


<b>NAME</b>	PRIYANKA NARAD		
<b>DESIGNATION</b>	Assistant Professor		
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<b>CONTACT NUMBER</b>	0120-4392410 (Office)		
<b>RESEARCH INTERESTS</b>	I am currently working in the area of stem cell bioinformatics. My research interests include construction and analysis of gene regulatory network describing human pluripotency and other stem cell related disorders. I am also proficient in analysis of microarray data using R language.		
<b>EDUCATIONAL QUALIFICATIONS:</b>			
Name of College / University	Degree	Year	
Delhi University	B.Sc(Hons) Botany	2006	
Birla Institute of Technology and Science, Mesra (Ranchi)	M.Sc Bioinformatics	2008	
Amity University, Uttar Pradesh	Ph.D	2017	
<b>Title of Ph.D. thesis: “Deciphering the interaction network describing pluripotency in human”</b>			
<b>EXPERIENCE (in chronological order)</b>			
Designation	Type of post held (teaching/ research)	Name of the Institute	Year (From – To)
Assistant Professor	Teaching	Centre for Bioinformatics and Computational Biology, Amity Institute of Biotechnology, Amity University, Noida.	2009-till date
PhD Scholar	Research	Stem Cell Bioinformatics, Centre for Bioinformatics, Amity Institute of Biotechnology, Amity University, Noida.	2013- 2017
Research Assistant	Research	Biotechnology Information Centre, DBT, Govt. of India, New Delhi	2008-2009
<b>PUBLICATIONS:16</b>	<ol style="list-style-type: none"> <li>Narad, P., Upadhyaya KC &amp; Som A. (2017). Reconstruction, visualization and explorative analysis of human pluripotency network. Network Biology, 7(3), 57.</li> <li>Charan, P. S., &amp; Narad, P. Insilico Analysis And Docking Studies Of Semenogelin 1 Targeting Senile Seminal Vesicle Amyloidosis (Ssva). Wjpmr, 2017,3(8), 182-186</li> <li><b>Narad, P.</b>, Chaurasia, A., Wadhwa, G., &amp; Upadhyayaa, K. C. (2016). Net2Align: An Algorithm For Pairwise Global Alignment of Biological Networks. Bioinformation, 12(12), 408-411.</li> <li><b>Narad, P.</b>, Wadhwa, G., Upadhyaya, KC.(2016);</li> </ol>		

Analyzing The Intervening Sequences Of Pluripotency Associated Genes To Identify Conserved Sequence Patterns In Human Using Integrative Bioinformatics, International J. of Pharma and BioSciences, Vol.8, Issue 1: B582-587.

5. Sengupta, A., & **Narad, P.** (2016, March). Glucose concentration varies logarithmically under both glycemic conditions in a computationally reconstructed human energy pool network (HEPNet). In Bioinformatics and Systems Biology (BSB), International Conference on (pp. 1-4). IEEE.
6. **Narad, P.**, Kumar, A., Chakraborty, A., Patni, P., Sengupta, A., Wadhwa, G., & Upadhyaya, K. C. (2016). Transcription Factor Information System (TFIS): A Tool for Detection of Transcription Factor Binding Sites. *Interdisciplinary Sciences: Computational Life Sciences*, 1-14.
7. Mitra, J; **Narad, P**; Paul, PK (2016); In silico, in vitro and in vivo approach in understanding the functional relationship between ergosterol and Rubisco. *Photosynthetica*, 1-8.
8. Bansal H, Kriti, Kumar M. Vimal, **Narad P**; (2016), Homology Modeling and Docking Studies on SEMA3A as A Receptor for Targeting Multiple Myeloma (2015), *Int J Phar Sc Rev Res*, Vol.36, Issue 1: 50-53.
9. Mitra, J., **Narad, P.**, Sengupta, A., Sharma, P. D., & Paul, P. K. (2015). In silico Identification of Ergosterol as a Novel Fungal Metabolite Enhancing RuBisCO Activity in *Lycopersicum esculentum*. *Interdisciplinary Sciences: Computational Life Sciences*, 1-12.
10. Jain A., Sengupta A., **Narad P.** (2015), Constitutively Activated Tyrosine Kinase Inhibitor Drug Design: Homology Modeling And Docking Studies On Chronic Myelogenous Leukemia Bcr-Abl Fusion Protein. *International J. of Pharma and BioSciences*, 6 (2): 1215-1225.
11. **Narad, P.**, & Upadhyaya, K. C. (2014). Integrative Bioinformatics Approaches to Analyze Molecular Events in Pluripotency. *Biology and Medicine*, 2014.
12. **Narad, P.**, Jain, A., Sengupta, A. (2014); Docking studies for tuberculosis taking alanine racemase as a receptor and a novel plant source quercetin as a potential drug source, *International J. of Pharma and BioSciences*, Vol.5, Issue 3: B31-B39.
13. Sengupta, A., Saxena, S., Singh, G., **Narad, P.**, Yadav,

	<p>A., &amp; Grover, M. (2014), A Computational Systems Biology Approach to Decipher Significant Intricacies of Dihydrolipoamide Dehydrogenase Deficiency in Human, International Journal of Soft Computing and Engineering (IJSCE), Volume-4, Issue-1,1-5.</p> <p>14. <b>Narad, P.</b>, Malpani, M., Chakraborty, V., &amp; Sengupta, A. (2012). Comparative Homology Modeling And Docking Of Lamin A Molecule And Its Incidence In Progeria. Int J Pharm Bio Sci, 1164-1170.</p> <p>15. <b>Narad, P.</b>, Sengupta, A., &amp; Wadhwa, G. (2011). Evolution of homeobox protein sequence (Hoxa9) across different species using phylogenetic analysis and expression analysis of the sequence in reference to the occurrence of Acute Myeloid Leukemia. Journal of Natural Science, Biology and Medicine, 2(3), 32.</p> <p>16. Wadhwa G, Singh R, Narad P, Gene Expression Analysis Studies for Acute Myeloid Leukemia to find out putative drug targets using in-silico approach, ISRST, ISBN: 978-1-60651-009-4, pg. 100-107.</p> <p><b>BOOK CHAPTER</b></p> <p>1. Biology of Useful Plants and Microbes (2013), ISBN-13: 978-8184872644</p>
<p><b>AWARDS &amp; HONOURS/ DISTINCTIONS</b></p>	<ul style="list-style-type: none"> <li>• DST SERB Young Scientist Travel Award</li> <li>• Selected for Advanced Course on In-silico Systems Biology at WellCome Trust Genome Campus, EMBL-EBI, UK.</li> <li>• Editorial Board- Biology Medicine Case Reports</li> <li>• Editorial Board- EC Proteomics and Bioinformatics</li> <li>• Reviewer: Journal of Pharmacy and Pharmacology</li> <li>• Reviewer: Interdisciplinary Sciences (Springer)</li> </ul>
<p><b>MEMBERSHIP</b> with Professional/ Academic bodies</p>	<ul style="list-style-type: none"> <li>• Member of Asia-Pacific Chemical, Biological&amp; Environmental Engineering Society (APCBEEES).</li> <li>• Member of American Society for Biochemistry and Molecular Biology.</li> </ul>