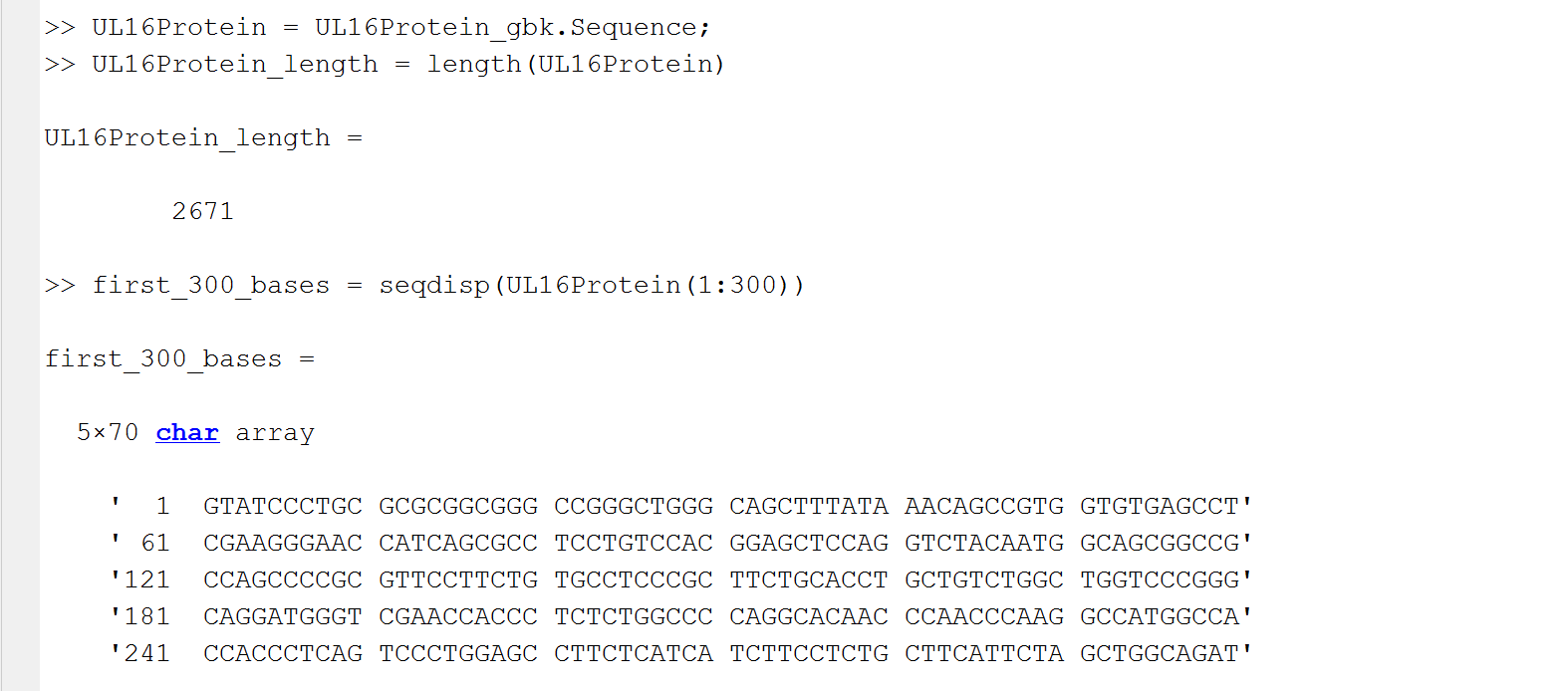
**MATLAB Tutorial – Bioinformatics Toolbox – Calculating & Visualizing Sequence Statistics – Tuesday, June 18, 2019**

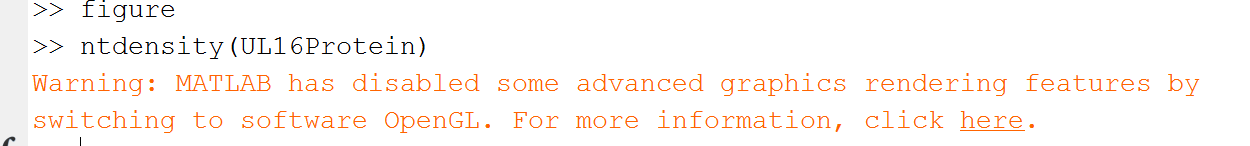
Link: <https://www.mathworks.com/help/bioinfo/examples/calculating-and-visualizing-sequence-statistics.html>

Box One:

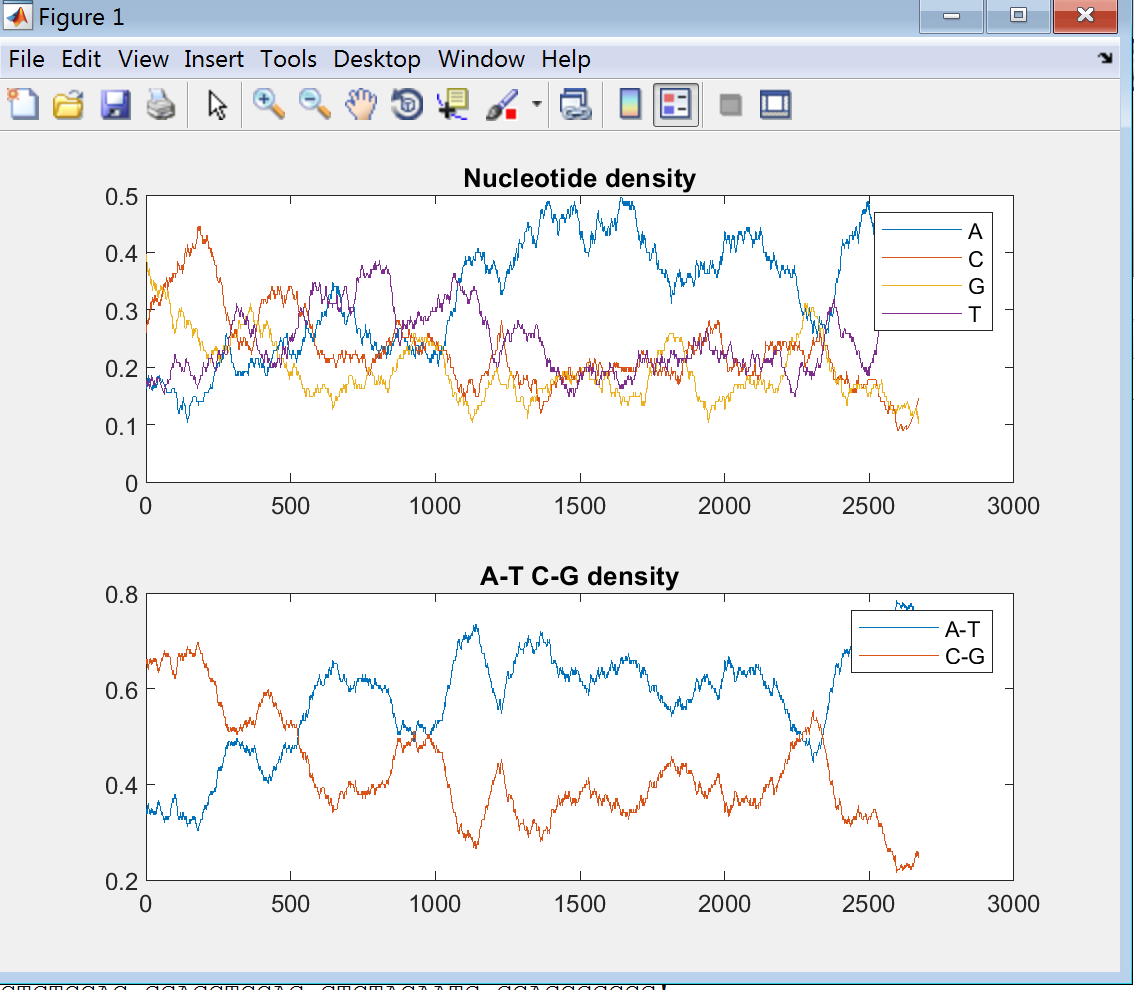




Box Two:



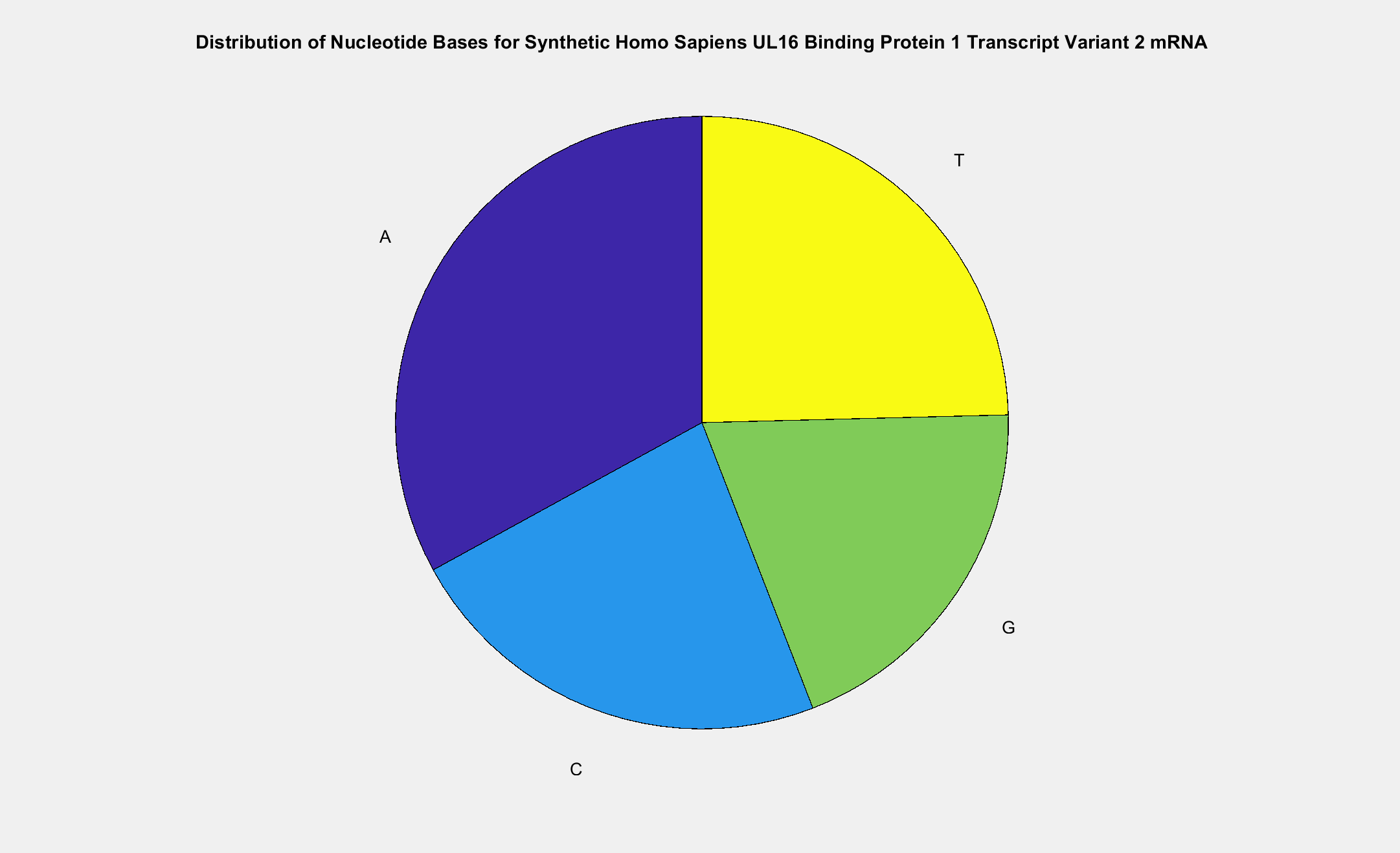
Nucleotide Density Figure 1:



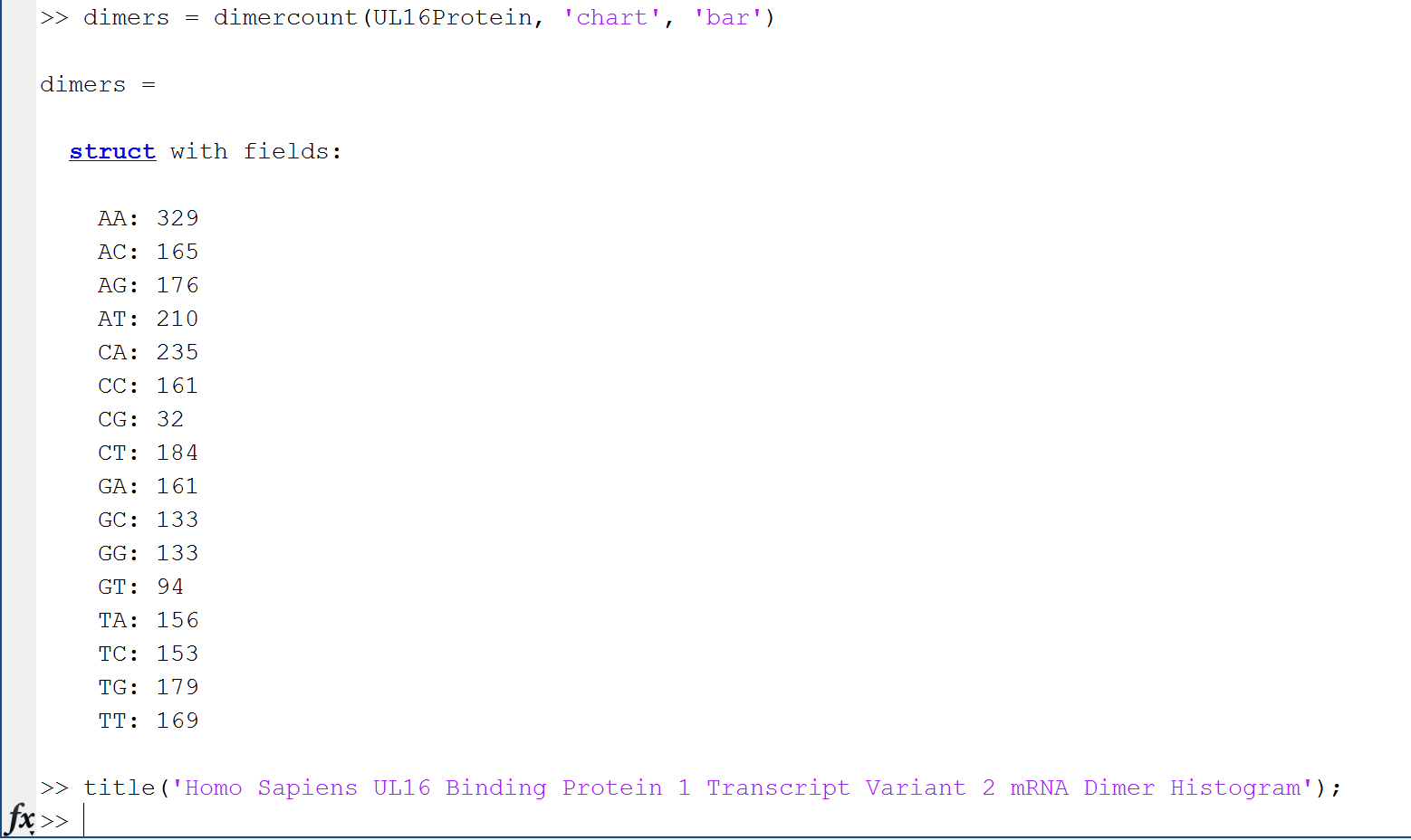
Box Three:



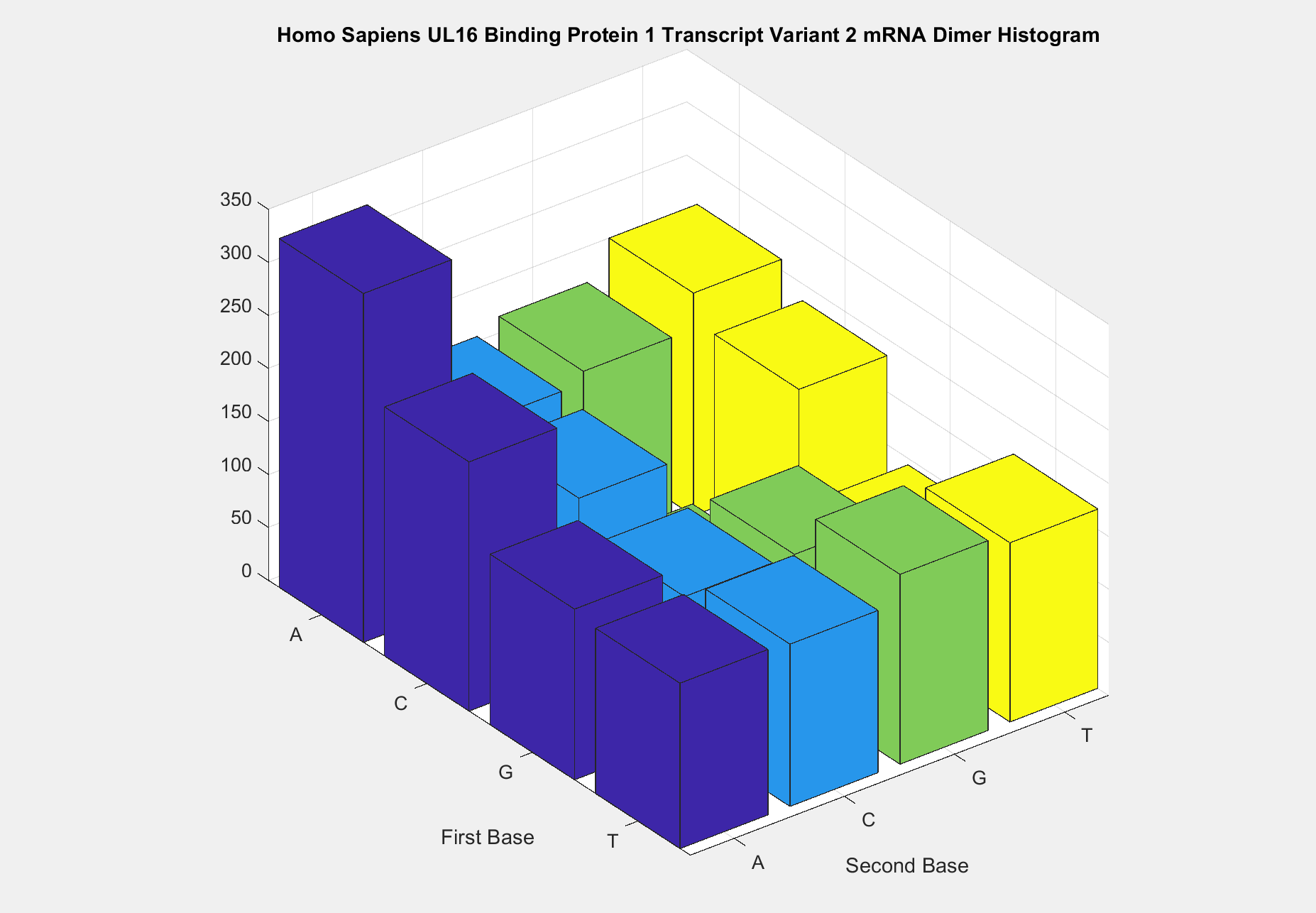
\*Distribution of Nucleotide Base for Synthetic Homo Sapiens UL16 Binding Protein 1 Transcript Variant 2 mRNA - Figure 2:



Box Four:



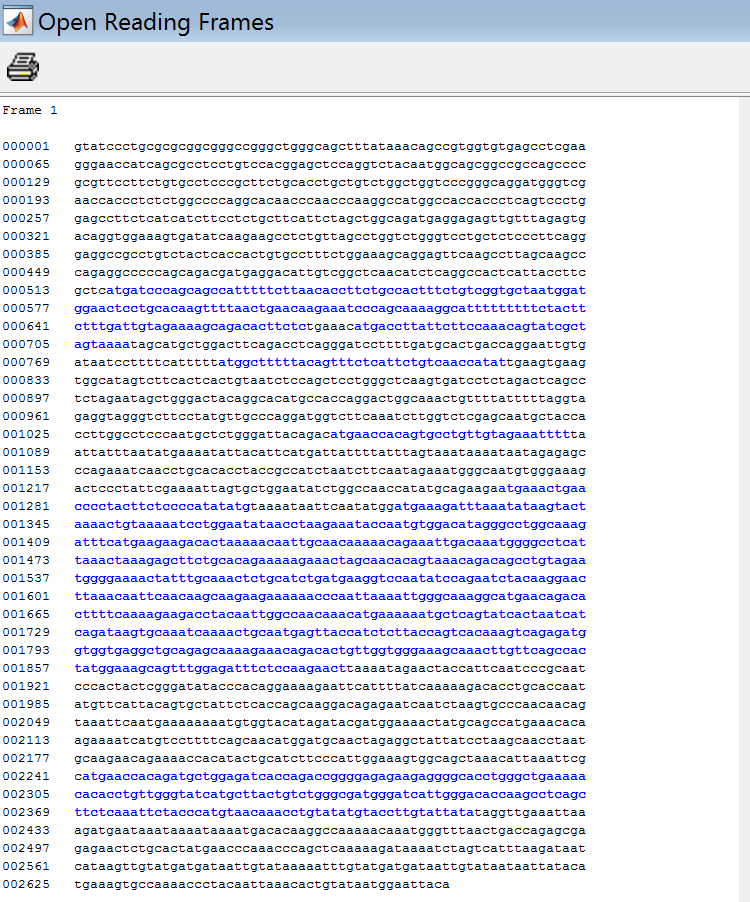
Homo Sapiens Ul16 Binding Protein 1 Transcript Variant 2 mRNA Dimer Histogram Figure:



Box Four:



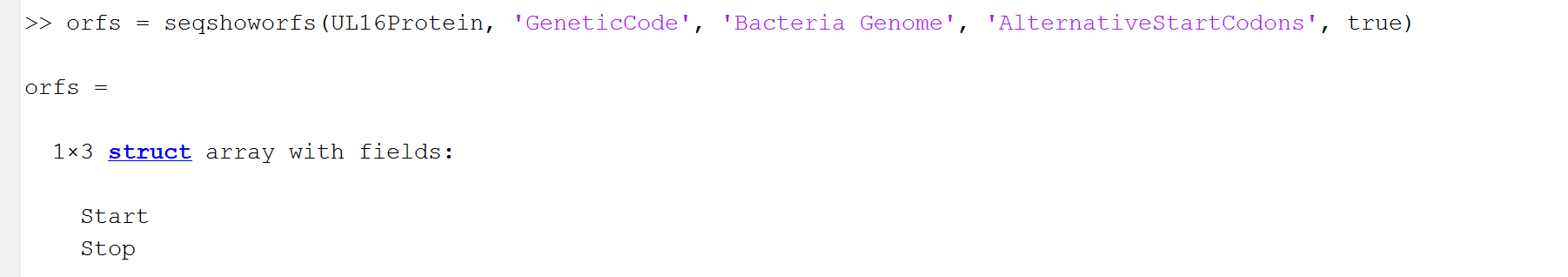
Sequence Open Reading Frames Figure:







Box :



Alternative Codons Open Reading Frame:

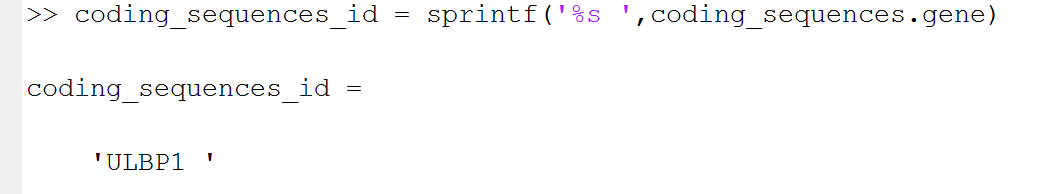






Box Five:





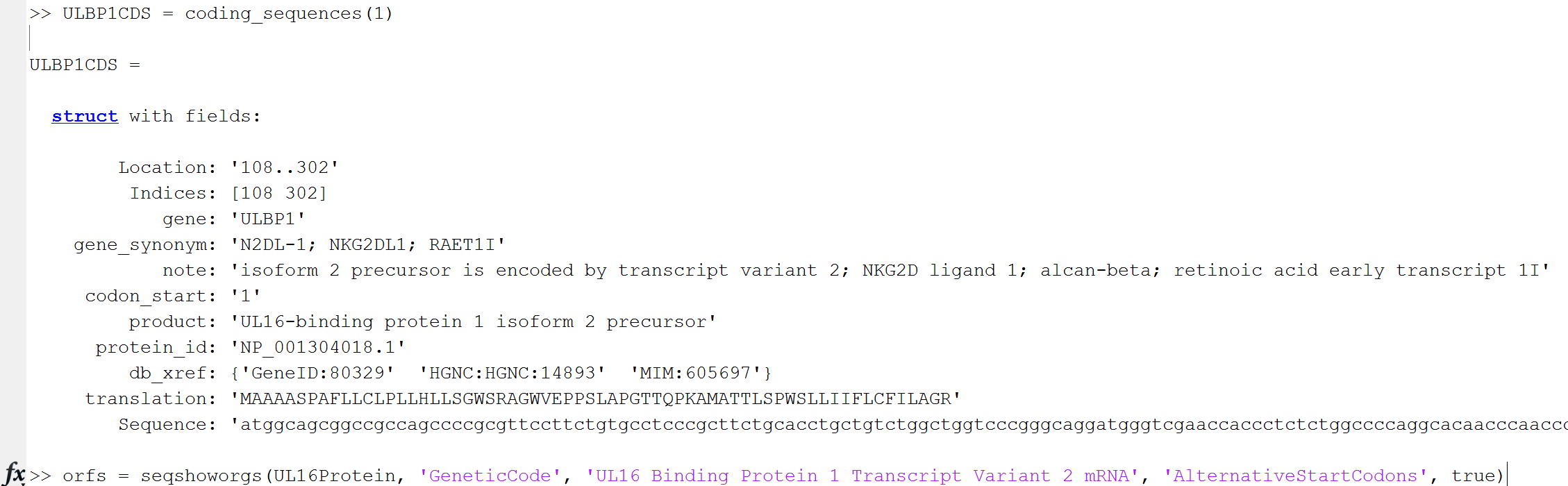
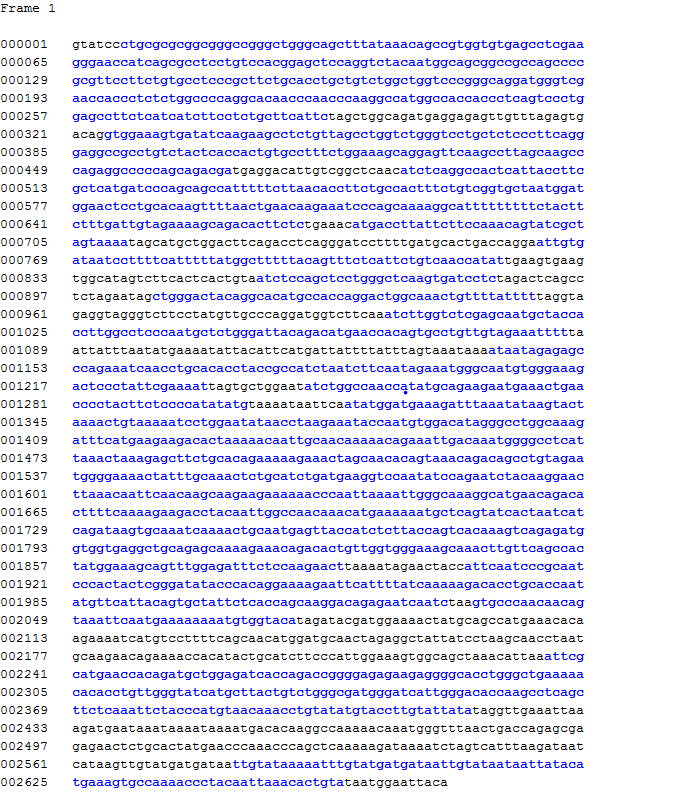


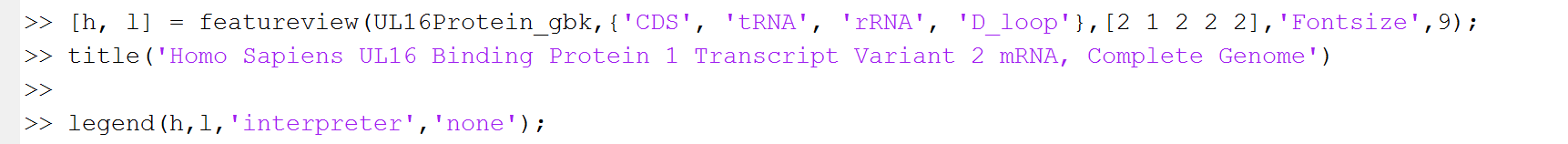
Figure:

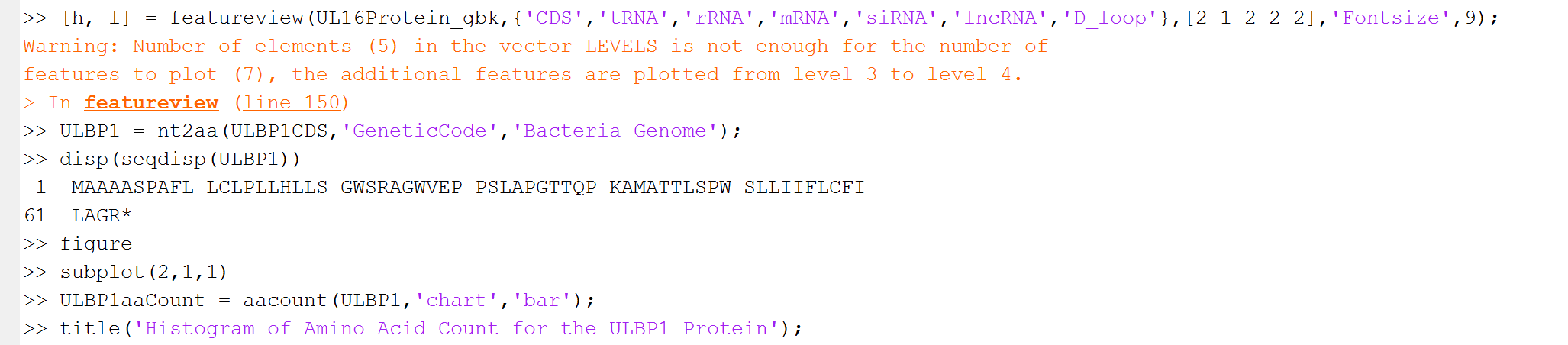




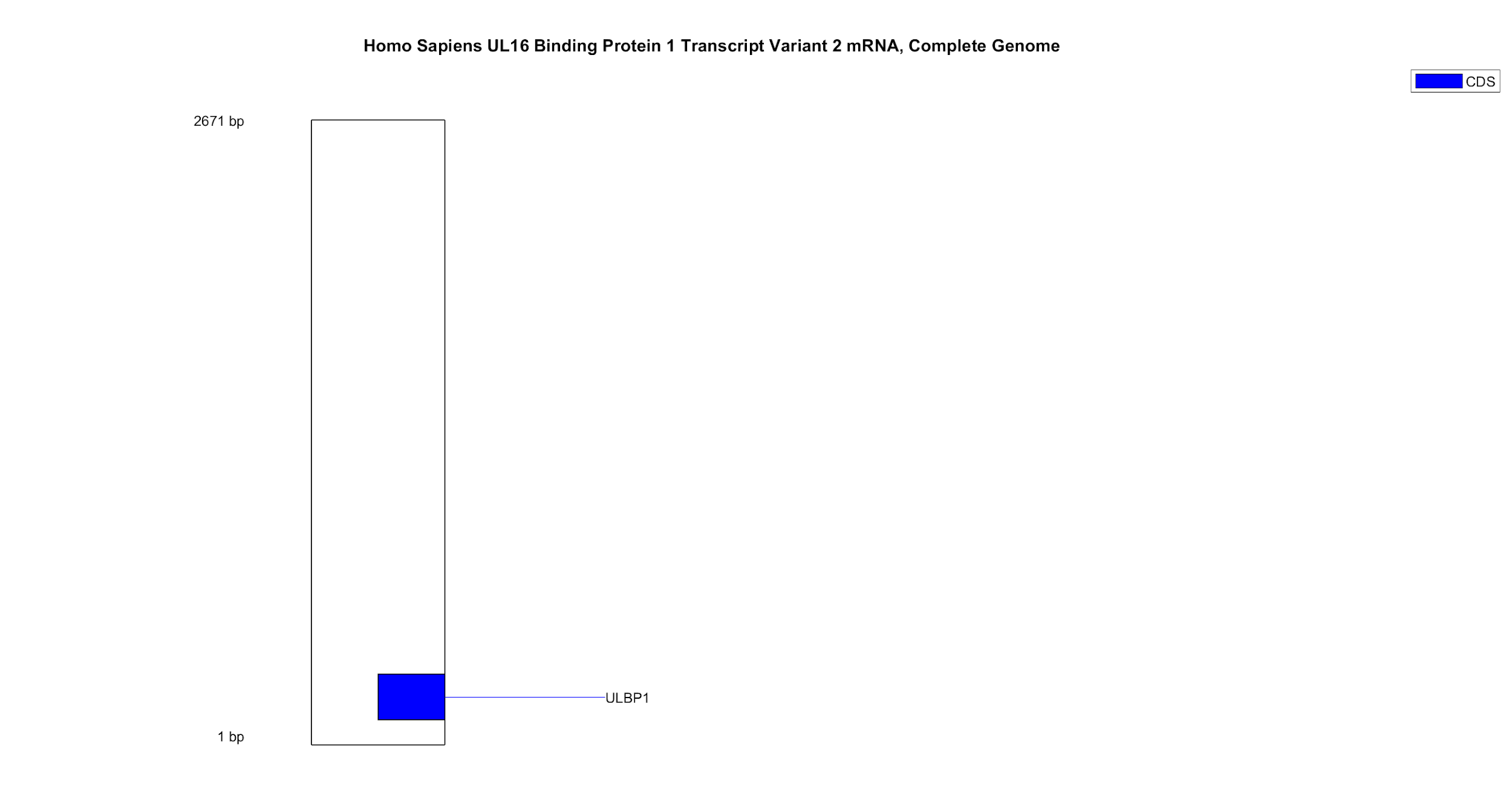


**Box:**

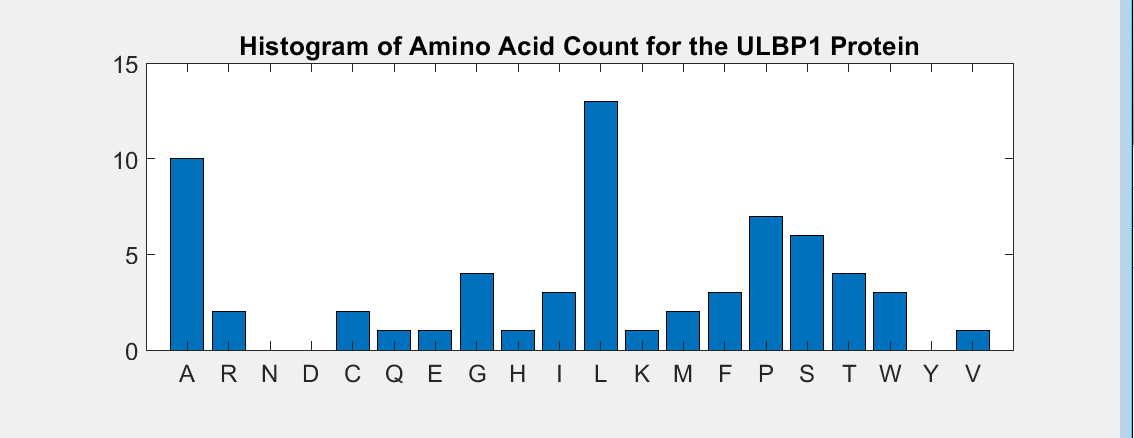




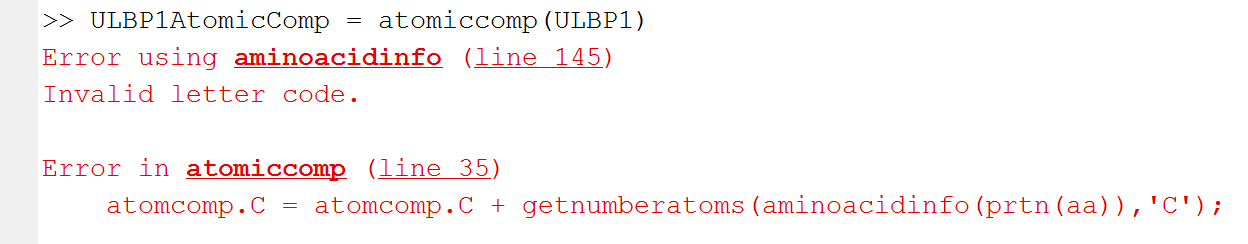
**Figure:**

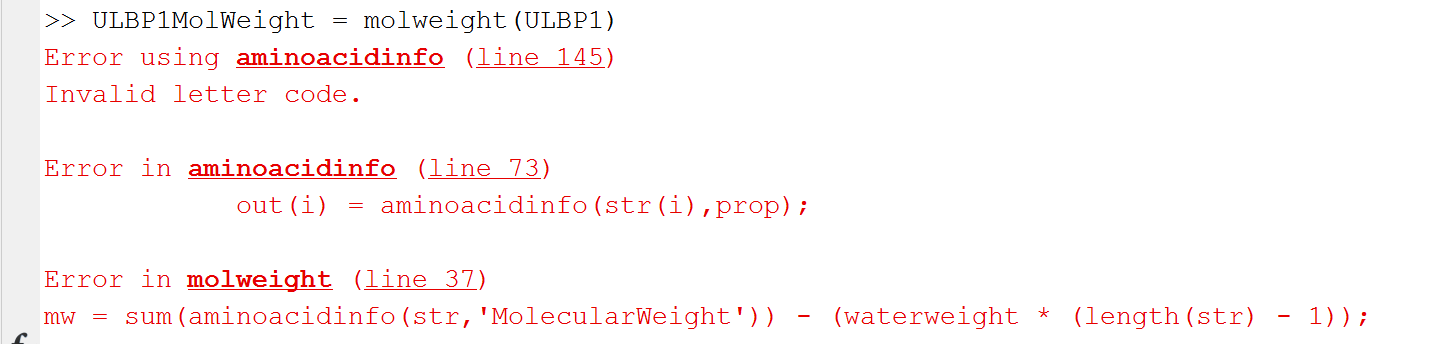


**Figure:**

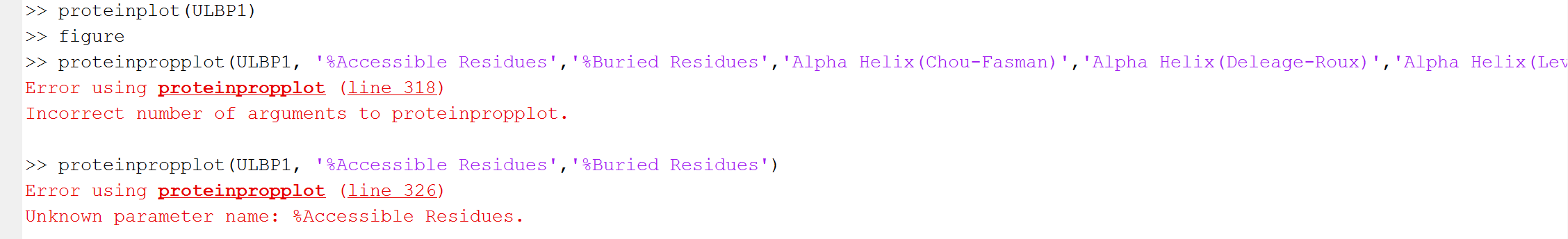


**Box:**





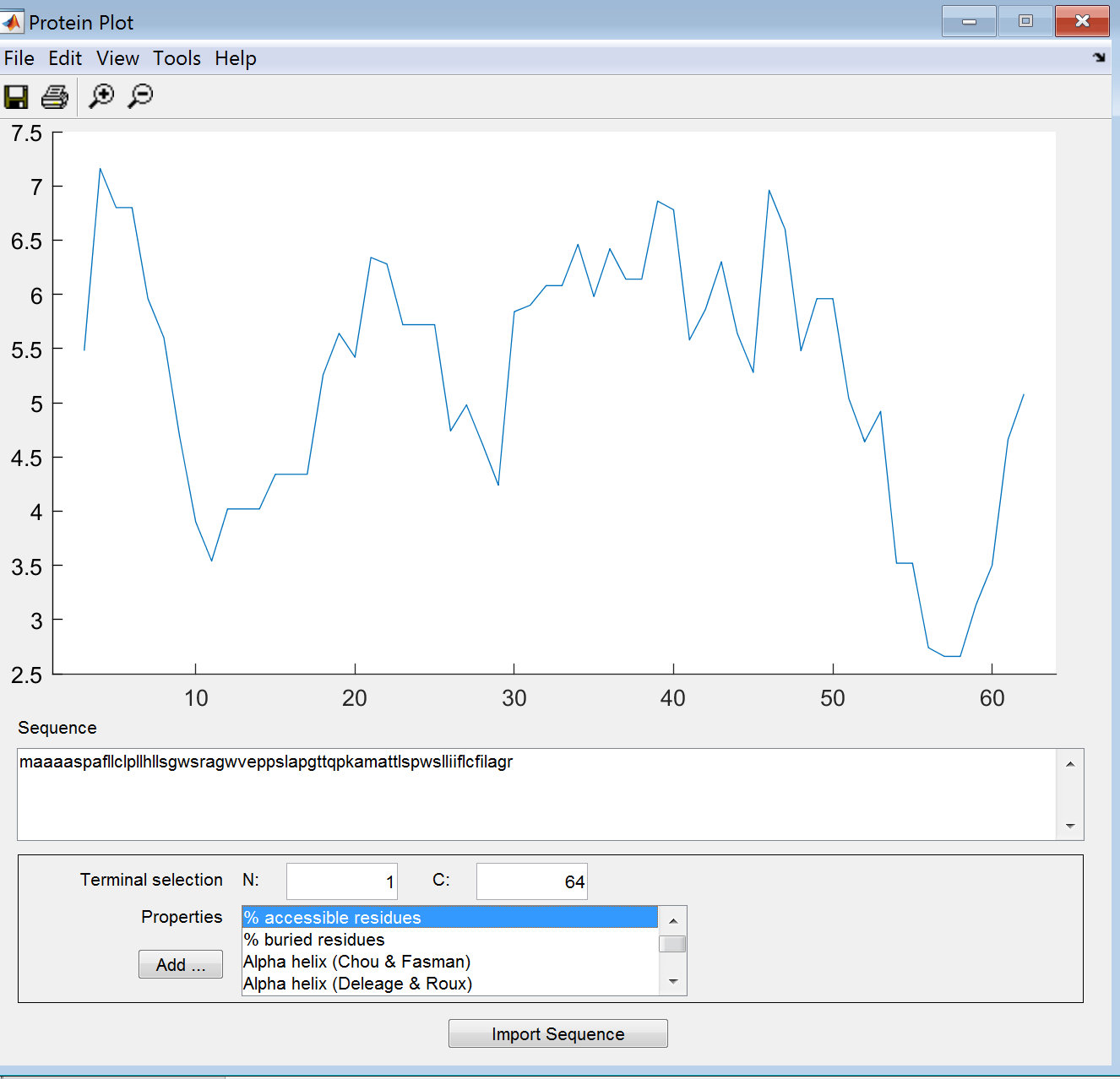
**Box:**



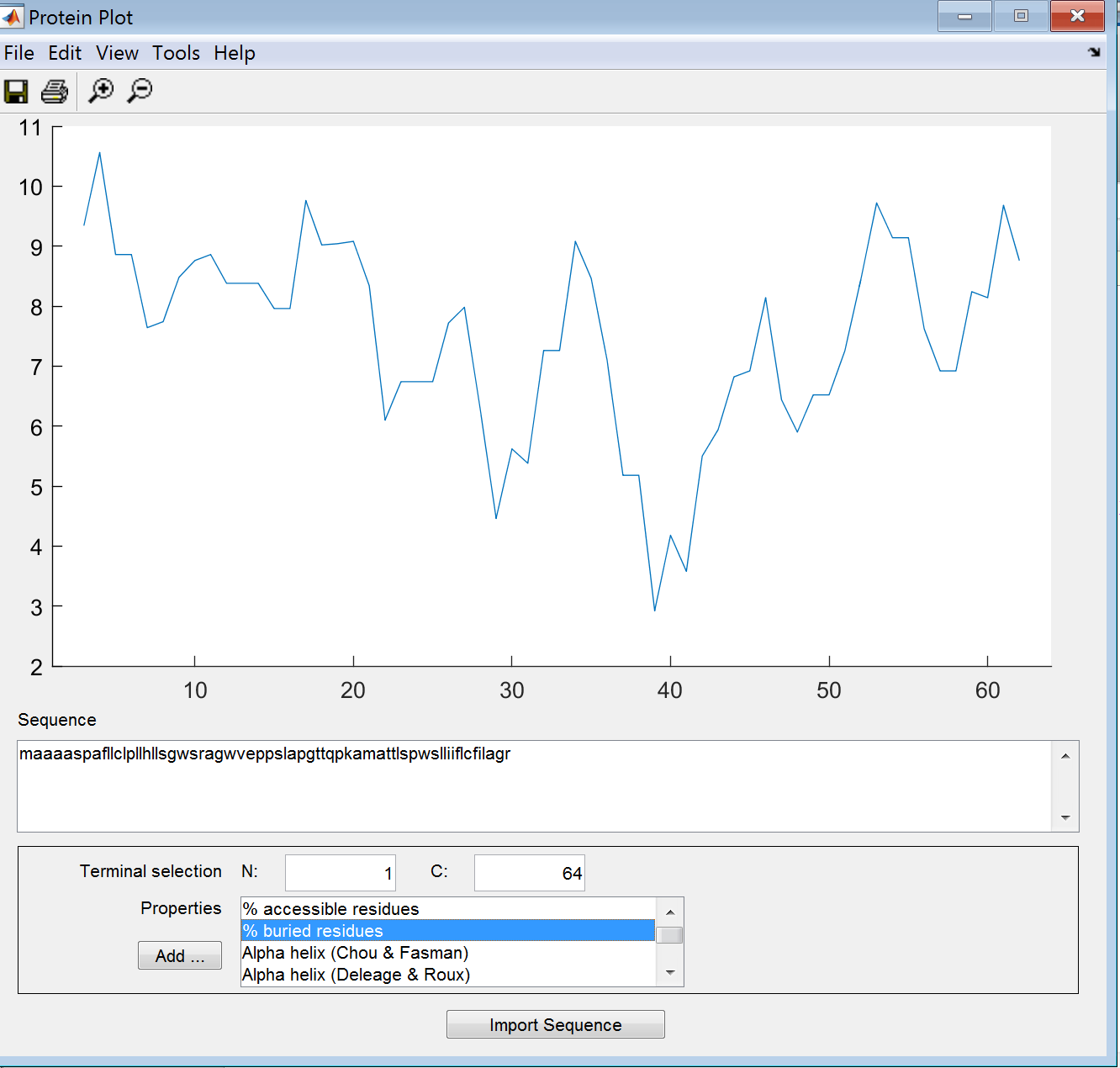


**Protein Plots (There Are A Lot of Them):**

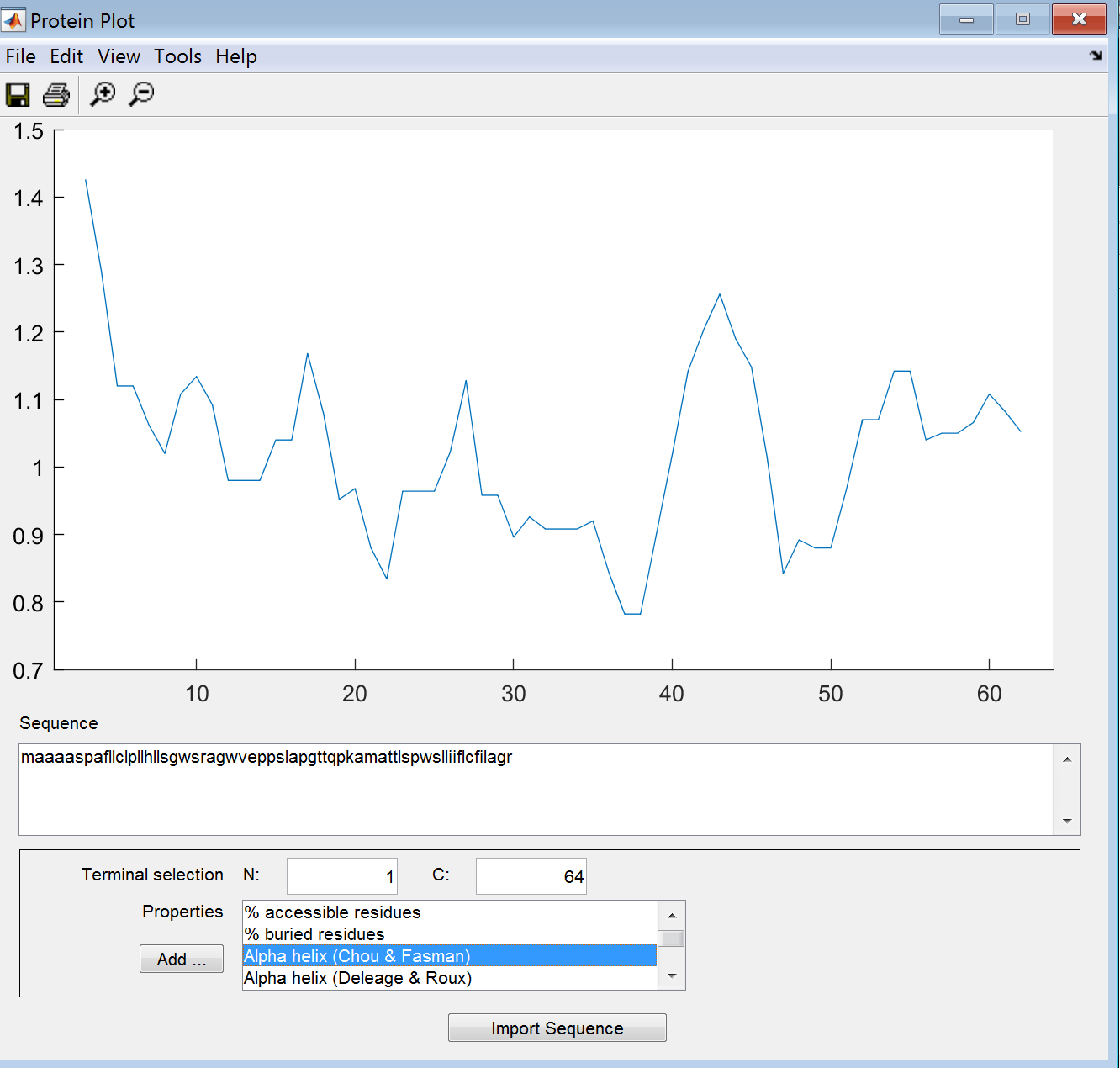
**%Accessible Residues**



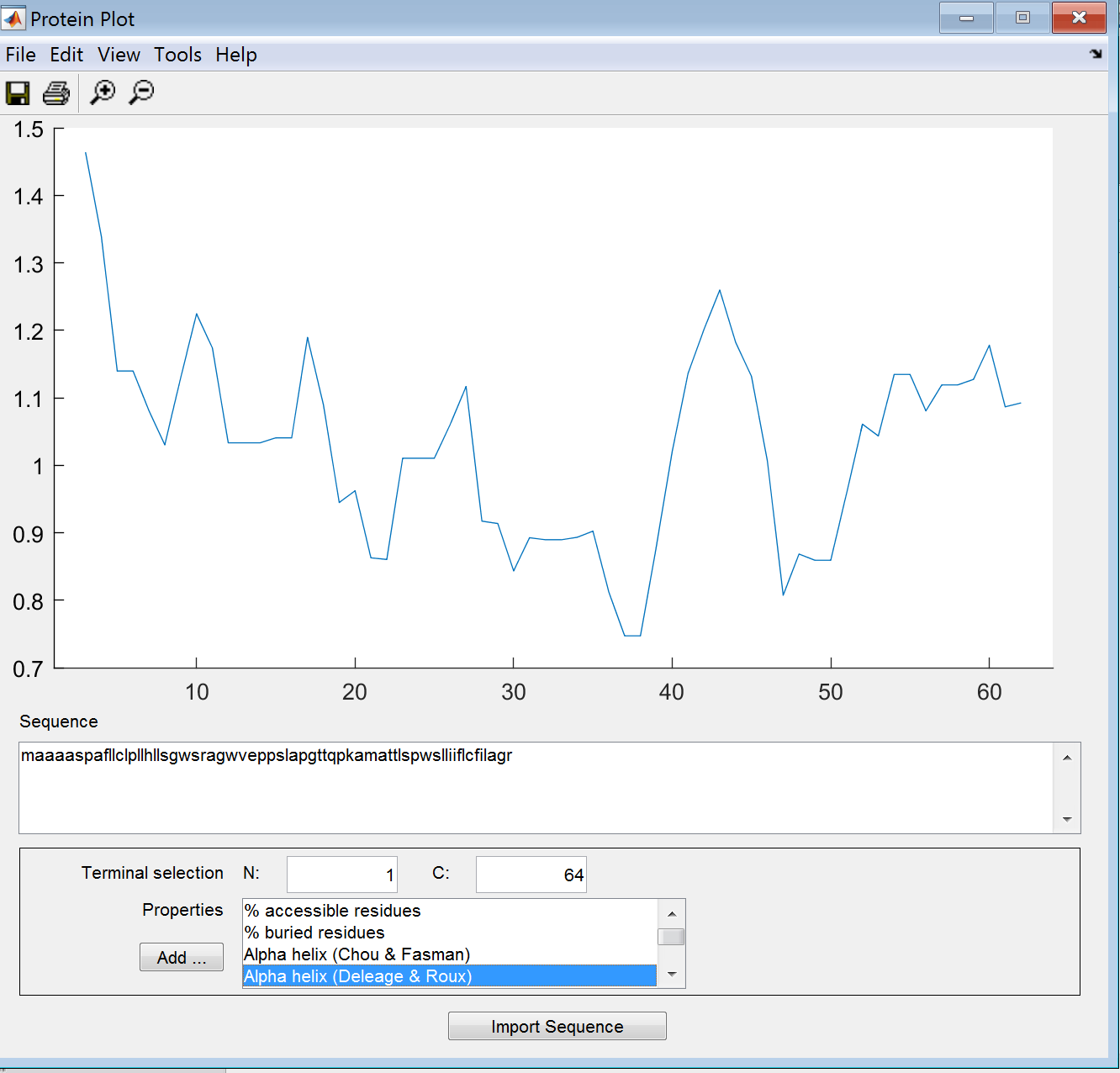
**%Buried Residues**



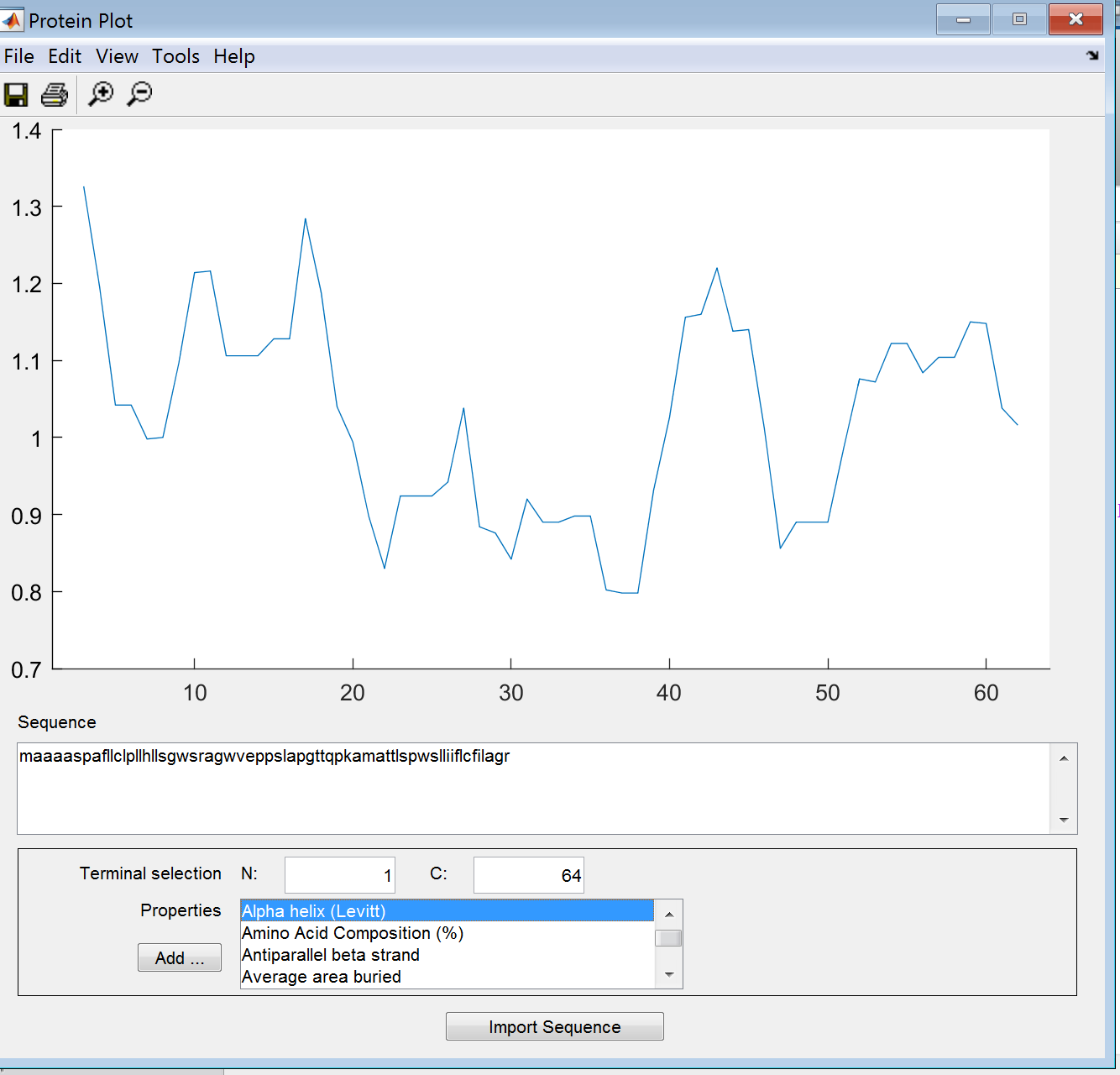
**Alpha Helix (Chou & Fasman)**



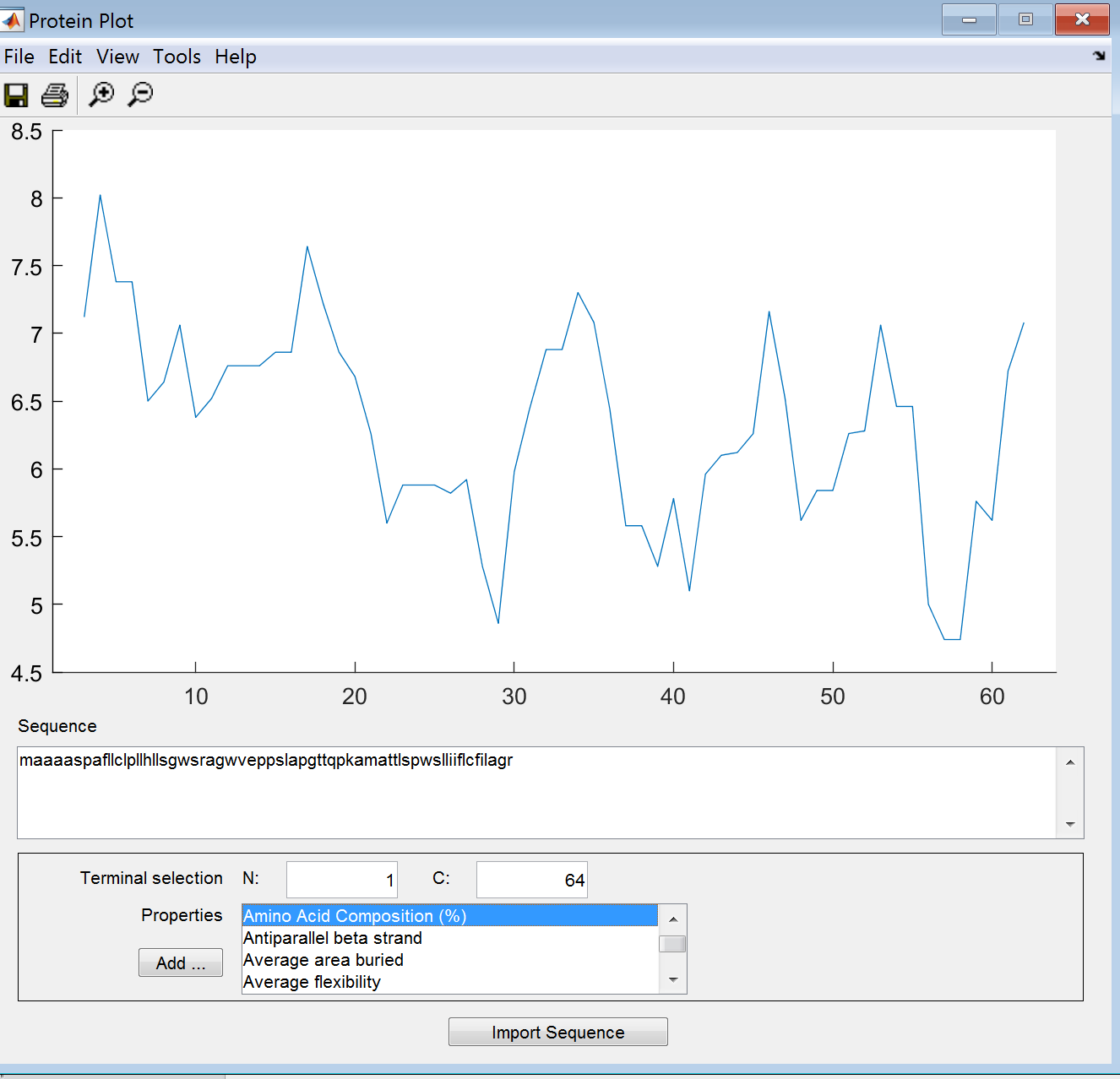
**Alpha Helix (Deleage-Roux)**



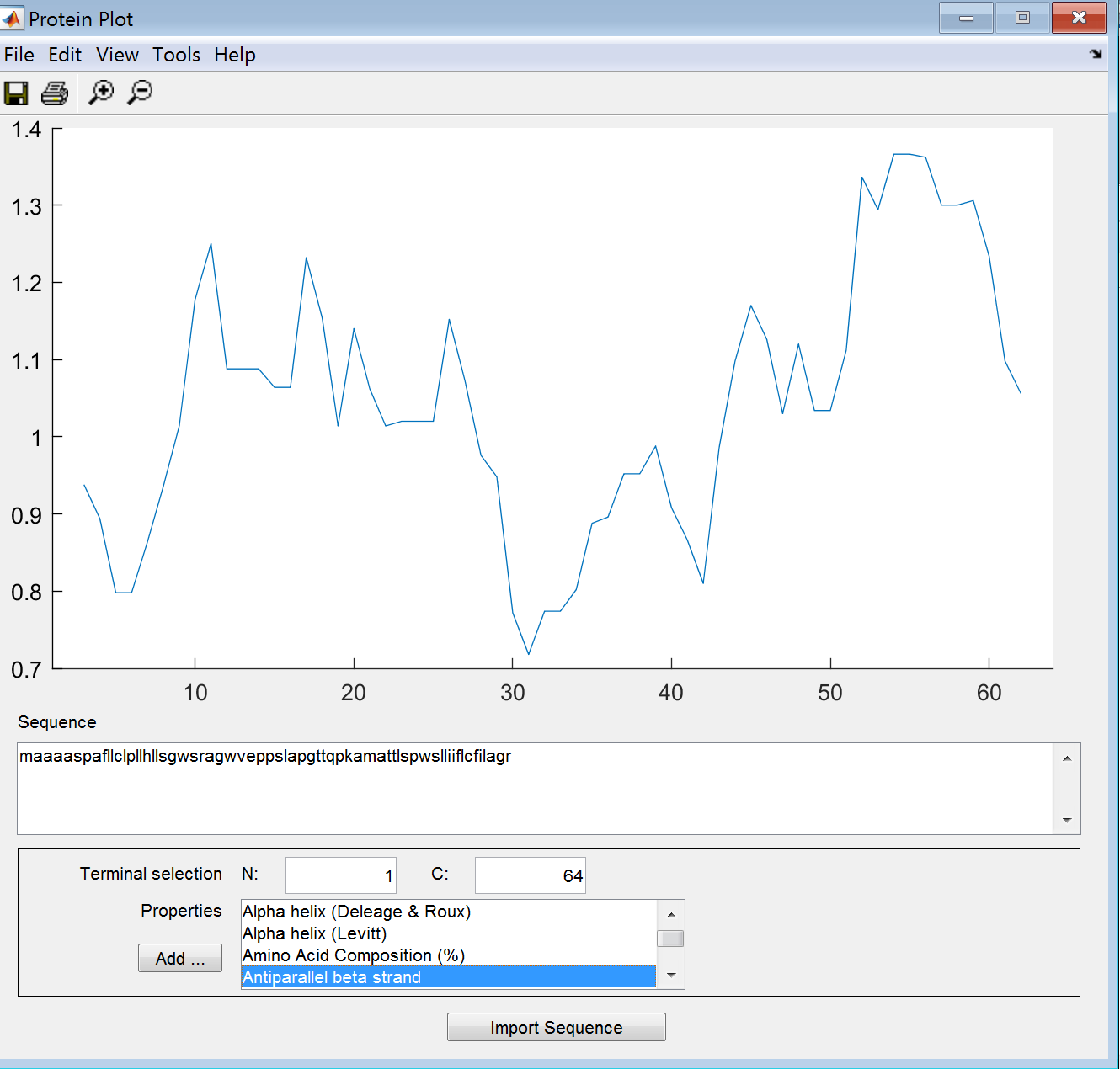
**Alpha Helix (LeVitt)**



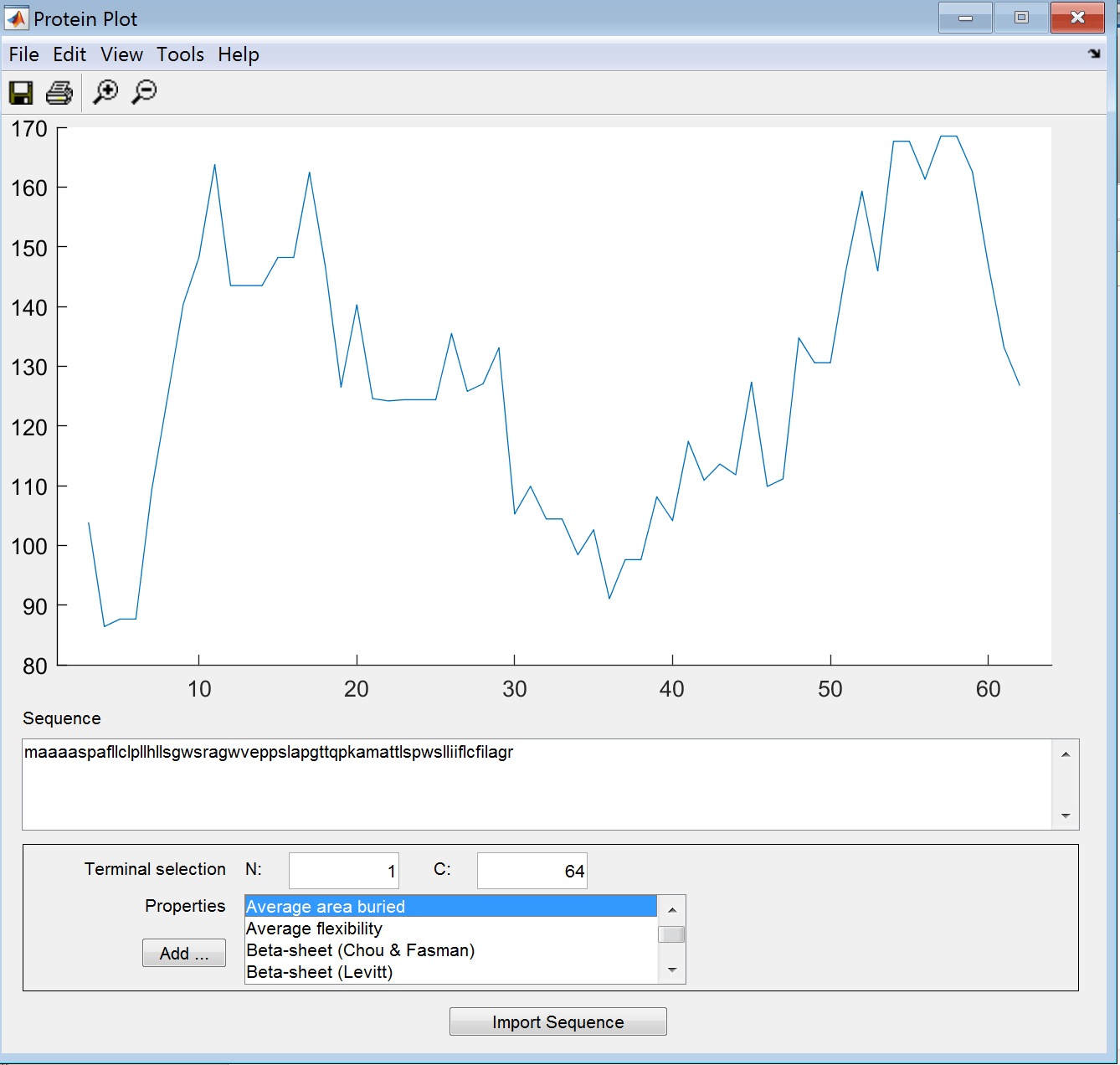
**Amino Acid Composition (%)**



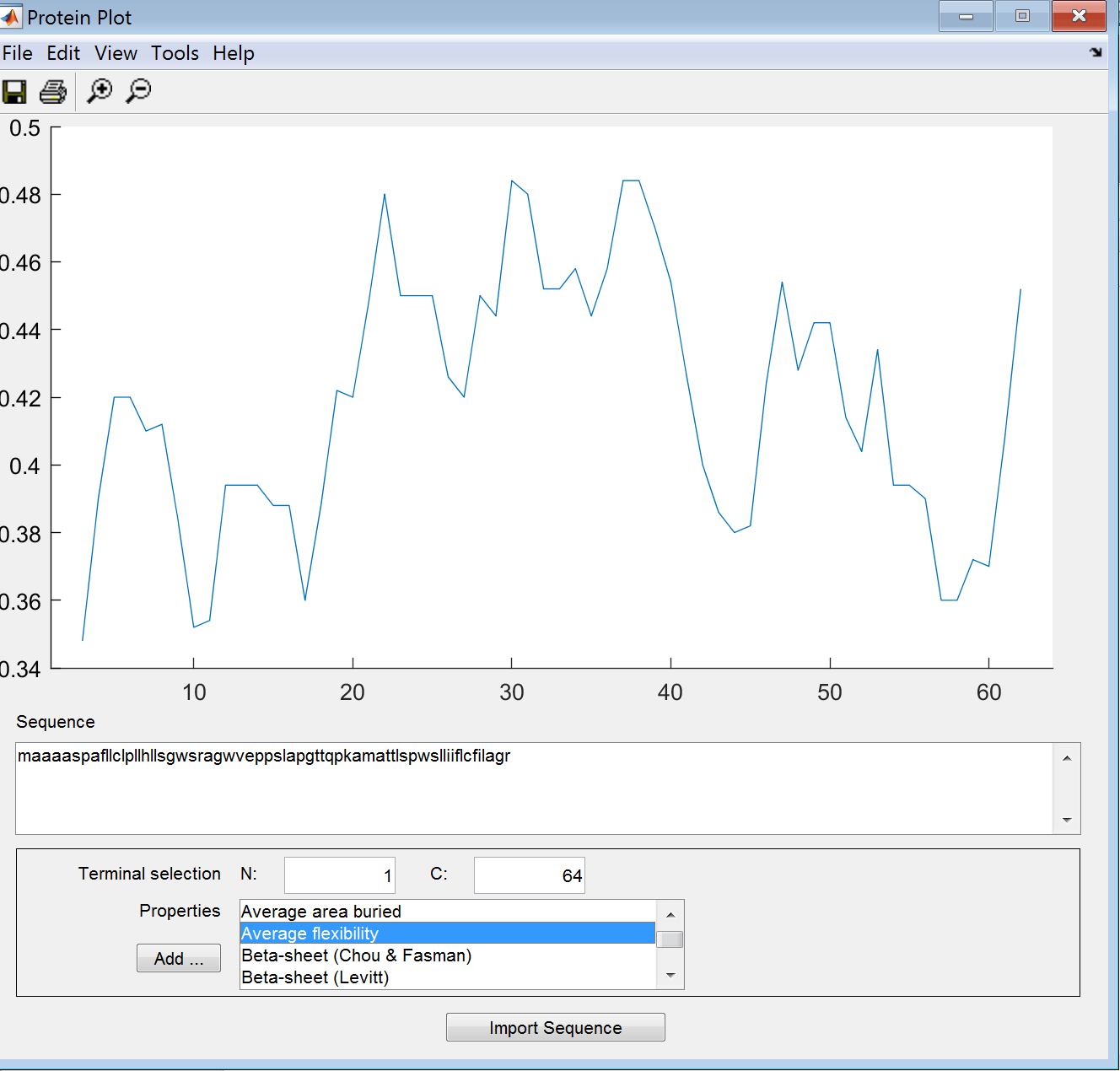
**Antiparallel Beta Strand**



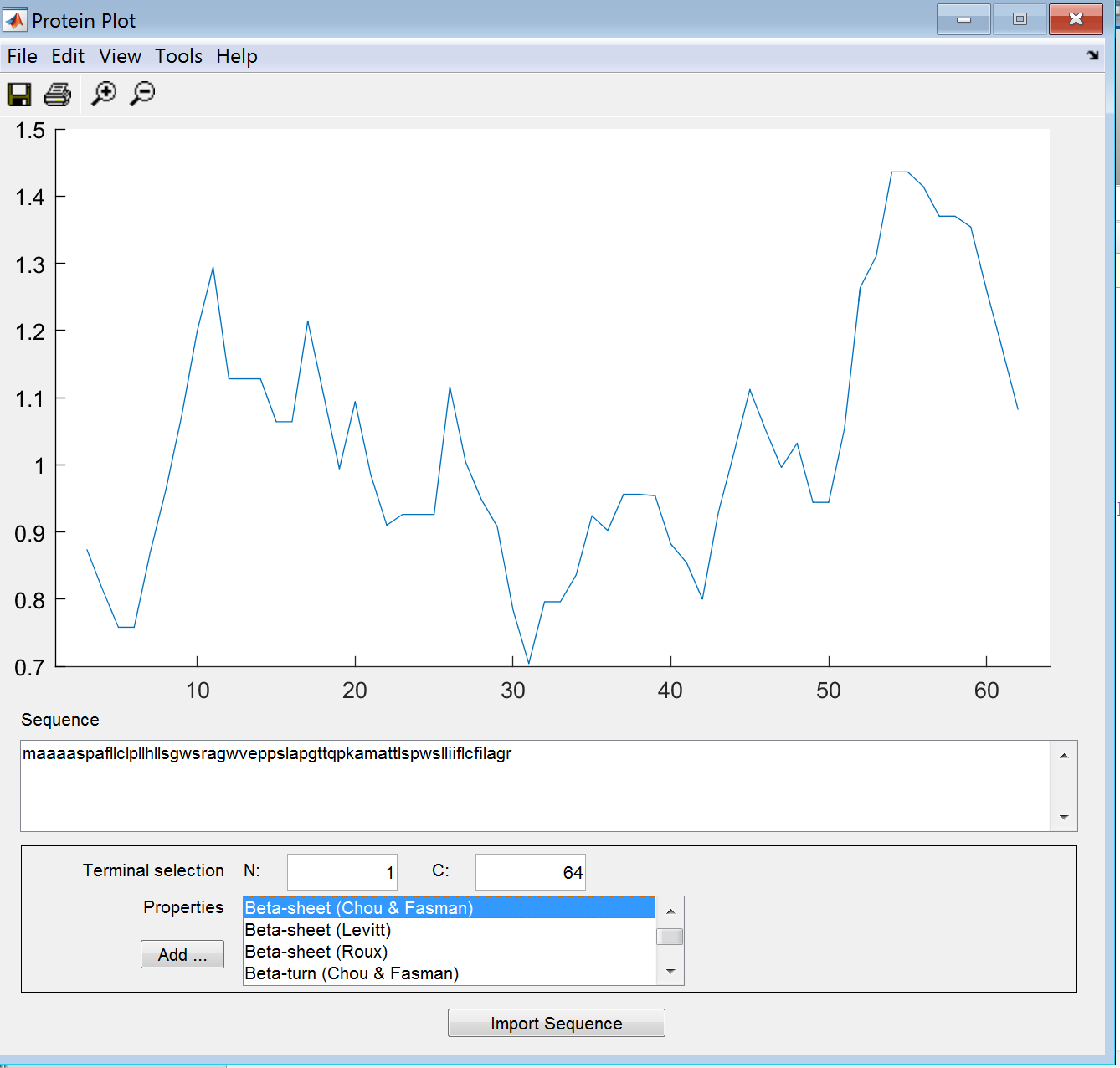
**Average Area Buried**



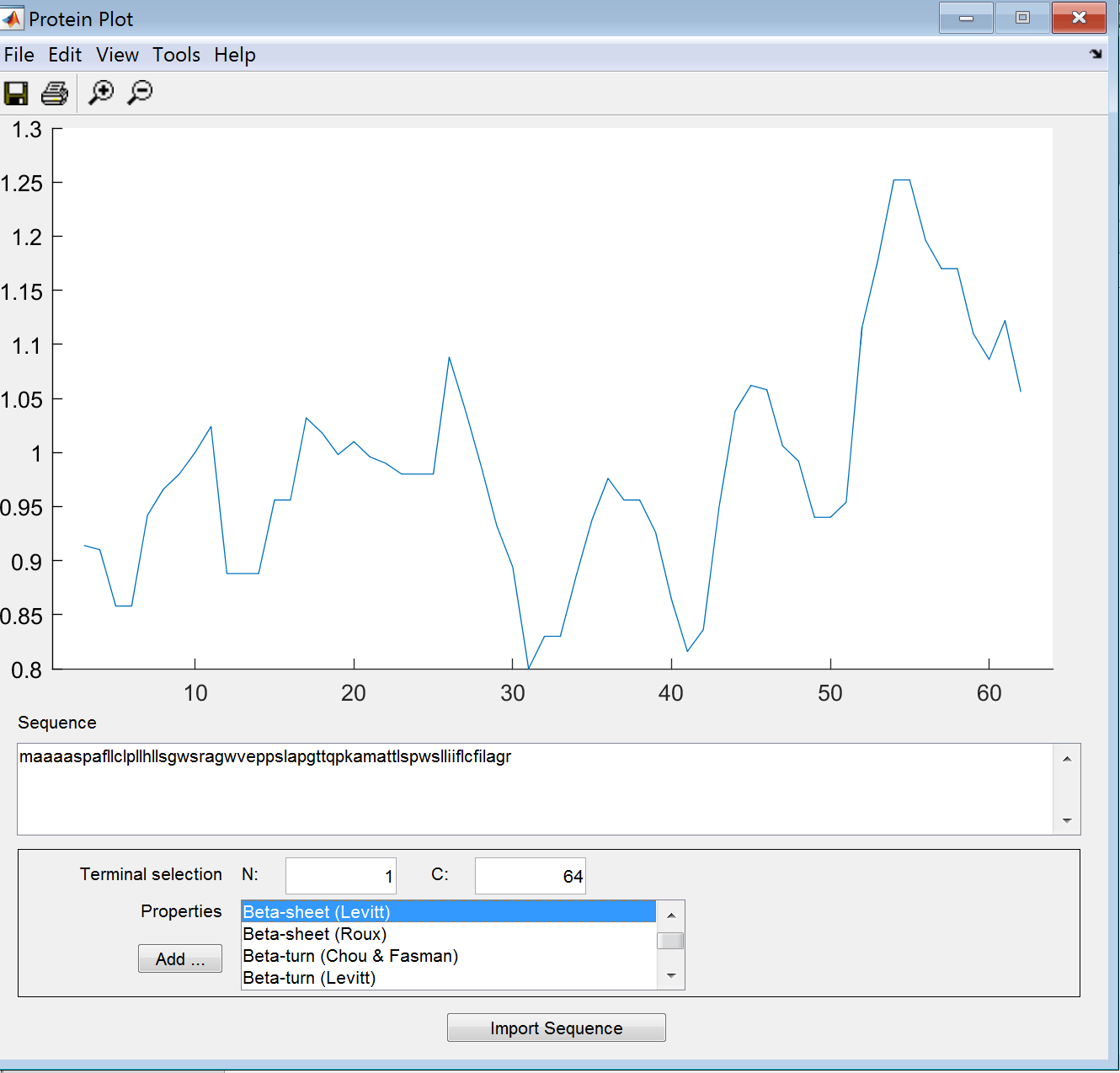
**Average Flexibility**



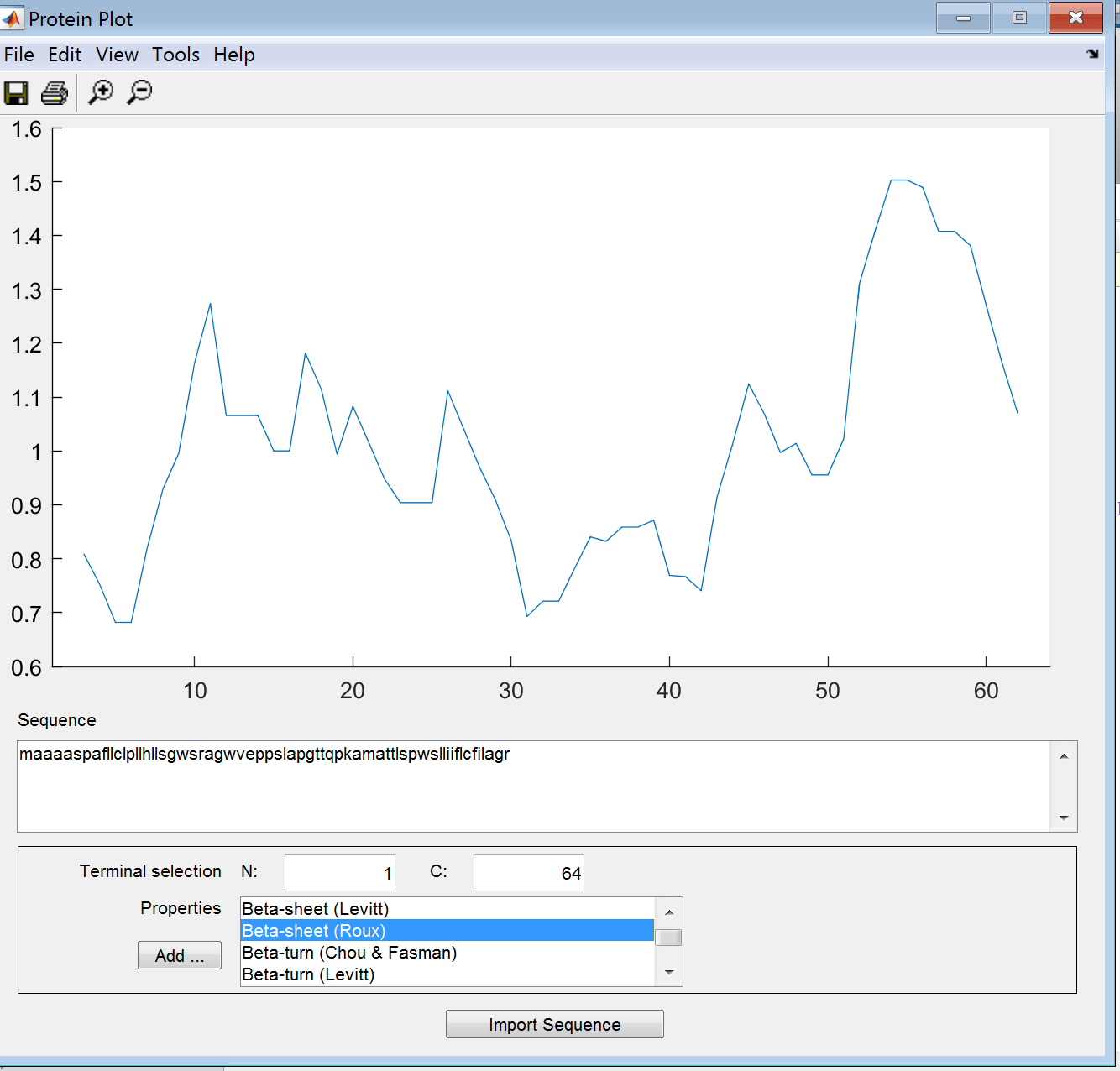
**Beta Sheet (Chou-Fasman)**



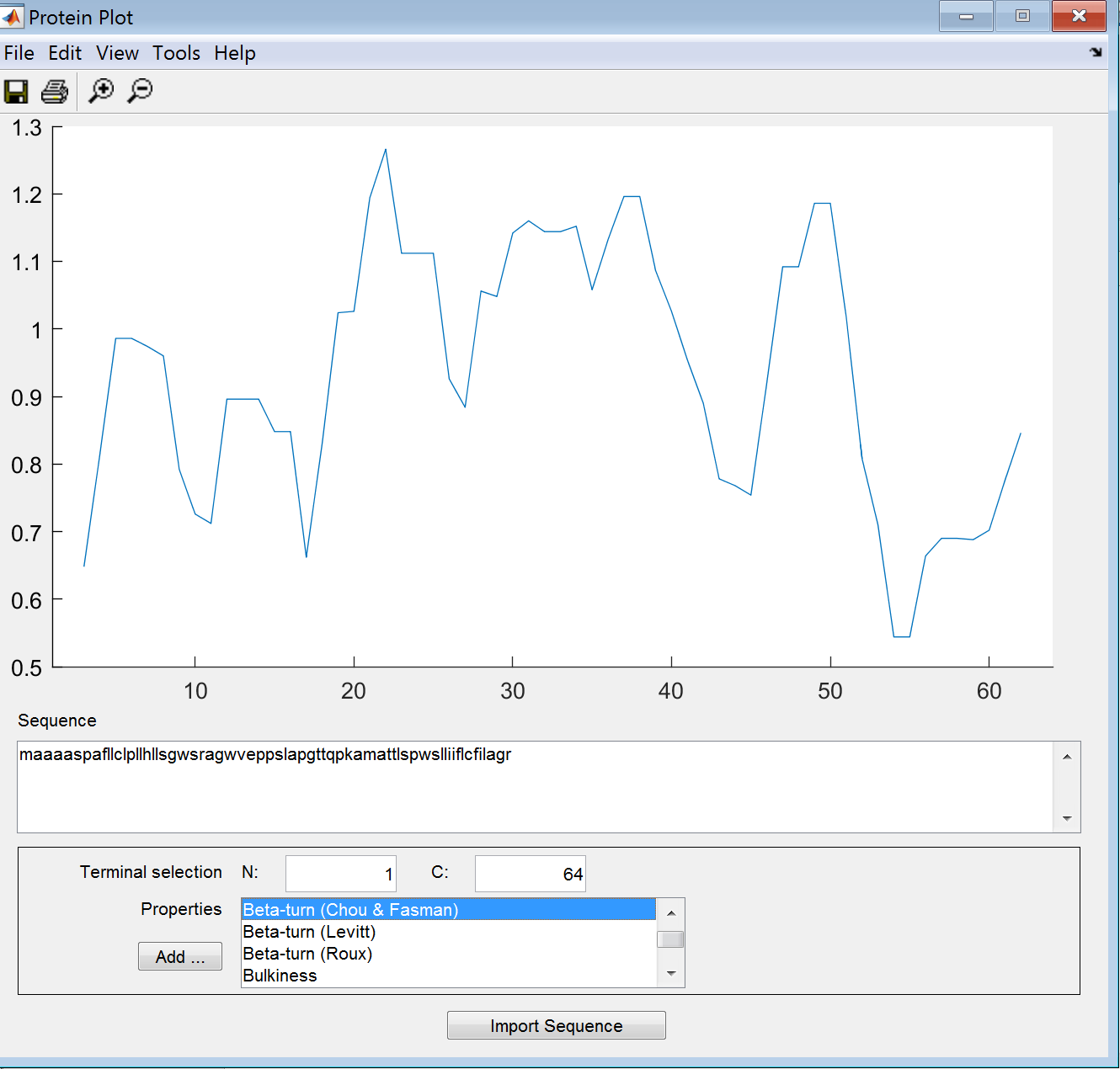
**Beta Sheet (LeVitt)**



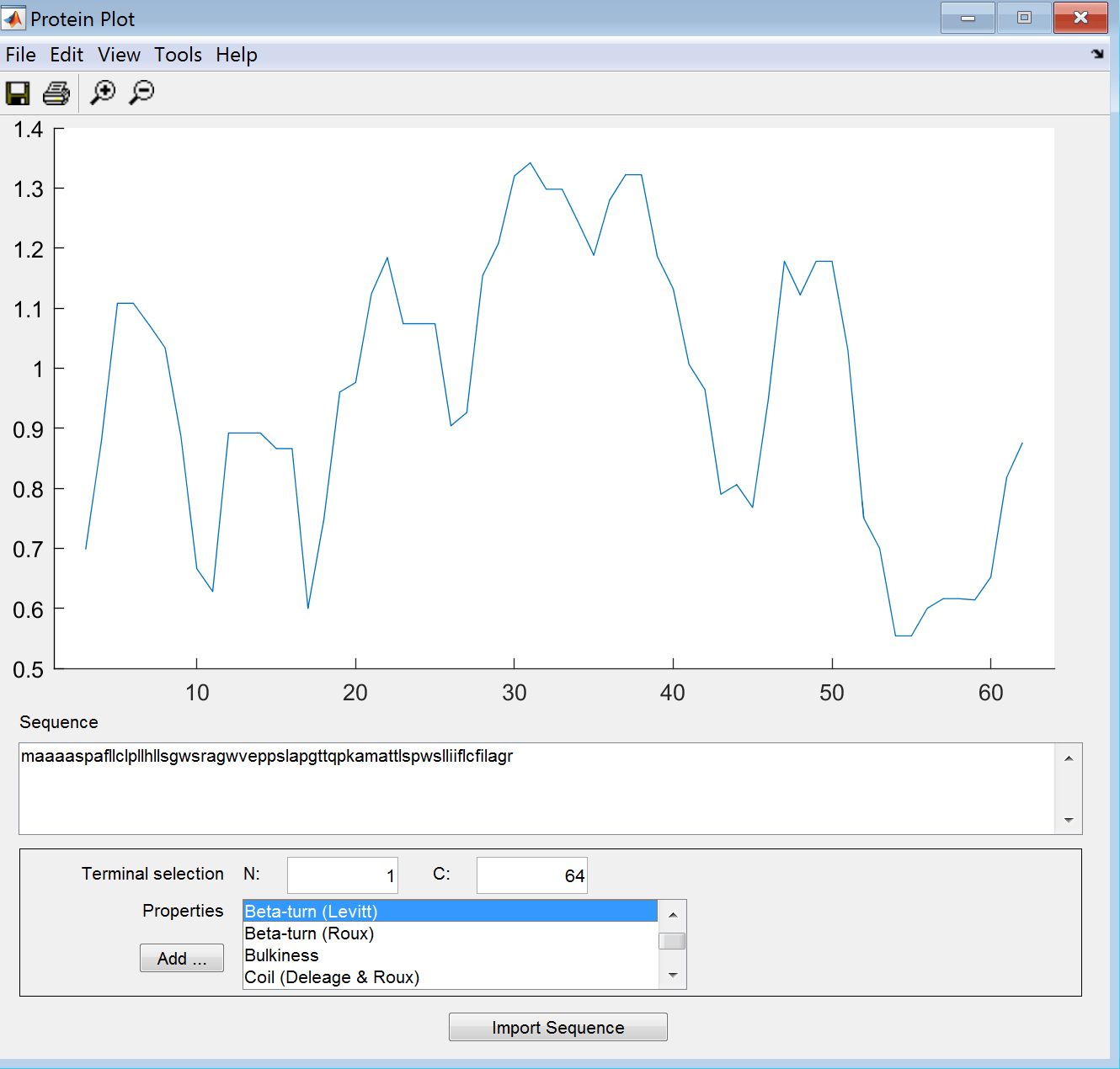
**Beta Sheet (Roux)**



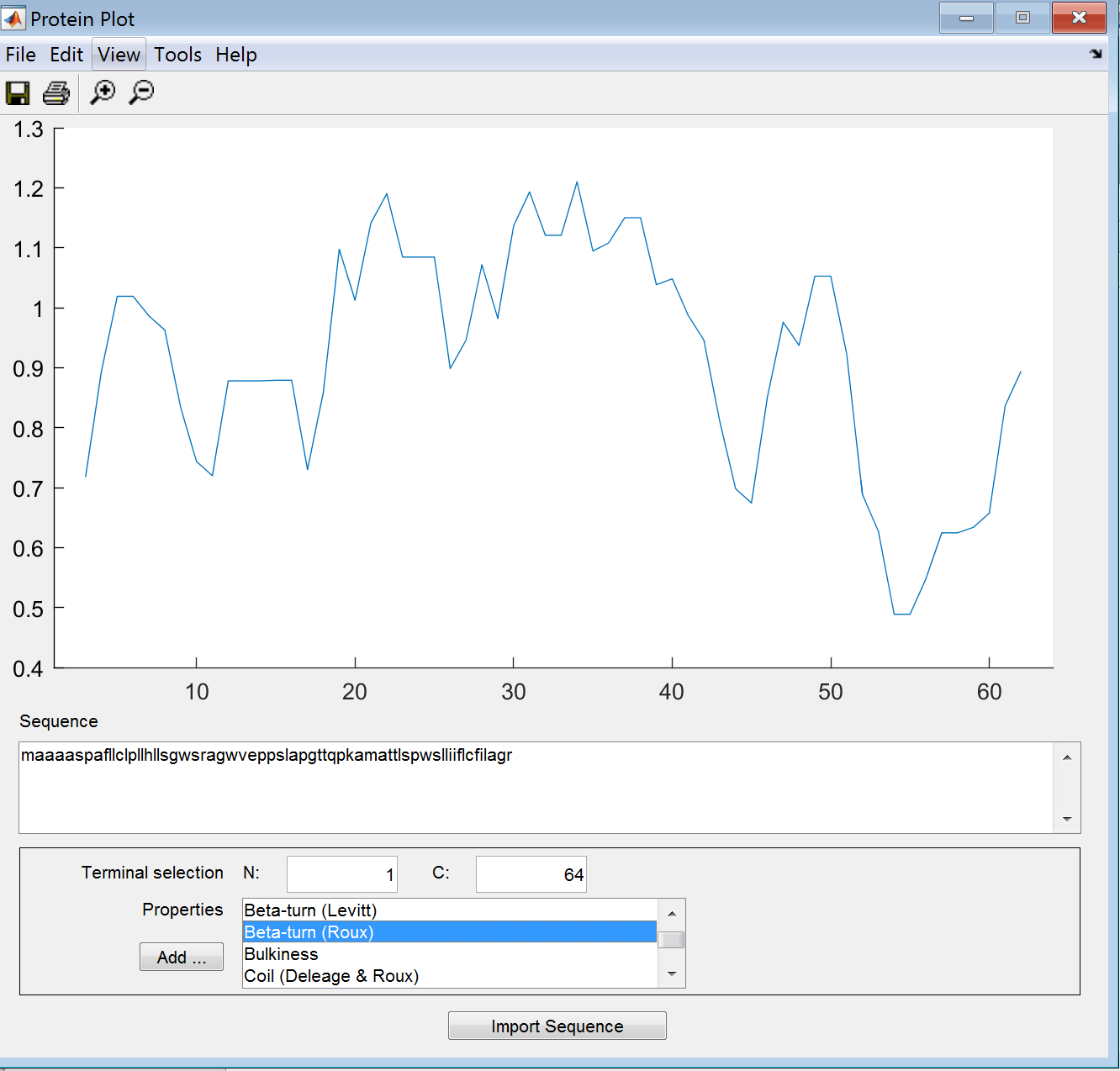
**Beta Turn (Chou-Fasman)**



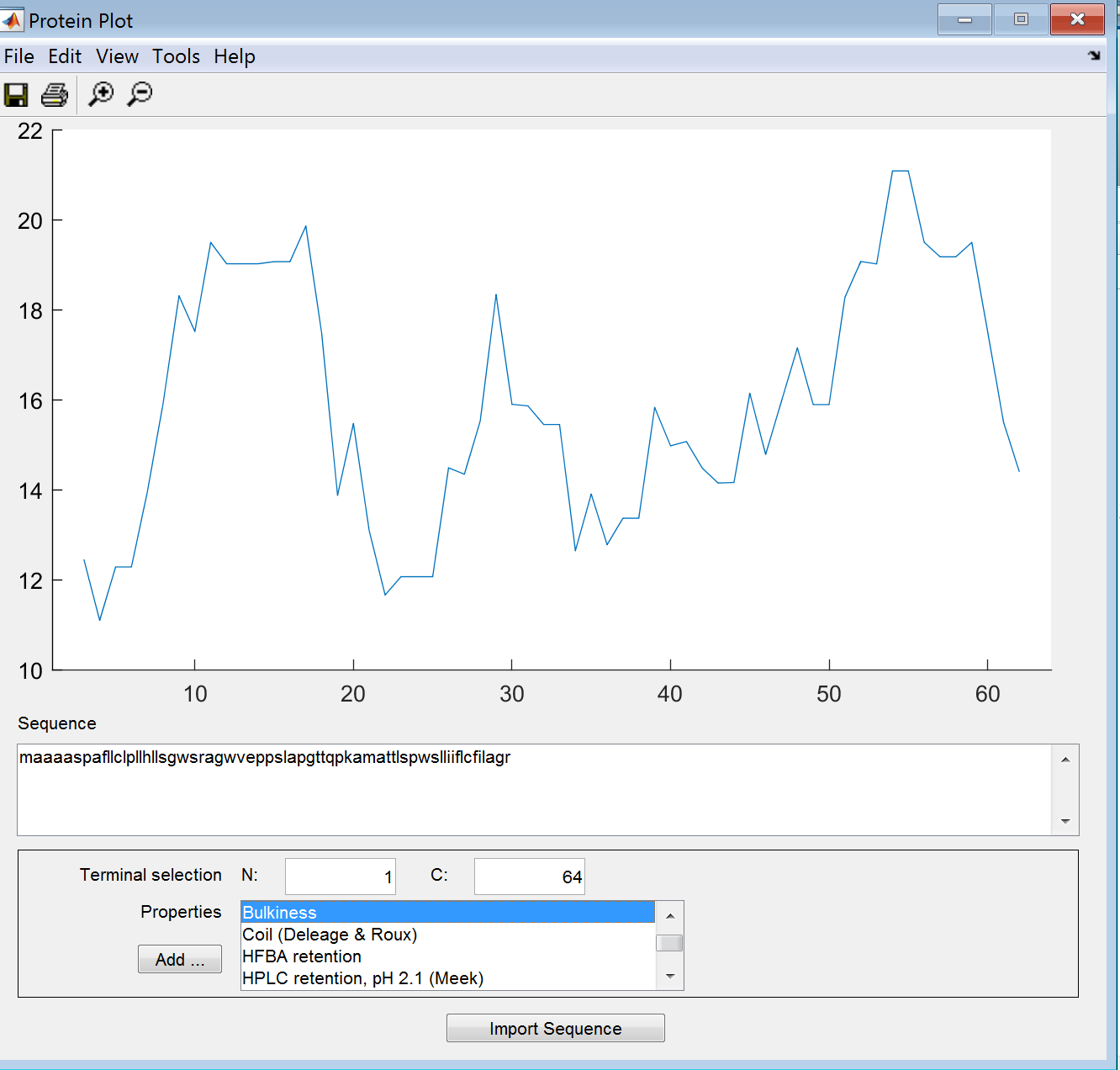
**Beta Turn (LeVitt)**



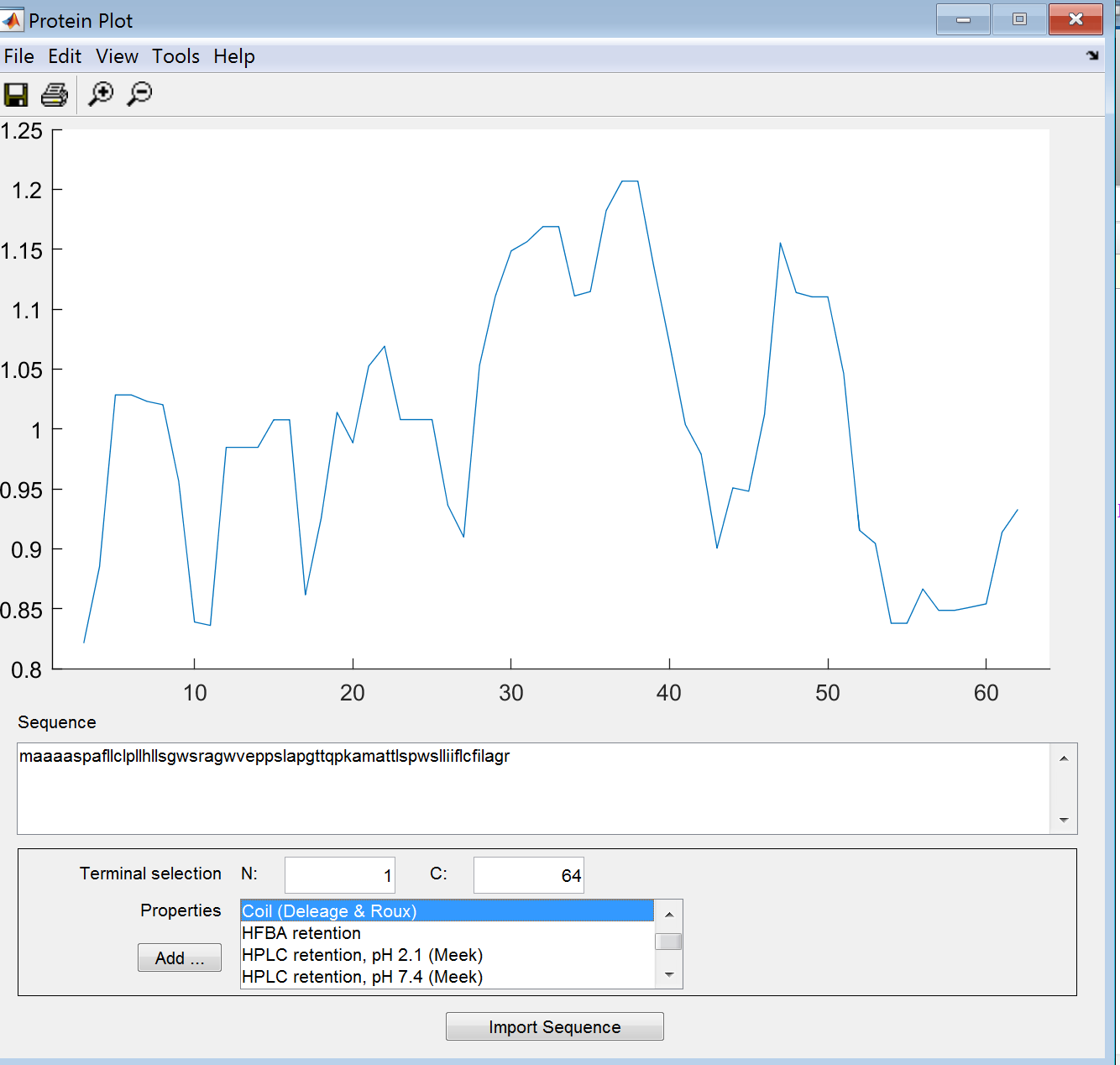
**Beta Turn (Roux)**



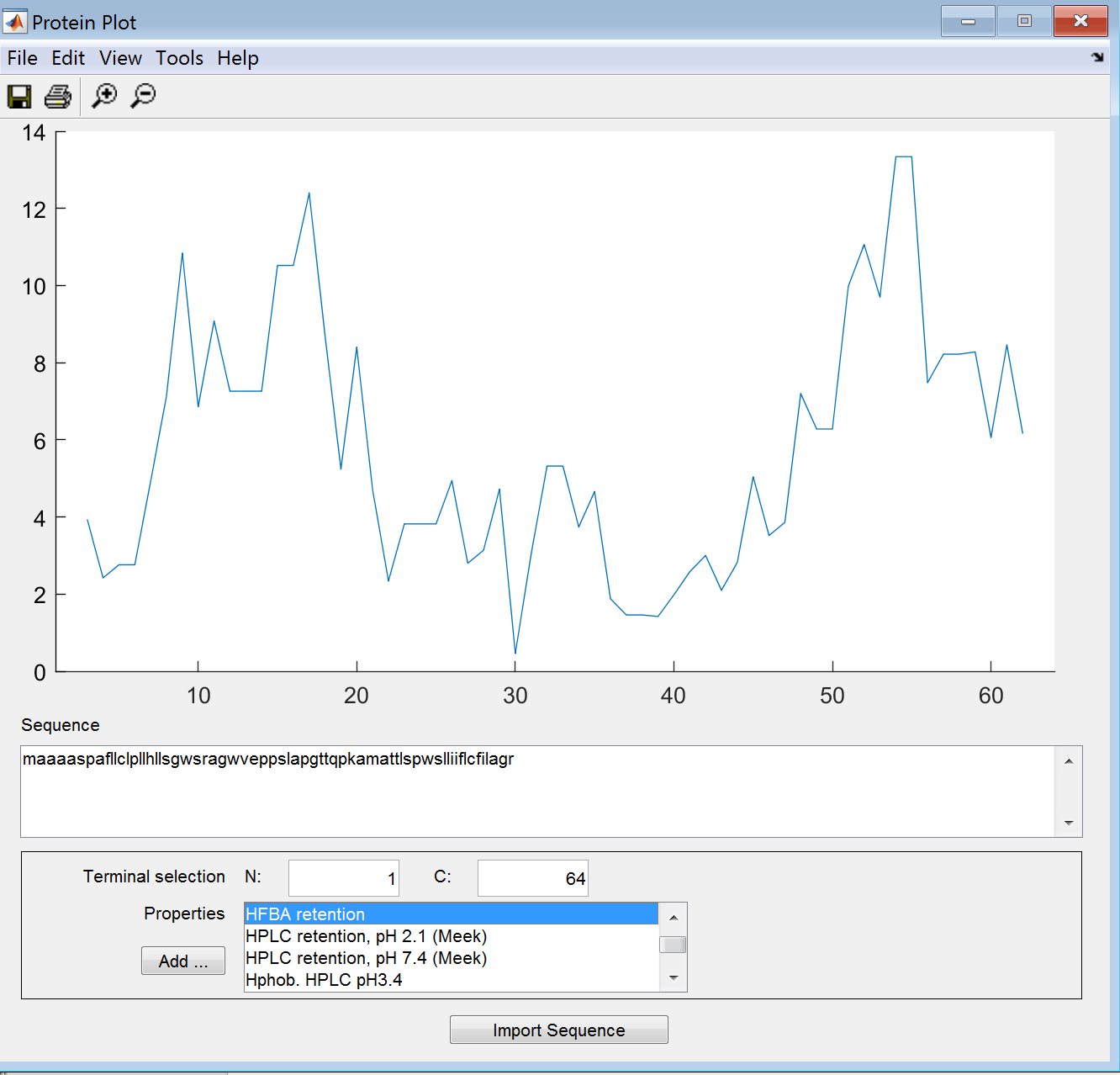
**Bulkiness**



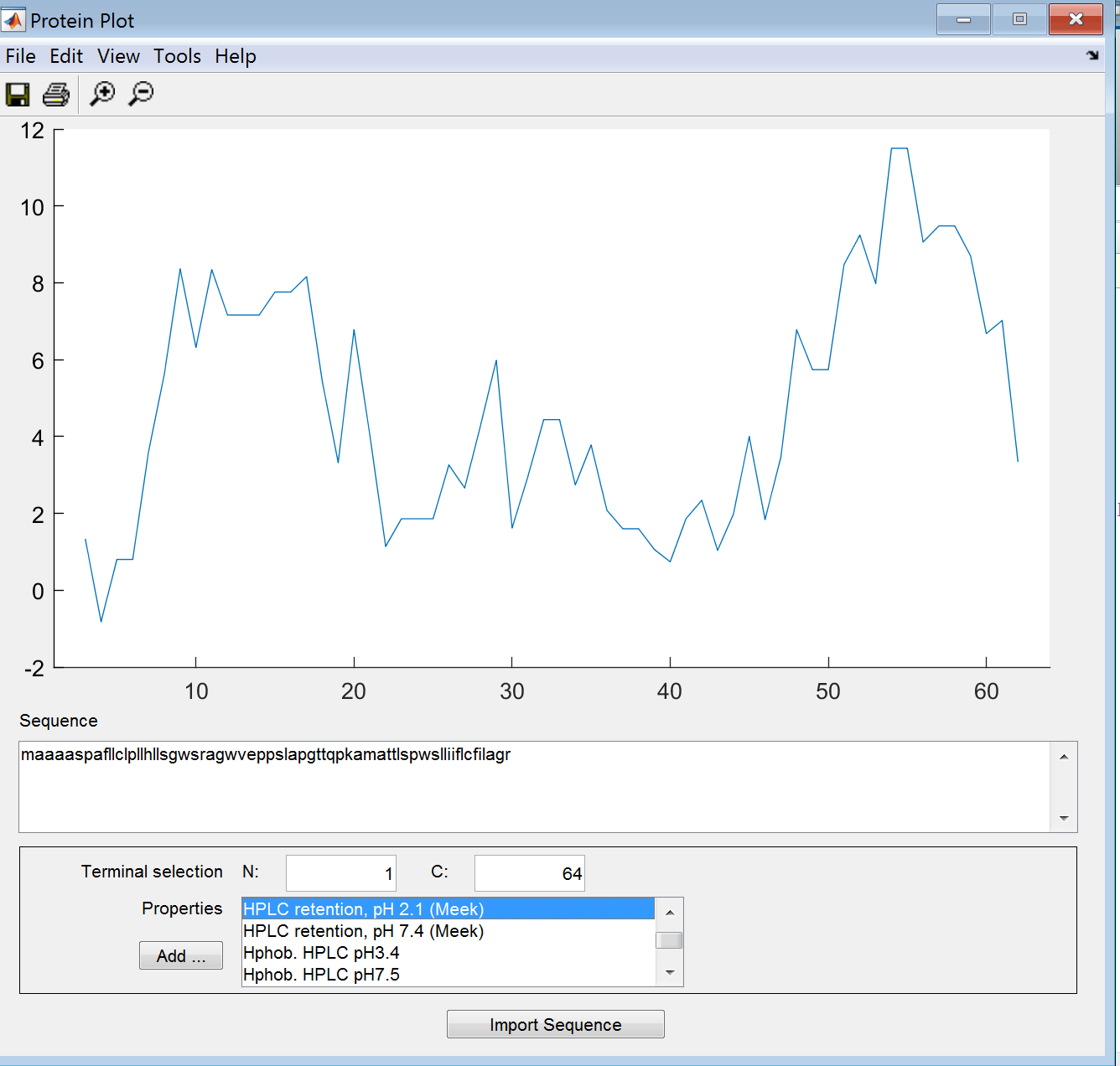
**Coil (Deleage-Roux)**



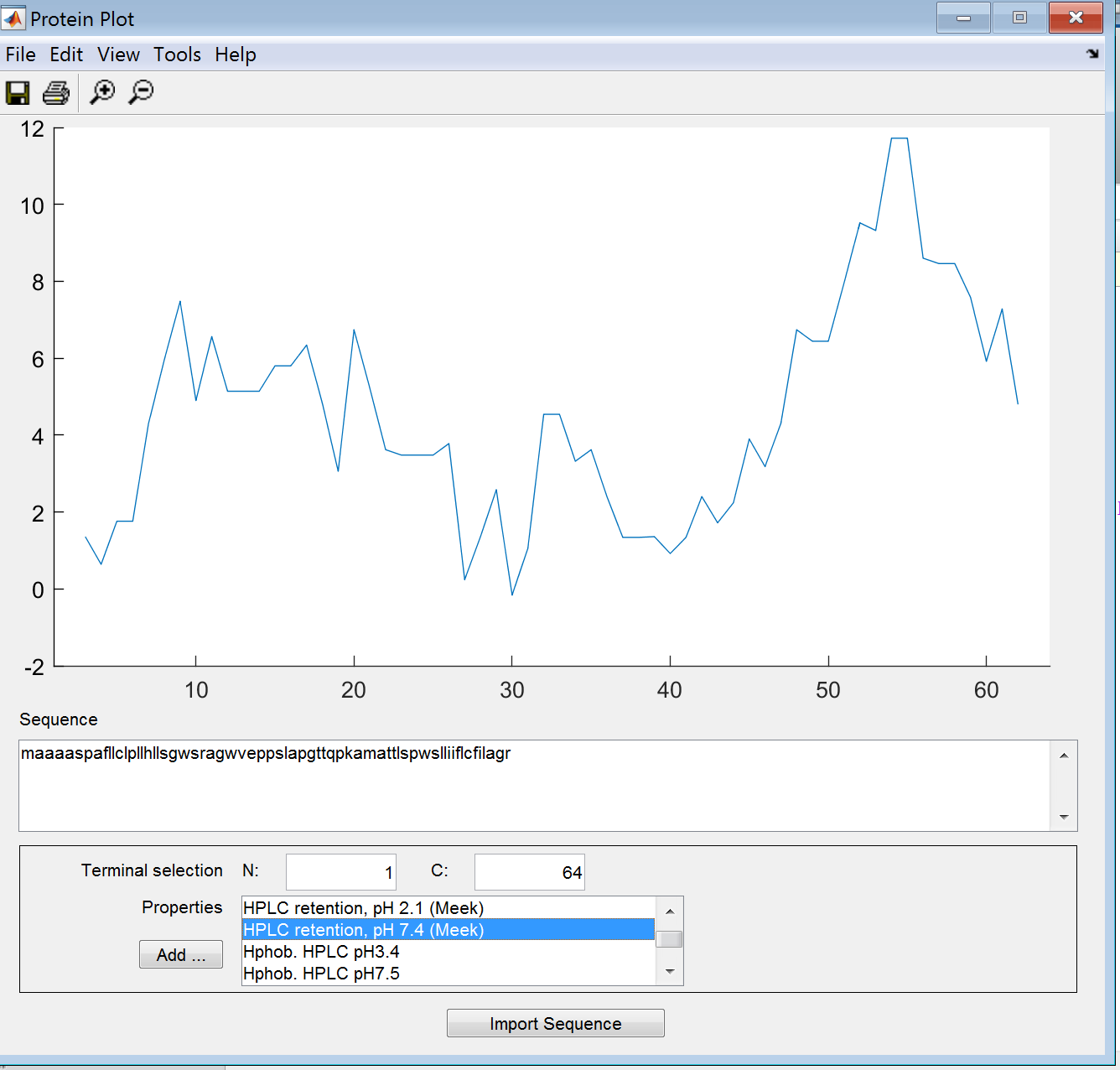
**HFBA Retention**



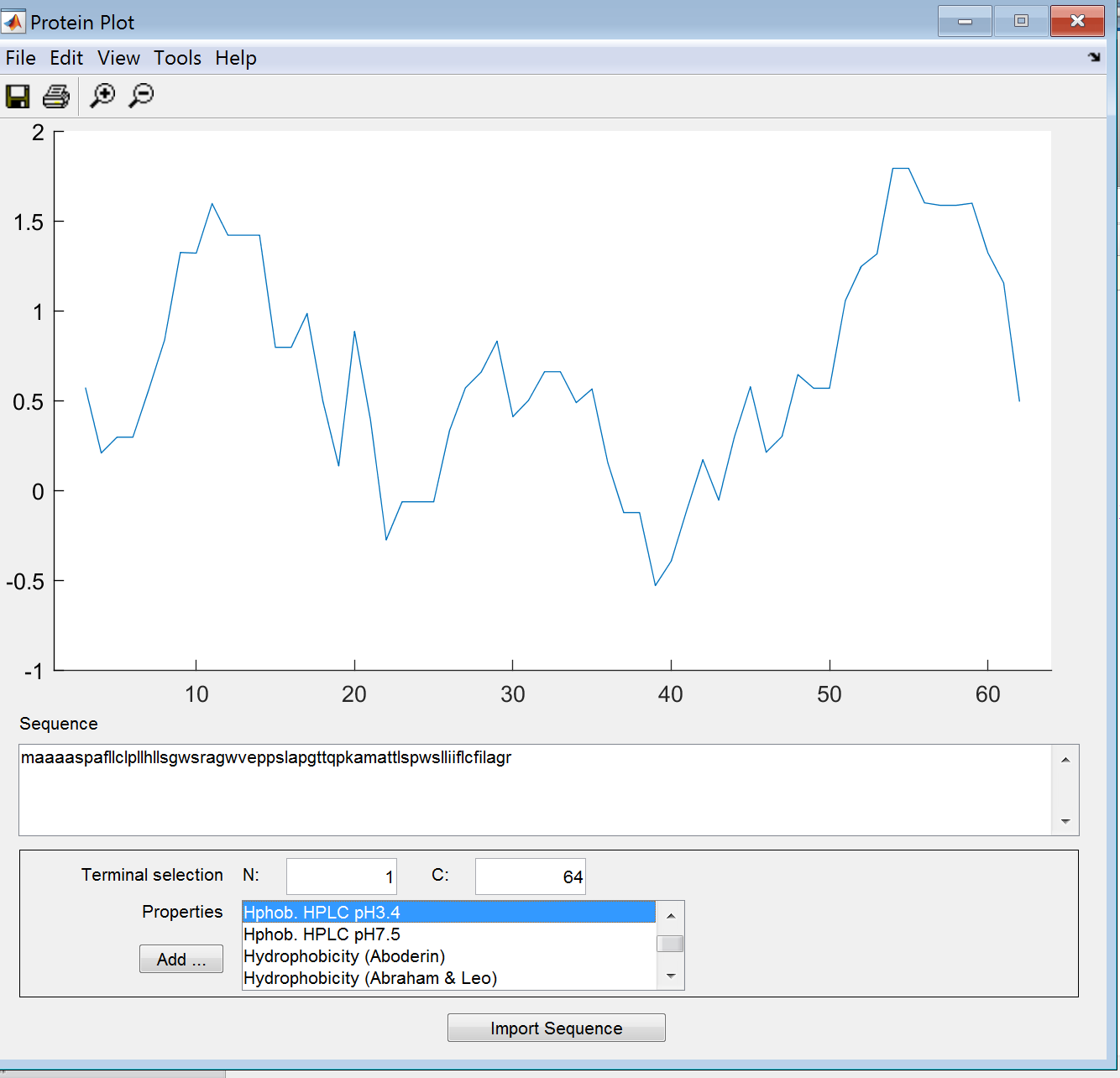
**HPLC Retention, pH 2.1 (Meek)**



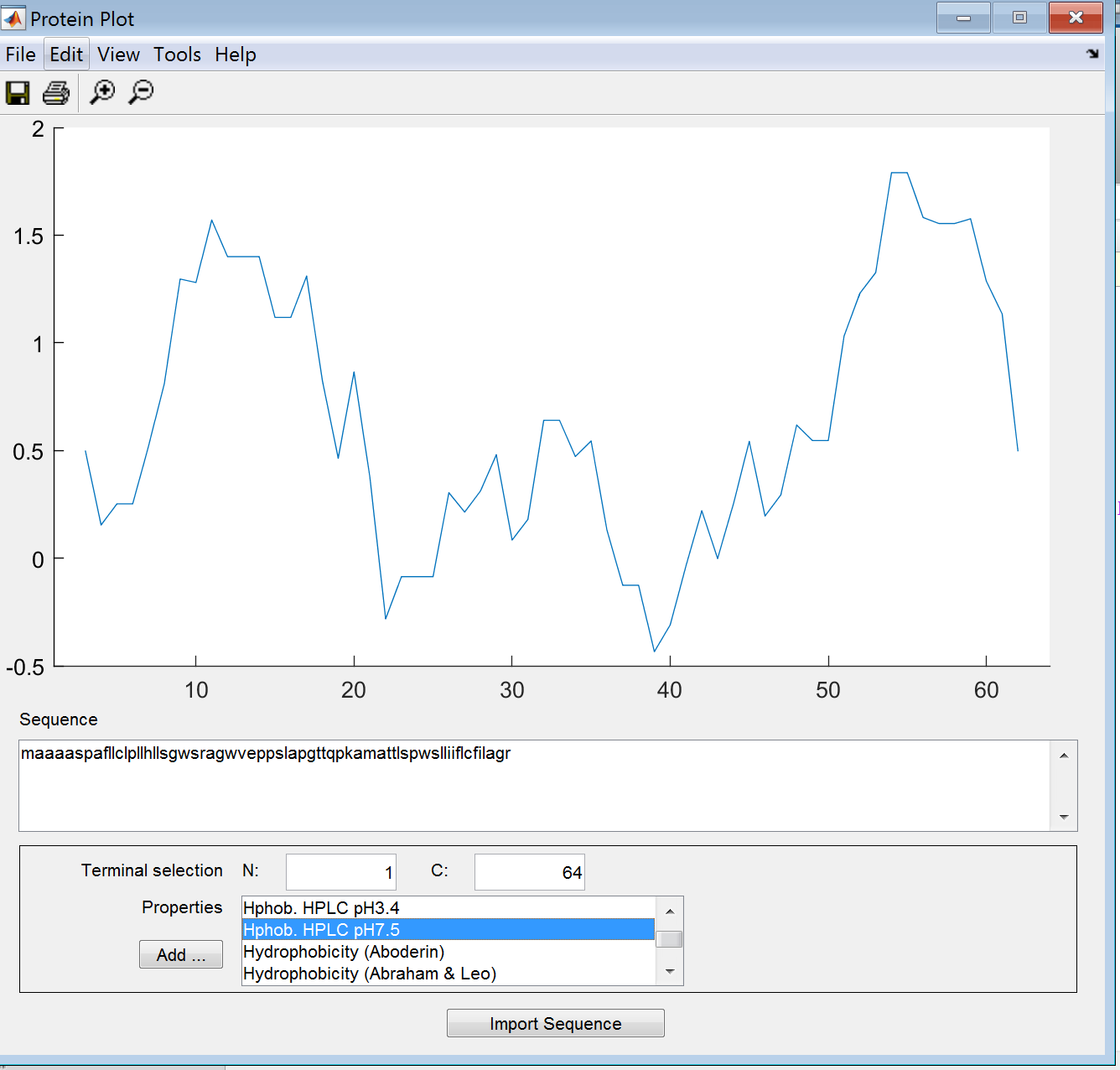
**HPLC Retention pH 7.4 (Meek)**



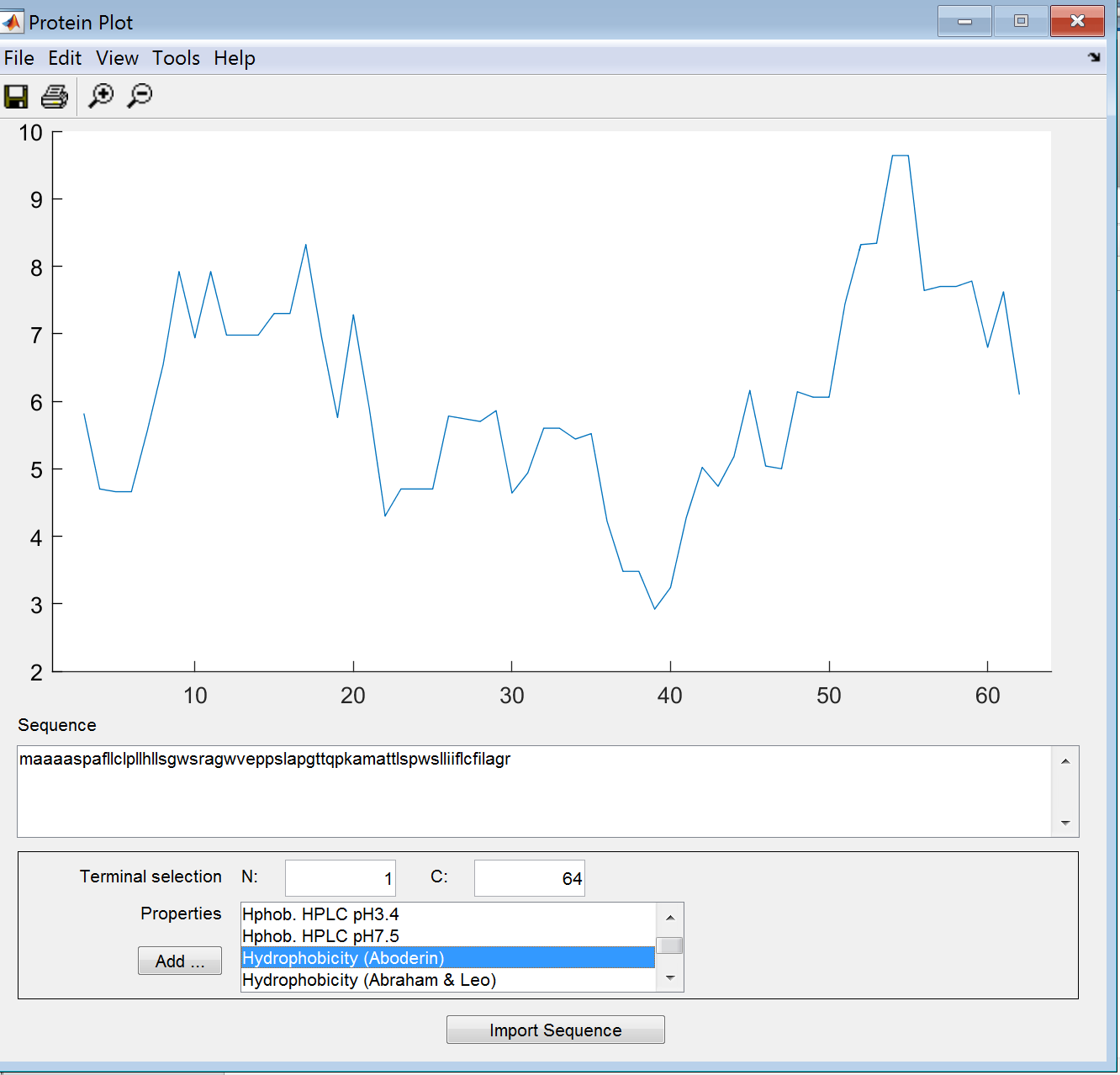
**Hphob, HPLC pH 3.4**



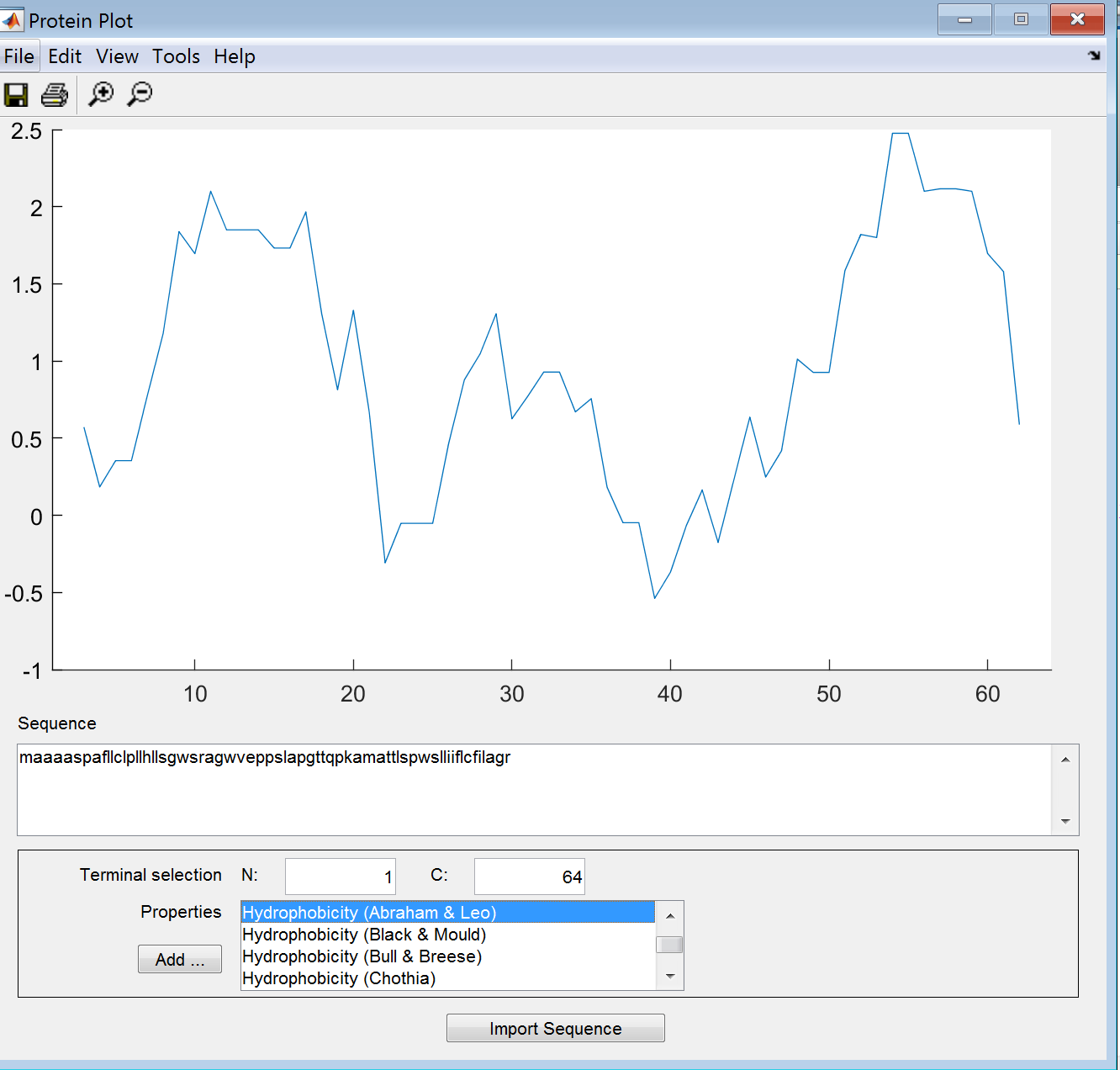
**Hphob HPLC pH 7.5**



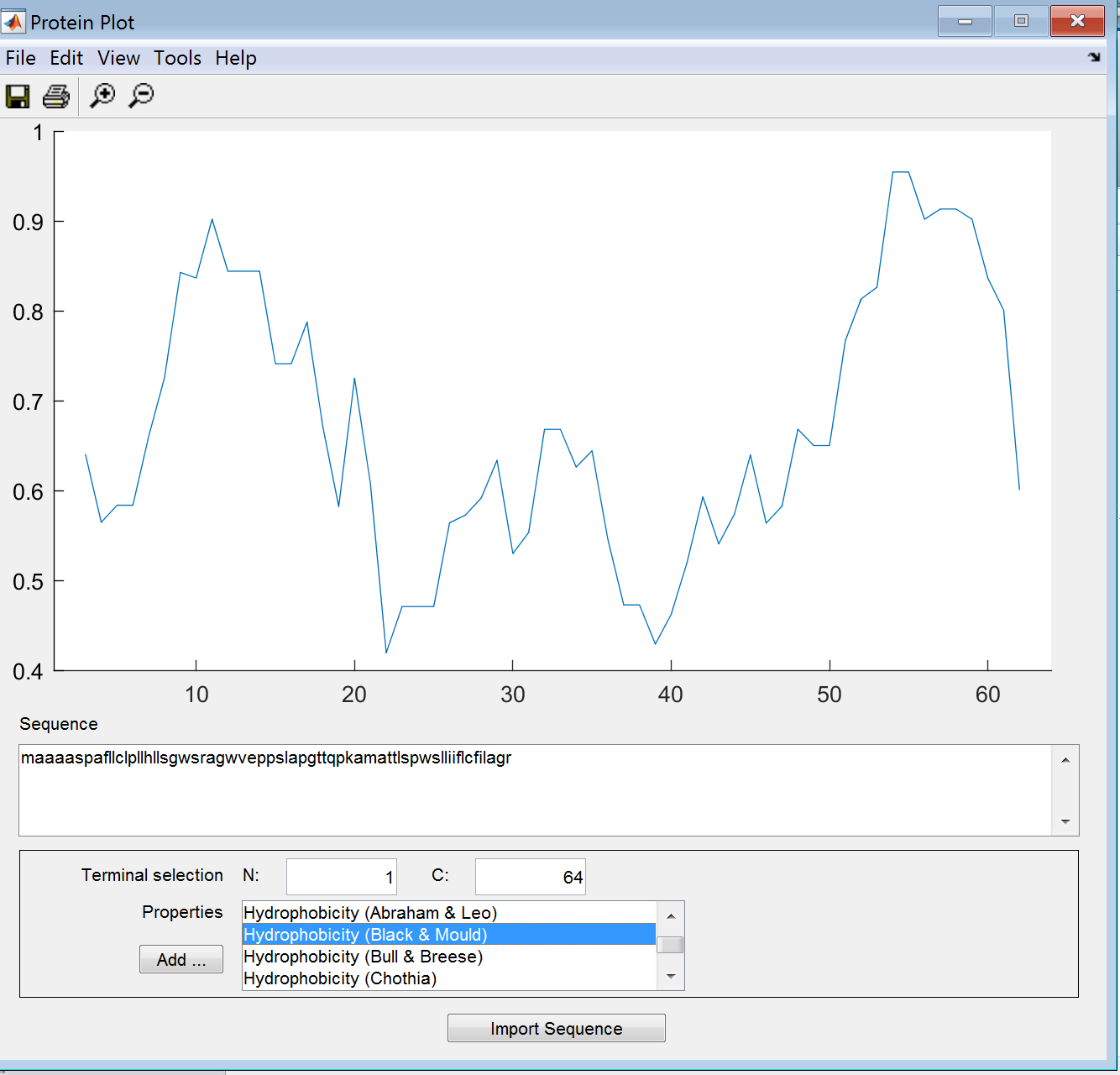
**Hydrophobicity (Aboderin)**



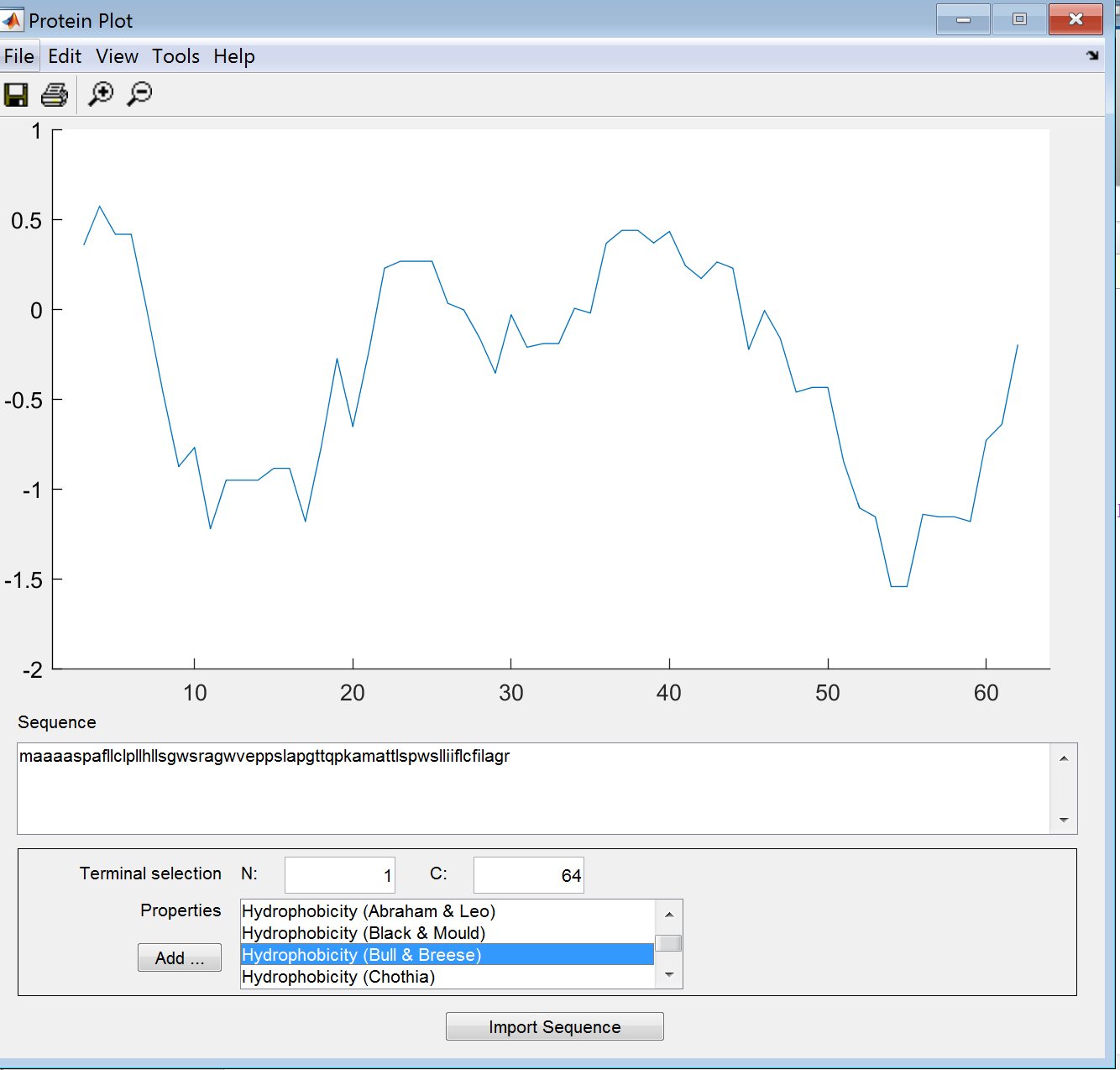
**Hydrophobicity (Abraham & Leo)**



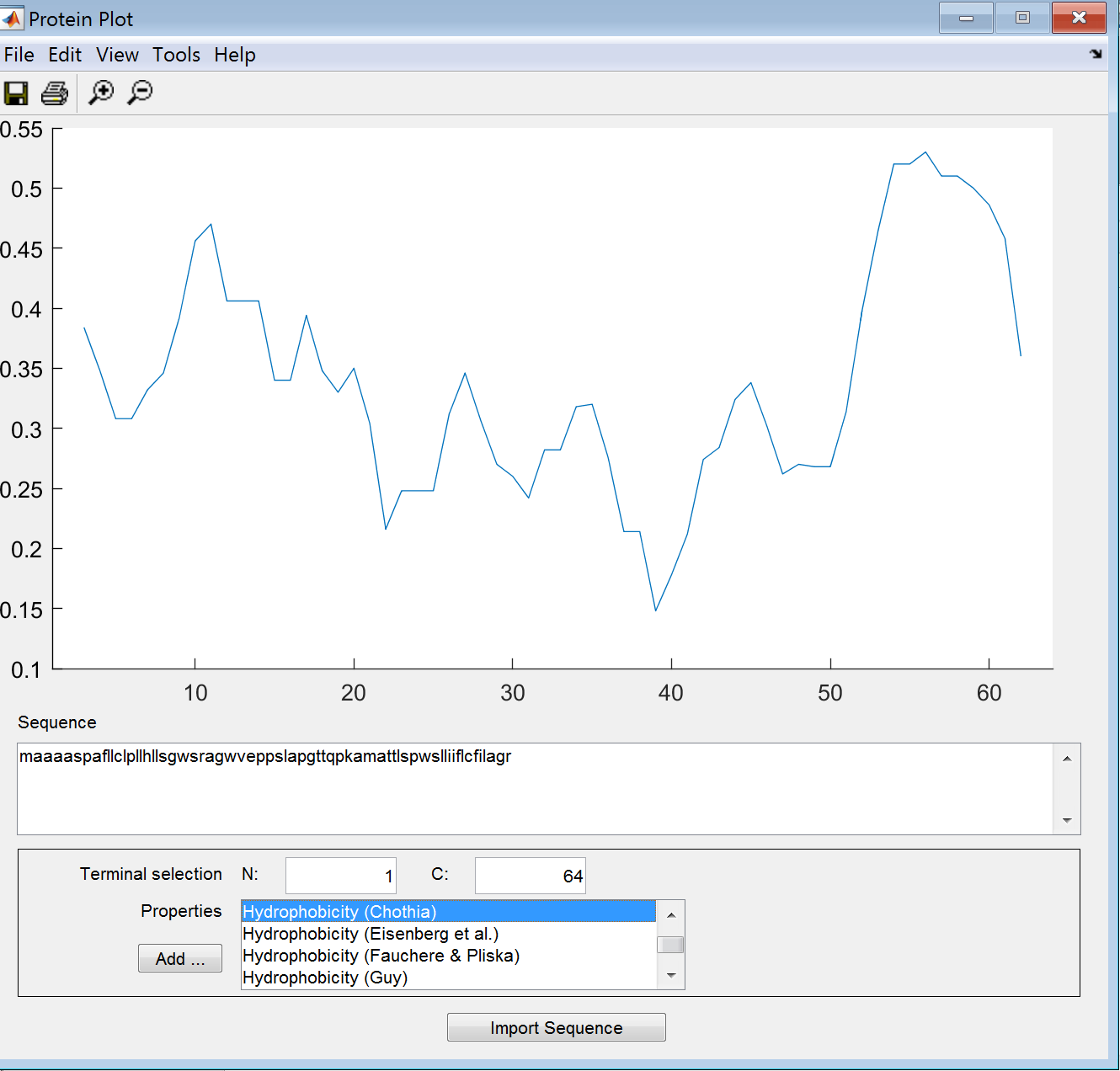
**Hydrophobicity (Black & Mould)**



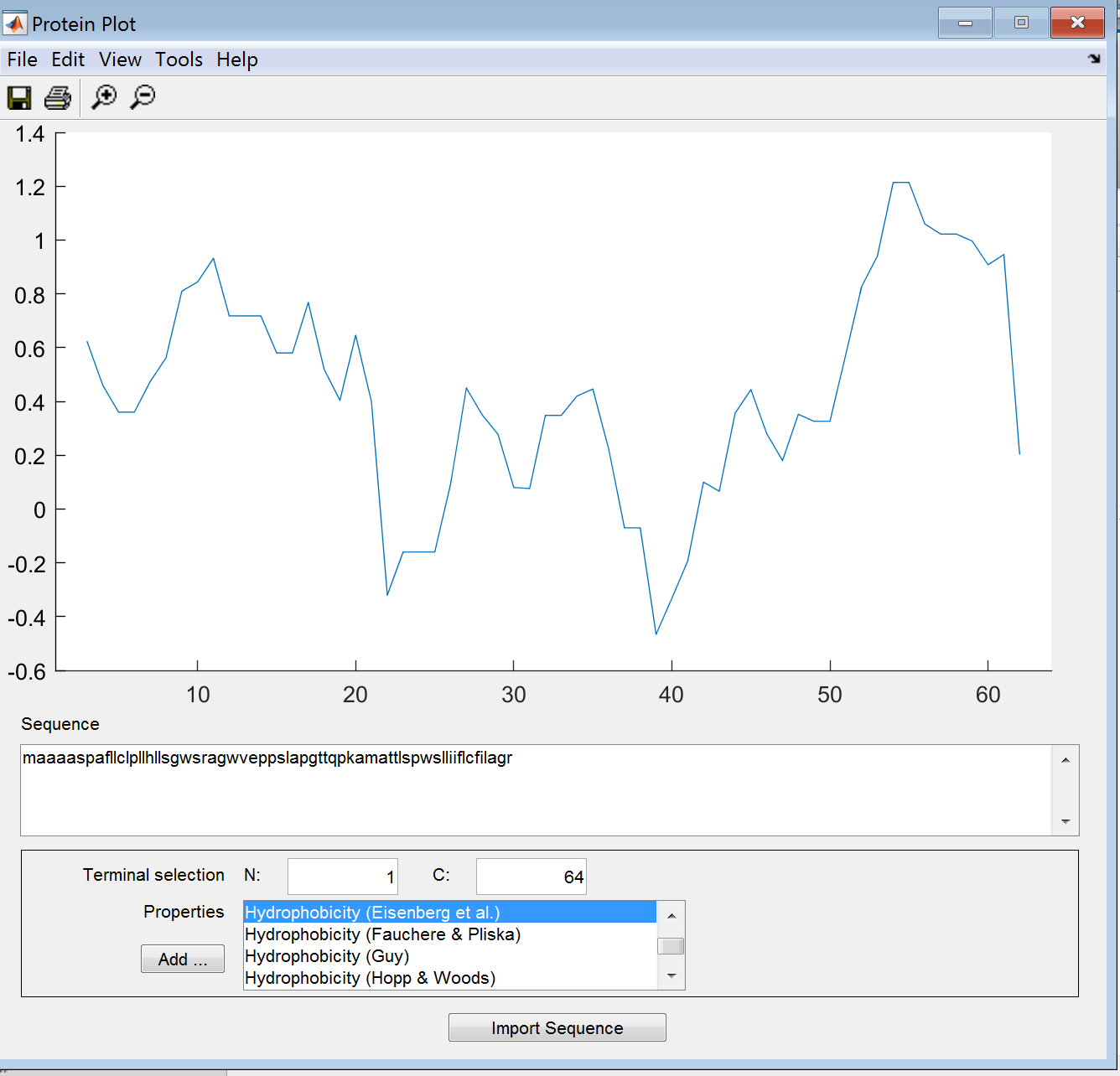
**Hydrophobicity (Bull & Breese)**



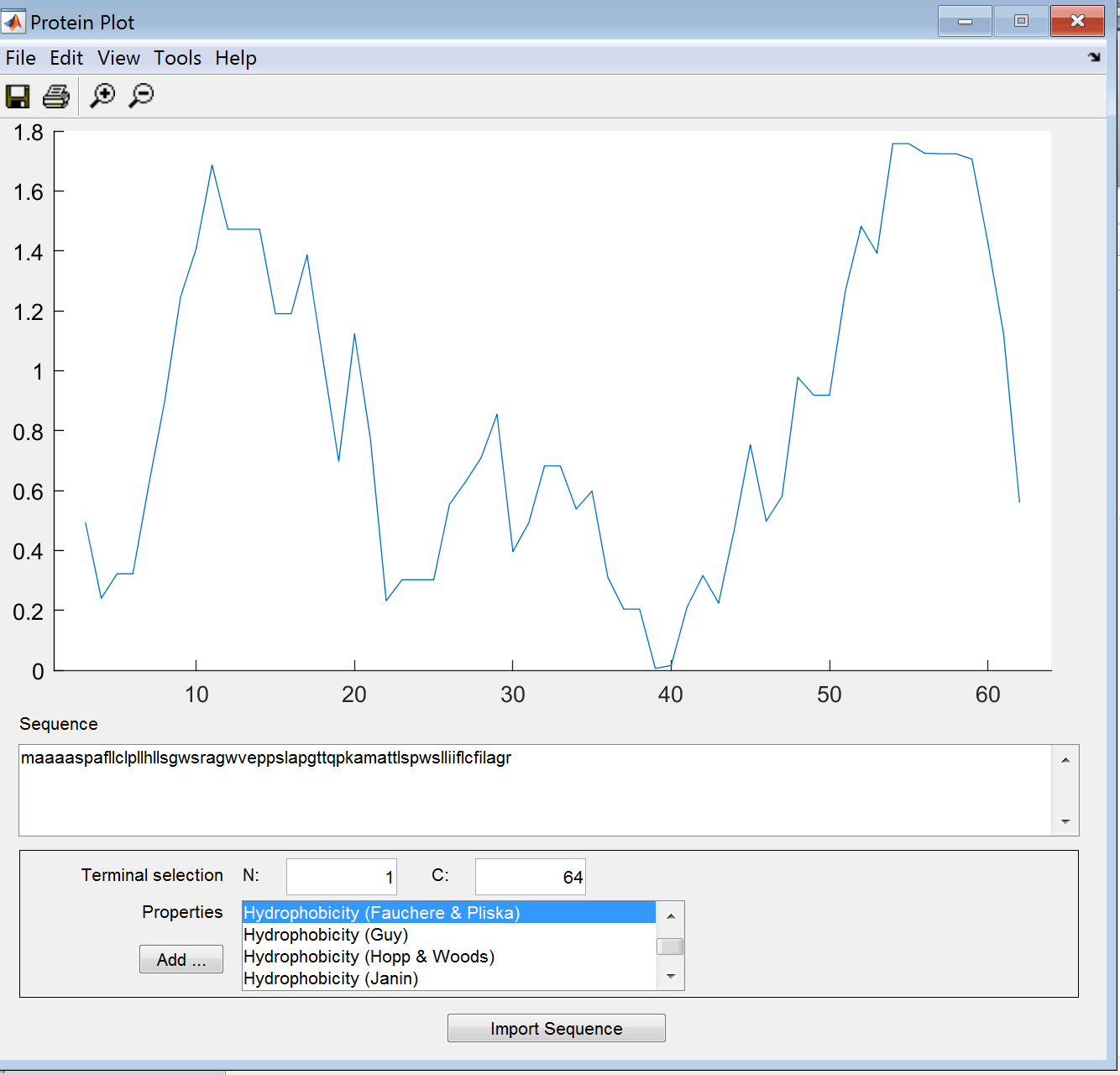
**Hydrophobicity (Chothia)**



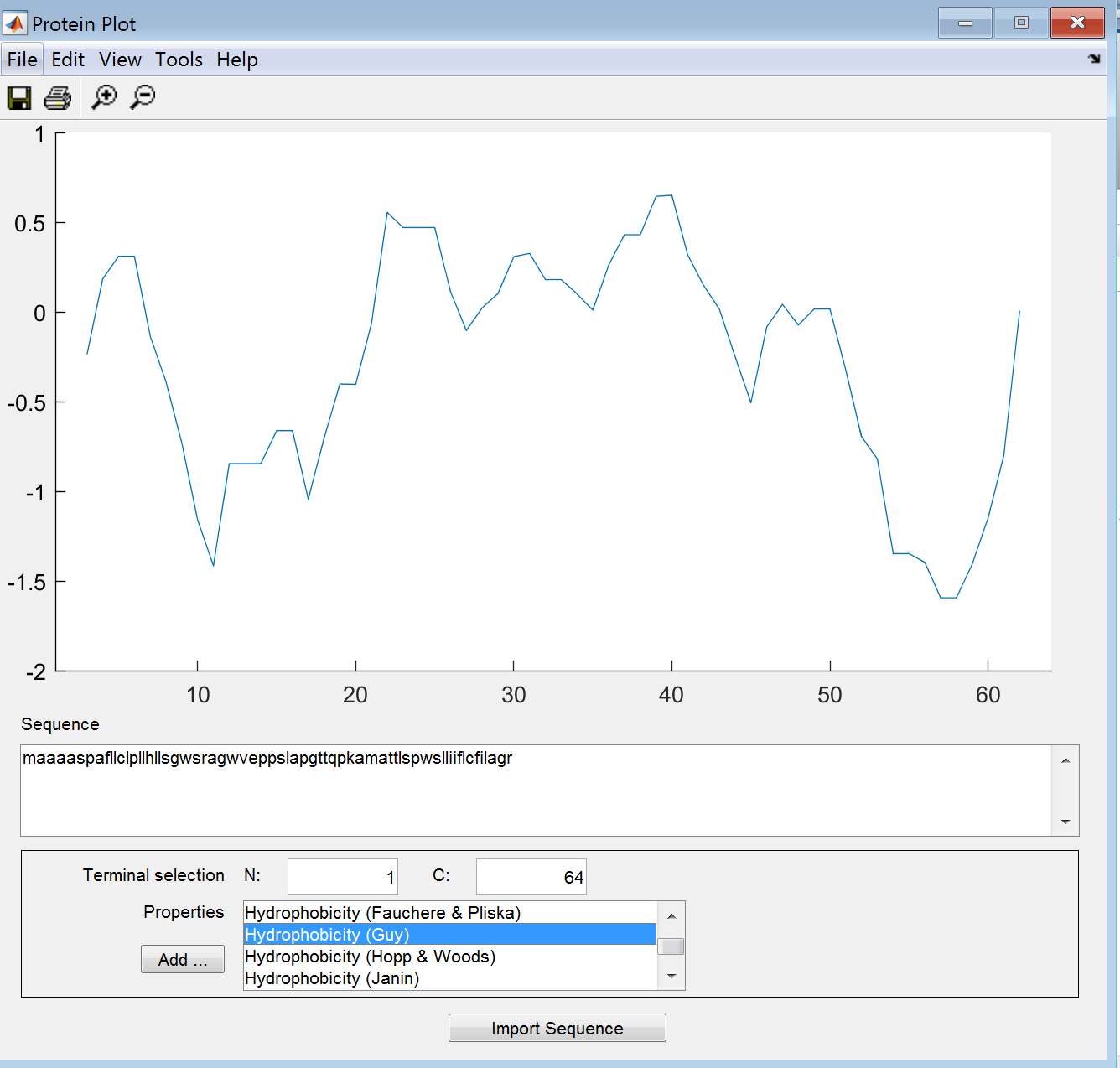
**Hydrophobicity (Eisenberg et. Al)**



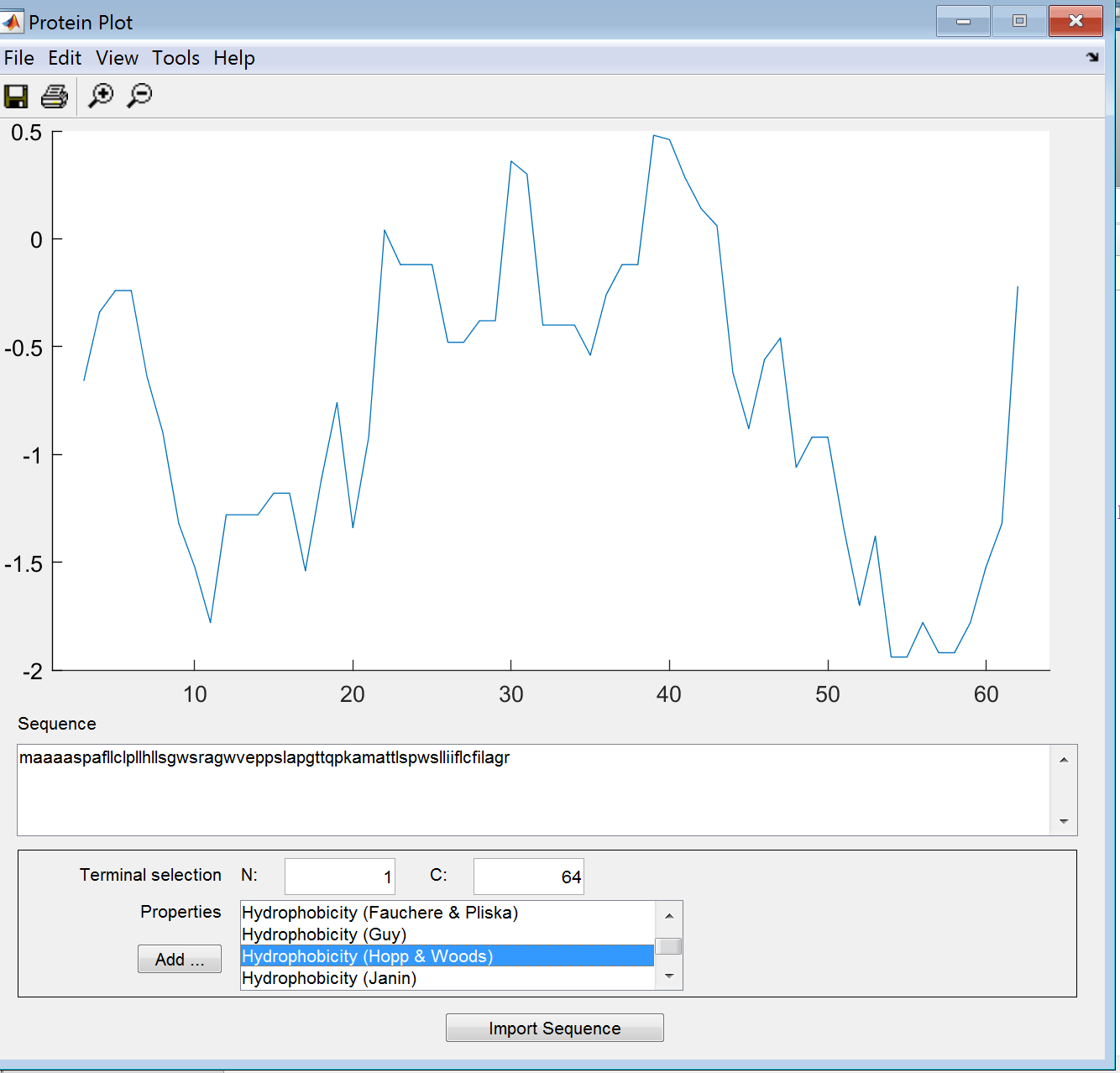
**Hydrophobicity (Fauchere & Pliska)**



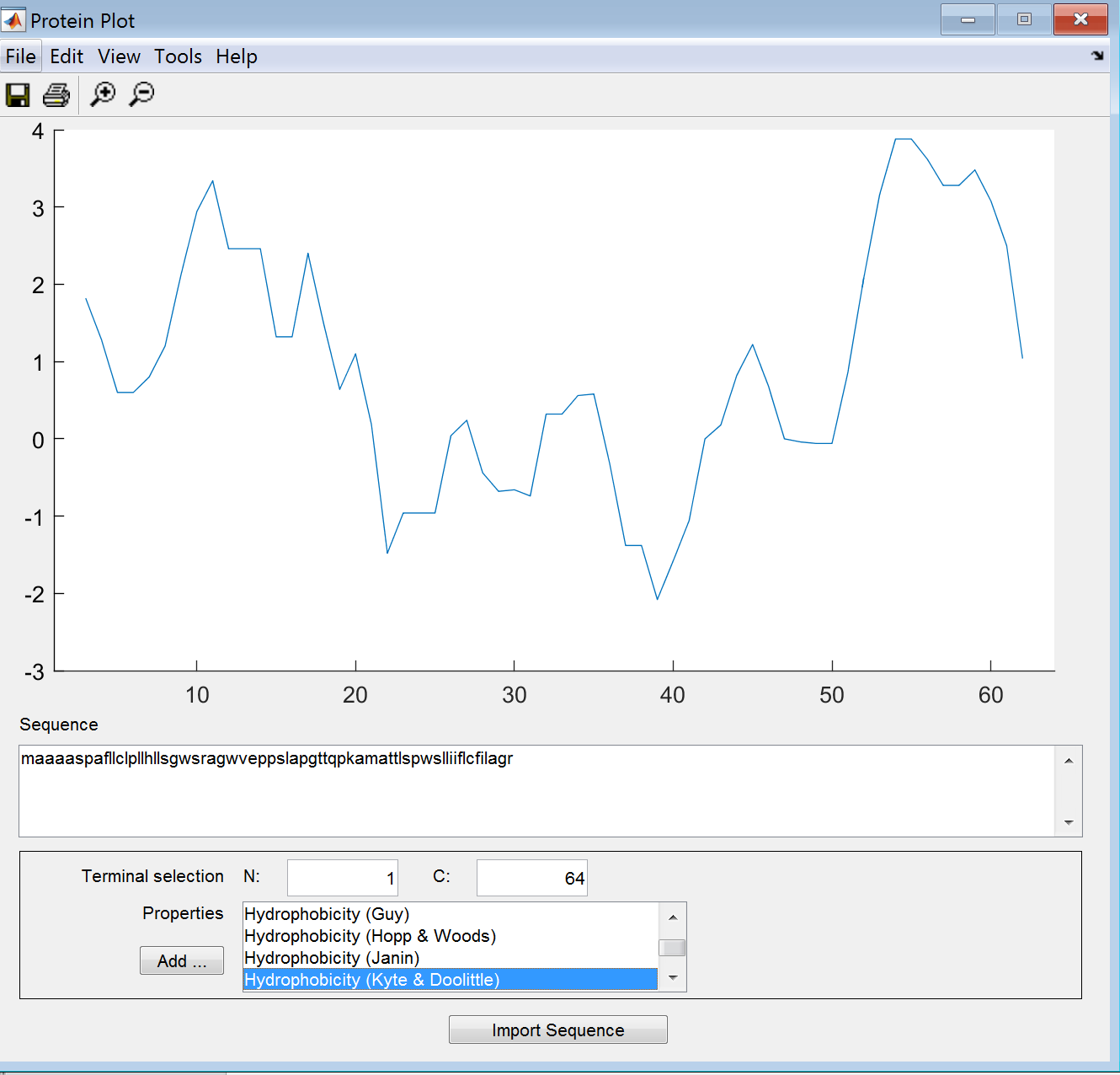
**Hydrophobicity (Guy)**



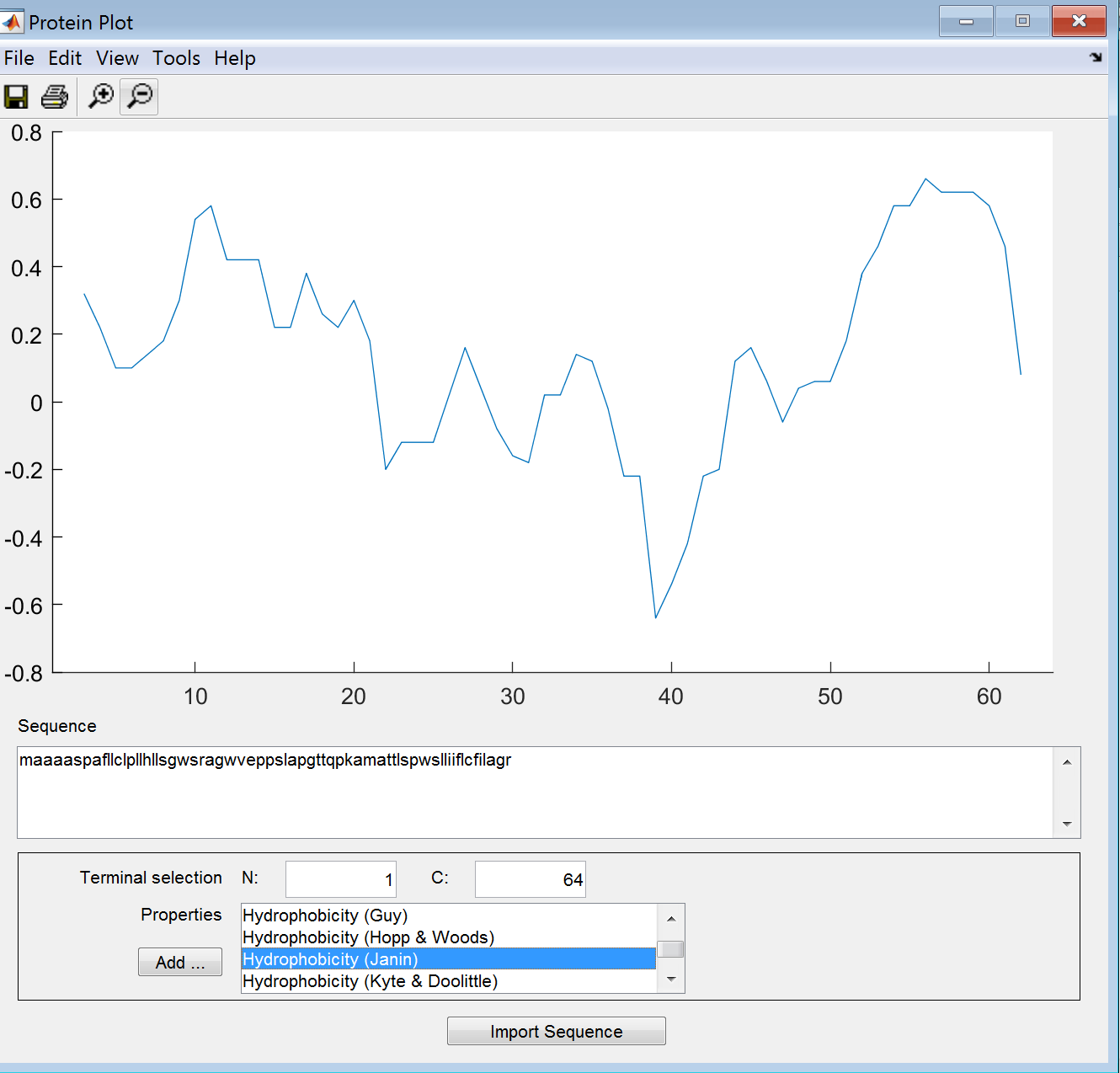
**Hydrophobicity (Hopp & Woods)**



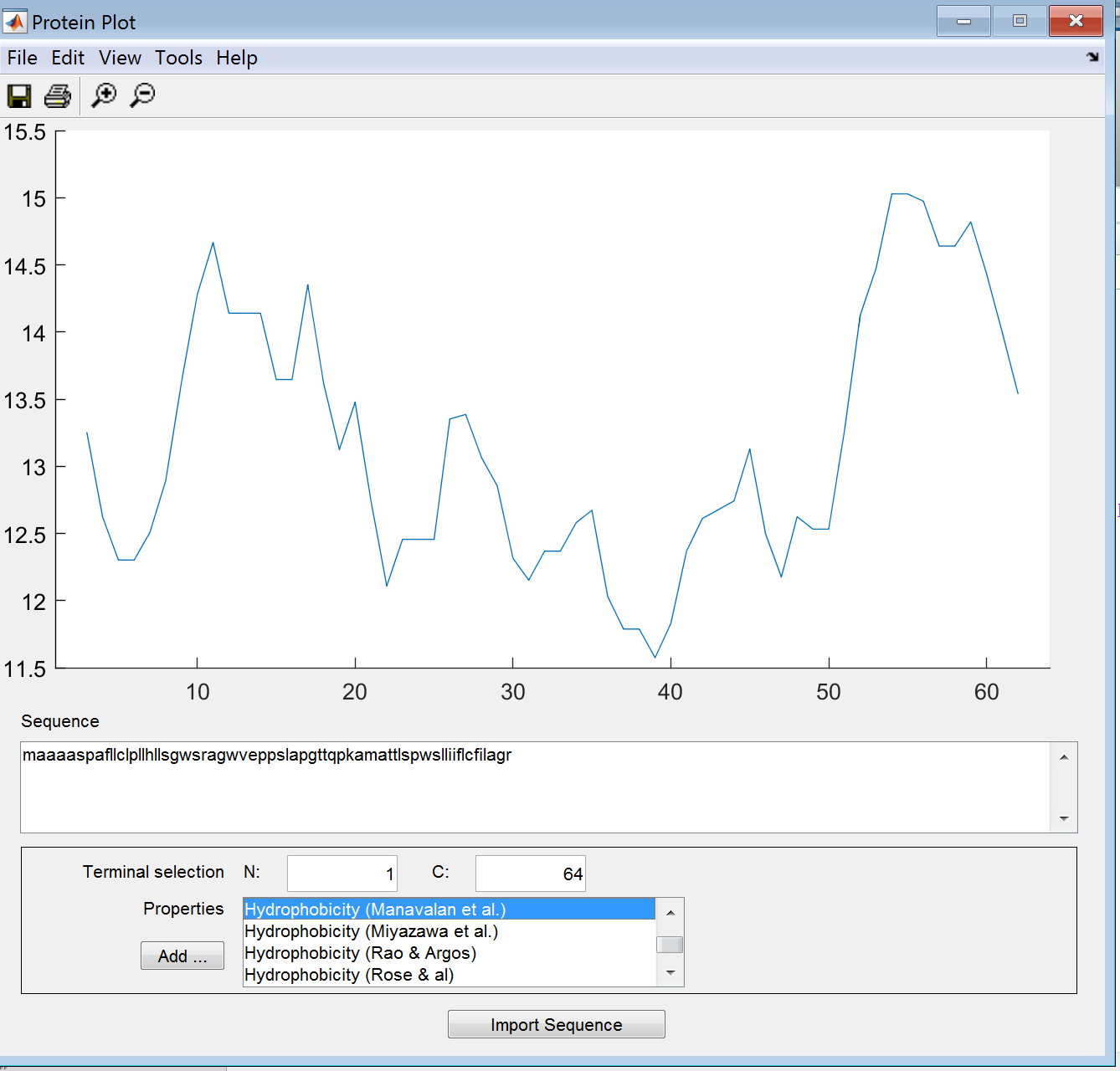
**Hydrophobicity (Kyle & Doolittle)**



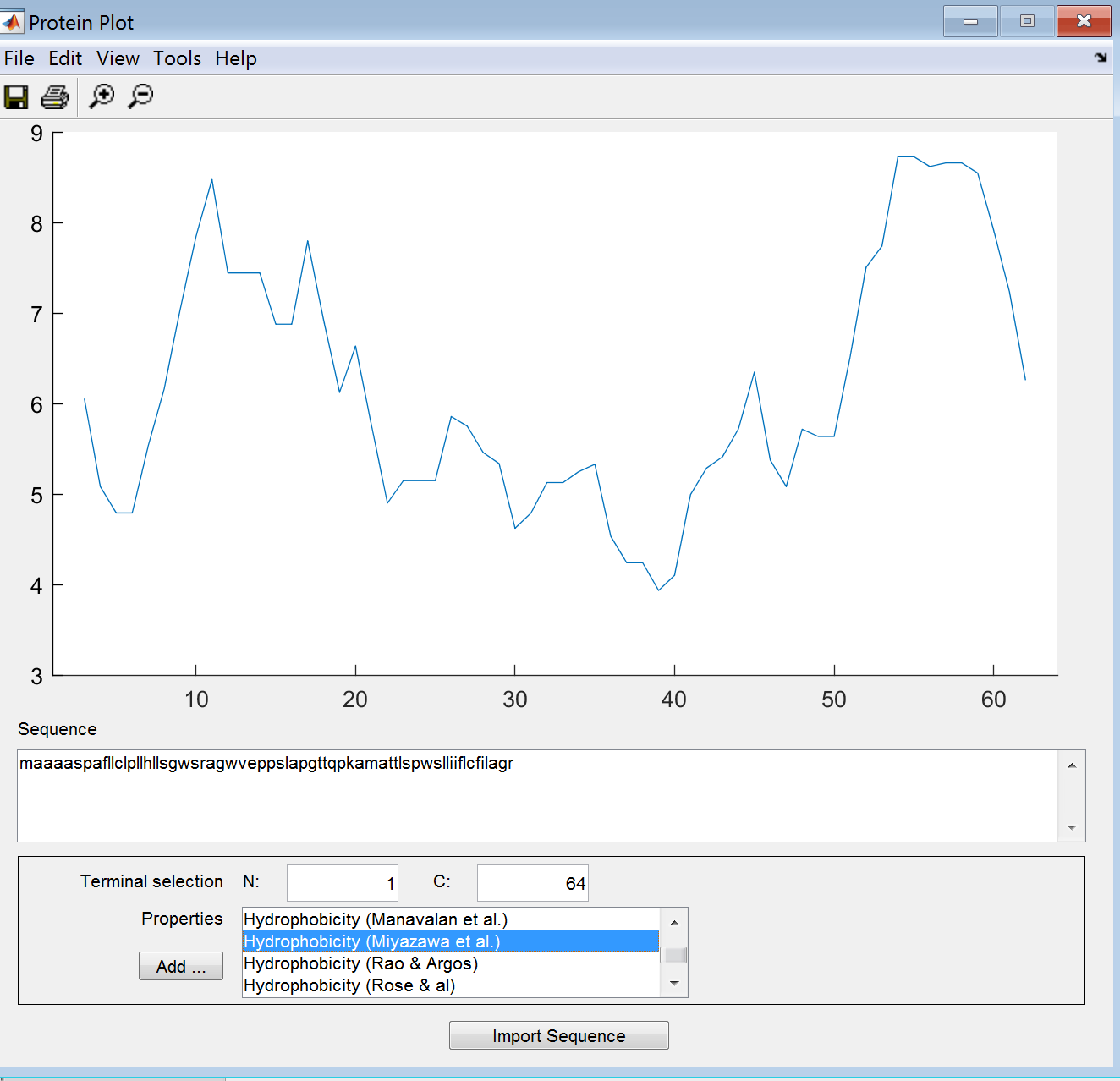
**Hydrophobicity (Janin)**



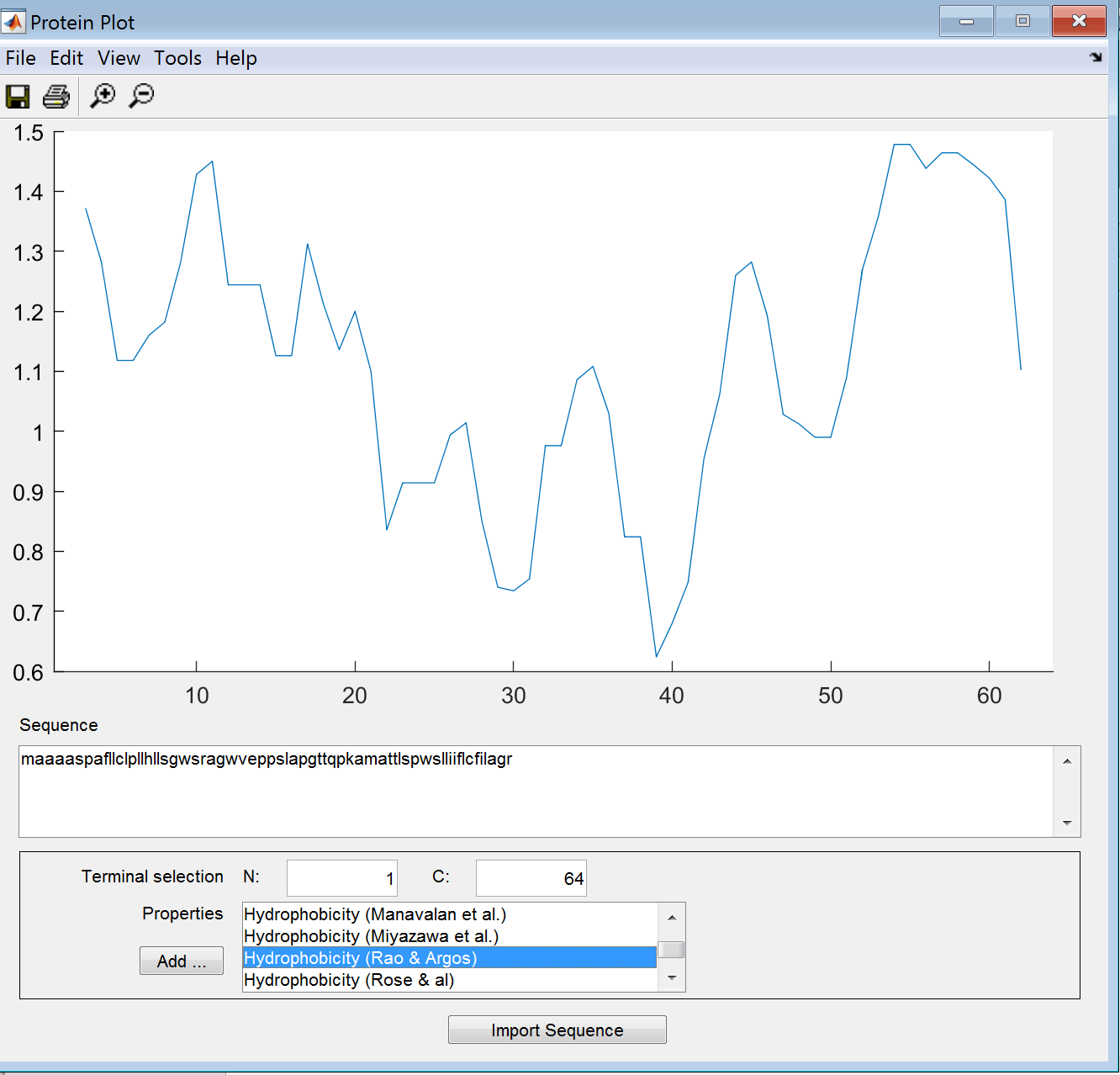
**Hydrophobicity (Manavalan et al)**



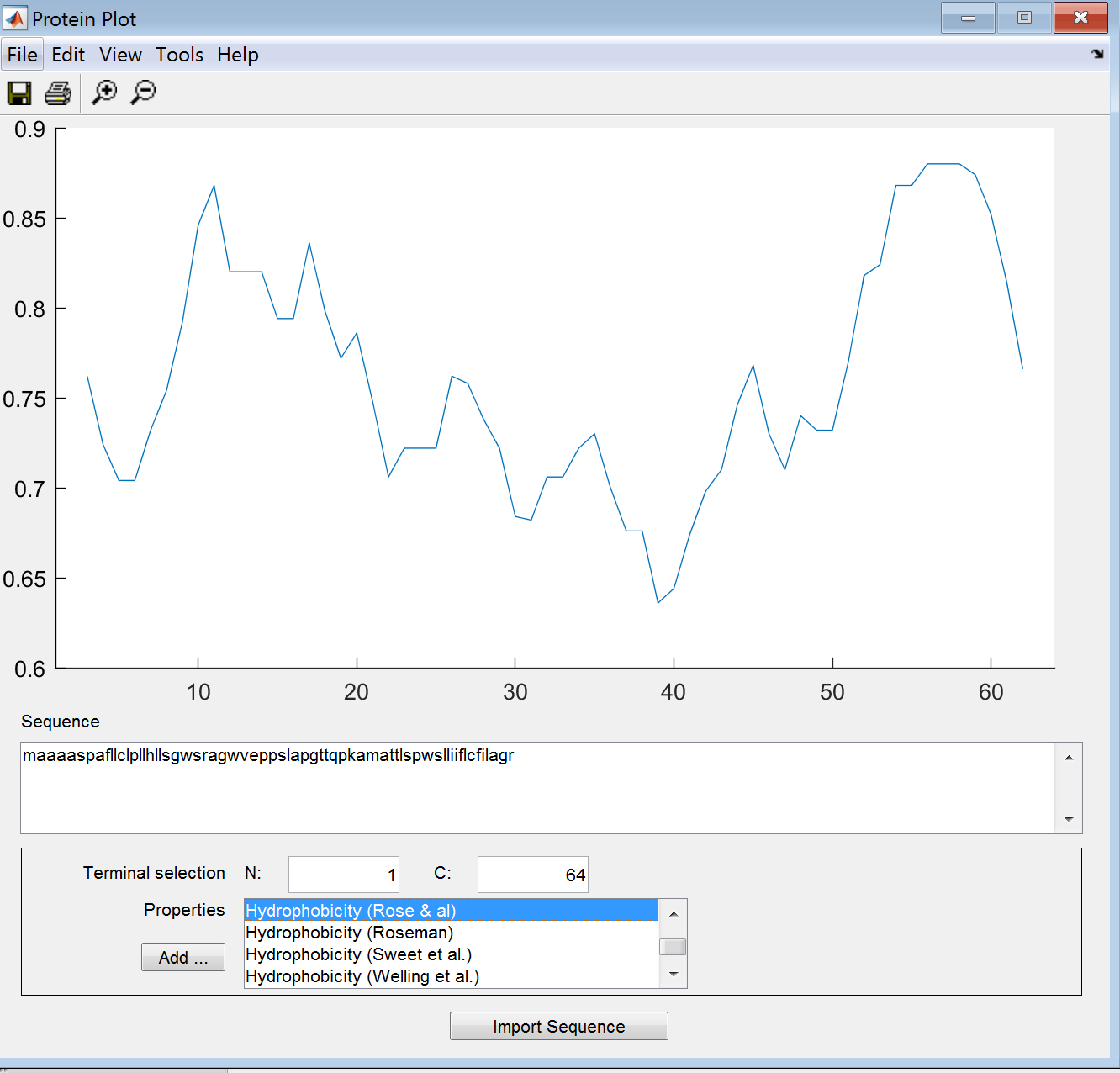
**Hydrophobicity (Miyazawa et al)**



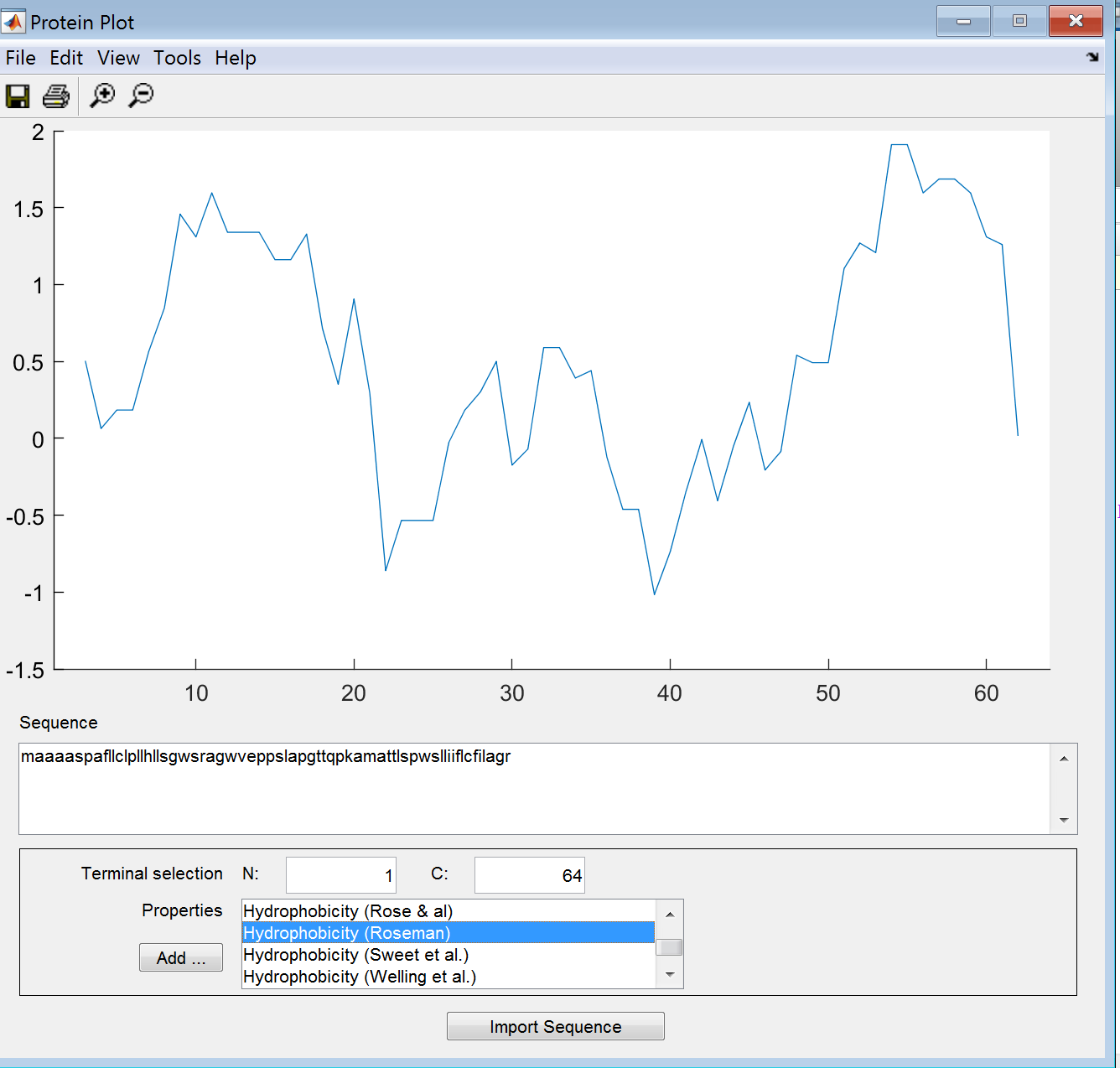
**Hydrophobicity (Rao & Argos)**



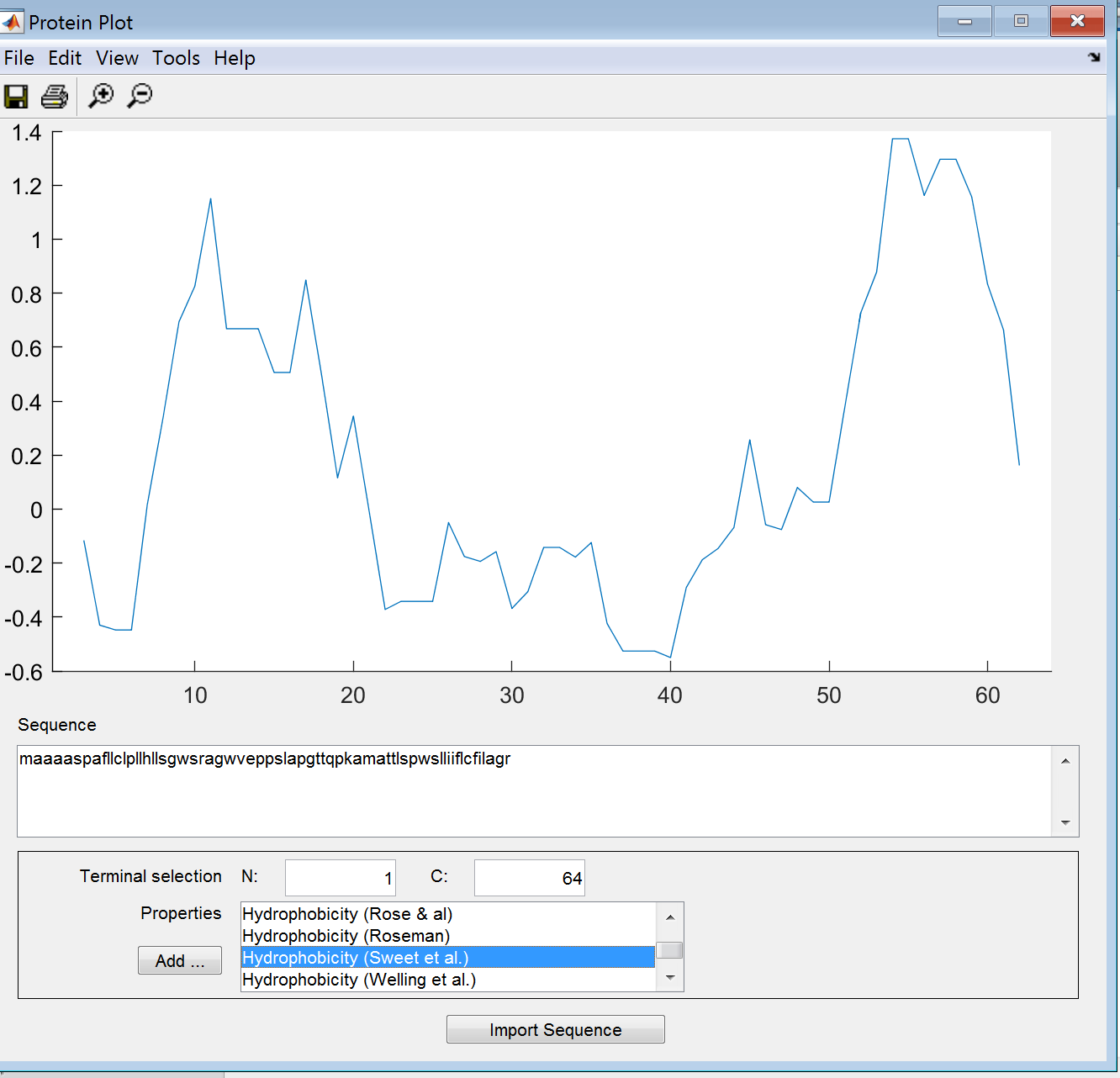
**Hydrophobicity (Rose & Al)**



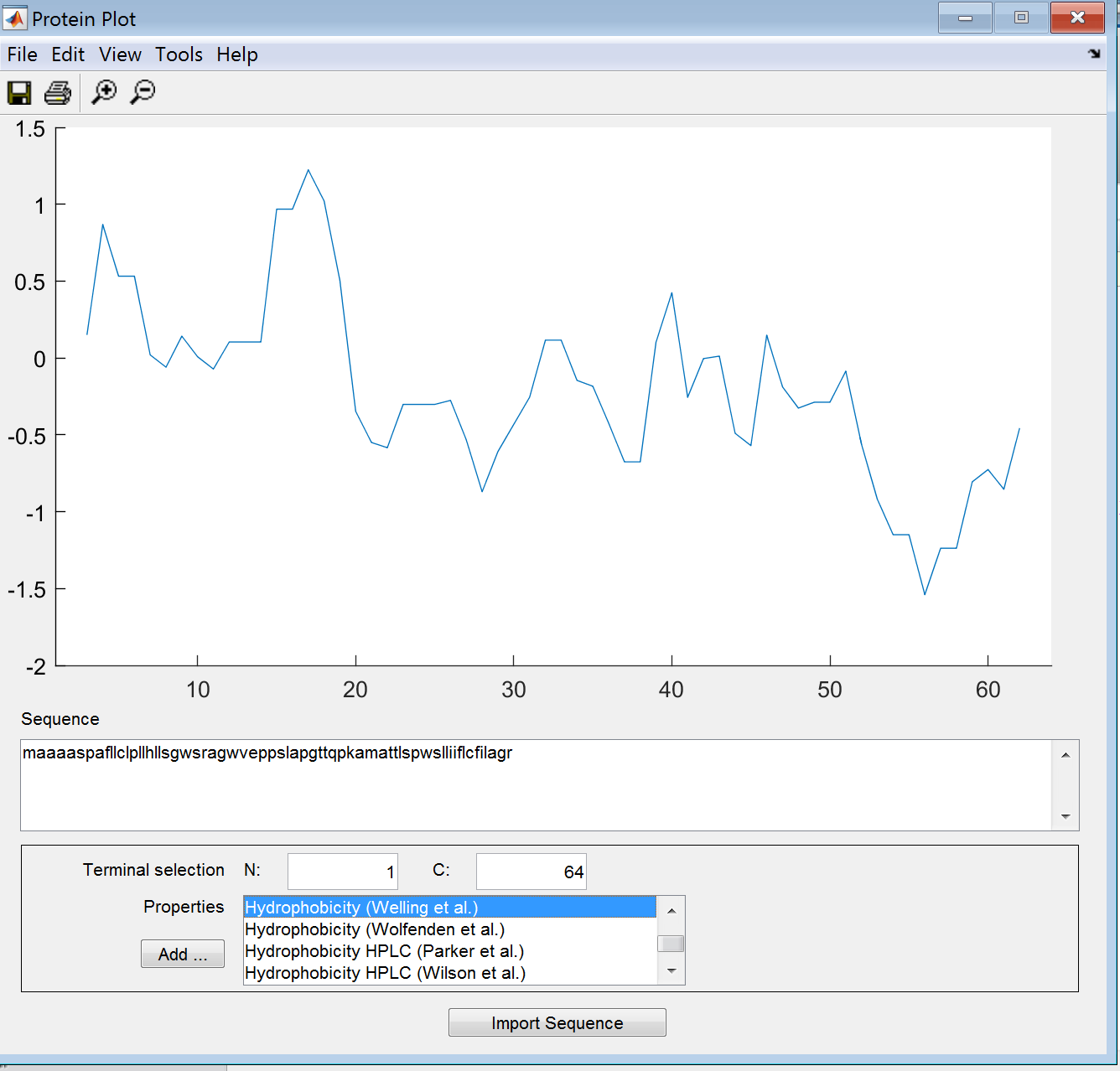
**Hydrophobicity (Roseman)**



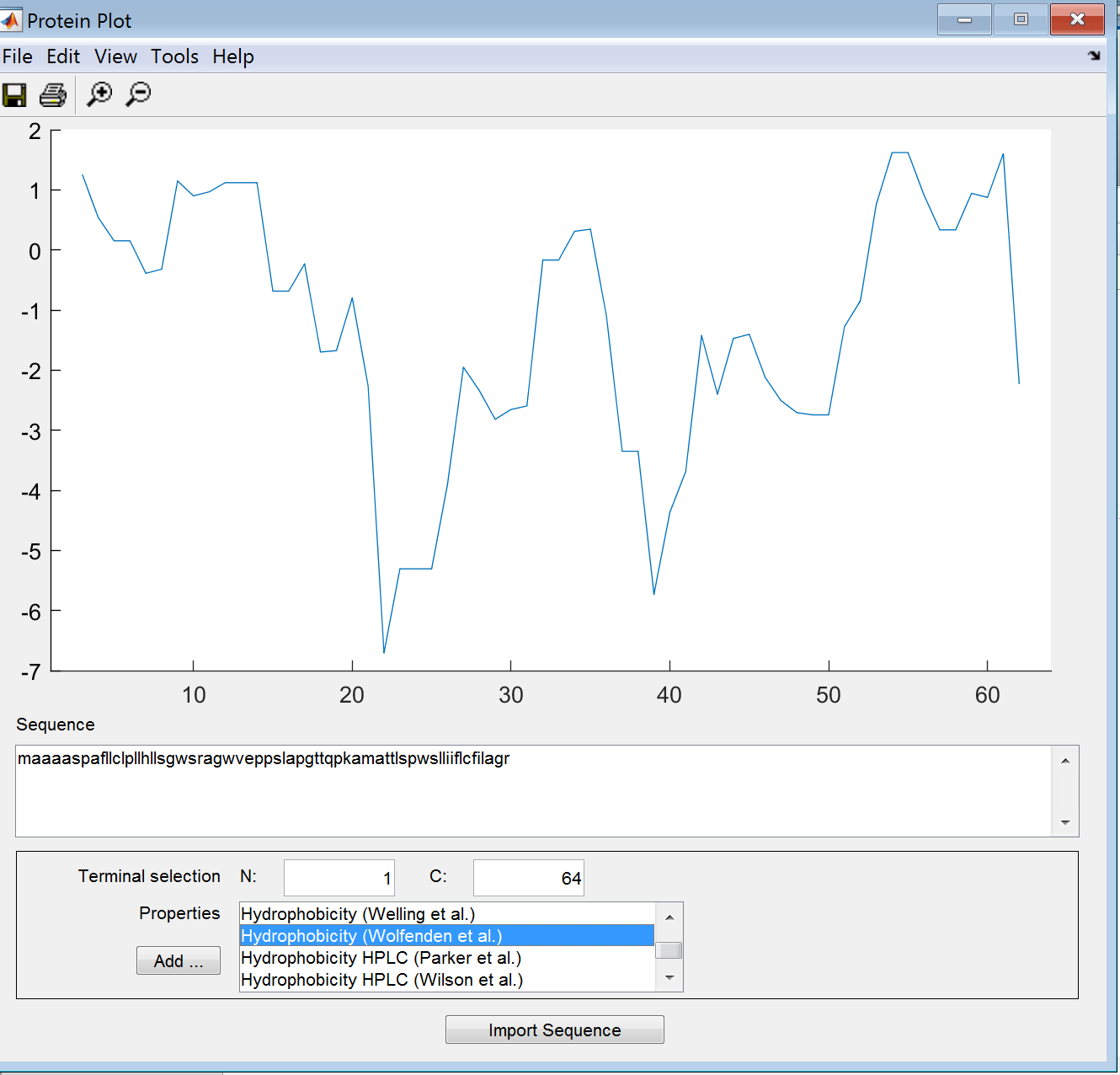
**Hydrophobicity (Sweet et Al)**



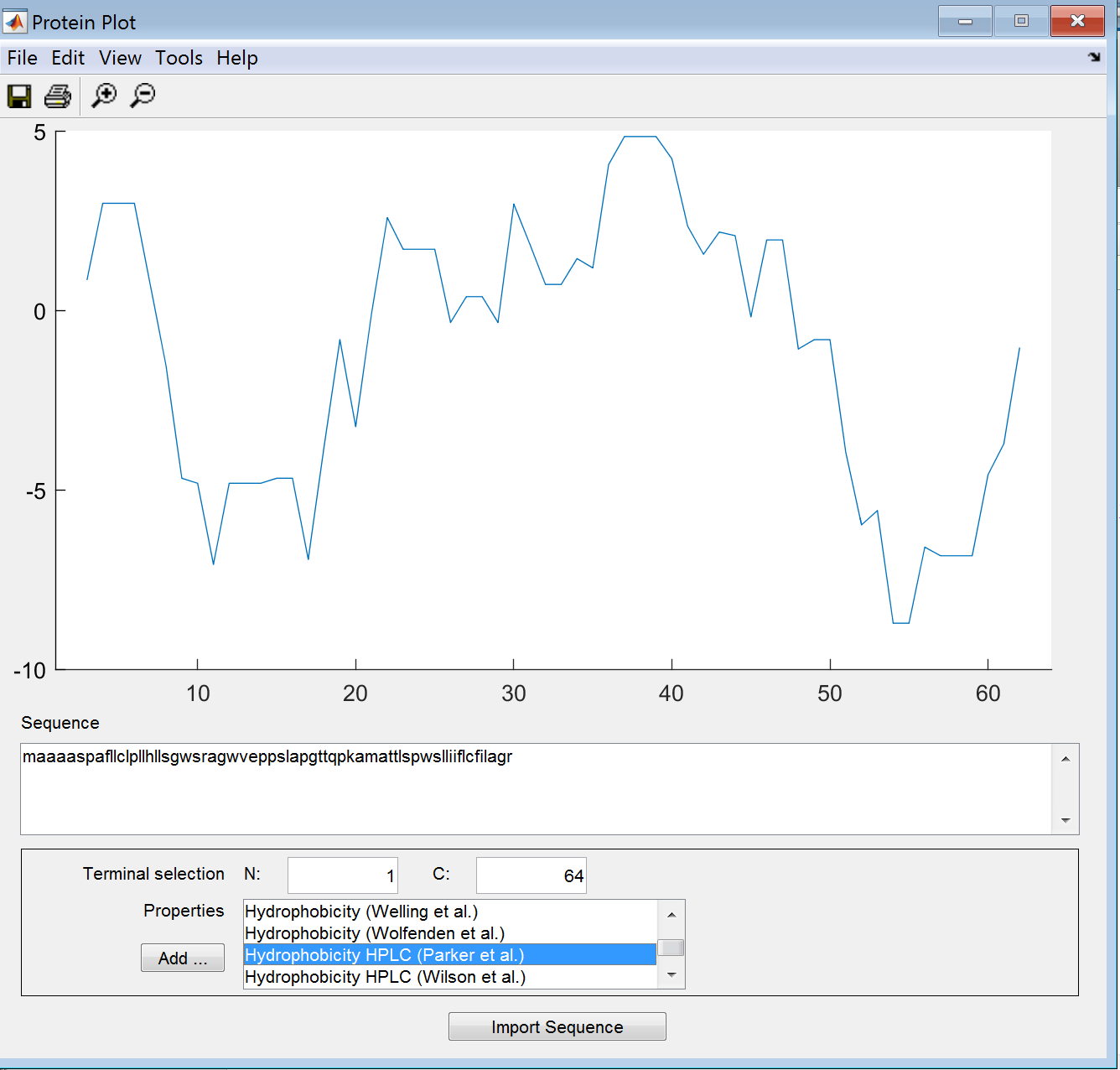
**Hydrophobicity (Welling et Al)**



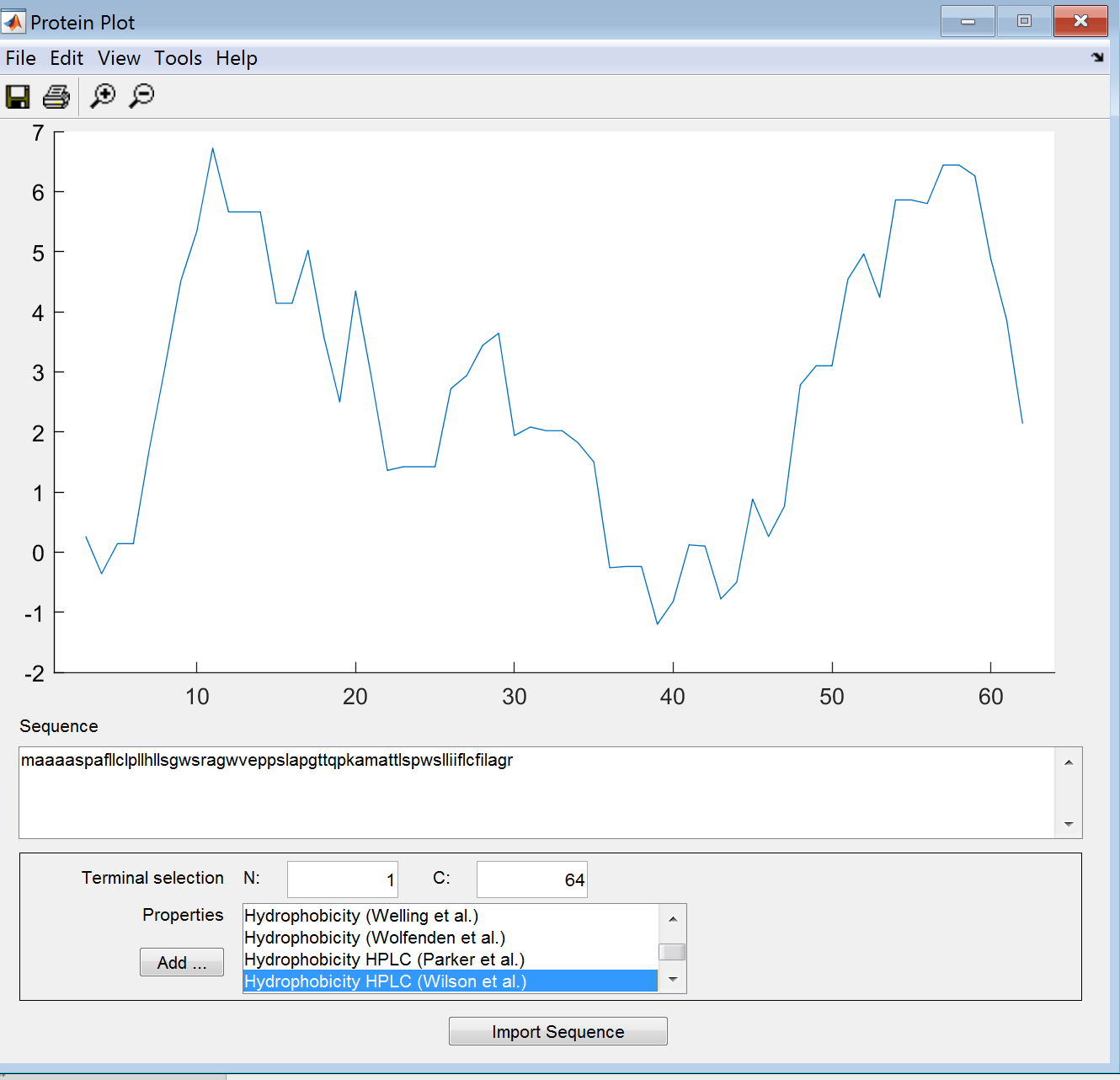
**Hydrophobicity (Wolfenden et Al)**



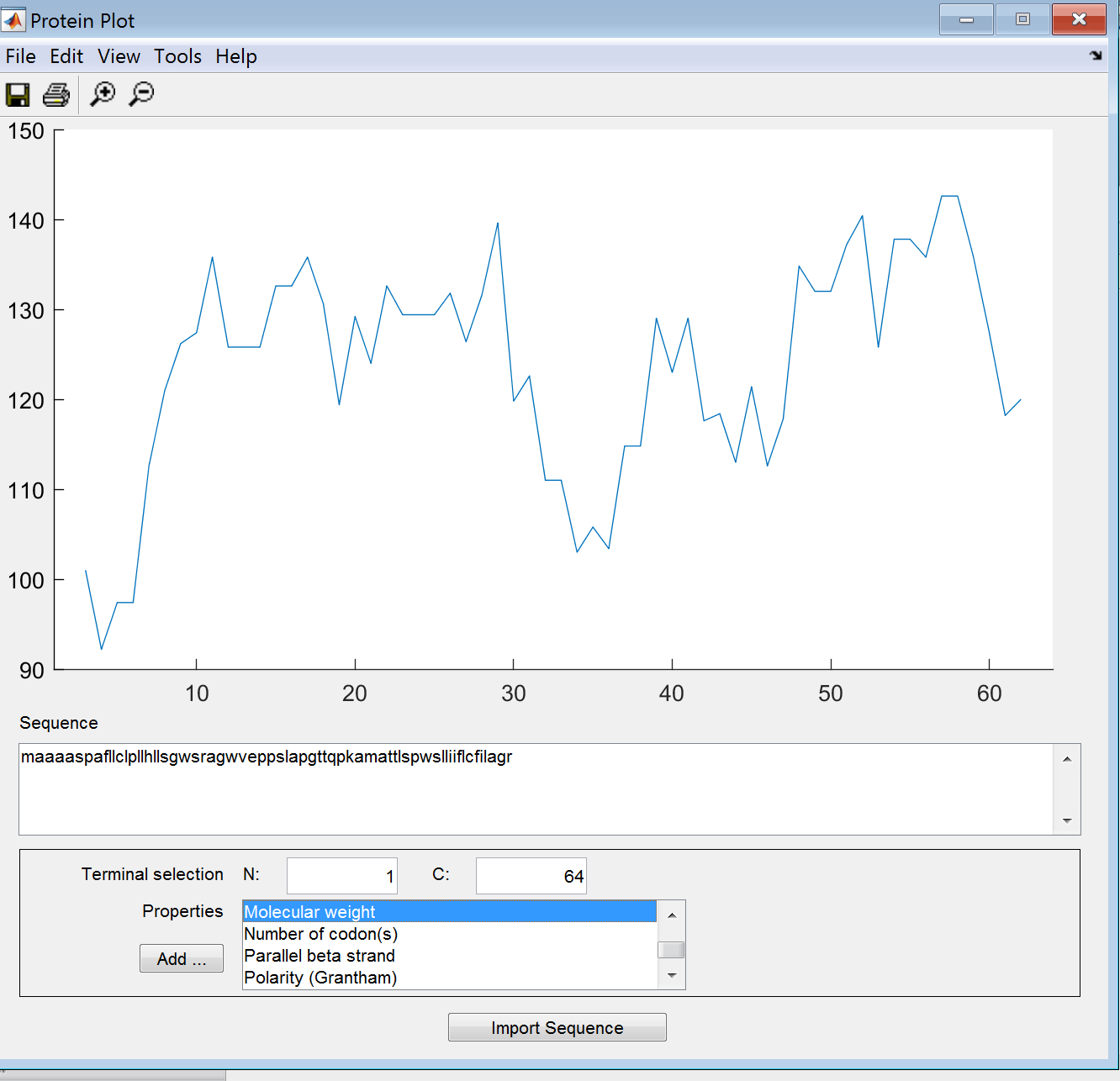
**Hydrophobicity (Parker et Al)**



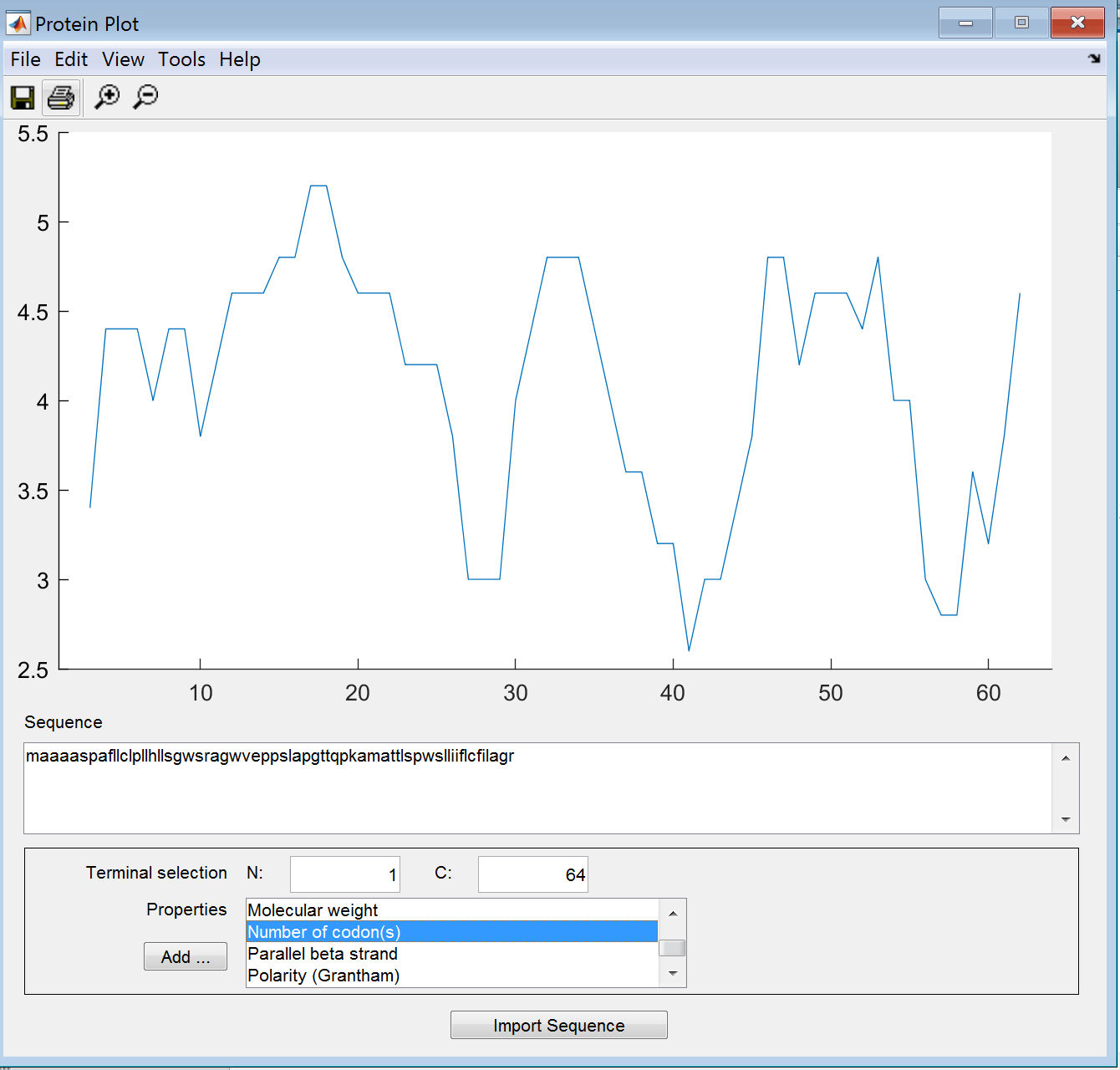
**Hydrophobicity HPLC (Wilson et Al)**



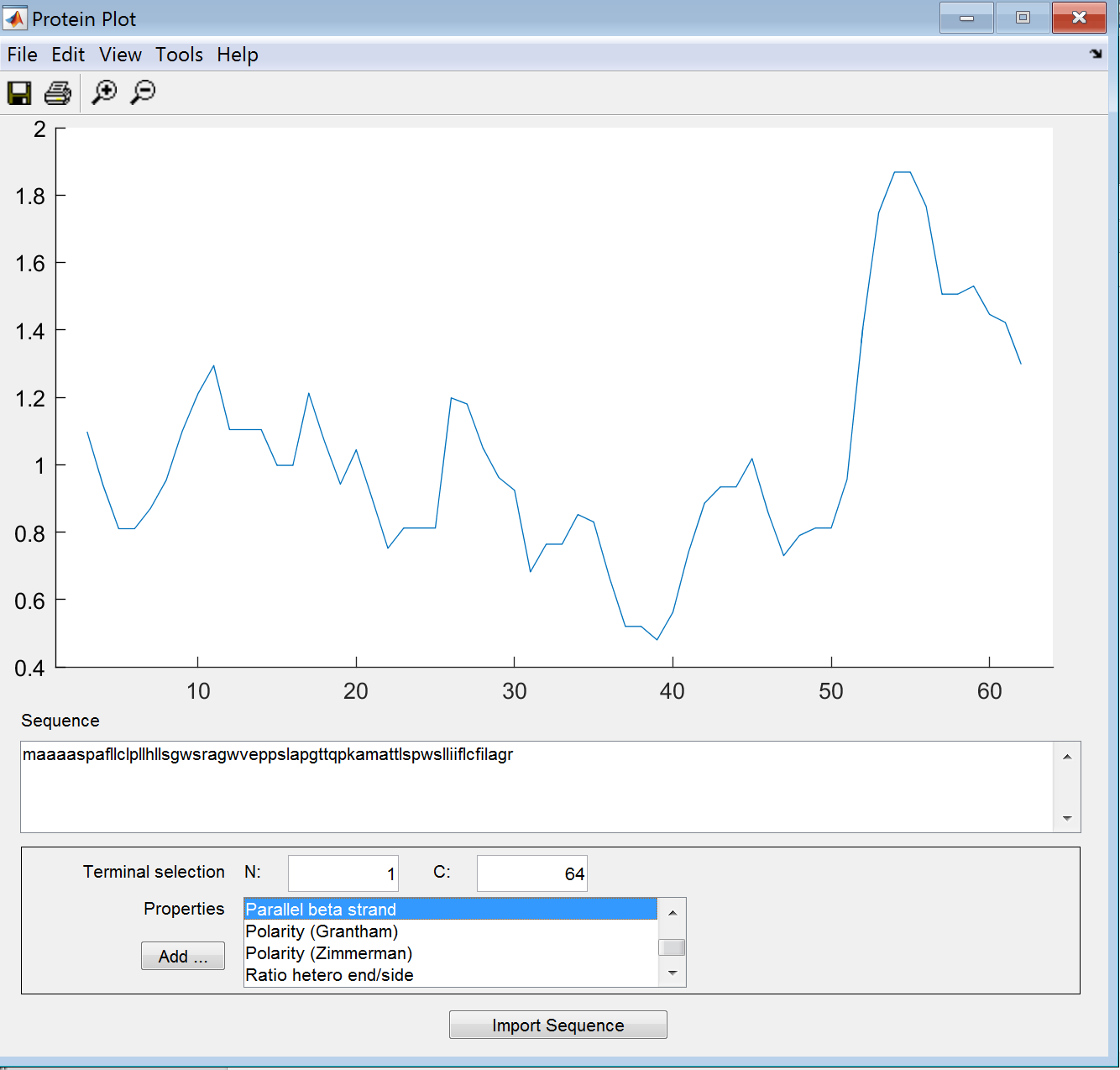
**Molecular Weight**



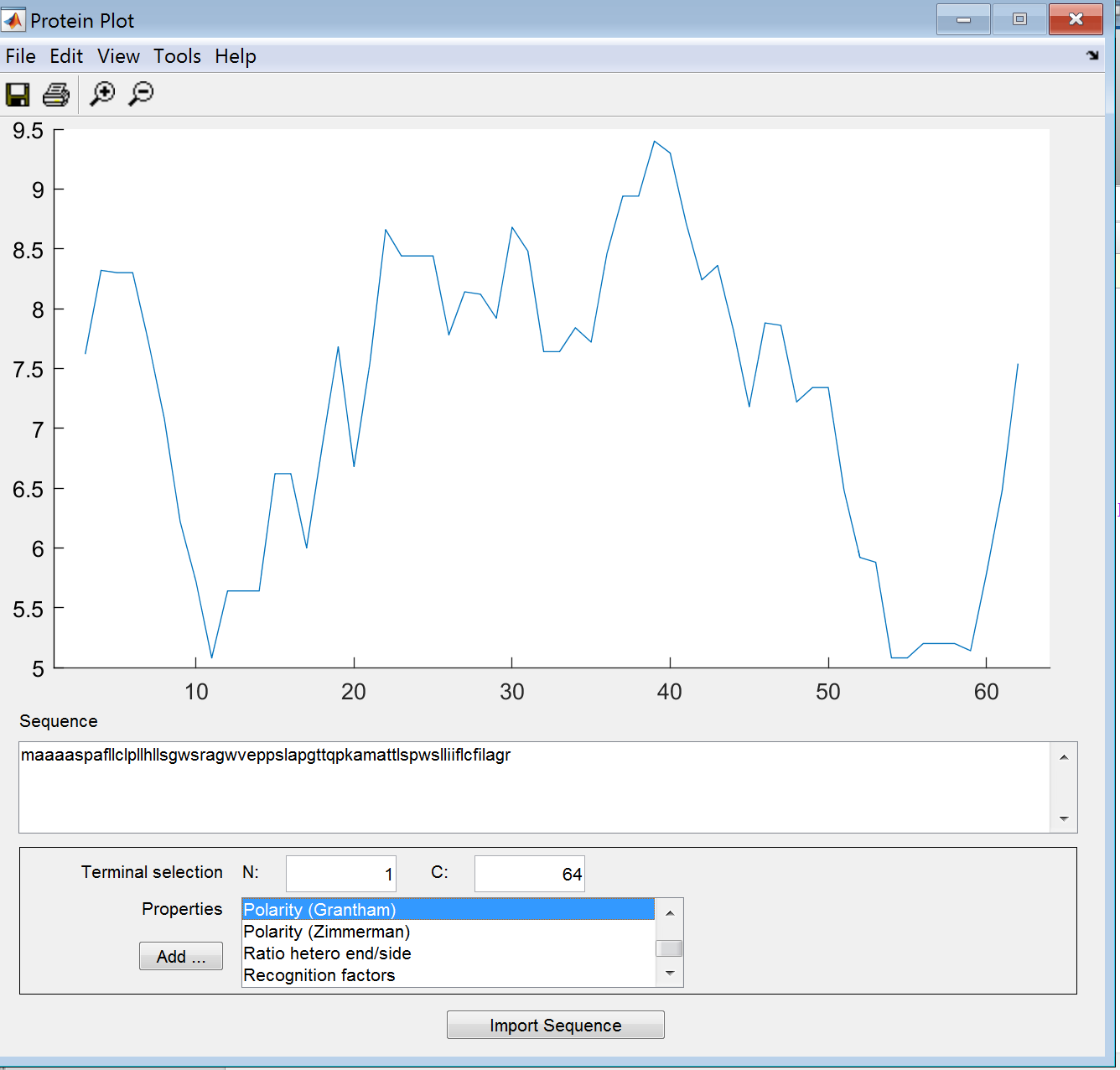
**Number of Codon(s)**



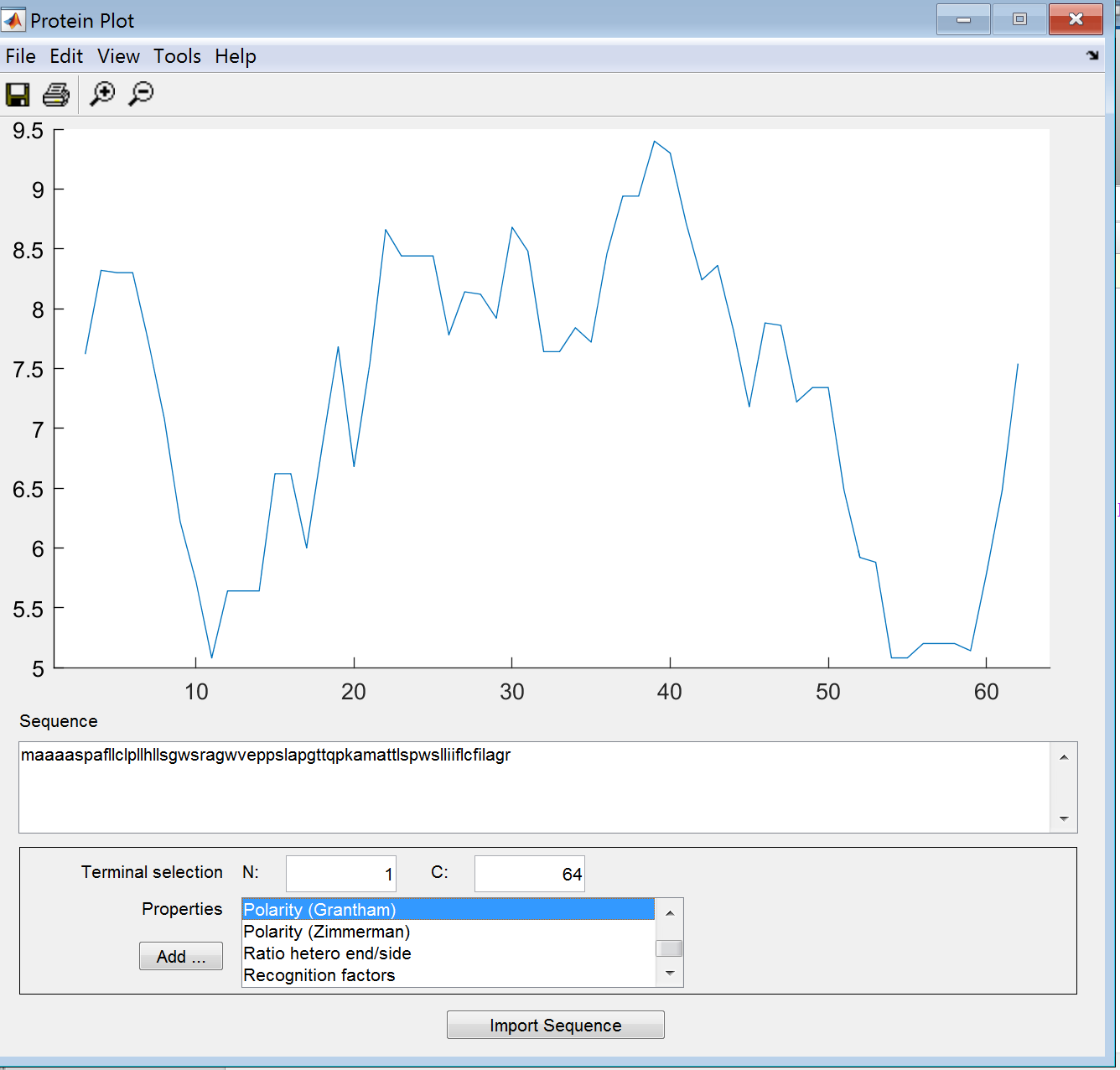
**Parallel Beta Strand**



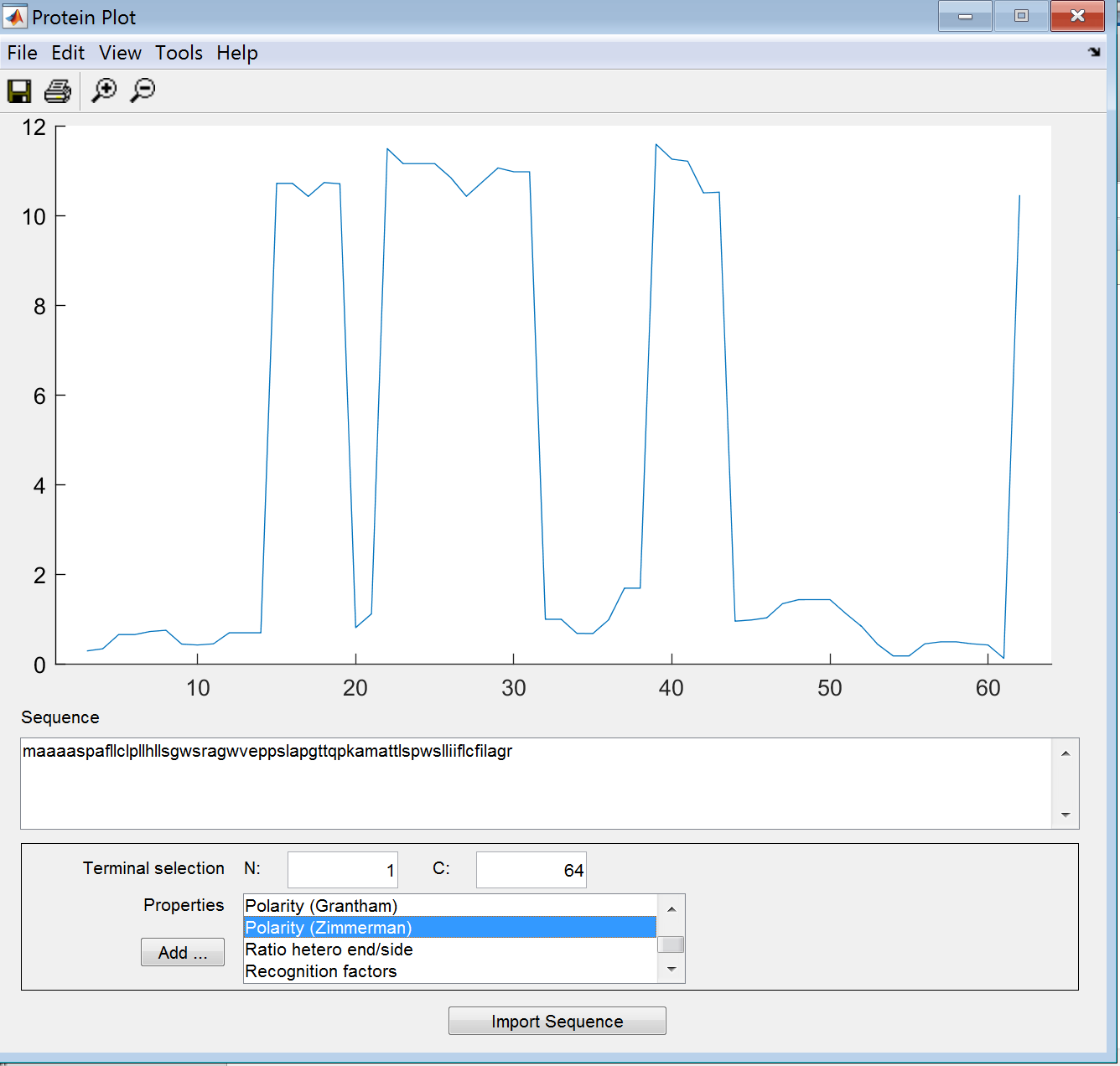
**Polarity (Grantham)**



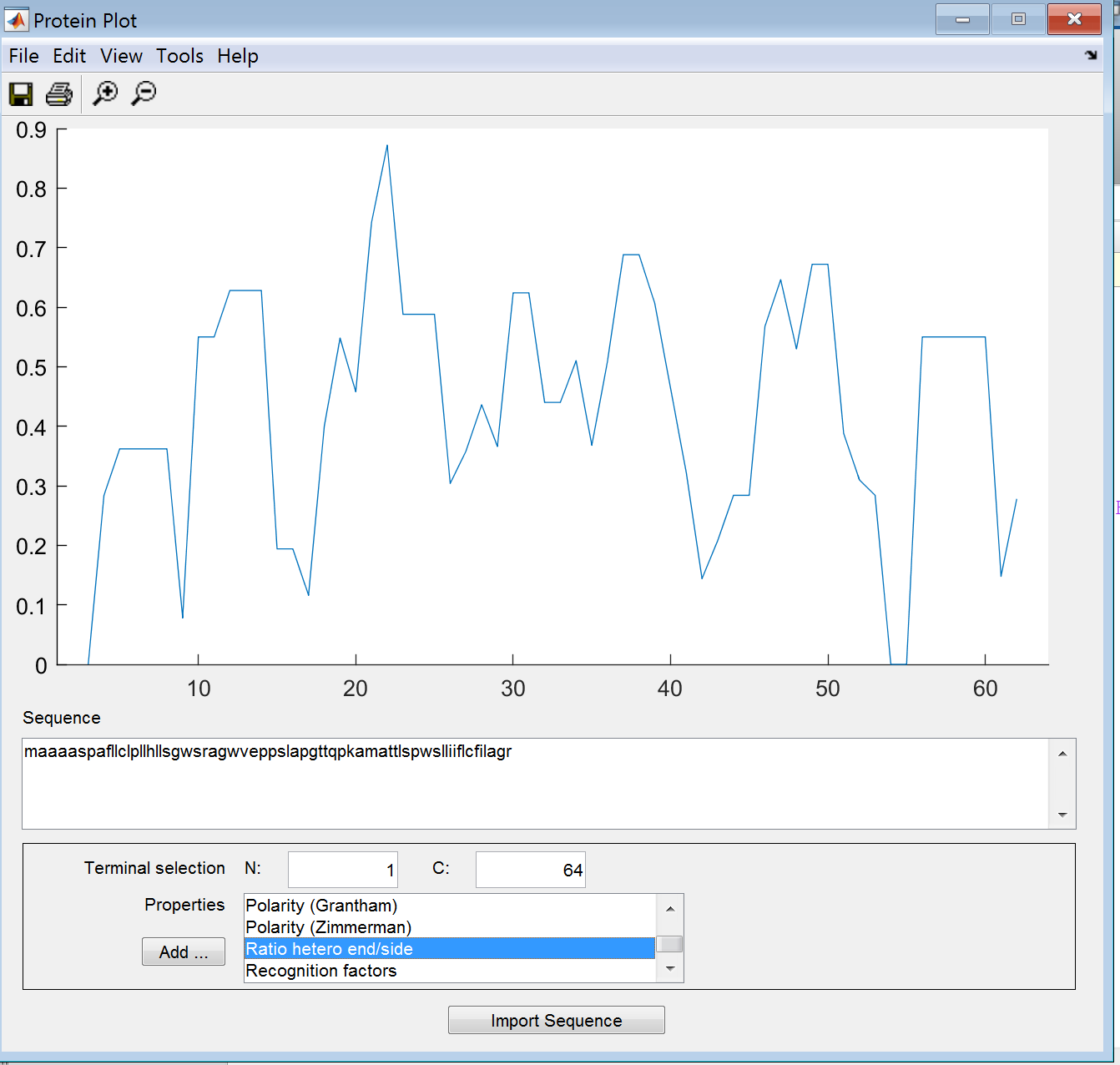
**Polarity (Zimmerman)**



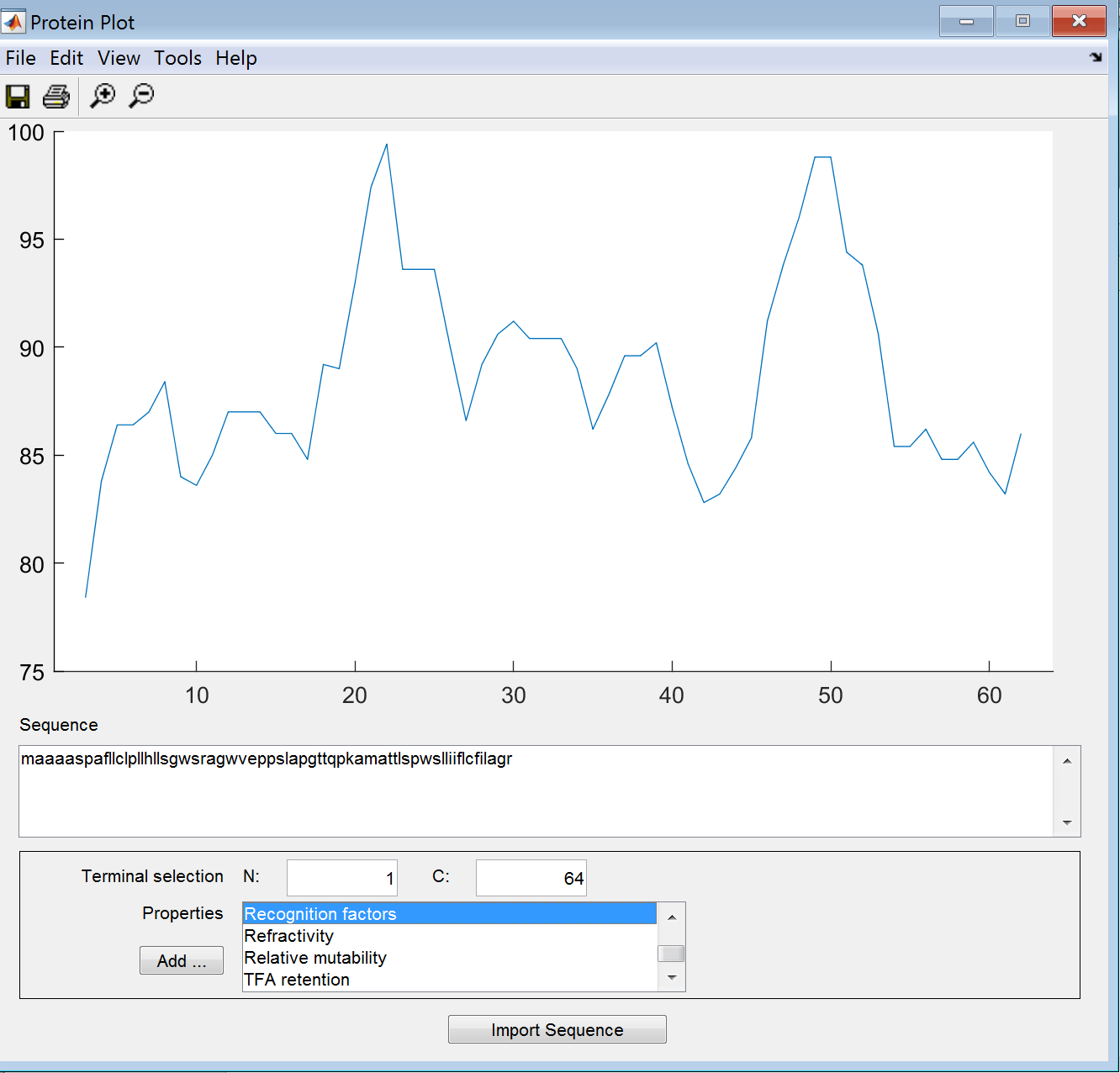
**Polarity (Zimmerman)**



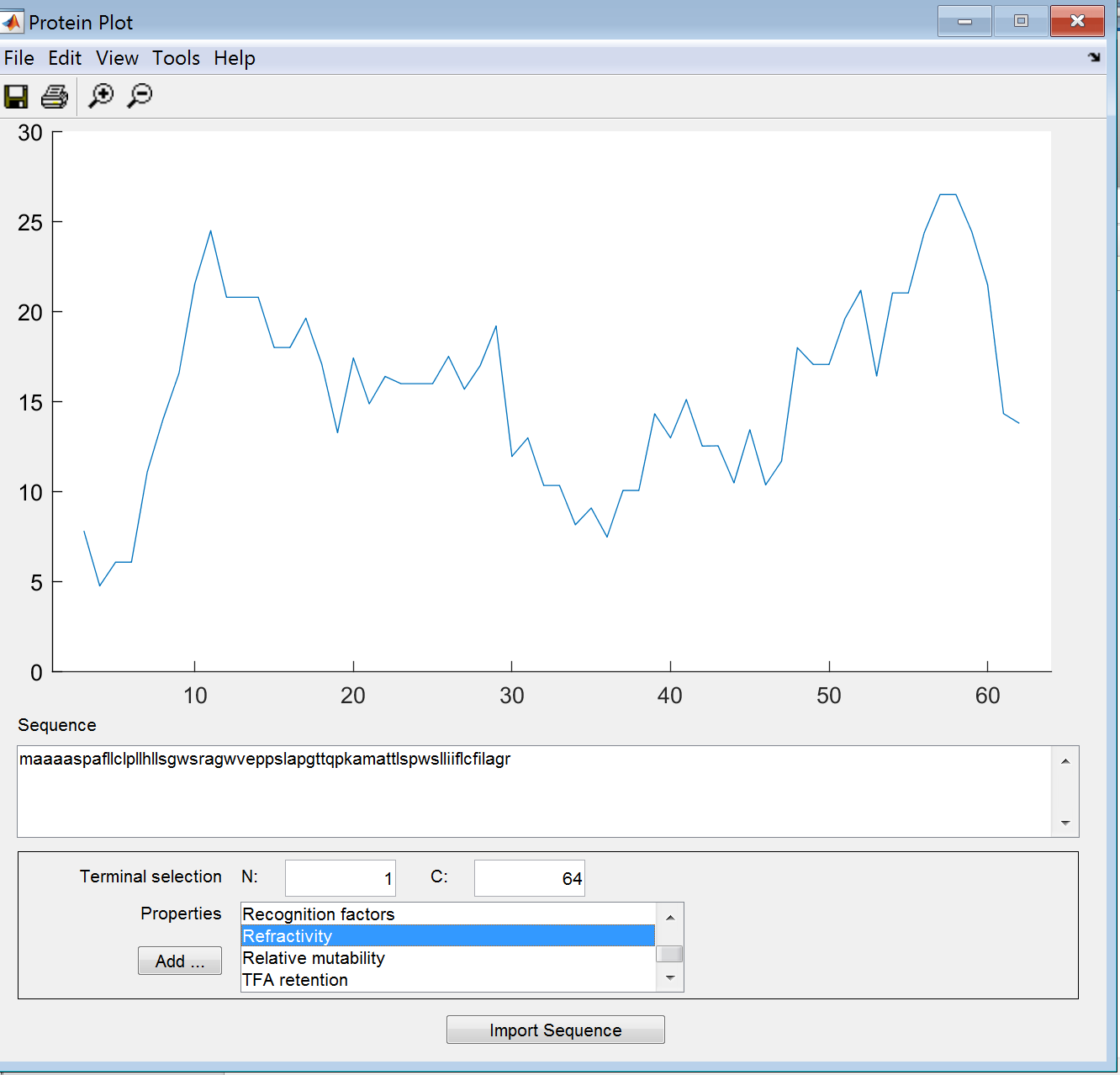
**Ratio Hetero End/Side**



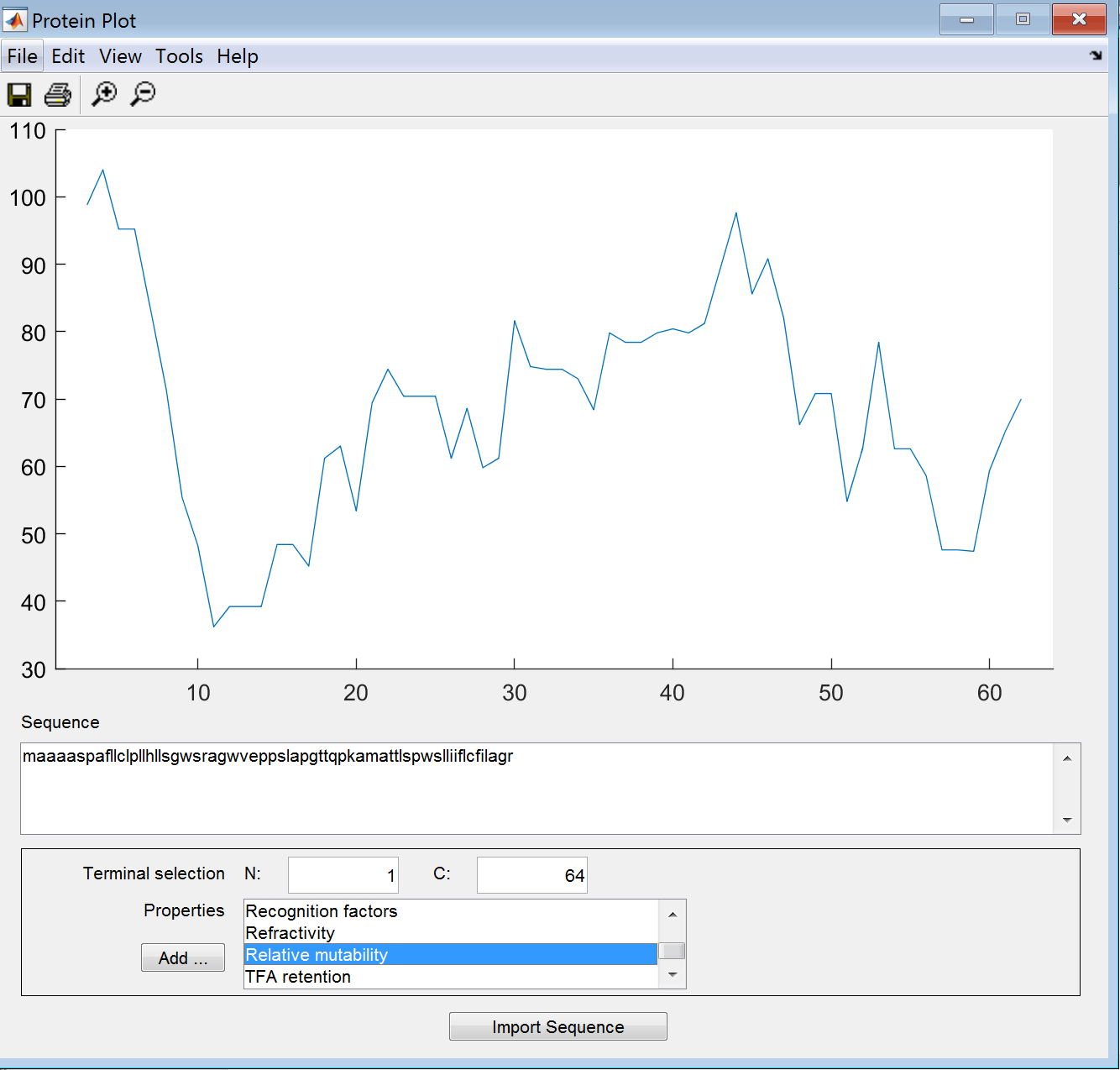
**Recognition Factors**



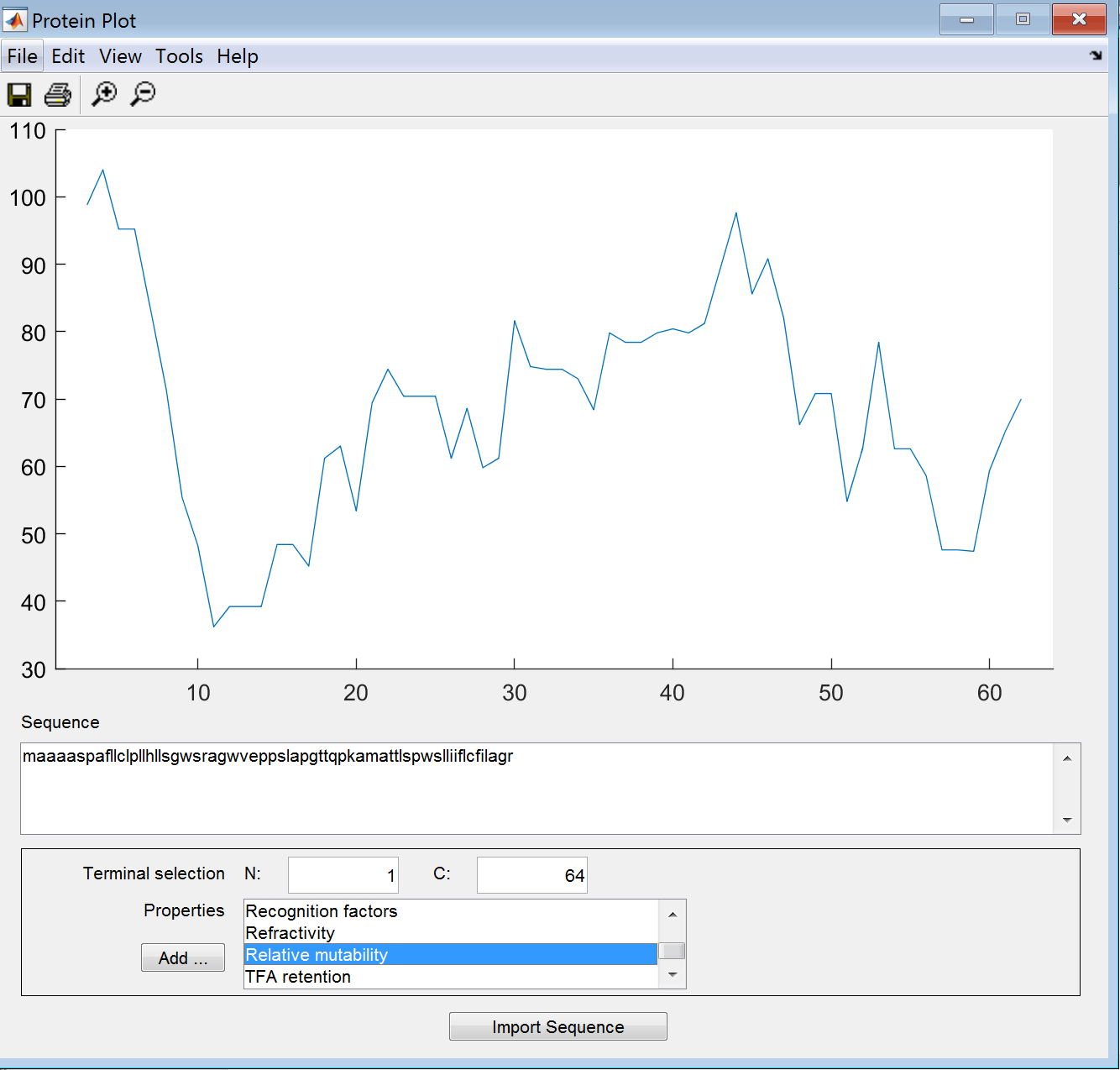
**Refractivity**



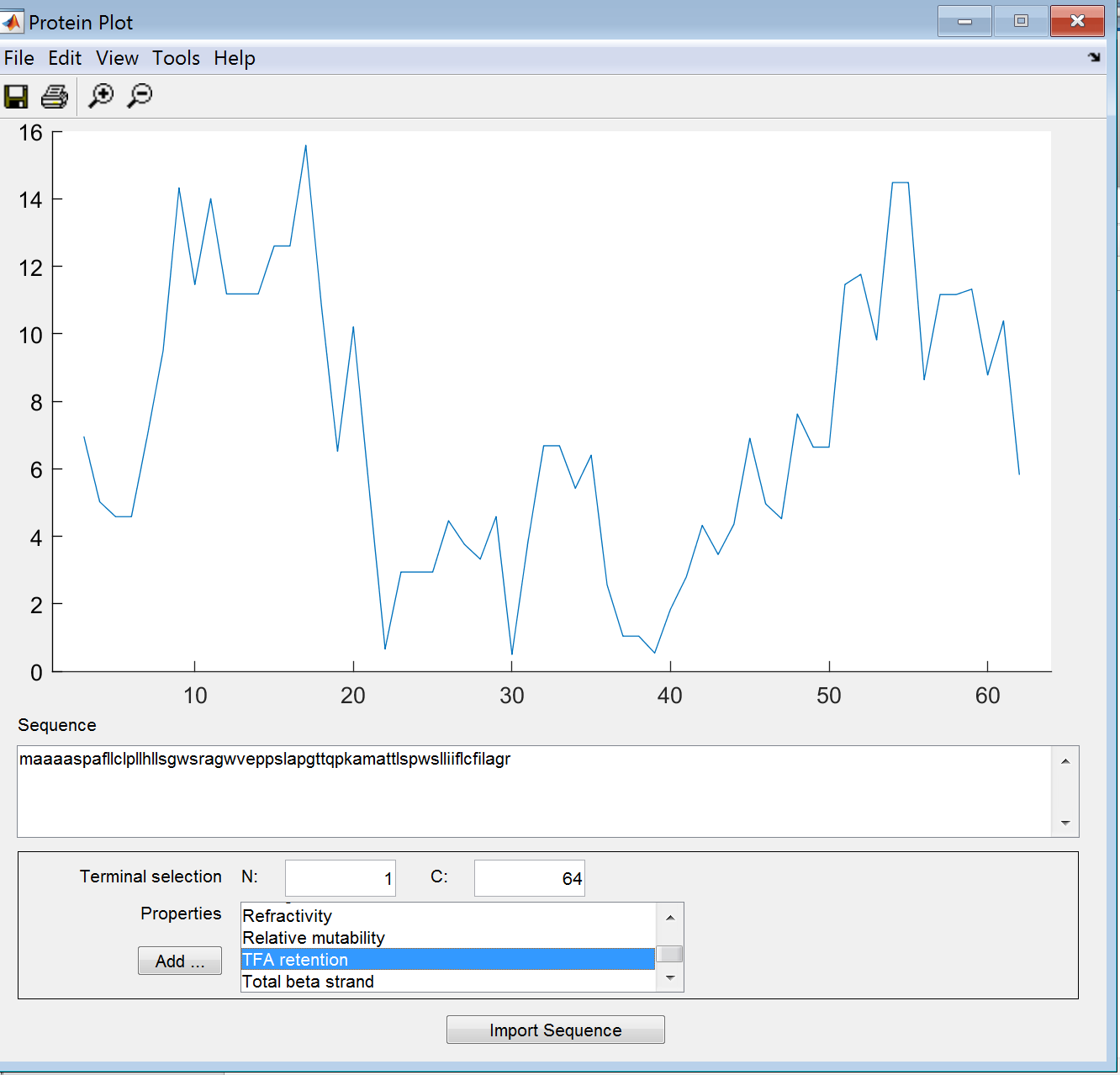
**Relative Mutability**



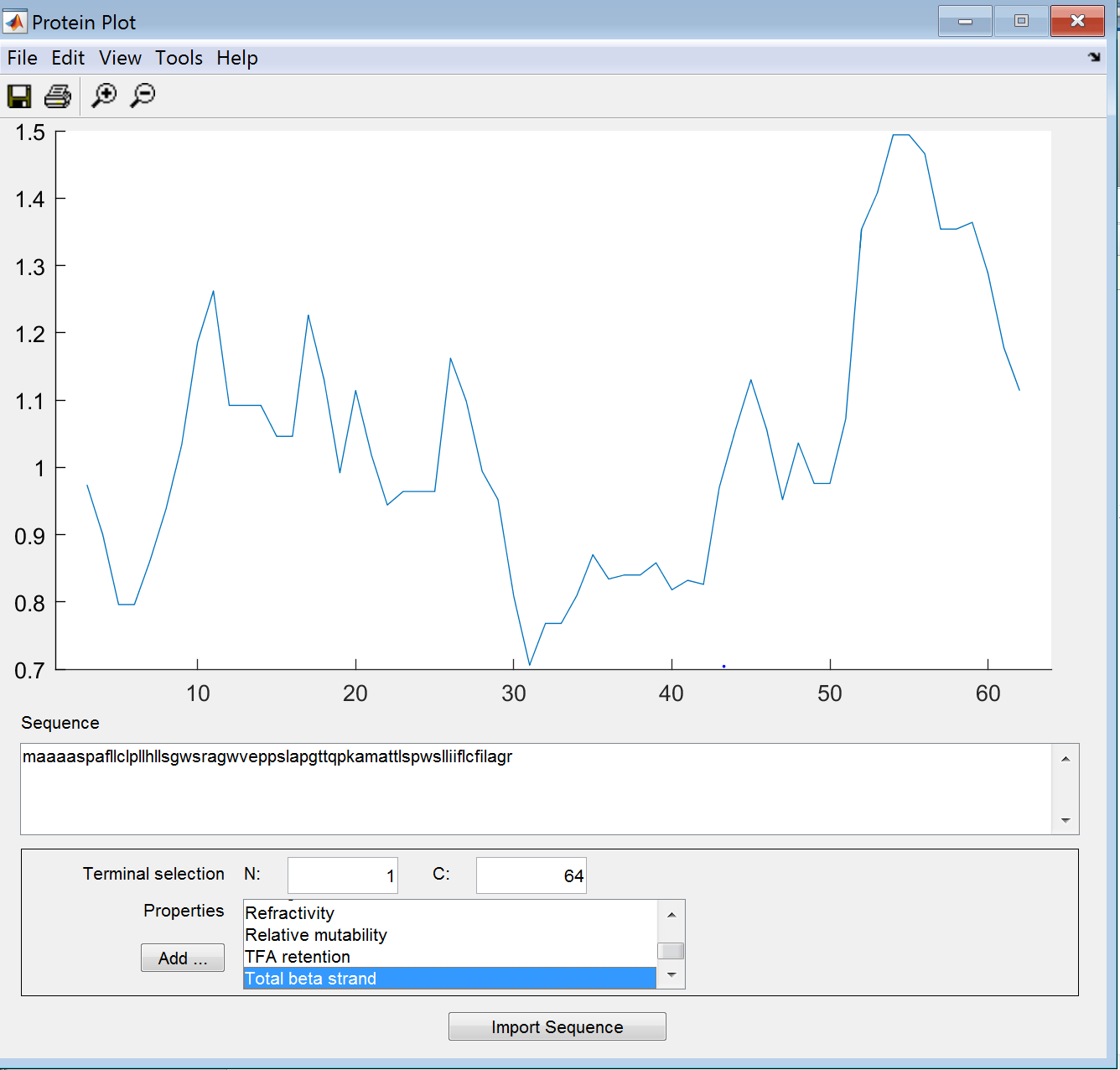
**Relative Mutability**



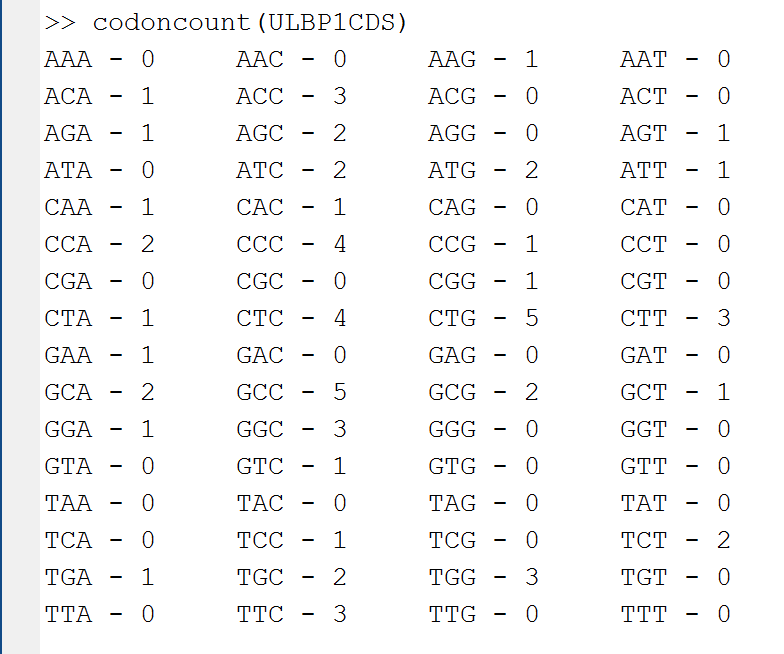
**TFA Retention**

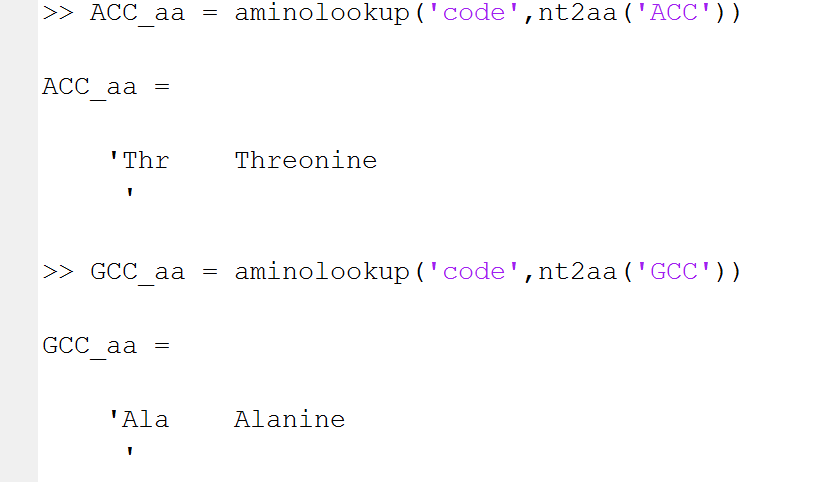


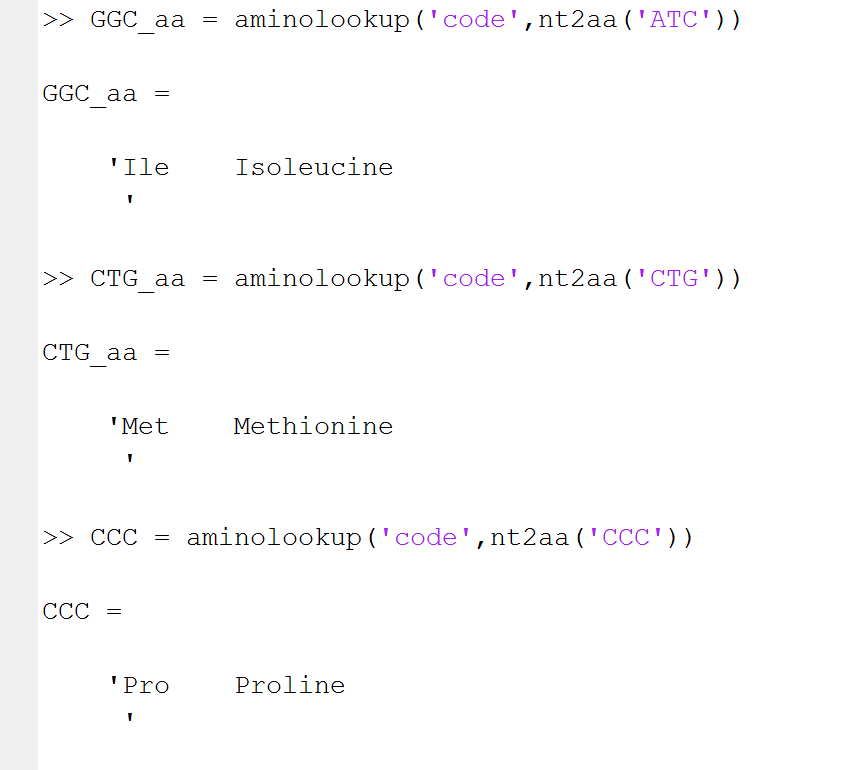
**Total Beta Strand**

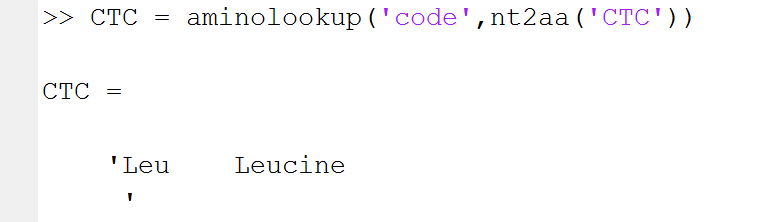


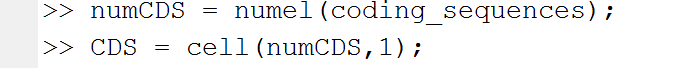
**Box:**

















**Figure:**

