Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 07:45 am BST

PDB ID	:	5N83
Title	:	Structure of the distal domain of mouse adenovirus 2 fibre, methylmercury chloride derivative
Authors	:	Singh, A.K.; van Raaij, M.J.
Deposited on	:	2017-02-22
Resolution	:	2.76 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 following versions of software and data (see references ⓘ) were used in the production of this report:

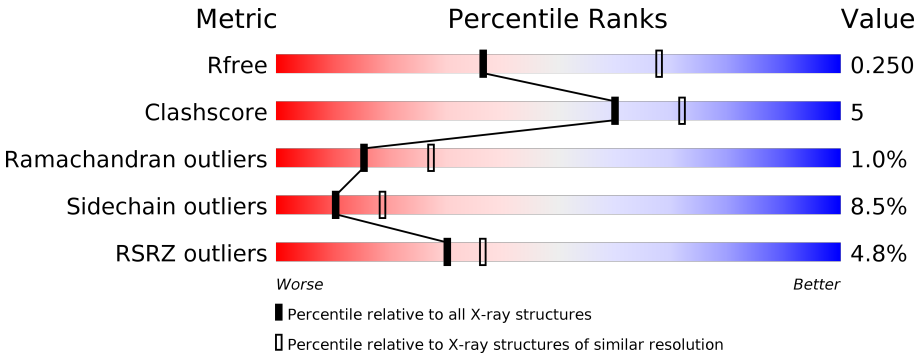
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.76 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}	130704	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 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 <=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	5% 66% 13% • 18%
1	B	237	3% 72% 10% • 18%
1	C	237	4% 68% 14% • 17%

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	HG	C	802	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4578 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	194	Total	C	N	O	S	0	0	0
			1505	957	242	295	11			
1	B	195	Total	C	N	O	S	0	0	0
			1510	960	243	296	11			
1	C	196	Total	C	N	O	S	0	0	0
			1514	962	244	297	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 MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Hg 1 1	0	0
2	A	2	Total Hg 2 2	0	0
2	C	2	Total Hg 2 2	0	0

- Molecule 3 is water.

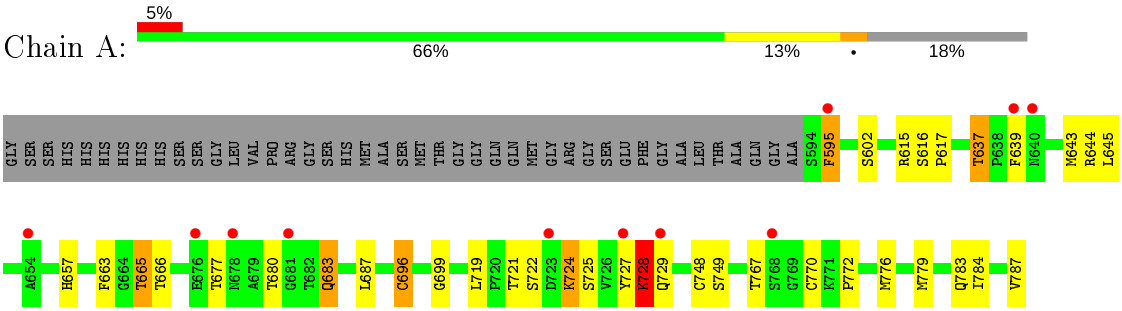
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	22	Total O 22 22	0	0
3	B	9	Total O 9 9	0	0
3	C	13	Total O 13 13	0	0

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.

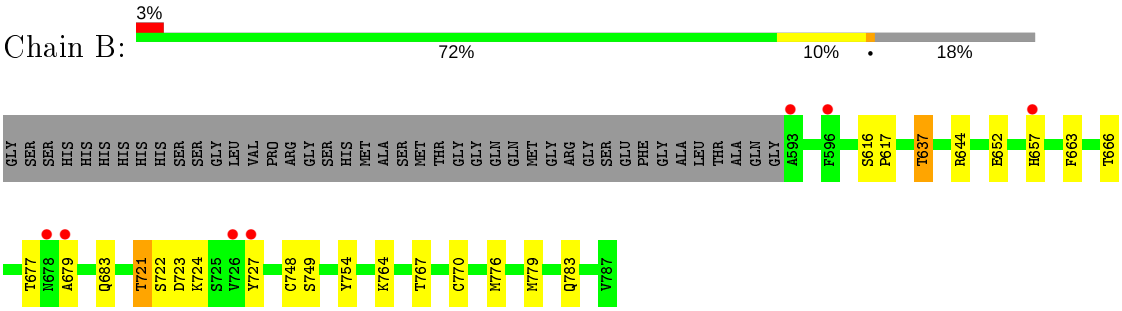
- Molecule 1: Fiber

Chain A:



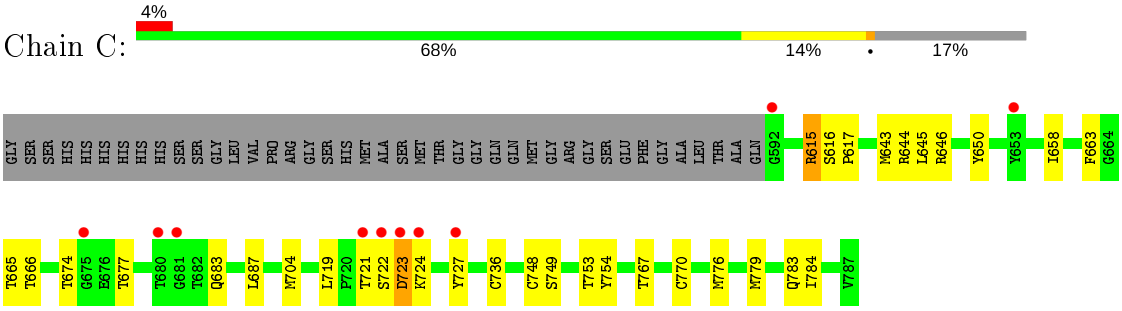
- Molecule 1: Fiber

Chain B:



- Molecule 1: Fiber

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	92.12Å 164.28Å 96.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	82.14 – 2.76 82.14 – 2.76	Depositor EDS
% Data completeness (in resolution range)	99.6 (82.14-2.76) 99.6 (82.14-2.76)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.03 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.203 , 0.248 0.206 , 0.250	Depositor DCC
R_{free} test set	985 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å^2)	57.7	Xtriage
Anisotropy	0.208	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 36.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.016 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.026 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4578	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: HG

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	0.51	0/1540	0.77	4/2091 (0.2%)
1	B	0.47	0/1545	0.70	0/2098
1	C	0.49	0/1549	0.70	0/2103
All	All	0.49	0/4634	0.73	4/6292 (0.1%)

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
1	A	0	1
1	B	0	1
1	C	0	1
All	All	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	663	PHE	CB-CA-C	-6.21	97.99	110.40
1	A	725	SER	N-CA-C	5.52	125.89	111.00
1	A	696	CYS	CA-CB-SG	5.05	123.08	114.00
1	A	595	PHE	CB-CG-CD1	5.01	124.31	120.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	728	LYS	Peptide
1	B	727	TYR	Peptide
1	C	723	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	1505	0	1456	18	0
1	B	1510	0	1461	10	0
1	C	1514	0	1464	14	0
2	A	2	0	0	2	0
2	B	1	0	0	1	0
2	C	2	0	0	3	0
3	A	22	0	0	2	0
3	B	9	0	0	0	0
3	C	13	0	0	1	0
All	All	4578	0	4381	41	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 (41) 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:C:736:CYS:SG	2:C:802:HG:HG	1.46	1.31
1:A:696:CYS:SG	2:A:801:HG:HG	1.57	1.22
1:B:748:CYS:SG	2:B:801:HG:HG	1.73	1.05
1:A:748:CYS:SG	2:A:802:HG:HG	1.89	0.91
1:C:748:CYS:SG	2:C:801:HG:HG	1.95	0.84
1:C:736:CYS:HG	2:C:802:HG:HG	1.20	0.84
1:B:652:GLU:CG	1:B:677:THR:HG21	2.19	0.71
1:B:652:GLU:HG3	1:B:677:THR:HG21	1.79	0.65
1:C:658:ILE:HD13	1:C:687:LEU:HD21	1.84	0.58
1:A:643:MET:HE1	1:A:687:LEU:HD22	1.86	0.56
1:B:749:SER:HB3	1:B:764:LYS:HB2	1.90	0.53
1:A:637:THR:HG21	1:A:657:HIS:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:637:THR:HG21	1:B:657:HIS:HA	1.90	0.53
1:A:696:CYS:SG	1:A:699:GLY:O	2.64	0.50
1:A:666:THR:HG21	1:A:779:MET:HE3	1.95	0.49
1:A:643:MET:CE	1:A:687:LEU:CD2	2.91	0.49
1:C:719:LEU:HB2	1:C:784:ILE:HD12	1.93	0.49
1:B:721:THR:HA	1:B:783:GLN:HG3	1.95	0.49
1:A:615:ARG:NH1	3:A:901:HOH:O	2.47	0.47
1:C:643:MET:HE3	1:C:645:LEU:HD21	1.96	0.47
1:A:665:THR:OG1	1:A:665:THR:O	2.31	0.47
1:A:639:PHE:HZ	1:C:665:THR:HG21	1.79	0.47
1:B:666:THR:HG21	1:B:779:MET:CE	2.46	0.46
1:A:683:GLN:NE2	1:A:772:PRO:HB3	2.31	0.46
1:C:666:THR:HG21	1:C:779:MET:CE	2.47	0.45
1:C:643:MET:CE	1:C:645:LEU:HD21	2.47	0.44
1:A:666:THR:HG21	1:A:779:MET:CE	2.46	0.44
1:B:724:LYS:HA	1:B:754:TYR:CD1	2.53	0.44
1:A:719:LEU:HB2	1:A:784:ILE:HD12	1.99	0.44
1:C:724:LYS:HA	1:C:754:TYR:CD2	2.52	0.44
1:A:643:MET:HE1	1:A:687:LEU:CD2	2.48	0.43
1:A:787:VAL:OXT	1:A:787:VAL:HG13	2.19	0.43
1:A:643:MET:CE	1:A:645:LEU:HD21	2.49	0.42
1:C:666:THR:HG21	1:C:779:MET:HE2	2.02	0.42
1:C:723:ASP:HA	1:C:724:LYS:HG3	2.01	0.41
1:C:615:ARG:NH2	3:C:901:HOH:O	2.54	0.41
1:C:616:SER:N	1:C:617:PRO:CD	2.84	0.41
1:B:616:SER:N	1:B:617:PRO:CD	2.84	0.40
1:A:616:SER:N	1:A:617:PRO:CD	2.84	0.40
1:A:724:LYS:NZ	3:A:902:HOH:O	2.53	0.40
1:B:666:THR:HG21	1:B:779:MET:HE3	2.03	0.40

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	192/237 (81%)	178 (93%)	11 (6%)	3 (2%)	9 16
1	B	193/237 (81%)	179 (93%)	12 (6%)	2 (1%)	15 27
1	C	194/237 (82%)	180 (93%)	13 (7%)	1 (0%)	29 47
All	All	579/711 (81%)	537 (93%)	36 (6%)	6 (1%)	15 27

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	721	THR
1	B	679	ALA
1	B	721	THR
1	C	721	THR
1	A	728	LYS
1	A	724	LYS

5.3.2 Protein sidechains (i)

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	168/198 (85%)	151 (90%)	17 (10%)	7 12
1	B	168/198 (85%)	159 (95%)	9 (5%)	22 38
1	C	168/198 (85%)	151 (90%)	17 (10%)	7 12
All	All	504/594 (85%)	461 (92%)	43 (8%)	10 19

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	595	PHE
1	A	602	SER
1	A	637	THR
1	A	644	ARG
1	A	665	THR
1	A	677	THR
1	A	680	THR

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Mol	Chain	Res	Type
1	A	683	GLN
1	A	722	SER
1	A	727	TYR
1	A	728	LYS
1	A	729	GLN
1	A	749	SER
1	A	767	THR
1	A	770	CYS
1	A	776	MET
1	A	783	GLN
1	B	637	THR
1	B	644	ARG
1	B	663	PHE
1	B	683	GLN
1	B	722	SER
1	B	723	ASP
1	B	767	THR
1	B	770	CYS
1	B	776	MET
1	C	615	ARG
1	C	644	ARG
1	C	646	ARG
1	C	650	TYR
1	C	663	PHE
1	C	674	THR
1	C	677	THR
1	C	683	GLN
1	C	704	MET
1	C	722	SER
1	C	727	TYR
1	C	749	SER
1	C	753	THR
1	C	767	THR
1	C	770	CYS
1	C	776	MET
1	C	783	GLN

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 95^{th} 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	194/237 (81%)	0.45	11 (5%)	23	28	33, 52, 100, 143	0
1	B	195/237 (82%)	0.45	7 (3%)	42	51	35, 55, 111, 137	0
1	C	196/237 (82%)	0.54	10 (5%)	28	34	36, 58, 116, 144	0
All	All	585/711 (82%)	0.48	28 (4%)	30	36	33, 56, 110, 144	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	727	TYR	5.8
1	A	727	TYR	5.0
1	C	723	ASP	4.5
1	C	592	GLY	4.5
1	B	678	ASN	4.0
1	A	723	ASP	3.8
1	C	680	THR	3.7
1	A	639	PHE	3.5
1	C	653	TYR	3.5
1	C	727	TYR	3.3
1	B	596	PHE	3.3
1	A	676	GLU	3.1
1	B	679	ALA	3.1
1	C	724	LYS	2.8
1	A	768	SER	2.7
1	C	681	GLY	2.7
1	A	678	ASN	2.5
1	B	593	ALA	2.5
1	C	721	THR	2.3
1	A	681	GLY	2.3
1	A	654	ALA	2.2
1	A	729	GLN	2.2
1	C	722	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	595	PHE	2.1
1	B	657	HIS	2.1
1	C	675	GLY	2.1
1	A	640	ASN	2.0
1	B	726	VAL	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)

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. The B-factors column lists the minimum, median, 95^{th} 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	HG	A	802	1/1	0.94	0.06	83,83,83,83	1
2	HG	B	801	1/1	0.98	0.04	47,47,47,47	1
2	HG	A	801	1/1	0.99	0.07	49,49,49,49	1
2	HG	C	802	1/1	0.99	0.13	88,88,88,88	1
2	HG	C	801	1/1	0.99	0.05	81,81,81,81	1

6.5 Other polymers (i)

There are no such residues in this entry.