

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

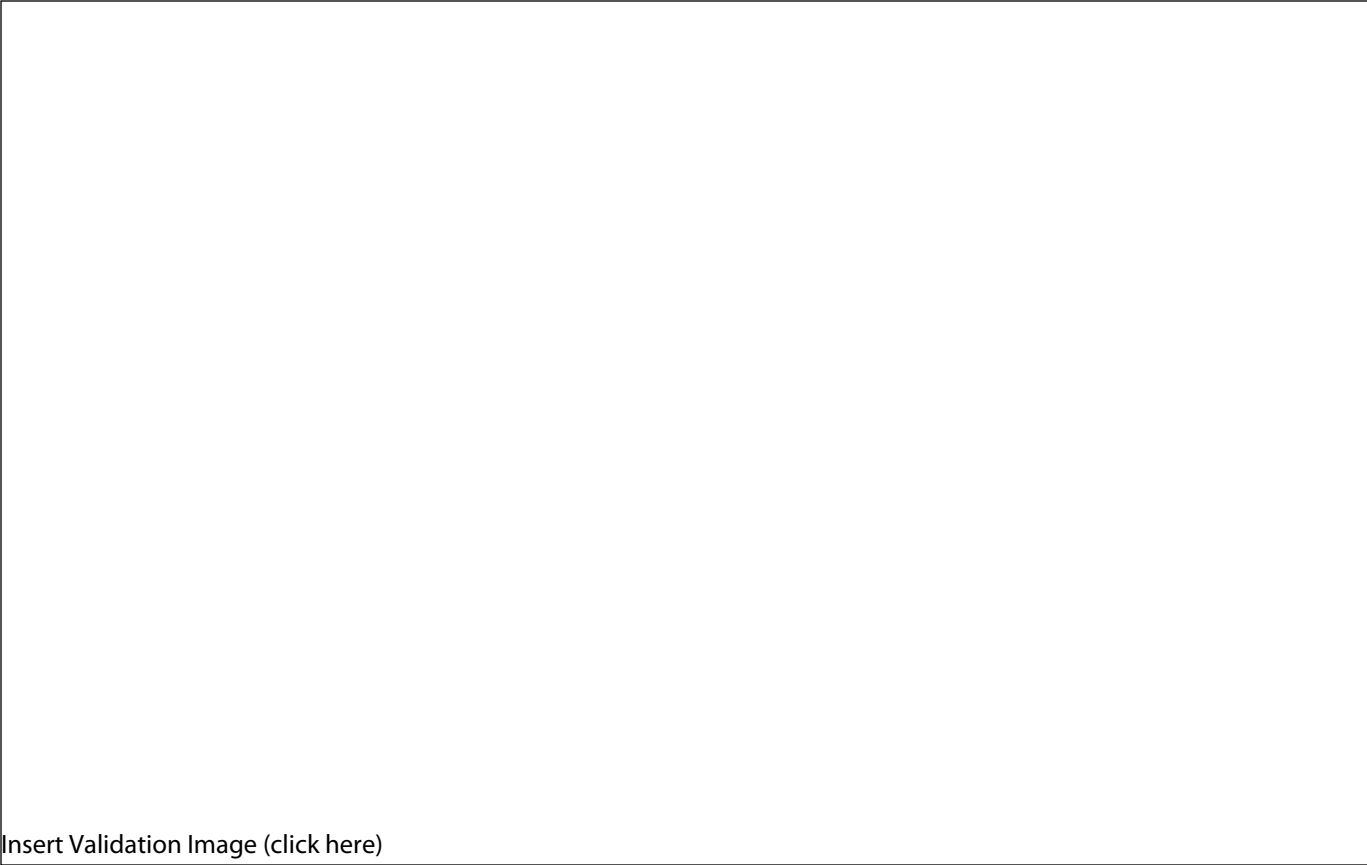
AA Position

Modification

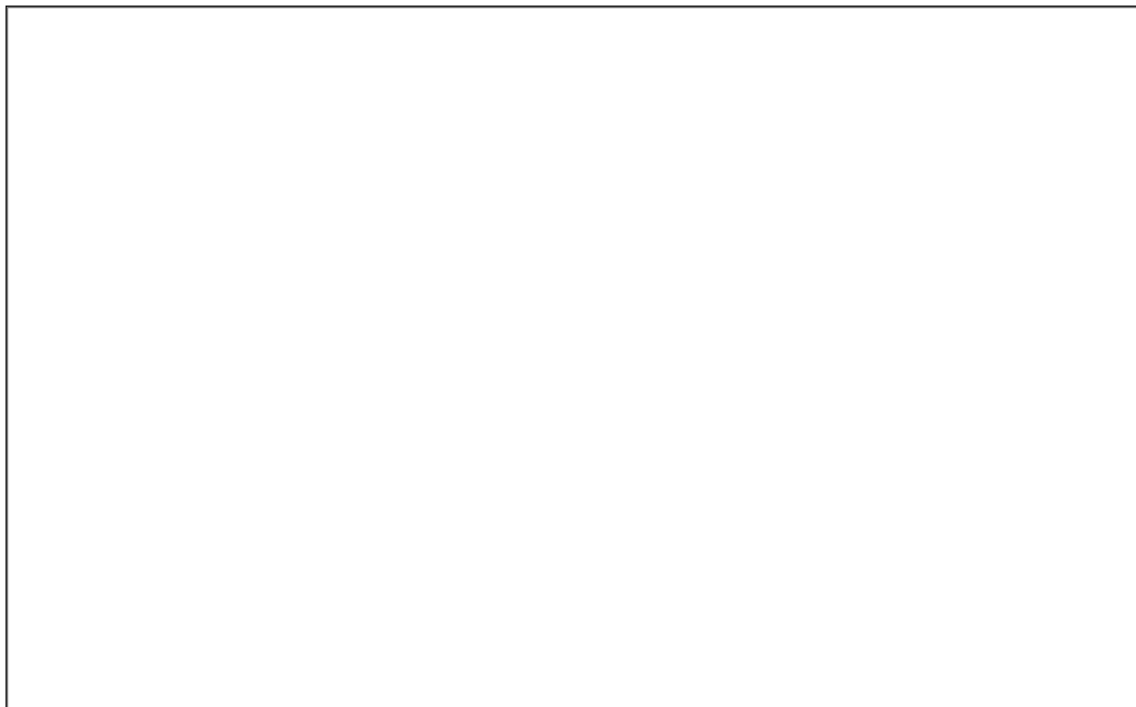
Validation #1
Analysis



Insert Validation Image (click here)



Validation #2
Analysis



Insert Validation Image (Click here)

15 entries (4 single hits) retrieved from
/home/TPP/tpp/20110218_Bowling/int-gb_20110218_LTQ_Bowling_IRF9-sequest.prot.xml

* corresponds to peptide is_nondegenerate_evidence flag

8a	UniRef100_P19474 1.0000 confidence: 1. coverage: 31. num unique p tot indep spec share of spect subsumed entries: 2 >52 kDa Ro protein n=1 Tax=Homo sapiens RepID=RO52_HUMAN	Length: 475aa
4a	UniRef100_C5I WV5 UniRef100_P00761 1.0000 confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 6.30% >Trypsinogen n=1 Tax=Sus scrofa RepID=C5I WV5_PIG >Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG	Length: 246aa
7a	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 >keratin, type I cytoskeletal 10 n=1 Tax=Homo sapiens RepID=UPI00017BCE7F	Length: 584aa
7b	UniRef100_P35527 1.0000 confidence: 1. coverage: 17. num unique p tot indep spec share of spectrum id's: 8.61% >Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN	Length: 623aa
6a	UniRef100_P04264 1.0000 confidence: 1. coverage: 14. 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
9a	UniRef100_Q00978 1.0000 confidence: 1 coverage: 12 num unique p tot indep spec share of spect subsumed entries: 2 >Interferon regulatory factor 9 n=2 Tax=Homo sapiens RepID=IRF9_HUMAN	Length: 393aa
14	UniRef100_P62805 UniRef100_UPI000186CBA9 UniRef100_UPI000186CBAA UniRef100_UPI000186DE6C 0.9838 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.77% >Histone H4 n=46 Tax=Bilateria RepID=H4_HUMAN >histone H4, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CBA9 >histone H4, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186CBAA >histone H4, putative n=1 Tax=Pediculus humanus corporis RepID=UPI000186DE6C	Length: 103aa
6b	UniRef100_P35908 1.0000 confidence: 1. coverage: 8.3 num unique p tot indep spec share of spectrum id's: 3.10% >Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens RepID=K22E_HUMAN	Length: 639aa
10	UniRef100_A0N5G3 UniRef100_A2NUT2 UniRef100_C6KXN3 UniRef100_Q6GMW3 UniRef100_Q6GMX4 UniRef100_Q6IPQ0 UniRef100_Q6PIQ7 UniRef100_Q6PJG0 UniRef100_Q8N355 UniRef100_Q8N5F4 UniRef100_Q96JD0 UniRef100_UPI0000112C31 UniRef100_UPI000158A17D UniRef100_UPI0001A5EC47 UniRef100_UPI0001BEF2DB UniRef100_UPI0001D63C0B 0.9988 confidence: 0. max coverage num unique p tot indep spec share of spectrum id's: 0.61% >Rheumatoid factor G9 light chain (Fragment) n=1 Tax=Homo sapiens RepID=A0N5G3_HUMAN >Lambda-chain (AA -20 to 215) n=1 Tax=Homo sapiens RepID=A2NUT2_HUMAN >Cyclosporin A transporter 1 (Fragment) n=1 Tax=Homo sapiens RepID=C6KXN3_HUMAN >IGL@ protein n=1 Tax=Homo sapiens RepID=Q6GMW3_HUMAN >IGL@ protein n=1 Tax=Homo sapiens RepID=Q6GMX4_HUMAN >IGL@ protein n=1 Tax=Homo sapiens RepID=Q6IPQ0_HUMAN >IGL@ protein n=1 Tax=Homo sapiens RepID=Q6PIQ7_HUMAN >Putative uncharacterized protein n=1 Tax=Homo sapiens RepID=Q6PJG0_HUMAN >IGL@ protein n=1 Tax=Homo sapiens RepID=Q8N355_HUMAN >IGL@ protein n=1 Tax=Homo sapiens RepID=Q8N5F4_HUMAN >Amyloid lambda 6 light chain variable region SAR (Fragment) n=1 Tax=Homo sapiens RepID=Q96JD0_HUMAN >BENCE-JONES PROTEIN RHE (LIGHT CHAIN) n=1 Tax=Homo sapiens RepID=UPI0000112C31 >Bence Jones KWR Protein - Immunoglobulin Ligh n=1 Tax=Homo sapiens RepID=UPI000158A17D >PREDICTED: hypothetical protein XP_002348153 n=1 Tax=Homo sapiens RepID=UPI0001A5EC47 >Fab 537-10D, light chain n=1 Tax=Homo sapiens RepID=UPI0001BEF2DB >Antibody PG9 light chain n=1 Tax=Homo sapiens RepID=UPI0001D63C0B	Length: 121aa
2a	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 confidence: 1. max coverage num unique p tot indep spec share of spectrum id's: 1.86% >cDNA FLJ78387 n=1 Tax=Homo sapiens RepID=A8K008_HUMAN >Ig gamma-1 chain C region n=1 Tax=Homo sapiens RepID=IGHG1_HUMAN	Length: 472aa

>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 gamma1 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

- 5a UniRef100_P02769 1.0000
 confidence: 1. coverage: 4.4' num unique p| tot indep spec share of spect subsumed entries: 1
 >Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa
- 13a UniRef100_B4DMJ6 UniRef100_P36578 UniRef100_Q53G74 UniRef100_Q59GY2 UniRef100_UPI0001AE68FD 0.9871
 confidence: 0. max coverage num unique p| tot indep spec share of spect subsumed entries: 2
 >cDNA FLJ50996, highly similar to 60S ribosomal protein L4 n=1 Tax=Homo sapiens RepID=B4DMJ6_HUMAN Length: 414aa
 >60S ribosomal protein L4 n=1 Tax=Homo sapiens RepID=RL4_HUMAN
 >Ribosomal protein L4 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q53G74_HUMAN
 >Ribosomal protein L4 variant (Fragment) n=1 Tax=Homo sapiens RepID=Q59GY2_HUMAN
 >UPI0001AE68FD related cluster n=1 Tax=Homo sapiens RepID=UPI0001AE68FD
- 15 UniRef100_B4DEI8 UniRef100_Q14CN4 UniRef100_Q14CN4-2 UniRef100_Q3SY84 UniRef100_Q7RTS7 UniRef100_Q86Y46
 UniRef100_Q86Y46-2 UniRef100_UPI00019912E7 0.9537
 confidence: 0. max coverage num unique p| tot indep spec share of spectrum id's: 0.39%
 >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
- 12 UniRef100_Q9HB75 UniRef100_Q9HB75-2 UniRef100_Q9HB75-3 UniRef100_Q9HB75-4 0.9891
 confidence: 0. max coverage num unique p| tot indep spec share of spectrum id's: 0.86%
 >Leucine-rich repeat and death domain-containing protein n=1 Tax=Homo sapiens RepID=PIDD_HUMAN Length: 910aa
 >Isoform 2 of Leucine-rich repeat and death domain-containing protein n=1 Tax=Homo sapiens RepID=Q9HB75-2
 >Isoform 3 of Leucine-rich repeat and death domain-containing protein n=1 Tax=Homo sapiens RepID=Q9HB75-3
 >Isoform 4 of Leucine-rich repeat and death domain-containing protein n=1 Tax=Homo sapiens RepID=Q9HB75-4
- 11 UniRef100_Q2M1Z1 UniRef100_Q8N3N3 UniRef100_Q9UHC1 UniRef100_Q9UHC1-2 UniRef100_UPI00001AE6A4 UniRef100_UPI00001AE6E0
 0.9891
 confidence: 0. max coverage num unique p| tot indep spec share of spectrum id's: 0.46%
 >MutL homolog 3 (E. coli) n=1 Tax=Homo sapiens RepID=Q2M1Z1_HUMAN Length: 1429aa
 >Putative uncharacterized protein DKFZp762L056 (Fragment) n=1 Tax=Homo sapiens RepID=Q8N3N3_HUMAN
 >DNA mismatch repair protein Mlh3 n=1 Tax=Homo sapiens RepID=MLH3_HUMAN
 >Isoform 2 of DNA mismatch repair protein Mlh3 n=1 Tax=Homo sapiens RepID=Q9UHC1-2
 >mutL homolog 3 isoform 2 n=1 Tax=Homo sapiens RepID=UPI00001AE6A4
 >mutL homolog 3 isoform 1 n=1 Tax=Homo sapiens RepID=UPI00001AE6E0