Eric Edward Bryant, PhD

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Education & Experience

2020—Pres. **Amgen, Postdoctoral Research Fellow**
- *Role:* Developed and executed a research plan studying the genetics of mammalian recombinant protein expression using CRISPR methods and transcriptomics.
- *Groups:* Mammalian Expression & Cell Engineering / Integrated Protein Design
- *Managers:* Irwin Chen & Rene Hubert
- *Keywords:* High-throughput mammalian expression / NGS / RNAseq / Arrayed & pooled CRISPR screening / Protein Engineering / Multispecifics / Biologics Discovery

2020 Spring **Roche/Genentech (Contract), Clinical Genomics Data Science Consultant**
- *Role:* Evaluated variant calling from RNAseq while on short-term contract.
- *Department:* Pharma Research & Early Development Informatics (pREDi)
- *Managers:* Venus So & Vitalay Fomin
- *Keywords:* Genome Analysis Toolkit (GATK) / RNAseq / Real World Data / High-performance computing cluster (HPC) / Bioinformatics / CWL, Nextflow, Seven Bridges Genomics

2011—'18 **PhD, Columbia University**
- *Department:* GSAS Biological Sciences
- *Thesis:* Systems genetics of DNA damage tolerance — cisplatin, *RAD5* & CRISPR-mediated nonsense
- *Mentor:* Rodney Rothstein
- *Co-Mentor:* Alberto Ciccia
- *Committee:* Songtao Jia, Elizabeth Miller & Matthew Weitzman
- *Keywords:* Systems genetics / Genetic interaction networks / Landscape enrichment analysis / Synthetic lethality / DNA replication, recombination & repair / Chromosome mobility / CRISPR iSTOP / Bioinformatics / R statistical programming, package and shiny app development

2009—'11 **Gene Oracle, Research Assistant**
- *Role:* De-novo gene synthesis & degenerate codon library construction.

2006—'09 **BS, University of California Los Angeles**
- *Department:* UCLA Microbiology, Immunology & Molecular Genetics

Software examples

2019 **screenmill R package: capture, annotate, quantify, review and analyze time-series colony growth.** This package was used for colony quantification and interaction analysis in Bryant et al. *NAR* 2019. A nice example analysis using screenmill can be found in Figure 1D. A shiny app is included to enable manual review of processed images.

2017 **iSTOP R package: design guides to introduce stop codons with CRISPR-mediated base editors.** This package was written to facilitate guide design for Billon et al. *Mol. Cell* 2017. iSTOP can be configured to generate any desired missense mutation using any hypothetical base editor. This package was used to design a base editing library for Cuella-Martin et al. *Cell* 2021.

Awards

2018 Departmental distinction for PhD dissertation defense
2017—'18 TL1 NIH training grant, clinical and translational research
2016—'17 T32 NIH training grant, cancer biology
2013—'15 T32 NIH training grant, biological sciences
2013 James Howard McGregor award (student with unusual promise as a teacher of zoology)

Publications

Lead contribution

2019-09-26 Rad5 dysregulation drives hyperactive recombination at replication forks resulting in cisplatin sensitivity and genome instability.
Bryant EE, Šunjevarić I, Berchowitz L, Rothstein R, Reid RJD.
Nucleic Acids Research. 2019 Sep 26;47(17):9144—9159
PMID: 31350889 – PMCID: PMC6753471 – DOI: 10.1093/nar/gkz631

2019-01-09 Systems genetics of DNA damage tolerance – Cisplatin, *RAD5* & CRISPR-mediated nonsense.
Bryant EE.
Columbia University.
DOI: 10.7916/d8-k1d0-kb09

2017-09-21 CRISPR-mediated base editing enables efficient disruption of eukaryotic genes through induction of STOP codons.
Billon P*, **Bryant EE***, Joseph SA, Nambiar TS, Hayward SB, Rothstein R, Ciccia A.
Molecular Cell. 2017 Sep 21;67(6):1068—1079.e4
PMID: 28890334 – PMCID: PMC5610906 – DOI: 10.1016/j.molcel.2017.08.008
*co-first authors

Supporting contribution

2022-03-24 Temporal coordination between chromosome mobility and homologous recombination.
Joseph F, Lee SJ, **Bryant EE**, Reid RJD, Šunjevarić I, Rothstein R.
BioRxiv: 10.1101/2022.03.24.485580v1 – DOI: 10.1101/2022.03.24.485580

2021-02-18 Functional interrogation of DNA damage response variants with base editing screens.
Cuella-Martin R, Hayward SB, Fan X, Chen Xiao, Huang JW, Taglialatela A, Leuzzi G, Zhao J, Rabadan R, Lu C, Shen Y, Ciccia A.
Cell. 2021 Feb 18;184(4):1081-1097.e19.
PMID: 33606978 – PMCID: PMC8018281 – DOI: 10.1016/j.cell.2021.01.041
** Acknowledged for bioinformatics support. I designed the CRISPR base editing guide library.*

2020-08-26 Measuring chromosome pairing during homologous recombination in yeast.
Joseph F, Lee SJ, **Bryant EE**, Rothstein R.
Methods in Molecular Biology. 2021;2153:253—265.
PMID: 32840785 – DOI: 10.1007/978-1-0716-0644-5_18

2019-10-01 DNA damage triggers increased mobility of chromosomes in G1 phase cells.
Smith MJ, **Bryant EE**, Joseph FJ, Rothstein R.
Molecular Biology of the Cell. 2019 Oct 1;30(21):2620—2625
PMID: 31483739 – PMCID: PMC6761769 – DOI: 10.1091/mbc.E19-08-0469

2018-09-01 Increased chromosomal mobility after DNA damage is controlled by interactions between the recombination machinery and the checkpoint.
Smith MJ, **Bryant EE**, Rothstein R.
Genes & Development. 2018 Sep 1;32(17-18):1242—1251
PMID: 30181361 – PMCID: PMC6120718 – DOI: 10.1101/gad.317966.118

2016-10-01 A synthetic dosage lethal genetic interaction between CKS1B and PLK1 is conserved in yeast and human cancer cells.
Reid RJD, Du X, Šunjevarić I, Rayannavar V, Dittmar J, **Bryant EE**, Maurer M, Rothstein R.
Genetics. 2016 Oct 1;204(2):807—819
PMID: 27558135 – PMCID: PMC5068864 – DOI: 10.1534/genetics.116.190231