



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:30 PM GMT

PDB ID : 1B4U
Title : PROTOCATECHUATE 4,5-DIOXYGENASE (LIGAB) IN COMPLEX
WITH PROTOCATECHUATE (PCA)
Authors : Sugimoto, K.; Senda, T.; Mitsui, Y.
Deposited on : 1998-12-29
Resolution : 2.20 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 (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

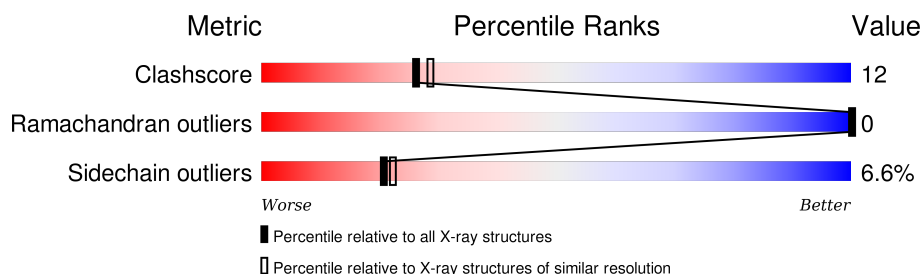
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)

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	139	
1	C	139	
2	B	302	
2	D	302	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6897 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 PROTOCATECHUATE 4,5-DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	132	Total	C	N	O	S	0	0	0
			1029	646	177	199	7			
1	C	132	Total	C	N	O	S	0	0	0
			1029	646	177	199	7			

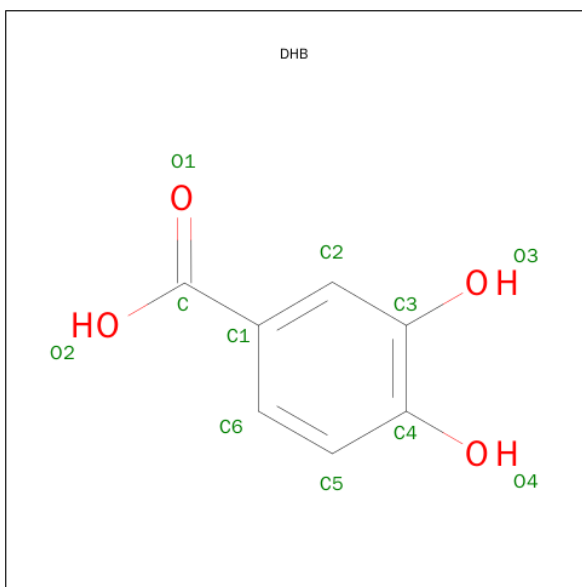
- Molecule 2 is a protein called PROTOCATECHUATE 4,5-DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	298	Total	C	N	O	S	0	0	0
			2313	1482	385	430	16			
2	D	298	Total	C	N	O	S	0	0	0
			2313	1482	385	430	16			

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Fe	0	0
			1	1		
3	D	1	Total	Fe	0	0
			1	1		

- Molecule 4 is 3,4-DIHYDROXYBENZOIC ACID (three-letter code: DHB) (formula: C₇H₆O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			11	7	4		
4	D	1	Total	C	O	0	0
			11	7	4		

- Molecule 5 is water.

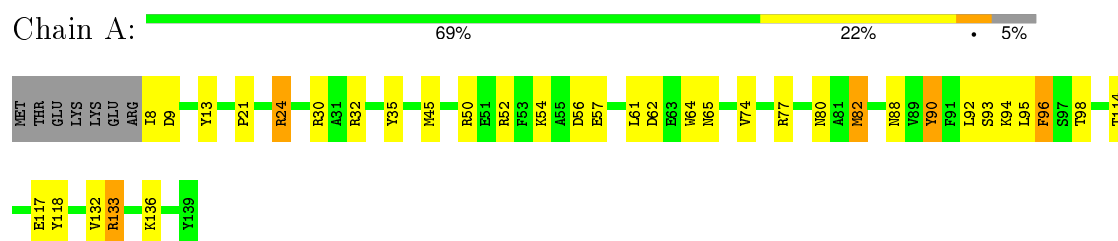
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total	O	0	0
			36	36		
5	B	68	Total	O	0	0
			68	68		
5	C	29	Total	O	0	0
			29	29		
5	D	56	Total	O	0	0
			56	56		

3 Residue-property plots

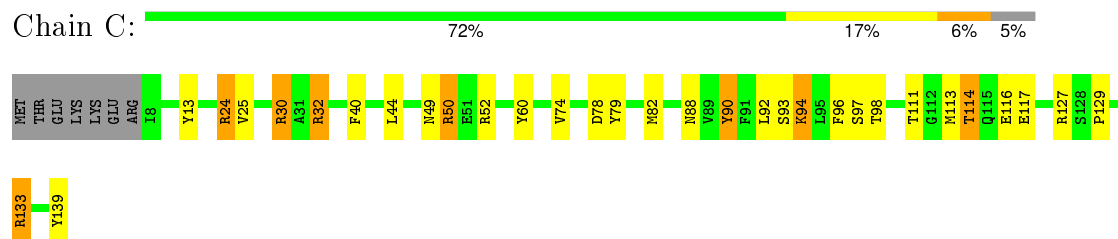
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($RSRZ > 2$). 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.

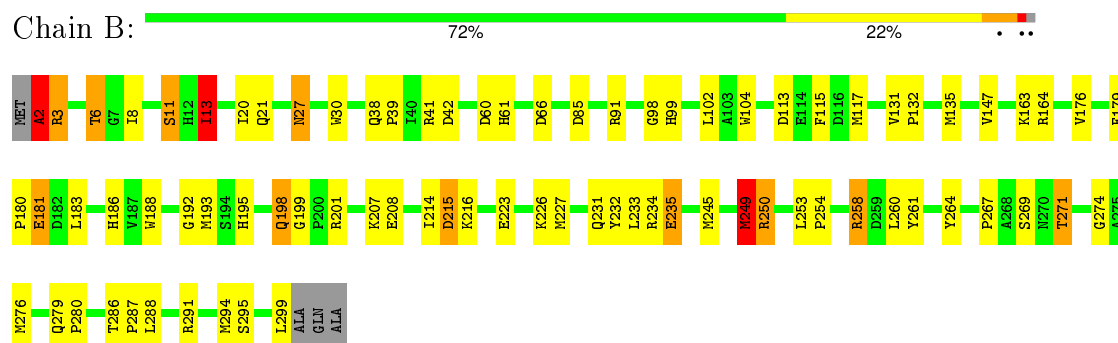
• Molecule 1: PROTOCATECHUATE 4,5-DIOXYGENASE



• Molecule 1: PROTOCATECHUATE 4,5-DIOXYGENASE



• Molecule 2: PROTOCATECHUATE 4,5-DIOXYGENASE



• Molecule 2: PROTOCATECHUATE 4,5-DIOXYGENASE



MET	A2	R3	T6	G7	I8	T9	S10	S11	H12	I13	P14	A15	L16	I20	M27	W30	G31	P32	Q38	P39	I40	R41	K45	Q46	P47	P51	D52	D66	M67	K82	R91	P92	V93	P94	D95	D101	L110	D113	E114	D124	V125	D126	V131	P132
M135	V155	P158	P159	R164	C165	D170	S171	I172	R173	A174	A175	V176	F179	L183	H186	V187	M188	G189	M193	S194	H195	Q196	L197	Q198	R201	L204	L205	N206	K207	E208	F209	N212	F213	I214	I218	E223	L224	M227	P228	H229	L233	R234	E235	
S236	G237	S238	E239	N245	I248	M249	L253	P254	E255	K256	D259	L260	Y261	T262	F263	T264	H265	I266	P267	A268	S269	N270	T271	G274	A275	H276	I277	L278	Q279	G285	P290	R291	K292	V293	N294	S295	G296	H297	S298	L299	ALA	GLN	ALA	

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.40 Å 66.50 Å 119.80 Å 90.00° 92.50° 90.00°	Depositor
Resolution (Å)	60.00 – 2.20	Depositor
% Data completeness (in resolution range)	91.0 (60.00-2.20)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.161 , 0.220	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6897	wwPDB-VP
Average B, all atoms (Å ²)	28.0	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: DHB, FE

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	0.88	0/1049	1.83	27/1408 (1.9%)
1	C	0.70	0/1049	1.61	14/1408 (1.0%)
2	B	0.88	0/2383	1.94	41/3253 (1.3%)
2	D	0.79	2/2383 (0.1%)	1.81	43/3253 (1.3%)
All	All	0.83	2/6864 (0.0%)	1.83	125/9322 (1.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	201	ARG	CD-NE	-5.84	1.36	1.46
2	D	245	MET	CG-SD	-5.68	1.66	1.81

The worst 5 of 125 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	291	ARG	CD-NE-CZ	38.73	177.83	123.60
2	B	258	ARG	CD-NE-CZ	24.80	158.33	123.60
2	B	91	ARG	CD-NE-CZ	22.01	154.42	123.60
2	B	234	ARG	NE-CZ-NH1	21.99	131.29	120.30
1	A	133	ARG	NE-CZ-NH1	20.57	130.59	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	2	ALA	Mainchain

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	1029	0	986	18	0
1	C	1029	0	986	29	0
2	B	2313	0	2252	60	0
2	D	2313	0	2252	64	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	B	11	0	4	3	0
4	D	11	0	4	2	0
5	A	36	0	0	0	0
5	B	68	0	0	0	0
5	C	29	0	0	1	0
5	D	56	0	0	0	0
All	All	6897	0	6484	162	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 12.

The worst 5 of 162 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)
2:B:249:MET:HE2	2:B:250:ARG:HA	1.40	1.01
1:C:74:VAL:HG22	1:C:82:MET:HE3	1.41	0.97
2:D:193:MET:HE3	2:D:274:GLY:HA3	1.44	0.95
1:C:114:THR:HG22	1:C:117:GLU:HG2	1.47	0.94
2:B:2:ALA:HB2	2:B:179:PHE:O	1.72	0.90

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	130/139 (94%)	126 (97%)	4 (3%)	0	100	100
1	C	130/139 (94%)	128 (98%)	2 (2%)	0	100	100
2	B	296/302 (98%)	286 (97%)	10 (3%)	0	100	100
2	D	296/302 (98%)	281 (95%)	15 (5%)	0	100	100
All	All	852/882 (97%)	821 (96%)	31 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	102/109 (94%)	98 (96%)	4 (4%)	39	48
1	C	102/109 (94%)	98 (96%)	4 (4%)	39	48
2	B	253/255 (99%)	237 (94%)	16 (6%)	22	24
2	D	253/255 (99%)	230 (91%)	23 (9%)	12	11
All	All	710/728 (98%)	663 (93%)	47 (7%)	21	22

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

Mol	Chain	Res	Type
1	C	94	LYS
2	D	11	SER
2	D	271	THR

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Mol	Chain	Res	Type
1	C	116	GLU
2	D	13	ILE

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

Mol	Chain	Res	Type
2	B	198	GLN
1	C	88	ASN
2	D	198	GLN
2	B	99	HIS
2	B	121	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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
4	DHB	B	503	3	8,11,11	0.61	0	11,15,15	2.09	4 (36%)
4	DHB	D	504	3	8,11,11	1.12	1 (12%)	11,15,15	1.19	1 (9%)

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
4	DHB	B	503	3	-	0/0/4/4	0/1/1/1
4	DHB	D	504	3	-	0/0/4/4	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	504	DHB	O3-C3	2.58	1.41	1.36

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	503	DHB	C1-C2-C3	-3.50	118.02	120.98
4	D	504	DHB	C2-C3-C4	-2.37	117.67	119.82
4	B	503	DHB	C5-C6-C1	-2.05	118.15	121.14
4	B	503	DHB	C5-C4-C3	2.42	122.79	119.72
4	B	503	DHB	C6-C1-C2	4.27	123.84	118.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	503	DHB	3	0
4	D	504	DHB	2	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

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

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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