



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3EEG / pdb\_00003eeg  
Title : Crystal structure of a 2-isopropylmalate synthase from *Cytophaga hutchinsonii*  
Authors : Sugadev, R.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center  
for Structural Genomics (NYSGXRC)  
Deposited on : 2008-09-04  
Resolution : 2.78 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

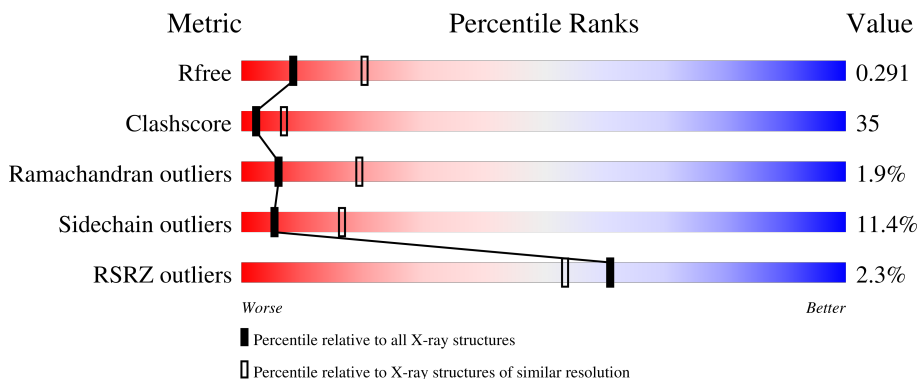
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.78 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))
$R_{free}$	180053	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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  $\geq 3$ , 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	325	
1	B	325	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4170 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 2-isopropylmalate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	267	2029	1267	358	391	5	8	0	0	0
1	B	273	2085	1301	371	400	5	8	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	expression tag	UNP Q11NN9
A	0	SER	-	expression tag	UNP Q11NN9
A	1	LEU	-	expression tag	UNP Q11NN9
A	316	GLU	-	expression tag	UNP Q11NN9
A	317	GLY	-	expression tag	UNP Q11NN9
A	318	HIS	-	expression tag	UNP Q11NN9
A	319	HIS	-	expression tag	UNP Q11NN9
A	320	HIS	-	expression tag	UNP Q11NN9
A	321	HIS	-	expression tag	UNP Q11NN9
A	322	HIS	-	expression tag	UNP Q11NN9
A	323	HIS	-	expression tag	UNP Q11NN9
B	-1	MSE	-	expression tag	UNP Q11NN9
B	0	SER	-	expression tag	UNP Q11NN9
B	1	LEU	-	expression tag	UNP Q11NN9
B	316	GLU	-	expression tag	UNP Q11NN9
B	317	GLY	-	expression tag	UNP Q11NN9
B	318	HIS	-	expression tag	UNP Q11NN9
B	319	HIS	-	expression tag	UNP Q11NN9
B	320	HIS	-	expression tag	UNP Q11NN9
B	321	HIS	-	expression tag	UNP Q11NN9
B	322	HIS	-	expression tag	UNP Q11NN9
B	323	HIS	-	expression tag	UNP Q11NN9

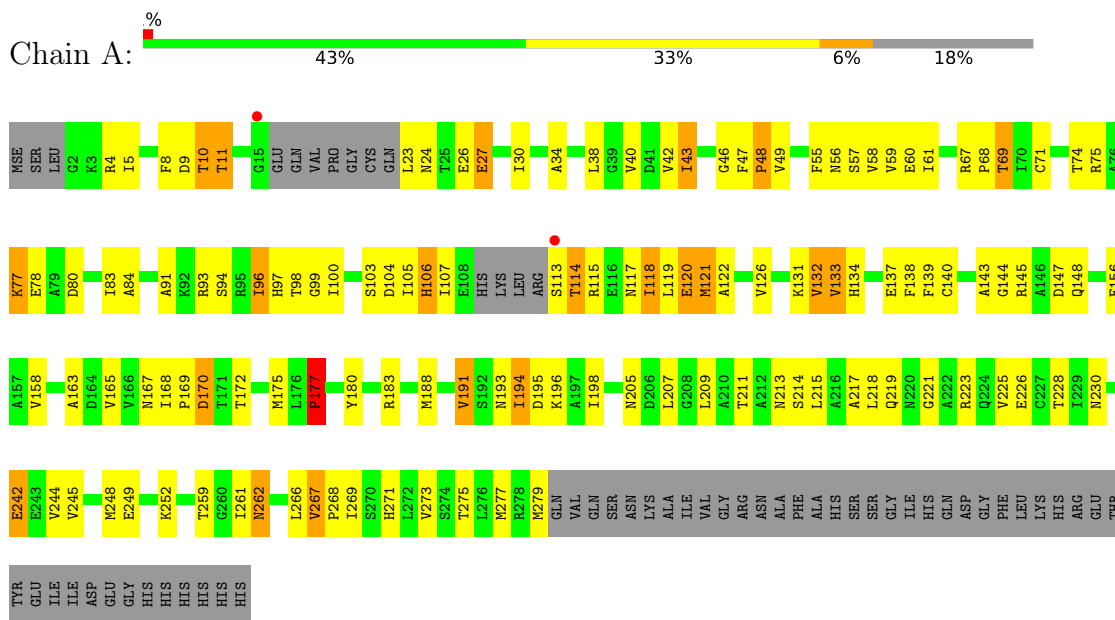
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	39	Total O 39 39	0	0
2	B	17	Total O 17 17	0	0

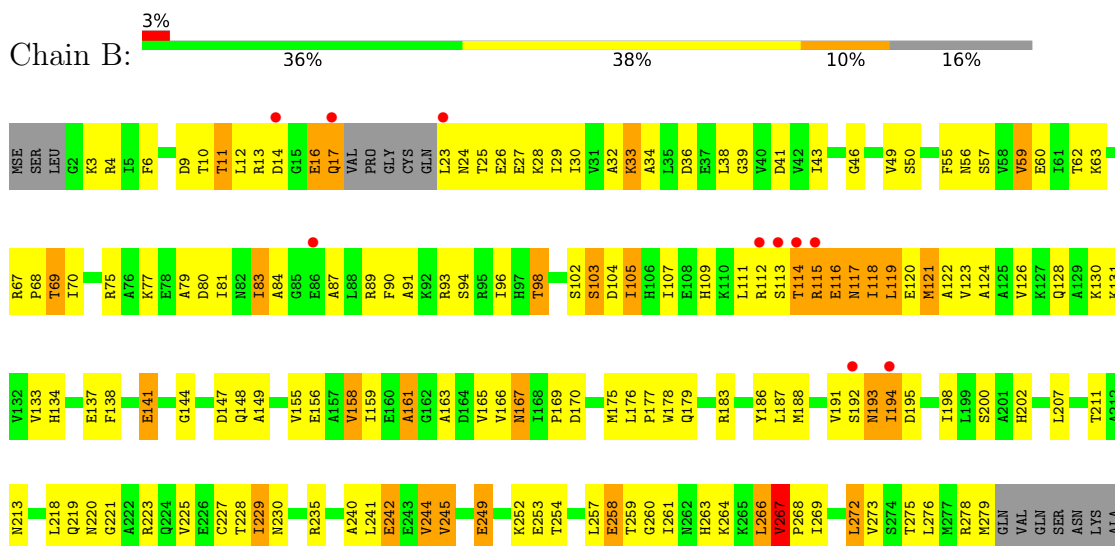
### 3 Residue-property plots [i](#)

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: 2-isopropylmalate synthase



- Molecule 1: 2-isopropylmalate synthase



ILE  
VAL  
GLY  
ARG  
ASN  
ALA  
PHE  
ALA  
HIS  
SER  
SER  
GLY  
ILE  
HIS  
GLN  
ASP  
GLY  
PHE  
LEU  
LYS  
HIS  
ARG  
GLU  
THR  
TYR  
GLU  
ILE  
ILE  
ASP  
GLU  
GLY  
HIS  
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	118.67Å 118.67Å 154.91Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.95 – 2.78 38.95 – 2.78	Depositor EDS
% Data completeness (in resolution range)	96.2 (38.95-2.78) 96.2 (38.95-2.78)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.59 (at 2.77Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.245 , 0.298 0.243 , 0.291	Depositor DCC
$R_{free}$ test set	655 reflections (3.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.7	Xtrriage
Anisotropy	0.124	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 50.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4170	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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 [i](#)

### 5.1 Standard geometry [i](#)

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	0.59	0/2045	1.10	19/2748 (0.7%)
1	B	0.53	1/2103 (0.0%)	1.06	12/2826 (0.4%)
All	All	0.56	1/4148 (0.0%)	1.08	31/5574 (0.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	267	VAL	CA-CB	5.11	1.56	1.54

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	121	MSE	N-CA-C	-13.20	95.86	112.88
1	A	121	MSE	N-CA-C	-9.00	102.85	112.93
1	B	104	ASP	N-CA-C	-7.06	103.92	112.54
1	A	27	GLU	N-CA-C	-7.02	103.39	112.23
1	B	235	ARG	CB-CA-C	-6.76	108.03	117.23

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	2029	0	2048	134	0
1	B	2085	0	2107	157	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	39	0	0	3	0
2	B	17	0	0	2	0
All	All	4170	0	4155	290	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 35.

The worst 5 of 290 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:B:103:SER:HB3	1:B:105:ILE:HG12	1.35	1.08
1:B:114:THR:HG23	1:B:118:ILE:HB	1.46	0.97
1:B:94:SER:H	1:B:134:HIS:HD2	1.13	0.96
1:B:170:ASP:HB2	1:B:175:MSE:HE3	1.45	0.96
1:A:9:ASP:OD1	1:A:11:THR:HG22	1.70	0.92

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	261/325 (80%)	236 (90%)	22 (8%)	3 (1%)	11	32
1	B	269/325 (83%)	235 (87%)	27 (10%)	7 (3%)	4	13
All	All	530/650 (82%)	471 (89%)	49 (9%)	10 (2%)	6	19

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	112	ARG
1	B	192	SER

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Mol	Chain	Res	Type
1	A	120	GLU
1	B	16	GLU
1	B	116	GLU

### 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	217/258 (84%)	199 (92%)	18 (8%)	10	29
1	B	223/258 (86%)	191 (86%)	32 (14%)	3	10
All	All	440/516 (85%)	390 (89%)	50 (11%)	5	16

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	118	ILE
1	B	207	LEU
1	B	275	THR
1	B	119	LEU
1	B	183	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	262	ASN
1	A	263	HIS
1	B	238	ASN
1	B	213	ASN
1	B	224	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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	259/325 (79%)	-0.10	2 (0%) 82 77	9, 24, 44, 50	0
1	B	265/325 (81%)	0.38	10 (3%) 44 37	16, 36, 56, 66	0
All	All	524/650 (80%)	0.14	12 (2%) 61 53	9, 30, 52, 66	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	112	ARG	3.0
1	B	114	THR	2.7
1	B	113	SER	2.6
1	B	23	LEU	2.6
1	B	17	GLN	2.5

### 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 oligosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.