

wwPDB X-ray Structure Validation Summary Report (i)

Jun 19, 2020 – 07:38 pm BST

PDB ID : 3F6G

Title: Crystal structure of the regulatory domain of LiCMS in complexed with

isoleucine - type II

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Deposited on : 2008-11-06

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
A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

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 : 2.11

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

Refmac: 5.8.0158

 $\begin{array}{cccc} & CCP4 & : & 7.0.044 \; (Gargrove) \\ Ideal \; geometry \; (proteins) & : & Engh \; \& \; Huber \; (2001) \end{array}$

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

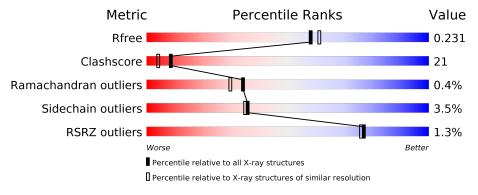
Validation Pipeline (wwPDB-VP) : 2.11

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 2.00 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
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 >=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	127	59%	31%	5% 5%			
1	В	127	65%	24%	• 9%			



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2054 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.

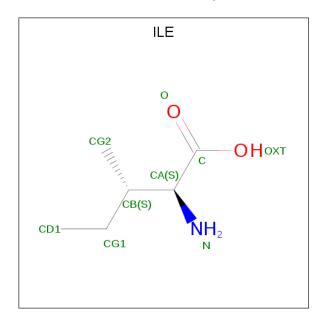
• Molecule 1 is a protein called Alpha-isopropylmalate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	В	115	Total			О		0	0	0
_			896	568	158	166	4		0	
1	Α	121	Total	С	N	О	S	0	0	0
	A	121	931	588	165	174	4	U	U	U

• Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0

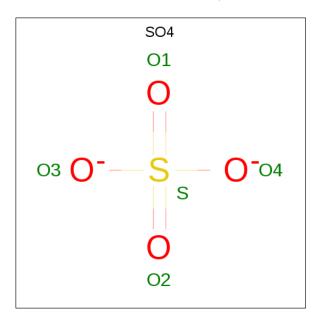
• Molecule 3 is ISOLEUCINE (three-letter code: ILE) (formula: $C_6H_{13}NO_2$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	В	1	Total 9	C 6		O 2	0	0
3	A	1	Total 9	C 6	N 1	O 2	0	0

 \bullet Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: $\mathrm{O_4S}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total O S 5 4 1	0	0
4	В	1	Total O S 5 4 1	0	0
4	В	1	Total O S 5 4 1	0	0
4	В	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0

• Molecule 5 is water.



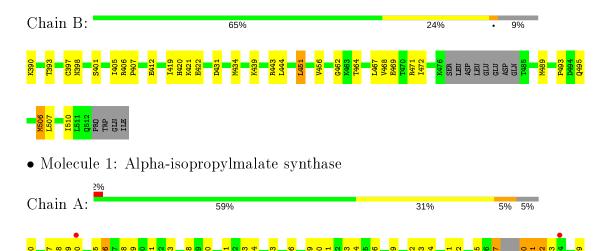
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	79	Total O 79 79	0	0
5	A	88	Total O 88 88	0	0



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 (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: Alpha-isopropylmalate synthase







4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	61.31Å 97.94Å 39.97Å	Depositor
a, b, c, α , β , γ	90.00° 91.38° 90.00°	Depositor
Resolution (Å)	20.00 - 2.00	Depositor
Resolution (A)	18.06 - 2.00	EDS
% Data completeness	97.8 (20.00-2.00)	Depositor
(in resolution range)	97.8 (18.06-2.00)	EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.53 \; ({\rm at} \; 2.00 {\rm \AA})$	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
υ .	0.226 , 0.263	Depositor
R, R_{free}	0.230 , 0.231	DCC
R_{free} test set	771 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.608	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.32 , 46.0	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.109 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2054	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 10.45% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: ZN, SO4

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	Boı	nd lengths	Bond angles		
Mol Chain		RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	0.50	2/946~(0.2%)	0.73	3/1277 (0.2%)	
1	В	0.35	0/911	0.61	0/1229	
All	All	0.43	$2/1857 \ (0.1\%)$	0.68	3/2506 (0.1%)	

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	3

All (2) bond length outliers are listed below:

$oxed{N}$	/Iol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
	1	A	482	GLU	C-O	5.33	1.33	1.23
	1	A	399	ILE	C-N	5.23	1.46	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	A	399	ILE	O-C-N	5.72	131.85	122.70
1	A	482	GLU	CA-C-N	5.21	128.67	117.20
1	A	481	GLU	C-N-CA	5.06	134.34	121.70

There are no chirality outliers.

All (3) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	480	LEU	Mainchain
1	A	481	GLU	Mainchain
1	A	482	GLU	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	931	0	940	56	0
1	В	896	0	920	36	0
2	A	1	0	0	0	0
2	В	1	0	0	0	0
3	A	9	0	13	0	0
3	В	9	0	13	0	0
4	A	20	0	0	1	0
4	В	20	0	0	1	0
5	A	88	0	0	6	0
5	В	79	0	0	3	0
All	All	2054	0	1886	78	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 21.

The worst 5 of 78 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{aligned}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:A:477:SER:HB2	1:A:480:LEU:CB	1.16	1.62
1:A:477:SER:CB	1:A:480:LEU:CB	2.03	1.34
1:A:477:SER:C	1:A:480:LEU:CB	2.25	1.05
1:A:506:MET:HE2	1:A:507:LEU:HA	1.42	0.97
1:B:506:MET:HE1	1:B:507:LEU:HA	1.56	0.87

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	${f Analysed}$	Favoured	Allowed	Outliers	Percenti	les
1	A	117/127 (92%)	115 (98%)	1 (1%)	1 (1%)	17 1	1
1	В	111/127~(87%)	109 (98%)	2 (2%)	0	100 10	00
All	All	$228/254 \ (90\%)$	224 (98%)	3 (1%)	1 (0%)	34 30)

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	483	ASP

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	${f Rotameric}$	Outliers	Percentiles
1	A	100/110 (91%)	97 (97%)	3 (3%)	41 41
1	В	98/110 (89%)	94 (96%)	4 (4%)	30 28
All	All	$198/220 \ (90\%)$	191 (96%)	7 (4%)	36 35

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	506	MET
1	A	506	MET
1	A	406	ARG
1	В	406	ARG
1	A	477	SER



Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	495	GLN
1	A	408	HIS
1	В	509	GLN
1	В	416	GLN
1	A	398	ASN

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 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	Т	Chain	Res	Link	В	ond leng	gths	В	ond ang	gles
MIOI	Type	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	A	1001	_	4,4,4	0.24	0	6,6,6	0.06	0
4	SO4	В	1007	-	4,4,4	0.27	0	6,6,6	0.06	0
4	SO4	A	1002	-	4,4,4	0.28	0	6,6,6	0.05	0
4	SO4	В	1006	-	4,4,4	0.25	0	6,6,6	0.09	0
4	SO4	A	1008	-	4,4,4	0.26	0	6,6,6	0.09	0
4	SO4	В	1005	-	4,4,4	0.29	0	6,6,6	0.05	0
4	SO4	В	1004	-	4,4,4	0.30	0	6,6,6	0.09	0
4	SO4	A	1003	-	4,4,4	0.28	0	6,6,6	0.07	0



There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1008	SO4	1	0
4	В	1004	SO4	1	0

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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(m \AA^2)$	Q < 0.9
1	A	121/127 (95%)	-0.34	3 (2%) 57 56	17, 29, 50, 71	0
1	В	$115/127 \ (90\%)$	-0.39	0 100 100	17, 31, 42, 54	0
All	All	$236/254 \ (92\%)$	-0.37	3 (1%) 77 76	17, 30, 47, 71	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	512	GLN	3.7
1	A	484	GLN	2.3
1	A	400	HIS	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 carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{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	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
4	SO4	Α	1008	5/5	0.76	0.34	72,73,73,74	0
4	SO4	В	1005	5/5	0.80	0.28	83,84,84,85	0

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Mol	Type	Chain	${ m Res}$	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q<0.9
4	SO4	A	1002	5/5	0.82	0.23	79,80,81,81	0
4	SO4	В	1004	5/5	0.84	0.31	88,89,89,90	0
4	SO4	В	1007	5/5	0.85	0.19	85,85,85,86	0
4	SO4	A	1003	5/5	0.93	0.10	64,64,66,66	0
4	SO4	A	1001	5/5	0.96	0.13	72,73,73,73	0
4	SO4	В	1006	5/5	0.96	0.13	70,70,70,71	0
3	ILE	A	1	9/9	0.97	0.09	17,19,24,27	0
2	ZN	A	359	1/1	0.98	0.29	35,35,35,35	1
3	ILE	В	1	9/9	0.98	0.09	20,20,23,25	0
2	ZN	В	358	1/1	0.99	0.21	23,23,23,23	1

6.5 Other polymers (i)

There are no such residues in this entry.

