)	807 (92%)	64 (7%)	5 (1%)	21	23

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	151	PRO
1	C	146	ALA
1	D	151	PRO
1	A	150	PRO
1	B	39	SER

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	187/187 (100%)	165 (88%)	22 (12%)	5	5
1	B	187/187 (100%)	163 (87%)	24 (13%)	4	4
1	C	187/187 (100%)	157 (84%)	30 (16%)	2	2
1	D	187/187 (100%)	162 (87%)	25 (13%)	4	3
All	All	748/748 (100%)	647 (86%)	101 (14%)	4	3

All (101) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	MET
1	A	35	MET
1	A	36	ARG
1	A	47	ILE
1	A	50	SER
1	A	60	ARG
1	A	61	ASP
1	A	74	ARG
1	A	81	GLN
1	A	90	LEU
1	A	92	ASN
1	A	93	ASN
1	A	117	SER
1	A	139	MET
1	A	143	ARG
1	A	148	ASP
1	A	177	ARG
1	A	195	SER
1	A	208	ILE
1	A	217	ILE
1	A	221	THR
1	A	223	LEU
1	B	27	ARG
1	B	30	MET
1	B	35	MET
1	B	47	ILE
1	B	50	SER
1	B	60	ARG
1	B	61	ASP
1	B	76	GLN
1	B	80	GLN
1	B	90	LEU
1	B	93	ASN
1	B	139	MET
1	B	147	HIS
1	B	150	PRO
1	B	161	THR
1	B	166	PHE
1	B	177	ARG
1	B	181	ILE
1	B	187	LYS
1	B	195	SER

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Mol	Chain	Res	Type
1	B	208	ILE
1	B	217	ILE
1	B	221	THR
1	B	222	ARG
1	C	23	GLN
1	C	34	GLN
1	C	35	MET
1	C	36	ARG
1	C	38(A)	ASN
1	C	38(B)	PRO
1	C	52	VAL
1	C	61	ASP
1	C	75	THR
1	C	76	GLN
1	C	90	LEU
1	C	110	SER
1	C	117	SER
1	C	125	GLN
1	C	135	GLN
1	C	147	HIS
1	C	148	ASP
1	C	153	GLN
1	C	165	PHE
1	C	177	ARG
1	C	181	ILE
1	C	195	SER
1	C	200	ILE
1	C	213	ASP
1	C	214	SER
1	C	221	THR
1	C	223	LEU
1	C	240	SER
1	C	242	LEU
1	C	243	ARG
1	D	16	ILE
1	D	23	GLN
1	D	27	ARG
1	D	30	MET
1	D	35	MET
1	D	47	ILE
1	D	59	LEU
1	D	60	ARG

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Mol	Chain	Res	Type
1	D	74	ARG
1	D	75	THR
1	D	93	ASN
1	D	104	LEU
1	D	107	GLN
1	D	113	ASN
1	D	135	GLN
1	D	143	ARG
1	D	154	VAL
1	D	166	PHE
1	D	177	ARG
1	D	178	PRO
1	D	195	SER
1	D	209	ILE
1	D	222	ARG
1	D	224	PHE
1	D	243	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	HIS
1	A	63(A)	GLN
1	A	65	ASN
1	A	92	ASN
1	A	93	ASN
1	A	101	ASN
1	A	113	ASN
1	A	153	GLN
1	A	179	HIS
1	A	210	GLN
1	B	65	ASN
1	B	76	GLN
1	B	113	ASN
1	B	156	GLN
1	C	38(A)	ASN
1	C	65	ASN
1	C	87	GLN
1	C	113	ASN
1	C	156	GLN
1	C	210	GLN
1	D	23	GLN

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Mol	Chain	Res	Type
1	D	63(A)	GLN
1	D	87	GLN
1	D	101	ASN
1	D	135	GLN
1	D	179	HIS
1	D	210	GLN

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 ⓘ

8 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	E	1	1,2	14,14,15	1.46	2 (14%)	17,19,21	1.94	6 (35%)
2	FUC	E	2	2	10,10,11	0.61	0	14,14,16	2.25	8 (57%)
2	NAG	F	1	1,2	14,14,15	1.33	3 (21%)	17,19,21	2.66	8 (47%)
2	FUC	F	2	2	10,10,11	0.75	0	14,14,16	2.42	5 (35%)
2	NAG	G	1	1,2	14,14,15	1.61	2 (14%)	17,19,21	1.64	4 (23%)
2	FUC	G	2	2	10,10,11	0.82	0	14,14,16	1.29	3 (21%)
2	NAG	H	1	1,2	14,14,15	1.64	3 (21%)	17,19,21	2.01	6 (35%)
2	FUC	H	2	2	10,10,11	0.70	0	14,14,16	2.11	4 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	1,2	-	4/6/23/26	0/1/1/1
2	FUC	E	2	2	-	-	0/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	FUC	F	2	2	-	-	0/1/1/1
2	NAG	G	1	1,2	-	4/6/23/26	0/1/1/1
2	FUC	G	2	2	-	-	0/1/1/1
2	NAG	H	1	1,2	-	4/6/23/26	0/1/1/1
2	FUC	H	2	2	-	-	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1	NAG	C8-C7	4.53	1.60	1.50
2	G	1	NAG	C8-C7	4.01	1.58	1.50
2	E	1	NAG	C8-C7	3.87	1.58	1.50
2	F	1	NAG	C8-C7	2.63	1.56	1.50
2	F	1	NAG	O5-C1	-2.48	1.39	1.43
2	E	1	NAG	O5-C1	-2.40	1.39	1.43
2	H	1	NAG	O5-C1	-2.30	1.39	1.43
2	F	1	NAG	C1-C2	2.18	1.55	1.52
2	H	1	NAG	O7-C7	2.13	1.28	1.23
2	G	1	NAG	C2-N2	2.13	1.49	1.46

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	NAG	O5-C5-C6	-5.17	97.61	107.66
2	F	2	FUC	O5-C1-C2	4.90	122.48	110.79
2	F	1	NAG	C3-C4-C5	-4.43	102.21	110.23
2	H	2	FUC	O5-C1-C2	3.86	120.00	110.79
2	F	2	FUC	C1-C2-C3	-3.84	104.05	109.64
2	E	2	FUC	O5-C1-C2	3.79	119.84	110.79
2	H	1	NAG	C1-O5-C5	-3.78	107.12	112.19
2	F	1	NAG	O7-C7-C8	3.76	128.75	122.05
2	E	1	NAG	C4-C3-C2	3.70	116.44	111.02
2	F	1	NAG	O4-C4-C5	3.65	118.32	109.32
2	E	2	FUC	O4-C4-C3	3.63	118.92	110.38
2	H	1	NAG	C4-C3-C2	3.46	116.09	111.02
2	G	1	NAG	O5-C5-C6	-3.45	100.95	107.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	2	FUC	C3-C4-C5	3.38	114.95	109.81
2	G	1	NAG	C2-N2-C7	3.34	127.38	122.90
2	H	1	NAG	O4-C4-C5	3.31	117.48	109.32
2	F	2	FUC	C6-C5-C4	-3.31	107.02	113.08
2	H	2	FUC	O4-C4-C3	3.19	117.91	110.38
2	G	1	NAG	C1-C2-N2	3.19	115.45	110.43
2	F	1	NAG	C8-C7-N2	-3.14	110.91	116.12
2	H	1	NAG	O5-C5-C6	-3.04	101.75	107.66
2	E	1	NAG	O5-C5-C6	-3.01	101.80	107.66
2	E	1	NAG	C2-N2-C7	2.99	126.91	122.90
2	E	1	NAG	O4-C4-C5	2.87	116.40	109.32
2	E	2	FUC	O5-C5-C6	2.82	113.52	107.40
2	F	1	NAG	O4-C4-C3	-2.79	103.79	110.38
2	F	2	FUC	O5-C5-C6	2.73	113.33	107.40
2	G	2	FUC	C2-C3-C4	2.73	115.65	110.86
2	E	2	FUC	O2-C2-C1	2.72	115.44	109.22
2	E	1	NAG	C1-C2-N2	-2.50	106.50	110.43
2	H	2	FUC	C2-C3-C4	2.49	115.24	110.86
2	H	1	NAG	C2-N2-C7	2.46	126.19	122.90
2	E	2	FUC	C2-C3-C4	2.41	115.10	110.86
2	H	1	NAG	C1-C2-N2	-2.40	106.65	110.43
2	E	2	FUC	C6-C5-C4	-2.40	108.69	113.08
2	G	1	NAG	O4-C4-C5	2.37	115.16	109.32
2	H	2	FUC	O3-C3-C2	2.30	114.75	110.05
2	F	1	NAG	C6-C5-C4	2.29	118.65	113.02
2	E	2	FUC	C3-C4-C5	2.25	113.23	109.81
2	G	2	FUC	C6-C5-C4	2.19	117.09	113.08
2	F	1	NAG	C1-O5-C5	-2.17	109.28	112.19
2	G	2	FUC	O4-C4-C3	2.10	115.32	110.38
2	E	1	NAG	C1-O5-C5	-2.05	109.44	112.19
2	E	2	FUC	O3-C3-C2	2.04	114.22	110.05

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	1	NAG	O7-C7-N2-C2
2	G	1	NAG	O5-C5-C6-O6
2	E	1	NAG	C8-C7-N2-C2
2	H	1	NAG	C8-C7-N2-C2
2	H	1	NAG	O7-C7-N2-C2
2	G	1	NAG	C4-C5-C6-O6

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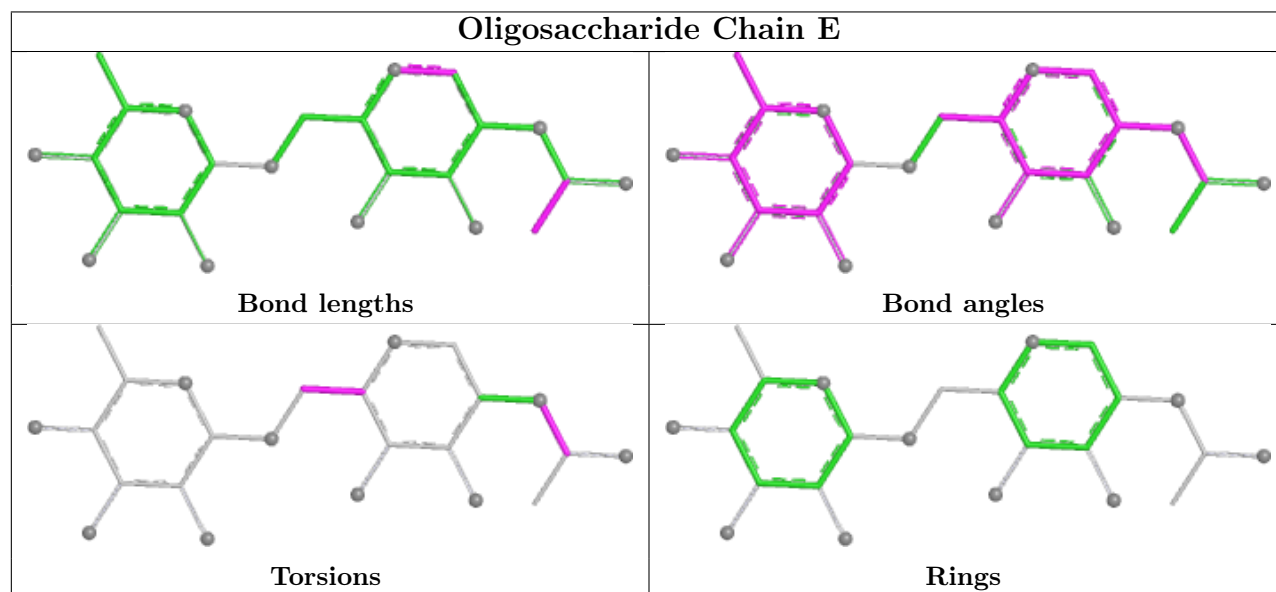
Mol	Chain	Res	Type	Atoms
2	F	1	NAG	O5-C5-C6-O6
2	G	1	NAG	O7-C7-N2-C2
2	E	1	NAG	O5-C5-C6-O6
2	H	1	NAG	O5-C5-C6-O6
2	F	1	NAG	C4-C5-C6-O6
2	G	1	NAG	C8-C7-N2-C2
2	H	1	NAG	C4-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6

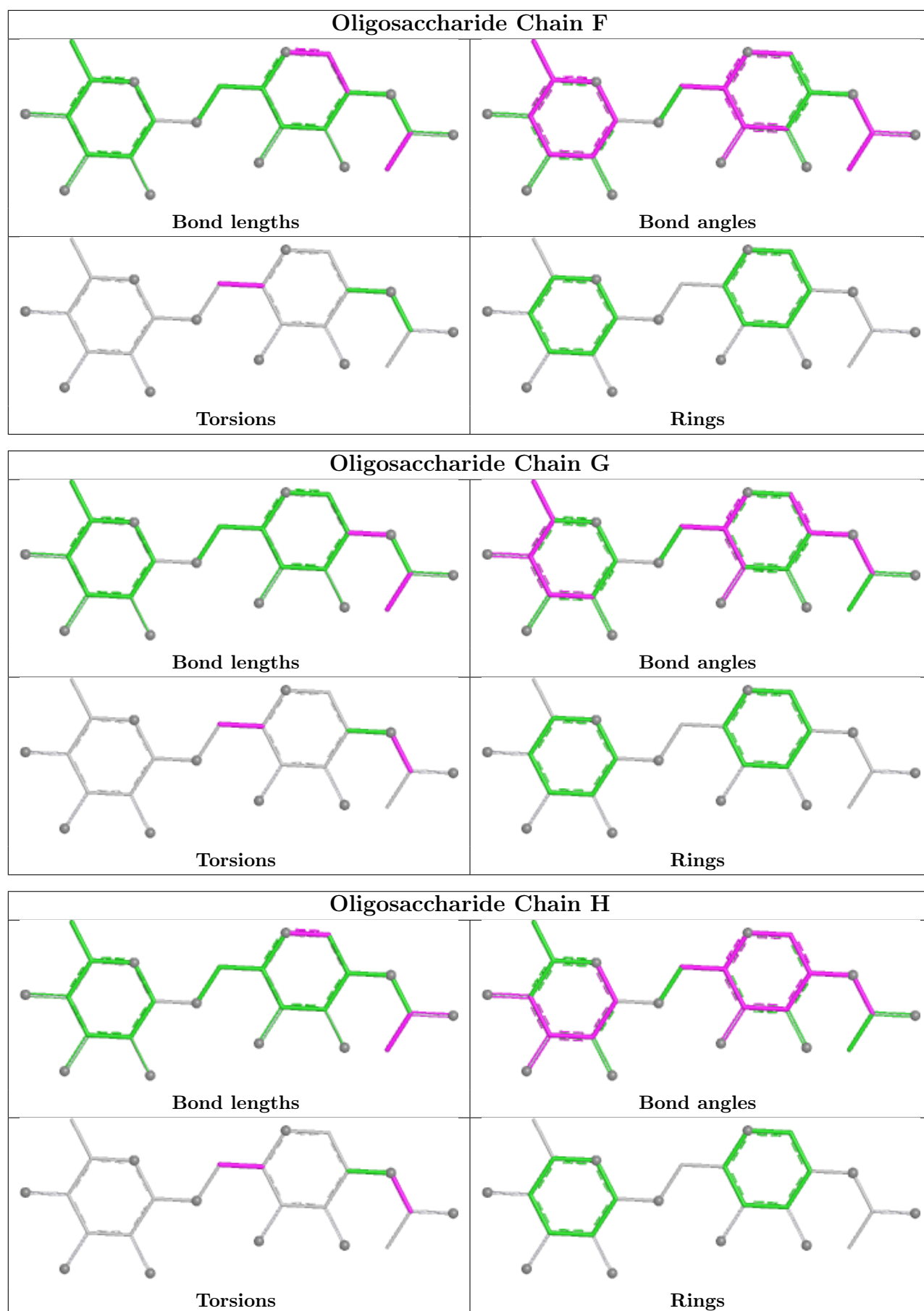
There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	2	FUC	2	0
2	H	2	FUC	1	0
2	G	2	FUC	1	0
2	E	2	FUC	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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	221/221 (100%)	-0.78	0 100 100	9, 24, 68, 100	0
1	B	221/221 (100%)	-0.70	1 (0%) 87 85	12, 28, 68, 98	0
1	C	221/221 (100%)	-0.72	1 (0%) 87 85	9, 26, 72, 100	0
1	D	221/221 (100%)	-0.70	1 (0%) 87 85	8, 27, 67, 100	0
All	All	884/884 (100%)	-0.72	3 (0%) 90 88	8, 27, 69, 100	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	150	PRO	6.4
1	B	148	ASP	3.6
1	C	146	ALA	2.6

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.

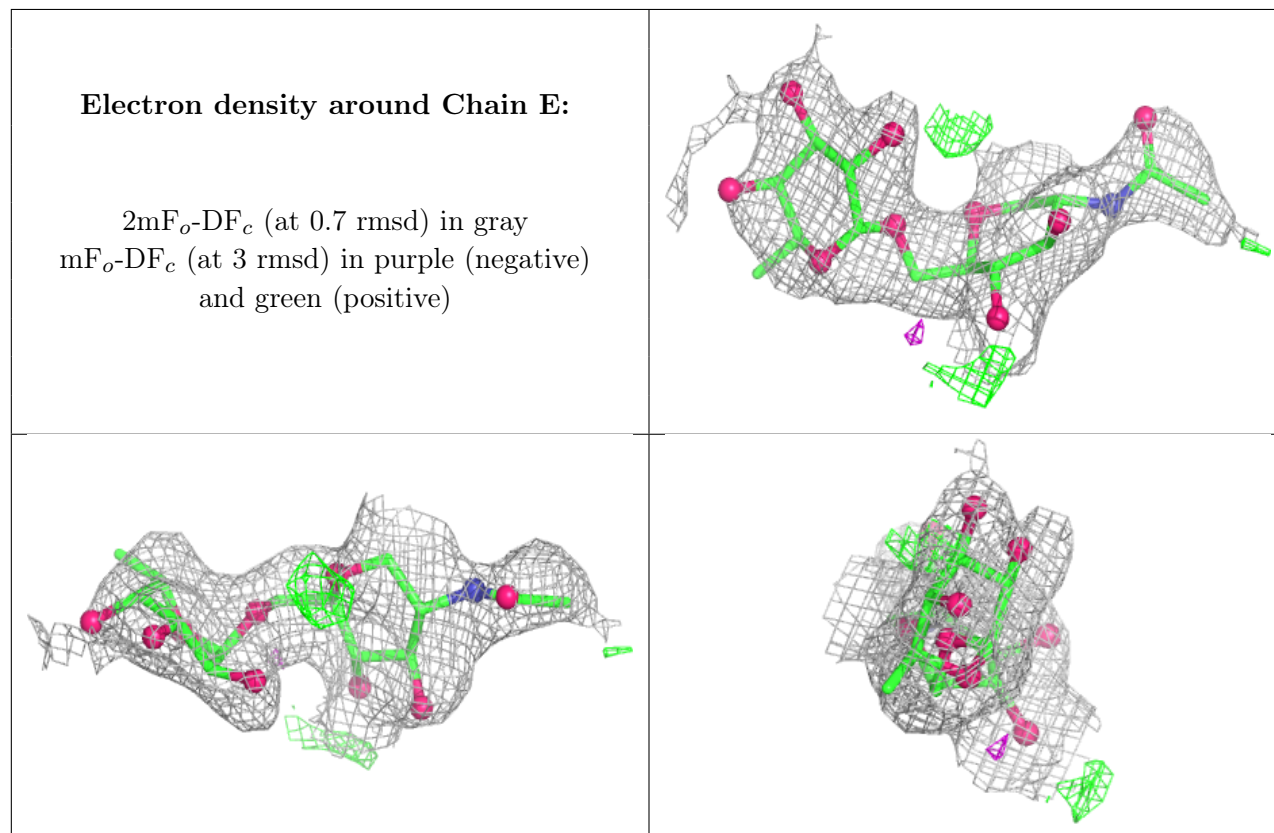
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	G	1	14/15	0.70	0.12	47,100,100,100	0
2	FUC	G	2	10/11	0.73	0.14	42,100,100,100	0
2	NAG	H	1	14/15	0.82	0.13	26,92,100,100	0
2	FUC	H	2	10/11	0.87	0.12	26,65,100,100	0

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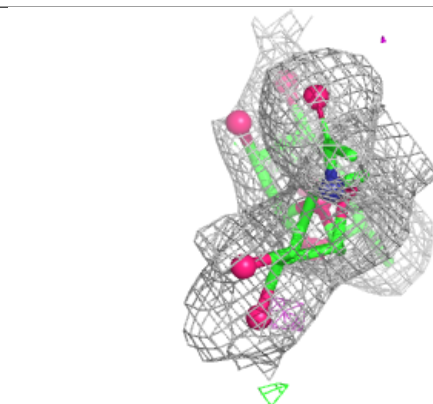
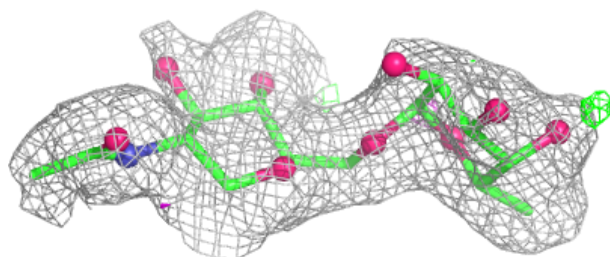
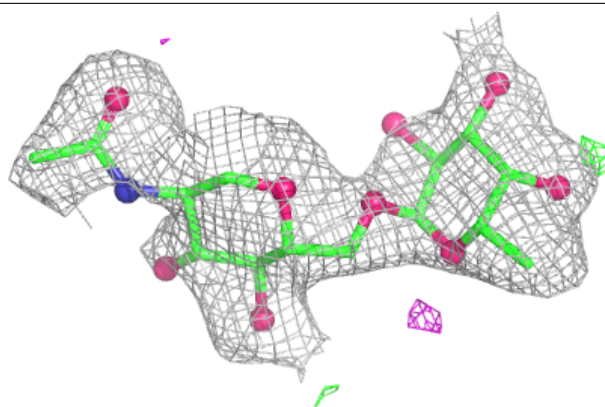
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	E	1	14/15	0.90	0.09	25,70,100,100	0
2	NAG	F	1	14/15	0.90	0.08	33,62,100,100	0
2	FUC	F	2	10/11	0.91	0.09	26,45,83,100	0
2	FUC	E	2	10/11	0.93	0.10	27,46,100,100	0

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

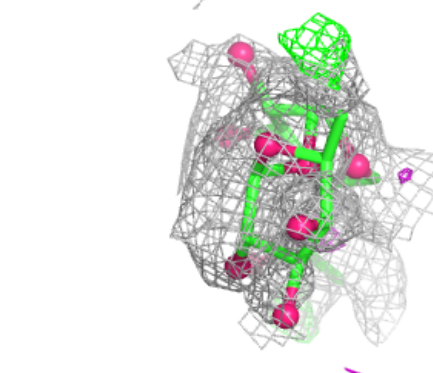
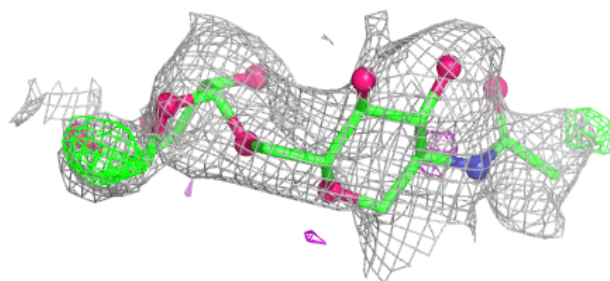
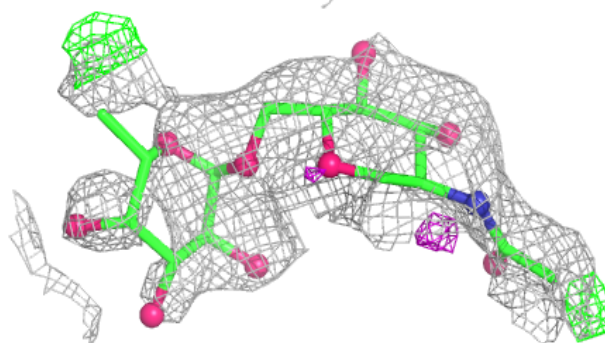


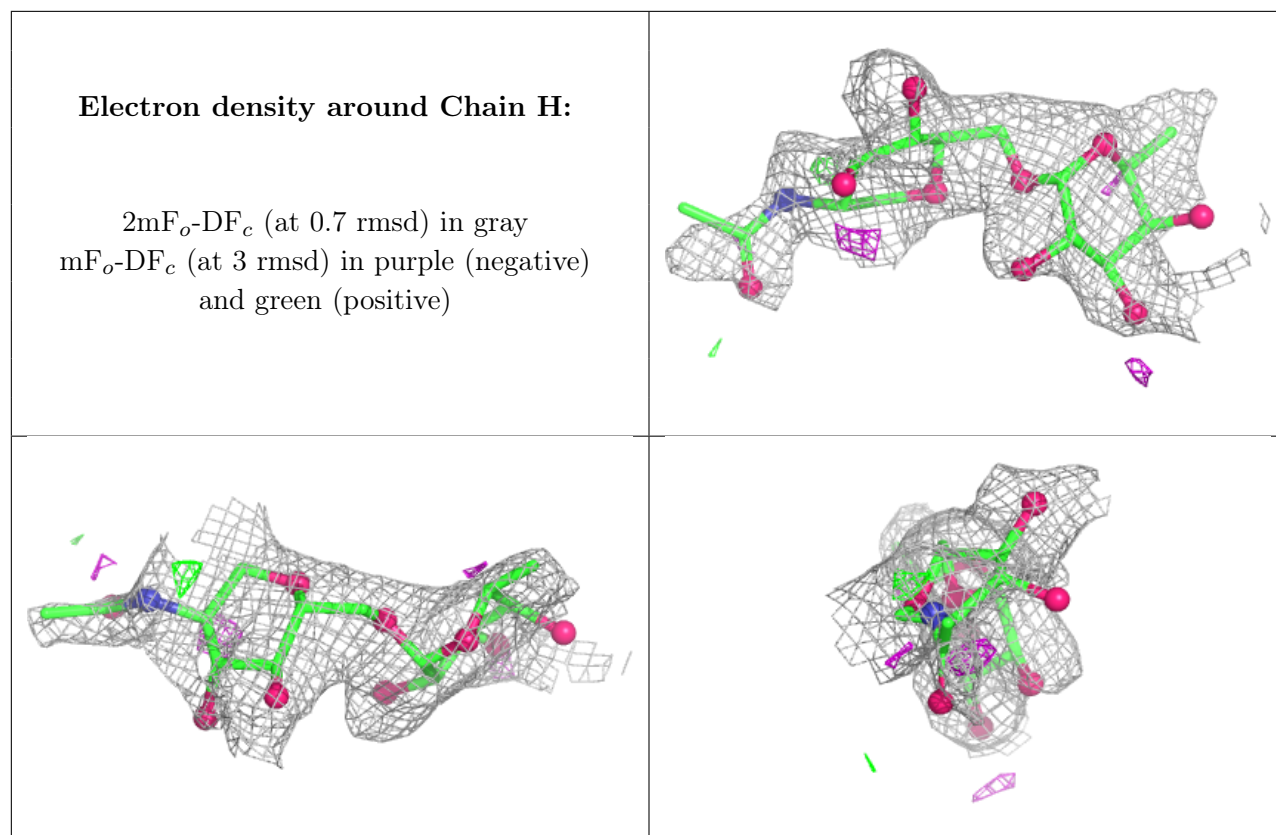
Electron density around Chain F:

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

**Electron density around Chain G:**

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





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.