

SUPPLEMENTARY DATA

ROCK2-specific inhibitor KD025 suppresses adipocyte differentiation by inhibiting casein kinase 2

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Supplemental Figures

(A)

NW Score		Identities		Positives		Gaps	
1306		242/263 (92%)		255/263 (96%)		0/263 (0%)	
ROCK1	76	YE	VVKVIGRGAFGEVQLVRHKSTRKVYAMKLLSKFEMIKRSDSAFFWEERDIMAFA	NSPW	135		
ROCK2	92	YD	VVKVIGRGAFGEVQLVRHKASQKVYAMKLLSKFEMIKRSDSAFFWEERDIMAFA	NSPW	151		
ROCK1	136	VV	QLFYAFQDDRYLYMVMEYMPGGDLVNLMNSNYDVPEKWARFYTA	EVVLA	195		
ROCK2	152	VV	QLFYAFQDDRYLYMVMEYMPGGDLVNLMNSNYDVPEKWA+FYTA	EVVLA	211		
ROCK1	196	HR	DKVDPNMLLDKSGHLKLADFGTCMKMKEGMVRC	DTAVGTPDYISPEVLKSQGGDGY	255		
ROCK2	212	HR	DKVDPNMLLDKSGHLKLADFGTCMKMDE	TGMVHCDTAVGTPDYISPEVLKSQGGDGY	271		
ROCK1	256	GRE	CDWWSVGVFLEYEMLVGDTPFYADSLVGTYSKIMNHKNSLTFPDDNDISKEAKNLICA	315			
ROCK2	272	GRE	CDWWSVGVFLEYEMLVGDTPFYADSLVGTYSKIM+HKNSLFP+D+ISKAKNLICA	331			
ROCK1	316	FL	TDREVLGRNGVEEIKRHLFF	338			
ROCK2	332	FL	TDREVLGRNGVEEIRQHPPF	354			

(B)

NW Score		Identities		Positives		Gaps	
1381		253/286 (88%)		271/286 (94%)		0/286 (0%)	
CK2α	39	YQ	LVRKLGRGKYSEVFEAINITNNEKVVVKILKPVKKKIKREIKILENLRGGPNITLA	98			
CK2α'	40	YQ	LVRKLGRGKYSEVFEAINITNNE+VVVKILKPVKKKIKRE+KILENLRGGNII	99			
CK2α	99	DI	VPVSRTPALVFEHVNNTDFKQLYQTLTDYDIRFYMYEILKALDYCHSMGIMHRDVK	158			
CK2α'	100	DI	VPVSRTPALVFEYINNTDFKQLYQTLTDYDIRFYMYELKALDYCHSGIMHRDVK	159			
CK2α	159	PH	NVMIDHEHRKRLRIDWGLAEFYHPGQEYNVRVASRYFKGPELLVDYQMYDYSLDMWSL	218			
CK2α'	160	PH	NVMIDH+KRLRIDWGLAEFYHPGQEYNVRVASRYFKGPELLVDYQMYDYSLDMWSL	219			
CK2α	219	GC	MLASMIFRKEPFFHGHNDYDQLVRIAKVLGTELDYIDKYNIELDPRFNDILGRHSR	278			
CK2α'	220	GC	MLASMIFRKEPFFHGHNDYDQLVRIAKVLGTELYGYLKKYHIDLPHFNDILGQHSR	279			
CK2α	279	KR	WERFVHSENQHLVSPEALDFDKLLRYDHQSRLTAREAMEHPYF	324			
CK2α'	280	KR	WENFIHSENRLVSPEALDLDKLLRYDHQRLTAKEAMEHPYF	325			

Figure S1. Pairwise alignment of kinase domains between ROCK1 and ROCK2 (A) and between CK2α and CK2α' (B). Protein sequences were aligned using NCBI BLAST global alignment tool (<https://blast.ncbi.nlm.nih.gov/>). NCBI protein ID: NP_005397.1 (ROCK1), NP_004841.2 (ROCK2), NP_001886.1 (CK2α), NP_001887.1 (CK2α').

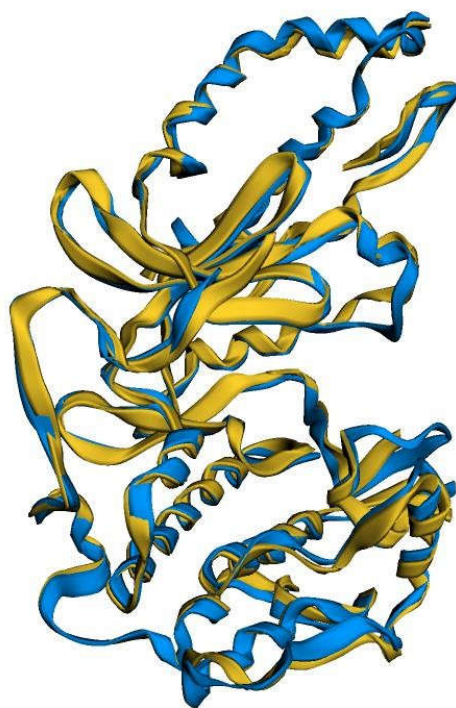


Figure S2. The structural alignment of ROCK1 and ROCK2. The structures were aligned using FATCAT program (<https://fatcat.godziklab.org/>). PDB IDs: 6E9W (ROCK1), 7JOV (ROCK2).