



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 20, 2023 – 02:31 PM EDT

PDB ID : 2I3T
Title : Bub3 complex with Mad3 (BubR1) GLEBS motif
Authors : Larsen, N.A.; Harrison, S.C.
Deposited on : 2006-08-20
Resolution : 2.80 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
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

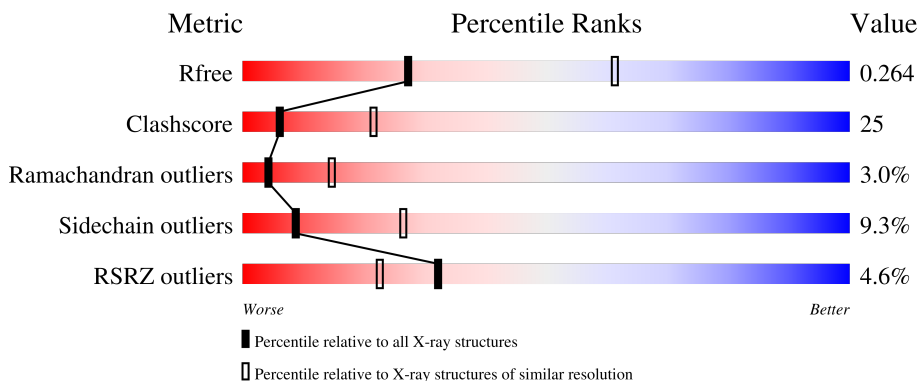
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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.



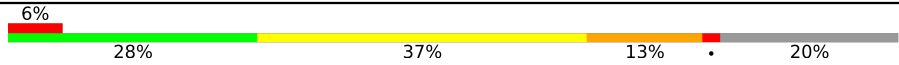
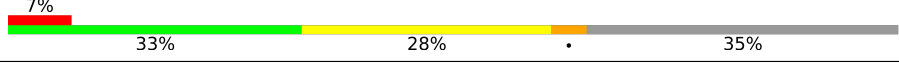
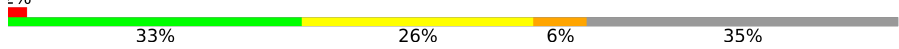
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	341	
1	C	341	
1	E	341	
1	G	341	
2	B	54	

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Mol	Chain	Length	Quality of chain
2	D	54	 <p>6% 28% 37% 13% 20%</p>
2	F	54	 <p>7% 33% 28% 35%</p>
2	H	54	 <p>2% 33% 26% 6% 35%</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 11816 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 Cell cycle arrest protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	334	2645	1677	443	512	13	0	0	0
1	C	334	2645	1677	443	512	13	0	0	0
1	E	334	2645	1677	443	512	13	0	0	0
1	G	334	2645	1677	443	512	13	0	0	0

- Molecule 2 is a protein called Spindle assembly checkpoint component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	35	294	191	47	53	3	0	0	0
2	D	43	354	224	59	68	3	0	0	0
2	F	35	294	191	47	53	3	0	0	0
2	H	35	294	191	47	53	3	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	353	MET	-	initiating methionine	UNP P47074
B	401	HIS	-	expression tag	UNP P47074
B	402	HIS	-	expression tag	UNP P47074
B	403	HIS	-	expression tag	UNP P47074
B	404	HIS	-	expression tag	UNP P47074
B	405	HIS	-	expression tag	UNP P47074
B	406	HIS	-	expression tag	UNP P47074
D	353	MET	-	initiating methionine	UNP P47074

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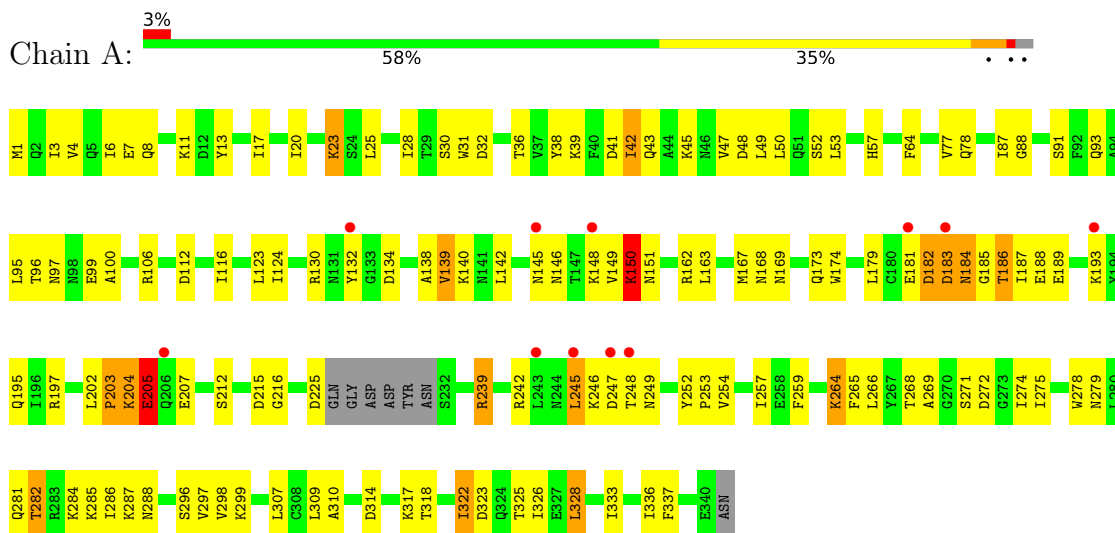
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Chain	Residue	Modelled	Actual	Comment	Reference
D	401	HIS	-	expression tag	UNP P47074
D	402	HIS	-	expression tag	UNP P47074
D	403	HIS	-	expression tag	UNP P47074
D	404	HIS	-	expression tag	UNP P47074
D	405	HIS	-	expression tag	UNP P47074
D	406	HIS	-	expression tag	UNP P47074
F	353	MET	-	initiating methionine	UNP P47074
F	401	HIS	-	expression tag	UNP P47074
F	402	HIS	-	expression tag	UNP P47074
F	403	HIS	-	expression tag	UNP P47074
F	404	HIS	-	expression tag	UNP P47074
F	405	HIS	-	expression tag	UNP P47074
F	406	HIS	-	expression tag	UNP P47074
H	353	MET	-	initiating methionine	UNP P47074
H	401	HIS	-	expression tag	UNP P47074
H	402	HIS	-	expression tag	UNP P47074
H	403	HIS	-	expression tag	UNP P47074
H	404	HIS	-	expression tag	UNP P47074
H	405	HIS	-	expression tag	UNP P47074
H	406	HIS	-	expression tag	UNP P47074

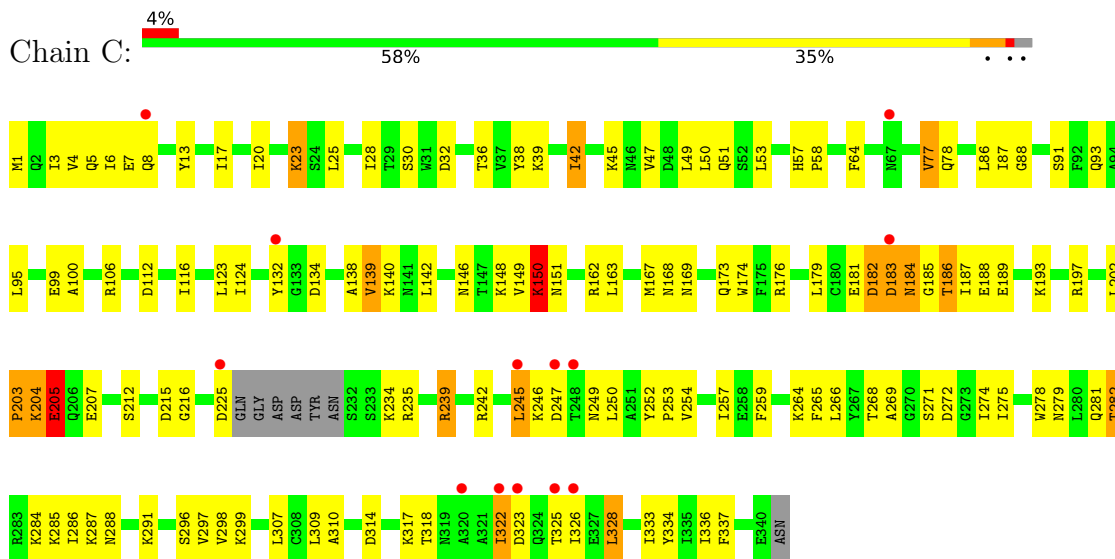
3 Residue-property plots i

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: Cell cycle arrest protein

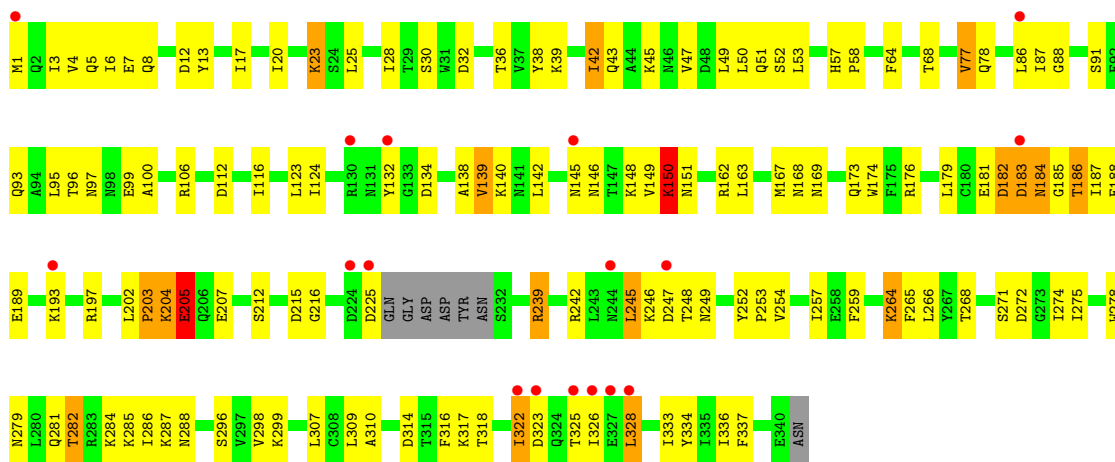


- Molecule 1: Cell cycle arrest protein

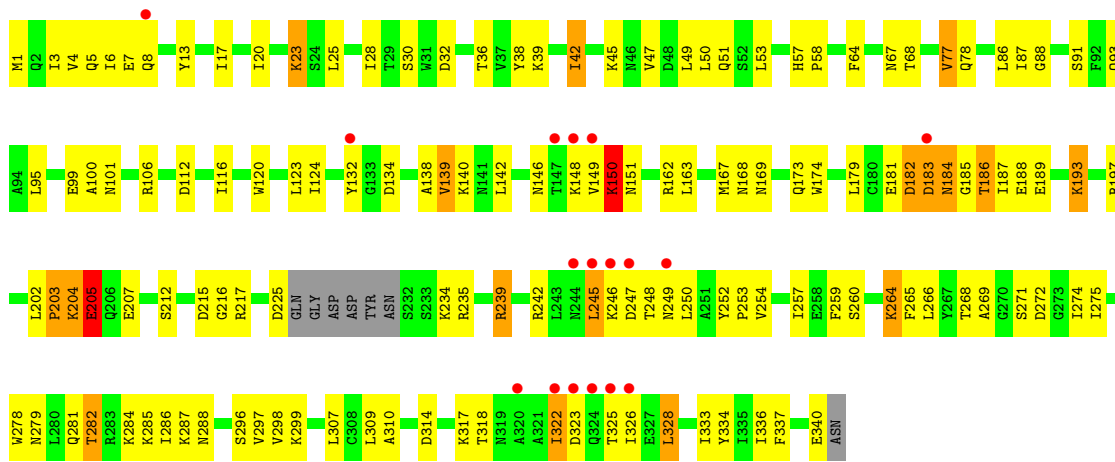


- Molecule 1: Cell cycle arrest protein

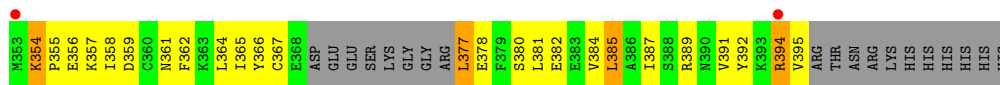
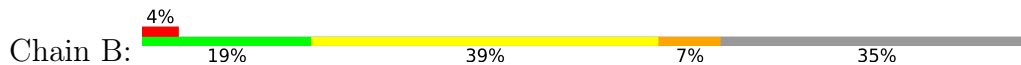




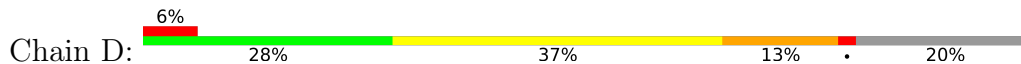
• Molecule 1: Cell cycle arrest protein



• Molecule 2: Spindle assembly checkpoint component

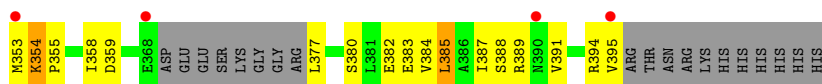


• Molecule 2: Spindle assembly checkpoint component

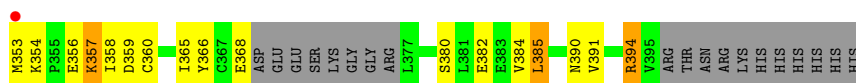
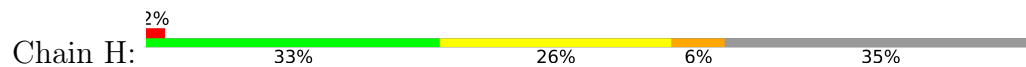


• Molecule 2: Spindle assembly checkpoint component





- Molecule 2: Spindle assembly checkpoint component



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.35Å 173.34Å 90.02Å 90.00° 95.30° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 49.04 – 2.69	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.80) 89.8 (49.04-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.69Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.238 , 0.267 0.236 , 0.264	Depositor DCC
R_{free} test set	1813 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	52.8	Xtrriage
Anisotropy	0.588	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11816	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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	0.43	0/2690	1.02	3/3640 (0.1%)
1	C	0.43	0/2690	0.72	3/3640 (0.1%)
1	E	0.43	0/2690	0.72	3/3640 (0.1%)
1	G	0.42	0/2690	0.72	3/3640 (0.1%)
2	B	0.53	0/297	0.70	0/395
2	D	0.47	0/358	0.73	0/476
2	F	0.51	0/297	0.81	0/395
2	H	0.55	0/297	0.79	0/395
All	All	0.43	0/12009	0.80	12/16221 (0.1%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	239	ARG	NE-CZ-NH1	-30.35	105.13	120.30
1	A	239	ARG	NE-CZ-NH2	29.07	134.83	120.30
1	A	239	ARG	CD-NE-CZ	17.96	148.74	123.60
1	C	239	ARG	NE-CZ-NH2	-10.62	114.99	120.30
1	E	239	ARG	NE-CZ-NH2	-10.03	115.29	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	2645	0	2638	143	0
1	C	2645	0	2638	128	0
1	E	2645	0	2638	134	0
1	G	2645	0	2638	148	0
2	B	294	0	303	26	0
2	D	354	0	357	36	0
2	F	294	0	303	13	0
2	H	294	0	303	18	0
All	All	11816	0	11818	582	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 25.

The worst 5 of 582 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:E:148:LYS:HD3	1:E:149:VAL:H	1.12	1.15
1:A:148:LYS:HD3	1:A:149:VAL:H	1.12	1.13
1:C:148:LYS:HD3	1:C:149:VAL:H	1.12	1.13
1:G:139:VAL:HG11	1:G:179:LEU:HD13	1.30	1.12
1:C:139:VAL:HG11	1:C:179:LEU:HD13	1.32	1.11

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	330/341 (97%)	294 (89%)	27 (8%)	9 (3%)	5 17
1	C	330/341 (97%)	295 (89%)	26 (8%)	9 (3%)	5 17
1	E	330/341 (97%)	296 (90%)	25 (8%)	9 (3%)	5 17
1	G	330/341 (97%)	293 (89%)	28 (8%)	9 (3%)	5 17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	31/54 (57%)	26 (84%)	3 (10%)	2 (6%)	1	3
2	D	41/54 (76%)	28 (68%)	8 (20%)	5 (12%)	0	1
2	F	31/54 (57%)	26 (84%)	5 (16%)	0	100	100
2	H	31/54 (57%)	28 (90%)	2 (6%)	1 (3%)	4	13
All	All	1454/1580 (92%)	1286 (88%)	124 (8%)	44 (3%)	4	15

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	183	ASP
1	A	204	LYS
2	B	394	ARG
1	C	183	ASP
1	C	204	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	299/305 (98%)	273 (91%)	26 (9%)	10	30
1	C	299/305 (98%)	273 (91%)	26 (9%)	10	30
1	E	299/305 (98%)	273 (91%)	26 (9%)	10	30
1	G	299/305 (98%)	273 (91%)	26 (9%)	10	30
2	B	34/51 (67%)	31 (91%)	3 (9%)	10	29
2	D	40/51 (78%)	34 (85%)	6 (15%)	3	9
2	F	34/51 (67%)	29 (85%)	5 (15%)	3	9
2	H	34/51 (67%)	28 (82%)	6 (18%)	2	5
All	All	1338/1424 (94%)	1214 (91%)	124 (9%)	9	26

5 of 124 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	371	GLU
1	G	281	GLN
1	E	162	ARG
1	G	264	LYS
2	H	356	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	361	ASN
1	G	184	ASN
1	E	151	ASN
1	G	263	HIS
1	G	146	ASN

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 monosaccharides 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	334/341 (97%)	0.13	11 (3%) 46 36	33, 53, 90, 104	0
1	C	334/341 (97%)	0.20	13 (3%) 39 29	34, 53, 89, 104	0
1	E	334/341 (97%)	0.22	17 (5%) 28 19	35, 55, 90, 103	0
1	G	334/341 (97%)	0.25	17 (5%) 28 19	36, 54, 89, 104	0
2	B	35/54 (64%)	0.43	2 (5%) 23 15	50, 66, 94, 108	0
2	D	43/54 (79%)	0.37	3 (6%) 16 9	51, 64, 108, 112	0
2	F	35/54 (64%)	0.89	4 (11%) 5 3	46, 61, 103, 114	0
2	H	35/54 (64%)	0.06	1 (2%) 51 41	39, 50, 69, 87	0
All	All	1484/1580 (93%)	0.23	68 (4%) 32 22	33, 55, 92, 114	0

The worst 5 of 68 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	353	MET	9.6
2	B	353	MET	8.4
1	G	323	ASP	6.3
1	E	326	ILE	5.1
1	C	326	ILE	4.8

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 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.