

Secondary Structure Predictions of mutated GBA sequence

PISPRED Secondary Structure Prediction

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WT: CCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCEEEEEEECCC
Mut.: CCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCEEEEEEECCC
AA: MEFSSPSREECPKPLSRVSIAGSLTGLLLLQAVSWASGARPCIPKSFSSYSSVVCVSNAT
      10      20      30      40      50      60

WT: CCCCCCCCCCCCCCEEEEEEECCCCCCCCCCCCCCCCCCCCCCCCCEEEEEEECCCCCEEEEE
Mut.: CCCCCCCCCCCCCCEEEEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEEEECCCCCEEEEE
AA: YCNISFDPPPTFPALGTFSTRYSRSTRSGRRMELSMGPIQANRTGTGLLLTLQPEQKFQKVKGF
      70      80      90     100     110     120

WT: EECCCHHHHHHHHCCCHHHHHHHHHHHCCCCCCCCCEEEEEEEEEECCCCCCCCCCCCCCCCCCCC
Mut.: EECCCHHHHHHHHCCCHHHHHHHHHHHCCCCCCCCCEEEEEEEEEECCCCCCCCCCCCCCCCCCCC
AA: GGAMTDAALNILALSPPAQNLKLSYFSEEGIGYNIIOVPMASCDFSIRTYTYADTPDD
      130     140     150     160     170     180

WT: CCCCCCCCCCCCCCHHHHHHHHHHHCCCCCEEEEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCC
Mut.: CCCCCCCCCCCCCCHHHHHHHHHHHCCCCCEEEEEEECCCCCCCCCEEEEECCCCCCCCCCCCCCCC
AA: FQLHNFSLPEEDTKLKIPLIHRALQLAQRVPSLLASPWTSLLTWLKTNGAVNGKGS LKGQP
      190     200     210     220     230     240

WT: CCHHHHHHHHHHHHHHHHHHHHHHCCCEEEEEEECCCCCCCCCCCCCCCCCCCCCHHHHHHHHH
Mut.: CCHHHHHHHHHHHHHHHHHHHHHHCCCEEEEEEECCCCCCCCCCCCCCCCCCCCCHHHHHHHHH
AA: GDIYHQTWARYFVKFLDAYAEHKLQFVAVTAENEPSAGLLSGYPFQCLGFTPEHQ RDFIA
      250     260     270     280     290     300

WT: HHHHHHHHC CCCCCCEEEEEEECCCCCCHHHHHHHHHCCCHHHHCCCCCEEEEEEECCCCCCCCCH
Mut.: HHHHHHHHC CCCCCCEEEEEEECCCCCCHHHHHHHHHCCCHHHHCCCCCEEEEEEECCCCCCCCCH
AA: RDLGPTLANNTHHNVRLLMLDDQRLLLPHWAKVVLTDPEAAKYVHGIAVRWYLD FLAPAK
      310     320     330     340     350     360

WT: HHHHHHHHCCCCCEEEEEEECCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHCCCEEEEEEE
Mut.: HHHHHHHHCCCCCEEEEEEECCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHCCCEEEEEEE
AA: ATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSDRGMQYSHSIITSLLYHVVGWTDW
      370     380     390     400     410     420

WT: CCCCCCCCCCCCCCCCCCCCCCEEEEEEECCCCCEEEEECHHHHHHHHHCCCCCCCCCEEEEEEECCC
Mut.: CCCCCCCCCCCCCCCCCCCCCCEEEEEEECCCCCEEEEECHHHHHHHHHCCCCCCCCCEEEEEEECCC
AA: NLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQPVFYHLGHFSKFIPEGSQRVGLVASQK
      430     440     450     460     470     480

WT: CCCEEEEEEECCCCCEEEEEEECCCCCEEEEEEEEEECCCCCEEEEEEECCCCCEEEEEEEEEECC
Mut.: CCCEEEEEEECCCCCEEEEEEECCCCCEEEEEEEEEECCCCCEEEEEEECCCCCEEEEEEEEEECC
AA: NDLDAVALMHPDGS AVVVV LNRSSKDVPTIKDPAVG FLETISP GYSIHTYLWRRQ
      490     500     510     520     530
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Secondary Structure Predictions of mutated GBA sequence

JPred3 Secondary Structure Prediction

Original	,	-----	-----HHH	HHHHHHHHHH	HHHHHHH---	-----
Mutation	,	-----	-----HHH	HHHHHHHHHH	HHHHHHH---	-----
Mut Seq	,	MEFSSPSREE	CPKPLSRVSI	MAGSLTGLLL	LQAVSWASGA	RPCIPKSF S Y
Original	,	--EEEE--	--	-----EEEE	E-----	-----
Mutation	,	--EEEE--	--	-----EEEE	EE-----	-----
Mut Seq	,	SSVVCVCNAT	YCNSFD P PPTF	PALGTFSRYE	STRSGRMEL	SMGPIQAN R T
Original	,	---EEEE--	---EEEEEE	EEHHHHHHHH	HH---HHHH	HHHHHHH---
Mutation	,	---EEEE--	---EEEEEE	EEHHHHHHHH	HH---HHHH	HHHHHHH---
Mut Seq	,	GTGLLLTLQP	EQKFQKVKGF	GGAMTDAAL	NILALSPPAQ	NLLLKSYFSE
Original	,	----EEEE	-----	-----	-----	----HHHHH
Mutation	,	----EEEE	-----	-----	-----	----HHHHH
Mut Seq	,	EGIGYNI I QV	PMASCD F SIR	TYTYADTPDD	FQLHN F SLPE	EDTKLKIPLI
Original	,	HHHHHH---	EEEE--	--EE--	-----	----HHHHH
Mutation	,	HHHHHH---	EEEE--	--EE--	-----	----HHHHH
Mut Seq	,	HRALQLAQR P	VSL L ASPWTS	L T WLKTNGAV	NGKGS L KGQP	GDIYHQ T WAR
Original	,	HHHHHHHHHH	H----EEEE	-----	-----	-HHHHHHHHH
Mutation	,	HHHHHHHHHH	H----EEEE	EE-----	-----	-HHHHHHHHH
Mut Seq	,	YFVKFLDAYA	EHKLQFWAVT	AENEPSAGLL	SGYPFQCLGF	TPEHQ R DFIA
Original	,	HHHHHHHHH-	----EEEE	-----HH	HHHH--HHH	HHHHHEEEE-
Mutation	,	HHHHHHHHH-	----EEEE	-----HH	HHHH--HHH	HHHHHEEEE-
Mut Seq	,	RDLGPTLANN	THHNVRL L ML	DDQRL L LPHW	AKVVL T DPEA	AKYV H GI A VR
Original	,	-----H	HHHHHHHHH-	----EEEE	EE-----	-----HHHH
Mutation	,	-----H	HHHHHHHHH-	----EEEE	EE-----	-----HHHH
Mut Seq	,	WYLDFLAPAK	ATLGETH R LF	PNTMLF A SEA	CVGSK F WEQS	VRLGS W DRGM
Original	,	HHHHHHHHHH	HHHHHHHHHH	HHH-----	-----E	EEEE----EE
Mutation	,	HHHHHHHHHH	HHHHHHHHHH	HH-----	-----EE	EEEE----EE
Mut Seq	,	QYSHS I I T SL	LYHVVGWTDW	NLALN P EGGP	NWVRN F VDSP	IIVDIT K DTF
Original	,	EE--HHHHH	HHH-----	EEEE-----	--EEEEEEE-	----EEEEEE
Mutation	,	EE--HHHHH	HHH-----	EEEE-----	--EEEEEEE-	----EEEEEE
Mut Seq	,	YKQPV F YHLG	HFSK F IPEGS	QRVGL V ASQK	NDLDA V ALMH	PDGSA V VVVL
Original	,	E-----EEEE	EEE---EEEE	EEE---EEE	EEEE--	
Mutation	,	E-----EEEE	EEE---EEEE	EEE---EEE	EEEE--	
Mut Seq	,	NRSSK D V P P T	IKDPA V G F LE	TISP G YSI H T	YLW R RQ	