Multiple structural and functional annotations based in-silico characterization of Q9BRX8 protein

Eiman Zahid
Muhammad Farhan Sarwar

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Multiple structural and functional annotations based in-silico characterization of Q9BRX8 protein

Abstract
Numerous proteins found in humans are poorly understood because there is a dearth of experimental evidence. Hypothetical proteins (HPs) or uncharacterized proteins are the terms used to describe these proteins. In this work, one of these proteins, Q9BRX8, is investigated using in-silico or bioinformatics tools to reveal its significant properties. In this regard, NCBI for the sequence retrieval, ProtParam tool for analysis of physiochemical properties, SOPMA for secondary structure prediction, SWISS-Model for homology modelling, STRING for protein-protein interaction and HDOCK for protein-protein docking analysis among other tools, were incorporated. The physiochemical characteristics indicated that Q9BRX8, which has an instability score of 32.57, is a stable protein. It was identified in other cellular compartments, such as the cytosol, mitochondria, etc., where it may be betrothed in a variety of cellular functions, according to the sub-cellular localization studies. In addition, its secondary structure consists of high percentage of alpha helices (44.10%), among other components. Additionally, it was discovered through protein-protein interactions that this protein belongs to FAM213A family suggesting that it may function as antioxidant and affect bone resorption among other crucial functions. While, molecular docking analysis indicated that Q9BRX8 had a larger degree of similarity with the HLA-G protein, scoring -332.53kcal/mol. It can be hypothesized that the functions of Q9BRX8 and the HLA-G may be associated as a result of this similarity.

Keywords
Characterization, Homo sapiens, Hypothetical protein, In-silico analysis, Q9BRX8 protein

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Multiple Structural and Functional Annotations Based *In-silico* Characterization of Q9BRX8 Protein

Eiman Zahid, Muhammad Farhan Sarwar*  

Department of Biotechnology, Knowledge Unit of Science, University of Management and Technology (UMT), Sialkot, Punjab, Pakistan

Abstract

Numerous proteins found in humans are poorly understood because there is a dearth of experimental evidence. Hypothetical proteins (HPs) or uncharacterized proteins are the terms used to describe these proteins. In this work, one of these proteins, Q9BRX8, is investigated using *in-silico* or bioinformatics tools to reveal its significant properties. In this regard, NCBI for the sequence retrieval, ProtParam tool for analysis of physiochemical properties, SOPMA for secondary structure prediction, SWISS-Model for homology modelling, STRING for protein–protein interaction and HDOCK for protein–protein docking analysis among other tools, were incorporated. The physiochemical characteristics indicated that Q9BRX8, which has an instability score of 32.57, is a stable protein. It was identified in other cellular compartments, such as the cytosol, mitochondria, etc., where it may be betrothed in a variety of cellular functions, according to the sub-cellular localization studies. In addition, its secondary structure consists of high percentage of alpha helices (44.10%), among other components. Additionally, it was discovered through protein–protein interactions that this protein belongs to FAM213A family suggesting that it may function as antioxidant and affect bone resorption among other crucial functions. While, molecular docking analysis indicated that Q9BRX8 had a larger degree of similarity with the HLA-G protein, scoring $\approx 332.53$ kcal/mol. It can be hypothesized that the functions of Q9BRX8 and the HLA-G may be associated as a result of this similarity.

Keywords: Characterization, *Homo sapiens*, Hypothetical protein, *In-silico* analysis, Q9BRX8 protein

1. Introduction

Hypothetical proteins (HPs) are those whose translation from a certain open reading frame (ORF) is predicted, but for which there is no experimental support. These hypothetical proteins (HPs) come in two different varieties. One class is comprised of uncharacterized protein families (UPFs), and the other encompasses the domain with unknown functions (DUFs). The majority of hypothetical proteins are produced via pseudogenes, hence it’s essential to have a method to identify HPs that have a high likelihood of being discovered [1]. These proteins, which fall under the category of “domains of unknown functions” (DUFs), have been experimentally identified yet lack any structural or functional domains. They may possess coiled-coil or transmembrane regions that make it impossible to attribute a function to them [2]. It is necessary to annotate them using various techniques in order to examine their properties. The use of these HPs as markers and pharmacological targets in the discovery, development, and testing of new medications is made possible by the annotations of new functions and pathways revealed by multiple analyses performed on these HPs [3].

In this regard, a variety of bioinformatics tools can be used to forecast the structural and functional characteristics of such proteins [4]. According to data from the Protein Data Bank (PDB), about 42.53% of entries are actually real examples of proteins with unknown characteristics, or uncharacterized proteins. 1465entities, however, can be reassessed in light of their direct functional characterization or structures, enabling the inference of computational function [5]. Microfluidics can be utilized in addition...
to the most popular bioinformatics techniques to represent the physiochemical properties of proteins. The four biological parents of the field of microfluidics are molecular analysis, biodefense, molecular biology, and microelectronics [6].

The Pfam database (http://pfam.xfam.org), which contains information about many protein families and their distinctive characteristics, is typically used to learn more about these proteins. Pfam provides functional annotation, database links, and literature citations for each family [7]. This database was mainly developed to give insights and increase or update the collected data regarding the related families of proteins over times [8]. Almost 22% of all protein domains in Pfam, there is a domain containing the proteins with uncharacterized features known as the domain of unknown functions (DUFs) [9].

One such uncharacterized protein, thought to be translated from the human chromosome 10 open reading frame 58 (C10orf58) gene, was subjected to this study. 'Q9BRX8' protein is the common designation under which it is listed in various databases. According to our findings, the protein Q9BRX8 inhibits the TNFSF11-induced activation of JUN, NFKB1, and osteoclast development in addition to acting as an antioxidant. The nucleus is anticipated to be its subcellular site. Additionally, it has been discovered to influence bone absorption and aid in preserving bone mass. The protein Q9BRX8 is anticipated to function as a suppressor of macrophage-induced inflammation by limiting the production of inflammatory cytokines, most likely through blocking the MAPK signaling pathway. The two reported alternatively spliced human isoforms. Additionally, Q9BRX8 protein is actually FAM213A-like protein which shows the antioxidant activity [10].

2. Materials and methods

2.1. Sequence retrieval

The sequence of this uncharacterized protein i.e. Q9BRX8 from human beings was obtained from NCBI (National Center for Biotechnology Information) using FASTA format (https://www.ncbi.nlm.nih.gov/) [11].

2.2. Physiochemical characterization

For physiochemical characterization of Q9BRX8 protein, ProtParam tool on ExPASy is employed [12] to find number of amino acids, isoelectric point, molecular weight, aliphatic index, extinction coefficient, total number of atoms, instability index as well as GRAVY (grand average of hydropathicity) of the uncharacterized protein (https://web.expasy.org/protparam/).

2.3. Subcellular localization prediction

The subcellular localization is predicted through COMPARTMENTS tool (https://compartments.jensenlab.org/) [13].

2.4. Structural analysis

SOPMA (Self-Optimized Prediction Method with Alignment) (https://npsa-prabi.ibcp.fr/NPSA/npsa_sopma.html) [14], an online tools is then further employed in order to forecast the secondary structure of Q9BRX8 protein. Moreover, to build a three dimensional (3D) model, SWISS-Model, an online structure prediction server is incorporated in this study (https://swissmodel.expasy.org/). SWISS-Model follows the comparative and homology modelling approach in order to build a three dimensional (3D) model of the given protein sequence. GMQE score, sequence identity and the coverage, are the parameters which are mostly considered to opt the predicted model.

2.5. Structure validation

For structure validation, PROCHECK server is employed (https://saves.mbi.ucla.edu/). This server analyzes the given.pdb format file of protein structure and then evaluate it through Ramachandran plot. This plot works on the basis of stereochemical properties of the amino acid residues of protein of interest and then plot them in one of the four quadrants. Steric hindrance and other properties of amino acid residues are analyzed in order to calculate their respective percentages in most favored, additionally allowed, generously allowed and disallowed region of Ramachandran plot [15].

2.6. Functional annotation

For further analysis and specifically to explore the functional sites in the Q9BRX8 protein, PredictProtein (https://predictprotein.org/) is utilized [16].

2.7. Protein family prediction

The protein family prediction analysis helps to give insights into the possible functions of the given protein. For this objective, the Pfam database (http://pfam.xfam.org/) which is now hosted by InterPro (https://www.ebi.ac.uk/interpro/search/sequence/)
is incorporated. Its results exhibit the detailed overview of the family and other important domains of the studied protein [17,18].

2.8. Prediction of phosphorylation sites

PhosphoSitePlus server (https://www.phosphosite.org/) is incorporated in order to predict the phosphorylation sites in Q9BRX8 protein.

2.9. Protein – protein interaction

Protein–protein interactions give a network of related proteins which further help in unveiling the functions of poorly understood proteins. This objective is achieved by utilizing an online tool named, ‘STRING’ which is available at https://stringdb.org/cgi/input?sessionId=boNvW0juxAXY &input_page_show_search=on [19].

2.10. Protein–protein docking analysis

To further validate the results of protein–protein interaction and assess the interaction affinities, protein–protein docking analysis is performed through a well-known online server, HDOCK SERVER (http://hdock.phys.hust.edu.cn/) [20]. All of the interacting proteins in the STRING protein network were docked with Q9BRX8 protein. The required structures were obtained one-by-one from the AlphaFold protein structure database (https://alphafold.ebi.ac.uk/). Furthermore, to perform docking analysis the.pdb files of the respective proteins were uploaded. The Q9BRX8 protein were kept as input receptor molecule while all the other proteins to be docked with it were uploaded in input ligand molecule section. The results of docking analysis represents the binding energies in kcal/mol which are analyzed to select the best docked protein.

3. Results

3.1. Amino acid composition & physiochemical characterization

The amino acid composition and physiochemical characterization are determined by ProtParam (https://web.expasy.org/protparam/). According to the findings, Q9BRX8 has a molecular weight of 25.76414 kDa and a predicted isoelectric point of 8.92. It also has 229 amino acids in it. Additionally, under this perspective, a total of 32 positively charged residues and 28 negatively charged residues are also predicted. Most importantly, it was discovered that the instability index was 32.57, suggesting that Q9BRX8 is a stable protein. Tables 1 and 2 provide detailed representations of additional significant parameters as follows:

<table>
<thead>
<tr>
<th>Table 1. Complete amino acid composition along their individual quantities and percentages in Q9BRX8 protein.</th>
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</thead>
<tbody>
<tr>
<td>Sr. no.</td>
</tr>
<tr>
<td>1.</td>
</tr>
<tr>
<td>2.</td>
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<tr>
<td>3.</td>
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<tr>
<td>4.</td>
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<tr>
<td>5.</td>
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<tr>
<td>6.</td>
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<td>10.</td>
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<tr>
<td>11.</td>
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<tr>
<td>12.</td>
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<tr>
<td>13.</td>
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<tr>
<td>14.</td>
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<tr>
<td>15.</td>
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<tr>
<td>16.</td>
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<tr>
<td>17.</td>
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<tr>
<td>18.</td>
</tr>
<tr>
<td>19.</td>
</tr>
<tr>
<td>20.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Table 2. The details of important physiochemical characteristics of Q9BRX8 protein.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sr. no.</td>
</tr>
<tr>
<td>1.</td>
</tr>
<tr>
<td>2.</td>
</tr>
<tr>
<td>3.</td>
</tr>
<tr>
<td>4.</td>
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<tr>
<td>5.</td>
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<tr>
<td>6.</td>
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<tr>
<td>7.</td>
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<tr>
<td>8.</td>
</tr>
<tr>
<td>9.</td>
</tr>
<tr>
<td>10.</td>
</tr>
</tbody>
</table>

3.2. Subcellular localization

The Q9BRX8 protein’s subcellular localization made a prediction that the protein would have a strong nuclear localization. It is discovered that it is also present in the cytosol in addition to the nucleus. This is relevant because ribosomes, the primary component of a cell’s machinery for synthesizing proteins, are found in the cytoplasm. The studies, however, also showed that this protein is expressed in the cytoskeleton, endoplasmic reticulum, mitochondria, and peroxisomes, among other cellular compartments (Table 3, Fig. 1).
3.3. Structure prediction

In this particular context, secondary structure and three dimensional (3D) model of Q9BRX8 protein is determined by SOPMA (https://npsa-prabi.ibcp.fr/NPSA/npsa_sopma.html) and SWISS-Model (https://swissmodel.expasy.org/) tools, respectively. The results of secondary structure prediction showed, the amino acid sequence length is 229. Secondary structure is predicted on the basis of parameters such as the number of confirmation states i.e. 4, the window width i.e. 17 as well the similarity threshold i.e. 8. The results of Q9BRX8 protein’s secondary structure estimation are displayed as (Fig. 2):

Following table shows respective number and percentages of alpha helices, beta sheets/strands, turns and coils in the secondary structure of Q9BRX8 protein (Table 4).

While, the tertiary structure of Q9BRX8 protein is obtained by subjecting the amino acid sequence of Q9BRX8 protein in FASTA format to SWISS-Model server. Two models were predicted in this regard. The first model was selected because its sequence identity was found to be 100% with that of the aligned template sequence. Moreover, its GMQE score was 0.88 which is considered to be a good value when choosing a protein structure from a

---

### Table 3. The details of subcellular localization by COMPARTMENT method.

<table>
<thead>
<tr>
<th>Sr. no.</th>
<th>Name</th>
<th>Z-score</th>
<th>Confidence</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Nucleus</td>
<td>3.9</td>
<td>2/5</td>
</tr>
<tr>
<td>2.</td>
<td>Mitochondrion</td>
<td>3.3</td>
<td>2/5</td>
</tr>
<tr>
<td>3.</td>
<td>Plasma Membrane</td>
<td>3.3</td>
<td>2/5</td>
</tr>
<tr>
<td>4.</td>
<td>Cytosol</td>
<td>3.2</td>
<td>2/5</td>
</tr>
<tr>
<td>5.</td>
<td>Cytoskeleton</td>
<td>3.2</td>
<td>2/5</td>
</tr>
<tr>
<td>6.</td>
<td>Extracellular region</td>
<td>3.6</td>
<td>2/5</td>
</tr>
<tr>
<td>7.</td>
<td>Protease Inhibitor Complex</td>
<td>3.0</td>
<td>2/5</td>
</tr>
<tr>
<td>8.</td>
<td>Peroxisome</td>
<td>1.9</td>
<td>1/5</td>
</tr>
<tr>
<td>9.</td>
<td>Vacuole</td>
<td>2.3</td>
<td>2/5</td>
</tr>
<tr>
<td>10.</td>
<td>Endoplasmic Reticulum</td>
<td>2.4</td>
<td>2/5</td>
</tr>
<tr>
<td>11.</td>
<td>BAX complex</td>
<td>1.8</td>
<td>1/5</td>
</tr>
<tr>
<td>12.</td>
<td>Cell wall</td>
<td>1.2</td>
<td>1/5</td>
</tr>
</tbody>
</table>

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![Fig. 1.](image1.jpg)

Fig. 1. The intensity of green color reveals the subcellular localization of Q9BRX8 protein in various cellular compartments in correspondence to the given scheme.

![Fig. 2.](image2.jpg)

Fig. 2. The figure shows the positions of alpha helices, beta sheets, turns and coils at their respective sites in the secondary structure of Q9BRX8 protein in the form of bars and peaks.
number of built structures. Following figure exhibits the 3D model or tertiary structure of Q9BRX8 protein (Fig. 3).

3.4. Evaluation of the protein model

After the construction of three dimensional protein model, it is highly necessary to evaluate its quality. For this particular objective, Ramachandran plot is incorporated. The results suggested that 90.4% of the total residues lie in the most favored region affirming the fact that the predicted model of Q9BRX8 protein is of good quality. While, 9.1% of the amino acid residues lie in the additionally allowed regions. The following figure demonstrates the Ramachandran plot. Moreover, its other calculated parameters are also represented in the figure below (see Fig. 4).

3.5. Functional sites

Every protein possess specific functional sites which assist it to interact with other proteins or other entities. To determine such sites in the Q9BRX8 protein we utilized a well-known tool named, PredictProtein. Since 1992, PredictProtein has predicted the structural and functional characteristics of the proteins as a meta-service for different analysis [21]. It examines current public sequence databases, generates alignments and makes predictions about multiple aspects of the protein. The users subject the query sequence and a single file including the results of database comparisons and prediction techniques is generated [22]. According to the results in Fig. 5, it was found that Q9BRX8 protein does not possess DNA and RNA binding sites while two protein binding sites were found between the amino acids 160 to 220. It reveals that the given protein is capable of interaction with the related proteins which can help to explore its functional characteristics.

Table 4. Summarized attributes of Q9BRX8 protein’s secondary structure.

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sequence Length</td>
<td>229</td>
</tr>
<tr>
<td>Alpha helix (Hh):</td>
<td>101 (44.10%)</td>
</tr>
<tr>
<td>3_10 helix (Gg):</td>
<td>0 (0.00%)</td>
</tr>
<tr>
<td>Pi helix (Ii):</td>
<td>0 (0.00%)</td>
</tr>
<tr>
<td>Beta bridge (Bb):</td>
<td>0 (0.00%)</td>
</tr>
<tr>
<td>Extended strand (Ee):</td>
<td>52 (22.71%)</td>
</tr>
<tr>
<td>Beta turn (Tt):</td>
<td>14 (6.11%)</td>
</tr>
<tr>
<td>Bend region (Ss):</td>
<td>0 (0.00%)</td>
</tr>
<tr>
<td>Random coil (Cc):</td>
<td>62 (27.07%)</td>
</tr>
<tr>
<td>Ambiguous states (?):</td>
<td>0 (0.00%)</td>
</tr>
<tr>
<td>Other states:</td>
<td>0 (0.00%)</td>
</tr>
<tr>
<td>Window width</td>
<td>17</td>
</tr>
<tr>
<td>Number of states</td>
<td>4</td>
</tr>
<tr>
<td>Similarity threshold</td>
<td>8</td>
</tr>
</tbody>
</table>

Fig. 3. Tertiary Structure Predicted by homology modelling approach in SWISS-Model.
Fig. 4. Ramachandran plot to evaluate the 3D model of Q9BRX8 protein.
3.6. Protein family of Q9BRX8

The results of family prediction of Q9BRX8 protein suggested that this protein possesses the peroxiredoxin like 2A/2B (PXL2A/2B) domain which infers that the given protein may play a crucial role in redox reaction in the cell. These results also suggest that it may also function in regulating various anti-inflammatory factors in the cell. Moreover, it can also be visualized in the following figure that Q9BRX8 protein also possesses the PRX-like2 residues. The possession of these results hypothesized that Q9BRX8 protein confer a protective antioxidant role in the cell. Furthermore, some of the important domains are also predicted in these results including the cytoplasmic, non-cytoplasmic and the transmembrane helices (Fig. 6).

![Predicted Features](image)

**Fig. 5. Predicted features by PredictProtein**

![Family prediction](image)

**Fig. 6. The result of protein family prediction. PXL2A/2B and PRX-like2 regions in Q9BRX8 protein can be visualized.**
3.7. Phosphorylation sites

Several phosphorylation sites are predicted in Q9BRX8 protein at different sites by PhosphoSitePlus online server (https://www.phosphosite.org/proteinAction?id=2410253&showAllSites=true). This server proposed some of the functions of our protein of interest including the antioxidant role, inhibition of TNFS11 induced NFKB1 and JUN activation. It also highlighted that Q9BRX8 protein belongs to PRXL2 family affirming its antioxidant function. Following figure demonstrates the results of PhosphoSitePlus server. It can be visualized that the given protein also possess the AhpC-TSA-2 region which also suggests that Q9BRX8 protein is an antioxidant protein (Fig. 7).

3.8. Protein—protein interactions

The results of protein—protein interaction in Fig. 5 were generated by STRING (https://string-db.org/). STRING subjects the amino acid sequence of the given protein to interact with the related protein in database and then presents the results in the form of a protein network. Protein—protein interactions showed that Q9BRX8 protein is interrelated with a variety of additional proteins too, including SELO, ACTB, GUSB and others. This protein—protein interaction showed its involvement in redox regulation of the cell and it may also work as an antioxidant agent in the cell. It is also found to be involved in the retarding the TNFSF11-induced NFKB1, activation of JUN as well as the osteoclast differentiation. These results also suggested that it may also play a role as a suppressor of the macrophages induced inflammation by retarding the macrophage specific production of inflammatory cytokines, most likely via an inhibiting MAPK signaling pathway. Moreover the interaction with the neighboring protein in the following protein network also shows its characteristic nature i.e., the peroxiredoxin-like FAM213A gene [23] (Fig. 8).

3.9. Protein—protein docking analysis

Protein—protein interactions are important for most of the biological roles. Protein—protein complexes functional mechanisms and roles in the cell can be understood by predicting three-dimensional structures of these complexes (docking). The complexes help in drug design by revealing...
information about the protein’s interfaces. The docking approach basically helps to infer the way of interacting macromolecules to elucidate the relevant phenomenon [24]. Based on the findings of STRING, docking analysis was carried out with the proteins in the network. Docking and confidence score were obtained in this context to figure out the best docked protein partners. It is usually

<table>
<thead>
<tr>
<th>Cartoon-cartoon view</th>
<th>Cartoon-surface view</th>
<th>Surface-surface view</th>
<th>Protein</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1" alt="Cartoon-cartoon view" /></td>
<td><img src="image2" alt="Cartoon-surface view" /></td>
<td><img src="image3" alt="Surface-surface view" /></td>
<td>PALM-Q9BRX8</td>
</tr>
<tr>
<td><img src="image4" alt="Cartoon-cartoon view" /></td>
<td><img src="image5" alt="Cartoon-surface view" /></td>
<td><img src="image6" alt="Surface-surface view" /></td>
<td>GUSB-Q9BRX8</td>
</tr>
<tr>
<td><img src="image7" alt="Cartoon-cartoon view" /></td>
<td><img src="image8" alt="Cartoon-surface view" /></td>
<td><img src="image9" alt="Surface-surface view" /></td>
<td>SELO-Q9BRX8</td>
</tr>
<tr>
<td><img src="image10" alt="Cartoon-cartoon view" /></td>
<td><img src="image11" alt="Cartoon-surface view" /></td>
<td><img src="image12" alt="Surface-surface view" /></td>
<td>GAPDH-Q9BRX8</td>
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<tr>
<td><img src="image13" alt="Cartoon-cartoon view" /></td>
<td><img src="image14" alt="Cartoon-surface view" /></td>
<td><img src="image15" alt="Surface-surface view" /></td>
<td>POTEF-Q9BRX8</td>
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<td><img src="image18" alt="Surface-surface view" /></td>
<td>ACTB-Q9BRX8</td>
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<tr>
<td><img src="image19" alt="Cartoon-cartoon view" /></td>
<td><img src="image20" alt="Cartoon-surface view" /></td>
<td><img src="image21" alt="Surface-surface view" /></td>
<td>HLA-G-Q9BRX8</td>
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</table>

Table 5. The figures in the following table display the results of docking analysis of Q9BRX8 protein with the interacting partners in the protein–protein network, in different layouts.
interpreted that if there is the highest negative docking score among two proteins then it would be preferred over others. Therefore, on the basis of such parameters, HLA-G showed the highest negative docking score i.e. −332.53 kcal/mol. It can be then hypothesized that Q9BRX8 protein may also possess the similar characteristics as that of HLA-G. The results of docking analysis are shown below in three different forms i.e. cartoon-surface view, cartoon—cartoon view and surface—surface view in the following table (Table 5).

4. Discussion

A putative protein from *Homo sapiens* called Q9BRX8 is specifically annotated in this work from a number of angles. Our research showed that the protein in question, with an instability score of 32.57, is a stable protein. This protein’s subcellular location is also predicted. It was decided to use the COMPARTMENT approach for this specific goal. Using this method, it was demonstrated that although the Q9BRX8 protein is mostly found in the nucleus, it is also present in other cellular components such as the cytosol and mitochondria and may be involved in a number of cellular metabolic pathways. It is predicted to be a nuclear protein because the projected score for its localization inside the nucleus was greatest. A related research work was done on hypothetical proteins from *Candida dubliniensis* in which various tools were employed in order to predict the sub-cellular localization of the targeted proteins [25].

Additionally, the results of SOPMA’s secondary structure prediction showed that the Q9BRX8 protein is made up of 44.10%, 22.71%, 6.11%, 27.07%, and 44.10%, respectively, of alpha helices, beta strands, twists, and random coils. In terms of the functional sites that were predicted for this protein, it was discovered that there were no sites for DNA or RNA binding, but that it did have two sites for protein binding between amino acids 160 and 220. A related study also reported the functions prediction of hypothetical proteins. The conclusive results of this study unveiled the non-pathogenesis related (NPR1)-like functions [26].

This study incorporates the protein family and phosphorylation sites predictions analyses in addition to the protein−protein interaction and protein−protein docking analysis to learn more about the Q9BRX8 protein, in particular, about its various characteristics. In this regard, initially it is inferred that Q9BRX8 protein belongs to PRXLA family proposing the possession of antioxidant function. Afterwards, the STRING-generated protein network of Q9BRX8 to get insights into the interacting protein members. This interaction was then subjected to protein−protein docking analysis which revealed to have a substantial relationship with the HLA-G protein. Since each of these proteins had a docking score of −332.53 kcal/mol, it was hypothesized that they might have comparable functions including the role in the immune system’s presentation of foreign antigens and in protecting the maternal fetus by fending off the negative effects of cytotoxic T lymphocytes, macrophages, and natural killer cells. The STRING approach also predicts that the Q9BRX8 protein will act as an antioxidant and delay the induction of NFKB1 by TNFSF11. Another study incorporating the protein−protein docking analysis was also performed to elucidate the interaction of sericin protein and cocoonase enzyme of silkworm for cocoon softening [27]. Our findings in this study can be helpful to get deeper insights into Q9BRX8 protein to explore more of its attributes so that it can be employed for various objectives.

5. Conclusion

In this study, we characterized the putative protein Q9BRX8 using a variety of *in-silico* approaches. In this regard, we found that the given protein is a nuclear protein when analyzed from the perspective of subcellular localization. With a low instability score of 32.57, it is predicted that this protein is stable. No DNA or RNA binding sites were found, although it does have two functional protein-binding sites between amino acids 160 and 220. An investigation of the protein−protein interaction also found significant interactions with the linked protein. The HLA-G protein, one of these proteins, showed the strongest relatedness among the others with a docking score of −332.53 kcal/mol.

The Q9BRX8 protein may perform similar tasks to the HLA-G protein, according to this docking score. On the basis of all of the findings of this study, it was therefore projected to draw the conclusion that Q9BRX8 protein may have important functions including the antioxidant role and regulating certain anti-inflammatory factors in the cell. This study will aid in the investigation of related proteins in a related manner. Thus, one could discover any significant function of the specified proteins in humans that might be of great interest due to its wide range of applications.

Funding

No funding was received in this study from any funding organization.
Conflict of interest

The author(s) declare(s) that they have no competing interests.

Acknowledgements

We appreciate the help of the colleagues of the Department of Biotechnology, University of Management and Technology (UMT) Sialkot, Pakistan.

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