



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 04:17 PM UTC

PDB ID : 5D13 / pdb\_00005d13  
Title : Third PDZ domain (PDZ3) of PSD-95 complexed with CFMOC-KKETEV peptide  
Authors : De, S.; Spaller, M.R.; Olson, R.  
Deposited on : 2015-08-03  
Resolution : 2.15 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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
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

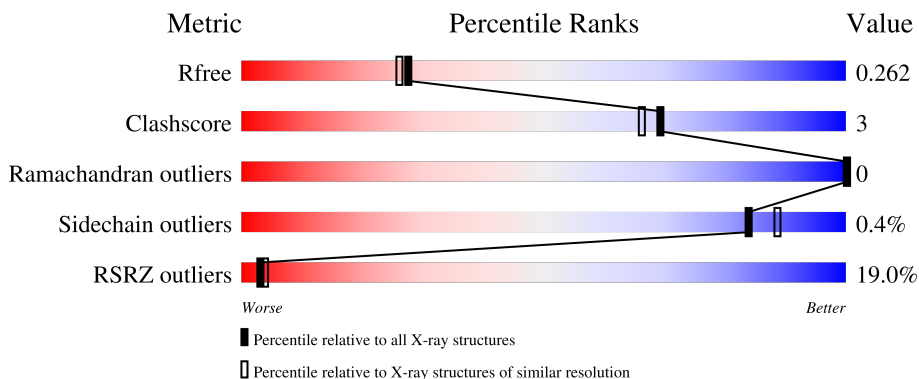
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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.



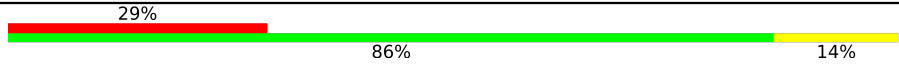
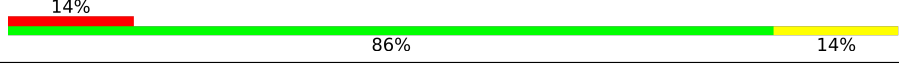
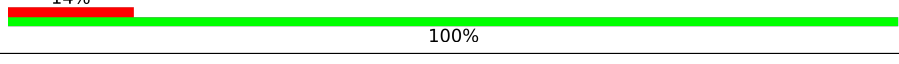
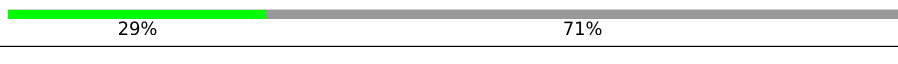
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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  $\geq 3$ , 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	119	
1	B	119	
1	C	119	
1	D	119	
2	E	7	

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Mol	Chain	Length	Quality of chain
2	F	7	 29% 86% 14%
2	G	7	 14% 86% 14%
2	H	7	 14% 100%
2	I	7	 29% 71%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5887 atoms, of which 2739 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 Disks large homolog 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
1	A	100	1357	440	644	134	139	0	0	0
1	B	100	1447	459	710	136	142	0	0	0
1	C	101	1398	450	666	137	145	0	0	0
1	D	100	1159	399	517	117	126	0	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	297	GLY	-	expression tag	UNP P31016
A	298	SER	-	expression tag	UNP P31016
A	299	PRO	-	expression tag	UNP P31016
A	300	GLU	-	expression tag	UNP P31016
A	301	PHE	-	expression tag	UNP P31016
A	403	ASN	-	expression tag	UNP P31016
A	404	SER	-	expression tag	UNP P31016
A	405	ARG	-	expression tag	UNP P31016
A	406	VAL	-	expression tag	UNP P31016
A	407	ASP	-	expression tag	UNP P31016
A	408	SER	-	expression tag	UNP P31016
A	409	SER	-	expression tag	UNP P31016
A	410	GLY	-	expression tag	UNP P31016
A	411	ARG	-	expression tag	UNP P31016
A	412	ILE	-	expression tag	UNP P31016
A	413	VAL	-	expression tag	UNP P31016
A	414	THR	-	expression tag	UNP P31016
A	415	ASP	-	expression tag	UNP P31016
B	297	GLY	-	expression tag	UNP P31016
B	298	SER	-	expression tag	UNP P31016
B	299	PRO	-	expression tag	UNP P31016

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Chain	Residue	Modelled	Actual	Comment	Reference
B	300	GLU	-	expression tag	UNP P31016
B	301	PHE	-	expression tag	UNP P31016
B	403	ASN	-	expression tag	UNP P31016
B	404	SER	-	expression tag	UNP P31016
B	405	ARG	-	expression tag	UNP P31016
B	406	VAL	-	expression tag	UNP P31016
B	407	ASP	-	expression tag	UNP P31016
B	408	SER	-	expression tag	UNP P31016
B	409	SER	-	expression tag	UNP P31016
B	410	GLY	-	expression tag	UNP P31016
B	411	ARG	-	expression tag	UNP P31016
B	412	ILE	-	expression tag	UNP P31016
B	413	VAL	-	expression tag	UNP P31016
B	414	THR	-	expression tag	UNP P31016
B	415	ASP	-	expression tag	UNP P31016
C	297	GLY	-	expression tag	UNP P31016
C	298	SER	-	expression tag	UNP P31016
C	299	PRO	-	expression tag	UNP P31016
C	300	GLU	-	expression tag	UNP P31016
C	301	PHE	-	expression tag	UNP P31016
C	403	ASN	-	expression tag	UNP P31016
C	404	SER	-	expression tag	UNP P31016
C	405	ARG	-	expression tag	UNP P31016
C	406	VAL	-	expression tag	UNP P31016
C	407	ASP	-	expression tag	UNP P31016
C	408	SER	-	expression tag	UNP P31016
C	409	SER	-	expression tag	UNP P31016
C	410	GLY	-	expression tag	UNP P31016
C	411	ARG	-	expression tag	UNP P31016
C	412	ILE	-	expression tag	UNP P31016
C	413	VAL	-	expression tag	UNP P31016
C	414	THR	-	expression tag	UNP P31016
C	415	ASP	-	expression tag	UNP P31016
D	297	GLY	-	expression tag	UNP P31016
D	298	SER	-	expression tag	UNP P31016
D	299	PRO	-	expression tag	UNP P31016
D	300	GLU	-	expression tag	UNP P31016
D	301	PHE	-	expression tag	UNP P31016
D	403	ASN	-	expression tag	UNP P31016
D	404	SER	-	expression tag	UNP P31016
D	405	ARG	-	expression tag	UNP P31016
D	406	VAL	-	expression tag	UNP P31016

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Chain	Residue	Modelled	Actual	Comment	Reference
D	407	ASP	-	expression tag	UNP P31016
D	408	SER	-	expression tag	UNP P31016
D	409	SER	-	expression tag	UNP P31016
D	410	GLY	-	expression tag	UNP P31016
D	411	ARG	-	expression tag	UNP P31016
D	412	ILE	-	expression tag	UNP P31016
D	413	VAL	-	expression tag	UNP P31016
D	414	THR	-	expression tag	UNP P31016
D	415	ASP	-	expression tag	UNP P31016

- Molecule 2 is a protein called CFMOC-KKETEV peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
2	G	7	Total	C	H	N	O	0	0	0
			120	44	56	7	13			
2	E	7	Total	C	H	N	O	0	0	0
			105	41	45	6	13			
2	H	7	Total	C	H	N	O	0	0	0
			105	41	45	6	13			
2	F	7	Total	C	H	N	O	0	0	0
			97	39	41	6	11			
2	I	2	Total	C	H	N	O	0	0	0
			41	22	15	2	2			

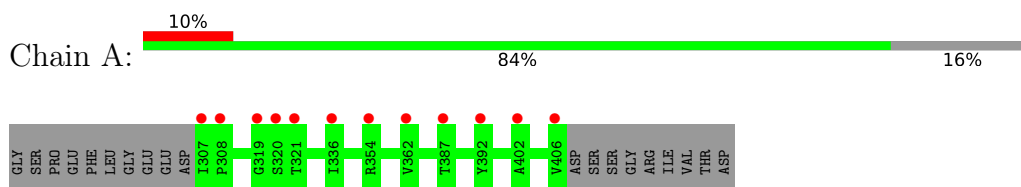
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	24	Total	O	0	0
			24	24		
3	C	19	Total	O	0	0
			19	19		
3	D	2	Total	O	0	0
			2	2		
3	G	5	Total	O	0	0
			5	5		
3	E	2	Total	O	0	0
			2	2		

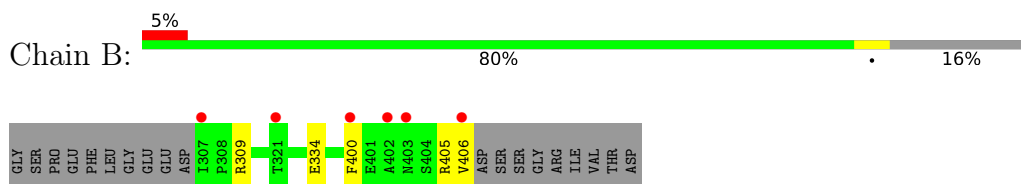
### 3 Residue-property plots [i](#)

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.

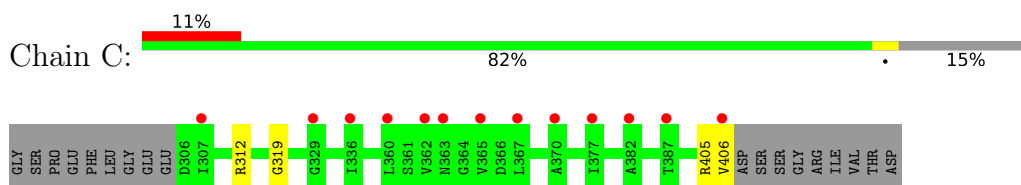
- Molecule 1: Disks large homolog 4



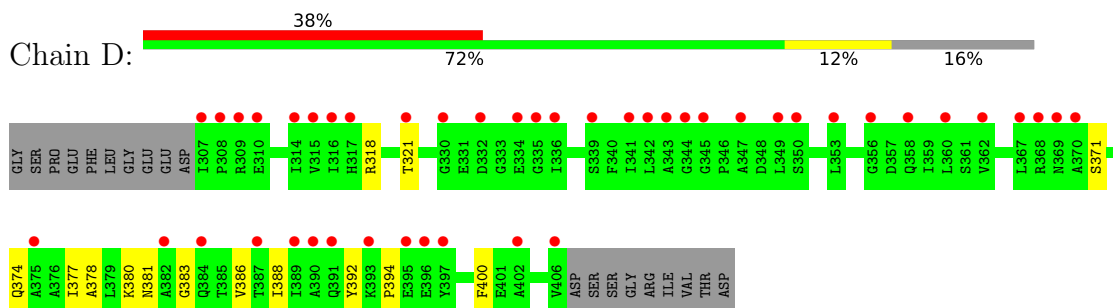
- Molecule 1: Disks large homolog 4



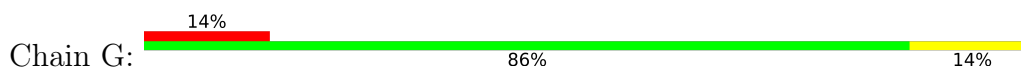
- Molecule 1: Disks large homolog 4

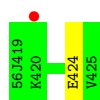


- Molecule 1: Disks large homolog 4

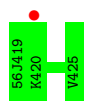


- Molecule 2: CFMOC-KKETEV peptide

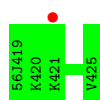




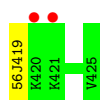
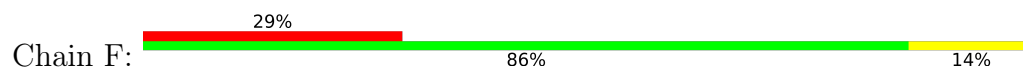
- Molecule 2: CFMOC-KKETEV peptide



- Molecule 2: CFMOC-KKETEV peptide



- Molecule 2: CFMOC-KKETEV peptide



- Molecule 2: CFMOC-KKETEV peptide



## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	84.94Å 84.94Å 210.19Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.50 – 2.15 36.50 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (36.50-2.15) 100.0 (36.50-2.15)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.11 (at 2.16Å)	Xtrriage
Refinement program	PHENIX 1.8.4	Depositor
R, $R_{free}$	0.210 , 0.257 0.220 , 0.262	Depositor DCC
$R_{free}$ test set	1530 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.7	Xtrriage
Anisotropy	0.728	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.43 , 95.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.000 for $-1/3^*h+1/3^*k+1/3^*l,-k,8/3^*h+4/3^*k+1/3^*l$ 0.012 for $-2/3^*h-1/3^*k-1/3^*l,-1/3^*h-2/3^*k+1/3^*l,-4/3^*h+4/3^*k+1/3^*l$ 0.000 for $-h,1/3^*h-1/3^*k-1/3^*l,-4/3^*h-8/3^*k+1/3^*l$ 0.000 for $-h,2/3^*h+1/3^*k+1/3^*l,4/3^*h+8/3^*k-1/3^*l$ 0.000 for $1/3^*h+2/3^*k-1/3^*l,-k,-8/3^*h-4/3^*k-1/3^*l$ 0.011 for $-1/3^*h-2/3^*k+1/3^*l,-2/3^*h-1/3^*k-1/3^*l,4/3^*h-4/3^*k-1/3^*l$ 0.039 for $-h-k,k,-l$	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5887	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	81.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.21 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5769e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 56J

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	0.62	0/724	0.80	0/981
1	B	0.85	0/748	0.91	0/1011
1	C	0.65	0/743	0.83	0/1004
1	D	0.45	0/652	0.86	0/891
2	E	0.45	0/42	0.61	0/55
2	F	0.36	0/38	0.56	0/50
2	G	0.70	0/46	1.03	0/59
2	H	0.33	0/42	0.67	0/55
2	I	0.51	0/8	0.59	0/8
All	All	0.66	0/3043	0.84	0/4114

There are no bond length outliers.

There are no bond angle outliers.

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	713	644	648	0	0
1	B	737	710	711	3	0
1	C	732	666	674	2	0
1	D	642	517	529	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	60	45	31	0	0
2	F	56	41	27	2	0
2	G	64	56	42	1	0
2	H	60	45	31	0	0
2	I	26	15	12	0	0
3	A	6	0	0	0	0
3	B	24	0	0	1	0
3	C	19	0	0	1	0
3	D	2	0	0	3	0
3	E	2	0	0	0	0
3	G	5	0	0	1	0
All	All	3148	2739	2705	20	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 3.

The worst 5 of 20 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:380:LYS:O	3:D:501:HOH:O	1.94	0.86
1:D:318:ARG:NH1	1:D:383:GLY:O	2.35	0.59
2:G:424:GLU:O	3:G:501:HOH:O	2.17	0.57
1:D:318:ARG:HD3	1:D:321:THR:C	2.33	0.54
1:D:374:GLN:O	1:D:378:ALA:N	2.30	0.52

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	98/119 (82%)	98 (100%)	0	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	98/119 (82%)	97 (99%)	1 (1%)	0	100	100
1	C	99/119 (83%)	98 (99%)	1 (1%)	0	100	100
1	D	98/119 (82%)	98 (100%)	0	0	100	100
2	E	4/7 (57%)	4 (100%)	0	0	100	100
2	F	4/7 (57%)	4 (100%)	0	0	100	100
2	G	4/7 (57%)	4 (100%)	0	0	100	100
2	H	4/7 (57%)	4 (100%)	0	0	100	100
All	All	409/504 (81%)	407 (100%)	2 (0%)	0	100	100

There are no Ramachandran outliers to report.

### 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	64/94 (68%)	64 (100%)	0	100	100
1	B	72/94 (77%)	72 (100%)	0	100	100
1	C	68/94 (72%)	67 (98%)	1 (2%)	57	64
1	D	47/94 (50%)	47 (100%)	0	100	100
2	E	4/6 (67%)	4 (100%)	0	100	100
2	F	3/6 (50%)	3 (100%)	0	100	100
2	G	5/6 (83%)	5 (100%)	0	100	100
2	H	4/6 (67%)	4 (100%)	0	100	100
2	I	1/6 (17%)	1 (100%)	0	100	100
All	All	268/406 (66%)	267 (100%)	1 (0%)	84	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	312	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	391	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	100/119 (84%)	1.09	12 (12%) 9 9	53, 77, 111, 152	0
1	B	100/119 (84%)	0.59	6 (6%) 27 31	42, 64, 94, 118	0
1	C	101/119 (84%)	0.86	13 (12%) 7 8	44, 76, 105, 117	0
1	D	100/119 (84%)	2.00	45 (45%) 0 1	76, 111, 149, 160	0
2	E	6/7 (85%)	0.82	1 (16%) 4 5	70, 77, 87, 108	0
2	F	6/7 (85%)	1.36	2 (33%) 1 1	92, 105, 114, 143	0
2	G	6/7 (85%)	0.43	1 (16%) 4 5	54, 56, 91, 92	0
2	H	6/7 (85%)	0.69	1 (16%) 4 5	77, 88, 112, 125	0
2	I	1/7 (14%)	0.51	0 100 100	69, 69, 69, 69	0
All	All	426/511 (83%)	1.11	81 (19%) 3 4	42, 81, 134, 160	0

The worst 5 of 81 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	336	ILE	5.0
1	D	390	ALA	5.0
1	B	402	ALA	4.9
1	A	321	THR	4.9
1	B	307	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 oligosaccharides 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.