



wwPDB X-ray Structure Validation Summary Report ⓘ

May 22, 2018 – 10:32 AM EDT

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

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031021

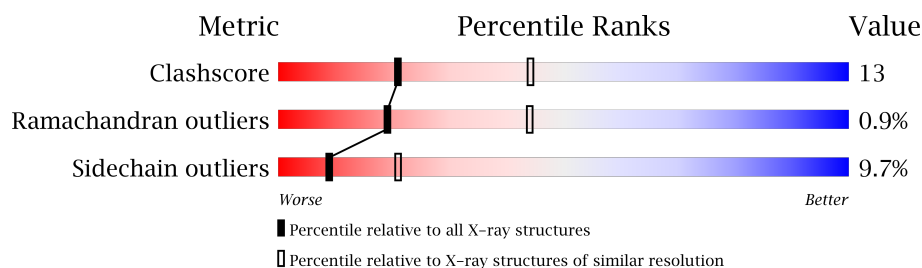
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	122126	2756 (2.70-2.70)
Ramachandran outliers	120053	2716 (2.70-2.70)
Sidechain outliers	120020	2716 (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 ≥ 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 $\leq 5\%$.

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

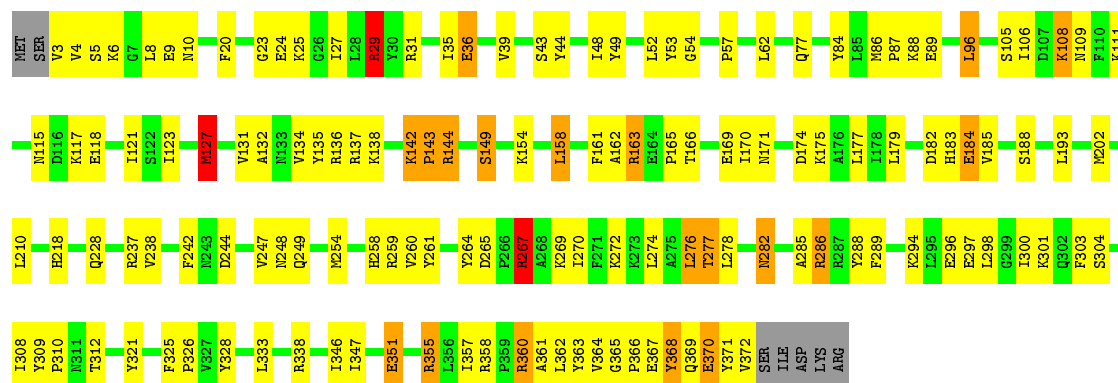
There is only 1 type of molecule in this entry. The entry contains 11738 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 CITRATE SYNTHASE.

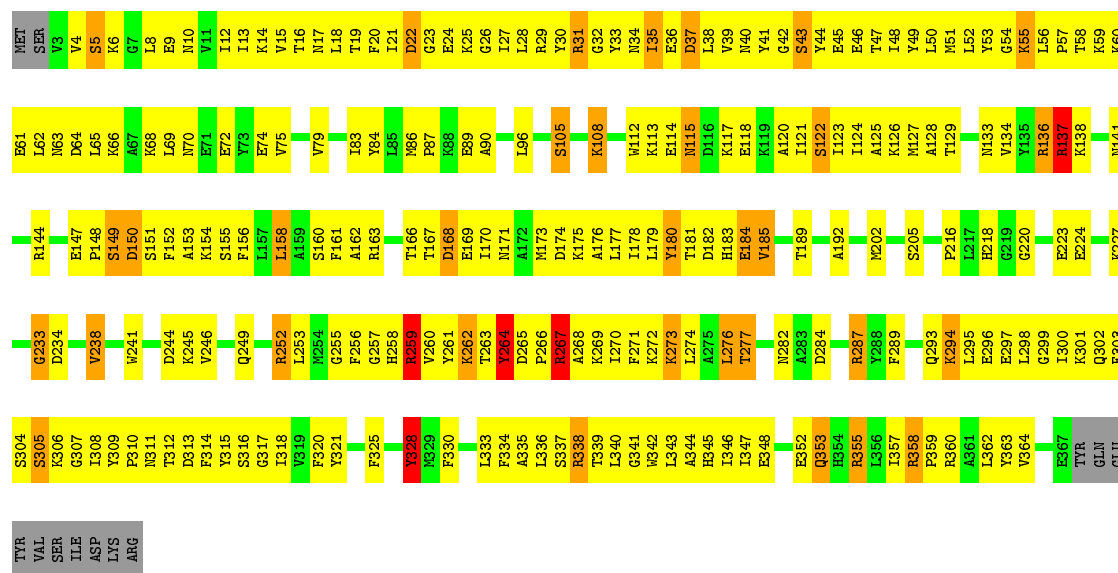
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	0	0
			2935	1897	487	544	7			
1	B	366	Total	C	N	O	S	0	0	0
			2926	1892	485	542	7			
1	C	370	Total	C	N	O	S	0	0	0
			2963	1916	490	550	7			
1	D	365	Total	C	N	O	S	0	0	0
			2914	1883	484	540	7			

Chain C:  60% 32% 5% ..



• Molecule 1: CITRATE SYNTHASE

Chain D:  34% 53% 9% ..



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.34 Å 97.86 Å 119.33 Å 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 ²)	37.0	wwPDB-VP

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	0.47	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 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	2935	0	2966	97	328
1	B	2926	0	2958	70	2668
1	C	2963	0	2990	91	240
1	D	2914	0	2949	84	2525

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	11738	0	11863	309	2931

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 13.

The worst 5 of 309 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: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	Interatomic distance (Å)	Clash overlap (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%)	21	47
1	B	364/377 (97%)	343 (94%)	18 (5%)	3 (1%)	21	47

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	368/377 (98%)	344 (94%)	22 (6%)	2 (0%)	31 58
1	D	363/377 (96%)	344 (95%)	14 (4%)	5 (1%)	12 31
All	All	1460/1508 (97%)	1369 (94%)	78 (5%)	13 (1%)	19 44

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%)	8 17
1	B	308/319 (97%)	284 (92%)	24 (8%)	14 32
1	C	312/319 (98%)	288 (92%)	24 (8%)	14 33
1	D	307/319 (96%)	267 (87%)	40 (13%)	4 11
All	All	1236/1276 (97%)	1116 (90%)	120 (10%)	9 21

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
1	D	293	GLN
1	C	77	GLN
1	C	183	HIS

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.