Zoology Legends

BIF401

Quiz No.3 Spring 2023

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Question # 1 of 5 (Start time: 10:09:26 AM, 16 July 2023) **Total Marks:** 1

The peptide sequence tags are .....

Select the correct option

Reload Math Equations

- ( ) The partial sequence of a peptide that can be revealed by consecutive peaks
- ( ) The variation in the fragmentation site of a peptide
- ( ) The mass difference between consecutive peaks in a peptide sequence
- (•) The sequence of a peptide that is produced after MS2

Click to Save Answer & Move to Next Question

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Draw | Read aloud | peptide sequence 1/15

$$M_b + M_y = R_P + \langle N \rangle + \langle C \rangle + 2H \ (= M_P + 2H)$$

$$M_a + M_x = R_P + \langle N \rangle - CO + \langle C \rangle + CO \ (= M_P)$$

$$M_c + M_z = R_P + \langle N \rangle + N + 3H + \langle C \rangle - N - H \ (= M_P + 2H)$$

Figure 22 Masses after Fragmentation by ECD

132 Peptide Sequence Tags

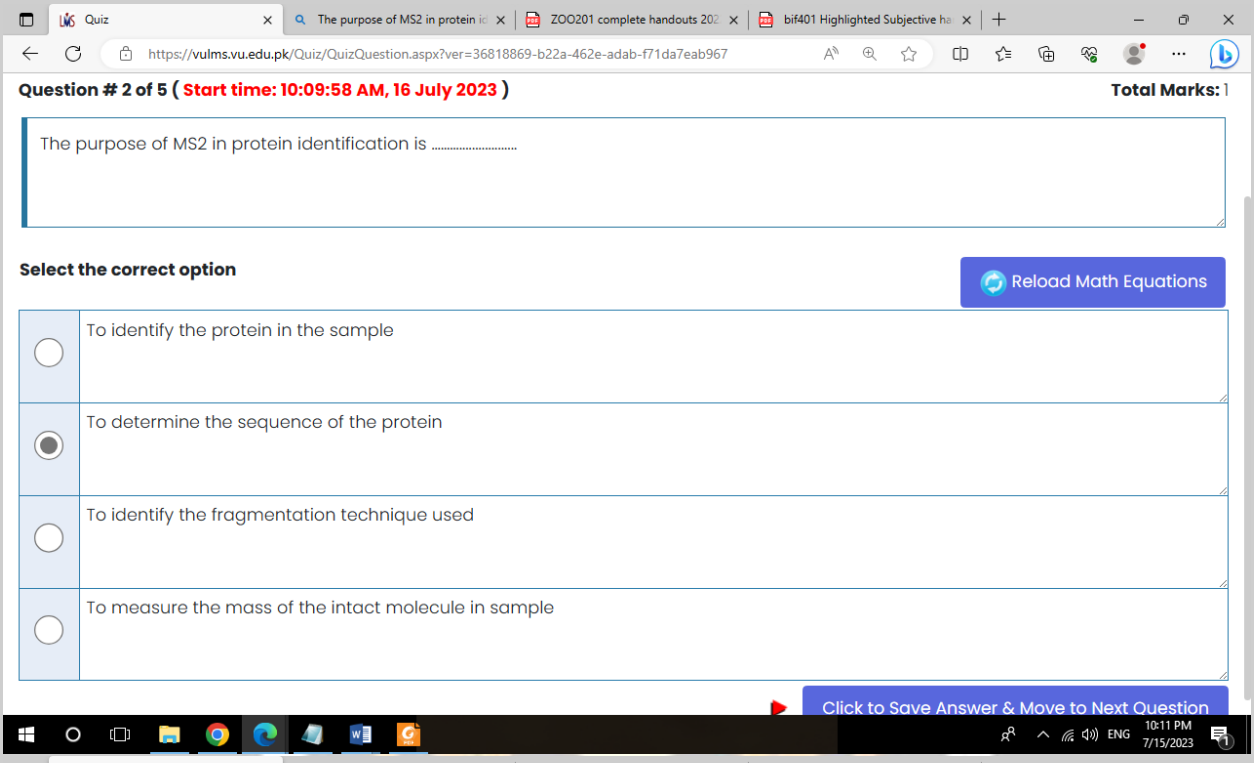
Peptide sequence tag are the sequence of peptide which are produced after MS2. We can obtain the sequence of peptide through variation in fragmentation site.

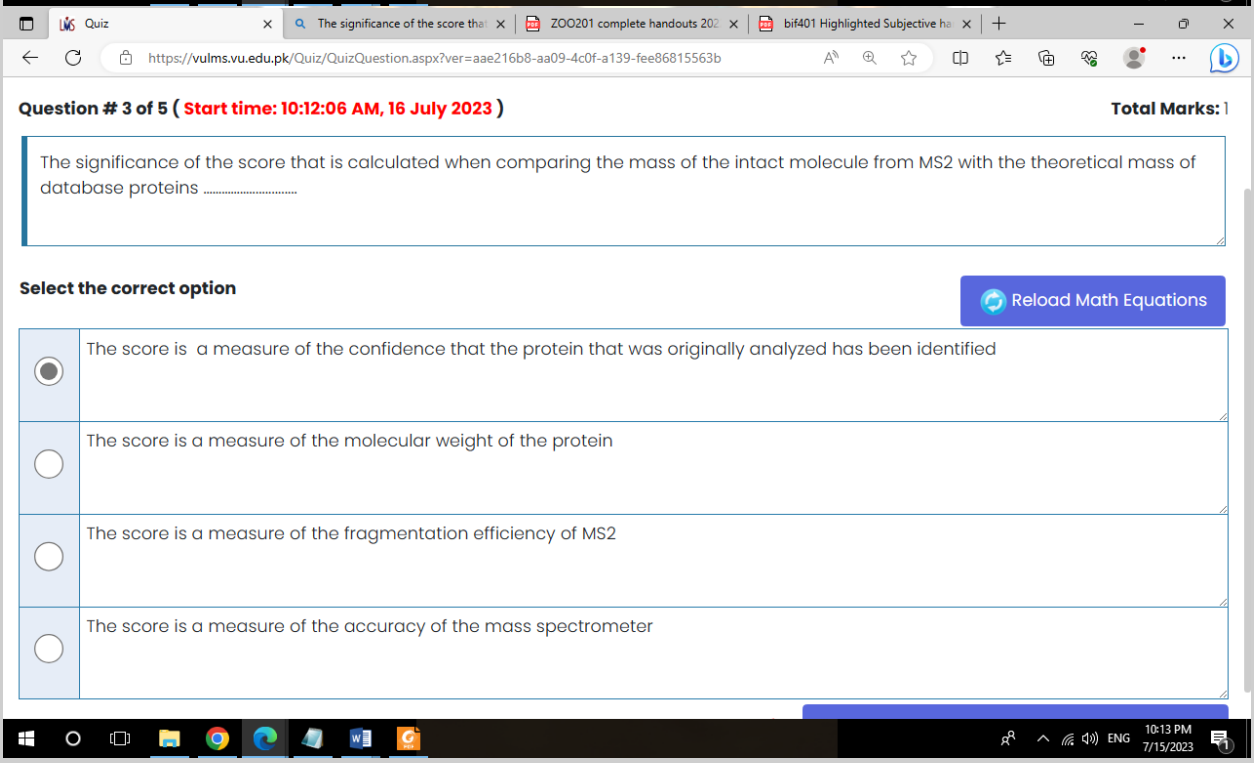
Mass Select: [375.0 , 377.0]
Protein Sequence: **"MQV..."**
Fragments formed may be **M, MQ, QV** etc.

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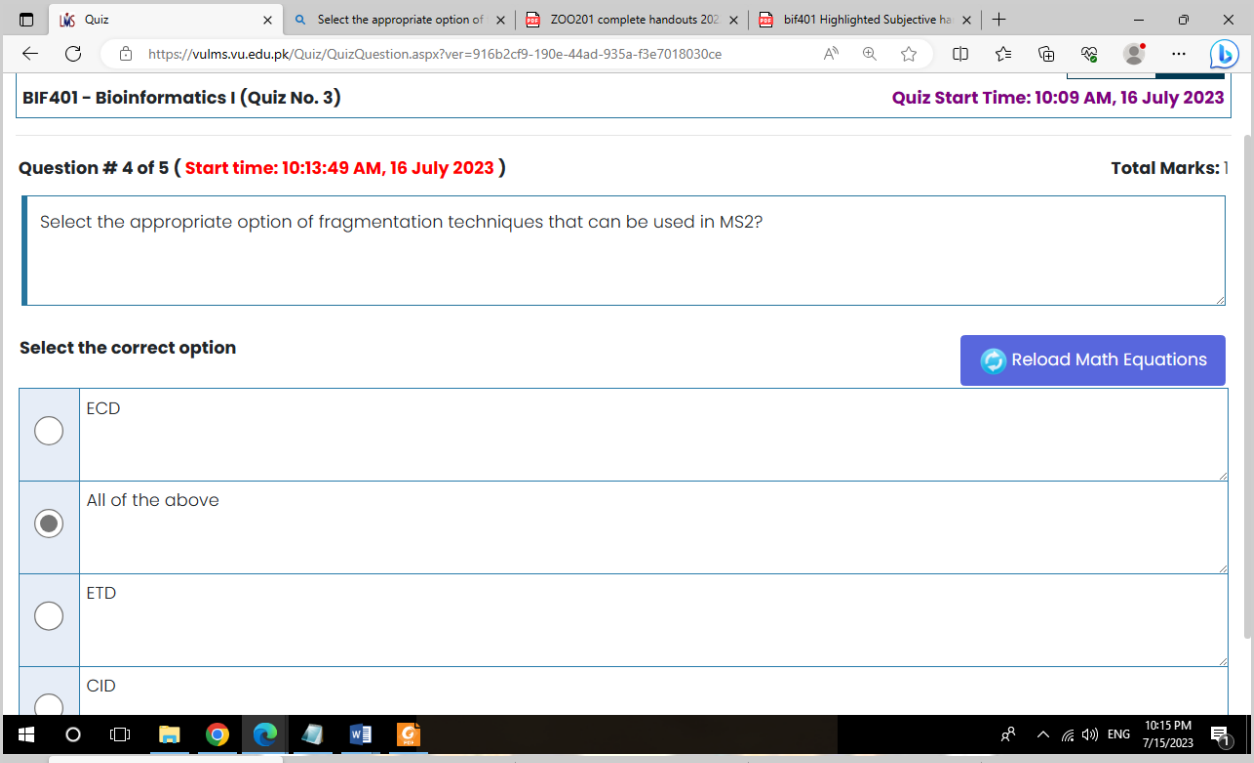
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BIF401 - Bioinformatics I (Quiz No. 3) **Quiz Start Time: 10:09 AM, 16 July 2023**

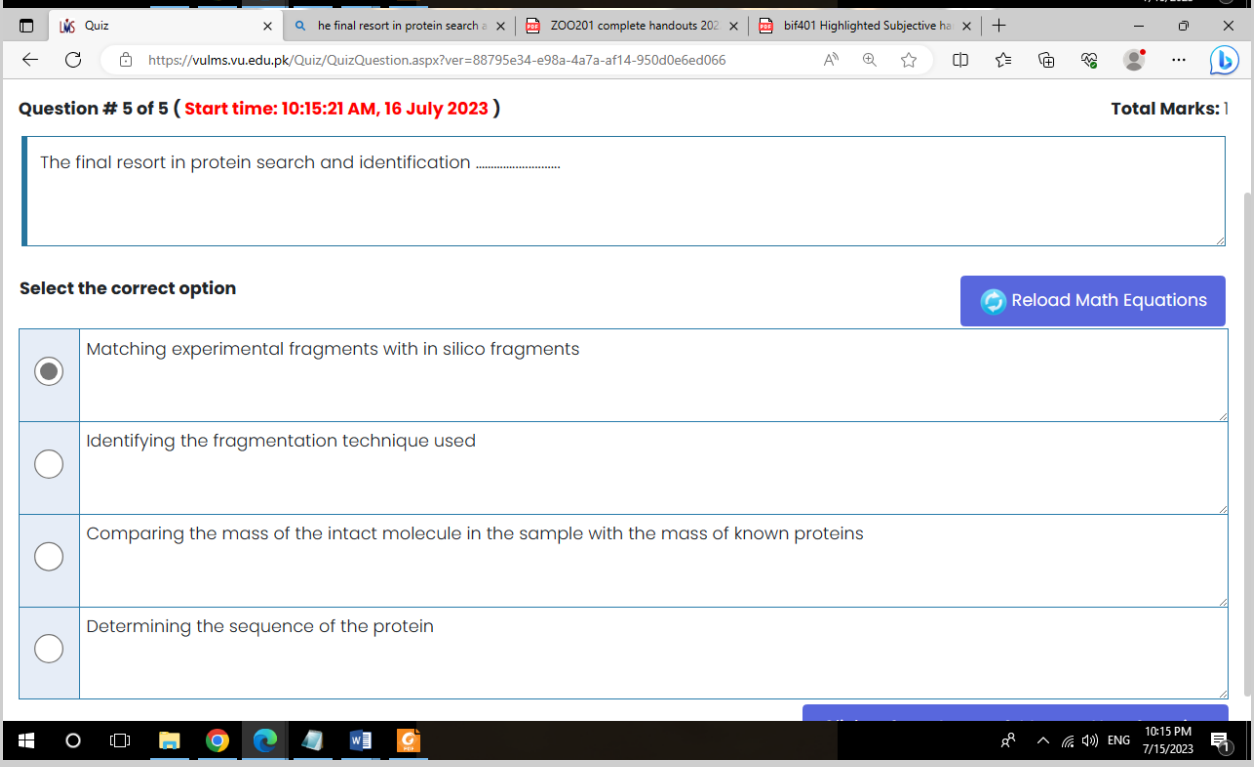
Question # 4 of 5 (Start time: 10:13:49 AM, 16 July 2023) **Total Marks:** 1

Select the appropriate option of fragmentation techniques that can be used in MS2?

Select the correct option

Reload Math Equations

- ○ ECD
- ● All of the above
- ○ ETD
- ○ CID



Quiz | he final resort in protein search | ZOO201 complete handouts 202 | bif401 Highlighted Subjective ha

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Question # 5 of 5 (Start time: 10:15:21 AM, 16 July 2023) **Total Marks:** 1

The final resort in protein search and identification .....

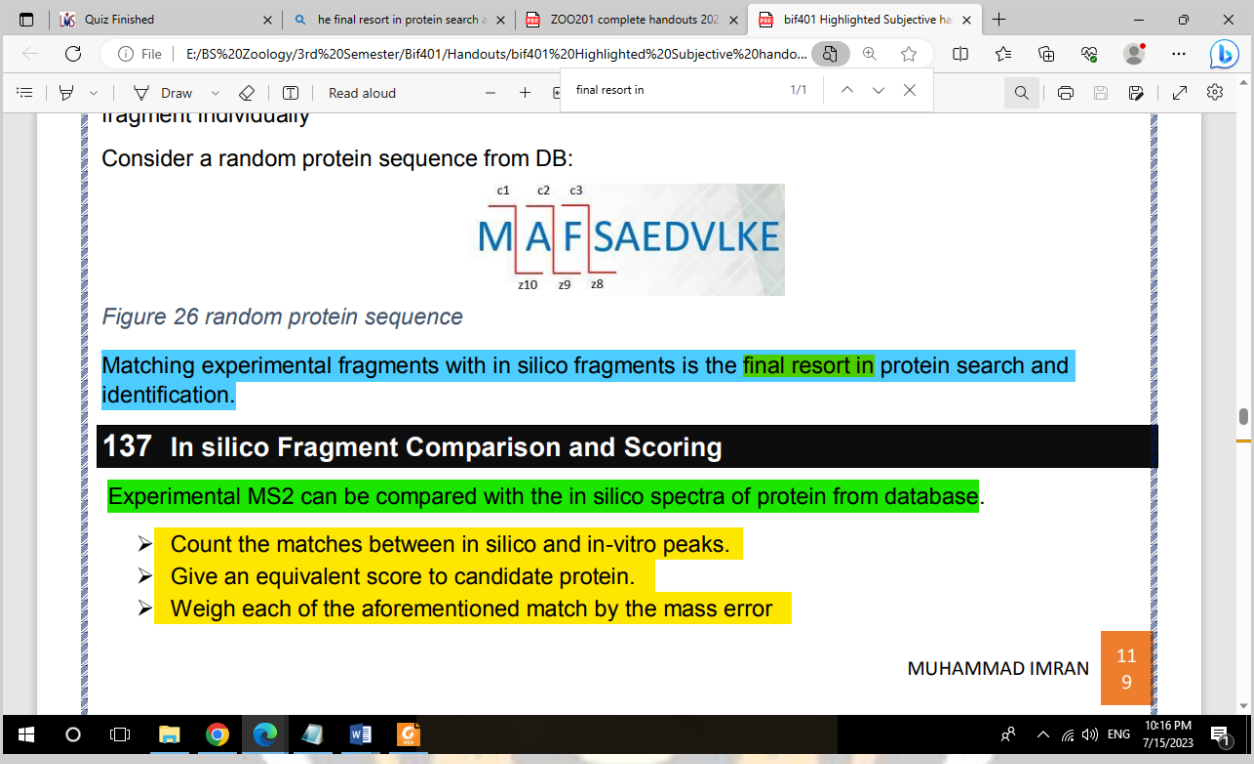
Select the correct option

Reload Math Equations

- ● Matching experimental fragments with in silico fragments
- ○ Identifying the fragmentation technique used
- ○ Comparing the mass of the intact molecule in the sample with the mass of known proteins
- ○ Determining the sequence of the protein

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Draw | Read aloud | final resort in 1/1

fragment individually

Consider a random protein sequence from DB:

Figure 26 random protein sequence

Matching experimental fragments with in silico fragments is the final resort in protein search and identification.

137 In silico Fragment Comparison and Scoring

Experimental MS2 can be compared with the in silico spectra of protein from database.

- Count the matches between in silico and in-vitro peaks.
- Give an equivalent score to candidate protein.
- Weigh each of the aforementioned match by the mass error

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Remember me in you Precious Prayer

Jazak Allah

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