



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 2, 2017 – 02:16 AM EDT

PDB ID : 1MOK
Title : NADPH DEPENDENT 2-KETOPROPYL COENZYME M OXIDOREDUCTASE/CARBOXYLASE
Authors : Nocek, B.; Jang, S.B.; Jeong, M.S.; Clark, D.D.; Ensign, S.A.; Peters, J.W.
Deposited on : unknown
Resolution : 2.80 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

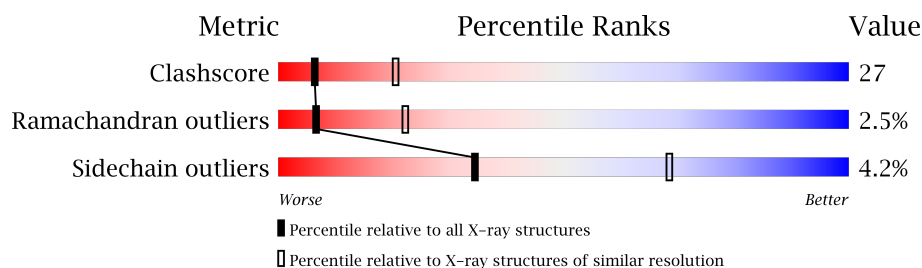
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)

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	523	
1	B	523	
1	C	523	
1	D	523	

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 16304 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 orf3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	522	Total	C	N	O	S	0	0	0
			4023	2546	699	755	23			
1	B	522	Total	C	N	O	S	0	0	0
			4023	2546	699	755	23			
1	C	522	Total	C	N	O	S	0	0	0
			4023	2546	699	755	23			
1	D	522	Total	C	N	O	S	0	0	0
			4023	2546	699	755	23			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).

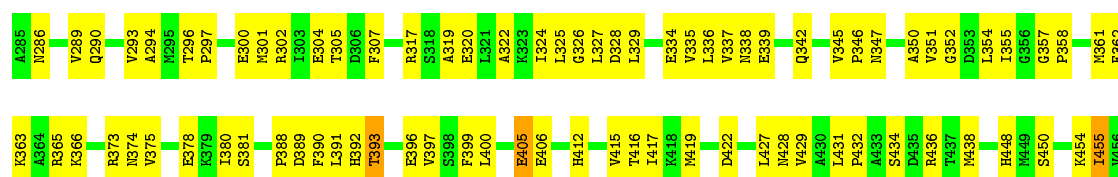


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0
			53	27	9	15	2	
2	B	1	Total	C	N	O	P	0
			53	27	9	15	2	

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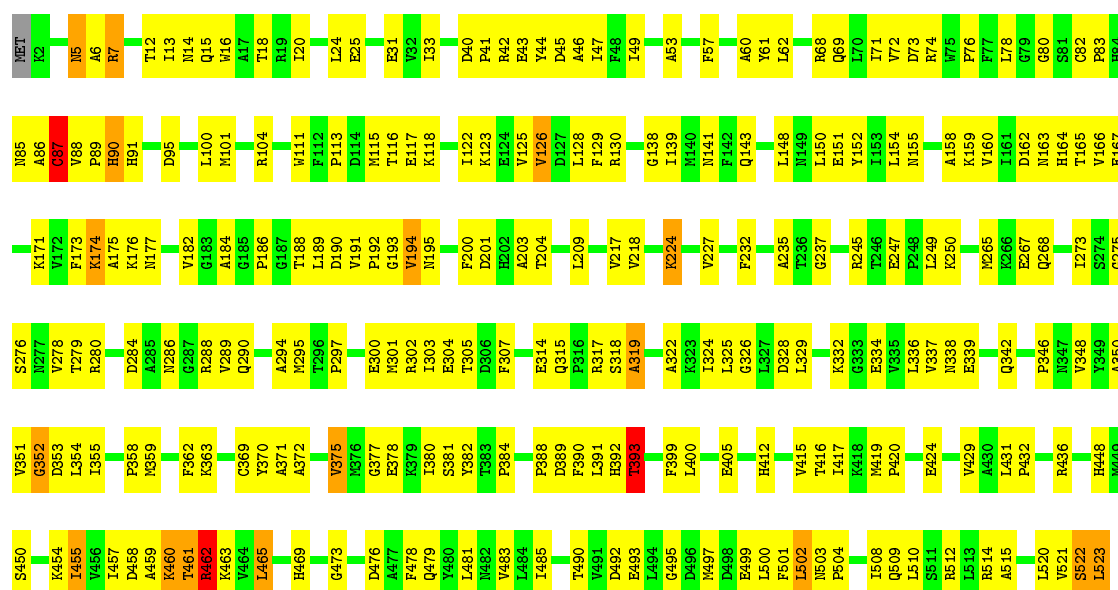
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		



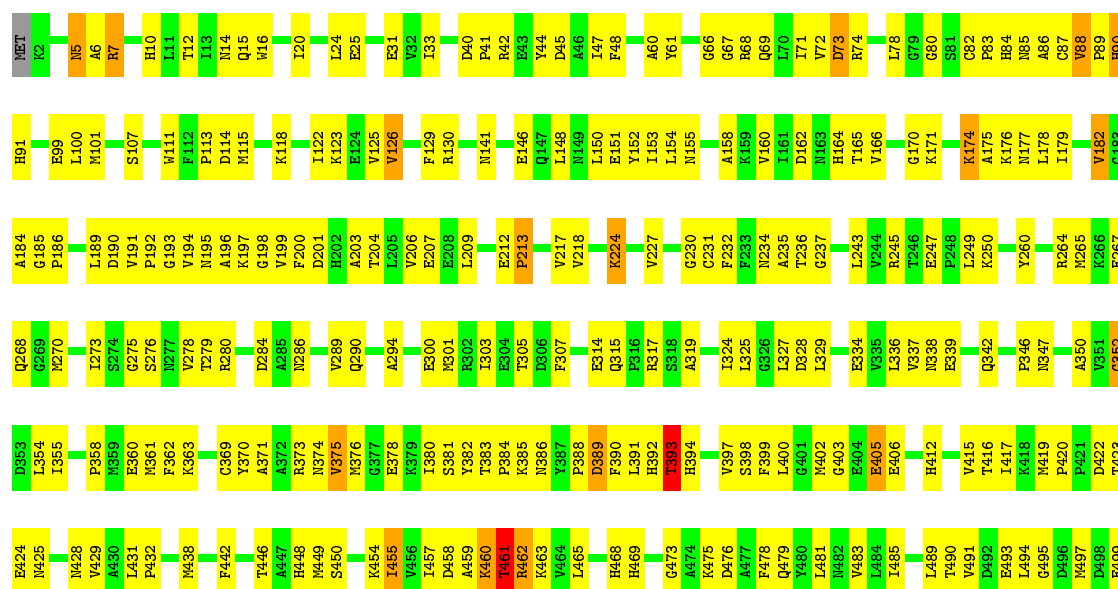
• Molecule 1: orf3

Chain C: 54% 42%



• Molecule 1: orf3

Chain D: 50% 45%



L500	F501	L502	J1503	P504	T505	H506	F507	L508	Q509	L510	S511	R512	L513	R514	V521	S522	L523
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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	65.60Å 87.50Å 100.70Å 72.00° 73.40° 69.81°	Depositor
Resolution (Å)	19.99 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (19.99-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.225 , 0.277	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16304	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.48	1/4106 (0.0%)	0.66	2/5556 (0.0%)
1	B	0.53	2/4106 (0.0%)	0.71	4/5556 (0.1%)
1	C	0.48	1/4106 (0.0%)	0.67	4/5556 (0.1%)
1	D	0.50	1/4106 (0.0%)	0.67	2/5556 (0.0%)
All	All	0.50	5/16424 (0.0%)	0.68	12/22224 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	523	LEU	C-O	-16.04	0.92	1.23
1	D	523	LEU	C-O	-15.27	0.94	1.23
1	C	523	LEU	C-O	-15.03	0.94	1.23
1	A	523	LEU	C-O	-14.81	0.95	1.23
1	B	73	ASP	C-N	-7.01	1.18	1.34

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	523	LEU	CA-C-O	12.25	145.82	120.10
1	D	523	LEU	CA-C-O	11.65	144.57	120.10
1	A	523	LEU	CA-C-O	10.93	143.06	120.10
1	C	523	LEU	CA-C-O	10.14	141.41	120.10
1	B	462	ARG	NE-CZ-NH2	7.37	123.98	120.30

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	4023	0	3980	222	0
1	B	4023	0	3979	217	0
1	C	4023	0	3980	234	0
1	D	4023	0	3980	231	0
2	A	53	0	31	6	0
2	B	53	0	31	6	0
2	C	53	0	31	9	0
2	D	53	0	31	12	0
All	All	16304	0	16043	864	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 27.

The worst 5 of 864 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:C:460:LYS:O	1:C:461:THR:HB	1.39	1.08
1:C:82:CYS:HA	1:C:86:ALA:HB3	1.38	1.05
1:A:82:CYS:HA	1:A:86:ALA:HB3	1.42	1.00
1:D:40:ASP:OD1	1:D:42:ARG:HG2	1.64	0.98
1:C:165:THR:HG22	1:C:174:LYS:HG3	1.46	0.97

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	520/523 (99%)	449 (86%)	60 (12%)	11 (2%)	8	27
1	B	520/523 (99%)	447 (86%)	62 (12%)	11 (2%)	8	27
1	C	520/523 (99%)	456 (88%)	51 (10%)	13 (2%)	6	22
1	D	520/523 (99%)	450 (86%)	54 (10%)	16 (3%)	5	16
All	All	2080/2092 (99%)	1802 (87%)	227 (11%)	51 (2%)	6	22

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	LYS
1	A	319	ALA
1	A	462	ARG
1	B	224	LYS
1	B	462	ARG

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	423/424 (100%)	407 (96%)	16 (4%)	38	72
1	B	423/424 (100%)	405 (96%)	18 (4%)	33	67
1	C	423/424 (100%)	407 (96%)	16 (4%)	38	72
1	D	423/424 (100%)	402 (95%)	21 (5%)	28	62
All	All	1692/1696 (100%)	1621 (96%)	71 (4%)	34	68

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	504	PRO
1	C	126	VAL
1	D	455	ILE
1	B	514	ARG
1	C	25	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	412	HIS
1	C	90	HIS
1	D	392	HIS
1	B	425	ASN
1	C	5	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
2	FAD	A	524	-	51,58,58	2.85	13 (25%)	54,89,89	2.44	13 (24%)
2	FAD	B	524	-	51,58,58	2.84	16 (31%)	54,89,89	2.42	13 (24%)
2	FAD	C	524	-	51,58,58	2.79	14 (27%)	54,89,89	2.37	13 (24%)
2	FAD	D	524	-	51,58,58	2.77	15 (29%)	54,89,89	2.47	12 (22%)

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	FAD	A	524	-	-	0/28/50/50	0/6/6/6
2	FAD	B	524	-	-	0/28/50/50	0/6/6/6
2	FAD	C	524	-	-	0/28/50/50	0/6/6/6
2	FAD	D	524	-	-	0/28/50/50	0/6/6/6

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	524	FAD	C1'-N10	-5.43	1.42	1.48
2	B	524	FAD	C1'-N10	-5.03	1.43	1.48
2	C	524	FAD	C1'-N10	-4.29	1.44	1.48
2	D	524	FAD	C1'-N10	-3.94	1.44	1.48
2	B	524	FAD	C5A-C4A	-3.93	1.31	1.40

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	524	FAD	C4X-C4-N3	-6.09	114.82	123.48
2	A	524	FAD	C4X-C4-N3	-6.01	114.93	123.48
2	B	524	FAD	C4X-C4-N3	-5.83	115.19	123.48
2	C	524	FAD	C4X-C4-N3	-5.51	115.64	123.48
2	B	524	FAD	N3A-C2A-N1A	-5.25	124.29	128.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	524	FAD	6	0
2	B	524	FAD	6	0
2	C	524	FAD	9	0
2	D	524	FAD	12	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	73:ASP	C	74:ARG	N	1.17

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.