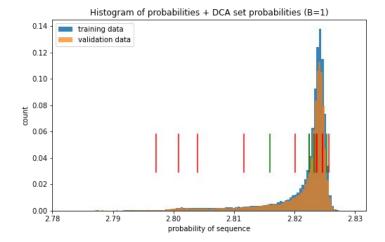
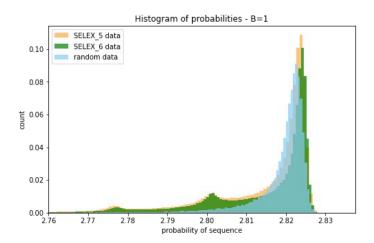
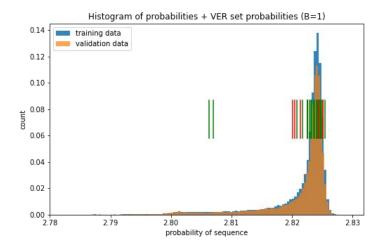
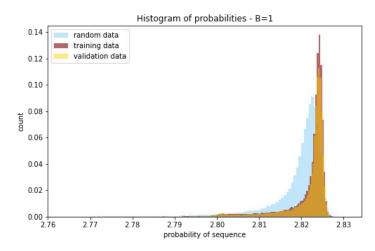
# DNA β-VAE results

 $\beta=1$ 

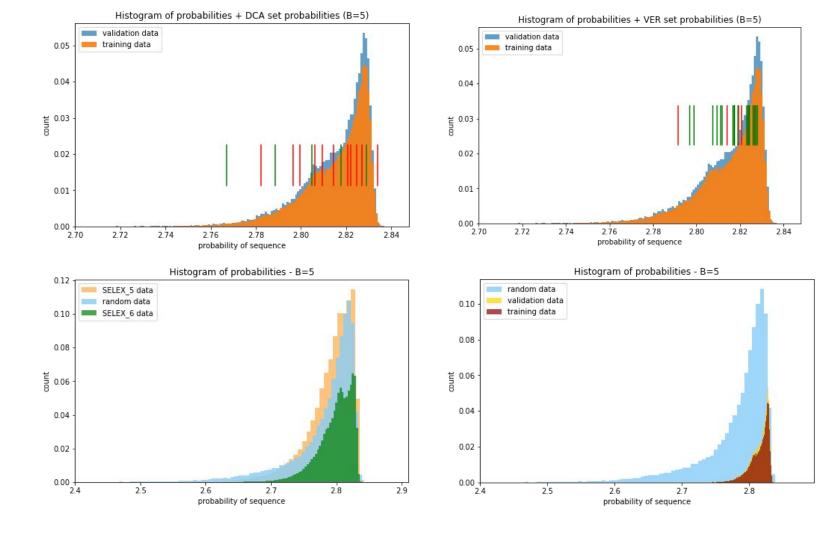




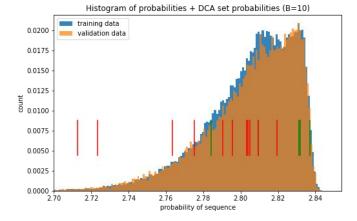


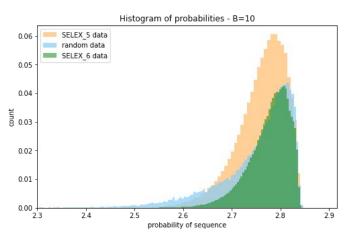


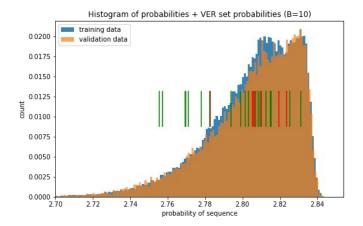
 $\beta=5$ 

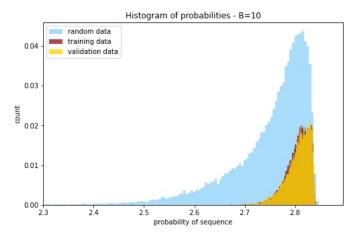


# β=10





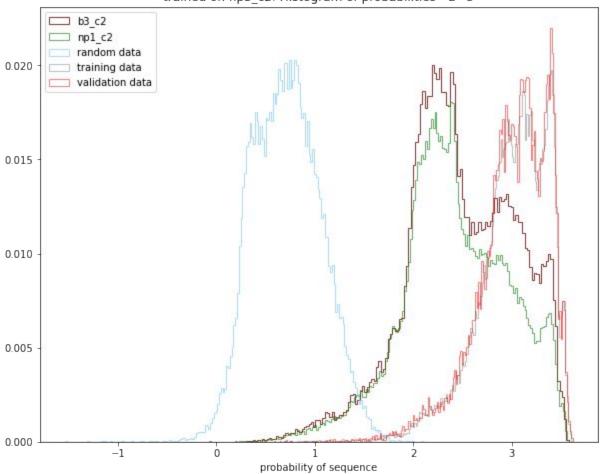




# Peptides β-VAE results

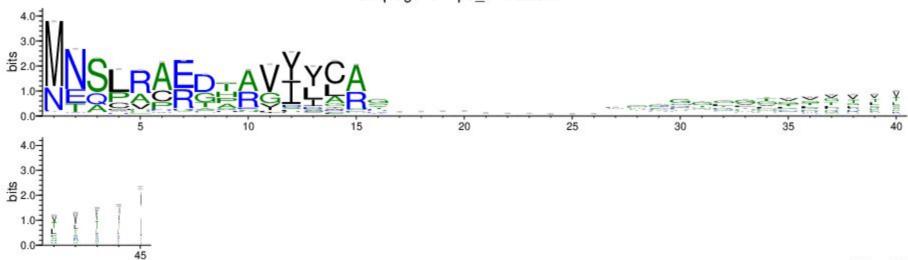
c2

trained on np3\_c2: Histogram of probabilities - B=5



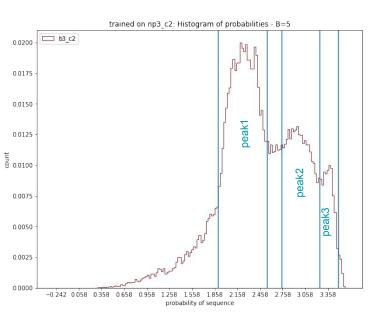
count

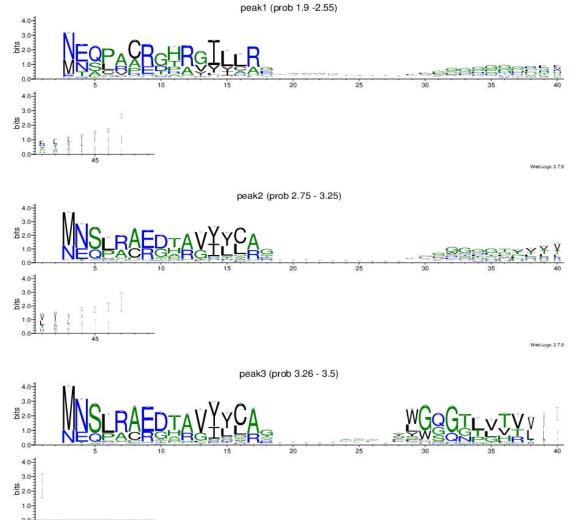
#### Seq logo for np3\_c2 dataset



WebLogo 3.7.9

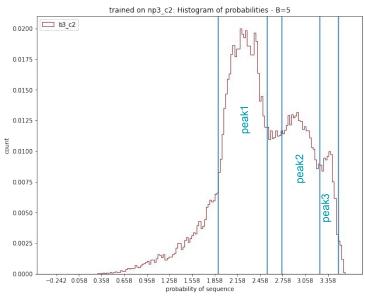
# b3\_c2

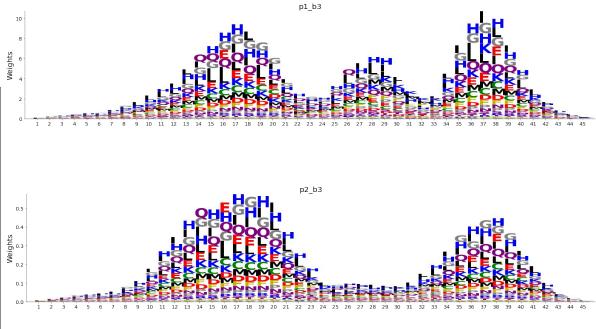


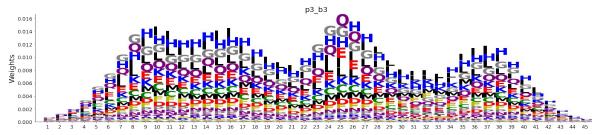


WebLogo 3.7.9

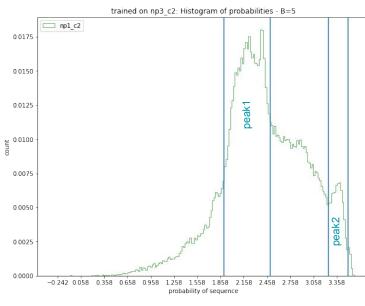
# b3\_c2: SALIENCY

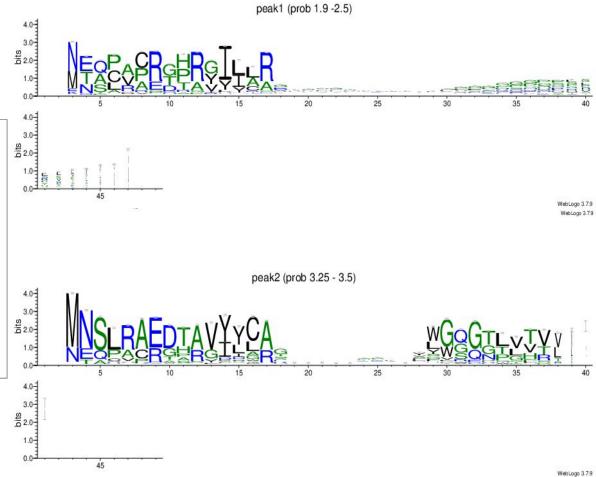




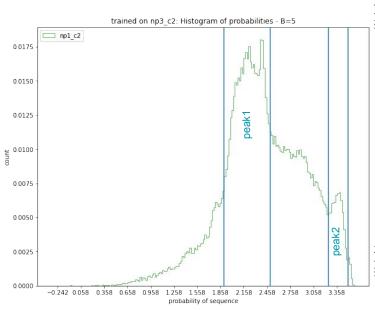


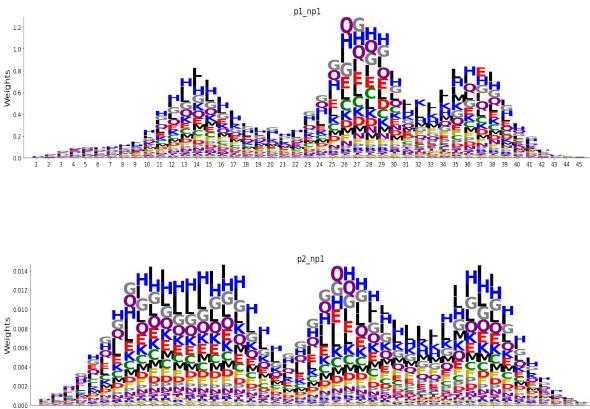




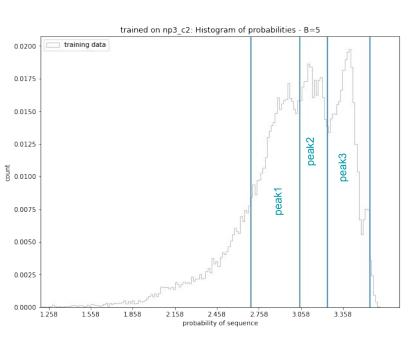


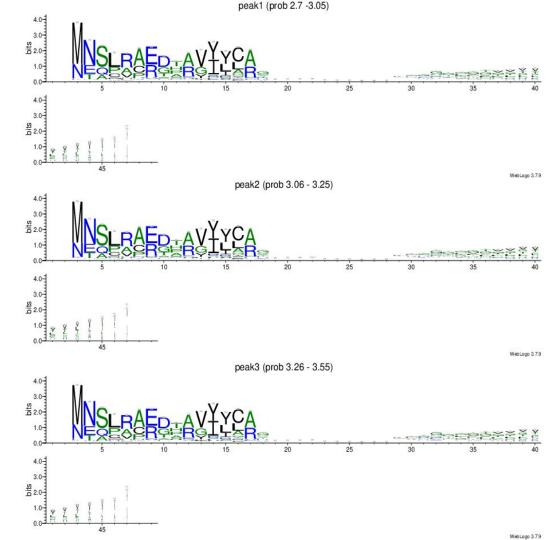
np1\_c2: SALIENCY



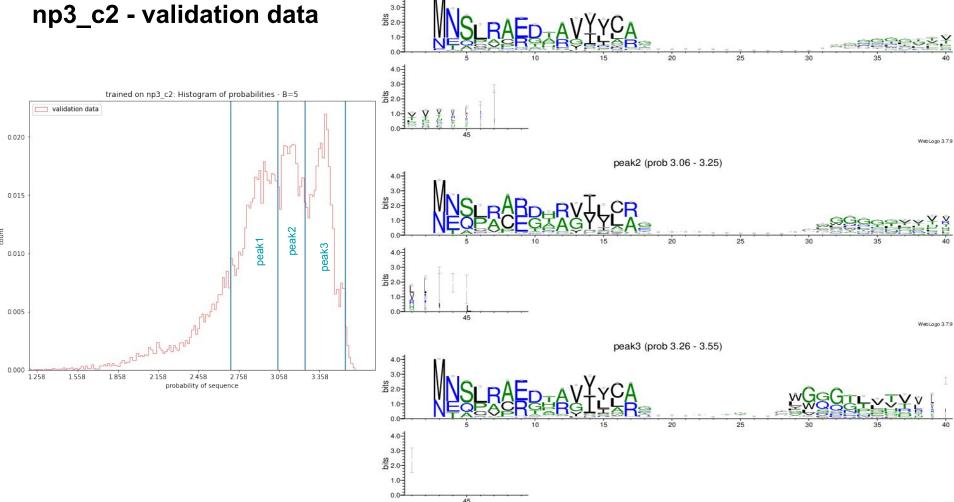


## np3\_c2 - training data





## np3\_c2 - validation data



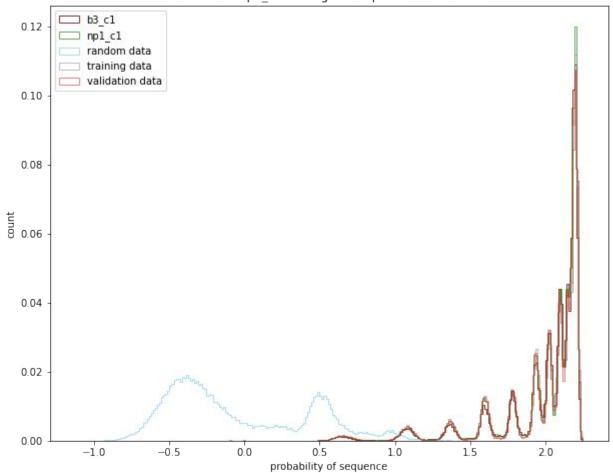
peak1 (prob 2.7 -3.05)

WebLogo 3.7.9

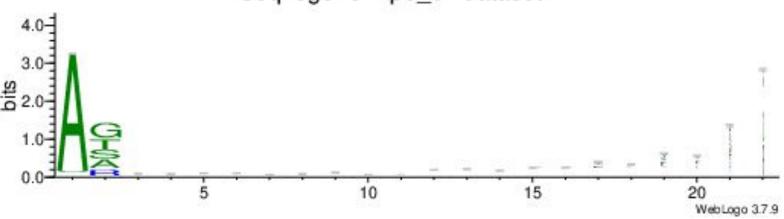
# Peptides β-VAE results

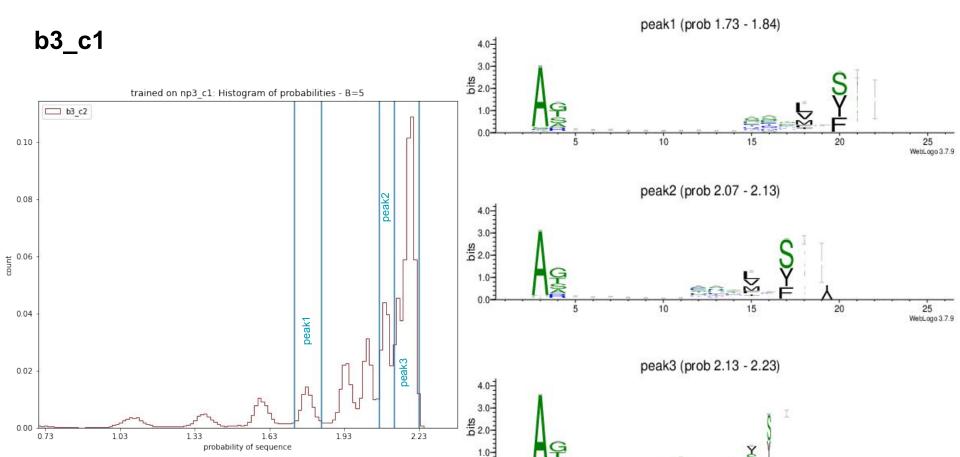
**C1** 

trained on np3\_c1: Histogram of probabilities - B=5



# Seq logo for np3\_c1 dataset





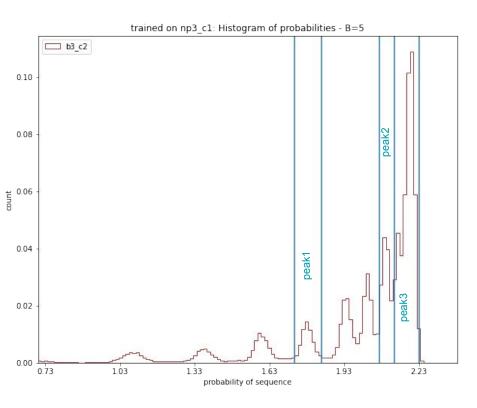
0.0-

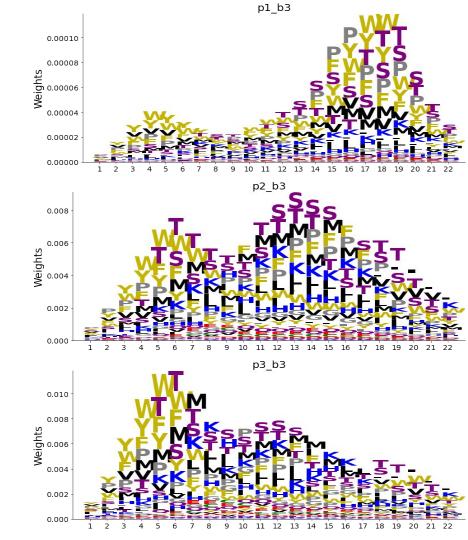
25 WebLogo 3.7.9

20

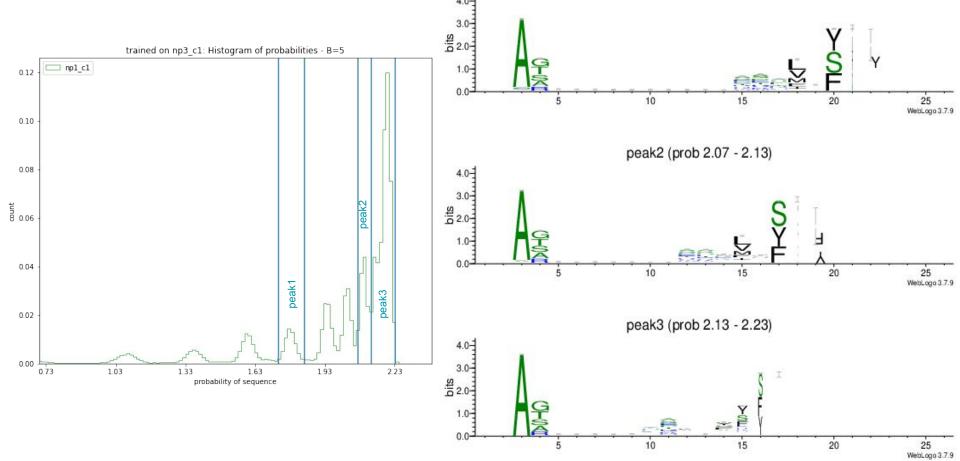
10

# b3\_c1: SALIENCY



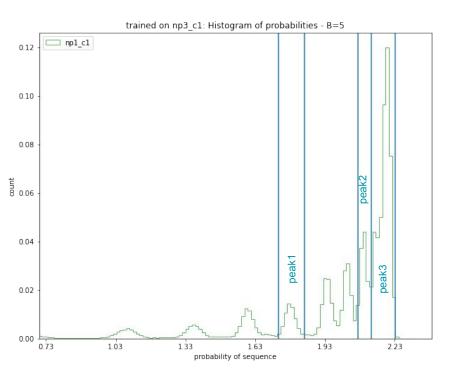


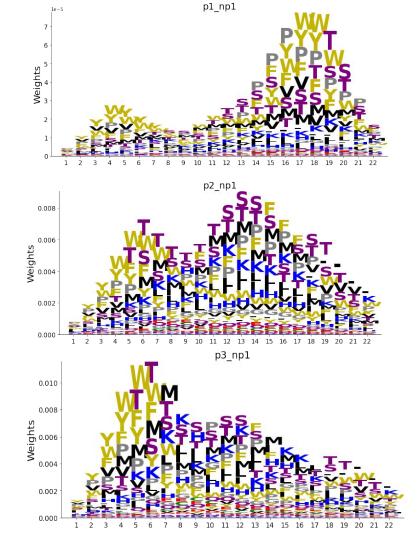




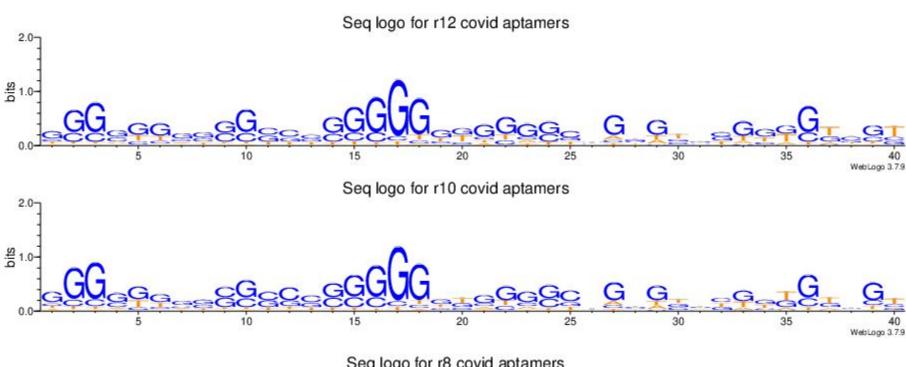
peak1 (prob 1.73 - 1.84)

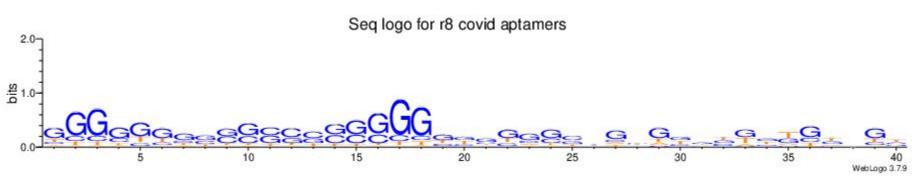
# np1\_c1: SALIENCY



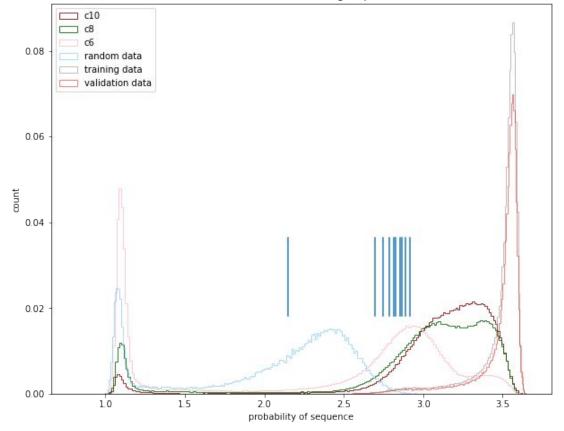


# Covid aptamers β-VAE results





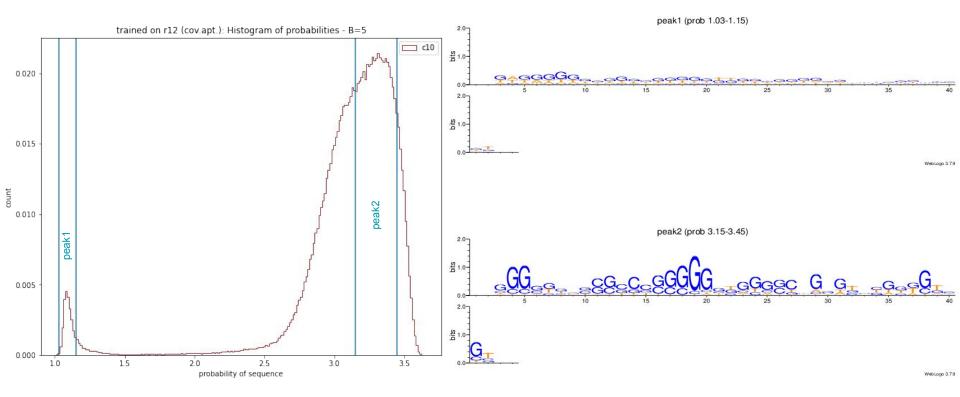
#### trained on covid aptamers 12: Histogram of probabilities - B=5 +vertical results of testing sequences



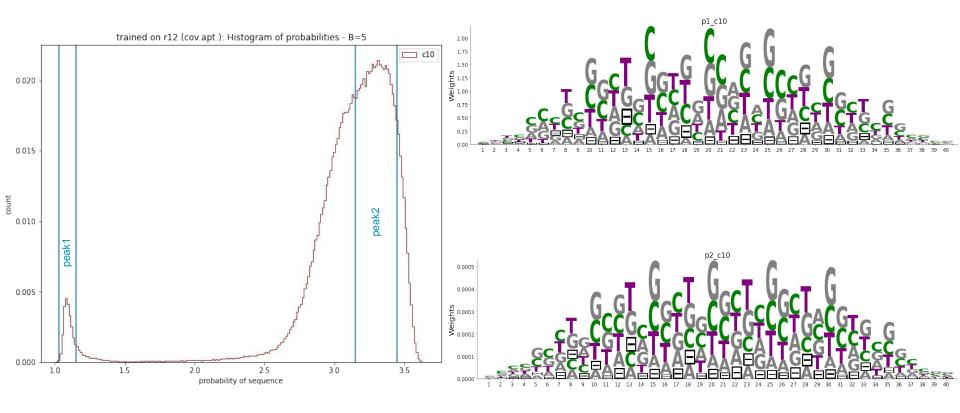
# vertical sequences + their probabilities:

>"SP5"	
TCAACCATGGTAGGTATTGCTTGGTAGGGATAGTGGGCTT >"SP6"	 2.147
CAACCCATGGTAGGTATTGCTTGGTAGGGATAGTGGGCTT >"SP7"	 2.856
CAAAGGAGGTAGTAGTGCTTGGTAGGGAAACTCCGCCG	 2.699
>"SP6C" CAACCCATGGTAGGTATTGCTTGGTAGCGATAGTGGGCTT	 2.747
>"SP634" AAACCCATGGTAGGTATTGCTTGGTAGGGATAGTGGGAAA	 2.784
>"SP634G" AAACCCATGGTAGGTATTGGTTGGTAGGGATAGTGGGAAA	 2.816
>"SP634C" AAACCCATGGTAGGTATTGCTTGGTAGCGATAGTGGGAAA	 2.914
>"SP634A" AAACCCATGGTAGGTATTGCATGGTAGGGATAGTGGGAAA	 2.827
>"SP630" AAAAACATGGTAGGTATTGCATGGTAGGGATAGTGAAAAA	 2.867
>"SP619" AAAAAAAAAAAAAATATTGCATGGTAGGGATAGAAAAAAA	 2.886

#### r10 of covid aptamers



# r10 of covid aptamers: SALIENCY



trained on covid aptamers 10: Histogram of probabilities - B=5 \_\_\_ c12 0.12 random data training data validation data 0.10 0.08 0.06 0.04 0.02 0.00 1.0 1.5 2.0 2.5 3.0 3.5

probability of sequence

count