



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:27 AM UTC

PDB ID : 3EAB / pdb_00003eab
Title : Crystal structure of Spastin MIT in complex with ESCRT III
Authors : Yang, D.; Rimanchi, N.; Renvoise, B.; Lippincott-Schwartz, J.; Blackstone, C.;
Hurley, J.H.
Deposited on : 2008-08-25
Resolution : 2.50 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

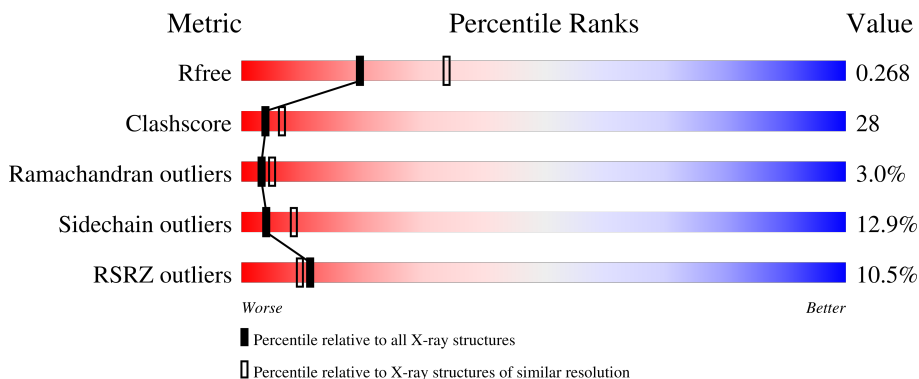
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	89	 11% 51% 37% 10% .
1	B	89	 8% 55% 35% 7% ..
1	C	89	 9% 58% 36% . .
1	D	89	 16% 52% 35% 11% ..
1	E	89	 10% 66% 26% . .

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Mol	Chain	Length	Quality of chain
1	F	89	
2	G	50	
2	H	50	
2	I	50	
2	J	50	
2	K	50	
2	L	50	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5977 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 Spastin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	89	719	448	129	136	6	0	0	0
1	B	88	711	443	128	135	5	0	0	0
1	C	89	719	448	129	136	6	0	0	0
1	D	88	709	443	128	132	6	0	0	0
1	E	86	701	438	126	132	5	0	0	0
1	F	87	701	437	127	131	6	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	108	MET	-	expression tag	UNP Q9UBP0
A	109	GLY	-	expression tag	UNP Q9UBP0
A	110	SER	-	expression tag	UNP Q9UBP0
A	111	MET	-	expression tag	UNP Q9UBP0
B	108	MET	-	expression tag	UNP Q9UBP0
B	109	GLY	-	expression tag	UNP Q9UBP0
B	110	SER	-	expression tag	UNP Q9UBP0
B	111	MET	-	expression tag	UNP Q9UBP0
C	108	MET	-	expression tag	UNP Q9UBP0
C	109	GLY	-	expression tag	UNP Q9UBP0
C	110	SER	-	expression tag	UNP Q9UBP0
C	111	MET	-	expression tag	UNP Q9UBP0
D	108	MET	-	expression tag	UNP Q9UBP0
D	109	GLY	-	expression tag	UNP Q9UBP0
D	110	SER	-	expression tag	UNP Q9UBP0
D	111	MET	-	expression tag	UNP Q9UBP0
E	108	MET	-	expression tag	UNP Q9UBP0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	109	GLY	-	expression tag	UNP Q9UBP0
E	110	SER	-	expression tag	UNP Q9UBP0
E	111	MET	-	expression tag	UNP Q9UBP0
F	108	MET	-	expression tag	UNP Q9UBP0
F	109	GLY	-	expression tag	UNP Q9UBP0
F	110	SER	-	expression tag	UNP Q9UBP0
F	111	MET	-	expression tag	UNP Q9UBP0

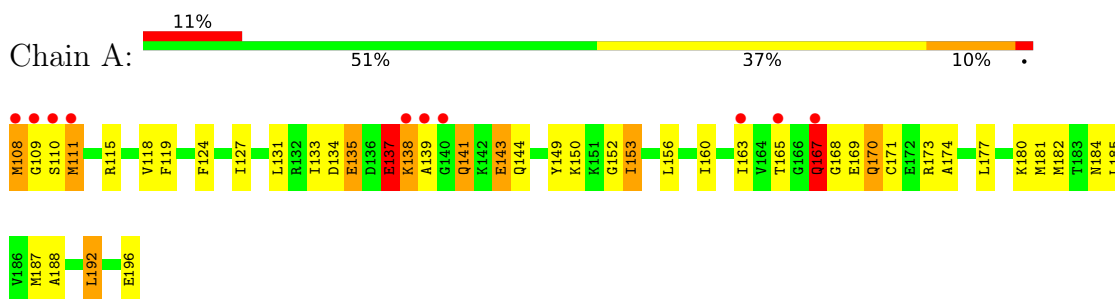
- Molecule 2 is a protein called CHMP1b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	G	40	Total 297	C 176	N 53	O 66	S 2	0	0	0
2	H	39	Total 290	C 170	N 51	O 67	S 2	0	0	0
2	I	41	Total 307	C 182	N 54	O 69	S 2	0	0	0
2	J	37	Total 271	C 160	N 47	O 62	S 2	0	0	0
2	K	38	Total 281	C 167	N 50	O 62	S 2	0	0	0
2	L	37	Total 271	C 162	N 47	O 60	S 2	0	0	0

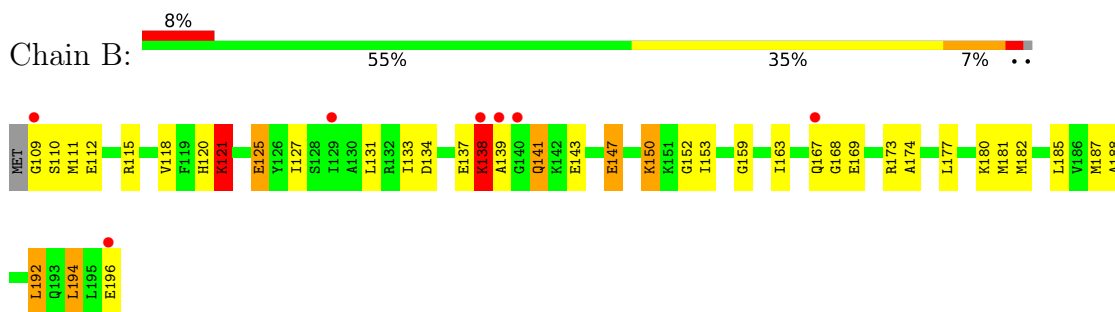
3 Residue-property plots [i](#)

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.

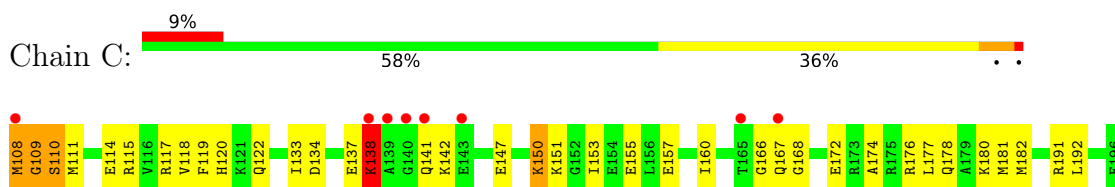
- Molecule 1: Spastin



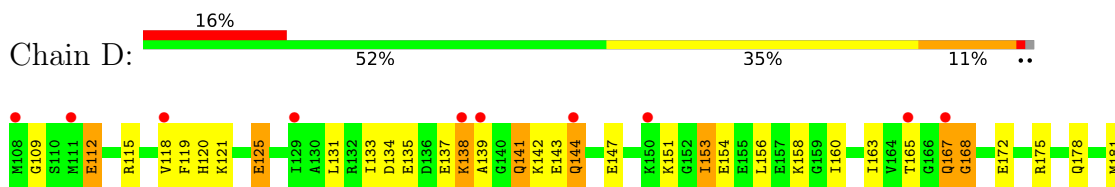
- Molecule 1: Spastin

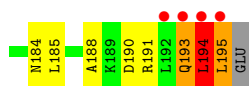


- Molecule 1: Spastin

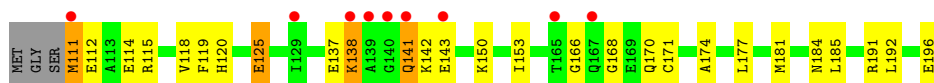


- Molecule 1: Spastin

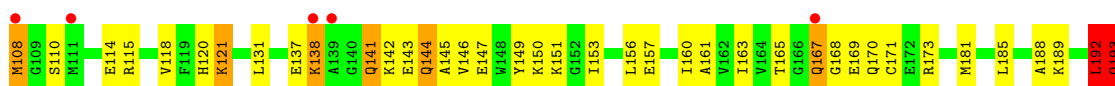




- Molecule 1: Spastin



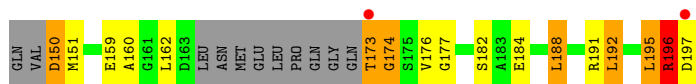
- Molecule 1: Spastin



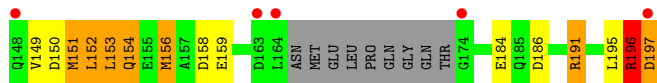
- Molecule 2: CHMP1b



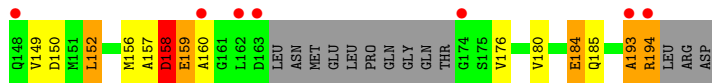
- Molecule 2: CHMP1b



- Molecule 2: CHMP1b



- Molecule 2: CHMP1b



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	151.97Å 95.49Å 100.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.65 – 2.50 47.65 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.7 (47.65-2.50) 93.7 (47.65-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 2.29Å)	Xtrriage
Refinement program	CNS, REFMAC	Depositor
R, R_{free}	0.232 , 0.268 0.232 , 0.268	Depositor DCC
R_{free} test set	2987 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	37.5	Xtrriage
Anisotropy	0.834	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 57.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.029 for -h,l,k	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5977	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.66% 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	0.53	0/725	0.76	0/963
1	B	0.79	2/717 (0.3%)	0.88	2/953 (0.2%)
1	C	0.76	1/725 (0.1%)	0.82	1/963 (0.1%)
1	D	0.56	0/715	0.86	0/951
1	E	0.55	0/707	0.74	1/940 (0.1%)
1	F	0.76	3/707 (0.4%)	0.89	3/940 (0.3%)
2	G	0.47	0/295	0.79	0/394
2	H	0.57	0/288	0.85	1/383 (0.3%)
2	I	0.50	0/305	0.78	0/406
2	J	0.55	0/269	0.86	1/359 (0.3%)
2	K	0.56	0/279	0.84	0/372
2	L	0.47	0/269	0.83	1/359 (0.3%)
All	All	0.63	6/6001 (0.1%)	0.83	10/7983 (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
1	A	0	1
1	B	0	1
1	C	0	2
1	E	0	2
1	F	0	1
2	J	0	2
All	All	0	9

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	150	LYS	CE-NZ	12.81	1.87	1.49
1	B	150	LYS	CE-NZ	12.27	1.86	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	121	LYS	CE-NZ	9.60	1.78	1.49
1	F	121	LYS	CD-CE	6.42	1.71	1.52
1	B	121	LYS	CE-NZ	6.41	1.68	1.49

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	167	GLN	OE1-CD-NE2	6.74	129.34	122.60
2	J	184	GLU	N-CA-C	6.12	117.62	111.07
1	F	121	LYS	CD-CE-NZ	-5.73	93.55	111.90
1	C	191	ARG	N-CA-C	-5.55	105.31	111.36
1	B	150	LYS	CD-CE-NZ	-5.54	94.19	111.90

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	167	GLN	Peptide
1	B	138	LYS	Peptide
1	C	138	LYS	Peptide
1	C	166	GLY	Peptide
1	E	166	GLY	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	719	0	733	45	0
1	B	711	0	724	69	1
1	C	719	0	733	29	0
1	D	709	0	727	44	1
1	E	701	0	716	31	0
1	F	701	0	716	48	1
2	G	297	0	288	19	0
2	H	290	0	275	22	0
2	I	307	0	296	17	0
2	J	271	0	257	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	281	0	273	15	0
2	L	271	0	264	23	1
All	All	5977	0	6002	337	3

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 28.

The worst 5 of 337 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:121:LYS:CE	1:B:121:LYS:NZ	1.68	1.51
1:F:121:LYS:CE	1:F:121:LYS:NZ	1.78	1.46
1:B:150:LYS:CE	1:B:150:LYS:NZ	1.86	1.39
1:C:150:LYS:NZ	1:C:150:LYS:CE	1.87	1.37
2:J:194:ARG:HD3	2:J:194:ARG:N	1.12	1.21

All (3) 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)
2:L:156:MET:CE	2:L:156:MET:CE[2_555]	1.72	0.48
1:B:147:GLU:OE2	1:D:144:GLN:NE2[4_457]	1.89	0.31
1:F:144:GLN:NE2	1:F:147:GLU:OE2[2_555]	2.17	0.03

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	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	3 4
1	B	86/89 (97%)	81 (94%)	4 (5%)	1 (1%)	10 20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	87/89 (98%)	85 (98%)	0	2 (2%)	5	8
1	D	86/89 (97%)	76 (88%)	6 (7%)	4 (5%)	2	2
1	E	84/89 (94%)	82 (98%)	1 (1%)	1 (1%)	10	20
1	F	85/89 (96%)	79 (93%)	3 (4%)	3 (4%)	3	4
2	G	36/50 (72%)	33 (92%)	3 (8%)	0	100	100
2	H	35/50 (70%)	30 (86%)	3 (9%)	2 (6%)	1	1
2	I	37/50 (74%)	33 (89%)	3 (8%)	1 (3%)	4	6
2	J	33/50 (66%)	30 (91%)	2 (6%)	1 (3%)	3	5
2	K	34/50 (68%)	29 (85%)	3 (9%)	2 (6%)	1	1
2	L	33/50 (66%)	29 (88%)	2 (6%)	2 (6%)	1	1
All	All	723/834 (87%)	665 (92%)	36 (5%)	22 (3%)	3	5

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	109	GLY
1	A	138	LYS
1	B	138	LYS
1	C	138	LYS
1	D	193	GLN

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	74/74 (100%)	61 (82%)	13 (18%)	2	3
1	B	73/74 (99%)	65 (89%)	8 (11%)	6	13
1	C	74/74 (100%)	69 (93%)	5 (7%)	14	31
1	D	73/74 (99%)	62 (85%)	11 (15%)	3	5
1	E	72/74 (97%)	67 (93%)	5 (7%)	14	30
1	F	72/74 (97%)	65 (90%)	7 (10%)	8	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	G	32/41 (78%)	27 (84%)	5 (16%)	2	5
2	H	31/41 (76%)	24 (77%)	7 (23%)	1	1
2	I	33/41 (80%)	25 (76%)	8 (24%)	1	1
2	J	29/41 (71%)	25 (86%)	4 (14%)	3	7
2	K	30/41 (73%)	24 (80%)	6 (20%)	1	2
2	L	29/41 (71%)	28 (97%)	1 (3%)	32	60
All	All	622/690 (90%)	542 (87%)	80 (13%)	4	9

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	188	LEU
2	J	159	GLU
2	H	195	LEU
2	I	156	MET
2	K	180	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	154	GLN
2	I	185	GLN
2	H	185	GLN
2	J	148	GLN
1	C	184	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 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	89/89 (100%)	0.69	10 (11%) 10 8	30, 53, 106, 120	0
1	B	88/89 (98%)	0.53	7 (7%) 18 16	29, 46, 92, 121	0
1	C	89/89 (100%)	0.42	8 (8%) 15 13	25, 44, 82, 119	0
1	D	88/89 (98%)	0.97	14 (15%) 5 4	34, 55, 92, 110	0
1	E	86/89 (96%)	0.45	9 (10%) 11 10	28, 47, 93, 124	0
1	F	87/89 (97%)	0.60	6 (6%) 23 20	37, 54, 85, 126	0
2	G	40/50 (80%)	0.49	4 (10%) 12 10	37, 50, 81, 95	0
2	H	39/50 (78%)	0.33	2 (5%) 33 29	28, 46, 88, 97	0
2	I	41/50 (82%)	0.53	5 (12%) 8 7	26, 45, 84, 94	0
2	J	37/50 (74%)	0.96	7 (18%) 3 2	34, 45, 89, 95	0
2	K	38/50 (76%)	0.63	5 (13%) 7 6	29, 43, 85, 98	0
2	L	37/50 (74%)	0.24	3 (8%) 18 15	34, 47, 69, 79	0
All	All	759/834 (91%)	0.58	80 (10%) 11 10	25, 49, 92, 126	0

The worst 5 of 80 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	164	LEU	8.1
2	K	174	GLY	5.3
2	J	160	ALA	5.3
1	D	139	ALA	4.4
1	A	108	MET	4.4

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 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.