



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 4, 2024 – 12:31 AM JST

PDB ID : 6JKW  
Title : Seleno-methionine PNGM-1 from deep-sea sediment metagenome  
Authors : Hong, M.K.; Park, K.S.; Jeon, J.H.; Lee, J.H.; Park, Y.S.; Lee, S.H.; Kang, L.W.  
Deposited on : 2019-03-02  
Resolution : 2.29 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>.

---

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

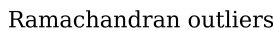
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

**i**

## X-RAY DIFFRACTION

A.

Metric	Percentile Rank	Value
--------	-----------------	-------



R <sub>free</sub>
Clashscore
Ramachandran outliers
Sidechain outliers
RSRZ outliers

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.

1	A	372	<div><div></div><div></div><div></div></div> <div>3%86%13%</div>
1	B	372	<div><div></div><div></div><div></div></div> <div>2%87%11%</div>
1	C	372	<div><div></div><div></div><div></div></div> <div>6%86%12%</div>
1	D	372	<div><div></div><div></div><div></div></div> <div>3%89%9%</div>
1	E	372	<div><div></div><div></div><div></div></div> <div>4%85%13%</div>
1	F	372	<div><div></div><div></div><div></div></div> <div>5%84%15%</div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	372	<div><div></div><div>5%</div><div>81%</div><div>18%</div><div>.</div></div>
1	H	372	<div><div></div><div>10%</div><div>76%</div><div>21%</div><div>..</div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 23910 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 Metallo-beta-lactamases PNGM-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	372	Total	C	N	O	S	Se	0	0	0
			2933	1853	506	554	3	17			
1	B	372	Total	C	N	O	S	Se	0	0	0
			2933	1853	506	554	3	17			
1	C	372	Total	C	N	O	S	Se	0	0	0
			2933	1853	506	554	3	17			
1	D	372	Total	C	N	O	S	Se	0	0	0
			2933	1853	506	554	3	17			
1	E	372	Total	C	N	O	S	Se	0	0	0
			2933	1853	506	554	3	17			
1	F	372	Total	C	N	O	S	Se	0	0	0
			2933	1853	506	554	3	17			
1	G	372	Total	C	N	O	S	Se	0	0	0
			2933	1853	506	554	3	17			
1	H	372	Total	C	N	O	S	Se	0	0	0
			2933	1853	506	554	3	17			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		
2	E	2	Total	Zn	0	0
			2	2		
2	F	2	Total	Zn	0	0
			2	2		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	2	Total 2	Zn 2	0	0
2	H	2	Total 2	Zn 2	0	0

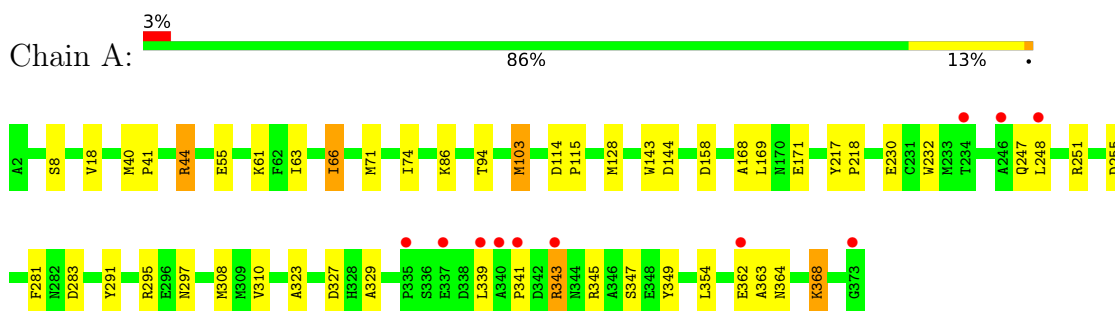
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	79	Total 79	O 79	0	0
3	B	81	Total 81	O 81	0	0
3	C	46	Total 46	O 46	0	0
3	D	63	Total 63	O 63	0	0
3	E	53	Total 53	O 53	0	0
3	F	43	Total 43	O 43	0	0
3	G	39	Total 39	O 39	0	0
3	H	26	Total 26	O 26	0	0

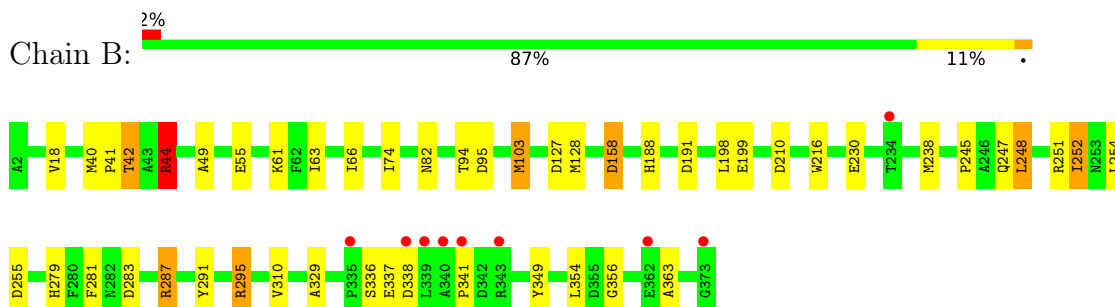
### 3 Residue-property plots [i](#)

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.

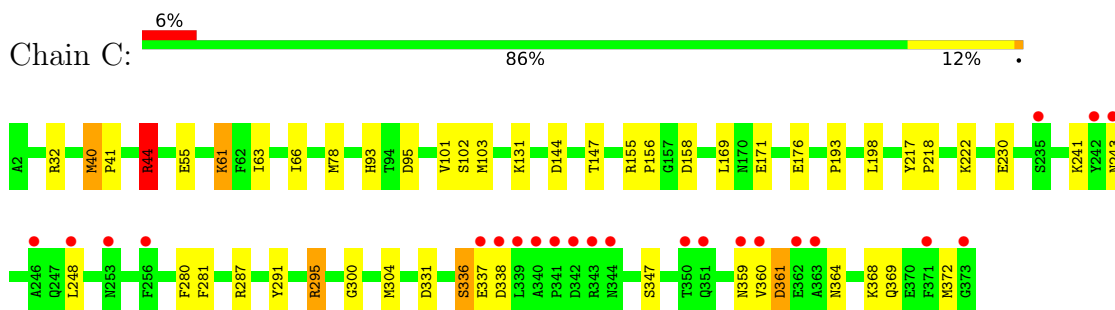
#### • Molecule 1: Metallo-beta-lactamases PNGM-1



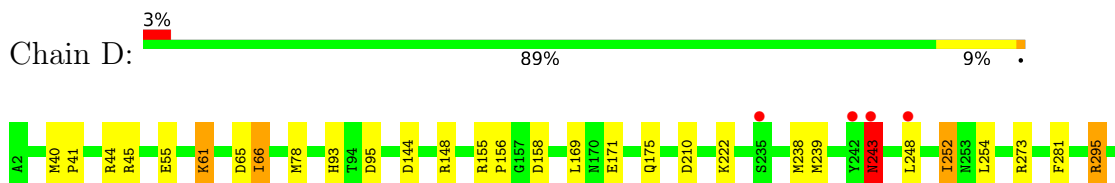
#### • Molecule 1: Metallo-beta-lactamases PNGM-1

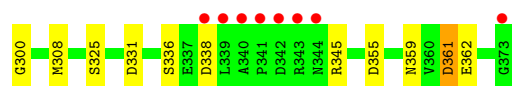


#### • Molecule 1: Metallo-beta-lactamases PNGM-1

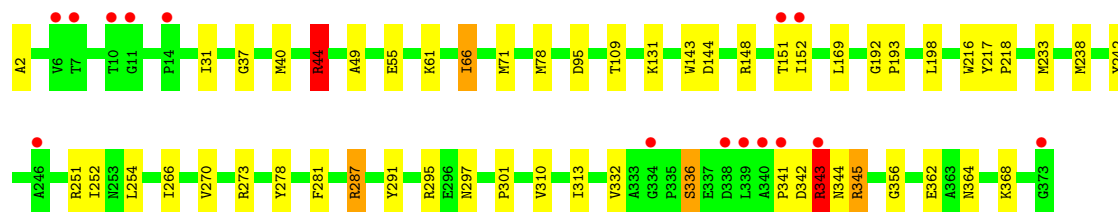
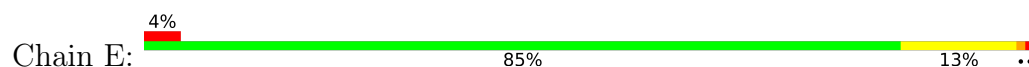


#### • Molecule 1: Metallo-beta-lactamases PNGM-1

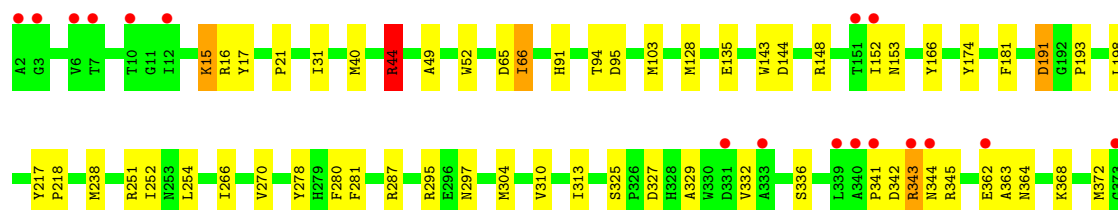
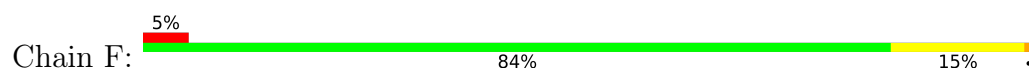




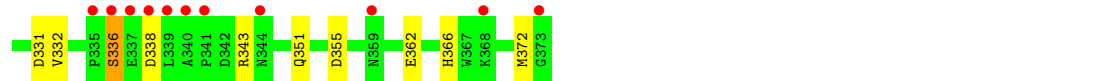
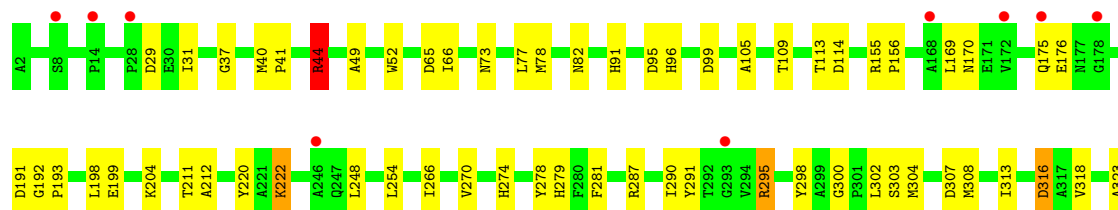
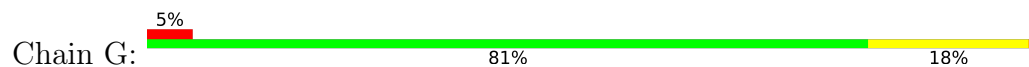
● Molecule 1: Metallo-beta-lactamases PNGM-1



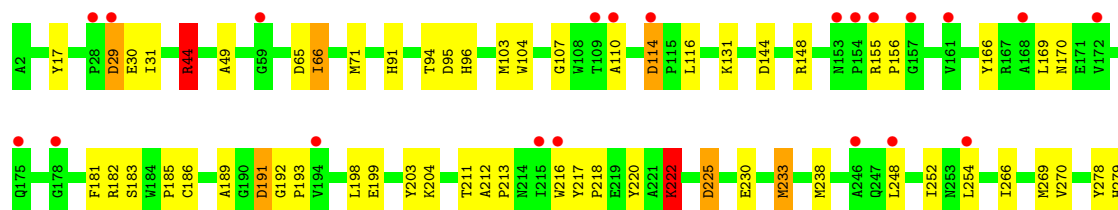
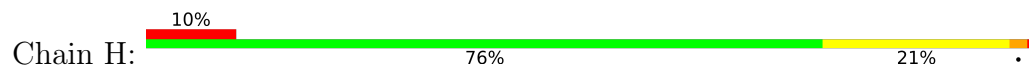
● Molecule 1: Metallo-beta-lactamases PNGM-1

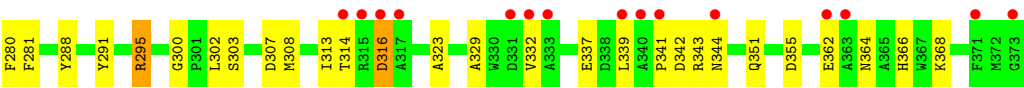


● Molecule 1: Metallo-beta-lactamases PNGM-1



● Molecule 1: Metallo-beta-lactamases PNGM-1







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.86Å 83.12Å 162.83Å 90.00° 110.18° 90.00°	Depositor
Resolution (Å)	34.93 – 2.29 34.93 – 2.29	Depositor EDS
% Data completeness (in resolution range)	97.4 (34.93-2.29) 98.0 (34.93-2.29)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	9.47 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.211 , 0.274 0.218 , 0.279	Depositor DCC
$R_{free}$ test set	6909 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.0	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 32.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	23910	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 89.79 % 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 2.9735e-08. 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: ZN

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	0.87	0/3002	0.90	4/4064 (0.1%)
1	B	0.89	0/3002	0.92	7/4064 (0.2%)
1	C	0.80	0/3002	0.89	5/4064 (0.1%)
1	D	0.83	0/3002	0.91	7/4064 (0.2%)
1	E	0.79	0/3002	0.89	5/4064 (0.1%)
1	F	0.80	1/3002 (0.0%)	0.91	9/4064 (0.2%)
1	G	0.80	1/3002 (0.0%)	0.88	4/4064 (0.1%)
1	H	0.76	0/3002	0.87	4/4064 (0.1%)
All	All	0.82	2/24016 (0.0%)	0.90	45/32512 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	52	TRP	CB-CG	-6.76	1.38	1.50
1	F	52	TRP	CB-CG	-5.16	1.41	1.50

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	295	ARG	NE-CZ-NH1	8.67	124.63	120.30
1	F	44	ARG	NE-CZ-NH2	-8.65	115.97	120.30
1	E	44	ARG	NE-CZ-NH2	-8.61	115.99	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	345	ARG	NE-CZ-NH2	-7.97	116.31	120.30
1	C	295	ARG	NE-CZ-NH1	7.87	124.24	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	151	THR	Peptide

## 5.2 Too-close contacts ⓘ

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	2933	0	2754	31	1
1	B	2933	0	2754	30	0
1	C	2933	0	2754	28	0
1	D	2933	0	2754	16	0
1	E	2933	0	2754	31	0
1	F	2933	0	2754	30	1
1	G	2933	0	2754	32	0
1	H	2933	0	2754	48	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
3	A	79	0	0	1	0
3	B	81	0	0	0	0
3	C	46	0	0	0	0
3	D	63	0	0	0	0
3	E	53	0	0	0	0
3	F	43	0	0	3	0
3	G	39	0	0	0	0
3	H	26	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	23910	0	22032	218	1

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.

The worst 5 of 218 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:E:66:ILE:HD11	1:E:71:MSE:HE1	1.36	1.02
1:A:66:ILE:HD11	1:A:71:MSE:HE1	1.64	0.80
1:D:359:ASN:ND2	1:D:361:ASP:OD1	2.16	0.79
1:F:342:ASP:O	1:F:344:ASN:N	2.17	0.77
1:G:295:ARG:NH2	1:G:300:GLY:O	2.15	0.76

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:347:SER:O	1:F:344:ASN:ND2[2_455]	2.19	0.01

## 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	370/372 (100%)	350 (95%)	18 (5%)	2 (0%)	25	32
1	B	370/372 (100%)	353 (95%)	14 (4%)	3 (1%)	16	20
1	C	370/372 (100%)	344 (93%)	23 (6%)	3 (1%)	16	20
1	D	370/372 (100%)	354 (96%)	13 (4%)	3 (1%)	16	20
1	E	370/372 (100%)	343 (93%)	23 (6%)	4 (1%)	12	13

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	370/372 (100%)	340 (92%)	24 (6%)	6 (2%)	8	7
1	G	370/372 (100%)	351 (95%)	14 (4%)	5 (1%)	9	9
1	H	370/372 (100%)	346 (94%)	19 (5%)	5 (1%)	9	9
All	All	2960/2976 (100%)	2781 (94%)	148 (5%)	31 (1%)	13	15

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	341	PRO
1	E	343	ARG
1	F	343	ARG
1	C	336	SER
1	D	243	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	302/285 (106%)	290 (96%)	12 (4%)	27	40
1	B	302/285 (106%)	290 (96%)	12 (4%)	27	40
1	C	302/285 (106%)	283 (94%)	19 (6%)	15	21
1	D	302/285 (106%)	288 (95%)	14 (5%)	23	33
1	E	302/285 (106%)	289 (96%)	13 (4%)	25	36
1	F	302/285 (106%)	291 (96%)	11 (4%)	30	44
1	G	302/285 (106%)	284 (94%)	18 (6%)	16	23
1	H	302/285 (106%)	280 (93%)	22 (7%)	11	16
All	All	2416/2280 (106%)	2295 (95%)	121 (5%)	20	30

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	44	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	H	248	LEU
1	F	44	ARG
1	H	233	MSE
1	H	344	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	344	ASN
1	H	344	ASN
1	E	75	GLN
1	E	344	ASN
1	F	82	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 oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 16 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

## 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	355/372 (95%)	-0.16	11 (3%) 51 53	9, 20, 58, 103	0
1	B	355/372 (95%)	-0.17	9 (2%) 58 59	9, 19, 56, 109	0
1	C	355/372 (95%)	0.14	23 (6%) 26 28	13, 27, 70, 122	0
1	D	355/372 (95%)	0.04	12 (3%) 48 50	13, 26, 62, 114	0
1	E	355/372 (95%)	0.21	15 (4%) 41 42	12, 29, 59, 108	0
1	F	355/372 (95%)	0.30	17 (4%) 36 37	13, 31, 62, 100	0
1	G	355/372 (95%)	0.64	20 (5%) 31 33	15, 35, 61, 114	0
1	H	355/372 (95%)	0.86	36 (10%) 14 15	18, 39, 67, 88	0
All	All	2840/2976 (95%)	0.23	143 (5%) 35 36	9, 29, 64, 122	0

The worst 5 of 143 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	373	GLY	6.7
1	G	339	LEU	6.1
1	G	341	PRO	5.6
1	F	152	ILE	5.2
1	F	343	ARG	5.2

### 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 monosaccharides in this entry.



## 6.4 Ligands

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<sup>th</sup> 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZN	G	401	1/1	0.97	0.04	41,41,41,41	0
2	ZN	A	402	1/1	0.98	0.03	21,21,21,21	0
2	ZN	C	401	1/1	0.98	0.03	39,39,39,39	0
2	ZN	A	401	1/1	0.98	0.03	30,30,30,30	0
2	ZN	H	401	1/1	0.98	0.05	45,45,45,45	0
2	ZN	H	402	1/1	0.98	0.03	33,33,33,33	0
2	ZN	D	401	1/1	0.99	0.03	37,37,37,37	0
2	ZN	E	401	1/1	0.99	0.02	33,33,33,33	0
2	ZN	E	402	1/1	0.99	0.03	24,24,24,24	0
2	ZN	F	401	1/1	0.99	0.03	36,36,36,36	0
2	ZN	F	402	1/1	0.99	0.02	24,24,24,24	0
2	ZN	B	402	1/1	0.99	0.03	19,19,19,19	0
2	ZN	G	402	1/1	0.99	0.03	26,26,26,26	0
2	ZN	B	401	1/1	0.99	0.03	33,33,33,33	0
2	ZN	C	402	1/1	0.99	0.02	28,28,28,28	0
2	ZN	D	402	1/1	1.00	0.01	25,25,25,25	0

## 6.5 Other polymers

There are no such residues in this entry.