https://doi.org/10.17952/37EPS.2024.P2268

PICKAPEP

Visualization and Calculation of Cyclized and Modified Peptidomimetics Made Easy

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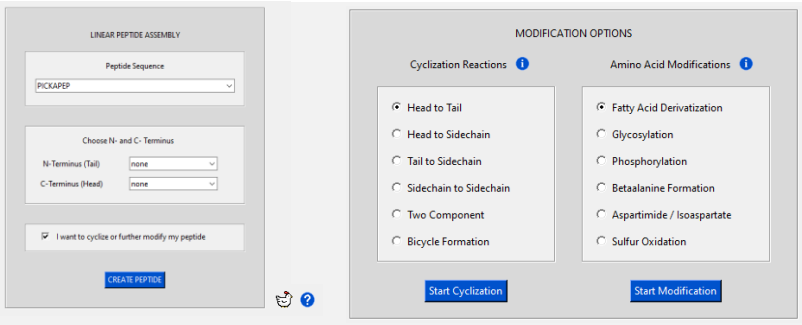
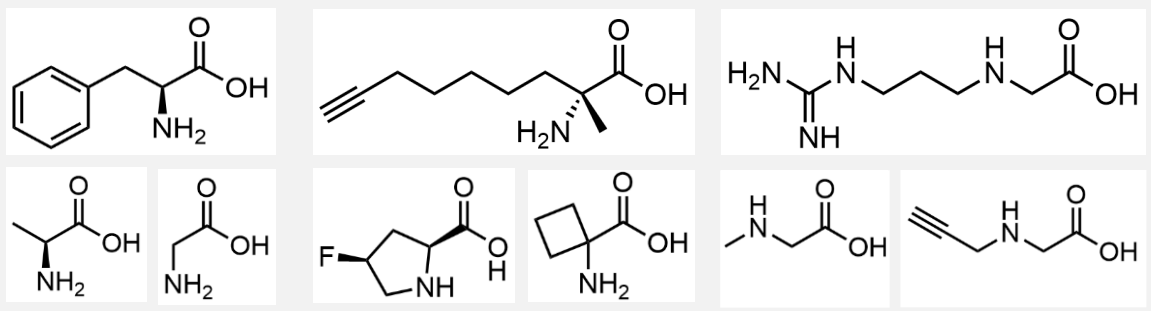
INTRODUCTION

Recently, the interest in peptides and peptidomimetic structures has risen enormously.[1] Novel modification strategies including nonnatural amino acids, sophisticated cyclization strategies, and side chain modifications to improve the pharmacokinetic properties of peptides are continuously arising. However, a calculator tool accompanying the current development in peptide sciences towards modified peptides is missing. Herein, we present the application **PICKAPEP**, enabling the virtual **construction** and **visualization** of peptidomimetics with regular and self-designed amino acids.[2] **Calculated** parameters include the molecular weight, the **LogP**, the **TPSA**, and the peptide **SMILES code**.[3] To our knowledge, **PICKAPEP** is the first tool allowing users to add custom amino acids (**AA**) as building blocks and also the only tool giving the possibility to process **large peptide libraries** and calculate parameters for multiple peptides at once.

USER FRIENDLY GRAPHICAL INTERFACE





- Enter sequence
- Modify N- & C-terminus
- Cyclize your peptide

AMINO ACID BUILDING BLOCKS

Non-Natural Amino Acids
- D- or N-methylated
- Peptoid building blocks
- Various

Own Amino Acids
Backbone template

Natural Amino Acids
One or three letter code

Beta alanine

Post-Translational Modifications
- Glycosylation
- Phosphorylation

Fatty Acid Derivatization
Spacer + Linker + Fatty (di)acid

AMINO ACID MODIFICATIONS

Common Side Products from Synthesis
- Sulfur oxidation
- Formation of aspartimide and isoaspartate

- > 100 predefined AAs
- Create your own AAs
- Modify side chains

CYCLIZATIONS

Backbone Involved
- Head to tail
- Head to sidechain
- Tail to sidechain

Multiple Cyclizations
- Bicycle formation
- Stitched peptides

Sidechain to Sidechain
- Natural and nonnatural
- Two component

C-/N-TERMINUS MODIFICATIONS

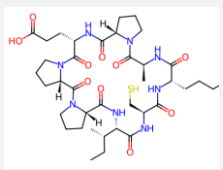
- Efficiently calculate multiple peptides at once
- Visualize your peptides in 2D and 3D
- Get all important parameters

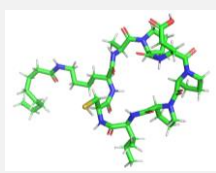
MULTIPLE PEPTIDE PROCESSING

	A	B	C	D	E	F	G	H	I
1	**Name**	**Input Linear Sequence**	**Nterm**	**Cterm**	**Cyclizations**	**Modifications**	**Status**	**Sequence**	**Linea**
2	**Angiotensin I**	D-R-V-Y-I-H-P-F-H-L					Done	N-Term ,	D-R-V
3	**Angiotensin II**	Asp-Arg-Val-Tyr-Ile-His-Pro-I					Done	N-Term ,	D-R-V
4	**Ciclosporin A**	V-Lnme-A-Ad-Lnme-Lnme-V			Head, Tail		Done	N-Term ,	*V-Lnr
5	**Linaclotide**	CCEYCCNPACTGCY			1, 6, disulfide; 2 , 10, c		Done	N-Term ,	C-C-E
6	**Liraglutide**	HAEGTFTSDVSSYLEGQAAKEFI				20, fa, 1, y-glu, c16ac	Done	N-Term ,	H-A-E
7	**Semaglutide**	HAibEGTFTSDVSSYLEGQAAKE				20, fa, 2, ado, 1, y-glu, c1	Done	N-Term ,	H-Aib
8	**Motixafortide**	Motix1-R-Motix3-C-Y-Cit-K-K		Am	4, 13, disulfide		Done	N-Term ,	Motix
9	**Zilucoplan**	K-V-E-R-F-D-Dnme-Ziluc8-Y-A	Ac		1, 6, amide	15, fa, 1, y-glu, c16 ac	Done	N-Term ,	Ac-K-
10									
11	**Peptide 1**	P-J-C-K-A-P-E-P					Unknown aminoacid: J		
12	**Peptide 2**	P-I-C-K-A-P-E-P			2, 8 , disulfide		Reaction 1 not possible		
13	**Peptide 3**	P-I-C-K-A-P-E-P				3, sulfiac; 7, a-D-GalNac	Glycosylation not possible		
14	**Peptide 4**	P-I-C-K-A-P-E-P	Am				N-Terminus not available		
15									

OUTPUT AND VISUALIZATION

Chemical Formula: $C_{38}H_{63}N_9O_{11}S$	Number of Amino Acids: 8
Molecular Weight: 854.04	LogP: -1.78
Exact Weight: 853.4368	TPSA: 298.77
$[M+H]^+$: 854.4446	Rotatable Bonds: 23
$[M+2H]^{2+}$: 427.7262	Number of HBA: 12
$[M+3H]^{3+}$: 285.4867	Number of HBD: 10
$[M+4H]^{4+}$: 214.367	Aromatic Rings: 0





CONCLUSION

With **PICKAPEP**, we provide an open-source tool which can be used to generate numerous types of cyclized and modified peptidomimetics. Combined with its user-friendly comprehensive GUI and various options, **PICKAPEP** can be used **without** substantial **computational expertise** or **knowledge in peptide chemistry**.

Resources and contact information

Resources

Open source software: ETH research collection

Source code: Github

Contact:

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ACKNOWLEDGEMENT

The authors thanks the organizing committee for giving a waiver for registration fee to V. Erckes.