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Poster presentation

Using Comparative Genomics & RNA Structure to Find RNA Editing Sites

Daniel Clutterbuck*

Address: MRC Human Genetics Unit, Western General Hospital, Edinburgh EH4 2XU, UK

Email: Daniel Clutterbuck* - daniel.clutterbuck@hgu.mrc.ac.uk

* Corresponding author

A-I RNA editing is the conversion of adenosine to inosine (which is read as guanosine) in pre-mRNAs. Editing has been shown to change the protein sequence or regulation of genes involved in several neurological diseases. Recently, reports demonstrate that editing is very widespread in human Alu-repeat sequences, however, there are still only a handful of specific protein recoding sites. We have generated a pipeline to identify mismatches from the public sequence databases and then prioritise them based on a series of features that correctly identify the known editing sites. These features include high sequence conservation around the proposed editing site and the ability of the region to form an RNA hairpin with neighbouring sequences. Using this pipeline we have identified and verified a novel RNA editing target, BC10, which is highly conserved across a range of metazoa and has been implicated in two forms of cancer. Furthermore we have used these features to predict novel targets in a range of species, without the use of mismatch data.