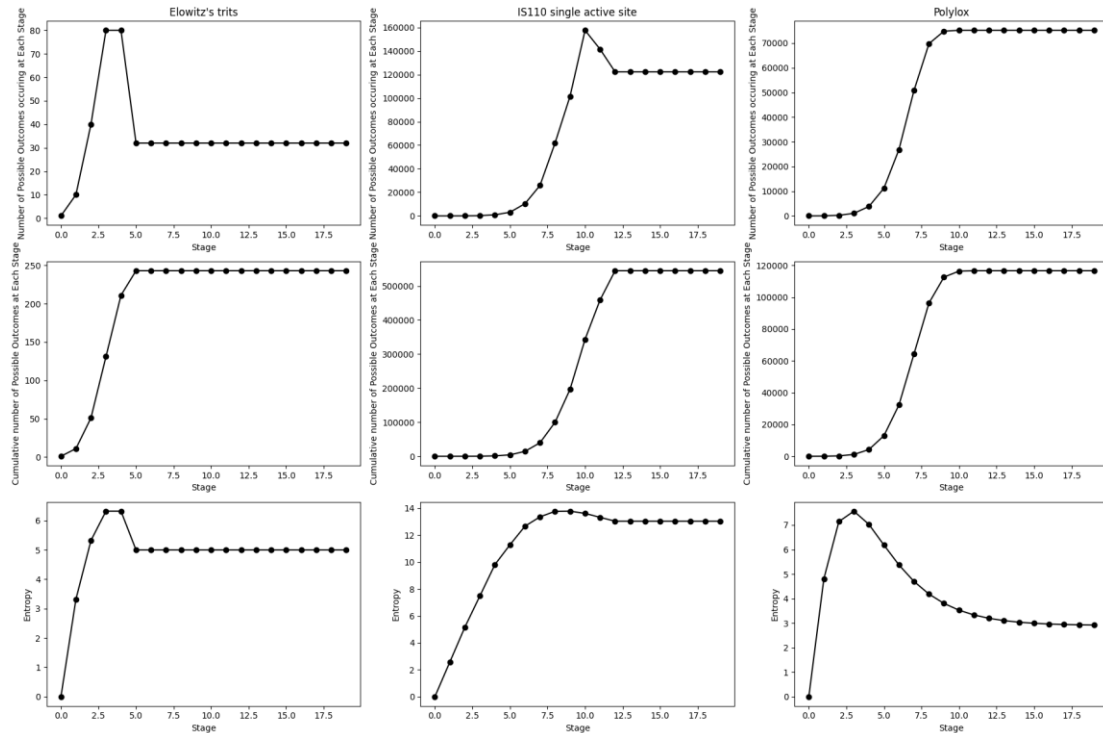


# SUMMARY PLOTS



All initial sequences in this study begin with five pairs of recombinase sites and are subjected to 20 rounds of recombinase activity, where each round (or "stage") represents a single recombinase event.

## Key Features of Each System:

- Elowitz's trits:**

This system produces fewer distinct barcodes, but the entropy of the barcode distribution converges to a higher value, indicating a more even spread among possible outcomes.
- Polylox:**

Polylox achieves a high number of unique barcodes, but its entropy converges to a lower value, suggesting that a few barcode types become dominant.
- IS110:**

IS110 generates a large variety of barcodes and maintains high entropy throughout the process.

The IS110 initial sequence is designed so that at every stage, only one site contains the active element GAMMA. This GAMMA site alternates its reaction partner between ALPHA and BETA in successive stages. After each recombinase event, one active A-ALPHA or B-BETA site is lost, ensuring that the process continues without the need of excision until all possible reactions are exhausted. Notice that although we can deactivate sites without excision, excisions still happen after more than two inversions. A possible way to continue the research is to design a technology where excisions cannot happen.

Another area that can be explored is the entropy and diversity of barcodes achieved by reverting or switching to a new rule set after a sequence has terminated using the initial rule set. For example, here we chose a random sequence generated from 5 pairs of IS110 sites after 14 stages and let it react with new rules.

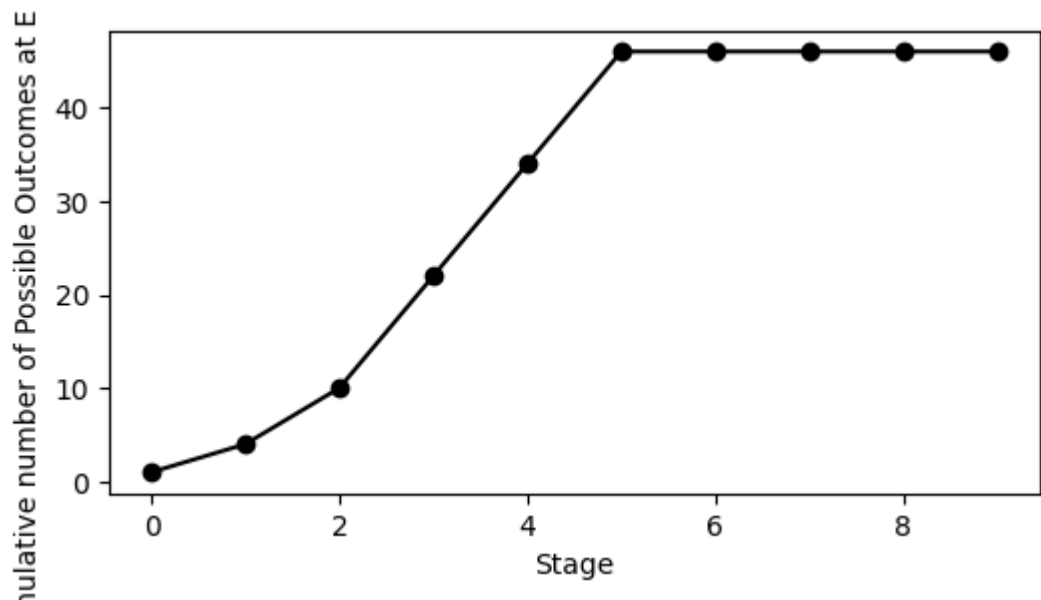
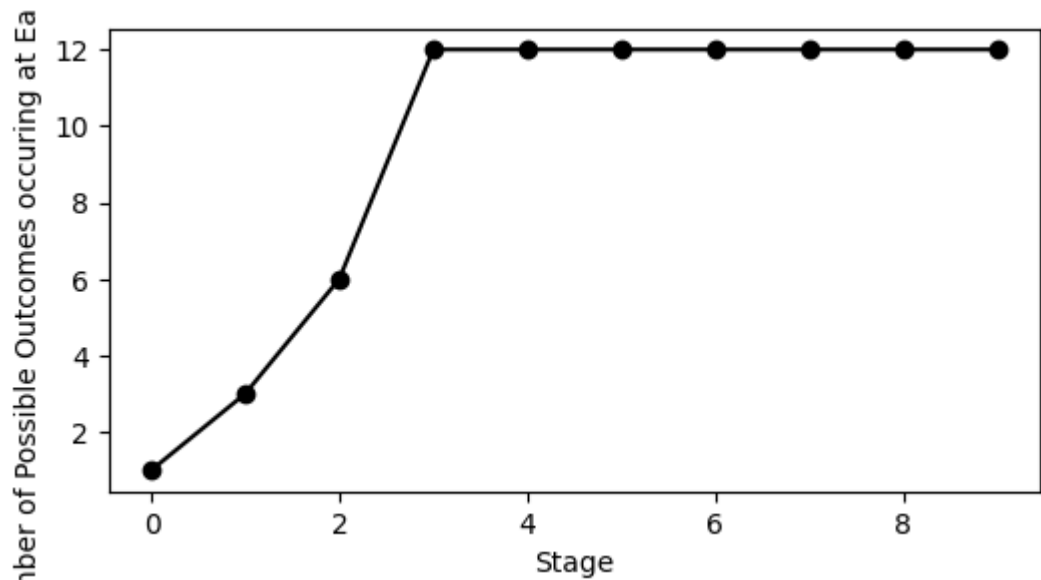
```

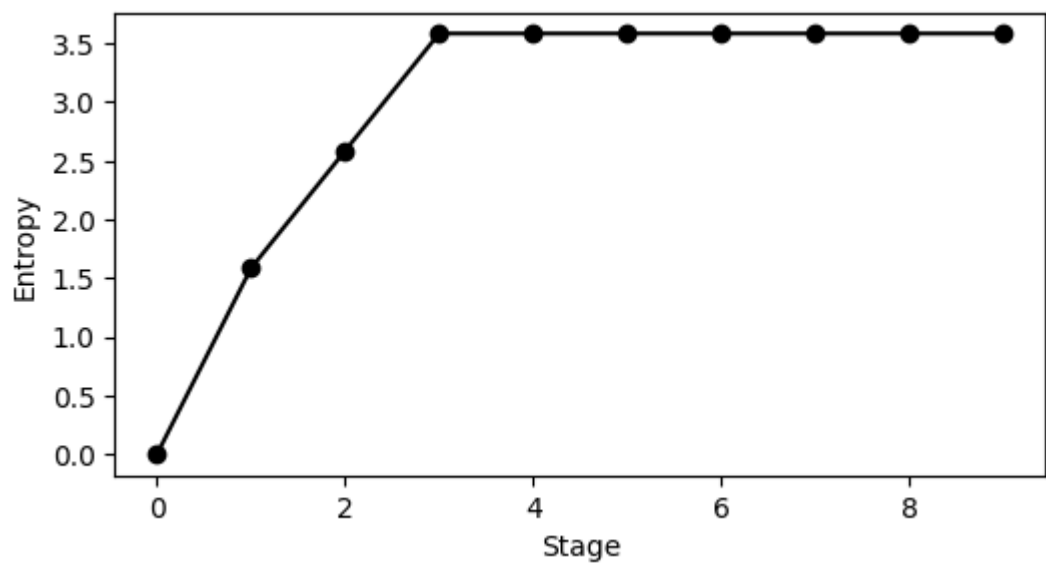
print("Reverse starts here")
for i in range(1):
    DNA_sequence_2 = list(random.choice(list(outcome_lists_1[-1].keys())))
    pairs_pool_2=[(['A','GAMMA'], ['B','ALPHA']),(['B','GAMMA'], ['A','BETA'])]
    outcome_lists_2= run_probability_calculation_and_plot_IS110(DNA_sequence_2,pairs_pool_2,numberofevents=10, plot=1,rank=1)

```

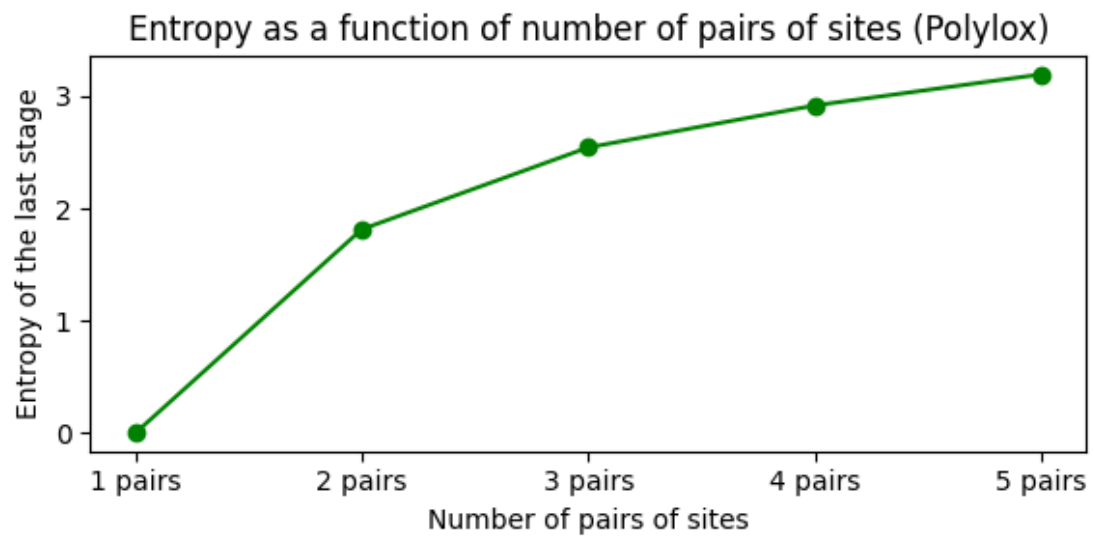
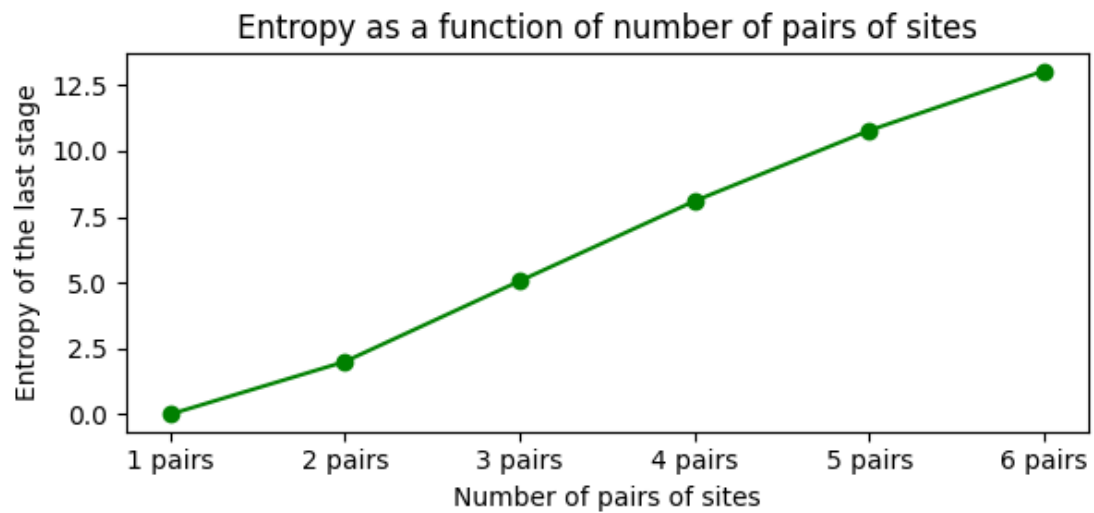
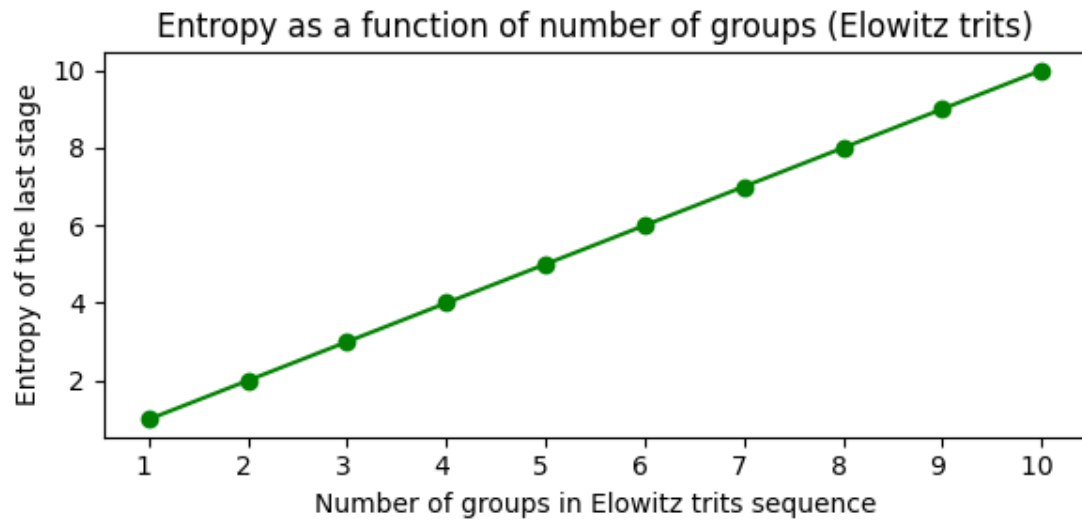
[43] ✓ 3.5s

... Reverse starts here





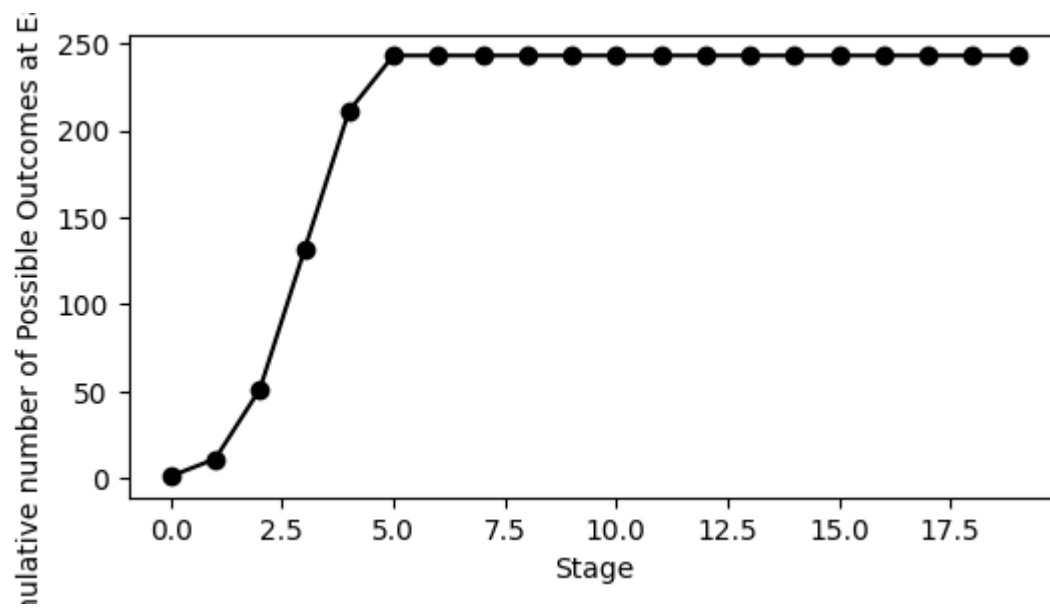
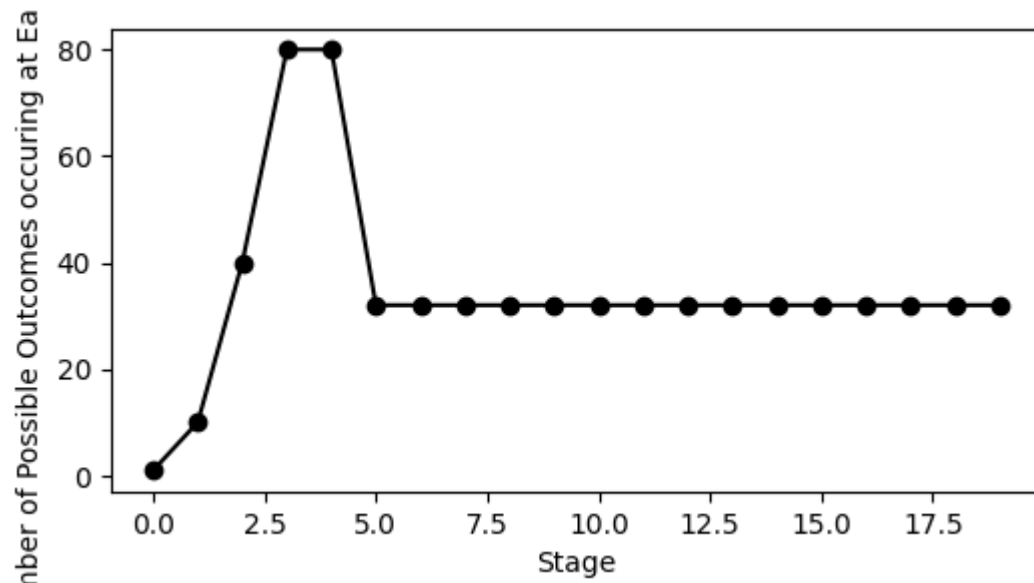
# Entropy as a function of number of pairs of sites

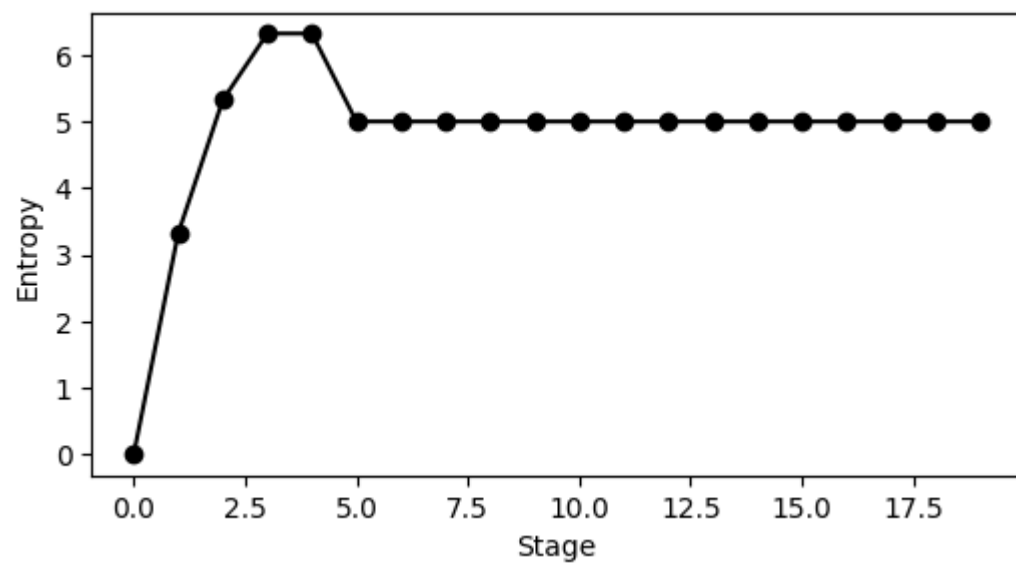


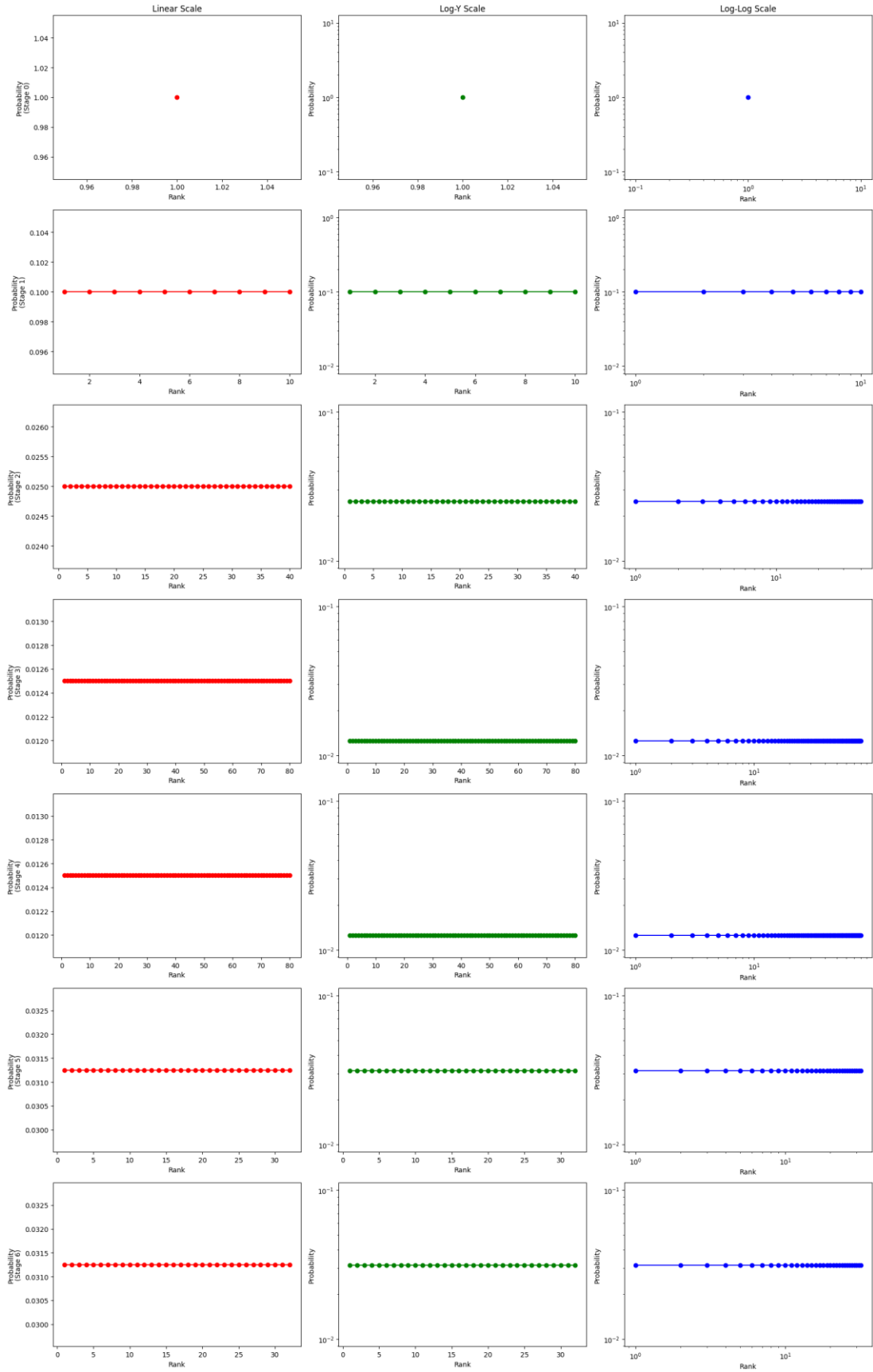
Note: Maximum number of pairs of sites limited by calculation power



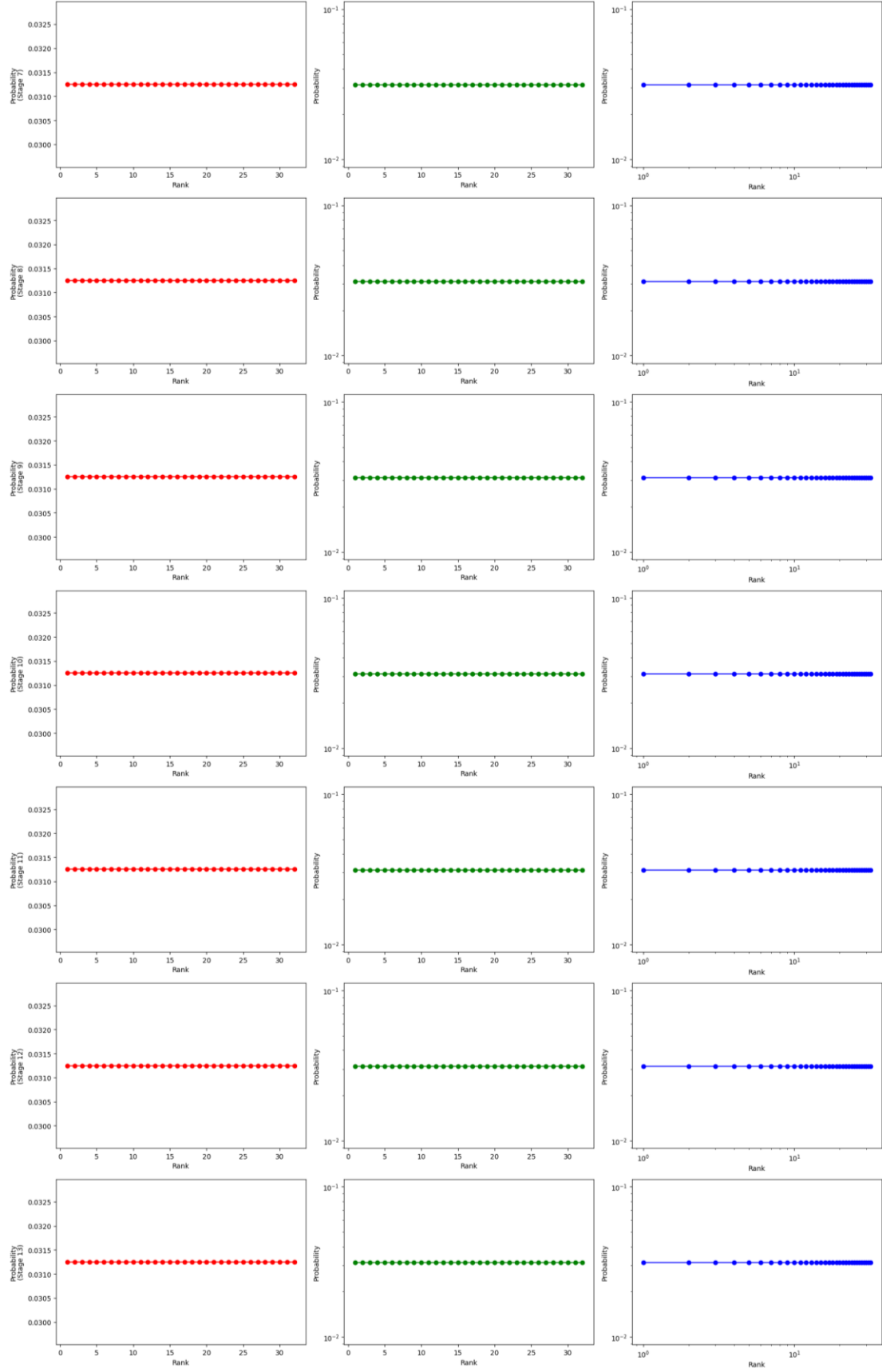
# Elowitz's trits sequence

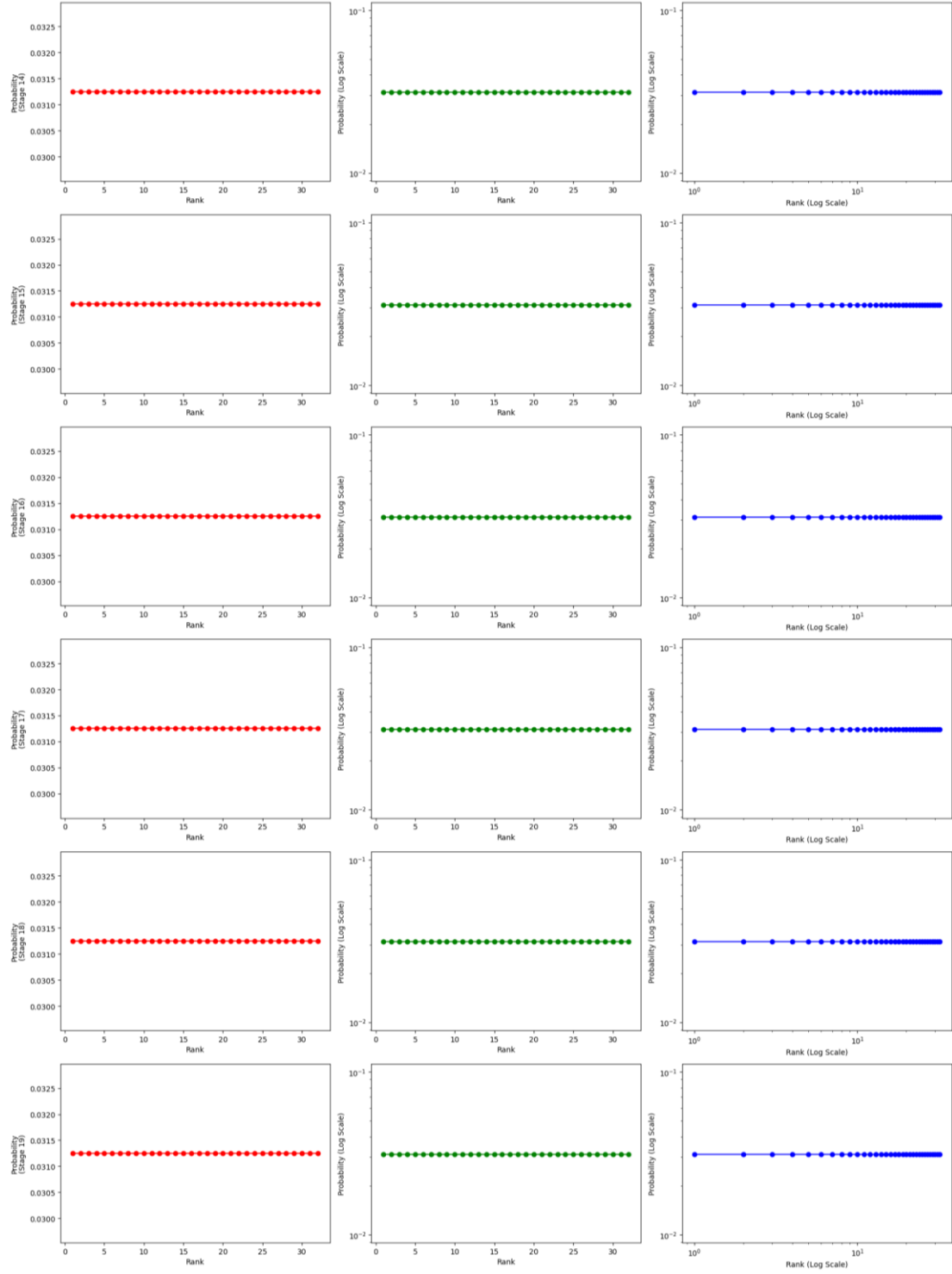




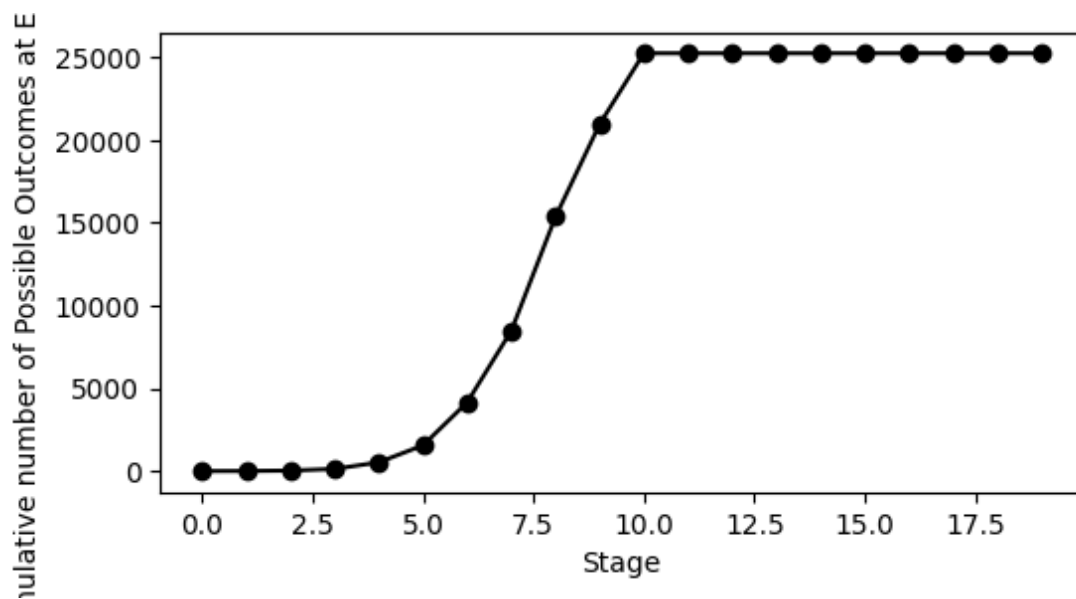
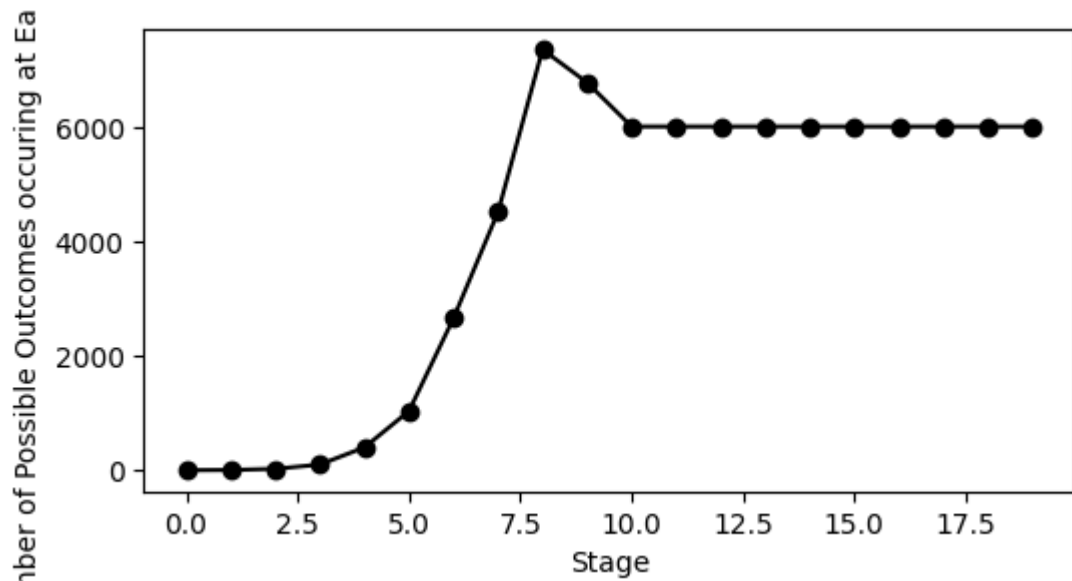


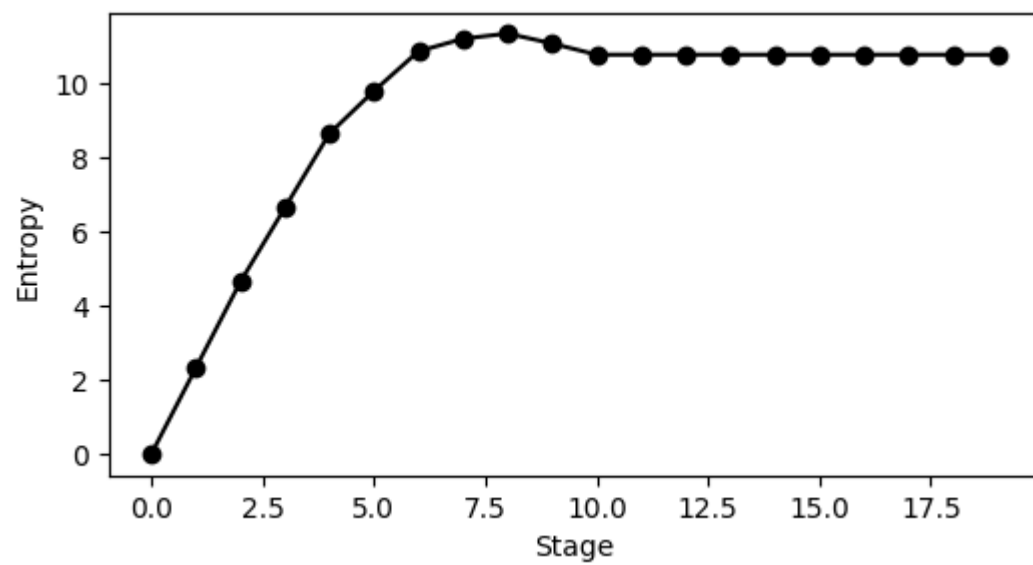


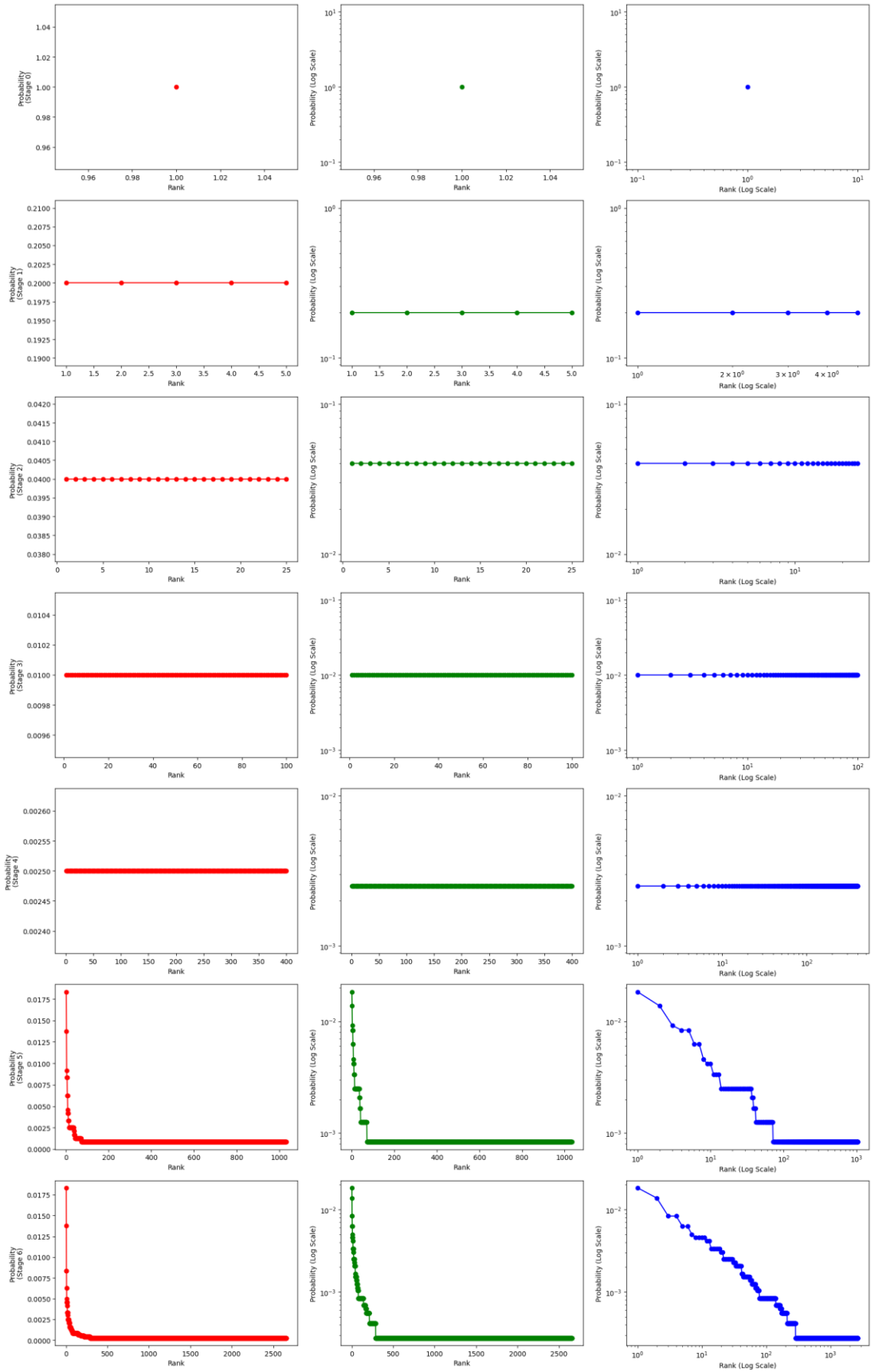


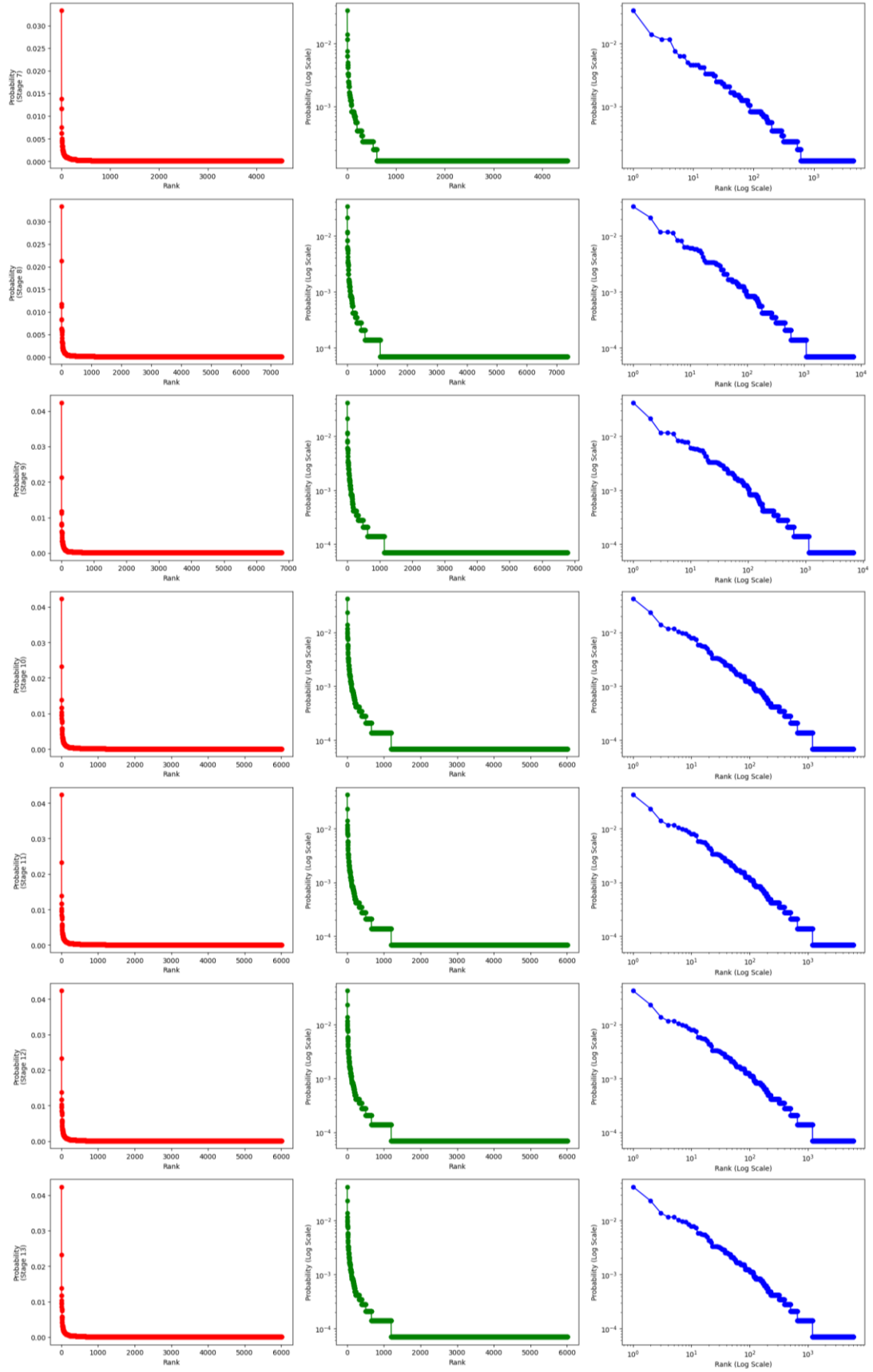


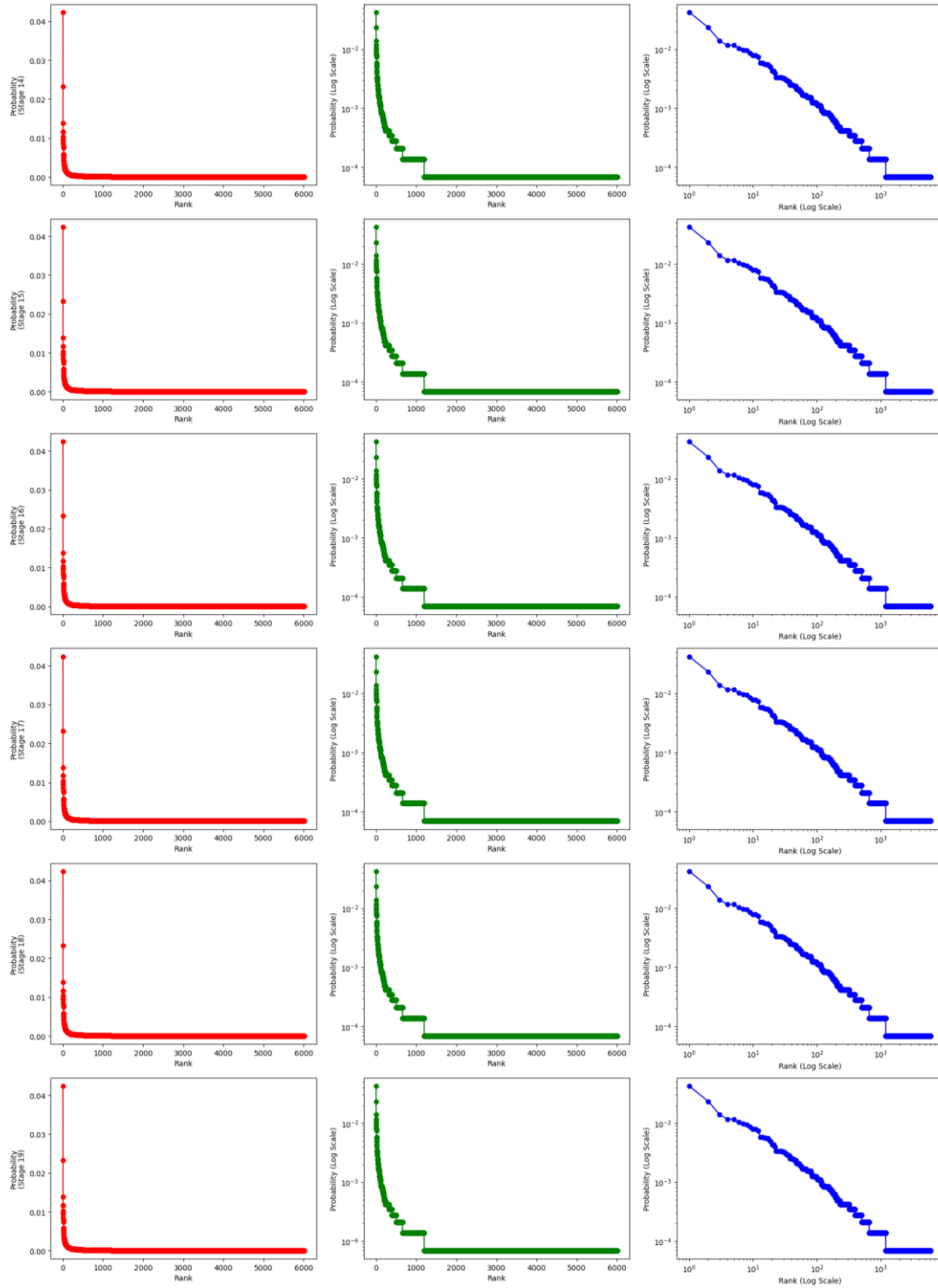
# IS110 single active site sequence











# Polylox sequence

