



# Nanos

Csa MALKTTKYNALNSPKNSYYFPAQLDSEIDNHLTGSYSSSSSTSGFISPKLSEAS--F---DNFSKFENKRGSDKNDLSSCFDSFNLDEKSTVLAKHWNIPENSFDWEQSINALFDP 110  
Ast MAESRCK-----TKQNDSAIMTSAL-----ESAIK 25  
Aae ME-----NVNSYYF---LAPAIAK-----SFNSSGDSFESDPSLI-----YSSSSSDVDNLTATFQELVIDVNGMV----- 59  
Aga MEVTKQN-----ASNNTTEEALWKLILAPYGWDEQMNEAARE 37  
Eba M-----YPDDM---YRNNVENN-----NENFGTFY-----GMN-CRQEYLEDTSTI----- 39  
Dme M-----F-----RSNLEGS-GAAAVGVANPPSLAQSGKIFQLQDNFSAFHARGGLNILGL----QDMYLDTSGANSSATLSPPITPVTPDPSTSA---- 81

Csa SSKQFIDFENFVQSSHGFSDCSL----FSYSPL-----SSLESISNDQNYND-----LYSDDLTYRMQQ-----ECIRREFEMNGKNVDEES--FY--- 186  
Ast FLQRYPELTQFVVN-----KSSYQFDI-----HSLIVDAKKMNL-AEA-----VEDIRKEFATNGSSSEFC----- 82  
Aae -----RE-----LFEKNTDLHRDT-----DSIRQDFIRNG----- 84  
Aga FLKNYSDFIPMLIG-----QSHYKIDL-----RSIIKEARANKWRNTT-----LDEICADFANGTTCEL-E----- 94  
Eba -----KEEDEISRSLKMFAMLTAYKTEPTQSNYQVDAIMQEFACNGFSCDEL---RY--- 88  
Dme QSTHF----PFLADSAATANSLLMQRQYHYHLLLQOQQQLAMAQHQLALAASAAAAASASHQQTDEIARSLKIFAQVTTGAAENAAGS--MQDVMQEFATNGYASDDLGRMSYGSA 189

Csa PLAMSTPFVERKSDQYKFNYSNREPTKVEFEPTKVFPSKQHQSALSIV---PFQPYNNITENIQFDSIYPPPYLVPSVFPDNKAGNKINGRKRGHQNSHGVLQNLQPMI--- 294  
Ast -----ENQGSLEHSVSIDPI-----KQNRQSEDALLTE-----DESTRVEEPANESAECNVLQ----- 130  
Aae -----IDSSMTECLSSRRLPPPGLGIVISKWPLSMCDNESS-----ATNPNGTKTDDSERKRNKGA----- 140  
Aga -----EEEVDLQA-----KHAPEMDGSELME-----AVDVAAELKNM-----VLQ----- 129  
Eba -----QRCNNNETTNNPDGVR-----NNVWKPKT----- 112  
Dme PPQVQMPQOQHQQOQLHLPLGRNPAQLQTNGGNLMP-----IPLATHW-LNNYRE-----HLNNVWRNMSYIPAAP-----NTMGLQAQTAATVSTNLGVGMGL 279

Csa -----NTNNSNYKFGAANEKMKDKNSIKKKKMD---DHCVFCKNNGADEILYKSHTVKDLKGRVLCPKLRAYQCPICGADGDQSHTVKYCPKKPIVMTMEDLKKLDAS 393  
Ast -----DITNHTKDRPR-RNLRK---NGSHPKHCVFCHNNGATREEYESHCKDEWGNVTCVPLQNFVCSRCNATGTNAHTAKYCPQKPIITPEDCVAIEKR 221  
Aae -----FQSSRRKR-----SKENE---DYCVFCYNNREEQETYLGHSCRDGEGFVVCVKLQRYVCPYQATGHLAHTKKYCPKKPIITPDDLRSMTVP 223  
Aga -----DISNQPKQSTTRPLRKRKNKSTCELDHCVFCFNKADREVEYESHCKDEAGNVTCPVLQTFVCMRCKATGTAHTAKYCPKPKPIITPEDCLAMELR 225  
Eba -----TNIAEYN---RKQPK--KRYNNNIKSGRYSVPRHCVFCENNNQPHAVVKSHNVRDIHDKVLCPKLRTYICPICATGDNAHTVKYCPQKPIITMEDAIKAE-S 208  
Dme GLPVQGEQLRGASNSSNNN---NNNNKVYKRYNSKAKEIS---RHCVFCENNNEPEAVINSHSVRDNFNRVLCPKLRTYVCPICGASGDSAHTIKYCPKKPIITMEDAIKAE-S 386

Csa -----KMINGYASTRF 404  
Ast WQQRRRRL--VQETIGANGQSKPIVETKATSRI RL 255  
Aae FDGP-----ANTSGRNRSVGRGKSLRF 246  
Aga RHKIHRKGVCTASEINLSAGSSSAIVHTK-KRLVRL 260  
Eba F-----RLSKSSYFKHHMKA 223  
Dme F-----RLAKSSYYKQOMKV 401

# Caudal

Aga MVS-YYNHFAMYPKNHSGNLPYSATTG--W-YPSNYQHQP--HPOFIGDGESSPOPA-----MYYPHPHVHFHPQ---SSPDWSSHENFSTPPQTSGLGSHG-----PSPGA-- 94  
Eli MVS-YYNSLSYSQKHSAPNLTYP SAPHQPW-FPTNYHPAAAANNQFLSSMDPQHH-----QPMYY-NPHMFH-QTAAAADLYAARENFSNLSAGPLTAHSQMFSTLPHNQQQQ 104  
Llu MVSSFYNTQPY SQKHHGINLPYS--TAQPW-FTSSYHPHP--NHQFLGD-DSPH---HHPQ--HMYYPSPHMFHQT---SAGDWHVPENYPNTAQAHM-LQ----- 88  
Mab MVS GYYNPLQY-QKHTSA---YP--PGN-W-FPPANYATPH-POQFLNDVHEQH---QAA--LTYYNQT-MF-----PPGDWHAPDTMQSPPTSHH-GSS-----HHM 82  
Eba MVS-YYNSLSYSQKHSAAANLPYP--AGQPWAWQSNYHP-PP-NHQFLGDVDSPHSVGHHP--Q-YYN--HMFGNH---PSADWHTTENFQNTAQSHL-LQH-----QHQ 91  
Dme MVSHYYNTLPY TQKHSAAANLAYASAAGQPWNWTPNYHHTPP--NHQFLGDVDS SHAAHAAAAHQMYYN SHHMFHSAAAAASAGEWHSP---ASSTADNF-VQNV-----PTSAHQ 105

Aga -----GGTGGGGGGGGGGIGSGALHLGQNP NLHHHHHHHHGNNGGGNGGGGGSGNAHD-HLADGL-HSIPSPPI TVSGSDMSSPG-APTGSSSPQI----- 185  
Eli QQQQQQQQQQQQQNGS-----HQNHQQCNHQNVGHGSGTGNN SPLDETSSADLLTDGI PSPAIT----NLNNGGGGAGGGGGGGSEISSP----- 187  
Llu -----QHNNVAG-----GNTQLNDSTSSSTGENNNNNNNN-----NNNTAHIAEGL---PSPPI TVSGSEISSPG-APASSSPHPLTNIN----- 159  
Mab LYQ-----SPATN-----SQTQLNETTSSNGDSNHNS-----HPTPNLTEAL---PSPPI TVSGSELSSPGAPVAASSPNGNIGSH----- 152  
Eba QHQQQQHQQHHQHQS-----GATQLNDSASSVGE-----PQIADGL---PSPPI TVSGSEISSPG-APASSSPHANMSTN----- 159  
Dme MQQH HHHHAHASSSSASSGSSSSGGAPGAPQLNETNSSIGVGGAGGGGGVGGATDGGPGSAPPNHQQHIAEGL---PSPPI TVSGSEISSPG-APTSASSPHHHLAHL SAVAN 215

Aga -----TPRPTPVKSPY--EWMKKQSYQS QPNPGKTRTKDKYRVVYTDQRLELEKEFYTRYITIRRKAELAQNQLSERQVKIWFQNRRAKD 270  
Eli -----GIPNASSSPQISVNGQQQQQRPTPCNSPYRYDWMKKPAYASQPNPGKTRTKDKYRVVYTDQRLELEKEYHTSRYITIRRKT ELAQGLQLSERQVKIWFQNRRAKE 292  
Llu -GNHTNSNNNNNSNN-----NNNNHRTSPVKSPY-YEWMKKPSYPTOPTPGKTRTKDKYRVVYTDYQRLELEKEYCTSRITIRRKT ELAQLQLSERQVKIWFQNRRAKE 263  
Mab -GRASPST-----KNVY-YDWMKKPSYPAOPTPGKTRTKDKYRVVYSDQRLELEKEYCTARYITIRRKS ELATSLQLSERQVKIWFQNRRAKE 239  
Eba -SNNNNNNSTTNNNNTSGNSTTINNTIRSSPVKSPY-YDWMKKQSYTAOPTPGKTRTKDKYRVVYTDQRLELEKEYCTSRITIRRKT ELAQLQLSERQVKIWFQNRRAKE 271  
Dme NNNNNNNNSPSTHNNNNNNNSVSNNN-RTSPSKPPY-FDWMKKPAYPAQOPQPGKTRTKDKYRVVYTDQRLELEKEYCTSRITIRRKS ELAQLTSLSERQVKIWFQNRRAKE 328

## Homeodomain

Aga RKQKKAETGSVG-----GGMGGLGGGQSLVAHAHQGNHPHGAAQSMSALLADTKPKLEPSLHLSH-----LHQ--MSAMSMGMSMGLHHHPGHHAALHAHLG 364  
Eli RKQTKKRDDSSSSINSSNGCIGQNGGVSGVGGGIS-----SATADDLVNFM-EPKPKLESGLH--HHL SHQHSFHHHQMMAATGMSPSMSGLQ---ALHHHHHGH LA 388  
Llu RKQNKRRDDP-----L--IGQNP-----LSNYM-DTKPKIEPSLH---L--QHSLHQ---MG-MSMSP-SFAIHH---LHQGHPLL- 326  
Mab RKQKRRDDP-----VPMMG-----ADYM-DTKPKIEPGAH---HL--LHQMQM-----HMAM-P-PMGLHHHG----- 291  
Eba RKQNKRRDDP-----MSAVVQHSD-----LASYM-DTKPKIEPLH---HL--QHSLHP---MSSMAMNM-PMSLHHHHSVLHHGHHP LA- 342  
Dme RKQNKKGSDPNV-----MGVGVQHAD-----YSQLL-DAKAKLEPLHLSHSL--AHSMPN---MAAMNI-P-AMRLEPH---LAAHSHSLAA 400

Aga VPTSQHH-----QLNQAAVAAAAASQVPSTSLSI-----M 394  
Eli AVAAAASGNSSTTQSQHMQH VYQOM-----TGIETIS 420  
Llu --PPPQHLHQSHAHTHS---HSHSHPQSHSHSQMSSSPNGVIGSGVGVGALSM 376  
Mab -----LHHPHAHTHALLOQSQHNLHPHISOMP GS-----VPTPPM 326  
Eba VPPAPQHLHQTHSQ-----MSAAAAASV GALSM 369  
Dme VAAHSHQLQQQS-----AOMSA-----AAAVGTLSM 427

# Orthodenticle

Tca-1	MWPPEAVHSLERFCYGNVNYRQRSSQPLKISCLKTPPPPEEDNRGCAASVGGESFYLPNMNQGFVKQQTAPHGPPYAPHPSLSSGLGGG-LSGMPMPALG-FGLG-HPLES--V	110
Tca-2	MWS-----NSLTAGC-----NPDSE-----LFP--GF--GSTCGSSSSSMAYLKSAP-----YPVPLGLHLGLPVDLSLHSSMA	59
Nvi-1	MAAAGAPNSV-----VGSQYHHQAVSHHPS-----HSAAAHHQIGMGPHPHGPSH--HPGLSGPFLTSHPHF-----HGHPDLAHMV	71
Nvi-2	MWP-----NSLGGG-----AGCGGASAAAAALKTSP-----Y-VGALGMP--PIEALHSSI-	44
Eba	MAA-----GFLKSGD-----LGPHPHSY-----GGPHPHSVPHGPLPPGM-----PMPSLGPFGLP-HGLEA--V	53
Dme	MAA-----GFLKSGD-----LGPHPHSY-----GGPHPHSVPHGPLPPGM-----PMPSLGPFGLP-HGLEA--V	53
Homeodomain		
Tca-1	P-FPQVYSYFAGVNPQRKRRERTTFTRAQLDLLEGLFAKTRYPDIFMREEVAVKINLPESRVQVWFKNRRAKCRQQLQQQQ-----	191
Tca-2	G-YP-----AGNQKRRERTTFTRAQLDVLEALFGKTRYPDIFMREEVAVKINLPESRVQVWFKNRRAKCRQQQKQHNQQQSVE-----KSSKLKNK	146
Nvi-1	ATFPQGM-----NQRKRRERTTFTRAQLDVLEALFLKTRYPDIFAREVALKINLPESRVQVWFKNRRAKVRQQASQQQAQQQQ-----	153
Nvi-2	G-YP-----GCNPRKRRERTTFTRAQLDVLEGLFSKTRYPDIFMREEVAVKINLPESRVQVWFKNRRAKCRQQQKQQQQQQQQ-----QQQQQQDK	130
Eba	G-FSQGMW--GVNTRKRRERTTFTRAQLDVLESLFGKTRYPDIFMREEVAVKINLPESRVQVWFKNRRAKCRQQLQQQQQSNLSNSSKGNSSGNVGS--GGNSGSSRNSNSN	161
Dme	G-FSQGMW--GVNTRKRRERTTFTRAQLDVLEALFGKTRYPDIFMREEVAVKINLPESRVQVWFKNRRAKCRQQLQQQQQSNLSNSSKKNASGGGSGNSCSCSSSSANSRNSN	164
Tca-1	-----NKSASRTTTSPTKVKKASKASPAAPRSVATP-----	222
Tca-2	SAPILTKTSP-----TPVSIINNNTSTSSSASSPSVTAAPHLRD-----SPNY-----	189
Nvi-1	-----QQQQQNLNEQKSAGRTQTNTQSSASAASNKQ-----	185
Nvi-2	SSRTSKKLQPSNPNGAVSGNPPPGKSPSIATTPATAAAATAAVPATTPLSGGTAGSAASSPALLRD-----SPQYKASAGG-----	207
Eba	NNSGNANNQNSS--GSGNSGTNSSNT-----PAKSSNNNNNNNNKSSANSA-----	206
Dme	GSSNNNTQSSGGNNSNKSSQKQNSQSSQGGSSGGNNSNNNSAAAAASAAAATAAQAQSIKTHHS--SFLSAAAAASGGTNTQSANNSNNNNQGNSTPNSSSSGGGGGSQAG	277
Tca-1	-----TGIPTPSTSASPPTVNI--KKE-----	248
Tca-2	-----IKPOLHVSTGTSTSPETIA-----SATYTNANSNS-I-----SPQMOSY	219
Nvi-1	-QLNAAAANN-SLQAIARRTSPCSPRPAKAPGNSPLV-----STTPSVASSSSNNNPVAAGYPRLGATPGA I-----	254
Nvi-2	-----ASSLLLAASTTPPSQLG-----GTVYSSGGSSSI-----	238
Eba	-----	206
Dme	GHLSAAAAAALNVTAHQNSPLLP-TPATSVSPVS-IVCKKEHLGGYSSVGGGGGGGASSGGLNLG-VGVGVGVGVGVGSQDLLRSPYDQLKDAGGDIGAGVHHHSIY	389
Tca-1	RP-----TGNITPHGSNTSSLIITPSPSAPLA-----YOHEYNSFN-WTANGHGHTSSHNYAQNYY--APTYYGQM	313
Tca-2	---WSPASIDS---FTLEQHR---SWCSSSQVPLSTTN-----STTNCY-----NN---YP-----RYSNM	262
Nvi-1	-----SNASSTVITPSPPTS-----DY-----HSF I---CIVSRYC--	284
Nvi-2	---WSPAVTESGAAGNGAGAAGFPGSEHQRLAAW---ATTS---SQOQCY-----QN---YS---SYYSNM	288
Eba	-----PVTMPSPQSAAVAHAAAAQAQAQSAHHSAA-AHSAYMNSHDSYNFVHWN-QY-NQ-----YPNNY-QTPSYYSQM	270
Dme	GSAAGSNPRLLPQG-----GNITPMDSSSS-I-TTPSPPIITPMSQSAAAA--AHAAQAQAQSAHHSAA-HSAAYMNSHDSYNFVHWN-QY-QQ-----YPNNYAQAQPSYYSQM	484
Tca-1	QPDYILNSQTTQ--HMQAMNMMAGT-YQMTGYSAMGMAAPHHQNFQ-----PRHPDCS-----MEFANMA	371
Tca-2	--DYLS--STMSHQFG-----NGLTSGWKSRSDES--SWF-YNS-GW-E-----RK	301
Nvi-1	-----YTLFSQVFPVRECRERERESKTKKLRKRR-----TATALARIMIIYIHSYIAL	335
Nvi-2	--DYLSPTSHQLNVVVGTRSSASSCFSESQGA-----NGLDNAWPRTRDESASSWF-YNSAGWGE-----RK	348
Eba	--EYFSNQ--QVNYNMG-HSGYSASNFLSPSSFTGTMSA-QAFSONGLDYMSPODK-----YVNMV	328
Dme	--EYFSNQ--QVNYNMG-HSGYTASNFLSPSPFTGTVSA-QAFSONSLIYMSPODK-----YANMV	542