



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 02:04 am BST

PDB ID : 5INF  
Title : Structural basis for acyl-CoA carboxylase-mediated assembly of unusual polyketide synthase extender units incorporated into the stambomycin antibiotics  
Authors : Valentic, T.R.; Ray, L.; Miyazawa, T.; Withall, D.M.; Song, L.; Osada, H.; Tsai, S.C.; Challis, G.L.  
Deposited on : 2016-03-07  
Resolution : 2.75 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.

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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	:	2.11
buster-report	:	1.1.7 (2018)
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)	:	2.11

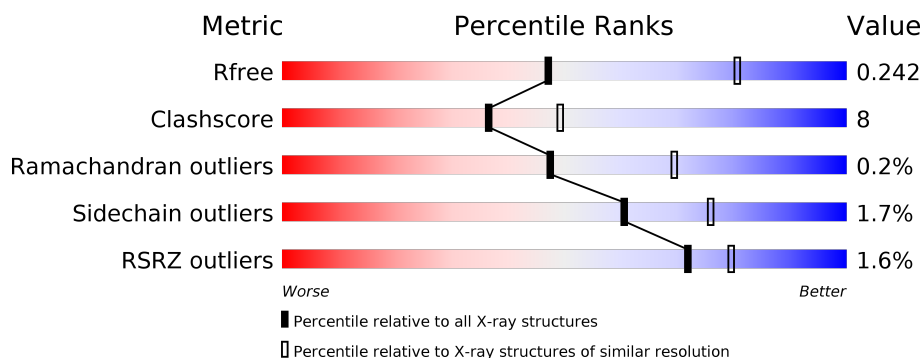
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 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	538	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 76%, yellow 12%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>76%</span> <span>12%</span> <span>• 11%</span> </div> </div>
1	B	538	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 77%, yellow 11%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>77%</span> <span>11%</span> <span>• 11%</span> </div> </div>
1	C	538	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 75%, yellow 13%, grey 10%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>75%</span> <span>13%</span> <span>• 10%</span> </div> </div>
1	D	538	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, green 73%, yellow 15%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>2%</span> <span>73%</span> <span>15%</span> <span>• 11%</span> </div> </div>
1	E	538	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, green 76%, yellow 13%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>2%</span> <span>76%</span> <span>13%</span> <span>• 11%</span> </div> </div>
1	F	538	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 75%, yellow 15%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>75%</span> <span>15%</span> <span>• 8%</span> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 23108 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 Carboxyl transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	478	Total	C	N	O	S	0	0	0
			3625	2281	642	684	18			
1	B	480	Total	C	N	O	S	0	0	0
			3632	2287	638	688	19			
1	C	486	Total	C	N	O	S	0	0	0
			3680	2314	651	696	19			
1	D	479	Total	C	N	O	S	0	0	0
			3634	2288	643	685	18			
1	E	481	Total	C	N	O	S	0	0	0
			3643	2293	643	689	18			
1	F	494	Total	C	N	O	S	0	0	0
			3750	2361	662	708	19			

There are 36 discrepancies between the modelled and reference sequences:

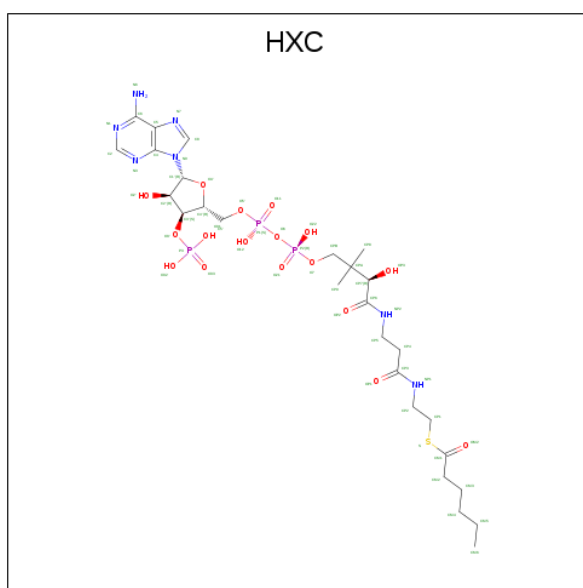
Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP A0ACI9
A	-4	ILE	-	expression tag	UNP A0ACI9
A	-3	ASP	-	expression tag	UNP A0ACI9
A	-2	PRO	-	expression tag	UNP A0ACI9
A	-1	PHE	-	expression tag	UNP A0ACI9
A	0	THR	-	expression tag	UNP A0ACI9
B	-5	GLY	-	expression tag	UNP A0ACI9
B	-4	ILE	-	expression tag	UNP A0ACI9
B	-3	ASP	-	expression tag	UNP A0ACI9
B	-2	PRO	-	expression tag	UNP A0ACI9
B	-1	PHE	-	expression tag	UNP A0ACI9
B	0	THR	-	expression tag	UNP A0ACI9
C	-5	GLY	-	expression tag	UNP A0ACI9
C	-4	ILE	-	expression tag	UNP A0ACI9
C	-3	ASP	-	expression tag	UNP A0ACI9
C	-2	PRO	-	expression tag	UNP A0ACI9
C	-1	PHE	-	expression tag	UNP A0ACI9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	THR	-	expression tag	UNP A0ACI9
D	-5	GLY	-	expression tag	UNP A0ACI9
D	-4	ILE	-	expression tag	UNP A0ACI9
D	-3	ASP	-	expression tag	UNP A0ACI9
D	-2	PRO	-	expression tag	UNP A0ACI9
D	-1	PHE	-	expression tag	UNP A0ACI9
D	0	THR	-	expression tag	UNP A0ACI9
E	-5	GLY	-	expression tag	UNP A0ACI9
E	-4	ILE	-	expression tag	UNP A0ACI9
E	-3	ASP	-	expression tag	UNP A0ACI9
E	-2	PRO	-	expression tag	UNP A0ACI9
E	-1	PHE	-	expression tag	UNP A0ACI9
E	0	THR	-	expression tag	UNP A0ACI9
F	-5	GLY	-	expression tag	UNP A0ACI9
F	-4	ILE	-	expression tag	UNP A0ACI9
F	-3	ASP	-	expression tag	UNP A0ACI9
F	-2	PRO	-	expression tag	UNP A0ACI9
F	-1	PHE	-	expression tag	UNP A0ACI9
F	0	THR	-	expression tag	UNP A0ACI9

- Molecule 2 is HEXANOYL-COENZYME A (three-letter code: HXC) (formula:  $C_{27}H_{46}N_7O_{17}P_3S$ ).

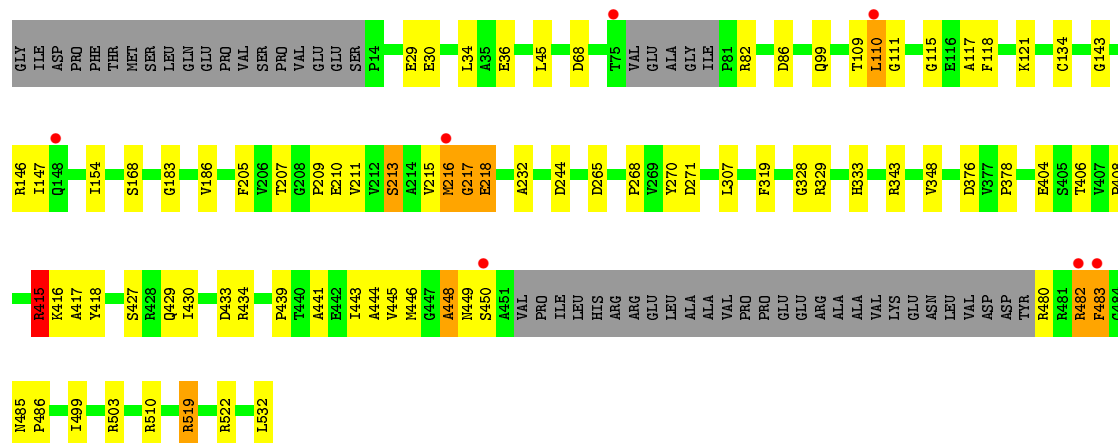


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	S	0	0
			55	27	7	17	3	1		

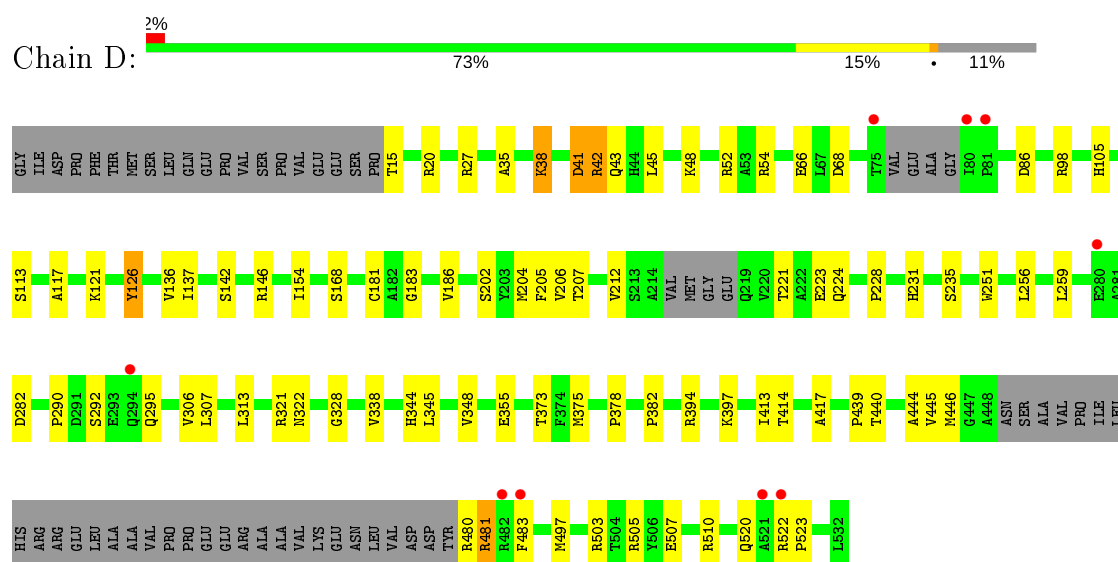
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	171	Total 171	O 171	0	0
3	B	181	Total 181	O 181	0	0
3	C	199	Total 199	O 199	0	0
3	D	172	Total 172	O 172	0	0
3	E	205	Total 205	O 205	0	0
3	F	161	Total 161	O 161	0	0

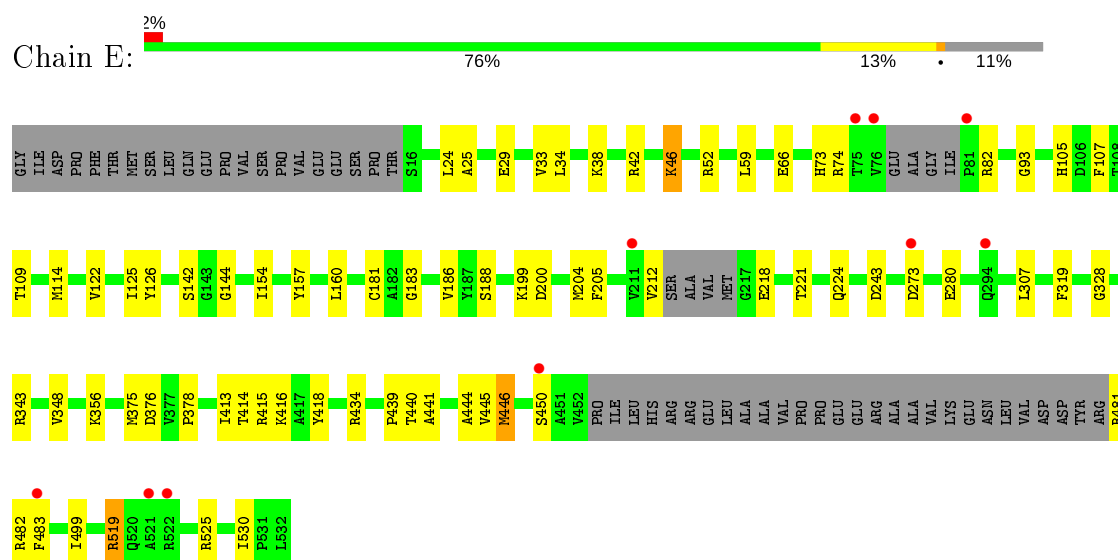




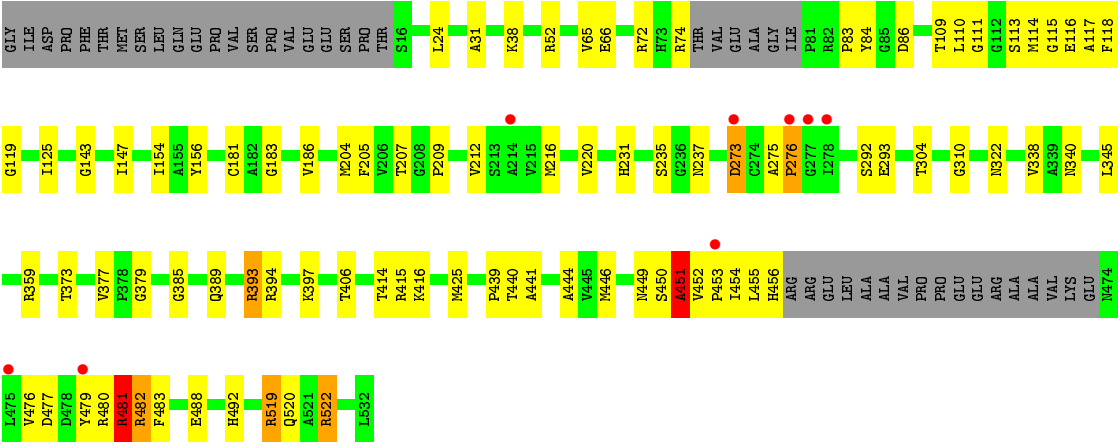
• Molecule 1: Carboxyl transferase



• Molecule 1: Carboxyl transferase



• Molecule 1: Carboxyl transferase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.07Å 165.45Å 190.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.22 – 2.75 44.55 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.6 (42.22-2.75) 90.6 (44.55-2.75)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.37 (at 2.77Å)	Xtriage
Refinement program	PHENIX (1.10 _2155: ???)	Depositor
R, $R_{free}$	0.184 , 0.244 0.186 , 0.242	Depositor DCC
$R_{free}$ test set	2000 reflections (2.21%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.6	Xtriage
Anisotropy	0.275	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 24.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	23108	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.57	0/3700	0.70	3/5025 (0.1%)
1	B	0.58	0/3708	0.68	0/5038
1	C	0.64	1/3757 (0.0%)	0.76	3/5103 (0.1%)
1	D	0.54	0/3709	0.67	2/5038 (0.0%)
1	E	0.62	0/3718	0.70	0/5050
1	F	0.61	0/3829	0.72	5/5203 (0.1%)
All	All	0.59	1/22421 (0.0%)	0.71	13/30457 (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
1	A	0	2
1	D	0	1
1	F	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	134	CYS	CB-SG	-7.32	1.69	1.82

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	483	PHE	N-CA-CB	-12.21	88.62	110.60
1	D	41	ASP	CB-CA-C	-9.33	91.74	110.40
1	A	482	ARG	NE-CZ-NH2	-8.36	116.12	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	482	ARG	NE-CZ-NH1	8.12	124.36	120.30
1	F	481	ARG	NE-CZ-NH2	-7.02	116.79	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	480	ARG	Peptide
1	A	481	ARG	Peptide
1	D	481	ARG	Peptide
1	F	481	ARG	Peptide

## 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	3625	0	3569	46	0
1	B	3632	0	3573	60	0
1	C	3680	0	3623	62	0
1	D	3634	0	3581	71	0
1	E	3643	0	3584	50	1
1	F	3750	0	3689	91	0
2	B	55	0	42	10	0
3	A	171	0	0	2	0
3	B	181	0	0	10	0
3	C	199	0	0	11	0
3	D	172	0	0	11	0
3	E	205	0	0	6	0
3	F	161	0	0	12	0
All	All	23108	0	21661	346	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 8.

The worst 5 of 346 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:D:41:ASP:O	1:D:45:LEU:CD2	1.88	1.22
2:B:601:HXC:C1'	2:B:601:HXC:O4'	1.69	1.13
1:C:209:PRO:O	1:C:213:SER:HB2	1.52	1.09
1:D:41:ASP:O	1:D:45:LEU:HD23	1.50	1.05
1:A:37:LYS:NZ	3:A:601:HOH:O	1.91	1.01

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)
1:E:46:LYS:NZ	1:E:280:GLU:OE2[4_555]	1.89	0.31

## 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	470/538 (87%)	450 (96%)	20 (4%)	0	100	100
1	B	474/538 (88%)	459 (97%)	15 (3%)	0	100	100
1	C	480/538 (89%)	450 (94%)	26 (5%)	4 (1%)	19	34
1	D	471/538 (88%)	454 (96%)	17 (4%)	0	100	100
1	E	473/538 (88%)	453 (96%)	20 (4%)	0	100	100
1	F	488/538 (91%)	463 (95%)	24 (5%)	1 (0%)	47	69
All	All	2856/3228 (88%)	2729 (96%)	122 (4%)	5 (0%)	47	69

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	217	GLY
1	C	448	ALA
1	F	451	ALA

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Mol	Chain	Res	Type
1	C	415	ARG
1	C	449	ASN

### 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	379/430 (88%)	375 (99%)	4 (1%)	73	84
1	B	380/430 (88%)	373 (98%)	7 (2%)	59	75
1	C	385/430 (90%)	373 (97%)	12 (3%)	40	60
1	D	380/430 (88%)	377 (99%)	3 (1%)	81	88
1	E	381/430 (89%)	374 (98%)	7 (2%)	59	75
1	F	393/430 (91%)	386 (98%)	7 (2%)	59	75
All	All	2298/2580 (89%)	2258 (98%)	40 (2%)	60	76

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	415	ARG
1	C	519	ARG
1	F	393	ARG
1	C	480	ARG
1	D	38	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	99	GLN
1	E	517	ASN
1	F	449	ASN

### 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 ⓘ

1 ligand is 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	HXC	B	601	-	49,57,57	4.16	10 (20%)	60,83,83	1.72	10 (16%)

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	HXC	B	601	-	-	22/52/72/72	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	HXC	O4'-C1'	19.99	1.69	1.41
2	B	601	HXC	C2'-C1'	-16.93	1.28	1.53
2	B	601	HXC	O4'-C4'	-6.88	1.29	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	HXC	CP6-NP2	5.75	1.46	1.33
2	B	601	HXC	CP3-NP1	5.07	1.44	1.33

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	HXC	CM2-CM1-S	6.56	121.09	113.46
2	B	601	HXC	N3-C2-N1	-4.42	121.76	128.68
2	B	601	HXC	OM2-CM1-S	-4.29	117.05	122.61
2	B	601	HXC	CP2-NP1-CP3	3.26	128.88	122.84
2	B	601	HXC	CP4-CP5-NP2	-2.42	107.00	111.90

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

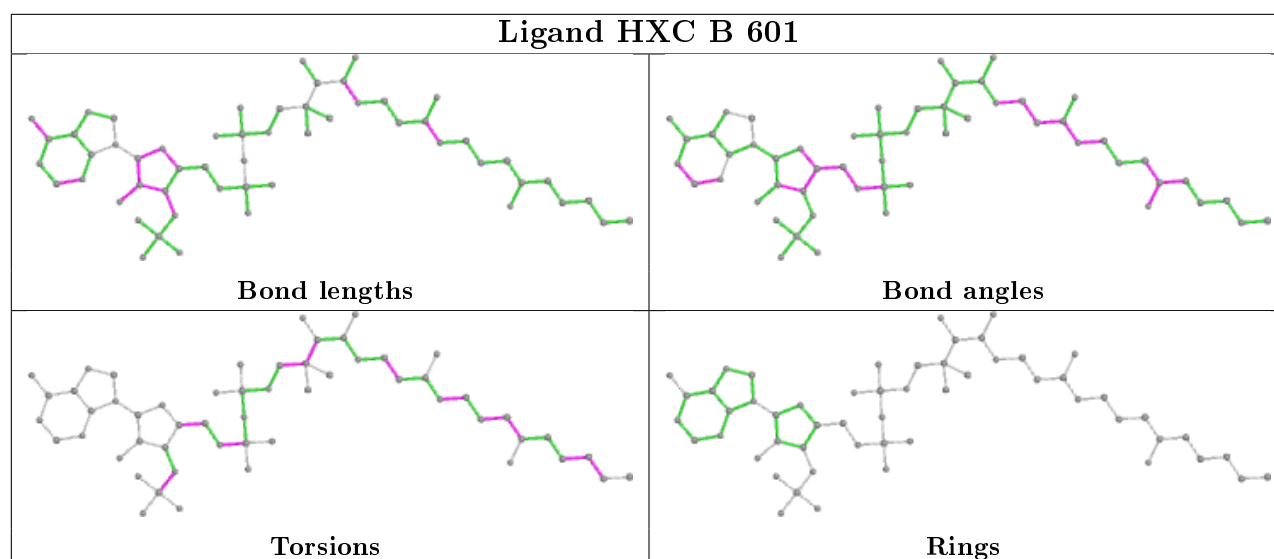
Mol	Chain	Res	Type	Atoms
2	B	601	HXC	C5'-O5'-P1-O11
2	B	601	HXC	C5'-O5'-P1-O12
2	B	601	HXC	C5'-O5'-P1-O6
2	B	601	HXC	CP6-CP7-CPA-CPB
2	B	601	HXC	OP3-CP7-CPA-CP9

There are no ring outliers.

1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	HXC	10	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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	478/538 (88%)	-0.53	6 (1%) 77 84	15, 25, 56, 82	0
1	B	480/538 (89%)	-0.56	5 (1%) 82 87	12, 23, 51, 72	0
1	C	486/538 (90%)	-0.53	7 (1%) 75 82	11, 22, 56, 84	0
1	D	479/538 (89%)	-0.46	9 (1%) 66 75	16, 26, 57, 95	0
1	E	481/538 (89%)	-0.49	10 (2%) 63 72	12, 21, 56, 100	0
1	F	494/538 (91%)	-0.43	8 (1%) 72 79	12, 23, 58, 102	0
All	All	2898/3228 (89%)	-0.50	45 (1%) 72 79	11, 23, 56, 102	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	450	SER	4.6
1	B	521	ALA	4.5
1	F	277	GLY	4.5
1	D	80	ILE	4.5
1	C	75	THR	4.3

### 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](#)

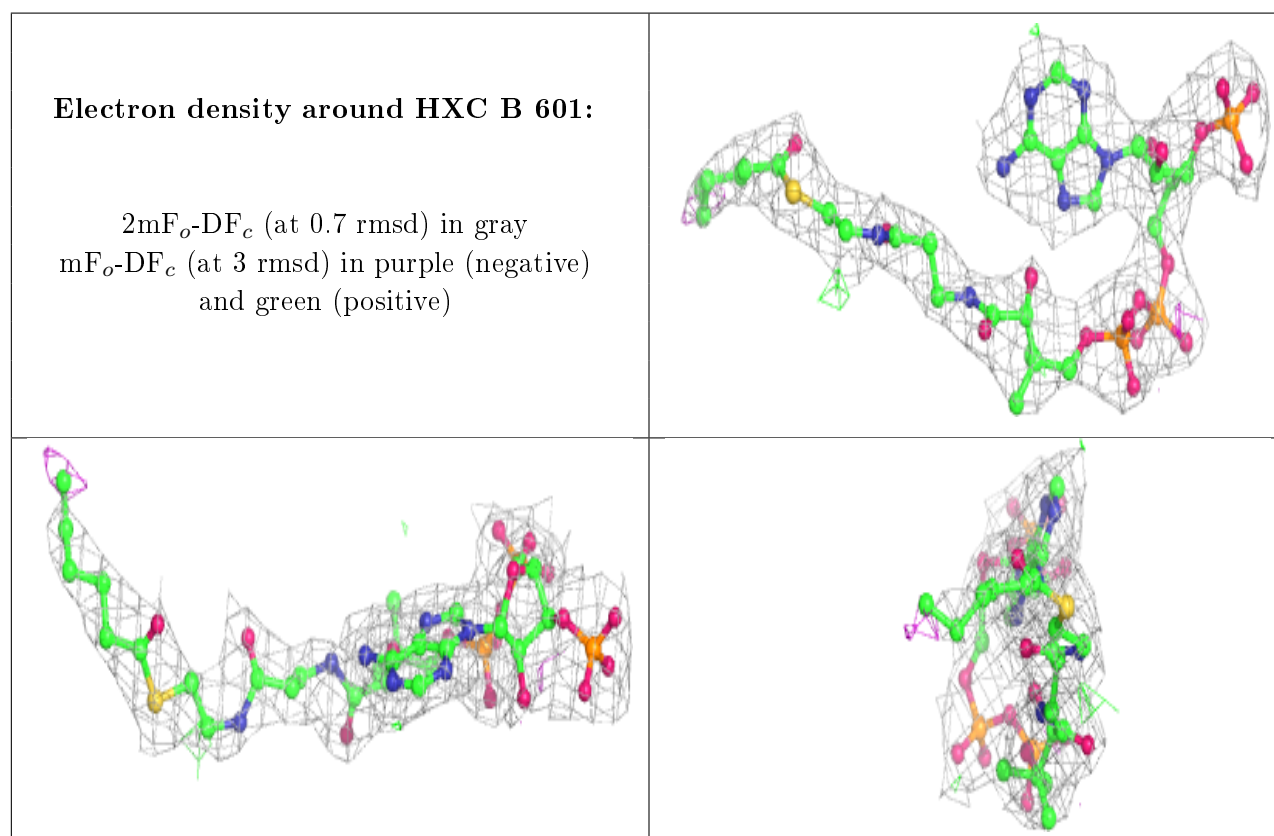
There are no carbohydrates in this entry.

## 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, 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	HXC	B	601	55/55	0.92	0.17	25,52,74,80	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.