Supplemental Information

S.cerevisiae: S.pombe: D.rerio: H.sapiens: A.thaliana:	MSSQEYTTFI M 	DIPVTRAQUE TLILTKNQUL MKKEQUV MKKEHUL MKEDEUN :*	HCSYSFWSSL HCQFSSWYSL NCQFSVWYPL HCQFSAWYPF RCQIQNWYPR .**	YPKYVPKSIV FRKLTPKAKV FKKHTIKSL- FRGVTIKSV- FKSLTIKTK- : . *:	LKSLPKKFIQ IKPIPATVLK ILPIPQNVID ILPLPQNVKD FHKLPESFIN : :*	YLEQDGIKLP YLHEDSIYVE YLLDDGTLVV YLLDDGTLVV YLLDDGTLVV YLIDDSGPFL ** :*.	QEENSRSVYT QPMNTVEEV- SGSENNNSQT SGRDDPPTHS LPHSVTNEDA	70 60 56 56 56
S.cerevisiae: S.pombe: D.rerio: H.sapiens: A.thaliana:	EEIIRN-E QANNSDSD QP-DSDDE MPNRVHNFEE	DNDYSDWEDD DSEED EEDIQWT-DD AEEIQWS-DD EDDFQVPEEA :	EDTATEFVQE EESAPAYYPE ETTTTVT ENTATLT SDDEPLN	VEPLIDFPEL REA APEFPEF APEFPEF RPSFPEL	HQKLKDALNE IQLIEKAIKE NVKVQEAINV ATKVQEAINS EIEIRESIET :::	-LGAVAPKLN LGGAVVPKLN LGGCIFPKLN LGGSVFPKLN LGGTIIPKLN * : ****	WSAPRDATWI WSTPKDALWI WSAPRDANWI WSAPRDAYWI WSSPKDAAWI **:*:**	136 108 117 116 120
S.cerevisiae: S.pombe: D.rerio: H.sapiens: A.thaliana:	LPNNTMKENE TTTGSLKETT ALNSSLQOQS AMNSSLKEKT SPSQNLSETC	VNELYLLLNA AEEVLLLLKS LSEIFLLFKS LSDIFLLFKS FNEIALLFRS .:: **:.:	SNYIMHDLQR SDFVAHDLNH SDFITHDLTQ SDFITRDFTQ SDSLTHDLFN *: : :*:	AFKGCVDGDD AFDDCKDFDN PFLHCSDDSP PFIHCTDDSP AYDSCSDKVS : * *	IKGLK ADGSVPKDFS DPTIN DPCIE SRPES	FDLVLRQWCD FELVLKEWFP YELVLRKWSE YELVLRKWCE FYLALRKWYP : *.*::*	-MNPALEFRV -MHASTEFRC -LIPGGEFRC -LIPGAEFRC SLKPEMEFRC : ***	200 177 181 180 185
S.cerevisiae: S.pombe: D.rerio: H.sapiens: A.thaliana:	FVKNAHIVGA FVKSKRLIAF FVKENKLIAI FVKENKLIGI FVKSNELVGI ***:.	TQRDL-NYYD CQRDD-NYYE CQRDYTQHYQ SQRDYTQYYD CQREVTTFYP **: .*	YLDELSDTFK FLKENIDCYE HIGKQEASIS HISKQKEEIR VLLNEKDLLK : :	DLIDEIVHDV KLISDLLKK- TSILQFFRDN RCIQDFFKKH GLIEEFFDDK * ::	VLPKEPDKSF -LDTEPDPDF IQYQEPDEDF IQYKELDEDF IRFEESENY *;	VLDVYIPRPF VFDVYIHK VLDVYRDSS- VFDIYRDSR- TFDVYVTKE- .:*:*	NKIFIVDINP DRAWLIDINP GRVWLIDFNP GKVWLIDFNP RRVKLIDFNT : ::*:*	269 242 250 249 254
S.cerevisiae: S.pombe: D.rerio: H.sapiens: A.thaliana:	cdc12 FARKTDSTLF FYPRTDGTLF FGEVTDSTLF FGEVTDSTLF WCGSTLPTMY : * *::	3-1 E283K SWNEIAAIAP SWSELESMNS TWEELTSGKN TWEELISENN TWEELEKIHG :*.*:	PKNDVE ENM LTANQTQEET LNGDFSEVDA ECD	DYELRL KPEIRL ALPDGPAFRC QEQDSPAFRC ELELRI :*	VTRHNTGRFA IPKGSMPSTG TNSEVTVQ TNSEVTVQ VESRLS	SKEHSENHVP SAKYYTNRVP PSPCLSYRIP PSPYLSYRIP VLPGLKTAVP :*	A327 J QDLVEASLNP FDMIAASE-G RDFLDLTT-G KDFVDLST-G YDYLDVSA-G * : :	331 300 317 316 308
S.cerevisiae: S.pombe: D.rerio: H.sapiens: A.thaliana:	EAIRELTQKW ENLLEFAQKW EDAYKLIDFL EDAHKLIDFL SGWAQVLKIV	KELLSQQAKE QDLTNKSNE- KLKRGQQEEE KLKRNQQEDD EEEFQKDD :	ESSDSENET- EESNEEGEEP QSSDEVA	- 360 - 319 Q 348 - 336 - 333				

Figure S1. Alignment of Cdc123 orthologs.

Cdc123 orthologs from Saccharomyces cerevisiae, Schizosaccharomyces pombe, Danio rerio, Homo sapiens and Arabidopsis thaliana were aligned with Clustal Ω (clustal consensus is shown below the aligned sequences). Residues that are conserved in 5 or 4 species are highlighted in black and grey, respectively. The amino acid substitution (E283K) resulting from the *cdc123-1* mutant allele (*G847A*) as well as the last residue of the truncated version encoded by the *cdc123/J327* mutant allele are indicated.

Table S1. Yeast strains

name	relevant	genotype	back- ground	used in Figure
BY4741	MATa	$his3\Delta 1 \ leu2\Delta 0 \ ura3\Delta 0 \ met15\Delta 0$	S288c	1A, 1B, 2D, 3A
W4050	<i>MAT</i> a	cdc123-1-ha3-URA3	S288c	1A
W3702	<i>MAT</i> a	cdc123/_327-ha3-natMX4	S288c	1A, 2D
W3439	ΜΑΤα	cdc123-1-ha3-URA3 can1∆::MFA1pr-HIS3-MFAalpha1pr-LEU2	S288c	1B
W3129	ΜΑΤα	cdc123∆327-ha3-natMX4 can1∆::MFA1pr-HIS3-MFAalpha1pr-LEU2	S288c	1B, 2B
YTH3 (1)	<i>MAT</i> a	CDC33(-198,1)::kanMX4-tTA-tetO7	S288c	1B
BY4742	MATα	$his3\Delta 1 \ leu2\Delta 0 \ ura3\Delta 0 \ lys2\Delta 0 \ MET15$	S288c	1C
W13221	MATα	cdc123/1327-ha3-natMX4 MET15	S288c	1C
W13224	MATα	cdc123-1-ha3-URA3 MET15	S288c	1C
W10897	MATα	p180	S288c	1D, 1E
W10898	<i>MAT</i> a	<i>cdc123A327-ha3-natMX4</i> p180	S288c	1D, 1E
W10899	<i>MAT</i> a	$gcn2\Delta::kanMX6$ p180	S288c	1D, 1E
W10900	<i>MAT</i> a	<i>gcn2</i> Δ:: <i>kanMX6 cdc123</i> Δ327- <i>ha3-natMX4</i> p180	S288c	1D, 1E
W10901	MATα	$gcn3\Delta::kanMX4$ p180	S288c	1D, 1E
W10902	MATα	gcn3∆::kanMX4 cdc123∆327-ha3-natMX4 p180	S288c	1D, 1E
W10903	<i>MAT</i> a	pWS3396	S288c	1D, 1E
W10904	<i>MAT</i> a	cdc123-1-ha3-URA3 pWS3396	S288c	1D, 1E
W10905	<i>MAT</i> a	$gcn2\Delta::kanMX6$ pWS3396	S288c	1D, 1E
W10906	MATα	gcn2∆::kanMX6 cdc123-1-ha3-URA3 pWS3396	S288c	1D, 1E
BY4743	MATa/α	his $3\Delta 1$ /his $3\Delta 1$ leu $2\Delta 0$ /leu $2\Delta 0$ ura $3\Delta 0$ /ura $3\Delta 0$ MET15/met15 $\Delta 0$ LYS2/lys $2\Delta 0$	S288c	2A
W4467	MATa/α	GCD11/GCD11-myc13-kanMX6	S288c	2A
W5471	MATa/α	cdc123∆327-ha3-natMX4/cdc123∆327-ha3-natMX4 GCD11/GCD11-myc13-kanMX6	S288c	2A
W5472	MATa/α	CDC123-ha3-HIS3MX6/CDC123-ha3-HIS3MX6 GCD11/GCD11-myc13-kanMX6	S288c	2A
W4177	<i>MAT</i> a	GCD11-myc13-kanMX6	S288c	2B, 3A
K699	MATa	ade2-1 can1-100 his3-11 leu2-3,-112 trp1-1 ura3-2 ssd1	W303	2C, 2E, 5C, 5D

Table S1 (contin	iued). Y	east	strains
------------------	----------	------	---------

name	relevant	genotype	back- ground	used in Figure
W12768	<i>MAT</i> a	kanMX4-pGCD11-flag3-GCD11	W303	2C
W12770	<i>MAT</i> a	kanMX4-pGCD11-flag3-GCD11 cdc123 Δ 327-ha3-HIS3MX6	W303	2C
W4444	MATα	cdc123∆::kanMX4 ura3::pGALL-cdc123-1-ha3-URA3	W303	2E
W5294	<i>MAT</i> a	CDC123-myc13-kanMX6	S288c	3A
W4887	<i>MAT</i> a	GCD1-myc13-HIS3MX6	S288c	3A
W4884	ΜΑΤα	GCD11-ha3-HIS3MX6	S288c	3B
W5288	ΜΑΤα	CDC123-ha3-HIS3MX6	S288c	3B
W5290	ΜΑΤα	SUI2-ha3-HIS3MX6	S288c	3B
W276	ΜΑΤα	his3 trp1 ura3::lexAop-lacZ leu2::lexAop-LEU2	W303	4A
W12626	MATa/α	$GCD11/gcd11\Delta$::kanMX6	W303	4C, 5A
W12784	MATa/α	GCD11/gcd11Δ::kanMX6 his3/his3::pGCD11-flag3- GCD11-tCYC1-HIS3	W303	4C, 4D, 5A
W12786	MATa/α	GCD11/gcd11Δ::kanMX6 his3/his3::pGCD11-flag3- GCD11(aa1-523)-tCYC1-HIS3	W303	4C, 4D
W12788	MATa/α	GCD11/gcd11Δ::kanMX6 his3/his3::pGCD11-flag3- GCD11(aa1-519)-tCYC1-HIS3	W303	4C, 4D, 5A
W12790	MATa/α	GCD11/gcd11Δ::kanMX6 his3/his3::pGCD11-flag3- GCD11(aa1-514)-tCYC1-HIS3	W303	4C, 4D
W12833	MATa/α	GCD11/gcd11∆::kanMX6 his3/his3::pGCD11-flag3- GCD11(aa1-519)-tCYC1-HIS3 leu2/leu2::pTEF2-CDC123- tCYC1-LEU2	W303	5A, 5B
W12949	MATa/a	GCD11/gcd11A::kanMX6 leu2/leu2::pTEF2-CDC123- tCYC1-LEU2	W303	5A
W12950	MATa/a	GCD11/gcd11∆::kanMX6 his3/his3::pGCD11-flag3- GCD11-tCYC1-HIS3 leu2/leu2::pTEF2-CDC123-tCYC1- LEU2	W303	5A
W5539	<i>MAT</i> a	cdc123∆::kanMX4 ura3::pTEF2-SUI2-tCYC1-URA3	W303	5C, 5D
W5495	<i>MAT</i> a	$cdc123\Delta$:: $kanMX4$ leu2:: $pTEF2$ -GCD11-tCYC1-LEU2	W303	5C, 5D
W5540	ΜΑΤα	cdc123∆::kanMX4 ura3::pTEF2-SUI2-tCYC1-URA3 leu2::pTEF2-GCD11-tCYC1-LEU2	W303	5C, 5D
W5544	<i>MAT</i> a	cdc123∆::kanMX4 trp1::pTEF2-SUI3-tCYC1-TRP1 leu2::pTEF2-GCD11-tCYC1-LEU2	W303	5C, 5D
W5592	ΜΑΤα	cdc123∆::kanMX4 ura3::pTEF2-SUI2-tCYC1-URA3 trp1::pTEF2-SUI3-tCYC1-TRP1 leu2::pTEF2-GCD11-tCYC1-LEU2	W303	5C, 5D

Table S2. Plasmids

name	description	vector	insert	used in Figure
p180 (2)	pGCN4-lacZ, URA3, ARS/CEN			1D, 1E
pWS3396	pGCN4-lacZ, LEU2, ARS/CEN	pRS315 (SalI/PstI)	SalI/PstI fragment of p180	1D, 1E
pWS1389	prha-his6-CDC123	pJOE4056.2 (BamHI/HindIII)	<i>CDC123</i> (BamHI/HindIII)	3C
pWS1483	prha-mbp-GCD11	pJOE2955 (BamHI/HindIII)	GCD11 (BamHI/HindIII)	3C
pWS1957	prha-mbp-GCD11-RBS-his6-CDC123	pWS1483 (HindIII)	RBS-his6- CDC123 (HindIII)	3C
pEG202 (3)	pADH-lexA-MCS, HIS3, 2µ			4A
pJG4-5 (3)	pGAL-NLS-AD-HA-MCS, TRP1, 2µ			4A
pWS1463	pADH-lexA-CDC123	pEG202 (EcoRI/XhoI)	CDC123 (EcoRI/XhoI)	4A
pWS1513	pGAL-NLS-AD-HA-GCD11	pJG4-5 (EcoRI/XhoI)	<i>GCD11</i> (<i>bp1-1584</i>) (EcoRI/SalI)	4A
pWS1535	pADH-lexA-SUI3	pEG202 (EcoRI/XhoI)	<i>SUI3</i> (MunI/XhoI)	4A
pWS1537	pADH-lexA-SUI2	pEG202 (EcoRI/XhoI)	<i>SUI2</i> (EcoRI/XhoI)	4A
pWS3413	pGAL-NLS-AD-HA-GCD11(aa410- 527)	pJG4-5 (EcoRI/XhoI)	GCD11 (bp1228-1584) (EcoRI/SalI)	4A
pWS3473	pGAL-NLS-AD-HA-GCD11(aa1-514)	pJG4-5 (EcoRI/XhoI)	GCD11(bp1- 1542+Stop) (EcoRI/SalI)	4A
pWS3917	pADH-lexA-hD123	pEG202 (EcoRI/XhoI)	<i>hD123</i> (EcoRI/XhoI)	4A

Table S3. Antibodies

antibody	description	used for immunoprecipitation	used for Western blot
		in Figure	in Figure
anti-Cdc123	affinity-purified polyclonal rabbit antiserum (this study)	-	3A, 4C, 5A
anti-flag	M2, mouse monoclonal (Sigma-Aldrich)	2C, 4C, 5A (agarose conjugate)	2C, 4C, 5A
anti-Gcd11	polyclonal rabbit antiserum (4)	-	2D, 2E, 5D
anti-Gcd11	affinity-purified polyclonal rabbit antiserum (this study)	-	3A, 3C
anti-ha	12CA5, mouse monoclonal	-	3B, 4A
anti-his	Tetra-His antibody, mouse monoclonal (Qiagen)	-	3C
anti-myc	9E10, mouse monoclonal	2A, 3A	2A, 3A
anti-Sui2	polyclonal rabbit antiserum (5)	2D, 2E	1E, 2A, 2D, 2E, 3A, 5D
anti-Sui2	polyclonal rabbit antiserum (this study)	-	2C, 4C, 5A
anti-Sui2-P	anti-eIF2α[phoshoS52] polyclonal rabbit antibody (Invitrogen, 44728G)	-	1E
anti-Sui3	polyclonal rabbit antiserum (6)	2D, 2E	2A, 2D, 2E, 3A, 5D
anti-Sui3	polyclonal rabbit antiserum (this study)	-	2C, 4C, 5A

Supplemental References

- 1. von der Haar, T., and McCarthy, J. E. (2002) Intracellular translation initiation factor levels in Saccharomyces cerevisiae and their role in cap-complex function. *Mol Microbiol* **46**, 531-544
- 2. Hinnebusch, A. G. (1985) A hierarchy of trans-acting factors modulates translation of an activator of amino acid biosynthetic genes in Saccharomyces cerevisiae. *Mol Cell Biol* **5**, 2349-2360
- Ausubel, F. M., Brent, R., Kingston, R. E., Moore, D. D., Seidman, J. G., Smith, J. A., and Struhl, K. (2005) *Current Protocols in Molecular Biology* (Harkins, E. W., Ed.), John Wiley & Sons, Inc.
- 4. Hannig, E. M., Cigan, A. M., Freeman, B. A., and Kinzy, T. G. (1993) GCD11, a negative regulator of GCN4 expression, encodes the gamma subunit of eIF-2 in Saccharomyces cerevisiae. *Mol Cell Biol* **13**, 506-520
- 5. Cigan, A. M., Pabich, E. K., Feng, L., and Donahue, T. F. (1989) Yeast translation initiation suppressor sui2 encodes the alpha subunit of eukaryotic initiation factor 2 and shares sequence identity with the human alpha subunit. *Proc Natl Acad Sci U S A* **86**, 2784-2788
- 6. Hashimoto, N. N., Carnevalli, L. S., and Castilho, B. A. (2002) Translation initiation at non-AUG codons mediated by weakened association of eukaryotic initiation factor (eIF) 2 subunits. *Biochem J* **367**, 359-368