

Table S3. Summary of model building for the human spliceosomal B 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	3.0~5.0	B
	Prp8/ <i>Spp42</i> /Prp8	2335	56:662/675:2026/2067:2335		HM	3.0~5.0	A
	Snu114/ <i>Cwf10</i> /Snu114	972	112:943	5XJC	HM	3.0~5.0	C
	Brr2	2136	404:2125		RD	4.5~9.0	D
	U5-40K/ <i>Cwf17</i> /-	357	WD40 domain		RD	8.0~10.0	E
	Dim1/ <i>Dim1</i> / <i>Dib1</i>	142	Thioredoxin-like	1QGV	HM	3.0~4.0	O
	SmB,D1,D2,D3,E,F,G	-	Sm fold	5XJC	RD	6.0~15.0	a-g
U6 snRNP	U6 snRNA	107 nt	1:97	5O9Z/5XJC	HM	3.0~4.5	F
	Lsm2-8	-	Sm fold	4M7A	RD	10.0~30.0	q-t, x-z
Pre-mRNA	Pre-mRNA	274 nt	76 nt	5XJC	HM	3.5~6.0	G
U4 snRNP	U4 snRNA	144 nt	1:145	3JCM/5O9Z	HM	3.0~8.0	I
	SmB,D1,D2,D3,E,F,G	-	Sm fold	5O9Z	RD	5.0~8.0	P-V
U2 snRNP	U2 RNA	188 nt	3:14/30:81/97:184	5XJC	RD	4.0~20.0	H
	U2-A'/ <i>Lea1</i> / <i>Lea1</i>	255	LRR domain	1A9N	RD	8.0~20.0	o
	U2-B'/ <i>Msl1</i> / <i>Msl1</i>	225	RRM domain	1A9N	RD	8.0~20.0	p
	SmB,D1,D2,D3,E,F,G	-	Sm fold	4WZJ	RD	8.0~20.0	h-n
	SF3a120/ <i>Sap114</i> /Prp21	793	160:294		RD	20.0~30.0	u
	SF3a66/ <i>Sap62</i> /Prp11	464	92:233	4DGW	RD	20.0~30.0	v
	SF3a60/ <i>Sap61</i> /Prp9	501	1:374/390:463/480:499		RD	20.0~30.0	w
	SF3b155/ <i>Sap155</i> / <i>Hsh155</i>	1304	HEAT repeat	5IFE	RD	10.0~20.0	l
	SF3b145/ <i>Sap145</i> / <i>Cus1</i>	895	461:600/604:692	5GM6	HM	10.0~20.0	2
	SF3b130/ <i>Sap130</i> / <i>Rse1</i>	1217	WD40 domain I/II/III	5IFE	RD	10.0~20.0	3
	SF3b49/ <i>Sap49</i> / <i>Hsh49</i>	424	RRM domain I/II	5LSB	RD	10.0~20.0	4
	SF3b14a/ <i>p14-like</i> /-	125	RRM domain	5IFE	RD	10.0~20.0	5
	SF3b14b/ <i>Ini1</i> / <i>Rds3</i>	110	PHF5 domain	5IFE	RD	10.0~20.0	6
	SF3b10/ <i>SF3b10</i> / <i>Ysf3</i>	86	15:80	5IFE	RD	10.0~20.0	7
Tri-snRNP specific proteins	Prp3	683	Ferredoxin-like domain		HM	3.0~5.0	J
	Prp4/ <i>Cwf3</i> / <i>Syfl</i>	522	WD40 domain		RD	3.0~5.0	K
	Prp31/ <i>Cwf7</i> / <i>Snt309</i>	499	Nop domain 52:432	3JCM	HM	3.0~5.0	L
	Snu13/ <i>Cdc5</i> / <i>Cef1</i>	128	5:128		HM	3.0~4.0	M
	Prp6/ <i>Cwf4</i> / <i>Cif1</i>	941	NTD; TPR repeat		HM	3.0~8.0	N
B specific	CypH/ <i>CypH</i> /-	177	Cyclophilin domain		RD	5.0~8.0	W
	FBP21/-/-	376	8:82	5O9Z	RD	4.0~6.0	X
	Smu1/-/-	513	WD40 domain		RD	4.0~6.0	Y
	Prp38	312	1:176	5F5S	RD	5.0~8.0	Z
	MFAP1/-/ <i>Spp381</i>	439	270:314		RD	5.0~8.0	0
	Snu23	199	79:134	5O9Z	RD	5.0~8.0	8
	Snu66	800	117:131/148:214/250:358	5NRL/5O9Z/4PYU	HM	4.0~6.0	9
	UBL5/-/ <i>Hub1</i>	73	Ubiquitin like domain	4PYU	RD	4.0~6.0	A0

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.