University of São Paulo São Carlos Institute of Physics Graduate Program

> Admission Test Biomolecular Physics First Semester 2025

Exam Booklet

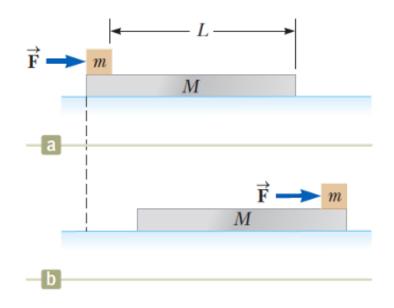
Candidate's Code:

Physics Questions (Multiple Choice)

Instructions: The Physics questions are multiple-choice. For these questions, please indicate your chosen answer directly in this exam booklet by marking the corresponding square with an "X" using a black or blue pen. Do not use this exam booklet for elaborating on your answers or as a draft. You may use the provided Notepaper for developing your answers or as a draft paper. The answers considered for correction will be the ones marked in the exam booklet.

Question 1:

A block of mass *m* is at rest at the left end of a block of mass *M*, which is also at rest, as shown in the figure below. The distance between the edge of the two blocks is L, as indicated in the figure. The coefficient of kinetic friction between the two blocks is $\mu = 1/2$, and the surface on which the block of mass *M* rests is frictionless. A constant horizontal force is applied to the block of mass *m*, setting it in motion as shown in the figure. Knowing that the force F = 2mg and that m = M/3 (where g is the local acceleration gravity), when the block of mass *m* reaches the end of the block of mass *M* (situation b in the figure), the edge of the block of mass *M* will have moved from its initial position by a distance D given by:



Place an 'X' in the square that corresponds to the correct answer.

$$\Box D = L/22$$

$$\Box D = L/8$$

$$\Box D = L/26$$

$$\Box D = L/4$$

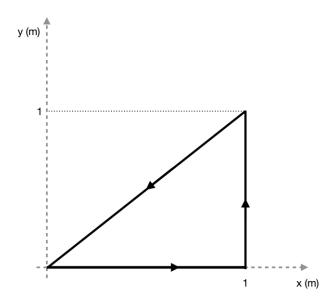
$$\Box D = L/3$$

The block of mass *m* has an acceleration given by $a_m = (F - Fat)/m = (F - \mu m g)/m$. The acceleration of the block of mass *M* is $a_M = (m/M)\mu g$. Both have the equation of motion $x(t) = (1/2) a t^2$, with their respective accelerations. Thus, the block of mass *m* takes a time $(t_f)^2 = 2L/(am - aM)$ to reach the end of the block of mass *M*. During this time, the block of mass M will travel a distance given by, using the data from the problem,

 $D = x(t_f) = (1/2) (m/M)\mu g 2L/(am - aM) = L/8$

Question 2:

A particle moves along the closed path in the xy-plane represented in the figure, starting its motion at the origin and performing one complete turn along this path, under the action of a force $\mathbf{F_1} = C (y^2 \mathbf{i} - 2xy \mathbf{j})$, with C = 10 J/m². Another particle follows the same path under the action of a different force $\mathbf{F_2} = C (y^2 \mathbf{i} + 2xy \mathbf{j})$. We are interested in the work W1 and W2 done by the forces $\mathbf{F_1}$ and $\mathbf{F_2}$, respectively, along the closed path shown in the figure, and in what can be concluded based only on the results obtained for W1 and W2.



Place an X' in the square that corresponds to the correct answer.

□ W1 = 0J, W2=0J. The two forces may be conservative □ W1 = 0J, W2 = -10/3J. The force F_1 is conservative. **X** W1= -20/3 J, W2=0J. The force F_2 may be conservative. □ W1= -20/3 J, W2=0J. The force F_2 is conservative.

 \Box W1= -20/3 J, W2=+10J. None of the forces is conservative.

We will split the calculation into 3 segments. The first segment goes from the origin to the point (x, y) = (1, 0), the second from (1, 0) to (1, 1), and the third from (1, 1) back to the origin, always following the path indicated in the figure. We denote the work done by force i in segment j by $W_{F_i}^{(j)}$. Recall that $\vec{F_1} = C(y^2\hat{i} - 2xy\hat{j})$ and $\vec{F_2} = C(y^2\hat{i} + 2xy\hat{j})$, with $C = 10 \text{ J/m}^2$.

Thus, in segment 1, we see that both forces are zero (since y = 0) and

$$W_{F_1}^{(1)} = W_{F_2}^{(1)} = 0 \,\mathrm{J}.$$

In segment 2, we have x = 1 and $d\vec{\ell_2} = dy\hat{j}$, and for the work done,

$$W^{(2)}_{F_1} = \int ec{F_1} \cdot dec{\ell_2} = C \int_0^1 (-2y \, dy) = -10 \, {
m J},$$

and for force 2,

$$W_{F_2}^{(2)} = \int \vec{F_2} \cdot d\vec{\ell_2} = C \int_0^1 (+2y \, dy) = +10 \,\mathrm{J}.$$

In segment 3, we have y = x and dx = dy. Thus,

$$W_{F_1}^{(3)} = C \int_1^0 x^2 \, dx - C \int_1^0 2x^2 \, dx = +\frac{10}{3} \,\mathrm{J},$$

$$W_{F_2}^{(3)} = C \int_1^0 x^2 \, dx + C \int_1^0 2x^2 \, dx = -10 \,\mathrm{J}.$$

For the total work, we have

$$W_{F_1} = \sum_{j=1}^3 W_{F_1}^{(j)} = -10 \,\mathrm{J} + \frac{10}{3} \,\mathrm{J} = -\frac{20}{3} \,\mathrm{J}.$$
$$W_{F_2} = \sum_{j=1}^3 W_{F_2}^{(j)} = 0 \,\mathrm{J}.$$

It is possible to conclude that the force \vec{F}_1 is not conservative and that the force \vec{F}_2 may be conservative (we cannot be certain based only on the calculation of the work for a specific closed path).

Question 3:

An object oscillates with angular frequency $\omega = 5.0$ rad/s. At t = 0 s, the object is at x = 10.0 cm with an initial velocity $v_x = -50$ cm/s. Find the phase constant of the motion e x as a function of time.

Place an 'X' in the square that corresponds to the correct answer.

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\Box \pi/8 \text{ rad}; x = (5.0 \text{ cm}) \cos[(10.0 \text{ s}^{-1})\text{t} + \pi/2]
\Box \pi/8 \text{ rad}; x = (20.0 \text{ cm}) [\sin(5.0 \text{ s}^{-1} t + \pi/4)]
X \pi/4 \text{ rad}; x = (10.0 \text{ cm}) [\cos(5.0 \text{ s}^{-1} t) - \sin(5.0 \text{ s}^{-1} t)]
\Box \pi/4 \text{ rad}; x = (4.0 \text{ cm}) [\cos(5.0 \text{ s}^{-1} t) + \sin(5.0 \text{ s}^{-1} t)]
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 \Box None of the previous answers

The initial position and velocity are related to the amplitude and phase constant.

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x = A \cos(\omega t + \delta) = v_x = -\omega A \sin(\omega t + \delta)

Then,

x_0 = A\cos(\delta)

and

v_{0x} = -\omega A \sin(\delta).

Thus,

v_{0x}/x_0 = -\omega A \sin(\delta) / A \cos(\delta) = -\omega \tan(\delta).

Therefore,

\tan(\delta) = -v_{0x}/\omega x_0

\delta = \tan^{-1}(-v_{0x}/\omega x_0) = \tan^{-1}(-(-50 \text{ cm/s})/(5.0 \text{ rad/s}) (10.0 \text{ cm})) = \pi/4 \text{ rad}

A = x_0 / \cos(\delta) = 10.0 \text{ cm/}\cos(\pi/4) = 20.0/\sqrt{2} \text{ cm}

x = (20,0/\sqrt{2} \text{ cm})\cos[(5.0 \text{ s}^{-1})t + \pi/4] = 10.0[\cos(5.0 \text{ s}^{-1} t) - \sin(5.0 \text{ s}^{-1} t)]
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Question 4:

 $v_{y,max} = 2.0 \text{ m / s}$

Consider a harmonic wave function in a string:

 $Y(x,t) = (0.25 \text{ m}) \text{ sen}[(2.0 \text{ m}-1)x - (8.0 \text{ s}^{-1})t]$

Find the wavelength, the frequency and the maximum speed at any point in the string.

Place an 'X' in the square that corresponds to the correct answer.

 $\Box 3\pi / 4 \text{ m}; 1/\pi \text{ s}; 1.0 \text{ m/s}$ $\boxed{\lambda} \pi \text{ m}; 4/\pi \text{ s}; 2.0 \text{ m/s}$ $\Box 2.0 \text{ m}; 1.5 \text{ s}; 3.0 \text{ m/s}$ $\Box 4.0 \text{ m}; 2.0 \text{ s}; 0.5\pi \text{ m/s}$ $\Box \text{ None of the previous answers}$ $\lambda = 2\pi/\text{k} = 2\pi/2.0 \text{ m}^{-1} = \pi \text{ m}$ $T = 2\pi/\omega = 2\pi/8.0 \text{ s}^{-1} = \pi/4 \text{ s}$ $f = 1/T = 4/\pi \text{ s}$ $A = 0.25 \text{ m} = \frac{1}{4} \text{ m}$ $v_{y} = (0.25 \text{ m}) (-8.0 \text{ s}^{-1}) \cos[(2.0 \text{ m}^{-1})x - (8.0 \text{ s}^{-1})t] = -(2.0 \text{ m/s}) \cos[(2.0 \text{ m}^{-1})x - (8.0 \text{ s}^{-1})t]$

Question 5:

Suppose that you have no heat source to heat a jar of water (500 ml) at initial temperature of 15 °C to make a coffee. You can heat water by shaking it inside a thermos flask. Considering that in each shake the water falls 30 cm and all mechanical energy is converted into heat. If you are able to making 30 shakes each minute, neglecting any loss of thermal energy by the flask, how long you must shake the flask before the water boils.

Place an 'X' in the square that corresponds to the correct answer.

X 2.7 days

 \Box 4.6 hours

□ 39.5 hours

□ 3.2 days

 $\hfill\square$ None of the proposed answers.

Each shake of the bottle provides: $E = mgh = 0.5 \text{ kg}*10 \text{ m/s}^2*0.3 \text{ m}=1.5 \text{ J}$ Every minute there are 30 shakes: E=30*1.5 J=45 J/min

To almost boil 500 ml of water: $Q = mc(T_{final} - T_{inicial}) = mc\Delta T$ Q(cal) = 500g*1 cal/g*(100-15) = 500*1*85 = ~42500 calE(J) = 42500 cal*4.18 J = ~177650 J

Therefore, the time it takes to shake the jar is: $177650/45 = \sim 3948$ min 3948 min = ~ 65.8 h = ~ 2.7 dias

QUESTIONS ON BIOLOGICAL SCIENCE AND BIOCHEMISTRY (Multiple Choice)

Instructions: The questions on biological science and biochemistry are multiple-choice. For these questions, please indicate your chosen answer directly in this exam booklet by marking the corresponding square with an "X" using a black or blue pen. Do not use this exam booklet for elaborating on your answers or as a draft. You may use the provided Notepaper for developing your answers or as a draft paper. **The answers considered for correction will be the ones marked in the exam booklet.**

Question 1:

The structure and chemical properties of amino acids directly influence the formation and stability of proteins and peptides. Considering these characteristics, which of the following alternatives describes the chemistry of amino acids and their peptides?

- □ The peptide bond has a purely simple character, allowing free rotation around the C–N axis, which facilitates the conformational flexibility of the protein.
- The primary sequence of a protein is responsible for the formation of disulfide bonds, which are stabilized between the side chains of methionine residues.
- The titration of an amino acid with distinct acidic and basic groups, such as lysine, presents two titration stages corresponding to the two ionizable amino groups.
- The acid-base behavior of a polypeptide is influenced by the nature of the amino acid residues, with the side chains of acidic and basic amino acids determining the isoelectric point.
- Aromatic amino acids, such as tyrosine and phenylalanine, are highly soluble in water due to the ability of their side chains to form hydrogen bonds with water molecules.

Correct answer: The acid-base behavior of a polypeptide is influenced by the nature of the amino acid residues, with the acidic and basic amino acid side chains determining the isoelectric point.

Question 2:

The Ramachandran diagram is a fundamental tool for analyzing the possible conformations of proteins. Based on this, which of the following alternatives correctly describes the use of the Ramachandran diagram and its relationship with the secondary structure of proteins?

- The Ramachandran diagram allows the prediction of hydrophobic interactions between amino acid residues in the tertiary structure of proteins.
- The diagram maps the torsion angles φ (phi) and ψ (psi) of peptide bonds, and specific regions of the diagram correspond to the favorable conformations of a-helices and β -sheets.
- □ The allowed regions in the Ramachandran diagram are identical for all types of amino acids, regardless of the size or polarity of the side chains.
- □ Amino acids such as proline are commonly found in regions outside the allowed areas in the diagram due to their high conformational flexibility.
- □ The Ramachandran diagram is useful for predicting protein-ligand interactions by analyzing bond angles in the active site.

Correct answer: The diagram maps the torsion angles φ (phi) and ψ (psi) of peptide bonds, and specific regions of the diagram correspond to favorable conformations of a-helices and β -sheets.

Question 3:

The three-dimensional structure of polysaccharides is complex and determines their biological functions. Considering the interactions and properties of carbohydrates, which of the following alternatives is true regarding the structure and function of polysaccharides?

- □ Cellulose and starch have identical secondary structures, since both are formed by glucose units linked by $a(1\rightarrow 4)$ glycosidic bonds.
- \Box Aldoses have an amino group while ketoses have a carbonyl group.
- In glycogen, branches occur through $a(1\rightarrow 6)$ glycosidic bonds, allowing rapid mobilization of glucose during glycogenolysis.
- The presence of branches in polysaccharides such as starch and glycogen results in lower solubility in water compared to cellulose, due to the greater compaction of the chains.
- \Box Hyaluronic acid, a glycosaminoglycan, is formed by repeating units of disaccharides linked by $\beta(1\rightarrow 3)$ bonds and is involved in energy storage in animals.

Correct answer: In glycogen, branching occurs through $a(1\rightarrow 6)$ glycosidic bonds, allowing rapid mobilization of glucose during glycogenolysis.

Question 4:

Nucleotides have several biological functions, such as providing energy to cells, participating in metabolism, and signaling. Based on this, which of the following statements is correct?

- During DNA replication, DNA polymerase can initiate the synthesis of a new strand without the need for a primer, using free nucleotides directly.
- The base pairing between adenine and thymine is maintained by three hydrogen bonds, making it more stable than the bond between cytosine and guanine.
- In RNA transcription, RNA polymerase uses both magnesium ions (Mg²⁺) and ATP as essential cofactors to catalyze the formation of phosphodiester bonds.
- The double helix structure of DNA is stabilized by hydrophobic interactions between nitrogenous bases and by the presence of metal ions, such as magnesium (Mg²⁺), which neutralize the negative charges of the phosphate backbone.
- \Box DNA is composed of ribose while RNA is composed of deoxyribose.

Correct answer: The double helix structure of DNA is stabilized by hydrophobic interactions between the nitrogenous bases and by the presence of metal ions, such as magnesium (Mg²⁺), which neutralize the negative charges of the phosphate backbone.

Question 5:

Membrane lipids are amphipathic molecules that make up the basic structure of cell membranes. Which of the following alternatives correctly describes the influence of lipids on the structural and functional organization of biological membranes?

- □ The increase in the proportion of saturated fatty acids in membranes increases their fluidity, facilitating protein transport.
- The presence of cholesterol in the membrane of animal cells reduces rigidity, making the membrane more permeable to ions and small molecules.
- Lipid domains, such as lipid rafts, are regions enriched in cholesterol and sphingolipids that play a role in cell signaling and protein trafficking.
- Membrane phospholipids are static, not moving laterally within the bilayer, which ensures the necessary structural rigidity.
- □ The lipid composition of a membrane does not affect the function of integral proteins, since these depend only on interactions with other proteins for their activity.

Correct answer: Lipid domains, such as lipid rafts, are regions enriched in cholesterol and sphingolipids that play a role in cell signaling and protein trafficking.