RDF friendly Chemical Taxonomies for Semantic Web (Using ORACLE/MySQL)

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<u>Downloads</u> <u>Query 3-D data</u> <u>Query 2-D data</u>

Prasanna MD, Vondrasek J, Wlodawer A, Rodriguez H, Bhat TN. Chemical compound navigator: a web-based chem-BLAST, chemical taxonomy-based search engine for browsing compounds. Proteins 2006;63(4):907-917.

Software Tools
Government Besources

BioSync

Dictionaries & File Formats

General Information
Acknowledgements

Frequently Asked Questions

Known Problems

Report Bugs/Comments

Prior work

A **narrated tutorial** illustrates how to search, navigate, browse, generate reports and visualize structures using this

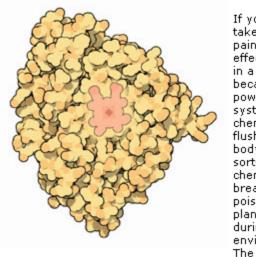
a more consistent and comprehensive archive.

that utilize the data resulting from origonia errorts to create

Information about compatible browsers can be found here.

new Site. [This requires the Macromedia Flash player download.]

Comments? info@rcsb.org



Molecule of the Month: Cytochrome p450

If you have a headache and take a drug to block the pain, you'll notice that the effects of the drug wear off in a few hours. This happens because you have a powerful detoxification system that finds unusual chemicals, like drugs, and flushes them out of your body. This system fights all sorts of unpleasant chemicals that we eat and breathe, including drugs, poisonous compounds in plants, carcinogens formed during cooking, and environmental pollutants. The cytochrome p450 enzymes are our first line of defense in this chemical battle.

■ More ...

■ Previous Features

17-October-2006
RCSB PDB Focus:
Exploring Domains in
Protein Structure

(at RCSB or PDBi)

PDB Exchange

Full Story

structures.

includes examples and

definitions provided in the

Dictionary as quides for

users depositing their

structural units from which proteins are assembled that retain properties of the whole protein, such as a hydrophobic core.

Domains can be thought

of as the smallest

various ways of exploring domains in protein structures.

The RCSB PDB offers

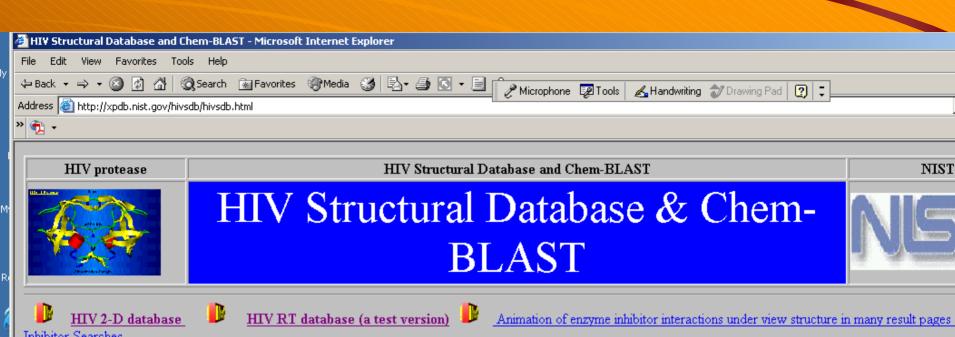
Full Story ...

The RCSB PDB is supported by funds from the National Science Foundation (NSF), the National Institute of General Medical Sciences (NIGMS), the Office of Science, Department of Energy (DOE), the National Library of Medicine (NLM), the National Cancer Institute (NCI), the National Center for Research Resources (NCRR), the National Institute of Biomedical Imaging and Bioengineering (NIBIB), National Institute of Neurological Disorders and Stroke

(NINDS), and the National Institute of Diabetes and Digestive and Kidney

to: H.M. Berman, J.
Westbrook, Z. Feng, G.
Gilliland, T.N. Bhat, H.
Weissig, I.N. Shindyalov, P.E.
Bourne: The Protein Data Bank.
Nucleic Acids Research, 28

In citing the PDB please refer-



Inhibitor Searches

HIV Structural Reference Database (102) and Chem-BLAST

Biotechnology Division, National Institute of Standards and Technology Gaithersburg, MD 20899 U.S.A.

In citing this work please use the following publications:

http://xpdb.nist.gov/hivsdb/hivsdb.html

1. Prasanna, M.D., Vondrasek, J., Wlodawer, A., Bhat, T. N. Application of InChI to curate, index and query 3-D structures. PROTEINS: Structure, Function, and Bioinformatics 60, 1-4 (2005).

2. Prasanna M.D., Vondrasek J., Wlodawer A., Rodriguez H., Bhat T.N. Chemical compound navigator: a web-based Chem-BLAST, chemical taxonomy-based search engineering browsing compounds. Proteins 63(4), 907-917(2006).

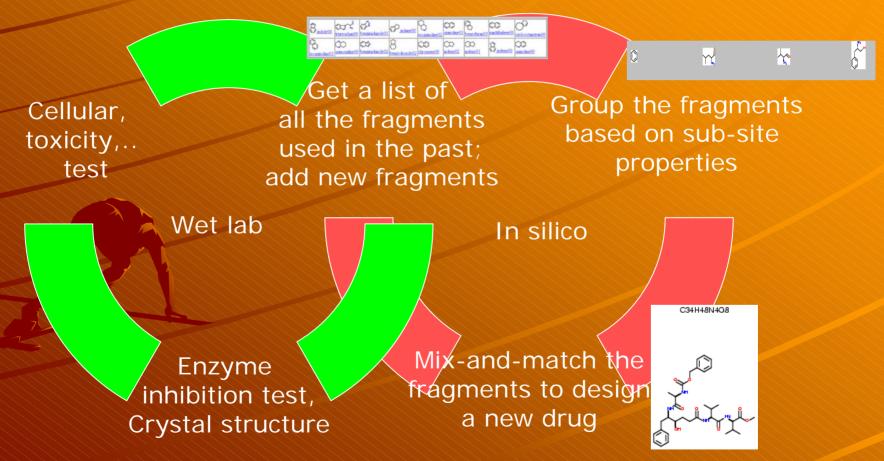
Information is available on the following topics:

- Show credits

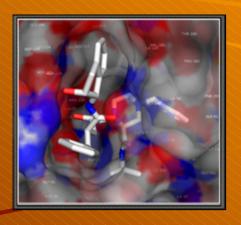
What is new in HIVSDB compared to what is out there?

- All the current AIDS drugs were developed based on structures of HIV proteins
 - There is no other database focused on structures of HIV proteins
- HIVSDB is a comprehensive resource of structures of AIDS proteins/complexes and of related info for drug design
 - 3-D data (X-ray or NMR)
 - Chemical structures (2-D, schematic drawing) of inhibitors obtained from literature
 - Synonyms, company names, IUPAC names
 - These are not ordinary structures that may or may not bind to a target enzyme
 - * EC50s less than 1 micro Molar with a Therapeutic Index between 1 and 800
 - Biological, cellular, anti-viral data, references for further reading from published literature
 - Not info of the type ' he said, they said '. One can see the citation as well
 - Drug resistance data (over 10,000 citations have been weaned through this year alone)
 - Drug resistance mutant 3-D models
 - Semantic chemical fragments for (in silico) SAR studies
 - To design new drugs
 - To compare drugs
 - Illustration of enzyme drug interactions
 - To enable SAR modeling
 - Animation to illustrate mutant effects
- HIVSDB narrates (attempts) the (complete) story of drug design efforts for AIDS on which the world has spent billions of \$ during the last two decades
- Database includes HIV protease, RT (incorporation of other proteins is planned)

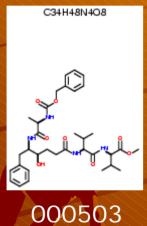
Drug design by mix-match-method

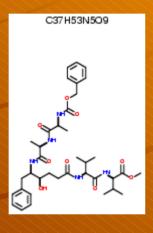


Data are chosen over a wide range of company, core type, and potency.

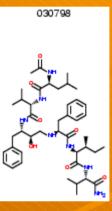


Inhibitors of HIV protease









000505

1A8K

030798



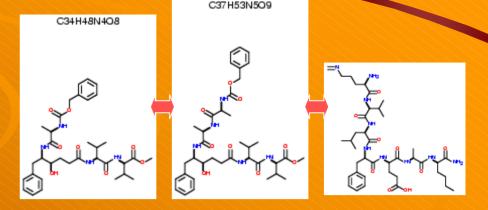






```
PDB Format
 HETATM 1 C1 A7700 800
                              3.484 3.332 10.744 1.00 19.36
 HETATM 10 C10 A7700 800
                              7.702 5.966 10.862 1.00 28.71
 HETATM 11 C11 A7700 800
                              8 525 6 077 9 751 1 00 30 20
 HETATM 54 C12 A7700 800
                              3.555 -8.734 19.771 1.00 26.67
 HETATM 56 C13 A7700 800
                              2.317 -8.344 20.282 1.00 25.95
 HETATM 57 C14 A7700 800
                              3.355 -6.296 20.983 1.00 31.02
 HETATM 58 C15 A7700 800
                              2.211 -7.098 20.901 1.00 28.97
 HETATM 51 C2 A7700 800
                              5.791 -8.392 16.839 1.00 22.59
 HETATM 13 C22 A7700 800
                              2.786 1.298 11.960 1.00 17.23
                              3.932 0.378 12.380 1.00 17.53
 HETATM 14 C23 A7700 800
 HETATM 16 C25 A7700 800
                                                   0 18.10
                              >30 years
 Mol format
 1HVC mol
  -ISIS-
             3D
 116119 0 0 0 0 0 0 0 0 0
   3.4840 3.3320 10.7440 C 0.0 0 0 0
   7.7020 5.9660 10.8620 C 0 0 0 0 0
   8.5250 6.0770 9.7510 C 0 0 0 0 0
   3.5550 -8.7340 19.7710 C 0.0 0 0 0
   2.3170 -8.3440 20.2820 C 0 0 0 0 0
   3.3550 -6.2960 20.9830 C 0 0 0 0 0
   2.2110 -7.0980 20.9010 C 0 0 0 0
                                      >15 years
 CML
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:date day="22" month="11" year="1995" />
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float builtin="v2">0.4329</float>
 </atom>
katom id="a2">
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                                     >5 years
 </atom>
 <float builtin="v2">0.9977</float>
```

</atom>



PDB + PDB = ? PDB - MOL = ? CML + CML = ? MOL - CML = ?

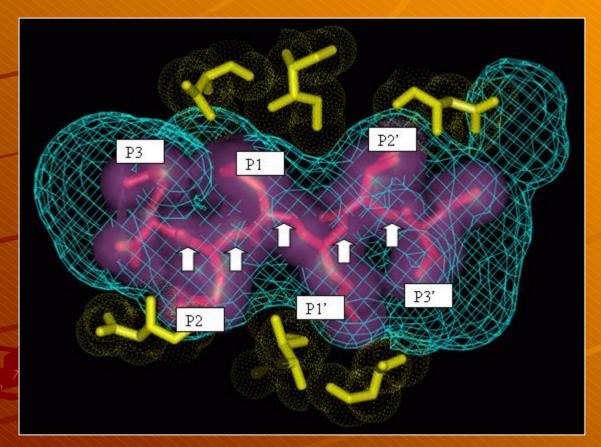
Problem

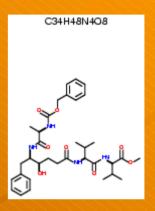
These formats need a wrapper to operate on them

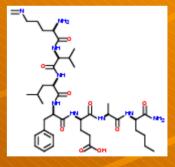
Goal

Eliminate the need of a wrapper and develop RDF statements that facilitate the above operations on structures in a database or Web environment to enable drug design

Elements of a RDF







http://esw.w3.org/topic/HCLS/ChemicalTaxonomiesUseCase

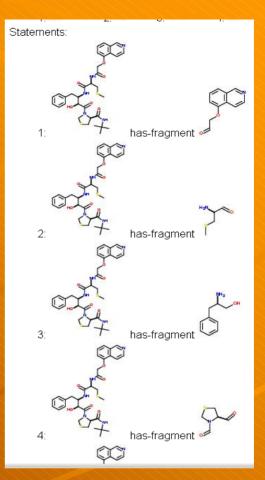
Each site such as P1, P2 is a building block for drug design These sites are used as the elements of RDF They are truly Semantic and mean 'some thing for drug design'

Statements: has-fragment has fragment has fragment has fragment

Chemical RDF

Can be added
Can be subtracted
Can be intersected

And, all, or, at least, all most



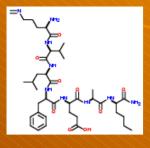
From these statements computers are capable of automatically answering questions such as (using SQL in ORACLE/MySQL)

What fragments are common between a set of compounds? (intersection)

What fragments are unique for a compound? (not in)

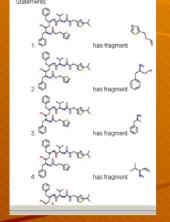
What are best neighbors of a compounds? (max(intersection))

We are now building a set of rules and schema for a Semantic Web for chemical compounds to answer these questions dynamically in a Web environment



A Review of Indexing Methods

- Proper indexing (ontology) of data is key in developing a database to support Semantic Web
 - Data indices are the only means by which a Web tool may hold, organize, select and display data
- * PDB (three-letter code, like naming of hurricanes), chemical abstracts (CAS number) are not suitable for machine reasoning
 - They are assigned by humans
 - They are not rule based
 - They have no structural rationale
 - * 3TC and 4TC may not be structurally more similar when compared to 3TC and 6DA
 - One may not use such indices to infer relationships
- IUPAC International Chemical Identifier (InChI) is machine assigned structure based identifier
 - 1/C10H10S/c1-2-5-9(6-3-1)10-7-4-8-11-10/h1-3,5-7H,4,8H2
 - Prasanna M, Vondrasek, J., Wlodawer, A., Bhat, TN. Application of InChI to curate, index and query 3-D structures. Proteins, Structure, Function, and Bioinformatics 2005; 60: 1-4.
 - Murray-Rust P, Rzepa HS, Stewart JJ, Zhang Y. A global resource for computational chemistry. J Mol Model (Online) 2005;11(6):532-541.



Indexing of Structures

InChI is Good but not Good Enough
Indexing using the RDF elements solves the problem

Use of InChI turned out to problematic for 3-D Structures

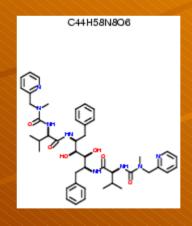
- InChI is sensitive to observed variations in structures
- 2. InChI uses a data tree of depth = 1
- Use InChI (Iupac International Chemical Identifier) Developed by NIST (Steve Stein)
 - Application of InChI to curate, index, and query 3-D structures. <u>Prasanna MD</u>, <u>Vondrasek J</u>, <u>Wlodawer A</u>, <u>Bhat TN</u>.

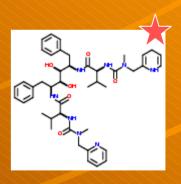
Proteins. 2005 Jul 1;60(1):1-4.

- InChI is an identifier using chemical connectivity, chirality,... of the molecule
 - 1/C10H10S/c1-2-5-9(6-3-1)10-7-4-8-11-10/h1-3,5-7H,4,8H2

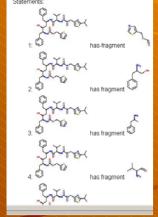
The problem is solved if indexed on elements of RDF statements Example RDF finds new related structure



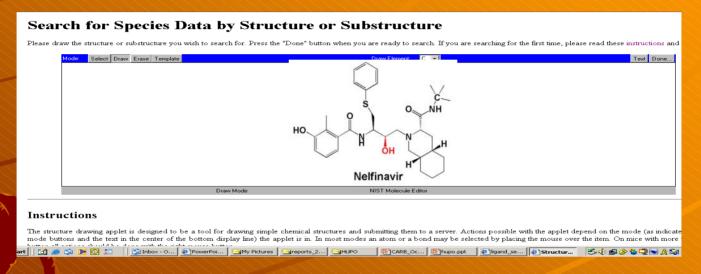




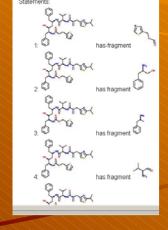
1HVC. Chemical & Crystallographic structures get different InChl



Current Query Technique

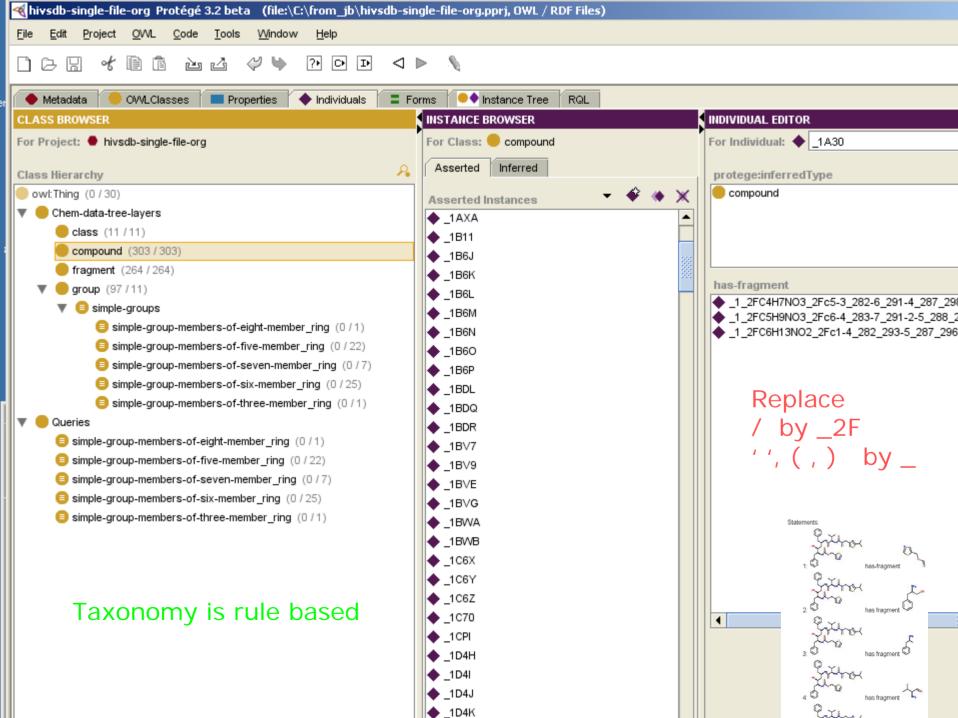


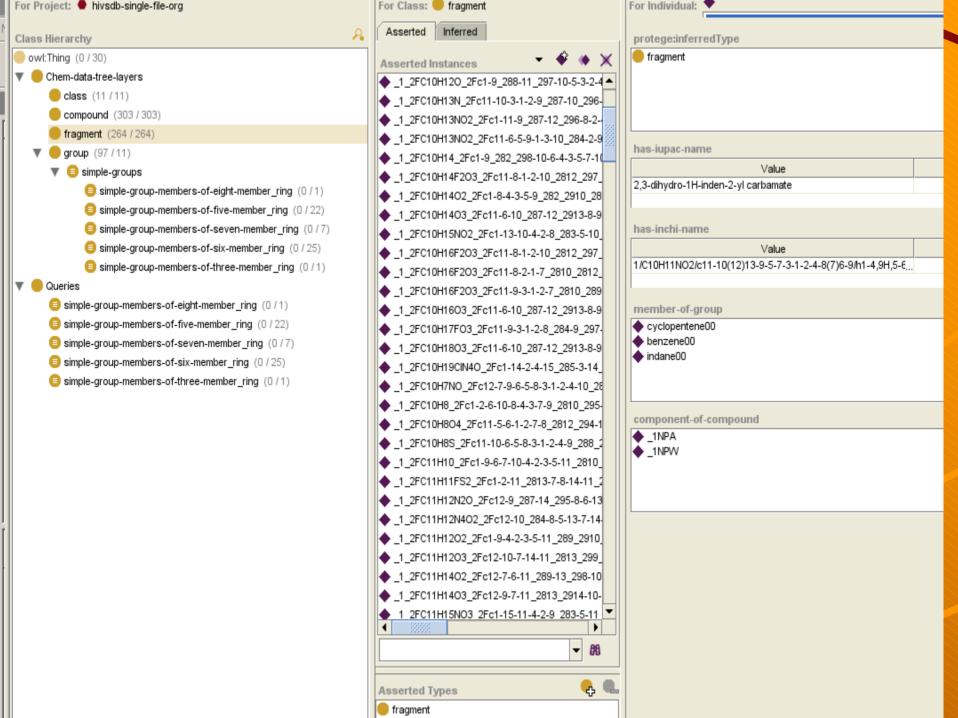
- These methods often lead to missed or overwhelming hits.
 - One need to know what is there in the database to query effectively using such method
 - If one queries simple group such as on a phenyl group every compound will be hit
 - In HIVSDB every structure has a phenyl group
 - If one queries a piperazine you may not get any hit



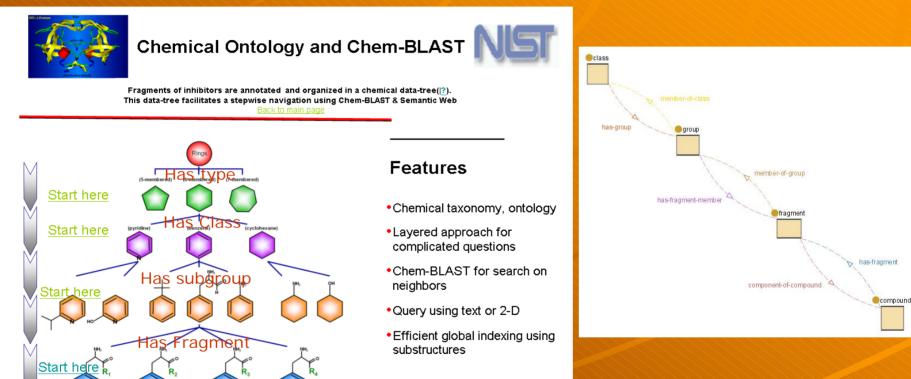
Current Query Technique is Difficult to Use

- At present there is miss-mach between the way drugs are indexed and the way drugs are queried in many databases e.g., PDB, Pub-CHEM,...
 - Drugs are indexed as a whole, for instance using InChl
 - However, 99% of the queries are based on fragments specified either by a drawing window or by an input text chosen from an IUPAC name
 - This miss match results in missed hits or overwhelming hits
 - If we use the proposed RDF based index, the problem is solved





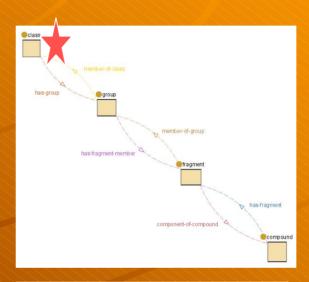
Layered data indexing using elements of RDF solves the problem

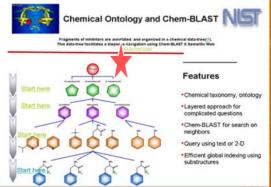


Layered query similar to Protégé or other Semantic Search engines Each element is uniquely indexed by a rule that is based on its structure

Class layer

sixdouble fused member ring ring nitrogen amino. acid containing fiveoxygen member containing ring sevensulfur lmember containing ring threephosphorus lmember containing ring

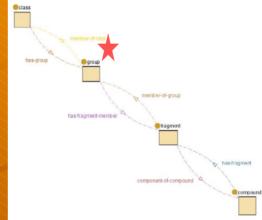


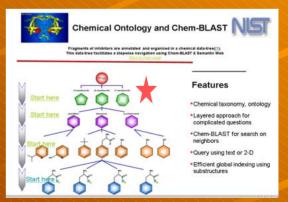


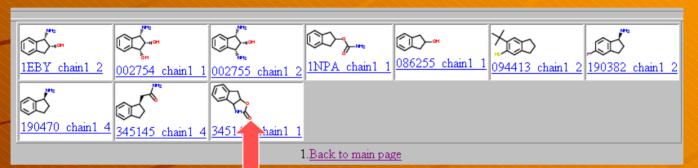
Fragment Layer for Fused Rings

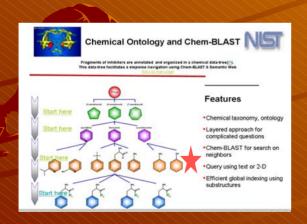
 A user gets to see all the rings of known drugs to query related compounds

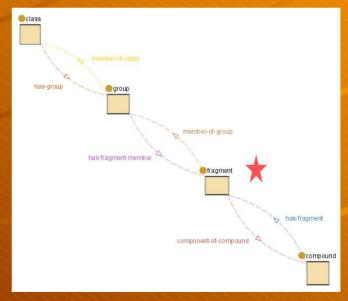






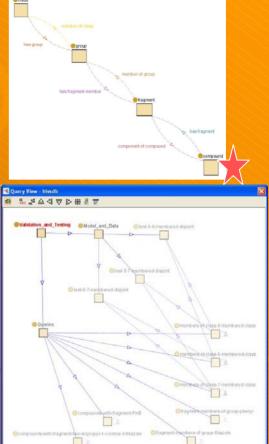


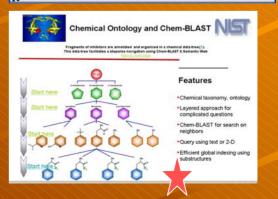




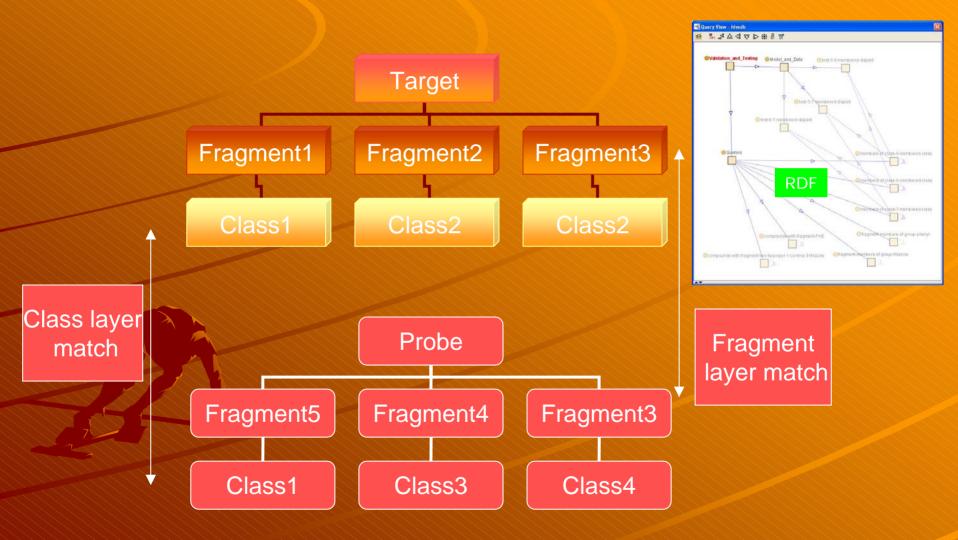


Elements of RDF can be used for complicated queries involving 'intersection', 'in', 'not in' type of searches in a database environment





Chem-BLAST
Chemical Block Layered Alignment of Substructure Technique



Chem-BLAST uses structure relationships (RDF) in a Oracle/ MySQL

Source Code

```
<?xml version="1.0"?>
<rdf:RDF xmlns="http://localhost/web/hiv-pdb/hivsdb-ind.owl#"
    xml:base="http://localhost/web/hiv-pdb/hivsdb-ind.owl"
    xmlns:pl="http://www.owl-ontologies.com/assert.owl#"
    xmlns:xsd="http://www.w3.org/2001/XMLSchema#"
    xmlns:dc="http://purl.org/dc/elements/1.1/"
    xmlns:rdfs="http://www.w3.org/2000/01/rdf-schema#"
    xmlns:daml="http://www.daml.org/2001/03/daml+oil#"
    xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
    xmlns:owl="http://www.w3.org/2002/07/owl#">
    <owl:Ontology rdf:about="">
        <rdfs:comment rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
            >alt;p style=aquot;margin-top: Oaquot;aqt;
    &lt:/p&gt:</rdfs:comment>
    </owl:Ontology>
    <fraqment rdf:ID=" 1 2FC12H1002 2Fc13-8-9-14-12-7-3-5-10-4-1-2-6-11 2810 2912 2Fh1-8H 2C9H2">
        <has-inchi-name rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
            >1/C12H1002/c13-8-9-14-12-7-3-5-10-4-1-2-6-11(10)12/h1-8H,9H2</has-inchi-name>
        <has-iupac-name rdf:datatvpe="http://www.w3.org/2001/XMLSchema#string"</pre>
            >(1-naphthyloxy)acetaldehyde</has-iupac-name>
        <component-of-compound rdf:resource="# 1HIV"/>
        <component-of-compound rdf:resource="# 1IVP"/>
        <component-of-compound rdf:resource="# HIV25NCI"/>
        <member-of-group rdf:resource="#benzene00"/>
        <member-of-group rdf:resource="#naphthalene00"/>
    </fragment>
   <fraqment rdf:ID=" 1 2FC12H17F02S 2Fc1-9 282 298-10 283 2916 2814 2C15 2912-6-4-11 2813 295-7-12 2Fh4-</p>
        <has-inchi-name rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
           >1/C12H17F02S/c1-9(2)8-10(3)16(14,15)12-6-4-11(13)5-7-12/h4-7,9-10H,8H2,1-3H3</has-inchi-name>
        <has-iupac-name rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</p>
           >(1R)-1,3-dimethylbutyl4-fluorophenylsulfone</has-iupac-name>
        <component-of-compound rdf:resource="# 1XL5"/>
        <member-of-group rdf:resource="#benzene00"/>
        <member-of-group rdf:resource="#oxosulfane oxide00"/>
        <member-of-group rdf:resource="#sulfur00"/>
    </fragment>
   <fragment rdf:ID=" 1 2FC10H1202 2Fc1-8-4-3-5-9 282 2910 288 2912-7-6-11 2Fh3-6H 2C7H2 2C1-2H3">
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```

Summary

- Structure based drug design method is described
- Current methods of indexing and querying of structures are reviewed
- * A novel chemical taxonomy for structure based drug design using Semantic Web concepts is proposed and illustrated for AIDS research
- Use of the rule based chemical taxonomy for developing RDF for Semantic Web is illustrated
- Implementation of this taxonomy is database (ORACLE & MySQL) friendly and it provides better on-line experience both for developers and users of the database
- The implementation is Web friendly and it reduces missed hits without producing overwhelming result pages
- In this approach a user need not wean through a large result set to get what he wants- Web page lays out the contents of the database in an orderly fashion for pick and choose
- This approach makes the contents of the database transparent to the users using the pictures of the molecules that are indexed with the commonly used concepts
- http://xpdb.nist.gov/hivsdb/advanced_query_files/slide0002.htm