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1  MPYQYPALTP  EQKKELSDIA  HRIVAPGKGI  LADESTGSI  AKRLQSIGTE
51  NTEENRRFYR  QLLLTADDRV  NPCIGGVILF  HETLYQKADD  GRPFPQVIKS
101 KGGVVGIVVD  KGVVPLAGTN  GETTTQGLDG  LSERCAQYKK  DGADFAKWRC
151 VLKIGEHTPS  ALAIMENANV  LARYASICQQ  NGIVPIVEPE  ILPDGDHDLK
201 RCQYVTEKVL  AAVYKALSDH  HIYLEGTLK  PNMVTPGHAC  TQKFSHEEIA
251 MATVTALRRT  VPPAVTGITF  LSGGQSEEEA  SINLNAINKC  PLLKPWALTF
301 SYGRALQASA  LKAWGGKKEN  LKAAQEYVVK  RALANSLACQ  GKYTSPGQAG
351 AAASESLFVS  NHAY

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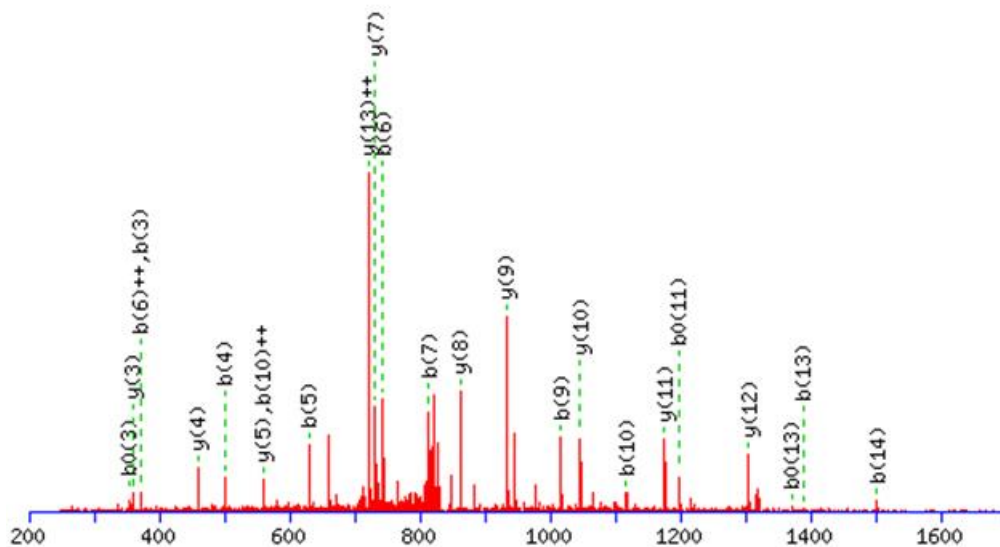
B

Figure 1: Peptide sequence data from actin cytoplasmic 1 (ACT B) showing (A) a representation of the ACT B tryptic digest peptide sequence that were identified in highlighted red, and (B) an example of the ACT B peptide fragmentation spectra with lead ions shown as red lines. These represent the fragmentation spectra where (b) ions represent a fragmentation from the amine-terminus and (y) ions are a representation of fragmentation from the carboxyl-terminus of the protein [68].

A

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1  MDDIAALVV  DNGSGMCKAG  FAGDDAPRAV  FPSIVGRPRH  QGVMVGMGQK
51  DSYVGDEAQS  KRGILTLYKYP  IEHGIVTNWD  DMEKIWHHTF  YNELRVAPPE
101  HPVLLTEAPL  NPKANREKMT  QIMFETFNTP  AMYVAIQAVL  SLYASGRITG
151  IVMDSGDGVV  HTVPIYEGYA  LPHAILRLDL  AGRDLTDYLM  KILTERGYSF
201  TTTAEREIVR  DIKEKLCYVA  LDFEQEMATA  ASSSSLEKSY  ELPDGQVITI
251  GNERFRCPEA  LFQPSFLGME  SCGIHETTFN  SIMKCDVDIR  KDLYANTVLS
301  GGTTPYPIA  DRMQKEITAL  APSTMKIKII  APPERKYSVW  IGGSILASLS
351  TFQQMWISKQ  EYDESGPSIV  HRKCF

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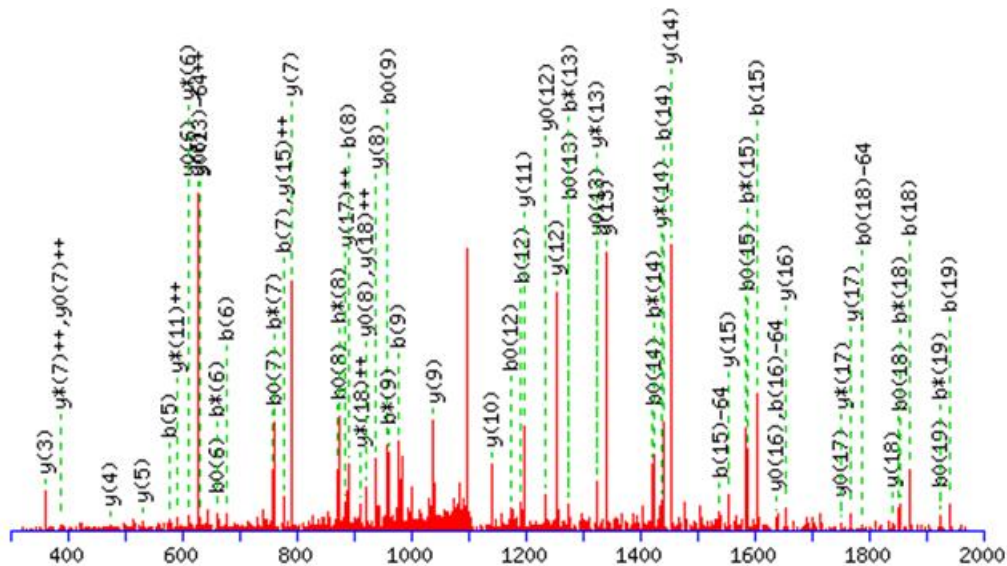
B

Figure 2: Peptide sequence data from fructose biphosphaste aldolase 1 (ALDO A) showing (A) a representation of the ALDO A tryptic digest peptide sequence that were identified in highlighted red, and (B) an example of the ALDO A peptide fragmentation spectra with lead ions shown as red lines. These represent the fragmentation spectra where (b) ions represent a fragmentation from the amine-terminus and (y) ions are a representation of fragmentation from the carboxyl-terminus of the protein [68].

A

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1 MASGVAVSDG VIKVFNDMKV RKSSTPEEVK KRKKAVLFCL SEDKKNIILE
51 EGKEILVGDV GQTVDDPYAT FVKMLPDKDC RYALYDATYE TKESKKEDLV
101 FIFWAPESAP LKSKMIYASS KDAIKKLTG IKHELQANCY EEVKDRCTLA
151 EKLGSAVIS LEGKPL

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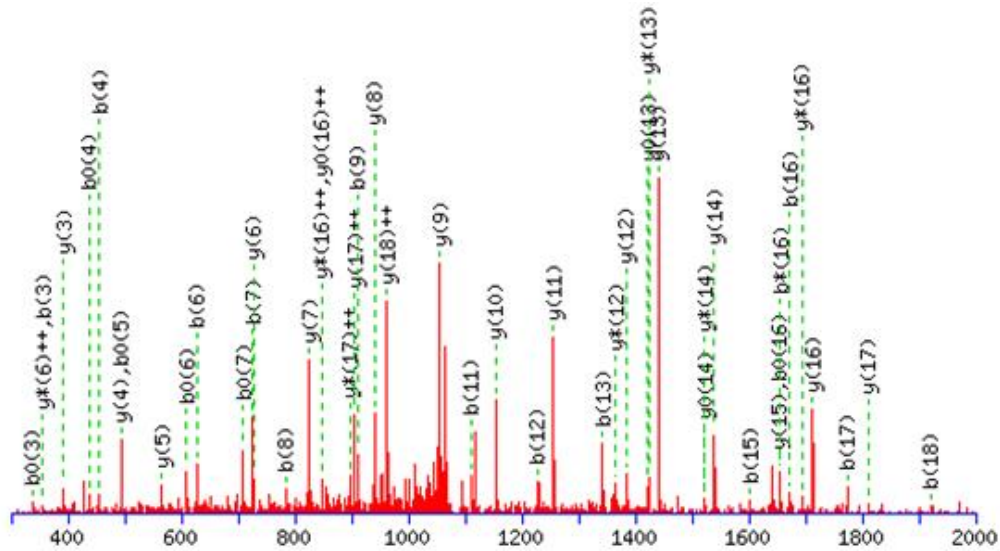
B

Figure 3: Peptide sequence data from cofilin 1 (CFL 1) showing (A) a representation of the CFL 1 tryptic digest peptide sequence that were identified in highlighted red, and (B) an example of the CFL 1 peptide fragmentation spectra with lead ions shown as red lines. These represent the fragmentation spectra where (b) ions represent a fragmentation from the amine-terminus and (y) ions are a representation of fragmentation from the carboxyl-terminus of the protein [68].

A

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1 MAGWNAVYIDN LMADGICQDA AIVGYKDSPS VWAAVPGKTF VNITPAEYGV
51 LVGKDRSSFY VNGLTLGGQK CSVIRDSLLQ DGEFSMDLRT KSTGGAPTFN
101 VTVTKIDKTL VLLMGKEGVH GGLINKKCYE MASHLRRSQY
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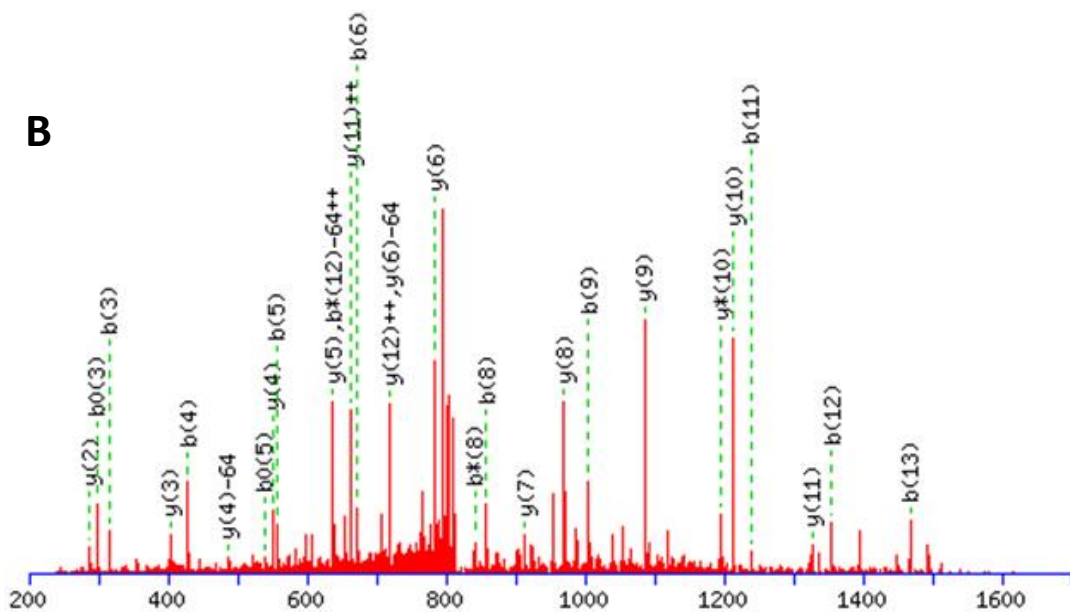
B

Figure 4: Peptide sequence data from profilin 1 (PFN 1) showing (A) a representation of the PFN 1 tryptic digest peptide sequence that were identified in highlighted red, and (B) an example of the PFN 1 peptide fragmentation spectra with lead ions shown as red lines. These represent the fragmentation spectra where (b) ions represent a fragmentation from the amine-terminus and (y) ions are a representation of fragmentation from the carboxyl-terminus of the protein [68].