



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:20 AM UTC

PDB ID : 4ZDN / pdb_00004zdn
Title : Streptomyces platensis isomigrastatin ketosynthase domain MgsF KS4
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Deposited on : 2015-04-17
Resolution : 2.51 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 ⓘ 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

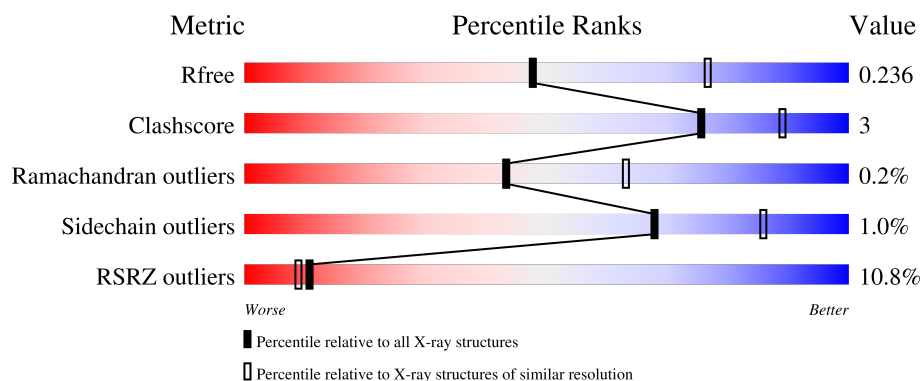
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	639	10% 85% 7% 8%

2 Entry composition [i](#)

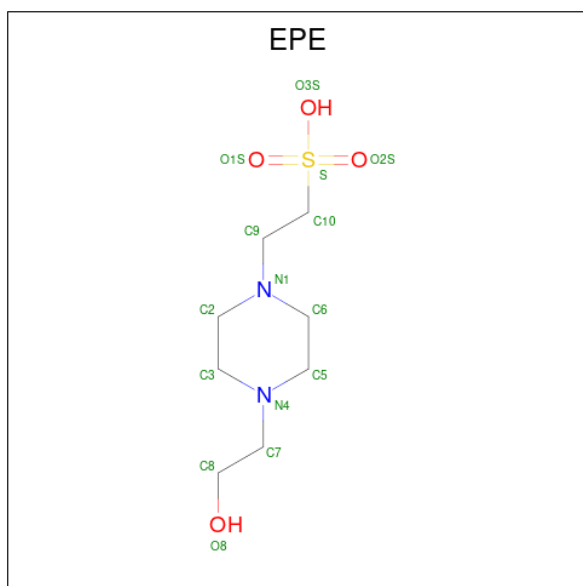
There are 4 unique types of molecules in this entry. The entry contains 4503 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 AT-less polyketide synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	589	4361	2748	787	813	7	6	0	1	0

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	15	8	2	4	1	0	0

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	126	Total 126	O 126	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	126.69Å 126.69Å 143.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.52 – 2.51 40.52 – 2.51	Depositor EDS
% Data completeness (in resolution range)	86.5 (40.52-2.51) 89.3 (40.52-2.51)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.40 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.187 , 0.226 0.199 , 0.236	Depositor DCC
R_{free} test set	1839 reflections (4.52%)	wwPDB-VP
Wilson B-factor (Å ²)	38.6	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4503	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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

5.1 Standard geometry

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

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	0.29	0/4472	0.72	0/6096

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

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	4361	0	4156	26	0
2	A	15	0	17	1	0
3	A	1	0	0	0	0
4	A	126	0	0	1	2
All	All	4503	0	4173	26	2

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 3.

All (26) 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:680:THR:HG22	1:A:905:ALA:HB2	1.77	0.67
1:A:664:ARG:NH2	4:A:1302:HOH:O	2.31	0.64
1:A:874:ILE:HD12	1:A:937:ILE:HD13	1.82	0.61
1:A:645:ARG:NH2	1:A:1176:PHE:O	2.37	0.56
1:A:689:PRO:HG2	1:A:697:PRO:HB2	1.88	0.55
1:A:727:CYS:HB2	1:A:970:GLY:HA2	1.89	0.53
1:A:787:GLY:HA2	1:A:866:THR:HG22	1.93	0.51
1:A:934:ASN:HB3	1:A:937:ILE:HD12	1.93	0.51
1:A:769:SER:HB2	1:A:771:MSE:HE2	1.92	0.51
1:A:578:ARG:NH1	1:A:923:GLU:OE1	2.46	0.49
1:A:629:PHE:O	2:A:1201:EPE:H52	2.13	0.48
1:A:759:HIS:CG	1:A:760:PRO:HD2	2.49	0.48
1:A:696:PRO:HA	1:A:697:PRO:HD3	1.82	0.47
1:A:1141:ALA:O	1:A:1145:LYS:HG2	2.16	0.46
1:A:646:LEU:HB3	1:A:794:VAL:HG21	1.98	0.44
1:A:912:LEU:CD1	1:A:980:VAL:HG21	2.48	0.44
1:A:853:ALA:HB3	1:A:884:ASP:HB2	2.00	0.43
1:A:862:HIS:N	1:A:873:GLU:OE1	2.46	0.43
1:A:763:TYR:CZ	1:A:790:PRO:HG2	2.54	0.43
1:A:843:ARG:HD2	1:A:843:ARG:HA	1.92	0.42
1:A:767:CYS:SG	1:A:772:LEU:HD12	2.60	0.41
1:A:731:LEU:HD12	1:A:731:LEU:HA	1.88	0.41
1:A:853:ALA:HB1	1:A:881:PHE:CD2	2.56	0.41
1:A:897:LYS:HE3	1:A:902:HIS:ND1	2.36	0.40
1:A:851:VAL:HG12	1:A:852:SER:O	2.22	0.40
1:A:874:ILE:HD12	1:A:937:ILE:HG21	2.04	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1422:HOH:O	4:A:1422:HOH:O[6_555]	2.15	0.05
4:A:1410:HOH:O	4:A:1410:HOH:O[5_655]	2.18	0.02

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	580/639 (91%)	565 (97%)	14 (2%)	1 (0%)	43 63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	904	GLU

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	421/468 (90%)	417 (99%)	4 (1%)	68 86

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	794	VAL
1	A	846	LEU
1	A	1122	GLU
1	A	1142	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	708	ASN

5.3.3 RNA ⓘ

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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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
2	EPE	A	1201	-	15,15,15	0.88	1 (6%)	19,20,20	1.76	4 (21%)

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
2	EPE	A	1201	-	-	2/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	EPE	C10-S	2.96	1.81	1.77

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	EPE	C5-N4-C3	4.26	118.01	108.84
2	A	1201	EPE	C7-N4-C3	3.62	120.89	111.24
2	A	1201	EPE	C7-N4-C5	3.23	119.85	111.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	EPE	O3S-S-C10	2.09	110.09	106.00

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1201	EPE	C10-C9-N1-C6
2	A	1201	EPE	C10-C9-N1-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	EPE	1	0

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

6.1 Protein, DNA and RNA chains

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	583/639 (91%)	0.43	63 (10%) 11 9	15, 50, 91, 118	1 (0%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	691	ALA	6.9
1	A	551	ALA	5.7
1	A	1160	THR	5.4
1	A	696	PRO	5.2
1	A	607	GLN	4.6
1	A	685	ASP	4.5
1	A	868	LEU	4.4
1	A	786	ASP	4.3
1	A	993	PRO	4.1
1	A	608	GLN	4.0
1	A	595	ASP	3.9
1	A	1180	PRO	3.7
1	A	884	ASP	3.6
1	A	1155	HIS	3.5
1	A	690	PRO	3.5
1	A	889	GLY	3.5
1	A	785	GLY	3.4
1	A	1178	PHE	3.4
1	A	930	ALA	3.3
1	A	931	GLU	3.3
1	A	1026	GLY	3.3
1	A	948	THR	3.3
1	A	960	GLY	3.2
1	A	604	ARG	3.2
1	A	589	ALA	3.2
1	A	770	ARG	3.1
1	A	958	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	768	ARG	3.0
1	A	606	VAL	3.0
1	A	1069	ASP	3.0
1	A	603	GLN	3.0
1	A	596	ALA	2.9
1	A	994	ALA	2.9
1	A	552	ASP	2.9
1	A	599	GLU	2.9
1	A	686	ARG	2.8
1	A	609	GLY	2.8
1	A	1179	GLY	2.7
1	A	927	THR	2.7
1	A	938	ASP	2.7
1	A	1099	GLU	2.7
1	A	578	ARG	2.6
1	A	1161	PRO	2.6
1	A	995	PRO	2.5
1	A	867	ARG	2.5
1	A	688	ARG	2.5
1	A	600	PRO	2.5
1	A	553	GLU	2.5
1	A	984	ARG	2.5
1	A	932	GLN	2.4
1	A	992	THR	2.4
1	A	590	GLU	2.3
1	A	635	ARG	2.3
1	A	878	THR	2.3
1	A	787	GLY	2.3
1	A	781	PHE	2.3
1	A	698	ALA	2.2
1	A	828	ASN	2.2
1	A	826	ARG	2.2
1	A	934	ASN	2.2
1	A	788	PHE	2.1
1	A	829	GLY	2.1
1	A	585	ARG	2.0

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

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($\text{\AA}^2$)	Q<0.9
2	EPE	A	1201	15/15	0.95	0.10	34,43,52,55	0
3	CL	A	1202	1/1	0.95	0.10	70,70,70,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.