

Supplementary information, Table S3. Summary of model building for the human spliceosomal ILS complex.

	Molecule	Length	Domain/Region	PDB code	Modeling	Resolution (Å)	Chain ID
	Human/ <i>S.pombe</i> / <i>S.cere</i>						
U5 snRNP	U5 snRNA	117	3:116		HM	2.8~4.0	B
	Prp8/ <i>Spp42</i> / <i>Prp8</i>	2335	56:662/675:2026		HM	2.8~4.0	A
	Snu114/ <i>Cwf10</i> / <i>Snu114</i>	972	112:943	5XJC	HM	2.8~4.0	C
	U5-40K/ <i>Cwf17</i> /-	357	WD40 domain		HM	3.5~4.5	E
	SmB,D1,D2,D3,E,F,G	-	Sm fold		RD	4.0~8.0	a-g
U6 snRNP	U6 snRNA	107 nt	1:97	5XJC	HM	2.8~4.0	F
Pre-mRNA	Pre-mRNA	-	70 nt	5XJC	HM	2.8~4.5	G
U2 snRNP	U2 RNA	188 nt	1:47		HM	3.0~5.0	
			54:184	5XJC	RD	8~15.0	H
	U2-A'/ <i>Lea1</i> / <i>Lea1</i>	255	LRR domain	1A9N	RD	8~15.0	o
	U2-B''/ <i>Msl1</i> / <i>Msl1</i>	225	RRM domain	1A9N	RD	8~15.0	p
	SmB,D1,D2,D3,E,F,G	-	Sm fold	4WZJ	RD	8~15.0	h-n
Prp19/ Complex	Prp19	504	3:137		RD	4.5~7.0	q-t
	Syf1/ <i>Cwf3</i> / <i>Syf1</i>	855	1:800		RD	4.5~8.0	I
	Syf3/ <i>Cwf4</i> / <i>Clf1</i>	848	179:215		HM	2.8~4.0	
			TPR domain (216:446)		HM	3.0~4.0	J
			TPR domain (447:740)	5XJC	RD	4.5~8.0	
	Spf27/ <i>Cwf7</i> / <i>Snt309</i>	225	14:222		HM	4.5~8.0	K
	Cdc5/ <i>Cde5</i> / <i>Cef1</i>	802	Myb Domain (6:108)		HM	2.8~3.0	L
			130:270		HM	3.0~4.0	
			689:795		RD	4.5~8.0	
NTC Related proteins	Syf2	201	113:243		HM	2.8~3.5	M
	G10/ <i>Cwf14</i> / <i>Bud31</i>	144	1:144		HM	3.0~4.0	N
	RBM22/ <i>Cwf5</i> / <i>Cwf2</i>	420	19:303		HM	3.0~3.5	O
			/Ecm2/Cwc2				
	Ad-002/ <i>Cwf15</i> / <i>Cwc15</i>	229	2:78/188:229	5XJC	HM	2.8~3.5	P
	SKIP/ <i>Prp45</i> / <i>Prp45</i>	536	51:316		HM	3.0~4.0	R
	PPIL1	166	Cyclophilin domain(8:166)		HM	3.0~3.5	S
IBC protein	PRL1/ <i>Prp5</i> / <i>Prp46</i>	514	WD40 domain (184:496)		HM	3.0~3.5	T
Known Splicing Factors	Aquarius/ <i>Cwf11</i> /-	1485	19:1381	5XJC	RD	6.0~10.0	Q
	CypE/-/-	301	RRM domain (6:84)	3MDF	RD	8.0~10.0	y
	Prp17	579	83:273		HM	3.0~4.0	
			(ILS1)WD40 domain (274:576)	5XJC	HM	4.0~5.0	W
	Cwf19L2/	894	536:894	3JB9	HM	3.0~4.0	U
	Prp43(ILS2)	795		5XDR	RD	15.0~20.0	V

Under the column labeled “Molecule”, proteins from human, *S. pombe*, and *S. cerevisiae* are colored black, red, and green, respectively. If the proteins from all three species have the same name, only a single name in black is indicated. Under the column labeled “Modeling”, HM stands for homology modelling; RD stands for rigid docking and refinement.