

1. Record Nr.	UNINA9910299705703321
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Titolo	Bioinformatics of Non Small Cell Lung Cancer and the Ras Proto-Oncogene // by Amita Kashyap, D. Bujamma, Naresh Babu M
Pubbl/distr/stampa	Singapore : , : Springer Singapore : , : Imprint : Springer, , 2015
ISBN	981-4585-08-4
Edizione	[1st ed. 2015.]
Descrizione fisica	1 online resource (79 p.)
Collana	SpringerBriefs in Forensic and Medical Bioinformatics, , 2196-8845
Disciplina	006.3 502.85 519 570285
Soggetti	Computational intelligence Bioinformatics Cancer - Research Biomedical engineering Medical informatics Applied mathematics Engineering mathematics Computational Intelligence Computational Biology/Bioinformatics Cancer Research Biomedical Engineering and Bioengineering Health Informatics Mathematical and Computational Engineering
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.
Nota di contenuto	Introduction -- Review of Literature -- Materials and Methods (Tools and Databases) -- Flowchart -- Conclusion.-References.
Sommario/riassunto	Cancer is initiated by activation of oncogenes or inactivation of tumor suppressor genes. Mutations in the K-ras proto-oncogene are responsible for 10–30% of adenocarcinomas. Clinical Findings point to a wide variety of other cancers contributing to lung cancer incidence.

Such a scenario makes identification of lung cancer difficult and thus identifying its mechanisms can contribute to the society. Identifying unique conserved patterns common to contributing proto-oncogenes may further be a boon to Pharmacogenomics and pharmacoinformatics. This calls for ab initio/de novo drug discovery that in turn will require a comprehensive in silico approach of Sequence, Domain, Phylogenetic and Structural analysis of the receptors, ligand screening and optimization and detailed Docking studies. This brief involves extensive role of the RAS subfamily that includes a set of proteins, which cause an over expression of cancer-causing genes like M-ras and initiate tumour formation in lungs. SNP Studies and Structure based drug discovery will also be undertaken.
