

## Supplemental Figure 1

### (A) 5 ms ETD only

ID/Gene	Length	Mass	Mass Diff.	PPM Diff.	C Ions	Z Ions	Total Ions	PDE Score	E-Value
▶ >sp P68082 MYG_HORSE Myoglobin OS=Equus caballus GN=MB PE=1 SV=2, ; . (Type: <i>basic</i> , Signal Peptide: <i>false</i> , Propep: <i>false</i> )									
1	1	16941	12.9262	762.433	56	44	100	121	6.42E-14

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1  G L S D G E W Q Q V L N V W G K V E A D I A G H G Q E V L I z124
31 R L F T T G H P E T T L E K F D K F K H L K T T E A E M K A S E D z94
61 L K K H G T V V L T A L G G I L K K K G H H E A E L K P L A z64
91 Q S H A T K H K I P I K Y L E F I S D A I I H V L H S K H P z34
121 G D F G A D A Q G A M T K A L E L F R N D I A A K Y K E L G z4
151 F Q G z1
  
```

### (B) 5 ms ETD + 20 ms IIPT

ID/Gene	Length	Mass	Mass Diff.	PPM Diff.	C Ions	Z Ions	Total Ions	PDE Score	E-Value
▶ >sp P68082 MYG_HORSE Myoglobin OS=Equus caballus GN=MB PE=1 SV=2, ; . (Type: <i>basic</i> , Signal Peptide: <i>false</i> , Propep: <i>false</i> )									
1	1	16941	12.9262	762.433	67	64	131	124	2.12E-14

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1  G L S D G E W Q Q V L N V W G K V E A D I A G H G Q E V L I z124
31 R L F T T G H P E T T L E K F D K F K H L K T T E A E M K A S E D z94
61 L K K H G T V V L T A L G G I L K K K G H H E A E L K P L A z64
91 Q S H A T K H K I P I K Y L E F I S D A I I H V L H S K H P z34
121 G D F G A D A Q G A M T K A L E L F R N D I A A K Y K E L G z4
151 F Q G z1
  
```

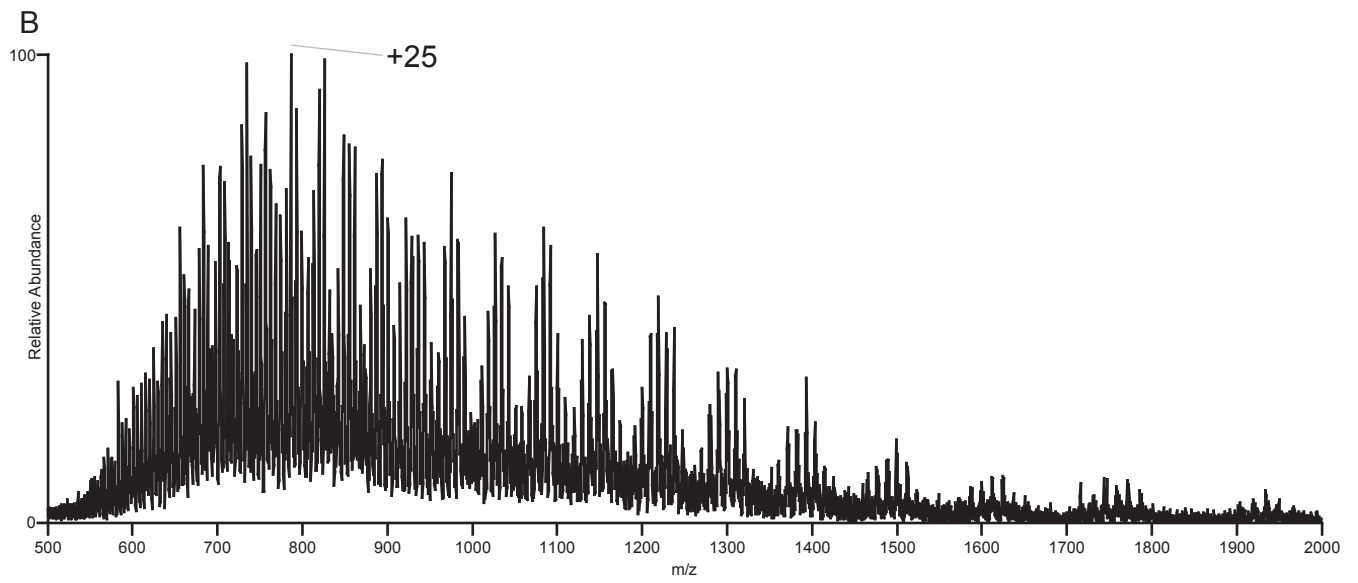
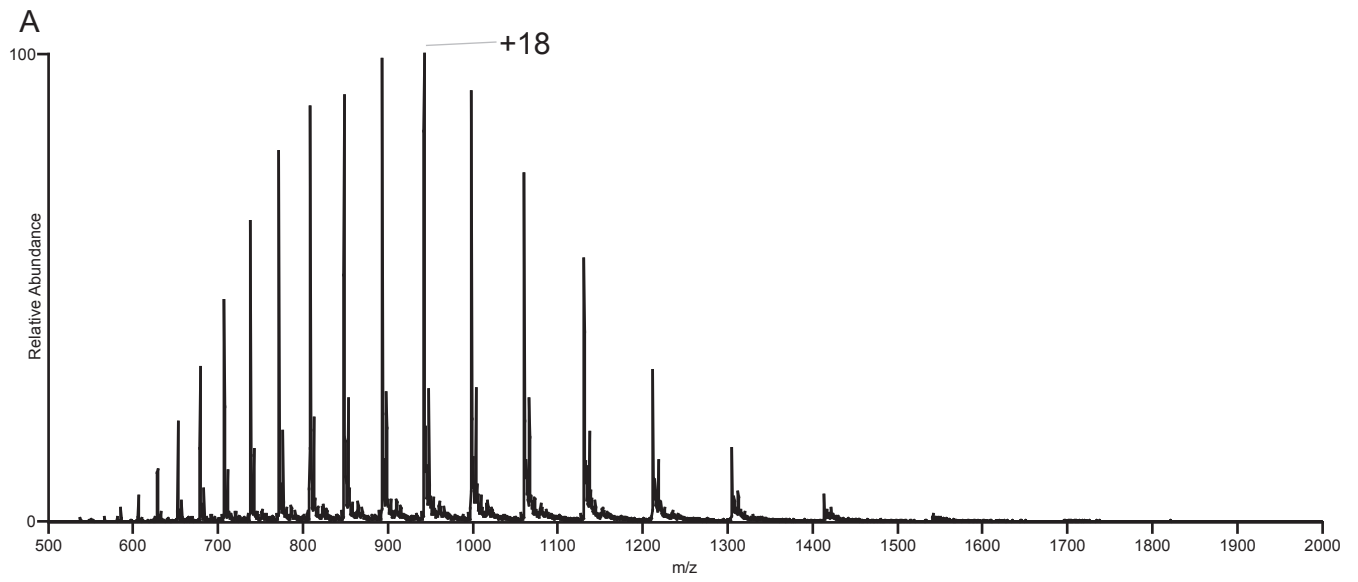
### (C) 5 ms ETD + 40 ms IIPT

ID/Gene	Length	Mass	Mass Diff.	PPM Diff.	C Ions	Z Ions	Total Ions	PDE Score	E-Value
▶ >sp P68082 MYG_HORSE Myoglobin OS=Equus caballus GN=MB PE=1 SV=2, ; . (Type: <i>basic</i> , Signal Peptide: <i>false</i> , Propep: <i>false</i> )									
1	1	16941	12.9262	762.433	77	73	150	145	4.01E-24

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1  G L S D G E W Q Q V L N V W G K V E A D I A G H G Q E V L I z124
31 R L F T T G H P E T T L E K F D K F K H L K T T E A E M K A S E D z94
61 L K K H G T V V L T A L G G I L K K K G H H E A E L K P L A z64
91 Q S H A T K H K I P I K Y L E F I S D A I I H V L H S K H P z34
121 G D F G A D A Q G A M T K A L E L F R N D I A A K Y K E L G z4
151 F Q G z1
  
```

# Supplemental Figure 2



## Supplemental Figure Legends

**Supplemental Figure 1 – Apomyoglobin sequence coverage determined by analysis of ETD and ETD/IIPT MS/MS spectra with ProSight PC™ software.** (A) Sequence coverage from 5 msec of ETD only. (B) Sequence coverage from 5 msec of ETD & 20 msec of IIPT. (C) Sequence coverage from 5 msec of ETD & 40 msec of IIPT. Searches were performed by using ProSightPC 3.0 (Thermo Fisher Scientific). Fragment mass tolerance was set to 2 Da.

**Supplemental Figure 2 – Electrospray Ionization mass spectra of unmodified and modified apomyoglobin.** Distribution of charge states observed for (A) apomyoglobin, and (B) apomyoglobin derivatized with aminoethylbenzimidazole.