PI Name(s) All	Institution	Title
IVANOVIC, TIJANA	BRANDEIS UNIVERSITY	Building mechanistic insight into evolvability of viral cell-entry functions
PORCO, TRAVIS CHRISTIAN	UNIVERSITY OF CALIFORNIA, SAN FRANCIS	Ebola modeling: behavior, asymptomatic infection, and contacts
NOVEMBRE, JOHN	UNIVERSITY OF CHICAGO	Extending Tools for Visualization of Geographic Structure in Population Ger
JENSEN, JEFFREY D	ARIZONA STATE UNIVERSITY-TEMPE CAMPU	Developing novel statistics and coalescent approaches for the improved s
BUCETA, JAVIER (contact); BOCCHIN	LEHIGH UNIVERSITY	Risk Assessment of Ebola Outbreaks through Probabilistic Modeling of Chiro
WANG, JIN	UNIVERSITY OF TENNESSEE CHATTANOOG/	Experimentally Guided Modeling and Simulation for Cholera Dynamics
MORDECAI, ERIN	STANFORD UNIVERSITY	Leveraging environmental drivers to predict vector-borne disease transmis
CALLAHAN, BENJAMIN JOHN	NORTH CAROLINA STATE UNIVERSITY RALEI	Quantitative Metagenomics and the Vaginal Microbiome of Preterm Birth
LANZAS, CRISTINA	NORTH CAROLINA STATE UNIVERSITY RALEI	Analytical pipelines for data and model integration: finding informed path
RABADAN, RAUL	COLUMBIA UNIVERSITY HEALTH SCIENCES	Uncovering Evolutionary History using the Topology of Genomic Data with A
DAHARI, HAREL (contact); BOODRAM	LOYOLA UNIVERSITY CHICAGO	Computational discovery of effective hepatitis C intervention strategies
SEGRE, DANIEL (contact); DELISI, CHA	BOSTON UNIVERSITY (CHARLES RIVER CAM	A platform for mining, visualization and design of microbial interaction netv
CHRISTOFFERSON, REBECCA CARRIERI	LOUISIANA STATE UNIV A&M COL BATON F	Characterization of temperature-driven heterogeneity in mosquito popula
NUISMER, SCOTT L	UNIVERSITY OF IDAHO	COLLABORATIVE RESEARCH: A MATHEMATICAL THEORY OF TRANSMISSIBLE V
WHITE, LAURA FORSBERG	BOSTON UNIVERSITY MEDICAL CAMPUS	Methods to Estimate the Effect of Interventions on the Incidence and Trans
BANSAL, SHWETA	GEORGETOWN UNIVERSITY	Vaccine hesitancy and erosion of herd immunity: harnessing big data to fo
LOPMAN, BENJAMIN A	EMORY UNIVERSITY	Integrating data streams with multi-scale modeling to guide norovirus vacc
QUINLAN, AARON R	UNIVERSITY OF UTAH	Software for exploring all forms of genetic variation in any species
SANTILLANA GUZMAN, MAURICIO	BOSTON CHILDREN'S HOSPITAL	Development of an Open-Source and Data-Driven Modeling Platform to M
REICH, NICHOLAS G	UNIVERSITY OF MASSACHUSETTS AMHERST	Statistical methods for real-time forecasts of infectious disease: dynamic tir
MAY, ERIC ROBERT	UNIVERSITY OF CONNECTICUT STORRS	Structural Dynamics of Viral Proteins: Computational Investigation of Capsi
BUCKEE, CAROLINE O'FLAHERTY	HARVARD SCHOOL OF PUBLIC HEALTH	New approaches to measuring and containing the spatial spread of huma
CAPRA, JOHN ANTHONY	VANDERBILT UNIVERSITY	The Evolution of Gene Regulation and Human Disease
SALZBERG, STEVEN L	JOHNS HOPKINS UNIVERSITY	Computational Methods for Microbial and Microbiome Sequence Analysis
BEDFORD, TREVOR BC	FRED HUTCHINSON CANCER RESEARCH C	Real-time tracking of virus evolution for vaccine strain selection and epide

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