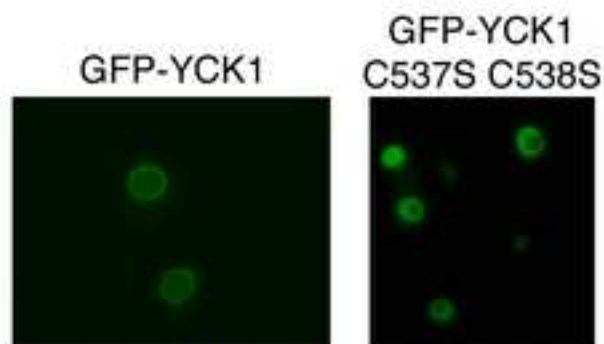



A**B**

 Kinase Domain
 Engineered Stop Codons

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YCK1      1  .... MSMP IASTT LAVNNLTN INGNANFNVOANKQLHHQAYDSPARSSMTATT AANSNSNSSRRDST I VGLHYKIGKKIGEGSFGVL 83
YCK2      1  MSQVQSPLTATNSGLAVNNNTMNSOMPNRNVRLVNGTLPSSLHVSSNLNHNHTGNSSASYSGSOSRDDST I VGLHYKIGKKIGEGSFGVL 90
YCK3      1  .... MSQRSSOH I VGIHYAVGPKIGEGSFGV I 28
HRR25     1  .... MDL RVGRKFR IGRKIGSBSFGD I 23

YCK1     84  FEGT --- NM I N --- GVPVA I XFEPRKTEAPQL RDEYKTYK I L NGTPN I PYAYYFGOEGLNH I L V I DLLGPSLEDL F 153
YCK2     91  FEGT --- NM I N --- GLPVA I XFEPRKTEAPQL KDEYRTYK I L ADTPG I POEY YFGOEGLNH I L V I DLLGPSLEDL F 160
YCK3     29  FEGE --- N I L HSCQAQTGSKRDSS I I MANEPVA I XFEPRHSDAPQL RDEFRAYR I L N GCVG I PHAYYFGOEGMHN I L I I DLLGPSLEDL F 115
HRR25    24  YHGTNL I S --- GEEVA I XLES I RSRHPQL DYESRVYR I L SGGVG I P F I RWFGREGEY NAMV I DLLGPSLEDL F 93

YCK1    154  DWCGRKF SVKT VVQVA VQMI TL I EDL RAHDL I YRDIKPNFL I GRPGQP --- DANN I HL I DFGMAKQYRDPKT KOH I 227
YCK2    161  DWCGRRF SVKT VVQVA VQMI TL I EDL RAHDL I YRDIKPNFL I GRPGQP --- DANKVHL I DFGMAKQYRDPKT KOH I 234
YCK3    116  EWCGRKF SVKT T CMVA KQMI DRVRA I HDHDL I YRDIKPNFL I SQYQR I SPEGKV I KSCASSSNDPNL I YMVDFGMAKQYRDPRT KOH I 205
HRR25    94  NYCHRRF SFKTY I MLALQMF CR I QY I HGRSF I HRDIKPNFL MGVGRG --- STVHV I DFGLSK KYRDFNT HRH I 165

YCK1    228  PYREK KSL SGTARYMS I NTHL GREQSRDDMEALGHVFF YFLRGHL PWQGLKAPNNKOKYK I GEKKRSTNVYDLAOG - - LPVDFGRYLE 315
YCK2    235  PYREK KSL SGTARYMS I NTHL GREQSRDDMEAMGHVFF YFLRGQL PWQGLKAPNNKOKYK I GEKKRLTNVYDLAOG - - LP I QDFGRYLE 322
YCK3    206  PYREK KSL SGTARYMS I NTHF GREQSRDDL ESLGHVFF YFLRGLS PWQGLKAPNNKLYEK I GMTKOKLNPDDL L NNA I PYQF AT YLK 295
HRR25    166  PYRENKSL TGTARYASV NTHLG I EQSRDDL ESLGYL I YFCGSL PWQGLKATT KOKY DR I MEKKLNVSVET L CSG - - LPLEQEYMA 253

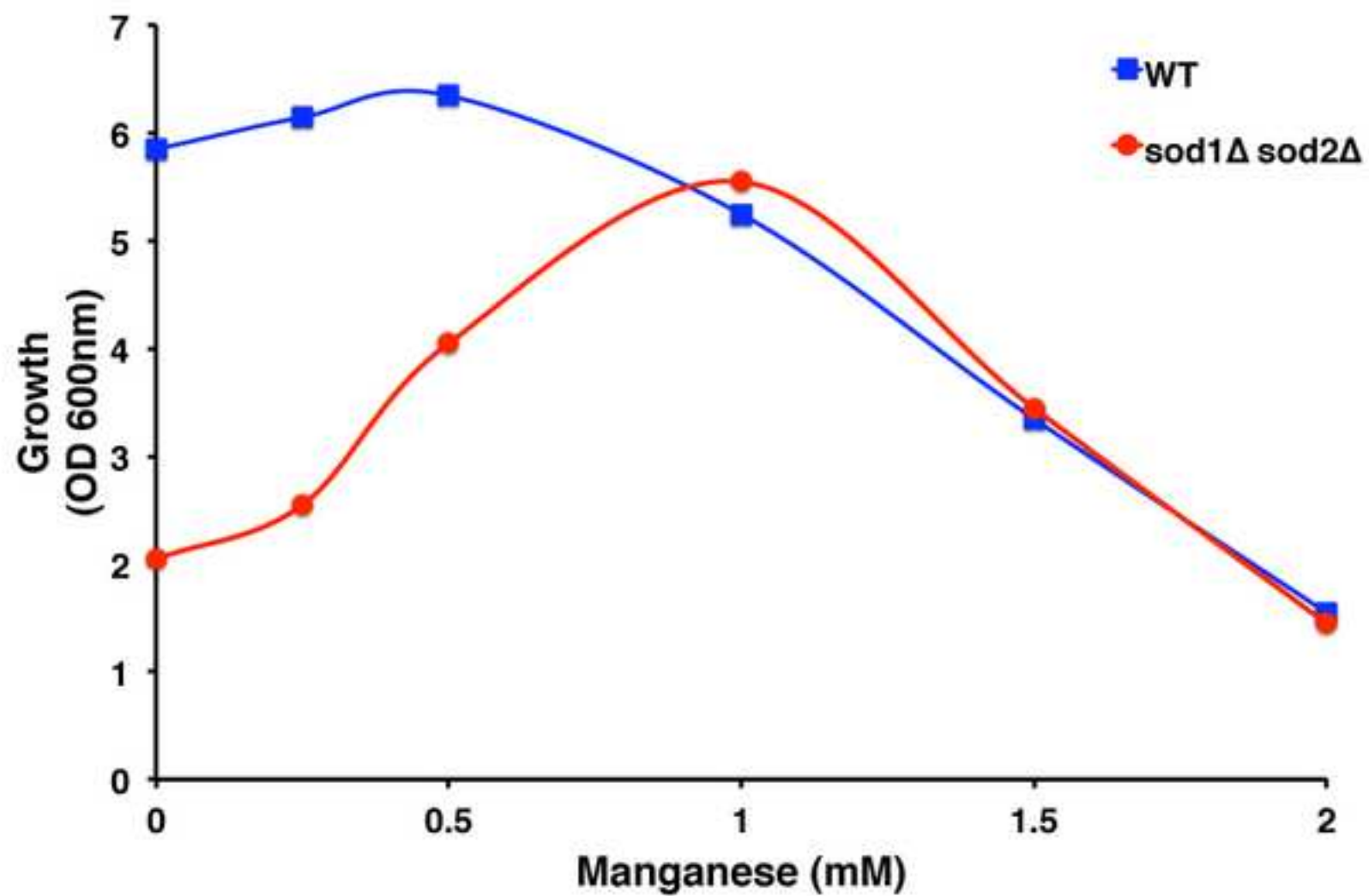
YCK1    316  I VRS L SFE CPDYEGYRK I L L SVL DDLGET ADGQYDWMK L NDGRGWDL N I N --- KKP NLHG YGHPNP - PNEKSKHRNKOLQMOQ 396
YCK2    323  I VRN L SFE ETPOYEGYRML I L L SVL DDLGET ADGQYDWMK L NGGRGWDL S I N --- KKP NLHG YGHPNP - PNEKSKHRNKHQYSS 403
YCK3    296  YARS L KFE DDPDYDYL I S L MDDALRLNDL KDDGHYDMD L NGGKGWN I K I N --- RRANLHG YGNPNPRVNGNTARNVNTNSKTR 377
HRR25    254  YCKN L KFE DKPDYLF LARL I FKDL S I KLEYHNDHL F DWTML RYTKAMVEKQRDLL I EKGD L NANSNAASASNST ONKSETFNK I KLLAMKK 343

YCK1    397  LQMQQLGQQQQQQYAQKTEADMRNSOYKPKLDPTSYEAYGHQTQOKY L QEQQKROQQK L QEQQLQEQQLQEQQLQEQQLQEQQLRATGQPPSQ 486
YCK2    404  PDHHHHYNQQQQQQQAQAQAQAQAQAKVQ - - OQQLGQAGAQQAANRYLOPPDDSHYDEEREASKLDPTSYEAYQQQTQOKYAGQQQKQM 490
YCK3    378  N TTPVATPKQQAQNSYNKDNKSKSR I SSNPQSFTKQOHV LKK I EPNSKY I PETHSNLQRP I KQSQSYDS I SHTQNSPFPVYSSSKANPKR 467
HRR25    344  FPTHFHYYKNEDKHNPSP E I KOOT I L N NNAASSLPEELLNALDKGMENLRQQQPQQVQSSQPQPQPQQLQDDPNGQRPNYYPEPLLQ 433

YCK1    487  PQAQTQSQQFGARYQPOQPSAALRTPEQHPNDDNSS - - - LAASHKGF FOKLGCC - - - - 538
YCK2    491  QQKSKQFANTGANGQTNKYPPYNAQPTANDEQNAKNAQAQRNSNKSSKGF FSKLGC - - - - 546
YCK3    468  S NNEHNLPNHYTNLANKN I NYOSORTNEQENDAYSODENDTFCSK I KYCCCCFC - - - - 524
HRR25    434  QQRDSQEQQQQVPMATTRATQYPPQ I NSNNFNTNQASVPPQMRSNPQQPPQDKPAGQS I WL 494

```

Supplemental Figure 3





Kinase Domain



SOD1 Interacting Degron



Lysines in SOD-Regulated Degron

		10	20	30	40	
YCK1	1	-----MSMPIASTTLAVN	NLTN	INGNANFN	VQANKQL	HHQAVD 38
YCK2	1	MSQVQSPLTATNSGLAVN	NNNTMNSQMPN	RSNVRLV	NGTLP	PPSLHV 45
CK1g3	1	-----			MENKKKKDKDKSD	12
		50	60	70	80	
YCK1	39	SPARSSMTATTAANSNSNS	SRDDST	I	VGLHYKIQKKIGEGSFGVL	83
YCK2	46	SSNLNHNTGNSSASYSQS	SRDDST	I	VGLHYKIQKKIGEGSFGVL	90
CK1g3	13	DRMARPSGRLGHNTRGTG	SSSGVLMVGP	NFRVQ	KKIGCGNFGEL	57
		100	110	120	130	
YCK1	84	FEGTNMINGVPVAIKFEP	RKTEAPQLRDEYKTYKILN	-GTPNIPY		127
YCK2	91	FEGTNMINGLPVAIKFEP	RKTEAPQLKDEYRTYKILA	-GTPGIPQ		134
CK1g3	58	RLGKNLVTNEYVAIKLE	PKSRAPQLHLEYRFYKQLG	-SGDGI	PQ	101
		140	150	160	170	
YCK1	128	AYYFGQEGLHNILVIDLL	GPSLEDFDWCGRKFSVKT	VVQVAVOM		172
YCK2	135	EYYFGQEGLHNILVIDLL	GPSLEDFDWCGRRFVKT	VVQVAVOM		179
CK1g3	102	VYYFGPCGKYNAMVLELL	GPSLEDFDLCORTFSLKTV	LMIAIQL		146
		190	200	210	220	
YCK1	173	ITLIEDLHAHDLIYRDI	KPDNFI	IGRPGQPDANNIHL	IDFGMAKQ	217
YCK2	180	ITLIEDLHAHDLIYRDI	KPDNFI	IGRPGQPDANKVHL	IDFGMAKQ	224
CK1g3	147	ISRMETVYVHSKNLIYR	QVKPENFI	IGRPGNKTOQVTHI	IDFGLAKE	191
		230	240	250	260	
YCK1	218	YRDPKTKQHI	PYREKKSLSGTARYMS	INTHLGREQSR	RDDMEALG	262
YCK2	225	YRDPKTKQHI	PYREKKSLSGTARYMS	INTHLGREQSR	RDDMEAMG	269
CK1g3	192	YIDRET	KKHPIPYREHKSLTGTARYMS	INTHLGKEQSR	RDDLEALG	236
		280	290	300	310	
YCK1	263	HVFFYFLRGHLPWQGL	KAPNNKQKYEKIGEK	KRSTNVYDL	AQGLP	307
YCK2	270	HVFFYFLRGQLPWQGL	KAPNNKQKYEKIGEK	KRLTNVYDL	AQGLP	314
CK1g3	237	HMEMYFLBGS	LPWQGLKAOTLKERYQK	IGDTKRATPIEVL	CENFP	281
		320	330	340	350	
YCK1	308	VQFGRYLEIVRSL	SFEPCPDYEGYRKLLSVL	DDLGETADGOYDW		352
YCK2	315	IQFGRYLEIVRNL	SFEETPDYEGYRMLLSVL	DDLGETADGOYDW		359
CK1g3	282	-EMATYLRV	VRRLEDFEKPDYDYL	RKLF	TDLFD	DRKGYMFDYEYDW 325
		370	380	390	400	
YCK1	353	MKLNDRGWDLN	INKKPNLHGYGHPNPPNEK	SRKHRNKQL	QMQL	397
YCK2	360	MKLNDRGWDLN	INKKPNLHGYGHPNPPNEK	SKRHRNKKNHQYSSP		404
CK1g3	326	IGKQLPTPVGAVQDP	-ALSSNREAH	PHRCKQSKN		360
		410	430	440		
YCK1	398	QMQLQQQQQQQY	AQKTEADM	RNSQYKPKLDPTSYEAYOHQTQQ		442
YCK2	405	DHHHHYNQQQQQQQ	AQAQAQAQAQAKVQ	- - -	QQQLQAQAQQGAN	446
CK1g3	361	-----			QVVSSTNGELNTDD	374
		460	470	480	490	
YCK1	443	KYLOEQQKROQQQK	LEEQQL	LEEQQLQQQQQQQL	RATGPPSOP	487
YCK2	447	RYQLQPDSSH	YDEEREASKLDPTS	SYEAYQQQTQ	QKYAQQQOKOMQ	491
CK1g3	375	PTAGRSNAPITAPTE	VEVMDETNCQKVL	NMWCCCF	KRRKRKTID	419
		500	510	520	530	
YCK1	488	QAQTQSQQFGARY	QPQQQPSAAL	RTPEQHPNDDN	SS - - -	LAASH 528
YCK2	492	QKSKQFANTGANG	QTNKYRYNAQPT	ANDEQNAKNA	AQDRNSNKSS	536
CK1g3	420	RHK - - - - -				422
		529	537			
YCK1	529	KGFFOKL	GCC			538
YCK2	537	KGFFSKL	GCC			546
CK1g3		-----				

IP: GFP-YCK1

GLU

GAL

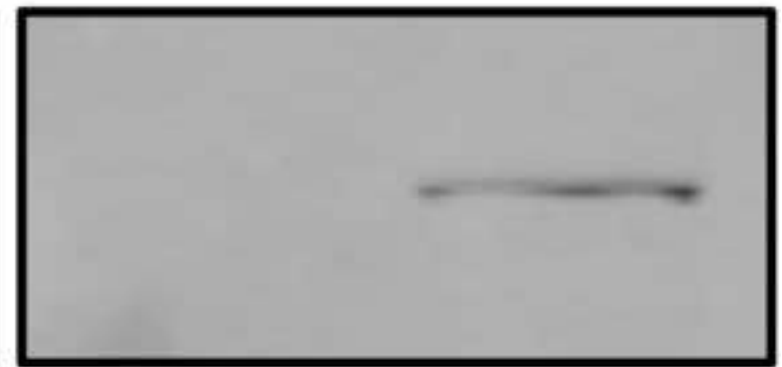
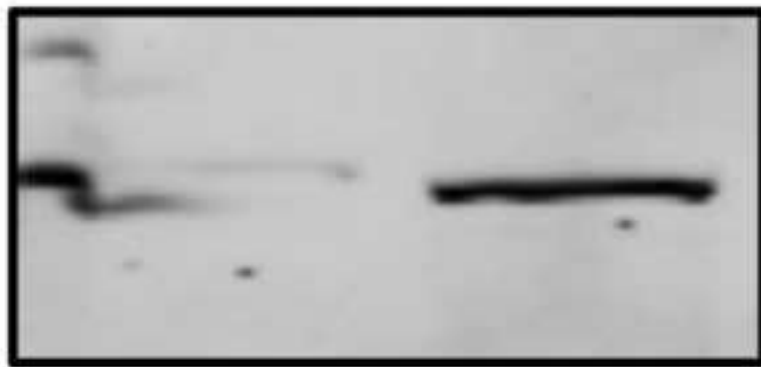
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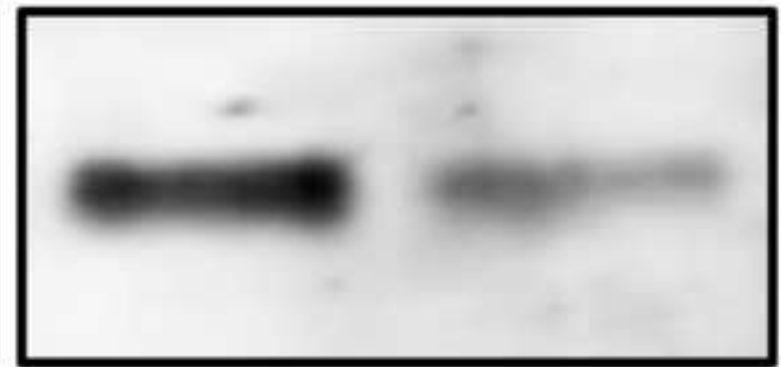
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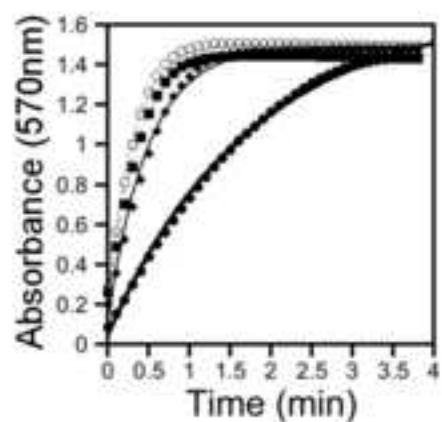
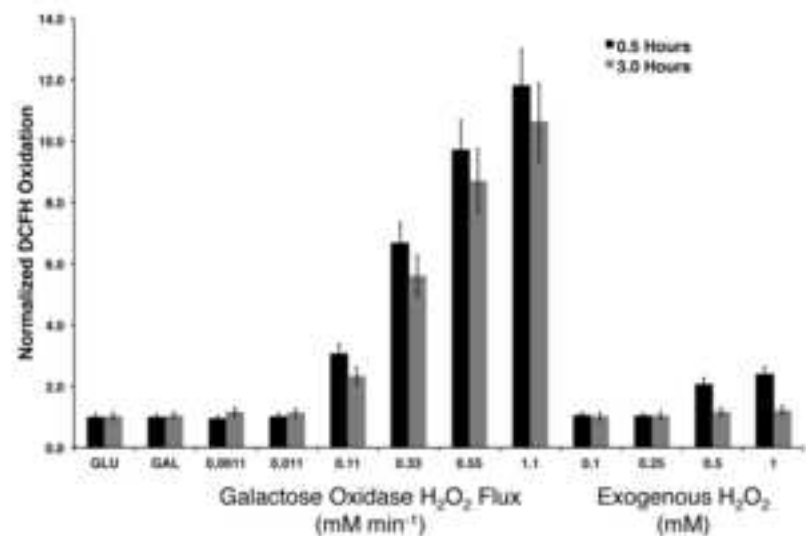
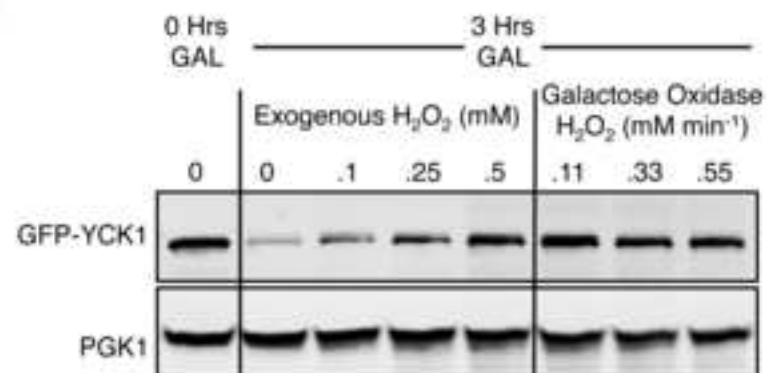
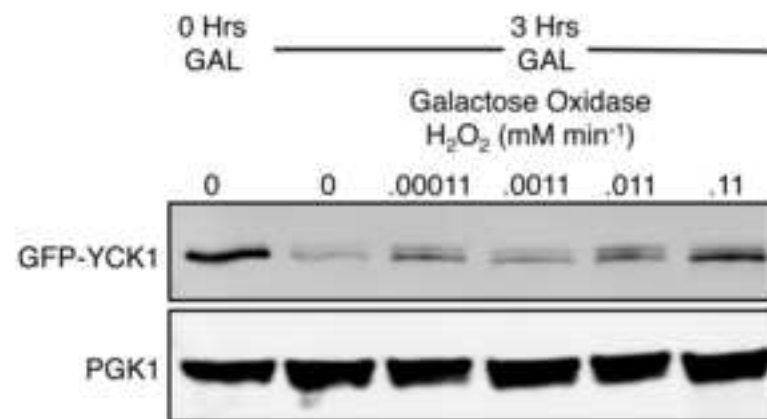
IP

α -GFP



α -SOD1



A**B****C****D****E**