1. Given the following segment of DNA, identify the various components and processes involved in the translation from DNA to protein.
   DNA coding sequence: ATGGCCGTAGGCTAAAAGGGTGCCCGATAG
   a) Identify the coding and template strands and write them down.

   b) Write down the mRNA sequence transcribed from the template strand. Indicate the directionality of the strand.

   c) List the sequence of codons in the mRNA and translate the codons into the corresponding amino acids using the genetic code chart.

   d) Write down the final protein sequence in single letter code in the direction of translation and comment the potential observations.

   e) Draw the polypeptide chain that would result from this mRNA strand.

2. Given the following list of amino acids, classify them based on their side chain properties:
   - Alanine (Ala)
   - Glutamic Acid (Glu)
   - Serine (Ser)
   - Valine (Val)
   - Lysine (Lys)
   - Tyrosine (Tyr)
   - Leucine (Leu)
   - Arginine (Arg)

   a) Which amino acids in the list have hydrophobic side chains and which amino acids have hydrophilic or charged side chains?

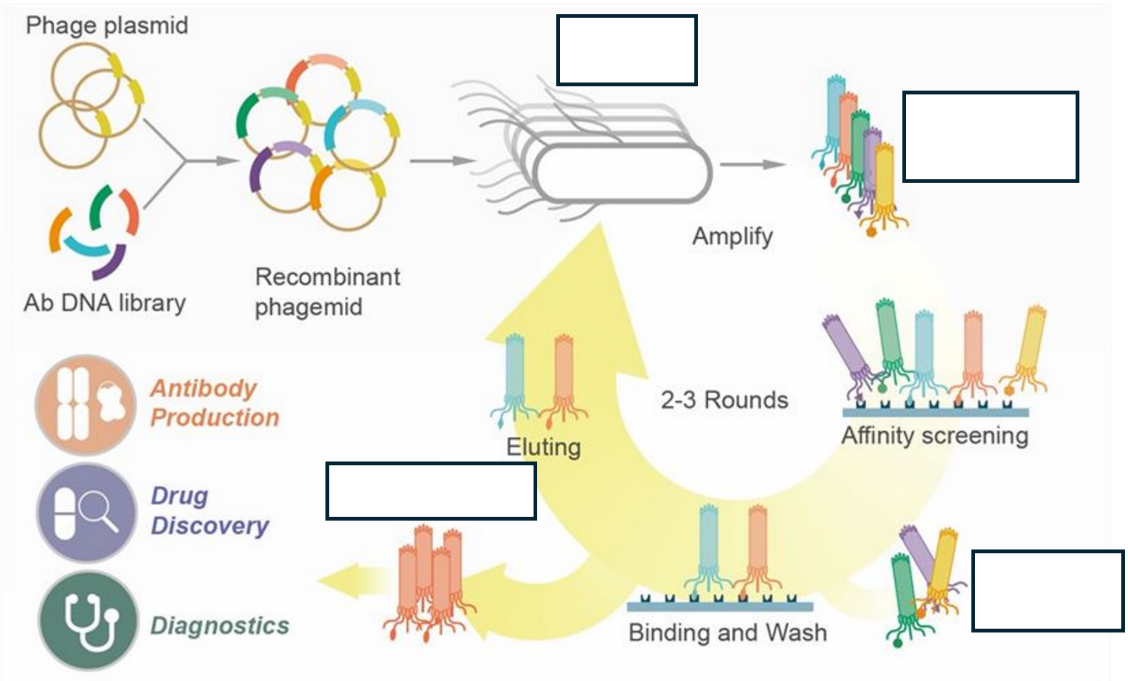
   b) Related to the side chain properties of Leucine and Lysine, where would they respectively most likely be found: in the transmembrane region of a cell or on the surface of a cytoplasmic protein?

3. What does the following DNA-sequence encode:
5′-CACCACCATCACCATCAC-3′

a) If we now want to couple such a tag to a protein of interest, how would you do this? What is this specific peptide chain used for in a research setting?

b) Please draw a plasmid and annotate the components in your cartoon.

c) When identifying strong binding partners (e.g. tags) for a specific target, which technique is often used? Below is a schematic illustration of this technique, please fill in the gray boxes with the steps or components they refer to.



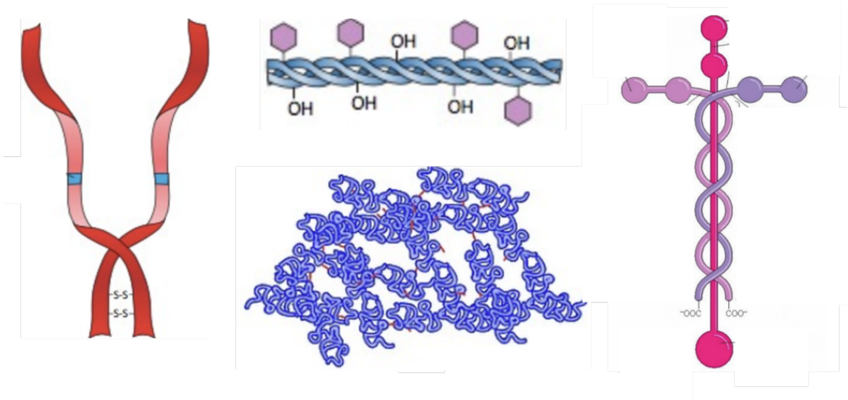
4. Draw a DNA origami scaffold in the shape of a star.

a) What is the most important feature that the DNA origami scaffold always has?

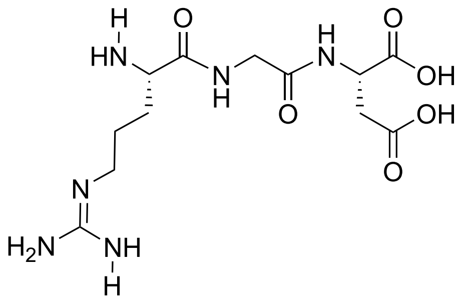
b) If I would like to functionalize a protein onto the surface of my DNA origami nanoparticle, how would I do this? Annotate on the DNA origami scaffold.

c) Assume that the sequence of the strand that you annotate in 4b) is: 5’-GGCTGAAAATCTCCTGACATG-3’. Please give the sequence of the DNA strand that should be conjugated to the protein.

5. Which of the following 4 ECM-proteins are involved in the connection between cells and the extra cellular matrix (ECM)?



a) Your cell of interest will connect to a particular 3 amino acid motif within this ECM protein using its integrin receptors. Please annotate the amino acids in the structure below in single letter code.



b) Please give a potential mRNA-sequence for this motif in 5′ to 3′ direction.

c) Please give the coding and template strand of this mRNA both in 5′ to 3′ direction.

6. Ligand and receptors

You are given data from an experiment where a ligand interacts with a receptor.

	Ligand concentration [L] (nM)	Receptor-ligand complex [LR] (nM)
Timepoint 1	10	8
Timepoint 2	20	15
Timepoint 3	50	30
Timepoint 4	80	30

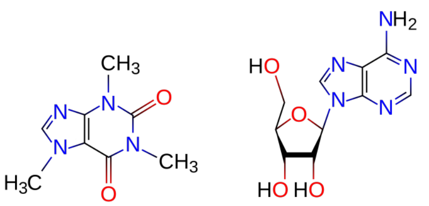
a) Use the provided experimental data to calculate the Kd with the following formula:
[R] = [LR] = 50% of max [LR]
Kd = ([L] * [R]) / [LR]

b) Use the provided data to calculate the Ka.

c) Would you consider the ligand and receptor strong binders, based on the Kd that you calculated?

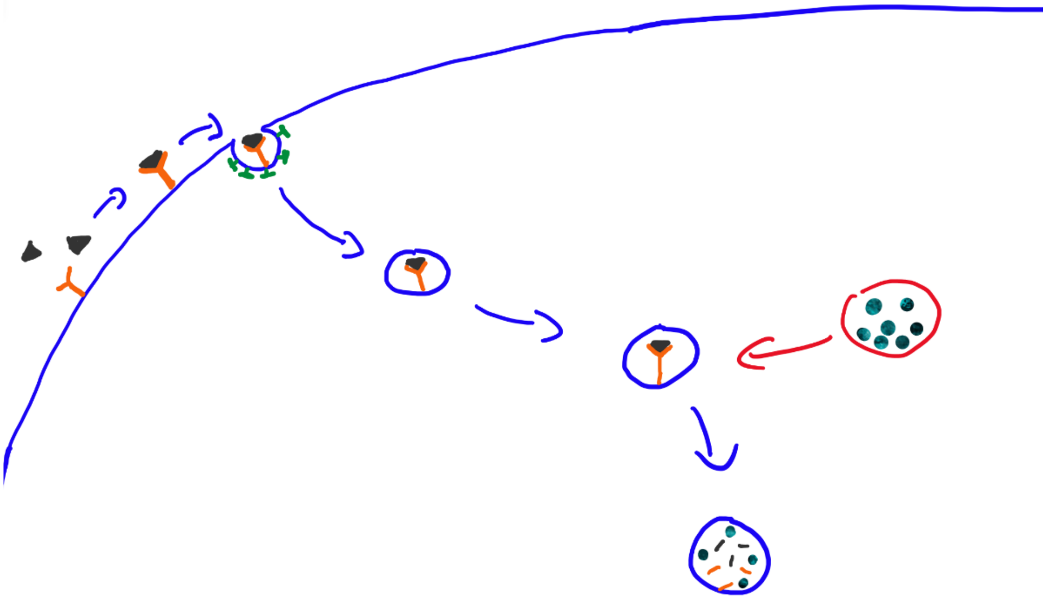
d) I want to functionalize this ligand on a nanoparticle to target the receptor. Would it be necessary to functionalize many ligands on the nanoparticle, and therefore leverage multivalent binding to ensure a stable interaction between the ligand and receptor? Why?

e) During the lecture you heard about adenosine, a natural molecule in our body. Naturally, it binds to adenosine-receptors and makes us feel tired. Often, we drink coffee to feel more awake and alert. Caffeine, a component of coffee, is a ligand for the adenosine-receptor. Based on the effect, is caffeine an agonist or antagonist for the adenosine receptor? Explain why?



Caféine Adénosine

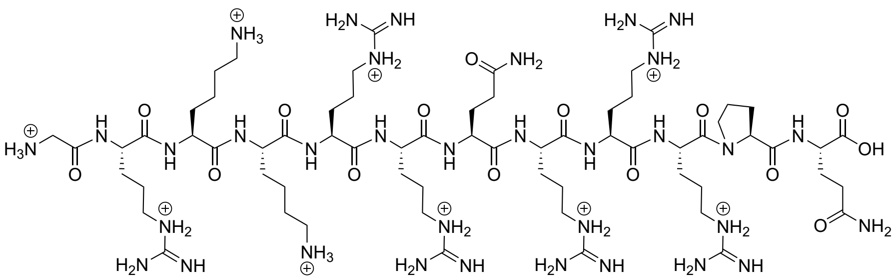
7. The following pathway is very important in the context of many therapeutic applications.



a. Please annotated the differently colored components.

b. During the whole process the pH of the vesicle is changing. Please indicate the trend and why this is important.

c. Nanoparticles of interest can be fused to the following peptide to allow for their escape from the endosome. Please name this peptide and give the amino acid sequence in single letter code.

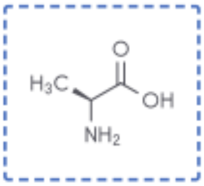


d. Another peptide with similar function has the single letter code N-RRRRRRRR-C. What do these two peptides have in common, that help them carry out the function?

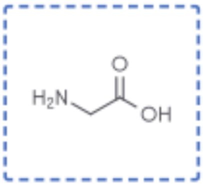
Chart Key

Alkyl | Aromatic | Neutral | Acidic | Basic | Essential | Non-Essential

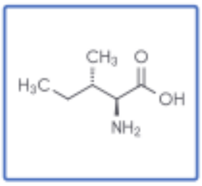
Note: The NH_2 and COOH values listed below are pK_a values.



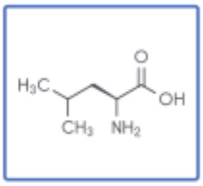
Alanine
Ala A
NH_2: 9.87 COOH: 2.35



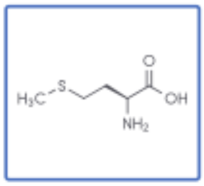
Glycine
Gly G
NH_2: 9.60 COOH: 2.34



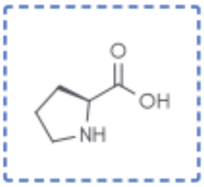
Isoleucine
Ile I
NH_2: 9.76 COOH: 2.32



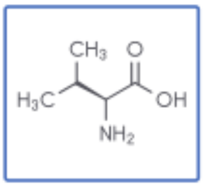
Leucine
Leu L
NH_2: 9.60 COOH: 2.36



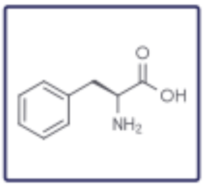
Methionine
Met M
NH_2: 9.21 COOH: 2.28



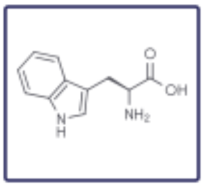
Proline
Pro P
NH_2: 10.60 COOH: 1.99



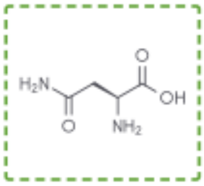
Valine
Val V
NH_2: 9.72 COOH: 2.29



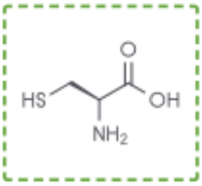
Phenylalanine
Phe F
NH_2: 9.24 COOH: 2.58



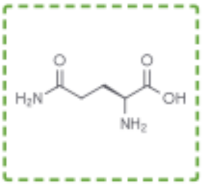
Tryptophan
Trp W
NH_2: 9.39 COOH: 2.38



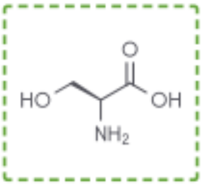
Asparagine
Asn N
NH_2: 8.80 COOH: 2.02



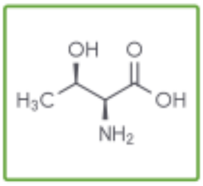
Cysteine
Cys C
NH_2: 10.78 COOH: 1.71



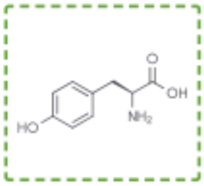
Glutamine
Gln Q
NH_2: 9.13 COOH: 2.17



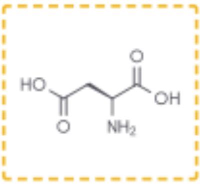
Serine
Ser S
NH_2: 9.15 COOH: 2.21



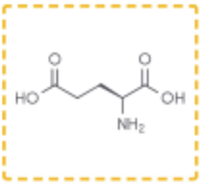
Threonine
Thr T
NH_2: 9.12 COOH: 2.15



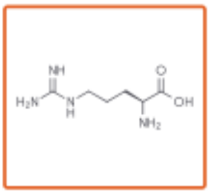
Tyrosine
Tyr Y
NH_2: 9.11 COOH: 2.20



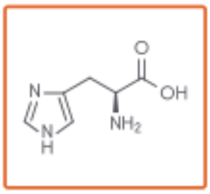
Aspartic Acid
Asp D
NH_2: 9.60 COOH: 1.88



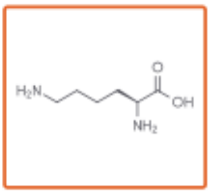
Glutamic Acid
Glu E
NH_2: 9.67 COOH: 2.19



Arginine
Arg R
NH_2: 9.09 COOH: 2.18



Histidine
His H
NH_2: 8.97 COOH: 1.78



Lysine
Lys K
NH_2: 10.28 COOH: 8.90

Second Position

First Position	T	C	A	G	Third Position
T	TTT, TTC: Phe TTA, TTG: Leu	TCT, TCC, TCA, TCG: Ser	TAT, TAC: Tyr TAA: ***STOP*** TAG: ***STOP***	TGT, TGC: Cys TGA: ***STOP*** TGG: Trp	T C A G
C	CTT, CTC, CTA, CTG: Leu	CCT, CCC, CCA, CCG: Pro	CAT, CAC: His CAA, CAG: Gln	CGT, CGC, CGA, CGG: Arg	T C A G
A	ATT, ATC, ATA: Ile ATG: Met	ACT, ACC, ACA, ACG: Thr	AAT, AAC: Asn AAA, AAG: Lys	AGT, AGC: Ser AGA, AGG: Arg	T C A G
G	GTT, GTC, GTA, GTG: Val	GCT, GCC, GCA, GCG: Ala	GAT, GAC: Asp GAA, GAG: Glu	GGT, GGC, GGA, GGG: Gly	T C A G