

# **Viral Dark Matter: Protein Structure Prediction Update**

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# Progress

- In process of optimizing window selection
- Selection “by hand” is difficult/inefficient

# “Windows”

310003126

CCEEEEECCCCHHHHHHHHHHHHH | CCCCEEEEECCCCCCCCHHHHHHHHH | CCCCCCCCCCEE  
EECCCC | HHHHHHHHHHHCCCCCEEEHHHH | CCCCCCCCCHHHHHHHHCHHHHHHHHHHHH  
HHH | CCCCEEEEECCCECCCCCCCCCCCCCCCC | HHHHHHHHHHHHHHHHHHHHHHCCCEE  
EEEE | CCCCCCCCCCCCCCHHHHHHHHHHCCCC | EEECCCCCCCCCCCCCEE | HHHHHHHHHH  
HHHH | CCCCCCCCCCCCCCEE | CCCCCCHHHHHHHHHHHH | CCCCCCEECCCCCCCCC  
EE | CCCHHHHHHCCCCCCC | HHHHHHHHHHHHHHCCCCC

MKRVLITGGAGFIAHHLIGQILETTDWEVITLDRLDYSGNLNLRLHDLMLSFDPEVRKRVRVHHDL  
KAELNPMVCREIGNVDYILHLAAGSHVDRSIEYPLEFVMDNVVGTCNILDFARTQKENLERFIYFST  
DEVFGPAPDGIKYKENDRYNSTNPYSASKAGGEELAVAYENTYGLPIYITHTMNVFGERQHPEKFIP  
MCIRKVRNGESVTIHSDSTKTVPGSRHYIHAEDVASAILFLVNHEGGFEPTWGNACPKFNIVGAE  
ELNNLELAQIIAESQGKELKYEMVDFHSSRPGHDLRYALDGDKMKELGWVPAKSVRERISEVTRW  
TLANERWL

# PEPFold

- Does not consistently generates PDB files
- Arbitrary (server issues?)

# Future

Create a utility that selects windows that meet certain criteria:

- 36 length maximum
- does not “break up” secondary structures