

Biomax™ Genome Analysis

Gene Report
LBA0005
DNA gyrase subunit B

Category	Value	General Properties	Prot. Function	Blast	Prot. Structure	Groups	Export
Contig Name	NC_006814						
Gene Position	4283-6244						
Protein Classifier	tox-component sensor histidine kinase-like protein						
Gene Name (by similarity)	gyrB						
Gene Synonyms (by similarity)	HMPPEF0492_0054						
Length [aa]	654						
Molecular Weight [Da]	73030.7						
Isoelectric Point	6.1						
GC Content	39.0 %						

Biological Processes

Accession	Description	Score
03.01.03	DNA synthesis and replication	L.monocytogenes_put 0.0
03.01.03.01	DNA topology	L.monocytogenes_put 0.0
03.01.05	DNA recombination and DNA repair	L.monocytogenes_put 0.0

Localisation

Accession	Description	Score
40.37	prokaryotic nucleoid	L.monocytogenes_put 0.0
5.99.1.3	DNA topoisomerase (ATP-hydrolyzing)	0.0

Molecular Function

Accession	Type	Description	Score
GO:0016853	H	isomerase activity	73.1
GO:0003916	H	DNA topoisomerase activity	43.3
GO:0003918	H	DNA topoisomerase (ATP-hydrolyzing) activity	29.9
GO:0000186	H	nucleotide binding	26.9
GO:0005524	H	ATP binding	13.4

COGS (blastp COGS)

Accession	Description	Score
COGS:COG0187	Type III topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit	0.0
PFAM:PF0204.17	DNA gyrase B	5.2E-04
PFAM:PF01986.13	DNA gyrase B subunit, carboxyl terminus	2.3E-37
PFAM:PF02518.18	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	4.2E-27
PFAM:PF01751.14	Toprim domain	3.5E-5

PROSITE patterns (ScanProsite)

Accession	Description	Score
PROSITE:PS000177 (1)	DNA topoisomerase II signature	2.7E-3
PROSITE:PS00003 (2)	Tyrosine sulfation site	2.5E-4
BLOCKS:IPB000595A	DNA gyrase subunit B signature	7.3E-5
BLOCKS:IPB000595B	DNA gyrase subunit B signature	7.3E-10
BLOCKS:IPB000595C	DNA gyrase subunit B signature	1.4E-9
BLOCKS:IPB000595D	DNA gyrase subunit B signature	1.4E-11
BLOCKS:IPB000595E	DNA gyrase subunit B signature	4.7E-4
BLOCKS:IPB000595F	DNA gyrase subunit B signature	4.2E-7
BLOCKS:IPB000595G	DNA gyrase subunit B signature	1.6E-2
BLOCKS:IPB000595H	DNA gyrase subunit B signature	9.8E-2
BLOCKS:IPB000595I	DNA gyrase subunit B signature	3E-9
BLOCKS:IPB002288A	DNA gyrase, subunit B, C-terminal	9.2E-33
BLOCKS:IPB002288B	DNA gyrase, subunit B, C-terminal	9.5E-17

Analysis results are displayed in an intuitive interface. A gene report is shown here.

Displayed sequence range
From: 272000 bp
To: 282000 bp

Zoom
50% +
50% -

con48_gene18_start:274240, st
A04c001

272000 275000

Enzymes

Contig structure

GENE (Watson strand)

GENE (Crick strand)

GC content panel

The DNA Viewer shows the data graphically.

Reliable, expert genome analysis services

Analyze

Turn sequence data into valuable knowledge

Biomax Informatics provides high-quality, comprehensive automatic and expert analysis of genome sequences and entire genomes to help researchers get the most out of their sequence data. With over ten years of experience in genome analysis for industry and academia, the Biomax annotation team represents one of the most skilled and experienced genome analysis teams available.

We offer the following levels of genome analysis, which can be tailored to your specific research perspectives and goals:

- > High-quality automatic analysis
- > Enhanced analysis
- > Customized analysis

Refine

Reveal the most relevant information

The Pedant-Pro™ Sequence Analysis Suite provides the automatic analysis results, which become a framework for further annotation. Biomax's team of multi-disciplinary scientists verify and improve the automatically generated data. The analysis results are delivered through a secure Web portal. In addition, the data are provided in GenBank and FASTA formats for download.

- > State-of-the-art methods with manual correction
- > Optimal gene prediction for prokaryotes or eukaryotes
- > Functional and structural classification
- > Cross-references to public and/or proprietary databases
- > Support for resequencing projects, for example, by integration of SNP and other variation data

Innovate

Use reliable analysis to speed research and innovation

High-quality analysis allows researchers to do the following:

- > Make sense of raw sequence data
- > Efficiently extract biologically significant information
- > Perform functional and structural analyses more effectively
- > Optimize the design of experiments to answer questions about molecular and genetic aspects
- > Narrow down options for drug targets or regions that should be further characterized and studied

Biomax™ Genome Analysis



The DNA Viewer



The Protein Viewer

High-quality automatic analysis

The automatic level of analysis involves gene prediction using the Pedant-Pro Sequence Analysis Suite. In addition to open reading frames (ORFs), tRNAs, rRNAs and other genetic elements are identified. For all automatically identified genes, the following analyses and annotation are performed:

- > Similarity searches against protein or DNA sequence databases
- > Functional classification of genes (GeneOntology)
- > Assignment of genes to the Enzyme Commission (EC) catalog
- > Assignment of genes to keyword classification
- > Assignment of genes to protein families
- > Analysis of local similarities, domains, patterns and motifs (Blocks, PROSITE, Pfam, and COGS)
- > Analysis of structural features (transmembrane domains and two- and three-dimensional features)

Enhanced analysis

Building on the high-quality automatic analysis results, the enhanced analysis verifies and improves the data through the following types of tasks:

- > Ensure ORFs have the correct start and stop and exon borders
- > Check intergenic regions for missed coding sequences
- > Find internal or overlapping ORFs

Customized analysis

A customized analysis extends the high-quality automatic and enhanced analyses to be tailored to your specific project goals. For example, a customized analysis could focus on a certain biological function, type of sequence or level of coverage using the following:

- > Verification of automatically predicted features and EC numbers
- > Identification of additional information about specific ORFs (e.g., catalytic activity, function and pathways)
- > Analysis for missing enzymes

Selected references

The Biomax annotation team has analyzed numerous genomes for clients worldwide. The following are a selection of Biomax analysis projects which have been published in peer-reviewed journals.

- Andersen MR, et al (2011) Comparative genomics of citric-acid-producing *Aspergillus niger* ATCC 1015 versus enzyme-producing CBS 513.88. *Genome Research* 21(6):885–97
- van den Berg MA, et al (2008) Genome sequencing and analysis of the filamentous fungus *Penicillium chrysogenum*. *Nature Biotechnology* 26(10):1161–8
- Pel HJ, et al (2007) Genome sequencing and analysis of the versatile cell factory *Aspergillus niger* CBS 513.88. *Nature Biotechnology* 25(2): 221–231
- Brzuszkiewicz E, et al (2006) How to become a uropathogen: comparative genomic analysis of extraintestinal pathogenic *Escherichia coli* strains. *Proc Natl Acad Sci U S A* 103(34):12879–84
- Ramezani-Rad M, et al (2003) The *Hansenula polymorpha* (strain CBS4732) genome sequencing and analysis. *FEMS Yeast Res* 4(2):207–15



Aspergillus niger project in Nature Biotechnology

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