



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 1, 2017 – 08:35 AM EDT

PDB ID : 1R35
Title : MURINE INDUCIBLE NITRIC OXIDE SYNTHASE OXYGENASE DIMER,
TETRAHYDROBIOPTERIN AND 4R-FLUORO-N6-ETHANIMIDOYL-L-
LYSINE
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Deposited on : unknown
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure 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/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

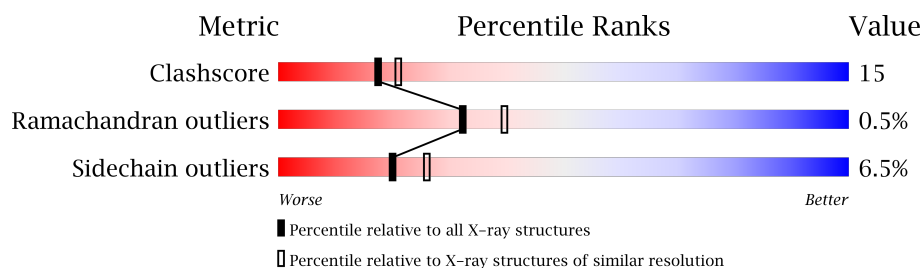
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)

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	433	
1	B	433	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7283 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 Nitric oxide synthase, inducible.

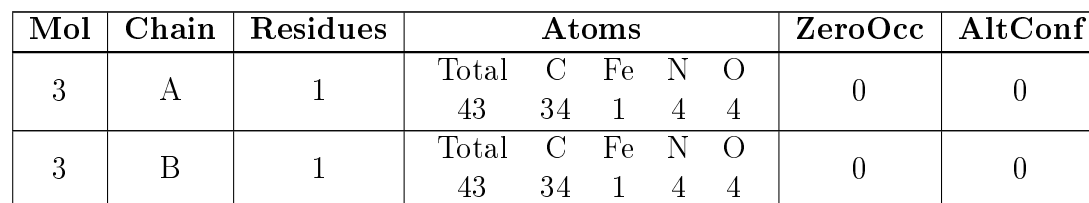
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	413	Total	C	N	O	S	0	0	0
			3368	2159	581	608	20			
1	B	413	Total	C	N	O	S	0	0	0
			3368	2159	581	608	20			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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- The chemical structure of H4B (Hydroxybenzoylserine) is shown with the following details:
- Atom Numbering:** Carbons are labeled C7, C8A, C2, C4A, C4, C6(P), C9(R), and C10(S). Nitrogens are labeled N8, N1, N2, N3, and N5. Oxygen atoms are labeled O9 and O4. Hydroxyl groups are labeled HO and OH.
 - Stereochemistry:** The hydroxyl group (HO) at C9(R) is shown with a dashed bond, indicating it is pointing away from the viewer. The hydroxyl group (OH) at C10(S) is shown with a wedged bond, indicating it is pointing towards the viewer.
 - Functional Groups:** The structure includes a benzamide group (N1, N2, N3, C2, C4, C4A) and a serine side chain (C6(P), C9(R), C10(S), N5, O9, OH).

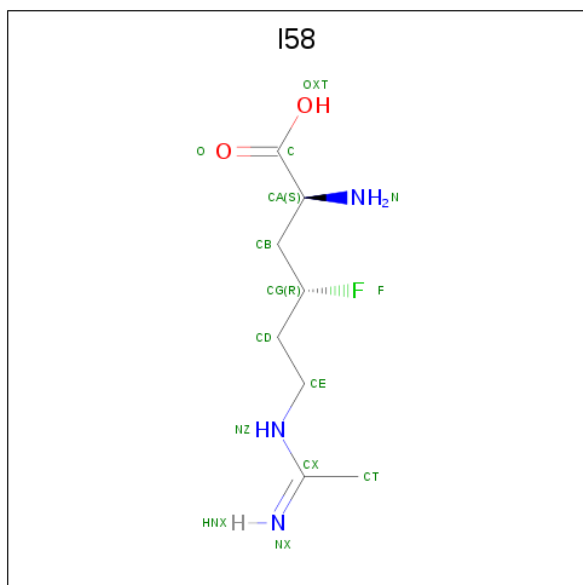
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	9	5	3		



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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 5 is 4R-FLUORO-N6-ETHANIMIDOYL-L-LYSINE (three-letter code: I58) (formula: C₈H₁₆FN₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	F	N	O	0
			14	8	1	3	2	0
5	B	1	Total	C	F	N	O	0
			14	8	1	3	2	0

- Molecule 6 is water.

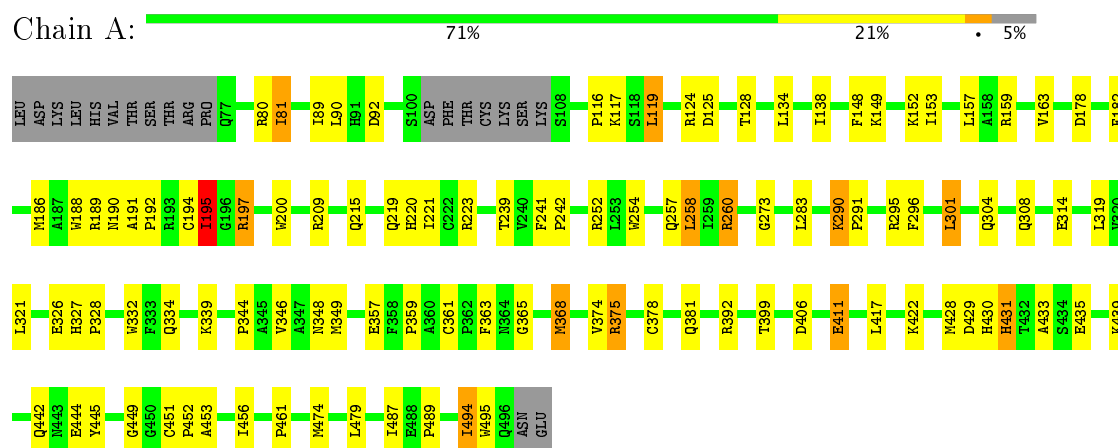
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	219	Total	O	0	0
			219	219		
6	B	175	Total	O	0	0
			175	175		

3 Residue-property plots [i](#)

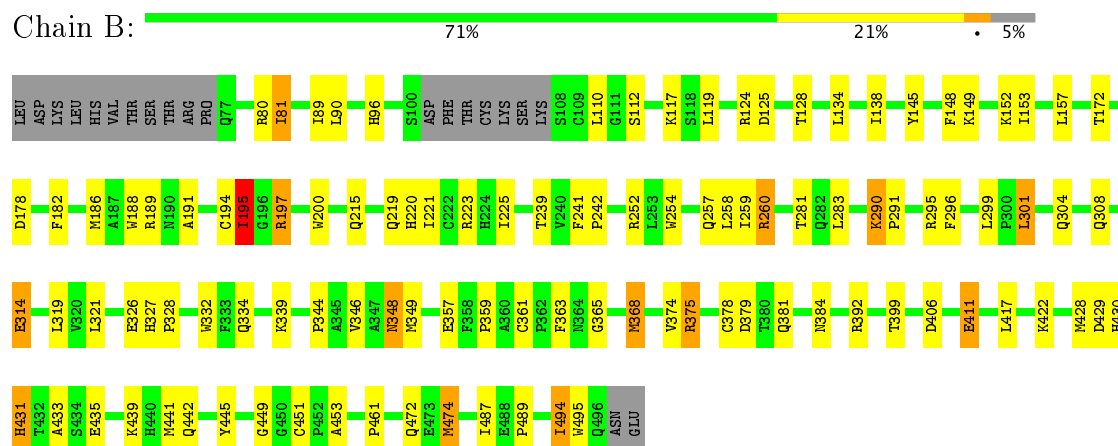
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

- Molecule 1: Nitric oxide synthase, inducible



- Molecule 1: Nitric oxide synthase, inducible



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	214.28Å 214.28Å 117.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.30	Depositor
% Data completeness (in resolution range)	73.3 (8.00-2.30)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 98.1	Depositor
R, R_{free}	0.252 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7283	wwPDB-VP
Average B, all atoms (Å ²)	54.0	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, SO4, H4B, I58

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	0/3466	0.65	3/4712 (0.1%)
1	B	0.39	0/3466	0.64	3/4712 (0.1%)
All	All	0.39	0/6932	0.64	6/9424 (0.1%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	365	GLY	N-CA-C	-5.56	99.19	113.10
1	B	195	ILE	CB-CA-C	-5.47	100.65	111.60
1	B	365	GLY	N-CA-C	-5.47	99.42	113.10
1	A	195	ILE	CB-CA-C	-5.30	101.01	111.60
1	A	368	MET	N-CA-C	-5.24	96.85	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	3368	0	3265	90	0
1	B	3368	0	3265	101	0
2	A	5	0	0	0	0
3	A	43	0	30	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	43	0	30	10	0
4	A	17	0	15	2	0
4	B	17	0	15	3	0
5	A	14	0	15	3	0
5	B	14	0	15	2	0
6	A	219	0	0	18	0
6	B	175	0	0	22	0
All	All	7283	0	6650	208	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 15.

The worst 5 of 208 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:346:VAL:HG11	1:A:349:MET:HE2	1.52	0.91
1:B:472:GLN:HG3	6:B:2023:HOH:O	1.73	0.88
1:B:299:LEU:HB2	6:B:1976:HOH:O	1.75	0.86
1:B:339:LYS:HG3	6:B:1982:HOH:O	1.80	0.80
1:A:296:PHE:HA	6:A:969:HOH:O	1.82	0.80

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	409/433 (94%)	386 (94%)	21 (5%)	2 (0%)	32	39
1	B	409/433 (94%)	383 (94%)	24 (6%)	2 (0%)	32	39
All	All	818/866 (94%)	769 (94%)	45 (6%)	4 (0%)	32	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	197	ARG
1	A	197	ARG
1	B	431	HIS
1	A	431	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	361/381 (95%)	338 (94%)	23 (6%)	20	27
1	B	361/381 (95%)	337 (93%)	24 (7%)	19	25
All	All	722/762 (95%)	675 (94%)	47 (6%)	20	26

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	494	ILE
1	B	149	LYS
1	B	417	LEU
1	B	81	ILE
1	B	178	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	486	GLN
1	B	95	HIS
1	B	348	ASN
1	A	348	ASN
1	A	430	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

7 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$
5	I58	A	800	-	7,13,13	2.07	3 (42%)	4,16,16	1.35	1 (25%)
3	HEM	A	901	1	28,50,50	1.60	5 (17%)	17,82,82	1.46	2 (11%)
4	H4B	A	902	-	14,18,18	1.51	2 (14%)	12,26,26	2.62	6 (50%)
2	SO4	A	903	-	4,4,4	0.52	0	6,6,6	0.07	0
5	I58	B	1800	-	7,13,13	2.08	3 (42%)	4,16,16	1.27	1 (25%)
4	H4B	B	1902	-	14,18,18	1.63	4 (28%)	12,26,26	2.56	7 (58%)
3	HEM	B	901	1	28,50,50	1.55	4 (14%)	17,82,82	1.44	2 (11%)

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
5	I58	A	800	-	-	0/9/14/14	0/0/0/0
3	HEM	A	901	1	-	1/6/54/54	0/0/8/8
4	H4B	A	902	-	-	0/8/17/17	0/2/2/2
2	SO4	A	903	-	-	0/0/0/0	0/0/0/0
5	I58	B	1800	-	-	0/9/14/14	0/0/0/0
4	H4B	B	1902	-	-	0/8/17/17	0/2/2/2
3	HEM	B	901	1	-	1/6/54/54	0/0/8/8

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	901	HEM	C3B-C2B	-4.04	1.35	1.40
3	B	901	HEM	C3B-C2B	-3.98	1.35	1.40
4	A	902	H4B	C4A-C8A	-3.43	1.34	1.41
4	B	1902	H4B	C4A-C8A	-3.35	1.35	1.41
3	A	901	HEM	C3C-CAC	-3.29	1.41	1.47

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	902	H4B	C6-C7-N8	-3.52	105.43	111.01
4	B	1902	H4B	C6-C7-N8	-3.15	106.02	111.01
3	B	901	HEM	CAD-C3D-C2D	-3.06	120.28	129.00
3	A	901	HEM	CAD-C3D-C2D	-3.03	120.34	129.00
4	A	902	H4B	C7-C6-N5	-2.48	105.21	110.31

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	901	HEM	C2D-C3D-CAD-CBD
3	A	901	HEM	C2D-C3D-CAD-CBD

There are no ring outliers.

6 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	800	I58	3	0
3	A	901	HEM	10	0
4	A	902	H4B	2	0
5	B	1800	I58	2	0
4	B	1902	H4B	3	0
3	B	901	HEM	10	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.