Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 11:59 AM EDT

PDB ID	:	6T8C
Title	:	Crystal structure of formate dehydrogenase FDH2 enzyme from Granulicella mallensis MP5ACTX8 in the apo form.
Authors	:	Robescu, M.S.; Rubini, R.; Filippini, F.; Bergantino, B.; Cendron, L.
Deposited on	:	2019-10-24
Resolution	:	1.97 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 ⓘ 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:

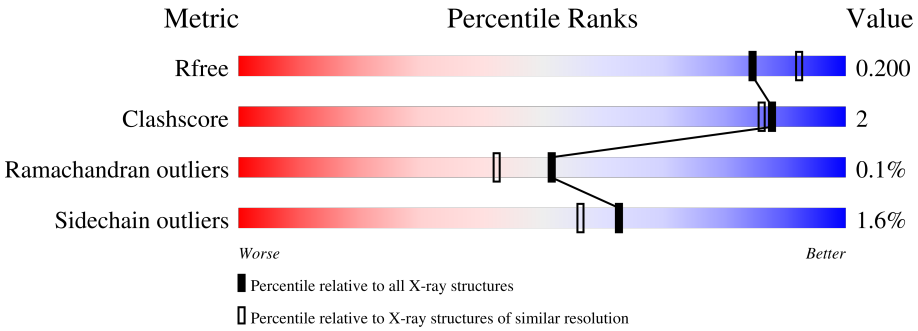
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.97 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	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)

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%

Mol	Chain	Length	Quality of chain
1	A	386	94%
1	B	386	92%
1	C	386	91% 6%
1	D	386	89% 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 12435 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 Formate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	0	2	0
			2927	1868	500	547	12			
1	B	373	Total	C	N	O	S	0	3	0
			2924	1866	500	546	12			
1	C	374	Total	C	N	O	S	0	0	0
			2911	1858	498	543	12			
1	D	373	Total	C	N	O	S	0	0	0
			2906	1855	497	542	12			

- Molecule 2 is water.

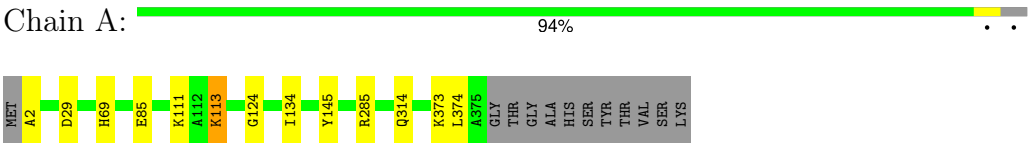
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	185	Total	O	0	0
			185	185		
2	B	193	Total	O	0	0
			193	193		
2	C	197	Total	O	0	0
			197	197		
2	D	192	Total	O	0	0
			192	192		

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. 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. 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.

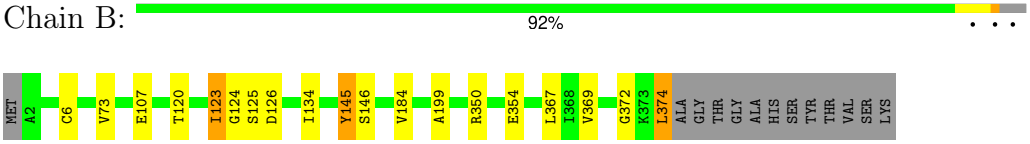
• Molecule 1: Formate dehydrogenase

Chain A:



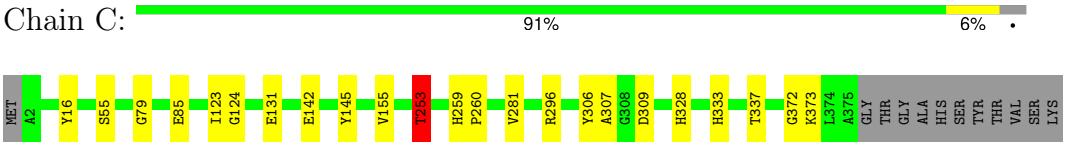
• Molecule 1: Formate dehydrogenase

Chain B:



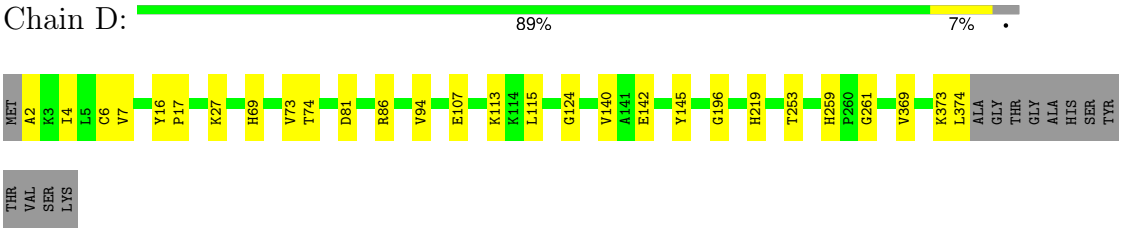
• Molecule 1: Formate dehydrogenase

Chain C:



• Molecule 1: Formate dehydrogenase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	99.36Å 112.49Å 147.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.95 – 1.97 48.95 – 1.97	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.95-1.97) 99.8 (48.95-1.97)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.95 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	(Not available) , (Not available) 0.167 , 0.200	Depositor DCC
R_{free} test set	5824 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	22.4	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 37.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	12435	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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

5.1 Standard geometry

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	0.54	0/2999	0.81	0/4081
1	B	0.54	0/2996	0.81	0/4076
1	C	0.51	0/2983	0.79	1/4059 (0.0%)
1	D	0.53	0/2978	0.81	0/4052
All	All	0.53	0/11956	0.81	1/16268 (0.0%)

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	B	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	253	THR	CB-CA-C	-5.47	96.83	111.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	125[A]	SER	Mainchain
1	B	125[B]	SER	Mainchain

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	2927	0	2913	7	0
1	B	2924	0	2913	15	0
1	C	2911	0	2900	13	0
1	D	2906	0	2895	13	0
2	A	185	0	0	2	0
2	B	193	0	0	5	0
2	C	197	0	0	3	0
2	D	192	0	0	1	0
All	All	12435	0	11621	46	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 2.

All (46) 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:123[B]:ILE:HD11	1:B:146:SER:N	2.00	0.77
1:B:123[A]:ILE:CD1	2:B:562:HOH:O	2.36	0.73
1:C:259:HIS:HB2	1:C:260:PRO:HD2	1.75	0.68
1:B:120:THR:HG21	1:B:124[A]:GLY:O	1.96	0.66
1:A:314:GLN:NE2	2:A:401:HOH:O	2.30	0.65
1:D:373:LYS:HG2	1:D:374:LEU:N	2.12	0.63
1:C:124:GLY:N	1:C:142:GLU:OE2	2.26	0.62
1:C:259:HIS:HB2	1:C:260:PRO:CD	2.32	0.59
1:B:123[B]:ILE:HD11	1:B:146:SER:H	1.66	0.59
1:A:134:ILE:HD13	1:A:374:LEU:HD11	1.87	0.57
1:C:79:GLY:O	1:C:85:GLU:HG3	2.07	0.55
1:C:123:ILE:HD13	2:C:500:HOH:O	2.06	0.54
1:D:140:VAL:HB	1:D:369:VAL:HG13	1.90	0.53
1:D:124:GLY:N	1:D:142:GLU:OE2	2.40	0.53
1:B:123[A]:ILE:HD12	2:B:422:HOH:O	2.09	0.52
1:C:155:VAL:HG11	1:C:253:THR:HG21	1.92	0.51
1:D:81:ASP:O	1:D:86:ARG:NH1	2.44	0.51
1:A:85:GLU:OE2	1:A:111:LYS:HE2	2.11	0.51
1:B:107:GLU:OE2	1:B:107:GLU:N	2.42	0.49
1:D:2:ALA:N	2:D:403:HOH:O	2.46	0.49
1:B:372:GLY:C	1:B:374:LEU:H	2.17	0.48
1:A:2:ALA:N	1:A:69:HIS:HD1	2.12	0.47
1:D:4:ILE:HD12	1:D:4:ILE:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:372:GLY:HA2	2:C:449:HOH:O	2.14	0.47
1:B:123[A]:ILE:HD11	2:B:562:HOH:O	2.10	0.47
1:B:123[B]:ILE:HG21	2:B:562:HOH:O	2.15	0.47
1:D:259:HIS:HD2	1:D:261:GLY:H	1.63	0.46
1:C:281:VAL:HA	1:C:307:ALA:O	2.17	0.45
1:D:7:VAL:HA	1:D:74:THR:O	2.17	0.45
1:A:124:GLY:HA3	2:A:540:HOH:O	2.17	0.44
1:B:123[A]:ILE:HG13	2:B:562:HOH:O	2.16	0.44
1:D:94:VAL:HG23	1:D:115:LEU:HD13	1.99	0.44
1:D:196:GLY:HA2	1:D:219:HIS:O	2.17	0.44
1:D:6:CYS:O	1:D:73:VAL:HA	2.18	0.43
1:D:2:ALA:N	1:D:69:HIS:HD1	2.16	0.43
1:B:123[B]:ILE:HD11	1:B:145:TYR:C	2.38	0.43
1:B:184:VAL:HG11	1:C:337:THR:HG23	2.00	0.43
1:B:6:CYS:O	1:B:73:VAL:HA	2.19	0.42
1:C:309:ASP:O	1:C:333:HIS:HA	2.20	0.42
1:D:16:TYR:CD1	1:D:17:PRO:HD2	2.54	0.42
1:C:16:TYR:CD1	1:C:55:SER:HB2	2.55	0.41
1:C:124:GLY:C	2:C:451:HOH:O	2.57	0.41
1:B:350:ARG:O	1:B:354:GLU:HG3	2.21	0.41
1:A:373:LYS:HE2	1:B:367:LEU:O	2.21	0.40
1:A:113:LYS:HA	1:A:113:LYS:HD2	1.80	0.40
1:C:306:TYR:O	1:C:328:HIS:HA	2.22	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	374/386 (97%)	361 (96%)	13 (4%)	0	100	100
1	B	374/386 (97%)	364 (97%)	9 (2%)	1 (0%)	41	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	372/386 (96%)	361 (97%)	11 (3%)	0	100 100
1	D	371/386 (96%)	358 (96%)	13 (4%)	0	100 100
All	All	1491/1544 (97%)	1444 (97%)	46 (3%)	1 (0%)	51 42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	199	ALA

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	315/322 (98%)	311 (99%)	4 (1%)	69 64
1	B	315/322 (98%)	308 (98%)	7 (2%)	52 46
1	C	313/322 (97%)	308 (98%)	5 (2%)	62 56
1	D	313/322 (97%)	308 (98%)	5 (2%)	62 56
All	All	1256/1288 (98%)	1235 (98%)	21 (2%)	62 53

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	ASP
1	A	113	LYS
1	A	145	TYR
1	A	285	ARG
1	B	123[A]	ILE
1	B	123[B]	ILE
1	B	126	ASP
1	B	134	ILE
1	B	145	TYR
1	B	369	VAL
1	B	374	LEU

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Mol	Chain	Res	Type
1	C	131	GLU
1	C	145	TYR
1	C	253	THR
1	C	296	ARG
1	C	373	LYS
1	D	27	LYS
1	D	107	GLU
1	D	113	LYS
1	D	145	TYR
1	D	253	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	259	HIS
1	D	259	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)

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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.