***Original Research Article***

**In Silico Structural and Functional Characterisation of Hypothetical Protein WP\_020728386.1 from *Mycobacterium marinum*: A Potential Dioxygenase Involved in Pathogenesis**

**ABSTRACT**

**Background:** *Mycobacterium marinum* is ubiquitous in aquatic environment and is mostly spread by coming into contact with fresh and salt water, such as from swimming pools, aquariums, and marine life. It is considered the most serious ﬁsh pathogen, known for triggering a variety of symptoms at a time, including uncoordinated swimming, abdominal swelling, weight loss, skin ulceration, the growth of white nodules in the liver, kidney, and spleen in both fresh and marine water ﬁsh.

**Aims:** The objective of this investigation was to assess the intended function of the hypothetical protein WP\_020728386.1.

**Methodology:** It is a computer-based in silico dry lab study utilising various software and manipulating databases. The study is conducted in a dry lab from 2024 to 2025.The projected tertiary structure was assessed using servers such as Swiss Model. The Swiss-Model Interactive Workplace, ProSA-web, PROCHEK, Ramachandran Plot, Z scores, and structural evaluations are used to choose the most suitable materials. To find out homologous proteins, different bioinformatics tools were used for searching sequence similarity.

**Results:** Fish dwelling in both fresh and saltwater are susceptible to infection from the opportunistic pathogen *Mycobacterium marinum.* This infection causes morbidity and mortality in fish by causing necrotising granuloma similar to tuberculosis. In humans, it causes nodular lymphangitis, skin nodules, and ulcers as signs of preliminary cutaneous infections that can progress to osteomyelitis, tenosynovitis, and arthritis, leading to serious health hazards. Because of the presence of the extradiol ring cleavage dioxygenase family protein, the protein WP\_020728386.1 present in *Mycobacterium marinum* has an enormous effect on catalysing the incorporation activity of molecular oxygen atoms into substrates, resulting in ring cleavage in aromatics. However, the protein has not yet been fully explicit. As a result, an in-silico method was developed in this study to record the structure and function of the unidentified protein WP\_020728386.1. The tertiary structure of the matrix protein was assessed employing the Ramachandran plot by the PROCHECK program. it can be said a valid model as 91.0% residues were found in the most favoured region. The analysis of physicochemical parameters, functional annotation, predicted active site of ligand binding, Ramachandran plot analysis, as well as overall fundamental features of the hypothetical protein provides an insight into the studied protein that it might be a very functional and potentially protein possessing a crucial role.

**Conclusions:** As a result of this research, the overall understanding of pathogenesis and pathophysiology will increase, and researchers will be able to concentrate on the protein complex, which might assist in the development of effective treatment drugs and vaccines against *Mycobacterium marinum* infections.

Keywords: *Mycobacterium marinum, in silico*, functional annotation, homology modelling, Ramachandran plot.

**1. INTRODUCTION**

Mycobacteria are the most common cause of granulomatous lesions in people and animals because mycobacteria are intracellular agents; the organism's immunological reaction takes the form of a histiocytic granuloma. A great number of macrophages accumulate in the region of the lesion during its early stages, and central macrophage necrosis can be seen (Alabaş et al., 2022). *Mycobacterium marinum*, a macrophage pathogen similar to *Mycobacterium tuberculosis*, causes a persistent, systemic disease in ectotherms that resembles tuberculosis. In 1926, Aronson isolated and identified this slow-growing nontuberculous Mycobacterium (NTM) from fish for the first time. (Haenen et al. 2013; Aroson 1926; Collins 1985). Later, in 1954, Collins et al. characterised *M. marinum* as an opportunistic pathogen that affects humans (Collins 1985; Linell, 1954). These bacteria are ubiquitous in the aquatic environment and are mostly spread by coming into contact with fresh and salt water, such as from swimming pools, aquariums, and marine life (Wayne 1992). It is considered as the most serious ﬁsh pathogen, known for triggering a variety of symptoms at a time, including uncoordinated swimming, abdominal swelling, weight loss, skin ulceration, the growth of white nodules in the liver, kidney, and spleen in both fresh and marine water ﬁsh (Ferguson [2006](#_bookmark159); El Amrani et al. [2010](#_bookmark156)). In fish, infection by *M. marinum* has long been referred to as fish tuberculosis. In humans, *Mycobacterium marinum* infections may cause treatment-refractory skin and soft tissue lesions, cutaneous manifestations like solitary papules or nodules, and in extreme cases, develop tenosynovitis. Diagnosis is difficult and requires a high index of suspicion, both from the clinician and from the lab. Treatment can be challenging and usually consists of a two or three-drug combination (Tsiolakkis et al., 2023).

Although *M*. *tuberculosis* is the most common macrophage, its slow growth hinders the discovery of new drugs. On the contrary, the fast-growing nature of *M*. *marinum* makes it suitable for use as a surrogate model for studyingthe pathogenesis of *M*. *tuberculosis*. Additionally, the feasibility of employing *M. marinum* as a model for assessing anti-TB activity has been explained (Dharra et al. 2019).

There is a dynamic interaction between the host immune system and pathogens, making it essential to understand the relationship between host and pathogen to study the effects of pathogens on the host (Iqbal et al., 2024). Although there exists an uncountable amount of biological data, for instance, genomic sequences, functional genomic data, etc., gathered from different high-throughput experiments, there is still a lack of functional annotation for most of the recently sequenced proteins. For instance, about half of the *Mycobacterium tuberculosis* genome is made up of proteins of unknown function (Mazandu et al. 2012**)**. It is now a crying need to extract information from this big data pool. For the exploitation of these data, there is a need for effective computational procedures/methods to get genome annotation to predict functional annotations of uncharacterized proteins. Hence, the experiment is conducted to characterise and annotate a hypothetical Protein from *Mycobacterium marinum* (WP\_020728386.1).

**2. MATERIALS AND METHODS**

**2.1 Sequence retrieval and Homology searching**

The sequence information of the selected hypothetical protein obtained from the protein database of the National Centre for Biotechnology Information (NCBI) (Sayers et al. 2022), having Accession no.WP\_020728386 (Version WP\_020728386.1),which contains 231 amino acids. After that, the sequence of amino acids was extracted in FASTA format for further analysis. To locate the protein's homologues, homology searching was done using the NCBI's BLASTp search tools (http://www.ncbi.nlm.nih.gov/) against the non-redundant database with default parameters (Altschul et al. 1990).

**2.2 Physicochemical properties analysis**

The physicochemical properties of the hypothetical protein, such as molecular weight, theoretical pI, amino acid composition, atomic composition, instability index, and grand average of hydropathicity (GRAVY), were evaluated using a web-based server named Protparam tool of ExPaSy server (Gasteiger et al. 2003). Furthermore, the theoretical isoelectric point (pI) of the hypothetical protein was measured using SMS Suite (v2.0) (Stothard, 2000).

**2.3 Subcellular location determination**

The subcellular location of the hypothetical protein was predicted by CELLO v.2.5 (Yu et al. 2006). The protein's location, such as its membrane, extracellular space, cytoplasm, or cell wall, is primarily predicted by the CELLO Prediction. The location is appropriately indicated by a higher reliability value.

**2.4 Functional annotation prediction**

We used the NCBI Conserved Domains Database (NCBI-CDD) (Wang et al. 2023) for functional annotation of the hypothetical protein from *Mycobacterium marinum.*

**2.5 Secondary structure prediction**

The secondary structure features for the selected hypothetical protein were predicted by the reliable PSIPRED server (McGuffin et al. 2000). For element prediction, the self-optimised prediction method with alignment (SOPMA) (Combet et al. 2000) was also used.

**2.6 Three-dimensional (3D) structure prediction and model quality validation**

The three-dimensional (tertiary) structure of the hypothetical protein under study was predicted using the Swiss-Model server (Waterhouse et al. 2018). Finally, the anticipated 3D structure of the hypothetical protein was assessed for quality using the PROCHECK service available in the SAVES (v6.0) server (Laskowski et al. 1996). Furthermore, the Z-score of the modelled structure for structural evaluation was calculated using the ProSA-Web server (Wiederstein& ProSA-Web, 2007)

**2.7 Active site detection**

CASTp server (Computed Atlas of Surface Topography of Protein) (Tian et al. 2018) was used to determine the active sites of the modelled protein. The CASTp web server delivers an online service for identifying, characterising, and measuring concave surface areas on three-dimensional structures of proteins.

**3. RESULTS AND DISCUSSION**

**3.1 Protein Sequence retrieval and homology Information**

The basic determinants of biological function and structure are protein sequences, which are the ultimate instrument in both cases of drug discovery and development. The NCBI protein sequence databank is a reservoir of protein sequences collected from different sources such as RefSeq, Genebank, TPA, etc. Here, the studied protein obtained from the NCBI protein database is present in the locus WP\_020728386.1, containing 231 amino acids (aa). However, additional information about the respective protein is shown in Table 1.

|  |  |
| --- | --- |
| **Parameters** |  **Information on Protein** |
| Locus | WP\_020728386.1 |
| Definition | Hypothetical protein WP\_020728386.1(*Mycobacterium marinum)* |
| Amino acid | 231 aa |
| Accession | WP\_020728386 |
| Version | WP\_020728386.1 |
| Source | *Mycobacterium marinum* |
| Keywords | RefSeq |
| Organism | [*Mycobacterium marinum*](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Tree&id=1781&lvl=3&keep=1&srchmode=1&unlock) |
| FASTA sequence | MLSAIAIIPSAPVLVPELTGLAGAEVADLRSAVVAAASSLPNHWVGIGVGPEDQVAGPDAVGTFAGFGVDVQVRLAPALGEQPGPPSDLPLCALLAGWVRGQIRPAATAKIQVYAHGRESEDALVQGKLLRAEIDRTADPVGVLVVADGVNTLTPSAPGGYDPTGAPAQLLLDDALAGGDVAALARLPERVLGRPAFQVLAGLCGAGPRSATELYRGAPFGVGCFVGVWQP |

**Table 1. Protein retrieval**

Well known NCBI BLASTp tools were used for analysing the homology search of our hypothetical protein. According to the homology analysis, our query protein shows structural similarities with other dioxygenase domain containing proteins from different Mycobacterium species. 5 results of homology searching is presented in the Table 2.

**Table 2. Protein similarity is shown by the BLASTp result.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Accession no.** | **Organism** | **Protein Name** | **Score** | **Percent Identity** | **E-Value** |
| WP\_198965783.1 | Mycobacterium shottsii | Hypothetical Protein | 434 | 99.13% | 8e-153 |
| WP\_011741159.1 | Mycobacterium ulcerans | Hypothetical Protein | 431 | 97.84% | 2e-151 |
| WP\_036411733.1 | Mycobacterium gastri | Hypothetical Protein | 290 | 67.10% | 8e-96 |
| WP\_103802134.1 | Mycobacterium kansasii | Hypothetical Protein | 288 | 69.26% | 8e-95 |
| WP\_083111484.1 | Mycobacterium Angelicum | Hypothetical Protein | 281 | 65.80% | 4e-92 |

**3.2 Physicochemical Characterisation**

The amino acid sequence of WP\_020728386.1 present in *Mycobacterium marinum* was retrieved in FASTA format for use as a query sequence to determine physicochemical parameters. The instability index of WP\_020728386 is 33.61(<40), indicating the stable nature of the protein (Guruprasad et al. 1990). The protein has a molecular weight of 23253.66 Da and is naturally acidic (pI 4.66\*). Cystine is present according to extinction coefficient values (21095). Higher aliphatic index values (106.49) suggest an eventual factor of increased thermo stability of the query protein for a wide temperature range. Since the protein is hydrophobic, the higher grand average of hydropathicity (GRAVY) index value (0.367) suggests that there may be less interaction with water (Table 3). The ExPASy ProtParam tool was put to use to determine the amino acid composition, where Alanine (16.5%) was the most prevalent amino acid, and methionine (0.4%) was the least abundant amino acid. The amino acid composition can help us to reveal the active amino acid pocket for drug and vaccine targeting against the protein (Saikat and Ripon 2020).

**Table 3. Physiochemical properties**

|  |  |
| --- | --- |
| **Characteristics** | **Value** |
| Molecular weight | 23253.66 |
| Theoretical pI | 4.66 |
| Total number of negatively charged residues (Asp + Glu) | 22 |
| Total number of positively charged residues (Arg + Lys) | 14 |
| Formula | C1042H1665N287O307S4 |
| Total number of atoms | 3305 |
| The estimated half-life | 1. 30 hours (mammalian reticulocytes, *in vitro*)
2. 20 hours (yeast, *in vivo*)
3. 10 hours (*Escherichia coli, in vivo*)
 |
| Instability index (II) | 33.61 |
| Aliphatic index | 106.49 |
| Grand average of hydropathicity (GRAVY) | 0.367 |

**3.3 Subcellular location determination**

Subcellular localisations dictate the circumstances in which proteins operate. This subcellular localisation is important as it can influence protein function through controlling a range of molecular interaction partners' accessibility and availability. A protein's subcellular localisation can be used to identify it as a therapeutic or vaccination target (Shahbaaz et al. 2013). The studied WP\_020728386.1 hypothetical protein is a membrane protein predicted by CELLO v.2.5. Also, this serverpredicted the localisation of physico-chemical comp., partitioned seq. comp., neighbouring seq. comp., amino acid comp. and N-peptide comp. values of 0.933, 0.743, 0.527, 0.634 and 0.570, respectively (Table 4). Proteins found in surface membranes may serve as potential vaccination targets, while cytoplasmic proteins are thought to be powerful pharmacological targets (Vetrivel et al. 2011). This type of subcellular identification research suggests that the hypothetical protein might be helpful in disease recovery through introducing various novel medicines.

**Table 4. Analysis of subcellular localization**

|  |  |  |
| --- | --- | --- |
| **Support Vector Machine (SVM)** | **Localization** | **Reliability** |
| Amino Acid Comp. | Cytoplasmic | 0.634 |
| N-peptide Comp. | Extracellular | 0.570 |
| Partitioned seq. Comp. | Membrane | 0.743 |
| Physico-chemical Comp. | Membrane | 0.933 |
| Neighboring seq. Comp. | Membrane | 0.527 |
| Subcellular localization Predictor (CELLO) value | Membrane | 2.543 \* |
| Cytoplasmic | 1.353 |
| Extracellular | 1.066 |
| CellWall | 0.038 |

\*CELLO predicted the subcellular location of the hypothetical protein as membrane

**3.4 Functional Annotation Assessment**

A component of NCBI's Entrez query and retrieval system, CDD (the Conserved Domain Database) annotates protein sequences with the location of conserved domain footprints and functional locations assumed from these footprints (Marchler-Bauer et al. 2012). According to the conserved domain search (CD-search), the chosen hypothetical protein had one domain. The anticipated domain is Extradiol\_Dioxygenase\_3B\_like super family, indicating class III extradiol ring-cleavage dioxygenase family protein (pfam accession: pfam cl00599, Interval: 7-229, E-value: 3.84\*1031). These family proteins can catalyze the incorporation of the atoms of molecular oxygen into substrates, leading to ring cleavage in aromatics by using different reaction mechanisms. Two main categories of dioxygenases exist as per the cleavage pattern of aromatic ring: Intradiol enzymes cleave the aromatic ring between two hydroxyl groups by utilising non-heme Fe (III), while extradiol enzymes cleave the aromatic ring between a hydroxylated carbon and an adjacent non-hydroxylated carbon by utilising non-heme Fe (II). Again, Extradiol dioxygenases are of three classes. Class I and II enzymes have sequence similarity while they are evolutionarily related, class II enzymes having two domains evolving from class I enzymes through the process of gene duplication. Class III enzymes have two subunits (A and B) and have differences in sequence and structure from the other two classes, I and II. This model includes the catalytic subunit B of extradiol dioxygenase class III enzymes. However, Class III enzymes belonging to this family include 2'-aminobiphenyl-2,3-diol 1,2-dioxygenase (CarB), Protocatechuate 4,5-dioxygenase (LigAB), 3,4-dihydroxyphenylacetate (homoprotocatechuate) 2,3-dioxygenase (HPCD) and 4,5-DOPA Dioxygenase, 2,3-dihydroxyphenylpropionate 1,2-dioxygenase.

Dioxygenases are required for the aerobic breakdown of aromatic compounds by bacteria as they catalyse the oxygenolytic fission of catecholic chemicals. Again, extradiol dioxygenases seem to be more adaptable than their intradiol equivalents. Nevertheless, Extradiol dioxygenases can cleave a greater range of substrates, have evolved on more structural scaffolds, and are found in a greater range of passageways, such as those that break down non-aromatic substances and biosynthetic pathways. (Vaillancourt et al. 2006).

Research conducted by Senda et al. (1996) and Han et al. (1995) revealed X-ray crystal structures of extradiol dioxygenases, which have come to be known as the 2-His-1-carboxylate facial triad motif for metal binding at the active site. More than 20 families of enzymes with a wide range of catalytic activity can use the motif.

**3.5 Secondary structure detection**

The structure and function of proteins are closely associated. Secondary structural components, namely helices, coils, sheets, and turns, exhibit a remarkable correlation with protein function, structure, and engagement. (Uchôa et al. 2004; Padjaseket al. 2020; Zhang et al. 2018; Rademaker et al. 2020; Wardah et al. 2019). The secondary structure prediction server SOPMA analyzed the proportions of alpha helix, extended strand, and the random coil of the studied protein as 36.36%, 17.32%, and 46.32%, respectively (Fig. 1). Again, The PSIPRED software estimates the helix, strand, and coil of the matrix protein (WP\_020728386.1) with more assurance (Fig. 2).



**Fig. 1. Predicted secondary structure from multiple alignments using SOPMA server.**



**Fig. 2. The target protein’s Secondary structure was determined using the PSIPRED server.**

**3.6 Tertiary structure prediction and validation:**

Homology modelling is an efficient technique for getting the three-dimensional structure (3D) of a hypothetical protein based on identity between the template and target protein sequences. The sequence of WP\_020728386.1 in FASTA format was inserted into the Swiss-Modelserver as input for homology modelling. The server completed the BLASTP search against each protein sequence to identify homologous templates, and the most suitable template (TK2203) was picked with a 100% probability rate. GMQE (Global Model Quality Estimation) is 0.60 for this template. The chosen model's GMQE and QMEAN values indicated that it might be a higher-quality and more dependable model. Fig. 3 represents the structure generated through SWISS\_MODEL.



**Fig. 3. Structure in three dimensions that is generated by the SWISS-Model tool.**

The tertiary structure of matrix protein was assessed employing the Ramachandran plot by PROCHECK program (Fig. 4a), which showed that 91.0 percent of the total residues (462) resided in the core [A, B, L]; 8.1 percent of residues were present in the additional allowed regions [a,b,l,p]; and 0.6 percent of residues were in the generously allowed regions [a,b,l,p]. There were 60 and 44 glycine and proline residues, respectively (Table 5). However, it can be said a valid model as 91.0% residues were found in the most favoured region. Hooda *et al* suggested that it is acceptable to have more than 90% of the residues in the most favoured regions, which is likely to be a valid 3D model (Hooda et al. 2012).

The Prosa-eb server was utilised for standard bond angles identification in the predicted tertiary structures of the studied protein WP\_020728386.1. Here, the constructed tertiary structures from the Swiss-Model server had a Z-score of -7.65 (Fig. 4b). Saikat et. al. reported that Z-scores obtained from the ProSA-web reveal the projected tertiary structures' "degree of nativeness" (Saikat et al. 2020).



**Fig. 4. a) Ramachandran plot of the structural model, verified by the PROCHECK program b) The overall model quality by Z-score (-7.65) obtained from the ProSA-web.**

**Table 5. Analysis of the hypothetical protein's Ramachandran plot statistics**

|  |  |  |
| --- | --- | --- |
| **Statistics** | **Residues** | **Percentage (%)** |
| Residues in the most favored regions [A, B, L] | 324 | 91 |
| Residues in the additional allowed regions [a, b, l, p] | 29 | 8.1 |
| Residues in the generously allowed regions [~a, ~b, ~l,~p] | 2 | 0.6 |
| Residues in disallowed regions | 1 | 0.3 |
| Number of nonglycine and nonproline residues | 356 | 100 |
| Number of end-residues (excl, Gly and Pro) | 2 |  |
| Number of glycine residues (shown as triangles) | 60 |  |
| Number of proline residues | 44 |  |
| Total number of residues | 462 |  |

**3.7 Active site determination:**

The active sites were identified for the hypothetical protein's amino acid residues through the Computer Atlas of Surface Topography of Protein (CASTp) website. According to the CASTp calculation result, a total of 141 {69(chain A), 72 (chain B)} amino acids are included in the potent active site. Based on the predicted active site of the protein, areas covered the best active site 3242.393 which occupied a volume of amino acids 5258.349. Residues of amino acids in the ligand binding site are presented in Fig. 5.



**Fig.5. Active site of the hypothetical protein WP\_020728386.1 (the active sites are highlighted by the red sphere).**

**4. CONCLUSION**

For manipulating biological processes, proteins functional annotation is indispensable. Predicting physicochemical parameters, the predicted active site of ligand binding, and overall fundamental features of the hypothetical protein provide insight into the studied protein, identifying it as functional and potentially useful. It is expected that a variety of useful therapeutic goods, as well as nutritious food items, could be produced from the selected hypothetical protein. Ultimately, this study may boost and broaden our knowledge of pathophysiology, which would help to develop potent therapeutic drugs and vaccines against the infection by *Mycobacterium marinum.*

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