

APC/C^{CDC20} and APC/C play pivotal roles in the process of embryonic development in *Artemia sinica*

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Supplementary Figure Legends

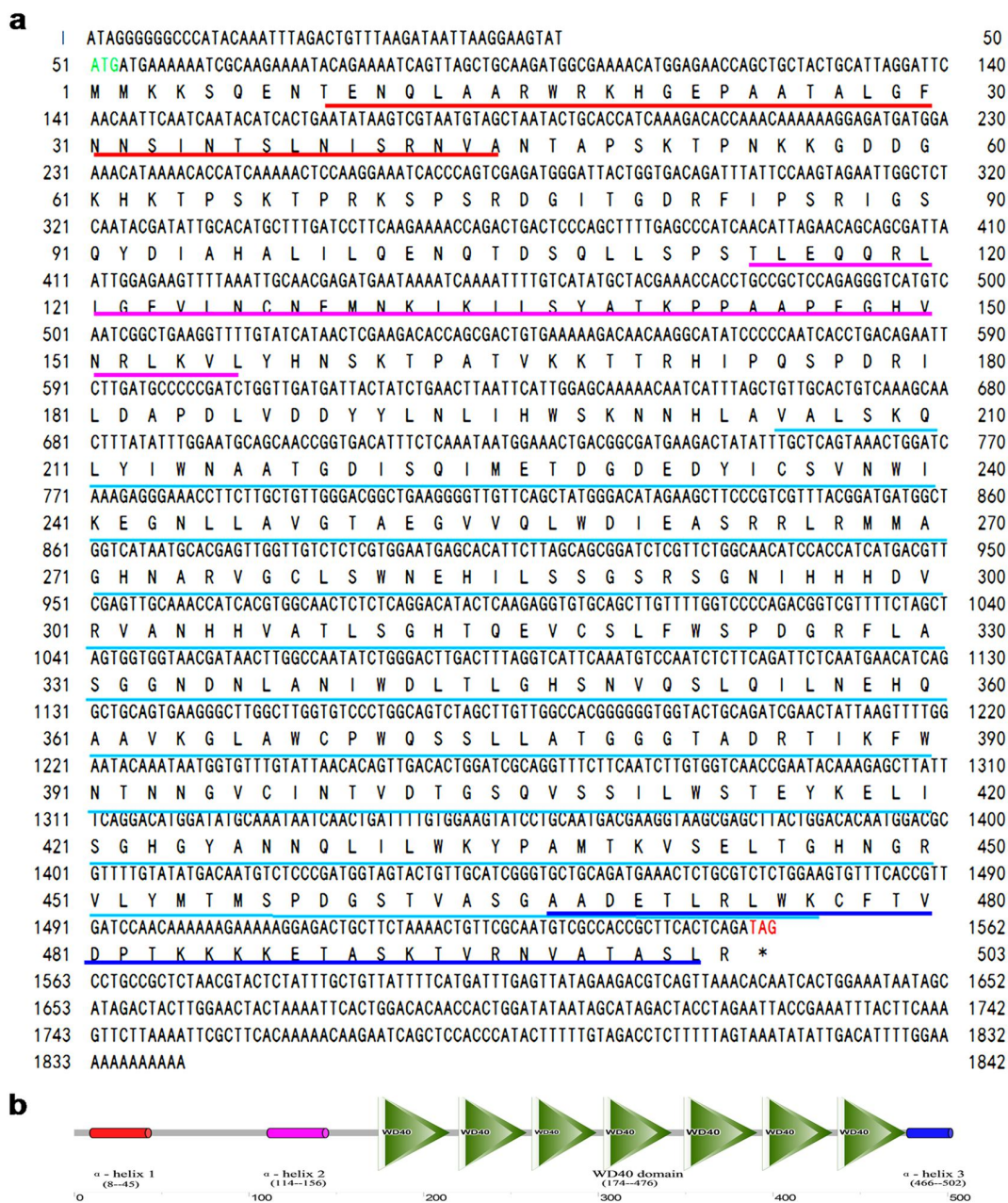


Fig. S1 The full-length cDNA and deduced amino acid sequences of *As-cdc20* and putative protein domains. (A) Sequence analysis of the cDNA and predicted peptide sequences of *As-cdc20*. The start codon is indicated in green; the stop codon is indicated in red; a blue straight line indicates the WD40 superfamily domain. (B) Domain analysis of the putative *As-CDC20* protein, which includes α -helices and seven WD40 repeats.

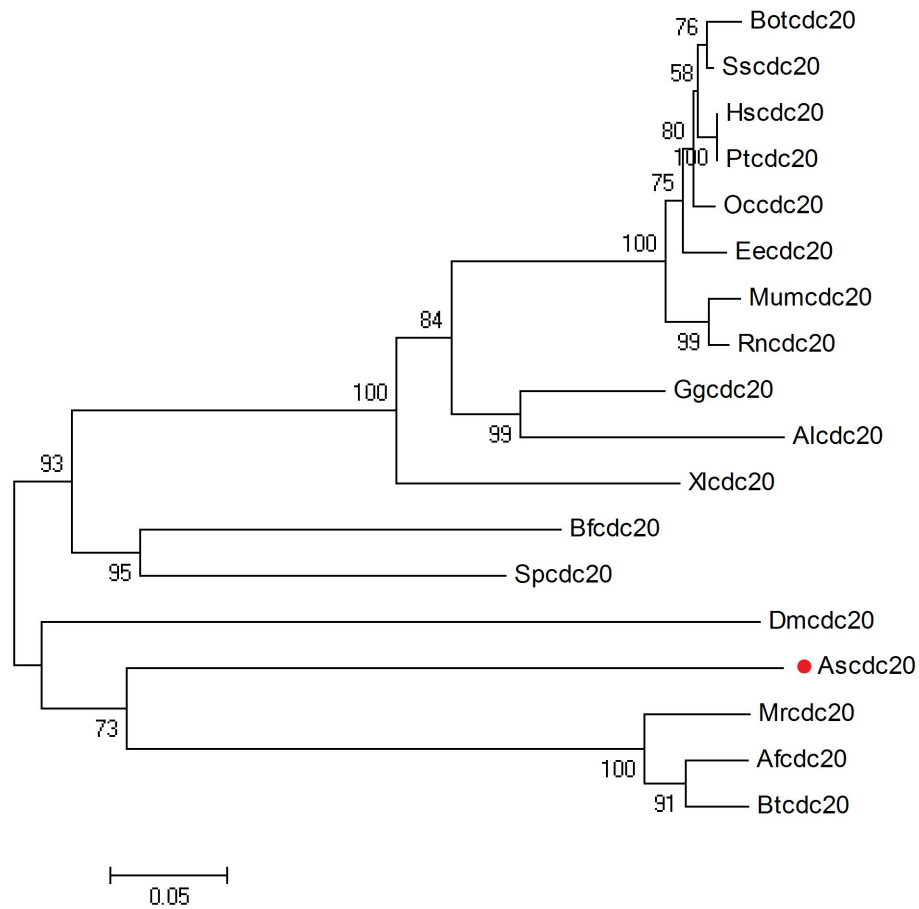


Fig. S2 Multiple sequence alignment of *As*-CDC20 protein. Alignment of known CDC20 sequences from 18 species. Identical amino acid residues are indicated by a black box. Less conserved residues are indicated by a gray box, whereas a pale gray box indicates somewhat similar residues. The sequence of the WD40 domain is shown in red. The sequences and their accession numbers are as follows: Alcdc20, *Alligator sinensis*, XP_006015910.1; Ggcdc20, *Gallus gallus*, NP_001006536.1; Afcdc20, *Apis florea*, XP_003697924.1; Btcdc20, *Bombus terrestris*, XP_003393065.1; Botcdc20, *Bos taurus*, NP_001075905.1; Bfcdc20, *Branchiostoma floridae*, AAO85336.1; Dmcdc20, *Drosophila melanogaster*, AAF53523.1; Eecdc20, *Erinaceus europaeus*, XP_007526147.1; Hscdc20, *Homo sapiens*, NP_001246.2; Mrcdc20, *Megachile*

rotundata, XP_003707890.1; Mumcdc20, *Mus musculus*, NP_075712.2; Occdc20, *Oryctolagus cuniculus*, XP_002715214.1; Ptcdc20, *Pan troglodytes*, JAA40139.1; Rncdc20, *Rattus norvegicus*, NP_741990.1; Spcdc20, *Strongylocentrotus purpuratus*, XP_781780.2; Sscdc20, *Sus scrofa*, NP_001116566.1; Xlcdc20, *Xenopus laevis*, NP_001081776.1; Asc dc20, *Artemia sinica*, KP162166.

Ggdc20 MAHFVFEALHGLKMLTPI.FNAFARWQRRAKESACF.....GFGFSAASMF...MKFANRSYSGK...TFSKTEK 70
 Alcd20 ...MVCASRVGHPTVAHR.HRCF.FLEFRRAALR.....ESRSPDFGEA...YGRFAAAG...GK 57
 Botcd20 NAQVFESLHSLQLLAPI.FNAFARWQRRAKESAG.....FAFSPMRAAN...SHSAGRTFGR.....TFGK 62
 Ssdc20 NAQVFESLHSLQLLAPI.FNAFARWQRRAKESAG.....FAFSPMRAAN...SHSAGRTFGR.....TFGK 62
 Hecdc20 NAQVFESLHSLQLLAPI.FNAFARWQRRAKESAG.....FAFSPMRAAN...SHSAGRTFGR.....TFGK 62
 Fcdc20 NAQVFESLHSLQLLAPI.FNAFARWQRRAKESAG.....FAFSPMRAAN...SHSAGRTFGR.....TFGK 62
 Ocdc20 NAQVFESLHSLQLLAPI.FNAFARWQRRAKESAG.....FAFSPMRAAN...SHSAGRTFGR.....TFGK 62
 Ecdc20 NAQVFESLHSLQLLAPI.FNAFARWQRRAKESAG.....FAFSPMRAAN...SHSAGRTFGR.....TFGK 62
 Mumcd20 NAQVFESLHSLQLLAPI.FNAFARWQRRAKESAG.....FAFSPMRAAN...SHSAGRTFGR.....TFGK 62
 Rnacd20 NAQVFESLHSLQLLAPI.FNAFARWQRRAKESAG.....FAFSPMRAAN...SHSAGRTFGR.....TFGK 62
 Xlcd20 NAQFAFETINSLKLTPI.TNAFLARWQRRAKESAG.....LNTSANTISLSEKASNR...SHSSSTFSK.....TFGK 71
 Bfcdc20 NSHLKFMKINNTTMEETI..KGHLPRWQRRAKESAG.....LNTSANTISLSEKASNR...SHSSSTFSK.....TFGK 96
 Spdc20 NSHLMKFMKINNTTMEETI..KGHLPRWQRRAKESAG.....LNTSANTISLSEKASNR...SHSSSTFSK.....TFGK 89
 Dmcd20 NSQTFMVDLGNLIMGETI..RGAHPRWQRRAKESAG.....LNTSANTISLSEKASNR...SHSSSTFSK.....TFGK 73
 Afcdc20 NSHLKFMKINNTTMEETI..KGHLPRWQRRAKESAG.....LNTSANTISLSEKASNR...SHSSSTFSK.....TFGK 75
 Btcd20 NSHLKFMKINNTTMEETI..KGHLPRWQRRAKESAG.....LNTSANTISLSEKASNR...SHSSSTFSK.....TFGK 77
 Mrcdc20 NSHLKFMKINNTTMEETI..KGHLPRWQRRAKESAG.....LNTSANTISLSEKASNR...SHSSSTFSK.....TFGK 77
 Ascdc20 MKKSCENTENCAARWRHGEAATALGNINNTSLN.....ISRNVAITAENKFR..KGDGRHTEK.....TFGK 71
 ConsensusK

Ggdc20 GSS..RVG...STTRKAGDRVIR..FTMQEMANLITKE..NDSE.....NSTI.....KREKAWALNNGFVEEAMVRLSGFPGN 146
 Alcd20 SAS..RTG...STFRAGDRVIR..DRAMQEVANLITKE..NDSE.....DTHI.....KREKAWALNNGFVEEAMVRLSGFPGN 133
 Botcd20 SSS..KIQ...TTFSPGDRVIR..DRASQMEVASLSEK..NQENS.....ETFI.....KREKAWALNNGFVEEAMVRLSGFPGN 139
 Ssdc20 SNS..KMG...TTFSPGDRVIR..DRASQMEVASLSEK..NQENS.....QTFI.....KREKAWALNNGFVEEAMVRLSGFPGN 139
 Hsdc20 SSS..RVG...TTFSPGDRVIR..DRASQMEVASLSEK..NQENS.....QTFI.....KREKAWALNNGFVEEAMVRLSGFPGN 139
 Fcdc20 SSS..RVG...TTFSPGDRVIR..DRASQMEVASLSEK..NQENS.....QTFI.....KREKAWALNNGFVEEAMVRLSGFPGN 139
 Ocdc20 SNS..KQG...TTFSPGDRVIR..DRASQMEVASLSEK..NQENS.....QTFI.....KREKAWALNNGFVEEAMVRLSGFPGN 139
 Ecdc20 GTS..RVG...TTFSPGDRVIR..DRASQMEVASLSEK..NQENS.....ETFI.....KREKAWALNNGFVEEAMVRLSGFPGN 139
 Mumcd20 SSS..RVG...TTFSPGDRVIR..DRASQMEVASLSEK..NQEDR.....GTFI.....KREKAWALNNGFVEEAMVRLSGFPGN 139
 Rnacd20 SNS..RVG...TTFSPGDRVIR..DRASQMEVASLSEK..NQEDG.....GTFI.....KREKAWALNNGFVEEAMVRLSGFPGN 139
 Xlcd20 SGF..KMG...GTFSPGDRVIR..DRASQMEVASLSEK..NEEVD.....TSET.....KREKAWALNNGFVEEAMVRLSGFPGN 147
 Bfcdc20 SKTFPGNAK...TF..KTFVDRGIR..DRASQMEVASLSEK..NEEVD.....MLSPS.....KREKAWALNNGFVEEAMVRLSGFPGN 175
 Spdc20 ...GSK...TFTRFPGDRVIR..DRASQMEVASLSEK..NEEVD.....MLSPS.....KREKAWALNNGFVEEAMVRLSGFPGN 161
 Dmcd20 KSNITFS...KTFGGDRVIR..DRASQMEVASLSEK..NEEVD.....MLSPS.....KREKAWALNNGFVEEAMVRLSGFPGN 66
 Afcdc20 TSKKSPSTISALTFSPGDRVIR..DRASQMEVASLSEK..NEEVD.....MLSPS.....KREKAWALNNGFVEEAMVRLSGFPGN 164
 Btcd20 TSKKSPSTISALTFSPGDRVIR..DRASQMEVASLSEK..NEEVD.....MLSPS.....KREKAWALNNGFVEEAMVRLSGFPGN 165
 Mrcdc20 GSKKSPSTISALTFSPGDRVIR..DRASQMEVASLSEK..NEEVD.....MLSPS.....KREKAWALNNGFVEEAMVRLSGFPGN 164
 Ascdc20 S.....PSRDGITDRVIR..DRASQMEVASLSEK..NEEVD.....MLSPS.....KREKAWALNNGFVEEAMVRLSGFPGN 144
 Consensus dr ip r q 1

Ggdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 246
 Alcd20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 233
 Botcd20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 239
 Ssdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 239
 Hecdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 239
 Fcdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 239
 Ocdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 239
 Ecdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 239
 Mumcd20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 239
 Rnacd20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 239
 Xlcd20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 247
 Bfcdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 275
 Spdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 261
 Dmcd20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 264
 Afcdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 262
 Btcd20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 264
 Mrcdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 263
 Ascdc20 FEVGNLRKLVDSQRTFSSRTKIG..IESLPRDLDAPIRDYINLINSQNALVAADNSYVHNSGGLLQLLQMECPGYSVAWVTEG 244
 Consensus pe n y tp r ip ldap dyyinl ws n aval y w g i y wi eq

Ggdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 346
 Alcd20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 333
 Botcd20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 339
 Ssdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 339
 Hecdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 339
 Fcdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 339
 Ocdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 339
 Ecdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 339
 Mumcd20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 339
 Rnacd20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 339
 Xlcd20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 347
 Bfcdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 375
 Spdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 361
 Dmcd20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 364
 Afcdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 362
 Btcd20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 364
 Mrcdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 363
 Ascdc20 LAAGSNAEVLWDVQQRFRNMTSSSRVGSLENNYVILSGRGGCHHBDVRAEHVATISEGVEVCHRAADHGLASGNDNLVWVBSA 344
 Consensus la g lwd r z m zv l wn sg r g i hbdvz t h qevc l w d laag ndn w

Ggdc20 RSDSG.FTHVQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 445
 Alcd20 RSDSG.FTHVQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 432
 Botcd20 FEGG..WVFLQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 437
 Ssdc20 FEGG..WVFLQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 437
 Hecdc20 FEGG..WVFLQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 437
 Fcdc20 FEGG..WVFLQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 437
 Ocdc20 FEGG..WVFLQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 437
 Ecdc20 FEGG..WVFLQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 437
 Mumcd20 FEGG..WVFLQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 437
 Rnacd20 FEGG..WVFLQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 437
 Xlcd20 RSDSG.FTHVQITFTHCAGAVAVWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 446
 Bfcdc20 FREG..NVVLSITFHQAVAVLWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 473
 Spdc20 FREG..NVVLSITFHQAVAVLWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 459
 Dmcd20 SGVGTATIDHKNENHQAVALWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 464
 Afcdc20 SVCSHTNITCIYSLNHQAVALWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 462
 Btcd20 SVCSHTNITCIYSLNHQAVALWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 464
 Mrcdc20 SVCSHTNITCIYSLNHQAVALWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 463
 Ascdc20 RSHN.VGSLQIRNHQAVALWCFWQSNLHGGGTDRHIFHWVCSGACLSAFAFSQVSIILSPHRELISHGAGNCLVWRYPMARUI 442
 Consensus hq av wcpwq la gggd di wn g d sqv s ke s ng a nql wky p m

Ggdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 506
 Alcd20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 493
 Botcd20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 498
 Ssdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 498
 Hecdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 498
 Fcdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 498
 Ocdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 498
 Ecdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 499
 Mumcd20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 498
 Rnacd20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 498
 Xlcd20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 506
 Bfcdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 535
 Spdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 523
 Dmcd20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 525
 Afcdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 522
 Btcd20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 524
 Mrcdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 523
 Ascdc20 IIRGHTARLNDMSPDGTVNSAETELRLMCPHDFIRKREKAKASAR..SS.IIHGG 502
 Consensus l qh r l hspdg s aetelrlw of dp

Fig. S3 The neighbor-joining phylogenetic analysis of *As*-CDC20 protein. The tree constructed based on the amino acid sequences of *As*-CDC20 (this study) and 17 other

species from GenBank using the sequence analysis tool MEGA 4.1. The sequences and their accession numbers refer to the legend of Supplementary Fig. S2. A red dot indicates *As*-CDC20.

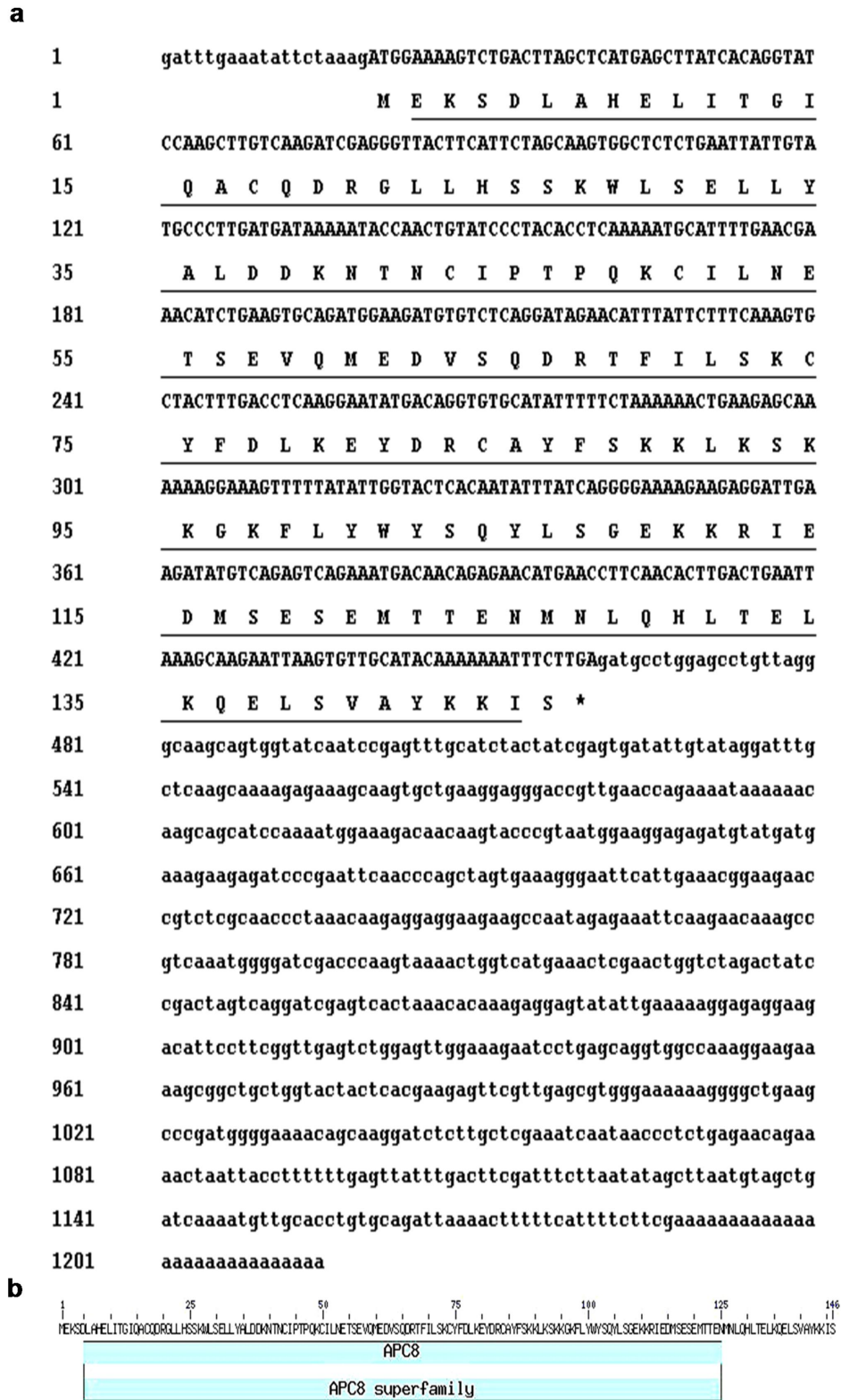


Fig. S4 The full-length cDNA and deduced amino acid sequences of *As-cdc23* and putative protein domains. (A) Sequence analysis of the cDNA and predicted peptide

sequences of *As-cdc23*. A black straight line indicates the ORF region. **(B)** Domain analysis of the putative *As-CDC23* protein. The mature protein includes an APC8 superfamily domain in the N-terminus.

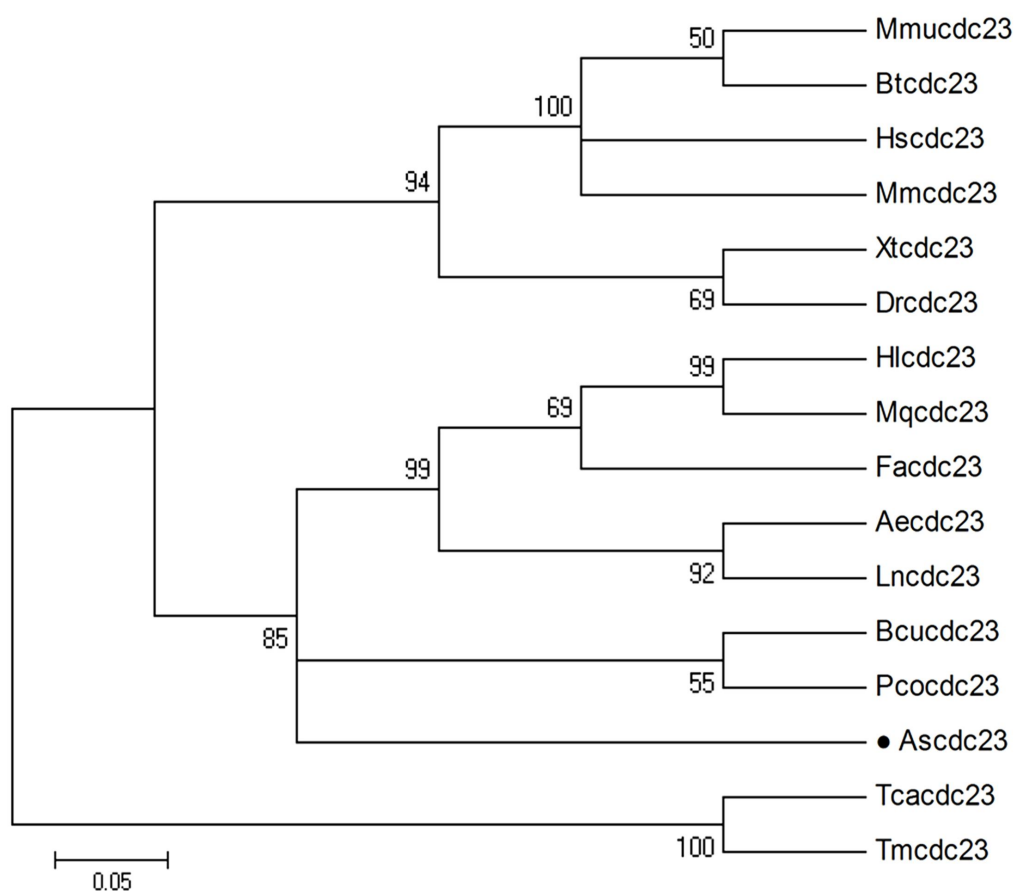


Fig. S5 Multiple sequence alignment of *As-CDC23* protein. Sequence alignment of known CDC23 sequences from 16 species. Identical amino acid residues are indicated by gray shading, and less conserved residues are indicated by pale gray shading. The sequence of the APC8 domain is shown in blue. The sequences and their accession numbers are as follows: Mmucdc23, *Mus musculus*, NP_848124.1; Btcdc23, *Bos taurus*, NP_001073735.1; Hscdc23, *Homo sapiens*, NP_004652.2; Mmcdc23, *Macaca mulatta*,

NP_001244486.1; Xtcdc23, *Xenopus tropicalis*, NP_001016759.1; Drcdc23, *Danio rerio*, NP_957227.1; Hlcdc23, *Habropoda laboriosa*, KOC68110.1; Mqcdc23, *Melipona quadrifasciata*, KOX74256.1; Facdc23, *Fopius arisanus*, JAG81156.1; Aecdc23, *Acromyrmex echinator*, EGI60542.1; Lncdc23, *Lasius niger*, KMQ88026.1; Bcucdc23, *Bactrocera cucurbitae*, JAC97421.1; Pcocdc23, *Pediculus corporis*, XP_002426290.1; Teacdc23, *Toxocara canis*, KHN78208.1; Tmcdc23, *Trichinella murrelli*, KRX39430.1; Ascsc23, *Artemia sinica*, KU986660.

Aecdc23VE.....KELLAHEITGQAGCQDGLHSSWLS...EELVNDKXNICTPTQKGLMETSVEQMEDVSQD.....RT...EELSKYFLENERC...YESSKLLKSKG	96
Aecdc23MDES.....KFMN...EVSDI...HAIREGSCQGLLHTTWLA...EHSYKRVNVDIDDLTIHAK...VPEVSEAEI.....VTLAKYFVLENYDRAAVYVINDVYSPRI	93
Bouc23MEEDLFN.....IPL...FVWRERRRGIVECQPRGLIGSARWLA...EMHGLSEVECDG...DVNRCQNFISINEGGQFLGIGSQAEYDN...MELAKSYFVLENYDRAAVYVINDVYSPRI	109
Drcdc23NAATR.....CSDFGDL...QIRKQISITACQRRERGLVHSRWLA...EAFSLDPLFNEIPPPP...LTERDAQDLDA...LCLAKSYFVLENYDRAAVYVINDVYSPRI	97
Facdc23MEVSM.....KFDI...EVMIDTLRAITEGSCQGLLHTTWLA...EHSYKRVNVDIDDLTIHAK...VPEVSEAEI.....VTLAKYFVLENYDRAAVYVINDVYSPRI	95
Hlcdc23MEEFV.....KFDI...EVMIDTLRAITEGSCQGLLHTTWLA...EHSYKRVNVDIDDLTIHAK...VPEVSEAEI.....VTLAKYFVLENYDRAAVYVINDVYSPRI	95
Lncdc23MDES.....KFMN...EVSDI...HAIREGSCQGLLHTTWLA...EHSYKRVNVDIDDLTIHAK...VPEVSEAEI.....VTLAKYFVLENYDRAAVYVINDVYSPRI	93
Mqcdc23MDES.....KFMN...EVSDI...HAIREGSCQGLLHTTWLA...EHSYKRVNVDIDDLTIHAK...VPEVSEAEI.....VTLAKYFVLENYDRAAVYVINDVYSPRI	93
Xtcdc23NARAT.....SGMPSDL...EIRKQISITACQRRERGLVHSRWLA...EAFSLDPLFNEIPPPP...LTERDAQDLDA...LCLAKSYFVLENYDRAAVYVINDVYSPRI	96
Pocdc23	MFDQNNKQDDEEN.....KIKIKKDESAI...KCLNRLIHTANWLS...EAFSLDPLFNEIPPPP...LTERDAQDLDA...LCLAKSYFVLENYDRAAVYVINDVYSPRI	99
Mmucdc23NAASTSVVAVVAVAVLSTNSDFSL...EIRKQISITACQRRERGLVHSRWLA...EAFSLDPLFNEIPPPP...LTERDAQDLDA...LCLAKSYFVLENYDRAAVYVINDVYSPRI	114
Toacdc23FLQRSLEKPNNSVWTLIGHEFMEQKNSAACLAY...KAVQSDFNDRVGYGL...CYLDILKMSYS...VYVQQAHCCKSDDSRMLVALG...VYTRLNRVSDAQKCLLKA...FVGVDE...TALMLL...GKLFK...GEGDQA...AVVE	139
Tmcdc23TAYANILMSVERSN.....ESLAAIAYESH...TNAFSDIEMVYGIYS...LYNDIQSK...ALHYRH...LANNSDSQA...WMLGHSI...QLMENS...V...AMFAYERA...E...RDPFF...V...ALY...IG...L...Y...Q...E...H...K...V...D...F	121
Bcucdc23NAASTSVVAVVAVAVLSTNSDFSL...EIRKQISITACQRRERGLVHSRWLA...EAFSLDPLFNEIPPPP...LTERDAQDLDA...LCLAKSYFVLENYDRAAVYVINDVYSPRI	114
Mmcdc23NAASTSVVAVVAVAVLSTNSDFSL...EIRKQISITACQRRERGLVHSRWLA...EAFSLDPLFNEIPPPP...LTERDAQDLDA...LCLAKSYFVLENYDRAAVYVINDVYSPRI	114
Hscdc23NAASTSVVAVVAVAVLSTNSDFSL...EIRKQISITACQRRERGLVHSRWLA...EAFSLDPLFNEIPPPP...LTERDAQDLDA...LCLAKSYFVLENYDRAAVYVINDVYSPRI	114
ConsensusNAASTSVVAVVAVAVLSTNSDFSL...EIRKQISITACQRRERGLVHSRWLA...EAFSLDPLFNEIPPPP...LTERDAQDLDA...LCLAKSYFVLENYDRAAVYVINDVYSPRI	114
Aecdc23	YELIYMSRY...LSGKRRK...I...E...D...M...S...E...M...T...E...M...N...L...Q...H...E...K...Q...E...S...V...A...Y...K...K...I...S	146
Aecdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	141
Bouc23	YELIYMSRY...LSGKRRK...I...D...S...T...D...R...S...N...L...N...D...Y...G...H...V...R...L...M...E...L...L...A...V...R...S...E...Y...S...H...G	159
Drcdc23	YELIYMSRY...LSGKRRK...I...D...E...T...V...D...S...L...G...F...L...E...G...Q...V...R...N...E...A...R...R...E...R...V...E...L...S...R...K...H...S...A...G...E	149
Facdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	143
Hlcdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	143
Lncdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	141
Mqcdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	143
Xtcdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	148
Pocdc23	YELIYMSRY...LSGKRRK...I...V...E...D...M...T...E...Q...T...C...L...L...D...S...Q...T...A...V...I...N...S...Q...N...E...L...A...K...E...R...T...O...N...S	150
Mmucdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	166
Toacdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	203
Tmcdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	185
Bcucdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	166
Mmcdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	166
Hscdc23	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	166
Consensus	YELIYMSRY...LSGKRRK...I...D...M...T...D...V...P...P...M...K...R...N...E...T...K...Y...C...A...D...R...S...D...H...L...A...S...K	166

Fig. S6 The neighbor-joining phylogenetic analysis of *As*-CDC23 protein. The tree constructed by the neighbor-joining method, based on the amino acid sequences of *As*-CDC23 and 15 other species from GenBank using the sequence analysis tool MEGA 4.1. The sequences and their accession numbers are shown in Supplementary Fig S5. A black dot (●) indicates *As*-CDC23.

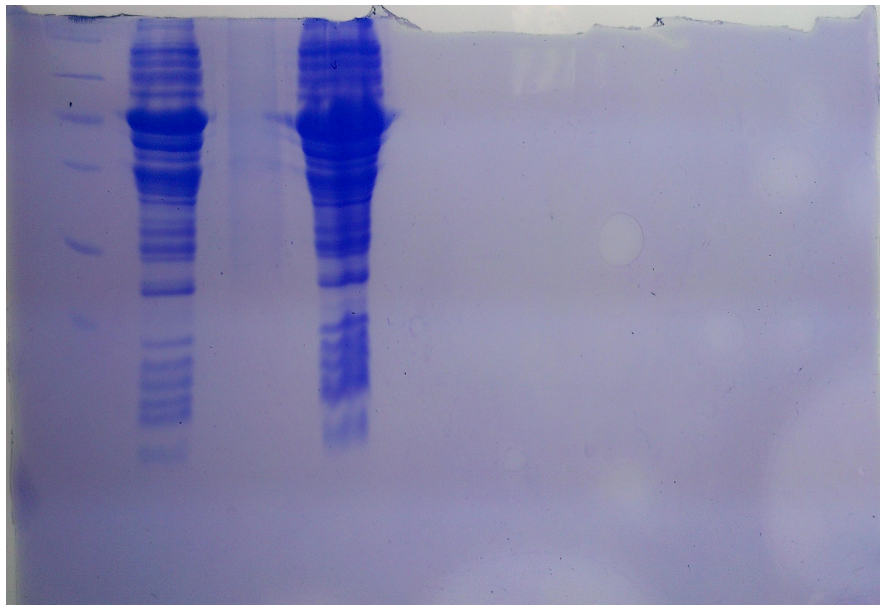
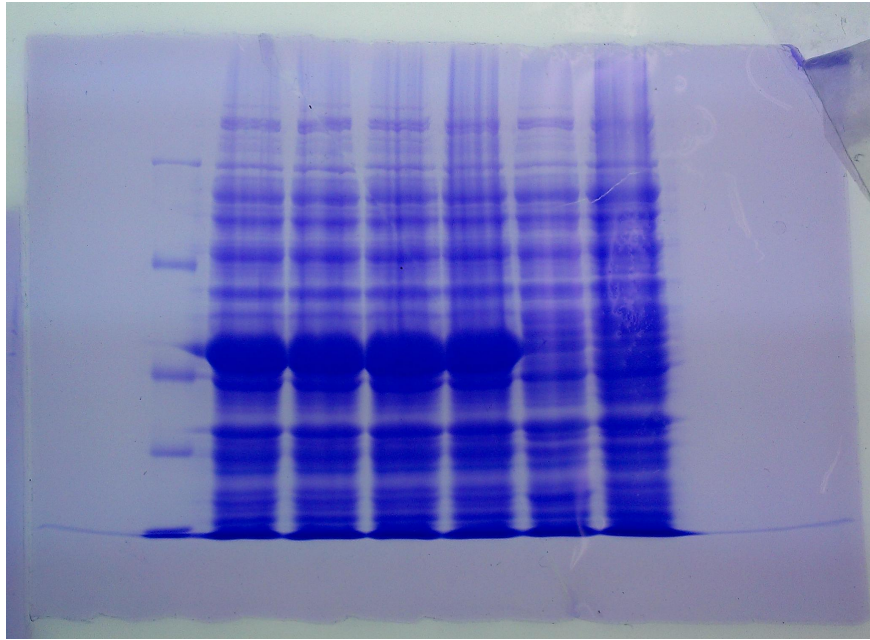
Equipment and settings

Fig.S1 and Fig.S4: We used DNAMAN to display the sequences, and using ORF Finder; the prosite tools of ExPASy and SMART predict the protein structural and functional domains.

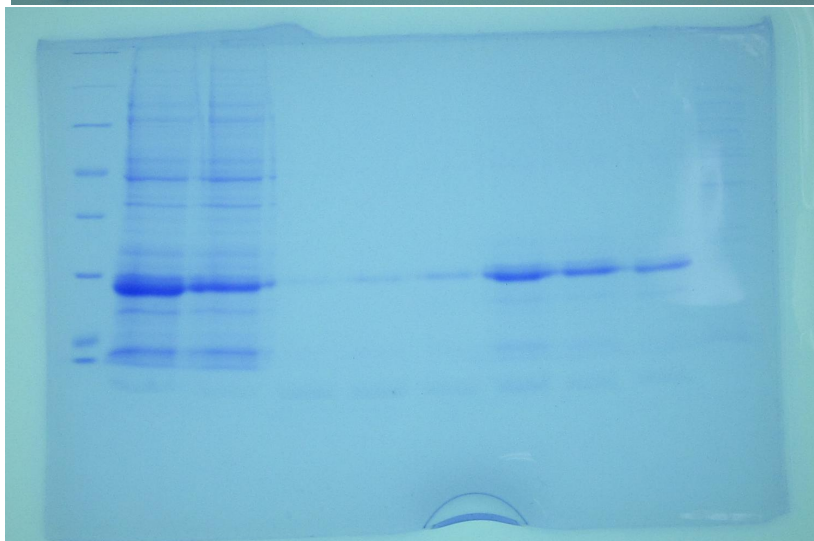
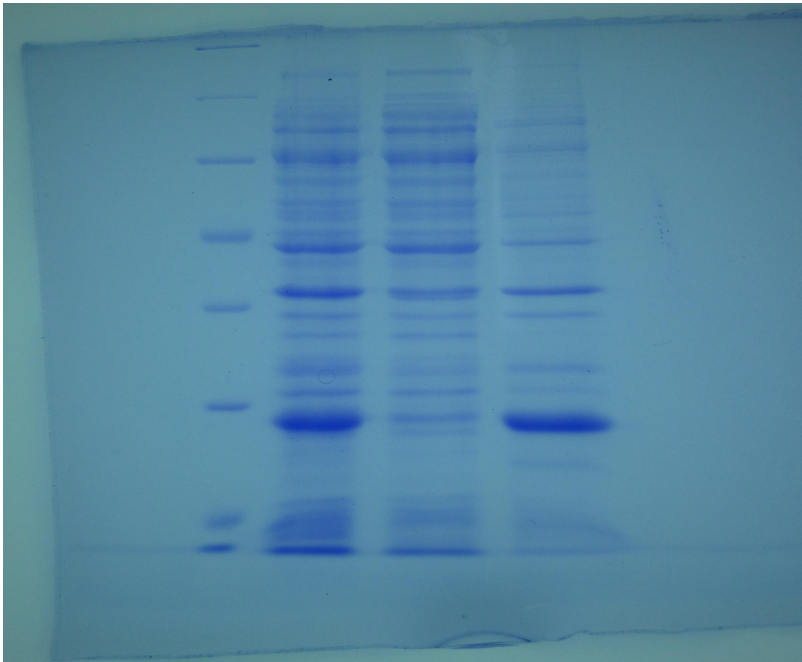
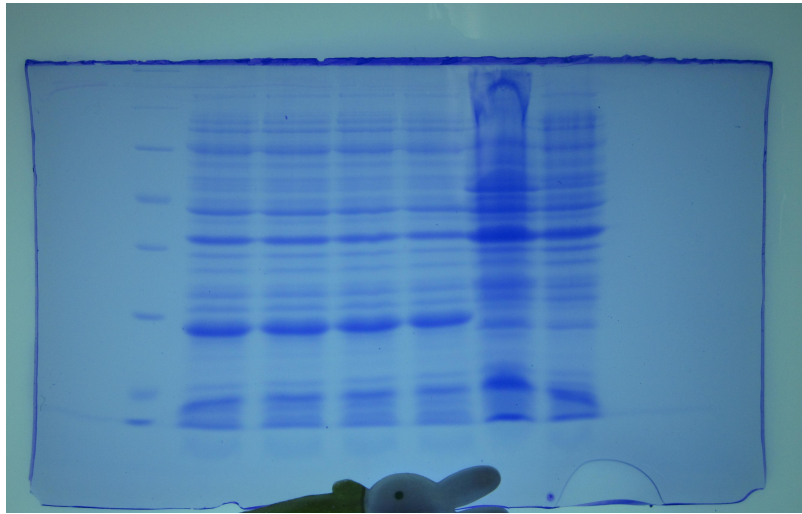
Fig.S2 and Fig.S5: MEGA4.1 software and ClustalX2.0 were used to construct a phylogenetic tree of the two proteins from different species using the neighbor-joining (NJ) method.

Fig.S3 and Fig.S6: Multiple sequence alignments were performed for the amino acid sequences of *As*-CDC20 and *As*-CDC23 with similar proteins from other species, using the ClustalX2.0 and DNAMAN.

Supplementary Figure 7: The full-length gels of *As*-CDC20 protein.

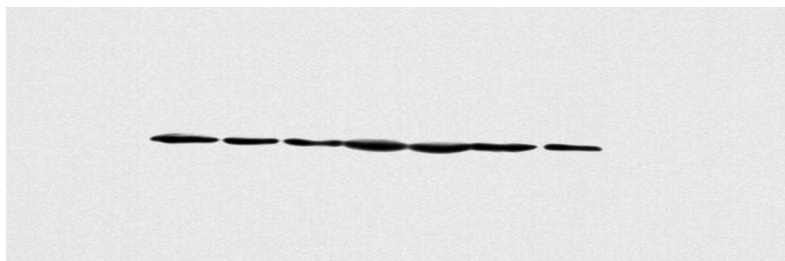


Supplementary Figure 8: The full-length gels of *As*-CDC23 protein.



Supplementary Figure 9: The full-length blots of western blotting analysis.

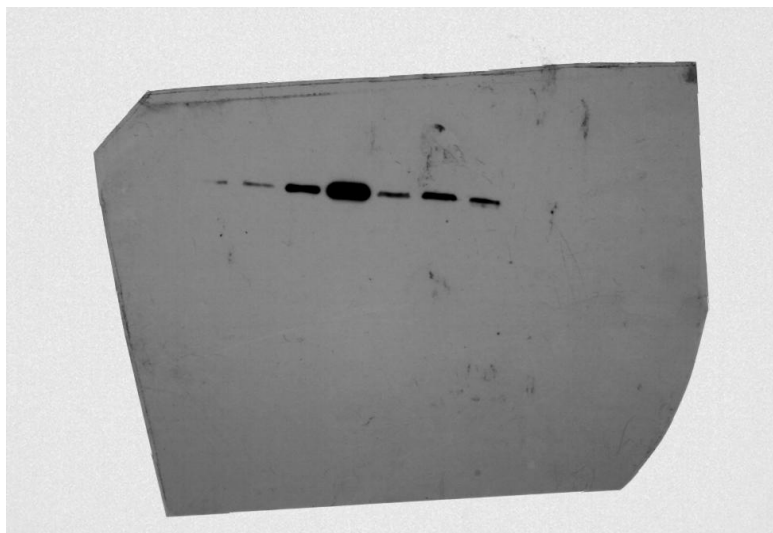
GAPDH



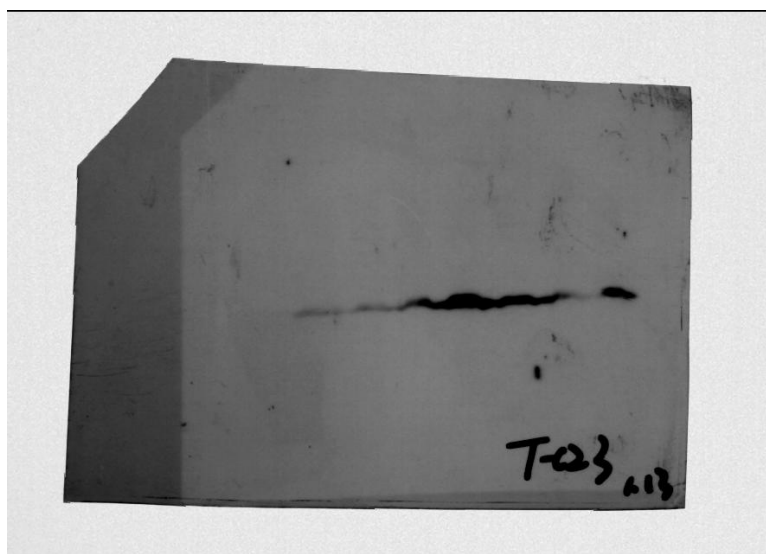
***As*-CDC20**



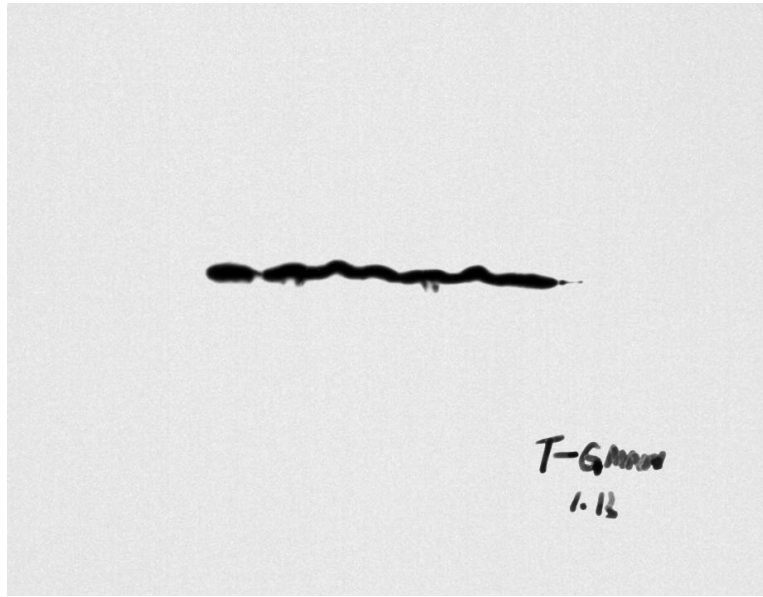
***As*-CDH1**



***As*-CDC23**



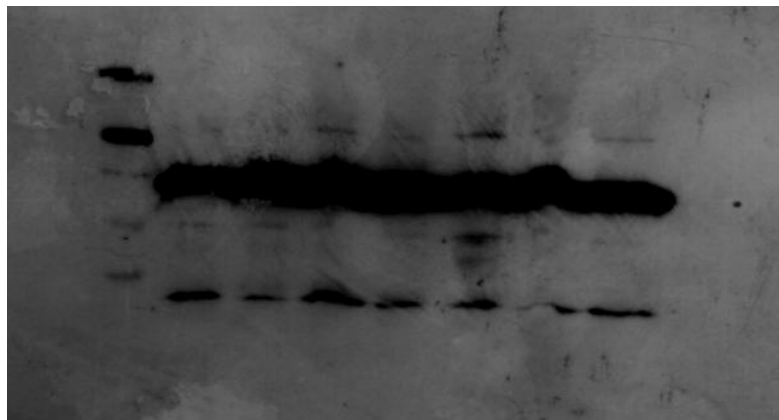
As-Geminin



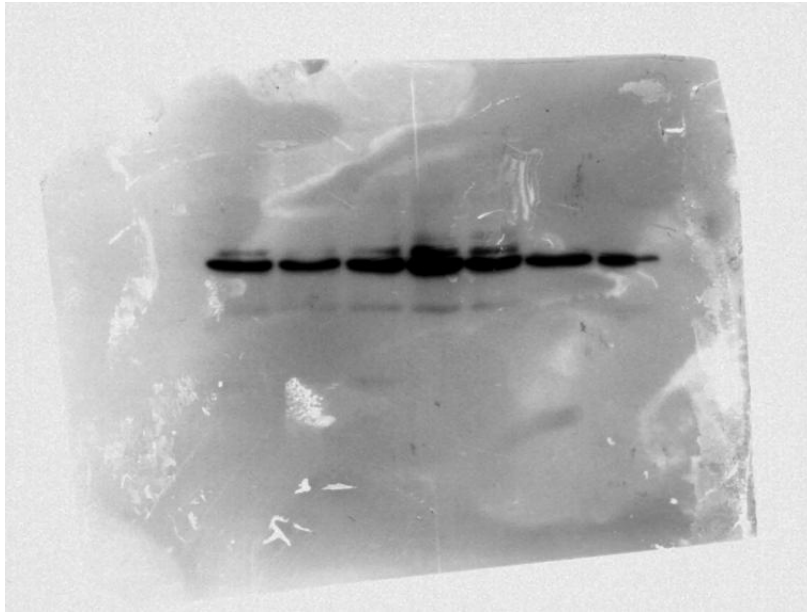
As-CDC14



As-securin



As-CDK1



As-Cyclin B

