

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: BCL11A_(SC-56011) IP-Mass Spec the 120 kDa band identified in IP-Western in Validation 1. Target protein was identified in entry number 19a with 0.9999% probability.

| Entry no. | Protein | Protein probability | Percent share of spectrum id's | Description |
|------------|---|---------------------|--------------------------------|---|
| 1 | UniRef100_A4QN18,UniRef100_A4QN19,UniRef100_O15027,UniRef100_O15027-2,UniRef100_O15027-3,UniRef100_O15027-4,UniRef100_O15027-5 | 1 | 0.77 | SEC16A protein (Fragment) |
| 2 | UniRef100_B3KMV5,UniRef100_B3KY56,UniRef100_Q9BSJ8,UniRef100_Q9BSJ8-2 | 1 | 0.79 | cDNA FLJ12728 fis, clone NT2R2P2000040, highly similar to Protein FAM62A |
| 3 | UniRef100_B3KPH8,UniRef100_B3KU28,UniRef100_B3KX55,UniRef100_B4DPX0,UniRef100_P36776,UniRef100_Q2VPA0,UniRef100_Q8N8K8 | 1 | 0.47 | Lon protease homolog |
| 4 | UniRef100_P00762 | 1 | 0.67 | Anionic trypsin-1 |
| 5 | UniRef100_P35527 | 1 | 2.67 | Keratin, type I cytoskeletal 9 |
| 6 | UniRef100_Q00610,UniRef100_Q00610-2,UniRef100_UPI0001AE66DF | 1 | 1.42 | Clathrin heavy chain 1 |
| 7 | UniRef100_Q96P70 | 1 | 0.32 | Importin-9 |
| 9a | UniRef100_A4D210,UniRef100_B4DV79,UniRef100_B4DXN6,UniRef100_P55884,UniRef100_P55884-2,UniRef100_UPI00015E042B | 1 | 0.84 | Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa |
| 10a | UniRef100_A8JZY9,UniRef100_B3KPS3,UniRef100_B3KT06,UniRef100_B7Z1K5,UniRef100_P68363,UniRef100_Q53GA7,UniRef100_Q8WU19,UniRef100_Q9BQE3 | 1 | 0.47 | cDNA FLJ78587 |
| 11a | UniRef100_A8K6M8,UniRef100_B3KMF6,UniRef100_B3KW21,UniRef100_Q8WU16,UniRef100_Q9Y678 | 1 | 0.47 | cDNA FLJ77708, highly similar to Homo sapiens coatomer protein complex, subunit gamma (COPG), mRNA |
| 12a | UniRef100_A8K7J7,UniRef100_B3KRA9,UniRef100_B3KXY9,UniRef100_P19367,UniRef100_P19367-2,UniRef100_P19367-3,UniRef100_P19367-4,UniRef100_UPI000013E942,UniRef100_UPI0001AE6D68 | 1 | 0.63 | cDNA FLJ78173, highly similar to Homo sapiens hexokinase 1 (HK1) mRNA |
| 13a | UniRef100_A8K8U1,UniRef100_Q86VP6,UniRef100_Q86VP6-2 | 1 | 1.73 | cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA |
| 14a | UniRef100_A8K9C4,UniRef100_B4DV42,UniRef100_P68104,UniRef100_Q53G85,UniRef100_Q53G89,UniRef100_Q53GE9,UniRef100_Q53HM9,UniRef100_Q53HQ7,UniRef100_Q53HR5,UniRef100_Q5VTE0,UniRef100_Q6IPN6,UniRef100_Q6IPT9,UniRef100_Q96RE1,UniRef100_Q9NZS6 | 1 | 0.47 | Elongation factor 1-alpha |
| 15a | UniRef100_A8MXP9,UniRef100_D6R991,UniRef100_D6REM6,UniRef100_P43243,UniRef100_Q68D11 | 1 | 0.47 | Putative uncharacterized protein MATR3 |
| 16a | UniRef100_B0I1T2,UniRef100_UPI00001D747C | 1 | 2.3 | Minor histocompatibility antigen HA-2 |
| 17a | UniRef100_B2R5W3,UniRef100_B4E0E1,UniRef100_P09874 | 1 | 2.04 | cDNA, FLJ92658, highly similar to Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA |
| 18a | UniRef100_B2R6D0,UniRef100_Q05BX4,UniRef100_Q05CW6,UniRef100_Q99460,UniRef100_Q99460-2 | 1 | 0.47 | cDNA, FLJ92896, highly similar to Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (PSMD1), mRNA |
| 19a | UniRef100_B3KNX8,UniRef100_B3KRW8,UniRef100_B4DMK8,UniRef100_Q9H165,UniRef100_Q9H165-2,UniRef100_Q9H165-6 | 0.9999 | 0.31 | cDNA FLJ30689 fis, clone FCBBF2000566, highly similar to B-cell lymphoma/leukemia 11A |
| 20a | UniRef100_B3KU67,UniRef100_B4E299,UniRef100_Q59FF0,UniRef100_Q7KZF4,UniRef100_UPI0001AE70F2 | 1 | 0.94 | cDNA FLJ39264 fis, clone OCBBF2009603, highly similar to Staphylococcal nuclease domain-containing protein 1 |
| 21a | UniRef100_B3KX72,UniRef100_B4DLR3,UniRef100_Q00839,UniRef100_Q00839-2,UniRef100_Q4R810 | 1 | 1.25 | cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclear ribonucleoprotein U |
| 22a | UniRef100_B3KXZ4,UniRef100_B4DSV5,UniRef100_P49736,UniRef100_UPI0001B797CF | 1 | 1.02 | cDNA FLJ46429 fis, clone THYMU3014372, highly similar to DNA replication licensing factor MCM2 |
| 23a | UniRef100_B4DH02,UniRef100_O14992,UniRef100_P34932,UniRef100_Q59GF8 | 1 | 0.94 | cDNA FLJ50510, highly similar to Heat shock 70 kDa protein 4 |
| 24a | UniRef100_B4DIM0,UniRef100_B4E3P0,UniRef100_P53396,UniRef100_UPI0000225CC0 | 1 | 1.43 | cDNA FLJ56442, highly similar to ATP-citrate synthase (EC 2.3.3.8) |

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|-----|---|--------|------|--|
| 25a | UniRef100_B4DS32,UniRef100_B4DUC5,UniRef100_P55060,UniRef100_P55060-3,UniRef100_UPI0001AE6604 | 0.9999 | 0.31 | cdNA FLJ56236, highly similar to Exportin-2 |
| 26a | UniRef100_B4E0R6,UniRef100_O00410,UniRef100_O0410-2 | 1 | 0.62 | cdNA FLJ54573, highly similar to Importin beta-3 |
| 27a | UniRef100_B7Z1H4,UniRef100_B7Z1V9,UniRef100_B7Z463,UniRef100_B7Z4B2,UniRef100_B7Z899,UniRef100_P55786 | 1 | 0.47 | cdNA FLJ56052, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) |
| 28a | UniRef100_C5IWV5,UniRef100_P00761 | 1 | 5.94 | Trypsinogen |
| 29a | UniRef100_O14980 | 1 | 1.72 | Exportin-1 |
| 30a | UniRef100_O95782,UniRef100_O95782-2,UniRef100_Q8N9K4 | 1 | 0.79 | AP-2 complex subunit alpha-1 |
| 31a | UniRef100_P02769 | 1 | 8.18 | Serum albumin |
| 32a | UniRef100_P04264 | 1 | 8.18 | Keratin, type II cytoskeletal 1 |
| 32b | UniRef100_P35908 | 1 | 3.03 | Keratin, type II cytoskeletal 2 epidermal |
| 32c | UniRef100_Q7RTS7,UniRef100_Q86Y46 | 0.9881 | 0.23 | Keratin, type II cytoskeletal 74 |
| 33a | UniRef100_P11586,UniRef100_UPI000013C6FA | 1 | 4.43 | Formyltetrahydrofolate synthetase |
| 34a | UniRef100_P13639 | 1 | 5.41 | Elongation factor 2 |
| 35a | UniRef100_P13645,UniRef100_UPI00017BCE7F | 1 | 7.52 | Keratin, type I cytoskeletal 10 |
| 36a | UniRef100_P14625,UniRef100_Q5CAQ5 | 1 | 6.4 | Endoplasmic reticulum chaperone |
| 36b | UniRef100_B4DGL0,UniRef100_B4DMA2,UniRef100_P08238 | 1 | 1.12 | cdNA FLJ53619, highly similar to Heatshock protein HSP 90-beta |
| 37a | UniRef100_P22102,UniRef100_Q3B7A7,UniRef100_Q59HH3 | 1 | 0.78 | Phosphoribosylglycinamide formyltransferase |
| 38a | UniRef100_P22314 | 1 | 2.66 | Ubiquitin-like modifier-activating enzyme 1 |
| 39a | UniRef100_P35579,UniRef100_P35579-2 | 1 | 0.78 | Myosin-9 |
| 40a | UniRef100_P53618 | 1 | 0.47 | Coatomer subunit beta |
| 41a | UniRef100_P55072 | 1 | 0.78 | Transitional endoplasmic reticulum ATPase |
| 42a | UniRef100_Q08211 | 1 | 0.78 | ATP-dependent RNA helicase A |
| 43a | UniRef100_Q12965 | 1 | 0.47 | Myosin-Ie |
| 44a | UniRef100_Q14152,UniRef100_Q24JU4 | 1 | 0.96 | Eukaryotic translation initiation factor 3 subunit A |
| 45a | UniRef100_Q14566 | 1 | 0.84 | DNA replication licensing factor MCM6 |
| 46a | UniRef100_Q8N8A2,UniRef100_Q8N8A2-2,UniRef100_UPI00015E0ACE | 1 | 0.37 | Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B |
| 47a | UniRef100_Q9P2I0 | 1 | 3.03 | Cleavage and polyadenylation specificity factor subunit 2 |
| 48a | UniRef100_UPI00017BDB43 | 1 | 0.78 | FabOX117 Heavy Chain Fragment |
| 49a | UniRef100_B4DIW2,UniRef100_B4DJ30,UniRef100_B4DSM6,UniRef100_B4DZ53,UniRef100_Q14697,UniRef100_Q14697-2 | 0.9998 | 0.31 | cdNA FLJ54035, highly similar to Neutral alpha-glucosidase AB |
| 50a | UniRef100_B4DM22,UniRef100_B4DX07,UniRef100_B4DX11,UniRef100_Q13200,UniRef100_Q53XQ4,UniRef100_Q59EG8,UniRef100_UPI000198CB9B | 0.999 | 0.43 | cdNA FLJ53357, highly similar to 26S proteasome non-ATPase regulatory subunit 2 |
| 51a | UniRef100_B4DUU6,UniRef100_P14618,UniRef100_UPI0001662C1E | 0.9998 | 0.39 | Pyruvate kinase |
| 52 | UniRef100_A8K2U2,UniRef100_P52789,UniRef100_Q53QX9,UniRef100_Q68E10 | 0.9996 | 0.22 | cdNA FLJ75392, highly similar to Homo sapiens hexokinase II (HKII) mRNA |
| 53 | UniRef100_A4QP80,UniRef100_B4E2M0,UniRef100_P46940,UniRef100_Q6P1N4 | 0.995 | 0.32 | IQ motif containing GTPase activating protein 1 |
| 54 | UniRef100_B2R6H7,UniRef100_B3KM69,UniRef100_B3KMX1,UniRef100_C9IZM0,UniRef100_Q4R785,UniRef100_Q9Y5L0,UniRef100_Q9Y5L0-3 | 0.995 | 0.16 | cdNA, FLJ92955, highly similar to Homo sapiens transportin SR (TRN-SR), mRNA |
| 55 | UniRef100_B3KMX0,UniRef100_B4DLA6,UniRef100_P33991,UniRef100_UPI0001AE6ED3 | 0.995 | 0.47 | cdNA FLJ12837 fis, clone NT2RP2003228, highly similar to DNA replication licensing factor MCM4 |
| 56 | UniRef100_B3KSY4,UniRef100_B3KUH7,UniRef100_B4DFD6,UniRef100_B4DKU9,UniRef100_P57737 | 0.995 | 0.47 | HCG1787779, isoform CRA_b |
| 57 | UniRef100_B4DSN3,UniRef100_P53992 | 0.995 | 0.47 | cdNA FLJ60345, highly similar to Protein transport protein Sec24C |
| 58 | UniRef100_B4E205,UniRef100_O95486 | 0.995 | 0.32 | cdNA FLJ61651, highly similar to Protein transport protein Sec24A |

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|----|--|--------|------|--|
| 59 | UniRef100_B7Z8Y3,UniRef100_D3DV75,UniRef100_D3DV76,UniRef100_P55265,UniRef100_P55265-2,UniRef100_P55265-3,UniRef100_P55265-4,UniRef100_Q59EC0,UniRef100_UPI00003665AC,UniRef100_UPI0001AE78F3,UniRef100_UPI0001AE78F4 | 0.995 | 0.16 | cDNA FLJ61696, highly similar to Double-stranded RNA-specific adenosine deaminase (EC 3.5.4.-) |
| 60 | UniRef100_UPI0000111654,UniRef100_UPI00017BDB3D,UniRef100_UPI00017BDB42 | 0.995 | 0.16 | MONOCLONAL ANTIBODY MAK33 |
| 61 | UniRef100_A8K674,UniRef100_B2RDW1,UniRef100_P62988,UniRef100_Q3MIH3,UniRef100_Q49A90,UniRef100_Q59EM9,UniRef100_Q5RKT7,UniRef100_Q5U5U6,UniRef100_Q5UGI3,UniRef100_Q66K58,UniRef100_Q96C32,UniRef100_Q96H31,UniRef100_Q96MH4,UniRef100_UPI000013DC28,UniRef100_UPI0001D63C67 | 0.9945 | 0.16 | cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA |
| 62 | UniRef100_B2R7C5,UniRef100_B4DUQ9,UniRef100_P25205,UniRef100_Q53HJ4,UniRef100_Q8NHX6 | 0.9945 | 0.16 | cDNA, FLJ93378, highly similar to Homo sapiens MCM3 minichromosome maintenance deficient 3 (<i>S. cerevisiae</i>) (MCM3), mRNA |
| 63 | UniRef100_B4DF00,UniRef100_B4DK55,UniRef100_B4DZ95,UniRef100_B4E2U9,UniRef100_B4E3E9,UniRef100_Q02218,UniRef100_Q4R5L8,UniRef100_UPI000198CDE7,UniRef100_UPI000198CDE8,UniRef100_UPI000198CDF6,UniRef100_UPI000198CDF7 | 0.9945 | 0.16 | cDNA FLJ53308, highly similar to 2-oxoglutarate dehydrogenase E1 component, mitochondrial (EC 1.2.4.2) |
| 64 | UniRef100_B4DFD5,UniRef100_Q05CW7,UniRef100_Q9H0A0,UniRef100_UPI000013CF8E,UniRef100_UPI0001929506,UniRef100_UPI0001AE6B62 | 0.994 | 0.16 | cDNA FLJ58528, highly similar to N-acetyltransferase 10 (EC 2.3.1.-) |
| 65 | UniRef100_A8MXQ4,UniRef100_B4DKQ2,UniRef100_C9J4M5,UniRef100_D3YTI4,UniRef100_P00338,UniRef100_P00338-2 | 0.9905 | 0.31 | L-lactate dehydrogenase |
| 66 | UniRef100_B2RBES,UniRef100_B4E2T6,UniRef100_Q58F05,UniRef100_Q9BXJ9,UniRef100_Q9BXJ9-4,UniRef100_UPI000004961C | 0.9905 | 0.31 | cDNA, FLJ95468, highly similar to Homo sapiens transcriptional coactivator tubedown-100 (TBDN100),transcript variant 1, mRNA |
| 67 | UniRef100_B4E2Z3,UniRef100_P08195,UniRef100_P08195-3,UniRef100_P08195-4,UniRef100_UPI0000405902,UniRef100_UPI00004EC298 | 0.9905 | 0.16 | cDNA FLJ54090, highly similar to 4F2 cell-surface antigen heavy chain |
| 68 | UniRef100_A6NC17,UniRef100_A8K492,UniRef100_B3KVK7,UniRef100_B4E0E9,UniRef100_P56192,UniRef100_UPI0001AE6AF3 | 0.99 | 0.16 | Putative uncharacterized protein MARS |
| 69 | UniRef100_B4DXN0,UniRef100_Q14764 | 0.99 | 0.16 | cDNA FLJ53371, highly similar to Major vault protein |
| 70 | UniRef100_B2R8R5,UniRef100_Q13263,UniRef100_Q13263-2 | 0.9821 | 0.16 | cDNA, FLJ94025, highly similar to Homo sapiens tripartite motif-containing 28 (TRIM28), mRNA |
| 71 | UniRef100_B3KTJ9,UniRef100_Q8N163,UniRef100_Q8N163-2 | 0.9806 | 0.31 | cDNA FLJ38393 fis, clone FEBRA2007212 |
| 72 | UniRef100_P01625,UniRef100_P06312,UniRef100_P06313,UniRef100_P06314,UniRef100_Q9NP29 | 0.9613 | 0.47 | Ig kappa chain V-IV region Len |