

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)

Validation 2: FOXM1_(SC-502) IP-Mass Spec of the 100 kDa band identified in IP-Western in Validation 1. Target protein (FOXM1) was identified in entry number 7a with 100% probability.

| Entry no. | Protein | Protein probability | Percent share of spectrum id's | Description |
|-----------|---|---------------------|--------------------------------|--|
| 1 | UniRef100_A0N5G3,UniRef100_A2NUT2,UniRef100_C6KXN3,UniRef100_Q6GMW3,UniRef100_Q6GMX4,UniRef100_Q6IPQ0,UniRef100_Q6PIQ7,UniRef100_Q6PJG0,UniRef100_Q8N355,UniRef100_Q8N5F4 | 1 | 1.26 | Rheumatoid factor G9 light chain (Fragment) |
| 2 | UniRef100_B2R8R5,UniRef100_Q13263,UniRef100_Q13263-2 | 1 | 1 | cdNA, FLJ94025, highly similar to Homo sapiens tripartite motif-containing 28 (TRIM28), mRNA |
| 3 | UniRef100_P04264 | 1 | 1.77 | Keratin, type II cytoskeletal 1 |
| 4 | UniRef100_Q8IYV2,UniRef100_Q8NEH0,UniRef100_Q8TDR3,UniRef100_Q9UHI6 | 1 | 1 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 |
| 5a | UniRef100_A8K008,UniRef100_P01857,UniRef100_P01860,UniRef100_Q5EBM2,UniRef100_Q5EFE5,UniRef100_Q6GMX6,UniRef100_Q6MZQ6,UniRef100_Q6MZV7,UniRef100_Q6N030, | 0.9999 | 2.01 | cdNA FLJ78387 |
| 6a | UniRef100_A8K3W4,UniRef100_A8K6U7,UniRef100_Q9BUJ2,UniRef100_Q9BUJ2-2,UniRef100_Q9BUJ2-4 | 1 | 9.71 | cdNA FLJ75163, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein U-like 1 (HNRPUL1), transcript variant 4, mRNA |
| 7a | UniRef100_A8K591,UniRef100_Q08050,UniRef100_Q08050-2 | 1 | 2.4 | Forkhead box protein M1 |
| 8a | UniRef100_B0YJC4,UniRef100_P08670,UniRef100_Q53HU8 | 1 | 1.95 | Vimentin variant 3 |
| 9a | UniRef100_B2R5W3,UniRef100_B4E0E1,UniRef100_P09874 | 1 | 5.81 | cdNA, FLJ92658, highly similar to Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA |
| 10a | UniRef100_B2R7D3,UniRef100_Q96D71,UniRef100_Q96D71-3 | 1 | 2.9 | cdNA, FLJ93390, highly similar to Homo sapiens RALBP1 associated Eps domain containing 1 (REPS1),mRNA |
| 11a | UniRef100_B3KU67,UniRef100_B4E299,UniRef100_Q59FF0,UniRef100_Q7KZF4,UniRef100_UPI0001AE70F2 | 1 | 0.67 | cdNA FLJ39264 fis, clone OCBBF2009603, highly similar to Staphylococcal nuclease domain-containing protein 1 |
| 12a | UniRef100_B3KX72,UniRef100_B4DLR3,UniRef100_Q00839,UniRef100_Q00839-2 | 1 | 5.48 | cdNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclear ribonucleoprotein U |
| 13a | UniRef100_C5IWW5,UniRef100_P00761 | 1 | 1.65 | Trypsinogen |
| 15a | UniRef100_O75400,UniRef100_O75400-2 | 0.9999 | 0.66 | Pre-mRNA-processing factor 40 homolog A |
| 16a | UniRef100_P02769,UniRef100_UPI000179EC85 | 1 | 2.97 | Serum albumin |
| 17a | UniRef100_P13639 | 1 | 6.66 | Elongation factor 2 |

| | | | | |
|-----|--|--------|-------|--|
| 17b | UniRef100_A8KAP3,UniRef100_B3KX19,UniRef100_B4DMC0,UniRef100_B4DZB1,UniRef100_Q15029,UniRef100_Q61BM8 | 1 | 1.79 | cDNA FLJ78483, highly similar to Homo sapiens elongation factor Tu GTP binding domain containing 2 (EFTUD2), mRNA |
| 18a | UniRef100_P13645,UniRef100_UPI00017BCE7F | 1 | 2.33 | Keratin, type I cytoskeletal 10 |
| 19a | UniRef100_P14625,UniRef100_Q59FC6,UniRef100_Q5CAQ5 | 1 | 1.46 | Endoplasmin |
| 20a | UniRef100_P35908 | 1 | 1.43 | Keratin, type II cytoskeletal 2 epidermal |
| 21a | UniRef100_Q02241,UniRef100_UPI00015DFCE3 | 1 | 8.38 | Kinesin-like protein KIF23 |
| 22a | UniRef100_Q14566 | 1 | 0.71 | DNA replication licensing factor MCM6 |
| 23a | UniRef100_Q14694,UniRef100_Q14694-2,UniRef100_Q14694-3,UniRef100_UPI0001AE68C9 | 1 | 0.66 | Ubiquitin carboxyl-terminal hydrolase 10 |
| 24a | UniRef100_Q9HCE1 | 1 | 13.25 | Putative helicase MOV-10 |
| 25a | UniRef100_Q9NZC9,UniRef100_UPI0000D49C5A | 1 | 1.31 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1 |
| 26a | UniRef100_Q9P2I0 | 1 | 2.74 | Cleavage and polyadenylation specificity factor subunit 2 |
| 27a | UniRef100_Q9UP52,UniRef100_Q9UP52-3 | 1 | 2.17 | Transferrin receptor protein 2 |
| 28 | UniRef100_A4D210,UniRef100_B4DV79,UniRef100_B4DXN6,UniRef100_P55884,UniRef100_P55884-2,UniRef100_Q59FS8, | 0.9964 | 0.33 | Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa |
| 29 | UniRef100_A8MXP9,UniRef100_D6R991,UniRef100_D6REM6,UniRef100_P43243,UniRef100_Q68D11 | 0.9964 | 0.67 | Putative uncharacterized protein MATR3 |
| 30 | UniRef100_B4DIW2,UniRef100_B4DJ30,UniRef100_B4DSM6,UniRef100_B4DZ53,UniRef100_Q14697,UniRef100_Q14697-2,UniRef100_Q9BS14 | 0.9964 | 0.33 | cDNA FLJ54035, highly similar to Neutral alpha-glucosidase AB |
| 31 | UniRef100_Q96LA8 | 0.9964 | 0.33 | Protein arginine N-methyltransferase 6 |
| 32 | UniRef100_A8K9K1,UniRef100_A8MYK9,UniRef100_D3DTJ8,UniRef100_P16615,UniRef100_P16615-2,UniRef100_P16615-3 | 0.9957 | 0.67 | cDNA FLJ77199, highly similar to Homo sapiens ATPase, Ca++ transporting, ubiquitous (ATP2A3), transcript variant 6, mRNA |
| 33 | UniRef100_A4FS09,UniRef100_B3KMX0,UniRef100_B4DLA6,UniRef100_P33991,UniRef100_UPI0001AE6ED3 | 0.9954 | 0.67 | Minichromosome maintenance protein 4 (Fragment) |
| 34 | UniRef100_B2RBR9,UniRef100_B7Z5M1,UniRef100_B7Z752,UniRef100_B7ZAV6,UniRef100_Q14974 | 0.9954 | 0.33 | cDNA, FLJ95650, highly similar to Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA |
| 35 | UniRef100_A4QN18,UniRef100_A4QN19,UniRef100_O15027,UniRef100_O15027-2, | 0.995 | 1 | SEC16A protein (Fragment) |
| 36 | UniRef100_B4DPI9,UniRef100_Q13823 | 0.9946 | 0.67 | cDNA FLJ54985, highly similar to Nucleolar GTP-binding protein 2 |
| 37 | UniRef100_B7Z8P5,UniRef100_C9J6I2,UniRef100_Q9H2U1,UniRef100_Q9H2U1-2,UniRef100_Q9H2U1-3,UniRef100_UPI0000EE21F9, | 0.9943 | 0.33 | cDNA FLJ51438, highly similar to Probable ATP-dependent RNA helicase DHX36 (EC 3.6.1.-) (Fragment) |

| | | | | |
|----|--|--------|------|---|
| 38 | UniRef100_B4DIM0,UniRef100_B4E3P0,UniRef100_P53396,UniRef100_UPI000225CC0,UniRef100_UPI0001D63C11 | 0.9939 | 0.33 | cDNA FLJ56442, highly similar to ATP-citrate synthase (EC 2.3.3.8) |
| 39 | UniRef100_P46934-4,UniRef100_Q96PU5,UniRef100_Q96PU5-2,UniRef100_Q96PU5-3, | 0.9939 | 0.33 | Isoform 4 of E3 ubiquitin-protein ligase NEDD4 |
| 40 | UniRef100_B4DHD2,UniRef100_B7Z5C1,UniRef100_Q4W4Y1,UniRef100_Q6NUS1,UniRef100_Q8WUM4,UniRef100_UPI00004121D3 | 0.9925 | 0.33 | cDNA FLJ55458, highly similar to Programmed cell death 6-interacting protein |
| 41 | UniRef100_Q2NL82 | 0.9922 | 0.67 | Pre-rRNA-processing protein TSR1 homolog |
| 42 | UniRef100_B2R7C5,UniRef100_B4DS46,UniRef100_B4DUQ9,UniRef100_P25205,UniRef100_Q53HJ4,UniRef100_Q8NHX6,UniRef100_UPI000186DE64 | 0.9911 | 0.66 | cDNA, FLJ93378, highly similar to Homo sapiens MCM3 minichromosome maintenance deficient 3 (<i>S. cerevisiae</i>) (MCM3), mRNA |
| 43 | UniRef100_D3DSF4,UniRef100_P22102,UniRef100_Q15374,UniRef100_Q3B7A7,UniRef100_Q59HH3 | 0.9911 | 0.66 | Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase, isoform CRA_c |
| 44 | UniRef100_A8K7J7,UniRef100_B3KRA9,UniRef100_B3KXY9,UniRef100_P19367,UniRef100_P19367-2, | 0.9907 | 0.33 | cDNA FLJ78173, highly similar to Homo sapiens hexokinase 1 (HK1) mRNA |
| 45 | UniRef100_A8K492,UniRef100_B3KVK7,UniRef100_B4DF61,UniRef100_B4E0E9,UniRef100_P56192,UniRef100_UPI0001AE6AF3 | 0.9841 | 1 | cDNA FLJ76789, highly similar to Homo sapiens methionine-tRNA synthetase (MARS), mRNA |
| 46 | UniRef100_UPI0000D9A9C4 | 0.9747 | 0.66 | PREDICTED: protease, serine, 1 (trypsin 1) |
| 47 | UniRef100_B4DGI6,UniRef100_B4DKV2,UniRef100_B4DM03,UniRef100_B4E300,UniRef100_Q4V9L5,UniRef100_Q59FS7, | 0.9665 | 0.33 | cDNA FLJ50498, highly similar to ATP-dependent RNA helicase DDX24 (EC 3.6.1.-) |
| 48 | UniRef100_D3DVA5,UniRef100_D3DVA6,UniRef100_Q5VY93,UniRef100_Q92974 | 0.6106 | 0.28 | Rho/rac guanine nucleotide exchange factor (GEF) 2, isoform CRA_a |
| 49 | UniRef100_A2BF21,UniRef100_A6NI54,UniRef100_B0UXE9,UniRef100_C9J3N1,UniRef100_C9J8W5,UniRef100_D3DT71,UniRef100_D3DT72,UniRef100_D3DT73,UniRef100_P12107,UniRef100_P12107-2, | 0.5059 | 0.57 | Collagen, type XI, alpha 2 (Fragment) |
| 50 | UniRef100_Q9Y5Q9,UniRef100_Q9Y5Q9-2 | 0.4582 | 0.25 | General transcription factor 3C polypeptide 3 |
| 51 | UniRef100_A8MUE1,UniRef100_C9JHA6,UniRef100_C9JST2,UniRef100_Q8NHJ6,UniRef100_Q8NHJ6-2,UniRef100_Q8NHJ6-3, | 0.3297 | 0.62 | Putative uncharacterized protein LILRB4 |
| 52 | UniRef100_UPI000186F3C6 | 0.3016 | 0.2 | ciliary dynein heavy chain, putative |
| 53 | UniRef100_B3KSE4,UniRef100_P49711,UniRef100_Q59EL8,UniRef100_UPI0001AE6829 | 0.2052 | 0.16 | cDNA FLJ36076 fis, clone TESTI2019760, highly similar to TRANSCRIPTIONAL REPRESSOR CTCF |