A

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        10         20         30         40         50         60
mAKSGGCGAG AGVGGGNGAL TWVNNAAKKE ESETANKNDS SKKLSVERVY QKKTQLEHIL
        70         80         90        100        110        120
LRPDTYIGSV EPLTQFmWVY DEDVGmNCRE VTFVPGLYKI FDEILVNAAD NKQRDKNmTC
       130        140        150        160        170        180
IKVSIDPESN IISIWNNGKG IPVVEHKVEK VYVPALIFGQ LLTSSNYDDD EKKVTGGRNG
       190        200        210        220        230        240
YGAKLCNIFS TKFTVETACK EYKHSFKQTW mnnmmKTSEA KIKHFDGEDY TCITFQPDLS
       250        260        270        280        290        300
KFKmEKLDKD IVALmTRRAY DLAGSCRGVK VmFNGKKLPV NGFRSYVDLY VKDKLDETGV
       310        320        330        340        350        360
ALKVIHELAN ERWDVCLTLS EKGFQQISFV NSIATTKGGR HVDYVVDQVV GKLIEVVKKK
       370        380        390        400        410        420
NKAGVSVKPF QVKNHIWVFI NCLIENPTFD SQTKENmTLQ PKSFGSKCQL SEKFFKAASN
       430        440        450        460        470        480
CGIVESILNW VKFKAQTQLN KKCSSVKYSK IKGIPKLDDA NDAGGKHSLE CTLILTEGDS
       490        500        510        520        530        540
AKSLAVSGLG VIGRDRYGVF PLRGKILNVR EASHKQImEN AEINNIIKIV GLQYKKSYDD
       550        560        570        580        590        600
AESLKTLRYG KImimTDQDQ DGSHIKGLLI NFIHHNWPSL LKHGFLEEFI TPIVKASKNK
       610        620        630        640        650      ↓ 660
QELSFYSIPE FDEWKKHIEN QKAWKIKYYK GLGTSTAKEA KEYFADmERH RILFRYAGPE
       670        680        690        700        710 ↓      720
DDAAITLAFS KKKIDDRKEW LTNFmEDRRQ RRLHGLPEQF LYGTATKHLT YNDFINKELI
       730        740        750        760        770        780
LFSNSDNERS IPSLVDGFKP GQRKVLFTCF KRNDKREVKV AQLAGSVAEm SAYHHGEQAL
       790        800        810        820        830        840
mmTIVNLAQN FVGSNNINLL QPIGQFGTRL HGGKDAASPR YIFTmLSTLA RLLFPAVDDN
       850        860        870        880        890        900
LLKFLYDDNQ RVEPEWYIPI IPmVLINGAE GIGTGWACKL PNYDAREIVN NVRRmLDGLD
       910        920        930        940        950        960
PHPmLPNYKN FKGTIQELGQ NQYAVSGEIF VVDRNTVEIT ELPVRTWTQV YKEQVLEPmL
       970        980        990       1000       1010       1020
NGTDKTPALI SDYKEYHTDT TVKFVVKmTE EKLAQAEAAG LHKVFKLQTT LTCNSmVLFD
      1030       1040       1050       1060       1070       1080
HmGCLKKYET VQDILKEFFD LRLSYYGLRK EWLVGmLGAE STKLNNQARF ILEKIQGKIT
      1090       1100       1110       1120       1130       1140
IENRSKKDLI QmLVQRGYES DPVKAWKEAQ EKAAEEDETQ NQHDDSSSDS GTPSGPDFNY
      1150       1160       1170       1180       1190       1200
ILNmSLWSLT KEKVEELIKQ RDAKGREVND LKRKSPSDLW KEDLAAFVEE LDKVESQERE
      1210       1220       1230       1240       1250       1260
DVLAGmSGKA IKGKVGKPKV KKLQLEETmP SPYGRRIIPE ITAmKADASK KLLKKKKGDL
      1270       1280       1290       1300       1310       1320
DTAAVKVEFD EEFSGAPVEG AGEEALTPSV PINKGPKPKR EKKEPGTRVR KTPTSSGKPS
      1330       1340       1350       1360       1370       1380
AKKVKKRNPW SDDESKSESD LEETEPVVIP RDSLLRRAAA ERPKYTFDFS EEEDDDADDD
      1390      ↓1400       1410       1420      ↓1430       1440
DDDNNDLEEL KVKASPITND GEDEFVPSDG LDKDEYTFSP GKSKATPEKS LHDKKSQDFG
      1450       1460       1470       1480       1490       1500
NLFSFPSYSQ KSEDDSAKFD SNEEDSASVF SPSFGLKQTD KVPSKTVAAK KGKPSSDTVP
      1510       1520       1530       1540     ↓ 1550       1560
KPKRAPKQKK VVEAVNSDSD SEFGIPKKTT TPKGKGRGAK KRKASGSENE GDYNPGRKTS
      1570       1580       1590       1600       1610       1620
KTTSKKPKKT SFDQDSDVDI FPSDFPTEPP SLPRTGRARK EVKYFAESDE EEDDVDFAmf
n
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B

Expected CNBr Peptides

Amino Acid #	MW	Amino Acid Sequence
2-77	8590.4	AKSGGCGAGAGVGGGNGALTWVNNAAKKEESETANKNDSSKKLSVERVYQKKTQLEHILLRPDTYIGSVEPLTQFM
78-86	1065.5	WVYDEDVGM
87-118	3692.9	NCREVTFVPGLYKIFDEILVNAADNKQRDKNM
119-211	10407.3	TCIKVSIDPESNIISIWNNGKGIPVVEHKVEKVYVPALIFGQLLTSSNYDDDEKKVTGGRNGYGAKLCNIFSTKFTVETACKEYKHSFKQTWM
216-244	3359.7	KTSEAKIKHFDGEDYTCITFQPDLSKFKM
245-255	1226.7	EKLDKDIVALM
256-272	1835.0	TRRAYDLAGSCRGVKVM
273-397	14127.5	FNGKKLPVNGFRSYVDLYVKDKLDETGVALKVIHELANERWDVCLTLSEKGFQQISFVNSIATTKGGRHVDYVVDQVVGKLIEVVKKKNKAGVSVKPFQVKNHIWVFINCLIENPTFDSQTKENM
398-518	13118.0	TLQPKSFGSKCQLSEKFFKAASNCGIVESILNWVKFKAQTQLNKKCSSVKYSKIKGIPKLDDANDAGGKHSLECTLILTEGDSAKSLAVSGLGVIGRDRYGVFPLRGKILNVREASHKQIM
519-553	4010.2	ENAEINNIIKIVGLQYKKSYDDAESLKTLRYGKIM
556-647	10774.5	TDQDQDGSHIKGLLINFIHHNWPSLLKHGFLEEFITPIVKASKNKQELSFYSIPEFDEWKKHIENQKAWKIKYYKGLGTSTAKEAKEYFADM
648-685	4533.4	ERHRILFRYAGPEDDAAITLAFSKKKIDDRKEWLTNFM
686-770	9817.1	EDRRQRRLHGLPEQFLYGTATKHLTYNDFINKELILFSNSDNERSIPSLVDGFKPGQRKVLFTCFKRNDKREVKVAQLAGSVAEM
771-781	1195.6	SAYHHGEQALM
783-825	4625.4	TIVNLAQNFVGSNNINLLQPIGQFGTRLHGGKDAASPRYIFTM
826-863	4470.4	LSTLARLLFPAVDDNLLKFLYDDNQRVEPEWYIPIIPM
864-895	3481.8	VLINGAEGIGTGWACKLPNYDAREIVNNVRRM
896-904	946.5	LDGLDPHPM
905-959	6364.3	LPNYKNFKGTIQELGQNQYAVSGEIFVVDRNTVEITELPVRTWTQVYKEQVLEPM
960-988	3266.7	LNGTDKTPALISDYKEYHTDTTVKFVVKM
989-1016	3014.6	TEEKLAQAEAAGLHKVFKLQTTLTCNSM
1017-1022	713.4	VLFDHM
1023-1056	4093.2	GCLKKYETVQDILKEFFDLRLSYYGLRKEWLVGM
1057-1092	4080.3	LGAESTKLNNQARFILEKIQGKITIENRSKKDLIQM
1093-1144	5765.6	LVQRGYESDPVKAWKEAQEKAAEEDETQNQHDDSSSDSGTPSGPDFNYILNM
1145-1206	7165.7	SLWSLTKEKVEELIKQRDAKGREVNDLKRKSPSDLWKEDLAAFVEELDKVESQEREDVLAGM
1207-1229	2449.5	SGKAIKGKVGKPKVKKLQLEETM
1230-1244	1652.9	PSPYGRRIIPEITAM
1245-1619	41192.6	KADASKKLLKKKKGDLDTAAVKVEFDEEFSGAPVEGAGEEALTPSVPINKGPKPKREKKEPGTRVRKTPTSSGKPSAKKVKKRNPWSDDESKSESDLEETEPVVIPRDSLLRRAAAERPKYTFDFSEEEDDDADDDDDDNNDLEELKVKASPITNDGEDEFVPSDGLDKDEYTFSPGKSKATPEKSLHDKKSQDFGNLFSFPSYSQKSEDDSAKFDSNEEDSASVFSPSFGLKQTDKVPSKTVAAKKGKPSSDTVPKPKRAPKQKKVVEAVNSDSDSEFGIPKKTTTPKGKGRGAKKRKASGSENEGDYNPGRKTSKTTSKKPKKTSFDQDSDVDIFPSDFPTEPPSLPRTGRARKEVKYFAESDEEEDDVDFAM

Supplemental Figure 1. (A) Amino acid sequence of topo IIβ. The position of methionine residues (cleavage with CNBr) is marked in red and lower case letters. The highlighted peptides correspond to those that were detected by LC-MS/MS analysis following tryptic digests of the CNBr peptides separated on a polyacrylamide gel. (B) Size and sequence of peptides that would be expected to be generated following cleavage with CNBr.