

CLUSTAL 2.1 multiple sequence alignment of pannier

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Dmel    MYHSSAVAAAYTDLAAAGSAAASAGVGVSGYHQAVNA-----PVYVPSN-----RQYN 49
Cvic    MYHSS--AGYDLSG-----SATGSGVSSYHQAAAAAAAAATVSAPVYVPSNRALTNQYQ 52
Ccap    MYHSS--TGYPDLTG-----GAAGNGG--YHHQTAMN-----APVYVPSNRALTQSQYN 45
Mabd    MFHST--SAYPDIS-----AGTGNVSSYHQQASAA-----PVYVPSNRALS--SQY- 43
Agam    MFHTS--AAYSDMTAA----VVATGNTGSYHQSAAAAAAAAAANAPVYVPSRRALPHSQYG 54
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Dmel    HVAAHFGSAAAQNAWTTEGFGSAHA----QFYSNAAVMMGSWRSAYPDPSG-FQRSSFYE 104
Cvic    HVAAHFGTAAAQNAWTSDFSFGTAHTQLPPQFYTQ-NAVMMGSWRAAYDPTG-FQRSSPYD 110
Cer     HVATHFGTAAAQNAWTTDSFGTAHAQLPAQFYT-----MGSWRAAYDPTG-FQRSSPYE 98
Mabd    ---SHFGTSAQAQNAWTADSFSSAHS----QFYAQ-NAMMMGSWRATFDPTAAFHQANPYD 95
Agam    ---AHSANFSAQNGWPTDGFGTHTQLPPQFYAQ--NVMMGSWR--AYDPTG-FQRTSPYD 107
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Dmel    SAMDFQFGEGRFCVNCGAI STPLWRRDGTGHYLCNACGLYHKMNGMNRPLIKPSKRLVSA 164
Cvic    SAIDFQFGEGRFCVNCGAI STPLWRRDGTGHYLCNACGLYHKMNGMNRPLIKPSKRLVSA 170
Ccap    NAIDFQFGEGRFCVNCGAI STPLWRRDGTGHYLCNACGLYHKMNGMNRPLIKPSKRLVSA 158
Mabd    SSMDFQFGEGRFCVNCGAI STPLWRRDGTGHYLCNACGLYHKMNGMNRPLIKPSKRLT-- 153
Agam    SAMDFQFGEGRFCVNCGAI STPLWRRDGTGHYLCNACGLYHKMNGMNRPLIKPSKRLVSO 167
      .::***** ***** ***** *****

Dmel    TATRRMGLCTNCGTRTTTLWRRNNDGEPVCNACGLYKLGHVNRPLAMRKDGIQTRKRK 224
Cvic    TATRRLLGLCTNCGTRTTTLWRRNNEGEPVCNACGLYFKLHGVRNPLAMRKDGIQTRKRK 230
Ccap    TATRRLLGLCTNCGTRTTTLWRRNNEGEPVCNACGLYFKLHGVRNPLAMRKDGIQTRKRK 218
Mabd    -ATRRLLGLSCTNCGTRTTTLWRRNNEGEPVCNACGLYFKLHGVRNPLAMRKDGIQTRKRK 212
Agam    TATRRLLGLCTNCGTRTTTLWRRNNDGEPVCNACGLYFKLHGVRNPLAMRKDGIQTRKRK 227
      ****:*.* ***** ***** ***** *****

Dmel    PKKTGSGSAVGAGTGS GTSTLEAIKECKEEHDLKPSLS---LERHSLSKLHTDMKSGTS 281
Cvic    PKKSGGSTENGKEIKDEDLKPSLGLERHSLPGSLASKLQNDLAAKASSSSSALHNLSLGS 290
Ccap    PKKSTSSSDVSKDGKDD-----GDNHNNTLGSMMN-----NNSLHNLSLNAINSSP 264
Mabd    PKKSG--SESGKDKEDD-----LKP TLQASSLSSKLG LP 244
Agam    PKKTGGSGGSADVMALVGGKDDGGIGDGLLQTRNG-----NSKNLTGSPKSNLSSP 281
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Dmel    SSSTLMG--HHSAQOQQOQQOQQOQQOQQOQSAHQOCFPLYGQT TTQQOHHQHGHSMT 339
Cvic    ATSALH----SSLSHMHLPH TSAQQTRLLNNVSSY TSA AHLGSSTNTSTS-STNGNSAH 345
Ccap    STGSLH----NSLSHHLHLP SAAAQQR--HSTISHTHAHALSSTNNTPTVHSAT TASSL 318
Mabd    TSPDLK----NNNLHQYTPSTFF TDLKK--NSTSPRTSDFNFCHQSNTPVVR--ATLASAT 297
Agam    TIRSLHISP HHGQSYGLGSSLGSAHHGGSAGT LGS L VGKYDLSALSPGSLGGVPGSIVS 341
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Dmel    S---SSG----QAHLSARHLHGAAG----- 357
Cvic    NNNLYSPSALAAQSNLSHSQLSGSFAFGTQ--KYEHL LGS SN----- 384
Ccap    NSNMYS P----QNNVNSAQLSASSFGSHGISKYEHL LSTSGSSGGGGVGVGNIGN 373
Mabd    R---ASP----SKNQSR TQ TPLN----- 313
Agam    SSAHQOHT---TAGLNSSHIYTPS----- 363
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Dmel      -----TQLYTPGSSSSGGGSASAYT-----SHSAETPALSNGTPSPHYQHHHHLGGTH 404
Cvic      -----ALSNGLSPSSTASSNYH-----AHHLHHHHHAAAAAHHAASAHHH--HHH 428
Ccap      LNNSSSTNAVSLNGLIS-SSTPSPNYHHSASAAAHLHHHHHHH---HPSASAAHHATSHHS 429
Mabd      -----NAYSNNNNPSATTPTDYN-----SYNTTNYTSSPSTASTPSNVNDMSVSGS 359
Agam      -----SNLSTQHSHPVNGYGNHPTGGSNLPGNNGGAGGGGSNTPSNHGALGNTQ 416

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Dmel      GHHVTAAAAHHHFHAAAA---VAAYGVKTEASATNY-DYVNNC---YFGGTFGALG--- 453
Cvic      SPSLSQHVPTSASSGGS---LGGYSVKSESATNY-DYVNNC---YFGSSFGAFG--- 476
Ccap      AAALSQHSGGSHISSGDGSGVGGYGVKSESATNY-DYVSNC---YFSSSFPLS--- 481
Mabd      SPNYSHHPHSHLSHQH-----HGYGVKSESYTSNY-DYMNC---YFGGNFGALS--- 406
Agam      NNAGGNQTPFGQIKSESNPLGGASTPTPSVPSSNGYGDYMNNCLOSGYFSGGFSSLHSHH 476

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Dmel      ----GAATTTA-----MAGGAAS--ELAGY-HHQHNVIQAACLMA 486
Cvic      ----GSTGSSS-----GVHGATAS--DMAGYHHQHNVIQAACLMA 511
Ccap      ----ASTAAAAAGTGMSMGMGVGVGMGMGMHGMHGSSELASYHHHQHNVIQAACLMA 537
Mabd      ----VAAASAG-----TGAS--ELAGY-HHQHNVIQAACLMA 436
Agam      SPHHVSPGMGSTVNGASLTHSHHAHPHHHHHHHHHPTAADLAGY-HHQHNVIQAACLMA 535

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Dmel      TS 488
Cvic      TS 513
Ccap      TS 539
Mabd      SS 438
Agam      SS 537
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Blue: putative GSK3/sgg phosphorylation sites
Yellow: zinc fingers