



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 24, 2026 – 04:08 PM JST

PDB ID : 9WEW / pdb_00009wew
Title : Aquifex aeolicus IscS2 with 5 mutations (5 mut)
Authors : Fujishiro, T.
Deposited on : 2025-08-20
Resolution : 3.70 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
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

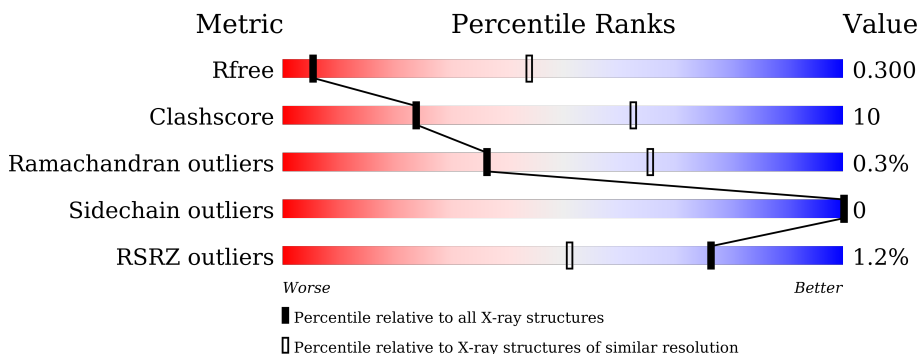
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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	1131 (3.80-3.60)
Clashscore	190562	1171 (3.80-3.60)
Ramachandran outliers	187476	1129 (3.80-3.60)
Sidechain outliers	187428	1126 (3.80-3.60)
RSRZ outliers	180081	1130 (3.80-3.60)

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	406	70%22%7%
1	G	406	% 69%23%8%
1	J	406	3% 67%25%8%
2	D	406	% 75%17%8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11766 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 cysteine desulfurase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	376	Total	C	N	O	S	0	0	0
			2957	1874	521	555	7			
1	G	373	Total	C	N	O	S	0	0	0
			2936	1862	517	550	7			
1	J	372	Total	C	N	O	S	0	0	0
			2929	1857	515	550	7			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	80	THR	ILE	engineered mutation	UNP O66947
A	159	ASN	ARG	engineered mutation	UNP O66947
A	189	GLN	PRO	engineered mutation	UNP O66947
A	212	LYS	LEU	engineered mutation	UNP O66947
A	361	ARG	VAL	engineered mutation	UNP O66947
G	80	THR	ILE	engineered mutation	UNP O66947
G	159	ASN	ARG	engineered mutation	UNP O66947
G	189	GLN	PRO	engineered mutation	UNP O66947
G	212	LYS	LEU	engineered mutation	UNP O66947
G	361	ARG	VAL	engineered mutation	UNP O66947
J	80	THR	ILE	engineered mutation	UNP O66947
J	159	ASN	ARG	engineered mutation	UNP O66947
J	189	GLN	PRO	engineered mutation	UNP O66947
J	212	LYS	LEU	engineered mutation	UNP O66947
J	361	ARG	VAL	engineered mutation	UNP O66947

- Molecule 2 is a protein called cysteine desulfurase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	372	Total	C	N	O	P S	0	0	0
			2941	1862	516	555	1 7			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	80	THR	ILE	engineered mutation	UNP O66947
D	159	ASN	ARG	engineered mutation	UNP O66947
D	189	GLN	PRO	engineered mutation	UNP O66947
D	212	LLP	LEU	engineered mutation	UNP O66947
D	361	ARG	VAL	engineered mutation	UNP O66947

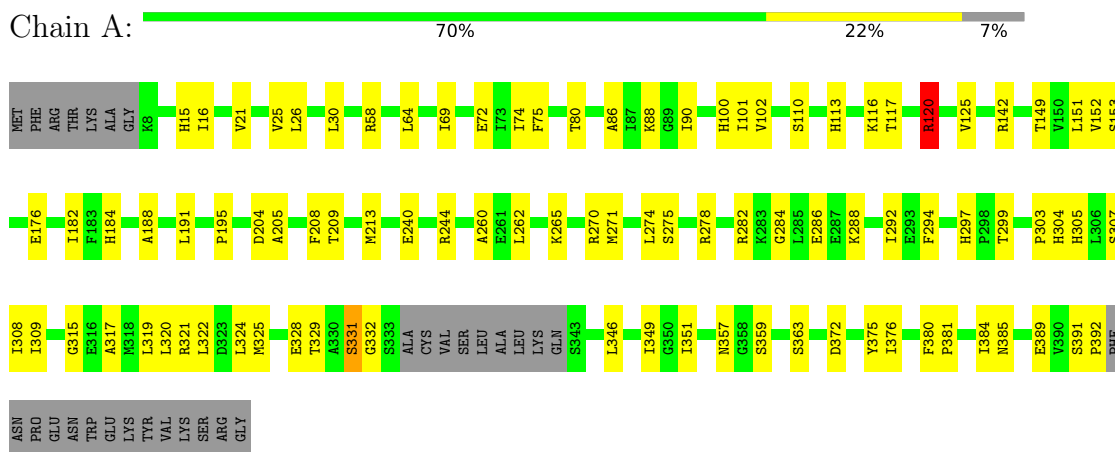
- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0
3	G	1	Total Cl 1 1	0	0
3	J	1	Total Cl 1 1	0	0

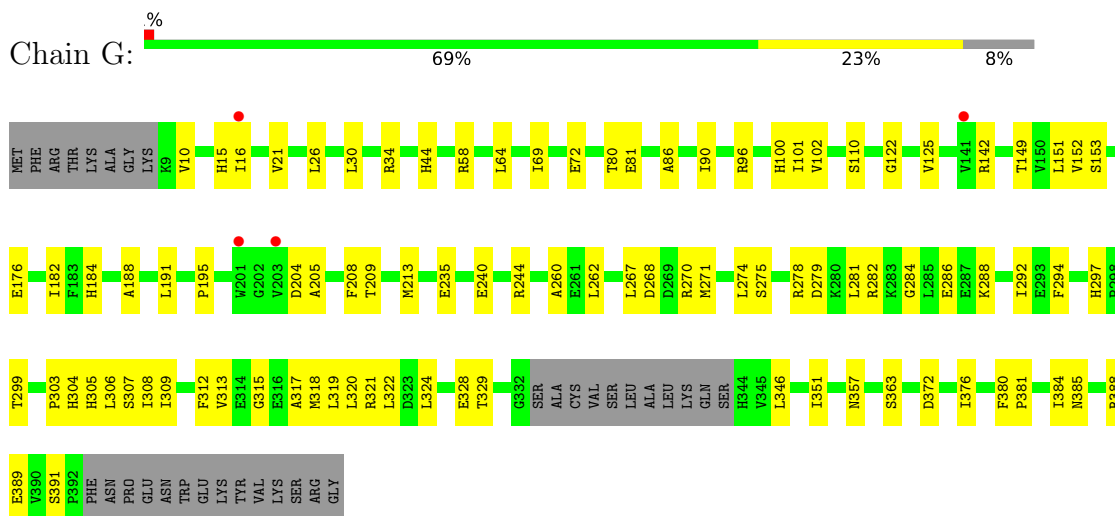
3 Residue-property plots

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.

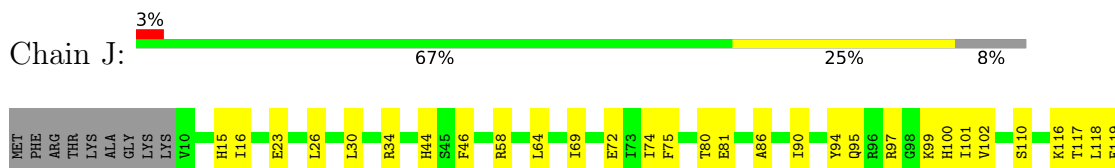
• Molecule 1: cysteine desulfurase

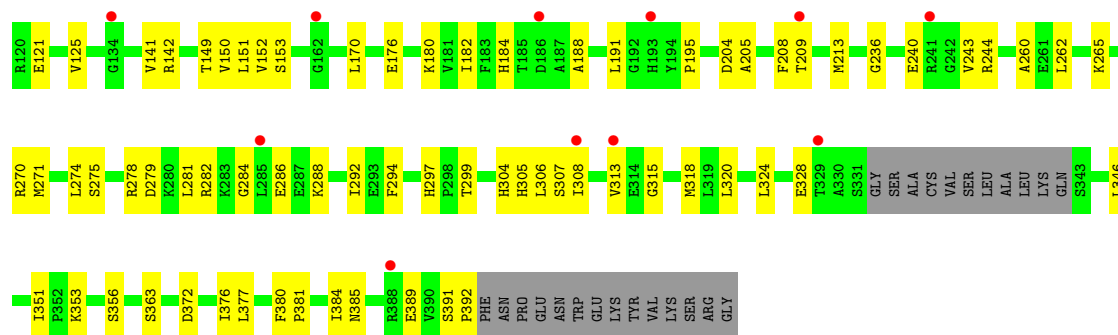


• Molecule 1: cysteine desulfurase

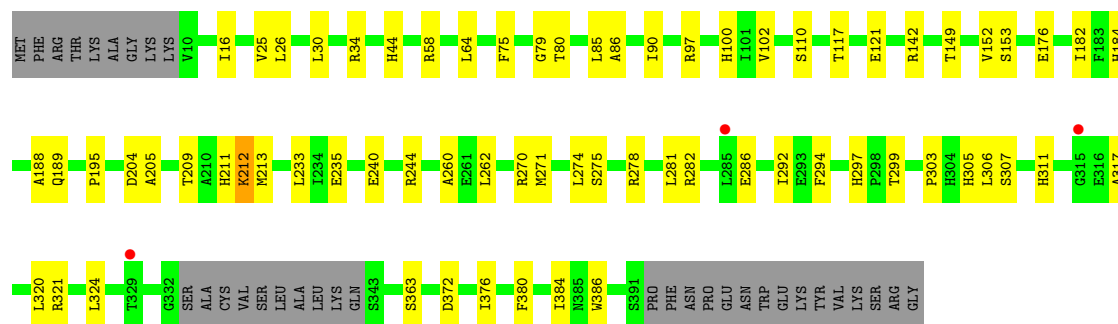
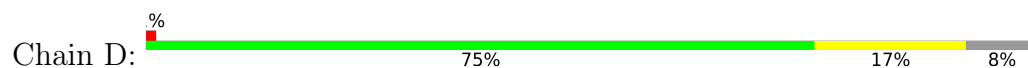


• Molecule 1: cysteine desulfurase





• Molecule 2: cysteine desulfurase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.12Å 61.91Å 209.65Å 90.00° 90.03° 90.00°	Depositor
Resolution (Å)	47.26 – 3.70 47.26 – 3.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.26-3.70) 99.8 (47.26-3.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 3.67Å)	Xtriage
Refinement program	PHENIX (1.21.1_5286: ???)	Depositor
R, R_{free}	0.267 , 0.300 0.267 , 0.300	Depositor DCC
R_{free} test set	898 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	97.4	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 96.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.009 for k,h,-l 0.000 for -k,-h,-l 0.227 for h,-k,-l	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	11766	wwPDB-VP
Average B, all atoms (Å ²)	106.0	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 21.89 % 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 6.3872e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

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

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	0.21	0/3018	0.50	1/4079 (0.0%)
1	G	0.19	0/2997	0.47	0/4052
1	J	0.19	0/2990	0.50	0/4044
2	D	0.22	0/2976	0.47	1/4023 (0.0%)
All	All	0.20	0/11981	0.49	2/16198 (0.0%)

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	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	120	ARG	CB-CA-C	-5.12	102.30	110.79
2	D	386	TRP	CA-CB-CG	5.05	123.19	113.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	120	ARG	Sidechain

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	2957	0	2963	64	0
1	G	2936	0	2940	69	0
1	J	2929	0	2929	70	0
2	D	2941	0	2929	52	0
3	A	1	0	0	0	0
3	G	1	0	0	0	0
3	J	1	0	0	0	0
All	All	11766	0	11761	238	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 10.

The worst 5 of 238 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:G:262:LEU:HD22	1:G:270:ARG:NH2	1.84	0.90
2:D:16:ILE:HD12	2:D:363:SER:OG	1.81	0.81
1:J:74:ILE:HD13	1:J:243:VAL:HG11	1.67	0.75
1:G:10:VAL:HG11	1:J:46:PHE:HE1	1.52	0.74
2:D:311:HIS:HE1	1:G:96:ARG:HH22	1.35	0.74

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	372/406 (92%)	353 (95%)	18 (5%)	1 (0%)	36	65
1	G	369/406 (91%)	348 (94%)	19 (5%)	2 (0%)	24	56
1	J	368/406 (91%)	350 (95%)	17 (5%)	1 (0%)	36	65
2	D	367/406 (90%)	350 (95%)	17 (5%)	0	100	100
All	All	1476/1624 (91%)	1401 (95%)	71 (5%)	4 (0%)	36	65

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	331	SER
1	J	236	GLY
1	G	122	GLY
1	G	391	SER

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	316/341 (93%)	316 (100%)	0	100	100
1	G	313/341 (92%)	313 (100%)	0	100	100
1	J	313/341 (92%)	313 (100%)	0	100	100
2	D	311/340 (92%)	311 (100%)	0	100	100
All	All	1253/1363 (92%)	1253 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	189	GLN
1	G	311	HIS
1	G	305	HIS
1	G	357	ASN

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Mol	Chain	Res	Type
2	D	63	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	LLP	D	212	2	23,24,25	1.48	2 (8%)	25,32,34	1.14	3 (12%)

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	LLP	D	212	2	-	3/16/17/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	212	LLP	C4'-NZ	4.83	1.43	1.27
2	D	212	LLP	C2-N1	2.39	1.38	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	212	LLP	C4-C4'-NZ	2.62	136.34	124.31
2	D	212	LLP	C5-C6-N1	-2.40	119.82	123.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	212	LLP	C3-C4-C5	2.06	119.84	118.26

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	212	LLP	C5'-OP4-P-OP2
2	D	212	LLP	C5'-OP4-P-OP3
2	D	212	LLP	C5'-OP4-P-OP1

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	212	LLP	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 ⓘ

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	376/406 (92%)	-0.10	0 100 100	55, 80, 112, 135	0
1	G	373/406 (91%)	0.10	4 (1%) 78 53	82, 107, 131, 154	0
1	J	372/406 (91%)	0.34	11 (2%) 52 32	86, 123, 173, 233	0
2	D	371/406 (91%)	-0.06	3 (0%) 82 60	66, 97, 145, 205	0
All	All	1492/1624 (91%)	0.07	18 (1%) 76 51	55, 103, 151, 233	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	285	LEU	3.4
1	J	186	ASP	3.3
2	D	315	GLY	3.0
1	J	134	GLY	2.9
1	J	209	THR	2.9

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
2	LLP	D	212	24/25	0.91	0.14	70,87,100,114	0

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
3	CL	J	501	1/1	0.69	0.09	73,73,73,73	0
3	CL	A	501	1/1	0.78	0.19	48,48,48,48	0
3	CL	G	501	1/1	0.84	0.18	75,75,75,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.