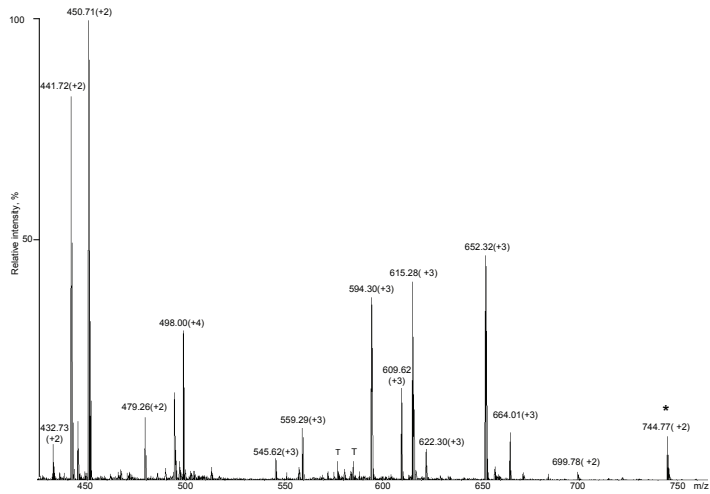
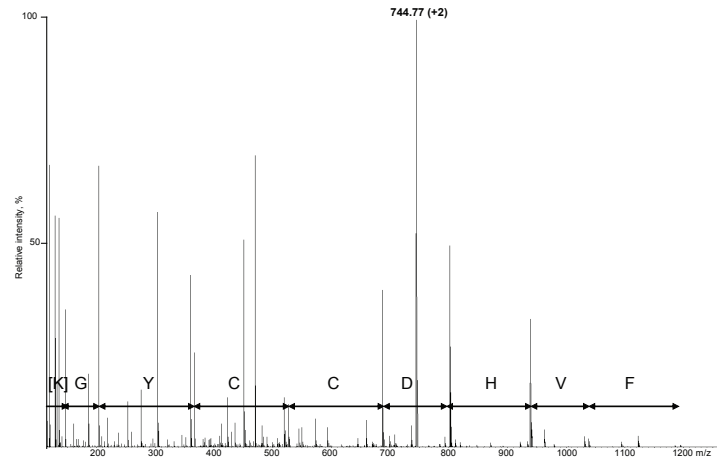


A**B****C**

m/z 652(+2): -BYFSYGCYCGLGGQGPR-GSYGCYCLGGL
 m/z 699(+2): -BXXFVHDCCYGK
 m/z 744(+2): -BXXXFVHDCCYGK
 m/z 545(+3): -BXXKDTYNLQYWLYQK-BXXKDTYNLKYWLYAGK
 m/z 664(+2): -BLTYNLQYWLYQK-BLTYNLKYWLYAGK
 m/z 479(+2): -BYGEGLYQK-BYGEGLYAGK
 m/z 441(+2): -BVVTTCFR
 m/z 432(+2): -BVAVLCFR
 m/z 615(+3): -BQLCECFVA
 m/z 609(+3): -BXXCECFV
 m/z 594(+3): -BXXLWQFGT

D

Q8QG87 Phospholipase A2 BITP01A(EC 3.1.1.4), Length = 138
 Total Score: 391

Score = 106
 Query: 2 BYFSYGCYCGLGGQGPR 19
 +YF YGCYCG GG+GQPR
 Sbjct: 36 KYFYYGICYCGWGGIGQPR 53

Score = 103
 Query: 87 BXXKDTYNLKYWLYGAK 103
 + KDTY+ KYWLYGAK
 Sbjct: 113 RDNKDTYDMKYWLYGAK 129

Score = 81
 Query: 43 BXXFVHDCCYGK 54
 + FVHDCCYGK
 Sbjct: 58 RCCFVHDCCYGK 69

Score = 58
 Query: 169 BQLCECFVA 178
 +Q+CECD VA
 Sbjct: 99 KQICECDRVA 108

Score = 43
 Query: 151 BVVTTCFR 158
 +V TCFR
 Sbjct: 106 RVAATCFR 113