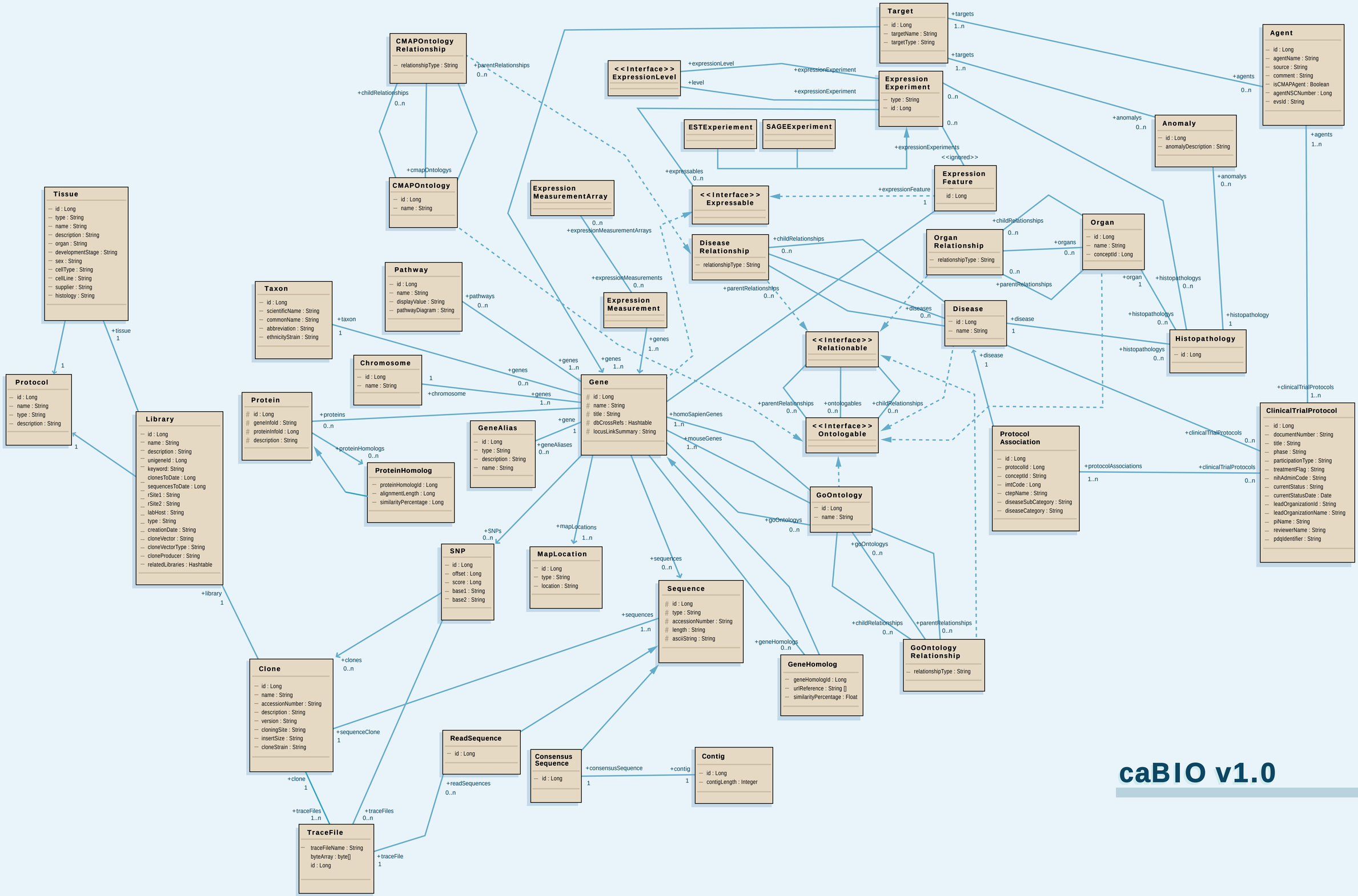
Target
id : Long
targetName : String
targetType : String
Agent
id : Long
agentName : String
source : String
comment : String
isCMAPAgent : Boolean
agentNSCNumber : Long
evsId : String
CMAPOntology Relationship
relationshipType : String
<<Interface>> ExpressionLevel
Expression Experiment
type : String
id : Long
Anomaly
id : Long
anomalyDescription : String
ESTExperiement
SAGEExperiment
CMAPOntology
id : Long
name : String
Expression Feature
id : Long
<<Interface>> Expressable
Expression MeasurementArray
Disease Relationship
relationshipType : String
Organ Relationship
relationshipType : String
Organ
id : Long
name : String
conceptId : Long
Tissue
id : Long
type : String
name : String
description : String
organ : String
developmentStage : String
sex : String
cellType : String
cellLine : String
supplier : String
histology : String
Pathway
id : Long
name : String
displayValue : String
pathwayDiagram : String
Taxon
id : Long
scientificName : String
commonName : String
abbreviation : String
ethnicityStrain : String
Expression Measurement
Disease
id : Long
name : String
<<Interface>> Relationable
Histopathology
id : Long
Chromosome
id : Long
name : String
Protocol
id : Long
name : String
type : String
description : String
Gene
id : Long
name : String
title : String
dbCrossRefs : Hashtable
locusLinkSummary : String
Protein
id : Long
geneInfold : String
proteinInfold : Long
description : String
Library
id : Long
name : String
description : String
unigeneId : Long
keyword: String
clonesToDate : Long
sequencesToDate : Long
rSite1 : String
rSite2 : String
labHost : String
type : String
creationDate : String
cloneVector : String
cloneVectorType : String
cloneProducer : String
relatedLibraries : Hashtable
GeneAlias
id : Long
type : String
description : String
name : String
<<Interface>> Ontologable
Protocol Association
id : Long
protocolId : Long
conceptId : String
imtCode : Long
ctepName : String
diseaseSubCategory : String
diseaseCategory : String
ClinicalTrialProtocol
id : Long
documentNumber : String
title : String
phase : String
participationType : String
treatmentFlag : String
nihAdminCode : String
currentStatus : String
currentStatusDate : Date
leadOrganizationId : String
leadOrganizationName : String
piName : String
reviewerName : String
pdqIdentifier : String
ProteinHomolog
proteinHomologId : Long
alignmentLength : Long
similarityPercentage : Long
GoOntology
id : Long
name : String
SNP
id : Long
offset : Long
score : Long
base1 : String
base2 : String
MapLocation
id : Long
type : String
location : String
Sequence
id : Long
type : String
accessionNumber : String
length : String
asciiString : String
GeneHomolog
geneHomologId : Long
urlReference : String []
similarityPercentage : Float
GoOntology Relationship
relationshipType : String
Clone
id : Long
name : String
accessionNumber : String
description : String
version : String
cloningSite : String
insertSize : String
cloneStrain : String
ReadSequence
id : Long
Consensus Sequence
id : Long
Contig
id : Long
contigLength : Integer
TraceFile
traceFileName : String
byteArray : byte[]
id : Long
+targets 1..n
+targets 1..n
+agents 0..n
+agents 1..n
+expressionLevel
+level
+expressionExperiment
+expressionExperiment
0..n
0..n
+expressionExperiments
<<ignored>>
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+expressionFeature 1
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+childRelationships 0..n
+organs 0..n
0..n
+parentRelationships
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+pathways 0..n
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1
1
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1
+chromosome
+proteins 0..n
+proteinHomologs 0..n
+gene 1
+geneAliases 0..n
+homoSapienGenes 1..n
+mouseGenes 1..n
+goOntologys 0..n
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+childRelationships 0..n
+parentRelationships 0..n
+geneHomologs 0..n
+SNPs 0..n
+mapLocations 1..n
+sequences 0..n
+sequences 1..n
+clones 0..n
+sequenceClone 1
+library 1
+clone 1
+traceFiles 1..n
+traceFiles 0..n
+traceFile 1
+readSequences 0..n
+consensusSequence 1
+contig 1

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