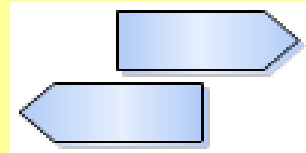
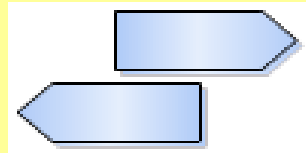


Genome Explorer



Genome Explorer



The Genome Explorer is a genome visualization tool for browsing and comparing enzyme annotations in full genomes. It closes the gap between genomic and enzymatic data and allows the alignment of genomes at a given enzyme-coding gene, thus allowing to visually compare the genomic environment of the gene in different organisms. The underlying genome database is compiled from EBI Genomes and ENSEMBL and supplemented by UniProt annotations.

Enzyme Database - BRENDA - Mozilla Firefox

http://134.169.106.62/index.php4

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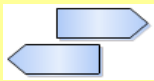
Release 2008.2

EC-Number Enzyme Name Organism Protein Full text Advanced Search

Search Display 10 entries

Latest BRENDA update: June 2008

| Nomenclature | Reaction & Specificity | Functional Parameters |
|---|---|--|
| Enzyme Names EC Number Common/ Recommended Name Systematic Name Synonyms CAS Registry Number | Pathway Catalysed Reaction Reaction Type Natural Substrates and Products Substrates and Products Substrates Natural Substrate Products Natural Product Inhibitors Cofactors | Km Value Ki Value IC50 Value pI Value Turnover Number Specific Activity pH Optimum pH Range Temperature Optimum Temperature Range |
| Isolation & Preparation | | Organism-related information |
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| | | Disease & References |
| | | Disease References |
| | | Application & Engineering |
| | | Engineering Application |

 **Genome Explorer:**
Search a total of more than 3000 complete genomes, plasmids and organelles for specific genes and proteins using some simple search criteria.

Java (at least version 1.4) has to be installed

Fertig

Start Enzyme Database - B... LEO Ergebnisse für "... TOSHIBA (F:) Short tutorial - Open... DE 11:33

Enzyme Database - BRENDA - Mozilla Firefox

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http://www.brenda-enzymes.info/

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Release 2008.1

Genome Explorer

Available genomes: **Archaea**
Acidianus ambivalens plasmid pDL10
Aeropyrum pernix K1 DNA
Archaeoglobus fulgidus DSM 4304
Caldiviga maquilingensis IC-167
Candidatus Methanoregula boonei 6A8
Cenarchaeum symbiosum A
Halorcula marismortui ATCC 43049 chromosome I

(Hold down CTRL or SHIFT to select multiple genomes)

Organism: begins with
EC Number: contains
UniProt Accession: contains
Protein Name: contains

Max. number of results: 50 Preview all results

Restrict your search: Search only in selected genomes

Extend your search: Display homolog proteins min. 50%

search/display

Combine the search criteria:
- EC number
- UniProt accession
- Protein name

Click [here](#) for information on the data sources used for the Genome Explorer.

Fertig

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Genome Explorer

Available genomes:

- Archaea
- Acidianus ambivalens plasmid pDL10
- Aeropyrum pernix K1 DNA
- Archaeoglobus fulgidus DSM 4304
- Caldivirus maquilingensis IC-167
- Candidatus Methanoregula boonei 6A8
- Cenarchaeum symbiosum A
- Haloarcula marismortui ATCC 43049 chromosome I

(Hold down CTRL or SHIFT to select multiple genomes)

Organism: begins with [input] [Filter] [Reset]

EC Number: begins with [input]

UniProt Accession: contains [input]

Protein Name: exact [input]
ends with [input]
use * as joker [input]

Max. number of results: 50 [input] Preview all results

Restrict your search: Search only in selected genomes

Extend your search: Display homolog proteins min. [input] [input]

Search modes:

- contains
- exact
- begins with
- ends with
- use * as a joker

Click here for information on the data sources used for the Genome Explorer

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Genome Explorer

Available genomes:

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- Acidianus ambivalens plasmid pDL10
- Aeropyrum pernix K1 DNA
- Archaeoglobus fulgidus DSM 4304
- Caldivirga maquilingensis IC-167
- Candidatus Methanothermobacter thermoautotrophicus strain ATCC 49619
- Cenarchaeum symbiosum A
- Haloarcula marismortui ATCC 43049 chromosome

(Hold down CTRL or SHIFT to select multiple)

Organism: begins with

EC Number: begins with

UniProt Accession: contains

Protein Name: exact, ends with, use * as joker

Max. number of results: 50 Preview all results

Restrict your search: Search only in selected genomes

Extend your search: Display homolog proteins

Genome selection:
Select one or more entries from the list of available genomes. (Use the CTRL (Strg) or SHIFT key.)

Click here for information on the data sources used for the Genome Explorer

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Available genomes:

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 - Acidianus ambivalens plasmid pDL10
 - Aeropyrum pernix K1 DNA
 - Archaeoglobus fulgidus DSM 4304
 - Caldivirga maquilingensis IC-167
 - Candidatus Methanoregula boonei 6A8
 - Cenarchaeum symbiosum A
 - Haloarcula marismortui ATCC 43049 chromosome I

(Hold down CTRL or SHIFT to select multiple genomes)

Organism: begins with

EC Number: begins with

UniProt Accession: contains

Protein Name: exact
ends with
use * as joker

Max. number of results: 50 Preview all results

Restrict your search: Search only in selected genomes

Extend your search: Display homolog proteins min. 50% 90%

Click [here](#) for information on the data sources used for the Genome Explorer.

Filter the contents of the select box. When the filter is applied, all matching genomes are automatically selected in the select box.

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Genome Explorer

Available genomes: *Archaea*

- Acidianus ambivalens plasmid pDL10
- Aeropyrum pernix K1 DNA
- Archaeoglobus fulgidus DSM 4304
- Caldivirga maquilingensis IC-167
- Candidatus Methanoregula boonei 6A8
- Cenarchaeum symbiosum A
- Haloarcula marismortui ATCC 43049 chromosome I

(Hold down CTRL or SHIFT to select multiple genomes)

Organism: begins with

EC Number: begins with

UniProt Accession: contains

Protein Name: exact
ends with
use * as joker

Max. number of results: 50 Preview all results

Restrict your search: Search only in selected genomes

Extend your search: Display homolog proteins min.

Check the "Search only in selected genomes" option to restrict your query to the genomes you have chosen from the list.

Click here for information on the data sources used for the Genome Explorer

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Genome Explorer

Available genomes:

- Archaea
- Acidianus ambivalens plasmid pDL10
- Aeropyrum pernix K1 DNA
- Archaeoglobus fulgidus DSM 4304
- Caldvirga maquilingensis IC-167
- Candidatus Methanoregula boonei 6A8
- Cenarchaeum symbiosum A
- Haloarcula marismortui ATCC 43049 chromosome I

(Hold down CTRL or SHIFT to select multiple genomes)

Organism: use * as joker [] Filter!

EC Number: contains 4.1.1.1

UniProt Accession: contains []

Protein Name: contains []

Max. number of results: 50 Preview all results

Restrict your search: Search only in selected genomes

Extend your search: Display homolog proteins min. 50%

Click [here](#) for information on the data sources used for the Genome Explorer.

Searching for a specific enzyme or class of enzymes: Enter an EC number or part of an EC number in the corresponding search field.

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Available genomes: **Archaea**
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Aeropyrum pernix K1 DNA
Archaeoglobus fulgidus DSM 4304
Caldivirga maquilingensis IC-167
Candidatus Methanoregula boonei 6A8
Cenarchaeum symbiosum A
Halorcula marismortui ATCC 43049 chromosome I
(Hold down CTRL or SHIFT to select multiple genomes)

Organism: begins with [] Filter! Reset
EC Number: contains []
UniProt Accession: exact [] Q6GHG1
Protein Name: contains []

Max. number of results: 50 [] Preview all results
Restrict your search: Search only in selected genomes
Extend your search: Display homolog proteins min. 50%

Click here for information on the data sources used for the Genome Explorer

Fertig

Start Enzyme Database - B... Short tutorial - Open... LEO Ergebnisse für "p... http://www.brenda-e... DE 10:00

Searching for a specific protein:
Enter the protein's
UniProt/Swiss-Prot accession.
Usually you look for an exact
match.

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Genome Explorer

Available genomes: *Archaea*

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- Aeropyrum pernix K1 DNA
- Archaeoglobus fulgidus DSM 4304
- Caldivirga maquilingensis IC-167
- Candidatus Methanoregula boonei 6A8
- Cenarchaeum symbiosum A
- Haloarcula marismortui ATCC 43049 chromosome I

(Hold down CTRL or SHIFT to select multiple genomes)

Organism: begins with [] [Filter!] [Reset]

EC Number: contains []

UniProt Accession: contains []

Protein Name: contains [Pyruvate decarboxylase]

Max. number of results: 50 [] Preview all results

Restrict your search: Search only in selected genomes

Extend your search: Display homolog proteins min. 50% 90% 100% []

Click [here](#) for information on the data sources used for the Genome Explorer.

**Protein name:
Search for proteins by their
description or their synonyms.**

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Click [here](#) for information on the data sources used

Organism: begins with [] Filter! Reset
EC Number: contains []
Accession: contains []
Enzyme Name: contains [Pyruvate decarboxylase]
Max. number of results: 50 [] Preview all results
Restrict your search: Search only in selected genomes
Extend your search: Display homolog proteins min. 50% 90% 100% sequence identity
search/display

"Extend your search" to find also proteins that are homolog to the proteins in the original result set, check the "display homolog proteins" option.

Specify the minimum level of homology by selecting either 50%, 90% or 100% sequence identity.

http://www.brenda-enzymes.info/genomeexplorer/index.php4

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- Archaeoglobus fulgidus DSM 4304
- Caldivirga maquilingensis IC-167
- Candidatus Methanoregula boonei 6A8
- Cenarchaeum symbiosum A
- Haloarcula marismortui ATCC 43049 chromosome I

(Hold down CTRL or SHIFT to select multiple genomes)

Organism: begins with Filter! Reset

EC Number: contains

UniProt Accession: contains

Protein Name: contains Pyruvate deca

Max. number of results: 50 Preview all results

Restrict your search: Search only in selected genomes

Extend your search: Display homolog proteins min. 50% 90% 100% sequence identity

search/display

Click on ? to get help.

i Click [here](#) for information on the data sources used for the Genome Explorer.

http://www.brenda-enzymes.info/genomeexplorer/index.php4

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Genome Explorer

Preview

Your search

EC Number contains **4.1.1.1**

yielded the following results.

You can now select the genes of interest to be visualized using the BRENDA Genome Explorer.

You have currently selected 1 gene from 1 genome.

Showing results **1 - 20** of **627** > >> Results per page:

| <input type="checkbox"/> | Organism | Gene | Product | EC Number | Accession |
|-------------------------------------|------------------------------------|-------------|---|-----------|-----------|
| <input type="checkbox"/> | Acidobacteria bacterium Ellin345 | | arginine decarboxylase | 4.1.1.19 | Q11QA5 |
| <input type="checkbox"/> | Acinetobacter sp. ADP1 | | putative ornithine decarboxylase | 4.1.1.17 | Q6F8V3 |
| <input type="checkbox"/> | Acinetobacter sp. ADP1 | panD | aspartate 1-decarboxylase precursor Aspartate 1-decarboxylase | 4.1.1.11 | Q6F8I6 |
| <input type="checkbox"/> | Agrobacterium rhizogenes | riorf52 | Riorf52 protein | 4.1.1.18 | Q9KWD2 |
| <input type="checkbox"/> | Agrobacterium tumefaciens str. C58 | panD | aspartate 1-decarboxylase Aspartate 1-decarboxylase precursor Aspartate alpha-decarboxylase | 4.1.1.11 | Q8U9Q9 |
| <input type="checkbox"/> | Agrobacterium tumefaciens str. C58 | AGR_L_2336p | Aspartate 1-decarboxylase precursor Aspartate alpha-decarboxylase | 4.1.1.11 | Q8U9Q9 |
| <input checked="" type="checkbox"/> | Agrobacterium tumefaciens str. C58 | speF | ornithine decarboxylase | | |
| <input type="checkbox"/> | Agrobacterium tumefaciens str. C58 | panD | aspartate 1-decarboxylase precursor Aspartate 1-decarboxylase | | |
| <input type="checkbox"/> | Alcanivorax borkumensis SK2 | panD | aspartate 1-decarboxylase precursor Aspartate 1-decarboxylase | | |
| <input type="checkbox"/> | Aquifex aeolicus VF5 | panD | aspartate 1-decarboxylase precursor Aspartate 1-decarboxylase | | |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | | glutamate decarboxylase Glutamate decarboxylase GAD 1 | | |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | AT4g34710 | arginine decarboxylase SPE2 Arginine decarboxylase 2 | 4.1.1.19 | O23141 |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | | ARGDC 2 ADC 2 ADC 1 | | |

Example for results: Select the genes you would like to view by marking the check box.

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Genome Explorer

Preview

Your search **EC Number** contains **4.1.1.1**

yielded the following results.

You can now select the genes of interest to be visualized using the BRENDA Genome Explorer.

You have currently selected 1 gene from 1 genome.

Visualize selected Visualize all

Showing results 1 - 20 of 7 > >>

| <input type="checkbox"/> | Organism | | | | |
|-------------------------------------|------------------------------------|-------------|-------------------------------------|----------|--------|
| <input type="checkbox"/> | Acidobacteria bacterium Ellin345 | | | | |
| <input type="checkbox"/> | Acinetobacter sp. ADP1 | | | | |
| <input type="checkbox"/> | Acinetobacter sp. ADP1 | panD | aspartate 1-decarboxylase | 4.1.1.11 | Q0VSR5 |
| <input type="checkbox"/> | Agrobacterium rhizogenes | riol | aspartate 1-decarboxylase | 4.1.1.11 | O66773 |
| <input type="checkbox"/> | Agrobacterium tumefaciens str. C58 | panD | aspartate 1-decarboxylase | 4.1.1.11 | O66773 |
| <input type="checkbox"/> | Agrobacterium tumefaciens str. C58 | AGR_L_2336p | Aspartate 1-decarboxylase precursor | 4.1.1.11 | Q8U9Q9 |
| <input type="checkbox"/> | Agrobacterium tumefaciens str. C58 | AGR_L_2336p | Aspartate alpha-decarboxylase | 4.1.1.11 | Q8U9Q9 |
| <input checked="" type="checkbox"/> | Agrobacterium tumefaciens str. C58 | speF | ornithine decarboxylase | 4.1.1.17 | Q8UB21 |
| <input type="checkbox"/> | Agrobacterium tumefaciens str. C58 | AGR_L_3227p | Ornithine decarboxylase | 4.1.1.17 | Q8UB21 |
| <input type="checkbox"/> | Alcanivorax borkumensis SK2 | panD | aspartate 1-decarboxylase | 4.1.1.11 | Q0VSR5 |
| <input type="checkbox"/> | Aquifex aeolicus VF5 | panD | aspartate 1-decarboxylase | 4.1.1.11 | O66773 |
| <input type="checkbox"/> | Aquifex aeolicus VF5 | panD | Aspartate 1-decarboxylase precursor | 4.1.1.11 | O66773 |
| <input type="checkbox"/> | Aquifex aeolicus VF5 | panD | Aspartate alpha-decarboxylase | 4.1.1.11 | O66773 |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | | glutamate decarboxylase 1 (GAD 1) | 4.1.1.15 | Q42521 |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | | Glutamate decarboxylase 1 | 4.1.1.15 | Q42521 |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | | GAD 1 | 4.1.1.15 | Q42521 |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | | arginine decarboxylase SPE2 | 4.1.1.19 | O23141 |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | AT4g34710 | Arginine decarboxylase 2 | 4.1.1.19 | O23141 |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | AT4g34710 | ARGDC 2 | 4.1.1.19 | O23141 |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | AT4g34710 | ADC 2 | 4.1.1.19 | O23141 |
| <input type="checkbox"/> | Arabidopsis thaliana (thale cress) | AT4g34710 | ADC M | 4.1.1.19 | O23141 |

Press "Visualize selected" to explore the genomic neighborhood of the selected genes, or "Visualize all" to display all genes found in your query.

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Click here to view the color legend

Operon detection: off
Color scheme: EC_Main

1-1545895 166204 176203
1.1.3.15 1.1.3.15 4.2.1.8 5.1.1.13 4.1.1.15 4.2.99.8
[AE017261] *Picrophilus torridus* DSM 9790, complete genome. (1545895 bp)

1-1545895 345795 355793
6.1.1.4 1.3.99.10
[AE017261] *Picrophilus torridus* DSM 9790, complete genome. (1545895 bp)

1-1661137 142881
1.1.1.205
strain S2, complete sequence. (1661137 bp)

1-1661137 1538228
2.5.1.16 3.5.9.11 1.1.1.95
strain S2, complete sequence. (1661137 bp)

1-2178400 719355
DSM 4304 complete genome. (2178400 bp)

1-2178400 121111
DSM 4304 complete genome. (2178400 bp)

1-2178400 8319
[AE000782] *Archaeoglobus fulgidus* DSM 4304 complete genome. (2178400 bp)

1-1751377 786833 796832
3.5.4.2 2.7.9.23 2.5.1.61
[AE000656] *Methanobacterium thermoautotrophicum* delta H complete g (1751377 bp)

1-1751377 717813 727811
2.7.9.2 2.4.2.9 2.4.2.9
[AE000656] *Methanobacterium thermoautotrophicum* delta H complete g (1751377 bp)

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Start Enzyme Database ... Enzyme Database ... http://www.brend... http://www.brend... TOSHIBA (F:) Short tutorial - Op... DE 11:46

Visualization of the genes on the selected genomes. Navigate through the genomes, view the gene annotations, perform various genome alignments, and follow a number of hyperlinks to additional sources of information.

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1545895 166204 176203
1.1.3.15 1.1.3.15
4.2.1.9 5.1.1.10 4.2.99.6
[AE017261] Picrophilus torridus DSM 9790, complete genome. (1545895 bp)

1545895 345795 355793
6.1.1.4 1.3.99.10
[AE017261] Picrophilus torridus DSM 9790, complete genome. (1545895 bp)

1661137 142881
1.1.1.205
[AE017261] Picrophilus torridus strain S2, complete sequence. (1661137 bp)

1661137 1538228
2.5.1.15 9.5.9.11 1.1.1.95
[AE017261] Picrophilus torridus strain S2, complete sequence. (1661137 bp)

2178400 719355
[AE017261] Picrophilus DSM 4304 complete genome. (2178400 bp)

2178400 121111
[AE017261] Picrophilus DSM 4304 complete genome. (2178400 bp)

2178400 8319
[AE017261] Picrophilus DSM 4304 complete genome. (2178400 bp)




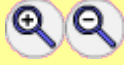


1751377 796832
3.1.9.25 2.7.1.23 2.5.1.61
[AF000656] Methanobacterium thermoautotrophicum delta H complete g (1751377 bp)

1751377 727811
4.1.2.9
[AF000656] Methanobacterium thermoautotrophicum delta H complete g (1751377 bp)

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Toolbar

-  Jump to the start/end in each genome
-  Navigate one page to the left/right in each genome
-  Navigate 1/10 of a page to the left/right in each genome
-  Zoom in/out of the genome view
-  Remove/keep the selected genomes
-  Sort the alignment by left/right neighborhood

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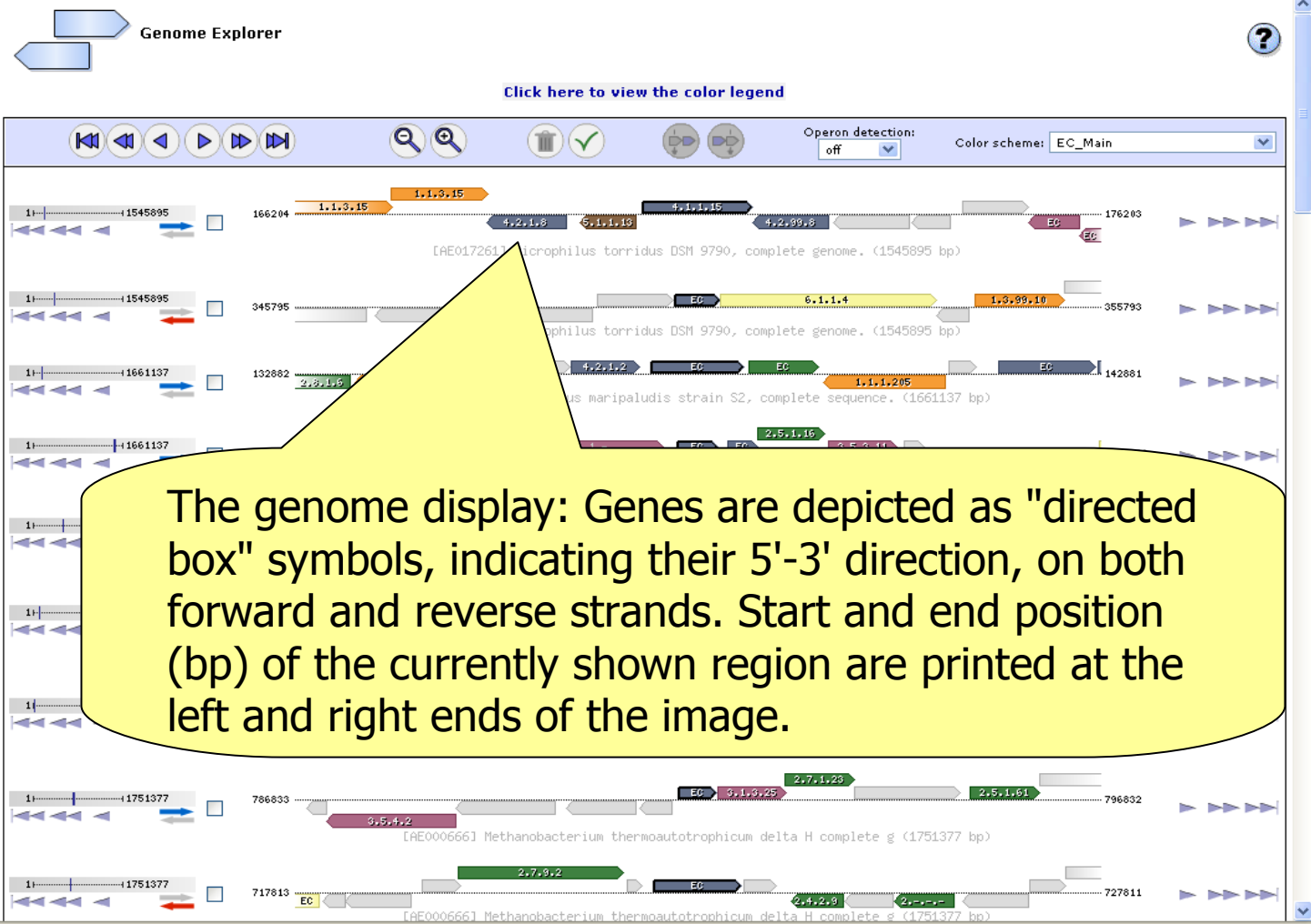


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The genome display: Genes are depicted as "directed box" symbols, indicating their 5'-3' direction, on both forward and reverse strands. Start and end position (bp) of the currently shown region are printed at the left and right ends of the image.

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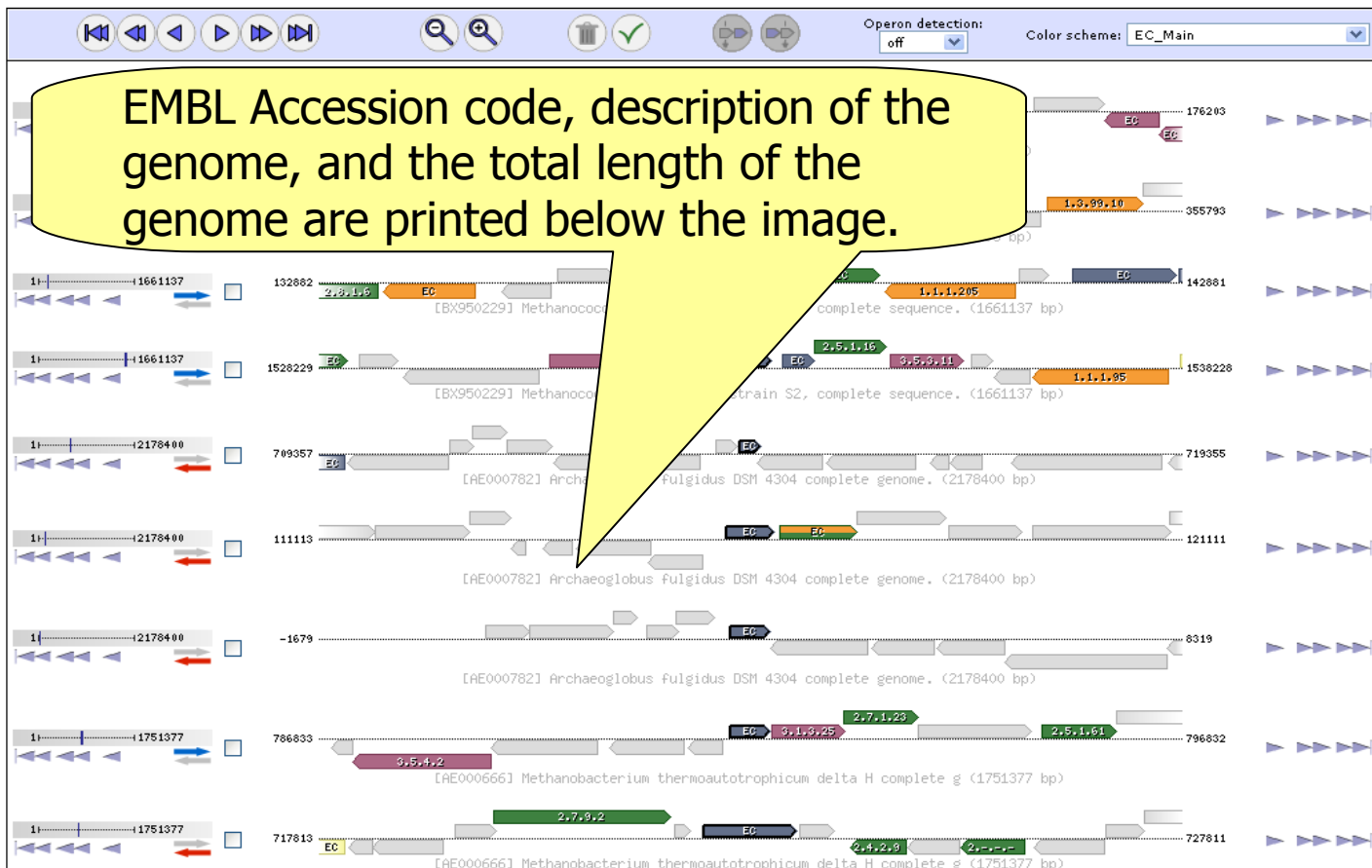
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Operon detection: off Color scheme: EC_Main

The genes are colored according to their functional classification. The color depends on which color scheme is selected. When a gene is annotated with an EC number, it is either printed inside the box or at least indicated by an "EC" label.

1-1545895 166204 176203
[AE017261] Picrophilus torridus DSM 9790, complete genome. (1545895 bp)

1-1545895 345795 355793
[AE017261] Picrophilus torridus DSM 9790, complete genome. (1545895 bp)

1-1661137 132882 142881
[BX950229] Methanococcus marisnigri strain S2, complete sequence. (1661137 bp)

1-1661137 1528229 1538228
[BX950229] Methanococcus marisnigri strain S2, complete sequence. (1661137 bp)

1-1751377 786833 796832
[AE000666] Methanobacterium thermoautotrophicum delta H complete g (1751377 bp)

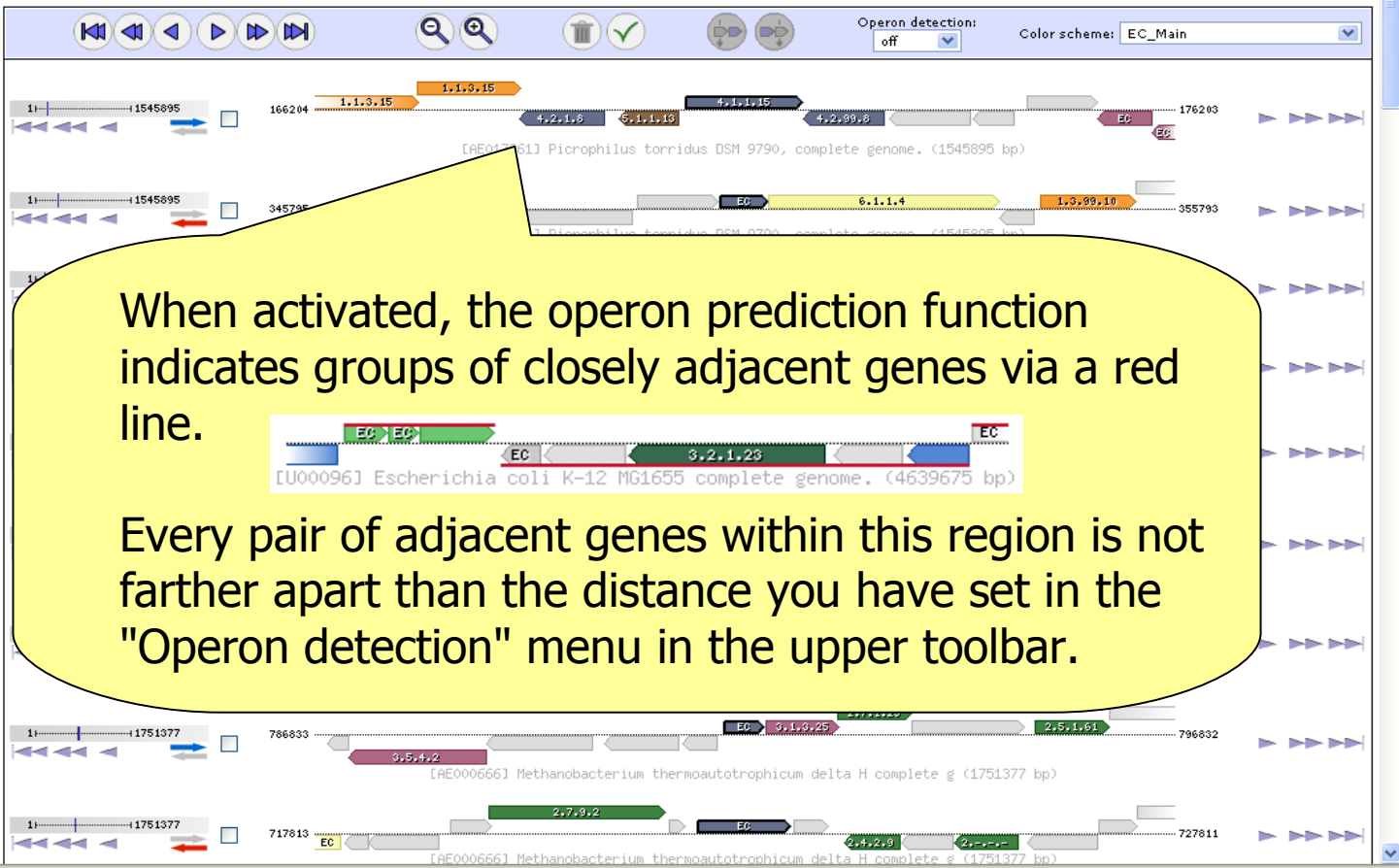
1-1751377 717813 727811
[AE000666] Methanobacterium thermoautotrophicum delta H complete g (1751377 bp)

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Operon detection: off
Color scheme: EC_Main

1-1545895 166204 176203
[AE017261] *Picrophilus torridus* DSM 9790, complete genome. (1545895 bp)

1-1545895 355793
[AE017261] *Picrophilus torridus* DSM 9790, complete genome. (1545895 bp)

1-1661137 142881
[AF0950229] *Methanococcus maripaludis* strain S2, complete sequence. (1661137 bp)

1538228
[AF0950229] *Methanococcus maripaludis* strain S2, complete sequence. (1661137 bp)

719355
[AF000666] *Methanobacterium thermoautotrophicum* delta H complete g (1751377 bp)

121111
[AF000666] *Methanobacterium thermoautotrophicum* delta H complete g (1751377 bp)

8319
[AF000666] *Methanobacterium thermoautotrophicum* delta H complete g (1751377 bp)



796833 796832
[AE000666] *Methanobacterium thermoautotrophicum* delta H complete g (1751377 bp)

717813 727811
[AF000666] *Methanobacterium thermoautotrophicum* delta H complete g (1751377 bp)

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Each genome is selectable via the checkbox. Use the "keep selected genomes" function  to display only the selected genomes, or the "remove selected genomes" function  to drop the selected genomes.

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1-1545895 166204 176203
1.1.3.15 1.1.3.15 4.1.1.15 4.2.9.9 6.1.1.9
[AE017261] *Picrophilus torridus* DSM 9790, complete genome. (1545895 bp)

1-1545895 345795 355793
6.1.1.4 1.3.99.10
[AE017261] *Picrophilus torridus* DSM 9790, complete genome. (1545895 bp)

1-1661137 132882 142881
2.2.1.5 EC 4.2.1.2 EC 1.1.1.205 EC
[BX950229] *Methanococcus marisnigri* strain S2, complete sequence. (1661137 bp)

1-1661137 1528229 1538228
EC 2.5.1.16 EC 3.5.9.11 1.1.1.95
[BX950229] *Methanococcus marisnigri* strain S2, complete sequence. (1661137 bp)

719355 719355
[AE000666] *Methanobacterium thermoautotrophicum* delta H complete genome. (2178400 bp)

121111 121111
[AE000666] *Methanobacterium thermoautotrophicum* delta H complete genome. (2178400 bp)

8319 8319
[AE000666] *Methanobacterium thermoautotrophicum* delta H complete genome. (2178400 bp)

796833 796833
9.5.4.2 2.7.1.23 2.5.1.61
[AE000666] *Methanobacterium thermoautotrophicum* delta H complete g (1751377 bp)

1-1751377 717813 727811
2.7.8.2 EC 2.4.2.9 2.5.1.61
[AE000666] *Methanobacterium thermoautotrophicum* delta H complete g (1751377 bp)

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Clicking on a non-EC gene will take you to the corresponding UniProt entry while clicking on an EC annotated gene will take you to the respective BRENDA entry.

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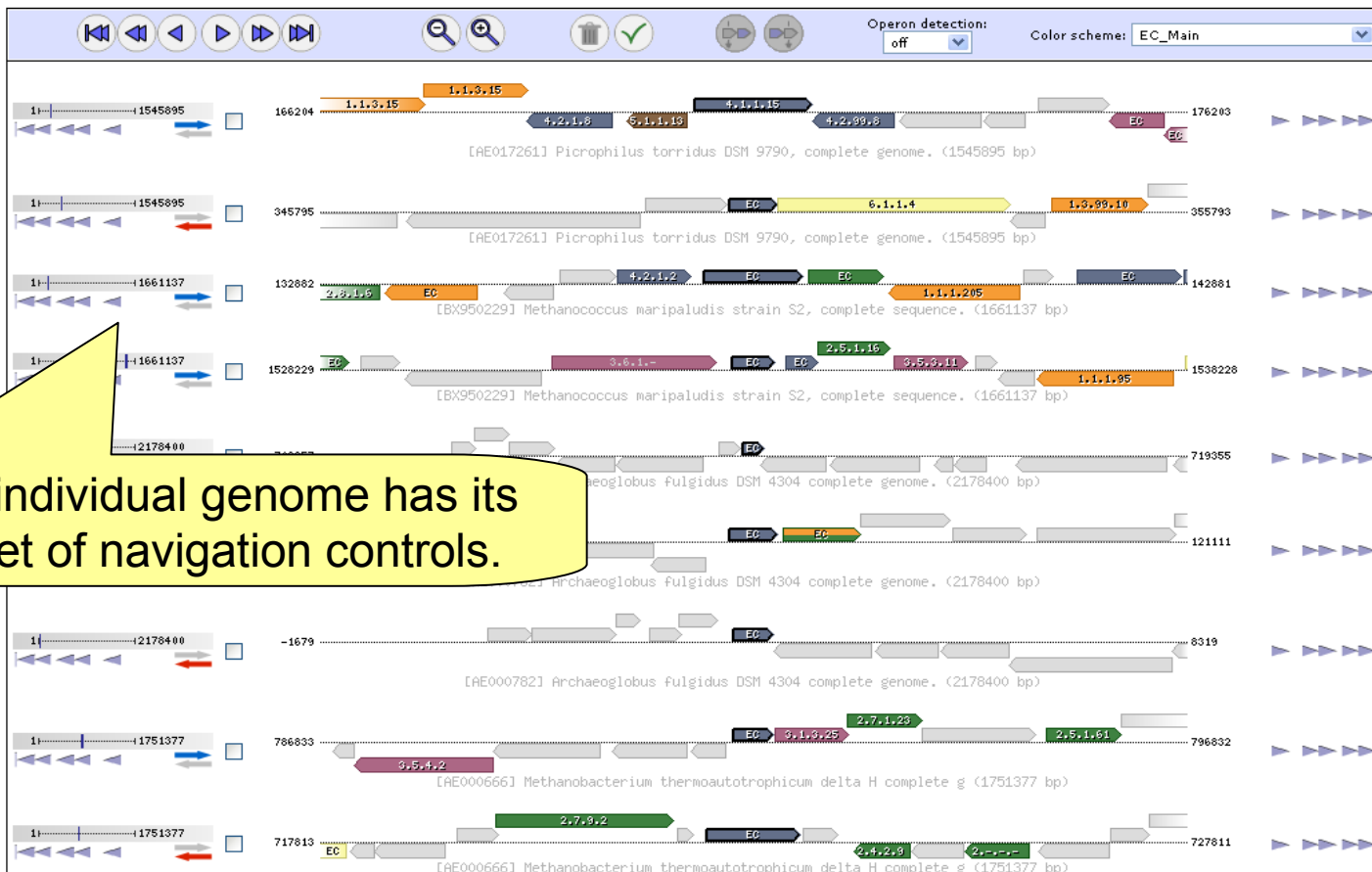
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Each individual genome has its own set of navigation controls.

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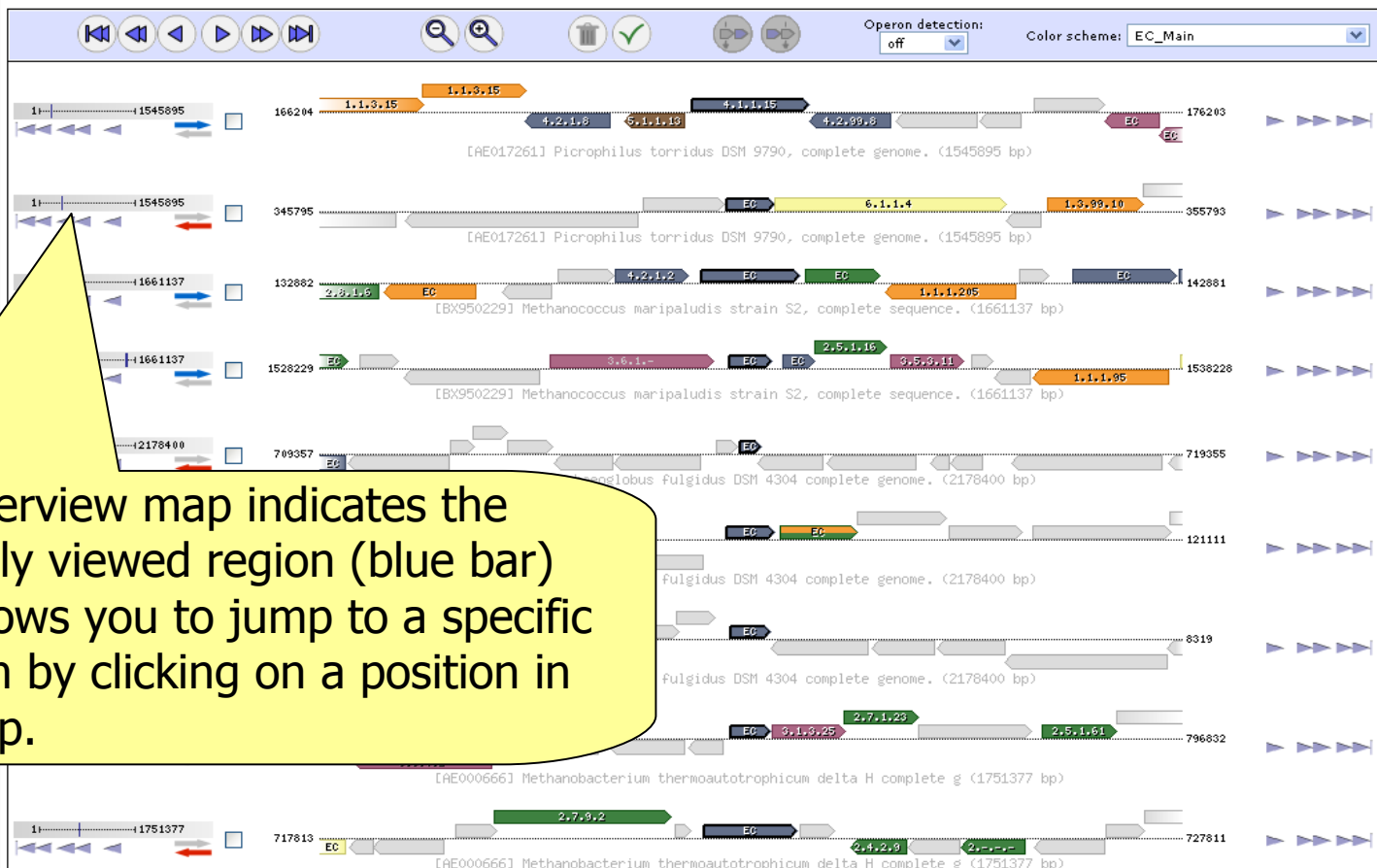


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The overview map indicates the currently viewed region (blue bar) and allows you to jump to a specific position by clicking on a position in the map.

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Each genome can be navigated individually using the local navigation controls.

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Color scheme: EC_Main

1545895
166204 176203
[AE017261] *Picrophilus torridus* DSM 9790, complete genome. (1545895 bp)

345795 355793
[AE017261] *Picrophilus torridus* DSM 9790, complete genome. (1545895 bp)

132882 142881
[BX950229] *Methanococcus maripaludis* strain S2, complete sequence. (1661137 bp)

1528229 1538228
[BX950229] *Methanococcus maripaludis* strain S2, complete sequence. (1661137 bp)

709357 719355
[BX950229] *Methanococcus maripaludis* strain S2, complete sequence. (1661137 bp)

121111
8319
796832
727811

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Genome direction:



Genome is displayed with its forward strand on top.



Genome is "flipped" and displayed with its reverse strand on top.

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COG_Modified
COG_Original
COG_Superclasses
EC_Main
KEGG_Pathway_Subclasses
KEGG_Pathway_Superclasses

1 |< 1765118
[AL096836] Pyrococcus abyssi complete genome (1765118 bp)

1 |< 2365589
[AE005176] Lactococcus lactis subsp. lactis IL1403, complete genom (2365589 bp)

1 |< 4857432
1.1.1.3 2.7.2.4 2.7.1.99 4.2.99.2 4.2.3.1

1 |< 2595221
[CR936257] Natronomonas pharaonis DSM 2160 complete genome (2595221 bp)

New search

Genes can be colored according to their products:

- COG classification (superclasses or subclasses)
- EC classification (main classes)
- KEGG pathway classification (superclasses or subclasses).

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- COG_Modified
- COG_Original
- COG_Superclasses
- EC_Main
- KEGG_Pathway_Subclasses
- KEGG_Pathway_Superclasses

The interface displays genomic tracks for several organisms, including Pyrococcus, Lactococcus lactis, Sinorhizobium meliloti, and Natronomonas pharaonis. Each track shows gene models with arrows indicating direction and color coding. A yellow callout box highlights the 'Click here to view the color legend' link at the top of the page.

To view the color legend of the current scheme, click on the "Click here to view the color legend" link on top of the page.

New search

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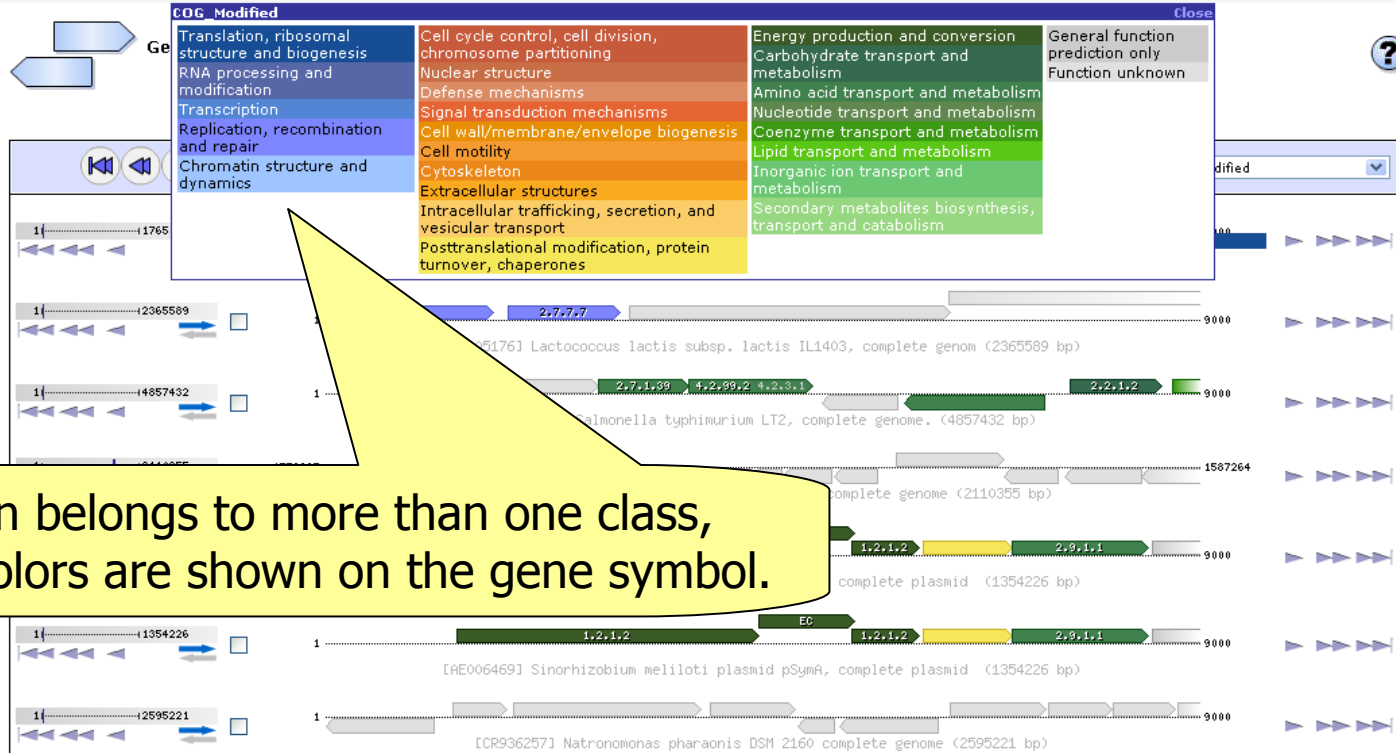
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COG_Modified

| | | | |
|---|---|--|----------------------------------|
| Translation, ribosomal structure and biogenesis | Cell cycle control, cell division, chromosome partitioning | Energy production and conversion | General function prediction only |
| RNA processing and modification | Nuclear structure | Carbohydrate transport and metabolism | Function unknown |
| Transcription | Defense mechanisms | Amino acid transport and metabolism | |
| Replication, recombination and repair | Signal transduction mechanisms | Nucleotide transport and metabolism | |
| Chromatin structure and dynamics | Cell wall/membrane/envelope biogenesis | Coenzyme transport and metabolism | |
| | Cell motility | Lipid transport and metabolism | |
| | Cytoskeleton | Inorganic ion transport and metabolism | |
| | Extracellular structures | Secondary metabolites biosynthesis, transport and catabolism | |
| | Intracellular trafficking, secretion, and vesicular transport | | |
| | Posttranslational modification, protein turnover, chaperones | | |



If a protein belongs to more than one class, multiple colors are shown on the gene symbol.

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[AL096836] *Pyrococcus abyssi* complete genome (1765118 bp)

CDS:
1882 - 3024:
DNA polymerase III, beta chain (EC 2.7.7.7)
DNA polymerase III, beta chain

EC Numbers:
2.7.7.7 (Source: SwissProt) [Show Reaction]

Database references:
GOA: Q9CJJ1
UniProt/Swiss-Prot: **Q9CJJ1**

COGs:
DNA polymerase sliding clamp subunit (homolog)

Pathways:
Purine metabolism
Pyrimidine metabolism
DNA polymerase

Browse homolog proteins:
min. 50% sequence identity

Moving the mouse over a gene symbol will bring up an information box providing useful functional annotations for the gene of interest.

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Gene Description:

- CDS:** 1882 - 3024
- EC Numbers:** 2.7.7.7 (Source: UniProt)
- Database reference:** GOA: Q9CJ11, UniProt/Swiss-Prot: [AE006468]
- COGs:** DNA polymerase subunit (PCNA homolog)
- Pathways:** Purine metabolism, Pyrimidine metabolism, DNA replication

Position of the gene on the genome and description of the gene product.

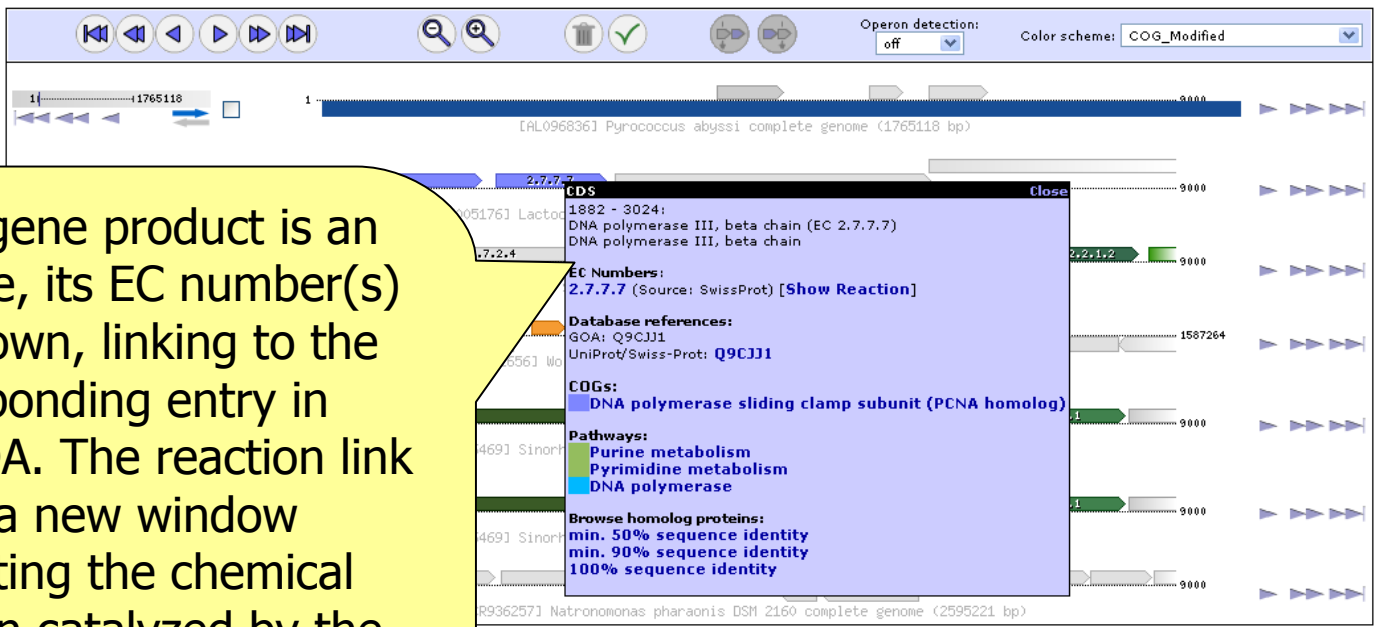
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If the gene product is an enzyme, its EC number(s) are shown, linking to the corresponding entry in BRENDA. The reaction link opens a new window illustrating the chemical reaction catalyzed by the enzyme.

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[AL096836] Pyrococcus abyssi complete genome (1765118 bp)

1882 - 3024:
DNA polymerase III, beta chain (EC 2.7.7.7)
DNA polymerase III, beta chain

EC Numbers:
2.7.7.7 (Source: SwissProt) [Show Reaction]

Database references:
GOA: Q9CJJ1
UniProt/Swiss-Prot: Q9CJJ1

COGs:
DNA polymerase sliding clamp subunit (PCNA homolog)

...one metabolism
...idine metabolism
...polymerase

...olog proteins:
...sequence identity

If the gene product has been categorized into a COG cluster, the description of the cluster is shown. Clicking on the description will align all proteins of the cluster in the Genome Explorer.

http://www.brenda-enzymes.info/php/result_flat.php4?ecno=2.7.7.7

Start Enzyme Database ... Enzyme Database ... http://www.brend... TOSHIBA (F:) Short tutorial - Op... http://www.brend... DE 13:23

Enzyme Database - BRENDA - Mozilla Firefox

http://www.brenda-enzymes.info/

Erste Schritte Aktuelle Nachrichten BRENDA™ Setup Wiz...

BRENDA home login history All enzymes

BRENDA
The Comprehensive Enzyme Information System

TU Braunschweig
Dept. of Bioinformatics

SEARCH-Navigator

- close all open all
- Nomenclature
- Reaction & Specificity
- Functional Parameters
- Organism related Information
- Enzyme Structure
- Isolation & Preparation
- Stability
- Disease & References
- Application & Engineering

Quick search
Fulltext search
Advanced search
Substructure search
TaxTree Explorer
EC Explorer
Sequence Search

Genome Explorer

[Click here to view the color legend](#)

Operon detection: off Color scheme: COG_Modified

[AL096836] Pyrococcus abyssi complete genome (1765118 bp)

[AE005176] Lactococcus lactis complete genome (2961916 bp)

[AE006468] Escherichia coli O157:H7 complete genome (4,845,872 bp)

[BX571656] Wolinella succinogenes complete genome (15,782,655 bp)

[S14691] Sinorhizobium lotum complete genome (25,952,221 bp)

1882 - 3024:
DNA polymerase III, beta chain (EC 2.7.7.7)
DNA polymerase III, beta chain

EC Numbers:
2.7.7.7 (Source: SwissProt) [Show Reaction]

Database references:
GOA: Q9CJJ1
UniProt/Swiss-Prot: Q9CJJ1

COGs:
DNA polymerase sliding clamp subunit (PCNA homolog)

Pathways:
Purine metabolism
Pyrimidine metabolism
DNA polymerase

Browse homolog proteins:
min. 50% sequence identity
min. 90% sequence identity
100% sequence identity

Natronomonas pharaonis DSM 2160 complete genome (2595221 bp)

http://www.brenda-enzymes.info/php/result_flat.php4?ecno=2.7.7.7

Start Enzyme Database ... Enzyme Database ... http://www.brend... TOSHIBA (F:) Short tutorial - Op... http://www.brend... DE 13:23

If the gene product is an enzyme, all KEGG pathways in which the enzyme is involved in are shown. Clicking on the pathway name will open a new window showing the pathway map with the highlighted enzyme.

SEARCH-Navigator

- close all open all
- Nomenclature
- Reaction & Specificity
- Functional Parameters
- Organism related Information
- Enzyme Structure
- Isolation & Purification
- Stability
- Disease & Application



Click here to view the color legend

The UniRef database groups closely related protein sequences into clusters sharing at least 50%, 90% and 100% sequence identity. Click on one of the three links to view all members of the same cluster in the Genome Explorer.

Operon detection: off Color scheme: COG_Modified

[AL096836] Pyrococcus abyssii complete genome (1765118 bp)

2.7.7.7

0051761 Lactococcus lactis subsp. lactis strain 10000
DNA polymerase III, beta chain (EC 2.7.7.7)
DNA polymerase III, beta chain

3 2.7.2.4 [AE006468] Escherichia coli strain O157:H7
DNA polymerase III, beta prime subunit

8X5716561 Wolinella succinogenes strain ATCC 4961
DNA polymerase III, beta prime subunit

E0064691 Sinorhizobium meliloti strain 1021
DNA polymerase III, beta prime subunit

[CR936257] Natronomonas pharaonis DSM 2160 complete genome (2595221 bp)

CDS

1882 - 3024:
DNA polymerase III, beta chain (EC 2.7.7.7)
DNA polymerase III, beta chain

EC Numbers:
2.7.7.7 (Source: SwissProt) [Show Reaction]

Database references:
GOA: Q9CJJ1
UniProt/Swiss-Prot: Q9CJJ1

COGs:
DNA polymerase sliding clamp subunit (PCNA homolog)

Pathways:
Purine metabolism
Pyrimidine metabolism
DNA polymerase

Browse homolog proteins:
min. 50% sequence identity
min. 90% sequence identity
100% sequence identity

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Ideas for *BRENDA's*
improvement welcome !!!