

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*

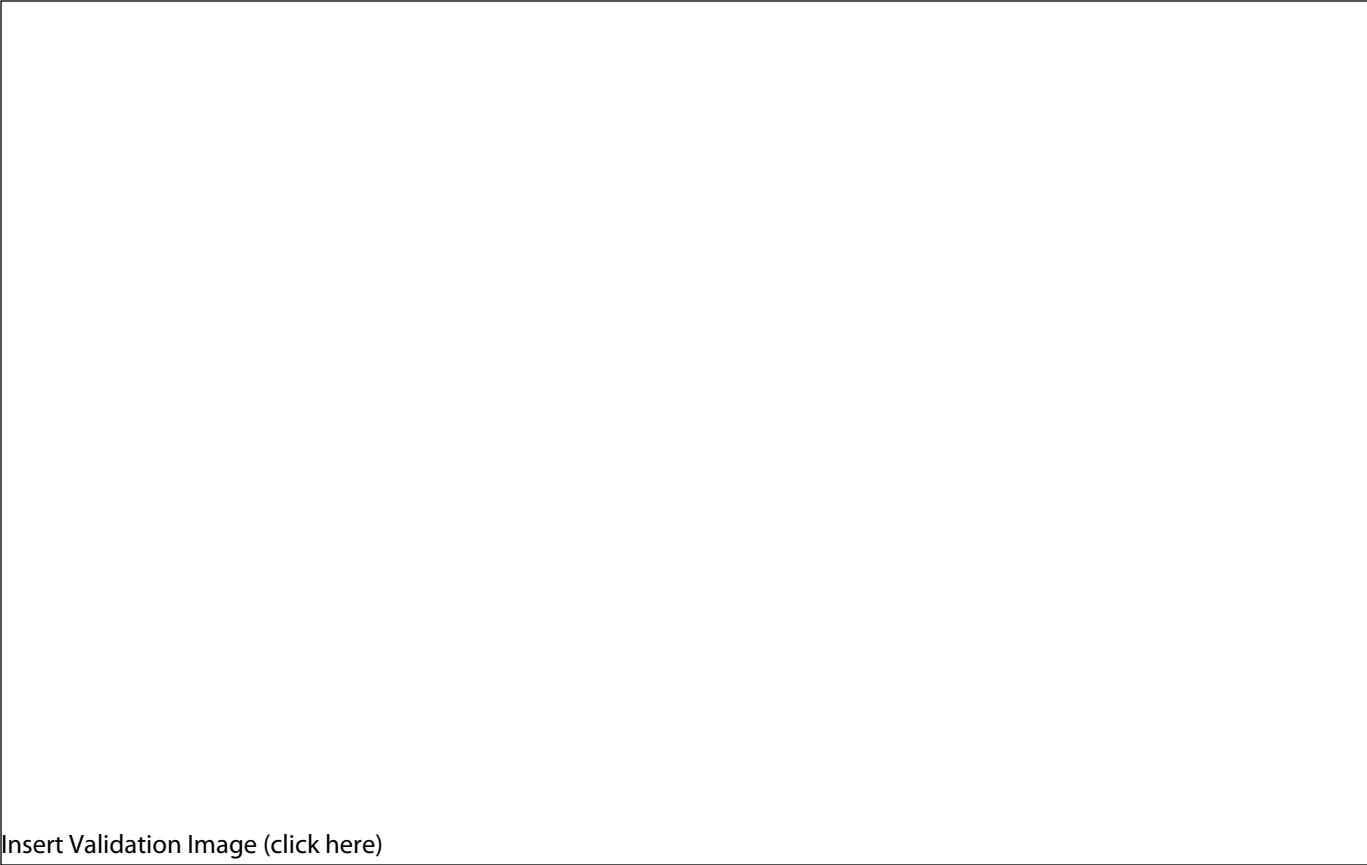
Histone Name

AA modified

AA Position

Modification

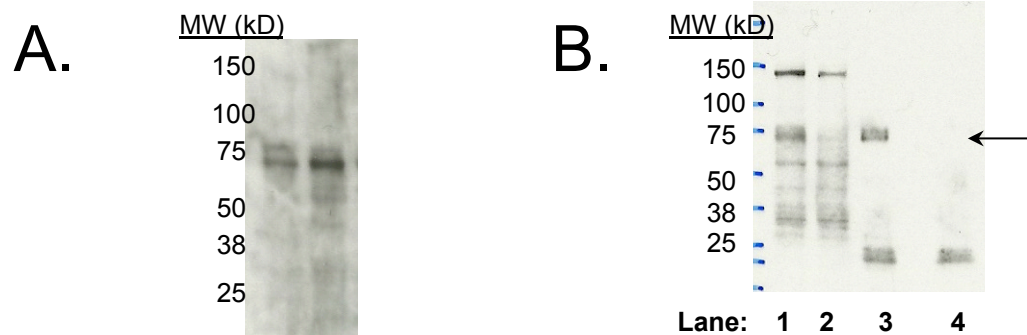
Validation #1
Analysis



Insert Validation Image (click here)

Antibody: HSF1 Source: Santa Cruz Biotechnology sc-17756

Validation 1: Immunoblotting/Immunoprecipitation



A. Western blot using sc-17756. Both shown lanes contain nuclear lysates from HepG2 cells stimulated with forskolin. (Lane 1), **B.** Immunoprecipitation of HSF1 from forskolin-stimulated HepG2 cells using sc-17756. Lane 1: input nuclear lysate, Lane 2: unbound material from immunoprecipitation with sc-17756, Lane 3: material immunoprecipitated with sc-17756, Lane 4: material immunoprecipitated using control IgG.

Validation #2
Analysis



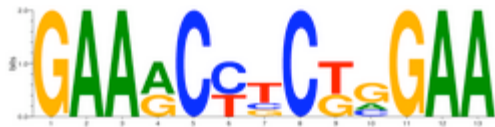
Insert Validation Image (Click here)

Table 1. HSF1 motif enrichment.

| Cell Line | Motif Enrichment (log2) | Enrichment p-value (-log10) | Fraction of peaks containing motif |
|-------------------|-------------------------|-----------------------------|------------------------------------|
| HepG2 (forskolin) | 2.65737 (Hsf_known3) | 55.9022 (Hsf_known2) | 0.160602 (Hsf_known2) |

Figure 2. Motif consensus sequences and position weight matrices for highly enriched HSF1 motif.

HSF1_known2

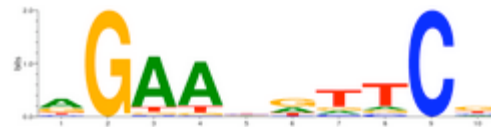


>Hsf_known2 HSF_transfac_M00641 -

Position/
Consensus

| | <u>A</u> | <u>C</u> | <u>G</u> | <u>T</u> |
|---|----------|----------|----------|----------|
| G | 0.000000 | 0.000000 | 1.000000 | 0.000000 |
| A | 1.000000 | 0.000000 | 0.000000 | 0.000000 |
| A | 1.000000 | 0.000000 | 0.000000 | 0.000000 |
| R | 0.600000 | 0.000000 | 0.400000 | 0.000000 |
| C | 0.000000 | 1.000000 | 0.000000 | 0.000000 |
| Y | 0.000000 | 0.600000 | 0.000000 | 0.400000 |
| B | 0.000000 | 0.200000 | 0.200000 | 0.600000 |
| C | 0.000000 | 1.000000 | 0.000000 | 0.000000 |
| K | 0.000000 | 0.000000 | 0.400000 | 0.600000 |
| V | 0.200000 | 0.200000 | 0.600000 | 0.000000 |
| G | 0.000000 | 0.000000 | 1.000000 | 0.000000 |
| A | 1.000000 | 0.000000 | 0.000000 | 0.000000 |
| A | 1.000000 | 0.000000 | 0.000000 | 0.000000 |

HSF1_known3



>Hsf_known3 HSF1_transfac_M00146 +

Position/
Consensus

| | <u>A</u> | <u>C</u> | <u>G</u> | <u>T</u> |
|---|----------|----------|----------|----------|
| R | 0.533333 | 0.088889 | 0.266667 | 0.111111 |
| G | 0.000000 | 0.000000 | 1.000000 | 0.000000 |
| A | 0.844445 | 0.022222 | 0.044444 | 0.088889 |
| A | 0.800001 | 0.022222 | 0.044444 | 0.133333 |
| B | 0.155556 | 0.311111 | 0.200000 | 0.333333 |
| D | 0.295455 | 0.045455 | 0.477273 | 0.181818 |
| T | 0.133333 | 0.088889 | 0.133333 | 0.644445 |
| T | 0.111111 | 0.088889 | 0.111111 | 0.688889 |
| C | 0.000000 | 1.000000 | 0.000000 | 0.000000 |
| K | 0.133333 | 0.155556 | 0.466667 | 0.244444 |