



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:28 PM UTC

PDB ID : 2CBG / pdb_00002cbg
Title : Crystal structure of the PMSF-inhibited thioesterase domain of the fengycin biosynthesis cluster
Authors : Samel, S.; Marahiel, M.A.; Essen, L.-O.
Deposited on : 2006-01-03
Resolution : 2.50 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 ⓘ 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	:	4-5-2 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

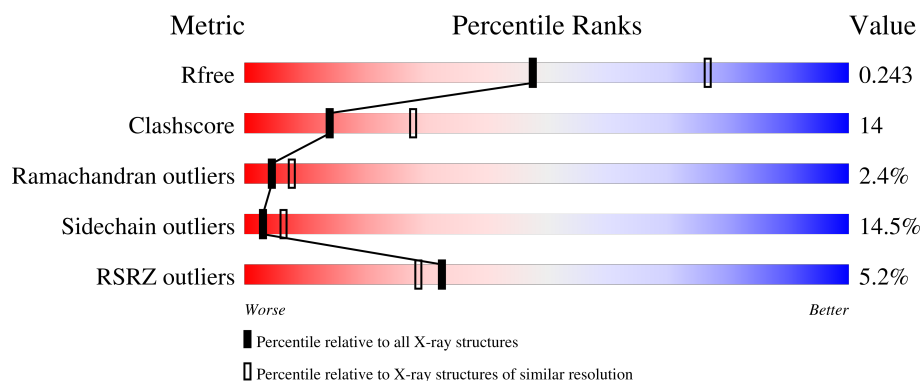
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 ≥ 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	244	5% 50% 23% 10% • 14%

2 Entry composition [i](#)

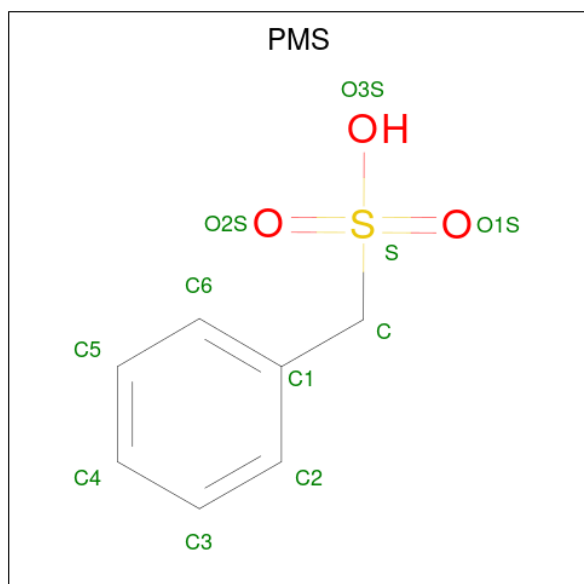
There are 3 unique types of molecules in this entry. The entry contains 1750 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FENGYCIN SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	0	0
			1665	1063	275	321	6			

- Molecule 2 is phenylmethanesulfonic acid (CCD ID: PMS) (formula: C₇H₈O₃S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			10	7	2	1		

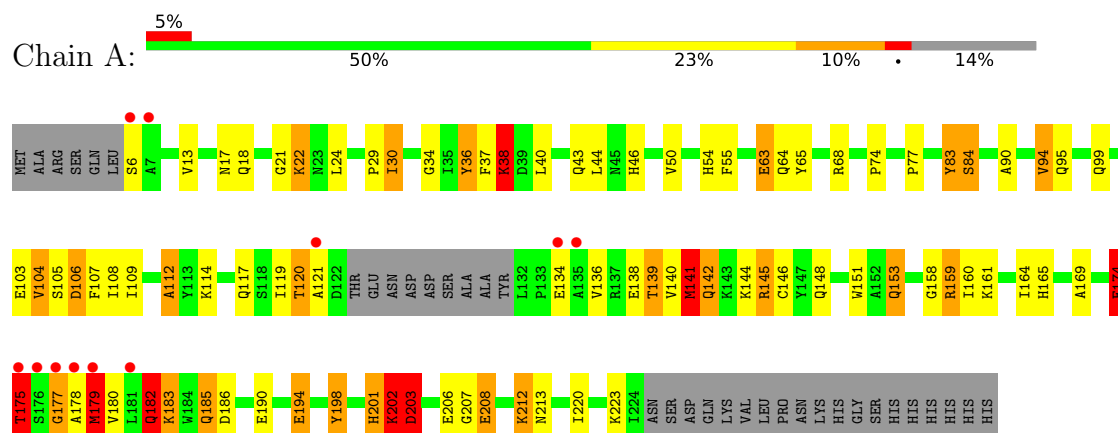
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	75	Total	O	0	0
			75	75		

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: FENGYCIN SYNTHETASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	72.35Å 72.35Å 96.33Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.00 – 2.50 24.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	92.2 (24.00-2.50) 92.2 (24.00-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.37 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.162 , 0.237 0.170 , 0.243	Depositor DCC
R_{free} test set	489 reflections (5.32%)	wwPDB-VP
Wilson B-factor (Å ²)	22.5	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.082 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1750	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

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

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	2.17	44/1698 (2.6%)	1.61	14/2290 (0.6%)

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	MET	SD-CE	14.90	2.16	1.79
1	A	141	MET	SD-CE	13.46	2.13	1.79
1	A	183	LYS	CE-NZ	11.92	1.85	1.49
1	A	108	ILE	CA-CB	11.49	1.67	1.54
1	A	220	ILE	CA-CB	8.17	1.64	1.54
1	A	104	VAL	CA-CB	8.07	1.62	1.53
1	A	83	TYR	C-O	7.62	1.32	1.24
1	A	161	LYS	CA-C	7.59	1.63	1.52
1	A	17	ASN	C-O	6.89	1.32	1.23
1	A	212	LYS	CE-NZ	6.87	1.70	1.49
1	A	112	ALA	C-O	6.81	1.32	1.23
1	A	174	GLU	CA-C	6.72	1.61	1.52
1	A	164	ILE	C-O	-6.69	1.16	1.24
1	A	174	GLU	C-O	6.57	1.32	1.24
1	A	38	LYS	CG-CD	6.56	1.72	1.52
1	A	50	VAL	CA-CB	6.47	1.61	1.54
1	A	208	GLU	C-O	6.42	1.32	1.24
1	A	94	VAL	C-O	6.37	1.31	1.24
1	A	106	ASP	CA-C	-6.26	1.44	1.52
1	A	145	ARG	NE-CZ	6.21	1.39	1.33
1	A	169	ALA	C-O	6.13	1.31	1.23
1	A	43	GLN	N-CA	6.08	1.53	1.46
1	A	175	THR	CA-CB	6.01	1.63	1.53
1	A	121	ALA	CA-CB	5.82	1.62	1.53
1	A	153	GLN	C-O	5.82	1.31	1.24
1	A	153	GLN	CD-OE1	5.79	1.34	1.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	99	GLN	CG-CD	5.74	1.66	1.52
1	A	30	ILE	CA-C	5.64	1.60	1.52
1	A	36	TYR	CA-C	5.61	1.60	1.52
1	A	194	GLU	CA-C	5.61	1.59	1.52
1	A	63	GLU	CD-OE1	5.55	1.35	1.25
1	A	22	LYS	CA-C	5.55	1.60	1.52
1	A	182	GLN	N-CA	5.53	1.52	1.46
1	A	142	GLN	CB-CG	-5.43	1.36	1.52
1	A	175	THR	N-CA	5.42	1.53	1.46
1	A	198	TYR	C-O	5.32	1.30	1.23
1	A	55	PHE	C-O	5.32	1.30	1.24
1	A	13	VAL	C-O	5.22	1.30	1.23
1	A	6	SER	N-CA	5.22	1.56	1.46
1	A	94	VAL	CA-C	5.17	1.59	1.52
1	A	24	LEU	CG-CD2	5.07	1.69	1.52
1	A	55	PHE	CA-C	5.07	1.59	1.52
1	A	105	SER	C-O	5.04	1.30	1.24
1	A	37	PHE	C-O	5.02	1.31	1.24

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	203	ASP	CB-CA-C	-8.01	98.12	111.02
1	A	203	ASP	N-CA-C	7.55	121.80	112.59
1	A	183	LYS	CD-CE-NZ	6.57	132.93	111.90
1	A	64	GLN	N-CA-C	5.82	118.40	111.71
1	A	120	THR	CB-CA-C	5.78	119.30	109.53
1	A	65	TYR	N-CA-C	-5.78	104.90	111.14
1	A	21	GLY	N-CA-C	-5.66	101.50	111.80
1	A	177	GLY	N-CA-C	5.49	126.20	113.18
1	A	178	ALA	CA-C-N	5.47	128.40	120.79
1	A	178	ALA	C-N-CA	5.47	128.40	120.79
1	A	139	THR	CA-C-N	5.47	127.95	120.46
1	A	139	THR	C-N-CA	5.47	127.95	120.46
1	A	208	GLU	CA-C-O	5.16	125.71	119.31
1	A	84	SER	CA-CB-OG	-5.01	101.08	111.10

There are no chirality outliers.

There are no planarity outliers.

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	1665	0	1614	47	0
2	A	10	0	7	2	0
3	A	75	0	0	10	0
All	All	1750	0	1621	47	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 14.

All (47) 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:A:212:LYS:CE	1:A:212:LYS:NZ	1.70	1.53
1:A:183:LYS:CE	1:A:183:LYS:NZ	1.85	1.38
1:A:141:MET:CE	1:A:141:MET:SD	2.13	1.36
1:A:179:MET:CE	1:A:179:MET:SD	2.16	1.33
1:A:34:GLY:H	1:A:54:HIS:HD2	1.15	0.92
1:A:185:GLN:HG3	3:A:2059:HOH:O	1.76	0.85
1:A:74:PRO:HD2	3:A:2027:HOH:O	1.79	0.82
1:A:141:MET:HA	1:A:141:MET:HE2	1.61	0.80
1:A:34:GLY:H	1:A:54:HIS:CD2	2.02	0.76
1:A:144:LYS:O	1:A:148:GLN:HG3	1.87	0.74
1:A:139:THR:O	1:A:142:GLN:HG2	1.90	0.71
1:A:142:GLN:O	1:A:146:CYS:HB2	1.91	0.70
1:A:34:GLY:N	1:A:54:HIS:HD2	1.89	0.68
1:A:141:MET:CE	1:A:141:MET:HA	2.23	0.68
1:A:202:LYS:HG3	1:A:203:ASP:OD1	1.94	0.67
1:A:106:ASP:OD1	1:A:165:HIS:HE1	1.81	0.63
1:A:151:TRP:CE2	2:A:1225:PMS:H4	2.39	0.58
1:A:185:GLN:CG	3:A:2059:HOH:O	2.45	0.57
1:A:198:TYR:H	1:A:213:ASN:HD21	1.52	0.57
1:A:151:TRP:CD2	2:A:1225:PMS:H4	2.41	0.56
1:A:38:LYS:O	1:A:38:LYS:HD3	2.07	0.55
1:A:179:MET:O	1:A:182:GLN:HB2	2.08	0.53
1:A:29:PRO:HG3	1:A:83:TYR:HD2	1.75	0.52
1:A:179:MET:O	1:A:182:GLN:N	2.35	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:LYS:HE3	3:A:2056:HOH:O	2.08	0.52
1:A:77:PRO:HA	1:A:103:GLU:O	2.11	0.51
1:A:68:ARG:HD2	3:A:2026:HOH:O	2.10	0.51
1:A:159:ARG:HD3	1:A:186:ASP:O	2.12	0.48
1:A:36:TYR:OH	3:A:2014:HOH:O	2.17	0.48
1:A:40:LEU:HD11	1:A:44:LEU:HD11	1.94	0.48
1:A:158:GLY:C	1:A:159:ARG:HG2	2.39	0.47
1:A:90:ALA:HB3	1:A:107:PHE:CE1	2.51	0.46
1:A:94:VAL:HG13	1:A:104:VAL:HG21	1.98	0.46
1:A:186:ASP:HA	3:A:2061:HOH:O	2.16	0.45
1:A:201:HIS:O	1:A:202:LYS:C	2.61	0.44
1:A:38:LYS:HD3	1:A:38:LYS:C	2.43	0.44
1:A:84:SER:O	1:A:112:ALA:HB2	2.18	0.43
1:A:175:THR:HG22	3:A:2058:HOH:O	2.18	0.43
1:A:18:GLN:HG3	1:A:46:HIS:CE1	2.53	0.43
1:A:95:GLN:HG3	1:A:160:ILE:HG22	2.00	0.42
1:A:30:ILE:HG23	1:A:144:LYS:HE3	2.01	0.42
1:A:114:LYS:O	1:A:182:GLN:HG3	2.19	0.42
1:A:141:MET:HE2	1:A:141:MET:CA	2.42	0.41
1:A:180:VAL:CG2	3:A:2058:HOH:O	2.67	0.41
1:A:206:GLU:O	1:A:207:GLY:C	2.64	0.40
1:A:29:PRO:HG3	1:A:83:TYR:CD2	2.54	0.40
1:A:180:VAL:HG21	3:A:2058:HOH:O	2.21	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	206/244 (84%)	192 (93%)	9 (4%)	5 (2%)	4 8

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	174	GLU
1	A	175	THR
1	A	177	GLY
1	A	201	HIS
1	A	202	LYS

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	172/202 (85%)	147 (86%)	25 (14%)	3 6

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LYS
1	A	38	LYS
1	A	63	GLU
1	A	109	ILE
1	A	117	GLN
1	A	119	ILE
1	A	120	THR
1	A	134	GLU
1	A	136	VAL
1	A	138	GLU
1	A	140	VAL
1	A	141	MET
1	A	145	ARG
1	A	153	GLN
1	A	159	ARG
1	A	174	GLU
1	A	179	MET
1	A	182	GLN
1	A	185	GLN
1	A	190	GLU
1	A	194	GLU
1	A	202	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	203	ASP
1	A	208	GLU
1	A	223	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	HIS
1	A	148	GLN
1	A	153	GLN
1	A	165	HIS
1	A	182	GLN
1	A	213	ASN
1	A	219	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PMS	A	1225	1	7,10,11	1.84	2 (28%)	11,12,15	1.49	2 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PMS	A	1225	1	-	1/4/4/5	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1225	PMS	C5-C6	3.07	1.44	1.38
2	A	1225	PMS	C3-C2	2.71	1.43	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1225	PMS	O2S-S-C	3.19	111.06	105.55
2	A	1225	PMS	C6-C1-C2	2.21	121.51	118.23

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1225	PMS	C1-C-S-O1S

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1225	PMS	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 95th 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	A	210/244 (86%)	-0.36	11 (5%) 33 29	21, 31, 76, 89	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	178	ALA	5.1
1	A	179	MET	3.6
1	A	181	LEU	3.3
1	A	176	SER	3.0
1	A	121	ALA	2.9
1	A	7	ALA	2.7
1	A	175	THR	2.5
1	A	177	GLY	2.4
1	A	135	ALA	2.1
1	A	6	SER	2.1
1	A	134	GLU	2.1

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 [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, 95th 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($\text{\AA}^2$)	Q<0.9
2	PMS	A	1225	10/11	0.99	0.06	26,28,32,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.