Supplemental data

Structure of GPN-loop GTPase Npa3 and implications for RNA polymerase II assembly

Jürgen Niesser[a,b], Felix R. Wagner[b], Dirk Kostrewa[b], Wolfgang Mühlbacher[a] and Patrick Cramer[a]

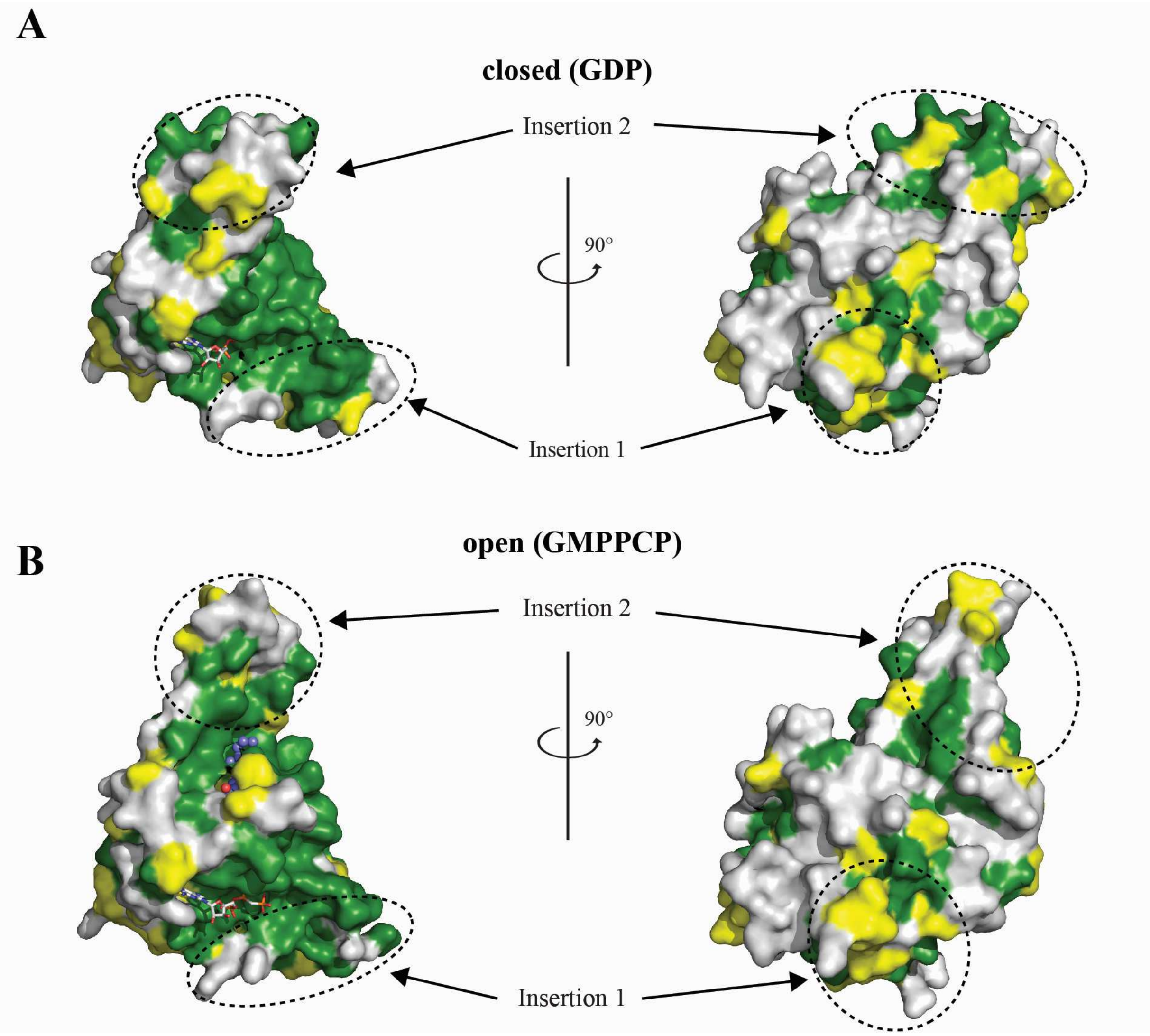
[a]Max-Planck-Institute for Biophysical Chemistry, Department of Molecular Biology, Göttingen, Germany.

[b]Gene Center and Department of Biochemistry, Ludwig-Maximilians-Universität München, Munich, Germany.

Running Head: Structure of GPN-loop GTPase and Pol II assembly

Address correspondence to Patrick Cramer, pcramer@mpibpc.mpg.de

Supplemental Figures

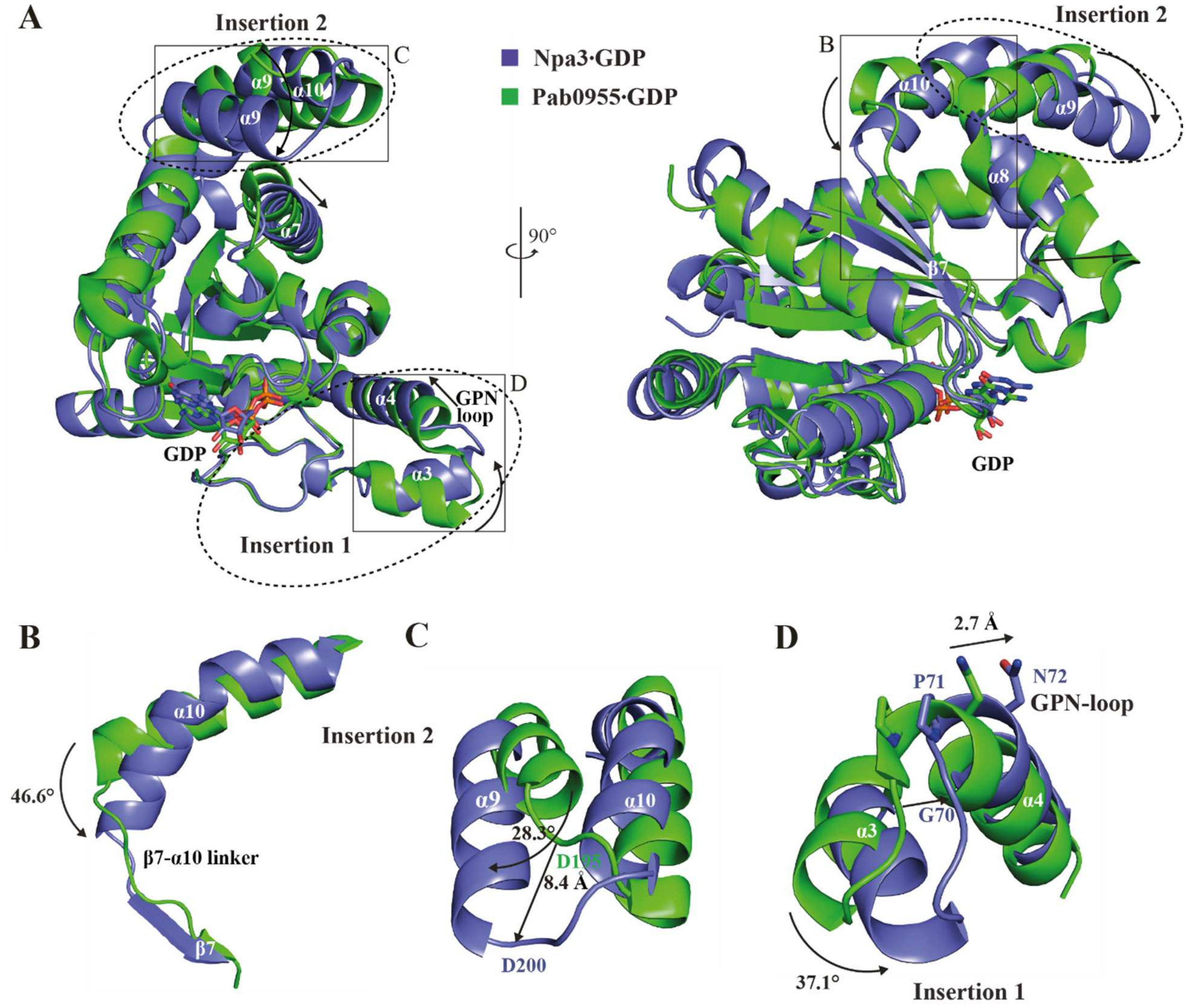


Supplemental Figure S1 Surface conservation of Npa3

A in the closed, GDP-bound and

B open, GMPPCP-bound state. The bound lipid is shown as stale blue spheres.

Invariant residues are shown in green, conserved residues in yellow and variable residues in grey.



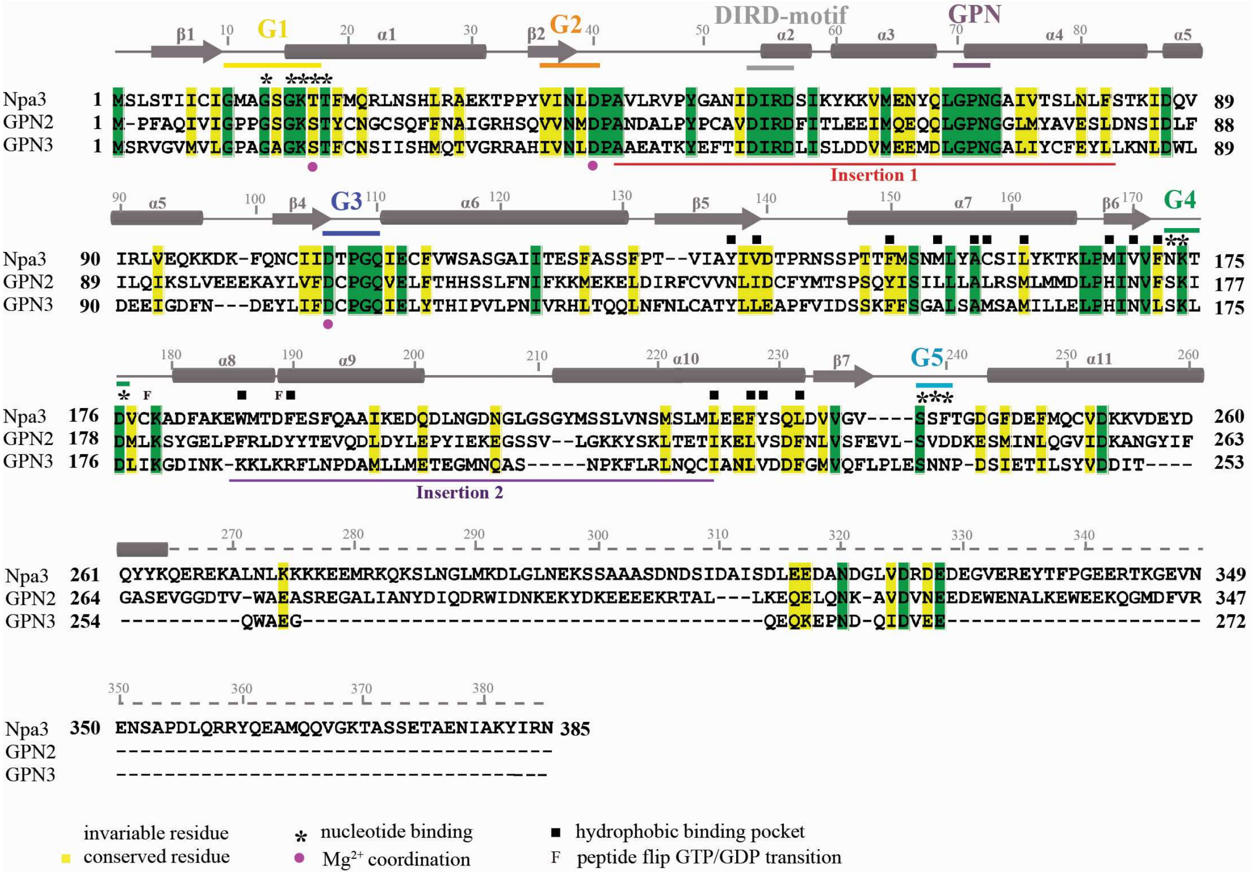
Supplemental Figure S2 Superposition of Npa3·GDP (blue) and the archaeal GPN-loop GTPase Pab0955·GDP (green) reveals eukaryote-specific structural features.

A Superposition of overall structures from Npa3·GDP and Pab0955·GDP (pdb code: 1YRB,(18)) shown as front view (left) and side view (right). Significant differences between the two structures are indicated with black arrows and the insertion regions are shown with dashed lines. Boxes highlight areas shown in B-D.

B The linker between strand β7 and helix α10 is shorter in Npa3 leading to a strong bending of helix α10.

C Helix α9 of Npa3 is rotated, leading to significant differences of insertion 2 compared to the archaeal GPN-loop GTPase.

D Helix α3 of insertion 1 is rotated and the GPN-loop is shifted.



Supplemental Figure S3 Amino acid sequence alignment of GPN-loop GTPases Npa3 from *S. cerevisiae* (*S.c.*), and its paralogs GPN2 and GPN3.

Secondary structure elements are indicated above the sequence (cylinders, α-helices; arrows, β-strands; dashed line, no structural data available). Numbering above the sequence corresponds to Npa3. Invariant residues are in green whereas conserved residues are in yellow. The G-domains G1-G5 and insertion regions are marked with bars, residues of the hydrophobic pocket with black squares, residues involved in nucleotide-binding with asterisks and residues involved in magnesium binding with pink spheres.

Supplemental Table S1 List of all 15meric (overlap: 11 amino acids; offset: 4 amino acids) Pol II-derived peptides, analyzed for Npa3 binding. ‘Start a.a.’ and ‘end a.a.’ depicts the first and last amino acid of the corresponding peptide in the respective Pol II subunit sequence. Peptides containing amino acids from two different subunits are shown in grey and were not further analyzed since they represent artificial sequences.

Pol II subunit	**Peptide No.**	**Start a.a.**	**End a.a.**	**Sequence**
Rpb1	1	1	15	MVGQQYSSAPLRTVK
	2	5	19	QYSSAPLRTVKEVQF
	3	9	23	APLRTVKEVQFGLFS
	4	13	27	TVKEVQFGLFSPEEV
	5	17	31	VQFGLFSPEEVRAIS
	6	21	35	LFSPEEVRAISVAKI
	7	25	39	EEVRAISVAKIRFPE
	8	29	43	AISVAKIRFPETMDE
	9	33	47	AKIRFPETMDETQTR
	10	37	51	FPETMDETQTRAKIG
	11	41	55	MDETQTRAKIGGLND
	12	45	59	QTRAKIGGLNDPRLG
	13	49	63	KIGGLNDPRLGSIDR
	14	53	67	LNDPRLGSIDRNLKC
	15	57	71	RLGSIDRNLKCQTCQ
	16	61	75	IDRNLKCQTCQEGMN
	17	65	79	LKCQTCQEGMNECPG
	18	69	83	TCQEGMNECPGHFGH
	19	73	87	GMNECPGHFGHIDLA
	20	77	91	CPGHFGHIDLAKPVF
	21	81	95	FGHIDLAKPVFHVGF
	22	85	99	DLAKPVFHVGFIAKI
	23	89	103	PVFHVGFIAKIKKVC
	24	93	107	VGFIAKIKKVCECVC
	25	97	111	AKIKKVCECVCMHCG
	26	101	115	KVCECVCMHCGKLLL
	27	105	119	CVCMHCGKLLLDEHN
	28	109	123	HCGKLLLDEHNELMR
	29	113	127	LLLDEHNELMRQALA
	30	117	131	EHNELMRQALAIKDS
	31	121	135	LMRQALAIKDSKKRF
	32	125	139	ALAIKDSKKRFAAIW
	33	129	143	KDSKKRFAAIWTLCK
	34	133	147	KRFAAIWTLCKTKMV
	35	137	151	AIWTLCKTKMVCETD
	36	141	155	LCKTKMVCETDVPSE
	37	145	159	KMVCETDVPSEDDPT
	38	149	163	ETDVPSEDDPTQLVS
	39	153	167	PSEDDPTQLVSRGGC
	40	157	171	DPTQLVSRGGCGNTQ
	41	161	175	LVSRGGCGNTQPTIR
Rpb1	42	165	179	GGCGNTQPTIRKDGL
	43	169	183	NTQPTIRKDGLKLVG
	44	173	187	TIRKDGLKLVGSWKK
	45	177	191	DGLKLVGSWKKDRAT
	46	181	195	LVGSWKKDRATGDAD
	47	185	199	WKKDRATGDADEPEL
	48	189	203	RATGDADEPELRVLS
	49	193	207	DADEPELRVLSTEEI
	50	197	211	PELRVLSTEEILNIF
	51	201	215	VLSTEEILNIFKHIS
	52	205	219	EEILNIFKHISVKDF
	53	209	223	NIFKHISVKDFTSLG
	54	213	227	HISVKDFTSLGFNEV
	55	217	231	KDFTSLGFNEVFSRP
	56	221	235	SLGFNEVFSRPEWMI
	57	225	239	NEVFSRPEWMILTCL
	58	229	243	SRPEWMILTCLPVPP
	59	233	247	WMILTCLPVPPPPVR
	60	237	251	TCLPVPPPPVRPSIS
	61	241	255	VPPPPVRPSISFNES
	62	245	259	PVRPSISFNESQRGE
	63	249	263	SISFNESQRGEDDLT
	64	253	267	NESQRGEDDLTFKLA
	65	257	271	RGEDDLTFKLADILK
	66	261	275	DLTFKLADILKANIS
	67	265	279	KLADILKANISLETL
	68	269	283	ILKANISLETLEHNG
	69	273	287	NISLETLEHNGAPHH
	70	277	291	ETLEHNGAPHHAIEE
	71	281	295	HNGAPHHAIEEAESL
	72	285	299	PHHAIEEAESLLQFH
	73	289	303	IEEAESLLQFHVATY
	74	293	307	ESLLQFHVATYMDND
	75	297	311	QFHVATYMDNDIAGQ
	76	301	315	ATYMDNDIAGQPQAL
	77	305	319	DNDIAGQPQALQKSG
	78	309	323	AGQPQALQKSGRPVK
	79	313	327	QALQKSGRPVKSIRA
	80	317	331	KSGRPVKSIRARLKG
	81	321	335	PVKSIRARLKGKEGR
	82	325	339	IRARLKGKEGRIRGN

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
Rpb1	83	329	343	LKGKEGRIRGNLMGK
	84	333	347	EGRIRGNLMGKRVDF
	85	337	351	RGNLMGKRVDFSART
	86	341	355	MGKRVDFSARTVISG
	87	345	359	VDFSARTVISGDPNL
	88	349	363	ARTVISGDPNLELDQ
	89	353	367	ISGDPNLELDQVGVP
	90	357	371	PNLELDQVGVPKSIA
	91	361	375	LDQVGVPKSIAKTLT
	92	365	379	GVPKSIAKTLTYPEV
	93	369	383	SIAKTLTYPEVVTPY
	94	373	387	TLTYPEVVTPYNIDR
	95	377	391	PEVVTPYNIDRLTQL
	96	381	395	TPYNIDRLTQLVRNG
	97	385	399	IDRLTQLVRNGPNEH
	98	389	403	TQLVRNGPNEHPGAK
	99	393	407	RNGPNEHPGAKYVIR
	100	397	411	NEHPGAKYVIRDSGD
	101	401	415	GAKYVIRDSGDRIDL
	102	405	419	VIRDSGDRIDLRYSK
	103	409	423	SGDRIDLRYSKRAGD
	104	413	427	IDLRYSKRAGDIQLQ
	105	417	431	YSKRAGDIQLQYGWK
	106	421	435	AGDIQLQYGWKVERH
	107	425	439	QLQYGWKVERHIMDN
	108	429	443	GWKVERHIMDNDPVL
	109	433	447	ERHIMDNDPVLFNRQ
	110	437	451	MDNDPVLFNRQPSLH
	111	441	455	PVLFNRQPSLHKMSM
	112	445	459	NRQPSLHKMSMMAHR
	113	449	463	SLHKMSMMAHRVKVI
	114	453	467	MSMMAHRVKVIPYST
	115	457	471	AHRVKVIPYSTFRLN
	116	461	475	KVIPYSTFRLNLSVT
	117	465	479	YSTFRLNLSVTSPYN
	118	469	483	RLNLSVTSPYNADFD
	119	473	487	SVTSPYNADFDGDEM
	120	477	491	PYNADFDGDEMNLHV
	121	481	495	DFDGDEMNLHVPQSE
	122	485	499	DEMNLHVPQSEETRA
	123	489	503	LHVPQSEETRAELSQ
	124	493	507	QSEETRAELSQLCAV
	125	497	511	TRAELSQLCAVPLQI
	126	501	515	LSQLCAVPLQIVSPQ
	127	505	519	CAVPLQIVSPQSNKP
	128	509	523	LQIVSPQSNKPCMGI
Rpb1	129	513	527	SPQSNKPCMGIVQDT
	130	517	531	NKPCMGIVQDTLCGI
	131	521	535	MGIVQDTLCGIRKLT
	132	525	539	QDTLCGIRKLTLRDT
	133	529	543	CGIRKLTLRDTFIEL
	134	533	547	KLTLRDTFIELDQVL
	135	537	551	RDTFIELDQVLNMLY
	136	541	555	IELDQVLNMLYWVPD
	137	545	559	QVLNMLYWVPDWDGV
	138	549	563	MLYWVPDWDGVIPTP
	139	553	567	VPDWDGVIPTPAIIK
	140	557	571	DGVIPTPAIIKPKPL
	141	561	575	PTPAIIKPKPLWSGK
	142	565	579	IIKPKPLWSGKQILS
	143	569	583	KPLWSGKQILSVAIP
	144	573	587	SGKQILSVAIPNGIH
	145	577	591	ILSVAIPNGIHLQRF
	146	581	595	AIPNGIHLQRFDEGT
	147	585	599	GIHLQRFDEGTTLLS
	148	589	603	QRFDEGTTLLSPKDN
	149	593	607	EGTTLLSPKDNGMLI
	150	597	611	LLSPKDNGMLIIDGQ
	151	601	615	KDNGMLIIDGQIIFG
	152	605	619	MLIIDGQIIFGVVEK
	153	609	623	DGQIIFGVVEKKTVG
	154	613	627	IFGVVEKKTVGSSNG
	155	617	631	VEKKTVGSSNGGLIH
	156	621	635	TVGSSNGGLIHVVTR
	157	625	639	SNGGLIHVVTREKGP
	158	629	643	LIHVVTREKGPQVCA
	159	633	647	VTREKGPQVCAKLFG
	160	637	651	KGPQVCAKLFGNIQK
	161	641	655	VCAKLFGNIQKVVNF
	162	645	659	LFGNIQKVVNFWLLH
	163	649	663	IQKVVNFWLLHNGFS
	164	653	667	VNFWLLHNGFSTGIG
	165	657	671	LLHNGFSTGIGDTIA
	166	661	675	GFSTGIGDTIADGPT
	167	665	679	GIGDTIADGPTMREI
	168	669	683	TIADGPTMREITETI
	169	673	687	GPTMREITETIAEAK
	170	677	691	REITETIAEAKKKVL
	171	681	695	ETIAEAKKKVLDVTK
	172	685	699	EAKKKVLDVTKEAQA
	173	689	703	KVLDVTKEAQANLLT
	174	693	707	VTKEAQANLLTAKHG

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
Rpb1	175	697	711	AQANLLTAKHGMTLR
	176	701	715	LLTAKHGMTLRESFE
	177	705	719	KHGMTLRESFEDNVV
	178	709	723	TLRESFEDNVVRFLN
	179	713	727	SFEDNVVRFLNEARD
	180	717	731	NVVRFLNEARDKAGR
	181	721	735	FLNEARDKAGRLAEV
	182	725	739	ARDKAGRLAEVNLKD
	183	729	743	AGRLAEVNLKDLNNV
	184	733	747	AEVNLKDLNNVKQMV
	185	737	751	LKDLNNVKQMVMAGS
	186	741	755	NNVKQMVMAGSKGSF
	187	745	759	QMVMAGSKGSFINIA
	188	749	763	AGSKGSFINIAQMSA
	189	753	767	GSFINIAQMSACVGQ
	190	757	771	NIAQMSACVGQQSVE
	191	761	775	MSACVGQQSVEGKRI
	192	765	779	VGQQSVEGKRIAFGF
	193	769	783	SVEGKRIAFGFVDRT
	194	773	787	KRIAFGFVDRTLPHF
	195	777	791	FGFVDRTLPHFSKDD
	196	781	795	DRTLPHFSKDDYSPE
	197	785	799	PHFSKDDYSPESKGF
	198	789	803	KDDYSPESKGFVENS
	199	793	807	SPESKGFVENSYLRG
	200	797	811	KGFVENSYLRGLTPQ
	201	801	815	ENSYLRGLTPQEFFF
	202	805	819	LRGLTPQEFFFHAMG
	203	809	823	TPQEFFFHAMGGREG
	204	813	827	FFFHAMGGREGLIDT
	205	817	831	AMGGREGLIDTAVKT
	206	821	835	REGLIDTAVKTAETG
	207	825	839	IDTAVKTAETGYIQR
	208	829	843	VKTAETGYIQRRLVK
	209	833	847	ETGYIQRRLVKALED
	210	837	851	IQRRLVKALEDIMVH
	211	841	855	LVKALEDIMVHYDNT
	212	845	859	LEDIMVHYDNTTRNS
	213	849	863	MVHYDNTTRNSLGNV
	214	853	867	DNTTRNSLGNVIQFI
	215	857	871	RNSLGNVIQFIYGED
	216	861	875	GNVIQFIYGEDGMDA
	217	865	879	QFIYGEDGMDAAHIE
	218	869	883	GEDGMDAAHIEKQSL
	219	873	887	MDAAHIEKQSLDTIG
	220	877	891	HIEKQSLDTIGGSDA
Rpb1	221	881	895	QSLDTIGGSDAAFEK
	222	885	899	TIGGSDAAFEKRYRV
	223	889	903	SDAAFEKRYRVDLLN
	224	893	907	FEKRYRVDLLNTDHT
	225	897	911	YRVDLLNTDHTLDPS
	226	901	915	LLNTDHTLDPSLLES
	227	905	919	DHTLDPSLLESGSEI
	228	909	923	DPSLLESGSEILGDL
	229	913	927	LESGSEILGDLKLQV
	230	917	931	SEILGDLKLQVLLDE
	231	921	935	GDLKLQVLLDEEYKQ
	232	925	939	LQVLLDEEYKQLVKD
	233	929	943	LDEEYKQLVKDRKFL
	234	933	947	YKQLVKDRKFLREVF
	235	937	951	VKDRKFLREVFVDGE
	236	941	955	KFLREVFVDGEANWP
	237	945	959	EVFVDGEANWPLPVN
	238	949	963	DGEANWPLPVNIRRI
	239	953	967	NWPLPVNIRRIIQNA
	240	957	971	PVNIRRIIQNAQQTF
	241	961	975	RRIIQNAQQTFHIDH
	242	965	979	QNAQQTFHIDHTKPS
	243	969	983	QTFHIDHTKPSDLTI
	244	973	987	IDHTKPSDLTIKDIV
	245	977	991	KPSDLTIKDIVLGVK
	246	981	995	LTIKDIVLGVKDLQE
	247	985	999	DIVLGVKDLQENLLV
	248	989	1003	GVKDLQENLLVLRGK
	249	993	1007	LQENLLVLRGKNEII
	250	997	1011	LLVLRGKNEIIQNAQ
	251	1001	1015	RGKNEIIQNAQRDAV
	252	1005	1019	EIIQNAQRDAVTLFC
	253	1009	1023	NAQRDAVTLFCCLLR
	254	1013	1027	DAVTLFCCLLRSRLA
	255	1017	1031	LFCCLLRSRLATRRV
	256	1021	1035	LLRSRLATRRVLQEY
	257	1025	1039	RLATRRVLQEYRLTK
	258	1029	1043	RRVLQEYRLTKQAFD
	259	1033	1047	QEYRLTKQAFDWVLS
	260	1037	1051	LTKQAFDWVLSNIEA
	261	1041	1055	AFDWVLSNIEAQFLR
	262	1045	1059	VLSNIEAQFLRSVVH
	263	1049	1063	IEAQFLRSVVHPGEM
	264	1053	1067	FLRSVVHPGEMVGVL
	265	1057	1071	VVHPGEMVGVLAAQS
	266	1061	1075	GEMVGVLAAQSIGEP

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
Rpb1	267	1065	1079	GVLAAQSIGEPATQM
	268	1069	1083	AQSIGEPATQMTLNT
	269	1073	1087	GEPATQMTLNTFHFA
	270	1077	1091	TQMTLNTFHFAGVAS
	271	1081	1095	LNTFHFAGVASKKVT
	272	1085	1099	HFAGVASKKVTSGVP
	273	1089	1103	VASKKVTSGVPRLKE
	274	1093	1107	KVTSGVPRLKEILNV
	275	1097	1111	GVPRLKEILNVAKNM
	276	1101	1115	LKEILNVAKNMKTPS
	277	1105	1119	LNVAKNMKTPSLTVY
	278	1109	1123	KNMKTPSLTVYLEPG
	279	1113	1127	TPSLTVYLEPGHAAD
	280	1117	1131	TVYLEPGHAADQEQA
	281	1121	1135	EPGHAADQEQAKLIR
	282	1125	1139	AADQEQAKLIRSAIE
	283	1129	1143	EQAKLIRSAIEHTTL
	284	1133	1147	LIRSAIEHTTLKSVT
	285	1137	1151	AIEHTTLKSVTIASE
	286	1141	1155	TTLKSVTIASEIYYD
	287	1145	1159	SVTIASEIYYDPDPR
	288	1149	1163	ASEIYYDPDPRSTVI
	289	1153	1167	YYDPDPRSTVIPEDE
	290	1157	1171	DPRSTVIPEDEEIIQ
	291	1161	1175	TVIPEDEEIIQLHFS
	292	1165	1179	EDEEIIQLHFSLLDE
	293	1169	1183	IIQLHFSLLDEEAEQ
	294	1173	1187	HFSLLDEEAEQSFDQ
	295	1177	1191	LDEEAEQSFDQQSPW
	296	1181	1195	AEQSFDQQSPWLLRL
	297	1185	1199	FDQQSPWLLRLELDR
	298	1189	1203	SPWLLRLELDRAAMN
	299	1193	1207	LRLELDRAAMNDKDL
	300	1197	1211	LDRAAMNDKDLTMGQ
	301	1201	1215	AMNDKDLTMGQVGER
	302	1205	1219	KDLTMGQVGERIKQT
	303	1209	1223	MGQVGERIKQTFKND
	304	1213	1227	GERIKQTFKNDLFVI
	305	1217	1231	KQTFKNDLFVIWSED
	306	1221	1235	KNDLFVIWSEDNDEK
	307	1225	1239	FVIWSEDNDEKLIIR
	308	1229	1243	SEDNDEKLIIRCRVV
	309	1233	1247	DEKLIIRCRVVRPKS
	310	1237	1251	IIRCRVVRPKSLDAE
	311	1241	1255	RVVRPKSLDAETEAE
	312	1245	1259	PKSLDAETEAEEDHM
Rpb1	313	1249	1263	DAETEAEEDHMLKKI
	314	1253	1267	EAEEDHMLKKIENTM
	315	1257	1271	DHMLKKIENTMLENI
	316	1261	1275	KKIENTMLENITLRG
	317	1265	1279	NTMLENITLRGVENI
	318	1269	1283	ENITLRGVENIERVV
	319	1273	1287	LRGVENIERVVMMKY
	320	1277	1291	ENIERVVMMKYDRKV
	321	1281	1295	RVVMMKYDRKVPSPT
	322	1285	1299	MKYDRKVPSPTGEYV
	323	1289	1303	RKVPSPTGEYVKEPE
	324	1293	1307	SPTGEYVKEPEWVLE
	325	1297	1311	EYVKEPEWVLETDGV
	326	1301	1315	EPEWVLETDGVNLSE
	327	1305	1319	VLETDGVNLSEVMTV
	328	1309	1323	DGVNLSEVMTVPGID
	329	1313	1327	LSEVMTVPGIDPTRI
	330	1317	1331	MTVPGIDPTRIYTNS
	331	1321	1335	GIDPTRIYTNSFIDI
	332	1325	1339	TRIYTNSFIDIMEVL
	333	1329	1343	TNSFIDIMEVLGIEA
	334	1333	1347	IDIMEVLGIEAGRAA
	335	1337	1351	EVLGIEAGRAALYKE
	336	1341	1355	IEAGRAALYKEVYNV
	337	1345	1359	RAALYKEVYNVIASD
	338	1349	1363	YKEVYNVIASDGSYV
	339	1353	1367	YNVIASDGSYVNYRH
	340	1357	1371	ASDGSYVNYRHMALL
	341	1361	1375	SYVNYRHMALLVDVM
	342	1365	1379	YRHMALLVDVMTTQG
	343	1369	1383	ALLVDVMTTQGGLTS
	344	1373	1387	DVMTTQGGLTSVTRH
	345	1377	1391	TQGGLTSVTRHGFNR
	346	1381	1395	LTSVTRHGFNRSNTG
	347	1385	1399	TRHGFNRSNTGALMR
	348	1389	1403	FNRSNTGALMRCSFE
	349	1393	1407	NTGALMRCSFEETVE
	350	1397	1411	LMRCSFEETVEILFE
	351	1401	1415	SFEETVEILFEAGAS
	352	1405	1419	TVEILFEAGASAELD
	353	1409	1423	LFEAGASAELDDCRG
	354	1413	1427	GASAELDDCRGVSEN
	355	1417	1431	ELDDCRGVSENVILG
	356	1421	1435	CRGVSENVILGQMAP
	357	1425	1439	SENVILGQMAPIGTG
	358	1429	1443	ILGQMAPIGTGAFDV

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
Rpb1	359	1433	1447	MAPIGTGAFDVMIDE
	360	1437	1451	GTGAFDVMIDEESLV
	361	1441	1455	FDVMIDEESLVKYMP
	362	1445	1459	IDEESLVKYMPEQKI
	363	1449	1463	SLVKYMPEQKITEIE
	364	1453	1467	YMPEQKITEIEDGQD
	365	1457	1471	QKITEIEDGQDGGVT
	366	1461	1475	EIEDGQDGGVTPYSN
	367	1465	1479	GQDGGVTPYSNESGL
	368	1469	1483	GVTPYSNESGLVNAD
	369	1473	1487	YSNESGLVNADLDVK
	370	1477	1491	SGLVNADLDVKDELM
	371	1481	1495	NADLDVKDELMFSPL
	372	1485	1499	DVKDELMFSPLVDSG
	373	1489	1503	ELMFSPLVDSGSNDA
	374	1493	1507	SPLVDSGSNDAMAGG
	375	1497	1511	DSGSNDAMAGGFTAY
	376	1501	1515	NDAMAGGFTAYGGAD
	377	1505	1519	AGGFTAYGGADYGEA
	378	1509	1523	TAYGGADYGEATSPF
	379	1513	1527	GADYGEATSPFGAYG
	380	1517	1531	GEATSPFGAYGEAPT
	381	1521	1535	SPFGAYGEAPTSPGF
	382	1525	1539	AYGEAPTSPGFGVSS
	383	1529	1543	APTSPGFGVSSPGFS
	384	1533	1547	PGFGVSSPGFSPTSP
	385	1537	1551	VSSPGFSPTSPTYSP
	386	1541	1555	GFSPTSPTYSPTSPA
	387	1545	1559	TSPTYSPTSPAYSPT
	388	1549	1563	YSPTSPAYSPTSPSY
	389	1553	1567	SPAYSPTSPSYSPTS
	390	1557	1571	SPTSPSYSPTSPSYS
	391	1561	1575	PSYSPTSPSYSPTSP
	392	1565	1579	PTSPSYSPTSPSYSP
	393	1569	1583	SYSPTSPSYSPTSPS
	394	1573	1587	TSPSYSPTSPSYSPT
	395	1577	1591	YSPTSPSYSPTSPSY
	396	1581	1595	SPSYSPTSPSYSPTS
	397	1585	1599	SPTSPSYSPTSPSYS
	398	1589	1603	PSYSPTSPSYSPTSP
	399	1593	1607	PTSPSYSPTSPSYSP
	400	1597	1611	SYSPTSPSYSPTSPS
	401	1601	1615	TSPSYSPTSPSYSPT
	402	1605	1619	YSPTSPSYSPTSPSY
	403	1609	1623	SPSYSPTSPSYSPTS
	404	1613	1627	SPTSPSYSPTSPSYS
Rpb1	405	1617	1631	PSYSPTSPSYSPTSP
	406	1621	1635	PTSPSYSPTSPSYSP
	407	1625	1639	SYSPTSPSYSPTSPS
	408	1629	1643	TSPSYSPTSPSYSPT
	409	1633	1647	YSPTSPSYSPTSPSY
	410	1637	1651	SPSYSPTSPSYSPTS
	411	1641	1655	SPTSPSYSPTSPSYS
	412	1645	1659	PSYSPTSPSYSPTSP
	413	1649	1663	PTSPSYSPTSPAYSP
	414	1653	1667	SYSPTSPAYSPTSPS
	415	1657	1671	TSPAYSPTSPSYSPT
	416	1661	1675	YSPTSPSYSPTSPSY
	417	1665	1679	SPSYSPTSPSYSPTS
	418	1669	1683	SPTSPSYSPTSPSYS
	419	1673	1687	PSYSPTSPSYSPTSP
	420	1677	1691	PTSPSYSPTSPSYSP
	421	1681	1695	SYSPTSPSYSPTSPN
	422	1685	1699	TSPSYSPTSPNYSPT
	423	1689	1703	YSPTSPNYSPTSPSY
	424	1693	1707	SPNYSPTSPSYSPTS
	425	1697	1711	SPTSPSYSPTSPGYS
	426	1701	1715	PSYSPTSPGYSPGSP
	427	1705	1719	PTSPGYSPGSPAYSP
	428	1709	1723	GYSPGSPAYSPKQDE
	429	1713	1727	GSPAYSPKQDEQKHN
	430	1717	1731	YSPKQDEQKHNENEN
Rpb1/2	431			QDEQKHNENENSRMS
	432			KHNENENSRMSDLAN
	433			NENSRMSDLANSEKY
	434			RMSDLANSEKYYDED
Rpb2	435	4	18	LANSEKYYDEDPYGF
	436	8	22	EKYYDEDPYGFEDES
	437	12	26	DEDPYGFEDESAPIT
	438	16	30	YGFEDESAPITAEDS
	439	20	34	DESAPITAEDSWAVI
	440	24	38	PITAEDSWAVISAFF
	441	28	42	EDSWAVISAFFREKG
	442	32	46	AVISAFFREKGLVSQ
	443	36	50	AFFREKGLVSQQLDS
	444	40	54	EKGLVSQQLDSFNQF
	445	44	58	VSQQLDSFNQFVDYT
	446	48	62	LDSFNQFVDYTLQDI
	447	52	66	NQFVDYTLQDIICED
	448	56	70	DYTLQDIICEDSTLI
	449	60	74	QDIICEDSTLILEQL
	450	64	78	CEDSTLILEQLAQHT

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
Rpb2	451	68	82	TLILEQLAQHTTESD
	452	72	86	EQLAQHTTESDNISR
	453	76	90	QHTTESDNISRKYEI
	454	80	94	ESDNISRKYEISFGK
	455	84	98	ISRKYEISFGKIYVT
	456	88	102	YEISFGKIYVTKPMV
	457	92	106	FGKIYVTKPMVNESD
	458	96	110	YVTKPMVNESDGVTH
	459	100	114	PMVNESDGVTHALYP
	460	104	118	ESDGVTHALYPQEAR
	461	108	122	VTHALYPQEARLRNL
	462	112	126	LYPQEARLRNLTYSS
	463	116	130	EARLRNLTYSSGLFV
	464	120	134	RNLTYSSGLFVDVKK
	465	124	138	YSSGLFVDVKKRTYE
	466	128	142	LFVDVKKRTYEAIDV
	467	132	146	VKKRTYEAIDVPGRE
	468	136	150	TYEAIDVPGRELKYE
	469	140	154	IDVPGRELKYELIAE
	470	144	158	GRELKYELIAEESED
	471	148	162	KYELIAEESEDDSES
	472	152	166	IAEESEDDSESGKVF
	473	156	170	SEDDSESGKVFIGRL
	474	160	174	SESGKVFIGRLPIML
	475	164	178	KVFIGRLPIMLRSKN
	476	168	182	GRLPIMLRSKNCYLS
	477	172	186	IMLRSKNCYLSEATE
	478	176	190	SKNCYLSEATESDLY
	479	180	194	YLSEATESDLYKLKE
	480	184	198	ATESDLYKLKECPFD
	481	188	202	DLYKLKECPFDMGGY
	482	192	206	LKECPFDMGGYFIIN
	483	196	210	PFDMGGYFIINGSEK
	484	200	214	GGYFIINGSEKVLIA
	485	204	218	IINGSEKVLIAQERS
	486	208	222	SEKVLIAQERSAGNI
	487	212	226	LIAQERSAGNIVQVF
	488	216	230	ERSAGNIVQVFKKAA
	489	220	234	GNIVQVFKKAAPSPI
	490	224	238	QVFKKAAPSPISHVA
	491	228	242	KAAPSPISHVAEIRS
	492	232	246	SPISHVAEIRSALEK
	493	236	250	HVAEIRSALEKGSRF
	494	240	254	IRSALEKGSRFISTL
	495	244	258	LEKGSRFISTLQVKL
	496	248	262	SRFISTLQVKLYGRE
Rpb2	497	252	266	STLQVKLYGREGSSA
	498	256	270	VKLYGREGSSARTIK
	499	260	274	GREGSSARTIKATLP
	500	264	278	SSARTIKATLPYIKQ
	501	268	282	TIKATLPYIKQDIPI
	502	272	286	TLPYIKQDIPIVIIF
	503	276	290	IKQDIPIVIIFRALG
	504	280	294	IPIVIIFRALGIIPD
	505	284	298	IIFRALGIIPDGEIL
	506	288	302	ALGIIPDGEILEHIC
	507	292	306	IPDGEILEHICYDVN
	508	296	310	EILEHICYDVNDWQM
	509	300	314	HICYDVNDWQMLEML
	510	304	318	DVNDWQMLEMLKPCV
	511	308	322	WQMLEMLKPCVEDGF
	512	312	326	EMLKPCVEDGFVIQD
	513	316	330	PCVEDGFVIQDRETA
	514	320	334	DGFVIQDRETALDFI
	515	324	338	IQDRETALDFIGRRG
	516	328	342	ETALDFIGRRGTALG
	517	332	346	DFIGRRGTALGIKKE
	518	336	350	RRGTALGIKKEKRIQ
	519	340	354	ALGIKKEKRIQYAKD
	520	344	358	KKEKRIQYAKDILQK
	521	348	362	RIQYAKDILQKEFLP
	522	352	366	AKDILQKEFLPHITQ
	523	356	370	LQKEFLPHITQLEGF
	524	360	374	FLPHITQLEGFESRK
	525	364	378	ITQLEGFESRKAFFL
	526	368	382	EGFESRKAFFLGYMI
	527	372	386	SRKAFFLGYMINRLL
	528	376	390	FFLGYMINRLLLCAL
	529	380	394	YMINRLLLCALDRKD
	530	384	398	RLLLCALDRKDQDDR
	531	388	402	CALDRKDQDDRDHFG
	532	392	406	RKDQDDRDHFGKKRL
	533	396	410	DDRDHFGKKRLDLAG
	534	400	414	HFGKKRLDLAGPLLA
	535	404	418	KRLDLAGPLLAQLFK
	536	408	422	LAGPLLAQLFKTLFK
	537	412	426	LLAQLFKTLFKKLTK
	538	416	430	LFKTLFKKLTKDIFR
	539	420	434	LFKKLTKDIFRYMQR
	540	424	438	LTKDIFRYMQRTVEE
	541	428	442	IFRYMQRTVEEAHDF
	542	432	446	MQRTVEEAHDFNMKL

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
Rpb2	543	436	450	VEEAHDFNMKLAINA
	544	440	454	HDFNMKLAINAKTIT
	545	444	458	MKLAINAKTITSGLK
	546	448	462	INAKTITSGLKYALA
	547	452	466	TITSGLKYALATGNW
	548	456	470	GLKYALATGNWGEQK
	549	460	474	ALATGNWGEQKKAMS
	550	464	478	GNWGEQKKAMSSRAG
	551	468	482	EQKKAMSSRAGVSQV
	552	472	486	AMSSRAGVSQVLNRY
	553	476	490	RAGVSQVLNRYTYSS
	554	480	494	SQVLNRYTYSSTLSH
	555	484	498	NRYTYSSTLSHLRRT
	556	488	502	YSSTLSHLRRTNTPI
	557	492	506	LSHLRRTNTPIGRDG
	558	496	510	RRTNTPIGRDGKLAK
	559	500	514	TPIGRDGKLAKPRQL
	560	504	518	RDGKLAKPRQLHNTH
	561	508	522	LAKPRQLHNTHWGLV
	562	512	526	RQLHNTHWGLVCPAE
	563	516	530	NTHWGLVCPAETPEG
	564	520	534	GLVCPAETPEGQACG
	565	524	538	PAETPEGQACGLVKN
	566	528	542	PEGQACGLVKNLSLM
	567	532	546	ACGLVKNLSLMSCIS
	568	536	550	VKNLSLMSCISVGTD
	569	540	554	SLMSCISVGTDPMPI
	570	544	558	CISVGTDPMPIITFL
	571	548	562	GTDPMPIITFLSEWG
	572	552	566	MPIITFLSEWGMEPL
	573	556	570	TFLSEWGMEPLEDYV
	574	560	574	EWGMEPLEDYVPHQS
	575	564	578	EPLEDYVPHQSPDAT
	576	568	582	DYVPHQSPDATRVFV
	577	572	586	HQSPDATRVFVNGVW
	578	576	590	DATRVFVNGVWHGVH
	579	580	594	VFVNGVWHGVHRNPA
	580	584	598	GVWHGVHRNPARLME
	581	588	602	GVHRNPARLMETLRT
	582	592	606	NPARLMETLRTLRRK
	583	596	610	LMETLRTLRRKGDIN
	584	600	614	LRTLRRKGDINPEVS
	585	604	618	RRKGDINPEVSMIRD
	586	608	622	DINPEVSMIRDIREK
	587	612	626	EVSMIRDIREKELKI
	588	616	630	IRDIREKELKIFTDA
Rpb2	589	620	634	REKELKIFTDAGRVY
	590	624	638	LKIFTDAGRVYRPLF
	591	628	642	TDAGRVYRPLFIVED
	592	632	646	RVYRPLFIVEDDESL
	593	636	650	PLFIVEDDESLGHKE
	594	640	654	VEDDESLGHKELKVR
	595	644	658	ESLGHKELKVRKGHI
	596	648	662	HKELKVRKGHIAKLM
	597	652	666	KVRKGHIAKLMATEY
	598	656	670	GHIAKLMATEYQDIE
	599	660	674	KLMATEYQDIEGGFE
	600	664	678	TEYQDIEGGFEDVEE
	601	668	682	DIEGGFEDVEEYTWS
	602	672	686	GFEDVEEYTWSSLLN
	603	676	690	VEEYTWSSLLNEGLV
	604	680	694	TWSSLLNEGLVEYID
	605	684	698	LLNEGLVEYIDAEEE
	606	688	702	GLVEYIDAEEEESIL
	607	692	706	YIDAEEEESILIAMQ
	608	696	710	EEEESILIAMQPEDL
	609	700	714	SILIAMQPEDLEPAE
	610	704	718	AMQPEDLEPAEANEE
	611	708	722	EDLEPAEANEENDLD
	612	712	726	PAEANEENDLDVDPA
	613	716	730	NEENDLDVDPAKRIR
	614	720	734	DLDVDPAKRIRVSHH
	615	724	738	DPAKRIRVSHHATTF
	616	728	742	RIRVSHHATTFTHCE
	617	732	746	SHHATTFTHCEIHPS
	618	736	750	TTFTHCEIHPSMILG
	619	740	754	HCEIHPSMILGVAAS
	620	744	758	HPSMILGVAASIIPF
	621	748	762	ILGVAASIIPFPDHN
	622	752	766	AASIIPFPDHNQSPR
	623	756	770	IPFPDHNQSPRNTYQ
	624	760	774	DHNQSPRNTYQSAMG
	625	764	778	SPRNTYQSAMGKQAM
	626	768	782	TYQSAMGKQAMGVFL
	627	772	786	AMGKQAMGVFLTNYN
	628	776	790	QAMGVFLTNYNVRMD
	629	780	794	VFLTNYNVRMDTMAN
	630	784	798	NYNVRMDTMANILYY
	631	788	802	RMDTMANILYYPQKP
	632	792	806	MANILYYPQKPLGTT
	633	796	810	LYYPQKPLGTTRAME
	634	800	814	QKPLGTTRAMEYLKF

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
Rpb2	635	804	818	GTTRAMEYLKFRELP
	636	808	822	AMEYLKFRELPAGQN
	637	812	826	LKFRELPAGQNAIVA
	638	816	830	ELPAGQNAIVAIACY
	639	820	834	GQNAIVAIACYSGYN
	640	824	838	IVAIACYSGYNQEDS
	641	828	842	ACYSGYNQEDSMIMN
	642	832	846	GYNQEDSMIMNQSSI
	643	836	850	EDSMIMNQSSIDRGL
	644	840	854	IMNQSSIDRGLFRSL
	645	844	858	SSIDRGLFRSLFFRS
	646	848	862	RGLFRSLFFRSYMDQ
	647	852	866	RSLFFRSYMDQEKKY
	648	856	870	FRSYMDQEKKYGMSI
	649	860	874	MDQEKKYGMSITETF
	650	864	878	KKYGMSITETFEKPQ
	651	868	882	MSITETFEKPQRTNT
	652	872	886	ETFEKPQRTNTLRMK
	653	876	890	KPQRTNTLRMKHGTY
	654	880	894	TNTLRMKHGTYDKLD
	655	884	898	RMKHGTYDKLDDDGL
	656	888	902	GTYDKLDDDGLIAPG
	657	892	906	KLDDDGLIAPGVRVS
	658	896	910	DGLIAPGVRVSGEDV
	659	900	914	APGVRVSGEDVIIGK
	660	904	918	RVSGEDVIIGKTTPI
	661	908	922	EDVIIGKTTPISPDE
	662	912	926	IGKTTPISPDEEELG
	663	916	930	TPISPDEEELGQRTA
	664	920	934	PDEEELGQRTAYHSK
	665	924	938	ELGQRTAYHSKRDAS
	666	928	942	RTAYHSKRDASTPLR
	667	932	946	HSKRDASTPLRSTEN
	668	936	950	DASTPLRSTENGIVD
	669	940	954	PLRSTENGIVDQVLV
	670	944	958	TENGIVDQVLVTTNQ
	671	948	962	IVDQVLVTTNQDGLK
	672	952	966	VLVTTNQDGLKFVKV
	673	956	970	TNQDGLKFVKVRVRT
	674	960	974	GLKFVKVRVRTTKIP
	675	964	978	VKVRVRTTKIPQIGD
	676	968	982	VRTTKIPQIGDKFAS
	677	972	986	KIPQIGDKFASRHGQ
	678	976	990	IGDKFASRHGQKGTI
	679	980	994	FASRHGQKGTIGITY
	680	984	998	HGQKGTIGITYRRED
Rpb2	681	988	1002	GTIGITYRREDMPFT
	682	992	1006	ITYRREDMPFTAEGI
	683	996	1010	REDMPFTAEGIVPDL
	684	1000	1014	PFTAEGIVPDLIINP
	685	1004	1018	EGIVPDLIINPHAIP
	686	1008	1022	PDLIINPHAIPSRMT
	687	1012	1026	INPHAIPSRMTVAHL
	688	1016	1030	AIPSRMTVAHLIECL
	689	1020	1034	RMTVAHLIECLLSKV
	690	1024	1038	AHLIECLLSKVAALS
	691	1028	1042	ECLLSKVAALSGNEG
	692	1032	1046	SKVAALSGNEGDASP
	693	1036	1050	ALSGNEGDASPFTDI
	694	1040	1054	NEGDASPFTDITVEG
	695	1044	1058	ASPFTDITVEGISKL
	696	1048	1062	TDITVEGISKLLREH
	697	1052	1066	VEGISKLLREHGYQS
	698	1056	1070	SKLLREHGYQSRGFE
	699	1060	1074	REHGYQSRGFEVMYN
	700	1064	1078	YQSRGFEVMYNGHTG
	701	1068	1082	GFEVMYNGHTGKKLM
	702	1072	1086	MYNGHTGKKLMAQIF
	703	1076	1090	HTGKKLMAQIFFGPT
	704	1080	1094	KLMAQIFFGPTYYQR
	705	1084	1098	QIFFGPTYYQRLRHM
	706	1088	1102	GPTYYQRLRHMVDDK
	707	1092	1106	YQRLRHMVDDKIHAR
	708	1096	1110	RHMVDDKIHARARGP
	709	1100	1114	DDKIHARARGPMQVL
	710	1104	1118	HARARGPMQVLTRQP
	711	1108	1122	RGPMQVLTRQPVEGR
	712	1112	1126	QVLTRQPVEGRSRDG
	713	1116	1130	RQPVEGRSRDGGLRF
	714	1120	1134	EGRSRDGGLRFGEME
	715	1124	1138	RDGGLRFGEMERDCM
	716	1128	1142	LRFGEMERDCMIAHG
	717	1132	1146	EMERDCMIAHGAASF
	718	1136	1150	DCMIAHGAASFLKER
	719	1140	1154	AHGAASFLKERLMEA
	720	1144	1158	ASFLKERLMEASDAF
	721	1148	1162	KERLMEASDAFRVHI
	722	1152	1166	MEASDAFRVHICGIC
	723	1156	1170	DAFRVHICGICGLMT
	724	1160	1174	VHICGICGLMTVIAK
	725	1164	1178	GICGLMTVIAKLNHN
	726	1168	1182	LMTVIAKLNHNQFEC

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
Rpb2	727	1172	1186	IAKLNHNQFECKGCD
	728	1176	1190	NHNQFECKGCDNKID
	729	1180	1194	FECKGCDNKIDIYQI
	730	1184	1198	GCDNKIDIYQIHIPY
	731	1188	1202	KIDIYQIHIPYAAKL
	732	1192	1206	YQIHIPYAAKLLFQE
	733	1196	1210	IPYAAKLLFQELMAM
	734	1200	1214	AKLLFQELMAMNITP
	735	1204	1218	FQELMAMNITPRLYT
	736	1208	1222	MAMNITPRLYTDRSR
Rpb2/3	737			ITPRLYTDRSRDFMS
	738			LYTDRSRDFMSEEGP
	739			RSRDFMSEEGPQVKI
	740			FMSEEGPQVKIREAS
Rpb3	741	4	18	EGPQVKIREASKDNV
	742	8	22	VKIREASKDNVDFIL
	743	12	26	EASKDNVDFILSNVD
	744	16	30	DNVDFILSNVDLAMA
	745	20	34	FILSNVDLAMANSLR
	746	24	38	NVDLAMANSLRRVMI
	747	28	42	AMANSLRRVMIAEIP
	748	32	46	SLRRVMIAEIPTLAI
	749	36	50	VMIAEIPTLAIDSVE
	750	40	54	EIPTLAIDSVEVETN
	751	44	58	LAIDSVEVETNTTVL
	752	48	62	SVEVETNTTVLADEF
	753	52	66	ETNTTVLADEFIAHR
	754	56	70	TVLADEFIAHRLGLI
	755	60	74	DEFIAHRLGLIPLQS
	756	64	78	AHRLGLIPLQSMDIE
	757	68	82	GLIPLQSMDIEQLEY
	758	72	86	LQSMDIEQLEYSRDC
	759	76	90	DIEQLEYSRDCFCED
	760	80	94	LEYSRDCFCEDHCDK
	761	84	98	RDCFCEDHCDKCSVV
	762	88	102	CEDHCDKCSVVLTLQ
	763	92	106	CDKCSVVLTLQAFGE
	764	96	110	SVVLTLQAFGESEST
	765	100	114	TLQAFGESESTTNVY
	766	104	118	FGESESTTNVYSKDL
	767	108	122	ESTTNVYSKDLVIVS
	768	112	126	NVYSKDLVIVSNLMG
	769	116	130	KDLVIVSNLMGRNIG
	770	120	134	IVSNLMGRNIGHPII
	771	124	138	LMGRNIGHPIIQDKE
	772	128	142	NIGHPIIQDKEGNGV
Rpb3	773	132	146	PIIQDKEGNGVLICK
	774	136	150	DKEGNGVLICKLRKG
	775	140	154	NGVLICKLRKGQELK
	776	144	158	ICKLRKGQELKLTCV
	777	148	162	RKGQELKLTCVAKKG
	778	152	166	ELKLTCVAKKGIAKE
	779	156	170	TCVAKKGIAKEHAKW
	780	160	174	KKGIAKEHAKWGPAA
	781	164	178	AKEHAKWGPAAAIEF
	782	168	182	AKWGPAAAIEFEYDP
	783	172	186	PAAAIEFEYDPWNKL
	784	176	190	IEFEYDPWNKLKHTD
	785	180	194	YDPWNKLKHTDYWYE
	786	184	198	NKLKHTDYWYEQDSA
	787	188	202	HTDYWYEQDSAKEWP
	788	192	206	WYEQDSAKEWPQSKN
	789	196	210	DSAKEWPQSKNCEYE
	790	200	214	EWPQSKNCEYEDPPN
	791	204	218	SKNCEYEDPPNEGDP
	792	208	222	EYEDPPNEGDPFDYK
	793	212	226	PPNEGDPFDYKAQAD
	794	216	230	GDPFDYKAQADTFYM
	795	220	234	DYKAQADTFYMNVES
	796	224	238	QADTFYMNVESVGSI
	797	228	242	FYMNVESVGSIPVDQ
	798	232	246	VESVGSIPVDQVVVR
	799	236	250	GSIPVDQVVVRGIDT
	800	240	254	VDQVVVRGIDTLQKK
	801	244	258	VVRGIDTLQKKVASI
	802	248	262	IDTLQKKVASILLAL
	803	252	266	QKKVASILLALTQMD
	804	256	270	ASILLALTQMDQDKV
	805	260	274	LALTQMDQDKVNFAS
	806	264	278	QMDQDKVNFASGDNN
	807	268	282	DKVNFASGDNNTASN
	808	272	286	FASGDNNTASNMLGS
	809	276	290	DNNTASNMLGSNEDV
	810	280	294	ASNMLGSNEDVMMTG
	811	284	298	LGSNEDVMMTGAEQD
	812	288	302	EDVMMTGAEQDPYSN
	813	292	306	MTGAEQDPYSNASQM
	814	296	310	EQDPYSNASQMGNTG
	815	300	314	YSNASQMGNTGSGGY
	816	304	318	SQMGNTGSGGYDNAW
Rpb3/4	817			NTGSGGYDNAWMNVS
	818			GGYDNAWMNVSTSTF

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
	819			NAWMNVSTSTFQTRR
Rpb4	820	2	16	NVSTSTFQTRRRRLK
	821	6	20	STFQTRRRRLKKVEE
	822	10	24	TRRRRLKKVEEEENA
	823	14	28	RLKKVEEEENAATLQ
	824	18	32	VEEEENAATLQLGQE
	825	22	36	ENAATLQLGQEFQLK
	826	26	40	TLQLGQEFQLKQINH
	827	30	44	GQEFQLKQINHQGEE
	828	34	48	QLKQINHQGEEEELI
	829	38	52	INHQGEEEELIALNL
	830	42	56	GEEEELIALNLSEAR
	831	46	60	ELIALNLSEARLVIK
	832	50	64	LNLSEARLVIKEALV
	833	54	68	EARLVIKEALVERRR
	834	58	72	VIKEALVERRRAFKR
	835	62	76	ALVERRRAFKRSQKK
	836	66	80	RRRAFKRSQKKHKKK
	837	70	84	FKRSQKKHKKKHLKH
	838	74	88	QKKHKKKHLKHENAN
	839	78	92	KKKHLKHENANDETT
	840	82	96	LKHENANDETTAVED
	841	86	100	NANDETTAVEDEDDD
	842	90	104	ETTAVEDEDDDLDED
	843	94	108	VEDEDDDLDEDDVNA
	844	98	112	DDDLDEDDVNADDDD
	845	102	116	DEDDVNADDDDFMHS
	846	106	120	VNADDDDFMHSETRE
	847	110	124	DDDFMHSETREKELE
	848	114	128	MHSETREKELESIDV
	849	118	132	TREKELESIDVLLEQ
	850	122	136	ELESIDVLLEQTTGG
	851	126	140	IDVLLEQTTGGNNKD
	852	130	144	LEQTTGGNNKDLKNT
	853	134	148	TGGNNKDLKNTMQYL
	854	138	152	NKDLKNTMQYLTNFS
	855	142	156	KNTMQYLTNFSRFRD
	856	146	160	QYLTNFSRFRDQETV
	857	150	164	NFSRFRDQETVGAVI
	858	154	168	FRDQETVGAVIQLLK
	859	158	172	ETVGAVIQLLKSTGL
	860	162	176	AVIQLLKSTGLHPFE
	861	166	180	LLKSTGLHPFEVAQL
	862	170	184	TGLHPFEVAQLGSLA
	863	174	188	PFEVAQLGSLACDTA
	864	178	192	AQLGSLACDTADEAK
	865	182	196	SLACDTADEAKTLIP
	866	186	200	DTADEAKTLIPSLNN
	867	190	204	EAKTLIPSLNNKISD
	868	194	208	LIPSLNNKISDDELE
	869	198	212	LNNKISDDELERILK
	870	202	216	ISDDELERILKELSN
	871	206	220	ELERILKELSNLETL
Rpb4/5	872			ILKELSNLETLYMDQ
	873			LSNLETLYMDQENER
	874			ETLYMDQENERNISR
Rpb5	875	1	15	MDQENERNISRLWRA
	876	5	19	NERNISRLWRAFRTV
	877	9	23	ISRLWRAFRTVKEMV
	878	13	27	WRAFRTVKEMVKDRG
	879	17	31	RTVKEMVKDRGYFIT
	880	21	35	EMVKDRGYFITQEEV
	881	25	39	DRGYFITQEEVELPL
	882	29	43	FITQEEVELPLEDFK
	883	33	47	EEVELPLEDFKAKYC
	884	37	51	LPLEDFKAKYCDSMG
	885	41	55	DFKAKYCDSMGRPQR
	886	45	59	KYCDSMGRPQRKMMS
	887	49	63	SMGRPQRKMMSFQAN
	888	53	67	PQRKMMSFQANPTEE
	889	57	71	MMSFQANPTEESISK
	890	61	75	QANPTEESISKFPDM
	891	65	79	TEESISKFPDMGSLW
	892	69	83	ISKFPDMGSLWVEFC
	893	73	87	PDMGSLWVEFCDEPS
	894	77	91	SLWVEFCDEPSVGVK
	895	81	95	EFCDEPSVGVKTMKT
	896	85	99	EPSVGVKTMKTFVIH
	897	89	103	GVKTMKTFVIHIQEK
	898	93	107	MKTFVIHIQEKNFQT
	899	97	111	VIHIQEKNFQTGIFV
	900	101	115	QEKNFQTGIFVYQNN
	901	105	119	FQTGIFVYQNNITPS
	902	109	123	IFVYQNNITPSAMKL
	903	113	127	QNNITPSAMKLVPSI
	904	117	131	TPSAMKLVPSIPPAT
	905	121	135	MKLVPSIPPATIETF
	906	125	139	PSIPPATIETFNEAA
	907	129	143	PATIETFNEAALVVN
	908	133	147	ETFNEAALVVNITHH
	909	137	151	EAALVVNITHHELVP
	910	141	155	VVNITHHELVPKHIR

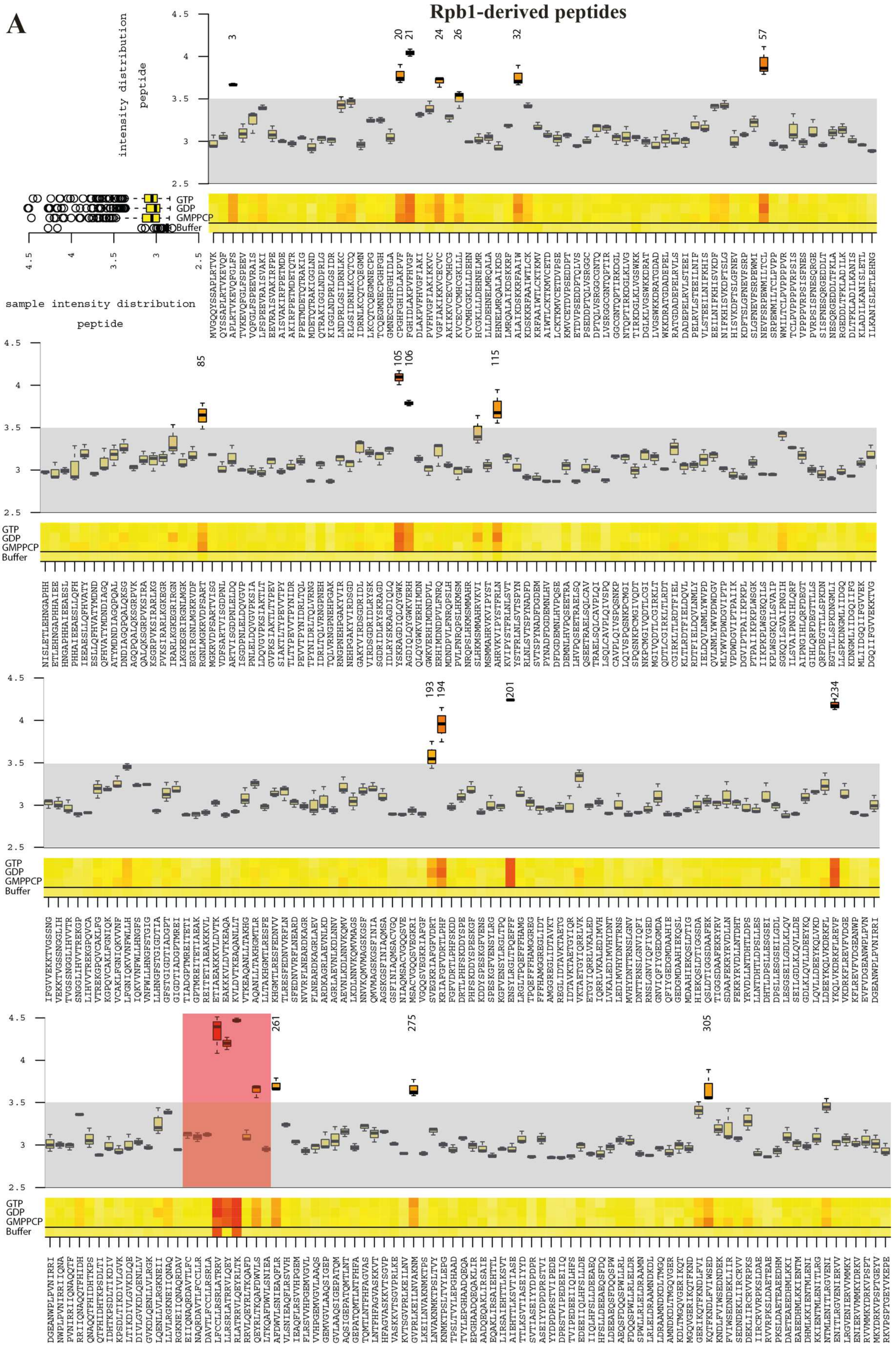
Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
	911	145	159	THHELVPKHIRLSSD
	912	149	163	LVPKHIRLSSDEKRE
	913	153	167	HIRLSSDEKRELLKR
	914	157	171	SSDEKRELLKRYRLK
	915	161	175	KRELLKRYRLKESQL
	916	165	179	LKRYRLKESQLPRIQ
	917	169	183	RLKESQLPRIQRADP
	918	173	187	SQLPRIQRADPVALY
	919	177	191	RIQRADPVALYLGLK
	920	181	195	ADPVALYLGLKRGEV
	921	185	199	ALYLGLKRGEVVKII
	922	189	203	GLKRGEVVKIIRKSE
	923	193	207	GEVVKIIRKSETSGR
	924	197	211	KIIRKSETSGRYASY
	925	201	215	KSETSGRYASYRICM
Rpb5/6	926			SGRYASYRICMMSDY
	927			ASYRICMMSDYEEAF
	928			ICMMSDYEEAFNDGN
Rpb6	929	2	16	SDYEEAFNDGNENFE
	930	6	20	EAFNDGNENFEDFDV
	931	10	24	DGNENFEDFDVEHFS
	932	14	28	NFEDFDVEHFSDEET
	933	18	32	FDVEHFSDEETYEEK
	934	22	36	HFSDEETYEEKPQFK
	935	26	40	EETYEEKPQFKDGET
	936	30	44	EEKPQFKDGETTDAN
	937	34	48	QFKDGETTDANGKTI
	938	38	52	GETTDANGKTIVTGG
	939	42	56	DANGKTIVTGGNGPE
	940	46	60	KTIVTGGNGPEDFQQ
	941	50	64	TGGNGPEDFQQHEQI
	942	54	68	GPEDFQQHEQIRRKT
	943	58	72	FQQHEQIRRKTLKEK
	944	62	76	EQIRRKTLKEKAIPK
	945	66	80	RKTLKEKAIPKDQRA
	946	70	84	KEKAIPKDQRATTPY
	947	74	88	IPKDQRATTPYMTKY
	948	78	92	QRATTPYMTKYERAR
	949	82	96	TPYMTKYERARILGT
	950	86	100	TKYERARILGTRALQ
	951	90	104	RARILGTRALQISMN
	952	94	108	LGTRALQISMNAPVF
	953	98	112	ALQISMNAPVFVDLE
	954	102	116	SMNAPVFVDLEGETD
	955	106	120	PVFVDLEGETDPLRI
	956	110	124	DLEGETDPLRIAMKE
	957	114	128	ETDPLRIAMKELAEK
	958	118	132	LRIAMKELAEKKIPL
	959	122	136	MKELAEKKIPLVIRR
	960	126	140	AEKKIPLVIRRYLPD
	961	130	144	IPLVIRRYLPDGSFE
	962	134	148	IRRYLPDGSFEDWSV
	963	138	152	LPDGSFEDWSVEELI
Rpb6/7	964			SFEDWSVEELIVDLM
	965			WSVEELIVDLMFFIK
	966			ELIVDLMFFIKDLSL
	967			DLMFFIKDLSLNITL
Rpb7	968	3	17	FIKDLSLNITLHPSF
	969	7	21	LSLNITLHPSFFGPR
	970	11	25	ITLHPSFFGPRMKQY
	971	15	29	PSFFGPRMKQYLKTK
	972	19	33	GPRMKQYLKTKLLEE
	973	23	37	KQYLKTKLLEEVEGS
	974	27	41	KTKLLEEVEGSCTGK
	975	31	45	LEEVEGSCTGKFGYI
	976	35	49	EGSCTGKFGYILCVL
	977	39	53	TGKFGYILCVLDYDN
	978	43	57	GYILCVLDYDNIDIQ
	979	47	61	CVLDYDNIDIQRGRI
	980	51	65	YDNIDIQRGRILPTD
	981	55	69	DIQRGRILPTDGSAE
	982	59	73	GRILPTDGSAEFNVK
	983	63	77	PTDGSAEFNVKYRAV
	984	67	81	SAEFNVKYRAVVFKP
	985	71	85	NVKYRAVVFKPFKGE
	986	75	89	RAVVFKPFKGEVVDG
	987	79	93	FKPFKGEVVDGTVVS
	988	83	97	KGEVVDGTVVSCSQH
	989	87	101	VDGTVVSCSQHGFEV
	990	91	105	VVSCSQHGFEVQVGP
	991	95	109	SQHGFEVQVGPMKVF
	992	99	113	FEVQVGPMKVFVTKH
	993	103	117	VGPMKVFVTKHLMPQ
	994	107	121	KVFVTKHLMPQDLTF
	995	111	125	TKHLMPQDLTFNAGS
	996	115	129	MPQDLTFNAGSNPPS
	997	119	133	LTFNAGSNPPSYQSS
	998	123	137	AGSNPPSYQSSEDVI
	999	127	141	PPSYQSSEDVITIKS
	1000	131	145	QSSEDVITIKSRIRV
	1001	135	149	DVITIKSRIRVKIEG
	1002	139	153	IKSRIRVKIEGCISQ

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
	1003	143	157	IRVKIEGCISQVSSI
	1004	147	161	IEGCISQVSSIHAIG
	1005	151	165	ISQVSSIHAIGSIKE
	1006	155	169	SSIHAIGSIKEDYLG
Rpb7/8	1007			AIGSIKEDYLGAIMS
	1008			IKEDYLGAIMSNTLF
	1009			YLGAIMSNTLFDDIF
	1010			IMSNTLFDDIFQVSE
Rpb8	1011	4	18	TLFDDIFQVSEVDPG
	1012	8	22	DIFQVSEVDPGRYNK
	1013	12	26	VSEVDPGRYNKVCRI
	1014	16	30	DPGRYNKVCRIEAAS
	1015	20	34	YNKVCRIEAASTTQD
	1016	24	38	CRIEAASTTQDQCKL
	1017	28	42	AASTTQDQCKLTLDI
	1018	32	46	TQDQCKLTLDINVEL
	1019	36	50	CKLTLDINVELFPVA
	1020	40	54	LDINVELFPVAAQDS
	1021	44	58	VELFPVAAQDSLTVT
	1022	48	62	PVAAQDSLTVTIASS
	1023	52	66	QDSLTVTIASSLNLE
	1024	56	70	TVTIASSLNLEDTPA
	1025	60	74	ASSLNLEDTPANDSS
	1026	64	78	NLEDTPANDSSATRS
	1027	68	82	TPANDSSATRSWRPP
	1028	72	86	DSSATRSWRPPQAGD
	1029	76	90	TRSWRPPQAGDRSLA
	1030	80	94	RPPQAGDRSLADDYD
	1031	84	98	AGDRSLADDYDYVMY
	1032	88	102	SLADDYDYVMYGTAY
	1033	92	106	DYDYVMYGTAYKFEE
	1034	96	110	VMYGTAYKFEEVSKD
	1035	100	114	TAYKFEEVSKDLIAV
	1036	104	118	FEEVSKDLIAVYYSF
	1037	108	122	SKDLIAVYYSFGGLL
	1038	112	126	IAVYYSFGGLLMRLE
	1039	116	130	YSFGGLLMRLEGNYR
	1040	120	134	GLLMRLEGNYRNLNN
	1041	124	138	RLEGNYRNLNNLKQE
	1042	128	142	NYRNLNNLKQENAYL
	1043	132	146	LNNLKQENAYLLIRR
Rpb8/9	1044			KQENAYLLIRRMTTF
	1045			AYLLIRRMTTFRFCR
	1046			IRRMTTFRFCRDCNN
Rpb9	1047	2	16	TTFRFCRDCNNMLYP
	1048	6	20	FCRDCNNMLYPREDK
	1049	10	24	CNNMLYPREDKENNR
	1050	14	28	LYPREDKENNRLLFE
	1051	18	32	EDKENNRLLFECRTC
	1052	22	36	NNRLLFECRTCSYVE
	1053	26	40	LFECRTCSYVEEAGS
	1054	30	44	RTCSYVEEAGSPLVY
	1055	34	48	YVEEAGSPLVYRHEL
	1056	38	52	AGSPLVYRHELITNI
	1057	42	56	LVYRHELITNIGETA
	1058	46	60	HELITNIGETAGVVQ
	1059	50	64	TNIGETAGVVQDIGS
	1060	54	68	ETAGVVQDIGSDPTL
	1061	58	72	VVQDIGSDPTLPRSD
	1062	62	76	IGSDPTLPRSDRECP
	1063	66	80	PTLPRSDRECPKCHS
	1064	70	84	RSDRECPKCHSRENV
	1065	74	88	ECPKCHSRENVFFQS
	1066	78	92	CHSRENVFFQSQQRR
	1067	82	96	ENVFFQSQQRRKDTS
	1068	86	100	FQSQQRRKDTSMVLF
	1069	90	104	QRRKDTSMVLFFVCL
	1070	94	108	DTSMVLFFVCLSCSH
	1071	98	112	VLFFVCLSCSHIFTS
	1072	102	116	VCLSCSHIFTSDQKN
	1073	106	120	CSHIFTSDQKNKRTQ
Rpb9/10	1074			FTSDQKNKRTQFSMI
	1075			QKNKRTQFSMIVPVR
	1076			RTQFSMIVPVRCFSC
	1077			SMIVPVRCFSCGKVV
Rpb10	1078	4	18	PVRCFSCGKVVGDKW
	1079	8	22	FSCGKVVGDKWESYL
	1080	12	26	KVVGDKWESYLNLLQ
	1081	16	30	DKWESYLNLLQEDEL
	1082	20	34	SYLNLLQEDELDEGT
	1083	24	38	LLQEDELDEGTALSR
	1084	28	42	DELDEGTALSRLGLK
	1085	32	46	EGTALSRLGLKRYCC
	1086	36	50	LSRLGLKRYCCRRMI
	1087	40	54	GLKRYCCRRMILTHV
	1088	44	58	YCCRRMILTHVDLIE
	1089	48	62	RMILTHVDLIEKFLR
	1090	52	66	THVDLIEKFLRYNPL
	1091	56	70	LIEKFLRYNPLEKRD
Rpb10/11	1092			FLRYNPLEKRDMNAP
	1093			NPLEKRDMNAPDRFE
	1094			KRDMNAPDRFELFLL

Pol II subunit	Peptide No.	Start a.a.	End a.a.	Sequence
Rpb11	1095	2	16	NAPDRFELFLLGEGE
	1096	6	20	RFELFLLGEGESKLK
	1097	10	24	FLLGEGESKLKIDPD
	1098	14	28	EGESKLKIDPDTKAP
	1099	18	32	KLKIDPDTKAPNAVV
	1100	22	36	DPDTKAPNAVVITFE
	1101	26	40	KAPNAVVITFEKEDH
	1102	30	44	AVVITFEKEDHTLGN
	1103	34	48	TFEKEDHTLGNLIRA
	1104	38	52	EDHTLGNLIRAELLN
	1105	42	56	LGNLIRAELLNDRKV
	1106	46	60	IRAELLNDRKVLFAA
	1107	50	64	LLNDRKVLFAAYKVE
	1108	54	68	RKVLFAAYKVEHPFF
	1109	58	72	FAAYKVEHPFFARFK
	1110	62	76	KVEHPFFARFKLRIQ
	1111	66	80	PFFARFKLRIQTTEG
	1112	70	84	RFKLRIQTTEGYDPK
	1113	74	88	RIQTTEGYDPKDALK
	1114	78	92	TEGYDPKDALKNACN
	1115	82	96	DPKDALKNACNSIIN
	1116	86	100	ALKNACNSIINKLGA
	1117	90	104	ACNSIINKLGALKTN
	1118	94	108	IINKLGALKTNFETE
	1119	98	112	LGALKTNFETEWNLQ
	1120	102	116	KTNFETEWNLQTLAA
	1121	106	120	ETEWNLQTLAADDAF
Rpb11/12	1122			NLQTLAADDAFMSRE
	1123			LAADDAFMSREGFQI
	1124			DAFMSREGFQIPTNL
Rpb12	1125	2	16	SREGFQIPTNLDAAA
	1126	6	20	FQIPTNLDAAAAGTS
	1127	10	24	TNLDAAAAGTSQART
	1128	14	28	AAAAGTSQARTATLK
	1129	18	32	GTSQARTATLKYICA
	1130	22	36	ARTATLKYICAECSS
	1131	26	40	TLKYICAECSSKLSL
	1132	30	44	ICAECSSKLSLSRTD
	1133	34	48	CSSKLSLSRTDAVRC
	1134	38	52	LSLSRTDAVRCKDCG
	1135	42	56	RTDAVRCKDCGHRIL
	1136	46	60	VRCKDCGHRILLKAR
	1137	50	64	DCGHRILLKARTKRL
	1138	54	68	RILLKARTKRLVQFE
	1139	56	70	LLKARTKRLVQFEAR

Supplemental Table S2 List of all 15meric Pol II-derived peptides, which interact with Npa3. 'Start a.a.' and 'End a.a.' depicts the first and last amino acid of the corresponding peptide in the respective Pol II subunit sequence.

Pol II subunit	Peptide No	Start a.a.	End a.a.	Sequence	Interface
Rpb1	3	9	23	APLRTVKEVQFGLFS	Yes
	20	77	91	CPGHFGHIDLAKPVF	Yes
	21	81	95	FGHIDLAKPVFHVGF	Yes
	24	93	107	VGFIAKIKKVCECVC	Yes
	26	101	115	KVCECVCMHCGKLLL	No
	32	125	139	ALAIKDSKKRFAAIW	No
	57	225	239	NEVFSRPEWMILTCL	Yes
	85	337	351	RGNLMGKRVDFSART	Yes
	105	417	431	YSKRAGDIQLQYGWK	Yes
	106	421	435	AGDIQLQYGWKVERH	Yes
	115	457	471	AHRVKVIPYSTFRLN	Yes
	193	769	783	SVEGKRIAFGFVDRT	Yes
	194	773	787	KRIAFGFVDRTLPHF	Yes
	201	801	815	ENSYLRGLTPQEFFF	Yes
	234	933	947	YKQLVKDRKFLREVF	Yes
	261	1041	1055	AFDWVLSNIEAQFLR	Yes
	275	1097	1111	GVPRLKEILNVAKNM	No
	305	1217	1231	KQTFKNDLFVIWSED	No
	375	1497	1511	DSGSNDAMAGGFTAY	Lacking in 1WCM
Rpb2	463	116	130	EARLRNLTYSSGLFV	Yes
	464	120	134	RNLTYSSGLFVDVKK	No
	465	124	138	YSSGLFVDVKKRTYE	No
	481	188	202	DLYKLKECPFDMGGY	Yes
	482	192	206	LKECPFDMGGYFIIN	Yes
	525	364	378	ITQLEGFESRKAFFL	No
	527	372	386	SRKAFFLGYMINRLL	No
	539	420	434	LFKKLTKDIFRYMQR	No
	547	452	466	TITSGLKYALATGNW	No
	630	784	798	NYNVRMDTMANILYY	Yes
	645	844	858	SSIDRGLFRSLFFRS	Yes
	646	848	862	RGLFRSLFFRSYMDQ	Yes
	647	852	866	RSLFFRSYMDQEKKY	Yes
	730	1184	1198	GCDNKIDIYQIHIPY	Yes
Rpb4	833	54	68	EARLVIKEALVERRR	Yes
	834	58	72	VIKEALVERRRAFKR	Yes
	837	70	84	FKRSQKKHKKKHLKH	Yes
	855	142	156	KNTMQYLTNFSRFRD	Yes
Rpb5	892	69	83	ISKFPDMGSLWVEFC	No
	921	185	199	ALYLGLKRGEVVKII	No
Rpb7	970	11	25	ITLHPSFFGPRMKQY	Yes
	971	15	29	PSFFGPRMKQYLKTK	Yes
	975	31	45	LEEVEGSCTGKFGYI	Yes
	976	35	49	EGSCTGKFGYILCVL	Yes
	977	39	53	TGKFGYILCVLDYDN	Yes
	984	67	81	SAEFNVKYRAVVFKP	Yes
Rpb8	1036	104	118	FEEVSKDLIAVYYSF	Yes
	1037	108	122	SKDLIAVYYSFGGLL	Yes
	1038	112	126	IAVYYSFGGLLMRLE	Yes
	1039	116	130	YSFGGLLMRLEGNYR	Yes
	1043	132	146	LNNLKQENAYLLIRR	Yes
Rpb9	1047	2	16	TTFRFCRDCNNMLYP	Yes
Rpb11	1106	46	60	IRAELLNDRKVLFAA	Yes
	1108	54	68	RKVLFAAYKVEHPFF	Yes
	1109	58	72	FAAYKVEHPFFARFK	Yes
	1110	62	76	KVEHPFFARFKLRIQ	Yes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sample intensity distribution
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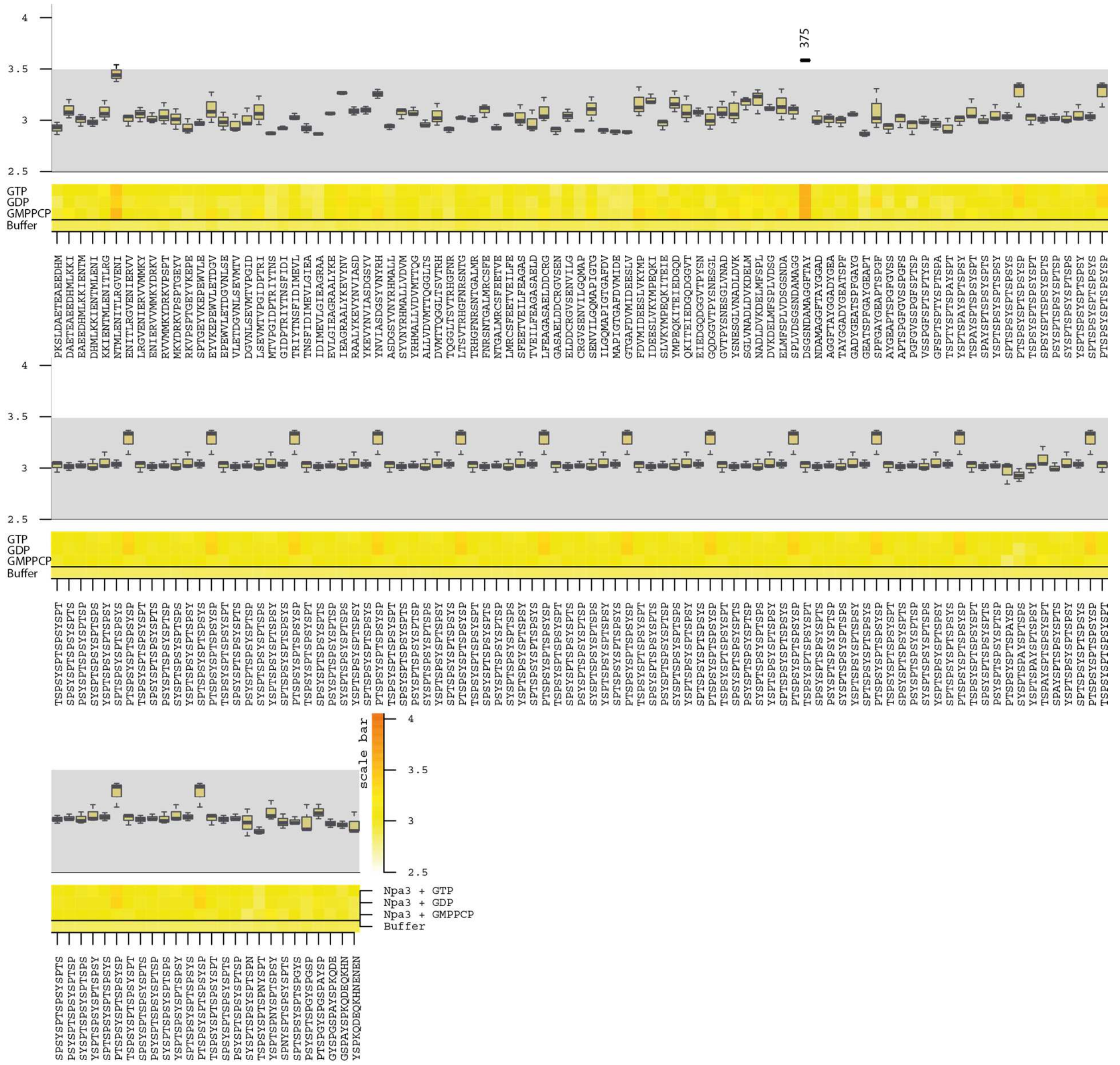
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RVVMMKYDRKVPSPT
MKYDRKVPSPTGEYV
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TRIYTNSFIDIMEVL
TNSFIDIMEVLGIEA
IDIMEVLGIEAGRAA
EVLGIEAGRAALYKE
IEAGRAALYKEVYNV
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TVEILFEAGASAELD
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ELDDCRGVSENVILG
CRGVSENVILGQMAP
SENVILGQMAPIGTG
ILGQMAPIGTGAFDV
MAPIGTGAFDVMIDE
GTGAFDVMIDEESLV
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SLVKYMPEQKITEIE
YMPEQKITEIEDGQD
QKITEIEDGQDGGVT
EIEDGQDGGVTPYSN
GQDGGVTPYSNESGL
GVTPYSNESGLVNAD
YSNESGLVNADLDVK
SGLVNADLDVKDELM
NADLDVKDELMFSPL
DVKDELMFSPLVDSG
ELMFSPLVDSGSNDA
SPLVDSGSNDAMAGG
DSGSNDAMAGGFTAY
NDAMAGGFTAYGGAD
AGGFTAYGGADYGEA
TAYGGADYGEATSPF
GADYGEATSPFGAYG
GEATSPFGAYGEAPT
SPFGAYGEAPTSPGF
AYGEAPTSPGFGVSS
APTSPGFGVSSPGFS
PGFGVSSPGFSPTSP
VSSPGFSPTSPTYSP
GFSPTSPTYSPTSPA
TSPTYSPTSPAYSPT
YSPTSPAYSPTSPSY
TSPAYSPTSPSYSPT
SPAYSPTSPSYSPTS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
4
3.5
3
2.5
GTP
GDP
GMPPCP
Buffer
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
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SPSYSPTSPSYSPTS
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YSPTSPSYSPTSPSY
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TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
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TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
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SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
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SPSYSPTSPSYSPTS
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PTSPSYSPTSPAYSP
SYSPTSPAYSPTSPS
YSPTSPAYSPTSPSY
TSPAYSPTSPSYSPT
SPAYSPTSPSYSPTS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
scale bar
4
3.5
3
2.5
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPS
YSPTSPSYSPTSPSY
SPTSPSYSPTSPSYS
PTSPSYSPTSPSYSP
TSPSYSPTSPSYSPT
SPSYSPTSPSYSPTS
PSYSPTSPSYSPTSP
SYSPTSPSYSPTSPN
TSPSYSPTSPNYSPT
YSPTSPNYSPTSPSY
SPNYSPTSPSYSPTS
SPTSPSYSPTSPGYS
PSYSPTSPGYSPGSP
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YSPKQDEQKHNENEN

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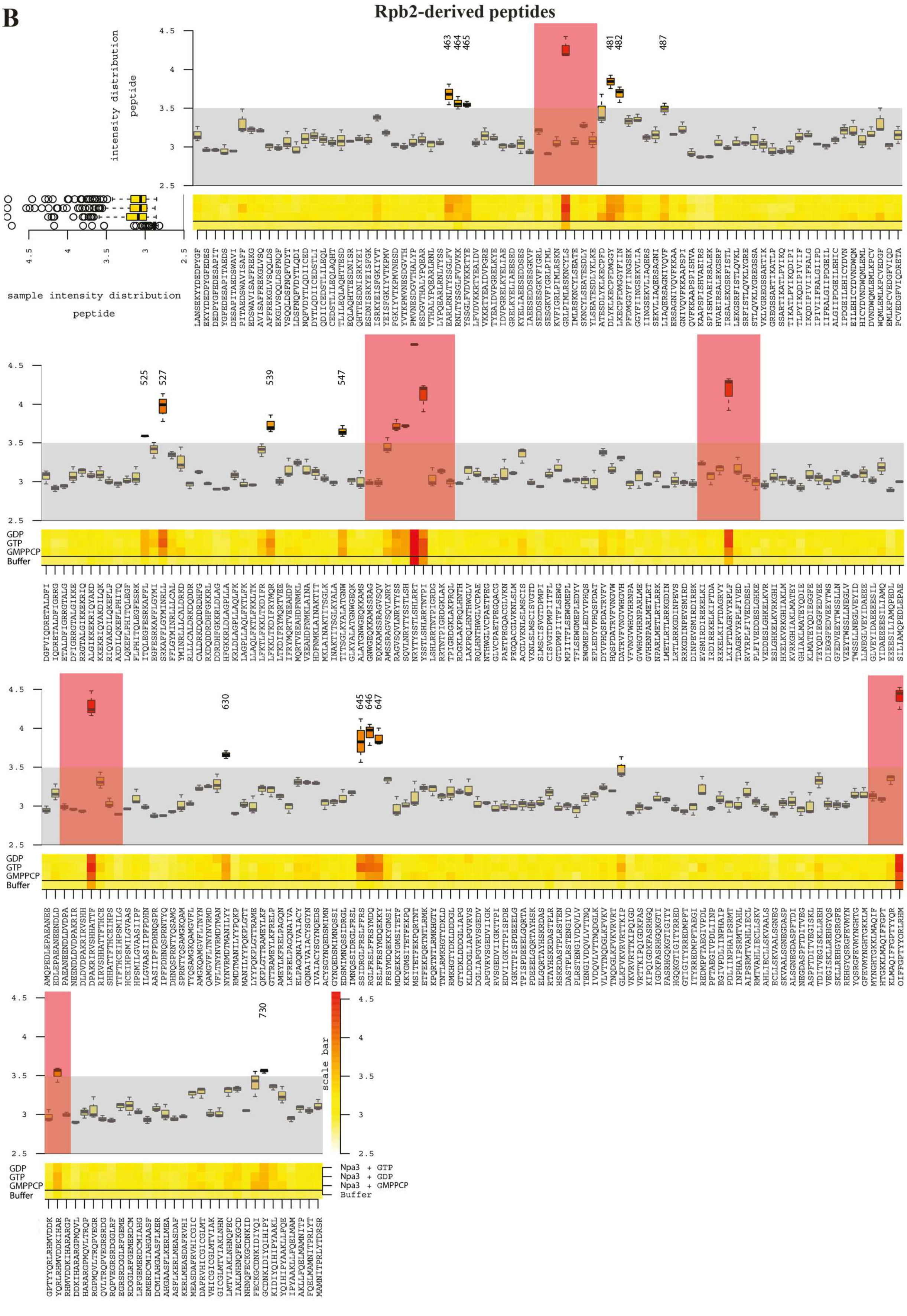
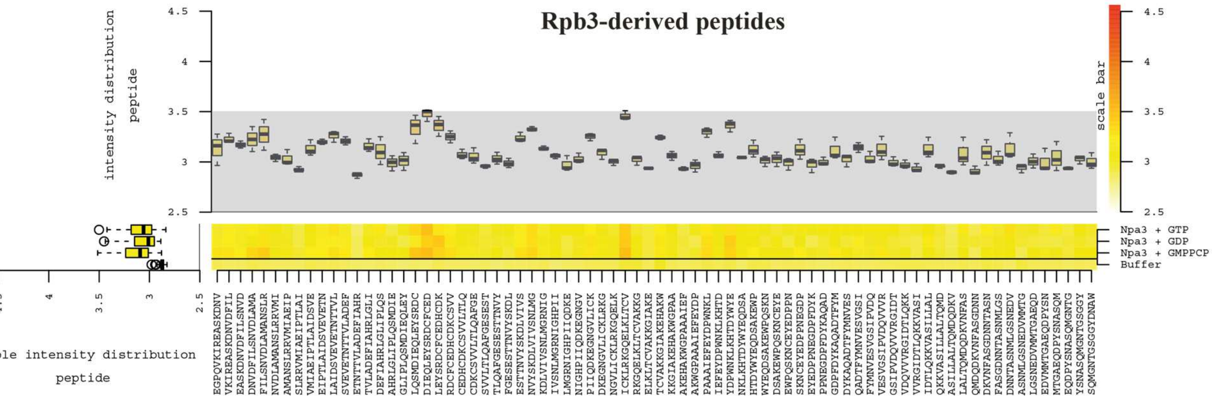
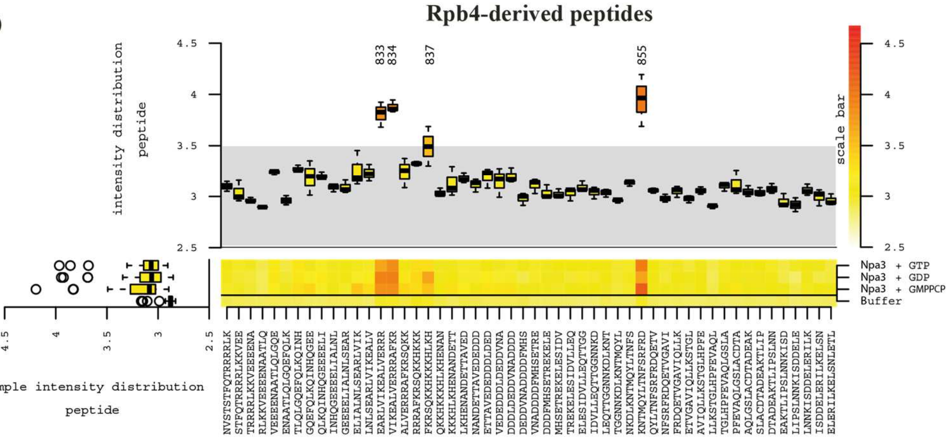

Rpb2-derived peptides
intensity distribution
peptide
sample intensity distribution
peptide
4.5
4
3.5
3
2.5
463
464
465
481
482
487
525
527
539
547
630
645
646
647
730
GDP
GTP
GMPPCP
Buffer
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer

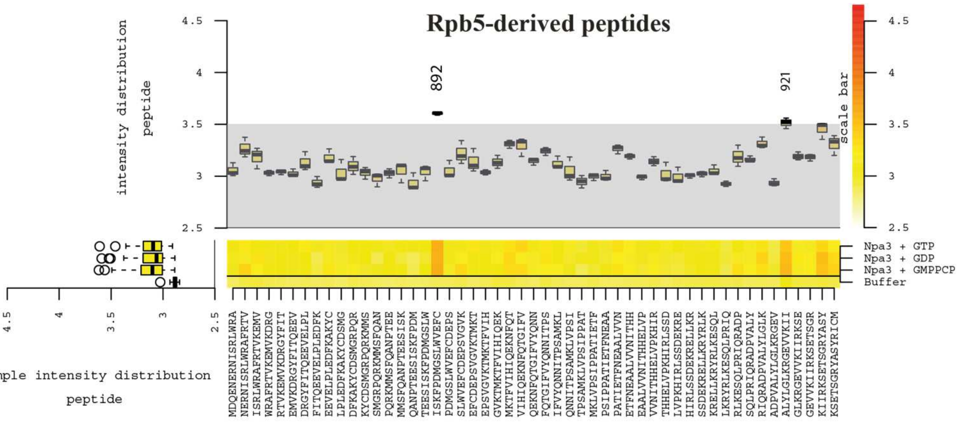
C


Rpb3-derived peptides
intensity distribution
peptide
4.5
4
3.5
3
2.5
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide

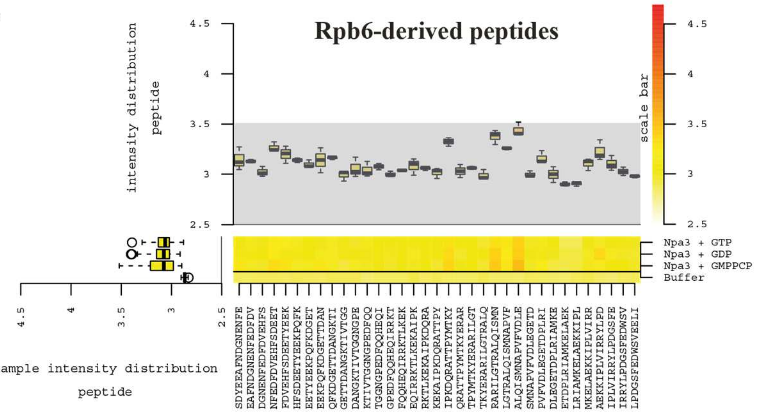
D


Rpb4-derived peptides
intensity distribution
peptide
833
834
837
855
4.5
4
3.5
3
2.5
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide

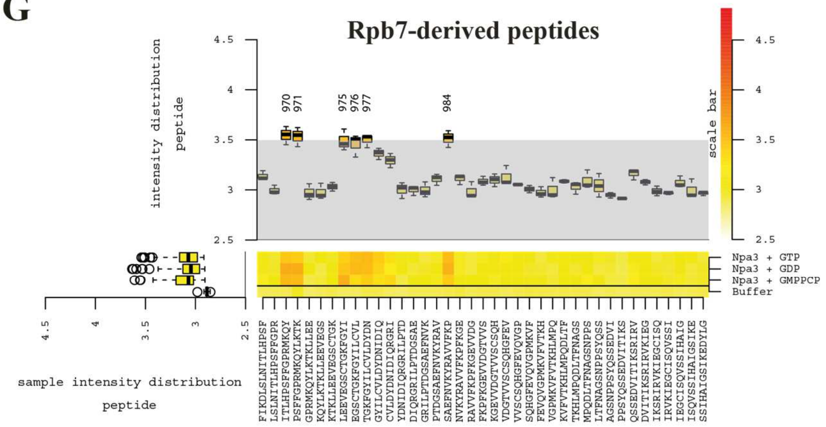
E


Rpb5-derived peptides
intensity distribution
peptide
892
921
4.5
4
3.5
3
2.5
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide

F


Rpb6-derived peptides
intensity distribution
peptide
4.5
4
3.5
3
2.5
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide

G


Rpb7-derived peptides
intensity distribution
peptide
4.5
4
3.5
3
2.5
970
971
975
976
977
984
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide
FIKDLSLNITLHPSF
LSLNITLHPSFFGPR
ITLHPSFFGPRMKQY
PSFFGPRMKQYLKTK
GPRMKQYLKTKLLEE
KQYLKTKLLEEVEGS
KTKLLEEVEGSCTGK
LEEVEGSCTGKFGYI
EGSCTGKFGYILCVL
TGKFGYILCVLDYDN
GYILCVLDYDNIDIQ
CVLDYDNIDIQRGRI
YDNIDIQRGRILPTD
DIQRGRILPTDGSAE
GRILPTDGSAEFNVK
PTDGSAEFNVKYRAV
SAEFNVKYRAVVFKP
NVKYRAVVFKPFKGE
RAVVFKPFKGEVVDG
FKPFKGEVVDGTVVS
KGEVVDGTVVSCSQH
VDGTVVSCSQHGFEV
VVSCSQHGFEVQVGP
SQHGFEVQVGPMKVF
FEVQVGPMKVFVTKH
VGPMKVFVTKHLMPQ
KVFVTKHLMPQDLTF
TKHLMPQDLTFNAGS
MPQDLTFNAGSNPPS
LTFNAGSNPPSYQSS
AGSNPPSYQSSEDVI
PPSYQSSEDVITIKS
QSSEDVITIKSRIRV
DVITIKSRIRVKIEG
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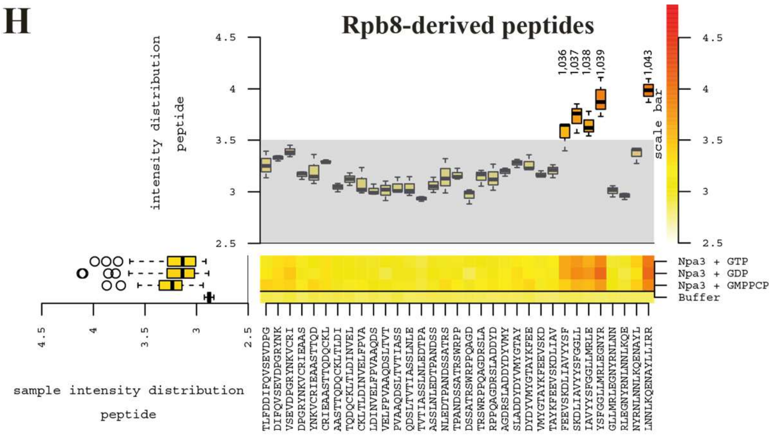
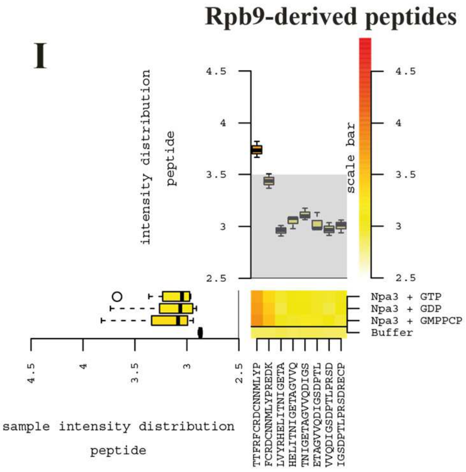
IRVKIEGCISQVSSI
IEGCISQVSSIHAIG
ISQVSSIHAIGSIKE
SSIHAIGSIKEDYLG

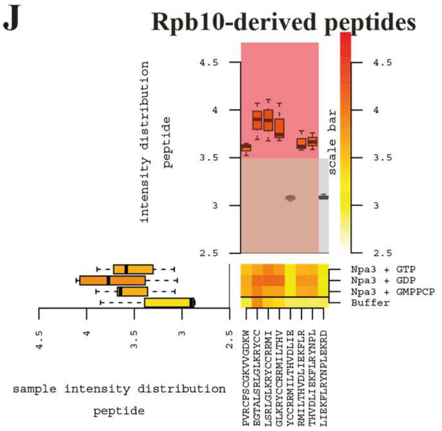
H


Rpb8-derived peptides
intensity distribution
peptide
4.5
4
3.5
3
2.5
1,036
1,037
1,038
1,039
1,043
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide
TLFDDIFQVSEVDPG
DIFQVSEVDPGRYNK
VSEVDPGRYNKVCRI
DPGRYNKVCRIEAAS
YNKVCRIEAASTTQD
CRIEAASTTQDQCKL
AASTTQDQCKLTLDI
TQDQCKLTLDINVEL
CKLTLDINVELFPVA
LDINVELFPVAAQDS
VELFPVAAQDSLTVT
PVAAQDSLTVTIASS
QDSLTVTIASSLNLE
TVTIASSLNLEDTPA
ASSLNLEDTPANDSS
NLEDTPANDSSATRS
TPANDSSATRSWRPP
DSSATRSWRPPQAGD
TRSWRPPQAGDRSLA
RPPQAGDRSLADDYD
AGDRSLADDYDVVMY
SLADDYDVVMYGTAY
DYDVVMYGTAYKFEE
VMYGTAYKFEEVSKD
TAYKFEEVSKDLIAV
FEEVSKDLIAVYYSF
SKDLIAVYYSFGGLL
IAVYYSFGGLLMRLE
YSFGGLLMRLEGNYR
GLLMRLEGNYRNLNN
RLEGNYRNLNNLKQE
NYRNLNNLKQENAYL
LNNLKQENAYLLIRR

I


Rpb9-derived peptides
intensity distribution
peptide
4.5
4
3.5
3
2.5
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide
TTFRFCRDCNNMLYP
FCRDCNNMLYPREDK
LVYRHELITNIGETA
HELITNIGETAGVVQ
TNIGETAGVVQDIGS
ETAGVVQDIGSDPTL
VVQDIGSDPTLPRSD
IGSDPTLPRSDRECP

J


Rpb10-derived peptides
intensity distribution
peptide
4.5
4
3.5
3
2.5
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide
PVRCFSCGKVVGDKW
EGTALSRLGLKRYCC
LSRLGLKRYCCRRMI
GLKRYCCRRMILTHV
YCCRRMILTHVDLIE
RMILTHVDLIEKFLR
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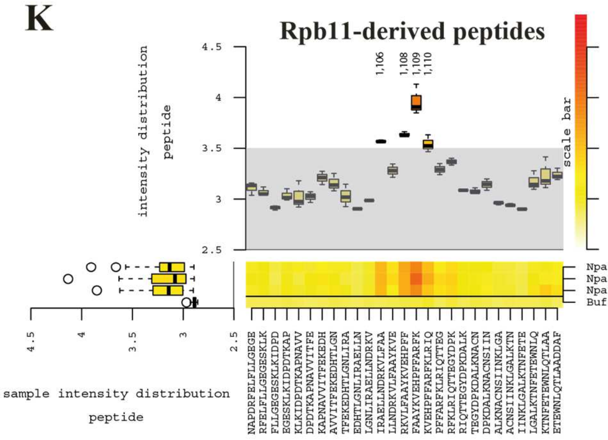
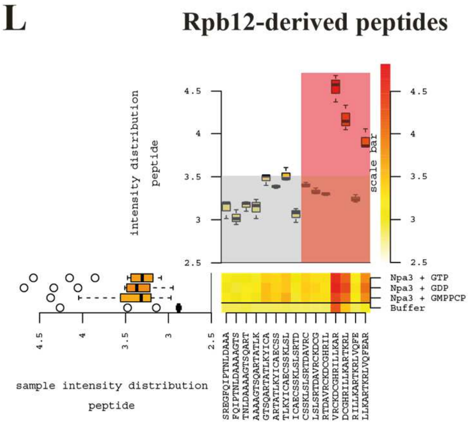
LIEKFLRYNPLEKRD

K


Rpb11-derived peptides
intensity distribution
peptide
4.5
4
3.5
3
2.5
1,106
1,108
1,109
1,110
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide
NAPDRFELFLLGEGE
RFELFLLGEGESKLK
FLLGEGESKLKIDPD
EGESKLKIDPDTKAP
KLKIDPDTKAPNAVV
DPDTKAPNAVVITFE
KAPNAVVITFEKEDH
AVVITFEKEDHTLGN
TFEKEDHTLGNLIRA
EDHTLGNLIRAELLN
LGNLIRAELLNDRKV
IRAELLNDRKVLFAA
LLNDRKVLFAAYKVE
RKVLFAAYKVEHPFF
FAAYKVEHPFFARFK
KVEHPFFARFKLRIQ
PFFARFKLRIQTTEG
RFKLRIQTTEGYDPK
RIQTTEGYDPKDALK
TEGYDPKDALKNACN
DPKDALKNACNSIIN
ALKNACNSIINKLGA
ACNSIINKLGALKTN
IINKLGALKTNFETE
LGALKTNFETEWNLQ
KTNFETEWNLQTLAA
ETEWNLQTLAADDAF

L


Rpb12-derived peptides
intensity distribution
peptide
4.5
4
3.5
3
2.5
scale bar
Npa3 + GTP
Npa3 + GDP
Npa3 + GMPPCP
Buffer
sample intensity distribution
peptide
SREGFQIPTNLDAAA
FQIPTNLDAAAAGTS
TNLDAAAAGTSQART
AAAAGTSQARTATLK
GTSQARTATLKYICA
ARTATLKYICAECSS
TLKYICAECSSKLSL
ICAECSSKLSLSRTD
CSSKLSLSRTDAVRC
LSLSRTDAVRCKDCG
RTDAVRCKDCGHRIL
VRCKDCGHRILLKAR
DCGHRILLKARTKRL
RILLKARTKRLVQFE
LLKARTKRLVQFEAR

Supplemental Figure S4 Heatmap and boxplot representation of Npa3 binding to 1,139 Pol II-derived peptides in the presence of GTP, GDP and GMPPCP, respectively. Results are shown individually for all 12 Pol II subunits Rpb1-Rpb12 (Supplemental Figures. S4 A-L, respectively). Control experiments were performed without Npa3 and nucleotides to test cross-reactivity of the anti-His antibody (Buffer). Red boxes indicate false-positive binding of the antibody to the peptides, either directly or in overlapping regions. These peptides were not used for further analysis. Intensity distributions are shown in logarithmic scale. Upper panels: Boxplot for each peptide showing the signal distribution of all samples. Left panels: Boxplot for each sample showing the signal distribution of all peptides from the corresponding Pol II subunit. Peptides with signal intensity <3.5 were defined as unbound (grey area). Peptide numbers are shown for Npa3 binding peptides above the boxplots (see Supplemental Tables S1 and S2).