

1. Record Nr.	UNINA9910451735303321
Autore	Norton O. Richard
Titolo	Field guide to meteors and meteorites [[electronic resource] /] / O. Richard Norton, Lawrence A. Chitwood
Pubbl/distr/stampa	London, : Springer, c2008
ISBN	1-281-37824-0 9786611378240 1-84800-157-6
Edizione	[1st ed. 2008.]
Descrizione fisica	1 online resource (292 p.)
Collana	Patrick Moore's practical astronomy series, , 1617-7185
Altri autori (Persone)	ChitwoodLawrence A
Disciplina	523.51
Soggetti	Meteors Astrogeology Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Includes indexes.
Nota di contenuto	pt. 1. Ancient fragments of the solar system -- pt. 2. The family of meteorites -- pt. 3. Collecting and analyzing meteorites.
Sommario/riassunto	Imagine the unique experience of being the very first person to hold a newly-found meteorite in your hand – a rock from space, older than Earth! "Weekend meteorite hunting" with magnets and metal detectors is becoming ever more popular as a pastime, but of course you can't just walk around and pick up meteorites in the same way that you can pick up seashells on the beach. Those fragments that survived the intense heat of re-entry tend to disguise themselves as natural rocks over time, and it takes a trained eye – along with the information in this book – to recognize them. Just as amateur astronomers are familiar with the telescopes and accessories needed to study a celestial object, amateur meteoritists have to use equipment ranging from simple hand lenses to microscopes to study a specimen, to identify its type and origins. Equipment and techniques are covered in detail here of course, along with a complete and fully illustrated guide to what you might find and where you might find it. In fact, the Field Guide to Meteors and Meteorites contains pretty much everything an amateur astronomer – or geologist – needs to know about meteors and

meteorites.

2. Record Nr.	UNINA9911018651603321
Autore	Wang Sufang
Titolo	Practical Bioinformatics : A Laboratory Manual // by Sufang Wang, Michael Gribskov
Pubbl/distr/stampa	Singapore : , : Springer Nature Singapore : , : Imprint : Springer, , 2025
ISBN	9789819679492
Edizione	[1st ed. 2025.]
Descrizione fisica	1 online resource (143 pages)
Altri autori (Persone)	GribskovMichael
Disciplina	616.042072
Soggetti	Genetics - Research Biology - Technique Genetics Molecular biology Biotechnology Genetics Research Biological Techniques Genetics and Genomics Molecular Biology
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Chapter 1. Introduction to Bioinformatics -- Chapter 2. Introduction to Antibiotic Resistance -- Chapter 3. Introduction to Evolution and Homology -- Chapter 4. Preparing your sequences -- Chapter 5. Investigating sequence comparison statistics -- Chapter 6. Finding homologous sequences using Blast -- Chapter 7. Finding homologous sequences using UniProt -- Chapter 8. Multiple Sequence Alignment -- Chapter 9. Identifying conserved sequence motifs -- Chapter 10. Building a phylogenetic tree -- Chapter 11. Gene expression analysis in RNA-seq -- Chapter 12. Machine learning methods in RNA-seq.
Sommario/riassunto	This book is a lab manual which can be integrated with bioinformatics course. The field of bioinformatics is advancing at a remarkable rate.

With the development of new analytical techniques that make use of the latest advances in machine learning and data science, today's biologists are gaining fantastic new insights into the natural world's most complex systems. This book includes a lab-based manual that can assist students handling large biological data. It aims to help students and researchers understand (1) the importance of horizontal transfer in the spread of antibiotic resistance, and in biology more broadly; (2) how protein and nucleic acid sequences are used to determine phylogenetic trees and the genetic relationship between organisms; (3) how sequence comparisons can be used to infer protein function; and (4) how to analyze high-throughput sequencing data to do gene expression analysis. This book is valuable for researchers, teachers and students, as well as any readers who are interested in bioinformatics.
