

Supplementary Materials

*Article*

**Purification and characterization of double-stranded nucleic acid-dependent ATPase activities of tagged Dicer-related helicase 1 and its short isoform in *Caenorhabditis elegans***

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Ce_DRH-1a	1	MRRKQCSLSLYDKETLLCLEPTYRDEKQDGFSELLPLGRDELKIOSEN	---	QDFSKQLYHDLKNSLSNA	DDRERYKDIIMTYLQYLPKCTFH	95		
Cbr_DRH-1	1	WRKKQCAALVLYREIIRCLPTIEPEPDRGHEFEELLTRGRIEELIGESEN	---	EMDFKLLFVELTSSPLSLA	DDRERYKDIIMTYLQYLPKCTFH	96		
Cla_DRH-1	1	WRKKQCAALVLYREIIRCLPTIEPEPDRGHEFEELLTRGRIEELIGESEN	---	AVDFSKLLFVELSESPLTRD	DEERLYKNIIMTYLQYLPKCTFH	97		
Cre_DRH-1	1	WRKKQCAALVLYREIIRCLPTIEPEPDRGHEFEELLTRGRIEELIGESEN	---	AVDFSKLLFVELSESPLTRD	DEERLYKNIIMTYLQYLPKCTFH	96		
Cbg_DRH-1	1	WRKKQCAALVLYREIIRCLPTIEPEPDRGHEFEELLTRGRIEELIGESEN	---	TTSFSSQLFHELDESPTSKA	DDRERYKNIIMTYLQYLPKCTFH	96		
Cni_DRH-1	1	WRKKQCAALVLYREIIRCLPTIEPEPDRGHEFEELLTRGRIEELIGESEN	---	PPNKKGSSQLFHELDESPTSKA	DDRERYKNIIMTYLQYLPKCTFH	99		
Ce_DRH-1a	96	KLLNCSREVKLSDFHYLDFHFGFLRFIEPKVLAFLDSYFQYDVAVALR	---	KEIER	---	NEEDNQSDFTKLLILRIVPLLGEDAVYDMMYIETSEKS	190	
Cbr_DRH-1	97	RIVSCSDKSIIRSEFCIKLRNLDNFRFLNPALGLGSPYPHYEDLVRVFNWRNTE	---	---	---	NEEDNQENMKKAILKMWPLGFEFAYDMMYIETSEHT	192	
Cla_DRH-1	98	KLLKCSDKIMRRQDFSTILNLDGFLRYSDEPTEILRYLDCYPHYKQVVALR	---	REIED	---	NRDDETEDEDFIKLLILRIVPLLGESSAYDMMYIETSENT	193	
Cre_DRH-1	97	KLLKCSDRTMRSQDFSTILNLDGFLRYSDEPTEILRYLDCYPHYDVMVALR	---	REIED	---	NRDDETEDEDFIKLLILRIVPLLGESSAYDMMYIETSENT	192	
Cbg_DRH-1	97	KLLKCSDRTMRCQDFGLLNLDGFLINYPDPNEVLYLDSYFQYDILVREL	---	RETERIVPE	---	EQQNTFELKKSILRIVPLLGESSAYDMMYALYDKP	193	
Cni_DRH-1	100	KLLKCSDRTMRCQDFGLLNLDGFLINYPDPNEVLYLDSYFQYDILVREL	---	RETERIMEOE	---	EQQNTFELKKSILRIVPLLGESSAYDMMYALYNNP	196	
Ce_DRH-1a	191	SNLNDVEAKDFIAKVLRLKNDGLREFY	---	QITNARROLNKRLYICPV	HESEATEM	---	YLGTAALNTRMYRMINIRYDNTIYQENSTIPRLVIESVRR	284
Cbr_DRH-1	193	TNDRQEKAFSIEDLLHLEGEFRRYGIFHFSOSINADRLDRNGMYICPTHESEATEM	---	YIGSPFN	---	TRMYRMINIRYDNTIYQENSTIPRLVIESVRR	292	
Cla_DRH-1	194	SNLNEEAKFTIENVLDLKRGGFKAFY	---	EFISADRRQCNKRLYICPTHESEATEM	---	VRLPEFNDSRYRMINIRYDNTIYQENSTIPRLVIESVRR	285	
Cre_DRH-1	193	SNLNEEAKFTIENVLDLKRGGFKAFY	---	EFISADRRQCNKRLYICPTHESEATEM	---	VRLPEFNDSRYRMINIRYDNTIYQENSTIPRLVIESVRR	284	
Cbg_DRH-1	194	SNLNEEARAFIEKILRLRPGSDFAFY	---	REVSDDRFRNGNITICPIHEATEM	---	ITARTPEVNRHYRMINIRYDNTIYQENSTIPRLVIESVRR	285	
Cni_DRH-1	197	SNLNEEARAFIEKILRLRPGSDFAFY	---	REVSDDRFRNGNITICPIHEATEM	---	ITARTPAVNRHYRMINIRYDNTIYQENSTIPRLVIESVRR	288	
Ce_DRH-1a	285	THDRQLCLRRYQEEELCVLALRGNTIVTAPTSGKTVIAANIKE	---	HFESRSSEK	---	RFKALFMTNPSMILKQQSDSISSYLDMY	369	
Cbr_DRH-1	293	TDQORQLCLRRYQEEELCVLALRGNTIVTAPTSGKTVIAANIKE	---	HFETREDR	---	QRFKALFMTNPSMILKQQSDSISSYLDMY	392	
Cla_DRH-1	286	THDRQLCLRRYQEEELCVLALRGNTIVTAPTSGKTVIAANIKE	---	HFETREDR	---	QRFKALFMTNPSMILKQQSDSISSYLDMY	370	
Cre_DRH-1	285	THDRQLCLRRYQEEELCVLALRGNTIVTAPTSGKTVIAANIKE	---	HFETREDR	---	QRFKALFMTNPSMILKQQSDSISSYLDMY	369	
Cbg_DRH-1	286	THDRQLCLRRYQEEELCVLALRGNTIVTAPTSGKTVIAANIKE	---	HFETREDR	---	QRFKALFMTNPSMILKQQSDSISSYLDMY	370	
Cni_DRH-1	289	THDRQLCLRRYQEEELCVLALRGNTIVTAPTSGKTVIAANIKE	---	HFETREDR	---	QRFKALFMTNPSMILKQQSDSISSYLDMY	373	
Ce_DRH-1a	370	HTDILQSDNVPTRNMQSKDLIVATPQMIVNLCEHRDLKDEES	---	RLDQFLSTFTIIFDFECHNT	---	KNPSY	452	
Cbr_DRH-1	393	HQIVQGADNIPVRAIAIKSKDLIVATPQMIVNLCEHRDLKDEES	---	RLDQFLSTFTIIFDFECHNT	---	KNPSY	477	
Cla_DRH-1	371	HQIVQGADNIPVRSIAIQSKDLIVATPQMIVNLCEHRDLKMAE	---	GVEQFLSTFTIIFDFECHNT	---	LKSPYA	453	
Cre_DRH-1	370	HQIVQGADNIPVRSIAIQSKDLIVATPQMIVNLCEHRDLKMAE	---	GVEQFLSTFTIIFDFECHNT	---	LKSPYA	452	
Cbg_DRH-1	371	HQIVQGADNIPVRAIAIQSKDLIVATPQMIVNLCEHRDLKTE	---	NEIGIEQFLSTFTIIFDFECHNT	---	KNPTPYACEPTIPVIMNFSDIMREYHTLK	470	
Cni_DRH-1	374	HQIVQGADNIPVRSIAIQSKDLIVATPQMIVNLCEHRDLKTE	---	NEIGIEQFLSTFTIIFDFECHNT	---	KNPTPY	458	
Ce_DRH-1a	453	MGNMPEGHSIPQIIGLTASLTGDKNCLDQVRYNIAGLCASMDVKLSLVKDLNLEELRGYSPVDPKVL	---	CLERS	---	FDGPGMFTNRLTLMOVEGLTRT	552	
Cbr_DRH-1	478	MGNMPEHHLPOIIGLTASLTGDKGNLGVKDIASLCAIMDKVLSLVKDLNLEELRGYSPVDPKVL	---	CLERS	---	FDGPGMFTNRLTLMOVEGLTRT	577	
Cla_DRH-1	454	MGNMPEGHHLPQIIGLTASLTGDKGNLGVKEHIASLCAIMDKVLSLVKDLNLEELRGYSPVDPKVL	---	CLERS	---	FDGPGMFTNRLTLMOVEGLTRT	553	
Cre_DRH-1	453	MGNMPEGHHLPQIIGLTASLTGDKGNLGVKEHIASLCAIMDKVLSLVKDLNLEELRGYSPVDPKVL	---	CLERS	---	FDGPGMFTNRLTLMOVEGLTRT	552	
Cbg_DRH-1	471	MGNMPEGHHLPQIIGLTASLTGDKGNLGVKEHIASLCAIMDKVLSLVKDLNLEELRGYSPVDPKVL	---	CLERS	---	FDGPGMFTNRLTLMOVEGLTRT	548	
Cni_DRH-1	459	MGNMPEGHHLPQIIGLTASLTGDKGNLGVKEHIASLCAIMDKVLSLVKDLNLEELRGYSPVDPKVL	---	CLERS	---	FDGPGMFTNRLTLMOVEGLTRT	558	
Ce_DRH-1a	553	ALRNEHTIEQRRLDLETT	---	ERDFRP	---	DSSFLDPADKEHAGYVNWVCQMLVSGTSTR	678	
Cbr_DRH-1	578	ALVNEHTIODEGQIQPR	---	FDREYAP	---	TNTFLTAPDEKHEGSLNWCQMLVSGTSTR	645	
Cla_DRH-1	554	ALAQEHTIYDQDQGRPT	---	DDRF	---	FGPINEFQAPNDKEHSGYLNWCQMLVSGTSTR	650	
Cre_DRH-1	553	ALAQEHTIYDQDQGRPT	---	DDRF	---	FGPINEFQAPNDKEHSGYLNWCQMLVSGTSTR	649	
Cbg_DRH-1	549	SFYENITPNDVQNVQNSLFDPRPYPAENFQAPNDKEHSGYLNWCQMLVSGTSTR	---	AKFN	---	RDGTIINEALEVLKCEYWTLSYNNFNPEVALRYLKS	648	
Cni_DRH-1	559	ALDQENITPNDVQNAQISLFDPRPYPAENFQAPNDKEHSGYLNWCQMLVSGTSTR	---	AKFN	---	RDGTIINEALEVLKCEYWTLSYNNFNPEVALRYLKS	658	
Ce_DRH-1a	649	EMEVYTPNFVWRIWIWER	---	YHNLVITG	---	TAQNPMITVEKKIIVQNSDQNSRSIIFVRYRYEATILNLELNKRETLERLGIKSE	733	
Cbr_DRH-1	676	EIEHNRARNFPEMSRIWQD	---	YHNLVITG	---	TAQNPMITVEKKIIVQNSDQNSRSIIFVRYRYEATILNLELNKRETLERLGIKSE	760	
Cla_DRH-1	651	EINLRSSNFPEMARIWDR	---	YHNLVITG	---	TAQNPMITVEKKIIVQNSDQNSRSIIFVRYRYEATILNLELNKRETLERLGIKSE	735	
Cre_DRH-1	650	EINLRSSNFPEMARIWDR	---	YHNLVITG	---	TAQNPMITVEKKIIVQNSDQNSRSIIFVRYRYEATILNLELNKRETLERLGIKSE	734	
Cbg_DRH-1	649	ELEBSANFTHTMSRIWESKFQFLLLLCIEISG	---	YHNLVITG	---	TAQNPMITVEKKIIVQNSDQNSRSIIFVRYRYEATILNLELNKRETLERLGIKSE	748	
Cni_DRH-1	659	ELEBSANFTHTMSRIWESKFQFLLLLCIEISG	---	YHNLVITG	---	TAQNPMITVEKKIIVQNSDQNSRSIIFVRYRYEATILNLELNKRETLERLGIKSE	743	
Ce_DRH-1a	734	WISGLNKSTASSADISASKQKQMEIKMFADETRILVSTISVAEEGLDVAE	---	CSLVIKY	---	KNATNEIAHVQRRGRGRANSTCVLITNSIPLRDEGANRDK	833	
Cbr_DRH-1	761	WISGLNKSTSSGSETAASQKQKREKRFANGELVSTISVAEEGLDVAE	---	CSLVIKY	---	KNATNEIAHVQRRGRGRANSTCVLITNSIPLRDEGANRDK	860	
Cla_DRH-1	736	WISGLNKSTASSADISASKQKQMEIKRKFASGETRVLVATSVAAEGLDVAE	---	CSLVIKY	---	KNATNEIAHVQRRGRGRANSTCVLITNSIPLRDEGANRDK	835	
Cre_DRH-1	735	WISGLNKSTASSADISASKQKQMEIKRKFASGETRVLVATSVAAEGLDVAE	---	CSLVIKY	---	KNATNEIAHVQRRGRGRANSTCVLITNSIPLRDEGANRDK	834	
Cbg_DRH-1	749	WISGLNKSTSSADISASKQKQMEIKRKFASGETRVLVATSVAAEGLDVAE	---	CSLVIKY	---	KNATNEIAHVQRRGRGRANSTCVLITNSIPLRDEGANRDK	848	
Cni_DRH-1	744	WISGLNKSTSSADISASKQKQMEIKRKFASGETRVLVATSVAAEGLDVAE	---	CSLVIKY	---	KNATNEIAHVQRRGRGRANSTCVLITNSIPLRDEGANRDK	843	
Ce_DRH-1a	834	ESLWSETISLTONSPAERKCVDESNKIPRILREDDTKAOKTEQINRNLVYKILCKKCEVFLCTN	---	DIRARNTQYLCRPEFWSLVKRVKVELSPAD	---	933		
Cbr_DRH-1	861	ENMNDALLKIQSNPFAFRDAVIAEASNIWNRI	---	REDTERAQIAEQIS	---	RNTYRILVCKKCEVFLCTNDIRARNTQYLCRPEFWSLVKRVKVELSPAD	958	
Cla_DRH-1	836	ENMNDALLKIQSNPFAFRDAVIAEASNIWNRI	---	REDTERAQIAEQIS	---	RNTYRILVCKKCEVFLCTNDIRARNTQYLCRPEFWSLVKRVKVELSPAD	933	
Cre_DRH-1	835	ENMNDALLKIQSNPFAFRDAVIAEASNIWNRI	---	REDTERAQIAEQIS	---	RNTYRILVCKKCEVFLCTNDIRARNTQYLCRPEFWSLVKRVKVELSPAD	932	
Cbg_DRH-1	849	ENMNDALLKIQSNPFAFRDAVIAEASNIWNRI	---	REDTERAQIAEQIS	---	RNTYRILVCKKCEVFLCTNDIRARNTQYLCRPEFWSLVKRVKVELSPAD	948	
Cni_DRH-1	844	ENMNDALLKIQSNPFAFRDAVIAEASNIWNRI	---	REDTERAQIAEQIS	---	RNTYRILVCKKCEVFLCTNDIRARNTQYLCRPEFWSLVKRVKVELSPAD	943	
Ce_DRH-1a	934	LKIYNATG	---	INC	---	RENCGLKGLIEVNTVLPCLSAEITVL	1010	
Cbr_DRH-1	959	VDRSHSTGRLYFOLLRCGANGCATTGLRLDINSVELPCLGAEGMFFELIRLYYHVEYSYRHRORWRGK	---	SNQEMENG	---	ILHFFTPVLRQLDQIKM	1057	
Cla_DRH-1	934	ADRCSTGK	---	VKCL	---	GRNGCATTGLRLDINSVELPCLSAEITVL	1011	
Cre_DRH-1	933	ADRCSTGK	---	VKCL	---	GRNGCATTGLRLDINSVELPCLSAEITVL	1010	
Cbg_DRH-1	949	TNKFHSTG	---	EKCL	---	GTNGCATTGLRLDINSVELPCLSAEITVL	1032	
Cni_DRH-1	944	RNKFHSTG	---	EKCL	---	GTNGCATTGLRLDINSVELPCLSAEITVL	1020	
Ce_DRH-1a	1011	RDADQARITPMVFEHFRANGVVALIREA	---	1037	---	1037		
Cbr_DRH-1	1058	RDASDNRAPINFEVHNGVIQINRDA	---	1084	---	1084		
Cla_DRH-1	1012	RDADQARASLNFEHFRANGIENINREI	---	1038	---	1038		
Cre_DRH-1	1011	RDADQARASLNFEHFRANGIENINREI	---	1037	---	1037		
Cbg_DRH-1	1033	RDANQTRITPFLNFEINNGELQNIITREA	---	1059	---	1059		
Cni_DRH-1	1021	RDANQTRITVFNFEINNGELQNIITREI	---	1047	---	1047		

**Figure S2.** Multiple alignment of DRH-1 sequences of six *Caenorhabditis* species. The accession numbers of DRH-1 sequences are NP\_501018 (*C. elegans*, Ce), EGT53499 (*C. brenneri*, Cbr), OZG19204 (*C. latens*, Cla), XP\_003096885 (*C. remanei*, Cre), CAP25885 (*C. briggsae*, Cbg), and PIC33712 (*C. nigoni*, Cni), respectively. Identical residues are shown by red boxes.