

Supplementary Table 1: Summary of sequence analysis of *N. meningitidis* serogroup B Proteins

Total number of proteins	2001
Duplicates (>60% identical)	62
Non-paralogs	1939
Number of proteins without hits in <i>H. sapiens</i>	1413
Number of proteins with matches in DEG	362
Number of uncharacterized proteins	36

Supplementary Table 2: Functional classification of putative uncharacterized proteins of *N. meningitidis* by using SVMProt web server.

SI No	Accession Number	Protein Function Protein Family Predicted by SVMProt	P value (%) [*]
1	Q7DD59	Transmembrane	99.0
		TC 2.A. Electrochemical Potential-driven transporters - Porters (uniporters, symporters, antiporters)	96.4
		TC 2.A.1 Major facilitator family (MFS)	58.6
		TC 3.A.3 P-type ATPase (P-ATPase) family	58.6
		TC 3.A.5 Type II (general) secretory pathway (IISP) family	58.6
2	Q7DD59	Transmembrane	99.0
		TC 2.A. Electrochemical Potential-driven transporters - Porters (uniporters, symporters, antiporters)	96.4
		TC 2.A.1 Major facilitator family (MFS)	58.6
		TC 3.A.3 P-type ATPase (P-ATPase) family	58.6
		TC 3.A.5 Type II (general) secretory pathway (IISP) family	58.6
3	Q7DD95	Zinc-binding	96.1
		Iron-binding	65.4
		Metal-binding	62.2
		DNA repair	58.6
4	Q9JXQ8	Zinc-binding	82.2
		Hydrolases - Acting on Acid Anhydrides	76.2
		Lyases - Carbon-Carbon Lyases	71.3
		Lyases - Carbon-Oxygen Lyases	65.4
		Metal-binding	62.2
		All DNA-binding	58.6
		Photosystem I	58.6

5	Q9JXZ5	Transferases – Glycosyltransferases	89.3
		Zinc-binding	86.8
		Cobalt-binding	86.8
		Oxidoreductases - Acting on iron-sulfur proteins as donors	82.2
		Iron-binding	73.8
		Oxidoreductases - Acting on the aldehyde or oxo group of donors	71.3
		Hydrolases - Acting on Ester Bonds	68.5
		Lyases - Carbon-Oxygen Lyases	65.4
		Transferases - Transferring Phosphorus-Containing Groups	62.2
		Manganese-binding	62.2
		Photosystem I	58.6
		Chlorophyll biosynthesis	58.6
		Metal-binding	58.6
		Calcium-binding	58.6
		DNA repair	58.6
		Copper-binding	58.6
		6	Q9JYI5
Hydrolases - Acting on peptide bonds (Peptidases)	76.2		
Metal-binding	65.4		
Potassium-binding	62.2		
All lipid-binding proteins	58.6		
TC 3.A. Primary Active Transporters - P-P-bond-hydrolysis-driven transporters	58.6		
Photosystem I	58.6		
Magnesium-binding	58.6		
7	Q9JYK2	Zinc-binding	97.7
		All lipid-binding proteins	96.1
		Metal-binding	65.4
		DNA repair	58.6
		Copper-binding	58.6
		Calcium-binding	58.6
8	Q9JYP7	Transmembrane	97.7
		TC 9.B. Incompletely Characterized Transport Systems - Putative uncharacterized transport proteins	95.7
		All lipid-binding proteins	82.2
		Lipid transport	71.3
		Motor protein	58.6
		Metal-binding	58.6
		DNA repair	58.6

9	Q9JYQ6	All lipid-binding proteins	96.4
		Zinc-binding	89.3
		Metal-binding	65.4
10	Q9JYS5	Oxidoreductases - Acting on the CH-OH group of donors	98.8
		Zinc-binding	96.4
		Iron-binding	92.1
		Lyases - Carbon-Carbon Lyases	88.1
		Lyases - Carbon-Oxygen Lyases	88.1
		Metal-binding	78.4
		Outer membrane	58.6
		Magnesium-binding	58.6
11	Q9JYZ0	Iron-binding	89.3
		All lipid-binding proteins	86.8
		Metal-binding	58.6
		DNA repair	58.6
12	Q9JYZ8	Zinc-binding	93.6
		Manganese-binding	78.4
		Transferases - Transferring Alkyl or Aryl Groups, Other than Methyl Groups	68.5
		RNA-binding Proteins	58.6
		Chlorophyll biosynthesis	58.6
		Metal-binding	58.6
		TC 1.C. Channels/Pores - Pore-forming toxins	58.6
		Outer membrane	78.4
		Motor protein	68.5
		Actin binding	58.6
		Magnesium-binding	58.6
13	Q9JZF6	Lipoprotein	97.7
		All lipid-binding proteins	90.3
		Hydrolases - Acting on Ester Bonds	78.4
		Hydrolases - Acting on peptide bonds (Peptidases)	68.5
		Lyases - Carbon-Carbon Lyases	58.6
		Transferases - Transferring One-Carbon Groups	58.6
		DNA repair	58.6
		Copper-binding	58.6
14	Q9JZQ6	All lipid-binding proteins	91.3
		Transferases – Glycosyltransferases	76.2
		Hydrolases - Acting on Ester Bonds	71.3
		RNA-binding Proteins	58.6
15	Q9K0A4	All DNA-binding	86.8
		Chlorophyll biosynthesis	58.6
		DNA condensation	58.6

16	Q9K0A8	Lyases - Carbon-Sulfur Lyases	88.1
		Hydrolases - Acting on peptide bonds (Peptidases)	73.8
		Transferases - Transferring Phosphorus-Containing Groups	71.3
		Transferases - Transferring Nitrogenous Groups	65.4
17	Q9K0H7	All lipid-binding proteins	97.7
		Manganese-binding	97.5
		Zinc-binding	89.3
		Transmembrane	86.8
		Hydrolases - Acting on Ester Bonds	78.4
		Iron-binding	76.2
		Metal-binding	62.2
		Chlorophyll biosynthesis	58.6
		TC 3.A.3 P-type ATPase (P-ATPase) family	58.6
		DNA repair	58.6
		Copper-binding	58.6
		Magnesium-binding	58.6
18	Q9K0H9	Transferases - Transferring Phosphorus-Containing Groups	98.0
		Zinc-binding	85.4
		Chlorophyll biosynthesis	58.6
19	Q9K0J7	Transmembrane	98.7
		TC 2.A. Electrochemical Potential-driven transporters - Porters (uniporters, symporters, antiporters)	89.3
		Iron-binding	82.2
		Photoreceptor	78.4
		All lipid-binding proteins	62.2
		TC 2.A.1 Major facilitator family (MFS)	58.6
		TC 3.A.3 P-type ATPase (P-ATPase) family	58.6
		Metal-binding	58.6
		Copper-binding	58.6
20	Q9K0Q5	Iron-binding	99.1
		Manganese-binding	96.7
		All lipid-binding proteins	93.6
		Lyases - Carbon-Carbon Lyases	92.1
		Zinc-binding	88.1
		Metal-binding	85.4
		Hydrolases - Acting on Ester Bonds	83.9
		Oxidoreductases - Acting on the CH-OH group of donors	83.9
		Lyases - Carbon-Oxygen Lyases	80.4
		Chlorophyll biosynthesis	58.6

		Calcium-binding	58.6
		Outer membrane	58.6
21	Q9K0T9	Iron-binding	96.4
		All lipid-binding proteins	71.3
		Metal-binding	62.2
		DNA repair	58.6
22	Q9K0V2	Iron-binding	96.4
		All lipid-binding proteins	71.3
		Metal-binding	62.2
		DNA repair	58.6
23	Q9K0V4	Zinc-binding	86.8
		Carbon-Oxygen Lyases	68.5
24	Q9K0W3	Transmembrane	99.1
		TC 2.A. Electrochemical Potential-driven transporters - Porters (uniporters, symporters, antiporters)	97.3
		Manganese-binding	68.5
		Zinc-binding	65.4
		TC 2.A.1 Major facilitator family (MFS)	58.6
		TC 3.A.3 P-type ATPase (P-ATPase) family	58.6
		Magnesium-binding	58.6
25	Q9K0X4	Transmembrane	99.0
		TC 2.A. Electrochemical Potential-driven transporters - Porters (uniporters, symporters, antiporters)	94.2
		All lipid-binding proteins	73.8
		TC 2.A.1 Major facilitator family (MFS)	58.6
		Metal-binding	58.6
		Calcium-binding	58.6
26	Q9K148	All DNA-binding	58.6
		DNA repair	58.6
27	Q9K0X7	Transmembrane	99.2
		TC 2.A. Electrochemical Potential-driven transporters - Porters (uniporters, symporters, antiporters)	98.9
		Sodium-binding	97.3
		Zinc-binding	71.3
		Iron-binding	68.5
		Metal-binding	65.4
		Calcium-binding	58.6
		TC 2.A.1 Major facilitator family (MFS)	58.6
		TC 2.A.3 Amino acid-polyamine-organocation	58.6

(APC) family			
28	Q9K162	Transmembrane	99.1
		Zinc-binding	65.4
		Metal-binding	58.6
		Magnesium-binding	58.6
29	Q9K1D2	Carbon-Carbon Lyases	71.3
		All lipid-binding proteins	68.5
		Metal-binding	62.2
		Actin binding	58.6
		Calcium-binding	58.6
30	Q9K1D3	TC 2.A. Electrochemical Potential-driven transporters - Porters	99.1
		Transmembrane	98.6
		Manganese-binding	71.3
		TC 3.A.3 P-type ATPase (P-ATPase) family	58.6
		7 transmembrane receptor (Secretin family)	58.6
31	Q9K1J6	Zinc-binding	65.4
		Motor protein	58.6
		Metal-binding	58.6
		DNA repair	58.6
		Transferases - Transferring One-Carbon Groups	58.6
		Copper-binding	58.6
32	Q9K1M7	Transmembrane	99.2
		TC 2.A. Electrochemical Potential-driven transporters - Porters	99.1
		Iron-binding	92.1
		Metal-binding	76.2
		Transferases - Transferring Phosphorus-Containing Groups	73.8
		Hydrolases - Acting on Acid Anhydrides	58.6
33	Q9K1N6	Transferases - Transferring Phosphorus-Containing Groups	62.2
		Zinc-binding	58.6
		All lipid-binding proteins	58.6
		Chlorophyll biosynthesis	58.6
		Magnesium-binding	58.6

(*P-value is the expected classification accuracy in terms of percentage.)

Supplementary Table 3: List of the outer membrane and periplasmic proteins of *N. meningitidis* serogroup B predicted by PA-SUB

Sl. No	Swiss prot ID	Protein Name
Outer Membrane Proteins		
1	Q9K187	LPS-assembly protein
2	Q7DDU3	Putative membrane-bound lytic murein transglycosylase A
3	Q7DD63	Outer membrane lipoprotein
4	Q9K1M2	Putative outer membrane protein NMB0088
5	Q9JXB7	Putative uncharacterized protein
6	Q9K1H0	Outer membrane protein omp85
7	Q06379	Lactoferrin-binding protein A
8	Q9K0U9	Transferrin-binding protein 1
9	Q9JYA8	Hemoglobin receptor
Periplasmic Proteins		
1	Q9K0M9	Thiamine biosynthesis lipoprotein ApbE
2	Q7DDU3	Putative membrane-bound lytic murein transglycosylase A
3	Q7DDG9	Ferredoxin, 2Fe-2S type
4	Q9K1A0	RlpA-like protein
5	Q9JY10	Penicillin-binding protein 3
6	Q9K0B1	Competence lipoprotein comL
7	Q9JS33	Sulfite reductase [NADPH] hemoprotein beta-component
8	P57068	Outer-membrane lipoprotein carrier protein
9	Q9JYG7	Spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein
10	Q9K0U8	Spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein
11	Q9JZK1	Sulfate ABC transporter, periplasmic sulfate-binding protein

Supplementary Table 4: List of essential enzymes from the pathways present exclusively in *Neisseria meningitidis* Serogroup B

<i>N. meningitidis</i> specific Pathways	Protein Name	SwissProt ID	Gene Name	EC	Involvement in Other Metabolic Pathways
C5-branched diabolic acid metabolism	Acetolactate synthase isozyme III large subunit	Q9JYI0	ilvI	2.2.1.6	Butanoate metabolism, leucine and isoleucine biosynthesis, Pantothenate and CoA biosynthesis
Oxidative phosphorylation	F0F1 ATP synthase subunit A	Q7DD64	atpB	3.6.3.14	
Carbon fixation in photosynthetic organisms	phosphoenolpyruvate carboxylase	Q9JXG5	ppc	4.1.1.31	Pyruvate metabolism, Reductive carboxylate cycle
D-Alanine metabolism	D-alanine-D-alanine ligase	Q9K0Y0	ddl	6.3.2.4	Peptidoglycan biosynthesis
Lipopolysaccharide biosynthesis	UDP-N-acetylglucosamine acyltransferase	P95379	lpxA	2.3.1.129	
	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	Q9K1Q3	lpxC	3.5.1.-	
	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	P95377	lpxD	2.3.1.-	
	UDP-2,3-diacylglucosamine hydrolase	Q9K0P2	lpxH	3.6.1.-	
	lipid-A-disaccharide synthase	Q9K1F5	lpxB	2.4.1.182	
	3-deoxy-D-manno-octulosonic-acid transferase	Q9K1Q6	kdtA	NA	
	tetraacyldisaccharide 4'-kinase	Q9K0D7	lpxK	2.7.1.130	
	lipid A biosynthesis lauroyl acyltransferase	Q9JY07	NA	2.3.1.-	
	3-deoxy-manno-octulosonate cytidyltransferase	Q9K0D6	kdsB	2.7.7.38	
	2-dehydro-3-deoxyphosphooctonate	Q9JZ55	kdsA	2.5.1.55	

	aldolase					
	D-beta-D-heptose 7-phosphate kinase	Q9JXF0	aut	2.7.1.-		
	lipopolysaccharide heptosyltransferase I	Q9JX98	rfaC	2.4.-.-		
	ADP-heptose:LPS heptosyltransferase II	Q9JYL5	rfaF	2.4.-.-		
Polyketide sugar unit biosynthesis	dTDP-4-keto-6-deoxy-D-glucose-3,6-epimerase	Q9K1M5	NA	5.1.3.13		
Streptomycin biosynthesis	dTDP-4-dehydrorhamnose 3,5-epimerase	Q9K1M5	NA	5.1.3.13	Streptomycin biosynthesis, Nucleotide sugars metabolism	
Novobiocin biosynthesis	histidinol-phosphate aminotransferase	Q9JYH7	hisC	2.6.1.9	Histidine metabolism, Tyrosine metabolism, Phenylalanine metabolism, tyrosine and tryptophan biosynthesis	
Type II secretion system	type IV pilus assembly protein	Q7DDR2	pilF			
	pilus assembly protein	Q7DDR1	pilG			
	twitching motility protein	Q7DDU1	pilT-1			
	twitching motility protein	Q9K053	pilT-2			
	competence protein	Q9K0B2	comA			
Phosphotransferase system (PTS)	phosphoenolpyruvate-protein phosphotransferase	Q9JXH7	ptsI	2.7.3.9		
	nitrogen regulatory IIA protein	Q9K082	ptsN	2.7.1.69		
Two-component system	LuxR family transcriptional regulator	Q7DDD4	narL	4.2.1.20		
	tryptophan synthase subunit alpha	Q9K0D4	trpA	4.2.1.20	tyrosine and tryptophan biosynthesis	
	tryptophan synthase subunit beta	Q9K0B5	trpB	4.2.1.20	tyrosine and tryptophan biosynthesis	

indole-3-glycerol-phosphate synthase	Q9K192	trpC	4.1.1.48	tyrosine and tryptophan biosynthesis tyrosine and tryptophan biosynthesis tyrosine and tryptophan biosynthesis
anthranilate phosphoribosyltransferase	P66995	trpD	2.4.2.18	
anthranilate synthase component I	P56995	trpE	4.1.3.27	
protein-PII uridylyltransferase nitrogen regulatory protein P-II 1	Q9JZB4 Q9JXK6	glnD glnB	2.7.7.59	
