Hu et al., Supplemental Figure S1. Peptide mass fingerprinting of the tryptic digest of the proteins (112, 76, 59, and 40 kDa) (A–D). The peptide band masses were matched to the theoretical masses. Using the MASCOT search engine, human PRTD-NY2 was identified with scores of 154, 137, 145, and 177 and sequence coverage of 31%, 29%, 29%, and 31% (A′–D′). The peptide band masses of the tryptic digest of the protein of 146kDa was identified with a score of 356 and a sequence coverage of 45% (E′).
Figure S1

**MATRIX** Mascot Search Results

**Protein View**

Match to: gi|12330995 Score: 154 Expect: 5.4e-011
PRTD-NY2 [Homo sapiens]

Nominal mass (M$_i$): 146679; Calculated pI value: 7.97
NCBI BLAST search of gi|12330995 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 99
Number of mass values matched: 36
Sequence Coverage: 31%

Matched peptides shown in **Bold Red**

1  MPEKRLTAEP PTITEEEFED SLATDDFLVD YPNEFLSLPT FSEAIFNAD
51  YGVEFVANDA PQFLEKQLKK ILQHQQPMPN IYDVRKEXKN EVKPVQMNAP
101 DEDETINNYN NIMLCSRQQ EIKWIKKERLQP AFLEDSCYFE YRLAKLVSQV
151 RWSKGMNFT VGSSFSSWIV KKPSSLPPPA TEEIDLASYT QTKDWFALAK
201 QSSQTVSTFS LPCCVFYNKL KSPAISSSVE NFIFDDGVHP RTKRDPSKT
251 KLISEEFEEEE GEEEEWSVSL QDTPSALLR VYLEKQKQED ESLTHFSTC
301 EEFLLSSYIF ILRGAIIQIVK GKPVEQRPDY INFNNITKVS FDDCFESIHG
401 KEKFFKFKFI RGTIERXXW LWMDIERKLV LKDFGRHQRH LEKMKCYLV
451 SNGDYLLSAE ILSEFKLLDG SQWNEEHLRN IQSEVLPQKLY WAPFRCVT
501 HSASTKYSYA ELKFWHLRQA KFLRDIQPFP QMTAILLPLRP KSCIPIQEI
551 QKEEFSLSQP PKSNKMSPEV KTATQPKWKR ELYPGSSKD DVIEKSGKM
601 SESSVIHULT SFTDISECLK PQDLRRYAYT EEPVVKTVSD VQALG6GSDME
651 HLLQSLYVEN RAGFHTTFKC EHSQHLWKD SVYFQFDLQA YHQLFYQETL
701 QFKKVCQKQV YLFATYVAPS ATLDIGLQE KKKEIYMIQK PPFDLFDFTA
751 EYIIILLLLE PUTHMKVDQ IAYKAVELVE ETTRQDSSTUF RKLQALHKET
801 FSKKAEQTTT EIGTGILSLS NVSKRTEYWD NUPAEYKHFK FSJPLNMLKET
851 FEMFQOFLET HSSSRTLCA D RHUSSGSEIT YRDNPQKAK SIYINKNYLN
901 KKYFFGPNSP ASLYQQNQVM HLSGGVWKIL HEQDLAPVVL EIQKHQONRL
951 ENWFLPLFLA SEQAERQIKI KVQMKDIAE EE LLLQKAEKKI GVUWFPESK
1001 ISSSSCIIAF RKALLMPVTS RQFQFQVFALK GDLLENGLFP WQEVQKYKDL
1051 CHSHCDETVI QRKTIITINC FINSSSIPAL QIDIPVEAQ KIIEHREKELG
1101 PVYFREGAQMT IFQVFKFQWP QCFEFRKNL T DENTHSVLER RQYRNQKQKK
1151 LAVLEDEKSG KDQIGKYANT SVPAIKTALL SDFSLQGQPY GROPTWCSYK
1201 YIEALEQERI LLKIQEELLEK KLFAGLQPLT NFKA SST M LKKNMSAHS
1251 QK
Mascot Search Results

Protein View

Match to: gi|12330995 Score: 137 Expect: 2.7e-009
PRTD-NY2 [Homo sapiens]

Nominal mass (M_r): 146679; Calculated pI value: 7.97
NCBI BLAST search of gi|12330995 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 98
Number of mass values matched: 34
Sequence Coverage: 29%

Matched peptides shown in Bold Red

1  MPKKRLTAEP PTITEEFEFD SLATDDFLVD YFNEFLSLPT FSEAIRFNAD  51  YGVFENANDA PQFLEKQKK ILQHNQQPRNP IYDVRKRGKN EVKPVQMNAP
101 DEDETVNY NIMCLESREEG IWKIKERLP AFLESDCYEF YRLAQLVSQV 151 RUSKSMNFT VGSSNFSSWV KPPSSLPPPA TEEDNLASYT QTKDWFALAK
201 QSQQTSTSTS LPCCVPYMNKL KSAISSVEH MFIFIDGVHVP RTKIDPSKTN 251 KLISEEEEVEEVEVSVL QDTPSQAQLR VYLEKQKVDQ ESLTMHFSSTC
301 EEFSSYYIF ILRGAIQQIV GKPVGETPDI INFNINIKVS FDDCFESIHG 351 KNFLSELVQT TKERSEEIEQ TSLSSKNESA GESPRAWCI SHRTYDIGHR
401 KEFERRKFI RGTLGERYW LWMDIERLKV LKDPGRHQRH LEKMKCCYLV 451 SNGDYLYLSEA ILSKFKLLDG SQWNEEHCLRN IQSEVULKPLL LYWAPRFCVT
501 HSASTYASA ELKEWHLRQA KPRKDIDPFP QMATLLPLRP KSCIPQ1PEI 551 QKEEFLS5QP PKPSNKSPVE KPQVBPWKR ELYPGSSKD DVIEKGSKYM
601 SSSWVHILT SPTDISECCK PQQDRRYYAT EEPVRKTVSD VGALGSSSDME 651 NLLQLSYYVEN RAGFFTKFC EHSNGNKLWD SVYFUFDLQA YHQLFYQETL
701 QFQKVCQKQA YLFATVPLS ATLDIQLQKE KKEIYMKIQ PFPEDLFDTA 751 EEYILLLLLE PUTKMVQSDQ IAYKVKEVLE ETRQLDSTYF RKLQALQHKT
801 FSKEAEDITTC EIGTQIGLVS NVSKRTETYWD HVPAEYKHFK FSDLNNKMLE 851 FEHRDFLET HSRRSLICAD RHUSSSGEIT YRQNLQKAK SIYIKKNLYN
901 KKYFPQGNSP ASLYQONQVM HLSGGWCKIL HEQLDAPVLU EIQKHWQVNL 951 ENWWLFLLA SEQFAARQKI KVQMDIAEE LLLQKAEKTI GVWKVESKU
1001 ISSSCHIIAF RKALLNPVTS RQRFQRFVALK DLDENGFLF WQEVQYKDL 1051 CSHEDCTV LKQITTIINC FINSSSIPAL QIDIPVEQAQ KIIERHKELG
1101 PYYFRKJQAMT IFGUVFKWFP QFCEFRRKLNQ DENIMSVLER RQMYNQKHKK 1151 LAVLEDEKSG KDGIKQYANT SVPAIKTALL SDFSGLGQPY GRQPTWCSYK
1201 YIEALEQERI LLKIQCEELEK KLFAGLQPLT NFKASSSTMS LKKNMSAHSS 1251 QR
Mascot Search Results

Protein View

Match to: gi|12330995 Score: 145 Expect: 4.3e-010
PRTD-NY2 [Homo sapiens]

Nominal mass (M): 146679; Calculated pI value: 7.97
NCBI BLAST search of gi|12330995 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 100
Number of mass values matched: 33
Sequence Coverage: 29%

Matched peptides shown in Bold Red

1  MPEKRLTAEP PTITEEFED SLATDDFLVD YPNEFLSLPT FSEAIRFPAD
51  YGUFFVEDANDA PQFLEKQKLK LLQHQQRHPN IYVDVRRKGKN EVKPQVMNAP
101  DEDETIVHNY NIMCLSREEG IKWKKERLPL APLESDCGYE YRLAKLVSQV
151  RWSKSMNFT VGSMFHSSWIV KPPSSLPPLPA TEEEDNASYT QTKDFALAK
201  QSOQTVSTFS LPCCCPYNKL KPSAISSVSE ATPFDGGVHP RTRKDPKSTN
251  KLISEFEEEE GEEEEEVSVL QDTPSQALLR VYLEKQDQVD ESLTMHFSTC
301  EEFLSYYLF ILRAIGQQIV GKPVEGDTPY IINFNNITKVS FDCCFEISHG
351  KNFLSLVQQT TKERSSEEQI TSLSSKNESA GPEPRADWCI SHRTPYDIHG
401  KEFERFPKFI RTGTLGERYZWW LRMIDIERLKV LKDPGRHQHR LEMKMKCYLV
451  SNGDYYLSAE ILSKFKLDLG SQWNEEHLRN IQSEVHKPLL LYWAPFRCVT
501  HSASTSKYASA ELASKWLHRQA KPRKDDPPFP QMATLPLLRF KSCIPQIEPI
551  QKEEFSLSQP PKSPNSPSFP KTATQKPSWKR ELYPGSSKDK DVEIEGSKYIM
601  SESSKVIHLT SFTDISECLK PQLDRRYAYT EEPVTKVSVD VQALGGSDME
651  HLLQSLYVEN RAGFFTXFC EHSGNKLMKD SVFYWFDLQA YHQLFYQETL
701  QPFQKCVQQK YTFLATIVAFS ATLDIGLQWE KKKEYIYNHK PPFDLFDTA
751  EEYLLLLEPFTKMKSVSQ IAYKKEVLE ETRQQLSTYF RKLQAMHKT
801  FSXKAEDTC EIGTGLLSF NVSKRTTEYWD NSPAEXKHFK FSDLNNKLE
851  FEHEROFLET HSSSRILCAD RHUSSSGEIT YRDRNQQKAK SIYIKKNYLN
901  KYFFGPNSP ASLYQQQNVN HLSGGWKGKL HEQLDAPVVL EIQHIVQRNL
951  ENNWLPFELA SEQFARQKIQ KVQMNDIAEE LLLQRAEKKI GUVKPSKESVW
1001  ISSSKCIIAF RRKALLPVSIQRFQFVALK GDLENGLLF WQEVQKYKDK
1051  CHSHDCTVI QKKTITIINC FINISSIPPA QDIDPVEQAQ KIEEHRKELG
1101  PYVYFRKAMT IFGVLFKWPQ QCEFREKNTL DENIMSVLER QRQYNQKXKK
1151  LAVLEEKSG KDGKQKYANT SVPAIKTALL SDFSLGQPY GRQTPWCSK
1201  YTEALEQERI LLLKIQELEEL KLFAGLQPLL NFKASSSTMS LKKNNMSAHSS
1251  QK
Mascot Search Results

Protein View

Match to: gi|12330995 Score: 177 Expect: 2.7e-013  
PRTD-NY2 [Homo sapiens]

Nominal mass (M): 146679: Calculated pI value: 7.97
NCBI BLAST search of gi|12330995 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 97
Number of mass values matched: 35
Sequence Coverage: 31%

Matched peptides shown in Bold Red

1  MPKKRLTAEP PTITEEFED SLATIDFLVD YFNEFLSLPT FSEAIRFNAD
10  YGVFEVANDA POFLAXQCKK ILQNIQPRNP YTVIRKRGKKN EVKPVNQMP
100  DLEDINVNY NJIMLSSREEG IKNWIKERLP AFLESDCYPF YRLAKIVSVQ
150  RWSKGSNHPT VGNSFSSSWV KKPPSLPPPA TEEDMNLASY TQTKDFALAX
200  QSSQHTSVTFS LPCCVPIYKL KSPIASSVSE HPFDGDUGHF RTRKDFSKTN
250  KLISPEEEDB GREEEVSSSL QDTPSAILR VYLEKQVDVL ESLTNHFSTC
300  EEFLSSYIFYL RAKIAQQTIV GKPGIEPTDY INFHNITKVS FDDCESIHING
350  KNFSLSIVTQ TERSSEIEEQ TSLSSKMNES GESRADWCI SHRTYIVGNR
400  KERPFRKFI RGTGLERTYWW LMMDIERKLV KLQPGHCRHE LEYNKCYLTV
450  SNGDYYSLSAE ILSXKLLDG SQWNEEHLRN IQSEVKLPLL LYWAPFCVT
500  HSAASYAKLA ELKFWHLRQA KPRKIDFPFP QMATLLPLRF KSCIPQIEPI
550  QKKEFLSLQP KSPPNSPEV KTATQKHKKR ELLYPGSSKD DVIEKGSYKM
600  SESSSIVHLTL SPTDISECLK PQDERRTAAT EEPVRKTVXDI VGALGGSNMD
650  MLISLQSLYVEN RAGFFTKFC EHSNKLWKKD SVTFWFDLQA THQLFYQETL
700  QPFKVKCQAO YLFATTVAFS ATLIDQLQEE KKKEIYMKIQ PPFEDLRTA
750  EEEYYLLLLE PUTXMKSDQ IAYKEVLEVE ETRQLDSTYE RKLQALHEET
800  FSKAEDYTSC EIGTGILSLS NUSKRTEYWD HWAEXYKHF FSDLLLNNKLE
850  FEHRFQPLET HSSSRILCAD RHWSSSGEIT YRDINQQRAK SIVYIKNYKLN
900  KKYFFGPNISP ASLYQNONQM HSLSGUGKIL BEQLOAPVUL EIQKIVQHNR
950  ENNWLPLPLA SQPQAPQKFI KVCNMDIAE LLLQXAEKIK GVQKFPVESK
1000 ISSSCKIIAF REALHPVIS RQFQFPVALK GDLLENGLLF WQSVQKYEDL
1050 CSCHDECETVI QKKTIININC FINSIPPAL QIDIPVECAQ KIIEHEFLKEL
1100 DIVVFEAQQMT IFGVLFHFKWP QCCEFRMLMT DEMINSYLER RQQYNHRKQIK
1150 LAVLEDKSK KDGIKQYANT SVPAIAKTL SEDSLGLQPY 6QQTPWCSYK
1200 YTEALEQERI LLLQKXEELEK KLFLAGLQLPT NFKAASSSTMS LKKNMHSBSS
1250 QK

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**Mascot Search Results**

**Protein View**

Match to: **qi12330995 Score: 356 Expect: 3.4e-031**  
**PRTD-NY2 [Homo sapiens]**

Nominal mass (M): **146679**; Calculated pI value: **7.97**

NCBI BLAST search of **qi12330995** against nr
Unformatted sequence string for pasting into other applications

**Taxonomy:** **Homo sapiens**

Fixed modifications: Carbamidomethyl (C)  
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of ER unless next residue is P
Number of mass values searched: **98**  
Number of mass values matched: **56**  
Sequence Coverage: **48%**  

Matched peptides shown in **Bold Red**

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<th>Peptide</th>
<th>Score</th>
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