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Paper Name: Proteomics and Metabolomics
Time: 2.5 Hours

Paper Code: MCSB DSE22
Maximum Marks: 60

Section A

Q.No.	Question	Marks	CO	BL
1.	What are theoretical plates in high performance liquid chromatography column? Why having high plate number gives better resolution in HPLC?	4	CO4	BL1, BL3
2.	Explain the followings: - Targeted metabolomics and untargeted metabolomics - What is a Mass analyser with at least two examples. - What do you understand by good and poor separation in HPLC	4	CO2	BL1, BL2
3.	What is time of flight mass spectrometry? what is the relationship between time of flight, t , and m/q (mass/charge) in time-of-flight mass analyser.	4	CO1	BL2, BL5
4.	Explain the following with reference to column chromatography: - Retention time - dead time - capacity factor - what is the major cause of peak broadening.	4	CO4	BL1 BL4
5.	A particle is traveling through a mass spectrometer in a region of space where the electric field is 1,500 V/m and magnetic field 0.034T. The magnetic and electric force exactly balances one another out so it follows a straight path. Calculate the speed of the particle.	4	CO3	BL4

Section B

Note: Attempt any four.

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1.	Calculate the following Mass of Alanine (till two decimal points) for with the help of given table: • Average Mass • Nominal Mass • Exact Mass • Mass Defect <table><thead><tr><th>Isotope</th><th>Mass [Da]</th><th>Nat. abundance [%]</th><th>Isotope</th><th>Mass [Da]</th><th>Nat. abundance [%]</th></tr></thead><tbody><tr><td>¹H</td><td>1.007 825 0322(6)</td><td>99.985</td><td>¹⁶O</td><td>15.994 914 620(2)</td><td>99.76</td></tr><tr><td>²H</td><td>2.014 101 7781(8)</td><td>0.015</td><td>¹⁷O</td><td>16.999 131 757(5)</td><td>0.038</td></tr><tr><td>¹²C</td><td>12 (exact)</td><td>98.90</td><td>¹⁸O</td><td>17.999 159 613(6)</td><td>0.2</td></tr><tr><td>¹³C</td><td>13.003 354 835(2)</td><td>1.1</td><td>³¹P</td><td>30.973 761 998(5)</td><td>100</td></tr><tr><td>¹⁴N</td><td>14.003 074 004(2)</td><td>99.63</td><td>³²S</td><td>31.972 071 174(9)</td><td>95.02</td></tr><tr><td>¹⁵N</td><td>15.000 108 899(4)</td><td>0.37</td><td>³³S</td><td>32.971 458 910(9)</td><td>0.75</td></tr><tr><td></td><td></td><td></td><td>³⁴S</td><td>33.967 8670(3)</td><td>4.21</td></tr></tbody></table>	Isotope	Mass [Da]	Nat. abundance [%]	Isotope	Mass [Da]	Nat. abundance [%]	¹ H	1.007 825 0322(6)	99.985	¹⁶ O	15.994 914 620(2)	99.76	² H	2.014 101 7781(8)	0.015	¹⁷ O	16.999 131 757(5)	0.038	¹² C	12 (exact)	98.90	¹⁸ O	17.999 159 613(6)	0.2	¹³ C	13.003 354 835(2)	1.1	³¹ P	30.973 761 998(5)	100	¹⁴ N	14.003 074 004(2)	99.63	³² S	31.972 071 174(9)	95.02	¹⁵ N	15.000 108 899(4)	0.37	³³ S	32.971 458 910(9)	0.75				³⁴ S	33.967 8670(3)	4.21	10	CO2	BL1 BL4
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2.	What is electron spray ionization (ESI) method? Explain the difference between soft ionization and hard ionization methods. When do we prefer positive and negative mode of ESI?	10	CO1	BL1 BL2 BL3																																																
3.	What do you understand by metabolic modelling? How do you construct a genome scale metabolic model of a species from its gene sequences?	10	CO3	BL2 BL4 BL5																																																
4.	How would you identify and quantify the proteins present in a sample with the help of mass spectrometry?	10	CO4	BL3																																																
5.	How yeast two hybrid system and protein fragment complementation assay are used to study protein-protein interaction?	10	CO2	BL1 BL3																																																
6.	What are different approaches in proteomics? Explain shotgun proteomics and peptide mass fingerprinting for identifying proteins present in a sample with the help of mass spectrometry.	10	CO3	BL1 BL2 BL3																																																