



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 12:10 PM UTC

PDB ID : 9D2T / pdb_00009d2t
Title : Crystal structure of S. aureus Threonine deaminase regulatory domain
Authors : Rock, C.O.; Yun, M.
Deposited on : 2024-08-09
Resolution : 2.80 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

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
Xtrriage (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

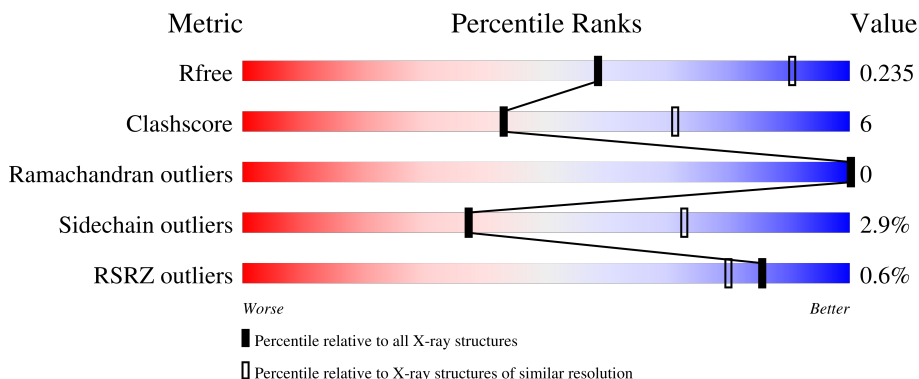
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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.



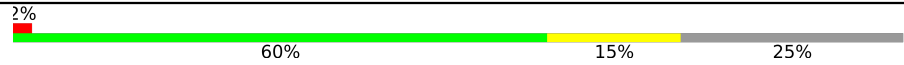


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 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	107	
1	B	107	
1	C	107	
1	D	107	
1	E	107	

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Mol	Chain	Length	Quality of chain
1	F	107	 <p>2% 60% 15% 25%</p>
1	G	107	 <p>61% 15% 24%</p>
1	H	107	 <p>63% 13% 22%</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 5429 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 L-threonine dehydratase biosynthetic IIvA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	85	Total 695	C 447	N 118	O 128	S 2	0	0	0
1	B	78	Total 643	C 417	N 107	O 117	S 2	0	0	0
1	C	85	Total 688	C 445	N 116	O 126	S 1	0	0	0
1	D	82	Total 675	C 436	N 113	O 124	S 2	0	0	0
1	E	85	Total 688	C 444	N 116	O 127	S 1	0	0	0
1	F	80	Total 666	C 431	N 111	O 122	S 2	0	0	0
1	H	83	Total 683	C 443	N 115	O 123	S 2	0	0	0
1	G	81	Total 677	C 440	N 114	O 121	S 2	0	0	0

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	316	MET	-	initiating methionine	UNP Q2FF63
A	317	GLY	-	expression tag	UNP Q2FF63
A	318	SER	-	expression tag	UNP Q2FF63
A	319	SER	-	expression tag	UNP Q2FF63
A	320	HIS	-	expression tag	UNP Q2FF63
A	321	HIS	-	expression tag	UNP Q2FF63
A	322	HIS	-	expression tag	UNP Q2FF63
A	323	HIS	-	expression tag	UNP Q2FF63
A	324	HIS	-	expression tag	UNP Q2FF63
A	325	HIS	-	expression tag	UNP Q2FF63
A	326	SER	-	expression tag	UNP Q2FF63
A	327	SER	-	expression tag	UNP Q2FF63
A	328	GLY	-	expression tag	UNP Q2FF63

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Chain	Residue	Modelled	Actual	Comment	Reference
A	329	LEU	-	expression tag	UNP Q2FF63
A	330	VAL	-	expression tag	UNP Q2FF63
A	331	PRO	-	expression tag	UNP Q2FF63
A	332	ARG	-	expression tag	UNP Q2FF63
A	333	GLY	-	expression tag	UNP Q2FF63
A	334	SER	-	expression tag	UNP Q2FF63
A	335	HIS	-	expression tag	UNP Q2FF63
B	316	MET	-	initiating methionine	UNP Q2FF63
B	317	GLY	-	expression tag	UNP Q2FF63
B	318	SER	-	expression tag	UNP Q2FF63
B	319	SER	-	expression tag	UNP Q2FF63
B	320	HIS	-	expression tag	UNP Q2FF63
B	321	HIS	-	expression tag	UNP Q2FF63
B	322	HIS	-	expression tag	UNP Q2FF63
B	323	HIS	-	expression tag	UNP Q2FF63
B	324	HIS	-	expression tag	UNP Q2FF63
B	325	HIS	-	expression tag	UNP Q2FF63
B	326	SER	-	expression tag	UNP Q2FF63
B	327	SER	-	expression tag	UNP Q2FF63
B	328	GLY	-	expression tag	UNP Q2FF63
B	329	LEU	-	expression tag	UNP Q2FF63
B	330	VAL	-	expression tag	UNP Q2FF63
B	331	PRO	-	expression tag	UNP Q2FF63
B	332	ARG	-	expression tag	UNP Q2FF63
B	333	GLY	-	expression tag	UNP Q2FF63
B	334	SER	-	expression tag	UNP Q2FF63
B	335	HIS	-	expression tag	UNP Q2FF63
C	316	MET	-	initiating methionine	UNP Q2FF63
C	317	GLY	-	expression tag	UNP Q2FF63
C	318	SER	-	expression tag	UNP Q2FF63
C	319	SER	-	expression tag	UNP Q2FF63
C	320	HIS	-	expression tag	UNP Q2FF63
C	321	HIS	-	expression tag	UNP Q2FF63
C	322	HIS	-	expression tag	UNP Q2FF63
C	323	HIS	-	expression tag	UNP Q2FF63
C	324	HIS	-	expression tag	UNP Q2FF63
C	325	HIS	-	expression tag	UNP Q2FF63
C	326	SER	-	expression tag	UNP Q2FF63
C	327	SER	-	expression tag	UNP Q2FF63
C	328	GLY	-	expression tag	UNP Q2FF63
C	329	LEU	-	expression tag	UNP Q2FF63
C	330	VAL	-	expression tag	UNP Q2FF63

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Chain	Residue	Modelled	Actual	Comment	Reference
C	331	PRO	-	expression tag	UNP Q2FF63
C	332	ARG	-	expression tag	UNP Q2FF63
C	333	GLY	-	expression tag	UNP Q2FF63
C	334	SER	-	expression tag	UNP Q2FF63
C	335	HIS	-	expression tag	UNP Q2FF63
D	316	MET	-	initiating methionine	UNP Q2FF63
D	317	GLY	-	expression tag	UNP Q2FF63
D	318	SER	-	expression tag	UNP Q2FF63
D	319	SER	-	expression tag	UNP Q2FF63
D	320	HIS	-	expression tag	UNP Q2FF63
D	321	HIS	-	expression tag	UNP Q2FF63
D	322	HIS	-	expression tag	UNP Q2FF63
D	323	HIS	-	expression tag	UNP Q2FF63
D	324	HIS	-	expression tag	UNP Q2FF63
D	325	HIS	-	expression tag	UNP Q2FF63
D	326	SER	-	expression tag	UNP Q2FF63
D	327	SER	-	expression tag	UNP Q2FF63
D	328	GLY	-	expression tag	UNP Q2FF63
D	329	LEU	-	expression tag	UNP Q2FF63
D	330	VAL	-	expression tag	UNP Q2FF63
D	331	PRO	-	expression tag	UNP Q2FF63
D	332	ARG	-	expression tag	UNP Q2FF63
D	333	GLY	-	expression tag	UNP Q2FF63
D	334	SER	-	expression tag	UNP Q2FF63
D	335	HIS	-	expression tag	UNP Q2FF63
E	316	MET	-	initiating methionine	UNP Q2FF63
E	317	GLY	-	expression tag	UNP Q2FF63
E	318	SER	-	expression tag	UNP Q2FF63
E	319	SER	-	expression tag	UNP Q2FF63
E	320	HIS	-	expression tag	UNP Q2FF63
E	321	HIS	-	expression tag	UNP Q2FF63
E	322	HIS	-	expression tag	UNP Q2FF63
E	323	HIS	-	expression tag	UNP Q2FF63
E	324	HIS	-	expression tag	UNP Q2FF63
E	325	HIS	-	expression tag	UNP Q2FF63
E	326	SER	-	expression tag	UNP Q2FF63
E	327	SER	-	expression tag	UNP Q2FF63
E	328	GLY	-	expression tag	UNP Q2FF63
E	329	LEU	-	expression tag	UNP Q2FF63
E	330	VAL	-	expression tag	UNP Q2FF63
E	331	PRO	-	expression tag	UNP Q2FF63
E	332	ARG	-	expression tag	UNP Q2FF63

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Chain	Residue	Modelled	Actual	Comment	Reference
E	333	GLY	-	expression tag	UNP Q2FF63
E	334	SER	-	expression tag	UNP Q2FF63
E	335	HIS	-	expression tag	UNP Q2FF63
F	316	MET	-	initiating methionine	UNP Q2FF63
F	317	GLY	-	expression tag	UNP Q2FF63
F	318	SER	-	expression tag	UNP Q2FF63
F	319	SER	-	expression tag	UNP Q2FF63
F	320	HIS	-	expression tag	UNP Q2FF63
F	321	HIS	-	expression tag	UNP Q2FF63
F	322	HIS	-	expression tag	UNP Q2FF63
F	323	HIS	-	expression tag	UNP Q2FF63
F	324	HIS	-	expression tag	UNP Q2FF63
F	325	HIS	-	expression tag	UNP Q2FF63
F	326	SER	-	expression tag	UNP Q2FF63
F	327	SER	-	expression tag	UNP Q2FF63
F	328	GLY	-	expression tag	UNP Q2FF63
F	329	LEU	-	expression tag	UNP Q2FF63
F	330	VAL	-	expression tag	UNP Q2FF63
F	331	PRO	-	expression tag	UNP Q2FF63
F	332	ARG	-	expression tag	UNP Q2FF63
F	333	GLY	-	expression tag	UNP Q2FF63
F	334	SER	-	expression tag	UNP Q2FF63
F	335	HIS	-	expression tag	UNP Q2FF63
H	316	MET	-	initiating methionine	UNP Q2FF63
H	317	GLY	-	expression tag	UNP Q2FF63
H	318	SER	-	expression tag	UNP Q2FF63
H	319	SER	-	expression tag	UNP Q2FF63
H	320	HIS	-	expression tag	UNP Q2FF63
H	321	HIS	-	expression tag	UNP Q2FF63
H	322	HIS	-	expression tag	UNP Q2FF63
H	323	HIS	-	expression tag	UNP Q2FF63
H	324	HIS	-	expression tag	UNP Q2FF63
H	325	HIS	-	expression tag	UNP Q2FF63
H	326	SER	-	expression tag	UNP Q2FF63
H	327	SER	-	expression tag	UNP Q2FF63
H	328	GLY	-	expression tag	UNP Q2FF63
H	329	LEU	-	expression tag	UNP Q2FF63
H	330	VAL	-	expression tag	UNP Q2FF63
H	331	PRO	-	expression tag	UNP Q2FF63
H	332	ARG	-	expression tag	UNP Q2FF63
H	333	GLY	-	expression tag	UNP Q2FF63
H	334	SER	-	expression tag	UNP Q2FF63

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Chain	Residue	Modelled	Actual	Comment	Reference
H	335	HIS	-	expression tag	UNP Q2FF63
G	316	MET	-	initiating methionine	UNP Q2FF63
G	317	GLY	-	expression tag	UNP Q2FF63
G	318	SER	-	expression tag	UNP Q2FF63
G	319	SER	-	expression tag	UNP Q2FF63
G	320	HIS	-	expression tag	UNP Q2FF63
G	321	HIS	-	expression tag	UNP Q2FF63
G	322	HIS	-	expression tag	UNP Q2FF63
G	323	HIS	-	expression tag	UNP Q2FF63
G	324	HIS	-	expression tag	UNP Q2FF63
G	325	HIS	-	expression tag	UNP Q2FF63
G	326	SER	-	expression tag	UNP Q2FF63
G	327	SER	-	expression tag	UNP Q2FF63
G	328	GLY	-	expression tag	UNP Q2FF63
G	329	LEU	-	expression tag	UNP Q2FF63
G	330	VAL	-	expression tag	UNP Q2FF63
G	331	PRO	-	expression tag	UNP Q2FF63
G	332	ARG	-	expression tag	UNP Q2FF63
G	333	GLY	-	expression tag	UNP Q2FF63
G	334	SER	-	expression tag	UNP Q2FF63
G	335	HIS	-	expression tag	UNP Q2FF63

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total O 4 4	0	0
2	C	3	Total O 3 3	0	0
2	D	4	Total O 4 4	0	0
2	E	1	Total O 1 1	0	0
2	F	1	Total O 1 1	0	0
2	H	1	Total O 1 1	0	0



I422

- Molecule 1: L-threonine dehydratase biosynthetic IlvA



- Molecule 1: L-threonine dehydratase biosynthetic IlvA



I422

4 Data and refinement statistics i

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	88.92Å 88.92Å 213.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.46 – 2.80 44.46 – 2.81	Depositor EDS
% Data completeness (in resolution range)	99.6 (44.46-2.80) 97.8 (44.46-2.81)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.81Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.192 , 0.239 0.190 , 0.235	Depositor DCC
R_{free} test set	1002 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	82.9	Xtrriage
Anisotropy	0.267	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 121.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	0.304 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5429	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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 [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	0.11	0/709	0.27	0/957
1	B	0.11	0/657	0.28	0/887
1	C	0.10	0/702	0.25	0/949
1	D	0.11	0/689	0.28	0/929
1	E	0.11	0/702	0.27	0/948
1	F	0.09	0/680	0.26	0/917
1	G	0.10	0/691	0.25	0/929
1	H	0.12	0/697	0.30	0/939
All	All	0.11	0/5527	0.27	0/7455

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	695	0	676	6	0
1	B	643	0	630	10	0
1	C	688	0	668	8	0
1	D	675	0	659	8	0
1	E	688	0	669	8	0
1	F	666	0	654	10	0
1	G	677	0	684	9	0
1	H	683	0	677	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	4	0	0	0	0
2	C	3	0	0	0	0
2	D	4	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	H	1	0	0	0	0
All	All	5429	0	5317	66	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.

The worst 5 of 66 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:F:388:LEU:HD21	1:F:397:LEU:HD22	1.69	0.74
1:B:360:LEU:HD21	1:B:386:ILE:HD13	1.72	0.71
1:E:388:LEU:HD11	1:E:397:LEU:HD22	1.79	0.65
1:F:342:ILE:HD11	1:F:421:LEU:HD21	1.79	0.64
1:G:346:PRO:HB2	1:G:348:ARG:HG2	1.81	0.62

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	81/107 (76%)	79 (98%)	2 (2%)	0	100	100
1	B	74/107 (69%)	72 (97%)	2 (3%)	0	100	100
1	C	81/107 (76%)	80 (99%)	1 (1%)	0	100	100
1	D	78/107 (73%)	75 (96%)	3 (4%)	0	100	100
1	E	81/107 (76%)	77 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	76/107 (71%)	75 (99%)	1 (1%)	0	100	100
1	G	77/107 (72%)	75 (97%)	2 (3%)	0	100	100
1	H	79/107 (74%)	76 (96%)	3 (4%)	0	100	100
All	All	627/856 (73%)	609 (97%)	18 (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	76/99 (77%)	73 (96%)	3 (4%)	28	64
1	B	71/99 (72%)	68 (96%)	3 (4%)	26	61
1	C	74/99 (75%)	73 (99%)	1 (1%)	59	85
1	D	74/99 (75%)	71 (96%)	3 (4%)	27	62
1	E	75/99 (76%)	75 (100%)	0	100	100
1	F	74/99 (75%)	73 (99%)	1 (1%)	59	85
1	G	76/99 (77%)	73 (96%)	3 (4%)	28	64
1	H	75/99 (76%)	72 (96%)	3 (4%)	28	63
All	All	595/792 (75%)	578 (97%)	17 (3%)	37	73

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	371	TYR
1	G	391	HIS
1	D	345	PHE
1	D	356	VAL
1	D	388	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	412	ASN
1	H	347	GLN
1	G	414	ASN
1	G	391	HIS
1	G	408	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](#)

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 [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	85/107 (79%)	0.14	1 (1%) 76 68	62, 82, 127, 160	0
1	B	78/107 (72%)	-0.08	0 100 100	60, 86, 118, 133	0
1	C	85/107 (79%)	0.13	0 100 100	67, 90, 129, 170	0
1	D	82/107 (76%)	0.31	1 (1%) 76 68	68, 89, 132, 141	0
1	E	85/107 (79%)	-0.06	0 100 100	53, 78, 120, 139	0
1	F	80/107 (74%)	0.22	2 (2%) 58 48	64, 97, 148, 177	0
1	G	81/107 (75%)	0.25	0 100 100	70, 96, 135, 153	0
1	H	83/107 (77%)	0.10	0 100 100	56, 91, 132, 155	0
All	All	659/856 (76%)	0.13	4 (0%) 85 80	53, 90, 132, 177	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	346	PRO	2.1
1	A	339	HIS	2.0
1	D	401	VAL	2.0
1	F	358	ASP	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 oligosaccharides 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.