ENCODE DCC Antibody Validation Document

Date of Submission: Aug 30, 2011

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Lab: Myers

Antibody Name: MBD4_(SC-271530)

Target: MBD4

Company/ Source: Santa Cruz Biotechnology

Catalog Number, database ID, laboratory: sc-271530

Lot Number: H1210

Antibody Description: Mouse monoclonal IgG, specific for an epitope mapping between a.a. 515-555 within an internal region of MBD4 of mouse origin.

Target Description: Methyl-CpG binding domain protein 4. Mol weight ~66 kDa

Entrez gene ID 8930

Species Target: Mouse

Species Host: Mouse

Validation Method #1: Western Blot

Validation Method #2: IP-Mass Spec

Purification Method:

Polyclonal/ Monoclonal:

Vendor URL: http://www.scbt.com/datasheet-271530-

Reference (PI/ Publication Information):

Please complete the following for antibodies to histone modifications:

if your specifications are not listed in the drop-down box, please write-in the appropriate information

Histone Name:

AA modified:

AA Position:

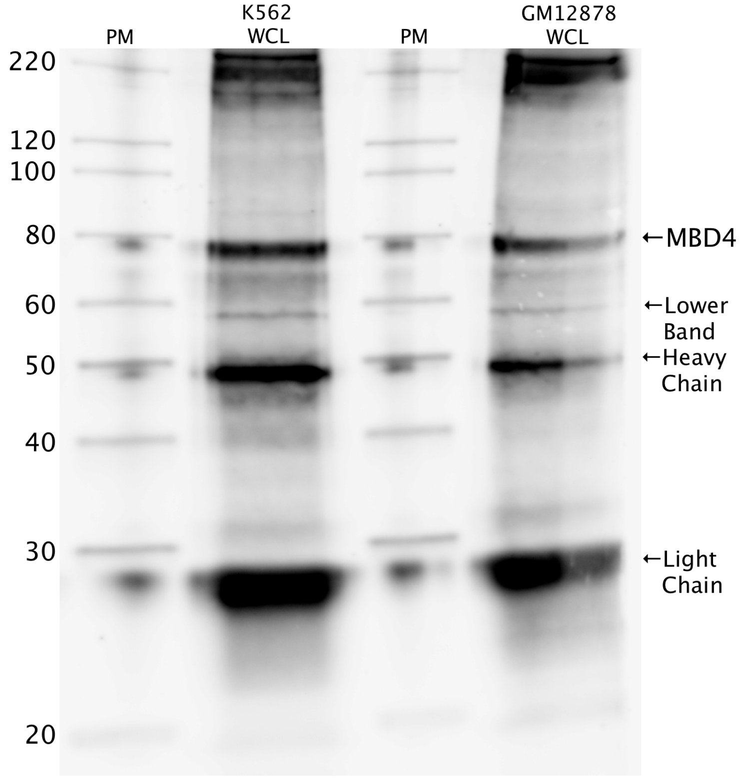
Modification:

Validation #1
Analysis

Western blot protocol:
Whole cell lysate was immunoprecipitated using primary antibody, and the IP fraction was loaded on a 12% acrylamide gel and separated with a Bio-Rad PROTEAN II xi system. After separation, the samples were transferred to a nitrocellulose membrane with an Invitrogen iBlot system. Blotting with primary (same as that used for IP) and secondary HRP-conjugated antibodies was performed on an Invitrogen BenchPro 4100 system. Visualization was achieved using SuperSignal West Femto solution (Thermo Scientific).

Results: Band of expected size visualized, representing strongest signal in the lane. Lower band also visualized at ~58 kDa. Both bands tested by IP-mass spec, but only the ~75 kDa band was positive for MBD4 (see below).

Figure legend: IP-western with sc-271530 in whole cell lysate (WCL) of K562 and GM12878; PM=protein marker. MBD4 band is indicated.



–Molecular Weight of MBD4: 66kDa

Insert Validation Image (click here)

Validation #2 Analysis

IP followed by mass spectrometry:
Briefly, K562 whole cell lysate was immunoprecipitated using primary antibody, and the IP fraction was loaded on a 12% acrylamide gel and separated with a Bio-Rad PROTEAN II xi system. Gel was stained with Coomassie Blue in order to visualize marker bands. Gel fragments corresponding to the bands indicated above in the western blot image were excised and sent to the University of Alabama at Birmingham Cancer Center Mass Spectrometry/Proteomics Shared Facility. There the samples were run on an LTQ XL Linear Ion Trap Mass Spectrometer by LC-ESI-MS/MS. Peptides were identified using SEQUEST tandem mass spectra analysis, with probability based matching at $p < 0.05$.

As per ENCODE data standards, all SEQUEST results are attached (ENCODE_HAIB_MBD4_sc271530_08252011_MassSpec.pdf), including common contaminants. Target protein is listed as hit 9 in the upper (~75kDa) band and absent from the lower (~58kDa) band.

Insert Validation Image (Click here)

Submit by Email

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MBD4 Mass Spec - upper band:

33 entries (12 single hits) retrieved from
/home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_MDB4-2-sequest.prot.xml


* corresponds to peptide is_nondegenerate_evidence flag



1     UniRef100_B4DUT7 UniRef100_B4DXV7 UniRef100_P49915 UniRef100_Q53F90 UniRef100_UPI0001B79651 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.40%
      >cDNA FLJ57604, highly similar to GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) n=1 Tax=Homo sapiens RepI Length: 642aa
      >cDNA FLJ57661, highly similar to GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) n=1 Tax=Homo sapiens RepID=B4DXV7_HUMAN
      >GMP synthase [glutamine-hydrolyzing] n=2 Tax=Homo sapiens RepID=GUAA_HUMAN
      >Guanine monophosphate synthetase variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53F90_HUMAN
      >GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (Glutamine amidotransferase) (GMP synthetase). n=1 Tax=Homo sapiens
                  RepID=UPI0001B79651

2     UniRef100_P35527 1.0000
      confidence: 1. coverage: 16. num unique p tot indep spec share of spectrum id's: 3.32%
      >Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN                                   Length: 623aa


3     UniRef100_P54886 UniRef100_P54886-2 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.74%
      >Gamma-glutamyl phosphate reductase n=2 Tax=Homo sapiens RepID=P5CS_HUMAN                               Length: 795aa
      >Isoform Short of Delta-1-pyrroline-5-carboxylate synthase n=1 Tax=Homo sapiens RepID=P54886-2


4     PROTEIN GROUP: 1 1.0000

a     UniRef100_A6H8Z4 UniRef100_A6NJK7 UniRef100_C9K008 UniRef100_Q76FK4 UniRef100_Q76FK4-4 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.50%
      >NOL8 protein n=1 Tax=Homo sapiens RepID=A6H8Z4_HUMAN                                                   Length: 1099aa
      >Putative uncharacterized protein NOL8 n=1 Tax=Homo sapiens RepID=A6NJK7_HUMAN
      >Putative uncharacterized protein NOL8 n=1 Tax=Homo sapiens RepID=C9K008_HUMAN
      >Nucleolar protein 8 n=3 Tax=Homo sapiens RepID=NOL8_HUMAN
      >Isoform 4 of Nucleolar protein 8 n=1 Tax=Homo sapiens RepID=Q76FK4-4


b     UniRef100_B4DM91 UniRef100_Q6AI50 UniRef100_UPI000059DA42 0.0000
      confidence: 0.9993          num unique p tot indep spectra: 0
      >cDNA FLJ60085, highly similar to Nucleolar protein 8 (Fragment) n=1 Tax=Homo sapiens RepID=B4DM91_HUMAN  Length: 933aa
      >Putative uncharacterized protein DKFZp686P12242 n=1 Tax=Homo sapiens RepID=Q6AI50_HUMAN
      >UPI000059DA42 related cluster n=1 Tax=Homo sapiens RepID=UPI000059DA42


5     PROTEIN GROUP: 2 1.0000

a     UniRef100_B1AHM1 UniRef100_B4DZQ7 UniRef100_C9J5E1 UniRef100_C9JMU5 UniRef100_Q92841-2 UniRef100_UPI0001AE634E
      UniRef100_UPI0001B79048 0.0000
      confidence: 1.0000          num unique p tot indep spectra: 0
      >DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 n=1 Tax=Homo sapiens RepID=B1AHM1_HUMAN                      Length: 652aa
      >cDNA FLJ58652, highly similar to Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DZQ7_HUMAN
      >Putative uncharacterized protein DDX17 n=1 Tax=Homo sapiens RepID=C9J5E1_HUMAN
      >Putative uncharacterized protein DDX17 n=1 Tax=Homo sapiens RepID=C9JMU5_HUMAN
      >Isoform 2 of Probable ATP-dependent RNA helicase DDX17 n=1 Tax=Homo sapiens RepID=Q92841-2
      >UPI0001AE634E related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE634E
      >UPI0001B79048 related cluster n=1 Tax=Homo sapiens RepID=UPI0001B79048


b     UniRef100_B1AHM2 0.0000
      confidence: 0.2536          num unique p tot indep spectra: 0
      >DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 (Fragment) n=1 Tax=Homo sapiens RepID=B1AHM2_HUMAN          Length: 174aa


c     UniRef100_B3KSF4 UniRef100_D6RCM4 UniRef100_Q9NQI0 UniRef100_Q9NQI0-2 UniRef100_UPI0000E0956E UniRef100_UPI0001BB0BF9
      UniRef100_UPI0001D3B259 0.0000
      confidence: 0.9992          num unique p tot indep spectra: 0
      >cDNA FLJ36120 fis, clone TESTI2022738, highly similar to Probable ATP-dependent RNA helicase DDX4 (EC 3.6.1.-) Length: 575aa
      >Putative uncharacterized protein DDX4 n=1 Tax=Homo sapiens RepID=D6RCM4_HUMAN
      >Probable ATP-dependent RNA helicase DDX4 n=1 Tax=Homo sapiens RepID=DDX4_HUMAN
      >Isoform 2 of Probable ATP-dependent RNA helicase DDX4 n=1 Tax=Homo sapiens RepID=Q9NQI0-2
      >probable ATP-dependent RNA helicase DDX4 isoform 4 n=1 Tax=Homo sapiens RepID=UPI0000E0956E
      >probable ATP-dependent RNA helicase DDX4 isoform 3 n=1 Tax=Homo sapiens RepID=UPI0001BB0BF9
      >UPI0001D3B259 related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3B259


d     UniRef100_B4DK29 0.0000
      confidence: 1.0000          num unique p tot indep spectra: 0
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        >cDNA FLJ59914, highly similar to ATP-dependent RNA helicase DDX3Y (EC 3.6.1.-) n=2 Tax=Homo sapiens RepID= Length: 291aa


e       UniRef100_B4DLU5 UniRef100_UPI0001AE6F7E 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >cDNA FLJ60675, highly similar to ATP-dependent RNA helicase DDX3X (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID= Length: 532aa
        >UPI0001AE6F7E related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6F7E


f       UniRef100_B4DLW8 UniRef100_B5BUE6 UniRef100_P17844 UniRef100_UPI0001AE6729 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0          subsumed entries: 4
        >cDNA FLJ59339, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) n=1 Tax=Homo sapiens Length: 535aa
        >ATP-dependent RNA helicase DDX5 (Fragment) n=1 Tax=Homo sapiens RepID=B5BUE6_HUMAN
        >Probable ATP-dependent RNA helicase DDX5 n=3 Tax=Eutheria RepID=DDX5_HUMAN
        >UPI0001AE6729 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6729


g       UniRef100_B4DN41 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >cDNA FLJ53366, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) n=1 Tax=Homo sapiens Length: 603aa


h       UniRef100_B4DNG2 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >cDNA FLJ59357, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) n=1 Tax=Homo sapiens Length: 544aa


i       UniRef100_B4DXX7 UniRef100_O15523 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >cDNA FLJ50912, highly similar to ATP-dependent RNA helicase DDX3Y (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID= Length: 657aa
        >ATP-dependent RNA helicase DDX3Y n=1 Tax=Homo sapiens RepID=DDX3Y_HUMAN


j       UniRef100_B4E010 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >cDNA FLJ53946, highly similar to ATP-dependent RNA helicase DDX3Y (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID= Length: 410aa


k       UniRef100_B4E132 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >cDNA FLJ53122, highly similar to ATP-dependent RNA helicase DDX3Y (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID= Length: 407aa


l       UniRef100_B4E3C4 0.0000
        confidence: 0.9989          num unique p tot indep spectra: 0
        >cDNA FLJ52848, highly similar to ATP-dependent RNA helicase DDX3X (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID= Length: 308aa


m       UniRef100_B4E3E8 UniRef100_B5BTY4 UniRef100_O00571 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0          subsumed entries: 9
        >cDNA FLJ60399, highly similar to ATP-dependent RNA helicase DDX3X (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID= Length: 646aa
        >ATP-dependent RNA helicase DDX3X n=1 Tax=Homo sapiens RepID=B5BTY4_HUMAN
        >ATP-dependent RNA helicase DDX3X n=3 Tax=Homo sapiens RepID=DDX3X_HUMAN


n       UniRef100_C1IK54 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >DEAD box polypeptide 5/ets variant protein 4 fusion protein n=1 Tax=Homo sapiens RepID=C1IK54_HUMAN        Length: 519aa


o       UniRef100_C9J081 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >Putative uncharacterized protein DDX3Y n=1 Tax=Homo sapiens RepID=C9J081_HUMAN                             Length: 250aa


p       UniRef100_Q4R4H4 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >Brain cDNA, clone: QtrA-14110, similar to human DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 (DDX17),transcript Length: 304aa


q       UniRef100_Q4R6G0 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >Testis cDNA, clone: QtsA-18104, similar to human DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 (DDX5), n=2 Tax=M Length: 509aa


r       UniRef100_Q4R9A4 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
        >Testis cDNA clone: QtsA-10416, similar to human DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked(DDX3X), tra Length: 480aa


s       UniRef100_Q59E92 UniRef100_Q7Z2V5 0.0000
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        confidence: 1.0000            num unique p tot indep spectra: 0
        >Putative uncharacterized protein (Fragment) n=2 Tax=Eutheria RepID=Q59E92_HUMAN                   Length: 457aa
        >Putative uncharacterized protein DKFZp686J01190 (Fragment) n=1 Tax=Homo sapiens RepID=Q7Z2V5_HUMAN


t       UniRef100_Q59F66 UniRef100_Q92841 UniRef100_Q92841-3 UniRef100_Q92841-4 UniRef100_UPI00003670EA UniRef100_UPI0001533DB4
        UniRef100_UPI0001AE634C 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0
        >DEAD box polypeptide 17 isoform p82 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59F66_HUMAN     Length: 737aa
        >Probable ATP-dependent RNA helicase DDX17 n=1 Tax=Homo sapiens RepID=DDX17_HUMAN
        >Isoform 3 of Probable ATP-dependent RNA helicase DDX17 n=1 Tax=Homo sapiens RepID=Q92841-3
        >Isoform 4 of Probable ATP-dependent RNA helicase DDX17 n=1 Tax=Homo sapiens RepID=Q92841-4
        >UPI00003670EA related cluster n=1 Tax=Homo sapiens RepID=UPI00003670EA
        >probable ATP-dependent RNA helicase DDX17 isoform 3 n=1 Tax=Homo sapiens RepID=UPI0001533DB4
        >Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) (DEAD box protein 17) (RNA-dependent helicase p72) (DEAD box protein p72). n=1
                 Tax=Homo sapiens RepID=UPI0001AE634C

u       UniRef100_Q5S4N1 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0
        >Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens RepID=Q5S4N1_HUMAN                Length: 362aa


v       UniRef100_UPI000186CE62 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0
        >DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CE62   Length: 579aa


w       UniRef100_UPI000186D4DD 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0
        >DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D4DD   Length: 684aa


x       UniRef100_UPI000186DD12 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0
        >DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186DD12   Length: 678aa


y       UniRef100_UPI000186EE68 UniRef100_UPI000186EEE2 UniRef100_UPI000186F2DC 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0
        >DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EE68   Length: 755aa
        >DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EEE2
        >DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186F2DC


6       PROTEIN GROUP: 3 1.0000

a       UniRef100_B4DG84 UniRef100_Q9ULH0-5 0.0000
        confidence: 0.9911            num unique p tot indep spectra: 0
        >cDNA FLJ56432, highly similar to Homo sapiens kinase D-interacting substance of 220 kDa (KIDINS220), mRNA n= Length: 625aa
        >Isoform 5 of Kinase D-interacting substrate of 220 kDa n=2 Tax=Homo sapiens RepID=Q9ULH0-5


b       UniRef100_B4DGY1 UniRef100_UPI0001B79857 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0
        >cDNA FLJ61245, highly similar to Homo sapiens kinase D-interacting substance of 220 kDa (KIDINS220), mRNA n= Length: 994aa
        >UPI0001B79857 related cluster n=1 Tax=Homo sapiens RepID=UPI0001B79857


c       UniRef100_B4DK94 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0
        >cDNA FLJ61593, highly similar to Homo sapiens kinase D-interacting substance of 220 kDa (KIDINS220), mRNA (F Length: 1218aa


d       UniRef100_Q7Z322 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0
        >Putative uncharacterized protein DKFZp686H14204 (Fragment) n=1 Tax=Homo sapiens RepID=Q7Z322_HUMAN    Length: 691aa


e       UniRef100_Q9ULH0 UniRef100_Q9ULH0-2 UniRef100_Q9ULH0-4 0.0000
        confidence: 1.0000            num unique p tot indep spectra: 0          subsumed entries: 6
        >Kinase D-interacting substrate of 220 kDa n=1 Tax=Homo sapiens RepID=KDIS_HUMAN                    Length: 1771aa
        >Isoform 2 of Kinase D-interacting substrate of 220 kDa n=1 Tax=Homo sapiens RepID=Q9ULH0-2
        >Isoform 4 of Kinase D-interacting substrate of 220 kDa n=1 Tax=Homo sapiens RepID=Q9ULH0-4


f       UniRef100_Q9ULH0-3 0.0000
        confidence: 0.9904            num unique p tot indep spectra: 0
        >Isoform 3 of Kinase D-interacting substrate of 220 kDa n=1 Tax=Homo sapiens RepID=Q9ULH0-3         Length: 1031aa


g       UniRef100_UPI0000371E3E 0.0000
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     confidence: 0.2659        num unique p tot indep spectra: 0
     >UPI0000371E3E related cluster n=1 Tax=Homo sapiens RepID=UPI0000371E3E                               Length: 151aa


7    PROTEIN GROUP: 4 1.0000

a    UniRef100_B7Z1V7 UniRef100_B7Z4V2 UniRef100_P38646 UniRef100_Q8N1C8 1.0000
     confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.22%
     >cDNA FLJ51811, highly similar to Stress-70 protein, mitochondrial n=1 Tax=Homo sapiens RepID=B7Z1V7_HUMAN Length: 437aa
     >cDNA FLJ51907, highly similar to Stress-70 protein, mitochondrial n=2 Tax=Homininae RepID=B7Z4V2_HUMAN
     >Stress-70 protein, mitochondrial n=1 Tax=Homo sapiens RepID=GRP75_HUMAN
     >HSPA9 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8N1C8_HUMAN


b    UniRef100_B7Z4T3 0.0000
     confidence: 0.0768        num unique p tot indep spectra: 0
     >cDNA FLJ51903, highly similar to Stress-70 protein, mitochondrial n=1 Tax=Homo sapiens RepID=B7Z4T3_HUMAN Length: 632aa


c    UniRef100_D6RJI2 0.0000
     confidence: 0.9999        num unique p tot indep spectra: 0
     >Putative uncharacterized protein HSPA9 n=2 Tax=Homo sapiens RepID=D6RJI2_HUMAN                       Length: 95aa


8    PROTEIN GROUP: 5 1.0000

a    UniRef100_C5IWV5 UniRef100_P00761 1.0000
     confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
     >Trypsinogen n=1 Tax=Sus scrofa RepID=C5IWV5_PIG                                                      Length: 246aa
     >Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG


b    UniRef100_A1A508 UniRef100_A6XMV8 UniRef100_A6XMV9 UniRef100_P07477 UniRef100_P07478 UniRef100_Q3SY19
     UniRef100_Q3SY20 UniRef100_Q45KI0 UniRef100_Q53ZX7 UniRef100_Q53ZX8 UniRef100_Q53ZX9 UniRef100_Q6PK75
     UniRef100_Q7Z5F3 UniRef100_Q86W17 UniRef100_Q86W20 UniRef100_Q8NHM4 UniRef100_UPI0000D9A9C8 UniRef100_UPI0001795EE3
     UniRef100_UPI0001AE7178 UniRef100_UPI0001AE7179 UniRef100_UPI0001B79292 UniRef100_UPI0001B79293 0.0000
     confidence: 0.0185        num unique p tot indep spectra: 0
     >PRSS3 protein n=1 Tax=Homo sapiens RepID=A1A508_HUMAN                                                Length: 247aa
     >Protease serine 2 preproprotein n=1 Tax=Homo sapiens RepID=A6XMV8_HUMAN
     >Protease serine 2 preproprotein n=1 Tax=Homo sapiens RepID=A6XMV9_HUMAN
     >Alpha-trypsin chain 2 n=1 Tax=Homo sapiens RepID=TRY1_HUMAN
     >Trypsin-2 n=2 Tax=Homo sapiens RepID=TRY2_HUMAN
     >PRSS1 protein n=1 Tax=Homo sapiens RepID=Q3SY19_HUMAN
     >Protease, serine, 2 (Trypsin 2) n=1 Tax=Homo sapiens RepID=Q3SY20_HUMAN
     >Trypsin I (Fragment) n=1 Tax=Homo sapiens RepID=Q45KI0_HUMAN
     >Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q53ZX7_HUMAN
     >Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q53ZX8_HUMAN
     >Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q53ZX9_HUMAN
     >PRSS2 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6PK75_HUMAN
     >Protease serine 2 isoform B n=1 Tax=Homo sapiens RepID=Q7Z5F3_HUMAN
     >Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q86W17_HUMAN
     >Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q86W20_HUMAN
     >Putative trypsin-6 n=1 Tax=Homo sapiens RepID=TRY6_HUMAN
     >PREDICTED: protease, serine, 2 (trypsin 2) isoform 1 n=1 Tax=Macaca mulatta RepID=UPI0000D9A9C8
     >PREDICTED: similar to anionic trypsinogen n=1 Tax=Equus caballus RepID=UPI0001795EE3
     >trypsinogen C (TRY6) on chromosome 7 n=1 Tax=Homo sapiens RepID=UPI0001AE7178
     >Trypsin-2 precursor (EC 3.4.21.4) (Trypsin II) (Anionic trypsinogen) (Serine protease 2). n=1 Tax=Homo sapiens RepID=UPI0001AE7179
     >UPI0001B79292 related cluster n=1 Tax=Homo sapiens RepID=UPI0001B79292
     >UPI0001B79293 related cluster n=1 Tax=Homo sapiens RepID=UPI0001B79293


c    UniRef100_A4UWM7 UniRef100_A8CED1 UniRef100_A8CED3 UniRef100_B1AN99 UniRef100_B5AEC7 UniRef100_B9WPP8
     UniRef100_C1KRJ0 UniRef100_D2D388 UniRef100_O42158 UniRef100_O42159 UniRef100_O42160 UniRef100_O42608
     UniRef100_P06871 UniRef100_P07146 UniRef100_P12788 UniRef100_P19799 UniRef100_P35030 UniRef100_P35030-2
     UniRef100_P35030-3 UniRef100_Q0PG34 UniRef100_Q6ISJ4 UniRef100_Q6R670 UniRef100_Q6R671 UniRef100_Q7T1R8
     UniRef100_Q7Z5F4 UniRef100_Q8N2U3 UniRef100_UPI000021129C UniRef100_UPI00004A5B07 UniRef100_UPI00005A2FD6
               UniRef100_UPI00005A2FD7
     UniRef100_UPI00005E8630 UniRef100_UPI0000D92B0D UniRef100_UPI0000D92B15 UniRef100_UPI0000E21E68 UniRef100_UPI0000F2E411
               UniRef100_UPI000194B97D
     UniRef100_UPI000194B9B7 UniRef100_UPI0001AE6E33 UniRef100_UPI0001AE7177 0.0000
     confidence: 0.9909        num unique p tot indep spectra: 0
     >Trypsinogen n=1 Tax=Oryzias latipes RepID=A4UWM7_ORYLA                                               Length: 242aa
     >Protease, serine, 3 (Mesotrypsin), isoform CRA_d n=1 Tax=Homo sapiens RepID=A8CED1_HUMAN
     >Trypsinogen 5 n=1 Tax=Homo sapiens RepID=A8CED3_HUMAN
     >Protease, serine, 3 (Fragment) n=1 Tax=Homo sapiens RepID=B1AN99_HUMAN
     >Trypsin (Fragment) n=2 Tax=Rhinichthys RepID=B5AEC7_9TELE
     >Trypsin (Fragment) n=1 Tax=Thunnus thynnus RepID=B9WPP8_THUTH
     >Trypsin (Fragment) n=1 Tax=Petenia splendida RepID=C1KRJ0_9CICH
     >Trypsinogen n=1 Tax=Culter alburnus RepID=D2D388_9TELE
     >Trypsinogen a2 n=1 Tax=Petromyzon marinus RepID=O42158_PETMA
     >Trypsinogen B1 (Fragment) n=1 Tax=Petromyzon marinus RepID=O42159_PETMA
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>Trypsinogen b2 (Fragment) n=1 Tax=Petromyzon marinus RepID=O42160_PETMA
>Trypsinogen A1 n=1 Tax=Petromyzon marinus RepID=O42608_PETMA
>Cationic trypsin n=1 Tax=Canis lupus familiaris RepID=TRY1_CANFA
>Anionic trypsin-2 n=2 Tax=Mus musculus RepID=TRY2_MOUSE
>Trypsin-4 n=1 Tax=Rattus norvegicus RepID=TRY4_RAT
>Trypsin n=1 Tax=Xenopus laevis RepID=TRY1_XENLA
>Trypsin-3 n=1 Tax=Homo sapiens RepID=TRY3_HUMAN
>Isoform B of Trypsin-3 n=1 Tax=Homo sapiens RepID=P35030-2
>Isoform C of Trypsin-3 n=1 Tax=Homo sapiens RepID=P35030-3
>Trypsin n=1 Tax=Spinibarbus sinensis RepID=Q0PG34_9TELE
>Mesotrypsinogen n=1 Tax=Homo sapiens RepID=Q6ISJ4_HUMAN
>Trypsin n=1 Tax=Oreochromis aureus RepID=Q6R670_OREAU
>Trypsin n=1 Tax=Oreochromis niloticus RepID=Q6R671_ORENI
>Trypsinogen n=1 Tax=Pangasianodon hypophthalmus RepID=Q7T1R8_9TELE
>Protease serine 4 isoform B n=1 Tax=Homo sapiens RepID=Q7Z5F4_HUMAN
>PRSS3 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8N2U3_HUMAN
>Trypsin-3 precursor (EC 3.4.21.4) (Trypsin III) (Brain trypsinogen) (Mesotrypsinogen) (Trypsin IV) (Serine protease 3) (Serine protease 4). n=1 Tax=Homo sapiens RepID=UPI000021129C
>PREDICTED: similar to trypsinogen 7 isoform 3 n=1 Tax=Canis lupus familiaris RepID=UPI00004A5B07
>PREDICTED: similar to trypsinogen 7 isoform 5 n=1 Tax=Canis lupus familiaris RepID=UPI00005A2FD6
>PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 6 n=1 Tax=Canis lupus familiaris RepID=UPI00005A2FD7
>PREDICTED: similar to Anionic trypsin n=1 Tax=Monodelphis domestica RepID=UPI00005E8630
>PREDICTED: similar to Cationic trypsin-3 precursor (Cationic trypsin III) (Pretrypsinogen III) n=1 Tax=Monodelphis domestica RepID=UPI0000D92B0D
>PREDICTED: similar to pancreatic anionic trypsinogen n=1 Tax=Monodelphis domestica RepID=UPI0000D92B15
>PREDICTED: similar to trypsinogen IV b-form n=1 Tax=Pan troglodytes RepID=UPI0000E21E68
>PREDICTED: similar to Cationic trypsin-3 precursor (Cationic trypsin III) (Pretrypsinogen III) n=1 Tax=Monodelphis domestica RepID=UPI0000F2E411
>PREDICTED: similar to Anionic trypsin n=1 Tax=Taeniopygia guttata RepID=UPI000194B97D
>PREDICTED: similar to Anionic trypsin n=1 Tax=Taeniopygia guttata RepID=UPI000194B9B7
>UPI0001AE6E33 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6E33
>UPI0001AE7177 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7177

d UniRef100_P00762 UniRef100_Q86W19 UniRef100_UPI0000D9A9C4 0.0000
confidence: 0.0003 num unique p tot indep spectra: 0
>Anionic trypsin-1 n=1 Tax=Rattus norvegicus RepID=TRY1_RAT Length: 246aa
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q86W19_HUMAN
>PREDICTED: protease, serine, 1 (trypsin 1) n=1 Tax=Macaca mulatta RepID=UPI0000D9A9C4

e UniRef100_P06872 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0
>Anionic trypsin n=2 Tax=Canis lupus familiaris RepID=TRY2_CANFA Length: 247aa

f UniRef100_Q7M754 0.0000
confidence: 0.9995 num unique p tot indep spectra: 0
>Try10-like trypsinogen n=1 Tax=Mus musculus RepID=Q7M754_MOUSE Length: 246aa

g UniRef100_UPI00005A2FD5 0.0000
confidence: 0.0022 num unique p tot indep spectra: 0
>PREDICTED: similar to trypsinogen 7 isoform 4 n=1 Tax=Canis lupus familiaris RepID=UPI00005A2FD5 Length: 138aa

9 PROTEIN GROUP: 6 1.0000

a UniRef100_D3DNC3 1.0000
confidence: coverage: 29 num unique tot indep spe share of spe subsumed entries: 2
>Methyl-CpG binding domain protein 4, isoform CRA_a n=2 Tax=Homo sapiens RepID=D3DNC3_HUMAN Length: 574aa

b UniRef100_B4DZN2 0.0000
confidence: 1.0000 num unique tot indep spectra: 0
>cDNA FLJ61001, highly similar to Methyl-CpG-binding domain protein 4 (EC 3.2.2.-) n=1 Tax=Homo sap Length: 572aa

c UniRef100_D6RBI7 0.0000
confidence: 1.0000 num unique tot indep spectra: 0
>Putative uncharacterized protein MBD4 n=1 Tax=Homo sapiens RepID=D6RBI7_HUMAN Length: 52aa

d UniRef100_D6RDL1 UniRef100_D6RE61 0.0000
confidence: 1.0000 num unique tot indep spectra: 0
>Putative uncharacterized protein MBD4 n=1 Tax=Homo sapiens RepID=D6RDL1_HUMAN Length: 86aa
>Putative uncharacterized protein MBD4 n=1 Tax=Homo sapiens RepID=D6RE61_HUMAN

e UniRef100_O95243 UniRef100_UPI000020A20A 0.0000
confidence: 1.0000 num unique tot indep spectra: 0 subsumed entries: 4

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      >Methyl-CpG-binding domain protein 4 n=2 Tax=Homo sapiens RepID=MBD4_HUMAN                    Length: 580aa
      >UPI000020A20A related cluster n=1 Tax=Homo sapiens RepID=UPI000020A20A


f     UniRef100_O95243-3 0.0000
      confidence: 1.0000        num unique  tot indep spectra: 0
      >Isoform 3 of Methyl-CpG-binding domain protein 4 n=1 Tax=Homo sapiens RepID=O95243-3          Length: 540aa


g     UniRef100_Q2MD36 0.0000
      confidence: 1.0000        num unique  tot indep spectra: 0
      >Putative methyl-CpG binding protein n=1 Tax=Homo sapiens RepID=Q2MD36_HUMAN                   Length: 262aa


h     UniRef100_Q4R3V5 0.0000
      confidence: 1.0000        num unique  tot indep spectra: 0
      >Testis cDNA clone: QtsA-13911, similar to human methyl-CpG binding domain protein 4 (MBD4), n=1 T Length: 498aa


i     UniRef100_UPI000186D3A2 0.0000
      confidence: 0.9998        num unique  tot indep spectra: 0
      >conserved hypothetical protein n=1 Tax=Pediculus humanus corporis RepID=UPI000186D3A2         Length: 168aa


10    PROTEIN GROUP: 7 1.0000

a     UniRef100_P02769 1.0000
      confidence: 1. coverage: 28. num unique p tot indep spec share of spect subsumed entries: 6
      >Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN                                             Length: 607aa


b     UniRef100_A6NBZ8 UniRef100_A8K9P0 UniRef100_B2RBS8 UniRef100_B4DPP6 UniRef100_B4DPR2 UniRef100_P02768
      UniRef100_UPI0001AE74F7 UniRef100_UPI0001D3B4DF 0.0000
      confidence: 1.0000        num unique p tot indep spectra: 0
      >Putative uncharacterized protein ALB n=1 Tax=Homo sapiens RepID=A6NBZ8_HUMAN                  Length: 627aa
      >cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA n=1 Tax=Homo sapiens RepID=A8K9P0_HUMAN
      >cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA n=1 Tax=Homo sapiens RepID=B2RBS8_HUMAN
      >cDNA FLJ54371, highly similar to Serum albumin n=1 Tax=Homo sapiens RepID=B4DPP6_HUMAN
      >cDNA FLJ50830, highly similar to Serum albumin n=1 Tax=Homo sapiens RepID=B4DPR2_HUMAN
      >Serum albumin n=2 Tax=Hominidae RepID=ALBU_HUMAN
      >UPI0001AE74F7 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE74F7
      >UPI0001D3B4DF related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3B4DF


c     UniRef100_B7WNR0 UniRef100_C9JKR2 UniRef100_D6RHD5 UniRef100_P02768-2 0.0000
      confidence: 1.0000        num unique p tot indep spectra: 0
      >Putative uncharacterized protein ALB n=1 Tax=Homo sapiens RepID=B7WNR0_HUMAN                  Length: 494aa
      >Albumin, isoform CRA_k n=1 Tax=Homo sapiens RepID=C9JKR2_HUMAN
      >Putative uncharacterized protein ALB n=1 Tax=Homo sapiens RepID=D6RHD5_HUMAN
      >Isoform 2 of Serum albumin n=1 Tax=Homo sapiens RepID=P02768-2


d     UniRef100_Q56G89 0.0000
      confidence: 1.0000        num unique p tot indep spectra: 0
      >Serum albumin n=1 Tax=Homo sapiens RepID=Q56G89_HUMAN                                         Length: 609aa


e     UniRef100_Q8IUK7 UniRef100_UPI000045722A 0.0000
      confidence: 1.0000        num unique p tot indep spectra: 0
      >ALB protein n=1 Tax=Homo sapiens RepID=Q8IUK7_HUMAN                                           Length: 396aa
      >Serum albumin precursor. n=1 Tax=Homo sapiens RepID=UPI000045722A


f     UniRef100_UPI0001610EBC 0.0000
      confidence: 0.9997        num unique p tot indep spectra: 0
      >UPI0001610EBC related cluster n=1 Tax=Homo sapiens RepID=UPI0001610EBC                        Length: 197aa


g     UniRef100_UPI000179EC85 0.0000
      confidence: 1.0000        num unique p tot indep spectra: 0
      >Serum albumin precursor (Allergen Bos d 6) (BSA). n=1 Tax=Bos taurus RepID=UPI000179EC85      Length: 609aa

11    PROTEIN GROUP: 8 1.0000

a     UniRef100_P04264 1.0000
      confidence: 1. coverage: 20. num unique p tot indep spec share of spectrum id's: 5.18%
      >Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN                         Length: 644aa


b     UniRef100_P35908 1.0000
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        confidence: 1. coverage: 10. num unique p tot indep spec share of spectrum id's: 1.85%
        >Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E_HUMAN                                   Length: 639aa


c       UniRef100_Q0IIN1 UniRef100_UPI00001D797A 0.7657
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.25%
        >Keratin 77 n=1 Tax=Homo sapiens RepID=Q0IIN1_HUMAN                                                                Length: 578aa
        >keratin, type II cytoskeletal 1b n=1 Tax=Homo sapiens RepID=UPI00001D797A


d       UniRef100_A8K2I0 UniRef100_B2R853 UniRef100_B4DKJ0 UniRef100_B4DKV4 UniRef100_B4DRR0 UniRef100_B4DRR7
        UniRef100_B4DRS2 UniRef100_B4DRU6 UniRef100_B4DRW1 UniRef100_B4DRY0 UniRef100_B4DWU6 UniRef100_P02538
        UniRef100_P19013 UniRef100_P48668 UniRef100_UPI0000D9FD95 UniRef100_UPI0001AE6B0A UniRef100_UPI0001AE6B0B 0.0000
        confidence: 0.1019             num unique p tot indep spectra: 0
        >cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA n=1 Tax=Homo sapiens RepID=A8K2I0 Length: 564aa
        >cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA n=1 Tax=Homo sapiens RepID=B2R853_HUMAN
        >cDNA FLJ58539, highly similar to Keratin, type II cytoskeletal 4 n=1 Tax=Homo sapiens RepID=B4DKJ0_HUMAN
        >cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B n=1 Tax=Homo sapiens RepID=B4DKV4_HUMAN
        >cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A n=1 Tax=Homo sapiens RepID=B4DRR0_HUMAN
        >cDNA FLJ59399, highly similar to Keratin, type II cytoskeletal 4 n=1 Tax=Homo sapiens RepID=B4DRR7_HUMAN
        >cDNA FLJ58275, highly similar to Keratin, type II cytoskeletal 4 n=1 Tax=Homo sapiens RepID=B4DRS2_HUMAN
        >cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A n=1 Tax=Homo sapiens RepID=B4DRU6_HUMAN
        >cDNA FLJ55805, highly similar to Keratin, type II cytoskeletal 4 n=1 Tax=Homo sapiens RepID=B4DRW1_HUMAN
        >cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E n=1 Tax=Homo sapiens RepID=B4DRY0_HUMAN
        >cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A n=1 Tax=Homo sapiens RepID=B4DWU6_HUMAN
        >Keratin, type II cytoskeletal 6A n=1 Tax=Homo sapiens RepID=K2C6A_HUMAN
        >Keratin, type II cytoskeletal 4 n=1 Tax=Homo sapiens RepID=K2C4_HUMAN
        >Keratin, type II cytoskeletal 6C n=1 Tax=Homo sapiens RepID=K2C6C_HUMAN
        >keratin, type II cytoskeletal 4 n=1 Tax=Homo sapiens RepID=UPI0000D9FD95
        >UPI0001AE6B0A related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6B0A
        >UPI0001AE6B0B related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6B0B


e       UniRef100_P04259 0.0000
        confidence: 0.9973             num unique p tot indep spectra: 0           subsumed entries: 1
        >Keratin, type II cytoskeletal 6B n=1 Tax=Homo sapiens RepID=K2C6B_HUMAN                                           Length: 564aa


f       UniRef100_Q7Z794 0.0000
        confidence: 0.0043             num unique p tot indep spectra: 0
        >Keratin, type II cytoskeletal 1b n=1 Tax=Homo sapiens RepID=K2C1B_HUMAN                                           Length: 576aa


12      PROTEIN GROUP: 9 1.0000

a       UniRef100_P11142 1.0000
        confidence: 1. coverage: 28. num unique p tot indep spec share of spect subsumed entries: 12
        >Heat shock cognate 71 kDa protein n=8 Tax=Eutheria RepID=HSP7C_HUMAN                                              Length: 646aa


b       UniRef100_P11021 1.0000
        confidence: 1. coverage: 13. num unique p tot indep spec share of spect subsumed entries: 2
        >78 kDa glucose-regulated protein n=1 Tax=Homo sapiens RepID=GRP78_HUMAN                                           Length: 654aa


c       UniRef100_UPI000186E8AE 0.9762
        confidence: 0. coverage: 3.1 num unique p tot indep spec share of spectrum id's: 0.43%
        >Heat shock cognate 71 kDa protein, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E8AE               Length: 635aa


d       UniRef100_UPI000186D0C5 0.8711
        confidence: 0. coverage: 2.7 num unique p tot indep spec share of spectrum id's: 0.35%
        >Heat shock protein 70 A2, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D0C5                        Length: 661aa


e       UniRef100_A4D111 0.0000
        confidence: 1.0000             num unique p tot indep spectra: 0
        >Similar to Chain , Heat-Shock Cognate 70kd Protein (44kd Atpase N-Terminal) (E.C.3.6.1.3) Mutant With Asp 206 R Length: 231aa


f       UniRef100_A8K7Q2 0.0000
        confidence: 1.0000             num unique p tot indep spectra: 0
        >cDNA FLJ77848 n=2 Tax=Homo sapiens RepID=A8K7Q2_HUMAN                                                             Length: 410aa


g       UniRef100_B2R6X5 UniRef100_B3KSM6 UniRef100_P17066 UniRef100_Q53FC7 0.0000
        confidence: 1.0000             num unique p tot indep spectra: 0
        >cDNA, FLJ93166, highly similar to Homo sapiens heat shock 70kDa protein 6 (HSP70B') (HSPA6), mRNA n=1 Tax=l Length: 643aa
        >cDNA FLJ36606 fis, clone TRACH2015654, highly similar to HEAT SHOCK 70 kDa PROTEIN 6 n=1 Tax=Homo sapiens RepID=B3KSM6_HUMAN
        >Heat shock 70 kDa protein 6 n=1 Tax=Homo sapiens RepID=HSP76_HUMAN
        >Heat shock 70kDa protein 6 (HSP70B') variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53FC7_HUMAN
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h      UniRef100_B2RCQ9 UniRef100_B4DI54 UniRef100_P34931 UniRef100_Q53FA3 UniRef100_UPI0001AE7148 UniRef100_UPI0001AE71DD
       UniRef100_UPI0001AE71EA 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA, FLJ96225, highly similar to Homo sapiens heat shock 70kDa protein 1-like (HSPA1L), mRNA n=1 Tax=Homo Length: 641aa
       >cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L n=1 Tax=Homo sapiens RepID=B4DI54_HUMAN
       >Heat shock 70 kDa protein 1-like n=1 Tax=Homo sapiens RepID=HS71L_HUMAN
       >Heat shock 70kDa protein 1-like (Fragment) n=1 Tax=Homo sapiens RepID=Q53FA3_HUMAN
       >UPI0001AE7148 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7148
       >UPI0001AE71DD related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE71DD
       >UPI0001AE71EA related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE71EA


i      UniRef100_B3KTT5 UniRef100_Q5SP16 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ38698 fis, clone KIDNE2002015, highly similar to HEAT SHOCK 70 kDa PROTEIN 1 n=1 Tax=Homo sapien Length: 476aa
       >Heat shock 70kDa protein 1A n=1 Tax=Homo sapiens RepID=Q5SP16_HUMAN


j      UniRef100_B3KTV0 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ38781 fis, clone LIVER2000216, highly similar to HEAT SHOCK COGNATE 71 kDa PROTEIN n=1 Tax=Hom Length: 621aa


k      UniRef100_B3KUS2 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ40505 fis, clone TESTI2045562, highly similar to HEAT SHOCK-RELATED 70 kDa PROTEIN 2 n=1 Tax=Hon Length: 413aa


l      UniRef100_B4DEF7 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ60062, highly similar to 78 kDa glucose-regulated protein n=1 Tax=Homo sapiens RepID=B4DEF7_HUMA Length: 278aa


m      UniRef100_B4DFN9 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ54303, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4DFN9_HUMAN      Length: 572aa


n      UniRef100_B4DHP5 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ51847, highly similar to Heat shock 70 kDa protein 6 n=1 Tax=Homo sapiens RepID=B4DHP5_HUMAN      Length: 619aa


o      UniRef100_B4DI39 UniRef100_B4DWK5 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ54328, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4DI39_HUMAN      Length: 618aa
       >cDNA FLJ54392, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4DWK5_HUMAN


p      UniRef100_B4DNT8 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ54370, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4DNT8_HUMAN      Length: 617aa


q      UniRef100_B4DNV4 UniRef100_P48741 0.0000
       confidence: 0.9996            num unique p tot indep spectra: 0
       >cDNA FLJ53071, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4DNV4_HUMAN      Length: 232aa
       >Putative heat shock 70 kDa protein 7 n=1 Tax=Homo sapiens RepID=HSP77_HUMAN


r      UniRef100_B4DNX1 UniRef100_UPI0001AE714A 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ53752, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4DNX1_HUMAN      Length: 417aa
       >UPI0001AE714A related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE714A


s      UniRef100_B4DTX2 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ59163, highly similar to Heat shock cognate 71 kDa protein n=2 Tax=Euarchontoglires RepID=B4DTX2_H Length: 210aa


t      UniRef100_B4DVU9 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ54389, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4DVU9_HUMAN      Length: 544aa


u      UniRef100_B4DXY3 0.0000
       confidence: 1.0000            num unique p tot indep spectra: 0
       >cDNA FLJ56517, highly similar to Heat shock 70 kDa protein 1L n=1 Tax=Homo sapiens RepID=B4DXY3_HUMAN    Length: 532aa
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v     UniRef100_B4E1S9 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >cDNA FLJ54283, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4E1S9_HUMAN      Length: 550aa


w     UniRef100_B4E1T6 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >cDNA FLJ54342, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4E1T6_HUMAN      Length: 398aa


x     UniRef100_B4E388 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >cDNA FLJ54407, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4E388_HUMAN      Length: 563aa


y     UniRef100_B4E3B6 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >cDNA FLJ54408, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4E3B6_HUMAN      Length: 586aa


z     UniRef100_C9IYE6 UniRef100_C9JCM4 UniRef100_UPI0001AE71DE 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >Putative uncharacterized protein ENSP00000392294 n=1 Tax=Homo sapiens RepID=C9IYE6_HUMAN                  Length: 238aa
      >Putative uncharacterized protein ENSP00000396508 n=1 Tax=Homo sapiens RepID=C9JCM4_HUMAN
      >UPI0001AE71DE related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE71DE


aa    UniRef100_P08107 UniRef100_Q59EJ3 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0          subsumed entries: 11
      >Heat shock 70 kDa protein 1A/1B n=3 Tax=Hominidae RepID=HSP71_HUMAN                                       Length: 641aa
      >Heat shock 70kDa protein 1A variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59EJ3_HUMAN


ab    UniRef100_P54652 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >Heat shock-related 70 kDa protein 2 n=1 Tax=Homo sapiens RepID=HSP72_HUMAN                                Length: 639aa


ac    UniRef100_Q4R8Y3 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >Testis cDNA clone: QtsA-11142, similar to human heat shock 70kDa protein 2 (HSPA2), n=1 Tax=Macaca fascicular Length: 302aa


ad    UniRef100_Q53GZ6 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >Heat shock 70kDa protein 8 isoform 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GZ6_HUMAN           Length: 646aa


ae    UniRef100_Q53HF2 UniRef100_UPI00015E00A1 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >Heat shock 70kDa protein 8 isoform 2 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53HF2_HUMAN           Length: 493aa
      >Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8). n=1 Tax=Homo sapiens RepID=UPI00015E00A1


af    UniRef100_Q96H53 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >HSPA8 protein (Fragment) n=2 Tax=Homo sapiens RepID=Q96H53_HUMAN                                          Length: 219aa


ag    UniRef100_Q9NWW3 UniRef100_Q9NZ87 0.0000
      confidence: 0.9999         num unique p tot indep spectra: 0
      >cDNA FLJ20564 fis, clone KAT12033 n=1 Tax=Homo sapiens RepID=Q9NWW3_HUMAN                                 Length: 129aa
      >Uncharacterized bone marrow protein BM034 n=1 Tax=Homo sapiens RepID=Q9NZ87_HUMAN


ah    UniRef100_Q9UQC1 0.0000
      confidence: 0.9998         num unique p tot indep spectra: 0
      >Heat shock protein 72 (Fragment) n=1 Tax=Homo sapiens RepID=Q9UQC1_HUMAN                                  Length: 151aa


ai    UniRef100_UPI000186CBE0 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >Heat shock 70 kDa protein cognate, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CBE0         Length: 660aa


aj    UniRef100_UPI000186D9DF 0.0000
      confidence: 0.0751         num unique p tot indep spectra: 0
      >Heat shock protein, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D9DF                       Length: 642aa
```

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ak    UniRef100_UPI000186E328 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >Heat shock 70 kDa protein cognate 3 precursor, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E Length: 656aa


al    UniRef100_UPI0001AE7147 UniRef100_UPI0001AE7283 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >UPI0001AE7147 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7147                    Length: 560aa
      >Heat shock 70 kDa protein 1L (Heat shock 70 kDa protein 1-like) (Heat shock 70 kDa protein 1-Hom) (HSP70-Hom). n=1 Tax=Homo sapiens
                RepID=UPI0001AE7283

am    UniRef100_UPI0001AE7149 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >UPI0001AE7149 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7149                    Length: 232aa


13    PROTEIN GROUP: 10 1.0000

a     UniRef100_P13639 UniRef100_Q8TA90 0.9999
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
      >Elongation factor 2 n=2 Tax=Hominidae RepID=EF2_HUMAN                                     Length: 858aa
      >Similar to Elongation factor 2b (Fragment) n=1 Tax=Homo sapiens RepID=Q8TA90_HUMAN


b     UniRef100_B4DPU3 UniRef100_Q6W6M8 0.0000
      confidence: 0.2837         num unique p tot indep spectra: 0
      >cDNA FLJ56548, highly similar to Elongation factor 2 n=1 Tax=Homo sapiens RepID=B4DPU3_HUMAN   Length: 566aa
      >Antigen MLAA-42 (Fragment) n=1 Tax=Homo sapiens RepID=Q6W6M8_HUMAN


c     UniRef100_B4DRE8 UniRef100_Q6PK56 0.0000
      confidence: 0.0809         num unique p tot indep spectra: 0
      >cDNA FLJ58164, highly similar to Elongation factor 2 n=1 Tax=Homo sapiens RepID=B4DRE8_HUMAN   Length: 505aa
      >EEF2 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6PK56_HUMAN


14    PROTEIN GROUP: 11 1.0000

a     UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
      >Keratin, type I cytoskeletal 10 n=1 Tax=Homo sapiens RepID=K1C10_HUMAN                    Length: 584aa
      >keratin, type I cytoskeletal 10 n=1 Tax=Homo sapiens RepID=UPI00017BCE7F


b     UniRef100_C9JT19 UniRef100_P02533 UniRef100_P08779 UniRef100_Q6ZPD6 UniRef100_Q7Z3Y7 UniRef100_Q7Z3Y8
      UniRef100_Q7Z3Y9 UniRef100_Q7Z3Z0 UniRef100_UPI0000E59F67 0.0000
      confidence: 0.1257         num unique p tot indep spectra: 0
      >Putative uncharacterized protein KRT25 n=1 Tax=Homo sapiens RepID=C9JT19_HUMAN            Length: 380aa
      >Keratin, type I cytoskeletal 14 n=1 Tax=Homo sapiens RepID=K1C14_HUMAN
      >Keratin, type I cytoskeletal 16 n=1 Tax=Homo sapiens RepID=K1C16_HUMAN
      >cDNA FLJ25992 fis, clone DMC03508 n=1 Tax=Homo sapiens RepID=Q6ZPD6_HUMAN
      >Keratin, type I cytoskeletal 28 n=1 Tax=Homo sapiens RepID=K1C28_HUMAN
      >Keratin, type I cytoskeletal 27 n=1 Tax=Homo sapiens RepID=K1C27_HUMAN
      >Keratin, type I cytoskeletal 26 n=1 Tax=Homo sapiens RepID=K1C26_HUMAN
      >Keratin, type I cytoskeletal 25 n=1 Tax=Homo sapiens RepID=K1C25_HUMAN
      >keratin 25 n=1 Tax=Homo sapiens RepID=UPI0000E59F67


15    PROTEIN GROUP: 12 1.0000

a     UniRef100_P14625 UniRef100_Q59FC6 UniRef100_Q5CAQ5 0.9999
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
      >Endoplasmin n=1 Tax=Homo sapiens RepID=ENPL_HUMAN                                         Length: 803aa
      >Tumor rejection antigen (Gp96) 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59FC6_HUMAN
      >Tumor rejection antigen (Gp96) 1 n=1 Tax=Homo sapiens RepID=Q5CAQ5_HUMAN


b     UniRef100_A8K3W9 UniRef100_Q5T9W5 UniRef100_Q9H6X9 UniRef100_UPI000059D8E5 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0
      >cDNA FLJ77842 n=1 Tax=Homo sapiens RepID=A8K3W9_HUMAN                                     Length: 362aa
      >Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5T9W5_HUMAN
      >cDNA: FLJ21717 fis, clone COL10322 n=1 Tax=Homo sapiens RepID=Q9H6X9_HUMAN
      >UPI000059D8E5 related cluster n=1 Tax=Homo sapiens RepID=UPI000059D8E5


c     UniRef100_B4DGL0 UniRef100_B4DMA2 UniRef100_P08238 0.0000
      confidence: 1.0000         num unique p tot indep spectra: 0          subsumed entries: 4
      >cDNA FLJ53619, highly similar to Heat shock protein HSP 90-beta n=1 Tax=Homo sapiens RepID=B4DGL0_HUMAN Length: 714aa
      >cDNA FLJ54023, highly similar to Heat shock protein HSP 90-beta n=1 Tax=Homo sapiens RepID=B4DMA2_HUMAN
      >Heat shock protein HSP 90-beta n=1 Tax=Homo sapiens RepID=HS90B_HUMAN
```

d UniRef100_B4DHT9 UniRef100_B4DU71 UniRef100_UPI0001AE6A99 0.0000
confidence: 0.1037 num unique p tot indep spectra: 0
>cDNA FLJ58812, highly similar to Endoplasmin (Heat shock protein 90kDa beta member 1) n=1 Tax=Homo sapiens Length: 468aa
>cDNA FLJ58626, highly similar to Endoplasmin (Heat shock protein 90 kDa beta member 1) n=1 Tax=Homo sapiens RepID=B4DU71_HUMAN
>UPI0001AE6A99 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6A99

e UniRef100_B4DR68 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0
>cDNA FLJ58608, highly similar to Heat shock protein 75 kDa, mitochondrial n=1 Tax=Homo sapiens RepID=B4DR6 Length: 651aa

f UniRef100_O00585 0.0000
confidence: 0.0003 num unique p tot indep spectra: 0
>C-C motif chemokine 21 n=3 Tax=Homo sapiens RepID=CCL21_HUMAN Length: 134aa

g UniRef100_O14942 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0
>Heat shock protein beta (Fragment) n=1 Tax=Homo sapiens RepID=O14942_HUMAN Length: 130aa

h UniRef100_O75322 UniRef100_Q86U12 0.0000
confidence: 0.9986 num unique p tot indep spectra: 0
>Hsp89-alpha-delta-N n=2 Tax=Homo sapiens RepID=O75322_HUMAN Length: 539aa
>Full-length cDNA clone CS0CAP007YF18 of Thymus of Homo sapiens (human) n=1 Tax=Homo sapiens RepID=Q86U12_HUMAN

i UniRef100_P07900 UniRef100_Q2VPJ6 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0
>Heat shock protein HSP 90-alpha n=2 Tax=Homo sapiens RepID=HS90A_HUMAN Length: 732aa
>HSP90AA1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q2VPJ6_HUMAN

j UniRef100_Q12931 UniRef100_Q53FS6 UniRef100_Q53G55 UniRef100_Q9BV61 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0 subsumed entries: 2
>Heat shock protein 75 kDa, mitochondrial n=2 Tax=Homo sapiens RepID=TRAP1_HUMAN Length: 704aa
>TNF receptor-associated protein 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53FS6_HUMAN
>TNF receptor-associated protein 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53G55_HUMAN
>TRAP1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q9BV61_HUMAN

k UniRef100_Q14568 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0
>Putative heat shock protein HSP 90-alpha A2 n=1 Tax=Homo sapiens RepID=HS902_HUMAN Length: 343aa

l UniRef100_Q58FF7 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0
>Putative heat shock protein HSP 90-beta-3 n=1 Tax=Homo sapiens RepID=H90B3_HUMAN Length: 597aa

m UniRef100_Q58FF8 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0
>Putative heat shock protein HSP 90-beta 2 n=1 Tax=Homo sapiens RepID=H90B2_HUMAN Length: 381aa

n UniRef100_Q58FG1 0.0000
confidence: 0.9985 num unique p tot indep spectra: 0
>Putative heat shock protein HSP 90-alpha A4 n=1 Tax=Homo sapiens RepID=HS904_HUMAN Length: 418aa

o UniRef100_Q59EK6 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0
>TNF receptor-associated protein 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59EK6_HUMAN Length: 703aa

p UniRef100_Q5CAQ4 0.0000
confidence: 1.0000 num unique p tot indep spectra: 0
>TNF receptor-associated protein 1 n=1 Tax=Homo sapiens RepID=Q5CAQ4_HUMAN Length: 495aa

q UniRef100_Q5T9W4 UniRef100_UPI000059D8E3 0.0000
confidence: 0.9998 num unique p tot indep spectra: 0
>Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5T9W Length: 170aa
>UPI000059D8E3 related cluster n=1 Tax=Homo sapiens RepID=UPI000059D8E3

r UniRef100_Q5T9W6 0.0000

```
      confidence: 1.0000           num unique p tot indep spectra: 0
      >Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5T9W Length: 141aa


s     UniRef100_Q6PK50 0.0000
      confidence: 1.0000           num unique p tot indep spectra: 0
      >HSP90AB1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6PK50_HUMAN                                      Length: 351aa


t     UniRef100_Q86SX1 0.0000
      confidence: 1.0000           num unique p tot indep spectra: 0
      >Full-length cDNA 5-PRIME end of clone CS0DN005YI08 of Adult brain of Homo sapiens (human) (Fragment) n=1 Ta Length: 262aa


u     UniRef100_Q8N9Z3 0.0000
      confidence: 1.0000           num unique p tot indep spectra: 0
      >cDNA FLJ36025 fis, clone TESTI2016701, highly similar to TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIAT Length: 579aa


v     UniRef100_Q8TBA7 0.0000
      confidence: 1.0000           num unique p tot indep spectra: 0
      >HSP90AA1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8TBA7_HUMAN                                      Length: 638aa


w     UniRef100_Q96GW1 0.0000
      confidence: 0.1512           num unique p tot indep spectra: 0
      >HSP90B1 protein n=1 Tax=Homo sapiens RepID=Q96GW1_HUMAN                                                  Length: 315aa


x     UniRef100_Q96HX7 0.0000
      confidence: 0.1142           num unique p tot indep spectra: 0
      >HSP90AA1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q96HX7_HUMAN                                      Length: 422aa


y     UniRef100_UPI000186D26E 0.0000
      confidence: 0.0001           num unique p tot indep spectra: 0
      >conserved hypothetical protein n=1 Tax=Pediculus humanus corporis RepID=UPI000186D26E                    Length: 718aa


z     UniRef100_UPI000186D735 0.0000
      confidence: 0.9959           num unique p tot indep spectra: 0
      >heat shock protein 75 kDa, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D735               Length: 689aa


aa    UniRef100_UPI000186EC3C 0.0000
      confidence: 0.0667           num unique p tot indep spectra: 0
      >Hsp90 protein, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EC3C                           Length: 725aa

16    PROTEIN GROUP: 13 1.0000

a     UniRef100_P27694 1.0000
      confidence: 1. coverage: 11. num unique p tot indep spec share of spect subsumed entries: 1
      >Replication protein A 70 kDa DNA-binding subunit n=1 Tax=Homo sapiens RepID=RFA1_HUMAN                  Length: 616aa


b     UniRef100_Q4R388 0.0000
      confidence: 0.1752           num unique p tot indep spectra: 0
      >Testis cDNA clone: QtsA-18675, similar to human replication protein A1, 70kDa (RPA1), n=1 Tax=Macaca fascicular Length: 268aa

17    PROTEIN GROUP: 14 1.0000

a     UniRef100_P52272 UniRef100_P52272-2 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
      >Heterogeneous nuclear ribonucleoprotein M n=1 Tax=Homo sapiens RepID=HNRPM_HUMAN                         Length: 730aa
      >Isoform 2 of Heterogeneous nuclear ribonucleoprotein M n=1 Tax=Homo sapiens RepID=P52272-2


b     UniRef100_B4DEG4 0.0000
      confidence: 1.0000           num unique p tot indep spectra: 0
      >cDNA FLJ60435, highly similar to Heterogeneous nuclear ribonucleoprotein M n=1 Tax=Homo sapiens RepID=B4DE Length: 366aa


c     UniRef100_Q59ES8 UniRef100_Q7KYM9 0.0000
      confidence: 1.0000           num unique p tot indep spectra: 0
      >Heterogeneous nuclear ribonucleoprotein M isoform a variant (Fragment) n=2 Tax=Homininae RepID=Q59ES8_HU Length: 615aa
      >ORF protein n=3 Tax=Homininae RepID=Q7KYM9_HUMAN


d     UniRef100_Q6P2D7 0.0000
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        confidence: 0.9993          num unique p tot indep spectra: 0
        >HNRPM protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6P2D7_HUMAN                                    Length: 285aa


18      PROTEIN GROUP: 15 1.0000

a       UniRef100_P54136 1.0000
        confidence: 1. coverage: 7.0 num unique p tot indep spec share of spect subsumed entries: 3
        >Arginyl-tRNA synthetase, cytoplasmic n=2 Tax=Homo sapiens RepID=SYRC_HUMAN                         Length: 660aa


b       UniRef100_B4DXW6 0.0000
        confidence: 0.9983          num unique p tot indep spectra: 0
        >cDNA FLJ50285, highly similar to Arginyl-tRNA synthetase (EC 6.1.1.19) n=1 Tax=Homo sapiens RepID=B4DXW6_ Length: 454aa


c       UniRef100_Q4R5J2 0.0000
        confidence: 0.1068          num unique p tot indep spectra: 0
        >Brain cDNA, clone: QflA-12413, similar to human arginyl-tRNA synthetase (RARS), n=1 Tax=Macaca fascicularis Re Length: 454aa


d       UniRef100_UPI000186D598 0.0000
        confidence: 0.0845          num unique p tot indep spectra: 0
        >Arginyl-tRNA synthetase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D598            Length: 575aa


19      PROTEIN GROUP: 16 1.0000

a       UniRef100_Q53GR7 UniRef100_Q546F9 UniRef100_Q9UJS0 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
        >Solute carrier family 25, member 13 (Citrin) variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GR7_HUMAN   Length: 675aa
        >Mitochondrial aspartate-glutamate carrier protein n=1 Tax=Homo sapiens RepID=Q546F9_HUMAN
        >Calcium-binding mitochondrial carrier protein Aralar2 n=2 Tax=Homininae RepID=CMC2_HUMAN


b       UniRef100_B3KMV8 UniRef100_B3KR64 UniRef100_O75746 UniRef100_UPI0001AE7767 0.0000
        confidence: 0.0849          num unique p tot indep spectra: 0
        >cDNA FLJ12766 fis, clone NT2RP2001520, highly similar to Calcium-binding mitochondrial carrier protein Aralar1 n= Length: 678aa
        >cDNA FLJ33752 fis, clone BRCAN2000364, highly similar to Calcium-binding mitochondrial carrier protein Aralar1 n=1 Tax=Homo sapiens
                        RepID=B3KR64_HUMAN
        >Calcium-binding mitochondrial carrier protein Aralar1 n=1 Tax=Homo sapiens RepID=CMC1_HUMAN
        >Calcium-binding mitochondrial carrier protein Aralar1 (Mitochondrial aspartate glutamate carrier 1) (Solute carrier family 25 member 12). n=1
                        Tax=Homo sapiens RepID=UPI0001AE7767

c       UniRef100_B7Z2E2 0.0000
        confidence: 0.9972          num unique p tot indep spectra: 0
        >cDNA FLJ54671, highly similar to Calcium-binding mitochondrial carrier protein Aralar2 n=1 Tax=Homo sapiens Rep Length: 567aa


d       UniRef100_Q75KX8 0.0000
        confidence: 0.1643          num unique p tot indep spectra: 0
        >Putative uncharacterized protein SLC25A13 (Fragment) n=1 Tax=Homo sapiens RepID=Q75KX8_HUMAN          Length: 288aa


20      PROTEIN GROUP: 17 1.0000

a       UniRef100_Q96PK6 1.0000
        confidence: 1. coverage: 12. num unique p tot indep spec share of spect subsumed entries: 3
        >RNA-binding protein 14 n=1 Tax=Homo sapiens RepID=RBM14_HUMAN                                       Length: 669aa


b       UniRef100_B0LM41 UniRef100_B8ZZ74 UniRef100_D6RAB9 UniRef100_D6RGD8 UniRef100_Q2PYN1 UniRef100_Q96PK6-2
        UniRef100_UPI0001881AEF UniRef100_UPI0001881AF0 0.0000
        confidence: 0.3410          num unique p tot indep spectra: 0
        >Transcriptional coactivator CoAZ n=1 Tax=Homo sapiens RepID=B0LM41_HUMAN                            Length: 339aa
        >Putative uncharacterized protein RBM14 n=1 Tax=Homo sapiens RepID=B8ZZ74_HUMAN
        >Putative uncharacterized protein RBM14 n=1 Tax=Homo sapiens RepID=D6RAB9_HUMAN
        >Putative uncharacterized protein RBM14 n=1 Tax=Homo sapiens RepID=D6RGD8_HUMAN
        >Coactivator regulator n=1 Tax=Homo sapiens RepID=Q2PYN1_HUMAN
        >Isoform 2 of RNA-binding protein 14 n=1 Tax=Homo sapiens RepID=Q96PK6-2
        >UPI0001881AEF related cluster n=1 Tax=Homo sapiens RepID=UPI0001881AEF
        >UPI0001881AF0 related cluster n=1 Tax=Homo sapiens RepID=UPI0001881AF0


c       UniRef100_B4DNG4 0.0000
        confidence: 0.9996          num unique p tot indep spectra: 0
        >cDNA FLJ59137, highly similar to RNA-binding protein 14 n=1 Tax=Homo sapiens RepID=B4DNG4_HUMAN     Length: 213aa


d       UniRef100_Q59GV2 0.0000
        confidence: 1.0000          num unique p tot indep spectra: 0
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        >RNA binding motif protein 14 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59GV2_HUMAN                        Length: 552aa


21      PROTEIN GROUP: 18 1.0000

a       UniRef100_Q9NZI8 1.0000
        confidence: 1. coverage: 11. num unique p tot indep spec share of spect subsumed entries: 3
        >Insulin-like growth factor 2 mRNA-binding protein 1 n=1 Tax=Homo sapiens RepID=IF2B1_HUMAN                     Length: 577aa


b       UniRef100_O00425 1.0000
        confidence: 1. coverage: 6.7 num unique p tot indep spec share of spect subsumed entries: 2
        >Insulin-like growth factor 2 mRNA-binding protein 3 n=1 Tax=Homo sapiens RepID=IF2B3_HUMAN                     Length: 579aa


c       UniRef100_B4DKT5 UniRef100_C9JLA6 UniRef100_O00425-2 UniRef100_Q9Y6M1 UniRef100_Q9Y6M1-1 UniRef100_Q9Y6M1-3
        UniRef100_Q9Y6M1-4 UniRef100_Q9Y6M1-5 0.0000
        confidence: 0.9997           num unique p tot indep spectra: 0
        >cDNA FLJ53054, highly similar to Insulin-like growth factor 2 mRNA-binding protein 2 n=1 Tax=Homo sapiens RepI Length: 300aa
        >Putative uncharacterized protein IGF2BP2 n=1 Tax=Homo sapiens RepID=C9JLA6_HUMAN
        >Isoform 2 of Insulin-like growth factor 2 mRNA-binding protein 3 n=1 Tax=Homo sapiens RepID=O00425-2
        >Insulin-like growth factor 2 mRNA-binding protein 2 n=1 Tax=Homo sapiens RepID=IF2B2_HUMAN
        >Isoform 2 of Insulin-like growth factor 2 mRNA-binding protein 2 n=1 Tax=Homo sapiens RepID=Q9Y6M1-1
        >Isoform 3 of Insulin-like growth factor 2 mRNA-binding protein 2 n=1 Tax=Homo sapiens RepID=Q9Y6M1-3
        >Isoform 4 of Insulin-like growth factor 2 mRNA-binding protein 2 n=1 Tax=Homo sapiens RepID=Q9Y6M1-4
        >Isoform 5 of Insulin-like growth factor 2 mRNA-binding protein 2 n=1 Tax=Homo sapiens RepID=Q9Y6M1-5


d       UniRef100_C9JT33 0.0000
        confidence: 1.0000           num unique p tot indep spectra: 0
        >Putative uncharacterized protein IGF2BP1 n=1 Tax=Homo sapiens RepID=C9JT33_HUMAN                               Length: 438aa


e       UniRef100_D3DTW3 0.0000
        confidence: 1.0000           num unique p tot indep spectra: 0
        >Insulin-like growth factor 2 mRNA binding protein 1, isoform CRA_a n=1 Tax=Homo sapiens RepID=D3DTW3_HUM Length: 441aa


f       UniRef100_UPI0001881463 0.0000
        confidence: 0.3696           num unique p tot indep spectra: 0
        >UPI0001881463 related cluster n=1 Tax=Homo sapiens RepID=UPI0001881463                                         Length: 81aa


g       UniRef100_UPI0001AE7064 0.0000
        confidence: 1.0000           num unique p tot indep spectra: 0
        >UPI0001AE7064 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7064                                         Length: 488aa


22      PROTEIN GROUP: 19 0.9997

a       UniRef100_C6KXN3 0.9985
        confidence: 0. coverage: 9.5 num unique p tot indep spec share of spect subsumed entries: 2
        >Cyclosporin A transporter 1 (Fragment) n=1 Tax=Homo sapiens RepID=C6KXN3_HUMAN                                 Length: 232aa


b       UniRef100_A0M8Q7 UniRef100_P01716 0.0000
        confidence: 0.0072           num unique p tot indep spectra: 0
        >V2-1 protein (Fragment) n=2 Tax=Homo sapiens RepID=A0M8Q7_HUMAN                                                Length: 95aa
        >Ig lambda chain V-IV region X n=1 Tax=Homo sapiens RepID=LV402_HUMAN


c       UniRef100_A0N5G3 UniRef100_A2NUT2 UniRef100_Q6GMW3 UniRef100_Q6GMX4 UniRef100_Q6IPQ0 UniRef100_Q6PIQ7
        UniRef100_Q6PJG0 UniRef100_Q8N355 UniRef100_Q8N5F4 UniRef100_Q96JD0 UniRef100_UPI0000112C31 UniRef100_UPI000158A17D
        UniRef100_UPI0001A5EC47 UniRef100_UPI0001BEF2DB UniRef100_UPI0001D63C0B 0.0000
        confidence: 0.3384           num unique p tot indep spectra: 0
        >Rheumatoid factor G9 light chain (Fragment) n=1 Tax=Homo sapiens RepID=A0N5G3_HUMAN                            Length: 121aa
        >Lambda-chain (AA -20 to 215) n=1 Tax=Homo sapiens RepID=A2NUT2_HUMAN
        >IGL@ protein n=1 Tax=Homo sapiens RepID=Q6GMW3_HUMAN
        >IGL@ protein n=1 Tax=Homo sapiens RepID=Q6GMX4_HUMAN
        >IGL@ protein n=1 Tax=Homo sapiens RepID=Q6IPQ0_HUMAN
        >IGL@ protein n=1 Tax=Homo sapiens RepID=Q6PIQ7_HUMAN
        >Putative uncharacterized protein n=1 Tax=Homo sapiens RepID=Q6PJG0_HUMAN
        >IGL@ protein n=1 Tax=Homo sapiens RepID=Q8N355_HUMAN
        >IGL@ protein n=1 Tax=Homo sapiens RepID=Q8N5F4_HUMAN
        >Amyloid lambda 6 light chain variable region SAR (Fragment) n=1 Tax=Homo sapiens RepID=Q96JD0_HUMAN
        >BENCE-JONES PROTEIN RHE (LIGHT CHAIN) n=1 Tax=Homo sapiens RepID=UPI0000112C31
        >Bence Jones KWR Protein - Immunoglobulin Ligh n=1 Tax=Homo sapiens RepID=UPI000158A17D
        >PREDICTED: hypothetical protein XP_002348153 n=1 Tax=Homo sapiens RepID=UPI0001A5EC47
        >Fab 537-10D, light chain n=1 Tax=Homo sapiens RepID=UPI0001BEF2DB
        >Antibody PG9 light chain n=1 Tax=Homo sapiens RepID=UPI0001D63C0B
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23   UniRef100_A6NFL3 UniRef100_A6NMA2 UniRef100_A8MSP6 UniRef100_B3KPB3 UniRef100_D2K8Q1 UniRef100_Q5SV15
     UniRef100_Q5SV24 UniRef100_Q5T9A2 UniRef100_Q5T9A4 UniRef100_Q5T9A4-2 UniRef100_Q5T9A4-3 UniRef100_Q96T67
     UniRef100_Q9H834 UniRef100_Q9NVI7 0.9901
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.18%
     >Putative uncharacterized protein ATAD3B n=1 Tax=Homo sapiens RepID=A6NFL3_HUMAN                    Length: 285aa
     >Putative uncharacterized protein ATAD3B n=1 Tax=Homo sapiens RepID=A6NMA2_HUMAN
     >Putative uncharacterized protein ATAD3B n=1 Tax=Homo sapiens RepID=A8MSP6_HUMAN
     >cDNA FLJ31537 fis, clone NT2RI2000704, highly similar to ATPase family AAA domain-containing protein 3A n=1 Tax=Homo sapiens
                RepID=B3KPB3_HUMAN
     >AAA domain containing 3A protein n=2 Tax=Homo sapiens RepID=D2K8Q1_HUMAN
     >ATPase family, AAA domain containing 3A (Fragment) n=1 Tax=Homo sapiens RepID=Q5SV15_HUMAN
     >ATPase family, AAA domain containing 3A (Fragment) n=3 Tax=Homo sapiens RepID=Q5SV24_HUMAN
     >ATPase family, AAA domain containing 3B n=1 Tax=Homo sapiens RepID=Q5T9A2_HUMAN
     >ATPase family AAA domain-containing protein 3B n=1 Tax=Homo sapiens RepID=ATD3B_HUMAN
     >Isoform 2 of ATPase family AAA domain-containing protein 3B n=1 Tax=Homo sapiens RepID=Q5T9A4-2
     >Isoform 3 of ATPase family AAA domain-containing protein 3B n=1 Tax=Homo sapiens RepID=Q5T9A4-3
     >TOB3 n=1 Tax=Homo sapiens RepID=Q96T67_HUMAN
     >cDNA FLJ13966 fis, clone Y79AA1001394, weakly similar to CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-) n=1 Tax=Homo sapiens
                RepID=Q9H834_HUMAN
     >ATPase family AAA domain-containing protein 3A n=1 Tax=Homo sapiens RepID=ATD3A_HUMAN


24   UniRef100_B4DMB5 UniRef100_B7Z9C4 UniRef100_P17812 0.9901
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.35%
     >cDNA FLJ60075, highly similar to CTP synthase 1 (EC 6.3.4.2) n=1 Tax=Homo sapiens RepID=B4DMB5_HUMAN   Length: 497aa
     >cDNA FLJ54863, highly similar to CTP synthase 1 (EC 6.3.4.2) n=1 Tax=Homo sapiens RepID=B7Z9C4_HUMAN
     >CTP synthase 1 n=2 Tax=Homo sapiens RepID=PYRG1_HUMAN


25   UniRef100_P56545 UniRef100_P56545-2 UniRef100_Q5SQP8 UniRef100_Q8IY44 0.9901
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.18%
     >C-terminal-binding protein 2 n=3 Tax=Catarrhini RepID=CTBP2_HUMAN                                   Length: 445aa
     >Isoform 2 of C-terminal-binding protein 2 n=1 Tax=Homo sapiens RepID=P56545-2
     >C-terminal binding protein 2 n=1 Tax=Homo sapiens RepID=Q5SQP8_HUMAN
     >CTBP2 protein n=1 Tax=Homo sapiens RepID=Q8IY44_HUMAN


26   UniRef100_Q92945 UniRef100_Q92945-2 0.9901
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.18%
     >Far upstream element-binding protein 2 n=1 Tax=Homo sapiens RepID=FUBP2_HUMAN                        Length: 710aa
     >Isoform 2 of Far upstream element-binding protein 2 n=1 Tax=Homo sapiens RepID=Q92945-2


27   UniRef100_A4D2A2 UniRef100_B2RBA6 UniRef100_B4DDF5 UniRef100_C6EMX8 UniRef100_P33993 UniRef100_Q4R3W8
     UniRef100_Q9H4N9 0.9891
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.35%
     >MCM7 minichromosome maintenance deficient 7 (S. cerevisiae) n=2 Tax=Homo sapiens RepID=A4D2A2_HUMAN   Length: 543aa
     >cDNA, FLJ95407, highly similar to Homo sapiens MCM7 minichromosome maintenance deficient 7 (S. cerevisiae) (MCM7), mRNA n=1
                Tax=Homo sapiens RepID=B2RBA6_HUMAN
     >cDNA FLJ55929, highly similar to DNA replication licensing factor MCM7 n=1 Tax=Homo sapiens RepID=B4DDF5_HUMAN
     >HsMcm7 n=1 Tax=Homo sapiens RepID=C6EMX8_HUMAN
     >DNA replication licensing factor MCM7 n=1 Tax=Homo sapiens RepID=MCM7_HUMAN
     >Testis cDNA clone: QtsA-13641, similar to human MCM7 minichromosome maintenance deficient 7 (S.cerevisiae) (MCM7), transcript variant 1,
                n=1 Tax=Macaca fascicularis RepID=Q4R3W8_MACFA
     >Clone CDABP0042 mRNA sequence n=1 Tax=Homo sapiens RepID=Q9H4N9_HUMAN


28   UniRef100_Q05CI5 UniRef100_Q08211 UniRef100_Q58F26 UniRef100_Q6PJK6 0.9891
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.18%
     >DHX9 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q05CI5_HUMAN                                     Length: 593aa
     >ATP-dependent RNA helicase A n=1 Tax=Homo sapiens RepID=DHX9_HUMAN
     >DHX9 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q58F26_HUMAN
     >DHX9 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6PJK6_HUMAN


29   UniRef100_A8MZ91 UniRef100_B2RDD7 UniRef100_B4DV00 UniRef100_B4DX49 UniRef100_B4DY30 UniRef100_C9JSX3
     UniRef100_O14744 UniRef100_UPI0001AE6957 0.9881
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.53%
     >Protein arginine methyltransferase 5, isoform CRA_d n=1 Tax=Homo sapiens RepID=A8MZ91_HUMAN          Length: 620aa
     >cDNA, FLJ96564, highly similar to Homo sapiens SKB1 homolog (S. pombe) (SKB1), mRNA n=1 Tax=Homo sapiens RepID=B2RDD7_HUMAN
     >cDNA FLJ54039, highly similar to Protein arginine N-methyltransferase 5 (EC 2.1.1.-) n=2 Tax=Catarrhini RepID=B4DV00_HUMAN
     >cDNA FLJ54566, highly similar to Protein arginine N-methyltransferase 5 (EC2.1.1.-) n=1 Tax=Homo sapiens RepID=B4DX49_HUMAN
     >cDNA FLJ54078, highly similar to Protein arginine N-methyltransferase 5 (EC 2.1.1.-) n=1 Tax=Homo sapiens RepID=B4DY30_HUMAN
     >Putative uncharacterized protein PRMT5 n=1 Tax=Homo sapiens RepID=C9JSX3_HUMAN
     >Protein arginine N-methyltransferase 5 n=3 Tax=Catarrhini RepID=ANM5_HUMAN
     >Protein arginine N-methyltransferase 5 (EC 2.1.1.125) (EC 2.1.1.-) (Shk1 kinase-binding protein 1 homolog) (SKB1Hs) (Jak-binding protein 1)
                (72 kDa ICln-binding protein). n=2 Tax=Homo sapiens RepID=UPI0001AE6957

30   UniRef100_A8K674 UniRef100_B2RDW1 UniRef100_P62988 UniRef100_Q3MIH3 UniRef100_Q49A90 UniRef100_Q59EM9
     UniRef100_Q5RKT7 UniRef100_Q5U5U6 UniRef100_Q5UGI3 UniRef100_Q66K58 UniRef100_Q96C32 UniRef100_Q96H31
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       UniRef100_Q96MH4 UniRef100_UPI000013DC28 UniRef100_UPI0001D63C67 0.9871
       confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.35%
       >cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA n=1 Tax=Homo sapiens RepID=A8K674_HU Length: 609aa
       >Ribosomal protein S27a, isoform CRA_c n=5 Tax=Tetrapoda RepID=B2RDW1_HUMAN
       >Ubiquitin n=40 Tax=Coelomata RepID=UBIQ_HUMAN
       >Ubiquitin A-52 residue ribosomal protein fusion product 1 n=8 Tax=Tetrapoda RepID=Q3MIH3_HUMAN
       >RPS27A protein n=1 Tax=Homo sapiens RepID=Q49A90_HUMAN
       >Ubiquitin C variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59EM9_HUMAN
       >Ribosomal protein S27a n=1 Tax=Homo sapiens RepID=Q5RKT7_HUMAN
       >Ubiquitin B n=5 Tax=Eutheria RepID=Q5U5U6_HUMAN
       >Ubiquitin C splice variant n=1 Tax=Homo sapiens RepID=Q5UGI3_HUMAN
       >Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens RepID=Q66K58_HUMAN
       >UBC protein n=4 Tax=Coelomata RepID=Q96C32_HUMAN
       >UBC protein (Fragment) n=2 Tax=Tetrapoda RepID=Q96H31_HUMAN
       >cDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9 n=1 Tax=Homo sapiens RepID=Q96MH4_HUMAN
       >ubiquitin C n=1 Tax=Homo sapiens RepID=UPI000013DC28
       >UBIQUITIN VARIANT UBV.21.4 n=1 Tax=Homo sapiens RepID=UPI0001D63C67


31     UniRef100_A6NCC1 UniRef100_A8JZY9 UniRef100_B3KPS3 UniRef100_B3KT06 UniRef100_B4DQK4 UniRef100_B7Z1K5
       UniRef100_P68363 UniRef100_Q4R546 UniRef100_Q53GA7 UniRef100_Q71U36 UniRef100_Q8N532 UniRef100_Q9BQE3
       UniRef100_UPI00015DFE80 0.9813
       confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.52%
       >Putative uncharacterized protein ENSP00000351411 n=1 Tax=Homo sapiens RepID=A6NCC1_HUMAN           Length: 437aa
       >cDNA FLJ78587 n=1 Tax=Homo sapiens RepID=A8JZY9_HUMAN
       >cDNA FLJ32131 fis, clone PEBLM2000267, highly similar to Tubulin alpha-ubiquitous chain n=1 Tax=Homo sapiens RepID=B3KPS3_HUMAN
       >cDNA FLJ37398 fis, clone BRAMY2027467, highly similar to Tubulin alpha-ubiquitous chain n=1 Tax=Homo sapiens RepID=B3KT06_HUMAN
       >cDNA FLJ53743, highly similar to Tubulin alpha-3 chain n=1 Tax=Homo sapiens RepID=B4DQK4_HUMAN
       >cDNA FLJ55956, highly similar to Tubulin alpha-6 chain n=1 Tax=Homo sapiens RepID=B7Z1K5_HUMAN
       >Tubulin alpha-1B chain n=10 Tax=Tetrapoda RepID=TBA1B_HUMAN
       >Brain cDNA, clone: QccE-19314, similar to human tubulin, alpha 3 (TUBA3), n=1 Tax=Macaca fascicularis RepID=Q4R546_MACFA
       >Tubulin alpha 6 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GA7_HUMAN
       >Tubulin alpha-1A chain n=7 Tax=Eutheria RepID=TBA1A_HUMAN
       >TUBA1C protein n=1 Tax=Homo sapiens RepID=Q8N532_HUMAN
       >Tubulin alpha-1C chain n=2 Tax=Homininae RepID=TBA1C_HUMAN
       >Tubulin alpha-1C chain (Tubulin alpha-6 chain) (Alpha-tubulin 6). n=1 Tax=Homo sapiens RepID=UPI00015DFE80


32     UniRef100_Q14686 UniRef100_UPI00015DF877 0.9755
       confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.20%
       >Nuclear receptor coactivator 6 n=1 Tax=Homo sapiens RepID=NCOA6_HUMAN                               Length: 2063aa
       >Nuclear receptor coactivator 6 (Amplified in breast cancer protein 3) (Cancer-amplified transcriptional coactivator ASC-2) (Activating signal
                   cointegrator 2) (ASC-2) (Peroxisome proliferator-activated receptor-interacting protein) (PPAR-interacting protei n=1
                  Tax=Homo sapiens RepID=UPI00015DF877
33     UniRef100_Q4W5K9 UniRef100_Q96HC4 UniRef100_Q96HC4-3 UniRef100_UPI00001401C7 0.9708
       confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.35%
       >Putative uncharacterized protein LIM (Fragment) n=1 Tax=Homo sapiens RepID=Q4W5K9_HUMAN            Length: 337aa
       >PDZ and LIM domain protein 5 n=1 Tax=Homo sapiens RepID=PDLI5_HUMAN
       >Isoform 3 of PDZ and LIM domain protein 5 n=1 Tax=Homo sapiens RepID=Q96HC4-3
       >PDZ and LIM domain protein 5 isoform a n=1 Tax=Homo sapiens RepID=UPI00001401C7

MBD4 Mass Spec - lower band

42 entries (14 single hits) retrieved from
/home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_MDB4-1-sequest.prot.xml


* corresponds to peptide is_nondegenerate_evidence flag


1      UniRef100_B2RDG1 UniRef100_Q8WVX9 UniRef100_Q9H600 UniRef100_UPI0001AE6B80 1.0000
       confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.69%
       >cDNA, FLJ96593 n=1 Tax=Homo sapiens RepID=B2RDG1_HUMAN                                              Length: 515aa
       >Fatty acyl-CoA reductase 1 n=2 Tax=Homo sapiens RepID=FACR1_HUMAN
       >cDNA: FLJ22728 fis, clone HSI15617 (Fragment) n=1 Tax=Homo sapiens RepID=Q9H600_HUMAN
       >Fatty acyl-CoA reductase 1 (EC 1.2.1.-) (Male sterility domain- containing protein 2). n=1 Tax=Homo sapiens RepID=UPI0001AE6B80


2      UniRef100_P06576 UniRef100_Q0QEN7 UniRef100_UPI000186EDED 1.0000
       confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 2.93%
       >ATP synthase subunit beta, mitochondrial n=1 Tax=Homo sapiens RepID=ATPB_HUMAN                      Length: 529aa
       >ATP synthase subunit beta (Fragment) n=1 Tax=Homo sapiens RepID=Q0QEN7_HUMAN
       >ATP synthase subunit beta, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EDED


3      UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000
       confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.63%
       >Keratin, type I cytoskeletal 10 n=1 Tax=Homo sapiens RepID=K1C10_HUMAN                              Length: 584aa
       >keratin, type I cytoskeletal 10 n=1 Tax=Homo sapiens RepID=UPI00017BCE7F
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4      UniRef100_P35527 1.0000
       confidence: 1. coverage: 4.7 num unique p tot indep spec share of spectrum id's: 1.00%
       >Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN                                   Length: 623aa


5a     UniRef100_A6NJK7 UniRef100_B4DM91 UniRef100_C9K008 UniRef100_Q76FK4 UniRef100_Q76FK4-4 1.0000
       confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 3
       >Putative uncharacterized protein NOL8 n=1 Tax=Homo sapiens RepID=A6NJK7_HUMAN                          Length: 1131aa
       >cDNA FLJ60085, highly similar to Nucleolar protein 8 (Fragment) n=1 Tax=Homo sapiens RepID=B4DM91_HUMAN
       >Putative uncharacterized protein NOL8 n=1 Tax=Homo sapiens RepID=C9K008_HUMAN
       >Nucleolar protein 8 n=3 Tax=Homo sapiens RepID=NOL8_HUMAN
       >Isoform 4 of Nucleolar protein 8 n=1 Tax=Homo sapiens RepID=Q76FK4-4


7a     UniRef100_A8K402 UniRef100_B5BTY7 UniRef100_B7Z243 UniRef100_B7Z7K4 UniRef100_B7ZAT2 UniRef100_P78371
                 1
       confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 2.58%
       >cDNA FLJ75037, highly similar to Homo sapiens chaperonin containing TCP1, subunit 2 (beta) (CCT2),mRNA n=1 T Length: 535aa
       >T-complex protein 1 subunit beta n=1 Tax=Homo sapiens RepID=B5BTY7_HUMAN
       >cDNA FLJ50480, highly similar to T-complex protein 1 subunit beta n=1 Tax=Homo sapiens RepID=B7Z243_HUMAN
       >cDNA FLJ52359, highly similar to T-complex protein 1 subunit beta n=1 Tax=Homo sapiens RepID=B7Z7K4_HUMAN
       >Chaperonin containing TCP1, subunit 2 (Beta), isoform CRA_c n=1 Tax=Homo sapiens RepID=B7ZAT2_HUMAN
       >T-complex protein 1 subunit beta n=3 Tax=Catarrhini RepID=TCPB_HUMAN


8a     UniRef100_A8K7D9 UniRef100_P52292 UniRef100_Q53YE3 UniRef100_Q6NVW7 UniRef100_Q7Z726 1.0000
       confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.49%
       >cDNA FLJ78270, highly similar to Homo sapiens karyopherin alpha 2 (RAG cohort 1, importin alpha 1)(KPNA2), mR Length: 529aa
       >Importin subunit alpha-2 n=1 Tax=Homo sapiens RepID=IMA2_HUMAN
       >Karyopherin alpha 2 (RAG cohort 1, importin alpha 1) n=1 Tax=Homo sapiens RepID=Q53YE3_HUMAN
       >Karyopherin alpha 2 (RAG cohort 1, importin alpha 1) n=1 Tax=Homo sapiens RepID=Q6NVW7_HUMAN
       >Karyopherin alpha 2 (RAG cohort 1, importin alpha 1) n=1 Tax=Homo sapiens RepID=Q7Z726_HUMAN


9a     UniRef100_A8MV96 UniRef100_B3KN20 UniRef100_B5MBY3 UniRef100_Q9BPX6 UniRef100_Q9BPX6-2 UniRef100_Q9BPX6-3
       UniRef100_UPI00015E0121 1.0000
       confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.17%
       >Putative uncharacterized protein CBARA1 n=1 Tax=Homo sapiens RepID=A8MV96_HUMAN                        Length: 478aa
       >cDNA FLJ13256 fis, clone OVARC1000834, highly similar to Homo sapiens calcium binding atopy-related autoantigen 1 (CBARA1), mRNA n=1
                 Tax=Homo sapiens RepID=B3KN20_HUMAN
       >Putative uncharacterized protein CBARA1 n=1 Tax=Homo sapiens RepID=B5MBY3_HUMAN
       >Calcium-binding atopy-related autoantigen 1 n=1 Tax=Homo sapiens RepID=CBAA1_HUMAN
       >Isoform 2 of Calcium-binding atopy-related autoantigen 1 n=1 Tax=Homo sapiens RepID=Q9BPX6-2
       >Isoform 3 of Calcium-binding atopy-related autoantigen 1 n=1 Tax=Homo sapiens RepID=Q9BPX6-3
       >calcium binding atopy-related autoantigen 1 n=1 Tax=Homo sapiens RepID=UPI00015E0121


10a    UniRef100_B0R0W4 UniRef100_B4DRH0 UniRef100_Q09028 UniRef100_Q16576 UniRef100_Q4R6M6 UniRef100_Q5JP00
       UniRef100_UPI000186D900 1.0000
       confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
       >Retinoblastoma binding protein 7 n=2 Tax=Catarrhini RepID=B0R0W4_HUMAN                                Length: 411aa
       >cDNA FLJ53908, highly similar to Histone-binding protein RBBP4 n=1 Tax=Homo sapiens RepID=B4DRH0_HUMAN
       >Histone-binding protein RBBP4 n=5 Tax=Eutheria RepID=RBBP4_HUMAN
       >Histone-binding protein RBBP7 n=5 Tax=Euarchontoglires RepID=RBBP7_HUMAN
       >Testis cDNA, clone: QtsA-17633, similar to human retinoblastoma binding protein 4 (RBBP4), n=1 Tax=Macaca fascicularis
                 RepID=Q4R6M6_MACFA
       >Retinoblastoma binding protein 7 n=1 Tax=Homo sapiens RepID=Q5JP00_HUMAN
       >retinoblastoma-binding protein, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D900


11a    UniRef100_B0V2L1 UniRef100_B4DP52 UniRef100_B4DX78 UniRef100_O00148 UniRef100_Q13838 UniRef100_Q13838-2
       UniRef100_Q4R5P7 1.0000
       confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
       >HLA-B associated transcript 1 (Fragment) n=2 Tax=Homo sapiens RepID=B0V2L1_HUMAN                       Length: 327aa
       >HCG2005638, isoform CRA_c n=1 Tax=Homo sapiens RepID=B4DP52_HUMAN
       >cDNA FLJ55484, highly similar to ATP-dependent RNA helicase DDX39 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DX78_HUMAN
       >ATP-dependent RNA helicase DDX39 n=2 Tax=Homo sapiens RepID=DDX39_HUMAN
       >Spliceosome RNA helicase BAT1 n=7 Tax=Eutheria RepID=UAP56_HUMAN
       >Isoform 2 of Spliceosome RNA helicase BAT1 n=1 Tax=Homo sapiens RepID=Q13838-2
       >Brain cDNA, clone: QccE-11261, similar to human HLA-B associated transcript 1 (BAT1), transcript variant1, n=1 Tax=Macaca fascicularis
                 RepID=Q4R5P7_MACFA

12a    UniRef100_B3KML9 1.0000
       confidence: 1. coverage: 49. num unique p tot indep spec share of spect subsumed entries: 6
       >cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain n=1 Tax=Homo sapiens RepID= Length: 397aa


12b    UniRef100_B2R6L0 UniRef100_Q13885 1.0000
       confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
       >cDNA, FLJ93005, highly similar to Homo sapiens tubulin, beta polypeptide (TUBB), mRNA n=1 Tax=Homo sapiens  Length: 445aa
       >Tubulin beta-2A chain n=4 Tax=Euarchontoglires RepID=TBB2A_HUMAN
```

12c UniRef100_B4DP54 UniRef100_Q9BUF5 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
>cDNA FLJ52712, highly similar to Tubulin beta-6 chain n=1 Tax=Homo sapiens RepID=B4DP54_HUMAN Length: 418aa
>Tubulin beta-6 chain n=1 Tax=Homo sapiens RepID=TBB6_HUMAN

13a UniRef100_B4DLW8 UniRef100_B4DN41 UniRef100_B4DNG2 UniRef100_B5BUE6 UniRef100_P17844 UniRef100_Q4R6G0
UniRef100_UPI0001AE6729 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
>cDNA FLJ59339, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) n=1 Tax=Homo sapiens Length: 535aa
>cDNA FLJ53366, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DN41_HUMAN
>cDNA FLJ59357, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DNG2_HUMAN
>ATP-dependent RNA helicase DDX5 (Fragment) n=1 Tax=Homo sapiens RepID=B5BUE6_HUMAN
>Probable ATP-dependent RNA helicase DDX5 n=3 Tax=Eutheria RepID=DDX5_HUMAN
>Testis cDNA, clone: QtsA-18104, similar to human DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 (DDX5), n=2 Tax=Macaca fascicularis
RepID=Q4R6G0_MACFA
>UPI0001AE6729 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6729

15a UniRef100_B7Z7P8 UniRef100_P62495 UniRef100_Q96CG1 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.85%
>cDNA FLJ56175, highly similar to Eukaryotic peptide chain release factor subunit1 n=1 Tax=Homo sapiens RepID=I Length: 423aa
>Eukaryotic peptide chain release factor subunit 1 n=7 Tax=Eutheria RepID=ERF1_HUMAN
>ETF1 protein n=2 Tax=Eutheria RepID=Q96CG1_HUMAN

16a UniRef100_B7Z8W6 UniRef100_P43490 1.0000
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.64%
>cDNA FLJ55038, highly similar to Nicotinamide phosphoribosyltransferase (EC 2.4.2.12) n=1 Tax=Homo sapiens Re Length: 241aa
>Nicotinamide phosphoribosyltransferase n=1 Tax=Homo sapiens RepID=NAMPT_HUMAN

17a UniRef100_C5IWV5 UniRef100_P00761 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 3
>Trypsinogen n=1 Tax=Sus scrofa RepID=C5IWV5_PIG Length: 246aa
>Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG

18a UniRef100_D3DSF4 UniRef100_P22102 UniRef100_Q15374 UniRef100_Q3B7A7 UniRef100_Q59HH3 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.88%
>Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazol Length: 433aa
>Phosphoribosylglycinamide formyltransferase n=2 Tax=Homo sapiens RepID=PUR2_HUMAN
>GARS protein n=1 Tax=Homo sapiens RepID=Q15374_HUMAN
>Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase n=1
Tax=Homo sapiens RepID=Q3B7A7_HUMAN
>Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase isoform 1
variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59HH3_HUMAN

19a UniRef100_D6RBM0 UniRef100_P31943 UniRef100_UPI00001AF4DD 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
>Putative uncharacterized protein HNRNPH1 n=3 Tax=Homo sapiens RepID=D6RBM0_HUMAN Length: 212aa
>Heterogeneous nuclear ribonucleoprotein H, N-terminally processed n=2 Tax=Homo sapiens RepID=HNRH1_HUMAN
>Heterogeneous nuclear ribonucleoprotein H (hnRNP H). n=1 Tax=Homo sapiens RepID=UPI00001AF4DD

20a UniRef100_P02769 1.0000
confidence: 1. coverage: 20. num unique p tot indep spec share of spect subsumed entries: 6
>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa

21a UniRef100_P05787 1.0000
confidence: 1. coverage: 41. num unique p tot indep spec share of spect subsumed entries: 6
>Keratin, type II cytoskeletal 8 n=1 Tax=Homo sapiens RepID=K2C8_HUMAN Length: 483aa

21b UniRef100_P04264 1.0000
confidence: 1. coverage: 18. num unique p tot indep spec share of spectrum id's: 3.97%
>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN Length: 644aa

21c UniRef100_B0YJC4 UniRef100_B3KRK8 UniRef100_P08670 UniRef100_Q53HU8 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
>Vimentin variant 3 n=1 Tax=Homo sapiens RepID=B0YJC4_HUMAN Length: 431aa
>cDNA FLJ34494 fis, clone HLUNG2005030, highly similar to VIMENTIN n=1 Tax=Homo sapiens RepID=B3KRK8_HUMAN
>Vimentin n=2 Tax=Homo sapiens RepID=VIME_HUMAN
>Vimentin variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53HU8_HUMAN

22a UniRef100_P06733 1.0000

```
        confidence: 1. coverage: 17. num unique p tot indep spec share of spect subsumed entries: 5
        >Alpha-enolase n=1 Tax=Homo sapiens RepID=ENOA_HUMAN                                                     Length: 434aa


23a     UniRef100_P14868 1.0000
        confidence: 1. coverage: 9.0 num unique p tot indep spec share of spect subsumed entries: 3
        >Aspartyl-tRNA synthetase, cytoplasmic n=4 Tax=Homo sapiens RepID=SYDC_HUMAN                             Length: 501aa


24a     UniRef100_P17987 1.0000
        confidence: 1. coverage: 11. num unique p tot indep spec share of spect subsumed entries: 1
        >T-complex protein 1 subunit alpha n=2 Tax=Homininae RepID=TCPA_HUMAN                                    Length: 556aa


25a     UniRef100_P19474 1.0000
        confidence: 1. coverage: 18. num unique p tot indep spec share of spect subsumed entries: 1
        >52 kDa Ro protein n=1 Tax=Homo sapiens RepID=RO52_HUMAN                                                 Length: 475aa


26a     UniRef100_P25705 1.0000
        confidence: 1. coverage: 22. num unique p tot indep spec share of spect subsumed entries: 3
        >ATP synthase subunit alpha, mitochondrial n=3 Tax=Homininae RepID=ATPA_HUMAN                            Length: 553aa


27a     UniRef100_P68366 1.0000
        confidence: 1. coverage: 26. num unique p tot indep spec share of spectrum id's: 5.18%
        >Tubulin alpha-4A chain n=8 Tax=Eutheria RepID=TBA4A_HUMAN                                               Length: 448aa


28a     UniRef100_Q9BZV1 1.0000
        confidence: 1. coverage: 7.7 num unique p tot indep spec share of spect subsumed entries: 1
        >UBX domain-containing protein 6 n=1 Tax=Homo sapiens RepID=UBXN6_HUMAN                                  Length: 441aa


14a     UniRef100_B4DNE0 UniRef100_P68104 UniRef100_Q05639 UniRef100_Q53G85 UniRef100_Q53GA1 UniRef100_Q53GE9
        UniRef100_Q53HM9 UniRef100_Q53HQ7 UniRef100_Q53HR5 UniRef100_Q5VTE0 UniRef100_Q6IPN6 UniRef100_Q6IPT9
        UniRef100_Q6IQ15 UniRef100_UPI00015E0621 UniRef100_UPI000186CC55 0.9999
        confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
        >Elongation factor 1-alpha n=1 Tax=Homo sapiens RepID=B4DNE0_HUMAN                                       Length: 395aa
        >Elongation factor 1-alpha 1 n=13 Tax=Eutheria RepID=EF1A1_HUMAN
        >Elongation factor 1-alpha 2 n=5 Tax=Eutheria RepID=EF1A2_HUMAN
        >Elongation factor 1-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q53G85_HUMAN
        >Elongation factor 1-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q53GA1_HUMAN
        >Elongation factor 1-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q53GE9_HUMAN
        >Elongation factor 1-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q53HM9_HUMAN
        >Elongation factor 1-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q53HQ7_HUMAN
        >Elongation factor 1-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q53HR5_HUMAN
        >Putative elongation factor 1-alpha-like 3 n=1 Tax=Homo sapiens RepID=EF1A3_HUMAN
        >Elongation factor 1-alpha n=1 Tax=Homo sapiens RepID=Q6IPN6_HUMAN
        >Elongation factor 1-alpha n=2 Tax=Homo sapiens RepID=Q6IPT9_HUMAN
        >Elongation factor 1-alpha n=1 Tax=Homo sapiens RepID=Q6IQ15_HUMAN
        >Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1) (Elongation factor Tu) (EF-Tu) (Leukocyte receptor cluster
                    member 7). n=1 Tax=Homo sapiens RepID=UPI00015E0621
        >elongation factor 1-alpha, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CC55


29a     UniRef100_A8K6N9 UniRef100_B3KTH7 UniRef100_B3KY86 UniRef100_O00561 UniRef100_Q13555 UniRef100_Q13555-2
        UniRef100_Q13555-3 UniRef100_Q13555-6 UniRef100_Q13555-7 UniRef100_Q13555-8 UniRef100_Q13555-9 UniRef100_Q5SWX3
        >cDNA FLJ77153, highly similar to Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II gam Length: 518aa
        >Calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma, isoform CRA_p n=1 Tax=Homo sapiens RepID=B3KTH7_HUMAN
        >Calcium/calmodulin-dependent protein kinase isoform A (Fragment) n=1 Tax=Homo sapiens RepID=O00561_HUMAN
        >Calcium/calmodulin-dependent protein kinase type II subunit gamma n=1 Tax=Homo sapiens RepID=KCC2G_HUMAN
        >Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit gamma n=1 Tax=Homo sapiens RepID=Q13555-2
        >Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit gamma n=1 Tax=Homo sapiens RepID=Q13555-3
        >Isoform 6 of Calcium/calmodulin-dependent protein kinase type II subunit gamma n=1 Tax=Homo sapiens RepID=Q13555-6
        >Isoform 7 of Calcium/calmodulin-dependent protein kinase type II subunit gamma n=1 Tax=Homo sapiens RepID=Q13555-7
        >Isoform 8 of Calcium/calmodulin-dependent protein kinase type II subunit gamma n=1 Tax=Homo sapiens RepID=Q13555-8
        >Isoform 9 of Calcium/calmodulin-dependent protein kinase type II subunit gamma n=1 Tax=Homo sapiens RepID=Q13555-9
        >Calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma n=2 Tax=Eutheria RepID=Q5SWX3_HUMAN
        >Calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma n=7 Tax=Eutheria RepID=Q5SWX4_HUMAN
        >CAMK2G protein (Fragment) n=2 Tax=Euarchontoglires RepID=Q8WU40_HUMAN


30      UniRef100_A8K3C3 UniRef100_B7Z2F4 UniRef100_B7Z2Z8 UniRef100_B7Z8B1 UniRef100_B7Z9L0 UniRef100_P50991
            0.9892
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.35%
        >T-complex protein 1 subunit delta n=1 Tax=Homo sapiens RepID=A8K3C3_HUMAN                               Length: 539aa
        >T-complex protein 1 subunit delta n=1 Tax=Homo sapiens RepID=B7Z2F4_HUMAN
        >T-complex protein 1 subunit delta n=1 Tax=Homo sapiens RepID=B7Z2Z8_HUMAN
        >T-complex protein 1 subunit delta n=1 Tax=Homo sapiens RepID=B7Z8B1_HUMAN
        >T-complex protein 1 subunit delta n=1 Tax=Homo sapiens RepID=B7Z9L0_HUMAN
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      >T-complex protein 1 subunit delta n=1 Tax=Homo sapiens RepID=TCPD_HUMAN


31    UniRef100_B4DJ63 UniRef100_B4DJQ3 UniRef100_B4DLV4 UniRef100_B4DP88 UniRef100_B4DW25 UniRef100_B4DWA7
      UniRef100_B4E1G2 UniRef100_B7Z9F1 UniRef100_P34897 UniRef100_Q53ET4 UniRef100_Q5BJF5 UniRef100_Q5HYG8
      UniRef100_Q8N1A5 UniRef100_UPI0001AE6AEA UniRef100_UPI0001AE6AEB 0.9892
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.35%
      >Serine hydroxymethyltransferase n=1 Tax=Homo sapiens RepID=B4DJ63_HUMAN                      Length: 378aa
      >Serine hydroxymethyltransferase n=1 Tax=Homo sapiens RepID=B4DJQ3_HUMAN
      >Serine hydroxymethyltransferase 2 (Mitochondrial), isoform CRA_h n=1 Tax=Homo sapiens RepID=B4DLV4_HUMAN
      >Serine hydroxymethyltransferase n=1 Tax=Homo sapiens RepID=B4DP88_HUMAN
      >Serine hydroxymethyltransferase n=1 Tax=Homo sapiens RepID=B4DW25_HUMAN
      >Serine hydroxymethyltransferase n=1 Tax=Homo sapiens RepID=B4DWA7_HUMAN
      >Serine hydroxymethyltransferase n=1 Tax=Homo sapiens RepID=B4E1G2_HUMAN
      >Serine hydroxymethyltransferase n=1 Tax=Homo sapiens RepID=B7Z9F1_HUMAN
      >Serine hydroxymethyltransferase, mitochondrial n=1 Tax=Homo sapiens RepID=GLYM_HUMAN
      >Serine hydroxymethyltransferase (Fragment) n=1 Tax=Homo sapiens RepID=Q53ET4_HUMAN
      >Serine hydroxymethyltransferase (Fragment) n=1 Tax=Homo sapiens RepID=Q5BJF5_HUMAN
      >Serine hydroxymethyltransferase n=1 Tax=Homo sapiens RepID=Q5HYG8_HUMAN
      >Serine hydroxymethyltransferase n=1 Tax=Homo sapiens RepID=Q8N1A5_HUMAN
      >UPI0001AE6AEA related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6AEA
      >UPI0001AE6AEB related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6AEB


32    UniRef100_P26196 0.9892
      confidence: 0. coverage: 2.5 num unique p tot indep spec share of spectrum id's: 0.17%
      >Probable ATP-dependent RNA helicase DDX6 n=2 Tax=Homo sapiens RepID=DDX6_HUMAN               Length: 483aa


33    UniRef100_P28838 UniRef100_P28838-2 UniRef100_UPI0001D3B21D 0.9892
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.17%
      >Cytosol aminopeptidase n=1 Tax=Homo sapiens RepID=AMPL_HUMAN                                 Length: 519aa
      >Isoform 2 of Cytosol aminopeptidase n=1 Tax=Homo sapiens RepID=P28838-2
      >UPI0001D3B21D related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3B21D


34    UniRef100_Q6ZNK3 0.9892
      confidence: 0. coverage: 2.4 num unique p tot indep spec share of spectrum id's: 0.17%
      >FLJ00304 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6ZNK3_HUMAN                          Length: 381aa


35    UniRef100_UPI0000111654 UniRef100_UPI00017BDB3D UniRef100_UPI00017BDB42 0.9892
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.17%
      >MONOCLONAL ANTIBODY MAK33 n=1 Tax=Homo sapiens RepID=UPI0000111654                           Length: 213aa
      >FabOX108 Light Chain Fragment n=1 Tax=Homo sapiens RepID=UPI00017BDB3D
      >FabOX117 Light Chain Fragment n=1 Tax=Homo sapiens RepID=UPI00017BDB42


36    UniRef100_B4DFL1 UniRef100_B4DMK9 UniRef100_P09622 UniRef100_UPI000198CF5D 0.9871
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.17%
      >Dihydrolipoyl dehydrogenase n=2 Tax=Homo sapiens RepID=B4DFL1_HUMAN                          Length: 459aa
      >cDNA FLJ56112, highly similar to Dihydrolipoyl dehydrogenase, mitochondrial (EC 1.8.1.4) n=1 Tax=Homo sapiens RepID=B4DMK9_HUMAN
      >Dihydrolipoyl dehydrogenase, mitochondrial n=1 Tax=Homo sapiens RepID=DLDH_HUMAN
      >UPI000198CF5D related cluster n=1 Tax=Homo sapiens RepID=UPI000198CF5D


37    UniRef100_A8K4G7 UniRef100_A8K5D8 UniRef100_O75351 UniRef100_Q6PIW4 UniRef100_Q6PIW4-2 UniRef100_Q9UN37
      UniRef100_UPI000186DC11 UniRef100_UPI000186E6CB UniRef100_UPI000186EE57 0.9850
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.52%
      >cDNA FLJ78528, highly similar to Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA n=1 Tax=Hom Length: 444aa
      >cDNA FLJ75934, highly similar to Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA n=1 Tax=Homo sapiens
                  RepID=A8K5D8_HUMAN
      >Vacuolar protein sorting-associated protein 4B n=1 Tax=Homo sapiens RepID=VPS4B_HUMAN
      >Fidgetin-like protein 1 n=2 Tax=Homo sapiens RepID=FIGL1_HUMAN
      >Isoform 2 of Fidgetin-like protein 1 n=2 Tax=Homo sapiens RepID=Q6PIW4-2
      >Vacuolar protein sorting-associated protein 4A n=1 Tax=Homo sapiens RepID=VPS4A_HUMAN
      >Katanin p60 ATPase-containing subunit, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186DC11
      >Katanin p60 ATPase-containing subunit A1, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E6CB
      >vacuolar sorting protein 4A, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EE57


38    UniRef100_Q9NP73-2 0.9850
      confidence: 0. coverage: 4.2 num unique p tot indep spec share of spectrum id's: 0.17%
      >Isoform 2 of UDP-N-acetylglucosamine transferase subunit ALG13 homolog n=1 Tax=Homo sapiens RepID=Q9NP7 Length: 165aa


39    UniRef100_Q92945 UniRef100_Q92945-2 0.9807
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.17%
      >Far upstream element-binding protein 2 n=1 Tax=Homo sapiens RepID=FUBP2_HUMAN                Length: 710aa
      >Isoform 2 of Far upstream element-binding protein 2 n=1 Tax=Homo sapiens RepID=Q92945-2
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21d UniRef100_B4DEI8 UniRef100_Q14CN4 UniRef100_Q14CN4-2 UniRef100_Q3SY84 UniRef100_Q7RTS7 UniRef100_Q86Y46
UniRef100_Q86Y46-2 UniRef100_UPI00019912E7 0.9775
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.40%
>cDNA FLJ60438, highly similar to Homo sapiens keratin protein K6irs (K6IRS2), mRNA n=1 Tax=Homo sapiens Rep Length: 469aa
>Keratin, type II cytoskeletal 72 n=1 Tax=Homo sapiens RepID=K2C72_HUMAN
>Isoform 2 of Keratin, type II cytoskeletal 72 n=1 Tax=Homo sapiens RepID=Q14CN4-2
>Keratin, type II cytoskeletal 71 n=1 Tax=Homo sapiens RepID=K2C71_HUMAN
>Keratin, type II cytoskeletal 74 n=1 Tax=Homo sapiens RepID=K2C74_HUMAN
>Keratin, type II cytoskeletal 73 n=1 Tax=Homo sapiens RepID=K2C73_HUMAN
>Isoform 2 of Keratin, type II cytoskeletal 73 n=1 Tax=Homo sapiens RepID=Q86Y46-2
>keratin, type II cytoskeletal 72 isoform 2 n=1 Tax=Homo sapiens RepID=UPI00019912E7

40 UniRef100_D4YW74 UniRef100_Q8WXH0 UniRef100_Q8WXH0-2 0.9745
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.17%
>Polytrophin n=1 Tax=Homo sapiens RepID=D4YW74_HUMAN Length: 6825aa
>Nesprin-2 n=1 Tax=Homo sapiens RepID=SYNE2_HUMAN
>Isoform 2 of Nesprin-2 n=1 Tax=Homo sapiens RepID=Q8WXH0-2

41 UniRef100_A0N5G3 UniRef100_A2NUT2 UniRef100_C6KXN3 UniRef100_Q6GMW3 UniRef100_Q6GMX4 UniRef100_Q6IPQ0
UniRef100_Q6PIQ7 UniRef100_Q6PJG0 UniRef100_Q8N355 UniRef100_Q8N5F4 UniRef100_Q96JD0 UniRef100_UPI0000112C31
UniRef100_UPI000158A17D UniRef100_UPI0001A5EC47 UniRef100_UPI0001BEF2DB UniRef100_UPI0001D63C0B 0.9673
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.34%
>Rheumatoid factor G9 light chain (Fragment) n=1 Tax=Homo sapiens RepID=A0N5G3_HUMAN Length: 121aa
>Lambda-chain (AA -20 to 215) n=1 Tax=Homo sapiens RepID=A2NUT2_HUMAN
>Cyclosporin A transporter 1 (Fragment) n=1 Tax=Homo sapiens RepID=C6KXN3_HUMAN
>IGL@ protein n=1 Tax=Homo sapiens RepID=Q6GMW3_HUMAN
>IGL@ protein n=1 Tax=Homo sapiens RepID=Q6GMX4_HUMAN
>IGL@ protein n=1 Tax=Homo sapiens RepID=Q6IPQ0_HUMAN
>IGL@ protein n=1 Tax=Homo sapiens RepID=Q6PIQ7_HUMAN
>Putative uncharacterized protein n=1 Tax=Homo sapiens RepID=Q6PJG0_HUMAN
>IGL@ protein n=1 Tax=Homo sapiens RepID=Q8N355_HUMAN
>IGL@ protein n=1 Tax=Homo sapiens RepID=Q8N5F4_HUMAN
>Amyloid lambda 6 light chain variable region SAR (Fragment) n=1 Tax=Homo sapiens RepID=Q96JD0_HUMAN
>BENCE-JONES PROTEIN RHE (LIGHT CHAIN) n=1 Tax=Homo sapiens RepID=UPI0000112C31
>Bence Jones KWR Protein - Immunoglobulin Ligh n=1 Tax=Homo sapiens RepID=UPI000158A17D
>PREDICTED: hypothetical protein XP_002348153 n=1 Tax=Homo sapiens RepID=UPI0001A5EC47
>Fab 537-10D, light chain n=1 Tax=Homo sapiens RepID=UPI0001BEF2DB
>Antibody PG9 light chain n=1 Tax=Homo sapiens RepID=UPI0001D63C0B

42 UniRef100_B0YIW6 UniRef100_B4E1X2 UniRef100_P48444 UniRef100_Q6MZV5 UniRef100_UPI000185BDB3 0.9632
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.17%
>Archain 1, isoform CRA_a n=1 Tax=Homo sapiens RepID=B0YIW6_HUMAN Length: 552aa
>cDNA FLJ51620, highly similar to Coatomer subunit delta n=1 Tax=Homo sapiens RepID=B4E1X2_HUMAN
>Coatomer subunit delta n=2 Tax=Homo sapiens RepID=COPD_HUMAN
>Putative uncharacterized protein DKFZp686M09245 n=1 Tax=Homo sapiens RepID=Q6MZV5_HUMAN
>coatomer subunit delta isoform 2 n=1 Tax=Homo sapiens RepID=UPI000185BDB3