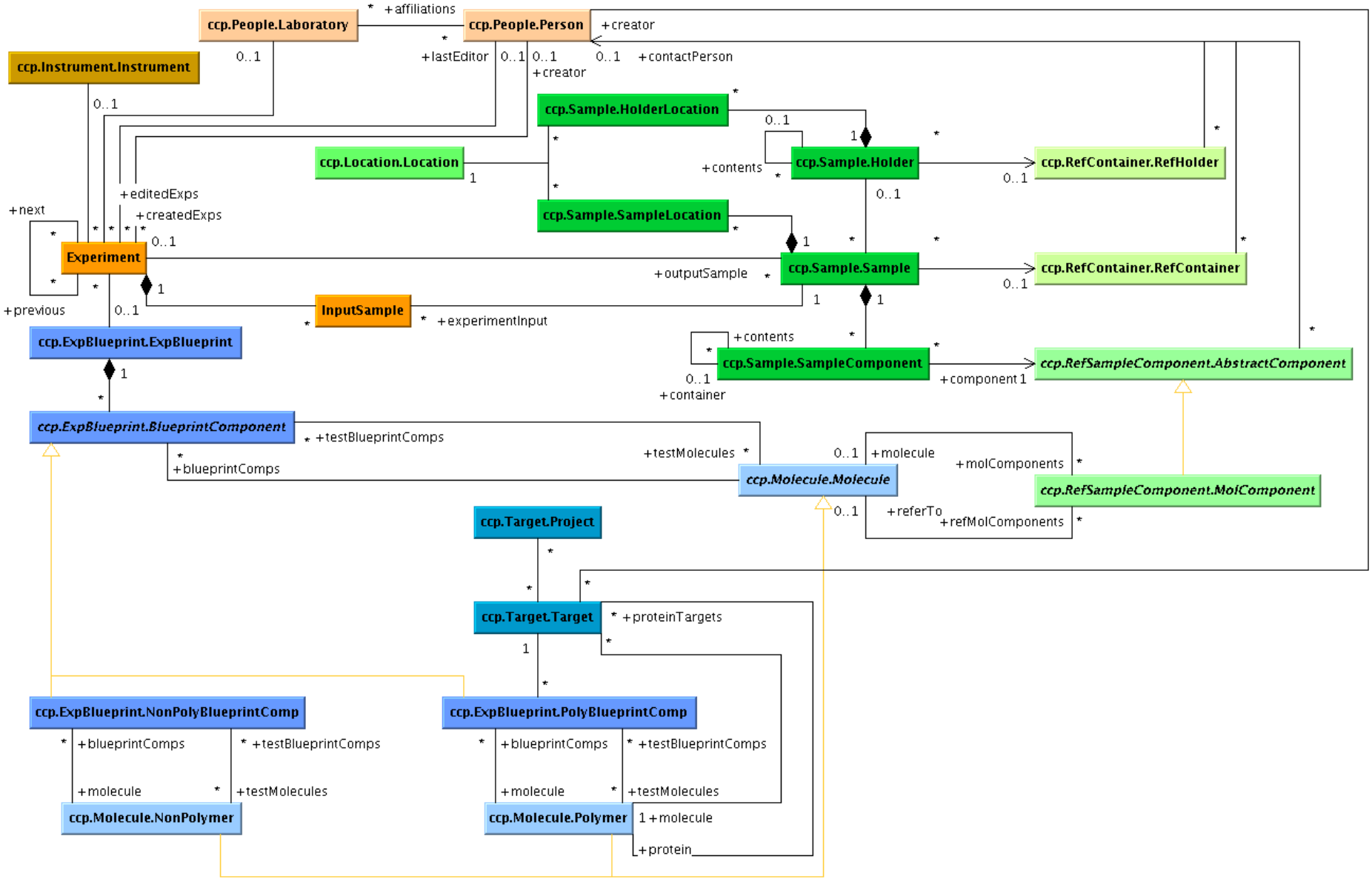
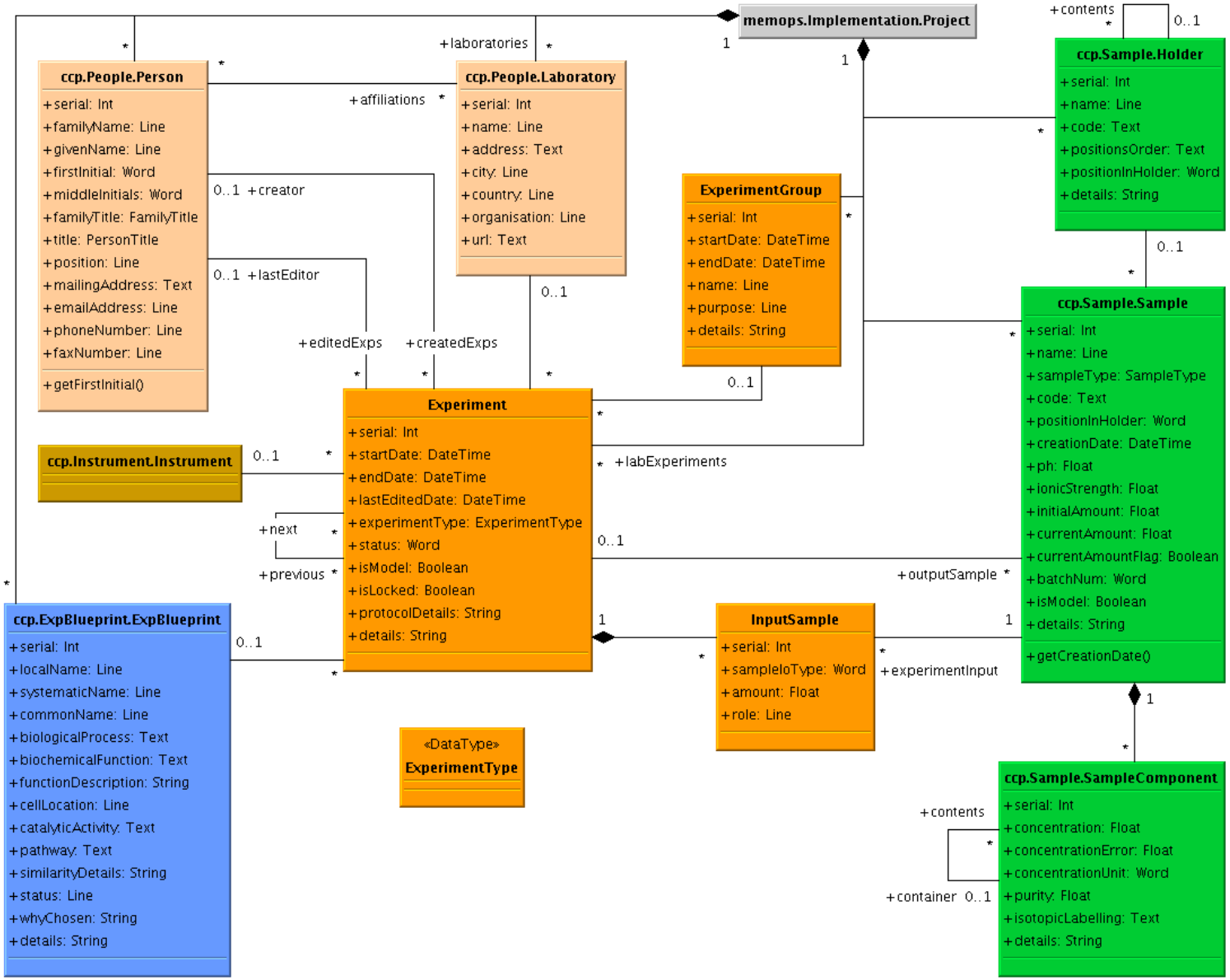
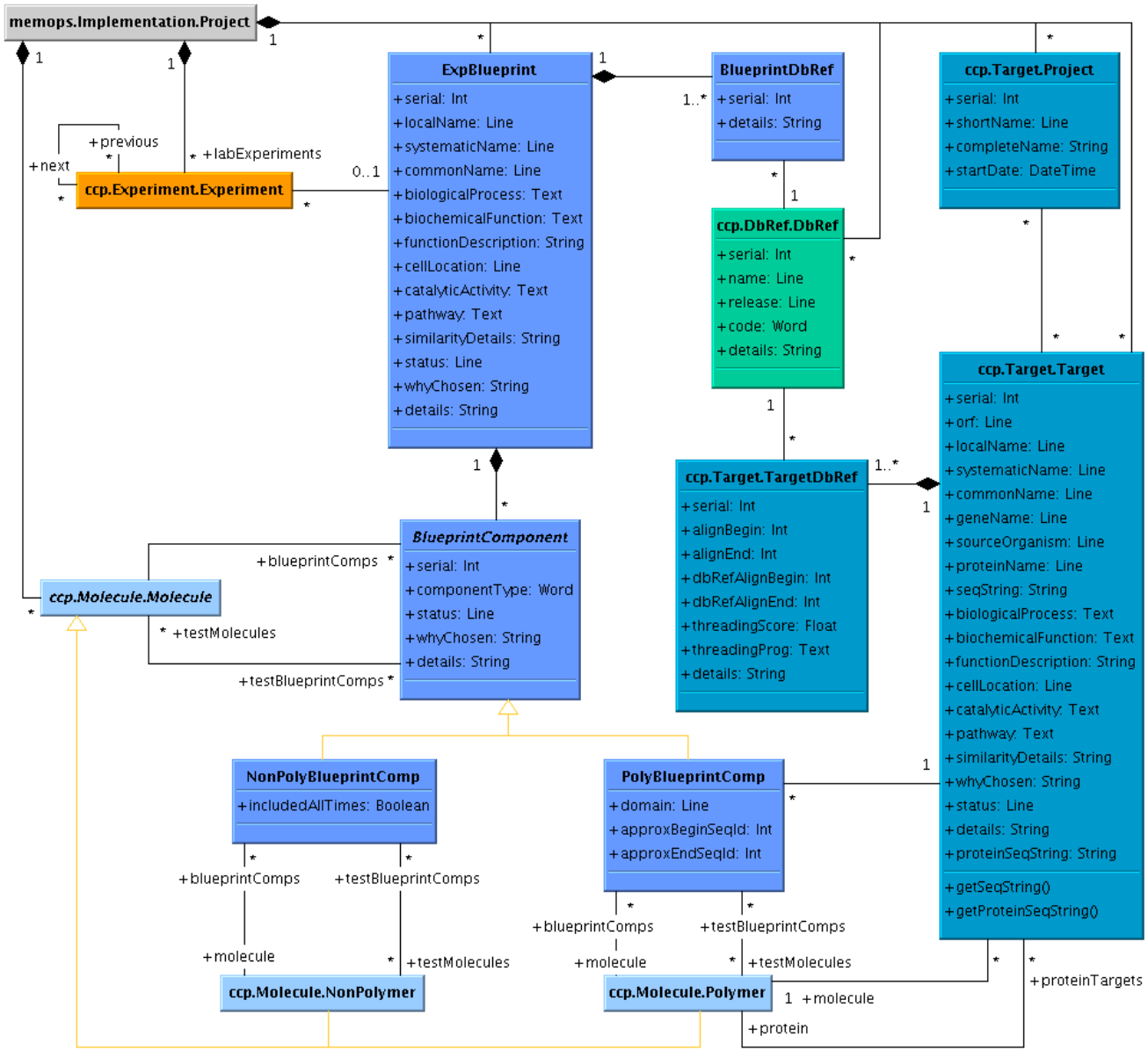
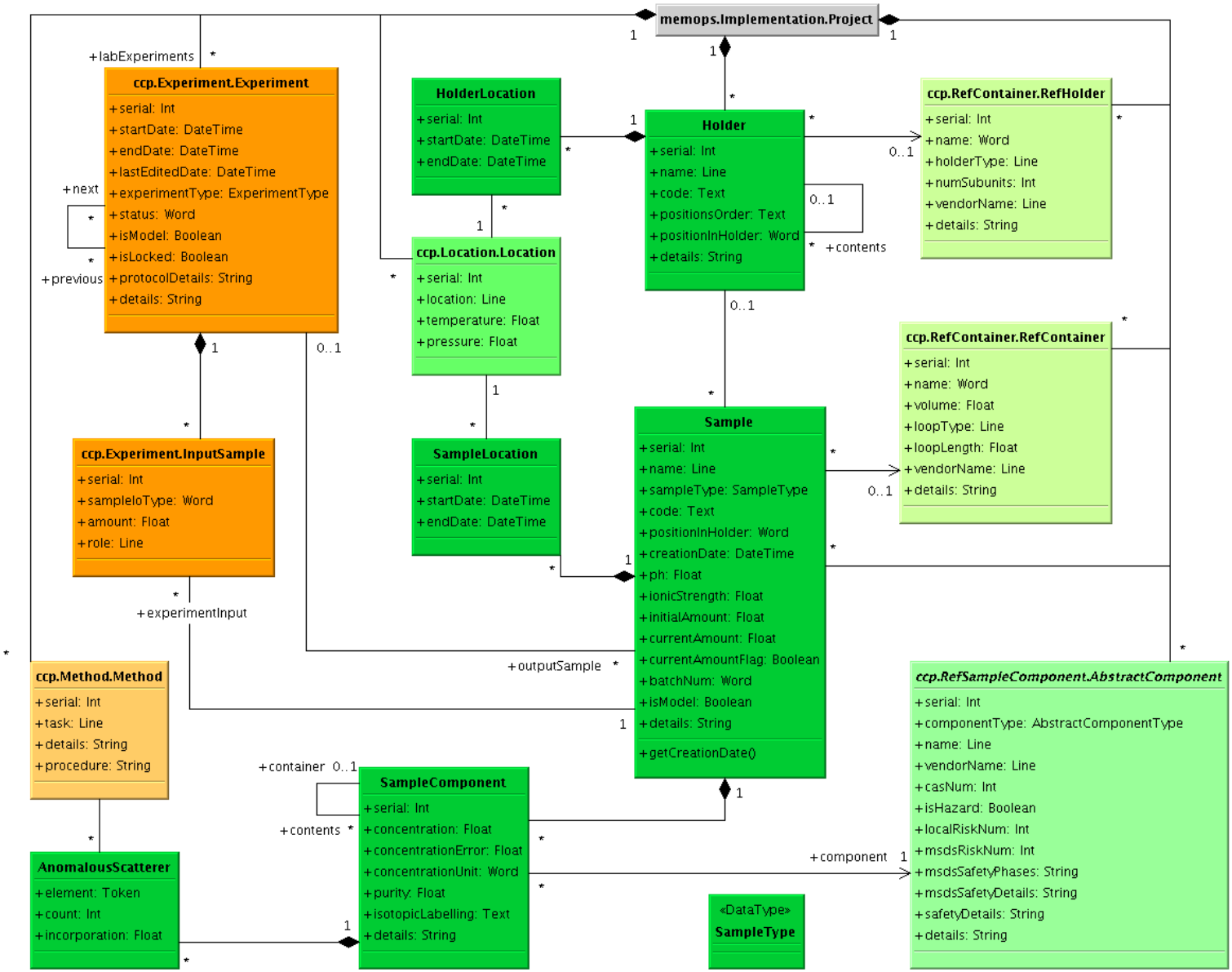
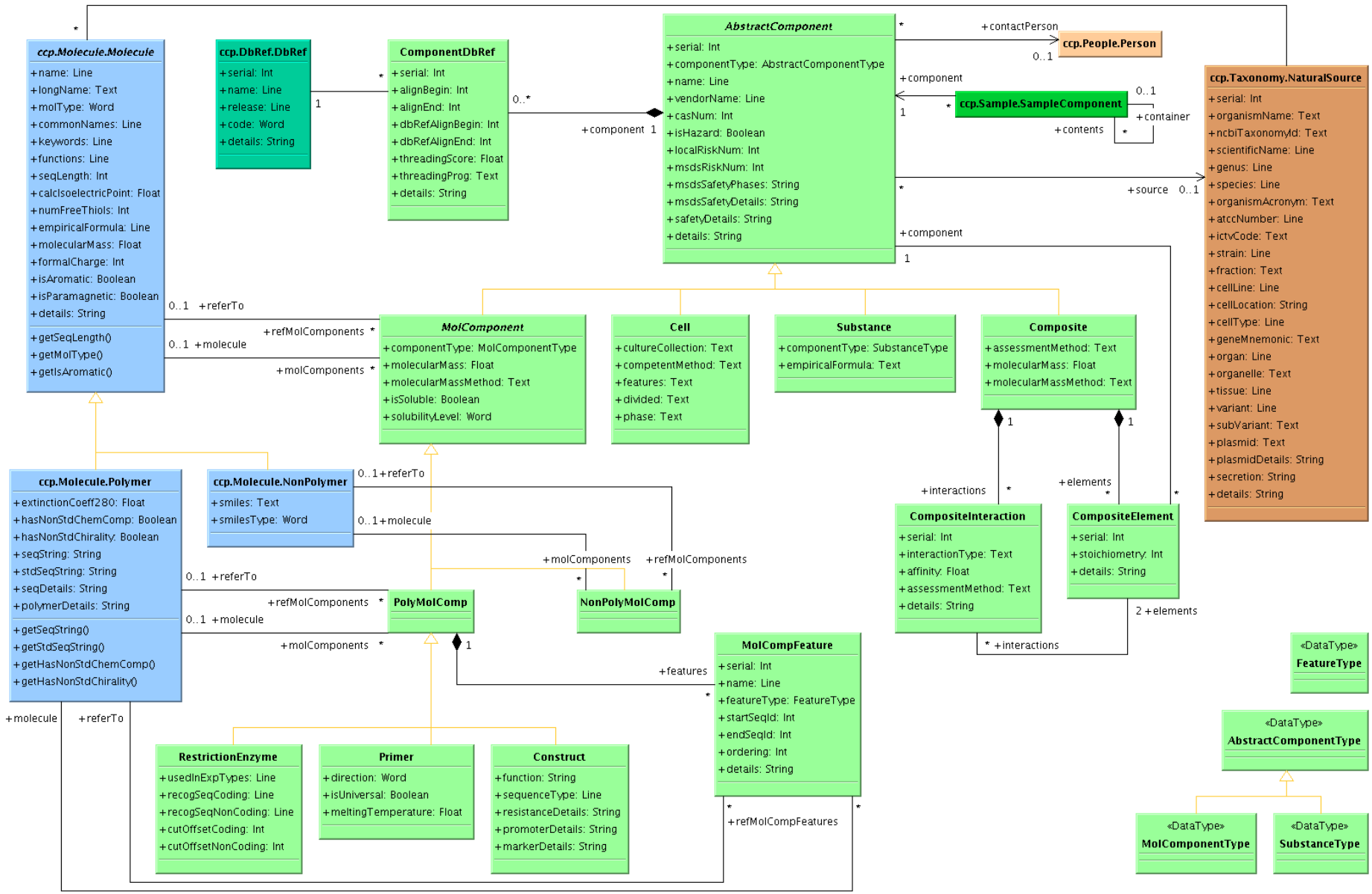
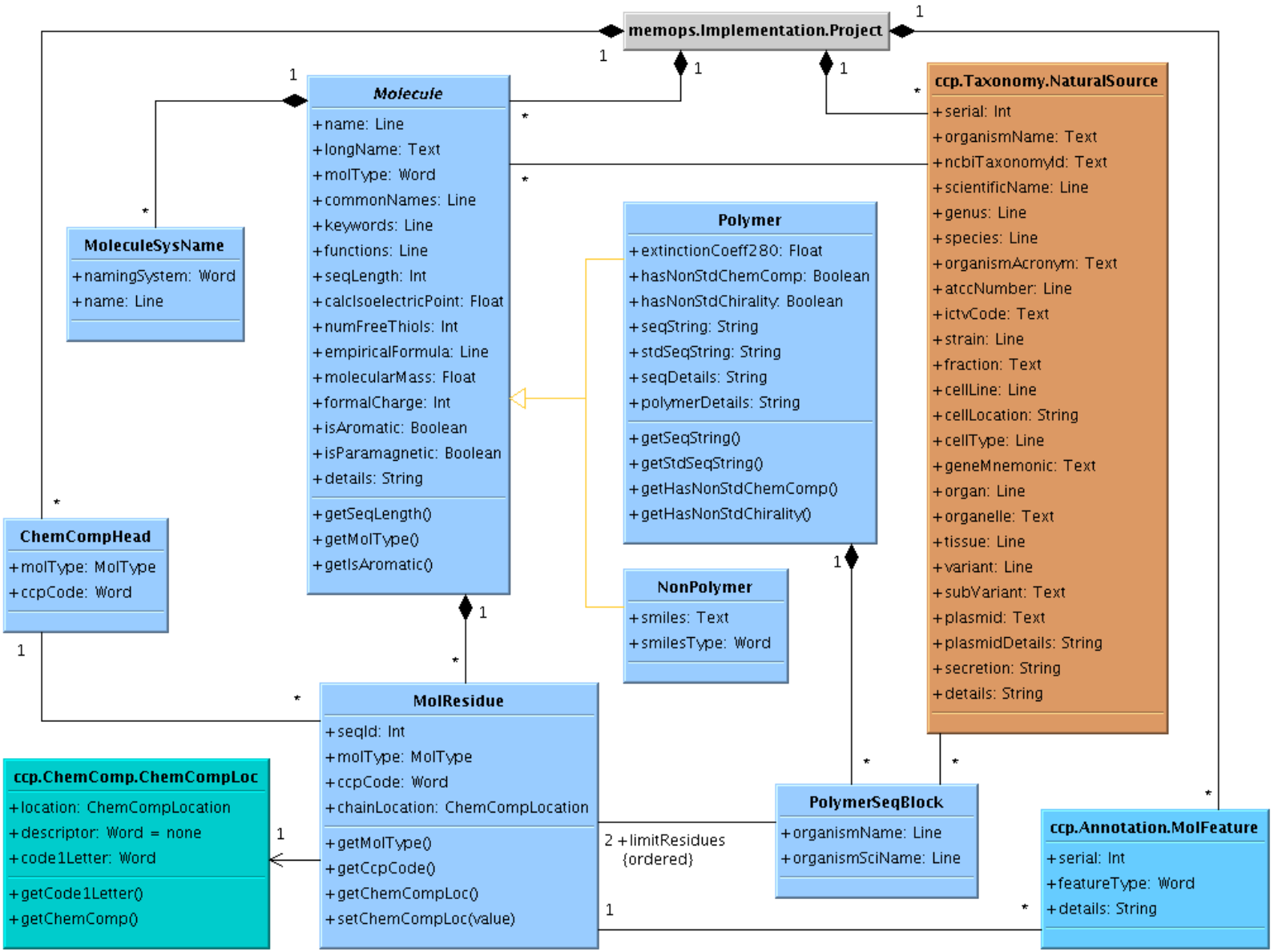

ccp.People.Laboratory
+affiliations
ccp.People.Person
+creator
ccp.Instrument.Instrument
+lastEditor
+contactPerson
ccp.Sample.HolderLocation
ccp.Location.Location
+contents
ccp.Sample.Holder
ccp.RefContainer.RefHolder
+editedExps
+createdExps
+next
ccp.Sample.SampleLocation
Experiment
+outputSample
ccp.Sample.Sample
ccp.RefContainer.RefContainer
+previous
InputSample
+experimentInput
ccp.ExpBlueprint.ExpBlueprint
+contents
ccp.Sample.SampleComponent
ccp.RefSampleComponent.AbstractComponent
+component
+container
ccp.ExpBlueprint.BlueprintComponent
+testBlueprintComps
+testMolecules
+molecule
+molComponents
+blueprintComps
ccp.Molecule.Molecule
ccp.RefSampleComponent.MolComponent
+referTo
+refMolComponents
ccp.Target.Project
ccp.Target.Target
+proteinTargets
ccp.ExpBlueprint.NonPolyBlueprintComp
ccp.ExpBlueprint.PolyBlueprintComp
+blueprintComps
+testBlueprintComps
+molecule
+testMolecules
ccp.Molecule.NonPolymer
ccp.Molecule.Polymer
+protein

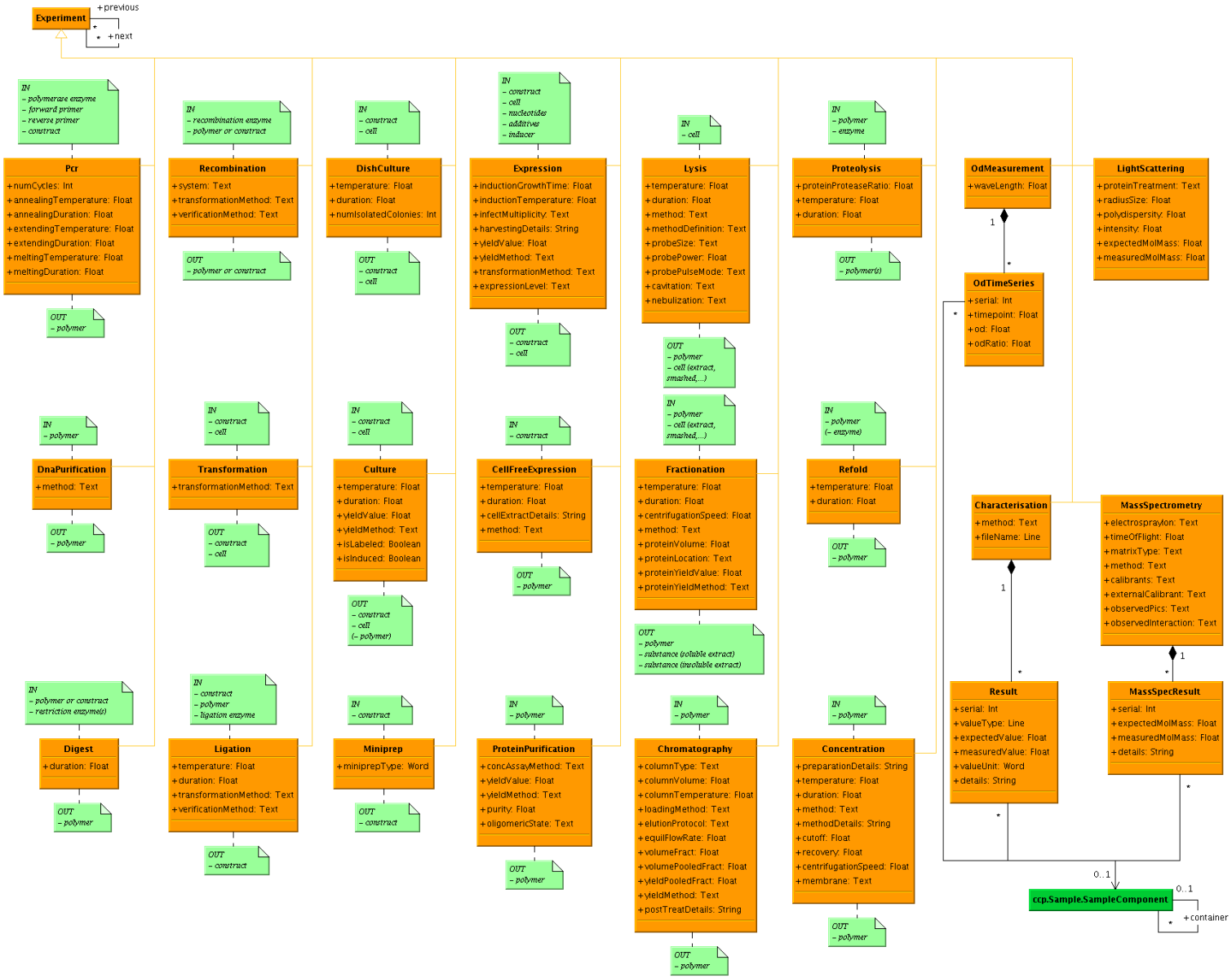

memops.Implementation.Project
ccp.People.Person
+serial: Int
+familyName: Line
+givenName: Line
+firstInitial: Word
+middleInitials: Word
+familyTitle: FamilyTitle
+title: PersonTitle
+position: Line
+mailingAddress: Text
+emailAddress: Line
+phoneNumber: Line
+faxNumber: Line
+getFirstInitial()
ccp.People.Laboratory
+serial: Int
+name: Line
+address: Text
+city: Line
+country: Line
+organisation: Line
+url: Text
+laboratories
+affiliations
0..1 +creator
0..1 +lastEditor
+editedExps
+createdExps
ccp.Sample.Holder
+serial: Int
+name: Line
+code: Text
+positionsOrder: Text
+positionInHolder: Word
+details: String
+contents
ExperimentGroup
+serial: Int
+startDate: DateTime
+endDate: DateTime
+name: Line
+purpose: Line
+details: String
ccp.Sample.Sample
+serial: Int
+name: Line
+sampleType: SampleType
+code: Text
+positionInHolder: Word
+creationDate: DateTime
+ph: Float
+ionicStrength: Float
+initialAmount: Float
+currentAmount: Float
+currentAmountFlag: Boolean
+batchNum: Word
+isModel: Boolean
+details: String
+getCreationDate()
Experiment
+serial: Int
+startDate: DateTime
+endDate: DateTime
+lastEditedDate: DateTime
+experimentType: ExperimentType
+status: Word
+isModel: Boolean
+isLocked: Boolean
+protocolDetails: String
+details: String
+labExperiments
ccp.Instrument.Instrument
+next
+previous
+outputSample
ccp.ExpBlueprint.ExpBlueprint
+serial: Int
+localName: Line
+systematicName: Line
+commonName: Line
+biologicalProcess: Text
+biochemicalFunction: Text
+functionDescription: String
+cellLocation: Line
+catalyticActivity: Text
+pathway: Text
+similarityDetails: String
+status: Line
+whyChosen: String
+details: String
InputSample
+serial: Int
+sampleIoType: Word
+amount: Float
+role: Line
+experimentInput
«DataType»
ExperimentType
ccp.Sample.SampleComponent
+serial: Int
+concentration: Float
+concentrationError: Float
+concentrationUnit: Word
+purity: Float
+isotopicLabelling: Text
+details: String
+contents
+container


memops.Implementation.Project
ExpBlueprint
+serial: Int
+localName: Line
+systematicName: Line
+commonName: Line
+biologicalProcess: Text
+biochemicalFunction: Text
+functionDescription: String
+cellLocation: Line
+catalyticActivity: Text
+pathway: Text
+similarityDetails: String
+status: Line
+whyChosen: String
+details: String
BlueprintDbRef
+serial: Int
+details: String
ccp.Target.Project
+serial: Int
+shortName: Line
+completeName: String
+startDate: DateTime
ccp.Experiment.Experiment
+previous
+next
+labExperiments
0..1
1..*
ccp.DbRef.DbRef
+serial: Int
+name: Line
+release: Line
+code: Word
+details: String
ccp.Target.Target
+serial: Int
+orf: Line
+localName: Line
+systematicName: Line
+commonName: Line
+geneName: Line
+sourceOrganism: Line
+proteinName: Line
+seqString: String
+biologicalProcess: Text
+biochemicalFunction: Text
+functionDescription: String
+cellLocation: Line
+catalyticActivity: Text
+pathway: Text
+similarityDetails: String
+whyChosen: String
+status: Line
+details: String
+proteinSeqString: String
+getSeqString()
+getProteinSeqString()
ccp.Target.TargetDbRef
+serial: Int
+alignBegin: Int
+alignEnd: Int
+dbRefAlignBegin: Int
+dbRefAlignEnd: Int
+threadingScore: Float
+threadingProg: Text
+details: String
BlueprintComponent
+serial: Int
+componentType: Word
+status: Line
+whyChosen: String
+details: String
+blueprintComps
+testMolecules
+testBlueprintComps
ccp.Molecule.Molecule
NonPolyBlueprintComp
+includedAllTimes: Boolean
PolyBlueprintComp
+domain: Line
+approxBeginSeqId: Int
+approxEndSeqId: Int
+molecule
+proteinTargets
+protein
ccp.Molecule.NonPolymer
ccp.Molecule.Polymer


memops.Implementation.Project
ccp.Experiment.Experiment
+serial: Int
+startDate: DateTime
+endDate: DateTime
+lastEditedDate: DateTime
+experimentType: ExperimentType
+status: Word
+isModel: Boolean
+isLocked: Boolean
+protocolDetails: String
+details: String
+labExperiments
+next
+previous
HolderLocation
+serial: Int
+startDate: DateTime
+endDate: DateTime
ccp.Location.Location
+serial: Int
+location: Line
+temperature: Float
+pressure: Float
Holder
+serial: Int
+name: Line
+code: Text
+positionsOrder: Text
+positionInHolder: Word
+details: String
+contents
ccp.RefContainer.RefHolder
+serial: Int
+name: Word
+holderType: Line
+numSubunits: Int
+vendorName: Line
+details: String
ccp.RefContainer.RefContainer
+serial: Int
+name: Word
+volume: Float
+loopType: Line
+loopLength: Float
+vendorName: Line
+details: String
ccp.Experiment.InputSample
+serial: Int
+sampleIoType: Word
+amount: Float
+role: Line
+experimentInput
SampleLocation
+serial: Int
+startDate: DateTime
+endDate: DateTime
Sample
+serial: Int
+name: Line
+sampleType: SampleType
+code: Text
+positionInHolder: Word
+creationDate: DateTime
+ph: Float
+ionicStrength: Float
+initialAmount: Float
+currentAmount: Float
+currentAmountFlag: Boolean
+batchNum: Word
+isModel: Boolean
+details: String
+getCreationDate()
+outputSample
ccp.Method.Method
+serial: Int
+task: Line
+details: String
+procedure: String
+container
+contents
SampleComponent
+serial: Int
+concentration: Float
+concentrationError: Float
+concentrationUnit: Word
+purity: Float
+isotopicLabelling: Text
+details: String
+component
ccp.RefSampleComponent.AbstractComponent
+serial: Int
+componentType: AbstractComponentType
+name: Line
+vendorName: Line
+casNum: Int
+isHazard: Boolean
+localRiskNum: Int
+msdsRiskNum: Int
+msdsSafetyPhases: String
+msdsSafetyDetails: String
+safetyDetails: String
+details: String
AnomalousScatterer
+element: Token
+count: Int
+incorporation: Float
«DataType»
SampleType


ccp.Molecule.Molecule
+name: Line
+longName: Text
+molType: Word
+commonNames: Line
+keywords: Line
+functions: Line
+seqLength: Int
+calcIsoelectricPoint: Float
+numFreeThiols: Int
+empiricalFormula: Line
+molecularMass: Float
+formalCharge: Int
+isAromatic: Boolean
+isParamagnetic: Boolean
+details: String
+getSeqLength()
+getMolType()
+getIsAromatic()
ccp.DbRef.DbRef
+serial: Int
+name: Line
+release: Line
+code: Word
+details: String
ComponentDbRef
+serial: Int
+alignBegin: Int
+alignEnd: Int
+dbRefAlignBegin: Int
+dbRefAlignEnd: Int
+threadingScore: Float
+threadingProg: Text
+details: String
AbstractComponent
+serial: Int
+componentType: AbstractComponentType
+name: Line
+vendorName: Line
+casNum: Int
+isHazard: Boolean
+localRiskNum: Int
+msdsRiskNum: Int
+msdsSafetyPhases: String
+msdsSafetyDetails: String
+safetyDetails: String
+details: String
+contactPerson
ccp.People.Person
+component
ccp.Sample.SampleComponent
+container
+contents
+source
ccp.Taxonomy.NaturalSource
+serial: Int
+organismName: Text
+ncbiTaxonomyId: Text
+scientificName: Line
+genus: Line
+species: Line
+organismAcronym: Text
+atccNumber: Line
+ictvCode: Text
+strain: Line
+fraction: Text
+cellLine: Line
+cellLocation: String
+cellType: Line
+geneMnemonic: Text
+organ: Line
+organelle: Text
+tissue: Line
+variant: Line
+subVariant: Text
+plasmid: Text
+plasmidDetails: String
+secretion: String
+details: String
+component
+referTo
+refMolComponents
+molecule
+molComponents
MolComponent
+componentType: MolComponentType
+molecularMass: Float
+molecularMassMethod: Text
+isSoluble: Boolean
+solubilityLevel: Word
Cell
+cultureCollection: Text
+competentMethod: Text
+features: Text
+divided: Text
+phase: Text
Substance
+componentType: SubstanceType
+empiricalFormula: Text
Composite
+assessmentMethod: Text
+molecularMass: Float
+molecularMassMethod: Text
+interactions
+elements
CompositeInteraction
+serial: Int
+interactionType: Text
+affinity: Float
+assessmentMethod: Text
+details: String
CompositeElement
+serial: Int
+stoichiometry: Int
+details: String
2 +elements
+interactions
ccp.Molecule.Polymer
+extinctionCoeff280: Float
+hasNonStdChemComp: Boolean
+hasNonStdChirality: Boolean
+seqString: String
+stdSeqString: String
+seqDetails: String
+polymerDetails: String
+getSeqString()
+getStdSeqString()
+getHasNonStdChemComp()
+getHasNonStdChirality()
ccp.Molecule.NonPolymer
+smiles: Text
+smilesType: Word
PolyMolComp
NonPolyMolComp
+features
MolCompFeature
+serial: Int
+name: Line
+featureType: FeatureType
+startSeqId: Int
+endSeqId: Int
+ordering: Int
+details: String
+refMolCompFeatures
+molecule
+referTo
RestrictionEnzyme
+usedInExpTypes: Line
+recogSeqCoding: Line
+recogSeqNonCoding: Line
+cutOffsetCoding: Int
+cutOffsetNonCoding: Int
Primer
+direction: Word
+isUniversal: Boolean
+meltingTemperature: Float
Construct
+function: String
+sequenceType: Line
+resistanceDetails: String
+promoterDetails: String
+markerDetails: String
«DataType»
FeatureType
«DataType»
AbstractComponentType
«DataType»
MolComponentType
«DataType»
SubstanceType


memops.Implementation.Project
Molecule
+name: Line
+longName: Text
+molType: Word
+commonNames: Line
+keywords: Line
+functions: Line
+seqLength: Int
+calcIsoelectricPoint: Float
+numFreeThiols: Int
+empiricalFormula: Line
+molecularMass: Float
+formalCharge: Int
+isAromatic: Boolean
+isParamagnetic: Boolean
+details: String
+getSeqLength()
+getMolType()
+getIsAromatic()
ccp.Taxonomy.NaturalSource
+serial: Int
+organismName: Text
+ncbiTaxonomyId: Text
+scientificName: Line
+genus: Line
+species: Line
+organismAcronym: Text
+atccNumber: Line
+ictvCode: Text
+strain: Line
+fraction: Text
+cellLine: Line
+cellLocation: String
+cellType: Line
+geneMnemonic: Text
+organ: Line
+organelle: Text
+tissue: Line
+variant: Line
+subVariant: Text
+plasmid: Text
+plasmidDetails: String
+secretion: String
+details: String
MoleculeSysName
+namingSystem: Word
+name: Line
Polymer
+extinctionCoeff280: Float
+hasNonStdChemComp: Boolean
+hasNonStdChirality: Boolean
+seqString: String
+stdSeqString: String
+seqDetails: String
+polymerDetails: String
+getSeqString()
+getStdSeqString()
+getHasNonStdChemComp()
+getHasNonStdChirality()
NonPolymer
+smiles: Text
+smilesType: Word
ChemCompHead
+molType: MolType
+ccpCode: Word
MolResidue
+seqId: Int
+molType: MolType
+ccpCode: Word
+chainLocation: ChemCompLocation
+getMolType()
+getCcpCode()
+getChemCompLoc()
+setChemCompLoc(value)
ccp.ChemComp.ChemCompLoc
+location: ChemCompLocation
+descriptor: Word = none
+code1Letter: Word
+getCode1Letter()
+getChemComp()
PolymerSeqBlock
+organismName: Line
+organismSciName: Line
2 +limitResidues
{ordered}
ccp.Annotation.MolFeature
+serial: Int
+featureType: Word
+details: String


Experiment
+previous
+next
Pcr
+numCycles: Int
+annealingTemperature: Float
+annealingDuration: Float
+extendingTemperature: Float
+extendingDuration: Float
+meltingTemperature: Float
+meltingDuration: Float
IN – polymerase enzyme – forward primer – reverse primer – construct
OUT – polymer
Recombination
+system: Text
+transformationMethod: Text
+verificationMethod: Text
IN – recombination enzyme – polymer or construct
OUT – polymer or construct
DishCulture
+temperature: Float
+duration: Float
+numIsolatedColonies: Int
IN – construct – cell
OUT – construct – cell
Expression
+inductionGrowthTime: Float
+inductionTemperature: Float
+infectMultiplicity: Text
+harvestingDetails: String
+yieldValue: Float
+yieldMethod: Text
+transformationMethod: Text
+expressionLevel: Text
IN – construct – cell – nucleotides – additives – inducer
OUT – construct – cell
Lysis
+temperature: Float
+duration: Float
+method: Text
+methodDefinition: Text
+probeSize: Text
+probePower: Float
+probePulseMode: Text
+cavitation: Text
+nebulization: Text
IN – cell
OUT – polymer – cell (extract, smashed,...)
Proteolysis
+proteinProteaseRatio: Float
+temperature: Float
+duration: Float
IN – polymer – enzyme
OUT – polymer(s)
OdMeasurement
+waveLength: Float
OdTimeSeries
+serial: Int
+timepoint: Float
+od: Float
+odRatio: Float
LightScattering
+proteinTreatment: Text
+radiusSize: Float
+polydispersity: Float
+intensity: Float
+expectedMolMass: Float
+measuredMolMass: Float
DnaPurification
+method: Text
IN – polymer
OUT – polymer
Transformation
+transformationMethod: Text
IN – construct – cell
OUT – construct – cell
Culture
+temperature: Float
+duration: Float
+yieldValue: Float
+yieldMethod: Text
+isLabeled: Boolean
+isInduced: Boolean
IN – construct – cell
OUT – construct – cell (– polymer)
CellFreeExpression
+temperature: Float
+duration: Float
+cellExtractDetails: String
+method: Text
IN – construct
OUT – polymer
Fractionation
+temperature: Float
+duration: Float
+centrifugationSpeed: Float
+method: Text
+proteinVolume: Float
+proteinLocation: Text
+proteinYieldValue: Float
+proteinYieldMethod: Text
IN – polymer – cell (extract, smashed,...)
OUT – polymer – substance (soluble extract) – substance (insoluble extract)
Refold
+temperature: Float
+duration: Float
IN – polymer (– enzyme)
OUT – polymer
Characterisation
+method: Text
+fileName: Line
MassSpectrometry
+electrospraylon: Text
+timeOfFlight: Float
+matrixType: Text
+method: Text
+calibrants: Text
+externalCalibrant: Text
+observedPics: Text
+observedInteraction: Text
Digest
+duration: Float
IN – polymer or construct – restriction enzyme(s)
OUT – polymer
Ligation
+temperature: Float
+duration: Float
+transformationMethod: Text
+verificationMethod: Text
IN – construct – polymer – ligation enzyme
OUT – construct
Miniprep
+miniprepType: Word
IN – construct
OUT – construct
ProteinPurification
+concAssayMethod: Text
+yieldValue: Float
+yieldMethod: Text
+purity: Float
+oligomericState: Text
IN – polymer
OUT – polymer
Chromatography
+columnType: Text
+columnVolume: Float
+columnTemperature: Float
+loadingMethod: Text
+elutionProtocol: Text
+equilFlowRate: Float
+volumeFract: Float
+volumePooledFract: Float
+yieldPooledFract: Float
+yieldMethod: Text
+postTreatDetails: String
IN – polymer
OUT – polymer
Concentration
+preparationDetails: String
+temperature: Float
+duration: Float
+method: Text
+methodDetails: String
+cutoff: Float
+recovery: Float
+centrifugationSpeed: Float
+membrane: Text
IN – polymer
OUT – polymer
Result
+serial: Int
+valueType: Line
+expectedValue: Float
+measuredValue: Float
+valueUnit: Word
+details: String
MassSpecResult
+serial: Int
+expectedMolMass: Float
+measuredMolMass: Float
+details: String
ccp.Sample.SampleComponent
+container
0..1
1
*