



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2023 – 10:15 am BST

PDB ID : 8H5M
Title : Crystal structure of PETase S121E/D186H/N233C/S242T/N246D/S282C mutant from Ideonella sakaiensis
Authors : Lee, S.H.; Seo, H.; Kim, K.-J.
Deposited on : 2022-10-13
Resolution : 1.89 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 : 4.02b-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

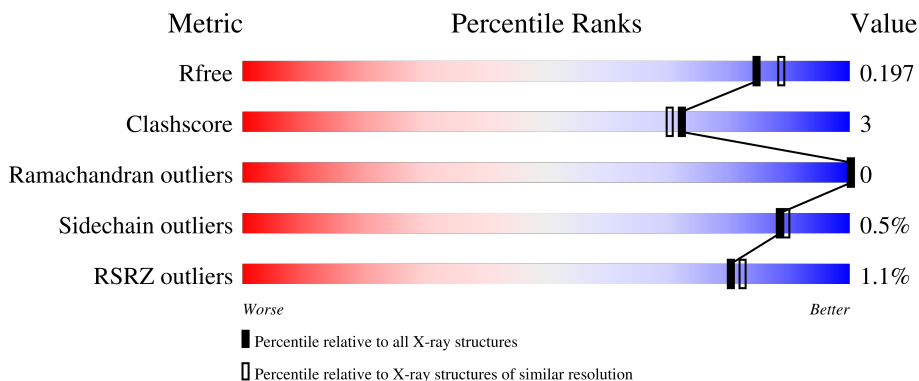
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 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}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	300	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2158 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 Poly(ethylene terephthalate) hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	261	1935	1194	347	380	14	0	2	0

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	MET	-	initiating methionine	UNP A0A0K8P6T7
A	14	GLY	-	expression tag	UNP A0A0K8P6T7
A	15	SER	-	expression tag	UNP A0A0K8P6T7
A	16	SER	-	expression tag	UNP A0A0K8P6T7
A	17	HIS	-	expression tag	UNP A0A0K8P6T7
A	18	HIS	-	expression tag	UNP A0A0K8P6T7
A	19	HIS	-	expression tag	UNP A0A0K8P6T7
A	20	HIS	-	expression tag	UNP A0A0K8P6T7
A	21	HIS	-	expression tag	UNP A0A0K8P6T7
A	22	HIS	-	expression tag	UNP A0A0K8P6T7
A	23	SER	-	expression tag	UNP A0A0K8P6T7
A	24	SER	-	expression tag	UNP A0A0K8P6T7
A	25	GLY	-	expression tag	UNP A0A0K8P6T7
A	26	LEU	-	expression tag	UNP A0A0K8P6T7
A	27	VAL	-	expression tag	UNP A0A0K8P6T7
A	28	PRO	-	expression tag	UNP A0A0K8P6T7
A	29	ARG	-	expression tag	UNP A0A0K8P6T7
A	30	GLY	-	expression tag	UNP A0A0K8P6T7
A	31	SER	-	expression tag	UNP A0A0K8P6T7
A	32	HIS	-	expression tag	UNP A0A0K8P6T7
A	33	MET	-	expression tag	UNP A0A0K8P6T7
A	121	GLU	SER	engineered mutation	UNP A0A0K8P6T7
A	186	HIS	ASP	engineered mutation	UNP A0A0K8P6T7
A	233	CYS	ASN	engineered mutation	UNP A0A0K8P6T7
A	242	THR	SER	engineered mutation	UNP A0A0K8P6T7
A	246	ASP	ASN	engineered mutation	UNP A0A0K8P6T7
A	282	CYS	SER	engineered mutation	UNP A0A0K8P6T7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	291	LEU	-	expression tag	UNP A0A0K8P6T7
A	292	GLU	-	expression tag	UNP A0A0K8P6T7
A	293	ASP	-	expression tag	UNP A0A0K8P6T7
A	294	PRO	-	expression tag	UNP A0A0K8P6T7
A	295	ALA	-	expression tag	UNP A0A0K8P6T7
A	296	ALA	-	expression tag	UNP A0A0K8P6T7
A	297	ASN	-	expression tag	UNP A0A0K8P6T7
A	298	LYS	-	expression tag	UNP A0A0K8P6T7
A	299	ALA	-	expression tag	UNP A0A0K8P6T7
A	300	ARG	-	expression tag	UNP A0A0K8P6T7
A	301	LYS	-	expression tag	UNP A0A0K8P6T7
A	302	GLU	-	expression tag	UNP A0A0K8P6T7
A	303	ALA	-	expression tag	UNP A0A0K8P6T7
A	304	GLU	-	expression tag	UNP A0A0K8P6T7
A	305	LEU	-	expression tag	UNP A0A0K8P6T7
A	306	ALA	-	expression tag	UNP A0A0K8P6T7
A	307	ALA	-	expression tag	UNP A0A0K8P6T7
A	308	ALA	-	expression tag	UNP A0A0K8P6T7
A	309	THR	-	expression tag	UNP A0A0K8P6T7
A	310	ALA	-	expression tag	UNP A0A0K8P6T7
A	311	GLU	-	expression tag	UNP A0A0K8P6T7
A	312	GLN	-	expression tag	UNP A0A0K8P6T7

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0

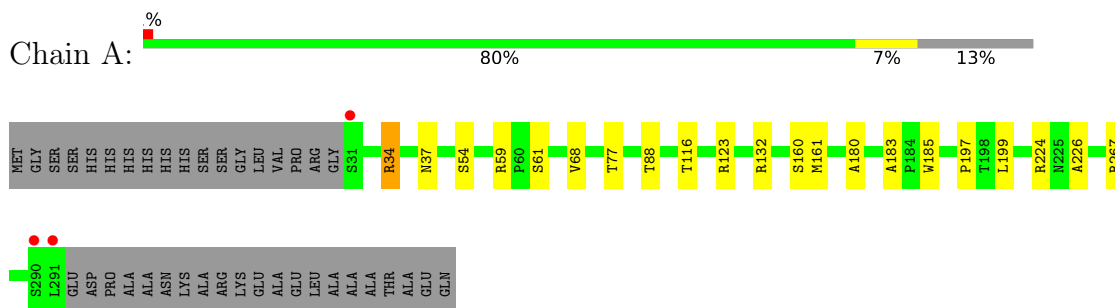
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	222	Total O 222 222	0	0

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Poly(ethylene terephthalate) hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.68Å 67.80Å 78.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.23 – 1.89 28.21 – 1.89	Depositor EDS
% Data completeness (in resolution range)	94.7 (28.23-1.89) 94.7 (28.21-1.89)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.73 (at 1.89Å)	Xtrriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.151 , 0.188 0.162 , 0.197	Depositor DCC
R_{free} test set	1130 reflections (5.34%)	wwPDB-VP
Wilson B-factor (Å ²)	14.5	Xtrriage
Anisotropy	0.055	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 52.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2158	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.91% 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](#)

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

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	0.49	0/1980	0.75	0/2694

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	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	123	ARG	Sidechain
1	A	132	ARG	Sidechain
1	A	224	ARG	Sidechain
1	A	34	ARG	Sidechain

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	1935	0	1854	13	0
2	A	1	0	0	0	0
3	A	222	0	0	2	0
All	All	2158	0	1854	13	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 3.

All (13) 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:37:ASN:HD22	1:A:267:ARG:HH11	1.47	0.60
1:A:37:ASN:HB3	3:A:693:HOH:O	2.00	0.60
1:A:37:ASN:ND2	1:A:267:ARG:HH11	2.09	0.51
1:A:54:SER:HA	1:A:68:VAL:O	2.13	0.48
1:A:160:SER:HA	1:A:183:ALA:O	2.14	0.47
1:A:161:MET:CE	1:A:185:TRP:CZ3	2.98	0.47
1:A:161:MET:HG2	1:A:185:TRP:CE3	2.51	0.46
1:A:88:THR:HA	1:A:116:THR:HB	1.99	0.45
1:A:34:ARG:CZ	1:A:77:THR:O	2.65	0.45
1:A:180:ALA:HA	1:A:199:LEU:O	2.18	0.44
1:A:59:ARG:NH2	3:A:508:HOH:O	2.52	0.43
1:A:161:MET:HE3	1:A:185:TRP:CZ3	2.55	0.41
1:A:197:PRO:HA	1:A:226:ALA:O	2.21	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 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	261/300 (87%)	251 (96%)	10 (4%)	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 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	210/236 (89%)	209 (100%)	1 (0%)	88 89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	HIS
1	A	37	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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.

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	261/300 (87%)	-0.17	3 (1%) 80 82	8, 14, 25, 43	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	291	LEU	4.0
1	A	290	SER	2.7
1	A	31	SER	2.3

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 monosaccharides 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	MG	A	401	1/1	1.00	0.13	6,6,6,6	0

6.5 Other polymers [i](#)

There are no such residues in this entry.