



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 10:06 PM GMT

PDB ID : 5CFF
Title : Crystal structure of Miranda/Staufen dsRBD5 complex
Authors : Shan, Z.; Wen, W.
Deposited on : 2015-07-08
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

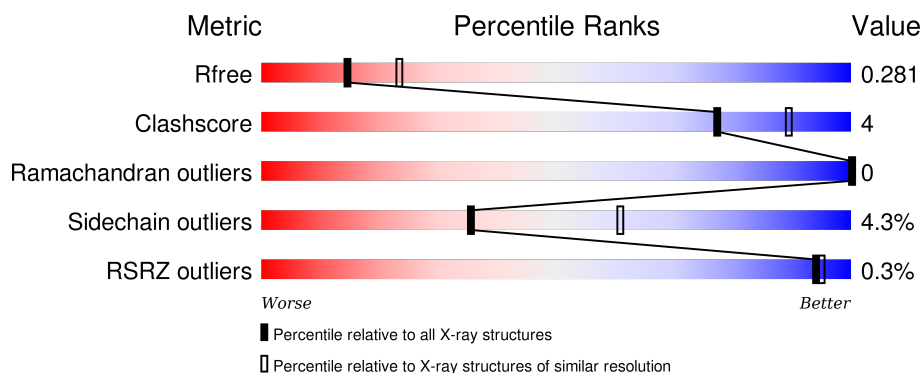
1 Overall quality at a glance

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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	95	<div> <div>%</div> <div> <div></div> <div>78%</div> <div>14%</div> <div>8%</div> </div> </div>
1	B	95	<div> <div></div> <div>78%</div> <div>14%</div> <div>7%</div> </div>
1	C	95	<div> <div>%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>8%</div> </div> </div>
1	D	95	<div> <div></div> <div>87%</div> <div>5%</div> <div>7%</div> </div>
2	E	72	<div> <div></div> <div>94%</div> <div></div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	72	<div><div></div><div>83%</div><div>11%</div><div></div><div></div></div>
2	G	72	<div><div></div><div>85%</div><div>11%</div><div></div><div></div></div>
2	H	72	<div><div></div><div>79%</div><div>11%</div><div>10%</div><div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4632 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 Miranda.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	87	Total	C	N	O	Se	0	0	0
			637	399	113	124	1			
1	B	88	Total	C	N	O	Se	0	0	0
			658	410	115	132	1			
1	C	87	Total	C	N	O	Se	0	0	0
			627	398	109	119	1			
1	D	88	Total	C	N	O	Se	0	1	0
			662	407	116	138	1			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	501	GLY	-	expression tag	UNP Q9VDR7
A	502	PRO	-	expression tag	UNP Q9VDR7
A	503	GLY	-	expression tag	UNP Q9VDR7
A	504	SER	-	expression tag	UNP Q9VDR7
A	505	GLU	-	expression tag	UNP Q9VDR7
A	506	PHE	-	expression tag	UNP Q9VDR7
A	507	GLU	-	expression tag	UNP Q9VDR7
A	508	LEU	-	expression tag	UNP Q9VDR7
A	509	ARG	-	expression tag	UNP Q9VDR7
A	510	ARG	-	expression tag	UNP Q9VDR7
A	511	GLN	-	expression tag	UNP Q9VDR7
A	512	ALA	-	expression tag	UNP Q9VDR7
A	513	SER	-	expression tag	UNP Q9VDR7
A	590	GLN	-	expression tag	UNP Q9VDR7
A	591	THR	-	expression tag	UNP Q9VDR7
A	592	LEU	-	expression tag	UNP Q9VDR7
A	593	GLN	-	expression tag	UNP Q9VDR7
A	594	SER	-	expression tag	UNP Q9VDR7
A	595	GLU	-	expression tag	UNP Q9VDR7
B	501	GLY	-	expression tag	UNP Q9VDR7
B	502	PRO	-	expression tag	UNP Q9VDR7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	503	GLY	-	expression tag	UNP Q9VDR7
B	504	SER	-	expression tag	UNP Q9VDR7
B	505	GLU	-	expression tag	UNP Q9VDR7
B	506	PHE	-	expression tag	UNP Q9VDR7
B	507	GLU	-	expression tag	UNP Q9VDR7
B	508	LEU	-	expression tag	UNP Q9VDR7
B	509	ARG	-	expression tag	UNP Q9VDR7
B	510	ARG	-	expression tag	UNP Q9VDR7
B	511	GLN	-	expression tag	UNP Q9VDR7
B	512	ALA	-	expression tag	UNP Q9VDR7
B	513	SER	-	expression tag	UNP Q9VDR7
B	590	GLN	-	expression tag	UNP Q9VDR7
B	591	THR	-	expression tag	UNP Q9VDR7
B	592	LEU	-	expression tag	UNP Q9VDR7
B	593	GLN	-	expression tag	UNP Q9VDR7
B	594	SER	-	expression tag	UNP Q9VDR7
B	595	GLU	-	expression tag	UNP Q9VDR7
C	501	GLY	-	expression tag	UNP Q9VDR7
C	502	PRO	-	expression tag	UNP Q9VDR7
C	503	GLY	-	expression tag	UNP Q9VDR7
C	504	SER	-	expression tag	UNP Q9VDR7
C	505	GLU	-	expression tag	UNP Q9VDR7
C	506	PHE	-	expression tag	UNP Q9VDR7
C	507	GLU	-	expression tag	UNP Q9VDR7
C	508	LEU	-	expression tag	UNP Q9VDR7
C	509	ARG	-	expression tag	UNP Q9VDR7
C	510	ARG	-	expression tag	UNP Q9VDR7
C	511	GLN	-	expression tag	UNP Q9VDR7
C	512	ALA	-	expression tag	UNP Q9VDR7
C	513	SER	-	expression tag	UNP Q9VDR7
C	590	GLN	-	expression tag	UNP Q9VDR7
C	591	THR	-	expression tag	UNP Q9VDR7
C	592	LEU	-	expression tag	UNP Q9VDR7
C	593	GLN	-	expression tag	UNP Q9VDR7
C	594	SER	-	expression tag	UNP Q9VDR7
C	595	GLU	-	expression tag	UNP Q9VDR7
D	501	GLY	-	expression tag	UNP Q9VDR7
D	502	PRO	-	expression tag	UNP Q9VDR7
D	503	GLY	-	expression tag	UNP Q9VDR7
D	504	SER	-	expression tag	UNP Q9VDR7
D	505	GLU	-	expression tag	UNP Q9VDR7
D	506	PHE	-	expression tag	UNP Q9VDR7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	507	GLU	-	expression tag	UNP Q9VDR7
D	508	LEU	-	expression tag	UNP Q9VDR7
D	509	ARG	-	expression tag	UNP Q9VDR7
D	510	ARG	-	expression tag	UNP Q9VDR7
D	511	GLN	-	expression tag	UNP Q9VDR7
D	512	ALA	-	expression tag	UNP Q9VDR7
D	513	SER	-	expression tag	UNP Q9VDR7
D	590	GLN	-	expression tag	UNP Q9VDR7
D	591	THR	-	expression tag	UNP Q9VDR7
D	592	LEU	-	expression tag	UNP Q9VDR7
D	593	GLN	-	expression tag	UNP Q9VDR7
D	594	SER	-	expression tag	UNP Q9VDR7
D	595	GLU	-	expression tag	UNP Q9VDR7

- Molecule 2 is a protein called Staufen.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	E	70	Total	C	N	O	S	Se	0	0	0
			527	333	86	106	1	1			
2	F	71	Total	C	N	O	S	Se	0	1	0
			522	333	87	100	1	1			
2	G	70	Total	C	N	O	S	Se	0	0	0
			507	324	83	98	1	1			
2	H	65	Total	C	N	O	S	Se	0	0	0
			465	299	76	88	1	1			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	947	GLY	-	expression tag	UNP P25159
E	948	PRO	-	expression tag	UNP P25159
E	949	GLY	-	expression tag	UNP P25159
E	950	SER	-	expression tag	UNP P25159
E	951	MSE	-	expression tag	UNP P25159
F	947	GLY	-	expression tag	UNP P25159
F	948	PRO	-	expression tag	UNP P25159
F	949	GLY	-	expression tag	UNP P25159
F	950	SER	-	expression tag	UNP P25159
F	951	MSE	-	expression tag	UNP P25159
G	947	GLY	-	expression tag	UNP P25159
G	948	PRO	-	expression tag	UNP P25159
G	949	GLY	-	expression tag	UNP P25159

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	950	SER	-	expression tag	UNP P25159
G	951	MSE	-	expression tag	UNP P25159
H	947	GLY	-	expression tag	UNP P25159
H	948	PRO	-	expression tag	UNP P25159
H	949	GLY	-	expression tag	UNP P25159
H	950	SER	-	expression tag	UNP P25159
H	951	MSE	-	expression tag	UNP P25159

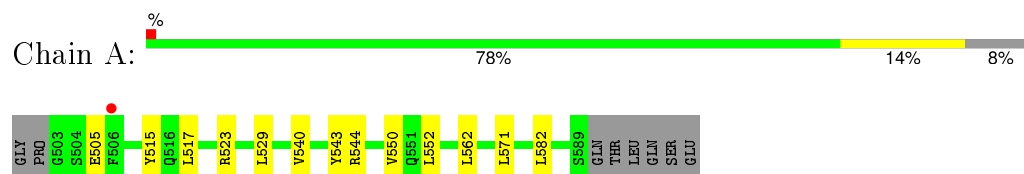
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total O 2 2	0	0
3	B	3	Total O 3 3	0	0
3	C	6	Total O 6 6	0	0
3	D	5	Total O 5 5	0	0
3	E	5	Total O 5 5	0	0
3	F	2	Total O 2 2	0	0
3	G	4	Total O 4 4	0	0

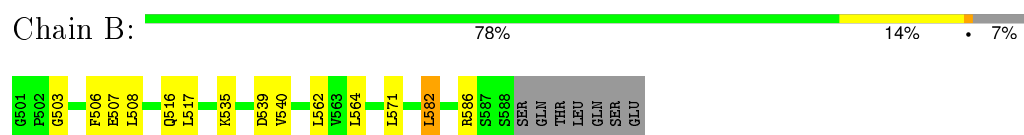
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

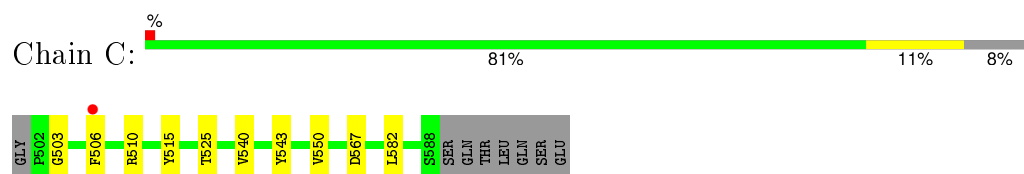
- Molecule 1: Miranda



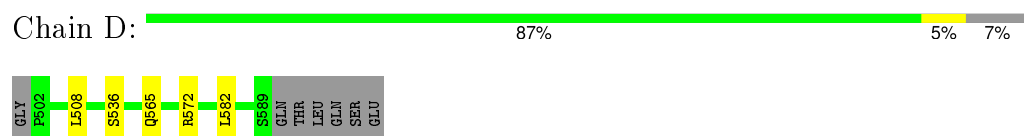
- Molecule 1: Miranda



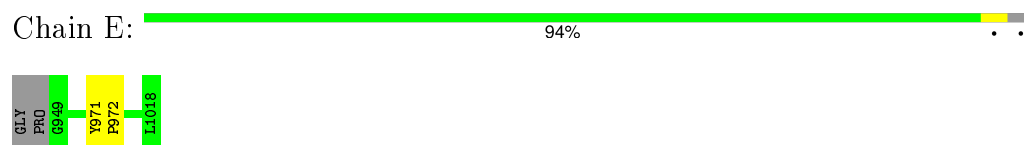
- Molecule 1: Miranda



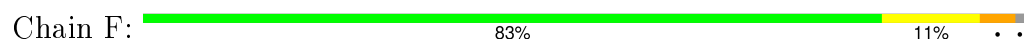
- Molecule 1: Miranda

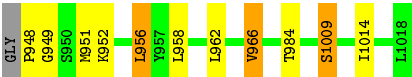


- Molecule 2: Staufen

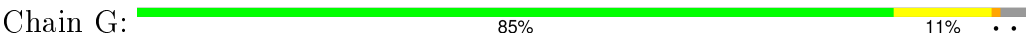


- Molecule 2: Staufen

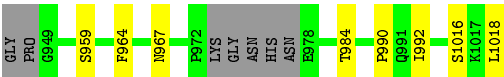
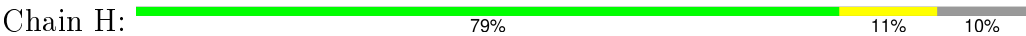




● Molecule 2: Staufen



● Molecule 2: Staufen



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	200.02Å 51.33Å 100.27Å 90.00° 90.56° 90.00°	Depositor
Resolution (Å)	27.66 – 2.50 27.66 – 2.49	Depositor EDS
% Data completeness (in resolution range)	93.7 (27.66-2.50) 94.8 (27.66-2.49)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.29 (at 2.51Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.242 , 0.281 0.252 , 0.281	Depositor DCC
R_{free} test set	1698 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	54.5	Xtriage
Anisotropy	0.409	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 19.6	EDS
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 34166 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4632	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.71% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.51	0/639	0.59	0/863
1	B	0.55	0/660	0.64	1/888 (0.1%)
1	C	0.53	0/629	0.57	0/845
1	D	0.59	0/666	0.60	0/898
2	E	0.52	0/536	0.61	0/726
2	F	0.51	0/531	0.60	0/721
2	G	0.46	0/516	0.58	0/700
2	H	0.45	0/472	0.56	0/642
All	All	0.52	0/4649	0.60	1/6283 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	582	LEU	CA-CB-CG	5.45	127.83	115.30

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	637	0	604	8	0
1	B	658	0	635	8	0
1	C	627	0	587	10	0
1	D	662	0	627	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	527	0	497	1	0
2	F	522	0	480	6	0
2	G	507	0	473	5	0
2	H	465	0	434	5	0
3	A	2	0	0	0	0
3	B	3	0	0	0	0
3	C	6	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	2	0	0	0	0
3	G	4	0	0	0	0
All	All	4632	0	4337	33	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 4.

The worst 5 of 33 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:F:951:MSE:HE3	2:F:1009:SER:HB2	1.68	0.75
2:G:978:GLU:HG3	2:G:996:VAL:HB	1.71	0.73
1:C:510:ARG:NH1	2:H:1018:LEU:O	2.28	0.66
1:A:544:ARG:HG3	1:C:543:TYR:HE2	1.59	0.64
1:B:582:LEU:HD23	1:D:582:LEU:HA	1.84	0.58

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	85/95 (90%)	85 (100%)	0	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	86/95 (90%)	86 (100%)	0	0	100	100
1	C	85/95 (90%)	85 (100%)	0	0	100	100
1	D	87/95 (92%)	87 (100%)	0	0	100	100
2	E	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
2	F	70/72 (97%)	69 (99%)	1 (1%)	0	100	100
2	G	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
2	H	61/72 (85%)	59 (97%)	2 (3%)	0	100	100
All	All	610/668 (91%)	604 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	57/81 (70%)	51 (90%)	6 (10%)	8	16
1	B	62/81 (76%)	57 (92%)	5 (8%)	15	27
1	C	53/81 (65%)	52 (98%)	1 (2%)	65	87
1	D	64/81 (79%)	63 (98%)	1 (2%)	70	90
2	E	58/63 (92%)	58 (100%)	0	100	100
2	F	52/63 (82%)	48 (92%)	4 (8%)	16	30
2	G	53/63 (84%)	52 (98%)	1 (2%)	65	87
2	H	48/63 (76%)	47 (98%)	1 (2%)	61	85
All	All	447/576 (78%)	428 (96%)	19 (4%)	35	61

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	517	LEU
1	B	562	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	F	1009	SER
1	B	516	GLN
2	F	1014	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates 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	86/95 (90%)	0.06	1 (1%) 81 83	30, 48, 67, 73	0
1	B	87/95 (91%)	-0.06	0 100 100	25, 36, 60, 67	0
1	C	86/95 (90%)	0.01	1 (1%) 81 83	26, 37, 68, 79	0
1	D	87/95 (91%)	0.01	0 100 100	26, 34, 66, 79	0
2	E	69/72 (95%)	-0.17	0 100 100	26, 38, 49, 59	0
2	F	70/72 (97%)	-0.22	0 100 100	27, 39, 51, 72	0
2	G	69/72 (95%)	-0.24	0 100 100	33, 43, 62, 67	0
2	H	64/72 (88%)	-0.03	0 100 100	33, 50, 67, 81	0
All	All	618/668 (92%)	-0.07	2 (0%) 94 95	25, 40, 66, 81	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	506	PHE	3.1
1	A	506	PHE	2.8

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 carbohydrates 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.