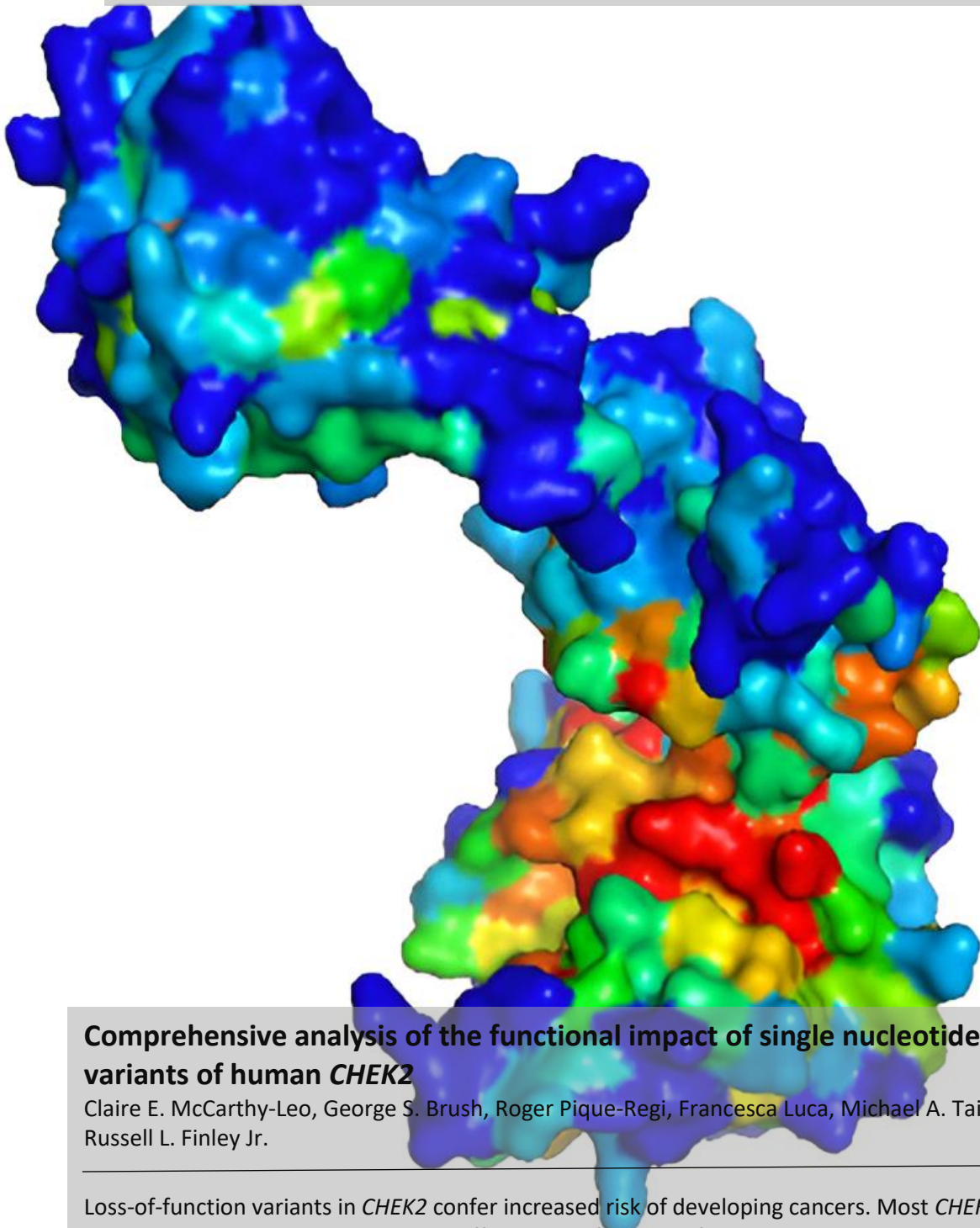


# PLOS GENETICS

Public Library of Science | plosgenetics.org | Volume 20 | Issue 8 | August 2024



## Comprehensive analysis of the functional impact of single nucleotide variants of human *CHEK2*

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Loss-of-function variants in *CHEK2* confer increased risk of developing cancers. Most *CHEK2* variants, however, have an unknown effect on the function of the Chk2 protein kinase. This study tested the functional impact of all possible variants in the *CHEK2* coding region. The protein structure is shown with a heat map overlay showing the fraction of variants at each position that were damaging to function; red positions indicate that all amino acid changes were damaging, while blue positions indicate all changes were tolerated. Regions the least tolerant to changes (red) include the catalytic site in the kinase domain.

Image credit: Claire E. McCarthy-Leo