



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 02:59 PM EDT

PDB ID : 6NF7 / pdb_00006nf7
Title : Crystal Structure of RT1.Aa-Bu31-10
Authors : Gras, S.
Deposited on : 2018-12-19
Resolution : 2.90 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
Xtriage (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

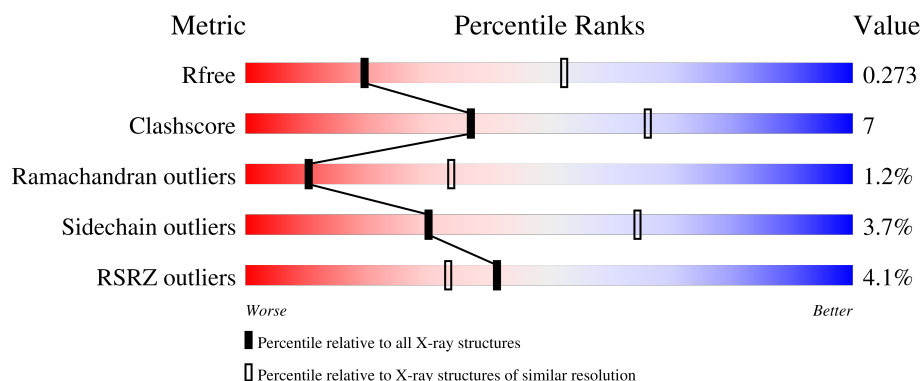
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	275	
1	D	275	
1	G	275	
1	J	275	
1	M	275	

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Mol	Chain	Length	Quality of chain
2	B	100	% 74% 23% ..
2	E	100	8% 72% 23% 5%
2	H	100	6% 70% 24% 6%
2	K	100	11% 74% 25% .
2	N	100	69% 29% ..
3	C	12	8% 67% 33%
3	F	12	25% 58% 25% 17%
3	I	12	17% 75% 8% 17%
3	L	12	25% 67% 8% 25%
3	O	12	8% 67% 8% 25%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15902 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 RT1A.a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2261	1420	401	432	8			
1	D	275	Total	C	N	O	S	0	0	0
			2261	1420	401	432	8			
1	G	275	Total	C	N	O	S	0	0	0
			2261	1420	401	432	8			
1	J	275	Total	C	N	O	S	0	0	0
			2261	1420	401	432	8			
1	M	275	Total	C	N	O	S	0	0	0
			2261	1420	401	432	8			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			821	528	137	152	4			
2	E	100	Total	C	N	O	S	0	0	0
			829	533	138	153	5			
2	H	100	Total	C	N	O	S	0	0	0
			829	533	138	153	5			
2	K	99	Total	C	N	O	S	0	0	0
			821	528	137	152	4			
2	N	99	Total	C	N	O	S	0	0	0
			821	528	137	152	4			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P07151
E	0	MET	-	initiating methionine	UNP P07151
H	0	MET	-	initiating methionine	UNP P07151
K	0	MET	-	initiating methionine	UNP P07151
N	0	MET	-	initiating methionine	UNP P07151

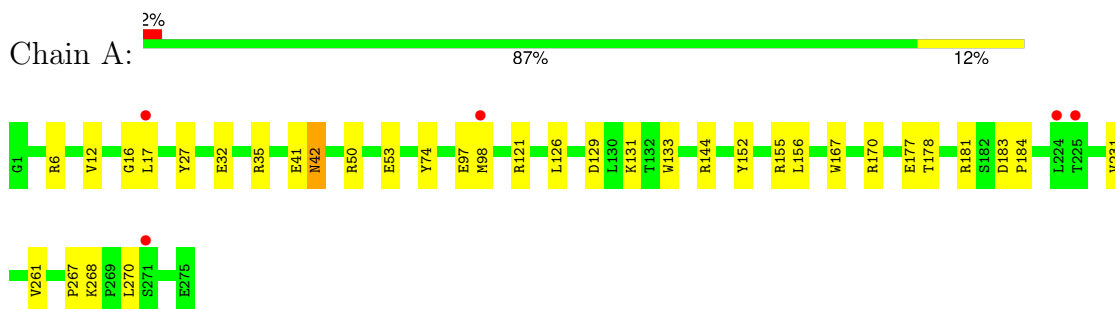
- Molecule 3 is a protein called Bu31-10 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	12	Total	C	N	O	0	0	0
			109	68	18	23			
3	F	10	Total	C	N	O	0	0	0
			98	61	16	21			
3	I	10	Total	C	N	O	0	0	0
			95	61	16	18			
3	L	9	Total	C	N	O	0	0	0
			87	57	15	15			
3	O	9	Total	C	N	O	0	0	0
			87	57	15	15			

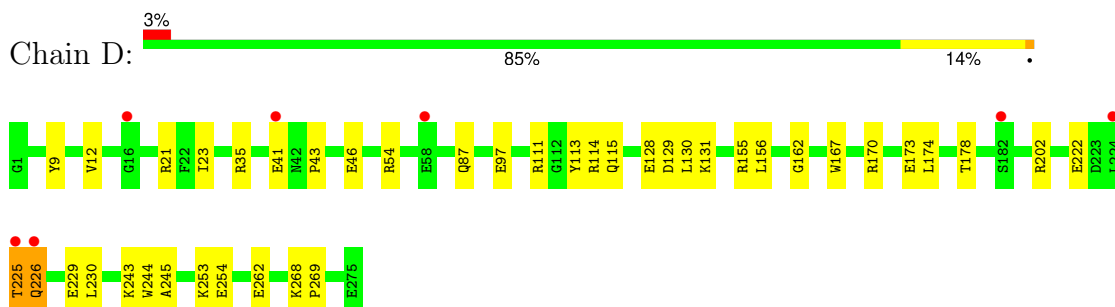
3 Residue-property plots [i](#)

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.

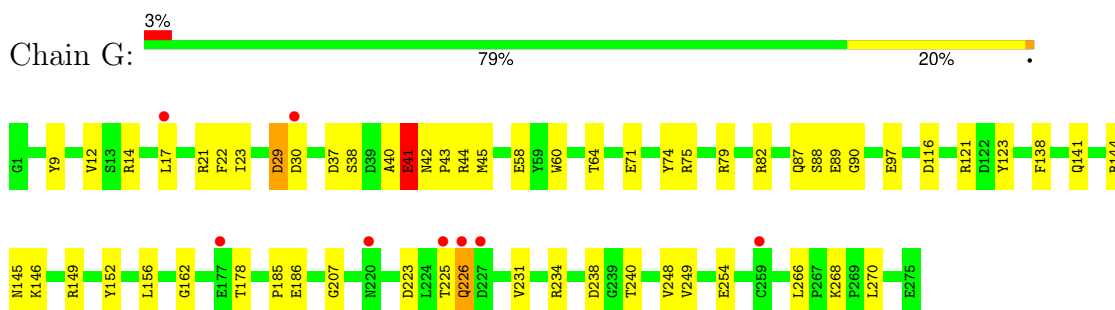
- Molecule 1: RT1A.a



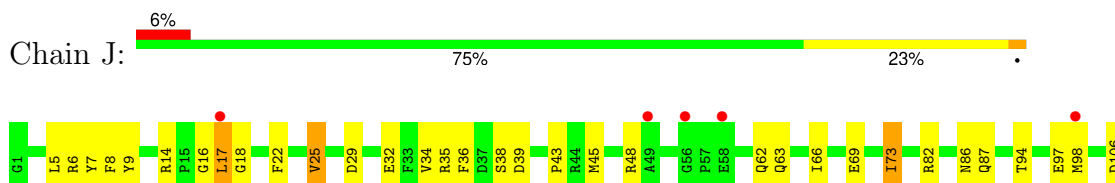
- Molecule 1: RT1A.a

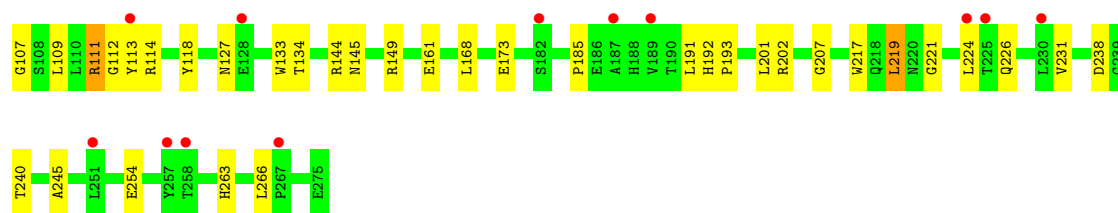


- Molecule 1: RT1A.a

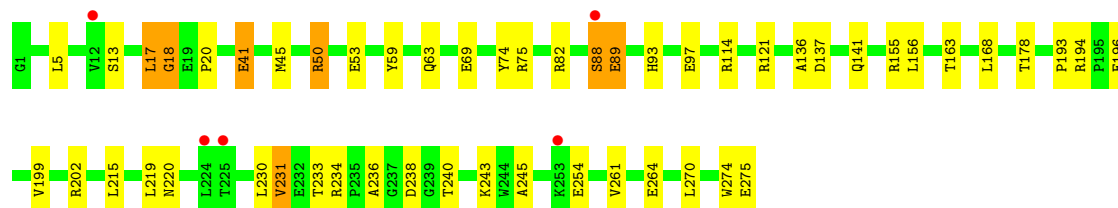
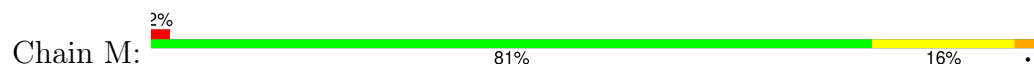


- Molecule 1: RT1A.a

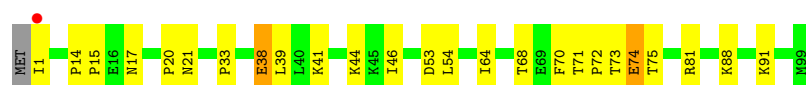




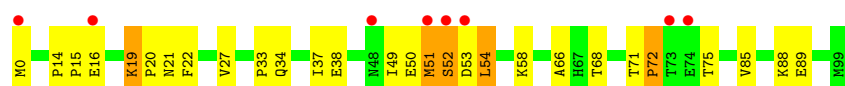
• Molecule 1: RT1A.a



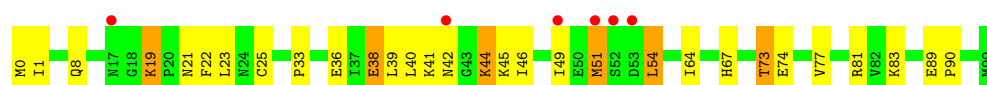
• Molecule 2: Beta-2-microglobulin



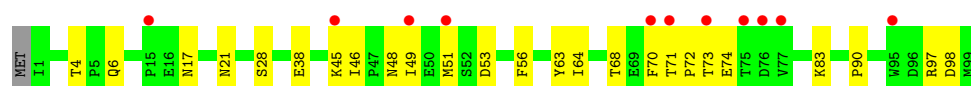
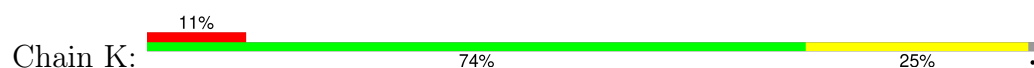
• Molecule 2: Beta-2-microglobulin



• Molecule 2: Beta-2-microglobulin



• Molecule 2: Beta-2-microglobulin



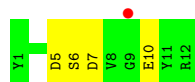
• Molecule 2: Beta-2-microglobulin

Chain N:  69% 29% ..



• Molecule 3: Bu31-10 peptide

Chain C:  8% 67% 33%



• Molecule 3: Bu31-10 peptide

Chain F:  25% 58% 25% 17%



• Molecule 3: Bu31-10 peptide

Chain I:  17% 75% 8% 17%



• Molecule 3: Bu31-10 peptide

Chain L:  25% 67% 8% 25%



• Molecule 3: Bu31-10 peptide

Chain O:  8% 67% 8% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.05Å 205.86Å 100.67Å 90.00° 103.25° 90.00°	Depositor
Resolution (Å)	47.86 – 2.90 47.86 – 2.90	Depositor EDS
% Data completeness (in resolution range)	94.1 (47.86-2.90) 94.5 (47.86-2.90)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.91Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.207 , 0.275 0.212 , 0.273	Depositor DCC
R_{free} test set	2673 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	35.3	Xtriage
Anisotropy	0.721	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	15902	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% 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	0.27	0/2322	0.71	2/3152 (0.1%)
1	D	0.28	0/2322	0.73	1/3152 (0.0%)
1	G	0.29	0/2322	0.75	3/3152 (0.1%)
1	J	0.28	0/2322	0.73	3/3152 (0.1%)
1	M	0.28	0/2322	0.70	0/3152
2	B	0.28	0/846	0.78	0/1149
2	E	0.32	0/854	0.80	2/1159 (0.2%)
2	H	0.29	0/854	0.75	1/1159 (0.1%)
2	K	0.29	0/846	0.76	0/1149
2	N	0.26	0/846	0.78	4/1149 (0.3%)
3	C	0.34	0/111	0.71	0/147
3	F	0.29	0/99	0.71	0/129
3	I	0.20	0/96	0.49	0/125
3	L	0.16	0/88	0.40	0/114
3	O	0.17	0/88	0.50	0/114
All	All	0.28	0/16338	0.73	16/22154 (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
2	E	0	1

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	89	GLU	CA-C-N	5.91	127.23	119.84
2	N	89	GLU	C-N-CA	5.91	127.23	119.84
1	J	29	ASP	CB-CA-C	-5.64	110.08	116.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	54	LEU	N-CA-C	5.49	117.98	110.24
1	D	162	GLY	N-CA-C	5.44	115.16	110.21

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	51	MET	Peptide

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	2261	0	2135	22	0
1	D	2261	0	2135	23	0
1	G	2261	0	2135	38	0
1	J	2261	0	2135	41	0
1	M	2261	0	2133	32	0
2	B	821	0	807	15	0
2	E	829	0	816	16	0
2	H	829	0	816	20	0
2	K	821	0	807	16	0
2	N	821	0	807	17	0
3	C	109	0	97	3	0
3	F	98	0	84	4	0
3	I	95	0	87	1	0
3	L	87	0	83	1	0
3	O	87	0	83	1	0
All	All	15902	0	15160	221	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 7.

The worst 5 of 221 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:D:131:LYS:HD2	1:G:226:GLN:HG2	1.46	0.95
2:E:58:LYS:H	2:E:58:LYS:HD2	1.38	0.88
1:J:35:ARG:HH22	2:K:53:ASP:HB2	1.44	0.80
1:D:114:ARG:HD2	1:D:156:LEU:HD21	1.68	0.75
1:J:35:ARG:HG3	1:J:48:ARG:HG3	1.70	0.73

There are no symmetry-related clashes.

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	273/275 (99%)	255 (93%)	18 (7%)	0	100	100
1	D	273/275 (99%)	257 (94%)	15 (6%)	1 (0%)	30	59
1	G	273/275 (99%)	256 (94%)	13 (5%)	4 (2%)	8	28
1	J	273/275 (99%)	256 (94%)	13 (5%)	4 (2%)	8	28
1	M	273/275 (99%)	249 (91%)	19 (7%)	5 (2%)	6	25
2	B	97/100 (97%)	92 (95%)	4 (4%)	1 (1%)	12	39
2	E	98/100 (98%)	85 (87%)	9 (9%)	4 (4%)	2	9
2	H	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
2	K	97/100 (97%)	92 (95%)	4 (4%)	1 (1%)	12	39
2	N	97/100 (97%)	92 (95%)	3 (3%)	2 (2%)	5	21
3	C	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
3	F	6/12 (50%)	3 (50%)	3 (50%)	0	100	100
3	I	6/12 (50%)	5 (83%)	1 (17%)	0	100	100
3	L	5/12 (42%)	3 (60%)	2 (40%)	0	100	100
3	O	5/12 (42%)	5 (100%)	0	0	100	100
All	All	1884/1935 (97%)	1751 (93%)	111 (6%)	22 (1%)	10	34

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	74	GLU
2	E	52	SER
1	G	29	ASP
1	G	41	GLU
2	N	17	ASN

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	234/234 (100%)	231 (99%)	3 (1%)	61	86
1	D	234/234 (100%)	225 (96%)	9 (4%)	29	64
1	G	234/234 (100%)	222 (95%)	12 (5%)	21	53
1	J	234/234 (100%)	225 (96%)	9 (4%)	29	64
1	M	234/234 (100%)	225 (96%)	9 (4%)	29	64
2	B	95/96 (99%)	91 (96%)	4 (4%)	26	60
2	E	96/96 (100%)	91 (95%)	5 (5%)	21	52
2	H	96/96 (100%)	90 (94%)	6 (6%)	16	45
2	K	95/96 (99%)	93 (98%)	2 (2%)	47	77
2	N	95/96 (99%)	93 (98%)	2 (2%)	47	77
3	C	11/11 (100%)	10 (91%)	1 (9%)	9	28
3	F	10/11 (91%)	10 (100%)	0	100	100
3	I	9/11 (82%)	9 (100%)	0	100	100
3	L	8/11 (73%)	8 (100%)	0	100	100
3	O	8/11 (73%)	8 (100%)	0	100	100
All	All	1693/1705 (99%)	1631 (96%)	62 (4%)	30	64

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	186	GLU
1	M	178	THR
2	H	38	GLU
1	M	69	GLU
1	M	264	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	48	ASN
1	J	63	GLN
1	M	145	ASN
1	J	62	GLN
1	J	87	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

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(Å ²)	Q<0.9
1	A	275/275 (100%)	0.21	5 (1%) 67 59	15, 30, 55, 94	0
1	D	275/275 (100%)	0.19	7 (2%) 58 48	16, 31, 56, 81	0
1	G	275/275 (100%)	0.30	8 (2%) 53 45	15, 29, 57, 76	0
1	J	275/275 (100%)	0.71	17 (6%) 26 21	30, 49, 76, 93	0
1	M	275/275 (100%)	0.44	5 (1%) 67 59	23, 41, 69, 84	0
2	B	99/100 (99%)	0.13	1 (1%) 79 73	17, 33, 55, 61	0
2	E	100/100 (100%)	0.52	8 (8%) 18 15	16, 36, 66, 79	0
2	H	100/100 (100%)	0.38	6 (6%) 27 21	17, 35, 60, 76	0
2	K	99/100 (99%)	0.88	11 (11%) 10 9	32, 54, 82, 90	0
2	N	99/100 (99%)	0.39	0 100 100	29, 45, 64, 71	0
3	C	12/12 (100%)	0.71	1 (8%) 17 14	20, 40, 67, 78	0
3	F	10/12 (83%)	0.92	3 (30%) 1 1	22, 31, 70, 73	0
3	I	10/12 (83%)	1.26	2 (20%) 3 2	24, 34, 65, 66	0
3	L	9/12 (75%)	1.17	3 (33%) 1 1	44, 53, 65, 68	0
3	O	9/12 (75%)	1.21	1 (11%) 10 9	29, 36, 65, 73	0
All	All	1922/1935 (99%)	0.41	78 (4%) 41 33	15, 38, 68, 94	0

The worst 5 of 78 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	8	VAL	4.7
1	A	225	THR	4.2
2	K	73	THR	4.0
1	J	113	TYR	3.9
2	H	52	SER	3.8

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.