



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 23, 2023 – 02:59 AM JST

PDB ID : 7YU0  
Title : Structure of 6-aminohexanoate-oligomer hydrolase NylC precursor,  
H130Y/N266A/T267A mutant  
Authors : Negoro, S.; Higuchi, Y.  
Deposited on : 2022-08-16  
Resolution : 1.35 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
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

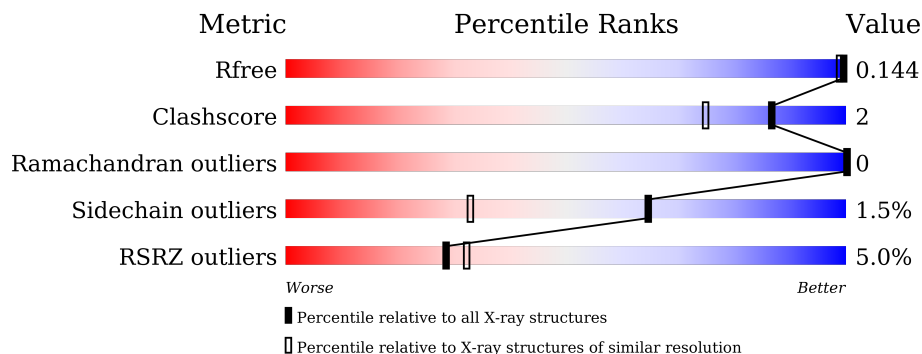
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.35 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	1509 (1.38-1.34)
Clashscore	141614	1551 (1.38-1.34)
Ramachandran outliers	138981	1530 (1.38-1.34)
Sidechain outliers	138945	1530 (1.38-1.34)
RSRZ outliers	127900	1487 (1.38-1.34)

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  $\geq 3$ , 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	355	 5% 89% 7%
1	B	355	 5% 87% 6% 6%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 10798 atoms, of which 5081 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.

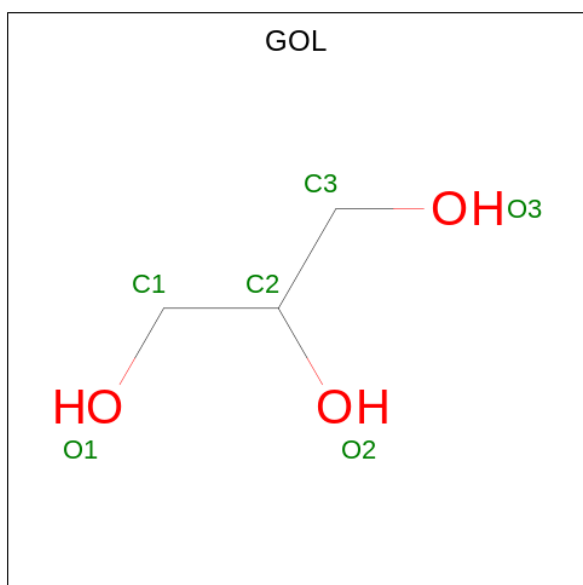
- Molecule 1 is a protein called 6-aminohexanoate-oligomer endohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	329	4994	1578	2485	449	473	9	60	14	0
1	B	333	5057	1601	2516	447	483	10	62	16	0

There are 6 discrepancies between the modelled and reference sequences:

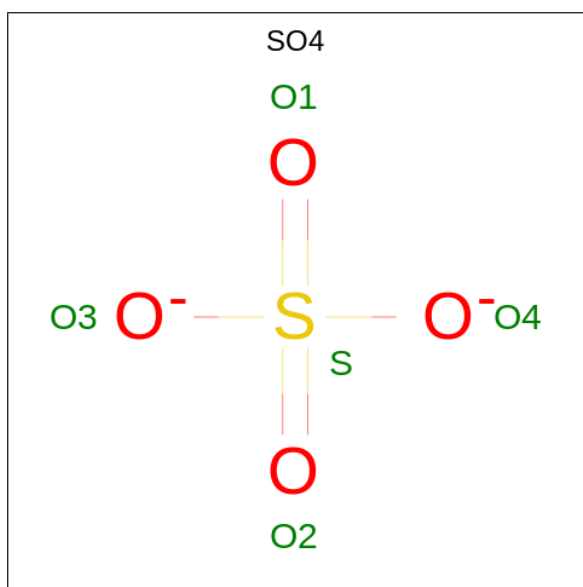
Chain	Residue	Modelled	Actual	Comment	Reference
A	130	TYR	HIS	engineered mutation	UNP Q79F77
A	266	ALA	ASN	engineered mutation	UNP Q79F77
A	267	ALA	THR	engineered mutation	UNP Q79F77
B	130	TYR	HIS	engineered mutation	UNP Q79F77
B	266	ALA	ASN	engineered mutation	UNP Q79F77
B	267	ALA	THR	engineered mutation	UNP Q79F77

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	2	0
			14	3	8	3		
2	A	1	Total	C	H	O	2	0
			14	3	8	3		
2	A	1	Total	C	H	O	2	0
			14	3	8	3		
2	A	1	Total	C	H	O	2	0
			14	3	8	3		
2	A	1	Total	C	H	O	2	0
			14	3	8	3		
2	B	1	Total	C	H	O	2	0
			14	3	8	3		
2	B	1	Total	C	H	O	2	0
			14	3	8	3		
2	B	1	Total	C	H	O	2	0
			14	3	8	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	2	Total Na 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	273	Total O 273 273	0	0
5	B	306	Total O 306 306	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.24Å 144.34Å 129.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.01 – 1.35 36.98 – 1.35	Depositor EDS
% Data completeness (in resolution range)	97.7 (37.01-1.35) 97.7 (36.98-1.35)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.89 (at 1.35Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.111 , 0.139 0.116 , 0.144	Depositor DCC
$R_{free}$ test set	7049 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.1	Xtrriage
Anisotropy	0.662	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.45 , 52.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	10798	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, NA, GOL

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	0.62	0/2606	0.75	0/3538
1	B	0.60	0/2632	0.77	0/3577
All	All	0.61	0/5238	0.76	0/7115

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	2509	2485	2491	8	1
1	B	2541	2516	2518	12	1
2	A	36	48	48	1	0
2	B	24	32	32	1	0
3	A	10	0	0	0	0
3	B	15	0	0	0	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
5	A	273	0	0	0	0
5	B	306	0	0	0	0
All	All	5717	5081	5089	21	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 2.

The worst 5 of 21 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:19:ASP:HB3	1:A:20:PRO:HA	1.72	0.72
1:A:19:ASP:HB3	1:A:20:PRO:CA	2.28	0.64
1:B:69:PRO:HB2	1:B:183[A]:MET:HG3	1.85	0.57
1:A:69:PRO:HB2	1:A:183[B]:MET:CG	2.40	0.52
1:B:67:GLU:O	1:B:153[A]:THR:HG21	2.11	0.50

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)
1:B:292[A]:SER:HG	1:B:302:HIS:HD2[3_857]	1.18	0.42
1:A:292[A]:SER:HG	1:A:302:HIS:HD2[3_857]	1.22	0.38

## 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	340/355 (96%)	329 (97%)	11 (3%)	0	100	100
1	B	346/355 (98%)	334 (96%)	12 (4%)	0	100	100
All	All	686/710 (97%)	663 (97%)	23 (3%)	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	255/260 (98%)	251 (98%)	4 (2%)	62	30
1	B	259/260 (100%)	254 (98%)	5 (2%)	57	23
All	All	514/520 (99%)	505 (98%)	9 (2%)	65	25

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	151[A]	ARG
1	B	151[B]	ARG
1	A	305[B]	MET
1	B	29	VAL
1	B	30	PHE

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	76	HIS
1	A	302	HIS

### 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 18 ligands modelled in this entry, 3 are monoatomic - leaving 15 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	GOL	A	1006	-	5,5,5	0.12	0	5,5,5	0.33	0
2	GOL	B	402	-	5,5,5	0.09	0	5,5,5	0.25	0
2	GOL	A	1003	-	5,5,5	0.13	0	5,5,5	0.28	0
3	SO4	A	1007	-	4,4,4	0.22	0	6,6,6	0.08	0
2	GOL	A	1002	-	5,5,5	0.18	0	5,5,5	0.28	0
3	SO4	A	1008	-	4,4,4	0.19	0	6,6,6	0.08	0
2	GOL	B	403	-	5,5,5	0.23	0	5,5,5	0.40	0
3	SO4	B	406	-	4,4,4	0.25	0	6,6,6	0.13	0
3	SO4	B	405	-	4,4,4	0.36	0	6,6,6	0.05	0
3	SO4	B	407	-	4,4,4	0.36	0	6,6,6	0.06	0
2	GOL	B	404	-	5,5,5	0.18	0	5,5,5	0.33	0
2	GOL	A	1005	-	5,5,5	0.12	0	5,5,5	0.28	0
2	GOL	A	1004	-	5,5,5	0.12	0	5,5,5	0.50	0
2	GOL	A	1001	-	5,5,5	0.17	0	5,5,5	0.50	0
2	GOL	B	401	-	5,5,5	0.10	0	5,5,5	0.27	0

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	GOL	A	1006	-	-	4/4/4/4	-
2	GOL	B	402	-	-	2/4/4/4	-
2	GOL	A	1003	-	-	2/4/4/4	-
2	GOL	A	1002	-	-	0/4/4/4	-
2	GOL	B	403	-	-	2/4/4/4	-
2	GOL	B	404	-	-	1/4/4/4	-
2	GOL	A	1005	-	-	1/4/4/4	-
2	GOL	A	1004	-	-	2/4/4/4	-
2	GOL	A	1001	-	-	4/4/4/4	-
2	GOL	B	401	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	GOL	O1-C1-C2-O2
2	A	1001	GOL	O1-C1-C2-C3
2	A	1001	GOL	C1-C2-C3-O3
2	B	401	GOL	O1-C1-C2-C3
2	A	1003	GOL	C1-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	404	GOL	1	0
2	A	1005	GOL	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	329/355 (92%)	-0.11	16 (4%) 29 33	14, 20, 36, 60	0
1	B	333/355 (93%)	-0.10	17 (5%) 28 31	13, 18, 31, 67	0
All	All	662/710 (93%)	-0.10	33 (4%) 28 32	13, 19, 34, 67	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	30	PHE	12.8
1	A	30	PHE	10.0
1	B	29	VAL	6.4
1	A	29	VAL	5.7
1	B	321	PRO	5.1

### 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, 95<sup>th</sup> 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	GOL	A	1006	6/6	0.73	0.23	43,55,57,57	2
2	GOL	A	1005	6/6	0.80	0.11	40,51,57,60	2
2	GOL	A	1001	6/6	0.80	0.16	35,41,48,53	2
2	GOL	B	403	6/6	0.81	0.16	29,33,50,50	2
2	GOL	B	402	6/6	0.85	0.22	47,57,67,70	2
2	GOL	B	401	6/6	0.87	0.09	47,51,59,65	2
3	SO4	A	1007	5/5	0.89	0.31	41,48,56,66	0
3	SO4	B	406	5/5	0.90	0.23	68,70,94,95	0
3	SO4	A	1008	5/5	0.91	0.29	60,67,78,88	0
4	NA	A	1009	1/1	0.92	0.12	51,51,51,51	0
2	GOL	A	1003	6/6	0.93	0.08	32,39,52,55	2
3	SO4	B	407	5/5	0.94	0.44	58,65,76,76	0
2	GOL	B	404	6/6	0.94	0.12	29,42,50,55	2
2	GOL	A	1004	6/6	0.95	0.11	26,39,47,48	2
2	GOL	A	1002	6/6	0.95	0.07	25,27,31,31	2
4	NA	B	409	1/1	0.95	0.06	50,50,50,50	0
3	SO4	B	405	5/5	0.96	0.31	60,65,69,75	0
4	NA	B	408	1/1	0.99	0.47	38,38,38,38	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.