

Table 2. Prediction of molecular change of substitutions by MutPred.

Variant ID	Mutation	Probability of deleterious mutation	Features
rs375095163	E308K	0.882	-
rs52804924	P299L	0.839	Gain of Helix (Pr = 0.31 P = 5.5e-03) Altered Ordered interface (Pr = 0.25 P = 0.03) Loss of allosteric site at Y302 (Pr = 0.21 P = 0.04) Altered Transmembraneprotein (Pr = 0.16 P = 0.01) Altered Metal binding (Pr = 0.14 P = 0.04)
rs760199460	D298H	0.874	Altered Ordered interface (Pr = 0.24 P = 0.04) Altered Transmembraneprotein (Pr = 0.23 P = 2.2e-03) Loss of allosteric site at Y302 (Pr = 0.19 P = 0.05) Altered Metal binding (Pr = 0.18 P = 0.04)
rs121913562	C271F	0.927	Altered Transmembraneprotein (Pr = 0.28 P = 4.6e-04) Loss of Helix (Pr = 0.28 P = 0.03) Altered ordered interface (Pr = 0.25 P = 0.02) Gain of sulfatation at Y268 (Pr = 0.03 P = 0.02)
rs1057517991	C271R	0.952	Altered Transmembraneprotein (Pr = 0.29 P = 2.6e-04) Loss of Helix (Pr = 0.29 P = 0.02) Gain of stand (Pr = 0.28 P = 8.9e-03) Gain of loop (Pr = 0.27 P = 0.02) Altered ordered interface (Pr = 0.26 P = 9.7e-03) Loss of sulfatation at Y268 (Pr = 0.03 P = 0.02)
rs1435358988	P260L	0.843	Loss of Strand (Pr = 0.30 P = 1.9e-03) Gain of Helix (Pr = 0.29 P = 0.01) Altered ordered interface (Pr = 0.27 P = 9.3e-03) Alteredtransmembraneprotein (Pr = 0.18 P = 8.0e-03) Altered Metal binding (Pr = 0.04 P = 0.04)
rs1333658154	T246N	0.885	Altered Transmembraneprotein (Pr = 0.30 P = 0.02) Gain of Helix (Pr = 0.27 P = 0.05) Loss of Stand (Pr = 0.26 P = 0.03) Loss of Catalytic site at K242 (Pr = 0.14 P = 0.03) Loss of methylationat K242 (Pr = 0.11 P = 0.04) Gain of N-linked glycosylation at T246 (Pr = 0.04 P = 0.02)
rs868309222	G243R	0.956	Gain of Helix (Pr = 0.32 P = 2.2e-03) Altered Transmembraneprotein (Pr = 0.29 P = 0.03) Altered Ordered interface (Pr = 0.29 P = 3.3e-03) Loss of Stand (Pr = 0.29 P = 3.3e-03) Loss of Catalytic site at K242 (Pr = 0.15 P = 0.02) Loss of methylationat K242 (Pr = 0.11 P = 0.04) Loss of GPI-anchor amidation at N240 (Pr = 0.05 P = 4.8e-03)
rs1191554117	C196Y	0.914	Altered Transmembraneprotein (Pr = 0.37 P = 9.7e-06) Altered Ordered interface (Pr = 0.27 P = 6.6e-03)
rs1159323398	W174C	0.946	Gain of Helix (Pr = 0.35 P = 5.3e-04) Altered Ordered interface (Pr = 0.32 P = 3.4e-03) Loss of strand (Pr = 0.31 P = 1.1e-03) Altered Transmembraneprotein (Pr = 0.19 P = 6.3e-03)
rs768916374	Y157S	0.915	Altered Ordered interface (Pr = 0.48 P = 2.7e-04) Altered Transmembraneprotein (Pr = 0.34 P = 4.4e-05) Loss of allosteric site at Y157 (Pr = 0.30 P = 4.3e-03) Altered Metal binding (Pr = 0.22 P = 0.02) Altered DNA binding (Pr = 0.14 P = 0.05)
rs766665118	T150I	0.834	Altered Disordered interface (Pr = 0.32 P = 0.02) Altered Transmembraneprotein (Pr = 0.29 P = 1.9e-04) Altered Ordered interface (Pr = 0.26 P = 0.01) Loss of allosteric site at R147 (Pr = 0.26 P = 0.01)
rs768806551	D126Y	0.925	Altered Ordered interface (Pr = 0.41 P = 2.5e-04) Altered Transmembraneprotein (Pr = 0.32 P = 7.3e-05) Gain of Strand (Pr = 0.28 P = 7.1e-03) Loss of Helix (Pr = 0.27 P = 0.04) Altered Metal binding (Pr = 0.14 P = 0.04) Gain of sulfation at D126 (Pr = 0.02 P = 0.04)
rs1598932350	D90G	0.918	Loss of Helix (Pr = 0.29 P = 0.01) Altered Transmembraneprotein (Pr = 0.10 P = 0.05)
rs1215552316	H76Y	0.877	Altered Ordered interface (Pr = 0.39 P = 4.1e-04) Altered Metal binding (Pr = 0.18 P = 0.04) Altered Transmembrane protein (Pr = 0.11 P = 0.04)