

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 16, 2026

NPS

RRID:SCR_010890

Type: Tool

Proper Citation

NPS (RRID:SCR_010890)

Resource Information

URL: <http://liulab.dfci.harvard.edu/NPS/>

Proper Citation: NPS (RRID:SCR_010890)

Description: A python software package that can identify nucleosome positions given histone-modification ChIP-seq or nucleosome sequencing at the nucleosome level.

Abbreviations: NPS

Synonyms: Nucleosome Positioning from Sequencing, NPS (Nucleosome Positioning from Sequencing)

Resource Type: software resource

Defining Citation: [PMID:19014516](#)

Keywords: bio.tools

Resource Name: NPS

Resource ID: SCR_010890

Alternate IDs: OMICS_00505, biotools:nps

Alternate URLs: <https://bio.tools/nps>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260912T195725+0000

Ratings and Alerts

No rating or validation information has been found for NPS.

No alerts have been found for NPS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 121 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Sahebi M, et al. (2014) Isolation and expression analysis of novel silicon absorption gene from roots of mangrove (*Rhizophora apiculata*) via suppression subtractive hybridization. *BioMed research international*, 2014, 971985.

Morito D, et al. (2014) Moyamoya disease-associated protein mysterin/RNF213 is a novel AAA+ ATPase, which dynamically changes its oligomeric state. *Scientific reports*, 4, 4442.

Dey P, et al. (2014) Functional characterization of two structurally novel diacylglycerol acyltransferase2 isozymes responsible for the enhanced production of stearate-rich storage lipid in *Candida tropicalis* SY005. *PloS one*, 9(4), e94472.

Kim YB, et al. (2014) Transcripts of anthocyanidin reductase and leucoanthocyanidin reductase and measurement of catechin and epicatechin in tartary buckwheat. *TheScientificWorldJournal*, 2014, 726567.

Wan L, et al. (2014) Molecular cloning, structural analysis and tissue expression of protein phosphatase 3 catalytic subunit alpha isoform (PPP3CA) gene in Tianfu goat muscle. *International journal of molecular sciences*, 15(2), 2346.

Yagi M, et al. (2014) Protective epitopes of the *Plasmodium falciparum* SERA5 malaria vaccine reside in intrinsically unstructured N-terminal repetitive sequences. *PloS one*, 9(6), e98460.

Gu HF, et al. (2014) Adaptive evolution of the circadian gene timeout in insects. *Scientific reports*, 4, 4212.

Zhang Y, et al. (2014) Transcription factor Nrf1 is topologically repartitioned across membranes to enable target gene transactivation through its acidic glucose-responsive domains. *PloS one*, 9(4), e93458.

Jacquier N, et al. (2014) Cell wall precursors are required to organize the chlamydial division septum. *Nature communications*, 5, 3578.

Liu Y, et al. (2014) Tc1-like transposable elements in plant genomes. *Mobile DNA*, 5, 17.

Kim YB, et al. (2014) Cloning and characterization of a flavonol synthase gene from *Scutellaria baicalensis*. *TheScientificWorldJournal*, 2014, 980740.

Bradshaw E, et al. (2013) Proteomic survey of the *Streptomyces coelicolor* nucleoid. *Journal of proteomics*, 83, 37.

Ksenofontov AL, et al. (2013) Partially disordered structure in intravirus coat protein of potyvirus potato virus A. *PloS one*, 8(7), e67830.

Puranik S, et al. (2013) Comprehensive genome-wide survey, genomic constitution and expression profiling of the NAC transcription factor family in foxtail millet (*Setaria italica* L.). *PloS one*, 8(5), e64594.

Favoino E, et al. (2013) Autoantibodies recognizing the amino terminal 1-17 segment of CENP-A display unique specificities in systemic sclerosis. *PloS one*, 8(4), e61453.

Wang X, et al. (2013) TaAbc1, a member of Abc1-like family involved in hypersensitive response against the stripe rust fungal pathogen in wheat. *PloS one*, 8(3), e58969.

Gouba N, et al. (2013) Plant and fungal diversity in gut microbiota as revealed by molecular and culture investigations. *PloS one*, 8(3), e59474.

Vlachakis D, et al. (2013) Molecular modeling and pharmacophore elucidation study of the Classical Swine Fever virus helicase as a promising pharmacological target. *PeerJ*, 1, e85.

Zhao G, et al. (2013) Identification and characterization of *Toxoplasma gondii* aspartic protease 1 as a novel vaccine candidate against toxoplasmosis. *Parasites & vectors*, 6, 175.

Zhang Y, et al. (2013) The membrane-topogenic vectorial behaviour of Nrf1 controls its post-translational modification and transactivation activity. *Scientific reports*, 3, 2006.