



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 12:33 am BST

PDB ID : 1D8I
Title : X-RAY CRYSTAL STRUCTURE OF YEAST RNA TRIPHOSPHATASE IN COMPLEX WITH A SULFATE ION.
Authors : Lima, C.D.; Wang, L.K.; Shuman, S.
Deposited on : 1999-10-24
Resolution : 2.05 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

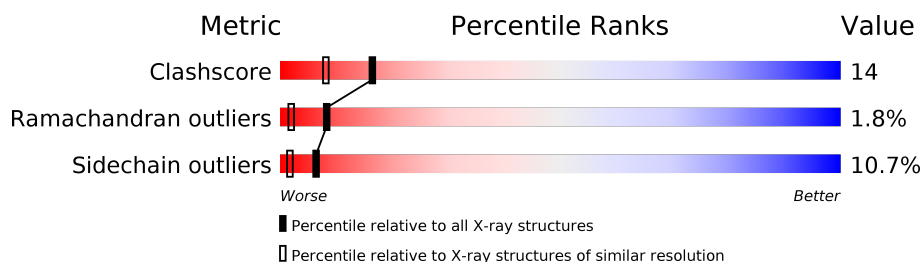
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)

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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	311	
1	B	311	
1	C	311	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7329 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 MRNA TRIPHOSPHATASE CET1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	0	0
			2295	1457	393	440	5			
1	B	288	Total	C	N	O	S	0	0	0
			2295	1457	393	440	5			
1	C	288	Total	C	N	O	S	0	0	0
			2295	1457	393	440	5			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	242	ARG	LYS	CONFLICT	UNP O13297
B	242	ARG	LYS	CONFLICT	UNP O13297
C	242	ARG	LYS	CONFLICT	UNP O13297

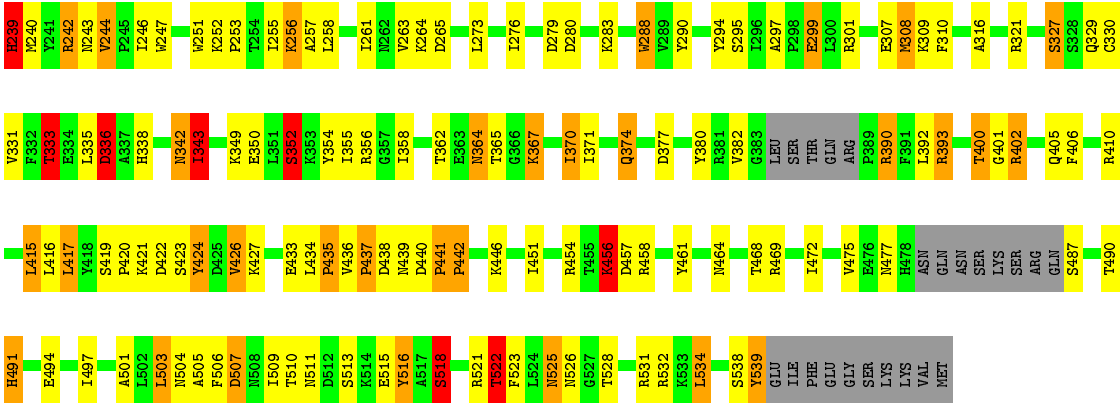
- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	121	Total	O	0	0
			121	121		
3	B	134	Total	O	0	0
			134	134		
3	C	159	Total	O	0	0
			159	159		



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	121.36Å 116.09Å 82.31Å 90.00° 110.25° 90.00°	Depositor
Resolution (Å)	25.00 – 2.05	Depositor
% Data completeness (in resolution range)	82.2 (25.00-2.05)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.203 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7329	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.99	2/2342 (0.1%)	2.17	84/3178 (2.6%)
1	B	0.93	1/2342 (0.0%)	2.00	72/3178 (2.3%)
1	C	1.00	6/2342 (0.3%)	2.08	85/3178 (2.7%)
All	All	0.98	9/7026 (0.1%)	2.08	241/9534 (2.5%)

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	18
1	B	0	15
1	C	0	19
All	All	0	52

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	332	PHE	N-CA	-10.36	1.25	1.46
1	C	330	CYS	CB-SG	-9.36	1.66	1.82
1	C	247	TRP	NE1-CE2	-6.76	1.28	1.37
1	C	295	SER	CB-OG	6.32	1.50	1.42
1	C	419	SER	CB-OG	5.82	1.49	1.42

The worst 5 of 241 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	321	ARG	NE-CZ-NH1	-20.80	109.90	120.30
1	B	531	ARG	NE-CZ-NH2	18.95	129.78	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	521	ARG	NE-CZ-NH1	-17.89	111.35	120.30
1	A	321	ARG	NE-CZ-NH2	17.59	129.10	120.30
1	A	458	ARG	NE-CZ-NH1	-16.57	112.02	120.30

There are no chirality outliers.

5 of 52 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	MET	Mainchain
1	A	242	ARG	Mainchain
1	A	243	ASN	Mainchain
1	A	273	LEU	Mainchain
1	A	294	TYR	Mainchain

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	2295	0	2274	74	0
1	B	2295	0	2273	66	0
1	C	2295	0	2274	60	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
2	C	10	0	0	0	0
3	A	121	0	0	18	0
3	B	134	0	0	16	1
3	C	159	0	0	8	1
All	All	7329	0	6821	197	1

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 14.

The worst 5 of 197 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:441:PRO:HB2	1:A:442:PRO:HD3	1.47	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:441:PRO:HB2	1:C:442:PRO:HD3	1.51	0.91
1:C:441:PRO:HB2	1:C:442:PRO:CD	2.04	0.86
1:C:538:SER:O	1:C:539:TYR:HB3	1.74	0.85
1:A:263:VAL:HA	3:A:701:HOH:O	1.77	0.84

All (1) 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)
3:B:723:HOH:O	3:C:662:HOH:O[2_657]	2.13	0.07

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	282/311 (91%)	260 (92%)	18 (6%)	4 (1%)	11	3
1	B	282/311 (91%)	264 (94%)	13 (5%)	5 (2%)	8	2
1	C	282/311 (91%)	260 (92%)	16 (6%)	6 (2%)	7	1
All	All	846/933 (91%)	784 (93%)	47 (6%)	15 (2%)	8	2

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	401	GLY
1	A	437	PRO
1	B	401	GLY
1	B	437	PRO
1	C	401	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	259/291 (89%)	232 (90%)	27 (10%)	7	2
1	B	259/291 (89%)	230 (89%)	29 (11%)	6	1
1	C	259/291 (89%)	232 (90%)	27 (10%)	7	2
All	All	777/873 (89%)	694 (89%)	83 (11%)	6	2

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	307	GLU
1	B	423	SER
1	C	487	SER
1	B	334	GLU
1	B	363	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	342	ASN
1	B	364	ASN
1	C	342	ASN
1	A	511	ASN
1	B	243	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](#)

6 ligands are 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	SO4	B	605	-	4,4,4	0.95	0	6,6,6	1.28	1 (16%)
2	SO4	B	602	-	4,4,4	0.63	0	6,6,6	0.26	0
2	SO4	A	601	-	4,4,4	0.63	0	6,6,6	0.24	0
2	SO4	C	606	-	4,4,4	0.39	0	6,6,6	0.61	0
2	SO4	C	603	-	4,4,4	0.57	0	6,6,6	0.47	0
2	SO4	A	604	-	4,4,4	0.64	0	6,6,6	1.03	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	605	SO4	O4-S-O2	2.42	121.92	109.31

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 ⓘ

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.