NAME: ROLL NO:

LS2103. Class Test-2. 24.10.2024 Time: 20 MINUTES. Clearly tick ONLY ONE OPTION (single right answer). Negative marks for wrong/ambiguous selection.

Use back page for any rough work.

- 1. Consider a protein system that can occupy one "active" (named A) state, and three different "inactive" (named I<sub>1</sub>, I<sub>2</sub>, I<sub>3</sub>) states. The *disorder* (or entropy) will be zero when:
- a) I<sub>1</sub>, I<sub>2</sub> and I<sub>3</sub> are identical
- b) 'A' is the only occupied state
- c) All four states are uniformly occupied
- d) Temperature is elevated by 10 K
- 2. A large number of protein molecules are tagged and their movements are monitored over a total time, *T*.
- a) The mean distance covered increases with protein size
- b) The distances covered should follow a Gaussian distribution centered at 0
- c) The squared distances covered should follow a Gaussian distribution centered at 0
- d) Only the positions of the protein molecules with time are required for estimating the diffusion coefficient
- 3. At a constant temperature, the diffusivity of free particles in a particular solvent medium is:
- a) Proportional to the viscous friction coefficient of the medium
- b) Proportional to the temperature
- c) Independent of thermal conditions
- d) Dependent on number of particles
- 4. The Stokes-Einstein relationship:
- a) Connects medium viscosity and particle diffusivity at constant temperature
- b) Is disconnected to the spatial dimensions
- Is disconnected to the movement of individual particles
- d) Connects medium viscosity and particle diffusivity at constant pressure
- 5. A large amino acid sequence (ie. a protein) emerges from the ribosome as a disordered chain. It takes some time to acquire the functionally folded form.
- a) The final end-to-end distances are all identical
- b) The final end-to-end distances obey a Normal distribution
- c) The final, mean squared end-to-end distances are independent of the number of amino acids
- d) The amino acids are assumed to be connected with highly non-uniform bonds