



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1XTM / pdb_00001xtm
Title : Crystal structure of the double mutant Y88H-P104H of a SOD-like protein from *Bacillus subtilis*.
Authors : Calderone, V.; Mangani, S.; Banci, L.; Benvenuti, M.; Bertini, I.; Fantoni, A.; Viezzoli, M.S.
Deposited on : 2004-10-22
Resolution : 1.60 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
Xtrriage (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

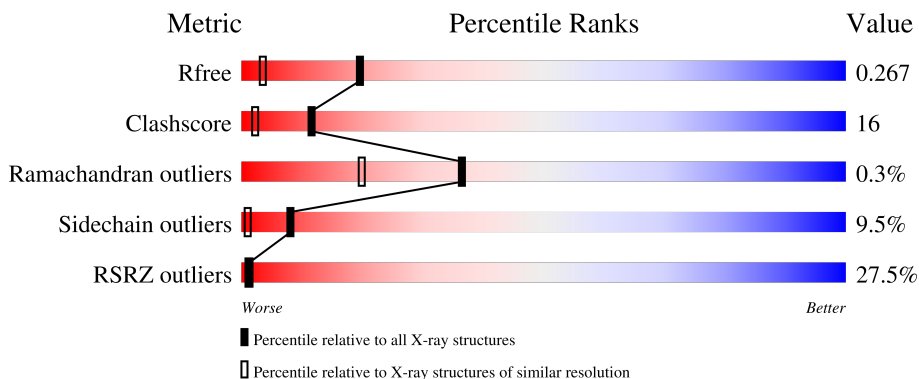
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	175	
1	B	175	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2507 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 Hypothetical superoxide dismutase-like protein yojM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	153	1140	705	206	225	4	0	0	0
1	A	152	1134	702	205	223	4	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	88	HIS	TYR	engineered mutation	UNP O31851
B	104	HIS	PRO	engineered mutation	UNP O31851
A	88	HIS	TYR	engineered mutation	UNP O31851
A	104	HIS	PRO	engineered mutation	UNP O31851

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cu	0	0
			1	1		
2	A	1	Total	Cu	0	0
			1	1		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	4	Total	Zn	0	0
			4	4		
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	142	Total 142	O 142	0	0
4	A	84	Total 84	O 84	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	52.46Å 104.35Å 58.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.60 – 1.60 25.60 – 1.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (25.60-1.60) 99.5 (25.60-1.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 1.60Å)	Xtrriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.253 , 0.266 0.253 , 0.267	Depositor DCC
R_{free} test set	6323 reflections (7.72%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtrriage
Anisotropy	0.495	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2507	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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: ZN, CU

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	1.78	3/1158 (0.3%)	1.39	7/1563 (0.4%)
1	B	1.29	2/1164 (0.2%)	1.34	14/1571 (0.9%)
All	All	1.55	5/2322 (0.2%)	1.37	21/3134 (0.7%)

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	2
1	B	0	3
All	All	0	5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	119	GLY	C-N	-43.04	0.76	1.33
1	A	120	HIS	C-N	32.74	1.78	1.33
1	B	143	PRO	C-N	23.16	1.66	1.33
1	B	144	ASP	C-N	12.75	1.50	1.33
1	A	121	HIS	C-O	-5.66	1.17	1.23

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	119	GLY	CA-C-N	19.01	147.71	120.71
1	A	119	GLY	C-N-CA	19.01	147.71	120.71
1	A	120	HIS	CA-C-O	16.94	139.82	121.19
1	A	119	GLY	O-C-N	-14.55	103.78	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	101	ALA	N-CA-C	13.93	129.37	112.38

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119	GLY	Peptide
1	A	132	ALA	Peptide
1	B	101	ALA	Peptide
1	B	102	GLY	Peptide
1	B	190	LEU	Peptide

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	1134	0	1074	47	0
1	B	1140	0	1081	24	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	4	0	0	0	0
4	A	84	0	0	7	0
4	B	142	0	0	3	0
All	All	2507	0	2155	71	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 16.

The worst 5 of 71 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:120:HIS:C	1:A:121:HIS:N	1.78	1.42
1:A:119:GLY:O	1:A:120:HIS:N	1.57	1.26
1:A:119:GLY:C	1:A:120:HIS:CA	2.14	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:GLY:CA	1:A:120:HIS:N	2.15	1.09
1:A:183:ARG:HG3	4:A:540:HOH:O	1.56	1.04

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	150/175 (86%)	136 (91%)	13 (9%)	1 (1%)	18 6
1	B	151/175 (86%)	141 (93%)	10 (7%)	0	100 100
All	All	301/350 (86%)	277 (92%)	23 (8%)	1 (0%)	36 20

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	133	ASP

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	120/143 (84%)	107 (89%)	13 (11%)	6 1
1	B	121/143 (85%)	111 (92%)	10 (8%)	10 1
All	All	241/286 (84%)	218 (90%)	23 (10%)	8 1

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	SER
1	A	108	LEU
1	A	100	SER
1	A	129	GLU
1	B	133	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	154	ASN
1	A	141	ASN
1	A	75	ASN
1	B	179	ASN
1	A	127	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	120:HIS	C	121:HIS	N	1.78
1	B	143:PRO	C	144:ASP	N	1.66
1	A	119:GLY	C	120:HIS	N	0.76

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	152/175 (86%)	2.08	70 (46%) 0 0	17, 32, 48, 51	0
1	B	153/175 (87%)	0.51	14 (9%) 14 14	11, 17, 30, 43	0
All	All	305/350 (87%)	1.29	84 (27%) 1 1	11, 25, 44, 51	0

The worst 5 of 84 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	102	GLY	8.0
1	A	101	ALA	5.5
1	A	160	GLY	5.1
1	B	65	ASP	4.9
1	A	156	LEU	4.6

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(\AA^2)	Q<0.9
3	ZN	B	505	1/1	0.86	0.08	26,26,26,26	1
2	CU	A	503	1/1	0.97	0.07	41,41,41,41	0
3	ZN	A	504	1/1	0.98	0.08	33,33,33,33	1
3	ZN	B	506	1/1	0.99	0.11	21,21,21,21	1
2	CU	B	500	1/1	0.99	0.03	23,23,23,23	0
3	ZN	B	502	1/1	1.00	0.08	21,21,21,21	0
3	ZN	B	501	1/1	1.00	0.07	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.