

# Pooran DEWARI

## Postdoc, University of Edinburgh

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 Edinburgh, UK  UK ILR work permit

Trained as a cancer molecular biologist and bioinformatician, I have collaborated with leading biotech companies (IDT, Twist Bioscience, Sphere Fluidics) to develop CRISPR genome-editing pipelines for efficient and scalable tagging of genes in mammalian stem cells. Using ChIP-seq and RNA-seq approaches, I am currently investigating how neurodevelopmental transcription factors fuel proliferation of brain tumour stem cells. Keen on transitioning into bioinformatics job and work in team environment wherein I can apply my research skills and interests.

## SKILLS

<b>Industry collaboration</b>	Collaborated with Integrated DNA Technologies, USA (2016-2018) and developed a CRISPR pipeline for epitope tagging in stem cells. Currently working in collaboration with Twist Bioscience and Sphere Fluidics (2018- present) to develop microfluidic benchtop CRISPR module for knock-in of fluorescent reporter genes in mammalian cells.
<b>Bioinformatics</b>	<b>ChIP-seq analysis</b> : QC and align reads to genome, peak calling, motif discovery, GO analysis, heatmap generation, data visualisation <b>RNA-seq analysis</b> : Align reads using STAR, DESeq differential expression analysis, data visualisation <b>R language</b> : tidyverse data wrangling, visualisation using ggplot2, analysis of RIME and ChIP-SICAP MS data using R packages, other packages : ChIPseeker, clusterProfiler <b>Programming languages</b> : Python (intermediate level) <b>Other software programs</b> : BEDTools, bamCoverage, Intervene, LaTeX, Snapgene, ImageJ, CellProfiler
<b>NGS sample preparation</b>	Perform ChIP pull-down and prepare barcoded libraries for sequencing
<b>CRISPR genome-editing</b>	Epitope and fluorescent reporter tagging in mammalian stem cells, gene knock-out
<b>Protein partners</b>	Identify protein partners using RIME
<b>Other techniques</b>	Fluorescence microscopy, Gibson and gateway cloning, real-time qPCR, DNA and RNA extraction, Western Blotting

## EDUCATION AND PROFESSIONAL EXPERIENCE

<b>June 2020-present</b>	<b>Health Data Science course, UNIVERSITY OF EDINBURGH, UK</b> <ul style="list-style-type: none"><li>&gt; Analyse health data using R programming language, including summarisation, visualisation and interpretation</li><li>&gt; Learn principles and methods of data science in health</li></ul>
<b>2014 - present</b>	<b>Postdoc, CRM-UNIVERSITY OF EDINBURGH, UK</b> <ul style="list-style-type: none"><li>&gt; In collaboration with IDT Inc. (USA) developed RNP-based CRISPR method and bioinformatics tool for scalable epitope knock-in in mammalian stem cells (2016-2018)</li><li>&gt; Scaled-up mCherry reporter knock-in in GSCs using CRISPR RNP approach (in collaboration with Twist Bioscience and Sphere Fluidics from 2018- present)</li><li>&gt; Identified genomic targets of key neurodevelopmental TFs in patient-derived glioma stem cells (GSCs) using ChIP-seq</li><li>&gt; Computed overlap between TFs binding to chromatin and their intersection with evolutionary conservation (phyloP score) and gene expression (RNA-seq)</li><li>&gt; Identified protein partners of TFs in GSCs using RIME</li></ul>
<b>2013-2014</b>	<b>Postdoc, CENTRE FOR CELLULAR AND MOLECULAR BIOLOGY, India</b> <ul style="list-style-type: none"><li>&gt; Set up zebrafish behavioural assays</li><li>&gt; Model zebrafish to study chronic alcoholism</li><li>&gt; Optimise ChIP using zebrafish brain tissue</li></ul>

2006-2013	<b>PhD, CENTRE FOR CELLULAR AND MOLECULAR BIOLOGY, India</b> <ul style="list-style-type: none"> <li>&gt; Identified role of yeast histone chaperone Asf1 in pol III transcription by ChIP-seq mapping</li> <li>&gt; Studied RNA pol III transcriptional regulation in budding yeast using genetics, biochemistry, and genomics approaches</li> <li>&gt; Purified core components of RNA polymerase III machinery- histones, chromatin assembly chaperone Asf1, yeast RNA polymerase III enzyme, yeast transcription factor C (TFIIIC), and developed assays to assemble chromatin in vitro</li> </ul>
2004-2006	<b>MSc, GB PANT UNIVERSITY OF AGRICULTURE AND TECHNOLOGY, India</b> <ul style="list-style-type: none"> <li>&gt; Final-year research project on 'Development of novel protein and DNA-based markers for identification of bamboo cultivars'</li> <li>&gt; Modules included enzymology, intermediary metabolism, principles in genetic engineering, and techniques in molecular biology</li> </ul>
2000-2003	<b>BSc, KUMAUN UNIVERSITY NAINITAL, India</b> <ul style="list-style-type: none"> <li>&gt; Major subjects : Zoology, Botany, and Chemistry</li> </ul>

## PUBLICATIONS

- 2020 **Dewari PS** et al. Systematic fluorescent reporter knock-in of human basal RNA polymerase II machinery using all-bespoke CRISPR approach. Manuscript in preparation
- 2020 McCarten K, **Dewari PS**, Pollard SM et al. RNA binding protein MYEF2 is a SOX2 interactor and involved in the tumorigenicity of glioblastoma. Manuscript to be submitted
- 2018 **Dewari PS**, Southgate B, McCarten K, Monogarov G, O'Duibhir E, Quinn N, Tyrer A, Leitner MC, Plumb C, Kalantzaki M et al. An efficient and scalable pipeline for epitope tagging in mammalian stem cells using Cas9 ribonucleoprotein. *Elife* 7
- 2017 Bressan RB, **Dewari PS**, Kalantzaki M, Gangoso E, Matjusaitis M, Garcia-Diaz C, Blin C, Grant V, Bulstrode H, Gogolok S et al. Efficient CRISPR/Cas9-assisted gene targeting enables rapid and precise genetic manipulation of mammalian neural stem cells. *Development* 144 : 635-648
- 2016 **Dewari PS**, Ajani F, Kushawah G, Kumar DS, Mishra RK. Reversible loss of reproductive fitness in zebrafish on chronic alcohol exposure. *Alcohol* 50 : 83-89
- 2014 **Dewari PS**, Bhargava P. Genome-wide mapping of yeast histone chaperone anti-silencing function 1 reveals its role in condensin binding with chromatin. *PLoS One* 9 : e108652
- 2011 Mahapatra S, **Dewari PS**, Bhardwaj A, Bhargava P. Yeast H2A.Z, FACT complex and RSC regulate transcription of tRNA gene through differential dynamics of flanking nucleosomes. *Nucleic Acids Res* 39 : 4023-4034

**Guest Blogger at Addgene**    Google Forums Round Up : First Impressions of NgAgo (2016)  
Hassle-free 96-well Format Epitope Tagging Using Cas9 Ribonucleoprotein (2018)

## HONOURS AND AWARDS

- 2020    Funding for Health Data Science course at Edinburgh University by the Scottish Funding Council (SFC)
- 2008-2011    Senior Research Fellowship awarded by Council of Scientific and Industrial Research, India
- 2006-2008    Junior Research Fellowship awarded by Council of Scientific and Industrial Research, India
- 2005-2006    University Teaching Assistant Fellowship during Masters
- 2003    Top-rank holder medal in Bachelor science faculty, Kumaun University, India

## CONFERENCES AND TALKS

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- 2018 Invited talk at The Roslin Institute, Edinburgh.  
Talk title : A practical guide to using Cas9 ribonucleoprotein (RNP) for efficient knock-in of protein tags
- 2018 Part of the UK delegation to enhance collaboration with universities in Japan, Edinburgh–Tsukuba–Kumamoto meetings
- 2017 Invited talk at the Bristol Neuroscience Forum, University of Bristol, UK.  
Talk title : An efficient and scalable CRISPR/Cas9 pipeline for epitope tagging in mammalian stem cells
- 2017 Short talk at Berlin Brain Tumor conference, Germany.  
Talk title : An efficient and scalable CRISPR/Cas9 pipeline for epitope tagging in neural and glioma stem cells
- 2016 Short talk at Edinburgh CRISPR/Cas9 workshop, UK
- 2011 Attended two-day SciComm workshop organised by The Wellcome Trust-DBT India Alliance, India

## TEACHING AND MENTORING

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- Edinburgh University** Mentored and supervised four dissertation students in Steve Pollard's lab in my current postdoc position  
Students learned tissue-culture techniques and CRISPR genome-editing in glioma stem cells  
Closely collaborated with Masters student to develop web-based TAG-IN bioinformatics tool
- CCMB, India** Supervised two Masters students during my PhD
- University Teaching Fellow** Supervised and demonstrated elementary biochemistry experiments to undergraduate students during my Masters degree

## REFERENCES

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**Steve Pollard**  
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