Supplementary material

A new disease-specific machine learning approach for the prediction of cancer-causing missense variants.

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Supplementary Table 1.

Method	URL	Ref.
CanPredict	http://www.cgl.ucsf.edu/Research/genentech/canpredict/	[1]
CHASM	http://wiki.chasmsoftware.org/i	[2]
LS-SNP	http://modbase.compbio.ucsf.edu/LS-SNP/	[3]
MutD	http://mud.tau.ac.il	[4]
MutPred	http://mutpred.mutdb.org/	[5]
nsSNPAnalyzer	http://snpanalyzer.uthsc.edu/	[6]
PANTHER	http://www.pantherdb.org/tools/csnpScoreForm.jsp	[7]
PhD-SNP	http://gpcr2.biocomp.unibo.it/cgi/predictors/PhD-SNP/PhD-SNP.cgi	[8]
PMUT	http://mmb2.pcb.ub.es:8080/PMut/	[9]
PolyPhen	http://genetics.bwh.harvard.edu/pph2/	[10]
SIFT	http://sift.jcvi.org/	[11]
SNAP	http://rostlab.org/services/snap/	[12]
SNPs3D	http://www.snps3d.org/	[13]
SNPs&GO	http://snps.uib.es/snps-and-go/	[14]

Web available servers for the prediction of deleterious missense variants.

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