



wwPDB EM Validation Summary Report ⓘ

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PDB ID : 9CQ0 / pdb_00009cq0
Title : Event-based electron counting microED structure of thiostrepton from a single crystal
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Deposited on : 2024-07-18
Resolution : 1.50 Å(reported)
Based on initial model : 1E9W

This is a wwPDB EM Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

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)
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

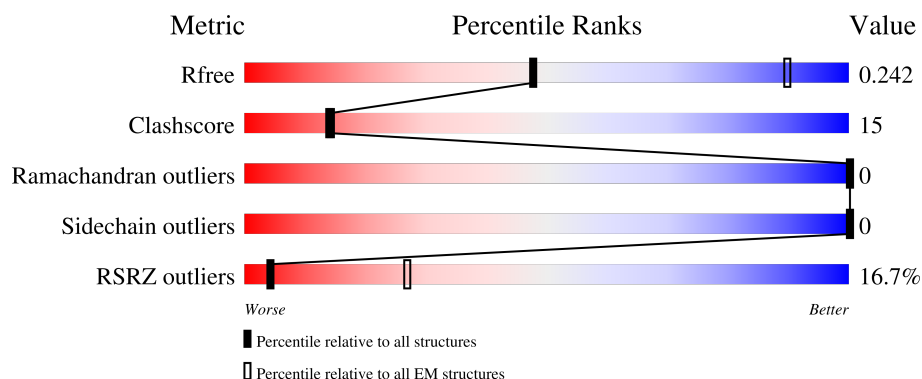
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON CRYSTALLOGRAPHY

The reported resolution of this entry is 1.50 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)	EM structures (#Entries)
R_{free}	180332	208
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RSRZ outliers	180361	209

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	19	5% 53% 26% 21%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 116 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Thiostrepton.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	19	Total	C	N	O	S	0	1
			114	72	19	18	5		

- Molecule 2 is water.

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

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Thiostrepton



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	26.47Å 26.47Å 27.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	18.72 – 1.50 18.72 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (18.72-1.50) 99.5 (18.72-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 1.50Å)	Xtriage
Refinement program	unknown	Depositor
R, R_{free}	0.201 , 0.217 0.224 , 0.242	Depositor DCC
R_{free} test set	174 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	12.8	Xtriage
Anisotropy	0.347	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.53 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.059 for -h,l,k 0.044 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	116	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 25.80 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9615e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: QUA, MH6, NH2, DBU, DCY, TS9, BB9, DHA

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	0.57	0/31	0.76	0/38

There are no bond length outliers.

There are no bond angle outliers.

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	114	0	80	3	0
2	A	2	0	0	0	0
All	All	116	0	80	3	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 15.

All (3) 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:17:DHA:O	1:A:18:DHA:HB1	1.97	0.64
1:A:6:SER:H	1:A:14:BB9:HN1	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:BB9:HN1	1:A:14:BB9:CA	2.33	0.41

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 PDB entries followed by that with respect to all EM entries.

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	5/19 (26%)	4 (80%)	1 (20%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	3/4 (75%)	3 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

11 non-standard protein/DNA/RNA residues 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
1	TS9	A	11	1	7,8,10	0.90	0	6,12,15	0.71	0
1	DHA	A	18	1	3,4,5	3.15	1 (33%)	2,4,6	3.28	2 (100%)
1	DHA	A	4	1	3,4,5	2.78	1 (33%)	2,4,6	3.11	1 (50%)
1	BB9	A	7	1	2,5,6	2.81	1 (50%)	1,5,7	3.16	1 (100%)
1	BB9	A	16	1	2,5,6	3.97	1 (50%)	1,5,7	5.23	1 (100%)
1	MH6	A	15	1	3,3,6	1.16	0	1,3,7	0.93	0
1	BB9	A	14	1	2,4,6	0.98	0	3,4,7	3.83	3 (100%)
1	DHA	A	17	1	3,4,5	3.31	1 (33%)	2,4,6	3.78	2 (100%)
1	BB9	A	12	1	2,5,6	2.97	1 (50%)	1,5,7	3.93	1 (100%)
1	DBU	A	9	1	3,4,6	1.44	1 (33%)	3,4,7	5.67	2 (66%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	TS9	A	11	1	-	1/9/12/16	-
1	DHA	A	18	1	-	0/0/2/4	-
1	DHA	A	4	1	-	0/0/2/4	-
1	BB9	A	7	1	-	0/0/4/6	-
1	BB9	A	16	1	-	0/0/4/6	-
1	BB9	A	14	1	-	0/0/2/6	-
1	DHA	A	17	1	-	0/0/2/4	-
1	BB9	A	12	1	-	0/0/4/6	-
1	DBU	A	9	1	-	0/1/2/6	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	17	DHA	C-CA	-5.59	1.35	1.45
1	A	18	DHA	C-CA	-5.43	1.35	1.45
1	A	16	BB9	C-CA	5.41	1.54	1.45
1	A	4	DHA	C-CA	-4.76	1.37	1.45
1	A	12	BB9	C-CA	4.01	1.51	1.45

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	9	DBU	CB-CA-N	8.77	128.03	122.88
1	A	16	BB9	O-C-CA	-5.23	118.83	125.39
1	A	17	DHA	O-C-CA	-4.90	116.33	125.53
1	A	4	DHA	O-C-CA	-4.27	117.52	125.53
1	A	14	BB9	C-CA-CB	4.24	129.25	121.45

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	11	TS9	CG2-CB-CG1-OD2

There are no ring outliers.

4 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	18	DHA	1	0
1	A	7	BB9	1	0
1	A	14	BB9	2	0
1	A	17	DHA	1	0

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.