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PENGANTAR BIOINFORMATIKA

IBT 431

By Seprianto S.Pi, M.Si



Pertemuan 5

Operasional Data Base

Sasaran Perkuliahan

- Mahasiswa Mampu menjelaskan mekanisme pengambilan data dan penyimpanan database berbasis online
- Mahasiswa dapat mengakses NCBI, EMBL dan DDBJ
- Mahasiswa mampu cara mencari dan mendapatkan data dari GenBank
- Mengetahui cara penyimpanan data dalam bentuk Notepad

Introduction... Access to NCBI

1. Where do I start ?
2. How do I find my gene ?
3. How do I find gene-related data ?
4. Where can I ask questions or submit suggestions ?

1. Where do I start ?

What kind of data is available ?

NCBI includes data from:

- external resources
model organism databases,
genome projects,
PubMed and GenBank
submissions, and datasets
provided by the
research community

- internal computation

- ongoing curation

- follow the "How to reach us" link to submit questions or submissions

Tools
Data mining

Research at
NCBI
People,
projects, and
seminars

Software
engineering
Tools, R&D,
and databases

Education
Teaching
resources and
on-line
tutorials

FTP site
Download data
and software

Contact
information
How to reach
us



National Center for Biotechnology Information

National Library of Medicine National Institutes of Health

PubMed Entrez BLAST OMIM Books TaxBrowser Structure

Search Entrez for Go

SITE MAP

Guide to NCBI
resources

About NCBI

An introduction
for
researchers,
educators and
the public

GenBank

Sequence
submission
support and
software

Literature databases

PubMed,
OMIM, Books,
and PubMed
Central

Molecular databases

Sequences,
structures, and
taxonomy

Genomic biology

The human
genome,
whole
genomes, and
related
resources

What does NCBI do?

Established in 1988 as a national resource for molecular biology information, NCBI creates public databases, conducts research in computational biology, develops software tools for analyzing genome data, and disseminates biomedical information - all for the better understanding of molecular processes affecting human health and disease. [More...](#)

Cancer Chromosomes

Find cytogenetic, clinical, and reference information in the new Cancer Chromosomes database. Cancer Chromosomes, part of the Entrez retrieval system, integrates information from the NCI Mitelman Database of Chromosome Aberrations in Cancer, the NCI Recurrent Aberrations in Cancer database, and the NCI/NCBI SKY/M-FISH & CGH Database.

Entrez Gene

You can now use Entrez to search for information centered on the concept of a gene, and connect to many sources of related information both within and outside NCBI.

PubMed Central

An archive of life sciences journals

- Free fulltext
- Over 300,000 articles from over 150 journals
- Linked to PubMed and fully searchable

Use of PubMed Central requires no registration or fee. Access it from any computer with an Internet connection.

NCBI Newsletter

FG++ enhanced NCBI training course

Slots available for FieldGuidePlus Training Course at NCBI

Hot Spots

- Clusters of orthologous groups
- Coffee Break, Genes & Disease, NCBI Handbook
- Electronic PCR
- Entrez Home
- Entrez Tools
- Gene expression omnibus (GEO)
- Human genome resources
- LocusLink
- Malaria genetics & genomics
- Map Viewer
- dbMHC
- Mouse genome resources
- ORF finder
- Rat genome resources
- Reference sequence project

- Reference sequence project
- Retrovirus resources
- SAGEmap
- SKY/CGH database
- Trace archive
- VecScreen
- NCI-CGAP

1. Where do I start ?

www.ncbi.nlm.nih.gov

- navigate to NCBI databases, resources and tools from links provided on NCBI's home page
- from NCBI's home page you can submit a query against any of the databases in the pulldown menu

The screenshot shows the NCBI homepage with a red circle highlighting the search bar and the 'Entrez' dropdown menu. The dropdown menu lists various databases and resources:

- Entrez
- NCBI Web Site
- PubMed
- Protein
- Nucleotide
- Structure
- Genome
- Books
- CancerChromosomes
- Conserved Domains
- 3D Domains
- Gene
- GEO Profiles
- GEO Datasets
- HomoloGene
- Journals
- LocusLink
- MeSH
- OMIM

The main content area includes sections for 'Molecular databases Sequences, structures, and taxonomy', 'Genomic biology The human genome, whole genomes, and related resources', and 'PubMed Central An archive of life sciences journals'. The PubMed Central section lists:

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Other features include 'NCBI Newsletter', 'FG++ enhanced NCBI training course', and 'Slots available for FieldGuidePlus Training Course at NCBI'.

NCBI Home Page

- begin searches from Entrez Home Page, the Genome Biology Page, or Taxonomy Page

- navigate by links provided on the NCBI home page

National Center for Biotechnology Information
National Library of Medicine National Institutes of Health

PubMed Entrez BLAST OMIM Books TaxBrowser Structure

Search **Entrez** for **Go**

SITE MAP
[Guide to NCBI resources](#)
[About NCBI](#)
 An introduction for researchers, educators and the public
[GenBank](#)
 Sequence submission support and software
[Literature databases](#)
 PubMed, OMIM, Books, and PubMed Central
[Molecular databases](#)
 Sequences, structures, and taxonomy
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 The human genome, whole genomes, and related resources

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1. Where do I start ?

- find out what is new at NCBI from the Highlights on the NCBI home page or from the NCBI newsletter



National Center for Biotechnology Information

National Library of Medicine National Institutes of Health
www.ncbi.nlm.nih.gov

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[NCBI Newsletter](#)

FG⁺⁺ enhanced NCBI training course

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1. Where do I start ?

- the Genome Biology page provides links to organism specific resource pages

The screenshot shows the NCBI website interface. At the top, there is a navigation bar with links for PubMed, Entrez, BLAST, OMIM, Books, TaxBrowser, and Structure. A search bar is present with 'Entrez' selected. Below the navigation bar, the 'Genomic Biology' section is highlighted. It features a 'Genomic-scale science' section with a paragraph about genomics and a 'Human Genome' section with a link to explore resources. To the right, there is a list of 'Organism-specific resources' including Bee, Cat, Chicken, Cow, Dog, Frog, Fruit fly, Human, Malaria parasite, Microbial Genomes, Mosquito, Mouse, Nematode, Pig, Plant Genomes Central, Rat, Retroviruses, Sea urchin, Sheep, and Zebrafish. A blue sidebar on the left contains several links: Site Map, Human Genome resources at NCBI, Entrez Genomes complete genome sequences, RefSeq the reference sequence project, Clusters of Orthologous Groups analysis of complete genomes, HomoloGene orthologs between pairs of organisms, and LocusLink access to a collection of gene-related information. At the bottom, there are links for Disclaimer and Privacy statement, and a revision date of April 21, 2004.

NCBI

Site Map
guide to NCBI
resources

Human Genome
resources at
NCBI

Entrez Genomes
complete
genome
sequences

RefSeq
the reference
sequence
project

Clusters of
Orthologous
Groups
analysis of
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HomoloGene
orthologs
between pairs
of organisms

LocusLink
access to a
collection of
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Genomic Biology

PubMed Entrez BLAST OMIM Books TaxBrowser Structure

Search Entrez for Go

Genomic-scale science

Genomics is a new and fascinating area of biology, enabled through the large-scale DNA sequencing efforts of many public and private organizations, including the [Human Genome Project](#). Genomics takes a holistic approach to molecular biology and evolution by studying the complete genome and its protein expression patterns.

Human Genome

Explore [human genome resources](#) or browse the human genome sequence using the [Map Viewer](#).

The SNP Database

Single nucleotide polymorphisms (SNPs) are the most common genetic variations and occur once every 100 to 300 bases. It is expected that SNPs will accelerate the identification of disease genes by allowing researchers to look for associations between a disease and specific differences (in the form of SNPs) for a given population. [dbSNP](#) is a GenBank-independent database for SNP information. More information on using this database can be found at the [dbSNP homepage](#).

Organism-specific resources:

- Bee **NEW**
- Cat **NEW**
- Chicken **NEW**
- Cow **NEW**
- Dog **NEW**
- Frog **NEW**
- Fruit fly
- Human
- Malaria parasite
- Microbial Genomes
- Mosquito
- Mouse
- Nematode
- Pig **NEW**
- Plant Genomes Central
- Rat
- Retroviruses
- Sea urchin **NEW**
- Sheep **NEW**
- Zebrafish

[Disclaimer](#) [Privacy statement](#)

Revised: April 21, 2004.

1. Untuk Membuka data base NCBI, klik www.ncbi.nlm.nih.gov Tampilan Utama

The screenshot displays the NCBI (National Center for Biotechnology Information) homepage. The browser's address bar shows the URL <https://www.ncbi.nlm.nih.gov>. The page features a navigation menu on the left with categories such as NCBI Home, Resource List (A-Z), All Resources, Chemicals & Bioassays, Data & Software, DNA & RNA, Domains & Structures, Genes & Expression, Genetics & Medicine, Genomes & Maps, Homology, Literature, Proteins, Sequence Analysis, Taxonomy, Training & Tutorials, and Variation. The main content area is titled "Welcome to NCBI" and includes a search bar, a "Sign in to NCBI" link, and several key service categories: Submit (Deposit data or manuscripts into NCBI databases), Download (Transfer NCBI data to your computer), Learn (Find help documents, attend a class or watch a tutorial), Develop (Use NCBI APIs and code libraries to build applications), Analyze (Identify an NCBI tool for your data analysis task), and Research (Explore NCBI research and collaborative projects). A "Popular Resources" section lists PubMed, Bookshelf, PubMed Central, PubMed Health, BLAST, Nucleotide, Genome, SNP, Gene, Protein, and PubChem. The "NCBI News & Blog" section features articles such as "April 11 webinar: Getting the most out of web BLAST tabular format" (dated 04 Apr 2018) and "BLAST+ database improved" (dated 02 Apr 2018). The Windows taskbar at the bottom shows the system clock at 13:39 on 09/04/2018.

2. Untuk mencari urutan nukleotida yang diinginkan, maka pada kontak AI database, pilih nucleotide dan pada kotak search tuliskan nukleotida yang ingin dicari misalnya SoX2

The screenshot shows the NCBI (National Center for Biotechnology Information) website. The browser address bar displays 'https://www.ncbi.nlm.nih.gov'. The search bar at the top contains 'SoX2' and is circled in red. A dropdown menu next to the search bar is set to 'All Databases'. The page features a navigation menu on the left, a central 'Welcome to NCBI' section with links for 'Submit', 'Download', 'Learn', 'Develop', 'Analyze', and 'Research', and a 'Popular Resources' section on the right listing PubMed, Bookshelf, and other tools. The Windows taskbar at the bottom shows various application icons and the system clock indicating 13:44 on 09/04/2018.

3. Maka akan muncul beberapa hasil pencarian terkait nukleotida Sox2 yang terdapat pada berbagai organisme, klik salah satunya (tanda merah)

The screenshot shows the NCBI Nucleotide search interface. The search term 'soX2' is entered in the search bar. The results page displays a list of nucleotide sequences. A red arrow points to the first result, which is for *Ornithorhynchus anatinus*. The search results are as follows:

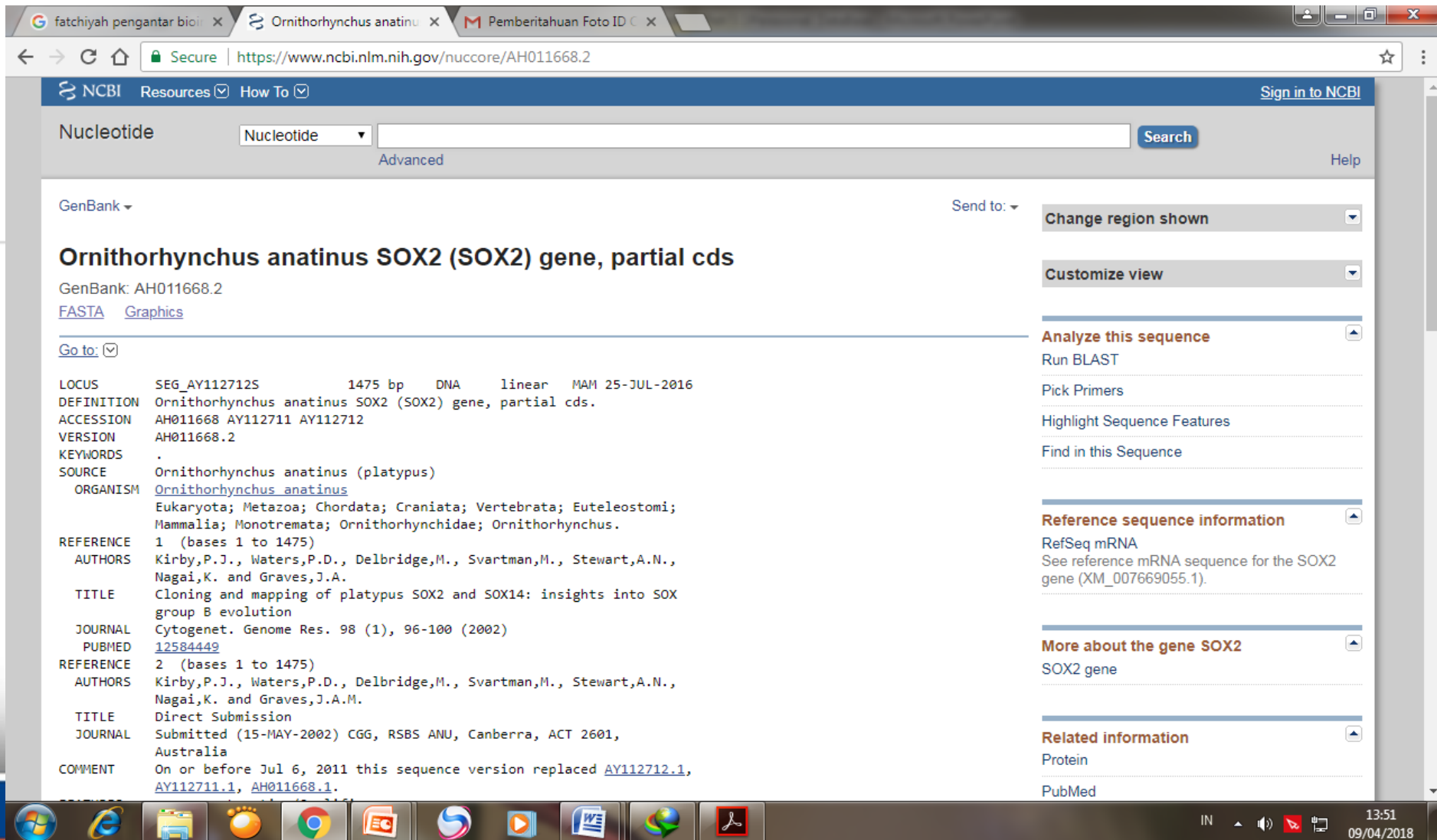
Items: 1 to 20 of 2222

Found 8592 nucleotide sequences. Nucleotide (2222) EST (6363) GSS (7)

- [Ornithorhynchus anatinus SOX2 \(SOX2\).gene..partial cds](#)
1. 1,475 bp linear DNA
Accession: AH011668.2 GI: 339511241
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)
- [Oreochromis mossambicus Sox2 \(Sox2\).gene..partial cds](#)
2. 597 bp linear DNA
Accession: EF431923.1 GI: 126723917
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)
- [Oreochromis karongae Sox2 \(Sox2\).gene..partial cds](#)
3. 664 bp linear DNA
Accession: EF431922.1 GI: 126723915
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)
- [Oreochromis aureus Sox2 \(Sox2\).gene..partial cds](#)

The right sidebar contains sections for 'Results by taxon', 'Find related data', 'Search details', and 'Recent activity'. The 'Search details' section shows the search term 'soX2[All Fields]'.

4. Hasil pencarian akan memunculkan *Oreochromis anatinus*, SoX2 gene, partial cds,



The screenshot shows a web browser window with the NCBI GenBank database. The search results for the entry AH011668.2 are displayed. The entry is for the *Ornithorhynchus anatinus* SOX2 (SOX2) gene, partial cds. The sequence is 1475 bp long, linear, and was submitted on July 25, 2016. The entry includes two references, both by Kirby, P.J., Waters, P.D., Delbridge, M., Svartman, M., Stewart, A.N., Nagai, K., and Graves, J.A. The first reference is from Cytogenet. Genome Res. 98 (1), 96-100 (2002), and the second is a direct submission to the GenBank database. The entry also includes a comment stating that the sequence version was replaced by AY112712.1, AY112711.1, and AH011668.1 on or before July 6, 2011.

GenBank Send to:

Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds

GenBank: AH011668.2
[FASTA](#) [Graphics](#)

Go to:

LOCUS SEG_AY112712S 1475 bp DNA linear MAM 25-JUL-2016
DEFINITION *Ornithorhynchus anatinus* SOX2 (SOX2) gene, partial cds.
ACCESSION AH011668 AY112711 AY112712
VERSION AH011668.2
KEYWORDS .
SOURCE *Ornithorhynchus anatinus* (platypus)
ORGANISM [Ornithorhynchus anatinus](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
REFERENCE 1 (bases 1 to 1475)
AUTHORS Kirby,P.J., Waters,P.D., Delbridge,M., Svartman,M., Stewart,A.N.,
Nagai,K. and Graves,J.A.
TITLE Cloning and mapping of platypus SOX2 and SOX14: insights into SOX
group B evolution
JOURNAL Cytogenet. Genome Res. 98 (1), 96-100 (2002)
PUBMED [12584449](#)
REFERENCE 2 (bases 1 to 1475)
AUTHORS Kirby,P.J., Waters,P.D., Delbridge,M., Svartman,M., Stewart,A.N.,
Nagai,K. and Graves,J.A.M.
TITLE Direct Submission
JOURNAL Submitted (15-MAY-2002) CGG, RSBS ANU, Canberra, ACT 2601,
Australia
COMMENT On or before Jul 6, 2011 this sequence version replaced [AY112712.1](#),
[AY112711.1](#), [AH011668.1](#).

Analyze this sequence

Run BLAST
Pick Primers
Highlight Sequence Features
Find in this Sequence

Reference sequence information

RefSeq mRNA
See reference mRNA sequence for the SOX2 gene (XM_007669055.1).

More about the gene SOX2

SOX2 gene


Related information

Protein
PubMed

Tampilan sekuens DNA dan posisi gen pada sekuens

/organism="Ornithorhynchus anatinus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9258"
gene <1..>1475
 /gene="SOX2"
 mRNA <1..>206
 /gene="SOX2"
 /product="SOX2"
CDS <1..>206
 /gene="SOX2"
 /note="HMG box"
 /codon_start=1
 /product="SOX2"
 /protein_id="AAMS1630.1"
 /translation="PMNAFMVWSRGQRKMAQENPKMHNSEISKRLGAEWKLLTDAEK
 RPFIDEAKRLRALHMKHPDYKYRP"
 gap 207..306
 /estimated_length=unknown
 mRNA <307..>1475
 /gene="SOX2"
 /product="SOX2"
 3'UTR <307..>1475
 /gene="SOX2"
ORIGIN
 1 cccatgaacg ccttcatggt ctggtcccgg gggcagcgtc ggaaaaatggc ccaggagaa
 61 cccaagatgc acaactcggg gatcagcaag cgtctggcgc ccgagtggaa actcttgacc
 121 gagcccgaga agcggccctt catcgacgag gccaaagcggc tgcgggcccct gcacatgaag
 181 gagcaccag attacaata ccggcc
 [gap 100 bp] [Expand Ns](#)
 307 aggg gaaggaccgg gaaggagggg agggactatt tttgtacaga gaaaactctg
 361 gggaggggag agaggaaactt gtatagatcc ggagggaacg aacgctacc aaaacttttt
 421 aaaagtcta gtggaacggt aggagctttg cagaaagtgt gcaaaagtct ttaccaataa
 481 tatttagagc tagtctccga gcgacggggg agggggggga gggaggggaa atgtttta
 541 atttgccagc agcttttgta cagtatttat cgagataaac atggcgatcc aaatgtccat
 601 cgtttataag ctgagaattt gccaatattt tccaaggaga gccttcttgc agaattttca
 661 tcagggaac cgacatttag agcggttgca aacgagaacg aggaaattag tcagatttgg
 721 acatcttaat ggtggagaaa ttgtacaaaa ggagggggga gtgggggaaag gttaggataa
 781 gtacttgcaa aaccatgtcc gtggttttct ataaaagggc aaaagttag attgtactaa
 841 attttttttt tactcttgtg taaaaagcga aaatggccac gcaggatgac accgttgata
 901 atttataata atagcttttg tttccaaatt tttcatcctg ttcagattaa aaaaaaacat
 961 gaattactet gtttgaata ttttctatg atttgaata tttctgtaa tttatcatga

5. Untuk mengetahui literatur jural yang digunakan dalam data urutan nukleotida tersebut, dapat klik PubMed pada lama *Related Information*



The screenshot shows a web browser window with the following elements:

- Browser Tabs:** fatchiyah pengantar bioi, Cloning and mapping of, Pemberitahuan Foto ID
- Address Bar:** Secure | https://www.ncbi.nlm.nih.gov/pubmed?LinkName=nucore_pubmed&from_uid=339511241
- NCBI Header:** NCBI Resources How To Sign in to NCBI
- Search Bar:** PubMed [Search] Help
- Format:** Abstract
- Links from Nucleotide:** Cytogenet Genome Res. 2002;98(1):96-100.
- Title:** Cloning and mapping of platypus SOX2 and SOX14: insights into SOX group B evolution.
- Authors:** Kirby PJ¹, Waters PD, Delbridge M, Svartman M, Stewart AN, Nagai K, Graves JA.
- Author information:** + Author information
- Abstract:** Group B SOX genes, the closest relatives to the sex-determining gene SRY, are thought to have evolved from a single ancestral SOX B by a series of duplications and translocations. The two SOX B genes SOX2 and SOX14 co-localize to chromosome 3q in humans. SOX2 and SOX14 homologues were cloned and characterized in the platypus, a monotreme mammal distantly related to man. The two genes were found to co-localize to chromosome 1q in this species. Proximity of the two related genes has therefore been conserved for 170 Myr, since humans and platypus diverged. The sequence similarity and conserved synteny of these group B genes provide clues to their origin. A simple model of SOX group B gene evolution is proposed.
- PMID:** 12584449 **DOI:** 10.1159/000068539
- Indexed for MEDLINE:** [Indexed for MEDLINE]
- Publication type, MeSH terms, Substances, Secondary source ID:** +
- LinkOut - more resources:** +
- Full text links:** KARGER Final Version
- Save items:** Add to Favorites
- Similar articles:**
 - Two distinct subgroups of Group B Sox genes for transcriptional activators and re [Mech Dev. 1999]
 - Sex determination in platypus and echidna: autosomal location of S [Chromosome Res. 2007]
 - The isolation and high-resolution chromosomal mapping of human SOX1 [Mamm Genome. 1999]
 - Review SOX genes: architects of development. [Mol Med. 1996]
 - Review Pairing SOX off: with partners in the regulation of embryonic dev [Trends Genet. 2000]
- Cited by 11 PubMed Central articles:** Spatiotemporal regulation of nervous system

7. Untuk membuka urutan nukleotida dalam format FASTA (kotak merah) maka klik FASTA kiri atas maka akan muncul nekleotida format FASTA

The screenshot shows a web browser window with the NCBI website open. The address bar shows the URL: <https://www.ncbi.nlm.nih.gov/nucleotide/AH011668.2?report=fasta>. The page title is "Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds". The main content area displays the FASTA sequence in a monospaced font. On the right side, there are several interactive panels: "Change region shown", "Customize view", "Analyze this sequence" (with sub-links for "Run BLAST" and "Pick Primers"), "Highlight Sequence Features", "Find in this Sequence", "Reference sequence information" (with a link for "RefSeq mRNA"), "More about the gene SOX2" (with a link for "SOX2 gene"), and "Related information" (with links for "Protein" and "PubMed").

FASTA

Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds

GenBank: AH011668.2

[GenBank](#) [Graphics](#)

```
>AH011668.2 Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds
CCCATGAACGCCTTCATGGTCTGGTCCCGGGGGCAGCGTCGGAAAATGGCCAGGAGAAGCCCAAGATGC
ACAACCTCGGAGATCAGCAAGCGTCTGGGCGCCGAGTGGAAACTCTTGACCGACCGCGAGAAGCGGCCCTT
CATCGACGAGGCCAAGCGGCTGCGGGCCCTGCACATGAAGGAGCACCCAGATTACAAATACCGGCCNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
GAAAACCTGCGGGAGGGCGAGAGGAACCTGTATAGATCCGGAGGGAACGAACGCTACCCAAAACCTTTT
AAAAGTTCTAGTGGAACGGTAGGAGCTTTGCAGAAAGTTGCAAAAGTCTTTACCAATAATATTTAGAGC
TAGTCTCCGAGCGACGGGGAGGGGGGGAGGGGAGGGGAAATGTTTAAATATTTGCCAGCAGCTTTGTGA
CAGTATTTATCGAGATAAACATGGCGATCCAAATGTCCATCGTTTATAAGCTGAGAATTTGCCAATATTT
TTCAAGGAGAGCCTTCTTGCAGAAATTTTTCACACGGCAACCCGACATTTAGAGCGGTGCAAAACGAGAACG
AGGAAATTAGTCAGATTTGGACATCTTAATGGTGGAGAAATTTACAAAAGGAGGGGGAGTGGGGAAAG
GTTAGGATAAGTACTTGCAAAACCATGTCGGTGGTTTTCTATAAAAGGGCAAAAGTTTAGATTGACTACTAA
ATTTTTTTTTTACTTCTTGTAAAAAGCGAAAATGGCCACGCAAGGATGACACCGTTGATAATTTATAATA
ATAGCTTTTGTTCAAAATTTTTCATCCTGTTGAGATTAAAAAAAACATGAATTAAGTGTGTTGAAATA
TTTTCTTATGGTTTGTAAATTTCTGTAATTTATCGTGATATTTAAAGTTTTTTTTCTCTCATTTCCG
TAGTTGTATTTAAAGATTCCGGCTCTGTGTTATTTGAATCAGTCTGCCGAGAGTCCATGTATATTTGA
ACTAATACCATCCTTATAACAGGTACATTTTCAACTTAAGTTTTTACTCCATTATGCACAGTTTGAGATA
AATAAATTTTTGAAATATGGACACTGAAATTCGGTTTGAGTCTTCGATTATTTGGGATCATGCAATGTGA
TTTTTCATAACTCGGGGACTAAAATCTCTCTGTTGACGGAGTTGATCTAAAAGCCACCGTAGTATT
CAAGCCGAGACGTGCAACATATGCTAATGTGACAGTTAGACCAAAAAAAAAAAAAACAACAATCAAAAAA
AAAAAAAAACAAGCAACCTTAAGTGAATAACTAATCGGGTAAAACGAAATACTCATGTGTTTAAATACG
AATTA
```

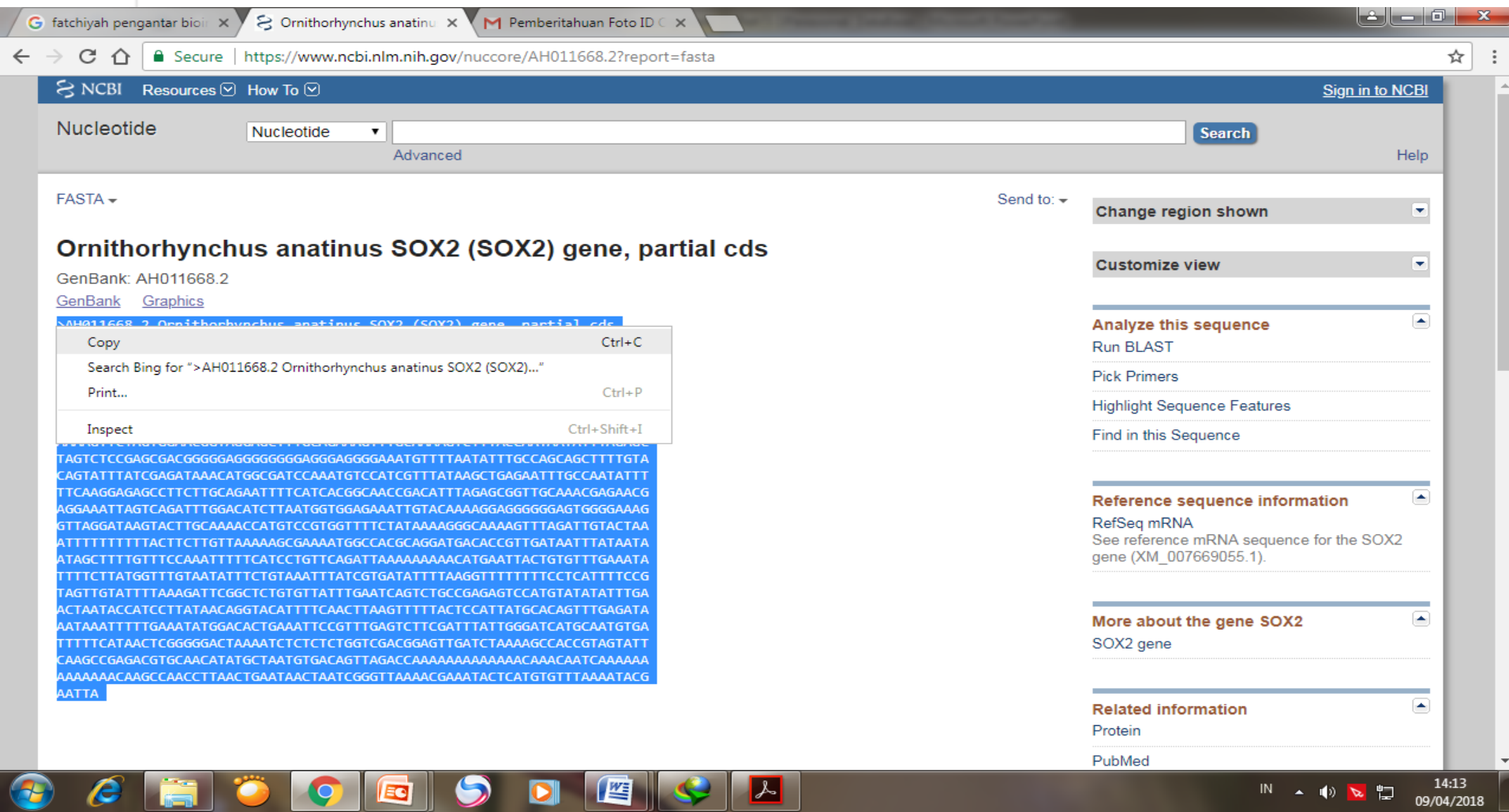
Terdapat berbagai cara untuk penyimpanan urutan nukleotida tersebut. Untuk menyimpan dalam format FASTA maka klik send Complete record → file FASTA

The screenshot shows the NCBI website interface. At the top, there are navigation links for 'NCBI Resources' and 'How To'. The main content area displays the 'Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds' with its GenBank ID 'AH011668.2'. Below the title, there is a 'Send to' dropdown menu that is open, showing three options: 'Complete Record' (selected), 'Coding Sequences', and 'Gene Features'. Under the 'Choose Destination' section, 'File' is selected, and the 'Format' is set to 'FASTA'. A 'Create File' button is visible at the bottom of the dropdown menu. The main content area also shows the FASTA sequence text starting with '>AH011668.2 Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds'.

8. Apabila telah memiliki akun NCBI, maka data FASTA tersebut dapat ditambahkan dalam akun dengan cara klik send Complete record Collection add to Collection

The screenshot shows the NCBI website interface. The main content area displays the FASTA sequence for the **Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds**. The GenBank ID is AH011668.2. The sequence is shown in a monospaced font, starting with >AH011668.2 Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds. A 'Send to' dropdown menu is open, showing options: Complete Record (selected), Coding Sequences, Gene Features, File, Clipboard, Collections (selected), and Analysis Tool. The 'Add to Collections' button is highlighted. The right sidebar contains sections for Reference sequence information, More about the gene SOX2, and Related information.

9. Penyimpana data juga dapat dilakukan dengan secara langsung mengcopy FASTA pada laman WEB



Browser tabs: fatchiyah pengantar bio... x, Ornithorhynchus anatinu... x, Pemberitahuan Foto ID C... x

Address bar: <https://www.ncbi.nlm.nih.gov/nucore/AH011668.2?report=fasta>

NCBI Resources How To Sign in to NCBI

Nucleotide Advanced Help

FASTA

Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds

GenBank: AH011668.2
[GenBank](#) [Graphics](#)

AH011668.2 Ornithorhynchus anatinus SOX2 (SOX2) gene, partial cds

- Copy
- Search Bing for ">AH011668.2 Ornithorhynchus anatinus SOX2 (SOX2)..."
- Print...
- Inspect

```

TAGTCTCCGAGCGACGGGGAGGGGGGGAGGGAGGGGAAATGTTTAAATATTTGCCAGCAGCTTTTGTACAGTATTTATCGAGATAAACATGGCGATCCAAATGTCCATCGTTTATAAGCTGAGAAATTTGCCAATATTTCAAGGAGAGCCTTCTGCGAAGATTTTCATCACGGCAACCACGACATTTAGAGCGGTTGCAAAACGAGAACGAGGAAATAGTCAGATTTGGACATCTTAATGGTGGAGAAATGTACAAAAGGAGGGGGAGTGGGAAAGGTTAGGATAAGTACTTGCAAAACCATGTCCTGGTGGTTTCTATAAAAAGGGCAAAAGTTAGATTGACTAAATTTTCTTACTCTTGTATAAAAGCGAAAATGGCCACGACAGGATGACACCGTTGATAATTTATAATAATAGCTTTGTTTCCAAATTTTCATCCTGTTGAGATTAATAAAAAAACAATGAATTAAGTGTGTTGAAATAATTTCTATAGGTTTGTAAATATTTCTGTAATTTATCGTGATATTTAAAGGTTTTTTTTCCTCATTTCCGTAGTTGATTTTAAAGATTCGGCTCTGTGTTATTTGAATCAGTCTGCCGAGAGTCCATGATATATTTGACTAATACCACCTTATAACAGGTACATTTCAACTAAGTTTTTACTCCATTATGCACAGTTTGAGATAAATAAATTTTGAATATGGACACTGAAATTCGGTTTGAGTCTTCGATTATTTGGGATCATGCAATGTGATTTTTCATAACTCGGGGACTAAAATCTCTCTCTGTTGTCGACGGAGTTGATCTAAAAGCCACCGTAGTATTCAAGCGAGACGTGCACATATGCTAATGTGACAGTTAGACCAAAAAAAAAAAAAACAAACAATCAAAAAA
AAAAAAAAACAAAGCCAACCTTAACCTGAATAACTAATCGGGTTAAAAACGAAATACTCATGTGTTAAAAATACG
AATTA

```

Change region shown

Customize view

Analyze this sequence

- Run BLAST
- Pick Primers
- Highlight Sequence Features
- Find in this Sequence

Reference sequence information

RefSeq mRNA
See reference mRNA sequence for the SOX2 gene (XM_007669055.1).

More about the gene SOX2

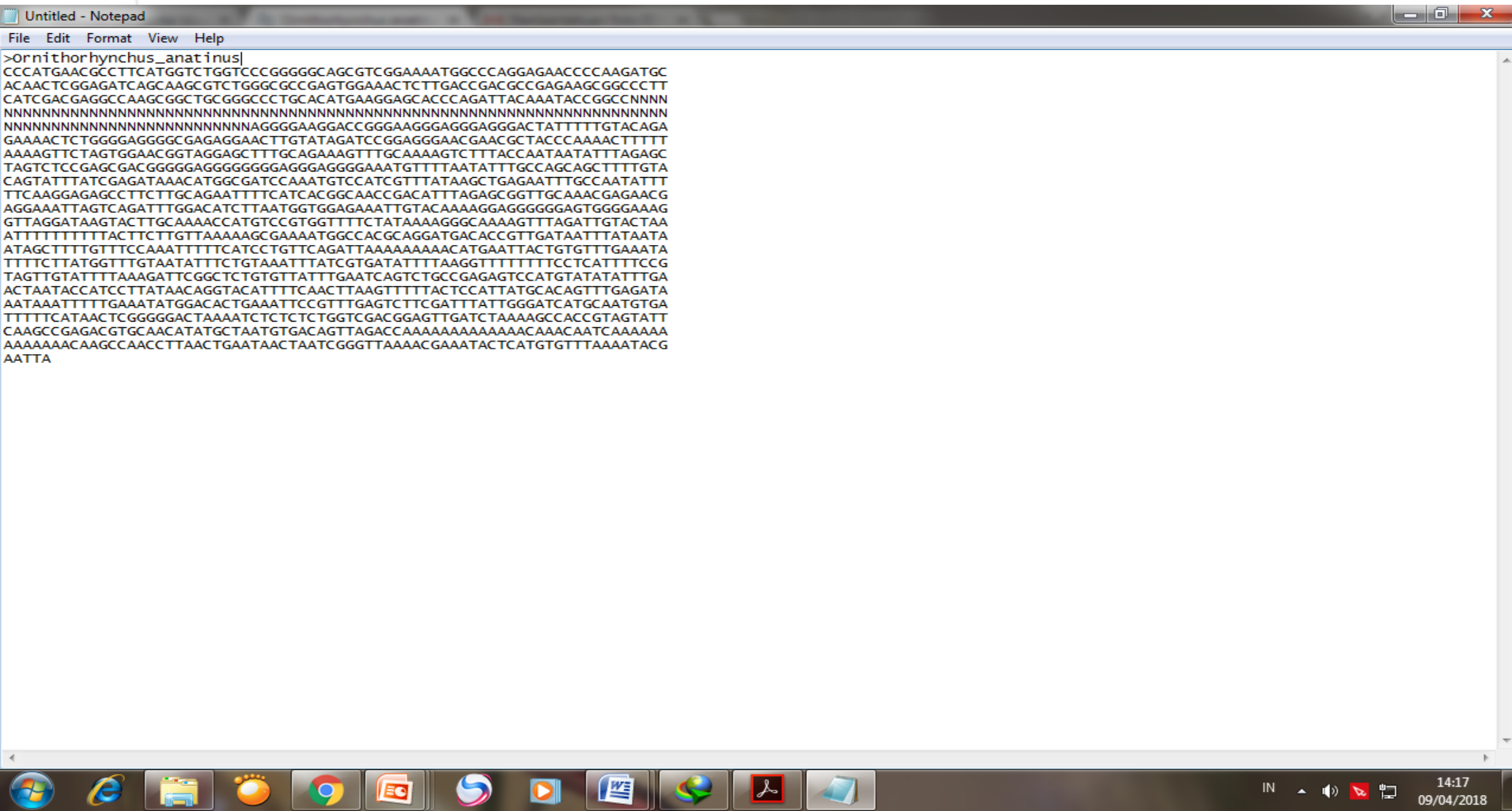
SOX2 gene

Related information

- Protein
- PubMed

Windows taskbar: 14:13 09/04/2018

9. FASTA yang sudah di copy, kemudian di Paste dalam Notepad dan di save . Data dapat digunakan sewaktu waktu untuk analisis lebih lanjut. Lakukan Hal yang sama untuk pencarian protein (pada all database “ nucleotide diganti Protein



Untitled - Notepad

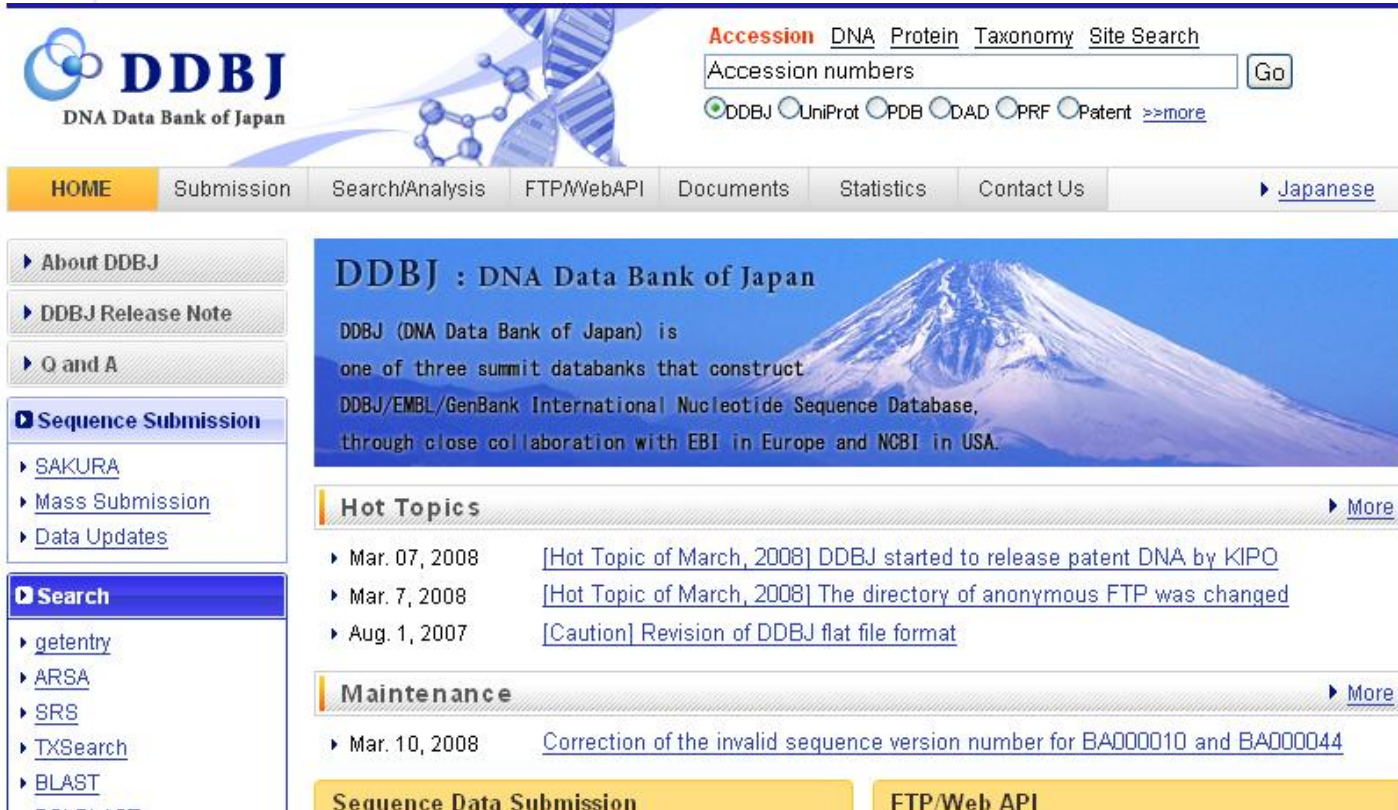
File Edit Format View Help

```
>Ornithorhynchus_anatinus|
CCCATGAACGCCTTCATGGTCTGGTCCC GGGGGCAGCGTCGGAAAATGGCCCAGGAGAACCCCAAGATGC
ACAAC TC GGAGATCAGCAAGCGTCTGGGCGCCGAGTGGAACTCTTGACCGACGCCGAGAAGCGGCCCTT
CATCGACGGAGCCAAGCGGCTGCGGGCC TGCACATGAAGGAGCACCCAGATTACAAATACCGCCNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
GAAAAC TC TGGGGAGGGCCGAGAGGAAC TTGTATAGATCCGGAGGGAACGAACGC TACCCAAAAC TTTT
AAAAGTTCTAGTGGAACGGTAGGAGCTTTCAGAAAAGTTTGC AAAAGTCTTTACCAATAATATTTAGAGC
TAGTCTCCGAGCGACGGGGGAGGGGGGGAGGGGAAATGTTTTAATATTTGCCAGCAGCTTTTGTA
CAGTATTTATC GAGATAAACATGGCGATCCAAATGTCCATCGTTTTAAGCTGAGAATTTGCCAATATTT
TTCAAGGAGAGCCTTCTTGCAGAATTTTCACACGGCAACC GACATTTAGAGCGGTTTGC AAACGAGAACG
AGGAAATTAGTCAGATTTGGACATCTTAATGGTGGAGAAATGTACAAAAGGAGGGGGGAGTGGGGAAAG
GTTAGGATAAGTACTTGCAAAACCATGTCCGTGTTTTCTATAAAAAGGGCAAAAAGTTTAGATTGTACTAA
ATTTTTTTTTTACTTCTGTTAAAAAGCGAAAATGGCCACGCAAGGATGACACCGTTGATAATTTATAATA
ATAGCTTTTGTTC CAAATTTTTTCATCCGTTTCAGATTA AAAAAAAAAACATGAATTACTGTGTTTGAATA
TTTTCTTATGGTTTGTAAATTTTCTGTAAATTTATCGTGATATTTAAGGTTTTTTTTCTCCATTTTCCG
TAGTTGATTTTTAAAGATTCGGCTCTGTGTTATTTGAATCAGTCTGCCGAGAGTCCATGTATATTTTGA
ACTAATACCATCCCTTATAACAGGTACATTTTCAACTTAAGTTTTTACTCCATTATGCACAGTTTGAGATA
AATAAATTTTTGAAAATATGGACACTGAAAATCCGTTTGAGTCTTCGATTTATTGGGATCATGCAATGTGA
TTTTTCATAAC TCGGGGGACTAAAATCTCTCTGGTGCACGGAGTTGATCTAAAAGCCACCGTAGTATT
CAAGCCGAGACGTGCAACATATGCTAATGTGACAGTTAGACCAAAAAAAAAAAAAACAAACAATCAAAAAA
AAAAAAAAACAAGCCAACCTTAACTGAATAACTTAATCGGGTTAAAACGAAATACTCATGTGTTTAAAAATACG
AATTA
```


CIB-DDBJ

Center for information biology

- <http://www.ddbj.nig.ac.jp/>
- Jepang



DDBJ
DNA Data Bank of Japan

[Accession](#) [DNA](#) [Protein](#) [Taxonomy](#) [Site Search](#)

Accession numbers

DDBJ UniProt PDB DAD PRF Patent [>>more](#)

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Sequence Submission
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[Data Updates](#)

Search
[getentry](#)
[ARSA](#)
[SRS](#)
[TXSearch](#)
[BLAST](#)

DDBJ : DNA Data Bank of Japan

DDBJ (DNA Data Bank of Japan) is one of three summit databanks that construct DDBJ/EMBL/GenBank International Nucleotide Sequence Database, through close collaboration with EBI in Europe and NCBI in USA.

Hot Topics [More](#)

- ▶ Mar. 07, 2008 [\[Hot Topic of March, 2008\] DDBJ started to release patent DNA by KIPO](#)
- ▶ Mar. 7, 2008 [\[Hot Topic of March, 2008\] The directory of anonymous FTP was changed](#)
- ▶ Aug. 1, 2007 [\[Caution\] Revision of DDBJ flat file format](#)

Maintenance [More](#)

- ▶ Mar. 10, 2008 [Correction of the invalid sequence version number for BA000010 and BA000044](#)

Sequence Data Submission **FTP/Web API**

The screenshot shows the ENA website interface. At the top, there is a navigation bar with links for Services, Research, Training, and About us. Below this is the ENA logo and a search bar with a 'Search' button. The search bar includes examples like 'BN000085, histone' and links for 'Advanced' and 'Sequence' search. A secondary navigation bar contains links for Home, Search & Browse, Submit & Update, Software, About ENA, and Support. The main content area features a large heading 'European Nucleotide Archive' followed by a descriptive paragraph and a link to 'More about ENA'. Below this is a 'Text Search' section with a search input field, examples, and a 'Search' button. A 'Sequence Search' section is also visible, with a prompt to 'Enter or paste a nucleotide sequence or accession number'. On the right side, there is a 'Popular' section with a list of links and a 'Latest ENA news' section with a news item dated '03 Apr 2017'.

EMBL-EBI

Services Research Training About us

ENA
European Nucleotide Archive

Search

Examples: BN000085, histone

Advanced
Sequence

Home Search & Browse Submit & Update Software About ENA Support

European Nucleotide Archive

The European Nucleotide Archive (ENA) provides a comprehensive record of the world's nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation. [More about ENA](#)

Access to ENA data is provided through the browser, through search tools, large scale file download and through the API.

Text Search

Search

Examples: BN000065, histone

Search

Advanced search

Sequence Search

Enter or paste a nucleotide sequence or accession number

Popular

- Submit and update
- Sequence submissions
- Genome assembly submissions
- Submitting environmental sequences
- Citing ENA data
- Rest URLs for data retrieval
- Rest URLs to search ENA

Latest ENA news

03 Apr 2017: [ENA Release 131](#)

Release 131 of ENA's assembled/annotated sequences now available

Interface dari European Nucleotide Archive

Terhubung dengan database lain seperti NCBI dan DDBJ

ENA relatif mudah diakses dengan pengelompokan data yang baik

EMBL-EBI European Nucleotide Archive

Services Research Training About us

Home Search & Browse Submit & Update Software About ENA Support

European Nucleotide Archive

The European Nucleotide Archive (ENA) provides a comprehensive record of the world's nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation. [More about ENA](#)

Access to ENA data is provided through the browser, through search tools, large scale file download and through the API.

Text Search

Examples: [BN000065](#), [histone](#)

[Search](#)

[Advanced search](#)

Sequence Search

Enter or paste a nucleotide sequence or accession number

Popular

- [Submit and update](#)
- [Sequence submissions](#)
- [Genome assembly submissions](#)
- [Submitting environmental sequences](#)
- [Citing ENA data](#)
- [Rest URLs for data retrieval](#)
- [Rest URLs to search ENA](#)

Latest ENA news

03 Apr 2017: [ENA Release 131](#)

Release 131 of ENA's assembled/annotated sequences now available

Step 1.

Gunakan kata kunci untuk mencari database transkriptomik dan genomik

Kasus A. Gunakan kata kunci . **Oryza officinalis**

Kasus B. Gunakan kata kunci. **Human Mycobacterium**

www.ebi.ac.uk/ena/data/search?query=oryza+officialis

Assembly (1)
Sequence (Update) (1)
Sequence (Release) (109,167)
Contig set
Genome assembly contig set (1)
Transcriptome assembly contig set (1)
Coding (Update) (37)
Coding (Release) (895)
Non-coding (Release) (105)
Read
Experiment (7)
Run (8)
Study (4)
Study (Sequence) (15)
Taxon (1)
Sample (17)
Submission

Assembly (1 results found)
GCA_000717455.1 O. officinalis chromosome 3 short arm assembly for Oryza officinalis
View all 1 results

Sequence (Update) (1 results found)
AP011469 Oryza officinalis genomic DNA, chromosome 6, BAC clone: OO_Ba0014A07, strain: IRGC 100896.
View all 1 results

Sequence (Release) (109,167 results found)
AC225786 Oryza officinalis, complete sequence.
View all 109,167 results

Genome assembly contig set (1 results found)
JJMQ01000000 Oryza officinalis, WGS project JJMQ01000000 data
View all 1 results

Transcriptome assembly contig set (1 results found)
GBRJ01000000 Oryza officinalis, TSA project GBRJ01000000 data
View all 1 results

Coding (Update) (37 results found)
BAX24998 Oryza officinalis hypothetical protein
View all 37 results

Step 2a. Kasus A. Kata kunci ? Oryza officinalis?

Klik data Transcriptome assembly contig set

Penting: Dalam analisis komparasi ekspresi gen, lebih mudah membandingkan data transkrip yang sudah valid seperti RNA sequencing

www.ebi.ac.uk/ena/data/view/GBRJ01000000

TSA Sequence Set: GBRJ01000000

Oryza officinalis, TSA project GBRJ01000000 data

View: [TEXT](#) [XML](#) Download: [XML](#) [TEXT](#)

Lineage	Molecule type	Topology	Data class	Taxonomic Division
Oryza officinalis	transcribed RNA	linear	SET	PLN

Number of sequences: 476 Set Version: 1

Keywords: Transcriptome Shotgun Assembly, TSA.

Lineage: Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza

Navigation: [Source Feature\(s\)](#) [Comments](#) [Publications](#) [Submission Details](#)

[1] **De novo assembly and characterization of Oryza officinalis leaf transcriptome by using RNA-seq.**
Bao Y., Xu S., Jing X., Meng L., Qin Z.
School of Life Science, Qufu Normal University, Qufu, Shandong 273165, China.
Biomed Res Int 2015982065 (2015)
[Show abstract](#)
[PubMed](#)
[PDF](#)
DOI: 10.1155/2015/982065
[doi](#)

Publications inherited from Study

[1] ~~De novo assembly and characterization of Oryza officinalis leaf transcriptome by using RNA-seq.~~

16:17 20-Apr-17

Step 3a. Kasus A. Kata kunci Oryza officinalis

Publikasi dari data tersebut dapat dicek pada laman **Publications**

www.ebi.ac.uk/ena/data/view/GBRJ01000000

rizaputranto - Yahoo | Gmail - Boîte de réception | Webmail - Main | Google Agenda | Facebook | Twitter / Accueil | Welcome! | LinkedIn | Riza Arief Putranto | Riza-Arief Putranto - | Google Maps

TSA Sequence Set: GBRJ01000000

Oryza officinalis, TSA project GBRJ01000000 data

View: [TEXT](#) [XML](#) Download: [XML](#) [TEXT](#)

Lineage	Molecule type	Topology	Data class	Taxonomic Division
Oryza officinalis	transcribed RNA	linear	SET	PLN

Number of sequences: 476
Set Version: 1

Keywords
Transcriptome Shotgun Assembly, TSA.

Lineage
[Eukaryota](#), [Viridiplantae](#), [Streptophyta](#), [Embryophyta](#), [Tracheophyta](#), [Spermatophyta](#), [Magnoliophyta](#), [Liliopsida](#), [Poales](#), [Poaceae](#), [BOP clade](#), [Oryzoideae](#), [Oryzeae](#), [Oryzinae](#), [Oryza](#)

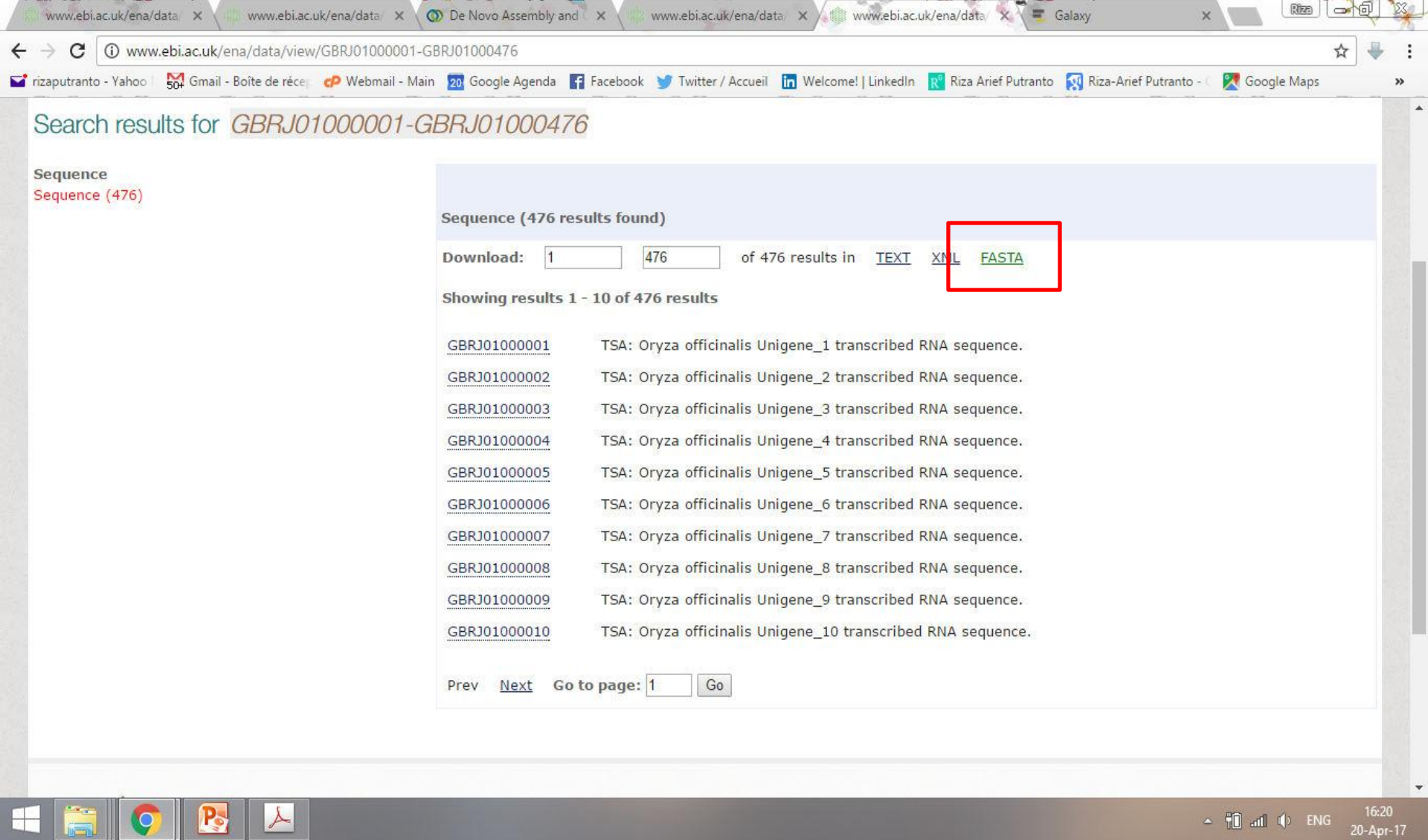
Navigation | Source Feature(s) | Comments | Publications | Submission Details

↓	Transcriptome assembly contig	GBRJ01000001-GBRJ01000476
↑	Study:	PRJNA261634
↓	Sample:	SAMN03074946
🏠	Taxon:	Taxon:4535

Windows taskbar: 16:16 20-Apr-17

Step 4a. Kasus A. Kata kunci Oryza officinalis

Data transkriptomik dapat diakses di laman **Navigation**
Klik kode sekuen **GBR1000001** untuk mengunduh data



Step 5a. Kasus A. Kata kunci **Oryza officinalis**

Data sekuen transkrip mRNA dapat diunduh dalam bentuk **.fasta** dengan langsung klik **FASTA**

PDB

Protein data bank



A MEMBER OF THE PDB

An Information Portal to Biological Macromolecular Structures

As of Tuesday Mar 11, 2008 there are 49426 Structures | [PDB Statistics](#) [CONTACT US](#) | [HELP](#) | [PRINT PAGE](#) PDB ID or keyword Author [Home](#) [Search](#)

Are you missing data updates? The PDB archive has moved to <ftp://ftp.wwpdb.org>.
For more information click [here](#).

Welcome to the RCSB PDB

The **RCSB** PDB provides a variety of tools and resources for studying the structures of biological macromolecules and their relationships to sequence, function, and disease.

The RCSB is a member of the **wwPDB** whose mission is to ensure that the PDB archive remains an international resource with uniform data.

News

- [Complete News](#)
- [Newsletter](#)
- [Discussion Forum](#)
- [Job Listings](#)

11-March-2008

Using RCSB PDB Tools and Resources

A chapter describing the various options and procedures for querying, downloading and

- <http://www.rcsb.org/pdb/home/home.do>
- 3D Struktur

- Home
- Getting Started
- ▶ Download Files
- ▶ Deposit and Validate
- ▶ Structural Genomics
- ▶ Dictionaries & File Formats
- ▶ Software Tools
- ▶ General Education
- ▶ Site Tutorials
- BioSync
- ▼ General Information
 - About the PDB

Situs website - Bioinformatika

protein database. <http://www.expasy.org/sprot/>

ExPASy - UniProt Knowledgebase: Swiss-Prot and TrEMBL

http://www.expasy.org/sprot/

Search for

Swiss-Prot
Protein knowledgebase
TrEMBL
Computer-annotated supplement to Swiss-Prot

UniProt
the universal protein resource

The UniProt Knowledgebase consists of:

- **UniProtKB/Swiss-Prot**; a curated protein sequence database which strives to provide a high level of annotation (such as the description of the function of a protein, its domains structure, post-translational modifications, variants, etc.), a minimal level of redundancy and high level of integration with other databases [[More details](#) / [References](#) / [Linking to Swiss-Prot](#) / [User manual](#) / [Recent changes](#) / [Disclaimer](#)].
- **UniProtKB/TrEMBL**; a computer-annotated supplement of Swiss-Prot that contains all the translations of EMBL nucleotide sequence entries not yet integrated in Swiss-Prot.

These databases are developed by the Swiss-Prot groups [at SIB](#) and [at EBI](#).

UniProt Knowledgebase Release 12.1 consists of:
UniProtKB/Swiss-Prot Release 54.1 of 21-Aug-2007:
277883 entries ([More statistics](#))
UniProtKB/TrEMBL Release 37.1 of 21-Aug-2007:
4754787 entries ([More statistics](#))

> Swiss-Prot headlines
More than 18'500 phosphorylation sites identified by mass spectrometry in UniProtKB/Swiss-Prot (Read [more...](#))

Access to the UniProt Knowledgebase

- **SRS** - Access to UniProtKB/Swiss-Prot, UniProtKB/TrEMBL and other databases using the Sequence Retrieval System
- **Full text search** in the UniProt Knowledgebase
- **Advanced search in the UniProt Knowledgebase** by description, gene name and organism (can be used to create html links to UniProt Knowledgebase queries)
- **Taxonomy browser (NEWT)**
- **BLAST** similarity search
- **by description or identification** (any word in the DE, OS, OG, GN and ID lines)
- **by citation** (RL line; UniProtKB/Swiss-Prot only)
- **Retrieve a list of UniProtKB entries**
- **Randomly retrieve a UniProtKB entry**
- **UniProtKB Sequence/Annotation Version Database** new!
- **Swiss-Prot ID tracker**

Documents and services

Swiss-Prot documents - user manual, release notes, indices and lots of other important documents and lists

1. Situs ini mengkhususkan pada protein database
2. Fasilitas meliputi : Blast, struktur dll

TUGAS PRAKTIKUM ---- KUMPULKAN MINGGU DEPAN

1. Setiap mahasiswa menetapkan gen atau protein yang ingin dicari , kemudian lakukan pencarian secara mandiri pada situs NCBI dan EBI. Kemudian pelajari data yang ada didalannya dengan benar. jangan ragu ragu untuk eksplorasi yang ada dalam database

THANK
YOU



607132.wordpress.com

Noviani's Blog

