

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)

PML lower band MS results:

18 entries (7 single hits) retrieved from
/home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_PML-1-sequest.prot.xml

* corresponds to peptide is_nondegenerate_evidence flag

- 1 UniRef100_P35527 1.0000
confidence: 1. coverage: 18.1 num unique p|tot indep spec share of spectrum id's: 7.31%
>Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN Length: 623aa
- 2 UniRef100_UPI000186E38A 1.0000
confidence: 1. coverage: 14.1 num unique p|tot indep spec share of spectrum id's: 3.59%
>Tropomyosin-2, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186E38A Length: 284aa
- 5a UniRef100_C5IWV5 UniRef100_P00761 1.0000
confidence: 1. max coverage num unique p|tot indep spec share of spect subsumed entries: 2
>Trypsinogen n=1 Tax=Sus scrofa RepID=C5IWV5_PIG Length: 246aa
>Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG
- 5b UniRef100_P06872 1.0000
confidence: 1. coverage: 6.9 num unique p|tot indep spec share of spectrum id's: 3.07%
>Anionic trypsin n=2 Tax=Canis lupus familiaris RepID=TRY2_CANFA Length: 247aa
- 6a UniRef100_P02769 1.0000
confidence: 1. coverage: 21.1 num unique p|tot indep spec share of spect subsumed entries: 6
>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa
- 7a UniRef100_P04264 1.0000
confidence: 1. coverage: 23.1 num unique p|tot indep spec share of spect subsumed entries: 1
>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN Length: 644aa
- 7b UniRef100_P35908 1.0000
confidence: 1. coverage: 12.1 num unique p|tot indep spec share of spectrum id's: 2.12%
>Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E_HUMAN Length: 639aa
- 8a UniRef100_P11021 1.0000
confidence: 1. coverage: 6.9 num unique p|tot indep spec share of spect subsumed entries: 2
>78 kDa glucose-regulated protein n=1 Tax=Homo sapiens RepID=GRP78_HUMAN Length: 654aa
- 9a UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000
confidence: 1. max coverage num unique p|tot indep spec share of spect subsumed entries: 2
>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_P29590 UniRef100_P29590-2 UniRef100_P29590-3 UniRef100_P29590-4 UniRef100_P29590-5 UniRef100_P29590-7
UniRef100_Q15959 UniRef100_Q9BZX7 UniRef100_Q9BZY3 1.0000**
confidence: 1. max coverage num unique p|tot indep spec share of spect subsumed entries: 2
>Probable transcription factor PML n=1 Tax=Homo sapiens RepID=PML_HUMAN Length: 882aa
>Isoform PML-2 of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-2
>Isoform PML-3 of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-3
>Isoform PML-3B of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-4
>Isoform PML-X of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-5
>Isoform PML-5 of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-7
>PML protein n=1 Tax=Homo sapiens RepID=Q15959_HUMAN
>Tripartite motif protein TRIM19 kappa n=1 Tax=Homo sapiens RepID=Q9BZX7_HUMAN
>Tripartite motif protein TRIM19 beta n=1 Tax=Homo sapiens RepID=Q9BZY3_HUMAN
- 11a UniRef100_P35579 UniRef100_P35579-2 1.0000
confidence: 1. max coverage num unique p|tot indep spec share of spect subsumed entries: 1
>Myosin-9 n=2 Tax=Homo sapiens RepID=MYH9_HUMAN Length: 1960aa
>Isoform 2 of Myosin-9 n=1 Tax=Homo sapiens RepID=P35579-2
- 4a UniRef100_B3KTV0 UniRef100_B4DTX2 UniRef100_P11142 UniRef100_Q53GZ6 UniRef100_Q53HF2 UniRef100_UPI00015E00A1
0.9999
confidence: 1. max coverage num unique p|tot indep spec share of spect subsumed entries: 1
>cDNA FLJ38781 fis, clone LIVER2000216, highly similar to HEAT SHOCK COGNATE 71 kDa PROTEIN n=1 Tax=Homo sapiens RepID=FLJ38781_HUMAN Length: 621aa
>cDNA FLJ59163, highly similar to Heat shock cognate 71 kDa protein n=2 Tax=Euarchontoglires RepID=B4DTX2_HUMAN

>Heat shock cognate 71 kDa protein n=8 Tax=Eutheria RepID=HSP7C_HUMAN
 >Heat shock 70kDa protein 8 isoform 1 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53GZ6_HUMAN
 >Heat shock 70kDa protein 8 isoform 2 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53HF2_HUMAN
 >Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8). n=1 Tax=Homo sapiens RepID=UPI00015E00A1

- 12a UniRef100_UPI0000111654 UniRef100_UPI00017BDB3D UniRef100_UPI00017BDB42 0.9998
 confidence: 1. max coverage num unique p_i tot indep spec share of spectrum id's: 1.36%
 >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
- 4b UniRef100_B2R6X5 UniRef100_B3KSM6 UniRef100_P17066 UniRef100_P48741 UniRef100_Q53FC7 0.9995
 confidence: 1. max coverage num unique p_i tot indep spec share of spectrum id's: 0.72%
 >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
 >Putative heat shock 70 kDa protein 7 n=1 Tax=Homo sapiens RepID=HSP77_HUMAN
 >Heat shock 70kDa protein 6 (HSP70B') variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53FC7_HUMAN
- 13 UniRef100_C6L245 0.9983
 confidence: 0. coverage: 5.3' num unique p_i tot indep spec share of spectrum id's: 1.04%
 >Putative trypsinogen n=1 Tax=Sus scrofa RepID=C6L245_PIG Length: 247aa
- 14 UniRef100_A5JHP3 UniRef100_P81605 0.9932
 confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 1.08%
 >Dermcidin isoform 2 n=1 Tax=Homo sapiens RepID=A5JHP3_HUMAN Length: 121aa
 >DCD-1 n=3 Tax=Euarchontoglires RepID=DCD_HUMAN
- 15 UniRef100_UPI000186D393 0.9932
 confidence: 0. coverage: 3.2' num unique p_i tot indep spec share of spectrum id's: 0.36%
 >conserved hypothetical protein n=1 Tax=Pediculus humanus corporis RepID=UPI000186D393 Length: 252aa
- 16 UniRef100_B4DVQ0 UniRef100_B4DW52 UniRef100_B4E335 UniRef100_B4E3A4 UniRef100_P60709 UniRef100_P63261
 UniRef100_Q4R4H6 UniRef100_Q53G76 UniRef100_Q53G99 UniRef100_Q53GK6 UniRef100_Q6PJ43 UniRef100_Q8WVW5
 UniRef100_UPI000186E470 0.9925
 confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.72%
 >cDNA FLJ58286, highly similar to Actin, cytoplasmic 2 n=1 Tax=Homo sapiens RepID=B4DVQ0_HUMAN Length: 333aa
 >cDNA FLJ55253, highly similar to Actin, cytoplasmic 1 n=1 Tax=Homo sapiens RepID=B4DW52_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
 >Actin, cytoplasmic 1, N-terminally processed n=24 Tax=Amniota RepID=ACTB_HUMAN
 >Actin, cytoplasmic 2, N-terminally processed n=9 Tax=Tetrapoda RepID=ACTG_HUMAN
 >Brain cDNA, clone: QfA-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
 >ACTG1 protein (Fragment) n=5 Tax=Eutheria RepID=Q6PJ43_HUMAN
 >Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8WVW5_HUMAN
 >Actin-5C n=1 Tax=Pediculus humanus corporis RepID=UPI000186E470
- 17 UniRef100_P27694 0.9925
 confidence: 0. coverage: 2.1' num unique p_i tot indep spec share of spectrum id's: 1.08%
 >Replication protein A 70 kDa DNA-binding subunit n=1 Tax=Homo sapiens RepID=RFA1_HUMAN Length: 616aa
- 18 UniRef100_P16159 UniRef100_P32936 0.9838
 confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.36%
 >Alpha-amylase/trypsin inhibitor CM16 n=2 Tax=Triticum aestivum RepID=IAC16_WHEAT Length: 143aa
 >Alpha-amylase/trypsin inhibitor CMB n=2 Tax=Hordeum vulgare RepID=IAAB_HORVU
- 5c UniRef100_P06871 UniRef100_UPI00004A5B07 UniRef100_UPI00005A2FD6 UniRef100_UPI00005A2FD7 0.9779
 confidence: 1. max coverage num unique p_i tot indep spec share of spect subsumed entries: 2
 >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

PML upper band MS results:

11 entries (5 single hits) retrieved from
 /home/TPP/tpp/20110617_Bowling/int-gb_20110617_LTQ_Bowling_PML-2-sequest.prot.xml

* corresponds to peptide is_nondegenerate_evidence flag

2a UniRef100_C5IWV5 UniRef100_P00761 1.0000
confidence: 1. max coverage num unique p_i tot indep spec share of spectrum id's: 28.10%
>Trypsinogen n=1 Tax=Sus scrofa RepID=C5IWV5_PIG Length: 246aa
>Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG

2b UniRef100_P06872 1.0000
confidence: 1. coverage: 6.9 num unique p_i tot indep spec share of spectrum id's: 3.64%
>Anionic trypsin n=2 Tax=Canis lupus familiaris RepID=TRY2_CANFA Length: 247aa

2c UniRef100_P00762 1.0000
confidence: 1. coverage: 8.1 num unique p_i tot indep spec share of spectrum id's: 0.77%
>Anionic trypsin-1 n=1 Tax=Rattus norvegicus RepID=TRY1_RAT Length: 246aa

3a UniRef100_P02769 1.0000
confidence: 1. coverage: 11. num unique p_i tot indep spec share of spect subsumed entries: 5
>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa

4a UniRef100_P04264 1.0000
confidence: 1. coverage: 25. num unique p_i tot indep spec share of spect subsumed entries: 1
>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN Length: 644aa

5a UniRef100_P14625 UniRef100_Q5CAQ5 1.0000
confidence: 1. max coverage num unique p_i tot indep spec share of spect subsumed entries: 1
>Endoplasmin n=1 Tax=Homo sapiens RepID=ENPL_HUMAN Length: 803aa
>Tumor rejection antigen (Gp96) 1 n=1 Tax=Homo sapiens RepID=Q5CAQ5_HUMAN

7a UniRef100_P35527 1.0000
confidence: 1. coverage: 17. num unique p_i tot indep spec share of spectrum id's: 8.18%
>Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN Length: 623aa

7b UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000
confidence: 1. max coverage num unique p_i tot indep spec share of spectrum id's: 7.08%
>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

8a UniRef100_P35579 UniRef100_P35579-2 1.0000
confidence: 0. max coverage num unique p_i tot indep spec share of spect subsumed entries: 1
>Myosin-9 n=2 Tax=Homo sapiens RepID=MYH9_HUMAN Length: 1960aa
>Isoform 2 of Myosin-9 n=1 Tax=Homo sapiens RepID=P35579-2

6a **UniRef100_P29590 UniRef100_P29590-2 UniRef100_P29590-3 UniRef100_P29590-4 UniRef100_P29590-5 UniRef100_P29590-7
UniRef100_Q15959 UniRef100_Q9BZX7 UniRef100_Q9BZX9 UniRef100_Q9BZY0 UniRef100_Q9BZY1 UniRef100_Q9BZY2
UniRef100_Q9BZY3 0.9999**
confidence: 1 max coverage num unique p_i tot indep spec share of spect subsumed entries: 1
>Probable transcription factor PML n=1 Tax=Homo sapiens RepID=PML_HUMAN Length: 882aa
>Isoform PML-2 of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-2
>Isoform PML-3 of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-3
>Isoform PML-3B of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-4
>Isoform PML-X of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-5
>Isoform PML-5 of Probable transcription factor PML n=1 Tax=Homo sapiens RepID=P29590-7
>PML protein n=1 Tax=Homo sapiens RepID=Q15959_HUMAN
>Tripartite motif protein TRIM19 kappa n=1 Tax=Homo sapiens RepID=Q9BZX7_HUMAN
>Tripartite motif protein TRIM19 zeta n=1 Tax=Homo sapiens RepID=Q9BZX9_HUMAN
>Tripartite motif protein TRIM19 epsilon n=1 Tax=Homo sapiens RepID=Q9BZY0_HUMAN
>Tripartite motif protein TRIM19 delta n=1 Tax=Homo sapiens RepID=Q9BZY1_HUMAN
>Tripartite motif protein TRIM19 gamma n=1 Tax=Homo sapiens RepID=Q9BZY2_HUMAN
>Tripartite motif protein TRIM19 beta n=1 Tax=Homo sapiens RepID=Q9BZY3_HUMAN

7c UniRef100_P02533 0.9999
confidence: 1. coverage: 10. num unique p_i tot indep spec share of spect subsumed entries: 6
>Keratin, type I cytoskeletal 14 n=1 Tax=Homo sapiens RepID=K1C14_HUMAN Length: 472aa

7d UniRef100_P08779 0.9999
confidence: 1. coverage: 10. num unique p_i tot indep spec share of spectrum id's: 1.39%
>Keratin, type I cytoskeletal 16 n=1 Tax=Homo sapiens RepID=K1C16_HUMAN Length: 473aa

- 9 UniRef100_UPI0000111654 UniRef100_UPI0000112158 UniRef100_UPI00017BDB3D UniRef100_UPI00017BDB42 0.9937
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 1.37%
>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
- 10 UniRef100_B4DR68 UniRef100_Q12931 UniRef100_Q53FS6 UniRef100_Q53G55 UniRef100_Q8N9Z3 UniRef100_Q9BV61
UniRef100_UPI000186D735 0.9886
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 1.37%
>cDNA FLJ58608, highly similar to Heat shock protein 75 kDa, mitochondrial n=1 Tax=Homo sapiens RepID=B4DR6; 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
>cDNA FLJ36025 fis, clone TESTI2016701, highly similar to TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN n=1
Tax=Homo sapiens RepID=Q8N9Z3_HUMAN
>TRAP1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q9BV61_HUMAN
>heat shock protein 75 kDa, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186D735
- 11 UniRef100_B4DVQ0 UniRef100_B4DW52 UniRef100_B4E335 UniRef100_B4E3A4 UniRef100_P60709 UniRef100_P63261
UniRef100_Q4R4H6 UniRef100_Q53G76 UniRef100_Q53G99 UniRef100_Q53GK6 UniRef100_Q6PJ43 UniRef100_Q8WVW5
UniRef100_UPI000186E470 0.9807
confidence: 0. max coverage num unique p_i tot indep spec share of spectrum id's: 0.46%
>cDNA FLJ58286, highly similar to Actin, cytoplasmic 2 n=1 Tax=Homo sapiens RepID=B4DVQ0_HUMAN Length: 333aa
>cDNA FLJ5253, highly similar to Actin, cytoplasmic 1 n=1 Tax=Homo sapiens RepID=B4DW52_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
>Actin, cytoplasmic 1, N-terminally processed n=24 Tax=Amniota RepID=ACTB_HUMAN
>Actin, cytoplasmic 2, N-terminally processed n=9 Tax=Tetrapoda RepID=ACTG_HUMAN
>Brain cDNA, clone: QfIA-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
>ACTG1 protein (Fragment) n=5 Tax=Eutheria RepID=Q6PJ43_HUMAN
>Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens RepID=Q8WVW5_HUMAN
>Actin-5C n=1 Tax=Pediculus humanus corporis RepID=UPI000186E470