Online Resource 2 List of matrices, *in silico* predictors and databases used for the current study and the score obtained for the *MEN1* variant c.703T>C (up-date November 2023).

Article title: A novel likely pathogenetic variant p.(Cys235Arg) of the *MEN1* gene in multiple endocrine neoplasia type 1 with multifocal glucagonomas

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Type of tool	Name	Website	Score
Matrix[1]	Grantham	https://gist.github.com/danielecook/501f03650bca6a3db31ff3af2d413d2a	180 (0 to 215)
	BLOSUM62	https://www.ncbi.nlm.nih.gov/Class/FieldGuide/BLOSUM62.txt	-3 (11 to -4)
Predictor[2]	CADD	https://cadd.gs.washington.edu/	Phred 26,8
	DANN	https://cbcl.ics.uci.edu/public_data/DANN/	0,99
	Align-GVGD	http://agvgd.hci.utah.edu/index.php	C65 (D, S)
	PolyPhen-2	http://genetics.bwh.harvard.edu/pph2/	HumVar 1 (D) HumDiv 0,99 (D)
	MutationTaster	https://www.mutationtaster.org/	94 | 6 (D)
	SIFT	https://sift.bii.a-star.edu.sg/	0 (D, P)
	PROVEAN	http://provean.jcvi.org/index.php	-10,84 (D, P)
	BayesDel	https://fengbj-laboratory.org/BayesDel/BayesDel.html	noAF 0.5674 (D, S) addAF 0.5606 (D, S)
	REVEL	https://sites.google.com/site/revelgenomics/	0.959 (D, S)
	MetaRNN	https://varsome.com/variant/hg38/NM_001370259.2%3Ac.688T%3EC?annotation-mode=germline	0.9916 (D, S)
	MetaLR	https://sites.google.com/site/jpopgen/dbNSFP	0.959 (D, P)
	DEOGEN2	http://deogen2.mutaframe.com/ https://bio.tools/DEOGEN2	0.9844 (D, S)
	MutPred2	http://mutpred.mutdb.org/	0.901 (D, S)
	FATHMM-MKL	https://fathmm.biocompute.org.uk/fathmmMKL.htm	0.9677 (D, M)
	M-CAP	http://bejerano.stanford.edu/mcap/	0.9335 (D, M)
	MVP	https://github.com/ShenLab/missense	0.9912 (D, M)
	EIGEN	http://www.columbia.edu/~ii2135/eigen.html	0.7171 (D, P)
	LRT	by Varsome	0 (D, P)
	PrimateAI	https://github.com/Illumina/PrimateAI	0.8331 (D, P)
	VARITY	https://sites.google.com/site/jpopgen/dbNSFP	0.98 (D)
	Franklin	https://franklin.genoox.com/clinical-db/home	Aggregated prediction 0.99 (D) Likely pathogenic
	Varsome	https://varsome.com/variant/hg38	Aggregated prediction 9 points (D) Likely pathogenic
	LIST-S2	https://list-s2.msl.ubc.ca/;jsessionid=686EBE2822265217A1638E5EF6B898F6?session=686EBE2822265217A1638E5EF6B898F6	0.8979 (U)
	MutationAssessor	http://mutationassessor.org/r3/	2.66 (U)
	Missense3D	http://missense3d.bc.ic.ac.uk/missense3d/	
	Phyre2	http://www.sbg.bio.ic.ac.uk/~phyre2/html/page.cgi?id=index	
Database	1000 genomes phase 3	https://www.internationalgenome.org/data-portal/data-collection/phase-3	

ESP	https://evs.gs.washington.edu/EVS/
gnomAD	https://gnomad.broadinstitute.org/
ClinVar	https://www.ncbi.nlm.nih.gov/clinvar/
Uniprot	https://www.uniprot.org/

[1]Scores range from the more tolerated to the less tolerated, [2]Score D for predicted deleterious effect [when available, the annotation is further divided in strong (S), moderate (M) or supportive (P) prediction], U for uncertain effect. None predictor gave a benign prediction.