

# ENCODE DCC Antibody Validation Document

Date of Submission

Name:

Email:

Lab

Antibody Name:

Target:

Company/  
Source:

Catalog Number, database ID, laboratory

Lot Number

Antibody  
Description:

Target  
Description:

Species Target

Species Host

Validation Method #1

Validation Method #2

Purification  
Method

Polyclonal/  
Monoclonal

Vendor URL:

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

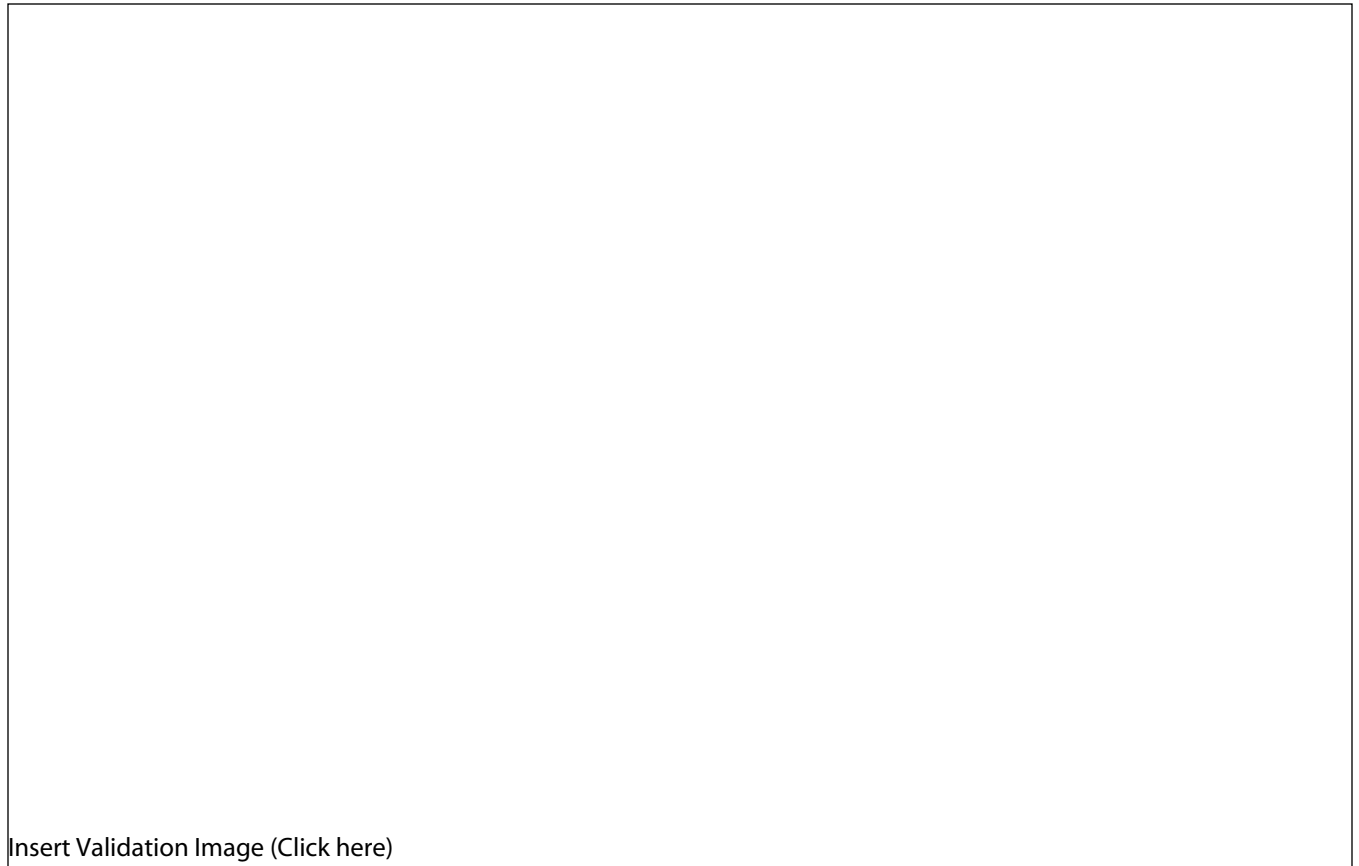
Validation #1  
Analysis



Insert Validation Image (click here)



Validation #2  
Analysis



Insert Validation Image (Click here)

35 entries (16 single hits) retrieved from  
/home/TPP/tpp/20110617\_Bowling/int-gb\_20110617\_LTQ\_Bowling\_AFT2-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: 2.34%  
>cDNA FLJ57604, highly similar to GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) n=1 Tax=Homo sapiens RepL 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=GUAH\_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: 0. coverage: 4.7 num unique p tot indep spec share of spectrum id's: 0.90%  
>Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9\_HUMAN Length: 623aa

3 UniRef100\_Q86UX7 UniRef100\_Q86UX7-2 1.0000  
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 2.16%  
>Fermitin family homolog 3 n=1 Tax=Homo sapiens RepID=URP2\_HUMAN Length: 667aa  
>Isoform 2 of Fermitin family homolog 3 n=1 Tax=Homo sapiens RepID=Q86UX7-2

4 PROTEIN GROUP: 1 1.0000

a UniRef100\_A1XP52 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Catecholamine-regulated protein 40 n=1 Tax=Homo sapiens RepID=A1XP52\_HUMAN Length: 350aa

b UniRef100\_B7Z1V7 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>cDNA FLJ51811, highly similar to Stress-70 protein, mitochondrial n=1 Tax=Homo sapiens RepID=B7Z1V7\_HUMAN Length: 437aa

c UniRef100\_B7Z4T3 0.0000  
confidence: 1.0000 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

d UniRef100\_B7Z4V2 UniRef100\_P38646 UniRef100\_Q8N1C8 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0 subsumed entries: 8  
>cDNA FLJ51907, highly similar to Stress-70 protein, mitochondrial n=2 Tax=Homininae RepID=B7Z4V2\_HUMAN Length: 665aa  
>Stress-70 protein, mitochondrial n=1 Tax=Homo sapiens RepID=GRP75\_HUMAN  
>HSPA9 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8N1C8\_HUMAN

e UniRef100\_D6RJ12 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Putative uncharacterized protein HSPA9 n=2 Tax=Homo sapiens RepID=D6RJ12\_HUMAN Length: 95aa

f UniRef100\_Q2F839 0.0000  
confidence: 0.9990 num unique p tot indep spectra: 0  
>Heat shock 70 kDa protein 9B (Fragment) n=1 Tax=Homo sapiens RepID=Q2F839\_HUMAN Length: 176aa

g UniRef100\_Q4R7F6 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Testis cDNA, clone: QtsA-15441, similar to human heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear qen Length: 455aa

h UniRef100\_UPI000186EA7C UniRef100\_UPI0001D63C17 0.0000  
confidence: 0.9990 num unique p tot indep spectra: 0  
>Heat shock 70 kDa protein cognate, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EA7C Length: 694aa  
>Stress-70 protein, mitochondrial n=1 Tax=Homo sapiens RepID=UPI0001D63C17

i UniRef100\_UPI0001D3B8BF 0.0000  
confidence: 0.2343 num unique p tot indep spectra: 0  
>UPI0001D3B8BF related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3B8BF Length: 102aa

5 PROTEIN GROUP: 2 1.0000

a UniRef100\_A4D7U3 UniRef100\_UPI0001881894 0.0000  
confidence: 1.0000 num unique tot indep spectra: 0  
>Activating transcription factor 2 splice variant ATF2-var0 n=1 Tax=Homo sapiens RepID=A4D7U3\_HUN Length: 377aa  
>UPI0001881894 related cluster n=1 Tax=Homo sapiens RepID=UPI0001881894

b UniRef100\_A4D7U4 UniRef100\_P15336 UniRef100\_Q4R5T2 0.0000  
confidence: 1.0000 num unique tot indep spectra: 0 subsumed entries: 5  
>Activating transcription factor 2 splice variant ATF2-var1 n=1 Tax=Homo sapiens RepID=A4D7U4\_HUN Length: 487aa  
>Cyclic AMP-dependent transcription factor ATF-2 n=2 Tax=Homo sapiens RepID=ATF2\_HUMAN  
>Testis cDNA, clone: QtsA-21051, similar to human activating transcription factor 2 (ATF2), n=1 Tax=Macaca fascicularis  
RepID=Q4R5T2\_MACFA

c UniRef100\_A4D7U7 0.0000  
confidence: 1.0000 num unique tot indep spectra: 0  
>Activating transcription factor 2 splice variant ATF2-var10 n=1 Tax=Homo sapiens RepID=A4D7U7\_HU Length: 289aa

d UniRef100\_A4D7U9 UniRef100\_A4D7V5 UniRef100\_B3KY57 UniRef100\_Q3B7B7 0.0000  
confidence: 1.0000 num unique tot indep spectra: 0  
>Activating transcription factor 2 splice variant ATF2-var6 n=1 Tax=Homo sapiens RepID=A4D7U9\_HUN Length: 399aa  
>Activating transcription factor 2 splice variant ATF2-var12 n=1 Tax=Homo sapiens RepID=A4D7V5\_HUMAN  
>cDNA FLJ46899 fis, clone UTERU3022588, highly similar to Cyclic AMP-dependent transcription factor ATF-2 n=1  
Tax=Homo sapiens RepID=B3KY57\_HUMAN  
>ATF2 protein n=1 Tax=Homo sapiens RepID=Q3B7B7\_HUMAN

e UniRef100\_A4D7V1 UniRef100\_Q8TAR1 UniRef100\_UPI0001881899 0.0000  
confidence: 1.0000 num unique tot indep spectra: 0  
>Activating transcription factor 2 splice variant ATF2-var11 n=2 Tax=Homo sapiens RepID=A4D7V1\_HU Length: 219aa  
>ATF2 protein n=1 Tax=Homo sapiens RepID=Q8TAR1\_HUMAN  
>UPI0001881899 related cluster n=1 Tax=Homo sapiens RepID=UPI0001881899

**f** UniRef100\_A5D6Y4 UniRef100\_Q8IVR8 0.0000  
confidence: 0.2070 num unique tot indep spectra: 0  
>ATF7 protein n=1 Tax=Homo sapiens RepID=A5D6Y4\_HUMAN Length: 117aa  
>ATF7 protein n=1 Tax=Homo sapiens RepID=Q8IVR8\_HUMAN

**g** UniRef100\_B2R8U0 UniRef100\_B2RMP1 UniRef100\_P17544 UniRef100\_P17544-2 UniRef100\_P17544-3 UniRef100\_P17544-4  
0  
confidence: 0.9971 num unique tot indep spectra: 0  
>cDNA, FLJ94063, highly similar to Homo sapiens activating transcription factor 7 (ATF7), mRNA n=1 Ta Length: 483aa  
>Activating transcription factor 7 n=1 Tax=Homo sapiens RepID=B2RMP1\_HUMAN  
>Cyclic AMP-dependent transcription factor ATF-7 n=1 Tax=Homo sapiens RepID=ATF7\_HUMAN  
>Isoform 1 of Cyclic AMP-dependent transcription factor ATF-7 n=1 Tax=Homo sapiens RepID=P17544-2  
>Isoform 2 of Cyclic AMP-dependent transcription factor ATF-7 n=1 Tax=Homo sapiens RepID=P17544-3  
>Isoform 4 of Cyclic AMP-dependent transcription factor ATF-7 n=1 Tax=Homo sapiens RepID=P17544-4

**h** UniRef100\_B4DU13 UniRef100\_B5BUH3 UniRef100\_Q02930 UniRef100\_Q02930-2 UniRef100\_Q02930-3 UniRef100\_Q96JT8  
UniRef100\_UPI0001AE707D 0.0000  
confidence: 0.1707 num unique tot indep spectra: 0  
>CAMP responsive element binding protein 5, isoform CRA\_a n=3 Tax=Homo sapiens RepID=B4DU13\_H Length: 369aa  
>cAMP responsive element binding protein 5 isoform alpha (CAMP responsive element binding protein 5, isoform CRA\_c)  
(Fragment) n=1 Tax=Homo sapiens RepID=B5BUH3\_HUMAN  
>Cyclic AMP-responsive element-binding protein 5 n=1 Tax=Homo sapiens RepID=CREB5\_HUMAN  
>Isoform 2 of Cyclic AMP-responsive element-binding protein 5 n=1 Tax=Homo sapiens RepID=Q02930-2  
>Isoform 3 of Cyclic AMP-responsive element-binding protein 5 n=2 Tax=Homo sapiens RepID=Q02930-3  
>Activating transcription factor 2 splice variant n=2 Tax=Homo sapiens RepID=Q96JT8\_HUMAN  
>UPI0001AE707D related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE707D

**i** UniRef100\_B8ZU6 0.0000  
confidence: 1.0000 num unique tot indep spectra: 0  
>Putative uncharacterized protein ATF2 n=1 Tax=Homo sapiens RepID=B8ZU6\_HUMAN Length: 389aa

**j** UniRef100\_C9JCI8 0.0000  
confidence: 0.1352 num unique tot indep spectra: 0  
>Putative uncharacterized protein ATF2 n=1 Tax=Homo sapiens RepID=C9JCI8\_HUMAN Length: 189aa

**k** UniRef100\_P15336-2 0.0000  
confidence: 1.0000 num unique tot indep spectra: 0  
>Isoform 2 of Cyclic AMP-dependent transcription factor ATF-2 n=1 Tax=Homo sapiens RepID=P15336- Length: 329aa

**6** PROTEIN GROUP: 3 1.0000

**a** 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

**b** UniRef100\_B4DGL0 UniRef100\_B4DMA2 UniRef100\_P08238 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0 subsumed entries: 3  
>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

**c** UniRef100\_B4DR68 UniRef100\_Q12931 UniRef100\_Q53FS6 UniRef100\_Q53G55 UniRef100\_Q9BV61 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=B4DR68 Length: 651aa  
>Heat shock protein 75 kDa, mitochondrial n=2 Tax=Homo sapiens RepID=TRAP1\_HUMAN  
>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

**d** UniRef100\_Q14942 UniRef100\_Q86SX1 0.0000  
confidence: 0.9995 num unique p tot indep spectra: 0  
>Heat shock protein beta (Fragment) n=1 Tax=Homo sapiens RepID=Q14942\_HUMAN Length: 130aa  
>Full-length cDNA 5-PRIME end of clone CS0DN005Y108 of Adult brain of Homo sapiens (human) (Fragment) n=1 Tax=Homo sapiens  
RepID=Q86SX1\_HUMAN

**e** UniRef100\_Q75322 UniRef100\_Q86U12 UniRef100\_Q96HX7 0.0000  
confidence: 0.9947 num unique p tot indep spectra: 0  
>Hsp89-alpha-delta-N n=2 Tax=Homo sapiens RepID=Q75322\_HUMAN Length: 539aa  
>Full-length cDNA clone CS0CAP007YF18 of Thymus of Homo sapiens (human) n=1 Tax=Homo sapiens RepID=Q86U12\_HUMAN  
>HSP90AA1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q96HX7\_HUMAN

**f** UniRef100\_P07900 UniRef100\_Q2VPJ6 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0 subsumed entries: 1  
>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

**g** UniRef100\_P14625 UniRef100\_Q59FC6 UniRef100\_Q5CAQ5 UniRef100\_Q96GW1 0.0000  
confidence: 0.0820 num unique p tot indep spectra: 0  
>Endoplasmic reticulum chaperone protein 90 kDa (Fragment) 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  
>HSP90B1 protein n=1 Tax=Homo sapiens RepID=Q96GW1\_HUMAN

**h** UniRef100\_Q14568 0.0000  
confidence: 0.9953 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

**i** UniRef100\_Q58FF7 0.0000  
confidence: 0.9836 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

**j** UniRef100\_Q58FF8 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0 subsumed entries: 1

>Putative heat shock protein HSP 90-beta 2 n=1 Tax=Homo sapiens RepID=H90B2\_HUMAN Length: 381aa

k UniRef100\_Q58FG1 0.0000  
confidence: 0.0613 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

l 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

m 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

n UniRef100\_Q5T9W4 UniRef100\_UPI000059D8E3 0.0000  
confidence: 0.1488 num unique p tot indep spectra: 0  
>Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5T9W4 Length: 170aa  
>UPI000059D8E3 related cluster n=1 Tax=Homo sapiens RepID=UPI000059D8E3

o UniRef100\_Q5T9W6 0.0000  
confidence: 0.9994 num unique p tot indep spectra: 0  
>Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5T9W6 Length: 141aa

p 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

q 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

r 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

s UniRef100\_UPI000186D735 0.0000  
confidence: 0.9846 num unique p tot indep spectra: 0  
>heat shock protein 75 kDa, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D735 Length: 689aa

7 PROTEIN GROUP: 4 1.0000

a UniRef100\_A8K9C4 UniRef100\_B4DNE0 UniRef100\_B4E2C5 UniRef100\_P68104 UniRef100\_Q05639 UniRef100\_Q504Z0  
UniRef100\_Q53G85 UniRef100\_Q53GA1 UniRef100\_Q53GE9 UniRef100\_Q53HM9 UniRef100\_Q53HQ7 UniRef100\_Q53HR1  
UniRef100\_Q53HR5 UniRef100\_Q59GP5 UniRef100\_Q5VTE0 UniRef100\_Q6IPN6 UniRef100\_Q6IPT9 UniRef100\_Q6IQ15  
UniRef100\_Q6P082 UniRef100\_Q8TBL1 UniRef100\_Q96CD8 UniRef100\_Q96RE1 UniRef100\_Q9NZS6 UniRef100\_UPI00015E0621  
UniRef100\_UPI000186CC55 0.9999  
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 0.35%  
>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  
>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  
>Elongation factor 1-alpha 2 n=5 Tax=Eutheria RepID=EF1A2\_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=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=Q53HR1\_HUMAN  
>Elongation factor 1-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q53HR5\_HUMAN  
>Eukaryotic translation elongation factor 1 alpha 2 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59GP5\_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  
>elongation factor 1-alpha, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CC55

b UniRef100\_A9X7H1 UniRef100\_B4DV42 UniRef100\_Q9H217 0.0000  
confidence: 0.1209 num unique p tot indep spectra: 0  
>Eukaryotic translation elongation factor 1 alpha (Fragment) n=1 Tax=Homo sapiens RepID=A9X7H1\_HUMAN Length: 177aa  
>Elongation factor 1-alpha n=1 Tax=Homo sapiens RepID=B4DV42\_HUMAN  
>Elongation factor 1-alpha n=1 Tax=Homo sapiens RepID=Q9H217\_HUMAN

c UniRef100\_Q14222 UniRef100\_Q16577 UniRef100\_Q53G89 UniRef100\_Q6W0R3 0.0000  
confidence: 0.1570 num unique p tot indep spectra: 0  
>EEF1A protein (Fragment) n=1 Tax=Homo sapiens RepID=Q14222\_HUMAN Length: 227aa  
>Elongation factor 1-alpha n=1 Tax=Homo sapiens RepID=Q16577\_HUMAN  
>Elongation factor 1-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q53G89\_HUMAN  
>Elongation factor-1 alpha (Fragment) n=2 Tax=Pediculus humanus RepID=Q6W0R3\_9NEOP

8 PROTEIN GROUP: 5 1.0000

a UniRef100\_B1AHC7 UniRef100\_B2RDN9 UniRef100\_P12956 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa) n=1 Tax=Homo s Length: 557aa  
>cDNA, FLJ96699, highly similar to Homo sapiens thyroid autoantigen 70kDa (Ku antigen) (G22P1), mRNA n=1 Tax=Homo sapiens  
RepID=B2RDN9\_HUMAN  
>X-ray repair cross-complementing protein 6 n=1 Tax=Homo sapiens RepID=XRCC6\_HUMAN

b UniRef100\_B1AHC8 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0

>X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa) n=1 Tax=Homo sz Length: 568aa

c UniRef100\_B1AHC9 UniRef100\_B4DE32 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa) n=1 Tax=Homo sz Length: 559aa  
>cDNA FLJ53970, highly similar to ATP-dependent DNA helicase 2 subunit 1 (EC3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DE32\_HUMAN

d UniRef100\_B4E356 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>cDNA FLJ54993, highly similar to ATP-dependent DNA helicase 2 subunit 1 (EC 3.6.1.-) n=1 Tax=Homo sapiens Ref Length: 476aa

e UniRef100\_Q4R673 UniRef100\_Q4R829 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Testis cDNA, clone: QtsA-19002, similar to human thyroid autoantigen 70kDa (Ku antigen) (G22P1), n=1 Tax=Maci Length: 609aa  
>Testis cDNA clone: QtsA-13665, similar to human thyroid autoantigen 70kDa (Ku antigen) (G22P1), n=1 Tax=Macaca fascicularis  
RepID=Q4R829\_MACFA

f UniRef100\_Q6IC76 0.0000  
confidence: 0.9984 num unique p tot indep spectra: 0  
>G22P1 protein n=1 Tax=Homo sapiens RepID=Q6IC76\_HUMAN Length: 227aa

9 PROTEIN GROUP: 6 1.0000

a UniRef100\_B4D132 UniRef100\_D6RAQ3 UniRef100\_P02545 UniRef100\_P02545-3 UniRef100\_Q516Y4 UniRef100\_Q516Y6  
UniRef100\_UPI0001AE794A 1.0000  
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1  
>cDNA FLJ56081, highly similar to Lamin-A/C n=1 Tax=Homo sapiens RepID=B4D132\_HUMAN Length: 574aa  
>Putative uncharacterized protein LMNA n=1 Tax=Homo sapiens RepID=D6RAQ3\_HUMAN  
>Lamin-A/C n=1 Tax=Homo sapiens RepID=LMNA\_HUMAN  
>Isoform ADelta10 of Lamin-A/C n=1 Tax=Homo sapiens RepID=P02545-3  
>Lamin A/C transcript variant 1 n=1 Tax=Homo sapiens RepID=Q516Y4\_HUMAN  
>Lamin A/C transcript variant 1 n=1 Tax=Homo sapiens RepID=Q516Y6\_HUMAN  
>UPI0001AE794A related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE794A

b UniRef100\_P20700 UniRef100\_UPI0000D4DAE5 0.9999  
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1  
>Lamin-B1 n=1 Tax=Homo sapiens RepID=LMNB1\_HUMAN Length: 586aa  
>Lamin-B1 n=1 Tax=Homo sapiens RepID=UPI0000D4DAE5

c UniRef100\_B4DFR3 UniRef100\_Q03252 0.0000  
confidence: 0.0981 num unique p tot indep spectra: 0  
>cDNA FLJ55771, highly similar to Lamin-A/C n=1 Tax=Homo sapiens RepID=B4DFR3\_HUMAN Length: 228aa  
>Lamin-B2 n=1 Tax=Homo sapiens RepID=LMNB2\_HUMAN

d UniRef100\_B4DZT3 0.0000  
confidence: 0.9948 num unique p tot indep spectra: 0  
>cDNA FLJ50934, highly similar to Lamin-B1 n=1 Tax=Homo sapiens RepID=B4DZT3\_HUMAN Length: 376aa

e UniRef100\_D3DVB0 UniRef100\_Q3BDU5 UniRef100\_Q516Y5 UniRef100\_Q5TC18 UniRef100\_Q5TC19 UniRef100\_Q5TCJ4  
UniRef100\_Q6UYC3 UniRef100\_Q8N519 0.0000  
confidence: 0.9920 num unique p tot indep spectra: 0  
>Lamin A/C, isoform CRA\_b n=2 Tax=Homo sapiens RepID=D3DVB0\_HUMAN Length: 572aa  
>Rhabdomyosarcoma antigen MU-RMS-40.12 n=1 Tax=Homo sapiens RepID=Q3BDU5\_HUMAN  
>Lamin A/C transcript variant 1 n=1 Tax=Homo sapiens RepID=Q516Y5\_HUMAN  
>Lamin A/C n=1 Tax=Homo sapiens RepID=Q5TC18\_HUMAN  
>Lamin A/C (Fragment) n=1 Tax=Homo sapiens RepID=Q5TC19\_HUMAN  
>Lamin A/C n=1 Tax=Homo sapiens RepID=Q5TCJ4\_HUMAN  
>Lamin A/C n=1 Tax=Homo sapiens RepID=Q6UYC3\_HUMAN  
>LMNA protein n=1 Tax=Homo sapiens RepID=Q8N519\_HUMAN

f UniRef100\_Q6DC98 0.0000  
confidence: 0.9965 num unique p tot indep spectra: 0  
>LMNB1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6DC98\_HUMAN Length: 333aa

10 PROTEIN GROUP: 7 1.0000

a UniRef100\_B4DL99 UniRef100\_P04843 UniRef100\_Q53EP4 UniRef100\_Q6IBR0 1.0000  
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.53%  
>cDNA FLJ51740, highly similar to Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit (EC Length: 581aa  
>Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 n=3 Tax=Homo sapiens RepID=RPN1\_HUMAN  
>Ribophorin I variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53EP4\_HUMAN  
>RPN1 protein n=1 Tax=Homo sapiens RepID=Q6IBR0\_HUMAN

b UniRef100\_B4DNJ5 UniRef100\_B7Z4L4 0.0000  
confidence: 0.0667 num unique p tot indep spectra: 0  
>cDNA FLJ51908, highly similar to Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit (EC Length: 378aa  
>cDNA FLJ50809, highly similar to Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit (EC 2.4.1.119) n=1  
Tax=Homo sapiens RepID=B7Z4L4\_HUMAN

11 PROTEIN GROUP: 8 1.0000

a UniRef100\_B4DRH6 UniRef100\_P40939 1.0000  
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1  
>cDNA FLJ54509, highly similar to Trifunctional enzyme subunit alpha, mitochondrial n=1 Tax=Homo sapiens RepID: Length: 717aa  
>Long chain 3-hydroxyacyl-CoA dehydrogenase n=1 Tax=Homo sapiens RepID=ECHA\_HUMAN

b UniRef100\_B4DDZ5 0.0000  
confidence: 0.9895 num unique p tot indep spectra: 0  
>cDNA FLJ53969, highly similar to Trifunctional enzyme subunit alpha, mitochondrial n=2 Tax=Homo sapiens RepID: Length: 573aa

c UniRef100\_B4DYP2 UniRef100\_Q53TA2 0.0000  
confidence: 0.1144 num unique p tot indep spectra: 0  
>cDNA FLJ52806, highly similar to Trifunctional enzyme subunit alpha, mitochondrial n=1 Tax=Homo sapiens RepID: Length: 260aa  
>Putative uncharacterized protein HADHA (Fragment) n=1 Tax=Homo sapiens RepID=Q53TA2\_HUMAN

12 PROTEIN GROUP: 9 1.0000

a UniRef100\_C5IWW5 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=C51WV5\_PIG Length: 246aa  
>Trypsin n=1 Tax=Sus scrofa RepID=TRYP\_PIG

b UniRef100\_P06871 UniRef100\_UPI00004A5B07 UniRef100\_UPI00005A2FD6 UniRef100\_UPI00005A2FD7 0.9711  
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 1  
>Cationic trypsin n=1 Tax=Canis lupus familiaris RepID=TRY1\_CANFA Length: 246aa  
>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

c UniRef100\_A1A508 UniRef100\_A6XMV8 UniRef100\_A6XMV9 UniRef100\_ABCE1 UniRef100\_ABCE3 UniRef100\_B1AN99  
UniRef100\_P07477 UniRef100\_P07478 UniRef100\_P35030 UniRef100\_P35030-2 UniRef100\_P35030-3 UniRef100\_Q3SY19  
UniRef100\_Q3SY20 UniRef100\_Q45K10 UniRef100\_Q53ZK7 UniRef100\_Q53ZK8 UniRef100\_Q53ZK9 UniRef100\_Q61S14  
UniRef100\_Q6PK75 UniRef100\_Q7Z5F3 UniRef100\_Q7Z5F4 UniRef100\_Q86W17 UniRef100\_Q86W20 UniRef100\_Q8N2U3  
UniRef100\_Q8NHM4 UniRef100\_UPI000021129C UniRef100\_UPI0000D9A9C8 UniRef100\_UPI0000E21E68 UniRef100\_UPI0001795EE3  
UniRef100\_UPI0001AE6E33  
UniRef100\_UPI0001AE7177 UniRef100\_UPI0001AE7178 UniRef100\_UPI0001AE7179 UniRef100\_UPI0001B79292  
UniRef100\_UPI0001B79293 0.0000  
confidence: 0.0010 num unique p tot indep spectra: 0 Length: 247aa  
>PRSS3 protein n=1 Tax=Homo sapiens RepID=A1A508\_HUMAN  
>Protease serine 2 preproprotein n=1 Tax=Homo sapiens RepID=A6XMV8\_HUMAN  
>Protease serine 2 preproprotein n=1 Tax=Homo sapiens RepID=A6XMV9\_HUMAN  
>Protease, serine, 3 (Mesotrypsin), isoform CRA\_d n=1 Tax=Homo sapiens RepID=ABCE1\_HUMAN  
>Trypsinogen 5 n=1 Tax=Homo sapiens RepID=ABCE3\_HUMAN  
>Protease, serine, 3 (Fragment) n=1 Tax=Homo sapiens RepID=B1AN99\_HUMAN  
>Alpha-trypsin chain 2 n=1 Tax=Homo sapiens RepID=TRY1\_HUMAN  
>Trypsin-2 n=2 Tax=Homo sapiens RepID=TRY2\_HUMAN  
>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  
>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=Q45K10\_HUMAN  
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q53ZK7\_HUMAN  
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q53ZK8\_HUMAN  
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q53ZK9\_HUMAN  
>Mesotrypsinogen n=1 Tax=Homo sapiens RepID=Q61S14\_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 4 isoform B n=1 Tax=Homo sapiens RepID=Q7Z5F4\_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  
>PRSS3 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8N2U3\_HUMAN  
>Putative trypsin-6 n=1 Tax=Homo sapiens RepID=TRY6\_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: protease, serine, 2 (trypsin 2) isoform 1 n=1 Tax=Macaca mulatta RepID=UPI0000D9A9C8  
>PREDICTED: similar to trypsinogen IV b-form n=1 Tax=Pan troglodytes RepID=UPI0000E21E68  
>PREDICTED: similar to anionic trypsinogen n=1 Tax=Equus caballus RepID=UPI0001795EE3  
>UPI0001AE6E33 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6E33  
>UPI0001AE7177 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7177  
>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

d UniRef100\_A4UWM7 UniRef100\_B9WPP8 UniRef100\_C1KRJ0 UniRef100\_O42158 UniRef100\_O42159 UniRef100\_O42160  
UniRef100\_O42608 UniRef100\_Q7T1R8 UniRef100\_UPI0000D92B0D UniRef100\_UPI0000F2E411 0.0000  
confidence: 0.0296 num unique p tot indep spectra: 0 Length: 242aa  
>Trypsinogen n=1 Tax=Oryzias latipes RepID=A4UWM7\_ORYLA  
>Trypsin (Fragment) n=1 Tax=Thunnus thynnus RepID=B9WPP8\_THUTH  
>Trypsin (Fragment) n=1 Tax=Petenia splendida RepID=C1KRJ0\_CICCH  
>Trypsinogen a2 n=1 Tax=Petromyzon marinus RepID=O42158\_PETMA  
>Trypsinogen B1 (Fragment) n=1 Tax=Petromyzon marinus RepID=O42159\_PETMA  
>Trypsinogen b2 (Fragment) n=1 Tax=Petromyzon marinus RepID=O42160\_PETMA  
>Trypsinogen A1 n=1 Tax=Petromyzon marinus RepID=O42608\_PETMA  
>Trypsinogen n=1 Tax=Pangasianodon hypophthalmus RepID=Q7T1R8\_9TELE  
>PREDICTED: similar to Cationic trypsin-3 precursor (Cationic trypsin III) (Pretrypsinogen III) n=1 Tax=Monodelphis domestica  
RepID=UPI0000D92B0D  
>PREDICTED: similar to Cationic trypsin-3 precursor (Cationic trypsin III) (Pretrypsinogen III) n=1 Tax=Monodelphis domestica  
RepID=UPI0000F2E411

e UniRef100\_C6L245 0.0000  
confidence: 0.0002 num unique p tot indep spectra: 0 Length: 247aa  
>Putative trypsinogen n=1 Tax=Sus scrofa RepID=C6L245\_PIG

f UniRef100\_P06872 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0 Length: 247aa  
>Anionic trypsin n=2 Tax=Canis lupus familiaris RepID=TRY2\_CANFA

g UniRef100\_Q7TT42 UniRef100\_UPI00001F381C 0.0000  
confidence: 0.0022 num unique p tot indep spectra: 0 Length: 246aa  
>Trypsinogen 5 n=1 Tax=Mus musculus RepID=Q7TT42\_MOUSE  
>trypsinogen 4 n=1 Tax=Mus musculus RepID=UPI00001F381C

h UniRef100\_UPI00005A2FD5 0.0000  
confidence: 0.2363 num unique p tot indep spectra: 0 Length: 138aa  
>PREDICTED: similar to trypsinogen 7 isoform 4 n=1 Tax=Canis lupus familiaris RepID=UPI00005A2FD5

13 PROTEIN GROUP: 10 1.0000

a UniRef100\_P02769 UniRef100\_UPI000179EC85 1.0000  
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 5 Length: 607aa  
>Serum albumin n=1 Tax=Bos taurus RepID=ALBU\_BOVIN  
>Serum albumin precursor (Allergen Bos d 6) (BSA), n=1 Tax=Bos taurus RepID=UPI000179EC85

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 Length: 627aa  
>Putative uncharacterized protein ALB n=1 Tax=Homo sapiens RepID=A6NBZ8\_HUMAN  
>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\_Q8IU7 UniRef100\_UPI000045722A 0.0000  
confidence: 0.9951 num unique p tot indep spectra: 0  
>ALB protein n=1 Tax=Homo sapiens RepID=Q8IU7\_HUMAN Length: 396aa  
>Serum albumin precursor. n=1 Tax=Homo sapiens RepID=UPI000045722A

f UniRef100\_UPI0001610EBC 0.0000  
confidence: 0.9986 num unique p tot indep spectra: 0  
>UPI0001610EBC related cluster n=1 Tax=Homo sapiens RepID=UPI0001610EBC Length: 197aa

14 PROTEIN GROUP: 11 1.0000

a UniRef100\_P04264 1.0000  
confidence: 1. coverage: 18.1 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

b UniRef100\_P35908 1.0000  
confidence: 1. coverage: 8.6 num unique p tot indep spec share of spectrum id's: 1.61%  
>Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E\_HUMAN Length: 639aa

c 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\_UPI00009FD95 UniRef100\_UPI0001AE6B0A UniRef100\_UPI0001AE6B0B 0.0000  
confidence: 0.0538 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=UPI00009FD95  
>UPI0001AE6B0A related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6B0A  
>UPI0001AE6B0B related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6B0B

d UniRef100\_P04259 0.0000  
confidence: 0.9899 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

e UniRef100\_Q0IIN1 UniRef100\_UPI00001D797A 0.0000  
confidence: 0.0436 num unique p tot indep spectra: 0  
>Keratin 77 n=1 Tax=Homo sapiens RepID=Q0IIN1\_HUMAN Length: 578aa  
>keratin, type II cytoskeletal 1b n=1 Tax=Homo sapiens RepID=UPI00001D797A

15 PROTEIN GROUP: 12 1.0000

a UniRef100\_P08107 1.0000  
confidence: 1. coverage: 37.1 num unique p tot indep spec share of spect subsumed entries: 17  
>Heat shock 70 kDa protein 1A/1B n=3 Tax=Hominidae RepID=HSP71\_HUMAN Length: 641aa

b UniRef100\_Q53GZ6 1.0000  
confidence: 1. coverage: 41.1 num unique p tot indep spec share of spectrum id's: 8.60%  
>Heat shock 70kDa protein 8 isoform 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GZ6\_HUMAN Length: 646aa

c UniRef100\_P11021 1.0000  
confidence: 1. coverage: 16.1 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

d UniRef100\_UPI000186CBE0 1.0000  
confidence: 1. coverage: 21.1 num unique p tot indep spec share of spectrum id's: 2.61%  
>Heat shock 70 kDa protein cognate, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CBE0 Length: 660aa

e UniRef100\_UPI000186DOC5 0.8701  
confidence: 1. coverage: 6.2 num unique p tot indep spec share of spectrum id's: 0.48%  
>Heat shock protein 70 A2, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186DOC5 Length: 661aa

f UniRef100\_UPI000186E8AE 0.5220  
confidence: 0. coverage: 3.1 num unique p tot indep spec share of spectrum id's: 0.19%  
>Heat shock cognate 71 kDa protein, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E8AE Length: 635aa

g UniRef100\_A4D110 0.0000  
confidence: 0.1898 num unique p tot indep spectra: 0  
>Putative uncharacterized protein n=1 Tax=Homo sapiens RepID=A4D110\_HUMAN Length: 127aa

h UniRef100\_A4D111 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Similar to Chain , Heat-Shock Coanate 70kd Protein (44kd Atbase N-Terminal) (E.C.3.6.1.3) Mutant With Asp 206 R Length: 231aa

i 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

j 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=I 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

k UniRef100\_B2RCQ9 UniRef100\_B4DI54 UniRef100\_P34931 UniRef100\_Q53FA3 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

l 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

m UniRef100\_B3KTV0 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>cDNA FLJ38781 fis, clone LIVER200216, highly similar to HEAT SHOCK COGNATE 71 kDa PROTEIN n=1 Tax=Hom Length: 621aa

n 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

o 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

p 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

q 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

r UniRef100\_B4DI39 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

s 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

t UniRef100\_B4DNV4 0.0000  
confidence: 1.0000 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

u UniRef100\_B4DNX1 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

v 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

w 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

x UniRef100\_B4DWK5 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>cDNA FLJ54392, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4DWK5\_HUMAN Length: 623aa

y 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

z 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

aa 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

ab 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

ac 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

ad UniRef100\_C9IYE6 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

ae UniRef100\_C9JCM4 UniRef100\_UPI0001AE71DE 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Putative uncharacterized protein ENSP00000396508 n=1 Tax=Homo sapiens RepID=C9JCM4\_HUMAN Length: 232aa  
>UPI0001AE71DE related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE71DE

af UniRef100\_P11142 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0 subsumed entries: 11  
>Heat shock cognate 71 kDa protein n=8 Tax=Eutheria RepID=HSP7C\_HUMAN Length: 646aa

ag UniRef100\_P48741 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Putative heat shock 70 kDa protein 7 n=1 Tax=Homo sapiens RepID=HSP77\_HUMAN Length: 367aa

ah 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

ai UniRef100\_Q4R8Y3 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Testis cDNA clone: OtsA-11142, similar to human heat shock 70kDa protein 2 (HSPA2), n=1 Tax=Macaca fascicular Length: 302aa

aj 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

ak UniRef100\_Q59EJ3 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Heat shock 70kDa protein 1A variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59EJ3\_HUMAN Length: 709aa

al 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

am UniRef100\_Q9NWW3 UniRef100\_Q9N287 0.0000  
confidence: 0.9991 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=Q9N287\_HUMAN

an UniRef100\_Q9UQC1 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Heat shock protein 72 (Fragment) n=1 Tax=Homo sapiens RepID=Q9UQC1\_HUMAN Length: 151aa

ao UniRef100\_UPI000186D9DF 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Heat shock protein, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D9DF Length: 642aa

ap 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

aq 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

ar UniRef100\_UPI0001AE7148 UniRef100\_UPI0001AE71DD UniRef100\_UPI0001AE71EA 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>UPI0001AE7148 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7148 Length: 583aa  
>UPI0001AE71DD related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE71DD  
>UPI0001AE71EA related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE71EA

as 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

at UniRef100\_UPI0001AE714A 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>UPI0001AE714A related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE714A Length: 563aa

16 PROTEIN GROUP: 13 1.0000

a UniRef100\_P10398 UniRef100\_Q96IIS 1.0000  
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 3  
>Serine/threonine-protein kinase A-Raf n=1 Tax=Homo sapiens RepID=ARAF\_HUMAN Length: 606aa  
>ARAF protein n=1 Tax=Homo sapiens RepID=Q96IIS\_HUMAN

b UniRef100\_B4DMG5 UniRef100\_Q59HC8 0.0000  
confidence: 0.1334 num unique p tot indep spectra: 0  
>cDNA FLJ59256, highly similar to A-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.11.1) n=1 Tax=Ho Length: 188aa  
>V-raf murine sarcoma 3611 viral oncogene homolog variant (Fragment) n=2 Tax=Homo sapiens RepID=Q59HC8\_HUMAN

c UniRef100\_B4DV85 0.0000

confidence: 1.0000 num unique p tot indep spectra: 0  
>cDNA FLJ53211, highly similar to A-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.11.1) n=1 Tax=Ho Length: 472aa

d UniRef100\_B4E0X2 UniRef100\_B4E1N6 UniRef100\_B6HY61 UniRef100\_B6HY62 UniRef100\_B6HY63 UniRef100\_B6HY64  
UniRef100\_B6HY65 UniRef100\_B6HY66 UniRef100\_C7TPG7 UniRef100\_P04049 UniRef100\_P04049-2 UniRef100\_P15056  
UniRef100\_Q5IBP5 UniRef100\_UPI000186EA42 UniRef100\_UPI0001B7927F UniRef100\_UPI0001B79280 0.0000  
confidence: 0.2335 num unique p tot indep spectra: 0  
>cDNA FLJ57286, highly similar to RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.11.1) n=1 Tax=Hom Length: 567aa  
>cDNA FLJ50355, highly similar to RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.11.1) n=1 Tax=Homo sapiens  
RepID=B4E1N6\_HUMAN  
>L-protein KIAA1549:BRAF 16\_9 n=1 Tax=Homo sapiens RepID=B6HY61\_HUMAN  
>L-protein KIAA1549:BRAF 16\_11 n=1 Tax=Homo sapiens RepID=B6HY62\_HUMAN  
>L-protein KIAA1549:BRAF 15\_9 n=1 Tax=Homo sapiens RepID=B6HY63\_HUMAN  
>S-protein KIAA1549:BRAF 16\_9 n=1 Tax=Homo sapiens RepID=B6HY64\_HUMAN  
>S-protein KIAA1549:BRAF 16\_11 n=1 Tax=Homo sapiens RepID=B6HY65\_HUMAN  
>S-protein KIAA1549:BRAF 15\_9 n=1 Tax=Homo sapiens RepID=B6HY66\_HUMAN  
>SRGAP3:RAF1 fusion protein n=1 Tax=Homo sapiens RepID=C7TPG7\_HUMAN  
>RAF proto-oncogene serine/threonine-protein kinase n=2 Tax=Hominidae RepID=RAF1\_HUMAN  
>Isoform 2 of RAF proto-oncogene serine/threonine-protein kinase n=1 Tax=Homo sapiens RepID=P04049-2  
>Serine/threonine-protein kinase B-raf n=2 Tax=Homininae RepID=BRAF\_HUMAN  
>AKAP9-BRAF fusion protein n=1 Tax=Homo sapiens RepID=Q5IBP5\_HUMAN  
>cAMP-dependent protein kinase catalytic subunit, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EA42  
>UPI0001B7927F related cluster n=1 Tax=Homo sapiens RepID=UPI0001B7927F  
>UPI0001B79280 related cluster n=1 Tax=Homo sapiens RepID=UPI0001B79280

17 PROTEIN GROUP: 14 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\_A1A4E9 UniRef100\_A8K2H9 UniRef100\_C9JA77 UniRef100\_P13646 UniRef100\_P13646-2 UniRef100\_P13646-3  
UniRef100\_Q2M215 UniRef100\_UPI0000E4FB59 UniRef100\_UPI0000E4FB5A 0.0000  
confidence: 0.0723 num unique p tot indep spectra: 0  
>Keratin 13 n=1 Tax=Homo sapiens RepID=A1A4E9\_HUMAN Length: 458aa  
>cDNA FLJ78503, highly similar to Homo sapiens keratin 13 (KRT13), transcript variant 1, mRNA n=1 Tax=Homo sapiens RepID=A8K2H9\_HUMAN  
>Putative uncharacterized protein KRT13 n=1 Tax=Homo sapiens RepID=C9JA77\_HUMAN  
>Keratin, type I cytoskeletal 13 n=1 Tax=Homo sapiens RepID=K1C13\_HUMAN  
>Isoform 2 of Keratin, type I cytoskeletal 13 n=1 Tax=Homo sapiens RepID=P13646-2  
>Isoform 3 of Keratin, type I cytoskeletal 13 n=1 Tax=Homo sapiens RepID=P13646-3  
>Keratin, type I cytoskeletal 24 n=1 Tax=Homo sapiens RepID=K1C24\_HUMAN  
>keratin, type I cytoskeletal 13 isoform b n=1 Tax=Homo sapiens RepID=UPI0000E4FB59  
>keratin, type I cytoskeletal 13 isoform a n=1 Tax=Homo sapiens RepID=UPI0000E4FB5A

c UniRef100\_Q7Z3Y7 UniRef100\_Q7Z3Y8 UniRef100\_Q7Z3Z0 0.0000  
confidence: 0.0568 num unique p tot indep spectra: 0  
>Keratin, type I cytoskeletal 28 n=1 Tax=Homo sapiens RepID=K1C28\_HUMAN Length: 464aa  
>Keratin, type I cytoskeletal 27 n=1 Tax=Homo sapiens RepID=K1C27\_HUMAN  
>Keratin, type I cytoskeletal 25 n=1 Tax=Homo sapiens RepID=K1C25\_HUMAN

18 PROTEIN GROUP: 15 1.0000

a UniRef100\_P52272 UniRef100\_P52272-2 UniRef100\_Q59ES8 UniRef100\_Q7KYM9 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  
>Heterogeneous nuclear ribonucleoprotein M isoform a variant (Fragment) n=2 Tax=Homininae RepID=Q59ES8\_HUMAN  
>ORF protein n=3 Tax=Homininae RepID=Q7KYM9\_HUMAN

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=B4DEG4 Length: 366aa

c UniRef100\_Q6P2D7 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>HNRPM protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6P2D7\_HUMAN Length: 285aa

d UniRef100\_Q8TCM5 0.0000  
confidence: 0.3948 num unique p tot indep spectra: 0  
>Putative uncharacterized protein DKFZp547H118 (Fragment) n=1 Tax=Homo sapiens RepID=Q8TCM5\_HUMAN Length: 50aa

19 PROTEIN GROUP: 16 1.0000

a UniRef100\_P54136 1.0000  
confidence: 1. coverage: 5.8 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: 0.9935 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: 0.0563 num unique p tot indep spectra: 0  
>Brain cDNA, clone: OflA-12413, similar to human arginyl-tRNA synthetase (RARS), n=1 Tax=Macaca fascicularis Re Length: 454aa

d UniRef100\_UPI000186D598 0.0000  
confidence: 0.0439 num unique p tot indep spectra: 0  
>Arginyl-tRNA synthetase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D598 Length: 575aa

20 PROTEIN GROUP: 17 1.0000

a UniRef100\_Q53GR7 UniRef100\_Q546F9 UniRef100\_Q9UJ50 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\_B7Z2E2 UniRef100\_Q75746 UniRef100\_UPI0001AE7767 0.0000  
confidence: 0.9896 num unique p tot indep spectra: 0  
>cDNA FLJ12766 fis, clone NT2RP2001520, highly similar to Calcium-binding mitochondrial carrier protein Aralar1 n=1 Length: 678aa  
>cDNA FLJ33752 fis, clone BRCAN2000364, highly similar to Calcium-binding mitochondrial carrier protein Aralar1 n=1 Tax=Homo sapiens  
RepID=B3KR64\_HUMAN  
>cDNA FLJ54671, highly similar to Calcium-binding mitochondrial carrier protein Aralar2 n=1 Tax=Homo sapiens RepID=B7Z2E2\_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\_Q75KX8 0.0000  
confidence: 0.0897 num unique p tot indep spectra: 0  
>Putative uncharacterized protein SLC25A13 (Fragment) n=1 Tax=Homo sapiens RepID=Q75KX8\_HUMAN Length: 288aa

d UniRef100\_UPI000186E1DC 0.0000  
confidence: 0.0394 num unique p tot indep spectra: 0  
>calcium-binding mitochondrial carrier Aralar1, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E1I Length: 630aa

21 PROTEIN GROUP: 18 1.0000

a UniRef100\_Q59F66 UniRef100\_Q92841 UniRef100\_Q92841-3 UniRef100\_Q92841-4 UniRef100\_UPI00003670EA UniRef100\_UPI0001533DB4  
UniRef100\_UPI0001AE634C 1.0000  
confidence: 1. max coverage num unique p tot indep spec share of spect subsumed entries: 7  
>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

b UniRef100\_B4DLW8 UniRef100\_B4DN41 UniRef100\_B5BUE6 UniRef100\_P17844 UniRef100\_UPI0001AE6729 1.0000  
confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 3.49%  
>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  
>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

c UniRef100\_B1AHM1 UniRef100\_C9J5E1 UniRef100\_C9JMU5 UniRef100\_Q92841-2 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  
>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  
>UPI0001B79048 related cluster n=1 Tax=Homo sapiens RepID=UPI0001B79048

d UniRef100\_B1AHM2 0.0000  
confidence: 0.9991 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

e UniRef100\_B3KSF4 UniRef100\_D6RCM4 UniRef100\_Q9NQI0 UniRef100\_Q9NQI0-2 UniRef100\_UPI0000E0956E UniRef100\_UPI0001BB0BF9  
0  
confidence: 0.9912 num unique p tot indep spectra: 0  
>cDNA FLJ36120 fis, clone TEST12022738, 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

f UniRef100\_B4DK29 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>cDNA FLJ59914, highly similar to ATP-dependent RNA helicase DDX3Y (EC 3.6.1.-) n=2 Tax=Homo sapiens RepID= Length: 291aa

g 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

h UniRef100\_B4DNG2 UniRef100\_Q4R6G0 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  
>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

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\_B4DZQ7 UniRef100\_UPI0001AE634E 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>cDNA FLJ58652, highly similar to Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) n=1 Tax=Homo sapien Length: 420aa  
>UPI0001AE634E related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE634E

k 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

l 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

m UniRef100\_B4E3C4 0.0000  
confidence: 0.0797 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

n 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

o UniRef100\_C1IK54 0.0000  
confidence: 0.0486 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

p UniRef100\_C9J081 UniRef100\_UPI0001D3B259 0.0000  
confidence: 0.1032 num unique p tot indep spectra: 0  
>Putative uncharacterized protein DDX3Y n=1 Tax=Homo sapiens RepID=C9J081\_HUMAN Length: 250aa  
>UPI0001D3B259 related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3B259

q UniRef100\_Q4R4H4 0.0000  
confidence: 1.0000 num unique p tot indep spectra: 0  
>Brain cDNA, clone: OtrA-14110, similar to human DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 (DDX17),transcript \ Length: 304aa

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  
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\_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

u UniRef100\_Q9UQL5 UniRef100\_UPI0000EE5B10 0.0000  
confidence: 0.1408 num unique p tot indep spectra: 0  
>DEAD-box protein p72 n=1 Tax=Homo sapiens RepID=Q9UQL5\_HUMAN Length: 183aa  
>probable ATP-dependent RNA helicase DDX17 isoform 4 n=1 Tax=Homo sapiens RepID=UPI0000EE5B10

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\_UPI000186D3DC 0.0000  
confidence: 0.0030 num unique p tot indep spectra: 0  
>DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D3DC Length: 1014aa

x 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

y 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

z UniRef100\_UPI000186EE4F 0.0000  
confidence: 0.7815 num unique p tot indep spectra: 0  
>pre-mRNA-splicing ATP-dependent RNA helicase prp28, putative n=1 Tax=Pediculus humanus corporis RepID=UPI0 Length: 788aa

aa UniRef100\_UPI000186EE68 UniRef100\_UPI000186F2DC 0.0000  
confidence: 0.9999 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=UPI000186F2DC

ab UniRef100\_UPI000186EE69 0.0000  
confidence: 0.8825 num unique p tot indep spectra: 0  
>DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EE69 Length: 610aa

ac UniRef100\_UPI000186EEE2 0.0000  
confidence: 0.8767 num unique p tot indep spectra: 0  
>DEAD box ATP-dependent RNA helicase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EEE2 Length: 630aa

22 PROTEIN GROUP: 19 1.0000

a UniRef100\_Q96PK6 1.0000  
confidence: 1. coverage: 13. 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\_B8Z74 UniRef100\_D6RAB9 UniRef100\_D6RGD8 UniRef100\_Q2PYN1 UniRef100\_Q96PK6-2  
UniRef100\_UPI0001881AEF UniRef100\_UPI0001881AF0 0.0000  
confidence: 0.2071 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=B8Z74\_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: 0.1206 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  
>RNA binding motif protein 14 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59GV2\_HUMAN Length: 552aa

23 PROTEIN GROUP: 20 1.0000

a UniRef100\_Q9NZI8 1.0000  
confidence: 1. coverage: 11.1 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: 9.0 num unique p tot indep spec share of spect subsumed entries: 3  
>Insulin-like growth factor 2 mRNA-binding protein 3 n=1 Tax=Homo sapiens RepID=IF2B3\_HUMAN Length: 579aa

c UniRef100\_A8K9C1 UniRef100\_D2IYL2 UniRef100\_Q0EFA5 UniRef100\_Q15517 UniRef100\_Q2L6G8 UniRef100\_UPI0000530311  
0  
confidence: 0.0163 num unique p tot indep spectra: 0  
>cDNA FLJ78714, highly similar to Homo sapiens corneodesmosin, mRNA n=1 Tax=Homo sapiens RepID=A8K9C1\_H Length: 528aa  
>Corneodesmosin n=1 Tax=Homo sapiens RepID=D2IYL2\_HUMAN  
>S protein n=1 Tax=Homo sapiens RepID=Q0EFA5\_HUMAN  
>Corneodesmosin n=1 Tax=Homo sapiens RepID=CDSN\_HUMAN  
>Corneodesmosin n=1 Tax=Homo sapiens RepID=Q2L6G8\_HUMAN  
>corneodesmosin precursor n=1 Tax=Homo sapiens RepID=UPI0000530311

d UniRef100\_B4DKT5 UniRef100\_C9JLA6 UniRef100\_Q9Y6M1 UniRef100\_Q9Y6M1-1 UniRef100\_Q9Y6M1-3 UniRef100\_Q9Y6M1-4  
UniRef100\_Q9Y6M1-5 0.0000  
confidence: 0.0859 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 RepID Length: 300aa  
>Putative uncharacterized protein IGF2BP2 n=1 Tax=Homo sapiens RepID=C9JLA6\_HUMAN  
>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

e 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

f 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

g UniRef100\_O00425-2 0.0000  
confidence: 0.9989 num unique p tot indep spectra: 0  
>Isoform 2 of Insulin-like growth factor 2 mRNA-binding protein 3 n=1 Tax=Homo sapiens RepID=O00425-2 Length: 198aa

h UniRef100\_UPI0001881463 0.0000  
confidence: 0.2746 num unique p tot indep spectra: 0  
>UPI0001881463 related cluster n=1 Tax=Homo sapiens RepID=UPI0001881463 Length: 81aa

i 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

24 UniRef100\_A6NKB8 UniRef100\_Q7RU04 UniRef100\_Q9H4A4 0.9905  
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.54%  
>Putative uncharacterized protein RNPEP n=1 Tax=Homo sapiens RepID=A6NKB8\_HUMAN Length: 611aa  
>Aminopeptidase B n=1 Tax=Homo sapiens RepID=Q7RU04\_HUMAN  
>Aminopeptidase B n=1 Tax=Homo sapiens RepID=AMPB\_HUMAN

25 UniRef100\_A6NMX6 UniRef100\_A8K4H1 UniRef100\_B4DR70 UniRef100\_B4E312 UniRef100\_P35637 UniRef100\_P35637-2  
UniRef100\_Q13344 UniRef100\_Q59H57 UniRef100\_Q5PQK2 UniRef100\_Q70T18 UniRef100\_Q8CFQ9 UniRef100\_Q8TBR3  
UniRef100\_Q92804 UniRef100\_Q92804-2 UniRef100\_UPI000040A0A0 UniRef100\_UPI00015558FA UniRef100\_UPI0001AE6817 0.9905  
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.54%  
>Putative uncharacterized protein FUS n=1 Tax=Homo sapiens RepID=A6NMX6\_HUMAN Length: 151aa  
>cDNA FLJ78268, highly similar to Homo sapiens fusion (involved in t(12;16) in malignant liposarcoma), transcript variant 1, mRNA n=1  
Tax=Homo sapiens RepID=A8K4H1\_HUMAN  
>cDNA FLJ58049, highly similar to RNA-binding protein FUS n=1 Tax=Homo sapiens RepID=B4DR70\_HUMAN  
>cDNA FLJ53422, highly similar to TATA-binding protein-associated factor 2N n=1 Tax=Homo sapiens RepID=B4E312\_HUMAN  
>RNA-binding protein FUS n=2 Tax=Homo sapiens RepID=FUS\_HUMAN  
>Isoform Short of RNA-binding protein FUS n=1 Tax=Homo sapiens RepID=P35637-2  
>Fus-like protein (Fragment) n=1 Tax=Homo sapiens RepID=Q13344\_HUMAN  
>Fusion (Involved in t(12;16) in malignant liposarcoma) isoform a variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59H57\_HUMAN  
>Fusion, derived from t(12;16) malignant liposarcoma (Human) n=1 Tax=Rattus norvegicus RepID=Q5PQK2\_RAT  
>BBF2H7/FUS protein (Fragment) n=1 Tax=Homo sapiens RepID=Q70T18\_HUMAN  
>Fusion, derived from t(12;16) malignant liposarcoma (Human) n=1 Tax=Mus musculus RepID=Q8CFQ9\_MOUSE  
>Fusion (Involved in t(12;16) in malignant liposarcoma) n=1 Tax=Homo sapiens RepID=Q8TBR3\_HUMAN  
>TATA-binding protein-associated factor 2N n=2 Tax=Homo sapiens RepID=RBP56\_HUMAN  
>Isoform Short of TATA-binding protein-associated factor 2N n=1 Tax=Homo sapiens RepID=Q92804-2  
>fused in sarcoma isoform 3 n=1 Tax=Homo sapiens RepID=UPI000040A0A0  
>PREDICTED: similar to Fusion, derived from t(12;16) malignant liposarcoma (human), partial n=1 Tax=Ornithorhynchus anatinus  
RepID=UPI00015558FA  
>UPI0001AE6817 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6817

26 UniRef100\_A8K5U9 UniRef100\_A8MW24 UniRef100\_A8MX97 UniRef100\_B5BU72 UniRef100\_C9JDZ4 UniRef100\_Q13492  
UniRef100\_Q13492-2 UniRef100\_Q13492-3 UniRef100\_Q4LE54 0.9905  
confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.18%  
>cDNA FLJ75056, highly similar to Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), m Length: 652aa  
>Putative uncharacterized protein PICALM n=1 Tax=Homo sapiens RepID=A8MW24\_HUMAN  
>Putative uncharacterized protein PICALM n=1 Tax=Homo sapiens RepID=A8MX97\_HUMAN  
>Phosphatidylinositol-binding clathrin assembly protein isoform 2 n=1 Tax=Homo sapiens RepID=B5BU72\_HUMAN  
>Putative uncharacterized protein PICALM n=1 Tax=Homo sapiens RepID=C9JDZ4\_HUMAN  
>Phosphatidylinositol-binding clathrin assembly protein n=1 Tax=Homo sapiens RepID=PICAL\_HUMAN  
>Isoform 2 of Phosphatidylinositol-binding clathrin assembly protein n=1 Tax=Homo sapiens RepID=Q13492-2  
>Isoform 3 of Phosphatidylinositol-binding clathrin assembly protein n=1 Tax=Homo sapiens RepID=Q13492-3  
>PICALM variant protein (Fragment) n=1 Tax=Homo sapiens RepID=Q4LE54\_HUMAN

27 UniRef100\_B1ANR0 UniRef100\_B1ANR1 UniRef100\_B3KT93 UniRef100\_B4DQX0 UniRef100\_B4DZW4 UniRef100\_P11940  
UniRef100\_P11940-2 UniRef100\_Q13310 UniRef100\_Q13310-2 UniRef100\_Q4VC03 UniRef100\_Q61Q30 0.9905

confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.36%  
 >Poly(A) binding protein, cytoplasmic 4 (Inducible form) n=1 Tax=Homo sapiens RepID=B1ANR0\_HUMAN Length: 615aa  
 >Poly(A) binding protein, cytoplasmic 4 (Inducible form) (Fragment) n=2 Tax=Eutheria RepID=B1ANR1\_HUMAN  
 >cDNA FLJ37875 fis, clone BRSSN2018771, highly similar to Poly(A)-binding protein 1 n=1 Tax=Homo sapiens RepID=B3KT93\_HUMAN  
 >cDNA FLJ59219, highly similar to Poly(A)-binding protein 1 n=1 Tax=Homo sapiens RepID=B4DQX0\_HUMAN  
 >cDNA FLJ57246, highly similar to Poly(A)-binding protein 1 n=1 Tax=Homo sapiens RepID=B4DZW4\_HUMAN  
 >Polyadenylate-binding protein 1 n=2 Tax=Eutheria RepID=PABP1\_HUMAN  
 >Isoform 2 of Polyadenylate-binding protein 1 n=1 Tax=Homo sapiens RepID=P11940-2  
 >Polyadenylate-binding protein 4 n=1 Tax=Homo sapiens RepID=PABP4\_HUMAN  
 >Isoform 2 of Polyadenylate-binding protein 4 n=1 Tax=Homo sapiens RepID=Q13310-2  
 >PABPC4 protein n=1 Tax=Homo sapiens RepID=Q4VC03\_HUMAN  
 >PABPC4 protein n=1 Tax=Homo sapiens RepID=Q6IQ30\_HUMAN

28 UniRef100\_B7Z2V6 UniRef100\_P38606 UniRef100\_UPI000186DABD 0.9905  
 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.18%  
 >cDNA FLJ53889, highly similar to Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (EC 3.6.3.14) n=1 Length: 334aa  
 >V-type proton ATPase catalytic subunit A n=3 Tax=Homo sapiens RepID=VATA\_HUMAN  
 >vacuolar ATP synthase catalytic subunit A, osteoclast isoform, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186DABD

29 UniRef100\_B7Z4C7 UniRef100\_P26038 UniRef100\_UPI00015E03E6 0.9905  
 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.36%  
 >cDNA FLJ57321, moderately similar to Moesin n=1 Tax=Homo sapiens RepID=B7Z4C7\_HUMAN Length: 204aa  
 >Moesin n=1 Tax=Homo sapiens RepID=MOES\_HUMAN  
 >Moesin (Membrane-organizing extension spike protein). n=1 Tax=Homo sapiens RepID=UPI00015E03E6

30 UniRef100\_A8K666 UniRef100\_B4DFM0 UniRef100\_B7ZB32 UniRef100\_Q4R569 UniRef100\_Q9BR63 UniRef100\_Q9NSD9  
 0.9895  
 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.36%  
 >cDNA FLJ75460, highly similar to Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit, mRNA n=1 Tax= Length: 589aa  
 >Phenylalanine-tRNA synthetase-like, beta subunit, isoform CRA\_c n=1 Tax=Homo sapiens RepID=B4DFM0\_HUMAN  
 >cDNA, FLJ79396, highly similar to Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) n=1 Tax=Homo sapiens RepID=B7ZB32\_HUMAN  
 >Brain cDNA, clone: Qccc-16621, similar to human phenylalanine-tRNA synthetase-like, beta subunit(FARSLB), n=1 Tax=Macaca fascicularis  
 RepID=Q4R569\_MACFA  
 >FARSB protein (Fragment) n=1 Tax=Homo sapiens RepID=Q9BR63\_HUMAN  
 >Phenylalanyl-tRNA synthetase beta chain n=1 Tax=Homo sapiens RepID=SYFB\_HUMAN

31 UniRef100\_A8MTP3 UniRef100\_A8MZ91 UniRef100\_B2RDD7 UniRef100\_B4DV00 UniRef100\_B4DX49 UniRef100\_B4DY30  
 UniRef100\_O14744 UniRef100\_UPI0001AE6957 0.9886  
 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.36%  
 >Protein arginine methyltransferase 5, isoform CRA\_c n=1 Tax=Homo sapiens RepID=A8MTP3\_HUMAN Length: 466aa  
 >Protein arginine methyltransferase 5, isoform CRA\_d n=1 Tax=Homo sapiens RepID=A8MZ91\_HUMAN  
 >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 (EC 2.1.1.-) 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  
 >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 ICL-binding protein). n=2 Tax=Homo sapiens RepID=UPI0001AE6957

32 UniRef100\_B4DMB5 UniRef100\_B4DR64 UniRef100\_B4E1E0 UniRef100\_P17812 0.9886  
 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.18%  
 >cDNA FLJ60075, highly similar to CTP synthase 1 (EC 6.3.4.2) n=1 Tax=Homo sapiens RepID=B4DMB5\_HUMAN Length: 497aa  
 >cDNA FLJ59392, highly similar to CTP synthase 1 (EC 6.3.4.2) n=1 Tax=Homo sapiens RepID=B4DR64\_HUMAN  
 >cDNA FLJ58563, highly similar to CTP synthase 1 (EC 6.3.4.2) n=1 Tax=Homo sapiens RepID=B4E1E0\_HUMAN  
 >CTP synthase 1 n=2 Tax=Homo sapiens RepID=PYRG1\_HUMAN

33 UniRef100\_UPI0000111654 UniRef100\_UPI0000112158 UniRef100\_UPI00017BDB3D UniRef100\_UPI00017BDB42 0.9886  
 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.36%  
 >MONOCLONAL ANTIBODY MAK33 n=1 Tax=Homo sapiens RepID=UPI0000111654 Length: 213aa  
 >monoclonal antibody light chain n=1 Tax=Homo sapiens RepID=UPI0000112158  
 >FabOX108 Light Chain Fragment n=1 Tax=Homo sapiens RepID=UPI00017BDB3D  
 >FabOX117 Light Chain Fragment n=1 Tax=Homo sapiens RepID=UPI00017BDB42

34 UniRef100\_A6NL74 UniRef100\_B4DT31 UniRef100\_B4DWL1 UniRef100\_B4E0X8 UniRef100\_C9JT73 UniRef100\_Q59FU3  
 UniRef100\_Q6PJY1 UniRef100\_Q96AE4 UniRef100\_Q96AE4-2 UniRef100\_UPI000059CF9 UniRef100\_UPI00015E0BF5 UniRef100\_UPI0001AE7889  
 0.9802  
 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.18%  
 >Putative uncharacterized protein FUBP1 n=1 Tax=Homo sapiens RepID=A6NL74\_HUMAN Length: 645aa  
 >cDNA FLJ53425, highly similar to Far upstream element-binding protein 1 n=1 Tax=Homo sapiens RepID=B4DT31\_HUMAN  
 >cDNA FLJ59240, highly similar to Far upstream element-binding protein 1 n=1 Tax=Homo sapiens RepID=B4DWL1\_HUMAN  
 >cDNA FLJ61021, highly similar to Far upstream element-binding protein 1 n=1 Tax=Homo sapiens RepID=B4E0X8\_HUMAN  
 >Putative uncharacterized protein FUBP1 n=1 Tax=Homo sapiens RepID=C9JT73\_HUMAN  
 >Far upstream element-binding protein variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59FU3\_HUMAN  
 >FUBP1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6PJY1\_HUMAN  
 >Far upstream element-binding protein 1 n=1 Tax=Homo sapiens RepID=FUBP1\_HUMAN  
 >Isoform 2 of Far upstream element-binding protein 1 n=1 Tax=Homo sapiens RepID=Q96AE4-2  
 >Far upstream element-binding protein 1 (FUSE-binding protein 1) (FBP) (DNA helicase V) (HDH V). n=1 Tax=Homo sapiens RepID=UPI000059CF9  
 >Far upstream element-binding protein 1 (FUSE-binding protein 1) (FBP) (DNA helicase V) (HDH V). n=1 Tax=Homo sapiens RepID=UPI00015E0BF5  
 >UPI0001AE7889 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7889

35 UniRef100\_B4DRE8 UniRef100\_P13639 UniRef100\_Q6PK56 UniRef100\_Q8TA90 0.9540  
 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.18%  
 >cDNA FLJ58164, highly similar to Elongation factor 2 n=1 Tax=Homo sapiens RepID=B4DRE8\_HUMAN Length: 505aa  
 >Elongation factor 2 n=2 Tax=Hominiidae RepID=EF2\_HUMAN  
 >EEF2 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6PK56\_HUMAN  
 >Similar to Elongation factor 2b (Fragment) n=1 Tax=Homo sapiens RepID=Q8TA90\_HUMAN