**Annotation**

Polyphen (Adzhubei *et al.* 2010)

<http://genetics.bwh.harvard.edu/pph2/>

SIFT (Vaser *et al.* 2016)

<https://sift.bii.a-star.edu.sg/>

CADD (Kircher *et al.* 2014)

Adzhubei I. A., Schmidt S., Peshkin L., Ramensky V. E., Gerasimova A., Bork P., Kondrashov A. S., Sunyaev S. R., 2010 A method and server for predicting damaging missense mutations a. Nat. Methods **7**: 248–249.

Kircher M., Witten D. M., Jain P., O’Roak B. J., Cooper G. M., Shendure J., 2014 A general framework for estimating the relative pathogenicity of human genetic variants. Nat. Genet. **46**: 310–5.

Vaser R., Adusumalli S., Leng S. N., Sikic M., Ng P. C., 2016 SIFT missense predictions for genomes. Nat. Protoc. **11**: 1–9.