



Interacts With

Surface Structure

The "active" system; the results obtained from and the processing carried out querying and manipulating rules

- Relationships calculated by the system from middle structure: "RPS1 is-a Molecule," derived from transitive chaining of "RPS1 is-a Protein" and "Protein is-a Molecule"
- Computation of Location relationships: overlapping genomic coordinates, location of test tubes in freezers, etc.
- Presentation of user interface elements
- Translation of RNA to protein sequence, etc.

Generate

Animation Procedures

- Read and manipulate rules
- Logical Deduction
 - Location Computation
 - RNA Translation, etc.

Middle Structure

- Contents of database tables; the "laws" of the system.
- Define entities, relationships, semantic networks, events, attributes, etc.; all the "things" and data the system should know about
- Define meta-rules that influence how rules are read and processed (e.g., how to perform logical deductions, location-based calculations)

Resource	Subject	Relationship	Object
IUPAC	Serine	is-a	Amino Acid
GFS Output #5	Precursor Ion 234	theoretically-derived-from	Peptide YRTSYK
NCBI Taxonomy	E. coli	genus	Escherichia

Drives

Constrains

Deep Structure

- Database tables, generally less than 50 total.
- Represent fundamental concepts and define syntax constraints for middle structure rules

