



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:20 AM UTC

PDB ID : 4HFU / pdb_00004hfu
Title : Crystal structure of Fab 8M2 in complex with a H2N2 influenza virus hemagglutinin
Authors : Xu, R.; Wilson, I.A.
Deposited on : 2012-10-05
Resolution : 3.11 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

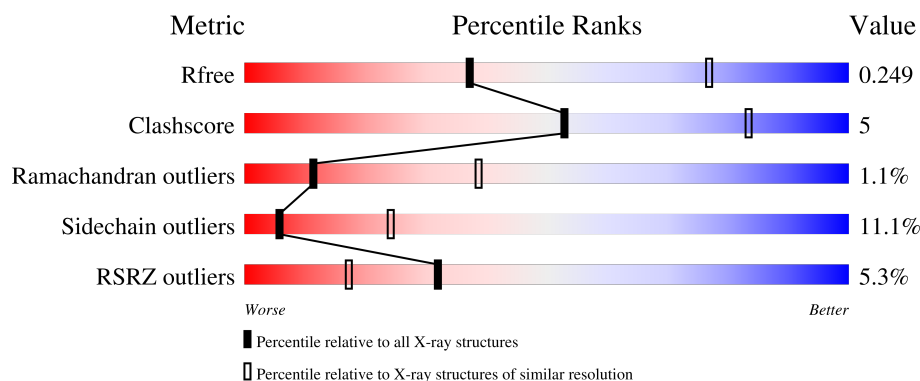
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.11 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	327	4% 80% 17% ..
2	B	174	2% 81% 14% ...
3	H	226	4% 74% 21% ..
4	L	215	10% 78% 19% ..
5	C	2	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7242 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 Hemagglutinin HA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	3	1	0
			2513	1584	434	480	15			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	PRO	-	expression tag	UNP Q67085

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	172	Total	C	N	O	S	0	0	0
			1396	871	237	279	9			

- Molecule 3 is a protein called Fab 8M2 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	224	Total	C	N	O	S	0	0	0
			1670	1051	280	332	7			

- Molecule 4 is a protein called Fab 8M2 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	213	Total	C	N	O	S	0	0	0
			1635	1024	280	327	4			

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

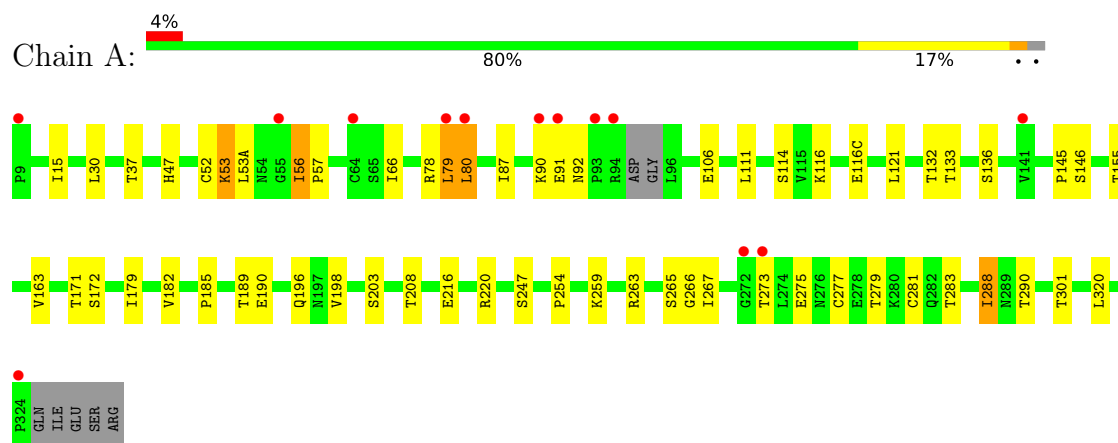


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

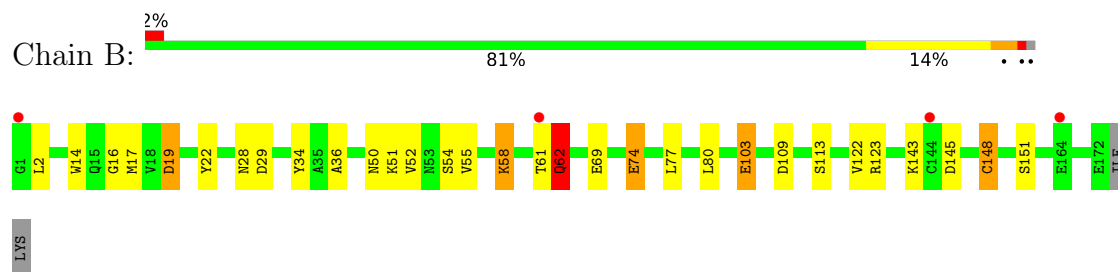
3 Residue-property plots [i](#)

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.

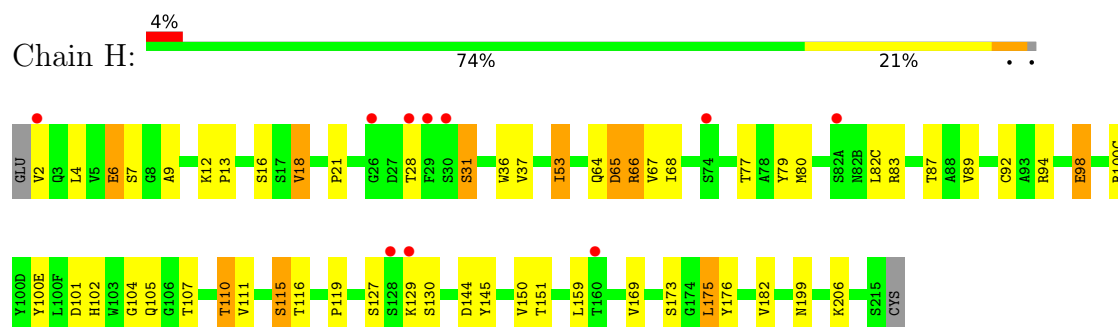
• Molecule 1: Hemagglutinin HA1



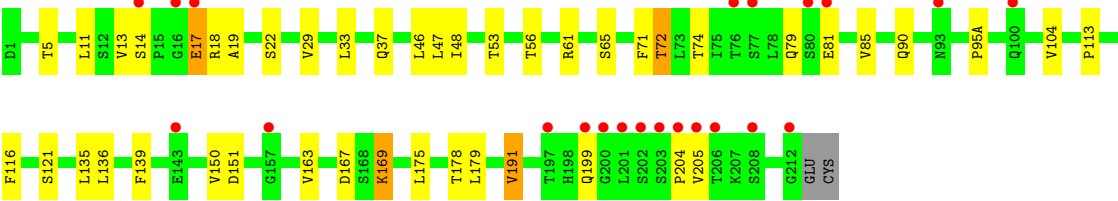
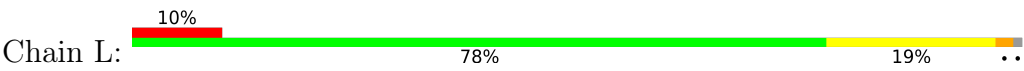
• Molecule 2: Hemagglutinin HA2



• Molecule 3: Fab 8M2 heavy chain



• Molecule 4: Fab 8M2 light chain



- 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	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	129.59Å 129.59Å 536.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.90 – 3.11 41.90 – 3.11	Depositor EDS
% Data completeness (in resolution range)	85.4 (41.90-3.11) 85.0 (41.90-3.11)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	18.25 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.8_1063	Depositor
R, R_{free}	0.193 , 0.251 0.193 , 0.249	Depositor DCC
R_{free} test set	1374 reflections (4.28%)	wwPDB-VP
Wilson B-factor (Å ²)	34.4	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 41.0	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	0.90	EDS
Total number of atoms	7242	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.30	0/2575	0.75	2/3494 (0.1%)
2	B	0.27	0/1424	0.68	0/1912
3	H	0.31	0/1713	0.76	1/2338 (0.0%)
4	L	0.30	0/1673	0.75	0/2277
All	All	0.30	0/7385	0.74	3/10021 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	31	SER	N-CA-C	-6.56	104.91	113.17
1	A	121	LEU	CA-C-N	5.38	125.39	119.90
1	A	121	LEU	C-N-CA	5.38	125.39	119.90

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	2513	0	2475	19	0
2	B	1396	0	1299	12	0
3	H	1670	0	1620	27	0
4	L	1635	0	1584	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	28	0	25	0	0
All	All	7242	0	7003	71	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 5.

All (71) 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:A:78:ARG:O	1:A:80:LEU:N	2.25	0.69
4:L:65:SER:HB3	4:L:72:THR:HG22	1.78	0.66
2:B:19:ASP:HB2	2:B:36:ALA:HB2	1.78	0.64
2:B:51:LYS:HE2	2:B:103:GLU:HG3	1.80	0.63
3:H:87:THR:HG23	3:H:110:THR:HA	1.83	0.61
3:H:159:LEU:HD21	3:H:182:VAL:HG11	1.83	0.60
4:L:11:LEU:HB3	4:L:104:VAL:HG12	1.84	0.60
2:B:28:ASN:HD22	2:B:145:ASP:HA	1.68	0.59
4:L:136:LEU:HD12	4:L:175:LEU:HD23	1.87	0.56
1:A:116:LYS:HE2	1:A:263:ARG:HD2	1.87	0.56
3:H:36:TRP:CE2	3:H:80:MET:HB2	2.41	0.55
1:A:15:ILE:HD11	2:B:122:VAL:HG21	1.87	0.55
1:A:53:LYS:HG2	1:A:277:CYS:O	2.07	0.54
2:B:74:GLU:HB3	2:B:77:LEU:HD13	1.88	0.53
2:B:145:ASP:H	2:B:148:CYS:HB3	1.73	0.53
3:H:7:SER:O	3:H:107:THR:OG1	2.21	0.53
4:L:33:LEU:HD22	4:L:71:PHE:CG	2.44	0.53
3:H:82(C):LEU:HD13	3:H:111:VAL:HG22	1.91	0.52
3:H:127:SER:H	3:H:130:SER:HB2	1.74	0.52
1:A:265:SER:OG	1:A:266:GLY:N	2.42	0.52
4:L:37:GLN:HB2	4:L:47:LEU:HD11	1.91	0.52
3:H:13:PRO:O	3:H:16:SER:OG	2.28	0.51
1:A:216:GLU:O	1:A:220:ARG:NH2	2.44	0.51
1:A:52:CYS:HB2	1:A:279:THR:HG22	1.93	0.50
1:A:116(C):GLU:HB3	1:A:259:LYS:HD3	1.94	0.50
4:L:163:VAL:HG22	4:L:175:LEU:HD13	1.93	0.50
3:H:6:GLU:O	3:H:105:GLN:NE2	2.46	0.49
2:B:14:TRP:HE3	2:B:17:MET:HE2	1.78	0.49
3:H:12:LYS:HG3	3:H:18:VAL:HG13	1.95	0.49
1:A:136:SER:HB2	3:H:98:GLU:OE1	2.13	0.48
4:L:13:VAL:HG13	4:L:17:GLU:HB3	1.95	0.48
3:H:31:SER:HA	3:H:53:ILE:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:115:SER:OG	3:H:116:THR:N	2.47	0.47
3:H:119:PRO:HB3	3:H:145:TYR:HB3	1.96	0.47
3:H:4:LEU:O	3:H:104:GLY:HA2	2.15	0.46
4:L:116:PHE:HD2	4:L:135:LEU:HD23	1.81	0.46
1:A:66:ILE:H	1:A:66:ILE:HD12	1.81	0.46
3:H:101:ASP:HA	4:L:46:LEU:HD22	1.96	0.46
1:A:87:ILE:HB	1:A:267:ILE:HG12	1.97	0.46
4:L:113:PRO:HB3	4:L:139:PHE:HB3	1.99	0.45
3:H:80:MET:HE3	3:H:80:MET:HB3	1.85	0.45
4:L:29:VAL:HG11	4:L:90:GLN:HB2	1.97	0.45
2:B:54:SER:O	2:B:58:LYS:HB2	2.17	0.45
4:L:14:SER:HB2	4:L:17:GLU:HB2	1.97	0.45
4:L:13:VAL:HG11	4:L:19:ALA:HB2	1.97	0.45
1:A:53:LYS:HB3	1:A:57:PRO:HA	1.98	0.45
3:H:64:GLN:C	3:H:66:ARG:H	2.25	0.43
3:H:21:PRO:HA	3:H:79:TYR:HD2	1.84	0.43
1:A:145:PRO:HG3	3:H:31:SER:HB3	2.00	0.43
4:L:169:LYS:HE3	4:L:169:LYS:HB2	1.86	0.43
3:H:12:LYS:HA	3:H:13:PRO:HD3	1.92	0.43
4:L:61:ARG:H	4:L:61:ARG:HG3	1.58	0.42
3:H:110:THR:HG21	3:H:176:TYR:OH	2.20	0.42
2:B:16:GLY:HA3	2:B:34:TYR:CE2	2.55	0.41
3:H:4:LEU:HD11	3:H:94:ARG:HB2	2.01	0.41
3:H:100(C):ARG:HB2	3:H:100(E):TYR:CE2	2.54	0.41
2:B:19:ASP:OD1	2:B:19:ASP:N	2.52	0.41
2:B:61:THR:HB	2:B:62:GLN:H	1.74	0.41
3:H:36:TRP:CZ3	3:H:92:CYS:HB3	2.55	0.41
3:H:2:VAL:HB	3:H:102:HIS:CE1	2.56	0.41
4:L:151:ASP:HA	4:L:191:VAL:HG13	2.03	0.41
4:L:167:ASP:OD1	4:L:169:LYS:HE2	2.21	0.40
1:A:179:ILE:O	1:A:254:PRO:HB3	2.21	0.40
1:A:281:CYS:SG	1:A:288:ILE:HD11	2.61	0.40
3:H:53:ILE:H	3:H:53:ILE:HG13	1.38	0.40
3:H:144:ASP:HB3	3:H:175:LEU:HD23	2.02	0.40
1:A:56:ILE:HG22	1:A:57:PRO:HD2	2.04	0.40
1:A:189:THR:HG21	4:L:95(A):PRO:HG3	2.03	0.40
1:A:52:CYS:HB3	1:A:277:CYS:O	2.21	0.40
1:A:185:PRO:HB3	1:A:190:GLU:HG3	2.03	0.40
2:B:2:LEU:HB2	2:B:109:ASP:OD1	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	317/327 (97%)	302 (95%)	11 (4%)	4 (1%)	9	35
2	B	170/174 (98%)	163 (96%)	5 (3%)	2 (1%)	10	37
3	H	222/226 (98%)	211 (95%)	8 (4%)	3 (1%)	9	34
4	L	211/215 (98%)	190 (90%)	20 (10%)	1 (0%)	24	57
All	All	920/942 (98%)	866 (94%)	44 (5%)	10 (1%)	11	39

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	79	LEU
1	A	80	LEU
1	A	273	THR
2	B	69	GLU
3	H	65	ASP
1	A	92	ASN
4	L	204	PRO
2	B	62	GLN
3	H	9	ALA
3	H	98	GLU

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	284/289 (98%)	252 (89%)	32 (11%)	5	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	149/151 (99%)	133 (89%)	16 (11%)	6	25
3	H	188/190 (99%)	166 (88%)	22 (12%)	5	22
4	L	182/184 (99%)	162 (89%)	20 (11%)	6	24
All	All	803/814 (99%)	713 (89%)	90 (11%)	6	24

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	LEU
1	A	37	THR
1	A	47	HIS
1	A	53	LYS
1	A	53(A)	LEU
1	A	56	ILE
1	A	79	LEU
1	A	90	LYS
1	A	91	GLU
1	A	106	GLU
1	A	111	LEU
1	A	114	SER
1	A	132	THR
1	A	133	THR
1	A	146	SER
1	A	155	THR
1	A	163	VAL
1	A	171	THR
1	A	172	SER
1	A	182	VAL
1	A	196	GLN
1	A	198	VAL
1	A	203[A]	SER
1	A	203[B]	SER
1	A	208	THR
1	A	247	SER
1	A	275	GLU
1	A	283	THR
1	A	288	ILE
1	A	290	THR
1	A	301	THR
1	A	320	LEU
2	B	19	ASP

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Mol	Chain	Res	Type
2	B	22	TYR
2	B	29	ASP
2	B	50	ASN
2	B	52	VAL
2	B	55	VAL
2	B	58	LYS
2	B	62	GLN
2	B	74	GLU
2	B	80	LEU
2	B	103	GLU
2	B	113	SER
2	B	123	ARG
2	B	143	LYS
2	B	148	CYS
2	B	151	SER
3	H	6	GLU
3	H	18	VAL
3	H	28	THR
3	H	37	VAL
3	H	53	ILE
3	H	65	ASP
3	H	66	ARG
3	H	67	VAL
3	H	68	ILE
3	H	77	THR
3	H	83	ARG
3	H	89	VAL
3	H	110	THR
3	H	115	SER
3	H	129	LYS
3	H	150	VAL
3	H	151	THR
3	H	169	VAL
3	H	173	SER
3	H	175	LEU
3	H	199	ASN
3	H	206	LYS
4	L	5	THR
4	L	17	GLU
4	L	18	ARG
4	L	22	SER
4	L	48	ILE

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Mol	Chain	Res	Type
4	L	53	THR
4	L	56	THR
4	L	72	THR
4	L	74	THR
4	L	79	GLN
4	L	81	GLU
4	L	85	VAL
4	L	121	SER
4	L	150	VAL
4	L	169	LYS
4	L	178	THR
4	L	179	LEU
4	L	191	VAL
4	L	199	GLN
4	L	205	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	289	ASN
2	B	15	GLN
2	B	50	ASN
2	B	142	HIS
2	B	154	ASN
2	B	171	ASN
3	H	102	HIS
3	H	171	GLN
3	H	192	GLN
3	H	204	ASN
4	L	3	GLN
4	L	93	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

2 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	0.52	0	17,19,21	0.80	0
5	NAG	C	2	5	14,14,15	0.53	0	17,19,21	0.59	0

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	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

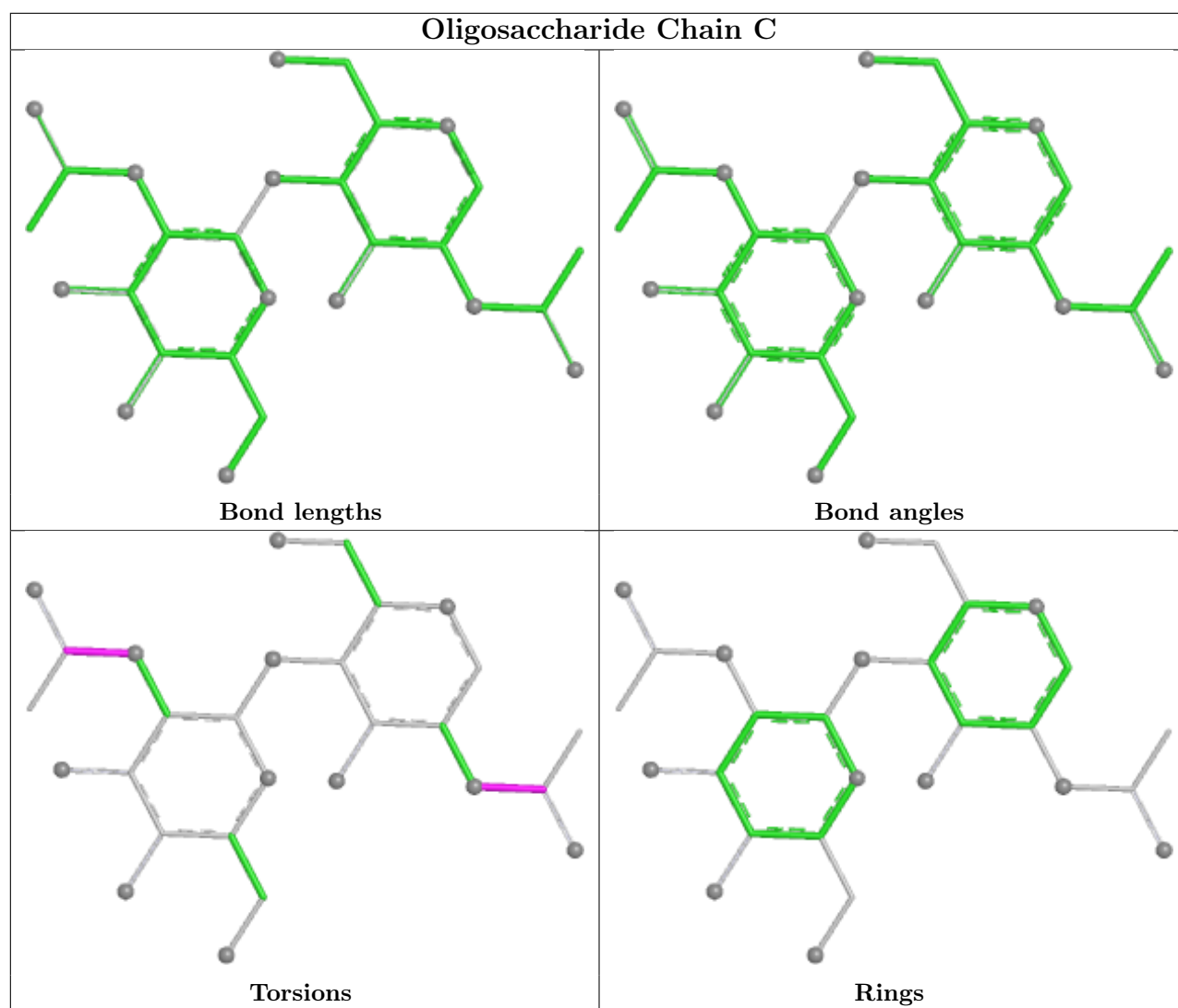
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	1	NAG	C8-C7-N2-C2
5	C	1	NAG	O7-C7-N2-C2
5	C	2	NAG	C8-C7-N2-C2
5	C	2	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

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	A	320/327 (97%)	0.09	13 (4%) 41 23	27, 52, 103, 150	1 (0%)
2	B	172/174 (98%)	-0.01	4 (2%) 61 39	20, 53, 86, 104	0
3	H	224/226 (99%)	0.22	10 (4%) 38 20	31, 61, 100, 137	0
4	L	213/215 (99%)	0.64	22 (10%) 12 6	36, 76, 120, 183	0
All	All	929/942 (98%)	0.23	49 (5%) 32 17	20, 59, 103, 183	1 (0%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	273	THR	4.9
1	A	93	PRO	4.5
1	A	79	LEU	4.4
4	L	197	THR	3.9
4	L	81	GLU	3.9
4	L	77	SER	3.8
4	L	199	GLN	3.8
3	H	28	THR	3.8
1	A	324	PRO	3.8
4	L	212	GLY	3.7
3	H	29	PHE	3.7
4	L	202	SER	3.6
4	L	203	SER	3.5
4	L	200	GLY	3.3
1	A	272	GLY	3.3
4	L	16	GLY	3.3
1	A	80	LEU	3.3
4	L	204	PRO	3.2
1	A	9	PRO	3.2
4	L	201	LEU	3.1
4	L	80	SER	2.9

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Mol	Chain	Res	Type	RSRZ
4	L	17	GLU	2.9
2	B	61	THR	2.7
3	H	128	SER	2.7
4	L	205	VAL	2.6
3	H	30	SER	2.6
3	H	82(A)	SER	2.6
3	H	129	LYS	2.5
1	A	91	GLU	2.5
3	H	160	THR	2.5
2	B	144	CYS	2.4
2	B	1	GLY	2.3
4	L	76	THR	2.3
3	H	74	SER	2.3
4	L	93	ASN	2.2
4	L	157	GLY	2.2
1	A	94	ARG	2.2
4	L	14	SER	2.1
4	L	208	SER	2.1
1	A	141	VAL	2.1
1	A	90	LYS	2.1
4	L	100	GLN	2.1
1	A	64	CYS	2.1
4	L	206	THR	2.1
1	A	55	GLY	2.1
3	H	26	GLY	2.0
2	B	164	GLU	2.0
3	H	2	VAL	2.0
4	L	143	GLU	2.0

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

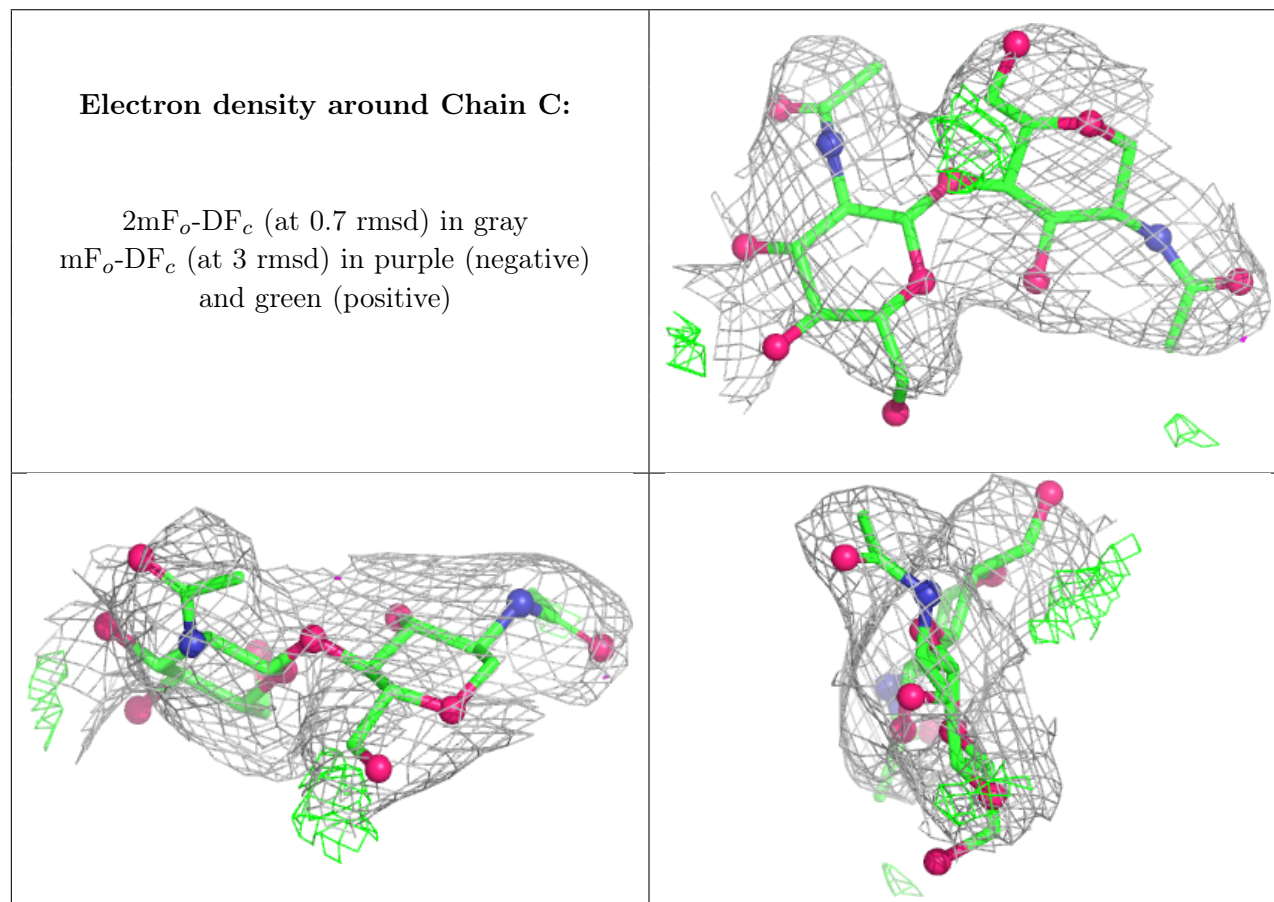
There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
5	NAG	C	1	14/15	-	-	47,60,73,82	0
5	NAG	C	2	14/15	-	-	74,106,117,122	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.



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.