α chain

Signal peptide

```
  1 MFSMRIVCLV LSVVGTAWTA DSGEGDFLAE GGGVRGPRVV ERHQSACKDS
 51 DWPFCSDEDW NYKCPSGCRM KGLIDEVNQD FTNRINKLKN SLFEYQKNNK
101 DSHSLTTNIM EILRGDFSSA NNRDNTYNRV SEDLRSRIEV LKRKVIEKVQ
151 HIQLLQKNVR AQLVDMKRLE VDIDIKIRSC RGSCSRALAR EVDLKDYEDQ
201 QKQLEQVIAK DLLPSRDRQH LPLIKMKPVP DLVPGNFKSQ LQKVPPEWKA
251 LTDMPQMRME LERPGGNEIT RGGSTSYGTG SETESPRNPS SAGSWNSGSS
301 GPGSTGNRNP GSSGTGGTAT WKPGSSGPGS TGSWNSGSSG TGSTGNQNPG
351 SPRPGSTGTW NPGSSERGSA GHWTSESSVS GSTGQWHSES GSFRPDSPGS
401 GNARPNNPDW GTFEEVSGNV SPGTRREYHT EKLVTSKGDK ELRTGKEKVT
451 SGSTTTTRRS CSKTVTKTVI GPDGHKEVTK EVVTSEDGSD CPEAMDLGTL
501 SGIGTLDGFR HRHPDEAAFF DTASTGKTFP GFFSPMLGEF VSETESRGSE
551 SGIFTNTKES SSHHPGIAEF PSRGKSSSYS KQFTSSTSYN RGDSTFESKS
601 YKMADEAGSE ADHEGTHSTK RGHAKSRPVR GIHTSPLGKP SLSP
```

→ Absent from the α-chain of circulating fibrinogen

Legend:
═══ Identified as semi-tryptic
···· Potential N-glycosylation site

β chain

Signal peptide

```
  1 MKRMVSWSFH KLKTMKHLLL LLLCVFLVKS QGVNDNEEGF FSARGHRPLD
 51 KKREEAPSLR PAPPPISGGG YRARPAKAAA TQKKVERKAP DAGGCLHADP
101 DLGVLCPTGC QLQEALLQQE RPIRNSVDEL NNNVEAVSQT SSSSFQYMYL
151 LKDLWQKRQK QVKDNENVVN EYSSELEKHQ LYIDETVNSN IPTNLRVLRS
201 ILENLRSKIQ KLESDVSAQM EYCRTPCTVS CNIPVVSGKE CEEIIRKGGE
251 TSEMYLIQPD SSVKPYRVYC DMNTENGGWT VIQNRQDGSV DFGRKWDPYK
301 QGFGNVATNT DGKNYCGLPG EYWLGNDKIS QLTRMGPTEL LIEMEDWKGD
351 KVKAHYGGFT VQNEANKYQI SVNKYRGTAG NALMDGASQL MGENRTMTIH
401 NGMFFSTYDR DNDGWLTSDP RKQCSKEDGG GWWYNRCHAA NPNGRYYWGG
451 QYTWDMAKHG TDDGVVWMNW KGSWYSMRKM SMKIRPFFPQ Q
```

γ chain

Signal peptide

```
  1 MSWSLHPRNL ILYFYALLFL SSTCVAYVAT RDNCCILDER FGSYCPTTCG
 51 IADFLSTYQT KVDKDLQSLE DILHQVENKT SEVKQLIKAI QLTYNPDESS
101 KPNMIDAATL KSRKMLEEIM KYEASILTHD SSIRYLQEIY NSNNQKIVNL
151 KEKVAQLEAQ CQEPCKDTVQ IHDITGKDCQ DIANKGAKQS GLYFIKPLKA
201 NQQFLVYCEI DGSGNGWTVF QKRLDGSVDF KKNWIQYKEG FGHLSPTGTT
251 EFWLGNEKIH LISTQSAIPY ALRVELEDWN GRTSTADYAM FKVGPEADKY
301 RLTYAYFAGG DAGDAFDGFD FGDDPSDKFF TSHNGMQFST WDNDNDKFEG
351 NCAEQDGSGW WMNKCHAGHL NGVYYQGGTY SKASTPNGYD NGIIWATWKT
401 RWYSMKKTTM KIIPFNRLTI GEGQQHHLGG AKQVRPEHPA ETEYDSLYPE
451 DDL
```

Fig S2. Sequence coverage upon nanoLC-ESI-ion trap-MS/MS analysis of Fibrinogen 1 (Fib 1). Peptides identified via proteomic analysis are indicated in red.