



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 5FTP / pdb_00005ftp
Title : sulfur SAD phasing of Cdc23Nterm: data collection with a tailored X- ray beam size at 2.69 Å wavelength (4.6 keV)
Authors : Cianci, M.; Groves, M.R.; Barford, D.; Schneider, T.R.
Deposited on : 2016-01-14
Resolution : 3.10 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

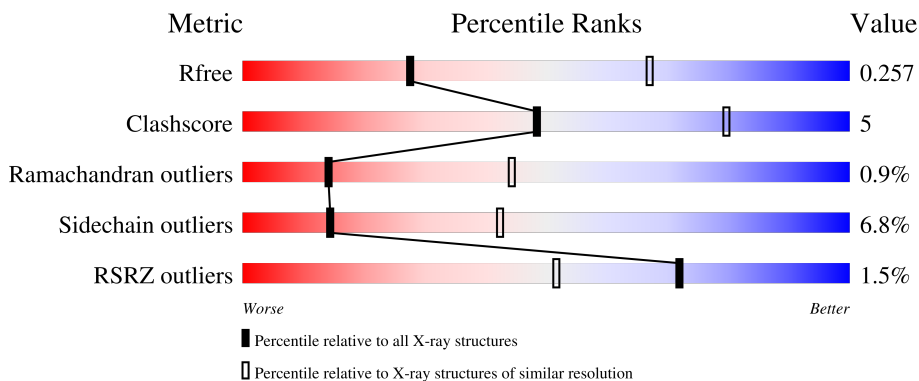
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	291	
1	B	291	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3866 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 ANAPHASE-PROMOTING COMPLEX SUBUNIT 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	230	1871	1207	307	348	9	0	0	0
1	B	242	1988	1280	328	371	9	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	MET	-	expression tag	UNP O94556
A	302	ALA	-	expression tag	UNP O94556
A	303	GLU	-	expression tag	UNP O94556
A	304	ASN	-	expression tag	UNP O94556
A	305	LEU	-	expression tag	UNP O94556
A	306	TYR	-	expression tag	UNP O94556
A	307	PHE	-	expression tag	UNP O94556
A	308	GLN	-	expression tag	UNP O94556
A	285	LEU	ASP	conflict	UNP O94556
B	18	MET	-	expression tag	UNP O94556
B	302	ALA	-	expression tag	UNP O94556
B	303	GLU	-	expression tag	UNP O94556
B	304	ASN	-	expression tag	UNP O94556
B	305	LEU	-	expression tag	UNP O94556
B	306	TYR	-	expression tag	UNP O94556
B	307	PHE	-	expression tag	UNP O94556
B	308	GLN	-	expression tag	UNP O94556
B	285	LEU	ASP	conflict	UNP O94556

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	O	0	0
			5	5		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	O	0	0
			2	2		

4 Data and refinement statistics i

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	61.25Å 61.25Å 151.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.25 – 3.10 61.25 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (61.25-3.10) 99.8 (61.25-3.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 3.13Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.187 , 0.260 0.198 , 0.257	Depositor DCC
R_{free} test set	510 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	62.5	Xtrriage
Anisotropy	0.010	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.069 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3866	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% 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](#)

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	0.65	0/1909	1.00	4/2577 (0.2%)
1	B	0.65	0/2028	1.00	2/2734 (0.1%)
All	All	0.65	0/3937	1.00	6/5311 (0.1%)

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	ARG	N-CA-C	10.62	125.98	112.92
1	B	232	SER	N-CA-C	-5.99	101.42	110.28
1	A	37	ARG	O-C-N	-5.47	115.77	122.34
1	A	40	VAL	N-CA-C	5.46	116.23	110.72
1	B	168	GLN	N-CA-C	-5.24	103.11	110.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	37	ARG	Peptide
1	B	234	HIS	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	1871	0	1870	22	0
1	B	1988	0	1981	22	0
2	A	5	0	0	0	0
2	B	2	0	0	0	0
All	All	3866	0	3851	42	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 5.

The worst 5 of 42 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:148:LEU:HD21	1:A:155:PHE:HE1	1.37	0.89
1:A:148:LEU:HD21	1:A:155:PHE:CE1	2.17	0.79
1:A:148:LEU:HD23	1:A:148:LEU:C	2.21	0.64
1:B:110:LEU:HD11	1:B:121:LEU:HD12	1.80	0.63
1:B:261:GLU:HA	1:B:264:ILE:CD1	2.32	0.59

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	224/291 (77%)	207 (92%)	16 (7%)	1 (0%)	30 61
1	B	234/291 (80%)	216 (92%)	15 (6%)	3 (1%)	9 35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	458/582 (79%)	423 (92%)	31 (7%)	4 (1%)	14	44

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	235	ILE
1	B	169	GLY
1	A	54	ASN
1	B	231	PRO

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	206/267 (77%)	194 (94%)	12 (6%)	18	48
1	B	219/267 (82%)	202 (92%)	17 (8%)	11	38
All	All	425/534 (80%)	396 (93%)	29 (7%)	14	42

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	83	LEU
1	B	264	ILE
1	B	121	LEU
1	B	250	GLN
1	B	110	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	275	GLN
1	B	299	ASN
1	B	308	GLN
1	A	275	GLN

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Mol	Chain	Res	Type
1	A	229	GLN

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](#)

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 [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	230/291 (79%)	-0.19	3 (1%)	75 56	31, 51, 78, 127	0
1	B	242/291 (83%)	-0.08	4 (1%)	69 48	31, 56, 85, 113	0
All	All	472/582 (81%)	-0.14	7 (1%)	72 52	31, 54, 83, 127	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	20	LEU	3.5
1	A	23	ILE	2.9
1	B	78	ALA	2.5
1	B	77	MET	2.3
1	A	56	ILE	2.2

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.