



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:03 PM UTC

PDB ID : 4A5W / pdb_00004a5w
Title : Crystal structure of C5b6
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Deposited on : 2011-10-28
Resolution : 3.50 Å(reported)

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

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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

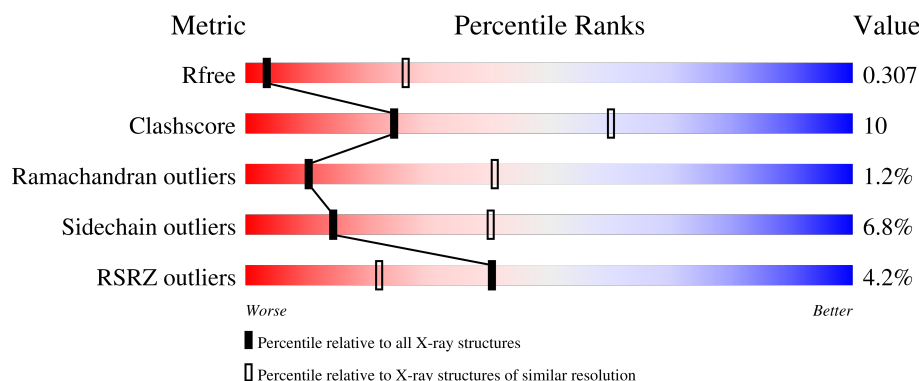
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	1580	 2% 71% 23% • •
2	B	913	 7% 63% 27% 5% • 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	MAN	B	1568	X	-	-	-
6	MAN	B	1571	X	-	-	-
6	MAN	B	1574	X	-	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 19028 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.

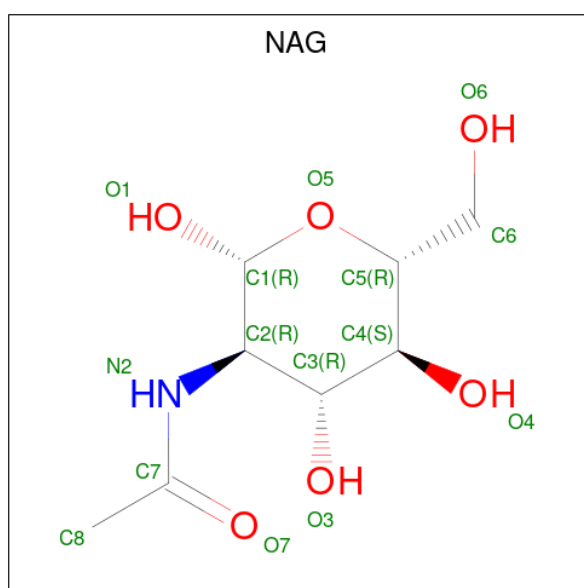
- Molecule 1 is a protein called COMPLEMENT C5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1528	Total	C	N	O	S	0	0	0
			12111	7768	1977	2321	45			

- Molecule 2 is a protein called COMPLEMENT COMPONENT C6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	871	Total	C	N	O	S	0	0	0
			6817	4206	1196	1344	71			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

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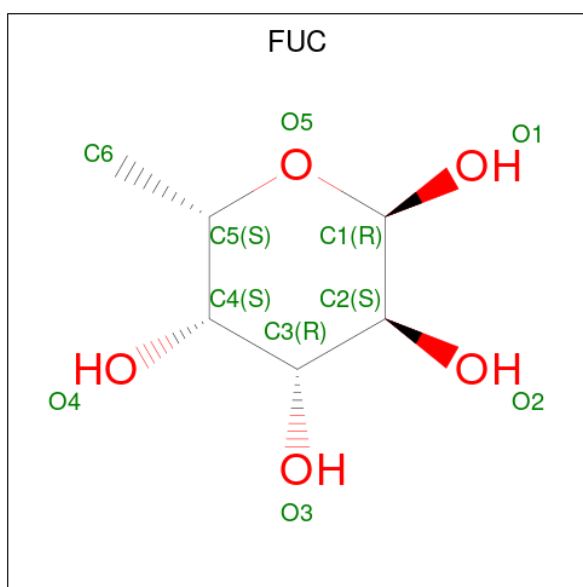
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

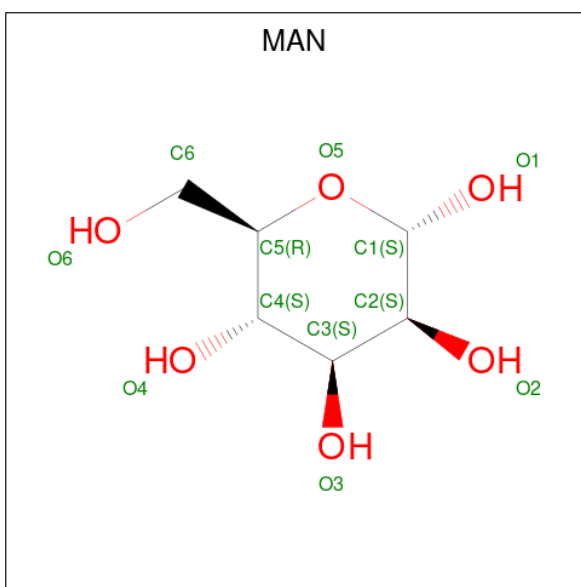
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		

- Molecule 5 is alpha-L-fucopyranose (CCD ID: FUC) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).

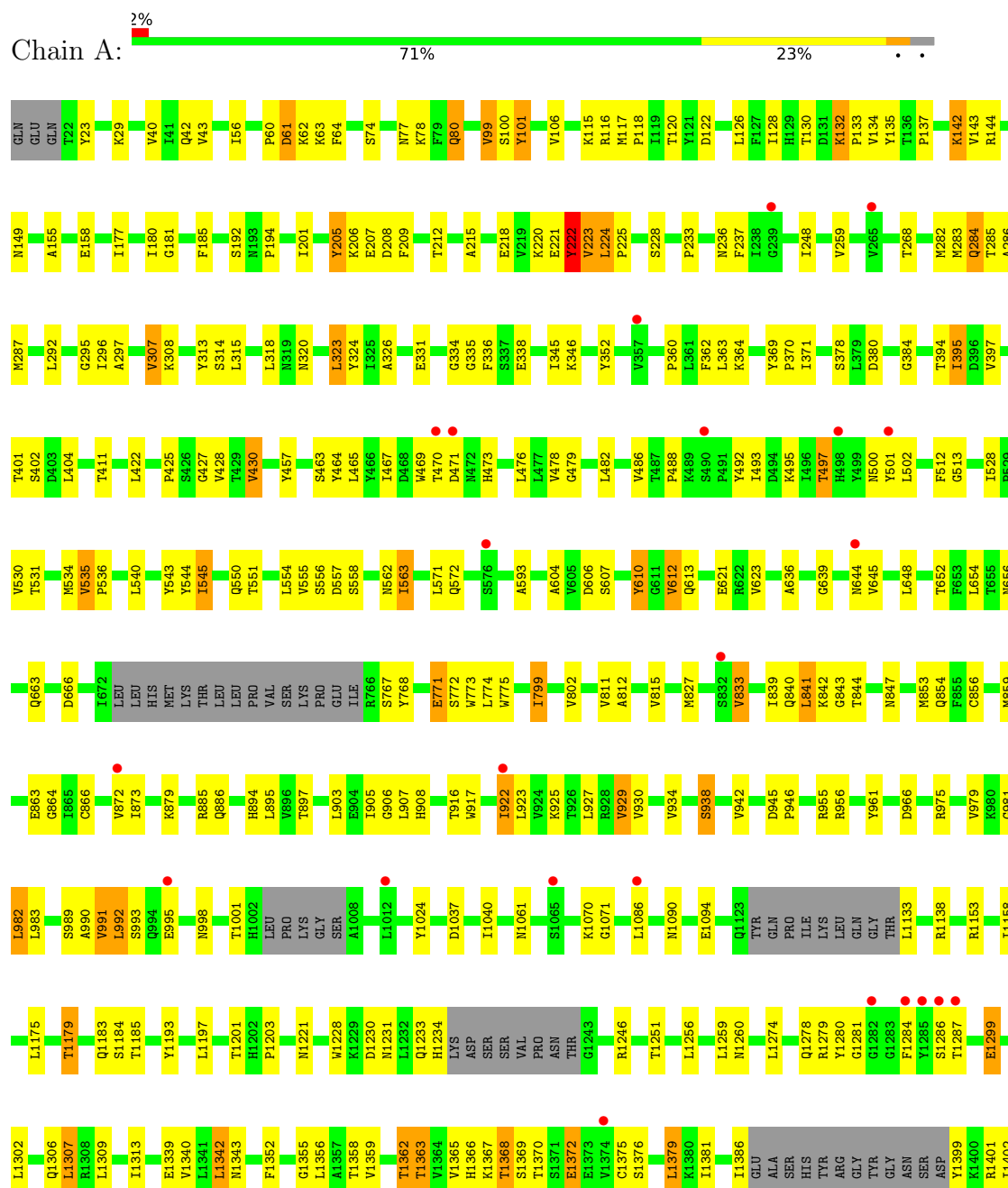


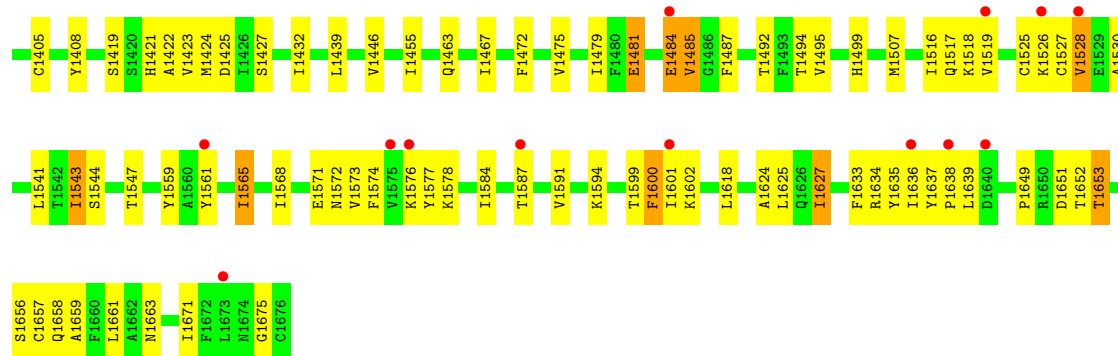
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			11	6	5		
6	B	1	Total	C	O	0	0
			11	6	5		
6	B	1	Total	C	O	0	0
			11	6	5		

3 Residue-property plots

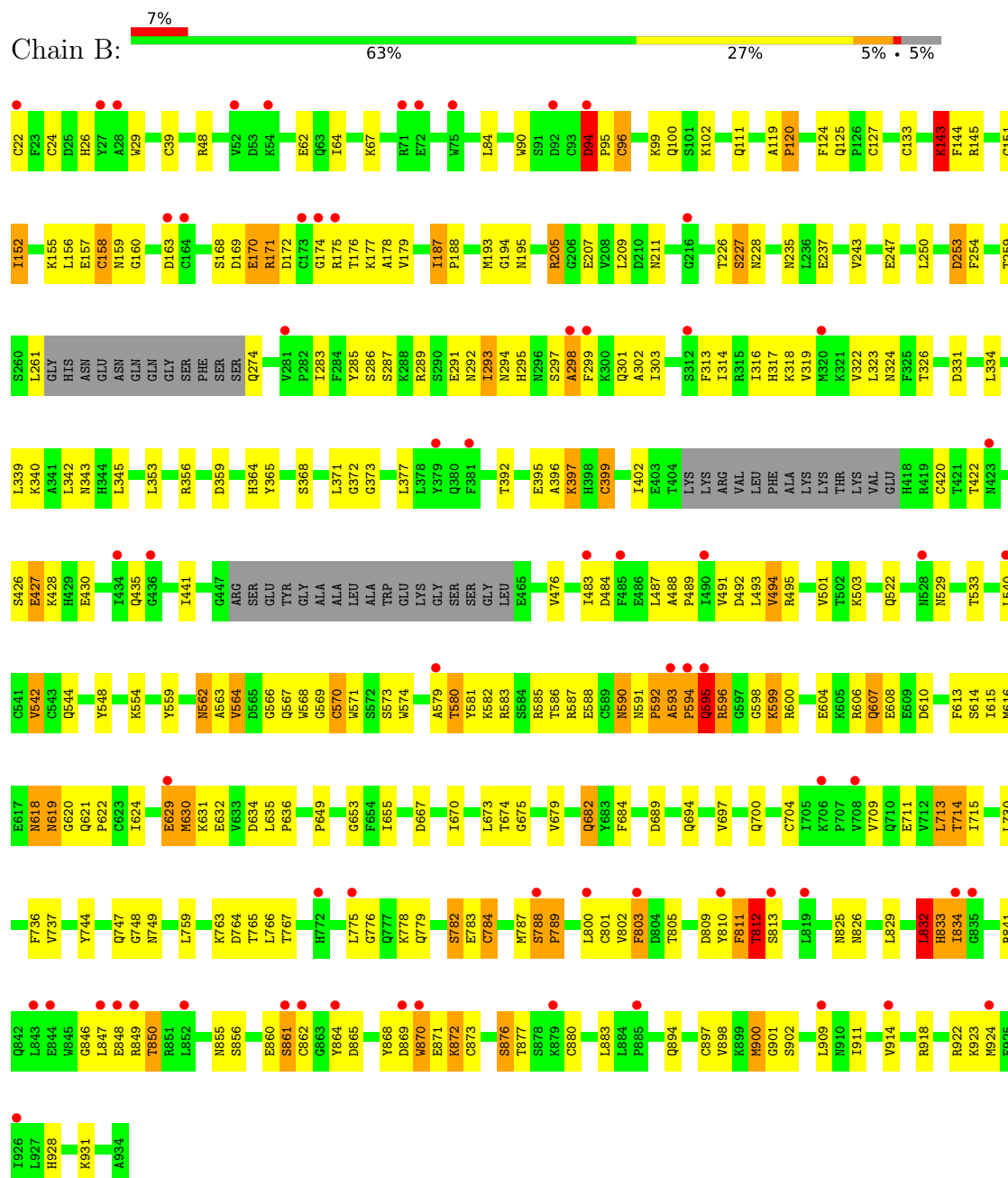
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: COMPLEMENT C5





• Molecule 2: COMPLEMENT COMPONENT C6



4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	154.22Å 230.75Å 269.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.19 – 3.50 46.19 – 3.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (46.19-3.50) 96.9 (46.19-3.50)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 3.48Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.256 , 0.270 0.295 , 0.307	Depositor DCC
R_{free} test set	3027 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	129.0	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 97.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	19028	wwPDB-VP
Average B, all atoms (Å ²)	157.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.12% 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: CA, FUC, NAG, 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	0.57	0/12375	1.03	35/16792 (0.2%)
2	B	0.60	0/6957	1.24	60/9392 (0.6%)
All	All	0.58	0/19332	1.11	95/26184 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

There are no bond length outliers.

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1370	THR	N-CA-C	-10.19	99.64	113.30
2	B	596	ARG	N-CA-C	-9.87	100.89	113.72
2	B	427	GLU	N-CA-C	9.12	124.47	113.16
2	B	848	GLU	N-CA-C	9.08	122.86	111.69
2	B	562	ASN	N-CA-C	9.06	121.15	111.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	94	ASP	Peptide

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	12111	0	12029	200	0
2	B	6817	0	6472	176	0
3	A	28	0	26	0	0
3	B	28	0	26	0	0
4	B	1	0	0	0	0
5	B	10	0	10	1	0
6	B	33	0	30	3	0
All	All	19028	0	18593	372	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 10.

The worst 5 of 372 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:992:LEU:HB3	1:A:993:SER:HA	1.42	1.02
1:A:1280:TYR:HB2	1:A:1281:GLY:HA2	1.51	0.90
2:B:294:ASN:HB3	2:B:295:HIS:HA	1.56	0.85
1:A:1286:SER:HB2	1:A:1287:THR:HA	1.65	0.79
1:A:1571:GLU:HB2	1:A:1572:ASN:HA	1.65	0.79

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	1516/1580 (96%)	1390 (92%)	113 (8%)	13 (1%)	14	47
2	B	863/913 (94%)	699 (81%)	148 (17%)	16 (2%)	6	33
All	All	2379/2493 (95%)	2089 (88%)	261 (11%)	29 (1%)	10	41

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	VAL
1	A	833	VAL
2	B	95	PRO
2	B	169	ASP
1	A	1627	ILE

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	1356/1403 (97%)	1267 (93%)	89 (7%)	15	41
2	B	775/810 (96%)	719 (93%)	56 (7%)	13	38
All	All	2131/2213 (96%)	1986 (93%)	145 (7%)	14	40

5 of 145 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	580	THR
2	B	911	ILE
2	B	629	GLU
2	B	803	PHE
1	A	922	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	26	HIS

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Mol	Chain	Res	Type
2	B	292	ASN
2	B	894	GLN
2	B	63	GLN
2	B	162	ASN

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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	1855	2	14,14,15	1.74	3 (21%)	17,19,21	3.46	6 (35%)
6	MAN	B	1574	2	11,11,12	1.33	2 (18%)	15,15,17	1.88	4 (26%)
5	FUC	B	1005	2	10,10,11	0.97	1 (10%)	14,14,16	2.25	6 (42%)
6	MAN	B	1571	2	11,11,12	1.59	2 (18%)	15,15,17	3.47	7 (46%)
6	MAN	B	1568	2	11,11,12	1.47	1 (9%)	15,15,17	3.88	7 (46%)
3	NAG	B	1324	2	14,14,15	3.48	4 (28%)	17,19,21	2.82	9 (52%)
3	NAG	A	1911	1	14,14,15	2.49	6 (42%)	17,19,21	2.31	6 (35%)
3	NAG	A	2630	1	14,14,15	2.25	2 (14%)	17,19,21	1.69	4 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	1855	2	-	1/6/23/26	0/1/1/1
6	MAN	B	1574	2	1/1/4/5	2/2/19/22	0/1/1/1
5	FUC	B	1005	2	-	-	0/1/1/1
6	MAN	B	1571	2	1/1/4/5	2/2/19/22	0/1/1/1
6	MAN	B	1568	2	1/1/4/5	2/2/19/22	0/1/1/1
3	NAG	B	1324	2	-	0/6/23/26	0/1/1/1
3	NAG	A	1911	1	-	1/6/23/26	0/1/1/1
3	NAG	A	2630	1	-	0/6/23/26	0/1/1/1

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1324	NAG	C1-C2	11.80	1.68	1.52
3	A	2630	NAG	C1-C2	7.26	1.62	1.52
3	A	1911	NAG	C1-C2	6.14	1.60	1.52
3	B	1855	NAG	C1-C2	4.83	1.58	1.52
3	B	1324	NAG	C3-C2	3.76	1.60	1.52

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1855	NAG	C1-O5-C5	11.90	128.14	112.19
6	B	1568	MAN	C1-O5-C5	11.21	127.22	112.19
6	B	1571	MAN	C1-O5-C5	8.39	123.42	112.19
3	B	1324	NAG	C1-O5-C5	7.84	122.69	112.19
6	B	1571	MAN	O4-C4-C3	-6.72	94.54	110.38

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	B	1568	MAN	C1
6	B	1571	MAN	C1
6	B	1574	MAN	C1

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	1568	MAN	O5-C5-C6-O6
6	B	1574	MAN	C4-C5-C6-O6
6	B	1574	MAN	O5-C5-C6-O6
6	B	1571	MAN	O5-C5-C6-O6
6	B	1568	MAN	C4-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1005	FUC	1	0
6	B	1571	MAN	2	0
6	B	1568	MAN	1	0

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, 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	1528/1580 (96%)	0.28	36 (2%) 59 35	66, 142, 207, 242	0
2	B	871/913 (95%)	0.62	65 (7%) 20 13	85, 182, 243, 264	0
All	All	2399/2493 (96%)	0.41	101 (4%) 40 22	66, 154, 231, 264	0

The worst 5 of 101 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	594	PRO	5.1
1	A	1285	TYR	4.7
2	B	834	ILE	4.4
2	B	483	ILE	4.4
1	A	1528	VAL	4.1

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](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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
3	NAG	A	2630	14/15	0.01	0.15	227,231,233,233	0
3	NAG	B	1324	14/15	0.31	0.16	190,194,197,197	0
5	FUC	B	1005	10/11	0.63	0.16	166,166,168,168	0
6	MAN	B	1574	11/12	0.74	0.14	188,190,191,193	0
6	MAN	B	1571	11/12	0.80	0.15	153,156,157,158	0
4	CA	B	1000	1/1	0.83	0.13	146,146,146,146	0
3	NAG	A	1911	14/15	0.85	0.09	118,122,124,125	0
3	NAG	B	1855	14/15	0.90	0.14	198,201,204,204	0
6	MAN	B	1568	11/12	0.93	0.11	169,172,173,174	0

6.5 Other polymers [i](#)

There are no such residues in this entry.