

# Functional Annotation & Beyond with Integrated Microbial Genomes (IMG)

**Rekha Seshadri**

## Abstract

Explore and compare two strains of *Dehalococcoides mccartyi* to discover putative gene(s) responsible for complete dechlorination of PCE to nontoxic end product, ethylene.

**Citation:** Rekha Seshadri Functional Annotation & Beyond with Integrated Microbial Genomes (IMG). **protocols.io**  
dx.doi.org/10.17504/protocols.io.fb4biqw

**Published:** 25 Jul 2016

## Guidelines

### Background:

Organohalides (e.g., tetrachloroethylene, polychlorinated biphenyls, dioxins) constitute a large proportion of environmental pollutants, and reductive dehalogenases encoded by obligate organohalide-respiring bacteria (OHRB), catalyze their dehalogenation to non-toxic metabolites. Corrinoid cobalamin (B12) is an essential cofactor of reductive dehalogenases. De novo biosynthesis of corrinoid is one of the most complicated metabolic pathways in nature, and OHRB have developed different strategies to cope with their need for this cofactor.

### Case Study:

Explore and compare two strains of *Dehalococcoides mccartyi* to discover putative gene(s) responsible for complete dechlorination of PCE to nontoxic end product, ethylene.

Strain 195 <sup>1</sup>	Strain CBDB1 <sup>2</sup>
1.467 Mbp	1.395 Mbp
Chloroethylenes, etc	Chlorobenzenes, etc
PCE->TCE->DCE->VC->Eth	PCE->TCE->DCE
17(+2) RDs	32 RDs

## REFERENCES

1. Genome sequence of the PCE-dechlorinating bacterium Dehalococcoides ethenogenes. Seshadri R, et al. Science, 2005 Jan 7. PMID 15637277
2. Genome sequence of the chlorinated compound-respiring bacterium Dehalococcoides species strain CBDB1. Kube M et. Al. Nat Biotechnol. 2005 Oct;23(10):1269-73.
3. Microbial species delineation using whole genome sequences, Varghese, N. et. al. Nucl. Acids Res. (2015)
4. Trichloroethene reductive dehalogenase from Dehalococcoides ethenogenes: sequence of tceA and substrate range characterization. Magnuson JK, et al. Appl Environ Microbiol, 2000 Dec. PMID 11097881
5. The Genomes OnLine Database (GOLD) v.5: a metadata management system based on a four level (meta)genome project classification. Reddy TBK, et. al., Nucl. Acids Res. (2014)
6. Discovery of Novel Plant Interaction Determinants from the Genomes of 163 Root Nodule Bacteria. Seshadri, R. et.al. Nat. Sci. Rep. 2015. 5:16825.

## Before start

If you do not have an existing JGI SSO account, make your request here:  
<https://contacts.jgi.doe.gov/registration/new>

## Protocol

### Question 1

#### Step 1.

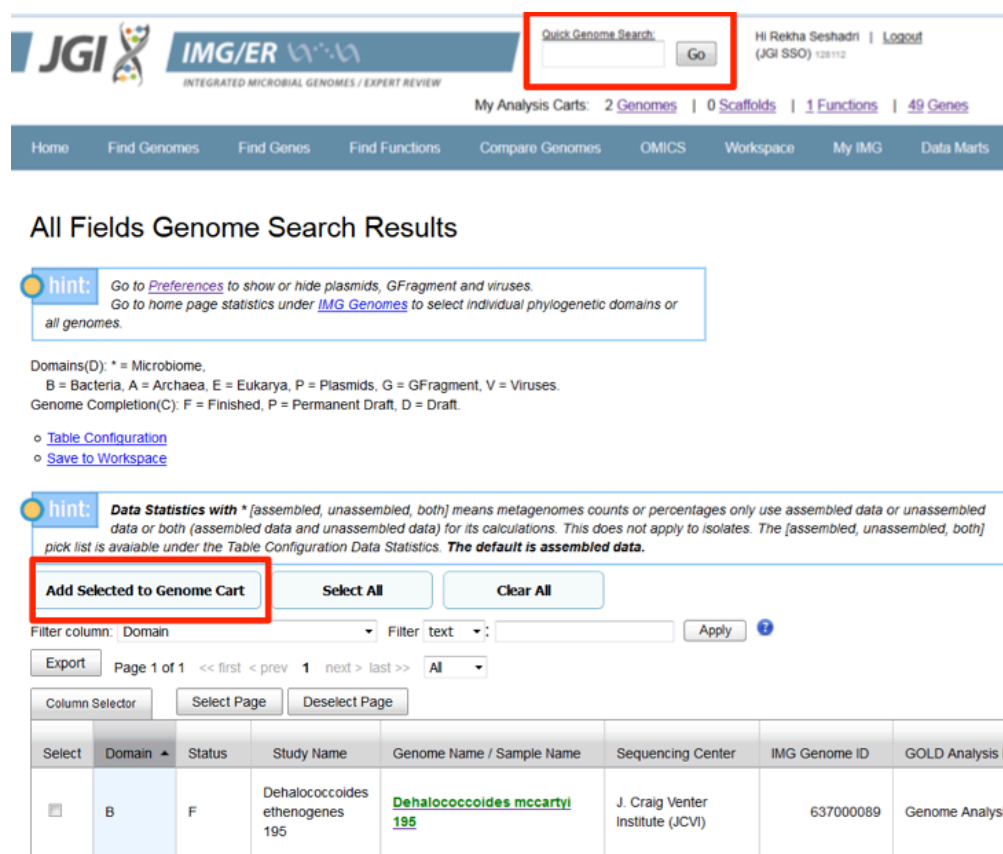
**Question 1:** Given that these are designated as strains of the same species based on 16S rRNA identity, what is the extent of conservation of gene order or “synteny”?

Strain 195 <sup>1</sup>	Strain CBDB1 <sup>2</sup>
1.467 Mbp	1.395 Mbp
Chloroethylenes, etc	Chlorobenzenes, etc
PCE->TCE->DCE-> <b>VC-&gt;Eth</b>	PCE->TCE->DCE

## Question 1

### Step 2.

Add the following 2 genomes to your genome cart using the 'Quick genome Search' box at the top of the page: [Dehalococcoides mccartyi CBDB1](#) and [Dehalococcoides mccartyi 195](#)



**JGI IMG/ER** INTEGRATED MICROBIAL GENOMES / EXPERT REVIEW

Quick Genome Search:

Hi Rekha Seshadri | Logout (JGI SSO) 128112

My Analysis Carts: 2 Genomes | 0 Scaffolds | 1 Functions | 49 Genes

Home Find Genomes Find Genes Find Functions Compare Genomes OMICS Workspace My IMG Data Marts

### All Fields Genome Search Results

**hint:** Go to [Preferences](#) to show or hide plasmids, GFragment and viruses.  
Go to home page statistics under [IMG Genomes](#) to select individual phylogenetic domains or all genomes.

Domains(D): \* = Microbiome,  
B = Bacteria, A = Archaea, E = Eukarya, P = Plasmids, G = GFragment, V = Viruses.  
Genome Completion(C): F = Finished, P = Permanent Draft, D = Draft.

- [Table Configuration](#)
- [Save to Workspace](#)

**hint:** Data Statistics with \* [assembled, unassembled, both] means metagenomes counts or percentages only use assembled data or unassembled data or both (assembled data and unassembled data) for its calculations. This does not apply to isolates. The [assembled, unassembled, both] pick list is available under the Table Configuration Data Statistics. **The default is assembled data.**

**Add Selected to Genome Cart**

Filter column: Domain Filter text:

Page 1 of 1 << first < prev 1 next > last >> All

Column Selector

Select	Domain	Status	Study Name	Genome Name / Sample Name	Sequencing Center	IMG Genome ID	GOLD Analysis F
<input type="checkbox"/>	B	F	Dehalococcoides ethenogenes 195	<a href="#">Dehalococcoides mccartyi 195</a>	J. Craig Venter Institute (JCVI)	637000089	Genome Analysis

## Question 1

### Step 3.

Use Compare Genomes > Synteny Viewers > Dot Plot

Home Find Genomes Find Genes Find Functions Compare Genomes OMICS Workspace My IMG Data Marts

Home > Find Genomes

**Fri. May. 6, 2016.** NERSC will be replacing IMG's web service on **Tue. May. 24, 2016.** NERSC and JGI quarterly maintenance. A inconvenience.

### All Fields Genome Search Results

**hint:** Go to [Preferences](#) to show or hide plasmids, GFragment and virus. Go to home page statistics under [IMG Genomes](#) to select individual genomes.

Domains(D): \* = Microbiome,  
B = Bacteria, A = Archaea, E = Eukarya, P = Plasmids, G = GFragment, V =  
Genome Completion(C): F = Finished, P = Permanent Draft, D = Draft.

- Table Configuration
- Save to Workspace

**hint:** Data Statistics with \* [assembled, unassembled, both] means means only use assembled data or unassembled data or both (assembled data and unassembled data) for its calculation. The default pick list is available under the Table Configuration Data Statistics. The default

Add Selected to Genome Cart Select All

Filter column: Domain Filter text:

Genome Statistics 1 Loaded

Synteny Viewers VISTA

Abundance Profiles Dot Plot

Phylogenetic Dist. Artemis ACT

Avg Nucleotide Ident.

Distance Tree

Function Profile

Genome Clustering

Genome Gene Best Hmigs

Phylo. Marker COGs

## Question 1

### Step 4.

Select and Add both genomes and click "Dotplot"

## DotPlot

**Dot Plot** employs [Mummer](#) to generate dotplot diagrams between two genomes. It uses input DNA sequences directly for comparing genomes with similar sequences (because the DNA sequence conserved as the amino acid translation).

Please select 2 genomes.

**Sequencing Status** All Finished, Permanent Draft and Draft **Domain** Genome Cart

☒ List ☐ Tree [Show](#)

Selected: 2

Search for: <enter a genome name to search>

Dehalococcoides mccartyi 195 (B) [F]  
Dehalococcoides mccartyi CBDB1 (B) [F]

Add >  
Add All >>

< Remove  
<< Remove All

**Selected Genomes**

Please select 2 genomes: 2 selected

Dehalococcoides mccartyi 195 (B) [F]  
Dehalococcoides mccartyi CBDB1 (B) [F]

**Algorithm:**

☒ Nucleotide sequence based comparisons  
☐ Protein sequence based comparisons

**Reference:**

☒ Use 1 as reference  
☐ Use 2 as reference

**Dotplot** **Reset**

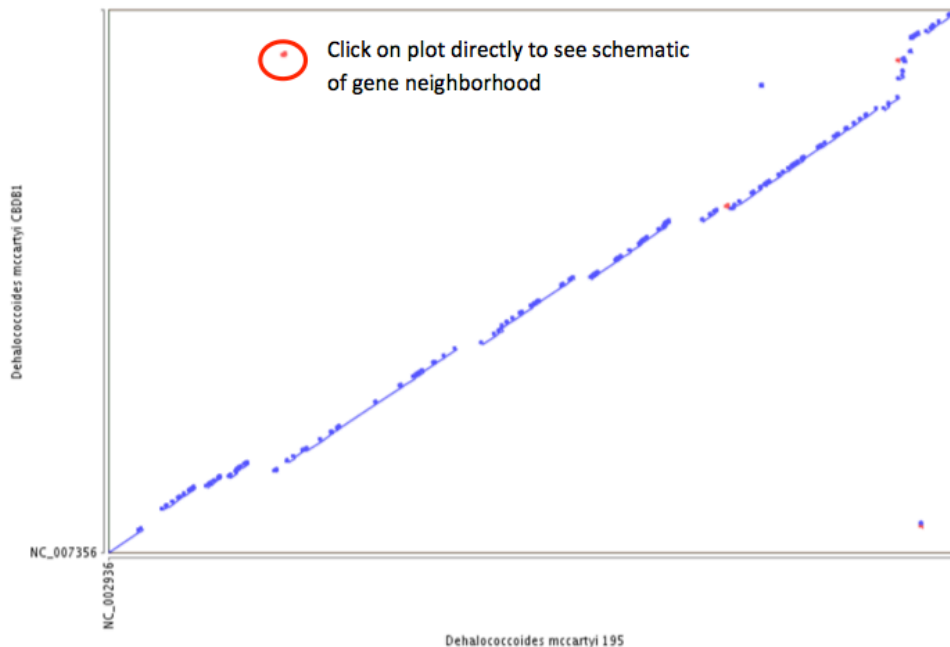
## Question 1

## Step 5.

Click on plot directly to see schematic of gene neighborhood

Dehalococcoides mccartyi 195 vs.  
Dehalococcoides mccartyi CBDB1

Using [nucmer](#) to compare genomes:



## Question 1

### Step 6.

**Answer 1:** Dot plot reveals extensive synteny with some gaps, rearrangement, transposition or inversion appears to involve reductive dehalogenase genes, key enzymes for their hallmark property.

## Question 2

### Step 7.

**Question 2:** What proportion of genes or proteins is conserved?

## Question 2

### Step 8.

Use Compare Genomes > Average Nucleotide Identity > Pairwise ANI

Home Find Genomes Find Genes Find Functions Compare Genomes OMICS Workspace My

**① Fri. May. 6, 2016.** NERSC will be replacing IMG's web serv  
**Tue. May. 24, 2016.** NERSC and JGI quarterly maintenance. A

**IMG/ER Content**

Datasets	JGI	All
Bacteria	6341	43427
Archaea	373	1174
Eukarya	31	257
Plasmids	1	1220
Viruses		5185
Genome Fragments		1201
Metagenome	4747	10147
metatranscriptome	837	1408
Total Datasets		62611
My Private Datasets		12530
Last Datasets Added On:		
Genome	2016-05-18	
Metagenome	2016-05-22	

Project Map  
 Metagenome Projects Map  
 System Requirements

Hands on training available at the

The **Integrated Microbial Gen**  
 analysis and annotation of geno  
 comparative context. The **IMG d**  
 datasets provided by IMG users  
 metagenome datasets.

**IMG/ER** provides users with tool  
 protected access) genome datas  
 and/or metagenome datasets (h  
 access) genome and metagenor

**IMG/ER Statistics**

Metagenome (excluding metatran

Sequenced at:	Engine	All
Metagenome	506	3189
Metatranscriptome	104	295

**IMG/ER** contains [246](#) public studies, 5180 public metagenome datasets ([4780](#) unique samples) distrib

Genome Statistics  
 Synteny Viewers  
 Abundance Profiles  
 Phylogenetic Dist.  
 Avg Nucleotide Ident. **Pairwise ANI**  
 Distance Tree  
 Function Profile  
 Genome Clustering  
 Genome Gene Best Hmigs  
 Phylo. Marker COGs

Periodically for a few minutes.  
 n for the day. Sorry for any in

community resource for  
 comprehensive  
 e and metagenome  
 ly available

Same Species Plot  
 ANI Cliques

dataset distribution.  
 -associated

## Question 2

### Step 9.

The Pairwise ANI page will look like this:

## Pairwise ANI

BBHs between a genome pair are computed as pairwise bidirectional best nSimScan hits of genes having 70% or more identity and at least 70% coverage of the shorter gene. You may either select genome(s) from IMG or you may upload a nucleotide sequence in FASTA format (using the [Upload File](#) button) to compute ANI to selected genome(s) in IMG

Please select up to 100 genomes:

Quick Search:


### Sequencing Status

All Finished, Permanent Draft and Draft

### Domain

Genome Cart

☒ List ☐ Tree

Show 

Selected: 1

Search for:

Dehalococcoides mccartyi 195 (B) [F]

Dehalococcoides mccartyi CBDB1 (B) [F]

## Selected Genomes

Pairwise 1: 1 selected

Dehalococcoides mccartyi 195 (B) [F]

Add

Upload Sets

Remove

Upload File

Pairwise 2: 1

Dehalococcoides mccartyi CBDB1 (B) [F]

Add

Upload Sets

Remove

ANI

## Pairwise ANI

Filter column: Genome1 ID Filter text:  Apply 

Export

Page 1 of 1 << first < prev 1 next > last >> All

Column Selector

Genome1 ID	Genome1 Name	Genome2 ID	Genome2 Name	ANI1->2	ANI2->1	AF1->2	AF2->1	Total BBH	Precomputed ?
637000089	<a href="#">Dehalococcoides mccartyi 195</a>	637000090	<a href="#">Dehalococcoides mccartyi CBDB1</a>	86.35	86.34	0.810	0.830	1251	Yes

Export

Page 1 of 1 << first < prev 1 next > last >> All

## Question 2

### Step 10.

To compare proteins, use Compare Genomes > Genome Genes Best HmIgs

Genome Gene Best Homologs ?

Percent Identity 60+ ▾

Sequencing Status All Finished, Permanent Draft and Draft ▾ Domain Genome Cart ▾

☒ List ☐ Tree  Selected: 1

Search for: <enter a genome name to search>

Dehalococcoides mccartyi 195 (B) [F]  
Dehalococcoides mccartyi CBDB1 (B) [F]

**Selected Genomes**

Reference Genome  
Dehalococcoides mccartyi 195 (B) [F]

Query Genomes (50 max) 1  
Dehalococcoides mccartyi CBDB1 (B) [F]

Excluded Genomes

## Question 2

### Step 11.

**Answer 2:** Both nucleotide and amino acid sequence based comparisons suggest about 70-80% of the genes and proteins are conserved based on best reciprocal hits.

## Question 3

### Step 12.

**Question 3:** How many genes or what functions appear to be unique to Strain 195?

## Question 3

### Step 13.

Use Find Genes > Phylogenetic Profiles > Single Genes



## Phylogenetic Profiler for Single Genes

Sequencing Status  
All Finished, Permanent Draft and Draft  
List Tree Show ⓘ

Domain  
Genome Cart  
Selected: 1

Search for: <enter a genome name to search>  
Dehalococcoides mccartyi 195 (B) [F]  
Dehalococcoides mccartyi CBDB1 (B) [F]

Find Genes In

Dehalococcoides mccartyi 195 (B) [F]

Add Remove ⓘ

With Homologs In

Add Remove

Without Homologs In 1

Dehalococcoides mccartyi CBDB1 (B) [F]

Add Remove

Submit

Advance Options  

Similarity Cutoffs

Max. E-value	1e-10
Min. Percent Identity	1e-2
Exclude Pseudo Genes	1e-5
Algorithm	By Present/Absent Homologs
Min. Taxon Percent With Homologs	100
Min. Taxon Percent Without Homologs	100

### Question 3

#### Step 14.

Results table filtered by Gene Name for "nitrogenase"

Select	Result	Gene Object ID	Locus Tag	Gene Name	Length	KEGG Map Name	KEGG Module Name
<input type="checkbox"/>	231	<a href="#">637120711</a>	DET1148	nitrogenase cofactor biosynthesis protein NifB, putative	276	-	-
<input type="checkbox"/>	234	<a href="#">637120714</a>	DET1151	dinitrogenase iron-molybdenum cofactor NifB/Y/X family protein	134	-	-
<input type="checkbox"/>	235	<a href="#">637120715</a>	DET1152	nitrogenase molybdenum-iron protein, beta subunit, putative	451	-	-
<input type="checkbox"/>	236	<a href="#">637120716</a>	DET1153	nitrogenase MoFe cofactor biosynthesis protein NifE	454	-	-
<input type="checkbox"/>	237	<a href="#">637120717</a>	DET1154	Mo-nitrogenase MoFe protein subunit NifK (EC 1.18.6.1)	461	Microbial metabolism in diverse environments Metabolic pathways Chloroalkane and chloroalkene degradation Nitrogen metabolism	Nitrogen fixation, nitrogen => ammonia Nitrogen fixation, nitrogen => ammonia Nitrogen fixation, nitrogen => ammonia Nitrogen fixation, nitrogen => ammonia
<input type="checkbox"/>	238	<a href="#">637120718</a>	DET1155	nitrogenase molybdenum-iron protein alpha chain	539	Microbial metabolism in diverse environments Chloroalkane and chloroalkene degradation Nitrogen metabolism Metabolic pathways	Nitrogen fixation, nitrogen => ammonia Nitrogen fixation, nitrogen => ammonia Nitrogen fixation, nitrogen => ammonia Nitrogen fixation, nitrogen => ammonia
<input type="checkbox"/>	239	<a href="#">637120721</a>	DET1158	Mo-nitrogenase iron protein subunit NifH (EC 1.18.6.1)	274	Nitrogen metabolism Metabolic pathways Chloroalkane and chloroalkene degradation Microbial metabolism in diverse environments	Nitrogen fixation, nitrogen => ammonia Nitrogen fixation, nitrogen => ammonia Nitrogen fixation, nitrogen => ammonia Nitrogen fixation, nitrogen => ammonia

### Question 3

#### Step 15.

**Answer 3:** About 300 genes appear to be unique to Strain 195 – these include a nitrogenase operon for nitrogen fixation, and a small number of reductive dehalogenases, that might correspond to observed differences in organohalide substrate specificities.

### Question 4

#### Step 16.

**Question 4:** The two strains have different dehalogenation profiles (i.e., preferences in halogenated substrate specificities), in particular, *D. mccartyi* strain195 is capable of COMPLETE dechlorination of PCE to ethylene, unlike Strain CBDB1. Can we identify the reductive dehalogenase(s) responsible for the terminal steps?

### Question 4

#### Step 17.

Use Compare Genomes > Abundance Profile Tools > Overview (All Functions) > Select Pfam (for function type)

Home Find Genomes Find Genes Find Functions Compare Genomes OMICS Workspace My

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**Tue. May. 24, 2016.** NERSC and JGI quarterly maintenance. All services will be down for the day. Sorry for any inconvenience.

**IMG/ER Content**

Datasets	JGI	All
Bacteria	6341	43427
Archaea	373	1174
Eukarya	31	257
Plasmids	1	1220
Viruses		5185
Genome Fragments		1201
Metagenome	4747	10147
metatranscriptome	837	1408
Total Datasets		62611
My Private Datasets		12530

Last Datasets Added On:  
 Genome 2016-05-18  
 Metagenome 2016-05-22

[Project Map](#)  
[Metagenome Projects Map](#)  
[System Requirements](#)

Hands on training available at the

The Integrated Microbial Genomes (IMG) system provides analysis and annotation of genomic data in a comparative context. The IMG datasets provided by IMG users and metagenome datasets.

IMG/ER provides users with tools for genome analysis (password protected access) g...  
[/42/D1/D560](#) and/or metagenome datasets. All public (free access) genome datasets.

**IMG/ER Statistics**

Metagenome (excluding metatranscriptome) dataset distribution:

Sequenced at	Engine	Associated
Metagenome	506	3189
Metatranscriptome	104	295

Genome Statistics  
 Synteny Viewers  
 Abundance Profiles  
 Phylogenetic Dist.  
 Avg Nucleotide Ident.  
 Distance Tree  
 Function Profile  
 Genome Clustering  
 Genome Gene Best Hmgs  
 Phylo. Marker COGs

Overview (All Functions)  
 Search  
 Function Comparisons  
 Function Category

## Question 4

### Step 18.

Selecting Pfam page:

## Abundance Profile Overview

### Display Options:

#### Output Type

☒ Heat Map

OR

☐ Matrix

#### Normalization Method <sup>3</sup>

☒ None

☐ Scale for genome size

*Since both genomes are of comparable size, no normalization is needed*

☒ Gene count

☐

Include all rows, including those without hits

☐ Estimated gene copies <sup>2</sup>

500

functions per page

(Slower)

Enter matching text for highlighting clusters/rows (E.g., "kinase")

### Function:

☐ COG

☐ Enzyme

☐ KO

☒ Pfam

☐ TIGRfam

### Genomes <sup>1</sup>:

MER-FS Metagenome: Assembled

Please select 1 to 100 genomes.

#### Sequencing Status

Finished

#### Domain

Genome Cart

☒ List ☐ Tree

Show

?

Selected: 2

Search for: <enter a genome name to search>

Dehalococcoides mccartyi 195 (B) [F]

Dehalococcoides mccartyi CBDB1 (B) [F]

Go

## Question 4

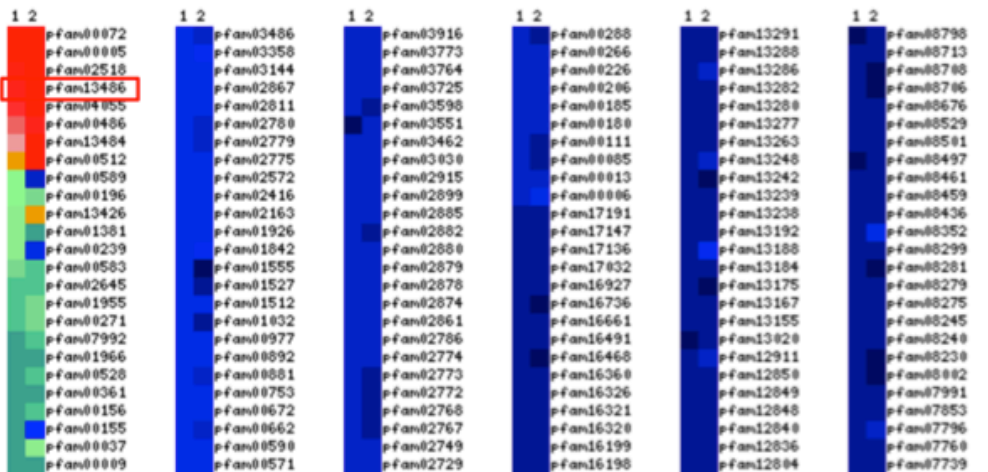
### Step 19.

Add genes corresponding to reductive dehalogenases (pfam13486) from both genomes to your gene cart

# Abundance Profile Overview Results (Gene Count)

Mouse over labels to see additional information.  
Clicking on the column number will sort rows for that column in descending gene count order.  
Clicking on row cluster ID will add the cluster to the appropriate analysis cart (if cart is supported).  
Mouse over heat map to see gene counts. Clicking in the heat map will take you to the gene list.

- 1 - [Dehalococcoides mccartyi 195](#)
- 2 - [Dehalococcoides mccartyi CBDB1](#)



## Question 4 Step 20.

From Gene Cart page, use the Sequence Alignment Tab and "Do alignment"

### Gene Cart

Only a maximum of 20000 genes can be in cart.  
49 gene(s) in cart

Genes in Cart

Functions

Upload & Export & Save

Chromosome Map

Sequence Alignment

Gene Neighborhoods

Profile & Alignment

Edit

Add Genomes of Selected Genes to Cart

Add Scaffolds of Selected Genes to Cart

Toggle Selected

Select All

Clear All

Remove Selected

49 of 49 rows selected

Filter column: Gene Product Name

Filter text

Apply

Export

Page 1 of 1

<< first

< prev

1

next >

last >>

All

Column Selector

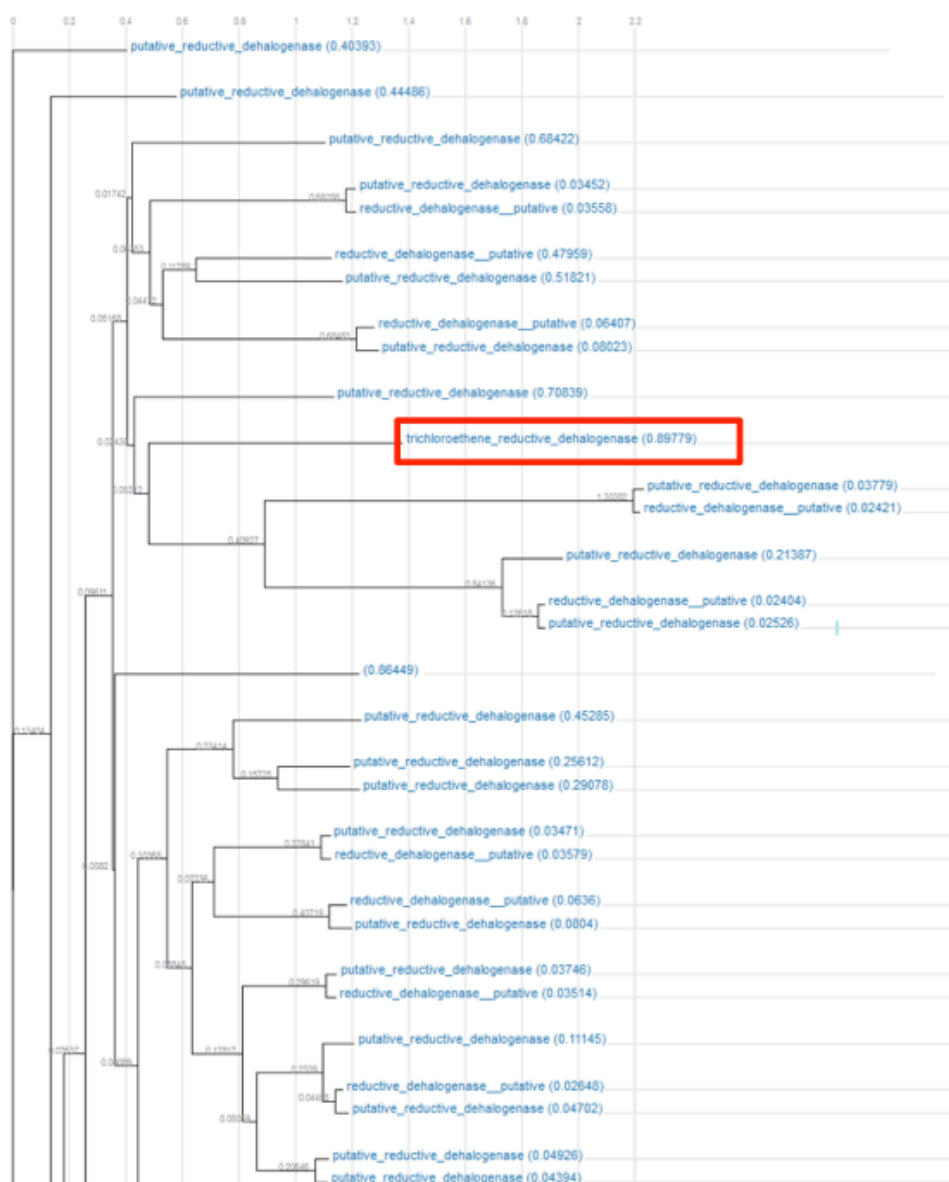
Select Page

Deselect Page

Select	Gene ID	Locus Tag	Gene Product Name	Genome ID	Genome Name	Batch <sup>1</sup>	Amino Acid Sequence Length (aa)
<input checked="" type="checkbox"/>	<a href="#">640733214</a>	DET0162		637000089	<a href="#">Dehalococcoides mccartyi 195</a>	3	486
<input checked="" type="checkbox"/>	<a href="#">637703851</a>	cbdb_A1491	putative reductive dehalogenase	637000090	<a href="#">Dehalococcoides mccartyi CBDB1</a>	2	482
<input checked="" type="checkbox"/>	<a href="#">637702640</a>	cbdb_A84	putative reductive dehalogenase	637000090	<a href="#">Dehalococcoides mccartyi CBDB1</a>	2	488
<input checked="" type="checkbox"/>	<a href="#">637703982</a>	cbdb_A1624	putative reductive dehalogenase	637000090	<a href="#">Dehalococcoides mccartyi CBDB1</a>	2	495
<input checked="" type="checkbox"/>	<a href="#">637703944</a>	cbdb_A1582	putative reductive dehalogenase	637000090	<a href="#">Dehalococcoides mccartyi CBDB1</a>	2	491

## Question 4 Step 21.

From the alignment results page, select "Rectangular Phylogram" tab to view tree



## Question 4

### Step 22.

**Answer 4:** From the tree, it is possible to discern a handful of divergent candidates in strain 195 relative to CBDB1- the gene described as “trichloroethene reductive dehalogenase” is experimentally validated to dehalogenate DCE and VC to ethylene

## Question 5

### Step 23.

**Question 5.** Corrinoid cobalamin (B12) is an essential cofactor of reductive dehalogenases. *De novo* biosynthesis of corrinoid is one of the most complicated metabolic pathways in nature (involving >30 enzymatic steps.), and dehalorespiring bacteria have developed different strategies to cope with their need for this cofactor. Are *D. mccartyi* strains capable of *de novo* cobalamin biosynthesis? Do they have partial pathways? Are they all auxotrophs? What is your conjecture based on your findings?

## Question 5

### Step 24.

Hint: Find Functions > KEGG > Pathways via KO terms > Select Porphyrin and chlorophyll metabolism under Metabolism of cofactors and vitamins > Switch Tab to “view map for selected genomes” > View maps individually for each genome > *On the KEGG map, focus on the **anaerobic portion of the pathway leading from precorrin to Vitamin B12***

The screenshot shows the IMG/ER website interface. The top navigation bar includes links for Home, Find Genomes, Find Genes, Find Functions, Compare Genomes, OMICS, and Worksp. A notification banner at the top left states: "Sat. June 11 to Sun. June 12 NERSC S during this time. Sorry for the inconvenience." On the left side, there is a section titled "IMG/ER Content" with a table of datasets:

Datasets	JGI	All
Bacteria	6341	43428
Archaea	373	1175
Eukarya	31	257
Plasmids	1	1220
Viruses		5185
Genome Fragments		1196
Metagenome & Metatranscriptome	4823	10175
Total Datasets		62636
My Private Datasets		12138

Below this table, there are links for "Project Map", "Metagenome Projects Map", and "System Requirements". A small image shows a person at a computer with the text "Hands on training available at the Microbial Genomics & Metagenomics Workshop".

The main content area shows a "Find Functions" dropdown menu. The menu options are: Function Search, Search Pathways, Secondary Metabolism, COG, KOG, Pfam, TIGRfam, Transporter Class., KEGG, IMG Networks, Enzyme, MetaCyc, Phenotypes, InterPro Browser, and Protein Family Comparison. The "KEGG" option is selected, and a sub-menu is displayed with the following options: KO List, KO List w/ Stats, KEGG Module List, KEGG Module List w/, Orthology KO Terms, and Pathways via KO Terms. The "Pathways via KO Terms" option is highlighted.

## Question 5

### Step 25.

KEGG Pathways Page:



# KEGG Orthology (KO) Terms and Pathways

[KEGG Orthology \(KO\) Terms](#) Based on [BRITe Hierarchy](#)  
[KEGG Pathways via KO Terms](#)

## KEGG Pathways via KO Terms

### 01 Metabolism

#### 02 Global and overview maps

- 03 [Metabolic pathways](#) (2632)
- 03 [Biosynthesis of secondary metabolites](#) (949)
- 03 [Microbial metabolism in diverse environments](#) (978)
- 03 [Biosynthesis of antibiotics](#) (738)
- 03 [Carbon](#)
- 03 [2-Oxoc](#)
- 03 [Fatty ac](#)
- 03 [Biosynt](#)
- 03 [Degrad](#)



#### 02 Metabolism of cofactors and vitamins

- 03 [Thiamine metabolism](#) (24)
- 03 [Riboflavin metabolism](#) (26)
- 03 [Vitamin B6 metabolism](#) (23)
- 03 [Nicotinate and nicotinamide metabolism](#) (61)
- 03 [Pantothenate and CoA biosynthesis](#) (36)
- 03 [Biotin metabolism](#) (23)
- 03 [Lipoic acid metabolism](#) (4)
- 03 [Folate biosynthesis](#) (47)
- 03 [One carbon pool by folate](#) (33)
- 03 [Retinol metabolism](#) (48)
- 03 [Porphyrin and chlorophyll metabolism](#) (107)
- 03 [Ubiquinone and other terpenoid-quinone biosynthesis](#) (55)

#### 02 Metabolism of terpenoids and polyketides

- 03 [Terpenoid backbone biosynthesis](#) (53)

### Question 5

#### Step 26.

Tab over to "View Map for Selected Genomes" from the KEGG Pathway details page:

## KEGG Pathway Details

Details for Pathway: *Porphyrin and chlorophyll metabolism*  
\*Showing counts for genomes in genome cart only

KO Terms in Pathway

Save to My Workspace

View Map for Selected Genomes

### KEGG Orthology (KO) Terms in Pathway

Add Selected to Function Cart

Select All

Clear All

Filter column: KO Term ID

Filter: text

Apply

Export

Page 1 of 2 << first < prev

1

2

next > last >>

100

Column Selector

Select Page

Deselect Page

Select	KO Term ID	KO Name	Definition	KO Module ID	KO Module Name
<input type="checkbox"/>	<a href="#">KO00214</a>	BLVRA, bvdR	biliverdin reductase [EC:1.3.1.24]		
<input type="checkbox"/>	<a href="#">KO00218</a>	E1.3.1.33, por	protochlorophyllide reductase [EC:1.3.1.33]		

### Question 5

#### Step 27.



View map for all 5 genomes INDIVIDUALLY:

## KEGG Pathway Details

Details for Pathway: *Porphyrin and chlorophyll metabolism*  
\*Showing counts for genomes in genome cart only

KO Terms in Pathway Save to My Workspace View Map for Selected Genomes

### KEGG Map for Selected Genomes

Sequencing Status: All Finished, Permanent Draft and Draft Domain: Genome Cart

List Tree Show Selected: 1

Search for: <enter a genome name to search>

- Dehalobacter restrictus DSM 9455 (B) [F]
- Dehalobacter sp. 11DCA (B) [F]
- Dehalobacter sp. CF (B) [F]
- Dehalococcoides mccartyi 195 (B) [F]
- Dehalogenimonas lykanthroporepellens BL-DC-9 (B) [F]

Add > Add All >> < Remove << Remove All

Selected Genomes

Please select genomes to highlight on KEGG Pathway Map:

MER-FS Metagenome: Assembled

☐ Genes in selected genome  
☒ Find missing enzymes  
☐ None

View Map Reset

## Question 5

### Step 28.

On the KEGG map displayed for "Porphyrin and chlorophyll metabolism," examine the "Anaerobic Pathway" leading from Precorrin to Vitamin B12:

