



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 03:49 am BST

PDB ID : 5Y9Y
Title : Crystal structure of the Kdo hydroxylase KdoO, a non-heme Fe(II) α -ketoglutarate dependent dioxygenase in complex with succinate and Co(II)
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Deposited on : 2017-08-29
Resolution : 1.60 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

<https://www.wwpdb.org/validation/2017/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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

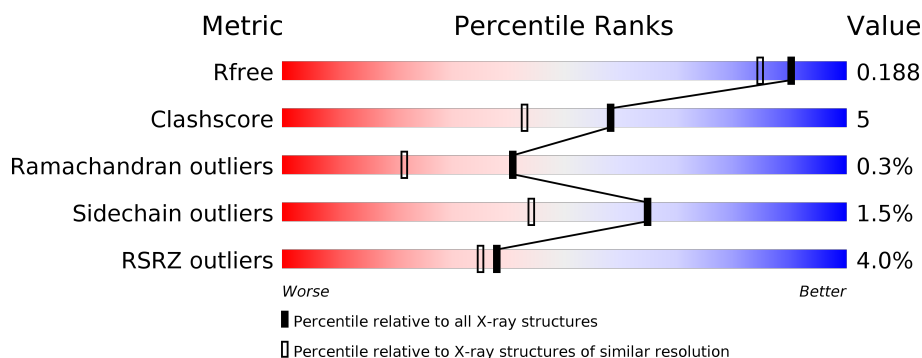
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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))
R_{free}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 respectively. 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	318	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PG4	A	405	-	X	-	-
6	ACT	A	409	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 2743 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 Uncharacterized protein KdoO.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total	C	N	O	S	0	6	0
			2417	1570	406	440	1			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	306	LYS	-	expression tag	UNP B3DUR4
A	307	LEU	-	expression tag	UNP B3DUR4
A	308	ALA	-	expression tag	UNP B3DUR4
A	309	ALA	-	expression tag	UNP B3DUR4
A	310	ALA	-	expression tag	UNP B3DUR4
A	311	LEU	-	expression tag	UNP B3DUR4
A	312	GLU	-	expression tag	UNP B3DUR4
A	313	HIS	-	expression tag	UNP B3DUR4
A	314	HIS	-	expression tag	UNP B3DUR4
A	315	HIS	-	expression tag	UNP B3DUR4
A	316	HIS	-	expression tag	UNP B3DUR4
A	317	HIS	-	expression tag	UNP B3DUR4
A	318	HIS	-	expression tag	UNP B3DUR4

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Co	0	0
			1	1		

- Molecule 3 is SUCCINIC ACID (three-letter code: SIN) (formula: C₄H₆O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	4	4		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



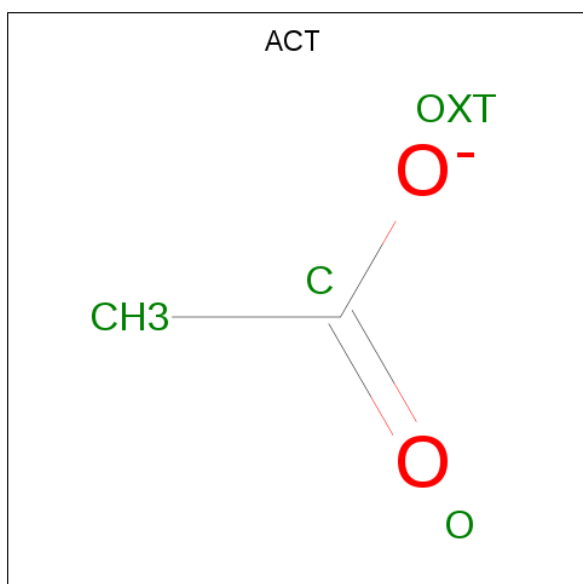
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Cl 1 1	0	0

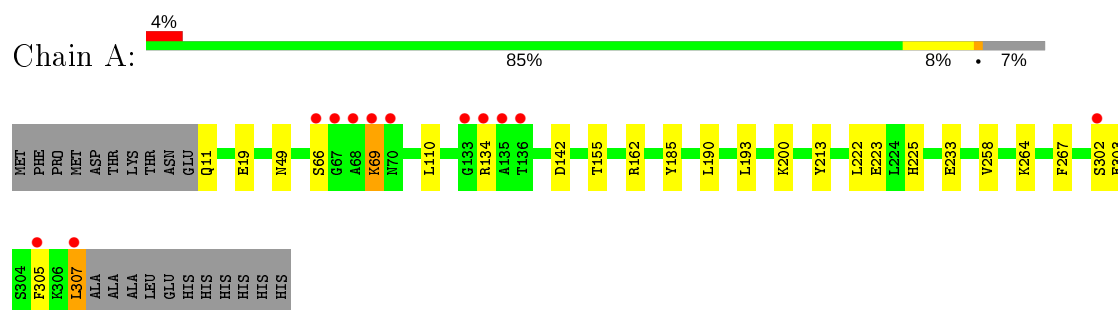
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	246	Total 246	O 246	0	0

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.

• Molecule 1: Uncharacterized protein KdoO



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	45.76 Å 59.32 Å 116.43 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.57 – 1.60 42.59 – 1.60	Depositor EDS
% Data completeness (in resolution range)	94.0 (23.57-1.60) 90.6 (42.59-1.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.63 (at 1.60 Å)	Xtriage
Refinement program	PHENIX 1.10.1 _2155	Depositor
R, R_{free}	0.159 , 0.194 0.159 , 0.188	Depositor DCC
R_{free} test set	2011 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	16.6	Xtriage
Anisotropy	0.582	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 56.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2743	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: GOL, CO, CL, PG4, SO4, ACT, SIN

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	0.99	3/2500 (0.1%)	0.78	1/3384 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	19	GLU	CD-OE1	-5.77	1.19	1.25
1	A	223	GLU	CD-OE1	-5.30	1.19	1.25
1	A	303	GLU	CD-OE1	-5.29	1.19	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	TYR	CA-CB-CG	5.12	123.13	113.40

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	2417	0	2440	22	0
2	A	1	0	0	0	0
3	A	8	0	4	0	0
4	A	6	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	38	0	46	4	0
6	A	16	0	12	6	0
7	A	10	0	0	0	0
8	A	1	0	0	0	0
9	A	246	0	0	7	0
All	All	2743	0	2510	24	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 5.

The worst 5 of 24 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:69:LYS:HE2	1:A:134:ARG:HD2	1.44	0.96
1:A:134:ARG:HH22	1:A:142:ASP:H	1.27	0.79
1:A:264:LYS:CE	6:A:409:ACT:OXT	2.34	0.76
1:A:69:LYS:HE2	1:A:134:ARG:CD	2.17	0.75
1:A:233:GLU:OE2	9:A:502:HOH:O	2.09	0.70

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	301/318 (95%)	296 (98%)	4 (1%)	1 (0%)	41 21

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	267	PHE

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	267/279 (96%)	263 (98%)	4 (2%)	65 44

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	SER
1	A	69	LYS
1	A	302	SER
1	A	307	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	A	225	HIS

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](#)

Of 15 ligands modelled in this entry, 2 are monoatomic - leaving 13 for Mogul analysis.

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$
6	ACT	A	409	-	1,3,3	0.99	0	0,3,3	0.00	-
5	PG4	A	407	-	3,3,12	0.83	0	2,2,11	1.28	0
6	ACT	A	411	-	1,3,3	0.72	0	0,3,3	0.00	-
4	GOL	A	403	-	5,5,5	0.31	0	5,5,5	0.51	0
6	ACT	A	410	-	1,3,3	0.50	0	0,3,3	0.00	-
5	PG4	A	406	-	3,3,12	0.64	0	2,2,11	0.68	0
7	SO4	A	413	-	4,4,4	0.31	0	6,6,6	0.87	0
6	ACT	A	412	-	1,3,3	1.04	0	0,3,3	0.00	-
5	PG4	A	405	-	6,6,12	0.77	0	5,5,11	2.13	3 (60%)
7	SO4	A	414	-	4,4,4	0.26	0	6,6,6	0.62	0
3	SIN	A	402	2	1,7,7	0.62	0	2,8,8	3.18	2 (100%)
5	PG4	A	404	-	9,9,12	0.90	0	8,8,11	1.99	4 (50%)
5	PG4	A	408	-	12,12,12	0.69	0	11,11,11	1.44	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
5	PG4	A	407	-	-	1/1/1/10	-
4	GOL	A	403	-	-	0/4/4/4	-
5	PG4	A	406	-	-	0/1/1/10	-
5	PG4	A	405	-	-	3/4/4/10	-
3	SIN	A	402	2	-	0/1/5/5	-
5	PG4	A	404	-	-	5/7/7/10	-
5	PG4	A	408	-	-	5/10/10/10	-

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	404	PG4	O3-C4-C3	3.73	126.46	110.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	SIN	C2-C3-C4	3.20	118.04	112.67
3	A	402	SIN	C3-C2-C1	3.16	117.97	112.67
5	A	405	PG4	O2-C3-C4	2.68	127.34	111.81
5	A	405	PG4	C5-O3-C4	2.66	124.81	113.29

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	404	PG4	O3-C5-C6-O4
5	A	404	PG4	O4-C7-C8-O5
5	A	408	PG4	O2-C3-C4-O3
5	A	404	PG4	O2-C3-C4-O3
5	A	407	PG4	O4-C7-C8-O5

There are no ring outliers.

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	409	ACT	3	0
5	A	407	PG4	1	0
6	A	411	ACT	1	0
4	A	403	GOL	1	0
6	A	410	ACT	1	0
5	A	406	PG4	1	0
6	A	412	ACT	1	0
5	A	405	PG4	1	0
5	A	408	PG4	1	0

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 [i](#)

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

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	297/318 (93%)	-0.25	12 (4%) 38 35	12, 21, 50, 106	1 (0%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	68	ALA	11.0
1	A	67	GLY	4.2
1	A	133	GLY	4.1
1	A	307	LEU	3.7
1	A	136	THR	3.7

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. 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	B-factors(Å ²)	Q<0.9
5	PG4	A	407	4/13	0.52	0.29	66,76,88,103	0
5	PG4	A	404	10/13	0.64	0.13	37,56,59,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	PG4	A	405	7/13	0.68	0.15	40,46,56,58	0
6	ACT	A	409	4/4	0.71	0.22	67,69,70,74	0
7	SO4	A	414	5/5	0.74	0.15	115,121,122,123	0
6	ACT	A	412	4/4	0.79	0.14	29,43,44,47	0
5	PG4	A	406	4/13	0.80	0.14	52,57,61,65	0
5	PG4	A	408	13/13	0.80	0.12	45,55,61,62	0
7	SO4	A	413	5/5	0.83	0.16	94,95,97,101	0
6	ACT	A	410	4/4	0.86	0.10	53,54,56,58	0
6	ACT	A	411	4/4	0.86	0.15	59,60,61,65	0
4	GOL	A	403	6/6	0.92	0.13	17,25,27,33	0
8	CL	A	415	1/1	0.96	0.05	28,28,28,28	1
3	SIN	A	402	8/8	0.98	0.06	17,19,21,26	0
2	CO	A	401	1/1	0.99	0.07	15,15,15,15	0

6.5 Other polymers ⓘ

There are no such residues in this entry.