WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Sep 26, 2023 – 07:23 PM EDT

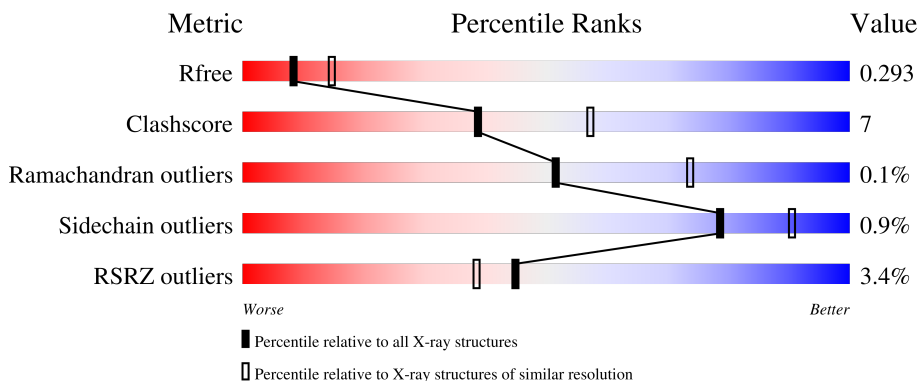|		
PDB ID	:	6BYH
Title	:	Ubiquitin Variant (UbV.Fl11.1) bound to a human Skp1-Fbl11 fragment complex.
Authors	:	Manczyk, N.; Sicheri, F.
Deposited on	:	2017-12-20
Resolution	:	2.61 Å(reported)

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 2.61 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.
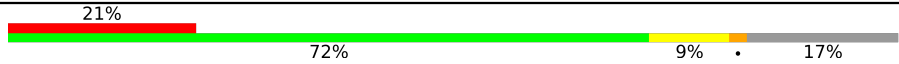
Metric	Percentile Ranks	Value
Rfree		0.293
Clashscore		7
Ramachandran outliers		0.1%
Sidechain outliers		0.9%
RSRZ outliers		3.4%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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 <=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	165	% 76% 12% 12%
1	B	165	% 73% 17% • 9%
1	G	165	7% 65% 12% 24%
2	E	47	4% 83% 13% •
2	F	47	85% 11% •

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Mol	Chain	Length	Quality of chain
2	I	47	21% 72% 9% · 17%
3	C	87	80% 15% · ·
3	D	87	77% 21% ·
3	H	87	% 84% 13% ·

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 6235 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 S-phase kinase-associated protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	145	Total	C	N	O	S	0	0	0
			1105	701	182	217	5			
1	B	150	Total	C	N	O	S	0	0	0
			1153	730	190	228	5			
1	G	126	Total	C	N	O	S	0	0	0
			909	582	150	172	5			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P63208
A	0	ALA	-	expression tag	UNP P63208
B	-1	GLY	-	expression tag	UNP P63208
B	0	ALA	-	expression tag	UNP P63208
G	-1	GLY	-	expression tag	UNP P63208
G	0	ALA	-	expression tag	UNP P63208

- Molecule 2 is a protein called Lysine-specific demethylase 2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	45	Total	C	N	O	S	0	0	0
			368	236	63	61	8			
2	F	45	Total	C	N	O	S	0	0	0
			377	242	62	65	8			
2	I	39	Total	C	N	O	S	0	0	0
			268	172	44	48	4			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	GLY	-	expression tag	UNP Q9Y2K7
E	0	ALA	-	expression tag	UNP Q9Y2K7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	GLY	-	expression tag	UNP Q9Y2K7
F	0	ALA	-	expression tag	UNP Q9Y2K7
I	-1	GLY	-	expression tag	UNP Q9Y2K7
I	0	ALA	-	expression tag	UNP Q9Y2K7

- Molecule 3 is a protein called Polyubiquitin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	84	Total 652	C 411	N 113	O 127	S 1	0	0	0
3	D	85	Total 670	C 422	N 117	O 130	S 1	0	0	0
3	H	84	Total 663	C 420	N 117	O 125	S 1	0	0	0

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP P0CG47
C	-1	SER	-	expression tag	UNP P0CG47
C	8	ARG	LEU	engineered mutation	UNP P0CG47
C	9	HIS	THR	engineered mutation	UNP P0CG47
C	10	SER	GLY	engineered mutation	UNP P0CG47
C	11	TYR	LYS	engineered mutation	UNP P0CG47
C	11a	LYS	-	insertion	UNP P0CG47
C	11b	HIS	-	insertion	UNP P0CG47
C	11c	GLY	-	insertion	UNP P0CG47
C	11d	LEU	-	insertion	UNP P0CG47
C	11e	ILE	-	insertion	UNP P0CG47
C	11f	GLU	-	insertion	UNP P0CG47
C	11g	ASN	-	insertion	UNP P0CG47
C	42	VAL	ARG	engineered mutation	UNP P0CG47
C	46	SER	ALA	engineered mutation	UNP P0CG47
C	47	ARG	GLY	engineered mutation	UNP P0CG47
C	49	ARG	GLN	engineered mutation	UNP P0CG47
C	68	ARG	HIS	engineered mutation	UNP P0CG47
C	72	VAL	ARG	engineered mutation	UNP P0CG47
C	73	PHE	LEU	engineered mutation	UNP P0CG47
C	74	GLY	ARG	engineered mutation	UNP P0CG47
C	75	ARG	GLY	engineered mutation	UNP P0CG47
C	76	ARG	GLY	engineered mutation	UNP P0CG47
D	-2	GLY	-	expression tag	UNP P0CG47

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	SER	-	expression tag	UNP P0CG47
D	8	ARG	LEU	engineered mutation	UNP P0CG47
D	9	HIS	THR	engineered mutation	UNP P0CG47
D	10	SER	GLY	engineered mutation	UNP P0CG47
D	11	TYR	LYS	engineered mutation	UNP P0CG47
D	11a	LYS	-	insertion	UNP P0CG47
D	11b	HIS	-	insertion	UNP P0CG47
D	11c	GLY	-	insertion	UNP P0CG47
D	11d	LEU	-	insertion	UNP P0CG47
D	11e	ILE	-	insertion	UNP P0CG47
D	11f	GLU	-	insertion	UNP P0CG47
D	11g	ASN	-	insertion	UNP P0CG47
D	42	VAL	ARG	engineered mutation	UNP P0CG47
D	46	SER	ALA	engineered mutation	UNP P0CG47
D	47	ARG	GLY	engineered mutation	UNP P0CG47
D	49	ARG	GLN	engineered mutation	UNP P0CG47
D	68	ARG	HIS	engineered mutation	UNP P0CG47
D	72	VAL	ARG	engineered mutation	UNP P0CG47
D	73	PHE	LEU	engineered mutation	UNP P0CG47
D	74	GLY	ARG	engineered mutation	UNP P0CG47
D	75	ARG	GLY	engineered mutation	UNP P0CG47
D	76	ARG	GLY	engineered mutation	UNP P0CG47
H	-2	GLY	-	expression tag	UNP P0CG47
H	-1	SER	-	expression tag	UNP P0CG47
H	8	ARG	LEU	engineered mutation	UNP P0CG47
H	9	HIS	THR	engineered mutation	UNP P0CG47
H	10	SER	GLY	engineered mutation	UNP P0CG47
H	11	TYR	LYS	engineered mutation	UNP P0CG47
H	11a	LYS	-	insertion	UNP P0CG47
H	11b	HIS	-	insertion	UNP P0CG47
H	11c	GLY	-	insertion	UNP P0CG47
H	11d	LEU	-	insertion	UNP P0CG47
H	11e	ILE	-	insertion	UNP P0CG47
H	11f	GLU	-	insertion	UNP P0CG47
H	11g	ASN	-	insertion	UNP P0CG47
H	42	VAL	ARG	engineered mutation	UNP P0CG47
H	46	SER	ALA	engineered mutation	UNP P0CG47
H	47	ARG	GLY	engineered mutation	UNP P0CG47
H	49	ARG	GLN	engineered mutation	UNP P0CG47
H	68	ARG	HIS	engineered mutation	UNP P0CG47
H	72	VAL	ARG	engineered mutation	UNP P0CG47
H	73	PHE	LEU	engineered mutation	UNP P0CG47

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Chain	Residue	Modelled	Actual	Comment	Reference
H	74	GLY	ARG	engineered mutation	UNP P0CG47
H	75	ARG	GLY	engineered mutation	UNP P0CG47
H	76	ARG	GLY	engineered mutation	UNP P0CG47

- Molecule 4 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	18	Total 18	O 18	0	0
4	B	16	Total 16	O 16	0	0
4	E	1	Total 1	O 1	0	0
4	F	5	Total 5	O 5	0	0
4	I	1	Total 1	O 1	0	0
4	C	5	Total 5	O 5	0	0
4	D	14	Total 14	O 14	0	0
4	H	10	Total 10	O 10	0	0

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.
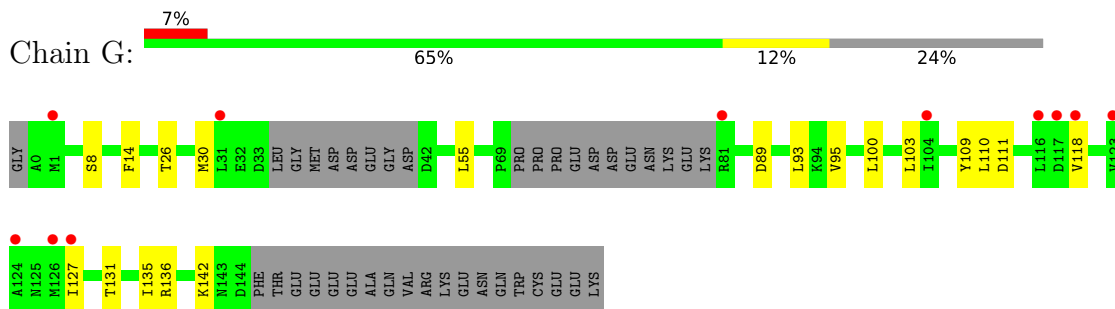
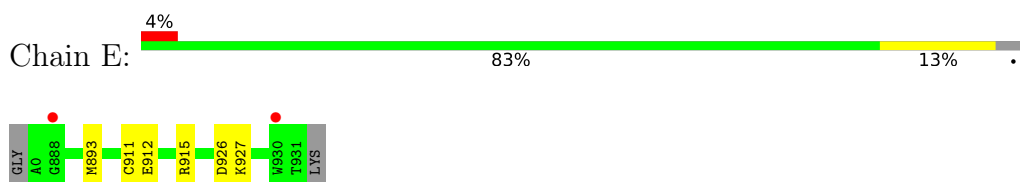• Molecule 1: S-phase kinase-associated protein 1
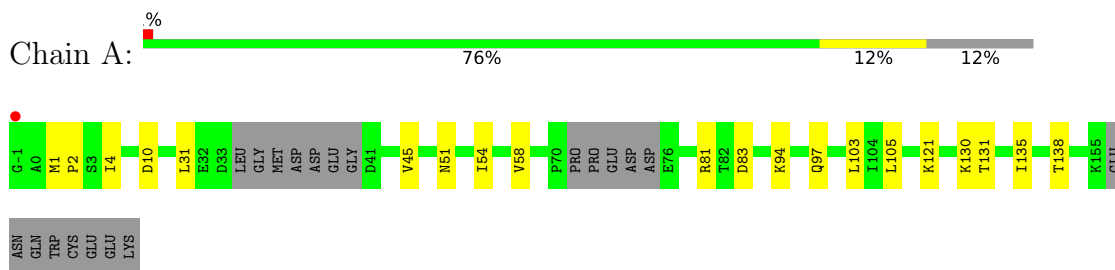
• Molecule 1: S-phase kinase-associated protein 1
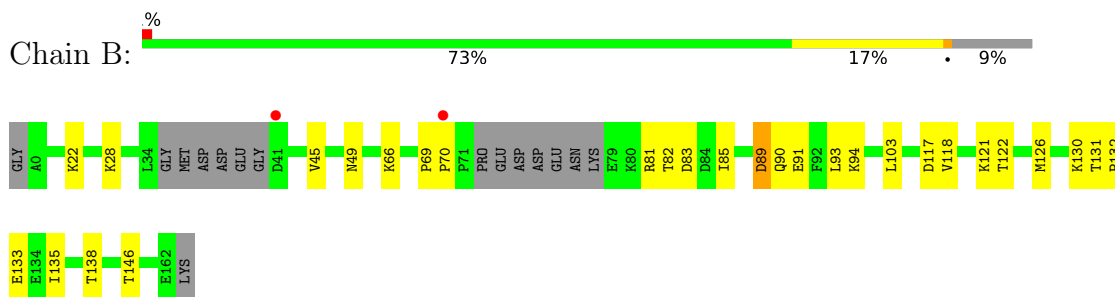
• Molecule 1: S-phase kinase-associated protein 1

• Molecule 2: Lysine-specific demethylase 2A
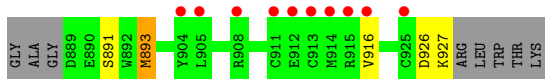
• Molecule 2: Lysine-specific demethylase 2A

Chain F:

• Molecule 2: Lysine-specific demethylase 2A

Chain I:

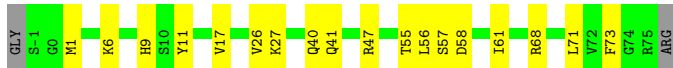

• Molecule 3: Polyubiquitin-B

Chain C:

• Molecule 3: Polyubiquitin-B

Chain D:

• Molecule 3: Polyubiquitin-B

Chain H:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	60.56Å 118.19Å 146.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.09 – 2.61 45.09 – 2.61	Depositor EDS
% Data completeness (in resolution range)	96.8 (45.09-2.61) 96.9 (45.09-2.61)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	2.80 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.235 , 0.294 0.235 , 0.293	Depositor DCC
R_{free} test set	1642 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å^2)	53.5	Xtriage
Anisotropy	0.342	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 43.5	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	6235	wwPDB-VP
Average B, all atoms (Å^2)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.95% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

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	0.36	0/1122	0.52	0/1525
1	B	0.34	0/1171	0.50	0/1590
1	G	0.31	0/924	0.53	0/1263
2	E	0.34	0/380	0.52	0/517
2	F	0.37	0/389	0.52	0/527
2	I	0.34	0/276	0.56	0/381
3	C	0.49	1/661 (0.2%)	0.65	1/894 (0.1%)
3	D	0.36	0/679	0.59	0/917
3	H	0.36	0/672	0.63	0/907
All	All	0.37	1/6274 (0.0%)	0.56	1/8521 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	73	PHE	CE2-CZ	5.23	1.47	1.37

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	73	PHE	CD1-CE1-CZ	-5.85	113.08	120.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1105	0	1072	15	0
1	B	1153	0	1118	23	1
1	G	909	0	842	11	0
2	E	368	0	324	2	1
2	F	377	0	341	6	0
2	I	268	0	185	6	0
3	C	652	0	642	10	0
3	D	670	0	668	19	0
3	H	663	0	667	7	0
4	A	18	0	0	0	0
4	B	16	0	0	0	0
4	C	5	0	0	0	0
4	D	14	0	0	1	0
4	E	1	0	0	0	0
4	F	5	0	0	1	0
4	H	10	0	0	0	0
4	I	1	0	0	0	0
All	All	6235	0	5859	87	1

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 7.

The worst 5 of 87 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)
2:I:891:SER:HB3	2:I:893:MET:SD	1.99	1.00
2:I:893:MET:SD	2:I:893:MET:N	2.43	0.92
1:B:130:LYS:NZ	1:B:138:THR:HG21	1.95	0.81
3:D:9:HIS:CD2	3:D:11:TYR:H	2.07	0.72
1:A:130:LYS:NZ	1:A:138:THR:OG1	2.23	0.71

All (1) 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:B:146:THR:OG1	2:E:912:GLU:OE2[4_545]	2.19	0.01

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	139/165 (84%)	131 (94%)	8 (6%)	0	100	100
1	B	144/165 (87%)	138 (96%)	6 (4%)	0	100	100
1	G	120/165 (73%)	116 (97%)	4 (3%)	0	100	100
2	E	43/47 (92%)	41 (95%)	1 (2%)	1 (2%)	6	10
2	F	43/47 (92%)	41 (95%)	2 (5%)	0	100	100
2	I	37/47 (79%)	36 (97%)	1 (3%)	0	100	100
3	C	82/87 (94%)	79 (96%)	3 (4%)	0	100	100
3	D	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
3	H	82/87 (94%)	78 (95%)	4 (5%)	0	100	100
All	All	773/897 (86%)	738 (96%)	34 (4%)	1 (0%)	51	74

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	927	LYS

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	119/150 (79%)	119 (100%)	0	100	100
1	B	125/150 (83%)	124 (99%)	1 (1%)	81	92
1	G	89/150 (59%)	86 (97%)	3 (3%)	37	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	36/44 (82%)	35 (97%)	1 (3%)	43	68
2	F	39/44 (89%)	39 (100%)	0	100	100
2	I	19/44 (43%)	18 (95%)	1 (5%)	22	43
3	C	71/80 (89%)	71 (100%)	0	100	100
3	D	74/80 (92%)	74 (100%)	0	100	100
3	H	72/80 (90%)	72 (100%)	0	100	100
All	All	644/822 (78%)	638 (99%)	6 (1%)	78	90

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	89	ASP
1	G	142	LYS
2	I	893	MET
2	E	926	ASP
1	B	89	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	9	HIS
3	H	62	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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(Å²)	Q<0.9
1	A	145/165 (87%)	-0.12	1 (0%)	87	85	32, 50, 101, 135	0
1	B	150/165 (90%)	-0.16	2 (1%)	77	73	31, 52, 98, 117	0
1	G	126/165 (76%)	0.23	11 (8%)	10	7	59, 83, 113, 129	0
2	E	45/47 (95%)	0.17	2 (4%)	34	28	41, 68, 100, 126	0
2	F	45/47 (95%)	-0.05	0	100	100	41, 62, 87, 104	0
2	I	39/47 (82%)	1.19	10 (25%)	0	0	80, 130, 152, 158	0
3	C	84/87 (96%)	-0.22	0	100	100	50, 69, 86, 123	0
3	D	85/87 (97%)	-0.09	0	100	100	39, 59, 85, 102	0
3	H	84/87 (96%)	-0.15	1 (1%)	79	76	34, 52, 73, 102	0
All	All	803/897 (89%)	0.00	27 (3%)	45	38	31, 64, 113, 158	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	905	LEU	3.6
2	I	911	CYS	3.6
1	B	41	ASP	3.6
2	E	930	TRP	3.6
2	I	908	ARG	3.5

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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.