

Біоінформатика.

A black and white line drawing of a multi-story brick building. A sign on the top left of the building reads "CREASEY & MOVER" with "FURNITURE WAREHOUSE" written below it. The building has several windows and a small awning over the entrance. The drawing is done in a sketchy, hand-drawn style.

**БАЗИ ДАНИХ.  
МОДЕЛЬ NSVI**

Lab.1

# Центральні питання

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

# National Center for Biotechnology Information

[www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)

The screenshot shows the NCBI homepage in a Firefox browser. The address bar displays "www.ncbi.nlm.nih.gov". The page features a navigation menu on the left with categories like "NCBI Home", "Resource List (A-Z)", and "All Resources". The main content area includes a "Welcome to NCBI" message, a "Get Started" section with links to Tools, Downloads, How-To's, and Submissions, and a "3D Structures" section with a molecular model. On the right, there are sections for "Popular Resources" (PubMed, Booksshelf, etc.) and "NCBI Announcements" (Now Available: NCBI Insights Blog!).

Firefox

www.ncbi.nlm.nih.gov

National Center for Biotechnology Infor... +

NCBI Resources How To Sign in to NCBI

NCBI National Center for Biotechnology Information

All Databases Search

**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
- Variation

**Welcome to NCBI**

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

[About the NCBI](#) | [Mission](#) | [Organization](#) | [Research](#) | [RSS Feeds](#)

**Get Started**

- [Tools](#): Analyze data using NCBI software
- [Downloads](#): Get NCBI data or software
- [How-To's](#): Learn how to accomplish specific tasks at NCBI
- [Submissions](#): Submit data to GenBank or other NCBI databases

**3D Structures**

Explore three-dimensional structures of proteins, DNA, and RNA molecules. Examine sequence-structure relationships, active sites, molecular interactions, biological activities of bound chemicals, and associated biosystems.

Popular Resources

- PubMed
- Booksshelf
- PubMed Central
- PubMed Health
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

**NCBI Announcements**

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,

# NCBI

- ❑ Фізична локація – м. Бетезда, штат Меріленд (США)
- ❑ Подвійна функція – сховище даних і сервер для аналізу

## Типи даних

### Біомедичні дані

PubMed

PubChem

Taxonomy

Chemicals and assays

Proteins

.....

### Геномні дані

Genome

Variations

SNP

OMIM

Genes and expression

.....

# PubMed

[www.ncbi.nlm.nih.gov/pubmed](http://www.ncbi.nlm.nih.gov/pubmed)

Firefox

www.ncbi.nlm.nih.gov/pubmed/

Home - PubMed - NCBI

NCBI Resources How To Sign in to NCBI

PubMed.gov  
US National Library of Medicine  
National Institutes of Health

PubMed

Advanced

Search

Help

### PubMed

PubMed comprises more than 22 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full-text content from PubMed Central and publisher web sites.

### PubReader

A whole new way to read scientific literature at PubMed Central

#### Using PubMed

- [PubMed Quick Start Guide](#)
- [Full Text Articles](#)
- [PubMed FAQs](#)
- [PubMed Tutorials](#)
- [New and Noteworthy](#)

#### PubMed Tools

- [PubMed Mobile](#)
- [Single Citation Matcher](#)
- [Batch Citation Matcher](#)
- [Clinical Queries](#)
- [Topic-Specific Queries](#)

#### More Resources

- [MeSH Database](#)
- [Journals in NCBI Databases](#)
- [Clinical Trials](#)
- [E-Utilities](#)
- [LinkOut](#)

You are here: NCBI > Literature > PubMed

Write to the Help Desk

# PubMed

The screenshot shows the PubMed website interface. At the top, the browser address bar displays "www.ncbi.nlm.nih.gov/pubmed/?term=streptomyces". The search bar contains the term "streptomyces" and is circled in red. To the left of the search bar, the "PubMed" dropdown menu is also circled in red. Below the search bar, the "Display Settings" are set to "Summary, 20 per page, Sorted by Recently Added". The search results are listed as "Results: 1 to 20 of 21536". The first result is titled "Two Novel Potent  $\alpha$ -Amylase Inhibitors from the Family of Acarviosatins Isolated from the Culture of *Streptomyces coelicoflavus* ZG0656." The left sidebar contains filter options such as "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...), and "Species" (Humans, Other Animals). This sidebar is circled in red, and a red arrow points from it to the search bar. On the right side, there is a "Results by year" bar chart, "Related searches" (streptomyces coelicolor, streptomyces clavuligerus, etc.), and "PMC Images search for streptomyces".

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

# PubMed

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

The screenshot shows the PubMed search interface. At the top left is the PubMed logo and the text 'US National Library of Medicine National Institutes of Health'. The search bar contains the query 'streptomyces AND peptidoglycan', which is circled in red. Below the search bar are links for 'RSS', 'Save search', and 'Advanced'. The main content area shows search settings: 'Display Settings: [checked] Summary, 20 per page, Sorted by Recently Added' and a 'Send to:' dropdown. The results section is titled 'Results: 1 to 20 of 174' and includes navigation buttons: '<< First', '< Prev', 'Page 1 of 9', 'Next >', and 'Last >>'. Four search results are listed, each with a checkbox, a title link, and publication details. A yellow arrow points to the fourth result, 'Glycopeptide sulfation evades resistance'.

PubMed.gov  
US National Library of Medicine  
National Institutes of Health

PubMed streptomyces AND peptidoglycan  
RSS Save search Advanced

Show additional filters

Display Settings: [checked] Summary, 20 per page, Sorted by Recently Added Send to: [checked]

Article types  
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

Clear all

Show additional filters

Results: 1 to 20 of 174 << First < Prev Page 1 of 9 Next > Last >>

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 cyclabdan enhances the potency of  \$\beta\$ -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

Firefox

www.ncbi.nlm.nih.gov/pubmed/23104813

Glycopeptide sulfation evades resistance... +

NCBI Resources How To Sign in to NCBI

PubMed.gov PubMed Search Help

US National Library of Medicine National Institutes of Health Advanced

Display Settings: Abstract Send to: JB FINAL VERSION

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. DeGrootte Institute for Infectious Disease Research, Department of Biochemistry and Biomedical Sciences, DeGrootte 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

Save items

Add to Favorites

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]

See reviews... See all...

Recent activity

Turn Off Clear

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](https://doi.org/10.1128/JB.01617-12): 10.1128/JB.01617-12. Epub 2012 Oct 26. PubMed [PMID](https://pubmed.ncbi.nlm.nih.gov/23104813/): 23104813; PubMed Central [PMCID](https://pubmed.ncbi.nlm.nih.gov/PMC3536170/): PMC3536170.

Ідентифікатори статті як цифрового об'єкта (ЦО):

- ❑ DOI (**D**igital **O**bject **I**dentification) – унікальна комбінація арабських цифр і латинських літер – жоден інший ЦО такої не має. Видавець звертається до [www.doi.org](http://www.doi.org), що видає первинний номер (10.1128/JB), який далі продовжується у міру появи нових ЦО. DOI можна присвоїти частинам статті (рисункам)
- ❑ PMID – присвоюється автоматично кожному посиланню, що потрапляє у базу PubMed
- ❑ PMCID – номери доступу до повних текстів статей, зібраних із доступних джерел фахівцями NCBI, і поміщених в PubMed Central

## Доступ до повних текстів статей

Сайт видавця

The screenshot shows the PubMed interface for the article "Glycopeptide sulfation evades resistance." The article is from *J. Bacteriol.*, 2013, Jan; 195(1):167-71. The authors are Kalan L, Perry J, Koteva K, Thaker M, Wright G. The abstract discusses the increasing incidence of antibiotic resistance and the role of glycopeptide sulfation in evading it. The article is available as a full-text PDF, indicated by the "JB FINAL VERSION" button, which is circled in red. The page also includes options to save items, related citations, and publication types.

NCBI Resources How To Sign in to NCBI

PubMed.gov PubMed Search Help

US National Library of Medicine National Institutes of Health Advanced

Display Settings: Abstract Send to:

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

**Abstract**

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

Publication Types, MeSH Terms, Substances, Grant Support

LinkOut - more resources

Save items

Add to Favorites

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]

See reviews...

See all...

**Деякі видання у галузі хімії не реферуються в PubMed**

## **Видавничий дім Elsevier**

- Журнали Open Access**
- NIH вимагає відкривати зміст усіх статей, де описано дослідження, що ними фінансувались – через певний період часу (зразу, півроку, рік)**
- Запит до автора статті (може переслати персональну копію для особистого вжитку)**
- Пошук через Google**
- Запит через наукові соцмережі (LinkedIn, ResearchGate)**

# GenBank

- ❑ 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).
- ❑ GenBank – підрозділ NCBI.  
[www.ncbi.nlm.nih.gov/genbank](http://www.ncbi.nlm.nih.gov/genbank)
- ❑ 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
- ❑ GenBank, ENA і DDBJ щоденно обмінюються інформацією, і зміст їхніх баз ідентичний

# GenBank

Firefox

www.ncbi.nlm.nih.gov/genbank/

GenBank Home

NCBI Resources How To Sign in to NCBI

GenBank Nucleotide Search

GenBank Submit Genomes WGS HTGs EST/GSS Metagenomes TPA TSA INSDC

## GenBank Overview

### What is GenBank?

GenBank<sup>®</sup> 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](#)

**Анотовані фрагменти геномів; анотовані геноми; неанотовані фрагменти і геноми; чернетки (драфти геномів), метагеномні дані....**

## Формат

### FASTA

>PM13114

TTAAGAAGCAATAGGTGTCCATAGTTCACСТААТТТАТАGТСССАСТ  
СТТТТGGТТТААТGGGAATGCGCCCCGCATТGGGGGTAAAGGTCATТ  
TCACTAAACAGTAGTGTGGТТТCTGACATТAAAAAATCGACCCGACA  
ATAGGCAAAACCGTTAGCTAATТТGTTGGCTAATGTGAGCATATТGT  
CAAATТGTAGCGGТТТТТCAATATATТCTGGGGTATТGGGATCTТCT  
AAAGTAAAAGGCTGTAATТGCCATТGTGTATCATAAACATТGATA

Шрифт Courier New



**Рядок анотації може займати кілька рядків, містити пробіли**

>WemR

MKKLKKYLTRKKKENYIIFSIIYYFIKVTSSIFISDSLRYKYIFKRKY  
KLNLKKPTSFNEKIHRYILNDHNPITYTKLADKLLVRDYVREKIGEKY  
LIKLINHYNTPSEINFNTLPKSFVLKCNHVDGSMIINDKSKINEKA  
IKKKLKIALKNNIYYQNREWHYKNIKPKIICEELINIFPHNKKNYPE  
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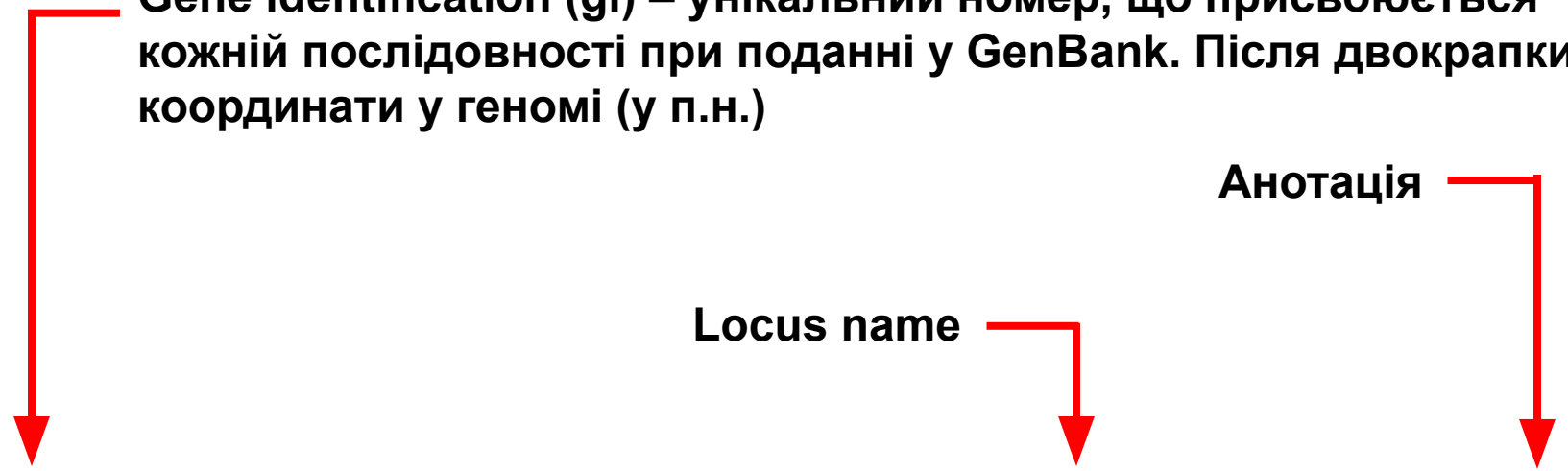


# GenBank

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

**Анотація**

**Locus name**



```
>gi|197283915:3424858-3425733|PMI3114| Proteus  
mirabilis HI4320 chromosome, complete genome  
TTAAGAAGCAATAGGTGTCCATAGTTCACCTAATTTATAGTCCCAC  
TCTTTTGGTTTAATGGGAATGCGCCCCGCATTGGGGGTAAAGGTCA  
TTTCACTAAACAGTAGTGTGGTTTCTGACATTAAAAAATCGACCCG  
ACAATAGGCAAAACCGTTAGCTAATTTGTTGGCTAATGTGAGCATA  
TTGTCAAATTGTAGCGGTTTTTCAATATATTCTGGGGTATTGGGAT  
CTTCTAAAGTAAAAGGCTGTAATTGCCATTGTGTATCATAAACATT  
GATA
```

# GenBank

Firefox

www.ncbi.nlm.nih.gov/nuccore/?term=moeH5

moeH5 - Nucleotide - NCBI

Nucleotide  Search

Save search Limits Advanced Help

Display Settings:  Summary, Sorted by Default order

Send to:  Filter your results:

Results: 5

- [Streptomyces clavuligerus ATCC 27064 plasmid pSCL4, whole genome shotgun sequence](#)  
1. 1,796,500 bp linear DNA  
Accession: NZ\_CM000914.1 GI: 294816545  
[GenBank](#) [FASTA](#) [Graphics](#)
- [Streptomyces clavuligerus ATCC 27064 supercont1.74 genomic scaffold, whole genome shotgun sequence](#)  
2. 30,051 bp linear DNA  
Accession: NZ\_DS570697.1 GI: 254392936  
[GenBank](#) [FASTA](#) [Graphics](#)
- [Streptomyces clavuligerus ATCC 27064 plasmid pSCL4, whole genome shotgun sequence](#)  
3. 1,796,500 bp linear DNA  
Accession: CM000914.1 GI: 294321360  
[GenBank](#) [FASTA](#) [Graphics](#)
- [Streptomyces clavuligerus ATCC 27064 supercont1.74 genomic scaffold, whole genome shotgun sequence](#)  
4. 30,051 bp linear DNA  
Accession: DS570697.1 GI: 169402358  
[GenBank](#) [FASTA](#) [Graphics](#)
- [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](#)  
5. 35,000 bp linear DNA  
Accession: DQ988994.1 GI: 116247579


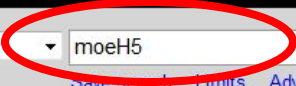
Manage Filters

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

LOCUS DQ988994 35000 bp DNA linear ECT 04-APR-2007  
 DEFINITION Streptomyces ghanensis putative transmembrane protein and putative transcriptional regulator genes, complete cds; see gene cluster 1, complete sequence; putative TetR family regulator, putative hydrolase, hypothetical protein, and putative dehydrogenase genes, complete cds.  
 ACCESSION DQ988994  
 VERSION DQ988994.1 GI:116247579  
 KEYWORDS .  
 SOURCE Streptomyces ghanensis ATCC 14672  
 ORGANISM Streptomyces ghanensis ATCC 14672  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyocineae; Streptomycetaceae; Streptomyces.  
 REFERENCE 1 (bases 1 to 35000)  
 AUTHORS Ostash,S., Saghatelyan,A. and Walker,S.  
 TITLE A streamlined metabolic pathway for the biosynthesis of moenomycin A  
 JOURNAL Chem. Biol. 14 (9), 257-267 (2007)  
 FORMED 17376411  
 REFERENCE 2 (bases 1 to 35000)  
 AUTHORS Orash,B.O. and Walker,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-SEP-2006) Microbiology and Molecular Genetics, Harvard Medical School, 200 Longwood Ave., Boston, MA 02115, USA

## HEADER

FEATURES  
 Location/Qualifiers  
 source  
 1..35000  
 /organism="Streptomyces ghanensis ATCC 14672"  
 /mol\_type="genomic DNA"  
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 /db\_xref="ATCC:14672"  
 /db\_xref="taxon:566461"  
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 /transl\_table=11  
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## FEATURES

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## SEQUENCE

# Структура GenBank FlatFile (GBFF) - флетфайл

# GenBank

## HEADER

LOCUS DQ988994 35000 bp DNA linear BCT 04-APR-2007  
DEFINITION *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.  
ACCESSION DQ988994  
VERSION DQ988994.1 GI:116247579  
KEYWORDS .  
SOURCE *Streptomyces ghanaensis* ATCC 14672  
ORGANISM *Streptomyces ghanaensis* ATCC 14672  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; *Streptomyces*.  
REFERENCE 1 (bases 1 to 35000)  
AUTHORS Ostash,B., Saghatelian,A. and Walker,S.  
TITLE A streamlined metabolic pathway for the biosynthesis of moenomycin A  
JOURNAL Chem. Biol. 14 (3), 257-267 (2007)  
PUBMED [17379141](#)  
REFERENCE 2 (bases 1 to 35000)  
AUTHORS Ostash,B.O. and Walker,S.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-2006) Microbiology and Molecular Genetics, Harvard Medical School, 200 Longwood Ave., Boston, MA 02115, USA

# GenBank

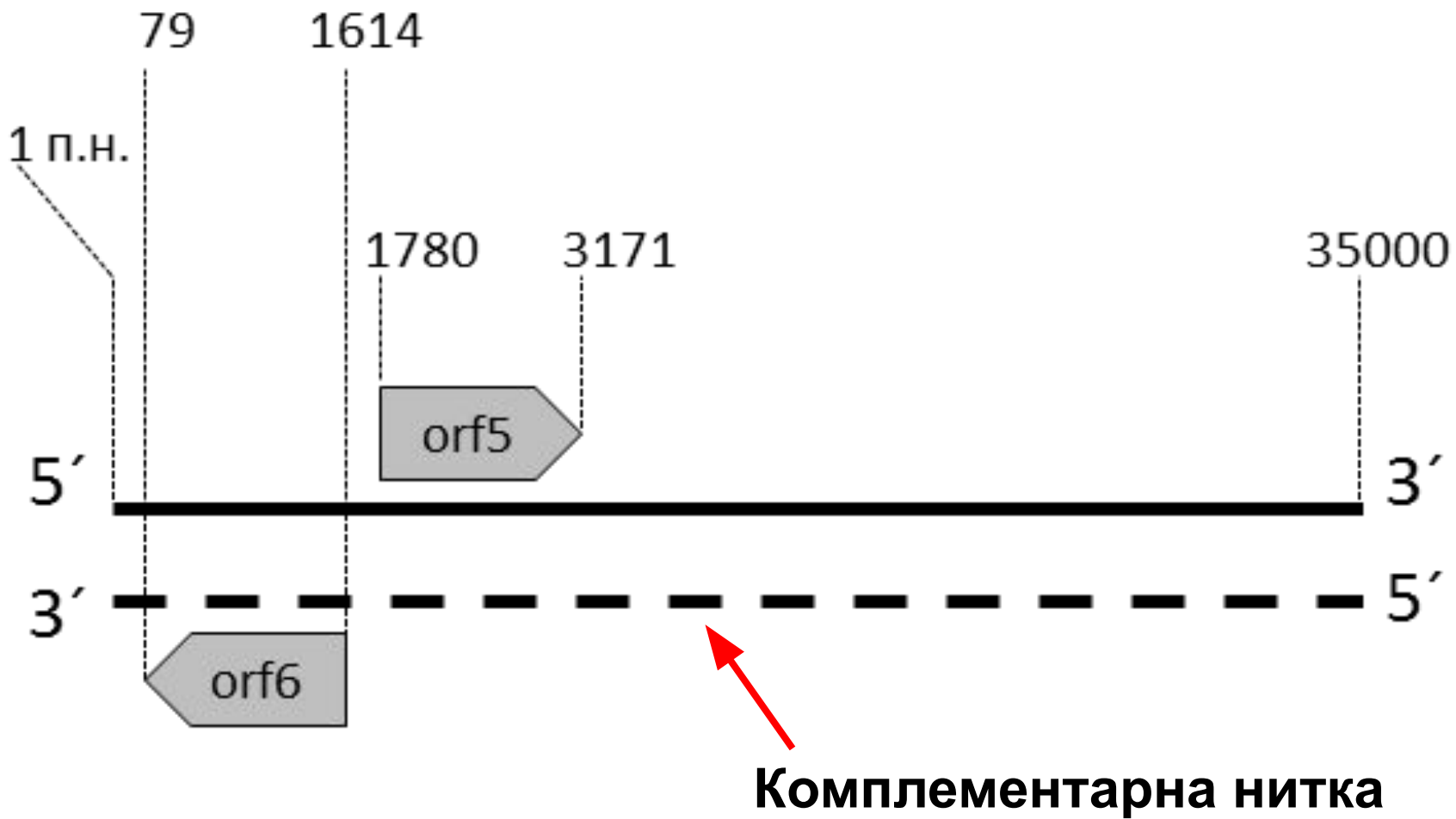
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complement(79..1614)

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# GenBank



# GenBank

## FEATURES

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# GenBank

## ORIGIN

ORIGIN

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# GenBank

## FEATURES

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# GenBank

## moeH5

www.ncbi.nlm.nih.gov/nuccore/DQ988994.1


nyses ghanaensis putative trans... +

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ARRRP"
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Feature 10 of 26 DQ988994 : 1 segment

Details Display: FASTA GenBank Help








## FASTA-файл для *moeH5* - гена

Display Settings:  FASTA

Send:

 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


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

```
>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
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## FASTA-файл для *moeH5* - гена

Display Settings:  FASTA

Send:

 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

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

```
>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
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# Прямий шлях до МоеН5

## Стартова сторінка NCBI

The screenshot shows the NCBI homepage in a Firefox browser. The address bar displays 'www.ncbi.nlm.nih.gov'. The page features a navigation menu on the left, a central 'Welcome to NCBI' section, and a right sidebar with 'Popular Resources' and 'NCBI Announcements'. A search bar at the top contains the text 'All Databases' and is circled in red. A red arrow points from the 'Protein' link in the left sidebar to the search bar. Another red arrow points from the search bar to the 'Protein' link in the right sidebar.

Вибрати Protein

Задати назву білка (МоеН5)

# Депонування НАП

Firefox

www.ncbi.nlm.nih.gov/genbank/

GenBank Home

NCBI Resources How To Sign in to NCBI

GenBank Nucleotide Search

GenBank Submit Genomes WGS HTGs EST/GSS Metagenomes TPA TSA INSDC

## GenBank Overview

### What is GenBank?

GenBank<sup>®</sup> 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
  - SeqIn** – 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 org (якщо є)
- Походження послідовності (що секвенували – хромосома, плазміда тощо; з якого організму)

1

167

CTAAAGGGGAACAAAAGCTGGAGCTCCACC GCGGTGGCGGCCGCTCTAGAACTAGTGGATCCGCAGGAAGCGAGAGCCCCGGGCCCTCCTATCCTGGGCGGGCGCGAA  
CGGCTTTCGGCCCGACGCGAACGACCGTAGGGGCAAAGGCCATCGGGGGATCGGTTTCAGC **ATG**GGCAAGGGCAAGGACAGCCAGGGGTACCCGGCGATGGAGGGCATA  
CGGCCGCTCGTGACC GGTTGACCCGGCGCGGATCGGGCCCTATCGGCTACTGGGACGGCTCGGTGCGGGCGGGATGGGCCGGGTGTACTGGCCCGTTTCGGCGGGCGG  
GCGCACCGTTCGCGGTGAAGGTGGTGCACGAGGAGCACATCGCGAACGGGGAGTTCCGGGCCCGCTTCCGTCGGGAGATCGAGGCCGCCGCCGCGTTCGGCGGGCGGT  
ACACCGCTCCCGTGTTCGACGCGGACGCGGACGCGAACGGCCCTGGGTGGCCACCGGCTACGTCGCCCGGCCCTCCCTCGAACAGGCCGTACGGGAGCACGGGCCG  
CTGCCCCGCCCTCGGTCAACGCCCTGGCCGAGGGGCTGTTGAGGGCCCTGCGCGGCATTTACGCGCCGGGATCGTCCACCGGGACCTCAAGCGTCCAACGTCTT  
GCTCACCGTTCGACGGGCCCGCGTCAATCGACTTCGGCATCGCCCGCGCTCCAGGTTCCGTTGGAGTCCCTGCTGACCAGTACGGGCATGGTCAATCGGCTCTCCCG  
GGTTCATGGCGCCCGAGCAGATCCTCGGGGAGGAGACCGGAGCGGGGGCGGACGTTCTCCCTCGGCTGTGTCTGATGTACGCGGCCACGGGGCGGCTGCCGTTT  
GGCGCCGGTTCGAGCAACCAGCACGCGGTGATGTTCCGGATCGTCCAGTCCCCGCCGGACCTCGACGCGGTGGAGGACGCTCCCTGCGCGAGCTGATCGAACGCTG  
CCTGACCAAAGCCGCCGCGAACGCCCGGGAGTGGACGAGCTGGTGGGGTGCCTGGCGCTGACC GGTTCCCGGACGCTTGGCTGGTGCCTGGCTGCCGCCGGTGC  
TCTTGGCCCCGGTGGCGCAGCAGTTCGGCGTGTGCTCGACGCGGATGTTCCGGAGACCTCGGACGTACCGCGCTGTGCGGGCGGGGGCGCCGAGGAGCTGCT  
TCTTTCGGTTGTTCTTCCGAGGCTCCCGTTGTTCTTCCGAGGCTCCCGTGCCTCGAGCCGCGTACCTCGGTACGGTTCGATTCGAGGCCGGCACCGGCGAAGGACGACGAGGC  
GGGCAGCTGTACCGGACCCGGCCCGGACCCGGACCCGGACTTCTCCCGGCATCGGCATCGGCATCGGGCCCGGCCCGGCCCTTGTCCCTGGTCCCGGAGGGG  
GCTGGTGCCTGCCGGTGGCGGGCGGACCGGCGAGGAAAGTGGGCTAGGCGTTCGTGCGTGGGTGCTGCGCGCAGTTCGTGTCGCGCTGCTGGTGGCTGCCGGGGCAC  
ACCGCTTCTCAACCGCGGCCCGGGTGGCGCCGACCCCGGGGGCGGAGAGGCTGCCGCGCCGCCCGCCGCGCCAGTACGGACCGTCCGGCGCCCGTCTCCCCGGC  
CGGGGAGGACGACTCCAAGGGCAGCGAGAAGGACAAGGGCAAGGACAAGGACAACGGCAAGGAAGACGGGAAGGACAAGGAAGGTACAGAAGAGGAGCAGGGCGGAG  
AGGACGGCGGGGACTCCGGCGGGCGGACGAGCGACGGGGCCGGTTCCGGCGAGGGCGCGTCTCGGGCGGAGGCGAGGGGGCCGGAGCTTCCGGCGGAGGCGGCACA  
CAGGACGGGTCCGGTTCGTCCGGTTTCGGGGGGCTCCGGCGGTGCCGCGAAGCCGCCCGCCAGGACCCCGCCCCGGACGGCCGGGTGCCGACGAGTTCGTTCGGGAC  
CTGGTCCATCGGTTCCAGTACGACGCCCTCCAGCCGACACCGTGGTCAATCCGGCGGGTGTGCGCCGGGACGTGGCGGTGACCTCATCGCCGACGTTCCAGGGGT  
CGGGGCACTGCGAGTACACGGCGAAGCTCAGCTCCGTTGGCGGACGGCGGGAAACCGGATCAACGTCGGTACCGCCGTTGGTGGACAAGGCCCGTTCCGGCGGGGTGTGC  
CGGACACCGACCCCTCGTTCTTACCGTTCGCGGGCTCCGGCATCTGCACGACGTCGGGCCCGCCACGGCAGCGGCTATCGTACAAACCGCGCT **TGA**CGGGGCC  
GTCACTCCGGAATCGACGGTCCGGAACCGGCCGACGTTCCGACGCCCG

2294

2239

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## Streptomyces coelicolor

Well-studied antibiotic-producing bacterium

Lineage: Bacteria[4068]; Actinobacteria[697]; Actinobacteria[697]; Actinobacteridae[646]; Actinomycetales[623]; Streptomycineae[67]; Streptomycetaceae[67]; Streptomycetes[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

- Community selected** : Streptomyces coelicolor
- 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
Plasm	SCP2	NC_003904.1	AL645771.1	0.031317	72.1	34	-	-	-	34	-
Plasm	SCP1	NC_003903.1	AL689148.1	0.356023	69.1	351	-	-	-	355	4

### Biological Properties

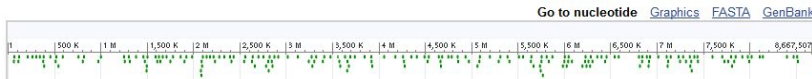
- Morphology
  - Gram : Positive
  - Shape : Tailed
  - Shape : Filamentous
  - Motility : Yes
- Environment
  - OxygenReq : Aerobic
  - OptimumTemperature : 25-35
  - TemperatureRange : Mesophilic
  - Habitat : Multiple
- Phenotype
  - Disease : None

### 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	PRJNA13296	-	○	-	-	-	-	-	-
Streptomyces coelicolor A3(2)	PRJNA57801, PRJNA242	ASM20383v1	●	1	2	9.05	72	8,300	8,153

### Genome Region



### Other BioProjects

Epigenomics	3
Other	3
Transcriptome or Gene expression	30
Variation	1

### Publications

- 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
- 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
- 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...](#)

### Related information

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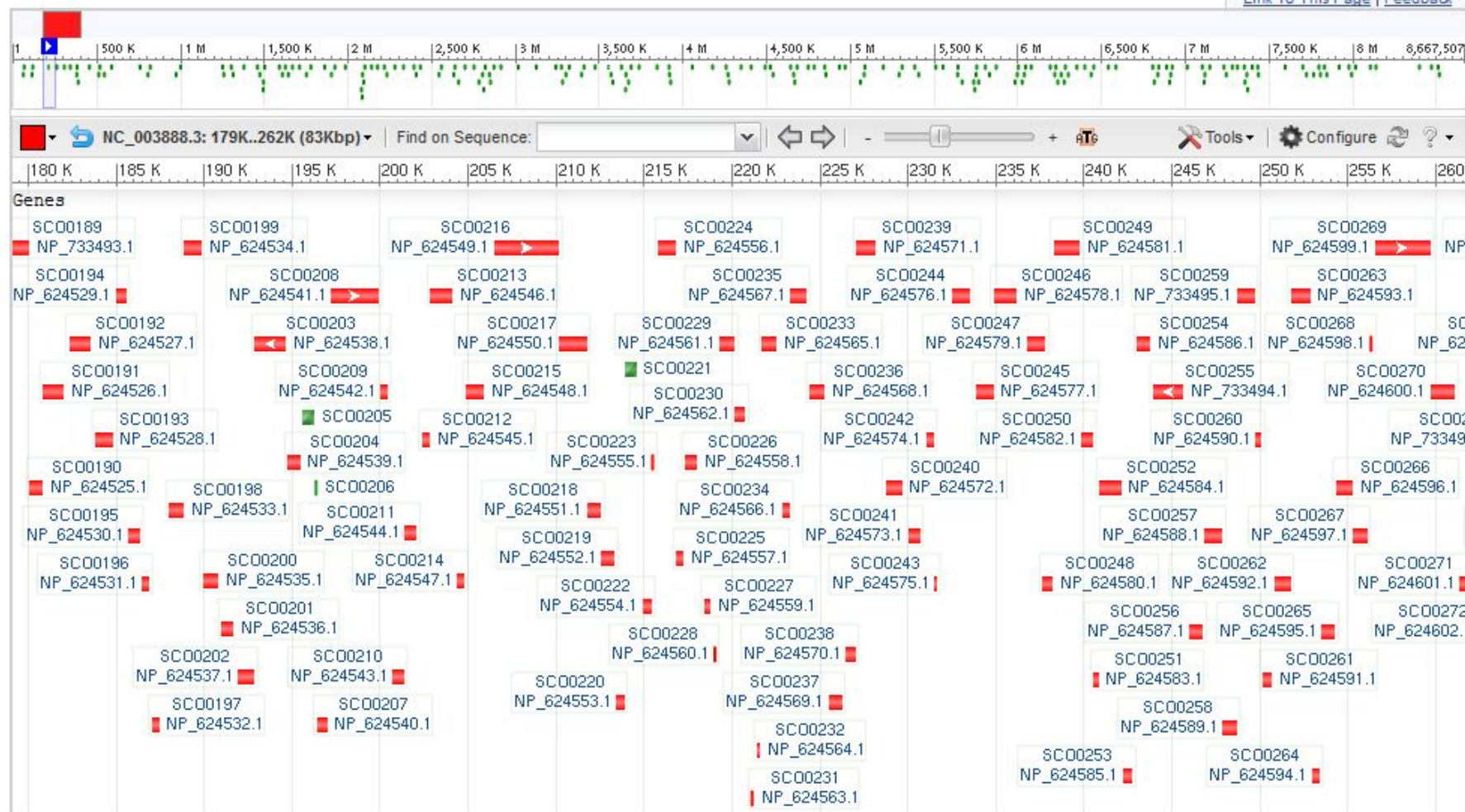
# Genome

## Streptomyces coelicolor A3(2) chromosome, complete genome

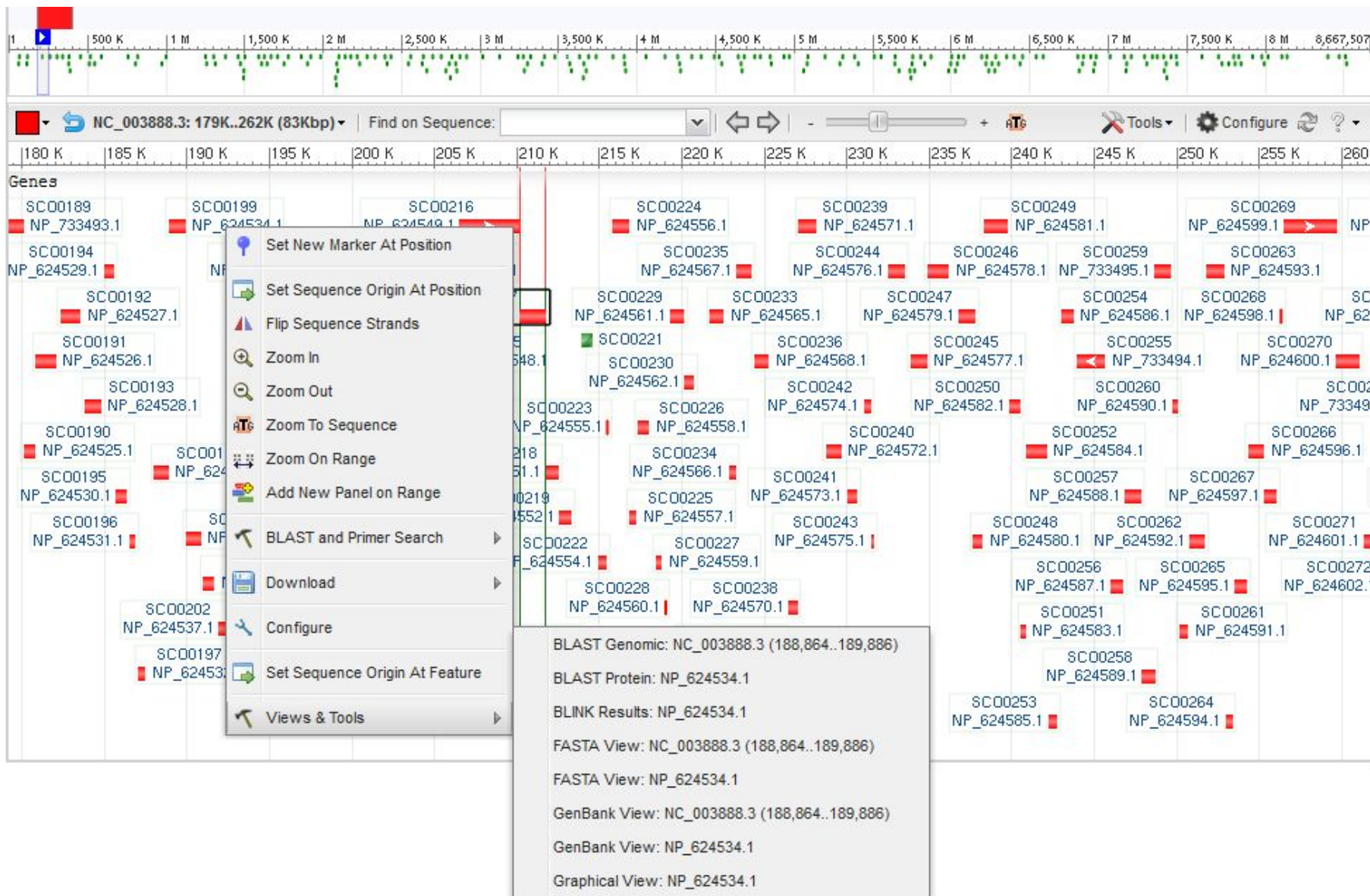
NCBI Reference Sequence: NC\_003888.3

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3nCD

...

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PubMed

Taxonomy

...