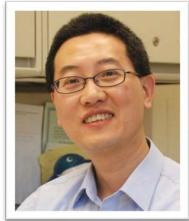
## CENTER FOR RNA BIOMEDICINE



RNA Innovation Seminar Thursday, May 4th at 4:00pm Forum Hall, Palmer Commons

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"Human coding RNA editing is generally nonadaptive"

## Abstract:

Impairment of RNA editing at a handful of coding sites causes severe disorders, prompting the view that coding RNA editing is highly advantageous. Recent genomic studies have expanded the list of human coding RNA editing sites by more than 100 times, raising the question of how common advantageous RNA editing is. Analyzing 1,783 human coding A-to-G editing sites, we show that both the frequency and level of RNA editing decrease as the importance of a site or gene increases; that during evolution, edited As are more likely than unedited As to be replaced with Gs but not with Ts or Cs; and that among nonsynonymously edited As, those that are evolutionarily least conserved exhibit the highest editing levels. These and other observations reveal the overall nonadaptive nature of coding RNA editing, despite the presence of a few sites in which editing is clearly beneficial. We propose that most observed human coding RNA editing results from tolerable promiscuous targeting by RNA editing enzymes, the original physiological functions of which remain elusive.

## Keywords:

Editing level, evolution, human, nonsynonymous, deleterious, neutral, synonymous