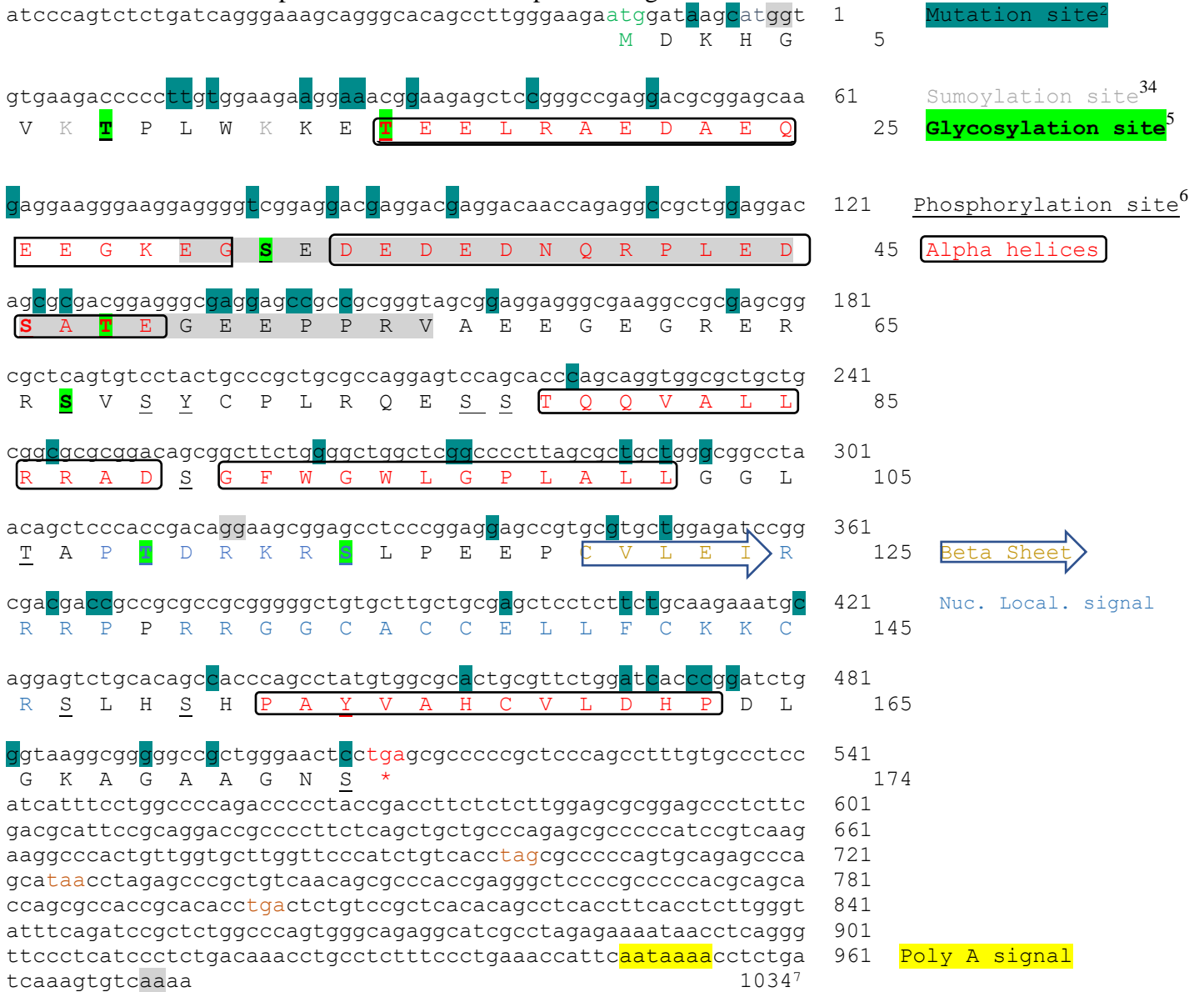


>NM_145272.3 Homo sapiens chromosome 17 open reading frame 50¹



Three different prediction programs (Swiss Model, Phyre2, and Ali2D) were used to predict the formation of alpha helices and beta sheets. Results with high probability that appeared in at least two of the programs are shown on the conceptual translation above.^{8,9,10}

¹ NCBI (National Center for Biotechnology Information) entry on C17orf50 [https://www.ncbi.nlm.nih.gov/nucore/NM_145272] Accessed 25 January 2018

² dbSNP: Short Genetic Variations (NCBI) [https://www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?locusId=146853] Accessed 21 April 2018

³ SUMOplot (Abgent) [http://www.abgent.com/sumoplot] Accessed 17 April 2018

⁴ SUMOsp (The Cuckoo Work Group) [http://sumosp.biocuckoo.org/showResult.php] Accessed 17 April 2018

⁵ NetOGlyc (Technical University of Denmark) [http://www.cbs.dtu.dk/cgi-bin/webface2.fcgi?jobid=5AD6A2ED000058DFF0F4FA61&wait=20] Accessed 3 April 2018

⁶ NetPhos [http://www.cbs.dtu.dk/cgi-bin/webface2.fcgi?jobid=5ACCC31E00002BAD07B0B71E&wait=20] Accessed 3 April 2018

⁷ ExPASy [https://web.expasy.org/cgi-bin/translate/dna_aa] Accessed 25 January 2018

⁸ Kelley, Lawrence and Sternberg, Michael. Phyre2 (Structural Bioinformatics Group) [http://www.sbg.bio.ic.ac.uk/phyre2/phyre2_output/f2cfa91423bbe83/summary.html] Accessed 19 April 2018

⁹ Swiss-Model (Swiss Institute of Bioinformatics) [https://swissmodel.expasy.org/interactive/wrtd7e/models/] Accessed 19 April 2018

¹⁰ Ali2D [https://toolkit.tuebingen.mpg.de/#/jobs/5792387] Accessed 17 April 2018