wwPDB X-ray Structure Validation Summary Report (i)

Dec 10, 2022 – 04:43 PM EST

PDB ID	:	1QCN
Title	:	CRYSTAL STRUCTURE OF FUMARYLACETOACETATE HYDROLASE
Authors	:	Timm, D.E.; Mueller, H.A.; Bhanumoorthy, P.; Harp, J.M.; Bunick, G.J.
Deposited on	:	1999-05-14
Resolution	:	1.90 Å(reported)

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

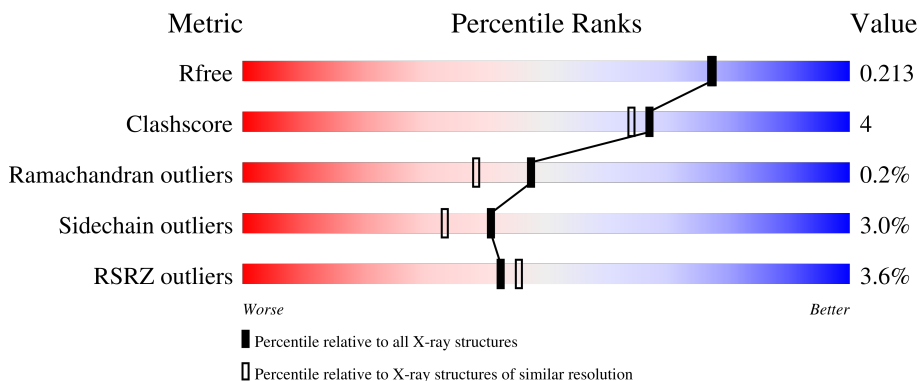|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 1.90 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	Percentile Ranks	Value
Rfree		0.213
Clashscore		4
Ramachandran outliers		0.2%
Sidechain outliers		3.0%
RSRZ outliers		3.6%

Worse — *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 <=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	421	3% / 88% / 10% ··
1	B	421	4% / 91% / 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACT	A	1004	-	-	X	-

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 7086 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 FUMARYLACETOACETATE HYDROLASE.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	417	Total 3222	C 2048	N 563	O 590	S 6	Se 15		0	0	1
1	B	420	Total 3241	C 2058	N 566	O 595	S 6	Se 16		0	0	1

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	cloning artifact	UNP P35505
A	0	SER	-	cloning artifact	UNP P35505
A	1	MSE	MET	modified residue	UNP P35505
A	71	MSE	MET	modified residue	UNP P35505
A	115	MSE	MET	modified residue	UNP P35505
A	140	MSE	MET	modified residue	UNP P35505
A	177	MSE	MET	modified residue	UNP P35505
A	180	MSE	MET	modified residue	UNP P35505
A	198	MSE	MET	modified residue	UNP P35505
A	202	MSE	MET	modified residue	UNP P35505
A	228	MSE	MET	modified residue	UNP P35505
A	231	MSE	MET	modified residue	UNP P35505
A	266	MSE	MET	modified residue	UNP P35505
A	270	MSE	MET	modified residue	UNP P35505
A	308	MSE	MET	modified residue	UNP P35505
A	322	MSE	MET	modified residue	UNP P35505
A	326	MSE	MET	modified residue	UNP P35505
A	362	MSE	MET	modified residue	UNP P35505
B	499	GLY	-	cloning artifact	UNP P35505
B	500	SER	-	cloning artifact	UNP P35505
B	501	MSE	MET	modified residue	UNP P35505
B	571	MSE	MET	modified residue	UNP P35505
B	615	MSE	MET	modified residue	UNP P35505
B	640	MSE	MET	modified residue	UNP P35505
B	677	MSE	MET	modified residue	UNP P35505

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Chain	Residue	Modelled	Actual	Comment	Reference
B	680	MSE	MET	modified residue	UNP P35505
B	698	MSE	MET	modified residue	UNP P35505
B	702	MSE	MET	modified residue	UNP P35505
B	728	MSE	MET	modified residue	UNP P35505
B	731	MSE	MET	modified residue	UNP P35505
B	766	MSE	MET	modified residue	UNP P35505
B	770	MSE	MET	modified residue	UNP P35505
B	808	MSE	MET	modified residue	UNP P35505
B	822	MSE	MET	modified residue	UNP P35505
B	826	MSE	MET	modified residue	UNP P35505
B	862	MSE	MET	modified residue	UNP P35505

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Ca 1	0	0
2	B	1	Total 1	Ca 1	0	0

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).
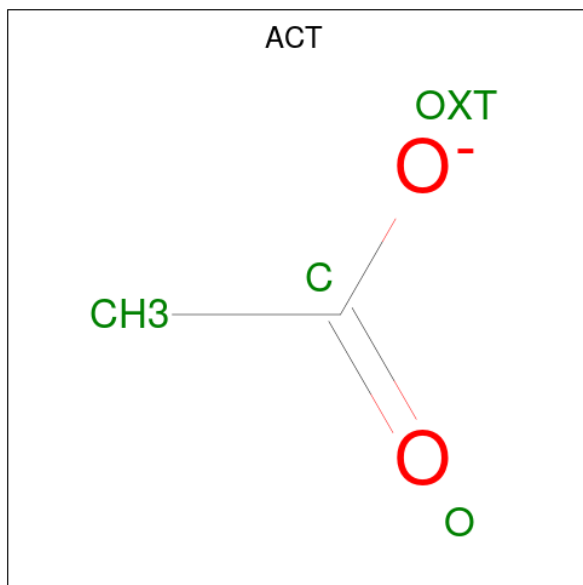
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0

- Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Ni 1	0	0

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	291	Total 291	O 291	0	0
5	B	313	Total 313	O 313	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: FUMARYLACETOACETATE HYDROLASE

Chain A:

- Molecule 1: FUMARYLACETOACETATE HYDROLASE

Chain B:
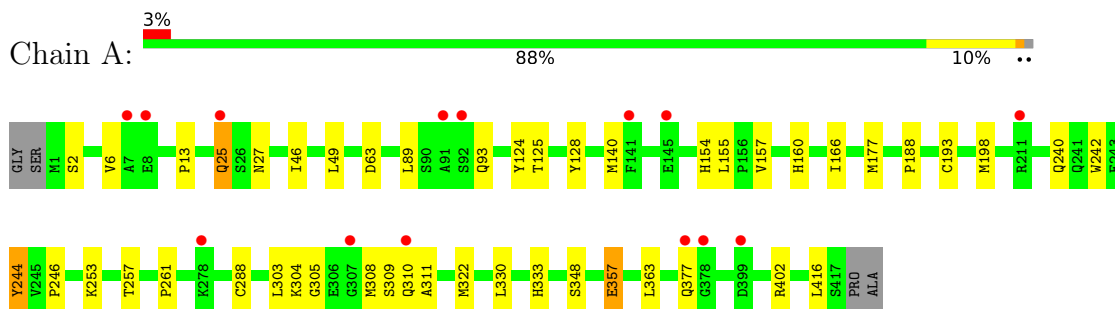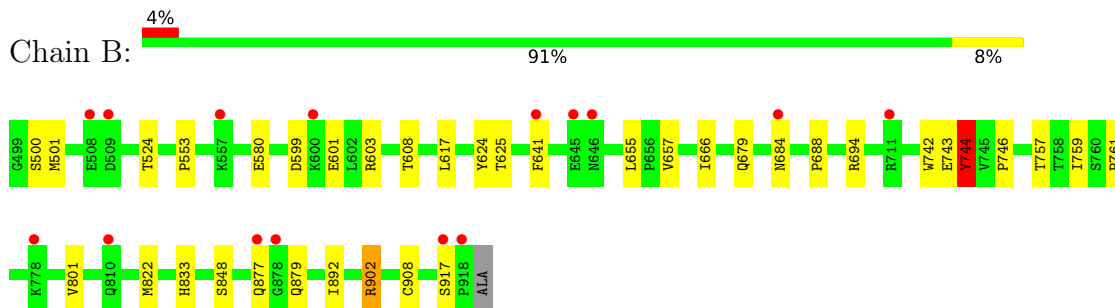
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	64.32Å 110.34Å 67.53Å 90.00° 102.38° 90.00°	Depositor
Resolution (Å)	22.00 – 1.90 22.30 – 1.89	Depositor EDS
% Data completeness (in resolution range)	96.2 (22.00-1.90) 97.9 (22.30-1.89)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.90 (at 1.89Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.191 , 0.220 0.185 , 0.213	Depositor DCC
R_{free} test set	3609 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	11.1	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 46.0	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.021 for l,-k,h	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7086	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, CA, NI

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	0.48	0/3296	0.69	2/4453 (0.0%)
1	B	0.49	0/3314	0.70	2/4474 (0.0%)
All	All	0.49	0/6610	0.70	4/8927 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	694	ARG	NE-CZ-NH1	-6.20	117.20	120.30
1	A	93	GLN	N-CA-C	-5.60	95.88	111.00
1	A	244	TYR	N-CA-C	5.30	125.31	111.00
1	B	744	TYR	N-CA-C	5.30	125.30	111.00

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	3222	0	3160	33	0
1	B	3241	0	3177	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	8	0	6	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	8	0	6	0	0
4	B	1	0	0	0	0
5	A	291	0	0	7	0
5	B	313	0	0	4	0
All	All	7086	0	6349	50	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 4.

The worst 5 of 50 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:A:240:GLN:HE22	3:A:1004:ACT:H3	1.37	0.87
1:A:253:LYS:HZ3	3:A:1004:ACT:H1	1.45	0.81
1:B:822:MSE:HE2	1:B:848:SER:HB2	1.64	0.77
1:B:761:PRO:HD2	5:B:1157:HOH:O	1.83	0.77
1:A:125:THR:OG1	1:A:333:HIS:HE1	1.69	0.76

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	415/421 (99%)	403 (97%)	12 (3%)	0	100	100
1	B	418/421 (99%)	404 (97%)	12 (3%)	2 (0%)	29	18
All	All	833/842 (99%)	807 (97%)	24 (3%)	2 (0%)	47	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	877	GLN
1	B	917	SER

5.3.2　Protein sidechains　ⓘ

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	350/338 (104%)	338 (97%)	12 (3%)	37	28
1	B	353/338 (104%)	344 (98%)	9 (2%)	47	41
All	All	703/676 (104%)	682 (97%)	21 (3%)	41	33

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	601	GLU
1	B	684	ASN
1	B	902	ARG
1	B	744	TYR
1	B	641	PHE

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

Mol	Chain	Res	Type
1	B	539	GLN
1	B	660	HIS
1	B	833	HIS
1	B	740	GLN
1	A	160	HIS

5.3.3　RNA　ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
3	ACT	B	1007	-	3,3,3	1.13	0	3,3,3	0.98	0
3	ACT	B	1006	2	3,3,3	1.27	0	3,3,3	0.93	0
3	ACT	A	1004	2	3,3,3	1.18	0	3,3,3	0.98	0
3	ACT	A	1005	-	3,3,3	1.17	0	3,3,3	0.96	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.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1004	ACT	4	0

5.7 Other polymers ⓘ

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 ⓘ

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	401/421 (95%)	-0.14	14 (3%)	44	47	4, 10, 23, 29	0
1	B	404/421 (95%)	-0.12	15 (3%)	41	44	4, 10, 22, 35	0
All	All	805/842 (95%)	-0.13	29 (3%)	42	45	4, 10, 23, 35	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	918	PRO	9.9
1	B	878	GLY	7.6
1	B	917	SER	5.2
1	B	646	ASN	4.6
1	B	877	GLN	4.5

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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, 95th 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	B-factors($Å^2$)	Q<0.9
3	ACT	B	1007	4/4	0.86	0.16	23,23,23,23	0
3	ACT	A	1004	4/4	0.87	0.15	11,12,12,13	0
3	ACT	B	1006	4/4	0.95	0.10	9,9,10,10	0
3	ACT	A	1005	4/4	0.96	0.07	12,13,13,13	0
4	NI	B	1003	1/1	0.98	0.05	13,13,13,13	0
2	CA	B	1002	1/1	0.99	0.05	8,8,8,8	0
2	CA	A	1001	1/1	0.99	0.05	6,6,6,6	0

6.5   Other polymers ⓘ

There are no such residues in this entry.