

Version ArchCandy-1.0

INPUT

To paste a protein sequence (one letter code) in the input window.

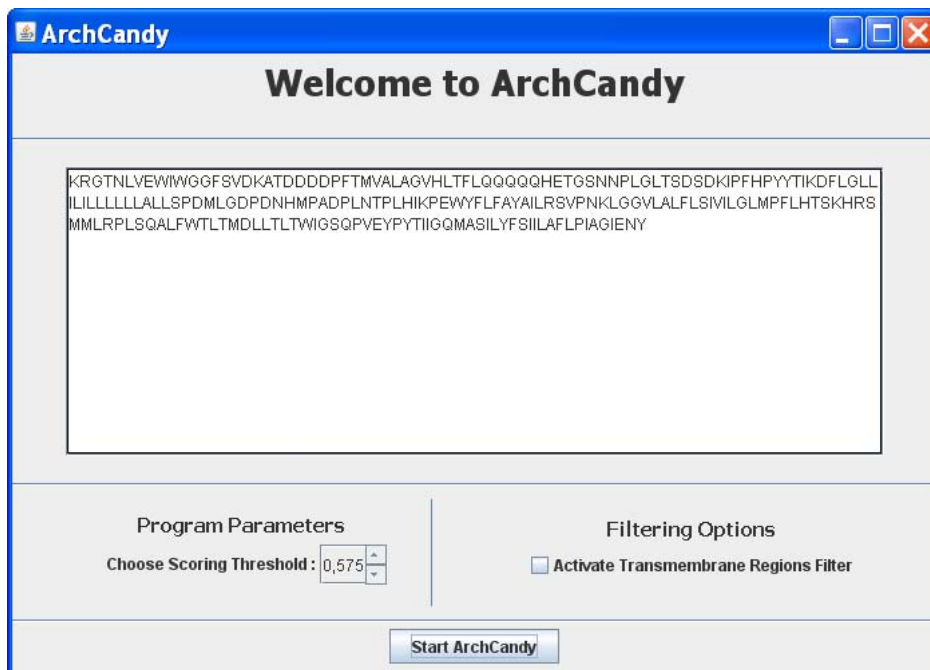
SEARCH OPTIONS

«Choose Scoring Threshold»

All predicted amyloidogenic regions have a score assigned to them. This option allows the user to output only those predictions that are higher than the specified value. The default value (recommended to distinguish between amyloidogenic and non-amyloidogenic sequences) is 0.575.

Filtering Option "Activate Transmembrane Regions Filter"

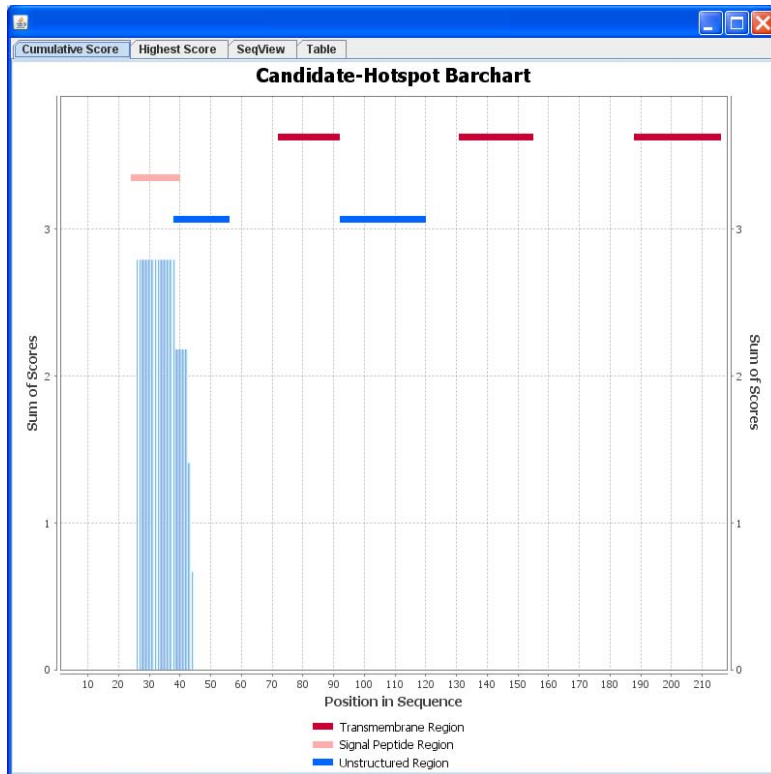
As transmembrane protein regions and signal peptides are located in the membranes in the alpha-helical conformation, it is unlikely that they will form amyloid fibrils. Therefore, if this option is activated, predictions are not made in these regions.



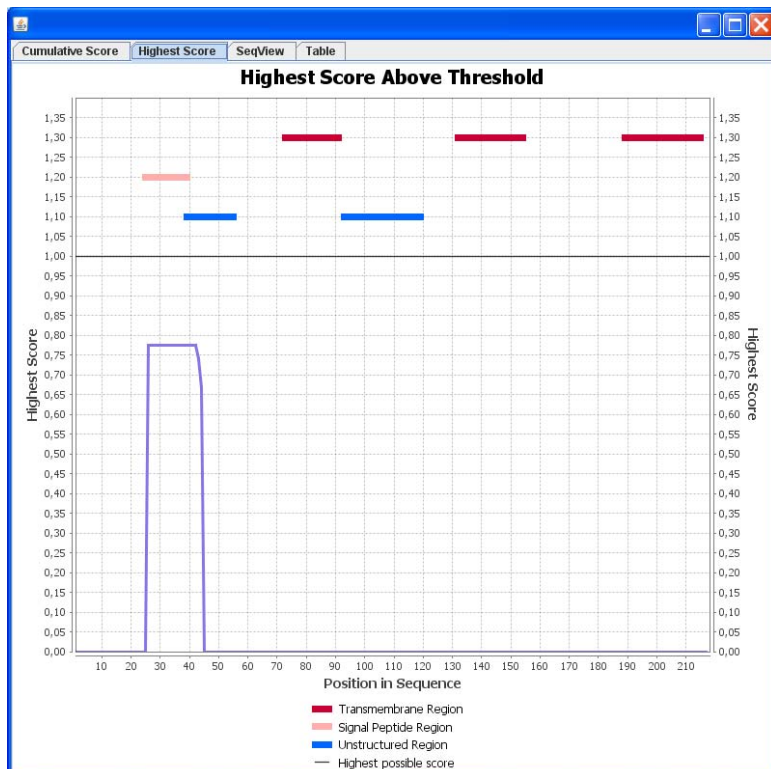
The screenshot shows the ArchCandy software window. The title bar reads "ArchCandy". The main window has a header "Welcome to ArchCandy". Below the header is a large text input area containing a protein sequence: KRGTNLVEWVWGGFSDKATDDDDPFTMVALAGVHLTFLQQQQQHETGSNNPLGLTSDSDKIPFFHPYYTIKDFLGLLILLLLLLLLALLSPDMLGDPDNHMPADPLNTPHLHKPEWYFLFAYAILRSVPNKLGGVLALFLSIVLGLMPFLHTSKHRSMMMLRPLSQALFWTLTMDLLTLTWIGSQPVEYPYTIIGQMASILYFSIILAFPLIAGIENY. Below the input area are two sections: "Program Parameters" with a "Choose Scoring Threshold" field set to 0,575, and "Filtering Options" with a checkbox for "Activate Transmembrane Regions Filter" which is currently unchecked. At the bottom center is a "Start ArchCandy" button.

OUTPUT WINDOWS

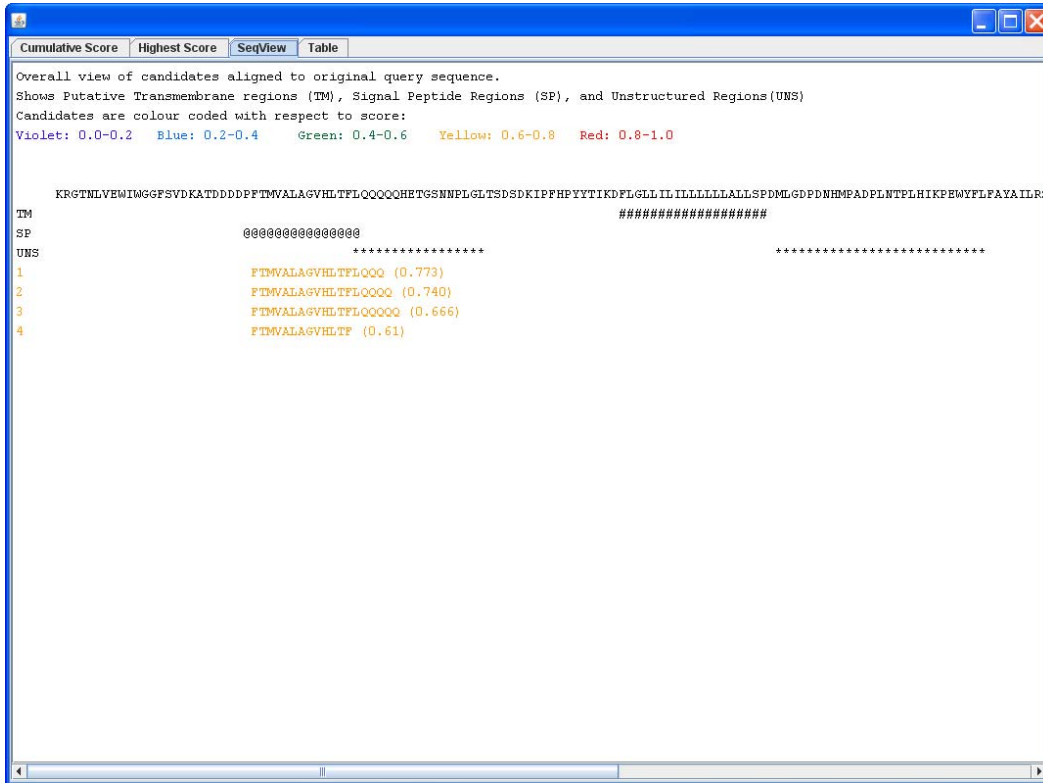
1. Cumulative Score: It is the sum of the scores of all amyloidogenic candidates at a given amino acid position.



2. Highest Score: It is the highest scores among all amyloidogenic candidates at a given amino acid position. Maximal possible value is 1.0



3. SeqView shows locations within the protein, scores and sequences of the amyloidogenic regions.



4. Table with 2D diagrams of the predicted beta-arches

Diagram	Number	Score	Arc Type	Position
<pre> H T L Q / \ / \ / \ L F Q Q V A A M F \ / \ / \ / G L V T </pre>	01	0.773	PPL	26-42
<pre> L F Q Q / \ / \ / \ H T L Q Q / V / \ \ A A M F \ / \ / \ / G L V T </pre>	02	0.740	GBPL	26-43
<pre> T L Q Q / \ / \ / \ L F Q Q Q \ H / V A A M F \ / \ / \ / G L V T </pre>	03	0.666	5 Res Arc	26-44
<pre> G H T / \ / \ / \ V L F A A H F \ / \ / \ / L V T </pre>	04	0.61	PPL	26-38

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