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SC|1I3Q_A      MVG-QQYS--SAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMDETQTR 47
HU|3J0K_A      MVG-QQYS--SAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMDETQTR 47
SP|3H0G_A      MSG-IQFSPSSVPLRRVEEVQFGLFSPEEIRSMVAKIEFPETMDESGQR 49
TBB|P17545     MSGGAALPVSQMELHKVNEVQFEIFKERQIKSYAVCLVEHAKSAYANA--A 48
TBG|XP_011773113.1|DAL972  MSGGAALPVSQMELHKVNEVQFEIFKERQIKSYAVCLVEHAKSERYER--R 48
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SC|1I3Q_A      AKIGGLNDPRLGS-IDRNLRKQTCEQEGMNECPGHFGHIDLAKPVFHVGF 96
HU|3J0K_A      AKIGGLNDPRLGS-IDRNLRKQTCEQEGMNECPGHFGHIDLAKPVFHVGF 96
SP|3H0G_A      PRVGGLLDPRLGT-IDRQFRKQTCEGETMADCPGHFGHIELAKPVFHIGFL 98
TBB|P17545     DQSGEAMICVWVPLTNSACETCHRKHPECPGHFGYIELAEPVFNIGVF 98
TBG|XP_011773113.1|DAL972  PVRGGINDLRMGT-TDFEFACTCHRKHPECPGHFGYIELAEPVFNIGVF 97
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Motif 1A
SC|1I3Q_A      AKIKKVCCEVCMHCGKLLLDDEHNELMRQALAIKDSKKRFAAIWTLCKTKM 146
HU|3J0K_A      AKIKKVCCEVCMHCGKLLLDDEHNELMRQALAIKDSKKRFAAIWTLCKTKM 146
SP|3H0G_A      SKIKKILECVCWNCGKLLIDSSNPKFNDTQRYRDPKNRLNAVWNVCKTKM 148
TBB|P17545     DLVLLVLCVKCKTCGALLLNTREQDVHKKLQHMTGLNRLRQVAKMAEAK- 147
TBG|XP_011773113.1|DAL972  DLVLLVLCVKCKTCGALLLNTREQDVHKKLQHMTGLNRLRQVAKMAEAK- 146
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Motif 2
First Zinc Finger (Zn)
SC|1I3Q_A      VCETDVPSRDD-----PTQLVSRG-----GCGNTQPTIRKDGKLL 181
HU|3J0K_A      VCETDVPSRDD-----PTQLVSRG-----GCGNTQPTIRKDGKLL 181
SP|3H0G_A      VCDTGLSAGSDNFDLSNPSANMGGH-----GCGAAQPTIRKDGRL 189
TBB|P17545     -CRVSTSTEDDMGIDGFDSPAFNGGSGMGPGATRGCASQPRVS----RF 192
TBG|XP_011773113.1|DAL972  -CRVSTSTEDDMGIDGFDSPAFNGGSGMGPGATRGCASQPRVS----RF 191
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Second Zinc Finger (Zn)
SC|1I3Q_A      VGSWKDRATGDAPELRLVSTEEILNIFKHISVKDFTSLGFNEVFSRP 231
HU|3J0K_A      VGSWKDRATGDAPELRLVSTEEILNIFKHISVKDFTSLGFNEVFSRP 231
SP|3H0G_A      WGSWK--RGKDESDLPEKRLLSPLEVHTIFTHISSEDLAHLGLNEQYARP 237
TBB|P17545     YGIYPTLVKAVHEEQD-AEWHADKVRQVLDREVSDDDARLMGFDPQRCHP 241
TBG|XP_011773113.1|DAL972  YGIYPTLVKAVHEEQD-AEWHADKVRQVLDREVSDDDARLMGFDPQRCHP 240
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Motif 1B
SC|1I3Q_A      EWMILTCLPVPPPVRPSISFNESQRGEDDLTFKLADILKANISETLEH 281
HU|3J0K_A      EWMILTCLPVPPPVRPSISFNESQRGEDDLTFKLADILKANISETLEH 281
SP|3H0G_A      DWMIITVLPVPPPVRPSISVDGTSRGEEDDLTHKLSDIKANANVRRCEQ 287
TBB|P17545     RDLVLTVLPVPPPQVRPAISFGG-LRSDELTHQIMSIVKRNNQLRR-DK 289
TBG|XP_011773113.1|DAL972  RDLVLTVLPVPPPQVRPAISFGG-LRSDELTHQIMSIVKRNNQLRR-DK 288
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SC|1I3Q_A      NGAPHHAEAEESLLQFHVATYMDNDIAGQPQALQKSGRPVKSIRARLKG 331
HU|3J0K_A      NGAPHHAEAEESLLQFHVATYMDNDIAGQPQALQKSGRPVKSIRARLKG 331
SP|3H0G_A      EGAPAHIVSEYEQLLQFHVATYMDNEIAGQPQALQKSGRPLKSIRARLKG 337
TBB|P17545     ESDVQAADRSRALLQEHVATYFNNASTYKPKTVNDTKKLSLTERLKG 339
TBG|XP_011773113.1|DAL972  ESDVQAADRSRALLQEHVATYFNNASTYKPKTVNDTKKLSLTERLKG 338
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Motif 3A
SC|1I3Q_A      KEGRIRGNLMGKRVDFSARTVI SGDPNLELDQVGVPKSI AKTLTYPEVVT 381
HU|3J0K_A      KEGRIRGNLMGKRVDFSARTVI SGDPNLELDQVGVPKSI AKTLTYPEVVT 381
SP|3H0G_A      KEGRIRGNLMGKRVDFSARTVI TGDPNLSLDLGVPRSIAKTLTYPETVT 387
TBB|P17545     KYGRIRGNLMGKRVDFSARTVI TGDPNIDVDEVGVPFVSAMTLTFPERVN 389
TBG|XP_011773113.1|DAL972  KYGRIRGNLMGKRVDFSARTVI TGDPNIDVDEVGVPFVSAMTLTFPERVN 388
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SC|1I3Q_A      PYNIDRLTQLVRNGPNEHPGAKYVIRDSGDRIDLRYSKRAGDIQLQYGWK 431
HU|3J0K_A      PYNIDRLTQLVRNGPNEHPGAKYVIRDSGDRIDLRYSKRAGDIQLQYGWK 431
SP|3H0G_A      PYNIYQLQELVRNGPDEHPGAKYI IRDTGERIDLRYHHRAGDIPRYGWR 437
TBB|P17545     TINKKRLTEFARR--TVYPSANYIHHPNGTITKLALLRDRSKVTLNIGDV 437
TBG|XP_011773113.1|DAL972  TVNKKRLTEFARR--TVYPSANYIHHPNGTITKLALLRDRSKVTLNIGDV 436
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CLAMP CORE

CLAMP HEAD

CLAMP CORE

ACTIVE SITE

Dock

SC|1I3Q_A SLDTIGGSD-----AAFEKRYRVDLLNTDHTLDPSSLLESQ-SEILGDLKL 925
HU|3J0K_A SLDTIGGSD-----AAFEKRYRVDLLNTDHTLDPSSLLESQ-SEILGDLKL 925
SP|3H0G_A VFDSLRLST-----KQFEKKYRIDLME-DRSLSLYMENS-----IENDSSV 927
TBB|P17545 QLFPLPFRDDKEMEDTYKYEYDVDGTFSGKVGNGYMDPHVRKMLRADPQN 934
TGB|XP_011773113.1|DAL972 QLFPLPFRDDKEMEDTYKYEYDVDGTFSGKVGNGYMDPHVRKMLRADPQN 933
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SC|1I3Q_A QVLLDEEYKQLVKDRKFLR-EVFDVG--EANWPLPVNIRRIQNAQQTFH 972
HU|3J0K_A QVLLDEEYKQLVKDRKFLR-EVFDVG--EANWPLPVNIRRIQNAQQTFH 972
SP|3H0G_A QDLLDEEYQTLVADRELLCKFI FPKG--DARWPLPVNVQRIQNALQIFH 975
TBB|P17545 VRKLEQEYEQTLADREWSRKMLDLEDRDKLKLNLVNPGRLIQNAARSTMG 984
TGB|XP_011773113.1|DAL972 VRKLEQEYEQTLADREWSRKMLDLEDRDKLKLNLVNPGRLIQNAARSTMG 983
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SC|1I3Q_A IDHTKPSDLTIKDIVLGVKDLQENLLVLRG-----KNEIIQNAQR 1012
HU|3J0K_A IDHTKPSDLTIKDIVLGVKDLQENLLVLRG-----KNEIIQNAQR 1012
SP|3H0G_A LEAKKPTDLLPSDI INGLNELIAKLTIFRG-----SDRITRDVQN 1015
TBB|P17545 KRSQ-VSNLSPITIIDHVRKQLQEDLMKLFPSYHRGGDGYIRNTLSRERIE 1033
TGB|XP_011773113.1|DAL972 KRSQ-VSNLSPITIIDHVRKQLQEDLMKLFPSYHRGGDGYIRNTLSRERIE 1032
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SC|1I3Q_A DAVTLFCCLLRSLRATRRVLQEYRLTKQAFDQVLSNIEAQFLRSVVHPGE 1062
HU|3J0K_A DAVTLFCCLLRSLRATRRVLQEYRLTKQAFDQVLSNIEAQFLRSVVHPGE 1062
SP|3H0G_A NATLLFQILLRSKFAVKRVIMEYRLNKVAFEWIMGEVEARFQAVVSPGE 1065
TBB|P17545 SALTFLFNHRLQLLASKRVLKEYKLNDRAFEYLLKEIRTKYHQSLTTPGE 1083
TGB|XP_011773113.1|DAL972 SALTFLFNHRLQLLASKRVLKEYKLNDRAFEYLLKEIRTKYHQSLTTPGE 1082
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Motif 4C

SC|1I3Q_A MVGVLAQSI GEPATQMTLNTFFHAGVASKKVTSGVPRLKEILNVAKNMK 1112
HU|3J0K_A MVGVLAQSI GEPATQMTLNTFFHAGVASKKVTSGVPRLKEILNVAKNMK 1112
SP|3H0G_A MVGTLAAQSI GEPATQMTLNTFFHAGVSSKNVTLGVPRLKEILNVAKNK 1115
TBB|P17545 NIGATAAQSC GEPATQMTLNTFFHNAGISSKNVTLGVPRLELLNVS RNQK 1133
TGB|XP_011773113.1|DAL972 NIGATAAQSC GEPATQMTLNTFFHNAGISSKNVTLGVPRLELLNVS RNQK 1132
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SC|1I3Q_A TPSLTVYLEPGHAADQEQAKLIRSAIEHTTLKSVTIASEIYYDPDRSTV 1162
HU|3J0K_A TPSLTVYLEPGHAADQEQAKLIRSAIEHTTLKSVTIASEIYYDPDRSTV 1162
SP|3H0G_A TPSLTIYLMFWIAANMDLAKNVQTQIEHTTLSTVTSATEIHYPDPQDVT 1165
TBB|P17545 HASMTVSLFPPYDEKRN-AQKAQHLEIYCTLESITRRIQFIYDPDRHTV 1182
TGB|XP_011773113.1|DAL972 HASMTVSLFPPYDEKRN-AQKAQHLEIYCTLESITRRIQFIYDPDRHTV 1181
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SC|1I3Q_A IPEDEEIIQLHFSLLDEE----AEQSFQQSPWLLRLELDRAAMNDKDLT 1208
HU|3J0K_A IPEDEEIIQLHFSLLDEE----AEQSFQQSPWLLRLELDRAAMNDKDLT 1208
SP|3H0G_A IEEDKDFVEAFFAIPDEE----VEENLYKQSPWLLRLELDRAKMLDKKLS 1211
TBB|P17545 VEADRDI LELEWNVMDSDAELRIQEVVAGSPWVVRLELDVDMVTDKALD 1232
TGB|XP_011773113.1|DAL972 VEADRDI LELEWNVMDSDAELRIQEVVAGSPWVVRLELDVDMVTDKALD 1231
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SC|1I3Q_A MGQVGERIKQTFKNDLFIWSEDNDEKLIIRCRVVRP---KSLDAETEAE 1255
HU|3J0K_A MGQVGERIKQTFKNDLFIWSEDNDEKLIIRCRVVRP---KSLDAETEAE 1255
SP|3H0G_A MSDVAGKIAESFERDLFTIWSEDNADKLIIRCRIIRDDDRKAEDDDNMIE 1261
TBB|P17545 MKDVKQAILRVDESIIETGMANNVRQRTIRMSRYN-----EGAD 1273
TGB|XP_011773113.1|DAL972 MKDVKQAILRVDESIIETGMANNVRQRTIRMSRYN-----EGAD 1272
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SC|1I3Q_A EDHMLKKIENTMLENITLRGVENIERVVMKY-DRKVPSPTEGYVKEPEW 1304
HU|3J0K_A EDHMLKKIENTMLENITLRGVENIERVVMKY-DRKVPSPTEGYVKEPEW 1304
SP|3H0G_A EDVFLKTI EGHMLESISLRGVENITRVYMMEH-KIVRQIEDGTFFERADEW 1310
TBB|P17545 SIPKLRKREIPALLARVHLRIGVRRALLKDTTEFTVDQATGKMSGNKIW 1323
TGB|XP_011773113.1|DAL972 SIPKLRKREIPALLARVHLRIGVRRALLKDTTEFTVDQATGKMSGNKIW 1322
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FOOT

CLEFT

JAW

SC|1I3Q_A
 HU|3J0K_A
 SP|3H0G_A
 TBB|P17545
 TBG|XP_011773113.1|DAL972

VLETDGVNLSEVMT-VPG-----IDPTRIYTNSFIDIMEVLGIEAGRAA 1347
 VLETDGVNLSEVMT-VPG-----IDPTRIYTNSFIDIMEVLGIEAGRAA 1347
 VLETDGINLTEAMT-VEG-----VDATRITYSNSFVEILQILGIEATRSA 1353
 AIDTDGTALRRAFIGVVGEDGKNIINAVKTSSNKVPEVCSLLGIEAARSK 1373
 AIDTDGTALRRAFIGVVGEDGKNIINAVKTSSNKVPEVCSLLGIEAARSK 1372
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SC|1I3Q_A
 HU|3J0K_A
 SP|3H0G_A
 TBB|P17545
 TBG|XP_011773113.1|DAL972

LYKEVYNVIASDGSYVNYRHMALLVDVMTTQGGLTSVTRHGFNRNNT-GA 1396
 LYKEVYNVIASDGSYVNYRHMALLVDVMTTQGGLTSVTRHGFNRNNT-GA 1396
 LLKELRNVIEFDGSYVNYRHLALLCDVMTSRGHLMAITRHGINRAET-GA 1402
 MLTELREAYLAYGLNINRYRHYTILVDTICQHGYLMAVSRSGINRSDTSGP 1423
 MLTELREAYLAYGLNINRYRHYTILVDTICQHGYLMAVSRSGINRSDTSGP 1422
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SC|1I3Q_A
 HU|3J0K_A
 SP|3H0G_A
 TBB|P17545
 TBG|XP_011773113.1|DAL972

LMRCSFEETVEILFEAGASAELEDDCRGVSENVILGQMAPIGTGAFDVMID 1446
 LMRCSFEETVEILFEAGASAELEDDCRGVSENVILGQMAPIGTGAFDVMID 1446
 LMRCSFEETVEILMDAAASGEKDDCKGISENIMLGQLAPMGTGAFDIYLD 1452
 LMRCSFEETVKVLMMAAASFGECDPVRGVSANLVLGNQARVGTGLFDLVLN 1473
 LMRCSFEETVKVLMMAAASFGECDPVRGVSANLVLGNQARVGTGLFDLVLN 1472
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SC|1I3Q_A
 HU|3J0K_A
 SP|3H0G_A
 TBB|P17545
 TBG|XP_011773113.1|DAL972

EESLVKYMPEQKITEIEDG-----QDGGVTPYSNESGLVNADLDVKDE 1489
 EESLVKYMPE----- 1455
 QDMLMNYSLGTAVPTLAGSGMGTSQLPEGAGTPYERSPMVDSGFVGPDA 1502
 MAALQAVPQAEAVAPCGKDVNVYHSLGSLTQQNIQSSIAYRPRDHDATPF 1523
 MAALQAVPQAEAVAPCGKDVNVYHSLGSLTQQNIQSSIAYRPRDHDATPF 1522



CLEFT

CLAMP CORE

LINKER