

# wwPDB X-ray Structure Validation Summary Report (i)

#### Sep 10, 2023 – 09:08 PM EDT

PDB ID : 4KUM

Title: Structure of LSD1-CoREST-Tetrahydrofolate complex

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Deposited on : 2013-05-22

Resolution : 3.05 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*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 (1)) 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 : 2.35.1 buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

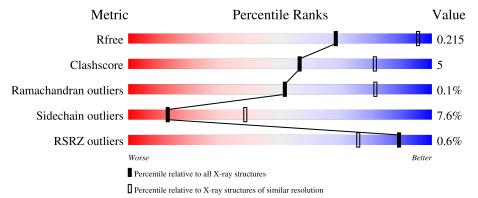
Validation Pipeline (wwPDB-VP) : 2.35.1

## 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 3.05 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
$R_{free}$	130704	1754 (3.10-3.02)
Clashscore	141614	1864 (3.10-3.02)
Ramachandran outliers	138981	1794 (3.10-3.02)
Sidechain outliers	138945	1793 (3.10-3.02)
RSRZ outliers	127900	1713 (3.10-3.02)

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	666		15%	•		
2	В	235	43%	13%	43%		-



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 6409 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 Lysine-specific histone demethylase 1A.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	٨	666	Total	С	N	О	S	0	9	0
1	A	000	5228	3330	910	968	20	U	2	

• Molecule 2 is a protein called REST corepressor 1.

$\mathbf{Mol}$	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	В	133	Total 1070	C 673	N 191	O 203	S 3	0	0	0

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	248	MET	-	expression tag	UNP J3KN32
В	249	GLY	-	expression tag	UNP J3KN32
В	250	SER	-	expression tag	UNP J3KN32
В	251	SER	-	expression tag	UNP J3KN32
В	252	HIS	-	expression tag	UNP J3KN32
В	253	HIS	-	expression tag	UNP J3KN32
В	254	HIS	-	expression tag	UNP J3KN32
В	255	HIS	-	expression tag	UNP J3KN32
В	256	HIS	-	expression tag	UNP J3KN32
В	257	HIS	-	expression tag	UNP J3KN32
В	258	SER	-	expression tag	UNP J3KN32
В	259	SER	-	expression tag	UNP J3KN32
В	260	GLY	-	expression tag	UNP J3KN32
В	261	LEU	-	expression tag	UNP J3KN32
В	262	VAL	-	expression tag	UNP J3KN32
В	263	PRO	-	expression tag	UNP J3KN32
В	264	ARG	-	expression tag	UNP J3KN32
В	265	GLY	-	expression tag	UNP J3KN32
В	266	SER		expression tag	UNP J3KN32
В	267	HIS	-	expression tag	UNP J3KN32

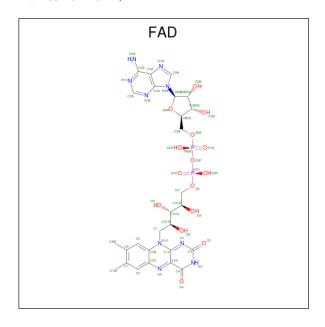
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Chain	Residue	Modelled	Actual	Comment	Reference
В	268	MET	-	expression tag	UNP J3KN32
В	269	ALA	-	expression tag	UNP J3KN32
В	270	SER	-	expression tag	UNP J3KN32
В	271	MET	-	expression tag	UNP J3KN32
В	272	THR	-	expression tag	UNP J3KN32
В	273	GLY	-	expression tag	UNP J3KN32
В	274	GLY	-	expression tag	UNP J3KN32
В	275	GLN	-	expression tag	UNP J3KN32
В	276	GLN	-	expression tag	UNP J3KN32
В	277	MET	-	expression tag	UNP J3KN32
В	278	GLY	-	expression tag	UNP J3KN32
В	279	ARG	-	expression tag	UNP J3KN32
В	280	GLY	-	expression tag	UNP J3KN32
В	281	SER	-	expression tag	UNP J3KN32
В	282	GLU	-	expression tag	UNP J3KN32
В	283	PHE	-	expression tag	UNP J3KN32
В	284	GLY	-	expression tag	UNP J3KN32
В	285	ARG	-	expression tag	UNP J3KN32

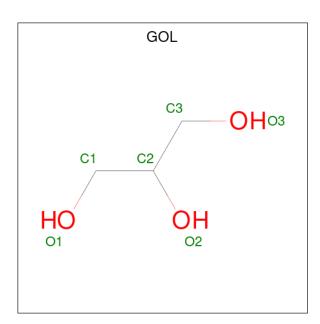
• Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
3	A	1	Total 53	C 27	N 9	O 15	P 2	0	0

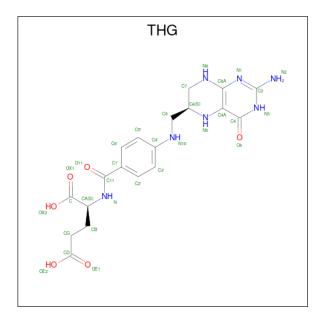
• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total C C 6 3 3	)	0	0

• Molecule 5 is (6S)-5,6,7,8-TETRAHYDROFOLATE (three-letter code: THG) (formula:  $C_{19}H_{23}N_7O_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total 32	C 19	N 7	O 6	0	0

• Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).



$\mathbf{Mol}$	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Cl 1 1	0	0

#### • Molecule 7 is water.

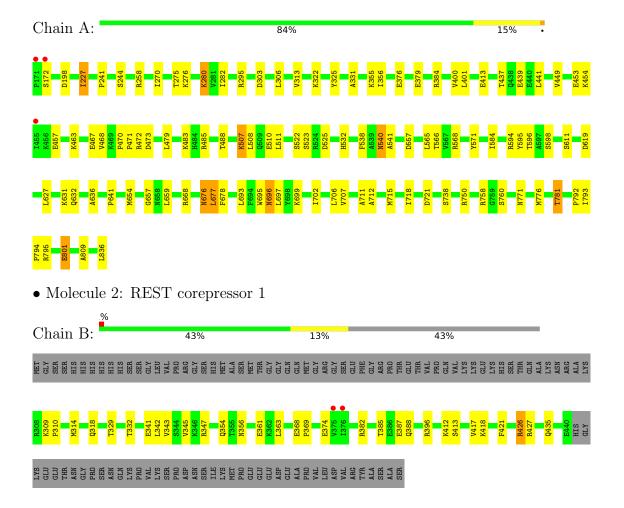
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	19	Total O 19 19	0	0



# 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: Lysine-specific histone demethylase 1A





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	123.86Å 179.37Å 235.05Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 - 3.05	Depositor
resolution (A)	46.90 - 3.03	EDS
% Data completeness	92.8 (40.00-3.05)	Depositor
(in resolution range)	91.7 (46.90-3.03)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.13	Depositor
$< I/\sigma(I) > 1$	3.34 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
D D.	0.196 , 0.217	Depositor
$R, R_{free}$	0.196 , $0.215$	DCC
$R_{free}$ test set	2376 reflections $(5.07\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	64.4	Xtriage
Anisotropy	1.037	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.33, 59.5	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.50, < L^2> = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6409	wwPDB-VP
Average B, all atoms $(Å^2)$	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.22% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: GOL, CL, THG, FAD

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		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.57	0/5342	0.79	0/7246	
2	В	0.45	0/1085	0.68	0/1464	
All	All	0.55	0/6427	0.77	0/8710	

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	5228	0	5264	57	0
2	В	1070	0	1080	12	0
3	A	53	0	31	4	0
4	A	6	0	8	2	0
5	A	32	0	21	0	0
6	A	1	0	0	0	0
7	A	19	0	0	2	0
All	All	6409	0	6404	64	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 5.



The worst 5 of 64 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$
1:A:760:SER:HB2	3:A:901:FAD:HM83	1.75	0.69
1:A:538:PHE:CE1	1:A:706:LEU:HD13	2.28	0.69
1:A:325:TYR:HB3	1:A:702:ILE:HD11	1.74	0.69
1:A:695:TRP:CE3	1:A:697:LEU:HD11	2.29	0.67
1:A:468:VAL:O	1:A:472:ARG:NH1	2.28	0.66

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	Perce	ntiles
1	A	$665/666 \ (100\%)$	644 (97%)	20 (3%)	1 (0%)	47	77
2	В	$131/235\ (56\%)$	125 (95%)	6 (5%)	0	100	100
All	All	796/901~(88%)	769 (97%)	26 (3%)	1 (0%)	51	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	792	PRO

#### 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	567/566 (100%)	529 (93%)	38 (7%)	16 43		
2	В	116/203 (57%)	102 (88%)	14 (12%)	5 17		
All	All	683/769 (89%)	631 (92%)	52 (8%)	13 38		

5 of 52 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	A	668	ARG
1	A	781	THR
2	В	396	ARG
1	A	676	ASN
1	A	699	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	В	318	GLN
2	В	348	GLN
2	В	435	GLN
2	В	354	GLN
1	A	532	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 monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	Mol Type Chain		in Res	Link	Bond lengths			Bond angles		
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
4	GOL	A	902	-	5,5,5	0.47	0	5,5,5	0.67	0
3	FAD	A	901	-	53,58,58	1.29	5 (9%)	68,89,89	1.45	12 (17%)
5	THG	A	903	-	32,34,34	1.50	2 (6%)	39,47,47	1.95	12 (30%)

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	GOL	A	902	-	-	0/4/4/4	-
3	FAD	A	901	-	-	9/30/50/50	0/6/6/6
5	THG	A	903	-	-	10/22/31/31	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
5	A	903	THG	C4A-C4	6.22	1.49	1.41
3	A	901	FAD	C9A-C5X	4.23	1.48	1.41
5	A	903	THG	C4A-C8A	4.00	1.49	1.41
3	A	901	FAD	C5X-N5	-3.19	1.33	1.39
3	A	901	FAD	C8-C7	2.78	1.47	1.40

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
5	A	903	THG	C4-C4A-N5	5.46	123.71	119.12
3	A	901	FAD	N3A-C2A-N1A	-4.21	122.09	128.68
5	A	903	THG	C2-N3-C4	4.05	122.37	115.93
5	A	903	THG	CA-N-C11	3.93	131.21	121.60
3	A	901	FAD	O4-C4-C4X	-3.62	117.00	126.60

There are no chirality outliers.



5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	901	FAD	C5B-O5B-PA-O1A
5	A	903	THG	C-CA-N-C11
5	A	903	THG	OX2-C-CA-N
3	A	901	FAD	C2'-C3'-C4'-O4'
5	A	903	THG	OX1-C-CA-N

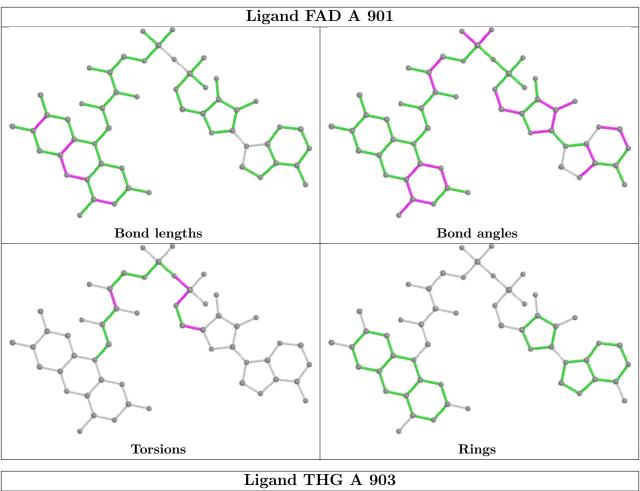
There are no ring outliers.

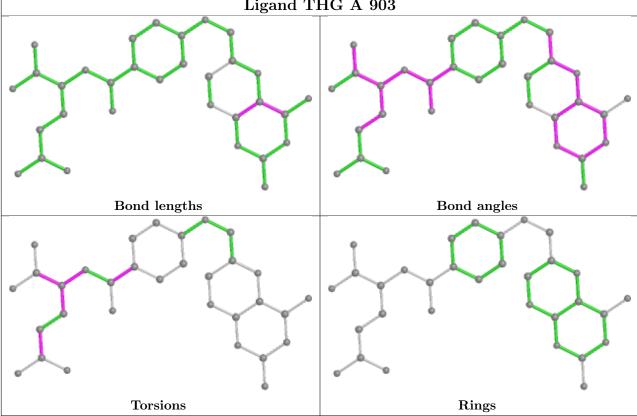
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	902	GOL	2	0
3	A	901	FAD	4	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,  $95^{th}$  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	666/666 (100%)	-0.11	3 (0%) 91 79	45, 83, 129, 156	0
2	В	133/235~(56%)	0.21	2 (1%) 73 51	79, 115, 140, 163	0
All	All	799/901 (88%)	-0.06	5 (0%) 89 76	45, 89, 133, 163	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	172	SER	2.9
2	В	375	VAL	2.5
1	A	171	PRO	2.4
2	В	376	ILE	2.3
1	A	455	ILE	2.0

### 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.

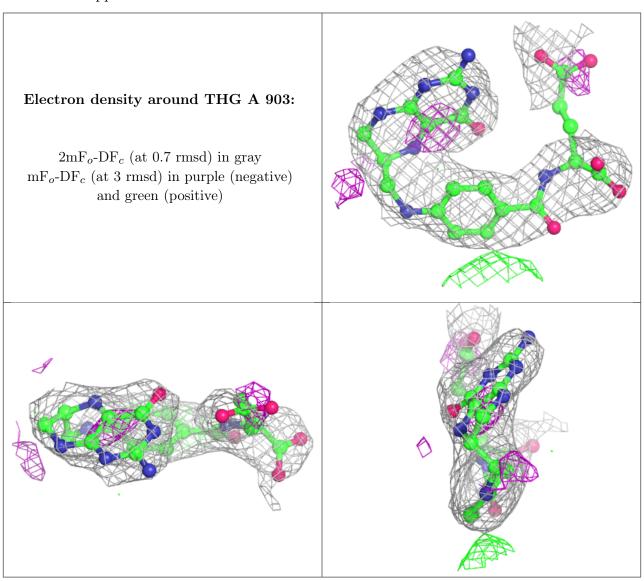
#### 6.4 Ligands (i)

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,  $95^{th}$  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.

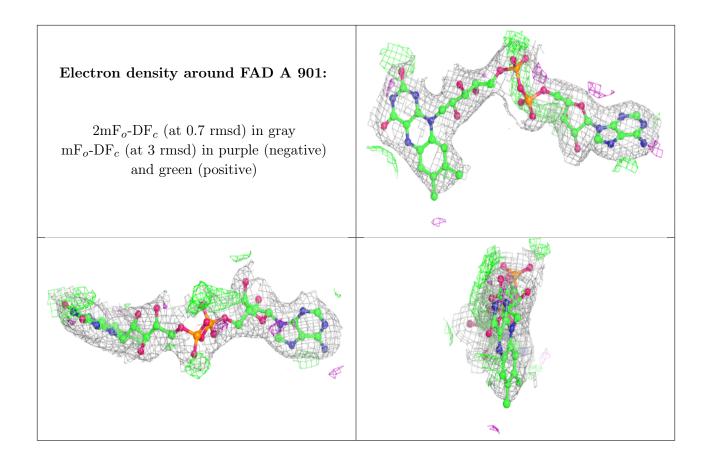


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
5	THG	A	903	32/32	0.85	0.29	102,119,136,142	0
4	GOL	A	902	6/6	0.94	0.18	65,70,73,75	0
6	CL	A	904	1/1	0.95	0.28	71,71,71,71	0
3	FAD	A	901	53/53	0.98	0.21	37,54,78,86	0

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.

