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Ce_CEH-86      -----MPTSSSTPPIVYETDLEPIYIYQDCYCHKELVFC-----KNMKFGGEIFKYNSSGTNSSIRRVQDCC-VY-----KDQEI DEEMSEKVKTFKGTIDF-----85
Ce_C35E7.2a    -----MNTSEYONPPSKYSTSTQTQPLPKV-----MNPNDQVSQKPKAEQS-----17
CBG08468      -----MNPNDQVSQKPKAEQS-----17
CRE_28417      -----MNPNDQVSQKPKAEQS-----17
CRE_28418      -----MNPNDQVSQKPKAEQS-----17
Ce_C35E7.5a    -----MNPNDQVSQKPKAEQS-----17
CBG08470      -----MNPNDQVSQKPKAEQS-----17
Ce_C35E7.3     -----MNPNDQVSQKPKAEQS-----17
CAEBREN_12536  -----MNPNDQVSQKPKAEQS-----17
CBG08472      -----MNPNDQVSQKPKAEQS-----17
CRE_28419      -----MNPNDQVSQKPKAEQS-----17
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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Ce_CEH-86      ROVVQNNCFOH--SPLYSKCEHYGHMIGF--FVNSLKDTVMAYDLADGLFQETKDCGC--CL-----HKDVLTLNHFIEKS--HRDEYQGTICNDIN--HTKEHGKMSIFFNSQGFGEYRNNRVQCKLKOLD212
Ce_C35E7.2a    ARIV-----PKYSVVCENSLEVLFGT--DNGVFGKRIY--KNNEFLKAPDCVQCISLR--ADDNLRTDSVBEVQGRATDKLHRGIDGQORLMCIGIS--NIGCKQSGVMDTFVNIHIGIKGYRKTPEGLLIK-DENKA150
CBG08468      EKPQKQPK-----EVYRSRVCEKTHTLIVFA--HGEDKGLGRYIP--TGSDPVKAPHCCECTCLN--DKFHNVSDFPHGALGNVGE--QHDSEFNRLIPISMK--HTTCRQRRARFVFAHENGSGRNVHSPEGYYPHSEPLKS147
CRE_28417      EVLKPIPTIRTVNLPKFSRVCKISLEVMVFA--NSKTKKLHRYVF--ENNDPKRADECCSDTCYVDPFIMISPSGRAFGDEKR--VDCYGEALINIGIT--HTKCRQTGSMDLFVHANGSIGIYV-KTKLGMQLFEMNDD180
CRE_28418      KELVDEENNNFFWIRPFHSDICLETNEIVIFCLIIYENKVLQAYSFDPKTQKFTKS--CCQCKKCNIT--DHTNSDGHSGQIGYRRS--HRDRNGLPLVCLAIT--N-KNSYEGLNIFCDEQGYIGRYEYNYDQKCDLLELLD200
Ce_C35E7.5a    ELEVDERRMNNLEIMCSEYCEQCEMTIFAK--DTDEEFPMTNPKTQSTYS-KCK--ECIENT--KFAIRRHYNQOISKLAGTFLPYQDRKGKELISLOUT--N-LNKEQGNMEYFVNPFGNISKYQNEKQYADHVRTLD148
CBG08470      NDVLMDMTANFLWLRFYSIDICSETNEVVVFLMKYPETKKLAAYSPNPETQYFLES--DCECKKCTET--NHTYNNMSSHSGQIGYQRT--HRDRNGLPLVCLAIT--N-KNSYEGLNIFCDEQGYIGRYEYNYDQKCDLLELLD267
Ce_C35E7.3     DELVDEDSGNFLWIQPKYSSICVKTNNAVIRTFPENFKLDAYTFDPETQKFEELS--NCKCDGCSNIT--DYSLSSEFFGAQIGYQRT--HRDQNGLPLVCLAIT--N-KNSYEGLNIFCDEQGYIGRYEYNYDQKCDLLELLD253
CAEBREN_12536  GRRVDEENGNCLWFQPVYSKNCENTOKITVFAGIYQOLDIYLPNFDLHQRNFVKS--ECRENCCKER--FLSALAPRTDFGNGQGCARS--HRDQAGRPLICLAIT--N-YNKEHGQMEIFMDQDGDIGRYEYNSRKCKFLQKLTLE195
CBG08472      DEMVDDSDSYLWIQPVFSKCEVTISKMAVFASVFPDVSRLVFNFDAGNKQFVRS--ICDADCCMEARNDD--GISPAADFSGSQGHYSRT--HRDQAGRPLICLAIT--N-YNKEHGQMEIFMDQDGDIGRYEYNSRKCKFLQKLTLE265
CRE_28419      DKPVDDDKYSYLWQPVFVSFKQNTGKIVTFASIKYPHQDRLLANFNDLEKLNVPFA--EQCEQCCOMTGFDRRISPRADFSGSQGHYSARS--HHDQAGRPLICLAIT--N-YNKEHGQMEIFMDQDGDIGRYEYNSRKCKFLQKLTLE266
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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CEH-86 homeodomain

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Ce_CEH-86      VKTTEYEVAADRDEDEKNWSSFSYDAIHLEQYRRTKYVSSDCKSEK-----HLEELIEKFRARRATS-----KREANSNEDLTSQYQOTKLTK-----304
Ce_C35E7.2a    IALPNFPIQNTQA-----IMEKDL-----LNTKICPHVSQKIYFKCTKTSKESVHVVLNKLTHFEILKCSVCTDKNLEIYDKDKTKLYAETVRCETTEKFAIRSAKNENFLSTYCPKTLT-----LKIQSPVAMEERKL282
CBG08468      IKCLPMESNIP-----IMDTEFT-----LSHAVFCAHKDKVYVC--TREGIMEQLIFNKTTHFERIKCKHCISD--KCG--DPAGRKYQAEIPTSXSDFVGYQANNQOWTKFNTNRR--FDVQSDMVLDCRS269
CRE_28417      VKMIPATNPPTGKE-----VMDSSFK-----LIDKQCMPLSVVTFMVRSIR--EGSTEQLVFNKTTDQFEMIRCEKCMQDRQKKG--KTVDGDLCEWVATNCEKYTVYRGEQGGKTKWVFTVTRQS--WEYCSKSVMDCRM309
CRE_28418      IRVSHSIQETEVKKR-----PDLLFDDCLR-----VLVYHSHCDQNLRTFFFGYHQMDDTMQKTFNEYSHQFEIFKCSDCKEHS--KVG--KPTAESVFPTPSLLTGKMGIRLMDKDRSEKTVQVNDYS--VKLEKAPIRNLHF333
Ce_C35E7.5a    VETLASGSINKMLG-----IVEEKS-----TAYAHARNRLIQVN-----TEQLWAGERSSS-----QLG-----SLPPVSKPEKKVLVQLQ-----215
CBG08470      VRVHSMNDME-----PR-----PELLDDDLR-----LFYIEHCREMKRDFFYGFHRKDKKPKQYTFNEVTLQDFLFCSDCHFDQK-KAQ--LYLEDKPALAS--TCKLITGRDITVSYGTNGVPKATIRGDSGSEIKMGKAPIRNLHY400
Ce_C35E7.3     VRVHKVLETSRSTSK-----PRLLIDDLF-----IYHKDNCKKLDMPYFYGHFEEGKTRKYLNNRTLOFERIKCPDCIDSRKIVR--SRALTDLAVTRCDLTSKIKKRRKPMGRVEKSETIRHGF--LPLGKAPIRFLKYL387
CAEBREN_12536  VRCNHHFYNKO--GDK-----KGLVDDDLR-----VMEHTKCPALKEDVYFCHLSDDGKTRKIYFDVTLQFVLVKCPCCSPTGG--YSA--NNTMVFTLGVVMPCATOGKVMILKDKDSMLKVMVTVYGTSS--VTMTSPIRMDSHL327
CBG08472      VRTMSHRYPSEEHET-----AEVLYDNELY-----LNTKNCSSLRDKIYFCWHINDGETQRYVFDSTNLQFALVKCPCCYS-----339
CRE_28419      VRTNHNNDCEEKIMK-----PEIWDYDGLR-----LYPKECPTLRTTFSSVHVKDGKTRKYVFNPICLPFNVVKCQCCVDAS-LII--DKEENTHVALYTCNTTSTKLMRSNKDGCINKEFLTAYAGEQ--RTLOKSPIRIDSHL400
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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Ce_CEH-86      -----DGTEGYFLRNKHEYFKKIVTVGF--SDGSVKPCVWIE-KISEYQIIDQETIRL-----KENSRVMAIDAEAREQVHRQR377
Ce_C35E7.2a    TN-----SESNH-----YNTKSCEENLEKCPANENHOTLVATEGATFGTIYMMNNENYK-----DPPKIAPT-----344
CBG08468      PLHEIQKR-----HRYIYNRKLGVLEELQSDGRFQIMYTEFNTTGEIVMKDTRDT-----ILPFSRSDLMGRTSFVEITAEQLHEKR350
CRE_28417      SMRDLLLR-----YHYERNRNASMNSRQVNVNRLAFIEDTTMGRIFFMMDSLNA-----VKPFELM--YV-----371
CRE_28418      DTEKLVEH--YASRKVVSQELPIQIESDETEKN-----ITTRHSSAVTVFLTGMDGKVKLHRIEN--NACDVKENKYLAVNEQGNVRKEDDKRIGRSISDSFVIPTETDISEPVVNTSTIVEGYTYCPHFQOILLYAFYDTH-----467
Ce_C35E7.5a    -----DGTECLVIRKDRVSSNGLYKIDTISF--KDGSVKPYRRND--TTRQYELKSEYEAAGLFSVETVEE-----SERVSLDWDLTPTKTVSCTHNDRTLFTAGNNFTQTDGFFYNSSTGHVHEHS332
CBG08470      EKDOLIAHFFSIRTYKNLLOFSET-----DGTEON-----NASSQEMDALIGDGOVKLRKVQ--PPESQSEEDG-----TDKDEMLOSLSEQDL-----481
Ce_C35E7.3     AVEDILKHYTPRRNCPDQYFQSFDSKNEEKFNFLNYSNLCEKKNNSAMIIIGMDGTIRNVLQD-----TKTKPQGHMKWKRYALDNDLLEPKSLQCIHSIVPIMFCNTSGMRGYVILDMRSGHIMEHP453
CAEBREN_12536  APNEIISR--RLAENIHITOMTQLFTAEGLEGVLRTRQRTSSDGCTOIGTMAL--MDGSVKPITIDC--NRYNFAIYHADCVNL-----TKTKPQGHMKWKRYALDNDLLEPKSLQCIHSIVPIMFCNTSGMRGYVILDMRSGHIMEHP467
CBG08472      -----YDD-----NPNMSFIATY-----353
CRE_28419      MPHEFGIR--RIEN--NVPHMIOILISKDEANVIRRRFRLGSDGKTATGTVVL--MDGSVKPFYDQ--KLMEYALFEPDCHDLAA--LKTNPNASPHVNCDRYALDNDLTPRSLAYCTHFNNHPTAYNH--TNSTHTYVYNGSTGHLHENS544
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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Ce_CEH-86      K-----LNSNEKRKEEEAEQEKLEKEMAELEIQ-----407
Ce_C35E7.2a    -----IPGTGTFLLISSLDFKSRKVIAS-----469
CBG08468      QKGAKIAALRCGEFQEQEAFDPASC-----DHCCNKRKGLKLEKQCVDRGAYGSGPYGSGHPS--DRPGDRARSMDAWPATIYIPFETLPQIPPPPRPINFPIASRQFP-----455
CRE_28417      -----PNSAEQTLLEIDPLTHRRKQEL-----394
CRE_28418      -----PIQLLLTSYLIQVKNCSCEKSRSGPHVLKVSNNMFPCEEGFAHRVYAKNRTIQKIEYDS--TKTWKDVHEYSIRLKGIEEENARKDIEINNDSPFKRCCCN-----571
Ce_C35E7.5a    GCSTC-----KSSVIDSSQVIASSIPFTRCAIILKTNKEGRFLKVLGNECSRKLYEAMALKVNVHVPVQSNHARKIOTVEDVLNVYKQVQEAANKKVDEVEKHERISSLEKECNMHLESLKMMNDSRKEFEVNAELEKKVFDL477
CBG08470      -----EESPLDRLENTYKQHSNRVSRGLAEM-----507
Ce_C35E7.3     -----SCA-----ANNTQSASIRVRERESRT-----453
CAEBREN_12536  GCQCELRDPTKIAPIAPSTVIFWISSPLSATDVVYATNSDGYLVKVSKNPVTEESGMIPLRLVTPD--EVNQFTGYQQQDQINQKLSAMENTLRQNLVQISLEVKISENTLE-----580
CBG08472      -----SCA-----ANNTQSASIRVRERESRT-----376
CRE_28419      GCETCQKE--RMYSIGPNOVIFGAASPOSKRAIILSTNSEGRLLKIGENSSKVVYCGMVPSPRVITEK-DV--QFLGEQNSKTEELIRSGRIPEKKLHEETVARLETRVMEAEKKIKDTETQNNMLSEEKTLLEKQIMELEQOIKOLNEGK690
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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Ce_CEH-86	EETTTKPEYRKLRMS-----RRKQNELLOKWLEKNTENTHA EKTNOEKK TENAVO-----EQLEOMMKMIOEERRAADSKNKLQEMVLEMKD KLDLAQETRIKELEEVIKS	683
Ce_C35E7.2a	TFFQQAPHPAPNAQT-----ANSMQSIABLLAQRGAPRPRRLTTEGGPK-----YNRVPPSPRIPSSTDKKEMLKSNDRFDKLRREEVSDVRTQLSGLEDTPFTFK	656
CBG08468	KLYVEALAKTKCVHNVT-----LAAGHOLA EKRELANEHLKSEKAKKO-----LQMHYEPSEIMHTDLLKYDARVKEVYFGESENDEKNKGSGPSTSSDPE	785
CRE_28417	QLAALVPPTNYQHYPF-----RTEDPREKLENELKNLEE-----MFRDNVTLCASSHGESSHAAVYAPRTKKTVMRMDMRSPMEKNQETOEPNLIVE	713
CRE_28418	KMLYEMDDVECTFKTKLYFLRFSLKNEFEFSQYOETEDFAGPTFPVEESERHKVFYSNANVLSTSIFMKS-----SESVFGEDDDDSHSSTNSIYSDVGGVGNNVITRSHSVYEGAFERSENNMNSVDH	956
Ce_C35E7.5a	EDNDAEYTSIALEPS-----DFEDNCDFESTATAVEPLDFEELSMDVTOQNSESFGVEHVED-----DTQSTTTTALEPSDIENDCNCDVESTTAVEPLDFEDDNSLDTQESDSLLEMEHVE	1069
CBG08470	DSGEVSDENSTDEHKA-----NRERNRDGPDDSETSFW-----KLYLOGGDDEPKOSNDSDALEE-----IWDILRKNGYSDEPAGSROSGLENCADGIEEDEVASDKGDVADEISDENAEDDVD	839
Ce_C35E7.3	-----EATQPSTSSVDF-----EKMAKERGOTLEEFS-----HLVSRYFYSEVVASNDVVSQPPPLRLKLEAPSDESEDSDLRVESIGIRDISDTESEETDDSSDISRIESIGIQDISDTETALEPELDELSELKIDEESSDDSD	492
CAEBREN 12536	DDEE	1441
CBG08472	-----THOSETATSNDIKCV-----E LIENDREDAESTA TALENDQEDVESTTALDHSDVEEDVEVDEDOMSTATATDGEODDVESTV TALDISDISDAEFVNEHDIDDASSTATAIEGDQDDVESTATALDVSDISDSA EFINGHD	393
CRE_284191510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650	1429

Ce_CEH-86	SGED	733
Ce_C35E7.2a	VQ	707
CBG08468	MNLDLD	832
CRE_28417	VNLDLD	770
CRE_28418	VDANVPPT	1017
Ce_C35E7.5a	MDIASDKESLVSESNYQDFMDPTIHSFTNSQIAEADONFPFGCILS	1182
CBG08470		892
Ce_C35E7.3		492
CAEBREN_12536	SGMDGDDEESFAEQEPFGSAHPDDVPAPQVDPINQQ	1590
CBG08472		393
CRE_28419	FSVNGDEPSESEMVKSNYEDCNDLGEAEPEGEERPVAQDANTCITS	1625
1810.....1820.....1830.....1840.....	

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