



wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 08:17 AM GMT

PDB ID : 1XPQ
Title : Crystal structure of fms1, a polyamine oxidase from yeast
Authors : Huang, Q.; Liu, Q.; Hao, Q.
Deposited on : 2004-10-09
Resolution : 2.60 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

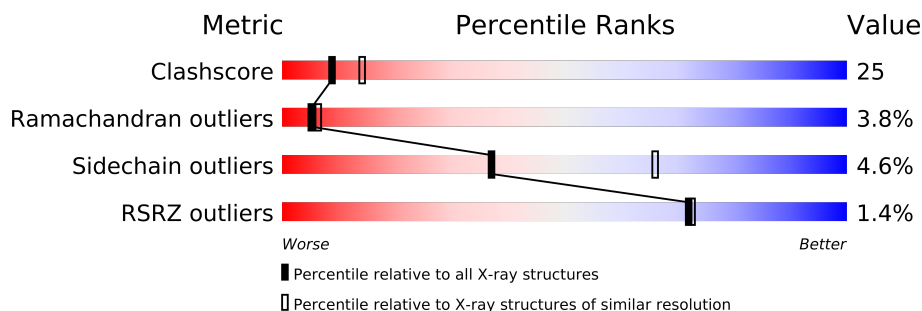
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

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	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	513	
1	B	513	
1	C	513	
1	D	513	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16332 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

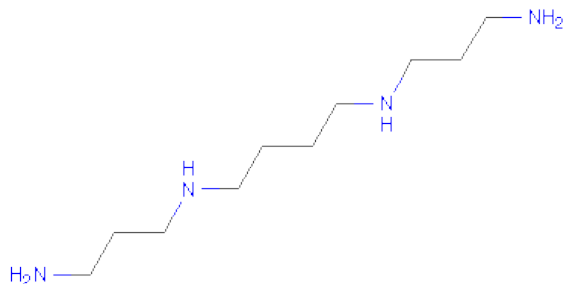
- Molecule 1 is a protein called FMS1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	498	Total	C	N	O	S	86	0	0
			3997	2526	699	750	22			
1	B	492	Total	C	N	O	S	144	0	0
			3946	2496	687	741	22			
1	C	495	Total	C	N	O	S	118	0	0
			3967	2509	690	746	22			
1	D	490	Total	C	N	O	S	144	0	0
			3929	2484	684	739	22			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	509	LEU	-	CLONING ARTIFACT	UNP P50264
A	510	GLU	-	CLONING ARTIFACT	UNP P50264
A	511	HIS	-	CLONING ARTIFACT	UNP P50264
A	512	HIS	-	CLONING ARTIFACT	UNP P50264
A	513	HIS	-	CLONING ARTIFACT	UNP P50264
B	509	LEU	-	CLONING ARTIFACT	UNP P50264
B	510	GLU	-	CLONING ARTIFACT	UNP P50264
B	511	HIS	-	CLONING ARTIFACT	UNP P50264
B	512	HIS	-	CLONING ARTIFACT	UNP P50264
B	513	HIS	-	CLONING ARTIFACT	UNP P50264
C	509	LEU	-	CLONING ARTIFACT	UNP P50264
C	510	GLU	-	CLONING ARTIFACT	UNP P50264
C	511	HIS	-	CLONING ARTIFACT	UNP P50264
C	512	HIS	-	CLONING ARTIFACT	UNP P50264
C	513	HIS	-	CLONING ARTIFACT	UNP P50264
D	509	LEU	-	CLONING ARTIFACT	UNP P50264
D	510	GLU	-	CLONING ARTIFACT	UNP P50264
D	511	HIS	-	CLONING ARTIFACT	UNP P50264
D	512	HIS	-	CLONING ARTIFACT	UNP P50264
D	513	HIS	-	CLONING ARTIFACT	UNP P50264

- Molecule 2 is SPERMINE (three-letter code: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	N	14	0
			14	10	4		
2	D	1	Total	C	N	14	0
			14	10	4		
2	B	1	Total	C	N	14	0
			14	10	4		
2	A	1	Total	C	N	14	0
			14	10	4		

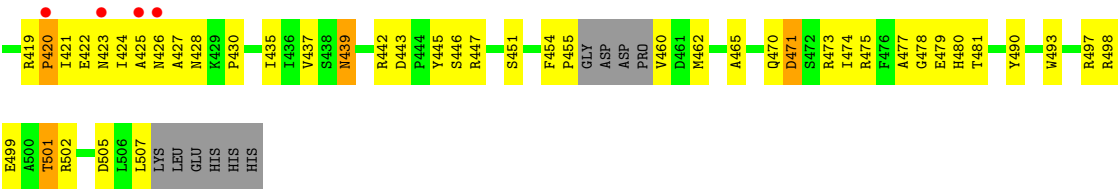
- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	55	Total	O	0	0
			55	55		
4	B	54	Total	O	0	0
			54	54		
4	C	66	Total	O	0	0
			66	66		
4	D	50	Total	O	0	0
			50	50		



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	103.05Å 98.13Å 123.83Å 90.00° 103.28° 90.00°	Depositor
Resolution (Å)	35.23 – 2.60 49.84 – 2.51	Depositor EDS
% Data completeness (in resolution range)	(Not available) (35.23-2.60) 73.5 (49.84-2.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.88 (at 2.51Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.232 , 0.309 0.252 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	43.7	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 26.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 66311 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16332	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SPM, FAD

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	0.39	0/4080	0.64	0/5515
1	B	0.39	0/4025	0.65	0/5441
1	C	0.40	0/4047	0.64	0/5471
1	D	0.38	0/4008	0.63	1/5419 (0.0%)
All	All	0.39	0/16160	0.64	1/21846 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	380	LEU	CA-CB-CG	5.92	128.90	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3997	0	3916	202	0
1	B	3946	0	3881	217	0
1	C	3967	0	3900	159	0
1	D	3929	0	3857	207	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	14	0	26	0	0
2	B	14	0	26	0	0
2	C	14	0	26	0	0
2	D	14	0	26	0	0
3	A	53	0	31	3	0
3	B	53	0	31	8	0
3	C	53	0	31	1	0
3	D	53	0	31	3	0
4	A	55	0	0	1	0
4	B	54	0	0	8	0
4	C	66	0	0	2	0
4	D	50	0	0	1	0
All	All	16332	0	15782	778	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 25.

The worst 5 of 778 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:292:GLY:H	1:A:451:SER:HA	1.00	1.07
1:A:289:ILE:HD11	1:A:462:MET:HG3	1.35	1.05
1:A:122:MET:HE1	1:A:145:VAL:HG22	1.39	1.05
1:D:32:ILE:HD12	1:D:507:LEU:HD12	1.40	1.02
1:D:278:LEU:HA	1:D:470:GLN:HE22	1.25	0.99

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	492/513 (96%)	418 (85%)	53 (11%)	21 (4%)	4 5
1	B	486/513 (95%)	420 (86%)	45 (9%)	21 (4%)	4 5
1	C	489/513 (95%)	426 (87%)	49 (10%)	14 (3%)	7 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	484/513 (94%)	404 (84%)	61 (13%)	19 (4%)	5	6
All	All	1951/2052 (95%)	1668 (86%)	208 (11%)	75 (4%)	5	6

5 of 75 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	289	ILE
1	A	290	HIS
1	A	291	PHE
1	A	420	PRO
1	B	133	HIS

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	439/454 (97%)	417 (95%)	22 (5%)	34	61
1	B	435/454 (96%)	415 (95%)	20 (5%)	37	66
1	C	437/454 (96%)	420 (96%)	17 (4%)	43	74
1	D	433/454 (95%)	412 (95%)	21 (5%)	35	64
All	All	1744/1816 (96%)	1664 (95%)	80 (5%)	37	66

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	377	GLN
1	C	124	LYS
1	D	291	PHE
1	B	382	ASN
1	B	471	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	255	GLN
1	B	439	ASN
1	D	329	ASN
1	B	259	ASN
1	B	362	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 ligands are modelled in this entry.

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	FAD	A	803	-	58,58,58	1.16	5 (8%)	85,89,89	1.34	8 (9%)
2	SPM	A	924	-	13,13,13	0.92	1 (7%)	12,12,12	0.56	0
3	FAD	B	804	-	58,58,58	1.27	6 (10%)	85,89,89	1.77	17 (20%)
2	SPM	B	923	-	13,13,13	0.95	1 (7%)	12,12,12	0.58	0
3	FAD	C	801	-	58,58,58	1.25	7 (12%)	85,89,89	1.95	14 (16%)
2	SPM	C	921	-	13,13,13	0.96	1 (7%)	12,12,12	0.59	0
3	FAD	D	802	-	58,58,58	1.15	6 (10%)	85,89,89	1.39	11 (12%)
2	SPM	D	922	-	13,13,13	0.96	1 (7%)	12,12,12	0.60	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FAD	A	803	-	-	0/34/50/50	0/1/6/6
2	SPM	A	924	-	-	0/11/11/11	0/0/0/0
3	FAD	B	804	-	-	0/34/50/50	0/1/6/6
2	SPM	B	923	-	-	0/11/11/11	0/0/0/0
3	FAD	C	801	-	-	0/34/50/50	0/1/6/6
2	SPM	C	921	-	-	0/11/11/11	0/0/0/0
3	FAD	D	802	-	-	0/34/50/50	0/1/6/6
2	SPM	D	922	-	-	0/11/11/11	0/0/0/0

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	802	FAD	C9A-N10	3.44	1.43	1.38
3	B	804	FAD	PA-O3P	3.36	1.66	1.59
3	B	804	FAD	C9A-N10	2.97	1.43	1.38
3	C	801	FAD	C9A-N10	2.78	1.43	1.38
3	C	801	FAD	C5X-N5	2.65	1.39	1.35

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	801	FAD	O2A-PA-O5B	-6.40	76.25	108.51
3	C	801	FAD	O5B-PA-O1A	6.20	133.67	109.37
3	C	801	FAD	O3P-PA-O1A	-5.30	73.27	111.28
3	C	801	FAD	O2A-PA-O1A	-5.09	83.80	112.21
3	B	804	FAD	C4B-O4B-C1B	-5.06	104.25	109.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	498/513 (97%)	-0.48	7 (1%) 72 72	20, 38, 63, 93	22 (4%)
1	B	492/513 (95%)	-0.45	4 (0%) 83 85	18, 37, 61, 79	37 (7%)
1	C	495/513 (96%)	-0.47	4 (0%) 83 85	19, 36, 63, 87	33 (6%)
1	D	490/513 (95%)	-0.39	13 (2%) 52 49	18, 40, 68, 92	34 (6%)
All	All	1975/2052 (96%)	-0.45	28 (1%) 72 72	18, 38, 65, 93	126 (6%)

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	423	ASN	5.2
1	D	134	LEU	3.9
1	B	135	GLY	3.7
1	A	424	ILE	3.5
1	B	425	ALA	3.3

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 carbohydrates 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. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	FAD	C	801	53/53	0.16	0.88	20,28,40,44	0
3	FAD	A	803	53/53	0.14	0.10	27,32,36,37	0
3	FAD	B	804	53/53	0.13	-0.11	23,32,40,41	0
3	FAD	D	802	53/53	0.12	-0.23	28,34,39,39	0
2	SPM	C	921	14/14	-	-	175,178,181,181	14
2	SPM	D	922	14/14	-	-	161,165,169,169	14
2	SPM	B	923	14/14	-	-	134,138,142,142	14
2	SPM	A	924	14/14	-	-	142,144,145,145	14

6.5 Other polymers ⓘ

There are no such residues in this entry.