

Kinase	Length	Alignment	Activation T-Loop Phosphorylation Site	Kinase Domain	Truncated Protein	Mutant Protein
MAP4K1	833	162-IGATLARRLSFIGTPYWMA-180	S171	17-274	1-500	1-500 S171D
MAP4K2	820	161-LTASVAKRRSFIGTPYWMA-179	S170	16-273	1-500	1-500 S170D
MAP4K3	894	161-ITATIAKRKSFIGTPYWMA-179	S170	16-273	1-500	1-500 S170D
MAP4K4	1239	178-LDRTVGRRNTFIGTPYWMA-196	T187	25-289	1-500	1-500 T187E
MAP4K5	846	165-ITATIAKRKSFIGTPYWMA-183	S174	20-277	1-400	1-400 S174D
MAP4K6	1233	178-QDRTVGRRNTFIGTPYWMA-196	T187	25-289	1-500	1-500 T187E
MAP4K7	1360	178-LDRTVGRRNTFIGTPYWMA-196	T187	25-289	1-500	1-500 T187E
PAK1	545	414-ITPEQSKRSTMVGTPTYWMA-432	T423	270-521		T423E
PAK2	524	393-ITPEQSKRSTMVGTPTYWMA-411	T402	249-499		T402E
PAK3	559	427-ITPEQSKRSTMVGTPTYWMA-445	T436	283-534		T436E
PAK4	591	465-VSKEVPRRKS LVGTPTYWMA-483	S474	321-572		S474D
PAK5	719	593-VSKEVPRRKS LVGTPTYWMA-611	S602	449-700	200-719	200-719 S602
PAK6	681	551-ISKDVPKRKSLVGTPTYWMA-569	S560	407-658		S560D
TAOK1	1001	172-SASMASPANSFVGTPYWMA-190	S181	28-281	1-500	1-500 S181D
TAOK2	898	172-SASIMAPANSFVGTPYWMA-190	S181	28-281	1-500	1-500 S181D
TAOK3	1235	168-SASMASPANSFVGTPYWMA-186	S177	24-277	1-500	1-500 S177D
MYO3A	1616	175-LTSTRHRRNTSVGTPFWMA-193	T184	21-287	1-500	1-500 T184E
MYO3B	1341	181-LTSTRLRNNTSVGTPFWMA-199	T190	27-293	1-500	1-500 T190E
STK2	1235	180-NTRTIQRRDSFIGTPYWMA-198	S189	34-292	1-535	1-535 S189D
STK10	968	182-NLKTQKRKDSFIGTPYWMA-200	S191	36-294	1-500	1-500 S191D
STK39	545	222-DVTRNKVRKTFVGTPCWMA-240	T231	63-337		T231E
OSR1	527	176-DITRNKVRKTFVGTPCWMA-194	T185	17-291		T185E
NRK	1582	202-VSRTNGRRNSFIGTPYWMA-220	S211	25-313	1-500	1-500 S211D
MST1	487	174-LTDTMAKRNTVIGTPFWMA-183	T183	30-281		
MST2	491	171-LTDTMAKRNTVIGTPFWMA-190	T180	27-287		
MST3	431	169-LTDTQIKRNTFVGTPTFWMA-188	T178	36-286		
MST4	416	169-LTDTQIKRNTFVGTPTFWMA-188	T178	24-274		
MST5	426	165-LTDTQIKRNTFVGTPTFWMA-184	T174	20-270		