



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 02:22 am BST

PDB ID : 2WGG  
Title : Crystal Structure of Mycobacterium tuberculosis C171Q KasA variant with bound TLM  
Authors : Luckner, S.R.; Kisker, C.  
Deposited on : 2009-04-17  
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

<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

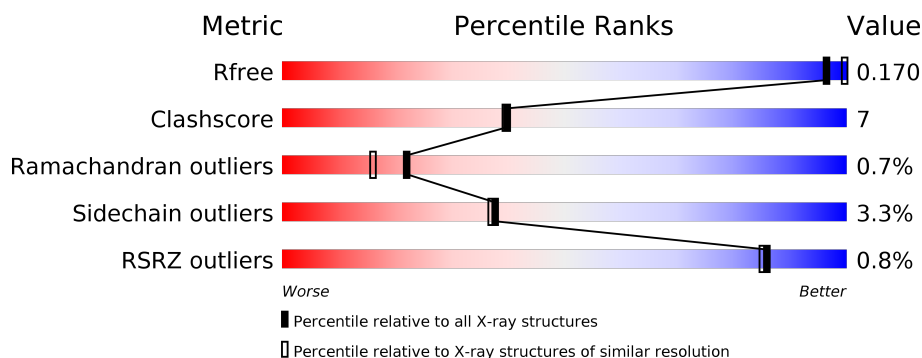
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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 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	416	<div> <div>%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>.</div> </div> </div>
1	B	416	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>9%</div> <div>.</div> </div> </div>
1	C	416	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>12%</div> <div>.</div> </div> </div>
1	D	416	<div> <div>%</div> <div> <div></div> <div>87%</div> <div>11%</div> <div>.</div> </div> </div>
1	E	416	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>12%</div> <div>.</div> </div> </div>
1	F	416	<div> <div>%</div> <div> <div></div> <div>87%</div> <div>12%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	416	<div> <div>%</div> <div> </div> <div>86% 12%</div> </div>
1	H	416	<div> <div> </div> <div>86% 13%</div> </div>

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
5	PEG	B	1423	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 25672 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.

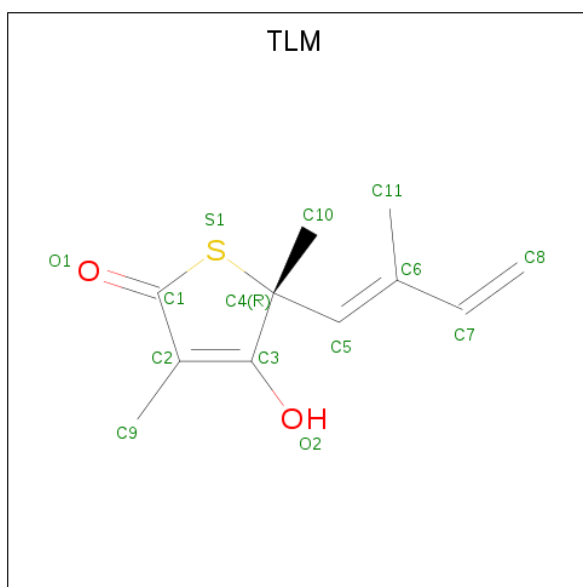
- Molecule 1 is a protein called 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	415	Total	C	N	O	S	0	3	0
			3047	1901	539	589	18			
1	B	415	Total	C	N	O	S	0	2	0
			3046	1900	542	587	17			
1	C	415	Total	C	N	O	S	0	2	0
			3042	1898	539	587	18			
1	D	415	Total	C	N	O	S	0	4	0
			3052	1905	539	589	19			
1	E	415	Total	C	N	O	S	0	2	0
			3040	1897	539	586	18			
1	F	415	Total	C	N	O	S	0	3	0
			3048	1902	539	589	18			
1	G	415	Total	C	N	O	S	0	1	0
			3037	1895	539	585	18			
1	H	415	Total	C	N	O	S	0	1	0
			3037	1895	539	585	18			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	171	GLN	CYS	engineered mutation	UNP P63454
B	171	GLN	CYS	engineered mutation	UNP P63454
C	171	GLN	CYS	engineered mutation	UNP P63454
D	171	GLN	CYS	engineered mutation	UNP P63454
E	171	GLN	CYS	engineered mutation	UNP P63454
F	171	GLN	CYS	engineered mutation	UNP P63454
G	171	GLN	CYS	engineered mutation	UNP P63454
H	171	GLN	CYS	engineered mutation	UNP P63454

- Molecule 2 is THIOLACTOMYCIN (three-letter code: TLM) (formula: C<sub>11</sub>H<sub>14</sub>O<sub>2</sub>S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			14	11	2	1		
2	B	1	Total	C	O	S	0	0
			14	11	2	1		
2	C	1	Total	C	O	S	0	0
			14	11	2	1		
2	D	1	Total	C	O	S	0	0
			14	11	2	1		
2	E	1	Total	C	O	S	0	0
			14	11	2	1		
2	F	1	Total	C	O	S	0	0
			14	11	2	1		
2	G	1	Total	C	O	S	0	0
			14	11	2	1		
2	H	1	Total	C	O	S	0	0
			14	11	2	1		

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

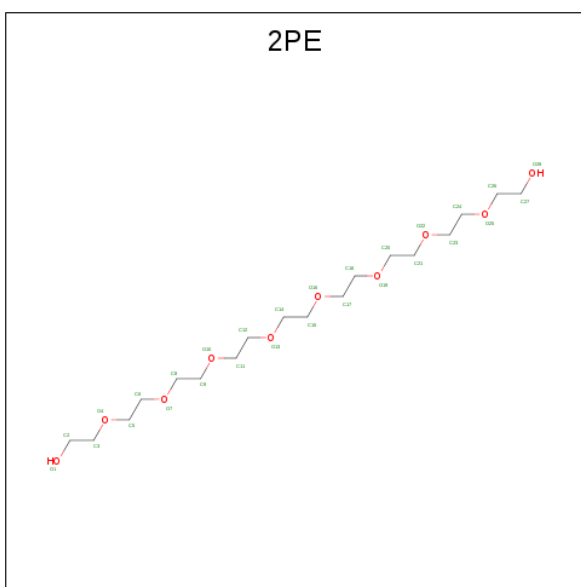
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Na	0	0
			1	1		
3	D	1	Total	Na	0	0
			1	1		
3	E	1	Total	Na	0	0
			1	1		
3	H	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Na 1	0	0
3	C	1	Total 1	Na 1	0	0
3	A	1	Total 1	Na 1	0	0
3	F	1	Total 1	Na 1	0	0

- Molecule 4 is NONAETHYLENE GLYCOL (three-letter code: 2PE) (formula: C<sub>18</sub>H<sub>38</sub>O<sub>10</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 28	C 18	O 10	0	0
4	B	1	Total 28	C 18	O 10	0	0
4	C	1	Total 28	C 18	O 10	0	0
4	D	1	Total 28	C 18	O 10	0	0
4	E	1	Total 28	C 18	O 10	0	0
4	F	1	Total 28	C 18	O 10	0	0
4	G	1	Total 28	C 18	O 10	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			28	18	10		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		
5	G	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	132	Total	O	0	0
			132	132		

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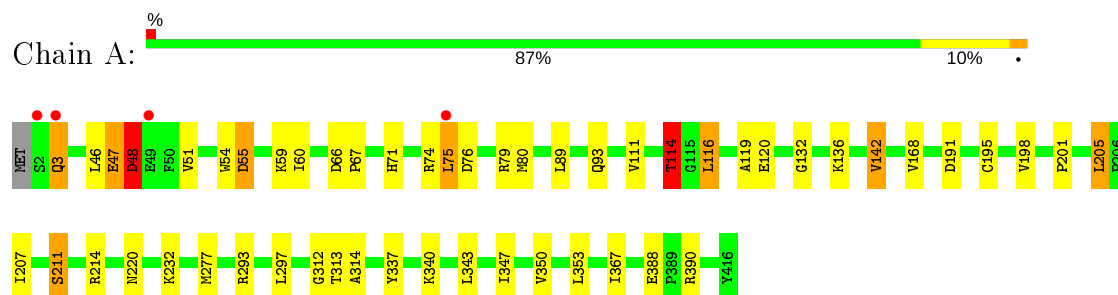
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	138	Total 138	O 138	0	0
6	C	112	Total 112	O 112	0	0
6	D	127	Total 127	O 127	0	0
6	E	108	Total 108	O 108	0	0
6	F	127	Total 127	O 127	0	0
6	G	93	Total 93	O 93	0	0
6	H	93	Total 93	O 93	0	0



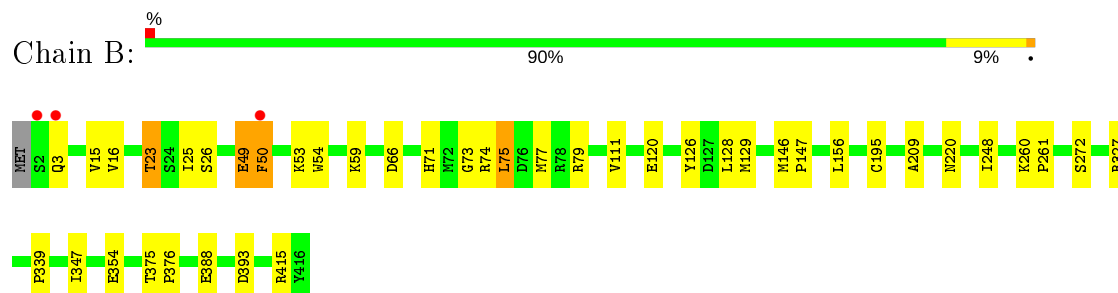
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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.

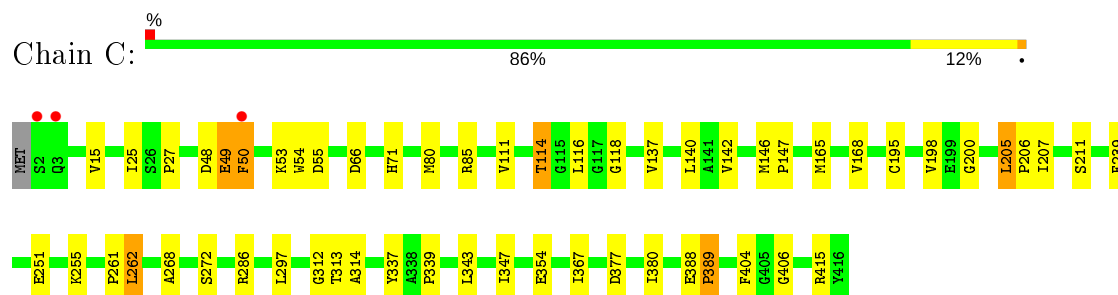
#### • Molecule 1: 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE 1



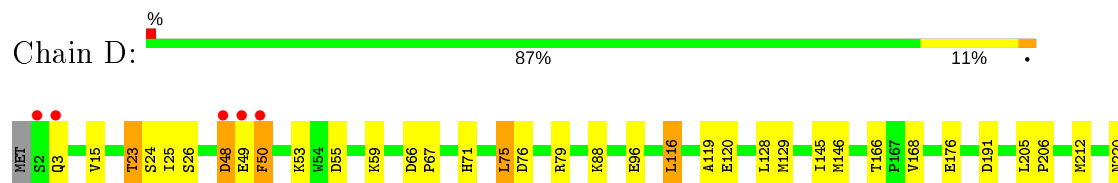
#### • Molecule 1: 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE 1



#### • Molecule 1: 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE 1

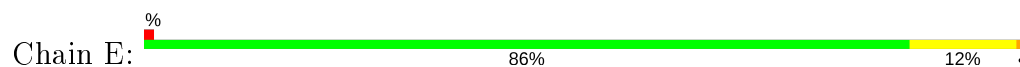


#### • Molecule 1: 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE 1

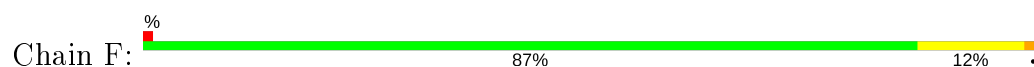




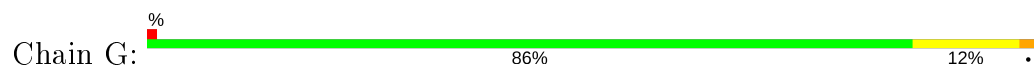
• Molecule 1: 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE 1



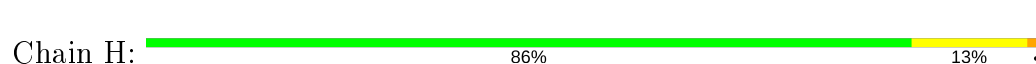
• Molecule 1: 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE 1



• Molecule 1: 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE 1



• Molecule 1: 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	151.28Å 151.28Å 147.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.16 – 2.00 46.16 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.16-2.00) 100.0 (46.16-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.73 (at 2.00Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.137 , 0.179 0.132 , 0.170	Depositor DCC
$R_{free}$ test set	13028 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.5	Xtriage
Anisotropy	0.353	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 31.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.079 for -h,-k,l 0.278 for h,-h-k,-l 0.079 for -k,-h,-l	Xtriage
Reported twinning fraction	0.287 for h,-h-k,-l	Depositor
Outliers	0 of 255871 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	25672	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.88% 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, PEG, 2PE, TLM

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	0.51	0/3116	0.69	3/4233 (0.1%)
1	B	0.49	0/3112	0.67	0/4227
1	C	0.49	0/3108	0.65	0/4222
1	D	0.49	0/3124	0.67	1/4244 (0.0%)
1	E	0.49	0/3106	0.64	1/4219 (0.0%)
1	F	0.49	0/3117	0.66	1/4234 (0.0%)
1	G	0.47	0/3100	0.65	0/4211
1	H	0.46	0/3100	0.66	0/4211
All	All	0.49	0/24883	0.66	6/33801 (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

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	75	LEU	CA-CB-CG	8.19	134.13	115.30
1	D	262	LEU	CA-CB-CG	6.42	130.07	115.30
1	A	48	ASP	N-CA-C	5.54	125.95	111.00
1	F	262	LEU	CA-CB-CG	5.28	127.44	115.30
1	A	114	THR	CB-CA-C	-5.13	97.75	111.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	47	GLU	Mainchain,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	3047	0	3002	42	0
1	B	3046	0	3004	28	0
1	C	3042	0	2998	44	0
1	D	3052	0	3011	39	0
1	E	3040	0	2999	48	0
1	F	3048	0	3004	41	0
1	G	3037	0	2994	50	0
1	H	3037	0	2994	56	0
2	A	14	0	13	3	0
2	B	14	0	13	2	0
2	C	14	0	13	1	0
2	D	14	0	13	1	0
2	E	14	0	13	1	0
2	F	14	0	13	0	0
2	G	14	0	13	1	0
2	H	14	0	13	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	28	0	38	5	0
4	B	28	0	38	7	0
4	C	28	0	38	6	0
4	D	28	0	38	5	0
4	E	28	0	38	8	0
4	F	28	0	38	2	0
4	G	28	0	38	9	0
4	H	28	0	38	7	0
5	A	7	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	21	0	30	10	0
5	C	7	0	10	1	0
5	F	7	0	10	1	0
5	G	7	0	10	1	0
6	A	132	0	0	3	0
6	B	138	0	0	1	0
6	C	112	0	0	2	0
6	D	127	0	0	0	0
6	E	108	0	0	2	0
6	F	127	0	0	2	0
6	G	93	0	0	5	0
6	H	93	0	0	1	0
All	All	25672	0	24484	360	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 7.

The worst 5 of 360 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:E:86:MET:CE	1:E:243:GLY:HA3	1.73	1.19
1:E:201:PRO:HD2	4:E:1419:2PE:H241	1.26	1.08
1:D:191[B]:ASP:OD2	1:D:253:HIS:HD2	1.43	1.01
1:H:317:ILE:HD11	6:H:2065:HOH:O	1.56	1.01
1:E:86:MET:HE3	1:E:243:GLY:CA	1.92	0.98

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	416/416 (100%)	401 (96%)	11 (3%)	4 (1%)	15	9
1	B	415/416 (100%)	401 (97%)	13 (3%)	1 (0%)	47	44
1	C	415/416 (100%)	402 (97%)	11 (3%)	2 (0%)	29	23
1	D	417/416 (100%)	401 (96%)	12 (3%)	4 (1%)	15	9
1	E	415/416 (100%)	399 (96%)	14 (3%)	2 (0%)	29	23
1	F	416/416 (100%)	404 (97%)	8 (2%)	4 (1%)	15	9
1	G	414/416 (100%)	401 (97%)	9 (2%)	4 (1%)	15	9
1	H	414/416 (100%)	397 (96%)	15 (4%)	2 (0%)	29	23
All	All	3322/3328 (100%)	3206 (96%)	93 (3%)	23 (1%)	22	16

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	ASP
1	D	49	GLU
1	G	49	GLU
1	A	55	ASP
1	A	312	GLY

### 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	310/308 (101%)	299 (96%)	11 (4%)	36	35
1	B	309/308 (100%)	300 (97%)	9 (3%)	42	43
1	C	309/308 (100%)	300 (97%)	9 (3%)	42	43
1	D	311/308 (101%)	299 (96%)	12 (4%)	32	30
1	E	309/308 (100%)	298 (96%)	11 (4%)	35	34
1	F	310/308 (101%)	301 (97%)	9 (3%)	42	43
1	G	308/308 (100%)	297 (96%)	11 (4%)	35	34
1	H	308/308 (100%)	298 (97%)	10 (3%)	39	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2474/2464 (100%)	2392 (97%)	82 (3%)	38 37

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	221	ASP
1	E	114	THR
1	H	75	LEU
1	D	232	LYS
1	E	3	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	157	GLN
1	D	253	HIS
1	H	157	GLN
1	D	220	ASN
1	E	71	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 31 ligands modelled in this entry, 8 are monoatomic - leaving 23 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
4	2PE	B	1417	-	27,27,27	0.92	0	26,26,26	0.71	0
5	PEG	B	1423	-	6,6,6	0.38	0	5,5,5	1.24	1 (20%)
5	PEG	C	1420	-	6,6,6	0.44	0	5,5,5	0.61	0
5	PEG	B	1424	-	6,6,6	0.49	0	5,5,5	0.85	0
2	TLM	D	1417	-	7,14,14	1.75	1 (14%)	10,21,21	2.65	4 (40%)
4	2PE	G	1417	-	27,27,27	0.58	0	26,26,26	0.78	0
4	2PE	F	1420	-	27,27,27	0.63	0	26,26,26	0.64	0
2	TLM	C	1417	-	7,14,14	1.90	2 (28%)	10,21,21	2.02	4 (40%)
2	TLM	B	1419	-	7,14,14	2.18	2 (28%)	10,21,21	2.35	5 (50%)
2	TLM	A	1417	-	7,14,14	1.75	1 (14%)	10,21,21	2.50	4 (40%)
2	TLM	F	1417	-	7,14,14	1.75	1 (14%)	10,21,21	2.85	4 (40%)
2	TLM	G	1419	-	7,14,14	2.53	2 (28%)	10,21,21	3.27	4 (40%)
4	2PE	D	1419	-	27,27,27	0.68	0	26,26,26	0.75	0
2	TLM	E	1417	-	7,14,14	1.87	1 (14%)	10,21,21	2.32	3 (30%)
4	2PE	C	1419	-	27,27,27	0.61	0	26,26,26	0.77	0
4	2PE	E	1419	-	27,27,27	0.62	0	26,26,26	0.45	0
5	PEG	F	1419	-	6,6,6	0.54	0	5,5,5	0.60	0
4	2PE	A	1419	-	27,27,27	0.60	0	26,26,26	0.83	1 (3%)
5	PEG	A	1420	-	6,6,6	0.53	0	5,5,5	0.20	0
2	TLM	H	1417	-	7,14,14	1.92	1 (14%)	10,21,21	2.18	4 (40%)
5	PEG	B	1425	-	6,6,6	0.72	0	5,5,5	0.25	0
5	PEG	G	1418	-	6,6,6	0.60	0	5,5,5	0.59	0
4	2PE	H	1419	-	27,27,27	0.68	0	26,26,26	0.62	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
4	2PE	B	1417	-	-	10/25/25/25	-
5	PEG	B	1423	-	-	1/4/4/4	-
5	PEG	C	1420	-	-	2/4/4/4	-
5	PEG	B	1424	-	-	2/4/4/4	-
2	TLM	D	1417	-	-	0/4/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	2PE	G	1417	-	-	14/25/25/25	-
4	2PE	F	1420	-	-	17/25/25/25	-
2	TLM	C	1417	-	-	0/4/26/26	0/1/1/1
2	TLM	B	1419	-	-	0/4/26/26	0/1/1/1
2	TLM	A	1417	-	-	0/4/26/26	0/1/1/1
2	TLM	F	1417	-	-	0/4/26/26	0/1/1/1
2	TLM	G	1419	-	-	0/4/26/26	0/1/1/1
4	2PE	D	1419	-	-	14/25/25/25	-
2	TLM	E	1417	-	-	0/4/26/26	0/1/1/1
4	2PE	C	1419	-	-	13/25/25/25	-
4	2PE	E	1419	-	-	14/25/25/25	-
5	PEG	F	1419	-	-	3/4/4/4	-
4	2PE	A	1419	-	-	14/25/25/25	-
5	PEG	A	1420	-	-	1/4/4/4	-
2	TLM	H	1417	-	-	0/4/26/26	0/1/1/1
5	PEG	B	1425	-	-	2/4/4/4	-
5	PEG	G	1418	-	-	3/4/4/4	-
4	2PE	H	1419	-	-	13/25/25/25	-

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	1419	TLM	C7-C6	-5.93	1.35	1.46
2	B	1419	TLM	C7-C6	-4.61	1.37	1.46
2	H	1417	TLM	C7-C6	-4.29	1.38	1.46
2	E	1417	TLM	C7-C6	-4.24	1.38	1.46
2	F	1417	TLM	C7-C6	-3.86	1.39	1.46

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1419	TLM	C8-C7-C6	-8.61	117.50	126.59
2	F	1417	TLM	C8-C7-C6	-6.10	120.15	126.59
2	D	1417	TLM	C8-C7-C6	-4.98	121.34	126.59
2	B	1419	TLM	C8-C7-C6	-4.63	121.70	126.59
2	A	1417	TLM	C8-C7-C6	-4.56	121.78	126.59

There are no chirality outliers.

5 of 123 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	1417	2PE	C9-C8-O7-C6
4	E	1419	2PE	C9-C8-O7-C6
4	H	1419	2PE	C9-C8-O7-C6
4	H	1419	2PE	C20-C21-O22-C23
4	C	1419	2PE	C17-C18-O19-C20

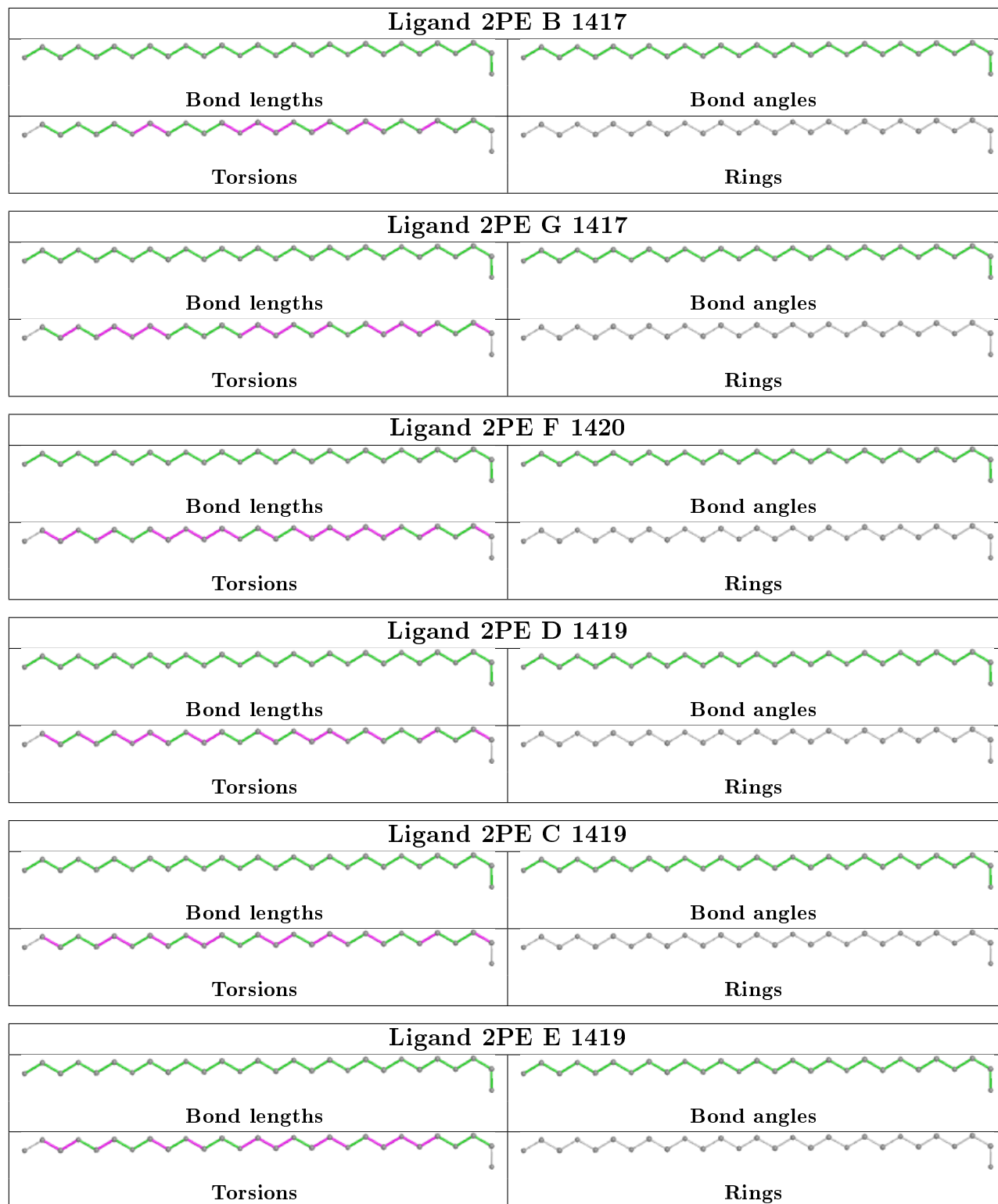
There are no ring outliers.

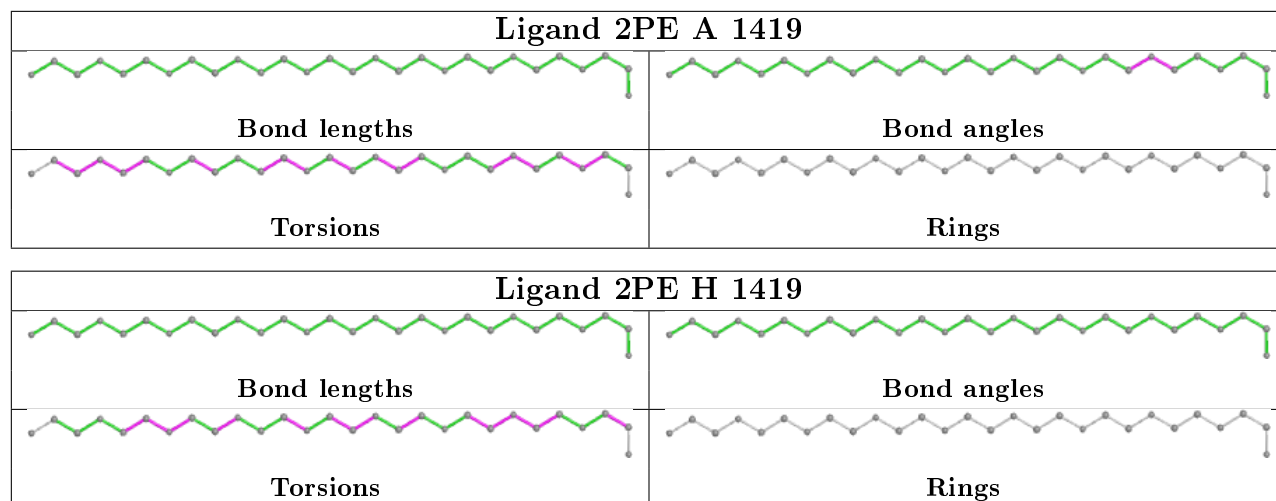
21 monomers are involved in 66 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1417	2PE	7	0
5	B	1423	PEG	6	0
5	C	1420	PEG	1	0
5	B	1424	PEG	1	0
2	D	1417	TLM	1	0
4	G	1417	2PE	9	0
4	F	1420	2PE	2	0
2	C	1417	TLM	1	0
2	B	1419	TLM	2	0
2	A	1417	TLM	3	0
2	G	1419	TLM	1	0
4	D	1419	2PE	5	0
2	E	1417	TLM	1	0
4	C	1419	2PE	6	0
4	E	1419	2PE	8	0
5	F	1419	PEG	1	0
4	A	1419	2PE	5	0
2	H	1417	TLM	1	0
5	B	1425	PEG	3	0
5	G	1418	PEG	1	0
4	H	1419	2PE	7	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	415/416 (99%)	-0.56	4 (0%) 82 81	15, 23, 47, 92	0
1	B	415/416 (99%)	-0.59	3 (0%) 87 87	14, 22, 42, 97	0
1	C	415/416 (99%)	-0.59	3 (0%) 87 87	15, 24, 47, 89	0
1	D	415/416 (99%)	-0.57	5 (1%) 79 78	15, 24, 47, 94	0
1	E	415/416 (99%)	-0.46	3 (0%) 87 87	19, 28, 51, 86	0
1	F	415/416 (99%)	-0.57	4 (0%) 82 81	16, 25, 46, 98	0
1	G	415/416 (99%)	-0.51	3 (0%) 87 87	19, 29, 52, 92	0
1	H	415/416 (99%)	-0.51	2 (0%) 91 90	16, 28, 52, 102	0
All	All	3320/3328 (99%)	-0.54	27 (0%) 86 85	14, 26, 49, 102	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	2	SER	7.0
1	B	2	SER	6.8
1	D	2	SER	5.3
1	A	2	SER	5.1
1	F	2	SER	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 carbohydrates in this entry.

## 6.4 Ligands ⓘ

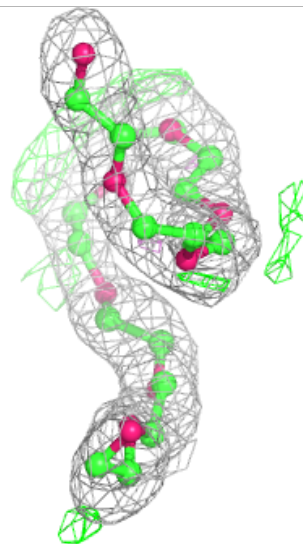
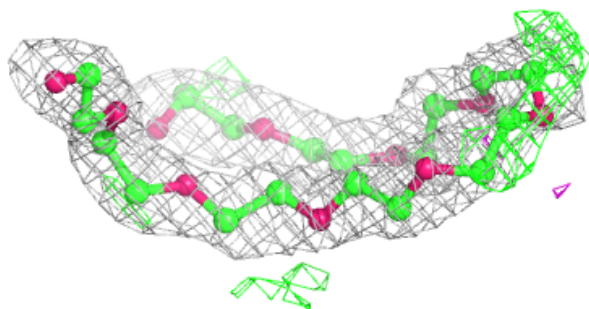
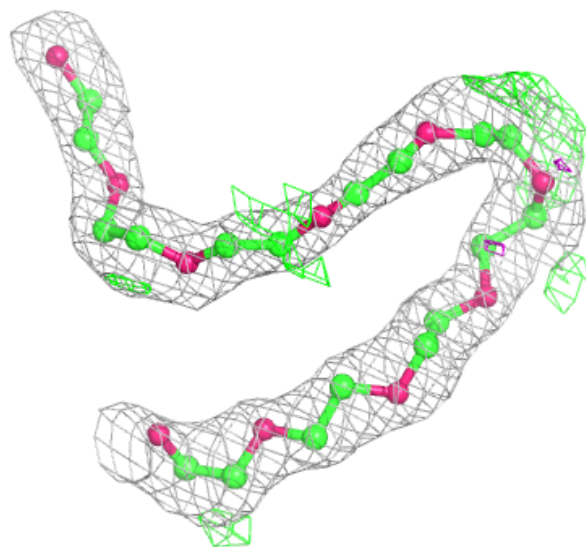
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	PEG	C	1420	7/7	0.87	0.21	25,38,49,49	0
5	PEG	F	1419	7/7	0.91	0.16	27,39,57,58	0
5	PEG	B	1425	7/7	0.91	0.29	34,39,57,63	0
4	2PE	B	1417	28/28	0.92	0.12	24,43,66,75	0
4	2PE	D	1419	28/28	0.93	0.11	26,41,72,78	0
5	PEG	B	1423	7/7	0.93	0.19	20,29,45,61	0
5	PEG	A	1420	7/7	0.93	0.16	29,36,40,43	0
4	2PE	F	1420	28/28	0.93	0.12	24,45,63,72	0
4	2PE	C	1419	28/28	0.94	0.13	23,44,61,84	0
4	2PE	E	1419	28/28	0.94	0.13	25,41,53,57	0
5	PEG	B	1424	7/7	0.94	0.22	36,53,55,56	0
4	2PE	A	1419	28/28	0.94	0.13	20,43,64,80	0
5	PEG	G	1418	7/7	0.94	0.15	34,44,57,69	0
4	2PE	G	1417	28/28	0.94	0.12	24,45,64,77	0
2	TLM	B	1419	14/14	0.95	0.09	20,27,33,45	0
2	TLM	F	1417	14/14	0.95	0.09	19,25,40,43	0
4	2PE	H	1419	28/28	0.95	0.12	23,46,65,80	0
2	TLM	C	1417	14/14	0.96	0.10	13,23,35,50	0
2	TLM	H	1417	14/14	0.96	0.09	23,29,45,53	0
2	TLM	E	1417	14/14	0.96	0.10	21,31,40,42	0
2	TLM	D	1417	14/14	0.96	0.12	17,29,44,47	0
2	TLM	G	1419	14/14	0.97	0.09	19,34,39,53	0
2	TLM	A	1417	14/14	0.97	0.10	19,27,32,34	0
3	NA	F	1418	1/1	0.99	0.18	9,9,9,9	0
3	NA	B	1420	1/1	1.00	0.17	7,7,7,7	0
3	NA	C	1418	1/1	1.00	0.20	10,10,10,10	0
3	NA	D	1418	1/1	1.00	0.19	11,11,11,11	0
3	NA	G	1420	1/1	1.00	0.18	16,16,16,16	0
3	NA	E	1418	1/1	1.00	0.14	12,12,12,12	0
3	NA	H	1418	1/1	1.00	0.20	14,14,14,14	0
3	NA	A	1418	1/1	1.00	0.18	10,10,10,10	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.

**Electron density around 2PE B 1417:**

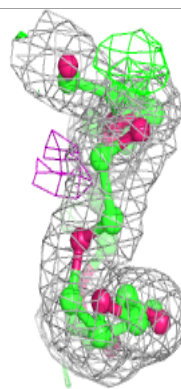
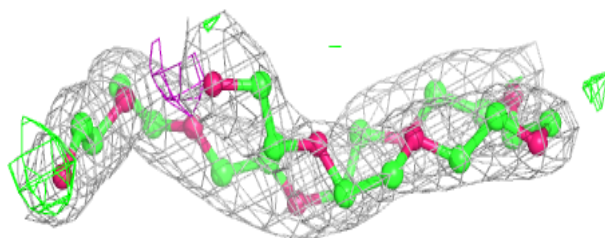
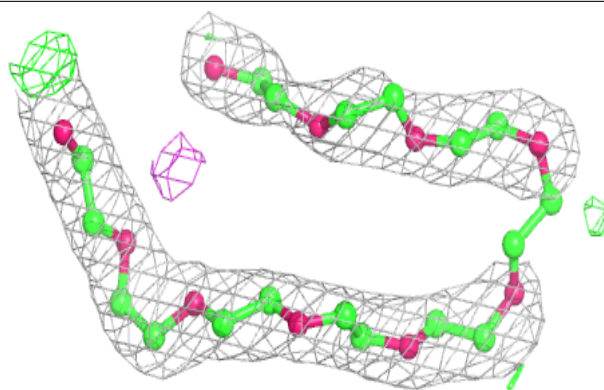
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



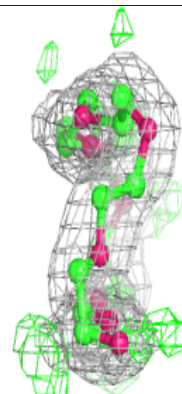
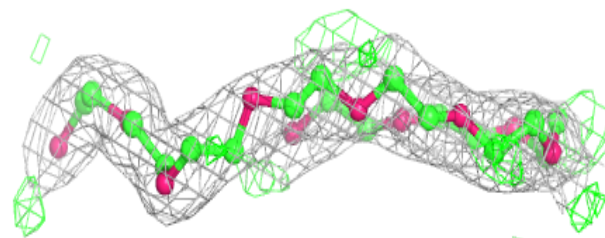
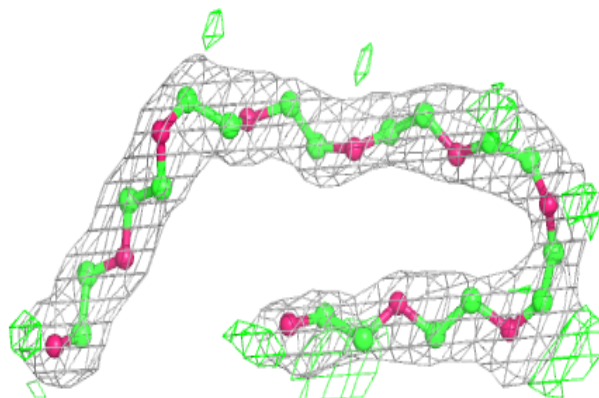


**Electron density around 2PE D 1419:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

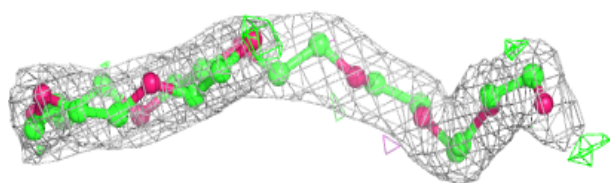
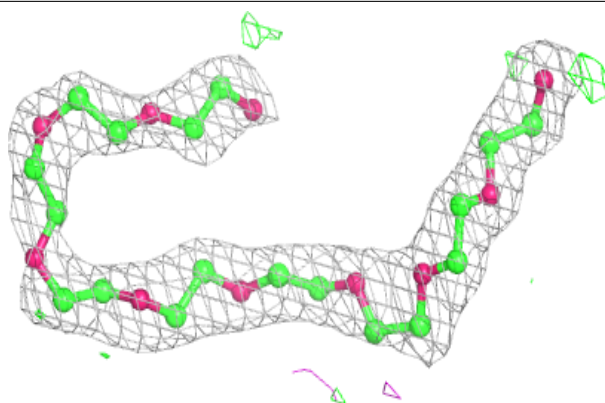
**Electron density around 2PE F 1420:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

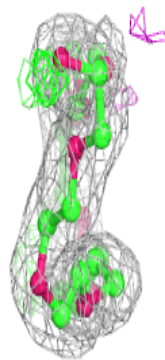
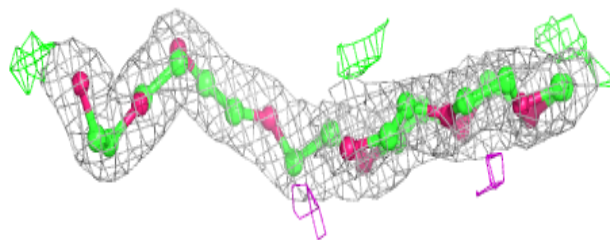
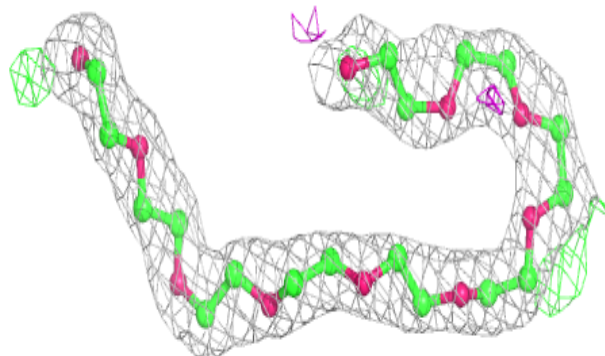


**Electron density around 2PE C 1419:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

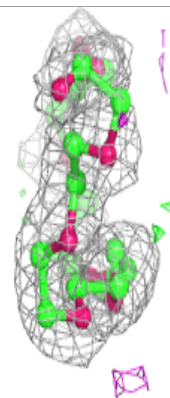
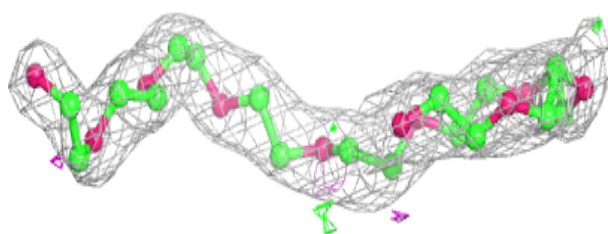
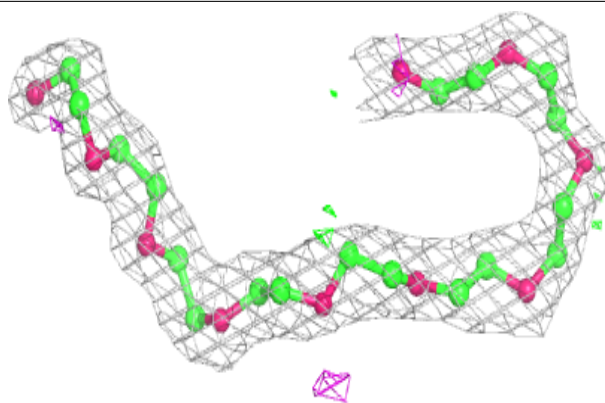
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

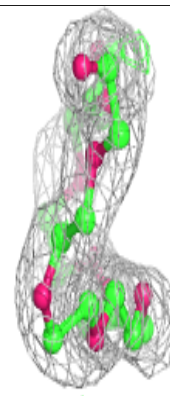
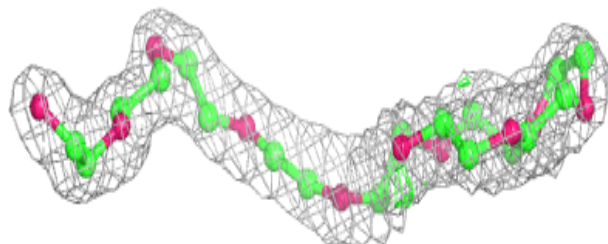
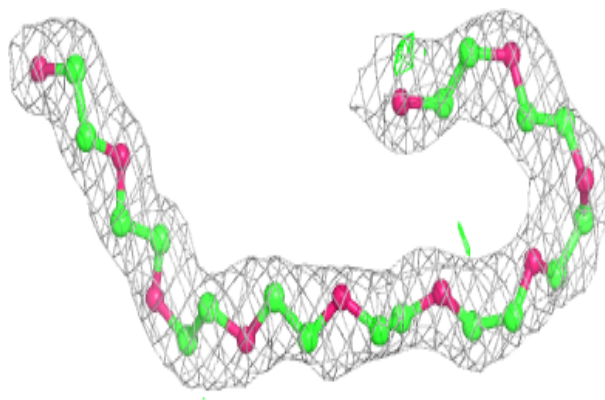


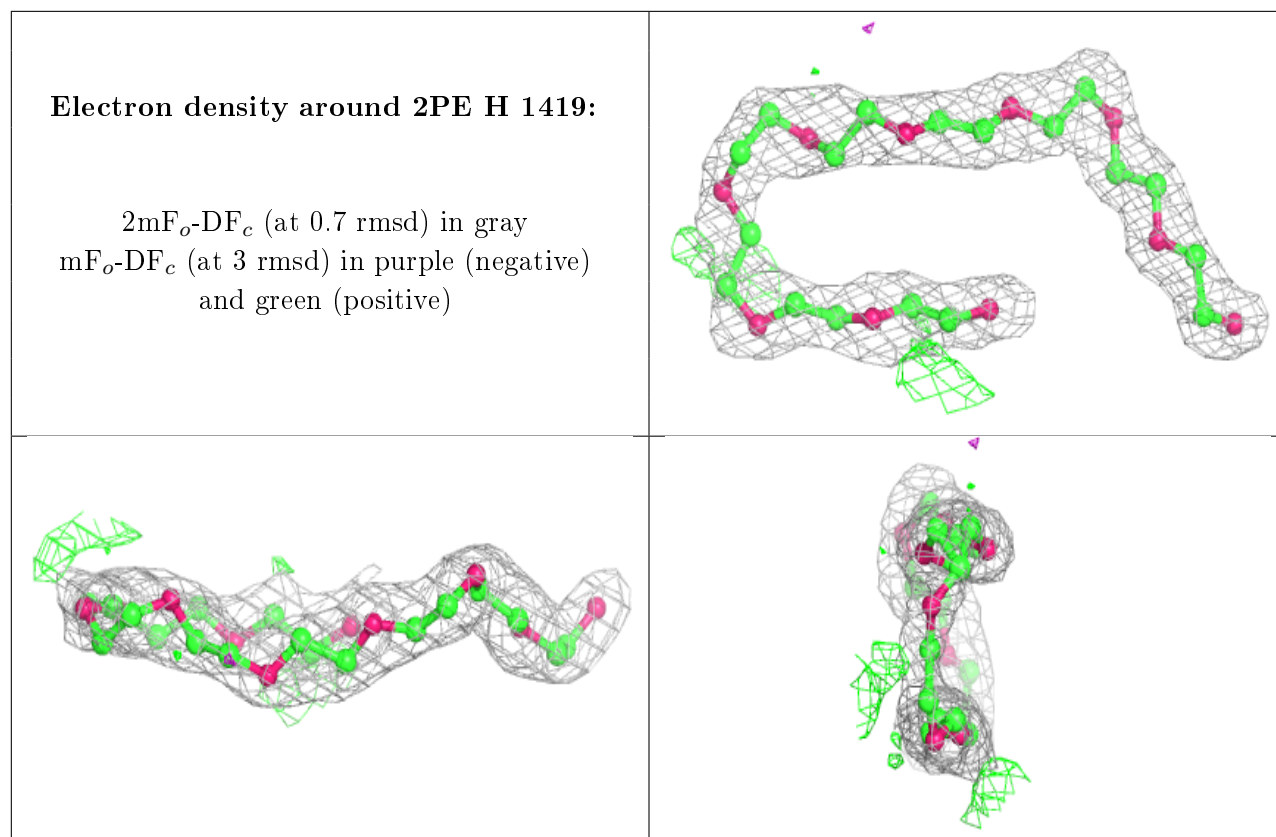
**Electron density around 2PE A 1419:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around 2PE G 1417:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.