Protein identification

retention time

"Big 5" method

MS1 scans (whole peptides = *precursor ions*)

MS2 scans (peptide fragments = *fragment ions*)

AAEK
AEAEAAPAAAK
AQTEEFYVITWEAK
ASSR
AVVVR
EQCLALTTQLR
EQIFEMPTGGAAIMR
FGK
FSGR
IGQNVNPIK
LTPCFYR
MMSPAEI
NKFK
PAAR
PAWTVPTLNPDTPSPIFGGSTGGLLR
QGPNLLK
TQAPAATR
VAVAAR
VFPDGK
VGANQNMR
VQYLHPADGVYPEK
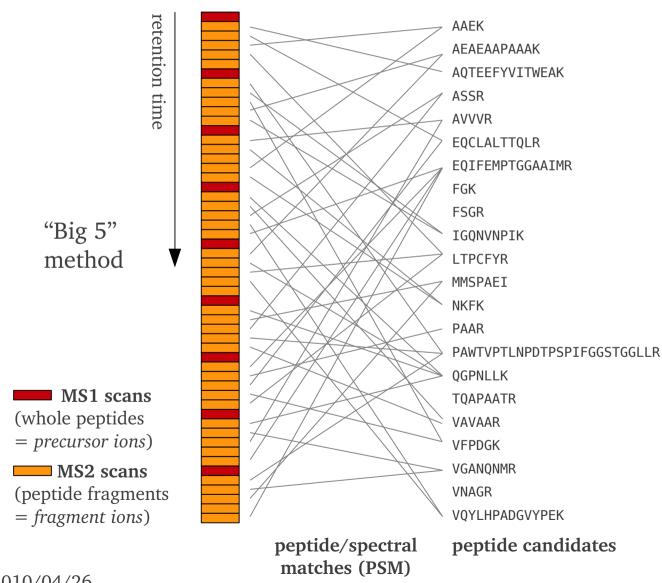
>PsaD
MRTQAPAATRASSRVAVAARPAARRAVVVRAEAEA
APAAAKKAAEKPAWTVPTLNPDTPSPIFGGSTGGL
LRKAQTEEFYVITWEAKKEQIFEMPTGGAAIMRQG
PNLLKFGKKEQCLALTTQLRNKFKLTPCFYRVFPD
GKVQYLHPADGVYPEKVNAGRVGANQNMRRIGQNV
NPIKVKFSGRMMSPAEI*
>LhcSR3
GVFDPAGFLATASIKDVRRWRESEITHGRVAMLAA
LGFVVGEQLQDFPLFFNWDGRVSGPAIYHFQQIGQ
GFWEPLLIAIGVAESYRVAVGWATPTGTGFNSLKD
DYEPGDLGFDPLGLKPTDPEELKVMQTKELNNGRL
AMIAIAAFVAQELVEQTEIFEHLALRFEKEAILEL
DDIERDLGLPVTPLPDNLKSL*

protein database

in silico digestion

peptide/spectral matches (PSM)

peptide candidates