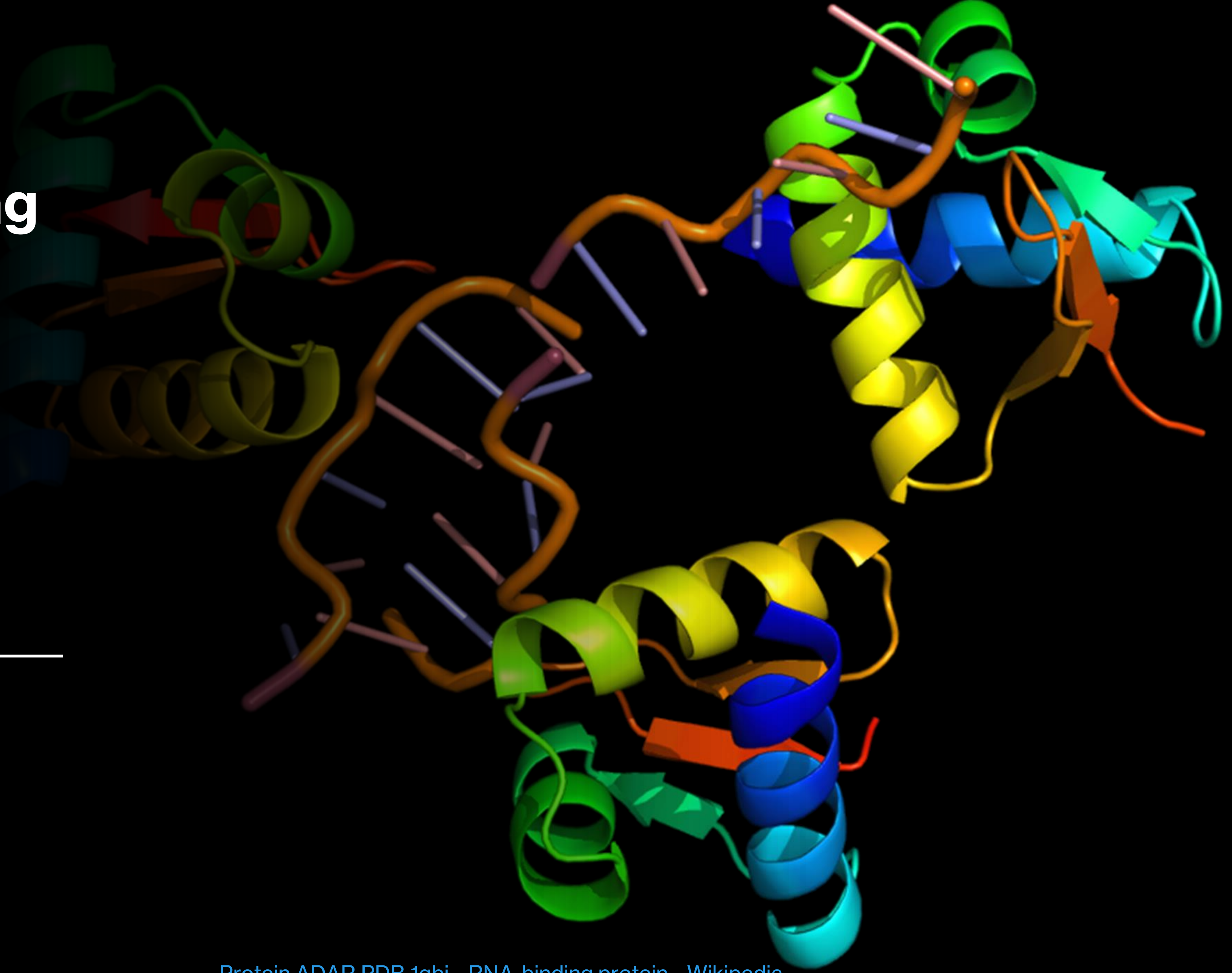
PureCLIP: capturing target-specific protein–RNA interaction footprints from single-nucleotide CLIP-seq data

Presentation by Yang Xie and Janus Mosbacher



Protein ADAR PDB 1qbj - RNA-binding protein - Wikipedia

RNA-Bi re they
inte

virus b

RESEARCH ARTICLE

The severe acute respiratory syndrome-coronavirus replicative protein nsp9 is a single-stranded RNA-b unit unique in the RNA virus world

Egloff, François Ferron, Valérie Campanacci, Sonia Lon

and affiliations

3796; https://doi.org/10.1073/pnas.0307877101

chool, Boston, MA, and approved January 28,

RNA-RNA and RNA-protein interactions in coronavirus replication and transcri

Isabel Sola [1], Pedro A Mateos-Gomez, Fernando A

Affiliations + expand

PMID: 21378501 PMCID: PMC323

L523S, an RNA-binding protein as a pot therapeutic target for lung cancer

T Wang, L Fan, Y Watanabe, P D McNeill, G G Moulton, C Bangur, G Persing & S G Reed

British Journal of Cancer **88**, 887–894 (2003) | Cite this article

859 Accesses | **88** Citations | **6** Altmetric | Metrics

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of SARS

Crystal structure of SARS nucleocapsid prot reveals poten

nen [a], Suhua Zhang [c], Hong Shan

A-Binding Proteins and

Article

The Matrix Protein VP40 from Ebola Virus Octamerizes into Pore-like Structures with Specific RNA Binding Properties

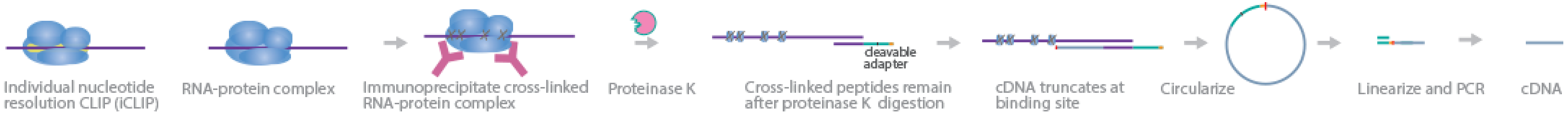
F.Xavier Gomis-Rüth [1,2], Andréa Dessen [1,4], Joanna Timmins [1], Andreas Bracher [1], Larissa Kolesnikowa [3], Stephan Becker [3], Hans-Dieter Klenk [3], Winfried Weissenhorn [1]

How to extract RNA-binding proteins/CLIP-data

- High throughput sequencing technologie Illumina
- RNA-protein interaction sequences can be enriched using iCLIP or eCLIP
- iCLIP and eCLIP are both new methods. With this methods it is possible to analyze truncated cDNAs, which is not possible with other CLIP-methods.

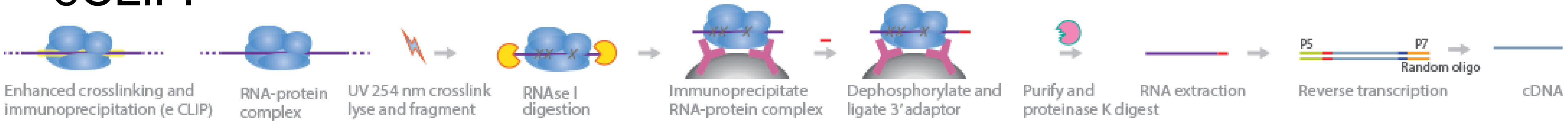
iCLIP vs eCLIP

- iCLIP:



[iCLIP (illumina.com)](illumina.com)

- eCLIP:

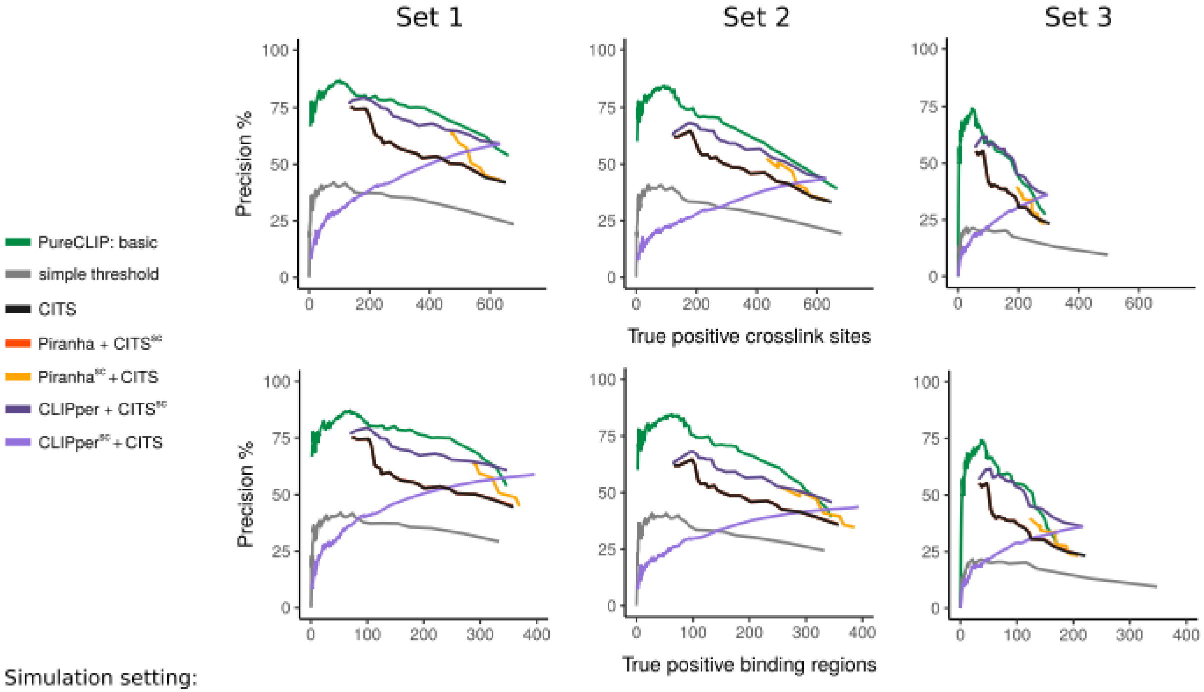


[eCLIP (illumina.com)](illumina.com)

Common methods and PureCLIP-The advantage

- eCLIP and iCLIP data shows a spatial dependency, which can be a problem using peak calling methods
- With PureCLIP this problem will be eliminated caused by the use of Hidden Markov Model. HMM ⟶ single nucleotide resolution
- inclusion of crosslink motifs and non-specific background signal increases the detection rate

Results



Simulation setting:			
Pull-down rate	100%	100%	50%
Background binding	✗	✓	✓

Conclusion

- The PureCLIP program based on Hidden Markov Models has a much higher precision in detecting target specific cross linking binding sites compared to the other methods described in the paper!

- With PureCLIP it is possible to get more detailed information about specific target protein-RNA interaction. For instance this is a very help- and powerful tool for medical research and could save life in future!

Sources

- Crystal structure of SARS-CoV-2 nucleocapsid protein RNA binding domain reveals potential unique drug targeting sites – ScienceDirect
- https://www.sciencedirect.com/science/article/pii/0042682286903053
- RNA-binding proteins of coronavirus MHV: Detection of monomeric and multimeric N protein with an RNA overlay-protein blot assay – ScienceDirect
- L523S, an RNA-binding protein as a potential therapeutic target for lung cancer | British Journal of Cancer (nature.com)
- The Matrix Protein VP40 from Ebola Virus Octamerizes into Pore-like Structures with Specific RNA Binding Properties - ScienceDirect

Thank you for your attention!

If you are interested in more detailed information about PureCLIP please ask and have a look at our Poster!