Supplementary Tables

Supplementary Table 1

All Y2H activators described in this study. The original Y2H study from which they were extracted (Uetz = [24] or Ito = [23]) and the measured activation strengths are given. LTH is the minimal concentration of 3-AT (in mM) that is required to suppress activator activity and thus a direct measure of activation strength. bGAL is the beta-Galactosidase activity measured as described in Materials and Methods, including the Standard Error Mean (SEM) resulting from 3 measurements. Proteins annotated to have the F-GO term "transcriptional activator activity" in the YPD database (Biobase) are indicated (YPD).

ORF	name	source	LTH (3-AT)	bGAL (+/- SEM)	YPD
YAL014C	YAL014C	Ito	>200	0.8685+/-0.0990	
YAL040C	CLN3	Ito	50	-0.029+/-0.0399	
YAR003W	YAR003W	Ito	100	0.1138+/-0.1060	
YAR014C	YAR014C	Ito & Uetz	50	NA	
YAR042W	SWH1	Ito	25	-0.073+/-0.0191	
YAR062W	YAR062W	Ito	50	0.2152+/-0.0601	
YAR074C		Ito	NA	NA	
YBL005W-A		Ito	NA	NA	
YBL007C	SLA1	Ito	>200	0.8809+/-0.0605	
YBL010C	YBL010C	Ito	100	NA	
YBL025W	RRN10	Ito	NA	NA	
YBL032W		Uetz	NA	NA	
YBL046W	YBL046W	Ito	10	NA	
YBL049W	YBL049W	Ito	NA	NA	
YBL051C	YBL051C	Ito	100	0.4275+/-0.1067	
YBL056W	PTC3	Ito	3	NA	
YBL074C	AAR2	Ito	NA	NA	
YBL079W	NUP170	Ito	100	0.2055+/-0.0769	
YBL081W	YBL081W	Ito	>200	0.8972+/-0.0431	
YBL093C	ROX3	Ito	>200	0.5879+/-0.0490	y
YBL097W	BRN1	Ito	10	NA	
YBR012C	YBR012C	Ito	NA	NA	
YBR028C		Uetz	10	NA	
YBR030W	YBR030W	Ito	100	0.5805+/-0.1252	
YBR045C	GIP1	Ito	NA	NA	
YBR050C	REG2	Ito & Uetz	NA	NA	
YBR057C	MUM2	Ito	NA	NA	
YBR058C	UBP14	Ito	50	0.6862+/-0.0742	
YBR061C	YBR061C	Ito	200	NA	
YBR062C	YBR062C	Ito	NA	NA	
YBR072W	HSP26	Ito	50	0.6162+/-0.1196	

YBR098W	YBR098W	Ito	100	0.0312+/-0.0478	y
YBR105C	VID24	Ito	NA	NA	
YBR125C		Uetz	3	NA	
YBR138C	YBR138C	Ito	100	0.5158+/-0.0970	
YBR156C		Uetz	NA	NA	
YBR193C	MED8	Ito	>200	0.8372+/-0.1316	y
YBR211C		Uetz	NA	NA	
YBR212W	NGR1	Ito	100	NA	
YBR239C		Uetz	3	NA	
YBR240C	THI2	Ito	50	NA	
YBR250W		Uetz	3	NA	
YBR271W	YBR271W	Ito	200	0.7195+/-0.1125	
YBR284W	YBR284W	Ito	50	-0.000+/-0.0249	
YBR289W	SNF5	Ito	100	NA	y
YCL012W		Ito	NA	NA	
YCL017C	NFS1	Ito	50	-0.137+/-0.0089	
YCL032W		Uetz	3	NA	
YCL043C		Uetz	NA	NA	
YCR065W	HCM1	Ito	100	0.1958+/-0.0279	y
YCR077C	PAT1	Ito	>200	0.5859+/-0.0760	
YCR082W	YCR082W	Ito	200	0.5496+/-0.0552	
YDL005C	MED2	Ito	NA	NA	
YDL017W	CDC7	Ito	100	0.2612+/-0.0748	
YDL020C	RPN4	Ito	25	NA	y
YDL028C		Uetz	3	NA	
YDL037C	YDL037c	Ito	NA	NA	
YDL065C	PEX19	Ito	200	0.1532+/-0.0317	
YDL081C	RPP1A	Ito	200	0.1932+/-0.0225	
YDL088C	ASM4	Ito	>200	0.0355+/-0.0473	
YDL106C	GRF10	Ito	NA	NA	
YDL115C	YDL115c	Ito	NA	NA	
YDL125C		Uetz	NA	NA	
YDL130W	RPP1B	Ito	100	0.1822+/-0.0318	
YDL134C	PPH21	Ito & Uetz	100	0.1252+/-0.0366	
YDL154W	MSH5	Ito	100	-0.080+/-0.0233	
YDL161W	YDL161w	Ito	>200	0.7565+/-0.1249	
YDL165W	CDC36	Ito	50	0.3929+/-0.1141	y
YDL188C	PPH22	Ito	25	-0.003+/-0.0198	
YDL215C	GDH2	Ito	3	NA	
YDL223C		Uetz	3	NA	
YDR016C	YDR016c	Ito	100	NA	
YDR022C	CIS1	Ito	100	0.0735+/-0.0341	
YDR031W	YDR031w	Ito	200	0.4646+/-0.0889	
YDR045C	YDR045C	Ito	10	0.0372+/-0.0526	
YDR073W	SNF11	Ito	100	0.3912+/-0.0466	y
YDR075W	YDR075W	Ito & Uetz	NA	NA	
YDR081C	PDC2	Ito	>200	0.0566+/-0.0424	
YDR082W	STN1	Ito	50	0.3036+/-0.0682	

YDR098C	YDR098C	Ito	3	0.0172+/-0.0266	
YDR103W	STE5	Ito	200	NA	
YDR111C		Uetz	3	NA	
YDR118W	APC4	Ito	>200	0.2609+/-0.0465	
YDR123C	YDR123C	Ito	NA	NA	y
YDR124W	YDR124W	Ito	NA	NA	
YDR132C		Uetz	10	NA	
YDR145W	YDR145W	Ito	NA	NA	y
YDR146C	SWI5	Ito	>200	0.5196+/-0.1306	y
YDR151C	YDR151C	Ito	NA	NA	
YDR162C	YDR162C	Ito	NA	NA	
YDR164C		Uetz	NA	NA	
YDR165W		Uetz	3	NA	
YDR167W	YDR167W	Ito	NA	NA	y
YDR183W	YDR183W	Ito	NA	NA	
YDR184C	ATC1	Ito	>200	0.5882+/-0.0313	
YDR189W		Uetz	3	NA	
YDR210W	YDR210W	Ito	100	NA	
YDR213W	YDR213W	Ito	>200	0.5049+/-0.1203	y
YDR216W	ADR1	Ito	>200	0.4752+/-0.2174	y
YDR221W	YDR221W	Ito	3	NA	
YDR223W	YDR223W	Ito	>200	0.5482+/-0.0435	
YDR253C	MET32	Ito	50	0.3632+/-0.0988	
YDR260C	YDR260C	Ito	200	-0.010+/-0.0371	
YDR273W	YDR273W	Ito	100	0.5725+/-0.0730	
YDR277C	MTH1	Ito	NA	NA	
YDR291W	YDR291W	Ito	>200	0.0675+/-0.0683	
YDR299W	BFR2	Ito	>200	0.5766+/-0.0529	
YDR308C	SRB7	Ito	25	0.0699+/-0.0375	
YDR318W	YDR318W	Ito	NA	NA	
YDR320C	YDR320C	Ito	>200	0.8629+/-0.0902	
YDR328C	SKP1	Ito	3	0.0399+/-0.0280	
YDR330W	YDR330W	Ito	200	0.2609+/-0.0773	
YDR373W		Uetz	3	NA	
YDR392W	SPT3	Ito	50	0.2372+/-0.1230	y
YDR423C	CAD1	Ito	100	0.0096+/-0.0185	y
YDR443C	SSN2	Ito	>200	0.7916+/-0.0357	
YDR448W	ADA2	Ito	NA	NA	y
YDR464W	SPP41	Ito	3	0.1369+/-0.0537	
YDR484W		Uetz	NA	NA	
YDR489W	YDR489W	Ito	>200	NA	
YDR518W		Uetz	NA	NA	
YDR520C	YDR520C	Ito	>200	0.8299+/-0.0179	
YDR527W	YDR527W	Ito	NA	NA	
YDR532C	YDR532C	Ito	100	0.2726+/-0.0802	
YEL053C	MAK10	Ito	3	NA	
YER008C	SEC3	Ito	50	0.0352+/-0.0300	
YER021W	RPN3	Ito	50	0.3698+/-0.2191	

YER027C	GAL83	Ito	100	0.0962+/-0.0576	
YER033C	YER033c	Ito	100	NA	
YER040W	GLN3	Ito	>200	NA	
YER045C	YER045c	Ito	>200	0.9192+/-0.0479	y
YER051W		Uetz	200	NA	
YER059W	PCL6	Ito	200	0.0992+/-0.1759	
YER089C		Uetz	3	NA	
YER096W	YER096w	Ito	100	0.4195+/-0.0440	
YER108C		Ito	NA	NA	
YER111C	SWI4	Ito	100	0.2982+/-0.1524	y
YER118C	YER118c	Ito	100	0.7692+/-0.0578	
YER122C		Uetz	3	NA	
YER125W	RSP5	Ito	>200	0.9515+/-0.0602	
YER130C	YER130c	Ito	10	NA	
YER149C	PEA2	Ito	25	NA	
YER151C	UBP3	Ito	>200	0.8425+/-0.0947	
YER167W	BCK2	Ito	>200	0.6002+/-0.2382	
YFL029C	CAK1	Ito	200	0.5335+/-0.0385	
YFL033C	RIM15	Ito	>200	0.4306+/-0.0764	
YFL049W	YFL049W	Ito	100	0.6852+/-0.1114	
YFR033C	QCR6	Ito	25	0.0139+/-0.0445	
YFR034C	PHO4	Ito	200	0.5952+/-0.0681	y
YFR043C	YFR043C	Ito	100	-0.101+/-0.0157	
YFR046C	YFR046C	Ito	NA	NA	
YGL003C	CDH1	Ito	100	NA	
YGL015C	YGL015C	Ito	100	0.0675+/-0.0458	
YGL019W	CKB1	Ito	50	0.2105+/-0.1388	
YGL036W	YGL036W	Ito	>200	0.5912+/-0.1001	
YGL043W	DST1	Ito	100	0.1785+/-0.1442	
YGL066W	YGL066W	Ito & Uetz	50 (3 Uetz)	0.7785+/-0.1077	
YGL070C	RPB9	Ito	100	0.0272+/-0.0506	
YGL073W	HSF1	Ito	>200	NA	
YGL079W	YGL079W	Ito	200	0.2138+/-0.0565	
YGL127C	SOH1	Ito	50	0.0412+/-0.0288	
YGL134W	PCL10	Ito	25	-0.054+/-0.0140	
YGL151W	YGL151W	Ito	NA	NA	
YGL154C	LYS5	Ito	10	0.3445+/-0.1086	
YGL161C		Uetz	NA	NA	
YGL166W	CUP2	Ito	>200	0.8069+/-0.1406	y
YGL170C	YGL170C	Ito	100	0.2252+/-0.1502	
YGL172W	NUP49	Ito	100	0.5799+/-0.0877	
YGL175C	SAE2	Ito	NA	NA	
YGL181W		Uetz	3	NA	y
YGL223C	YGL223C	Ito	200	NA	
YGL227W	YGL227W	Ito	NA	NA	
YGL229C	SAP4	Ito	100	NA	
YGR052W		Uetz	3	NA	
YGR070W		Uetz	NA	NA	

YGR077C	PEX8	Ito	25	0.0188+/-0.0190	
YGR120C	YGR120C	Ito	>200	NA	
YGR130C	YGR130C	Ito	>200	0.4559+/-0.0909	
YGR160W		Uetz	25	NA	
YGR163W	YGR163W	Ito	NA	NA	
YGR188C		Uetz	3	NA	
YGR241C	YAP1802	Ito	>200	0.2015+/-0.0863	
YGR251W	YGR251W	Ito	50	NA	
YGR253C	PUP2	Ito	200	0.1598+/-0.0615	
YGR256W		Uetz	3	NA	
YGR269W	YGR269W	Ito	25	NA	
YGR274C	YGR274C	Ito	NA	NA	y
YGR288W	YGR288W	Ito	25	NA	y
YHL009C	YAP3	Ito	NA	NA	
YHL012W	YHL012W	Ito	200	NA	
YHL018W	YHL018W	Ito	3	NA	
YHR030C	SLT2	Ito	100	0.5042+/-0.0686	
YHR056C	YHR056C	Ito	25	NA	
YHR086W	NAM8	Ito	3	NA	
YHR124W	NDT80	Ito	3	0.0272+/-0.0281	
YHR135C		Uetz	3	NA	
YHR149C	YHR149C	Ito	10	NA	
YHR160C	YHR160C	Ito	>200	1.0002+/-0.0941	
YHR167W		Uetz	3	NA	
YHR170W	NMD3	Ito	3	NA	
YHR183W		Uetz	10	NA	
YHR184W	SSP1	Ito	25	NA	
YHR185C	YHR185C	Ito	25	NA	
YHR187W	IKI1	Ito	200	0.8495+/-0.0858	
YHR205W	SCH9	Ito	200	0.1552+/-0.0475	
YIL007C		Uetz	50	NA	
YIL019W	YIL019W	Ito	200	0.2692+/-0.0706	
YIL021W	RPB3	Ito	>200	0.6482+/-0.0357	
YIL034C	CAP2	Ito	100	0.2682+/-0.0399	
YIL036W	YIL036W	Ito	100	0.2162+/-0.0778	y
YIL046W		Uetz	NA	NA	
YIL062C	ARC15	Ito	100	-0.047+/-0.0183	
YIL071W		Ito	NA	NA	
YIL079C	YIL079C	Ito	>200	0.9892+/-0.0207	
YIL093C	YIL093C	Ito	3	-0.042+/-0.0378	
YIL119C	RPI1	Ito	>200	0.9349+/-0.0426	y
YIL123W	SIM1	Ito	3	NA	
YIL135C	YIL135C	Ito	3	NA	
YIL151C	YIL151C	Ito	NA	NA	
YIR010W	YIR010W	Ito	100	0.0122+/-0.0233	
YIR025W	YIR025W	Ito	3	-0.092+/-0.0238	
YJL029C	YJL029C	Ito	>200	NA	
YJL058C	YJL058C	Ito	50	0.0046+/-0.0229	

YJL069C	YJL069C	Ito	100	-0.019+/-0.0421	
YJL070C	YJL070C	Ito	NA	NA	
YJL084C	YJL084C	Ito	50	NA	
YJL098W	YJL098W	Ito	10	NA	
YJL100W		Uetz	100	NA	
YJL103C	YJL103C	Ito	50	-0.056+/-0.0198	
YJL106W	IME2	Ito	10	NA	
YJL116C	NCA3	Ito	200	0.6629+/-0.1065	
YJL126W		Uetz	3	NA	
YJL127C	SPT10	Ito	25	-0.076+/-0.0166	y
YJL146W	IDS2	Ito	>200	0.2022+/-0.1395	
YJL147C	YJL147C	Ito	3	NA	
YJL159W	HSP150	Ito	NA	NA	
YJL176C	SWI3	Ito	200	0.0189+/-0.0175	
YJL181W	YJL181W	Ito	>200	0.1689+/-0.0668	
YJL185C	YJL185C	Ito	50	0.0228+/-0.0163	
YJL187C	SWE1	Ito	25	0.0969+/-0.0519	
YJL204C		Uetz	3	NA	
YJL218W	YJL218W	Ito	100	NA	
YJR002W	MPP10	Ito	25	-0.006+/-0.0353	
YJR042W	YJR042W	Ito	NA	NA	
YJR056C		Uetz	3	NA	
YJR063W	RPA12	Ito	200	-0.011+/-0.0032	
YJR067C	YAE1	Ito	3	NA	
YJR070C	YJR070C	Ito & Uetz	200 (3 Uetz)	NA	
YJR082C	YJR082C	Ito	3	0.0038+/-0.0197	
YJR093C	FIP1	Ito	100	-0.134+/-0.0214	
YJR094C	IME1	Ito	200	NA	
YJR112W	NNF1	Ito	10	NA	
YJR119C	YJR119C	Ito	200	0.2019+/-0.1009	
YJR125C	YJR125C	Ito	3	NA	
YJR141W		Uetz	10	NA	
YKL002W	YKL002W	Ito	100	NA	
YKL015W	PUT3	Ito	200	0.3072+/-0.0846	y
YKL025C	PAN3	Ito	100	0.2319+/-0.0485	
YKL028W	TFA1	Ito	100	0.3572+/-0.1658	
YKL038W	YKL038W	Ito	NA	NA	y
YKL048C		Uetz	10	NA	
YKL059C	YKL059C	Ito	200	0.1292+/-0.0985	
YKL061W	YKL061W	Ito	100	0.3545+/-0.1920	
YKL062W	MSN4	Ito	100	0.7522+/-0.0354	y
YKL068W	NUP100	Ito	200	0.3679+/-0.0517	
YKL093W	MBR1	Ito	200	-0.132+/-0.0142	
YKL109W	HAP4	Ito	200	0.6056+/-0.0597	y
YKL135C	APL2	Ito	>200	0.1112+/-0.0662	
YKL143W	LTV1	Ito	200	0.5272+/-0.0376	
YKL161C	YKL161C	Ito	3	0.0465+/-0.0765	
YKL165C	MCD4	Ito	>200	0.3156+/-0.0892	

YKL171W	YKL171W	Ito	200	NA	
YKL173W	SNU114	Ito	100	0.1232+/-0.0124	
YKL190W		Uetz	25	NA	
YKR017C	YKR017C	Ito	50	0.0619+/-0.0165	
YKR021W	YKR021W	Ito	50	0.3116+/-0.0905	
YKR022C		Uetz	100	NA	
YKR027W	YKR027W	Ito	50	0.2616+/-0.0432	
YKR048C	NAP1	Ito	200	0.6022+/-0.0544	
YKR060W	YKR060W	Ito	>200	NA	
YKR064W	YKR064W	Ito	200	-0.024+/-0.0423	
YKR077W	YKR077W	Ito	>200	0.9899+/-0.0390	
YLL013C	YLL013C	Ito	>200	0.7076+/-0.0934	
YLR016C		Uetz	50	NA	
YLR019W	YLR019W	Ito	100	NA	
YLR024C	YLR024C	Ito	100	0.1615+/-0.0752	
YLR038C	COX12	Ito	3	NA	
YLR053C	YLR053C	Ito	3	NA	
YLR071C	RGR1	Ito	50	NA	y
YLR085C	ARP6	Ito	25	NA	
YLR095C	YLR095C	Ito	100	0.2445+/-0.0776	
YLR098C	CHA4	Ito	200	0.6499+/-0.0856	y
YLR102C	APC9	Ito	100	NA	
YLR113W	HOG1	Ito	100	0.1389+/-0.0362	
YLR119W	SRN2	Ito	3	NA	
YLR131C	ACE2	Ito	>200	NA	y
YLR135W	YLR135W	Ito	>200	0.7172+/-0.1206	
YLR144C	ACF2	Ito	>200	NA	
YLR154C	YLR154C	Ito	3	-0.099+/-0.0144	
YLR182W	SWI6	Ito	100	NA	y
YLR192C	YLR192C	Ito	>200	0.8849+/-0.0641	
YLR212C	TUB4	Ito	100	0.2939+/-0.0491	
YLR215C		Uetz	100	NA	
YLR226W		Uetz	NA	NA	
YLR228C	ECM22	Ito	>200	0.7762+/-0.1344	y
YLR273C	PIG1	Ito	100	NA	
YLR285W	YLR285W	Ito	>200	0.9469+/-0.0781	
YLR288C	MEC3	Ito	25	NA	
YLR300W	EXG1	Ito	25	NA	
YLR321C	SFH1	Ito	100	0.2722+/-0.0064	
YLR331C	YLR331C	Ito	100	1.0302+/-0.0364	
YLR371W		Uetz	3	NA	
YLR403W	SFP1	Ito	3	0.0022+/-0.0089	
YLR417W	VPS36	Ito	25	0.0082+/-0.0187	
YLR424W	YLR424W	Ito	100	-0.011+/-0.0300	
YLR435W	YLR435W	Ito	10	-0.028+/-0.0141	
YLR445W	YLR445W	Ito	200	0.1456+/-0.0112	
YLR451W	LEU3	Ito	100	0.3956+/-0.1238	y
YML037C	YML037C	Ito	200	0.0382+/-0.0207	

YML058W	SML1	Ito	3	NA	
YML068W	YML068W	Ito	3	-0.098+/-0.0059	
YML081W	YML081W	Ito	3	-0.061+/-0.0332	
YML091C	YML091C	Ito	NA	NA	
YML099C	ARG81	Ito	100	NA	y
YML128C	YML128C	Ito	100	0.3646+/-0.0531	
YMR004W	MVP1	Ito	>200	0.3639+/-0.0600	
YMR022W		Uetz	3	NA	
YMR030W	YMR030W	Ito	>200	0.0425+/-0.0698	y
YMR037C	MSN2	Ito	>200	1.1689+/-0.1381	y
YMR048W	YMR048W	Ito	>200	0.1739+/-0.0609	
YMR080C	NAM7	Ito	200	0.0282+/-0.0298	
YMR081C	ISF1	Ito	200	0.2389+/-0.0471	
YMR091C	NPL6	Ito	25	NA	
YMR112C	YMR112C	Ito	100	0.2012+/-0.0585	
YMR133W	REC114	Ito	200	-0.035+/-0.0319	
YMR179W	SPT21	Ito	>200	-0.009+/-0.0390	
YMR181C	YMR181C	Ito	>200	0.8592+/-0.0775	
YMR195W	YMR195W	Ito	>200	0.3746+/-0.0845	
YMR223W	UBP8	Ito	50	0.6462+/-0.1722	
YMR227C	YMR227C	Ito	NA	NA	
YMR236W	YMR236W	Ito	NA	NA	y
YMR270C	RRN9	Ito	100	NA	
YMR277W	FCP1	Ito	200	0.1342+/-0.0405	
YMR295C	YMR295C	Ito	>200	NA	
YMR297W	PRC1	Ito	25	NA	
YMR299C	YMR299C	Ito	200	0.0979+/-0.0148	
YMR323W	YMR323W	Ito	3	-0.014+/-0.0122	
YNL004W	HRB1	Ito	3	-0.062+/-0.0235	
YNL025C	SSN8	Ito	100	0.2122+/-0.0517	
YNL027W	CRZ1	Ito	>200	0.8595+/-0.0728	
YNL032W	SIW14	Ito	200	0.7252+/-0.1191	
YNL074C	YNL074C	Ito	NA	NA	
YNL075W		Uetz	25	NA	
YNL091W	YNL091W	Ito	50	-0.014+/-0.0416	
YNL092W	YNL092W	Ito	3	-0.045+/-0.0169	
YNL103W	MET4	Ito	>200	0.7636+/-0.0770	y
YNL127W	YNL127W	Ito	3	0.0485+/-0.0240	
YNL151C	RPC31	Ito	50	-0.026+/-0.0369	
YNL161W	CBK1	Ito	100	0.3809+/-0.1267	
YNL164C	YNL164C	Ito	3	0.0162+/-0.0497	
YNL192W	YNL192W	Ito	NA	NA	
YNL199C	GCR2	Ito	100	0.5216+/-0.0662	y
YNL204C	SPS18	Ito	100	0.0242+/-0.0378	
YNL223W	YNL223W	Ito	NA	NA	
YNL225C	CNM67	Ito	100	0.1709+/-0.0875	
YNL236W	SIN4	Ito	>200	0.1229+/-0.0694	
YNL245C		Uetz	NA	NA	

YNL308C		Uetz	3	NA	
YNL309W	STB1	Ito	100	NA	y
YNL314W	DAL82	Ito	100	-0.047+/-0.0655	y
YNL330C	RPD3	Ito	10	NA	
YNR003C	RPC34	Ito	3	NA	
YNR004W	YNR004W	Ito	10	0.0165+/-0.0629	
YNR010W	CSE2	Ito	200	0.3445+/-0.0819	
YNR017W	MAS6	Ito	200	0.5209+/-0.1233	
YNR023W	SNF12	Ito	NA	NA	
YNR032W	PPG1	Ito	200	NA	
YNR063W	YNR063W	Ito	100	0.0312+/-0.0368	
YNR069C	YNR069C	Ito	>200	0.9416+/-0.3435	
YOL044W		Uetz	3	NA	
YOL051W	GAL11	Ito	200	0.9772+/-0.0244	y
YOL067C	RTG1	Ito	>200	0.5925+/-0.0651	y
YOL082W	YOL082W	Ito	NA	NA	
YOL083W	YOL083W	Ito	NA	NA	
YOL108C	INO4	Ito	100	NA	y
YOL112W	MSB4	Ito	200	0.4759+/-0.1309	
YOL135C	MED7	Ito	50	0.0815+/-0.0151	
YOL136C	PFK27	Ito	200	0.3526+/-0.0579	
YOL148C	SPT20	Ito	100	0.4402+/-0.1069	y
YOR032C	HMS1	Ito	NA	NA	
YOR066W	YOR066W	Ito	>200	0.5309+/-0.1226	
YOR069W		Uetz	NA	NA	
YOR070C	GYP1	Ito	>200	-0.070+/-0.0176	
YOR113W		Uetz	NA	NA	y
YOR128C	ADE2	Ito	NA	NA	
YOR151C	YOR151C	Ito & Uetz	NA	NA	
YOR162C	YRR1	Ito	100	0.0812+/-0.0411	y
YOR166C	YOR166C	Ito	200	0.0519+/-0.0395	
YOR174W	MED4	Ito	>200	0.1035+/-0.0747	
YOR177C		Uetz	3	NA	
YOR178C	GAC1	Ito	>200	0.5292+/-0.0982	
YOR194C	TOA1	Ito	>200	NA	
YOR197W	YOR197W	Ito	100	0.1565+/-0.0919	
YOR212W	STE4	Ito	NA	NA	
YOR262W	YOR262W	Ito	200	0.5596+/-0.0335	
YOR281C	YOR281C	Ito	100	NA	
YOR290C	SNF2	Ito	200	0.7139+/-0.1587	
YOR299W	BUD7	Ito	50	0.1079+/-0.0420	
YOR329C	SCD5	Ito	>200	0.2706+/-0.0516	
YOR339C		Uetz	NA	NA	
YOR344C	TYE7	Ito	100	0.3559+/-0.1249	y
YOR352W	YOR352W	Ito	100	0.2375+/-0.0558	
YOR355W	GDS1	Ito	100	0.2076+/-0.0304	
YOR370C	MRS6	Ito	>200	0.5295+/-0.1343	
YOR382W	YOR382W	Ito	3	-0.023+/-0.0297	

YPL011C	YPL011C	Ito	NA	NA	
YPL014W	YPL014W	Ito	3	0.0819+/-0.0381	
YPL026C	SKS1	Ito	50	-0.025+/-0.0102	
YPL038W	MET31	Ito	50	0.0242+/-0.0316	
YPL042C	SSN3	Ito	NA	NA	
YPL054W	LEE1	Ito	50	-0.041+/-0.0251	
YPL055C	YPL055C	Ito	3	-0.047+/-0.0301	
YPL075W	GCR1	Ito	50	0.0769+/-0.0356	y
YPL089C	RLM1	Ito	200	NA	
YPL105C	YPL105C	Ito	200	0.0619+/-0.0482	
YPL124W	YPL124W	Ito	NA	NA	
YPL174C	NIP100	Ito	100	-0.056+/-0.0151	
YPL184C	YPL184C	Ito	100	0.5069+/-0.1525	
YPL202C	YPL202C	Ito	NA	NA	y
YPL229W	YPL229W	Ito & Uetz	200	0.0929+/-0.0316	
YPL233W	YPL233W	Ito	200	NA	
YPL250C	YPL250C	Ito	>200	0.5319+/-0.1199	
YPL254W	HFI1	Ito	100	0.2372+/-0.1030	y
YPL256C	CLN2	Ito	NA	NA	
YPL278C	YPL278C	Ito	100	0.3419+/-0.0477	
YPR007C	YPR007C	Ito	3	-0.013+/-0.0290	
YPR008W	YPR008W	Ito	>200	0.8622+/-0.1090	
YPR040W		Uetz	3	NA	
YPR046W	MCM16	Ito	50	0.0815+/-0.0187	
YPR066W	YPR066W	Ito	NA	NA	
YPR070W	YPR070W	Ito	NA	NA	
YPR076W	YPR076W	Ito	100	0.4306+/-0.0696	
YPR103W	PRE2	Ito	100	0.0619+/-0.0151	
YPR105C		Uetz	3	NA	
YPR119W		Uetz	3	NA	
YPR144C	YPR144C	Ito & Uetz	50	NA	
YPR168W	NUT2	Ito	100	0.0442+/-0.0305	
YPR179C	YPR179C	Ito	>200	0.8885+/-0.0251	
YPR180W	AOS1	Ito	>200	-0.048+/-0.1139	
YPR187W	RPO26	Ito	100	0.0695+/-0.0532	
YPR192W	YPR192W	Ito	NA	NA	

Supplementary Table 2

Influence of „specific“ physicochemical properties onto activation properties. The mean difference of several „specific“ physicochemical properties in the nuclear sets of activators and non-activators evaluated. The table shows the analyzed properties, together with their raw p-value of a Student’s t-test and the p-values after correction for multiple testing (Bonferroni correction and Holm’s correction). Significance after Holm’s correction at a level of $p<0.05$ is indicated. Significant groups are labelled yellow.

		raw p-value	Bonferroni correction	Holm's correction
Over-/underrepresentation of amino-acid groups indicated by one letter code (calculated using SAPS programm)	KR	6.98E-04	3.28E-02	2.65E-02
	O	6.09E-01	1.00E+00	1.00E+00
	KR_ED	1.12E-05	5.27E-04	4.71E-04
	LVIFM	1.37E-01	1.00E+00	1.00E+00
	ST	8.32E-02	1.00E+00	1.00E+00
	AGP	5.70E-01	1.00E+00	1.00E+00
	FIKMNY	5.14E-01	1.00E+00	1.00E+00
	ED	9.17E-02	1.00E+00	1.00E+00
	KRED	6.09E-01	1.00E+00	1.00E+00
segments or clusters of physicochemical properties (charge, hydrophobicity) (calculated with SAPS program)	positive cluster	8.18E-02	1.00E+00	1.00E+00
	negative cluster	1.64E-02	7.73E-01	5.26E-01
	hydrophobic segment	2.63E-01	1.00E+00	1.00E+00
	transmembrane segment	6.40E-01	1.00E+00	1.00E+00
clusters of amino-acids indicated by one letter code (calculated with SAPS program)	AAClusterQ	2.03E-03	9.56E-02	7.52E-02
	AAClusterN	3.37E-01	1.00E+00	1.00E+00
	AAClusterH	6.06E-05	2.85E-03	2.36E-03
	AAClusterY	8.94E-01	1.00E+00	1.00E+00
	AAClusterP	2.36E-01	1.00E+00	1.00E+00
	AAClusterW	4.61E-01	1.00E+00	1.00E+00
	AAClusterF	3.19E-01	1.00E+00	1.00E+00
	AAClusterS	4.64E-03	2.18E-01	1.62E-01
	AAClusterT	8.33E-02	1.00E+00	1.00E+00
Over-/underrepresentation of specific amino-acids indicated by one letter code	L	7.77E-01	1.00E+00	1.00E+00
	A	3.02E-05	1.42E-03	1.21E-03
	G	4.60E-06	2.16E-04	2.02E-04
	S	5.74E-06	2.70E-04	2.47E-04
	V	5.06E-13	2.38E-11	2.38E-11
	K	9.55E-12	4.49E-10	4.39E-10
	E	2.95E-01	1.00E+00	1.00E+00
	T	6.45E-01	1.00E+00	1.00E+00
	D	4.43E-03	2.08E-01	1.59E-01
	I	1.31E-01	1.00E+00	1.00E+00
	R	7.70E-02	1.00E+00	1.00E+00
	P	7.51E-03	3.53E-01	2.48E-01
	N	2.46E-10	1.16E-08	1.11E-08
	R	4.46E-01	1.00E+00	1.00E+00
	Q	1.55E-05	7.29E-04	6.36E-04
	Y	3.28E-01	1.00E+00	1.00E+00
	H	9.15E-02	1.00E+00	1.00E+00
	M	6.56E-02	1.00E+00	1.00E+00
	C	6.55E-01	1.00E+00	1.00E+00
	W	7.06E-03	3.32E-01	2.40E-01

Supplementary Table 3

Functional groups among Y2H activators. GO terms in the set of Y2H activators were compared to the whole yeast genome using the program FuncAssociate [32]. GO terms are ranked according to the significance of their overrepresentation in this dataset.

See http://llama.med.harvard.edu/cgi/func/funcassociate for technical details.

Rank	position in the attribute list ranked by significance of association
N	number of genes in your query with this attribute;
X	number of genes overall with this attribute;
LOD	the natural log of the odds ratio; positive and negative values indicate over- and underrepresentation, respectively;
P	single hypothesis one-sided P-value of the association between attribute and query (based on Fisher's Exact Test);
P-adj	adjusted P-value: fraction (as a %) of 1000 null-hypothesis simulations having attributes with this single-hypothesis P value or smaller

Rank	N	X	LOD	P	P-adj	GO Attribute
1	92	319	0.816	5.7e-35	<0.001	0030528: transcription regulator activity
2	105	461	0.684	3.4e-30	<0.001	0006350: transcription
3	95	429	0.657	3.5e-26	<0.001	0006351: transcription, DNA-dependent
4	72	265	0.759	1.9e-25	<0.001	0006366: transcription from Pol II promoter
5	47	123	0.959	8.9e-24	<0.001	0003702: RNA polymerase II transcription factor activity
6	233	1940	0.430	1.9e-23	<0.001	0005634: nucleus
7	83	426	0.573	5.4e-19	<0.001	0050789: regulation of biological process/regulation
8	29	62	1.095	6e-18	<0.001	0016251: general RNA polymerase II transcription factor activity
9	87	516	0.494	9.3e-16	<0.001	0007049: cell cycle/cell-division cycle
10	60	283	0.602	1.4e-15	<0.001	0005654: nucleoplasm
11	70	376	0.536	5.8e-15	<0.001	0050791: regulation of physiological process
12	70	376	0.536	5.8e-15	<0.001	0019222: regulation of metabolism
13	91	588	0.449	4.2e-14	<0.001	0008283: cell proliferation
14	27	74	0.910	1.6e-13	<0.001	0016591: DNA-directed RNA polymerase II, holoenzyme
15	45	206	0.608	2.2e-12	<0.001	0000278: mitotic cell cycle
16	166	1492	0.314	6.6e-12	<0.001	0006139: nucleobase, nucleoside, nucleotide and nucleic acid

						metabolism
17	55	297	0.522	8.3e-12	<0.001	0006355: regulation of transcription, DNA-dependent
18	56	306	0.516	8.6e-12	<0.001	0045449: regulation of transcription
19	57	315	0.511	8.9e-12	<0.001	0019219: regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism
20	13	20	1.392	3.9e-11	<0.001	0016455: RNA polymerase II transcription mediator activity
21	38	172	0.609	8.8e-11	<0.001	0006357: regulation of transcription from Pol II promoter
22	228	2378	0.263	4.7e-10	<0.001	0009987: cellular process
23	18	47	0.937	7.7e-10	<0.001	0000082: G1/S transition of mitotic cell cycle
24	222	2312	0.259	9.4e-10	<0.001	0050875: cellular physiological process
25	13	24	1.206	9.7e-10	<0.001	0000119: mediator complex/TRAP complex
26	15	36	0.995	5.2e-09	<0.001	0016563: transcriptional activator activity/transcription activating factor
27	209	2201	0.241	1.6e-08	<0.001	0008151: cell growth and/or maintenance/cell physiology
28	16	44	0.900	1.7e-08	<0.001	0006367: transcription initiation from Pol II promoter
29	44	258	0.470	1.7e-08	<0.001	0000279: M phase/M-phase
30	27	124	0.594	7.1e-08	<0.001	0000074: regulation of cell cycle/cell cycle control
31	17	55	0.796	9.5e-08	<0.001	0003700: transcription factor activity
32	40	239	0.457	1.3e-07	<0.001	0000280: nuclear division
33	15	45	0.843	1.8e-07	<0.001	0045944: positive regulation of transcription from Pol II promoter
34	17	59	0.752	3e-07	<0.001	0009893: positive regulation of metabolism
35	12	30	0.964	3.2e-07	<0.001	0004722: protein serine/threonine phosphatase activity
36	16	53	0.781	3.3e-07	<0.001	0045893: positive regulation of transcription, DNA-dependent
37	15	48	0.802	4.6e-07	<0.001	0004721: phosphoprotein phosphatase activity/protein phosphatase activity
38	9	17	1.181	5.4e-07	<0.001	0000124: SAGA complex/Spt-Ada-Gcn5-acetyltransferase complex
39	16	55	0.758	5.7e-07	<0.001	0006352: transcription initiation
40	24	114	0.574	7.4e-07	<0.001	0005667: transcription factor complex
41	14	44	0.813	8.8e-07	<0.001	0003704: specific RNA polymerase II transcription factor activity
42	16	57	0.736	9.8e-07	<0.001	0045935: positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism
43	16	57	0.736	9.8e-07	<0.001	0045941: positive regulation of transcription

44	23	108	0.580	1e-06	<0.001	0006468: protein amino acid phosphorylation
45	8	14	1.248	1.1e-06	<0.001	0000114: G1-specific transcription in mitotic cell cycle
46	54	398	0.353	1.1e-06	<0.001	0006464: protein modification
47	31	181	0.465	2.2e-06	0.001	0006793: phosphorus metabolism
48	31	181	0.465	2.2e-06	0.001	0006796: phosphate metabolism
49	24	128	0.510	6.4e-06	0.007	0007126: meiosis
50	11	33	0.842	8.1e-06	0.007	0000086: G2/M transition of mitotic cell cycle
51	12	42	0.746	1.9e-05	0.011	0000075: cell cycle checkpoint
52	7	15	1.076	3e-05	0.023	0000079: regulation of cyclin dependent protein kinase activity/regulation of CDK activity
53	8	21	0.930	4.8e-05	0.031	0000080: G1 phase of mitotic cell cycle
54	25	153	0.437	4.9e-05	0.031	0030234: enzyme regulator activity/enzyme modulator
55	15	68	0.597	5.1e-05	0.032	0007059: chromosome segregation
56	24	145	0.444	5.6e-05	0.034	0016310: phosphorylation
57	30	202	0.389	5.7e-05	0.035	0003677: DNA binding
58	12	47	0.680	6.4e-05	0.037	0000123: histone acetyltransferase complex

Supplementary Table 4A

Proteins co-occurring in protein complexes with nuclear activators

Proteins significantly overrepresented in protein complexes with nuclear Y2H activators (N=181) are shown. The list is sorted by the percentage [%] of nuclear Y2H activators found to be in at least one protein complex with the respective ORF. For example, the large subunit of RNA polymerase II, YDL140C, was found in a complex with 17.7% of all nuclear Y2H activators. The percent [%] ratio is the previous percentage devided by the percentage of nuclear non-activators (in other words: the [%] ratio is the enrichment compared to nuclear non-activators). A significant co-occurrence was assessed using Fisher's exact test comparing the set of nuclear Y2H activators with nuclear non-activators (P). The P value was adjusted (P_{adj}) for multiple testing using Holm's procedure [37]. Only the top 20 significance list ranked by percentage is shown.

ORF	%	% ratio	Definition	Description	P	P_{adj}
YDL140C	17,7	3,8	RNA polymerase II core subunit	RNA polymerase II large subunit	4,95E-09	1,02E-05
YOL086C	17,7	2,9	alcohol dehydrogenase	Adh protein catalyzes activities for the production of certain carboxylate esters.	1,29E-06	2,63E-03
YGL112C	16,0	4,5	TATA-binding protein-associated-factor	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4	1,53E-09	3,17E-06
YBR081C	15,5	4,7	histone acetyltransferase SAGA complex member|transcription factor	Subunit of the SAGA transcriptional regulatory complex, involved in proper assembly of the complex; also present as a C-terminally truncated form in the SLIK/SALSA transcriptional regulatory complex	1,75E-09	3,61E-06
YML007W	14,4	8,0	jun-like transcription factor	bZip transcription factor required for oxidative stress tolerance and localized to the nucleus in response to the presence of oxidants.	2,52E-12	5,22E-09
YGR252W	14,4	6,5	histone acetyltransferase	functions in the Ada and SAGA (Spt/Ada) complexes to acetylate nucleosomal histones	4,63E-11	9,60E-08
YDR448W	13,8	6,1	transcription factor	transcription factor, member of ADA and SAGA, two transcriptional adaptor/HAT (histone acetyltransferase)complexes	3,36E-10	6,95E-07
YNL236W	13,8	5,7	RNA polymerase II holoenzyme/mediator subunit	involved in positive and negative regulation of transcription, possibly via changes in chromatin structure; regulation of YGP1 expression	8,88E-10	1,84E-06
YOR174W	13,8	3,4	RNA polymerase II holoenzyme/mediator subunit	Member of RNA Polymerase II transcriptional regulation mediator	1,72E-06	3,51E-03
YHR174W	10,5	3,9	enolase	Enolase II, catalyzes the first common step of glycolysis and gluconeogenesis; expression is induced in response to glucose	6,61E-06	1,35E-02
YHR147C	9,4	8,0		Mitochondrial ribosomal protein of the large subunit	2,11E-08	4,36E-05
YNL025C	9,4	4,0	C-type cyclin|associates with the Ssn3p cyclin-dependent kinase	Component of RNA polymerase II holoenzyme, involved in RNA pol II carboxy-terminal domain phosphorylation. Activity of the kinase (SSN3)/cyclin (SSN8) pair required, along with SSN6 & TUP1, for transcriptional repression of a-specific genes	1,84E-05	3,73E-02
YBR198C	8,8	4,3		Subunit (90 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification	1,53E-05	3,12E-02
YKL060C	8,8	4,3	aldolase	Fructose 1,6-bisphosphate adolase, required for glycolysis and gluconeogenesis	1,53E-05	3,12E-02

YGL025C	8,3	9,6		Probable transcription factor, polyglutamine domain protein	3,43E-08	7,09E-05
YBR253W	8,3	9,6	part of Srb/Mediator complex|transcription factor	involved in transcription as part of Srb/Mediator complex	3,43E-08	7,09E-05
YHR058C	8,3	9,6		RNA polymerase II transcriptional regulation mediator	3,43E-08	7,09E-05
YER022W	8,3	9,6	RNA polymerase II holoenzyme/mediator subunit	subunit of RNA polymerase II holoenzyme/mediator complex	3,43E-08	7,09E-05
YPL042C	8,3	8,8	cyclin (SSN8)-dependent serine/threonine protein kinase	Component of RNA polymerase II holoenzyme, involved in RNA pol II carboxy-terminal domain phosphorylation. Activity of the kinase (SSN3)/cyclin (SSN8) pair required, along with SSN6 & TUP1, for transcriptional repression of a-specific genes	6,89E-08	1,42E-04
YCR081W	8,3	8,8		activation mediator subcomplex of RNA polymerase I holoenzyme	6,89E-08	1,42E-04

Supplementary Table 4B

Binary interactions of Y2H activators

Proteins interacting with nuclear Y2H activators (N=181). Only the twenty highest significant proteins are shown. The list is sorted by the percentage [%] of nuclear Y2H activators found to interact with the respective ORF. For example, 5.5% of all nuclear Y2H activators interact with YDR167W, a subunit of TFIID and SAGA. The percent [%] ratio compares this percentage with the percentage for nuclear non activators (**NA** – the % ratio could not be calculated because no interaction with non activator set was found). A significant interaction was assessed using Fisher's exact test comparing the set of nuclear Y2H activators with nuclear non activators (P). When the P value was adjusted (P_{adj}) for multiple testing using Holm's procedure [37], none of these interaction were significant, most likely due to a limited interaction data set.

ORF	%	% ratio	Definition	Description	p
YDR167W	5,5	4,7	TFIID subunit	Subunit (145 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification	4,24E-04
YLR055C	3,9	9,9	probable member of histone acetyltransferase SAGA complex|transcription factor	Subunit of the SAGA transcriptional regulatory complex but not present in SAGA-like complex SLIK/SALSA, required for SAGA-mediated inhibition at some promoters	1,89E-04
YBR081C	3,9	9,9	histone acetyltransferase SAGA complex member|transcription factor	Subunit of the SAGA transcriptional regulatory complex, involved in proper assembly of the complex; also present as a C-terminally truncated form in the SLIK/SALSA transcriptional regulatory complex	1,89E-04
YGR252W	3,9	9,9	histone acetyltransferase	functions in the Ada and SAGA (Spt/Ada) complexes to acetylate nucleosomal histones	1,89E-04
YGL112C	3,9	8,2	TATA-binding protein-associated-factor	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4	3,67E-04
YBR198C	3,9	8,2		Subunit (90 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification	3,67E-04
YHR099W	3,9	6,2	ATM/Mec1/TOR1/TOR2-related|NuA4 complex component	TRA1 is the homolog of the human protein TRRAP which we have isolated as an essential cofactor of c-Myc.	1,11E-03
YDR176W	3,9	5,5		Involved in glucose repression of GAL4p-regulated transcription	1,76E-03
YOR174W	3,3	14,1	RNA polymerase II holoenzyme/mediator subunit	Member of RNA Polymerase II transcriptional regulation mediator	2,09E-04
YDR145W	3,3	7,0	TFIID subunit	Subunit (61/68 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, similar to histone H2A	1,66E-03
YPL254W	3,3	7,0	Ada/Gcn5 protein complex member|transcription factor	Adaptor protein required for structural integrity of the SAGA complex, a histone acetyltransferase-coactivator complex that is involved in global regulation of gene expression through acetylation and transcription functions	1,66E-03
YMR236W	3,3	7,0	TFIID subunit	Subunit (17 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, similar to histone H3	1,66E-03
YDR392W	3,3	6,0	histone acetyltransferase SAGA complex member|transcription factor	Subunit of the SAGA and SAGA-like transcriptional regulatory complexes,	2,76E-03

				interacts with Spt15p to activate transcription of some RNA polymerase II-dependent genes, also functions to inhibit trancription at some promoters	
YOL135C	2,8	17,6	RNA polymerase II holoenzyme/mediator subunit	Member of RNA Polymerase II transcriptional regulation mediator	4,81E-04
YPR040W	2,2	NA		SDF1 the first obserwed null phenotype was Sporulation DeFiciency	2,33E-04
YGL025C	2,2	28,2		Probable transcription factor, polyglutamine domain protein	1,05E-03
YBR270C	2,2	28,2			1,05E-03
YDL132W	2,2	14,1		Cullin, structural protein of SCF complexes (which also contain Skp1p, Cdc34p, and an F-box protein) involved in ubiquitination; SCF promotes the G1-S transition by targeting G1 cyclins and the Cln-CDK inhibitor Sic1p for degradation	2,84E-03
YIL021W	2,2	14,1	RNA polymerase II 45 kDa subunit	RNA polymerase II core subunit	2,84E-03
YDR054C	2,2	14,1	ubiquitin-conjugating enzyme	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F-box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation	2,84E-03
YDR308C	1,7	NA	RNA polymerase II holoenzyme/mediator subunit	Suppressor of RNA polymerase II, possible component of the holoenzyme	1,90E-03

Supplementary Table 5

Domains of Y2H activators. Domains over-represented in the Y2H activator set ranked by their significance are shown. The number of Y2H activators containing the domain (#) and enrichment of this domain in the set of Y2H activators compared to the whole genome are shown. The significance level indicates significant over-representation using Fisher's exact test only ($P<0.05$, *) or also after correction for multiple testing using Holm's procedure ($P<0.05$, **).

Domain	Description	#	enrich-ment	significance level
HLH	helix loop helix domain	6	6,64	**
ZnF_C2C2	C2C2 Zinc finger	4	8,85	**
GAL4	GAL4-like Zn(II)2Cys6 (or C6 zinc) binuclear cluster DNA-binding domain	16	2,53	*
RPOL9	RNA polymerase subunit 9	3	8,85	*
ZnF_C2H2	zinc finger	13	2,30	*
ZnF_C2HC	zinc finger	5	4,02	*
IBR	In Between Ring fingers	2	8,85	*
BRLZ	basic region leucin zipper	5	2,95	*
ArfGap	Putative GTP-ase activating proteins for the small GTPase, ARF	3	4,43	*
PP2C_SIG	Sigma factor PP2C-like phosphatases	3	4,43	*
STYKc	Protein kinase; unclassified specificity.	10	2,06	*
CNH	Domain found in NIK1-like kinases, mouse citron and yeast ROM1, ROM2	2	5,90	*
Cu_FIST	Copper-Fist	2	5,90	*
S_TK_X	Extension to Ser/Thr-type protein kinases	4	2,95	*
PP2Ac	Protein phosphatase 2A homologues, catalytic domain.	4	2,95	*