



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 03:03 PM GMT

PDB ID : 3T5O
Title : Crystal Structure of human Complement Component C6
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Deposited on : 2011-07-27
Resolution : 2.87 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

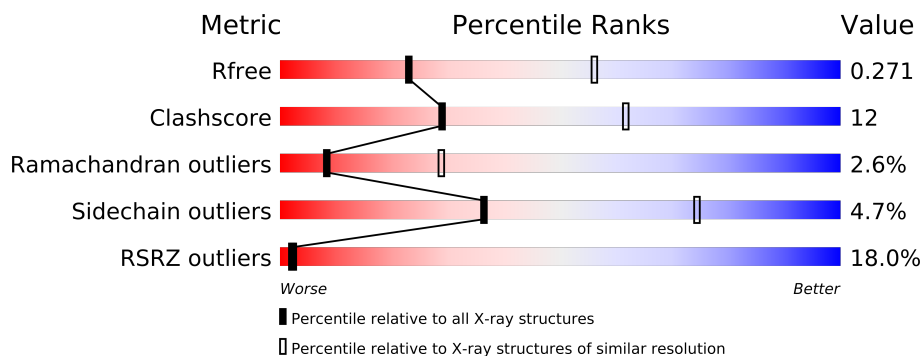
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.87 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}	66092	1524 (2.90-2.82)
Clashscore	79885	1879 (2.90-2.82)
Ramachandran outliers	78287	1824 (2.90-2.82)
Sidechain outliers	78261	1827 (2.90-2.82)
RSRZ outliers	66119	1526 (2.90-2.82)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	913	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	FUL	A	1004	-	X

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 6934 atoms, of which 0 are hydrogen and 0 are deuterium.

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 component C6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	871	Total	C	N	O	S	0	0	0
			6830	4222	1203	1336	69			

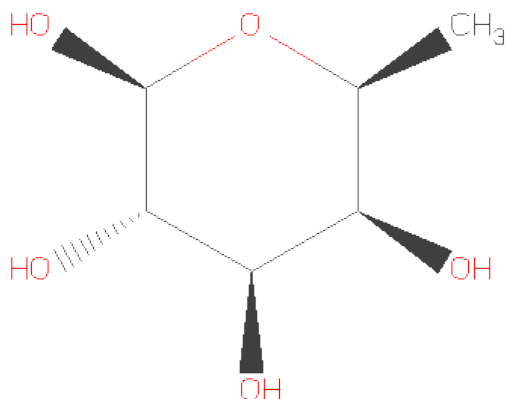
- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cd	0	0
			1	1		

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is SUGAR (BETA-L-FUCOSE) (three-letter code: FUL) (formula: C₆H₁₂O₅).

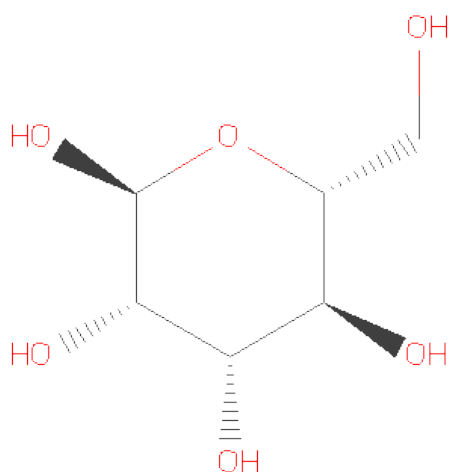


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	2	Total	C	O	0	0
			21	12	9		

- Molecule 6 is SUGAR (ALPHA-D-MANNOSE) (three-letter code: MAN) (formula: C₆H₁₂O₆).

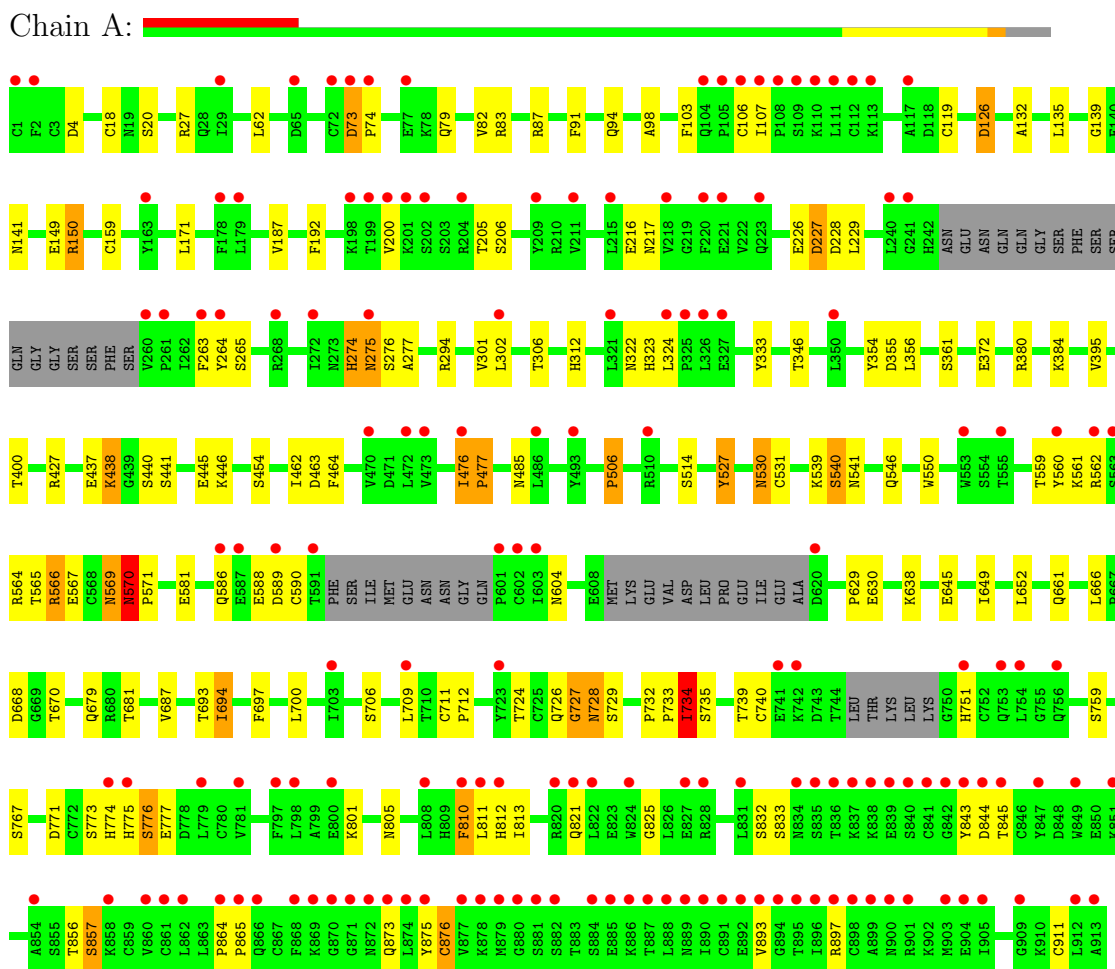


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 component C6



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	146.81Å 180.15Å 60.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.06 – 2.87 47.53 – 2.87	Depositor EDS
% Data completeness (in resolution range)	94.9 (43.06-2.87) 94.9 (47.53-2.87)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.86Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.222 , 0.276 0.219 , 0.271	Depositor DCC
R_{free} test set	2180 reflections (6.10%)	DCC
Wilson B-factor (Å ²)	82.3	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 74.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 35749 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6934	wwPDB-VP
Average B, all atoms (Å ²)	121.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BGC, NAG, CD, FUC, FUL, 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	0.50	1/6973 (0.0%)	0.67	3/9409 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	531	CYS	CB-SG	5.23	1.91	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	652	LEU	CA-CB-CG	-6.84	99.56	115.30
1	A	570	ASN	N-CA-C	-5.68	95.67	111.00
1	A	666	LEU	CA-CB-CG	-5.07	103.64	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6830	0	0	86	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	28	0	0	0	0
4	A	10	0	0	1	0
5	A	21	0	0	0	0
6	A	44	0	0	0	0
All	All	6934	0	0	86	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (86) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:570:ASN:CB	1:A:571:PRO:CD	2.33	1.05
1:A:567:GLU:O	1:A:569:ASN:OD1	1.84	0.96
1:A:126:ASP:OD1	1:A:150:ARG:NH2	2.19	0.76
1:A:734:ILE:N	1:A:734:ILE:CD1	2.51	0.72
1:A:205:THR:O	1:A:205:THR:CG2	2.42	0.68
1:A:733:PRO:O	1:A:735:SER:N	2.28	0.66
1:A:569:ASN:OD1	1:A:569:ASN:N	2.30	0.65
1:A:726:GLN:NE2	1:A:729:SER:OG	2.29	0.64
1:A:726:GLN:O	1:A:728:ASN:N	2.30	0.64
1:A:728:ASN:C	1:A:728:ASN:OD1	2.38	0.60
1:A:73:ASP:N	1:A:74:PRO:CD	2.65	0.60
1:A:139:GLY:N	1:A:149:GLU:OE2	2.35	0.60
1:A:464:PHE:O	1:A:464:PHE:CD1	2.57	0.58
1:A:274:HIS:O	1:A:276:SER:N	2.37	0.58
1:A:810:PHE:CD2	1:A:811:LEU:N	2.73	0.57
1:A:440:SER:OG	1:A:441:SER:N	2.39	0.56
1:A:564:ARG:NH2	1:A:586:GLN:OE1	2.40	0.55
1:A:812:HIS:CD2	1:A:813:ILE:O	2.60	0.54
1:A:638:LYS:NZ	1:A:645:GLU:OE1	2.40	0.54
1:A:801:LYS:NZ	1:A:844:ASP:OD1	2.40	0.53
1:A:832:SER:OG	1:A:833:SER:N	2.39	0.53
1:A:476:ILE:CB	1:A:477:PRO:CD	2.87	0.53
1:A:774:HIS:O	1:A:775:HIS:C	2.48	0.52
1:A:546:GLN:CB	1:A:571:PRO:CG	2.87	0.52
1:A:821:GLN:O	1:A:825:GLY:N	2.43	0.52
1:A:567:GLU:C	1:A:569:ASN:OD1	2.48	0.51
1:A:739:THR:CG2	1:A:740:CYS:N	2.74	0.51
1:A:274:HIS:O	1:A:277:ALA:N	2.45	0.50
1:A:333:TYR:CE2	1:A:485:ASN:CB	2.95	0.50
1:A:372:GLU:N	4:A:1004:FUL:C1	2.75	0.50
1:A:4:ASP:OD1	1:A:27:ARG:NH1	2.44	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:83:ARG:NH2	1:A:98:ALA:O	2.45	0.50
1:A:751:HIS:CG	1:A:751:HIS:O	2.65	0.50
1:A:301:VAL:O	1:A:302:LEU:CD1	2.60	0.49
1:A:106:CYS:SG	1:A:107:ILE:N	2.85	0.49
1:A:527:TYR:CD2	1:A:527:TYR:N	2.80	0.49
1:A:734:ILE:O	1:A:735:SER:C	2.51	0.49
1:A:727:GLY:O	1:A:728:ASN:OD1	2.30	0.49
1:A:873:GLN:NE2	1:A:875:TYR:CE1	2.81	0.49
1:A:427:ARG:N	1:A:454:SER:OG	2.47	0.48
1:A:294:ARG:NH2	1:A:355:ASP:OD1	2.46	0.48
1:A:876:CYS:CA	1:A:911:CYS:CB	2.93	0.47
1:A:767:SER:N	1:A:771:ASP:OD2	2.48	0.47
1:A:776:SER:O	1:A:777:GLU:C	2.53	0.47
1:A:569:ASN:O	1:A:570:ASN:C	2.52	0.47
1:A:264:TYR:CD1	1:A:265:SER:O	2.68	0.46
1:A:380:ARG:NH1	1:A:380:ARG:CG	2.79	0.46
1:A:306:THR:N	1:A:346:THR:O	2.50	0.45
1:A:91:PHE:CD1	1:A:530:ASN:ND2	2.84	0.45
1:A:560:TYR:CB	1:A:589:ASP:CB	2.94	0.45
1:A:581:GLU:OE1	1:A:581:GLU:CA	2.65	0.45
1:A:629:PRO:O	1:A:630:GLU:C	2.55	0.45
1:A:192:PHE:CE2	1:A:312:HIS:CD2	3.05	0.44
1:A:354:TYR:CZ	1:A:356:LEU:CD1	3.01	0.44
1:A:226:GLU:O	1:A:228:ASP:N	2.51	0.44
1:A:205:THR:O	1:A:206:SER:OG	2.36	0.44
1:A:560:TYR:O	1:A:590:CYS:N	2.51	0.44
1:A:810:PHE:CG	1:A:811:LEU:N	2.86	0.43
1:A:550:TRP:CZ2	1:A:566:ARG:NE	2.87	0.43
1:A:856:THR:O	1:A:857:SER:CB	2.66	0.43
1:A:694:ILE:CG2	1:A:709:LEU:CD1	2.95	0.43
1:A:559:THR:C	1:A:561:LYS:N	2.71	0.43
1:A:171:LEU:N	1:A:171:LEU:CD1	2.81	0.43
1:A:697:PHE:C	1:A:697:PHE:CD2	2.92	0.43
1:A:216:GLU:O	1:A:217:ASN:ND2	2.51	0.43
1:A:801:LYS:O	1:A:805:ASN:CB	2.67	0.43
1:A:562:ARG:NH2	1:A:588:GLU:OE1	2.52	0.43
1:A:864:PRO:N	1:A:865:PRO:CD	2.81	0.42
1:A:226:GLU:O	1:A:229:LEU:N	2.52	0.42
1:A:437:GLU:O	1:A:438:LYS:C	2.56	0.42
1:A:226:GLU:O	1:A:227:ASP:C	2.57	0.42
1:A:322:ASN:C	1:A:324:LEU:N	2.72	0.42
1:A:589:ASP:OD1	1:A:589:ASP:N	2.53	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:462:ILE:O	1:A:463:ASP:C	2.57	0.42
1:A:539:LYS:O	1:A:540:SER:O	2.38	0.41
1:A:132:ALA:O	1:A:135:LEU:N	2.54	0.41
1:A:773:SER:OG	1:A:774:HIS:N	2.53	0.41
1:A:79:GLN:O	1:A:103:PHE:CA	2.69	0.41
1:A:843:TYR:N	1:A:844:ASP:CA	2.83	0.41
1:A:263:PHE:CD2	1:A:263:PHE:N	2.88	0.41
1:A:62:LEU:N	1:A:87:ARG:O	2.54	0.40
1:A:706:SER:OG	1:A:724:THR:OG1	2.40	0.40
1:A:893:VAL:CG1	1:A:897:ARG:CZ	2.99	0.40
1:A:445:GLU:O	1:A:446:LYS:C	2.60	0.40
1:A:274:HIS:O	1:A:275:ASN:C	2.60	0.40
1:A:322:ASN:O	1:A:324:LEU:N	2.54	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	861/913 (94%)	734 (85%)	105 (12%)	22 (3%)	8	29

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	ARG
1	A	540	SER
1	A	570	ASN
1	A	712	PRO
1	A	727	GLY
1	A	734	ILE
1	A	141	ASN
1	A	275	ASN
1	A	323	HIS
1	A	668	ASP

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Mol	Chain	Res	Type
1	A	857	SER
1	A	227	ASP
1	A	810	PHE
1	A	438	LYS
1	A	759	SER
1	A	506	PRO
1	A	687	VAL
1	A	20	SER
1	A	476	ILE
1	A	477	PRO
1	A	73	ASP
1	A	732	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	772/810 (95%)	736 (95%)	36 (5%)	36 74

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	CYS
1	A	82	VAL
1	A	94	GLN
1	A	119	CYS
1	A	126	ASP
1	A	159	CYS
1	A	187	VAL
1	A	200	VAL
1	A	274	HIS
1	A	361	SER
1	A	384	LYS
1	A	395	VAL
1	A	400	THR
1	A	506	PRO
1	A	514	SER
1	A	527	TYR

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Mol	Chain	Res	Type
1	A	530	ASN
1	A	541	ASN
1	A	565	THR
1	A	566	ARG
1	A	569	ASN
1	A	604	ASN
1	A	649	ILE
1	A	661	GLN
1	A	670	THR
1	A	679	GLN
1	A	681	THR
1	A	693	THR
1	A	694	ILE
1	A	700	LEU
1	A	711	CYS
1	A	728	ASN
1	A	734	ILE
1	A	776	SER
1	A	845	THR
1	A	876	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

4 carbohydrates 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	$\# Z > 2$
3	NAG	A	1002	1,3	12,14,15	0.74	1 (8%)	15,19,21	0.76	0
3	NAG	A	1003	3	12,14,15	0.62	0	15,19,21	0.96	1 (6%)
5	FUC	A	1005	1,5	9,10,11	0.85	0	10,14,16	1.84	3 (30%)
5	BGC	A	1006	5	10,11,12	0.97	1 (10%)	11,15,17	1.56	2 (18%)

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	A	1002	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1003	3	-	0/6/23/26	0/1/1/1
5	FUC	A	1005	1,5	-	0/0/17/20	0/1/1/1
5	BGC	A	1006	5	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1006	BGC	O5-C5	-2.72	1.40	1.45
3	A	1002	NAG	O5-C5	-2.29	1.41	1.45

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1006	BGC	O5-C5-C4	-3.33	106.42	110.65
5	A	1005	FUC	C6-C5-C4	-3.30	107.70	113.06
5	A	1005	FUC	O5-C5-C6	3.19	113.17	108.03
3	A	1003	NAG	O5-C5-C6	3.06	110.19	106.98
5	A	1005	FUC	O4-C4-C5	-2.16	104.78	109.78
5	A	1006	BGC	C3-C4-C5	-2.11	106.44	110.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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$
4	FUL	A	1004	1	9,10,11	0.69	0	10,14,16	0.83	0
6	MAN	A	1007	1	10,11,12	1.11	1 (10%)	11,15,17	1.82	3 (27%)
6	MAN	A	1008	1	10,11,12	1.36	1 (10%)	11,15,17	2.10	4 (36%)
6	MAN	A	1009	1	10,11,12	0.78	0	11,15,17	1.65	2 (18%)
6	MAN	A	1010	1	10,11,12	0.66	0	11,15,17	1.53	2 (18%)

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	FUL	A	1004	1	-	0/0/17/20	0/1/1/1
6	MAN	A	1007	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1008	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1009	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1010	1	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1008	MAN	O5-C5	-2.93	1.40	1.45
6	A	1007	MAN	O5-C5	-2.50	1.40	1.45

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1008	MAN	O5-C5-C6	4.08	111.27	106.98
6	A	1007	MAN	O5-C5-C6	4.01	111.19	106.98
6	A	1010	MAN	C4-C3-C2	-3.80	105.40	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1009	MAN	O5-C5-C4	3.57	115.18	110.65
6	A	1008	MAN	O4-C4-C3	-3.21	103.16	110.35
6	A	1009	MAN	C3-C4-C5	3.19	115.90	110.20
6	A	1007	MAN	O5-C5-C4	-3.07	106.76	110.65
6	A	1008	MAN	O5-C5-C4	-2.69	107.23	110.65
6	A	1007	MAN	O4-C4-C3	-2.54	104.65	110.35
6	A	1008	MAN	O4-C4-C5	-2.24	103.37	109.28
6	A	1010	MAN	O5-C5-C4	2.04	113.24	110.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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	871/913 (95%)	1.12	159 (18%) 2 2	41, 107, 238, 291	0

All (159) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	888	LEU	14.5
1	A	840	SER	13.5
1	A	913	ALA	13.4
1	A	843	TYR	12.4
1	A	842	GLY	11.7
1	A	905	ILE	11.5
1	A	874	LEU	10.7
1	A	111	LEU	10.5
1	A	871	GLY	10.1
1	A	893	VAL	10.1
1	A	892	GLU	10.1
1	A	873	GLN	9.9
1	A	879	MET	9.9
1	A	861	CYS	9.5
1	A	865	PRO	8.7
1	A	870	GLY	8.5
1	A	110	LYS	8.5
1	A	753	GLN	8.1
1	A	260	VAL	7.9
1	A	587	GLU	7.8
1	A	862	LEU	7.8
1	A	884	SER	7.7
1	A	889	ASN	7.7
1	A	473	VAL	7.6
1	A	775	HIS	7.6
1	A	875	TYR	7.4
1	A	838	LYS	7.3

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Mol	Chain	Res	Type	RSRZ
1	A	903	MET	7.1
1	A	742	LYS	7.0
1	A	105	PRO	6.9
1	A	887	THR	6.8
1	A	264	TYR	6.8
1	A	824	TRP	6.7
1	A	899	ALA	6.7
1	A	73	ASP	6.7
1	A	834	ASN	6.6
1	A	200	VAL	6.6
1	A	877	VAL	6.6
1	A	261	PRO	6.2
1	A	860	VAL	6.2
1	A	827	GLU	6.1
1	A	602	CYS	6.0
1	A	847	TYR	6.0
1	A	326	LEU	5.9
1	A	601	PRO	5.9
1	A	885	GLU	5.8
1	A	836	THR	5.8
1	A	820	ARG	5.8
1	A	811	LEU	5.6
1	A	886	LYS	5.5
1	A	754	LEU	5.5
1	A	896	ILE	5.5
1	A	880	GLY	5.3
1	A	912	LEU	5.3
1	A	553	TRP	5.1
1	A	808	LEU	5.0
1	A	112	CYS	5.0
1	A	562	ARG	4.9
1	A	831	LEU	4.8
1	A	849	TRP	4.8
1	A	878	LYS	4.7
1	A	486	LEU	4.6
1	A	835	SER	4.6
1	A	868	PHE	4.6
1	A	810	PHE	4.6
1	A	204	ARG	4.6
1	A	882	SER	4.5
1	A	223	GLN	4.4
1	A	211	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	864	PRO	4.4
1	A	837	LYS	4.3
1	A	895	THR	4.2
1	A	854	ALA	4.2
1	A	591	THR	4.2
1	A	781	VAL	4.2
1	A	563	SER	4.1
1	A	869	LYS	4.1
1	A	272	ILE	4.1
1	A	797	PHE	4.0
1	A	821	GLN	4.0
1	A	324	LEU	3.9
1	A	201	LYS	3.9
1	A	891	CYS	3.9
1	A	839	GLU	3.8
1	A	179	LEU	3.5
1	A	845	THR	3.5
1	A	109	SER	3.5
1	A	890	ILE	3.5
1	A	220	PHE	3.5
1	A	894	GLY	3.4
1	A	72	CYS	3.4
1	A	751	HIS	3.3
1	A	198	LYS	3.3
1	A	107	ILE	3.3
1	A	822	LEU	3.2
1	A	828	ARG	3.1
1	A	709	LEU	3.1
1	A	756	GLN	3.1
1	A	221	GLU	3.1
1	A	555	THR	3.0
1	A	113	LYS	3.0
1	A	897	ARG	2.9
1	A	858	LYS	2.9
1	A	703	ILE	2.8
1	A	900	ASN	2.8
1	A	268	ARG	2.8
1	A	178	PHE	2.8
1	A	774	HIS	2.8
1	A	812	HIS	2.8
1	A	327	GLU	2.8
1	A	108	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	325	PRO	2.7
1	A	904	GLU	2.7
1	A	851	LYS	2.7
1	A	218	VAL	2.7
1	A	321	LEU	2.7
1	A	881	SER	2.7
1	A	472	LEU	2.6
1	A	163	TYR	2.6
1	A	909	GLY	2.6
1	A	510	ARG	2.6
1	A	104	GLN	2.5
1	A	241	GLY	2.5
1	A	470	VAL	2.5
1	A	1	CYS	2.5
1	A	779	LEU	2.5
1	A	106	CYS	2.4
1	A	841	CYS	2.4
1	A	215	LEU	2.4
1	A	77	GLU	2.4
1	A	117	ALA	2.4
1	A	898	CYS	2.3
1	A	800	GLU	2.3
1	A	589	ASP	2.3
1	A	586	GLN	2.3
1	A	603	ILE	2.3
1	A	209	TYR	2.3
1	A	65	ASP	2.2
1	A	199	THR	2.2
1	A	872	ASN	2.2
1	A	350	LEU	2.2
1	A	844	ASP	2.2
1	A	560	TYR	2.2
1	A	275	ASN	2.2
1	A	74	PRO	2.2
1	A	476	ILE	2.1
1	A	202	SER	2.1
1	A	620	ASP	2.1
1	A	723	TYR	2.1
1	A	901	ARG	2.1
1	A	493	TYR	2.1
1	A	2	PHE	2.1
1	A	741	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	302	LEU	2.0
1	A	263	PHE	2.0
1	A	240	LEU	2.0
1	A	798	LEU	2.0
1	A	866	GLN	2.0
1	A	29	ILE	2.0

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

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

6.3 Carbohydrates ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	BGC	A	1006	11/12	0.21	2.26	51,62,72,80	0
3	NAG	A	1002	14/15	0.21	-0.88	120,151,163,169	0
5	FUC	A	1005	10/11	0.18	-1.98	47,56,68,78	0
3	NAG	A	1003	14/15	0.41	-2.76	148,174,183,187	0

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	FUL	A	1004	10/11	0.28	2.55	154,162,169,172	0
6	MAN	A	1007	11/12	0.23	1.12	73,87,95,102	0
2	CD	A	1001	1/1	0.20	0.17	133,133,133,133	0
6	MAN	A	1008	11/12	0.20	-0.33	58,71,81,107	0
6	MAN	A	1009	11/12	0.17	-0.37	152,162,169,172	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	MAN	A	1010	11/12	0.18	-0.45	127,137,142,143	0

6.5 Other polymers ⓘ

There are no such residues in this entry.