Návrh protospaceru pomocí skriptu

1. Instalace Pythonu

Stáhněte si a nainstalujte verzi Pythonu vhodnou pro váš operační systém ze stránky: <u>https://www.python.org/downloads/</u>



2. Stažení skriptu

Ze stránky <u>https://github.com/ahatoum/CRISPR-Cas10-Protospacer-Selector</u> si stáhněte skripty MainScript.py, GNfunctions.py. Oba skripty si uložte ve stejné složce.

GitHub, Inc. [US] github.com/ahatoum/CRISPR-Cas10-Protospacer-Selector								
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	This is a tool to select optimal protospacers for CRISPR-Cas10 targeting. This tool can be used in conjunction with recombineering to edit phage (or other) genomes.							
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3. Stažení sekvence Major Capsid proteinu (MCP)

Na stránkách Genbank si pod přístupovým kódem MH844528 najděte sekvenci Major capsid proteinu. Uložte si kódující sekvenci proteinu spolu s 500 bp upstream a downstream ve Fasta formátu.

>MH844528_phi812_MCP_500upanddown

4. Otevřete skript MainScript.py ve vhodném editoru, můžete použít například Notepad. Upravte sekvenci tag, pokud využíváte jiný Cas editační systém a Váš tag se liší.



gene =

poscount, Data = GNfunctions.AnalyzeSpacer(mask, gene)

#poscount represents the number of possible targets in the gene

WRITE FILE

file = open("Results_MCP.txt", "w")

5. Dále vložte sekvenci MCP a okolního lokusu jako plain text do proměnné gene. Nezapomeňte ponechat uvozovky.

MainScript MCP – Poznámkový blok

Soubor Úpravy Formát Zobrazení Nápověda

import GNfunctions

tag = ['A', 'C', 'G', 'A', 'G', 'A', 'C'] # Corresponding (Reverse Complemented)
mask = [nuc for nuc in reversed(GNfunctions.comp(tag))]
print(mask)



poscount, Data = GNfunctions.AnalyzeSpacer(mask, gene)

#poscount represents the number of possible targets in the gene

WRITE FILE

file = open("Results_MCP.txt", "w")

- 6. Uložte změny a spusťte skript.
- 7. Ve stejné složce jako jsou uloženy skripty by se vám měl zobrazit soubor Results.txt, ve kterém naleznete sekvence možných protospacerů.

Length of Sequence: 324

Possible Protospacers: 57

Tag Input: ACGAGAAC

Sequence Input:

1	ATGGCAGAAGAAGAAAAAATTATTAAAGAAGAACC	AACGAATG	GGTTCTTCTTTAATAATTTTTTCTTCTTCTGCCAT
7	GAAGAAGAAAAAATTATTAAAGAAGAACCAACGAA	TGAAGAAA	TTCGTTGGTTCTTCTTTAATAATTTTTTCTTCTTC
9	AGAAGAAAAAATTATTAAAGAAGAACCAACGAATG	AAGAAACA	CATTCGTTGGTTCTTCTTTAATAATTTTTTCTTCT
13	GAAAAAATTATTAAAGAAGAACCAACGAATGAAGA	AACAGAAC	TCTTCATTCGTTGGTTCTTCTTTAATAATTTTTTC
14	AAAAAATTATTAAAGAAGAACCAACGAATGAAGAA	ACAGAACA	TTCTTCATTCGTTGGTTCTTCTTTAATAATTTTTT
16	AAAATTATTAAAGAAGAACCAACGAATGAAGAAAC	AGAACAAC	GTTTCTTCATTCGTTGGTTCTTCTTTAATAATTTT
22	ATTAAAGAAGAACCAACGAATGAAGAAACAGAACA	ACCAGAAA	TGTTCTGTTTCTTCATTCGTTGGTTCTTCTTTAAT
23	TTAAAGAAGAACCAACGAATGAAGAAACAGAACAA	CCAGAAAA	TTGTTCTGTTTCTTCATTCGTTGGTTCTTCTTTAA
24	TAAAGAAGAACCAACGAATGAAGAAACAGAACAAC	CAGAAAAA	GTTGTTCTGTTTCTTCATTCGTTGGTTCTTCTTTA
25	AAAGAAGAACCAACGAATGAAGAAACAGAACAACC	AGAAAAAA	GGTTGTTCTGTTTCTTCATTCGTTGGTTCTTCTTT
28	GAAGAACCAACGAATGAAGAAACAGAACAACCAGA	AAAAATTG	TCTGGTTGTTCTGTTTCTTCATTCGTTGGTTCTTC
34	CCAACGAATGAAGAAACAGAACAACCAGAAAAAAT	TGAAAGTG	ATTTTTTCTGGTTGTTCTGTTTCTTCATTCGTTGG
40	AATGAAGAAACAGAACAACCAGAAAAAATTGAAAG	TGCAGAAG	CTTTCAATTTTTTCTGGTTGTTCTGTTTCTTCATT
43	GAAGAAACAGAACAACCAGAAAAAATTGAAAGTGC	AGAAGATG	GCACTTTCAATTTTTTCTGGTTGTTCTGTTTCTTC
46	GAAACAGAACAACCAGAAAAAATTGAAAGTGCAGA	AGATGTTG	TCTGCACTTTCAATTTTTTCTGGTTGTTCTGTTTC
55	CAACCAGAAAAAATTGAAAGTGCAGAAGATGTTGT	AACTGAAC	ACAACATCTTCTGCACTTTCAATTTTTTCTGGTTG
61	GAAAAAATTGAAAGTGCAGAAGATGTTGTAACTGA	ACCTGAAA	TCAGTTACAACATCTTCTGCACTTTCAATTTTTTC