Captify™ Nucleosome Full Panel

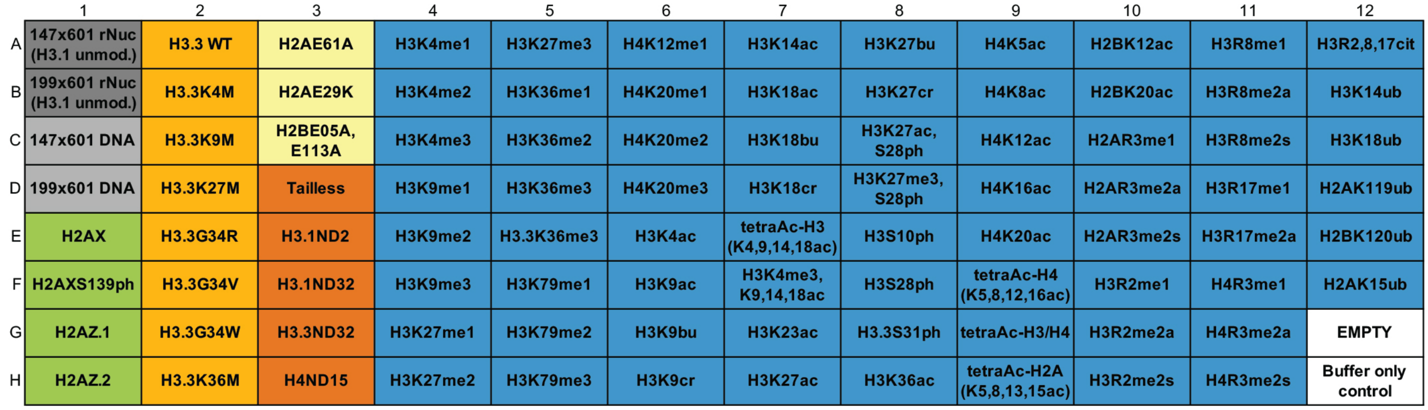
Catalog No	16-9001	**Pack Size**	96-well plate
Lot No	23090003-81		

DESCRIPTION

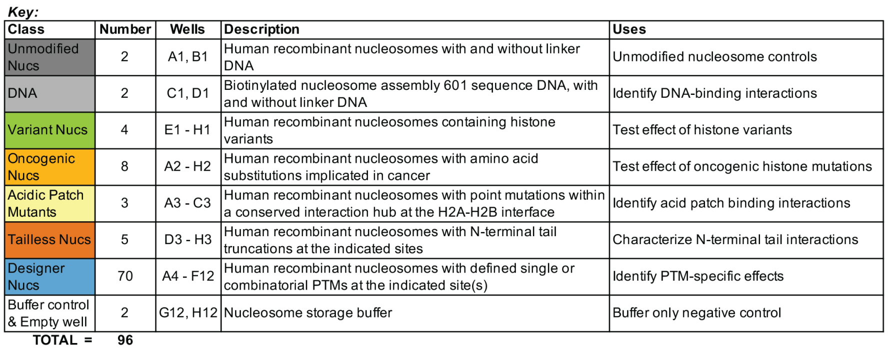
Understanding epigenetic reader proteins and their binding preference for post-translational modifications (PTMs) is key to unveiling how these proteins regulate genome processes and how their dysregulation may be contributing to disease. The Captify™ Nucleosome Panel enables access to epigenetic diversity in a physiologically relevant context, the nucleosome, where chromatin reader activity can be accurately interrogated. The 96-well plate contains recombinant mononucleosomes as well as appropriate controls. Human histones expressed in *E. coli* bearing single and combinatorial histone post-translational modifications (PTMs) are wrapped by 147 or 199 base pair DNA with a 5' biotin-TEG group and a central 601-positioning sequence, identified by Lowary and Widom [1].

All nucleosomes in the panel are subjected to EpiCypher's rigorous quality control metrics, including: ESI-TOF mass spectrometry analysis of the modified histones, SDS-PAGE to confirm octamer composition and purity, native PAGE to confirm nucleosome assembly, and western blot analysis of the PTM, histone mutation, or histone variant (if applicable). For the full list of nucleosomes in the panel, including individual catalog numbers of full-size (50 µg) products, see the associated excel sheet on the product page at www.epicypher.com/16-9001.

Full plate layout and key:



	1	2	3	4	5	6	7	8	9	10	11	12
A	147x601 rNuc (H3.1 unmod.)	H3.3 WT	H2AE61A	H3K4me1	H3K27me3	H4K12me1	H3K14ac	H3K27bu	H4K5ac	H2BK12ac	H3R8me1	H3R2,8,17cit
B	199x601 rNuc (H3.1 unmod.)	H3.3K4M	H2AE29K	H3K4me2	H3K36me1	H4K20me1	H3K18ac	H3K27cr	H4K8ac	H2BK20ac	H3R8me2a	H3K14ub
C	147x601 DNA	H3.3K9M	H2BE05A, E113A	H3K4me3	H3K36me2	H4K20me2	H3K18bu	H3K27ac, S28ph	H4K12ac	H2AR3me1	H3R8me2s	H3K18ub
D	199x601 DNA	H3.3K27M	Tailless	H3K9me1	H3K36me3	H4K20me3	H3K18cr	H3K27me3, S28ph	H4K16ac	H2AR3me2a	H3R17me1	H2AK119ub
E	H2AX	H3.3G34R	H3.1ND2	H3K9me2	H3.3K36me3	H3K4ac	tetraAc-H3 (K4,9,14,18ac)	H3S10ph	H4K20ac	H2AR3me2s	H3R17me2a	H2BK120ub
F	H2AXS139ph	H3.3G34V	H3.1ND32	H3K9me3	H3K79me1	H3K9ac	H3K4me3, K9,14,18ac	H3S28ph	tetraAc-H4 (K5,8,12,16ac)	H3R2me1	H4R3me1	H2AK15ub
G	H2AZ.1	H3.3G34W	H3.3ND32	H3K27me1	H3K79me2	H3K9bu	H3K23ac	H3.3S31ph	tetraAc-H3/H4	H3R2me2a	H4R3me2a	EMPTY
H	H2AZ.2	H3.3K36M	H4ND15	H3K27me2	H3K79me3	H3K9cr	H3K27ac	H3K36ac	tetraAc-H2A (K5,8,13,15ac)	H3R2me2s	H4R3me2s	Buffer only control



Key:

Class	Number	Wells	Description	Uses
Unmodified Nucs	2	A1, B1	Human recombinant nucleosomes with and without linker DNA	Unmodified nucleosome controls
DNA	2	C1, D1	Biotinylated nucleosome assembly 601 sequence DNA, with and without linker DNA	Identify DNA-binding interactions
Variant Nucs	4	E1 - H1	Human recombinant nucleosomes containing histone variants	Test effect of histone variants
Oncogenic Nucs	8	A2 - H2	Human recombinant nucleosomes with amino acid substitutions implicated in cancer	Test effect of oncogenic histone mutations
Acidic Patch Mutants	3	A3 - C3	Human recombinant nucleosomes with point mutations within a conserved interaction hub at the H2A-H2B interface	Identify acid patch binding interactions
Tailless Nucs	5	D3 - H3	Human recombinant nucleosomes with N-terminal tail truncations at the indicated sites	Characterize N-terminal tail interactions
Designer Nucs	70	A4 - F12	Human recombinant nucleosomes with defined single or combinatorial PTMs at the indicated site(s)	Identify PTM-specific effects
Buffer control & Empty well	2	G12, H12	Nucleosome storage buffer	Buffer only negative control
TOTAL =	96			

REFERENCES

[1] Lowary & Widom *J. Mol. Biol.* (1998). PMID: 9514715
[2] Weinberg et al. *Nature* (2019). PMID: 31485078
[3] Weinberg et al. *Nat. Genet.* (2021). PMID: 33986537
[4] Dilworth et al. *Nat. Chem. Biol.* (2022). PMID: 34782742
[5] Albanese et al. *ACS Chem. Biol.* (2020). PMID: 31634430

TECHNICAL INFORMATION

Storage	Stable for six months at -80°C from date of receipt. Avoid freeze/thaws.
Formulation	The material included in this 96-well plate is provided at 1.5 µM in 5 µL of nucleosome storage buffer (10 mM Tris-HCl pH 7.5, 25 mM NaCl, 1 mM EDTA, 2 mM DTT*, & 20% glycerol). *dNucs containing crotonyl-lysine are stored in nucleosome storage buffer without DTT. MW = ~200,000 Da

APPLICATION NOTES

Access to epigenetic diversity in the context of a physiological nucleosome enables broad end-user applications, including nucleosome binding studies (e.g. chromatin reader binding preferences [2-4]; *see data below*), enzyme screening assays (e.g. identification of preferred substrates), and antibody specificity testing (e.g. for applications where histone peptide specificity is an insufficient surrogate). The biotin group on the DNA facilitates a wide variety of applications involving streptavidin capture.

GENE & PROTEIN INFORMATION

UniProt ID

H2A - P04908 (alt. names: H2A type 1-B/E, H2A.2, H2A/a, H2A/m)
H2B - O60814 (alt. names: H2B K, HIRA-interacting protein 1)
H3.1 - P68431 (alt. names: H3, H3/a, H3/b, H3/c, H3/d)
H3.2 - Q71DI3
H3.3 - P84243
H4 - P62805

VALIDATION DATA

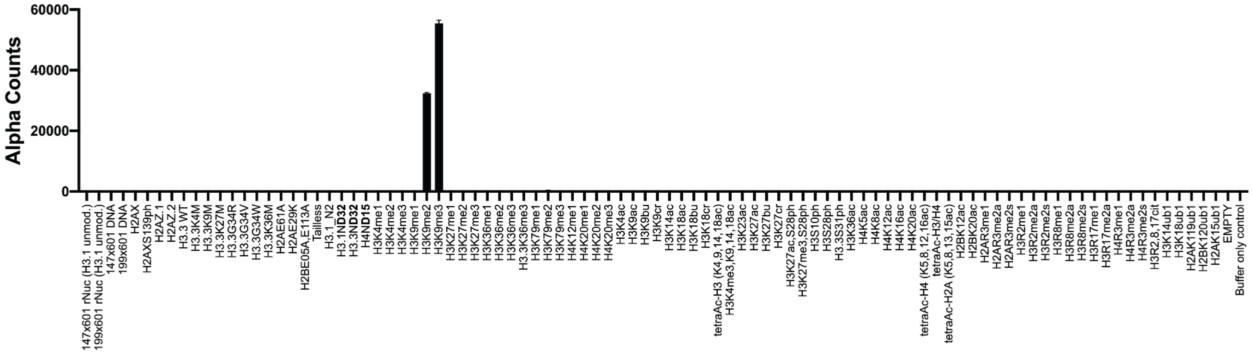


FIGURE 1 **Chromatin reader binding data.** GST-tagged HP1β (100 nM, EpiCypher 15-0074) was assayed with AlphaScreen (PerkinElmer) technology to measure binding to nucleosomes (x-axis) in the Captify nucleosome Panel (10 nM). HP1β shows binding to the H3K9me3 and H3K9me2 dNucs, consistent with its reported binding preference [5].