



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 04:59 PM UTC

PDB ID : 117E / pdb_0000117e
Title : THE R78K AND D117E ACTIVE SITE VARIANTS OF SACCHAROMYCES CEREVISIAE SOLUBLE INORGANIC PYROPHOSPHATASE: STRUCTURAL STUDIES AND MECHANISTIC IMPLICATIONS
Authors : Tuominen, V.; Heikinheimo, P.; Kajander, T.; Torkkel, T.; Hyytia, T.; Kapyla, J.; Lahti, R.; Cooperman, B.S.; Goldman, A.
Deposited on : 1998-09-15
Resolution : 2.15 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

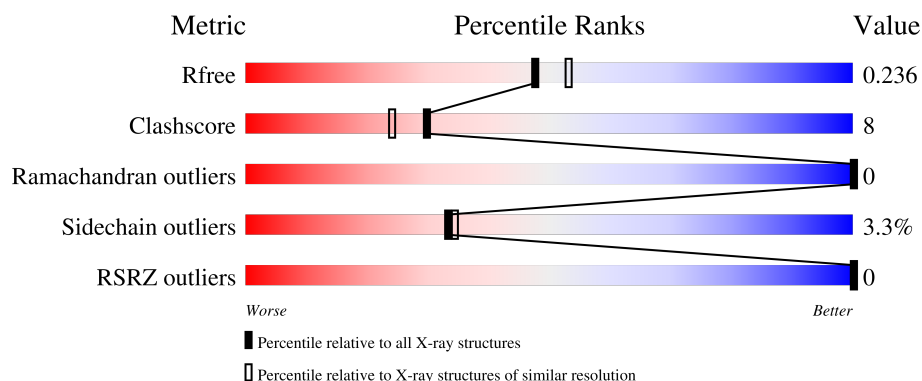
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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 of 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 $\leq 5\%$. 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	286	 76% 20% ..
1	B	286	 77% 20% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4943 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 PROTEIN (INORGANIC PYROPHOSPHATASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	282	Total	C	N	O	S	0	0	0
			2232	1435	363	431	3			
1	B	282	Total	C	N	O	S	0	0	0
			2234	1437	367	427	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	117	GLU	ASP	engineered mutation	UNP P00817
B	1117	GLU	ASP	engineered mutation	UNP P00817

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Mn	0	0
			4	4		
2	B	4	Total	Mn	0	0
			4	4		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	216	Total	O	0	0
			216	216		
4	B	238	Total	O	0	0
			238	238		

i

- Molecule 1: PROTEIN (INORGANIC PYROPHOSPHATASE)

[illegible]

A1144	A1145	W1153	K1154	W1155	A1156	A1157	I1158	A1165	P1166	I1171	E1187	R1190	I1191	I1194	P1195	K1198	P1199	E1200	N1201	Q1202	P1203	K1220	W1226	L1247	I1261	L1266	K1267	K1274	D1277	K1278	I1282	SR	GLY	SR	VAL					
T1001	Y1002	I1007	G1008	A1009	K1016	Y1017	Y1018	K1021	F1029	H1030	A1036	W1044	P1050	L1057	T1060	T1064	L1065	N1066	P1067	I1068	I1069	Q1070	R1078	P1103	H1107	P1108	E1109	T1110	K1111	N1116	L1122	E1126	T1127	I1128	A1129	Q1133	Q1136	G1141	T1142	W1143

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.40Å 102.80Å 116.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.15 8.00 – 2.15	Depositor EDS
% Data completeness (in resolution range)	87.0 (8.00-2.15) 85.1 (8.00-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.62 (at 2.11Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.182 , 0.240 0.181 , 0.236	Depositor DCC
R_{free} test set	1807 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	8.1	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.49 , 75.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4943	wwPDB-VP
Average B, all atoms (Å ²)	9.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MN, PO4

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	0/2290	0.92	10/3119 (0.3%)
1	B	0.49	0/2292	0.89	7/3120 (0.2%)
All	All	0.48	0/4582	0.91	17/6239 (0.3%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1036	ALA	N-CA-C	-7.13	102.55	112.45
1	B	1171	ILE	N-CA-C	6.97	117.68	110.36
1	A	171	ILE	N-CA-C	6.69	118.25	110.62
1	B	1278	LYS	N-CA-C	6.61	120.07	110.42
1	B	1247	LEU	CA-C-N	6.53	126.22	119.56

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	2232	0	2182	37	0
1	B	2234	0	2193	39	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	10	0	0	0	0
3	B	5	0	0	0	0
4	A	216	0	0	0	0
4	B	238	0	0	1	0
All	All	4943	0	4375	75	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 8.

The worst 5 of 75 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:1001:THR:N	1:B:1021:LYS:HZ2	1.85	0.73
1:A:141:GLY:HA3	1:A:171:ILE:HD13	1.74	0.69
1:B:1141:GLY:HA3	1:B:1171:ILE:HD13	1.76	0.67
1:A:44:ASN:ND2	1:A:136:GLN:HE21	1.92	0.66
1:B:1007:ILE:HB	1:B:1016:LYS:HB2	1.81	0.62

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	280/286 (98%)	273 (98%)	7 (2%)	0	100	100
1	B	280/286 (98%)	273 (98%)	7 (2%)	0	100	100
All	All	560/572 (98%)	546 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	240/248 (97%)	231 (96%)	9 (4%)	29	29
1	B	240/248 (97%)	233 (97%)	7 (3%)	37	39
All	All	480/496 (97%)	464 (97%)	16 (3%)	33	34

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1220	LYS
1	B	1198	LYS
1	A	267	LYS
1	B	1158	ILE
1	A	233	LYS

Sometimes 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	1030	HIS
1	B	1044	ASN
1	A	54	ASN
1	A	98	GLN
1	A	161	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 8 are monoatomic - leaving 3 for Mogul analysis.

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	$\# Z > 2$
3	PO4	A	3001	2	4,4,4	0.91	0	6,6,6	0.73	0
3	PO4	B	3004	2	4,4,4	0.80	0	6,6,6	0.67	0
3	PO4	A	3002	2	4,4,4	0.79	0	6,6,6	0.67	0

There are no bond length outliers.

There are no bond angle outliers.

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 [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	282/286 (98%)	-0.70	0 100 100	3, 8, 15, 21	0
1	B	282/286 (98%)	-0.67	0 100 100	3, 8, 16, 20	0
All	All	564/572 (98%)	-0.68	0 100 100	3, 8, 15, 21	0

There are no RSRZ outliers to report.

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MN	B	2008	1/1	0.96	0.03	8,8,8,8	0
2	MN	B	2007	1/1	0.97	0.04	14,14,14,14	0
2	MN	B	2006	1/1	0.97	0.03	6,6,6,6	0
3	PO4	A	3001	5/5	0.97	0.08	12,12,19,19	0
3	PO4	A	3002	5/5	0.97	0.08	4,6,11,11	0
2	MN	A	2001	1/1	0.98	0.02	7,7,7,7	0
3	PO4	B	3004	5/5	0.98	0.08	4,6,10,11	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MN	A	2004	1/1	0.99	0.02	6,6,6,6	0
2	MN	B	2005	1/1	0.99	0.01	6,6,6,6	0
2	MN	A	2002	1/1	0.99	0.03	10,10,10,10	0
2	MN	A	2003	1/1	0.99	0.03	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.