



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 27, 2019 – 08:02 PM EDT

PDB ID : 1E3H
Title : SeMet derivative of Streptomyces antibioticus PNPase/GPSI enzyme
Authors : Symmons, M.F.; Jones, G.H.; Luisi, B.F.
Deposited on : 2000-06-15
Resolution : 2.60 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : 1.13
EDS : 2.4
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

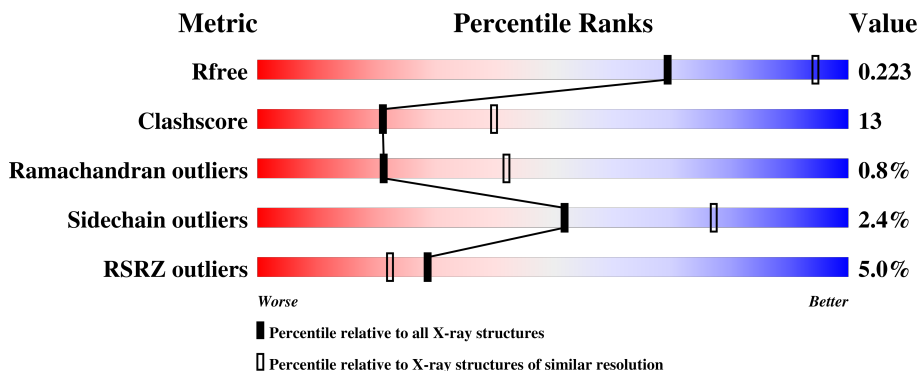
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	111664	2767 (2.60-2.60)
Clashscore	122126	3110 (2.60-2.60)
Ramachandran outliers	120053	3062 (2.60-2.60)
Sidechain outliers	120020	3062 (2.60-2.60)
RSRZ outliers	108989	2706 (2.60-2.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	757	<div> <div>4%</div> <div>61%</div> <div>18%</div> <div>•</div> <div>21%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	904	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4842 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 GUANOSINE PENTAPHOSPHATE SYNTHETASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	601	4506	2828	790	868	3	17	0	1	0

There are 39 discrepancies between the modelled and reference sequences:

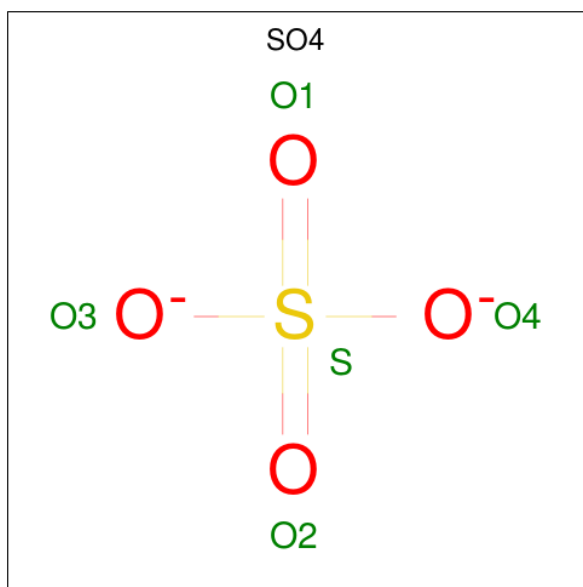
Chain	Residue	Modelled	Actual	Comment	Reference
A	31	ARG	LYS	conflict	UNP Q53597
A	156	ILE	TYR	conflict	UNP Q53597
A	210	ILE	VAL	conflict	UNP Q53597
A	260	PHE	PRO	conflict	UNP Q53597
A	261	LEU	SER	conflict	UNP Q53597
A	262	ASP	SER	conflict	UNP Q53597
A	263	TYR	THR	conflict	UNP Q53597
A	264	GLN	THR	conflict	UNP Q53597
A	265	ASP	ARG	conflict	UNP Q53597
A	267	VAL	THR	conflict	UNP Q53597
A	268	LEU	THR	conflict	UNP Q53597
A	269	GLU	SER	conflict	UNP Q53597
A	323	ALA	PRO	conflict	UNP Q53597
A	324	LEU	TRP	conflict	UNP Q53597
A	325	THR	PRO	conflict	UNP Q53597
A	326	LYS	SER	conflict	UNP Q53597
A	328	LEU	SER	conflict	UNP Q53597
A	329	VAL	SER	conflict	UNP Q53597
A	330	ARG	ALA	conflict	UNP Q53597
A	335	ALA	LYS	conflict	UNP Q53597
A	409	TYR	ILE	conflict	UNP Q53597
A	-15	MSE	MET	modified residue	PDB 1E3H
A	-9	MSE	MET	modified residue	PDB 1E3H
A	1	MSE	MET	modified residue	UNP Q53597
A	46	MSE	MET	modified residue	UNP Q53597
A	74	MSE	MET	modified residue	UNP Q53597
A	125	MSE	MET	modified residue	UNP Q53597

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Chain	Residue	Modelled	Actual	Comment	Reference
A	184	MSE	MET	modified residue	UNP Q53597
A	199	MSE	MET	modified residue	UNP Q53597
A	200	MSE	MET	modified residue	UNP Q53597
A	382	MSE	MET	modified residue	UNP Q53597
A	385	MSE	MET	modified residue	UNP Q53597
A	401	MSE	MET	modified residue	UNP Q53597
A	464	MSE	MET	modified residue	UNP Q53597
A	472	MSE	MET	modified residue	UNP Q53597
A	490	MSE	MET	modified residue	UNP Q53597
A	519	MSE	MET	modified residue	UNP Q53597
A	565	MSE	MET	modified residue	UNP Q53597
A	566	MSE	MET	modified residue	UNP Q53597

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	291	Total	O	0	0
			291	291		

4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	133.61Å 133.61Å 344.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.99 – 2.60 38.99 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.99-2.60) 99.7 (38.99-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.71 (at 2.61Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.201 , 0.226 0.197 , 0.223	Depositor DCC
R_{free} test set	1790 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	46.2	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.008 for $-1/3^*h+1/3^*k+1/3^*l, -k, 8/3^*h+4/3^*k+1/3^*l$ 0.017 for $-2/3^*h-1/3^*k-1/3^*l, -1/3^*h-2/3^*k+1/3^*l, -4/3^*h+4/3^*k+1/3^*l$ 0.012 for $-h, 1/3^*h-1/3^*k-1/3^*l, -4/3^*h-8/3^*k+1/3^*l$	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4842	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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: SO4

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	0.33	0/4563	0.59	0/6159

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	4506	0	4520	118	0
2	A	45	0	0	2	0
3	A	291	0	0	9	0
All	All	4842	0	4520	118	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 13.

The worst 5 of 118 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:112:LYS:H	1:A:112:LYS:HD3	1.20	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ARG:HH21	1:A:423:ARG:HD3	1.32	0.94
1:A:100:ARG:NH2	1:A:423:ARG:HD3	1.84	0.93
1:A:613:GLU:H	1:A:626:ALA:HB3	1.38	0.87
1:A:285:ILE:HB	1:A:291:ARG:HB2	1.61	0.83

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	596/757 (79%)	556 (93%)	35 (6%)	5 (1%)	21	42

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	459	ASN
1	A	630	PRO
1	A	461	SER
1	A	626	ALA
1	A	625	GLY

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	462/577 (80%)	451 (98%)	11 (2%)	52 77

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	132	LEU
1	A	152	PHE
1	A	289	GLN
1	A	112	LYS
1	A	276	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	HIS
1	A	381	ASN
1	A	495	GLN
1	A	502	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

9 ligands 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	$\# Z > 2$
2	SO4	A	901	-	4,4,4	0.34	0	6,6,6	0.10	0
2	SO4	A	902	-	4,4,4	0.35	0	6,6,6	0.07	0
2	SO4	A	903	-	4,4,4	0.43	0	6,6,6	0.13	0
2	SO4	A	904	-	4,4,4	0.37	0	6,6,6	0.09	0
2	SO4	A	905	-	4,4,4	0.35	0	6,6,6	0.07	0
2	SO4	A	906	-	4,4,4	0.34	0	6,6,6	0.08	0
2	SO4	A	907	-	4,4,4	0.35	0	6,6,6	0.06	0
2	SO4	A	908	-	4,4,4	0.35	0	6,6,6	0.10	0
2	SO4	A	909	-	4,4,4	0.34	0	6,6,6	0.14	0

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.

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	585/757 (77%)	-0.09	29 (4%) 29 22	24, 43, 98, 100	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	626	ALA	8.1
1	A	623	TYR	5.6
1	A	612	ALA	5.4
1	A	624	ILE	5.3
1	A	611	GLY	4.0

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 carbohydrates 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(Å ²)	Q<0.9
2	SO4	A	903	5/5	0.75	0.35	62,63,70,70	5
2	SO4	A	908	5/5	0.78	0.36	61,61,63,64	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	A	907	5/5	0.82	0.28	69,69,71,71	5
2	SO4	A	901	5/5	0.86	0.19	66,66,68,69	5
2	SO4	A	905	5/5	0.91	0.21	65,66,67,67	5
2	SO4	A	904	5/5	0.94	0.44	83,83,85,86	5
2	SO4	A	906	5/5	0.94	0.43	72,73,73,73	5
2	SO4	A	909	5/5	0.94	0.23	43,46,48,48	5
2	SO4	A	902	5/5	0.96	0.14	59,60,61,61	5

6.5 Other polymers [i](#)

There are no such residues in this entry.