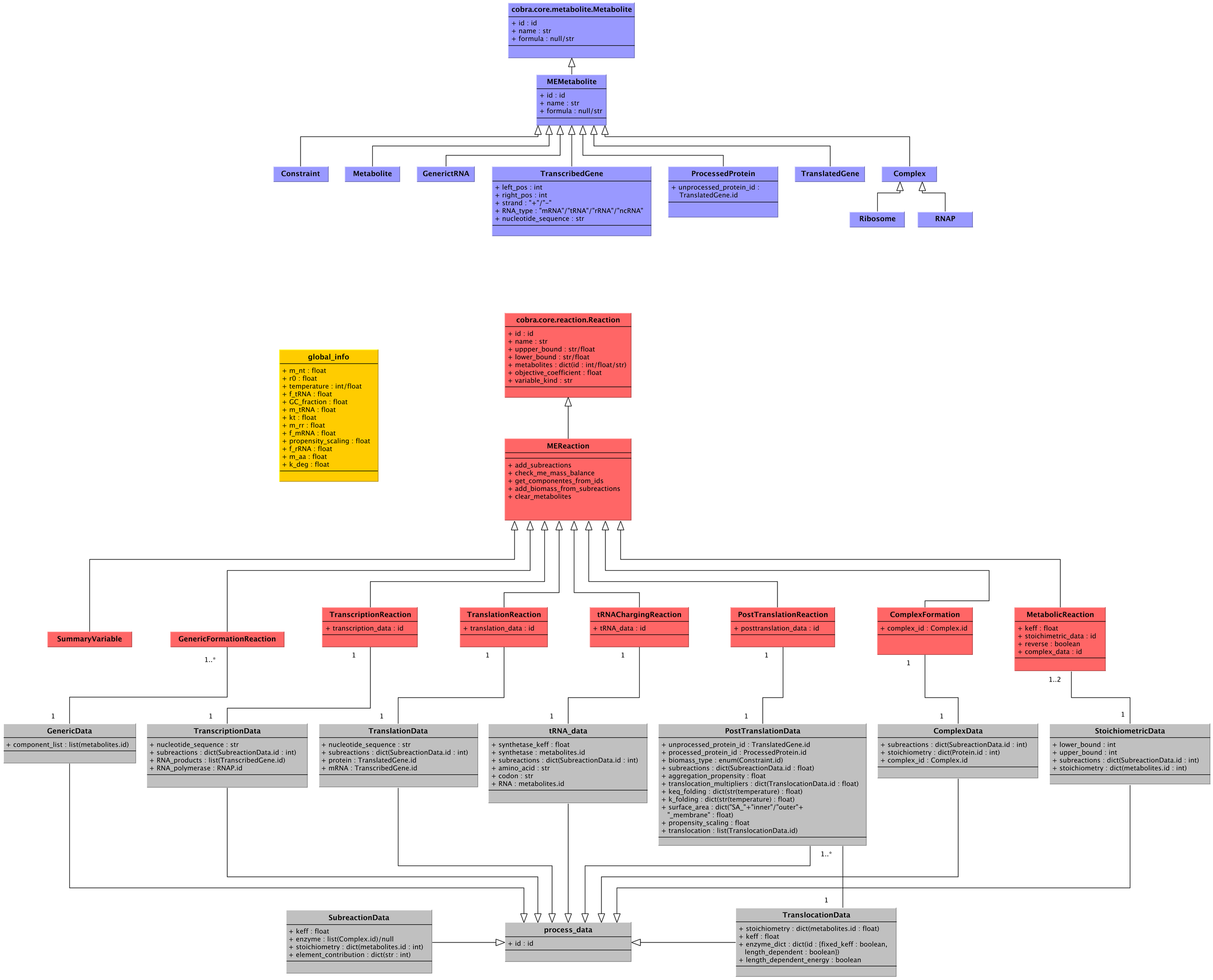
cobra.core.metabolite.Metabolite
+ id : id
+ name : str
+ formula : null/str
MEMetabolite
+ id : id
+ name : str
+ formula : null/str
Constraint
Metabolite
GenerictRNA
TranscribedGene
+ left_pos : int
+ right_pos : int
+ strand : "+"/"-"
+ RNA_type : "mRNA"/"tRNA"/"rRNA"/"ncRNA"
+ nucleotide_sequence : str
ProcessedProtein
+ unprocessed_protein_id : TranslatedGene.id
TranslatedGene
Complex
Ribosome
RNAP
global_info
+ m_nt : float
+ r0 : float
+ temperature : int/float
+ f_tRNA : float
+ GC_fraction : float
+ m_tRNA : float
+ kt : float
+ m_rr : float
+ f_mRNA : float
+ propensity_scaling : float
+ f_rRNA : float
+ m_aa : float
+ k_deg : float
cobra.core.reaction.Reaction
+ id : id
+ name : str
+ uppper_bound : str/float
+ lower_bound : str/float
+ metabolites : dict(id : int/float/str)
+ objective_coefficient : float
+ variable_kind : str
MEReaction
+ add_subreactions
+ check_me_mass_balance
+ get_componentes_from_ids
+ add_biomass_from_subreactions
+ clear_metabolites
SummaryVariable
GenericFormationReaction
TranscriptionReaction
+ transcription_data : id
TranslationReaction
+ translation_data : id
tRNAChargingReaction
+ tRNA_data : id
PostTranslationReaction
+ posttranslation_data : id
ComplexFormation
+ complex_id : Complex.id
MetabolicReaction
+ keff : float
+ stoichimetric_data : id
+ reverse : boolean
+ complex_data : id
1..*
1
1
1
1
1
1..2
1
1
1
1
1
1
1
1..*
1
GenericData
+ component_list : list(metabolites.id)
TranscriptionData
+ nucleotide_sequence : str
+ subreactions : dict(SubreactionData.id : int)
+ RNA_products : list(TranscribedGene.id)
+ RNA_polymerase : RNAP.id
TranslationData
+ nucleotide_sequence : str
+ subreactions : dict(SubreactionData.id : int)
+ protein : TranslatedGene.id
+ mRNA : TranscribedGene.id
tRNA_data
+ synthetase_keff : float
+ synthetase : metabolites.id
+ subreactions : dict(SubreactionData.id : int)
+ amino_acid : str
+ codon : str
+ RNA : metabolites.id
PostTranslationData
+ unprocessed_protein_id : TranslatedGene.id
+ processed_protein_id : ProcessedProtein.id
+ biomass_type : enum(Constraint.id)
+ subreactions : dict(SubreactionData.id : float)
+ aggregation_propensity : float
+ translocation_multipliers : dict(TranslocationData.id : float)
+ keq_folding : dict(str(temperature) : float)
+ k_folding : dict(str(temperature) : float)
+ surface_area : dict("SA_"+"inner"/"outer"+ "_membrane" : float)
+ propensity_scaling : float
+ translocation : list(TranslocationData.id)
ComplexData
+ subreactions : dict(SubreactionData.id : int)
+ stoichiometry : dict(Protein.id : int)
+ complex_id : Complex.id
StoichiometricData
+ lower_bound : int
+ upper_bound : int
+ subreactions : dict(SubreactionData.id : int)
+ stoichiometry : dict(metabolites.id : int)
SubreactionData
+ keff : float
+ enzyme : list(Complex.id)/null
+ stoichiometry : dict(metabolites.id : int)
+ element_contribution : dict(str : int)
process_data
+ id : id
TranslocationData
+ stoichiometry : dict(metabolites.id : float)
+ keff : float
+ enzyme_dict : dict(id : {fixed_keff : boolean, length_dependent : boolean})
+ length_dependent_energy : boolean