NGA User Guide

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Introduction

Natural gas analysis for hydrocarbons and hydrogen sulfide (H₂S) is required to avoid natural gas and oil escaping from the hole and is part of the ship's standard drilling safety plan.

The absolute quantity of hydrocarbons is the primary safety risk during shipboard operations. Gas monitoring via gas chromatography is a means of quantifying the hydrocarbon risk. H_2S is another significant risk factor for individuals working in the area. Emergency monitors on the drill floor provide early detection of H_2S , while later quantification is performed on the natural gas analyzer (NGA). A primary method of monitoring safety conditions is the concentration ratio of methane to ethane versus temperature (Figure 1).

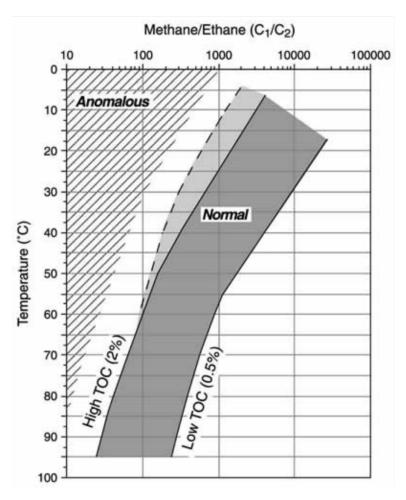


Figure 1. Risk Assessment for Drilling Safety (IODP).

Hydrocarbon Generation

Hydrocarbon generation in sediments is a result of thermal decomposition (maturation) of biogenic organic matter. C₁–C₄ hydrocarbons may be generated in significant quantities in sediment via two processes:

- Biogenic: biogenic hydrocarbons, typically characterized by methane, are produced in a sulfate-free environment via the reduction of dissolved bicarbonate.
- **Thermogenic:** thermogenic hydrocarbons are produced in sediments in direct proportion to temperature. C₅ and other heavier hydrocarbons are almost always the result of thermal generation of hydrogen-rich organic matter at temperatures typically ~100°C or greater.

The evolution of sedimentary biogenic organic matter under increasing burial depth and consequent temperature rise is divided into three stages:

- Diagenesis
 - biological, physical, and chemical alteration of sedimentary organic matter that occurs at low temperature (<50°C) in relatively recently deposited sediments (Peters et al., 2005).
- Catagenesis
 - o principal zone of oil formation, refers to a temperature range of 50°C~150°C. Liquid and gaseous hydrocarbons together with organic compounds with heteroatoms (oxygen, sulfur, and nitrogen) are released from the kerogen (*Figure* 2), so the catagenesis stage is called the "oil window."
- Metagenesis
 - Dry gases (mainly methane) are derived from liquid hydrocarbon accumulation in the crust (*Figure 3*). C₁–C₄ hydrocarbons may be generated in significant quantities in sediment via biogenic and thermogenic processes.

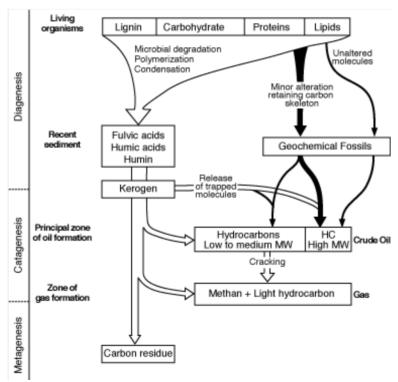


Figure 2. Hydrocarbon Formation Pathways in Geological Situations (Rullkotter, 1993).

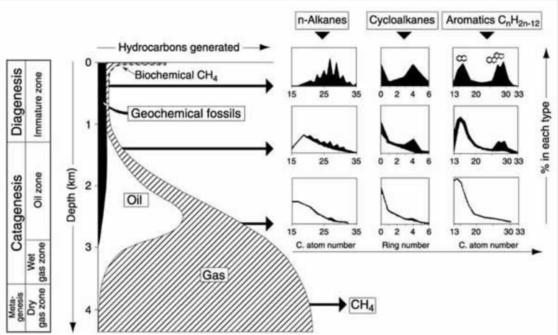


Figure 3. Hydrocarbon Generation Resulting from Burial of Organic Matter during Geologic Time.

Hydrogen Sulfide

Sulfate-reducing bacteria produce hydrogen sulfide in euxinic sediments. This may occur in a relatively shallow part of the sediment. Thermochemical sulfate reduction of sulfate by hydrocarbons in reservoirs occurs under high temperature (>127°C ~ 140°C).

Instruments

The NGA systems are both based on an Agilent 7890 GCs. These systems were further customized with specialized gas injection inlets and various column, detector, and valving systems for gas monitoring

Gases

The GC requires that hydrogen and air are connected to the marked fittings on the back of the instrument. The type of makeup gas must be identified in the method file.

- Air, compressed (Zero-Air +): >50 psi
- Helium, compressed (99.9995% +): >50 psi
- Hydrogen, compressed (99.9995% +): >50 psi

Method

Theory of method

The NGA gas chromatograph is equipped with 2 detectors:

- Flame ionization detector (FID)
- Thermal conductivity detector (TCD)

The TCD flow path travels through a 6 ft x 2.0 mm ID stainless steel (SS) column packed with Poropak T (50/80 mesh), a 3 ft x 2.0 mm ID SS column packed with molecular sieve 13x (60/80 mesh), and 6 ft x 2.0 mm ID SS column packed with 80/100 mesh HayeSep R (acid washed). The FID flow path traverses a 60 m x 0.25 mm ID capillary column with 0.25 µm DB-1 film.

This instrument measures C₁-C₇ hydrocarbons as well as some additional compounds:

- Methane (CH₄)
- Ethene (C₂H₄)
- Ethane (C₂H₆)
- Propene (C₃H₆)
- Popane (C₃H₈)
- n-Butane (C₄H₁₀)
- iso-Butane (CH₃-C₃H₇)
- n-Pentane (C₅H₁₂)
- iso-Pentane (CH₃-C₄H₉)
- n-Hexane (C₆H₁₄)
- iso-Hexane (CH₃-C₅H₁₁)
- n-Heptane (C₇H₁₆)
- iso-Heptane (CH₃-C₆H₁₃)
- Nitrogen (N₂)
- Oxygen (O₂)
- Carbon dioxide (CO₂)

NGA Sample Flow Schematics

Standby Mode

He gas flow for standby mode (green lines).

- Line 1: Aux-3—V1-4—V2-5—V2-3—capillary column—V2-4—V2-1—FID
 Line 2: Aux-4—sample inlet—V1-2—V1-3—V1-6—V1-1—V3-3—V3-4—V3-1—V4-3—V4-2—V4-5—V4-4—Vent
- Line 3: Front inlet—V3-5—V3-6—HaySep R column—V3-8—V3-7—V4-9—V4-8—TCD
 Line 4: Back inlet—V4-6—V4-7—MolSieve column—V4-1—V4-10—Vent

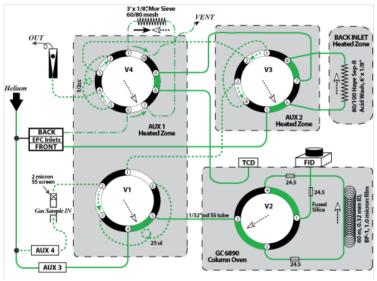


Figure 9. NGA in Standby Mode.

Injection mode

He carrier gas (green line) and sample gas (red line) flows in the NGA in injection mode. Sample gas fills the sample loops connected to V1 (25 µL), V3 (1 cm³), and V4 (0.5 cm³). He flushes the separation columns. He gas flow (green):

- Line 1: Aux-3—V1-4—V1-5—V2-3—V2-2—capillary column—V2-4—V2-1—FID
- Line 3: Front inlet—V3-5—V3-6—HaySep R column—V3-8—V3-7—V4-9—V4-8—TCD
 Line 4: Back inlet—V4-6—V4-7—MolSieve column—V4-1—V4-10—Vent

Sample gas flow (purge; red):

• Sample inlet—V1-2—V1-3—V1-6—V1-1—V3-3—V3-4—V3-1—V3-2—V4-3—V4-2—V4-5—V4-4—Vent

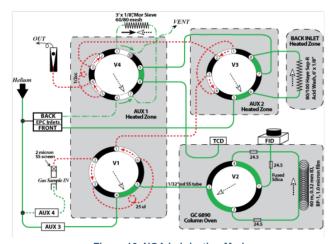


Figure 10. NGA in Injection Mode.

Run Mode at 0.01 min (open Valve V4)

He (green) and sample gas (red) flows in the NGA 0.01 min after start of run. Sample gas remains in the sample loop connected to V1 (25 µL) and V3 (1 cm3). After V4 opens, He returning from the back inlet pushes the sample gas out of the sample loop and into the molecular sieve column. Separated elements are detected by TCD. He gas flow:

• Line 1: Aux-3—V1-4—V1-5—V2-3—V2-2—capillary column—V2-4—V2-1—FID

- Line 2: Aux-4—V1-2
- Line 3: Front inlet—V3-5—V3-6—HayeSep R column—V3-8—V3-7—V4-9—V4-10—Vent
- Line 4: Back inlet—V4-6—V4-5

Sample gas flow (purge):

• V1-2—V1-3—V1-6—V1-1—V3-3—V3-4—V3-1—V3-2—V4-3—V4-4—out

Sample gas flow with He:

• V4-5—V4-2—V4-1—MolSieve column—V4-7—V4-8—TCD

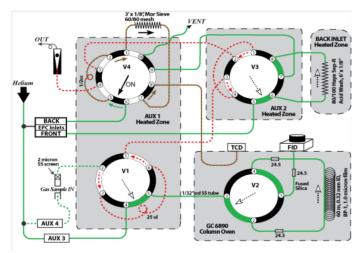


Figure 11. NGA in Run Mode: 0.01 min after starting run.

Run Mode at 0.07 min (open Valves V1 and V2)

He (green) and sample gas (red) flows in the NGA 0.07–1.79 min after start of run. Sample gas remains in the sample loop connected to V3 (1 cm³). After V1 and V2 open, He from Aux-3 pushes the sample gas out of the sample loop connected to V1 (25 µL) and into the capillary column (60 m) through V2, where it passes into the FID. He gas flow:

- Line 1: Aux-3—V1-4Line 2: Aux-4—V1-2
- Line 3: Front inlet—V3-5—V3-6—HaySep R column—V3-8—V3-7—V4-9—V4-10—vent
 Line 4: Back inlet—V4-6—V4-5—V4-2—V4-1—MolSieve column—V4-7—V4-8

Sample gas flow (purge):

• V3-4—V3-1—V3-2—V4-3—V4-4—out

Sample gas flow with He:

- V4-8—TCD
 V1-3—V1-6—V1-5—V2-3—V2-4—capillary column—V2-2—V2-1—FID
 V1-1—V3-3

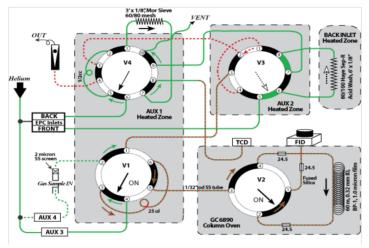


Figure 12. NGA in Run Mode: 0.07-1.79 min after starting run.

Run Mode at 1.80 min (open Valve V3)

He (green) and sample gas (red) flows in the NGA 1.80-1.82 min after start of run. After V3 opens, He from the front inlet pushes the sample gas out of the 1 cm³ sample loop into the HaySep column. He gas flow:

- Line 1: Aux-3—V1-4—V1-3—V1-6—V1-5—V2-3—V2-4
- Line 2: Aux-4—V1-2—V1-1—V3-3—V3-2—V4-3—V4-4—out
- Line 3: Front inlet—V3-5—V3-4
- Line 4: Back inlet—V4-6—V4-5—V4-2—V4-1—MolSieve column—V4-7—V4-8—TCD

Sample gas flow with He:

- Capillary column—V2-2—V2-1—FID
- B3-4—V3-1—V3-8—HaySep R column—V3-6—V3-7

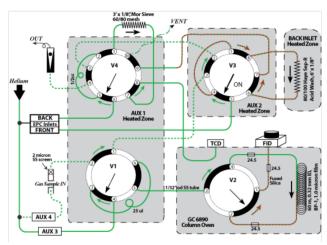


Figure 13. NGA in Run Mode: 1.80-1.82 min after starting run.

Run Mode at 1.83 min (close Valve V4)

He (green) and sample gas (red) flows in the NGA 1.83-8.49 min after start of run. After V4 closes, He from the back inlet flushes the molecular sieve column (backflush). Gas samples separated by the HaySep column enter the TCD through V4. Helium gas flow:

- Line 1: Aux-3—V1-4—V1-3—V1-6—V1-5—V2-3—V2-4—capillary column—V2-2—V2-1—FID
 Line 2: Aux-4—V1-2—V1-1—V3-3—V3-2—V4-3—V4-2—V4-5—V4-4—out
- Line 3: Front inlet—V3-5—V3-4—V3-1—V3-8

Sample gas flow with He:

• HaySep R column—V3-6—V3-7—V4-9—V4-8—TCD

Backflush:

• Line 4: Back inlet—V4-6—V4-7—MolSieve column—V4-1—V4-10—vent

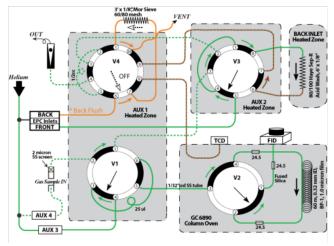


Figure 14. NGA in Run Mode: 1.83-8.49 min after starting run.

Run Mode at 8.50 min (close Valve V3)

He gas (green) and sample gas (red) flows in the NGA 8.50–9.09 min after start of run. After V3 closes, He from the front inlet flushes the HaySep column and the line leading to the TCD (backflush). He gas flow:

- Line 1: Aux-3—V1-4—V1-3—V1-6—V1-5—V2-3—V2-4—capillary column—V2-2—V2-1—FID
 Line 2: Aux-4—V1-2—V1-1—V3-3—V3-4—V3-1—V3-2—V4-3—V4-2—V4-5—V4-4—out
- Line 3: Back inlet—V4-6—V4-7—MolSieve column—V4-1—V4-10—vent

Backflush:

• Line 3: Front inlet—V3-5—V3-6—HaySep R column—V3-8—V3-7—V4-9—V4-8—TCD

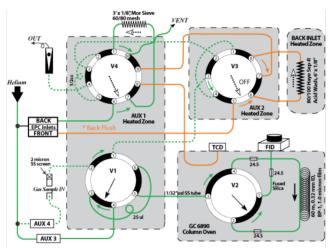


Figure 15. NGA in Run Mode: 8.50-9.09 min after starting run.

Run Mode at 10.0 min (close Valves V1 and V2)

He (green) and sample gas (red) flows in the NGA 9.09–10.0 min after start of run. After V1 and V2 close, He flow returns to standby mode. He gas flow:

- Line 1: Aux-3—V1-4—V1-5—V2-3—V2-2—capillary column—V2-4—V2-1—FID
- Line 2: Aux-4—V1-2—V1-3—V1-6—V1-1—V3-3—V3-4—V3-1—V3-2—V4-3—V4-2—V4-5—V4-4—out
- Line 3: Front inlet—V3-5—V3-6—HaySep R column—V3-8—V3-7—V4-9—V4-8—TCD
- Line 4: Back inlet—V4-6—V4-7—MolSieve column—V4-1—V4-10—vent

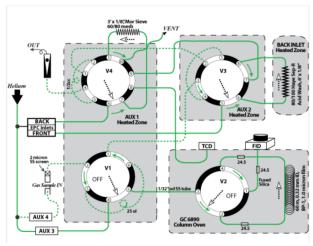


Figure 16. NGA in Run Mode: 9.09-10.0 min after starting run.

NGA Startup

The chromatography application ChemStation controls GC data acquisition and processing. It can be run either online or offline. Offline mode can be run without communication with the GCs, so it is useful for reintegrating or reprocessing chromatograms. Online mode requires communication with the GC.

- Turn on the GC. WARNING: Before turning on the GC, make sure the gas lines are open.
 The 6890 GC performs a comprehensive self-evaluation and shows real-time diagnostics on the screen. Warning, Fault, or Bad Main Board & Fatal Error messages require troubleshooting before moving to the next step (see Maintenance & Troubleshooting (HP6890GC)).
- Click the Agilent Control Panel, then select NGA1 or NGA2, then Launch to start ChemStation. The Method and Run Control window opens. At startup, ChemStation uses the method last used (shown on the main screen). In addition, the GC LCD shows the loaded settings from ChemStation. Settings changed on the GC using the GC control panel are also made to ChemStation, and parameter changes entered into ChemStation are made to the GC. ChemStation will prompt to save changes.
- To load a different method in Chemstation:
 - ° Click Method > Load Method, select the method from the list, and press OK or
 - Click the Method tab on the left side of the window and select a method to load
- The system automatically loads the new method selected in ChemStation to the appropriate GC. Oven and detector temperatures may
 increase immediately after a new method is loaded, and the FID will ignite when the detector temperature reaches 150°C. Sometimes, the
 GC beeps because the FID flame is out, especially after a long idle period. See Maintenance & Troubleshooting (HP6890GC).
- If the GC has been turned off for longer than a week, then bake the column for 8 hr with gas flowing (manually set the oven temperature to 175°C for GC3 or 275°C for NGA).

Instrument Operation

Before unknown samples can be analyzed for headspace gases, each GC system must have a valid calibration curve and the calibration curve must have been verified using a calibration verification standard.

Creating a Calibration Curve

1 Prepare 5-7 registered standard gases. 2 Activate NGA LIMS uploader located at Start > Program Files > IODP > MegaUploadaTron. The uploader must be activated before the calibration is run. 3 In the ChemStation Main menu, click Run Control > Sample Info. Fill in the specific fields on the screen as follows: Operator name: LIMS user account (your last name) Sample name: name of the standard (e.g., STD_D) and the replicate number (STD_D-1, STD_D-2, etc.) Comment: text ID of the standard (scan the label) Click **OK** to close screen. Slowly inject 5000 µL of the first standard gas and observe the floating ball in the flow meter move upward. Keep the outflow rate on the flow meter <80 mL/min. When the ball in the flow meter indicates flow has fallen to just above 0 (is about to hit 0), press the Start button on the control panel of the GC. 7 When the run has finished, open the Data Analysis screen in ChemStation and click Calibration. 8 On the *Main* ChemStation menu, select **Calibration** > **Recalibrate**. On the Recalibration screen, select Level # and Replace (or Average) as applicable for that level. 9 10 Repeat Steps 5–9 for 3 replicate standards (CH₄: A 25%, B = 50%, C 75%, D = 99%). 11 Click **OK** to change the calibration value. For NGA calibration, the same standard can be applied to both the appropriate TCD and FID level;

Running a Calibration Verification Standard

you do not need separate standards for TCD and FID.

1	Ensure the uploader is activated and the CV standard is registered in LIMS.			
2	Click Run Control in the main menu of ChemStation and select Sample Info.			
3	Fill in the specific section on the window as follows: • Operator name: LIMS user account (your last name) • Sample name: common name for standard (e.g., STD_D-1) • Comment: text ID of the standard (scan the label) Click OK to close the sample info screen.			
4	Prepare the CV standard at approximately the mid-point concentration of the curve.			
5	Slowly inject 5000 μL of the standard gas, keeping the outflow rate <80 mL/min.			
6	Press Start on the GC control panel when the flow meter is just above 0.			
7	When the run is finished, the report will automatically display the values. Click Upload in the uploader to submit the data to LIMS.			

Running a Blank

1	To run a blank, in the Main menu click RunControl > Sample Info.
2	Fill in the following fields: Operator name: your last name Sample name: "BLANK" Comment: text ID of the blank (scan the label) Click OK to close window and save information.
3	Prepare laboratory air (5000 µL) and inject it into the GC in the same fashion as the standards above when the ChemStation software shows Re ady.
4	Press the Start button on the GC control panel to start the run.
5	Confirm the chromatogram on the screen shows no peaks. If peaks are present, the system contamination must be found (injector, detector, sample loop, etc.).

Running a Gas Sample

Ensure the uploader has been activated.
Click Run Control in the main menu of ChemStation and select Sample Info.
Fill in the specific section on the window as follows:

Operator name: LIMS user account (your last name)
Sample name: Exp/site/hole/core/coretype/section/interval (e.g., 324-U1351A 5H4 32-35)
Comment: text ID of sample (scan label)
Click OK to close sample info screen.

Prepare a headspace or void gas sample.
Slowly inject 5000 μL of the gas sample, keeping the maximum gas outflow <80 mL/min.
Press Start on the GC control panel when the ball on the flow meter is just above 0.

Sample Preparation

There are two primary sample types used for natural gas analysis.

- Headspace gas, which is obtained from core samples by heating a sample to ~70°C.
- Void gas collected with a vacuum vial.

Occasionally, cores that come on deck have voids with large amounts of free gas. Free gas must be sampled using a sampling device that penetrates the liner and provides a channel for the gas to be drawn into a gas-tight syringe, vacuum vial, or gas sampling bag.

Headspace Gas

Collect samples from a freshly cut core section at a position within 0.5 inch of the inner side of the core liner (where sample has not been disturbed by contact with drilling fluid or core liner). In addition, the sample must be taken prior to the use of acetone or any other organic solvent in the catwalk area.

The curator authorizes the sampling plan before coring; therefore, the chemistry specialist must know the catwalk sampling plan before taking samples.

Locate a freshly sectioned core (consult with the curator).

Gently push the sample coring tool into the core section slightly inward of the edge.

Gently pull out the tool. If the sample recovery (% of coring tool with sample) is >80% (~5–7 cm³), proceed; otherwise repeat Steps 1 and 2.

Place the open end of the sample coring tool over a clean headspace gas vial and use the plunger to push the sediment into the vial.

Immediately place a gasket with a crimp top over the vial and crimp shut.

After sealing the vial, immediately write down the sampling interval, location, and any other information for the sample that was just taken. Generate a proper label and apply it to the vial as soon as possible.

Place the vial with the sample in a 70°C oven for 30 min to degas the sediment (use timer).

Inject extracted gas sample into the GC using syringe (see Running a Sample).

Collecting a Void Gas Sample

Use the puncture tool to make a hole in the core liner to make a channel for the gas.
 Quickly collect a free gas sample from the small hole with a syringe.
 Immediately introduce the gas sample into the GC instruments in the same manner as the headspace samples.

Data Upload

Data is uploaded from the NGA via a multi-step process:

- 1. When the run is complete, a macro (NGA_MUT.MAC) is automatically called, as configured in the method file. The macro copies information from the method directory to C:\LIMS\NGA\data
- 2. An in-house program called MegaUploadaTron (MUT) monitors the data folder locations and when a file is copied in initiates the next steps of the upload process.
- The file is opened and read, and data points are uploaded to LIMS
- The data files are compressed (zipped) and uploaded as well
- LIMS analysis codes are NGAFID, and NGATCD
- 1. After the upload to LIMS is complete, MUT moves the data files to an archive directory at C:\DATA\GC3\archive or C:\DATA\NGA\archive.
- 2. If an upload error occurs, the files are not archived and MUT will report the error in the main window (only).

Quality Assurance/Quality Control

QA/QC for GC3/NGA analysis consists of instrument calibration and continuing calibration verification using check standards, instrument blanks, and replicate samples.

Analytical Batch

An analytical batch is a method-defined number of samples with which QC samples including calibration verification, blank, and replicate samples are run. Samples are implicitly grouped into batches based on the spacing between CV samples.

QC Samples

Blank

- The blank determines the level of contamination originating from the laboratory environment (air) and sample path in the GC (injection port with screen, sample loop, and separation column).
- Run a blank with each batch of samples by injecting 5 mL of ambient laboratory air into the GC using the same syringe used to inject headspace gas samples.
- All calibrated values other than O₂ and N₂ should be nondetectable in the blank. If aberrant peaks appear, bake the column for 8 hr and repeat the blank analysis.

Calibration Sample

- Five to seven levels of calibration samples (standard gases) are used to create a calibration curve, which is saved with the measurement data (see *Instrument Calibration/Calibration Verification*).
- Correlation coefficient values for calibration curves should be 0.99 or better, except O₂ and N₂, which should be 0.95 or better.

Calibration Verification (CV) Sample

- Select one of the 5–7 calibration samples from the calibration curve for the calibration verification sample.
- Run a CV sample at least every shift that samples are taken (see Instrument Calibration/Calibration Verification).
- The CV should fall within 3% of the calibrated value; O₂ and N₂ should be within 10% of the calibrated value.

Control Limits

For a system to be considered in control, all QA/QC samples (blank and calibration verification) must be in control.

In Control

A QA/QC sample is in control when the sample analysis result is within a certain tolerance of acceptable limits (see above). Calibration verification samples should be within acceptable limits of the actual value calculated against the calibration curve (see *Calibration Verification (CV) Sample*) and blanks should be within acceptable limits of background levels of headspace hydrocarbons and gases (see *Blank*). When the system is in control, as indicated by acceptable results on QA/QC samples, analytical results for unknown samples are considered to be reliable.

Out of Control

If the control limits are exceeded, the instrument system is considered out of control and all samples in the current analytical batch are invalid and must be rerun after the system is proved to be in control.

LIMS Integration

LIMS Components

Analysis	Component	Unit	Description
GC3	dat_asman_id	_	Serial number of chromatographic data file in digital asset management database (ASMAN)

	dat_filename		File name of chromatographic data file containing measurements
	run_test		Test number of related calibration or QA/QC test
	propene	ppmv	Relative concentration of propene in the sample
	· ·		Relative concentration of properle in the sample
	propane	ppmv	
	ethene	ppmv	Relative concentration of ethene in the sample
	ethane	ppmv	Relative concentration of ethane in the sample
000 0100	methane	ppmv	Relative concentration of methane in the sample
GC3_QAQC	dat_asman_id		Serial number of chromatographic data file in ASMAN
	dat_filename		File name of chromatographic data file containing measurements
	run_test		Test number of related calibration or QA/QC test
	propene	ppmv	Relative concentration of propene in the sample
	propane	ppmv	Relative concentration of propane in the sample
	ethene	ppmv	Relative concentration of ethene in the sample
	ethane	ppmv	Relative concentration of ethane in the sample
	methane	ppmv	Relative concentration of methane in the sample
GC3_QCAL	mtd_asman_id		Serial number of chromatographic method in ASMAN
	mtd_filename		File name of the chromatographic method file containing measurements
	ethene_corr2	R ²	Ethene calibration coefficient
	ethene_intercept	_	Intercept of ethene calibration curve
	ethene_slope	_	Slope of ethene calibration curve
	ethane_corr2	R ²	Ethane calibration coefficient
	ethane_intercept	_	Intercept of ethane calibration curve
	ethane_slope	_	Slope of ethane calibration curve
	propene_corr2	R ²	Propene calibration coefficient
	propene_intercept	_	Intercept of propene calibration curve
	propene_slope	_	Slope of propene calibration curve
	propane_corr2	R ²	Propane calibration coefficient
	propane_intercept	_	Intercept of propane calibration curve
	propane_slope	_	Slope of propene calibration curve
	methane_corr2	R ²	Methane calibration coefficient
	methane_intercept	_	Intercept of methane calibration curve
	methane_slope	_	Slope of methane calibration curve
NGAFID	dat_asman_id	_	Serial number of chromatographic data file in ASMAN
	dat_filename	_	File name of chromatographic data file containing measurements
	run_test	_	Test number of related calibration or QA/QC test
	iso_butane	ppmv	Concentration of iso_butane in a sample
	iso_heptane	ppmv	Concentration of iso heptane in a sample
	iso_hexane	ppmv	Concentration of iso_hexane in a sample
	iso_pentane	ppmv	Concentration of iso_pentane in a sample
	n_butane	ppmv	Concentration of n_butane in a sample
	n_heptane	ppmv	Concentration of n_heptane in a sample
	n_hexane	ppmv	Concentration of n_hexane in a sample
	n_pentane	ppmv	Concentration of n_pentane in a sample
	ethane_ethene	ppmv	Concentration of H_peritarie in a sample Concentration of ethane + ethene in a sample
	propane_propene	ppmv	Concentration of entaile + enterte in a sample Concentration of propane + propene in a sample
	methane	ppmv	Concentration of methane in a sample

NGAFID_QA	dat_asman_id	_	Serial number of chromatographic data file in ASMAN
	dat_filename	_	File name of chromatographic data file containing measurements
	run_test	_	Test number of related calibration or QA/QC test
	iso_butane	ppmv	Concentration of iso_butane in a sample
	iso_heptane	ppmv	Concentration of iso_heptane in a sample
	iso_hexane	ppmv	Concentration of iso_hexane in a sample
	iso_pentane	ppmv	Concentration of iso_pentane in a sample
	n_butane	ppmv	Concentration of n_butane in a sample
	n_heptane	ppmv	Concentration of n_heptane in a sample
	n_hexane	ppmv	Concentration of n_hexane in a sample
	n_pentane	ppmv	Concentration of n_pentane in a sample
	ethane_ethene	ppmv	Concentration of ethane + ethene in a sample
	propane_propene	ppmv	Concentration of propane + propene in a sample
	methane	ppmv	Concentration of methane in a sample
NGAFID_QC	mtd_asman_id	_	Serial number of chromatographic method in ASMAN
	mtd_filename	_	File name of the chromatographic method file containing measurements
	iso_butane_corr2	R ²	Iso-butane calibration coefficient
	iso_butane_intercept	_	Intercept of iso-butane calibration curve
	iso_butane_slope	_	Slope of iso-butane calibration curve
	iso_heptane_corr2	R ²	Iso-heptane calibration coefficient
	iso_heptane_intercept	_	Intercept of iso-heptane calibration curve
	iso_heptane_slope	_	Slope of iso-heptane calibration curve
	iso_hexane_corr2	R ²	Iso-hexane calibration coefficient
	iso_hexane_intercept	_	Intercept of iso-hexane calibration curve
	iso_hexane_slope	_	Slope of iso-hexane calibration curve
	iso_pentane_corr2	R ²	Iso-pentane calibration coefficient
	iso_pentane_intercept	_	Intercept of iso-pentane calibration curve
	iso_pentane_slope	_	Slope of iso-pentane calibration curve
	n_butane_corr2	R ²	n-butane calibration coefficient
	n_butane_intercept	_	Intercept of n-butane calibration curve
	n_butane_slope	_	Slope of n-butane calibration curve
	n_heptane_corr2	R ²	n-heptane calibration coefficient
	n_heptane_intercept	_	Intercept of n-heptane calibration curve
	n_heptane_slope	_	Slope of n-heptane calibration curve
	n hexane corr2	R ²	n-hexane calibration coefficient
	n_hexane_intercept	_	Intercept of n-hexane calibration curve
	n_hexane_slope	_	Slope of n-hexane calibration curve
	n pentane corr2	R ²	n-pentane calibration coefficient
	n_pentane_intercept	—	Intercept of n-pentane calibration curve
			Slope of n-pentane calibration curve
	n_pentane_slope ethane_ethene_corr2	R ²	Ethane + ethene calibration coefficient
	ethane_ethene_intercept	_	Intercept of ethane + ethene calibration curve
	ethane_ethene_slope	- -	Slope of ethane + ethene calibration curve
	propane_propene_corr2	R ²	Propane + propene calibration coefficient
	propane_propene_intercept	_	Intercept of propane + propene calibration curve
	propane_propene_slope	_	Slope of propane + propene calibration curve

NGAFID_QC	methane_corr2	R ²	Methane calibration coefficient
	methane_intercept	_	Intercept of methane calibration curve
	methane_slope	_	Slope of methane calibration curve
NGATCD	dat_asman_id	_	Serial number of chromatographic data file in ASMAN
	dat_filename	_	File name of chromatographic data file containing measurements
	run_test	_	Test number of related calibration or QA/QC test
	carbon_dioxide	ppmv	Concentration of carbon dioxide in a sample
	ethane	ppmv	Concentration of ethane in a sample
	ethene	ppmv	Concentration of ethene in a sample
	hydrogen_sulfide	ppmv	Concentration of hydrogen sulfide in a sample
	methane	ppmv	Concentration of methane in a sample
	nitrogen	ppmv	Concentration of nitrogen in a sample
	oxygen	ppmv	Concentration of oxygen in a sample
	propane	ppmv	Concentration of propane in a sample
	propene	ppmv	Concentration of propene in a sample

Health, Safety & Environment

Safety

- · The following parts are dangerously hot. Avoid touching these areas and cool completely to room temperature before servicing them:
- Inlets
- Oven
- Detectors
- Column nuts
- · Be careful when working behind the instrument; during cooldown cycle the oven emits hot exhaust that can cause burns.
- Do not place temperature-sensitive items (e.g., gas cylinders, chemicals, regulators, and plastic tubing) in the path of the heated exhaust.
- Insulation around inlets, detectors, and valve box contains refractory ceramic fibers. Avoid inhaling particles and wear personal protective
 equipment including gloves, safety glasses, and dust/mist respirator when working in these areas.
- Do not leave flammable gas flows on if GC will be unmonitored for long periods of time (however, leave carrier gas on for column flow).
- Always operate the instrument with the cover properly installed.

Maintenance & Troubleshooting (HP6890GC)

Use the Status and Info keys on the GC keypad as a first check when something goes wrong.

Troubleshooting

Faults

- Beeping instrument (cancel beep by pressing Clear on the instrument keyboard)
- One beep: instrument fault, warning, or shutdown
- Series of beeps: gas flow cannot reach setpoint and flow will be shut down after 1–2 min
- Continuous beep: thermal shutdown
- Blinking setpoint on GC display
- Control table setpoint blinking: gas flow, valve, or oven shutdown
- Detector On/Off line blinking: pneumatics or detector failure
- Instrument screen messages (press Clear to remove message)
- · Caution: configuration problems
- Error: setpoint out of range or incorrect hardware
- Popup: shutdown, fault, or warning (see error table)
- FID will not stay lit
- Make sure the dessicant in the hydrogen generator is not saturated with water (replace/recharge as necessary).
- · Check water level in hydrogen generator

Leak Checking

When checking for leaks, check both parts of the system:

- External leaks: gas cylinders, gas purifiers/traps, regulator fittings, supply shutoff valves, GC supply fittings.
- GC leaks: inlets, purge vents; column connections to inlets, detectors, valves, splitters, adapters, and unions.

For safe leak-checking and flow measurement:

- Purge flowmeters with inert gas after measuring a flammable gas (such as hydrogen).
- Measure gases individually.
- Turn off detectors while measuring gas flows.

Column Size and Carrier Gas Flow Rate

Column type	Column	Carrier gas flow rate (mL /min)	
		Hydrogen	Helium
Packed	1/8 inch		30
	1/4 inch		60
Capillary	50 µm	0.5	0.4
	100 μm	1.0	0.8
	200 μm	2.0	1.6
	250 µm	2.5	2.0
	320 µm	3.2	2.6
	530 µm	5.3	4.2
These flow rates at normal temperature and pressure (25°C and 1 atm) are recommended for all column temperatures. For capillary columns, flow rates are proportional to column diameter and are 20% lower for helium than for hydrogen.			

LIMS Component Tables

The following tables represent all of the LIMS components for the following analysis codes:

- NGAFID C1-C7 hydrocarbons by flame ionization detector
- NGATCD C1-C3 hydrocarbons and fixed gases by thermal conductivity detector
 GC3 (legacy) C1-C3 hydrocarbons by flame ionization detector; this system is no longer aboard, but at the time was faster than the previous version of the NGA; the Agilent 7890 NGA GCs are fast enough to make the separate GC3 unnecessary

ANAL YSIS	TABLE	NAME	ABOUT TEXT
NGAF ID	SAMPLE	Exp	Exp: expedition number
NGAF ID	SAMPLE	Site	Site: site number
NGAF ID	SAMPLE	Hole	Hole: hole number
NGAF ID	SAMPLE	Core	Core: core number
NGAF ID	SAMPLE	Туре	Type: type indicates the coring tool used to recover the core (typical types are F, H, R, X).
NGAF ID	SAMPLE	Sect	Sect: section number
NGAF ID	SAMPLE	A/W	A/W: archive (A) or working (W) section half.
NGAF ID	SAMPLE	text_id	Text_ID: automatically generated database identifier for a sample, also carried on the printed labels. This identifier is guaranteed to be unique across all samples.
NGAF ID	SAMPLE	sample_numb er	Sample Number: automatically generated database identifier for a sample. This is the primary key of the SAMPLE table.
NGAF ID	SAMPLE	label_id	Label identifier: automatically generated, human readable name for a sample that is printed on labels. This name is not guaranteed unique across all samples.
NGAF ID	SAMPLE	sample_name	Sample name: short name that may be specified for a sample. You can use an advanced filter to narrow your search by this parameter.

NGAF ID	SAMPLE	x_sample_state	Sample state: Single-character identifier always set to "W" for samples; standards can vary.
NGAF ID	SAMPLE	x_project	Project: similar in scope to the expedition number, the difference being that the project is the current cruise, whereas expedition could refer to material/results obtained on previous cruises
NGAF ID	SAMPLE	x_capt_loc	Captured location: "captured location," this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2
NGAF ID	SAMPLE	location	Location: location that sample was taken; this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2
NGAF ID	SAMPLE	x_sampling_to ol	Sampling tool: sampling tool used to take the sample (e.g., syringe, spatula)
NGAF ID	SAMPLE	changed_by	Changed by: username of account used to make a change to a sample record
NGAF ID	SAMPLE	changed_on	Changed on: date/time stamp for change made to a sample record
NGAF ID	SAMPLE	sample_type	Sample type: type of sample from a predefined list (e.g., HOLE, CORE, LIQ)
NGAF ID	SAMPLE	x_offset	Offset (m): top offset of sample from top of parent sample, expressed in meters.
NGAF ID	SAMPLE	x_offset_cm	Offset (cm): top offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset, converted to cm)
NGAF ID	SAMPLE	x_bottom_offs et_cm	Bottom offset (cm): bottom offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset + length, converted to cm)
NGAF ID	SAMPLE	x_diameter	Diameter (cm): diameter of sample, usually applied only to CORE, SECT, SHLF, and WRND samples; however this field is null on both Exp. 390 and 393, so it is no longer populated by Sample Master
NGAF ID	SAMPLE	x_orig_len	Original length (m): field for the original length of a sample; not always (or reliably) populated
NGAF ID	SAMPLE	x_length	Length (m): field for the length of a sample [as entered upon creation]
NGAF ID	SAMPLE	x_length_cm	Length (cm): field for the length of a sample. This is a calculated field (length, converted to cm).
NGAF ID	SAMPLE	status	Status: single-character code for the current status of a sample (e.g., active, canceled)
NGAF ID	SAMPLE	old_status	Old status: single-character code for the previous status of a sample; used by the LIME program to restore a canceled sample
NGAF ID	SAMPLE	original_sample	Original sample: field tying a sample below the CORE level to its parent HOLE sample
NGAF ID	SAMPLE	parent_sample	Parent sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR)
NGAF ID	SAMPLE	standard	Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T)
NGAF ID	SAMPLE	login_by	Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created])
NGAF ID	SAMPLE	login_date	Login date: creation date of the sample
NGAF ID	SAMPLE	legacy	Legacy flag: T/F indicator for when a sample is from a previous expedition and is locked/uneditable on this expedition
NGAF ID	TEST	test changed_on	TEST changed on: date/time stamp for a change to a test record.
NGAF ID	TEST	test status	TEST status: single-character code for the current status of a test (e.g., active, in process, canceled)
NGAF ID	TEST	test old_status	TEST old status: single-character code for the previous status of a test; used by the LIME program to restore a canceled test
NGAF ID	TEST	test test_number	TEST test number: automatically generated database identifier for a test record. This is the primary key of the TEST table.
NGAF ID	TEST	test date_received	TEST date received: date/time stamp for the creation of the test record.
NGAF ID	TEST	test instrument	TEST instrument [instrument group]: field that describes the instrument group (most often this applies to loggers with multiple sensors); often obscure (e.g., user_input)
NGAF	TEST	test analysis	TEST analysis: analysis code associated with this test (foreign key to the ANALYSIS table)

NGAF ID	TEST	test x_project	TEST project: similar in scope to the expedition number, the difference being that the project is the current cruise, whereas expedition could refer to material/results obtained on previous cruises
NGAF ID	TEST	test sample_numb er	TEST sample number: the sample_number of the sample to which this test record is attached; a foreign key to the SAMPLE table
NGAF ID	CALCU LATED	Top depth CSF-A (m)	Top depth CSF-A (m): position of observation expressed relative to the top of the hole.
NGAF ID	CALCU LATED	Bottom depth CSF-A (m)	Bottom depth CSF-A (m): position of observation expressed relative to the top of the hole.
NGAF ID	CALCU LATED	Top depth CSF-B (m)	Top depth [other] (m): position of observation expressed relative to the top of the hole. The location is presented in a scale selected by the science party or the report user.
NGAF ID	CALCU LATED	Bottom depth CSF-B (m)	Bottom depth [other] (m): position of observation expressed relative to the top of the hole. The location is presented in a scale selected by the science party or the report user.
NGAF ID	RESULT	data_asman_id	RESULT data ASMAN_ID: serial number of the ASMAN link for the data file (binary format)
NGAF ID	RESULT	data_filename	RESULT data filename: file name of the data file (binary format)
NGAF ID	RESULT	ethane (ppmv)	RESULT ethane (ppmv): ethane (C2H6, also shown as C2) concentration of the headspace or void space
NGAF ID	RESULT	ethene (ppmv)	RESULT ethene (ppmv): ethene (C2H4, also shown as C2=) concentration of the headspace or void space
NGAF ID	RESULT	iso_butane (ppmv)	RESULT iso-butane (ppmv): iso-butane (HC(CH3)3) concentration of the headspace or void space; also known as 2-methyl propane
NGAF ID	RESULT	iso_heptane (ppmv)	RESULT iso-heptane (ppmv): iso-heptane (HC(CH3)6) concentration of the headspace or void space; also known as 2-methyl hexane
NGAF ID	RESULT	iso_hexane (ppmv)	RESULT iso-hexane (ppmv): iso-hexane (HC(CH3)5) concentration of the headspace or void space; also known as 2-methyl pentane
NGAF ID	RESULT	iso_pentane (ppmv)	RESULT iso-pentane (ppmv): iso-pentane (HC(CH3)4) concentration of the headspace or void space; also known as 2-methyl butane
NGAF ID	RESULT	methane (ppmv)	RESULT methane (ppmv): methane (CH4, also shown as C1) concentration of the headspace or void space
NGAF ID	RESULT	method_asma n_id	RESULT method ASMAN_ID: serial number of the ASMAN link for the method file (binary format)
NGAF ID	RESULT	method_filena me	RESULT method filename: file name of the method file (binary format)
NGAF ID	RESULT	n_butane (ppmv)	RESULT n-butane (ppmv): n-butane (C4H10) concentration of the headspace or void space
NGAF ID	RESULT	n_heptane (ppmv)	RESULT n-heptane (ppmv): n-heptane (C7H16) concentration of the headspace or void space
NGAF ID	RESULT	n_hexane (ppmv)	RESULT n-hexane (ppmv): n-hexane (C6H14) concentration of the headspace or void space
NGAF ID	RESULT	n_pentane (ppmv)	RESULT n-pentane (ppmv): n-pentane (C5H12) concentration of the headspace or void space
NGAF ID	RESULT	n_propane	RESULT n-propane (ppmv): n-propane (C3H8) concentration of the headspace or void space
NGAF ID	RESULT	propene (ppmv)	RESULT propene (ppmv): propene (C3H6, also shown as C3=) concentration of the headspace or void space
NGAF ID	RESULT	run_test	RESULT run test: number of the run, not always populated
NGAF ID	SAMPLE	sample description	SAMPLE comment: contents of the SAMPLE.description field, usually shown on reports as "Sample comments"
NGAF ID	TEST	test test_comment	TEST comment: contents of the TEST.comment field, usually shown on reports as "Test comments"
NGAF ID	RESULT	result comments	RESULT comment: contents of a result parameter with name = "comment," usually shown on reports as "Result comments"
ANAL YSIS	TABLE	NAME	ABOUT TEXT
NGAT CD	SAMPLE	Ехр	Exp: expedition number
NGAT CD	SAMPLE	Site	Site: site number

NGAT CD	SAMPLE	Hole	Hole: hole number
NGAT CD	SAMPLE	Core	Core: core number
NGAT CD	SAMPLE	Туре	Type: type indicates the coring tool used to recover the core (typical types are F, H, R, X).
NGAT CD	SAMPLE	Sect	Sect: section number
NGAT CD	SAMPLE	A/W	A/W: archive (A) or working (W) section half.
NGAT CD	SAMPLE	text_id	Text_ID: automatically generated database identifier for a sample, also carried on the printed labels. This identifier is guaranteed to be unique across all samples.
NGAT CD	SAMPLE	sample_numb er	Sample Number: automatically generated database identifier for a sample. This is the primary key of the SAMPLE table.
NGAT CD	SAMPLE	label_id	Label identifier: automatically generated, human readable name for a sample that is printed on labels. This name is not guaranteed unique across all samples.
NGAT CD	SAMPLE	sample_name	Sample name: short name that may be specified for a sample. You can use an advanced filter to narrow your search by this parameter.
NGAT CD	SAMPLE	x_sample_state	Sample state: Single-character identifier always set to "W" for samples; standards can vary.
NGAT CD	SAMPLE	x_project	Project: similar in scope to the expedition number, the difference being that the project is the current cruise, whereas expedition could refer to material/results obtained on previous cruises
NGAT CD	SAMPLE	x_capt_loc	Captured location: "captured location," this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2
NGAT CD	SAMPLE	location	Location: location that sample was taken; this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2
NGAT CD	SAMPLE	x_sampling_to ol	Sampling tool: sampling tool used to take the sample (e.g., syringe, spatula)
NGAT CD	SAMPLE	changed_by	Changed by: username of account used to make a change to a sample record
NGAT CD	SAMPLE	changed_on	Changed on: date/time stamp for change made to a sample record
NGAT CD	SAMPLE	sample_type	Sample type: type of sample from a predefined list (e.g., HOLE, CORE, LIQ)
NGAT CD	SAMPLE	x_offset	Offset (m): top offset of sample from top of parent sample, expressed in meters.
NGAT CD	SAMPLE	x_offset_cm	Offset (cm): top offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset, converted to cm)
NGAT CD	SAMPLE	x_bottom_offs et_cm	Bottom offset (cm): bottom offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset + length, converted to cm)
NGAT CD	SAMPLE	x_diameter	Diameter (cm): diameter of sample, usually applied only to CORE, SECT, SHLF, and WRND samples; however this field is null on both Exp. 390 and 393, so it is no longer populated by Sample Master
NGAT CD	SAMPLE	x_orig_len	Original length (m): field for the original length of a sample; not always (or reliably) populated
NGAT CD	SAMPLE	x_length	Length (m): field for the length of a sample [as entered upon creation]
NGAT CD	SAMPLE	x_length_cm	Length (cm): field for the length of a sample. This is a calculated field (length, converted to cm).
NGAT CD	SAMPLE	status	Status: single-character code for the current status of a sample (e.g., active, canceled)
NGAT CD	SAMPLE	old_status	Old status: single-character code for the previous status of a sample; used by the LIME program to restore a canceled sample
NGAT CD	SAMPLE	original_sample	Original sample: field tying a sample below the CORE level to its parent HOLE sample
NGAT CD	SAMPLE	parent_sample	Parent sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR)
NGAT CD	SAMPLE	standard	Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T)
NGAT CD	SAMPLE	login_by	Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created])

NGAT CD	SAMPLE	login_date	Login date: creation date of the sample
NGAT CD	SAMPLE	legacy	Legacy flag: T/F indicator for when a sample is from a previous expedition and is locked/uneditable on this expedition
NGAT CD	TEST	test changed_on	TEST changed on: date/time stamp for a change to a test record.
NGAT CD	TEST	test status	TEST status: single-character code for the current status of a test (e.g., active, in process, canceled)
NGAT CD	TEST	test old_status	TEST old status: single-character code for the previous status of a test; used by the LIME program to restore a canceled test
NGAT CD	TEST	test test_number	TEST test number: automatically generated database identifier for a test record. This is the primary key of the TEST table.
NGAT CD	TEST	test date_received	TEST date received: date/time stamp for the creation of the test record.
NGAT CD	TEST	test instrument	TEST instrument [instrument group]: field that describes the instrument group (most often this applies to loggers with multiple sensors); often obscure (e.g., user_input)
NGAT CD	TEST	test analysis	TEST analysis: analysis code associated with this test (foreign key to the ANALYSIS table)
NGAT CD	TEST	test x_project	TEST project: similar in scope to the expedition number, the difference being that the project is the current cruise, whereas expedition could refer to material/results obtained on previous cruises
NGAT CD	TEST	test sample_numb er	TEST sample number: the sample_number of the sample to which this test record is attached; a foreign key to the SAMPLE table
NGAT CD	CALCU LATED	Top depth CSF-A (m)	Top depth CSF-A (m): position of observation expressed relative to the top of the hole.
NGAT CD	CALCU LATED	Bottom depth CSF-A (m)	Bottom depth CSF-A (m): position of observation expressed relative to the top of the hole.
NGAT CD	CALCU LATED	Top depth CSF-B (m)	Top depth [other] (m): position of observation expressed relative to the top of the hole. The location is presented in a scale selected by the science party or the report user.
NGAT CD	CALCU LATED	Bottom depth CSF-B (m)	Bottom depth [other] (m): position of observation expressed relative to the top of the hole. The location is presented in a scale selected by the science party or the report user.
NGAT CD	RESULT	carbon_dioxid e (ppmv)	RESULT carbon dioxide (ppmv): concentration of CO2 in the headspace or void space
NGAT CD	RESULT	data_asman_id	RESULT data ASMAN_ID: serial number of the ASMAN link for the data file (binary format)
NGAT CD	RESULT	data_filename	RESULT data filename: file name of the data file (binary format)
NGAT CD	RESULT	ethane (ppmv)	RESULT ethane (ppmv): ethane (C2H6, also shown as C2) concentration of the headspace or void space
NGAT CD	RESULT	ethene (ppmv)	RESULT ethene (ppmv): ethene (C2H4, also shown as C2=) concentration of the headspace or void space
NGAT CD	RESULT	hydrogen_sulfi de (ppmv)	RESULT hydrogen sulfide (ppmv): concentration of H2S in the headspace or void space
NGAT CD	RESULT	methane (ppmv)	RESULT methane (ppmv): methane (CH4, also shown as C1) concentration of the headspace or void space
NGAT CD	RESULT	method_asma n_id	RESULT method ASMAN_ID: serial number of the ASMAN link for the method file (binary format)
NGAT CD	RESULT	method_filena me	RESULT method filename: file name of the method file (binary format)
NGAT CD	RESULT	nitrogen (ppmv)	RESULT nitrogen (ppmv): concentration of N2 in the headspace or void space
NGAT CD	RESULT	oxygen (ppmv)	RESULT oxygen (ppmv): concentration of O2 in the headspace or void space
NGAT CD	RESULT	propane (ppmv)	RESULT n-propane (ppmv): propane (C3H8) concentration of the headspace or void space
NGAT CD	RESULT	propene (ppmv)	RESULT propene (ppmv): propene (C3H6, also shown as C3=) concentration of the headspace or void space
NGAT CD	RESULT	run_test	RESULT run test: number of the run, not always populated
NGAT	SAMPLE	sample description	SAMPLE comment: contents of the SAMPLE.description field, usually shown on reports as "Sample comments"

NGAT CD	TEST	test test_comment	TEST comment: contents of the TEST.comment field, usually shown on reports as "Test comments"
NGAT CD	RESULT	result comments	RESULT comment: contents of a result parameter with name = "comment," usually shown on reports as "Result comments"

No. No.	ΔΝΑΙ	TADIE	NAME	ADOLIT TEYT
CCC SAMPLE Site Site site number CCC SAMPLE Hole Hole Concern unmber CCC SAMPLE Type: type indicates the coring tool used to recover the core (typical types are F, H, R, X). CCC SAMPLE Sect Sect section number CCC SAMPLE SAMPLE AVI Available (A) or working (W) section half. CCC SAMPLE SAMPLE SAMPLE build Total_UD-automated to be unique across all samples. CCC SAMPLE Sample_numb Care_UD-automated to be unique across all samples. CCC SAMPLE Sample_numb Sample_number build unique across all samples. CCC SAMPLE sample_number automated by generated database identifier for a sample. This is the primary key of the SAMPLE table. CCC SAMPLE sample_number. Sample_number automated by samples. CCC SAMPLE sample_number schot harm that may be specified for a sample. You can use an advanced filler to name you reserve by samples. CCC SAMPLE x_sample_number schot harm that may be specified for a sample. You can use an advanced filler to name you reserve by samples. CCC SAMPLE x_sam	ANAL YSIS	TABLE	NAME	ABOUT TEXT
CCG SAMPLE Hole Holes hole number CCG SAMPLE Core Core core number CCG SAMPLE Type Type: type indicates the coring bool used to recover the core (typical types are F, H, R, X). CCG SAMPLE Sect Sect section number CCG SAMPLE Sect Sect section number CCG SAMPLE Sect Sect section number CCG SAMPLE to the July Available (A) or working (W) section half. CCG SAMPLE baseline (A) Sect (A) or working (W) section half. CCG SAMPLE baseline (A) Sample number: automatically generated database identifier for a sample, also carried on the printed labels. This is dentifier is controlled to the printed labels. This is dentifier in sample and printed in the printed labels. This is dentifier in sample. This is the printed the SAMPLE table. CCG SAMPLE baseling (B) Sample number: automatically generated database identifier for a sample, also carried on the printed labels. This is dentifier in sample and printed labels. This is dentifier in sample and printed labels. This is dentifier in sample and printed labels. CCG SAMPLE baseling (B) Sample (A) Sample (A) Sample (A) <td>GC3</td> <td>SAMPLE</td> <td>Ехр</td> <td>Exp: expedition number</td>	GC3	SAMPLE	Ехр	Exp: expedition number
GCG SAMPLE Core Core core number GCG SAMPLE Type Type: type indicates the coring tool used to recover the core (typical types are F, H, R, X). GCG SAMPLE Sext Sext Sext Sext Sext Sext Sext Sext	GC3	SAMPLE	Site	Site: site number
GCG SAMPLE Type Type: type indicates the coring tool used to recover the core (typical types are F, H, R, X). GCG SAMPLE Sect. section number GCG SAMPLE AVW AVX: survive (A) or working (W) section half. GCG SAMPLE bart Library Ext. Library Type: type of sample. GCG SAMPLE bart Library Sample numb Sample numb Sample numb cancers all samples. GCG SAMPLE sample_numb Sample numb cancers all samples. Intelligence the sample for a sample. This is the primary key of the SAMPLE table. GCG SAMPLE sample_numb Label deterifier: automatically generated, human readable name for a sample. This is the primary key of the SAMPLE table. GCG SAMPLE x_sample_state Sample name: short name that may be specified for a sample. You can use an advanced filler to narrow your search by this parameter. GCG SAMPLE x_sample_state Sample name: short name that may be specified for a sample. You can use an advanced filler to narrow your search by this parameter. GCG SAMPLE x_sample_state Sample states: Simple-character identifier always set to Wf for samples: standards can vary. GCG SAMPLE	GC3	SAMPLE	Hole	Hole: hole number
GC3 SAMPLE Sect Sect section number GC3 SAMPLE Lext. id AVM: archive (A) or working (M) section half. GC3 SAMPLE text. id Text. ID: automatically generated database identifier for a sample, also carried on the printed labels. This identifier is guaranteed for the unique across all samples. GC3 SAMPLE ample, numb Sample, numb cartonatically generated database identifier for a sample. This is the primary key of the SAMPLE table. GC3 SAMPLE ample, numb Sample numb cartonatically generated, human readable name for a sample. This is the primary key of the SAMPLE table. GC3 SAMPLE ample, name Sample names short name that may be specified for a sample. You can use an advanced filter to natronational guaranteed. GC3 SAMPLE ample, name Sample names short name that may be specified for a sample. You can use an advanced filter to natronational guaranteed. GC3 SAMPLE ample, name Project similar in scope to the expecition number, the difference being that the project is the current cruise, whereas expedition countries. GC3 SAMPLE ample, name and countries and countries. Sample, number ending in 1, and GCR ending in 2 GC3 SAMPLE ample, name and countries. Sample, number ending in 1, and GCR ending in 2 GC3 SAMPLE ample, name and countries.	GC3	SAMPLE	Core	Core: core number
GC3 SAMPLE AVW AVX: archive (A) or working (W) section hast. GC3 SAMPLE text_id text_	GC3	SAMPLE	Туре	Type: type indicates the coring tool used to recover the core (typical types are F, H, R, X).
GC3 SAMPLE text_ID: automatically generated database identifier or a sample, also carried on the printed labels. This identifier is guaranteed to be unique across all samples. GC3 SAMPLE sample, mmb Sample number controlled by generated database identifier for a sample. This is the primary key of the SAMPLE table. GC3 SAMPLE babel_id Label identifier: automatically generated, human readable name for a sample that is printed on labels. This name is not guaranteed unique across all samples. GC3 SAMPLE ample, state Sample name: short name that may be specified for a sample. You can use an advanced filter to narrow your search by this parameter. GC3 SAMPLE project Sample state: Single-character identifier always set to VW for samples; standards can vary. GC3 SAMPLE project Project: similar in sopre to the expedition number, the difference being that the project is the current cruise, whereas expedition of the sample control of the control of the sample control of the sample control of the sample control of the sample. The sample control of the	GC3	SAMPLE	Sect	Sect: section number
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GC3 SAMPLE Isolated and Label Identifier: automatically generated, human readable name for a sample that is printed on labels. This name is not guaranteed unique across all samples. GC3 SAMPLE sample_name Sample name: short name that may be specified for a sample. You can use an advanced filter to narrow your search by this parameter. GC3 SAMPLE x_sample_state Sample state: Single-character identifier always set to "W" for samples; standards can vary. GC3 SAMPLE x_project Project similar in scope to the expedition number, the difference being that the project is the current cruise, whereas expedition outled refer to materiar/lesults obtained on previous cruises GC3 SAMPLE x_capt_loc Captured location: 'captured location,' this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2 GC3 SAMPLE chasing the change of the control of the sample is state; this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2 GC3 SAMPLE chasing d_by Changed by: username of account used to make a change to a sample record GC3 SAMPLE changed_by Changed on: date/time stamp for change made to a sample record GC3 SAMPLE cyffset Offset (m): top offset of sample f	GC3	SAMPLE	text_id	
GC3 SAMPLE sample_name parameted unique across all samples. GC3 SAMPLE sample_name parameter parameter parameter sample sample parameter. GC3 SAMPLE sample_state Sample states Single-character identifier always set to "W" for samples; standards can vary. GC3 SAMPLE sample_state Sample states Single-character identifier always set to "W" for samples; standards can vary. GC3 SAMPLE sample_state Sample states Single-character identifier always set to "W" for samples; standards can vary. GC3 SAMPLE sample_pole Captured location: "captured location," this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2 GC3 SAMPLE sample_gold Captured location: location that sample was taken; this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2 GC3 SAMPLE sample_gold Changed by: Username of account used to make a change to a sample record GC3 SAMPLE sample_gold Changed by: Username of account used to make a change to a sample record GC3 SAMPLE sample_gold Changed by: Use of sample from a predefined list (e.g., HOLE, CORE, LIO) GC3 SAMPLE sample_gold Coffset (cm): top offset of sample from top of parent sample, expressed in meters.	GC3	SAMPLE	. –	Sample Number: automatically generated database identifier for a sample. This is the primary key of the SAMPLE table.
GCG SAMPLE x_sample_state Sample states isnigle-character identifier always set to "W" for samples; standards can vary. GCG SAMPLE x_project Project: similar in scope to the expedition number, the difference being that the project is the current cruise, whereas expedition GCG SAMPLE x_capt_loc Captured location: 'captured location,' this field is usually rull and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2 GCG SAMPLE x_sampling_to Cocation: location that sample was taken; this field is usually rull and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2 GCG SAMPLE x_sampling_tool: sampling tool used to take the sample (e.g., syringe, spatula) GCG SAMPLE changed_by Changed by: username of account used to make a change to a sample record GCG SAMPLE changed_by Changed by: username of account used to make a change record GCG SAMPLE x_offset Offset (m): top offset of sample from top of parent sample record GCG SAMPLE x_offset Offset (m): top offset of sample from top of parent sample, expressed in meters. GCG SAMPLE x_offset_m Offset (m): top offset of sample from top of parent	GC3	SAMPLE	label_id	
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GC3 SAMPLE x_capt_loc Captured location: "captured location," this field is usually null and is unnecessary because any sample captured on the JR has a sample. GC3 SAMPLE location: Location: location that sample was taken; this field is usually null and is unnecessary because any sample captured on the JR has a sample. GC3 SAMPLE Location: Location: location that sample was taken; this field is usually null and is unnecessary because any sample captured on the JR has a sample. GC3 SAMPLE x_sampling_to Sampling tool: sampling tool used to take the sample (e.g., syringe, spatula) GC3 SAMPLE x_ample_type Changed by: username of account used to take the sample (e.g., syringe, spatula) GC3 SAMPLE changed_on Changed by: username of account used to take the sample record GC3 SAMPLE changed_on Changed on: data/time stamp for change made to a sample record GC3 SAMPLE x_offset Offset (m): top offset of sample from a predefined list (e.g., HOLE, CORE, LIQ) GC3 SAMPLE x_offset Offset (m): top offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset, converted to cm) GC3 SAMPLE x_offset Offset (m): top offset of sample from top of paren	GC3	SAMPLE	x_sample_state	Sample state: Single-character identifier always set to "W" for samples; standards can vary.
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SAMPLE changed_by Changed by: username of account used to make a change to a sample record CG3 SAMPLE changed_on Changed on: date/time stamp for change made to a sample record CG3 SAMPLE sample_type Sample type of sample from a predefined list (e.g., HOLE, CORE, LIQ) CG3 SAMPLE v_offset Offset (m): top offset of sample from top of parent sample, expressed in meters. CG3 SAMPLE v_offset_cm Offset (cm): top offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset, converted to cm) CG3 SAMPLE v_bottom_offset (cm): bottom offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset + length, converted to cm) CG3 SAMPLE v_diameter Diameter (cm): diameter of sample, usually applied only to CORE, SECT, SHLF, and WRND samples; however this field is null on both Exp. 390 and 393, so it is no longer populated by Sample Master CG3 SAMPLE v_length Diameter (cm): diameter of sample, usually applied only to CORE, SECT, SHLF, and WRND samples; however this field is null on both Exp. 390 and 393, so it is no longer populated by Sample Master CG3 SAMPLE v_length Length (m): field for the original length of a sample; not always (or reliably) populated CG3 SAMPLE v_length Length (m): field for the length of a sample, as aclculated field (length, converted to cm). CG3 SAMPLE status Status: single-character code for the current status of a sample (e.g., active, canceled) CG4 SAMPLE original_sample Original sample: field tying a sample below the CORE level to its parent HOLE sample CG5 SAMPLE parent_sample Parent sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR) CG5 SAMPLE login_by Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created])	GC3	SAMPLE	location	
SAMPLE sample_type	GC3	SAMPLE		Sampling tool: sampling tool used to take the sample (e.g., syringe, spatula)
SAMPLE sample_type Sample type: type of sample from a predefined list (e.g., HOLE, CORE, LIQ) SAMPLE x_offset Offset (m): top offset of sample from top of parent sample, expressed in meters. SAMPLE x_offset_cm Offset (cm): top offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset, converted to cm) SAMPLE x_bottom_offs et_cm Diameter (cm): bottom offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset + length, converted to cm) SAMPLE x_diameter Diameter (cm): diameter of sample, usually applied only to CORE, SECT, SHLF, and WRND samples; however this field is null on both Exp. 390 and 393, so it is no longer populated by Sample Master GC3 SAMPLE x_orig_len Original length (m): field for the original length of a sample; not always (or reliably) populated GC3 SAMPLE x_length Length (m): field for the length of a sample [as entered upon creation] GC3 SAMPLE x_length Length (m): field for the length of a sample. This is a calculated field (length, converted to cm). GC3 SAMPLE status Status: Single-character code for the current status of a sample; used by the LIME program to restore a canceled sample GC3 SAMPLE original_sample Original sample: field tying a sample below the CORE level to its parent HOLE sample GC3 SAMPLE parent_sample Parent_sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR) GC3 SAMPLE standard Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T) GC3 SAMPLE login_by Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created))	GC3	SAMPLE	changed_by	Changed by: username of account used to make a change to a sample record
SAMPLE x_offset Cm): top offset of sample from top of parent sample, expressed in meters. SAMPLE x_offset_cm	GC3	SAMPLE	changed_on	Changed on: date/time stamp for change made to a sample record
SAMPLE x_offset_cm Offset (cm): top offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset, converted to cm) SAMPLE x_bottom_offs et_cm	GC3	SAMPLE	sample_type	Sample type: type of sample from a predefined list (e.g., HOLE, CORE, LIQ)
converted to cm) GC3 SAMPLE x_bottom_offs et_cm	GC3	SAMPLE	x_offset	Offset (m): top offset of sample from top of parent sample, expressed in meters.
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GC3 SAMPLE x_length_cm Length (cm): field for the length of a sample. This is a calculated field (length, converted to cm). GC3 SAMPLE status Status: single-character code for the current status of a sample (e.g., active, canceled) GC3 SAMPLE old_status Old status: single-character code for the previous status of a sample; used by the LIME program to restore a canceled sample GC3 SAMPLE original_sample Original sample: field tying a sample below the CORE level to its parent HOLE sample GC3 SAMPLE parent_sample Parent sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR) GC3 SAMPLE standard Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T) GC3 SAMPLE login_by Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created]) GC3 SAMPLE login_date Login date: creation date of the sample	GC3	SAMPLE	x_orig_len	Original length (m): field for the original length of a sample; not always (or reliably) populated
GC3 SAMPLE status Status: single-character code for the current status of a sample (e.g., active, canceled) GC3 SAMPLE old_status Old status: single-character code for the previous status of a sample; used by the LIME program to restore a canceled sample GC3 SAMPLE original_sample Original sample: field tying a sample below the CORE level to its parent HOLE sample GC3 SAMPLE parent_sample Parent sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR) GC3 SAMPLE standard Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T) GC3 SAMPLE login_by Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created]) GC3 SAMPLE login_date Login date: creation date of the sample	GC3	SAMPLE	x_length	Length (m): field for the length of a sample [as entered upon creation]
GC3 SAMPLE old_status Old status: single-character code for the previous status of a sample; used by the LIME program to restore a canceled sample GC3 SAMPLE original_sample Original sample: field tying a sample below the CORE level to its parent HOLE sample GC3 SAMPLE parent_sample Parent sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR) GC3 SAMPLE standard Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T) GC3 SAMPLE login_by Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created]) GC3 SAMPLE login_date Login date: creation date of the sample	GC3	SAMPLE	x_length_cm	Length (cm): field for the length of a sample. This is a calculated field (length, converted to cm).
GC3 SAMPLE original_sample Original sample: field tying a sample below the CORE level to its parent HOLE sample GC3 SAMPLE parent_sample Parent sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR) GC3 SAMPLE standard Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T) GC3 SAMPLE login_by Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created]) GC3 SAMPLE login_date Login date: creation date of the sample	GC3	SAMPLE	status	Status: single-character code for the current status of a sample (e.g., active, canceled)
GC3 SAMPLE parent_sample Parent sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR) GC3 SAMPLE standard Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T) GC3 SAMPLE login_by Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created]) GC3 SAMPLE login_date Login date: creation date of the sample	GC3	SAMPLE	old_status	Old status: single-character code for the previous status of a sample; used by the LIME program to restore a canceled sample
another PWDR) GC3 SAMPLE standard Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T) GC3 SAMPLE login_by Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created]) GC3 SAMPLE login_date Login date: creation date of the sample	GC3	SAMPLE	original_sample	Original sample: field tying a sample below the CORE level to its parent HOLE sample
GC3 SAMPLE login_by Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created]) GC3 SAMPLE login_date Login date: creation date of the sample	GC3	SAMPLE	parent_sample	
created]) GC3 SAMPLE login_date Login date: creation date of the sample	GC3	SAMPLE	standard	Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T)
	GC3	SAMPLE	login_by	
GC3 SAMPLE legacy Legacy flag: T/F indicator for when a sample is from a previous expedition and is locked/uneditable on this expedition	GC3	SAMPLE	login_date	Login date: creation date of the sample
	GC3	SAMPLE	legacy	Legacy flag: T/F indicator for when a sample is from a previous expedition and is locked/uneditable on this expedition

GC3	TEST	test changed_on	TEST changed on: date/time stamp for a change to a test record.
GC3	TEST	test status	TEST status: single-character code for the current status of a test (e.g., active, in process, canceled)
GC3	TEST	test old_status	TEST old status: single-character code for the previous status of a test; used by the LIME program to restore a canceled test
GC3	TEST	test test_number	TEST test number: automatically generated database identifier for a test record. This is the primary key of the TEST table.
GC3	TEST	test date_received	TEST date received: date/time stamp for the creation of the test record.
GC3	TEST	test instrument	TEST instrument [instrument group]: field that describes the instrument group (most often this applies to loggers with multiple sensors); often obscure (e.g., user_input)
GC3	TEST	test analysis	TEST analysis: analysis code associated with this test (foreign key to the ANALYSIS table)
GC3	TEST	test x_project	TEST project: similar in scope to the expedition number, the difference being that the project is the current cruise, whereas expedition could refer to material/results obtained on previous cruises
GC3	TEST	test sample_numb er	TEST sample number: the sample_number of the sample to which this test record is attached; a foreign key to the SAMPLE table
GC3	CALCU LATED	Top depth CSF-A (m)	Top depth CSF-A (m): position of observation expressed relative to the top of the hole.
GC3	CALCU LATED	Bottom depth CSF-A (m)	Bottom depth CSF-A (m): position of observation expressed relative to the top of the hole.
GC3	CALCU LATED	Top depth CSF-B (m)	Top depth [other] (m): position of observation expressed relative to the top of the hole. The location is presented in a scale selected by the science party or the report user.
GC3	CALCU LATED	Bottom depth CSF-B (m)	Bottom depth [other] (m): position of observation expressed relative to the top of the hole. The location is presented in a scale selected by the science party or the report user.
GC3	RESULT	data_asman_id	RESULT data ASMAN_ID: serial number of the ASMAN link for the data file (binary format)
GC3	RESULT	data_filename	RESULT data filename: file name of the data file (binary format)
GC3	RESULT	ethane (ppmv)	RESULT ethane (ppmv): ethane (C2H6, also shown as C2) concentration of the headspace or void space
GC3	RESULT	ethene (ppmv)	RESULT ethene (ppmv): ethene (C2H4, also shown as C2=) concentration of the headspace or void space
GC3	RESULT	methane (ppmv)	RESULT methane (ppmv): methane (CH4, also shown as C1) concentration of the headspace or void space
GC3	RESULT	method_asma n_id	RESULT method ASMAN_ID: serial number of the ASMAN link for the method file (binary format)
GC3	RESULT	method_filena me	RESULT method filename: file name of the method file (binary format)
GC3	RESULT	propane (ppmv)	RESULT propane (ppmv): propane (C3H8, also shown as C3) concentration of the headspace or void space
GC3	RESULT	propene (ppmv)	RESULT propene (ppmv): propene (C3H6, also shown as C3=) concentration of the headspace or void space
GC3	RESULT	run_test	RESULT run test: number of the run, not always populated
GC3	RESULT	ssup_asman_id	RESULT spreadsheet uploader ASMAN_ID: serial number of the ASMAN link for the spreadsheet uploader file
GC3	RESULT	ssup_filename	RESULT spreadsheet uploader filename: file name for the spreadsheet uploader file
GC3	RESULT	c1_c2_gc3	RESULT C1/C2 ratio (unitless): ratio of the C1 (methane) peak to the total C2 (ethane + ethene) peak
GC3	RESULT	c1_heavy	RESULT C1/heavy ratio (unitless): ratio of the C1 (methane) peak to the total of all heavier hydrocarbon peaks
GC3	SAMPLE	sample description	SAMPLE comment: contents of the SAMPLE.description field, usually shown on reports as "Sample comments"
GC3	TEST	test test_comment	TEST comment: contents of the TEST.comment field, usually shown on reports as "Test comments"
GC3	RESULT	result comments	RESULT comment: contents of a result parameter with name = "comment," usually shown on reports as "Result comments"

Archive Version

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