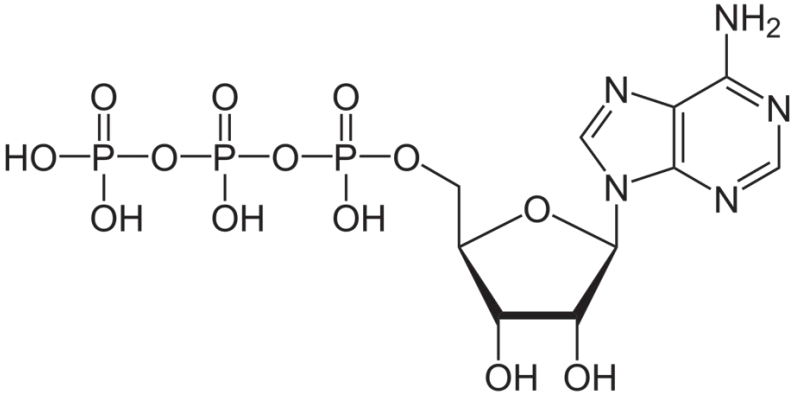
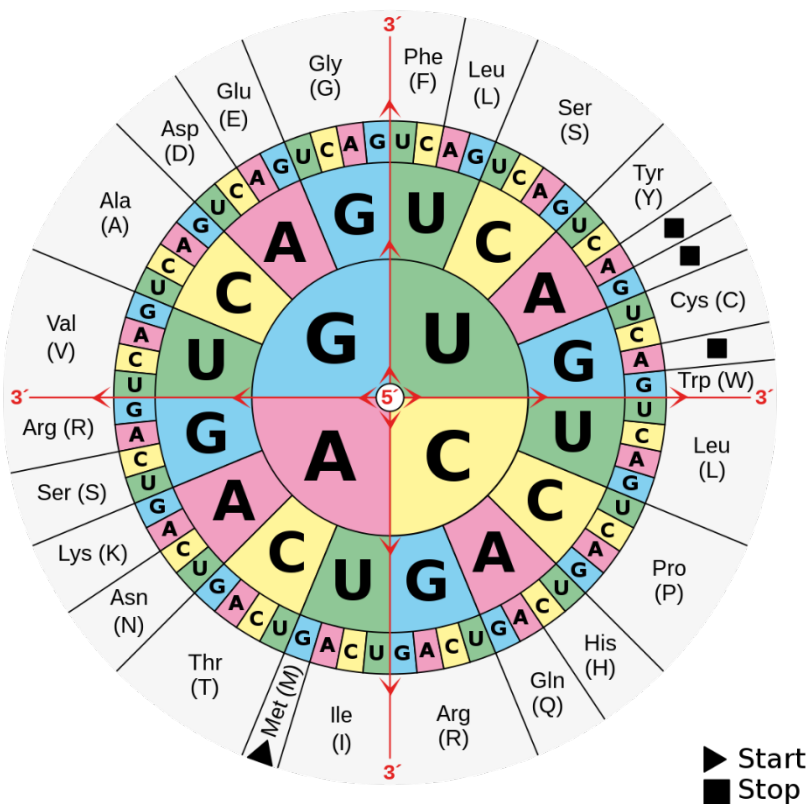


Exam:

1	<p>You are preparing a PCR reaction. All components (template DNA, primers, nucleotides, buffer, polymerase) are in place. Now you need to program the thermal cycler.</p> <p>On the axes below (X = time, Y = temperature), draw a typical temperature profile for one complete PCR cycle.</p> <ul style="list-style-type: none">• Label the individual steps of the cycle clearly.• Briefly explain what happens at each step (one sentence per step is sufficient). <p>Note: The exact duration of each step is not important. What matters is the correct order of events and the approximate temperature at each stage.</p>	3 P

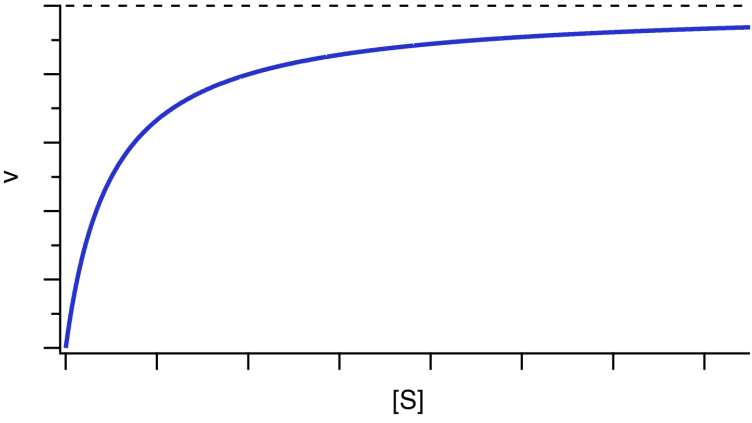
2	<p>Below is the structure of a central molecule of life.</p> <p>On the structure, please label or circle the following and add the corresponding letter:</p> <ul style="list-style-type: none"> • A: The glycosidic bond • B: The portion that makes up the nucleoside • C: The chemical feature that would define it being incorporated into RNA or DNA. 	3 P
		

3	<p>In plasmid cloning, restriction enzymes are commonly used that recognize specific DNA sequences, typically palindromic 6-base (6-mer) or 8-base (8-mer) target sites. Assume the DNA sequence of an 8,000 bp plasmid is completely random, with each base (A, T, G, and C) occurring with equal probability.</p> <p>a) On average, how many times would a restriction enzyme that recognizes a 6-base sequence cut the plasmid?</p> <p>b) How many times less likely is it for an enzyme that recognizes an 8-base sequence to cut the plasmid, compared to a 6-base cutter?</p> <p>c) Why is it relevant for this calculation that enzymes recognizing palindromic sequences are used?</p>	3 P

4	<p>Below is a segment of an mRNA sequence (5' → 3') and a codon table is provided for your reference.</p> <p><u>Identify the longest open reading frame (ORF) in the sequence and write down the resulting amino acid sequence using one-letter codes.</u></p> 	2 P
5	<p>While exploring the genome of a newly discovered alien species, you notice something remarkable: Its genome is structured much like ours - made of nucleic acids, transcribed and translated. But surprisingly, it only uses two nucleotides in its genome: A and U.</p> <p>Mass spectrometry of the alien proteins shows that it uses the same 20 amino acids as Earth-based life. Further analysis shows the presence of three distinct stop signals as well.</p> <p>Assuming this alien species uses fixed-length codons, what is the minimum number of bases per codon that their genetic code must use to encode all required amino acids and stop signals?</p> <p>Let's assume the alien genetic code uses the minimal number of nucleotides per codon needed to encode 20 amino acids and 3 stop codons, how would it compare to our genome in terms of degeneracy?</p>	2 P

6	<p>Give the precise technical terms that correspond to each of the following descriptions.</p> <ul style="list-style-type: none"> a) Organelle responsible for ATP production via oxidative phosphorylation b) Organelle responsible for protein sorting and modification, especially for secretion c) Organelle that digests macromolecules using hydrolytic enzymes at low pH d) Large protein complex that degrades ubiquitinated proteins e) Organelle that organizes microtubules and is important in spindle formation during cell division f) Organelle covered with ribosomes, involved in the synthesis of membrane and secreted proteins 	3 P
7	<p>A mutation arises in a gene that alters the structure of the inner mitochondrial membrane, making it significantly more permeable to protons (H^+ ions).</p> <ul style="list-style-type: none"> a) How would this mutation affect mitochondrial ATP synthesis? Explain your reasoning. b) Oxygen consumption by mitochondria in these mutant cells remains normal or even elevated. How can this observation be explained? c) Suggest one metabolic adjustment or pathway that the cell might upregulate in response to this defect, and explain why. 	3 P
8	<p>A popular restriction enzyme used for cloning is NcoI, which recognizes the motif CCATGG. It is often positioned so that it contains the actual start codon, since it creates a Kozak motif.</p> <ul style="list-style-type: none"> a) Briefly explain what a Kozak motif is. b) What is the constraint of using this enzyme at this position? 	2 P

9	<p>In an alien world each glucose molecule yields 10 ATP during aerobic respiration and only 2 ATP during low-oxygen anaerobic conditions. The following pseudocode calculates the total ATP produced from glucose metabolism under varying oxygen levels:</p> <p>What is the value of totalATP printed at the end? Show your work, i.e . provide the individual values of “yield”!</p>	3 P

10	<p>Consider the Michaelis-Menten reaction $E + S \rightleftharpoons ES \rightarrow E + P$. Assume the enzyme concentration $[E]$ is fixed.</p>  <p>(1) In the rate graph above, clearly mark K_M.</p> <p>(2) What does the dashed black line represent?</p> <p>(3) An inhibitor specifically slows down the $ES \rightarrow E + P$ rate of the reaction. Sketch the expected overall production rate in the graph above.</p> <p>(4) Is this type of inhibition (a) competitive or (b) non-competitive?</p>	4 P

11	<p><u>You need to prepare 1000mL of a specific buffer that should have the following composition</u></p> <p>200mM NaCl 20mM Tris-HCl (pH7.5) 2% (v/v) glycerol 1mM EDTA</p> <p><u>In the lab you find the following:</u></p> <p>Sodium chloride as a salt (molecular weight Mw=58 g/mol) A 2 liter bottle of 1M Tris-HCl pH 8.0 stock solution A 500mL-bottle of 40% v/v glycerol solution A 1 liter bottle of 0.5M EDTA Unlimited supply of double-distilled water (ddH₂O)</p> <p>a) How much of the individual ingredients do you need to prepare the desired buffer? b) For a second experiment you need 100 mL of a buffer with exactly half the concentration of all ingredients, and you decide to simply dilute your buffer with ddH₂O (50mL+50mL). Will the pH change upon dilution?</p>	3 P
12	<p>Antibody synthesis and secretion:</p> <p>a. Which feature in their amino acid sequence is guiding the antibody subunits (IgG, heavy and light chains, 50 KDa and 25 KDa, respectively) to the endoplasmic reticulum? b. What covalent (non-peptide) bond is stabilizing the quaternary structure of the antibody and where in the cell is it formed? c. The purified antibody is analyzed on a denaturing SDS-PAGE. How many bands and at what apparent molecular weight can you expect to see under reducing and non-reducing conditions?</p>	3 P

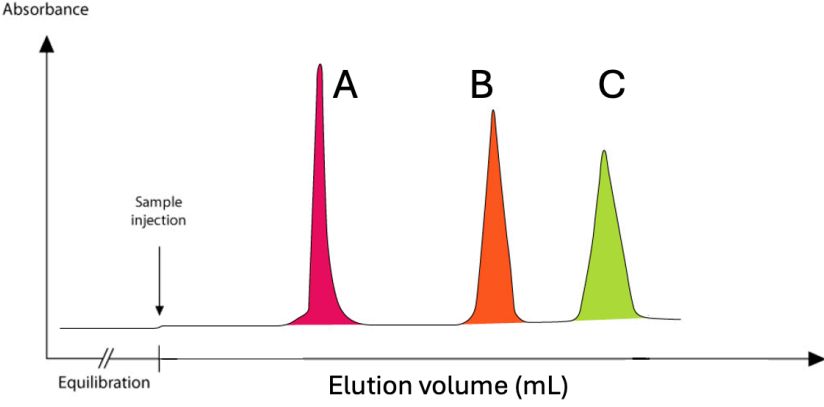
13	<p>Which of the three 20-amino acid sequences listed below (single letter code amino acid code) is the most likely candidate for</p> <ul style="list-style-type: none"> a) Being part of a soluble solvent exposed part of a protein b) form a transmembrane domain (α-helix) of a transmembrane protein c) An intrinsically disordered region <p>Briefly explain your answer!</p> <p>Sequence 1: LVLWVLSLCL GLLNGVCSL Sequence 2: HSLHPESIWD CPERGHGAKE Sequence 3: PQQQPQPQGK SPQPKPGSPQ</p>	3 P

14	<p>Match each of the 12 entities with the appropriate process of either</p> <ul style="list-style-type: none"> a) Replication b) Transcription c) Translation 	3 P
<ol style="list-style-type: none"> 1. TATA-box 2. Single-stranded-DNA binding protein 3. Requires tRNA 4. Promotor 5. Requires poly-A tail 6. Helicase 7. generates RNA 8. substrates are NTPs 9. P-site 10. Okazaki-fragments 11. Sliding clamp 12. Substrates are dNTPs 		

15	<p>You express a protein in <i>E. coli</i> and subsequently purify it using an affinity tag. To determine the concentration of your purified protein you measure an UV-spectrum in a photometer (with the respective buffer as a proper reference; wavelength range 230-320 nm). The operating instructions for the photometer cuvette state "path length = 1 cm".</p> <p>a) What additional information do you need to determine the concentration of the protein?</p> <p>b) What wavelength are you looking at / where do you expect the peak?</p> <p>c) You notice that the peak is somehow not at the expected wavelength (b), but at 260 nm. What could be the reason for this?</p>	3 P

16	<p>Proteins can be post translationally modified by (A)phosphorylation and (B) ubiquitylation. Please name for each type of modification the type of enzyme and the corresponding modified amino acids!</p>	2 P

17	Describe the structure and composition of a nucleosome!	2 P

18	<p>You have analyzed a mixture of proteins (BSA 66kDa, Myoglobin 16.7 kDa, and Hexokinase 100 kDa) by a size-exclusion chromatography run. Which of the peaks A-C in the following elution profile of the size-exclusion column corresponds to which protein?</p> 	1 P

Exam:

19	Name the four phases of the cell cycle and briefly describe the main function of each phase.	4 P
20	A cell is observed to have duplicated DNA, but it does not proceed to mitosis. In which phase is the cell likely arrested, and what could be the reason?	2P
21	Explain three ways a low error rate is achieved during DNA replication!	3P
22	<i>How do importins mediate the transport of nuclear proteins through the nuclear pore, and what role does the protein Ran play in this process?</i>	3 P