ENCODE DCC Antibody Validation Document

Date of Submission: Sep 1, 2011

Name: Florencia Pauli

Email: fpauli@hudsonalpha.org

Lab: Myers

Antibody Name: NFATC1_(SC-17834)

Target: NFATC1

Company/ Source: Santa Cruz Biotechnology

Catalog Number, database ID, laboratory: sc-17834

Lot Number: G2007

Antibody Description: Mouse monoclonal IgG, raised against amino acids 1-110 of NFATc1 of human origin.

Target Description: The product of this gene is a component of the nuclear factor of activated T cells DNA-binding transcription complex.

Entrez gene ID 4772; 90/110/140 kDa

Species Target: Human

Species Host: Mouse

Validation Method #1: Western Blot

Validation Method #2: IP-Mass Spec

Purification Method:

Polyclonal/ Monoclonal: Monoclonal

Vendor URL: http://www.scbt.com/datasheet-17834-

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:

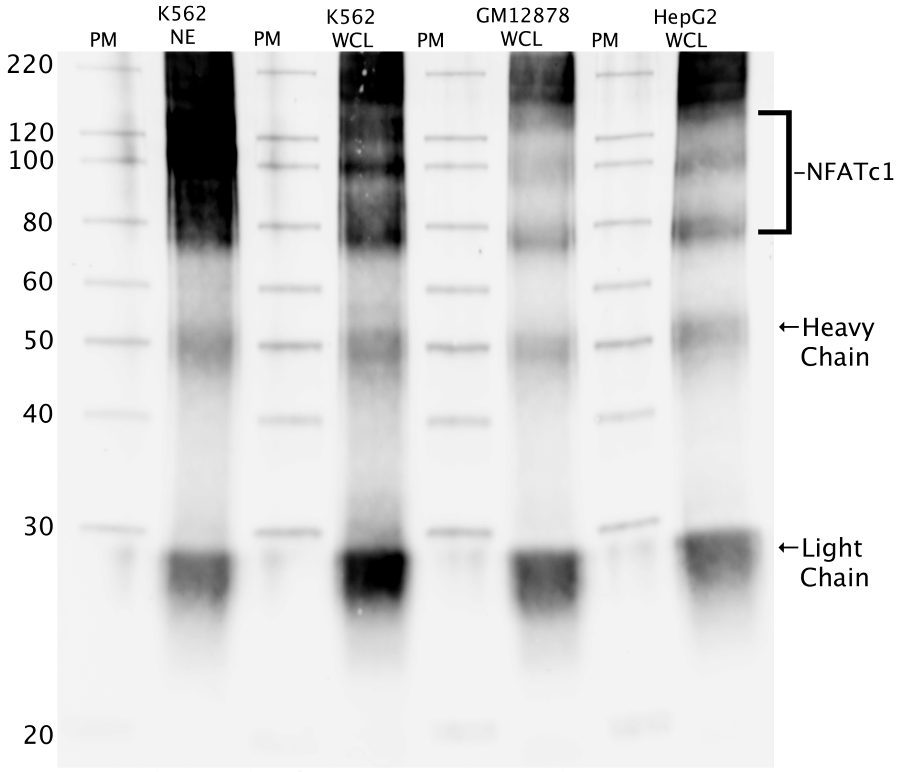
Modification:

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: Bands of expected size visualized, representing strongest signal in the lane.

Figure legend: IP-western with sc-17834 in nuclear extract (NE) of K562 and whole cell lysate (WCL) of K562, GM12878 and HepG2; PM=protein marker. NFATC1 bands are indicated.



–Molecular Weight of NFATc1: 90/110/140kDa

Insert Validation Image (click here)

Validation #2
Analysis

IP followed by mass spectrometry:
Briefly, K562 whole cell lysates were 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 (lower bands at ~85-100kDa, and upper bands at ~105-200kDa) 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_NFATC1_sc17834_09012011_MassSpec.pdf), including common contaminants. Target protein is listed as hit 16a in lower (~85-100 kDa) bands and 27a in upper (~105-200 kDa) bands.

Insert Validation Image (Click here)

Submit by Email

NFATC1 lower band MS results:

49 entries (20 single hits) retrieved from
/home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_NFATC1-1-sequest.prot.xml

* corresponds to peptide is_nondegenerate_evidence flag

```
1       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 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.64%
        >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


2       UniRef100_A8K897 UniRef100_Q4R8S7 UniRef100_Q8N1F7 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.86%
        >cDNA FLJ78686, highly similar to Homo sapiens nucleoporin 93kDa (NUP93), mRNA n=1 Tax=Homo sapiens RepID Length: 819aa
        >Testis cDNA clone: QtsA-11571, similar to human nucleoporin 93kDa (NUP93), n=1 Tax=Macaca fascicularis RepID=Q4R8S7_MACFA
        >Nuclear pore complex protein Nup93 n=2 Tax=Homo sapiens RepID=NUP93_HUMAN


3       UniRef100_P35527 1.0000
        confidence: 1. coverage: 24. num unique p tot indep spec share of spectrum id's: 4.41%
        >Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN                          Length: 623aa


5a      UniRef100_A8K3S3 UniRef100_B7Z6Q6 UniRef100_Q99661 UniRef100_Q99661-2 1.0000
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.58%
        >cDNA FLJ75664, highly similar to Homo sapiens kinesin family member 2C (KIF2C), mRNA n=1 Tax=Homo sapiens Length: 725aa
        >cDNA FLJ54088, highly similar to Kinesin-like protein KIF2C n=1 Tax=Homo sapiens RepID=B7Z6Q6_HUMAN
        >Kinesin-like protein KIF2C n=1 Tax=Homo sapiens RepID=KIF2C_HUMAN
        >Isoform 2 of Kinesin-like protein KIF2C n=2 Tax=Homo sapiens RepID=Q99661-2


6a      UniRef100_A8K3W4 UniRef100_A8K6U7 UniRef100_Q9BUJ2 UniRef100_Q9BUJ2-2 UniRef100_Q9BUJ2-3 UniRef100_Q9BUJ2-4
                  1
        confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.02%
        >cDNA FLJ75163, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein U-like 1 (HNRPUL1), tran Length: 756aa
        >cDNA FLJ78252, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein U-like 1 (HNRPUL1), transcript variant 1, mRNA n=1
                   Tax=Homo sapiens RepID=A8K6U7_HUMAN
        >Heterogeneous nuclear ribonucleoprotein U-like protein 1 n=1 Tax=Homo sapiens RepID=HNRL1_HUMAN
        >Isoform 2 of Heterogeneous nuclear ribonucleoprotein U-like protein 1 n=1 Tax=Homo sapiens RepID=Q9BUJ2-2
        >Isoform 3 of Heterogeneous nuclear ribonucleoprotein U-like protein 1 n=1 Tax=Homo sapiens RepID=Q9BUJ2-3
        >Isoform 4 of Heterogeneous nuclear ribonucleoprotein U-like protein 1 n=2 Tax=Homo sapiens RepID=Q9BUJ2-4


10a     UniRef100_A8K6Q8 1.0000
        confidence: 1. coverage: 9.5 num unique p tot indep spec share of spect subsumed entries: 3
        >cDNA FLJ75881, highly similar to Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA n=1 Tax=Homo sa Length: 760aa


11a     UniRef100_A8K9U6 UniRef100_C9J6P4 UniRef100_Q7Z2W4 UniRef100_Q7Z2W4-2 UniRef100_Q7Z2W4-3 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.41%
        >cDNA FLJ76121, highly similar to Homo sapiens zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 1, Length: 902aa
        >Putative uncharacterized protein ZC3HAV1 n=1 Tax=Homo sapiens RepID=C9J6P4_HUMAN
        >Zinc finger CCCH-type antiviral protein 1 n=1 Tax=Homo sapiens RepID=ZCCHV_HUMAN
        >Isoform 2 of Zinc finger CCCH-type antiviral protein 1 n=1 Tax=Homo sapiens RepID=Q7Z2W4-2
        >Isoform 3 of Zinc finger CCCH-type antiviral protein 1 n=1 Tax=Homo sapiens RepID=Q7Z2W4-3
```

14a UniRef100_B4DM22 UniRef100_B4DX07 UniRef100_B4DXY1 UniRef100_Q13041 UniRef100_Q13200 UniRef100_Q4R8E4
UniRef100_Q53XQ4 UniRef100_Q59EG8 UniRef100_UPI00015E0965 UniRef100_UPI000198CB9B 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.58%
>cDNA FLJ53357, highly similar to 26S proteasome non-ATPase regulatory subunit 2 n=1 Tax=Homo sapiens RepID Length: 900aa
>cDNA FLJ54077, highly similar to 26S proteasome non-ATPase regulatory subunit 2 n=1 Tax=Homo sapiens RepID=B4DX07_HUMAN
>cDNA FLJ55045, highly similar to 26S proteasome non-ATPase regulatory subunit 2 n=1 Tax=Homo sapiens RepID=B4DXY1_HUMAN
>P67 n=1 Tax=Homo sapiens RepID=Q13041_HUMAN
>26S proteasome non-ATPase regulatory subunit 2 n=2 Tax=Homininae RepID=PSMD2_HUMAN
>Testis cDNA clone: QtsA-12648, similar to human proteasome (prosome, macropain) 26S subunit, non-ATPase,2 (PSMD2), n=1 Tax=Macaca fascicularis RepID=Q4R8E4_MACFA
>Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 2 n=1 Tax=Homo sapiens RepID=Q53XQ4_HUMAN
>Proteasome 26S non-ATPase subunit 2 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59EG8_HUMAN
>26S proteasome non-ATPase regulatory subunit 2 (26S proteasome regulatory subunit RPN1) (26S proteasome regulatory subunit S2) (26S proteasome subunit p97) (Tumor necrosis factor type 1 receptor- associated protein 2) (55.11 protein). n=1 Tax=Homo sapiens RepID=UPI00015E0965
>UPI000198CB9B related cluster n=1 Tax=Homo sapiens RepID=UPI000198CB9B

15a UniRef100_B4DP70 UniRef100_Q92499 UniRef100_UPI0000E1F26E 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
>cDNA FLJ51017, highly similar to ATP-dependent RNA helicase DDX1 (EC 3.6.1.-) (Fragment) n=1 Tax=Homo sapie Length: 529aa
>ATP-dependent RNA helicase DDX1 n=2 Tax=Homo sapiens RepID=DDX1_HUMAN
>PREDICTED: similar to DEAD box protein RB - human isoform 4 n=1 Tax=Pan troglodytes RepID=UPI0000E1F26E

16a UniRef100_B5B2M5 UniRef100_O95644 UniRef100_UPI00015DFAC5 1.0000
confidence: max coverag num unique tot indep spe share of spe subsumed entries: 3
>Nuclear factor of activated T-cells c1 isoform IB-IXL n=5 Tax=Homo sapiens RepID=B5B2M5_HUMAN Length: 930aa
>Nuclear factor of activated T-cells, cytoplasmic 1 n=7 Tax=Homo sapiens RepID=NFAC1_HUMAN
>Nuclear factor of activated T-cells, cytoplasmic 1 (NFAT transcription complex cytosolic component) (NF-ATc1) (NF-ATc). n=1 Tax=Homo sapiens RepID=UPI00015DFAC5

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

19a UniRef100_P02769 1.0000
confidence: 1. coverage: 12. num unique p tot indep spec share of spect subsumed entries: 5
>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa

20a UniRef100_P04264 1.0000
confidence: 1. coverage: 44. num unique p tot indep spec share of spect subsumed entries: 2
>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN Length: 644aa

20b UniRef100_P35908 1.0000
confidence: 1. coverage: 18. num unique p tot indep spec share of spectrum id's: 2.75%
>Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E_HUMAN Length: 639aa

21a UniRef100_P08238 1.0000
confidence: 1. coverage: 39. num unique p tot indep spec share of spect subsumed entries: 13
>Heat shock protein HSP 90-beta n=1 Tax=Homo sapiens RepID=HS90B_HUMAN Length: 724aa

21b UniRef100_P07900 1.0000
confidence: 1. coverage: 29. num unique p tot indep spec share of spect subsumed entries: 8
>Heat shock protein HSP 90-alpha n=2 Tax=Homo sapiens RepID=HS90A_HUMAN Length: 732aa

22a UniRef100_P13010 UniRef100_Q53T09 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 2.46%
>X-ray repair cross-complementing protein 5 n=1 Tax=Homo sapiens RepID=XRCC5_HUMAN Length: 732aa
>Putative uncharacterized protein XRCC5 (Fragment) n=1 Tax=Homo sapiens RepID=Q53T09_HUMAN

23a UniRef100_P13639 1.0000
confidence: 1. coverage: 14. num unique p tot indep spec share of spect subsumed entries: 8
>Elongation factor 2 n=2 Tax=Hominidae RepID=EF2_HUMAN Length: 858aa

24a UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 5.20%
>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


25a     UniRef100_P14625 UniRef100_Q5CAQ5 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
        >Endoplasmin n=1 Tax=Homo sapiens RepID=ENPL_HUMAN                                           Length: 803aa
        >Tumor rejection antigen (Gp96) 1 n=1 Tax=Homo sapiens RepID=Q5CAQ5_HUMAN


26a     UniRef100_Q08211 1.0000
        confidence: 1. coverage: 9.6 num unique p tot indep spec share of spect subsumed entries: 4
        >ATP-dependent RNA helicase A n=1 Tax=Homo sapiens RepID=DHX9_HUMAN                          Length: 1270aa


27a     UniRef100_Q2NKK4 UniRef100_Q9Y6A5 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 5
        >Transforming, acidic coiled-coil containing protein 3 n=1 Tax=Homo sapiens RepID=Q2NKK4_HUMAN  Length: 838aa
        >Transforming acidic coiled-coil-containing protein 3 n=1 Tax=Homo sapiens RepID=TACC3_HUMAN


28a     UniRef100_Q4W4Y1 UniRef100_Q6NUS1 UniRef100_Q8WUM4 UniRef100_UPI00004121D3 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 5
        >Dopamine receptor interacting protein 4 n=1 Tax=Homo sapiens RepID=Q4W4Y1_HUMAN            Length: 868aa
        >PDCD6IP protein n=1 Tax=Homo sapiens RepID=Q6NUS1_HUMAN
        >Programmed cell death 6-interacting protein n=1 Tax=Homo sapiens RepID=PDC6I_HUMAN
        >programmed cell death 6-interacting protein isoform 2 n=1 Tax=Homo sapiens RepID=UPI00004121D3


29a     UniRef100_Q96S55 UniRef100_Q96S55-2 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
        >ATPase WRNIP1 n=1 Tax=Homo sapiens RepID=WRIP1_HUMAN                                        Length: 665aa
        >Isoform 2 of ATPase WRNIP1 n=1 Tax=Homo sapiens RepID=Q96S55-2


30a     UniRef100_Q9NR30 1.0000
        confidence: 1. coverage: 7.8 num unique p tot indep spec share of spect subsumed entries: 1
        >Nucleolar RNA helicase 2 n=2 Tax=Homo sapiens RepID=DDX21_HUMAN                             Length: 783aa


7a      UniRef100_A8K492 UniRef100_P56192 0.9999
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.53%
        >cDNA FLJ76789, highly similar to Homo sapiens methionine-tRNA synthetase (MARS), mRNA n=1 Tax=Homo sapie Length: 900aa
        >Methionyl-tRNA synthetase, cytoplasmic n=1 Tax=Homo sapiens RepID=SYMC_HUMAN


12a     UniRef100_B2RDF5 UniRef100_B3KMZ6 UniRef100_Q9UBT2 0.9998
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.56%
        >cDNA, FLJ96587, highly similar to Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), mRNA n=1 Tax=Ho Length: 640aa
        >cDNA FLJ13058 fis, clone NT2RP3001587, highly similar to Ubiquitin-like 1-activating enzyme E1B n=1 Tax=Homo sapiens
                        RepID=B3KMZ6_HUMAN
        >SUMO-activating enzyme subunit 2 n=1 Tax=Homo sapiens RepID=SAE2_HUMAN


13a     UniRef100_B4DKR1 UniRef100_B4DQY2 UniRef100_B4DT20 UniRef100_B8ZZQ7 UniRef100_B9A067 UniRef100_Q16891
        UniRef100_Q16891-2 UniRef100_Q16891-3 0.9997
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.41%
        >cDNA FLJ51884, highly similar to Mitochondrial inner membrane protein n=1 Tax=Homo sapiens RepID=B4DKR1_H Length: 746aa
        >cDNA FLJ59388, highly similar to Mitochondrial inner membrane protein n=1 Tax=Homo sapiens RepID=B4DQY2_HUMAN
        >cDNA FLJ59418, highly similar to Mitochondrial inner membrane protein n=1 Tax=Homo sapiens RepID=B4DT20_HUMAN
        >Putative uncharacterized protein IMMT n=1 Tax=Homo sapiens RepID=B8ZZQ7_HUMAN
        >Putative uncharacterized protein IMMT n=1 Tax=Homo sapiens RepID=B9A067_HUMAN
        >Mitochondrial inner membrane protein n=1 Tax=Homo sapiens RepID=IMMT_HUMAN
        >Isoform 2 of Mitochondrial inner membrane protein n=1 Tax=Homo sapiens RepID=Q16891-2
        >Isoform 3 of Mitochondrial inner membrane protein n=1 Tax=Homo sapiens RepID=Q16891-3


31      UniRef100_A8K3A8 UniRef100_B4DNN3 UniRef100_B4DTH6 UniRef100_B4DWJ2 UniRef100_B7Z840 UniRef100_C9J165
        UniRef100_C9JSG9 UniRef100_P47897 UniRef100_Q53HS0 UniRef100_UPI000198CA8A UniRef100_UPI0001AE75DA 0.9906
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%
        >cDNA FLJ75085, highly similar to Homo sapiens glutaminyl-tRNA synthetase (QARS), mRNA n=1 Tax=Homo sapien Length: 775aa
        >cDNA FLJ54453, highly similar to Glutaminyl-tRNA synthetase (EC 6.1.1.18) n=1 Tax=Homo sapiens RepID=B4DNN3_HUMAN
        >cDNA FLJ54881, highly similar to Glutaminyl-tRNA synthetase (EC 6.1.1.18) n=1 Tax=Homo sapiens RepID=B4DTH6_HUMAN
        >cDNA FLJ54314, highly similar to Glutaminyl-tRNA synthetase (EC 6.1.1.18) n=1 Tax=Homo sapiens RepID=B4DWJ2_HUMAN
        >cDNA FLJ55601, highly similar to Glutaminyl-tRNA synthetase (EC 6.1.1.18) n=1 Tax=Homo sapiens RepID=B7Z840_HUMAN
        >Putative uncharacterized protein QARS n=1 Tax=Homo sapiens RepID=C9J165_HUMAN
        >Putative uncharacterized protein QARS n=1 Tax=Homo sapiens RepID=C9JSG9_HUMAN
        >Glutaminyl-tRNA synthetase n=1 Tax=Homo sapiens RepID=SYQ_HUMAN
```

>Glutaminyl-tRNA synthetase variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53HS0_HUMAN
>UPI000198CA8A related cluster n=1 Tax=Homo sapiens RepID=UPI000198CA8A
>UPI0001AE75DA related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE75DA

32 UniRef100_A8K949 UniRef100_Q8N1G2 0.9906
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.29%
>cDNA FLJ77620 n=1 Tax=Homo sapiens RepID=A8K949_HUMAN Length: 835aa
>S-adenosyl-L-methionine-dependent methyltransferase FTSJD2 n=2 Tax=Hominidae RepID=FTSJ2_HUMAN

33 UniRef100_A8K9K1 UniRef100_A8MYK9 UniRef100_D3DTJ8 UniRef100_P16615 UniRef100_P16615-2 UniRef100_P16615-3 UniRef100_P16615-4 UniRef100_P16615-5 UniRef100_Q93084 UniRef100_Q93084-2 UniRef100_Q93084-4 UniRef100_Q93084-5 UniRef100_Q93084-6 0.9906
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%
>cDNA FLJ77199, highly similar to Homo sapiens ATPase, Ca++ transporting, ubiquitous (ATP2A3), transcript varian Length: 998aa
>Putative uncharacterized protein ATP2A3 n=1 Tax=Homo sapiens RepID=A8MYK9_HUMAN
>ATPase, Ca++ transporting, ubiquitous, isoform CRA_d n=2 Tax=Homo sapiens RepID=D3DTJ8_HUMAN
>Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 n=1 Tax=Homo sapiens RepID=AT2A2_HUMAN
>Isoform 2 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 n=1 Tax=Homo sapiens RepID=P16615-2
>Isoform 3 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 n=1 Tax=Homo sapiens RepID=P16615-3
>Isoform 4 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 n=1 Tax=Homo sapiens RepID=P16615-4
>Isoform 5 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 n=1 Tax=Homo sapiens RepID=P16615-5
>Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 n=1 Tax=Homo sapiens RepID=AT2A3_HUMAN
>Isoform SERCA3A of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 n=1 Tax=Homo sapiens RepID=Q93084-2
>Isoform SERCA3D of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 n=1 Tax=Homo sapiens RepID=Q93084-4
>Isoform SERCA3E of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 n=1 Tax=Homo sapiens RepID=Q93084-5
>Isoform SERCA3F of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 n=2 Tax=Homo sapiens RepID=Q93084-6

34 UniRef100_A8KAN9 UniRef100_Q9ULK0 UniRef100_UPI000059D191 0.9906
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%
>cDNA FLJ78030 n=1 Tax=Homo sapiens RepID=A8KAN9_HUMAN Length: 1009aa
>Glutamate receptor delta-1 subunit n=2 Tax=Homo sapiens RepID=GRID1_HUMAN
>Glutamate receptor delta-1 subunit precursor (GluR delta-1). n=1 Tax=Homo sapiens RepID=UPI000059D191

35 UniRef100_B0AZS5 UniRef100_B4DM85 UniRef100_D3DW97 UniRef100_O00139 UniRef100_O00139-2 UniRef100_O00139-4 UniRef100_UPI000186E36F 0.9906
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%
>cDNA, FLJ79515, highly similar to Kinesin-like protein KIF2 n=1 Tax=Homo sapiens RepID=B0AZS5_HUMAN Length: 660aa
>cDNA FLJ56002, highly similar to Kinesin-like protein KIF2 n=1 Tax=Homo sapiens RepID=B4DM85_HUMAN
>Kinesin heavy chain member 2, isoform CRA_b n=3 Tax=Homo sapiens RepID=D3DW97_HUMAN
>Kinesin-like protein KIF2A n=1 Tax=Homo sapiens RepID=KIF2A_HUMAN
>Isoform 2 of Kinesin-like protein KIF2A n=1 Tax=Homo sapiens RepID=O00139-2
>Isoform 4 of Kinesin-like protein KIF2A n=1 Tax=Homo sapiens RepID=O00139-4
>kif-2, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E36F

36 UniRef100_B2RDX5 UniRef100_B3KTN2 UniRef100_B4DEG8 UniRef100_B4DKZ9 UniRef100_P26639 UniRef100_Q53GX7 UniRef100_Q5M7Z9 UniRef100_UPI0001AE7343 0.9906
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.44%
>cDNA, FLJ96812, highly similar to Homo sapiens threonyl-tRNA synthetase (TARS), mRNA n=1 Tax=Homo sapiens Length: 711aa
>cDNA FLJ38533 fis, clone HCHON2001108, highly similar to Threonyl-tRNA synthetase, cytoplasmic (EC 6.1.1.3) n=1 Tax=Homo sapiens RepID=B3KTN2_HUMAN
>cDNA FLJ53464, highly similar to Threonyl-tRNA synthetase, cytoplasmic (EC 6.1.1.3) n=1 Tax=Homo sapiens RepID=B4DEG8_HUMAN
>cDNA FLJ55705, highly similar to Threonyl-tRNA synthetase, cytoplasmic (EC 6.1.1.3) n=1 Tax=Homo sapiens RepID=B4DKZ9_HUMAN
>Threonyl-tRNA synthetase, cytoplasmic n=1 Tax=Homo sapiens RepID=SYTC_HUMAN
>Threonyl-tRNA synthetase variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GX7_HUMAN
>TARS protein (Fragment) n=1 Tax=Homo sapiens RepID=Q5M7Z9_HUMAN
>UPI0001AE7343 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7343

37 UniRef100_B3KX72 UniRef100_B4DLR3 UniRef100_Q00839 UniRef100_Q00839-2 UniRef100_Q4R810 UniRef100_Q5RI19 0.9906
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.29%
>cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclear ribonucleoprotein U n=1 Tax=H Length: 750aa
>cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U n=1 Tax=Homo sapiens RepID=B4DLR3_HUMAN
>Heterogeneous nuclear ribonucleoprotein U n=3 Tax=Homo sapiens RepID=HNRPU_HUMAN
>Isoform Short of Heterogeneous nuclear ribonucleoprotein U n=1 Tax=Homo sapiens RepID=Q00839-2
>Testis cDNA clone: QtsA-13832, similar to human heterogeneous nuclear ribonucleoprotein U (scaffoldattachment factor A) (HNRPU), transcript variant 2, n=1 Tax=Macaca fascicularis RepID=Q4R810_MACFA
>Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A) n=2 Tax=Homo sapiens RepID=Q5RI19_HUMAN

38 UniRef100_P54886 UniRef100_P54886-2 0.9906
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%

```
    >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


39  UniRef100_Q00610 UniRef100_Q00610-2 UniRef100_UPI0001AE66DF 0.9906
    confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.29%
    >Clathrin heavy chain 1 n=3 Tax=Eutheria RepID=CLH1_HUMAN                                          Length: 1675aa
    >Isoform 2 of Clathrin heavy chain 1 n=1 Tax=Homo sapiens RepID=Q00610-2
    >UPI0001AE66DF related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE66DF


24b UniRef100_P02533 0.9900
    confidence: 1. coverage: 4.7 num unique p tot indep spec share of spect subsumed entries: 2
    >Keratin, type I cytoskeletal 14 n=1 Tax=Homo sapiens RepID=K1C14_HUMAN                            Length: 472aa


40  UniRef100_A5JHP3 UniRef100_P81605 0.9896
    confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%
    >Dermcidin isoform 2 n=1 Tax=Homo sapiens RepID=A5JHP3_HUMAN                                       Length: 121aa
    >DCD-1 n=3 Tax=Euarchontoglires RepID=DCD_HUMAN


41  UniRef100_B4E0S6 UniRef100_O43143 UniRef100_UPI000186D713 0.9896
    confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%
    >cDNA FLJ55635, highly similar to pre-mRNA-splicing factorATP-dependent RNA helicase DHX15 (EC 3.6.1.-) n=1 Ta Length: 784aa
    >Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 n=1 Tax=Homo sapiens RepID=DHX15_HUMAN
    >ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D713


42  UniRef100_D6RDP7 UniRef100_P27824 UniRef100_Q16094 UniRef100_UPI000179A8F1 UniRef100_UPI0001D3BB3C UniRef100_UPI0001D3BB3E
        0.9896
    confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.44%
    >Putative uncharacterized protein CANX n=4 Tax=Homo sapiens RepID=D6RDP7_HUMAN                     Length: 168aa
    >Calnexin n=3 Tax=Homo sapiens RepID=CALX_HUMAN
    >Calnexin (Fragment) n=1 Tax=Homo sapiens RepID=Q16094_HUMAN
    >Calnexin precursor (Major histocompatibility complex class I antigen- binding protein p88) (p90) (IP90). n=1 Tax=Homo sapiens
              RepID=UPI000179A8F1
    >UPI0001D3BB3C related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3BB3C
    >UPI0001D3BB3E related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3BB3E


43  UniRef100_UPI00004EC03F 0.9896
    confidence: 0. coverage: 4.1 num unique p tot indep spec share of spectrum id's: 0.44%
    >4m5.3 anti-fluorescein single chain antibody n=1 Tax=Homo sapiens RepID=UPI00004EC03F              Length: 268aa


44  UniRef100_Q8TA92 UniRef100_Q9Y4W6 0.9887
    confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%
    >Similar to AFG3 ATPase family gene 3-like 2 (Yeast) (Fragment) n=1 Tax=Homo sapiens RepID=Q8TA92_HUMAN    Length: 812aa
    >AFG3-like protein 2 n=2 Tax=Homo sapiens RepID=AFG32_HUMAN


45  UniRef100_B4DJW8 UniRef100_B4DRA5 UniRef100_B4DSQ5 UniRef100_Q15436 UniRef100_Q15437 UniRef100_Q5QPE2
    UniRef100_UPI0001C552C9 0.9878
    confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%
    >cDNA FLJ55697, highly similar to Protein transport protein Sec23B n=1 Tax=Homo sapiens RepID=B4DJW8_HUMA Length: 749aa
    >cDNA FLJ61346, highly similar to Protein transport protein Sec23B n=1 Tax=Homo sapiens RepID=B4DRA5_HUMAN
    >cDNA FLJ53608, highly similar to Protein transport protein Sec23A n=1 Tax=Homo sapiens RepID=B4DSQ5_HUMAN
    >Protein transport protein Sec23A n=1 Tax=Homo sapiens RepID=SC23A_HUMAN
    >Protein transport protein Sec23B n=2 Tax=Homo sapiens RepID=SC23B_HUMAN
    >Sec23 homolog B (S. cerevisiae) (Fragment) n=1 Tax=Homo sapiens RepID=Q5QPE2_HUMAN
    >protein transport protein Sec23B isoform 2 n=1 Tax=Homo sapiens RepID=UPI0001C552C9


46  UniRef100_Q59EK6 UniRef100_Q5CAQ4 0.9804
    confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.29%
    >TNF receptor-associated protein 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59EK6_HUMAN          Length: 703aa
    >TNF receptor-associated protein 1 n=1 Tax=Homo sapiens RepID=Q5CAQ4_HUMAN


47  UniRef100_UPI0000110496 0.9795
    confidence: 0. coverage: 5.0 num unique p tot indep spec share of spectrum id's: 0.44%
    >ANTIBODY A5B7 (HEAVY CHAIN) n=1 Tax=Homo sapiens RepID=UPI0000110496                              Length: 220aa


48  UniRef100_A8K6M8 UniRef100_B3KMF6 UniRef100_B3KND4 UniRef100_B3KW21 UniRef100_Q2NLA0 UniRef100_Q8WUI6
    UniRef100_Q9H9B7 UniRef100_Q9NUP3 UniRef100_Q9UBF2 UniRef100_Q9Y678 0.9579
```

```
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.15%
        >cDNA FLJ77708, highly similar to Homo sapiens coatomer protein complex, subunit gamma (COPG), mRNA n=1 Ta Length: 874aa
        >cDNA FLJ10862 fis, clone NT2RP4001574, highly similar to Coatomer subunit gamma n=1 Tax=Homo sapiens RepID=B3KMF6_HUMAN
        >cDNA FLJ14352 fis, clone Y79AA1000346, highly similar to Coatomer subunit gamma-2 n=1 Tax=Homo sapiens RepID=B3KND4_HUMAN
        >cDNA FLJ41945 fis, clone PLACE6019676, highly similar to Coatomer subunit gamma n=1 Tax=Homo sapiens RepID=B3KW21_HUMAN
        >COPG2 protein n=1 Tax=Homo sapiens RepID=Q2NLA0_HUMAN
        >COPG protein (Fragment) n=2 Tax=Homininae RepID=Q8WUI6_HUMAN
        >cDNA FLJ12872 fis, clone NT2RP2003760, highly similar to COATOMER GAMMA SUBUNIT n=1 Tax=Homo sapiens RepID=Q9H9B7_HUMAN
        >cDNA FLJ11224 fis, clone PLACE1008273, moderately similar to COATOMER GAMMA SUBUNIT n=1 Tax=Homo sapiens RepID=Q9NUP3_HUMAN
        >Coatomer subunit gamma-2 n=1 Tax=Homo sapiens RepID=COPG2_HUMAN
        >Coatomer subunit gamma n=2 Tax=Homo sapiens RepID=COPG_HUMAN


49      UniRef100_UPI000186DB8B 0.9501
        confidence: 0. coverage: 0.4 num unique p tot indep spec share of spectrum id's: 0.43%
        >conserved hypothetical protein n=1 Tax=Pediculus humanus corporis RepID=UPI000186DB8B                 Length: 1928aa
```

NFATC1 upper band MS results:

```
77 entries (25 single hits) retrieved from
/home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_NFATC1-2-sequest.prot.xml


* corresponds to peptide is_nondegenerate_evidence flag


1       UniRef100_A4D210 UniRef100_B4DV79 UniRef100_B4DXN6 UniRef100_P55884 UniRef100_P55884-2 UniRef100_Q59FS8
        UniRef100_Q96G38 UniRef100_UPI00015E042B 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.50%
        >Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa n=1 Tax=Homo sapiens RepID=A4D210_HUMAN    Length: 775aa
        >cDNA FLJ53410, highly similar to Eukaryotic translation initiation factor 3 subunit 9 n=1 Tax=Homo sapiens RepID=B4DV79_HUMAN
        >cDNA FLJ53461, highly similar to Eukaryotic translation initiation factor 3 subunit 9 n=1 Tax=Homo sapiens RepID=B4DXN6_HUMAN
        >Eukaryotic translation initiation factor 3 subunit B n=1 Tax=Homo sapiens RepID=EIF3B_HUMAN
        >Isoform 2 of Eukaryotic translation initiation factor 3 subunit B n=1 Tax=Homo sapiens RepID=P55884-2
        >Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa isoform b variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59FS8_HUMAN
        >EIF3B protein (Fragment) n=1 Tax=Homo sapiens RepID=Q96G38_HUMAN
        >Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) (eIF3b) (Prt1 homolog) (hPrt1). n=1 Tax=Homo sapiens
                  RepID=UPI00015E042B

2       UniRef100_B4DSR0 UniRef100_P42704 1.0000
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.75%
        >cDNA FLJ60080, highly similar to 130 kDa leucine-rich protein (LRP 130) (Fragment) n=1 Tax=Homo sapiens RepI Length: 1087aa
        >Leucine-rich PPR motif-containing protein, mitochondrial n=1 Tax=Homo sapiens RepID=LPPRC_HUMAN


3       UniRef100_O95782 UniRef100_O95782-2 UniRef100_Q8N9K4 1.0000
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.48%
        >AP-2 complex subunit alpha-1 n=1 Tax=Homo sapiens RepID=AP2A1_HUMAN                                   Length: 977aa
        >Isoform B of AP-2 complex subunit alpha-1 n=1 Tax=Homo sapiens RepID=O95782-2
        >cDNA FLJ36998 fis, clone BRACE2007295, highly similar to ALPHA-ADAPTIN A n=1 Tax=Homo sapiens RepID=Q8N9K4_HUMAN


4       UniRef100_P35527 1.0000
        confidence: 1. coverage: 13. num unique p tot indep spec share of spectrum id's: 1.77%
        >Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN                                  Length: 623aa


5       UniRef100_Q15058 1.0000
        confidence: 1. coverage: 5.8 num unique p tot indep spec share of spectrum id's: 1.23%
        >Kinesin-like protein KIF14 n=1 Tax=Homo sapiens RepID=KIF14_HUMAN                                     Length: 1648aa


6       UniRef100_UPI00004EC03F 1.0000
        confidence: 1. coverage: 6.0 num unique p tot indep spec share of spectrum id's: 0.86%
        >4m5.3 anti-fluorescein single chain antibody n=1 Tax=Homo sapiens RepID=UPI00004EC03F                 Length: 268aa


7       UniRef100_UPI00017BDB3E UniRef100_UPI00017BDB43 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.24%
        >FabOX108 Heavy Chain Fragment n=1 Tax=Homo sapiens RepID=UPI00017BDB3E                                Length: 229aa
        >FabOX117 Heavy Chain Fragment n=1 Tax=Homo sapiens RepID=UPI00017BDB43


8a      UniRef100_A0RZB8 UniRef100_B9ZVX0 UniRef100_O60610 UniRef100_O60610-2 UniRef100_Q17RN4 UniRef100_Q6URC4
        UniRef100_UPI0000EA87E7 UniRef100_UPI000155D622 UniRef100_UPI0001AE73A7 UniRef100_UPI0001AE73A8 1.0000
        confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
```

```
      >Diaphanous-1 n=1 Tax=Homo sapiens RepID=A0RZB8_HUMAN                                              Length: 1262aa
      >Diaphanous homolog 1 (Drosophila), isoform CRA_a n=1 Tax=Homo sapiens RepID=B9ZVX0_HUMAN
      >Protein diaphanous homolog 1 n=1 Tax=Homo sapiens RepID=DIAP1_HUMAN
      >Isoform 2 of Protein diaphanous homolog 1 n=1 Tax=Homo sapiens RepID=O60610-2
      >DIAPH1 protein n=1 Tax=Homo sapiens RepID=Q17RN4_HUMAN
      >Diaphanous 1 n=1 Tax=Homo sapiens RepID=Q6URC4_HUMAN
      >protein diaphanous homolog 1 isoform 2 n=1 Tax=Homo sapiens RepID=UPI0000EA87E7
      >Protein diaphanous homolog 1 (Diaphanous-related formin-1) (DRF1). n=1 Tax=Homo sapiens RepID=UPI000155D622
      >Protein diaphanous homolog 1 (Diaphanous-related formin-1) (DRF1). n=1 Tax=Homo sapiens RepID=UPI0001AE73A7
      >Protein diaphanous homolog 1 (Diaphanous-related formin-1) (DRF1). n=1 Tax=Homo sapiens RepID=UPI0001AE73A8


9a    UniRef100_A2RRR4 UniRef100_B2RCM2 UniRef100_B4DER1 UniRef100_B4E266 UniRef100_Q2TU79 UniRef100_Q9H8E3
      UniRef100_Q9P2J5 UniRef100_UPI0001AE73C3 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.35%
      >LARS protein n=1 Tax=Homo sapiens RepID=A2RRR4_HUMAN                                              Length: 485aa
      >cDNA, FLJ96156, highly similar to Homo sapiens leucyl-tRNA synthetase (LARS), mRNA n=1 Tax=Homo sapiens RepID=B2RCM2_HUMAN
      >cDNA FLJ58157, highly similar to Leucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.4) n=1 Tax=Homo sapiens RepID=B4DER1_HUMAN
      >cDNA FLJ58466, highly similar to Leucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.4) n=1 Tax=Homo sapiens RepID=B4E266_HUMAN
      >Cell proliferation-inducing protein 57 n=3 Tax=Homo sapiens RepID=Q2TU79_HUMAN
      >cDNA FLJ13715 fis, clone PLACE2000404, moderately similar to PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) n=1 Tax=Homo sapiens
                  RepID=Q9H8E3_HUMAN
      >Leucyl-tRNA synthetase, cytoplasmic n=3 Tax=Homo sapiens RepID=SYLC_HUMAN
      >UPI0001AE73C3 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE73C3


11a   UniRef100_A8K492 UniRef100_B3KVK7 UniRef100_B4E0E9 UniRef100_P56192 UniRef100_UPI0001AE6AF3 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
      >cDNA FLJ76789, highly similar to Homo sapiens methionine-tRNA synthetase (MARS), mRNA n=1 Tax=Homo sapie Length: 900aa
      >cDNA FLJ16674 fis, clone THYMU3008136, highly similar to Methionyl-tRNA synthetase (EC 6.1.1.10) n=1 Tax=Homo sapiens
                  RepID=B3KVK7_HUMAN
      >cDNA FLJ55046, highly similar to Methionyl-tRNA synthetase (EC 6.1.1.10) n=1 Tax=Homo sapiens RepID=B4E0E9_HUMAN
      >Methionyl-tRNA synthetase, cytoplasmic n=1 Tax=Homo sapiens RepID=SYMC_HUMAN
      >UPI0001AE6AF3 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6AF3


12a   UniRef100_A8K9C4 UniRef100_B4DNE0 UniRef100_B4DV42 UniRef100_B4E2C5 UniRef100_P68104 UniRef100_Q504Z0
      UniRef100_Q53G85 UniRef100_Q53GE9 UniRef100_Q53HM9 UniRef100_Q53HQ7 UniRef100_Q53HR5 UniRef100_Q5VTE0
      UniRef100_Q6IPN6 UniRef100_Q6IPT9 UniRef100_Q6IQ15 UniRef100_Q6P082 UniRef100_Q8TBL1 UniRef100_Q96CD8
      UniRef100_Q96RE1 UniRef100_Q9NZS6 UniRef100_UPI00015E0621 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.85%
      >Elongation factor 1-alpha n=1 Tax=Homo sapiens RepID=A8K9C4_HUMAN                                 Length: 462aa
      >Elongation factor 1-alpha n=1 Tax=Homo sapiens RepID=B4DNE0_HUMAN
      >Elongation factor 1-alpha n=1 Tax=Homo sapiens RepID=B4DV42_HUMAN
      >cDNA FLJ54032, highly similar to Elongation factor 1-alpha 1 n=1 Tax=Homo sapiens RepID=B4E2C5_HUMAN
      >Elongation factor 1-alpha 1 n=13 Tax=Eutheria RepID=EF1A1_HUMAN
      >EEF1A1 protein n=3 Tax=Simiiformes RepID=Q504Z0_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=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
      >EEF1A1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6P082_HUMAN
      >Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8TBL1_HUMAN
      >Putative uncharacterized protein (Fragment) n=2 Tax=Homo sapiens RepID=Q96CD8_HUMAN
      >Elongation factor 1-alpha n=4 Tax=Eutheria RepID=Q96RE1_HUMAN
      >Elongation factor 1-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q9NZS6_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

13a   UniRef100_A8MXP9 UniRef100_P43243 UniRef100_Q68D11 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.99%
      >Putative uncharacterized protein MATR3 n=1 Tax=Homo sapiens RepID=A8MXP9_HUMAN                    Length: 895aa
      >Matrin-3 n=2 Tax=Homo sapiens RepID=MATR3_HUMAN
      >Putative uncharacterized protein DKFZp686K23100 n=1 Tax=Homo sapiens RepID=Q68D11_HUMAN


15a   UniRef100_B2R5W3 UniRef100_B4E0E1 UniRef100_P09874 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.73%
      >cDNA, FLJ92658, highly similar to Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA r Length: 1014aa
      >cDNA FLJ53442, highly similar to Poly (ADP-ribose) polymerase 1 (EC 2.4.2.30) n=1 Tax=Homo sapiens RepID=B4E0E1_HUMAN
      >Poly [ADP-ribose] polymerase 1 n=1 Tax=Homo sapiens RepID=PARP1_HUMAN
```

```
16a   UniRef100_B2R8R5 UniRef100_Q13263 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.87%
      >cDNA, FLJ94025, highly similar to Homo sapiens tripartite motif-containing 28 (TRIM28), mRNA n=1 Tax=Homo sa Length: 835aa
      >Transcription intermediary factor 1-beta n=1 Tax=Homo sapiens RepID=TIF1B_HUMAN


17a   UniRef100_B2RU10 UniRef100_B4DGF1 UniRef100_B4DSI9 UniRef100_D3DNT2 UniRef100_D3DNT5 UniRef100_Q04637
      UniRef100_Q04637-5 UniRef100_Q4LE58 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.91%
      >EIF4G1 protein n=2 Tax=Homo sapiens RepID=B2RU10_HUMAN                                                   Length: 1606aa
      >cDNA FLJ56479, highly similar to Eukaryotic translation initiation factor 4 gamma 1 n=1 Tax=Homo sapiens RepID=B4DGF1_HUMAN
      >cDNA FLJ56483, highly similar to Eukaryotic translation initiation factor 4 gamma 1 n=1 Tax=Homo sapiens RepID=B4DSI9_HUMAN
      >Eukaryotic translation initiation factor 4 gamma, 1, isoform CRA_c n=5 Tax=Homo sapiens RepID=D3DNT2_HUMAN
      >Eukaryotic translation initiation factor 4 gamma, 1, isoform CRA_g n=3 Tax=Homo sapiens RepID=D3DNT5_HUMAN
      >Eukaryotic translation initiation factor 4 gamma 1 n=3 Tax=Homo sapiens RepID=IF4G1_HUMAN
      >Isoform D of Eukaryotic translation initiation factor 4 gamma 1 n=3 Tax=Homo sapiens RepID=Q04637-5
      >EIF4G1 variant protein (Fragment) n=2 Tax=Homo sapiens RepID=Q4LE58_HUMAN


18a   UniRef100_B3KMX0 UniRef100_B4DLA6 UniRef100_P33991 UniRef100_UPI0001AE6ED3 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
      >cDNA FLJ12837 fis, clone NT2RP2003228, highly similar to DNA replication licensing factor MCM4 n=1 Tax=Homo s Length: 863aa
      >cDNA FLJ54365, highly similar to DNA replication licensing factor MCM4 n=1 Tax=Homo sapiens RepID=B4DLA6_HUMAN
      >DNA replication licensing factor MCM4 n=1 Tax=Homo sapiens RepID=MCM4_HUMAN
      >UPI0001AE6ED3 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6ED3


19a   UniRef100_B3KQ43 UniRef100_B7Z700 UniRef100_Q9HCE1 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.50%
      >cDNA FLJ32791 fis, clone TESTI2002365, highly similar to helicase MOV-10 (EC 3.6.1.-) n=1 Tax=Homo sapiens Re Length: 417aa
      >cDNA FLJ54557, highly similar to helicase MOV-10 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B7Z700_HUMAN
      >Putative helicase MOV-10 n=2 Tax=Homo sapiens RepID=MOV10_HUMAN


20a   UniRef100_B3KU67 UniRef100_Q59FF0 UniRef100_Q7KZF4 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.85%
      >cDNA FLJ39264 fis, clone OCBBF2009603, highly similar to Staphylococcal nuclease domain-containing protein 1 n Length: 900aa
      >EBNA-2 co-activator variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59FF0_HUMAN
      >Staphylococcal nuclease domain-containing protein 1 n=2 Tax=Homo sapiens RepID=SND1_HUMAN


22a   UniRef100_B4DGL0 UniRef100_B4DMA2 UniRef100_P08238 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
      >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


23a   UniRef100_B4DH02 UniRef100_O14992 UniRef100_P34932 UniRef100_Q59GF8 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
      >cDNA FLJ50510, highly similar to Heat shock 70 kDa protein 4 n=1 Tax=Homo sapiens RepID=B4DH02_HUMAN      Length: 840aa
      >HS24/P52 n=1 Tax=Homo sapiens RepID=O14992_HUMAN
      >Heat shock 70 kDa protein 4 n=3 Tax=Homo sapiens RepID=HSP74_HUMAN
      >Heat shock 70kDa protein 4 isoform a variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59GF8_HUMAN


23b   UniRef100_B4DF68 UniRef100_B4DYH1 UniRef100_B4DZB4 UniRef100_Q92598 UniRef100_Q92598-2 UniRef100_Q92598-3
      UniRef100_UPI0001AE69C1 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.49%
      >cDNA FLJ55325, highly similar to Heat-shock protein 105 kDa n=1 Tax=Homo sapiens RepID=B4DF68_HUMAN       Length: 755aa
      >Heat shock 105kDa/110kDa protein 1, isoform CRA_b n=1 Tax=Homo sapiens RepID=B4DYH1_HUMAN
      >cDNA FLJ51707, highly similar to Heat-shock protein 105 kDa n=1 Tax=Homo sapiens RepID=B4DZB4_HUMAN
      >Heat shock protein 105 kDa n=1 Tax=Homo sapiens RepID=HS105_HUMAN
      >Isoform Beta of Heat shock protein 105 kDa n=1 Tax=Homo sapiens RepID=Q92598-2
      >Isoform 3 of Heat shock protein 105 kDa n=1 Tax=Homo sapiens RepID=Q92598-3
      >UPI0001AE69C1 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE69C1


24a   UniRef100_B4DIM0 UniRef100_B4E3P0 UniRef100_P53396 UniRef100_UPI0000225CC0 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.62%
      >cDNA FLJ56442, highly similar to ATP-citrate synthase (EC 2.3.3.8) n=1 Tax=Homo sapiens RepID=B4DIM0_HUMA Length: 1145aa
      >cDNA FLJ55447, highly similar to ATP-citrate synthase (EC 2.3.3.8) n=2 Tax=Homo sapiens RepID=B4E3P0_HUMAN
      >ATP-citrate synthase n=2 Tax=Homo sapiens RepID=ACLY_HUMAN
      >ATP-citrate synthase isoform 2 n=2 Tax=Homo sapiens RepID=UPI0000225CC0
```

25a UniRef100_B4DLR3 UniRef100_Q00839 UniRef100_Q00839-2 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 3
>cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U n=1 Tax=Homo sapiens RepID=B4DL Length: 784aa
>Heterogeneous nuclear ribonucleoprotein U n=3 Tax=Homo sapiens RepID=HNRPU_HUMAN
>Isoform Short of Heterogeneous nuclear ribonucleoprotein U n=1 Tax=Homo sapiens RepID=Q00839-2

27a UniRef100_B5B2M5 UniRef100_O95644 UniRef100_UPI00015DFAC5 1.0000
confidence: : max coverag num unique tot indep spe share of spe subsumed entries: 3
>Nuclear factor of activated T-cells c1 isoform IB-IXL n=5 Tax=Homo sapiens RepID=B5B2M5_HUMAN Length: 930aa
>Nuclear factor of activated T-cells, cytoplasmic 1 n=7 Tax=Homo sapiens RepID=NFAC1_HUMAN
>Nuclear factor of activated T-cells, cytoplasmic 1 (NFAT transcription complex cytosolic component) (NF-ATc1) (NF-ATc). n=1 Tax=Homo sapiens RepID=UPI00015DFAC5

28a UniRef100_B7Z1H4 UniRef100_B7Z1V9 UniRef100_B7Z463 UniRef100_B7Z4B2 UniRef100_B7Z899 UniRef100_P55786
1
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
>cDNA FLJ56052, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) n=1 Tax=Homo sapiens RepID Length: 602aa
>cDNA FLJ53310, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) n=1 Tax=Homo sapiens RepID=B7Z1V9_HUMAN
>cDNA FLJ53354, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) n=1 Tax=Homo sapiens RepID=B7Z463_HUMAN
>cDNA FLJ56108, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) n=1 Tax=Homo sapiens RepID=B7Z4B2_HUMAN
>cDNA FLJ55506, highly similar to Puromycin-sensitive aminopeptidase (EC3.4.11.-) n=1 Tax=Homo sapiens RepID=B7Z899_HUMAN
>Puromycin-sensitive aminopeptidase n=1 Tax=Homo sapiens RepID=PSA_HUMAN

29a UniRef100_C5IWV5 UniRef100_P00761 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 5.41%
>Trypsinogen n=1 Tax=Sus scrofa RepID=C5IWV5_PIG Length: 246aa
>Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG

30a UniRef100_C9JMV5 UniRef100_O00410 UniRef100_Q4R8T7 UniRef100_UPI0001B790BA 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
>Putative uncharacterized protein IPO5 n=1 Tax=Homo sapiens RepID=C9JMV5_HUMAN Length: 165aa
>Importin-5 n=2 Tax=Homo sapiens RepID=IPO5_HUMAN
>Testis cDNA clone: QtsA-11503, similar to human karyopherin (importin) beta 3 (KPNB3), n=1 Tax=Macaca fascicularis RepID=Q4R8T7_MACFA
>UPI0001B790BA related cluster n=1 Tax=Homo sapiens RepID=UPI0001B790BA

31a UniRef100_O14980 1.0000
confidence: 1. coverage: 4.4 num unique p tot indep spec share of spect subsumed entries: 2
>Exportin-1 n=1 Tax=Homo sapiens RepID=XPO1_HUMAN Length: 1071aa

32a UniRef100_O75694 UniRef100_UPI0001D3B217 1.0000
confidence: 0. max coverage num unique p tot indep spec share of spect subsumed entries: 1
>Nuclear pore complex protein Nup155 n=3 Tax=Homo sapiens RepID=NU155_HUMAN Length: 1391aa
>UPI0001D3B217 related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3B217

33a UniRef100_P02769 UniRef100_UPI000179EC85 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 3
>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa
>Serum albumin precursor (Allergen Bos d 6) (BSA). n=1 Tax=Bos taurus RepID=UPI000179EC85

34a UniRef100_P04264 1.0000
confidence: 1. coverage: 25. num unique p tot indep spec share of spect subsumed entries: 1
>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN Length: 644aa

34b UniRef100_P35908 1.0000
confidence: 1. coverage: 12. num unique p tot indep spec share of spectrum id's: 1.37%
>Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E_HUMAN Length: 639aa

35a UniRef100_P07814 1.0000
confidence: 1. coverage: 11. num unique p tot indep spec share of spect subsumed entries: 3
>Prolyl-tRNA synthetase n=1 Tax=Homo sapiens RepID=SYEP_HUMAN Length: 1512aa

36a UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 3
>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

```
37a   UniRef100_P22102 UniRef100_Q3B7A7 UniRef100_Q59HH3 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 8
      >Phosphoribosylglycinamide formyltransferase n=2 Tax=Homo sapiens RepID=PUR2_HUMAN                    Length: 1010aa
      >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

38a   UniRef100_P22314 1.0000
      confidence: 0. coverage: 4.2 num unique p tot indep spec share of spect subsumed entries: 1
      >Ubiquitin-like modifier-activating enzyme 1 n=1 Tax=Homo sapiens RepID=UBA1_HUMAN                    Length: 1058aa


39a   UniRef100_P27694 1.0000
      confidence: 1. coverage: 6.5 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


40a   UniRef100_P49327 1.0000
      confidence: 0. coverage: 1.3 num unique p tot indep spec share of spect subsumed entries: 1
      >Oleoyl-[acyl-carrier-protein] hydrolase n=1 Tax=Homo sapiens RepID=FAS_HUMAN                         Length: 2511aa


41a   UniRef100_P53621 UniRef100_P53621-2 1.0000
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.50%
      >Proxenin n=1 Tax=Homo sapiens RepID=COPA_HUMAN                                                       Length: 1224aa
      >Isoform 2 of Coatomer subunit alpha n=1 Tax=Homo sapiens RepID=P53621-2


42a   UniRef100_Q00610 UniRef100_Q00610-2 UniRef100_UPI0001AE66DF 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
      >Clathrin heavy chain 1 n=3 Tax=Eutheria RepID=CLH1_HUMAN                                             Length: 1675aa
      >Isoform 2 of Clathrin heavy chain 1 n=1 Tax=Homo sapiens RepID=Q00610-2
      >UPI0001AE66DF related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE66DF


43a   UniRef100_Q05BS0 UniRef100_Q14152 UniRef100_Q24JU4 UniRef100_Q3B770 UniRef100_Q6P1R0 UniRef100_Q7Z5T5
                1
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
      >EIF3A protein (Fragment) n=1 Tax=Homo sapiens RepID=Q05BS0_HUMAN                                     Length: 634aa
      >Eukaryotic translation initiation factor 3 subunit A n=1 Tax=Homo sapiens RepID=EIF3A_HUMAN
      >Eukaryotic translation initiation factor 3, subunit A n=1 Tax=Homo sapiens RepID=Q24JU4_HUMAN
      >EIF3A protein (Fragment) n=1 Tax=Homo sapiens RepID=Q3B770_HUMAN
      >EIF3A protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6P1R0_HUMAN
      >EIF3A protein (Fragment) n=1 Tax=Homo sapiens RepID=Q7Z5T5_HUMAN


44a   UniRef100_Q08211 1.0000
      confidence: 1. coverage: 29. num unique p tot indep spec share of spect subsumed entries: 4
      >ATP-dependent RNA helicase A n=1 Tax=Homo sapiens RepID=DHX9_HUMAN                                   Length: 1270aa


45a   UniRef100_Q14566 1.0000
      confidence: 1. coverage: 6.2 num unique p tot indep spec share of spect subsumed entries: 1
      >DNA replication licensing factor MCM6 n=2 Tax=Homo sapiens RepID=MCM6_HUMAN                          Length: 821aa


46a   UniRef100_Q14694 UniRef100_Q14694-2 UniRef100_Q14694-3 UniRef100_UPI0001AE68C9 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.11%
      >Ubiquitin carboxyl-terminal hydrolase 10 n=1 Tax=Homo sapiens RepID=UBP10_HUMAN                      Length: 798aa
      >Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10 n=1 Tax=Homo sapiens RepID=Q14694-2
      >Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 n=1 Tax=Homo sapiens RepID=Q14694-3
      >Ubiquitin carboxyl-terminal hydrolase 10 (EC 3.1.2.15) (Ubiquitin thioesterase 10) (Ubiquitin-specific-processing protease 10) (Deubiquitinating
                  enzyme 10). n=1 Tax=Homo sapiens RepID=UPI0001AE68C9

47a   UniRef100_Q24JQ7 UniRef100_Q2M2R5 UniRef100_Q99700 UniRef100_Q99700-2 UniRef100_UPI0000E5996A 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1
      >ATXN2 protein n=1 Tax=Homo sapiens RepID=Q24JQ7_HUMAN                                                Length: 1006aa
      >ATXN2 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q2M2R5_HUMAN
      >Ataxin-2 n=2 Tax=Homo sapiens RepID=ATX2_HUMAN
      >Isoform 2 of Ataxin-2 n=1 Tax=Homo sapiens RepID=Q99700-2
      >Ataxin-2 (Spinocerebellar ataxia type 2 protein) (Trinucleotide repeat-containing gene 13 protein). n=1 Tax=Homo sapiens
                  RepID=UPI0000E5996A

48a   UniRef100_Q2NKK4 UniRef100_Q9Y6A5 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 6
      >Transforming, acidic coiled-coil containing protein 3 n=1 Tax=Homo sapiens RepID=Q2NKK4_HUMAN        Length: 838aa
```

```
      >Transforming acidic coiled-coil-containing protein 3 n=1 Tax=Homo sapiens RepID=TACC3_HUMAN


49a   UniRef100_Q6PIQ7 1.0000
      confidence: 1. coverage: 6.8 num unique p tot indep spec share of spect subsumed entries: 2
      >IGL@ protein n=1 Tax=Homo sapiens RepID=Q6PIQ7_HUMAN                                          Length: 236aa


50a   UniRef100_Q7L2E3 UniRef100_Q7L2E3-2 UniRef100_Q7L2E3-3 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
      >Putative ATP-dependent RNA helicase DHX30 n=2 Tax=Homo sapiens RepID=DHX30_HUMAN              Length: 1194aa
      >Isoform 2 of Putative ATP-dependent RNA helicase DHX30 n=1 Tax=Homo sapiens RepID=Q7L2E3-2
      >Isoform 3 of Putative ATP-dependent RNA helicase DHX30 n=1 Tax=Homo sapiens RepID=Q7L2E3-3


51a   UniRef100_Q92900 UniRef100_Q92900-2 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 2
      >Regulator of nonsense transcripts 1 n=1 Tax=Homo sapiens RepID=RENT1_HUMAN                    Length: 1129aa
      >Isoform 2 of Regulator of nonsense transcripts 1 n=1 Tax=Homo sapiens RepID=Q92900-2


52a   UniRef100_UPI0000111654 UniRef100_UPI00017BDB3D UniRef100_UPI00017BDB42 1.0000
      confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.22%
      >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


14a   UniRef100_B0V043 UniRef100_P26640 UniRef100_UPI000173A15D 0.9999
      confidence: 0. max coverage num unique p tot indep spec share of spect subsumed entries: 1
      >Valyl-tRNA synthetase n=2 Tax=Homo sapiens RepID=B0V043_HUMAN                                  Length: 1264aa
      >Valyl-tRNA synthetase n=1 Tax=Homo sapiens RepID=SYVC_HUMAN
      >UPI000173A15D related cluster n=1 Tax=Homo sapiens RepID=UPI000173A15D


21a   UniRef100_B3KXZ4 UniRef100_B7Z8Z6 UniRef100_P49736 UniRef100_UPI0001B797CF 0.9999
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.41%
      >cDNA FLJ46429 fis, clone THYMU3014372, highly similar to DNA replication licensing factor MCM2 n=1 Tax=Homo s Length: 808aa
      >cDNA FLJ53276, moderately similar to DNA replication licensing factor MCM2 n=1 Tax=Homo sapiens RepID=B7Z8Z6_HUMAN
      >DNA replication licensing factor MCM2 n=1 Tax=Homo sapiens RepID=MCM2_HUMAN
      >UPI0001B797CF related cluster n=1 Tax=Homo sapiens RepID=UPI0001B797CF


53    UniRef100_P06872 0.9967
      confidence: 1. coverage: 6.9 num unique p tot indep spec share of spectrum id's: 0.60%
      >Anionic trypsin n=2 Tax=Canis lupus familiaris RepID=TRY2_CANFA                                Length: 247aa


34c   UniRef100_P04259 0.9901
      confidence: 1. coverage: 7.6 num unique p tot indep spec share of spect subsumed entries: 4
      >Keratin, type II cytoskeletal 6B n=1 Tax=Homo sapiens RepID=K2C6B_HUMAN                        Length: 564aa


54    UniRef100_A5HIR6 0.9896
      confidence: 0. coverage: 5.4 num unique p tot indep spec share of spectrum id's: 0.12%
      >Trypsin (Fragment) n=1 Tax=Metapenaeus ensis RepID=A5HIR6_METEN                                Length: 185aa


55    UniRef100_A6NDW8 UniRef100_B3KU37 UniRef100_B4DG92 UniRef100_B4DU15 UniRef100_Q14671 UniRef100_Q14671-2
      UniRef100_Q53HH5 UniRef100_Q5T1Z3 UniRef100_Q5T1Z4 UniRef100_Q5T1Z8 0.9896
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
      >Putative uncharacterized protein PUM1 n=1 Tax=Homo sapiens RepID=A6NDW8_HUMAN                  Length: 927aa
      >cDNA FLJ39157 fis, clone OCBBF2002083, highly similar to Pumilio homolog 1 n=1 Tax=Homo sapiens RepID=B3KU37_HUMAN
      >cDNA FLJ56067, highly similar to Pumilio homolog 1 n=1 Tax=Homo sapiens RepID=B4DG92_HUMAN
      >cDNA FLJ54549, highly similar to Pumilio homolog 1 n=1 Tax=Homo sapiens RepID=B4DU15_HUMAN
      >Pumilio homolog 1 n=2 Tax=Homo sapiens RepID=PUM1_HUMAN
      >Isoform 2 of Pumilio homolog 1 n=1 Tax=Homo sapiens RepID=Q14671-2
      >Pumilio homolog 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53HH5_HUMAN
      >Pumilio homolog 1 (Drosophila) n=1 Tax=Homo sapiens RepID=Q5T1Z3_HUMAN
      >Pumilio homolog 1 (Drosophila) n=1 Tax=Homo sapiens RepID=Q5T1Z4_HUMAN
      >Pumilio homolog 1 (Drosophila) n=1 Tax=Homo sapiens RepID=Q5T1Z8_HUMAN


56    UniRef100_A8K0G3 UniRef100_A8K916 UniRef100_B4DWG4 UniRef100_B4E261 UniRef100_C9J1E7 UniRef100_P63010
      UniRef100_Q10567 UniRef100_Q10567-2 UniRef100_Q10567-3 UniRef100_Q68DI0 UniRef100_Q86X54 UniRef100_UPI0000457067
          0.9896
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
```

```
      >cDNA FLJ78733, highly similar to Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), transc Length: 951aa
      >cDNA FLJ78481, highly similar to Homo sapiens adaptor-related protein complex 2, beta 1 subunit, mRNA n=1 Tax=Homo sapiens
                 RepID=A8K916_HUMAN
      >cDNA FLJ53223, highly similar to Adapter-relatedprotein complex 2 beta-1 subunit n=1 Tax=Homo sapiens RepID=B4DWG4_HUMAN
      >cDNA FLJ55646, highly similar to Adapter-relatedprotein complex 2 beta-1 subunit n=1 Tax=Homo sapiens RepID=B4E261_HUMAN
      >Putative uncharacterized protein AP1B1 n=1 Tax=Homo sapiens RepID=C9J1E7_HUMAN
      >AP-2 complex subunit beta n=3 Tax=Euarchontoglires RepID=AP2B1_HUMAN
      >AP-1 complex subunit beta-1 n=1 Tax=Homo sapiens RepID=AP1B1_HUMAN
      >Isoform B of AP-1 complex subunit beta-1 n=1 Tax=Homo sapiens RepID=Q10567-2
      >Isoform C of AP-1 complex subunit beta-1 n=1 Tax=Homo sapiens RepID=Q10567-3
      >Putative uncharacterized protein DKFZp781K0743 n=1 Tax=Homo sapiens RepID=Q68DI0_HUMAN
      >AP1B1 protein n=1 Tax=Homo sapiens RepID=Q86X54_HUMAN
      >AP-1 complex subunit beta-1 (Adapter-related protein complex 1 beta-1 subunit) (Beta-adaptin 1) (Adaptor protein complex AP-1 beta-1
                 subunit) (Golgi adaptor HA1/AP1 adaptin beta subunit) (Clathrin assembly protein complex 1 beta large chain). n=1 Tax=Homo
                 sapiens RepID=UPI0000457067
57    UniRef100_A8K8U1 UniRef100_Q86VP6 UniRef100_Q86VP6-2 0.9896
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.25%
      >cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA n Length: 1230aa
      >Cullin-associated NEDD8-dissociated protein 1 n=3 Tax=Eutheria RepID=CAND1_HUMAN
      >Isoform 2 of Cullin-associated NEDD8-dissociated protein 1 n=1 Tax=Homo sapiens RepID=Q86VP6-2


58    UniRef100_B3KPH8 UniRef100_B3KU28 UniRef100_B3KXS5 UniRef100_B4DPX0 UniRef100_P36776 UniRef100_Q2VPA0
      UniRef100_Q8N8K8 0.9896
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
      >Lon protease homolog n=1 Tax=Homo sapiens RepID=B3KPH8_HUMAN                                  Length: 763aa
      >Lon protease homolog n=1 Tax=Homo sapiens RepID=B3KU28_HUMAN
      >Lon protease homolog n=1 Tax=Homo sapiens RepID=B3KXS5_HUMAN
      >Lon protease homolog n=1 Tax=Homo sapiens RepID=B4DPX0_HUMAN
      >Lon protease homolog, mitochondrial n=1 Tax=Homo sapiens RepID=LONM_HUMAN
      >Lon protease homolog (Fragment) n=1 Tax=Homo sapiens RepID=Q2VPA0_HUMAN
      >Lon protease homolog n=1 Tax=Homo sapiens RepID=Q8N8K8_HUMAN


59    UniRef100_B4DKW0 UniRef100_B4DTW8 UniRef100_B5A952 UniRef100_P35590 UniRef100_UPI0000470B88 0.9896
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
      >cDNA FLJ52321, highly similar to Tyrosine-protein kinase receptor Tie-1 (EC 2.7.10.1) n=1 Tax=Homo sapiens Rep Length: 783aa
      >cDNA FLJ53921, highly similar to Tyrosine-protein kinase receptor Tie-1 (EC 2.7.10.1) n=1 Tax=Homo sapiens RepID=B4DTW8_HUMAN
      >Soluble TIE1 variant 5 n=1 Tax=Homo sapiens RepID=B5A952_HUMAN
      >Tyrosine-protein kinase receptor Tie-1 n=1 Tax=Homo sapiens RepID=TIE1_HUMAN
      >Tyrosine-protein kinase receptor Tie-1 precursor (EC 2.7.10.1). n=1 Tax=Homo sapiens RepID=UPI0000470B88


60    UniRef100_B4DM67 UniRef100_B4DS32 UniRef100_B4DUC5 UniRef100_P55060 UniRef100_P55060-3 UniRef100_UPI0001AE6604
          0.9896
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.25%
      >cDNA FLJ59343, highly similar to Exportin-2 n=1 Tax=Homo sapiens RepID=B4DM67_HUMAN              Length: 599aa
      >cDNA FLJ56236, highly similar to Exportin-2 n=1 Tax=Homo sapiens RepID=B4DS32_HUMAN
      >cDNA FLJ53202, highly similar to Exportin-2 n=1 Tax=Homo sapiens RepID=B4DUC5_HUMAN
      >Exportin-2 n=1 Tax=Homo sapiens RepID=XPO2_HUMAN
      >Isoform 3 of Exportin-2 n=1 Tax=Homo sapiens RepID=P55060-3
      >UPI0001AE6604 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6604


61    UniRef100_B4DMU8 UniRef100_B4DQN9 UniRef100_B4DXZ5 UniRef100_B4DY90 UniRef100_B4E052 UniRef100_B7ZAF0
      UniRef100_B7ZAK1 UniRef100_P07437 UniRef100_Q1KSF8 UniRef100_Q5JP53 UniRef100_Q5ST81 UniRef100_Q96B85
      UniRef100_UPI0001AE713B UniRef100_UPI0001AE72AC 0.9896
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.25%
      >cDNA FLJ53063, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DMU8_HUMAN    Length: 317aa
      >cDNA FLJ50617, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DQN9_HUMAN
      >cDNA FLJ52029, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DXZ5_HUMAN
      >cDNA FLJ56903, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DY90_HUMAN
      >cDNA FLJ52378, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4E052_HUMAN
      >cDNA, FLJ79164, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B7ZAF0_HUMAN
      >cDNA, FLJ79215, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B7ZAK1_HUMAN
      >Tubulin beta chain n=12 Tax=Amniota RepID=TBB5_HUMAN
      >XTP3TPA-transactivated protein 1 n=1 Tax=Homo sapiens RepID=Q1KSF8_HUMAN
      >Tubulin beta polypeptide n=1 Tax=Homo sapiens RepID=Q5JP53_HUMAN
      >Tubulin beta polypeptide n=3 Tax=Hominidae RepID=Q5ST81_HUMAN
      >TUBB protein (Fragment) n=1 Tax=Homo sapiens RepID=Q96B85_HUMAN
      >UPI0001AE713B related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE713B
      >UPI0001AE72AC related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE72AC


62    UniRef100_B5BUJ7 UniRef100_B5M0B4 UniRef100_D3DWQ9 UniRef100_P45984 UniRef100_P45984-2 UniRef100_P45984-3
          0.9896
      confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
```

```
        >Mitogen-activated protein kinase 9 isoform JNK2 alpha2 (Fragment) n=1 Tax=Homo sapiens RepID=B5BUJ7_HUMA Length: 424aa
        >Mitogen-activated protein kinase 9 isoform JNK2 gamma n=1 Tax=Homo sapiens RepID=B5M0B4_HUMAN
        >Mitogen-activated protein kinase 9, isoform CRA_b n=2 Tax=Homo sapiens RepID=D3DWQ9_HUMAN
        >Mitogen-activated protein kinase 9 n=2 Tax=Homo sapiens RepID=MK09_HUMAN
        >Isoform Alpha-1 of Mitogen-activated protein kinase 9 n=1 Tax=Homo sapiens RepID=P45984-2
        >Isoform Beta-1 of Mitogen-activated protein kinase 9 n=1 Tax=Homo sapiens RepID=P45984-3


63      UniRef100_B7Z809 UniRef100_P11586 UniRef100_UPI000013C6FA 0.9896
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
        >cDNA FLJ56016, highly similar to C-1-tetrahydrofolate synthase, cytoplasmic n=1 Tax=Homo sapiens RepID=B7Z8 Length: 1020aa
        >Formyltetrahydrofolate synthetase n=1 Tax=Homo sapiens RepID=C1TC_HUMAN
        >C-1-tetrahydrofolate synthase, cytoplasmic n=1 Tax=Homo sapiens RepID=UPI000013C6FA


64      UniRef100_B7Z8Y3 UniRef100_D3DV75 UniRef100_D3DV76 UniRef100_P55265 UniRef100_P55265-2 UniRef100_P55265-3
        UniRef100_P55265-4 UniRef100_Q59EC0 UniRef100_UPI00003665AC UniRef100_UPI0001AE78F3 UniRef100_UPI0001AE78F4 0.9896
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
        >cDNA FLJ61696, highly similar to Double-stranded RNA-specific adenosine deaminase (EC 3.5.4.-) n=1 Tax=Homo  Length: 970aa
        >Adenosine deaminase, RNA-specific, isoform CRA_b n=1 Tax=Homo sapiens RepID=D3DV75_HUMAN
        >Adenosine deaminase, RNA-specific, isoform CRA_a n=2 Tax=Homo sapiens RepID=D3DV76_HUMAN
        >Double-stranded RNA-specific adenosine deaminase n=1 Tax=Homo sapiens RepID=DSRAD_HUMAN
        >Isoform 2 of Double-stranded RNA-specific adenosine deaminase n=1 Tax=Homo sapiens RepID=P55265-2
        >Isoform 3 of Double-stranded RNA-specific adenosine deaminase n=1 Tax=Homo sapiens RepID=P55265-3
        >Isoform 4 of Double-stranded RNA-specific adenosine deaminase n=1 Tax=Homo sapiens RepID=P55265-4
        >Adenosine deaminase, RNA-specific isoform ADAR-a variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59EC0_HUMAN
        >Double-stranded RNA-specific adenosine deaminase (EC 3.5.4.-) (DRADA) (136 kDa double-stranded RNA-binding protein) (P136) (K88DSRBP)
                    (Interferon-inducible protein 4) (IFI-4 protein). n=1 Tax=Homo sapiens RepID=UPI00003665AC
        >UPI0001AE78F3 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE78F3
        >UPI0001AE78F4 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE78F4


65      UniRef100_B7ZLC9 UniRef100_Q8TEQ6 0.9896
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
        >GEMIN5 protein n=1 Tax=Homo sapiens RepID=B7ZLC9_HUMAN                                    Length: 1507aa
        >Gem-associated protein 5 n=1 Tax=Homo sapiens RepID=GEMI5_HUMAN


66      UniRef100_D3DVA5 UniRef100_D3DVA6 UniRef100_Q5VY93 UniRef100_Q92974 0.9896
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
        >Rho/rac guanine nucleotide exchange factor (GEF) 2, isoform CRA_a n=1 Tax=Homo sapiens RepID=D3DVA5_HUM Length: 1030aa
        >Rho/rac guanine nucleotide exchange factor (GEF) 2, isoform CRA_b n=3 Tax=Homo sapiens RepID=D3DVA6_HUMAN
        >Rho/rac guanine nucleotide exchange factor (GEF) 2 n=1 Tax=Homo sapiens RepID=Q5VY93_HUMAN
        >Rho guanine nucleotide exchange factor 2 n=1 Tax=Homo sapiens RepID=ARHG2_HUMAN


67      UniRef100_Q6ZQY3 UniRef100_Q6ZQY3-3 UniRef100_UPI0001AE75C9 0.9896
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
        >Glutamate decarboxylase-like protein 1 n=1 Tax=Homo sapiens RepID=GADL1_HUMAN             Length: 521aa
        >Isoform 2 of Glutamate decarboxylase-like protein 1 n=1 Tax=Homo sapiens RepID=Q6ZQY3-3
        >glutamate decarboxylase-like 1 n=1 Tax=Homo sapiens RepID=UPI0001AE75C9


68      UniRef100_Q9NUW1 UniRef100_Q9NV23 0.9896
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
        >Augmented in rheumatoid arthritis 1 n=1 Tax=Homo sapiens RepID=Q9NUW1_HUMAN               Length: 318aa
        >S-acyl fatty acid synthase thioesterase, medium chain n=1 Tax=Homo sapiens RepID=SAST_HUMAN


69      UniRef100_Q9NZC9 UniRef100_UPI0000D49C5A 0.9896
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
        >SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1 n=1 Tax=Ho Length: 954aa
        >SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1 (EC 3.6.1.-) (Sucrose nonfermenting
                   protein 2-like 1) (HepA-related protein) (hHARP). n=1 Tax=Homo sapiens RepID=UPI0000D49C5A

70      UniRef100_UPI0000D8BAE1 UniRef100_UPI0001A2D139 0.9896
        confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
        >Novel protein similar to human alpha 2 type V collagen (COL5A2) n=1 Tax=Danio rerio RepID=UPI0000D8BAE1     Length: 1252aa
        >Novel protein similar to human alpha 2 type V collagen (COL5A2) n=1 Tax=Danio rerio RepID=UPI0001A2D139


71      UniRef100_UPI000186E341 0.9896
        confidence: 0. coverage: 1.0 num unique p tot indep spec share of spectrum id's: 0.12%
        >DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E341      Length: 821aa


72      UniRef100_A8K674 UniRef100_B2RDW1 UniRef100_P62988 UniRef100_Q3MIH3 UniRef100_Q49A90 UniRef100_Q59EM9
```

```
     UniRef100_Q5RKT7 UniRef100_Q5U5U6 UniRef100_Q5UGI3 UniRef100_Q66K58 UniRef100_Q96C32 UniRef100_Q96H31
     UniRef100_Q96MH4 UniRef100_UPI000013DC28 UniRef100_UPI0001D63C67 0.9885
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.37%
     >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


73   UniRef100_B3KXH0 UniRef100_B7Z2N4 UniRef100_B7Z766 UniRef100_B7Z909 UniRef100_Q05D91 UniRef100_Q6IN67
     UniRef100_Q9Y4L1 0.9885
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
     >cDNA FLJ45395 fis, clone BRHIP3027191, highly similar to 150 kDa oxygen-regulated protein (Orp150) n=1 Tax=H Length: 991aa
     >cDNA FLJ56074, highly similar to 150 kDa oxygen-regulated protein (Orp150) n=1 Tax=Homo sapiens RepID=B7Z2N4_HUMAN
     >cDNA FLJ54564, highly similar to 150 kDa oxygen-regulated protein (Orp150) n=1 Tax=Homo sapiens RepID=B7Z766_HUMAN
     >cDNA FLJ54708, highly similar to 150 kDa oxygen-regulated protein (Orp150) n=1 Tax=Homo sapiens RepID=B7Z909_HUMAN
     >HYOU1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q05D91_HUMAN
     >HYOU1 protein n=1 Tax=Homo sapiens RepID=Q6IN67_HUMAN
     >Hypoxia up-regulated protein 1 n=2 Tax=Homo sapiens RepID=HYOU1_HUMAN


74   UniRef100_B4DHD2 UniRef100_B7Z5C1 UniRef100_Q4W4Y1 UniRef100_Q6NUS1 UniRef100_Q8WUM4 UniRef100_UPI00004121D3
         0.9885
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
     >cDNA FLJ55458, highly similar to Programmed cell death 6-interacting protein n=1 Tax=Homo sapiens RepID=B4D Length: 683aa
     >cDNA FLJ56126, highly similar to Programmed cell death 6-interacting protein n=1 Tax=Homo sapiens RepID=B7Z5C1_HUMAN
     >Dopamine receptor interacting protein 4 n=1 Tax=Homo sapiens RepID=Q4W4Y1_HUMAN
     >PDCD6IP protein n=1 Tax=Homo sapiens RepID=Q6NUS1_HUMAN
     >Programmed cell death 6-interacting protein n=1 Tax=Homo sapiens RepID=PDC6I_HUMAN
     >programmed cell death 6-interacting protein isoform 2 n=1 Tax=Homo sapiens RepID=UPI00004121D3


75   UniRef100_B4DN49 UniRef100_B4DSB9 UniRef100_P43246 UniRef100_Q4R336 UniRef100_Q53FK0 UniRef100_Q53GS1
     UniRef100_UPI000011DDE0 UniRef100_UPI00005793AE UniRef100_UPI0001AE767E 0.9875
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.25%
     >cDNA FLJ50998, highly similar to DNA mismatch repair protein Msh2 n=1 Tax=Homo sapiens RepID=B4DN49_HUM Length: 865aa
     >cDNA FLJ51069, highly similar to DNA mismatch repair protein Msh2 n=1 Tax=Homo sapiens RepID=B4DSB9_HUMAN
     >DNA mismatch repair protein Msh2 n=3 Tax=Homo sapiens RepID=MSH2_HUMAN
     >Testis cDNA clone: QtsA-19940, similar to human mutS homolog 2, colon cancer, nonpolyposis type 1 (E.coli) (MSH2), n=1 Tax=Macaca
               fascicularis RepID=Q4R336_MACFA
     >MutS homolog 2 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53FK0_HUMAN
     >MutS homolog 2 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GS1_HUMAN
     >UPI000011DDE0 related cluster n=1 Tax=Homo sapiens RepID=UPI000011DDE0
     >UPI00005793AE related cluster n=1 Tax=Homo sapiens RepID=UPI00005793AE
     >UPI0001AE767E related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE767E


76   UniRef100_A5JHP3 UniRef100_P81605 0.9855
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
     >Dermcidin isoform 2 n=1 Tax=Homo sapiens RepID=A5JHP3_HUMAN                                       Length: 121aa
     >DCD-1 n=3 Tax=Euarchontoglires RepID=DCD_HUMAN


77   UniRef100_A8K3I2 UniRef100_Q32P42 UniRef100_Q92878 UniRef100_Q92878-2 UniRef100_UPI000066DA06 UniRef100_UPI000173A2B5
         0.9814
     confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.12%
     >cDNA FLJ75532, highly similar to Homo sapiens RAD50 homolog (S. cerevisiae) (RAD50), transcript variant 1, mRN Length: 615aa
     >RAD50 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q32P42_HUMAN
     >DNA repair protein RAD50 n=2 Tax=Homo sapiens RepID=RAD50_HUMAN
     >Isoform 2 of DNA repair protein RAD50 n=1 Tax=Homo sapiens RepID=Q92878-2
     >UPI000066DA06 related cluster n=1 Tax=Homo sapiens RepID=UPI000066DA06
     >UPI000173A2B5 related cluster n=1 Tax=Homo sapiens RepID=UPI000173A2B5
```