1.

Record Nr.	UNINA9910146341203321
Titolo	Statistical modelling : proceedings of the 19th International workshop on statistical modelling, Florence (Italy), 4-8 July, 2004 / / Annibale Biggeri ... [et al.] [[electronic resource]]
Pubbl/distr/stampa	Firenze, : Firenze university press, 2004
ISBN	88-8453-192-6
Descrizione fisica	1 online resource (xix, 503 p.)
Altri autori (Persone)	BiggeriAnnibale
Disciplina	519
Soggetti	Linear models (Statistics) Linear models (Statistics) - Data processing
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Proceedings. On cover: Dipartimento di statistica Giuseppe Parenti.
Nota di bibliografia	Includes bibliographical references.

2.	Record Nr.	UNINA9910253933903321
	Autore	Stübler Sabine
	Titolo	Modelling Proteasome Dynamics in a Bayesian Framework / / by Sabine Stübler
	Pubbl/distr/stampa	Wiesbaden : , : Springer Fachmedien Wiesbaden : , : Imprint : Springer Spektrum, , 2017
	ISBN	3-658-20167-3
	Edizione	[1st ed. 2017.]
	Descrizione fisica	1 online resource (XV, 96 p. 30 illus., 10 illus. in color.)
	Collana	BestMasters, , 2625-3577
	Disciplina	616.079
	Soggetti	Immunology Bioinformatics Cytology Cell Biology
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Nota di bibliografia	Includes bibliographical references.
	Nota di contenuto	Structure and Function of the Proteasome -- Approaches to Model Proteasome Dynamics -- Comparison of the Dynamics of Proteasome Subtypes -- Inhibitor Influence on the Catalytic Subunits -- Inhibitor Influence on a Compartmentalised Short Fluorogenic Peptide Model . .
	Sommario/riassunto	Sabine Stübler compares different proteasome isoforms and subtypes in terms of their transport and active site-related parameters applying an existing computational model. In a second step, the author extends this model to be able to describe the influence of proteasome inhibitors in in vitro experiments. The computational model, which describes the hydrolysis of short fluorogenic peptides by the 20S proteasome, is calibrated to experimental data from different proteasome isoforms using an approximate Bayesian computation approach. The dynamics of proteasome inhibitors are included into the model in order to demonstrate how to modulate the inhibitor's transport parameters for strong or isoform-specific inhibition. Contents Structure and Function of the Proteasome Approaches to Model Proteasome Dynamics Comparison of the Dynamics of Proteasome Subtypes Inhibitor Influence on the Catalytic Subunits Inhibitor Influence on a Compartmentalised Short Fluorogenic Peptide Model Target Groups Lecturers and students of systems biology, immunology and cell

biology Practitioners from the fields of systems biology, immunology and cell biology About the Author Sabine Stübler works as PhD student in the Computational Physiology Group at the Institute of Biochemistry and Biology, University of Potsdam. Her research focus currently is on developing a novel systems pharmacology model.