

Supplementary tables and figures

Supplementary Table 1: tRNA introns in human fungal pathogens.

Species	Number of isodecoders	Number of isodecoders with an intron in all genes #
<i>S. cerevisiae</i>	41	10
<i>C. albicans</i>	41	23
<i>C. auris</i>	40	10*
<i>A. fumigatus</i>	44	19
<i>H. capsulatum</i>	45	27
<i>P. jirovecii</i>	45	27
<i>C. neoformans</i>	41	39
<i>R. arrhizus</i>	41	2
<i>M. circinelloides</i>	43	2

Some additional isodecoders have an intron in some genes. For example, the *C. albicans* genome contains five genes for Lys tRNA with a UUU anticodon, but only one of those genes has an intron and thus this tRNA is not counted in the table and Figure 1C.

* In *C. auris*, the elongator Met tRNA genes have an intron (and are included in the count), while the initiator Met tRNA genes do not have an intron.

Supplementary Table 2: tRNA splicing machinery in pathogenic fungi

	<i>TRL1</i> orthologs	tRNA splicing endonuclease		2'-phospho Transferase	Alternative ligases	
	Trl1	Sen2	Sen34	Tpt1	RTCB	RLIG1
<i>S. cerevisiae</i>	Y	Y	Y	Y	N	N
<i>C. albicans</i>	Y	Y	Y	Y	N	N
<i>C. auris</i>	Y	Y	Y	Y	N	N
<i>A. fumigatus</i>	Y	Y	Y	Y	N	N
<i>H. capsulatum</i>	Y	Y	Y	Y	N	N
<i>P. jirovecii</i>	Y	Y	Y	Y	N	N
<i>C. neoformans</i>	Y	Y	Y	Y	N	N
<i>R. arrhizus</i>	Truncated (sealing-only)	Y	Y	Y	N	N
<i>M. circinelloides</i>	Truncated (sealing-only)	Y	Y	Y	N	N
<i>R. irregularis</i>	Y	Y	Y	Y	N	N

Y: Orthologs present, N: No ortholog present

Supplementary Table 3: Plasmids used

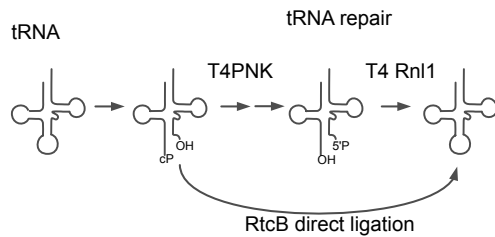
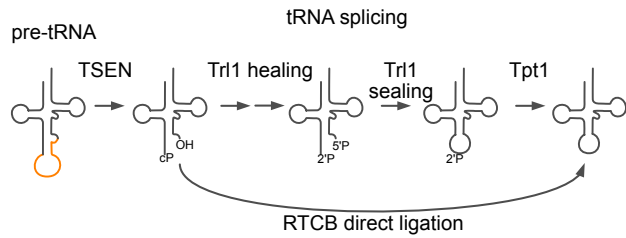
Plasmid	Plasmid description	Plasmid construction
p425GPD	Empty vector	(Mumberg et al. 1995)
pRS413	Empty vector	(Sikorski and Hieter 1989)
pAv1512	p425GPD-ScTRL1	<i>S. cerevisiae</i> <i>TRL1</i> gene amplified from genomic DNA and cloned in pRS425GPD.
pAv1655	p425GPD-CalbTRL1	<i>C. albicans</i> <i>TRL1</i> gene amplified from genomic DNA and cloned in pRS425GPD digested with Sall and XhoI.
pAv1656	p425GPD-CaurTRL1	<i>C. auris</i> <i>TRL1</i> gene amplified from genomic DNA and cloned in pRS425GPD digested with Sall and XhoI.
pAv1880	p425GPD-AfumTRL1	Codon-optimized <i>A. fumigatus</i> <i>TRL1</i> was amplified and Gibson assembled in pRS425GPD digested with BamHI and XhoI.
pAv1881	p425GPD-HcapTRL1	Codon-optimized <i>H. capsulatum</i> <i>TRL1</i> was amplified and Gibson assembled in pRS425GPD digested with BamHI and XhoI.
pAv1882	p425GPD-CneoTRL1	Codon-optimized <i>C. neoformans</i> <i>TRL1</i> was amplified and Gibson assembled in pRS425GPD digested with BamHI and XhoI.
pAv1883	p425GPD-RarrTRL1	Codon-optimized <i>R. arrhizus</i> <i>TRL1</i> was amplified and Gibson assembled in pRS425GPD digested with BamHI and XhoI.
pAv1884	p425GPD-McirTRL1	Codon-optimized <i>M. circinelloides</i> <i>TRL1</i> was amplified and Gibson assembled in pRS425GPD digested with BamHI and XhoI.
pAv1885	p425GPD-RirrTRL1	Codon-optimized <i>R. irregularis</i> <i>TRL1</i> was amplified and Gibson assembled in pRS425GPD digested with BamHI and XhoI.
pAv1909	p425GPD-PjirTRL1	Codon-optimized <i>P. jirovecii</i> <i>TRL1</i> was amplified and co-transformed into yeast with pRS425GPD digested with BamHI and XhoI.
pAv1630	pRS413- <i>trl1</i> -K114A	<i>S. cerevisiae</i> <i>trl1</i> -K114A was amplified with mutation-specific primers and Gibson assembled in pRS413 digested with Sall and SacI.
pAv1616	pRS413- <i>trl1</i> -K404AT405A	<i>S. cerevisiae</i> <i>trl1</i> -K404AT405A was amplified with mutation-specific primers and Gibson assembled in pRS413 digested with Sall and SacI.

pAv1614	pRS413- <i>trl1-H777A</i>	<i>S. cerevisiae trl1-H777A</i> was amplified with mutation-specific primers, and Gibson assembled in pRS413 digested with Sall and SacI.
pAv1886	p425GPD-Rarr <i>trl1-K116A</i>	<i>K116A</i> mutation was introduced in <i>R. arrhizus TRL1</i> using QuikChange Site-Directed Mutagenesis Kits (Agilent).
pAv1887	p425GPD-Mcir <i>trl1-K118A</i>	<i>K118A</i> mutation was introduced in <i>M. circinelloides TRL1</i> using QuikChange Site-Directed Mutagenesis Kits (Agilent).

Supplementary Table 4: Strains used

Strain	Genotype
BY4741	<i>matA, ura3-Δ0, leu2-Δ0, his3-Δ1, lys2-Δ0</i>
yAv4576	<i>matA, ura3-Δ0, leu2-Δ0, his3-Δ1, lys2-Δ0, trl1Δ::NEO, [TRL1, URA3]</i>
yAv4415	<i>matA, ura3-Δ0, leu2-Δ0, his3-Δ1, lys2-Δ0, ire1Δ::NEO, hac1Δ::NAT</i>
yAv4154	<i>matA, ura3-Δ0, leu2-Δ0, his3-Δ1, lys2-Δ0, ire1Δ::NEO</i>

Supplementary Figure 1: The tRNA splicing pathway is related to tRNA repair pathways in *E. coli* and its T4 phage. Top panel: the pre-tRNA splicing pathway from Figure 1A. Bottom panel: In bacteria and eukaryotes, tRNAs that have been cut by endonucleases are repaired. The *E. coli* pathway carried out by RtcB is very similar to the human pathway (carried out by RTCB). The T4 phage uses a heal and seal pathway, but the sealing activity of its polynucleotide kinase creates a 2' 3' OH instead of the 2'PO4 in yeast. The T4 Rnl1 ligase is active on this end, while yeast Trl1 requires a 2' PO4. Because of this difference in ligase, the T4 pathway doesn't require Tpt1.



Supplementary Figure 2: Multiple sequence alignment of Trl1 orthologs. The following orthologs were aligned using CLUSTAL O(1.2.4): *S. cerevisiae* (Scer; YJL087C), *C. albicans* (Calb; C7_02060W_A), *C. auris* (Caur; B9J08_004868), *A. fumigatus* (Afum; XP_752336.1), *H. capsulatum* (Hcap; XP_001544422.1), *P. jirovecii* (Pjir; XP_018228553.1), *C. neoformans* (Cneo; XP_012049418.1), *R. arrhizus* (Rarr; KAG0748437.1), *M. circinelloides* (Mcir; EPB83728.1), and *R. irregularis* (Rirr; PKK72613.1). The conserved peptide motifs (motif I, Ia, III, IV, V) in the ligase domain of Trl1 orthologs are indicated with blue boxes.

Scer	-----MP	2	Scer	AEFETWDMKDVSMQASKYGFRCVQCITNTLEDLKKFLDNCSATGSFEGQIEGFVIRCH	273
Calb	-----	0	Calb	ITFKTLPMDQVLQFAKEWGFYVSYLTDNAEDLFLFKHKGCESTGYNREIEGFVIRCH	283
Caur	-----ML--EPIP	6	Caur	IQFHSYPMKNVAVADYFGFKRVYEQYDSFTDLSWFLFEEKSRTGIFQGRIEGFVIRAK	276
Afum	-----	0	Afum	PQFATLPSSEVHNFADTWGFKKAKYLVYDDIHSVKFLDHCAETGTWDGRETGFVIRCO	277
Hcap	-----MD	2	Hcap	PEFATLPSLEVHNFADTWGFKKAKYLVYDDIHSVKFLDHCAETGTWDGRETGFVIRCO	275
Pjir	-----MPPPPP	7	Pjir	PAFSTAPFNVEVCSFGVEWGFQVDYIIFESLLELRNFIEDSEKSGSYHGREGVEGFVIRCK	276
Cneo	-----MNNINP	7	Cneo	PHFSTSSPSVAFAKFEFGIQTKYIQLESLSQVRSFADLAQSGTWEGEMIEGFVIRCT	423
Rarr	-----MVDGIDIP	7	Rarr	STLQTLPSAIVQVALAFGHHTSFETSSIEKVKYFADMQRSTGYLNRGIEGFVIRCK	275
Mcir	-----	6	Mcir	SELYLTPVSVVEQTAKEFGHATDFTVDTAEQVKFEGHVMQQTGYNREIEGFVIRCK	277
Rirr	MDLNLSTLFIIVVFIYRFRKTSISTKNNNDTRNVGDENASDEIKKSTKSDTSQDSIQID	60	Rirr	VDLKTWPKSLVTFNAKEWGFNPVYVQVDEVKSFIVNIEKRVLDREIEGFVIRCK	325
Scer	SP----YDGKRTVTLVNELEKAEKLSGRG--RAYRR-----VCDLS-----HSNKK	43	Scer	LKST-----EKPFEEKYKFEPEYLYRQWREVTKDYISNK-SRV---F---	312
Calb	-M----KDSQSDIELCNKLNEATLKRNG--KSIKL-----TNFVS-----NTQIK	40	Calb	RQSTNGDTD-----GDCFFPKYKFEQYLLYRQFREVTKQLLNGTPIINS---I---	319
Caur	V----FRDSEADLRDFVDLENSLIRKER-----STR---KQYKFPFTT---NGEAV	49	Caur	DKEDD-----DFFPKYKFEPEYLYRQWREVTKDYISNK-SRV---F---	312
Afum	-M----VQDDPQEVAVHLVGALEASSKKNRSEGRKTFCK---KSTFAVAG---SDNIS	47	Afum	LGEGG---VGP-----YRDWFFPKYKFEPEYLYRQWREVTKDYISNK-SRV---F---	316
Hcap	-M----VQDDGHEVTRLVHLSLEAASGKKKQLGKKTFSCK---KSTFPVSG---SD-IS	46	Hcap	LSGGG---VGP-----YRDWFFPKYKFEPEYLYRQWREVTKDYISNK-SRV---F---	316
Pjir	SR----KSEVPEAQELISRIEKAENDQNRNSKSVLKH-----TFTL---KNGTK	46	Pjir	SKNSDE-DTC-----FRDFFPKYKFEPEYLYRQWREVTKDYISNK-SRV---F---	318
Cneo	POPSTYASKHPSTPRLLNALRDL---HATDPKAI RTTVHRYPAALYAHGQDDHARDRF	63	Cneo	VKSGDGMQSGAPPYHANSFPFFPKYKFEPEYLYRQWREVTKDYISNK-SRV---F---	413
Rarr	AI----DLK--DQVHNIYVEK--YHEIK---ESSKDVRCR-----DFIL---EDEIK	45	Rarr	R--DG-----NDMFPKIK-NEQYLYRQWREVTKDYISNK-SRV---F---	315
Mcir	HF----TVD--QARVQHVIEQLYQVKL---DTPKELRSK-----DFVL---EDGQV	46	Mcir	R--NG-----MDMFPKIK-NEQYLYRQWREVTKDYISNK-SRV---F---	317
Rirr	PV----TQKDLTEADELISNLYKS-----KGGKVKRN-----EFVHK---SSGVT	98	Rirr	TVSTG-----QDFPKIKYDEPYLYRQWREVTKDYISNK-SRV---F---	360
Scer	VIWKFNEDWYKNTITLPCNARGLFISSD-TT-----NPPVIVAR	82	Scer	---KFRKHKFITNKYLDFAIPILESSPKICENYKLGFGVIELRNLFLQSYGMS-GLEILN	368
Calb	LDSWKFLEWDYKPSVQLPIQARGLFTLNN-----DTIAVR	76	Calb	---KIKKKNKPIITKYLQFVEKLFQEPPEIARNFENGFDIIRKVLQFLQSLNENGMNLLS	386
Caur	VDSWKFNEFAYGTDI-ELPSQARGLFTRDG-----KIAR	83	Caur	---EQRKHARIVQAYLDFVEKLFSEQPELAEQYLEKGIHKVRKMFLLKIDGLDQ--DGMG	375
Afum	VDSWRFDWDYK--RSNLPYARGLFTSKRRKDG-----TPEIIVR	85	Afum	---NIRKHKQITTEYLHARQRLSQNPKLGDLYQNHGII SMREGFLKERGLKGS-DIIA	372
Hcap	VDSWRFDWDYK--RDDLPYARGLFTSKRNEKN-----QVEIAIR	84	Hcap	---KIKKHVAITEQYLYARQFADPKLAKLYQNHGII SMRDFGLKERGMKS-DIIA	374
Pjir	IDSWKLFPEFGSKTFT-KTLDIRGLFTSKRNEKN-----HHEIVIR	85	Pjir	---FSTSDIEITKQYAKWRLLKKEPDLKLYQNHGII SMRDFGLKERGMKS-DIIA	374
Cneo	ITSWKTEHMYFKKLSVFTLARGLFTTEVLEGDMPPLETCSHQSESNPDAPNERIVLR	123	Cneo	KKVRSRAKREPVKYSYTWGEMMKKEPELEFDYIN--RGVIRVREERFLKWAEDDGKMWDD	541
Rarr	WTSWIVRESVYKPKHLPALARGLFTTKKT-NG-----KHSIVVR	84	Rarr	PTQAKYKYEKTKFYIDWLKKEVKEPEWFKYKAEKGIQTRQEFEEYKWTGS-SAAT	374
Mcir	WTSWIMRESVYKPKHLPALARGLFTTKKT-NG-----QYQIMVR	86	Mcir	PKKMKQEKTRFYIEWLKRVADHPEWFLKAEKGIQTRQEFEEYKWTGS-SAAT	372
Rirr	LSSWKMNEDWYK--KHRTPTQARGLFTRET-NS-----KNEIVIR	135	Rirr	---KPRTTYALSKQYLEWTEKIKTHPKLFEYKGNKGIIFVRDMFLEYLNKGD-IQTF	416
Scer	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	142	Scer	HEKVAELE---LKNADYDKVDERTKFLIFPISVIGCGKTTTQSLVNLNFPDSWGHQND	425
Calb	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	136	Calb	IDSELSDQKLNLANGLNGLSTTKYIFVPIATIGCGKTTTQSLVNLNFPDSWGHQND	445
Caur	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	142	Caur	LVALNNE---KLTKRNFEEVEVKRYLFPFIAPVGGKTTTQSLVNLNFPDSWGHQND	432
Afum	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	145	Afum	MEAGKPV-----DEVTRDVLAPASLGGKTTTQSLVNLNFPDSWGHQND	416
Hcap	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	144	Hcap	MELAQGE-----GTSPLAKVTQDIVLVVVASIGCGKTTTQSLVNLNFPDSWGHQND	422
Pjir	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	144	Pjir	LLNMM-----TDDLEDRSILVVTIGTIGCGKTTTQSLVNLNFPDSWGHQND	420
Cneo	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	145	Cneo	ARAGVKD-----EQRTGNRDLPKKMIWVPAAPGCGKTTTQSLVNLNFPDSWGHQND	594
Rarr	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	146	Rarr	EK-----	376
Mcir	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	145	Mcir	AK-----	372
Rirr	GYDKFNVGVEVNTKWNNEIENCTGYPDVTIKANGCIIIFISGLEDDGLVVCCKHSTGPRA	146	Rirr	AK-----IPQEEIKTLVPGTIGCGKTTTQSLVNLNFPDSWGHQND	457
Scer	DV-----DRNHAEAGE	144	Scer	DITGKDKSMLKKSLELLSKKEIKCVIVDRNNHQFRERKQFLFELWNLKEDYLVYDNIK	485
Calb	DDNESDKTTT-----	146	Calb	NISKAKLKICDLTLLALEDDQSVLFDNRNSASRERQIFPTIDQKRDEHLDVTDLK	505
Caur	IESDG-----	147	Caur	NYSAPK-----EFRNSCVKSLADSPLLLDRNNSRKRERQSLDIDFQMRNCVLPVNVGLR	488
Afum	DTNL-----	149	Afum	NIPKQKPKRFAFEIANLLADKPVVIADRNHHQRERQSLMEDI LPGAIP-----GAK	469
Hcap	DVTL-----	148	Hcap	NIQAPKPKRFAFEIANLLADKPVVIADRNHHQRERQSLMEDI LPGAIP-----GAK	473
Pjir	CGIS-----	149	Pjir	NITGKTKIQKFTVSTIEALMHYVVIADRNHHQRERQSLMEDI LPGAIP-----GAK	473
Cneo	AAEGVDSGTEKLIKDKPKAPKQCNESAPEKISQIRPIPSFPPTVKLPDEFKNNLTLEQS	243	Cneo	DITTKRTAPT-FIKNVITLTVHVVADRNHHQRERQSLMEDI LPGAIP-----GAK	473
Rarr	TDIK-----	148	Rarr	-----EDKKLQKFDTR	649
Mcir	TDVK-----	150	Rarr	-----	376
Rirr	-NAL-----	198	Mcir	-----	372
Scer	-----DRNHAEAGE	153	Rirr	NIIGKKARIE-FYRSINESSSHSGVLADRNHHI IELRKTLEIAVAKSNLS-----NVR	509
Calb	-----ATATATATRNHAKQGE	163	Scer	VIGVSAFAPYDKL-----SEIRIDTLQRVIRKGNHNSQIKWDELGEKKVVGIMNGF	535
Caur	-----KGRSRYERAK	157	Calb	YIAINFPEPDL-----EELWDTYVNRVGRDNHNSQIKWDELGEKKVVGIMNGF	555
Afum	-----SHAQGE	156	Caur	RVGINFTACDD-----KEKFSKVIKREIARGDNHNSQIKWDELGEKKVVGIMNGF	537
Hcap	-----SHAQGE	155	Afum	FVALHYVHEPKDVL-----LPSIREVTRKRLERGDNHNSQIKWDELGEKKVVGIMNGF	522
Pjir	-----SHAQGE	156	Hcap	FVALHYVHEPKDVL-----LHDIKVQVQARVLRGDNHNSQIKWDELGEKKVVGIMNGF	528
Cneo	QASQSLKSNALKAEKAAKLYQKMMNKGSEKSSQSTTAEKKEIKEHEEAQHAVVGR	303	Pjir	FIALYHYHDKDASLCKKQELNKILKITQDRVFARGSNHQITIDASPNIKAVLGMNGF	533
Rarr	-----AHAGVGY	155	Cneo	LICVWDLDTFF-----YRLLRILSDRVVARGENHQITLRLDPLDAEHAUVGKF	700
Mcir	-----AHAGVGY	157	Rarr	-----	376
Rirr	-----AHAVVGE	205	Mcir	-----	372
Scer	QQLLRQAAMNINRSDFARMYLTHTVAVAEYDDEFEHILEYPLEKAGLYLHGIVNKK	213	Rirr	IVAIYWNHEDRT-----KNEIFKITSKRVVSRGENHNSQIKWDELGEKKVVGIMNGF	557
Calb	FELLQDFDQDQKQVQLAHYLYENNTLVVAELDDDEFEHIVLPPKDKSGLYVHGLNYNT	223	Scer	LKRYQPV-----NLDSKPNDFMLMELDFGQA-----DSSLTNAKQILNEI	577
Caur	KTVYHLEKAGKLAEEALFTLYKHNITVAELDDDEFEHILEYPLEKAGLYLHGIVNKK	217	Calb	IQRYPPI-----NTRSPDQDFDHIYHLKLSKDNSSKSLNENVI I IDDL	601
Afum	KWVERHVAAGVGRMADLAKALRKNLTAVALGELDDDEFEHIVLPPKDKSGLYVHGLNYNT	216	Caur	EARLQPTLVASAPKNKVKGDELESPDSSFYSIMNFIDIT-----KSSLEIAKEIWAY	591
Hcap	NWAKRHVAAGVGRMADLAKALRKNLTAVALGELDDDEFEHIVLPPKDKSGLYVHGLNYNT	215	Afum	LKRFEGV-----NREPEPDSGFDDHIVLDLVA-----ASSRENLETVNVAL	562
Pjir	TWLDRLHLSVGRTRKQLARVLRKKNLTVLSELDDDEFEHILEYPLEKAGLYLHGIVNKK	216	Hcap	LSRFEAI-----DNLNYPDGGDFDHIYHLKLSKDNSSKSLNENVI I IDDL	568
Cneo	RWLKRTLESSGKTEELARLWKNLTAVALGELDDDEFEHIVLPPKDKSGLYVHGLNYNT	363	Pjir	LSRFEAI-----DRSKEPDSLFENVI ILDP-----KDRYLNLEIVVRLK	573
Rarr	NWVTKHLASVDKKEDEALWLFKFGVITVAELDDDEFEHILEYPLEKAGLYLHGIVNKK	215	Mcir	IRDYTPP-----D-----PAIFSDIISVNMV-----DSAKVTLTKVVQGL	735
Mcir	NWVTKHLASVDKKEDEALWLFKFGVITVAELDDDEFEHILEYPLEKAGLYLHGIVNKK	217	Rarr	-----	376
Rirr	QWLKHLKVVGRTEELANFLYKRNSTAVAEYDDEFEHIVLPPKDKSGLYVHGLNYNT	265			

Mcir ----- 372
 Rirr LNDFQPL-----NSNNKIDNQFDHVIEDVA-----NDVKTNLETVINEL 597

 Scer HKAYPILVP-EIPKDEIETAFRRS-LDYKPTVRKIVGKGNNOQK----- 621
 Calb VQNFPLIK-EKPADELINCFQKA-LDYKPTFKVNMNTANTIK-K----- 643
 Caur LSQLOQFNDERDPTTEEWQRAYQEA-LDYKPTFKKVVSSK----- 630
 Afum HSFPDQLLR-RVPTSQELDDAVTWAMTEYHVQLDLSYSGSSKPRQNLNKNKQNDGAST 621
 Hcap HSSFPQMEGKMPSSDLDNAIDDMKNKYVDTKHDLKFSNSN----- 611
 Pjir HEIIPKYIT-EIPTAFQMDNAVSSALNDYRPCISSVFPC----- 611
 Cneo VKSLGL---TMPSEDAINQGLEAA-SLYKTTTFVHPAA----- 769
 Rarr ----- 376
 Mcir ----- 372
 Rirr KPILGF---EKPSDEKIEK-VLEEISDYKPTVRKI---VG----- 630

 Scer -----TPKLIKPTYISAKIENY--DEIIEI--VKRCIASDAELTEKFKHLLA 664
 Calb -----DPTYYGIAM-HY--SSILEN--LEI--VSH--NEHFQ--NI 673
 Caur -----NLGDKRPEYGVRIEDV--SGLID-----GVSTKLGEQKMWQSMRA 669
 Afum AAHAQPQEPFSPPEALAQKIEYFCISIPAEVTTLLHS--LFPSP--TPPEKARLYHHLVN 678
 Hcap -KFSKQAPRESPDQLAKRIEYFNI SLNSNQITLLAS--LFSSTIPPERKLYHHLKN 668
 Pjir -----FSQTPYFAIVLKDNL-ALYVEE--IM--QGQSEKRTFWHELKS 651
 Cneo -----RHGKSTRYFAVAPEINLYELTSKAIEPFRDTEKQSAWSFLDELYK 815
 Rarr ----- 376
 Mcir ----- 372
 Rirr -----NKPPKVSFYGIKDFN-VQEF LSD--YY--NKHPNEDSGIFKLVQ 671

 Scer SGKVQKELHITLGHVMSREKE--A-----KWLKSYCNRY 698
 Calb KSHIQTEFHVTLGHIASSKQDK--AG-----RVKWKLVKTL 708
 Caur NDRVQRELHVTIGHKNSIYAF--SL-----KDKWELARRF 704
 Afum SRRVQPTFHVTLIHRASKTERV-----DIWDRYANQY 710
 Hcap SRRQTSFHVTLIHRASKTHP-----DIWAYYTNLY 700
 Pjir LSRVQHTFHVTLIHRADSKYK-----EIWYSYLSRI 683
 Cneo RGRITARPHVTLSHENNVKVEEARSRTGAPENKDDSELVRSRPGPEEILWETCKSIA 875
 Rarr ----- 376
 Mcir ----- 372
 Rirr GERIGFEHHVTLIHSKELKIDPLYK-----KWLWEQYEKI- 707

Scer TDQITEYNNNRIENAQSGSNNQNTQVKTTDKLNFRLR-KLCWDEKIIAIVVELSKDKDGC 757
 Calb G-----KGDPNKPK---SALKF-----FADVKLLQIV--INTDKLAC 740
 Caur AMQVAKKESKE---DKF-----VPVKFCD--VHVKKLVVFDNKLVTLSVQIPQTYKKE 753
 Afum IAKMKEQSQQAHTASP-----VLTPTLAPARVRLR-RLIWDDRIMAFVARIMPDRRE 763
 Hcap KAAIQKEQPN-PANGYV-----LETPI LGTTRVRIE-RLVWDDRIMAFVARICPR---E 749
 Pjir DK-----HGVICQANVEFT--HLVWNSRIMALAAKIDAQ--- 716
 Cneo -----TSKYPPLYSFLT--HLVWDDRTMAFICISLSPVISS 910
 Rarr ----- 376
 Mcir ----- 372
 Rirr -----CKDLPQVKVHIN-KIVFDSQIMALVVDRIVPSE-- 739

 Scer I IDEN-----NEKIKGLCCQNKIPHITLCKL-----ESGVKAVYSNVLCEKV 799
 Calb IKVEILK---IYDTNDVLQSEIEPINKQLHITIGCIPPATAVESNITLLELYDNPDEQEL 797
 Caur GEN-----IILQNPALPEPLNEHLHITVGTVS-----SSVSNADSNVLLHEL 794
 Afum QPD-----WPCANPIPHVTVGTAS-----AEVKPKESNDLLRRW 797
 Hcap GDS-----WPCANDIPHITVGTAA-----PEVKPKESNDLLRRW 783
 Pjir KKK-----LISVNLYPHATIGTEN-----KMI FAKESNDLLAFW 750
 Cneo TPDEPDGAASLSVCPDLDVLPQATRITLHVTVGTRD-----ADVPAPESRSLVKV 962
 Rarr ----- 376
 Mcir ----- 372
 Rirr -----ICSTNKIMHVITIGTVD-----NNVKHFQANTVCESA 770

 Scer ES---AEVDENIKVVKLDNS--KEFVGSVYLN----- 827
 Calb KPDGTYKCGDDTLHVFNDPDLKLSQQLFVAYQ----- 832
 Caur SKKYGD--V-----LA--DGEYPLKATIARVYSFDRLEKQVFIFFSYTF 836
 Afum LEVGSQ--GDTGIWEAEI--PGVKVVQSGVGMVMSRGKLLK----- 834
 Hcap LEVGAG--AETGIWEAEV--PSVTMLEGSGVGMVMSRGLMK----- 815
 Pjir KSHPHD--SSI--MALVL--TPRLFSGIAVAVYPTKSTI----- 783
 Cneo RERLEAGEQEIEELVANGGSKWIK--VGPARGRIRGMA----- 1003
 Rarr ----- 376
 Mcir ----- 372
 Rirr LSKENQ--S--EICVTNL--ENELVVDGTVKAFY----- 798

Supplemental references

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