

PiTou 皮头 computational Furin cleavage sites prediction tool

Download guide:

1. PiTou is a computational Furin cleavage sites prediction tool. PiTou is available as a stand-alone software package to install and run on windows platform at the user's own computer. Users can have fast predictions of Furin cleavage sites on hundreds of proteins.
2. This are 3 possible applications users may consider using 20-residues Furin cleavage motif and this tool:
 - predict Furin cleavage sites on proteins sequences.
 - engineer amino acids (physical property of amino acids) and reach desirable Furin cleavage sites for different purpose, e.g. drug delivery.
 - predict loss/gain of Furin cleavage sites in human disease as results of detected genomic mutations.
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5. The name 皮头 PiTou originated from 小绰皮 XiaoChuoPi, a local dialect used in ancient China Yuan dynasty (1271-1368) 元朝 (1271年-1368年). This word roughly means “a little gangster on the street”. This is how a real PiTou looks like in modern time http://www.nuolan.net/pitou_picture.html.

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