

Supplementary data

Legends to Supplementary Figures

Supplementary Figure S1 Secondary structures of the conserved domain (the 1070 rRNA region) of 23S/28S rRNA to which the stalk protein complexes bind.

(A) The domain of *P. horikoshii* 23S rRNA containing the residues 1142-1240. (B) The domain of rat 28S rRNA containing the residues 1841-1939. (C) The domain of *E. coli* 23S rRNA containing the residues 1029-1127. A possible binding site for EF-G/eEF-2 is arrowed.

Supplementary Figure S2 Comparison of amino acid sequences of L10-like proteins

(A) Amino acid sequence alignment of P0 homologues from *P. horikoshii* (Pho), silkworm (*Bombyx mori*, Bmo), yeast (*Saccharocyces cerevisiae*, Sce) and human (*Homo sapiens*, Hsa). The sequences were aligned using T-coffee (Supplementary references 1) and Genetyx-Mac (ver. 12.2.0) programs. The similar and identical amino acid residues are indicated with dots and asterisks, respectively. (B) The sequence of *Escherichia coli* (Eco) L10. Because of its small size and low sequence identity with the P0-like proteins from eukaryotes and archaeobacteria, this sequence is shown separately. Putative homologous amino acids are indicated with large dots.

Supplementary Figure S3 Comparison of amino acid sequences of L7/L12-like protein

Amino acid sequence alignments of P1 (A) and P2 (B) homologues from silkworm (*B. mori*, Bmo), yeast (*S. cerevisiae*, Sce) and human (*H. sapiens*, Hsa), together with *P. horikoshii* (Pho) Ph-L12. The sequences were aligned as described in Supplementary Fig. 2. The similar and identical amino acid residues are indicated with dots and asterisks, respectively. (C) The sequence of *E. coli* (Eco) L7/L12. Because of the very low sequence identity with its eukaryotic and archaeobacterial counterparts, this sequence is shown separately.

Supplementary Figure S4 Comparison of amino acid sequences of L11-like protein

(A) Amino acid sequence alignment of L11-like proteins from *P. horikoshii* (Pho), silkworm (*B. mori*, Bmo), yeast (*S. cerevisiae*, Sce), human (*H. sapiens*, Hsa), and *E. coli* (Eco). The sequences were aligned as described in Supplementary Fig. 2. The similar and identical amino acid residues are indicated by dots and asterisks, respectively.

Supplementary reference

- 1 Notredame, C., Higgins, D. G. and Heringa, J. (2000) T-Coffee: A novel method for fast and accurate multiple sequence alignment. *J. Mol. Biol.* **302**, 205-217

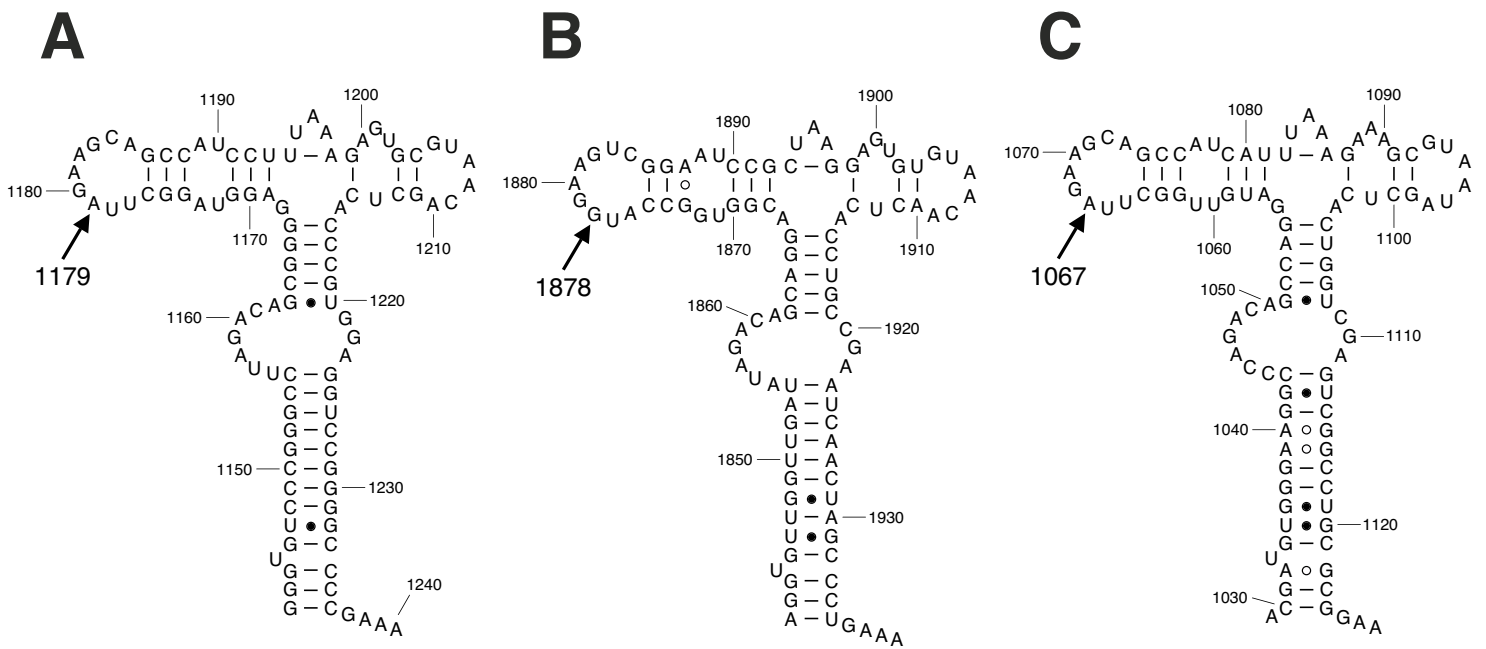


Figure S1

A

Pho P0	1	M--AHVAEWKKKEVEELAKLIKSYPVIALVDVSSMPAYPLSQMRRILIREN	48
Bmo P0	1	MGREDKATWKSNYFVKIIQLLDEYPKCFIVGADNVGSQQMQQIRISLRGS	50
Scce P0	1	M--GGIREKKAEYFAKLREYLEEYKSLFVVGVDNVSSQQMHVVRKELRGR	48
Hsa P0	1	MPREDRATWKSNYFLKIIQLLDDYPKCFIVGADNVGSKQMQQIRMSLRGK	50
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Pho P0	49	GLLLRVSRNTLIELAIKKAAKELGKPELEKLV EYIDRGAGILVTNMNPFK	98
Bmo P0	51	SIVL-MGKNTMMRKAIKDHLD--NNPALEKLLPHIKGNVGFVTRGDLVE	97
Scce P0	49	AVVL-MGKNTMVRRAIRGFLS--DLPDFEKL LPFVKGNVGFVFTNEPLTE	95
Hsa P0	51	AVVL-MGKNTMMRKAIRGHLE--NNPALEKLLPHIRGNVGFVFTKEDLTE	97
		* . . . ** . . ** . . * . *** * . . . * . . .	
Pho P0	99	LYKFLQQRQPAPAKPGAVVPKDVVVPAGPTPLAPGPIVGMQALGIPAR	148
Bmo P0	98	VRDKLLENKVQAPARPGAIAPLSVVIPAHNTGLGPEK-TSFFQALS IPTK	146
Scce P0	96	IKNVIVSNRVAAPARAGAVAPEDIWVRVAVNTGMEPGK-TSFFQALGVPTK	144
Hsa P0	98	IRDMLLANKVPAAARAGAIAPCEVTVPAQNTGLGPEK-TSFFQALGITTK	146
		. * . * . * . ** * . . . * . * . . * ***	
Pho P0	149	IEKGVITIQDTTVLKAGEVITPELANILNALGIQPLEVGLDVLAVYEDG	198
Bmo P0	147	ISKGTIEIINDVHILKPGDKVGASEATLLNMLNISPFSYGLVVKQVYDSG	196
Scce P0	145	IARGTIEIVSDVKVVDAGNKVGQSEASLLNLLNISPFTFGLTVVQVYDNG	194
Hsa P0	147	ISRGTIEILSDVQLIKTGDKVGASEATLLNMLNISPFSFGLVIQQVFDNG	196
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Pho P0	199	IVYTPDVLAIDEQEYIDMLQKAYMHAFNLAVNIA YPTPETIEAIIQKAFL	248
Bmo P0	197	TIFAPEILDIKPEDLRAKFQAGVANVAALSLAIGYPTIASAPHSIANGFK	246
Scce P0	195	QVFPSSILDITDEELVSHFVSAVSTIASISLAIGYPTLPSVGH TLINNYK	244
Hsa P0	197	SIYNPEVLDITEETLHSRFL EGVNRVASVCLQIGYPTVASVPHSIINGYK	246
		. * . * * . ***	
Pho P0	249	NAKTVAIEAGYITKETIQDIIGRAF RAMELLLAQQLPEDVLDEKTKELLSA	298
Bmo P0	247	NLLAIAAVTEVEFEFEE-ATTIKEFI-----KDP SKFAA	277
Scce P0	245	DLLAVAIAASYHYPE-IEDLVDR I-----ENPEKYAA	275
Hsa P0	247	RVLALSVETDYTFPL-AEKVKAF L-----ADPSAFVA	277
		. *	
Pho P0	299	QAQ-VAVATQPSEEEKKEEEKTEEE EKEEEEASEEEALAGLSALFG	342
Bmo P0	278	VAAAVAPSAAAAPAEKKEEKKE-EKEE-EE-SDDDMGFG---LFD	316
Scce P0	276	AAP-AATSAASGDAAPAE EAAA-E-EE-EE-SDDDMGFG---LFD	312
Hsa P0	278	AAPVAAATTAAPAAAAAPAKVE-AKEESEE-SDEDMGFG---LFD	317
		* * * . ** * * . ** .	

B

Eco L10	1	MALNLQDKQAIVAEVSEVAKGALS AVVADSRGVTVDKMT ELRKAGREAGV	50
		● ● ● ●	
	51	YMRVVRNTLLRRAVEGTPFECLKDAFVGPTLIAYSMEHPGAAARLFKEFA	100
		● ● ● ●	
	101	KANAKFEVKAAAFEGELIPASQIDRLATLPTYEEAIARLMATMKEASAGK	150
		● ● ● ●	
	151	LVRTLAAVRDAKEEA	165

Figure S2

A

Pho L12	1	M-----EYVYAALLLHSVGKEINEENLKAVLQAAGVEPEEARIKALVAA	44
Bmo P1	1	MVSKAELACVYSALILVDDDDVAVTGEKISTILKAAAVDVEPYWPLFAKA	50
Scs P1A	1	M--STESALSYAALILADSEIEISSEKLLTLTNAANVPVENIWADIFAKA	48
Scs P1B	1	M---SDSIISFAAFILADAGLEITSDNLLTITKAAGANVDNVWADVAKA	47
Hsa P1	1	MASVSELACIYSALILHDDEVTVTEDKINALIKAAGVNVPEFPWPLFAKA	50
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Pho L12	45	LEGVNIDEVIEKAA---MPVAVAAAPAAAPAEAGGEEKKEEEKKEEEEEKE	91
Bmo P1	51	LEGINVRDLITNIGSGVGAAPA---AGGAPAAAAAGAPAEKKEEKKEE	97
Scs P1A	49	LDGQNLKDLLVNF-S---AGAAAPAGVAGGVAGGEAGEAEAEKEEEE---E	91
Scs P1B	48	LEGKDLKEILSGFHN---AGPVAGAGAASGAAAAGGDAAAEEEEEKEE---E	91
Hsa P1	51	LAVNIGSLICNVGAG-GPAPAAGAAPAGGPAPSTAAAPAEKKEKVEAKKE	99
		* * * *	
Pho L12	92	E-EVSEEEALAGLSALFG	108
Bmo P1	98	EPEESDDDMGFG---LFD	112
Scs P1A	92	AKEESDDDMGFG---LFD	106
Scs P1B	92	AAEESDDDMGFG---LFD	106
Hsa P1	100	ESEESDDDMGFG---LFD	114
		. * . * * *	

B

Pho L12	1	MEYVYAALLLHSVGKEI-NEENLKAVLQAAGVEPEEARIKALVAALEGV-	48
Bmo P2	1	MRYVAAYLLAVLGGKTPAAADVEKILSSVGIEADAELKKKVVITELNGK-	49
Scs P2A	1	MKYLAAYLLLNAAAGNT-PDATKIKAILESVGIEIEDEKVSSVLSALEGK-	48
Scs P2B	1	MKYLAAYLLLQGGNAAPSAADIKAVVESVGAEVDEARINELLSLEGKG	50
Hsa P2	1	MRYVASYLALALGGNSSPSAKDIKKILDSVGIEADDDRLNKVISELNGK-	49
		* * . . . * . * * . * . . . *	
Pho L12	49	NIDEVIEK-----AAMP-----VAVAAAPAAAPAEAGGEEKKEEEKK	85
Bmo P2	50	DVEQLIAAGREKLSSMPVGGG-----APAAAAAAPAA-AAAEEKKEDKK	93
Scs P2A	49	SVDELITEGNEKLAAPVPA-----AGPASAGGAAAA-SGDAAAEEEEEKE	89
Scs P2B	51	SLEETIAEGQKKFATVPTGG-----ASSAAAGAAGAA-AGGDAAAEEEEEKE	93
Hsa P2	50	NIEDVIAQGIGKLVAPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEKK	99
		. . * * * *	
Pho L12	86	EEEEEEEEVSEEEALAGLSALFG	108
Bmo P2	94	EKKEDSE-SDDDMGFG---LFD	112
Scs P2A	90	EEAAE--E-SDDDMGFG---LFD	106
Scs P2B	94	EEAKE--E-SDDDMGFG---LFD	110
Hsa P2	100	EESEE---SDDDMGFG---LFD	115
		** . . * * *	

C

Eco L7/L12	1	MSITKDQIIEAVAAMSVMVVELISAMEEKFGVSAAAA VAVAAGPVEAAE	50
	51	EKTEFDVILKAAGANKVAVIKAVRGATGLGLKEAKDLVESAPAALKEGVS	100
	101	KDDAEALKKALEEAGAEVEVK	121

Figure S3

Pho L11	1	M-----KKQVVEVLVEGGKATPGPPLGPAIGPLGLNVKQVVDKI-NEA	42
Bmo eL12	1	MPPKFDPNKIKIVNLRVGGVEGATSSSLAPKIGPLGLSPKKVGGDI-AGA	49
Scs eL12	1	MPPKFDPNKIKVLYLRAVGGVEGASALAPKIGPLGLSPKKVGGDI-AGA	49
Hsa eL12	1	MPPKFDPNKIKVVYLRCTGGEVGSALAPKIGPLGLSPKKVGGDI-AGA	49
Eco L11	1	M----AKKVQAYVKLQVAAGMANPSPVGPALGQQGVNIMEFCKAFNAKT	46
	*.....*	
Pho L11	43	TKEFAGMQVPVKIIVDPVTKQFEIEV-GVPPTSQLIKKELGLEKGSGEPK	91
Bmo eL12	50	TSDWKGLKITVQLTVQ--NRQAQIAV--VPSAAALIIRALKEPPRDRKKQ	95
Scs eL12	50	TKEFKGKIVTVQLKIQ--NRQAAASV--VPSASSLVITALKEPPRDRKKD	95
Hsa eL12	50	TGDWKGLRITVKLTIQ--NRQAQIEV--VPSASALIICALKEPPRDRKKQ	95
Eco L11	47	DSIEKGLPIPVVITVY--ADRSFTFVTKTPPAAVLLKKA--AGIKSGSGK	92
		.*...*.....*.....*	
Pho L11	92	HNIV--GNLTMEQVIKIAKMKRSQMLALTLKAAAKEVIGTALSMGVTVEG	139
Bmo eL12	96	KNIKHNGNISLEDVVGIAKIMRNRSMARYLSGSVKEILGTAQSVGCTVEG	145
Scs eL12	96	KNVKHSGNIQLDEIIEIARQMRDKSFGRTLASVTKEILGTAQSVGCRVDF	145
Hsa eL12	96	KNIKHSGNITFDEIVNIARQMRHRSARELSGTIKEILGTAQSVGCNVDG	145
Eco L11	93	PNKDKVGGKISRQLQEIQAQTKAADMTGADIEAMTRSIEGTARSMGLVVED	142
		.*...*.....**.....***.*.*.*..	
Pho L11	140	KDPRIVQREIDEGVYDELFEKAEKE	164
Bmo eL12	146	RPPHDLIDDINSGALTIDE-----	164
Scs eL12	146	KNPHDIIEGINAGEIEIPEN-----	165
Hsa eL12	146	RHPHDIIDDINSGAVECPAS-----	165
Eco L11	142	-----	142
		

Figure S4