

## H2BS6ar2 Recombinant Nucleosome, Biotinylated

|                      |             |                |                                |
|----------------------|-------------|----------------|--------------------------------|
| <b>Catalog No</b>    | 16-0423     | <b>Species</b> | Human                          |
| <b>Lot No</b>        | 25221001-01 | <b>Source</b>  | <i>E. coli</i> & synthetic DNA |
| <b>Pack Size</b>     | 25 µg       | <b>Tag</b>     | Biotinylated                   |
| <b>Concentration</b> | 4.61 µM     | <b>MW</b>      | 201,938.5 Da                   |

### DESCRIPTION

ADP-ribosylation (ADPr) is a reversible histone modification that regulates chromatin structure, transcription, DNA replication, and DNA damage repair [1]. Occurring as either mono- or poly-ADP-ribose, ADPr supports recruitment of DNA repair proteins and chromatin remodelers [1]. Recombinant ADPr nucleosomes provide a defined platform for studying biological, chromatin-based functions of ADP-ribosylation.

#### Product Highlights:

- **Physiologically relevant binding** – Nucleosomes provide a physiologically relevant substrate for studying chromatin biology, capturing the multivalent binding environment that many chromatin-associated proteins require.
- **Built for versatility** – Designed for broad biochemical assays, these nucleosome substrates enable robust, quantitative analysis of protein binding, enzymatic activity, and chromatin interactions in a defined relevant format.
- **Research ready performance** – Built on deep nucleosome design expertise: EpiCypher's designer nucleosomes are supported by > 1,000 publications across diverse research applications including immunology, cancer, and molecular biology.

H2BS6ar2 (histone H2B serine 6 di-ADPr) Recombinant Nucleosome, Biotinylated consists of 147 base pairs of 601 sequence DNA [2] wrapped around an octamer of core histone proteins (two each of H2A, H2B, H3.1, and H4) to form a nucleosome, the basic repeating unit of chromatin. The DNA contains a 5' biotin-TEG group. H2BS6ar2 nucleosome contains H2B with di-ADP-ribosylated serine at position 6. H2BS6ar2 is ADP-ribosylated by poly-ADPr polymerase 1 (PARP1) and PARP2, and ADPr removal is achieved by the glycohydrolase ARH3 [1].

### TECHNICAL INFORMATION

|                    |   |
|--------------------|---|
| <b>Storage</b>     | Stable for six months at -80°C from date of receipt. For best results, aliquot and avoid freeze/thaws   |
| <b>Formulation</b> | 0.93 mg/mL mononucleosome in 26.9 µL 10 mM Tris HCl pH 7.5, 25 mM NaCl, 1 mM EDTA, 2 mM DTT, 20% glycerol (13.7 µg protein, 25 µg DNA + protein). |

### APPLICATION NOTES

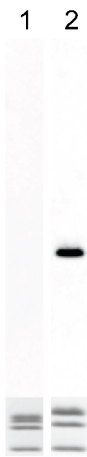
H2BS6ar2 nucleosome is highly purified and suitable for a variety of applications, including use as a substrate in enzyme assays, high-throughput screening and inhibitor testing, chromatin binding studies, protein-protein interaction assays, structural studies, and in effector protein binding experiments. For a corresponding unmodified control, we recommend EpiCypher 16-0006.

### GENE & PROTEIN INFORMATION

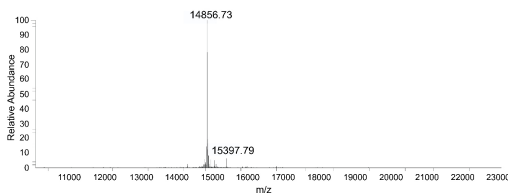
|                   |  |
|-------------------|--|
| <b>UniProt ID</b> | H2A - P04908 (alt. names: H2A type 1-B/E, H2A.2, H2A/a, H2A/m)<br>H2B - P62807 (alt. names: H2B type 1-C/E/F/G/I)<br>H3.1 - P68431 (alt. names: H3, H3/a, H3/b, H3/d)<br>H4 - P62805 |
|-------------------|--|

### REFERENCES

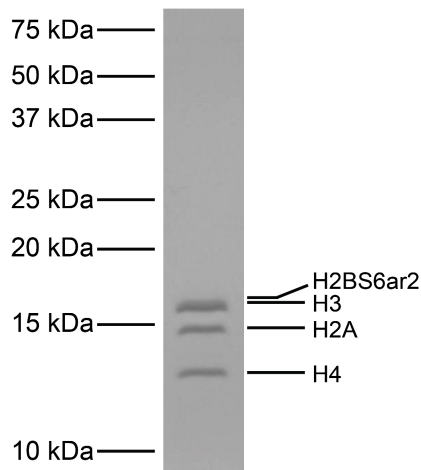
- [1] Longarini & Matic *DNA Repair*. (2022). PMID: 35963141  
[2] Lowary & Widom *J. Mol. Biol.* (1998). PMID: 9514715



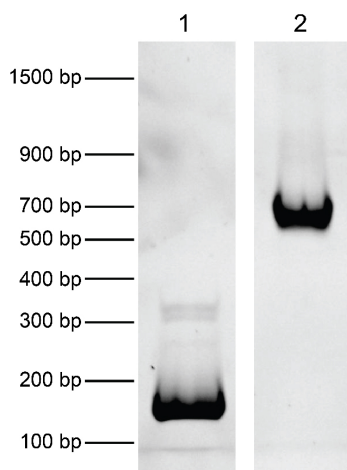
**FIGURE 1 Western blot data.** Western analysis of H2BS6ar2 nucleosome. All lanes were resolved on a single gel. **Top Panel:** Unmodified (EpiCypher 16-0006; Lane 1) and H2BS6ar2 (Lane 2) nucleosomes were probed with an anti-Poly/Mono-ADP Ribose antibody and analyzed via enhanced chemiluminescence (ECL). Only the H2BS6ar2 sample produced a detectable signal. **Bottom Panel:** Detail from Coomassie stained gel showing unmodified (Lane 1) and H2BS6ar2 (Lane 2) nucleosomes.



**FIGURE 2 Mass spec data.** H2BS6ar2 histone analyzed by high resolution mass spectrometry. Expected mass = 14857.11 Da. Determined mass = 14856.73 Da.



**FIGURE 3 Protein gel data.** Coomassie stained SDS-PAGE gel of proteins in H2BS6ar2 nucleosome (2 µg) demonstrates the purity of histones in the preparation. Sizes of molecular weight markers and positions of the core histones (H2A, H2BS6ar2, H3.1, and H4) are indicated. H2BS6ar2 nearly co-migrates with H3.



**FIGURE 4 DNA gel data.** H2BS6ar2 nucleosome resolved via native PAGE and stained with ethidium bromide to visualize DNA. All lanes were resolved on a single gel. **Lane 1:** Free DNA (EpiCypher 18-0005; 100 ng). **Lane 2:** Intact H2BS6ar2 nucleosomes (400 ng).