

Bioinformatics up to Date

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COVER STORY

Dr Shailesh Nayak, Secretary, Ministry of Earth Sciences, Govt of India visited tCSIR-NEIST during 2 – 3 June 2011. He delivered the 12th CSIR-NEIST Golden Jubilee Lecture series on “Societal Benefits of Earth System Science” at NEIST auditorium. The function was attended by Dr PG Rao, Director, CSIR-NEIST as well as distinguished guests and dignitaries from national, regional research institutes, universities, scientists, research scholars, school teachers, students, the scientific fraternity of CSIR-NEIST and others. Dr PG Rao, Director, CSIR-NEIST welcomed the audience while Dr Sourav Baruah, Scientist, CSIR-NEIST gave the introduction of the honored guest to the audience. In his vivid and illuminating talk Dr Nayak mentioned about the Earth System Science Processes and its interactions and in that connection he also mentioned about the importance of the Earth Science and stressed on the scientific understanding of the earth system so as to be able to improve prediction of climate, weather and natural hazards. On the event of World Environment Day to be held on 5 June 2011, Dr Nayak also planted a Neem sapling in the Golden Jubilee Garden of CSIR-NEIST on 3 June 2011.



BIOINFY QUIZ

- Unrecognised functional elements are present in-
 - Non-coding DNA
 - Non-coding RNA
 - Intron
- When the DNA is surrounding the coding region of a gene, promoter analysis involves the identification and study of:
 - Bioinformatics
 - Protein
 - Sequence motif
- Massive sequencing efforts are used to identify previously unknown point mutations in a variety of genes in :
 - Metastasis
 - Cancer
 - Chemotherapy
- Owen White, who was part of the team at The Institute for Genomic Research that sequenced and analyzed the first genome of a free-living organism to be decoded, the bacterium
 - Pathogenic bacteria
 - Haemophilus influenza
 - Typhoid fever
- The virtual evolution that attempts to understand evolutionary processes via the computer simulation of simple (artificial) life forms. Is also known as:
 - Formal methods
 - Artificial life
 - Requirements analysis

Answers on page 5

COMPUTATIONAL CHEMISTRY

CHEMGENOME 2.0

An ab-initio Gene Prediction Software

Chemgenome is an ab-initio gene prediction software, which find genes in prokaryotic genomes in all six reading frames. The methodology follows a physico-chemical approach and has been validated on 372 prokaryotic genomes.

Chemgenome is based on the hypothesis that both the structure of the DNA and its interactions with regulatory proteins and polymerases decide the function of a DNA sequence. It uses a simple three-parameter model based on Watson-Crick hydrogen-bonding energy, base-pair stacking energy, and a third parameter which is related to Protein-Nucleic Acid interactions. Each of these parameters acts as a dimension for a three-dimensional unit vector, whose orientation differs for each trinucleotide. DNA sequence is made up of set of four bases (A, T, G, C) which combine in different possible manner to give 64 unique codons. Each of the 64 codons(trinucleotides) are assigned a X(Hydrogen Bonding Energy), Y(Stacking Energy) and Z(protein-Nucleic acid interaction).

PROTEOMICS

Make2D-DB II P

A package to build a web-based proteomics database

Make2D-DB II is an environment to create, convert, publish, interconnect and keep up-to-date **two-dimensional gel electrophoresis** (2D-PAGE) databases. It converts data from various formats into a **relational** format. The tool offers the possibility to automatically update data related to numerous **external data resources** in a highly consistent manner. It is also possible with this tool to **dynamically interconnect** several remote databases or projects to form a virtual global database accessible from one single entry point.

Make2D-DB II can also be used without any local data, as a personal and a configurable **Web portal**, to link simultaneously to several remote 2D resources. Finally, this tool can be easily used to build up a 2-DE **repository**, accessible by any

BIOSERVER

NetSurfP Server

NetSurfP server predicts the surface accessibility and secondary structure of amino acids in an amino acid se. The method also simultaneously predicts the reliability for each prediction, in the form of a Z-score. The Z-score is related to the surface prediction, and not the secondary structure.

A newer and faster version of NetSurfP is now available. Please use [NetSurfP-1.1](#)

[Instructions](#)

[Output format](#)

Jobs typically take around 5 minutes to be processed. If there is no response after 2 hours please email bent [at] cbs.dtu.dk

Paste in sequence data (maximum 500 sequences)

or upload sequence data

Valid format examples: [Fasta](#)

All sequences must be submitted in amino acid format and have a unique sequence id!

Addition to output

COMPUTERS FOR BIOLOGISTS

SIFT: predicTion Tool For amino acid SubSTiTution

SIFT predicts whether an amino acid substitution affects protein function based on sequence homology and the physical properties of amino acids. SIFT can be applied to naturally occurring nonsynonymous polymorphisms and laboratory-induced missense mutations. The various tools in it includes: Batch tools, Genome tools, Single protein tool..

User Input

Homo sapiens NCBI 36 ▾

Chromosome Coordinates
Paste in comma separated list of chromosome coordinates, orientation (1,-1) and alleles see [\[sample format\]](#)

-or-

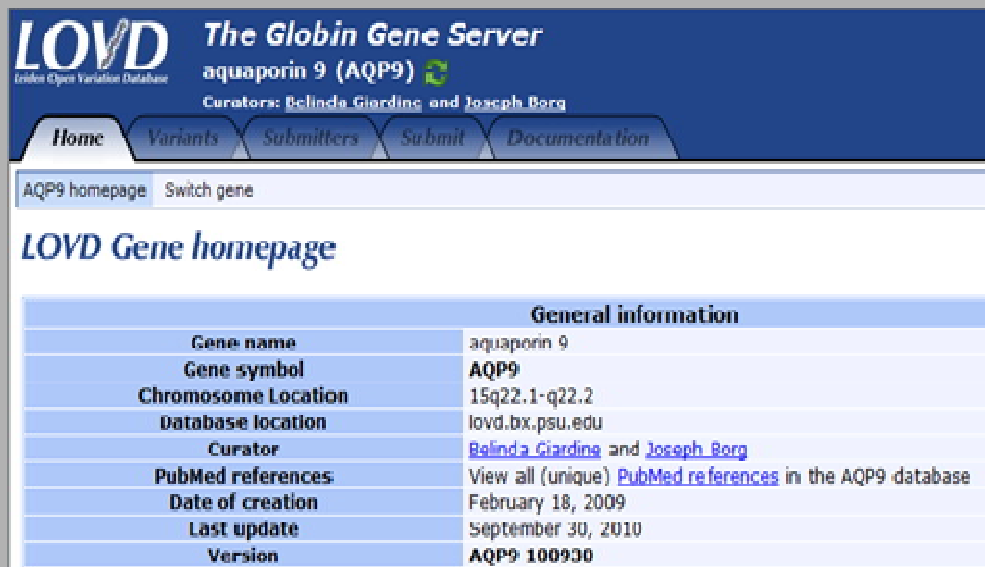
Upload file containing chromosome coordinates and nucleotide substitutions (size limit: 10M)

Enter your email address if you want the results through email :
Please check that your address is correct and your mailbox is not full.

GENOMICS

LOVD

LOVD stands for **L**eiden **O**pen (source) **V**ariation **D**atabase. LOVD is designed to provide a flexible, freely available tool for gene-centered collection and display of DNA variations.. LOVD was developed approaching the "LSDB-in-a-Box" idea for the easy creation and maintenance of a fully web-based gene sequence variation database, that is platform-independent and uses PHP and MySQL open source software only. The basic gene-centered and modular design of the database follows the recommendations of the Human Genome Variation Society (HGVS) and focuses on the collection and display of the DNA sequence variations but it is extendable with clinical data with minimal effort.



LOVD The Globin Gene Server
Leiden Open Variation Database
aquaporin 9 (AQP9)
Curators: [Balinda Giardina](#) and [Joseph Borg](#)

[Home](#) [Variants](#) [Submitters](#) [Submit](#) [Documentation](#)

[AQP9 homepage](#) [Switch gene](#)

LOVD Gene homepage

General information	
Gene name	aquaporin 9
Gene symbol	AQP9
Chromosome Location	15q22.1-q22.2
Database location	lovd.bx.psu.edu
Curator	Balinda Giardina and Joseph Borg
PubMed references:	View all (unique) PubMed references in the AQP9 database
Date of creation	February 18, 2009
Last update	September 30, 2010
Version	AQP9 100930

UPCOMING EVENTS

Indo-US Workshop on Biocomputing (ISB 2011)

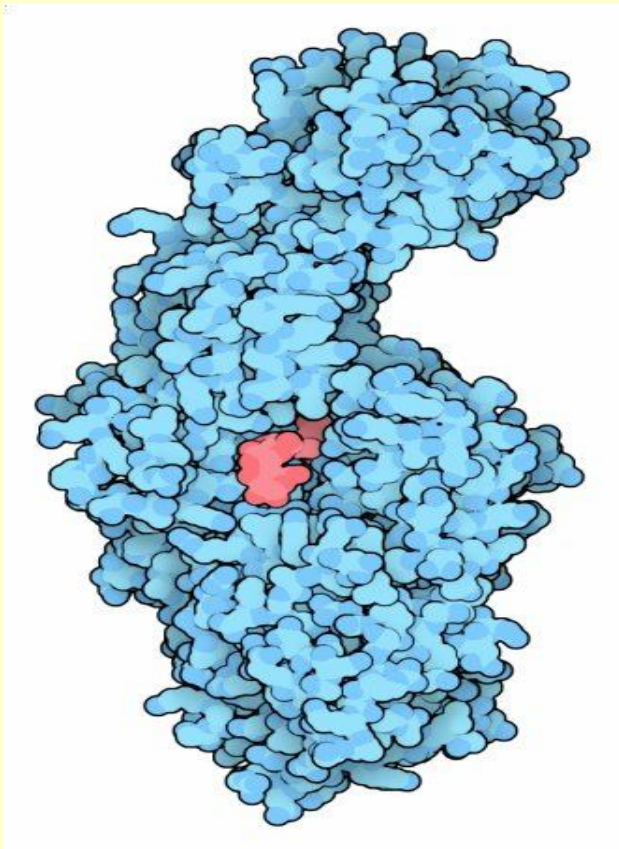
12 to 13 September 2011
Calicut, Kerala, India

Website: <http://www.isb2011.in>
Contact name: ISB 2011 Secretariat

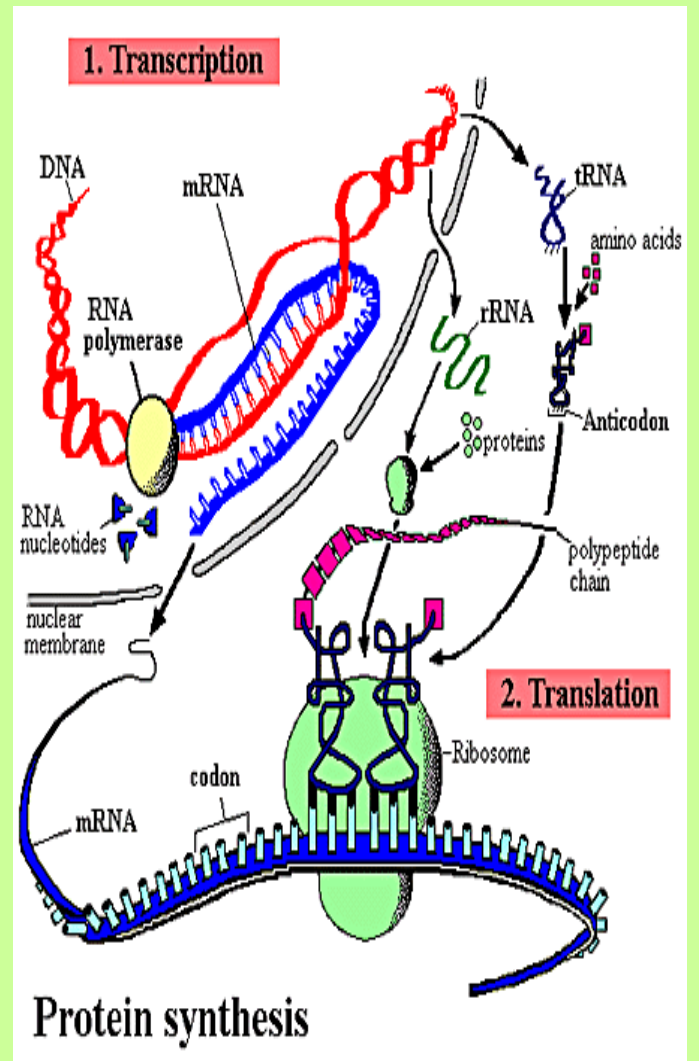
MOLECULE OF THE MONTH

The bacteria in our teeth use the enzyme glucansucrase to build long, sticky chains of sugars called glucans, using the sugar in our diet. These glucans glue the bacteria to the surfaces of our teeth, forming a biofilm that is difficult to remove.

PDB ID:3aic
Method: X-Ray diffraction



Protein transcription



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Answers of Bioinfy Quiz

1) A 2) C 3) B 4) B 5) B