

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)

19 entries (9 single hits) retrieved from
/home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_MTA3-sequest.prot.xml

* corresponds to peptide is_nondegenerate_evidence flag

1 UniRef100_B4DHT9 UniRef100_B4DU71 UniRef100_P14625 UniRef100_Q59FC6 UniRef100_Q5CAQ5 UniRef100_UPI0001AE6A99
1
confidence: 1. max coverage num unique p| tot indep spec share of spectrum id's: 2.00%
>cDNA FLJ58812, highly similar to Endoplasmin (Heat shock protein 90kDa beta member 1) n=1 Tax=Homo sapiens Length: 468aa
>cDNA FLJ58626, highly similar to Endoplasmin (Heat shock protein 90 kDa beta member 1) n=1 Tax=Homo sapiens RepID=B4DU71_HUMAN
>Endoplasmin n=1 Tax=Homo sapiens RepID=ENPL_HUMAN
>Tumor rejection antigen (Gp96) 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59FC6_HUMAN
>Tumor rejection antigen (Gp96) 1 n=1 Tax=Homo sapiens RepID=Q5CAQ5_HUMAN
>UPI0001AE6A99 related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE6A99

2 UniRef100_P35527 1.0000
confidence: 1. coverage: 11. num unique p| tot indep spec share of spectrum id's: 3.72%
>Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN Length: 623aa

4a UniRef100_B3GQS7 UniRef100_B7Z597 UniRef100_B7Z5E7 UniRef100_P10809 1.0000
confidence: 1. max coverage num unique p| tot indep spec share of spectrum id's: 3.68%
>Mitochondrial heat shock 60kD protein 1 variant 1 n=1 Tax=Homo sapiens RepID=B3GQS7_HUMAN Length: 569aa
>cDNA FLJ54373, highly similar to 60 kDa heat shock protein, mitochondrial n=1 Tax=Homo sapiens RepID=B7Z597_HUMAN
>cDNA FLJ51046, highly similar to 60 kDa heat shock protein, mitochondrial n=1 Tax=Homo sapiens RepID=B7Z5E7_HUMAN
>60 kDa heat shock protein, mitochondrial n=1 Tax=Homo sapiens RepID=CH60_HUMAN

5a UniRef100_B4DNL5 UniRef100_P07237 1.0000
confidence: 1. max coverage num unique p| tot indep spec share of spect subsumed entries: 6
>cDNA FLJ59361, highly similar to Protein disulfide-isomerase (EC 5.3.4.1) n=1 Tax=Homo sapiens RepID=B4DNL5 Length: 492aa
>Protein disulfide-isomerase n=1 Tax=Homo sapiens RepID=PDIA1_HUMAN

6a UniRef100_C5I WV5 UniRef100_P00761 1.0000
confidence: 1. max coverage num unique p| tot indep spec share of spect subsumed entries: 1
>Trypsinogen n=1 Tax=Sus scrofa RepID=C5I WV5_PIG Length: 246aa
>Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG

7a UniRef100_P02769 1.0000
confidence: 1. coverage: 31. num unique p| tot indep spec share of spect subsumed entries: 1
>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa

8a UniRef100_P04264 1.0000
confidence: 1. coverage: 25. num unique p| tot indep spec share of spectrum id's: 9.99%
>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN Length: 644aa

8b UniRef100_P35908 1.0000
confidence: 1. coverage: 16. num unique p| tot indep spec share of spectrum id's: 2.37%
>Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E_HUMAN Length: 639aa

8c UniRef100_P13647 1.0000
confidence: 1. coverage: 12. num unique p| tot indep spec share of spect subsumed entries: 2
>Keratin, type II cytoskeletal 5 n=1 Tax=Homo sapiens RepID=K2C5_HUMAN Length: 590aa

9a UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000
confidence: 1. max coverage num unique p| tot indep spec share of spect subsumed entries: 1
>Keratin, type I cytoskeletal 10 n=1 Tax=Homo sapiens RepID=K1C10_HUMAN Length: 584aa
>keratin, type I cytoskeletal 10 n=1 Tax=Homo sapiens RepID=UPI00017BCE7F

10a UniRef100_P14618 1.0000
confidence: 1. coverage: 10. num unique p| tot indep spec share of spect subsumed entries: 9
>Pyruvate kinase isozymes M1/M2 n=2 Tax=Homininae RepID=KP YM_HUMAN Length: 531aa

12a UniRef100_Q9BTC8 UniRef100_Q9BTC8-2 UniRef100_UPI0000D4CDC7 UniRef100_UPI0001881589 1.0000
confidence: 1. max coverage num unique p| tot indep spe share of spe subsumed entries: 6
>Metastasis-associated protein MTA3 n=3 Tax=Homininae RepID=MTA3_HUMAN Length: 594aa
>Isoform 2 of Metastasis-associated protein MTA3 n=1 Tax=Homo sapiens RepID=Q9BTC8-2
>UPI0000D4CDC7 related cluster n=1 Tax=Homo sapiens RepID=UPI0000D4CDC7
>UPI0001881589 related cluster n=1 Tax=Homo sapiens RepID=UPI0001881589

13a UniRef100_UPI0000111654 UniRef100_UPI00017BDB3D UniRef100_UPI00017BDB42 1.0000
confidence: 1. max coverage num unique pi tot indep spec share of spectrum id's: 0.56%
>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

11a UniRef100_P30101 0.9999
confidence: 1. coverage: 5.3' num unique pi tot indep spec share of spect subsumed entries: 2
>Protein disulfide-isomerase A3 n=2 Tax=Hominidae RepID=PDIA3_HUMAN Length: 505aa

6b UniRef100_P06872 0.9998
confidence: 1. coverage: 6.9' num unique pi tot indep spec share of spectrum id's: 1.82%
>Anionic trypsin n=2 Tax=Canis lupus familiaris RepID=TRY2_CANFA Length: 247aa

8d UniRef100_A8K2I0 UniRef100_B2R853 UniRef100_B4DRR0 UniRef100_B4DRU6 UniRef100_B4DRY0 UniRef100_B4DWU6
UniRef100_P02538 UniRef100_P48668 UniRef100_UPI0001AE6B0A UniRef100_UPI0001AE6B0B 0.9998
confidence: 1. max coverage num unique pi tot indep spec share of spectrum id's: 1.23%
>cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA n=1 Tax=Homo sapiens RepID=A8K2I0 Length: 564aa
>cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA n=1 Tax=Homo sapiens RepID=B2R853_HUMAN
>cDNA 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 FLJ54379, highly similar to Keratin, type II cytoskeletal 6E n=1 Tax=Homo sapiens RepID=B4DRY0_HUMAN
>cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A n=1 Tax=Homo sapiens RepID=B4DWU6_HUMAN
>Keratin, type II cytoskeletal 6A n=1 Tax=Homo sapiens RepID=K2C6A_HUMAN
>Keratin, type II cytoskeletal 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

9b UniRef100_P02533 0.9998
confidence: 1. coverage: 7.0' num unique pi tot indep spec share of spect subsumed entries: 2
>Keratin, type I cytoskeletal 14 n=1 Tax=Homo sapiens RepID=K1C14_HUMAN Length: 472aa

9c UniRef100_P08779 0.9998
confidence: 1. coverage: 6.8' num unique pi tot indep spec share of spectrum id's: 0.84%
>Keratin, type I cytoskeletal 16 n=1 Tax=Homo sapiens RepID=K1C16_HUMAN Length: 473aa

14a UniRef100_UPI000186EE46 0.9998
confidence: 0. coverage: 4.9' num unique pi tot indep spec share of spect subsumed entries: 1
>UDP-glucose 6-dehydrogenase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186EE46 Length: 473aa

15 UniRef100_B4DI25 UniRef100_B7Z2E9 UniRef100_B7Z9Y8 UniRef100_Q05BL1 UniRef100_Q13625 UniRef100_Q13625-2
UniRef100_UPI0000D620BA UniRef100_UPI00015E0CE3 0.9911
confidence: 0. max coverage num unique pi tot indep spec share of spectrum id's: 0.56%
>cDNA FLJ51856, highly similar to Apoptosis-stimulating of p53 protein 2 n=1 Tax=Homo sapiens RepID=B4DI25_H Length: 723aa
>cDNA FLJ50500, highly similar to Apoptosis-stimulating of p53 protein 2 n=1 Tax=Homo sapiens RepID=B7Z2E9_HUMAN
>cDNA, FLJ79002, highly similar to Apoptosis-stimulating of p53 protein 2 n=1 Tax=Homo sapiens RepID=B7Z9Y8_HUMAN
>TP53BP2 protein n=1 Tax=Homo sapiens RepID=Q05BL1_HUMAN
>Apoptosis-stimulating of p53 protein 2 n=2 Tax=Homo sapiens RepID=ASPP2_HUMAN
>Isoform 2 of Apoptosis-stimulating of p53 protein 2 n=2 Tax=Homo sapiens RepID=Q13625-2
>Apoptosis-stimulating of p53 protein 2 (Tumor suppressor p53-binding protein 2) (p53BP2) (53BP2) (Bcl2-binding protein) (Bbp) (Renal carcinoma antigen NY-REN-51). n=1 Tax=Homo sapiens RepID=UPI0000D620BA
>Apoptosis-stimulating of p53 protein 2 (Tumor suppressor p53-binding protein 2) (p53-binding protein 2) (p53BP2) (53BP2) (Bcl2-binding protein) (Bbp) (Renal carcinoma antigen NY-REN-51). n=1 Tax=Homo sapiens RepID=UPI00015E0CE3

16 UniRef100_UPI0000E1F682 0.9911
confidence: 0. coverage: 2.7' num unique pi tot indep spec share of spectrum id's: 0.85%
>PREDICTED: similar to [Human Iq rearranged gamma chain mRNA, V-J-C region and complete cds.], gene product Length: 415aa

17 UniRef100_UPI000186CD8C 0.9911
confidence: 0. coverage: 1.3' num unique pi tot indep spec share of spectrum id's: 0.29%
>protein disulfide isomerase, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CD8C Length: 630aa

18 UniRef100_A5JHP3 UniRef100_P81605 0.9893
confidence: 0. max coverage num unique pi tot indep spec share of spectrum id's: 0.29%
>Dermcidin isoform 2 n=1 Tax=Homo sapiens RepID=A5JHP3_HUMAN Length: 121aa
>DCD-1 n=3 Tax=Euarchontoglires RepID=DCD_HUMAN

19 UniRef100_A8K854 UniRef100_B2RBD5 UniRef100_B3KML9 UniRef100_B4DE77 UniRef100_B4DQ99 UniRef100_B4DY90
UniRef100_B4E052 UniRef100_B7ZAF0 UniRef100_B7ZAK1 UniRef100_P04350 UniRef100_P07437 UniRef100_P68371
UniRef100_Q13509 UniRef100_Q1KSF8 UniRef100_Q3ZCR3 UniRef100_Q53G92 UniRef100_Q5JP53 UniRef100_Q5ST81

UniRef100_Q6LC01 UniRef100_Q7KZS6 UniRef100_Q8IWP6 UniRef100_Q8IZ29 UniRef100_Q8N6N5 UniRef100_UPI000186CB60
UniRef100_UPI000186D036 0.9893
confidence: 0. max coverage num unique p| tot indep spec share of spectrum id's: 0.57%
>HCG1983504, isoform CRA_f n=1 Tax=Homo sapiens RepID=A8K854_HUMAN Length: 378aa
>cDNA, FLJ95457, highly similar to Homo sapiens tubulin, beta, 4 (TUBB4), mRNA n=1 Tax=Homo sapiens RepID=B2RBD5_HUMAN
>cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain n=1 Tax=Homo sapiens RepID=B3KML9_HUMAN
>cDNA FLJ55189, highly similar to Tubulin beta-4 chain n=1 Tax=Homo sapiens RepID=B4DE77_HUMAN
>cDNA FLJ50617, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DQN9_HUMAN
>cDNA FLJ56903, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4DY90_HUMAN
>cDNA FLJ52378, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B4E052_HUMAN
>cDNA, FLJ79164, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B7ZAF0_HUMAN
>cDNA, FLJ79215, highly similar to Tubulin beta-7 chain n=1 Tax=Homo sapiens RepID=B7ZAK1_HUMAN
>Tubulin beta-4 chain n=5 Tax=Eutheria RepID=TBB4_HUMAN
>Tubulin beta chain n=12 Tax=Amniota RepID=TBB5_HUMAN
>Tubulin beta-2C chain n=3 Tax=Eutheria RepID=TBB2C_HUMAN
>Tubulin beta-3 chain n=4 Tax=Eutheria RepID=TBB3_HUMAN
>XTP3TPA-transactivated protein 1 n=1 Tax=Homo sapiens RepID=Q1KSF8_HUMAN
>TUBB3 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q3ZCR3_HUMAN
>Tubulin, beta, 4 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53G92_HUMAN
>Tubulin beta polypeptide n=1 Tax=Homo sapiens RepID=Q5JP53_HUMAN
>Tubulin beta polypeptide n=3 Tax=Hominidae RepID=Q5ST81_HUMAN
>MRNA encoding beta-tubulin. (from clone D-beta-1) (Fragment) n=1 Tax=Homo sapiens RepID=Q6LC01_HUMAN
>HCG2042771 n=1 Tax=Homo sapiens RepID=Q7KZS6_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
>tubulin beta chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CB60
>tubulin beta chain, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D036

6c

UniRef100_P06871 UniRef100_UPI00004A5B07 UniRef100_UPI00005A2FD6 UniRef100_UPI00005A2FD7 0.9618
confidence: 1. max coverage num unique p| tot indep spec share of spect subsumed entries: 1
>Cationic trypsin n=1 Tax=Canis lupus familiaris RepID=TRY1_CANFA Length: 246aa
>PREDICTED: similar to trypsinogen 7 isoform 3 n=1 Tax=Canis lupus familiaris RepID=UPI00004A5B07
>PREDICTED: similar to trypsinogen 7 isoform 5 n=1 Tax=Canis lupus familiaris RepID=UPI00005A2FD6
>PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 6 n=1 Tax=Canis lupus familiaris RepID=UPI00005A2FD7