Біоінформатика.

БАЗИ ДАНИХ. МОДЕЛЬ NCBI

Lab.1

Центральні питання

- ☐ Де знайти літературу про ген/білок, що цікавить
- ☐ Де можна знайти послідовність гена/генома, що цікавить?
- ☐ Що таке депонування НАП?

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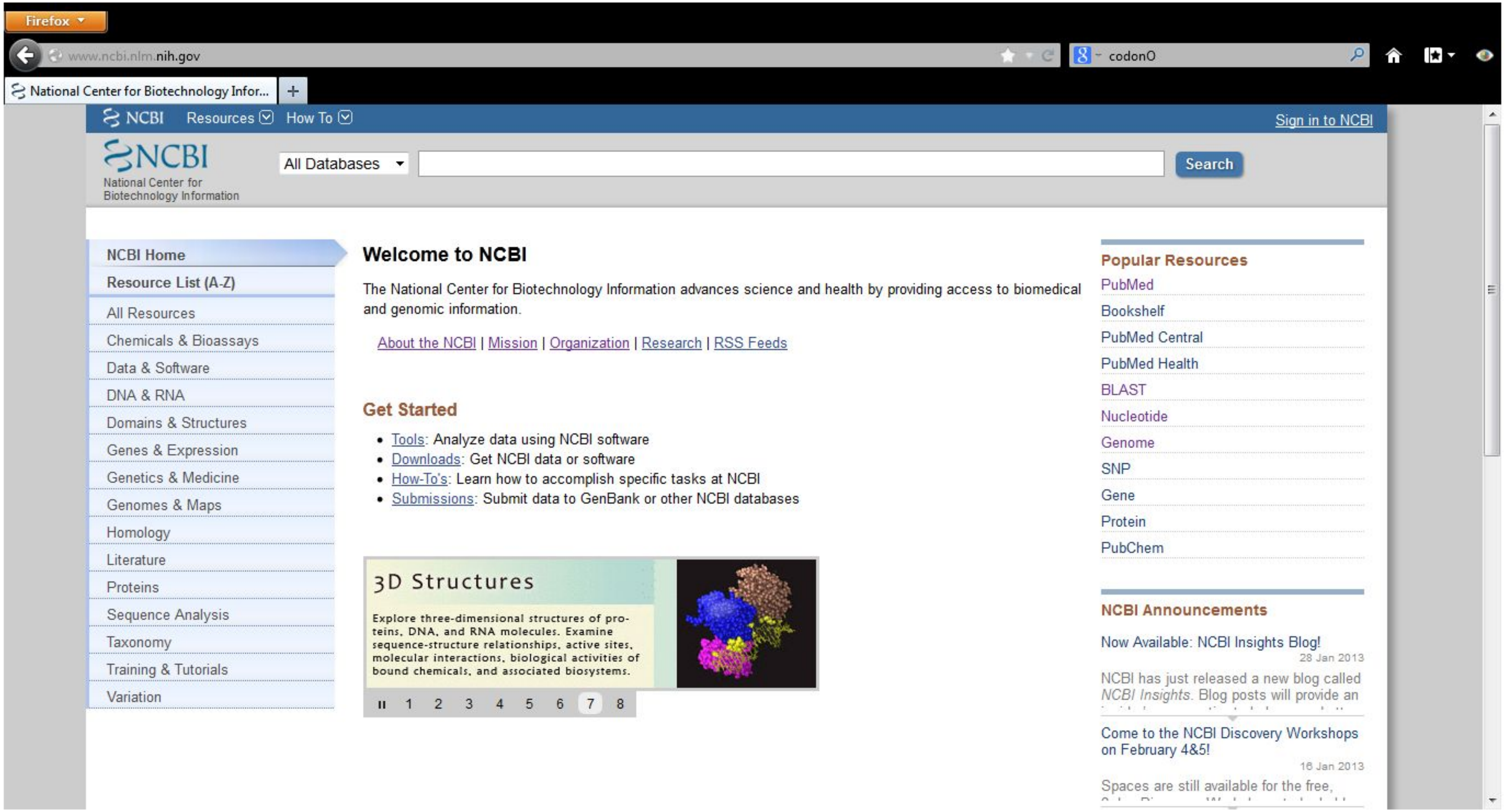

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- Submissions: Submit data to GenBank or other NCBI databases

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28 Jan 2013

NCBI has just released a new blog called *NCBI Insights*. Blog posts will provide an

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16 Jan 2013

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NCBI

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Chemicals and assays
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…..

Геномні дані

Genome
Variations
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OMIM
Genes and expression
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PubMed

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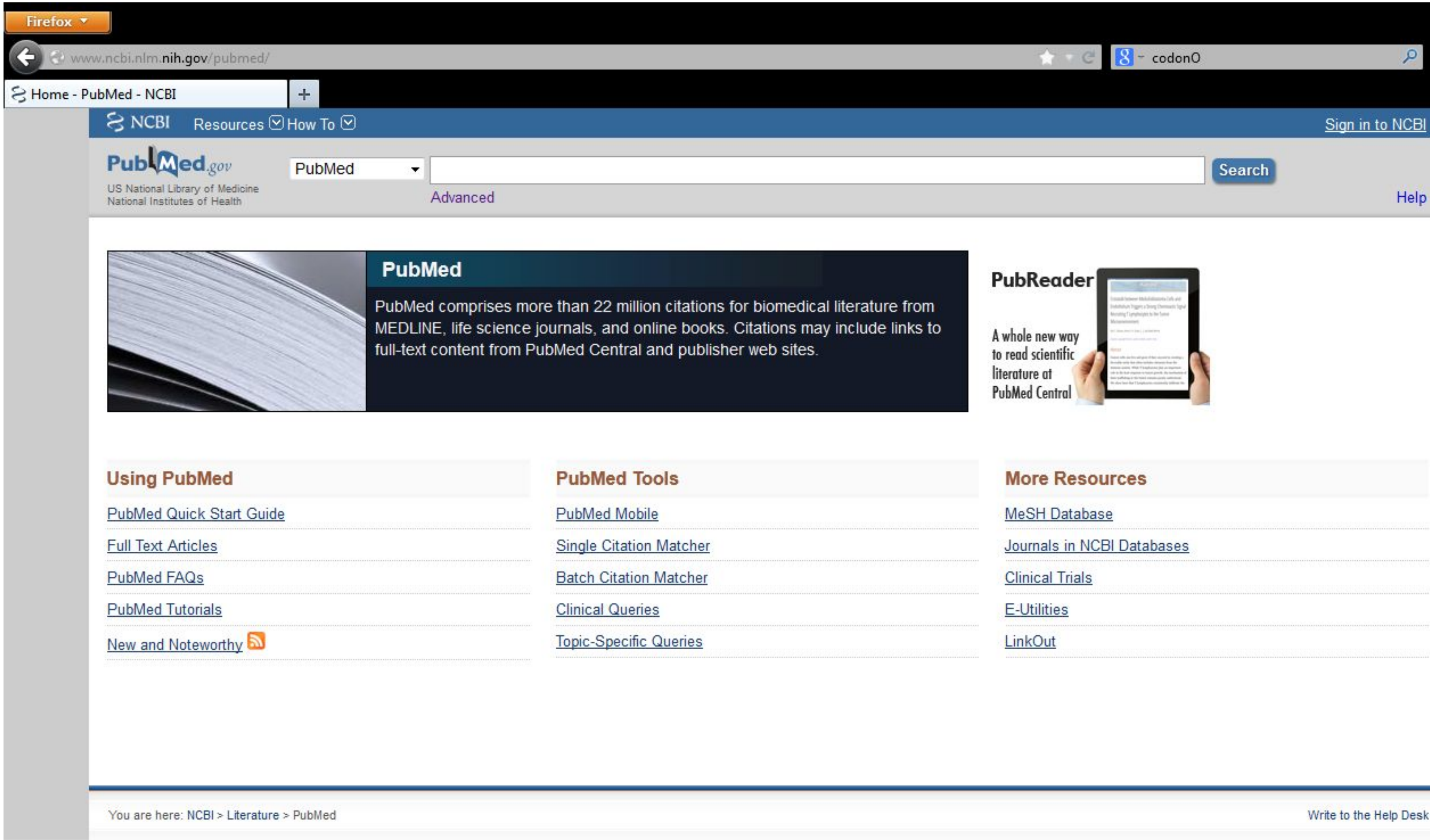

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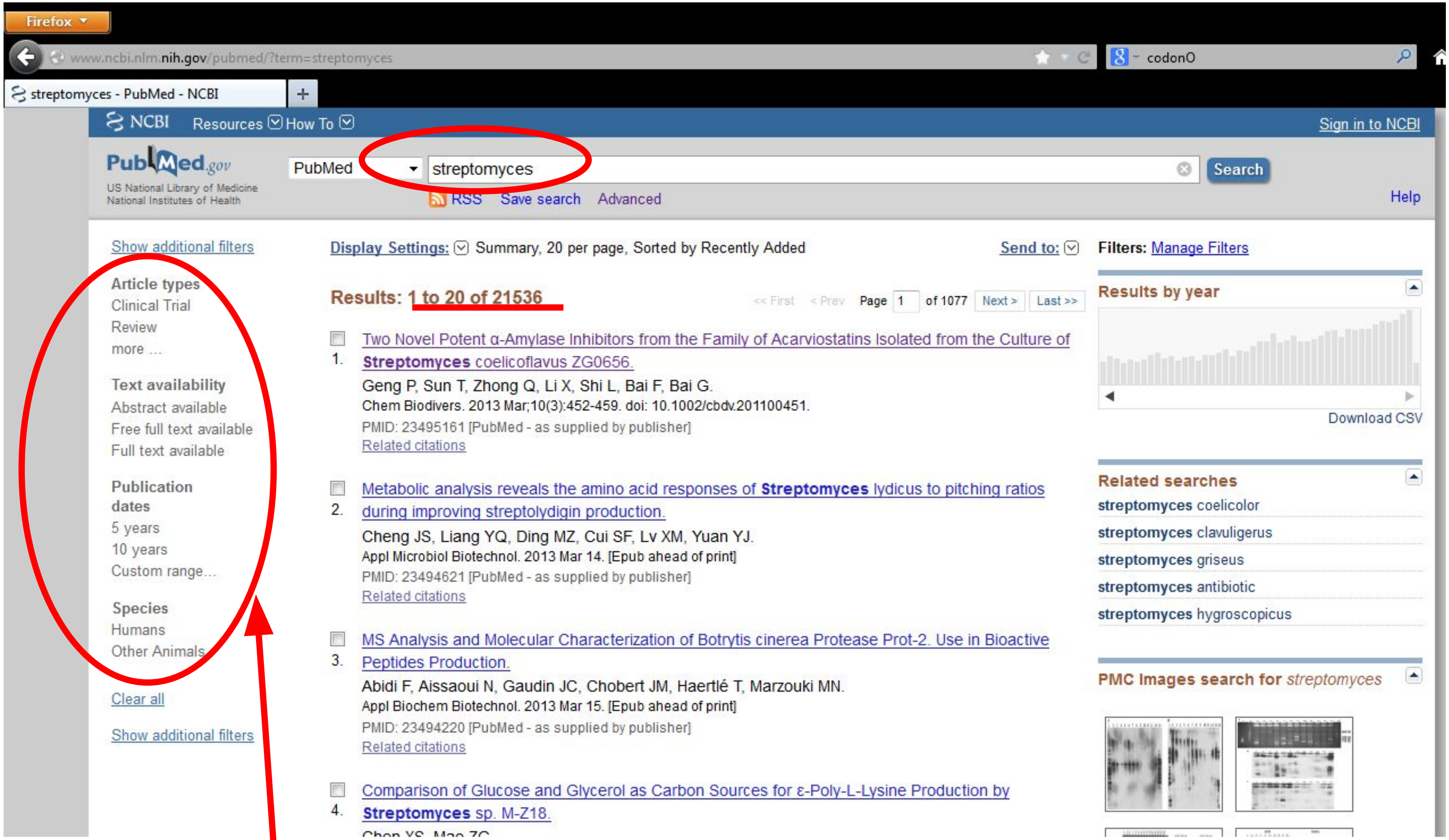


streptomyces

Display Settings: Summary, 20 per page, Sorted by Recently Added

Results: 1 to 20 of 21536

Article types
Clinical Trial
Review
more ...

Text availability
Abstract available
Free full text available
Full text available

Publication dates
5 years
10 years
Custom range...

Species
Humans
Other Animals

☐ 1. Two Novel Potent α-Amylase Inhibitors from the Family of Acarviostatins Isolated from the Culture of **Streptomyces** coelicoflavus ZG0656.
Geng P, Sun T, Zhong Q, Li X, Shi L, Bai F, Bai G.
Chem Biodivers. 2013 Mar;10(3):452-459. doi: 10.1002/cbdv.201100451.
PMID: 23495161 [PubMed - as supplied by publisher]
Related citations

☐ 2. Metabolic analysis reveals the amino acid responses of **Streptomyces** lydicus to pitching ratios during improving streptolydigin production.
Cheng JS, Liang YQ, Ding MZ, Cui SF, Lv XM, Yuan YJ.
Appl Microbiol Biotechnol. 2013 Mar 14. [Epub ahead of print]
PMID: 23494621 [PubMed - as supplied by publisher]
Related citations

☐ 3. MS Analysis and Molecular Characterization of Botrytis cinerea Protease Prot-2. Use in Bioactive Peptides Production.
Abidi F, Aissaoui N, Gaudin JC, Chobert JM, Haertlé T, Marzouki MN.
Appl Biochem Biotechnol. 2013 Mar 15. [Epub ahead of print]
PMID: 23494220 [PubMed - as supplied by publisher]
Related citations

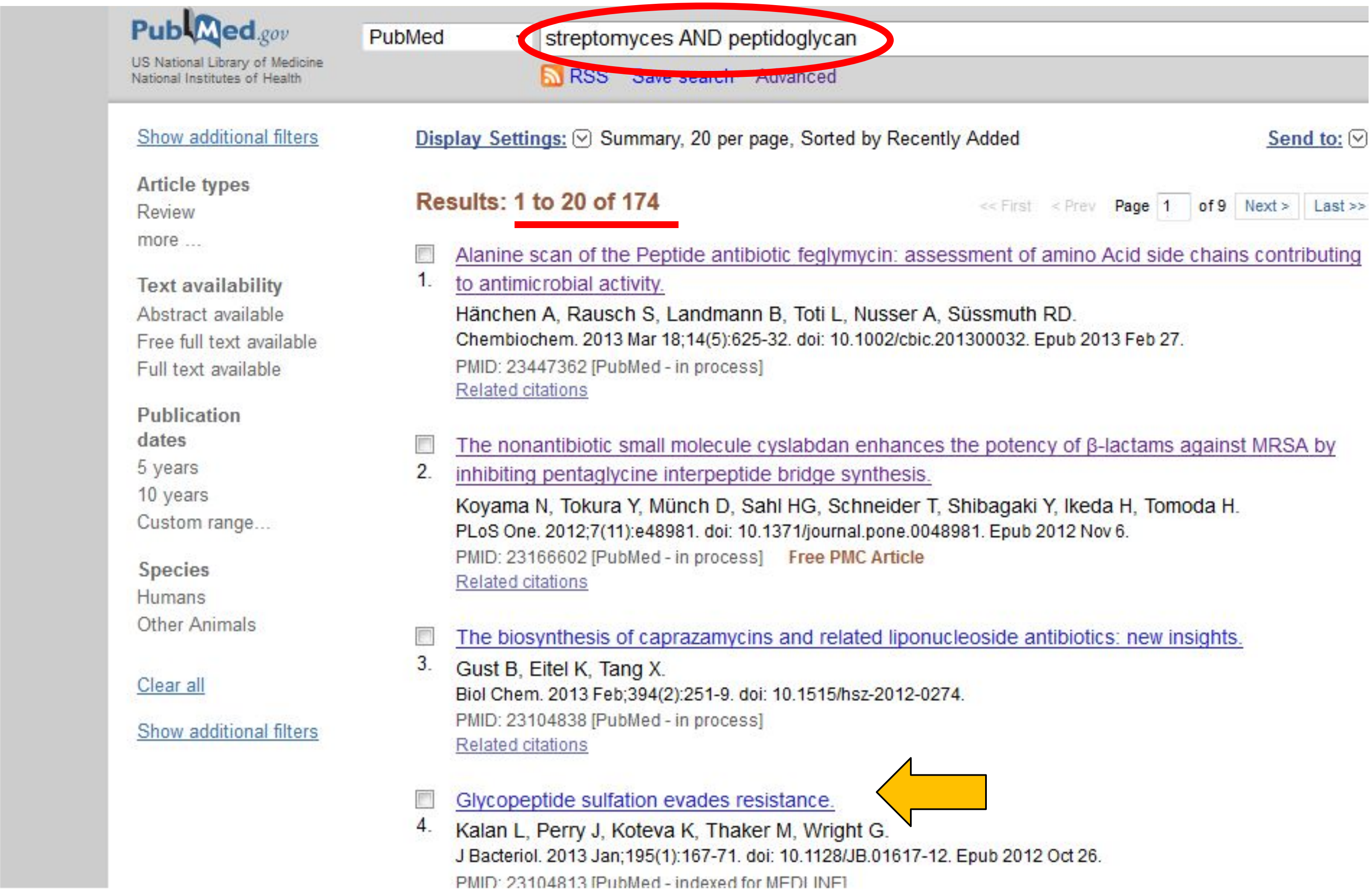
☐ 4. Comparison of Glucose and Glycerol as Carbon Sources for ε-Poly-L-Lysine Production by **Streptomyces** sp. M-Z18.

Related searches
streptomyces coelicolor
streptomyces clavuligerus
streptomyces griseus
streptomyces antibiotic
streptomyces hygroscopicus

Можна звузити коло пошуку до статей, що відповідають певним вимогам (напр., шукати тільки огляди - review)

PubMed

Логічні оператори: AND, OR, *.
Streptomyces; strepto*. * = будь-що



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PubMed | streptomyces AND peptidoglycan

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more ...

Text availability
Abstract available
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Publication dates
5 years
10 years
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Species
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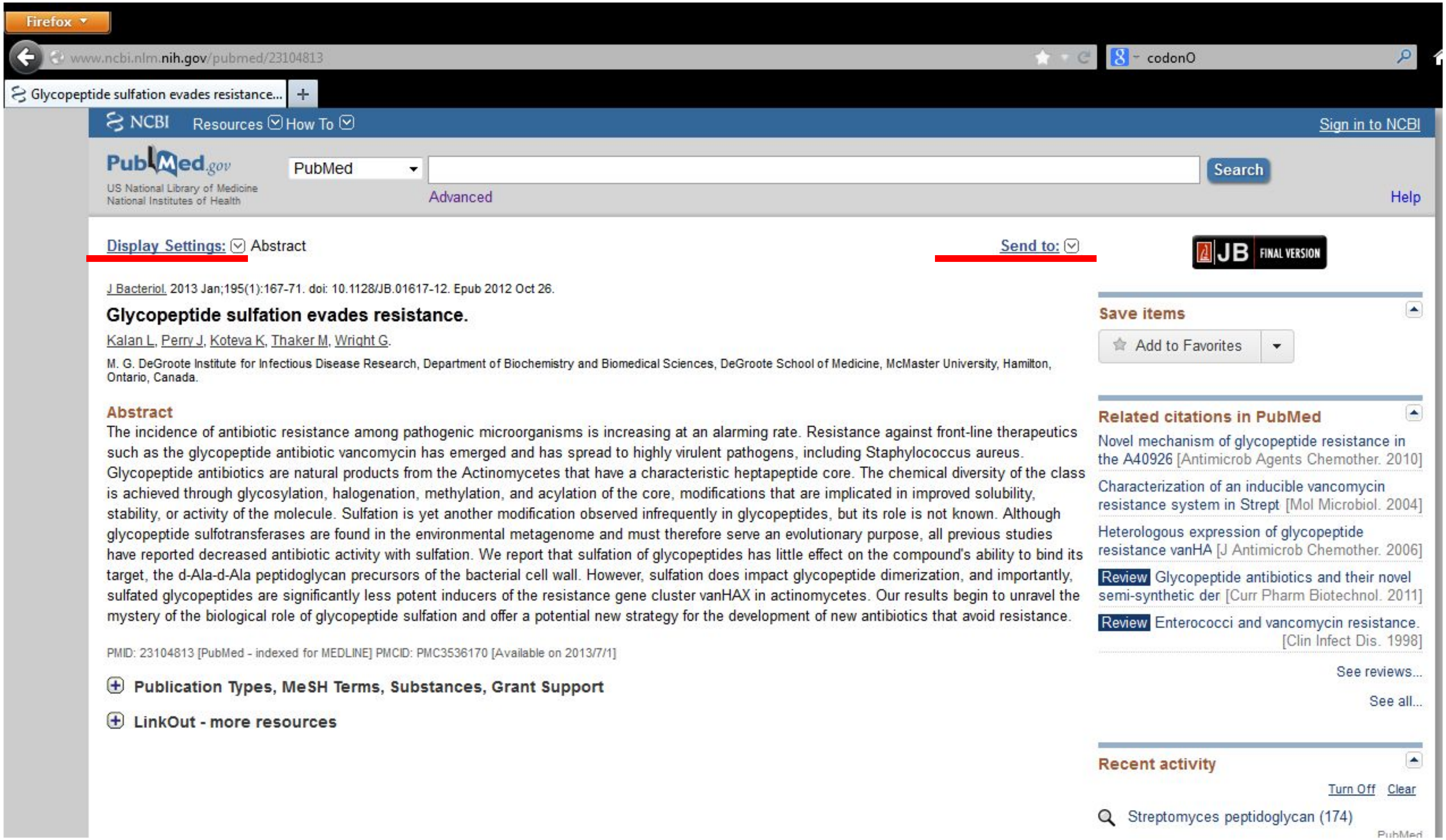
☐ 1. Alanine scan of the Peptide antibiotic feglymycin: assessment of amino Acid side chains contributing to antimicrobial activity.
Hänchen A, Rausch S, Landmann B, Toti L, Nusser A, Süssmuth RD.
Chembiochem. 2013 Mar 18;14(5):625-32. doi: 10.1002/cbic.201300032. Epub 2013 Feb 27.
PMID: 23447362 [PubMed - in process]
Related citations

☐ 2. The nonantibiotic small molecule cyslabdan enhances the potency of β-lactams against MRSA by inhibiting pentaglycine interpeptide bridge synthesis.
Koyama N, Tokura Y, Münch D, Sahl HG, Schneider T, Shibagaki Y, Ikeda H, Tomoda H.
PLoS One. 2012;7(11):e48981. doi: 10.1371/journal.pone.0048981. Epub 2012 Nov 6.
PMID: 23166602 [PubMed - in process] **Free PMC Article**
Related citations

☐ 3. The biosynthesis of caprazamycins and related liponucleoside antibiotics: new insights.
Gust B, Eitel K, Tang X.
Biol Chem. 2013 Feb;394(2):251-9. doi: 10.1515/hsz-2012-0274.
PMID: 23104838 [PubMed - in process]
Related citations

☐ 4. Glycopeptide sulfation evades resistance.
Kalan L, Perry J, Koteva K, Thaker M, Wright G.
J Bacteriol. 2013 Jan;195(1):167-71. doi: 10.1128/JB.01617-12. Epub 2012 Oct 26.
PMID: 23104813 [PubMed - indexed for MEDLINE]

PubMed



Display Settings: Abstract

J Bacteriol. 2013 Jan;195(1):167-71. doi: 10.1128/JB.01617-12. Epub 2012 Oct 26.

Glycopeptide sulfation evades resistance.

Kalan L, Perry J, Koteva K, Thaker M, Wright G.

M. G. DeGroote Institute for Infectious Disease Research, Department of Biochemistry and Biomedical Sciences, DeGroote School of Medicine, McMaster University, Hamilton, Ontario, Canada.

Abstract

The incidence of antibiotic resistance among pathogenic microorganisms is increasing at an alarming rate. Resistance against front-line therapeutics such as the glycopeptide antibiotic vancomycin has emerged and has spread to highly virulent pathogens, including Staphylococcus aureus. Glycopeptide antibiotics are natural products from the Actinomycetes that have a characteristic heptapeptide core. The chemical diversity of the class is achieved through glycosylation, halogenation, methylation, and acylation of the core, modifications that are implicated in improved solubility, stability, or activity of the molecule. Sulfation is yet another modification observed infrequently in glycopeptides, but its role is not known. Although glycopeptide sulfotransferases are found in the environmental metagenome and must therefore serve an evolutionary purpose, all previous studies have reported decreased antibiotic activity with sulfation. We report that sulfation of glycopeptides has little effect on the compound's ability to bind its target, the d-Ala-d-Ala peptidoglycan precursors of the bacterial cell wall. However, sulfation does impact glycopeptide dimerization, and importantly, sulfated glycopeptides are significantly less potent inducers of the resistance gene cluster vanHAX in actinomycetes. Our results begin to unravel the mystery of the biological role of glycopeptide sulfation and offer a potential new strategy for the development of new antibiotics that avoid resistance.

PMID: 23104813 [PubMed - indexed for MEDLINE] PMCID: PMC3536170 [Available on 2013/7/1]

⊕ **Publication Types, MeSH Terms, Substances, Grant Support**

⊕ **LinkOut - more resources**

Related citations in PubMed

- Novel mechanism of glycopeptide resistance in the A40926 [Antimicrob Agents Chemother. 2010]
- Characterization of an inducible vancomycin resistance system in Strept [Mol Microbiol. 2004]
- Heterologous expression of glycopeptide resistance vanHA [J Antimicrob Chemother. 2006]
- Review Glycopeptide antibiotics and their novel semi-synthetic der [Curr Pharm Biotechnol. 2011]
- Review Enterococci and vancomycin resistance. [Clin Infect Dis. 1998]

Recent activity

Streptomyces peptidoglycan (174)

PubMed

Скориставшись лінками, що підкреслено на попередньому слайді, можна отримати бібліографічний опис статті:

1: Kalan L, Perry J, Koteva K, Thaker M, Wright G. Glycopeptide sulfation evades resistance. J Bacteriol. 2013 Jan;195(1):167-71. doi: 10.1128/JB.01617-12. Epub 2012 Oct 26. PubMed PMID: 23104813; PubMed Central PMCID: PMC3536170.

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J Bacteriol. 2013 Jan;195(1):167-71. doi: 10.1128/JB.01617-12. Epub 2012 Oct 26.

Glycopeptide sulfation evades resistance.

Kalan L, Perry J, Koteva K, Thaker M, Wright G.

M. G. DeGroote Institute for Infectious Disease Research, Department of Biochemistry and Biomedical Sciences, DeGroote School of Medicine, McMaster University, Hamilton, Ontario, Canada.

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Novel mechanism of glycopeptide resistance in the A40926 [Antimicrob Agents Chemother. 2010]

Characterization of an inducible vancomycin resistance system in Strept [Mol Microbiol. 2004]

Heterologous expression of glycopeptide resistance vanHA [J Antimicrob Chemother. 2006]

Review Glycopeptide antibiotics and their novel semi-synthetic der [Curr Pharm Biotechnol. 2011]

Review Enterococci and vancomycin resistance. [Clin Infect Dis. 1998]

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- ☐ Ця база є частиною міжнародного консорціуму INSDC (International Nucleotide Sequence Databases Collaboration; http://www.insdc.org/), куди входять European Nucleotide Archive (ENA) і DNA Data Base of Japan (DDBJ).
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- ☐ Т.зв. первинна, або архівна, база даних – метою є збереження нуклеотидних послідовностей (і продуктів їхньої концептуальної трансляції), що подаються (депонуються) дослідниками з усього світу. Зміст поданої інформації загалом не перевіряється – це відповідальність авторів депонування
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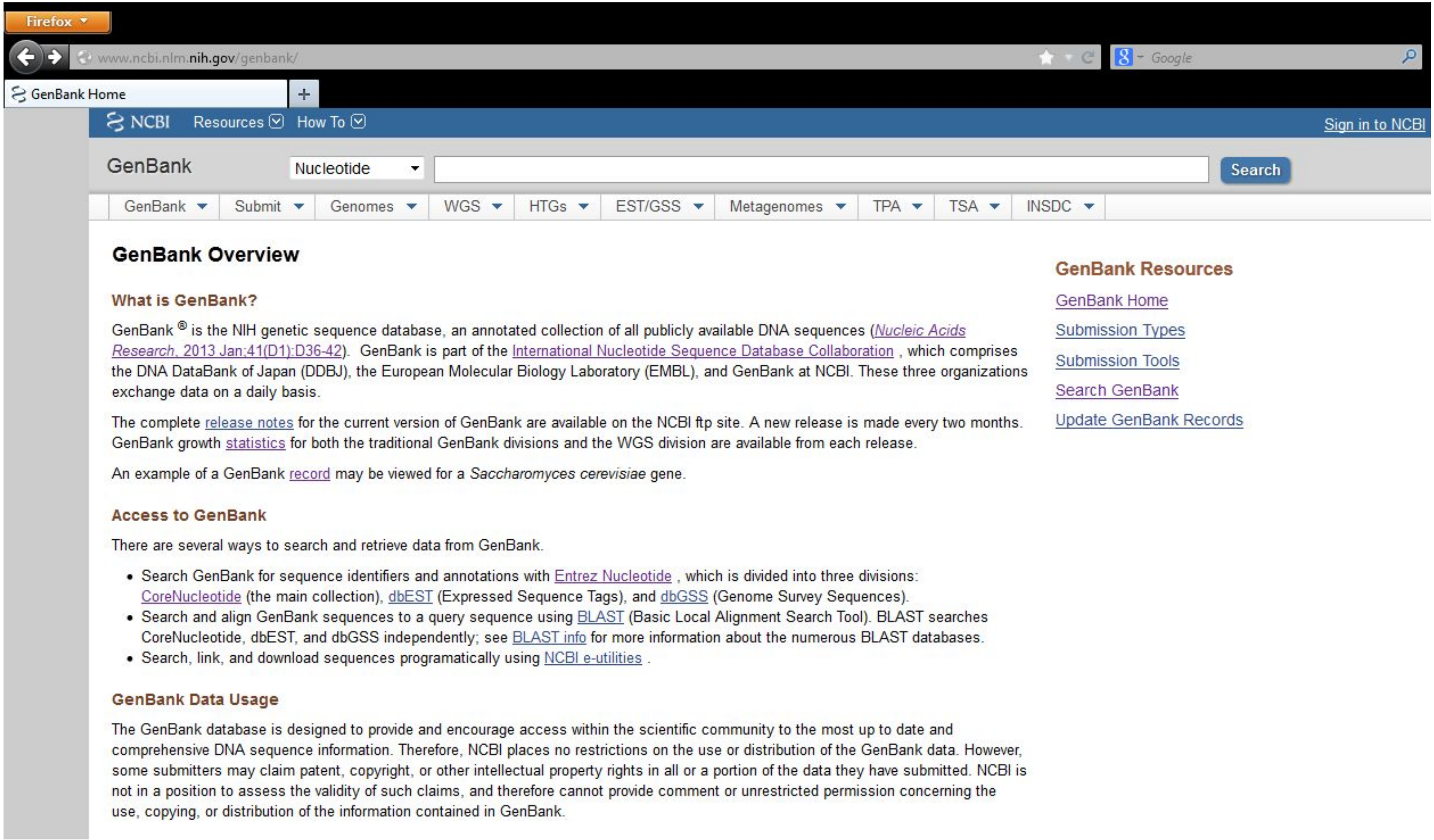

GenBank Overview

What is GenBank?

GenBank ® is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences (*Nucleic Acids Research*, 2013 Jan;41(D1):D36-42). GenBank is part of the International Nucleotide Sequence Database Collaboration , which comprises the DNA DataBank of Japan (DDBJ), the European Molecular Biology Laboratory (EMBL), and GenBank at NCBI. These three organizations exchange data on a daily basis.

The complete release notes for the current version of GenBank are available on the NCBI ftp site. A new release is made every two months. GenBank growth statistics for both the traditional GenBank divisions and the WGS division are available from each release.

An example of a GenBank record may be viewed for a *Saccharomyces cerevisiae* gene.

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There are several ways to search and retrieve data from GenBank.

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- Search and align GenBank sequences to a query sequence using BLAST (Basic Local Alignment Search Tool). BLAST searches CoreNucleotide, dbEST, and dbGSS independently; see BLAST info for more information about the numerous BLAST databases.
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- Update GenBank Records

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GenBank

Формат FASTA

Шрифт `Courier New`

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Рядок анотації може займати кілька рядків, містити пробіли

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GenBank

Gene identification (gi) – унікальний номер, що присвоюється кожній послідовності при поданні у GenBank. Після двокрапки – координати у геномі (у п.н.)

Анотація

Locus name

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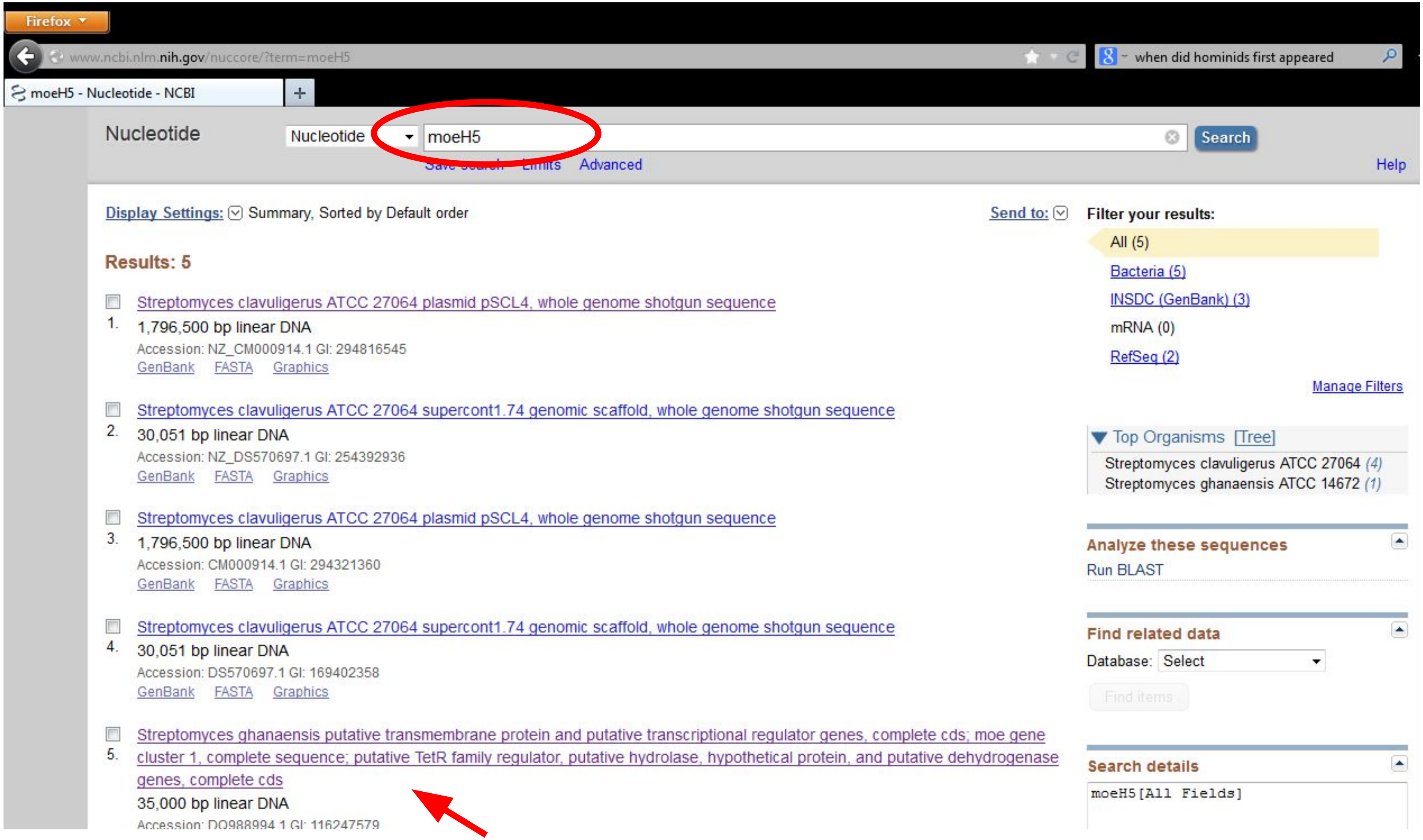
GenBank



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1. ☐ Streptomyces clavuligerus ATCC 27064 plasmid pSCL4, whole genome shotgun sequence
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   GenBank FASTA Graphics

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   GenBank FASTA Graphics

4. ☐ Streptomyces clavuligerus ATCC 27064 supercont1.74 genomic scaffold, whole genome shotgun sequence
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   GenBank FASTA Graphics

5. ☐ Streptomyces ghanaensis putative transmembrane protein and putative transcriptional regulator genes, complete cds; moe gene cluster 1, complete sequence; putative TetR family regulator, putative hydrolase, hypothetical protein, and putative dehydrogenase genes, complete cds
   35,000 bp linear DNA
   Accession: DQ988994.1 GI: 116247579

Filter your results:

All (5)
Bacteria (5)
INSDC (GenBank) (3)
mRNA (0)
RefSeq (2)

Manage Filters

Top Organisms [Tree]

Streptomyces clavuligerus ATCC 27064 (4)
Streptomyces ghanaensis ATCC 14672 (1)

Analyze these sequences

Run BLAST

Find related data

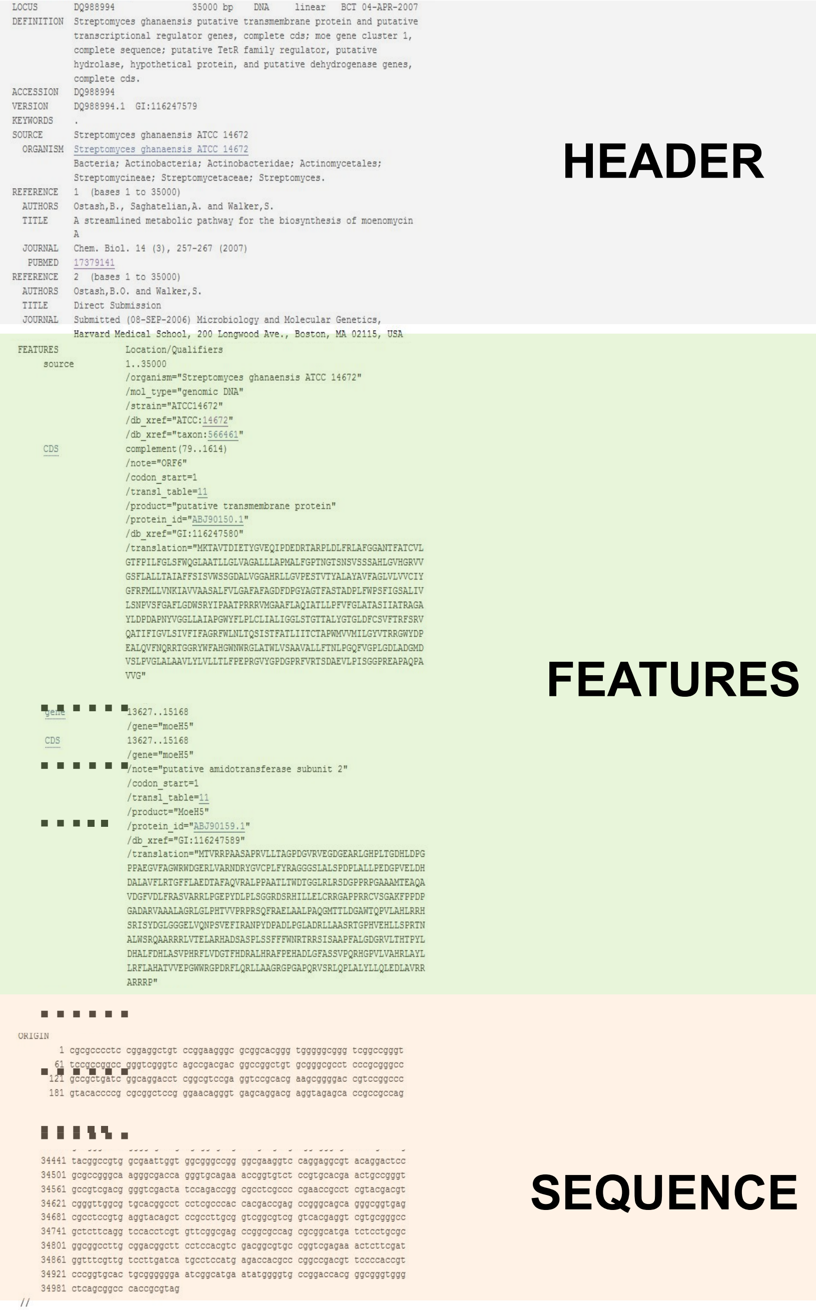
Database: Select

Find items

Search details

moeH5[All Fields]

GenBank



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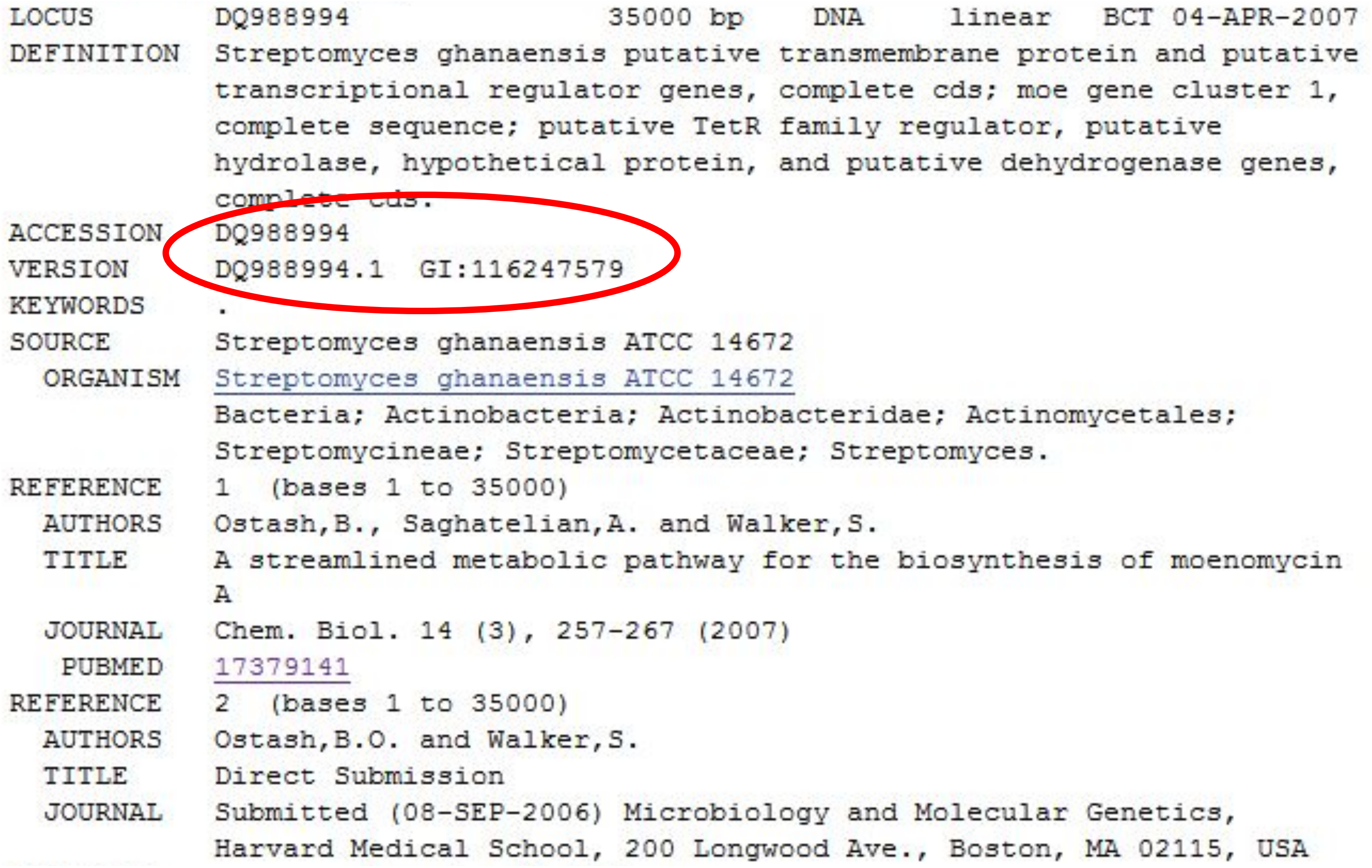

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  AUTHORS   Ostash,B., Saghatelian,A. and Walker,S.
  TITLE     A streamlined metabolic pathway for the biosynthesis of moenomycin
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  JOURNAL   Chem. Biol. 14 (3), 257-267 (2007)
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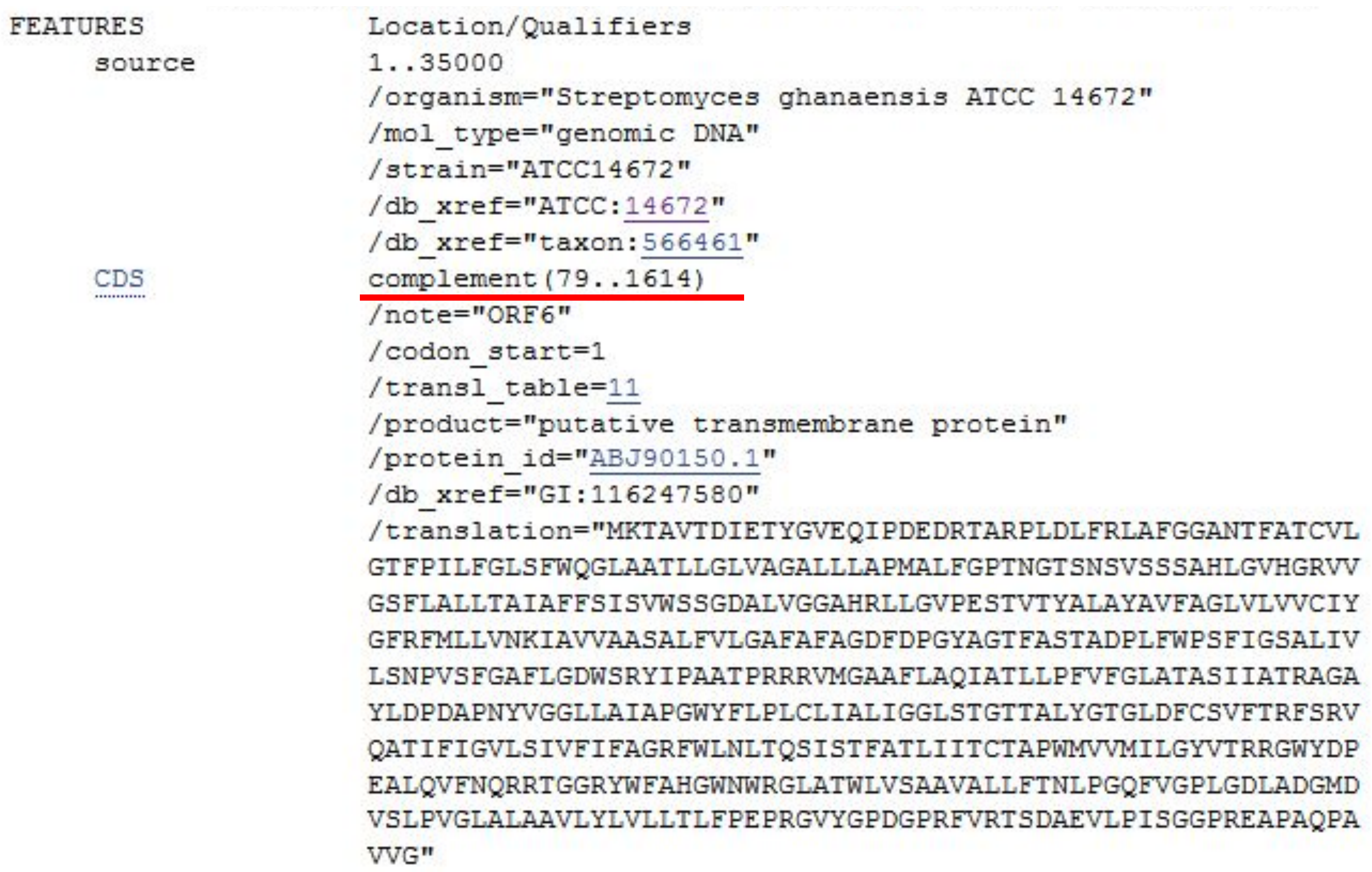

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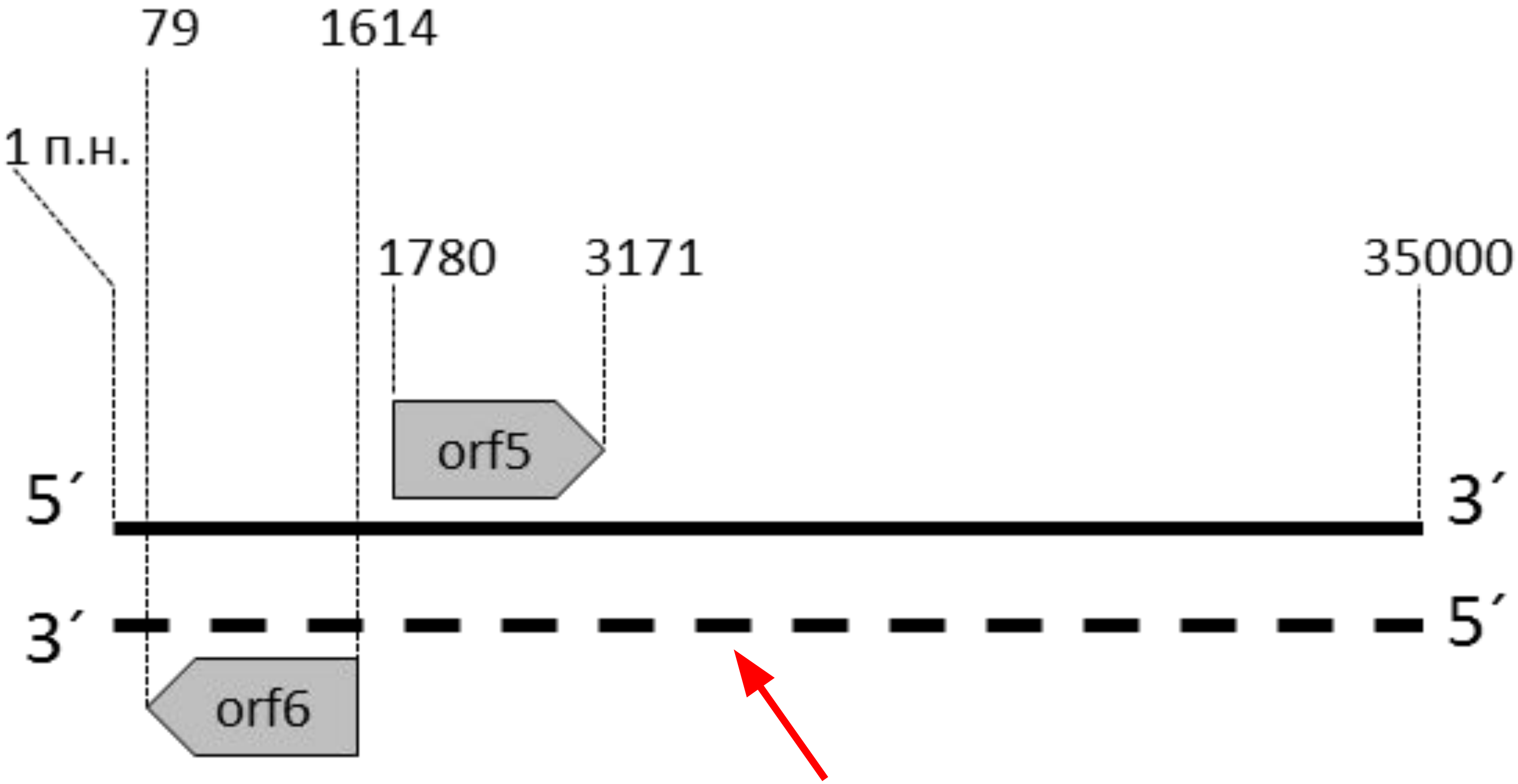

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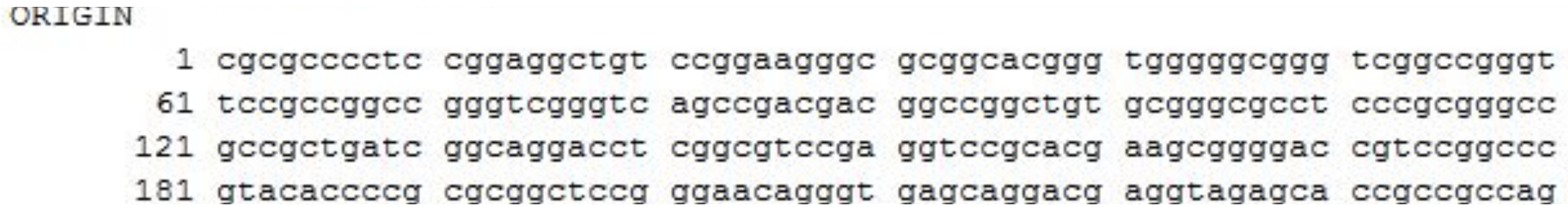

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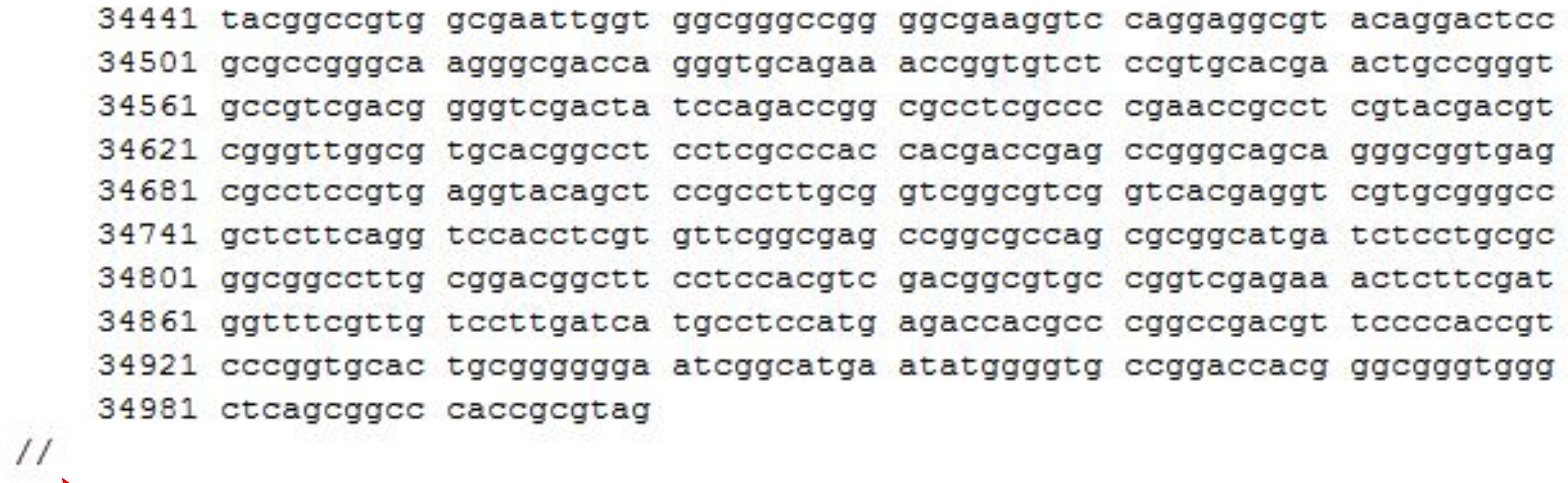

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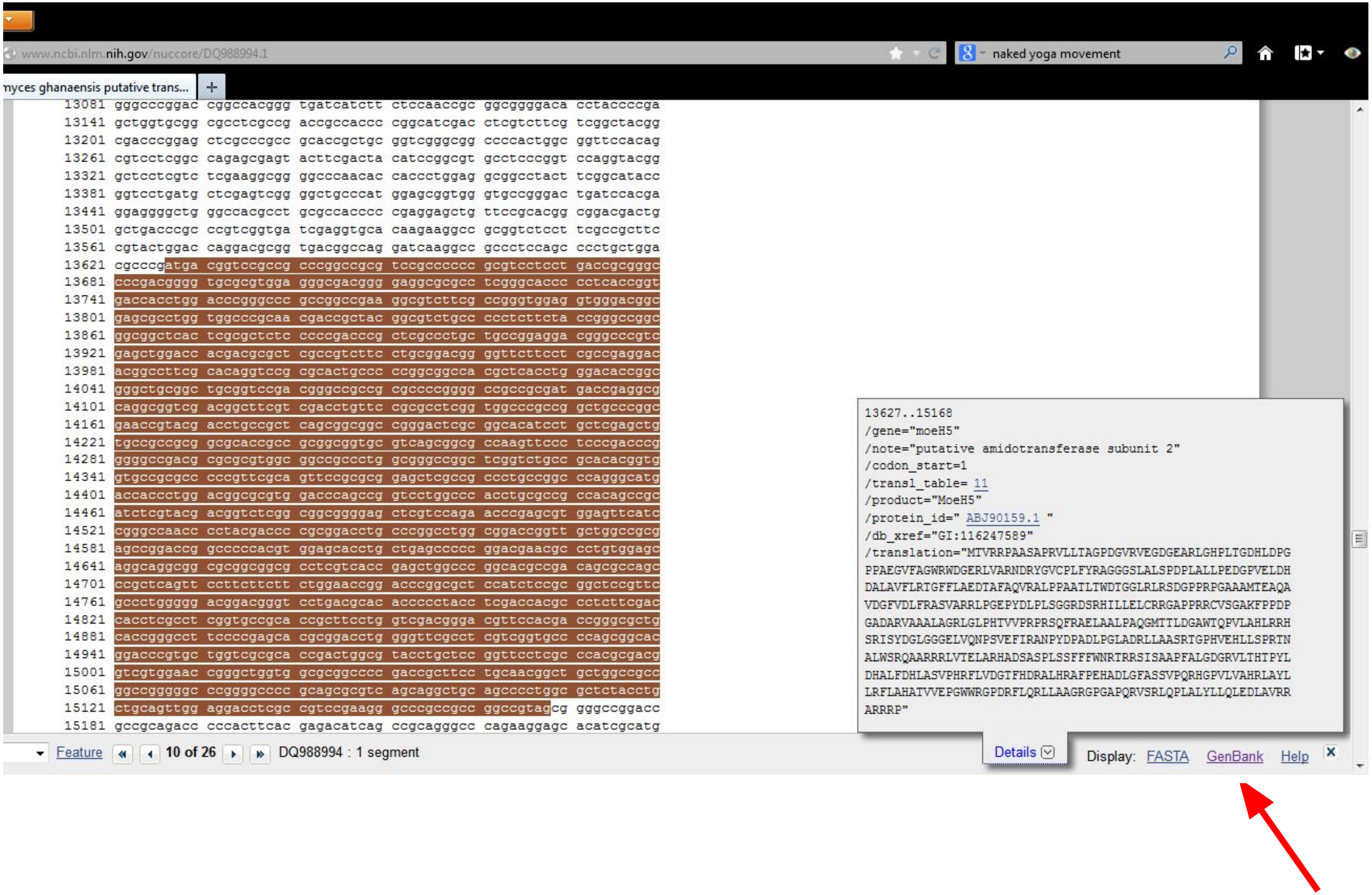

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GenBank

GBFF для *moeH5* - гена

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Streptomyces ghanaensis putative transmembrane protein and putative transcriptional regulator genes, complete cds; moe gene cluster 1, complete sequence; putative TetR family regulator, putative hydrolase, hypothetical protein, and putative dehydrogenase genes, complete cds

GenBank: DQ988994.1

FASTA Graphics

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  TITLE     A streamlined metabolic pathway for the biosynthesis of moenomycin
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  JOURNAL   Chem. Biol. 14 (3), 257-267 (2007)
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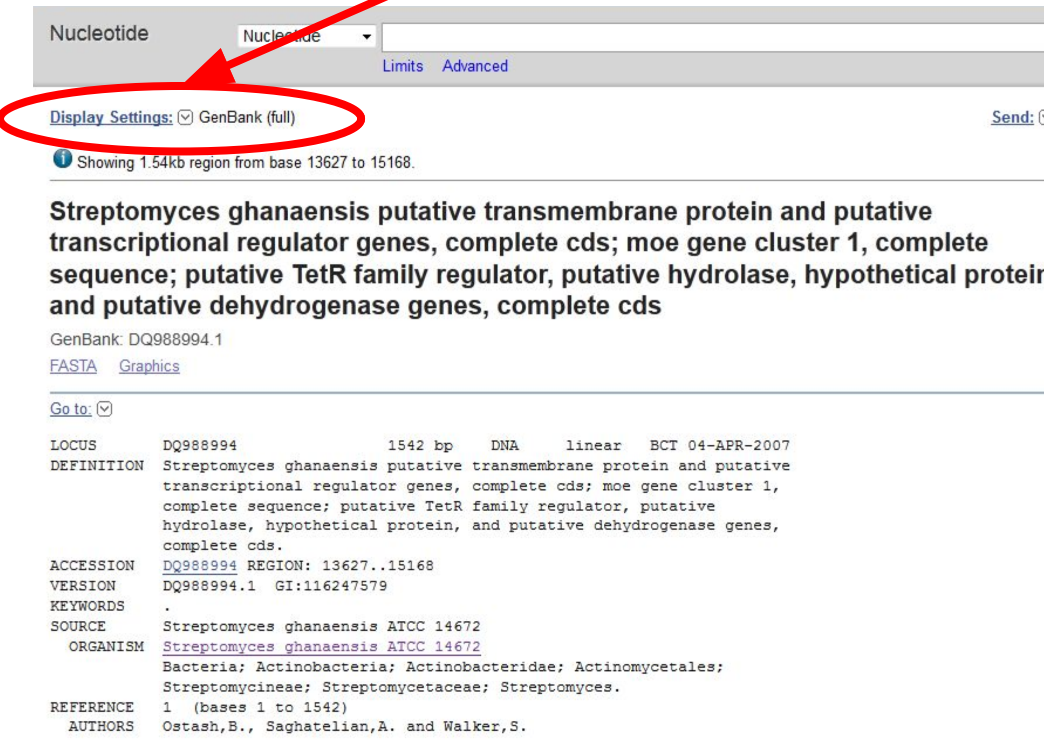

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Showing 1.54kb region from base 13627 to 15168.

Streptomyces ghanaensis putative transmembrane protein and putative transcriptional regulator genes, complete cds; moe gene cluster 1, complete sequence; putative TetR family regulator, putative hydrolase, hypothetical protein and putative dehydrogenase genes, complete cds

GenBank: DQ988994.1

FASTA Graphics

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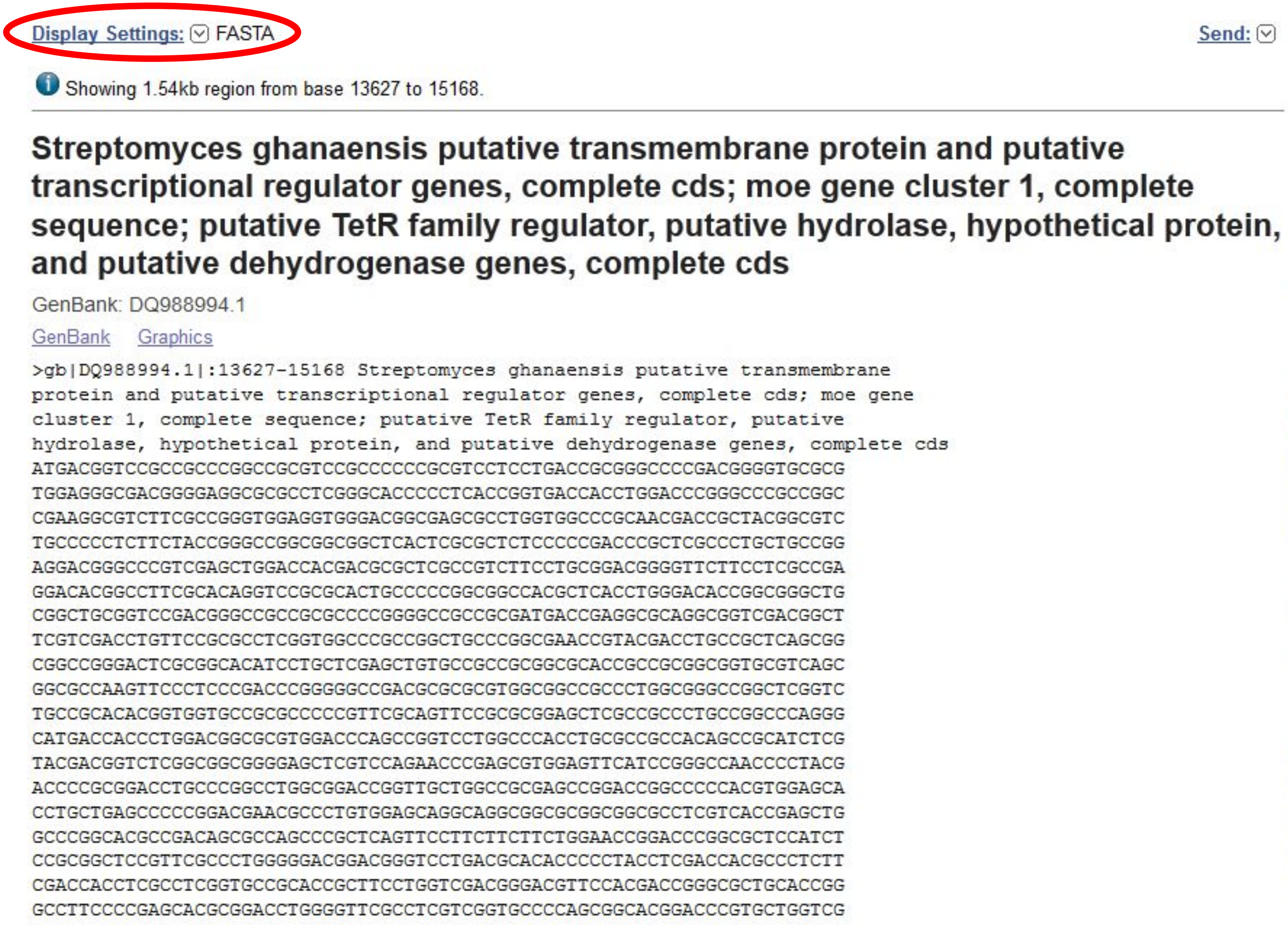
GenBank

FASTA-файл для *moeH5* - гена



Showing 1.54kb region from base 13627 to 15168.

Streptomyces ghanaensis putative transmembrane protein and putative transcriptional regulator genes, complete cds; moe gene cluster 1, complete sequence; putative TetR family regulator, putative hydrolase, hypothetical protein, and putative dehydrogenase genes, complete cds

GenBank: DQ988994.1

```
>gb|DQ988994.1|:13627-15168 Streptomyces ghanaensis putative transmembrane
protein and putative transcriptional regulator genes, complete cds; moe gene
cluster 1, complete sequence; putative TetR family regulator, putative
hydrolase, hypothetical protein, and putative dehydrogenase genes, complete cds
ATGACGGTCCGCCGCCCGGCCGCGTCCGCCCCCCGCGTCCTCCTGACCGCGGGCCCCGACGGGGTGCGCG
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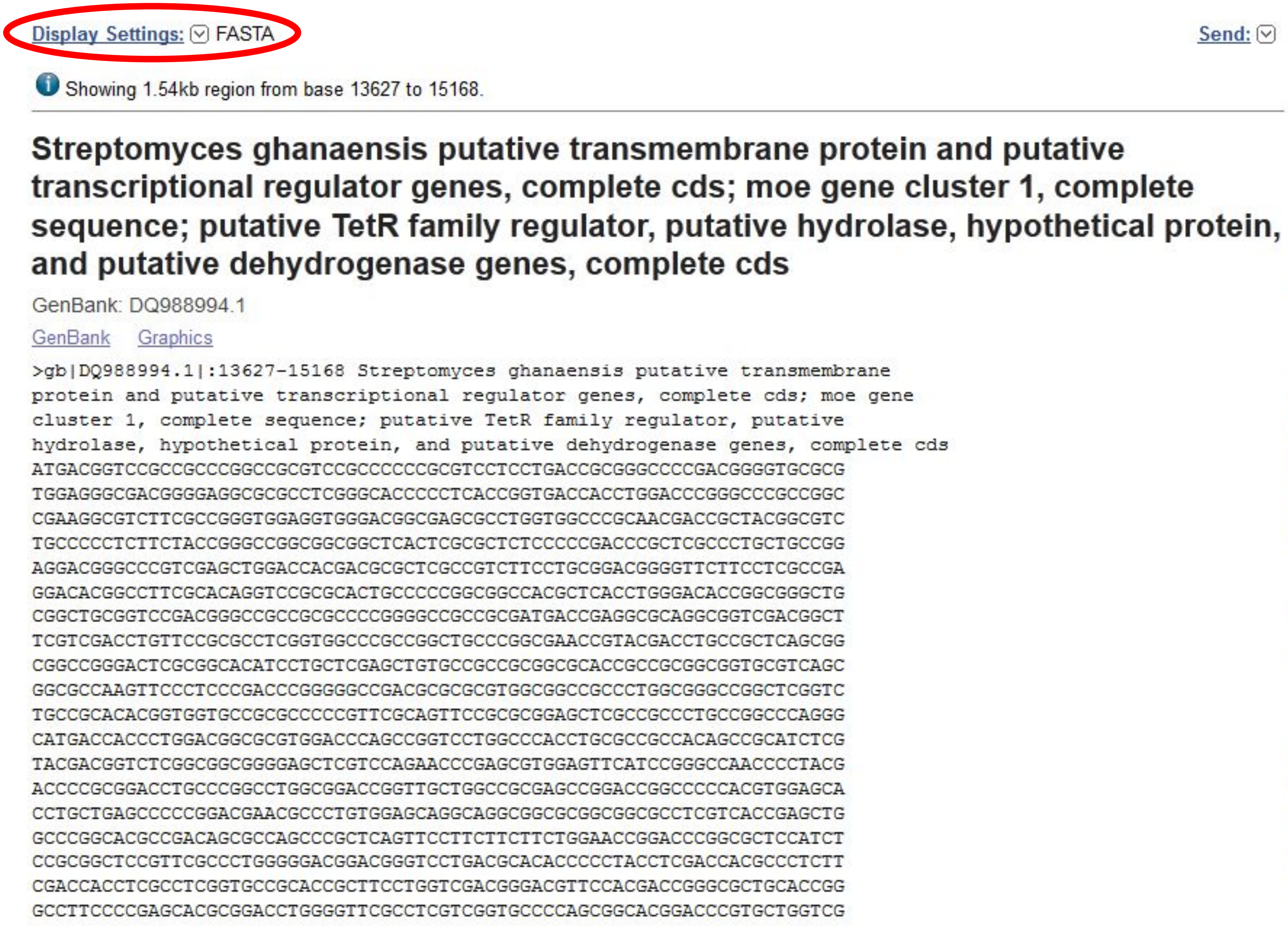
GenBank

FASTA-файл для *moeH5* - гена



Showing 1.54kb region from base 13627 to 15168.

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protein and putative transcriptional regulator genes, complete cds; moe gene
cluster 1, complete sequence; putative TetR family regulator, putative
hydrolase, hypothetical protein, and putative dehydrogenase genes, complete cds
ATGACGGTCCGCCGCCCGGCCGCGTCCGCCCCCCGCGTCCTCCTGACCGCGGGCCCCGACGGGGTGCGCG
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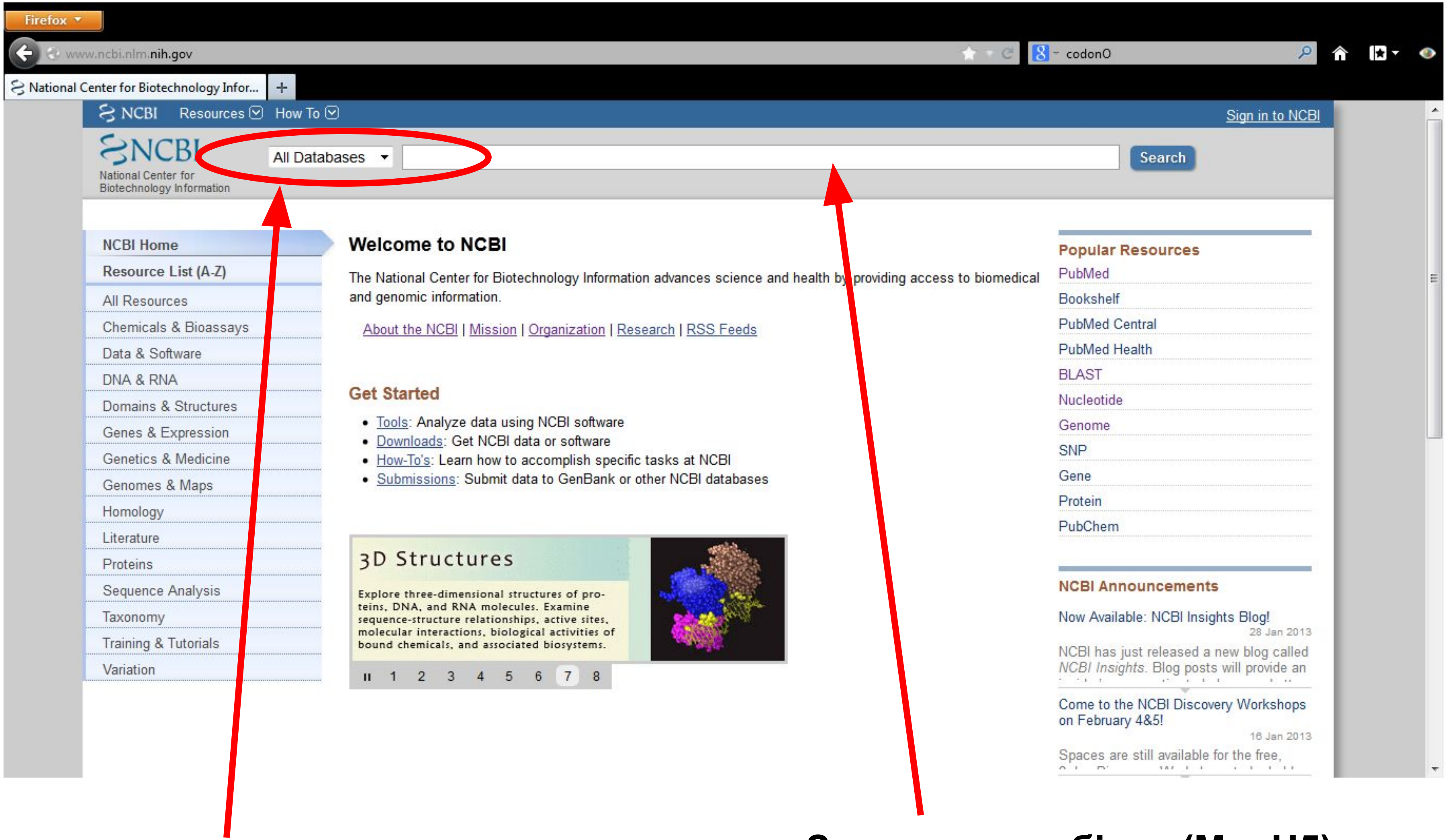
Прямий шлях до MoeH5

Стартова сторінка NCBI



Welcome to NCBI

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- Submissions: Submit data to GenBank or other NCBI databases

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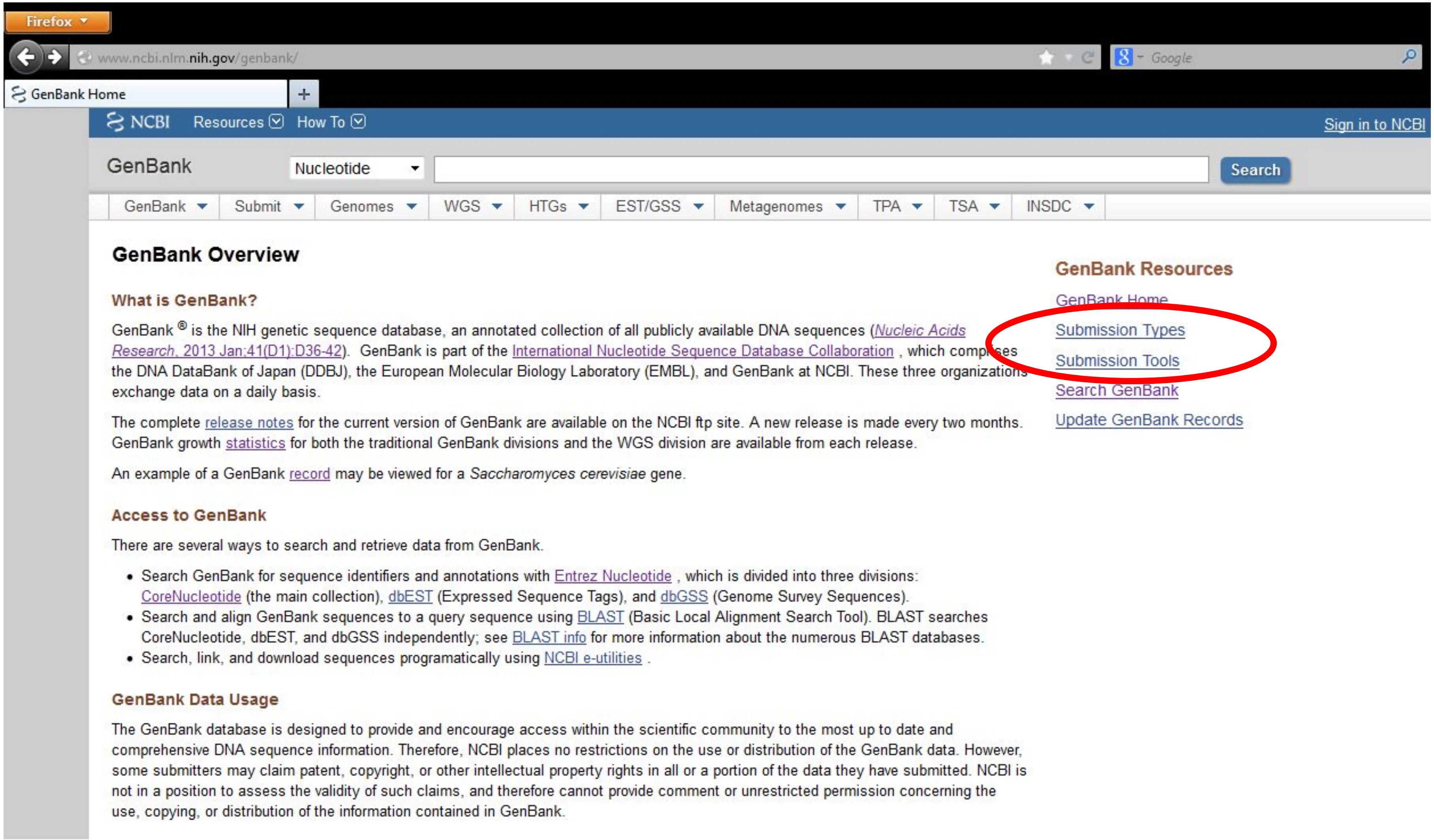
Now Available: NCBI Insights Blog!
28 Jan 2013
NCBI has just released a new blog called *NCBI Insights*. Blog posts will provide an

Come to the NCBI Discovery Workshops on February 4&5!
16 Jan 2013
Spaces are still available for the free,

Вибрати Protein

Задати назву білка (MoeH5)

Депонування НАП



GenBank Overview

What is GenBank?

GenBank ® is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences (*Nucleic Acids Research*, 2013 Jan;41(D1):D36-42). GenBank is part of the International Nucleotide Sequence Database Collaboration , which comprises the DNA DataBank of Japan (DDBJ), the European Molecular Biology Laboratory (EMBL), and GenBank at NCBI. These three organizations exchange data on a daily basis.

The complete release notes for the current version of GenBank are available on the NCBI ftp site. A new release is made every two months. GenBank growth statistics for both the traditional GenBank divisions and the WGS division are available from each release.

An example of a GenBank record may be viewed for a *Saccharomyces cerevisiae* gene.

Access to GenBank

There are several ways to search and retrieve data from GenBank.

- Search GenBank for sequence identifiers and annotations with Entrez Nucleotide , which is divided into three divisions: CoreNucleotide (the main collection), dbEST (Expressed Sequence Tags), and dbGSS (Genome Survey Sequences).
- Search and align GenBank sequences to a query sequence using BLAST (Basic Local Alignment Search Tool). BLAST searches CoreNucleotide, dbEST, and dbGSS independently; see BLAST info for more information about the numerous BLAST databases.
- Search, link, and download sequences programatically using NCBI e-utilities .

GenBank Data Usage

The GenBank database is designed to provide and encourage access within the scientific community to the most up to date and comprehensive DNA sequence information. Therefore, NCBI places no restrictions on the use or distribution of the GenBank data. However, some submitters may claim patent, copyright, or other intellectual property rights in all or a portion of the data they have submitted. NCBI is not in a position to assess the validity of such claims, and therefore cannot provide comment or unrestricted permission concerning the use, copying, or distribution of the information contained in GenBank.

GenBank Resources

- GenBank Home
- Submission Types
- Submission Tools
- Search GenBank
- Update GenBank Records

Депонування НАП

- Нуклеотидні послідовності – у базу, що входить INSDC - GenBank, ENA, DDBJ
- Білкові – SWISSPROT
- GenBank має різні знаряддя для депонування:
  - **BankIt** – для подання відносно коротких і простих (безінтронних) послідовностей
  - **SequIn** – подання складних послідовностей
  - Та інші (тут не розглядаються)
- Подання геномів – окрема історія (див. далі)
- При поданні нуклеотидних послідовностей потрібно знати мінімум інформації про неї, зокрема локалізацію в ній (координати) orf
- У результаті подання послідовності присвоюється номер доступу в GenBank

Депонування НАП

Мінімум інформації про послідовність

- **Розмір (у п.н.)**
- **Локалізація orf (якщо є)**
- **Походження послідовності (що секвенували – хромосома, плазміда тощо; з якого організму)**

1

167

```
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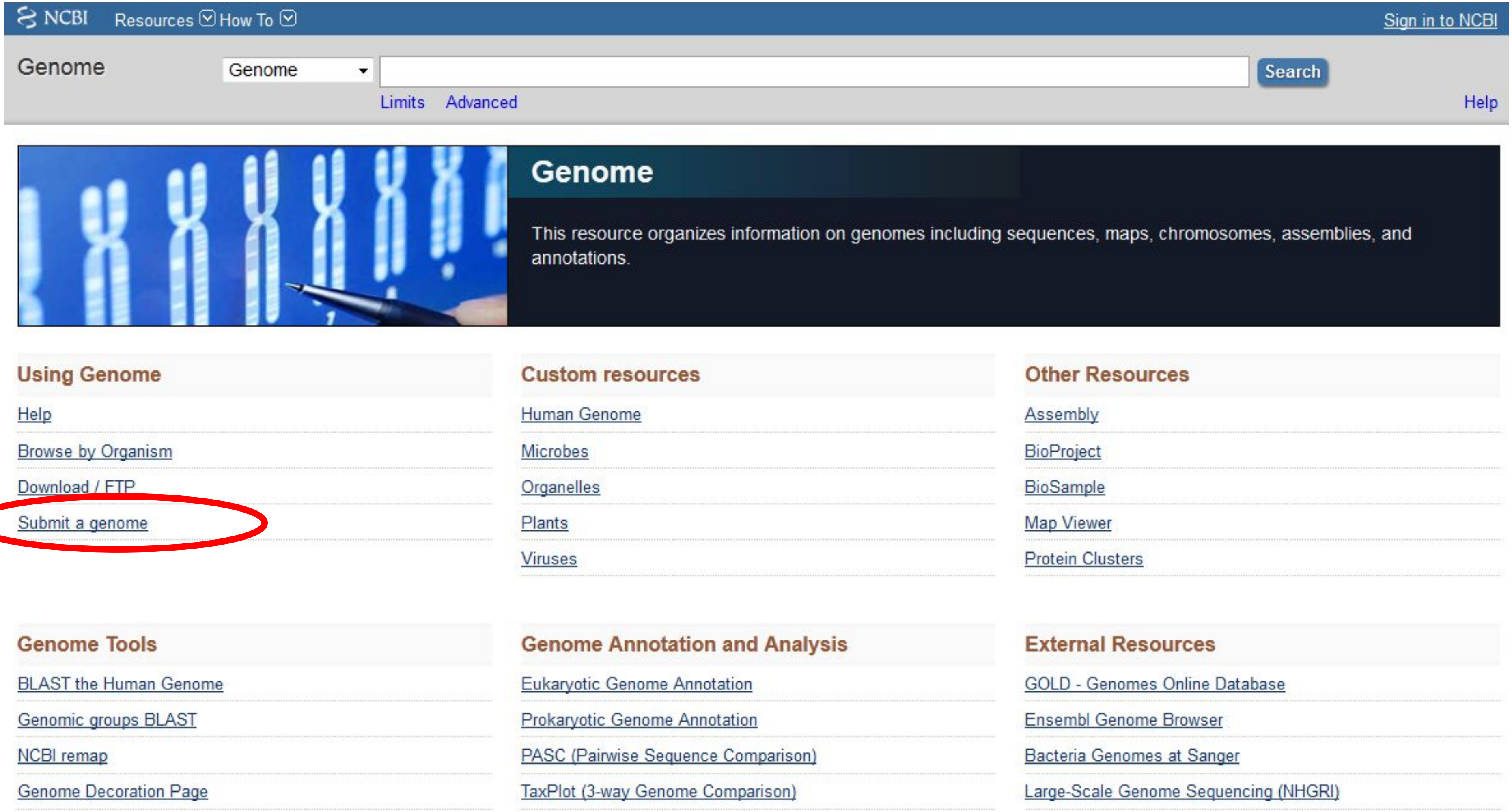
2239

2294

Genome

www.ncbi.nlm.nih.gov/genome



Genome

This resource organizes information on genomes including sequences, maps, chromosomes, assemblies, and annotations.

Using Genome

- Help
- Browse by Organism
- Download / FTP
- Submit a genome

Custom resources

- Human Genome
- Microbes
- Organelles
- Plants
- Viruses

Other Resources

- Assembly
- BioProject
- BioSample
- Map Viewer
- Protein Clusters

Genome Tools

- BLAST the Human Genome
- Genomic groups BLAST
- NCBI remap
- Genome Decoration Page

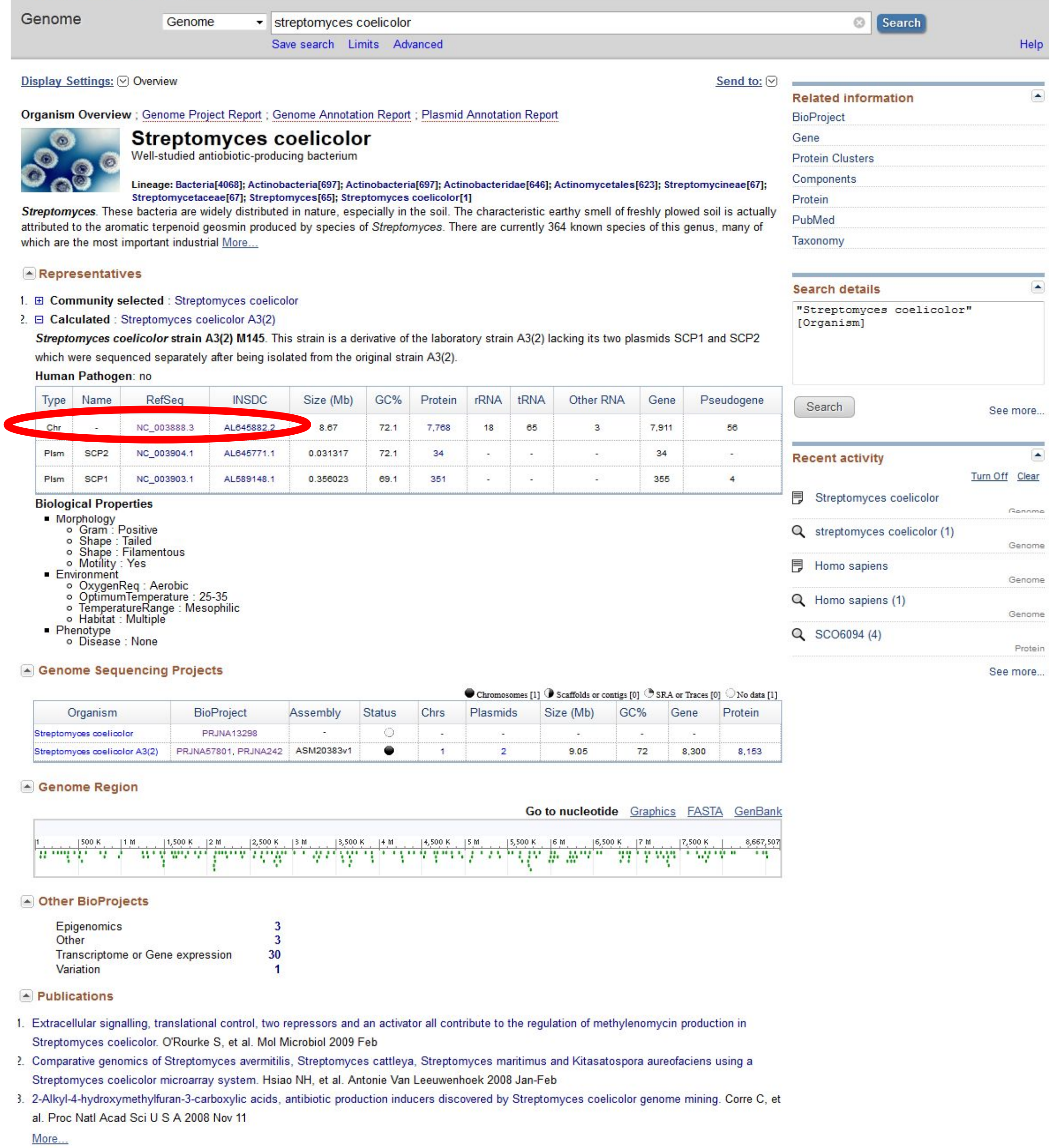
Genome Annotation and Analysis

- Eukaryotic Genome Annotation
- Prokaryotic Genome Annotation
- PASC (Pairwise Sequence Comparison)
- TaxPlot (3-way Genome Comparison)

External Resources

- GOLD - Genomes Online Database
- Ensembl Genome Browser
- Bacteria Genomes at Sanger
- Large-Scale Genome Sequencing (NHGRI)

Genome



streptomyces coelicolor

Display Settings: Overview

Organism Overview ; Genome Project Report ; Genome Annotation Report ; Plasmid Annotation Report

Streptomyces coelicolor

Well-studied antibiotic-producing bacterium

Lineage: Bacteria[4068]; Actinobacteria[697]; Actinobacteria[697]; Actinobacteridae[646]; Actinomycetales[623]; Streptomycineae[67]; Streptomycetaceae[67]; Streptomyces[65]; Streptomyces coelicolor[1]

Streptomyces. These bacteria are widely distributed in nature, especially in the soil. The characteristic earthy smell of freshly plowed soil is actually attributed to the aromatic terpenoid geosmin produced by species of *Streptomyces*. There are currently 364 known species of this genus, many of which are the most important industrial More...

Representatives

1. ⊞ **Community selected** : Streptomyces coelicolor
2. ⊟ **Calculated** : Streptomyces coelicolor A3(2)

***Streptomyces coelicolor* strain A3(2) M145**. This strain is a derivative of the laboratory strain A3(2) lacking its two plasmids SCP1 and SCP2 which were sequenced separately after being isolated from the original strain A3(2).

Human Pathogen: no

Type	Name	RefSeq	INSDC	Size (Mb)	GC%	Protein	rRNA	tRNA	Other RNA	Gene	Pseudogene
Chr	-	NC_003888.3	AL645882.2	8.67	72.1	7,768	18	65	3	7,911	56
Plsm	SCP2	NC_003904.1	AL645771.1	0.031317	72.1	34	-	-	-	34	-
Plsm	SCP1	NC_003903.1	AL589148.1	0.356023	69.1	351	-	-	-	355	4

Biological Properties

- Morphology
  - Gram : Positive
  - Shape : Tailed
  - Shape : Filamentous
  - Motility : Yes
- Environment
  - OxygenReq : Aerobic
  - OptimumTemperature : 25-35
  - TemperatureRange : Mesophilic
  - Habitat : Multiple
- Phenotype
  - Disease : None

Genome Sequencing Projects

● Chromosomes [1] ◑ Scaffolds or contigs [0] ◔ SRA or Traces [0] ○ No data [1]

Organism	BioProject	Assembly	Status	Chrs	Plasmids	Size (Mb)	GC%	Gene	Protein
Streptomyces coelicolor	PRJNA13298	-	○	-	-	-	-	-	
Streptomyces coelicolor A3(2)	PRJNA57801, PRJNA242	ASM20383v1	●	1	2	9.05	72	8,300	8,153

Genome Region

Go to nucleotide Graphics FASTA GenBank

Other BioProjects

Epigenomics	3
Other	3
Transcriptome or Gene expression	30
Variation	1

Publications

1. Extracellular signalling, translational control, two repressors and an activator all contribute to the regulation of methylenomycin production in Streptomyces coelicolor. O'Rourke S, et al. Mol Microbiol 2009 Feb
2. Comparative genomics of Streptomyces avermitilis, Streptomyces cattleya, Streptomyces maritimus and Kitasatospora aureofaciens using a Streptomyces coelicolor microarray system. Hsiao NH, et al. Antonie Van Leeuwenhoek 2008 Jan-Feb
3. 2-Alkyl-4-hydroxymethylfuran-3-carboxylic acids, antibiotic production inducers discovered by Streptomyces coelicolor genome mining. Corre C, et al. Proc Natl Acad Sci U S A 2008 Nov 11

More...

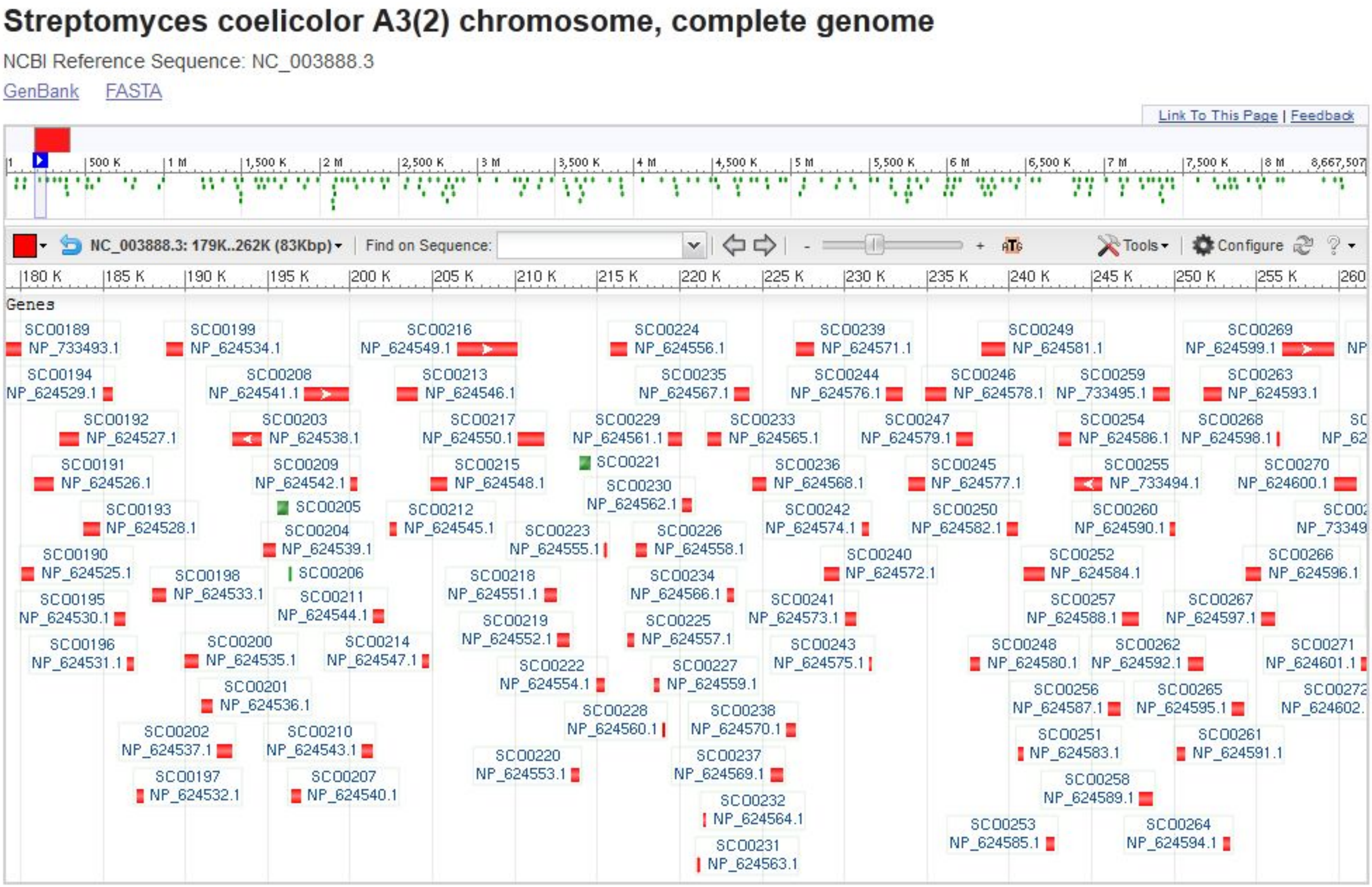
Search details

"Streptomyces coelicolor"[Organism]

Recent activity

- Streptomyces coelicolor — Genome
- streptomyces coelicolor (1) — Genome
- Homo sapiens — Genome
- Homo sapiens (1) — Genome
- SCO6094 (4) — Protein

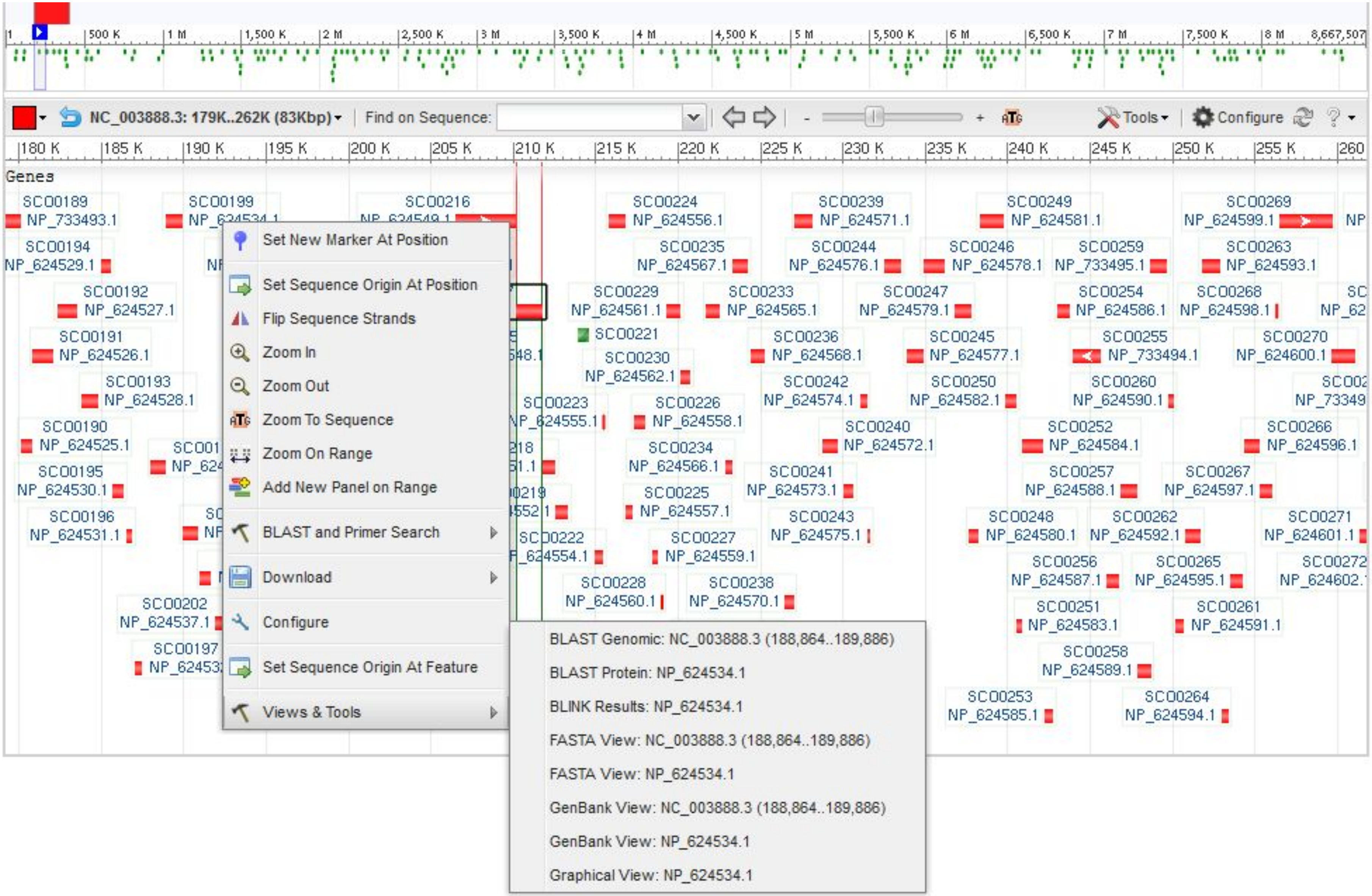
Genome



Streptomyces coelicolor A3(2) chromosome, complete genome

NCBI Reference Sequence: NC_003888.3

Genome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2 M
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3 M
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4 M
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5 M
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6 M
6,500 K
7 M
7,500 K
8 M
8,667,507
NC_003888.3: 179K..262K (83Kbp)
Find on Sequence:
Tools
Configure
180 K
185 K
190 K
195 K
200 K
205 K
210 K
215 K
220 K
225 K
230 K
235 K
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SCO0253 NP_624585.1
SCO0264 NP_624594.1
Set New Marker At Position
Set Sequence Origin At Position
Flip Sequence Strands
Zoom In
Zoom Out
Zoom To Sequence
Zoom On Range
Add New Panel on Range
BLAST and Primer Search
Download
Configure
Set Sequence Origin At Feature
Views & Tools
BLAST Genomic: NC_003888.3 (188,864..189,886)
BLAST Protein: NP_624534.1
BLINK Results: NP_624534.1
FASTA View: NC_003888.3 (188,864..189,886)
FASTA View: NP_624534.1
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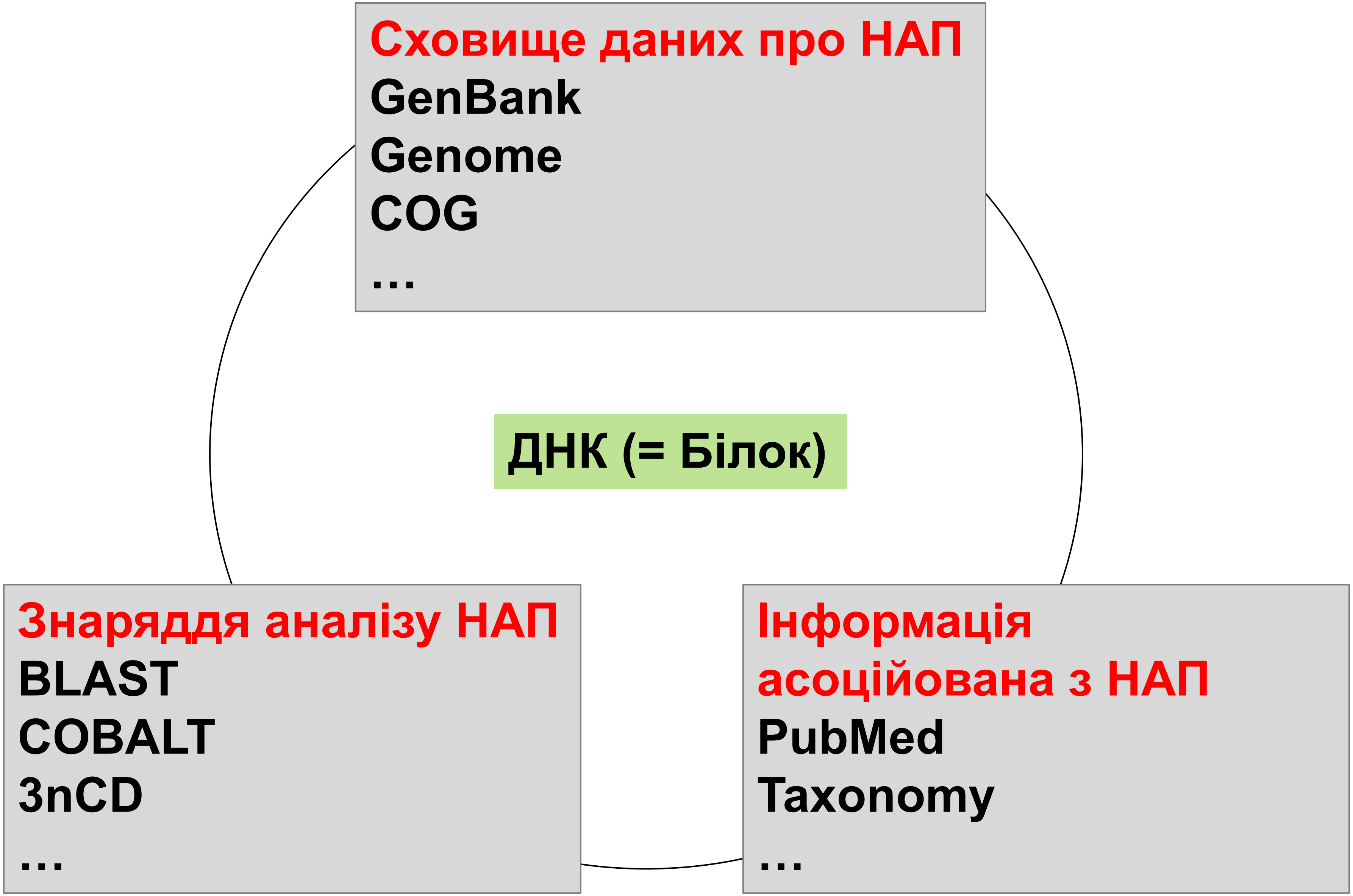
Graphical View: NP_624534.1

Модель NCBI



Сховище даних про НАП

GenBank
Genome
COG
…

ДНК (= Білок)

Знаряддя аналізу НАП

BLAST
COBALT
3nCD
…

Інформація асоційована з НАП

PubMed
Taxonomy
…