I am inclined to change a start from that called by GM, in favor of the next one which definitely has a better RBS score, but then this question of curiosity comes to my mind: Often, we annotators will scan the sequence to look for the best RBS score. However, ribosomes are “machines” which I would expect to bind at the earliest strong binding site they can find along their path down the sequence. It is understandable for places with z values below 2, but from the resource guide, “A Z-value higher than 2 is getting good”. If ribosomes do not go back and forth, first taking a “dry run” through the sequence like us humans to choose the best RBS score, what would then make a ribosome to skip start 2 in the figure below (Z= 2.018, Fs -5.536, called by GM), for example, and go several bases down the road to choose start 3, which has a better RBS score (Z=3.053, -2.645)? Please advise.

