

# Matthew Carter

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<b>Education</b>	<b>Cornell University</b> , College of Engineering, Ithaca, NY Bachelor of Science, <i>Cum Laude</i> , Biological Engineering (GPA: 3.69) 2013 Kessler Fellow	<b>May 2014</b>
<b>Technical Skills</b>	<b>Laboratory skills:</b> DNA and RNA purification, PCR, gel electrophoresis, molecular cloning, NGS library preparation, RNA-seq <b>Bioinformatics tools:</b> BWA, Bowtie, SAMtools, HH-suite, Clustal <b>Programming languages:</b> Python, Javascript, Bash <b>Web development:</b> HTML/CSS, Apache, MySQL, MongoDB	
<b>Research Experience</b>	<b>Caribou Biosciences, Inc.</b> , Berkeley, CA <i>Research Associate</i> , Technology Development Group	<b>March 2017 - Present</b>
	<ul style="list-style-type: none"><li>– Developed <i>E. coli</i> cell-based assays in order to validate predicted activities of proteins discovered <i>in silico</i>.</li></ul>	
	<b>Caribou Biosciences, Inc.</b> , Berkeley, CA <i>Bioinformatics Programmer</i> , Computational Biology Group	<b>August 2014 - March 2017</b>
	<ul style="list-style-type: none"><li>– Built an NGS pipeline to quantify and classify DNA repair outcomes from Cas9-mediated breaks in human cell lines and primary cells.</li><li>– Architected a web-based Laboratory Information Management System consisting of back-end SQL databases for storing experimental data and interactive, front-end visualization tools.</li></ul>	
	<b>Caribou Biosciences, Inc.</b> , Berkeley, CA <i>Summer Fellow</i>	<b>May 2013 - August 2013</b>
	<ul style="list-style-type: none"><li>– Designed computational tool for generating <i>in silico</i> off-target site predictions for CRISPR-Cas9 guide RNA sequences.</li></ul>	
	<b>Lucks Lab for RNA Engineering</b> , Cornell University, Ithaca, NY <i>Undergraduate Researcher</i>	<b>September 2011 - May 2014</b>
	<ul style="list-style-type: none"><li>– Created framework for visualizing RNA secondary structures based on SHAPE-Seq data.</li><li>– Designed pipeline for detecting putative <i>trans</i>-acting RNA activators endogenous to bacterial and viral genomes based on homology with bacterial terminator sequences.</li></ul>	
<b>Publications</b>	Cameron, P.*, Fuller, C.K.*, Donohoue, P.D., Jones, B.N., Thompson, M.S., <b>Carter, M.M.</b> , Gradia, S., Vidal, B., Garner, E., Slorach, E.M., Lau, E., Banh, L.M., Lied, A.M., Edwards L.S., Settle A.H., Capurso D., Llaca, V., Deschamps, S., Cigan, M., Young, J.K., May, A.P. "Mapping the genomic landscape of CRISPR-Cas9 cleavage." <i>Nature Methods</i> <b>14(6)</b> (2017): 600-606. PMID: 28459459.  van Overbeek, M.*, Capurso, D.*, <b>Carter, M.M.</b> , Thompson, M.S., Frias, E., Russ, C., Reece-Hoyes, J.S., Nye, C., Gradia, S., Vidal, B., Zheng, J., Hoffman, G.R., Fuller, C.K., May, A.P. "DNA Repair Profiling Reveals Nonrandom Outcomes at Cas9-Mediated Breaks." <i>Molecular Cell</i> <b>63(4)</b> (2016): 633-646. PMID: 27499295.	
<b>Patents Issued</b>	Andrew P. May, Rachel E. Haurwitz, Jennifer A. Doudna, James M. Berger, <b>Matthew M. Carter</b> , Paul Donohoue. Compositions and methods of nucleic acid-targeting nucleic acids. <b>US9260752</b> , Feb 2016; <b>US9410198</b> , Aug 2016; <b>US9725714</b> , Aug 2017; <b>US9803194</b> , Oct 2017; <b>US9809814</b> , Nov 2017.	
<b>Patents Pending</b>	<b>Matthew M. Carter</b> , Megan van Overbeek, Andrew P. May. Directed nucleic acid repair. <b>US20170058272</b> , Mar 2017.	