

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

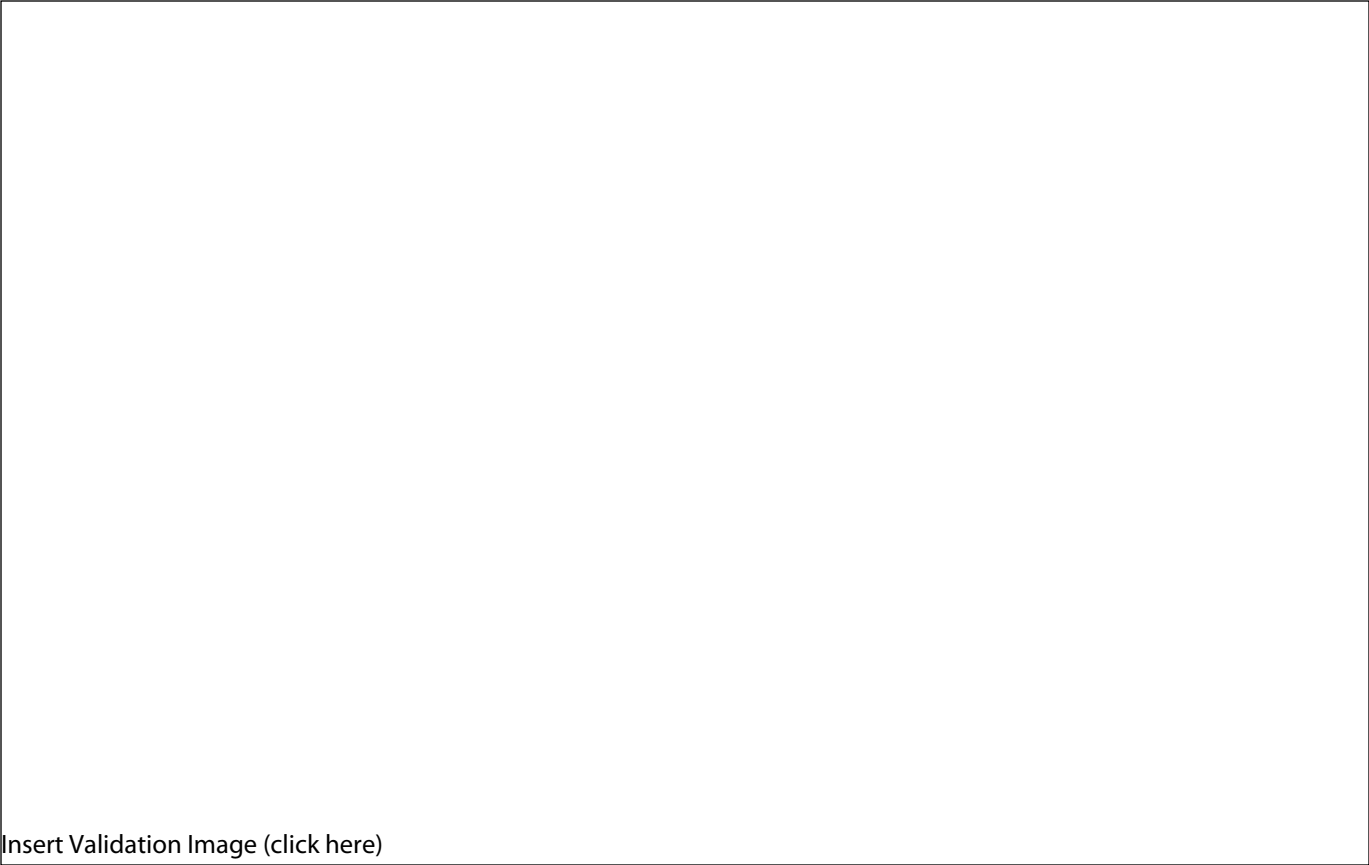
AA Position

Modification

Validation #1
Analysis



Insert Validation Image (click here)



Validation #2
Analysis



Insert Validation Image (Click here)

MS results for lower band (~120 kDa):

1

UniRef100_C5I WV5 UniRef100_P00761 1.0000

confidence: 1.00 max coverage: 30.3% num unique peps: 20tot indep
spectra: 51 share of spectrum id's: 14.90%

>Trypsinogen n=1 Tax=Sus scrofa RepID=C5I WV5_PIG Length: 246aa

>Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG

2

UniRef100_P04264 1.0000

confidence: 1.00 coverage: 21.1% num unique peps: 12tot indep spectra: 30
share of spectrum id's: 14.79% subsumed entries: 1

>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN
Length: 644aa

3

UniRef100_P02769 1.0000

confidence: 1.00 coverage: 20.6% num unique peps: 12tot indep spectra: 23
share of spectrum id's: 11.85% subsumed entries: 1

>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa

4

UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000

confidence: 1.00 max coverage: 20.5% num unique peps: 10tot indep
spectra: 25 share of spectrum id's: 12.86% 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

5

UniRef100_P35908 1.0000

confidence: 1.00 coverage: 20.3% num unique peps: 7 tot indep spectra: 9
share of spectrum id's: 6.42% subsumed entries: 2

>Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens
RepID=K22E_HUMAN Length: 639aa

6

UniRef100_B4DVQ0 UniRef100_B4DW52 UniRef100_B4E335
UniRef100_B4E3A4 UniRef100_P60709 UniRef100_P63261

UniRef100_Q4R4H6 UniRef100_Q53G76 UniRef100_Q53G99 UniRef100_Q53GK6
UniRef100_Q8WVW5 UniRef100_UPI000186E470

1.0000

confidence: 1.00 max coverage: 19.5% num unique peps: 5 tot indep
spectra: 6 share of spectrum id's: 2.94% subsumed entries: 4

>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: Qf1A-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

>Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens
RepID=Q8WVW5_HUMAN

>Actin-5C n=1 Tax=Pediculus humanus corporis RepID=UPI000186E470

7

UniRef100_B4DWU0 UniRef100_B4E2J5 UniRef100_P08779 1.0000

confidence: 1.00 max coverage: 19.3% num unique peps: 2 tot indep
spectra: 4 share of spectrum id's: 2.11% subsumed entries: 1

>cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 n=1 Tax=Homo
sapiens RepID=B4DWU0_HUMAN Length: 135aa

>cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 n=1 Tax=Homo
sapiens RepID=B4E2J5_HUMAN

>Keratin, type I cytoskeletal 16 n=1 Tax=Homo sapiens RepID=K1C16_HUMAN

8

UniRef100_P35527 1.0000

confidence: 1.00 coverage: 17.3% num unique peps: 6 tot indep spectra: 12
share of spectrum id's: 6.20%

>Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN
Length: 623aa

9

UniRef100_A5JHP3 UniRef100_P81605 0.9897

confidence: 0.37 max coverage: 10.0% num unique peps: 1 tot indep
spectra: 3 share of spectrum id's: 1.56%

>Dermcidin isoform 2 n=1 Tax=Homo sapiens RepID=A5JHP3_HUMAN
Length: 121aa

>DCD-1 n=3 Tax=Euarchontoglires RepID=DCD_HUMAN

10

UniRef100_B4E205 UniRef100_O95486 1.0000

confidence: 1.00 max coverage: 8.4% num unique peps: 5 tot indep spectra: 7
share of spectrum id's: 3.34%

>cDNA FLJ61651, highly similar to Protein transport protein Sec24A n=1 Tax=Homo
sapiens RepID=B4E205_HUMAN Length: 857aa

>Protein transport protein Sec24A n=1 Tax=Homo sapiens RepID=SC24A_HUMAN

11

UniRef100_P35579 1.0000

confidence: 1.00 coverage: 6.0% num unique peps: 8 tot indep spectra: 14
share of spectrum id's: 7.14% subsumed entries: 5

>Myosin-9 n=2 Tax=Homo sapiens RepID=MYH9_HUMAN Length: 1960aa

12

UniRef100_UPI0001D34140 0.9663

confidence: 0.21 coverage: 5.8% num unique peps: 1 tot indep spectra: 2
share of spectrum id's: 1.03%

>fab fragment of anti-Shh 5E1 mouse/human chim n=1 Tax=Mus musculus
RepID=UPI0001D34140 Length: 223aa

13

UniRef100_P19474 1.0000

confidence: 1.00 coverage: 5.7% num unique peps: 3 tot indep spectra: 5
share of spectrum id's: 2.59% subsumed entries: 1

>52 kDa Ro protein n=1 Tax=Homo sapiens RepID=RO52_HUMAN Length:
475aa

14

UniRef100_P13647 0.9993

confidence: 1.00 coverage: 5.6% num unique peps: 1 tot indep spectra: 1
share of spectrum id's: 1.51%

>Keratin, type II cytoskeletal 5 n=1 Tax=Homo sapiens RepID=K2C5_HUMAN
Length: 590aa

15

UniRef100_D3Y298 0.9754

confidence: 0.23 coverage: 4.9% num unique peps: 1 tot indep spectra: 2
share of spectrum id's: 1.04%

>Trypsinon (Fragment) n=1 Tax=Branchiostoma belcheri RepID=D3Y298_BRABE
Length: 204aa

16

UniRef100_A0JLS9 UniRef100_B2RBI8 UniRef100_B4DGU2
UniRef100_B4DJV0 UniRef100_B4DS26 UniRef100_B4DSB8
UniRef100_B4DUW9 UniRef100_P37275 UniRef100_Q13088
UniRef100_Q2KJ05 UniRef100_Q32Q63 UniRef100_Q5VZ84

UniRef100_Q8NB68 UniRef100_UPI000175911C UniRef100_UPI0001CE91A2
UniRef100_UPI0001CE91A3 0.9883

confidence: 0.10 max coverage: 2.0% num unique peps: 1 tot
indep spectra: 1 share of spectrum id's: 0.52%

>ZEB1 protein (Fragment) n=1 Tax=Homo sapiens RepID=A0JLS9_HUMAN
Length: 1059aa

>cDNA, FLJ95535, highly similar to Homo sapiens transcription factor 8
(represses interleukin 2 expression) (TCF8), mRNA n=1 Tax=Homo sapiens
RepID=B2RBI8_HUMAN

>cDNA FLJ61244, highly similar to Transcription factor 8 n=1 Tax=Homo
sapiens RepID=B4DGU2_HUMAN

>cDNA FLJ50550, highly similar to Transcription factor 8 (Fragment) n=1
Tax=Homo sapiens RepID=B4DJV0_HUMAN

>cDNA FLJ50636, highly similar to Transcription factor 8 n=1 Tax=Homo
sapiens RepID=B4DS26_HUMAN

>cDNA FLJ50640, highly similar to Transcription factor 8 (Fragment) n=1
Tax=Homo sapiens RepID=B4DSB8_HUMAN

>cDNA FLJ50696, highly similar to Transcription factor 8 n=1 Tax=Homo
sapiens RepID=B4DUW9_HUMAN

>Zinc finger E-box-binding homeobox 1 n=1 Tax=Homo sapiens
RepID=ZEB1_HUMAN

>ZEB (Fragment) n=1 Tax=Homo sapiens RepID=Q13088_HUMAN

>Zinc finger E-box binding homeobox 1 n=1 Tax=Homo sapiens
RepID=Q2KJ05_HUMAN

>ZEB1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q32Q63_HUMAN

>Zinc finger E-box binding homeobox 1 n=2 Tax=Homo sapiens
RepID=Q5VZ84_HUMAN

>cDNA FLJ34159 fis, clone FCBBF3013623, highly similar to NIL-2-A ZINC
FINGER PROTEIN n=1 Tax=Homo sapiens RepID=Q8NB68_HUMAN

>zinc finger E-box-binding homeobox 1 isoform a n=2 Tax=Homo sapiens
RepID=UPI000175911C

>zinc finger E-box-binding homeobox 1 isoform d n=1 Tax=Homo sapiens
RepID=UPI0001CE91A2

**>zinc finger E-box-binding homeobox 1 isoform e n=1 Tax=Homo sapiens
RepID=UPI0001CE91A3**

MS results for upper band (~200 kDa):

1

UniRef100_P04264 1.0000

confidence: 1.00 coverage: 50.3% num unique peps: 41tot indep spectra:
106 share of spectrum id's: 23.02% subsumed entries: 1

>Keratin, type II cytoskeletal 1 n=1 Tax=Homo sapiens RepID=K2C1_HUMAN
Length: 644aa

2

UniRef100_P35527 1.0000

confidence: 1.00 coverage: 44.6% num unique peps: 25tot indep spectra: 58
share of spectrum id's: 12.41%

>Keratin, type I cytoskeletal 9 n=1 Tax=Homo sapiens RepID=K1C9_HUMAN
Length: 623aa

3

UniRef100_P13645 UniRef100_UPI00017BCE7F 1.0000

confidence: 1.00 max coverage: 35.4% num unique peps: 23tot indep
spectra: 62 share of spectrum id's: 13.17%

>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

4

UniRef100_P02769 1.0000

confidence: 1.00 coverage: 32.6% num unique peps: 22tot indep spectra: 47
share of spectrum id's: 9.82% subsumed entries: 6

>Serum albumin n=1 Tax=Bos taurus RepID=ALBU_BOVIN Length: 607aa

5

UniRef100_C5I WV5 UniRef100_P00761 1.0000

confidence: 1.00 max coverage: 28.6% num unique peps: 18tot indep
spectra: 45 share of spectrum id's: 6.62%

>Trypsinogen n=1 Tax=Sus scrofa RepID=C5I WV5_PIG Length: 246aa

>Trypsin n=1 Tax=Sus scrofa RepID=TRYP_PIG

6

UniRef100_P35908 1.0000

confidence: 1.00 coverage: 25.8% num unique peps: 12tot indep spectra: 29
share of spectrum id's: 6.42%

>Keratin, type II cytoskeletal 2 epidermal n=1 Tax=Homo sapiens

RepID=K22E_HUMAN Length: 639aa

7

UniRef100_P02533 1.0000

confidence: 1.00 coverage: 25.0% num unique peps: 4 tot indep spectra: 7
share of spectrum id's: 2.78% subsumed entries: 10

>Keratin, type I cytoskeletal 14 n=1 Tax=Homo sapiens RepID=K1C14_HUMAN
Length: 472aa

8

UniRef100_A1E282 UniRef100_B4DVQ0 UniRef100_B4E335

UniRef100_B4E3A4 UniRef100_P60709 UniRef100_P63261

UniRef100_Q4R4H6 UniRef100_Q53G76 UniRef100_Q53G99 UniRef100_Q53GK6

UniRef100_Q8WVW5 UniRef100_UPI0000E0A7CD

UniRef100_UPI000186E470 0.9990

confidence: 1.00 max coverage: 24.0% num unique peps: 2 tot indep
spectra: 2 share of spectrum id's: 0.40%

>Beta-actin (Fragment) n=4 Tax=Coelomata RepID=A1E282_HUMAN Length:
121aa

>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

>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: 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

>Putative uncharacterized protein (Fragment) n=1 Tax=Homo sapiens
RepID=Q8WVW5_HUMAN

>UPI0000E0A7CD related cluster n=1 Tax=Homo sapiens RepID=UPI0000E0A7CD

>Actin-5C n=1 Tax=Pediculus humanus corporis RepID=UPI000186E470

9

UniRef100_P08779 1.0000

confidence: 1.00 coverage: 20.9% num unique peps: 3 tot indep spectra: 5
share of spectrum id's: 2.33% subsumed entries: 2

>Keratin, type I cytoskeletal 16 n=1 Tax=Homo sapiens RepID=K1C16_HUMAN
Length: 473aa

10

UniRef100_P13647 1.0000

confidence: 1.00 coverage: 17.3% num unique peps: 7 tot indep spectra: 13
share of spectrum id's: 3.72% subsumed entries: 2

>Keratin, type II cytoskeletal 5 n=1 Tax=Homo sapiens RepID=K2C5_HUMAN
Length: 590aa

11

UniRef100_P35579 1.0000

confidence: 1.00 coverage: 14.3% num unique peps: 24tot indep spectra: 47
share of spectrum id's: 10.22% subsumed entries: 10

>Myosin-9 n=2 Tax=Homo sapiens RepID=MYH9_HUMAN Length: 1960aa

12

UniRef100_P19474 1.0000

confidence: 1.00 coverage: 9.7% num unique peps: 4 tot indep spectra: 10
share of spectrum id's: 2.23% subsumed entries: 1

>52 kDa Ro protein n=1 Tax=Homo sapiens RepID=RO52_HUMAN Length:
475aa

13

UniRef100_A8K008 UniRef100_P01857 UniRef100_P01859
UniRef100_P01861 UniRef100_Q5EFE5 UniRef100_Q6GMX6

UniRef100_Q6MZU6 UniRef100_Q6MZV7 UniRef100_Q6MZX7 UniRef100_Q6N089
UniRef100_Q6N093 UniRef100_UPI00001125A4

UniRef100_UPI000173A69D UniRef100_UPI000173A69E
UniRef100_UPI000195C290 UniRef100_UPI0001A5EB10 1.0000

confidence: 1.00 max coverage: 8.3% num unique peps: 3 tot indep spectra: 7
share of spectrum id's: 1.33%

>cDNA FLJ78387 n=1 Tax=Homo sapiens RepID=A8K008_HUMAN Length:
472aa

>Ig gamma-1 chain C region n=1 Tax=Homo sapiens RepID=IGHG1_HUMAN

>Ig gamma-2 chain C region n=1 Tax=Homo sapiens RepID=IGHG2_HUMAN

>Ig gamma-4 chain C region n=1 Tax=Homo sapiens RepID=IGHG4_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 DKFZp686C15213 n=1 Tax=Homo sapiens
RepID=Q6MZU6_HUMAN

>Putative uncharacterized protein DKFZp686C11235 n=1 Tax=Homo sapiens
RepID=Q6MZV7_HUMAN

>Putative uncharacterized protein DKFZp686M24218 n=1 Tax=Homo sapiens
RepID=Q6MZX7_HUMAN

>Putative uncharacterized protein DKFZp686P15220 n=1 Tax=Homo sapiens
RepID=Q6N089_HUMAN

>Putative uncharacterized protein DKFZp686I04196 (Fragment) n=1 Tax=Homo
sapiens RepID=Q6N093_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

>IG GAMMA-1 CHAIN C REGION n=1 Tax=Homo sapiens RepID=UPI000195C290

>PREDICTED: similar to immunoglobulin lambda-like polypeptide 1 n=1 Tax=Homo
sapiens RepID=UPI0001A5EB10

14

**UniRef100_A0JLS9 UniRef100_B2RBI8 UniRef100_B4DS26
UniRef100_B4DSB8 UniRef100_B4DUW9 UniRef100_P37275**

**UniRef100_Q13088 UniRef100_Q2KJ05 UniRef100_Q32Q63
UniRef100_Q5VZ84 UniRef100_Q8NB68 UniRef100_UPI000175911C**

UniRef100_UPI0001CE91A2 UniRef100_UPI0001CE91A3 0.9663

**confidence: 0.08 max coverage: 5.1% num unique peps: 1 tot
indep spectra: 1 share of spectrum id's: 0.22%**

**>ZEB1 protein (Fragment) n=1 Tax=Homo sapiens RepID=A0JLS9_HUMAN
Length: 1059aa**

**>cDNA, FLJ95535, highly similar to Homo sapiens transcription factor 8
(represses interleukin 2 expression) (TCF8), mRNA n=1 Tax=Homo sapiens
RepID=B2RBI8_HUMAN**

**>cDNA FLJ50636, highly similar to Transcription factor 8 n=1 Tax=Homo
sapiens RepID=B4DS26_HUMAN**

**>cDNA FLJ50640, highly similar to Transcription factor 8 (Fragment) n=1
Tax=Homo sapiens RepID=B4DSB8_HUMAN**

**>cDNA FLJ50696, highly similar to Transcription factor 8 n=1 Tax=Homo
sapiens RepID=B4DUW9_HUMAN**

>Zinc finger E-box-binding homeobox 1 n=1 Tax=Homo sapiens
RepID=ZEB1_HUMAN

>ZEB (Fragment) n=1 Tax=Homo sapiens RepID=Q13088_HUMAN

>Zinc finger E-box binding homeobox 1 n=1 Tax=Homo sapiens
RepID=Q2KJ05_HUMAN

>ZEB1 protein (Fragment) n=1 Tax=Homo sapiens RepID=Q32Q63_HUMAN

>Zinc finger E-box binding homeobox 1 n=2 Tax=Homo sapiens
RepID=Q5VZ84_HUMAN

>cDNA FLJ34159 fis, clone FCBBF3013623, highly similar to NIL-2-A ZINC
FINGER PROTEIN n=1 Tax=Homo sapiens RepID=Q8NB68_HUMAN

>zinc finger E-box-binding homeobox 1 isoform a n=2 Tax=Homo sapiens
RepID=UPI000175911C

>zinc finger E-box-binding homeobox 1 isoform d n=1 Tax=Homo sapiens
RepID=UPI0001CE91A2

>zinc finger E-box-binding homeobox 1 isoform e n=1 Tax=Homo sapiens
RepID=UPI0001CE91A3

15

UniRef100_Q5DT20 UniRef100_Q86YZ3 1.0000

confidence: 0.89 max coverage: 1.7% num unique peps: 2 tot indep spectra: 2
share of spectrum id's: 0.44%

>Hornerin n=1 Tax=Homo sapiens RepID=Q5DT20_HUMAN Length: 2850aa

>Hornerin n=1 Tax=Homo sapiens RepID=HORN_HUMAN