

RESEARCH ARTICLE

Structure and function prediction in uncharacterized protein of *Neisseria meningitidis* Z2491

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Manuscript Details

Received : 18 June,2014
 Revised : 23 June, 2014
 Revised received: 29 June, 2014
 Accepted: 07 June, 2014
 Published: 09 July, 2014

ISSN: 2322-0015

Editor: Dr. Arvind Chavhan

Cite this article as:

Tauseef Ahmad. Structure and function prediction in uncharacterized protein of *Neisseria meningitidis* Z2491, *Int. Res. J. of Sci. and Engg.*, 2014 ; 2(4): 131-138

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ABSTRACT

Computational biology avails us to prognosticate the functionality in the uncharacterized proteins sequence utilizing the various strategies of comparative proteomics *Neisseria meningitidis* (Z2491) isolated into different serogroups on the substructure of the immunochemistry of their capsular polysaccharides; Serogroup A strains are in charge of pandemics of meningococcal illness, and in this manner dressiness and mortality connected with this infection. Our endeavour is to prognosticate the structure and function of uncharacterized proteins present in the genome of *Neisseria meningitidis* by the application of computational methods and Bioinformatics web tool. The probable function prognostication of the uncharacterized protein was done by utilizing Bioinformatics web implements like CDD-BLAST, INTERPROSCAN, PFAM and COGs by probing sequence databases for the presence of orthologous enzymatic conserved domains in the hypothetical sequences. While 3D structures were constructed utilizing PS2 Server (Protein Structure Prediction server). In this study investigate presences of enzymatic conserved domain in selected 200 uncharacterized proteins; s their function was unknown. These deciphered enzymatic information of uncharacterized proteins c might be used for the advance study of structural, functional, and evolutionary history of *N. meningitidis* and its life cycle.

Keywords: *Neisseria meningitidis* (Z2491) Bioinformatics web tools, Hypothetical protein Conserved, Domains Structure prediction.

INTRODUCTION

Neisseria meningitidis (Z2491) is intracellular human-categorical pathogens which are responsible for septicaemia and meningitis after crossing of the blood brain barrier, *Neisseria meningitidis* (Z2491) is a major causal agent of morbidity and mortality throughout the globe. (Shobana, 2011). It has been responsible for epidemics throughout the Asia and Africa (Genco, 2010) Computational biology avails us to prognosticate the functionality in the uncharacterized sequences using

various procedure of comparative proteomics (Gore, 2009). The program's capability of homology testing by utilizing defined databases and culling standard parameters, the presence of the enzymatic conserved domain/s in the sequences could be probed out and it may avail in the categorizing protein into categorical enzymatic family. Conserved domain databases like CDD-BLAST, INTERPROSCAN, PFAM and COGs can search the orthologous sequence in database for the query sequence, while assisting in the categorization of the target sequence in particular families. (Gore D G 2010) This study will avail us to understand the probable functions of uncharacterized proteins in *Neisseria meningitidis* (Z2491). Several online machine driven servers are available which can construct 3D structures for selected sequences by utilizing the strategy of aligning target sequences with orthologous sequences by virtue of sequence homology and predicated on that, constructs the 3D structure for target protein utilizing best scored template of orthologous family member. Here, we have presaged 3-D structure utilizing Protein Structure Prediction Server (PS2 server).

MATERIALS AND METHODS

Data collection:

The complete protein coding sequences of first two hundred uncharacterized proteins of *Neisseria meningitidis* (Z2491) were selected and downloaded from the website www.genome.jp/kegg/.

Functional Annotations:

uncharacterized proteins were screened for the presence of enzymatic conserved domains utilizing sequence homogeneous attribute search with close orthologous family members available in sundry protein databases utilizing the web-implements. Four bioinformatics web tools like: CDD-BLAST (www.ncbi.nlm.nih.gov/BLAST) Altschul (1997) INTERPROSCAN (www.abi.ac.uk/interpro) Zdob (2001), Pfam (www.pfam.sanger.ac.uk) Bateman (2000), COGs (www.ncbi.nlm.nih.gov/cog) Roman (2000) were utilized, which shows the ability to probe the defined conserved domains in the sequences and avail in the relegation of proteins in opportune family.

Functional categorization:

Screening of uncharacterized proteins by four web implements shown variable results for the presence of

enzymatic conserved domains in target sequences, resultant functional hypothetical sequences can be categorized into different confidence levels on the substructure of collective results of web implements utilizing following parameters:-

- 1) If the given four implements show the same functions then the confidence level were to be 100 percent.
- 2) If the given three implements show the same functions then the confidence level were to be 75 percent.
- 3) If the given two implements show the same functions and remaining two shows different function then the confidence level were to be 50 percent.
- 4) If the given four implements show the all different functions then the confidence level were to be 25 percent.

Protein structure prediction:

Several online automated protein structure prediction servers are available. Out of that, online PS2 (Protein Structure Prediction) Server was used. (www.ps2.life.nctu.edu.tw/) Chen (2006) this server accept input the protein (query) sequences in standard FASTA format and utilizes the both strategies of alignment by combining the filtering power of the programs PSI-BLAST, IMPALA and T-COFFEE in both target – template selection and alignment and new target proteins 3D structures were constructed utilizing structural situating information of atomic coordinates for kenneled template in PDB format utilizing best scored alignment data. Template selection was prognosticated on the constant conserved domain in the functional annotations that should be accessible in the structure alignment for modeling purport.

RESULTS AND DISCUSSION

Bioinformatics web implements results used to annotated 131 hypothetical proteins out of 200 protein sequences into particular Enzymatic family predicated on query sequence shown homology with kenneled enzyme sequence and categorized with variable confidence levels which are represented in Table 1 and derived Functional Percentage Classification of whole proteins are represented in Table 2.

Protein structure prediction:

The (PS)2 Server constructs the three dimensional structure of uncharacterized proteins in PDB format. Where in 200 uncharacterized protein sequences of *Neisseria meningitidis* (Z2491) analyzed, (PS)2

satisfactorily prognosticated structures of '89' uncharacterized proteins utilizing best scored orthologous template. The templates which scored best with hypothetical sequences are represented by their features such as KEGG number, template, identity, score

and E-value as in Table 3. Where out of 200 sequences (PS)2 fail to construct protein structures of 111 protein sequences because absence of copacetic template for structure building.

Table1: Function prediction to uncharacterized protein.

KEGG NO.	CDD	INTERPROSCAN	PFAM	COGs	% AGE
NMA0003	NO	NO	NO	NADH dehydrogenase	25%
NMA0004	Fic/DOC family	Fido domain	Fic/DOC family	Fic/DOC family	100%
NMA0011	GIY-YIG_	GIY-YIG endonuclease	GIY-YIG catalytic	GIY-YIG nuclease	100%
NMA0014	nuoF	NADH dehydrogenase	SLBB domain	NuoF	50%
NMA0023	unintegrated	unintegrated	Immunity protein	NO	25%
NMA0025	SMI1_KNR4	SMI1_KNR4	SMI1 / KNR4	NO	75%
NMA002	Allophanate hydrolase	Allophanate hydrolase	Allophanate	DUR1	75%
NMA0029	Allophanate hydrolase	Allophanate hydrolase	Allophanate	DUR1	75%
NMA0033	Helix-turn-helix	Integrase	Helix-turn-helix	Transposase	50%
NMA0071	S1_RNase_E: RNase E and RNase	S1 RNA binding	S1 RNA binding	CafA	75%
NMA0086	periplasmic chaperone	Chaperone protein	Outer membrane protein	HlpA	50%
NMA0089	Abi-like protein	AbiF-like	Abi-like protein	NO	75%
NMA0131	Rat sarcoma	GTP binding	GTPase	Ras_like_GTPase	75%
NMA0132	Rat sarcoma (Ras)	GTP binding	GTPase	Predicted GTPase	50%
NMA0153	Helix-turn-helix	helix-turn-helix	Helix-turn-helix	Helix-turn-helix	100%
NMA0155	NO	NO	glycosylase	NO	25%
NMA0165	Lysine Motif	lysin domain	LysM domain	LysM domain	100%
NMA0169	DUF3579	GNAT domain	DUF3579	RimI	25%
NMA0170	K_trans	NO	RNA polymerase	NO	25%
NMA0173	Peptidase_C39G	Peptidase	Peptidase C39	Peptidase C39	100%
NMA0181	cyanate hydratase	DNA-binding domain	(DUF746)	NO	25%
NMA0183	Sel1-like repeats	Sel1 repeat	Sel1 repeat	NO	75%
NMA0227	PLPDE_III_Yggs_like	Alanine racemase,	Alanine racemase,	NO	50%
NMA0239	NO	NO	glycoprotein E2	NO	25%
NMA0240	UPF0029	Impact, N-terminal	Uncharacterized protein family	Uncharacterized conserved protein	25%
NMA0249	AAA_13	NO	Adhesion protein FadA	Smc	25%
NMA0281	Peptidase_M75	Cupredoxin	Cupredoxin	periplasmic lipoprotein	50%
NMA0282	iron-dependent peroxidase	Twin-arginine translocation	peroxidase	peroxidase	50%
NMA0289	Competence-damaged protein	CinA, C-terminal	Competence-damaged protein	CinA	100%
NMA0292	GIY-YIG domain of	GIY-YIG nuclease	GIY-YIG catalytic	The GIY-YIG nuclease	100%
NMA0293	<i>Neisseria</i> _PilC	PilC beta-propeller domain	(DUF490)	PilY1	50%
NMA099	Lipoprotein	transferrin-binding protein	Lipoprotein	NO	50%
NMA0304	Competence-damaged protein.	Molybdopterin binding	Probable molybdopterin binding	MoCF_BD	50%
NMA0307	SMI1_KNR4 super	NO	SMI1	NO	50%
NMA0316	NO	NO	Immunity protein	NO	25%
NMA0320	NO	SMI1/KNR4	SMI1/ KNR4	NO	50%
NMA0330	cyclo-ligase	cyclo-ligase	cyclo-ligase fa	cyclo-ligase	100%
NMA0331	Acetyltransf	GNAT domain	Acetyltransferase	Acetyltransferases	75%
NMA038	halo_surf_glyco	Unintegrated	inner membrane protein	NO	25%
NMA0342	tetrapyrrole methylases	tetrapyrrole methylases	Tetrapyrrole Methylas	methyltransferases	100%
NMA0350	Ser_hydrolase	DUF1234	Serine hydrolase	NO	50%
NMA0358	NO	Nop25	Ryanodine Receptor TM 4-6	NO	25%

Table 1: Continued...

KEGG NO.	CDD	INTERPROSCAN	PFAM	COGs	% AGE
NMA0376	NO	NO	bZIP transcription factor	NO	25%
NMA0377	zapA	zapA	ZapA	protein ZapA	100%
NMA0382	NO	Ngg1p, NIF3	NIF3 (NGG1p interacting	NO	50%
NMA0386	RmuC	RmuC	RmuC	NO	75%
NMA0401	RmuC	RmuC	Antidote-toxin recognition Maze	NO	50%
NMA0415	beta_CA_cladeD	Carbonic anhydrase	Carbonic anhydrase	Carbonic anhydrase	75%
NMA0416	NMNAT	Cytidyltransferase	Cytidyltransferase	Adenyltransferase	50%
NMA0417	iojap-like ribosome	Protein Iojap/ribosomal silencing factor RsfS	Oligomerisation	Oligomerisation	50%
NMA0419	Fe	Fe(II) trafficking protein YggX Fe	Bacterial Fe(2+) trafficking	Uncharacterized protein conserved in bacteria	75%
NMA0428	Histidine kinase-like ATPases;	Histidine kinase-like ATPases;	Histidine kinase-, DNA gyrase B-, and HS	Molecular chaperone, HSP90 family	75%
NMA0432	NO	NO	integrase	NO	25%
NMA0434	Voltage gated	Voltage gated	Voltage gated	EriC	75%
NMA0436	LrgB	LrgB	LrgB	LrgB	100%
NMA0437	LrgA	LrgA/CidA	LrgA	LrgA	100%
NMA0440	NlpC/P60 family;	Endopeptidase, NLPC/P60	NlpC/P60	Spr	75%
NMA0442	NO	CBS domain	MgtE intracellular	MgtE	50%
NMA0449	TRM1	NO	NO	TRM1	50%
NMA0459	Fic/DOC	Fic/DOC	Fic/DOC	Fic	100%
NMA0482	NO	NO	Haemocyanin	NO	25%
NMA0489	STAS_anti-anti-sigma_factors	STAS_anti-anti-sigma_factors	STAS_anti-anti-sigma_factors	Anti-Sigma factor	100%
NMA0492	NO	NO	Thioesterase	FcbC	25%
NMA0510	NO	NO	lipoprotein-	NO	25%
NMA0529	Inositol-monophosphatase-	Inositol-monophosphatase	Inositol monophosphatase	SuhB	75%
NMA0545	PRTases_type	Phosphoribosyl transferase	Phosphoribosyl transferase	NO	75%
NMA0547	Tetrapyrrole (Corrin/Porphyrin) Methylas ...	Tetrapyrrole (Corrin/Porphyrin) Methylas ...	Tetrapyrrole (Corrin/Porphyrin) Methylas ...	Methyltransferases	100%
NMA0549	hypothetical protein; Provisional	Putative membrane protein insertion efficiency factor	Haemolytic domain	Haemolytic domain	50%
NMA0556	NO	NO	L,D-transpeptidase catalytic domain	NO	25%
NMA0562	HtpX	Peptidase M48	Peptidase family M48	HtpX	50%
NMA0571	GAF domain	GAF domain	GAF domain	GAF domain-containing protein	100%
NMA0573	RHOD_2	RHOD_2	RHOD_2	PspE	75%
NMA0576	Mannose-6-phosphate isomerise	Mannose-6-phosphate isomerase	Cupin domain	Mannose-6-phosphate isomerase	75%
NMA0581	zinc_ribbon	Zinc finger/thioredoxin putative	Zinc finger/thioredoxin putative	NO	75%
NMA0585	proteases,	Gcp-like	Glycoprotease	Proteases	50%
NMA0604	PRTases_type	Phosphoribosyltransferase	NO	phosphoribosyltransferases	75%
NMA0607	NO	NO	NO	Lactoylglutathione lyase	25%
NMA0629	CRISPR/Cas system-associated protein Cas2	CRISPR associated protein Cas2	CRISPR associated protein Cas2	CRISPR-associated protein	100%
NMA0630	CRISPR Cas1	CRISPR Cas1	CRISPR Cas1	CRISPR-associated protein	100%
NMA0631	CRISPR/Cas system	CRISPR	HNH endonuclease	CRISPR	75%
NMA0640	Glycosyltransferase	NO	Glycosyl transferase	Glycosyltransferase	75%

Table 1: Continued...

KEGG NO.	CDD	INTERPROSCAN	PFAM	COGs	% AGE
NMA0641	Glycosyltransferas	Glycosyltransferas	Glycosyl transferase	Glycosyltransferase	100%
NMA0659	ResB-like family	ResB-like domain	ResB-like family	ResB	100%
NMA0660	cytochrome	Cytochrome C	Cytochrome C	Cytochrome	100%
NMA0687	ShlB-type	Haemolysin activator HlyB	ShlB-type	FhaC	50%
NMA0688	FhaB	VENN motif	haemagglutination	FhaB	50%
NMA0689	NO	NO	Costars	NO	25%
NMA0690	DUF637	VENN motif	hemagglutinin	FhaB	25%
NMA0691	NO	NO	NO	NO	0%
NMA0692	DUF637	VENN motif	hemagglutinin	FhaB	25%
NMA0694	NO	NO	Double zinc ribbon	NO	25%
NMA0695	PT-VENN	VENN motif	Pre-toxin VENN	NO	75%
NMA0696	NO	unintegrated	Immunity protein	NO	0%
NMA0702	ExsB	Rossmann-like alpha/beta/alpha	Queuosine	PP-loop	25%
NMA0704	6-pyruvoyl tetrahydropterin	6-pyruvoyl tetrahydropterin	6-pyruvoyl tetrahydropterin	6-pyruvoyl-tetrahydropterin	100%
NMA0707	Radical SAM	Radical SAM	4Fe-4S single cluster	NrdG	50%
NMA0712	membrane protein	No hits found.	SNARE	membrane protein	50%
NMA0716	CBS_pair	CBS_pair	CBS domain	CorC	75%
NMA0717	NO	Endoribonuclease YbeY	NO	NO	75%
NMA0721	zinc-finger	Zinc finger, CHCC-type	Zinc-finger	Zinc-finger	100%
NMA0737	NO	No hits found.	HdeA/HdeB family	NO	25%
NMA0740	NO	No hits found.	NO	NO	0%
NMA0753	Anion permease ArsB/NhaD	Citrate transporter	Citrate transporter	ArsB	50%
NMA0767	Peptidase	Peptidase	Peptidase	glycine peptidase	75%
NMA0774	Zonular occludens	Zonular occludens	Zonular occludens	NO	0%
NMA0785	NO	No hits found.	EAP30/Vps36	NO	25%
NMA0795	Ribosomal protein S16	Ribosomal protein S16	Ribosomal protein S16	Ribosomal protein S16	100%
NMA0810	Histone deacetylases	Histone deacetylase	Histone deacetylase	AcuC	75%
NMA0827	Preprotein translocase	Preprotein translocase YajC	Preprotein translocase subunit	Kinase/pyrophosphorylase	75%
NMA0833	LbH_gamma_CA_	transferase hexapeptide	transferase hexapeptide	anhydrases/acyltransferases	50%
NMA0854	NO	Immunity protein	Immunity protein	NO	50%
NMA0855	Colicin-DNase	NO	DNase/tRNase domain of colicin	NO	50%
NMA0861	YjgF_YER057c_UK114_family	Enamine/imine deaminase YjgF-like	Endoribonuclease L-PSP	YjgF, YER057c, and UK114	100%
NMA0866	NO	NO	ZipA, C-terminal FtsZ-binding domain	NO	25%
NMA0868	yceG_like	YceG-like	YceG-like family	Aminodeoxychorismate lyase	75%
NMA0874	Uncharacterized	UPF0434/Trm112	Trm112p-like protein	Trm112p-like protein	75%
NMA0881	CNP1[NMA0881	CNP1-like family	NO	50%
NMA0882	SirA_YedF_YeeD	NO	Sulfurtransferase TusA	SirA, YedF, and YeeD.	50%
NMA0903	UDG_MUG	glycosylase	NO	Mug	75%
NMA0919	RDD family	RDD	NO	NO	50%
NMA0924	NO	Inner membrane protein YedI	NO	NhaP-type Na+	25%
NMA0935	ABC_DR	AAA domain	AAA domain	Predicted ATPases	50%
NMA0941	Chorismate lyase	Chorismate lyase	Chorismate lyase	NO	75%

Table 1: Continued...

KEGG NO.	CDD	INTERPROSCAN	PFAM	COGs	% AGE
NMA0944	ATPase protein family	ATPase protein family	ATPase	Chorismate lyase	75%
NMA0948	ATPase protein family	ATPase, P-loop-	P-loop ATPase	Predicted P-loop	100%
NMA0951	scpB	ScpB	Putative transcriptional regulators	Putative transcriptional regulators	50%
NMA0954	NAD(P)-binding Rossmann	Aromatic-ring hydroxylase	Oxidoreductase	DadA	25%
NMA0960	AdoMet_MTases	Putative rRNA methylase	Putative rRNA methylase	Methylase	100%
NMA0970	Uncharacterized conserved protein	Cytochrome	Cytochrome C	Cytochrome C	75%
NMA0982	TatD_DNase	TatD family	TatD related DNase	metallo-dependent hydrolases	75%
NMA0989	PRK10920	HemX	HemX	HemX	75%

Table 2: Percentage classification of enzymatic uncharacterized proteins

No. of proteins	27	36	30	34	73
Percentage of similarity	100%	75%	50%	25%	0%

Table 3: Structure Prediction for uncharacterized protein

KEGG NO.	TEMPLATE	IDENTITY	SCORE	E-VALUE
NMA0004	2g03A	100	147	3.00E-36
NMA0011	1zg2A	22	94	9.00E-21
NMA0014	2fug1	48	521	1.00E-148
NMA0023	2prvA	15	81	2.00E-16
NMA0025	2phcB	35	276	2.00E-75
NMA0028	2phcB	35	276	2.00E-75
NMA0033	1c6vA	15	43	7.00E-05
NMA0086	1u2mC	21	87	1.00E-18
NMA0131	1mkyA	15	123	2.00E-29
NMA0132	1tq4A	15	127	2.00E-30
NMA0153	1y9qA	14	59	5.00E-10
NMA0169	2beiB	20	113	4.00E-26
NMA0173	3b79A	17	95	2.00E-20
NMA0181	dw9A	14	37	7.00E-04
NMA0184	1xi4A	12	42	2.00E-04
NMA0240	1vi7A	29	217	1.00E-57
NMA0245	1xqbA	30	184	2.00E-47
NMA0281	2d3qA	20	168	1.00E-42
NMA0282	2ov0A	22	44	6.00E-05
NMA0289	2a9sA	48	176	3.00E-45
NMA0292	1zg2A	28	107	6.00E-25
NMA0299	1ys5A	20	79	3.00E-15
NMA0304	1di6A	15	58	2.00E-09
NMA0307	2prvA	12	35	0.009
NMA0320	2prvA	13	39	7.00E-04
NMA0330	1wkcA	28	115	1.00E-26
NMA0331	2z10A	30	157	7.00E-40
NMA0342	1s4dE	18	119	8.00E-28
NMA0350	3bdvA	20	158	4.00E-40
NMA0358	2qzvA	16	42	2.00E-04
NMA0376	1deqB	12	38	7.00E-04
NMA0377	1t3uB	25	105	2.00E-24
NMA0382	1nmoA	48	301	8.00E-83
NMA0386	1y1uA	12	54	1.00E-09
NMA0401	1ub4C	16	48	5.00E-07
NMA0415	1g5cA	35	153	3.00E-38
NMA0416	1yumA	33	207	1.00E-54

Table 3: Continued...

KEGG NO.	TEMPLATE	IDENTITY	SCORE	E-VALUE
NMA0417	2id1A	65	128	6.00E-31
NMA0419	1yhdA	43	151	3.00E-38
NMA0428	1y4sA	17	237	3.00E-63
NMA0434	1otsA	24	222	7.00E-59
NMA0440	2evrA	26	121	1.00E-28
NMA0442	2yvxA	30	401	1.00E-112
NMA0449	2glzA	12	38	0.002
NMA0459	3cucB	16	141	8.00E-35
NMA0492	1njka	39	110	2.00E-25
NMA0493	2hyxA	18	146	2.00E-36
NMA0529	2p3nA	29	216	4.00E-57
NMA0547	1wyzB	43	191	1.00E-49
NMA0562	3c37A	22	198	9.00E-52
NMA0571	1vhmB	42	143	3.00E-35
NMA0573	1qxnA	25	96	2.00E-21
NMA0576	2i45D	98	121	2.00E-29
NMA0585	1okjB	30	193	2.00E-50
NMA0604	1ecfB	16	134	1.00E-32
NMA0605	1cw0A	17	99	2.00E-22
NMA0607	2p7oA	30	52	3.00E-08
NMA0630	2yzsB	17	200	3.00E-52
NMA0634	2gekA	16	175	9.00E-45
NMA0689	2qdzA	20	255	2.00E-68
NMA0702	3bl5E	56	264	8.00E-72
:NMA0703	2qsdC	30	200	1.00E-52
NMA0704	2obaB	26	143	2.00E-35
NMA0707	1tv8A	18	77	3.00E-15
NMA0716	2pliA	97	88	2.00E-18
NMA0717	1xm5A	44	174	8.00E-45
NMA0721	2jvmA	29	41	6.00E-05
NMA0767	3b79A	17	69	6.00E-13
NMA0774	2r2aA	31	130	4.00E-31
NMA0795	2gy9P	66	123	7.00E-30
NMA0810	2rddB	35	50	9.00E-08
NMA0833	1v3wA	45	207	1.00E-54
NMA0850	1f9zA	30	162	1.00E-41
NMA0861	1j7hA	50	175	1.00E-45
NMA0866	1f46B	15	153	4.00E-38
NMA0868	2r1fA	42	316	3.00E-87
NMA0873	2jr6A	98	97	6.00E-22
NMA0882	1dcjA	27	105	2.00E-24
NMA0903	2c2qA	17	96	9.00E-21
NMA0924	2pliA	19	40	1.00E-04
NMA0935	1e69A	13	68	2.00E-12
NMA0944	1tt8A	24	128	6.00E-31
NMA0948	1zp6A	14	42	2.00E-04
NMA0951	2z99A	31	145	7.00E-36
NMA0960	1wg8A	16	52	1.00E-07
NMA0982	1yixA	43	334	9.00E-93
NMA0989	2i1kA	5	40	0.001

The analysis of the uncharacterized proteins is proved only on expression of the selective gene through cloning. The results obtained are concluded on the

bases of available information in different databases and we can presage the structure and function of any organisms by utilizing web implements.

CONCLUSION

This study sorted 131 functional proteins out of 200 uncharacterized proteins of *Neisseria meningitidis* (Z2491) by applying the parameters of confidence level and pair-wise sequence alignment along with structure prognostication implements, In out of 200, only 89 3-D structures for uncharacterized proteins were constructed utilizing (PS)2 servers as expeditious automated homology modelling web server. This prognosticated 3-D structures may avail in establishing their role in life cycle of *Neisseria meningitidis* (Z2491) whose exact role in phage-host lifecycle is still obscure and can be utilized in future for the study of virulence and evolution of both phage-host systems.

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