

A

Kinase	Length	Alignment	Activation T-Loop Phosphorylation Site	Kinase Domain	Truncated Protein
SIK1	783	176-SGEPLSTWCGSPPYAAPEV-194	T182	27-278	1-500
SIK2	926	169-SGELLATWCGSPPYAAPEV-187	T175	20-271	1-500
SIK3	1321	215-PGQLLKTWCGSPPYAAPEL-233	T221	66-317	59-558
AMPK $\alpha$ 1	559	177-DGEFLRTSCGSPNYAAPEV-195	T183	27-279	
AMPK $\alpha$ 2	552	166-DGEFLRTSCGSPNYAAPEV-184	T172	16-268	
BRSK1	778	183-GDSLLETSCGSPHYACPEV-201	T189	34-285	
BRSK2	736	168-GDSLLETSCGSPHYACPEV-186	T174	19-270	1-256
MARK1	795	209-TGNKLDTFCGSPPYAAPEL-227	T215	60-211	
MARK2	788	202-TGNKLDTFCGSPPYAAPEL-220	T208	53-304	$\Delta$ 505-560
MARK3	753	205-TGGKLDTFCGSPPYAAPEL-223	T211	56-307	
MARK4	752	208-LGSKLDTFCGSPPYAAPEL-226	T214	59-310	
NUAK1	661	205-KDKFLQTFCGSPLYASPEI-223	T211	55-306	
NUAK2	628	202-QGKFLQTFCGSPLYASPEI-220	T208	53-303	
MELK	651	161-KDYHLQTCCGSLAYAAPEL-179	T167	11-263	