



# wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 02:26 PM GMT

PDB ID : 1O7X  
Title : CITRATE SYNTHASE FROM SULFOLOBUS SOLFATARICUS  
Authors : Bell, G.S.; Russell, R.J.M.; Connaris, H.; Hough, D.W.; Danson, M.J.; Taylor, G.L.  
Deposited on : 2002-11-19  
Resolution : 2.70 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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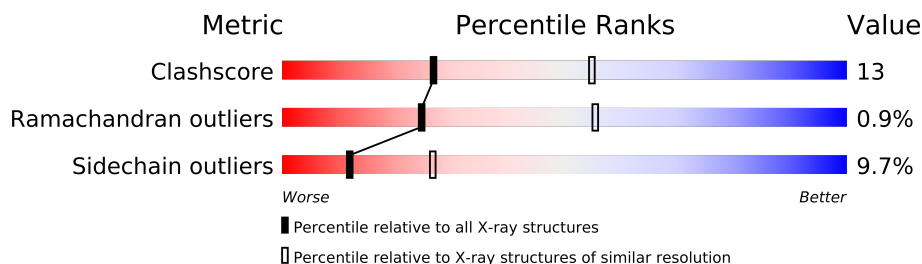
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.70 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))
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	377	
1	B	377	
1	C	377	
1	D	377	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 11738 atoms, of which 0 are hydrogen and 0 are deuterium.

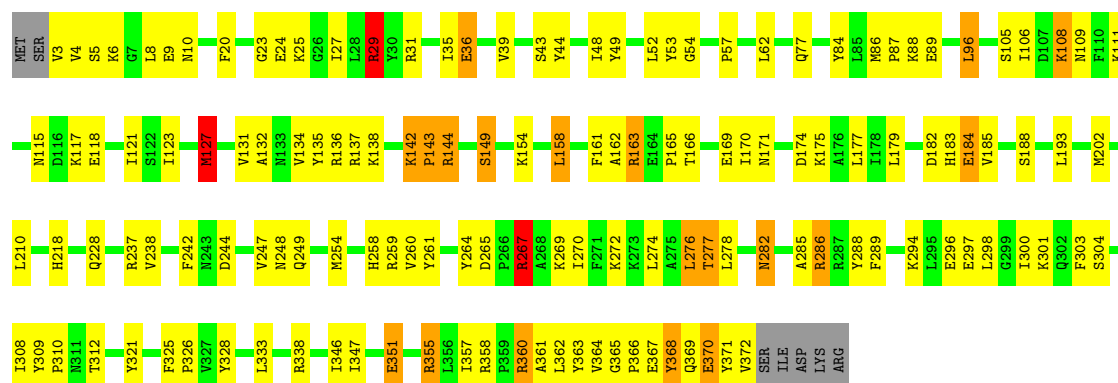
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CITRATE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	0	0
			2935	1897	487	544	7			
1	B	366	Total	C	N	O	S	0	0	0
			2926	1892	485	542	7			
1	C	370	Total	C	N	O	S	0	0	0
			2963	1916	490	550	7			
1	D	365	Total	C	N	O	S	0	0	0
			2914	1883	484	540	7			



## Chain C:



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.34Å 97.86Å 119.33Å 90.00° 107.60° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	88.6 (20.00-2.70)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.208 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11738	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

## 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	0.47	0/2998	1.31	19/4055 (0.5%)
1	B	0.53	0/2989	1.45	29/4043 (0.7%)
1	C	0.48	0/3027	1.36	22/4095 (0.5%)
1	D	0.52	0/2976	1.44	32/4025 (0.8%)
All	All	0.50	0/11990	1.39	102/16218 (0.6%)

There are no bond length outliers.

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	355	ARG	NE-CZ-NH2	-12.70	113.95	120.30
1	D	252	ARG	NE-CZ-NH1	12.03	126.32	120.30
1	B	281	ARG	CD-NE-CZ	11.05	139.08	123.60
1	A	267	ARG	CD-NE-CZ	10.93	138.90	123.60
1	B	338	ARG	NE-CZ-NH1	10.67	125.64	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2935	0	2966	97	328
1	B	2926	0	2958	70	2668

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2963	0	2990	91	240
1	D	2914	0	2949	84	2525
All	All	11738	0	11863	309	2931

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 13.

The worst 5 of 309 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:358:ARG:HD2	1:B:259:ARG:NH1	1.81	0.96
1:D:35:ILE:HD11	1:D:266:PRO:HB2	1.55	0.88
1:A:358:ARG:NH1	1:B:259:ARG:HD2	1.89	0.87
1:A:358:ARG:HD2	1:B:259:ARG:HH11	1.40	0.87
1:C:258:HIS:HD2	1:C:260:VAL:H	1.20	0.86

The worst 5 of 2931 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	Distance(Å)	Clash(Å)
1:B:312:THR:OG1	1:D:28:LEU:CB[2_546]	0.15	2.05
1:B:44:TYR:N	1:D:31:ARG:NH2[2_546]	0.18	2.02
1:A:365:GLY:C	1:D:152:PHE:O[2_546]	0.21	1.99
1:B:48:ILE:N	1:D:49:TYR:O[2_546]	0.22	1.98
1:B:49:TYR:CB	1:D:53:TYR:CE1[2_546]	0.24	1.96

## 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	365/377 (97%)	338 (93%)	24 (7%)	3 (1%)	27 58
1	B	364/377 (97%)	343 (94%)	18 (5%)	3 (1%)	27 58
1	C	368/377 (98%)	344 (94%)	22 (6%)	2 (0%)	38 70
1	D	363/377 (96%)	344 (95%)	14 (4%)	5 (1%)	16 41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1460/1508 (97%)	1369 (94%)	78 (5%)	13 (1%)	25 55

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	247	VAL
1	B	247	VAL
1	D	233	GLY
1	B	109	ASN
1	D	238	VAL

### 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	309/319 (97%)	277 (90%)	32 (10%)	10 23
1	B	308/319 (97%)	284 (92%)	24 (8%)	18 40
1	C	312/319 (98%)	288 (92%)	24 (8%)	18 40
1	D	307/319 (96%)	267 (87%)	40 (13%)	6 15
All	All	1236/1276 (97%)	1116 (90%)	120 (10%)	12 27

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	286	ARG
1	C	111	LYS
1	D	294	LYS
1	B	290	GLU
1	C	24	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	354	HIS
1	C	115	ASN

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Mol	Chain	Res	Type
1	D	293	GLN
1	C	77	GLN
1	C	183	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.