

MetaHCR v1.0

Users Guide

This document is the users guide for the Metagenomics on Hydrocarbon Resources (MetaHCR) web application. Administrators should consult the Administrators Guide.


Note that the pages and examples in this Users Guide are based on the use of a public version of the MetaHCR database.

Overview


MetaHCR is a web application interface to a relational database that stores the inter-relationships amongst Hydrocarbon Resource Samples, their Single Gene and Metagenome Analyses and the Organisms found via these analyses. Ancillary tables provide metadata.

Accessing MetaHCR and Logging On

Your system administrator will have given you a URL to use to access the web server that is hosting the MetaHCR application. Accessing this URL with a browser will result in the Home page being displayed:

**MetaHCR** **Metagenomics on Hydrocarbon Resources** [Register](#) | [Login](#)
Database:

[Home](#) [Browse](#) [Search](#) [Upload](#) [Admin](#)



The MetaHCR Project

The area of molecular microbiology and metagenomics in particular holds great potential that could be used in the oil and gas industry. The MetaHCR project aims to be a platform for the cataloguing, storage and analysis of microorganisms that have been identified in hydrocarbon-rich environments, and are related to hydrocarbon degradation, oil souring, metal corrosion and methane emissions.

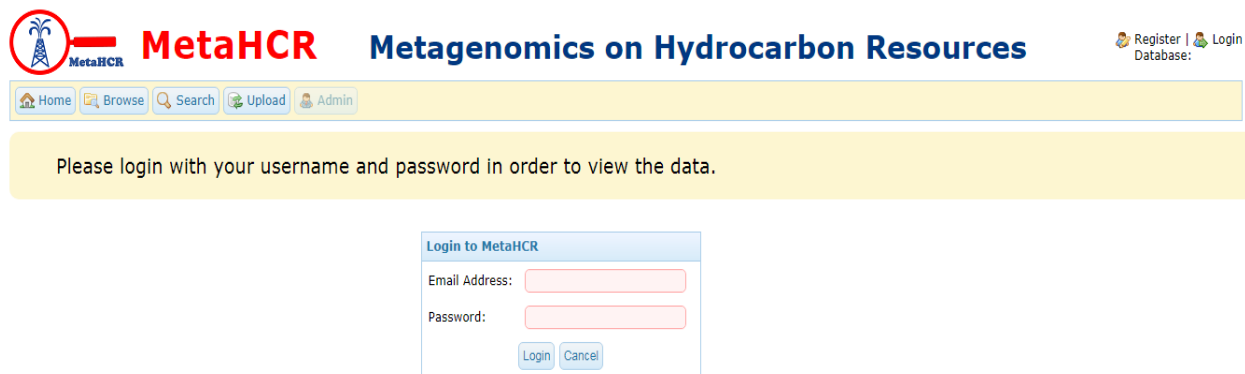
MetaHCR Milestones

- Development of a database containing microbial species, taxonomic and functional marker genes identified in the literature or the analyzed samples
- Implementation of a cyber-infrastructure to be used for data storage, analysis and sharing
- Creation of a user-friendly front-end allowing easy access to the data by the non-expert

» Read more about this project on the [about MetaHCR page](#).

Pumpjack during sunset. Monahans, Texas USA, 2013
(Photo: Laura Upshaw)

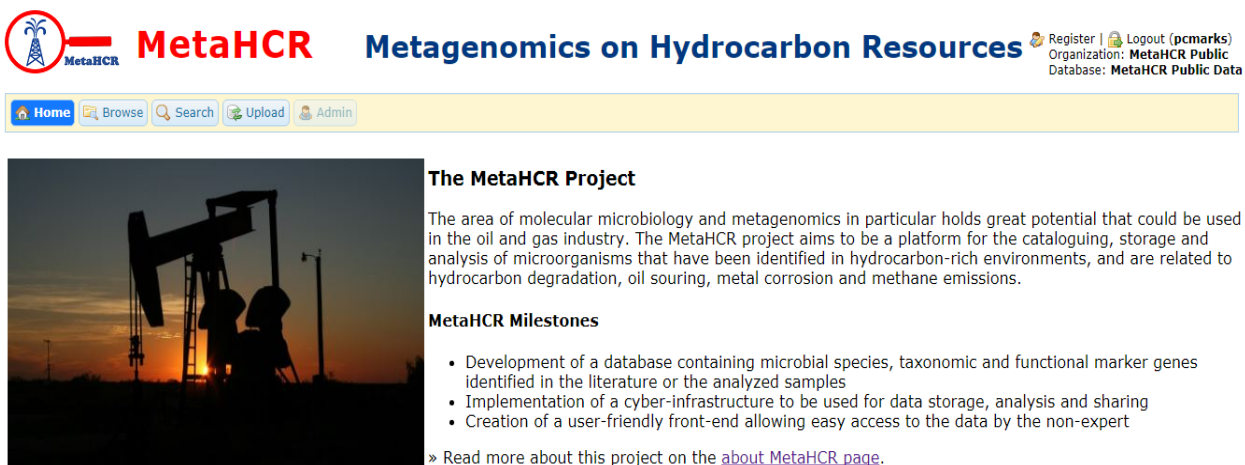
You must login to access MetaHCR's facilities. Click on the Login icon in the upper right-hand corner of the web page. You will be presented with the following dialog:



The image shows the MetaHCR website header and a login dialog box. The header includes the MetaHCR logo, the title "MetaHCR Metagenomics on Hydrocarbon Resources", and links for "Register" and "Login Database:". Below the header is a navigation bar with "Home", "Browse", "Search", "Upload", and "Admin" buttons. A yellow banner below the navigation bar contains the text: "Please login with your username and password in order to view the data." The login dialog box, titled "Login to MetaHCR", has two input fields: "Email Address:" and "Password:". Below these fields are "Login" and "Cancel" buttons.

Note if you are using a freshly-installed version of the public database, you should log in with user name of guest and the password of guest.

Enter your email address and password and click on the Login button. If the login is successful the Home page will be re-displayed:



The image shows the MetaHCR website home page. The header is identical to the previous image, but the "Login" link is replaced by "Logout (pcmarks)". The organization is listed as "MetaHCR Public" and the database as "MetaHCR Public Data". The navigation bar is also identical. Below the navigation bar, there is a large image of an oil pumpjack at sunset. To the right of the image, the text reads: "The MetaHCR Project" followed by a paragraph describing the project's goals. Below this, the "MetaHCR Milestones" section lists three bullet points: "Development of a database containing microbial species, taxonomic and functional marker genes identified in the literature or the analyzed samples", "Implementation of a cyber-infrastructure to be used for data storage, analysis and sharing", and "Creation of a user-friendly front-end allowing easy access to the data by the non-expert". A link "» Read more about this project on the [about MetaHCR page](#)." is provided at the bottom.

In the upper right hand corner, your user name, organization and the name of the database that you are currently accessing is displayed. In addition, there is an icon for logging out.

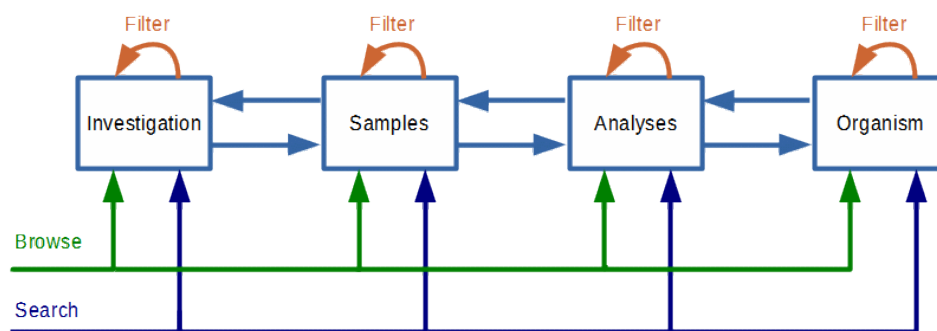
MetaHCR's Major Functional Areas

There are four major functional areas in MetaHCR: Browsing, Searching, Uploading and Administration. Each can be reached by selected the corresponding menu item at the top of the page. Each function gives you access to one or more of the following data resources: Investigations, Sample, Analyses (Single Gene and Metagenome), Organisms, and Hydrocarbon Resources. The primary data resource in the MetaHCR database are the following:

- Investigations which contain Samples,
- Samples which contain Analyses, and
- Analyses which contain Organisms

Browsing gives you the ability to examine all the entries in all of the data sources. In addition, various filters can be applied to these data to create subsets.

Searching gives you the ability to search for occurrences of one of the primary data resources and to then follow the relationships listed above. For example, searching for a particular Organism can lead to the Analyses in which it was identified. The Analyses, in turn, could lead to the Samples and ultimately to the Investigation that collected these Samples. Below is a diagram of how you can traverse the primary data resources in MetaHCR.



Traversal of the MetaHCR Primary Data Resources

Uploading provide facilities for uploading both Single Genome and Metagenome Analyses associated with a particular Sample. The use of each of the functional areas follows.

For a description of the Administration functions and usage, please consult the MetaHCR Administrators Guide.

Browsing and Filtering

Clicking on the *Browse* menu button will result in the following page being displayed:

Home

Browse

Search

Upload

Admin

Investigations

Samples

Analyses

Organisms

Hydrocarbon Resources

Name	Description
Halfdan corrosion study	Microbial profiling of produced water from 32 wells of the Halfdan field.
Produced water analysis f	Wang L - Molecular analysis of the microbial community structures in water-flooding petroleum reservoirs with different temper
Produced water analysis f	Lenchi N - Diversity of Microbial Communities in Production and Injection Waters of Algerian Oilfields Revealed by 16S
Produced water analysis f	Wang L - Comparison of bacterial community in aqueous and oil phases of water-flooded petroleum reservoirs using pyrosequen
Produced water analysis f	Gittel A - Prokaryotic Community Structure and Sulfate Reducer Activity in Water from High-Temperature Oil Reservoirs with an
Produced water analysis f	Gittel A - Prokaryotic Community Structure and Sulfate Reducer Activity in Water from High-Temperature Oil Reservoirs with an
Produced water analysis f	Piceno Y - Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydroca
Produced water analysis f	Gao P - Differences in microbial community composition between..
Produced water analysis f	Piceno Y - Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydroca
Produced water analysis f	Gao P - Differences in microbial community composition between..

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Page 1

of 4

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Download

Displaying 1 to 10 of 33 items

There are five tabs corresponding to Investigations, Samples, Analyses, Organisms, and Hydrocarbon Resources. Selecting any one of these tabs will display a list of all of the entries for that particular data resource. All of the lists provide the following sets of functions: Basic, Infosheets, and Nested Data.

Basic Functions

- The lists may be paged through and the number of entries per page can be changed: (10 – 50).
- The data for each displayed field, for example, Name and Description on the Investigations page, can be sorted by clicking on the up and down arrows next to the field name.
- Below each field name is an area that you can enter characters that will be used as filters. So, for example, typing “water” (without the quotes) into the Name field on an Investigation page will result in a new list of Investigations that contain these characters in their Name field. Note that as you type, each character triggers a search in the database, so you may experience a small “lag” in response.

Nested Data

Clicking on the “plus” sign in the leftmost column – if it is present – will result in the line opening up and displaying information about data that data resource “contains”. For example, clicking on the plus sign of the first Investigation entry will result in the display of two lines describing the two Samples that are part of this Investigation:

Home	Browse	Search	Upload	Admin
Investigations	Samples	Analyses	Organisms	Hydrocarbon Resources
Name	Description			
+	water			
-	Produced water analysis f Wang L - Molecular analysis of the microbial community structures in water-flooding petroleum reservoirs with different temper			
	Source Mat ID	Type	Subtype Description	Comment
+	BAO.PW.S2	produce	Sample S2A from Baolige field	
+	BAO.PW.S3	produce	Sample S3A from Baolige field	
+	Produced water analysis f Lenchi N - Diversity of Microbial Communities in Production and Injection Waters of Algerian Oilfields Revealed by 16S			
+	Produced water analysis f Wang L - Comparison of bacterial community in aqueous and oil phases of water-flooded petroleum reservoirs using pyrosequen			

Depending on the data being displayed further plus signs may appear. For Investigations, if the Samples have Analyses associated with them then clicking on the Sample's plus sign will show the analysis(es):

+	Halfdan corrosion study	Microbial profiling of produced water from 32 wells of the Halfdan field.							
-	Produced water analysis f Wang L - Molecular analysis of the microbial community structures in water-flooding petroleum reservoirs with different temper								
	Source Mat ID	Type	Subtype Description				Comment		
-	BAO.PW.S2	produce	Sample S2A from Baolige field						
	ID	Sample Analysis Name	Analysis Name	Type	Analysis Date	Upload Date	Uploaded By	Sequencing Center	
	453	BAO.PW.S2.16S.A	S2A	Single Gene		2017/05/15	pcmarks	Unknown	
	459	BAO.PW.S2.16S.B	S2B	Single Gene		2017/05/15	pcmarks	Unknown	
+	BAO.PW.S3	produce	Sample S3A from Baolige field						

Infosheets

Selecting a list entry will result in an “Infosheet” being displayed at the bottom of the page. An Infosheet will display all of the data fields associated with the list entry:

Produced water analysis f Piceno Y - Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydroca		
Produced water analysis f Gao P - Differences in microbial community composition between..		
10 ▾	Page 1 of 4	Download
Displaying 1 to 10 of 33 items		
Investigation		
MetaHCR information sheet for investigation Produced water analysis from Kuparuk River field		
INVESTIGATION ATTRIBUTES		HYDROCARBON RESOURCE
Name	Produced water analysis from Kuparuk River field	Type Oil Reservoir
Description	Piceno Y - Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydrocarbon reservoirs	Hcr Abbrev. KUP
Completion date	not completed yet	Basin North Slope
Submitted to INSDC	No	Field Milne Point
Publication	Piceno Y - Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydrocarbo	Reservoir Kuparuk River
		HCR Temps. 47.0 - 70.0
		Lithology Clastic
		Depos. Env. Transitional
		Hcr Geol. Age Cretaceous
		Salinity Today Brackish
		MINERALOGY
		CURATOR DETAILS
		E-mail

The infosheet can be collapsed or expanded by clicking on the title line containing the name of the data resource. For Investigations, the title line contains “Investigation”; similarly for the other data resources.

On the Infosheet title line, to the far right, is an “eye” icon. Clicking on this icon will toggle between showing the infosheet fields that contain data (the default) to displaying all of the fields, irrespective of their values. Compare the following infosheet with the previous:

Investigation		
MetaHCR information sheet for investigation Produced water analysis from Kuparuk River field		
INVESTIGATION ATTRIBUTES		HYDROCARBON RESOURCE
Name	Produced water analysis from Kuparuk River field	Type Oil Reservoir
Description	Piceno Y - Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydrocarbon reservoirs	Hcr Abbrev. KUP
Experimental Factor	n/a	Temperature Range
Type	n/a	HC Produced
NCBI Project ID		Basin North Slope
GOLD project ID		Field Milne Point
Reference		Reservoir Kuparuk River
Keywords		HCR Temps. 47.0 - 70.0
Status		Tvdss of Hcr Temp. 0.0
Availability		Hcr Pressure 0.0
Start date		Tvdss of Hcr Pressure 0.0
Completion date	not completed yet	Permeability 0.0
Submitted to INSDC	No	Porosity 0.0
Quality	None	Lithology Clastic
Purpose		Depos. Env. Transitional
Env		Hcr Geol. Age Cretaceous
		OWC Tvdss 0.0
		Hcr FW Salinity 0.0
		Sr. Kerog Type
		Sr. Lithology
		Sr. Dep. Env.
		Sr. Geol. Age
		Hcr Satur. PC.
		Drive Mech.
		MINERALOGY
		Analysis Date
		Anhydrite
		Carbonate
		Carbonate Cement
		Clay
		Dolomite
		Feldspar
		Mica
		Quartz
		Siderite
		Hematite
		Chlorite
		Illite
		Magnetite
		Smectite
		CURATOR DETAILS
		Firstname
		Lastname
		E-mail
		Comment

Sample and Analysis Infosheets

The infosheets for Samples and Analyses are the same: it is an accordion display with the following five expandable/collapsible panel. There are two types of Analyses: Single Gene and

Metagenome. Since, all analyses need to be associated with a Sample, the Sample's infosheet is available as well in the infosheet area. The panels are:

- *Metadata* – metadata for the Sample.
- *Single Gene Analysis* – metadata for the selected Analysis, if present
- *Single Gene Analysis Organisms* – a list of the Organisms found in the selected Analysis, ordered by abundance.
- *Metagenome Analysis* – metadata for the selected Analysis, if present
- *Metagenome Results* – metagenome results. A list of genes and associated data.

An example of a Single Gene Analysis infosheet:

Infosheet			
MetaHCR information sheet for sample MHC.PW.SRR088854			
Metadata			
Single Gene Analysis - Uploaded on May 15, 2017, midnight by pcmarks			
BIOLOGICAL ANALYSIS ATTRIBUTES		SINGLE GENE ANALYSIS ATTRIBUTES	
Sample Analysis Name	MHC.PW.SRR088854.16S.U	Chimera Check	Chimera Slayer
Analysis Name	SRR088854	Target Gene	16s rRNA
Type	Single Gene	Target Subfragment	
Seq. Method	454	PCR Primers	FWD:{ACGGGCGGTGTGTRC} REV:{ }
Seq. Quality Filtering Method		PCR Cond.	
Mid Names		SOP	
Mid		Nested PCR Required	False
Nucl. Acid Ext.	FastDNA Kit for Soil		
Adapters			
Nucl. Acid Amp.			
Url			
Reads Count	0		
Comment			
Reference			
Status Id			
Sequencing Center	GV		
Taxonomic Group	U		
Upload Date	May 15, 2017, midnight		
Uploaded By	pcmarks		

An example of a Single Gene Analysis Organisms infosheet:

Infosheet										
MetaHCR information sheet for sample MHC.PW.SRR088854										
Metadata										
Single Gene Analysis - Uploaded on May 15, 2017, midnight by pcmarks										
Single Gene Analysis Organisms - Uploaded on May 15, 2017, midnight by pcmarks										
Kingdom	Phylum	Class	Order	Family	Genus	Species	Strain	Abundance %	Metabolism Type	Threat
Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	Methanosaetaceae	Methanosaeta			15.01		MIC
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Magnetospirillum			9.04		MIC
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Defluviimonas			7.87		
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Desulfobulbus			5.18		H2S/MIC
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium			3.86		BF
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Ruegeria			3.75		MIC
Archaea	Euryarchaeota	Thermoplasmata	014H09-A-SD-P15	uncultured bacterium	uncultured bacterium			3.72		
Archaea	Euryarchaeota	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	Methanolinea			3.06		MIC
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Labrenzia			2.91		BF
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured			2.82		
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An example of a Metagenome Results infosheet:

Sample								
MetaHCR information sheet for sample HAL.PW.HDA5								
Metadata								
Single Gene Analysis (select under Sample if present)								
Metagenome Analysis - Uploaded on May 11, 2017, midnight by pcmarks								
Metagenome Results								
Gene Name	Scaffold ID	Length	COG ID	Pfam ID	EC Number	KO ID	Kingdom	Phylum
Uncharacterized protein involved in tolerance to divalent cations	Ga0070767_1094890	130879	COG1324	pfam03091		KO:K03926	Bacteria	Proteobacteria
NADPH-dependent FMN reductase	Ga0070767_1094890	130879	COG0655	pfam03358			Bacteria	Proteobacteria
NAD-dependent protein deacetylases, SIR2 family	Ga0070767_1094890	130879	COG0846	pfam02146	EC:3.5.1.-	KO:K12410	Bacteria	Proteobacteria
Prephenate dehydratase	Ga0070767_1094890	130879	COG0287	pfam02153			Bacteria	Proteobacteria
Putative transcriptional regulator, homolog of Bvg accessory factor	Ga0070767_1094890	130879	COG1521	pfam03309	EC:2.7.1.33	KO:K03525	Bacteria	Proteobacteria
Uncharacterized protein conserved in bacteria	Ga0070767_1094890	130879	COG3807	pfam06347			Bacteria	Proteobacteria
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Ga0070767_1094890	130879	COG2204	pfam00072			Bacteria	Proteobacteria
Predicted membrane protein - COG3762	Ga0070767_1094890	130879	COG3762	pfam04536		KO:K08988	Bacteria	Proteobacteria
Glycosyl transferase family 2	Ga0070767_1094890	130879	COG3551	pfam13469			Bacteria	Proteobacteria
PIIZ domain	Ga0070767_1094890	130879		pfam07238			Bacteria	Proteobacteria
<div> 10 Page 3 of 14031 Download </div>								
							Displaying 21 to 30 of 140307 ite	

Nested Data

- Clicking on the “plus” sign in the leftmost column – if it is present – will result in the line opening up and displaying information about data that data resource “contains”. For

example, clicking on the plus sign of the first Investigation entry will result in the display of two lines describing the two Samples that are part of this Investigation:

Home

Browse

Search

Upload

Admin

Investigations

Samples

Analyses

Organisms

Hydrocarbon Resources

Name ▾		Description ▾		
water				
Produced water analysis f Wang L - Molecular analysis of the microbial community structures in water-flooding petroleum reservoirs with different temper				
	Source Mat IC Type ▾	Subtype	Description ▾	Comment ▾
+	BAO.PW.S2	produce	Sample S2A from Baolige field	
+	BAO.PW.S3	produce	Sample S3A from Baolige field	
Produced water analysis f Lenchi N - Diversity of Microbial Communities in Production and Injection Waters of Algerian Oilfields Revealed by 16S				
Produced water analysis f Wang L - Comparison of bacterial community in aqueous and oil phases of water-flooded petroleum reservoirs using pyrosequen				

- Depending on the data being displayed further plus signs may appear. For Investigations, if the Samples have Analyses associated with them then clicking on the Sample's plus sign will show the analysis(es):

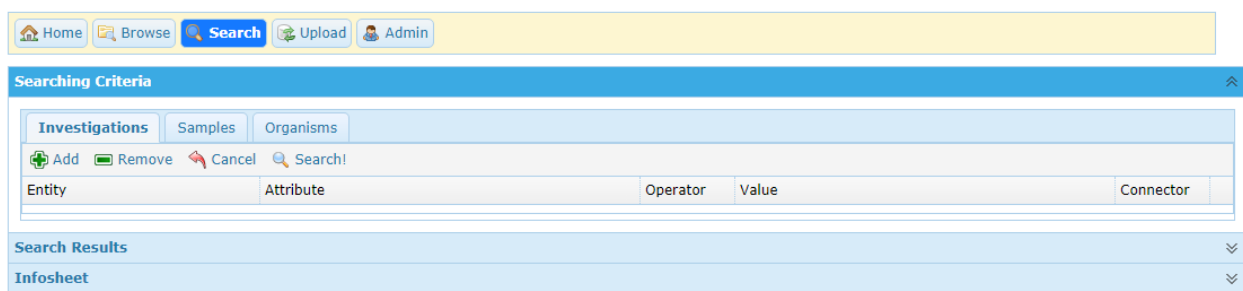
+		Halfdan corrosion study Microbial profiling of produced water from 32 wells of the Halfdan field.							
-		Produced water analysis f Wang L - Molecular analysis of the microbial community structures in water-flooding petroleum reservoirs with different temper							
		Source Mat IC Type	Subtype	Description	Comment				
-		BAO.PW.S2	produce	Sample S2A from Baolige field					
		ID	Sample Analysis Name	Analysis Name	Type	Analysis Date	Upload Date	Uploaded By	Sequencing Center
		453	BAO.PW.S2.16S.A	S2A	Single Gene		2017/05/15	pcmarks	Unknown
		459	BAO.PW.S2.16S.B	S2B	Single Gene		2017/05/15	pcmarks	Unknown
+		BAO.PW.S3	produce	Sample S3A from Baolige field					

- For all of these types of expansions, the infosheet for the respective data resource that is selected will display at the bottom of the page.

Searching

The search functions give you the ability to follow the relationships between Investigations, Samples and their Analyses, and Organisms. You can search for instances of each of these data resources using various criteria and then display the other data that these instances are part of. For instance, searching for organisms by taxonomy or by their characteristics will result in a list of Organisms. If these Organisms have appeared in any Analyses then these Analyses and their associated Samples and their Investigations may all be displayed. You may search for Investigations which will lead to Samples/Analyses then to Organisms. And, you can search for Samples/Analyses which will lead to their Investigations and Organisms.

The initial page for the Search function is shown below.



The screenshot shows the initial page for the Search function. At the top is a navigation bar with links: Home, Browse, Search, Upload, and Admin. Below this is the 'Searching Criteria' section, which is an accordion area. It contains three tabs: 'Investigations', 'Samples', and 'Organisms'. The 'Investigations' tab is currently selected. Below the tabs are four buttons: 'Add' (with a plus icon), 'Remove' (with a minus icon), 'Cancel' (with a red X icon), and 'Search!' (with a magnifying glass icon). Below these buttons is a table with four columns: 'Entity', 'Attribute', 'Operator', 'Value', and 'Connector'. The 'Entity' column is currently empty. Below the table are two more accordion areas: 'Search Results' and 'Infosheet', both of which are currently collapsed.

There are three accordion areas entitled Searching Criteria, Search Results, and Infosheet. Each can be collapsed or expanded by clicking on these titles. Searching begins in the Searching Criteria area. There are three tabs corresponding to which data resource will be searched for first. Below each of these tabs are four buttons that allow you to set up the search criteria. The criteria, when they exist, appear below these buttons. Clicking Add will create a new criterion; Remove deletes the currently selected criterion; Cancel cancels the entry of a criterion; and Search! initiates the search. Finally, below these buttons are the search criteria:

- Entity – is one or more data resources, depending on the tab chosen;
- Attributes – the fields associated with the selected data resource;
- Operator – depending on the data type of the Attribute this will be an operator such as '=', 'contains', etc.;
- Value – the particular value to be used in the search;
- Connector – either 'and' (the default) or 'or' which serves to combine two criteria.

A typical search is described in the following paragraphs. You will start with a search for a particular organism, find its Samples/Analyses and their Investigations.

Click on the Organisms tab. Next, click on the Add button – this section of the page should like: the following:

The screenshot shows the 'Searching Criteria' interface. At the top, there are three tabs: 'Investigations', 'Samples', and 'Organisms'. The 'Organisms' tab is selected. Below the tabs, there are four buttons: 'Add' (with a plus icon), 'Remove' (with a minus icon), 'Cancel' (with a red X icon), and 'Search!' (with a magnifying glass icon). Below these buttons is a table with five columns: 'Entity', 'Attribute', 'Operator', 'Value', and 'Connector'. Each column has a dropdown menu. Below the table, there are two sections: 'Search Results' and 'Infosheet', both with expand/collapse arrows.

Click on the Entity drop-down menu:

This screenshot shows the 'Entity' dropdown menu open in the 'Searching Criteria' interface. The menu lists two options: 'Organism' and 'Metabolism Type'. The 'Organisms' tab remains selected at the top of the interface.

Select Organism for the Entity with which you will begin the search. Next, select the Attribute drop-down menu – it will have changed to match the Entity – Organism - that you selected:

This screenshot shows the 'Attribute' dropdown menu open in the 'Searching Criteria' interface. The menu lists various attributes related to organisms, including 'A 16S Sequence', 'Accession No Cultured', 'Accession No Uncultured', 'Bio Class', 'Bio Order', 'Biotic Relationship', 'Cell Arrangement', 'Cell Diameter', 'Cell Length', and 'Cell Shape'. The 'Organisms' tab remains selected at the top.

You can either scroll down to the Attribute or begin typing the name of the attributes. Type the single letter 'g' – the drop-down menu for the Attribute becomes:

Searching Criteria

Investigations Samples **Organisms**

+ Add - Remove Cancel Search!

Entity	Attribute	Operator	Value	Connector
Organism	g			

Search Results

Infosheet

Genus
Genus Synonyms
Gold Project Id
Gram Staining
Grow Postgate

Choose 'Genus' and then click on the Operator drop-down menu. In this menu choose 'contains' which will, for character string attributes, search for the occurrence of the search string within the Attribute's value. Finally, type 'pelobacter' in the Value field. Note, if the Attribute is a Controlled Vocabulary item then the Value field turns into a drop-down menu with the allowable values. Your search criteria should look like this:

Searching Criteria

Investigations Samples **Organisms**

+ Add - Remove Cancel Search!

Entity	Attribute	Operator	Value	Connector
Organism	Genus	contains	pelobacter	and

Click on the **Search!** button just above the search criterion. The search is initiated and if any organisms have the string 'pelobacter' in their genus field, they will displayed in the Search Results area of the page:

Search Results

Investigations Samples **Organisms From Search**

Y Get Samples Y Get Investigation Y Get Organisms

ID	Name	Description

Source Mat. ID	Description

ID	Family	Genus
987	Desulfuromonadaceae	Pelobacter
6876	Pelobacteraceae	Pelobacter
6914	Pelobacteraceae	Pelobacter
7336	Pelobacteraceae	Pelobacter
42108	M113	unculture
42116	uncultured Pelobacter sp.	unculture
42784	Pelobacteraceae	Pelobacter
45836	Pelobacteraceae	Pelobacter

10 Page 1 of 1

Displaying 1 to 10 of 10 items

In Sample Analysis

In the right-most column of the Search Results you will see a paginated list of the matching Organisms. Selecting the plus sign will open up the Organism list entry and display the rest of the organism's taxonomy as well as some of its attributes.

Those Organisms that appear in one or more Analyses will have their ID highlighted. Select the first Organism in the list (ID = 987) – this will also result in an Infosheet for this organism to be displayed at the bottom of the page. Next click on the *Get Samples* button above the list. This action will result in a list of Samples, whose Analyses contain this organism, appearing in the middle column of the Search Results area:

Samples for organism species		Organisms From Search		
Y Get Investigation Y Get Organisms		From Search Y Get Samples Get Taxonomy		
Source Mat. ID	Description	ID	Family	Genus
MHC.PW.SRR088835	31A_MM aqueous phase	987	Desulfuromonadaceae	Pelobacter
MHC.PW.SRR088837	32O_MM oil phase	6876	Pelobacteraceae	Pelobacter
MHC.PW.SRR088839	34A_BB aqueous phase	6914	Pelobacteraceae	Pelobacter
MHC.PW.SRR088840	35O_BB oil phase	7336	Pelobacteraceae	Pelobacter
MHC.PW.SRR088842	A3-1_BB aqueous phase	42108	M113	uncultured Pelob
MHC.PW.SRR088844	O3_BB oil phase	42116	uncultured Pelobacter sp.	uncultured Pelob
MHC.PW.SRR088845	A4_BB aqueous phase	42784	Pelobacteraceae	Pelobacter
MHC.PW.SRR088846	O4_BB oil phase	45836	Pelobacteraceae	Pelobacter
MHC.PW.SRR088847	A13_BB aqueous phase			
MHC.PW.SRR088848	O13_BB oil phase			
MHC.PW.SRR088850	A19_BB aqueous phase			
MHC.PW.SRR088852	O19_BB oil phase			
MHC.PW.SRR088854	A27_BB aqueous phase			

10 Page 1 of 1 Displaying 1 to 10 of 10 items

In Sample Analysis

Clicking on the plus sign and/or selecting a Sample or an Analysis exhibits the same behavior as on the Browsing pages. For a more detailed description of this behavior, please see the Browsing section of this document.

In the center list of Samples and Analyses, you can select a Sample and click on the *Get Investigations* button to display the Investigation that this Sample is associated with. The Investigation will appear in the left-most area of the Search Results:

Search Results		
Investigations for sample MHC.PW.SRR088835		Samples for organism species
Y Get Samples		Y Get Investigation Y Get Organisms
Id	Name	Source Mat. ID
1	SRP004915 Metagenomics for Greener Production and Ex	MHC.PW.SRR088835
		MHC.PW.SRR088837
		MHC.PW.SRR088839
		MHC.PW.SRR088840
		MHC.PW.SRR088842
		MHC.PW.SRR088844
		MHC.PW.SRR088845
		MHC.PW.SRR088846
		MHC.PW.SRR088847
		MHC.PW.SRR088848
		MHC.PW.SRR088850
		MHC.PW.SRR088852
		MHC.PW.SRR088854

The above describes a search that begins with finding Organisms that have certain characteristics. Similar types of searches can be performed for Investigations and Samples. The results of these searches will appear in the left-most and center columns, respectively. From the Investigations list, you can get its Samples by clicking on the *Get Samples* button. From the Samples/Analyses list, you can get the Organisms found by an Analysis by clicking on the *Get Organisms* button.

Uploading

This set of functions can be reached by selecting the *Upload* menu button at the top of the M2SC page. Uploading allows you to:

1. Upload a Single Gene Analyses and associate it with a Sample.
2. Upload a Metagenomic Analysis and associate it with a Sample
3. Maintain (delete) previously uploaded Analyses

The Uploading page is divided into two areas:

1. A list of the Samples in the current database
2. An area for Analyses Uploading and Maintenance

[Home](#) [Browse](#) [Search](#) [Upload](#) [Admin](#)

To upload Single Gene and Metagenome Analyses results:

1. Choose either the Single Gene or Metagenome tab to the right.
2. Follow the instructions in the tab area.

Samples				
Source Mat. ID	Type	Sub Type	Description	Comment
ARD.CT.SRR097670	rock trimn		CBM exploration core - ARDLEY FM 324	KB_QS_CB_
ARD.CT.SRR098452	rock trimn		Cuttings from Quicksilver, Ardely forma	KB_QS_CB_
ARD.CT.SRR098465	rock trimn		Cuttings from Quicksilver, Ardely forma	KB_QS_CB_
BAK.PW.SRR090536	produced		Bakerfields Produced Water	GV_BaP_PL
BAK.PW.SRR090537	produced		Bakerfields Produced Water	GV_BaP_PL

Analyses Uploading and Maintenance »
[Single Gene Analysis](#) [Metagenome Analysis](#) [Analyses Maintenance](#)

Step 1. Choose and open (verify) a single gene analysis file.

L6 upload file: [Choose File](#) No file chosen

[Verify](#)

You choose the type of analysis to be uploaded by selecting one of tabs in the right-most column.

Single Gene Analysis Uploading

Single Gene Analysis has been designed to upload so-called “L6” files. A description of this file is located in the Administrator's Guide.

There are three steps involved in uploading Single Gene Analyses:

1. Choosing and verifying the analyses file.
2. Uploading the analyses file.
3. Examining the upload log file

They are outlined in the Single Gene Analysis tab:

Analyses Uploading and Maintenance

Single Gene Analysis

Metagenome Analysis

Analyses Maintenance

Step 1. Choose and open (verify) a single gene analysis file.

L6 upload file:

Choose File

No file chosen

Verify

Step 2. Examine sample names. Click on Upload to begin upload.

Samples present in the analysis file: **None**

Sample Names

Open an analysis file.

Upload

Step 3. Examine the upload log file.

Download SGA log file.

Metagenome Analysis Uploading

Metagenome Analysis uploading has been designed to upload a group of three separate data files: Scaffold file, Gene Function file, and RNA file. Descriptions of these files are located in the Administrator's Guide.

There are three steps involved in uploading Metagenome Analyses:

4. Choosing and verifying the three analyses files.
5. Uploading the analyses file.
6. Examining the upload log file

They are outlined in the Single Gene Analysis tab:

Analyses Uploading and Maintenance >>

Single Gene Analysis

Metagenome Analysis

Analyses Maintenance

Step 1. Locate and choose the three metagenome analysis files - scaffold, gene function and rna. Press the Verify button to preload and verify these files.

Scaffold file:

Choose File

No file chosen

Gene function file:

Choose File

No file chosen

Rna file:

Choose File

No file chosen

Verify

Step 2. Select a sample from the list to the left. Click on Upload to begin reading the analysis files and creating the analysis.

Upload

Step 3. Examine the upload log file.

Download the MGA log file.

MetaHCR creates a log file for every analysis.

MetaHCR can be configured to upload copies of the analyses files to Amazon's AWS S3 storage. These settings are in the applications settings.py file and description of them is available in the Administrators Guide.



Analyses Maintenance

This part of uploading gives you the ability to delete analyses and to download log files that were created during an upload. This function is accessed by clicking on the *Analyses Maintenance* tab:

Analyses Uploading and Maintenance >>

Single Gene AnalysisMetagenome Analysis**Analyses Maintenance**

- To delete an analysis, select the analysis and then press the delete button.
- To download a analysis upload log file, select the analysis and then press the 'Download Log File' button.

 Delete  Download Log File

Type ▾	Analysis Name ▾	Upload Date	Uploaded By	Sequ
All ▾				
Metagenome	HAL.PW.HDA5.METGNM2.U	2017/05/11	pcmarks	STCH
Metagenome	HAL.PW.HDA9.METGNM.U	2017/05/10	pcmarks	STCH
Metagenome	HAL.PW.HBA7.METGNM.U	2017/05/10	pcmarks	STCH
Metagenome	HAL.PW.HDA3.METGNM.U	2017/05/10	pcmarks	STCH
Metagenome	TUN.PW.Tuna.METGNM.U	2017/05/11	pcmarks	Univ
Metagenome	HAL.PW.HDA13.METGNM.U	2017/05/10	pcmarks	STCH
Metagenome	HAL.PW.HBA5.METGNM.U	2017/05/10	pcmarks	STCH
Metagenome	HAL.PW.HDA6.METGNM.U	2017/05/11	pcmarks	STCH
Metagenome	TUN.PW.Tuna2.METGNM.U	2017/05/11	pcmarks	Univ
Metagenome	HAL.PW.HBB9.METGNM.U	2017/05/10	pcmarks	STCH

10 ▾

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Displaying 1 to 10 of 492 items

A list of the current Analyses is shown along with instructions for deleting an analysis or downloading the log file for an analysis.