Pathway Tools Schema and Semantic Inference Layer

Compounds, Reactions, Proteins and RNAs

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References

- **Pathway Tools User's Guide, Volume I**
  - Appendix A: Guide to the Pathway Tools Schema
- **Ontology Papers section of http://biocyc.org/publications.shtml**
  - "An Evidence Ontology for use in Pathway/Genome Databases,"
  - "An ontology for biological function based on molecular interactions,"
  - "Representations of metabolic knowledge: Pathways,"
  - "Representations of metabolic knowledge,"

Use GKB Editor to Inspect the Pathway Tools Ontology

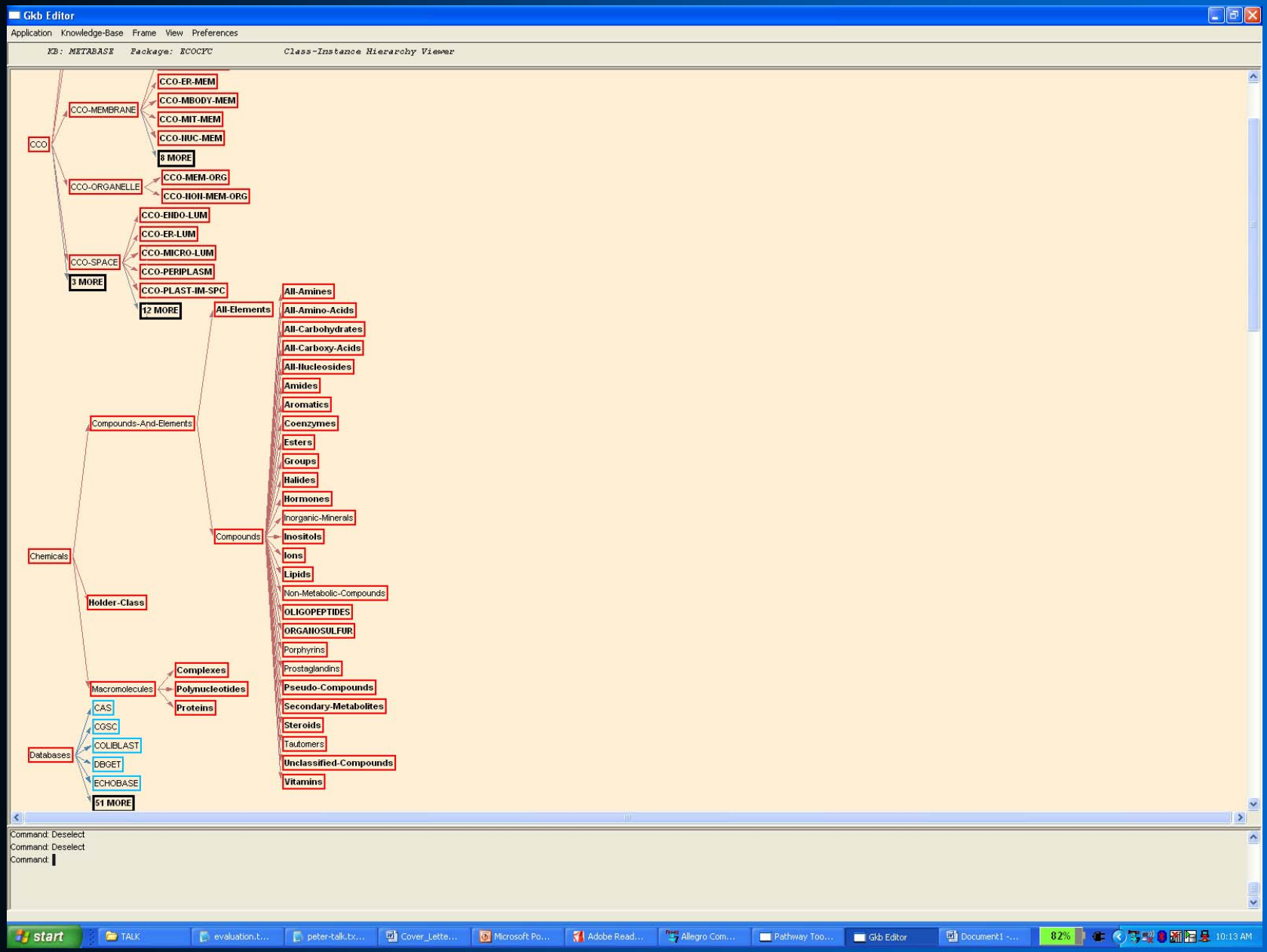
- **GKB Editor = Generic Knowledge Base Editor**
- **Type in Navigator window: (GKB) or**
- **[Right-Click] Edit->Ontology Editor**

- **View->Browse Class Hierarchy**
- **[Middle-Click] to expand hierarchy**
- **To view classes or instances, select them and:**
  - Frame -> List Frame Contents
  - Frame -> Edit Frame

Slots

- **Describe an attribute or a property of the object that the frame represents.**
  - Slots valid in only a particular set of classes
  - Slots valid in multiple classes
    - Common-Name
      - Primary name by which an on object is known
    - Synonyms
      - Names by which one may attempt to retrieve this object
    - Names
      - Values combined from all other name related slots
    - Comment
      - Stores the general comment about the object
    - Citations
      - Lists general citations pertaining to the object.
    - Database links
      - Links to variety of other databases

Compounds



SRI International Bioinformatics

BioCyc Database Collection

Compounds

- **Very few things come from within the compound editor**
  - MW, formula calculated from edited structure
- **Most traits defined in other editors**
  - “In pathway reactions” comes from reaction editing followed by pathway editing
  - activator, etc come from the enzymatic reaction editor

-- Instance TRP ---

Types: |Amino-Acid|, |Aromatic-Amino-Acids|, |Non-polar-amino-acids|

APPEARS-IN-LEFT-SIDE-OF: RXN0-287, TRANS-RXN-76, TRYPTOPHAN-RXN, TRYPTOPHAN--TRNA-LIGASE-RXN

APPEARS-IN-RIGHT-SIDE-OF: RXN0-2382, RXN0-301, TRANS-RXN-76, TRYPSYN-RXN

CHEMICAL-FORMULA: (C 11), (H 12), (N 2), (O 2)

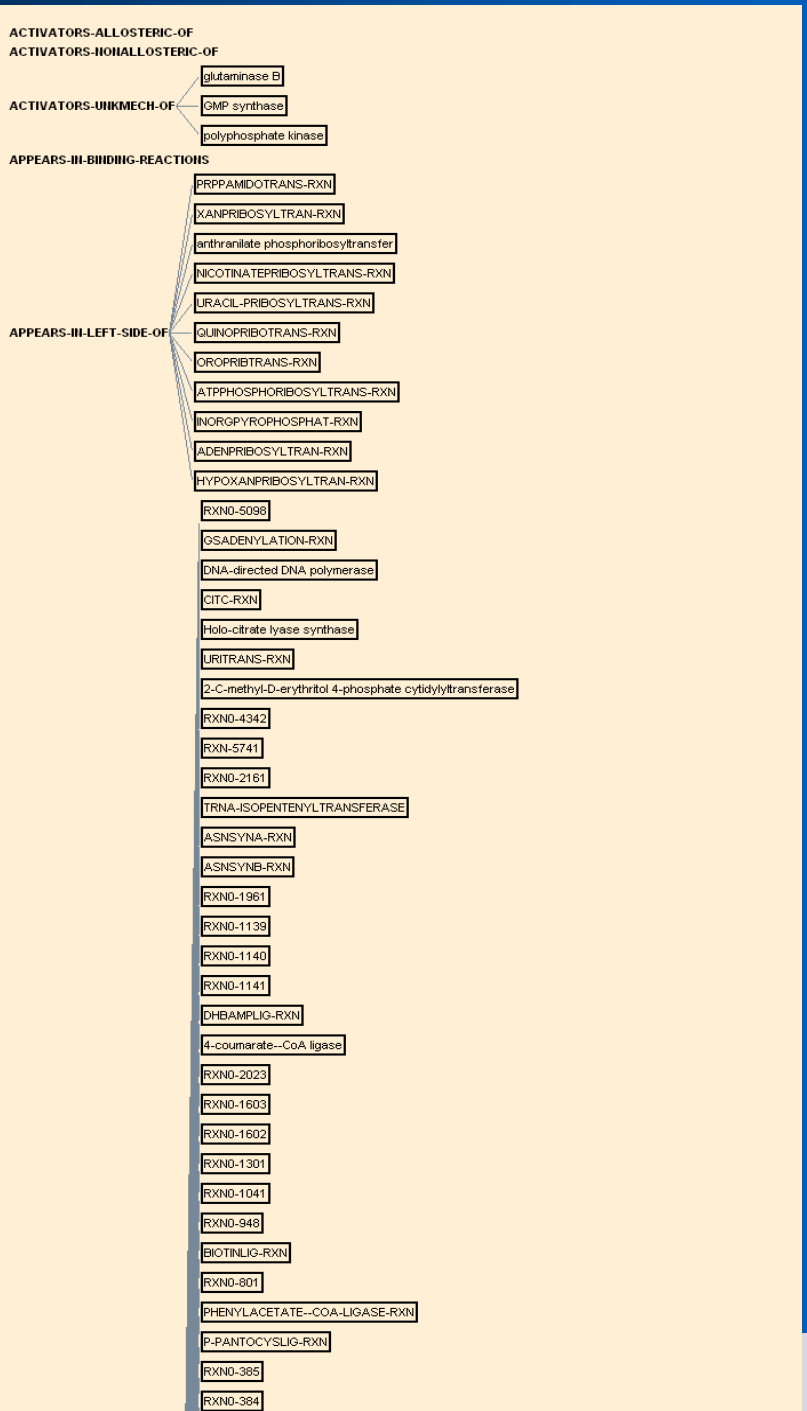
COMMON-NAME: "L-tryptophan"

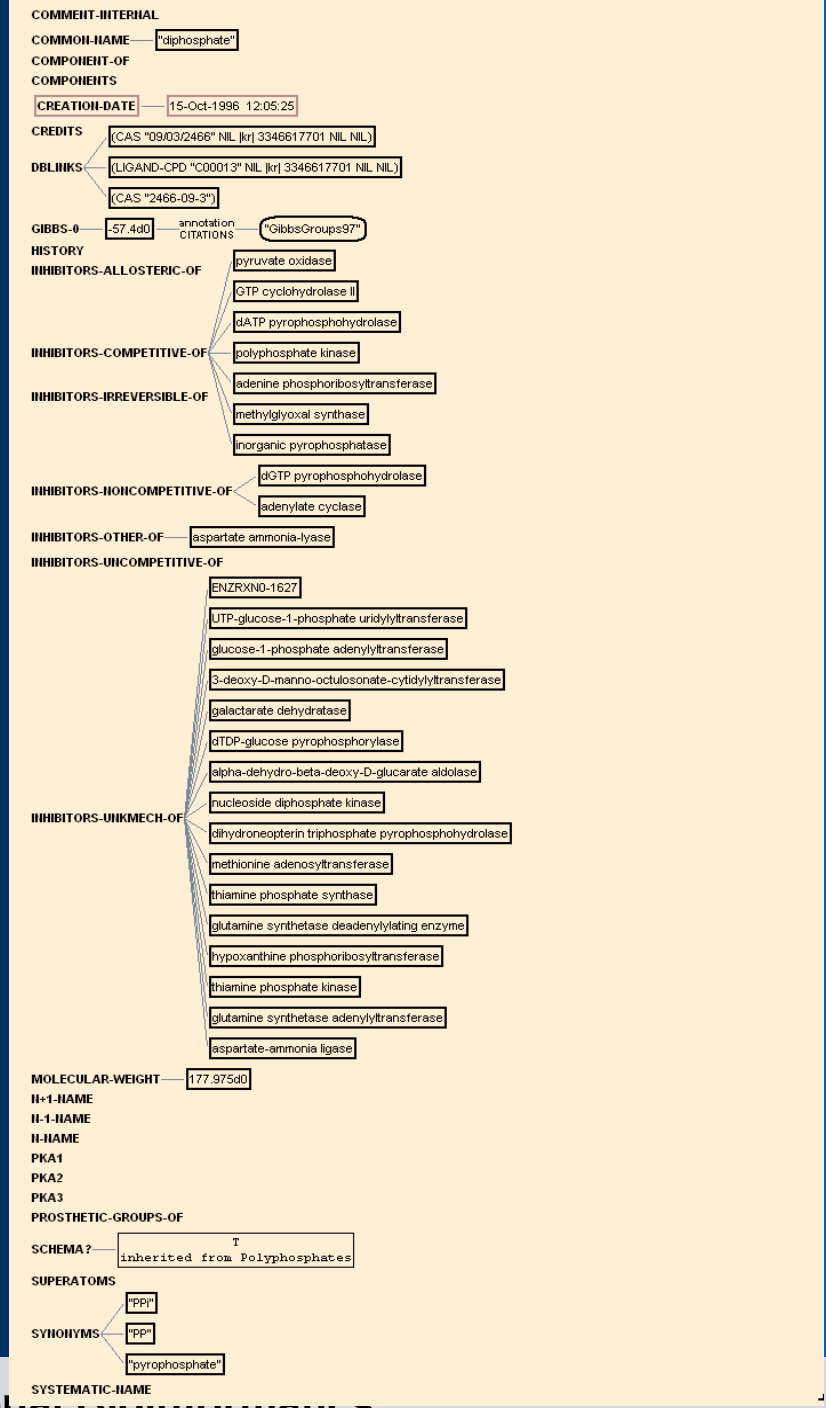
DBLINKS: (LIGAND-CPD "C00078" NIL |kaipa| 3311532640 NIL NIL), (CAS "6912-86-3"), (CAS "73-22-3")

NAMES: "L-tryptophan", "W", "tryptacin", "trofan", "trp", "tryptophan", "2-amino-3-indolylpropanic acid"

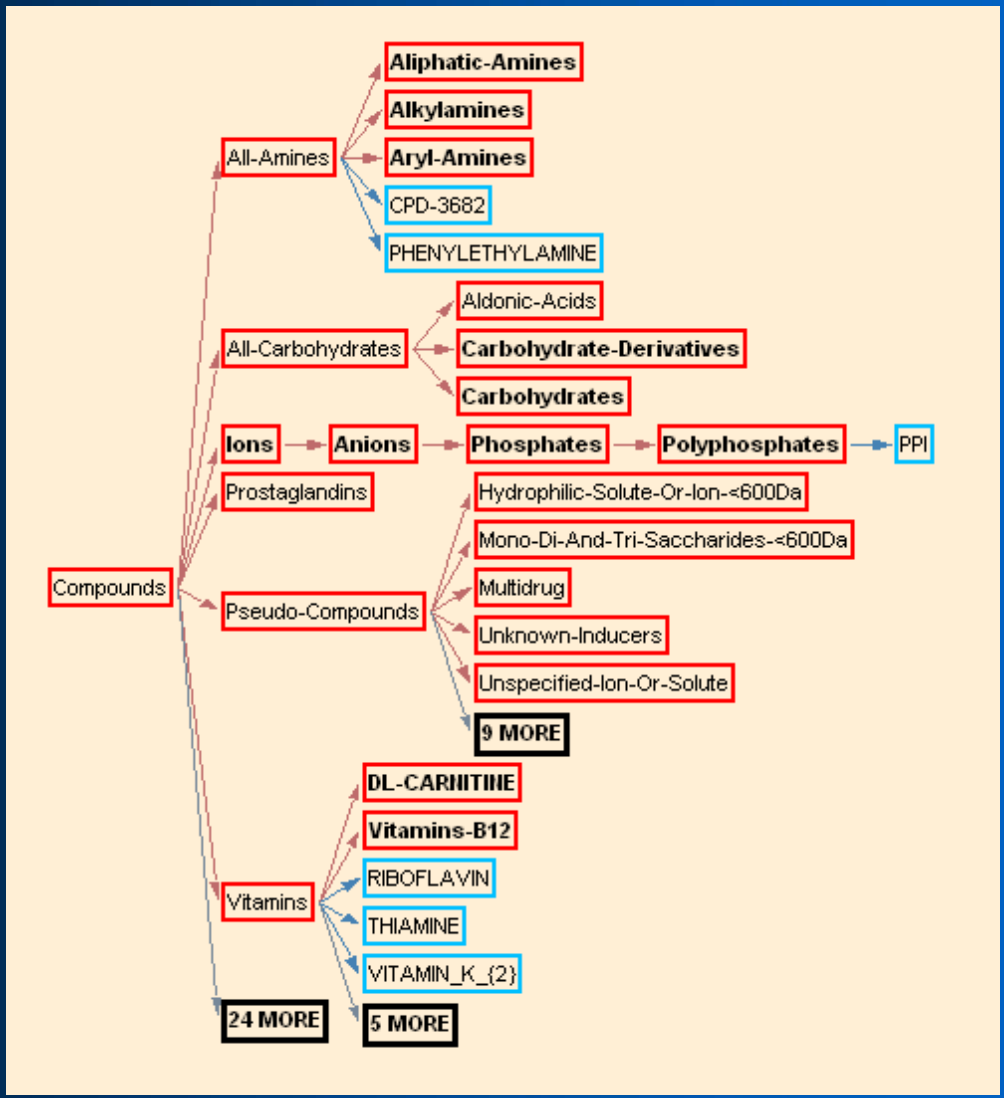
SMILES: "c1(c(CC(N)C(=O)O)c2(c([nH]1)cccc2))"

SYNONYMS: "W", "tryptacin", "trofan", "trp", "tryptophan", "2-amino-3-indolylpropanic acid"





Where is diphosphate in the ontology?



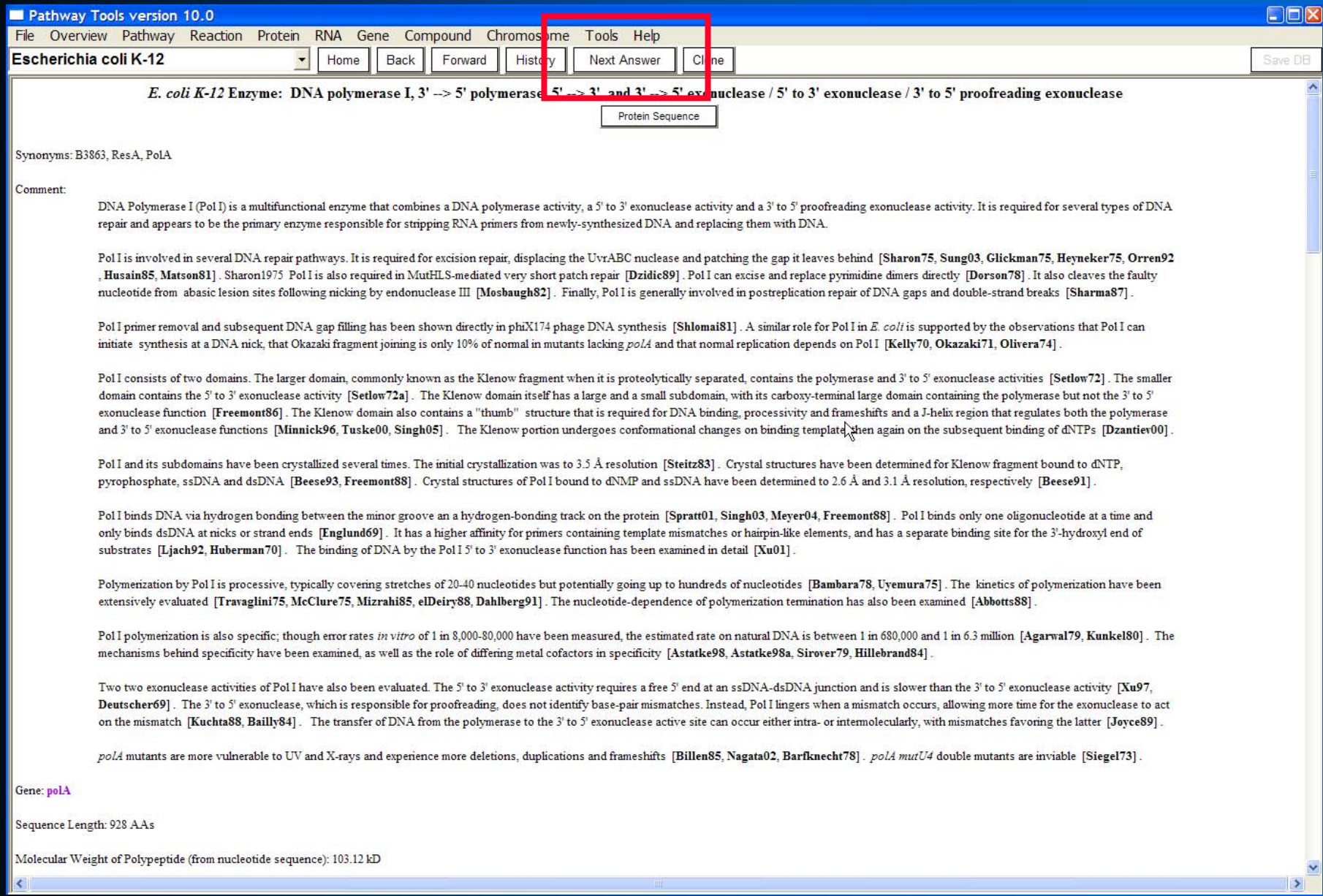
Semantic Inference Layer

- **Reactions-of-compound (cpd)**
- **Pathways-of-compound (cpd)**
- **is-substrate-an-autocatalytic-enzyme-p (cpd)**
- **Activated/inhibited by? (cpds slots)**
  - Returns a list of enzrxns for which a cpd in cpds is a modulator (example slots: activators-all, activators-allosteric)
- **All-substrates (rxns)**
  - All unique substrates specified in the given rxns
- **Has-structure-p? (cpd)**
- **Obtain-cpd-stats**
  - Returns two values:
    - Length of :all-cpds, cpds with structures

Miscellaneous things….

- **History List**
  - Back/Forward and History buttons
  - Default list is 50 items

- **Show frame**
- **(print-frame ‘frame)**


Pathway Tools version 10.0
File Overview Pathway Reaction Protein RNA Gene Compound Chromosome Tools Help
Escherichia coli K-12
Home Back Forward History Next Answer Clone
Save DB
E. coli K-12 Enzyme: DNA polymerase I, 3' --> 5' polymerase, 5' --> 3' and 3' --> 5' exonuclease / 5' to 3' exonuclease / 3' to 5' proofreading exonuclease
Protein Sequence
Synonyms: B3863, ResA, PolA
Comment:
DNA Polymerase I (Pol I) is a multifunctional enzyme that combines a DNA polymerase activity, a 5' to 3' exonuclease activity and a 3' to 5' proofreading exonuclease activity. It is required for several types of DNA repair and appears to be the primary enzyme responsible for stripping RNA primers from newly-synthesized DNA and replacing them with DNA.
Pol I is involved in several DNA repair pathways. It is required for excision repair, displacing the UvrABC nuclease and patching the gap it leaves behind [Sharon75, Sung03, Glickman75, Heyneker75, Orren92, Husain85, Matson81]. Sharon1975 Pol I is also required in MutHLS-mediated very short patch repair [Dzidic89]. Pol I can excise and replace pyrimidine dimers directly [Dorson78]. It also cleaves the faulty nucleotide from abasic lesion sites following nicking by endonuclease III [Mosbaugh82]. Finally, Pol I is generally involved in postreplication repair of DNA gaps and double-strand breaks [Sharma87].
Pol I primer removal and subsequent DNA gap filling has been shown directly in phiX174 phage DNA synthesis [Shlomai81]. A similar role for Pol I in E. coli is supported by the observations that Pol I can initiate synthesis at a DNA nick, that Okazaki fragment joining is only 10% of normal in mutants lacking polA and that normal replication depends on Pol I [Kelly70, Okazaki71, Olivera74].
Pol I consists of two domains. The larger domain, commonly known as the Klenow fragment when it is proteolytically separated, contains the polymerase and 3' to 5' exonuclease activities [Setlow72]. The smaller domain contains the 5' to 3' exonuclease activity [Setlow72a]. The Klenow domain itself has a large and a small subdomain, with its carboxy-terminal large domain containing the polymerase but not the 3' to 5' exonuclease function [Freemont86]. The Klenow domain also contains a "thumb" structure that is required for DNA binding, processivity and frameshifts and a J-helix region that regulates both the polymerase and 3' to 5' exonuclease functions [Minnick96, Tuske00, Singh05]. The Klenow portion undergoes conformational changes on binding template, then again on the subsequent binding of dNTPs [Dzantiev00].
Pol I and its subdomains have been crystallized several times. The initial crystallization was to 3.5 Å resolution [Steitz83]. Crystal structures have been determined for Klenow fragment bound to dNTP, pyrophosphate, ssDNA and dsDNA [Beese93, Freemont88]. Crystal structures of Pol I bound to dNMP and ssDNA have been determined to 2.6 Å and 3.1 Å resolution, respectively [Beese91].
Pol I binds DNA via hydrogen bonding between the minor groove an a hydrogen-bonding track on the protein [Spratt01, Singh03, Meyer04, Freemont88]. Pol I binds only one oligonucleotide at a time and only binds dsDNA at nicks or strand ends [Englund69]. It has a higher affinity for primers containing template mismatches or hairpin-like elements, and has a separate binding site for the 3'-hydroxyl end of substrates [Ljach92, Huberman70]. The binding of DNA by the Pol I 5' to 3' exonuclease function has been examined in detail [Xu01].
Polymerization by Pol I is processive, typically covering stretches of 20-40 nucleotides but potentially going up to hundreds of nucleotides [Bambara78, Uyemura75]. The kinetics of polymerization have been extensively evaluated [Travaglini75, McClure75, Mizrahi85, elDeiry88, Dahlberg91]. The nucleotide-dependence of polymerization termination has also been examined [Abbotts88].
Pol I polymerization is also specific; though error rates in vitro of 1 in 8,000-80,000 have been measured, the estimated rate on natural DNA is between 1 in 680,000 and 1 in 6.3 million [Agarwal79, Kunkel80]. The mechanisms behind specificity have been examined, as well as the role of differing metal cofactors in specificity [Astatke98, Astatke98a, Sirover79, Hillebrand84].
Two two exonuclease activities of Pol I have also been evaluated. The 5' to 3' exonuclease activity requires a free 5' end at an ssDNA-dsDNA junction and is slower than the 3' to 5' exonuclease activity [Xu97, Deutscher69]. The 3' to 5' exonuclease, which is responsible for proofreading, does not identify base-pair mismatches. Instead, Pol I lingers when a mismatch occurs, allowing more time for the exonuclease to act on the mismatch [Kuchta88, Bailly84]. The transfer of DNA from the polymerase to the 3' to 5' exonuclease active site can occur either intra- or intermolecularly, with mismatches favoring the latter [Joyce89].
polA mutants are more vulnerable to UV and X-rays and experience more deletions, duplications and frameshifts [Billen85, Nagata02, Barfknecht78]. polA mutU4 double mutants are inviable [Siegel73].
Gene: polA
Sequence Length: 928 AAs
Molecular Weight of Polypeptide (from nucleotide sequence): 103.12 kD

Queries with Multiple Answers

- **Navigator queries:**
  - Example: Substring search for “pyruvate”
  - Selected list is placed on the Answer list
  - Use “Next Answer” button to view each one of them

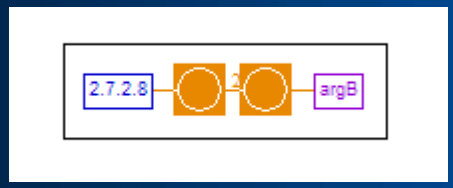
- **Lisp queries:**

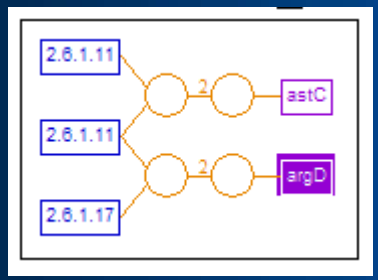
Example : Find reactions involving pyruvate as a substrate

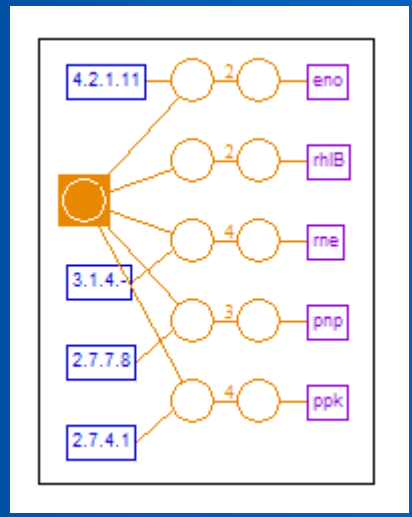
- (get-class-all-instances ‘|Compounds|)

```
(loop for rxn in (get-class-all-instances ‘|Reactions|)
      when (member ‘pyruvate (get-slot-values rxn ‘substrates)
        collect rxn)
      (replace-answer-list  * )
```

Gene Reaction Schematic





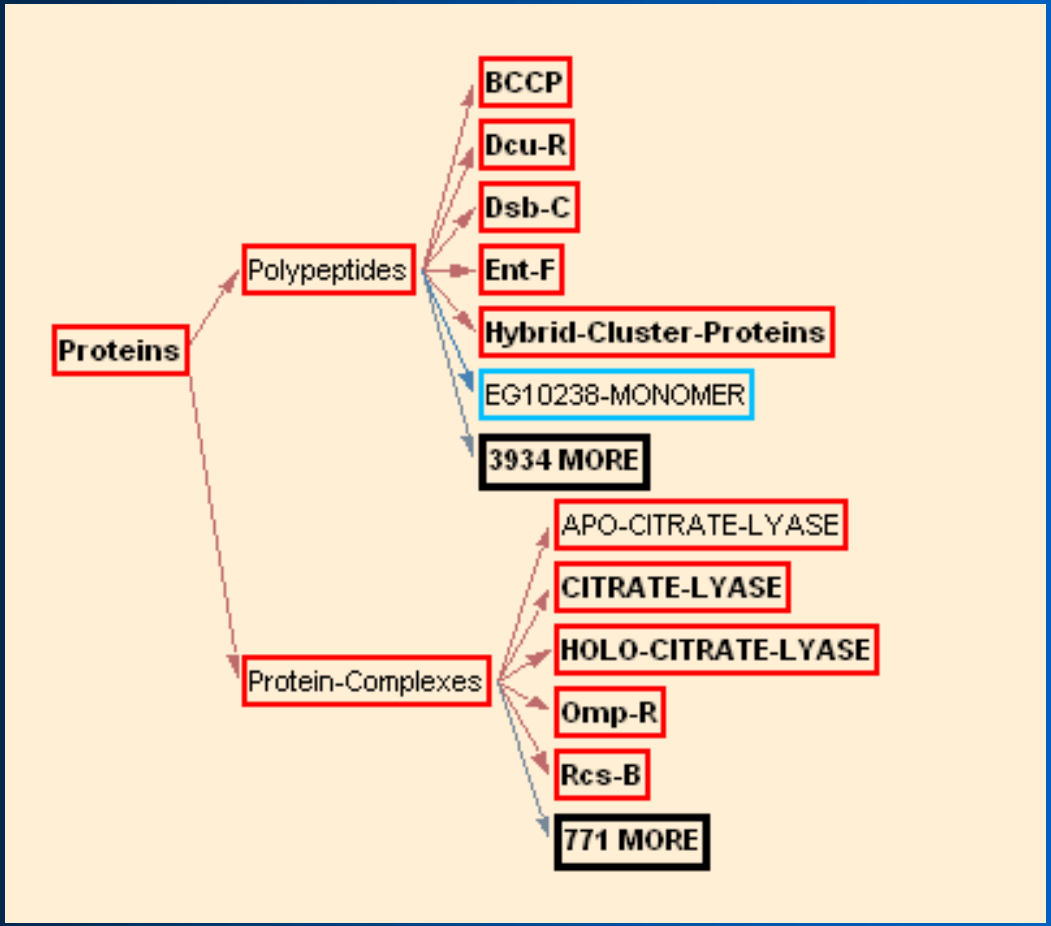


Proteins

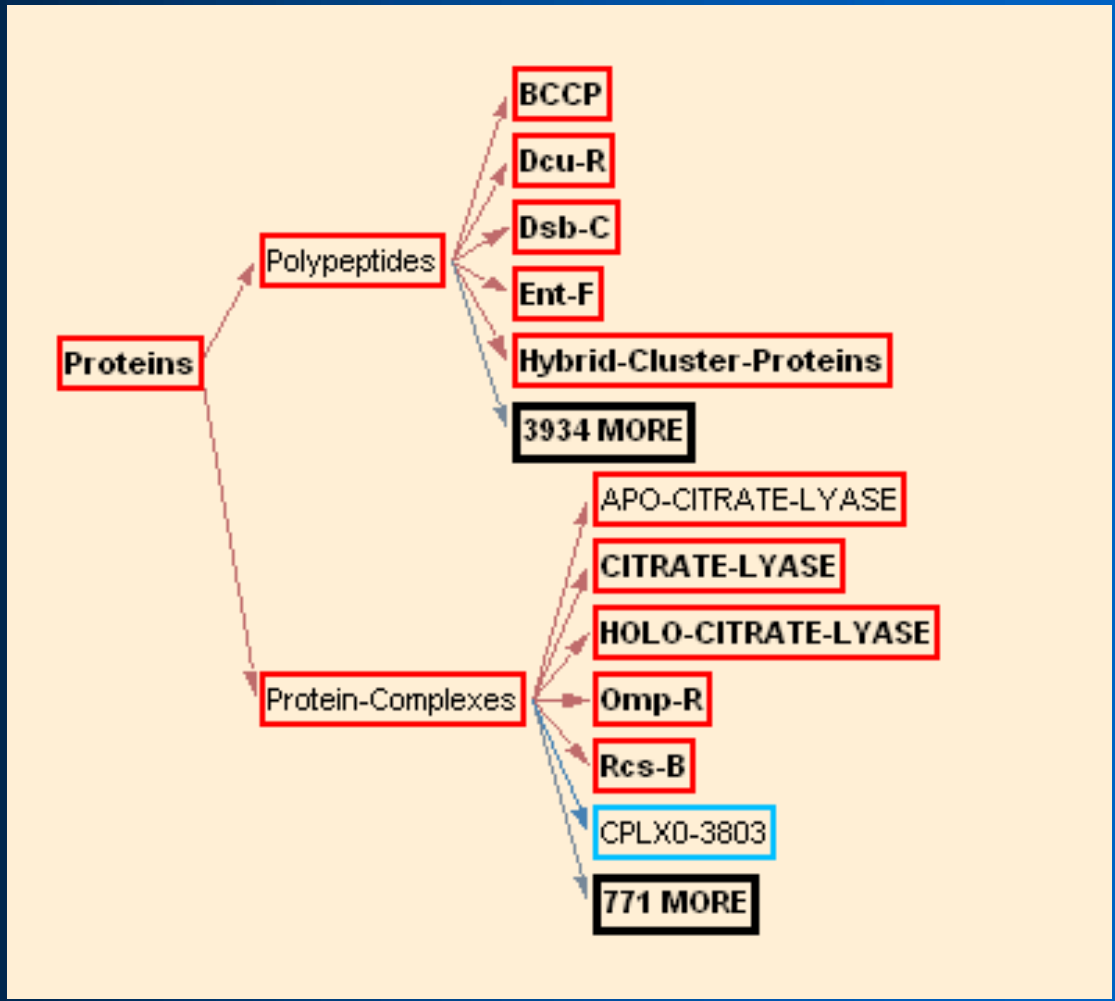
Proteins and Protein Complexes

- **Polypeptide: the monomer protein product of a given (may have multiple isoforms, as indicated at gene level)**
- **Protein complex: proteins consisting of multiple polypeptides or protein complexes**
- **Example: DNA pol III**
  - DnaE is a polypeptide
  - pol III core is DnaE and two other polypeptides
  - pol III holoenzymes is several protein complexes combined

Where is DnaE in the ontology?



Where is pol III in the ontology?



Features of a protein at the frame level (DnaE)

- catalyzes
- Is it an activator/reactant/etc?
- comments
- component-of
- dblinks
- features (edited in feature editor)

- Many other features possible

ACTIVATORS-ALLOSTERIC-OF
ACTIVATORS-NONALLOSTERIC-OF
ACTIVATORS-UNKMECH-OF
APPEARS-IN-BINDING-REACTIONS
APPEARS-IN-LEFT-SIDE-OF
APPEARS-IN-RIGHT-SIDE-OF
CATALYZES — ENZRXN0-6081
CHEMICAL-FORMULA
CITATIONS — "6288664"
COFACTORS-OF
COFACTORS-OR-PROSTHETIC-GROUPS-OF
COMMENT — "The alpha subunit of DNA polymerase III catalyzes the polymerase activity of the holoenzyme complex |CITS: [2997151]|. Replicative 5' to 3' polymerization of DNA requires dNTPs and template DNA with a bound RNA primer |CITS: [4560196][4589895]|. The newly polymerized DNA is covalently attached to the RNA primer |CITS: [1089643]|. The presence of the epsilon subunit increases the polymerase activity of the alpha subunit two-fold |CITS: [3037519]|.

The alpha subunit is required for misincorporation and bypass during UV mutagenesis |CITS: [2184308][2184309]|.

The middle portion of the alpha subunit (residues 542-991) is involved in binding to the polymerase III beta subunit. Deletion of the amino-terminal portion of alpha (residues 1-542) actually increases its affinity for beta |CITS: [8702820]|. The carboxy-terminus of alpha is required for binding to the polymerase III tau subunit |CITS: [8702819]|. The amino-terminal php domain of alpha is required for binding to the epsilon subunit |CITS: [16517598]|.

Transcription of dnaE is induced by nalidixic acid, but not by mitomycin C, and induction does not require LexA |CITS: [11544210]|.

Overproduction of alpha can compensate for an otherwise lethal deficiency in DNA polymerase I |CITS: [1597430]|."
COMMENT-INTERNAL
COMMON-NAME — "DNA polymerase III, α subunit"
COMPONENT-OF — DNA polymerase III, core enzyme
COMPONENTS
CREATION-DATE — 24-Jan-2000 10:28:54
CREATOR — pkarp
CREDITS
DBLINKS — (MODBASE "P10443" NIL |pkarp| 3355444109 NIL NIL)
(SWISSMODEL "P10443" NIL |pkarp| 3355444109 NIL NIL)
(PFAM "PF02231" IN-FAMILY |pkarp| 3346700315 NIL NIL)
(REFSEQ "NP_414726" NIL NIL NIL NIL NIL)
(UNIPROT "P10443" NIL |paley| 3169408120)
DNA-FOOTPRINT-SIZE
FEATURES — Protein-Binding-Region
Metal-Binding-Site
FUNCTIONAL-ASSIGNMENT-COMMENT
FUNCTIONAL-ASSIGNMENT-STATUS

A complex at the frame level (pol III)

- **Same features as polypeptide frame, different use**

- **comment**
- **component-of and components**
  - note coefficients

ACTIVATORS-ALLOSTERIC-OF
ACTIVATORS-NONALLOSTERIC-OF
ACTIVATORS-UNKMECH-OF
APPEARS-IN-BINDING-REACTIONS
APPEARS-IN-LEFT-SIDE-OF
APPEARS-IN-RIGHT-SIDE-OF
CATALYZES
CHEMICAL-FORMULA
CITATIONS
COFACTORS-OF
COFACTORS-OR-PROSTHETIC-GROUPS-OF

COMMENT — "The DNA polymerase III core enzyme contains one each of the alpha, epsilon and theta subunits and can carry out the basic polymerase and exonuclease activities of polymerase III |CITS: [368075]|.

Based on yeast two-hybrid data, both alpha and theta interact with epsilon, but not each other |CITS: [9515927]|. The interaction between epsilon and theta has been examined via lanthanide-labeling NMR |CITS: [16536542]|."

COMMENT-INTERNAL

COMMON-NAME — "DNA polymerase III, core enzyme"

COMPONENT-OF — DNA polymerase III, holoenzyme

COMPONENTS — DNA polymerase III, alpha subunit — annotation COEFFICIENT — 1
COMPONENTS — DNA polymerase III, epsilon subunit — annotation COEFFICIENT — 1
COMPONENTS — DNA polymerase III, theta subunit — annotation COEFFICIENT — 1

CREATION-DATE — 25-Jun-2004 15:54:36

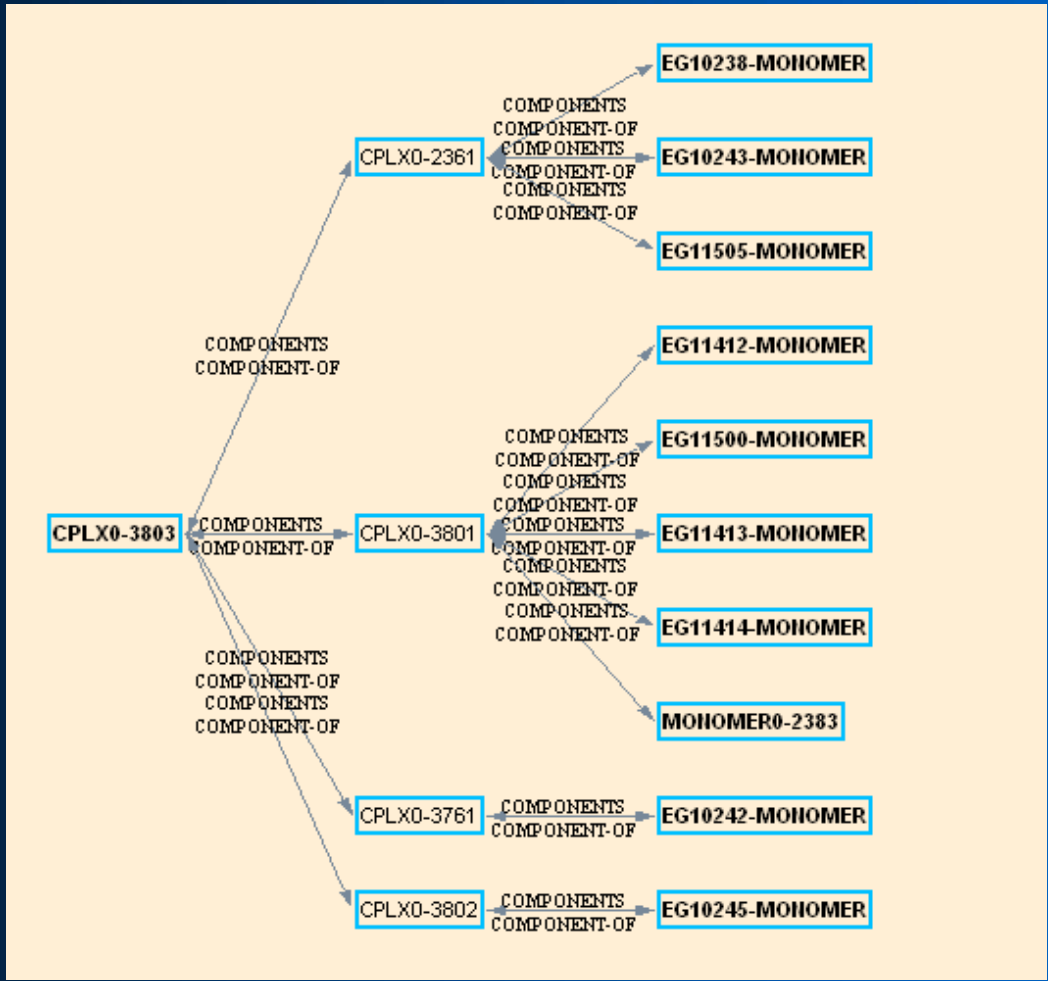
CREATOR — keseler

CREDITS
DBLINKS
DNA-FOOTPRINT-SIZE
HISTORY
INHIBITORS-ALLOSTERIC-OF
INHIBITORS-COMPETITIVE-OF
INHIBITORS-IRREVERSIBLE-OF
INHIBITORS-NONCOMPETITIVE-OF
INHIBITORS-OTHER-OF
INHIBITORS-UNCOMPETITIVE-OF
INHIBITORS-UNKMECH-OF
ISOZYME-SEQUENCE-SIMILARITY

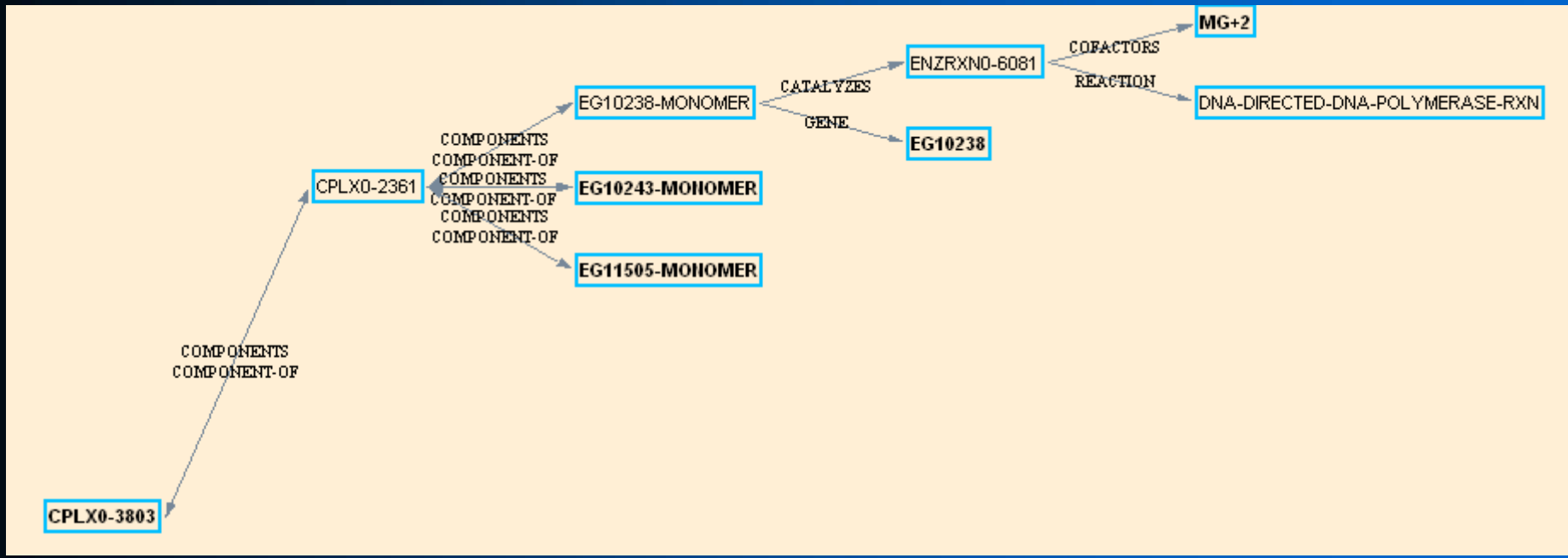
LOCATIONS — cytoplasm

MODIFIED-FORM
MOLECULAR-WEIGHT
MOLECULAR-WEIGHT-EXP
MOLECULAR-WEIGHT-SEQ
N+1-NAME
N-1-NAME
N-NAME
NEIDHARDT-SPOT-NUMBER
PI

Protein complex relationships



Protein complex relationships



Relationships are defined in many places

- component-of comes from creating a complex
- appears-in-left-side-of comes from defining a reaction (as do modified forms)
- inhibitor-of comes from an enzymatic reaction
- can only edit dna-footprint if protein has been associated with a TU

Semantic Inference Layer

- **Reactions-of-protein (pro)**
  - Returns a list of rxns this protein catalyzes
- **Transcription-units-of-proteins(pro)**
  - Returns a list of TU's activated/inhibited by the given protein
- **transporter? (pro)**
  - Is this protein a transporter
- **Polypeptide-or-homomultimer?**
- **Is this protein a transcription factor? (pro)**
- **Obtain-protein-stats**
  - Returns 5 values
    - Length of : all-polypeptides, complexes, transporters, enzymes, etc…

Sample

- **Find all enzymes that use pyridoxal phosphate as a cofactor or prosthetic group**
  - (loop for protein in (get-class-all-instances '|Proteins|)

    For enzrxn = (get-slot-value protein 'enzymatic-reaction)

    when (and enzrxn

    (or (member-slot-value-p enzrxn 'cofactors 'pyridoxal_phosphate)

    (member-slot-value-p enzrxn 'prosthetic-groups 'pyridoxal_phosphate))

    collect protein)

    (member-slot-value-p frame slot value) : T if Value is one of the values of Slot of Frame.

Sample

- **Find all proteins without a comment anywhere**

```
(defun proteins-sans-comments-al ()
  (replace-answer-list
   (loop for x in (get-class-all-instances '|Proteins|)
       for cmnts = (slot-has-value-p x 'comment)
       for rxn = (enz-rxn-comments x)
       for cplx = (complex-with-comments x)
       for cplx2 = (slot-has-value-p x 'components)
       for modform = (modified-form-comments x)
       for modform2 = (slot-has-value-p x 'unmodified-form)
       unless (or cmnts rxn cplx cplx2 modform modform2)
       collect x)
   )
  )

(defun enz-rxn-comments (subj-protein)
  (loop for x in (get-slot-values subj-protein 'catalyzes)
      for cmnts = (slot-has-value-p x 'comment)
      when cmnts
      collect x)
  )

(defun complex-with-comments (subj-protein)
  (loop for x in (get-slot-values subj-protein 'component-of)
      for rxn = (enz-rxn-comments x)
      for cmnts = (slot-has-value-p x 'comment)
      when (or cmnts rxn)
      collect x)
  )

(defun modified-form-comments (subj-protein)
  (loop for x in (get-slot-values subj-protein 'modified-form)
      for cmnts = (slot-has-value-p x 'comment)
      for rxn = (enz-rxn-comments x)
      for cplx = (complex-with-comments x)
      when (or cmnts rxn cplx)
      collect x)
  )
```

Reactions

Enzymatic reactions (DnaE and 2.7.7.7)

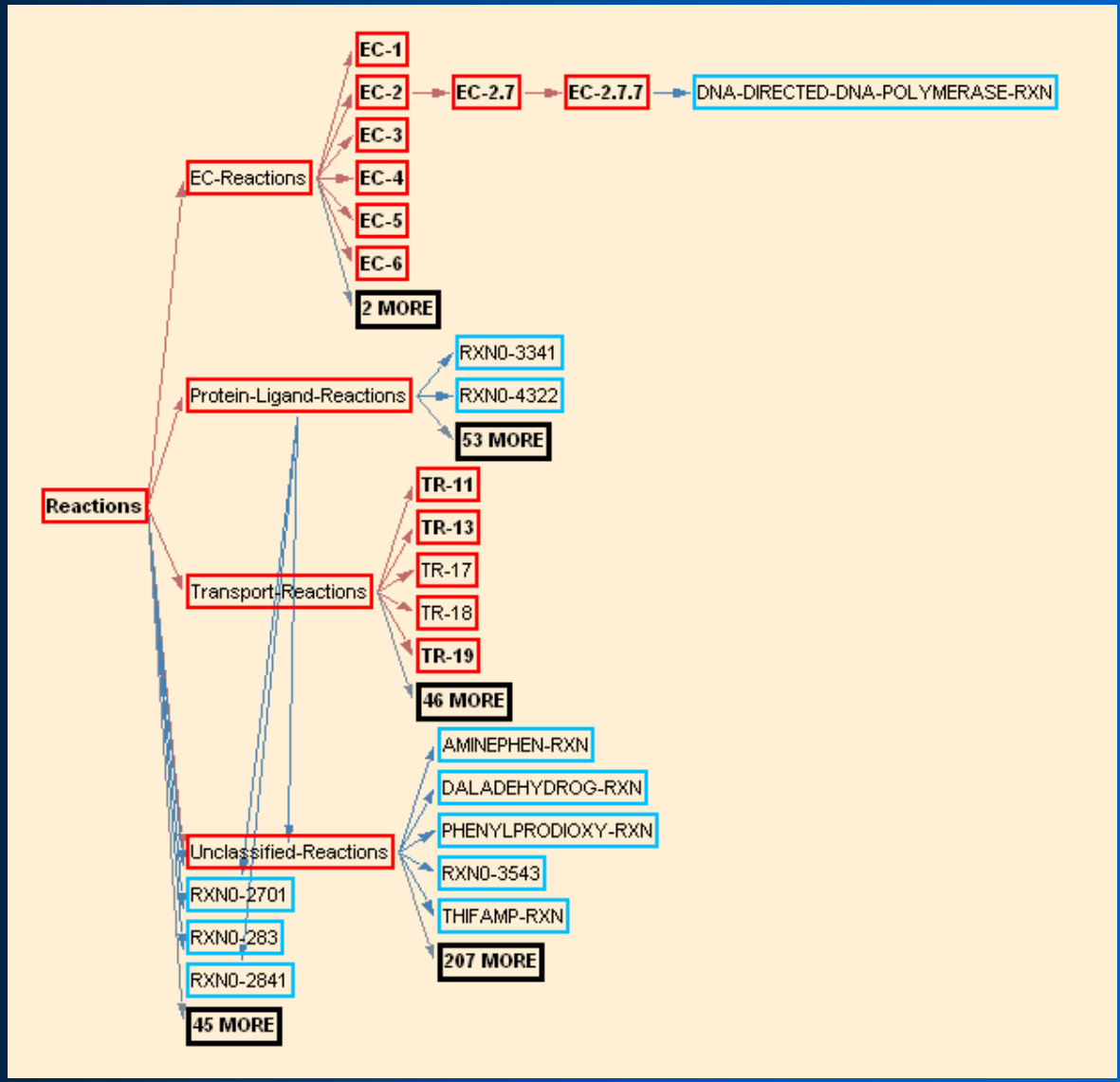
- **A necessary bridge between enzymes and "generic" versions of reactions**
- **Carries specific reaction features:**
  - activators
  - inhibitors
  - cofactors
  - alternative substrates
- **Frame generated when protein associated with reaction (protein or reaction editor)**

ACTIVATORS-ALLOSTERIC
ACTIVATORS-NONALLOSTERIC
ACTIVATORS-UNKMECH
ALTERNATIVE-COFACTORS
ALTERNATIVE-SUBSTRATES
BASIS-FOR-ASSIGNMENT
CITATIONS — "4560196"
CITATIONS — "1089643:EV-EXP-IDA-PURIFIED-PROTEIN:3336919499:shearer"
COFACTOR-BINDING-COMMENT
COFACTORS — Mg2+ — annotation CITATIONS — "4560196"
COFACTORS-OR-PROSTHETIC-GROUPS
COMMENT — "This enzyme can also use divalent manganese ion as a cofactor |CITS: [788784]|."
COMMENT-INTERNAL
COMMON-NAME
COMPONENT-OF
COMPONENTS
CREATION-DATE — 28-Sep-2005 10:55:45
CREATOR — shearer
CREDITS
DBLINKS
ENZYME — DNA polymerase III, alpha subunit
HISTORY
INHIBITORS-ALLOSTERIC
INHIBITORS-COMPETITIVE
INHIBITORS-IRREVERSIBLE
INHIBITORS-NONCOMPETITIVE
INHIBITORS-OTHER
INHIBITORS-UNCOMPETITIVE
INHIBITORS-UNKMECH
KM
PH-OPT
PHYSIOLOGICALLY-RELEVANT
PROSTHETIC-GROUPS
REACTION — DNA-directed DNA polymerase
REACTION-DIRECTION
REQUIRED-PROTEIN-COMPLEX
SCHEMA? — T
inherited from Enzymatic-Reactions
SYNONYMS
TEMPERATURE-OPT

Reactions

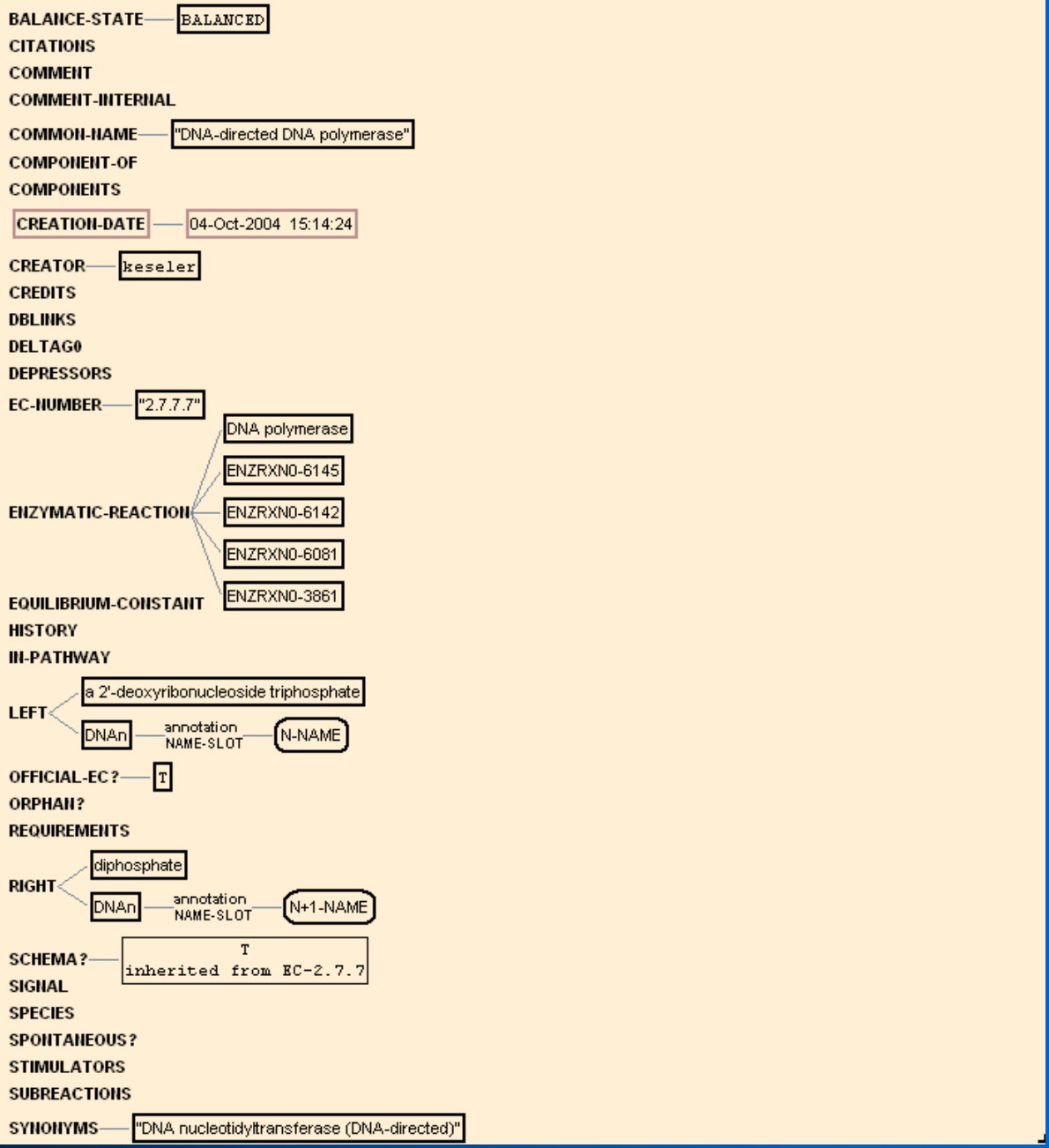
- **Represent the “generic” form of the reaction**
- **Connected to proteins via enzymatic reaction frames**
- **Classified with EC system when possible**
- **Example: 2.7.7.7 – DNA-directed DNA polymerization**
  - Carried out by five enzymes in *E. coli*

Where is 2.7.7.7 in the ontology?

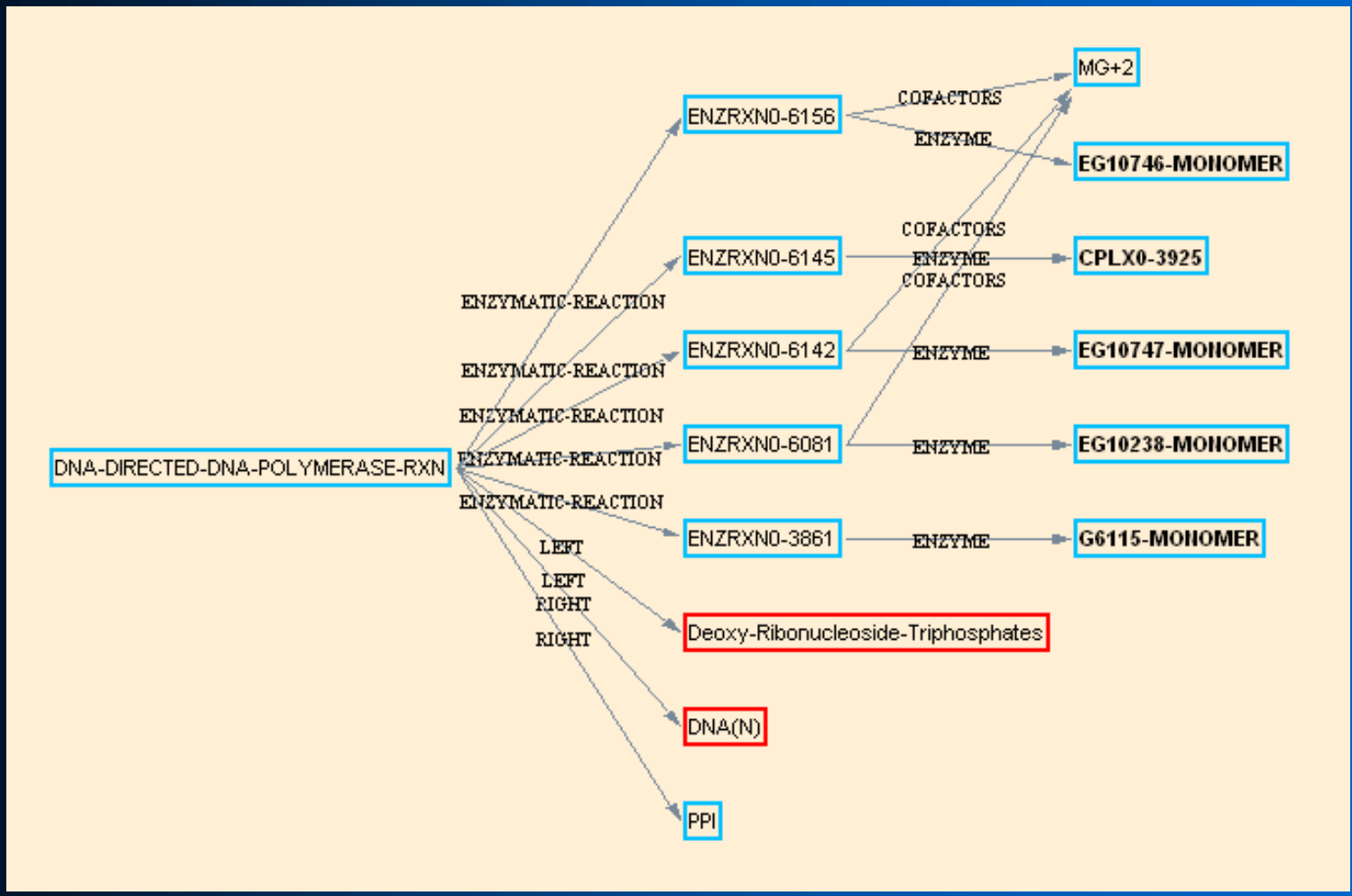


Features of a reaction at the frame level

- **balance-state**
- **ec-number**
- **enzymatic-reaction**
  - Generated in protein or reaction editor
- **in-pathway**
  - Generated in pathway editor
- **left and right-side compounds**
  - Can make modified forms of proteins, RNAs, etc here
  - Not all reactants/products need to be frames


BALANCE-STATE
BALANCED
CITATIONS
COMMENT
COMMENT-INTERNAL
COMMON-NAME
"DNA-directed DNA polymerase"
COMPONENT-OF
COMPONENTS
CREATION-DATE
04-Oct-2004 15:14:24
CREATOR
keseler
CREDITS
DBLINKS
DELTAG0
DEPRESSORS
EC-NUMBER
"2.7.7.7"
ENZYMATIC-REACTION
DNA polymerase
ENZRXN0-6145
ENZRXN0-6142
ENZRXN0-6081
ENZRXN0-3861
EQUILIBRIUM-CONSTANT
HISTORY
IN-PATHWAY
LEFT
a 2'-deoxyribonucleoside triphosphate
DNAn
annotation
NAME-SLOT
N-NAME
OFFICIAL-EC?
T
ORPHAN?
REQUIREMENTS
RIGHT
diphosphate
DNAn
annotation
NAME-SLOT
N+1-NAME
SCHEMA?
T
inherited from EC-2.7.7
SIGNAL
SPECIES
SPONTANEOUS?
STIMULATORS
SUBREACTIONS
SYNONYMS
"DNA nucleotidyltransferase (DNA-directed)"

Reaction relationships



Semantic Inference Layer

- **Genes-of-reaction (rxn)**
- **Substrates-of-reaction (rxn)**
- **Enzymes-of-reaction (rxn)**
- **Lacking-ec-number (organism)**
  - Returns list of rxns with no ec numbers in that database
- **Get-reaction-direction-in-pathway (pwy rxn)**
- **Reaction type? (rxn)**
    - Small molecule rxn, transport rxn, protein-small-molecule rxn (one substrate is protein and one is a small molecule), protein rxn (all substrates are proteins), etc.
- **(all-rxns :type)**
  - Specify the type of reaction (see above for type)
- **Obtain-rxn-stats**
  - Returns six values
    - Length of : all-rxns, transport, non-transport, etc…

Orphan reactions in an organism:

```
(defun orphan-reactions (&optional (verbose? t))

    (loop for r in (all-rxns :small-molecule)
        when (and (not (slot-has-value-p r 'enzymatic-reaction))
                  (not (get-slot-value r 'spontaneous?)))
        collect r)
)
```

RNAs

RNAs

- **Currently only represent RNAs that are the "terminal gene product"**
  - tRNAs
  - rRNAs
  - miscellaneous small RNAs
- **Frame features similar to proteins**
- **tRNAs can have an anticodon**

ACTIVATORS-ALLOSTERIC-OF
ACTIVATORS-NONALLOSTERIC-OF
ACTIVATORS-UNKMECH-OF
ANTICODON — "UUU"
APPEARS-IN-BINDING-REACTIONS
APPEARS-IN-LEFT-SIDE-OF
APPEARS-IN-RIGHT-SIDE-OF
CHEMICAL-FORMULA
CITATIONS
CODONS
COFACTORS-OF
COFACTORS-OR-PROSTHETIC-GROUPS-OF

COMMENT —

"tRNA(lysT) is one of six lysine tRNAs.

tRNAs are the adapters that allow synthesis of proteins from mRNAs.
Each tRNA carries a specific amino acid to the ribosome for protein synthesis.
There, the tRNA recognizes an RNA codon with its own three-nucleotide
anticodon, thus allowing synthesis of a specific peptide based on an mRNA
template.

tRNAs are processed to their active, mature forms by RNA cleavage
and by modification of their bases. RNA cleavage consists of
removal of both 5' and 3' extensions in a multistep process involving
many RNases |CITS: [11252717]|. RNases taking part in tRNA processing include |FRAME: CPLX0-3461|,
|FRAME: CPLX0-3601|, |FRAME: EG10858-MONOMER|, |FRAME: EG11620-MONOMER|, |FRAME: EG11620-MONOMER|,
|FRAME: EG11620-MONOMER|, and |FRAME: CPLX0-3602|. tRNAs are also subject to a
wide variety of base modifications catalyzed by proteins such as
|FRAME: EG11932-MONOMER|, |FRAME: EG10595-MONOMER|, |FRAME: G6364-MONOMER|, |FRAME: EG11344-MONOMER|,
|FRAME: G7199-MONOMER|, |FRAME: CPLX0-1101|, |FRAME: EG11779-MONOMER|, |FRAME: G7422-MONOMER|,
|FRAME: G7449-MONOMER|, |FRAME: EG11177-MONOMER|, |FRAME: EG10454-MONOMER|, |FRAME: EG10967-MONOMER|,
and |FRAME: EG11022-MONOMER|.

NMR analyses of the fully modified anticodon stem-loop domain of tRNA(lysT)
show that base modifications play an important role in maintaining the structure of
that domain |CITS: [11027137][15924427]|.

Mature tRNAs are linked via a 3' CCA sequence to their cognate
amino acid in an ATP-dependent fashion by the appropriate
amino-acid-tRNA synthetase, as shown in the |FRAME: TRNA-CHARGING-PWY|.
Subsequently, these charged tRNAs interact with the ribosome
and template mRNA to generate polypeptides. The discovery of the
role of tRNA in protein synthesis is reviewed in detail in |CITS: [7033244]|."

COMMENT-INTERNAL
COMMON-NAME — "tRNA^{lysT}"
COMPONENT-OF
COMPONENTS
CREATION-DATE — 25-Mar-1997 12:16:58
CREDITS — SRI International — annotation LAST-CURATED — 3355079216
CREDITS — shearer — annotation LAST-CURATED — 3355079216
DBLINKS
GENE — lysT
HISTORY
INHIBITORS-ALLOSTERIC-OF
INHIBITORS-COMPETITIVE-OF
INHIBITORS-IRREVERSIBLE-OF
INHIBITORS-NONCOMPETITIVE-OF
INHIBITORS-OTHER-OF
INHIBITORS-UNCOMPETITIVE-OF
INHIBITORS-UNKMECH-OF — 3'-nucleotidase inherited from RNA
INHIBITORS-UNKMECH-OF — 2',3'-cyclic nucleotide 2'-phosphodiesterase inherited from RNA
MODIFIED-FORM — L-lysyl-tRNAlysT
MOLECULAR-WEIGHT
N+1-NAME
N-1-NAME
N-NAME
PROSTHETIC-GROUPS-OF
SCHEMA? — T inherited from LYS-tRNAs
SPLICE-FORM-INTRONS
SYNONYMS

SRI International Bioinformatics

BioCyc Database Collection

The RNA ontology is simple (right now)