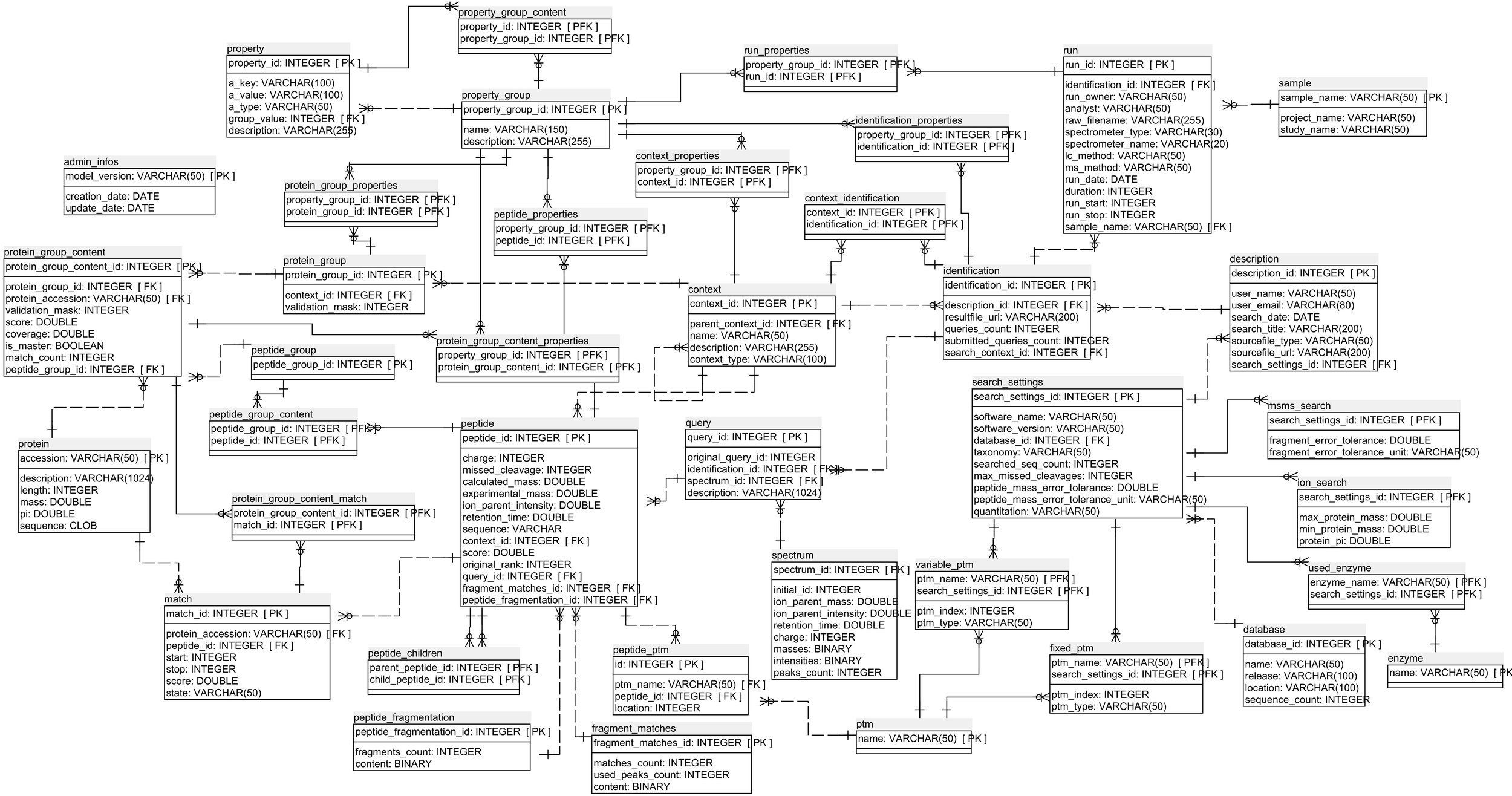
property_group_content
property_id: INTEGER [PFK]
property_group_id: INTEGER [PFK]
property
property_id: INTEGER [PK]
a_key: VARCHAR(100)
a_value: VARCHAR(100)
a_type: VARCHAR(50)
group_value: INTEGER [FK]
description: VARCHAR(255)
property_group
property_group_id: INTEGER [PK]
name: VARCHAR(150)
description: VARCHAR(255)
run_properties
property_group_id: INTEGER [PFK]
run_id: INTEGER [PFK]
run
run_id: INTEGER [PK]
identification_id: INTEGER [FK]
run_owner: VARCHAR(50)
analyst: VARCHAR(50)
raw_filename: VARCHAR(255)
spectrometer_type: VARCHAR(30)
spectrometer_name: VARCHAR(20)
lc_method: VARCHAR(50)
ms_method: VARCHAR(50)
run_date: DATE
duration: INTEGER
run_start: INTEGER
run_stop: INTEGER
sample_name: VARCHAR(50) [FK]
sample
sample_name: VARCHAR(50) [PK]
project_name: VARCHAR(50)
study_name: VARCHAR(50)
identification_properties
property_group_id: INTEGER [PFK]
identification_id: INTEGER [PFK]
admin_infos
model_version: VARCHAR(50) [PK]
creation_date: DATE
update_date: DATE
protein_group_properties
property_group_id: INTEGER [PFK]
protein_group_id: INTEGER [PFK]
peptide_properties
property_group_id: INTEGER [PFK]
peptide_id: INTEGER [PFK]
context_properties
property_group_id: INTEGER [PFK]
context_id: INTEGER [PFK]
context_identification
context_id: INTEGER [PFK]
identification_id: INTEGER [PFK]
protein_group_content
protein_group_content_id: INTEGER [PK]
protein_group_id: INTEGER [FK]
protein_accession: VARCHAR(50) [FK]
validation_mask: INTEGER
score: DOUBLE
coverage: DOUBLE
is_master: BOOLEAN
match_count: INTEGER
peptide_group_id: INTEGER [FK]
protein_group
protein_group_id: INTEGER [PK]
context_id: INTEGER [FK]
validation_mask: INTEGER
context
context_id: INTEGER [PK]
parent_context_id: INTEGER [FK]
name: VARCHAR(50)
description: VARCHAR(255)
context_type: VARCHAR(100)
identification
identification_id: INTEGER [PK]
description_id: INTEGER [FK]
resultfile_url: VARCHAR(200)
queries_count: INTEGER
submitted_queries_count: INTEGER
search_context_id: INTEGER [FK]
description
description_id: INTEGER [PK]
user_name: VARCHAR(50)
user_email: VARCHAR(80)
search_date: DATE
search_title: VARCHAR(200)
sourcefile_type: VARCHAR(50)
sourcefile_url: VARCHAR(200)
search_settings_id: INTEGER [FK]
protein_group_content_properties
property_group_id: INTEGER [PFK]
protein_group_content_id: INTEGER [PFK]
peptide_group
peptide_group_id: INTEGER [PK]
search_settings
search_settings_id: INTEGER [PK]
software_name: VARCHAR(50)
software_version: VARCHAR(50)
database_id: INTEGER [FK]
taxonomy: VARCHAR(50)
searched_seq_count: INTEGER
max_missed_cleavages: INTEGER
peptide_mass_error_tolerance: DOUBLE
peptide_mass_error_tolerance_unit: VARCHAR(50)
quantitation: VARCHAR(50)
msms_search
search_settings_id: INTEGER [PFK]
fragment_error_tolerance: DOUBLE
fragment_error_tolerance_unit: VARCHAR(50)
peptide_group_content
peptide_group_id: INTEGER [PFK]
peptide_id: INTEGER [PFK]
peptide
peptide_id: INTEGER [PK]
charge: INTEGER
missed_cleavage: INTEGER
calculated_mass: DOUBLE
experimental_mass: DOUBLE
ion_parent_intensity: DOUBLE
retention_time: DOUBLE
sequence: VARCHAR
context_id: INTEGER [FK]
score: DOUBLE
original_rank: INTEGER
query_id: INTEGER [FK]
fragment_matches_id: INTEGER [FK]
peptide_fragmentation_id: INTEGER [FK]
query
query_id: INTEGER [PK]
original_query_id: INTEGER
identification_id: INTEGER [FK]
spectrum_id: INTEGER [FK]
description: VARCHAR(1024)
protein
accession: VARCHAR(50) [PK]
description: VARCHAR(1024)
length: INTEGER
mass: DOUBLE
pi: DOUBLE
sequence: CLOB
protein_group_content_match
protein_group_content_id: INTEGER [PFK]
match_id: INTEGER [PFK]
ion_search
search_settings_id: INTEGER [PFK]
max_protein_mass: DOUBLE
min_protein_mass: DOUBLE
protein_pi: DOUBLE
spectrum
spectrum_id: INTEGER [PK]
initial_id: INTEGER
ion_parent_mass: DOUBLE
ion_parent_intensity: DOUBLE
retention_time: DOUBLE
charge: INTEGER
masses: BINARY
intensities: BINARY
peaks_count: INTEGER
variable_ptm
ptm_name: VARCHAR(50) [PFK]
search_settings_id: INTEGER [PFK]
ptm_index: INTEGER
ptm_type: VARCHAR(50)
used_enzyme
enzyme_name: VARCHAR(50) [PFK]
search_settings_id: INTEGER [PFK]
match
match_id: INTEGER [PK]
protein_accession: VARCHAR(50) [FK]
peptide_id: INTEGER [FK]
start: INTEGER
stop: INTEGER
score: DOUBLE
state: VARCHAR(50)
peptide_children
parent_peptide_id: INTEGER [PFK]
child_peptide_id: INTEGER [PFK]
peptide_ptm
id: INTEGER [PK]
ptm_name: VARCHAR(50) [FK]
peptide_id: INTEGER [FK]
location: INTEGER
fixed_ptm
ptm_name: VARCHAR(50) [PFK]
search_settings_id: INTEGER [PFK]
ptm_index: INTEGER
ptm_type: VARCHAR(50)
database
database_id: INTEGER [PK]
name: VARCHAR(50)
release: VARCHAR(100)
location: VARCHAR(100)
sequence_count: INTEGER
enzyme
name: VARCHAR(50) [PK
peptide_fragmentation
peptide_fragmentation_id: INTEGER [PK]
fragments_count: INTEGER
content: BINARY
fragment_matches
fragment_matches_id: INTEGER [PK]
matches_count: INTEGER
used_peaks_count: INTEGER
content: BINARY
ptm
name: VARCHAR(50) [PK]