



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 02:27 PM UTC

PDB ID : 6RYA / pdb_00006rya
Title : Structure of Dup1 mutant H67A:Ubiquitin complex
Authors : Donghyuk, S.; Ivan, D.
Deposited on : 2019-06-10
Resolution : 2.21 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 : 4-5-2 with Phenix2.0
Xtrriage (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

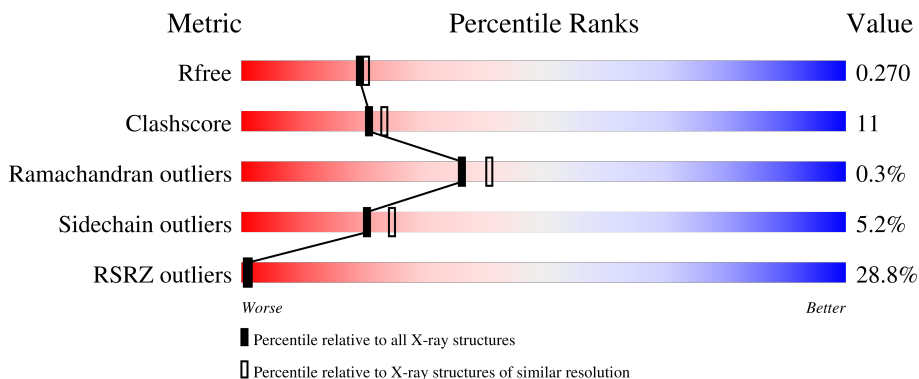
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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	343	 26% 71% 17% 10%
1	C	343	 28% 60% 27% 10%
1	E	343	 25% 71% 17% 10%
2	B	76	 33% 72% 24% 10%
2	D	76	 13% 79% 18% 10%

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Mol	Chain	Length	Quality of chain
2	F	76	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '36%', a green segment in the middle labeled '84%', and a yellow segment on the right labeled '14%'. A small black dot is located at the far right end of the bar.</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 9240 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 Septation initiation protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	308	2472	1569	435	459	9	0	0	0
1	C	308	2472	1569	435	459	9	0	0	0
1	E	308	2472	1569	435	459	9	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	SER	-	expression tag	UNP A0A3A6VNK6
A	67	ALA	HIS	conflict	UNP A0A3A6VNK6
A	228	ASP	ALA	conflict	UNP A0A3A6VNK6
C	3	SER	-	expression tag	UNP A0A3A6VNK6
C	67	ALA	HIS	conflict	UNP A0A3A6VNK6
C	228	ASP	ALA	conflict	UNP A0A3A6VNK6
E	3	SER	-	expression tag	UNP A0A3A6VNK6
E	67	ALA	HIS	conflict	UNP A0A3A6VNK6
E	228	ASP	ALA	conflict	UNP A0A3A6VNK6

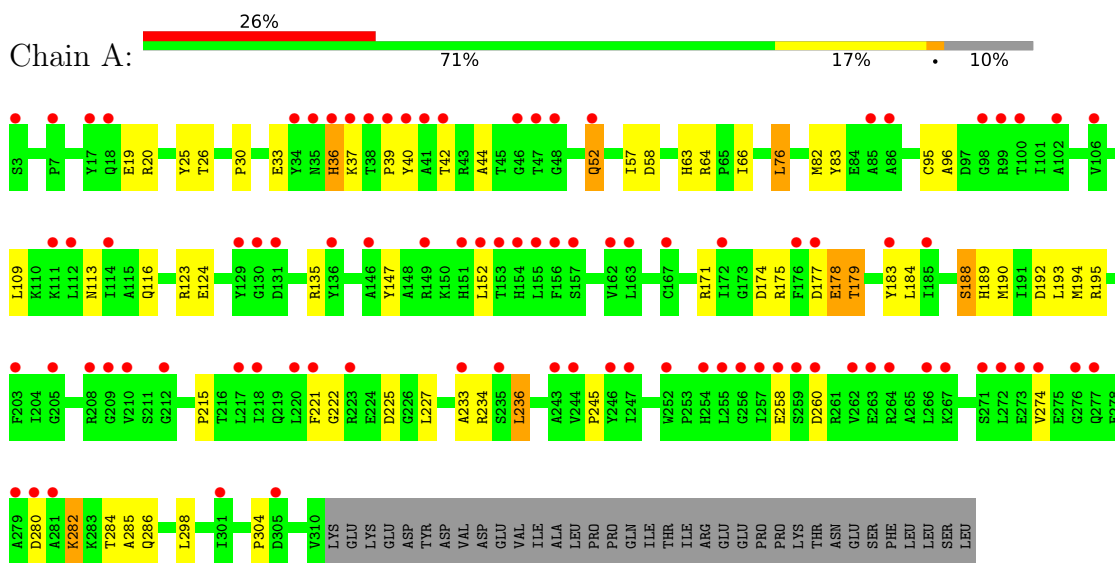
- Molecule 2 is a protein called Polyubiquitin-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	76	608	383	106	118	1	0	1	0
2	D	76	608	383	106	118	1	0	1	0
2	F	76	608	383	106	118	1	0	1	0

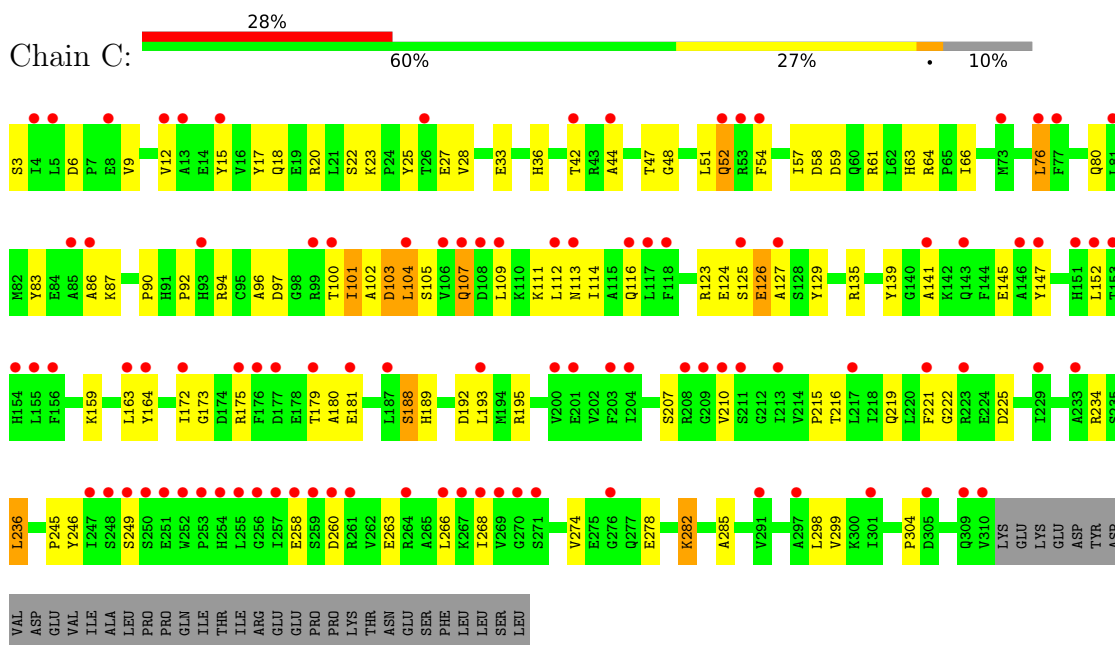
3 Residue-property plots [i](#)

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.

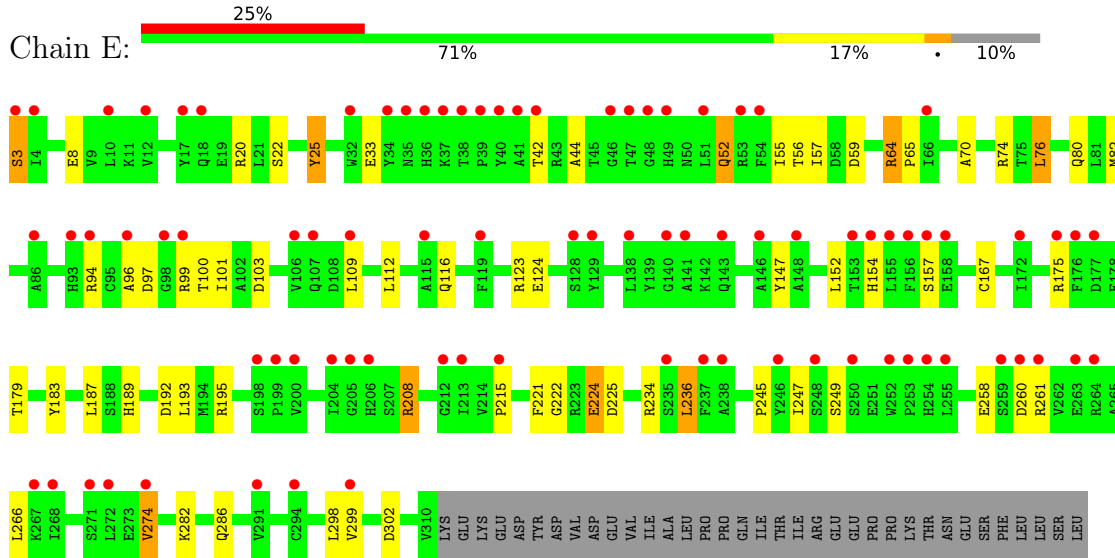
- Molecule 1: Septation initiation protein



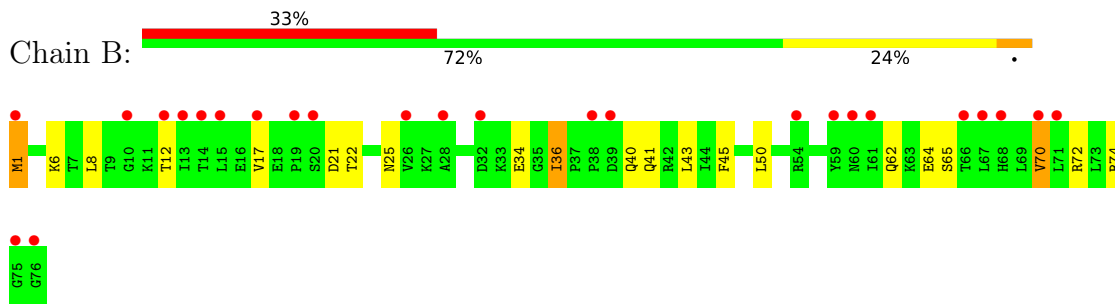
- Molecule 1: Septation initiation protein



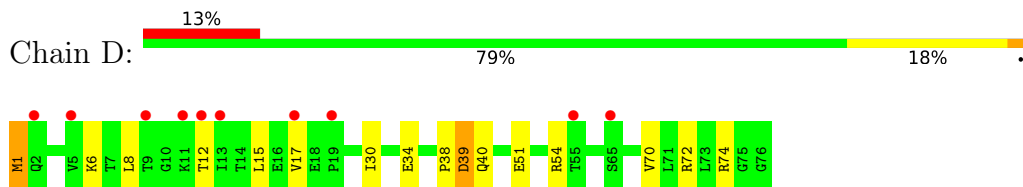
- Molecule 1: Septation initiation protein



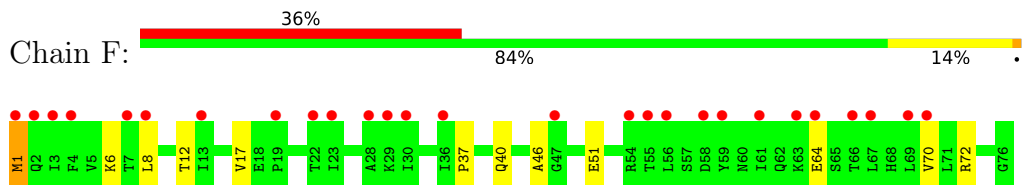
- Molecule 2: Polyubiquitin-C



- Molecule 2: Polyubiquitin-C



- Molecule 2: Polyubiquitin-C



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	116.33Å 67.14Å 182.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.07 – 2.21 49.07 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.07-2.21) 99.7 (49.07-2.21)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.209 , 0.289 (Not available) , 0.270	Depositor DCC
R_{free} test set	3463 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	40.9	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 33.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.108 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.115 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.058 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.057 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.046 for -h,-k,l	Xtriage
Reported twinning fraction	0.176 for H, K, L 0.169 for h,-k,-l 0.162 for -1/2H-3/2K, -1/2H+1/2K, -L 0.167 for -1/2H+3/2K, 1/2H+1/2K, -L 0.159 for 1/2H-3/2K, -1/2H-1/2K, -L 0.167 for 1/2H+3/2K, 1/2H-1/2K, -L	Depositor
Outliers	0 of 71216 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9240	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.66% 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

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	1.16	1/2534 (0.0%)	1.55	3/3430 (0.1%)
1	C	1.16	2/2534 (0.1%)	1.54	5/3430 (0.1%)
1	E	1.16	3/2534 (0.1%)	1.55	7/3430 (0.2%)
2	B	1.19	1/617 (0.2%)	1.54	3/827 (0.4%)
2	D	1.15	0/617	1.51	0/827
2	F	1.19	0/617	1.57	4/827 (0.5%)
All	All	1.16	7/9453 (0.1%)	1.55	22/12771 (0.2%)

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	C	0	2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	THR	C-O	6.83	1.32	1.23
1	E	179	THR	C-O	6.08	1.31	1.23
1	C	189	HIS	CE1-NE2	5.40	1.38	1.32
2	B	36	ILE	N-CA	5.30	1.50	1.46
1	E	25	TYR	C-O	5.18	1.30	1.24

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	222	GLY	CA-C-O	-7.55	116.18	122.29
1	C	222	GLY	CA-C-O	-6.64	116.91	122.29
1	E	222	GLY	CA-C-O	-6.48	116.61	122.57
1	E	167	CYS	CB-CA-C	-6.40	100.74	110.92
1	C	58	ASP	CA-CB-CG	6.32	118.92	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	173	GLY	Peptide
1	C	188	SER	Mainchain

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	2472	0	2405	58	0
1	C	2472	0	2405	81	17
1	E	2472	0	2405	38	0
2	B	608	0	642	16	0
2	D	608	0	642	17	0
2	F	608	0	642	5	0
All	All	9240	0	9141	202	17

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 11.

The worst 5 of 202 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:96:ALA:HB2	1:A:175:ARG:NH2	1.50	1.24
1:C:101:ILE:HD11	1:C:180:ALA:O	1.39	1.21
1:C:100:THR:OG1	1:C:103:ASP:OD2	1.61	1.16
1:A:96:ALA:CB	1:A:175:ARG:HH21	1.59	1.13
1:C:27:GLU:HB2	1:C:125:SER:HB3	1.22	1.13

The worst 5 of 17 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:103:ASP:N	1:C:103:ASP:CG[2_455]	0.66	1.54
1:C:103:ASP:CA	1:C:103:ASP:CG[2_455]	0.94	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:103:ASP:N	1:C:103:ASP:OD1[2_455]	1.25	0.95
1:C:102:ALA:C	1:C:103:ASP:OD1[2_455]	1.32	0.88
1:C:103:ASP:CA	1:C:103:ASP:OD2[2_455]	1.32	0.88

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	306/343 (89%)	290 (95%)	14 (5%)	2 (1%)	18	18
1	C	306/343 (89%)	282 (92%)	23 (8%)	1 (0%)	36	41
1	E	306/343 (89%)	288 (94%)	18 (6%)	0	100	100
2	B	75/76 (99%)	72 (96%)	3 (4%)	0	100	100
2	D	75/76 (99%)	74 (99%)	1 (1%)	0	100	100
2	F	75/76 (99%)	73 (97%)	2 (3%)	0	100	100
All	All	1143/1257 (91%)	1079 (94%)	61 (5%)	3 (0%)	36	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	GLU
1	A	304	PRO
1	C	304	PRO

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	259/293 (88%)	245 (95%)	14 (5%)	20	23
1	C	259/293 (88%)	242 (93%)	17 (7%)	15	17
1	E	259/293 (88%)	247 (95%)	12 (5%)	24	30
2	B	69/68 (102%)	66 (96%)	3 (4%)	26	33
2	D	69/68 (102%)	66 (96%)	3 (4%)	26	33
2	F	69/68 (102%)	67 (97%)	2 (3%)	37	49
All	All	984/1083 (91%)	933 (95%)	51 (5%)	21	25

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	215	PRO
2	D	38	PRO
2	F	1	MET
1	C	216	THR
1	C	274	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	41	GLN
2	D	62	GLN
1	C	36	HIS
1	E	36	HIS
2	D	40	GLN

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	308/343 (89%)	1.55	89 (28%) 1 1	28, 47, 83, 121	0
1	C	308/343 (89%)	1.57	96 (31%) 1 1	24, 48, 80, 105	0
1	E	308/343 (89%)	1.52	85 (27%) 1 1	26, 48, 77, 116	0
2	B	76/76 (100%)	1.70	25 (32%) 1 0	26, 52, 84, 109	1 (1%)
2	D	76/76 (100%)	0.98	10 (13%) 7 5	24, 46, 66, 74	1 (1%)
2	F	76/76 (100%)	1.58	27 (35%) 1 0	23, 54, 80, 100	1 (1%)
All	All	1152/1257 (91%)	1.52	332 (28%) 1 1	23, 48, 81, 121	3 (0%)

The worst 5 of 332 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	155	LEU	7.0
1	C	209	GLY	6.6
1	C	270	GLY	6.5
1	A	209	GLY	5.9
1	C	156	PHE	5.8

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.