

seq_annot_details

sag_info
Primary Key: sag_id INT(11)
Attributes: sag_name VARCHAR(50), accession VARCHAR(50), cluster VARCHAR(50), sequencing_effort DOUBLE, contigs INT(11), assembly_size DOUBLE, genome_recovery DOUBLE, estimated_genome_size DOUBLE, protein_coding_genes INT(11), gc DOUBLE, location TEXT, comments TEXT
Indexes

seq
Primary Key: seq_id INT(11)
Attributes: display_id VARCHAR(500), seq LONGTEXT, description TEXT
Indexes
Triggers

sfams_annot
Primary Key: sfams_annot_id INT(11)
Attributes: sfams_id INT(11), method VARCHAR(20), score DOUBLE, evaluate DOUBLE
Indexes

sfams_info
Primary Key: sfams_id INT(11)
Attributes: interpro_accession TEXT
Indexes

tax_nodes
Primary Key: taxon_id INT(11)
Attributes: parent_taxon_id INT(11), rank VARCHAR(50), embl_code VARCHAR(20), division_id INT(11), inherited_div_flag SMALLINT(6), genetic_code_id SMALLINT(6), inherited_gc_flag SMALLINT(6), mitochondrial_genetic_code_id SMALLINT(6), inherited_mgc_flag SMALLINT(6), genbank_hidden_flag SMALLINT(6), hidden_subtree_root_flag SMALLINT(6), comments TEXT
Indexes

tax_division
Primary Key: division_id INT(11)
Attributes: division_cde VARCHAR(10), division_name VARCHAR(200), comments TEXT
Indexes

tax_gencode
Primary Key: genetic_code_id SMALLINT(6)
Attributes: abbreviation VARCHAR(50), name VARCHAR(200), cde VARCHAR(500), starts VARCHAR(200)
Indexes

tax_full_lineage
Primary Key: taxon_id INT(11)
Attributes: full_lineage TEXT
Indexes

tax_names
Primary Key: taxon_id INT(11)
Attributes: name VARCHAR(500), uniqueness VARCHAR(100), class VARCHAR(50)
Indexes

interpro_info
Primary Key: interpro_accession VARCHAR(50)
Attributes: description TEXT
Indexes

tigrfams_annot
Primary Key: tigrfams_annot_id INT(11)
Attributes: tigrfams_name VARCHAR(50), tigrfams_accession VARCHAR(50), description TEXT, interpro_accession VARCHAR(50), method VARCHAR(20), score DOUBLE, evaluate DOUBLE
Indexes

phylodb_annot
Primary Key: phylodb_annot_id INT(11)
Attributes: subject_id VARCHAR(200), method VARCHAR(20), percent_identity DOUBLE, alignment_length INT(11), mismatches INT(11), gap_opening INT(11), query_start INT(11), query_end INT(11), subject_start INT(11), subject_end INT(11), evaluate DOUBLE, bit_score DOUBLE, phylodb_protein VARCHAR(1000), phylodb_taxon_id INT(11)
Indexes

swissprot_annot
Primary Key: swissprot_annot_id INT(11)
Attributes: swissprot_name VARCHAR(50), swissprot_accession VARCHAR(50), description TEXT, interpro_accession VARCHAR(50), method VARCHAR(20), score DOUBLE, evaluate DOUBLE
Indexes

superfamily_annot
Primary Key: superfamily_annot_id INT(11)
Attributes: superfamily_id VARCHAR(50), scop_id VARCHAR(50), method VARCHAR(20), description TEXT, score DOUBLE, evaluate DOUBLE
Indexes

pfam_annot
Primary Key: pfam_annot_id INT(11)
Attributes: pfam_name VARCHAR(50), pfam_accession VARCHAR(50), description TEXT, interpro_accession VARCHAR(50), method VARCHAR(20), score DOUBLE, evaluate DOUBLE
Indexes

seq_annot
Primary Key: seq_id INT(11)
Attributes: organism VARCHAR(500), taxon_id INT(11), original_annot TEXT, sfams_annot_id INT(11), protcluster_annot_id INT(11), sag_info_id INT(11), phylodb_annot_id INT(11), pfam_annot_id INT(11), superfamily_annot_id INT(11), swissprot_annot_id INT(11), tigrfams_annot_id INT(11)
Indexes

protcluster_annot
Primary Key: protcluster_annot_id INT(11)
Attributes: protcluster_accession VARCHAR(20), subject_length INT(11), method VARCHAR(20), evaluate DOUBLE, bit_score DOUBLE, score DOUBLE, identity DOUBLE
Indexes

protcluster_info
Primary Key: protcluster_id INT(11)
Attributes: accession VARCHAR(20), proteins INT(11), name VARCHAR(200), conserved_in VARCHAR(200), genera INT(11), organisms INT(11), paralogs INT(11), publications INT(11), domain_description TEXT, cog_category TEXT
Indexes

