



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 03:52 AM UTC

PDB ID : 4E4G / pdb_00004e4g
Title : Crystal structure of putative Methylmalonate-semialdehyde dehydrogenase from *Sinorhizobium meliloti* 1021
Authors : Malashkevich, V.N.; Bhosle, R.; Toro, R.; Hillerich, B.; Gizzi, A.; Garforth, S.; Kar, A.; Chan, M.K.; Laffuer, J.; Patel, H.; Matikainen, B.; Chamala, S.; Lim, S.; Celikgil, A.; Villegas, G.; Evans, B.; Zenchek, W.; Love, J.; Fiser, A.; Khafizov, K.; Seidel, R.; Bonanno, J.B.; Almo, S.C.; New York Structural Genomics Research Consortium (NYSGRC)
Deposited on : 2012-03-12
Resolution : 2.90 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 ⓘ 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 ⓘ](#)) 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)

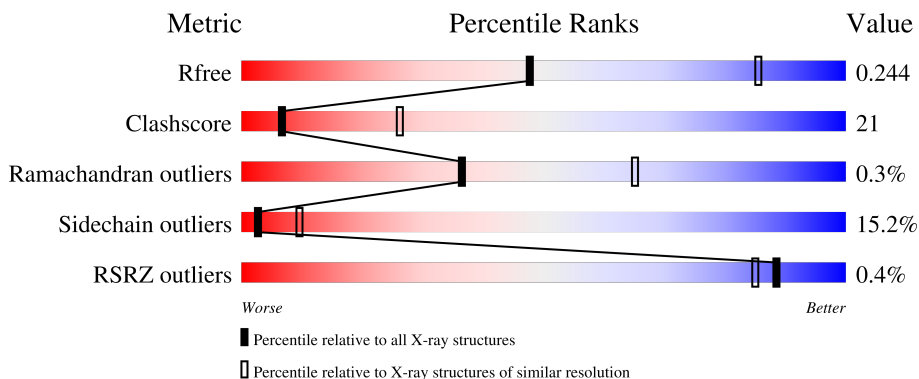
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 $\leq 5\%$. 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	521	
1	B	521	
1	C	521	

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
1	D	521	<p>55% 31% 8% 6%</p>
1	E	521	<p>% 47% 35% 11% 7%</p>
1	F	521	<p>2% 46% 37% 9% 7%</p>
1	G	521	<p>57% 29% 6% 7%</p>
1	H	521	<p>55% 32% 6% 7%</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 29653 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 Methylmalonate-semialdehyde dehydrogenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	488	3681	2325	640	693	5	18	0	0	0
1	B	486	3665	2316	638	689	5	17	0	0	0
1	C	486	3664	2315	637	689	5	18	0	0	0
1	D	488	3681	2325	640	693	5	18	0	0	0
1	E	486	3665	2316	638	689	5	17	0	0	0
1	F	484	3644	2301	635	686	5	17	0	0	0
1	G	485	3660	2312	636	688	5	19	0	0	0
1	H	485	3653	2307	637	687	5	17	0	0	0

There are 184 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MSE	-	expression tag	UNP Q92RW4
A	-23	HIS	-	expression tag	UNP Q92RW4
A	-22	HIS	-	expression tag	UNP Q92RW4
A	-21	HIS	-	expression tag	UNP Q92RW4
A	-20	HIS	-	expression tag	UNP Q92RW4
A	-19	HIS	-	expression tag	UNP Q92RW4
A	-18	HIS	-	expression tag	UNP Q92RW4
A	-17	SER	-	expression tag	UNP Q92RW4
A	-16	SER	-	expression tag	UNP Q92RW4
A	-15	GLY	-	expression tag	UNP Q92RW4
A	-14	VAL	-	expression tag	UNP Q92RW4
A	-13	ASP	-	expression tag	UNP Q92RW4
A	-12	LEU	-	expression tag	UNP Q92RW4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	GLY	-	expression tag	UNP Q92RW4
A	-10	THR	-	expression tag	UNP Q92RW4
A	-9	GLU	-	expression tag	UNP Q92RW4
A	-8	ASN	-	expression tag	UNP Q92RW4
A	-7	LEU	-	expression tag	UNP Q92RW4
A	-6	TYR	-	expression tag	UNP Q92RW4
A	-5	PHE	-	expression tag	UNP Q92RW4
A	-4	GLN	-	expression tag	UNP Q92RW4
A	-3	SER	-	expression tag	UNP Q92RW4
A	-2	MSE	-	expression tag	UNP Q92RW4
B	-24	MSE	-	expression tag	UNP Q92RW4
B	-23	HIS	-	expression tag	UNP Q92RW4
B	-22	HIS	-	expression tag	UNP Q92RW4
B	-21	HIS	-	expression tag	UNP Q92RW4
B	-20	HIS	-	expression tag	UNP Q92RW4
B	-19	HIS	-	expression tag	UNP Q92RW4
B	-18	HIS	-	expression tag	UNP Q92RW4
B	-17	SER	-	expression tag	UNP Q92RW4
B	-16	SER	-	expression tag	UNP Q92RW4
B	-15	GLY	-	expression tag	UNP Q92RW4
B	-14	VAL	-	expression tag	UNP Q92RW4
B	-13	ASP	-	expression tag	UNP Q92RW4
B	-12	LEU	-	expression tag	UNP Q92RW4
B	-11	GLY	-	expression tag	UNP Q92RW4
B	-10	THR	-	expression tag	UNP Q92RW4
B	-9	GLU	-	expression tag	UNP Q92RW4
B	-8	ASN	-	expression tag	UNP Q92RW4
B	-7	LEU	-	expression tag	UNP Q92RW4
B	-6	TYR	-	expression tag	UNP Q92RW4
B	-5	PHE	-	expression tag	UNP Q92RW4
B	-4	GLN	-	expression tag	UNP Q92RW4
B	-3	SER	-	expression tag	UNP Q92RW4
B	-2	MSE	-	expression tag	UNP Q92RW4
C	-24	MSE	-	expression tag	UNP Q92RW4
C	-23	HIS	-	expression tag	UNP Q92RW4
C	-22	HIS	-	expression tag	UNP Q92RW4
C	-21	HIS	-	expression tag	UNP Q92RW4
C	-20	HIS	-	expression tag	UNP Q92RW4
C	-19	HIS	-	expression tag	UNP Q92RW4
C	-18	HIS	-	expression tag	UNP Q92RW4
C	-17	SER	-	expression tag	UNP Q92RW4
C	-16	SER	-	expression tag	UNP Q92RW4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-15	GLY	-	expression tag	UNP Q92RW4
C	-14	VAL	-	expression tag	UNP Q92RW4
C	-13	ASP	-	expression tag	UNP Q92RW4
C	-12	LEU	-	expression tag	UNP Q92RW4
C	-11	GLY	-	expression tag	UNP Q92RW4
C	-10	THR	-	expression tag	UNP Q92RW4
C	-9	GLU	-	expression tag	UNP Q92RW4
C	-8	ASN	-	expression tag	UNP Q92RW4
C	-7	LEU	-	expression tag	UNP Q92RW4
C	-6	TYR	-	expression tag	UNP Q92RW4
C	-5	PHE	-	expression tag	UNP Q92RW4
C	-4	GLN	-	expression tag	UNP Q92RW4
C	-3	SER	-	expression tag	UNP Q92RW4
C	-2	MSE	-	expression tag	UNP Q92RW4
D	-24	MSE	-	expression tag	UNP Q92RW4
D	-23	HIS	-	expression tag	UNP Q92RW4
D	-22	HIS	-	expression tag	UNP Q92RW4
D	-21	HIS	-	expression tag	UNP Q92RW4
D	-20	HIS	-	expression tag	UNP Q92RW4
D	-19	HIS	-	expression tag	UNP Q92RW4
D	-18	HIS	-	expression tag	UNP Q92RW4
D	-17	SER	-	expression tag	UNP Q92RW4
D	-16	SER	-	expression tag	UNP Q92RW4
D	-15	GLY	-	expression tag	UNP Q92RW4
D	-14	VAL	-	expression tag	UNP Q92RW4
D	-13	ASP	-	expression tag	UNP Q92RW4
D	-12	LEU	-	expression tag	UNP Q92RW4
D	-11	GLY	-	expression tag	UNP Q92RW4
D	-10	THR	-	expression tag	UNP Q92RW4
D	-9	GLU	-	expression tag	UNP Q92RW4
D	-8	ASN	-	expression tag	UNP Q92RW4
D	-7	LEU	-	expression tag	UNP Q92RW4
D	-6	TYR	-	expression tag	UNP Q92RW4
D	-5	PHE	-	expression tag	UNP Q92RW4
D	-4	GLN	-	expression tag	UNP Q92RW4
D	-3	SER	-	expression tag	UNP Q92RW4
D	-2	MSE	-	expression tag	UNP Q92RW4
E	-24	MSE	-	expression tag	UNP Q92RW4
E	-23	HIS	-	expression tag	UNP Q92RW4
E	-22	HIS	-	expression tag	UNP Q92RW4
E	-21	HIS	-	expression tag	UNP Q92RW4
E	-20	HIS	-	expression tag	UNP Q92RW4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-19	HIS	-	expression tag	UNP Q92RW4
E	-18	HIS	-	expression tag	UNP Q92RW4
E	-17	SER	-	expression tag	UNP Q92RW4
E	-16	SER	-	expression tag	UNP Q92RW4
E	-15	GLY	-	expression tag	UNP Q92RW4
E	-14	VAL	-	expression tag	UNP Q92RW4
E	-13	ASP	-	expression tag	UNP Q92RW4
E	-12	LEU	-	expression tag	UNP Q92RW4
E	-11	GLY	-	expression tag	UNP Q92RW4
E	-10	THR	-	expression tag	UNP Q92RW4
E	-9	GLU	-	expression tag	UNP Q92RW4
E	-8	ASN	-	expression tag	UNP Q92RW4
E	-7	LEU	-	expression tag	UNP Q92RW4
E	-6	TYR	-	expression tag	UNP Q92RW4
E	-5	PHE	-	expression tag	UNP Q92RW4
E	-4	GLN	-	expression tag	UNP Q92RW4
E	-3	SER	-	expression tag	UNP Q92RW4
E	-2	MSE	-	expression tag	UNP Q92RW4
F	-24	MSE	-	expression tag	UNP Q92RW4
F	-23	HIS	-	expression tag	UNP Q92RW4
F	-22	HIS	-	expression tag	UNP Q92RW4
F	-21	HIS	-	expression tag	UNP Q92RW4
F	-20	HIS	-	expression tag	UNP Q92RW4
F	-19	HIS	-	expression tag	UNP Q92RW4
F	-18	HIS	-	expression tag	UNP Q92RW4
F	-17	SER	-	expression tag	UNP Q92RW4
F	-16	SER	-	expression tag	UNP Q92RW4
F	-15	GLY	-	expression tag	UNP Q92RW4
F	-14	VAL	-	expression tag	UNP Q92RW4
F	-13	ASP	-	expression tag	UNP Q92RW4
F	-12	LEU	-	expression tag	UNP Q92RW4
F	-11	GLY	-	expression tag	UNP Q92RW4
F	-10	THR	-	expression tag	UNP Q92RW4
F	-9	GLU	-	expression tag	UNP Q92RW4
F	-8	ASN	-	expression tag	UNP Q92RW4
F	-7	LEU	-	expression tag	UNP Q92RW4
F	-6	TYR	-	expression tag	UNP Q92RW4
F	-5	PHE	-	expression tag	UNP Q92RW4
F	-4	GLN	-	expression tag	UNP Q92RW4
F	-3	SER	-	expression tag	UNP Q92RW4
F	-2	MSE	-	expression tag	UNP Q92RW4
G	-24	MSE	-	expression tag	UNP Q92RW4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-23	HIS	-	expression tag	UNP Q92RW4
G	-22	HIS	-	expression tag	UNP Q92RW4
G	-21	HIS	-	expression tag	UNP Q92RW4
G	-20	HIS	-	expression tag	UNP Q92RW4
G	-19	HIS	-	expression tag	UNP Q92RW4
G	-18	HIS	-	expression tag	UNP Q92RW4
G	-17	SER	-	expression tag	UNP Q92RW4
G	-16	SER	-	expression tag	UNP Q92RW4
G	-15	GLY	-	expression tag	UNP Q92RW4
G	-14	VAL	-	expression tag	UNP Q92RW4
G	-13	ASP	-	expression tag	UNP Q92RW4
G	-12	LEU	-	expression tag	UNP Q92RW4
G	-11	GLY	-	expression tag	UNP Q92RW4
G	-10	THR	-	expression tag	UNP Q92RW4
G	-9	GLU	-	expression tag	UNP Q92RW4
G	-8	ASN	-	expression tag	UNP Q92RW4
G	-7	LEU	-	expression tag	UNP Q92RW4
G	-6	TYR	-	expression tag	UNP Q92RW4
G	-5	PHE	-	expression tag	UNP Q92RW4
G	-4	GLN	-	expression tag	UNP Q92RW4
G	-3	SER	-	expression tag	UNP Q92RW4
G	-2	MSE	-	expression tag	UNP Q92RW4
H	-24	MSE	-	expression tag	UNP Q92RW4
H	-23	HIS	-	expression tag	UNP Q92RW4
H	-22	HIS	-	expression tag	UNP Q92RW4
H	-21	HIS	-	expression tag	UNP Q92RW4
H	-20	HIS	-	expression tag	UNP Q92RW4
H	-19	HIS	-	expression tag	UNP Q92RW4
H	-18	HIS	-	expression tag	UNP Q92RW4
H	-17	SER	-	expression tag	UNP Q92RW4
H	-16	SER	-	expression tag	UNP Q92RW4
H	-15	GLY	-	expression tag	UNP Q92RW4
H	-14	VAL	-	expression tag	UNP Q92RW4
H	-13	ASP	-	expression tag	UNP Q92RW4
H	-12	LEU	-	expression tag	UNP Q92RW4
H	-11	GLY	-	expression tag	UNP Q92RW4
H	-10	THR	-	expression tag	UNP Q92RW4
H	-9	GLU	-	expression tag	UNP Q92RW4
H	-8	ASN	-	expression tag	UNP Q92RW4
H	-7	LEU	-	expression tag	UNP Q92RW4
H	-6	TYR	-	expression tag	UNP Q92RW4
H	-5	PHE	-	expression tag	UNP Q92RW4

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-4	GLN	-	expression tag	UNP Q92RW4
H	-3	SER	-	expression tag	UNP Q92RW4
H	-2	MSE	-	expression tag	UNP Q92RW4

- Molecule 2 is water.

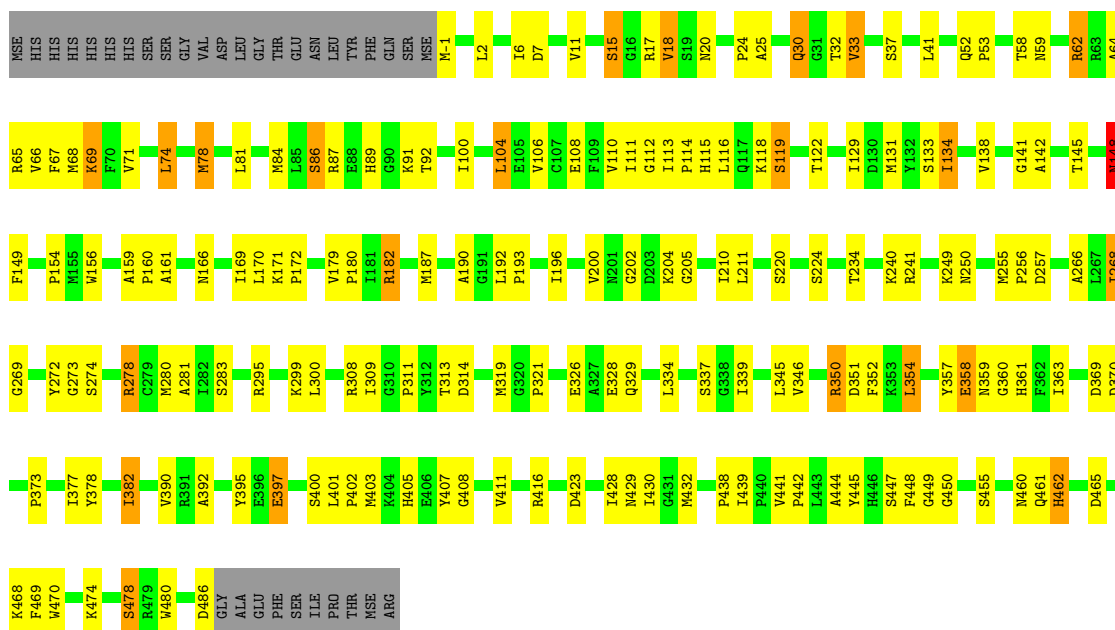
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	58	Total O 58 58	0	0
2	B	44	Total O 44 44	0	0
2	C	51	Total O 51 51	0	0
2	D	35	Total O 35 35	0	0
2	E	33	Total O 33 33	0	0
2	F	35	Total O 35 35	0	0
2	G	42	Total O 42 42	0	0
2	H	42	Total O 42 42	0	0

3 Residue-property plots

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.

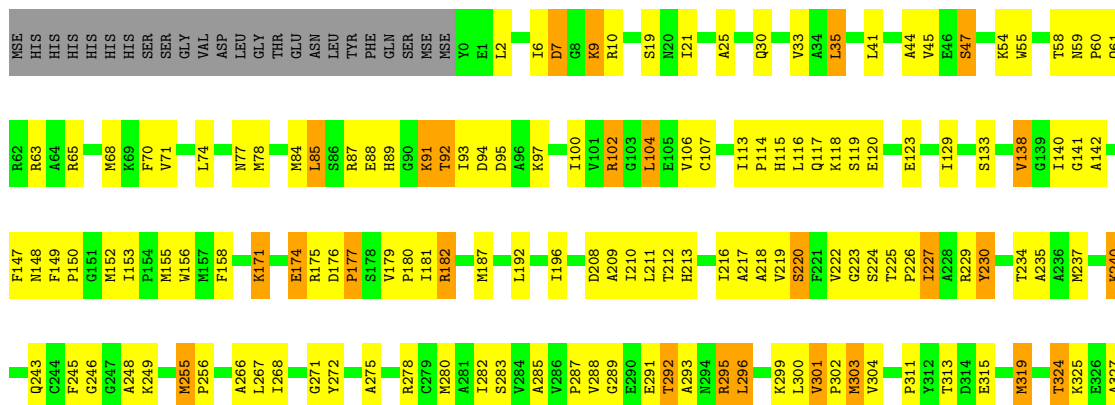
- Molecule 1: Methylmalonate-semialdehyde dehydrogenase

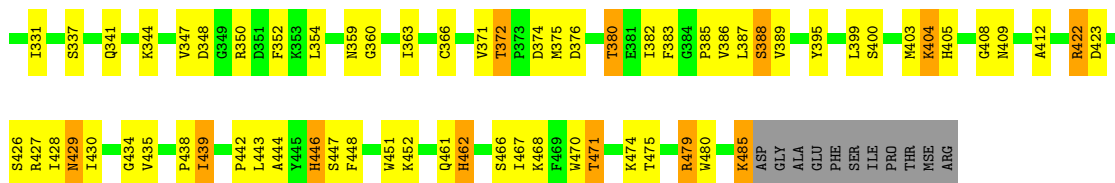
Chain A: 



- Molecule 1: Methylmalonate-semialdehyde dehydrogenase

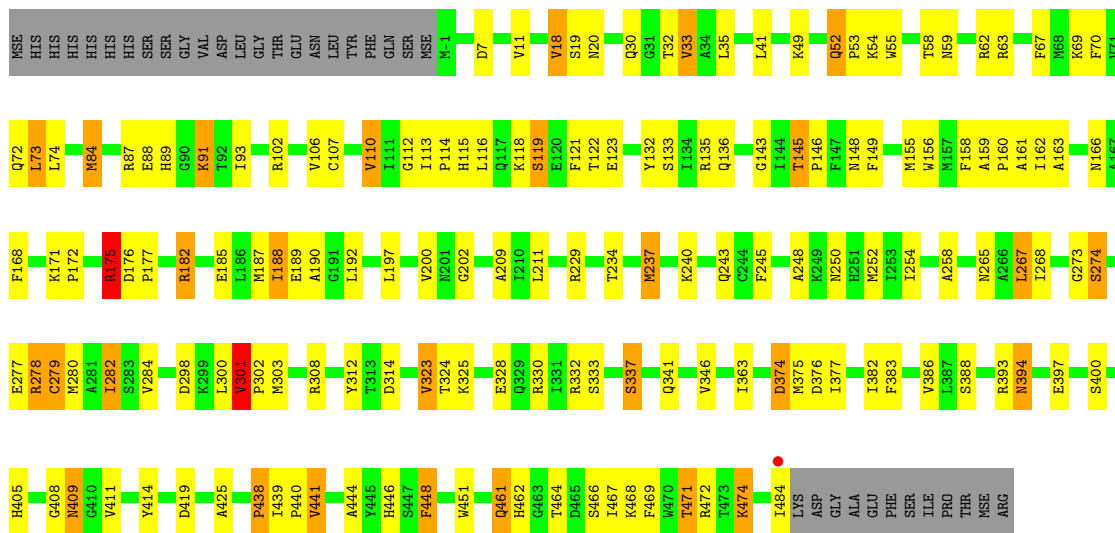
Chain B: 





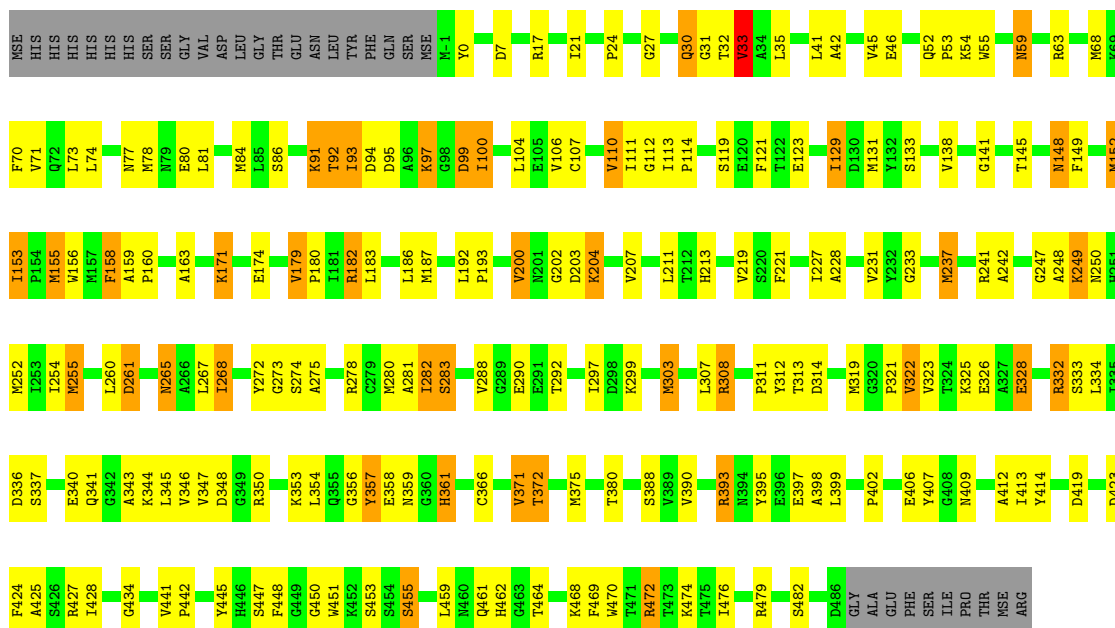
- Molecule 1: Methylmalonate-semialdehyde dehydrogenase

Chain C: 63% 25% 5% 7%



- Molecule 1: Methylmalonate-semialdehyde dehydrogenase

Chain D: 55% 31% 8% 6%

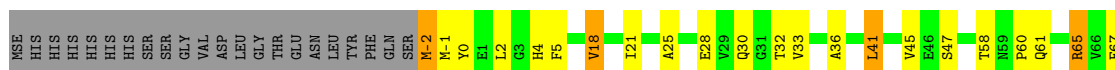


- Molecule 1: Methylmalonate-semialdehyde dehydrogenase



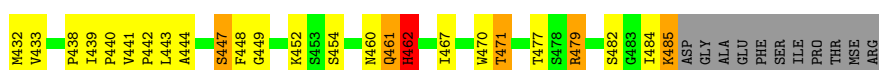
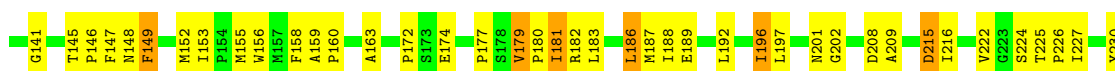
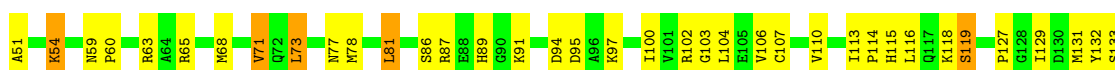
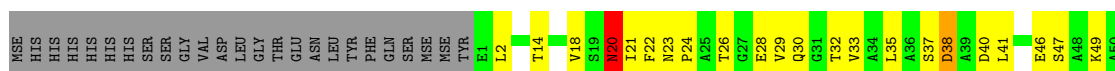
● Molecule 1: Methylmalonate-semialdehyde dehydrogenase

Chain G: 57% 29% 6% 7%



● Molecule 1: Methylmalonate-semialdehyde dehydrogenase

Chain H: 55% 32% 6% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	197.44Å 171.28Å 159.69Å 90.00° 124.03° 90.00°	Depositor
Resolution (Å)	19.97 – 2.90 19.97 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.6 (19.97-2.90) 98.6 (19.97-2.90)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.06 (at 2.88Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.188 , 0.269 (Not available) , 0.244	Depositor DCC
R_{free} test set	4795 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	43.1	Xtrriage
Anisotropy	0.059	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 41.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	29653	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 38.02 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.9244e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.80	1/3742 (0.0%)	1.07	9/5043 (0.2%)
1	B	0.83	3/3726 (0.1%)	1.07	7/5022 (0.1%)
1	C	0.83	6/3725 (0.2%)	1.08	6/5021 (0.1%)
1	D	0.86	5/3742 (0.1%)	1.05	10/5043 (0.2%)
1	E	0.84	4/3726 (0.1%)	1.14	18/5022 (0.4%)
1	F	0.96	9/3704 (0.2%)	1.14	13/4993 (0.3%)
1	G	0.84	4/3720 (0.1%)	1.06	9/5012 (0.2%)
1	H	0.88	6/3713 (0.2%)	1.10	11/5004 (0.2%)
All	All	0.85	38/29798 (0.1%)	1.09	83/40160 (0.2%)

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	31	GLY	C-N	8.97	1.46	1.33
1	B	446	HIS	CG-ND1	-8.24	1.29	1.38
1	F	357	TYR	CG-CD2	8.20	1.56	1.39
1	G	446	HIS	CG-ND1	-7.78	1.29	1.38
1	F	30	GLN	CA-C	-7.53	1.42	1.52

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	229	ARG	N-CA-C	-13.83	96.20	111.28
1	F	349	GLY	N-CA-C	12.64	128.95	112.77
1	F	273	GLY	N-CA-C	-11.67	98.50	111.93
1	F	125	ALA	N-CA-C	-9.89	100.50	111.28
1	E	323	VAL	N-CA-C	8.44	119.22	110.36

There are no chirality outliers.

There are no planarity outliers.

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	3681	0	3652	113	0
1	B	3665	0	3639	167	0
1	C	3664	0	3635	117	0
1	D	3681	0	3652	143	0
1	E	3665	0	3639	226	1
1	F	3644	0	3617	258	1
1	G	3660	0	3630	132	0
1	H	3653	0	3630	152	0
2	A	58	0	0	2	0
2	B	44	0	0	2	0
2	C	51	0	0	3	0
2	D	35	0	0	1	0
2	E	33	0	0	1	0
2	F	35	0	0	2	0
2	G	42	0	0	2	0
2	H	42	0	0	5	0
All	All	29653	0	29094	1253	1

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 1253 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:F:70:PHE:CE1	1:F:187:MSE:SE	2.30	1.33
1:H:110:VAL:CG1	1:H:163:ALA:HB2	1.78	1.13
1:F:126:GLY:HA3	1:F:129:ILE:HB	1.28	1.12
1:F:68:MSE:HE1	1:H:71:VAL:HG11	1.14	1.11
1:F:152:MSE:HE2	1:F:153:ILE:HD11	1.29	1.09

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:298:ASP:O	1:F:299:LYS:NZ[4_446]	2.14	0.06

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	486/521 (93%)	457 (94%)	28 (6%)	1 (0%)	43	72
1	B	484/521 (93%)	455 (94%)	28 (6%)	1 (0%)	43	72
1	C	484/521 (93%)	457 (94%)	25 (5%)	2 (0%)	30	59
1	D	486/521 (93%)	457 (94%)	28 (6%)	1 (0%)	43	72
1	E	484/521 (93%)	451 (93%)	31 (6%)	2 (0%)	30	59
1	F	482/521 (92%)	450 (93%)	31 (6%)	1 (0%)	43	72
1	G	483/521 (93%)	456 (94%)	25 (5%)	2 (0%)	30	59
1	H	483/521 (93%)	452 (94%)	28 (6%)	3 (1%)	21	51
All	All	3872/4168 (93%)	3635 (94%)	224 (6%)	13 (0%)	36	65

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	462	HIS
1	A	462	HIS
1	C	462	HIS
1	D	462	HIS
1	E	462	HIS

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	383/391 (98%)	343 (90%)	40 (10%)	7	23
1	B	381/391 (97%)	326 (86%)	55 (14%)	3	11
1	C	381/391 (97%)	332 (87%)	49 (13%)	4	13
1	D	383/391 (98%)	317 (83%)	66 (17%)	2	7
1	E	381/391 (97%)	307 (81%)	74 (19%)	1	5
1	F	379/391 (97%)	303 (80%)	76 (20%)	1	4
1	G	381/391 (97%)	322 (84%)	59 (16%)	2	9
1	H	380/391 (97%)	336 (88%)	44 (12%)	5	18
All	All	3049/3128 (98%)	2586 (85%)	463 (15%)	3	9

5 of 463 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	182	ARG
1	H	288	VAL
1	F	18	VAL
1	H	237	MSE
1	G	330	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	446	HIS
1	G	446	HIS
1	E	115	HIS
1	G	361	HIS
1	H	243	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, 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	470/521 (90%)	-0.69	0 100 100	17, 36, 55, 71	0
1	B	469/521 (90%)	-0.58	0 100 100	19, 38, 58, 76	0
1	C	468/521 (89%)	-0.79	1 (0%) 91 89	15, 28, 49, 79	0
1	D	470/521 (90%)	-0.49	0 100 100	15, 43, 75, 93	0
1	E	469/521 (90%)	0.03	4 (0%) 81 75	21, 57, 81, 97	0
1	F	467/521 (89%)	0.17	10 (2%) 63 54	29, 59, 87, 107	0
1	G	466/521 (89%)	-0.69	0 100 100	18, 35, 53, 70	0
1	H	468/521 (89%)	-0.63	0 100 100	18, 38, 57, 74	0
All	All	3747/4168 (89%)	-0.46	15 (0%) 88 85	15, 40, 73, 107	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	31	GLY	2.9
1	E	377	ILE	2.8
1	F	35	LEU	2.8
1	F	174	GLU	2.8
1	F	349	GLY	2.6

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.