1.
Record Nr.	UNINA9910300426803321
Autore	Karschau Jens
Titolo	Mathematical Modelling of Chromosome Replication and Replicative Stress [[electronic resource] /] / by Jens Karschau
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2015
ISBN	3-319-08861-0
Edizione	[1st ed. 2015.]
Descrizione fisica	1 online resource (89 p.)
Collana	Springer Theses, Recognizing Outstanding Ph.D. Research, , 2190-5053
Disciplina	572.8645
Soggetti	Biophysics
	Biological physics
	Statistical physics
	Dynamical systems
	Nucleic acids
	Genetic engineering
	Physics
	Biological and Medical Physics, Biophysics
	Complex Systems
	Nucleic Acid Chemistry
	Genetic Engineering
	Numerical and Computational Physics, Simulation
	Statistical Physics and Dynamical Systems
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references at the end of each chapters.
Nota di contenuto	Introduction -- Optimal Origin Placement for Minimal Replication Time -- Actively Replicating Domains Randomly Associate into Replication Factories -- Summary and Conclusions.
Sommario/riassunto	DNA replication is arguably the most crucial process at work in living cells. It is the mechanism by which organisms pass their genetic information from one generation to the next, and life on Earth would be unthinkable without it. Despite the discovery of DNA structure in the 1950s, the mechanism of its replication remains rather elusive. This

work makes important contributions to this line of research. In particular, it addresses two key questions in the area of DNA replication: which evolutionary forces drive the positioning of replication origins in the chromosome; and how is the spatial organization of replication factories achieved inside the nucleus of a cell?   A cross-disciplinary approach uniting physics and biology is at the heart of this research. Along with experimental support, statistical physics theory produces optimal origin positions and provides a model for replication fork assembly in yeast. Advances made here can potentially further our understanding of disease mechanisms such as the abnormal replication in cancer.