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1 55

(1) -MSRLLWRKVAGATVGP GPVPA PGRWVSSSV PASDPSDG QRRRQQQQQQQQQQQQ
(1) -MSRLLWRKVAGATVGP GPVPA PGRWVSSSV PASDPSDG QRRRQQQQQQQQQQ
(1) -MSRLLW~~R~~KVAGAKVASGPVPA TARWVSSSVLDPVPSDG R-----
(1) -MSRLLW~~R~~KVAGAKVASGPVPA TGRWVSSSVLDPVPSDG Q-----
(1) -MN~~R~~LQGTSLVPSWRTRGCYRRCSYA PQLHAKELMETS-----
(1) -MFYKACPSTLTC SKWIHSIIKTK KFLYCRHYSSK-----SFIDNAP-----
(1) -MTKLMVSECMRLMVRRRPLRVQFCARWFSTKNTABAP-----
(1) MLTPVRCC~~T~~V~~P~~NATVATAARVLRRANLF SRYPRQLGHLRWDSTIAQVLE-----

56 110

(55) QPQQPQVILSSEGGQIPRHNP~~LDI~~QMLSRGLHEQIFGQ----GGEMPGEAAVRRSVE
(53) -PQQPQVILSSEGGQIPRHNP~~LDI~~QMLSRGLHEQIFGQ----GGEMPGEAAVRRSVE
(40) --PPSQMP~~SSEN~~QIRLNPLLIQMLSRGLHEQIFGC----GGEMPDEAAVQR~~SVE~~
(40) --PQSQMP~~SSEN~~QIRLNPLHIQMLSRGLHEQIFGC----GGDV~~P~~DEAAVQR~~SIE~~
(42) -----QRRM~~N~~PLNIQMLSKGFHEQIFRG----KQVQHAEEDVQ~~SIT~~
(42) -----IRINPVGVQY~~I~~SPALQNQVF~~P~~Q----QNTQISQLHDLAKF
(40) -----RINPVGQYQYLGESIQRQVF~~G~~SCGGKDEVEQSDKLMELSKK
(50) ---RKGLGVPS-T~~A~~HNEIGVQQLSEHLYKQLF~~P~~RG---NTDP~~F~~PAPELIELAKD

111 165

(106) H~~L~~QKHGIWGQP~~A~~VPLPDVELRLP~~L~~PPLYGD~~N~~LDQHFRLLAQKQSI~~P~~YLEAA~~N~~LLIQ~~A~~
(103) H~~L~~QKHGIWGQP~~A~~VPLPDVELRLP~~L~~PPLYGD~~N~~LDQHFRLLAQKQSI~~P~~YLEAA~~N~~LLIQ~~A~~
(89) H~~L~~QKHGIWGQP~~A~~ATPLPDVELRLP~~R~~LFEGGNLDQHFRLLAQKQSL~~P~~YLEAAASLSEA
(89) H~~L~~RKHGIWGQP~~T~~PLPDV~~Q~~LR~~L~~PLFEGGNLDQHFRLLAQKQSL~~P~~YLEAAASLSEA
(80) H~~L~~KNHEI~~W~~GOETST~~V~~PDVELQ~~L~~KMYGN~~I~~E~~H~~FQ~~I~~LAQKQSL~~P~~YLEAA~~N~~DLINC
(79) H~~L~~A~~K~~HQI~~L~~NKET~~I~~KLPSFNFR~~L~~P~~I~~Q~~G~~K~~T~~I~~S~~E~~H~~Y~~N~~IGLEFAEPH~~I~~SKAIKF~~SKI~~
(80) S~~L~~KDHGIWGKKT~~I~~ITDP~~I~~S~~F~~PL~~P~~Q~~G~~RS~~L~~D~~H~~FQ~~K~~I~~G~~RF~~N~~SE~~P~~YKSFCE~~D~~K~~FTE~~
(97) H~~L~~ARHD~~L~~LGKT~~T~~DK~~T~~P~~I~~A~~F~~Q~~L~~P~~A~~LV~~G~~D~~T~~L~~D~~H~~F~~HKLGVD~~A~~E~~P~~LTHAKQF~~ADA~~

166 220

(161) QLPPK~~P~~PAWA~~A~~WAE~~G~~WTRY~~G~~PEGEAV~~P~~VAI~~P~~EER~~A~~LV~~F~~D~~V~~E~~V~~C~~L~~AEGTC~~P~~TL~~A~~V~~A~~
(158) QLPPK~~P~~PAWA~~A~~WAE~~G~~WTRY~~G~~PEGEAV~~P~~VAI~~P~~EER~~A~~LV~~F~~D~~V~~E~~V~~C~~L~~AEGTC~~P~~TL~~A~~V~~A~~
(144) QLPPEPK~~S~~WA~~A~~WAE~~G~~WTRY~~G~~PEGEAE~~P~~VAI~~P~~EER~~A~~LV~~F~~D~~V~~E~~V~~C~~L~~AEGTC~~P~~TL~~A~~V~~A~~
(144) QLPPQPRK~~W~~V~~A~~E~~G~~WTRY~~G~~PEGEAE~~P~~VAI~~P~~EER~~A~~LV~~F~~D~~V~~E~~V~~C~~L~~AEGTC~~P~~TL~~A~~V~~A~~
(135) QLPAMPQ~~T~~WAWQSGWTRY~~T~~ATGEKELVDFP~~D~~E~~K~~AMVFD~~V~~VC~~V~~TEG~~C~~CP~~T~~LA~~V~~A~~A~~
(134) DT~~P~~VQPK~~W~~KRQP~~G~~WT~~K~~YAKDG~~S~~ISC~~V~~P~~Y~~FD~~S~~DCM~~V~~FD~~V~~E~~V~~L~~Y~~KVSP~~F~~AV~~V~~AT~~A~~
(135) MVAR-PAE~~W~~LRKP~~G~~WT~~K~~YVP~~G~~MAP~~V~~E~~V~~AYP~~D~~EELVV~~V~~FD~~V~~E~~T~~LYNVSDY~~P~~T~~I~~A~~T~~
(152) H~~L~~PPK~~P~~TSW~~V~~RRS~~G~~WT~~K~~YNRD~~G~~TTEND~~V~~L~~E~~Q~~G~~NMMC~~F~~D~~V~~E~~V~~MYKDN~~P~~YAV~~M~~ACAG

221 275

(216) SPSA~~W~~Y~~S~~W~~S~~QRLVEERY~~Y~~SW~~T~~SQL~~S~~PADL~~I~~PLEVPTGASSPTQRDWQEQLVV~~G~~H~~N~~

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(213) SPSA**WYSWCSQRLVEERYSQLSPADIPLPEVPASASSPTQRDWQEQLVVGHN**
 (199) SPSA**WYSWCSRRLVEERYSQLSPADIPLGGSTSASSSTKQDGQEQLVVGHN**
 (199) SPSA**WYSWCSRRLVEERYSQLSPADIPLGVSASASSSTQQDWQEQLVVGHN**
 (190) SPQN**WYSWCSRRLTGTYTWSKEILLSDIFPLETSMNCNYMTKNNNTTERLVVGHN**
 (189) SEDA**WYCWLSPWLIGK--SENDRQLIPS-----NPKGAIFVGHN**
 (189) SSTA**WYWLSPFI CGGDDPAALIPLNTLN-----KEQVII GHN**
 (207) TPD**AWYAWLSPWLICE--TENKAQLVPMGD-----PTVDRIIVGHN**

276 330

(271) VSF**DRAHIREEQYLIQGSRMRFIDTMSMHMAISGLSSFORSLWIAAKQGKHK---**
 (268) VSF**DRAHIREEQYLIQGSRMRFIDTMSMHMAISGLSSFORSLWIAAKQGKHK---**
 (254) VSF**DRAHIREEQYLIQDSRMRFIDTMSMHMAISGLSSFORSLWMGAKQGKHK---**
 (254) VSF**DRAHIREEQYLIQGSRMHFIDTMSMHMAISGLSSFORSLWMGAKQGKHK---**
 (245) VSF**DRAHIREEQYLIKGSKTRFMDTMSMHMAISGLTGFQRTILWMASKYGKK---**
 (226) VSF**DRQRIREEEYNIKSSRNVFIDTMSLHVATHGMCSRQKPTWFKARKAYIR--SQ**
 (227) VAY**DRARVLEEEYNFRDSKAFFIDTQSILHIAASFGLCSRORPMEFKNN---**
 (246) IGY**DRAKILEEYDLKQTRNFIDTMSLHVAVNGMCSSQORPTWMKHKKARELREKA**

331 385

(322) VOPPT**KQGQKSQRKARRGPAISSLWDLDISSVNSLAEVHRLYVGGPPLKEEREL**
 (319) VOPST**KQGQKSQRKARRGPAISSLWDLDISSVNSLAEVHRLYVGGPPLKEEREL**
 (305) TQ**QSTKRGQKSPRKAN-GPAISSLWDWMDISSANNLADVHNLYVGGPPLKEEREL**
 (305) TQHP**TKRGQKSKQKNA-GPAISSLWDWMDISSANNLADVHNLYVGGPPLAKEEREL**
 (296) GLQE**VKQHIKKTRSNFSGSPISSWDWVNIISSINNLADVHALYVGGPPLKEAREL**
 (279) STET**SEDDDSSSFDDDYQNYLKQEPWLAHSSVNSLKDVAKFHCN-ITLDKSKRDD**
 (273) --KK**KEAEVESEVHPEISIEDYDDPWLNVSALNSLKDVAKFHC-KIDLDTDRDF**
 (301) EHE**SASVELQEVLQCGSLTAEEADLWVDKSSINSLRDVQAQFHIN-VKIDKDIRDV**

386 440

(377) FVKG**TMKDIRENFQDIIMOYCAQDVWAATHEVFQQQLFLFLERCPHPVTLAGMLEMG**
 (374) FVKG**TMKDIRENFQDIIMOYCAQDVWAATHEVFQQQLFLFLERCPHPVTLAGMLEMG**
 (359) FVKG**SMRDIRENFQDIIMOYCARDVWATFEVFQQQLFLFLERCPHPVTLAGMLEMG**
 (359) FVKG**SMRDIRENFQDIIMEYCARDVWATFEVFQQQLFLFLERCPHPVTLAGMLEMG**
 (351) FVKG**SMSDIRETEFQEIIMRYCALDVQATHEVFQEQQFFLMERCPHPVTLSGMLEMG**
 (333) FASL**EKEPILQKLNELITYCAHDTYSTHQVKKVFPQFLEVCPHPATFSAMISLG**
 (325) FASTDKSTII**ENFQKLVNYCATDVTATSQVDEIFFVFLKKC PHPVSFAGIKSLS**
 (355) EAETDRNV**ILNOLDLDTYCAAADVQVTHQVYQVVFENLGVCPHEVSFAAIRHLA**

441 495

(432) VSY**LPVNQN-WERYLAEAQGTYEELQREMKKSLMDLANDACQLLSG-ERYKEDPW**
 (429) VSY**LPVNQN-WERYLAEAQGTYEELQREMKKSLMDLANDACQLLSG-ERYKDDPW**
 (414) VSY**LPVNQN-WERYLTEAQNTYEELQREMKKSLMDLANDACQLLSG-ERYKEDPW**

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(414) VSYLPVNQNLWERYLTTEAQSTIYEELQREMKKSLMELANDACQLLSG-ERYKEDPW

(406) VSYLPVNQNLWERYLDEAQTSYEELOKEMKKSLMELANDACQLITK-DAYKEDPW

(388) SVFLPVNHS-WTRYINGVEEQYQQMIQLVDQKLSQYAEKAQDLINTKDTVLKDPW

(380) KCIILPTKLNWDNYLINSSESLYQQSKVQIESKIVQIKDIVLLDKPFDYLIKDPW

(410) SVILPVNKT-WDTYIETAEATYLOMLHGVQERLFTLMERTLDYKADPEKYLSDPW

496

550

(485) IWDLEWDLQEFKQKKAKKVKKEPATASKLPIEGAGAPGDPMDQEDLGPCSEEEEF

(482) IWDLEWDLQEFKQKKAKKVKKEPATASKLPIEGAGAPGDPMDQEDLGPCSEEEEF

(467) IWDLEWDLQEFKQKKAKKVKK-PASASKLPIEGAGPFGDPMDQEDPGPPSEEEEL

(467) IWDLEWDLQEFKQKKAKKVKK-TASASKLPIEGAGPFGDPMDQEDPGPPSEEEEL

(459) IWDLEWDIQLQESKQKTKISKK--QKKANEAAESVGNKLVEDHNEDPGPPTEKEES

(442) IRLQLDWTPCNCYRKLKAT-----

(435) ISQLDWTTKPLRLTKKGVP-----

(464) ISQLDWSGQEIKMAKPKKKGD-----

551

605

(540) QQDVMARACLQKLKGTTTELLPKRPQHLPGHPGWYRKLCPRLDDPAWTPGP-----

(537) QQDVMARACLQKLKGTTTELLPKRPQHLPGHPGWYRKLCPRLDDPAWTPGP-----

(521) QRSVTAHNRLQQLRSSTDLLPKRPQHLPGHPGWYRKLCPRLDDPAWAPGP-----

(521) QNIMAHTRLQQLKSTTDLLPKRPQHLPGHPGWYRKLCPRLDDPAWTPGP-----

(512) RPSMGKLYLEDLKLKTLPLPKRNQHLPGHPGWYRKLCPKLEDPDWLPGP-----

(461) -----OEVPVVPKWYKKAYCKTEKRAV-----

(454) -----AKCQKLPGFPEWYRQLFPSKDTVEP-----

(485) -----VER-----P-ALNQKLPGYFQWYKDLFVFKVPKELSGLDEPDKEQ-----

606

660

(590) -----SLLSLQMRVTPKIMALTWDGFPLHYSERHGWGYLVPGRRDNIAKLP-----

(587) -----SLLSLQMRVTPKIMALTWDGFPLHYSERHGWGYLVPGRRDNIAKLP-----

(571) -----SLLSLQMRVTPKIMALTWDGFPLHYSDSHGWGYLVPGRRDNIITEPP-----

(571) -----SLLSLQMRVTPKIMALTWDGFPLHYSDSHGWGYLVPGRRDNIATELP-----

(562) -----GLISLQMRRLTPKIMRLTWDGYPYLHYSEKHGWGYLVPGR-----KNNK-----

(483) -----I-TAKSRLAPIIIRLKWKHPLAWSDTYGWVFSVER-----

(479) -----KITIKSRIIPIIIFKLSWENSPVIWSKESGWCFNVEHEQ-----

(523) ENRKARHEFINLTVRSRIAFLIKLSWEGYPLFWSDQFGWTFQVRE-----

661

715

(636) TGTILESAVVCPYRAIESLYFKHCLEQGKQQLMPQEAGLAEEFLLTDNSAIWQT-----

(633) TGTILESAVVCPYRAIESLYFKHCLEQGKQQLMPQEAGLAEEFLLTDNSAIWQT-----

(617) VSPTEVESAATVCPYRAIESLYFKHCLEQGKQQLEPQEVDLAEEFLLTDSSAMWQT-----

(617) VSPTEVESAATVCPYRAIESLYFRHCLDQGKQQLETQETDLAEEFLLTDS-AMWQT-----

(604) LNNEESEEITIPCPYRAIEDIYAEYSKNTKDGCLSQHSTIPEEFMLTDNSMWOK-----

S. pombe pol gamma	(518)	- - - - -	TS
Copy of scyeast pol gamma mip1	(517)	- - - - -	VET
Copy of Neurospora pol gamma	(570)	- - - - -	KA
	716		770
Copy of hum pol gamma aa seq	(691)	VEELDYLEVEAEAKMENLRAAVPGQ--PIALTARGPKDTQPSYHHGNGPYNDVD	
Pan troglodytes (chimpanzee)	(688)	VEELDYLEVEAEAKMENLRAAVPGQ--PIALTARGPKDTQPSYHHGNGPYNDVD	
mus pol gamma	(672)	VEELGCLDVEAEAKMEE--NSGLSQ--PIVLPAACAPKSSQPTYHHGNGPYNDVN	
rat pol gamma	(671)	VEELGCLDVEAEATV--SSGLSQ--PIVPPTACAPKTSQPTYHHGNGPYNDVN	
Copy of Xenopus pol gamma	(659)	VEELSRTEMDSLSEVPATAKAKRNNNSSEHPVKLEMEDFDSLPDNHHGNSPCGDVN	
S. pombe pol gamma	(520)	KDEIEMILDQGLVPCS-----REEDTKLD	
Copy of scyeast pol gamma mip1	(520)	YKAKNYVIADSVSQEE-----EE-----IRTHNGL	
Copy of Neurospora pol gamma	(572)	ETFIQRQMTPVQFEDP-----DVDDRRLRM	
	771		825
Copy of hum pol gamma aa seq	(744)	IPGCWFFKLPHKDGSNCNVGSPFAKDFLPKMEDGTIQQAGPGGASGPRALEINKMI	
Pan troglodytes (chimpanzee)	(741)	IPGCWFFKLPHKDGSNCNVGSPFAKDFLPKMEDGTIQQAGPGGASGPRALEINKMI	
mus pol gamma	(722)	IPGCWFFKLPHKDGSNNYNVGSPFAKDFLPKMEDGTIQQAGPGGASGPRALEINKMI	
rat pol gamma	(721)	IPGCWFFKLPHKDGSNNYNVGSPFAKDFLPKMEDGTIQQAGPGGARGPRALEINKMI	
Copy of Xenopus pol gamma	(714)	VSGCWFYKLPHKDGSNNANNVGSPFAKDFLPKMEDGTIQQASTGDSATRALEINKMI	
S. pombe pol gamma	(544)	YNNYIIFKVPHKDGPEARCVRHSPNHTHTSKRVFYNQIMK--WLKKALEMSASC	
Copy of scyeast pol gamma mip1	(546)	QCTGVLFKVPHPNGPTFNCTNLLTKSYNHFFEKGVIKSESE--LAHQALQINSSG	
Copy of Neurospora pol gamma	(596)	DVDHKYFKLPHKDGSNARCVNEMAKGYLFYFEKGILSSEYPP--YAKEALEMSASC	
	826		880
Copy of hum pol gamma aa seq	(799)	SEWRNAHKRISSQMVVWLPRSLALPRAVIRHPDYDEE---GLYGAILPQVVTAGTI	
Pan troglodytes (chimpanzee)	(796)	SEWRNAHKRISSQMVVWLPRSLALPRAVIRHPDYDEE---GLYGAILPQVVTAGTI	
mus pol gamma	(777)	SEWRNAHKRISSQMVVWLPRSLALPRAVTRHPSFDEE---GHYGAILPQVVTAGTI	
rat pol gamma	(776)	SEWRNAHKRISSQMVVWLPRSLALPRAVTRHPSFDEE---SHYGAILPQVVTAGTI	
Copy of Xenopus pol gamma	(769)	SEWRNAHKRISSQMVVWMKKNEIHRTITRDPEFDEE---NKYGAILAQVVSAGTI	
S. pombe pol gamma	(597)	SYWSSARDRIRSQMVVWDKDAELIG---VPSSV---DGFGIILPCIIPMGTV	
Copy of scyeast pol gamma mip1	(599)	SYWMSARERIQSQFVWPSCKFPEFQSLSAKSSLNEKTNDLAIIPKIVPMGTV	
Copy of Neurospora pol gamma	(649)	SYWISARERIKNQMVVYEDQLPPSQRFVNKDADSNT---PIGFVLPQVIPMGTV	
	881		935
Copy of hum pol gamma aa seq	(851)	TRRAVEPTWLTASNARPDRVGSELKAMVQAPPGYTLVGADVDSQELWIAAVLGDA	
Pan troglodytes (chimpanzee)	(848)	TRRAVEPTWLTASNARPDRVGSELKAMVQAPPGYTLVGADVDSQELWIAAVLGDA	
mus pol gamma	(829)	TRRAVEPTWLTASNARPDRVGSELKAMVQAPPGYVLVGADVDSQELWIAAVLGDA	
rat pol gamma	(828)	TRRAVEPTWLTASNARPDRVGSELKAMVQAPPGYVLVGADVDSQELWIAAVLGDA	
Copy of Xenopus pol gamma	(821)	TRRAVEPTWLTASNARPDRVGSELKAMVQPPGYHIIGADVDSQELWIAATGEA	
S. pombe pol gamma	(642)	TRRAVENIWLTASNPKNRIGSELKAMIFAPDGYTFVGADVDSEELWIVALMGDS	
Copy of scyeast pol gamma mip1	(654)	TRRAVENAWLTASNPKNRIGSELKTQVKAPPGYCFVGADVDSEELWIASLVGDS	

Copy of Neurospora pol gamma	(701)	T R R A V E R I W L T A S N A K K N R V G S E L K A M V R A P P G Y V F V G A D V D S E E L W I A S V M G D A	
	936		990
Copy of hum pol gamma aa seq	(906)	H F A G M H G C T A F G W M T I Q G R K S R G T D L H S K T A T T V G I S R E H A K I F N Y G R I Y G A G Q P	
Pan troglodytes (chimpanzee)	(903)	H F A G M H G C T A F G W M T I Q G R K S R G T D L H S K T A T T V G I S R E H A K I F N Y G R I Y G A G Q P	
mus pol gamma	(884)	H F A G M H G C T A F G W M T I Q G R K S R G T D L H S K T A A T V G I S R E H A K I F N Y G R I Y G A G Q S	
rat pol gamma	(883)	H F A G M H G C T A F G W M T I Q G R K S R G T D L H S K T A A T V G I S R E H A K V F N Y G R I Y G A G Q S	
Copy of Xenopus pol gamma	(876)	H F A G I H G C T A F G W M T I Q G K K S S G T D L H S K T A S T V G I S R E H A K V F N Y G R I Y G A G Q P	
S. pombe pol gamma	(697)	Q E R - L H G A A P A L G M M T I E G K K S E G T D L H S K T A A I L G V S R D S A K V F N Y G R I Y G A G L K	
Copy of scyeast pol gamma mip1	(709)	I F N - V H G G T A I G W M C I E G T K N E G T D L H T K T A Q I L G C S R N E A K I F N Y G R I Y G A G A K	
Copy of Neurospora pol gamma	(756)	T F K - L H G G N A I G F M T I E G T K S Q G T D L H S R T A S I L G I T R N D A K V F N Y G R I Y G A G L K	
	991		1045
Copy of hum pol gamma aa seq	(961)	F A E R L L M Q F N H R L T Q Q E A A E K A Q Q M Y A A T K G L R W Y R L S D E G E W L V R E L N I P V D R T	
Pan troglodytes (chimpanzee)	(958)	F A E R L L M Q F N H R L T Q Q E A A E K A Q Q M Y A A T K G L R W Y R L S D E G E W L V R E L N I P V D R T	
mus pol gamma	(939)	F A E R L L M Q F N H R L T R Q Q E A A E K A Q Q M Y A V T K G L R R Y R L S A D G E W L V K Q L N L P V D R T	
rat pol gamma	(938)	F A E R L L M Q F N H R L S R Q Q E A A D K A Q Q M Y A V T K G L R R Y R L S D D G E W L V K Q L N V P V D R T	
Copy of Xenopus pol gamma	(931)	F A E R L L M Q F N H R L T Q Q E A A E K A Q Q M Y A V T K G I R R Y I L S K E G E W L V E E L G I S V E R G	
S. pombe pol gamma	(751)	H T T L I M N P T L K T A E A K E L K K S K M S K R - - - - - L Q - - - - -	
Copy of scyeast pol gamma mip1	(763)	F A S Q K R E N P S I T D E E T K K I A K E N K T K R S K - - - - -	
Copy of Neurospora pol gamma	(810)	F A S Q L L I R Q N P S I T E A E T T A I T K D A K T N R K S - - - - -	
	1046		1100
Copy of hum pol gamma aa seq	(1016)	E G G W I S L Q D L R K V Q R E T A R K S Q W K K W E V V A E R A W K G G T E S E M F N K L E S I A T S D I P	
Pan troglodytes (chimpanzee)	(1013)	E G G W I S L Q D L R K V Q R E T A R K S Q W K K W E V V A E R A W K G G T E S E M F N K L E S I A T S D I P	
mus pol gamma	(994)	E D G W V S L Q D L R M I R R E A S R K S R W K K W E V V A S E R A W T G C T E S E M F N K L E S I A M S D T P	
rat pol gamma	(993)	E D G W V S L Q D L R K I R R E A S R K S R W K K W E V V T E R A W T G C T E S E M F N K L E S I A M S D T P	
Copy of Xenopus pol gamma	(986)	E E N S V N L Q D L R K I Q K D A T K R S - R K W N L V S R R I W T G C T E S Q M F N K L E T I A M S P S P	
S. pombe pol gamma	(792)	- - - - - E M G I P K L T F W S Q C T E S F V F N K L E A M A Q L P S P	
Copy of scyeast pol gamma mip1	(800)	- - - - - I F K K F W Y G G S E S I L F N K L E S I A E Q E T P	
Copy of Neurospora pol gamma	(848)	- - - - - I Y K R P F W R G C T E S F V F N M L E E F A E Q E R P	
	1101		1155
Copy of hum pol gamma aa seq	(1071)	R T P V L G C C I S R A L E P - S A V Q E E E M T S R N W V V Q S S A V D Y L H L M L V A M K W L F E E F A	
Pan troglodytes (chimpanzee)	(1068)	R T P V L G C C I S R A L E P - S A V Q E E E M T S R N W V V Q S S A V D Y L H L M L V A M K W L F E E F A	
mus pol gamma	(1049)	R T P V L G C C I S R A L E P - S V V Q G E E I T S R V N W V V Q S S A V D Y L H L M L V A M K W L F E E F A	
rat pol gamma	(1048)	R T P V L G C C I S R A L E P - S V V Q G E E M T S R V N W V V Q S S A V D Y L H L M L V A M K W L F E E F A	
Copy of Xenopus pol gamma	(1040)	R T P V L G C R I S R A L E P - I A V K G E E I T S R V N W V V Q S S A V D Y L H L M L V A M K W L F E E A Y D	
S. pombe pol gamma	(823)	R T P V L D A G I Q Q A L S S K N L S K N S P M T S R V N W A I Q S S A V D Y L H L L L V S M N H L I K K Y Y	
Copy of scyeast pol gamma mip1	(827)	R T P V L G C G I T Y S L M K K N L R A N S F L P S R I N W A I Q S S G V D Y L H L L L C C S M E Y I I K K Y N	
Copy of Neurospora pol gamma	(876)	R T P V L G A G I T E A L M S R W V S K G G F L T S R I N W A I Q S S G V D Y L H L L I I A M D Y L T R R F N	
	1156		1210

Copy of hum pol gamma aa seq	(1125)	IDG <small>GRFCISI</small> H <small>DEVRYI</small> V <small>REEDF</small> YRAALALQITNL <small>TFCM</small> FAYKIGLNDLPQSVAF	
Pan troglodytes (chimpanzee)	(1122)	IDG <small>GRFCISI</small> H <small>DEVRYI</small> V <small>REEDF</small> YRAALALQITNL <small>TFCM</small> FAYKIGLNDLPQSVAF	
mus pol gamma	(1103)	IDG <small>GRFCISI</small> H <small>DEVRYI</small> V <small>REEDF</small> YRAALALQITNL <small>TFCM</small> FAYKIGLNDLPQSVAF	
rat pol gamma	(1102)	IDG <small>GRFCISI</small> H <small>DEVRYI</small> V <small>REEDF</small> YRAALALQITNL <small>TFCM</small> FAYKIGLNDLPQSVAF	
Copy of Xenopus pol gamma	(1094)	IDG <small>GRFCISI</small> H <small>DEVRYI</small> V <small>HSKD</small> YRAALALQITNL <small>TFCM</small> FASRLGIQDVPCSVAF	
S. pombe pol gamma	(878)	LEARLSLTVH <small>DEVRYI</small> SSDKDKYRVAFALQVANLWTRAFFCQRGINELPQSVAF	
Copy of scyeast pol gamma mip1	(882)	LEARLCISI <small>HDEIR</small> RELVSEKD KYRAAMALQISNI WTRAMFCQQMGINELPQNCAF	
Copy of Neurospora pol gamma	(931)	IACRRLAIVH <small>DEVRYI</small> LAEEPD KYRVAMALQIANL WTRVMEAQQVGIQDLPQCAF	
	1211		1265
Copy of hum pol gamma aa seq	(1180)	FSAVDidRCLRK <small>EVT</small> MDCKTPSNPTGMERRYGIPQGEALDIYQIEELTKGSLEK-	
Pan troglodytes (chimpanzee)	(1177)	FSAVDidRCLRK <small>EVT</small> MDCKTPSNPTGMERRYGIPQGEALDIYQIEELTKGSLEK-	
mus pol gamma	(1158)	FSAVDidQCLRK <small>EVT</small> MDCKTPSNPTGMERRYGIPQGEALDIYQIEELTKGSLEK-	
rat pol gamma	(1157)	FSAVDidQCLRK <small>EVT</small> MDCKTPSNPTGMERKYGIPQGEALDIYQIEELTKGSLEK-	
Copy of Xenopus pol gamma	(1149)	FSAVDidKCLRK <small>EVT</small> MDCTPSNPTGMEKRYGIPQGEALDIYQILKVTKGVI---	
S. pombe pol gamma	(933)	FSSVDidHVLRKDVKMDCVTPSNK-----VPIPPGEETIESVLEKLEQS-----	
Copy of scyeast pol gamma mip1	(937)	FSQVDIDSVIRKEVNMDCITPSNK-----TAIPHGEALDINQLLDKSNSKLGKP	
Copy of Neurospora pol gamma	(986)	FSAVDidHVLRKEVDMDCITPSNB-----IPIAHGESIDIFQILEKGDDAKLD-	
	1266		1320
Copy of hum pol gamma aa seq	(1234)	-----RSQPGP-----	
Pan troglodytes (chimpanzee)	(1231)	-----RSQPGP-----	
mus pol gamma	(1212)	-----RSQPGP-----	
rat pol gamma	(1211)	-----RSQPGP-----	
Copy of Xenopus pol gamma	(1201)	-----	
S. pombe pol gamma	(978)	-----GQSLEPLEQIQCFVDVKATTSAEITEEDKKNIAYLKAQAFY-----	
Copy of scyeast pol gamma mip1	(986)	NLDIDSKVSQYAYNYREPVFEEYNKSYTPEFLKYFLAMQVQSDKRDVNRLDEYL	
Copy of Neurospora pol gamma	(1034)	-----DSIVPQSQYAPRLENIPYTPRVPVMQRLRERAEGDHQAFLRFIRAQTNS	
	1321		1375
Copy of hum pol gamma aa seq	(1240)	-----	
Pan troglodytes (chimpanzee)	(1237)	-----	
mus pol gamma	(1218)	-----	
rat pol gamma	(1217)	-----	
Copy of Xenopus pol gamma	(1201)	-----	
S. pombe pol gamma	(1019)	-----	
Copy of scyeast pol gamma mip1	(1041)	RECTSKEYARDGNTAEYSLLDYIKDVEKGKRTKVRIMGSNFLDGTNAKADQRIR	
Copy of Neurospora pol gamma	(1085)	DEELKRIIAETRYSDPYGAFLASNGRVSGNPHQRHAHVASTKAAAPSKPSIA	
	1376		1430
Copy of hum pol gamma aa seq	(1240)	-----	
Pan troglodytes (chimpanzee)	(1237)	-----	

	mus pol gamma	(1218)	- - - - -	
	rat pol gamma	(1217)	- - - - -	
Copy of Xenopus pol gamma		(1201)	- - - - -	
S. pombe pol gamma		(1019)	- - - - -	
Copy of scyeast pol gamma mip1		(1096)	LPVNMPDYPTLHKIANDSAIPEKQLLENRRKKENRIDDENKKLTRKKNTTPMER	
Copy of Neurospora pol gamma		(1140)	SRFDSVSQASRIKSVAAGSDEPTIRATKAQGKAMAKASGTKLAASTKDTVLNVTI	1431
				1485
Copy of hum pol gamma aa seq		(1240)	- - - - -	
Pan troglodytes (chimpanzee)		(1237)	- - - - -	
	mus pol gamma	(1218)	- - - - -	
	rat pol gamma	(1217)	- - - - -	
Copy of Xenopus pol gamma		(1201)	- - - - -	
S. pombe pol gamma		(1019)	- - - - -	
Copy of scyeast pol gamma mip1		(1151)	KYKRVYGGGRKAFEAFYECANKPLDYTLETEKQFFNIPIDGVIDDVLNDKSNYKKK	
Copy of Neurospora pol gamma		(1195)	KKKVAAPEMAAVPSTSSESSESKSATTSTTTENATASPSSSSNVDAKKTSKTK	1486
				1540
Copy of hum pol gamma aa seq		(1240)	- - - - -	
Pan troglodytes (chimpanzee)		(1237)	- - - - -	
	mus pol gamma	(1218)	- - - - -	
	rat pol gamma	(1217)	- - - - -	
Copy of Xenopus pol gamma		(1201)	- - - - -	
S. pombe pol gamma		(1019)	- - - - -	
Copy of scyeast pol gamma mip1		(1206)	PSQARTASSSPIRKTAKAVHSKKLPARKSSTTNRNILVELERDITISREY-----	
Copy of Neurospora pol gamma		(1250)	PTHKKETEGEPEFPSLDDPVIAARLEAVSKTSPGTRASVAAKLDALASFCHASCCG	1541
Copy of hum pol gamma aa seq		(1240)	-	
Pan troglodytes (chimpanzee)		(1237)	-	
	mus pol gamma	(1218)	-	
	rat pol gamma	(1217)	-	
Copy of Xenopus pol gamma		(1201)	-	
S. pombe pol gamma		(1019)	-	
Copy of scyeast pol gamma mip1		(1255)	-	
Copy of Neurospora pol gamma		(1305)	C	