



Full wwPDB X-ray Structure Validation Report i

Oct 25, 2023 – 04:30 AM EDT

PDB ID : 2ZKY
Title : Crystal structure of human Cu-Zn superoxide dismutase mutant G93A
Authors : Yoshikawa, S.; Kukimoto-Niino, M.; Ito, K.; Shirouzu, M.; Urushitani, M.; Takahashi, R.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2008-03-31
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 i 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](#) ①) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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Mol	Chain	Length	Quality of chain			
1	F	159	%	80%	15%	..
1	G	159	3%	72%	23%	..
1	H	159		87%	8%	..
1	I	159	4%	81%	15%	.
1	J	159	%	82%	14%	..

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	66	Total O 66 66	0	0
3	E	60	Total O 60 60	0	0
3	F	69	Total O 69 69	0	0
3	G	21	Total O 21 21	0	0
3	H	42	Total O 42 42	0	0
3	I	28	Total O 28 28	0	0
3	J	34	Total O 34 34	0	0

5.5 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [\(i\)](#)

Of 10 ligands modelled in this entry, 10 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 [\(i\)](#)

There are no chain breaks in this entry.

