



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 05:10 am GMT

PDB ID : 1TQY  
Title : The Actinorhodin Ketosynthase/Chain Length Factor  
Authors : Keatinge-Clay, A.T.; Maltby, D.A.; Medzihradsky, K.F.; Khosla, C.; Stroud, R.M.  
Deposited on : 2004-06-18  
Resolution : 2.00 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

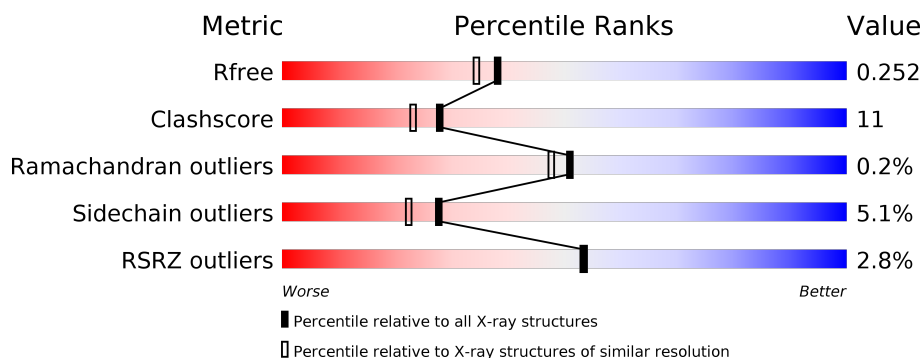
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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  $\geq 3$ , 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	424	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>24%</div> <div>..</div> </div> </div>
1	C	424	<div> <div>4%</div> <div> <div></div> <div>78%</div> <div>20%</div> <div>..</div> </div> </div>
1	E	424	<div> <div>6%</div> <div> <div></div> <div>74%</div> <div>24%</div> <div>..</div> </div> </div>
1	G	424	<div> <div>3%</div> <div> <div></div> <div>75%</div> <div>21%</div> <div>..</div> </div> </div>
2	B	415	<div> <div>2%</div> <div> <div></div> <div>72%</div> <div>22%</div> <div>..</div> </div> </div>
2	D	415	<div> <div>%</div> <div> <div></div> <div>79%</div> <div>16%</div> <div>..</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	F	415	 2% 74% 20% . .
2	H	415	 % 76% 19% . .

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
3	NA	D	1092	-	-	-	X
4	MG	A	1095	-	-	-	X
5	ACE	A	633	-	-	-	X
5	ACE	E	633	-	-	X	-
5	ACE	G	633	-	-	X	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 25535 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 Beta-Ketoacyl synthase/Acyl transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	0	0
			3140	1936	570	618	16			
1	C	421	Total	C	N	O	S	0	0	0
			3140	1936	570	618	16			
1	E	421	Total	C	N	O	S	0	0	0
			3140	1936	570	618	16			
1	G	421	Total	C	N	O	S	0	0	0
			3140	1936	570	618	16			

- Molecule 2 is a protein called Actinorhodin polyketide putative beta-ketoacyl synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	402	Total	C	N	O	S	0	0	0
			2970	1863	537	565	5			
2	D	402	Total	C	N	O	S	0	0	0
			2970	1863	537	565	5			
2	F	402	Total	C	N	O	S	0	0	0
			2970	1863	537	565	5			
2	H	402	Total	C	N	O	S	0	0	0
			2970	1863	537	565	5			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	MET	-	Flag-tag	UNP Q02062
B	-6	ASP	-	Flag-tag	UNP Q02062
B	-5	TYR	-	flag tag	UNP Q02062
B	-4	LYS	-	flag tag	UNP Q02062
B	-3	ASP	-	flag tag	UNP Q02062
B	-2	ASP	-	flag tag	UNP Q02062
B	-1	ASP	-	flag tag	UNP Q02062
B	0	ASP	-	flag tag	UNP Q02062

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1	LYS	-	flag tag	UNP Q02062
D	-7	MET	-	flag tag	UNP Q02062
D	-6	ASP	-	flag tag	UNP Q02062
D	-5	TYR	-	flag tag	UNP Q02062
D	-4	LYS	-	flag tag	UNP Q02062
D	-3	ASP	-	flag tag	UNP Q02062
D	-2	ASP	-	flag tag	UNP Q02062
D	-1	ASP	-	flag tag	UNP Q02062
D	0	ASP	-	flag tag	UNP Q02062
D	1	LYS	-	flag tag	UNP Q02062
F	-7	MET	-	flag tag	UNP Q02062
F	-6	ASP	-	flag tag	UNP Q02062
F	-5	TYR	-	flag tag	UNP Q02062
F	-4	LYS	-	flag tag	UNP Q02062
F	-3	ASP	-	flag tag	UNP Q02062
F	-2	ASP	-	flag tag	UNP Q02062
F	-1	ASP	-	flag tag	UNP Q02062
F	0	ASP	-	flag tag	UNP Q02062
F	1	LYS	-	flag tag	UNP Q02062
H	-7	MET	-	flag tag	UNP Q02062
H	-6	ASP	-	flag tag	UNP Q02062
H	-5	TYR	-	flag tag	UNP Q02062
H	-4	LYS	-	flag tag	UNP Q02062
H	-3	ASP	-	flag tag	UNP Q02062
H	-2	ASP	-	flag tag	UNP Q02062
H	-1	ASP	-	flag tag	UNP Q02062
H	0	ASP	-	flag tag	UNP Q02062
H	1	LYS	-	?	UNP Q02062

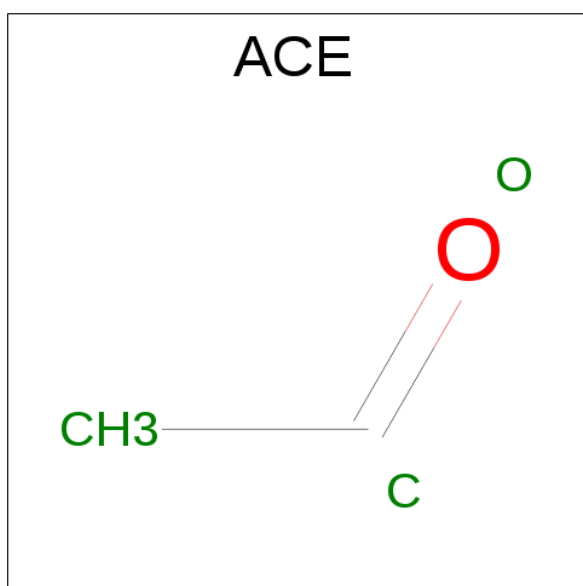
- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total Na 1 1	0	0
3	B	1	Total Na 1 1	0	0
3	D	1	Total Na 1 1	0	0
3	F	1	Total Na 1 1	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0
4	E	1	Total Mg 1 1	0	0

- Molecule 5 is ACETYL GROUP (three-letter code: ACE) (formula: C<sub>2</sub>H<sub>4</sub>O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 3 2 1	0	0
5	C	1	Total C O 3 2 1	0	0
5	E	1	Total C O 3 2 1	0	0
5	G	1	Total C O 3 2 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	99	Total O 99 99	0	0
6	B	144	Total O 144 144	0	0

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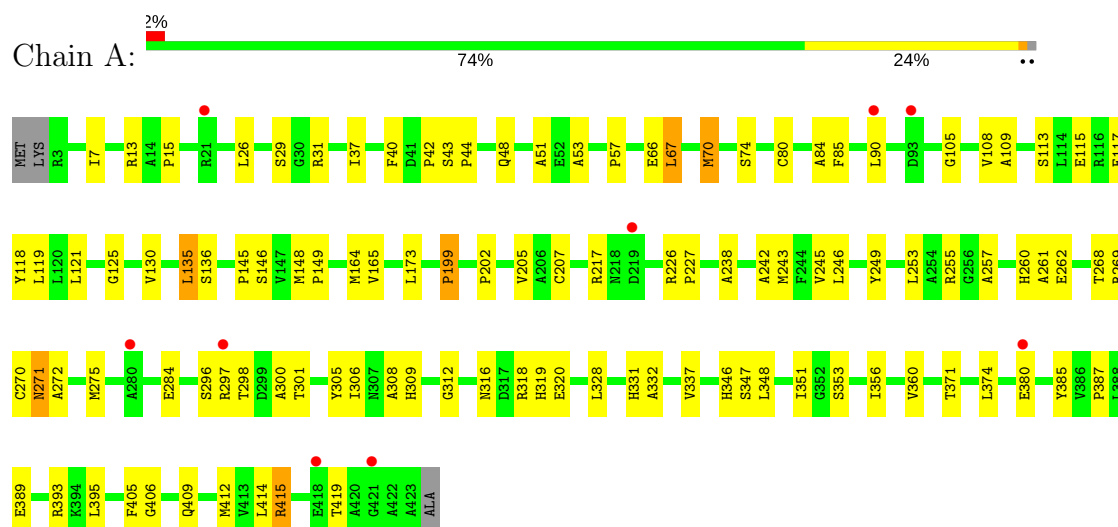
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	105	Total 105	O 105	0	0
6	D	187	Total 187	O 187	0	0
6	E	62	Total 62	O 62	0	0
6	F	157	Total 157	O 157	0	0
6	G	110	Total 110	O 110	0	0
6	H	211	Total 211	O 211	0	0

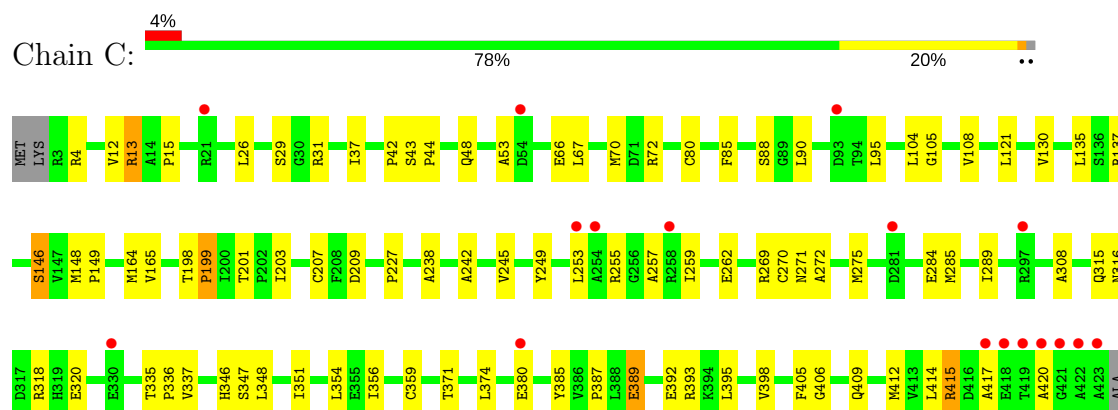
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

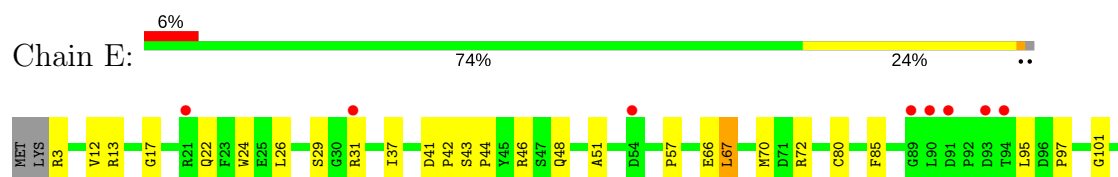
#### • Molecule 1: Beta-Ketoacyl synthase/Acyl transferase



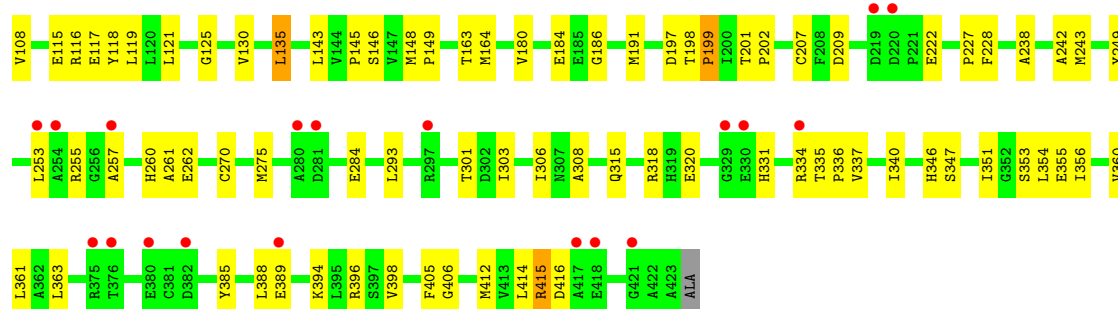
#### • Molecule 1: Beta-Ketoacyl synthase/Acyl transferase



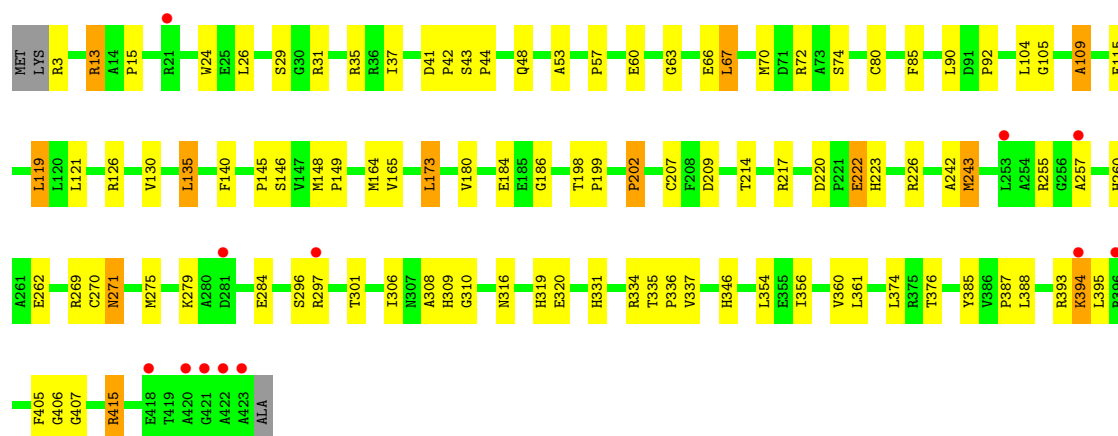
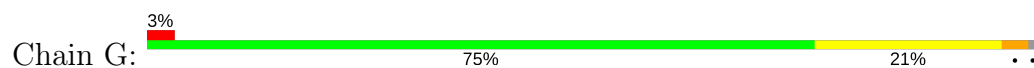
#### • Molecule 1: Beta-Ketoacyl synthase/Acyl transferase



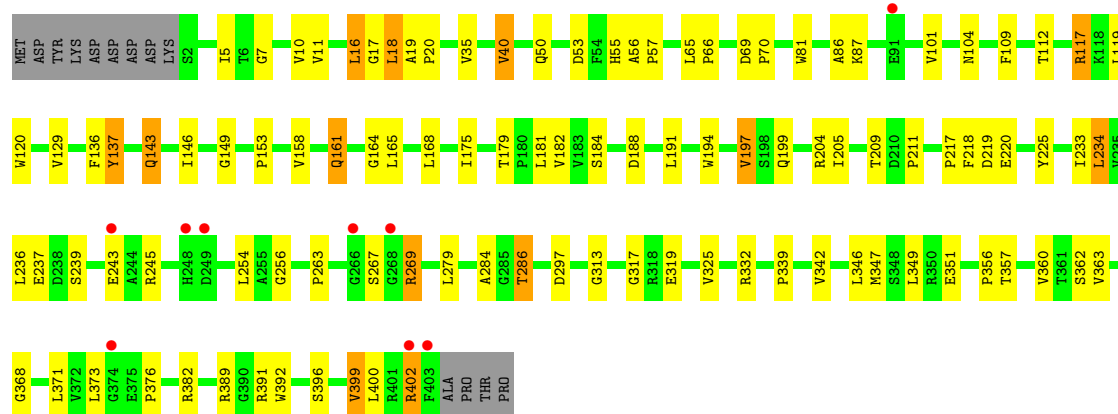




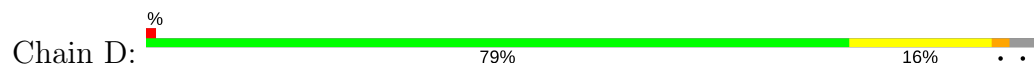
- Molecule 1: Beta-Ketoacyl synthase/Acyl transferase

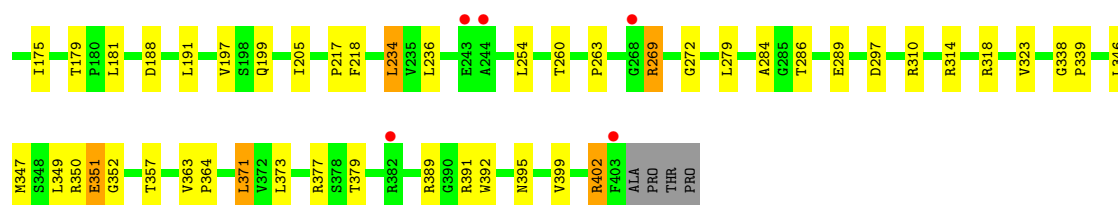


- Molecule 2: Actinorhodin polyketide putative beta-ketoacyl synthase 2



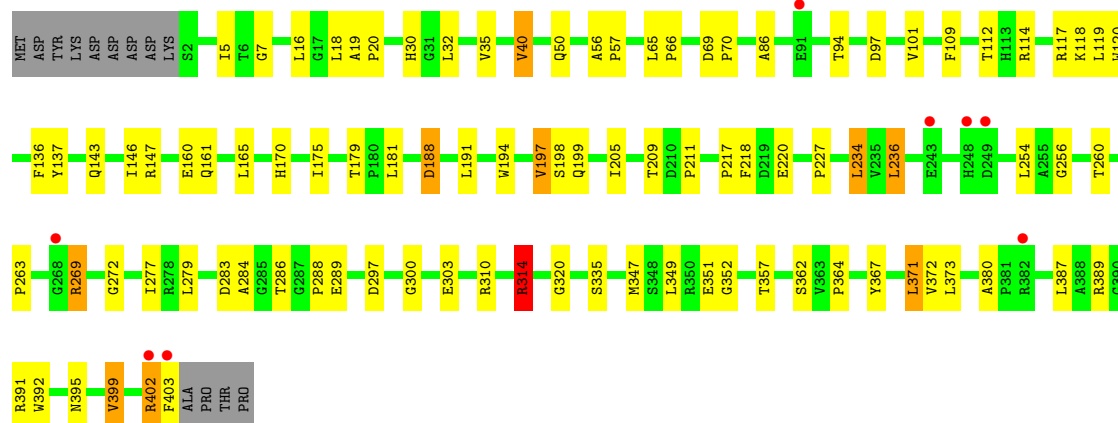
- Molecule 2: Actinorhodin polyketide putative beta-ketoacyl synthase 2





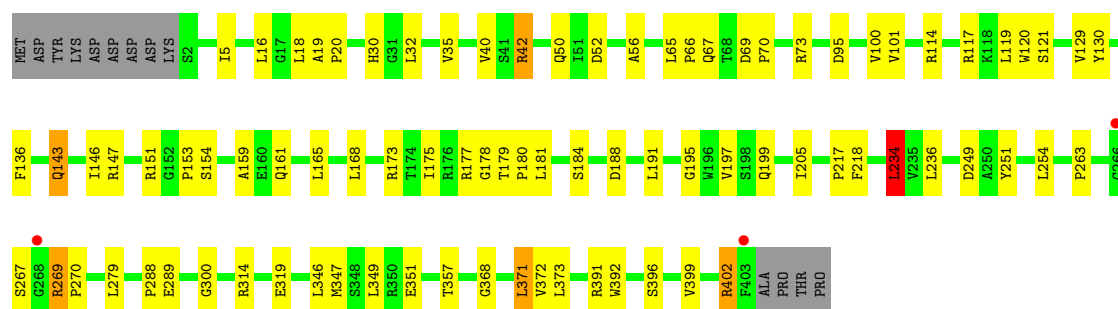
• Molecule 2: Actinorhodin polyketide putative beta-ketoacyl synthase 2

Chain F: 74% 20%



• Molecule 2: Actinorhodin polyketide putative beta-ketoacyl synthase 2

Chain H: 76% 19%



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	262.70Å 262.70Å 224.03Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.00 49.65 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.7 (50.00-2.00) 98.5 (49.65-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.70 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.233 , 0.253 0.233 , 0.252	Depositor DCC
$R_{free}$ test set	38543 reflections (10.03%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.2	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 42.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	25535	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.06% 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: NA, MG, ACE

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	0.38	0/3199	0.65	2/4346 (0.0%)
1	C	0.37	0/3199	0.62	0/4346
1	E	0.34	0/3199	0.59	0/4346
1	G	0.38	0/3199	0.64	1/4346 (0.0%)
2	B	0.37	0/3041	0.64	0/4151
2	D	0.41	0/3041	0.68	0/4151
2	F	0.37	0/3041	0.95	5/4151 (0.1%)
2	H	0.40	0/3041	0.89	5/4151 (0.1%)
All	All	0.38	0/24960	0.72	13/33988 (0.0%)

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
2	B	0	1
2	F	0	2
All	All	0	3

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	314	ARG	NE-CZ-NH2	-32.84	103.88	120.30
2	F	314	ARG	NE-CZ-NH1	30.51	135.55	120.30
2	H	314	ARG	NE-CZ-NH2	-27.43	106.59	120.30
2	H	314	ARG	NE-CZ-NH1	25.06	132.83	120.30
1	A	298	THR	CA-CB-CG2	8.28	123.99	112.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	137	TYR	Sidechain
2	F	137	TYR	Sidechain
2	F	314	ARG	Sidechain

## 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	3140	0	3032	78	0
1	C	3140	0	3032	69	0
1	E	3140	0	3032	77	0
1	G	3140	0	3032	80	0
2	B	2970	0	2903	76	0
2	D	2970	0	2903	61	0
2	F	2970	0	2903	73	0
2	H	2970	0	2903	69	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
5	A	3	0	3	1	0
5	C	3	0	3	1	0
5	E	3	0	3	2	0
5	G	3	0	3	2	0
6	A	99	0	0	1	0
6	B	144	0	0	2	1
6	C	105	0	0	9	0
6	D	187	0	0	11	0
6	E	62	0	0	1	0
6	F	157	0	0	7	1
6	G	110	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	H	211	0	0	4	0
All	All	25535	0	23752	538	1

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 11.

The worst 5 of 538 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)
2:D:402:ARG:HG3	6:D:1237:HOH:O	1.39	1.21
1:G:376:THR:HG23	6:G:1143:HOH:O	1.47	1.13
1:C:392:GLU:HB2	6:C:1124:HOH:O	1.50	1.11
1:G:275:MET:HE1	1:G:406:GLY:HA2	1.15	1.06
1:C:146:SER:HB2	6:D:1189:HOH:O	1.54	1.05

All (1) 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)
6:B:1122:HOH:O	6:F:1120:HOH:O[9_554]	2.14	0.06

## 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	419/424 (99%)	397 (95%)	22 (5%)	0	100	100
1	C	419/424 (99%)	393 (94%)	25 (6%)	1 (0%)	51	48
1	E	419/424 (99%)	394 (94%)	24 (6%)	1 (0%)	51	48
1	G	419/424 (99%)	399 (95%)	17 (4%)	3 (1%)	25	18
2	B	400/415 (96%)	379 (95%)	21 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	400/415 (96%)	383 (96%)	16 (4%)	1 (0%)	44	40
2	F	400/415 (96%)	385 (96%)	15 (4%)	0	100	100
2	H	400/415 (96%)	381 (95%)	18 (4%)	1 (0%)	44	40
All	All	3276/3356 (98%)	3111 (95%)	158 (5%)	7 (0%)	51	48

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	310	GLY
1	G	388	LEU
1	E	388	LEU
1	G	109	ALA
1	C	146	SER

### 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	319/321 (99%)	307 (96%)	12 (4%)	38	35
1	C	319/321 (99%)	310 (97%)	9 (3%)	49	49
1	E	319/321 (99%)	308 (97%)	11 (3%)	42	40
1	G	319/321 (99%)	302 (95%)	17 (5%)	26	21
2	B	297/309 (96%)	275 (93%)	22 (7%)	16	10
2	D	297/309 (96%)	277 (93%)	20 (7%)	19	13
2	F	297/309 (96%)	279 (94%)	18 (6%)	22	16
2	H	297/309 (96%)	280 (94%)	17 (6%)	24	18
All	All	2464/2520 (98%)	2338 (95%)	126 (5%)	28	22

5 of 126 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	254	LEU

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Mol	Chain	Res	Type
1	E	346	HIS
2	H	188	ASP
2	D	279	LEU
1	E	13	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	67	GLN
2	D	248	HIS
1	G	316	ASN
1	C	373	ASN
2	H	55	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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
5	ACE	A	633	1	2,2,2	0.68	0	1,1,1	0.26	0
5	ACE	C	633	1	2,2,2	0.68	0	1,1,1	0.26	0
5	ACE	E	633	1	2,2,2	0.68	0	1,1,1	0.26	0
5	ACE	G	633	1	2,2,2	0.70	0	1,1,1	0.26	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
5	ACE	A	633	1	-	0/0/0/0	0/0/0/0
5	ACE	C	633	1	-	0/0/0/0	0/0/0/0
5	ACE	E	633	1	-	0/0/0/0	0/0/0/0
5	ACE	G	633	1	-	0/0/0/0	0/0/0/0

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.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	633	ACE	1	0
5	C	633	ACE	1	0
5	E	633	ACE	2	0
5	G	633	ACE	2	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, 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	421/424 (99%)	-0.08	9 (2%) 64 63	20, 30, 45, 63	0
1	C	421/424 (99%)	0.05	17 (4%) 39 39	18, 29, 49, 79	0
1	E	421/424 (99%)	0.26	27 (6%) 20 20	20, 37, 56, 66	0
1	G	421/424 (99%)	-0.11	12 (2%) 52 52	18, 28, 46, 62	0
2	B	402/415 (96%)	-0.14	9 (2%) 62 61	18, 27, 43, 56	0
2	D	402/415 (96%)	-0.26	6 (1%) 74 73	16, 23, 39, 56	0
2	F	402/415 (96%)	-0.19	8 (1%) 65 65	19, 28, 45, 62	0
2	H	402/415 (96%)	-0.21	3 (0%) 87 87	17, 24, 41, 59	0
All	All	3292/3356 (98%)	-0.08	91 (2%) 53 53	16, 28, 48, 79	0

The worst 5 of 91 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	403	PHE	6.2
1	C	422	ALA	5.1
1	C	421	GLY	4.8
1	G	297	ARG	4.5
1	G	422	ALA	4.4

### 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 ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	ACE	G	633	3/3	0.87	0.22	4.91	46,46,47,47	0
4	MG	A	1095	1/1	0.35	0.20	4.62	51,51,51,51	0
3	NA	D	1092	1/1	0.94	0.13	4.58	38,38,38,38	0
5	ACE	A	633	3/3	0.85	0.20	2.91	52,52,52,52	0
3	NA	F	1093	1/1	0.96	0.11	1.50	45,45,45,45	0
5	ACE	C	633	3/3	0.93	0.15	1.36	52,52,53,53	0
4	MG	E	1097	1/1	0.83	0.14	1.06	47,47,47,47	0
5	ACE	E	633	3/3	0.93	0.13	0.30	47,47,48,48	0
3	NA	B	1091	1/1	0.70	0.09	0.22	39,39,39,39	0
3	NA	H	1094	1/1	0.97	0.06	-1.75	36,36,36,36	0
4	MG	C	1096	1/1	0.86	0.08	-2.90	39,39,39,39	0
4	MG	G	1098	1/1	0.96	0.07	-4.21	35,35,35,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.