Full wwPDB X-ray Structure Validation Report (i)

Oct 23, 2021 – 10:31 AM EDT

PDB ID	:	1YFM
Title	:	RECOMBINANT YEAST FUMARASE
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Deposited on	:	1998-01-07
Resolution	:	2.60 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

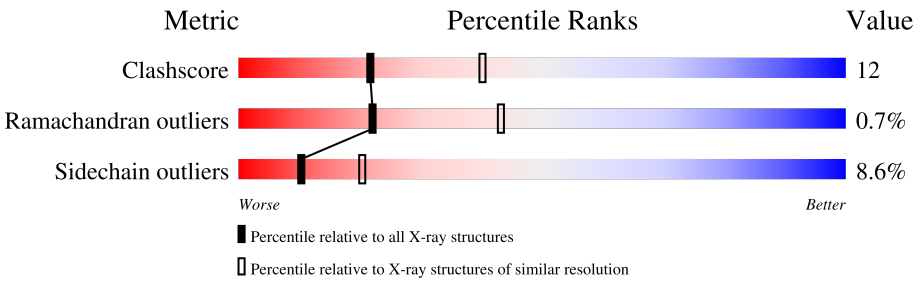
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.60 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))
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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	488	64% 24% • 8%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 3439 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 FUMARASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	450	3439	2166	602	656	15	0	0	0

There is a discrepancy between the modelled and reference sequences:

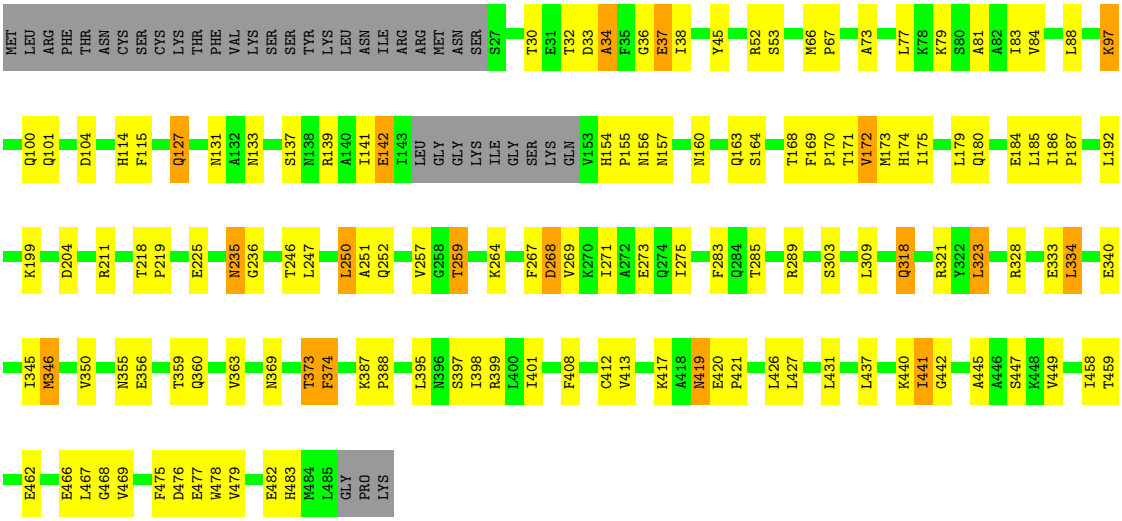
Chain	Residue	Modelled	Actual	Comment	Reference
A	289	ARG	LYS	engineered mutation	UNP P08417

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: FUMARASE

Chain A: 64% 24% • 8%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α, β, γ	95.19Å 95.19Å 100.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 47.59 – 2.60	Depositor EDS
% Data completeness (in resolution range)	60.0 (30.00-2.60) 88.6 (47.59-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.15	Depositor
$< I/\sigma(I) >$ [1]	0.95 (at 2.61Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.196 , 0.315 0.307 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	28.9	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 32.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.82	EDS
Total number of atoms	3439	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% 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 (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	0.44	3/3502 (0.1%)	0.68	3/4741 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	285	THR	C-N	-6.01	1.20	1.34
1	A	468	GLY	C-N	5.81	1.47	1.34
1	A	426	LEU	C-N	5.06	1.45	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	426	LEU	O-C-N	-6.12	112.90	122.70
1	A	427	LEU	C-N-CA	-5.66	107.55	121.70
1	A	427	LEU	O-C-N	5.11	130.88	122.70

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	3439	0	3441	82	0
All	All	3439	0	3441	82	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 12.

All (82) 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:77:LEU:HD21	1:A:168:THR:HG23	1.39	1.05
1:A:345:ILE:HG23	1:A:346:MET:HG2	1.60	0.83
1:A:139:ARG:NH1	1:A:142:GLU:HG2	2.00	0.77
1:A:139:ARG:HH11	1:A:142:GLU:HG2	1.52	0.74
1:A:33:ASP:HB3	1:A:52:ARG:HH22	1.54	0.72
1:A:38:ILE:HD12	1:A:52:ARG:HG2	1.75	0.69
1:A:133:ASN:ND2	1:A:160:ASN:HB2	2.08	0.69
1:A:269:VAL:O	1:A:273:GLU:HB2	1.97	0.65
1:A:387:LYS:HB2	1:A:388:PRO:HD3	1.76	0.65
1:A:84:VAL:HG21	1:A:271:ILE:HA	1.77	0.65
1:A:37:GLU:H	1:A:37:GLU:CD	2.01	0.64
1:A:73:ALA:HB3	1:A:172:VAL:HG22	1.81	0.62
1:A:137:SER:O	1:A:141:ILE:HG12	2.00	0.61
1:A:257:VAL:HG23	1:A:259:THR:HB	1.82	0.61
1:A:479:VAL:HG13	1:A:479:VAL:O	2.00	0.60
1:A:115:PHE:HA	1:A:131:ASN:HD21	1.66	0.60
1:A:356:GLU:O	1:A:360:GLN:HG3	2.02	0.60
1:A:397:SER:O	1:A:401:ILE:HG13	2.03	0.58
1:A:440:LYS:HD3	1:A:478:TRP:CE2	2.38	0.58
1:A:180:GLN:O	1:A:184:GLU:HB2	2.03	0.58
1:A:458:ILE:HG13	1:A:462:GLU:OE1	2.04	0.57
1:A:53:SER:HB2	1:A:127:GLN:NE2	2.20	0.57
1:A:267:PHE:O	1:A:271:ILE:HG22	2.05	0.56
1:A:374:PHE:CD1	1:A:374:PHE:N	2.75	0.54
1:A:466:GLU:HG3	1:A:467:LEU:HD13	1.89	0.54
1:A:437:LEU:O	1:A:441:ILE:HG22	2.08	0.53
1:A:169:PHE:O	1:A:172:VAL:HG12	2.09	0.53
1:A:441:ILE:HD11	1:A:469:VAL:CG1	2.39	0.53
1:A:225:GLU:OE1	1:A:323:LEU:HD21	2.09	0.52
1:A:369:ASN:O	1:A:373:THR:HG23	2.09	0.52
1:A:475:PHE:O	1:A:479:VAL:HG12	2.10	0.52
1:A:445:ALA:O	1:A:449:VAL:HG23	2.09	0.51
1:A:88:LEU:HD13	1:A:264:LYS:HB2	1.93	0.51
1:A:81:ALA:HB1	1:A:163:GLN:HE22	1.75	0.51
1:A:66:MET:SD	1:A:67:PRO:HD2	2.51	0.51
1:A:32:THR:HG22	1:A:33:ASP:N	2.26	0.51
1:A:133:ASN:HD21	1:A:160:ASN:HB2	1.75	0.51
1:A:97:LYS:NZ	1:A:101:GLN:HE21	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:ASN:O	1:A:163:GLN:HG2	2.12	0.50
1:A:355:ASN:HD22	1:A:355:ASN:N	2.09	0.50
1:A:271:ILE:O	1:A:275:ILE:HG13	2.12	0.50
1:A:303:SER:OG	1:A:369:ASN:ND2	2.45	0.50
1:A:83:ILE:HG12	1:A:100:GLN:NE2	2.28	0.49
1:A:441:ILE:HD11	1:A:469:VAL:HG13	1.94	0.49
1:A:441:ILE:HG23	1:A:442:GLY:N	2.28	0.49
1:A:419:ASN:HD22	1:A:421:PRO:HD2	1.78	0.48
1:A:458:ILE:HG23	1:A:462:GLU:HB2	1.94	0.48
1:A:97:LYS:HZ2	1:A:101:GLN:HE21	1.62	0.48
1:A:175:ILE:O	1:A:179:LEU:HG	2.14	0.48
1:A:268:ASP:OD1	1:A:269:VAL:HG23	2.14	0.47
1:A:318:GLN:NE2	1:A:321:ARG:HH21	2.14	0.46
1:A:170:PRO:HA	1:A:173:MET:SD	2.56	0.46
1:A:186:ILE:HB	1:A:187:PRO:HD3	1.97	0.46
1:A:475:PHE:CE2	1:A:479:VAL:HG11	2.49	0.46
1:A:180:GLN:HB3	1:A:398:ILE:HG21	1.98	0.45
1:A:482:GLU:H	1:A:482:GLU:CD	2.21	0.45
1:A:236:GLY:HA3	1:A:309:LEU:HD13	1.98	0.44
1:A:359:THR:O	1:A:363:VAL:HG23	2.18	0.44
1:A:355:ASN:N	1:A:355:ASN:ND2	2.65	0.44
1:A:441:ILE:CG2	1:A:442:GLY:N	2.80	0.44
1:A:250:LEU:HD22	1:A:283:PHE:HB3	1.99	0.43
1:A:420:GLU:HB2	1:A:421:PRO:HD3	2.00	0.43
1:A:211:ARG:HH22	1:A:333:GLU:CD	2.21	0.43
1:A:154:HIS:HA	1:A:155:PRO:HD3	1.88	0.43
1:A:417:LYS:HE2	1:A:417:LYS:HB3	1.79	0.43
1:A:437:LEU:HB3	1:A:441:ILE:HG21	2.00	0.43
1:A:154:HIS:HD2	1:A:157:ASN:CG	2.21	0.43
1:A:408:PHE:O	1:A:412:CYS:HB3	2.18	0.43
1:A:154:HIS:CD2	1:A:157:ASN:H	2.37	0.42
1:A:164:SER:O	1:A:168:THR:HB	2.20	0.42
1:A:199:LYS:HE3	1:A:413:VAL:O	2.18	0.42
1:A:45:TYR:H	1:A:114:HIS:CD2	2.38	0.42
1:A:171:THR:O	1:A:175:ILE:HG13	2.19	0.42
1:A:235:ASN:HD22	1:A:235:ASN:N	2.17	0.42
1:A:459:THR:HG23	1:A:462:GLU:H	1.85	0.42
1:A:77:LEU:CD2	1:A:168:THR:HG23	2.28	0.41
1:A:174:HIS:ND1	1:A:247:LEU:HA	2.35	0.41
1:A:79:LYS:HD2	1:A:104:ASP:HB2	2.02	0.41
1:A:323:LEU:HB3	1:A:334:LEU:HD22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:ALA:C	1:A:36:GLY:H	2.25	0.40
1:A:218:THR:HB	1:A:219:PRO:HD2	2.03	0.40
1:A:251:ALA:O	1:A:252:GLN:C	2.59	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	446/488 (91%)	402 (90%)	41 (9%)	3 (1%)	22 43

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	441	ILE
1	A	34	ALA
1	A	185	LEU

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	373/407 (92%)	341 (91%)	32 (9%)	10 20

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	THR
1	A	37	GLU
1	A	97	LYS
1	A	127	GLN
1	A	142	GLU
1	A	156	ASN
1	A	172	VAL
1	A	192	LEU
1	A	204	ASP
1	A	235	ASN
1	A	246	THR
1	A	250	LEU
1	A	259	THR
1	A	268	ASP
1	A	289	ARG
1	A	318	GLN
1	A	323	LEU
1	A	328	ARG
1	A	334	LEU
1	A	340	GLU
1	A	346	MET
1	A	350	VAL
1	A	373	THR
1	A	374	PHE
1	A	395	LEU
1	A	399	ARG
1	A	419	ASN
1	A	431	LEU
1	A	447	SER
1	A	476	ASP
1	A	477	GLU
1	A	483	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	ASN
1	A	85	ASN
1	A	101	GLN
1	A	114	HIS
1	A	127	GLN
1	A	131	ASN
1	A	138	ASN

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Mol	Chain	Res	Type
1	A	154	HIS
1	A	183	ASN
1	A	191	ASN
1	A	235	ASN
1	A	262	ASN
1	A	318	GLN
1	A	351	ASN
1	A	354	GLN
1	A	355	ASN
1	A	369	ASN
1	A	393	ASN
1	A	419	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 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	285:THR	C	286:ALA	N	1.20

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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

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

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

6.3 Carbohydrates (i)

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

6.4 Ligands (i)

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

6.5 Other polymers (i)

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