

CLUSTAL 2.0.12 multiple sequence alignment of scute

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Dmel      -----MKNNNNTTKSTTMSSSVLSTNETFPTTINSATKIFRYQHIMPAPSPL 47
Dsim      -----MKNNNNTTKSITMSSSVLSTNDTFPTTINSATKIFRYQHIMPAPSPL 47
Dyak      -----MSSSVLSTNDTFPTTINSATKIFRYQHIMPAPSPL 35
Dmoj      -----MSSVVFNASAVGKNAAEFPTTIGGATKMFYQHIMPAPPELK 42
Dqua      -----APTPQ---QPQQQHQLQ---K 18
Sleb      -----MSSVVFNTNPSAKGNSISINASNDLFPTTIGGATKMYRYQHIMPAMPNP 49
Ccap      MVKMSSAIFTKSNTALQYYSKSSNNHNNNNNTTAHPQQQLSAAVKMFYQNIAPATMP 60
Mdom      -----MSSVSCNQTNVQQPQHIFPTTIVTPGKMPKYPHIQPHPIAE 41
Cvic      -----MSSVSCNQNTAQ-QHLFPTTIVAATKMMKYPHIQPHPIAE 40
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Dmel      IPGGN---QNQPAGTMPKIKRKYTPRGMALTRCSESVSLSLPGSSP-----APYNVDQS 98
Dsim      IPGGN---QNQPGGTMPKIKRKYTPRGMALTRCSESVSLSLPGSSP-----APYNVDQS 98
Dyak      LPVGN---QNQPGGTMPKIKRKYTPRGMALTRCSESVSLSLPGSSP-----APYNVDQS 86
Dmoj      SSSNGV---GGGGGGGAAIKRKYTPRGMALANASSNSNSSSSSSSCS---SPYNVDQS 98
Dqua      S-----LMKTRKYTPRGMALATAAGAATCHTTATS-----APYSVDQS 56
Sleb      DQSQSTTALTAMGGIGIKTRKYSPRGSSSSGSSNNSSSGGI AVHSGNNGGAPYSVDQS 109
Ccap      LSLG-----CAGAEIKRKYTPRAPSNGG-----GPFSDQT 92
Mdom      DG-----KNRKVTR-----SQPYNADQS 59
Cvic      DG-----QARKVPANC-----PAPYNPDQT 60
          : ** . * : . ** :
    
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Dmel      Q-SVQRRNARERNRVKQVNNSFARLRQHIPQSIITDLTKGGGRGPHKKISKVDTLRIAVE 157
Dsim      Q-SVQRRNARERNRVKQVNNSFARLRQHIPQSIITDLTKGGGRGPHKKISKVDTLRIAVE 157
Dyak      Q-SVQRRNARERNRVKQVNNSFARLRQHIPQSIITDLTKGGGRGPHKKISKVDTLRIAVE 145
Dmoj      Q-SVQRRNARERNRVKQVNNSFARLRQHIPQSI IADLTKGGGRGPHKKISKVDTLRIAVE 157
Dqua      Q-SVQRRNARERNRVKQVNNSFARLRQHIPQTI IADLTKGGGRGPHKKISKVDTLRIAVE 115
Sleb      Q-SVQRRNARERNRVKQVNNSFARLRQHIPQSI IADLTKGGGRGPHKKISKVDTLRIAVE 168
Ccap      Q-SVQRRNARERNRVKQVNNSFARLRQHIPQTIITDLLKGGGRGPQKKISKVDTLRIAVE 151
Mdom      QHSVLRNARERNRVKQVNNSFARLRQHIPQTI IADLTKGGGRGPQKKISKVDTLRIAVE 119
Cvic      Q-SVLRNARERNRVKQVNNSFARLRQHIPQSI IADLTKGGGRGPQKKISKVDTLRIAVE 119
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Dmel      YIRRLQDLVDDLNGGSNIG----ANN-AVTQLQLCLDES-----SSHSSSSSTCSS 203
Dsim      YIRRLQDLVDDLNGGSNND----ATNNAVTQLQLCLDES-----SSHSSSSSTCSS 204
Dyak      YIRRLQDLVDDLNGGSNIG----ATSNAVTQLQLCLDES-----SSHSSSSSTCSS 192
Dmoj      YIRRLQDLVDDLNGGPSTN---SCTPTAAQFNLCLDET-----SSQSSSSSSST 204
Dqua      YIRRLQDLVDDLNGGSNTSNANATAAAHVAQLNLCLDET-----SSQCESSSSST 166
Sleb      YIRRLQDLVDDLNGGSNGGS--ANNSLPLPISSLCHDDDDDDDDDLISNNSSSSSSLSA 226
Ccap      YIRRLQDLVDDLNGSSGAGAVQSKYSTARGSSGLLMAATS DNNTTSSNSSFSNSSASS 211
Mdom      YIRRLLEDLDDLNGGVSS---SNEQYDLQTNNSCNDTAS-----NSSFSSSSSSSA 168
Cvic      YIRRLQDLLEDLNGGSSTQ--PQQQYESQANG-HCDSAS-----NSSFSSSSSTGSS 168
          ***** : * : * * * . * . * : * :
    
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Dmel      S-----GHNTYYQNTISVS-----PLOQQQQQLQRQQFN 231
Dsim      S-----GHNTYYQNTITVS-----PLOQQQQQLQRQQFN 232
Dyak      S-----GHNSYYQNTINVS-----PLOQQQQQLQRQQFN 220
Dmoj      -----ASSSA---SQQLAQLYSSALLT---QANATATPTALQQQQQLQRQQYP 248
Dqua      NGSSSHSHSSSNL----SASLAQLYNSNINTALQQQQQQQQQLQQQQQLQRQQYP 222
Scap      SSSSFNTITTTSTA---ATTVGSQPATTTSMPLP-LYSSSTLAATPLOQQQQQLTRQQFP 281
Ccap      NLSLLSPDSPTPNAPCADGLAAEQLYFASTANSA---LQAAFQQQQQEQQQHQQQFT 267
Mdom      SSTYN-----TTSQTPVYYTPQSTSP---LPSLMDVNLG-HLN-PYSSS 209
Cvic      SPSSS-----YTSTNTPVYYT-QPSSP---LPSLMDANLQVSHLNNPYNNS 210
          :
    
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Dmel      HQPLTALSLNTN-----LVGTSVPGGDAGCVSTSKN-QQTCHSPTSSFNSS-MSFD-- 280
Dsim      HQPLTALSLNTN-----LVGTSVTGGDAGCVSTSNN-QQTCHSPTSSFNSS-MSFD-- 281
Dyak      HQPLTALSLNTN-----LVGTSVPGGDAGCVSTSNN-QQTCHSPTSSFNSS-MSFD-- 269
Dmoj      NHPLTPITLNANNAQTAI PATTTTTTSSMMSSTAT TNIAGGCHSPTSSFNSS-MSFD-- 305
Dqua      NHPLMPIIPNTN----MPLVATTAVVAPGGTTTV-----CHSPTSSFNSS-MSFD-- 267
Sleb      NHPLTPISLNAY-----SPPTQVNSIAVGATLETAG----CHSPTSSFNSS-MSFD-- 327
Ccap      AALLTAEALQAY-----ASPOPQTQTQTQLDIG----CPSPTSSFNSS-MSFD-- 311
Mdom      TTLLSPVSMNSY-----SPQHN--AGYENNG----CHSPTSSFNSSNLSYEA 251
Cvic      TTLLSPVSLNSY-----SPPHNQAAPLENTG----SHSPSSSFNSS-LSYD-- 251
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Agam GGCYAPIAGGFKHEPYDIYVDPSSSPTPSFGSDHGIGGVTSSSVHLHTGGHSTVLGSATD

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Dmel      SGTYEGV-----PQQ-----ISTHLDRLDHLD---NELHTHSQLQLKFEPYEH 320
Dsim      SGTYEGV-----PQQ-----ISTHLDRMDHLD---NELHTHSQLQLKFEPYEH 321
Dyak      SGTYEAA-----PQQ-----ISTHLDRLDHLD---NEGHSHSQLQLKFEPYEH 309
Dmoj      SGTYEAQ-----PQQ-----LSP-----PVAAMDAQLQLKFEPYEH 336
Dqua      SGTFEAA-----PQQ-----LSPTEAI ISSGTSPASSSTLDAQLQLKFEPYEH 310
Sleb      SGTYEAA-----PQQ-----LSPPAAPGVEAH--AQQSPLDAHLQLKFEPYEH 368
Ccap      SGTFFVHSPV-----PQQQLSALRHGTASEAQRGSENNNASASQIDANLQLKFEPYDN 364
Mdom      AASFEOQQQSLADLPTQQQQQHSHHQQQQPHHHHQISADAATLAFDTNIQLKFEPYDN 311
Cvic      SPNFEPQPH---QQPTVQELQHFQONQQTTPPH-----FDGNLQLKFEPYDN 296
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Dmel      FQLDEEDCTPDDEEILDYISLWQEQ 345
Dsim      FQLDEEDCTPDDEEILDYISLWQEQ 346
Dyak      FQLDEEDCTPDDEEILDYISLWQEQ 334
Dmoj      FQLDEEDCTPDDEEILDYISLWQEQ 361
Dqua      FQLDEEDCTPDE----- 322
Scap      FNLEEDCTPDDEEILDYISLWQSQ 393
Ccap      FNLHEEDCTPDDEEILDYISLWQEQ 389
Mdom      FTLDEEDCTPDDEEILDYISLWQEQ 336
Cvic      FTLDEEDCTPDDEEILDYISLWQEQ 321
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Green: putative GSK3 sites

Blue: putative priming phosphate site