Supplementary Information for

Structural Basis of Nucleosome Assembly by the Abo1 AAA+ ATPase Histone Chaperone

Cho et al.,

Vta7(S cerevisiae)		
Abol (S. pombe)		
lex-1(C.elegans)	1	MPRSDGFSPRKNLF
ATAD2 (D. rerio)	1	MVNTRKSSEHKPSSPFISGRTRSSQRNNPNLDEHNSRKEPSSDANSSSPRLSPF
ATAD2A(M.musculus)		
ATADZA(H.sapiens)	1	MVVLR55LELHNHSAASATG5LDL55DFL5LEHIGRRRLR5AGAAQRRPAATTARAGDG55VREVET
Yta7(S.cerevisiae)	1	MARNLRNRRGSDVEDASNAKVGYETQIKDENGIIHTTTRSLRKINYA
Abo1(S.pombe)		
lex-1(C.elegans)	15	RSARDHSRSYAGQCNEDFDDMYAPSSRRSSGGVDGNGYTRSGRKINHNRYYEEEYHEAISSEEDERRYF DWDWD DOWDDCGDDWGDCSCOC
ATAD2(D.Terio) ATAD2A(M.musculus)	55	FRAIRRUIFF551D13F5F25RURG.SWIM5RUIRLSIGALQN
ATAD2A(H.sapiens)	68	YHRTRALRSLRKDAQNSSDSSFEKNVEITEQLAN
Abol(S.cerevisiae)	48	EIEKVFDFLEDDQVMDKDETPVDVTSDEHHNNNQKGDDEDDDVDLVSPHENART
lex-1(C.elegans)	85	TRRSSNSMTYROOVMOAIDESKRNOKVPPAKRKRIYLSDEEEEDFAEAAHVENTVE
ATAD2 (D. rerio)	99	.GHTIGRM
ATAD2A(M.musculus)		
ATAD2A(H.sapiens)	102	.GRHFTRQLARQQADKKK.EEHREDKVIPVTRSLRARNIVQSTEHLHEDNGDVE
Yta7(S.cerevisiae)	102	NEELTNERNLRKRK. AHDPEEDDESFHEEDVDDDEEEEEADEFEDEYLDEDSKDNNRRRAADRKFVVF
Abol(S.pombe)	25	SDEMPNNAKR <mark>R</mark> RRSQSMIANKRIHQAFQEDEGDEDWEEEEHKPKAKRRYNT.
<pre>lex-1(C.elegans)</pre>	141	ERATRRST <mark>R</mark> RR.SSMHEELGVSEQEEESPVRRTR.KAAKRL
ATAD2 (D. rer10)	126	LKRSR <mark>R</mark> VR.KSQFEHLNQSLLFDQLVNSTAEAVLQEMDNISSIRQSREVERL
ATADZA(M.musculus) ATADZA(H.sapiens)	154	VRRSCRI. RSRYS. GVNOSMLFDKLITNTAEAVLOKMDDMKKMRRORMRELEDL
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Yta7(S.cerevisiae)	170	DPDDDEEYDEDDEEGDRISHSA.SSKRLKRANSRRTRS.SRHPETPPPVRRALRSRI
Abol(S.pombe)	170	RSNESFSEGDDEPFEVSESSALEDELSDSEDSFIRSVRSKPKIRPGTRRSTRLRN
ATAD2(D.rerio)	177	
ATAD2A(M.musculus)		
ATAD2A(H.sapiens)	206	GVFN <mark>E</mark> TEESNLNMYTRGKQKDIQRTDEETTDNQEGSVESSEEGEDQEH
Yta7(S.cerevisiae)	225	RHSRTSNEENDDENDNSRNEALTLADEI. RELORDSPIREKRF <mark>I.R</mark> TKPVN Y KT.PPPI.TASNAFFFI
Abo1(S.pombe)	131	RRSQDEEESEEEHRPILRERTSRINYSVPLAFPPVDEMDC
lex-1(C.elegans)	232	A E E D E Q . S G E K D P E E E D D S S N A E S S E E S T A P R Q Y S L R R Q P V V Q F N A S E A R E N R R A R
ATAD2(D.rerio)	225	TEESNEE.GEEDEDVEADDDDEDDEGDEA.EEAGEENDRPYN <mark>LR</mark> QRKTVQR <mark>Y</mark> EAPPIEPVNRKQS
ATAD2A(M.musculus)	254	
ATADZA(H.Sapiens)	234	
Yta7(S.cerevisiae)	293	KNNNALSFHNPSPARRGRGGWNASQNSGPTRRLFPTGGPFGGNDVTTIFGKN.TNFYNQ V P <mark>SA</mark> F
Abo1(S.pombe)	171	DPSSQVNQSRSRKTHSELAITKLLRQQVSSFMPYIDSSGSES
lex-1(C.elegans)	289	VCT FDRUBCDA
ATAD2(D.Terio) ATAD2A(M.musculus)	200	MS
ATAD2A(H.sapiens)	318	PNIFYSGPASPARPRY.RLSSAGPRSPYCKRMNRRHA <mark>I</mark> H <mark>SS</mark> D <mark>S</mark> TSSSS
		AAA1
W-7/0	257	
Yta7(S.cerevisiae)	357	AAA1
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans)	357 213 317	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTOKKKKKKPETADLDPLGVD ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVD DSDDMVLPRPDKROSRPHMHNGERERGRFMPIMMTEKELOSAOHILMDRMKKTDAGOGASDIDPMSVDS
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio)	357 213 317 319	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKPEIADLDPLGVDR ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVDS DSDDMVLPRPDKRQSRPHMHNRGERERGRFMPINMTEKELQSAQHILMDRMRKTDAGQGASDIDPMSVDS SSDEERFERRKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMMEDT
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus)	357 213 317 319 22	AAA1 DNNNNKLIIDSDSSDDEI <mark>LPLG</mark> VTPKTKKENTQKKKKKKPE <mark>IADLDPL</mark> GVDR ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVD DSDDNVLPRPDKRQSRPHMHNRGERERGRFMPINMTEKELQSAQHILMDRMKTDAQGASDIDPMSVDS SSDEERFERRKKSMSRARNRCLPMNLRAEDLAS.GVLKDRVKVGASLADVDPMNLD SE.DDCFE <mark>R</mark> RKIGASLADVDPMQLD
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	357 213 317 319 22 366	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDK ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVDS DSDDMVLPRPDKRQSRPHMHNRGERERGRFMPINMTKELQSAQHILMDRMKTDAGGGASDIDPMSVDS SSDEERFERRKSKSMSRARNRCLPMNLRAEDLAS.GVLKDRVKIGASLADVDPMQLDT SE.DDCFERRKKRSRNRAINRCLPLNFRKDEL.K.GIYKDRMKIGASLADVDPMQLDT
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	357 213 317 319 22 366	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPTADLDPLGVDR ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVD SDDDVVLPRPDKRQSRPHMHNGERERGRFMPINMTEKELQSAQHILMDRMKTDAGQGASDIDPMNDD SSDEERFERRKSKSMSRANNCLPMNLAEDLAS.GVLKDRVKVGASLADVDPMNDD SE.DDCFERRKKSRNRAINRCLPLNFRKDEI.R.GIYKDRMKIGASLADVDPMQDD SEDQHFERRKKRSNRAINRCLPLNFRKDEL.K.GIYKDRMKIGASLADVDPMQDD AAA1
Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae)	357 213 317 319 22 366 409	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDE ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDLGVDS SDSDMVLPRPDKRQSRPHMHNGERERGFMPINMTEKELQSAQHILMDRMKKTDAGQGASDIDPMSVDS SSDEERFERKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMOLDT SE.DDCFERRKKRSRNRAINRCLPLNFRKDEI.RGIYKDRMKIGASLADVDPMOLDT SEDQHFERRRKRSRNRAINRCLPLNFRKDEI.KGIYKDRMKIGASLADVDPMOLDT AAA1 NVNDDDIGGLDNYHDOKKEMVALPLUYEELYONNNTPPRGVLFHGPPGTGKTLMARALAASCSSDERKI
Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe)	357 213 317 319 22 366 409 262	AAA1 DNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDIDPNSVD SDDDWVLPRPDKRQSRPHMHNGERERGFMPINMTEKELQSAQHILMDRMKKTDAGQGASDIDPMNVD SSDEERFERRKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMNLDT SE.DDCFERRKKSKMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMQDD SEDEQHFERRKIGASLADVDPMQDD AAA1 NVNFDDIGGLDNYLDQLKEMVALPLLYPELYQNFNTFPRGVLFHGPPGTGKTLMARALAASSSENKKY
Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans)	357 213 317 319 22 366 409 262 387	AAA1 DNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPEIADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVDS DSDDMVLPRPDKRQSRPHMHNRGERERGRFMPINMTEKELQSAQHILMDRMRKTDAGQGASDIDPMSVD SSDEERFERRKSKSMSARARNCLPMNLRAEDLASGVLRDRVKVGASLADVDPMQLDT SE.DDCFERRKKSMSRARNCLPMNLRAEDLASGVLRDRVKIGASLADVDPMQLDT SE.DDCFERRKKSMSRARNCLPMNLRAEDLASGVLRDRVKIGASLADVDPMQLDT SE.DDCFERRKSKSMSRARNCLPMNLRAEDLASGVLRDRVKIGASLADVDPMQLDT SE.DDCFERRKSKSMSRARNCLPMNLRAEDLASGVLRDRVKIGASLADVDPMQLDT SE.DDCFERRKSKSMSRARNCLPMNLRAEDLASGVLRDRVKIGASLADVDPMQLDT SE.DDCFERRKSKSMSRARNCLPMNFRDEI.KGIYKDRMKIGASLADVDPMQLDT SE.DDCFERRKSKSMSRARNCLPMNFRDEI.KGIYKDRMKIGASLADVDPMQLDT SE.DCGLGHFERRKIGASLADVDPMQLDT SE.GDCGLGLDYINQLKEMVMLPLLYPELYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKKY SVGFDQVGLGHHLQSLKEVVIFPMLYPEVFEKFRINPFKQVFYGPPGTGKTLVARALAACSSENKKY
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens) Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio)	357 213 317 319 22 366 409 262 387 376	AAA1 DNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVDF SDDUVLPRPDKRQSRPHMHNGERERGRFMPINMTKELQSAQHILUNDRMKTDAGQGASDIDPMSVDS SSDEERFERRKSKSMSRARNRCLPMNLRAEDLAS.GVLKDRVKVGASLADVDPMNDDT SE.DDCFERRTKRNRNRAINRCLPLNFRKDEI.R.GIYKDRMKIGASLADVDPMODD SEDDQHFERRKKSSNRAINRCLPLNFRKDEL.K.GIYKDRMKIGASLADVDPMODD AAA1 NVNFDDIGGLDNYLDQLKEMVALPLYPELYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SLSFESVGGLDNYLDQLKEMVALPLLYPEIFQRFNMOPPRGVLFHGPPGTGKTLMARALAACSSENKKV SVGFDGVGGLGHHIQSLKEVVLFFMLYPEVFEKFRINPPRGVVFYGPFTGKTLWARALAACSGDRKN SVGFDSVGGLGHHIQSLKEVVLFPLYPEVFEKFRINPPRGVCFGCTGKTLVARALANECRGGNKV
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens) Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2A(D.rerio) ATAD2A(H.sapiens)	357 213 317 22 366 409 262 387 376 77 422	AAA1 DNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDLGVDF SDDDMVLPRPDKRQSRPHMHNGERERGRFMPINMTKELQSAQHILMDRMKTDAGQGASDIDPMSVDS SSDEERFERKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMQLDT SE.DDCFERRKKSKNSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMQLDT SEDDGHFERRKKSKNSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMQLDT SEDDGHFERRKSKSMSRARNRCLPMNFRDEL.KGIVKDRMKIGASLADVDPMQLDT SEDSOGLDNYLDQLKEMVMLPLLYPELYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SJSFESVGGLDNYLDQLKEMVMLPLLYPELYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SVKFDSVGGLSSHLALKEMVVFPLLYPEVFEKFKIOPPRGCLFYGPPGTGKTLVARALANECSQGDRKV SVKFDSVGGLSSHLAALKEMVVFPLLYPEVFEKFKIOPPRGCLFYGPPGTGKTLVARALANECSGDKRV
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Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens)	357 213 317 319 22 366 409 262 387 376 77 422	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVDG SDDMVLPRPDKRQSRPHMHNGERERGRFMPINMTEKELQSAQHILMDRMRKTDAGQCASDIDPMSVDE SSDEERFERRKSKSMSRARNRCLPMNLRAEDLAS.GVLRDRVKVGASLADVDPMCDD SE.DDCFERRTKRNRNAINRCLPLNFRKDEI.R.GIYKDRMKIGASLADVDPMCDD SEDQHFFERRKRSRNRAINRCLPLNFRKDEI.K.GIYKDRMKIGASLADVDPMCDD AAA1 NVNFDDIGGLDNYIDQLKEMVALPLLYPEIYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SLSFESVGGLDNYINQLKEMVMLPLLYPEIFQRFNMQPPRGVLFHGPPGTGKTLMARALAACSSENKKV SVKFDSVGGLGHHIQSLKEMVVFPLLYPEVFEKFRIDPFRGVLFYGPPGTGKTLVARALANECSGDRKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFEKFRIOPPRGCLFYGPPGTGKTLVARALANECSGDRKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFEKFRIOPPRGCLFYGPPGTGKTLVARALANECSGDRKV
Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol (S. pombe)	357 213 317 319 22 366 409 262 387 376 77 422 479 332	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGDG SDDDMVLPRPDKRQSRPHMHNGERERGRFMPINMTEKELQSAQHILMDRMKKTDAGQGASDIDPMSVD SSDEERFERRKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMNLDT SE.DDCFERRTKRNRNAINRCLPLNFRKDEI.RGIYKDRMKIGASLADVDPMQDD SEDQHFERRRKRSRNRAINRCLPNNFRDEI.KGIYKDRMKIGASLADVDPMQDD AAA1 NVNFDDJIGGLDNYIDQLKEMVALPLLYPELYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKT SJSFSSVGGLDNYINQLKEMVMLPLLYPEIFQRFNMOPPRGVLFHGPPGTGKTLMARALAASSSENKKX SVGFDQVGGLGHHIQSLKEWVNFPLLYPEVFEKFKIDPPRGVLFHGPPGTGKTLVARALANECRGANKX SVKFDSVGGLSHHIQSLKEWVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKX SVRFDSVGGLSHHAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKX SVRFDSVGGLSHHAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKX SVRFDSVGGLSHHAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKX SVRFDSVGGLSHHAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKX
Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans)	357 213 317 319 22 366 409 262 387 376 77 422 479 332 457	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVD SDDDVVLPRPDKRQSRPHMHNGERERGRFMPINMTKELQSAQHILMDRMKTDAGQGASDIDPMSVD SSDEERFERKSKSMSRARNRCLPMNLRAEDLASGVLKDRVKVGASLADVDPMNDD SE.DDCFERTKRNRNRAINRCLPLNFRKDEI.RGIYKDRMKIGASLADVDPMQDD SEDDQHFERKKSKSKRANNCLPLNFRKDEL.KGIYKDRMKIGASLADVDPMQDD SEDDQHFERKKSKSKRANNCLPLNFRKDEL.KGIYKDRMKIGASLADVDPMQDD SEDQGHFERKKSKNRAINRCLPLNFRKDEL.KGIYKDRMKIGASLADVDPMQDD SKEDQGHFERKKSKSKRAINRCLPLNFRKDEL.KGIYKDRMKIGASLADVDPMQDD SEDQGHGENKKSKSKRAINRCLPLNFRKDEL.KGIYKDRMKIGASLADVDPMQDD SKEDQGFERKKSKNRAINRCLPLNFRKDEL.KGIYKDRMKIGASLADVDPMQDD SKEDQGGUDNYLDQLKEMVALPLLYPEJFQFFKFRINPPRGVLFHGPPGTGKTLMARALAASCSSDRKKV SVGFDQVGGLGHHQSLKEVVLFPLLYPEJFQFFKFRINPPKGVVFYGPTGKTLVARALANECSGGDKKV SVKFDSVGGLSSHIAALKEMVVFPLLYPEVFEKFRINPPKGVLFYGPPGTGKTLVARALANECSRGDKKV SVRFDSVGGLSSHIAALKEMVVFPLLYPEVFEKFKIQPPRGCLFYGPPGTGKTLVARALANECSRGDKKV AAA1 TFFMRKGADCLSKWVCGAERQLRLLFEEAKKHQPSIIFPDEIDGLAPVRSSKQEQIHASIVSTLLALMDG
Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2 (D.rerio)	357 213 317 22 366 409 262 387 376 77 422 479 332 457 446	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPTADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDLGVDG SDDDMVLPRPDKRQSRPHMHNGERERGRFMPINMTKEKELQSAQHILMDRMKKTDAGQGASDIDPMSVDS SSDEERFERRKSKSMSRARNRCLPMNLAEDLASGVLRDRVKVGASLADVDPMDDD SE.DDCPERRTKRNRNRAINRCLPLNFRKDEI.RGIYKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKSKRARNRCLPMNFRKDEL.KGIYKDRMKIGASLADVDPMQDD AAA1 NVNFDDIGGLDNYIDQLKEMVALPLLYPELYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SJSFSVGGLDNYINQLKEMVALPLLYPEIYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SVGFDQVGGLGHHIQSLKEVVLFPMLYPEVFEKFRIDPPRGVLFHGPPGTGKTLWARALANECSGDKKV SVGFDSVGGLSHIHALKEMVVFPLLYPEYFEKFRIDPPRGCLFYGPPGTGKTLWARALANECSGDKKV SVRFDSVGGLSHIHALKEMVVFPLLYPEVFEKFRIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFEKFRIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSHIGALKEMVVFPLLYPEVFEKFKLDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSSHIAALKEMVVFPLLYPEVFEKFKLDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFEKFKLDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFEKFKLDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFEKFKLDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFEKFKLDPPRGCLFYGPFGTGKTLWARALANECSQGDKKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFEKFKLDPPRGCLFYGPFGTGKTLWARALANECSQGDKKV
Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2 (D.rerio) ATAD2 (M.musculus)	357 213 317 22 366 409 262 387 376 77 422 479 332 457 446 147	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPTADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVD SDDMVLPRPDKRQSRPHMHNGEREGGFMPINMTEKELQSAQHILMDRMKKTDAGQCASDIDPMSVD SSDEERFERKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMCDD SE.DDCFERRTKRNRNAANRCLPLNFRKDEI.RGIXKDRMKIGASLADVDPMCDD SE.DDCFERRRKRSRNRAINRCLPLNFRKDEI.KGIXKDRMKIGASLADVDPMCDD AAA1 NVNFDDIGGLDNYIDQLKEMVMLPLLYPEIYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SLSFESVGGLDNYINQLKEMVMLPLLYPEIYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SVGFDQVGGLGHHIGSLKEVVLFPMLYBVFKFKIDPPRGCLFYGPPGTGKTLVARALANECSGDKKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFKFKIDPPRGCLFYGPPGTGKTLVARALANECSGDKKV SVRFDSVGGLSHIAALKEMVVFPLLYPEVFKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKV
Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (M.renio) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2 (M.musculus)	357 213 319 22 366 409 262 387 376 77 422 479 332 457 447 492	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVD SDDMVLPRPDKRQSRPHMHNGERERGRFMPINMTEKELQSAQHILMDRMKKTDAGQCASDIDPMSVD SSDEERFERRKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMCDD SE.DDCFERRTKRNRNAINRCLPLNFRKDEI.RGIYKDRMKIGASLADVDPMCDD SEDQHFFERRKRSRNRAINRCLPLNFRKDEI.KGIYKDRMKIGASLADVDPMCDD AAA1 NVNFDDIGGLDNYIDQLKEMVALPLLYPEIYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SLSFESVGGLDNYINQLKEMVMLPLLYPEIFQRFNMOPPRGVLFHGPPGTGKTLMARALAASCSSDERKI SVKFDSVGGLGHHIQSLKEMVVFPLLYPEVFKFRIDPFKGVVFYGPPGTGKTLVARALANECSQGDKKV SVKFDSVGGLSHHALKEMVVFPLLYPEVFKFRIDPFKGVLFYGPPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSHHAALKEMVVFPLLYPEVFKFRIDPFRGCLFYGPPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSHHAALKEMVVFPLLYPEVFKFRIDPFRGCLFYGPPGTGKTLVARALANECSQGDKKV AAA1 TFFMRKGADCLSKWVCEAERQLRLLFEEAKSTQPSIIFPDEIDGLAPVRSSKQEQIHASIVSTLLALMOG AFFMRKGADCLSKWVCESERQLRLLFPQAYQMRPAIIFPDEIDGLAPVRSSKQEQIHASIVSTLLALMOG AFFMRKGADCLSKWVCESERQLRLLFPQAYQMRPAIIFPDEIDGLAPVRSSKQEQIHASIVSTLLALMOG
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Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae)	357 213 317 319 22 366 409 262 387 376 422 457 422 457 446 147 492 549	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPTADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVDF SDDDWUPRPDKRQSRPHMHNGEREGGFMPINMTKELQSAQHILDMRMKTDAGQGASDIDPMSVD SSDEERFERKSKSMSRARNRCLPMNLAEDLASGVLKDRVKVGASLADVDPMNLDD SE.DDCFERRKKSKNSRARNRCLPMNFRKDEIR.GIVKDRMKIGASLADVDPMQLD SE.DDCFERRKKSKNSRARNRCLPLNFRKDEIR.GIVKDRMKIGASLADVDPMQLD SEDEQHFERRKKSKNSRARNRCLPLNFRKDEI.KGIVKDRMKIGASLADVDPMQLD SEDEQHFERRKKSKNSRARNRCLPLNFRKDEI.KGIVKDRMKIGASLADVDPMQLD SEDEQHFERRKKSKNSRARNRCLPLNFRKDEI.KGIVKDRMKIGASLADVDPMQLD SEDEQHFERRKKSKNSRARNRCLPLNFRKDEI.KGIVKDRMKIGASLADVDPMQLD SEDEQHFERRKKSKNSRARNRCLPLNFRKDEI.KGIVKDRMKIGASLADVDPMQLD SKEDSVGGLDNYLDQLKEMVMLPLLYPEIFQNFNITPPRGVLFHGPPGTGKTLWARALAASCSSDEKKI SVGFDQVGGLGHHQSLKEVVLFPLLYPEYFKFKIOPPRGVLFHGPPGTGKTLWARALAASCSSDEKKI SVKFDSVGGLSSHLAALKEMVVFPLLYPEVFEKFKIOPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSSHLAALKEMVVFPLLYPEVFEKFKIOPPRGCLFYGPPGTGKTLWARALANECSQGDKKV AAA1 TFFMRKGADCLSKWVCEAERQLRLFEEAKKHQPSIIFPDEIDGLAPVRSSKQEQIHASIVSTLLALMDG SFYMRKGADCLSKWVCESERQLRLFDQAYMRPSIIFPDEIDGLAPVRSSKQEQIHASIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSKQEQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSKQEQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSKQEQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSKQEQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSKQEQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSRQDQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSRQDQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSRQDQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSRQDQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSRQDQIHSIVSTLLALMDG AFFMRKGADCLSKWVCESERQLRLFDQAYQMRPSIIFPDEIDGLAPVRSSRQDQIHSIVSTLLALMDG
Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe)	357 213 319 22 366 409 262 387 376 422 479 332 457 446 147 492 549 402	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPTADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVDF SDDDMVLPRPDKRQSRPHMHNGERERGRFMINIMTKELQSAQHILMDRMKKTDAGQGASDIDPMSVDS SSDEERFERKSKSMSRARNRCLPMNIRAEDLASGVLRDRVKVGASLADVDPMIDD SE.DDCPERRTKRNRNAINRCLPLNFRKDEI.RGIYKDRMKIGASLADVDPMCDD SE.DDCPERRKKSKSKRRNRICLPMNIRAEDLASGYLRDRVKVGASLADVDPMCDD SE.DDCPERRKKSKSKRRNRICLPMNIRAEDLASGYLRDRVKVGASLADVDPMCDD SE.DDCPERRKKSKSKRRNRICLPMNIRAEDLASGYLRDRVKVGASLADVDPMCDD SE.DDCPERRKKSKSKSRRNRICLPMNIRAEDLASGYLRDRVKVGASLADVDPMCDD SE.DDCPERRKKSKSKSRRNRICLPNFRKDEI.KGIYKDRMKIGASLADVDPMCDD SE.DDCPERRKKSKSKSRRNRICLPNFRKDEI.KGIYKDRMKIGASLADVDPMCDD SE.DDCPERRKKSKSKSKSKSKSKSKSKSKSKSKSKSKSKSKSK
Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (H.sapiens)	357 213 317 319 22 366 409 262 387 77 422 457 446 479 332 457 442 2527 549 902 527	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPTADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVD SDDDMVLPRPDKRQSRPHMHNGEREGGFMPINTBEKELQSAQHILMDRMKKTDAGQCASDIDPMSVD SSDEERFERKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMCDD SE.DDCFERRKKSMSRARNRCLPMNLRAEDLASGVLRDRVKVGASLADVDPMCDD SE.DDCFERRKKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKIGASLADVDPMCDD SE.DDCFERRKKSKSMSRARNRCLPMNLRAEDLASGVLRDRVKIGASLADVDPMCDD SE.DDCFERRKKSKSMSRARNRCLPMNFRDEI.RGIXKDRMKIGASLADVDPMCDD SE.DDCFERRKKSKSMSRARNRCLPMNFRDEI.KGIXKDRMKIGASLADVDPMCDD SE.DDCFERRKKSKSMSRARNRCLPMNFRDEI.KGIXKDRMKIGASLADVDPMCDD SE.DDCFERRKKSKSMSRANNCLPLNFRKDEI.KGIXKDRMKIGASLADVDPMCDD SE.DDCFERRRKRSRNRAINRCLPLNFRKDEI.KGIXKDRMKIGASLADVDPMCDD SE.DCFERRRKRSRNRAINRCLPLNFRKDEI.KGIXKDRMKIGASLADVDPMCDD SE.DCFERRRKRSRNRAINRCLPLNFRKDPRGVLFHGPPGTGKTLMARALAASCSSDERKI SLSFBSVGGLDNYINOLKEMVMLPLLYPEIPQVFEKFRNDPRGVLFHGPPGTGKTLWARALANECSSGDEKKI SVGFDQVGGLGHHIGSLKEVVUFPLLYPEVFEKFRKIDPRGCLFYGPPGTGKTLWARALANECSGCDKKV SVRFDSVGGLSHHALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSGODKKV SVRFDSVGGLSHHALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFKIDPPRGCLFYGPGTGKTLVARALANECSQGDKKV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFNOPPRGCLFYGPGTGKTLVARALANECSQODKXV SVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFNOPPRGCLFYGPGTGKTLVARALANECSRGDVANGAALANECSGODKXV SVRFDSVGGLSNUGASERQLANDVFFNITPPDEIDGLAPVRSSKOOTHASIVSTLALMDG AFFMRKGADCLSKWVCESERVESENDVFFNITPPDAALANECSQODYN
Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.sapiens)	357 213 317 319 22 336 409 262 332 409 262 37 376 422 479 332 457 446 457 446 452 549 402 527 516	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPEDFGRIREKSDLADSDPLGVD SDDDVLPRPDKRQSRPHMHNRGEREGRFMPINMTKELQSAQHILDMRKKTDAGQGASDIDPMSVD SSDEERFERKSKSMSRARNRCLPMNLRAEDLASGVLHDRVKVGASLADVDPMNLDT SE.DDCFERKKSKSRRANRCLPLNFRKDEI.RGIYKDRMKIGASLADVDPMNLDT SEDDCHFERKKSKSRRANRCLPLNFRKDEI.KGIYKDRMKIGASLADVDPMQDD <i>AAA1</i> NVNFDDJGGLDNYLDQLKEMVALPLLYPELYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDRKV SVKFDSVGGLDNYLDQLKEMVALPLLYPEJFQFFKFRINPPRGVLFHGPPGTGKTLMARALAASCSSDRKV SVKFDSVGGLDNYLDQLKEMVALPLLYPEJFQFFKFRINPFKGVVFYGPFGTGKTLVARALAACSSCBNKV SVKFDSVGGLSHLAALKEMVVFPLLYPVFKFRINPFKGVVFYGPFGTGKTLVARALANECRGGANKV SVKFDSVGGLSHLAALKEMVVFPLLYPVFKFRINPFKGVFYGPPGTGKTLVARALANECSGGDKKV AAA1 TFFMRKGADCLSKWVCEAERQLRLLFEEAKKHQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDC SFYMRKGADCLSKWVCESERQLRLFFEEAKKHQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDC SFFMRKGADCLSKWVCESERQLRLLFPEAKKTQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDC AFFMRKGADCLSKWVGESERQLRLLFPEAKKTQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDC AFFMRKGADCLSKWVGESERQLRLLFPEAKKTQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDC AFFMRKGADCLSKWVGESERQLRLFPGATGFDREFYFPLPDEIDGLAPVRSSKQEQIHSIVSTLLALMDC AFFMRKGADCLSKWVGESERQLRLFPGATGFDREFYFPLPDEIDGLAPVRSSKQEQIHSIVSTLLALMDC AAFMRKGADCLSKWVGESERQLRLFPGATGFDREFYFPLPDEIDGLAPVRSSKQEQIHSIVSTLLALMDC SFRMRKGADCLSKWVGESERQLRLFPGATGFDREFYFPLPDEIDGLAPVRSSKQEQIHSIVSTLLALMDC AAFMRKGADCLSKWVGESERQLRLFPGATGFDREFYFPLPDEIDGLAPVRSSKQEQIHSIVSTLLALMDC SFRMRKGADCLSKWVGESERQLRLFPGATGFDREFYFPLPDATGLAPVRSSKQEQIHSIVSTLLALMDC AAFMRKGADCLSKWVGESERQLRLFPGAFFDREFYFPLPDATARQUTDITATKWSS.PLSTNFIDKLAFF
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Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (H.sapiens)	357 213 317 319 22 3366 3366 777 422 457 332 446 147 492 549 402 527 516 217 562	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPTADLDPLGVDF ESDNTRI.KKSSAKTIKALTDPANSGGPDFGRIREKSDLADSDPLGVDF SDDDMVLPRPDKRQSRPHMHNGERERGRFMINIMTKEKEQSAQHILDMRMKTDAGGGASDIDPMSVDS SSDEERFERKSKSMSRARNRCLPMNLAEDLASGVLRDRVKVGASLADVDPMQDD SE.DDCFERRKKSKSNSRARNRCLPMNLAEDLASGVLRDRVKVGASLADVDPMQDD SE.DDCFERRKKSKSNSRARNRCLPMNLAEDLASGVLRDRVKVGASLADVDPMQDD SE.DDCFERRKKSKSNSRARNRCLPMNTRKDEI.KGIVKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKVUPPLUYPELYPNFRKDEI.KGIVKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKNSRARNRCLPMNFRNDEL.KGIVKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKNSRARNRCLPNFRKDEI.KGIVKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKNSRARNRCLPNFRKDEI.KGIVKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKNSRARNRCLPNFRKDEI.KGIVKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKNSRARNRCLPNFRKDEI.KGIVKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKNSRARNRCLPNFRKDEI.KGIVKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKNSRARNRCLPNFRKDEI.KGIVKDRMKIGASLADVDPMQDD SE.DDCFERRKKSKNSRARNRCLPNFRKDEINGLYNSKUGAKTWARLAASCSSDEKKI SVKFDDVGGLDNYINOCKWVIPLUYPELYPEYFKFKIDPRGVLFHGPPGTGKTLWARALAASSSENKKV SVKFDSVGGLSSHLALKEMVVFPLLYPEYFKFKIDPRGCLFYGPPGTGKTLWARALAASCSGGDKKV SVKFDSVGGLSSHLAALKEMVVFPLLYPEYFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSSHLAALKEMVVFPLLYPEYFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHLAALKEMVVFPLLYPEYFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHLAALKEMVVFPLLYPEYFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHLAALKEMVVFPLLYPEYFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHLAALKEMVVFPLLYPEYFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHLAALKEMVVFPLLYPEYFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNHLAALKEMVVFPLLYPEYFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNLAALKEMVVFPLLYPEYFEKFKIDPPRGCLFYGPPGTGKTLWARALANECSQGDKKV SVRFDSVGGLSNLAALKEMVVGFACGACGLSKWVGSSERQLLLFPQQAYMRPSIIFFDEIDGLAPVRSSKQDQIHSSIVSTLLALMDG AFFMRKGADCLSKWVGESERQLLLFPQQAYQMRPSIIFFDEIDGLAPVRSSRQDQIHSSIVSTLLALMDG AFFMRKGADCLSKWVGSSERQLLFPQQAYQMRPSIIFFDEIDGLAPVRSSRQDQIHSSI
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Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2 (M.musculus) ATAD2 (H.sapiens)	357 213 317 319 22 366 409 262 387 77 422 457 442 457 492 549 9402 527 516 217 562 618	AAA1 DNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPETADDPLGVDF GSDDTRI.KKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVD SDDDVLPRPDKRQSRPHMHNRGEREGRFMPINMTKELQSAQHILMDRMRKTDAGQGASDIDPMSVD SSDEERFERKSKSMSRARNRCLPMNLRAEDLAS.GVLKDRVKVGASLADVDPMNDCD SE.DDCFERKKSKSRRANRCLPMNLRAEDLAS.GVLKDRVKVGASLADVDPMNDCD SE.DDCFERKKSKSRRANRCLPMNLRAEDLAS.GVLKDRVKVGASLADVDPMODD SE.DDCFERKKSRSRRAINCLPLNFRKDEL.K.GIVKDRMKIGASLADVDPMODD SEDCHFERKKSKSRRANRCLPMNFKDELK.GVKDRMKIGASLADVDPMODD SEDCHFERKKSKSNSRANRCLPMNFKDEL.K.GIVKDRMKIGASLADVDPMODD SEDCHFERKKSKSNSRANRCLPMNFKDEL.K.GIVKDRMKIGASLADVDPMODD SEDCHFERKKSSNSRANRINCLPLNFRKDEL.K.GIVKDRMKIGASLADVDPMODD SEDCHFERKKSSNSRANRINCLPLNFRKDEL.K.GIVKDRMKIGASLADVDPMODD SEDCGLDNYINOLKEMVMLPLLYPEJFORFKRINPKGVVFYGDFGTGKTLVARALAASSSENKKV SVKFDSVGGLDNYINOLKEMVMLPLLYPEJFORFKFRINPKGVVFYGDFGTGKTLVARALAASSSENKKV SVKFDSVGGLSHLALKEMVVFPLLYPEVFEKFRINPKGVVFYGDPGTGKTLVARALAASCSSENKKV SVKFDSVGGLSHLAALKEMVVFPLLYPEVFEKFRINPKGVPFGCLFYGPFGTGKTLVARALANECSQGDKRV AAA1 TFFMRKGADCLSKWVGEAEROLRLLFPLYNFPLYPEVFEKFKIOPPRGCLFYGPPGTGKTLVARALANECSQGDKRV AAA1 MDNRCOLSKWVGESEROLRLLFPDQAYAMPSIIFPDEIDGLAPVRSSKODOIHASIVSTLLALMDG SFFMRKGADCLSKWVGESEROLRLLFPDQAYLMPSIIFPDEIDGLAPVRSSKODOIHASIVSTLLALMDG AAFFMRKGADCLSKWVGESEROLRLLFPDQAYLMPSIIFPDEIDGLAPVRSSKODOIHASIVSTLLALMDG AAFFMRKGADCLSKWVGESEROLRLLFPDQAYLMPSIIFPDEIDGLAPVRSSKODOIHSSIVSTLLALMDG AAFFMRKGADCLSKWVGESEROLRLLFPDQAYLMPSIIFPDEIDGLAPVRSSKODOIHSSIVSTLLALMDG AAFFMRKGADCLSKWVGESEROLRLLFPDQAYLMPSIIFPDEIDGLAPVRSSKODOIHSSIVSTLLALMDG AAFFMRKGADCLSKWVGESEROLRLLFPGRPREFYFPLPDENDGLAPVRSSKODOIHSSIVSTLLALMDG AAFFMRKGADCLSKWVGESEROLRLLFPGRPREFYFPLPDEIDGLAPVRSSKODOIHSSIVSTLLALMDG AAFMRCGADCLSKWVGESEROLRLLFPGRPREFYFPLPDEIDGLAPVRSSKODOIHSSIVSTLLALMDG AAFFMRKGADCLSKWVGESEROLRLLFPGRPREFYFPLPDEIDGLAPVRSSKODOIHSSIVSTLLALMDG SFFMRRGADCLSKWVGESEROLRLLFPGRPREFYFPLPDEIDGLAPVRSSKODOIHSSIVSTLLALMDG AAFMRCGADCLSKWVGESEROLRLLFPGRPREFYFPLPDEIDGLAPVRSSKODOIHSSIVSTLLALMDG AAFMRKGADCLSKWVGESEROLRLFPGRPREFYFPLPDEIDGLAPVRSSKODOIHSSIVSTLALMDG
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Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol(S.pombe) lex-1 (C.elegans) ATAD2A (M.sapiens)	357 213 317 319 22 366 409 262 336 777 422 479 332 446 147 492 549 402 527 516 217 556 216 217 562	AAA1 DNNNKLIID
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Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (M.musculus) ATAD2A (M.musculus) ATAD2A (M.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (H.sapiens) Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2A (H.sapiens)	357 213 317 319 22 336 409 262 336 422 479 332 422 479 332 422 479 332 549 402 217 516 6217 585 527 516 631 631 638 631	AAA1 DNNNKLIIDSDSDDEIFELGUYPKIKKENTYKKKKKYPETADDPTGUVE ESDNTRI, KKSDSDDEIFELGUYPKIKKENTYKKKKKYPETADDPTGUVE ESDNTRI, KKSSAKIKLATTEN GEREGERFMEINMTEKELGSAGHILMDKRKTDAGGGASDIPPKSVD SSDEERFERKSKSNRARNCIPUNTEKELGSAGHILMDKRKTDAGGGASDIPPKSVD SSDEERFERKSKSNRARNCIPUNTEKELGSAGHILMDKRKTDAGGGASDIPPKSVD SE.DDCFERRKSKSNRARNCIPUNTEKELGSAGHILMDKRKTDAGGGASDIPPKSVD SE.DDCFERRKSKSNRARNCIPUNFKELJPNITEKELGSAGHILMDKRKTDAGGGASDIPPKSVD SE.DDCFERRKSKSNRARNCIPUNFKELJPNITEKELGSAGHILMDKRKTDAGGGASDIPPKVD SE.DDCFERRKSKSNRARNCIPUNFKELJPNITEKELGSAGHILMDKKKI KIGASLADVOPMOLD SEDDGHFERKSKSNRARNCIPUNFKELJPNITEKELGSAGHILMDKKKI KIGASLADVOPMOLD SEDDGHFERKSKSNRARNCIPUNFKELJPNITEKELGSAGHILMDKKKI KIGASLADVOPMOLD SEDDGHFERKKSKSNRARNCIPUNFKEKI VENKIKKI KKI GIYKDMKIGASLADVOPMOLD SEDGGHIGHIGSK KEWUHPLIPUNFKKI VENKIKI VGPGGKTTMARALAASSESDEKK SVGGDGVGGIGHIGSK KEWUHPLIPUPVEKKKI VPEKKKI VGPGGCKTU ARALAACSSENKKX SVGPDSVGGLSHINGSK KEWUYFPLLYPVEKKKI VPEKKKI VGPRGCLYVGPGGKTTU ARALAACSGODKXX SVKPDSVGGLSHINGSK KEWUYFPLLYPVEKKKI VPEKKKI VGPRGCLYVGPGGKTTU ARALAACSGODKXX SVKPDSVGGLSHINAALKEMUVFPLLYPVEKKKI VPEKKKI VGPRGCLYGPGGKTTU ARALAACSGODKXX SVRPDSVGGLSHINAALKEMUVFPLLYPVEKKKI VPEKKKI VGPRGCLYGPGGKTTU ARALAACSGODKXX SVRPDSVGGLSNNGA EROURLLPEAKKI VGPSI IFFDBIDGLAPVRSSKOOCI HASI VSTLLALMOC SPRKGADCLSKWVGB EROURLLPEAKKI VGPSI IFFDBIDGLAPVRSSKOOCI HASI VSTLLALMOC SPRKGADCLSKWVGB EROURLLPEAKKI VGPSI IFFDBIDGLAPVRSSKOOCI HASI VSTLLALMOC SPRKGADCLSKWVGB EROURLLPEAKKI VGPSI IFFDBIDGLAPVRSSKOOCI HSSI VSTLLALMOC AAPPMRKGADCLSKWVGB EROURLLPEAKKI VGPI FDEIDGLAPVRSSKOOCI HSSI VSTLLALMOC SPRKGADCLSKWVGB EROURLLPEAKKI VGPSI IFFDBIDGLAPVRSSKOOCI HSSI VSTLLALMOC AAPPMRKGADCLSKWVGB EROURLLPEAKKI VGPD FYND FDEIDGLAPVRSSKOOCI HSSI VSTLLALMOC AAPPMRKGADCLSKWVGB EROURLLPEAKKI VGPD FYND FDEIDGLAPVRSSKOOCI HSSI VSTLLALMOC AAPPMRKGADCLSKWVGB EROURLLPEAKKI VGPD FYND FDEIDGLAPVRSSROOCI HSSI VSTLLALMOC SPRKKGADCLSKWVGB EROURLLPEAKKI VGPD FYND FDEIDGLAPVRSSROOCI HSSI VSTLLALMOC SPRKKGADCLSKWVGB EROURLLPEAKKI VGPD FYND FDEIDGLAPVRS

		AAA2
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	748 582 702 723 421 766	EDTSSFRSYEFF.ESMAESQICKPRLLINGPKCNGO.OYVGAAILNYLEEFNVONLDLASLVS .KENDFEYQQRL.ETFETLRIYKPRFLICGRKGLGO.TALGPAILQQYEGVHVQSFDMSTLLQ SSELEQVVRALEPNPTVPAIRLLCGSEQLADGGOTSYVLPAILAKLDHLPVFSLSVSSLLT KKAASCTTHKPFLHFTTSAYQOPTSYRPRLLITGPQGAGOSTHLAPALLHHLEKFTVHRLDLPTLYS KENLNFLHINRNACYQPMSFRPRLLIVGEPGFGQSHLAPAVIHALEKFTVYTLDIPVLFG KSSHKAKDNFNFLHLNRNACYQPMSFRPRLLIVGEPGFGQSHLAPAVIHALEKFTVYTLDIPVLFG AAA2
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	809 642 764 790 482 833	ESSRTIEAAVVOSFMEAKKROPSVVFIPNLDIMINTIPENVILVLSGLFRSLOSNEKILLICLAENL DSTOSIETSIIHLFLEVRHTPSIIVIPDLDIMINVLPLTAITTFSSMLERLDFSDQILFALSS.S .DCRPEAFSMAIGSAMRASATGG-CIMLLPSIDEMIKVIPVSVOHMLITLESMTGFTPILFISTLD.T VSAKTPEESCAQVFREARRCVPSIIVMPHISAWWEAISETVKSSFLMLLQDVPSFTPLLIATAE.S ISTTSPEEACSQMIREARRTAPSIVVPHIHLWWEIVGPTLKATFTTLLQTIPSFAPVLLATSE.K VSTSPEETCAQVIREARRTAPSIVVPHIHLWWEIVGPTLKATFTTLLQVIPSFAPVLLATSE.K AAA2
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	876 708 831 856 548 899	DISEVKNGILSDFAFD.KNIFQLHKFSKENITRYSNLIELLKTKFSDIPMKKRRVK.PLPELQKVTSNA PLSELHPQLREWFSSK.QSVYSLQYPTRDSIIAFEOPILELIKASPTELPGGIPRKRRVLPELPLAP SFEDAPEYVTEIFRHANCIT.LMPSRRTIRQKYEHVIEKINTPFKVFDPTVVEMPLPD VYQQLPDELKCIFSRSYGEVFCLSMPGEEARRKFSDLILVQAAKAPPRRRKS.ACALEVLTLSE PYSALPEEVQELFTHDYGEIFNVQLPDKEERTKFEDLILKQASKPPVSQKKAVLQALEVLPVAP PHSALPEEVQELFIRDYGEIFNVQLPDKEERTKFEDLILKQASKPPVSQKKAVLQALEVLPVAP Iinker arm Bromodomain
Yta7 (S.cerevisiae) Abol (S.pombe) lex-1 (C.elegans) ATAD2 (D.rerio) ATAD2A (M.musculus) ATAD2A (H.sapiens)	944 774 889 920 613 964	APTNFDENGEPLSEKVVLRRKLKSFOHODMRLKNVLKIKLSGLMDLFKNRVKRERKPPIDDAFLVHLF DPPFTSOKITIKQTKQADMRLINKIKIKLNALIG.SLRARVKREKKPLIDFNDIVC.V DDSPDSKPSRKLNDDET.RELLKMVTALQROMRLFKERLTRLMRDRRVEVEPVEPV DPGPRQLSAEEQ.RRLEEQEENTLRELRIFLRDVTKRLATDKRPQIESKPV PPEPRPLTAEEV.KRLEEQEEDTFRELRIFLRNVTHRLAIDKRPRVETKPV PPEPRSLTAEEV.KRLEEQEEDTFRELRIFLRNVTHRLAIDKRPRVETKPV PPEPRSLTAEEV.KRLEEQEEDTFRELRIFLRNVTHRLAIDKRPRVETKPV
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	1012 831 944 970 663 1014	EPETSND PNWQPAYIKDENMILEVSTGRKFFNMDLDIVEERLWNGYYSEPKQFLKDIELIYRDANTIG DPETGHSYRSREECHYEFVDDVVKQIGSDQKFSMMSLEEIEKRTWDNCYCHTPKOPVHDIKLILBAALQLE DPDEAEDYYEI
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	1080 901 995 1021 714 1065	DRERVIKISEMFANAQMGTEEISTPDFIQECKATRQRDLERQELFLE.DE DSETIKRAQEMYANVLLGVEDMEDDQFSQRCERMALREAERRKLRHG.KLQKHL.D PSTTKDGKLIRQMANTLRDAIDDLECELDESVERIETVSRMLQDAGVT. PDKDPGDKIIRHRACSLKDTAHAMASELDPEFDRMCEEIKESRRKRAPQTAPQPPVTPSTV PDRDPGDRLIRHRACALRDTAYAIIKEELDEDFEQLCEEIQESRKKRGCSSSKYAPSYYHVMPKQNSPPV PDRDPGDRLIRHRACALRDTAYAIIKEELDEDFEQLCEEIQESRKKRGCSSSKYAPSYYHVMPKQNSTLV
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	1129 955 1045 1083 784 1135	EKRAAMELEAKEQSQENILQEPDLKDNKANEF ETKADMQFTSEKPTSDKLLTEIPKGFARKKAWSMTNSLAKEIE.QWTSER ATRKPMGEEAGLSSSQGDGVDKHCSNNIKRKFRRPIWGRGIIRKKKSYKKEEAEEDDEPEEEE GDKKPDQEQNEKLKVPCTPVACSTPAQLKRKFHKKSKWHVGTKIKRRKISQAKDNSLNAMNSSSRS GDKRSDPEQNEKLKTPSTPVACSTPAQLKRKIRKKSNWYLGTIKKRRKISQAKDDSQNAIDHKIES
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	1161 979 1082 1147 850 1201	GVAAGNQLQAQLQTTINTASIVNNSEVPQPIDTNLYKKEIPAATPSAVDKEKAVI AIKDGPPVLAETLT.NSLME.DVGPENVDMDIEDNEIFTNQSTMSVPSMLVEN EAENQKMLSKLGVAAPTLELVVVPVEDMKSEEGTSTSTDGVPAS.AGNKKKL.LKKK GAEDSTV.MAQGDACLTLDESSCDTMELHPERQPLQANGHVLSTEEENSCEPTAARDA DTEDSQHTHAEHTEPGNTDE.SSVESSDKQ.NRLESNIDLKNNSSSNI DTEETQDTSVDHNETGNTGE.SSVEENEKQQNASESKLELRNNSNTCNI
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegnas) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	1216 1030 1137 1204 897 1249	
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	1263 1076 1158 1266 919 1270	EENFSKIDANTNNINHVKEIQSVNKPNSLHETV.EKRERSPI.PKEV.V.VEPEQGKKSDKELI SNGRADIPVD.TLITSPADVPNNAPTDAHNITSADGHIENI.EQEV.V. DAGEDTIVENLEIKKN.QETPNSEHDIEMKDASKDSTFSVQISIAEKELI CSTGENTRTAEAVASDGDHEKEGSSKGKECGKGLSEVQAEEPAVRLQEAVQLPPPDLV CRGDASASQVTDIPEDSESKEMDFLRMTLARGSQVEQQELISMEQALAILSQPTPSLV CNGDASSSQIIHISDENEGKEMCVLRMTRARSQVEQQQLITVEKALAILSQPTPSLV C-terminal domain
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	1322 1126 1207 1325 977 1328	LTPEQTKKVSACLIEHCONFTVSQTEDVHSSVAKITWKSKSAWDKTGTVDETIKFLSE. FDEDRLTPLKQLLIDSTTGFTVDQTLHLHSFLYQITWNTKSEWNRNSVVDECERAVKEFMINALQ VSKPATCELIQCCVEKSEGWSVSETERLSSVLSHTERFRDEWNRENLPAQLTQIVREWQTADDSNNTIV VDHQRLKALLEQAVVKSGFSVDHIEVVFSALSQCTYVHRRDVDKTRLIEAMERQVEHFEFL LDHKQLTNILKTVVKKSQKYNIFQTENLYAVISQCTYEHRRDYDKTRLIEAMERQVEHFGSSS VDHERLKNLLKTVVKKSQNYNIFQTENLYAVISQCTYRHRKDHDKTSLIQKMEQEVENFSSS
Yta7(S.cerevisiae) Abol(S.pombe) lex-1(C.elegans) ATAD2(D.rerio) ATAD2A(M.musculus) ATAD2A(H.sapiens)	1277	NGTLNKSNGNLANGH

Supplementary Fig. 1 Sequence alignment shows the conserved domain organization of the

ATAD2 family.

Multiple alignment of ATAD2 genes from different species. ATAD2 homologs from S. cerevisiae (Yta7), S. pombe (Abo1), C. elegans (lex-7), D. rerio, M. musculus, and H. sapiens were aligned using the Clustal W program and displayed using ESPRIPT3.0. The conserved domains are labeled. Red represents 100% identity among sequences, yellow represents a similarity score of > 0.7.



Supplementary Fig. 2 Characteristics of Abo1-mediated H3-H4 DNA deposition.

a. Histogram of H3-H4 loading positions on DNA, which was built up by collecting the center coordinates of 2 D Gaussian function for fitting fluorescence intensity of individual Cy5-H3-H4 histones in Fig. 2b. Distribution of peak positions show the sequence independence of Abo1- mediated H3-H4 loading (N=597 molecules). Error bars were obtained by bootstrapping with a 70% confidence interval.

b. Results of MNase digestion of 269 bp DNA when mixed with histone H3-H4, CAF-1+H3-H4, Abo1+H3-H4, or Abo1. MNase digestion products were separated by 8% native PAGE. Major digestion products of CAF-1 are labeled with an arrow, and major protected fragments of Abo1 and histone H3-H4 are labeled with asterisks.



Supplementary Fig. 3 Absence of H3-H4 unloading from DNA by Abo1.

a Image of DNA curtains, on which Cy5-H3-H4 histones were loaded by yCAF-1.

b Image of DNA curtains after 15-minute Abo1 incubation with Cy5-H3-H4 pre-loaded by

yCAF-1 in the above (Full movies shown in Video S3 and S4).

c DNA fractions with bound H3-H4, which were quantified from DNA curtain data when H3-H4 was loaded onto DNA by yCAF-1 (in a) and when Abo1 is subsequently added to the pre-loaded H3-H4 by yCAF-1 (in b). (DNA molecules analyzed for each experiment are 200, N=200). The data were obtained from three independent experiments and error bars represent SD.



Supplementary Fig. 4 Workflow of cryo-EM data processing and cryo-EM data validation for the ATP-Abo1 Walker B mutant

a Workflow of cryo-EM data processing of ATP-Abo1 Walker B mutant. All processing was performed with cisTEM.

b Gold standard FSC curve of the cryo-EM reconstruction.

- c Angular distribution plot of particles for the final refinement.
- **d** Local resolution distribution of the cryo-EM map analyzed by ResMap.



Supplementary Fig. 5 Electron density map and fit of the ATP-Abo1 structural model

a Overall cryo-EM map of ATP-Abo1 Walker B mutant with the Abo1 structure built *de novo*.

b Cryo-EM density and structure of subunit E.

c- f Cryo-EM densities and structures of a.a. 330-367 (**c**), a.a. 662-730 (**d**), a.a. 1132-1166 (**e**), and a.a. 491-566 (**f**).



Supplementary Fig. 6 Electron density fit of nucleotides with conserved AAA+ residues

a-f Cryo-EM density and fit of nucleotides of subunit A-F. ATP molecules were built for subunits B-F, while an ADP molecule was built for subunit A. Side chains of K313 in the Walker A motif, Q372 in the Walker B motif, N415 in the sensor I motif, R480 in the sensor II motif and R429 of the arginine finger are depicted in each figure, and labeled in figure (**f**).



Supplementary Fig. 7 Electrostatic potential surface map of an individual Abo1 subunit.

The Abo1 electrostatic potential surface map of an Abo1 subunit (subunit E) highlighting the positive charge surface of the "hole" and the negative charge surface of the knob.



Supplementary Fig. 8 Structure and position of the AAA2 knob insert

a The α 0- β 1 insert (teal) in the Abo1 AAA2 domain that forms the "knob" structure that inserts into the "hole" of the adjacent AAA subunit. α 0 and β 1 are depicted in hot pink.

b, **c** Corresponding view of the NSF (PDB ID: 3j94) and p97 (PDB ID: 5ftm) AAA2 domains with $\alpha 0$ and $\beta 1$ in hot pink.



Supplementary Fig. 9 Workflow of cryo-EM data processing and validation for ADP-Abo1.

- a Workflow of cryo-EM data processing of ADP-Abo1 performed with cisTEM.
- **b** Gold standard FSC curve of the cryo-EM reconstruction.
- c Angular distribution plot of particles for the final refinement.
- d Local resolution distribution of the cryo-EM map analyzed by ResMap (8).



Supplementary Fig. 10 Workflow of cryo-EM data processing and validation for apo-Abo1.

- a Workflow of cryo-EM data processing of apo-Abo1 performed with cisTEM.
- **b** Gold standard FSC curve of the cryo-EM reconstruction.
- c Angular distribution plot of particles for the final refinement.
- d Local resolution distribution of the cryo-EM map analyzed by ResMap.

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Supplementary Fig. 11 Workflow of cryo-EM data processing and validation for apo-Abo1 structure with improved bromodomain density.

- a Workflow of cryo-EM data processing of apo-Abo1 performed with Relion 3.0.
- **b** Gold standard FSC curve of the cryo-EM reconstruction.
- c Angular distribution plot of particles for the final refinement.
- d Local resolution distribution of the cryo-EM map analyzed by ResMap.



Supplementary Fig. 12 Structure of the Abo1 bromodomains

a Side view of Abo1 in the apo state showing discrete densities for the bromodomain (top) and the AAA+ ring (bottom).

b Top view of the bromodomain, showing six lobes of density arranged in a ring around a lobe of central density.



Supplementary Fig. 13 MDFF fit of ADP-Abo1 and apo-Abo1 structures

a Fit of the ADP-Abo1 model created by MDFF into the cryo-EM density map, shown with the bottom (AAA2) view (top panel), and side view (bottom panel).

b Fit of the apo-Abo1 model created by MDFF into the cryo-EM density map, shown with the

bottom (AAA2) view (top panel), and side view (bottom panel).



Supplementary Fig. 14 Examples of Abo1 AAA+ ring at more than one position.

HS-AFM snapshots (bottom) and subunit analysis (top) of transient states where more than one Abo1 subunit seems to disappear from the field of view.



Supplementary Fig. 15 Dwell time analysis of Abo1 ring opening and closing

a, **b** Histograms of dwell times for open (a) and closed (b) states in the presence of 2mM ATP (N=90 for opening, N=102 for closing). Both distributions were fitted with a single exponential decay function, A * exp (-t/ τ), where τ is the time constant. Based on these constants, the rate of ring opening is 1.5 s⁻¹, and closing is 0.99 s⁻¹.



Supplementary Fig. 16 HS-AFM movie frames of Abo1 Walker B mutant with ATP.

a, **b** Two examples of Abo1 Walker B mutant molecules in the presence of 2mM ATP. Both molecules undergo a symmetry breaking event to produce an asymmetric spiral as in the cryo-EM structure, and are stuck in the same asymmetric state.





a, b Two examples of Abo1 molecules undergoing symmetry breaking in the presence of 2mM ATP. The positions (gray boxes) at which ring symmetry breaks shows a stochastic pattern in both molecules. Movies were taken at a rate of 0.2sec/frame. Scale bars represent 5nm.



Supplementary Fig. 18 Preparation of Abo-H3-H4 sample for crosslinking mass spectrometry analysis.

Native gel analysis of DSS-crosslinked and sucrose gradient fractionated Abo1-H3H4 complex. Abo1-H3H4 complex was separated from Abo1 by sucrose gradients and fractions 6 and 7 were used for mass spectrometric analysis.



Supplementary Fig. 19 Binding affinity and ATPase activity of Abo1 pore loop mutants. a Binding affinities of wild-type and pore loop mutant Abo1 for H3-H4 as measured by changes in fluorescence anisotropy. The respective binding affinities (Kd) of wild-type, W345A, and E385A are, 13 ± 3 nM, 14 ± 9 nM, and 19 ± 16 nM. Measurements are from three independent experiments and error bars represent SEM.

b Steady-state ATPase activity of wild-type and pore loop mutant Abo1. Measurements are from three independent experiments and error bars represent SEM.



Supplementary Fig. 20 Abo1-mediated DNA loading of tailless histone H3-H4

a Coomassie stained SDS-PAGE of Cy5-labeled-H3-H4* cleaved with trypsin. Cy5 was labeled

on histone H4 aa 71 and indicated with asterisks.

b Cy5 scan of SDS-PAGE of Cy5-labeled-H3-H4* cleaved with trypsin.

c Comparison of the H3-H4 loading activity on DNA by quantification of fraction DNA bound with labeled H3-H4.

	ATP-Walker B (E372Q) Abo1	ADP wtAbo1	Apo wtAbo1	Apo wtAbo1 -2
Data collection				
Microscope		Titan Krios		Titan Krios with VPP
Detector	Falcon3	Falcon3	Gatan K2	Gatan K2
Mode		Electron Co	unting	
Voltage (kV)		300		
Total electron exposure $(e^{-}/Å^2)$	59	48.96	75	40.60
Frames (used/collected)	39/59	47/48	39/50	39/40
Dose per fraction (e ⁻ /Å ² /sec)	1.00	1.02	1.50	1.04
Exposure time (sec)	120	37.75	10	10 sec
Defocus range (µm)	1-3.5	1.5-3.5	1-3.5	1-3.5
Pixel size (Å/pixel)	1.12	0.673	1.06	1.04
Micrographs (used/collected)	918/1032	1159/1589	2761/3222	901/1158
Data processing				
Symmetry imposed	C1	C1	C1	C1
Initial particle (no.)	425,696	115,089	823,421	120,779
Final particle images (no.)	99,421	53,582	125,874	23,581
Final map resolution (Å)	3.54	4.44	4.27	6.9
Model Validation				
Bonds (RMSD) - length (Å) - angles (°)	0.010 1.258	0.043 3.542	0.057 3.727	N/A
Ramachandran plot (% outliers/allowed/favored)	0.6/13.5/85.9	4.5/10.0/85.5	4.3/9.9/85.8	N/A
CC between map and model	0.85	0.80	0.78	N/A

Supplementary Table 1. Cryo-EM data collection, processing, and validation statistics

Crosslinked peptide sequence	Protein1	Protein2	Position1	Position2	LD score
GADCLSKWVGEAER-TKQTAR	abo1	H3	344	4	33.56
KKIIEIHTR-TKQTAR	abo1	Н3	446	4	33.14
K <mark>K</mark> IIEIHTR- <mark>K</mark> QLATK	abo1	Н3	446	18	30.31
KPLIDFNDIYCVDPETGHSYR- KLPFQR	abo1	Н3	819	64	28.98
KQLATK-LLNKLK	Н3	abo1	18	798	28.64
KIIEIHTR- <mark>K</mark> STGGK	abo1	H3	446	9	28.56
FKKPLIDFNDIYCVDPETGHSYR- KLPFQR	abo1	Н3	819	64	28.21
F <mark>K</mark> KPLIDFNDIYCVDPETGHSYR- KLPFQR	abo1	Н3	818	64	27.6
KIIEIHTR-STGGKAPR	abo1	H3	446	14	27.18
LRHG <mark>K</mark> LQK-STGG <mark>K</mark> APR	abo1	H3	948	14	26.38
RLQIDP <mark>K</mark> TIK- <mark>K</mark> STGGK	abo1	H3	510	9	26.07
KKIIEIHTR-KSTGGKAPR	abo1	Н3	446	14	25.97
DAVTYTEHA <mark>K</mark> R-I <mark>K</mark> LNALLGSLR	H4	abo1	77	802	24.65
DALQLEDSETIKR-DNIQGITKPAIR-	abo1	H4	906	31	23.46
DALQLEDSETIKR-VTIMPKDIQLAR	abo1	H3	906	122	22.96
SREECHYEFVDDVV <mark>K</mark> QIGSDQK- T <mark>K</mark> QTAR	abo1	Н3	854	4	21.26

Supplementary Table 2. Intermolecular crosslinks between Abo1 and H3-H4

* Only Abo1-histone peptide crosslinks with an LD-score higher than 20 are shown.

** Position denotes amino acid number in each protein.

Crosslinked peptide sequence	Position1	Position2	Domain	LD score
LLN <mark>K</mark> LK-I <mark>K</mark> LNALLGSLR	798	802	bromo-bromo	38.99
QT <mark>K</mark> QADMR-I <mark>K</mark> LNALLGSLR	789	802	bromo-bromo	35.77
KGADCLSK-LLNKLK	337	798	AAA1-bromo	34.62
ITLKQTK-LLNKLK	786	798	bromo-bromo	34.48
ITL <mark>K</mark> QTK-IKLNALLGSLR	786	802	bromo-bromo	33.94
KVSFYMR-IKLNALLGSLR	329	802	AAA1-bromo	29.46
KGADCLSK-IKLNALLGSLR	337	802	AAA1-bromo	28.98
KVSFYMR-KKIIEIHTR	330	446	AAA1-AAA1	24.93
QT <mark>K</mark> QADMR-HG <mark>K</mark> LQK	789	948	bromo-bromo	24.68
GVLFHGPPGTG <mark>K</mark> TLMAR-LLN <mark>K</mark> LK	313	798	AAA1-bromo	24.00
KGADCLSK-KKIIEIHTR	337	446	AAA1-AAA1	23.57
ITL <mark>K</mark> QTK-HG <mark>K</mark> LQK	786	948	bromo-bromo	23.35
DFVMSM <mark>K</mark> R-IKLNALLGSLR	524	802	AAA1-bromo	23.13
I <mark>K</mark> LNALLGSLR-DALQLEDSETI <mark>K</mark> R	802	906	bromo-bromo	21.82
ITL <mark>K</mark> QTK-LRHG <mark>K</mark> LQK-	786	948	bromo-bromo	21.72
GADCLSKWVGEAER-TLQKLMPVASK	344	562	AAA1-AAA1	20.99
KVSFYMR-KGADCLSK	329	337	AAA1-AAA1	20.88
QFVHDIKLILR-LQ <mark>K</mark> HLDETK	890	951	bromo-bromo	20.00

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* Only Abo1-histone peptide crosslinks with an LD-score higher than 20 are shown.