



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2018 – 07:39 PM EST

PDB ID : 5NC1
Title : Structure of the distal domain of mouse adenovirus 2 fibre bound to N-acetyl-glucosamine
Authors : Singh, A.K.; van Raaij, M.J.
Deposited on : 2017-03-03
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

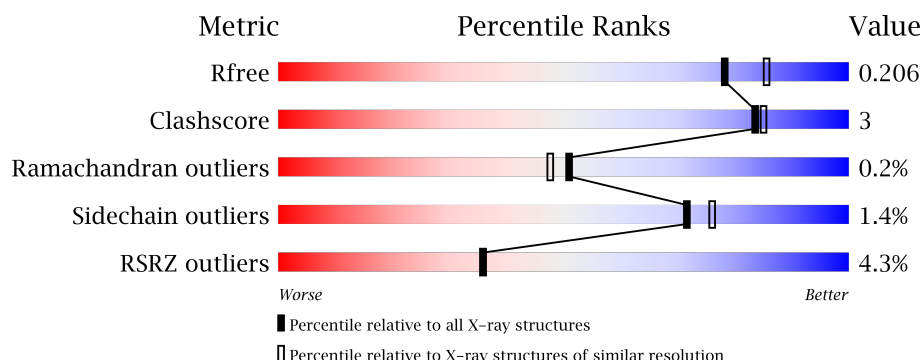
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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. 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	237	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> % </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 73% 8% 19% </div> </div>
1	B	237	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> 5% </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 77% • • 19% </div> </div>
1	C	237	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> 5% </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 77% • 19% </div> </div>

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
2	NAG	B	801	-	-	-	X
3	SO4	A	804	-	-	-	X
3	SO4	B	806	-	-	-	X
3	SO4	C	803	-	-	-	X
4	GOL	B	807	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5036 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 Fiber.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	193	Total	C	N	O	S	0	3	0
			1510	962	241	296	11			
1	B	193	Total	C	N	O	S	0	6	0
			1541	982	249	298	12			
1	C	193	Total	C	N	O	S	0	6	0
			1529	974	244	300	11			

There are 105 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	551	GLY	-	expression tag	UNP E7CH51
A	552	SER	-	expression tag	UNP E7CH51
A	553	SER	-	expression tag	UNP E7CH51
A	554	HIS	-	expression tag	UNP E7CH51
A	555	HIS	-	expression tag	UNP E7CH51
A	556	HIS	-	expression tag	UNP E7CH51
A	557	HIS	-	expression tag	UNP E7CH51
A	558	HIS	-	expression tag	UNP E7CH51
A	559	HIS	-	expression tag	UNP E7CH51
A	560	SER	-	expression tag	UNP E7CH51
A	561	SER	-	expression tag	UNP E7CH51
A	562	GLY	-	expression tag	UNP E7CH51
A	563	LEU	-	expression tag	UNP E7CH51
A	564	VAL	-	expression tag	UNP E7CH51
A	565	PRO	-	expression tag	UNP E7CH51
A	566	ARG	-	expression tag	UNP E7CH51
A	567	GLY	-	expression tag	UNP E7CH51
A	568	SER	-	expression tag	UNP E7CH51
A	569	HIS	-	expression tag	UNP E7CH51
A	570	MET	-	expression tag	UNP E7CH51
A	571	ALA	-	expression tag	UNP E7CH51
A	572	SER	-	expression tag	UNP E7CH51
A	573	MET	-	expression tag	UNP E7CH51

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Chain	Residue	Modelled	Actual	Comment	Reference
A	574	THR	-	expression tag	UNP E7CH51
A	575	GLY	-	expression tag	UNP E7CH51
A	576	GLY	-	expression tag	UNP E7CH51
A	577	GLN	-	expression tag	UNP E7CH51
A	578	GLN	-	expression tag	UNP E7CH51
A	579	MET	-	expression tag	UNP E7CH51
A	580	GLY	-	expression tag	UNP E7CH51
A	581	ARG	-	expression tag	UNP E7CH51
A	582	GLY	-	expression tag	UNP E7CH51
A	583	SER	-	expression tag	UNP E7CH51
A	584	GLU	-	expression tag	UNP E7CH51
A	585	PHE	-	expression tag	UNP E7CH51
B	551	GLY	-	expression tag	UNP E7CH51
B	552	SER	-	expression tag	UNP E7CH51
B	553	SER	-	expression tag	UNP E7CH51
B	554	HIS	-	expression tag	UNP E7CH51
B	555	HIS	-	expression tag	UNP E7CH51
B	556	HIS	-	expression tag	UNP E7CH51
B	557	HIS	-	expression tag	UNP E7CH51
B	558	HIS	-	expression tag	UNP E7CH51
B	559	HIS	-	expression tag	UNP E7CH51
B	560	SER	-	expression tag	UNP E7CH51
B	561	SER	-	expression tag	UNP E7CH51
B	562	GLY	-	expression tag	UNP E7CH51
B	563	LEU	-	expression tag	UNP E7CH51
B	564	VAL	-	expression tag	UNP E7CH51
B	565	PRO	-	expression tag	UNP E7CH51
B	566	ARG	-	expression tag	UNP E7CH51
B	567	GLY	-	expression tag	UNP E7CH51
B	568	SER	-	expression tag	UNP E7CH51
B	569	HIS	-	expression tag	UNP E7CH51
B	570	MET	-	expression tag	UNP E7CH51
B	571	ALA	-	expression tag	UNP E7CH51
B	572	SER	-	expression tag	UNP E7CH51
B	573	MET	-	expression tag	UNP E7CH51
B	574	THR	-	expression tag	UNP E7CH51
B	575	GLY	-	expression tag	UNP E7CH51
B	576	GLY	-	expression tag	UNP E7CH51
B	577	GLN	-	expression tag	UNP E7CH51
B	578	GLN	-	expression tag	UNP E7CH51
B	579	MET	-	expression tag	UNP E7CH51
B	580	GLY	-	expression tag	UNP E7CH51

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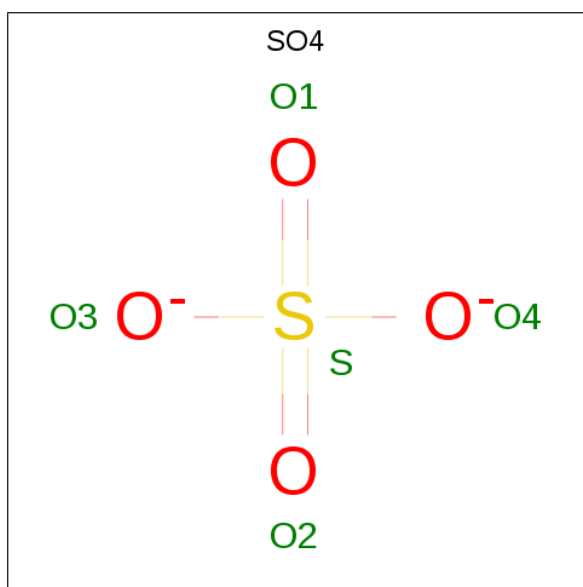
Chain	Residue	Modelled	Actual	Comment	Reference
B	581	ARG	-	expression tag	UNP E7CH51
B	582	GLY	-	expression tag	UNP E7CH51
B	583	SER	-	expression tag	UNP E7CH51
B	584	GLU	-	expression tag	UNP E7CH51
B	585	PHE	-	expression tag	UNP E7CH51
C	551	GLY	-	expression tag	UNP E7CH51
C	552	SER	-	expression tag	UNP E7CH51
C	553	SER	-	expression tag	UNP E7CH51
C	554	HIS	-	expression tag	UNP E7CH51
C	555	HIS	-	expression tag	UNP E7CH51
C	556	HIS	-	expression tag	UNP E7CH51
C	557	HIS	-	expression tag	UNP E7CH51
C	558	HIS	-	expression tag	UNP E7CH51
C	559	HIS	-	expression tag	UNP E7CH51
C	560	SER	-	expression tag	UNP E7CH51
C	561	SER	-	expression tag	UNP E7CH51
C	562	GLY	-	expression tag	UNP E7CH51
C	563	LEU	-	expression tag	UNP E7CH51
C	564	VAL	-	expression tag	UNP E7CH51
C	565	PRO	-	expression tag	UNP E7CH51
C	566	ARG	-	expression tag	UNP E7CH51
C	567	GLY	-	expression tag	UNP E7CH51
C	568	SER	-	expression tag	UNP E7CH51
C	569	HIS	-	expression tag	UNP E7CH51
C	570	MET	-	expression tag	UNP E7CH51
C	571	ALA	-	expression tag	UNP E7CH51
C	572	SER	-	expression tag	UNP E7CH51
C	573	MET	-	expression tag	UNP E7CH51
C	574	THR	-	expression tag	UNP E7CH51
C	575	GLY	-	expression tag	UNP E7CH51
C	576	GLY	-	expression tag	UNP E7CH51
C	577	GLN	-	expression tag	UNP E7CH51
C	578	GLN	-	expression tag	UNP E7CH51
C	579	MET	-	expression tag	UNP E7CH51
C	580	GLY	-	expression tag	UNP E7CH51
C	581	ARG	-	expression tag	UNP E7CH51
C	582	GLY	-	expression tag	UNP E7CH51
C	583	SER	-	expression tag	UNP E7CH51
C	584	GLU	-	expression tag	UNP E7CH51
C	585	PHE	-	expression tag	UNP E7CH51

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		
2	C	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 3 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



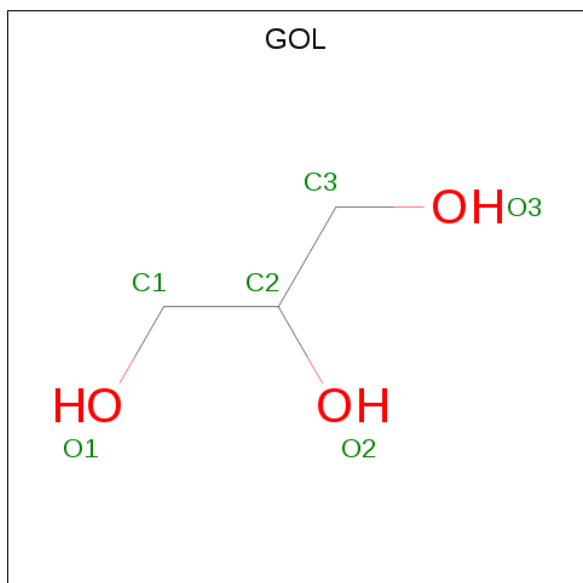
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		

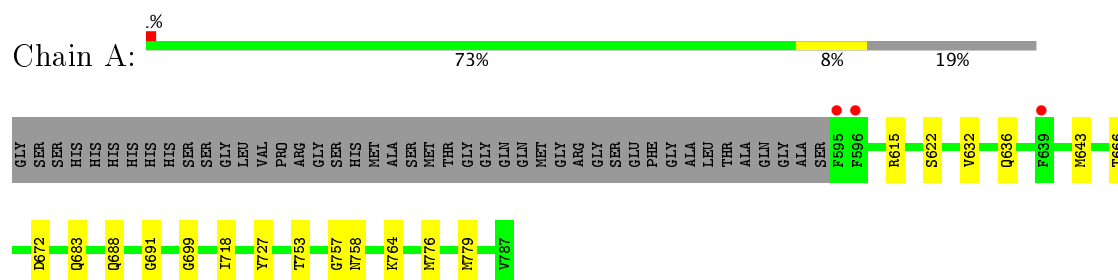
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	127	Total 127	O 127	0	0
5	B	132	Total 132	O 132	0	0
5	C	91	Total 91	O 91	0	0

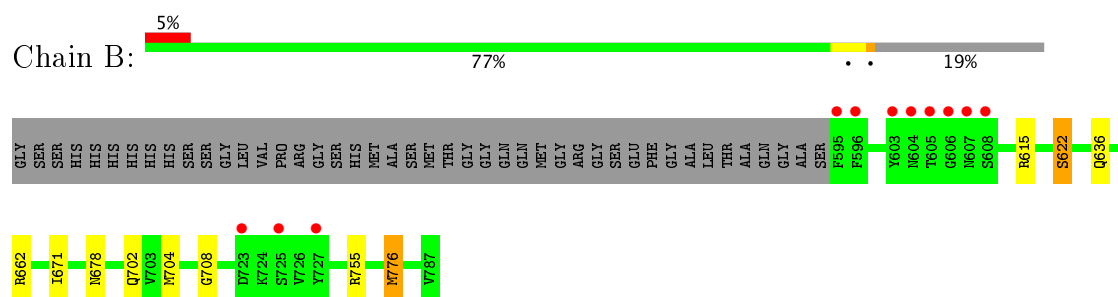
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

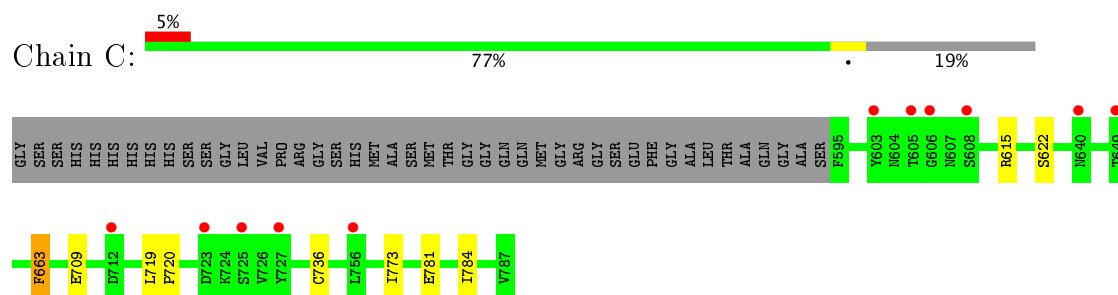
- Molecule 1: Fiber



- Molecule 1: Fiber



- Molecule 1: Fiber



4 Data and refinement statistics

Property	Value	Source
Space group	I 21 3	Depositor
Cell constants a, b, c, α , β , γ	163.41Å 163.41Å 163.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.00 – 2.00 28.89 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (28.00-2.00) 100.0 (28.89-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.76 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.165 , 0.205 0.173 , 0.206	Depositor DCC
R_{free} test set	2413 reflections (5.19%)	DCC
Wilson B-factor (Å ²)	23.5	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.048 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5036	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% 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: GOL, NAG, SO4

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	0.55	0/1554	0.76	0/2111
1	B	0.54	0/1591	0.71	2/2157 (0.1%)
1	C	0.49	0/1582	0.66	0/2147
All	All	0.53	0/4727	0.71	2/6415 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	662	ARG	NE-CZ-NH2	-5.45	117.57	120.30
1	B	662	ARG	NE-CZ-NH1	5.40	123.00	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1510	0	1471	14	0
1	B	1541	0	1511	7	0
1	C	1529	0	1494	10	0
2	A	15	0	15	0	0
2	B	15	0	15	0	0
2	C	15	0	15	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	15	0	0	0	0
3	B	25	0	0	1	0
3	C	15	0	0	1	0
4	B	6	0	8	0	0
5	A	127	0	0	1	0
5	B	132	0	0	0	0
5	C	91	0	0	2	0
All	All	5036	0	4529	26	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 3.

The worst 5 of 26 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:B:615:ARG:NH1	1:C:622:SER:OG	2.17	0.76
1:A:622:SER:OG	1:C:615[B]:ARG:NH1	2.27	0.68
1:A:727:TYR:CD2	1:A:753[A]:THR:HG22	2.34	0.62
1:B:755[B]:ARG:HG3	3:B:805:SO4:O2	2.00	0.61
1:A:615:ARG:NH1	1:B:622:SER:OG	2.37	0.58

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	194/237 (82%)	191 (98%)	3 (2%)	0	100	100
1	B	197/237 (83%)	191 (97%)	6 (3%)	0	100	100
1	C	197/237 (83%)	189 (96%)	7 (4%)	1 (0%)	32	26
All	All	588/711 (83%)	571 (97%)	16 (3%)	1 (0%)	51	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	720	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	170/198 (86%)	167 (98%)	3 (2%)	64	68
1	B	173/198 (87%)	170 (98%)	3 (2%)	66	70
1	C	173/198 (87%)	172 (99%)	1 (1%)	89	92
All	All	516/594 (87%)	509 (99%)	7 (1%)	71	76

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	622	SER
1	C	663	PHE
1	B	678	ASN
1	A	718	ILE
1	B	776	MET

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 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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

15 ligands 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	A	801	-	15,15,15	0.37	0	21,21,21	1.55	4 (19%)
3	SO4	A	802	-	4,4,4	0.37	0	6,6,6	0.36	0
3	SO4	A	803	-	4,4,4	0.41	0	6,6,6	0.32	0
3	SO4	A	804	-	4,4,4	0.44	0	6,6,6	0.25	0
2	NAG	B	801	-	15,15,15	0.78	0	21,21,21	1.02	1 (4%)
3	SO4	B	802	-	4,4,4	0.18	0	6,6,6	0.51	0
3	SO4	B	803	-	4,4,4	0.42	0	6,6,6	0.26	0
3	SO4	B	804	-	4,4,4	0.19	0	6,6,6	0.38	0
3	SO4	B	805	-	4,4,4	0.39	0	6,6,6	0.24	0
3	SO4	B	806	-	4,4,4	0.44	0	6,6,6	0.11	0
4	GOL	B	807	-	5,5,5	0.61	0	5,5,5	0.42	0
2	NAG	C	801	-	15,15,15	0.50	0	21,21,21	0.97	2 (9%)
3	SO4	C	802	-	4,4,4	0.39	0	6,6,6	0.22	0
3	SO4	C	803	-	4,4,4	0.44	0	6,6,6	0.35	0
3	SO4	C	804	-	4,4,4	0.47	0	6,6,6	0.20	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
2	NAG	A	801	-	-	0/6/26/26	0/1/1/1
3	SO4	A	802	-	-	0/0/0/0	0/0/0/0
3	SO4	A	803	-	-	0/0/0/0	0/0/0/0
3	SO4	A	804	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	801	-	-	0/6/26/26	0/1/1/1
3	SO4	B	802	-	-	0/0/0/0	0/0/0/0
3	SO4	B	803	-	-	0/0/0/0	0/0/0/0
3	SO4	B	804	-	-	0/0/0/0	0/0/0/0
3	SO4	B	805	-	-	0/0/0/0	0/0/0/0
3	SO4	B	806	-	-	0/0/0/0	0/0/0/0
4	GOL	B	807	-	-	0/4/4/4	0/0/0/0
2	NAG	C	801	-	-	0/6/26/26	0/1/1/1
3	SO4	C	802	-	-	0/0/0/0	0/0/0/0
3	SO4	C	803	-	-	0/0/0/0	0/0/0/0
3	SO4	C	804	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	NAG	C1-C2-C3	-3.64	105.59	110.54
2	A	801	NAG	C1-O5-C5	-3.11	107.77	113.39
2	A	801	NAG	O4-C4-C3	-2.77	104.32	110.36
2	C	801	NAG	O1-C1-O5	-2.01	104.24	110.20
2	C	801	NAG	O5-C1-C2	2.03	111.56	109.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	805	SO4	1	0
3	C	802	SO4	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	193/237 (81%)	-0.63	3 (1%) 72 71	15, 22, 42, 67	0
1	B	193/237 (81%)	-0.25	11 (5%) 24 25	17, 24, 51, 73	0
1	C	193/237 (81%)	-0.04	11 (5%) 24 25	20, 31, 57, 84	0
All	All	579/711 (81%)	-0.31	25 (4%) 36 36	15, 26, 54, 84	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	727	TYR	8.7
1	B	727	TYR	6.1
1	B	595	PHE	5.6
1	C	606	GLY	4.9
1	B	596	PHE	4.7

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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	SO4	B	806	5/5	0.92	0.43	13.13	35,36,38,39	5
4	GOL	B	807	6/6	0.81	0.17	9.61	33,40,44,44	0
3	SO4	C	803	5/5	0.81	0.19	5.72	42,42,42,45	5
3	SO4	A	804	5/5	0.91	0.19	4.26	36,37,40,41	5
2	NAG	B	801	15/15	0.93	0.14	2.50	24,28,32,34	0
3	SO4	A	802	5/5	0.89	0.17	1.54	43,45,46,48	5
3	SO4	C	802	5/5	0.92	0.18	1.46	41,41,42,43	5
3	SO4	B	802	5/5	0.99	0.10	1.04	28,30,33,34	0
3	SO4	B	805	5/5	0.89	0.25	0.60	39,40,41,42	5
2	NAG	A	801	15/15	0.96	0.09	0.40	22,23,26,30	0
2	NAG	C	801	15/15	0.95	0.11	0.30	34,35,38,43	0
3	SO4	B	803	5/5	0.98	0.07	-0.06	52,54,59,61	0
3	SO4	B	804	5/5	0.99	0.07	-0.49	28,30,31,34	0
3	SO4	A	803	5/5	0.94	0.22	-	74,76,77,80	0
3	SO4	C	804	5/5	0.89	0.16	-	37,41,42,43	5

6.5 Other polymers [i](#)

There are no such residues in this entry.