



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:52 PM GMT

PDB ID : 1D06
Title : STRUCTURAL BASIS OF DIMERIZATION AND SENSORY MECHANISMS OF OXYGEN-SENSING DOMAIN OF RHIZOBIUM MELILOTI FIXL DETERMINED AT 1.4Å RESOLUTION
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Deposited on : 1999-09-09
Resolution : 1.40 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

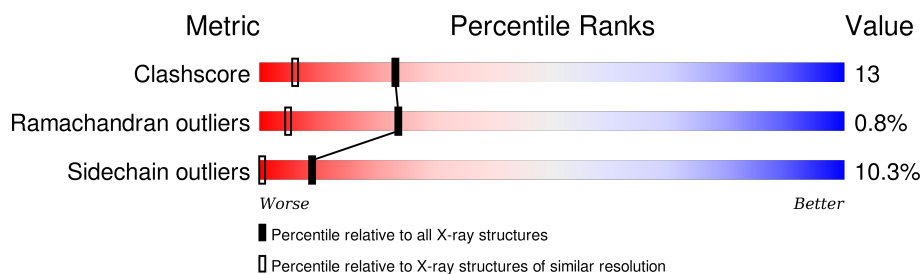
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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	102246	1295 (1.40-1.40)
Ramachandran outliers	100387	1259 (1.40-1.40)
Sidechain outliers	100360	1258 (1.40-1.40)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	130	 75% 22% •

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1135 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 nitrogen fixation regulatory protein fixL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	130	1019	633	186	195	5	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	122	GLY	ARG	ENGINEERED	UNP P10955
A	123	SER	ARG	ENGINEERED	UNP P10955
A	124	HIS	ALA	ENGINEERED	UNP P10955
A	125	MET	ILE	ENGINEERED	UNP P10955
A	126	LEU	ASP	ENGINEERED	UNP P10955
A	127	GLU	ARG	ENGINEERED	UNP P10955

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is water.

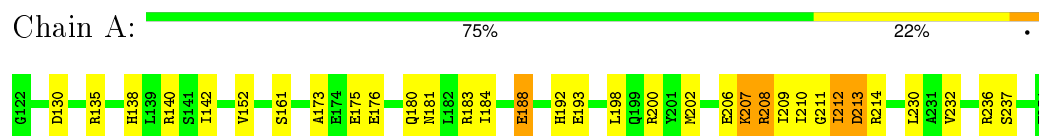
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	73	Total	O	0	0
			73	73		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

Note EDS was not executed.

- Molecule 1: nitrogen fixation regulatory protein fixL



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	60.60 Å 37.15 Å 53.99 Å 90.00° 115.43° 90.00°	Depositor
Resolution (Å)	20.00 – 1.40	Depositor
% Data completeness (in resolution range)	98.9 (20.00-1.40)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.224 , 0.275	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1135	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.42	0/1036	0.64	0/1394

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	1019	0	1000	28	0
2	A	43	0	30	2	0
3	A	73	0	0	3	0
All	All	1135	0	1030	28	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 13.

All (28) 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:210:ILE:HG12	1:A:232:VAL:HG23	1.35	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:GLU:HG3	3:A:65:HOH:O	1.68	0.93
1:A:210:ILE:HG12	1:A:232:VAL:CG2	2.08	0.82
1:A:181:ASN:HD22	1:A:183:ARG:H	1.32	0.78
1:A:175:GLU:H	1:A:175:GLU:CD	1.93	0.71
1:A:209:ILE:HG23	1:A:232:VAL:HG21	1.76	0.68
1:A:181:ASN:ND2	1:A:183:ARG:H	1.96	0.64
1:A:207:LYS:CG	1:A:210:ILE:HB	2.31	0.61
1:A:209:ILE:HG23	1:A:232:VAL:CG2	2.31	0.61
1:A:173:ALA:O	1:A:176:GLU:HB2	2.03	0.59
1:A:211:GLY:C	1:A:212:ILE:HG13	2.24	0.56
1:A:209:ILE:HG22	2:A:501:HEM:CGD	2.37	0.55
1:A:188:GLU:HB2	3:A:67:HOH:O	2.06	0.55
1:A:152:VAL:HB	1:A:161:SER:HB3	1.90	0.54
1:A:209:ILE:CD1	1:A:230:LEU:HD23	2.39	0.52
1:A:213:ASP:OD1	1:A:213:ASP:N	2.44	0.50
1:A:207:LYS:HG3	1:A:210:ILE:HB	1.94	0.49
1:A:209:ILE:HD13	1:A:230:LEU:HD23	1.96	0.47
1:A:207:LYS:HG2	1:A:210:ILE:HB	1.97	0.47
1:A:210:ILE:HG23	1:A:232:VAL:O	2.16	0.46
1:A:138:HIS:O	1:A:142:ILE:HG13	2.16	0.45
1:A:200:ARG:HH22	1:A:206:GLU:CD	2.20	0.45
1:A:208:ARG:NH1	3:A:56:HOH:O	2.50	0.43
1:A:192:HIS:CE1	1:A:193:GLU:HG3	2.54	0.42
1:A:198:LEU:O	1:A:202:MET:HG2	2.19	0.42
1:A:181:ASN:O	1:A:184:ILE:HG12	2.19	0.42
1:A:208:ARG:HD3	2:A:501:HEM:O1A	2.21	0.41
1:A:209:ILE:HD11	1:A:230:LEU:HD23	2.04	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	128/130 (98%)	124 (97%)	3 (2%)	1 (1%)	24 5

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	ILE

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	107/107 (100%)	96 (90%)	11 (10%)	9 0

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	ASP
1	A	135	ARG
1	A	140	ARG
1	A	180	GLN
1	A	188	GLU
1	A	207	LYS
1	A	208	ARG
1	A	213	ASP
1	A	214	ARG
1	A	236	ARG
1	A	237	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	169	GLN
1	A	180	GLN
1	A	181	ASN
1	A	199	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	$\# Z > 2$
2	HEM	A	501	1	30,50,50	2.47	12 (40%)	24,82,82	2.42	10 (41%)

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
2	HEM	A	501	1	-	0/10/54/54	0/0/8/8

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C2D-C3D	-6.42	1.35	1.54
2	A	501	HEM	C3B-CAB	-4.96	1.42	1.51
2	A	501	HEM	C3C-CAC	-4.78	1.42	1.51
2	A	501	HEM	C3D-C4D	-4.63	1.45	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C3B-C4B	-3.36	1.48	1.51
2	A	501	HEM	C2C-C1C	-3.13	1.46	1.52
2	A	501	HEM	C2B-C1B	-2.36	1.44	1.51
2	A	501	HEM	C2D-C1D	-2.17	1.44	1.51
2	A	501	HEM	CBC-CAC	2.12	1.41	1.29
2	A	501	HEM	CBB-CAB	2.32	1.42	1.29
2	A	501	HEM	C1C-NC	2.52	1.39	1.36
2	A	501	HEM	C4C-NC	3.64	1.40	1.36

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	HEM	CBD-CAD-C3D	-2.84	105.28	113.55
2	A	501	HEM	CBA-CAA-C2A	-2.06	108.84	112.53
2	A	501	HEM	CMD-C2D-C3D	2.64	126.02	114.35
2	A	501	HEM	C3C-CAC-CBC	2.92	128.93	124.46
2	A	501	HEM	C2D-C3D-C4D	3.47	107.38	101.50
2	A	501	HEM	C3B-CAB-CBB	3.73	130.18	124.46
2	A	501	HEM	CAD-C3D-C4D	3.83	125.99	112.47
2	A	501	HEM	CMB-C2B-C3B	3.99	126.50	116.53
2	A	501	HEM	CAD-C3D-C2D	4.66	126.62	113.22
2	A	501	HEM	CMC-C2C-C3C	5.12	129.32	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	2	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.