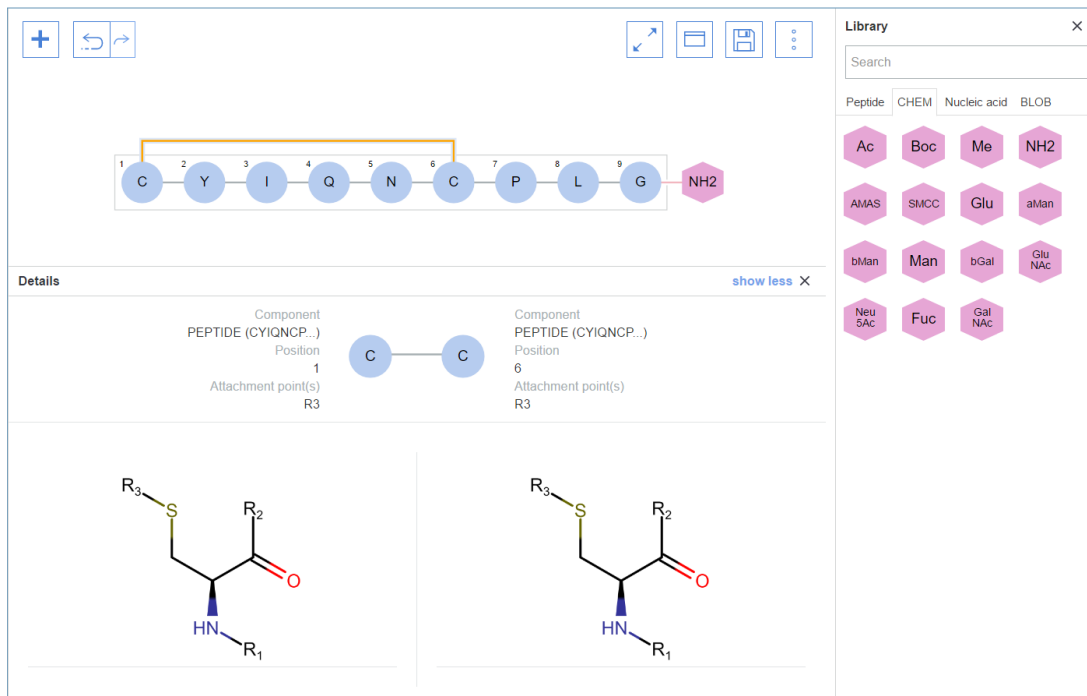
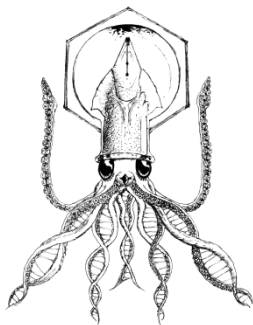




Tim Parrott
Roland Knispel

BIOEDDIE AND BIOMOLECULE TOOLKIT

- JS application for all major browsers
- Easy editing
- No-structure components
- Native support for MOL/HELM/sequence



The screenshot displays the BioEddie web application interface. At the top, there are navigation icons: a plus sign, a left arrow, and a right arrow. Below these is a peptide sequence editor showing a sequence of amino acids: C (1), Y (2), I (3), Q (4), N (5), C (6), P (7), L (8), G (9), and NH2. An orange bracket highlights the C6 and C9 positions. Below the sequence editor is a 'Details' section with a 'show less' link. It contains two component details for 'PEPTIDE (CYIQNCP...)' at position 6, showing attachment points R3 and C. Below the details are two chemical structures of a peptide backbone fragment, each with substituents R1, R2, and R3. The right side of the interface features a 'Library' panel with a search bar and tabs for 'Peptide', 'CHEM', 'Nucleic acid', and 'BLOB'. The 'Peptide' tab is active, showing a grid of chemical groups: Ac, Boc, Me, NH2, AMAS, SMCC, Glu, aMan, bMan, Man, bGal, Glu NAC, Neu 5Ac, Fuc, and Gal NAC.

+

↶ ↷

Toolbar


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Canvas



BioEddie
by ChemAxon

Library

Local Library

Search

Peptide Chem Nucleic acid BLOB

X	A	C	D	E
F	G	H	I	K
L	M	N	O	P
Q	R	S	T	V
W	Y	dC	dD	dE
dD	dE	dF	dG	dI
dK	dL	dM	dN	dP
dQ	dR	dS	dT	dV
dW	dY	Aib	B-Ala	Cit
Dha	g-Abu	Gla	Glp	Hse
Hyp	Nle	Nva	Orn	Sar
Aha	2Nia	meA	meC	meD

Library/
Annotations
panel

HELM Details

SSSSV2.0

HELM/Details view

Library Components

Library ×

Local Library ▼ ⚙️

Search

Peptide Chem Nucleic acid **BLOB**

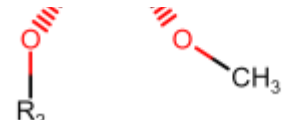
PEG

5kP EG-1 5kP EG-2

GNP

mAb

Glycosylation



The image shows a software interface for library components. At the top, there is a 'Library' header with a close button (X) and a 'Local Library' dropdown menu with a settings icon (gear). Below this is a search bar. A navigation bar contains tabs for 'Peptide', 'Chem', 'Nucleic acid', and 'BLOB', with 'BLOB' currently selected. The main content area is divided into sections: 'PEG', 'GNP', 'mAb', and 'Glycosylation'. The 'PEG' section is highlighted and contains two green circular icons labeled '5kP EG-1' and '5kP EG-2'. Below the 'Glycosylation' section, two chemical structures are shown: one with a red wavy line representing a PEG chain attached to an oxygen atom, which is further attached to an R2 group; the other shows a red wavy line representing a PEG chain attached to an oxygen atom, which is further attached to a methyl group (CH3).

https://bioeditor-demo.chemaxon.com

The screenshot displays the BioEditor web interface. At the top, the browser address bar shows the URL `https://bioeditor-demo.chemaxon.com`. The main workspace contains a peptide sequence represented by 11 numbered circles (1-11) connected by lines. The residues are: 1 (BMT with a pink Me group), 2 (g-Abu), 3 (Sar), 4 (meL), 5 (meL with an inline chemical structure of a methyl group), 6 (meL), 7 (A), 8 (dA), 9 (meL), 10 (meL), and 11 (meV). A blue box highlights the inline chemical structure of the 5th residue, which is a methyl group (H₃C-CH₂-). A green arrow points from a text box labeled "Inline chemistry" to this structure. Below the peptide sequence, there is a HELM viewer with a "Details" tab. The HELM string is: `PEPTIDE1([BMT].[g-Abu].[Sar].[meL].V.[meL].A.[dA].[meL].[meL].[meV])CHEM1([Me])$PEPTIDE1,PEPTIDE1,11:R2-1:R1|PEPTIDE1,CHEM1,1:R3-1:R1$$$V2.0`. A green arrow points from a text box labeled "HELM viewer with selection highlights" to the HELM string. To the right of the peptide sequence is a "Library" panel with a search bar and a grid of monomer buttons. A green arrow points from a text box labeled "Monomer preview on library hover-over" to a tooltip for "L-Tyrosine" (R1: H, R2: OH) which shows its chemical structure. A text box labeled "Context-dependent display options" has arrows pointing to the peptide sequence and the HELM viewer. The ChemAxon logo is in the bottom right corner.

Me

1 BMT 2 g-Abu 3 Sar 4 meL 5 meL 6 meL 7 A 8 dA 9 meL 10 meL 11 meV

Inline chemistry

Context-dependent display options

HELM Details

PEPTIDE1([BMT].[g-Abu].[Sar].[meL].V.[meL].A.[dA].[meL].[meL].[meV])CHEM1([Me])\$PEPTIDE1,PEPTIDE1,11:R2-1:R1|PEPTIDE1,CHEM1,1:R3-1:R1\$\$\$V2.0

HELM viewer with selection highlights

Monomer preview on library hover-over

L-Tyrosine
R1: H, R2: OH

Library

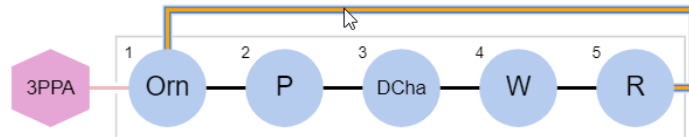
Search

Peptide CHEM Nucleic acid BLOB

X A C D
E F G H
I K L M
N O P Q
R S T V
W Y U dA
dD dE dF
dI dK dL
dN dP dQ
dS BMT dV
dW dY Aib B-Ala
Cit Dba g- Glu

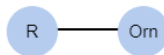
ChemAxon

Linkage Details

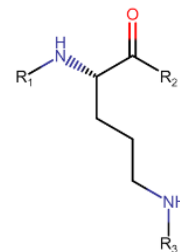
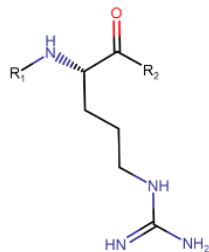


.M Details

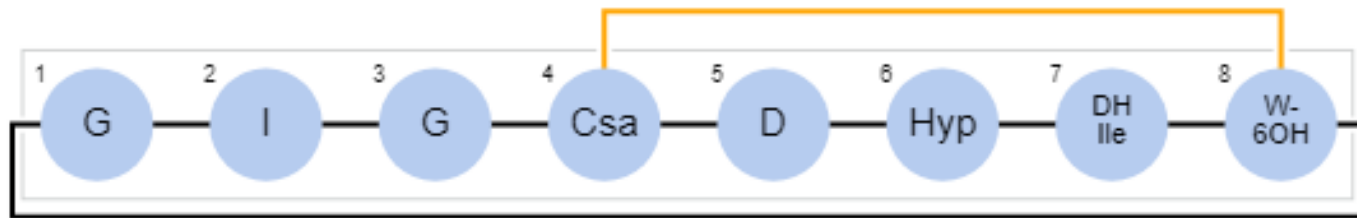
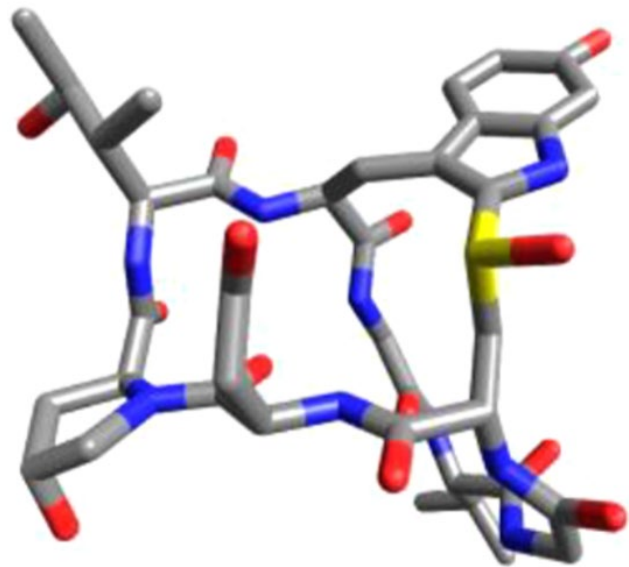
Component
PEPTIDE (OrnPDChaWR)
Position
5
Attachment point(s)
R2



Component
PEPTIDE (OrnPDChaWR)
Position
1
Attachment point(s)
R3

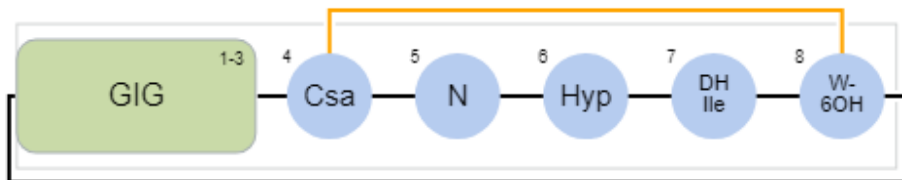


Bicyclic peptides

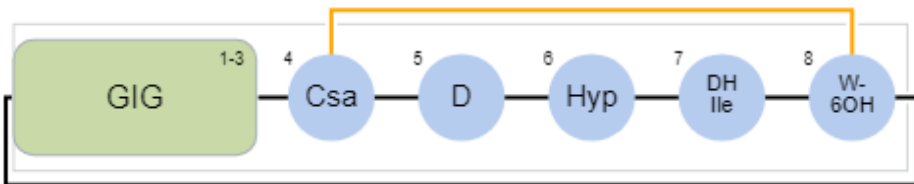


β -Amanitin

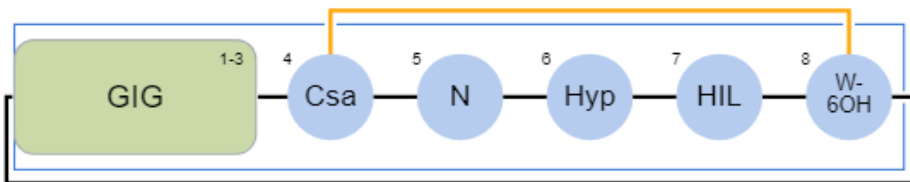
Sequence Comparisons



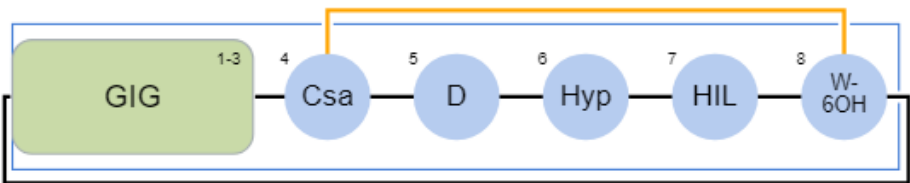
α -Amanitin



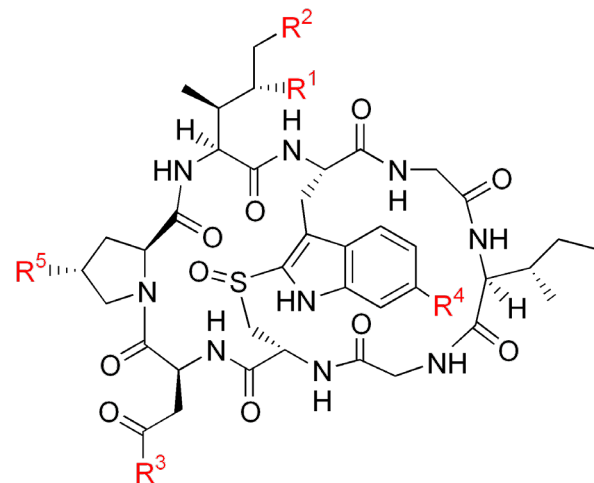
β -Amanitin



γ -Amanitin

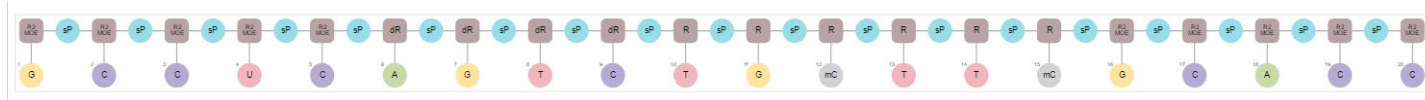


ϵ -Amanitin

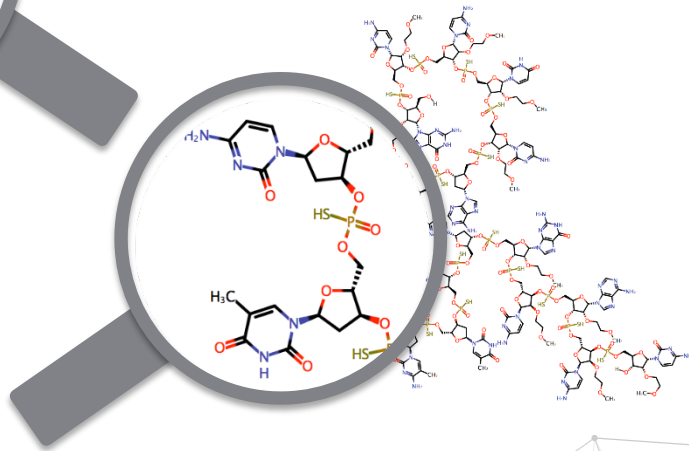
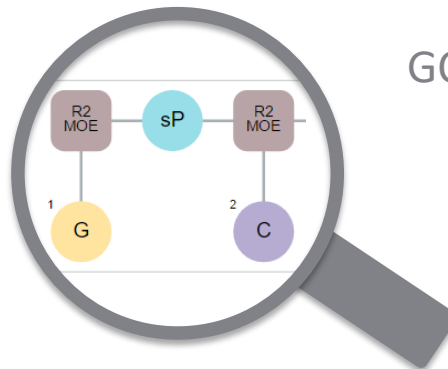


Name	R ¹	R ²	R ³	R ⁴	R ⁵
α -Amanitin	OH	OH	NH ₂	OH	OH
β -Amanitin	OH	OH	OH	OH	OH
γ -Amanitin	OH	H	NH ₂	OH	OH
ϵ -Amanitin	OH	H	OH	OH	OH

Oligonucleotides



GCCUCAGTCTGCTTCGCACC



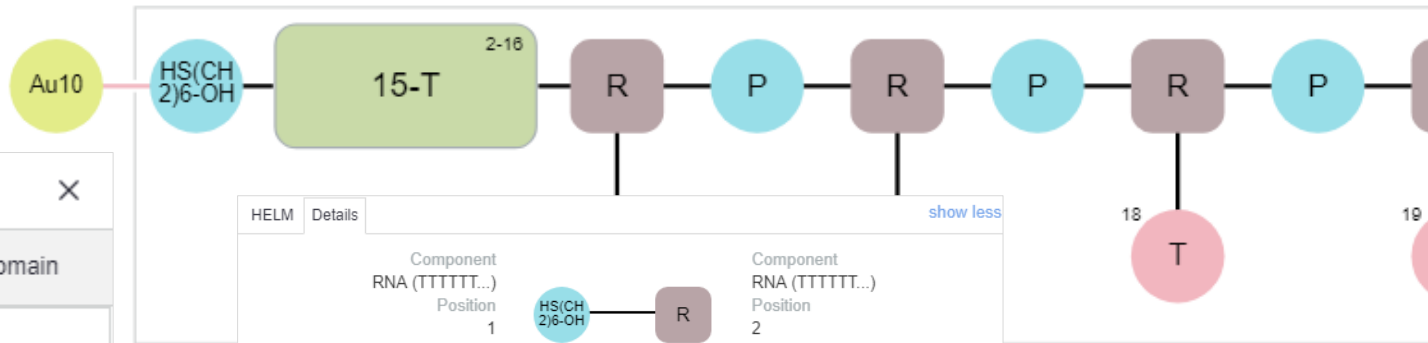
- Natural or modified bases
- Natural or modified sugars
- backbone chain chemistries



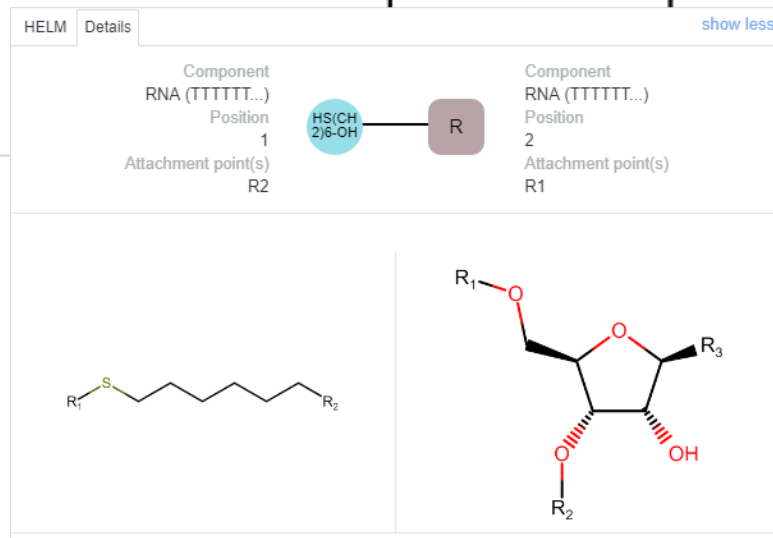
Mipomersen (Kynamro)

FDA approved to treat homozygous familial hypercholesterolemia

Gold Nanoparticles



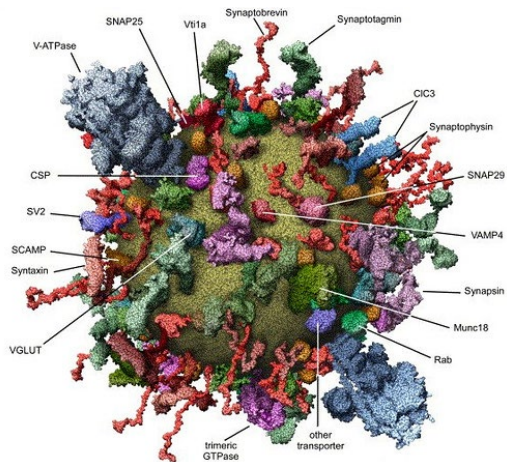
Annotations	
Macromolecule	Component
size (nm)	10
Number of particles /ml (OD=1)	4.8-E12
agent	citric acid
functionalized	no
OD /ml	1



J. Am. Chem. Soc., 2004, 126 (38), pp 11768–11769

DOI: 10.1021/ja046970u

Biomolecule Toolkit



API (Java and REST-ful) for

- Native HELM support (HELM, HELM2, xHELM)
- Standardization
- Centralized DB storage
- Registration of entities and batches with custom business logic
- Search by sequence/chemical structure/metadata
- Conversion to/from Mol/FASTA/HELM
- Property calculations

New: Similarity-based searching

- Distance-based

TGRWLQAKGV	TG-WIQAKGVW	3
Query sequence	Target sequence	Edit distance

- BLAST (P,N)
 - Using NCBI BLAST binaries
 - Experimenting with BLAST DB updates for large datasets

New: Sequence enumeration

- Ala-Scan
- Exhaustive enumeration of residue replacements

MTGCRLCYWEC

Position

Substitutions

MT **V** CRLCYWEC

3

V,A,Dha,Hse

MT **A** CRLCYWEC

6

I,V

MT **[Dha]** CRLCYWEC

MT **[Hse]** CRLCYWEC

MT **V** CRICYWEC

MT **A** CRICYWEC

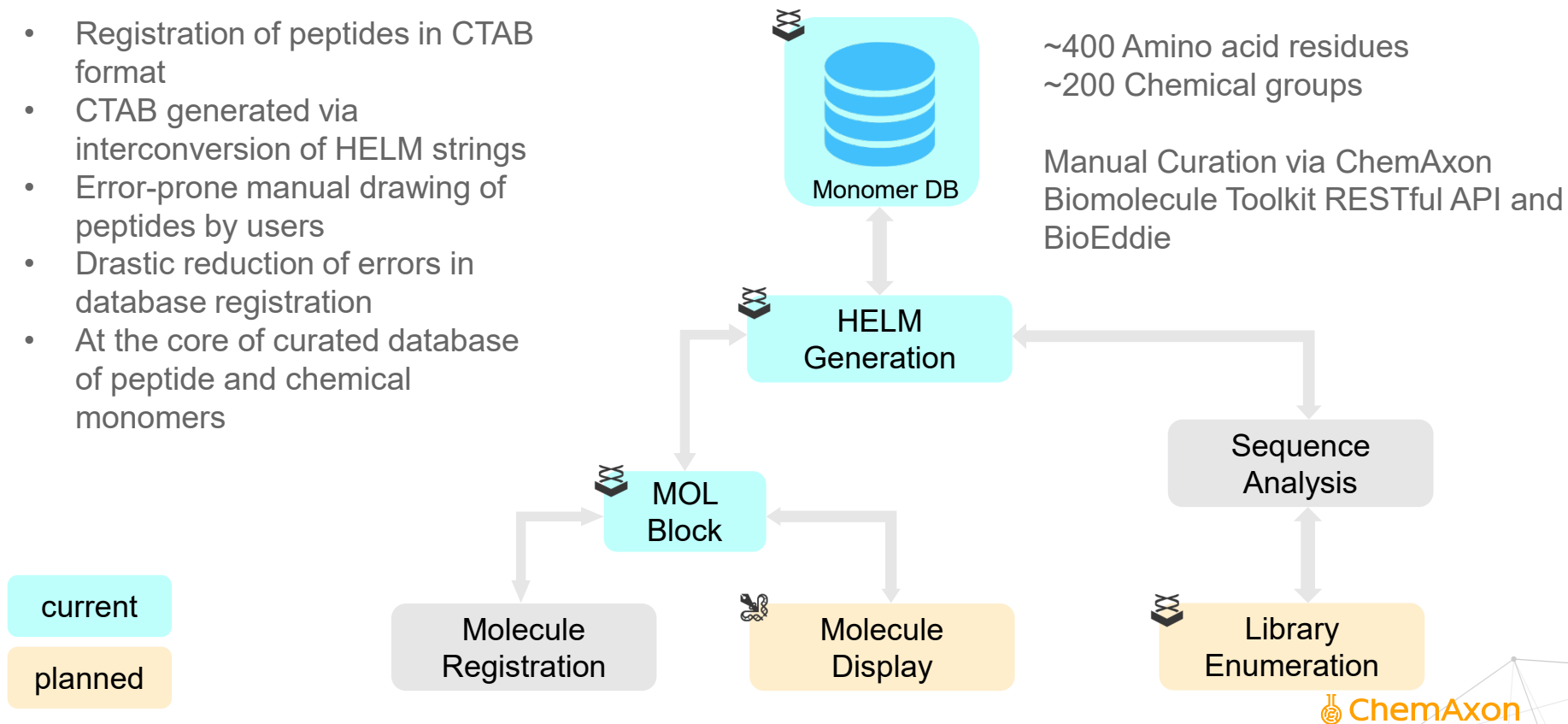
...



USE CASES

Biomolecule Toolkit Integration at Heptares*

- Registration of peptides in CTAB format
- CTAB generated via interconversion of HELM strings
- Error-prone manual drawing of peptides by users
- Drastic reduction of errors in database registration
- At the core of curated database of peptide and chemical monomers



*See Conor Scully, Heptares, UGM presentation, 2018, Budapest

Overview

Snapshot

SWITCH

Add property

#4

Anoplin (G1A, L3V, K4Om, R5dR, K7Or n, T8S, L10V) novel, stable

#3

Anoplin (K4Om, K7Om) novel

#2

Anoplin (K4Om)

#1

Anoplin (UniProtKB P0C005)

+

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1 A 2 L 3 V 4 Om 5 dR 6 I 7 Orn 8 S 9 L 10 V NH2

Details - Sequence ×

1 ALVRIKSLV

Library

Search

Peptide	CHEM	Nucleic acid	BLOB
N	O	P	
Q	R	S	
T	V	W	
Y	U	dA	
dC	dD	dE	
dF	dH	dI	
dK	dL	dM	

Sequence alignment

0

A	L	V	R	I	K	L	V
G	L	L	R	I	K	L	V

Molweight

	Current	Pinned
Molweight	1097.419	1153.527

Isoelectric Point

pl	Current	Pinned
	11.69	11.69

Antimicrobial activity

Matches: 3. Showing page 1 of 3. [Prev](#) [Next](#)

#3116 Anoplin

Target Species	Activity Measure	Activity
Staphylococcus aureus ATCC 6538	MIC	50 µg/ml
Staphylococcus aureus ATCC 6538	MIC	>75 µg/ml
Staphylococcus aureus ATCC 25923	MIC	5 µg/ml

Reference: Konno K., et al, *Biochim Biophys Acta*, 2001, 1550, 70-80

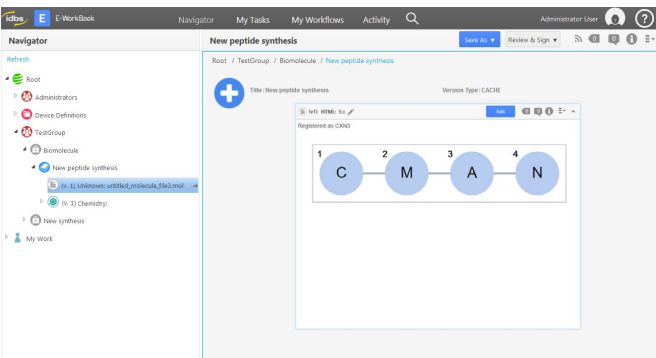
PDB ID: 2MJQ

Last edited by Borkenkäfer 36m

From designing small molecules towards designing peptides

Prototype for enhancing Marvin Live with peptide-specific data plugins featured by public data sources and Biomolecule Toolkit capabilities

Integration with IDBS EWB



- Registration directly from ELN (in production for 3 US customers)
- Biomolecule Toolkit integrated through REST API
- BioEddie default sketcher for chemically modified sequences

Next steps

- ELN-wide search for sequences
- Add support for bio-synthesis reactions
- Add Support for high-availability cloud deployments (e.g. clustering, distributed transactions)

Biomolecule Toolkit Roadmap

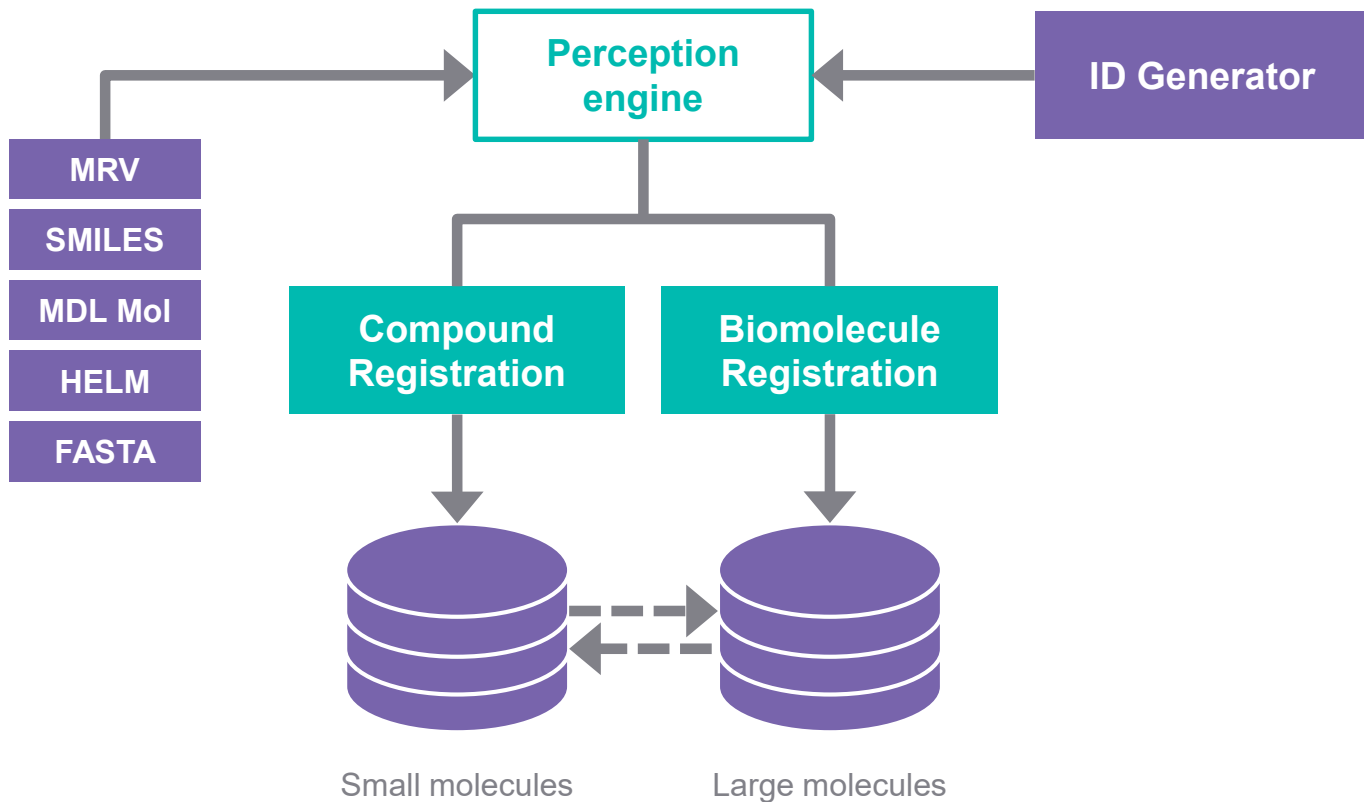
H1 2019

- Role-based authorization
- ✓ Docker image
- ✓ BLAST integration
- Genealogy capture
- Distributed deployment in cloud environments

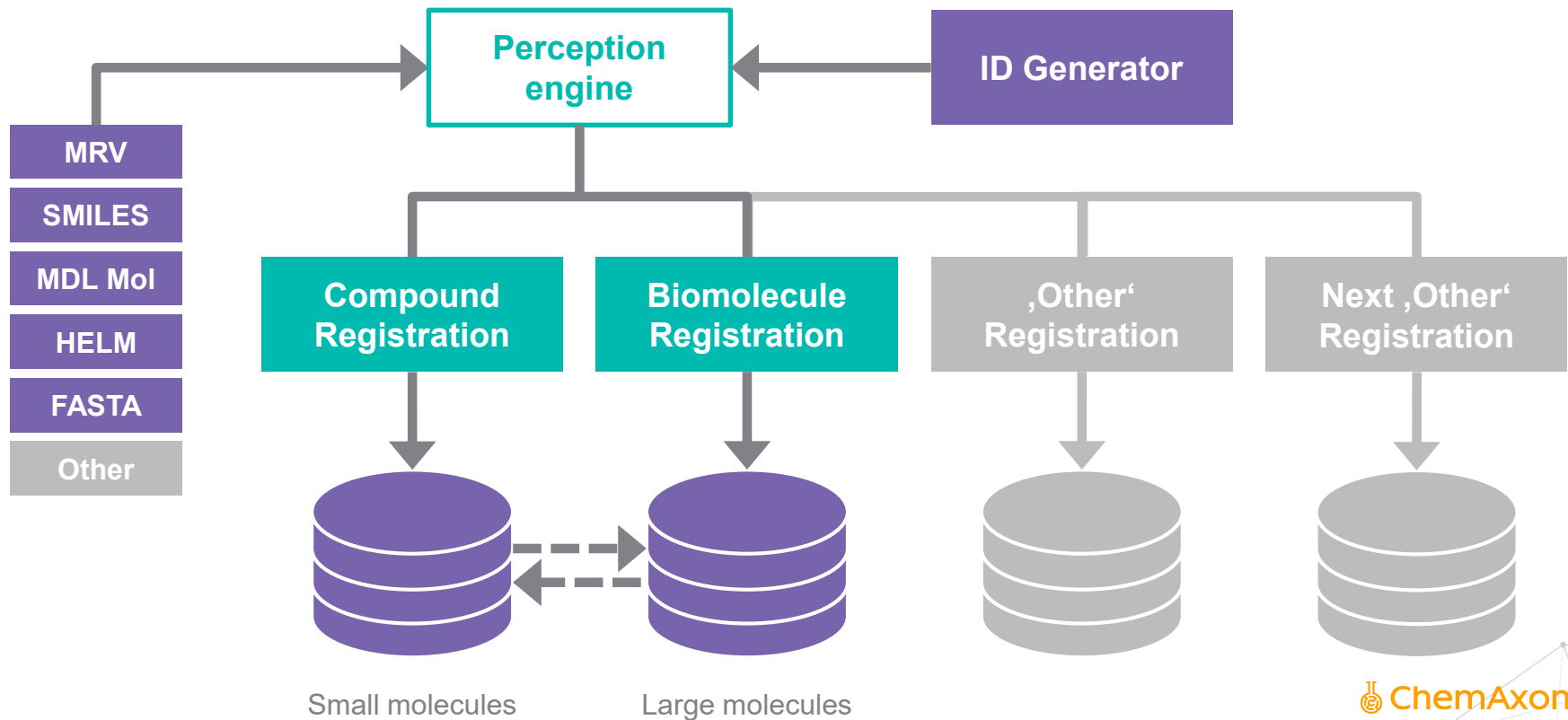
H2 2019

- Focus on agnostic registration and dependent requirements

Longterm plans – Agnostic registration



Longterm plans – Agnostic registration





GET IN TOUCH

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