



# Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 03:03 pm BST

PDB ID : 4YZE  
Title : Crystal structure of E.coli NemR reduced form  
Authors : Li, Y.; Gray, M.J.; Jakob, U.; Xu, Z.  
Deposited on : 2015-03-24  
Resolution : 2.20 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

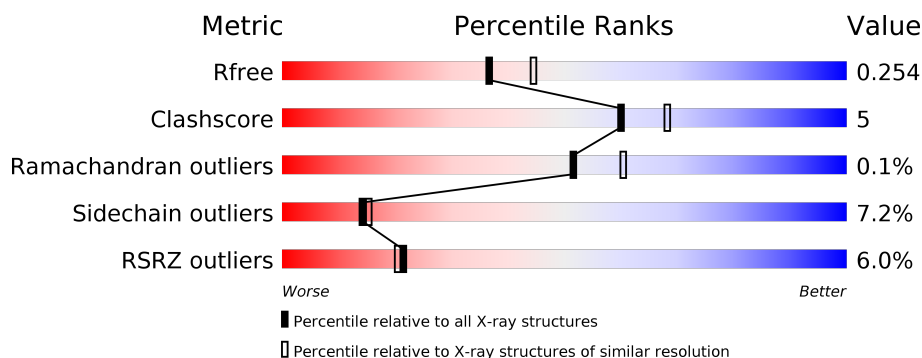
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	201	<div> <div>5%</div> <div> <div></div> <div>83%</div> <div>13%</div> <div>•</div> </div> </div>
1	B	201	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>7%</div> </div> </div>
1	C	201	<div> <div>8%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>• 6%</div> </div> </div>
1	D	201	<div> <div>6%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>• 6%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5786 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 HTH-type transcriptional repressor NemR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	193	Total	C	N	O	S	0	0	0
			1473	928	262	278	5			
1	B	186	Total	C	N	O	S	0	0	0
			1389	888	241	255	5			
1	C	189	Total	C	N	O	S	0	0	0
			1439	910	250	274	5			
1	D	188	Total	C	N	O	S	0	0	0
			1366	872	236	253	5			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P67430
A	0	SER	-	expression tag	UNP P67430
A	21	SER	CYS	engineered mutation	UNP P67430
A	98	SER	CYS	engineered mutation	UNP P67430
A	116	SER	CYS	engineered mutation	UNP P67430
A	149	SER	CYS	engineered mutation	UNP P67430
A	153	SER	CYS	engineered mutation	UNP P67430
B	-1	GLY	-	expression tag	UNP P67430
B	0	SER	-	expression tag	UNP P67430
B	21	SER	CYS	engineered mutation	UNP P67430
B	98	SER	CYS	engineered mutation	UNP P67430
B	116	SER	CYS	engineered mutation	UNP P67430
B	149	SER	CYS	engineered mutation	UNP P67430
B	153	SER	CYS	engineered mutation	UNP P67430
C	-1	GLY	-	expression tag	UNP P67430
C	0	SER	-	expression tag	UNP P67430
C	21	SER	CYS	engineered mutation	UNP P67430
C	98	SER	CYS	engineered mutation	UNP P67430
C	116	SER	CYS	engineered mutation	UNP P67430
C	149	SER	CYS	engineered mutation	UNP P67430
C	153	SER	CYS	engineered mutation	UNP P67430

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	GLY	-	expression tag	UNP P67430
D	0	SER	-	expression tag	UNP P67430
D	21	SER	CYS	engineered mutation	UNP P67430
D	98	SER	CYS	engineered mutation	UNP P67430
D	116	SER	CYS	engineered mutation	UNP P67430
D	149	SER	CYS	engineered mutation	UNP P67430
D	153	SER	CYS	engineered mutation	UNP P67430

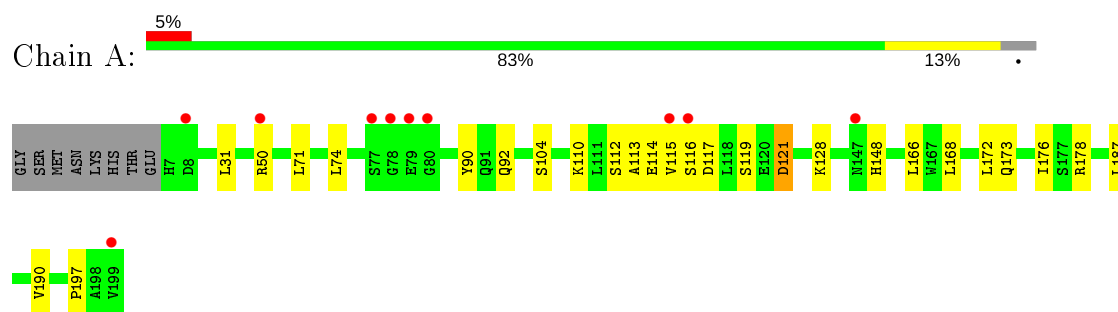
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	44	Total O 44 44	0	0
2	B	38	Total O 38 38	0	0
2	C	27	Total O 27 27	0	0
2	D	10	Total O 10 10	0	0

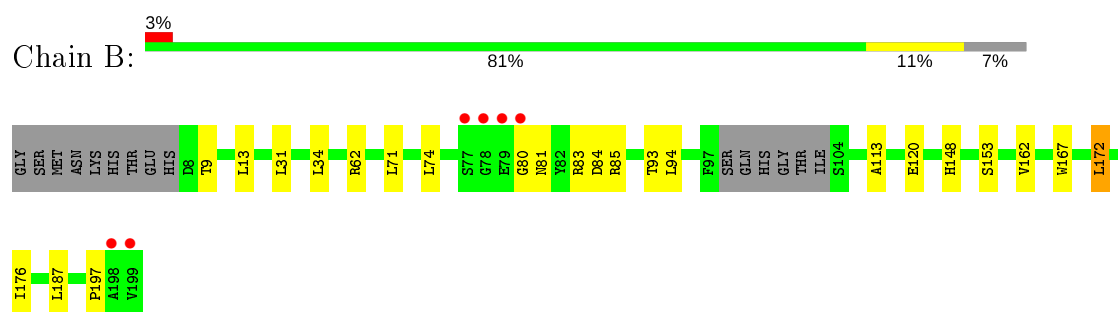
### 3 Residue-property plots [i](#)

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

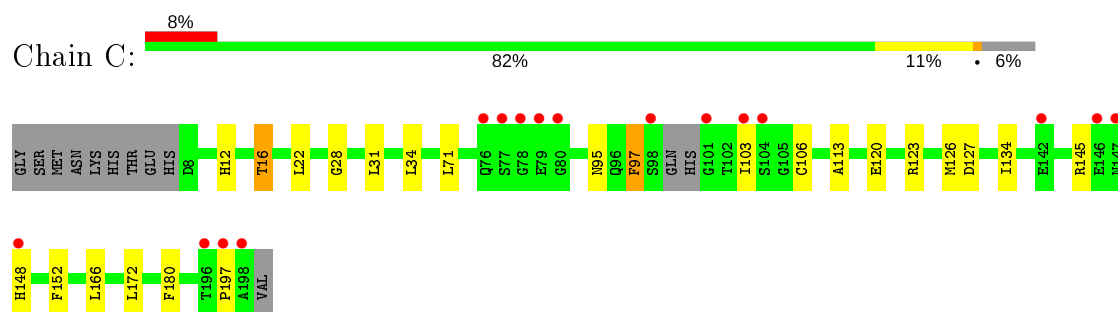
- Molecule 1: HTH-type transcriptional repressor NemR



- Molecule 1: HTH-type transcriptional repressor NemR

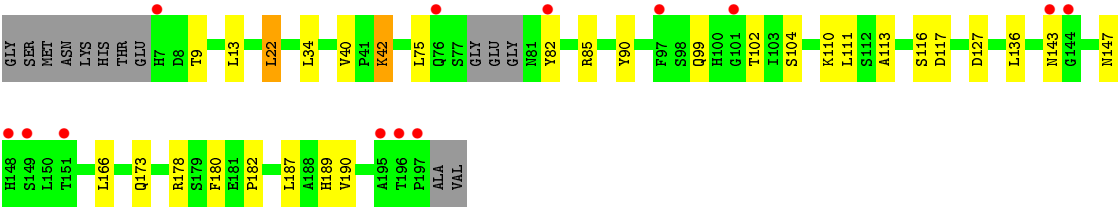


- Molecule 1: HTH-type transcriptional repressor NemR



- Molecule 1: HTH-type transcriptional repressor NemR





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.44Å 67.44Å 213.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.50 – 2.20 48.99 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.50-2.20) 99.8 (48.99-2.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.73 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.8.2 _1309	Depositor
R, $R_{free}$	0.205 , 0.255 0.204 , 0.254	Depositor DCC
$R_{free}$ test set	2564 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.1	Xtriage
Anisotropy	0.493	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 51.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.037 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5786	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.79% 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	0.41	0/1499	0.54	0/2026
1	B	0.40	0/1413	0.54	0/1909
1	C	0.38	0/1464	0.52	0/1979
1	D	0.33	0/1392	0.47	0/1890
All	All	0.38	0/5768	0.52	0/7804

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	1473	0	1429	18	0
1	B	1389	0	1345	11	0
1	C	1439	0	1388	18	0
1	D	1366	0	1270	15	0
2	A	44	0	0	3	0
2	B	38	0	0	0	0
2	C	27	0	0	1	0
2	D	10	0	0	1	0
All	All	5786	0	5432	51	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 5.



All (51) 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:93:THR:HG21	1:B:167:TRP:HE1	1.52	0.72
1:D:104:SER:O	2:D:201:HOH:O	2.06	0.72
1:A:121:ASP:OD1	2:A:201:HOH:O	2.07	0.71
1:C:123:ARG:HA	1:C:126:MET:HE2	1.75	0.68
1:D:143:ASN:O	1:D:147:ASN:ND2	2.28	0.66
1:A:104:SER:O	2:A:202:HOH:O	2.14	0.66
1:B:81:ASN:HD22	1:B:84:ASP:H	1.44	0.64
1:B:80:GLY:O	1:B:85:ARG:NH2	2.31	0.62
1:D:75:LEU:O	1:D:85:ARG:NH1	2.35	0.59
1:C:97:PHE:HB3	1:C:180:PHE:CE1	2.39	0.57
1:A:121:ASP:N	1:A:121:ASP:OD1	2.37	0.57
1:A:113:ALA:HB3	1:C:113:ALA:HB2	1.89	0.54
1:A:178:ARG:NH1	2:A:204:HOH:O	2.41	0.54
1:C:145:ARG:NH2	1:C:152:PHE:O	2.41	0.54
1:C:97:PHE:HB3	1:C:180:PHE:HE1	1.72	0.54
1:D:22:LEU:O	1:D:110:LYS:HE3	2.08	0.53
1:A:178:ARG:NH2	1:C:120:GLU:OE2	2.44	0.51
1:B:81:ASN:HD21	1:B:83:ARG:HB3	1.76	0.51
1:A:110:LYS:NZ	1:C:113:ALA:O	2.44	0.51
1:C:12:HIS:O	1:C:16:THR:HG23	2.11	0.50
1:A:90:TYR:CE2	1:A:190:VAL:HG21	2.47	0.50
1:A:112:SER:OG	1:A:113:ALA:N	2.46	0.48
1:B:81:ASN:ND2	1:B:83:ARG:HB3	2.27	0.48
1:C:97:PHE:HD2	1:C:180:PHE:CD1	2.32	0.48
1:A:119:SER:HB3	1:D:42:LYS:HD3	1.96	0.47
1:A:112:SER:HB2	1:C:172:LEU:HD22	1.97	0.47
1:C:123:ARG:HA	1:C:126:MET:CE	2.43	0.46
1:A:112:SER:O	1:A:115:VAL:HG22	2.15	0.46
1:D:13:LEU:HD11	1:D:40:VAL:HG21	1.99	0.45
1:A:173:GLN:HE22	1:C:134:ILE:HD11	1.81	0.45
1:D:90:TYR:CZ	1:D:190:VAL:HG21	2.52	0.45
1:B:148:HIS:O	1:B:197:PRO:HG3	2.16	0.45
1:A:176:ILE:HG22	1:C:127:ASP:OD1	2.16	0.44
1:A:112:SER:HB2	1:C:172:LEU:CD2	2.47	0.44
1:B:162:VAL:HG21	1:D:189:HIS:CG	2.53	0.44
1:B:120:GLU:OE2	1:D:178:ARG:NH1	2.51	0.43
1:D:99:GLN:N	1:D:102:THR:O	2.38	0.43
1:A:114:GLU:O	1:A:117:ASP:N	2.50	0.43
1:D:173:GLN:HG3	1:D:182:PRO:HG3	2.00	0.42
1:B:81:ASN:HB3	1:B:84:ASP:OD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:28:GLY:N	2:C:203:HOH:O	2.42	0.42
1:A:172:LEU:HA	1:A:172:LEU:HD23	1.81	0.42
1:B:172:LEU:O	1:B:176:ILE:HG12	2.20	0.41
1:D:82:TYR:CE2	1:D:143:ASN:HB3	2.56	0.41
1:C:148:HIS:O	1:C:197:PRO:HG3	2.21	0.41
1:D:136:LEU:HD23	1:D:136:LEU:HA	1.93	0.41
1:B:113:ALA:HB3	1:D:113:ALA:HB2	2.03	0.41
1:C:22:LEU:HD23	1:C:22:LEU:HA	1.88	0.40
1:A:148:HIS:O	1:A:197:PRO:HG2	2.21	0.40
1:C:103:ILE:O	1:C:106:CYS:HB2	2.22	0.40
1:D:22:LEU:HD13	1:D:22:LEU:HA	1.95	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	191/201 (95%)	188 (98%)	3 (2%)	0	100	100
1	B	182/201 (90%)	178 (98%)	4 (2%)	0	100	100
1	C	185/201 (92%)	180 (97%)	4 (2%)	1 (0%)	29	31
1	D	184/201 (92%)	176 (96%)	8 (4%)	0	100	100
All	All	742/804 (92%)	722 (97%)	19 (3%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	95	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	147/165 (89%)	136 (92%)	11 (8%)	13	14
1	B	130/165 (79%)	119 (92%)	11 (8%)	10	10
1	C	143/165 (87%)	137 (96%)	6 (4%)	30	38
1	D	125/165 (76%)	114 (91%)	11 (9%)	10	10
All	All	545/660 (83%)	506 (93%)	39 (7%)	14	15

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LEU
1	A	50	ARG
1	A	71	LEU
1	A	74	LEU
1	A	92	GLN
1	A	116	SER
1	A	121	ASP
1	A	128	LYS
1	A	166	LEU
1	A	168	LEU
1	A	187	LEU
1	B	9	THR
1	B	13	LEU
1	B	31	LEU
1	B	34	LEU
1	B	62	ARG
1	B	71	LEU
1	B	74	LEU
1	B	94	LEU
1	B	153	SER
1	B	172	LEU
1	B	187	LEU
1	C	16	THR
1	C	31	LEU

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Mol	Chain	Res	Type
1	C	34	LEU
1	C	71	LEU
1	C	97	PHE
1	C	166	LEU
1	D	9	THR
1	D	22	LEU
1	D	34	LEU
1	D	42	LYS
1	D	111	LEU
1	D	116	SER
1	D	117	ASP
1	D	127	ASP
1	D	166	LEU
1	D	180	PHE
1	D	187	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	81	ASN
1	D	147	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

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	193/201 (96%)	0.26	10 (5%) 27 26	25, 55, 89, 111	0
1	B	186/201 (92%)	0.15	6 (3%) 47 45	28, 51, 86, 124	0
1	C	189/201 (94%)	0.30	16 (8%) 10 9	28, 55, 94, 108	0
1	D	188/201 (93%)	0.46	13 (6%) 16 15	29, 73, 114, 143	0
All	All	756/804 (94%)	0.29	45 (5%) 21 20	25, 57, 101, 143	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	148	HIS	6.6
1	C	198	ALA	6.6
1	B	199	VAL	5.4
1	B	80	GLY	5.4
1	C	104	SER	5.2
1	C	197	PRO	4.6
1	B	198	ALA	4.4
1	D	197	PRO	4.4
1	B	78	GLY	4.3
1	B	79	GLU	4.1
1	A	78	GLY	4.1
1	D	76	GLN	3.6
1	A	80	GLY	3.6
1	D	82	TYR	3.2
1	C	98	SER	3.1
1	C	77	SER	3.1
1	D	143	ASN	3.1
1	A	79	GLU	3.0
1	A	50	ARG	3.0
1	C	78	GLY	2.9
1	A	77	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	148	HIS	2.8
1	D	144	GLY	2.7
1	A	116	SER	2.7
1	D	101	GLY	2.7
1	C	101	GLY	2.7
1	C	76	GLN	2.7
1	C	79	GLU	2.6
1	C	196	THR	2.6
1	A	199	VAL	2.6
1	C	103	ILE	2.5
1	C	146	GLU	2.4
1	C	147	ASN	2.4
1	D	149	SER	2.4
1	A	115	VAL	2.3
1	A	8	ASP	2.3
1	D	196	THR	2.2
1	D	195	ALA	2.2
1	D	7	HIS	2.1
1	C	142	GLU	2.1
1	A	147	ASN	2.1
1	D	97	PHE	2.1
1	C	80	GLY	2.1
1	D	151	THR	2.0
1	B	77	SER	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.