Tailless Recombinant Nucleosome with Linker DNA, Biotinylated

Catalog No	16-2027	**Species**	Human
Lot No	23347001-01	**Source**	*E. coli* & synthetic DNA
Pack Size	50 µg	**Tag**	Biotinylated
Concentration	4.6 µM	**MW**	215,300 Da

DESCRIPTION

Recombinant mononucleosomes consist of 199 base pairs of DNA wrapped around an octamer core of histone proteins (two each of H2A, H2B, H3.1, and H4) to form a nucleosome, the basic repeating unit of chromatin. The 5' biotin-TEG DNA consists of a core 147 bp 601 nucleosome assembly sequence [1] flanked by 26 bp linker sequences as underlined below. After assembly, histone tails were enzymatically removed. This product is ideal for use as a negative control in binding assays

TECHNICAL INFORMATION

Storage	Stable for six months at -80°C from date of receipt. For best results, aliquot and avoid freeze/thaws.
Formulation	0.99 mg/mL mononucleosome in 50.5 µL 10 mM Tris-HCl pH 7.5, 25 mM NaCl, 1 mM EDTA, 2 mM DTT, 20% glycerol. (21.4 µg protein, 50 µg DNA + protein).

APPLICATION NOTES

Tailless Recombinant Nucleosome with Linker DNA is highly purified and suitable for use as a negative control or substrate in enzyme screening assays and nucleosome binding experiments. The biotinylated DNA enables affinity binding applications.

DNA SEQUENCE

5'-Bio-TEG
GGACCCTATACGCGGCCGCCGAATTCCTGGAGAATCCCGGTCTGCAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCG
CTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATA
TACATCCTGTGGATCCGCCGGTCGCGAACAGCGACC3'

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) H4 - P62805

REFERENCES

[1] Lowary & Widom *J. Mol. Biol.* (1998). PMID: 9514715

VALIDATION DATA

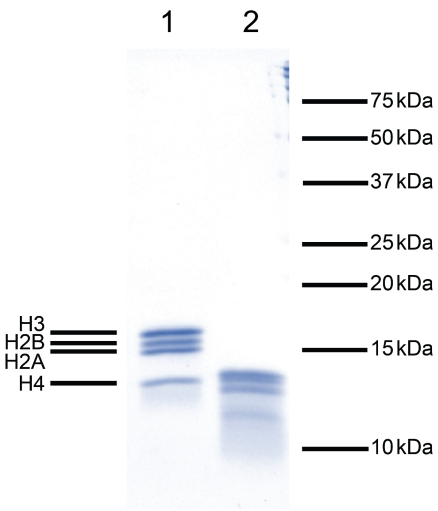

FIGURE 1 **Protein gel data.** Coomassie stained SDS-PAGE gel of proteins in Tailless Nucleosome (1 µg) demonstrates the purity of histones in the preparation. **Lane 1:** Histone proteins in the nucleosome before enzymatic removal of tails. Sizes of molecular weight markers and positions of the intact core histones (H2A, H2B, H3, and H4) are indicated. **Lane 2:** Histone proteins in the nucleosome after tail removal via trypsin-digestion. Heterogeneity of the trypsin-treated histone proteins can be observed.

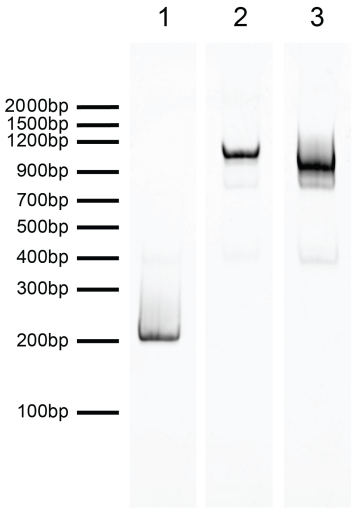

FIGURE 2 **DNA gel data.** Tailless Nucleosomes resolved via native PAGE and stained with ethidium bromide to visualize DNA. All lanes are from the same gel. **Lane 1:** Free DNA (EpiCypher 18-2044; 100 ng). **Lane 2:** Intact nucleosomes (400 ng). **Lane 3:** Nucleosomes after enzymatic removal of histone tails.