

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



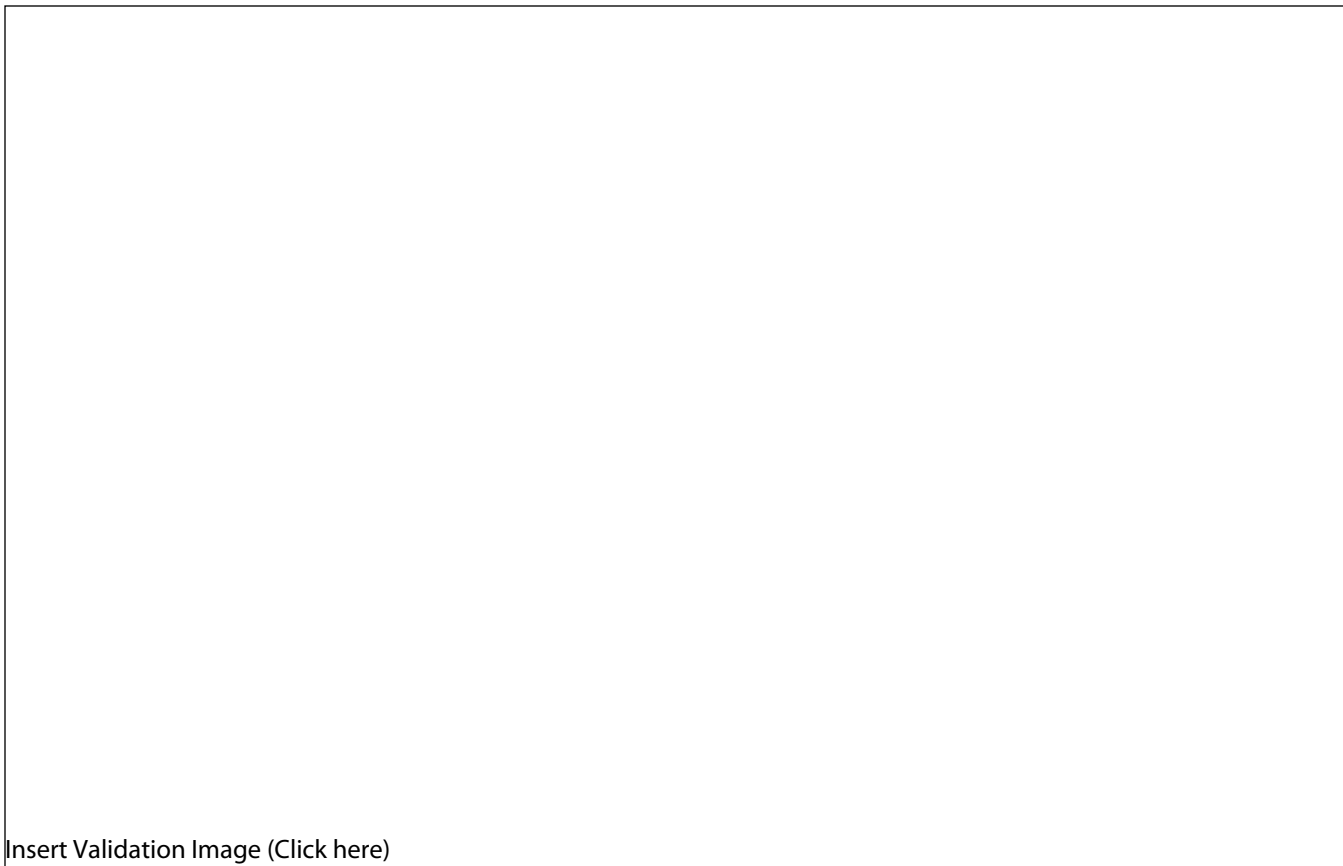
Insert Validation Image (click here)



Validation #2
Analysis



Insert Validation Image (Click here)



NFIC mass spec results - lower band (~55kDa):

24 entries (9 single hits) retrieved from
/home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_NFIC-1-sequest.prot.xml

* corresponds to peptide is_nondegenerate_evidence flag

1 PROTEIN GROUP: 1 1.0000

a UniRef100_A6NBZ8 UniRef100_A8K9P0 UniRef100_B2RBS8 UniRef100_B4DPP6 UniRef100_B4DPR2 UniRef100_P02768
UniRef100_P02769 UniRef100_Q56G89 UniRef100_UPI000179EC85 UniRef100_UPI0001AE74F7 UniRef100_UPI0001D3B4DF 1.0000
confidence: 1. max coverage num unique p_i tot indep spec share of spectrum id's: 0.68%
>Putative uncharacterized protein ALB n=1 Tax=Homo sapiens RepID=A6NBZ8_HUMAN Length: 627aa
>cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA n=1 Tax=Homo sapiens RepID=A8K9P0_HUMAN
>cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA n=1 Tax=Homo sapiens RepID=B2RBS8_HUMAN
>cDNA FLJ54371, highly similar to Serum albumin n=1 Tax=Homo sapiens RepID=B4DPP6_HUMAN
>cDNA FLJ50830, highly similar to Serum albumin n=1 Tax=Homo sapiens RepID=B4DPR2_HUMAN
>Serum albumin n=2 Tax=Hominidae RepID=ALBU_HUMAN
>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN
>Serum albumin n=1 Tax=Homo sapiens RepID=Q56G89_HUMAN
>Serum albumin precursor (Allergen Bos d 6) (BSA). n=1 Tax=Bos taurus RepID=UPI000179EC85
>UPI0001AE74F7 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE74F7
>UPI0001D3B4DF related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3B4DF

b UniRef100_B7WNR0 UniRef100_C9JKR2 UniRef100_D6RHD5 UniRef100_P02768-2 UniRef100_Q8IUK7 UniRef100_UPI000045722A
0
confidence: 0.0892 num unique p_i 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
>ALB protein n=1 Tax=Homo sapiens RepID=Q8IUK7_HUMAN
>Serum albumin precursor. n=1 Tax=Homo sapiens RepID=UPI000045722A

c UniRef100_UPI0001610EBC 0.0000
confidence: 0.9994 num unique p_i tot indep spectra: 0
>UPI0001610EBC related cluster n=1 Tax=Homo sapiens RepID=UPI0001610EBC Length: 197aa

2 PROTEIN GROUP: 2 1.0000

a UniRef100_B3KML9 UniRef100_P68371 UniRef100_Q8IWP6 UniRef100_Q8IZ29 UniRef100_Q8N6N5 1.0000
confidence: 1. max coverage num unique p_i tot indep spec share of spect subsumed entries: 1
>cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain n=1 Tax=Homo sapiens RepID=f Length: 397aa
>Tubulin beta-2C chain n=3 Tax=Eutheria RepID=TBB2C_HUMAN
>Class IVb beta tubulin n=1 Tax=Homo sapiens RepID=Q8IWP6_HUMAN
>Tubulin, beta 2C n=1 Tax=Homo sapiens RepID=Q8IZ29_HUMAN
>Tubulin, beta 2C n=1 Tax=Homo sapiens RepID=Q8N6N5_HUMAN

b UniRef100_A1L195 UniRef100_A1L196 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>TUBB2B protein (Fragment) n=1 Tax=Homo sapiens RepID=A1L195_HUMAN Length: 188aa
>Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens RepID=A1L196_HUMAN

c UniRef100_A4UCT2 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Tubulin beta 2C (Fragment) n=1 Tax=Homo sapiens RepID=A4UCT2_HUMAN Length: 88aa

d UniRef100_A5D906 UniRef100_A5D907 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>TUBB2A protein (Fragment) n=1 Tax=Homo sapiens RepID=A5D906_HUMAN Length: 253aa
>TUBB2A protein (Fragment) n=1 Tax=Homo sapiens RepID=A5D907_HUMAN

e UniRef100_A6NKZ8 UniRef100_Q5SQY1 UniRef100_Q9H4B7 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Putative tubulin beta chain-like protein ENSP00000290377 n=1 Tax=Homo sapiens RepID=YI016_HUMAN Length: 372aa
>Novel protein similar to beta-tubulin 4Q (TUBB4Q) (LOC253936) (Fragment) n=1 Tax=Homo sapiens RepID=Q5SQY1_HUMAN
>Tubulin beta-1 chain n=1 Tax=Homo sapiens RepID=TBB1_HUMAN

f UniRef100_A6NNZ2 UniRef100_C9JAA5 UniRef100_Q5SQY0 UniRef100_UPI0001B1A4B1 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0

>Tubulin beta-8 chain B n=1 Tax=Homo sapiens RepID=TBB8B_HUMAN Length: 444aa
>Putative uncharacterized protein ENSP00000418077 n=1 Tax=Homo sapiens RepID=C9JAA5_HUMAN
>Novel protein similar to beta-tubulin 4Q (TUBB4Q) (LOC253936) n=1 Tax=Homo sapiens RepID=Q5SQY0_HUMAN
>tubulin beta-8 chain isoform 2 n=1 Tax=Homo sapiens RepID=UPI0001B1A4B1

g UniRef100_A8K854 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>HCG1983504, isoform CRA_f n=1 Tax=Homo sapiens RepID=A8K854_HUMAN Length: 378aa

h UniRef100_B2R6L0 UniRef100_Q13885 UniRef100_Q9BVA1 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA, FLJ93005, highly similar to Homo sapiens tubulin, beta polypeptide (TUBB), mRNA n=1 Tax=Homo sapiens f Length: 445aa
>Tubulin beta-2A chain n=4 Tax=Euarchontoglires RepID=TBB2A_HUMAN
>Tubulin beta-2B chain n=6 Tax=Eutheria RepID=TBB2B_HUMAN

i UniRef100_B2RBD5 UniRef100_Q13509 UniRef100_Q53G92 UniRef100_Q7KZS6 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0 subsumed entries: 2
>cDNA, FLJ95457, highly similar to Homo sapiens tubulin, beta, 4 (TUBB4), mRNA n=1 Tax=Homo sapiens RepID=B Length: 450aa
>Tubulin beta-3 chain n=4 Tax=Eutheria RepID=TBB3_HUMAN
>Tubulin, beta, 4 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53G92_HUMAN
>HCG2042771 n=1 Tax=Homo sapiens RepID=Q7KZS6_HUMAN

j UniRef100_B3KS31 UniRef100_B4DP54 UniRef100_Q9BUF5 UniRef100_UPI000186CCD1 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Tubulin, beta 6, isoform CRA_a n=1 Tax=Homo sapiens RepID=B3KS31_HUMAN Length: 374aa
>cDNA FLJ52712, highly similar to Tubulin beta-6 chain n=1 Tax=Homo sapiens RepID=B4DP54_HUMAN
>Tubulin beta-6 chain n=1 Tax=Homo sapiens RepID=TBB6_HUMAN
>tubulin beta-3 chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CCD1

k UniRef100_B4DE77 UniRef100_P04350 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ55189, highly similar to Tubulin beta-4 chain n=1 Tax=Homo sapiens RepID=B4DE77_HUMAN Length: 409aa
>Tubulin beta-4 chain n=5 Tax=Eutheria RepID=TBB4_HUMAN

l UniRef100_B4DFH6 UniRef100_UPI0001AE63E3 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ52536, highly similar to Tubulin beta-4 chain n=1 Tax=Homo sapiens RepID=B4DFH6_HUMAN Length: 236aa
>UPI0001AE63E3 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE63E3

m UniRef100_B4DJ43 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ53341, highly similar to Tubulin beta-4 chain n=1 Tax=Homo sapiens RepID=B4DJ43_HUMAN Length: 362aa

n UniRef100_B4DMJ5 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ53012, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DMJ5_HUMAN Length: 242aa

o UniRef100_B4DMU8 UniRef100_UPI0001AE72AC 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ53063, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DMU8_HUMAN Length: 317aa
>UPI0001AE72AC related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE72AC

p UniRef100_B4DNW1 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ59940, highly similar to Tubulin beta-2C chain n=1 Tax=Homo sapiens RepID=B4DNW1_HUMAN Length: 193aa

q UniRef100_B4DQN9 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ50617, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DQN9_HUMAN Length: 372aa

r UniRef100_B4DXZ5 UniRef100_Q96B85 UniRef100_UPI0001AE713B 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ52029, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DXZ5_HUMAN Length: 271aa
>TUBB protein (Fragment) n=1 Tax=Homo sapiens RepID=Q96B85_HUMAN
>UPI0001AE713B related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE713B

s UniRef100_B4DY90 UniRef100_B7ZAF0 UniRef100_P07437 UniRef100_Q5JP53 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0 subsumed entries: 16

>cDNA FLJ56903, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DY90_HUMAN Length: 464aa
>cDNA, FLJ79164, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B7ZAF0_HUMAN
>Tubulin beta chain n=12 Tax=Amniota RepID=TBB5_HUMAN
>Tubulin beta polypeptide n=1 Tax=Homo sapiens RepID=Q5JP53_HUMAN

t UniRef100_B4E052 UniRef100_Q5ST81 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ52378, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4E052_HUMAN Length: 353aa
>Tubulin beta polypeptide n=3 Tax=Hominidae RepID=Q5ST81_HUMAN

u UniRef100_B7Z4N1 UniRef100_O43209 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ53906, highly similar to Tubulin beta chain n=1 Tax=Homo sapiens RepID=B7Z4N1_HUMAN Length: 354aa
>Homo sapiens clone 23678 (Fragment) n=3 Tax=Homininae RepID=O43209_HUMAN

v UniRef100_B7ZAK1 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA, FLJ79215, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B7ZAK1_HUMAN Length: 372aa

w UniRef100_C9JN87 UniRef100_UPI000046D38F 0.0000
confidence: 0.9998 num unique p_i tot indep spectra: 0
>Putative uncharacterized protein ENSP00000311042 n=1 Tax=Homo sapiens RepID=C9JN87_HUMAN Length: 119aa
>putative tubulin beta-4q chain n=1 Tax=Homo sapiens RepID=UPI000046D38F

x UniRef100_Q1KSF8 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>XTP3TPA-transactivated protein 1 n=1 Tax=Homo sapiens RepID=Q1KSF8_HUMAN Length: 208aa

y UniRef100_Q3ZCM7 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Tubulin beta-8 chain n=1 Tax=Homo sapiens RepID=TBB8_HUMAN Length: 444aa

z UniRef100_Q3ZCR3 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>TUBB3 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q3ZCR3_HUMAN Length: 280aa

aa UniRef100_Q6LC01 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>MRNA encoding beta-tubulin. (from clone D-beta-1) (Fragment) n=1 Tax=Homo sapiens RepID=Q6LC01_HUMAN Length: 437aa

ab UniRef100_Q6P602 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>TUBB protein n=4 Tax=Euarchontoglires RepID=Q6P602_HUMAN Length: 124aa

ac UniRef100_Q96HX0 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>TUBB2C protein (Fragment) n=2 Tax=Homo sapiens RepID=Q96HX0_HUMAN Length: 227aa

ad UniRef100_Q99867 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Putative tubulin beta-4q chain n=1 Tax=Homo sapiens RepID=TBB4Q_HUMAN Length: 434aa

ae UniRef100_Q9UGA2 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Putative uncharacterized protein DKFZp566F223 (Fragment) n=1 Tax=Homo sapiens RepID=Q9UGA2_HUMAN Length: 325aa

af UniRef100_UPI00005E77FA UniRef100_UPI000155D184 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>PREDICTED: similar to likely orthologue of Homo sapiens tubulin beta 1 (TUBB1) n=1 Tax=Monodelphis domestica Length: 449aa
>PREDICTED: similar to likely orthologue of Homo sapiens tubulin beta 1 (TUBB1) n=1 Tax=Ornithorhynchus anatinus RepID=UPI000155D184

ag UniRef100_UPI000186CB60 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>tubulin beta chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CB60 Length: 429aa

ah UniRef100_UPI000186CFD7 0.0000

confidence: 1.0000 num unique p_i tot indep spectra: 0
 >tubulin beta chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CFD7 Length: 444aa

ai UniRef100_UPI000186D036 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >tubulin beta chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D036 Length: 457aa

aj UniRef100_UPI000186D037 0.0000
 confidence: 0.9960 num unique p_i tot indep spectra: 0
 >tubulin beta-2 chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D037 Length: 492aa

ak UniRef100_UPI000186DC1C 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >tubulin beta-1 chain n=1 Tax=Pediculus humanus corporis RepID=UPI000186DC1C Length: 447aa

al UniRef100_UPI000186E8F0 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >tubulin beta-2 chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E8F0 Length: 445aa

am UniRef100_UPI0001AE713A 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >UPI0001AE713A related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE713A Length: 243aa

3 PROTEIN GROUP: 3 1.0000

a UniRef100_B4DGL0 UniRef100_B4DMA2 UniRef100_P07900 UniRef100_P08238 UniRef100_Q2VPJ6 UniRef100_Q8TBA7
 0.9999
 confidence: 0. max coverage num unique p_i tot indep spec share of spect subsumed entries: 1
 >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-alpha n=2 Tax=Homo sapiens RepID=HS90A_HUMAN
 >Heat shock protein HSP 90-beta n=1 Tax=Homo sapiens RepID=HS90B_HUMAN
 >HSP90AA1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q2VPJ6_HUMAN
 >HSP90AA1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8TBA7_HUMAN

b UniRef100_A8K3W9 UniRef100_B4DR68 UniRef100_O75322 UniRef100_Q12931 UniRef100_Q53FS6 UniRef100_Q53G55
 UniRef100_Q5T9W4 UniRef100_Q5T9W5 UniRef100_Q5T9W6 UniRef100_Q86U12 UniRef100_Q8N9Z3 UniRef100_Q96HX7
 UniRef100_Q9BV61 UniRef100_Q9H6X9 UniRef100_UPI000059D8E3 UniRef100_UPI000059D8E5 UniRef100_UPI000186D735 0.0000
 confidence: 0.2305 num unique p_i tot indep spectra: 0
 >cDNA FLJ77842 n=1 Tax=Homo sapiens RepID=A8K3W9_HUMAN Length: 362aa
 >cDNA FLJ58608, highly similar to Heat shock protein 75 kDa, mitochondrial n=1 Tax=Homo sapiens RepID=B4DR68_HUMAN
 >Hsp89-alpha-delta-N n=2 Tax=Homo sapiens RepID=O75322_HUMAN
 >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
 >Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5T9W4_HUMAN
 >Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5T9W5_HUMAN
 >Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5T9W6_HUMAN
 >Full-length cDNA clone CS0CAP007YF18 of Thymus of Homo sapiens (human) n=1 Tax=Homo sapiens RepID=Q86U12_HUMAN
 >cDNA FLJ36025 fis, clone TESTI2016701, highly similar to TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN n=1
 Tax=Homo sapiens RepID=Q8N9Z3_HUMAN
 >HSP90AA1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q96HX7_HUMAN
 >TRAP1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q9BV61_HUMAN
 >cDNA: FLJ21717 fis, clone COL10322 n=1 Tax=Homo sapiens RepID=Q9H6X9_HUMAN
 >UPI000059D8E3 related cluster n=1 Tax=Homo sapiens RepID=UPI000059D8E3
 >UPI000059D8E5 related cluster n=1 Tax=Homo sapiens RepID=UPI000059D8E5
 >heat shock protein 75 kDa, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D735

c UniRef100_O14942 UniRef100_Q14568 UniRef100_Q58FF8 UniRef100_Q6PK50 UniRef100_Q86SX1 0.0000
 confidence: 0.2476 num unique p_i tot indep spectra: 0
 >Heat shock protein beta (Fragment) n=1 Tax=Homo sapiens RepID=O14942_HUMAN Length: 130aa
 >Putative heat shock protein HSP 90-alpha A2 n=1 Tax=Homo sapiens RepID=HS902_HUMAN
 >Putative heat shock protein HSP 90-beta 2 n=1 Tax=Homo sapiens RepID=H90B2_HUMAN
 >HSP90AB1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6PK50_HUMAN
 >Full-length cDNA 5-PRIME end of clone CSODN005YI08 of Adult brain of Homo sapiens (human) (Fragment) n=1 Tax=Homo sapiens
 RepID=Q86SX1_HUMAN

d UniRef100_Q58FF7 0.0000
 confidence: 0.0324 num unique p_i tot indep spectra: 0
 >Putative heat shock protein HSP 90-beta-3 n=1 Tax=Homo sapiens RepID=H90B3_HUMAN Length: 597aa

4 PROTEIN GROUP: 4 1.0000

a UniRef100_B4DRT3 UniRef100_B4DUU6 UniRef100_P14618 UniRef100_UPI0001662C1E 1.0000
confidence: 1. max coverage num unique pi tot indep spec share of spect subsumed entries: 1
>Pyruvate kinase n=1 Tax=Homo sapiens RepID=B4DRT3_HUMAN Length: 511aa
>Pyruvate kinase n=1 Tax=Homo sapiens RepID=B4DUU6_HUMAN
>Pyruvate kinase isozymes M1/M2 n=2 Tax=Homininae RepID=KPYM_HUMAN
>PREDICTED: similar to pyruvate kinase, muscle n=1 Tax=Homo sapiens RepID=UPI0001662C1E

b UniRef100_B4DNK4 UniRef100_B4DPM0 UniRef100_O75758 UniRef100_P30613 UniRef100_P30613-2 UniRef100_Q16716
UniRef100_Q504U3 UniRef100_Q8WUW7 UniRef100_UPI00015DFCEC UniRef100_UPI00015E0C3E UniRef100_UPI0001AE6926
UniRef100_UPI0001AE6927 UniRef100_UPI0001AE791F 0.0000
confidence: 0.0961 num unique pi tot indep spectra: 0
>Pyruvate kinase n=1 Tax=Homo sapiens RepID=B4DNK4_HUMAN Length: 457aa
>Pyruvate kinase n=1 Tax=Homo sapiens RepID=B4DPM0_HUMAN
>Pyruvate kinase n=1 Tax=Homo sapiens RepID=O75758_HUMAN
>Pyruvate kinase isozymes R/L n=3 Tax=Homo sapiens RepID=KPYR_HUMAN
>Isoform L-type of Pyruvate kinase isozymes R/L n=2 Tax=Homo sapiens RepID=P30613-2
>Pyruvate kinase n=2 Tax=Homo sapiens RepID=Q16716_HUMAN
>Pyruvate kinase n=1 Tax=Homo sapiens RepID=Q504U3_HUMAN
>Pyruvate kinase (Fragment) n=1 Tax=Homo sapiens RepID=Q8WUW7_HUMAN
>Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase muscle isozyme) (Pyruvate kinase 2/3) (Cytosolic thyroid
hormone-binding protein) (CTHBP) (THBP1). n=1 Tax=Homo sapiens RepID=UPI00015DFCEC
>UPI00015E0C3E related cluster n=1 Tax=Homo sapiens RepID=UPI00015E0C3E
>UPI0001AE6926 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6926
>UPI0001AE6927 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6927
>UPI0001AE791F related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE791F

5 PROTEIN GROUP: 5 1.0000

a UniRef100_C5I WV5 UniRef100_P00761 1.0000
confidence: 1. max coverage num unique pi tot indep spec share of spect subsumed entries: 1
>Trypsinogen n=1 Tax=Sus scrofa RepID=C5I WV5_PIG Length: 246aa
>Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG

b UniRef100_A8CED1 UniRef100_A8CED3 UniRef100_B1AN99 UniRef100_B5AEC7 UniRef100_D2D388 UniRef100_P07146
UniRef100_P12788 UniRef100_P19799 UniRef100_P35030 UniRef100_P35030-2 UniRef100_P35030-3 UniRef100_Q0PG34
UniRef100_Q6ISJ4 UniRef100_Q6R670 UniRef100_Q6R671 UniRef100_Q7Z5F4 UniRef100_Q8N2U3 UniRef100_UPI000021129C
UniRef100_UPI00005E8630 UniRef100_UPI0000D92B15 UniRef100_UPI0000E21E68 UniRef100_UPI000194B97D UniRef100_UPI000194B9B7
UniRef100_UPI0001AE6E33 UniRef100_UPI0001AE7177 0.0000
confidence: 0.0518 num unique pi tot indep spectra: 0
>Protease, serine, 3 (Mesotrypsin), isoform CRA_d n=1 Tax=Homo sapiens RepID=A8CED1_HUMAN Length: 304aa
>Trypsinogen 5 n=1 Tax=Homo sapiens RepID=A8CED3_HUMAN
>Protease, serine, 3 (Fragment) n=1 Tax=Homo sapiens RepID=B1AN99_HUMAN
>Trypsin (Fragment) n=2 Tax=Rhinichthys RepID=B5AEC7_9TELE
>Trypsinogen n=1 Tax=Culter alburnus RepID=D2D388_9TELE
>Anionic trypsin-2 n=2 Tax=Mus musculus RepID=TRY2_MOUSE
>Trypsin-4 n=1 Tax=Rattus norvegicus RepID=TRY4_RAT
>Trypsin n=1 Tax=Xenopus laevis RepID=TRY1_XENLA
>Trypsin-3 n=1 Tax=Homo sapiens RepID=TRY3_HUMAN
>Isoform B of Trypsin-3 n=1 Tax=Homo sapiens RepID=P35030-2
>Isoform C of Trypsin-3 n=1 Tax=Homo sapiens RepID=P35030-3
>Trypsin n=1 Tax=Spinibarbus sinensis RepID=Q0PG34_9TELE
>Mesotrypsinogen n=1 Tax=Homo sapiens RepID=Q6ISJ4_HUMAN
>Trypsin n=1 Tax=Oreochromis aureus RepID=Q6R670_OREAU
>Trypsin n=1 Tax=Oreochromis niloticus RepID=Q6R671_ORENI
>Protease serine 4 isoform B n=1 Tax=Homo sapiens RepID=Q7Z5F4_HUMAN
>PRSS3 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8N2U3_HUMAN
>Trypsin-3 precursor (EC 3.4.21.4) (Trypsin III) (Brain trypsinogen) (Mesotrypsinogen) (Trypsin IV) (Serine protease 3) (Serine protease 4).
n=1 Tax=Homo sapiens RepID=UPI000021129C
>PREDICTED: similar to Anionic trypsin n=1 Tax=Monodelphis domestica RepID=UPI00005E8630
>PREDICTED: similar to pancreatic anionic trypsinogen n=1 Tax=Monodelphis domestica RepID=UPI0000D92B15
>PREDICTED: similar to trypsinogen IV b-form n=1 Tax=Pan troglodytes RepID=UPI0000E21E68
>PREDICTED: similar to Anionic trypsin n=1 Tax=Taeniopygia guttata RepID=UPI000194B97D
>PREDICTED: similar to Anionic trypsin n=1 Tax=Taeniopygia guttata RepID=UPI000194B9B7
>UPI0001AE6E33 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6E33
>UPI0001AE7177 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7177

c UniRef100_P06872 0.0000
confidence: 0.9960 num unique pi tot indep spectra: 0
>Anionic trypsin n=2 Tax=Canis lupus familiaris RepID=TRY2_CANFA Length: 247aa

d UniRef100_Q7M754 0.0000
confidence: 0.1374 num unique pi tot indep spectra: 0
>Try10-like trypsinogen n=1 Tax=Mus musculus RepID=Q7M754_MOUSE Length: 246aa

6

PROTEIN GROUP: 6 1.0000

a

UniRef100_C9JSM6 UniRef100_C9JSM7 UniRef100_O00712 UniRef100_Q5VW26 UniRef100_Q5VW27 UniRef100_Q5VW29
 UniRef100_Q5VW30 UniRef100_Q6ZNF9 1.0000
 confidence: 1 max coverage num unique | tot indep spe share of spe subsumed entries: 2
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=C9JSM6_HUMAN Length: 494aa
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=C9JSM7_HUMAN
 >Nuclear factor 1 B-type n=2 Tax=Homo sapiens RepID=NFIB_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q5VW26_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q5VW27_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q5VW29_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q5VW30_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q6ZNF9_HUMAN

b

UniRef100_B1AKN5 UniRef100_B1AKN6 UniRef100_B1AKN7 UniRef100_B1AKN8 UniRef100_B4DHW2 UniRef100_B4DM25
 UniRef100_B4DRN9 UniRef100_B4DS53 UniRef100_B5MDB4 UniRef100_B7Z4T6 UniRef100_B7Z4U5 UniRef100_C9JE99
 UniRef100_C9JSM5 UniRef100_C9JWJ8 UniRef100_D2DXM9 UniRef100_P08651 UniRef100_P08651-2 UniRef100_P08651-3
 UniRef100_P08651-4 UniRef100_P08651-5 UniRef100_Q12857 UniRef100_Q12857-2 UniRef100_Q13051 UniRef100_Q14938
 UniRef100_Q14938-2 UniRef100_Q14938-3 UniRef100_Q14938-5 UniRef100_Q6FI30 UniRef100_Q7Z3K7
 UniRef100_UPI0001AE789E 0
 confidence: 0.2280 num unique | tot indep spectra: 0
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B1AKN5_HUMAN Length: 487aa
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B1AKN6_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B1AKN7_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B1AKN8_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DHW2_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DM25_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DRN9_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DS53_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B5MDB4_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B7Z4T6_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B7Z4U5_HUMAN
 >Putative uncharacterized protein NFIA n=1 Tax=Homo sapiens RepID=C9JE99_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=C9JSM5_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=C9JWJ8_HUMAN
 >Nuclear factor 1 n=3 Tax=Catarrhini RepID=D2DXM9_HUMAN
 >Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=NFIC_HUMAN
 >Isoform 1 of Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=P08651-2
 >Isoform 2 of Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=P08651-3
 >Isoform 3 of Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=P08651-4
 >Isoform 5 of Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=P08651-5
 >Nuclear factor 1 A-type n=2 Tax=Homo sapiens RepID=NFIA_HUMAN
 >Isoform 2 of Nuclear factor 1 A-type n=1 Tax=Homo sapiens RepID=Q12857-2
 >Nuclear factor I (Fragment) n=1 Tax=Homo sapiens RepID=Q13051_HUMAN
 >Nuclear factor 1 X-type n=1 Tax=Homo sapiens RepID=NFIX_HUMAN
 >Isoform 2 of Nuclear factor 1 X-type n=1 Tax=Homo sapiens RepID=Q14938-2
 >Isoform 3 of Nuclear factor 1 X-type n=1 Tax=Homo sapiens RepID=Q14938-3
 >Isoform 5 of Nuclear factor 1 X-type n=1 Tax=Homo sapiens RepID=Q14938-5
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q6FI30_HUMAN
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q7Z3K7_HUMAN
 >UPI0001AE789E related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE789E

c

UniRef100_B4DS74 0.0000
 confidence: 0.9968 num unique | tot indep spectra: 0
 >Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DS74_HUMAN Length: 445aa

d

UniRef100_Q5W0Y9 0.0000
 confidence: 0.9986 num unique | tot indep spectra: 0
 >Nuclear factor I/B n=1 Tax=Homo sapiens RepID=Q5W0Y9_HUMAN Length: 200aa

7

PROTEIN GROUP: 7 1.0000

a

UniRef100_D6RBM0 UniRef100_D6RIH9 UniRef100_D6RIT2 UniRef100_P31943 UniRef100_UPI00001AF4DD 1.0000
 confidence: 1 max coverage num unique | tot indep spec share of spect subsumed entries: 1
 >Putative uncharacterized protein HNRNPH1 n=3 Tax=Homo sapiens RepID=D6RBM0_HUMAN Length: 212aa
 >Putative uncharacterized protein HNRNPH1 n=4 Tax=Homo sapiens RepID=D6RIH9_HUMAN
 >Putative uncharacterized protein HNRNPH1 n=5 Tax=Eutheria RepID=D6RIT2_HUMAN
 >Heterogeneous nuclear ribonucleoprotein H, N-terminally processed n=2 Tax=Homo sapiens RepID=HNRH1_HUMAN
 >Heterogeneous nuclear ribonucleoprotein H (hnRNP H). n=1 Tax=Homo sapiens RepID=UPI00001AF4DD

b

UniRef100_D6R9D3 0.0000
 confidence: 0.5407 num unique | tot indep spectra: 0
 >Putative uncharacterized protein HNRNPH1 n=1 Tax=Homo sapiens RepID=D6R9D3_HUMAN Length: 40aa

c

UniRef100_P55795 0.0000

confidence: 0.9967 num unique p_i tot indep spectra: 0
 >Heterogeneous nuclear ribonucleoprotein H2 n=3 Tax=Catarrhini RepID=HNRH2_HUMAN Length: 449aa

8 PROTEIN GROUP: 8 1.0000

a UniRef100_P05787 1.0000
 confidence: 1. coverage: 51. num unique p_i tot indep spec share of spect subsumed entries: 6
 >Keratin, type II cytoskeletal 8 n=1 Tax=Homo sapiens RepID=K2C8_HUMAN Length: 483aa

b UniRef100_P04264 1.0000
 confidence: 1. coverage: 25. num unique p_i tot indep spec share of spectrum id's: 5.78%
 >Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN Length: 644aa

c UniRef100_P08729 UniRef100_UPI000013CF9E 1.0000
 confidence: 1. max coverage num unique p_i tot indep spec share of spect subsumed entries: 5
 >Keratin, type II cytoskeletal 7 n=1 Tax=Homo sapiens RepID=K2C7_HUMAN Length: 469aa
 >keratin, type II cytoskeletal 7 n=1 Tax=Homo sapiens RepID=UPI000013CF9E

d UniRef100_P35908 1.0000
 confidence: 1. coverage: 16. num unique p_i tot indep spec share of spectrum id's: 1.58%
 >Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E_HUMAN Length: 639aa

e UniRef100_Q0IIN1 UniRef100_UPI00001D797A 0.9884
 confidence: 1. max coverage num unique p_i tot indep spec share of spectrum id's: 0.49%
 >Keratin 77 n=1 Tax=Homo sapiens RepID=Q0IIN1_HUMAN Length: 578aa
 >keratin, type II cytoskeletal 1b n=1 Tax=Homo sapiens RepID=UPI00001D797A

f UniRef100_A5Z217 UniRef100_B0YJC4 UniRef100_B0YJC5 UniRef100_B3KRK8 UniRef100_B3KWQ6 UniRef100_P08670
 UniRef100_P17661 UniRef100_P41219 UniRef100_P41219-2 UniRef100_Q45VM6 UniRef100_Q45VM7 UniRef100_Q45VM8
 UniRef100_Q4R7K6 UniRef100_Q53HU8 UniRef100_Q549R7 UniRef100_Q549R8 UniRef100_Q549R9 0.0000
 confidence: 0.9992 num unique p_i tot indep spectra: 0 Length: 470aa
 >Mutant desmin n=1 Tax=Homo sapiens RepID=A5Z217_HUMAN
 >Vimentin variant 3 n=1 Tax=Homo sapiens RepID=B0YJC4_HUMAN
 >Vimentin variant 4 n=1 Tax=Homo sapiens RepID=B0YJC5_HUMAN
 >cDNA FLJ34494 fis, clone HLUNG2005030, highly similar to VIMENTIN n=1 Tax=Homo sapiens RepID=B3KRK8_HUMAN
 >cDNA FLJ43599 fis, clone SMINT2017781, highly similar to PERIPHERIN n=1 Tax=Homo sapiens RepID=B3KWQ6_HUMAN
 >Vimentin n=2 Tax=Homo sapiens RepID=VIME_HUMAN
 >Desmin n=2 Tax=Homo sapiens RepID=DESM_HUMAN
 >Peripherin n=1 Tax=Homo sapiens RepID=PERI_HUMAN
 >Isoform 2 of Peripherin n=1 Tax=Homo sapiens RepID=P41219-2
 >Mutant desmin n=1 Tax=Homo sapiens RepID=Q45VM6_HUMAN
 >Mutant desmin n=1 Tax=Homo sapiens RepID=Q45VM7_HUMAN
 >Mutant desmin n=1 Tax=Homo sapiens RepID=Q45VM8_HUMAN
 >Testis cDNA, clone: QtsA-15009, similar to human desmin (DES), n=1 Tax=Macaca fascicularis RepID=Q4R7K6_MACFA
 >Vimentin variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53HU8_HUMAN
 >Mutant desmin n=1 Tax=Homo sapiens RepID=Q549R7_HUMAN
 >Mutant desmin n=1 Tax=Homo sapiens RepID=Q549R8_HUMAN
 >Mutant desmin n=1 Tax=Homo sapiens RepID=Q549R9_HUMAN

g UniRef100_A8K2I0 UniRef100_B4DRR0 UniRef100_B4DRU6 UniRef100_B4DWU6 UniRef100_P02538 UniRef100_P48668
 UniRef100_UPI0001AE6B0A UniRef100_UPI0001AE6B0B 0.0000
 confidence: 1.0000 num unique p_i 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 FLJ53910, highly similar to Keratin, type II cytoskeletal 6A n=1 Tax=Homo sapiens RepID=B4DRR0_HUMAN
 >cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A n=1 Tax=Homo sapiens RepID=B4DRU6_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 6C n=1 Tax=Homo sapiens RepID=K2C6C_HUMAN
 >UPI0001AE6B0A related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6B0A
 >UPI0001AE6B0B related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6B0B

h UniRef100_B2R853 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA n=1 Tax=Homo sapiens RepID=B2R85 Length: 564aa

i UniRef100_B3KY79 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >cDNA FLJ46620 fis, clone TLUNG2000654, highly similar to Keratin, type II cytoskeletal 7 n=1 Tax=Homo sapiens F Length: 445aa

j UniRef100_B4DEI8 UniRef100_Q14CN4 UniRef100_Q14CN4-2 UniRef100_Q3SY84 UniRef100_Q7RTS7 UniRef100_Q86Y46
 UniRef100_Q86Y46-2 UniRef100_UPI00019912E7 0.0000

confidence: 0.0853 num unique p_i tot indep spectra: 0
 >cDNA FLJ60438, highly similar to Homo sapiens keratin protein K6irs (K6IRS2), mRNA n=1 Tax=Homo sapiens Rep Length: 469aa
 >Keratin, type II cytoskeletal 72 n=1 Tax=Homo sapiens RepID=K2C72_HUMAN
 >Isoform 2 of Keratin, type II cytoskeletal 72 n=1 Tax=Homo sapiens RepID=Q14CN4-2
 >Keratin, type II cytoskeletal 71 n=1 Tax=Homo sapiens RepID=K2C71_HUMAN
 >Keratin, type II cytoskeletal 74 n=1 Tax=Homo sapiens RepID=K2C74_HUMAN
 >Keratin, type II cytoskeletal 73 n=1 Tax=Homo sapiens RepID=K2C73_HUMAN
 >Isoform 2 of Keratin, type II cytoskeletal 73 n=1 Tax=Homo sapiens RepID=Q86Y46-2
 >keratin, type II cytoskeletal 72 isoform 2 n=1 Tax=Homo sapiens RepID=UPI00019912E7

k UniRef100_B4DKV4 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B n=1 Tax=Homo sapiens RepID=B4DKV4_HUMAN Length: 526aa

l UniRef100_B4DL32 0.0000
 confidence: 0.9958 num unique p_i tot indep spectra: 0
 >cDNA FLJ59922, highly similar to Keratin, type II cytoskeletal 5 n=1 Tax=Homo sapiens RepID=B4DL32_HUMAN Length: 234aa

m UniRef100_B4DRY0 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E n=1 Tax=Homo sapiens RepID=B4DRY0_HUMAN Length: 547aa

n UniRef100_B4E1T1 UniRef100_P13647 UniRef100_UPI0001AE6B0C 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 n=1 Tax=Homo sapiens RepID=B4E1T1_HUMAN Length: 555aa
 >Keratin, type II cytoskeletal 5 n=1 Tax=Homo sapiens RepID=K2C5_HUMAN
 >UPI0001AE6B0C related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6B0C

o UniRef100_O95678 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0 subsumed entries: 2
 >Keratin, type II cytoskeletal 75 n=1 Tax=Homo sapiens RepID=K2C75_HUMAN Length: 551aa

p UniRef100_P04259 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0 subsumed entries: 7
 >Keratin, type II cytoskeletal 6B n=1 Tax=Homo sapiens RepID=K2C6B_HUMAN Length: 564aa

q UniRef100_P12035 UniRef100_Q01546 UniRef100_UPI000013EEC8 0.0000
 confidence: 0.9705 num unique p_i tot indep spectra: 0
 >Keratin, type II cytoskeletal 3 n=1 Tax=Homo sapiens RepID=K2C3_HUMAN Length: 629aa
 >Keratin, type II cytoskeletal 2 oral n=1 Tax=Homo sapiens RepID=K22O_HUMAN
 >keratin, type II cytoskeletal 3 n=1 Tax=Homo sapiens RepID=UPI000013EEC8

r UniRef100_Q147W7 UniRef100_Q7Z794 0.0000
 confidence: 0.9907 num unique p_i tot indep spectra: 0
 >KRT1B protein n=1 Tax=Homo sapiens RepID=Q147W7_HUMAN Length: 345aa
 >Keratin, type II cytoskeletal 1b n=1 Tax=Homo sapiens RepID=K2C1B_HUMAN

s UniRef100_Q3B834 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >KRT7 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q3B834_HUMAN Length: 112aa

t UniRef100_Q3KNV1 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >KRT7 protein n=1 Tax=Homo sapiens RepID=Q3KNV1_HUMAN Length: 132aa

u UniRef100_Q5XKE5 0.0000
 confidence: 0.9948 num unique p_i tot indep spectra: 0
 >Keratin, type II cytoskeletal 79 n=1 Tax=Homo sapiens RepID=K2C79_HUMAN Length: 535aa

v UniRef100_Q7L4M3 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >KRT8 protein n=1 Tax=Homo sapiens RepID=Q7L4M3_HUMAN Length: 279aa

w UniRef100_Q8IWY7 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Tau-tubulin kinase n=1 Tax=Homo sapiens RepID=Q8IWY7_HUMAN Length: 1649aa

x UniRef100_Q969I0 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>KRT8 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q969I0_HUMAN Length: 365aa

y UniRef100_Q96GE1 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens RepID=Q96GE1_HUMAN Length: 207aa

z UniRef100_Q9H319 0.0000
confidence: 0.0661 num unique p_i tot indep spectra: 0
>Mutant desmin n=1 Tax=Homo sapiens RepID=Q9H319_HUMAN Length: 470aa

aa UniRef100_Q9H552 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Keratin-8-like protein 1 n=1 Tax=Homo sapiens RepID=Q9H552_HUMAN Length: 499aa

ab UniRef100_Q9NSB2 0.0000
confidence: 0.9924 num unique p_i tot indep spectra: 0
>Keratin, type II cuticular Hb4 n=1 Tax=Homo sapiens RepID=KRT84_HUMAN Length: 600aa

ac UniRef100_UPI0000EE2053 0.0000
confidence: 0.1124 num unique p_i tot indep spectra: 0
>PREDICTED: similar to hCG1643231 n=1 Tax=Homo sapiens RepID=UPI0000EE2053 Length: 313aa

ad UniRef100_UPI00016622D6 0.0000
confidence: 0.9984 num unique p_i tot indep spectra: 0
>PREDICTED: similar to hCG1643231 n=1 Tax=Homo sapiens RepID=UPI00016622D6 Length: 315aa

ae UniRef100_UPI0001AE6B07 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>UPI0001AE6B07 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6B07 Length: 445aa

9 PROTEIN GROUP: 9 1.0000

a UniRef100_P06576 UniRef100_Q0QEN7 1.0000
confidence: 1. max coverage num unique p_i tot indep spec share of spectrum id's: 4.07%
>ATP synthase subunit beta, mitochondrial n=1 Tax=Homo sapiens RepID=ATPB_HUMAN Length: 529aa
>ATP synthase subunit beta (Fragment) n=1 Tax=Homo sapiens RepID=Q0QEN7_HUMAN

b UniRef100_UPI000186EDED 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>ATP synthase subunit beta, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EDED Length: 550aa

10 PROTEIN GROUP: 10 1.0000

a UniRef100_P06733 1.0000
confidence: 1. coverage: 25. num unique p_i tot indep spec share of spect subsumed entries: 7
>Alpha-enolase n=1 Tax=Homo sapiens RepID=ENOA_HUMAN Length: 434aa

b UniRef100_A4QMW8 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Enolase (Fragment) n=1 Tax=Homo sapiens RepID=A4QMW8_HUMAN Length: 135aa

c UniRef100_A4UCS8 0.0000
confidence: 0.9996 num unique p_i tot indep spectra: 0
>Enolase (Fragment) n=1 Tax=Homo sapiens RepID=A4UCS8_HUMAN Length: 166aa

d UniRef100_A8K3B0 UniRef100_B4DUJ6 UniRef100_B7Z2X9 UniRef100_P09104 UniRef100_UPI00015552D9 UniRef100_UPI000186E3EE
UniRef100_UPI0001AE669F 0.0000
confidence: 0.1284 num unique p_i tot indep spectra: 0
>Enolase n=1 Tax=Homo sapiens RepID=A8K3B0_HUMAN Length: 434aa
>Enolase n=1 Tax=Homo sapiens RepID=B4DUJ6_HUMAN
>Enolase n=1 Tax=Homo sapiens RepID=B7Z2X9_HUMAN
>Gamma-enolase n=2 Tax=Homo sapiens RepID=ENOG_HUMAN
>PREDICTED: similar to human gamma enolase, partial n=1 Tax=Ornithorhynchus anatinus RepID=UPI00015552D9
>Enolase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E3EE
>UPI0001AE669F related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE669F

e UniRef100_D3DTL2 UniRef100_P13929 UniRef100_P13929-2 UniRef100_P13929-3 UniRef100_UPI0001AE669E 0.0000
confidence: 0.9975 num unique p_i tot indep spectra: 0
>Enolase n=1 Tax=Homo sapiens RepID=D3DTL2_HUMAN Length: 434aa
>Beta-enolase n=1 Tax=Homo sapiens RepID=ENOB_HUMAN
>Isoform 2 of Beta-enolase n=1 Tax=Homo sapiens RepID=P13929-2
>Isoform 3 of Beta-enolase n=1 Tax=Homo sapiens RepID=P13929-3
>UPI0001AE669E related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE669E

f UniRef100_D3DTL4 UniRef100_Q9NPL4 0.0000
confidence: 0.2147 num unique p_i tot indep spectra: 0
>Enolase n=1 Tax=Homo sapiens RepID=D3DTL4_HUMAN Length: 341aa
>Enolase (Fragment) n=1 Tax=Homo sapiens RepID=Q9NPL4_HUMAN

g UniRef100_P06733-2 UniRef100_Q9BT62 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Isoform MBP-1 of Alpha-enolase n=1 Tax=Homo sapiens RepID=P06733-2 Length: 341aa
>Enolase (Fragment) n=1 Tax=Homo sapiens RepID=Q9BT62_HUMAN

h UniRef100_Q96GV1 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Enolase (Fragment) n=1 Tax=Homo sapiens RepID=Q96GV1_HUMAN Length: 184aa

11 PROTEIN GROUP: 11 1.0000

a UniRef100_P19474 1.0000
confidence: 1. coverage: 14. num unique p_i tot indep spec share of spect subsumed entries: 1
>52 kDa Ro protein n=1 Tax=Homo sapiens RepID=RO52_HUMAN Length: 475aa

b UniRef100_Q5XPV5 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Sjogren syndrome antigen A1 n=1 Tax=Homo sapiens RepID=Q5XPV5_HUMAN Length: 475aa

12 PROTEIN GROUP: 12 1.0000

a UniRef100_P25705 1.0000
confidence: 1. coverage: 25. num unique p_i tot indep spec share of spect subsumed entries: 3
>ATP synthase subunit alpha, mitochondrial n=3 Tax=Homininae RepID=ATPA_HUMAN Length: 553aa

b UniRef100_B4DGW3 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ54625, highly similar to ATP synthase subunit alpha, mitochondrial (EC 3.6.3.14) n=1 Tax=Homo sapiens Length: 167aa

c UniRef100_B4DY56 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>ATP synthase subunit alpha n=1 Tax=Homo sapiens RepID=B4DY56_HUMAN Length: 531aa

d UniRef100_UPI000186DC4D 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>ATP synthase subunit alpha, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186DC4D Length: 552aa

13 PROTEIN GROUP: 13 1.0000

a UniRef100_P68366 1.0000
confidence: 1. coverage: 21. num unique p_i tot indep spec share of spectrum id's: 3.53%
>Tubulin alpha-4A chain n=8 Tax=Eutheria RepID=TBA4A_HUMAN Length: 448aa

b UniRef100_A6NCC1 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Putative uncharacterized protein ENSP00000351411 n=1 Tax=Homo sapiens RepID=A6NCC1_HUMAN Length: 437aa

c UniRef100_A6NHL2 UniRef100_A6NHL2-2 0.0000
confidence: 0.0871 num unique p_i tot indep spectra: 0
>Tubulin alpha chain-like 3 n=1 Tax=Homo sapiens RepID=TBAL3_HUMAN Length: 446aa
>Isoform 2 of Tubulin alpha chain-like 3 n=1 Tax=Homo sapiens RepID=A6NHL2-2

d UniRef100_A6NHY4 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0

>Putative uncharacterized protein TUBA4A n=1 Tax=Homo sapiens RepID=A6NH4_HUMAN Length: 266aa

e UniRef100_A8JZY9 UniRef100_B3KPS3 UniRef100_B3KT06 UniRef100_P68363 UniRef100_Q71U36 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0 subsumed entries: 6
>cDNA FLJ78587 n=1 Tax=Homo sapiens RepID=A8JZY9_HUMAN Length: 451aa
>cDNA FLJ32131 fis, clone PEBLM2000267, highly similar to Tubulin alpha-ubiquitous chain n=1 Tax=Homo sapiens RepID=B3KPS3_HUMAN
>cDNA FLJ37398 fis, clone BRAMY2027467, highly similar to Tubulin alpha-ubiquitous chain n=1 Tax=Homo sapiens RepID=B3KT06_HUMAN
>Tubulin alpha-1B chain n=10 Tax=Tetrapoda RepID=TBA1B_HUMAN
>Tubulin alpha-1A chain n=7 Tax=Eutheria RepID=TBA1A_HUMAN

f UniRef100_B3KPW9 UniRef100_C9J2C0 UniRef100_Q7Z3M3 UniRef100_Q9NY65 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Tubulin, alpha 8, isoform CRA_b n=1 Tax=Homo sapiens RepID=B3KPW9_HUMAN Length: 383aa
>Putative uncharacterized protein TUBA8 n=1 Tax=Homo sapiens RepID=C9J2C0_HUMAN
>Putative uncharacterized protein DKFZp686L04275 (Fragment) n=1 Tax=Homo sapiens RepID=Q7Z3M3_HUMAN
>Tubulin alpha-8 chain n=1 Tax=Homo sapiens RepID=TBA8_HUMAN

g UniRef100_B4DDU2 UniRef100_Q9UQM3 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ60097, highly similar to Tubulin alpha-ubiquitous chain n=1 Tax=Homo sapiens RepID=B4DDU2_HUMAN Length: 298aa
>Alpha-tubulin (Fragment) n=1 Tax=Homo sapiens RepID=Q9UQM3_HUMAN

h UniRef100_B4DN58 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ53765, highly similar to Tubulin alpha chain n=1 Tax=Homo sapiens RepID=B4DN58_HUMAN Length: 182aa

i UniRef100_B4DQK4 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ53743, highly similar to Tubulin alpha-3 chain n=1 Tax=Homo sapiens RepID=B4DQK4_HUMAN Length: 385aa

j UniRef100_B7Z1K5 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ55956, highly similar to Tubulin alpha-6 chain n=1 Tax=Homo sapiens RepID=B7Z1K5_HUMAN Length: 519aa

k UniRef100_C9JDL2 UniRef100_C9K0S6 UniRef100_Q6QMJ5 0.0000
confidence: 0.3804 num unique p_i tot indep spectra: 0
>Putative uncharacterized protein TUBA4A n=1 Tax=Homo sapiens RepID=C9JDL2_HUMAN Length: 120aa
>Putative uncharacterized protein TUBA8 n=1 Tax=Homo sapiens RepID=C9K0S6_HUMAN
>Tubulin alpha-1 (Fragment) n=1 Tax=Homo sapiens RepID=Q6QMJ5_HUMAN

l UniRef100_C9JJQ8 UniRef100_C9JQ00 0.0000
confidence: 0.9991 num unique p_i tot indep spectra: 0
>Putative uncharacterized protein TUBA4A n=1 Tax=Homo sapiens RepID=C9JJQ8_HUMAN Length: 198aa
>Putative uncharacterized protein TUBA4A n=2 Tax=Homo sapiens RepID=C9JQ00_HUMAN

m UniRef100_D3DX41 0.0000
confidence: 0.1849 num unique p_i tot indep spectra: 0
>Alpha tubulin-like, isoform CRA_a n=1 Tax=Homo sapiens RepID=D3DX41_HUMAN Length: 157aa

n UniRef100_Q13748 UniRef100_Q13748-2 UniRef100_Q4R4C4 UniRef100_UPI000186DDE4 UniRef100_UPI000186E399 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Tubulin alpha-3C/D chain n=6 Tax=Euarchontoglires RepID=TBA3C_HUMAN Length: 450aa
>Isoform 2 of Tubulin alpha-3C/D chain n=1 Tax=Homo sapiens RepID=Q13748-2
>Testis cDNA clone: QtsA-11061, similar to human alpha-tubulin isotype H2-alpha (H2-ALPHA), n=1 Tax=Macaca fascicularis
RepID=Q4R4C4_MACFA
>tubulin alpha-3 chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186DDE4
>tubulin alpha-1 chain n=1 Tax=Pediculus humanus corporis RepID=UPI000186E399

o UniRef100_Q15670 0.0000
confidence: 0.3097 num unique p_i tot indep spectra: 0
>Alpha-tubulin isotype H2-alpha (Fragment) n=1 Tax=Homo sapiens RepID=Q15670_HUMAN Length: 98aa

p UniRef100_Q4R546 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Brain cDNA, clone: Qccc-19314, similar to human tubulin, alpha 3 (TUBA3), n=1 Tax=Macaca fascicularis RepID=Q Length: 251aa

q UniRef100_Q53GA7 UniRef100_Q9BQE3 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0 subsumed entries: 1

>Tubulin alpha 6 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GA7_HUMAN Length: 449aa
>Tubulin alpha-1C chain n=2 Tax=Homininae RepID=TBA1C_HUMAN

r UniRef100_Q6PEY2 0.0000
confidence: 1.0000 num unique p| tot indep spectra: 0
>Tubulin alpha-3E chain n=1 Tax=Homo sapiens RepID=TBA3E_HUMAN Length: 450aa

s UniRef100_Q8N532 UniRef100_UPI00015DFE80 0.0000
confidence: 1.0000 num unique p| tot indep spectra: 0
>TUBA1C protein n=1 Tax=Homo sapiens RepID=Q8N532_HUMAN Length: 325aa
>Tubulin alpha-1C chain (Tubulin alpha-6 chain) (Alpha-tubulin 6). n=1 Tax=Homo sapiens RepID=UPI00015DFE80

t UniRef100_Q8WU19 0.0000
confidence: 1.0000 num unique p| tot indep spectra: 0
>TUBA1B protein n=1 Tax=Homo sapiens RepID=Q8WU19_HUMAN Length: 335aa

u UniRef100_UPI000186DF3F 0.0000
confidence: 0.0781 num unique p| tot indep spectra: 0
>predicted protein n=1 Tax=Pediculus humanus corporis RepID=UPI000186DF3F Length: 452aa

v UniRef100_UPI000186EB2A 0.0000
confidence: 1.0000 num unique p| tot indep spectra: 0
>tubulin alpha-1 chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EB2A Length: 450aa

w UniRef100_UPI0001AE6ACC 0.0000
confidence: 1.0000 num unique p| tot indep spectra: 0
>UPI0001AE6ACC related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6ACC Length: 182aa

14 PROTEIN GROUP: 14 1.0000

a UniRef100_Q04695 1.0000
confidence: 1. coverage: 40. num unique p| tot indep spec share of spect subsumed entries: 10
>Keratin, type I cytoskeletal 17 n=1 Tax=Homo sapiens RepID=K1C17_HUMAN Length: 432aa

b UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000
confidence: 1. max coverage num unique p| tot indep spec share of spectrum id's: 3.82%
>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

c UniRef100_P35527 1.0000
confidence: 1. coverage: 14. num unique p| tot indep spec share of spectrum id's: 2.67%
>Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN Length: 623aa

d UniRef100_A1A4E9 UniRef100_A8K2H9 UniRef100_B3KRA2 UniRef100_B3KVF5 UniRef100_B4DL17 UniRef100_P13646
UniRef100_P13646-3 UniRef100_P35900 UniRef100_UPI0000E4FB59 UniRef100_UPI0000E4FB5A 0.0000
confidence: 0.9990 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
>cDNA FLJ33920 fis, clone CTONG2016904, highly similar to KERATIN, TYPE I CYTOSKELETAL 15 n=3 Tax=Homo sapiens
RepID=B3KRA2_HUMAN
>cDNA FLJ16494 fis, clone CTONG3004576, highly similar to Keratin, type I cytoskeletal 15 n=1 Tax=Homo sapiens RepID=B3KVF5_HUMAN
>cDNA FLJ52558, highly similar to Keratin, type I cytoskeletal 13 n=1 Tax=Homo sapiens RepID=B4DL17_HUMAN
>Keratin, type I cytoskeletal 13 n=1 Tax=Homo sapiens RepID=K1C13_HUMAN
>Isoform 3 of Keratin, type I cytoskeletal 13 n=1 Tax=Homo sapiens RepID=P13646-3
>Keratin, type I cytoskeletal 20 n=1 Tax=Homo sapiens RepID=K1C20_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

e UniRef100_A8MW45 0.0000
confidence: 1.0000 num unique p| tot indep spectra: 0
>Putative uncharacterized protein ENSP00000382160 n=1 Tax=Homo sapiens RepID=A8MW45_HUMAN Length: 441aa

f UniRef100_B4DE59 0.0000
confidence: 1.0000 num unique p| tot indep spectra: 0
>cDNA FLJ60424, highly similar to Junction plakoglobin n=1 Tax=Homo sapiens RepID=B4DE59_HUMAN Length: 563aa

g UniRef100_B4DJM5 UniRef100_UPI0001AE665F 0.0000

confidence: 1.0000 num unique p_i tot indep spectra: 0
 >cDNA FLJ61294, highly similar to Keratin, type I cytoskeletal 17 n=1 Tax=Homo sapiens RepID=B4DJM5_HUMAN Length: 177aa
 >UPI0001AE665F related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE665F

h UniRef100_B4DWU0 UniRef100_B4E204 UniRef100_B4E2J5 UniRef100_Q99456 0.0000
 confidence: 0.9995 num unique p_i tot indep spectra: 0
 >cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 n=1 Tax=Homo sapiens RepID=B4DWU0_HUMAN Length: 135aa
 >cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 n=1 Tax=Homo sapiens RepID=B4E204_HUMAN
 >cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 n=1 Tax=Homo sapiens RepID=B4E2J5_HUMAN
 >Keratin, type I cytoskeletal 12 n=1 Tax=Homo sapiens RepID=K1C12_HUMAN

i UniRef100_B4E2P9 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >cDNA FLJ56708, highly similar to Keratin, type I cytoskeletal 17 n=1 Tax=Homo sapiens RepID=B4E2P9_HUMAN Length: 172aa

j UniRef100_C9JH30 UniRef100_UPI00001AECF3 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Putative uncharacterized protein ENSP00000319235 n=1 Tax=Homo sapiens RepID=C9JH30_HUMAN Length: 433aa
 >UPI00001AECF3 related cluster n=1 Tax=Homo sapiens RepID=UPI00001AECF3

k UniRef100_C9JM50 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Putative uncharacterized protein KRT19 n=1 Tax=Homo sapiens RepID=C9JM50_HUMAN Length: 196aa

l UniRef100_C9JT19 UniRef100_Q6ZPD6 UniRef100_Q7Z3Y9 UniRef100_UPI0000E59F67 0.0000
 confidence: 0.9976 num unique p_i tot indep spectra: 0
 >Putative uncharacterized protein KRT25 n=1 Tax=Homo sapiens RepID=C9JT19_HUMAN Length: 380aa
 >cDNA FLJ25992 fis, clone DMC03508 n=1 Tax=Homo sapiens RepID=Q6ZPD6_HUMAN
 >Keratin, type I cytoskeletal 26 n=1 Tax=Homo sapiens RepID=K1C26_HUMAN
 >keratin 25 n=1 Tax=Homo sapiens RepID=UPI0000E59F67

m UniRef100_P02533 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0 subsumed entries: 6
 >Keratin, type I cytoskeletal 14 n=1 Tax=Homo sapiens RepID=K1C14_HUMAN Length: 472aa

n UniRef100_P08727 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Keratin, type I cytoskeletal 19 n=1 Tax=Homo sapiens RepID=K1C19_HUMAN Length: 400aa

o UniRef100_P08779 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Keratin, type I cytoskeletal 16 n=1 Tax=Homo sapiens RepID=K1C16_HUMAN Length: 473aa

p UniRef100_P19012 UniRef100_UPI000013CE0E UniRef100_UPI0001AE6659 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Keratin, type I cytoskeletal 15 n=1 Tax=Homo sapiens RepID=K1C15_HUMAN Length: 456aa
 >Keratin, type I cytoskeletal 15 (Cytokeratin-15) (CK-15) (Keratin-15) (K15). n=1 Tax=Homo sapiens RepID=UPI000013CE0E
 >Keratin, type I cytoskeletal 13 (Cytokeratin-13) (CK-13) (Keratin-13) (K13). n=1 Tax=Homo sapiens RepID=UPI0001AE6659

q UniRef100_Q13092 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Epidermal type I keratin (Fragment) n=1 Tax=Homo sapiens RepID=Q13092_HUMAN Length: 157aa

r UniRef100_Q14666 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Radiated keratinocyte mRNA 266 (keratin-related protein) (Fragment) n=1 Tax=Homo sapiens RepID=Q14666_HUI Length: 266aa

s UniRef100_Q7Z3Y7 UniRef100_Q7Z3Y8 UniRef100_Q7Z3Z0 0.0000
 confidence: 1.0000 num unique p_i 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

t UniRef100_Q8N1A0 0.0000
 confidence: 0.1162 num unique p_i tot indep spectra: 0
 >Keratin-like protein KRT222 n=2 Tax=Homo sapiens RepID=KT222_HUMAN Length: 295aa

u UniRef100_UPI00015DFB49 0.0000
confidence: 0.0012 num unique p_i tot indep spectra: 0
>Keratin, type I cytoskeletal 15 (Cytokeratin-15) (CK-15) (Keratin-15) (K15). n=1 Tax=Homo sapiens RepID=UPI00015DFB49 Length: 178aa

15 PROTEIN GROUP: 15 1.0000

a UniRef100_UPI0000111654 UniRef100_UPI00017BDB3D UniRef100_UPI00017BDB42 0.9999
confidence: 1. max coverage num unique p_i tot indep spec share of spectrum id's: 0.66%
>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

b UniRef100_UPI0000112158 0.0000
confidence: 0.1590 num unique p_i tot indep spectra: 0
>monoclonal antibody light chain n=1 Tax=Homo sapiens RepID=UPI0000112158 Length: 217aa

16 UniRef100_A2AB30 UniRef100_B0V2L1 UniRef100_B0V2L2 UniRef100_B4DP52 UniRef100_B4DX78 UniRef100_O00148
UniRef100_Q13838 UniRef100_Q13838-2 UniRef100_Q4R5P7 UniRef100_Q5STA0 UniRef100_Q69YT6 UniRef100_UPI000186D19E
0.9908
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.17%
>HLA-B associated transcript 1 (Fragment) n=11 Tax=Eutheria RepID=A2AB30_HUMAN Length: 186aa
>HLA-B associated transcript 1 (Fragment) n=2 Tax=Homo sapiens RepID=B0V2L1_HUMAN
>HLA-B associated transcript 1 (Fragment) n=2 Tax=Homo sapiens RepID=B0V2L2_HUMAN
>HCG2005638, isoform CRA_c n=1 Tax=Homo sapiens RepID=B4DP52_HUMAN
>cDNA FLJ55484, highly similar to ATP-dependent RNA helicase DDX39 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DX78_HUMAN
>ATP-dependent RNA helicase DDX39 n=2 Tax=Homo sapiens RepID=DDX39_HUMAN
>Spliceosome RNA helicase BAT1 n=7 Tax=Eutheria RepID=UAP56_HUMAN
>Isoform 2 of Spliceosome RNA helicase BAT1 n=1 Tax=Homo sapiens RepID=Q13838-2
>Brain cDNA, clone: QccE-11261, similar to human HLA-B associated transcript 1 (BAT1), transcript variant1, n=1 Tax=Macaca fascicularis
RepID=Q4R5P7_MACFA
>HLA-B associated transcript 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5STA0_HUMAN
>Putative uncharacterized protein DKFZp547B159 (Fragment) n=1 Tax=Homo sapiens RepID=Q69YT6_HUMAN
>ATP-dependent RNA helicase WM6, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D19E

17 UniRef100_B3KY95 UniRef100_B7Z254 UniRef100_B7Z4M8 UniRef100_Q15084 UniRef100_Q15084-2 0.9908
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.17%
>cDNA FLJ16143 fis, clone BRAMY2038516, highly similar to Protein disulfide-isomerase A6 (EC 5.3.4.1) n=1 Tax=H Length: 488aa
>cDNA FLJ58502, highly similar to Protein disulfide-isomerase A6 (EC 5.3.4.1) n=1 Tax=Homo sapiens RepID=B7Z254_HUMAN
>cDNA FLJ58023, highly similar to Protein disulfide-isomerase A6 (EC 5.3.4.1) n=1 Tax=Homo sapiens RepID=B7Z4M8_HUMAN
>Protein disulfide-isomerase A6 n=2 Tax=Homo sapiens RepID=PDIA6_HUMAN
>Isoform 2 of Protein disulfide-isomerase A6 n=2 Tax=Homo sapiens RepID=Q15084-2

18 UniRef100_B4DL86 UniRef100_B4E2U0 UniRef100_P52209 0.9908
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.17%
>6-phosphogluconate dehydrogenase, decarboxylating n=1 Tax=Homo sapiens RepID=B4DL86_HUMAN Length: 429aa
>6-phosphogluconate dehydrogenase, decarboxylating n=1 Tax=Homo sapiens RepID=B4E2U0_HUMAN
>6-phosphogluconate dehydrogenase, decarboxylating n=3 Tax=Homo sapiens RepID=6PGD_HUMAN

19 PROTEIN GROUP: 16 0.9908

a UniRef100_UPI000173A694 0.9811
confidence: 0. coverage: 11. num unique p_i tot indep spec share of spectrum id's: 0.17%
>UPI000173A694 related cluster n=1 Tax=Homo sapiens RepID=UPI000173A694 Length: 123aa

b UniRef100_P30101 UniRef100_UPI0000408869 UniRef100_UPI0000E59C11 0.0000
confidence: 0.3804 num unique p_i tot indep spectra: 0
>Protein disulfide-isomerase A3 n=2 Tax=Hominidae RepID=PDIA3_HUMAN Length: 505aa
>UPI0000408869 related cluster n=1 Tax=Homo sapiens RepID=UPI0000408869
>UPI0000E59C11 related cluster n=1 Tax=Homo sapiens RepID=UPI0000E59C11

20 UniRef100_A8K2Y2 UniRef100_B2R5N2 UniRef100_P41091 UniRef100_Q53HK3 UniRef100_UPI000059DADF 0.9898
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.17%
>cDNA FLJ78120, highly similar to Homo sapiens eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa Length: 472aa
>cDNA, FLJ92541, highly similar to Homo sapiens eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa (EIF2S3), mRNA n=1
Tax=Homo sapiens RepID=B2R5N2_HUMAN
>Eukaryotic translation initiation factor 2 subunit 3 n=1 Tax=Homo sapiens RepID=IF2G_HUMAN
>Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53HK3_HUMAN
>UPI000059DADF related cluster n=1 Tax=Homo sapiens RepID=UPI000059DADF

21 UniRef100_A8K7F6 UniRef100_B4DNH2 UniRef100_P60842 UniRef100_Q14240 UniRef100_Q96B07 UniRef100_Q9NZE6
UniRef100_UPI000186D356 0.9880
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.17%

>cDNA FLJ78244, highly similar to Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA Length: 406aa
 >cDNA FLJ58596, highly similar to Eukaryotic initiation factor 4A-I (EC 3.6.1.-) n=3 Tax=Euarchoptoglyres RepID=B4DNH2_HUMAN
 >Eukaryotic initiation factor 4A-I n=8 Tax=Eutheria RepID=IF4A1_HUMAN
 >Eukaryotic initiation factor 4A-II n=8 Tax=Eutheria RepID=IF4A2_HUMAN
 >EIF4A2 protein n=5 Tax=Eutheria RepID=Q96B07_HUMAN
 >BM-010 n=1 Tax=Homo sapiens RepID=Q9NZE6_HUMAN
 >eukaryotic initiation factor 4A-II, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D356

22 UniRef100_A8K259 UniRef100_B4DN87 UniRef100_P50454 0.9835
 confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.34%
 >cDNA FLJ78501, highly similar to Homo sapiens serpin peptidase inhibitor, clade H (heat shock protein 47), membe Length: 418aa
 >cDNA FLJ52569, highly similar to Collagen-binding protein 2 n=1 Tax=Homo sapiens RepID=B4DN87_HUMAN
 >Serpin H1 n=1 Tax=Homo sapiens RepID=SERPH_HUMAN

23 UniRef100_Q9N0W4 UniRef100_Q9N0W6 0.9519
 confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.51%
 >Anti-human A33 heavy chain domain (Fragment) n=1 Tax=Orctolagus cuniculus RepID=Q9N0W4_RABIT Length: 124aa
 >Anti-human A33 heavy chain domain (Fragment) n=1 Tax=Orctolagus cuniculus RepID=Q9N0W6_RABIT

24 UniRef100_UPI000186D2C2 0.9510
 confidence: 0. coverage: 5.4 num unique p_i tot indep spec share of spectrum id's: 0.27%
 >conserved hypothetical protein n=1 Tax=Pediculus humanus corporis RepID=UPI000186D2C2 Length: 314aa

NFIC mass spec results - upper band (~60kDa):

19 entries (10 single hits) retrieved from
 /home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_NFIC-2-sequest.prot.xml

* corresponds to peptide is_nondegenerate_evidence flag

1 PROTEIN GROUP: 1 1.0000

a UniRef100_A1XP52 UniRef100_Q4R7F6 0.0000
 confidence: 0.9985 num unique p_i tot indep spectra: 0
 >Catecholamine-regulated protein 40 n=1 Tax=Homo sapiens RepID=A1XP52_HUMAN Length: 350aa
 >Testis cDNA, clone: QtsA-15441, similar to human heat shock 70kDa protein 9B (mortalin-2) (HSPA9B),nuclear gene encoding mitochondrial protein, n=1 Tax=Macaca fascicularis RepID=Q4R7F6_MACFA

b UniRef100_B7Z1V7 0.0000
 confidence: 1.0000 num unique p_i 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_i 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_i tot indep spectra: 0 subsumed entries: 4
 >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_D6RJI2 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Putative uncharacterized protein HSPA9 n=2 Tax=Homo sapiens RepID=D6RJI2_HUMAN Length: 95aa

2 PROTEIN GROUP: 2 1.0000

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

b UniRef100_A8K3W9 UniRef100_Q58FF7 UniRef100_Q5T9W5 UniRef100_Q9H6X9 UniRef100_UPI000059D8E5 0.0000
 confidence: 0.4569 num unique p_i tot indep spectra: 0
 >cDNA FLJ77842 n=1 Tax=Homo sapiens RepID=A8K3W9_HUMAN Length: 362aa
 >Putative heat shock protein HSP 90-beta-3 n=1 Tax=Homo sapiens RepID=H90B3_HUMAN
 >Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) n=2 Tax=Homo sapiens RepID=Q5T9W5_HUMAN

>cDNA: FLJ21717 fis, clone COL10322 n=1 Tax=Homo sapiens RepID=Q9H6X9_HUMAN
>UPI000059D8E5 related cluster n=1 Tax=Homo sapiens RepID=UPI000059D8E5

- c UniRef100_O14942 0.0000
confidence: 0.4930 num unique p_i tot indep spectra: 0
>Heat shock protein beta (Fragment) n=1 Tax=Homo sapiens RepID=O14942_HUMAN Length: 130aa
- d UniRef100_O75322 UniRef100_Q86U12 0.0000
confidence: 0.2180 num unique p_i tot indep spectra: 0
>Hsp89-alpha-delta-N n=2 Tax=Homo sapiens RepID=O75322_HUMAN Length: 539aa
>Full-length cDNA clone CS0CAP007YF18 of Thymus of Homo sapiens (human) n=1 Tax=Homo sapiens RepID=Q86U12_HUMAN
- e UniRef100_P07900 UniRef100_Q2VPJ6 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Heat shock protein HSP 90-alpha n=2 Tax=Homo sapiens RepID=HS90A_HUMAN Length: 732aa
>HSP90AA1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q2VPJ6_HUMAN
- f UniRef100_Q14568 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>Putative heat shock protein HSP 90-alpha A2 n=1 Tax=Homo sapiens RepID=HS902_HUMAN Length: 343aa
- g UniRef100_Q58FF8 UniRef100_Q6PK50 UniRef100_Q8TBA7 0.0000
confidence: 0.9998 num unique p_i tot indep spectra: 0
>Putative heat shock protein HSP 90-beta 2 n=1 Tax=Homo sapiens RepID=H90B2_HUMAN Length: 381aa
>HSP90AB1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6PK50_HUMAN
>HSP90AA1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8TBA7_HUMAN
- h UniRef100_Q58FG1 0.0000
confidence: 0.2009 num unique p_i tot indep spectra: 0
>Putative heat shock protein HSP 90-alpha A4 n=1 Tax=Homo sapiens RepID=HS904_HUMAN Length: 418aa
- i UniRef100_Q86SX1 0.0000
confidence: 0.9999 num unique p_i tot indep spectra: 0
>Full-length cDNA 5-PRIME end of clone CSODN005YI08 of Adult brain of Homo sapiens (human) (Fragment) n=1 Ta Length: 262aa
- 3 PROTEIN GROUP: 3 1.0000
- a UniRef100_B4DR68 UniRef100_Q12931 UniRef100_Q53FS6 UniRef100_Q53G55 UniRef100_Q9BV61 0.0000
confidence: 1.0000 num unique p_i 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
- b UniRef100_Q59EK6 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>TNF receptor-associated protein 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59EK6_HUMAN Length: 703aa
- c UniRef100_Q5CAQ4 0.0000
confidence: 0.9995 num unique p_i tot indep spectra: 0
>TNF receptor-associated protein 1 n=1 Tax=Homo sapiens RepID=Q5CAQ4_HUMAN Length: 495aa
- d UniRef100_Q8N9Z3 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA FLJ36025 fis, clone TESTI2016701, highly similar to TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIAT Length: 579aa
- e UniRef100_UPI000186D735 0.0000
confidence: 0.9990 num unique p_i tot indep spectra: 0
>heat shock protein 75 kDa, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D735 Length: 689aa
- 4 PROTEIN GROUP: 4 1.0000
- a UniRef100_B4DXX7 UniRef100_B4E132 UniRef100_B4E3E8 UniRef100_B5BTY4 UniRef100_O00571 UniRef100_O15523
UniRef100_Q5S4N1 1.0000
confidence: 1. max coverage num unique p_i tot indep spec share of spect subsumed entries: 1
>cDNA FLJ50912, highly similar to ATP-dependent RNA helicase DDX3Y (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID= Length: 657aa
>cDNA FLJ53122, highly similar to ATP-dependent RNA helicase DDX3Y (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4E132_HUMAN

>cDNA FLJ60399, highly similar to ATP-dependent RNA helicase DDX3X (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4E3E8_HUMAN
>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
>ATP-dependent RNA helicase DDX3Y n=1 Tax=Homo sapiens RepID=DDX3Y_HUMAN
>Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens RepID=Q5S4N1_HUMAN

b UniRef100_B4DLU5 UniRef100_B4E010 UniRef100_UPI0001AE6F7E 0.0000
confidence: 0.0564 num unique p1 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
>cDNA FLJ53946, highly similar to ATP-dependent RNA helicase DDX3Y (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4E010_HUMAN
>UPI0001AE6F7E related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6F7E

c UniRef100_Q4R9A4 0.0000
confidence: 0.9977 num unique p1 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

5 PROTEIN GROUP: 5 1.0000

a UniRef100_C5IWV5 UniRef100_P00761 1.0000
confidence: 1. max coverage num unique p1 tot indep spec share of spectrum id's: 14.11%
>Trypsinogen n=1 Tax=Sus scrofa RepID=C5IWV5_PIG Length: 246aa
>Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG

b UniRef100_P06871 UniRef100_UPI00004A5B07 UniRef100_UPI00005A2FD6 UniRef100_UPI00005A2FD7 0.9792
confidence: 1. max coverage num unique p1 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_Q86W20 0.0000
confidence: 0.9166 num unique p1 tot indep spectra: 0
>PRSS3 protein n=1 Tax=Homo sapiens RepID=A1A508_HUMAN Length: 247aa
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q86W20_HUMAN

d UniRef100_A4UWM7 UniRef100_B9WPP8 UniRef100_C1KRJ0 UniRef100_O42158 UniRef100_O42159 UniRef100_O42160
UniRef100_O42608 UniRef100_Q7T1R8 UniRef100_UPI0000D92B0D UniRef100_UPI0000F2E411 0.0000
confidence: 0.1960 num unique p1 tot indep spectra: 0
>Trypsinogen n=1 Tax=Oryzias latipes RepID=A4UWM7_ORYLA Length: 242aa
>Trypsin (Fragment) n=1 Tax=Thunnus thynnus RepID=B9WPP8_THUTH
>Trypsin (Fragment) n=1 Tax=Petenia splendida RepID=C1KRJ0_9CICH
>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_A6XMV8 UniRef100_A6XMV9 UniRef100_P07477 UniRef100_P07478 UniRef100_Q3SY19 UniRef100_Q3SY20
UniRef100_Q45KI0 UniRef100_Q53ZX7 UniRef100_Q53ZX8 UniRef100_Q53ZX9 UniRef100_Q6PK75 UniRef100_Q7Z5F3
UniRef100_Q86W17 UniRef100_Q8NHM4 UniRef100_UPI0000D9A9C8 UniRef100_UPI0001795EE3 UniRef100_UPI0001AE7178
UniRef100_UPI0001AE7179 UniRef100_UPI0001B79292 UniRef100_UPI0001B79293 0.0000
confidence: 0.0058 num unique p1 tot indep spectra: 0
>Protease serine 2 preproprotein n=1 Tax=Homo sapiens RepID=A6XMV8_HUMAN Length: 246aa
>Protease serine 2 preproprotein n=1 Tax=Homo sapiens RepID=A6XMV9_HUMAN
>Alpha-trypsin chain 2 n=1 Tax=Homo sapiens RepID=TRY1_HUMAN
>Trypsin-2 n=2 Tax=Homo sapiens RepID=TRY2_HUMAN
>PRSS1 protein n=1 Tax=Homo sapiens RepID=Q3SY19_HUMAN
>Protease, serine, 2 (Trypsin 2) n=1 Tax=Homo sapiens RepID=Q3SY20_HUMAN
>Trypsin I (Fragment) n=1 Tax=Homo sapiens RepID=Q45KI0_HUMAN
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q53ZX7_HUMAN
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q53ZX8_HUMAN
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q53ZX9_HUMAN
>PRSS2 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q6PK75_HUMAN
>Protease serine 2 isoform B n=1 Tax=Homo sapiens RepID=Q7Z5F3_HUMAN
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q86W17_HUMAN
>Putative trypsin-6 n=1 Tax=Homo sapiens RepID=TRY6_HUMAN
>PREDICTED: protease, serine, 2 (trypsin 2) isoform 1 n=1 Tax=Macaca mulatta RepID=UPI0000D9A9C8
>PREDICTED: similar to anionic trypsinogen n=1 Tax=Equus caballus RepID=UPI0001795EE3
>trypsinogen C (TRY6) on chromosome 7 n=1 Tax=Homo sapiens RepID=UPI0001AE7178
>Trypsin-2 precursor (EC 3.4.21.4) (Trypsin II) (Anionic trypsinogen) (Serine protease 2). n=1 Tax=Homo sapiens RepID=UPI0001AE7179
>UPI0001B79292 related cluster n=1 Tax=Homo sapiens RepID=UPI0001B79292

>UPI0001B79293 related cluster n=1 Tax=Homo sapiens RepID=UPI0001B79293

f UniRef100_A8CED1 UniRef100_A8CED3 UniRef100_B1AN99 UniRef100_P35030 UniRef100_P35030-2 UniRef100_P35030-3
UniRef100_Q6ISJ4 UniRef100_Q7Z5F4 UniRef100_Q8N2U3 UniRef100_UPI000021129C UniRef100_UPI0000E21E68 UniRef100_UPI0001AE6E33
0
confidence: 1.0000 num unique p| tot indep spectra: 0 subsumed entries: 2
>Protease, serine, 3 (Mesotrypsin), isoform CRA_d n=1 Tax=Homo sapiens RepID=A8CED1_HUMAN Length: 304aa
>Trypsinogen 5 n=1 Tax=Homo sapiens RepID=A8CED3_HUMAN
>Protease, serine, 3 (Fragment) n=1 Tax=Homo sapiens RepID=B1AN99_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
>Mesotrypsinogen n=1 Tax=Homo sapiens RepID=Q6ISJ4_HUMAN
>Protease serine 4 isoform B n=1 Tax=Homo sapiens RepID=Q7Z5F4_HUMAN
>PRSS3 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8N2U3_HUMAN
>Trypsin-3 precursor (EC 3.4.21.4) (Trypsin III) (Brain trypsinogen) (Mesotrypsinogen) (Trypsin IV) (Serine protease 3) (Serine protease 4).
n=1 Tax=Homo sapiens RepID=UPI000021129C
>PREDICTED: similar to trypsinogen IV b-form n=1 Tax=Pan troglodytes RepID=UPI0000E21E68
>UPI0001AE6E33 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6E33

g UniRef100_B5AEC7 UniRef100_D2D388 UniRef100_P07146 UniRef100_P12788 UniRef100_P19799 UniRef100_Q0PG34
UniRef100_Q6R670 UniRef100_Q6R671 UniRef100_UPI00005E8630 UniRef100_UPI0000D92B15 UniRef100_UPI000194B97D
UniRef100_UPI000194B9B7 UniRef100_UPI0001AE7177 0.0000
confidence: 0.3122 num unique p| tot indep spectra: 0
>Trypsin (Fragment) n=2 Tax=Rhinichthys RepID=B5AEC7_9TELE Length: 74aa
>Trypsinogen n=1 Tax=Culter alburnus RepID=D2D388_9TELE
>Anionic trypsin-2 n=2 Tax=Mus musculus RepID=TRY2_MOUSE
>Trypsin-4 n=1 Tax=Rattus norvegicus RepID=TRY4_RAT
>Trypsin n=1 Tax=Xenopus laevis RepID=TRY1_XENLA
>Trypsin n=1 Tax=Spinibarbus sinensis RepID=Q0PG34_9TELE
>Trypsin n=1 Tax=Oreochromis aureus RepID=Q6R670_OREAU
>Trypsin n=1 Tax=Oreochromis niloticus RepID=Q6R671_ORENI
>PREDICTED: similar to Anionic trypsin n=1 Tax=Monodelphis domestica RepID=UPI00005E8630
>PREDICTED: similar to pancreatic anionic trypsinogen n=1 Tax=Monodelphis domestica RepID=UPI0000D92B15
>PREDICTED: similar to Anionic trypsin n=1 Tax=Taeniopygia guttata RepID=UPI000194B97D
>PREDICTED: similar to Anionic trypsin n=1 Tax=Taeniopygia guttata RepID=UPI000194B9B7
>UPI0001AE7177 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7177

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

i UniRef100_Q7M754 0.0000
confidence: 0.3239 num unique p| tot indep spectra: 0
>Try10-like trypsinogen n=1 Tax=Mus musculus RepID=Q7M754_MOUSE Length: 246aa

j UniRef100_Q7TT42 UniRef100_UPI00001F381C 0.0000
confidence: 0.0007 num unique p| tot indep spectra: 0
>Trypsinogen 5 n=1 Tax=Mus musculus RepID=Q7TT42_MOUSE Length: 246aa
>trypsinogen 4 n=1 Tax=Mus musculus RepID=UPI00001F381C

k UniRef100_Q86W18 UniRef100_UPI00006D1D23 UniRef100_UPI0000D9A9BD 0.0000
confidence: 0.0009 num unique p| tot indep spectra: 0
>Protease serine 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q86W18_HUMAN Length: 84aa
>PREDICTED: protease, serine, 2 (trypsin 2) isoform 2 n=1 Tax=Macaca mulatta RepID=UPI00006D1D23
>PREDICTED: protease, serine, 2 (trypsin 2) isoform 1 n=1 Tax=Macaca mulatta RepID=UPI0000D9A9BD

l UniRef100_UPI00005A2FD5 0.0000
confidence: 0.9994 num unique p| tot indep spectra: 0
>PREDICTED: similar to trypsinogen 7 isoform 4 n=1 Tax=Canis lupus familiaris RepID=UPI00005A2FD5 Length: 138aa

6 PROTEIN GROUP: 6 1.0000

a UniRef100_C9JSM6 UniRef100_C9JSM7 UniRef100_O00712 UniRef100_Q5VW26 UniRef100_Q5VW27 UniRef100_Q5VW29
UniRef100_Q5VW30 UniRef100_Q6ZNF9 1.0000
confidence: : max coverage num unique | tot indep spe share of spe subsumed entries: 1
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=C9JSM6_HUMAN Length: 494aa
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=C9JSM7_HUMAN
>Nuclear factor 1 B-type n=2 Tax=Homo sapiens RepID=NFIB_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q5VW26_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q5VW27_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q5VW29_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q5VW30_HUMAN

>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q6ZNF9_HUMAN

b UniRef100_B1AKN5 UniRef100_B1AKN6 UniRef100_B1AKN7 UniRef100_B1AKN8 UniRef100_B4DHW2 UniRef100_B4DM25 UniRef100_B4DRN9 UniRef100_B4DS53 UniRef100_B4DS74 UniRef100_B5MDB4 UniRef100_B7Z4T6 UniRef100_B7Z4U5 UniRef100_C9JE99 UniRef100_C9JSM5 UniRef100_C9JWJ8 UniRef100_D2DXM9 UniRef100_P08651 UniRef100_P08651-2 UniRef100_P08651-3 UniRef100_P08651-4 UniRef100_P08651-5 UniRef100_Q12857 UniRef100_Q12857-2 UniRef100_Q13051 UniRef100_Q14938 UniRef100_Q14938-2 UniRef100_Q14938-3 UniRef100_Q14938-5 UniRef100_Q5W0Y9 UniRef100_Q6FI30 UniRef100_Q7Z3K7 UniRef100_UPI0001AE789E 0.0000
confidence: 0.4663 num unique | tot indep spectra: 0
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B1AKN5_HUMAN Length: 487aa
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B1AKN6_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B1AKN7_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B1AKN8_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DHW2_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DM25_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DRN9_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DS53_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B4DS74_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B5MDB4_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B7Z4T6_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=B7Z4U5_HUMAN
>Putative uncharacterized protein NFIA n=1 Tax=Homo sapiens RepID=C9JE99_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=C9JSM5_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=C9JWJ8_HUMAN
>Nuclear factor 1 n=3 Tax=Catarrhini RepID=D2DXM9_HUMAN
>Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=NFIC_HUMAN
>Isoform 1 of Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=P08651-2
>Isoform 2 of Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=P08651-3
>Isoform 3 of Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=P08651-4
>Isoform 5 of Nuclear factor 1 C-type n=1 Tax=Homo sapiens RepID=P08651-5
>Nuclear factor 1 A-type n=2 Tax=Homo sapiens RepID=NFIA_HUMAN
>Isoform 2 of Nuclear factor 1 A-type n=1 Tax=Homo sapiens RepID=Q12857-2
>Nuclear factor I (Fragment) n=1 Tax=Homo sapiens RepID=Q13051_HUMAN
>Nuclear factor 1 X-type n=1 Tax=Homo sapiens RepID=NFIX_HUMAN
>Isoform 2 of Nuclear factor 1 X-type n=1 Tax=Homo sapiens RepID=Q14938-2
>Isoform 3 of Nuclear factor 1 X-type n=1 Tax=Homo sapiens RepID=Q14938-3
>Isoform 5 of Nuclear factor 1 X-type n=1 Tax=Homo sapiens RepID=Q14938-5
>Nuclear factor I/B n=1 Tax=Homo sapiens RepID=Q5W0Y9_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q6FI30_HUMAN
>Nuclear factor 1 n=1 Tax=Homo sapiens RepID=Q7Z3K7_HUMAN
>UPI0001AE789E related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE789E

7 PROTEIN GROUP: 7 1.0000

a UniRef100_P02769 1.0000
confidence: 1. coverage: 16. num unique | tot indep spec share of spect subsumed entries: 1
>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa

b UniRef100_A6NBZ8 UniRef100_A8K9P0 UniRef100_B2RBS8 UniRef100_B4DPR2 UniRef100_P02768 UniRef100_UPI0001AE74F7 UniRef100_UPI0001D3B4DF 0.0000
confidence: 1.0000 num unique | tot indep spectra: 0
>Putative uncharacterized protein ALB n=1 Tax=Homo sapiens RepID=A6NBZ8_HUMAN Length: 627aa
>cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA n=1 Tax=Homo sapiens RepID=A8K9P0_HUMAN
>cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA n=1 Tax=Homo sapiens RepID=B2RBS8_HUMAN
>cDNA 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_B4DPP6 0.0000
confidence: 1.0000 num unique | tot indep spectra: 0
>cDNA FLJ54371, highly similar to Serum albumin n=1 Tax=Homo sapiens RepID=B4DPP6_HUMAN Length: 618aa

d UniRef100_B7WNR0 UniRef100_C9JKR2 UniRef100_D6RHD5 UniRef100_P02768-2 UniRef100_Q8IUK7 UniRef100_UPI000045722A 0
confidence: 1.0000 num unique | 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
>ALB protein n=1 Tax=Homo sapiens RepID=Q8IUK7_HUMAN
>Serum albumin precursor. n=1 Tax=Homo sapiens RepID=UPI000045722A

e UniRef100_Q56G89 0.0000
confidence: 1.0000 num unique | tot indep spectra: 0

>Serum albumin n=1 Tax=Homo sapiens RepID=Q56G89_HUMAN Length: 609aa

f UniRef100_UPI0001610EBC 0.0000
confidence: 0.3827 num unique p_i tot indep spectra: 0
>UPI0001610EBC related cluster n=1 Tax=Homo sapiens RepID=UPI0001610EBC Length: 197aa

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

8 PROTEIN GROUP: 8 1.0000

a UniRef100_P04264 1.0000
confidence: 1. coverage: 14. num unique p_i tot indep spec share of spect subsumed entries: 3
>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN Length: 644aa

b UniRef100_P04259 0.0000
confidence: 0.1663 num unique p_i tot indep spectra: 0
>Keratin, type II cytoskeletal 6B n=1 Tax=Homo sapiens RepID=K2C6B_HUMAN Length: 564aa

c UniRef100_P35908 0.0000
confidence: 0.9991 num unique p_i tot indep spectra: 0
>Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E_HUMAN Length: 639aa

d UniRef100_Q0IIN1 UniRef100_UPI00001D797A 0.0000
confidence: 0.1612 num unique p_i 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

9 PROTEIN GROUP: 9 1.0000

a UniRef100_P08107 1.0000
confidence: 1. coverage: 23. num unique p_i tot indep spec share of spect subsumed entries: 14
>Heat shock 70 kDa protein 1A/1B n=3 Tax=Hominidae RepID=HSP71_HUMAN Length: 641aa

b UniRef100_P11021 1.0000
confidence: 1. coverage: 19. num unique p_i tot indep spec share of spect subsumed entries: 2
>78 kDa glucose-regulated protein n=1 Tax=Homo sapiens RepID=GRP78_HUMAN Length: 654aa

c UniRef100_UPI000186E8AE 0.9914
confidence: 1. coverage: 3.1. num unique p_i tot indep spec share of spectrum id's: 1.08%
>Heat shock cognate 71 kDa protein, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E8AE Length: 635aa

d UniRef100_A4D111 0.0000
confidence: 0.9997 num unique p_i tot indep spectra: 0
>Similar to Chain , Heat-Shock Cognate 70kd Protein (44kd Atpase N-Terminal) (E.C.3.6.1.3) Mutant With Asp 206 R Length: 231aa

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

f UniRef100_B2R6X5 UniRef100_B3KSM6 UniRef100_P17066 UniRef100_Q53FC7 0.0000
confidence: 1.0000 num unique p_i 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

g UniRef100_B2RCQ9 UniRef100_B4DI54 UniRef100_P34931 UniRef100_Q53FA3 UniRef100_UPI0001AE7148 UniRef100_UPI0001AE71DD
UniRef100_UPI0001AE71EA 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>cDNA, FLJ96225, highly similar to Homo sapiens heat shock 70kDa protein 1-like (HSPA1L), mRNA n=1 Tax=Homo Length: 641aa
>cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L n=1 Tax=Homo sapiens RepID=B4DI54_HUMAN
>Heat shock 70 kDa protein 1-like n=1 Tax=Homo sapiens RepID=HS71L_HUMAN
>Heat shock 70kDa protein 1-like (Fragment) n=1 Tax=Homo sapiens RepID=Q53FA3_HUMAN
>UPI0001AE7148 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7148
>UPI0001AE71DD related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE71DD
>UPI0001AE71EA related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE71EA

h UniRef100_B3KTT5 UniRef100_Q5SP16 0.0000
confidence: 1.0000 num unique p i 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

i UniRef100_B3KTV0 0.0000
confidence: 1.0000 num unique p i tot indep spectra: 0
>cDNA FLJ38781 fis, clone LIVER2000216, highly similar to HEAT SHOCK COGNATE 71 kDa PROTEIN n=1 Tax=Homo sapiens RepID=B3KTV0_HUMAN Length: 621aa

j UniRef100_B3KUS2 0.0000
confidence: 1.0000 num unique p i tot indep spectra: 0
>cDNA FLJ40505 fis, clone TESTI2045562, highly similar to HEAT SHOCK-RELATED 70 kDa PROTEIN 2 n=1 Tax=Homo sapiens RepID=B3KUS2_HUMAN Length: 413aa

k UniRef100_B4DEF7 0.0000
confidence: 1.0000 num unique p i tot indep spectra: 0
>cDNA FLJ60062, highly similar to 78 kDa glucose-regulated protein n=1 Tax=Homo sapiens RepID=B4DEF7_HUMAN Length: 278aa

l UniRef100_B4DFN9 0.0000
confidence: 1.0000 num unique p i 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

m UniRef100_B4DHP5 0.0000
confidence: 1.0000 num unique p i 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

n UniRef100_B4DI39 0.0000
confidence: 1.0000 num unique p i 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

o UniRef100_B4DNT8 0.0000
confidence: 1.0000 num unique p i 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

p UniRef100_B4DNV4 UniRef100_P48741 UniRef100_UPI0001AE7149 0.0000
confidence: 0.9999 num unique p i tot indep spectra: 0
>cDNA FLJ53071, highly similar to Heat shock 70 kDa protein 1 n=1 Tax=Homo sapiens RepID=B4DNV4_HUMAN Length: 232aa
>Putative heat shock 70 kDa protein 7 n=1 Tax=Homo sapiens RepID=HSP77_HUMAN
>UPI0001AE7149 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE7149

q UniRef100_B4DNX1 0.0000
confidence: 1.0000 num unique p i 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

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

s UniRef100_B4DVU9 0.0000
confidence: 1.0000 num unique p i 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

t UniRef100_B4DWK5 0.0000
confidence: 1.0000 num unique p i 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

u UniRef100_B4DXY3 0.0000
confidence: 1.0000 num unique p i 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

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

w UniRef100_B4E1T6 0.0000

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

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

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

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

aa UniRef100_P11142 UniRef100_Q53GZ6 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0 subsumed entries: 8
 >Heat shock cognate 71 kDa protein n=8 Tax=Eutheria RepID=HSP7C_HUMAN Length: 646aa
 >Heat shock 70kDa protein 8 isoform 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GZ6_HUMAN

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

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

ad UniRef100_Q53HF2 UniRef100_UPI00015E00A1 0.0000
 confidence: 1.0000 num unique p_i 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

ae UniRef100_Q59EJ3 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Heat shock 70kDa protein 1A variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59EJ3_HUMAN Length: 709aa

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

ag UniRef100_Q9NWW3 UniRef100_Q9NZ87 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >cDNA FLJ20564 fis, clone KAT12033 n=1 Tax=Homo sapiens RepID=Q9NWW3_HUMAN Length: 129aa
 >Uncharacterized bone marrow protein BM034 n=1 Tax=Homo sapiens RepID=Q9NZ87_HUMAN

ah UniRef100_Q9UQC1 0.0000
 confidence: 1.0000 num unique p_i tot indep spectra: 0
 >Heat shock protein 72 (Fragment) n=1 Tax=Homo sapiens RepID=Q9UQC1_HUMAN Length: 151aa

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

aj UniRef100_UPI000186D0C5 UniRef100_UPI000186D9DF 0.0000
 confidence: 0.1456 num unique p_i tot indep spectra: 0
 >Heat shock protein 70 A2, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D0C5 Length: 661aa
 >Heat shock protein, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D9DF

ak UniRef100_UPI000186E328 0.0000
 confidence: 0.9991 num unique p_i tot indep spectra: 0
 >Heat shock 70 kDa protein cognate 3 precursor, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E Length: 656aa

al UniRef100_UPI0001AE7147 UniRef100_UPI0001AE7283 0.0000

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

am UniRef100_UPI0001AE714A 0.0000
confidence: 1.0000 num unique p_i tot indep spectra: 0
>UPI0001AE714A related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE714A Length: 563aa

10 PROTEIN GROUP: 10 1.0000

a UniRef100_Q53GR7 UniRef100_Q546F9 UniRef100_Q9UJS0 1.0000
confidence: 1. max coverage num unique p_i tot indep spec share of spect subsumed entries: 1
>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_O75746 UniRef100_UPI0001AE7767 0.0000
confidence: 0.1639 num unique p_i tot indep spectra: 0
>cDNA FLJ12766 fis, clone NT2RP2001520, highly similar to Calcium-binding mitochondrial carrier protein Aralar1 n= Length: 678aa
>cDNA FLJ33752 fis, clone BRCAN2000364, highly similar to Calcium-binding mitochondrial carrier protein Aralar1 n=1 Tax=Homo sapiens
RepID=B3KR64_HUMAN
>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: 0.2927 num unique p_i tot indep spectra: 0
>Putative uncharacterized protein SLC25A13 (Fragment) n=1 Tax=Homo sapiens RepID=Q75KX8_HUMAN Length: 288aa

11 PROTEIN GROUP: 11 1.0000

a UniRef100_Q96PK6 1.0000
confidence: 1. coverage: 11. num unique p_i tot indep spec share of spect subsumed entries: 3
>RNA-binding protein 14 n=1 Tax=Homo sapiens RepID=RBM14_HUMAN Length: 669aa

b UniRef100_B0LM41 UniRef100_B8ZZ74 UniRef100_D6RAB9 UniRef100_D6RGD8 UniRef100_Q2PYN1 UniRef100_Q96PK6-2
UniRef100_UPI0001881AEF UniRef100_UPI0001881AF0 0.0000
confidence: 0.5197 num unique p_i tot indep spectra: 0
>Transcriptional coactivator CoAZ n=1 Tax=Homo sapiens RepID=B0LM41_HUMAN Length: 339aa
>Putative uncharacterized protein RBM14 n=1 Tax=Homo sapiens RepID=B8ZZ74_HUMAN
>Putative uncharacterized protein RBM14 n=1 Tax=Homo sapiens RepID=D6RAB9_HUMAN
>Putative uncharacterized protein RBM14 n=1 Tax=Homo sapiens RepID=D6RGD8_HUMAN
>Coactivator regulator n=1 Tax=Homo sapiens RepID=Q2PYN1_HUMAN
>Isoform 2 of RNA-binding protein 14 n=1 Tax=Homo sapiens RepID=Q96PK6-2
>UPI0001881AEF related cluster n=1 Tax=Homo sapiens RepID=UPI0001881AEF
>UPI0001881AF0 related cluster n=1 Tax=Homo sapiens RepID=UPI0001881AF0

c UniRef100_B4DNG4 0.0000
confidence: 0.3632 num unique p_i 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_i tot indep spectra: 0
>RNA binding motif protein 14 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59GV2_HUMAN Length: 552aa

12 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 0.9929
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 1.17%
>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

13 UniRef100_B1AHM1 UniRef100_B4DLW8 UniRef100_B4DN41 UniRef100_B4DNG2 UniRef100_B4DZQ7 UniRef100_B5BUE6
UniRef100_C9J5E1 UniRef100_C9JMU5 UniRef100_P17844 UniRef100_Q4R6G0 UniRef100_Q59E92 UniRef100_Q59F66
UniRef100_Q7Z2V5 UniRef100_Q92841 UniRef100_Q92841-2 UniRef100_Q92841-3 UniRef100_Q92841-4 UniRef100_UPI00003670EA
UniRef100_UPI0001533DB4 UniRef100_UPI0001AE634C UniRef100_UPI0001AE634E UniRef100_UPI0001AE6729
UniRef100_UPI0001B790480.9929
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 1.17%
>DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 n=1 Tax=Homo sapiens RepID=B1AHM1_HUMAN Length: 652aa
>cDNA FLJ59339, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DLW8_HUMAN
>cDNA FLJ53366, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DN41_HUMAN
>cDNA FLJ59357, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DNG2_HUMAN
>cDNA FLJ58652, highly similar to Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) n=1 Tax=Homo sapiens RepID=B4DZQ7_HUMAN
>ATP-dependent RNA helicase DDX5 (Fragment) n=1 Tax=Homo sapiens RepID=B5BUE6_HUMAN
>Putative uncharacterized protein DDX17 n=1 Tax=Homo sapiens RepID=C9J5E1_HUMAN
>Putative uncharacterized protein DDX17 n=1 Tax=Homo sapiens RepID=C9JMU5_HUMAN
>Probable ATP-dependent RNA helicase DDX5 n=3 Tax=Eutheria RepID=DDX5_HUMAN
>Testis cDNA, clone: QtsA-18104, similar to human DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 (DDX5), n=2 Tax=Macaca fascicularis
RepID=Q4R6G0_MACFA
>Putative uncharacterized protein (Fragment) n=2 Tax=Eutheria RepID=Q59E92_HUMAN
>DEAD box polypeptide 17 isoform p82 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59F66_HUMAN
>Putative uncharacterized protein DKFZp686J01190 (Fragment) n=1 Tax=Homo sapiens RepID=Q7Z2V5_HUMAN
>Probable ATP-dependent RNA helicase DDX17 n=1 Tax=Homo sapiens RepID=DDX17_HUMAN
>Isoform 2 of Probable ATP-dependent RNA helicase DDX17 n=1 Tax=Homo sapiens RepID=Q92841-2
>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
>UPI0001AE634E related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE634E
>UPI0001AE6729 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6729
>UPI0001B79048 related cluster n=1 Tax=Homo sapiens RepID=UPI0001B79048

14 UniRef100_B4DI32 UniRef100_D6RAQ3 UniRef100_P02545 UniRef100_P02545-3 UniRef100_Q5I6Y4 UniRef100_Q5I6Y6
UniRef100_UPI0001AE794A 0.9929
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.39%
>cDNA FLJ56081, highly similar to Lamin-A/C n=1 Tax=Homo sapiens RepID=B4DI32_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=Q5I6Y4_HUMAN
>Lamin A/C transcript variant 1 n=1 Tax=Homo sapiens RepID=Q5I6Y6_HUMAN
>UPI0001AE794A related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE794A

15 UniRef100_P13645 UniRef100_UPI00017BCE7F 0.9929
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.39%
>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

16 UniRef100_P54136 UniRef100_UPI000186D598 0.9929
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.78%
>Arginyl-tRNA synthetase, cytoplasmic n=2 Tax=Homo sapiens RepID=SYRC_HUMAN Length: 660aa
>Arginyl-tRNA synthetase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D598

17 UniRef100_Q6IPW8 UniRef100_Q8NBj5 0.9929
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.39%
>GLT25D1 protein (Fragment) n=2 Tax=Homo sapiens RepID=Q6IPW8_HUMAN Length: 222aa
>Procollagen galactosyltransferase 1 n=1 Tax=Homo sapiens RepID=GT251_HUMAN

18 UniRef100_Q9N0W4 UniRef100_Q9N0W6 0.9702
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 1.16%
>Anti-human A33 heavy chain domain (Fragment) n=1 Tax=Oryctolagus cuniculus RepID=Q9N0W4_RABIT Length: 124aa
>Anti-human A33 heavy chain domain (Fragment) n=1 Tax=Oryctolagus cuniculus RepID=Q9N0W6_RABIT

19 UniRef100_UPI0000111654 UniRef100_UPI0000112158 UniRef100_UPI00017BDB3D UniRef100_UPI00017BDB42 0.9621
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.77%
>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