



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 25, 2021 – 08:07 PM EST

PDB ID : 6VY9
Title : Crystal structure of NotF prenyltransferase
Authors : Dan, Q.; Smith, J.L.
Deposited on : 2020-02-25
Resolution : 3.19 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
Xtriage (Phenix)	:	1.13
EDS	:	2.16
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)	:	2.16

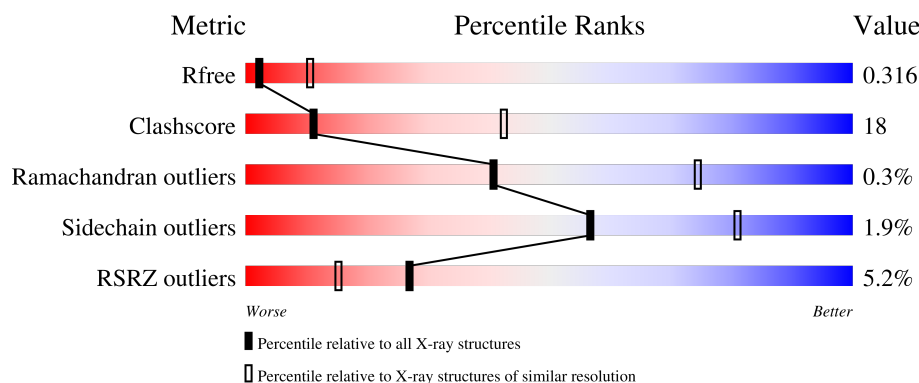
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	472	<div> <div>5%</div> <div> <div></div> <div>54%</div> <div>29%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	472	<div> <div>4%</div> <div> <div></div> <div>54%</div> <div>29%</div> <div>•</div> <div>16%</div> </div> </div>
1	C	472	<div> <div>6%</div> <div> <div></div> <div>54%</div> <div>29%</div> <div>•</div> <div>16%</div> </div> </div>
1	D	472	<div> <div>5%</div> <div> <div></div> <div>55%</div> <div>28%</div> <div>•</div> <div>16%</div> </div> </div>
1	E	472	<div> <div>4%</div> <div> <div></div> <div>55%</div> <div>28%</div> <div>•</div> <div>16%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	472	 3% 55% 28% • 16%
1	G	472	 3% 53% 29% • 16%
1	H	472	 5% 54% 29% • 16%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 25720 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 Deoxybrevianamide E synthase notF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	0	0
			3215	2083	541	584	7			
1	B	396	Total	C	N	O	S	0	0	0
			3215	2083	541	584	7			
1	G	396	Total	C	N	O	S	0	0	0
			3215	2083	541	584	7			
1	H	396	Total	C	N	O	S	0	0	0
			3215	2083	541	584	7			
1	F	396	Total	C	N	O	S	0	0	0
			3215	2083	541	584	7			
1	D	396	Total	C	N	O	S	0	0	0
			3215	2083	541	584	7			
1	E	396	Total	C	N	O	S	0	0	0
			3215	2083	541	584	7			
1	C	396	Total	C	N	O	S	0	0	0
			3215	2083	541	584	7			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP E0Y3X1
A	-18	GLY	-	expression tag	UNP E0Y3X1
A	-17	SER	-	expression tag	UNP E0Y3X1
A	-16	SER	-	expression tag	UNP E0Y3X1
A	-15	HIS	-	expression tag	UNP E0Y3X1
A	-14	HIS	-	expression tag	UNP E0Y3X1
A	-13	HIS	-	expression tag	UNP E0Y3X1
A	-12	HIS	-	expression tag	UNP E0Y3X1
A	-11	HIS	-	expression tag	UNP E0Y3X1
A	-10	HIS	-	expression tag	UNP E0Y3X1
A	-9	SER	-	expression tag	UNP E0Y3X1
A	-8	SER	-	expression tag	UNP E0Y3X1
A	-7	GLY	-	expression tag	UNP E0Y3X1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP E0Y3X1
A	-5	VAL	-	expression tag	UNP E0Y3X1
A	-4	PRO	-	expression tag	UNP E0Y3X1
A	-3	ARG	-	expression tag	UNP E0Y3X1
A	-2	GLY	-	expression tag	UNP E0Y3X1
A	-1	SER	-	expression tag	UNP E0Y3X1
A	0	HIS	-	expression tag	UNP E0Y3X1
B	-19	MET	-	initiating methionine	UNP E0Y3X1
B	-18	GLY	-	expression tag	UNP E0Y3X1
B	-17	SER	-	expression tag	UNP E0Y3X1
B	-16	SER	-	expression tag	UNP E0Y3X1
B	-15	HIS	-	expression tag	UNP E0Y3X1
B	-14	HIS	-	expression tag	UNP E0Y3X1
B	-13	HIS	-	expression tag	UNP E0Y3X1
B	-12	HIS	-	expression tag	UNP E0Y3X1
B	-11	HIS	-	expression tag	UNP E0Y3X1
B	-10	HIS	-	expression tag	UNP E0Y3X1
B	-9	SER	-	expression tag	UNP E0Y3X1
B	-8	SER	-	expression tag	UNP E0Y3X1
B	-7	GLY	-	expression tag	UNP E0Y3X1
B	-6	LEU	-	expression tag	UNP E0Y3X1
B	-5	VAL	-	expression tag	UNP E0Y3X1
B	-4	PRO	-	expression tag	UNP E0Y3X1
B	-3	ARG	-	expression tag	UNP E0Y3X1
B	-2	GLY	-	expression tag	UNP E0Y3X1
B	-1	SER	-	expression tag	UNP E0Y3X1
B	0	HIS	-	expression tag	UNP E0Y3X1
G	-19	MET	-	initiating methionine	UNP E0Y3X1
G	-18	GLY	-	expression tag	UNP E0Y3X1
G	-17	SER	-	expression tag	UNP E0Y3X1
G	-16	SER	-	expression tag	UNP E0Y3X1
G	-15	HIS	-	expression tag	UNP E0Y3X1
G	-14	HIS	-	expression tag	UNP E0Y3X1
G	-13	HIS	-	expression tag	UNP E0Y3X1
G	-12	HIS	-	expression tag	UNP E0Y3X1
G	-11	HIS	-	expression tag	UNP E0Y3X1
G	-10	HIS	-	expression tag	UNP E0Y3X1
G	-9	SER	-	expression tag	UNP E0Y3X1
G	-8	SER	-	expression tag	UNP E0Y3X1
G	-7	GLY	-	expression tag	UNP E0Y3X1
G	-6	LEU	-	expression tag	UNP E0Y3X1
G	-5	VAL	-	expression tag	UNP E0Y3X1

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-4	PRO	-	expression tag	UNP E0Y3X1
G	-3	ARG	-	expression tag	UNP E0Y3X1
G	-2	GLY	-	expression tag	UNP E0Y3X1
G	-1	SER	-	expression tag	UNP E0Y3X1
G	0	HIS	-	expression tag	UNP E0Y3X1
H	-19	MET	-	initiating methionine	UNP E0Y3X1
H	-18	GLY	-	expression tag	UNP E0Y3X1
H	-17	SER	-	expression tag	UNP E0Y3X1
H	-16	SER	-	expression tag	UNP E0Y3X1
H	-15	HIS	-	expression tag	UNP E0Y3X1
H	-14	HIS	-	expression tag	UNP E0Y3X1
H	-13	HIS	-	expression tag	UNP E0Y3X1
H	-12	HIS	-	expression tag	UNP E0Y3X1
H	-11	HIS	-	expression tag	UNP E0Y3X1
H	-10	HIS	-	expression tag	UNP E0Y3X1
H	-9	SER	-	expression tag	UNP E0Y3X1
H	-8	SER	-	expression tag	UNP E0Y3X1
H	-7	GLY	-	expression tag	UNP E0Y3X1
H	-6	LEU	-	expression tag	UNP E0Y3X1
H	-5	VAL	-	expression tag	UNP E0Y3X1
H	-4	PRO	-	expression tag	UNP E0Y3X1
H	-3	ARG	-	expression tag	UNP E0Y3X1
H	-2	GLY	-	expression tag	UNP E0Y3X1
H	-1	SER	-	expression tag	UNP E0Y3X1
H	0	HIS	-	expression tag	UNP E0Y3X1
F	-19	MET	-	initiating methionine	UNP E0Y3X1
F	-18	GLY	-	expression tag	UNP E0Y3X1
F	-17	SER	-	expression tag	UNP E0Y3X1
F	-16	SER	-	expression tag	UNP E0Y3X1
F	-15	HIS	-	expression tag	UNP E0Y3X1
F	-14	HIS	-	expression tag	UNP E0Y3X1
F	-13	HIS	-	expression tag	UNP E0Y3X1
F	-12	HIS	-	expression tag	UNP E0Y3X1
F	-11	HIS	-	expression tag	UNP E0Y3X1
F	-10	HIS	-	expression tag	UNP E0Y3X1
F	-9	SER	-	expression tag	UNP E0Y3X1
F	-8	SER	-	expression tag	UNP E0Y3X1
F	-7	GLY	-	expression tag	UNP E0Y3X1
F	-6	LEU	-	expression tag	UNP E0Y3X1
F	-5	VAL	-	expression tag	UNP E0Y3X1
F	-4	PRO	-	expression tag	UNP E0Y3X1
F	-3	ARG	-	expression tag	UNP E0Y3X1

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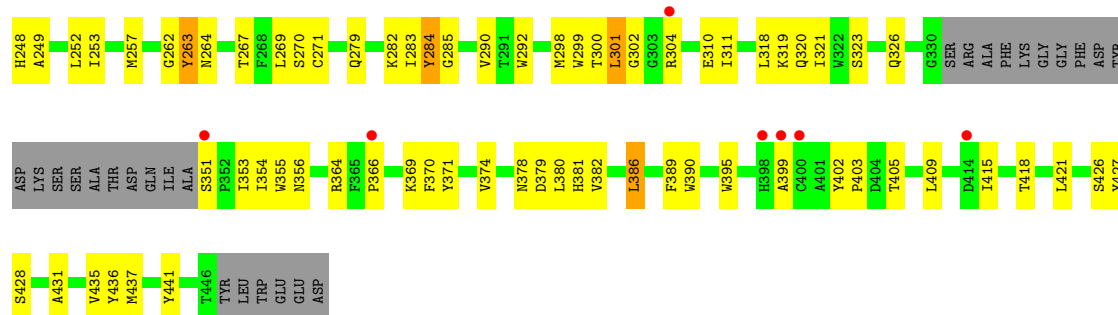
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Chain	Residue	Modelled	Actual	Comment	Reference
F	-2	GLY	-	expression tag	UNP E0Y3X1
F	-1	SER	-	expression tag	UNP E0Y3X1
F	0	HIS	-	expression tag	UNP E0Y3X1
D	-19	MET	-	initiating methionine	UNP E0Y3X1
D	-18	GLY	-	expression tag	UNP E0Y3X1
D	-17	SER	-	expression tag	UNP E0Y3X1
D	-16	SER	-	expression tag	UNP E0Y3X1
D	-15	HIS	-	expression tag	UNP E0Y3X1
D	-14	HIS	-	expression tag	UNP E0Y3X1
D	-13	HIS	-	expression tag	UNP E0Y3X1
D	-12	HIS	-	expression tag	UNP E0Y3X1
D	-11	HIS	-	expression tag	UNP E0Y3X1
D	-10	HIS	-	expression tag	UNP E0Y3X1
D	-9	SER	-	expression tag	UNP E0Y3X1
D	-8	SER	-	expression tag	UNP E0Y3X1
D	-7	GLY	-	expression tag	UNP E0Y3X1
D	-6	LEU	-	expression tag	UNP E0Y3X1
D	-5	VAL	-	expression tag	UNP E0Y3X1
D	-4	PRO	-	expression tag	UNP E0Y3X1
D	-3	ARG	-	expression tag	UNP E0Y3X1
D	-2	GLY	-	expression tag	UNP E0Y3X1
D	-1	SER	-	expression tag	UNP E0Y3X1
D	0	HIS	-	expression tag	UNP E0Y3X1
E	-19	MET	-	initiating methionine	UNP E0Y3X1
E	-18	GLY	-	expression tag	UNP E0Y3X1
E	-17	SER	-	expression tag	UNP E0Y3X1
E	-16	SER	-	expression tag	UNP E0Y3X1
E	-15	HIS	-	expression tag	UNP E0Y3X1
E	-14	HIS	-	expression tag	UNP E0Y3X1
E	-13	HIS	-	expression tag	UNP E0Y3X1
E	-12	HIS	-	expression tag	UNP E0Y3X1
E	-11	HIS	-	expression tag	UNP E0Y3X1
E	-10	HIS	-	expression tag	UNP E0Y3X1
E	-9	SER	-	expression tag	UNP E0Y3X1
E	-8	SER	-	expression tag	UNP E0Y3X1
E	-7	GLY	-	expression tag	UNP E0Y3X1
E	-6	LEU	-	expression tag	UNP E0Y3X1
E	-5	VAL	-	expression tag	UNP E0Y3X1
E	-4	PRO	-	expression tag	UNP E0Y3X1
E	-3	ARG	-	expression tag	UNP E0Y3X1
E	-2	GLY	-	expression tag	UNP E0Y3X1
E	-1	SER	-	expression tag	UNP E0Y3X1

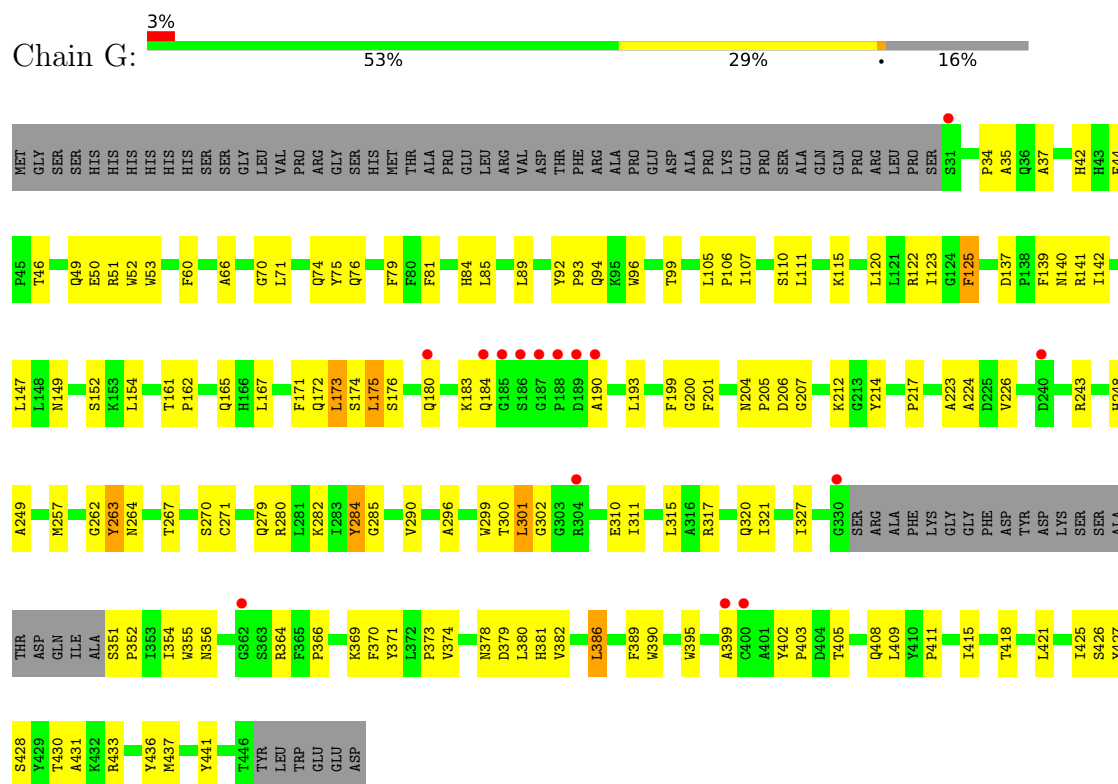
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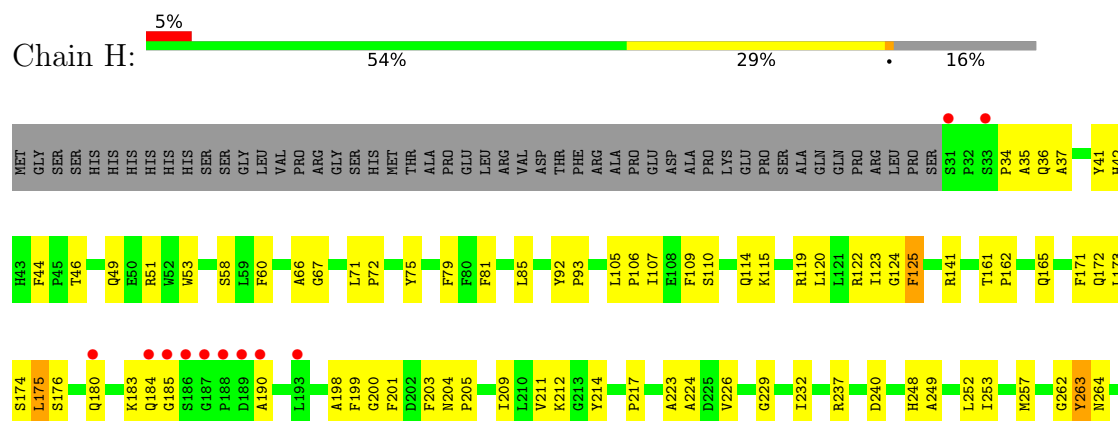
Chain	Residue	Modelled	Actual	Comment	Reference
E	0	HIS	-	expression tag	UNP E0Y3X1
C	-19	MET	-	initiating methionine	UNP E0Y3X1
C	-18	GLY	-	expression tag	UNP E0Y3X1
C	-17	SER	-	expression tag	UNP E0Y3X1
C	-16	SER	-	expression tag	UNP E0Y3X1
C	-15	HIS	-	expression tag	UNP E0Y3X1
C	-14	HIS	-	expression tag	UNP E0Y3X1
C	-13	HIS	-	expression tag	UNP E0Y3X1
C	-12	HIS	-	expression tag	UNP E0Y3X1
C	-11	HIS	-	expression tag	UNP E0Y3X1
C	-10	HIS	-	expression tag	UNP E0Y3X1
C	-9	SER	-	expression tag	UNP E0Y3X1
C	-8	SER	-	expression tag	UNP E0Y3X1
C	-7	GLY	-	expression tag	UNP E0Y3X1
C	-6	LEU	-	expression tag	UNP E0Y3X1
C	-5	VAL	-	expression tag	UNP E0Y3X1
C	-4	PRO	-	expression tag	UNP E0Y3X1
C	-3	ARG	-	expression tag	UNP E0Y3X1
C	-2	GLY	-	expression tag	UNP E0Y3X1
C	-1	SER	-	expression tag	UNP E0Y3X1
C	0	HIS	-	expression tag	UNP E0Y3X1

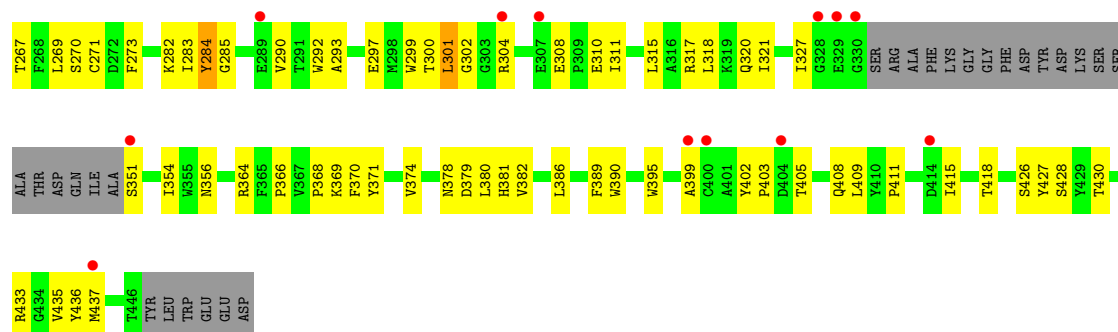


• Molecule 1: Deoxybrevianamide E synthase notF

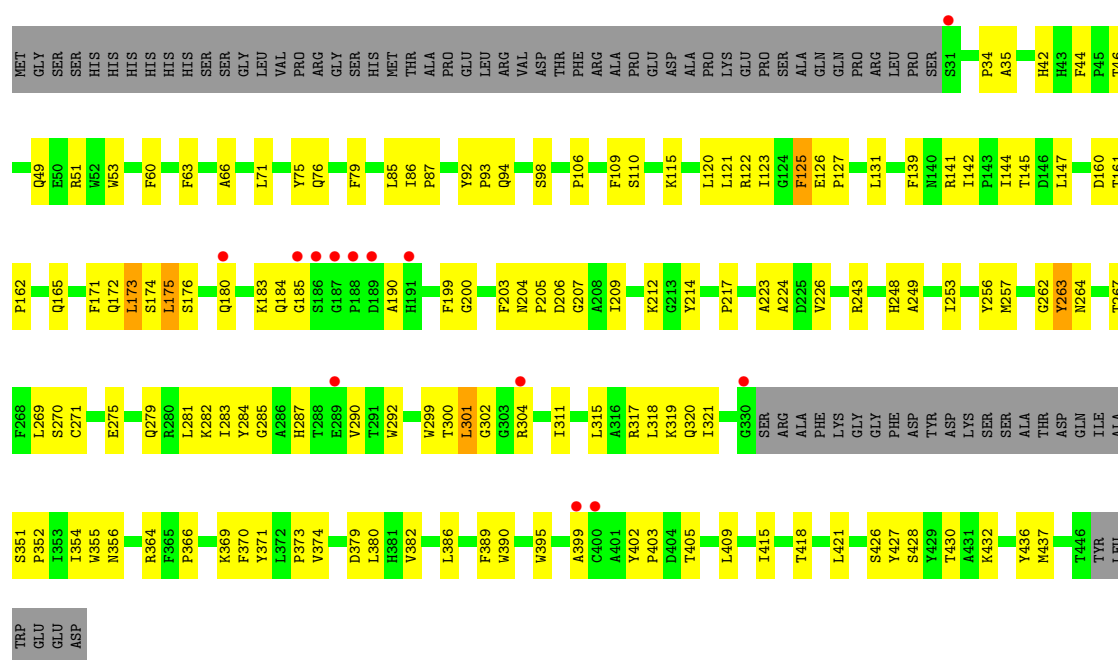


• Molecule 1: Deoxybrevianamide E synthase notF

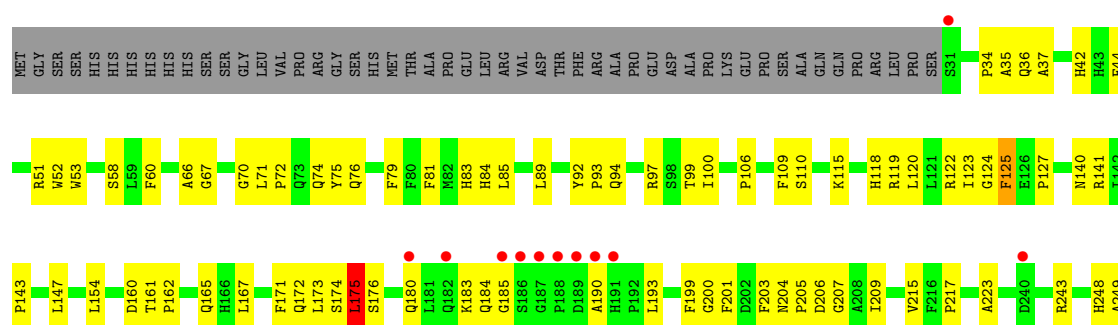


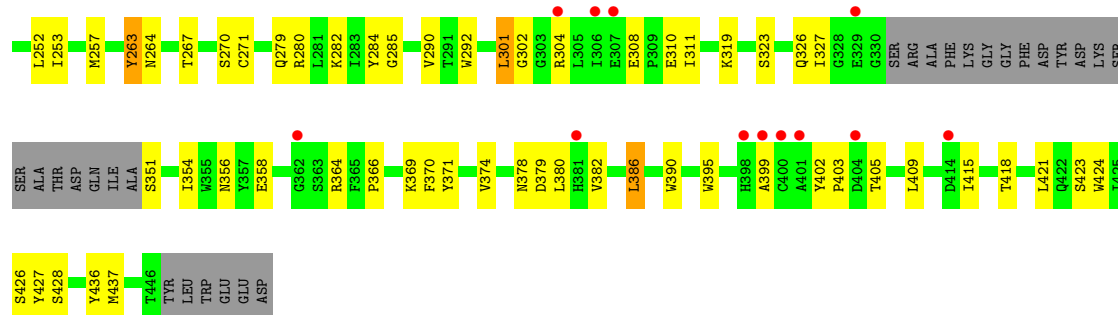


• Molecule 1: Deoxybrevianamide E synthase notF

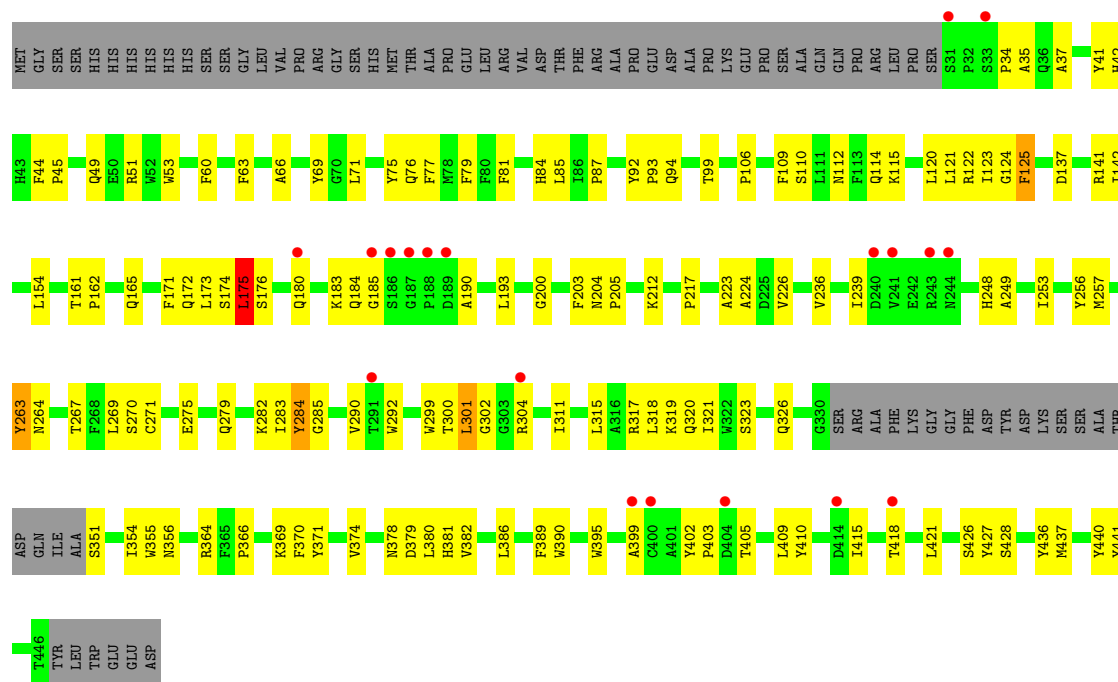


• Molecule 1: Deoxybrevianamide E synthase notF

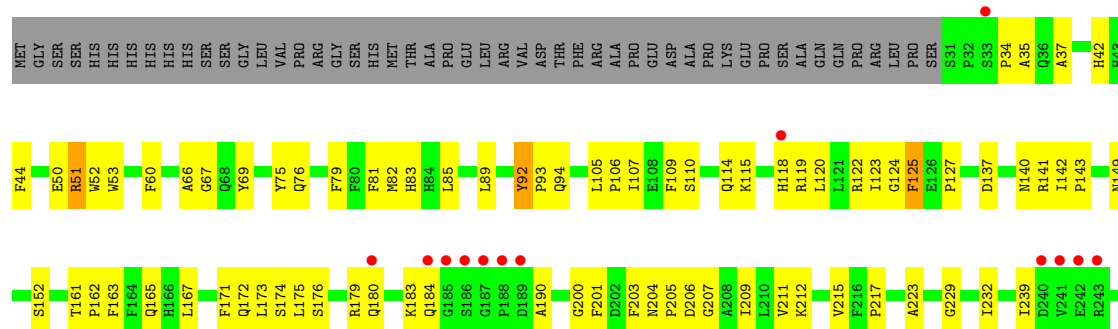


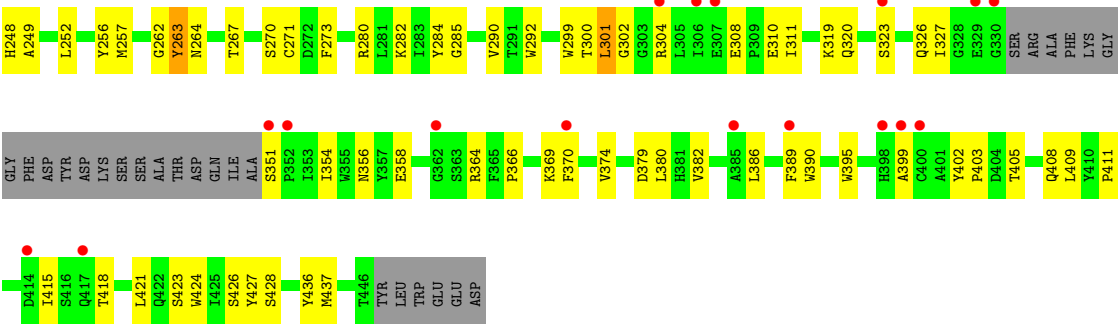


• Molecule 1: Deoxybrevianamide E synthase notF



• Molecule 1: Deoxybrevianamide E synthase notF





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	153.59Å 208.29Å 217.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.32 – 3.19 49.32 – 3.19	Depositor EDS
% Data completeness (in resolution range)	93.4 (49.32-3.19) 92.5 (49.32-3.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.307 , 0.316 0.307 , 0.316	Depositor DCC
R_{free} test set	1902 reflections (1.64%)	wwPDB-VP
Wilson B-factor (Å ²)	81.6	Xtriage
Anisotropy	0.657	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.002 for -h,l,k	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	25720	wwPDB-VP
Average B, all atoms (Å ²)	102.0	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 35.84 % 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 5.4788e-04. 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

5.1 Standard geometry

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	0.43	0/3319	0.65	2/4514 (0.0%)
1	B	0.44	0/3319	0.66	3/4514 (0.1%)
1	C	0.47	2/3319 (0.1%)	0.73	4/4514 (0.1%)
1	D	0.42	0/3319	0.65	3/4514 (0.1%)
1	E	0.43	0/3319	0.64	1/4514 (0.0%)
1	F	0.45	0/3319	0.67	3/4514 (0.1%)
1	G	0.43	0/3319	0.67	2/4514 (0.0%)
1	H	0.43	0/3319	0.66	2/4514 (0.0%)
All	All	0.44	2/26552 (0.0%)	0.67	20/36112 (0.1%)

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	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	51	ARG	CA-CB	-6.24	1.40	1.53
1	C	92	TYR	CE1-CZ	5.80	1.46	1.38

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	51	ARG	NE-CZ-NH1	14.62	127.61	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	51	ARG	CB-CG-CD	9.84	137.18	111.60
1	C	51	ARG	NE-CZ-NH2	-9.53	115.53	120.30
1	E	301	LEU	CA-CB-CG	7.16	131.77	115.30
1	F	301	LEU	CA-CB-CG	6.99	131.37	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	175	LEU	Peptide
1	E	175	LEU	Peptide
1	F	175	LEU	Peptide
1	G	175	LEU	Peptide
1	H	175	LEU	Peptide

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	3215	0	3093	128	0
1	B	3215	0	3093	131	0
1	C	3215	0	3093	123	0
1	D	3215	0	3093	121	0
1	E	3215	0	3093	122	0
1	F	3215	0	3093	116	0
1	G	3215	0	3093	126	0
1	H	3215	0	3093	117	0
All	All	25720	0	24744	903	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 18.

The worst 5 of 903 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:162:PRO:HG2	1:G:174:SER:HB3	1.35	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:290:VAL:HG21	1:G:351:SER:HB2	1.45	0.98
1:H:290:VAL:HG21	1:H:351:SER:HB2	1.48	0.95
1:F:165:GLN:HG3	1:C:172:GLN:HE22	1.31	0.94
1:B:174:SER:HB3	1:H:162:PRO:HG2	1.48	0.94

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	392/472 (83%)	368 (94%)	23 (6%)	1 (0%)	41	74
1	B	392/472 (83%)	368 (94%)	22 (6%)	2 (0%)	29	67
1	C	392/472 (83%)	367 (94%)	24 (6%)	1 (0%)	41	74
1	D	392/472 (83%)	370 (94%)	21 (5%)	1 (0%)	41	74
1	E	392/472 (83%)	366 (93%)	25 (6%)	1 (0%)	41	74
1	F	392/472 (83%)	365 (93%)	26 (7%)	1 (0%)	41	74
1	G	392/472 (83%)	366 (93%)	25 (6%)	1 (0%)	41	74
1	H	392/472 (83%)	366 (93%)	25 (6%)	1 (0%)	41	74
All	All	3136/3776 (83%)	2936 (94%)	191 (6%)	9 (0%)	41	74

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	34	PRO
1	E	34	PRO
1	C	34	PRO
1	A	34	PRO
1	G	34	PRO

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	344/408 (84%)	338 (98%)	6 (2%)	60	83
1	B	344/408 (84%)	337 (98%)	7 (2%)	55	80
1	C	344/408 (84%)	338 (98%)	6 (2%)	60	83
1	D	344/408 (84%)	337 (98%)	7 (2%)	55	80
1	E	344/408 (84%)	338 (98%)	6 (2%)	60	83
1	F	344/408 (84%)	338 (98%)	6 (2%)	60	83
1	G	344/408 (84%)	338 (98%)	6 (2%)	60	83
1	H	344/408 (84%)	337 (98%)	7 (2%)	55	80
All	All	2752/3264 (84%)	2701 (98%)	51 (2%)	57	81

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	209	ILE
1	F	175	LEU
1	C	184	GLN
1	H	284	TYR
1	F	184	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	422	GLN
1	F	248	HIS
1	C	172	GLN
1	F	76	GLN
1	F	279	GLN

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 monosaccharides 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.

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	396/472 (83%)	0.31	22 (5%) 24 13	61, 98, 168, 261	0
1	B	396/472 (83%)	0.24	20 (5%) 28 16	58, 94, 169, 261	0
1	C	396/472 (83%)	0.42	30 (7%) 13 7	64, 101, 169, 261	0
1	D	396/472 (83%)	0.36	23 (5%) 23 13	63, 100, 169, 261	0
1	E	396/472 (83%)	0.25	19 (4%) 30 18	59, 97, 169, 261	0
1	F	396/472 (83%)	0.18	13 (3%) 46 30	60, 96, 169, 261	0
1	G	396/472 (83%)	0.25	15 (3%) 40 26	58, 94, 169, 261	0
1	H	396/472 (83%)	0.40	23 (5%) 23 13	62, 101, 170, 261	0
All	All	3168/3776 (83%)	0.30	165 (5%) 27 15	58, 97, 169, 261	0

The worst 5 of 165 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	330	GLY	11.5
1	A	399	ALA	10.8
1	A	400	CYS	10.0
1	C	188	PRO	9.9
1	C	399	ALA	9.3

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.