

Introduction to cBioPortal

Tutorial for 59M/68M MSc students

Introduction and Learning Objectives

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Session structure

- 10.00 Introduction and Learning Objectives
- 10.05 cBioPortal website demonstration
- 10.15 Problem-solving tasks
- 10.40 Recap and Further Resources
- 10.45 Accessing and using underlying cBioPortal data
- 10.55 Close

Learning objectives

- 1 Recognise the applications and utility of cBioPortal for cancer research
- 2 Operate and explore the cBioPortal website to identify cancer data of interest
- 3 Complete two cancer biology problem-solving tasks using cBioPortal
- 4 Recognise the process for accessing and analysing cBioPortal data

What is cBioPortal?



Public website for exploratory analysis, visualisation and download of large cancer omics datasets, with clinical metadata

Data derived from large consortia, as well as highlighted studies



Data annotated by external reference databases

Depending on the dataset, includes mutations, CNA, gene expression, methylation data *etc.*

When using cBioPortal, cite the following papers, plus the reference papers for datasets used: [Cerami *et al.* 2012](#), [Gao *et al.* 2013](#)



Why use cBioPortal?



Access to the largest, publicly available cancer sequencing studies, all in one place

Explore broader relevance of laboratory/animal studies across cancer types

Hypothesis generation, including student projects

Data visualisation

Exploration of clinical data

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cBioPortal website demo

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