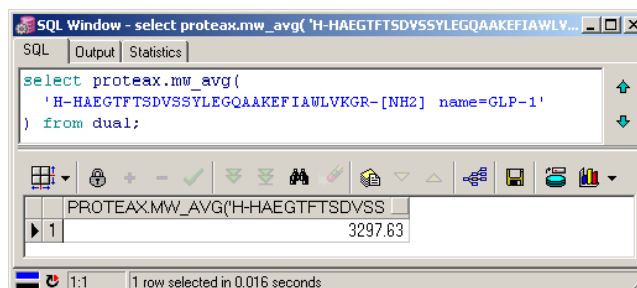


Proteax Cartridge - protein chemistry for Oracle® databases

Proteax® Cartridge lets you work with chemically or post-translationally modified protein sequences in Oracle® databases via normal SQL statements.

- Directly supports modified residues, terminals, disulfide bridges and lactam cyclizations.
- Average and mono-isotopic molecular weights based on the actual molecular structure of the protein entries.
- Sequence and structural identity checks.
- Protein comparison, manipulation, and SAR table reports via DerNot (**Derivatives Notation**) expressions.
- On-the-fly generation of 2D chemical structures for visualization or chemical indexing.

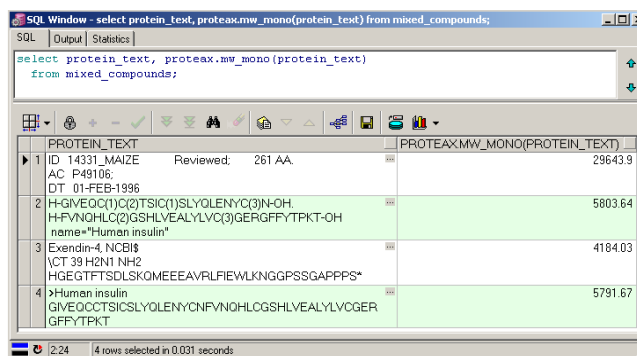


A simple SQL statement that calculates the average molecular weight of the GLP-1 molecule.

Industry standard formats

Proteax Cartridge accepts protein entries in the following standard protein file formats:

- UniProt - the UniProt Consortium
<http://www.uniprot.org>
- GPMW - by Lighthouse Data
<http://www.gpmw.com>
- FASTA - (unmodified sequences only)
<http://www.ncbi.nlm.nih.gov/blast/fasta.shtml>



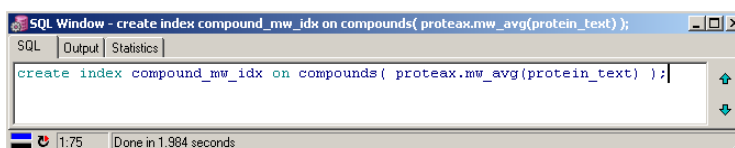
Any supported protein input format is accepted.

In addition, Biochemfusion's own PLN format lets you work with complex protein structures in an easily read format. The PLN notation was designed with specific attention to trouble-free e-mail and spreadsheet exchange of protein entries.

Protein entries can be freely converted to any of the formats PLN, UniProt, and GPMW without loss of chemical information.

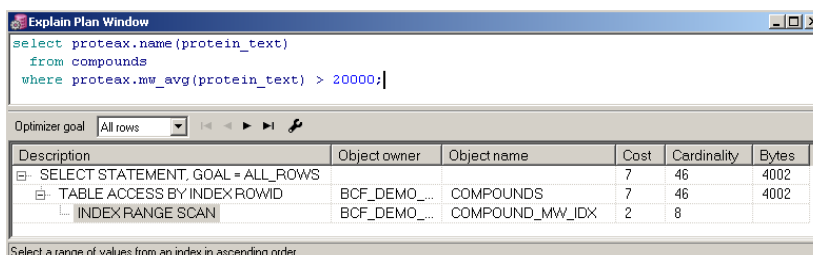
Functional indexing

Proteax Cartridge provides a number of functions that can be indexed by standard Oracle commands.



Indexes are created by normal SQL commands.

By leveraging Oracle's advanced support for functional indexes seamless integration into the Oracle optimizer is ensured.



Indexed Proteax functions are utilized as expected by the Oracle cost-based optimizer.

Protein identity checks

Proteax Cartridge contains powerful normalization functions that can be used to determine the identity of two protein entries even in the presence of cyclic chains. Normalization can be done to check sequence identity or to obtain a good measure of structural identity.

The normalization functions can be indexed to ensure excellent performance of identity checks.

Comparison and manipulation of protein entries

From January 2010 the Proteax Cartridge will support DerNot expressions. DerNot expressions specify a set of edit operations - residue substitutions, insertions, deletions, terminal modifications, and chain extensions. By applying DerNot expressions you can create new derivatives from existing entries or you can let Proteax calculate the DerNot expressions that describe the difference between proteins.

More details about DerNot expressions can be found in the *Proteax for Spreadsheets* product flyer.

Open Source visualization tools

Sequence visualization tools can be downloaded for free from the Biochemfusion web site. The tools are released with source code under a BSD-style license which lets you adapt and translate the tools to your environment of choice. Note that the tools are only hundreds of lines of code, not thousands.

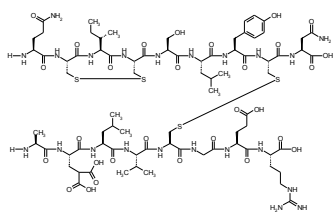
The Proteax demo site shows how these tools can be used to visualize protein sequences.

Rendering	Molecular weights	Da
1 GIVEQCCTSIICSLYQLENYC 21 NFVNQHLCGSHLVEALYLVC 41 GERGFPHYTKT	Average	5807.57022
	Standard UniProt	5795.64974

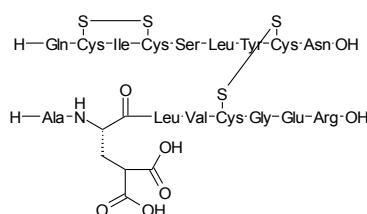
Part of the Proteax Live demo web page showing sequence graphics created by Biochemfusion's Flash rendering tool.

Chemical indexing

Proteax Cartridge can effectively extend the usable molecular size range of existing chemistry cartridges. Chemistry databases will readily index small peptides but will normally not scale well to large proteins. Proteax Cartridge can produce *condensed representation* molecules - a format that enhances registration and search performance by orders of magnitude. This will allow your chemistry database to store and chemically search protein structures with thousands of residues.



Full-structure representation of
 $H-QC(1)IC(1)SLYC(3)N-OH.H-A[G1a]LVC(3)GER-OH$




Equivalent condensed representation. All unmodified residues are represented by single "pseudo atoms". Graph complexity is reduced considerably and chemical indexing is therefore much faster.

Proteax Cartridge generates condensed chemical structures that adhere to the rules defined in the article "Building a BioChemformatics Database", Jan H. Jensen, Thomas Hoeg-Jensen and Søren B. Padkjær, *J. Chem. Inf. Model.*, November 2008, <http://pubs.acs.org/doi/abs/10.1021/ci800128b>.

System requirements

Proteax Cartridge installs on servers running a 32- or 64-bit version of Linux® or Windows®. In order to install Proteax Cartridge you will also need to have an existing Oracle 10g or 11g database running on your server. The following Oracle configurations are supported.

	Oracle 10gR2	Oracle 11gR1	Oracle XE (10g)
Windows	32-bit ✓ 64-bit ✓	32-bit ✓ 64-bit ✓	32-bit ✓
Linux 	32-bit ✓ 64-bit ✓	32-bit ✓ 64-bit ✓	32-bit ✓

Licensing

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The Tux penguin logo is the creation of Larry Ewing, lewing@isc.tamu.edu

Try the online demo at <http://www.biochemfusion.com/demo>
Contact info@biochemfusion.com or call +45 2063 4029 to obtain a free trial license.

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