ORIGINAL RESEARCH

Identification and analysis of potential targets in *Streptococcus sanguinis* using computer aided protein data analysis

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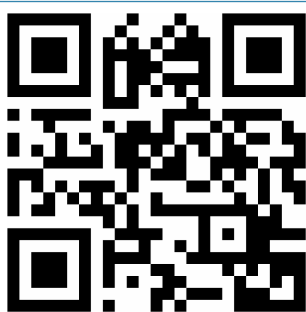
Point your SmartPhone at the code above. If you have a QR code reader the video abstract will appear. Or use:
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Purpose: *Streptococcus sanguinis* is a Gram-positive, facultative aerobic bacterium that is a member of the viridans streptococcus group. It is found in human mouths in dental plaque, which accounts for both dental cavities and bacterial endocarditis, and which entails a mortality rate of 25%. Although a range of remedial mediators have been found to control this organism, the effectiveness of agents such as penicillin, amoxicillin, trimethoprim–sulfamethoxazole, and erythromycin, was observed. The emphasis of this investigation was on finding substitute and efficient remedial approaches for the total destruction of this bacterium.

Materials and methods: In this computational study, various databases and online software were used to ascertain some specific targets of *S. sanguinis*. Particularly, the Kyoto Encyclopedia of Genes and Genomes databases were applied to determine human nonhomologous proteins, as well as the metabolic pathways involved with those proteins. Different software such as Phyre2, CastP, DoGSiteScorer, the Protein Function Predictor server, and STRING were utilized to evaluate the probable active drug binding site with its known function and protein–protein interaction.

Results: In this study, among 218 essential proteins of this pathogenic bacterium, 81 nonhomologous proteins were accrued, and 15 proteins that are unique in several metabolic pathways of *S. sanguinis* were isolated through metabolic pathway analysis. Furthermore, four essentially membrane-bound unique proteins that are involved in distinct metabolic pathways were revealed by this research. Active sites and druggable pockets of these selected proteins were investigated with bioinformatic techniques. In addition, this study also mentions the activity of those proteins, as well as their interactions with the other proteins.

Conclusion: Our findings helped to identify the type of protein to be considered as an efficient drug target. This study will pave the way for researchers to develop and discover more effective and specific therapeutic agents against *S. sanguinis*.

Keywords: *Streptococcus sanguinis,* essential proteins, unique metabolic pathways, therapeutic targets

Introduction

Streptococcus sanguinis, known earlier as *Streptococcus sanguis*, is a facultative, aerobic, Gram-positive, coccoid bacterium.[1] It is one of the microorganisms that pioneers the colonizing process because it binds to specific receptors on the obtained pellicle of the enamel surface.[2] Many species of viridans streptococcus cause endocarditis, although these bacteria rarely cause meningitis.[3] An intimate association between *S. sanguinis* and infection has been stated, and it has been seen that the clinical presentation and outcome are very much influenced by this bacterium.[4–8] *S. sanguinis*, moreover, is considered one of the most widespread agents of infective endocarditis

among the viridans streptococci.[9–11] It is a typical occupant of the human mouth and is predominantly found in dental plaque. It makes its surroundings favorable for other strains of *Streptococcus*, such as *S. mutans*, that are capable of causing cavities. An advantageous role within the oral cavity is normally played by the oral streptococci. Because of their habitation, the oral streptococci can be injected into the bloodstream through oral surgery or daily actions such as chewing and brushing.[12,13] Blood-borne bacteria may perhaps colonize in the endocardium or the cardiac valves that have been weakened by congenital circumstances or degenerative developments; this could result in transferable endocarditis.[14,15]

Oral streptococci are continuously subjected to environmental stressors. Saliva flow and intake of food cause vacillations in nutrient supply, pH, temperature, and other environmental conditions. *S. sanguinis* has the aptitude to use and integrate free extracellular DNA from the environments, an attribute also known as genetic competence.[16] This characteristic is shared by certain other bacteria, including more than a few oral streptococcal species.[17]

This study investigated the essential nonhuman homologue proteins of the unique pathways of *S. sanguinis* to determine their functions, their druggable pockets, the details of their metabolic pathways, and their associated proteins in other organisms.

Materials and methods

The methodical designation and delineation of the purported drug target of *S. sanguinis* was done strategically by the following methods.

Recognition of probable target proteins

Reclamation of indispensable proteins of *S. sanguinis*

In the beginning, with the help of the database of essential genes (DEG), 218 crucial genes of *S. sanguinis* were retrieved from the National Center for Biotechnology Information in FASTA format.[18,19]

Identifying human nonhomologous essential proteins in *S. sanguinis*

While the default constraints were kept unchanged, the retrieved 218 crucial proteins were put through BlastP at the National Center for Biotechnology Information server against *Homo sapiens*. To distinguish human nonhomologous essential proteins of *S. sanguinis*, proteins that have dissimilarities in threshold expectation values greater than 10^4 were considered. To do this, a protein database named Refseq was utilized.[20] Thus, the

human nonhomologous essential proteins of *S. sanguinis* were screened, as they form the bacterium's 218 crucial proteins.

Metabolic pathway analysis of human nonhomologous essential proteins in *S. sanguinis*

The screened human nonhomologous proteins of *S. sanguinis* were then subjected to a metabolic pathway investigation; this investigation was carried out by the KEGG Automatic Annotation Server (KAAS) at the Kyoto Encyclopedia of Genes and Genomes. The functional footnotes of the genes were made available by KAAS, along with the physically pastured KEGG GENES database. The functional annotation was also carried out by this server through a BlastP comparison of the genes.[21] Genes were separated according to their metabolic functions.

Exclusive metabolic pathway identification for *S. sanguinis*

Then, we identified those pathways of *S. sanguinis* that were not present in *H. sapiens*. Confrontation and comparisons of metabolic pathways of both *S. sanguinis* and *H. sapiens* were done by the use of the KEGG Genome Database, and incomparable metabolic pathways of *S sanguinis* were identified.[22] Among the distinct metabolic pathways of *S. sanguinis*, human nonhomologue essential proteins were identified.

Target protein identification of *S. sanguinis*

Subcellular localization of exclusive metabolic proteins (essential nonhuman homologues) of *S. sanguinis* was done by PSORTb to spot the proteins that are or might be available on the surface membrane.[23] Such an approach can be helpful to discover putative therapeutic targets.

Uncharacterized membrane-bound protein characterization

SVM-PORT was used for the depiction of uncharacterized membrane-bound hypothetical proteins.[24]

Characterization of target proteins

Three-dimensional structure development of target proteins

The three-dimensional (3D) structure for each of those four proteins was developed using Phyre2.[25] Phyre2 generates homology models by detecting homologues of known 3D structures. This is called template-based homology modeling, or protein recognition. Protein Data Bank files of those proteins were also downloaded from here.

Active site prediction of target proteins

CastP, a Web-based tool, was utilized in forecasting the active sites of the sequences of interest.[26] For the weighted Delaunay triangulation and the contour measurements of the alpha complex, CastP was utilized to identify and measure the surface attainable pockets, as well as accessible interior cavities of proteins and other molecules. Methodologically, it determines the volume, as well as the area of each cavity and pocket. Both the molecular surface (Connolly's surface) and the solvent accessible surface (Richards' surface) are calculated. For each pocket, the number of mouth openings, the circumferences of the mouth lips, and the areas of the openings – both the solvent accessible surface and the molecular surface – can be calculated with this tool.[27]

Druggable pocket identification

DoGSiteScorer is a Web-based tool that can provide qualitatively and quantitatively valuable data for druggability assessment.[28] By the use of this tool, the druggability of a pocket can be automatically predicted on the basis of size, shape, and chemical features. Moreover, DoGSiteScorer is helpful to assess amino acid composition, functional groups, and elements that can be present on the targeted pocket. Considering all descriptors, DoGSiteScorer provides a drug score value (0–1) for a selected pocket. The higher the score, the more druggable the pocket is estimated to be.

Functional properties analysis of target proteins

A specially designed tool, the Protein Function Prediction server from Kihara Bioinformatics Laboratory (Purdue University, West Lafayette, IN, USA), was utilized for the functional analysis of these proteins.[29] The amino acid sequences that were used as the input data were taken in FASTA format.

Protein–protein interaction predictions for target proteins

For conceding and prognosticating protein–protein interactions, an infallible database named STRING (Search Tools for the Retrieval of Interacting Genes/Proteins) was used.[30] The association of both physical and functional traits was assembled from four sources: Genomic Context; High-throughput Experiments; (Conserved) Co-expression; and Previous Knowledge. STRING quantitatively consolidates data interaction from these sources for a large number of organisms and sends information between these organisms when it is pertinent. This database covers 5,214,234 proteins from 1,133 organisms.[31]

Results and discussion

The present study revealed 81 essential nonhomologous metabolic proteins, of which 17 are membrane-bound proteins and 15 are metabolic proteins in unique pathways. Of these 15 proteins, only four proteins are essential nonhuman homologous membrane-bound proteins and, therefore, can be potential drug targets. For more specification, we have also examined the active sites of these four proteins, as well as their interactions with other proteins. On the basis of these results, drugs can be synthesized to more specifically target and more effectively kill *S. sanguinis* without harming the host.

This study was conducted with the intention of establishing possible therapeutic targets for alternative treatments of MRSA (methicillin-resistant *S. aureus*) and also to classify and investigate the targets. Utilization of the subtractive genomic approach was carried out in this study. The fundamental principle of the subtractive genomic approach is "a good therapeutic target is a gene/protein essential for the bacterial survival, [but] which cannot be found in host".[32] At the beginning, indispensable proteins of *S. sanguinis* were recovered from the DEG. The definition of essential genes is a minimal set of genes that is sufficient for the continued existence of a cellular life form under complementary conditions.[33]

With an intention to avoid any cross-reactivity of the recognized drug with the human host, BlastP was performed alongside the 218 essential proteins and then the 81 nonhuman homologue proteins having a threshold expectation value greater than 10^4. To find out additional characteristics of the nonhuman homologous vital proteins of *S. sanguinis*, a metabolic pathway investigation was carried out by the KAAS server at the KEGG. The outcome was a set of 65 proteins that were involved in 37 metabolic pathways that were particularly classified into 12 classes (Table 1). With an aim to determine which of the 65 metabolic proteins were possible drug targets, a comparative study was carried out in the metabolic pathways of human host and *S. sanguinis* in the KEGG Genome database. This analysis revealed 15 exclusive pathways; this finding indicated that these metabolic pathways are in *S. sanguinis*, but not in the human host. Also, 15 proteins were found that are involved in these exclusive pathways. Four of the 15 proteins in these pathways were found in cytoplasmic membranes. We examined these four proteins for more details. Those 15 proteins were present on four dissimilar, distinctive pathways. Eight out of the 15 proteins are in the peptidoglycan biosynthesis pathway, four of them are in the photosynthesis pathway, two of them are in the D-alanine

Table I Metabolic pathways of human nonhomologous proteins

Pathways	Related gene (KO number)
I. Energy metabolism	
a. Oxidative phosphorylation	K02110, K15986, K02110, K02109, K02113, K02114
b. Methane metabolism	K01624
c. Carbon fixation in photosynthetic organism	K01624
d. Carbon fixation pathways in prokaryotes	K01962
e. Photosynthesis	K02109, K02113, K02114, K02110
2. Carbohydrate metabolism	
a. Pentose phosphate pathways	K01624
b. Glycolysis	K01624
c. Fructose and mannose metabolism	K01624
d. Pyruvate metabolism	K01962
e. Propionate metabolism	K01962
3. Lipid metabolism	
a. Glycerolipid metabolism	K00655, K08591
b. Glycerophospolipid metabolism	K00655, K08591
c. Fatty acid biosynthesis	K01962, K02372, K02371, K00648
4. Nucleotide metabolism	
a. Purine metabolism	K02338, K03076, K02340, K02337, K02341, K03763
b. Pyrimidine metabolism	K02338, K03076, K02340, K02337, K02341, K00943, K03763
5. Amino acid metabolism	
a. Lysine biosynthesis	K01929, K01928
6 Metabolism of other amino acids:	
a. D-alanine metabolism	K01775, K01921
b. D-glutamine and D-glutamate metabolism	K01925, K01924, K01776
7. Glycan biosynthesis and metabolism	
a. Peptidoglycan biosynthesis	K01925, K02563, K01921, K01929, K01928, K05363, K05362, K01924
8. Membrane transport	
a. ABC transport	K09811, K02040, K02038
b. Bacterial secretion system	K03076, K03070, K03075, K03073
9. Protein export	K03076, K03070, K03075, K03073
10. Genetic information processing	
a. DNA replication	K02338, K03111, K02340, K02316, K02337, K02341, K03763, K02314
b. Mismatch repair	K02338, K03111, K02340, K02337, K02341, K03763
c. Homologous recombination	K02338, K03111, K02340, K02337, K02341, K03763
d. Ribosome	K02982, K02881, K02990, K02961, K02892
e. RNA polymerase	K03076
f. Amioacyl tRNA biosynthesis	K02435, K01879, K01878
II. Vitamin biosynthesis	
a. Folate biosynthesis	K00796, K00950
b. Pentothenate and CoA biosynthesis	K00997, K00954
c. Biotin	K02372
d. Nicotinate and nicotinamide metabolism	K01916

(*Continued*)

Table I (*Continued*)

Pathways	Related gene (KO number)
12. Other	
a. Tuberculosis	K02040
b. Cell-cycle caulobacter	K02313, K02563, K03531, K03588, K02314
c. Tetracycline biosynthesis	K01962
d. Two-component system	K02313, K02040, K07668
e. Terpenoid backbone biosynthesis	K00938

Abbreviations: KO, KEGG organism; ABC, adenosine triphosphate binding cassette; tRNA, transfer RNA; CoA, coenzyme A.

metabolism pathway, and the remaining one is in the tetracycline biosynthesis pathway. For additional categorization and forecasting, the subcellular localization of pathogenic proteins and computational characterization of hypothetical proteins were carried out, and this provided a faster way to recognize cell surface drug targets (Table 2).[34]

Our investigation uncovered 15 essential nonhuman homologue proteins, of which four are membranous proteins. The four proteins are undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase (gene reference 125717508), polysaccharide biosynthesis protein (gene reference 125718537), adenosine triphosphate (ATP) synthase F0F1 subunit C (gene reference 125717630), and ATP synthase F0F1 subunit B (gene reference 125717632). These four proteins can be potential targets against *S. sanguinis*.

We have discovered indispensable metabolic nonhuman homologue proteins in the exclusive metabolism pathways. Both in vitro and in vivo studies indicate that inhibitors that are designed for targeting these proteins have the potential to efficiently hold back bacterial growth by passing the bacterial mutation site for drug confrontation. The reason behind such activity is that almost all existing antibiotics are able to target just four pathways (cell wall synthesis, protein synthesis, nucleic acid synthesis, and folate synthesis).[35] Thus, such frequent contact with the same site amplifies the possibility of mutation to the site; this results in mutant bacteria.[35,36] Targets among these pathways have revealed their potential for antibacterial agents (for example, oligomycin, antimycin A), but are not utilized in human cases because of the unsafe outcomes for both bacteria and humans. However, the proteins that are revealed in this study are human nonhomologues and, therefore, can be used as drug targets to reduce the baneful consequences of the drug for the human host.[36]

Membrane proteins received particular consideration because among all the drug targets, 60% are membrane proteins. Membrane proteins are also easier to explore by means of computational techniques rather than experimental methods

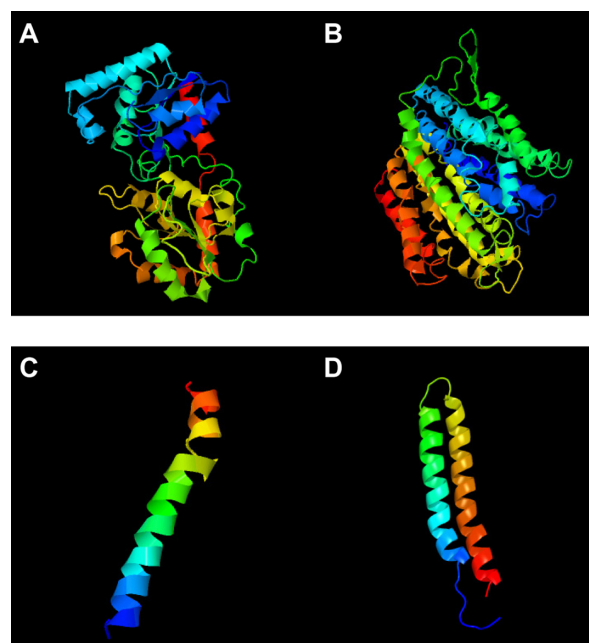**Table 2** Unique metabolism pathways and related proteins

Metabolism pathways	Gene reference	KO code	Membrane-bound
D-alanine metabolism	125717409	K01775	No
D-alanine metabolism	125717545	K01921	No
Peptidoglycan biosynthesis	125717507	K01925	No
Peptidoglycan biosynthesis	125717508	K02563	Yes
Peptidoglycan biosynthesis	125717545	K01921	No
Peptidoglycan biosynthesis	125717546	K01929	No
Peptidoglycan biosynthesis	125717649	K01928	No
Peptidoglycan biosynthesis	125717705	K05363	No
Peptidoglycan biosynthesis	125718537	K05362	Yes
Peptidoglycan biosynthesis	125718599	K01924	No
Tetracycline biosynthesis	125718722	K01962	No
Photosynthesis	125717632	K02109	Yes
Photosynthesis	125717630	K02110	Yes
Photosynthesis	125717633	K02113	No
Photosynthesis	125717637	K02114	No

Abbreviation: KO, KEGG organism.

Figure 1 3D structures.
Notes: (**A**) Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase; (**B**) polysaccharide biosynthesis protein; (**C**) ATP synthase F0F1 subunit B; and (**D**) ATP synthase F0F1 subunit C.
Abbreviations: 3D, three-dimensional; ATP, adenosine triphosphate.

because of their standardized interactions and structures. Proteins have a high tendency to assemble secondary structures consecutively, which lowers the difficulty of predicting the protein structure by computational means. If an elevated resolution structure is not established, computer-based structure forecasting can be done easily with membrane proteins, and the prediction of a structure-based drug can be carried out.[37]

The 3D structure of undecaprenyldiphospho-muramoyl-pentapeptide beta-N- acetylglucosaminyltransferase was developed based on the d1f0ka template. Here, 96% of the sequence was covered with 100% confidence (Figure 1A). In the case of the polysaccharide biosynthesis protein, coverage was 80%, but the confidence level was 100%. Here, the c41z9A template was used (Figure 1B). However, the confidence level was much lower in the case of ATP synthase F0F1 subunit B. The c1b9uA template was used here as a base (Figure 1C). The last target protein developed was based on c1wu0A, and the confidence level and coverage were 99.9% and 98%, respectively (Figure 1D).

In this study, we have also evaluated the best active site area of the aforementioned four experimental proteins, along with the number of amino acids involved with that site.

Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase is a human nonhomologous essential protein involved in a unique metabolism pathway named peptidoglycan biosynthesis. This can be found on the inner membrane, the organelle membrane, or the cell membrane. This enzyme is responsible for some biological functions, such as apocarotenoid metabolism, cell wall synthesis, regulation of gene expression via a specific molecular function such as transferase activity, binding, and undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase activity (Table 3 and Figure 2A).[8]

In *S. sanguinis* SK36, the polysaccharide biosynthesis protein is also a human nonhomologous protein that plays an identical role in peptidoglycan biosynthesis. Its cellular components include the nucleotide excision repair complex. Besides the biological function of peptidoglycan, the protein shows renilla-luciferin 2-monooxygenase activity as a molecular function (Table 3 and Figure 2B).

ATP synthase F0F1 subunit B is a common enzyme found in various species. This enzyme also shows unique activity in *S. sanguinis* SK36. Similar to ATP synthase F0F1 subunit C, ATP synthase F0F1 subunit B is also involved in photosynthesis. The hydrogen-translocating F-type ATPase complex and proton-transporting ATP synthase complex are some examples of its cellular components. Nucleoside triphosphate

Table 3 Molecular function, biological process, and cellular components of selected proteins

Proteins	Molecular function	Biological process	Cellular component
Undecaprenyldiphospho-muramoylpentapeptide beta-N acetylglucosaminyltransferase	Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase activity	Apocarotenoid metabolism	Inner membrane
	Binding	Cell wall biosynthesis	Organelle membrane
	Transferase activity	Regulation of gene expression, epigenetic	Cell wall
	Transferase activity, transferring hexosyl groups	Regulation of biological process	Membrane
	DNA clamp loader activity		
Polysaccharide biosynthesis protein	Renilla-luciferin2-monooxygenase activity	Peptide metabolism	Nucleotide excision repair complex
ATP synthase F0F1 subunit B	Hydrolase activity, acting on acid anhydrides	Energy-coupled proton transport, against electrochemical gradient	Hydrogen-translocating F-type ATPase complex
	Cation-transporting ATPase activity	Regulation of biological process	Proton-transporting ATP synthase complex
	ATPase activity, coupled to transmembrane movement of ions	Nucleoside triphosphate biosynthesis	Proton-transporting ATP synthase complex, coupling factor F(o)
ATP synthase F0F1 subunit C	Cation-transporting ATPase activity	Hydrogen transport	Proton-transporting ATP synthase complex (sensuEukaryota)
	Transition metal ion transporter activity	Energy-coupled proton transport, against electrochemical gradient	Hydrogen-translocating F-type ATPase complex
	Hydrolase activity, acting on acid anhydrides	ATP metabolism	Intracellular organelle
	Intramolecularlyase activity	Purine nucleoside triphosphate metabolism	Proton-transporting ATP synthase complex
		Regulation of metabolism	Intracellular membrane-bound organelle
		ATP synthesis coupled proton transport	Proton-transporting ATP synthase complex, coupling factor F(o)
		Phosphorus metabolism	
		Nucleoside triphosphate biosynthesis	
		Regulation of cellular physiological process	

Abbreviation: ATP, adenosine triphosphate.

biosynthesis, regulation of biological processes, and energy-coupled proton transport against electrochemical gradients are the biological activities of this subunit. The ATP synthase F0F1 subunit B also performs some molecular functions, such as hydrolase activity, by acting on acid anhydridescation-transporting ATPase (Table 3 and Figure 2C).

ATP synthase F0F1 subunit C is also a membranous protein responsible for photosynthesis. This enzyme is a component of the proton-transporting ATP synthase complex (sensu Eukaryota), and intracellular organelle proton-transporting ATP synthase complex. ATP synthase F0F1 subunit C is responsible for hydrogen transport, ATP metabolism, phosphorus metabolism, and purine

nucleoside triphosphate metabolism. ATP synthase F0F1 subunit C is responsible for specific molecular functions such as cation-transporting ATPase activity, transition metal ion transporter activity, intramolecular lyase activity, hydrolase activity, and acting on acid anhydrides (Table 3 and Figure 2D).

Pockets are the surface concavities of protein where a substrate might bind. The prediction of protein druggability has been a widely discussed topic in the pharmaceutical community over the past few decades. The pharmaceutical industry has an urgent need to prioritize suitable drug targets because of the high attrition rate and failure rates in drug discovery and development. In our study, we have already discussed four
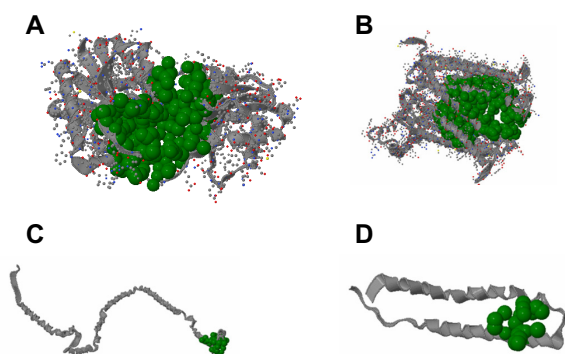
Figure 2 Active site information by CASTp.
Notes: (**A**) Active site information of undecaprenyldiphospho-muramoylpentapeptide beta-N acetylglucosaminyltransferase by CASTp. Green color shows the active site most highly positioned in area 1941.1 and volume 3,271.6 with the β-sheet in between them and the 3D representation of the best active site of undecaprenyldiphospho-muramoylpentapeptide beta-N acetylglucosaminyltransferase generated using CASTp. (**B**) Active site information of polysaccharide biosynthesis protein by CASTp. Green color shows the active site most highly positioned in area 3,802.1 and volume 6,383.1 with the β-sheet in between them and the 3D representation of the best active site polysaccharide biosynthesis protein generated using CASTp. (**C**) Active site information of ATP synthase F0F1 subunit B by CASTp. Green color shows the active site most highly positioned in area 189.1 and volume 410.2 with the β-sheet in between them, and the 3D representation of the best active site for ATP synthase F0F1 subunit B generated using CASTp. (**D**) Active site information of ATP synthase F0F1 subunit C by CASTp. Green color shows the active site most highly positioned in area 111.9 and volume 151.3 with the β-sheet in between them and the 3D representation of the best active site for ATP synthase F0F1 subunit C generated using CASTp.
Abbreviations: 3D, three-dimensional; ATP, adenosine triphosphate; CASTp, computed area of surface tomography of protein.

Figure 3 Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyl-transferase protein pockets 1 and 2, and polysaccharide biosynthesis protein pockets 6 and 7.
Notes: (**A**) Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyl-transferase protein, pocket 1. (**B**) Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase protein, pocket 2. (**C**) Polysaccharide biosynthesis protein, pocket 6. (**D**) Polysaccharide biosynthesis protein, pocket 7.

targeted proteins for *S. sanguinis* drug targets. These proteins have been further investigated to determine the specific pockets that are best able to bind with a drug. Using DoGSiteScorer, we uncovered 13 pockets from the undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase protein. Furthermore, the polysaccharide biosynthesis protein
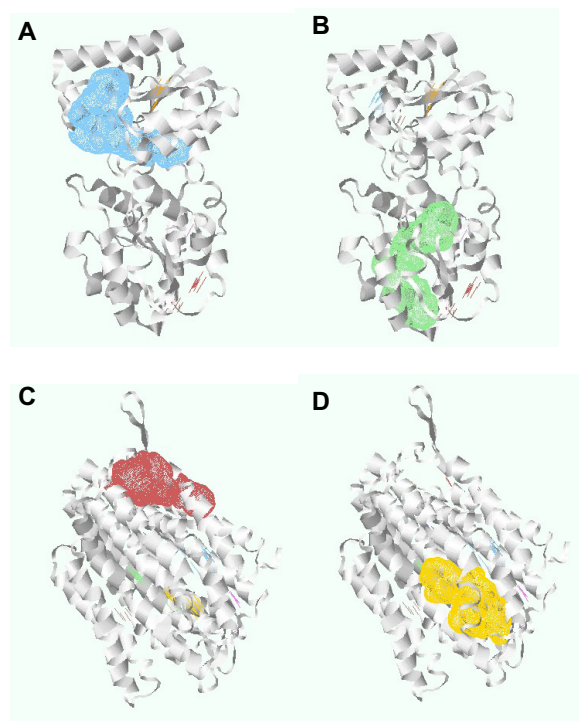
has 12 pockets, and ATP synthase F0F1 subunit B and ATP synthase F0F1 subunit C have one pocket each. Among these pockets, we have selected four pockets that have the highest druggability (Figure 3). To determine druggability, we have

Table 4 Identified drug targetable pockets of selected proteins

Protein name	Pocket	Volume (Å³)	Surface (Å²)	Liposurface (Å²)	Depth (Å)	Drug score
Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	P1	753.41	1036.76	736.97	29.21	0.87*
	P2	365.06	481.62	335.60	25.59	0.87*
	P3	256.96	338.37	223.16	19.53	0.74
	P4	279.55	445.01	319.37	16.87	0.68
	P5	420.86	675.73	362.61	12.38	0.62
Polysaccharide biosynthesis protein	P6	599.04	917.73	726.70	22.95	0.86*
	P7	466.18	726.57	617.61	23.49	0.85*
	P8	1,184.83	1,254.56	943.12	21.62	0.81
	P9	552.77	869.57	579.77	19.79	0.81
	P10	590.85	900.69	818.72	15.70	0.78
	P11	274.85	481.73	421.39	16.37	0.67
ATP synthase F0F1 subunit B	P12	87.68	306.12	289.77	11.15	0.34
ATP synthase F0F1 subunit C	P13	510.46	1,086.74	781.97	16.71	0.77

Note: *Drug score value higher than 0.85.
Abbreviation: ATP, adenosine triphosphate.

Table 5 Amino acid composition of selected pockets

Proteins	Targeted Pocket	Apolar amino acid ratio	Polar amino acid ratio	Positive amino acid ratio	Negative amino acid ratio
Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	P1	0.38	0.36	0.18	0.09
	P2	0.53	0.45	0.00	0.03
	P6	0.62	0.21	0.13	0.05
Polysaccharide biosynthesis protein	P7	0.56	0.41	0.03	0.00

taken pocket volume, surface area, liposurface area, and depth into consideration (Table 4). According to our inspection, undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase protein has two pockets with druggability scores of 0.87 each. Similarly, the polysaccharide biosynthesis protein has two pockets whose druggability scores are 0.86 and 0.85.

There are still no gold standards to individualize binding pocket properties, although many studies have showed different parameters. For instance, Volkamer et al[38] have shown that large pocket volume, high depth, and a high apolar amino acid ratio are effective parameters to determine druggability. Pocket volumes of selected pockets, namely P1, P2, P6, and P7, are 753.41, 365.06, 599.04, and 466.18, respectively, and the depths of the pockets are more than 20 Å (Table 4). Again, a high apolar amino acid ratio also suggests that those pockets could be potential drug targets (Table 5).

Today, in the postgenomic period, computational analysis of the complex networks formed by interactions between

proteins are one of the major challenges. Protein–protein interaction databases are useful to explore biological pathways and networks in cells. We also studied the protein–protein interactions of the selected proteins by STRING. The protein undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase (ID gi |125717508) was found to interact with cell division protein FtsA; putative, phospho-N-acetylmuramoyl-pentapeptide-transferase, cell division protein FtsW; and putative, undecaprenyl diphospho (UDP)-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase. Another protein of peptidoglycan biosynthesis, polysaccharide biosynthesis protein (ID gi |125718537), was seen to interact with UDP-N-acetylmuramoyl-L-alanyl-D-glutamate–L-lysine ligase, cation efflux family protein, L-cysteine desulfhydrase, and cystathionine gamma-synthase. ATP synthase F0F1 subunit B, (ID gi |125717632) can interact with F0F1 ATP synthase subunit A, F0F1 ATP synthase subunit epsilon, F0F1 ATP synthase subunit gamma, and proton-translocating ATPase. The remaining protein, ATP synthase F0F1 subunit C

Table 6 Interacting proteins with target proteins

Protein	Interacting protein
Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase; cell wall formation (murD)
	Phospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)
	Cell division protein FtsW, putative (ftsW)
	Cell division protein FtsA, putative (ftsA)
	UDP-N-acetylmuramoylalanyl-D-glutamate–L-lysine ligase (murE)
Polysaccharide biosynthesis protein	Cation efflux family protein (SSA_0851)
	Cystathionine gamma-synthase (metB)
	L-cysteine desulfhydrase (SSA_1736)
	F0F1 ATP synthase subunit A (uncB)
	Proton-translocating ATPase (uncA)
ATP synthase F0F1 subunit B	F0F1 ATP synthase subunit gamma (atpG)
	F0F1 ATP synthase subunit epsilon (atpC)
	Putative manganese-dependent inorganic pyrophosphatase (ppaC)
ATP synthase F0F1 subunit C	Adenylate kinase (adk)
	F0F1 ATP synthase subunit A (uncB)
	F0F1 ATP synthase subunit B (atpF)

Abbreviations: UDP, undecaprenyl diphospho; ATP, adenosine triphosphate.

(ID gi |125717630), was also found to interact with F0F1 ATP synthase subunit B, adenylate kinase, F0F1 ATP synthase subunit A, and putative manganese-dependent inorganic pyrophosphatase (Table 6). Thus, these target proteins have associations and functions in different and important metabolic processes of *S. sanguinis*. Therefore, the outcomes of this study will expose a new horizon in the treatment against *S. sanguinis*.

Conclusion

This study focuses on several sections of the *S. sanguinis* genome to reveal essential nonhomologous metabolic membrane-bound proteins as potential drug targets. Molecular modeling and analysis of the targets helped to uncover the best possible active sites that can be targeted for drug design. This pathogen-specific drug will not be lethal to the host because a subtractive genomic approach was applied in this study. Computational screening against these novel targets will be beneficial in the discovery of potential therapeutic agents against *S. sanguinis*.

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Author contributions

Md Rabiul Hossain Chowdhury: data collection; data analysis; literature review. Md IqbalKaiser Bhuiyan: data collection; data interpretation. Ayan Saha: research design; data analysis; literature review; manuscript correction. Ivan MHAI Mosleh: table and figure preparation; manuscript writing. Sobuj Mondol: manuscript writing. C M Sabbir Ahmed: software selection; data collection; literature review. All authors contributed toward data analysis, drafting and revising the paper and agree to be accountable for all aspects of the work.

Disclosure

The authors report no conflicts of interest in this work.

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