



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 06:38 am GMT

PDB ID : 1QZX
Title : Crystal structure of the complete core of archaeal SRP and implications for inter-domain communication
Authors : Rosendal, K.R.; Wild, K.; Montoya, G.; Sinning, I.
Deposited on : 2003-09-18
Resolution : 4.00 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtrriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

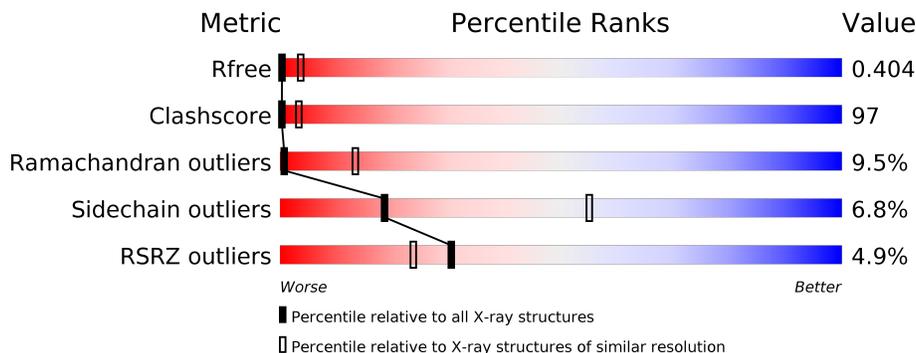
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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}	100719	1088 (4.40-3.60)
Clashscore	112137	1187 (4.40-3.60)
Ramachandran outliers	110173	1139 (4.40-3.60)
Sidechain outliers	110143	1126 (4.40-3.60)
RSRZ outliers	101464	1099 (4.40-3.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	440	 5% 21% 63% 11% . .
1	B	440	 5% 22% 62% 11% . .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6698 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 Signal recognition 54 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	425	3349	2142	565	628	14	0	0	0
1	B	425	3349	2142	565	628	14	0	0	0

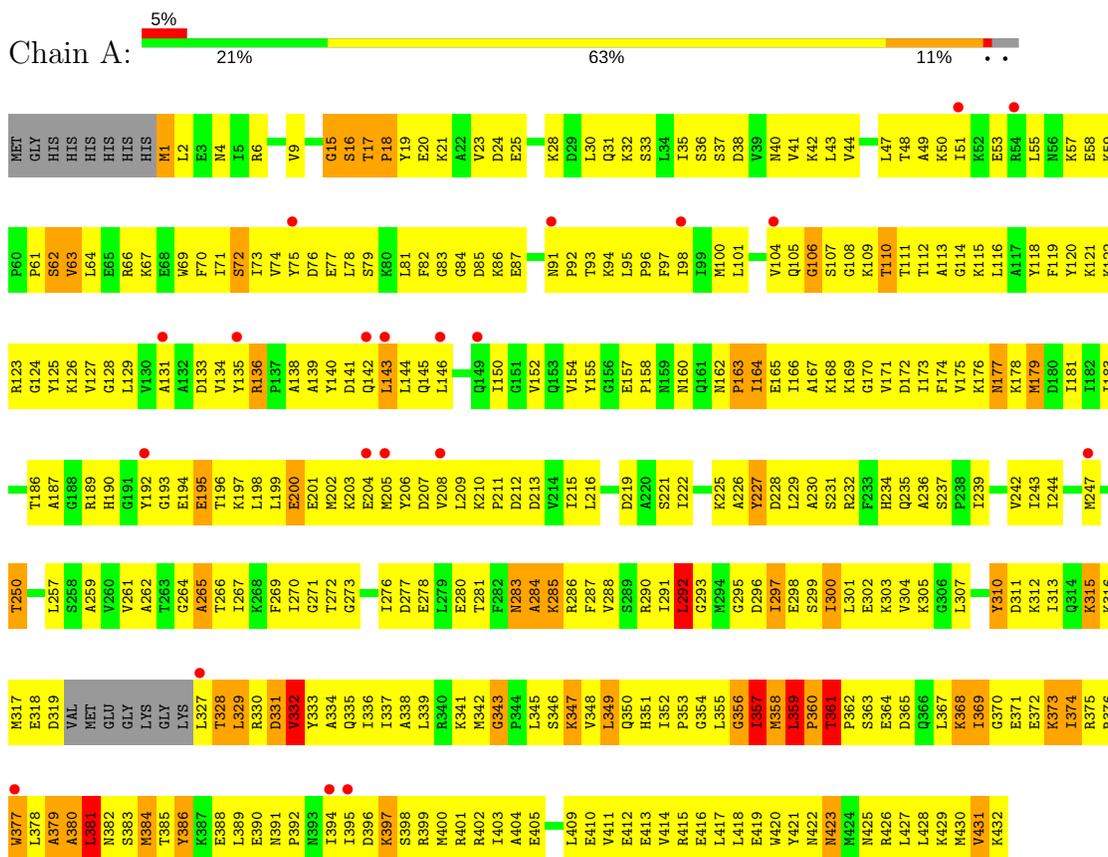
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	EXPRESSION TAG	UNP Q97ZE7
A	-6	GLY	-	EXPRESSION TAG	UNP Q97ZE7
A	-5	HIS	-	EXPRESSION TAG	UNP Q97ZE7
A	-4	HIS	-	EXPRESSION TAG	UNP Q97ZE7
A	-3	HIS	-	EXPRESSION TAG	UNP Q97ZE7
A	-2	HIS	-	EXPRESSION TAG	UNP Q97ZE7
A	-1	HIS	-	EXPRESSION TAG	UNP Q97ZE7
A	0	HIS	-	EXPRESSION TAG	UNP Q97ZE7
B	-7	MET	-	EXPRESSION TAG	UNP Q97ZE7
B	-6	GLY	-	EXPRESSION TAG	UNP Q97ZE7
B	-5	HIS	-	EXPRESSION TAG	UNP Q97ZE7
B	-4	HIS	-	EXPRESSION TAG	UNP Q97ZE7
B	-3	HIS	-	EXPRESSION TAG	UNP Q97ZE7
B	-2	HIS	-	EXPRESSION TAG	UNP Q97ZE7
B	-1	HIS	-	EXPRESSION TAG	UNP Q97ZE7
B	0	HIS	-	EXPRESSION TAG	UNP Q97ZE7

3 Residue-property plots i

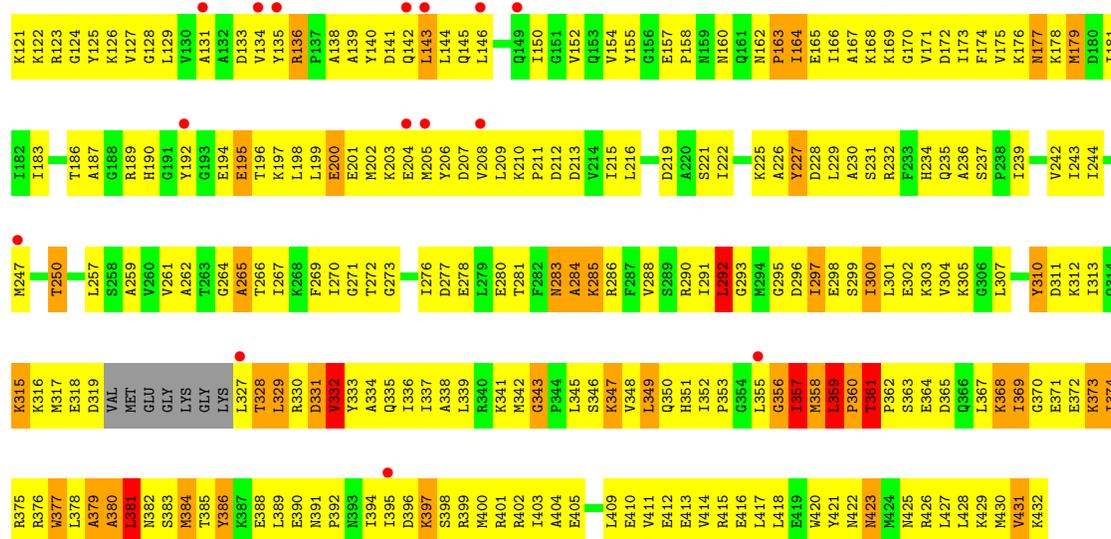
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

- Molecule 1: Signal recognition 54 kDa protein



- Molecule 1: Signal recognition 54 kDa protein





4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	197.91Å 197.91Å 64.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 4.00 38.81 – 4.00	Depositor EDS
% Data completeness (in resolution range)	89.0 (40.00-4.00) 97.9 (38.81-4.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 3.99Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.313 , 0.383 0.402 , 0.404	Depositor DCC
R_{free} test set	725 reflections (6.88%)	DCC
Wilson B-factor (Å ²)	171.1	Xtrriage
Anisotropy	0.085	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 26.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.428 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	6698	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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

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	0.71	5/3399 (0.1%)	0.88	4/4569 (0.1%)
1	B	0.71	5/3399 (0.1%)	0.88	4/4569 (0.1%)
All	All	0.71	10/6798 (0.1%)	0.88	8/9138 (0.1%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	361	THR	CB-CG2	-6.78	1.29	1.52
1	B	361	THR	CB-CG2	-6.78	1.29	1.52
1	B	227	TYR	CD2-CE2	-5.99	1.30	1.39
1	A	227	TYR	CD2-CE2	-5.96	1.30	1.39
1	A	361	THR	CA-CB	5.92	1.68	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	292	LEU	CA-CB-CG	-5.79	101.99	115.30
1	B	292	LEU	CA-CB-CG	-5.77	102.03	115.30
1	B	361	THR	N-CA-CB	5.21	120.20	110.30
1	A	361	THR	N-CA-CB	5.20	120.19	110.30
1	B	332	VAL	N-CA-C	-5.16	97.06	111.00

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	3349	0	3486	713	43
1	B	3349	0	3486	708	43
All	All	6698	0	6972	1324	43

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 97.

The worst 5 of 1324 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:B:362:PRO:HD3	1:B:367:LEU:CD2	1.43	1.47
1:B:190:HIS:CD2	1:B:197:LYS:HD2	1.49	1.45
1:A:190:HIS:CD2	1:A:197:LYS:HD2	1.49	1.44
1:A:362:PRO:HD3	1:A:367:LEU:CD2	1.43	1.43
1:B:359:LEU:CG	1:B:360:PRO:HD3	1.49	1.42

The worst 5 of 43 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:360:PRO:CB	1:B:362:PRO:CA[8_454]	1.18	1.02
1:A:362:PRO:CA	1:B:360:PRO:CB[8_454]	1.24	0.96
1:A:200:GLU:CB	1:B:203:LYS:CB[6_555]	1.41	0.79
1:A:203:LYS:CB	1:B:200:GLU:CB[6_555]	1.45	0.75
1:A:360:PRO:CB	1:B:362:PRO:CB[8_454]	1.57	0.63

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	421/440 (96%)	294 (70%)	87 (21%)	40 (10%)	1 13
1	B	421/440 (96%)	293 (70%)	88 (21%)	40 (10%)	1 13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	842/880 (96%)	587 (70%)	175 (21%)	80 (10%)	1 13

5 of 80 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	VAL
1	A	236	ALA
1	A	265	ALA
1	A	332	VAL
1	A	343	GLY

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	365/377 (97%)	340 (93%)	25 (7%)	18 55
1	B	365/377 (97%)	340 (93%)	25 (7%)	18 55
All	All	730/754 (97%)	680 (93%)	50 (7%)	18 55

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	384	MET
1	B	17	THR
1	B	381	LEU
1	A	386	TYR
1	B	1	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	350	GLN
1	B	31	GLN
1	B	350	GLN

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Mol	Chain	Res	Type
1	A	351	HIS
1	B	4	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 carbohydrates 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	425/440 (96%)	0.31	21 (4%) 30 24	80, 85, 85, 85	0
1	B	425/440 (96%)	0.26	21 (4%) 30 24	80, 85, 85, 85	0
All	All	850/880 (96%)	0.29	42 (4%) 30 24	80, 85, 85, 85	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	192	TYR	5.4
1	A	142	GLN	5.2
1	B	142	GLN	4.7
1	A	205	MET	4.7
1	B	192	TYR	4.6

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.