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Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division)
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Inside…..

About us

The Bioinformatics Infrastructure Facility (BIF) at Biotechnology division, CSIR NEIST, Jorhat runs under the Biotechnology Information System Network (BTISnet) programme of DBT, Ministry of Science & Technology, and Government of India. The Centre was established on 2nd February, 2008 to promote innovation in Biological research and education through Bioinformatics accomplishment. The main goal is to facilitate and expose students and researchers from different academic institutions of North East India in Bioinformatics. The center conduct training and workshops for enlightening the use of bioinformatics applications in biological research and development. The Centre has access to global information through 24 hour high speed internet facility, and also e-journal facilities with DeLCON, Science Direct etc. To date the Centre has profoundly extended support in R & D work with a great intensity to different biological discipline including medicinal chemistry, computer aided drug design, genomics and proteomic data analysis etc.

Draft Genome Sequence of *Micromonospora* sp. Strain HK10

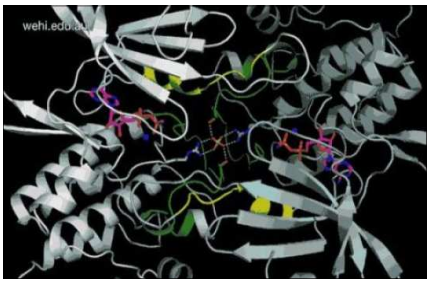
The Environmental biotechnology research group of BSTD, CSIR-NEIST has reported a 6.92-Mbp genome sequence of Micromonospora sp. HK10, isolated from soil samples collected from Kaziranga National Park, Assam, India. The work published in journal *Genome Announcements*, August 2016.

The full genome of strain Micromonospora sp. strain HK10 consists of 6,911,179 bp with 73.39% GC content, 6,196 protein-coding genes, and 86 RNAs. The Micromonospora sp. HK10 genome was sequenced with the Illumina NextSeq 500 format using a paired-end 2 150-bp library. The raw data has trimmed using Trimmomatic version 0.30 (8) for high-quality read length (cutoff quality score, 20). A total of 8,896,194 high-quality vector-filtered reads has used for assembly with CLC Genomics Workbench version 6 (CLC bio, Denmark). The final assembly contains 294 contigs with a total size of 6,911,179 bp, a GC content of 73.39%, and an N50 contig length of 61,860 bp; the longest contig assembled measures 352,445 bp. The draft genome of Micromonospora sp. HK10 has annotated for protein-coding genes with the help of Prodigal version 2.60 (9), and a total of 6,282 CDSs has been predicted. The gene annotation also reveals the presence of various pigments (porphyrin, carotenoid), antibiotic coding clusters (ansamycins, tetracycline, vancomycin group of antibiotics, neomycin, novobiocin, penicillin, and cephalosporin), and polyketide synthase coding genes.

[Courtesy: Genome Announc 4(4):e00559-15. doi:10.1128/genomeA.00559-15]

First 3-D Map of Cell-Building Protein Linked to Cancer

A team of researchers of Walter and Eliza Hall Institute, Australia have revealed for the first time the three-dimensional molecular 'map' of a protein that has been pinpointed as a driver of many types of cancers. The unrivalled view of the protein double cortin kinase like domain 1 (DCLK1) could provide clues to how it contributes to cancer formation and progression.DCLK1 is a protein that



assembles microtubules within cells. These rope-like structures give cells shape, enable movement and cell division, and are crucial in enabling the growth and spread of cancer cells. More than one in 10 stomach cancers have defective forms of DCLK1, which have also been found in kidney, rectal and pancreatic cancers.

Walter and Eliza Hall Institute scientists Dr. Onisha Patel and Dr Isabelle Lucet used the Australian Synchrotron to reveal the three-dimensional structure of a part of DCLK1 known as the 'kinase domain.The research was published Aug. 18 in the journal Structure.

In healthy cells, DCLK1 can control its own function, ensuring it only assembles microtubules at the right time.The kinase domain sits separately from the part of the protein that assembles microtubules, and can switch microtubule assembly on or off as needed. These mutations can lead to a non-stop microtubule building by DCLK1, and consequently chaotic cell division that is a hallmark of cancer.The protein structure they have generated allows to pinpoint a crucial three dimensional pocket within DCLK1.This will provide a first step towards designing a drug that will precisely target DCLK1, and prevent it from driving cancer growth. Similar protein structures have been used to design anti-cancer agents that are now been used clinically.

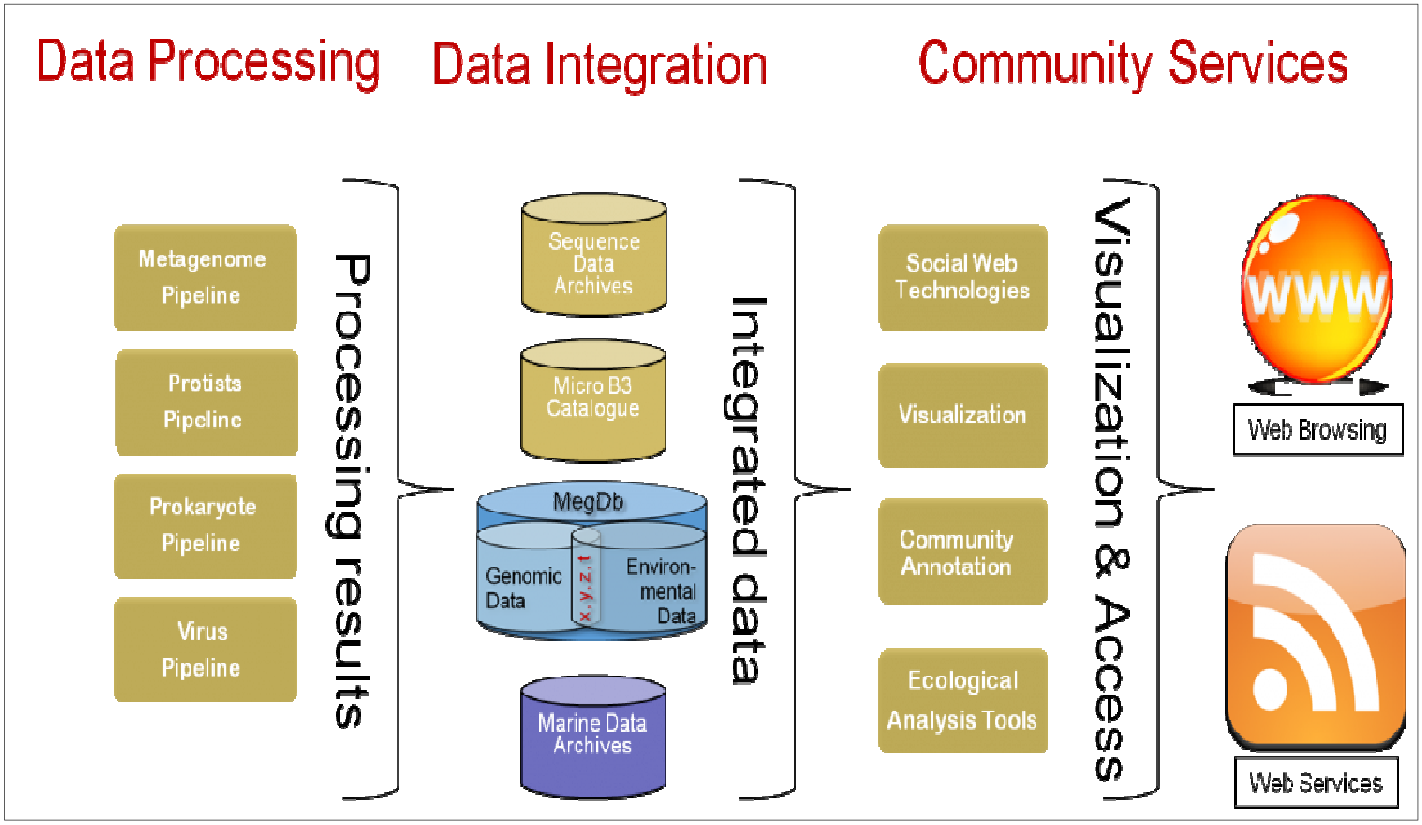
*[source: **Biochemical and Structural Insights into Doublecortin-like Kinase Domain 1.** Onisha Patel et al. Structure (Aug 22, 2016)]*

BioC viewer: a web-based tool for displaying and merging annotations in BioC

A group of researchers from Department of Biomedical Informatics (korea), National Center for Biotechnology Information (USA) and Deptartment of Computer Engineering (korea) designed BioC is an XML-based format to provide interoperability for text mining tools and manual curation results. BioC as a standard format is to align annotations from multiple systems is a challenge. Ideally, this should not be a major problem if users follow guidelines given by BioC key files. Nevertheless, the misalignment between text and annotations happens quite often because different systems tend to use different software development environments, e.g. ASCII vs. Unicode.

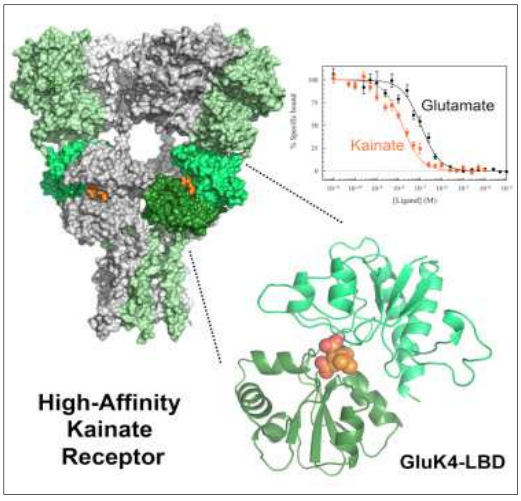
They first implemented the BioC Viewer to assist BioGRID curators as a part of the BioCreative V BioC track (Collaborative Biocurator Assistant Task). For the BioC track, the BioC Viewer helped curate protein-protein interaction and genetic interaction pairs appearing in full-text articles. The BioC Viewer itself as well as improvements made to the BioC Viewer since the BioCreative V Workshop to address the misalignment issue of BioC annotations. While uploading BioC files, a BioC merge process is offered when there are files from the same full-text article. If there is a mismatch between an annotated offset and text, the BioC Viewer adjusts the offset to correctly align with the text. The BioC Viewer has a user-friendly interface, where most operations can be performed within a few mouse clicks. The feedback from BioGRID curators has been positive for the web interface, particularly for its usability and learnability.

[Source: Database (Oxford). 2016 Aug 10;2016. pii: baw106. doi: 10.1093/database/baw106]



Kainate Receptor: GluK4 Ligand-Binding Domain

Ionotropic glutamate receptors play a key role in fast neurotransmission in the CNS and have been linked to several neurological diseases and disorders. One subfamily is the kainate receptors, which are grouped into low-affinity (GluK1-3) and high-affinity (GluK4-5) receptors based on their affinity for kainate. Although structures of the ligand-binding domain (LBD) of all low-affinity kainate receptors have been reported, no structures of the high-affinity receptor subunits are available. Here, we present the X-ray structure of GluK4-LBD with kainate at 2.05 Å resolution, together with thermofluor and radiolabel binding affinity data. Whereas binding-site residues in GluK4 are most similar to the AMPA receptor subfamily, the domain closure and D1-D2 interlobe contacts induced by kainate are similar to the low-affinity kainate receptor GluK1. These observations provide a likely explanation for the high binding affinity of kainate at GluK4-LBD.



Method: X-RAY DIFFRACTION
Resolution: 2.05 Å
R-Value Free: 0.262
R-Value Work: 0.191
Deposited: 2016-03-03
Released: 2016-08-24

[Source: Structure. 2016, 6;24(9):1582-9. doi: 10.1016/j.str.2016.06.019]

Upcoming events

International Conference on Molecular Signaling Basics to Applications | January 10–12, 2017

International Seminar on 'New Frontiers in Cytogenetics' and XIII Conference of the Society of Cytologists and Geneticists

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Patents

Data Semanticizer

US20060136194A1

Inventor: Patrick Armstrong et al.

Abstract

A computer-implemented method of defining a set of annotation elements to map a concept to electronic data as input data; generating a mapping rule, according to the set of annotation elements defined and a sample of the input data; mapping the concept to the input data by applying the mapping rule to the input data; and generating a semantic instance of the input data based upon the mapping of the concept to the input data. The set of annotation elements to map the concept to the input data are a selected ontology corresponding to the input data, a selected ontology concept from the selected ontology, a mapping of a word or word phrase in the sample input data to the selected ontology concept from the selected ontology, and a pattern of the mapped word or word phrase relative to a structure of the sample input data.

Kindly send us your feedback to

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