

International Conference on **Transcriptomics**

July 27-29, 2015 Orlando, USA

SSFinder: High throughput CRISPR-Cas target sites prediction tool

Shailesh Sharma

National Agri-Food Biotechnology Institute, India

Clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated protein (Cas) system facilitates targeted genome editing in organisms. Despite high demand of this system, finding a reliable tool for the determination of specific target sites in large genomic data remained challenging. Here, we report SSFinder, a python script to perform high throughput detection of specific target sites in large nucleotide datasets. The SSFinder is a user-friendly tool compatible with Windows, Mac OS and Linux operating systems and freely available online. We report SSFinder a comprehensive tool for the identification of specific CRISPR-Cas target sites with high reliability. It is a freeware, easy to edit and low memory demand tool compatible with many commonly used operating systems. Our tool is very useful in high throughput inhouse screening applications of large genomes in limited time. This can accelerate the functional genomics research based on the application of CRISPR-Cas system.

Biography

Shailesh Sharma completed his PhD in Structural Biology from the Magnetic Resonance Center of the University of Florence, Italy. His research interests are in computational biology and during PhD were focused on the investigation of structural, functional and dynamic properties of metalloproteins. He was a Postdoctoral Scientist in US-India joint research training program hosted by Seattle Biomedical Research Institute at the University of Washington in USA and at the International Centre for Genetic Engineering and Biotechnology in New. Currently he is a Scientist in Department of Biotechnology in Government of India. His research focuses on protein structure, genome annotation and Molecular Dynamics simulations.

shailesh.sharma@nabi.res.in

Notes: