

CHD4/706-1230 1790 VD-----PTVKYERQPEYLDA-TGGTLHPYQMEGLNWLRFSAWAQGTDTILADEMGLGKTIVQTAVFLYSLYKEGHSKGPFLVSAPLSTIIINW 790
CHD5/680-1204 1764 VD-----PTVKFDKQWPWYIDS-TGGTLHPYQLEGLNWLRFSAWAQGTDTILADEMGLGKTIVQTIVFLYSLYKEGHSKGPFLVSAPLSTIIINW 764
CHD3/716-1240 1716 ND-----PTVKYETQPRFITA-TGGTLHMYQLEGLNWLRFSAWAQGTDTILADEMGLGKTIVQTIVFLYSLYKEGHTKGPFLVSAPLSTIIINW 800
CHD1/460-980 1460 RP-----RFVALKKQPSYIGGHEGLELRDYLQNLGNLWLHAHWCNKGNSCILADEMGLGKTIVQTIVFLNYLFHEHQLYGPFLLVPLSTLTLSW 545
CHD2/464-983 1464 RP-----RFVALKKQPAYLGG-ENLELRDYLQLEGLNWLHAHWCNNSVILADEMGLGKTIVQTIVFLSYLFHQHQLYGPFLIVVPLSTLTLSW 548
Chd1/358-880 1358 RP-----RFEKLSVQPPFIKG---GELRDYFQLTGINWMAFLWSKGDNGILADEMGLGKTIVQTIVAFISWLIIFARRQNGPHIIVVPLSTMPAW 440
Isw1/181-686 181-----IEFQFSRESPAYVNG---QLRPPYQIQGVNWLVS LHKNKIAGILADEMGLGKTIVQTIVSFLGYLRYIEKIPGPFLVIAPKSTLNNW 260
Snf2/742-1268 1268 VDYYNVAHRIKEDIKQPSILVGV---GTLKDQYIKGLGMVSLFNNHLNGILADEMGLGKTIVQTIVSLTLYEMKNIRGPFLVIVPLSTLSNFW 831
CHD6/443-967 1443 SD-----SWQKLEKSREYKNS---NQLRREYQLEGMNWLFLNWNRNKNCILADEMGLGKTIVQTIVFLSEIF-LRGIHGPFLLIIAPLSTITNW 524
CHD7/950-1475 1475 AD-----DWKKSSESSREYKNN---NKLREYQLEGMNWLFLNWNMRNCILADEMGLGKTIVQTIVFLYEIY-LKGIHGPFLLIIAPLSTIPNW 1031
CHD9/842-1367 1367 SN-----IWKIDQSDRYKNG---NQLRREYQLEGLNWLFLNWNRRNCILADEMGLGKTIVQTIVFLYEIY-LTGIHGPFLLIIAPLSTIANW 923
CHD8/793-1318 1318 AS-----AWKKLELSHEYKNR---NQLRREYQLEGMNWLFLNWNRRNCILADEMGLGKTIVQTIVFLQEVY-NVGIHGPFLLIIAPLSTITNW 874

I (Walker A, P-loop)

Ia

CHD4/706-1230 1230 EREFEMWAPDMYVVTYVGDKDSRAIIRENEFSFEDNIRSGKKASRMKKEASVKFHVLLTSYELITIDMAILGSDIWACLIVDEAHLRKNQ 883
CHD5/680-1204 1204 EREFEMWAPDYFYVVTYGDKESRSVIRENEFSFEDNIRSGKKVFRMKKEVQIKFHVLLTSYELITIDQAILGSIWACLIVDEAHLRKNQ 857
CHD3/716-1240 1240 EREFQMWAPKFYVVTYTDKDSRAIIRENEFSFEDNIRSGKKAFKMKREAVQKFKHVLLTSYELITIDQAAIGSIRWACLIVDEAHLRKNQ 893
CHD1/460-980 1460 QREIQTWASQMNNAVYVLDGINSRNMIRTHEWTH-----HQTKRLLKFNILLTYEILLKDKAFLGGLNWAFIGVDEAHLRKNDD 624
CHD2/464-983 1464 QREFEIIWAPIENVVVYIGDLSRNTIREYEWI-----SQTKRLLKFNILLTYEILLKDKTVLGSINWAFIGVDEAHLRKNDD 627
Chd1/358-880 1358 LDTFEKWAIDLNCIYMGNQKSRDTRIIEYFYTNPR-----KGGKTMKFNVLITTYEILLKDRAGELSGIKQGFMAVDEAHLRKNDE 523
Isw1/181-686 1686 LEINRWITPDVNAIFLQGDKEERAEILQ-----KKLLGCDFDVVIASIEYIIREKSLPKKINWEYIIDEAHRIMKNEE 334
Snf2/742-1268 1268 SSEFAKWAPTLRTISFKGSPNERKAKQ-----AKIRAGEFDVVLITTFEYIYIKERALLSKVKKWHMIDEAHRIMKNEE 904
CHD6/443-967 1443 EREFRTWT-EMNAIVYHGSQISRQMQQYEMVYRDAQG-----NPLSGVFKFHVVIITTFEMILADCPPELKKIHWSCVIIDEAHLRKNRNC 608
CHD7/950-1475 1475 EREFRTWT-ELNVVVYHGSQASRRTIQLYEMYFKDPQG-----RVIKGSYKFHAIITTFEMILADCPPELRNIPWRCVIIDEAHLRKNRNC 1115
CHD9/842-1367 1367 EREFRTWT-ELNVVVYHGSLSISRQMQQYEMYFRDPSQG-----RIIRGAYRFQAIITTFEMILGDCPELNAIEWRCVIIDEAHLRKNK 1007
CHD8/793-1318 1318 EREFNTWT-EMNTIVYHGSLSISRQMQQYEMYCKDSRG-----RLIPGAYKFDALITTFEMILSDCPELREIEWRCVIIDEAHLRKNRNC 958

Loop (residues 832-837)

Ic

II (Walker B + IIa)

CHD4/706-1230 1230 KFFRVLN-GYSLQHKLLLTGTPLQNNLEELFHLNLFNLTPERFHNLEGFLE-----EFADIAKEQDIKKLHDMLGPHMLRRLK 960
CHD5/680-1204 1204 KFFRVLN-SYKIDYKLLLTGTPLQNNLEELFHLNLFNLTPERFNNLEGFLE-----EFADISKEQDIKKLHDLGLPHMLRRLK 934
CHD3/716-1240 1240 KFFRVLN-GYKIDHKLLLTGTPLQNNLEELFHLNLFNLTPERFNNLEGFLE-----EFADISKEQDIKKLHDLGLPHMLRRLK 970
CHD1/460-980 1460 LLYKTLI-DFKSNHRLIITGTPLQNSLKEWLSLHFIMPEKFSWEDFEE-----EHGK-GREYGYASLHKELEPFLLRRVKK 700
CHD2/464-983 1464 LLYKTLI-DFKSNHRLIITGTPLQNSLKEWLSLHFIMPEKFEWEDFEE-----DHGK-GRENGYQSLHKKLEPFLLRRVKK 703
Chd1/358-880 1358 SLYESLN-SFKVANRLIITGTPLQNNIKELAAVNFIMPGRFTIDQEDF-----ENQDEEQEYIHDHRRRIOPFILLRRLK 600
Isw1/181-686 1686 MLSQVLR-EFTSRNRLIITGTPLQNNLHELWALLNLFLLPDI FSDAQDFDDWFS-----ESTEEQDQKIVKQLHTVLPFLLRRLK 415
Snf2/742-1268 1268 KLSLTLNTHYHADRYLITGTPLQNNLELWALLNLFVLPKIFNSVQKDFEWFNTPFANTGGQDKILESEETLLVIRRLHKLRLPFLLRRLK 997
CHD6/443-967 1443 KLLLEGLK-LMALEHKVLLTGTPLQNSVEELFSLNLFLESPFSETAFL-----EFGDLKTEEQVKQLQSLKPFMMRLRLK 685
CHD7/950-1475 1475 KLLLEGLK-MMDLEHKVLLTGTPLQNTVEELFSLNLFLESPFSETFMQ-----EFGDLKTEEQVKQLQALKPFMMRLRLK 1192
CHD9/842-1367 1367 KLLLEGLK-LMNLLEHKVLLTGTPLQNTVEELFSLNLFLESPFSETFMQ-----EFGDLKTEEQVKQLQALKPFMMRLRLK 1084
CHD8/793-1318 1318 KLLDSLK-HMDLEHKVLLTGTPLQNTVEELFSLNLFLESPFSESEFLK-----DFGDLKTEEQVKQLQALKPFMMRLRLK 1035

III

Asn1010

CHD4/706-1230 1230 DVFKNMPSTKELIVRVELSPMKKKYKYILTRNFEALNARGGGNQV---SLLNVVMDLKCCCNHPYLFVPAAMEA-----PKMPNGMYD 1041
CHD5/680-1204 1204 DVFKNMPAKTELIVRVELSPMKKKYKYILTRNFEALNSKGGGNQV---SLLNIMMDLKCCCNHPYLFVPAAVEA-----PVLPNGSYD 1015
CHD3/716-1240 1240 DVFKNMPAKTELIVRVELSPMKKKYKYILTRNFEALNSKGGGNQV---SLLNIMMDLKCCCNHPYLFVPAAMES-----PKLPSGAYE 1051
CHD1/460-980 1460 DVEKSLPAKVQELIRVEMSAQKKYKYKWLTRNYKALSKGSGSTSGFLNIMMELKKCCCNHCYLIK---PPDEN-----NEFYNKQEA 779
CHD2/464-983 1464 DVEKSLPAKVQELIRVEMSAQKKYKYKWLTRNYKALSKGTRGSTSGFLNIMMELKKCCCNHCYLIK---PPEE-----NERENGQEI 782
Chd1/358-880 1358 DVEKSLPAKTEELIEVELTNIQKKYYRAILEKNFSLSKGAGHTNM---PNLNTMMELKKCCCNHPYLIK---GAEKILGEFRDYNPAASDFH 1173
Isw1/181-686 1686 DVETSLPLPKKELNLYVGMSSMKQKWKYKILEKDLDAVNGSNGSKESKTRLLNIMMQLKCCCNHPYLFDF---GAEP-----GPPYTTDE 495
Snf2/742-1268 1268 DVEKLEPDKVEKVVVKMSALQKQIMYQMLKYRRLIFGDQNNKMMVLRGNNQIMMLKKICCNHPVFVE---EVEDQI-----NPTRETDN 1080
CHD6/443-967 1443 DVEKNLAPKQETIIEVELTNIQKKYYRAILEKNFSLSKGAGHTNM---PNLNTMMELKKCCCNHPYLIK---GAEKILEDFRKTHTSPADPDF 774
CHD7/950-1475 1475 DVEKNLAPKEETIIEVELTNIQKKYYRAILEKNFSLSKGAGHTNM---PNLNTMMELKKCCCNHPYLIK---GAEKILEEFKETHNASPDF 1281
CHD9/842-1367 1367 DVEKNLAPKEETIIEVELTNIQKKYYRAILEKNFSLSKGAGHTNM---PNLNTMMELKKCCCNHPYLIK---GAEKILEEFKETHNASPDF 1281
CHD8/793-1318 1318 DVEKNLAPKQETIIEVELTNIQKKYYRAILEKNFSLSKGAGHTNM---PNLNTMMELKKCCCNHPYLIK---GAEKILETFEACHIIIPHDFH 1124

Arg1127

CHD4/706-1230 1230 GSALIRASGKLLLLQKMLKNLKEGGHRLVIFSQMTKMLDLLEDFLIEHEGYKYERIDGGITGNMRQEAIDRFNAPGAQQFCFLLSTRAGGLGIN 1134
CHD5/680-1204 1204 GSSLVKSSGKMLMLLQKMLKKLRDEGHRVLI F SQMTKMLDLLEDFLIEHEGYKYERIDGGITGGLRQEAIDRFNAPGAQQFCFLLSTRAGGLGIN 1108
CHD3/716-1240 1240 GGALLKSSGKMLMLLQKMLRKLKEGGHRLVIFSQMTKMLDLLEDFLIDYEGYKYERIDGGITGALRQEAIDRFNAPGAQQFCFLLSTRAGGLGIN 1144
CHD1/460-980 1460 LQHLIRSSGKLLLDKLLILRLRERGNRVLI F SQMVRLDILAEYLKYRQFPFQRLDGSIKGELRQALDHFAEGSEDFCFLLSTRAGGLGIN 872
CHD2/464-983 1464 LLSLLIRSSGKLLLDKLLTLRLRERGNRVLI F SQMVRLDILAEYLTKHYPFQRLDGSIKGEIRQALDHFNADGSEDFCFLLSTRAGGLGIN 875
Chd1/358-880 1358 LRGLIMSSGKMLLDQLLTLRLKKDGHRVLI F SQMVRLDILAGDYLISKHINFORLDGTVPSAQRISIDHENS PDSNDFVLLSTRAGGLGIN 779
Isw1/181-686 1686 --HLVYNAAKLQVLDKLLKLLKEGSRVLI F SQMSRLDILLEDYCYFRNVEYCRIDGSTAHEDRIQAIDDYNA PDSKKFVLLSTRAGGLGIN 586
Snf2/742-1268 1268 --DIWRVAGKFLDLRLIPKLKATGHRVLI F FQMTQIMDILEDYIRYINIKYLRDGHGTSKDSERSELLRFNA PDSSEYLCFLLSTRAGGLGIN 1171
CHD6/443-967 1443 LQAMQVAGKLLVLDKLLPKLKIAGGHKVLIFSQMVRLDILEDYLIQRRYTYERIDGRVVRGNLRQAAIDRFCKPDSDRFVLLSTRAGGLGIN 867
CHD7/950-1475 1475 LQAMQVAGKLLVLDKLLPKLKIAGGHKVLIFSQMVRLDILEDYLIQRRYTYERIDGRVVRGNLRQAAIDRFCKPDSDRFVLLSTRAGGLGIN 1374
CHD9/842-1367 1367 LQAMQVAGKLLVLDKLLPKMKAGGHKVLIFSQMVRLDILEDYLIQRRYTYERIDGRVVRGNLRQAAIDRFCKPDSDRFVLLSTRAGGLGIN 1266
CHD8/793-1318 1318 LQAMVRSAGKLLVLDKLLPKLKAGGHKVLIFSQMVRLDILEDYLIQRRYTYERIDGRVVRGNLRQAAIDRFCKPDSDRFVLLSTRAGGLGIN 1217

Trp1148

'Arg fingers' IV

IVa

V

CHD4/706-1230 1230 LATADTVIIFDSDWNPNDIQAFSRAHRIGQNKVMYIRYFVTRASVEERIITQVAKKMMMLTHLVVRPGLG-----SKTGSMSKQEL 1215
CHD5/680-1204 1204 LATADTVIIFDSDWNPNDIQAFSRAHRIGQNKVMYIRYFVTRASVEERIITQVAKKMMMLTHLVVRPGLG-----SKSGSMTKQEL 1189
CHD3/716-1240 1240 LATADTVIIFDSDWNPNDIQAFSRAHRIGQNKVMYIRYFVTRASVEERIITQVAKKMMMLTHLVVRPGLG-----SKAGSMSKQEL 1225
CHD1/460-980 1460 LASADTVIIFDSDWNPNDLQAQARAHRIGQKQVNIYRVLTKGVEEEDILERAKKMVLHDHLVIQRMDTGTGTVLHTGTSAPSSSTPFNKQEL 965
CHD2/464-983 1464 LASADTVIIFDSDWNPNDLQAQARAHRIGQKQVNIYRVLTKGVEEEDILERAKKMVLHDHLVIQRMDTGTGTVLHTGTSAPSSSTPFNKQEL 968
Chd1/358-880 1358 LMTADTVIIFDSDWNPNDLQAQARAHRIGQKQVNIYRVLTKGVEEEDILERAKKMVLHDHLVIQRMDTGTGTVLHTGTSAPSSSTPFNKQEL 968
Isw1/181-686 1686 LTSADVVVLYDSDWNPQADLQAMDRAHRIGQKQVVKVRLVTDNSEEKILERATQKRLRDQLVIQNRSTSLKK-----KENKADSKDAL 671
Snf2/742-1268 1268 LQTADTVIIFDSDWNPNDLQAQARAHRIGQKQVNIYRVLTKGVEEEDILERAKKMVLHDHLVIQNRSTSLKK-----NKSTSEEQAL 1253
CHD6/443-967 1443 LTAADTCIIFDSDWNPNDLQAQARAHRIGQKQVVKVYRLITRNSYEREMFDKASLKLGLDKALQDIN-RKGGT-----NGVQQLSKMEV 952
CHD7/950-1475 1475 LTAADTCIIFDSDWNPNDLQAQARAHRIGQKQVVKVYRLITRNSYEREMFDKASLKLGLDKALQDIN-RKGGT-----NGVQQLSKMEV 952
CHD9/842-1367 1367 LTAADTCIIFDSDWNPNDLQAQARAHRIGQKQVVKVYRLITRNSYEREMFDKASLKLGLDKALQDIN-RKGGT-----NGVQQLSKMEV 952
CHD8/793-1318 1318 LTAADTCIIFDSDWNPNDLQAQARAHRIGQKQVVKVYRLITRNSYEREMFDKASLKLGLDKALQDIN-RKGGT-----TGIIQQFSKKEL 1303

Va

VI

CHD4/706-1230 1230 DDILKFGTEELFKDE 1230
CHD5/680-1204 1204 DDILKFGTEELFKDD 1204
CHD3/716-1240 1240 DDILKFGTEELFKDE 1240
CHD1/460-980 966 SAILKFGAEELFKEP 980
CHD2/464-983 969 TAILKFGAEDLFKEL 983
Chd1/358-880 866 SAILKFGAGNMFAT 980
Isw1/181-686 672 LSMIQHGAADVFKSG 686
Snf2/742-1268 1254 LRSLLDAEEERRKKR 1268
CHD6/443-967 953 EDLLRKGAYGALMDE 967
CHD7/950-1475 1461 EDLLRKGAYGALMDE 1475
CHD9/842-1367 1353 EDLLRKGAYGALMEE 1367
CHD8/793-1318 1304 EDLLRKGAYGALMEE 1318