An Introduction to SeqHound

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What is SeqHound?

SeqHound

Access Methods

User

http://blueprint.org
What is SeqHound?

SeqHound acts as a database interface that connects various data sources, including GenBank, Taxonomy, GO, LocusLink, CDD, MMDB, MedLine, and BIND, to an application programming interface (API) that can be accessed remotely.
Remote API

Over 140 calls including

- SHoundGetFasta
- SHoundGetDefLine
- SHoundGetGenBankff
- SHoundGetPDB3D
- SHoundProteinsFromTaxID
- SHoundRedundantGroup
- SHoundNeighboursFromFromGi
- SHoundGOIDFromGi
- SHoundGetDomainsFromGi

Sequence
Structure
Complete Genomes
Identity/Similarity
Annotation
Remote API

Perl
Java
C
C++
Getting started with the remote API

Perl and Java
Follow the links to the sourceforge ftp site.
Instructions included with release package.

C and C++
Follow the links to the sourceforge ftp site.
Instructions included in the SeqHound manual.
Yes
Testing

Yes
Updating

Yes
Physical architecture:

Unrestricted 24/7 global access
Supported systems:

BIND Interaction Viewer
BIND Index
BIND BLAST
BIND curation
MMDBIND

In house research

BioMOBY services

Great teaching tool
An open source local installation based on MySQL:

Introduced with Release 3.0
More information:

http://blueprint.org

Blueprint booth (#33)

Software demo (9:30 Sunday morning)

Poster (C-11)

seqhound.usergroup email list

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