CoV2K AREAS, their *Entities* and `attributes`

VARIANTS area

Variant (`variant_id`)

Naming (`naming_id, org, v_class`)

Context (`context_id, owner, rule_description`)

EFFECTS area

Effect (`effect_id, type, lv, method`)

Evidence (`evidence_id, citation, type, uri, publisher`)

POSITIONS OF INTEREST area

Nuc Positional Mutation (`nuc_positional_mutation_id, reference, position, alternative, type, length`)

Aa Positional Change (`aa_positional_change_id, protein_id, reference, position, alternative, type, length`)

Aa Change Group (`aa_change_group_id`)

STRUCTURE area

Nuc. Annotation (`nuc_annotation_id, name, start_on_ref, stop_on_ref`)

Protein (`protein_id, aa_length, aa_sequence`)

Protein Region (`protein_region_id, name, type, category, protein_id, start_on_protein, stop_on_protein`)

RESIDUES area

Aa Residue Change (`aa_residue_change_id, reference, alternative, grantham_distance, type`)

Aa Residue (`aa_residue_id, molecular_weight, isoelectric_point, hydrophobicity, potential_side_chain_h_bonds, polarity, r_group_structure, charge, essentiality, side_chain_flexibility, chemical_group_in_the_side_chain`)

SEQUENCE DATA area

Sequence (`sequence_id, accession_id, source_database, length, n_percentage, gc_percentage`)

Host Sample (`host_sample_id, continent, country, region, collection_date, host_species`)

Nuc. Mutation (`nuc_mutation_id, reference, position, alternative, type, length`)

Aa Change (`aa_change_id, protein_id, reference, position, alternative, type, length`)

EPITOPES area

Epitope (`epitope_id, protein_id, host_species, epitope_start, epitope_stop`)

Assay (`assay_id, assay_type, mhc_class, hla_restriction`)