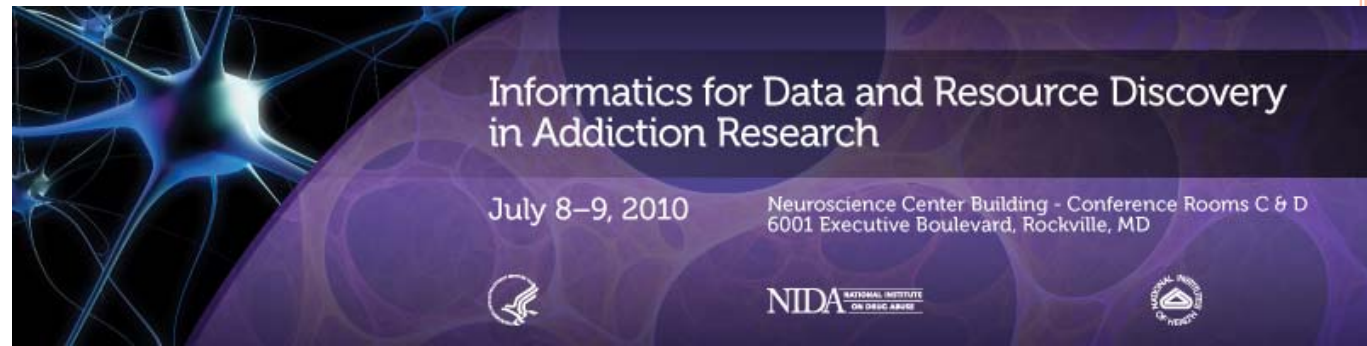


# RESOURCES TO UNDERSTAND THE ROLE OF NEUROPEPTIDES IN DRUG ABUSE

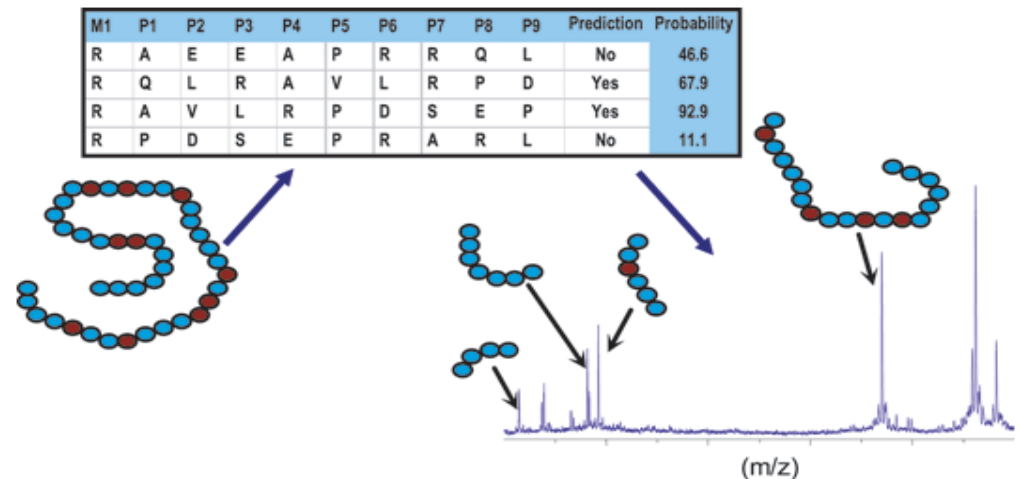
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Champaign



# BACKGROUND

- **Neuropeptides: messenger molecules critical in neural communication & substance abuse**
- **The cleavage of neuropeptides from prohormone precursors is a complex process**
- **Empirical data varies with peptide and species**
- **Our research**
  - **Funding: NIDA P30 DA 018310 and R21 DA027548**
  - **Neuroproteomics Center on Cell-Cell Signaling (<http://neuroproteomics.scs.illinois.edu/>)**
  - **predict neuropeptides, annotate prohormone genes, integrate proteomic data for neuropeptide identification and characterization**
- **Mass spectrometry**
  - **NeuroPred**
  - **SwePep**
- **Gene expression**
  - **Beehive**
  - **<http://stagbeetle.animal.uiuc.edu/beehive>**



# INTERNAL RESOURCES: NEUROPred

<http://neuroproteomics.scs.illinois.edu/neuropred.html>

Continual update of:  
prohormone sequences,  
cleavage information,  
prediction models

UIUC Neuroproteomics >> Welcome to NeuroPred >> NeuroPred Application

[Input Documentation](#) >> [Output Documentation](#) >> [Sequences](#)

## NeuroPred: Prediction of cleavage sites and mass from neuropeptide precursors

Please enter sequence into the sequence submission box below

```
adm precursor (proadrenomedullin) ADML_BOVIN (062827)
>sp|062827|ADM precursor (proadrenomedullin) Bos taurus SignalP=21
MKLVFVALMYLGSALFLGVDIARLDVAAEFRRKWKWALSRGKRELRESSYPTGLADVK
AGPVQTLIRPQDVKGASRSPQASSPDAARIRVKRYRQSLNMFQGLRSFGCRFGTCTVQKL
AHQIYHFDTKDKDGSAPRSKISPPQGYGRRRRSLPEAGLGRITLLQPPEPKLRGAPDSRVH
```

OR from a file named:   (Note that a file takes priority over the textbox)

### Model Selection and Output Selection Tasks

#### Model Selection

Known Motif  
 Mollusc\_Complex  
 Mollusc\_Basic  
 Mammalian  
 Apis  
 Drosophila

#### Output Selection Tasks

Predict Cleavage Sites Only  
 Predict Cleavage Sites and Calculate Model Accuracy Statistics  
 Predict Cleavage Sites and Obtain Mass of Predicted Peptides

### Options for Modeling and Mass Calculations

Threshold cleavage probability (0-1.0):  Confidence interval significance level (0.005-0.20):

Minimum number of amino acids: Before  and After  cleavage site.

Number of amino acids in the signal sequence:  Signal length identifier:

Lower mass value (Da):  Upper mass value (Da):

Maximum number of amino acids in a peptide:  Degree of peptide extension:

Sort output:  No  Alternatively, sort on:  Average Mass  Monoisotopic Mass  Sequence

### Post-Translational Modifications (PTMs)

Trim C-terminal K and R

#### Most Common PTMs

Amidation  
 Pyroglutamination  
 Acetylation  
 Sulfation of Y

O-linked Glycosylation of S  
 O-linked Glycosylation of T  
 Dipeptidase  
 Carboxylation of E  
 DiAcetylation

#### Less Common PTMs

N-linked Glycosylation of S  
 N-linked Glycosylation of T  
 Hydroxylation of P  
 Phosphorylation of S  
 Phosphorylation of T  
 Bromination of W  
 Methylation of E  
 Methylation of H  
 Methylation of K  
 Methylation of R

# EXTERNAL RESOURCES: SWEPEP

[http://www.swep  
ep.org/thegpm/s  
eq.html](http://www.swep<br/>ep.org/thegpm/s<br/>eq.html)

Empirically  
confirmed peptide  
sequences



Swepep uses code adapted from GPMDB to store and visualize MS/MS spectra  
powered by SwePep  
send us [email](#)

The SwePep MS/MS Database  
Swepep uses code adapted from GPMDB to store and visualize MS/MS spectra

Search by peptide sequence

Sequence  [View matches](#)

Examples [YGGFMRSL](#)  
[SANSNPAMAPRE](#)  
[SLSAASAPLVETSTPLRL](#)

Search by molecular mass

m+h  [View matches](#)

parent  $\delta m$    Da  ppm



4 matches for m+h: 1200

Best matches shown. [Show all](#)

#	log(e)	m+h	delta	z	peptide
1.	-3.3	1202.59	-0.299	2	200 <a href="#">QLEDEAKELQ</a> <sup>209</sup>
2.	-2.0	1202.59	-0.219	2	200 <a href="#">QLEDEAKELQ</a> <sup>209</sup>
3.	-1.8	1202.59	-0.239	2	200 <a href="#">QLEDEAKELQ</a> <sup>209</sup>
4.	-1.6	1197.663	-0.102	3	222 <a href="#">EKNAIKNAH</a> <sup>231</sup>



# RELATIONSHIP BETWEEN INTERNAL AND EXTERNAL INFORMATION

- Integration of NeuroPred and SwePep
  - Facilitated by the complete disclosure of information between resources
- Integration of information from UniProt and NCBI Entrez
  - may not be cross-referenced
  - For example OX26 (orexigenic neuropeptide QRFP)
- Integration of quantitative experimental information
  - Multiple labs



# OBSTACLES TO USE AND SHARE DATA AND RESOURCES

- Unavailability of universal public repository of proteomic experiments
  - Follow the example of gene expression microarray experiments
- Expectation of availability of proteomic experimental data in a public and timely manner
  - Enforced by some journals
- Diverse nomenclature across repositories, species
- Value of NIDA-centric catalogue of resources (tools, software, websites, repositories)



# REFERENCES

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