



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:37 PM GMT

PDB ID : 4FMO
Title : Structure of the C-terminal domain of the *Saccharomyces cerevisiae* MUTL
alpha (MLH1/PMS1) heterodimer bound to a fragment of exo1
Authors : Gueneau, E.; Legrand, P.; Charbonnier, J.B.
Deposited on : 2012-06-18
Resolution : 3.04 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

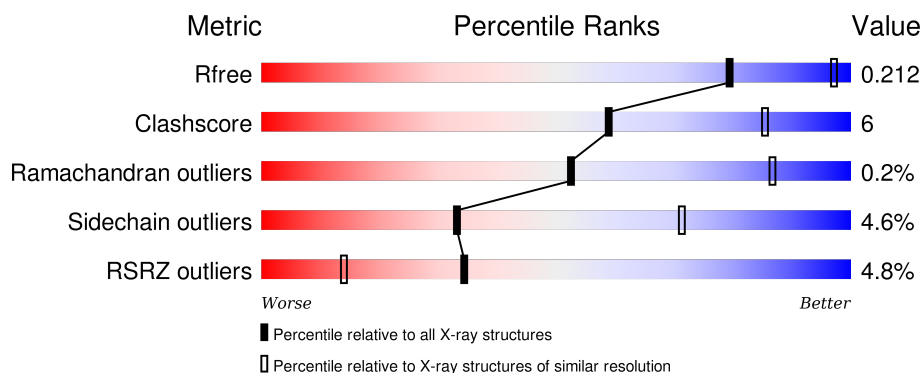
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.04 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}	91344	1995 (3.08-3.00)
Clashscore	102246	2351 (3.08-3.00)
Ramachandran outliers	100387	2272 (3.08-3.00)
Sidechain outliers	100360	2275 (3.08-3.00)
RSRZ outliers	91569	2013 (3.08-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	288	<div> <div>10%</div> <div>76% 14% • 8%</div> </div>
2	B	240	<div> <div>10%</div> <div>77% 9% • 13%</div> </div>
3	C	8	<div> <div>50% 38% 13%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3936 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 DNA mismatch repair protein MLH1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	0	0
			2156	1388	351	410	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	482	GLY	-	EXPRESSION TAG	UNP P38920
A	483	ALA	-	EXPRESSION TAG	UNP P38920
A	484	MET	-	EXPRESSION TAG	UNP P38920

- Molecule 2 is a protein called DNA mismatch repair protein PMS1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	208	Total	C	N	O	S	0	0	0
			1658	1062	284	302	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	634	GLY	-	EXPRESSION TAG	UNP P14242

- Molecule 3 is a protein called DNA repair peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	7	Total	C	N	O	0	0	0
			63	41	12	10			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total 2	Zn 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	39	Total 39	O 39	0	0
6	B	11	Total 11	O 11	0	0
6	C	6	Total 6	O 6	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	193.70Å 66.14Å 74.47Å 90.00° 91.28° 90.00°	Depositor
Resolution (Å)	48.41 – 3.04 48.08 – 3.04	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.41-3.04) 99.6 (48.08-3.04)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 3.07Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.180 , 0.196 0.199 , 0.212	Depositor DCC
R_{free} test set	1021 reflections (5.94%)	DCC
Wilson B-factor (Å ²)	62.0	Xtriage
Anisotropy	1.026	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 67.3	EDS
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 18219 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3936	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, MG

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	0.51	0/2195	0.75	0/2966
2	B	0.49	0/1687	0.68	0/2267
3	C	0.57	0/64	0.73	0/83
All	All	0.50	0/3946	0.72	0/5316

There are no bond length outliers.

There are no bond angle outliers.

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	2156	0	2175	30	0
2	B	1658	0	1641	17	0
3	C	63	0	61	4	0
4	A	1	0	0	0	0
5	B	2	0	0	0	0
6	A	39	0	0	1	0
6	B	11	0	0	0	0
6	C	6	0	0	0	0
All	All	3936	0	3877	45	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 6.

All (45) 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)
2:B:734:SER:HG	2:B:738:GLU:N	1.74	0.85
1:A:616:ILE:HG23	1:A:674:GLY:HA3	1.62	0.82
2:B:742:LEU:HD21	2:B:785:PHE:CZ	2.26	0.70
1:A:522:ASP:HA	1:A:525:ILE:HD12	1.73	0.69
2:B:785:PHE:CE2	2:B:789:ILE:HD11	2.31	0.66
1:A:748:HIS:CD2	1:A:749:ILE:HD13	2.31	0.65
1:A:555:LEU:HD22	1:A:760:PRO:HD3	1.79	0.63
1:A:512:THR:HG1	3:C:443:THR:N	1.98	0.60
1:A:526:HIS:HD2	1:A:747:ARG:HG2	1.66	0.60
1:A:629:GLU:OE1	3:C:447:PHE:HZ	1.86	0.58
1:A:691:ARG:NH2	6:A:905:HOH:O	2.05	0.56
2:B:742:LEU:HD21	2:B:785:PHE:HZ	1.67	0.56
2:B:754:LYS:HB2	2:B:771:SER:HB2	1.88	0.56
2:B:665:THR:HG23	2:B:666:VAL:HG23	1.86	0.55
2:B:742:LEU:HD11	2:B:789:ILE:HG12	1.89	0.55
1:A:626:MET:HB2	3:C:447:PHE:CG	2.43	0.54
2:B:785:PHE:O	2:B:789:ILE:HG13	2.08	0.54
1:A:748:HIS:HD2	1:A:749:ILE:HD13	1.73	0.52
1:A:547:ARG:NH2	2:B:870:ASP:OD2	2.35	0.51
1:A:640:LEU:HD23	1:A:642:ASN:H	1.76	0.51
1:A:526:HIS:CD2	1:A:747:ARG:HG2	2.45	0.50
1:A:663:LEU:HB3	1:A:666:LEU:HD22	1.92	0.50
1:A:511:LEU:HD13	1:A:513:SER:HB2	1.93	0.50
2:B:733:LEU:HD21	2:B:789:ILE:HD13	1.94	0.49
1:A:626:MET:HB2	3:C:447:PHE:CD2	2.49	0.47
1:A:600:LEU:HD13	1:A:670:ILE:HD13	1.97	0.47
1:A:669:PHE:O	1:A:673:LEU:HB2	2.14	0.47
1:A:600:LEU:CD1	1:A:670:ILE:HD13	2.45	0.46
2:B:669:ASN:HA	2:B:672:LYS:HE3	1.96	0.46
1:A:555:LEU:CD2	1:A:759:LEU:HB2	2.45	0.46
2:B:734:SER:OG	2:B:738:GLU:N	2.44	0.46
2:B:742:LEU:CD2	2:B:785:PHE:HZ	2.29	0.45
1:A:536:LEU:HG	1:A:740:LYS:HG3	1.98	0.45
1:A:555:LEU:HD23	1:A:759:LEU:HB2	1.99	0.45
1:A:552:GLN:HG3	2:B:680:PHE:HE2	1.82	0.44
1:A:511:LEU:HA	1:A:511:LEU:HD23	1.86	0.43
2:B:723:GLN:HB2	2:B:774:THR:HG21	2.01	0.42
2:B:723:GLN:HB2	2:B:774:THR:CG2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:786:ASN:HA	2:B:789:ILE:HD12	2.01	0.42
1:A:555:LEU:HD23	1:A:759:LEU:HD12	2.02	0.42
1:A:601:LEU:HD21	1:A:670:ILE:HG22	2.01	0.41
1:A:514:ILE:HG13	1:A:578:PHE:CD2	2.55	0.41
1:A:709:ASP:HB3	1:A:712:LEU:HD13	2.02	0.41
1:A:607:LEU:O	1:A:613:LYS:HE3	2.21	0.41
1:A:559:LEU:HD13	1:A:756:ILE:HD13	2.02	0.41

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	262/288 (91%)	252 (96%)	10 (4%)	0	100	100
2	B	198/240 (82%)	190 (96%)	7 (4%)	1 (0%)	34	74
3	C	5/8 (62%)	5 (100%)	0	0	100	100
All	All	465/536 (87%)	447 (96%)	17 (4%)	1 (0%)	52	87

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	692	ASP

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	246/265 (93%)	235 (96%)	11 (4%)	34	72
2	B	183/224 (82%)	175 (96%)	8 (4%)	35	73
3	C	7/8 (88%)	6 (86%)	1 (14%)	4	18
All	All	436/497 (88%)	416 (95%)	20 (5%)	33	71

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	510	ASN
1	A	511	LEU
1	A	592	SER
1	A	610	ASP
1	A	625	SER
1	A	666	LEU
1	A	709	ASP
1	A	714	GLU
1	A	715	ASP
1	A	727	ILE
1	A	749	ILE
2	B	691	VAL
2	B	731	VAL
2	B	734	SER
2	B	767	VAL
2	B	771	SER
2	B	782	LEU
2	B	809	ARG
2	B	864	TRP
3	C	444	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	642	ASN
1	A	683	GLN
1	A	748	HIS

5.3.3 RNA ⓘ

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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 ⓘ

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	264/288 (91%)	-0.26	0 100 100	55, 78, 132, 183	0
2	B	208/240 (86%)	0.67	23 (11%) 7 2	53, 112, 196, 214	0
3	C	7/8 (87%)	0.09	0 100 100	78, 82, 108, 114	0
All	All	479/536 (89%)	0.15	23 (4%) 34 14	53, 86, 181, 214	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	742	LEU	5.8
2	B	725	LEU	5.6
2	B	755	LEU	5.1
2	B	757	ILE	4.2
2	B	740	VAL	4.1
2	B	769	LEU	4.0
2	B	726	ILE	3.8
2	B	739	LEU	3.5
2	B	731	VAL	3.5
2	B	756	LYS	3.2
2	B	751	ASN	3.1
2	B	665	THR	3.0
2	B	753	PHE	2.9
2	B	785	PHE	2.9
2	B	788	LEU	2.8
2	B	654	ASP	2.7
2	B	724	LYS	2.6
2	B	792	ILE	2.4
2	B	765	SER	2.3
2	B	661	TYR	2.2
2	B	732	GLU	2.2
2	B	771	SER	2.1
2	B	723	GLN	2.0

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 carbohydrates in this entry.

6.4 Ligands [i](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
5	ZN	B	902	1/1	0.99	0.17	-1.02	75,75,75,75	0
4	MG	A	801	1/1	0.99	0.10	-2.87	46,46,46,46	0
5	ZN	B	901	1/1	0.99	0.18	-	74,74,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.