

# Full wwPDB X-ray Structure Validation Report (i)

#### May 26, 2020 – 01:30 pm BST

PDB ID	:	3DC7
Title	:	Crystal structure of the protein Q88SR8 from Lactobacillus plantarum. North-
		east Structural Genomics consortium target LpR109.
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		L.; Ciccosanti, C.; Xiao, R.; Nair, R.; Baran, M.C.; Acton, T.B.; Rost, B.;
		Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Con-
		$\operatorname{sortium}(\operatorname{NESG})$
Deposited on		
$\operatorname{Resolution}$	:	2.12  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* A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

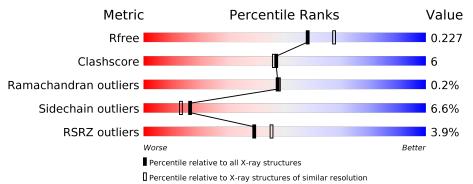
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\rm CCP4$	:	7.0.044  (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
$R_{free}$	130704	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705(2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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 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 <=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	А	232	4% 78%	12%	1	• 8%
1	В	232	4% 73%	14%	•	10%
1	С	232	3% 75%	12%	•	10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	А	235	-	-	Х	Х



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5071 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.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1	Λ	213	Total	С	Ν	Ο	S	$\mathbf{Se}$	0	3 0	0
	Л	213	1674	1062	293	312	1	6	0		0
1	В	209	Total	С	Ν	Ο	S	$\mathbf{Se}$	0	0	0
	D	209	1607	1019	274	307	1	6			
1	C	20.8	Total	С	Ν	0	S	Se	0	n	0
	U	$\mathbb{C}$ 208	1617	1028	277	305	1	6	0	2	0

• Molecule 1 is a protein called Putative uncharacterized protein lp\_3323.

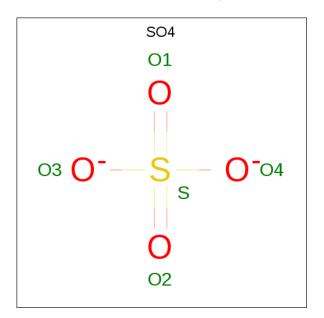
Chain	Residue	Modelled	Actual	Comment	Reference
А	225	LEU	-	expression tag	UNP Q88SR8
А	226	GLU	-	expression tag	UNP Q88SR8
А	227	HIS	-	expression tag	UNP Q88SR8
А	228	HIS	-	expression tag	UNP Q88SR8
А	229	HIS	-	expression tag	UNP Q88SR8
А	230	HIS	-	expression tag	UNP Q88SR8
A	231	HIS	-	expression tag	UNP Q88SR8
A	232	HIS	-	expression tag	UNP Q88SR8
В	225	LEU	-	expression tag	UNP Q88SR8
В	226	GLU	-	expression tag	UNP Q88SR8
В	227	HIS	-	expression tag	UNP Q88SR8
В	228	HIS	-	expression tag	UNP Q88SR8
В	229	HIS	-	expression tag	UNP Q88SR8
В	230	HIS	-	expression tag	UNP Q88SR8
В	231	HIS	-	expression tag	UNP Q88SR8
В	232	HIS	-	expression tag	UNP Q88SR8
С	225	LEU	-	expression tag	UNP Q88SR8
С	226	GLU	-	expression tag	UNP Q88SR8
С	227	HIS	-	expression tag	UNP Q88SR8
С	228	HIS	-	expression tag	UNP Q88SR8
С	229	HIS	-	expression tag	UNP Q88SR8
С	230	HIS	-	expression tag	UNP Q88SR8
С	231	HIS	_	expression tag	UNP Q88SR8

There are 24 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
С	232	HIS	-	expression tag	UNP Q88SR8

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total Na 1 1	0	0
3	С	1	Total Na 1 1	0	0

• Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total Mg 1 1	0	0



• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	56	$\begin{array}{cc} {\rm Total} & {\rm O} \\ 56 & 56 \end{array}$	0	0
5	В	40	$\begin{array}{cc} \text{Total} & \text{O} \\ 40 & 40 \end{array}$	0	0
5	С	59	Total O 59 59	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.

- Chain A: 78% 12% 8% • • Molecule 1: Putative uncharacterized protein lp 3323 4% Chain B: 73% 14% 10% MSE TILE MSE MSE MSE GLY GLY GLY MSE ALA MSE ALA MSE ALA ALA ALA ASN MSE RSSER GLY GLY HIS HIS HIS HIS HIS HIS • Molecule 1: Putative uncharacterized protein lp 3323 Chain C: 75% 12% 10% MSE ALA ALA ALA MSE SLY MSE ALA ALA ALA SER SER SSER SSER SSER
- Molecule 1: Putative uncharacterized protein lp\_3323



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	48.61Å $101.44$ Å $125.55$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	19.74 - 2.12	Depositor
Resolution (A)	19.74 - 2.12	EDS
% Data completeness	100.0 (19.74-2.12)	Depositor
(in resolution range)	86.0(19.74-2.12)	EDS
R <sub>merge</sub>	0.08	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.49 (at 2.13 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
D D.	0.184 , $0.224$	Depositor
$R, R_{free}$	0.186 , $0.227$	DCC
$R_{free}$ test set	1572 reflections $(5.10%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	27.5	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.40 , $40.3$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.48, \langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5071	wwPDB-VP
Average B, all atoms $(Å^2)$	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.48% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: NA, MG, SO4

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	Bond lengths		nd angles
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.47	0/1721	0.59	0/2331
1	В	0.48	0/1643	0.65	2/2227~(0.1%)
1	С	0.52	0/1657	0.65	1/2245~(0.0%)
All	All	0.49	0/5021	0.63	3/6803~(0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	С	75	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	В	75	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	В	37	LEU	CA-CB-CG	5.34	127.58	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	А	1674	0	1583	20	0
1	В	1607	0	1519	25	0
1	С	1617	0	1535	17	0
2	А	10	0	0	2	0
2	С	5	0	0	0	0



Mol	Chain	Non-H	$\rm H(model)$	H(added)	Clashes	Symm-Clashes
3	В	1	0	0	0	0
3	С	1	0	0	0	0
4	В	1	0	0	0	0
5	А	56	0	0	0	0
5	В	40	0	0	0	0
5	С	59	0	0	0	0
All	All	5071	0	4637	59	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 6.

All (59) 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:C:50:TRP:HE1	1:C:217:GLN:HE22	1.17	0.92
1:C:140:ILE:H	1:C:159:GLN:HE22	1.26	0.80
1:B:117:MSE:HE3	1:B:169:MSE:HE1	1.62	0.80
1:B:18:HIS:HD2	1:B:221:ASP:OD2	1.64	0.79
1:A:107:CYS:HB3	1:A:117:MSE:SE	2.44	0.68
1:B:18:HIS:CD2	1:B:221:ASP:OD2	2.47	0.67
1:C:58:LEU:O	1:C:75:ARG:NH2	2.28	0.66
1:A:226:GLU:HB2	1:B:214:ARG:NE	2.11	0.66
1:B:58:LEU:O	1:B:75:ARG:NH2	2.31	0.63
1:A:68:ARG:H	1:A:99:GLN:HE22	1.46	0.62
1:B:119:LEU:HD13	1:B:134:PHE:HZ	1.66	0.60
1:C:205:ASN:HD22	1:C:205:ASN:C	2.06	0.59
1:B:205:ASN:ND2	1:B:208:GLY:H	1.99	0.59
1:B:124:GLN:HA	1:B:124:GLN:HE21	1.69	0.57
1:B:136:SER:O	1:B:180:LEU:HB2	2.04	0.57
1:A:31:ILE:O	1:A:41:HIS:HD2	1.89	0.56
1:A:119:LEU:HD13	1:A:134[A]:PHE:HZ	1.70	0.56
1:C:37:LEU:HD12	1:C:37:LEU:H	1.71	0.56
1:A:110:THR:HG22	1:A:111:THR:HG23	1.89	0.55
1:C:205:ASN:ND2	1:C:208:GLY:H	2.04	0.55
1:A:108:ASP:OD1	1:A:110:THR:HB	2.08	0.54
1:B:205:ASN:HD22	1:B:205:ASN:C	2.12	0.53
1:A:71:ALA:HB3	1:A:74:VAL:HG12	1.93	0.51
1:A:65:ILE:HD11	1:A:134[B]:PHE:HZ	1.76	0.50
1:B:109:MSE:HG3	1:B:118:MSE:SE	2.61	0.50
1:C:136:SER:HB2	1:C:179:SER:HA	1.94	0.50
1:C:46:LEU:HD11	1:C:216:LEU:HD23	1.95	0.49



Continued from prev		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:205:ASN:HD22	1:B:208:GLY:H	1.60	0.48
1:C:205:ASN:HD22	1:C:208:GLY:H	1.61	0.47
1:A:226:GLU:HB2	1:B:214:ARG:CZ	2.43	0.47
1:C:70:ASP:O	1:C:75:ARG:HD3	2.14	0.46
1:A:186:MSE:HE1	1:A:211:VAL:HG21	1.97	0.46
1:B:60:ILE:HD12	1:B:75:ARG:NE	2.31	0.46
1:B:160:SER:HA	1:B:163:GLU:HB3	1.97	0.46
1:B:119:LEU:HD13	1:B:134:PHE:CZ	2.48	0.46
1:A:119:LEU:HD13	1:A:134[A]:PHE:CZ	2.50	0.45
1:A:200:ASP:OD2	1:A:203:HIS:HD2	1.98	0.45
1:A:171:ALA:HA	2:A:235:SO4:O2	2.15	0.45
1:C:96:GLY:O	1:C:147:SER:HB2	2.17	0.45
1:C:124:GLN:HE21	1:C:124:GLN:HA	1.81	0.45
1:A:160:SER:HA	1:A:163:GLU:HB3	2.00	0.44
2:A:235:SO4:O1	1:B:182:ARG:HB3	2.17	0.44
1:C:186:MSE:HB3	1:C:186:MSE:HE2	1.85	0.44
1:A:108:ASP:C	1:A:108:ASP:OD1	2.56	0.44
1:B:124:GLN:NE2	1:B:132:LYS:NZ	2.67	0.43
1:B:104:TYR:OH	1:C:158[A]:ARG:NH1	2.51	0.43
1:B:70:ASP:HB3	1:B:75:ARG:HD2	2.00	0.43
1:C:141:GLY:HA2	1:C:150:ALA:HB2	2.01	0.43
1:A:108:ASP:O	1:A:114:GLY:HA3	2.19	0.42
1:B:151:VAL:HG12	1:B:152:THR:HG23	2.01	0.42
1:B:34:ASN:N	1:B:34:ASN:OD1	2.47	0.42
1:B:68:ARG:H	1:B:99:GLN:HE22	1.66	0.42
1:B:126:ASN:HB2	1:B:127:TRP:CE3	2.55	0.42
1:C:52:VAL:HG21	1:C:55:SER:HB2	2.02	0.42
1:A:136:SER:OG	1:A:163:GLU:OE1	2.36	0.41
1:A:46:LEU:CD1	1:A:216:LEU:HD23	2.50	0.41
1:B:117:MSE:HB2	1:B:169:MSE:HE2	2.03	0.41
1:C:34:ASN:C	1:C:34:ASN:HD22	2.23	0.41
1:A:45:ILE:HD13	1:A:210[B]:ARG:HD2	2.02	0.41

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	Perce	ntiles
1	А	214/232~(92%)	205~(96%)	8 (4%)	1 (0%)	29	25
1	В	207/232 (89%)	198~(96%)	9 (4%)	0	100	100
1	С	208/232~(90%)	204 (98%)	4 (2%)	0	100	100
All	All	629/696~(90%)	607~(96%)	21 (3%)	1 (0%)	47	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	35	ASN

#### 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	А	172/173~(99%)	167~(97%)	5(3%)	42 44
1	В	165/173~(95%)	150 (91%)	15 (9%)	9 6
1	С	166/173~(96%)	153~(92%)	13 (8%)	12 9
All	All	503/519~(97%)	470 (93%)	33 (7%)	16 13

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	89	PHE
1	А	108	ASP
1	А	110	THR
1	А	119	LEU
1	А	133	LEU
1	В	27	LEU
1	В	34	ASN
1	В	37	LEU



Mol	Chain	Res	Type
1	В	89	PHE
1	В	92	VAL
1	В	101	LEU
1	В	108	ASP
1	В	119	LEU
1	В	124	GLN
1	В	136	SER
1	В	153	ASN
1	В	187	THR
1	В	205	ASN
1	В	216	LEU
1	В	220	LEU
1	С	22	LYS
1	С	27	LEU
1	С	30	SER
1	С	34	ASN
1	С	37	LEU
1	C C C C C C C C C C C C C C C C	89	PHE
1	С	101	LEU
1	С	108	ASP
1	С	116	LEU
1	С	136	SER
1	С	182	ARG
1	С	187	THR
1	С	205	ASN
			·

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	41	HIS
1	А	93	ASN
1	А	99	GLN
1	А	203	HIS
1	В	18	HIS
1	В	99	GLN
1	В	103	GLN
1	В	124	GLN
1	В	153	ASN
1	В	205	ASN
1	С	34	ASN
1	С	124	GLN
1	С	159	GLN



Continued from previous page...

Mol	Chain	Res	Type
1	С	168	GLN
1	С	193	GLN
1	С	205	ASN
1	C	217	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 carbohydrates in this entry.

#### 5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Type Chain		Link	Bond lengths				Bond angles		
	Type	Cham	$\mathbf{Res}$		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
2	SO4	А	233	-	4,4,4	0.12	0	$^{6,6,6}$	0.29	0	
2	SO4	С	234	-	4,4,4	0.16	0	$^{6,6,6}$	0.37	0	
2	SO4	А	235	-	4,4,4	0.14	0	$^{6,6,6}$	0.26	0	

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.



There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	235	SO4	2	0

### 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,  $95^{th}$  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	А	207/232~(89%)	0.22	9 (4%) 35 41	21, 27, 41, 61	0
1	В	203/232 (87%)	0.31	9 (4%) 34 40	20, 30, 43, 51	0
1	С	202/232~(87%)	0.06	6 (2%) 50 56	17, 24, 38, 48	0
All	All	612/696~(87%)	0.20	24 (3%) 39 45	17, 27, 42, 61	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	35	ASN	5.7
1	В	36	GLY	5.3
1	В	35	ASN	4.7
1	А	35	ASN	4.4
1	В	37	LEU	4.3
1	С	34	ASN	4.3
1	А	226	GLU	4.2
1	А	228	HIS	3.8
1	С	107	CYS	3.6
1	А	107	CYS	3.2
1	А	81	GLU	3.2
1	А	229	HIS	3.1
1	С	37	LEU	3.0
1	В	34	ASN	3.0
1	А	18	HIS	2.9
1	В	108	ASP	2.9
1	В	51	ASP	2.8
1	А	51	ASP	2.8
1	А	34	ASN	2.5
1	В	39	THR	2.4
1	В	49	ASP	2.2
1	В	65	ILE	2.1
1	С	225	LEU	2.0



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Mol	Chain	$\mathbf{Res}$	Type	RSRZ
1	С	18	HIS	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)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} extsf{-}\mathbf{B} extsf{-}\mathbf{factors}(\mathbf{A}^2)$	Q < 0.9
2	SO4	A	235	5/5	0.74	0.44	$94,\!94,\!95,\!95$	0
3	NA	В	233	1/1	0.75	0.34	33,33,33,33	0
2	SO4	С	234	5/5	0.81	0.34	$54,\!55,\!58,\!59$	0
2	SO4	А	233	5/5	0.89	0.28	72,72,73,73	0
4	MG	В	234	1/1	0.93	0.31	42,42,42,42	0
3	NA	С	233	1/1	0.93	0.31	$29,\!29,\!29,\!29$	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

