



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 7, 2024 – 12:39 PM EDT

PDB ID : 3UPU
Title : Crystal structure of the T4 Phage SF1B Helicase Dda
Authors : He, X.; Yun, M.K.; Pemble IV, C.W.; Kreuzer, K.N.; Raney, K.D.; White, S.W.
Deposited on : 2011-11-18
Resolution : 3.30 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

<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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

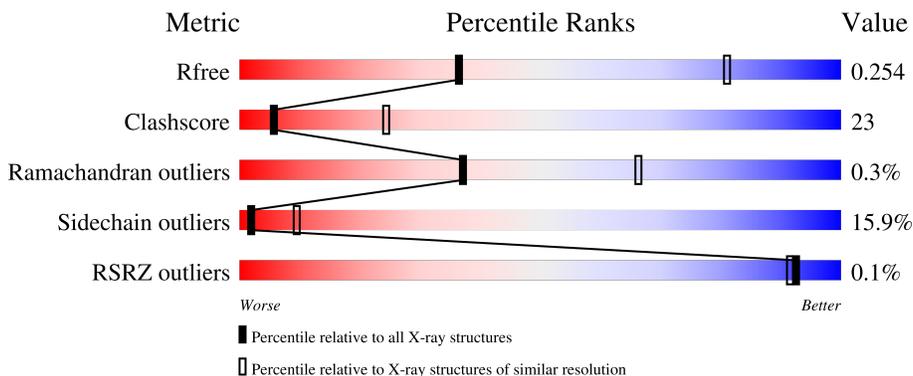
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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}	164625	1085 (3.32-3.28)
Clashscore	180529	1128 (3.32-3.28)
Ramachandran outliers	177936	1125 (3.32-3.28)
Sidechain outliers	177891	1124 (3.32-3.28)
RSRZ outliers	164620	1085 (3.32-3.28)

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	459	
1	B	459	
1	C	459	
2	D	8	
2	E	8	

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Mol	Chain	Length	Quality of chain
2	F	8	 A horizontal bar chart representing the quality of the chain. The bar is divided into two equal segments: the left segment is green and labeled '50%', and the right segment is yellow and labeled '50%'.

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 11054 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 ATP-dependent DNA helicase dda.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	439	3529	2280	582	655	5	7	0	1	0
1	B	439	3522	2275	580	655	5	7	0	0	0
1	C	439	3522	2275	580	655	5	7	0	0	0

There are 75 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MSE	-	expression tag	UNP P32270
A	-18	GLY	-	expression tag	UNP P32270
A	-17	SER	-	expression tag	UNP P32270
A	-16	SER	-	expression tag	UNP P32270
A	-15	HIS	-	expression tag	UNP P32270
A	-14	HIS	-	expression tag	UNP P32270
A	-13	HIS	-	expression tag	UNP P32270
A	-12	HIS	-	expression tag	UNP P32270
A	-11	HIS	-	expression tag	UNP P32270
A	-10	HIS	-	expression tag	UNP P32270
A	-9	SER	-	expression tag	UNP P32270
A	-8	SER	-	expression tag	UNP P32270
A	-7	GLY	-	expression tag	UNP P32270
A	-6	LEU	-	expression tag	UNP P32270
A	-5	VAL	-	expression tag	UNP P32270
A	-4	PRO	-	expression tag	UNP P32270
A	-3	ARG	-	expression tag	UNP P32270
A	-2	GLY	-	expression tag	UNP P32270
A	-1	SER	-	expression tag	UNP P32270
A	0	HIS	-	expression tag	UNP P32270
A	38	ALA	LYS	engineered mutation	UNP P32270
A	54	GLU	GLY	SEE REMARK 999	UNP P32270
A	151	ASP	GLU	SEE REMARK 999	UNP P32270

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Chain	Residue	Modelled	Actual	Comment	Reference
A	196	ILE	ASN	SEE REMARK 999	UNP P32270
A	357	GLY	ALA	SEE REMARK 999	UNP P32270
B	-19	MSE	-	expression tag	UNP P32270
B	-18	GLY	-	expression tag	UNP P32270
B	-17	SER	-	expression tag	UNP P32270
B	-16	SER	-	expression tag	UNP P32270
B	-15	HIS	-	expression tag	UNP P32270
B	-14	HIS	-	expression tag	UNP P32270
B	-13	HIS	-	expression tag	UNP P32270
B	-12	HIS	-	expression tag	UNP P32270
B	-11	HIS	-	expression tag	UNP P32270
B	-10	HIS	-	expression tag	UNP P32270
B	-9	SER	-	expression tag	UNP P32270
B	-8	SER	-	expression tag	UNP P32270
B	-7	GLY	-	expression tag	UNP P32270
B	-6	LEU	-	expression tag	UNP P32270
B	-5	VAL	-	expression tag	UNP P32270
B	-4	PRO	-	expression tag	UNP P32270
B	-3	ARG	-	expression tag	UNP P32270
B	-2	GLY	-	expression tag	UNP P32270
B	-1	SER	-	expression tag	UNP P32270
B	0	HIS	-	expression tag	UNP P32270
B	38	ALA	LYS	engineered mutation	UNP P32270
B	54	GLU	GLY	SEE REMARK 999	UNP P32270
B	151	ASP	GLU	SEE REMARK 999	UNP P32270
B	196	ILE	ASN	SEE REMARK 999	UNP P32270
B	357	GLY	ALA	SEE REMARK 999	UNP P32270
C	-19	MSE	-	expression tag	UNP P32270
C	-18	GLY	-	expression tag	UNP P32270
C	-17	SER	-	expression tag	UNP P32270
C	-16	SER	-	expression tag	UNP P32270
C	-15	HIS	-	expression tag	UNP P32270
C	-14	HIS	-	expression tag	UNP P32270
C	-13	HIS	-	expression tag	UNP P32270
C	-12	HIS	-	expression tag	UNP P32270
C	-11	HIS	-	expression tag	UNP P32270
C	-10	HIS	-	expression tag	UNP P32270
C	-9	SER	-	expression tag	UNP P32270
C	-8	SER	-	expression tag	UNP P32270
C	-7	GLY	-	expression tag	UNP P32270
C	-6	LEU	-	expression tag	UNP P32270
C	-5	VAL	-	expression tag	UNP P32270

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	PRO	-	expression tag	UNP P32270
C	-3	ARG	-	expression tag	UNP P32270
C	-2	GLY	-	expression tag	UNP P32270
C	-1	SER	-	expression tag	UNP P32270
C	0	HIS	-	expression tag	UNP P32270
C	38	ALA	LYS	engineered mutation	UNP P32270
C	54	GLU	GLY	SEE REMARK 999	UNP P32270
C	151	ASP	GLU	SEE REMARK 999	UNP P32270
C	196	ILE	ASN	SEE REMARK 999	UNP P32270
C	357	GLY	ALA	SEE REMARK 999	UNP P32270

- Molecule 2 is a DNA chain called 5'-D(*TP*TP*TP*TP*TP*TP*TP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	8	Total	C	N	O	P	0	0	0
			157	80	16	54	7			
2	E	8	Total	C	N	O	P	0	0	0
			157	80	16	54	7			
2	F	8	Total	C	N	O	P	0	0	0
			157	80	16	54	7			

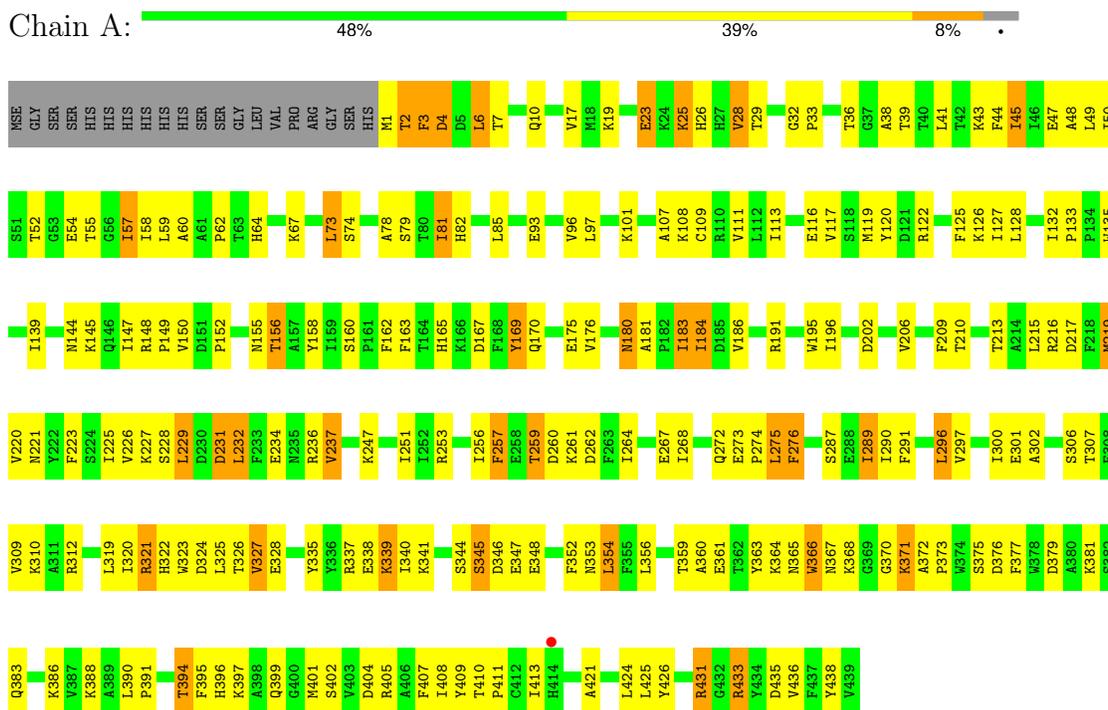
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	O	0	0
			4	4		
3	B	2	Total	O	0	0
			2	2		
3	D	2	Total	O	0	0
			2	2		
3	E	1	Total	O	0	0
			1	1		
3	F	1	Total	O	0	0
			1	1		

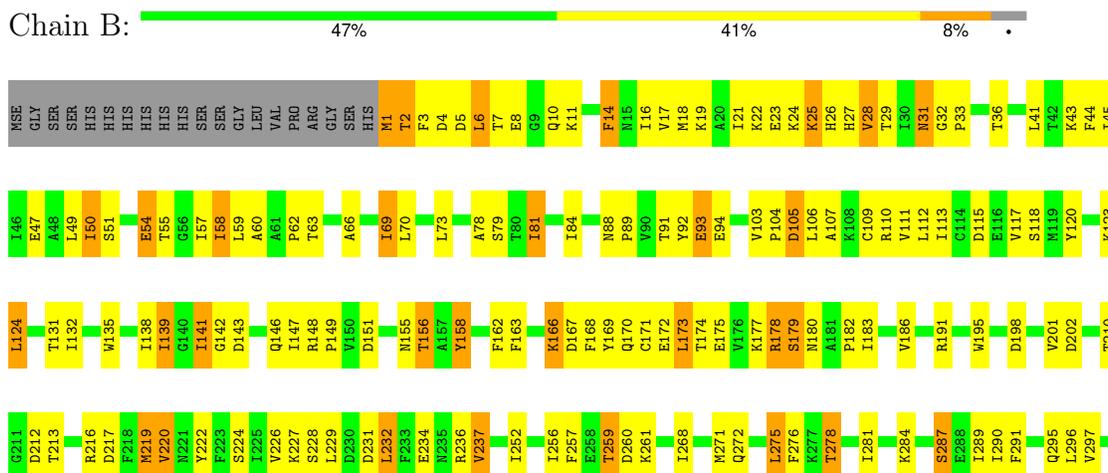
3 Residue-property plots

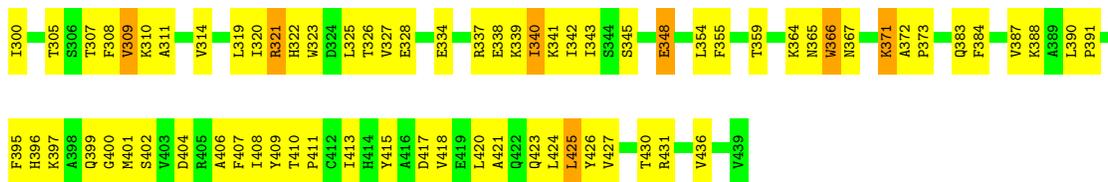
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



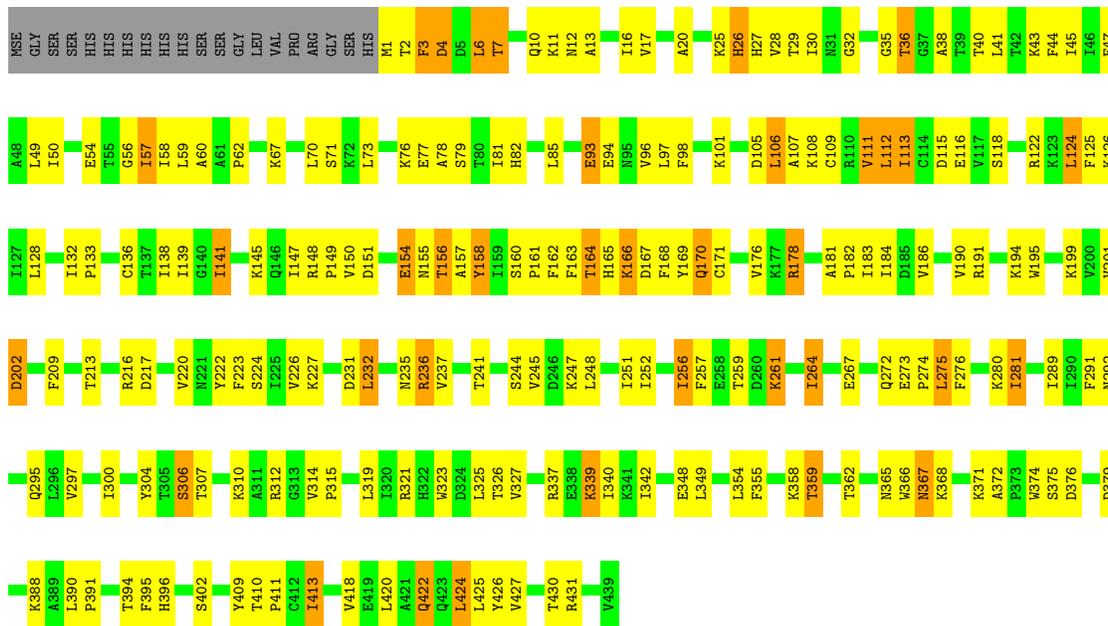
- Molecule 1: ATP-dependent DNA helicase dda





- Molecule 1: ATP-dependent DNA helicase dda

Chain C: 50% 38% 8%



- Molecule 2: 5'-D(*TP*TP*TP*TP*TP*TP*TP*T)-3'

Chain D: 25% 75%



- Molecule 2: 5'-D(*TP*TP*TP*TP*TP*TP*TP*T)-3'

Chain E: 50% 50%



- Molecule 2: 5'-D(*TP*TP*TP*TP*TP*TP*TP*T)-3'

Chain F: 50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	225.54Å 107.25Å 85.47Å 90.00° 94.13° 90.00°	Depositor
Resolution (Å)	32.27 – 3.30 32.27 – 3.30	Depositor EDS
% Data completeness (in resolution range)	91.1 (32.27-3.30) 90.7 (32.27-3.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.81 (at 3.32Å)	Xtrriage
Refinement program	PHENIX 1.7_650	Depositor
R, R_{free}	0.204 , 0.258 0.201 , 0.254	Depositor DCC
R_{free} test set	1466 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	92.4	Xtrriage
Anisotropy	0.443	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 64.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11054	wwPDB-VP
Average B, all atoms (Å ²)	110.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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

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	0.28	0/3607	0.51	0/4869
1	B	0.26	0/3596	0.47	0/4854
1	C	0.25	0/3596	0.47	0/4854
2	D	0.51	0/172	1.48	0/264
2	E	0.50	0/172	1.42	0/264
2	F	0.52	0/172	1.39	0/264
All	All	0.28	0/11315	0.57	0/15369

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	4
1	C	0	1
All	All	0	5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	259	THR	Peptide
1	A	344	SER	Peptide
1	A	366	TRP	Peptide
1	A	4	ASP	Peptide
1	C	108	LYS	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	3529	0	3549	175	0
1	B	3522	0	3542	163	0
1	C	3522	0	3542	156	0
2	D	157	0	98	8	0
2	E	157	0	98	5	0
2	F	157	0	98	9	0
3	A	4	0	0	0	0
3	B	2	0	0	0	0
3	D	2	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
All	All	11054	0	10927	504	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 23.

The worst 5 of 504 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:6:LEU:HD12	1:B:11:LYS:HG2	1.31	1.07
1:B:276:PHE:HE1	1:B:289:ILE:HG12	1.18	1.04
1:B:321:ARG:HG3	1:B:321:ARG:HH11	1.22	1.00
1:A:232:LEU:H	1:A:232:LEU:HD22	1.26	0.95
1:B:276:PHE:CE1	1:B:289:ILE:HG12	2.05	0.92

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	438/459 (95%)	408 (93%)	29 (7%)	1 (0%)	44	71
1	B	437/459 (95%)	397 (91%)	39 (9%)	1 (0%)	44	71
1	C	437/459 (95%)	402 (92%)	33 (8%)	2 (0%)	25	56
All	All	1312/1377 (95%)	1207 (92%)	101 (8%)	4 (0%)	37	66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	93	GLU
1	C	93	GLU
1	A	93	GLU
1	C	256	ILE

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	386/394 (98%)	330 (86%)	56 (14%)	2	12
1	B	385/394 (98%)	316 (82%)	69 (18%)	1	7
1	C	385/394 (98%)	326 (85%)	59 (15%)	2	10
All	All	1156/1182 (98%)	972 (84%)	184 (16%)	2	9

5 of 184 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	348	GLU
1	C	118	SER
1	B	367	ASN
1	C	28	VAL
1	C	166	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20

such sidechains are listed below:

Mol	Chain	Res	Type
1	C	95	ASN
1	C	272	GLN
1	C	353	ASN
1	C	295	GLN
1	B	82	HIS

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](#)

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 [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	432/459 (94%)	-0.68	1 (0%) 92 88	42, 98, 136, 169	1 (0%)
1	B	432/459 (94%)	-0.60	0 100 100	64, 106, 159, 184	0
1	C	432/459 (94%)	-0.57	0 100 100	81, 115, 154, 180	0
2	D	8/8 (100%)	-0.75	0 100 100	86, 91, 111, 160	0
2	E	8/8 (100%)	-0.75	0 100 100	95, 104, 149, 197	0
2	F	8/8 (100%)	-0.51	0 100 100	106, 112, 161, 217	0
All	All	1320/1401 (94%)	-0.62	1 (0%) 92 91	42, 107, 155, 217	1 (0%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	414[A]	HIS	2.4

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 monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.