Full wwPDB X-ray Structure Validation Report (i)

Oct 22, 2023 – 10:36 PM EDT

PDB ID	:	2ZMD
Title	:	Crystal structure of human Mps1 catalytic domain T686A mutant in complex with SP600125 inhibitor
Authors	:	Chu, M.L.H.; Chavas, L.M.G.; Douglas, K.T.; Eyers, P.A.; Tabernero, L.
Deposited on	:	2008-04-16
Resolution	:	2.88 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

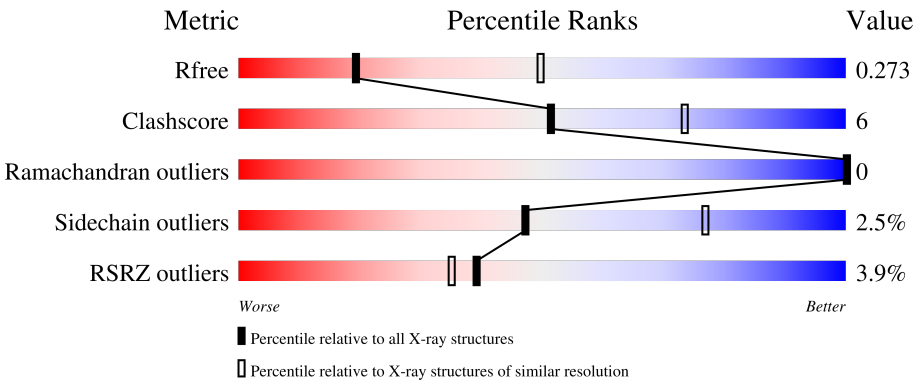
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.88 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	2691 (2.90-2.86)
Clashscore	141614	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)
RSRZ outliers	127900	2629 (2.90-2.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	390	3% 58% 8% 34%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2170 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 Dual specificity protein kinase TTK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	259	2111	1356	351	391	13	0	0	0

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	468	HIS	-	expression tag	UNP P33981
A	469	HIS	-	expression tag	UNP P33981
A	470	HIS	-	expression tag	UNP P33981
A	471	HIS	-	expression tag	UNP P33981
A	472	HIS	-	expression tag	UNP P33981
A	473	HIS	-	expression tag	UNP P33981
A	474	SER	-	expression tag	UNP P33981
A	475	SER	-	expression tag	UNP P33981
A	476	GLY	-	expression tag	UNP P33981
A	477	LEU	-	expression tag	UNP P33981
A	478	VAL	-	expression tag	UNP P33981
A	479	PRO	-	expression tag	UNP P33981
A	480	ARG	-	expression tag	UNP P33981
A	481	GLY	-	expression tag	UNP P33981
A	482	SER	-	expression tag	UNP P33981
A	483	GLY	-	expression tag	UNP P33981
A	484	MET	-	expression tag	UNP P33981
A	485	LYS	-	expression tag	UNP P33981
A	486	GLU	-	expression tag	UNP P33981
A	487	THR	-	expression tag	UNP P33981
A	488	ALA	-	expression tag	UNP P33981
A	489	ALA	-	expression tag	UNP P33981
A	490	ALA	-	expression tag	UNP P33981
A	491	LYS	-	expression tag	UNP P33981
A	492	PHE	-	expression tag	UNP P33981
A	493	GLU	-	expression tag	UNP P33981
A	494	ARG	-	expression tag	UNP P33981

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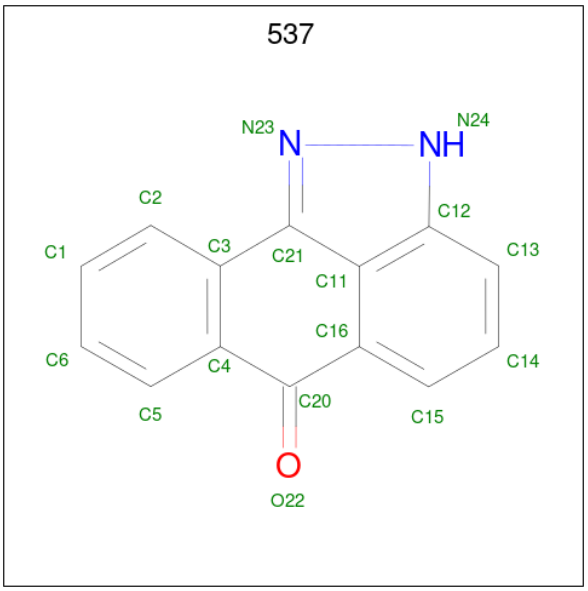
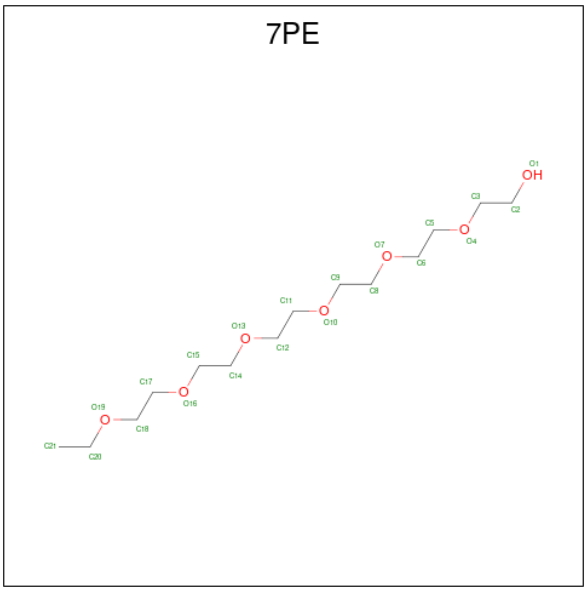
Chain	Residue	Modelled	Actual	Comment	Reference
A	495	GLN	-	expression tag	UNP P33981
A	496	HIS	-	expression tag	UNP P33981
A	497	MET	-	expression tag	UNP P33981
A	498	ASP	-	expression tag	UNP P33981
A	499	SER	-	expression tag	UNP P33981
A	500	PRO	-	expression tag	UNP P33981
A	501	ASP	-	expression tag	UNP P33981
A	502	LEU	-	expression tag	UNP P33981
A	503	GLY	-	expression tag	UNP P33981
A	504	THR	-	expression tag	UNP P33981
A	505	ASP	-	expression tag	UNP P33981
A	506	ASP	-	expression tag	UNP P33981
A	507	ASP	-	expression tag	UNP P33981
A	508	ASP	-	expression tag	UNP P33981
A	509	LYS	-	expression tag	UNP P33981
A	686	ALA	THR	engineered mutation	UNP P33981

- Molecule 2 is 2,6-DIHYDROANTHRA/1,9-CD/PYRAZOL-6-ONE (three-letter code: 537) (formula: $C_{14}H_8N_2O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	17	14	2	1	0	0

- Molecule 3 is 2-(2-(2-(2-(2-(2-ETHOXYETHOXY)ETHOXY)ETHOXY)ETHOXY)ETHOXY)ETHANOL (three-letter code: 7PE) (formula: $C_{14}H_{30}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	16	10	6	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	26	26	26	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Dual specificity protein kinase TTK

Chain A: 3% 58% 8% 34%

HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG GLY SER GLY MET LYS GLU THR ALA ALA ALA LYS PHE GLU ARG GLN HIS MET ASP SER PRO ASP LEU GLY THR ASP ASP ASP ASP LYS ALA SER SER SER ALA ASN E516 C517 I527 L528 G532 G535 S536 V542

L543 L557 L565 L575 L578 Q579 R587 E603 L613 K617 S618 I619 W622 W628 M631 H641 L654 N669 Q670 M671 GLN PRO ASP THR THR SER VAL VAL LYS D681 S682 Q683 V684 V687 D697 M698 SER SER SER ARG GLU ASN GLY LYS

SER LYS SER LYS I711 S712 Y726 G730 Q740 P789 I793 Q794 T795 HIS PRO VAL ASN GLN MET ALA LYS GLY THR THR GLU GLU MET LYS TYR VAL LEU GLY GLN LEU VAL GLY LEU ASN SER PRO ASN SER ILE LEU LYS ALA ALA LYS THR LEU TYR GLU HIS TYR SER

GLY GLY GLU SER HIS ASN SER SER SER SER LYS THR PHE GLU LYS LYS ARG GLY LYS LYS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	70.60Å 105.17Å 111.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.49 – 2.88 40.49 – 2.88	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.49-2.88) 99.7 (40.49-2.88)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.78 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.221 , 0.261 0.226 , 0.273	Depositor DCC
R_{free} test set	468 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å^2)	67.4	Xtriage
Anisotropy	0.344	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 42.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	2170	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.09% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 537, 7PE

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	0.33	0/2156	0.50	0/2912

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2111	0	2124	24	0
2	A	17	0	8	1	0
3	A	16	0	20	0	0
4	A	26	0	0	0	0
All	All	2170	0	2152	24	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 6.

All (24) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:613:LEU:CD2	1:A:619:ILE:HD11	2.23	0.67
1:A:682:SER:HB2	1:A:684:VAL:HG23	1.76	0.66
1:A:535:GLY:N	1:A:536:SER:HA	2.13	0.63
1:A:682:SER:HB3	1:A:683:GLN:HB3	1.80	0.63
1:A:682:SER:CB	1:A:684:VAL:HG23	2.35	0.57
1:A:557:LEU:HD22	1:A:565:LEU:HD23	1.89	0.54
1:A:587:ARG:HB2	1:A:603:GLU:HB2	1.91	0.53
1:A:527:ILE:HA	1:A:542:VAL:HG12	1.91	0.53
1:A:682:SER:HB3	1:A:683:GLN:CB	2.40	0.52
1:A:528:LEU:HD11	1:A:543:LEU:HD11	1.96	0.47
1:A:687:VAL:HG11	1:A:740:GLN:OE1	2.15	0.47
1:A:628:TRP:HA	1:A:631:MET:HE2	1.97	0.47
1:A:794:GLN:HA	1:A:795:THR:HG22	1.97	0.46
1:A:654:LEU:HD11	2:A:900:537:C3	2.46	0.45
1:A:557:LEU:HD22	1:A:565:LEU:CD2	2.47	0.45
1:A:578:LEU:HD21	1:A:641:HIS:CG	2.54	0.43
1:A:613:LEU:HD13	1:A:726:TYR:CD2	2.54	0.43
1:A:682:SER:HB3	1:A:683:GLN:CA	2.49	0.42
1:A:789:PRO:HB3	1:A:793:ILE:HD12	2.01	0.42
1:A:578:LEU:HD21	1:A:641:HIS:CD2	2.55	0.42
1:A:682:SER:CB	1:A:683:GLN:HB3	2.49	0.42
1:A:575:LEU:O	1:A:579:GLN:HG2	2.21	0.41
1:A:682:SER:HB3	1:A:683:GLN:C	2.40	0.41
1:A:613:LEU:HD13	1:A:726:TYR:HD2	1.85	0.40

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	253/390 (65%)	246 (97%)	7 (3%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	238/350 (68%)	232 (98%)	6 (2%)	47 77

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	517	CYS
1	A	669	ASN
1	A	671	MET
1	A	681	ASP
1	A	712	SER
1	A	795	THR

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

Mol	Chain	Res	Type
1	A	530	GLN
1	A	541	GLN
1	A	683	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	$\#\|Z\| > 2$
3	7PE	A	1	-	15,15,20	0.47	0	14,14,19	0.25	0
2	537	A	900	-	16,20,20	1.45	2 (12%)	23,30,30	1.80	4 (17%)

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
3	7PE	A	1	-	-	4/13/13/18	-
2	537	A	900	-	-	-	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	900	537	N23-N24	2.82	1.43	1.37
2	A	900	537	C16-C11	-2.58	1.38	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	900	537	C15-C16-C20	5.26	124.09	119.61
2	A	900	537	C13-C12-N24	4.40	137.35	130.19
2	A	900	537	C11-C16-C20	-3.20	117.28	119.92
2	A	900	537	C3-C21-C11	2.31	123.60	121.92

There are no chirality outliers.

All (4) torsion outliers are listed below:

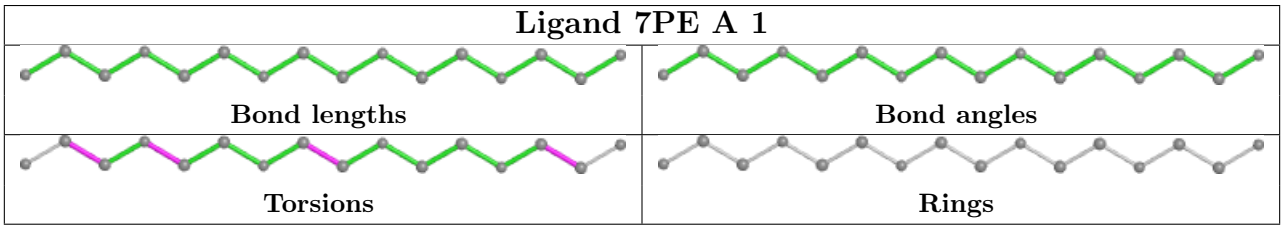
Mol	Chain	Res	Type	Atoms
3	A	1	7PE	O10-C11-C12-O13
3	A	1	7PE	O16-C17-C18-O19
3	A	1	7PE	O4-C5-C6-O7
3	A	1	7PE	C9-C8-O7-C6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	537	1	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 then 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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	259/390 (66%)	0.25	10 (3%) 39 35	53, 59, 69, 73	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	622	TRP	3.1
1	A	536	SER	2.8
1	A	618	SER	2.8
1	A	619	ILE	2.3
1	A	795	THR	2.3
1	A	516	GLU	2.2
1	A	532	GLY	2.2
1	A	617	LYS	2.2
1	A	730	GLY	2.1
1	A	697	ASP	2.1

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 monosaccharides in this entry.

6.4 Ligands (i)

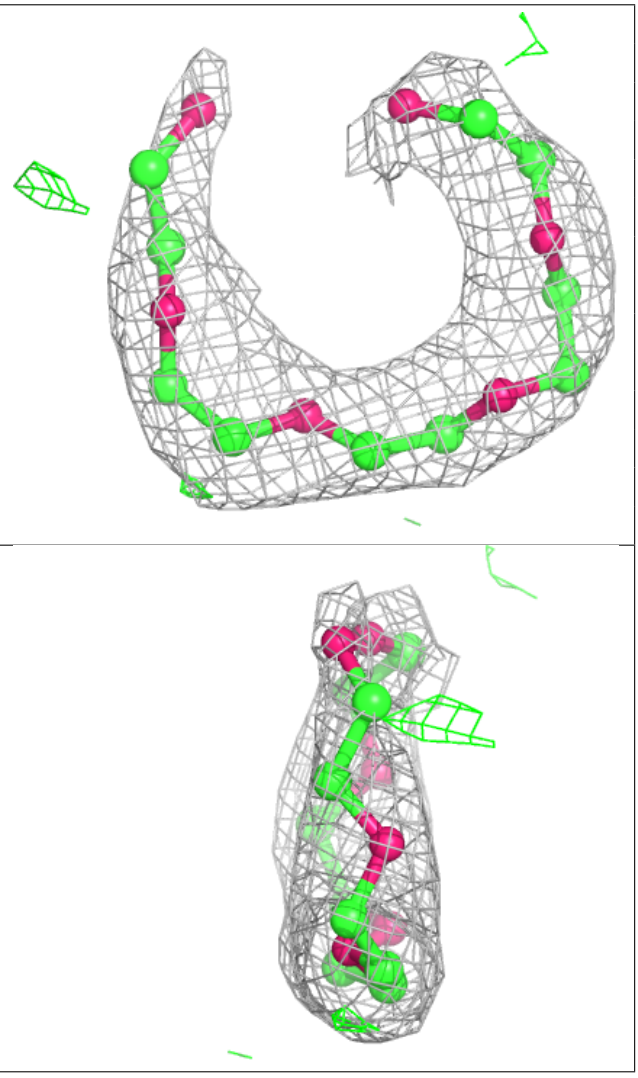
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	7PE	A	1	16/21	0.90	0.25	70,71,72,72	0
2	537	A	900	17/17	0.94	0.21	62,62,62,62	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 7PE A 1:

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.