Associate Editors

Salvador Capella Gutierrez – Barcelona Supercomputing. Computational aspects of personal medicine initiative, appears to include sequencing. PhD in bioinformatics. OK choice

Ana Maria Rojas – PI publishing bioinformatics sequencing methiods. Publishes miARma-Seq, which is a tool for RNA seq data. TreeDet, a web server to explore sequence space. Also works in molecular evolution. First choice so far Group Leader, Bioinformatics and Computational Biology, CABD-CSIC Sevilla

**First Choice – Ana Maria Rojas**

**Second Choice – Salvador Capella**

Reviewers

Expertise on mutation signatures

Ludmil Alexandrov. Assistant professor UCSD.

[**l2alexandrov@ucsd.edu**](mailto:l2alexandrov@ucsd.edu)

variant-calling expertise and user

Ignaty Leshchiner. Group leader Cancer Genome Analysis Group, Broad Institute

**igleshch@broadinstitute.org**

Somatic evolution in tumors

Inigo Martincorena. Group Leader Wellcome Trust – Sanger Institute UK

Probably too senior to do it, but may have people he can pass it off to, and it may be interesting enough for him to do that.

[**Inigo.martincorena@sanger.ac.uk**](mailto:Inigo.martincorena@sanger.ac.uk)

Pointed out how variant calling affects tumor biology inferences

Jeff Chuang, The Jackson Laboratory

Jeff.chuang@jax.org