

**Table S2. Summary of model building for the human spliceosomal pre-B complex.**

|                                            | Molecule<br>Human/ <i>S.pombe</i> / <i>S.cere</i> | Length | Domain/Region              | PDB<br>code | Modeling | Resolution<br>(Å) | Chain<br>ID |
|--------------------------------------------|---------------------------------------------------|--------|----------------------------|-------------|----------|-------------------|-------------|
| <b>U5 snRNP</b>                            | U5 snRNA                                          | 117    | 3:116                      |             | HM       | 4.0~5.0           | B           |
|                                            | Prp8/ <i>Spp42</i> / <i>Prp8</i>                  | 2335   | 56:662/675:2026/2067:2335  |             | HM       | 4.0~5.0           | A           |
|                                            | Snu114/ <i>Cwf10</i> / <i>Snu114</i>              | 972    | 112:943                    | From        | HM       | 4.0~5.0           | C           |
|                                            | Brr2                                              | 2136   | 404:2125                   | B           | RD       | 6.0~9.0           | 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           |             | HM       | 4.0~6.0           | O           |
|                                            | SmB,D1,D2,D3,E,F,G                                | -      | Sm fold                    |             | RD       | 6.0~15.0          | a-g         |
| <b>U6 snRNP</b>                            | U6 snRNA                                          | 107 nt | 1:97                       | From        | RD       | 4.0~6.0           | F           |
|                                            | Lsm2-8                                            | -      | Sm fold                    | B           | RD       | 9.0~20.0          | q-t, x-z    |
| <b>Pre-mRNA</b>                            | Pre-mRNA                                          | -      | 59 nt                      | 5XJC        | RD       | 4.0~6.0           | G           |
| <b>U4 snRNP</b>                            | U4 snRNA                                          | 144 nt | 1:145                      | From        | HM       | 4.0~8.0           | I           |
|                                            | SmB,D1,D2,D3,E,F,G                                | -      | Sm fold                    | B           | RD       | 5.0~8.0           | P-V         |
| <b>U2 snRNP</b>                            | U2 RNA                                            | 188 nt | 1:47/54:184                | 5XJC        | RD       | 8.0~20.0          | H           |
|                                            | U2-A'/ <i>Lea1</i> / <i>Lea1</i>                  | 255    | LRR domain                 | 1A9N        | RD       | 20.0~30.0         | o           |
|                                            | U2-B'/ <i>Msl1</i> / <i>Msl1</i>                  | 225    | RRM domain                 | 1A9N        | RD       | 20.0~30.0         | p           |
|                                            | SmB,D1,D2,D3,E,F,G                                | -      | Sm fold                    | 4WZJ        | RD       | 20.0~30.0         | h-n         |
|                                            | SF3a120/ <i>Sap114</i> / <i>Prp21</i>             | 793    | 160:294                    |             | RD       | 20.0~30.0         | u           |
|                                            | SF3a66/ <i>Sap62</i> / <i>Prp11</i>               | 464    | 92:233                     | 4DGW        | RD       | 20.0~30.0         | v           |
|                                            | SF3a60/ <i>Sap61</i> / <i>Prp9</i>                | 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         | 1           |
|                                            | SF3b145/ <i>Sap145</i> / <i>Cus1</i>              | 895    | 461:600/604:692            | 5GM6        | RD       | 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           |
| <b>Tri-snRNP<br/>specific<br/>proteins</b> | Prp3                                              | 683    | Ferredoxin-like domain     |             | RD       | 4.0~8.0           | J           |
|                                            | Prp4/ <i>Cwf3</i> / <i>Syfl</i>                   | 522    | WD40 domain                | From        | RD       | 4.0~8.0           | K           |
|                                            | Prp31/ <i>Cwf7</i> / <i>Snt309</i>                | 499    | Nop domain 52:432          | B           | RD       | 4.0~8.0           | L           |
|                                            | Snu13/ <i>Cdc5</i> / <i>Cefl</i>                  | 128    | 5:128                      |             | RD       | 4.0~8.0           | M           |
|                                            | Prp6/ <i>Cwf4</i> / <i>Cifl</i>                   | 941    | NTD; TPR repeat            |             | RD       | 4.0~8.0           | N           |
| <b>ATPase/Helicase</b>                     | Sad1/Ubp10/Sad1                                   | 565    | 103:565                    | 4MSX        | RD       | 4.0~8.0           | W           |
| <b>U1 snRNP</b>                            | Prp28                                             | 1061   | ATP-dependent RNA helicase | 4NHO        | RD       | 6.0~15.0          | X           |
|                                            | U1 snRNP molecules                                | -      | -                          | 5UZ5        | RD       | 20.0~40.0         | -           |

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.