MAIN DATA

- SLiMFinder results (per dataset)
- Occurrences
- Pairwise PPI
- Domain PPI
- ID Mapping
- (Sequence file)

CompariMotif
GO : Gene

GO : GO

~~Class~~ SLIM (Pattern)
- ~~GO~~ Gene Hubs
- Hub - Domain Hubs
  - Random (Hubs)
  - Spokes

} Lists linking to pages

- GO x 3
- Hub Dataset → Results
- ~~Spoke~~ Gene → Occurrences
- CompariMotif → CompariMotif
- ~~Interface~~ Interactome (?) → ~~Hubs~~ & ~~Spokes~~ connected (DATASETS)
- UniFab (?) = Hub

GENE
- GO
- Hub (SF & Occ)
- Spoke
- Interactors
- Domains
- Interactome
- UPC (Hub)
- UniFab (Hub)
- RSet
- RUPC

GO (DATASET)
- Relationships
- Genes
- Domains
- Hubs
- Spokes
- SLiMs

} Lists

(+ Results as dataset)

DOMAIN
- GO
- Hub (SF & Occ)
- Genes (Hub)
- Interactors

RANDOM (DATASET) x 2
- Genes / Patterns
- Dataset (Hub) → Results
- ~~Spoke~~ → Occurrences

SLiMFinder - (Main) Results table = Dataset-level results

- RunID
- ~~Analysis~~ - parent run
- Dataset - dataset name
- Type - type of "hub" used to make dataset
- Pattern - returned SLiM predicted

} Fudge this to work.

(Main) Occurrence table = Protein-level results
- RunID
- Dataset
- Pattern
- ~~Pos~~ Seq
- StartPos
- EndPos

PAPER
Paper
RunID

DATASETS
- ~~Hub~~ Dataset
- ~~Spoke~~ Gene
- Type
- ~~Species~~

NEW
- ~~Seq~~ / ~~Gene~~
- Gene
- Species

Pairwise PPI Table
- Hub
- Spoke

Domain PPI
- Domain
- Spoke

ID Mapping Table = linking to external sites via Gene
- Gene
- ~~EnsLoci~~

GO Mapping
Gene
GOID

GO Relationship
- GOID 1
- GOID 2
- Relationship

GO
GOID
...

CompariMotif
Pattern
...