# **GeneOntolo**

```
-goID: string = go:0005739
```

-goTerm: string = mitochondrion

-goAspect: char = C

+proteinGOAnnotations: list = Pi

gy

roteinGOAnnotation.id

eOntology

# **KEGGB**thw

```
-keggID: string = path:hsa00232
```

-keggName: string = Caffeine met

-annotedProteins: foreign key =



KEGG 0..N



abolism ProteinKEGGAnnotation

G

Annotation

S	V	n	0	n	V
	7		_		_

nation /naimonal forcion

mGeneSyr	mbol
----------	------

Y 1 G0Ar 0..N

# **ProteinGQ**nnot

-protein: foreign key = pr
-go: foreign key = GeneOnt
-evidenceCode: string = IE

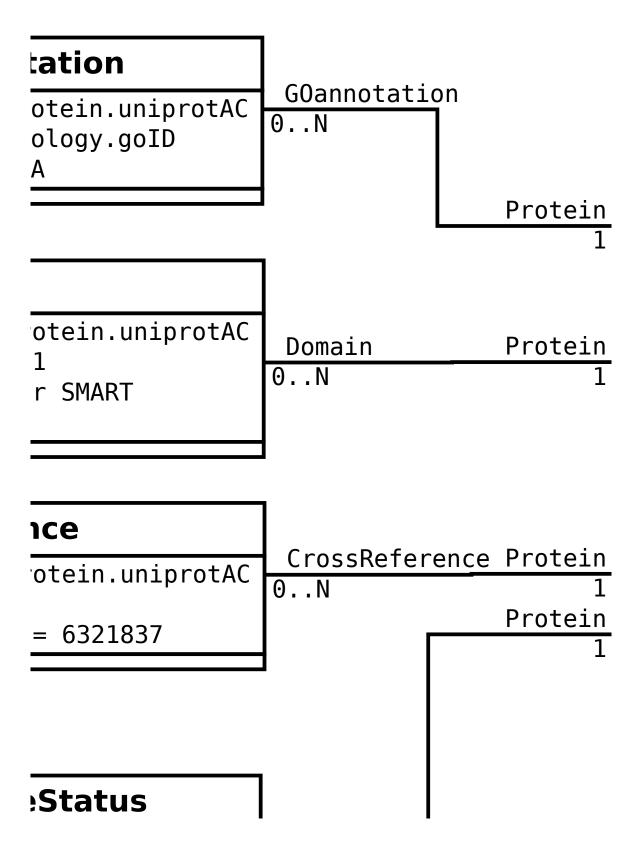
#### **ProteinDomain**

```
-protein (primary): foreign key = Pr
-domainID (primary): string = PF0007
-sourceDB (primary): string = Pfam o
-domainName: string = Ras
```

#### **ProteinCrossReferer**

```
-protein (primary): foreign key = Pr
-sourceDB (primary): string = GI
-crossReferenceID (primary): string
```

inotation



#### **ProteinKEGGAnn**

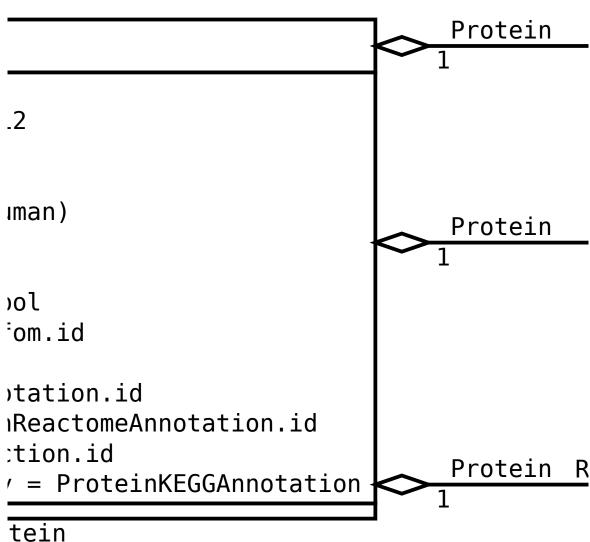
```
-protein: foreign key = Protε-crossReferenceID: string = h-keggPathway: foreign key = k
```

KEGG 0..N Pro 1

## **Protein**

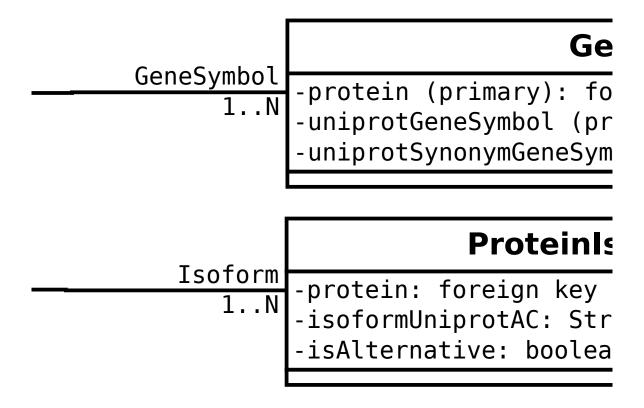
- -dbSource: string = sp or tr
- -uniprotAC (primary): string = P0111
- -uniprotID: string = RASH HUMAN
- -uniprotName: string = GTPase HRas
- -organism: string = Homo Sapiens (Hu
- -proteinLength: int = 199
- -idFragment: boolean = False
- -uniprotGeneSymbols: list = GeneSymb
- -uniprotIsoforms: list = ProteinIsof
- -domains: list = ProteinDomain.id
- -goAnnotations: list = ProteinGOAnno
- -reactomeAnnotations: list = Protein
- -interactions: list = ProteinInterac
- -keggPathwayAnnotations: foreign key

# otation in.uniprotAC isa:10 (EGGPathway.keggID Annotation tein



ProteinNetworkModule

```
-protein (primary): toreign r
-geneSymbol (primary): foreiq
-uniprotSynonymGeneSymbol (pr
```



# eactomeAnnotation

#### **ProteinReacto**

-protein: foreign key -reactome: foreign key key = GeneSymbol.protein\_ia
jn key = GeneSymbol.uniprotGeneSymbol
rimary): String = HSF2L

Synonym 0..N GeneSymbol 1

# neSymbol

reign key = Protein.uniprotAC

imary): String = HSFY1

bols: list = SynonymGeneSymbol

#### soform

= Protein.uniprotAC
ing = P01112-2
n = False

#### meAnnotation

- = Protein.uniprotAC
- = Reactome.reactomeID

ReactomeAnnotation
0..N
Reactome

-tableName: String-tableStatus: Stri-tableSource: Stri

-interactor/ -interactor/ -detectionMe -pubmedID: s -interactior -sourceDB: s -confidences

```
= <class name>
ng = error/ok
ng = <filename>
```

Interaction
0..N

#### **ProteinInteraction**

```
A: foreign key = protein.uniprotAC
3: foreign key = protein.uniprotAC
2thod: string = psi-mi:'MI:0006' (anti bastring = pubmed:1323411
1Type: string = psi-mi:'MI:0915' (physicastring = Intact
5core: string = 0.95
```

Interaction
1..N

Network
1

### **PPINetwork**

-Name (primary): string = Cocomplex

-protein (primary -networkModule (p

ait coimmunoprecipitation)

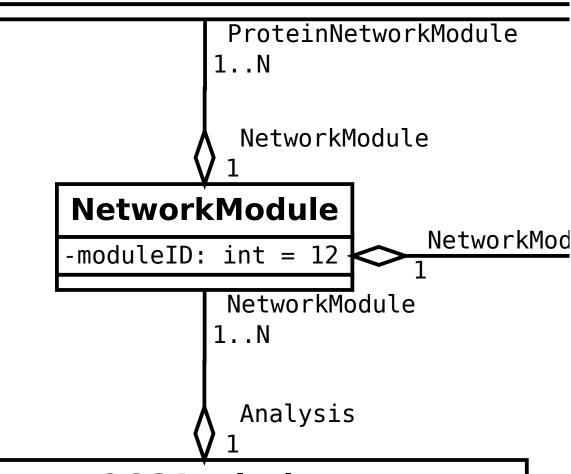
al association)

-alpha: -networ

Network PartitionAnaly

#### **ProteinNetworkModule**

/): foreign key = Protein.uniprotAC
primary): foreign\_key = NetworkModule.mod



# **OCGAnalysis**

float = 1.3 kModules: list = Table NetworkModule

**PrtitionAnalysis PrtitionAnalysis** 

duleID	

### Reac

-reactomeID: string = REACT\_27

-reactomeName: string = mycoth

-proteinAnnotations: list = Ta

#### lule Annotation

# NetworkMo

-networkModule: forein annotationName: String



#### tome

7106 niol metabolism able ProteinReactomeAnnotation

# duleAnnotation