



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2PZZ
Title : 2.2 Å resolution crystal structure of UPF0201 protein from *Methanococcus jannaschii*
Authors : Rao, K.N.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2007-05-18
Resolution : 2.20 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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

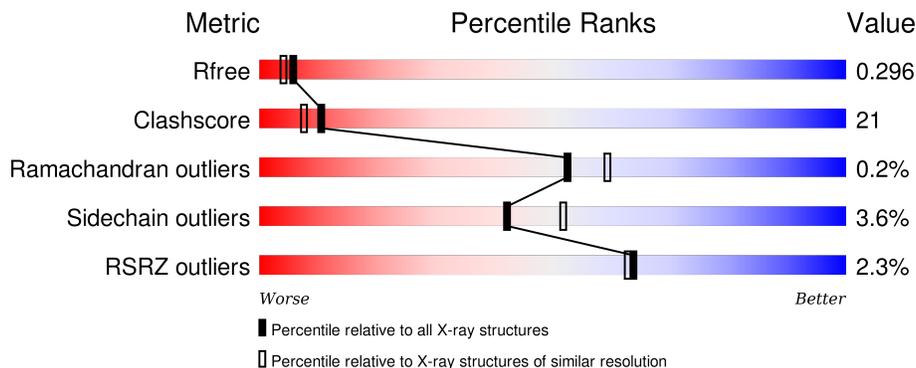
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	147	 66% 23% 10%
1	B	147	 56% 27% 16%
1	C	147	 44% 31% 22%
1	D	147	 44% 31% 24%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3926 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 UPF0201 protein MJ1564.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	133	1056	683	175	195	3	0	0	0
1	B	124	990	642	161	184	3	0	0	0
1	C	114	912	596	147	167	2	0	0	0
1	D	111	885	580	144	159	2	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	CLONING ARTIFACT	UNP Q58959
A	2	LEU	-	CLONING ARTIFACT	UNP Q58959
A	69	MSE	MET	MODIFIED RESIDUE	UNP Q58959
A	75	MSE	MET	MODIFIED RESIDUE	UNP Q58959
A	117	MSE	MET	MODIFIED RESIDUE	UNP Q58959
A	141	GLY	-	CLONING ARTIFACT	UNP Q58959
A	142	HIS	-	CLONING ARTIFACT	UNP Q58959
A	143	HIS	-	CLONING ARTIFACT	UNP Q58959
A	144	HIS	-	CLONING ARTIFACT	UNP Q58959
A	145	HIS	-	CLONING ARTIFACT	UNP Q58959
A	146	HIS	-	CLONING ARTIFACT	UNP Q58959
A	147	HIS	-	CLONING ARTIFACT	UNP Q58959
B	1	SER	-	CLONING ARTIFACT	UNP Q58959
B	2	LEU	-	CLONING ARTIFACT	UNP Q58959
B	69	MSE	MET	MODIFIED RESIDUE	UNP Q58959
B	75	MSE	MET	MODIFIED RESIDUE	UNP Q58959
B	117	MSE	MET	MODIFIED RESIDUE	UNP Q58959
B	141	GLY	-	CLONING ARTIFACT	UNP Q58959
B	142	HIS	-	CLONING ARTIFACT	UNP Q58959
B	143	HIS	-	CLONING ARTIFACT	UNP Q58959
B	144	HIS	-	CLONING ARTIFACT	UNP Q58959

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Chain	Residue	Modelled	Actual	Comment	Reference
B	145	HIS	-	CLONING ARTIFACT	UNP Q58959
B	146	HIS	-	CLONING ARTIFACT	UNP Q58959
B	147	HIS	-	CLONING ARTIFACT	UNP Q58959
C	1	SER	-	CLONING ARTIFACT	UNP Q58959
C	2	LEU	-	CLONING ARTIFACT	UNP Q58959
C	69	MSE	MET	MODIFIED RESIDUE	UNP Q58959
C	75	MSE	MET	MODIFIED RESIDUE	UNP Q58959
C	117	MSE	MET	MODIFIED RESIDUE	UNP Q58959
C	141	GLY	-	CLONING ARTIFACT	UNP Q58959
C	142	HIS	-	CLONING ARTIFACT	UNP Q58959
C	143	HIS	-	CLONING ARTIFACT	UNP Q58959
C	144	HIS	-	CLONING ARTIFACT	UNP Q58959
C	145	HIS	-	CLONING ARTIFACT	UNP Q58959
C	146	HIS	-	CLONING ARTIFACT	UNP Q58959
C	147	HIS	-	CLONING ARTIFACT	UNP Q58959
D	1	SER	-	CLONING ARTIFACT	UNP Q58959
D	2	LEU	-	CLONING ARTIFACT	UNP Q58959
D	69	MSE	MET	MODIFIED RESIDUE	UNP Q58959
D	75	MSE	MET	MODIFIED RESIDUE	UNP Q58959
D	117	MSE	MET	MODIFIED RESIDUE	UNP Q58959
D	141	GLY	-	CLONING ARTIFACT	UNP Q58959
D	142	HIS	-	CLONING ARTIFACT	UNP Q58959
D	143	HIS	-	CLONING ARTIFACT	UNP Q58959
D	144	HIS	-	CLONING ARTIFACT	UNP Q58959
D	145	HIS	-	CLONING ARTIFACT	UNP Q58959
D	146	HIS	-	CLONING ARTIFACT	UNP Q58959
D	147	HIS	-	CLONING ARTIFACT	UNP Q58959

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	28	Total O 28 28	0	0
2	B	27	Total O 27 27	0	0
2	C	12	Total O 12 12	0	0
2	D	16	Total O 16 16	0	0

Q87	Y94	Y95	F96	D97	ILE	ASP	THR	HIS	G102	L109	ALA	ASP	GLU	ASN	GLU	ASP	ILE	PRO	LYS	I119	I120	K121	D122	I123	A124	P125	ARG	THR	LYS	GLY	GLY	VAL	ILE	ILE	ASN	GLU	ASP	GLU	LEU	GLU	GLU	GLY	HIS	HIS	HIS	HIS	HIS	HIS
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	46.52Å 50.15Å 73.82Å 70.34° 72.61° 84.30°	Depositor
Resolution (Å)	47.23 – 2.20 47.23 – 2.19	Depositor EDS
% Data completeness (in resolution range)	95.8 (47.23-2.20) 85.5 (47.23-2.19)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.36 (at 2.20Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.249 , 0.299 0.249 , 0.296	Depositor DCC
R_{free} test set	864 reflections (2.96%)	DCC
Wilson B-factor (Å ²)	37.0	Xtrriage
Anisotropy	0.217	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.6	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Outliers	0 of 30128 reflections	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3926	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.40	0/1067	0.65	0/1424
1	B	0.40	0/1001	0.61	0/1336
1	C	0.39	0/921	0.62	0/1227
1	D	0.39	0/894	0.58	0/1190
All	All	0.39	0/3883	0.61	0/5177

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

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	1056	0	1118	36	0
1	B	990	0	1042	38	0
1	C	912	0	967	62	0
1	D	885	0	947	52	0
2	A	28	0	0	0	0
2	B	27	0	0	0	0
2	C	12	0	0	1	0
2	D	16	0	0	1	0
All	All	3926	0	4074	169	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 21.

The worst 5 of 169 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:C:51:VAL:HG23	1:C:55:LYS:HE3	1.58	0.83
1:D:51:VAL:HG23	1:D:55:LYS:HE3	1.62	0.82
1:B:13:THR:H	1:D:87:GLN:HE22	1.26	0.82
1:A:128:LYS:HG3	1:A:133:ILE:HD11	1.62	0.81
1:D:61:GLN:HE22	1:D:94:VAL:H	1.27	0.81

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	131/147 (89%)	124 (95%)	7 (5%)	0	100	100
1	B	122/147 (83%)	118 (97%)	4 (3%)	0	100	100
1	C	108/147 (74%)	105 (97%)	3 (3%)	0	100	100
1	D	105/147 (71%)	101 (96%)	3 (3%)	1 (1%)	19	16
All	All	466/588 (79%)	448 (96%)	17 (4%)	1 (0%)	52	59

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	77	GLU

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	114/124 (92%)	110 (96%)	4 (4%)	43	53
1	B	107/124 (86%)	102 (95%)	5 (5%)	32	39
1	C	98/124 (79%)	93 (95%)	5 (5%)	29	34
1	D	95/124 (77%)	94 (99%)	1 (1%)	80	89
All	All	414/496 (84%)	399 (96%)	15 (4%)	42	52

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	77	GLU
1	B	113	ASN
1	C	97	ASP
1	B	68	ARG
1	C	68	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	113	ASN
1	D	87	GLN
1	C	87	GLN
1	B	39	ASN
1	C	61	GLN

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	130/147 (88%)	0.23	1 (0%) 87 87	24, 39, 57, 67	0
1	B	121/147 (82%)	0.30	2 (1%) 73 72	29, 43, 53, 66	0
1	C	112/147 (76%)	0.45	5 (4%) 37 36	29, 48, 69, 71	0
1	D	109/147 (74%)	0.38	3 (2%) 56 55	36, 50, 66, 74	0
All	All	472/588 (80%)	0.33	11 (2%) 64 63	24, 44, 66, 74	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	100	THR	4.8
1	C	2	LEU	2.8
1	C	35	ILE	2.5
1	D	73	LYS	2.4
1	B	97	ASP	2.4

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.