Supplementary Material: Full sequence alignment for the RPB7 family

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RPOE_METMA|21226698       ----------------------------------------------MYKLMKLVDTVRIP 14
RPOE_METAC|20092492       ----------------------------------------------MYKLMKLIDTVRIP 14
RPOE_METBA|23051810       ----------------------------------------------MYKMMKLVDTVRIP 14
RPOE_ARCFU|11498717       ----------------------------------------------MYARIKLRDTVRVP 14
RPOE_METTH|15678292       ----------------------------------------------MYYVTKIVDTVRIP 14
RPOE_PYRHO|14591652       ----------------------------------------------MYKIVTVKDVVRIP 14
RPOE_PYRAB|14521883       ----------------------------------------------MYKIVTVKDVVRIP 14
RPOE_PYRFU|18976628       ----------------------------------------------MYKIVTVKDVVRIP 14
RPOE_METJA|15668573       ----------------------------------------------MYKILEIADVVKVP 14
RPOE_HALO|15790905        ----------------------------------------------MYKRARLKDTIEVP 14
RPOE_THEAC|16082590       ----------------------------------------------MYMLVEDKYIARVP 14
RPOE_THEVO|13541317       ----------------------------------------------MYMMVEDKYIARIP 14
RPOE_FERAC|22406866       ----------------------------------------------MYILLEDEYVIRVP 14
RPOE_METKA|20094887       ----------------------------------------------MYELVELETTVRIP 14
RPOE_SULTO|15920582       ----------------------------------------------MFKLIKAKGIIRIP 14
RPOE_SULAC|730613         ----------------------------------------------MFKLVRAKGIVRIP 14
RPOE_SULSO|15897347       ----------------------------------------------MYKLIKARSIVRIP 14
RPOE_PYRAE|18314155       ---------------------------------------------MPFRLVEAEDYVRVP 15
RPOE_AERPE|14600570       ---------------------------------------------MYYEYVVEEWIGMEP 15
RPC25_YEAST|6322705       ----------------------------------------------MFILSKIADLVRIP 14
RPC25_SCHPO|19112860      ----------------------------------------------MFLLSRFSDIISIH 14
RPC25_MOUSE|21313542      ----------------------------------------------MFVLVEMVDTVPIP 14
RPC25_HUMAN|22068810      ----------------------------------------------MFVLVEMVDTVRIP 14
RPC25_DROME|7294695       ----------------------------------------------MFVLAELKDNVRIA 14
PPC25_ARATH|15222202      ----------------------------------------------MFYLSELEHSLRVP 14
RPC25_CAEEL|17566938      ----------------------------------------------MFILSLLHDTVAIQ 14
RPB7_SCHPO|19114885       ---------------------------------------------MPFFLKELSLTISLH 15
RPB7_CANAL|12655858       ----------------------------------------------MFFLKDLSLNLTLH 14
RPB7_YEAST|6320612        ----------------------------------------------MFFIKDLSLNITLH 14
RPB7_DROME|23171325       ----------------------------------------------MFYHISLEQEILLH 14
RPB7_ANOGA|21288656       ----------------------------------------------MFYHISLEHEILLH 14
RPB7_HUMAN|4505947        ----------------------------------------------MFYHISLEHEILLH 14
RPB7_CAEEL|17510349       ----------------------------------------------MFFHLSLDHEVCLH 14
RPB7_ARATH|15237831       ----------------------------------------------MFFHIVLERNMQLH 14
RPB7_SOYBN|1173137        ----------------------------------------------MFFHIVLERNMQLH 14
RPB7_ENCCU|19074596       ----------------------------------------------MFFVRDFVQNIHLS 14
RPB7_PLAFA|23508072       ----------------------------------------------MYFVIEEWKNVIIK 14
RPB7_PLAYO|23481815       ----------------------------------------------MYFVIEEWKNVIIK 14
RPB7_GILTH|13811986       ----------------------------------------------MYAIMTLNQNLFIP 14
RPA43_YEAST|6324916       ----------MSQVKRANENRETARFIKKHKKQVTNPIDEKNGTSNCIVRVPIALYVSLA 50
RPA43_SCHPO|19113457      ------------------------------------------MPDLSLYKQTVDLYLSIA 18
RPA43_DROME|7297185       ---------------MAKILQKYIKFSVKELENYAS------SPESCVRCITTDMHLAMG 39
RPA43_ANOGA|21288304      --------------MHRTTIAKYTKFSAEELQKSTA------DPLSCVAAVQLNEILSLR 40
RPA43_HUMAN|20539462      MAAGCSEAPRPAAASDGSLVGQAGVLPCLELPTYAAACALVNSRYSCLVAGPHQRHIALS 60
RPA43_MOUSE|20847950      MAAGSVESQRSQAASERPVAGQAGVLPCLELPSYAAACALVGSRYSCLVAAPHRRHIALS 60
RPA43_ARATH|18410907      --------------------------------------------MEGLKLSEAELMIFIH 16
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RPOE_METMA|21226698       PTLLGEEIMPTIKNALREKLEGQ----------VDKKLGSLVAVYNIDEVG--------- 55
RPOE_METAC|20092492       PTLLGEEIMPTIKNALREKLEGQ----------VDKKLGSLVAVYNIDEVG--------- 55
RPOE_METBA|23051810       PTLLGEEVTQTVKNALREKLEGQ----------VDKKLGSLVAICKIVEIG--------- 55
RPOE_ARCFU|11498717       PSKLGEDIEKVINSLLWEQFEGR----------LDREYGMIIGIESIEEIG--------- 55
RPOE_METTH|15678292       PDRFEEPLEEVAVEVLNETYVGR----------MDKNLGQLITVKEIEDIG--------- 55
RPOE_PYRHO|14591652       PRMFTMDPKEAAMLVLRDTYEGT----------YDRDEGVILSIVEVKEVG--------- 55
RPOE_PYRAB|14521883       PRMFTMDPKEAAMLVLRETYEGK----------YDKDEGVILSIVEVKEVG--------- 55
RPOE_PYRFU|18976628       PTMFTMDPKEAAKIILRETYEGT----------YDKDEGVILSILEVKDIK--------- 55
RPOE_METJA|15668573       PEEFGKDLKETVKKILMEKYEGR----------LDKDVGFVLSIVDVKDIG--------- 55
RPOE_HALO|15790905        PEYLGAVGPDLVKRLLQDKLEGR----------MDEDVGSIVTVTEVHDLG--------- 55
RPOE_THEAC|16082590       PEMLGEDYDVAVREVTKRSLEGRLVDVINEKTSQNEGKYLVISVLYTESIG--------- 65
RPOE_THEVO|13541317       PDMLGEDYDKAVEEVTKRSLEGKLVDVVNEKTGVNEGKYLVISIISTKAVG--------- 65
RPOE_FERAC|22406866       PELLNDNYSDAVAEASKSTLEGKLVDI--QEGQKNIGKSYIVSVNSIEMKG--------- 63
RPOE_METKA|20094887       PTQFTSDVEDAVLKALENDVEGKLFRE----DDTGEPIGFVVFVDEILDVE--------- 61
RPOE_SULTO|15920582       PEYFGQPLDEIALQILRQEYQEK----------MIKDLGLVLAVLDAKVSE--------- 55
RPOE_SULAC|730613         PEYFGQSVDEIAIKILRQEYQEK----------LIKDIGVVLGIVNAKASE--------- 55
RPOE_SULSO|15897347       PNEFGKPLNEIALNELRQQYQEK----------ILKDLGLVLAILNVKTSE--------- 55
RPOE_PYRAE|18314155       PTEFGKPLEDIALSQLKSRYEGK----------VLREVGYIVAVLNVKVGR--------- 56
RPOE_AERPE|14600570       ASIYSSEDLDKAALEHLRRLEGR----------IDEEMGVIVAVLDAKIVG--------- 56
RPC25_YEAST|6322705       PDQFHRDTISAITHQLNNKFANK----------IIPNVGLCITIYDLLTVE--------- 55
RPC25_SCHPO|19112860      PSNFWKPTKEALAEEIHKKYANK----------VIQNIGLAICVYDFLKIG--------- 55
RPC25_MOUSE|21313542      PWQFERKLNDSIAEELNKKLANK----------VVYNVGLCICLFDITKLE--------- 55
RPC25_HUMAN|22068810      PWQFERKLNDSIAEELNKKLANK----------VVYNVGLCICLFDITKLE--------- 55
RPC25_DROME|7294695       PDQFHLKLVDAVRDEIDRKLANK----------VLLNVGLCIALKDIVSLK--------- 55
PPC25_ARATH|15222202      PHLLNLPLEDAIKSVLQNVFLDK----------VLADLGLCVSIYDIKSVE--------- 55
RPC25_CAEEL|17566938      PHQLSSDQQIVIKKRLNERLANK----------IIPDLGLCICVYDINEIG--------- 55
RPB7_SCHPO|19114885       PSYFGPRMQDYLKAKLLADVEGT----------CSGQYGYIICVLDSNTID--------- 56
RPB7_CANAL|12655858       PSFFGPQMDQYLREKLLSDVEGT----------CTGQFGYIVCVLDSMNID--------- 55
RPB7_YEAST|6320612        PSFFGPRMKQYLKTKLLEEVEGS----------CTGKFGYILCVLDYDNID--------- 55
RPB7_DROME|23171325       PRYFGPQLLETVKQKLYSEVEGT----------CTGKYGFVIAVTTIDQI---------- 54
RPB7_ANOGA|21288656       PRYFGPQLIETVKQKLYTEVEGT----------CTGKYGFVIAVTTIDDI---------- 54
RPB7_HUMAN|4505947        PRYFGPNLLNTVKQKLFTEVEGT----------CTGKYGFVIAVTTIDNI---------- 54
RPB7_CAEEL|17510349       PKYFGPNLNETIKMKLFNEVEGT----------CTGKYGFVIAVTTIDTI---------- 54
RPB7_ARATH|15237831       PRFFGRNLKENLVSKLMKDVEGT----------CSGRHGFVVAITGIDTI---------- 54
RPB7_SOYBN|1173137        PRYFGRNLRDNLVSKLMKDVEGT----------CSGRHGFVVAVTGIENI---------- 54
RPB7_ENCCU|19074596       PNYLGPNIQALIEEYLLSKVEGS----------CSSS-GYVVMVLSIDEI---------- 53
RPB7_PLAFA|23508072       PSQLGPRYQQYIEDMLRNSVEGQ----------CSVKYGYVICVIRIIHS---------- 54
RPB7_PLAYO|23481815       PSQLGPKYQQYIEDMLRNSIEGQ----------CTEKYGYIICVIRIMHS---------- 54
RPB7_GILTH|13811986       AKLLNNQLKSTLIAQLITLTEGL----------PFGNVGSIIMIINIDNQK--------- 55
RPA43_YEAST|6324916       PMYLENPLQGVMKQHLNPLVMKY----------NNKVGGVVLGYEGLKILDADPLSKEDT 100
RPA43_SCHPO|19113457      PGHSRDPLNAI-QEHMDSMILSK----------LPRINGIVLAYDNIRFL---------- 57
RPA43_DROME|7297185       PYGMANFKHALHELLIRTKVGFY----------DSGLDGIVLGIKNIKVL---------- 79
RPA43_ANOGA|21288304      PRDCEHIVKGVKRC-VTDKIGRY----------HAKLNGIVLGYAKIRVD---------- 79
RPA43_HUMAN|20539462      PRYLNRKRTGIREQ-LDAELLRY----------SESLLGVPIAYDNIKVV---------- 99
RPA43_MOUSE|20847950      PRYLSRKRTGIREQ-LDAELLRY----------SESLLGVPIAYDNIRVV---------- 99
RPA43_ARATH|18410907      PSQSRNVFQGICRELSSLLFQYN----------ETFDGVLLAYDATVKSK---------- 56
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RPOE_METMA|21226698       ---EGHILVGDGAVYYDVTFEAIMFYPDLQEIIEGEVVEAVGFGVFIGM-GPMDGLLHVS 111
RPOE_METAC|20092492       ---EGHILVGDGAVYYDVTFEAIMFIPELQEIIEGEVVEAVGFGVFVGM-GPMDGLLHVS 111
RPOE_METBA|23051810       ---EGHILVGDGAVYYDVTFEAIMFVPELQEIIEGEVVETVGFGVFVGM-GPMDGLLHVS 111
RPOE_ARCFU|11498717       ---EGRIIEGDGGVYFDVVFNAICFRPLHQEVVEGEVIEIVEFGAFVSI-GPFDALLHMS 111
RPOE_METTH|15678292       ---IGKVIMGDGAAYHEVTFTALFFKPELHEIVEGEVIEIAEFGAFVRI-GPVDGLVHVS 111
RPOE_PYRHO|14591652       ---DGIIVPGDGATYHEVVFDVLVWEPKRDEVVEGTVVDVVPFGAFIRI-GPMDGLVHIS 111
RPOE_PYRAB|14521883       ---DGIIVPGDGATYHEVVFDVLVWEPKQQEVVEGTVVDAVPFGAFVRI-GPMDGLVHIS 111
RPOE_PYRFU|18976628       ---DGIIIPGDGATYHEVVFDVLVWEPKIHEVVEGYVADVMPFGAFIRI-GPIDGLVHIS 111
RPOE_METJA|15668573       ---EGKVVHGDGSAYHPVVFETLVYIPEMYELIEGEVVDVVEFGSFVRL-GPLDGLIHVS 111
RPOE_HALO|15790905        ---EGAVLPNRPGVYYEAEFDAVTFEPEMQEVVDGEVVEVVSFGAFVGI-GPVDGLLHVS 111
RPOE_THEAC|16082590       ---EGTIVHGDGGVYQEVKYRALVYYPEMQEIVDGEVVSVQKFGAFIKF-SSFEGLLHIS 121
RPOE_THEVO|13541317       ---EGSIVHGDGGVYQEVKYSALVFYPEMQEIVDGEVVSVQKFGAFVKF-SSFEGLLHIS 121
RPOE_FERAC|22406866       ---EGTIVHGDGGVYQSIKYSALAYFPKMHEVVDGIVVAVQKFGAFIKF-GPFEGLLHIS 119
RPOE_METKA|20094887       ---NEGIFPGDGASYHRVRFRALVFRPVEREVVVGEVTRVKEYGAFVRL-GPLDGLLHVS 117
RPOE_SULTO|15920582       ---EGYIIFGDGATYHEVSFEMLAFVPIIQEVVEGEVNQVDNYGVYVNI-GPVDGLAHIS 111
RPOE_SULAC|730613         ---EGFIIFGDGATYHEVEFDMLVYTPIIHEVIEGEVSQVDNYGVYVNM-GPVDGLVHIS 111
RPOE_SULSO|15897347       ---EGILVFGDGATYHEVEFDMITYVPVVQEVVEGEVLQVDNYGIFVNL-GPMDGLVHIS 111
RPOE_PYRAE|18314155       ---EGKIVFGDGGTYHRAVFTMLAFMPLDGEVVEGVVENAREMGMLVRI-GPILGFINKI 112
RPOE_AERPE|14600570       -DGIIPPVSGDPSIYYPVRYRVLAFKPVQLEIVRGVVTRADDFGLVVNL-GPLDGKVHRN 114
RPC25_YEAST|6322705       ---EGQLKPGDGSSYINVTFRAVVFKPFLGEIVTGWISKCTAEGIKVSLLGIFDDIFIPQ 112
RPC25_SCHPO|19112860      ---EGIIKYGDGSSYMNVVFRLIIFRPFRGEVMLGKIKSCSEEGIRVTI-SFFDDIFIPK 111
RPC25_MOUSE|21313542      ---DAYVFPGDGASHTKVHFRYVVFHPFLDEILIGKIKGCSPEGVHVSL-GFFDDILIPP 111
RPC25_HUMAN|22068810      ---DAYVFPGDGASHTKVHFRCVVFHPFLDEILIGKIKGCSPEGVHVSL-GFFDDILIPP 111
RPC25_DROME|7294695       ---DSIILPGDGASHTEVLFRYVVFRPMVGTVITGKIRNCSREGVHVTL-GFFDDILIPH 111
PPC25_ARATH|15222202      ---GGFVLPGDGAATYKVGLRIVVFRPFVGEVIAAKFKESDANGLRLTL-GFFDDIYVPA 111
RPC25_CAEEL|17566938      ---DSYILPGEGDCRARVKFRMIVFRPFVDEVIEAKVIGSSRQGLCLTI-QFFEDIFVPA 111
RPB7_SCHPO|19114885       -IDKGRVVPGQGFAEFEVKYRAVLWRPFRGEVVDAIVTTVNKMGFFANI-GPLNVFVSSH 114
RPB7_CANAL|12655858       -VGKGRIIPSTGMAEFEVKYRAVVWKPFKGEVVDAVVTTVNKMGFFADV-GPLSVFVSTH 113
RPB7_YEAST|6320612        -IQRGRILPTDGSAEFNVKYRAVVFKPFKGEVVDGTVVSCSQHGFEVQV-GPMKVFVTKH 113
RPB7_DROME|23171325       --GSGVIQPGQGFVVYPVKYKAIVFRPFKGEVLDAVVKQINKVGMFAEI-GPLSCFISHH 111
RPB7_ANOGA|21288656       --GSGTIQPGQGFVVYPVKYKAIVFRPFKGEVLDATVKQVNKVGMFAEI-GPLSCFISHH 111
RPB7_HUMAN|4505947        --GAGVIQPGRGFVLYPVKYKAIVFRPFKGEVVDAVVTQVNKVGLFTEI-GPMSCFISRH 111
RPB7_CAEEL|17510349       --GHGLIQPGRGFVIYPVRYKAIVFRPFKGQVVDGVVTQVNKVGIFCDI-GPLSCFISRH 111
RPB7_ARATH|15237831       --GKGLIRDGTGFVTFPVKYQCVVFRPFKGEILEAVVTLVNKMGFFAEA-GPVQIFVSKH 111
RPB7_SOYBN|1173137        --GKGLIRDGTGFVTFPVKYQCVVFRPFKGEILEAVVTMVNKMGFFAEA-GPVQIFVSNH 111
RPB7_ENCCU|19074596       --SESRIIL-TGETIFTVKYKALTLKPLKGEVIDANVVETNKMGVFASV-GPLTVFISNH 109
RPB7_PLAFA|23508072       --EPGRVQDGTGMIVVKVKYQAIVFKPFKDEVLDAIVTDVNKLGFFAQA-GPLKIFISRT 111
RPB7_PLAYO|23481815       --EPGRVQDGTGMIVVKVKYQAIVFKPFKDEVLDAIVTDVNKLGFFAQA-GPLKIFISRT 111
RPB7_GILTH|13811986       --LYGKILPGFSSVLFKVNFQAVVLKIFKGEIIDAIVKNITSFGIFASA-GILNIFISNK 112
RPA43_YEAST|6324916       SEKLIKITPDTPFGFTWCHVNLYVWQPQVGDVLEGYIFIQSASHIGLLIHDAFNASIKKN 160
RPA43_SCHPO|19113457      -EKSAKVMYDSPFSFIWVRVDVLVFSPKKGDCLEGKINLVSPSHIGLLILGIFNASIPRK 116
RPA43_DROME|7297185       -GQTAGLRADDPTMHLVINADFYVFRPKAGAILSGVVRHISRHHVSAVIYRVFNTSIRFT 138
RPA43_ANOGA|21288304      -NALSALRLDSPYLHVRTTIDYYVFQPRIGSTLRGTVNYVSKNFVSAVIYRVFNVTVKLG 138
RPA43_HUMAN|20539462      -GELGDIYDDQGHIHLNIEADFVIFCPEPGQKLMGIVNKVSSSHIGCLVHGCFNASIPKP 158
RPA43_MOUSE|20847950      -GELGDIYDDQGHIHLNIEADFVIFCPEPGQTLMGTVNKVSSSHIGCLVHGCFNASIPKP 158
RPA43_ARATH|18410907      --QAKILTGLHPYFGVRVNTRLLLFDPKPKSFVEGKIVKISPESIHVIVLGFSAAVITDV 114
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RPOE_METMA|21226698        QITDD------FISYDAKNARLVTKS----------GGKSIAEGDHVRARIVAVS----- 150
RPOE_METAC|20092492        QITDD------FISYDAKNARLVTKN----------GGKSIAEGDHVRARIVAVS----- 150
RPOE_METBA|23051810        QITDD------FISYDAKNARLVTKN----------GGKSIAEGDHVRARVVAVS----- 150
RPOE_ARCFU|11498717        QVTDD------YMVFDEKNKRLVGRE----------TKKVLQEGDKVRARIVSLS----- 150
RPOE_METTH|15678292        QVTDD------YITYDPKKGSLTGKE----------SGRRLDEGDLVRARIVALS----- 150
RPOE_PYRHO|14591652        QLMDD------YVVYDERNKQFVGKE----------KKYLLKIGDAVRARIITVS----- 150
RPOE_PYRAB|14521883        QLMDD------YVVYDERNKQFVGKE----------KKYLLKIGDAVRARIITVS----- 150
RPOE_PYRFU|18976628        QLMDD------YVVYDERNKQFVGKE----------KKYLLKIGDLVRARIINIS----- 150
RPOE_METJA|15668573        QIMDD------YVSYDPKREAIIGKE----------TGKVLEIGDYVRARIVAIS----- 150
RPOE_HALO|15790905         QISDE------YLAFDEENQQLASRE----------SNQVLGTGDSVRARIVTKS----- 150
RPOE_THEAC|16082590        QIMDD------RIDIDLENKRFIGKE----------TKRDLKVGDRVRVRIVAMN----- 160
RPOE_THEVO|13541317        QIMDD------RIDVDLENKRFIGKD----------TKRDLKVGDKVRVRIVALN----- 160
RPOE_FERAC|22406866        QIMDD------AINIDMENQRIVGKD----------SKMELKVGDKIRVRIVALN----- 158
RPOE_METKA|20094887        QILDE------YMYYDGAREALVGEE----------TGRELKRGDVIKVMIIGVS----- 156
RPOE_SULTO|15920582        QITDD------NLKFDQNRGILIGER----------SKKIIQKGDRVRARIISV------ 149
RPOE_SULAC|730613          QITDD------NLKFDSNRGILIGEK----------SKKSITKGDRVRAMIISA------ 149
RPOE_SULSO|15897347        QITDD------TLKYDNVRGIIFGEK----------SKKVIQKGDKVRARVISVA----- 150
RPOE_PYRAE|18314155        HIMDDP-----NIFFDASTKSYIGER----------TKRRVSVGDVVRARITGVSFTT-- 155
RPOE_AERPE|14600570        QIMDE------GVELLPDRSGFVGLA----------SKREIRVGDVVRARVVHVS----- 153
RPC25_YEAST|6322705        NMLF------EGCYYTPEESAWIWPMDEE-------TKLYFDVNEKIRFRIEREVFVDVK 159
RPC25_SCHPO|19112860       DMLF------DPCVFRPDERAWVWKIEGEDGSEG--TELYFDIDEEIRFQIESEDFVDIS 163
RPC25_MOUSE|21313542       ESLQ------QPAKFDEAEQVWVWEYETEEGA----HDLYMDTGEEIRFRVVDESFVDTS 161
RPC25_HUMAN|22068810       ESLQ------QPAKFDEAEQVWVWEYETEEGA----HDLYMDTGEEIRFRVVDESFVDTS 161
RPC25_DROME|7294695        AALQ------HPSRFDEAEQAWVWEYPLEDGAK---HDLFMDVGEPIKFRVSREIFEETS 162
PPC25_ARATH|15222202       PLMPKPNRC-EPDPYNRKQMIWVWEY----GEPK--EDYIVDDACQIKFRVESISYPSVP 164
RPC25_CAEEL|17566938       EKLP------EPHVFEEEGQVWYWEYAQEDGEPP--AKLYMDPGKIVRFRVTEIIFKDLK 163
RPB7_SCHPO|19114885        LVPPD-------MKFDPTANPPNYSGEDQ----------VIEKGSNVRLKIVGTR----- 152
RPB7_CANAL|12655858        LIPSD-------MKFNPSANPPAYVSPDE----------NIEKGSRVRLKIVGTR----- 151
RPB7_YEAST|6320612         LMPQD-------LTFNAGSNPPSYQSSED----------VITIKSRIRVKIEGCI----- 151
RPB7_DROME|23171325        SIPAD-------MQFCPNGNPPCYKSKDED--------VVISGEDKIRLKIVGTR----- 151
RPB7_ANOGA|21288656        SIPAD-------MQFCPNGAPPCYRAINGE--------SVIAAEDKIRLKIVGTR----- 151
RPB7_HUMAN|4505947         SIPSE-------MEFDPNSNPPCYKTMDED--------IVIQQDDEIRLKIVGTR----- 151
RPB7_CAEEL|17510349        CIPPD-------MEFDPNSEKPCYKTNDEA--------NVIRNDDEIRVKLIGTR----- 151
RPB7_ARATH|15237831        LIPDD-------MEF-QAGDMPNYTTSDGS--------VKIQKECEVRLKIIGTR----- 150
RPB7_SOYBN|1173137         LIPDD-------MEF-QSGDMPNYTTSDGS--------VKIQKDSEVRLKIIGTR----- 150
RPB7_ENCCU|19074596        QIP--------------------NFLLENE----------ITKNVMIRLKIIGTK----- 134
RPB7_PLAFA|23508072        AIPKY-------FEYSEDLHYPCFSSGDY----------NIKPQTTVRIKLQGIR----- 149
RPB7_PLAYO|23481815        AIPKY-------FEYNEDAHYPCFSSGSH----------NIKPQTTVRLKLQGIR----- 149
RPB7_GILTH|13811986        FISQD-------LISQQSQTLFNFKNSTI----------NIKKNDIIRCKILNLK----- 150
RPA43_YEAST|6324916        NIPVDWTF----VHNDVEEDADVINTDENNGNNNNEDNKDSNGGSNSLGKFSFGNRSLGH 216
RPA43_SCHPO|19113457       SIPKDWIF----IEPDTTEEQGRWKTN-----------DGNILEPGKDLEFVVDG----- 149
RPA43_DROME|7297185        NQSASRE----DIAMDQEIKIRIKNFD------------ISNLMPYIEGELLLENGEAPK 182
RPA43_ANOGA|21288304       QQTARLH----ALKNGSDISFTVNSCD------------MKSELPVIEGELVLNGVIPVR 182
RPA43_HUMAN|20539462       EQLSAEQWQTMEINMGDELEFEVFRLD-----------SDAAGVFCIRGKLNITSLQFKR 207
RPA43_MOUSE|20847950       EQMSYEEWQTLEIHVGDELEFDVFRLD-----------SDSAGVFCIRGKLSTTSLQLKH 207
RPA43_ARATH|18410907       DIREEF-----KYRVRDGEGSFVSR--------------SHKRHALKLGTMLRLQVQSFD 155
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RPOE_METMA|21226698       ------------------------------------INEREPKESKIGLTMRQTALGKLQ 174
RPOE_METAC|20092492       ------------------------------------INEREPKESKIGLTMRQTALGKLQ 174
RPOE_METBA|23051810       ------------------------------------INEREPKESKIGLTMRQTALGKLQ 174
RPOE_ARCFU|11498717       ------------------------------------LKEREPEKSKIGLTMRQPWLGALK 174
RPOE_METTH|15678292       ------------------------------------LKGRR-EGVKVGLTMRQPGLGKFE 173
RPOE_PYRHO|14591652       ------------------------------------PKSRVIRENRIGLTMRQPGLGKFE 174
RPOE_PYRAB|14521883       ------------------------------------AKSRIIRENRIGLTMRQPGLGKFE 174
RPOE_PYRFU|18976628       ------------------------------------AKSKVIRENRIGLTMRQPGLGKFE 174
RPOE_METJA|15668573       ------------------------------------LKAERKRGSKIALTMRQPYLGKLE 174
RPOE_HALO|15790905        ------------------------------------IDERNPRESKIGLTAKQPGLGKHG 174
RPOE_THEAC|16082590       ------------------------------------LASSSISDSKIGFTMKQVGLGKLD 184
RPOE_THEVO|13541317       ------------------------------------LASSSVEDSKIGFTMKQVGLGKLE 184
RPOE_FERAC|22406866       ------------------------------------LSSASLSDSKIGFTAKQPGLGKLE 182
RPOE_METKA|20094887       ------------------------------------LNEERPRDSKIALTVKRPGLGKPE 180
RPOE_SULTO|15920582       -------------------------------------STSGGRMPRIALTMKQPYLGKIE 172
RPOE_SULAC|730613         -------------------------------------SMSSGRLPRIALTMKQPYLGKNR 172
RPOE_SULSO|15897347       -------------------------------------STVTGRLPRIALTMRQPYLGKLE 173
RPOE_PYRAE|18314155       ------------------------------------PREGTDLLIRVTLTMRSPGLGKLE 179
RPOE_AERPE|14600570       ------------------------------------RPSRTAQIIGIGLTMRQPYLGKEE 177
RPC25_YEAST|6322705       PKSPKERELE----------ERAQLENEIEGKNEETPQNEKPPAYALLGSCQTDGMGLVS 209
RPC25_SCHPO|19112860      PK-----------------------RNKNATAITGTEALESVSPYTLIASCSRDGLGIPA 210
RPC25_MOUSE|21313542      PTGP----------------------SSAEAASSSEELPKKEAPYTLVGSISEPGLGLLS 199
RPC25_HUMAN|22068810      PTGP----------------------SSADATTSSEELPKKEAPYTLVGSISEPGLGLLS 199
RPC25_DROME|7294695       PIGPPKTE------------AQTQQGASTSAAVASATSQEVKTPYRIIGAINESGLGVLS 210
PPC25_ARATH|15222202      TERA--------------------------------EDAKPFAPMVVTGNMDDDGLGPVS 192
RPC25_CAEEL|17566938      PELTH-------------------------------EERKTEKSMEIKGTMASTGLGCIG 192
RPB7_SCHPO|19114885       ---------------------------------------TDATEIFAIATMKEDYLGVL- 172
RPB7_CANAL|12655858       ---------------------------------------TDVNEIYAIGSIKEDYLGPSP 172
RPB7_YEAST|6320612        ---------------------------------------SQVSSIHAIGSIKEDYLGAI- 171
RPB7_DROME|23171325       ---------------------------------------VDATGIFAIGTLMDDYLGLVS 172
RPB7_ANOGA|21288656       ---------------------------------------VDATGIFAIGTLMDDYLGLVG 172
RPB7_HUMAN|4505947        ---------------------------------------VDKNDIFAIGSLMDDYLGLVS 172
RPB7_CAEEL|17510349       ---------------------------------------VDANDIFAIGTLMDDFLGLCQ 172
RPB7_ARATH|15237831       ---------------------------------------VDATAIFCVGTIKDDFLGVIN 171
RPB7_SOYBN|1173137        ---------------------------------------VDATEIFCIGTIKDDFLGVIN 171
RPB7_ENCCU|19074596       ---------------------------------------IDSTRIYAVGTLNDDSLGIIS 155
RPB7_PLAFA|23508072       ---------------------------------------YDLSNMFAIATINNEYLGCIE 170
RPB7_PLAYO|23481815       ---------------------------------------YDLSNMFAIATINNEYLGCIE 170
RPB7_GILTH|13811986       ---------------------------------------YNTGSIQAIGCIDDKYLGKL- 170
RPA43_YEAST|6324916       ----------------------------------WVDSNGEPIDGKLRFTVRNVHTTGRV 242
RPA43_SCHPO|19113457      ------------------------------------------IQREAGLTMVQGTLANS- 173
RPA43_DROME|7297185       NKSIKFGSP-----------PPEEKEVKKEDPDEMLDALITEIKKEPEFTPRKKTSTKRK 231
RPA43_ANOGA|21288304      IKT------------------EPGEQNGDCDEVEEIAMETDTIVKQEPKTPKKKASKKSK 235
RPA43_HUMAN|20539462      SEVAAKKP---KKKKKKKSEEVTENGTEEDPETYEVDSGTTKLADDADDTPMEESALQNT 275
RPA43_MOUSE|20847950      SAVSEDVAETVVEEVVEKTPKKKKKKKDKDTDTCGTVDSVTEVADVTDVTPQEETDIPCS 278
RPA43_ARATH|18410907      ---------------------------------------EEVMHIAGSLLPENTGCVKWL 187
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RPOE_METMA|21226698       WLEEARRKKQPQETPGEEAA---------------------------------------- 194
RPOE_METAC|20092492       WLEEARRKKQPQEAPGKEAA---------------------------------------- 194
RPOE_METBA|23051810       WLEEARKKKQSHEAVPEGAA---------------------------------------- 194
RPOE_ARCFU|11498717       WIEEEIEKLMKESGV--------------------------------------------- 189
RPOE_METTH|15678292       WIEEEKRKSKK------------------------------------------------- 184
RPOE_PYRHO|14591652       WIEKEKRKEKEGKK---------------------------------------------- 188
RPOE_PYRAB|14521883       WIEKEKRKEKEGKK---------------------------------------------- 188
RPOE_PYRFU|18976628       WIEKEKKKEKEEGKK--------------------------------------------- 189
RPOE_METJA|15668573       WIEEEKAKKQNQE----------------------------------------------- 187
RPOE_HALO|15790905        WLQADREQADAASEGE-------------------------------------------- 190
RPOE_THEAC|16082590       WLAKEASQ---------------------------------------------------- 192
RPOE_THEVO|13541317       WLEKEAQA---------------------------------------------------- 192
RPOE_FERAC|22406866       WMKKENVNN--------------------------------------------------- 191
RPOE_METKA|20094887       WWE--------------------------------------------------------- 183
RPOE_SULTO|15920582       WISQELTKASK------------------------------------------------- 183
RPOE_SULAC|730613         MDKSRNSKGEK------------------------------------------------- 183
RPOE_SULSO|15897347       WITQTKK----------------------------------------------------- 180
RPOE_PYRAE|18314155       WVKEKKPAAKKA------------------------------------------------ 191
RPOE_AERPE|14600570       WVAPEAKKG--------------------------------------------------- 186
RPC25_YEAST|6322705       WWE--------------------------------------------------------- 212
RPC25_SCHPO|19112860      WWK--------------------------------------------------------- 203
RPC25_MOUSE|21313542      WWTSN------------------------------------------------------- 204
RPC25_HUMAN|22068810      WWTS-------------------------------------------------------- 204
RPC25_DROME|7294695       WWDQQGKDDEQDDEEDEEYDDEDGEGACEE------------------------------ 240
PPC25_ARATH|15222202      WWDS---------YEQVDQEE--------------------------------------- 204
RPC25_CAEEL|17566938      WWAAEDEDDEAVEDEQDEQEEVIQPKEEIRQPQEEVRQPVKIKEEPV------------- 239
RPB7_SCHPO|19114885       ------------------------------------------------------------
RPB7_CANAL|12655858       M----------------------------------------------------------- 173
RPB7_YEAST|6320612        ------------------------------------------------------------
RPB7_DROME|23171325       N----------------------------------------------------------- 173
RPB7_ANOGA|21288656       S----------------------------------------------------------- 173
RPB7_HUMAN|4505947        ------------------------------------------------------------ 172
RPB7_CAEEL|17510349       AE---------------------------------------------------------- 174
RPB7_ARATH|15237831       DPAAA------------------------------------------------------- 176
RPB7_SOYBN|1173137        DPATV------------------------------------------------------- 176
RPB7_ENCCU|19074596       ------------------------------------------------------------
RPB7_PLAFA|23508072       SNILQVM----------------------------------------------------- 177
RPB7_PLAYO|23481815       SNALQVM----------------------------------------------------- 177
RPB7_GILTH|13811986       ------------------------------------------------------------
RPA43_YEAST|6324916       VSVDGTLISDAADEEGNGYNSSRADEEGNGYNSSRSQAESLPIVSNKKIVFDDEVSIENK 289
RPA43_SCHPO|19113457      ------------------------------------------------------------
RPA43_DROME|7297185       NGENGDTTKTKKVKKEIKSEPI-------------------------------------- 253
RPA43_ANOGA|21288304      EKSNGGPVETVRIKQEVLSSDDDEPSAVVEQQPTASTQGKAKSKKNGTNGVHLNGSAATP 284
RPA43_HUMAN|20539462      NNANGIWEEEPKKKKKKKKHQEVQDQDPVFQGSDSSGYQSDHKKKKKKRKHSEEAEFTPP 324
RPA43_MOUSE|20847950      DNVNDFFEEEPKKKKKKKKRHQ-EDQDPIFQASDSSGYQSDHNKKKKKRKHSEEANFESP 326
RPA43_ARATH|18410907      EKKSEEALPTDRDHKRRKLA---------------------------------------- 196
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RPOE_METMA|21226698       -------------------------------------
RPOE_METAC|20092492       -------------------------------------
RPOE_METBA|23051810       -------------------------------------
RPOE_ARCFU|11498717       -------------------------------------
RPOE_METTH|15678292       -------------------------------------
RPOE_PYRHO|14591652       -------------------------------------
RPOE_PYRAB|14521883       -------------------------------------
RPOE_PYRFU|18976628       -------------------------------------
RPOE_METJA|15668573       -------------------------------------
RPOE_HALO|15790905        -------------------------------------
RPOE_THEAC|16082590       -------------------------------------
RPOE_THEVO|13541317       -------------------------------------
RPOE_FERAC|22406866       -------------------------------------
RPOE_METKA|20094887       -------------------------------------
RPOE_SULTO|15920582       -------------------------------------
RPOE_SULAC|730613         -------------------------------------
RPOE_SULSO|15897347       -------------------------------------
RPOE_PYRAE|18314155       -------------------------------------
RPOE_AERPE|14600570       -------------------------------------
RPC25_YEAST|6322705       -------------------------------------
RPC25_SCHPO|19112860      -------------------------------------
RPC25_MOUSE|21313542      -------------------------------------
RPC25_HUMAN|22068810      -------------------------------------
RPC25_DROME|7294695       -------------------------------------
PPC25_ARATH|15222202      -------------------------------------
RPC25_CAEEL|17566938      -------------------------------------
RPB7_SCHPO|19114885       -------------------------------------
RPB7_CANAL|12655858       -------------------------------------
RPB7_YEAST|6320612        -------------------------------------
RPB7_DROME|23171325       -------------------------------------
RPB7_ANOGA|21288656       -------------------------------------
RPB7_HUMAN|4505947        -------------------------------------
RPB7_CAEEL|17510349       -------------------------------------
RPB7_ARATH|15237831       -------------------------------------
RPB7_SOYBN|1173137        -------------------------------------
RPB7_ENCCU|19074596       -------------------------------------
RPB7_PLAFA|23508072       -------------------------------------
RPB7_PLAYO|23481815       -------------------------------------
RPB7_GILTH|13811986       -------------------------------------
RPA43_YEAST|6324916       ESHKELDLPEVKEDNGSEIVYEENTSESNDGESSDSD 326
RPA43_SCHPO|19113457      -------------------------------------
RPA43_DROME|7297185       -------------------------------------
RPA43_ANOGA|21288304      ASADAANGETTTTT----------------------- 298
RPA43_HUMAN|20539462      LKCSPKRKGKSNFL----------------------- 338
RPA43_MOUSE|20847950      KKRQ--------------------------------- 330
RPA43_ARATH|18410907      -------------------------------------
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