

chem	
◆	mz DOUBLE
◆	element_formulae_c INT(11)
◆	element_formulae_h INT(11)
◆	element_formulae_o INT(11)
◆	element_formulae_n INT(11)
◆	element_formulae_s INT(11)
◆	element_formulae_p INT(11)
◆	compound_intensity DOUBLE
◆	compound_index DOUBLE
◆	sample_id VARCHAR(20)
Indexes	

sample_info	
◆	sample_id VARCHAR(20)
◆	location TEXT
◆	date DATE
◆	time_point ENUM(...)
◆	replicate ENUM('1','2','3')
◆	treatment ENUM(...)
◆	notes TEXT
Indexes	

climate	
◆	nesdis_id CHAR(8)
◆	nwslid CHAR(5)
◆	date DATETIME
◆	year SMALLINT(6)
◆	month TINYINT(4)
◆	day TINYINT(4)
◆	hour TINYINT(4)
◆	minute TINYINT(4)
◆	mean_temp_air DOUBLE
◆	flag_mean_temp_air CHAR(1)
◆	max_temp_air DOUBLE
◆	flag_max_temp_air CHAR(1)
◆	min_temp_air DOUBLE
◆	flag_min_temp_air CHAR(1)
◆	humidity DOUBLE
◆	flag_humidity CHAR(1)
◆	baro_press DOUBLE
◆	flag_baro_press CHAR(1)
◆	wind_speed DOUBLE
◆	flag_wind_speed CHAR(1)
◆	wind_dir DOUBLE
◆	flag_wind_dir CHAR(1)
◆	sd_wind_direction DOUBLE
◆	flag_sd_wind_direction CHAR(1)
◆	max_wind_speed DOUBLE
◆	flag_max_wind_speed CHAR(1)
◆	precipitation DOUBLE
◆	flag_precipitation CHAR(1)
◆	total_par DOUBLE
◆	flag_total_par CHAR(1)
◆	mean_par DOUBLE
◆	flag_mean_par CHAR(1)
◆	total_solar_rad DOUBLE
◆	flag_total_solar_rad CHAR(1)
◆	total_solar_rad_kw DOUBLE
◆	flag_total_solar_rad_kw CHAR(1)
◆	sample_info_sample_id VARCH...
Indexes	

metatrans_seqs	
◆	seq_id INT(11)
◆	display_id VARCHAR(60)
◆	len TEXT
◆	sample_id VARCHAR(20)
◆	notes TEXT
Indexes	

Metatrans Sequence Functional Annotation

cog_annot	
◆	query VARCHAR(60)
◆	subject VARCHAR(50)
◆	identity DOUBLE
◆	aln_len INT(11)
◆	mismatch INT(11)
◆	gap_openings INT(11)
◆	qstart INT(11)
◆	qend INT(11)
◆	sstart INT(11)
◆	send INT(11)
◆	log_evalue DOUBLE
◆	bit_score DOUBLE
Indexes	

cog_function	
◆	protein VARCHAR(50)
◆	organism_abbreviation CHAR(3)
◆	functional_classification CHAR(5)
◆	cog_name CHAR(10)
◆	function TEXT
Indexes	

marineref_annot	
◆	query VARCHAR(60)
◆	subject INT(11)
◆	identity DOUBLE
◆	aln_len INT(11)
◆	mismatch INT(11)
◆	gap_openings INT(11)
◆	qstart INT(11)
◆	qend INT(11)
◆	sstart INT(11)
◆	send INT(11)
◆	log_evalue DOUBLE
◆	bit_score DOUBLE
Indexes	

marineref_function	
◆	seq_id INT(11)
◆	organism VARCHAR(500)
◆	sfams_id INT(11)
◆	sfams_interpro_annotation TEXT
◆	seq_description TEXT
Indexes	

kegg_annot	
◆	query VARCHAR(60)
◆	subject VARCHAR(50)
◆	identity DOUBLE
◆	aln_len INT(11)
◆	mismatch INT(11)
◆	gap_openings INT(11)
◆	qstart INT(11)
◆	qend INT(11)
◆	sstart INT(11)
◆	send INT(11)
◆	log_evalue DOUBLE
◆	bit_score DOUBLE
Indexes	

kegg_function	
◆	protein VARCHAR(50)
◆	kegg_entry VARCHAR(20)
◆	function TEXT
Indexes	

