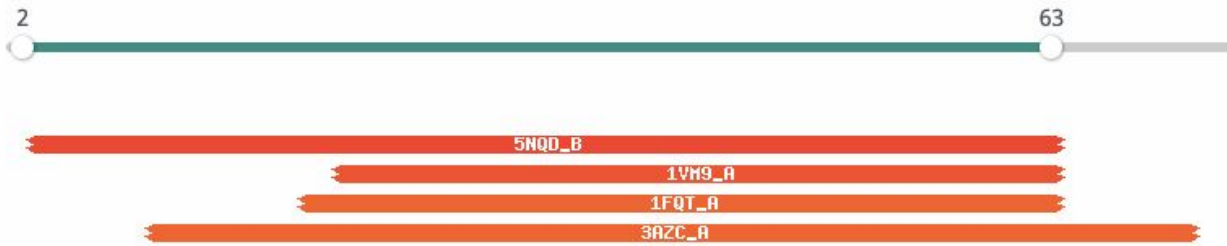


Details for gene Secretariat_Draft_79	
Phage	Secretariat · Cluster DJ · 57731 bp
Gene	Secretariat_Draft_79
Pham (click for Pham view →)	22354
Starterator	Pham 22354 report
Genome Position	51192 to 51419 (Forward)
Length	228 base pairs 75 amino acids
Amino Acid Sequence	Click to View
Notes	
Members (2) of Pham 22354	
Schwartz33_Draft_83	Secretariat_Draft_79

Secretariat\_Draft gene 79 (51192 - 51419 ) | pham 7579

DNA    PROTEIN    DOMAINS    CLUSTERS    FUNCTION

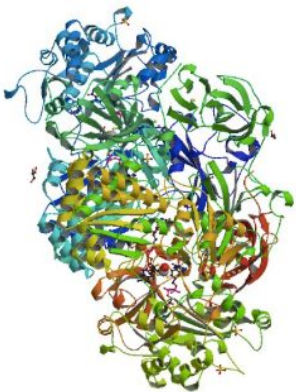
>Secretariat\_Draft gp79  
MNHTYVIDPENDIFDVVRLSVRTGDGQFTDVTHRCGNAKVRPAMVINKETVDCLTCGSQFDLYPEGENLEQQAS



Hit	Name	Probability	E-value	SS	Cols	Target Length
5NQD_B	Arsenite oxidase large subunit AioA; Arsenite oxidase, DMSOR family, Rieske; HET: GOL, MGD, EDO, PGE, P33, F3S, FES, SO4; 2.2A {Rhizobium sp. NT-26}; Related PDB entries: 5NQD_H 5NQD_F 5NQD_D	93.43	0.15	4.7	62	132
1VM9_A	protein; STRUCTURAL GENOMICS, CESH, PROTEIN STRUCTURE; HET: EDO; 1.48A {Pseudomonas mendocina} SCOP: b.33.1.1; Related PDB entries: 1SJG_A 4P1C_I 4P1C_H 2Q3W_A 4P1B_I 4P1B_H	92.62	0.15	3.4	44	111

1. **5NQD\_B** Arsenite oxidase large subunit AioA; Arsenite oxidase, DMSOR family, Rieske; HET: GOL, MGD, EDO, PGE, P33, F3S, FES, SO4; 2.2A {Rhizobium sp. NT-26}; Related PDB entries: 5NQD\_H 5NQD\_F 5NQD\_D  
Probability: 93.43%, E-value: 0.15, Score: 29.92, Aligned cols: 62, Identities: 16%, Similarity: 0.147,

Biological Assembly 1 ?



3D View: [Structure](#) | [Electron Density](#) |

## 5NQD




Arsenite oxidase AioAB from Rhizobium sp. str. NT-26 mutant AioBF108A  
DOI: [10.2210/pdb5NQD/pdb](https://doi.org/10.2210/pdb5NQD/pdb)  
Classification: [OXIDOREDUCTASE](#)  
Organism(s): [Rhizobium sp. NT-26](#)  
Expression System: [Escherichia coli](#)

Deposited: 2017-04-20 Released: 2018-05-30  
Deposition Author(s): [Santos-Silva, T.](#), [Romao, M.](#), [Vieira, M.](#), [Marques, A.T.](#)  
Funding Organization(s): FCT; PT2020

Experimental Data Snapshot

Method: X-RAY DIFFRACTION  
Resolution: 2.2 Å  
R-Value Free: 0.217  
R-Value Work: 0.172

wwPDB Validation

Metric	Percentile Rank
Rfree	
Clashscore	
Ramachandran outliers	

**arsenate reductase**

*Chemosphere*, 2016 Nov;163:400-412. doi: 10.1016/j.chemosphere.2016.08.044. Epub 2016 Aug 24.

### Genetic identification of arsenate reductase and arsenite oxidase in redox transformations carried out by arsenic metabolising prokaryotes - A comprehensive review.

Kumari N<sup>1</sup>, Jagadevan S<sup>2</sup>.

⊕ Author information

#### Abstract

Arsenic (As) contamination in water is a cause of major concern to human population worldwide, especially in Bangladesh and West Bengal, India. Arsenite (As(III)) and arsenate (As(V)) are the two common forms in which arsenic exists in soil and groundwater, the former being more mobile and toxic. A large number of arsenic metabolising microorganisms play a crucial role in microbial transformation of arsenic between its different states, thus playing a key role in remediation of arsenic contaminated water. This review focuses on advances in biochemical, molecular and genomic developments in the field of arsenic metabolising bacteria - covering recent developments in the understanding of structure of arsenate reductase and arsenite oxidase enzymes, their gene and operon structures and their mechanism of action. The genetic and molecular studies of these microbes and their proteins may lead to evolution of successful strategies for effective implementation of bioremediation programs.

Copyright © 2016 Elsevier Ltd. All rights reserved.

**KEYWORDS:** Arsenate reductase; Arsenic; Arsenite oxidase; Bioremediation; Genes; Operon

PMID: 27565307 DOI: [10.1016/j.chemosphere.2016.08.044](https://doi.org/10.1016/j.chemosphere.2016.08.044)

[Indexed for MEDLINE]

Protein

Gene

Organism

Submitted name: **Arsenite oxidase subunit AioB**

**aioB**

*Gordonia rubripertincta (Rhodococcus corallinus)*

GO - Molecular function<sup>i</sup>

- 2 iron, 2 sulfur cluster binding ⓘ Source: InterPro
- arsenate reductase (azurin) activity ⓘ Source: UniProtKB-EC
- oxidoreductase activity, acting on diphenols and related substances as donors ⓘ Source: InterPro

Keywords<sup>i</sup>

Molecular function	Oxidoreductase ⓘ Imported ▾
--------------------	-----------------------------

Names & Taxonomy<sup>i</sup>

Protein names <sup>i</sup>	Submitted name: Arsenite oxidase subunit AioB ⓘ Imported ▾ (EC:1.20.9.1 ⓘ Imported ▾ )
Gene names <sup>i</sup>	Name: <b>aioB</b> ⓘ Imported ▾ ORF Names: GCWB2_15850 ⓘ Imported ▾
Organism <sup>i</sup>	Gordonia rubripertincta (Rhodococcus corallinus) ⓘ Imported ▾
Taxonomic identifier <sup>i</sup>	36822 [NCBI]
Taxonomic lineage <sup>i</sup>	Bacteria > Actinobacteria > Corynebacteriales > Gordoniaceae > Gordonia ⓘ
Proteomes <sup>i</sup>	UP000264305 Component <sup>i</sup> : Chromosome

Subcellular location<sup>i</sup>

Topology

Feature key	Position(s)	Description	Actions	Graphical view	Length
Transmembrane <sup>i</sup>	56 – 76	Helical ⓘ Sequence analysis ▾	ⓘ Add ⓘ BLAST		21
Transmembrane <sup>i</sup>	96 – 117	Helical ⓘ Sequence analysis ▾	ⓘ Add ⓘ BLAST		22
Transmembrane <sup>i</sup>	163 – 187	Helical ⓘ Sequence analysis ▾	ⓘ Add ⓘ BLAST		25