



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 15, 2016 – 04:21 PM EDT

PDB ID : 5LP7  
Title : Crystal structure of 3-Ketoacyl-CoA Thiolase (MmgA) from Bacillus subtilis.  
Authors : Baker, G.E.; Race, P.R.  
Deposited on : 2016-08-11  
Resolution : 2.20 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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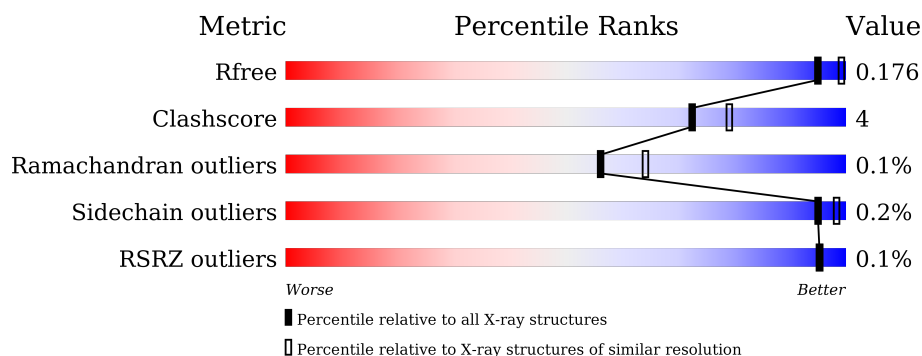
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027939  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : rb-20027939

**i**

## X-RAY DIFFRACTION

A.





Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

Mol	Chain	Length	Quality of chain
1	A	393	<div><div style="width: 79%;">79%</div><div style="width: 15%;">15%</div><div>• • •</div></div>
1	B	393	<div><div style="width: 82%;">82%</div><div style="width: 14%;">14%</div><div>• • •</div></div>
1	C	393	<div><div style="width: 80%;">80%</div><div style="width: 17%;">17%</div><div>• •</div></div>
1	D	393	<div><div style="width: 81%;">81%</div><div style="width: 15%;">15%</div><div>• •</div></div>
1	E	393	<div><div style="width: 80%;">80%</div><div style="width: 17%;">17%</div><div>• •</div></div>
1	F	393	<div><div style="width: 79%;">79%</div><div style="width: 16%;">16%</div><div>• •</div></div>

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Mol	Chain	Length	Quality of chain
1	G	393	 80% 16% ...
1	H	393	 79% 17% ..

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
2	GOL	A	401	-	-	-	X
2	GOL	B	401	-	-	-	X
2	GOL	B	402	-	-	-	X
2	GOL	C	401	-	-	-	X
2	GOL	D	401	-	-	-	X
2	GOL	E	401	-	-	-	X
2	GOL	F	401	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22740 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 Acetyl-CoA acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	386	Total	C	N	O	S	0	0	0
			2733	1707	484	524	18			
1	E	386	Total	C	N	O	S	0	0	0
			2740	1702	490	531	17			
1	A	386	Total	C	N	O	S	0	0	0
			2730	1703	486	523	18			
1	B	388	Total	C	N	O	S	0	0	0
			2753	1716	491	528	18			
1	C	387	Total	C	N	O	S	0	0	0
			2749	1713	497	522	17			
1	F	380	Total	C	N	O	S	0	0	0
			2641	1648	468	507	18			
1	G	385	Total	C	N	O	S	0	0	0
			2728	1702	482	528	16			
1	D	386	Total	C	N	O	S	0	0	0
			2740	1710	491	521	18			

- 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	E	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	82	Total	O	0	0
			82	82		
3	E	80	Total	O	0	0
			80	80		
3	A	110	Total	O	0	0
			110	110		
3	B	146	Total	O	0	0
			146	146		

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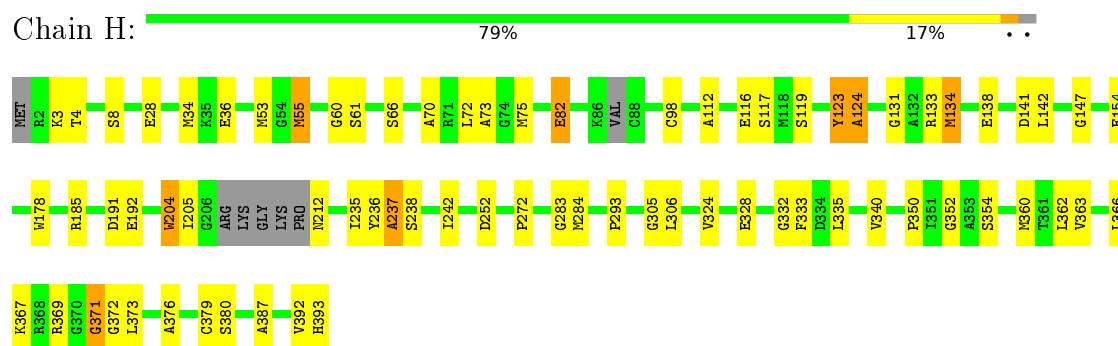
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	136	Total 136	O 136	0	0
3	F	80	Total 80	O 80	0	0
3	G	119	Total 119	O 119	0	0
3	D	125	Total 125	O 125	0	0

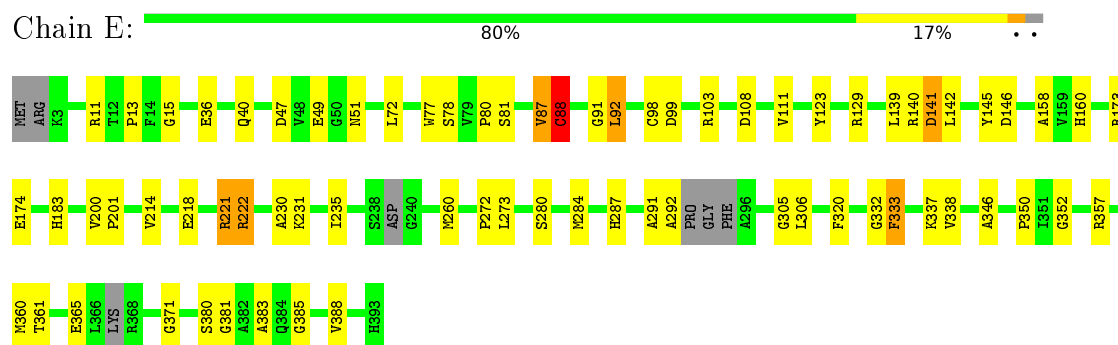
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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.

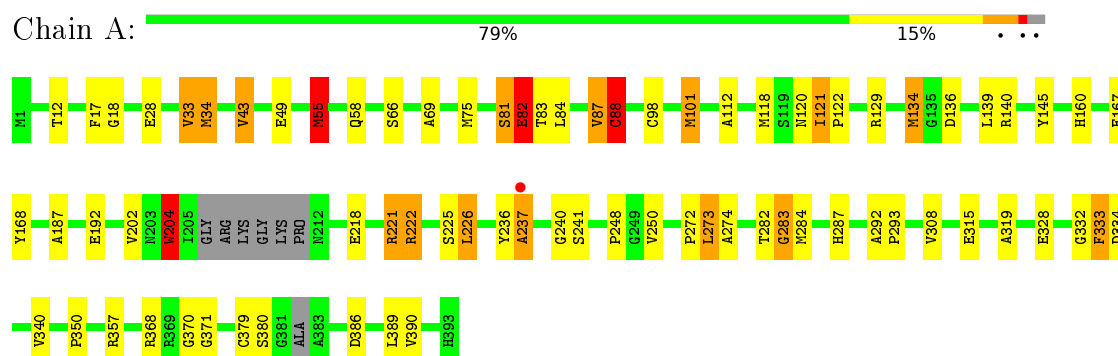
#### • Molecule 1: Acetyl-CoA acetyltransferase



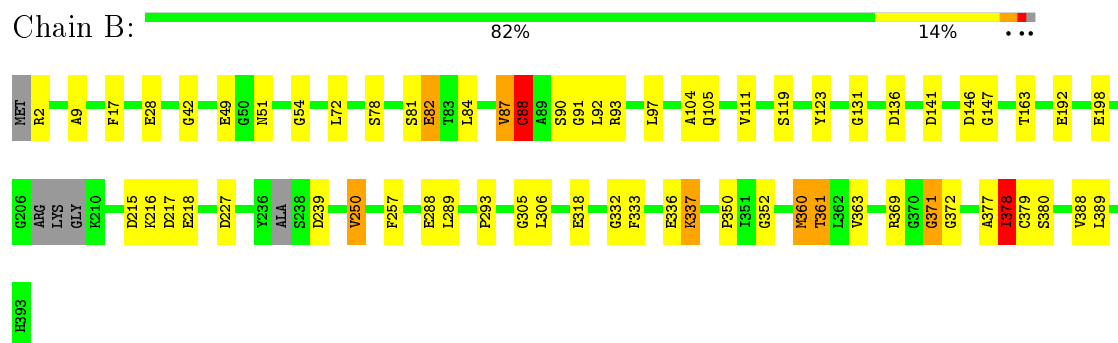
#### • Molecule 1: Acetyl-CoA acetyltransferase



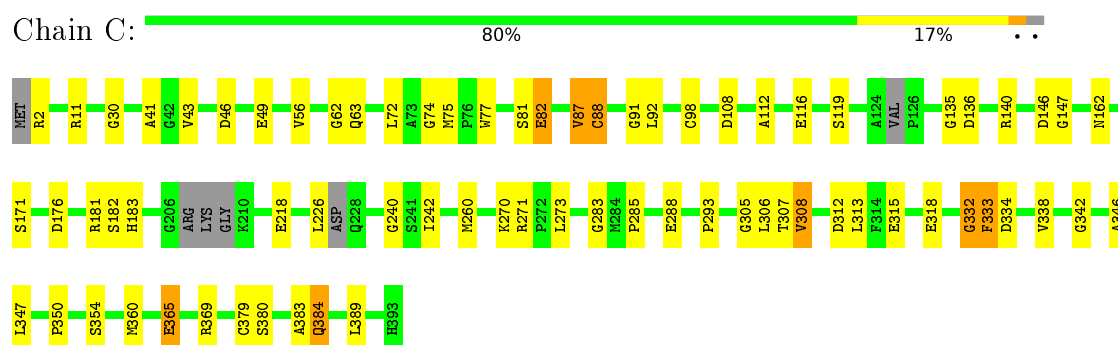
#### • Molecule 1: Acetyl-CoA acetyltransferase



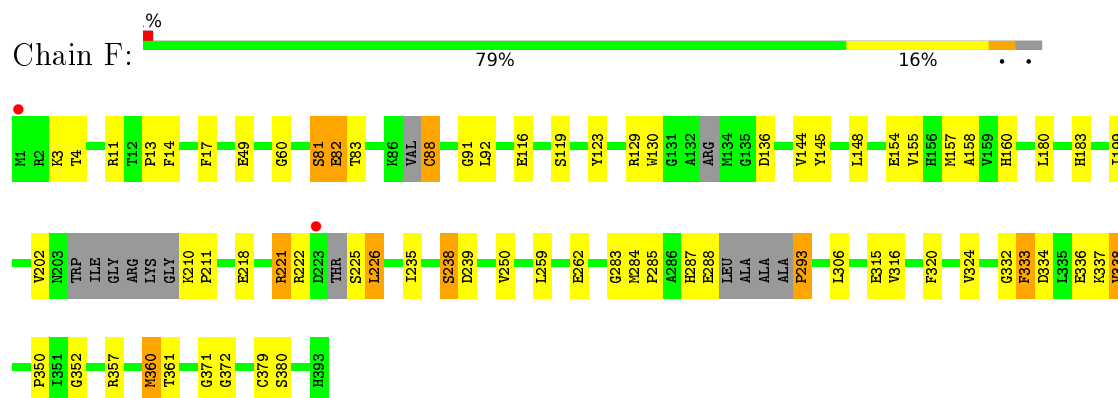
- Molecule 1: Acetyl-CoA acetyltransferase



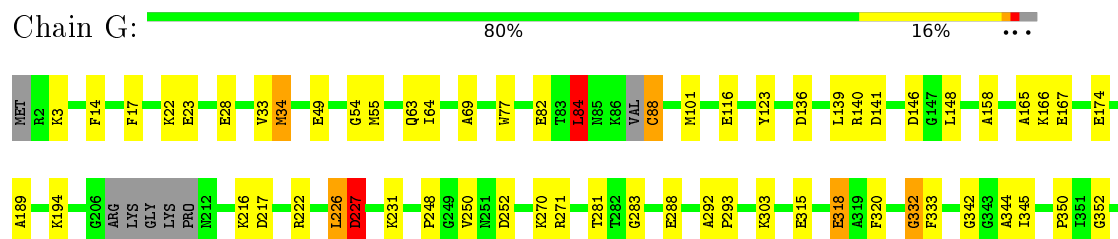
- Molecule 1: Acetyl-CoA acetyltransferase



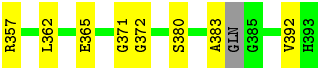
- Molecule 1: Acetyl-CoA acetyltransferase



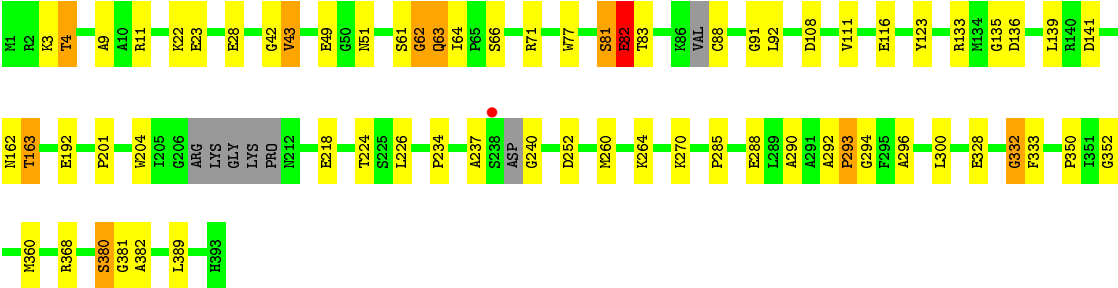
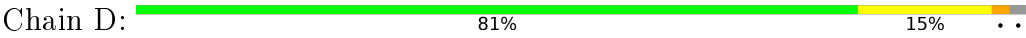
- Molecule 1: Acetyl-CoA acetyltransferase







● Molecule 1: Acetyl-CoA acetyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.18Å 141.12Å 211.46Å 90.00° 89.98° 90.00°	Depositor
Resolution (Å)	31.92 – 2.20 33.91 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.3 (31.92-2.20) 98.3 (33.91-2.20)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.93 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, $R_{free}$	0.150 , 0.205 0.170 , 0.176	Depositor DCC
$R_{free}$ test set	7962 reflections (5.20%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.3	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 10.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.426 for h,-k,-l	Xtriage
Reported twinning fraction	0.425 for H, K, L 0.575 for -H, -K, L	Depositor
Outliers	5 of 161152 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	22740	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.99% 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: 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	1.91	39/2769 (1.4%)	1.49	52/3742 (1.4%)
1	B	1.88	34/2792 (1.2%)	1.34	39/3773 (1.0%)
1	C	1.86	43/2787 (1.5%)	1.33	38/3762 (1.0%)
1	D	1.86	31/2778 (1.1%)	1.31	30/3753 (0.8%)
1	E	1.81	28/2777 (1.0%)	1.42	35/3756 (0.9%)
1	F	1.80	30/2675 (1.1%)	1.33	34/3614 (0.9%)
1	G	1.82	35/2766 (1.3%)	1.33	39/3733 (1.0%)
1	H	1.77	33/2772 (1.2%)	1.35	40/3741 (1.1%)
All	All	1.84	273/22116 (1.2%)	1.36	307/29874 (1.0%)

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	9
1	B	0	6
1	C	0	4
1	D	0	6
1	E	0	4
1	F	0	4
1	G	0	3
1	H	0	2
All	All	0	38

The worst 5 of 273 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	22	LYS	C-N	-20.02	0.88	1.34
1	B	336	GLU	C-N	-19.16	0.90	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	307	THR	C-N	-18.98	0.90	1.34
1	B	87	VAL	C-N	-18.74	0.91	1.34
1	B	91	GLY	C-N	-18.54	0.91	1.34

The worst 5 of 307 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	222	ARG	O-C-N	-28.82	76.58	122.70
1	E	222	ARG	CA-C-N	23.47	168.84	117.20
1	H	237	ALA	CB-CA-C	17.79	136.79	110.10
1	A	333	PHE	O-C-N	15.26	147.12	122.70
1	D	82	GLU	O-C-N	-15.00	98.70	122.70

There are no chirality outliers.

5 of 38 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	221	ARG	Mainchain
1	E	222	ARG	Mainchain
1	E	88	CYS	Mainchain
1	H	134	MET	Mainchain
1	H	55	MET	Mainchain

## 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	2730	0	2587	33	0
1	B	2753	0	2625	18	0
1	C	2749	0	2635	20	0
1	D	2740	0	2639	20	0
1	E	2740	0	2618	28	0
1	F	2641	0	2475	30	0
1	G	2728	0	2598	20	0
1	H	2733	0	2614	18	0
2	A	6	0	8	0	0
2	B	12	0	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	6	0	8	0	0
2	D	6	0	8	0	0
2	E	6	0	8	0	0
2	F	6	0	8	0	0
2	G	6	0	8	0	0
3	A	110	0	0	0	0
3	B	146	0	0	0	0
3	C	136	0	0	0	0
3	D	125	0	0	0	0
3	E	80	0	0	0	0
3	F	80	0	0	0	0
3	G	119	0	0	0	0
3	H	82	0	0	0	0
All	All	22740	0	20855	181	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 4.

The worst 5 of 181 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:62:GLY:C	1:D:63:GLN:N	1.70	1.45
1:A:66:SER:OG	1:A:82:GLU:O	1.62	1.15
1:F:333:PHE:CD1	1:F:338:VAL:HG21	1.90	1.05
1:F:333:PHE:CE1	1:F:338:VAL:HG21	1.93	1.03
1:E:333:PHE:CD1	1:E:338:VAL:HG21	1.95	1.01

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	380/393 (97%)	375 (99%)	4 (1%)	1 (0%)	46	50
1	B	382/393 (97%)	374 (98%)	7 (2%)	1 (0%)	46	50
1	C	379/393 (96%)	373 (98%)	5 (1%)	1 (0%)	46	50
1	D	378/393 (96%)	370 (98%)	8 (2%)	0	100	100
1	E	378/393 (96%)	370 (98%)	7 (2%)	1 (0%)	46	50
1	F	368/393 (94%)	361 (98%)	7 (2%)	0	100	100
1	G	377/393 (96%)	370 (98%)	7 (2%)	0	100	100
1	H	380/393 (97%)	374 (98%)	6 (2%)	0	100	100
All	All	3022/3144 (96%)	2967 (98%)	51 (2%)	4 (0%)	56	64

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	87	VAL
1	B	87	VAL
1	C	87	VAL
1	A	87	VAL

### 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	256/291 (88%)	255 (100%)	1 (0%)	93	97
1	B	259/291 (89%)	258 (100%)	1 (0%)	93	97
1	C	255/291 (88%)	255 (100%)	0	100	100
1	D	255/291 (88%)	254 (100%)	1 (0%)	93	97
1	E	259/291 (89%)	259 (100%)	0	100	100
1	F	239/291 (82%)	239 (100%)	0	100	100
1	G	256/291 (88%)	255 (100%)	1 (0%)	93	97
1	H	257/291 (88%)	257 (100%)	0	100	100
All	All	2036/2328 (88%)	2032 (100%)	4 (0%)	95	98

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	368	ARG
1	B	239	ASP
1	G	84	LEU
1	D	133	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	384	GLN

### 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 ⓘ

8 ligands are 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	GOL	A	401	-	5,5,5	0.58	0	5,5,5	0.93	0
2	GOL	B	401	-	5,5,5	0.44	0	5,5,5	1.65	2 (40%)
2	GOL	B	402	-	5,5,5	0.38	0	5,5,5	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GOL	C	401	-	5,5,5	0.33	0	5,5,5	0.77	0
2	GOL	D	401	-	5,5,5	0.44	0	5,5,5	0.79	0
2	GOL	E	401	-	5,5,5	0.79	0	5,5,5	0.67	0
2	GOL	F	401	-	5,5,5	0.20	0	5,5,5	0.51	0
2	GOL	G	401	-	5,5,5	0.49	0	5,5,5	0.93	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	401	-	-	0/4/4/4	0/0/0/0
2	GOL	B	401	-	-	0/4/4/4	0/0/0/0
2	GOL	B	402	-	-	0/4/4/4	0/0/0/0
2	GOL	C	401	-	-	0/4/4/4	0/0/0/0
2	GOL	D	401	-	-	0/4/4/4	0/0/0/0
2	GOL	E	401	-	-	0/4/4/4	0/0/0/0
2	GOL	F	401	-	-	0/4/4/4	0/0/0/0
2	GOL	G	401	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	GOL	O2-C2-C3	2.10	118.54	108.47
2	B	401	GOL	O3-C3-C2	2.87	124.53	109.97

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 ⓘ

There are no such residues in this entry.



## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	17
1	E	16
1	G	13
1	D	13
1	F	13
1	H	11
1	B	11
1	C	11

The worst 5 of 105 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	62:GLY	C	63:GLN	N	1.70
1	H	204:TRP	C	205:ILE	N	1.20
1	F	82:GLU	C	83:THR	N	1.20
1	H	363:VAL	C	364:TYR	N	1.19
1	B	217:ASP	C	218:GLU	N	1.19

## 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	386/393 (98%)	-0.77	1 (0%) 94 94	11, 21, 36, 58	0
1	B	388/393 (98%)	-0.86	0 100 100	10, 18, 32, 48	0
1	C	387/393 (98%)	-0.84	0 100 100	9, 17, 30, 62	0
1	D	386/393 (98%)	-0.80	1 (0%) 94 94	10, 19, 37, 53	0
1	E	386/393 (98%)	-0.80	0 100 100	11, 21, 37, 51	0
1	F	380/393 (96%)	-0.72	2 (0%) 91 91	12, 22, 40, 62	0
1	G	385/393 (97%)	-0.80	0 100 100	11, 19, 34, 58	0
1	H	386/393 (98%)	-0.81	0 100 100	10, 19, 33, 49	0
All	All	3084/3144 (98%)	-0.80	4 (0%) 95 95	9, 19, 35, 62	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	223	ASP	2.8
1	F	1	MET	2.5
1	A	237	ALA	2.5
1	D	238	SER	2.4

### 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. 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
2	GOL	B	401	6/6	0.94	0.18	7.85	25,25,28,32	0
2	GOL	F	401	6/6	0.88	0.19	3.72	49,52,56,63	0
2	GOL	E	401	6/6	0.93	0.16	3.41	25,29,35,38	0
2	GOL	B	402	6/6	0.91	0.18	3.40	36,37,40,42	0
2	GOL	C	401	6/6	0.94	0.15	3.13	35,43,45,50	0
2	GOL	A	401	6/6	0.83	0.18	3.10	28,32,34,36	0
2	GOL	D	401	6/6	0.94	0.12	2.94	31,35,36,38	0
2	GOL	G	401	6/6	0.96	0.09	0.50	14,16,17,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.