

# 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)

Lower band MS results:

33 entries (11 single hits) retrieved from  
[/home/TPP/tpp/20110617\\_Bowling/int-gb\\_20110617\\_LTQ\\_Bowling\\_CEBPD-1-sequest.prot.xml](http://home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_CEBPD-1-sequest.prot.xml)

\* corresponds to peptide is\_nondegenerate\_evidence flag

1 UniRef100\_B4DFE6 UniRef100\_P36542 **1.0000**  
max share of  
confidence: coverage: num unique tot indep spectrum  
1.00 14.0% peps: 2 spectra: 2 id's: 0.65%  
>cDNA FLJ59861, highly similar to ATP synthase gamma chain, mitochondrial (EC 3.6.3.14) n=1 Length:  
Tax=Homo sapiens RepID=B4DFE6\_HUMAN 143aa  
>ATP synthase subunit gamma, mitochondrial n=5 Tax=Homo sapiens RepID=ATPG\_HUMAN

2 UniRef100\_D6RAE9 UniRef100\_D6RFI0 UniRef100\_Q9H9B4 **1.0000**  
max share of  
confidence: coverage: num unique tot indep spectrum  
1.00 39.3% peps: 2 spectra: 3 id's: 0.95%  
Length:  
>Putative uncharacterized protein SFXN1 n=1 Tax=Homo sapiens RepID=D6RAE9\_HUMAN 56aa  
>Putative uncharacterized protein SFXN1 n=3 Tax=Hominidae RepID=D6RFI0\_HUMAN  
>Sideroflexin-1 n=2 Tax=Homo sapiens RepID=SFXN1\_HUMAN

3 UniRef100\_P06576 UniRef100\_Q0QEN7 UniRef100\_UPI000186EDED **1.0000**  
max share of  
confidence: coverage: num unique tot indep spectrum  
1.00 5.6% peps: 2 spectra: 4 id's: 1.32%  
Length:  
>ATP synthase subunit beta, mitochondrial n=1 Tax=Homo sapiens RepID=ATPB\_HUMAN 529aa  
>ATP synthase subunit beta (Fragment) n=1 Tax=Homo sapiens RepID=Q0QEN7\_HUMAN  
>ATP synthase subunit beta, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EDED

4 UniRef100\_P08729 UniRef100\_UPI000013CF9E **1.0000**  
max share of  
confidence: coverage: num unique tot indep spectrum  
1.00 5.3% peps: 2 spectra: 3 id's: 1.00%  
Length:  
>Keratin, type II cytoskeletal 7 n=1 Tax=Homo sapiens RepID=K2C7\_HUMAN 469aa  
>keratin, type II cytoskeletal 7 n=1 Tax=Homo sapiens RepID=UPI000013CF9E

6a UniRef100\_A8K008 UniRef100\_P01857 UniRef100\_P01860 UniRef100\_Q5EBM2 UniRef100\_Q5EFE5 UniRef100\_Q6GMX6  
UniRef100\_Q6MZQ6 UniRef100\_Q6MZV7 UniRef100\_Q6N030 UniRef100\_Q6N089 UniRef100\_Q6N094 UniRef100\_Q6N095  
UniRef100\_Q6N096 UniRef100\_Q6N097 UniRef100\_Q7Z351 UniRef100\_Q86TT2 UniRef100\_Q8NF17 UniRef100\_UPI00001125A4  
UniRef100\_UPI000173A69D UniRef100\_UPI000173A69E UniRef100\_UPI000173A69F UniRef100\_UPI000195C290 **1.0000**  
max share of  
confidence: coverage: num unique tot indep spectrum  
1.00 4.5% peps: 3 spectra: 7 id's: 2.20%  
Length:  
>cDNA FLJ78387 n=1 Tax=Homo sapiens RepID=A8K008\_HUMAN 472aa  
>Ig gamma-1 chain C region n=1 Tax=Homo sapiens RepID=IGHG1\_HUMAN  
>Ig gamma-3 chain C region n=1 Tax=Homo sapiens RepID=IGHG3\_HUMAN  
>Putative uncharacterized protein n=1 Tax=Homo sapiens RepID=Q5EBM2\_HUMAN  
>Anti-Rhd monoclonal T125 gammal heavy chain n=1 Tax=Homo sapiens RepID=Q5EFE5\_HUMAN  
>IGH@ protein n=1 Tax=Homo sapiens RepID=Q6GMX6\_HUMAN  
>Putative uncharacterized protein DKFZp686G11190 n=1 Tax=Homo sapiens RepID=Q6MZQ6\_HUMAN  
>Putative uncharacterized protein DKFZp686C11235 n=1 Tax=Homo sapiens RepID=Q6MZV7\_HUMAN  
>Putative uncharacterized protein DKFZp686I15212 n=1 Tax=Homo sapiens RepID=Q6N030\_HUMAN  
>Putative uncharacterized protein DKFZp686P15220 n=1 Tax=Homo sapiens RepID=Q6N089\_HUMAN  
>Putative uncharacterized protein DKFZp686O01196 n=1 Tax=Homo sapiens RepID=Q6N094\_HUMAN  
>Putative uncharacterized protein DKFZp686K03196 n=1 Tax=Homo sapiens RepID=Q6N095\_HUMAN  
>Putative uncharacterized protein DKFZp686I15196 n=1 Tax=Homo sapiens RepID=Q6N096\_HUMAN  
>Putative uncharacterized protein DKFZp686H20196 n=1 Tax=Homo sapiens RepID=Q6N097\_HUMAN  
>Putative uncharacterized protein DKFZp686N02209 n=1 Tax=Homo sapiens RepID=Q7Z351\_HUMAN  
>Full-length cDNA clone CS0DI019YF20 of Placenta of Homo sapiens (human) (Fragment) n=2 Tax=Homo sapiens RepID=Q86TT2\_HUMAN  
>FLJ00385 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8NF17\_HUMAN  
>IGG1 MCG INTACT ANTIBODY (HEAVY CHAIN) n=1 Tax=Homo sapiens RepID=UPI00001125A4  
>Immunoglobulin heavy chain C gene segment n=1 Tax=Homo sapiens RepID=UPI000173A69D  
>Immunoglobulin heavy chain C gene segment n=1 Tax=Homo sapiens RepID=UPI000173A69E  
>Immunoglobulin heavy chain C gene segment n=1 Tax=Homo sapiens RepID=UPI000173A69F  
>IG GAMMA-1 CHAIN C REGION n=1 Tax=Homo sapiens RepID=UPI000195C290

UniRef100\_A8K4Z4 UniRef100\_P05388 UniRef100\_Q3B7A4 UniRef100\_Q53HK9 UniRef100\_Q53HW2 UniRef100\_Q6NSF2  
**UniRef100\_Q8NHW5 1.0000**

confidence:	coverage:	num unique	tot indep	share of
1.00	16.9%	peps: 3	spectra: 7	spectrum id's: 2.32%

>cDNA FLJ75549, highly similar to Homo sapiens ribosomal protein, large, P0 (RPLP0), transcript variant 1, mRNA n=1 Tax=Homo sapiens RepID=A8K4Z4\_HUMAN Length: 317aa  
>60S acidic ribosomal protein P0 n=1 Tax=Homo sapiens RepID=RLA0\_HUMAN  
>RPLP0 protein n=1 Tax=Homo sapiens RepID=Q3B7A4\_HUMAN  
>Ribosomal protein P0 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53HK9\_HUMAN  
>Ribosomal protein P0 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53HW2\_HUMAN  
>RPLP0 protein n=1 Tax=Homo sapiens RepID=Q6NSF2\_HUMAN  
>60S acidic ribosomal protein P0-like n=1 Tax=Homo sapiens RepID=RLA0L\_HUMAN

9a UniRef100\_B2RA03 UniRef100\_P05783 **1.0000**

confidence:	coverage:	num unique	tot indep	share of
1.00	4.9%	peps: 2	spectra: 4	spectrum id's: 1.32%

>cDNA, FLJ94640, highly similar to Homo sapiens keratin 18 (KRT18), mRNA n=1 Tax=Homo sapiens RepID=B2RA03\_HUMAN Length: 430aa  
>Keratin, type I cytoskeletal 18 n=1 Tax=Homo sapiens RepID=K1C18\_HUMAN

11a UniRef100\_B4DJI1 UniRef100\_P00338 UniRef100\_UPI0001AE6BAB **1.0000**

confidence:	coverage:	num unique	tot indep	share of	
1.00	23.0%	peps: 8	spectra: 21	spectrum id's: 7.09%	<a href="#">subsumed entries: 2</a>

>L-lactate dehydrogenase n=1 Tax=Homo sapiens RepID=B4DJI1\_HUMAN Length: 305aa  
>L-lactate dehydrogenase A chain n=3 Tax=Homo sapiens RepID=LDHA\_HUMAN  
>UPI0001AE6BAB related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6BAB

11b [UniRef100\\_P07195 1.0000](#)

confidence:	coverage:	num unique	tot indep	share of
1.00	12.6%	peps: 3	spectra: 5	spectrum id's: 2.14%

>L-lactate dehydrogenase B chain n=4 Tax=Catarrhini RepID=LDHB\_HUMAN Length: 334aa

13a UniRef100\_B4DY90 UniRef100\_B7ZAF0 UniRef100\_P07437 UniRef100\_Q5JP53 UniRef100\_Q6LC01 **1.0000**

confidence:	coverage:	num unique	tot indep	share of	
1.00	5.8%	peps: 2	spectra: 3	spectrum id's: 0.99%	<a href="#">subsumed entries: 2</a>

>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  
>MRNA encoding beta-tubulin. (from clone D-beta-1) (Fragment) n=1 Tax=Homo sapiens RepID=Q6LC01\_HUMAN

14a UniRef100\_C5IWV5 UniRef100\_P00761 **1.0000**

confidence:	coverage:	num unique	tot indep	share of
1.00	25.1%	peps: 29	spectra: 72	spectrum id's: 16.72%

>Trypsinogen n=1 Tax=Sus scrofa RepID=C5IWV5\_PIG Length: 246aa  
>Trypsin n=1 Tax=Sus scrofa RepID=TRYP\_PIG

15a [UniRef100\\_O95639 1.0000](#)

confidence:	coverage:	num unique	tot indep	share of	
1.00	17.5%	peps: 4	spectra: 10	spectrum id's: 3.15%	<a href="#">subsumed entries: 3</a>

>Cleavage and polyadenylation specificity factor subunit 4 n=1 Tax=Homo sapiens RepID=CPSF4\_HUMAN Length: 269aa

16a UniRef100\_P02769 UniRef100\_UPI000179EC85 **1.0000**

confidence:	coverage:	num unique	tot indep	share of	
1.00	17.6%	peps: 12	spectra: 27	spectrum id's: 8.68%	<a href="#">subsumed entries: 5</a>

>Serum albumin n=1 Tax=Bos taurus RepID=ALBU\_BOVIN Length: 607aa  
>Serum albumin precursor (Allergen Bos d 6) (BSA). n=1 Tax=Bos taurus RepID=UPI000179EC85

17a [UniRef100\\_P04264 1.0000](#)

confidence:	coverage:	num unique	tot indep	share of	
0.99	3.3%	peps: 2	spectra: 4	spectrum	<a href="#">subsumed</a>
				id's: 1.30%	<a href="#">entries: 1</a>

>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1\_HUMAN

Length:  
644aa

  

18a UniRef100\_P04406 UniRef100\_Q2TSD0 UniRef100\_UPI0000D4D340 **1.0000**

confidence:	coverage:	num unique	tot indep	share of	
1.00	16.5%	peps: 3	spectra: 7	spectrum	<a href="#">subsumed</a>
				id's: 2.25%	<a href="#">entries: 3</a>

>Glyceraldehyde-3-phosphate dehydrogenase n=1 Tax=Homo sapiens RepID=G3P\_HUMAN  
>Glyceraldehyde-3-phosphate dehydrogenase n=1 Tax=Homo sapiens RepID=Q2TSD0\_HUMAN  
>Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH). n=1 Tax=Homo sapiens RepID=UPI0000D4D340

Length:  
335aa

  

19a UniRef100\_P05787 UniRef100\_Q7L4M3 UniRef100\_Q969I0 **1.0000**

confidence:	coverage:	num unique	tot indep	share of	
1.00	11.5%	peps: 3	spectra: 5	spectrum	
				id's: 1.66%	

>Keratin, type II cytoskeletal 8 n=1 Tax=Homo sapiens RepID=K2C8\_HUMAN  
>KRT8 protein n=1 Tax=Homo sapiens RepID=Q7L4M3\_HUMAN  
>KRT8 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q969I0\_HUMAN

Length:  
483aa

  

20a UniRef100\_P12004 UniRef100\_Q6FHF5 UniRef100\_Q6FI35 **1.0000**

confidence:	coverage:	num unique	tot indep	share of	
1.00	30.3%	peps: 6	spectra: 15	spectrum	<a href="#">subsumed</a>
				id's: 4.96%	<a href="#">entries: 2</a>

>Proliferating cell nuclear antigen n=3 Tax=Catarrhini RepID=PCNA\_HUMAN  
>Proliferating cell nuclear antigen (Fragment) n=1 Tax=Homo sapiens RepID=Q6FHF5\_HUMAN  
>Proliferating cell nuclear antigen n=1 Tax=Homo sapiens RepID=Q6FI35\_HUMAN

Length:  
261aa

  

21a [UniRef100\\_P23396 1.0000](#)

confidence:	coverage:	num unique	tot indep	share of	
1.00	32.9%	peps: 7	spectra: 20	spectrum	<a href="#">subsumed</a>
				id's: 6.55%	<a href="#">entries: 3</a>

>40S ribosomal protein S3 n=4 Tax=Eukaryota RepID=RS3\_HUMAN

Length:  
243aa

  

22a UniRef100\_Q99623 UniRef100\_UPI00015DFE52 **1.0000**

confidence:	coverage:	num unique	tot indep	share of	
1.00	30.8%	peps: 11	spectra: 27	spectrum	<a href="#">subsumed</a>
				id's: 8.81%	<a href="#">entries: 1</a>

>Prohibitin-2 n=3 Tax=Euarchontoglires RepID=PHB2\_HUMAN  
>Prohibitin-2 (B-cell receptor-associated protein BAP37) (Repressor of estrogen receptor activity) (D-prohibitin). n=1 Tax=Homo sapiens RepID=UPI00015DFE52

Length:  
299aa

  

23 [UniRef100\\_P35527 0.9951](#)

confidence:	coverage:	num unique	tot indep	share of	
0.06	2.6%	peps: 1	spectra: 3	spectrum	
				id's: 1.00%	

>Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9\_HUMAN

Length:  
623aa

  

24 UniRef100\_Q01650 UniRef100\_Q2MCL6 UniRef100\_Q8IV97 **0.9951**

confidence:	coverage:	num unique	tot indep	share of	
0.40	19.7%	peps: 1	spectra: 1	spectrum	
				id's: 0.33%	

>Large neutral amino acids transporter small subunit 1 n=1 Tax=Homo sapiens RepID=LAT1\_HUMAN  
>Large neutral amino acids transporter 1 (Fragment) n=1 Tax=Homo sapiens RepID=Q2MCL6\_HUMAN  
>Solute carrier family 7 (Cationic amino acid transporter, y+ system), member 5 n=1 Tax=Homo sapiens RepID=Q8IV97\_HUMAN

Length:  
507aa

  

25 UniRef100\_B8ZZ37 UniRef100\_P22626 **0.9937**

		max			share of	
	confidence:	coverage:	num unique	tot indep	spectrum	
	0.12	3.2%	peps: 1	spectra: 1	id's: 0.33%	
						Length:
						317aa
						>Putative uncharacterized protein HNRNPA2B1 n=1 Tax=Homo sapiens RepID=B8ZZ37_HUMAN
						>Heterogeneous nuclear ribonucleoproteins A2/B1 n=1 Tax=Homo sapiens RepID=ROA2_HUMAN
26	UniRef100_P62753	UniRef100_Q96DV6	UniRef100_Q9BZU1	<b>0.9937</b>		
		max			share of	
	confidence:	coverage:	num unique	tot indep	spectrum	
	0.37	15.2%	peps: 1	spectra: 3	id's: 1.00%	
						Length:
						249aa
						>40S ribosomal protein S6 n=8 Tax=Eutheria RepID=RS6_HUMAN
						>Ribosomal protein S6 n=1 Tax=Homo sapiens RepID=Q96DV6_HUMAN
						>PNAS-20 n=1 Tax=Homo sapiens RepID=Q9BZU1_HUMAN
27	UniRef100_A6NMY6	UniRef100_P07355		<b>0.9932</b>		
		max			share of	
	confidence:	coverage:	num unique	tot indep	spectrum	
	0.11	3.2%	peps: 1	spectra: 2	id's: 0.66%	
						Length:
						339aa
						>Putative annexin A2-like protein n=1 Tax=Homo sapiens RepID=AXA2L_HUMAN
						>Annexin A2 n=3 Tax=Hominidae RepID=ANXA2_HUMAN
28	<a href="#">UniRef100_P49716</a>	<a href="#">0.9932</a>				
		max			share of	
	confidence:	coverage:	num unique	tot indep	spectrum	
	0.14	3.7%	peps: 1	spectra: 2	id's: 0.66%	
						Length:
						269aa
						>CCAAT/enhancer-binding protein delta n=1 Tax=Homo sapiens RepID=CEBPD_HUMAN
29	UniRef100_B4DY56	UniRef100_P25705		<b>0.9864</b>		
		max			share of	
	confidence:	coverage:	num unique	tot indep	spectrum	
	0.07	2.3%	peps: 1	spectra: 1	id's: 0.33%	
						Length:
						531aa
						>ATP synthase subunit alpha n=1 Tax=Homo sapiens RepID=B4DY56_HUMAN
						>ATP synthase subunit alpha, mitochondrial n=3 Tax=Homininae RepID=ATPA_HUMAN
30	UniRef100_B4DIR3	UniRef100_B4DTW7	UniRef100_Q6UN15	UniRef100_Q6UN15-3	UniRef100_Q6UN15-4	UniRef100_UPI0000D9B14D
		max				<b>0.9817</b>
	confidence:	coverage:	num unique	tot indep	spectrum	
	0.16	5.0%	peps: 1	spectra: 3	id's: 0.98%	
						Length:
						588aa
						>cDNA FLJ56493, highly similar to Pre-mRNA 3'-end-processing factor FIP1 n=1 Tax=Homo sapiens RepID=B4DIR3_HUMAN
						>cDNA FLJ61400, highly similar to Pre-mRNA 3'-end-processing factor FIP1 n=1 Tax=Homo sapiens RepID=B4DTW7_HUMAN
						>Pre-mRNA 3'-end-processing factor FIP1 n=1 Tax=Homo sapiens RepID=FIP1_HUMAN
						>Isoform 3 of Pre-mRNA 3'-end-processing factor FIP1 n=1 Tax=Homo sapiens RepID=Q6UN15-3
						>Isoform 4 of Pre-mRNA 3'-end-processing factor FIP1 n=1 Tax=Homo sapiens RepID=Q6UN15-4
						>FIP1 like 1 isoform 2 n=1 Tax=Homo sapiens RepID=UPI0000D9B14D
31	UniRef100_A8K4W0	UniRef100_B7Z3M5	UniRef100_D6RB09	UniRef100_D6RG13	UniRef100_D6RGE0	UniRef100_P61247
	UniRef100_Q6NXR8	UniRef100_UPI0001D3B8ED	UniRef100_UPI0001D3B8EF	<b>0.9685</b>		
		max			share of	
	confidence:	coverage:	num unique	tot indep	spectrum	
	0.41	13.8%	peps: 1	spectra: 2	id's: 0.66%	
						Length:
						264aa
						>cDNA FLJ78591, highly similar to Homo sapiens ribosomal protein S3A (RPS3A), mRNA n=1 Tax=Homo sapiens RepID=A8K4W0_HUMAN
						>cDNA FLJ51870, highly similar to 40S ribosomal protein S3a n=3 Tax=Homo sapiens RepID=B7Z3M5_HUMAN
						>Putative uncharacterized protein RPS3A n=1 Tax=Homo sapiens RepID=D6RB09_HUMAN
						>Putative uncharacterized protein RPS3A n=1 Tax=Homo sapiens RepID=D6RG13_HUMAN
						>Putative uncharacterized protein RPS3A n=2 Tax=Homo sapiens RepID=D6RGE0_HUMAN
						>40S ribosomal protein S3a n=5 Tax=Eutheria RepID=RS3A_HUMAN
						>Ribosomal protein S3A n=1 Tax=Homo sapiens RepID=Q6NXR8_HUMAN
						>UPI0001D3B8ED related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3B8ED
						>UPI0001D3B8EF related cluster n=1 Tax=Homo sapiens RepID=UPI0001D3B8EF
	UniRef100_A1E282	UniRef100_A6NL76	UniRef100_A8K3K1	UniRef100_B3KUD3	UniRef100_B3KW67	UniRef100_B4DUI8
	UniRef100_B4DVQ0	UniRef100_B4E335	UniRef100_B4E3A4	UniRef100_B7Z6P1	UniRef100_B8ZZJ2	UniRef100_C9JFL5
	UniRef100_P60709	UniRef100_P62736	UniRef100_P63261	UniRef100_P63267	UniRef100_P68032	UniRef100_P68133

UniRef100\_Q4R4H6 UniRef100\_Q53G76 UniRef100\_Q53G99 UniRef100\_Q53GK6 UniRef100\_Q5T8M7 UniRef100\_Q5T8M8  
 UniRef100\_Q5T9N7 UniRef100\_Q7Z7J6 UniRef100\_Q8WVW5 UniRef100\_UPI000041FCA6 UniRef100\_UPI0000E0A7CD UniRef100\_UPI000186E470  
 UniRef100\_UPI00018815CC 0.9680

32

confidence:	max coverage:	num unique	tot indep	share of spectrum
0.29	9.1%	peps: 1	spectra: 1	ids: 0.33%

>Beta-actin (Fragment) n=4 Tax=Coelomata RepID=A1E282\_HUMAN  
 >Putative uncharacterized protein ACTA1 n=1 Tax=Homo sapiens RepID=A6NL76\_HUMAN  
 >cDNA FLJ78096, highly similar to Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA n=1  
 Tax=Homo sapiens RepID=A8K3K1\_HUMAN  
 >cDNA FLJ39583 fis, clone SKMUS2004897, highly similar to ACTIN, ALPHA SKELETAL MUSCLE n=1  
 Tax=Homo sapiens RepID=B3KUD3\_HUMAN  
 >cDNA FLJ42347 fis, clone UTERU2003399, highly similar to Actin, gamma-enteric smooth muscle n=1  
 Tax=Homo sapiens RepID=B3KW67\_HUMAN  
 >cDNA FLJ52761, highly similar to Actin, aortic smooth muscle n=2 Tax=Euteleostomi  
 RepID=B4DUI8\_HUMAN  
 >cDNA FLJ58286, highly similar to Actin, cytoplasmic 2 n=1 Tax=Homo sapiens RepID=B4DVQ0\_HUMAN  
 >cDNA FLJ52842, highly similar to Actin, cytoplasmic 1 n=1 Tax=Homo sapiens RepID=B4E335\_HUMAN  
 >cDNA FLJ57283, highly similar to Actin, cytoplasmic 2 n=1 Tax=Homo sapiens RepID=B4E3A4\_HUMAN  
 >cDNA FLJ53662, highly similar to Actin, alpha skeletal muscle n=1 Tax=Homo sapiens  
 RepID=B7Z6P1\_HUMAN  
 >Putative uncharacterized protein ACTG2 n=1 Tax=Homo sapiens RepID=B8ZZJ2\_HUMAN  
 >Putative uncharacterized protein ACTG2 n=1 Tax=Homo sapiens RepID=C9JFL5\_HUMAN  
 >Actin, cytoplasmic 1, N-terminally processed n=24 Tax=Amniota RepID=ACTB\_HUMAN  
 >Actin, aortic smooth muscle n=12 Tax=Eukaryota RepID=ACTA\_HUMAN  
 >Actin, cytoplasmic 2, N-terminally processed n=9 Tax=Tetrapoda RepID=ACTG\_HUMAN  
 >Actin, gamma-enteric smooth muscle n=7 Tax=Amniota RepID=ACTH\_HUMAN  
 >Actin, alpha cardiac muscle 1 n=10 Tax=Tetrapoda RepID=ACTC\_HUMAN  
 >Actin, alpha skeletal muscle n=8 Tax=Amniota RepID=ACTS\_HUMAN  
 >Brain cDNA, clone: QflA-11253, similar to human actin, gamma 1 (ACTG1), n=1 Tax=Macaca  
 fascicularis RepID=Q4R4H6\_MACFA  
 >Beta actin variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53G76\_HUMAN  
 >Beta actin variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53G99\_HUMAN  
 >Beta actin variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GK6\_HUMAN  
 >Actin, alpha 1, skeletal muscle n=1 Tax=Homo sapiens RepID=Q5T8M7\_HUMAN  
 >Actin, alpha 1, skeletal muscle n=1 Tax=Homo sapiens RepID=Q5T8M8\_HUMAN  
 >Actin, alpha 2, smooth muscle, aorta (Fragment) n=2 Tax=Eutheria RepID=Q5T9N7\_HUMAN  
 >Actin alpha 1 skeletal muscle protein n=1 Tax=Homo sapiens RepID=Q7Z7J6\_HUMAN  
 >Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8WVW5\_HUMAN  
 >Actin, alpha skeletal muscle (Alpha-actin-1). n=1 Tax=Homo sapiens RepID=UPI000041FCA6  
 >UPI0000E0A7CD related cluster n=1 Tax=Homo sapiens RepID=UPI0000E0A7CD  
 >Actin-5C n=1 Tax=Pediculus humanus corporis RepID=UPI000186E470  
 >UPI00018815CC related cluster n=1 Tax=Homo sapiens RepID=UPI00018815CC

Length:  
121aa

33

UniRef100\_B2RE88 UniRef100\_Q00325 UniRef100\_Q00325-2 UniRef100\_Q53HC3 UniRef100\_Q8NCF7 0.9611

confidence:	max coverage:	num unique	tot indep	share of spectrum
0.10	3.3%	peps: 1	spectra: 1	ids: 0.33%

>cDNA, FLJ96465, highly similar to Homo sapiens solute carrier family 25 (mitochondrial carrier;phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA n=1 Tax=Homo sapiens RepID=B2RE88\_HUMAN  
 >Phosphate carrier protein, mitochondrial n=1 Tax=Homo sapiens RepID=MPCP\_HUMAN  
 >Isoform B of Phosphate carrier protein, mitochondrial n=1 Tax=Homo sapiens RepID=Q00325-2  
 >Solute carrier family 25 member 3 isoform b variant (Fragment) n=1 Tax=Homo sapiens  
 RepID=Q53HC3\_HUMAN  
 >cDNA FLJ90278 fis, clone NT2RP1000325, highly similar to Phosphate carrier protein, mitochondrialprecursor n=1 Tax=Homo sapiens RepID=Q8NCF7\_HUMAN

Length:  
361aa

Upper band MS results:

8 entries (2 single hits) retrieved from

[/home/TPP/tpp/20110617\\_Bowling/int-gb\\_20110617\\_LTQ\\_Bowling\\_CEBPD-2-sequest.prot.xml](/home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_CEBPD-2-sequest.prot.xml)

\* corresponds to peptide is\_nondegenerate\_evidence flag

1 UniRef100\_P35527 1.0000

confidence:	coverage:	num unique	tot indep	share of spectrum
1.00	19.4%	peps: 12	spectra: 26	ids: 9.61%

>Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9\_HUMAN

Length:  
623aa

UniRef100\_A8K008 UniRef100\_P01857 UniRef100\_P01860 UniRef100\_Q5EBM2 UniRef100\_Q5EFE5 UniRef100\_Q6GMX6  
 UniRef100\_Q6MZQ6 UniRef100\_Q6MZV7 UniRef100\_Q6N030 UniRef100\_Q6N089 UniRef100\_Q6N094 UniRef100\_Q6N095



UniRef100\_Q6N096 UniRef100\_Q6N097 UniRef100\_Q7Z351 UniRef100\_Q86TT2 UniRef100\_Q8NF17 UniRef100\_UPI00001125A4  
 2a UniRef100\_UPI000173A69D UniRef100\_UPI000173A69E UniRef100\_UPI000173A69F UniRef100\_UPI000195C290 **1.0000**  
 max  
 confidence: coverage: num unique tot indep share of  
 1.00 4.5% peps: 3 spectra: 7 id's: 2.54%  
 Length: 472aa  
 >cDNA FLJ78387 n=1 Tax=Homo sapiens RepID=A8K008\_HUMAN  
 >Ig gamma-1 chain C region n=1 Tax=Homo sapiens RepID=IGHG1\_HUMAN  
 >Ig gamma-3 chain C region n=1 Tax=Homo sapiens RepID=IGHG3\_HUMAN  
 >Putative uncharacterized protein n=1 Tax=Homo sapiens RepID=Q5EBM2\_HUMAN  
 >Anti-RhD monoclonal T125 gammal heavy chain n=1 Tax=Homo sapiens RepID=Q5EFE5\_HUMAN  
 >IGH@ protein n=1 Tax=Homo sapiens RepID=Q6GMX6\_HUMAN  
 >Putative uncharacterized protein DKFZp686G11190 n=1 Tax=Homo sapiens RepID=Q6MZQ6\_HUMAN  
 >Putative uncharacterized protein DKFZp686C11235 n=1 Tax=Homo sapiens RepID=Q6MZV7\_HUMAN  
 >Putative uncharacterized protein DKFZp686I15212 n=1 Tax=Homo sapiens RepID=Q6N030\_HUMAN  
 >Putative uncharacterized protein DKFZp686P15220 n=1 Tax=Homo sapiens RepID=Q6N089\_HUMAN  
 >Putative uncharacterized protein DKFZp686O01196 n=1 Tax=Homo sapiens RepID=Q6N094\_HUMAN  
 >Putative uncharacterized protein DKFZp686K03196 n=1 Tax=Homo sapiens RepID=Q6N095\_HUMAN  
 >Putative uncharacterized protein DKFZp686I15196 n=1 Tax=Homo sapiens RepID=Q6N096\_HUMAN  
 >Putative uncharacterized protein DKFZp686H20196 n=1 Tax=Homo sapiens RepID=Q6N097\_HUMAN  
 >Putative uncharacterized protein DKFZp686N02209 n=1 Tax=Homo sapiens RepID=Q7Z351\_HUMAN  
 >Full-length cDNA clone CSODI019YF20 of Placenta of Homo sapiens (Fragment) n=2 Tax=Homo sapiens RepID=Q86TT2\_HUMAN  
 >FLJ00385 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8NF17\_HUMAN  
 >IGG1 MCG INTACT ANTIBODY (HEAVY CHAIN) n=1 Tax=Homo sapiens RepID=UPI00001125A4  
 >Immunoglobulin heavy chain C gene segment n=1 Tax=Homo sapiens RepID=UPI000173A69D  
 >Immunoglobulin heavy chain C gene segment n=1 Tax=Homo sapiens RepID=UPI000173A69E  
 >Immunoglobulin heavy chain C gene segment n=1 Tax=Homo sapiens RepID=UPI000173A69F  
 >IG GAMMA-1 CHAIN C REGION n=1 Tax=Homo sapiens RepID=UPI000195C290

UniRef100\_C5IWV5 UniRef100\_P00761 **1.0000**  
 max  
 confidence: coverage: num unique tot indep share of subsumed  
 1.00 25.1% peps: 28 spectra: 59 id's: 16.91% entries: 1  
 Length: 246aa  
 >Trypsinogen n=1 Tax=Sus scrofa RepID=C5IWV5\_PIG  
 >Trypsin n=1 Tax=Sus scrofa RepID=TRYP\_PIG

[UniRef100\\_P02769 1.0000](#)  
 confidence: coverage: num unique tot indep share of subsumed  
 1.00 17.3% peps: 12 spectra: 29 id's: 11.42% entries: 1  
 Length: 607aa  
 >Serum albumin n=1 Tax=Bos taurus RepID=ALBU\_BOVIN

[UniRef100\\_P04264 1.0000](#)  
 confidence: coverage: num unique tot indep share of subsumed  
 1.00 28.3% peps: 19 spectra: 47 id's: 18.09% entries: 1  
 Length: 644aa  
 >Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1\_HUMAN

[UniRef100\\_P35908 1.0000](#)  
 confidence: coverage: num unique tot indep share of spectrum  
 1.00 12.2% peps: 4 spectra: 5 id's: 3.34%  
 Length: 639aa  
 >Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E\_HUMAN

UniRef100\_P13645 UniRef100\_UPI00017BCE7F **1.0000**  
 max  
 confidence: coverage: num unique tot indep share of subsumed  
 1.00 18.2% peps: 10 spectra: 24 id's: 10.20% entries: 2  
 Length: 584aa  
 >Keratin, type I cytoskeletal 10 n=1 Tax=Homo sapiens RepID=K1C10\_HUMAN  
 >keratin, type I cytoskeletal 10 n=1 Tax=Homo sapiens RepID=UPI00017BCE7F

UniRef100\_P31327 UniRef100\_Q59HF8 UniRef100\_Q5R206 UniRef100\_Q5R208 UniRef100\_Q5R210 **1.0000**  
 max  
 confidence: coverage: num unique tot indep share of subsumed  
 1.00 11.4% peps: 16 spectra: 35 id's: 14.46% entries: 4  
 Length: 1500aa  
 >Carbamoyl-phosphate synthase [ammonia], mitochondrial n=4 Tax=Homo sapiens RepID=CPSM\_HUMAN  
 >Carbamoyl-phosphate synthetase 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59HF8\_HUMAN

>Carbamoylphosphate synthetase I n=1 Tax=Homo sapiens RepID=Q5R206\_HUMAN  
>Carbamoylphosphate synthetase I n=1 Tax=Homo sapiens RepID=Q5R208\_HUMAN  
>Carbamoylphosphate synthetase I n=2 Tax=Homo sapiens RepID=Q5R210\_HUMAN

6b

[UniRef100\\_P02533\\_0.9998](#)

confidence:	coverage:	num unique	tot indep	share of	
1.00	5.1%	peps: 1	spectra: 2	spectrum	<a href="#">subsumed</a>
				id's: 1.54%	<a href="#">entries: 3</a>

>Keratin, type I cytoskeletal 14 n=1 Tax=Homo sapiens RepID=K1C14\_HUMAN

Length:  
472aa

8 [UniRef100\\_UPI000186DEBF\\_0.9882](#)

confidence:	coverage:	num unique	tot indep	share of	
0.12	2.3%	peps: 1	spectra: 1	spectrum	
				id's: 0.42%	

>class A rhodopsin-like G-protein coupled receptor GPRnpy3, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186DEBF