

**Table S2.** Summary of model building for the human spliceosomal B<sup>act</sup> complex.

	Molecule	State			Length	Domain/Region	PDB code	Modeling	Resolution (Å)	Chain ID
	Human/ <i>S.pombe</i> / <i>S.cere</i>	early	mature	late						
U5 snRNP	U5 snRNA	✓	✓	✓	117	8:71/85:104		RD	4.0~5.0	B
	Prp8/ <i>Spp42</i> / <i>Prp8</i>	✓	✓	✓	2335	25:2335		RD	4.0~5.0	A
	Snu114/ <i>Cwf10</i> / <i>Snu114</i>	✓	✓	✓	972	54:943	5XJC	RD	4.0~5.0	C
	Brr2	✓	✓	✓	2136	404:2125		RD	4.0~9.0	D
	U5-40K/ <i>Cwf17</i> /-	✓	✓	✓	357	WD40 domain		RD	4.0~6.0	E
	SmB,D1,D2,D3,E,F,G	✓	✓	✓	-	Sm fold		RD	6.0~15.0	a-g
U6 snRNP	U6 snRNA	✓	✓	✓	107 nt	1:97	5XJC	RD	3.8~4.5	F
Pre-mRNA	Pre-mRNA	✓	✓	✓	-	59 nt	5XJC	RD	4.0~6.0	G
U2 snRNP	U2 RNA	✓	✓	✓	188 nt	1:47/54:184	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> / <i>Prp21</i>	✓	✓	✓	793	SURP1/2,-		RD	20.0~30.0	u
	SF3a66/ <i>Sap62</i> / <i>Prp11</i>	✓	✓	✓	464	ZF,-	4DGW	RD	20.0~30.0	v
	SF3a60/ <i>Sap61</i> / <i>Prp9</i>	✓	✓	✓	501	-		RD	20.0~30.0	w
	SF3b155/ <i>Sap155</i> / <i>Hsh155</i>	✓	✓	✓	1307	HEAT repeat	5IFE	RD	3.8~4.5	1
	SF3b145/ <i>Sap145</i> / <i>Cus1</i>	✓	✓	✓	895	-	5GM6	HM	3.8~4.5	2
	SF3b130/ <i>Sap130</i> / <i>Rse1</i>	✓	✓	✓	1217	WD40 domain I/II/III	5IFE	RD	3.8~4.5	3
	SF3b49/ <i>Sap49</i> / <i>Hsh49</i>	✓	✓	✓	424	RRM domain I/II	5LSB	RD	6.0~15.0	4
SF3b14a/ <i>p14-like</i> /-	✓	✓	✓	125	RRM domain	5IFE	RD	3.8~4.5	5	
SF3b14b/ <i>Ini1</i> / <i>Rds3</i>	✓	✓	✓	110	PHF5 domain	5IFE	RD	3.8~4.5	6	
SF3b10/ <i>SF3b10</i> / <i>Ysf3</i>	✓	✓	✓	86	-	5IFE	RD	3.8~4.5	7	
NTC/ Prp19 Complex	Prp19	X	✓	✓	504	3:137		RD	6.0~15.0	q-t
	Syf1/ <i>Cwf3</i> / <i>Syf1</i>	X	✓	✓	855	TPR repeat		RD	6.0~15.0	I
	Syf3/ <i>Cwf4</i> / <i>Chf1</i>	✓	✓	✓	848	TPR repeat	5XJC	RD	5.0~15.0	J
	Spf27/ <i>Cwf7</i> / <i>Snt309</i>	X	✓	✓	225	14:222		RD	6.0~15.0	K
	Cdc5/ <i>Cdc5</i> / <i>Cef1</i>	✓	✓	✓	802	Myb domain/-	5XJC	RD	4.0~15.0	L
NTC Related proteins	G10/ <i>Cwf14</i> / <i>Bud31</i>	X	✓	✓	144	1:144		RD	4.0~6.0	N
	RBM22/ <i>Cwf5</i> / <i>Cwf2</i> / <i>Ecm2</i> / <i>Cwc2</i>	X	✓	✓	420	19:303		RD	4.0~6.0	O
	Ad002/ <i>Cwf15</i> / <i>Cwc15</i>	✓	✓	✓	229	2:78/188:229	5XJC	RD	4.0~6.0	P
	Skip/ <i>Prp45</i> / <i>Prp45</i>	✓	✓	✓	536	51:316		RD	4.0~6.0	R
	Pr11/ <i>Prp5</i> / <i>Prp46</i>	✓	✓	✓	514	WD40 domain		RD	4.0~6.0	T
IBC protein	Aquarius/ <i>Cwf11</i> /-	X	✓	✓	1485	19:1381	5XJC	RD	7.0~15.0	Q
Known Splicing Factors	Prp2	✓	✓	✓	1061	ATP-dependent RNA helicase	5GM6	RD	8.0~15.0	S
	RNF113A/ <i>Cwf24</i> / <i>Cwc24</i>	✓	✓	X	343	ZF	5XJC	HM	4.0~6.0	M
	SRm300/ <i>Cwf21</i> / <i>Cwc21</i>	X	✓	✓	2296	1:26		RD	4.0~5.0	U
	Cwc22/ <i>Cwf22</i> / <i>Cwc22</i>	✓	✓	✓	908	MIF4G/ MA3		RD	4.0~10.0	V
Step II factors	Prp17	X	✓	✓	579	NTD (83:273);WD40 (274:576)	5XJC	RD	5.0~7.0	W
RES complex	SNIP1/-/ <i>Pml1</i>	✓	✓	✓	396	FHA domain		RD	4.0~6.0	X
	RBMX2/ <i>Cwf29</i> / <i>Snu17</i>	✓	✓	✓	322	RRM domain	5GM6	RD	4.0~6.0	Y
	Bud13/ <i>Cwf26</i> / <i>Bud13</i>	✓	✓	✓	619	-		RD	4.0~8.0	Z
PPI proteins	PPIL1/ <i>Cyp1</i> /-	✓	✓	✓	166	PPI domain	5XJC	RD	4.5~8.0	x
	CypE/-/-	X	✓	✓	301	RRM/PPI domain	3MDF/2R99	RD	8.0~15.0	y
	NY-CO- 10/ <i>Cyp7</i> / <i>Cwc27</i>	✓	✓	X	472	PPI domain	4R3E	RD	5.0~8.0	z

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.