



Peptides detected by MS/MS

MQVSRVLAAL CGMLLCASGL FAASGDFCDS SLCLNGGTCL TGQDNDIYCL 050
 -----|-----|-----E1-----
 CPEGFTGLVC NETERGPCSE NPCYNDKCL VTLDTQRGDI FTEYICQCPV 100
 -----|-----|-----E2-----
 GYSGIHCETE TNYYNLDGEY MFTTAVPNTA VPTPAPTPDL SNNLASRCST 150
 -----|-----|-----C1-----
 QLGMEGGAIA DSQISASSVY MGFMLQRWG PELARLYRTG IVNAWTASNY 200
 -----|-----|-----
 DSKPWIQVNL LRKMRVSGVM TQGASRAGRA EYLKTFKVAY SLDGRKFEFI 250
 -----|-----|-----
 QDESGGDKEF LGNLDNNSLK VNMFNPTLEA QYIKLYPVSC HRGCTLRFEL 300
 -----|-----|-----C2-----
 LGCELHGCSE PLGLKNNTIP DSQMSASSY KTWNLRAFGW YPHLGRLDNQ 350
 -----|-----|-----Medin-----
 GKINAWTAQS NSAKEWLQVD LGTQRQVTGI ITQGARDFGH IQYVASYKVA 400
 -----|-----|-----
 HSDDGVQWTV YEEQGSSKVF QGNLDNNSHK KNIFEKPFMA RYVRVLPVSW 450
 -----|-----|-----
 HNRITLRLEL LGC

Domain structure and coverage of the murine MFG-E8 sequence and the peptides detected by mass spectrometry. Yellow blocks indicate sequences covered with peptides found in MS/MS runs.