Table Name	Column Name	Column Comment
22. Chem_Gas		
Table Name	**Column Name**	**Column Comment**
Chem_Calib_Method	calib_method	method used for calibrating analytical instruments
Chem_Gas_Analysis	run_id	a unique identifier that will allow duplicates to be run from the same sample
	gas_analysis_code	code describing the type of analysis used to analyze a gas sample, such as C1, C2, H2S, etc.
	gas_analysis_result	the result of the analysis of a gas sample
Chem_Gas_Analysis_Type	gas_analysis_code	code describing the type of analysis used to analyze a gas sample, such as C1, C2, H2S, etc.
	gas_analysis_name	The name associated with an analysis code for a gas sample analysis.
	analysis_units	the measurement units used for an analysis, such as grams or milliliters, etc.
	analysis_code_order	used to determine the order that analysis codes will appear on a spreadsheet or report.
Chem_Gas_Calib	calib_id	internal identifier used to associate related data
	datetime	Generic date/time. Often used for keys when multiple comments, etc can be entered.
	method_code	A code for the method or instrument used for analyzing a sample, used in spreadsheets or input screens
	calib_method	method used for calibrating analytical instruments
	gas_comments	comments concerning a gas calibration
Chem_Gas_Chk_Result	calib_id	internal identifier used to associate related data
	gas_std_type	The name of the standard used for a gas calibrations or checks
	gas_analysis_code	code describing the type of analysis used to analyze a gas sample, such as C1, C2, H2S, etc.
	gas_std_class	defines the standard as a standard, a blank, or an unknown check.
	chk_sequence	identifies the order of measurements
	gas_analysis_result	the result of the analysis of a gas sample
Chem_Gas_Lipids	run_id	a unique identifier that will allow duplicates to be run from the same sample
	sample_id	Unique id attached to a sample - Allows multiple samples to be taken with same top and bottom interval
	location	
	lipid_volume	the volume of a lipid sample, in ul
	lipid_comments	comments concerning a sample analyzed for lipids
Chem_Gas_Sample	run_id	a unique identifier that will allow duplicates to be run from the same sample
	sample_id	Unique id attached to a sample - Allows multiple samples to be taken with same top and bottom interval
	location	
	sequence_identifier	allows ordering of samples when duplicate analysis are stored.
	gas_sample_method	The method used for obtaining a gas sample. HS is for headspace sample, VAC is for Vacutainer, O for Other
	vol_solid	Tthe volume of solid to be analyzed in ml or cc
	vol_hs	The volume of the headspace sample to be analyzed in ml or cc. Volume of the headspace equals volume of the vial minus volume of the solid.
	cal_id	internal identifier used to associate related data
	method_code	A code for the method or instrument used for analyzing a sample, used in spreadsheets or input screens

	gas_detector_signal	The type of signal, FID or TCD. The default value is FID.
Chem_Gas_Std	gas_std_type	The name of the standard used for a gas calibrations or checks
	gas_analysis_code	code describing the type of analysis used to analyze a gas sample, such as C1, C2, H2S, etc.
	gas_std_value	The value for a gas standard and analysis code.
Chem_Lipid_Results	run_id	a unique identifier that will allow duplicates to be run from the same sample
	gas_analysis_code	code describing the type of analysis used to analyze a gas sample, such as C1, C2, H2S, etc.
	lipid_analysis_level	The level of lipids in a sample. Options will be major, minor, trace, not present, or not determined
	lipid_concentration	The concentration of a lipid, derived from GC2 output
Chem_Method	method_code	A code for the method or instrument used for analyzing a sample, used in spreadsheets or input screens
	method_name	The name of the method or instrument used for analyzing a sample
Sample	sample_id	Unique id attached to a sample - Allows multiple samples to be taken with same top and bottom interval
	location	
	sam_archive_working	same as archive_working but allowed to be null for the sample application
	top_interval	
	bottom_interval	Distance in meters from the top of the section to the bottom of the sample. The value is stored in the database as meters, but usually appears in the Janus application as centimeters.
	piece	Additional identifier for hard rock samples. Each individual piece of rock within a section is numbered consecutively starting at the top of the section.
	sub_piece	Additional identifier for hard rock samples. When a piece is broken, the individual fragments are given consecutive letter designations. Note that subpiece assignments must be made in conjunction with piece numbers.
	beaker_id	The number on the moisture density beaker, such as "P267" or "Al1344". This value is entered on the sample table and the beaker_id is associated to the sample.
	volume	Volume of sample
	entered_by	Indicates who entered the row into the database
	sample_depth	depth of the sample
	sample_comment	A comment about the sample
	sam_repository	Repository where sample is stored.
	s_c_leg	Number identifying the cruise during which a particular core was retrieved. Nullable role of the attribute leg.
	s_c_sampling_code	Code used to identify the classify for whom the sample was taken.
	sam_sample_code_lab	Code to indicate the shipboard lab that will perform the initial analysis.
	section_id	
	timestamp	CHAR(18)