

**Proteins**

**proteinsUniprot**

- uniProtID CHAR(15)
- entryName VARCHAR(45)
- reviewed TINYINT(1)
- proteinName MEDIUMTEXT
- alternateNames JSON
- geneNamePreferred VARCHAR(45)
- geneNamesAlternative JSON
- geneNamesAll JSON
- interactsWith JSON
- taxid INT
- organism VARCHAR(100)
- 6 more...

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**meropsSubsUniprot**

- uniProtID CHAR(15)
- entryName VARCHAR(45)
- geneNamePreferred VARCHAR(45)
- geneNamesAlternative JSON
- taxid INT
- organism VARCHAR(100)

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**Structures & Drugs**

**uniprotPdbJoin**

- uniProtID CHAR(15)
- pdbID CHAR(5)
- chain VARCHAR(25)

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**pdb**

- pdbID CHAR(5)
- method VARCHAR(45)

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**pdbDrugBank**

- pdbID CHAR(5)
- drugBankID CHAR(15)
- drugShort CHAR(5)
- drugLong VARCHAR(256)

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**pdbBindingSites**

- pdbID CHAR(5)
- siteID CHAR(5)
- structResidNum INT
- uniprotResidNum INT
- residue CHAR(12)
- residChain CHAR(2)
- ligandResidNum INT
- ligandShort CHAR(5)
- 2 more...

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**Neo4j Graph**

**Node From**

- Protein Properties ...
- From UniProt & ...
- Substrate DBs ...

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**Edge (Interaction)**

- Interaction Properties ...
- From Substrate DBs ...

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**Node To**

- Protein Properties ...
- From UniProt & ...
- Substrate DBs ...

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**Interface**

**PDBs, Drugs, Binding Sites**

- MySQL Query of ...
- UniProt ID Submitted ...
- to Graph ...

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**Graph & Graph Table**

- Cypher Query of Neo4j DB ...
- From R to Interface ...

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**SQL Interface**

- Submit MySQL Query ...
- All Tables & Columns ...

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**Substrate Databases**

**Substrate\_search**

- cleavageID VARCHAR(10)
- code VARCHAR(8)
- Substrate\_name VARCHAR(128)
- Substrate\_formula VARCHAR(250)
- Site\_P4 VARCHAR(64)
- Site\_P3 VARCHAR(64)
- Site\_P2 VARCHAR(64)
- Site\_P1 VARCHAR(65)
- Site\_P1prime VARCHAR(64)
- Site\_P2prime VARCHAR(64)
- Site\_P3prime VARCHAR(64)
- Site\_P4prime VARCHAR(64)
- Ref VARCHAR(55)
- Uniprot VARCHAR(45)
- 11 more...

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**depodPhosphatase**

- uniProtIDPPase CHAR(15)
- geneNamePreferredPPase VARCHAR(45)
- ppaseTaxid INT
- ppaseOrganism VARCHAR(45)
- uniProtIDSub CHAR(15)
- geneNamePreferredSub VARCHAR(45)
- subTaxid INT
- subOrganism VARCHAR(45)
- subDephosphoSites VARCHAR(256)
- sitePlusMinus5AA VARCHAR(256)
- inVivo TINYINT(1)
- inVivo TINYINT(1)
- literature VARCHAR(256)
- reliabilityScore INT

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**kinasePhosphoSitePlus**

- uniProtIDKin CHAR(15)
- geneNamePreferredKin VARCHAR(45)
- kinTaxid INT
- kinOrganism VARCHAR(45)
- uniProtIDSub CHAR(15)
- geneNamePreferredSub VARCHAR(45)
- geneNameAltSub VARCHAR(45)
- subTaxid INT
- subOrganism VARCHAR(45)
- subModSite CHAR(10)
- sitePlusMinus7AA CHAR(20)
- inVivo TINYINT(1)
- inVivo TINYINT(1)

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**intact**

- interactionID CHAR(15)
- interactorA VARCHAR(25)
- interactorB VARCHAR(25)
- geneNamePreferredA MEDIUMTEXT
- geneNamePreferredB MEDIUMTEXT
- alternateNamesA JSON
- alternateNamesB JSON
- geneNamesAlternativeA JSON
- geneNamesAlternativeB JSON
- taxidA INT
- taxidB INT
- organismA VARCHAR(100)
- organismB VARCHAR(100)
- detectionMethod TINYTEXT
- 7 more...

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