

→ DMAP1 binding domain

-----MPARSAAPPPALP-----PALR--RRLKDLERDEDSLSEKETT 36
KEKLNLLHEFLQTEIKNQLCDLETKLRKEELSEGYLAKVKSLLNKDLSLENGAHA--MPARTAPARVPTLAVPAISLPDDVR--RRLKDLERD--SLTEKECV 42
MILGYRLSPFGTSPPPRPDWDGRRRLRSSPLPIGFRAKSRGACAATAASAEASEMPARTAPARVPTLAVPAISLPDDVR--RRLKDLERD--SLTEKECV 97
-----MPARTAPARVAAALASRAFLSFPDDVR--RRLKDLERH--SLTEKECV 42
-----MPARTAPARVPALASRAFLSFPDDVR--RRLKDLERD--SLTEKECV 42
-----MPARTAPARVPALALPAFLSFPDDVRSRRLKDLERD--SLTEKECV 43
-----MPARTAPARVPALASPAGSLPDHVR--RRLKDLERD--GLTEKECV 42
-----MPARTAPARVPALASPAGSLPDHVR--RRLKDLERD--GLTEKECV 42
-----MPARTGPAVVAAPGSPALQLPPEEVR--RRLKDLKEDIEDILTEKECI 44
-----MPTKTS-----LSLPEDVK--ERLQVLDDEGGDSLSEECV 33

QEKLRTRCFRAVQRRISALDADVRCRELSSEFRYLAKVKALRRELAAENGDAKLFPSRASNGCAGNGEEWERGGRCEDGAMEVEVEAAASS----- 130
KEKLNLLHEFLQTEIKNQLCDLETKLRKEELSEGYLAKVKSLLNKDLSLENGAHA--YNEVNGRLENGNOARSEARVGMADANSPKPLSKPRTPRR 140
KEKLNLLHEFLQTEIKNQLCDLETKLRKEELSEGYLAKVKSLLNKDLSLENGAHA--YNEVNGRLENGNOARSEARVGMADANSPKPLSKPRTPRR 195
KEKLNLLHEFLQTEIKNQLCDLETKLRKEELSEGYLAKVKSLLNKDLSLENGAHA--FSREVNGYLENGSQTSGEDRVMMAEENKSPKPVSRIGLTPRR 140
KEKLNLLHEFLRTEIKNQLCDLETKLRKEELSEGYLAKVKSLLNKDLSLENGAHA--FSREANGCLENGSQTSGEDCRVMAEKGKPKPVSRLYTTPRR 140
KEKLNLLHEFLQTEIKNQLCDLETKLRKEELSEGYLAKVTSLLNKDLSLENGAFA--FSREVNGCLGNGSQARGEDRVRVMAEENKSPKLVSKLGTTPRR 141
KEKLNLLHEFLQTEIKSQCLETKLRKEELSEGYLAKVKTLLNKDLSLENGTSL--LTQKANGCPANGSRP---TWKAEMADSNRSRPSRPPKPRGPRR 137
REKLNLLHEFLQTEIKSQCLETKLRKEELSEGYLAKVKSLLNKDLSLENGTHT--LTQKANGCPANGSRP---TWKAEMADSNRSRPSRPPKPRGPRR 137
KKKLSLLHEFLQAVQHQFDLBTIKLRKEELSEGYLAKVKFLLNKDLSLENGDHT--LNQKANGCLENGTYTSD-----EDFEKSIIEEDSAVE----- 131
KEKLRLLQEFLLADTDQDKNLEDKLKSSELSTVYMSEVKAVKKALGVGKEGDGVEQNGHNSGFSENGSHKDNGEQEGAMDQD----- 119

-----SSSSSSSSSSSSSSSSSLLPAPRAKARRSRNNGEESKKSPPASS-----RVTRSSGQOPTIIS----- 189
SKSDGEAKRSRDPASASQVTGIRAEPSPPRITRKSTRQTTITSHFAKGPAPKRPQEESEKASDESKEEDKDQDEKRRRVTSRERVARPLP-AEEPE 239
SKSDGEAK-----PEPSPPRITRKSTRQTTITSHFAKGPAPKRPQEESEKASDESKEEDKDQDEKRRRVTSRERVARPLP-AEEPE 278
SKSDGEAKSA-----EVSSSPRITRQTTITSHFTRGPGKRPKEEDTAKAKPDSVVEEEDKQDEKRRRVTSRDSVAGLLP-TEEPE 224
SKSDGETKS-----EVSSSPRITRKTTRQTTITSHFPRGPAPKRPKEEPEKVSDDSDVEE-KDQDEKRRRVTSRERVAGLLP-AEEPE 222
SRGDGEPK-----AEVSSSPRITRQTTITSHFARGPAKRPKEEELERADNSVDEE-KDQDEKRRRVTSRERVARPLP-AEEDP 223
SKSDSETMI-----EASSSVATRRTTRQTTITSHFKGPAPKRPKEDESEKGNANESAAAE-RDQDKRRRVAGTESASRAGESVEKPE 219
SKSDSDTLF-----ETSPPSVATRRTTRQTTITAHFTKGPTRKRPKEESEGNSAESAAAE-RDQDKRRRVDTESGAAAA--VEKLE 217
-----MEEATGSSTLSKS-----RKPRRSKSDGETKKSASS-----RVTRSSGQOPTIIVS----- 178
-----EGDAIKSPS-----APKGRGRRSKADSEPKKSPPASS-----RVTRNTGKQOPTIIVS----- 165

-----VFSKGSTKRKS--EVNGAVKPEVSAEKDEE-----EELEKEEQD 229
RAKSGTRTEKEEERDEKEEKR--LRSQTKBPTPKOKLKEEPDREARAGVQADEDEDG-DEKDEKRRHSQPKDLAAKRRPEEKEPEKVNPOISDEKDEDEKE 337
RAKSGTRTEKEEERDEKEEKR--LRSQTKBPTPKOKLKEEPDREARAGVQADEDEDG-DEKDEKRRHSQPKDLAAKRRPEEKEPEKVNPOISDEKDEDEKE 376
RVRPPTHME-----DDKEEKR--LRSQTKELTPKOKIKEELDRSTRPGGAQPGTNE--EDKDEKRRHSQPKGLACKRRPEEKEPEKRIKQVSDKDEDEKE 317
RVRPPTHMEEG-RDDKEEKR--LRSQTKBPTPKOKLKEEPDREARAGVQADEDEDG-EDKDEKRRHSQPKDLAAKRRPEEKEPEKRVKPOVSDKDEDEKE 319
RVRPPTHTEEEEREDREKR--VRSQTKBPTPKOKLKEEPDREARAGVQADEDEDG-EERDEKRRHSQPKDLAAKRRPEEKEPEKRVKPOVSDKDEDEKE 321
RVRPQTQLQEEQEQEDDRR--PRQTRRLASRKRSDPDREARPGTHLDVDDDEKRRSSRPSQPRDLATKRRPKKE--EVVQITPEPPEGKDEDEDE 317
EVTAGTQLGPEEPECEQEDDNRSLRRTRELSLRKSKEDPDREARPEHLDEDEDGKDKRRSSRPSQPRDPAKRRPKKEAPEQVAPETPEDRDEDEDE 317
-----LFSKGSSKRKS--EGATGKIKQEMNVEK-----EDDLEKEEQG 214
-----MFSRVPRKRSDELNGEPANGDTEIKT-----EETITEVRE 201

EKRRIKETKEG-----SEIKDEITQVKTSTPA--KTIIPPKCVDRCQYLDLDPDLKFFGDPDDALEEPEMLTDERLSIFDANEDGFESYEDLPQHKLTVS 320
EKRRKTPKEP-----TEKMMARAKTVMNS--KTHPPKCIQCGQYLDLDPDLKYGO--HPPDAVDEPQMLTNEKLSIFDANESGFESYEAALPQHKLTC 425
EKRRKTPKEP-----TEKMMARAKTVMNS--KTHPPKCIQCGQYLDLDPDLKYGO--HPPDAVDEPQMLTNEKLSIFDANESGFESYEAALPQHKLTC 464
EKRRRTTYKEP-----TEKKLARTKTAIVSTKADLKCQCQGYLDLDAELKYEQ--HPPDAVEITQLLTNERLSIFDANESGFESYEAALPQHKLTC 406
EKRRRTTYREL-----TEKMMTRKIAIVS--KTNPPKCEQLQYLDLDPDLRYEQ--HPPDAVEITQLLTNERLSIFDANESGFESYEDLPQHKLTC 407
EKRRKTSKEP-----MEKMMARAKTVLSS--KIHPPRCVCGQYLDLDAELKYEQ--HPPDAVEITQLLTNERLSIFDANESGFESYEAALPQHKLTC 409
EKRRKTRKKEPELSIPVQSRVPRKAAQSKS--VIP--KINSPKCPCCGQYLDLDPDLKYQO--HPPDAVDEPQMLTNEALSVEFDSNSWTFVSSMHHKFTF 415
EKRRKTRKLESHTVPVQSRSERKAAQSKS--VIP--KINSPKCPCCGQYLDLDPDLKYQO--HPPDAVDEPQMLTNEALSVEFDSNSWTFVSSMHHKFTF 414
EKKMKFEVKEG-----SEIK--EVVQKAVPPV--KSTPPKCMDCRQYLDLDPDLKFFGDPDGDALDEPEMLTDERLSIFDANEDGFESYEDLPQHKLTVS 304
EKRLKTEDEKP-----EAENAANLKPVSTAKTPPKCPDCRQYLDLDPDLKFFGDPDGDALDEPEMLTDERLSIFDANSNEDGFESYEDLPQHKLTVS 290

Replication foci domain

FSVYDKRGHLCPFDTGLIEKNIELYFSGAVKPIYDDNPELDDGGVRAKILGPIINAWWITGFDGGEKALIGFTTAFADYILMPESEBEYAPIFALMQEKIYMS 420
FSVYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDNPSLEGGVNGKNLGPIINAWWITGFDGGEKALIGFSTSAFAEYILMDPSPPEYAPIFGLMQEKIYIS 525
FSVYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDNPSLEGGVNGKNLGPIINAWWITGFDGGEKALIGFSTSAFAEYILMDPSPPEYAPIFGLMQEKIYIS 564
FSVYCKRGHLCPIDTGLIEKDVLEFFSGSAKPIYEDDPSLEGGVNGKNLGPIINAWWITGFDGGEKALIGFSTSAFAEYILMDPSPPEYAPIFSVMQEKIYIS 506
FSVYCKRGHLCPIDTGLIEKDVLEFFSGSAKPIYEDDPSLEGGVNGKNLGPIINAWWITGFDGGEKALIGFSTSAFAEYILMDPSPPEYAPIFSVMQEKIYIS 507
FSVYCKRGHLCPIDTGLIEKNIELFFSGSAKPIYDDNPSLEGGVNGKNLGPIINAWWITGFDGGEKALIGFSTSAFAEYILMDPSPPEYAPIFSVMQEKIYIS 509
FSVYCSRGHLCPVDTGLIEKNVLYFSGCAKATHDENPSMEGGTNGKNLGPIINAWWLSGFDGGEKVLIGFSTAFAYEFLMEPSPPEYAPIFGLMQEKIYIS 515
FSVYCSRGHLCPVDTGLIEKNVLYFSGCAKATHDENPSMEGGTNGKNLGPIINAWWLSGFDGGEKVLIGFSTAFAYEFLMEPSPPEYAPIFGLMQEKIYIS 514
FSVYDKKGHLCPIFDTGLIEKNIELYFSGAVKPIYDDNPELDDGGVRAKILGPIINAWWITGFDGGEKALIGFTTAFADYILMPESEBEYAPIFALMQEKIYMS 404
FSVYDKRGHLCPFDGLIEKNIELYFSGAVKPIYDDNPELDDGGVRAKILGPIINAWWITGFDGGEKALIGFTTAFADYILMDPSEBEYAPIFALMQEKIYMS 390

KIVVEFLQNNRDSYEDLNKIETTVPVGLNFRNRTFEDSLLRHAQFVVEQVESYDEAGDSDEQPVLLITPCMRDLIKLAGVTLGKRRAV--RRAQIRHPTR 519
KIVVEFLQNSDSTYEDLNKIETTVPVPSGLNLRFTFEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQRRARQARRQTRHSTR 625
KIVVEFLQNSDSTYEDLNKIETTVPVPSGLNLRFTFEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQRRARQARRQTRHSTR 664
KIVVEFLQNNPDSTYEDLNKIETTVPVSVLNLNRFTEFEDSLLRHAQFVVEQVESYDQAGDSDEQPIFLTPCMRDLIKLAGVTLGKRRAE--RRRTIGHSTK 605
KIVVEFLQNSPDSTYEDLNKIETTVPVCMNLNLRFTFEDSLLRHAQFVVEQVESYDRAGDSDEQPIFLSPCMRDLIKLAGVTLGKRRAE--RRQTRQPAK 606

KIVVEFLQSNPDSTYEDL INKIETTVPSPV LNLNRFTEDSLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGKRRAE--RROTIGHSAK 608  
KIVVEFLQSNPDVAYEDL INKIETTVPSPVAINVNRFTEDSLRHAQFVVSQVESYDDAKDDDETPIFLSPCMRSLIHLAGVSLCQRRAAT--RRRLVINSAK 613  
KIVVEFLQSNPDVAYEDL INKIETTVPSPVSTINVRFTEDSLRHAQFVVSQVESYDEAKDDDETPIFLSPCMRALIHLAGVSLCQRRAAT--RR--VMGATK 611  
KIVVEFLQSNPDVSYEDL INKIETTVPSPVAGLNFNRFTEDSLRHAQFVVEQVESYDEAGDSDEQPIIITPCMRDLIKLAGVTLGKRRAA--RRQAIRHPFK 503  
KIVVEFLQSNQDATYEDL INKIETTVPSPVAGLNFNRFTEDTLRHAQFVVEQVESYDEAGDSDEQPIIITPCMRDLIKLAGVTLGKRRAA--RROAVRHPFK 489

→ CXXC zinc finger domain ←

ID--KDKGPTKATTTKLVYQLFDFTFFSEQIEKDEEREDDKENAMKRRRCGVCVEVCQQPECGKCKACKQNMVVKFGGSRGSKQACLRRCPCNLAVREADEEDDEV 618  
E--KDRGPTKATTTKLVYQIFDFTFFAEQIEKDDRED--KENAFKRRRCGVCVEVCQQPECGKCKACKDMVKFGGSRGSKQACQERRCPNMAKKEADDEEVD 722  
E--KDRGPTKATTTKLVYQIFDFTFFAEQIEKDDRED--KENAFKRRRCGVCVEVCQQPECGKCKACKDMVKFGGSRGSKQACQERRCPNMAKKEADDEEVD 761  
E--KDKGPTKATTTKLVYQIFDFTFFAEQIEKDDKED--KENAFKRRRCGVCVEVCQQPECGKCKACKDMVKFGGSRGSKQACQERRCPNMAKKEADDEEVD 702  
E--KDKGPTKATTTKLVYQIFDFTFFAEQIEKDDKED--KENAFKRRRCGVCVEICQQPECGKCKACKDMVKFGGSRGSKQACQKRRCPNMAKKEADDEEVD 703  
E--KDKGPTKATTTKLVYQIFDFTFFAEQIEKDDRED--KENAFKRRRCGVCVEVCQQPECGKCKACKDMVKFGGSRGSKQACQERRCPNMAKKEADDEEVD 705  
V--KRKGPATKATTTKLVYQIFDFTFFSEQIEKDDKED--KENTMRRRCGVCVEVCQQPECGKCKACKDMVKFGGTGRSKQACLKRRCPNLAVKEADEDEAD 710  
E--KDKAPTATKATTTKLVYQIFDFTFFSEQIEKYDKED--KENAMKRRRCGVCVEVCQQPECGKCKACKDMVKFGGTGRSKQACLKRRCPNLAVKEADDEEAD 708  
ID--KDKGPTKATTTKLVYQLFDFTFFSEQIEKNEEREDDKENAMKRRRCGVCVEVCQQPECGKCKACKQDMVKFGGSRGSKQACLRRCPCNLAVKEADEEDDEV 602  
IEKDNKGPATKATTTKLVYHLIFDFTFFSDQIQDNNKDG----GVKRRQRCGVCVEVCQAPDCGKCSACKDMIKFGGSRGSKQACQKRRCPNLAVKEADEEDENMD 585

→ BAH domain

DN--IPEMPSPKMLQCRKKKQNKSRISWVGEPDKSDGKKDFYQRCIDSETLEVGDCVSVSPDDPTKPLYLARVTAMWEDSSG--QMFHAHWFCEGSDTVL 716  
DN--IPEMPSPKMHQGKKKQNKNRISWVGEAVKTDGKKSYKKVCIDAEETLEVGDCVSVIPDDSSKPLYLARVTALWEDSSNGQMFHAHWFCACTDTVL 821  
DN--IPEMPSPKMHQGKKKQNKNRISWVGEAVKTDGKKSYKKVCIDAEETLEVGDCVSVIPDDSSKPLYLARVTALWEDSSNGQMFHAHWFCACTDTVL 860  
DN--IPEMPSPKMHQGKKKQNKDRISWVGEAVKTDGKKIYKKVCIDSETLEVGDCVSVIPDDSSKPLYLARVTALWEDSSNGQMFHAHWFCACTDTVL 801  
DN--IPEMPSPKMHQGKKKQNKNRISWVGDVAVKTDGKKSYKKVCIDSETLEVGDCVSVIPDDSSKPLYLARVTALWEDSSNGQMFHAHWFCACTDTVL 802  
DN--IPEMPSPKMHQGKKKQNKNRITWVGDVAVKTDGKKSFYKVCIDSETLEVGDCVSVIPDDSSKPLYLARVTALWEDSSNGQMFHAHWFCACTDTVL 804  
DD--PELSPKHLHQGKKKQNKDRISWVGEAVKTDGKKIENRTYQKVSIDETLEVGDCVSVIPDDSSKPLYLARVTALWEDKNGQMFHAHWFCACTDTVL 808  
DD--VSEMPSPKHLHQGKKKQNKDRISWVGEAVKTDGKKIENRTYQKVSIDEMLEVGDCVSVIPDDSSKPLYLARVTALWEDKNGQMFHAHWFCACTDTVL 807  
DN--IPEMPSPKMLQCRKKKQNKTRISWVGEAVKTDGKKSDGKKDYQKVCIDSETLEVGDCVSVSPDDPTKPLYLARVTALWEDSSG--QMFHAHWFCACTDTVL 700  
EEDVLPVKDTKMSCTKKKQTKNKISWVGEPLKTEGKKEYYMKVRVENEVLEVGDCVSVSPDDPSHPLYLARVTALWEDDGEK--MFHAHWFCACTDTVL 683

GATSDPLEFLVDECEDMQLSYIHGKVNVIYKPPSENWAMEGGLDMEIKMV--EDDGRTYFYQMYDQYARFETPPRAQPMEDNKYKFCSCARLAEVPH 815  
GATSDPLEFLVDECEDMQLSYIHSKVKVIYKAPSENWAMEGMDPESELE--GDDGKTYFYQLWYDQYARFESPPKTOPTEDNKFKFCVSCARLAEVRQ 920  
GATSDPLEFLVDECEDMQLSYIHSKVKVIYKAPSENWAMEGMDPESELE--GDDGKTYFYQLWYDQYARFESPPKTOPTEDNKFKFCVSCARLAEVRQ 959  
GATSDPLEFLVDECEDMQLSYIHSKVKVIYKAPSENWALEGMDPEALMS--KDDGKTYFYQLWYDQYARFESPPKTOPTEDNKFKFCVSCARLAEVRQ 900  
GATSDPLEFLVDECEDMQLSYIHSKVKVIYKAPSENWAMEGMDPEALMS--EDDGRTYFYQLWYDQYARFESPPKTOPTEDNKYKFCSCARLAEVRQ 901  
GATSDPLEFLVDECEDMQLSYIHSKVKVIYKAPSENWALEGMDPEALMS--EDDGRTYFYQLWYDQYARFESPPKTOPTEDNKYKFCSCARLAEVRQ 903  
GATSDPLEFLVDECEDMQLSYIHSKVKVIYKAPSENWALEGMDPEALMS--EDDGRTYFYQLWYDQYARFESPPKTOPTEDNKYKFCSCARLAEVRQ 908  
GATSDPLEFLVDECEDMQLSYIHSKVKVIYKAPSENWAMEGMDPEALMS--EDDGRTYFYQLWYDQYARFESPPKTOPTEDNKHKFCLSCIRLAEVRQ 907  
GATSDPLEFLVDECEDMQLSYIHGKVNVIYKAPSENWAMEGGLDMEIKMV--EDDGRTYFYQMYDQYARFESPPKTOPTEDNKYKFCSCARLAEVRQ 799  
GESDPLEFLVDECEDMQLSFIHIGKVNVIYKAPSENWAMEGMDPESELE--DDDGESFFYQLWYDQYARFETPPKVTPESEDCKYKFCSCARLAEVRQ 782

→ BAH domain

KEIPKVAEPLDE--GDCKMFYAMATKNGVQYRVGDSVYLLPEAFSFSMTPASPAAKR--PKKEAVDEDLYPEHYRKYSEYIKGSNLDAPEPYRIGRIKEIFC 912  
KEIPRVLEQLED--LDSRVLYSATKNGILYRVGDGVYLPPEAFTFNKLSPPVKR--PRKEPVDEDLYPEHYRKYSDYIKGSNLDAPEPYRIGRIKEIFC 1017  
KEIPRVLEQLED--LDSRVLYSATKNGILYRVGDGVYLPPEAFTFNKLSPPVKR--PRKEPVDEDLYPEHYRKYSDYIKGSNLDAPEPYRIGRIKEIFC 1056  
KEIPRVMEQLED--LDGRVLYSSATKNGIYRVGDGVYLPPEAFTFNKLSPPVKG--PRKEPVDEDLYPEHYRKYSDYIKGSNLDAPEPYRIGRIKEIFC 997  
KEIPRVVEQLQD--LEGRVLYSLATKNGVQYRVGDSVYLLPEAFTFNKLSPPVKR--PRKEPVDEDLYPEHYRKYSDYIKGSNLDAPEPYRIGRIKEIFC 998  
KEIPRVLEQLED--LDGRVLYSSATKNGIYRVGDGVYLPPEAFTFNKLSPPVKR--PRKEPVDEDLYPEHYRKYSDYIKGSNLDAPEPYRIGRIKEIFC 1000  
KEMPVLEQLEE--VDGRVYCSSITKNGVYVYRLGDSVYLLPEAFTFNKMASPKR--SKRDPVNEDLYPEHYRKYSDYIKGSNLDAPEPYRIGRIKEIFC 1005  
KEMPVLEQLEE--VDGRVYCSSITKNGVYVYRLGDSVYLLPEAFTFNKMASPKR--SKRDPVNEDLYPEHYRKYSDYIKGSNLDAPEPYRIGRIKEIFC 1004  
KEIPKVTPELEE--LDHKVLYGLAMKNGVQYRTGDGVFFLPEAFGNMCLCSPTKR--SKKESVDEDLYPEHYRKYSEYIKGSNLDAPEPYRIGRIKEIFC 896  
ESVTHAYEPLDEEESDSKVFYGLVNYKEBOYKVGDSVYLLPEAFTFNKMASPKR--SKRDPVNEDLYPEHYRKYSDYIKGSNLDAPEPYRIGRIKEIFC 882

HIRTNGKPNADIKLRILYKFRYPENTHKSMTATYHADINLLYSDEEATVDFCAVQGRCTVYVGEDLLETSIQDYSAGGLDRFYFLEAYNAKTSFEDPPN 1012  
PKKSNGRPNETDIKIRVNFYRYPENTHKSSTPASYHADINLLYSDEEAVVDFKAVQGRCTVEYGEDLPECVQVYSMGGPNRFYFLEAYNAKTSFEDPPN 1117  
PKKSNGRPNETDIKIRVNFYRYPENTHKSSTPASYHADINLLYSDEEAVVDFKAVQGRCTVEYGEDLPECVQVYSMGGPNRFYFLEAYNAKTSFEDPPN 1156  
TKKSNKPNETDIKIRLNFYRYPENTHKSSTPASYHADINLLYSDEEAVVDFKAVQGRCTVEYGEDLPECLODFSAAGPDRFYFLEAYNAKTSFEDPPN 1097  
SKKSNGRPNETDIKIRVNFYRYPENTHKSSTPASYHADINLLYSDEEAVVDFKAVQGRCTVEYGEDLPECLODFSAAGPDRFYFLEAYNAKTSFEDPPN 1098  
IKKSNGRPNETDIKIRLNFYRYPENTHKSSTPASYHADINLLYSDEEAVVDFKAVQGRCTVEYGEDLPECLODFSAAGPDRFYFLEAYNAKTSFEDPPN 1100  
GKKKGKVNADIKLRILYKFRYPENTHKSSTPASYHADINLLYSDEEAVVDFSDVQGRCTVEYGEDLLETSIQDYSQGGPDRFYFLEAYNAKTSFEDPPN 1105  
KEMKVGQIEE--VDGRVYCSSITKNGVYVYRLGDSVYLLPEAFTFNKMASPKR--SKRDPVNEDLYPEHYRKYSDYIKGSNLDAPEPYRIGRIKEIFC 1103  
SKRSNGKPNADIKLRVNFYRYPENTHKSMTKASHHADINLLYSDEEAVVDFKAVQGRCTVEYGEDLLETSIQDYSAGGSDRFYFLEAYNAKTSFEDPPN 996  
NKRNGKPDTEIKLRILYKFRYPENTHKGPKGAYHSDINQLYSDEEAVVDFKAVQGRCTVEYGEDLLETSIQDYSAGGSDRFYFLEAYNAKTSFEDPPN 982

→ DNA Methylase domain

HARSSGNKGGKGGKGGKGGKGSSTTCEQSEPEPETELKLPKRLTLDVFSGCCGLSEGPHQAGVSETLWAIEMWEPAAQAFRLNPNPGTTFVTEDCNVLLKL 1112  
HARSPGNKGGKGGKGGKGGKPKSOA---CEPSEPE--IEIKLPKRLTLDVFSGCCGLSEGPHQAGISDTLWAIEMWDPAAQAFRLNPNPGTTFVTEDCNILLKL 1213  
HARSPGNKGGKGGKGGKGGKPKSOA---CEPSEPE--IEIKLPKRLTLDVFSGCCGLSEGPHQAGISDTLWAIEMWDPAAQAFRLNPNPGTTFVTEDCNILLKL 1252  
HARSPGNKGGKGGKGGKGGKSRKTSOT---CEPSELE--TEIKLPKRLTLDVFSGCCGLSEGPHQAGISDTLWAIEMWDPAAHAFRLNPNPGTTFVTEDCNVLLKL 1193  
HARSTGNKGGKGGKGGKGNRTKSOT---CEPSELE--TEIKLPKRLTLDVFSGCCGLSEGPHQAGISDTLWAIEMWDPAAQAFRLNPNPGTTFVTKDCNVLLKL 1194  
HARSPGNKGGKGGKGGKGGKAKSOV---CEPSEPK--AEIKLPKRLTLDVFSGCCGLSEGPHQAGISDTLWAIEMWDPAAQAFRLNPNPGTTFVTEDCNVLLKL 1196  
HARSPGNKGGKGGKGGKGGKGPQV---SEPKEPE--AAIKLPKRLTLDVFSGCCGLTEGPHQAGISDTLWAIEMWEPAAQAFRLNPNPGTTFVTEDCNVLLKL 1201  
HARSPGNKGGKGGKGGKGGKGGKQV---SEPKEPE--AAIKLPKRLTLDVFSGCCGLSEGPHQAGISDTLWAIEMWDPAAQAFRLNPNPGTTFVTEDCNVLLKL 1199  
HARSPGNKGGKGGKGGKGGKSRGKS--IAVPESEHETIEVKKPKRLTLDVFSGCCGLSEGPHQAGISDTLWAIEMWEPAAQAFRLNPNPGTTFVTEDCNVLLKL 1095  
HARSAVNKGGKGGKGGKGGKGGKQ--RSRTTGSQAQEPVVPKRLTLDVFSGCCGLSEGPHQAGISETHWAIEMWDPAAQAFRLNPNPGTTFVTEDCNVLLKL 1080

VMSEKTKNSLGQKLPQKGDVEMLCGGPPCQGFSGMNRFNRSRTYSKFKNSLVVSVLSYCDYRPRFFLEENVRNFVSFKRSMVLKLTLRCLVRMGYQCTFG 1212  
VMAGETTNSRGQRLLPQKGDVEMLCGGPPCQGFSGMNRFNRSRTYSKFKNSLVVSVLSYCDYRPRFFLEENVRNFVSFKRSMVLKLTLRCLVRMGYQCTFG 1313  
VMAGETTNSRGQRLLPQKGDVEMLCGGPPCQGFSGMNRFNRSRTYSKFKNSLVVSVLSYCDYRPRFFLEENVRNFVSFKRSMVLKLTLRCLVRMGYQCTFG 1352  
VMAGEVTNSRGQKLLPQKGDVEMLCGGPPCQGFSGMNRFNRSRTYSKFKNSLVVSVLSYCDYRPRFFLEENVRNFVSFKRSMVLKLTLRCLVRMGYQCTFG 1293  
VMAGEVTNSRGQKLLPQKGDVEMLCGGPPCQGFSGMNRFNRSRTYSKFKNSLVVSVLSYCDYRPRFFLEENVRNFVSFKRSMVLKLTLRCLVRMGYQCTFG 1294  
VMAGEVTNSRGQKLLPQKGDVEMLCGGPPCQGFSGMNRFNRSRTYSKFKNSLVVSVLSYCDYRPRFFLEENVRNFVSFKRSMVLKLTLRCLVRMGYQCTFG 1296  
VMAGEVTNSRGQKLLPQKGDVEMLCGGPPCQGFSGMNRFNRSRTYSKFKNSLVVSVLSYCDYRPRFFLEENVRNFVSFKRSMVLKLTLRCLVRMGYQCTFG 1301  
VMAGEVTNSRGQKLLPQKGDVEMLCGGPPCQGFSGMNRFNRSRTYSKFKNSLVVSVLSYCDYRPRFFLEENVRNFVSFKRSMVLKLTLRCLVRMGYQCTFG 1299  
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VMSEKTKNSLGQKLPQKGDVEMLCGGPPCQGFSGMNRFNRSRTYSKFKNSLVVSVLSYCDYRPRFFLEENVRNFVSFKRSMVLKLTLRCLVRMGYQCTFG 1180

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ARMREESGAAVAPPAPKMEEMTAAAD 1537aa, chickenDNMT1  
AKARESASAKIK--EEEAAKD----- 1632aa, humanDNMT1  
-----RHGI----- 1502aa, chimpanzeeDNMT1  
AKARESASVKVK--EEETTKD----- 1610aa, pigDNMT1  
AKARESASAKIK--EEEAAKD----- 1611aa, cattleDNMT1  
AKAQESASVRVK--EEKTTAD----- 1615aa, horseDNMT1  
ASAQESASAVKGEETTTED----- 1621aa, ratDNMT1  
SSARESASAAVKAKEEAATKD----- 1619aa, mouseDNMT1  
AKLKEN---ATEKIQEHFESTD--- 1514aa, opossumDNMT1  
EKMRENATEPVKQEKMELESD----- 1499aa, zebrafishDNMT1