	410 *	430	- 40	. 500	* 520		600
aIF5B Hmar :	LRTPIVAVLGHVDHGKTS	LLDKIRGSAVTAGESCAIT	HIGATAVPL20LLFIDTPG	HHS <mark>FSTLR</mark> SRCGALADIAILVVDV	JDGFQPOTLEAIDILKRTQTPFI	ANKIDTVP58	PVSAETS
aIF5B Mmar :	LRCPIVSVLGHVDHGKTS	LLDKIRRTRVTOREAGGIT	HIGASEIPI22ILVIDTPG	HEAFTSLEKRCGALADIAILVVDI	EGFKPOTIEAINILKOCKTPFI	ANKVORIP59	PVSAMTG
aIF5B Aful :	LRTPINAVLGHVDHGKTT	LLDRIRKSKVVAKEAGCIT	HIGATEVPL19LLFIDTPG	HKAFTNLERRCGALADLATLIVDI	JEGEKPOTEEAU SILRTEKTPEV	AANKIDRIP58	PISALKG
aTE58 Mthe :	TRSPTVSVLGHVDHCKTT	LLDHTRCSAVASRDACCTT	HIGATEIPM22LEEIDTPC	HEAPTTLEKECGALADIATLIVDI	JE GEKPOTOEAUNTLEMYRTPEV	ANKIDRTH58	PTSATTC
aTESE Nomi	TROPILTTLCHVDHCKTT	LI DKTRKTAVAOKEACCTT	HTCATEVET	FARSNUR RECCETADIATION	IF CTMPOTIKE ATE I CKOEPUPET	TANKIDKTP57	TUSNETC
alF5B Aper :	LEOPTWVI CHVDHCKTT	LLDKTERTAWAAKEACCTT	HICASTURA22LLETDTPC	HELESNI PRECOSVADEATIAVD	FCFKPOTYPALFLIKFRRUPFL	AANKTORTP58	PUSARTO
alF5B Ddie :	VPSPTTCTLCHVDTCKTS	LLDKTRNTNVOCCEARCTT	OTCASET PV22 LLI TOTPC	HESENNI PSPCSCI CDI ATLATI	HCT OA OTT DSTNLL PMPKTPET	ALNEVORTY58	TSANTC
oIF5B Scor :	TREPTCOTLCHVDTCKTK	LIDKTROTNVOCCENCCT			ANGI FOOT TRETKI I POPKA PEV	VALNETDRIV-58	TSAUTC
eirob Scer .	TROPICOTI CHUDTCKTK	LIDKTROTNUOF CENCOTT				AT NEADED V 59	DTSAUTC
erros cole .	TREPUTOUL CHUDTCKTK	MIDTERTAN			HOLEFONT BOOKLERERKIFF		DTONET C
eirsb cere .	TRADIT OUT CHUDTCKTY						TO TO ALLE
errss Hinus :	TRAPTICVIGHVD1GK1K					SERVICE E	PISARIG
elros Hsap :	LRAPTI CVLGHVD TGKTR		OTGATN PL22MEIIDTPG	ESISNLENEGSSICUTATLVVD1	HGLEPOTIDSINLLKSKRCPFI	ALNKIDELI58	PTSAHTG
mitirz_sce :	RRAPVVTIMGHVDHGRTT	IID ILRKSSVVAQBHGGIT	HIGAFOITA6ITFLDTPG	HAAFLKNRERGANTTDTTVLVVSVI	DSLMPOTDSALKHAKNSGNEMI	ATTRIDEIP32	PISARTG
IF2_Ttherm :	RRPPVVVIMGHVDHGRTT	LLDYLIRKSKI AEKBAGGI T	HVGAFEVRT4VVFIDTPG	HEAPTTIRORCARVADIAVIVIAA	DGIMPOTEDALAHAKAAGAKLI	MINKIDL28	PISAKTG
IF2_Ecol1 :	PRAPVVTIMGHVDHGKTS	IIIDYIIRSIIKVASGBAGGI T	HIGAYHVET4ITFLDTPG	HAADIISMRARCAQATDIIVVLVVAAI	DGVMPOTIBAIQHAKAAQVPVV	VAVNKIDK28	HVSAKAG
IF2_Styph :	PRAPVVTIMGHVDHGKTS	LLDY IRSTKVASGEAGGI T	HIGAYHVET4ITFLDTPG	AADUSMRARCAQATDIVVLVVAAI	DGVMPOTIEAUQHAKAAGVPVV	VAVNIKIDIK28	HVSAKAG
IF2_Bdent :	PRPPVVTVMGHVDHGKTR	LLD TIRSTNVIARE AGG I T	RIGAYOVTV8ITFLDTPG	HEAISTAMRARCAEL TOVALLVVAAI	DGVMPOTVEAUNHAQAAHVPIV	VAVNKIDK28	DISAKQG
IF2_Bsupt :	IRPPVVTIMGHVDHGKTT	LLDSIRKTKVVEGEAGGIT	CHIGAYQIEE4ITFLDTPG	AAFTTMRARGAEVTDI TILVVAAI	DGVMPOTVEAUNHAKAAEVPII	VAVNKIDK28	PLSALTG
	-					Sec. 1	
	P loop	Switch 1		Switch 2		G4	G5
	760	* 78	* 800	* 820	* 840 *	860	*
aIF5B Hmar :	TTOEEGVVIKADTLESLE	ALSSTTEEEE TPV	RAEVCAVAPROVRVAETAGES	TNOATLARSVDVLDDARDLAEOED	KI FEDDVILYOLVESYDDHVTAT	EFACOFOILENITRPAN	FRILODH
aTE58 Mmar :	LTDDEGT TTKADTMCSLE	ALANEL RKVNAKT	KKAEVODTSKKDVTEASSYASSNP	INGUT TSPNTKVLADAKAE TEKSD	KULEGKUTYKUVEEYEEWTKEM	ELMKSDE INRLTKPAN	TKTLPNC
aTF5B Aful :	RTDEEGVUKTDTLOSLE	TINET ROEGTPT	KKAEVCDVDKRDVVDASANKDEI	INKUVI APNVKULPOVEEEAKKYO	RTESHETTY TI TESEVKWREEE	RLAREROKVEALTKPC	TRLIKEF
aTE58 Mthe :	DTDEAGYYYKADTLOSIE		KVADICOVSERDVVNAGIALOEDE	VYGATTAPNYKYTPSAAOELKNSD	KI FOGNUTURI MEEVEEWVRGT	FERKKKWMEATTKPAS	TRI.TPKT.
aTESB Negu :	FEEKEGLYWKADTLOULE	ATVNTTKSKGTKV	SKAGTCETTKEDITKAOSOKDEI	KYRVII APNVSDIFSD	PTITYDNUTYPILEKYEEFIKOL	FORKLSTLDRITEVAR	TETTPCL
alF5B Aper :	L DDT D DDT HT TO ID T D DT	Horto Horto					TTT DOV
AIF5B Ddie :	RTENICYVVKADTLENTE	ALVEAN RRRGVPV	RLADICPUSESDVLDAAVTEKTDP	VI.CVVI ADNVKVI.PEAEEEASRAC	KTERES TYKLTEDYEEWYKKE	KEAFRI.KALNSI.TRPGH	PRILE PLAT
aIF5B Scar :	RTENIGVVVKADTLGTLE	ALVEALRRRGVPV	RLADIC PVSRSDVLDAAVTRKIDP	YLGV <mark>VLAENVK</mark> VLPEAEEEASRAG	KIFRESMIYKLIEDYEEWVKKE	KEAERLKALNSLIRPG	EVTN
	RTENIGVVVKADTLGTLE ETSGIGVSVQASTLGSLE	ALVEALRRRGVPV AFLNFLKKIKIPV ALLDFLKDMKIPV	RLADICPVSRSDVLDAAVTRKIDP ANVAICPVHKKHIMNASIMLDKDP MSICICPVYKPDVMKASTMLEKAP	YLGVVLAENVKVLPEAEEEASRAG KYAILLAEDVKIEESAIQAANEMK	KIFRESMIYKLIEDYEEWVKKE OVLSDETIYLFEEKLKKHFGAI KIFNADVINH FDSFTAVOFKI	KEAERLKALNSLIRPGH KEKLRAETASICVWPCI	LEVTN
aIF5B Cthe :	RTENIGVVVKADTLGTLE ETSGIGVSVQASTLGSLE DTTGKGVVVQASTLGSLE FKTGKGVSVQASTLGSLE	ALVEALRRRGVPV AFLNFLKKIKIPV ALLDFLKDMKIPV	RLADIC PVSRSDVLDAAVTRKID P ANVAIG PVHKKHIMNASIMLDKD P MSIGLG PVYKRDVMKASTMLEKA P ANVGLG PVYKRDVMCCGIMIEKA P	YLGVULAENVKVLPEAEEEASRAG KYAILUAEDVKIEESAIQAANEMK EYAVMLCEDVKVDKEAEQYAEQEG	K <mark>IFRESMIYKLIEDYEEWVKKE</mark> OVLSDETIYLFEEKLKKHFGAI KIFNADVIYHLFDSFTAYQEKL KIFNADVIYHLFDSFTAYQEKL	KEAERLKALNSLIRPGH KEKLRAETASICVWPCI LEERRKDFLDYAIFPCV	LEVTN
eIF5B Cthe :	RTENIGVVVKADTLGTLE ETSGIGVSVQASTLGSLE DTTGKGVVVQASTLGSLE EKTGKGVSVQASTLGSLE EKTGKGVSVQASTLGSLE	ALVEAD RRRGV PV AFLNFL KKIKI PV ALLDFL KDMKI PV ALLDFL KDCKI PV	RLADIC PVSRSDVLDAAV TRKIDP ANVALC PVHKKHIMNASIMLDKDP MSIGLC PVYKRDVMKASTMLEKAPI ANVGLC PVYKRDVMQCGIMLEKAPI	YLGVVLAENVKVLPEAEEEASRAG KYAILLAEDVKIEESAIQAANEMK EYAWICEDVKVDKEAEQYAEQEG DYAVMICEDVKVDKEAEQYADENG DYAVMICEDVKVDKEAQQYADENG	KIFRESMIYKLIEDYEEWVKKE OVLSDETIYLFEEKLKKHFGAI KIFNADVIYHLFDSFTAYQEKL KIFTADIIYHLFDSFTAYQEKL	KEAERLKALNSLIRPGE KEKLRAETASICVWPCI LEERRKDFLDYAIFPCV LEKKKEESKMLAVFPCV VEVAPPNEHIAVFPCV	LEVTN LQTLQ LNPVA
eIF5B Cthe : eIF5B Cele :	RTENIGVVVKADTLGTLE ETSGIGVSVQASTLGSLE DTTGKGVVVQASTLGSLE EKTGKGVSVQASTLGSLE RKKPEGVYVQASTLGSLE	ALVEALRRRGVPV AFLNFIKKIKIPV ALLDFIKDMKIPV ALLDFIKSQNIPY ALLEFIKSQNIPY	RLADICEPVSRSDVLDAAVIRKIDEP ANVALGPVHKKHIMNASIMLDKDPI MSIGLEPVYKRDVMKASIMLEKAPI ANVGIGPVYKRDVMCGIMLEKAPI SNVNIGPVHKKDVQKASAMKEHKAJ	YLGVVIADVKVLPEAEEEASRAG KYAILLADVKIEESAIQAANEMK EVAVMLCDVKVDKEAEQYAEQEG DYAVMLCDVKVDKEAQQYADENG EVACVIADVKVEREAQIFADHEG	KIFRESMIYKLIEDYEEWVKKE OVLSDETIYLFEEKLKKHFGAI KIFNADVIYHLFDSFTAYQEKL KIFTADIIYHLFDSFTKHQEQ KVFQADIIYHLQDAFLKHQEQ KVFQADIIYHLQDAFLKHQEQ	KEAERLKALNSLIRPGH KEKLRAETASICVWPCI LEERRKDFLDYAIFPCV LEKKKEESKMLAVFPCV KEKARRDNEHLAIFPCV	LEVTN LQTLQ LNPVA
eIF5B_Cthe : eIF5B_Cele : eIF5B_Mmus :	RTENIGVVKADTLGTLE ETSGIGVSVQASTLGSLE DTTGKGVVVQASTLGSLE EKTGKGVSVQASTLGSLE RKKPEGVYVQASTLGSLE KLEEKGVVVQASTLGSLE	ALVEAT RRGVPV AFLNFI KKIKI PV ALLDFI KDMKI PV ALLEFI KDCKI PV ALLEFI KTSEV PY ALLEFI KTSEV PY	RLADIG PVSKSDVLDAAVTRKIDP ANVAIG PVKKHIMNASIMLDKDPI MSIGLOPVYKRDVMKASTMLEKAPI ANVGIG PVYKRDVMQCGIMLEKAPI SNVNIC PVHKKDVQKASAMKEHKAI AGINIC PVHKKDVQKASAMKEHDPI AGINIC PVHKKDVMKASVMLEHDPI	Y LOVULAENVKU LPEAEEEASAG KYATIL AEDVKI EESAIQAANEMK EYAVME OFDVKVDKEAEQYAEQEG OYAVME OFDVKVDKEAEQYADENG EYACVLAEDVKVDKEAQQYADENG EYACVLAEDVKVEREAQI FADHEG QYAVITI AEDVRIERDAQEMADSLG OYAVITI AEDVRIERDAQEMADSLG	KIFRESMINKLIEDYEEWVKKE OVLSDETIYLFEEKLKKHFGAI KIFNADVIYHLFDSFTAYQEKL KIFTADIIYHLFDSFTKHMOBQ KVFQADIIYHLQDAFLKYREEL RIFSAEIIYHLFDAFTKYRQDY FFAATUWLFDAFTKYRQDY	KEAERLKALNSLIRPGH KEKLRAETASICVWPCI LEERRKDFLDYAIFPCV LEKKKEESKMLAVFPCV KEKARRDNEHLAIFPCI KKQKQEEFKHIAVFPCI	LEVTN LQTLQ LNPVA CLRVLPNH MKILPQY
eIF5B_Cthe : eIF5B_Cele : eIF5B_Mmus : eIF5B_Hsap : mitIF2_Sco	RTENIGVVVKADILGTER ETSGIGVSVASTLGSLE DTTGKGVVVASTLGSLE EKTGKGVSVASTLGSLE RKKPEGVVVASTLGSLE KLEEKGVVVASTLGSLE KLEEKGVVVASTLGSLE CREIGVVVASTLGSLE	ALVEAU AFLNFU	RLADIE GY SKEDU LDAAV THE ID PY MAN I GY VIKKH INNAS I MLDKD PI MSIG I GYY Y KRDVMKASTMLE KAPI SI SI Y KRDVMKASTMLE KAPI SI NY I GYV I KRDVMKASTMLE HD PI AGI NI GYV H KKDVMKASTMLE HD PI	YLGWITARNYKYLPEAEEEASRAC KYATIDARDYKIEESAIQAANEMK SYAMICODYKYNKEAEQYAEQEG DYAWITCODYKYNKEAEQYADENG EYACYDARDYKVEREAQIFADHEG DYAVITARDYRIERDAQEMADSLG DYAVITARDYRIERDAQEMADSLG DYAVITARDYRIERDAQEMADSLG	KIFRESKINKLIEDYEEWVKKE OVLSDETIVLFEEKLKKHFGAI KIFNADIVHIFDSFTAVQEKL KIFTADIIVHIFDSFTKHMQEQ KVFQADIIVHLQQAFLKYREEL KIFSAEIVHIFDAFTKYRQDY RIFSAEIVHIFDAFTKYRQDY	KEAERLKALNSLIRPGH KEKLRAETASICVWPCI LEERRKDFLDYAIFPCU LEEKKKEESKMLAVFPCU KEKARRDNEHLAIFPCI KKQKQEEFKHIAVFPCI KKQKQEEFKHIAVFPCI	LEVTN LQTLQ LNPVA CLRVLPNH MKILPQY
eIF5B_Cthe : eIF5B_Cele : eIF5B_Mmus : eIF5B_Hsap : mitIF2_Sce : IF2_Tthere	RTENIGVVVKADTIGTLE ETSGIGVSVQASTLGSLE DTTGKGVVQASTLGSLE EKTGKGVSVQASTLGSLE RKTPEGVVQASTLGSLE KLEEKGVVQASTLGSLE KLEEKGVVQASTLGSLE GFKLINYIKCDVSGSAE	AUVEAD	RLADIGEV SISDU LDAAV TIK ID DP MANA GEVIKKHIMAS ILDKOPI MSI GLOFVYKRDVMKASTMLEKAPI NAVG GEVYKRDVMQCGIMLEKAPI NAVG GEVIKKDVMKASAMKEIKAJ GINI GEVIKKDVMKASAMKEIHAJ GINI GEVIKKDVMKASVMLEHDP ISSS VGI PTS DLIMAGIT	VLGWITA SNYKVLPEAEEEASEAG VYATILA SNYKVESAI OANNEMK EYAVILG SDVKYDKEAEQYAEQEG YYAVILG SDVKYDKEAEQYAEQEG YYAVILG SDVKYDKEAQYADENG YYAVILA SDVKISEAQIF FADHEG YYAVILA SDVKISEAQIF FADHEG YYAVILA SDVKISEAQAEMADSLG -ESTILG SNLGNLPS - EVINNEAG	KIFRESMINKLIEDYEEWVKKE QULSDETIVLFEEKLKKHFGAI KIFNADVIHLFDSFTAVQEKL KIFTADITYHLFDSFTKHQEQ KVFQADITYHLQDAFLKYREEL RIFSAEITYHLFDAFTKYRQDY KISAEITHLFDAFTKYRQDY KIKQYNVIYKLIEDVTETL	KEAERLKALNSLIRPGH KEKLRAETASICUPCI LEERKKDFLDYAIFPC LEKKKESSKMLAVFPC KEKARRDBEHLAIFPC KKQKQEEFKHIAVFPC KKQKQEEFKHIAVFPC FENLRVIFEKKIVSTVI	LEVTN LQTLQ LNPVA CLRVLPNH MKILPQY CIKILPQY VRETFDF
eIF5B_Cthe : eIF5B_Cele : eIF5B_Mmus : eIF5B_Hsap : mitIF2_Sce : IF2_Ttherm : IF2_Ttherm :	RTENIGVVVKADTLGTLE ETSGIGVSVQASTLGSLE DTTGKGVVQASTLGSLE EKTGKGVSVQASTLGSLE KLEEKGVVQASTLGSLE KLEEKGVVQASTLGSLE KLEEKGVVQASTLGSLE GFKLINUIKCDVSGAE GFKELNLIPADTQGSLE	AUVEAD	RLADIE EV SISDILDAAV THEIDEY MSIG JOPVY KRDVMKASTMLEKAPI MSIG JOPVY KRDVMKASTMLEKAPI MSIG JOPVY KRDVMKASTMLEKAPI NIVOLEVY KRDVMKASTMLEKAPI AGINI GPVHKKDVMKASTMLEHDP GGINI GPVHKKDVMKASTMLEHDP JOS JOP JFIS SDULLAOTA LLAOV GAPTES DLKMQ IT	VLOVUADWIVUPEAEEASEAG VILOVUADWIVUPEAEEASIAO SIAVICOUVIVUEAEQIAEOSO VIAVICOUVIVUEAEQIAEOSO VIAVICOUVIVUEAEQIAEOSO VIAVIAOUVIEEAOIFADHEG QIAVITAGUVIEEAOAQEMADSLG VIAVITAGUVIEEAOAQEMADSLG VIAVITAGUVIEEAOAQEMADSLG -NAATIAGUVIEEAOAQEMADSLG -NAATIAGUVIEEAOAQEMADSLG -NAATIAGUVIEEAOA	KUPRESKIYKLIEDYBEWVKKE QULSDETTULFEKLIKKIFGAT KUPADUTHIFDSTTAVQEKLI KUPADI TYHLFDQTFKIMQED KUPADI TYHLFDQTFKIMQED RUPSAE TYHLFDAFTKYRQDY RUPSAE TYHLFDAFTKYRQDY KUPYNYTKIEDYTE	KEAERLKALNSLIRPG KEKLRAETASICWPCI LEERRKDFLDVAIPPCV LEERKKEESKMLAVPPCC KEKARRDNEHLAIPPC KKQKQEEFKHIAVPPCC KKQKQEEFKHIAVPCC TENLKPIFEKKIVSTVI KQQREPQYKEEVLGQA	LEVTN LQTLQ LNPVA CRVLPNH MKILPQY VRETFDF VRA
eIF5B_Cthe : eIF5B_Ctele : eIF5B_Mmus : eIF5B_Hsap : mitIF2_Sce : IF2_Ttherm : IF2_Ecoli : VT2_Ctere	RTENIGWYKADTLOTE ETSGIGVSVAASTLOSE DTTGKGWYVASTLOSE EKTCKGVSVASTLOSE RKKPEGVYVASTLOSE KLEEKGVYVASTLOSE KLEEKGVYVASTLOSE GPKLINYIKCDVSGSA GRKELALIRADTOGSE EVHEVNIVKADVASVS	ALVERI	KLADICEPVSRBULDAATTKKIDE NAVAIGEPVIKKITNANSITULDKOPI 85 DICEPVIKBUVNKISTULEKAPI 85 DICEPVIKBUVNGCGINLEKAPI 80 NNICEPVIKKUVQKISAMKEHKAJ 60 TINEEPVIKKUVVKISVULEHDOPI 15 SS VETPTESDLKANQIT- LLAQVEAPTESDLKANQIT- LLAQVEAPTESDLKANQIT- LLAQVEAPTESDLKANQIT- LLAQVEAPTESDLKANQIT-	VLGV VADSWYVLPEABEEASENG VYATULADWYVLPEABEASENG SYAVMI COVYVDKEAQYADEG DYAVMI COVYVDKEAQYADEG SYAVMI COVYVDKEAQYADEG YAVTI ADWYTERDAQEMADSLG -SSTICTALOWICKIERDAQEMADSLG -SSTICTALOWICKIERDAQEMADSLG -SSTICTALOWICKIERDAQEMADSLG -NATLAGENVFADASARKVITAES	KUPERSKI VK. IEDVERWYKKE OVSOET VUEEKLKHFGAI KUPNADU VHIEDSFTAYQEKL KUPNADI VHIEDSFTAYQEKL KUPADI VHIEDSFTAYQEKL KUPADI VHIEDSFTKYRODY KUPADI VHIEDSFTKYRODY KUPNEVK. IEDVFETK KUPKTEKLEDVECKAAM	KEAERLKALNSLIPPG KEKLRAFTASICWPCI LEERKKDFLDYAIFPC KEKARRDNEHLAIFPC KKQKQEEFKHIAVFPC KKQKQEEFKHIAVFPC FENLKPIFEKKIVSTVI KGQREPTKKEVLGQA SGMLBFELKQQIIGLA	LEVTN LQTLQ LNPVA CLRVLPNH MKILPQY CIKILPQY VRETFDF VRA VRA
eIF5B_Cthe : eIF5B_Cthe : eIF5B_Mmus : eIF5B_Hsap : mitIF2_Sce : IF2_Ttherm : IF2_Ecoli : IF2_Styph :	RTENIGWYKADIGTE ETSGIGWSOASTIGSIE ETGGWSOASTIGSIE EKTGKUSOASTIGSIE EKTGKUSOASTIGSIE KKEPEGWYOASTIGSIE KLEEKGWYOASTIGSIE GPKLINYI KCDVSGSIE GPKLINYI KCDVSGSIE EVHENNIYKADVSGSIE EVHENNIYKADVSGSIE	AUVENI	RLADICEPVSRBUDDAAVTEKIDP MANATEPVHKEHTMANSTMLDKDP MSTGLEPVYKBUVMQCGIMLEKAP MANGIOPVYKBUVMQCGIMLEKAP MSTNITEPVHKKUVMCSGIMLEKAP MSTNITEPVHKKUVMCSSVMLEHDP GSTNITEPVHKKUVMCSSVMLEHDP JISSSVGITPTSDLKMAQIT LLAQVGAPTSBUTLAQTA	VLGV VADANVKVLPEABEEASEAG VATALLADVVKULPEABEASEAG EYAVHI CSDVKVDKEABQYAEQEG DYAVHI CSDVKVDKEAQYAEQEG DYAVHI CSDVKVDKEAQYAEAG DYAVHI ABDVKIERDAQEMADSLG QYAVHI ABDVKIERDAQEMADSLG ESTILCONLCNLPS-EVINNRAG ESTILCONLCNLPS-EVINNRAG -NAAHAGVMENVADASARKVIEAES 	KUPERSKYKLIEDYBEWYKKE QUESDETVLPEKLKHFGAT KEPADUTHEPSTYDEKL KUPADITHEPSTYDEKL KUPADITHEPSTYNGEL KUPADITHEPSTKINGO KUPADITHEOATKYRGDI KUPADITHEOATKYRGDI KUPADITHEFAT KUPADITHEOATKYRGT KUPADITHEOATKYRG	KE ERLKALNSLIPPG KEKLRAETASIC WPCI LEERKKOFLDYAFPCC LEKKKESSMILAYPPC KKQKQEEFKHLAYPPC KKQKQEEFKHLAYPPC KKQKQEEFKHLAYPPC FENLKPIFKKTISTU SGMLSPELKQQIIGLA SGMLSPELKQQIIGLA	VRD VRD VRD VRD VRD VRD
eIF5B_Cthe : eIF5B_Cthe : eIF5B_Mmus : eIF5B_Hsap : mitIF2_Sce : IF2_Ttherm : IF2_Ecoli : IF2_Styph : IF2_Bdent :	RTENIGWYKADTIGTE ETSGIGWSOASTIGTE ETSGIGWSOASTIGTE EKTGKGWSOASTIGTE KLEEKGWYOASTIGTE KLEEKGWYOASTIGTE GPKLINYI KCDWSSA GPKLINYI KCDWSSA EVHENNIYKADWOSSA EVHENNIYKADWOSSA EVHENNIYKADWOSSA	AUVEALREKIE (WA ALDE)KOKE (WA ALDE)KOKE (WA ALDE)KOKE (WA ALDE)KOKE (WA ALDE)KOKE (WA ALDE)	RLADICEVSRBULDAATTKELDE MANATEEVHKETIMAASTILLOKDE SEGLEPVTKEDVIKKISTILLEKAP INNVETEEVYTKEDVIKSISTILLEKAP INNVETEEVHKEDVIKSISTILLEKAP INNVETEVHKEDVIKSISTILLEKAP ISSISTICEVHKEDVIKSISTILLEHDE ISSISTICEVHKEDVIKSISTILLEHDE ISSISTICETETDATLAAS ILLAQUEAPTESDILLAQUEA ISSISTICETETDATLAASS- IIIRGVEATETDATLAASS-	VLGV VADAVIVUPEABEEASEAG VATILA DOWNUPEADEASEAG YAMIL COUNVOIERAQIADEKG YAMIL COUNVOIERAQIADEKG YAMIL COUNVOIERAQIADEKG YAMILADUNI ERADQUMADELG ESTILCONLONLES-EVINNAG ESTILCONLONLES-EVINNAG -RATILAGONUPEOSVIKIAEEKG -NATILAGONUPEOSVIKIAEEKG -KAVILI CONVENDASARVUTEES -KAVILI CONVENDASARVUTESE	KUPESKIYKIIEDYREWYKKU VISOETYVIIERKIKHFGAI KUPNADIYHIFDSFTAYQEKI KUPNADIYHIFDSFTAYQEKI KUPADIYHIFDSFTAYQEKI RUPADIYHIFDAFTKYRODY RUPASHIYHIFDAFTKYRODY KUKYNYYKIIEDXFTXYRODY KUKYNYYKIIEDXFTXYRODY DIYYSYYNIIDEVKAAM DIYYSYYNIIDEVKASL DIYYSYYNIIDEVKASL	KEAERLKALNSLIPPC KEKLRAETASICWPCI LEERKKDEJAVIPCI LEEKKKESIMLAVFPCK KKOKOZEFKHIAVFPCK KKOKOZEFKHIAVFPCC FRILKPIFEKKIVSTVI KGQREPQYKEEVLGQAF SGMLSPELKQOIIGLAA SGMLSPELKQOIIGLAA	LEVTN VLQTLQ VLQTLPVA CLRVLPNH MKILPQY VKETFDF VRA VRD VRD IRE

Figure S3. Sequence alignment of the G domains (upper panel) and domains III (lower panel) from different aIF5B, eIF5B and IF2 homologues. Highly conserved residues are highlighted in blue; conserved residues that are directly involved in the stable contacts between switch 2 and domain III in inactive (apo and GDP-bound) eIF5B are highlighted in red. P-loop (G1 motif), switch 1 (with the G2 motif containing Thr439), switch 2 (with the G3 motif "DTPG") and motifs G4 and G5 in the G domain are indicated. The numbering above the sequences is according to the eIF5B homologue from Saccharomyces cerevisiae. Residues within the G domain that are implicated in nucleotide binding and the GTPdependent molecular switch in eIF5B are universally conserved among all three orthologs. Domain III is significantly less well conserved than the G domain; however, the N-terminal part of helix α9 (residues 763-768 in eIF5B) is highly conserved, particularly in those residues involved in the interactions with switch 2. Species names are abbreviated as follows: Hmar. Haloarcula marismortui; Mmar, Methanococcus maripaludis; Aful, Archaeoglobus fulgidus; Mthe, Methanothermobacter thermoautotrophicum; Nequi, Nanoarchaeum equitans; Aper, Aeropyrum pernix; Ddis, Dictyostelium discoideum; Scer, Saccharomyces cerevisiae; Cter, Chaetomium thermophilum; Cele, Caenorhabditis elegans; Mmus, Mus musculus; Hsap, Homo sapiens; Ttherm, Thermus thermophilus; Ecoli, Escherichia coli; Styph, Salmonella typhimurium; Bdent, Bifidobacterium dentium; Bsupt, Bacillus subtilis; mitIF2_Sce, mitochondrial IF2 from S. cerevisiae.