

SeqHound: An open source bioinformatics application-programming platform  
Blueprint Initiative at Mount Sinai Hospital, Canada

SeqHound is a bioinformatics programming platform offering daily-updated contents of Entrez sequences, 3-D structures, sequence redundancies and neighbours, taxonomy, complete genomes, Entrez Gene contents, conserved domains, Gene Ontology annotations, database cross-references, interaction data, PubMed links and literature co-occurrence data.

SeqHound may be set up locally using a freely available user manual and software. SeqHound is ODBC compliant and employs the MySQL database engine. SeqHound is also accessible via a remote API (Perl, BioPerl, Java, C/C++). Source code is freely available under GNU public license (<http://www.blueprint.org/seqhound/>).