

Supplemental Data

Structural Biology of RNA Polymerase III:

Subcomplex C17/25 X-ray Structure

and 11 Subunit Enzyme Model

Anna J. Jasiak, Karim-Jean Armache, Birgit Martens, Ralf-Peter Jansen, and Patrick Cramer

Figure S1. Structure-guided sequence alignments of core subunits

Sequences of Pol II subunits Rpb1, Rpb2, Rpb3, Rpb11 were aligned, guided by the Pol II structural context, with homologous subunits in Pol III (compare text). Regions of conserved fold as detected by inspection in the three-dimensional context are underlined and colored in orange.

Rpb1-C160 (Rpc1)

sp|P04050|RPB1_YEAST MVGQQYSSAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMETQTRAKIG-GLNDPRLG 59
sp|P04051|RPC1_YEAST -MKEVVVSETPKRIKGLEFSALSAAIDVAQSEVEVSTRDLDFLEKDRAPKANGALDPKMG 59
: : * . : : * : * . : * * . : : : * : * * . * * : * :

sp|P04050|RPB1_YEAST SIDRNLCQTCQEGMNECPGHFGHIDLAKVPFVHGFIAKIKKVCECVMHCGLLLEHN 119
sp|P04051|RPC1_YEAST VSSSLECATCHGNLASCHGHFGLKALPVPFHIGYFKATIQLQGICKNCSAILLSETD 119
. . * : * * * : . : . * * * * : . * * * * : : : : : * : * . : * * . * :

sp|P04050|RPB1_YEAST -----ELMRQALAIKDSKKRFAAIWTLCKTKMVCETDVPSEDDPTQLVSRGGCGNTQPT 173
sp|P04051|RPC1_YEAST KRQFLHELRRPGVDNLRMRGILKILDDQCKKQRRCLHCGALNG--VVKAAAGAGSAALK 177
* * * . : : * * * : * . : . . . : . * . * : .

sp|P04050|RPB1_YEAST IRKDGLKLVG-----SWKKDRATGDAPELIR-----VLSTEEILNIFKHISVK 217
sp|P04051|RPC1_YEAST I IHDTFRWVGKKSAPKEDIWVGEWKEVLAHNPELERYVVKRCMDLLNPLKTLNLFKQIKSA 237
* : * : * * * : * : * : * * * . * . : * * * * : *

sp|P04050|RPB1_YEAST DFTSLGFNEVFS--RPEWMILTCLPVPVPPVVRPSISFNES--QRGEDDLTFKLADILKANI 274
sp|P04051|RPC1_YEAST DCELLGIDATVPSGRPETYIWRYPAPPVCIRPSVMMQDPSANEDDLTVKLEIIVTSS 297
* * * : . . . * * * * * * * : * * * : * * * . * * * * * : * * : .

sp|P04050|RPB1_YEAST SLETLEHNGAPHHAIEEAESLLQPHVATYMDNDIAGQPQALQKSG---RPVKSIRARL 329
sp|P04051|RPC1_YEAST LIKAGLDKGISINMMEHWDYLLQTVAMYINSDSVNPAMLPGSSNGGGKVKPIRGFCQRL 357
: : * . : * : * . * * : * * * : * . . . * . : * : * : * *

sp|P04050|RPB1_YEAST KGKEGRIRGNLMGKRVDFSARTVISGDPNLELDQVGVPKSIAKTLTYPEVVTPYNIDRLT 389
sp|P04051|RPC1_YEAST KGKQGRFRGNLSGKRVDFSRTVISDPNLSIDEVAVPDRVAKVLTYPEKVTYRNRHKLQ 417
* * * : * * * * * * * * * * * * * * * * * * : * : * * * . : * * * * * * * * * * * * : *

sp|P04050|RPB1_YEAST QLVRNGPNEHPGAKYVIR-DSGDRIDLRYSKRAGDIQ-LQYGWKVERHIMDNDPVLFNRO 447
sp|P04051|RPC1_YEAST ELIVNGPNVHPGANLYLKRNEDARRNLRYGDRMKLAKNLQIGDVVERHLEDGVDVLFNRO 477
: * : * * * * * * * : : : . . * : * * * . * : * * * * * * * : * * * * * * * :

sp|P04050|RPB1_YEAST PSLHKMSMAHRVKVIPYSTFRNLNSVTSPYNADFDGDEMNLHVPQSEETRAELSOLCAV 507
sp|P04051|RPC1_YEAST PSLHRLSILSHYAKIRPWRTRFRLNECVCTPYNADFDGDEMNLHVPQTEEARAEAINLMGV 537
* * * : : * : * * . * : * * * * * * * * * * * * * * * * * * : * . *

sp|P04050|RPB1_YEAST PLQIVSPQSNKPCMGIVQDTLCGIRKTLRDTFIELDQVLNMLYWVPD--WDGVIPTPAI 565
sp|P04051|RPC1_YEAST KNNLTPKSGEPIIAATQDFITGYSYLISHKDSFYDRATLTQLLSMMSDGIEHFDIPPAI 597
: : * : * * : . . * * : * : * * : : * * : * . * * * * :

sp|P04050|RPB1_YEAST IKPKPLWSGKQILSVAIP--NGIHLQRFDEGTTLLSP-----KDNGMLIIDG- 610
sp|P04051|RPC1_YEAST MKPYLWTKGQVFSLLIKPNHNSPVVINLDAKNKVFVPPKSKSLPNEMSQNDGFVIIRGS 657
: * * * * * * * : * * . : : * . : : * : * * * * * * * : * * * * * * *

sp P04050 RPB1_YEAST	<u>QIFGVVEKKTVGSSN-GGLIHVVTREKGPQVCAKLFGNIQKVVFLLHNGFSTGIGDT</u>	669
sp P04051 RPC1_YEAST	<u>QILSGVMDKSVLGDGKHKHSVFYTTILRDYGPQEAANAMNRMAKLCARFLGNGRFGFSIGINDV</u>	717
	** : *** : * . . * . . : . : : : : * : ** * . * : . . : * : : * : . * * * * . * .	
sp P04050 RPB1_YEAST	<u>IADGPTMREITETIAEAKKKVLDVTKEAQANLLTAKHGMLRESFEDNVVRFLENEARDKA</u>	729
sp P04051 RPC1_YEAST	<u>TPADDLKQKKEELVEIAYHKCDELITLFLNKGELETQPGCNEEQTLEAKIGLLSKVREEV</u>	777
	. . . : : * : * : * * : : . : . * : : * . . : : : * : : : * : : . * : : .	
sp P04050 RPB1_YEAST	<u>GRLAEVNLKDLNNVKQMVMAGSKGSFINIAQMSACVQQSVEGKRIAFGFVDRTLPHFSK</u>	789
sp P04051 RPC1_YEAST	<u>GDVCINELDNWNAPLIMATCGSKGSTLNVSQMVAVVGQIIISGNRVPDGFQDRSLPHFPK</u>	837
	* . . : * . : * . . * * * * . * : : * * * * * * * : . * : . * * * : * * * * . *	
sp P04050 RPB1_YEAST	<u>DDYSPESKGFVENSYLRLTPQEFFFHAMGGREGLIDTAVKTAETGYIQRLVKALEDIM</u>	849
sp P04051 RPC1_YEAST	<u>NSKTPQSKGFVRSFFSGLSPPEFLFHAISGREGLVDTAVKTAETGYMSRRLMKSLEDLS</u>	897
	: . : * : * * * * . * * : * : * * * * * : *	
sp P04050 RPB1_YEAST	<u>VHYDNTTRNSLGNVIQFIYGEDGMDAAHIEKQSLDITIGGSDAAFEKRYRVDLLNTDHTLD</u>	909
sp P04051 RPC1_YEAST	<u>CQYDNTVRTSANGIVQFTYGGDGLDPLEMEGNAQPVN--FNRSWDHAYNITFNNQDKGLL</u>	955
	: * * * * . * . * . : : * * * * * . . * : : . . . : : : : * . : : * * : *	
sp P04050 RPB1_YEAST	P-S <u>LLESGESEILGDLKQLVLLDEEYKQLVKDRKFLREVFVDGEANWLPVNIRRIQNAQ</u>	968
sp P04051 RPC1_YEAST	<u>PYAIMETANEILGPLEERLVRYDMSGCLVKREDLNKAEYVD-----QYDAERDFYHSR</u>	996
	* : : : : . * * * * * * : : : : : * * * * . . . : : * *	
sp P04050 RPB1_YEAST	<u>QTFHIDHTKPSDLTIKDIVLGVKDLQENLLVLRGKNEIIQNAQRDAVTLFCCLLRSRLAT</u>	1028
sp P04051 RPC1_YEAST	<u>EYIN-----GKATALANLRKSRGLGELLEPPAKELQGIIDPDETVPDNVK</u>	1053
	* * * * * * * * * * : : : . : : : : . . .	
sp P04050 RPB1_YEAST	<u>RRVLQEQYRLTKQAFDVLVSNIEAQFLRSVHPGEMVGLAAQSIGEPATQMTLNTFHFAG</u>	1088
sp P04051 RPC1_YEAST	<u>TSVSQLYRISEKSVRKFLEIALFKYRKARLEPGTAIGAIGAQSIGEPGTQMTLKTFFHAG</u>	1113
	* * * * : : : : . . * . . : : : : * * : . : * * * * * . * * * * * * * * * *	
sp P04050 RPB1_YEAST	<u>VASKKVTSQVPRKEIILNVAKNMKTPSLTVYLEPGHAADQEQAKLIRSAIEHTTLKSVTI</u>	1148
sp P04051 RPC1_YEAST	<u>VASMNVTLGVPRIKEIINASKVISTPIINAVLVN--DNDEARAARVVKGRVEKTLSDVAF</u>	1171
	* * * * * * * * * * * * * : * * * * . . * . . * : . * * : : : . : * * * * . * : : :	
sp P04050 RPB1_YEAST	<u>ASEIYYDPDRSTVIPLEDEEIIQLHFSLLDDEEAEQSFDQQSPWLLRLELDRAAMNDKDLT</u>	1208
sp P04051 RPC1_YEAST	<u>YVQDVYKDN-----LSFIQVRIDLGTIDKQLQELTIEDIA</u>	1206
	: * . . : : : . . : . * * * * * * : : : : . : * :	
sp P04050 RPB1_YEAST	<u>MGQVGERIKQTFKNDLFIWSEDNDEKLIIRCVRVVRPKSLDAETEAEEDHMLKKIEN-TM</u>	1267
sp P04051 RPC1_YEAST	<u>VAITRASKLKIQASDVNIIGKDRIAIVFPEGYKAKSISTSACEPSENDFVFYRMQQLRRA</u>	1266
	: . . : : * : * : : : : . . . * . * : * * * : : : :	

sp|P04050|RPB1_YEAST LENITLRGVENIERVVMKYDRKVPSPTEGYVKEPEWVLETDGVNLSEVMTVPGIDPTRI 1327
sp|P04051|RPC1_YEAST LPDVVVVGLPDISRAVINIRD-----DGKRELLVEGYGLRDVMTDGVIGSRT 1314
* :.:.*: :*.*.*: * . :.:. . : : * .:* .* :** . * : *

sp|P04050|RPB1_YEAST YTNSFIDIMEVLGIEAGRAALYKEVYVNIASDGSYVNYRHMALLVDVMTTQGGLTSTVRH 1387
sp|P04051|RPC1_YEAST TTNHVLEVFVSLGIEAARYSIIREINYTMSNHGMSVDPRIQLLGDVMTYKGEVLGITRF 1374
** .:.:.*:**.* : :*: .:.* * : **: ** ***** :* : .:***.

sp|P04050|RPB1_YEAST GFNRSNTGALMRCSEETVEILFEAGASAELEDDCRGVSENVILGQMAPIGTGAFDVMIDE 1447
sp|P04051|RPC1_YEAST GLSKMRDVLQLASFEKTTDHLFDAAFYMKKDAVEGVSECIILGQTMSIGTGSFKVVKG- 1433
*.:. . . * .***:*. : **:* . : * .**** :**** .****:*. : ..

sp|P04050|RPB1_YEAST ESLVKYMPEQKITEIEDGQDGGVTPYSNESGLVNADLDVKDELMSPLVDSGSNDAMAGG 1507
sp|P04051|RPC1_YEAST -----TNISEKDLVPKRCLFESLSNEAALKA 1459
. : : : . : . . . : : . : . ** : * .:* **:* .

sp|P04050|RPB1_YEAST FTAYGGADYGEATSPFGAYGEAPTSPGFGVSSPGFSPTSPTYSPTSPTSPTSPTS 1567
sp|P04051|RPC1_YEAST NCLUSTAL----- 1467
. * .:.:. . : .:.:. . : .:.. :.:. :.:. :.:. :.:. :.:.

Rpb2-C128 (Rpc2)

sp|P08518|RPB2_YEAST ---MSDLANSEKYYDEDPYGFEDESAPI-----TAEDSWAVISAFFREKGLVSQ 46
sp|P22276|RPC2_YEAST MVAATKRKRKTHIHKHVKDEAFDILLKPVYKGGKLTDEINTAQDKWHLLPAPFLKVKGLVKQ 60
: . : : : . . . : * * : * : * : * : *

sp|P08518|RPB2_YEAST QLDSFNQFVDYTLQDIICEDSTLILEQLAQHTTESDNISRKYEISFGKIYVTKPMVNESD 106
sp|P22276|RPC2_YEAST HLDSFNYPVDTLKKIIKAN-----QLILSDVDPEFYLYVDIRVGGKSSSS 107
: * * * * * * : * : * : * : * : * : * : *

sp|P08518|RPB2_YEAST GVTHALYPQEARLRNLTYSSGLFVDVKKRTYEAIIDVPGRELKYELIAEESDDESSESGKVF 166
sp|P22276|RPC2_YEAST TKDYLTPHECLRDMTYSSAPIYDIEYTR-----GR----NIIMHKD-----VE 148
: * : * : * : * : * : * : * : * : * : *

sp|P08518|RPB2_YEAST IGRLPIMLRSKNCYLSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF 226
sp|P22276|RPC2_YEAST IGRMPIMLRSNKCILYDADESKMAKLNECPLDPGGYFIVNGTEKVLVQEQLSKNRIIVE 208
* * * * * * : * : * : * : * : * : * : * : * : * : *

sp|P08518|RPB2_YEAST KKAAPSPISHVAEIRSALEKGSRFISTLQVKLYGREGSSARTIKATLPYIKQDIPIVIIF 286
sp|P22276|RPC2_YEAST ADEK---GIVQASVTSS--THERKSKTYVITKNGK-----TYLKHNSIAEEIPIAIVL 257
: . . * * * * * : * : * : * : * : * : *

sp|P08518|RPB2_YEAST RALGIIPDGEILEHICYDNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKE 346
sp|P22276|RPC2_YEAST KACGILSDLEIMQLVCGNDSSYQDIFAVNLEESSKLDIYTQQALEYIGAKVKTMRRQKL 317
: * * : * : * : * : * : * : * : * : * : * : *

sp|P08518|RPB2_YEAST KRIQYAKDILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRL 406
sp|P22276|RPC2_YEAST TILQEGIEAIATTVIAHLTVEALDFREKALYIAMMTRRVVMAMYNPKMIDDRDYVGNKRL 377
: * : * : * : * : * : * : * : * : * : *

sp|P08518|RPB2_YEAST DLAGPLLAQLFKTLFKKLTKDIFRYMQRTVEEAH---DFNMKLAINAKT--ITSGLKYAL 461
sp|P22276|RPC2_YEAST ELAGQLISLLFEDLFKKFNNDFKLSIDKVLKKNRAMEYDALLSINVHSNNITSGLNRAI 437
: * * : * : * : * : * : * : * : * : * : * : *

sp|P08518|RPB2_YEAST ATGNWGEQKKAMSSRAGVSVQLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGL 521
sp|P22276|RPC2_YEAST STGNWS-LKRFKMERAGVTHVLSRLSYISALGMMTRISSQFEKSRKVSGPRALQPSQFGM 496
: * * : * : * : * : * : * : * : * : * : * : *

sp|P08518|RPB2_YEAST VCPAETPEGQACGLVKNLSLMSCISVGTDPMPITFLSEWGMPELEDYVPHQSPDATRVF 581
sp|P22276|RPC2_YEAST LCTADTPEGEACGLVKNLALMTHITTDDEEPIKKLCYVLGVEDITLIDSASLHLNYGVY 556
: * : * : * : * : * : * : * : * : * : *

sp|P08518|RPB2_YEAST VNGVWHGVHRNPARLMETLRLTRRRKGDINPEVSMIRDIREKELKIFTDAGRVRPLPFIVE 641
 sp|P22276|RPC2_YEAST LNGLTIGSIRFPFKFVTQFRHLRRTGKVSEFISISYNSHQMAVHIATDGGRICRPLIIVS 616
 :*. * * *::: :* **.*.:. :*: : : : :* **.*: **:*

sp|P08518|RPB2_YEAST DDESLGHKELKVRKGGHIAKLMATEYQDIEGGFEDVEEYTWSSLLNEGLVEYIDAEEEEESI 701
 sp|P22276|RPC2_YEAST DGQSR-----VKDIHLRKLDD-----GELDFDDFLKGLVEYLDVNEENDS 657
 .: *.: *:* **:* * :.:*: ******.:**:.

sp|P08518|RPB2_YEAST LIAMQPEDLEPAEANEENDLDVDPAKRIRVSHHATTFTHCEIHPSMILGVAASIIIPFDH 761
 sp|P22276|RPC2_YEAST YIALLYEKDIVP-----SMTHLEIEPFTIILGAVAGLIPYPHH 693
 : .*: * : **.* **.*.:**:*

sp|P08518|RPB2_YEAST NQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMANILYYPQKPLGTTRAMEYLFKRELPAQO 821
 sp|P22276|RPC2_YEAST NQSPRNTYQCAMGKQAI GAIAYNQFKRIDTLLYLMTYPQQPMVKTKTIELIDYDKLPAGQ 753
 *****.*:.* * :***: : :***: :.:** :. :*****

sp|P08518|RPB2_YEAST NAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQEKYGMSITETFEKPQRTN 881
 sp|P22276|RPC2_YEAST NATVAVMSYSGYDIEDALVLNKSSIDRGFRCETRKRKTTTLKRYANHTQDIIGG-MRVD 812
 ** *: .****: **:::*.*****: * . * . *:* : : *.:

sp|P08518|RPB2_YEAST TLRMKHGTYDKLDDGLIAPGVRVSGEDVIIGKTPIS-PDEEELGQRTAYHSKRDASTP 940
 sp|P22276|RPC2_YEAST ENGDPiWQHQSLGPDGLGEVGMKVQSGQIYINKSVPINSADAPNPNVNVQTYREAPVI 872
 :.:* .*** *.:*.. : :*.*.* . .* : : . . *:*..

sp|P08518|RPB2_YEAST LRSTENGIVDQVLVTINQDGLKFKVVRVTRTKIPQIGDKFASRHGQKGTIGITYRREDMP 1000
 sp|P22276|RPC2_YEAST YRGPESHIDQVMMSVSDNDQALIKVLLRQNRPELGDKFSRRHGQKGVCGIIVKQEDMP 932
 .. . :***:~:~:~: :**:* . : :*****:*****. ** :****

sp|P08518|RPB2_YEAST FTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFDTITVEGISKLLR 1060
 sp|P22276|RPC2_YEAST FNDQGIVPDIIMNPHGFPSRMTVGKMIELISGKAGVLNGTLEYGTCFPGSKLEDMSKILV 992
 * . :*****:***:~:~:~: :** : *..*.* . : * . :*.:**:*

sp|P08518|RPB2_YEAST EHGYQSRGFVEMYNGHTGKKLMAQIFFGPTYQRLRHMVDDKI HARARGPMQVLRQPVE 1120
 sp|P22276|RPC2_YEAST DQGFNYSGKDMLYSGITGECLQAYIFFGPIYYQKLMVLDKMHARARGPRAVLTRQPT 1052
 :~:~:~: * :~:~:~: * * * ***** **:*:*** **:****** *****.*

sp|P08518|RPB2_YEAST GRSRDGGRLRFGEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMTVIAKLNHNQF 1180
 sp|P22276|RPC2_YEAST GRSRDGGRLRFGEMERDCVIAYGASQLLLERLMISSDAFEVDVCDKCGLMGYSG----- 1105
 *****:*****:~:~:~: :* ** * :***.*.:. **** .

sp|P08518|RPB2_YEAST ECKGCDNKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF 1224
 sp|P22276|RPC2_YEAST WCTTCKSAENI IKMTIPYAAKLLFQELLSMNIAPRLRLLEDIFQQ 1149
 * . * . :* : : *****:~:~:~: : * :

Rpb11-AC19 (Rpc9)

```
sp|P38902|RPBY_YEAST -----MNAPDRFELFLLGEGES-----KLKIDPDTKAPNA 30
sp|P28000|RPC9_YEAST MTEDIEQKKTATEVTPQEPKHIQEEEEQDVTGDEEQEEEPDREKIKLQTQATSEDGTS 60
:: :. :: : * : * . ** :. :: . :
```

```
sp|P38902|RPBY_YEAST VVITFEKEDHTLGNLIRAEELNDRKVLFAAYKVEHPFFARFKLRIQTTEGYDPKDALKNA 90
sp|P28000|RPC9_YEAST ASFQIVEEDHTLGNALRYVIMKNPDVEFCGYSIPHPSENLLNIRIQTYGETTAVDALQKG 120
. : : :***** : * : : : . * * . * . : * * : :***** . *** : .
```

```
sp|P38902|RPBY_YEAST CNSIINKLGALKTNFETEWNLQTLAADDAF 120
sp|P28000|RPC9_YEAST LKDLMDLCDVVESKFTTEKIKSM----- 142
: : : : . : : : * : : : : : : :
```

Rpb3-AC40 (Rpc5)

```
sp|P16370|RPB3_YEAST -----MSEEGP-----QVKIREASKDNVDFILSNVD 26
sp|P07703|RPC5_YEAST MSNIVGIEYNRVTNTTSTDFPGFSKDAENENVEKFKKDFE VNISSLDAREANFDLINID 60
                        :*::.                :*: * . . :*: * *:*

sp|P16370|RPB3_YEAST LAMANSLRRVMIAEIPTLAIDSVEVETNTTVLADEFIAHRLGLIPLQSMDIEQLEYSRDC 86
sp|P07703|RPC5_YEAST TSIANAFRRIMISEVPSVAAEYVYFFNNTSVIQDEVLAHRIGLVPLK-VDPDMLTWVDSN 119
                        :*:*:*:*:*:*:*: * . .*:*: * *:***:***:***:***:*** : * : .

sp|P16370|RPB3_YEAST FCED--HCDKCSVVLTLQAFGESE-----STTNVYSKDLVIVSNLMGRNIG 130
sp|P07703|RPC5_YEAST LPDDEKFTDENTIVLSLNVKCTRNPDPAPKGSTDPKELYNNAHVYARDLKFEPQGRQSTTF 179
                        : * . * :*:*:*. : . .:***:*** : : .

sp|P16370|RPB3_YEAST HPIIQDKEGNGVLICKLRKQELKLTCAKKGIAKEHAKWGPAAAEFEYDPWNKLKH-- 188
sp|P07703|RPC5_YEAST ADCPVVPADPDILLAKLRPGQEISLKAHCILGIGGDHAKFSPVSTASYRLLPQINILQPI 239
                        . .*:*.*** **:. * . . * . :***:*. : : . * : :

sp|P16370|RPB3_YEAST -----TDYWYEQDSAKEWPQSKNCEYEDPPNEGDPFDYKAQAD 226
sp|P07703|RPC5_YEAST KGESARRFQKCFPPGVIGIDEGSDEAYVKDARKDTVSREVLRYEEFADK--VKLGRVRN 296
                        :* * :*: * : . : .** : : : . . . . . :

sp|P16370|RPB3_YEAST TFYMNVESVGSIPVDQVVVRGIDTLQKKVASIL-LALTQMDQDKVNFASGDNNTASN-- 282
sp|P07703|RPC5_YEAST HFIFNVESAGAMTPEEIFFKSVRILKNKAEYLNCPITQMTEDIEQKKTATEVTPQEPKH 356
                        * :***. * : : : : : * : * : : : : * : :

sp|P16370|RPB3_YEAST -MLGSNEDVMMTG--AEQDPYSNASQMGNTGSG--GYDNAW----- 318
sp|P07703|RPC5_YEAST IQEEEEQDVDMTGDEEQEEEPDREKIKLLTQATSEDTGSASFQIVEEDHTLGNALRYVIM 416
                        . :** ** * : * : : . . . * . : :

sp|P16370|RPB3_YEAST -----
sp|P07703|RPC5_YEAST KNPDVEFCGYSIPHPSENLLNIRIQTYGETTAVDALQKGLKDLMDLDCDVVESKFTTEKIKSM 477
```


Figure S2. Comparison of domain folds in C17/25 and Rpb4/7

(A) Comparison of C25 and Rpb7 based on superposition of their tip domains.

(B) Superposition of HRDC domains in C17 (pink) and Rpb4 (silver).

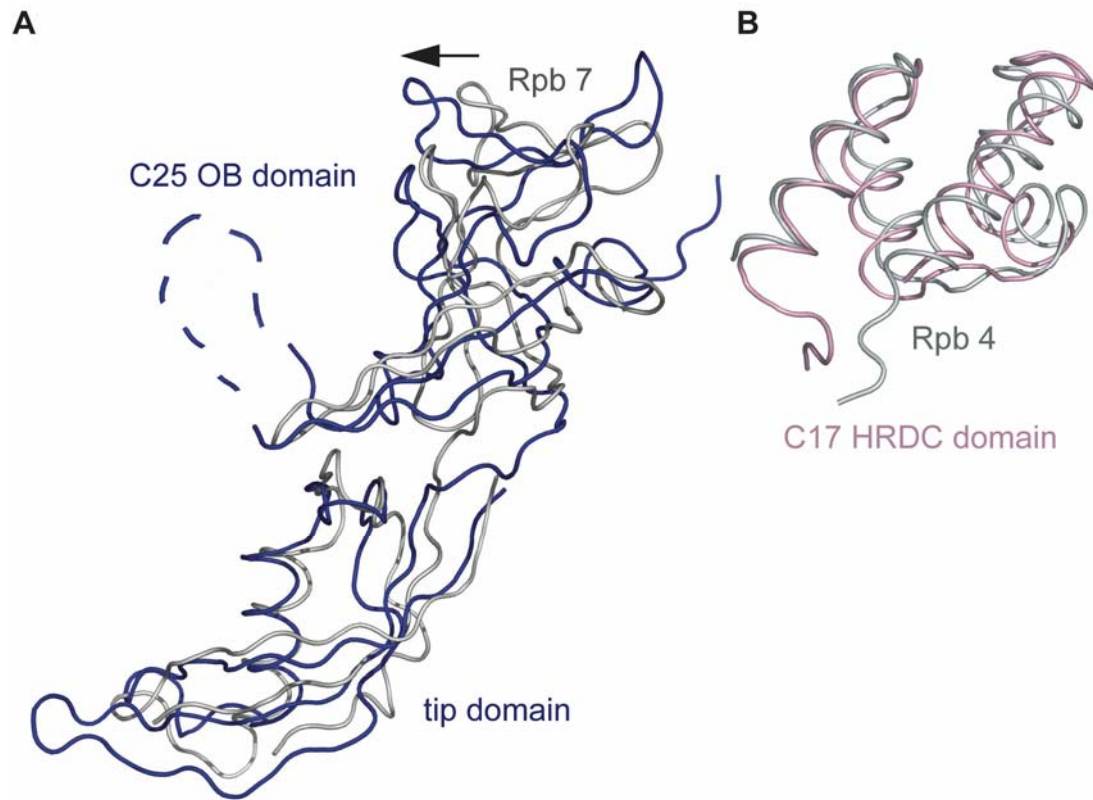


Figure S3. Alignment of C25 and C17 from different species

Conserved residues are highlighted according to decreasing conservation from green, through orange, to yellow. Residues that contribute to the C25-C17 HRDC interface are indicated with a red dot.

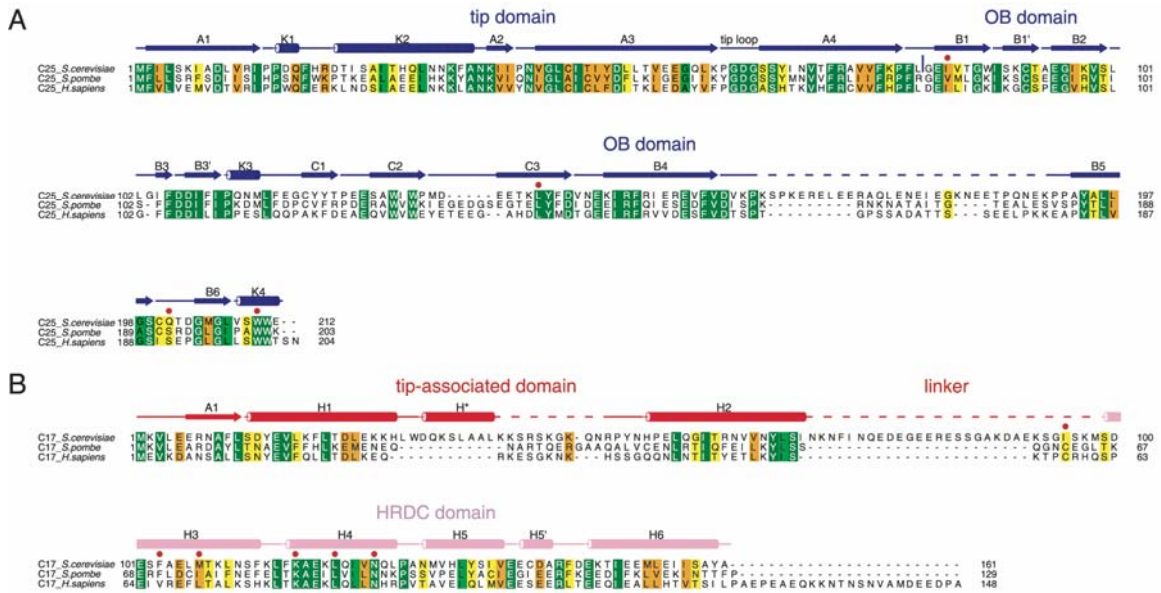


Table S1: Invariant contacts between common and homologous polymerase subunits

Common polymerase subunit	Residues	Contacted homologous subunit in Pol II, I, III	Invariant contact residues in homologous subunits (numbering of Pol II)	
Rpb5	Y168	Rpb1, A190, C160	R857	
	Y168, Y211		F866	
Rpb6	Y88, A91	Rpb1, A190, C160	L504	
	E89, T81, R136		Y852	
	G95,		A499	
	N104,		T381	
	I120		Y383	
Rpb8	100, 103	Rpb7, A43, C25	G66	
	Y20, N21, K22, V23	Rpb1, A190, C160	D538	
	N43		F540	
	L46		L571	
	N43, L46, D94, Y95,		K567	
	V96		P563	
	W79		W572	
	W79		P568	
	D94		I565	
	V96		I566	
Rpb10	I2		Rpb3, AC40	L143
	E19	Y114		
	D55, E58, I57	K146		
	F60, L61	V57		
	L61, R62, Y63, N64	R148		
	Y44	Rpb2, A135, C128		I1006
	R48	D1009		
Rpb12	R54	Rpb2, A135, C128	E116	
	K58		D896	
	R60, F67		Rpb3, AC40	D60