



# Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 05:32 pm BST

PDB ID : 3E7D  
Title : Crystal Structure of Precorrin-8X Methyl Mutase CbiC/CobH from *Brucella melitensis*  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2008-08-18  
Resolution : 1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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.

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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	:	2.11
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)	:	2.11

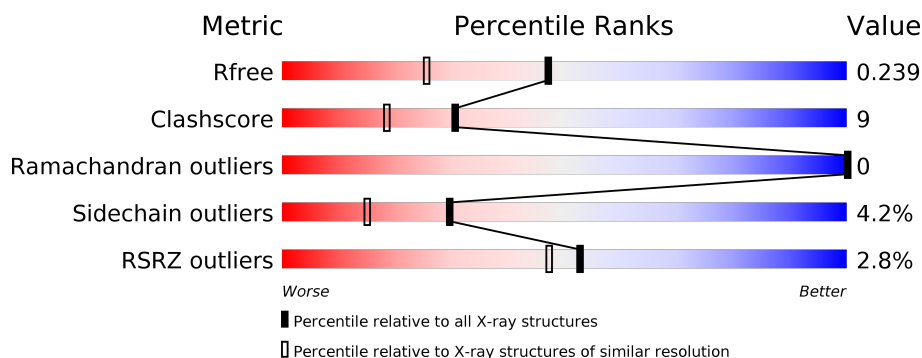
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 on 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	212	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 8%, green 72%, yellow 11%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>8%</span> <span>84%</span> <span>11%</span> <span>5%</span> </div> </div>
1	B	212	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 84%, yellow 11%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>84%</span> <span>11%</span> <span>• •</span> </div> </div>
1	C	212	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 8%, green 67%, yellow 18%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>8%</span> <span>75%</span> <span>18%</span> <span>• •</span> </div> </div>
1	D	212	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 8%, green 66%, yellow 21%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>8%</span> <span>74%</span> <span>21%</span> <span>• •</span> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6557 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 CobH, precorrin-8X methylmutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	0	0
			1469	926	265	272	6			
1	B	204	Total	C	N	O	S	0	0	0
			1487	936	273	272	6			
1	C	203	Total	C	N	O	S	0	0	0
			1483	934	268	275	6			
1	D	204	Total	C	N	O	S	0	0	0
			1470	926	268	270	6			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q57CK9
A	-2	PRO	-	expression tag	UNP Q57CK9
A	-1	GLY	-	expression tag	UNP Q57CK9
A	0	SER	-	expression tag	UNP Q57CK9
B	-3	GLY	-	expression tag	UNP Q57CK9
B	-2	PRO	-	expression tag	UNP Q57CK9
B	-1	GLY	-	expression tag	UNP Q57CK9
B	0	SER	-	expression tag	UNP Q57CK9
C	-3	GLY	-	expression tag	UNP Q57CK9
C	-2	PRO	-	expression tag	UNP Q57CK9
C	-1	GLY	-	expression tag	UNP Q57CK9
C	0	SER	-	expression tag	UNP Q57CK9
D	-3	GLY	-	expression tag	UNP Q57CK9
D	-2	PRO	-	expression tag	UNP Q57CK9
D	-1	GLY	-	expression tag	UNP Q57CK9
D	0	SER	-	expression tag	UNP Q57CK9

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	195	Total 195	O 195	0	0
2	B	173	Total 173	O 173	0	0
2	C	165	Total 165	O 165	0	0
2	D	115	Total 115	O 115	0	0



- Molecule 1: CobH, precorrin-8X methylmutase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.72Å 68.93Å 103.20Å 90.00° 95.88° 90.00°	Depositor
Resolution (Å)	50.00 – 1.80 34.84 – 1.80	Depositor EDS
% Data completeness (in resolution range)	91.2 (50.00-1.80) 91.2 (34.84-1.80)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.80 (at 1.81Å)	Xtriage
Refinement program	REFMAC refmac_5.4.0067	Depositor
R, $R_{free}$	0.232 , 0.260 0.238 , 0.239	Depositor DCC
$R_{free}$ test set	3392 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.3	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 52.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6557	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% of the height of the origin peak. No significant pseudotranslation is detected.*

<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](#)

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	0.54	0/1492	0.72	0/2028
1	B	0.57	0/1510	0.70	0/2051
1	C	0.72	0/1507	0.74	0/2048
1	D	0.60	0/1494	0.80	2/2033 (0.1%)
All	All	0.61	0/6003	0.74	2/8160 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	207	ARG	NE-CZ-NH2	7.10	123.85	120.30
1	D	6	ARG	NE-CZ-NH1	-5.91	117.34	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	1469	0	1496	17	0
1	B	1487	0	1518	22	0
1	C	1483	0	1507	35	0
1	D	1470	0	1479	40	0
2	A	195	0	0	1	0
2	B	173	0	0	1	0
2	C	165	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	115	0	0	1	0
All	All	6557	0	6000	109	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 9.

All (109) 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:206:GLU:O	1:D:207:ARG:HB2	1.41	1.15
1:A:112:ASN:HD22	1:A:113:THR:H	1.11	0.96
1:C:87:ARG:NH1	1:C:205:SER:HB3	1.82	0.94
1:C:112:ASN:HD22	1:C:113:THR:H	1.21	0.89
1:B:24:ASP:OD1	1:B:26:ARG:HD3	1.76	0.85
1:B:20:ARG:HH12	1:B:207:ARG:NH2	1.76	0.83
1:C:121:LEU:HD12	1:C:121:LEU:N	1.95	0.81
1:A:112:ASN:ND2	1:A:113:THR:H	1.82	0.77
1:D:153:LYS:HE3	1:D:179:ARG:O	1.88	0.73
1:A:112:ASN:HD22	1:A:113:THR:N	1.86	0.73
1:C:112:ASN:ND2	1:C:113:THR:H	1.87	0.71
1:B:206:GLU:O	1:B:207:ARG:CB	2.39	0.71
1:D:12:TYR:CZ	1:D:16:PHE:HE1	2.09	0.71
1:D:39:VAL:HG13	1:D:195:MET:HG2	1.75	0.68
1:C:112:ASN:HD22	1:C:113:THR:N	1.89	0.68
1:D:93:ARG:HG2	1:D:95:ILE:HD11	1.76	0.66
1:C:56:GLU:OE2	2:C:390:HOH:O	2.13	0.66
1:C:47:ASP:OD1	1:C:47:ASP:C	2.35	0.66
1:D:12:TYR:CZ	1:D:16:PHE:CE1	2.84	0.66
1:C:105:GLU:OE2	1:C:109:LYS:HE3	1.95	0.65
1:D:206:GLU:O	1:D:207:ARG:CB	2.29	0.65
1:D:161:PRO:HD2	1:D:171:LYS:HD3	1.79	0.64
1:C:121:LEU:N	1:C:121:LEU:CD1	2.61	0.63
1:C:92:ASN:HD22	1:C:92:ASN:H	1.47	0.62
1:D:18:ILE:O	1:D:22:GLU:HG3	1.99	0.62
1:D:12:TYR:CE1	1:D:16:PHE:HE1	2.18	0.62
1:B:112:ASN:HD22	1:B:113:THR:H	1.48	0.61
1:D:66:LEU:HD21	1:D:72:ILE:HD11	1.83	0.61
1:D:12:TYR:CE1	1:D:16:PHE:CE1	2.90	0.60
1:B:40:ILE:HG12	1:B:48:VAL:HG12	1.84	0.59
1:C:16:PHE:O	1:C:20:ARG:HG3	2.03	0.58
1:A:101:PRO:HG2	2:A:303:HOH:O	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:206:GLU:O	1:B:207:ARG:HB2	2.04	0.57
1:B:112:ASN:ND2	1:B:113:THR:H	2.03	0.57
1:C:47:ASP:OD1	1:C:48:VAL:N	2.37	0.57
1:D:123:LEU:HB2	1:D:124:PRO:HD3	1.87	0.57
1:D:89:PRO:HD2	1:D:92:ASN:ND2	2.18	0.57
1:C:92:ASN:ND2	1:C:92:ASN:H	2.03	0.56
1:A:88:LEU:HB3	1:A:92:ASN:HD22	1.72	0.55
1:D:103:VAL:HG12	1:D:114:ARG:HG2	1.87	0.55
1:D:93:ARG:CG	1:D:95:ILE:HD11	2.37	0.54
1:D:112:ASN:HD22	1:D:113:THR:H	1.55	0.53
1:C:103:VAL:HG12	1:C:114:ARG:HG2	1.90	0.53
1:D:121:LEU:N	1:D:121:LEU:HD12	2.22	0.53
1:B:207:ARG:HG3	2:B:329:HOH:O	2.07	0.53
1:D:50:ASN:OD1	2:D:276:HOH:O	2.19	0.53
1:D:140:LEU:HD22	1:D:144:PHE:CZ	2.45	0.52
1:D:12:TYR:CE2	1:D:16:PHE:HE1	2.27	0.52
1:C:47:ASP:OD1	1:C:190:ARG:NH1	2.41	0.51
1:C:105:GLU:HA	1:C:105:GLU:OE1	2.10	0.51
1:A:173:GLU:HA	1:A:173:GLU:OE1	2.11	0.50
1:B:20:ARG:NH1	1:B:207:ARG:NH2	2.54	0.50
1:D:35:LEU:HA	1:D:202:ALA:CB	2.41	0.50
1:C:78:MET:HE2	1:D:78:MET:CE	2.41	0.50
1:A:96:TYR:CZ	1:A:98:LEU:HB3	2.47	0.49
1:D:89:PRO:HD2	1:D:92:ASN:HD21	1.76	0.49
1:D:96:TYR:CZ	1:D:98:LEU:HB3	2.48	0.49
1:D:38:ARG:HH22	1:D:207:ARG:HD2	1.77	0.48
1:B:112:ASN:HD22	1:B:113:THR:N	2.11	0.47
1:D:121:LEU:N	1:D:121:LEU:CD1	2.77	0.47
1:B:35:LEU:C	1:B:35:LEU:HD23	2.35	0.47
1:B:206:GLU:O	1:B:207:ARG:HB3	2.15	0.46
1:A:105:GLU:OE1	1:A:105:GLU:HA	2.16	0.46
1:C:160:MET:N	1:C:161:PRO:CD	2.79	0.46
1:C:78:MET:HE2	1:D:78:MET:HE1	1.97	0.46
1:C:15:SER:O	1:C:19:ILE:HG13	2.17	0.45
1:C:23:ALA:HA	1:C:46:VAL:HG13	1.98	0.45
1:D:96:TYR:CE1	1:D:98:LEU:HB3	2.51	0.45
1:C:98:LEU:HD11	1:C:114:ARG:HB3	1.98	0.45
1:C:14:ARG:NH1	1:C:18:ILE:HD11	2.31	0.45
1:B:96:TYR:CZ	1:B:98:LEU:HB3	2.51	0.45
1:C:87:ARG:HH12	1:C:205:SER:HB3	1.77	0.45
1:A:81:GLU:OE1	1:B:81:GLU:OE2	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:23:ALA:HA	1:C:46:VAL:CG1	2.46	0.44
1:D:90:ALA:C	1:D:92:ASN:N	2.70	0.44
1:B:73:LEU:CD1	1:B:73:LEU:N	2.81	0.44
1:D:112:ASN:ND2	1:D:113:THR:H	2.14	0.44
1:D:38:ARG:NH2	1:D:207:ARG:HD2	2.33	0.44
1:A:160:MET:N	1:A:161:PRO:CD	2.80	0.44
1:A:92:ASN:ND2	1:A:92:ASN:H	2.16	0.44
1:C:73:LEU:HD23	1:C:122:TRP:HB3	1.98	0.44
1:A:71:PRO:HB2	1:A:95:ILE:HD12	1.99	0.43
1:C:142:ARG:O	1:C:145:GLU:HB2	2.18	0.43
1:A:123:LEU:HD23	1:A:123:LEU:HA	1.78	0.43
1:D:77:ARG:O	1:D:81:GLU:HG3	2.19	0.43
1:C:38:ARG:HD2	1:C:202:ALA:HB2	2.01	0.43
1:D:67:LEU:HD23	1:D:67:LEU:HA	1.93	0.43
1:A:78:MET:HE3	1:B:81:GLU:HB3	2.01	0.42
1:D:162:VAL:HG22	1:D:163:GLY:N	2.34	0.42
1:B:160:MET:N	1:B:161:PRO:CD	2.83	0.42
1:B:22:GLU:OE2	1:D:22:GLU:OE2	2.37	0.42
1:C:90:ALA:H	1:C:92:ASN:ND2	2.18	0.42
1:C:123:LEU:HA	1:C:123:LEU:HD23	1.79	0.42
1:A:60:LYS:NZ	1:A:64:ASN:HD21	2.18	0.41
1:C:206:GLU:O	1:C:206:GLU:HG3	2.19	0.41
1:D:47:ASP:OD1	1:D:47:ASP:C	2.59	0.41
1:C:135:ASN:O	1:C:137:PRO:HD3	2.21	0.41
1:A:47:ASP:OD1	1:A:47:ASP:C	2.59	0.41
1:B:100:ASP:HB3	1:B:103:VAL:HG23	2.03	0.41
1:C:123:LEU:HB2	1:C:124:PRO:HD3	2.02	0.41
1:A:127:GLU:HB2	1:A:152:PRO:HB2	2.02	0.41
1:D:93:ARG:CG	1:D:95:ILE:CD1	2.99	0.41
1:C:29:PRO:HG2	1:C:32:LEU:HB2	2.02	0.41
1:D:123:LEU:HA	1:D:123:LEU:HD23	1.93	0.41
1:D:84:THR:O	1:D:87:ARG:HB2	2.20	0.40
1:B:123:LEU:N	1:B:124:PRO:CD	2.84	0.40
1:C:162:VAL:HG22	1:C:163:GLY:N	2.36	0.40
1:B:40:ILE:HD11	1:B:49:ALA:HB2	2.02	0.40
1:B:20:ARG:HH12	1:B:207:ARG:HH21	1.63	0.40

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	200/212 (94%)	195 (98%)	5 (2%)	0	100	100
1	B	202/212 (95%)	198 (98%)	4 (2%)	0	100	100
1	C	201/212 (95%)	195 (97%)	6 (3%)	0	100	100
1	D	202/212 (95%)	193 (96%)	9 (4%)	0	100	100
All	All	805/848 (95%)	781 (97%)	24 (3%)	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	144/155 (93%)	140 (97%)	4 (3%)	43	30
1	B	145/155 (94%)	138 (95%)	7 (5%)	25	11
1	C	146/155 (94%)	141 (97%)	5 (3%)	37	22
1	D	141/155 (91%)	133 (94%)	8 (6%)	20	8
All	All	576/620 (93%)	552 (96%)	24 (4%)	30	15

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	48	VAL

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Mol	Chain	Res	Type
1	A	112	ASN
1	A	121	LEU
1	B	14	ARG
1	B	15	SER
1	B	48	VAL
1	B	109	LYS
1	B	112	ASN
1	B	140	LEU
1	B	207	ARG
1	C	38	ARG
1	C	56	GLU
1	C	105	GLU
1	C	112	ASN
1	C	140	LEU
1	D	14	ARG
1	D	33	GLU
1	D	38	ARG
1	D	56	GLU
1	D	109	LYS
1	D	112	ASN
1	D	140	LEU
1	D	207	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
1	A	64	ASN
1	A	92	ASN
1	A	112	ASN
1	B	92	ASN
1	B	112	ASN
1	C	27	HIS
1	C	50	ASN
1	C	92	ASN
1	C	112	ASN
1	D	50	ASN
1	D	92	ASN
1	D	112	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 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 ⓘ

### 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, 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	202/212 (95%)	0.17	2 (0%) 82 80	17, 24, 34, 39	0
1	B	204/212 (96%)	0.15	1 (0%) 91 89	16, 23, 35, 42	0
1	C	203/212 (95%)	0.20	3 (1%) 73 70	18, 24, 35, 39	0
1	D	204/212 (96%)	0.47	17 (8%) 11 8	18, 25, 36, 49	0
All	All	813/848 (95%)	0.25	23 (2%) 53 47	16, 24, 35, 49	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	5	ILE	4.2
1	D	4	TYR	4.0
1	D	68	ALA	3.8
1	D	67	LEU	3.6
1	D	7	ASP	3.6
1	D	93	ARG	3.2
1	D	89	PRO	3.0
1	D	205	SER	2.7
1	C	91	ASP	2.7
1	D	30	ALA	2.5
1	D	11	ILE	2.4
1	D	9	GLN	2.3
1	D	90	ALA	2.3
1	A	7	ASP	2.3
1	D	206	GLU	2.2
1	D	27	HIS	2.2
1	D	203	LEU	2.2
1	C	67	LEU	2.1
1	C	79	VAL	2.1
1	B	206	GLU	2.1
1	D	88	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	84	THR	2.0
1	A	12	TYR	2.0

## 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.