

A

CLUSTAL 2.1 multiple sequence alignment

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sp|P67775|PP2AA_HUMAN      MDEKVFTKELDQWIEQLNECKQLSESQVKSLCEKAKEILLTKESNVQEVRC 50
sp|O00743|PPP6_HUMAN      ----MAPLDLDKYVEIARLCKYLPENDLKRLCDYVCDLLLEESNVQPVST 46
                               : . :***** . ** *.*.:* ** : . :*: :***** *

sp|P67775|PP2AA_HUMAN      PVTVCGDVHGQFHDLMELFRIGGKSPDTNYLFMGDYVDRGYYSVETVLL 100
sp|O00743|PPP6_HUMAN      PVTVCGDIHGQFYDLCELFRTGGQVPDTNYIFMGDFVDRGYYSLETFTYL 96
*****:*****:* **** ** : *****:*****:*****:***_* *

sp|P67775|PP2AA_HUMAN      VALKVRYRERITILRGNHESRQITQVYGFYDECLRKYGNANVWKYFTDLF 150
sp|O00743|PPP6_HUMAN      LALKAKWPDRITLLRGNHESRQITQVYGFYDECQTKYGNANAWRYCTKVF 146
*****.: :***:*****:*****:***** *****.*:* *.:*

sp|P67775|PP2AA_HUMAN      DYLPLTTALVDGQIFCLHGGLSPSIDTLDHIRALDRLQEVPHEGPMCDLLW 200
sp|O00743|PPP6_HUMAN      DMLTVAALIDEQILCVHGGLSPDIKTLQIRTIERNQEIPHKGAFCDLVW 196
* *.:***:* **:*:*****.*.***:***:*** **:*:*.:***:*

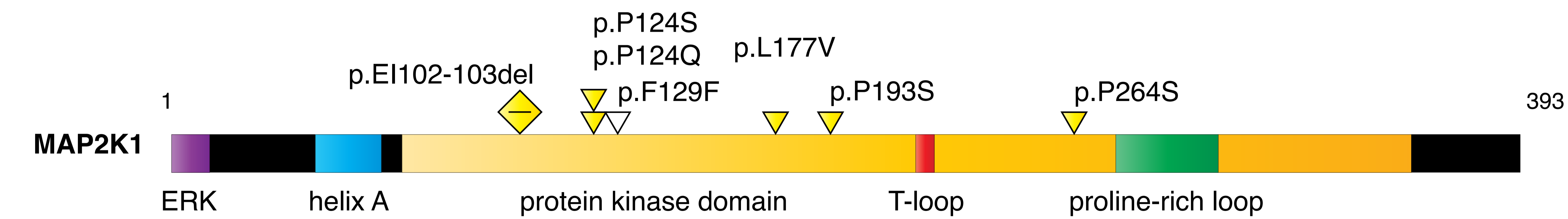
sp|P67775|PP2AA_HUMAN      SDPDDRGGWGISPRGAGYTFGQDISETFNHANGLTVSRAHQLVMEGYNW 250
sp|O00743|PPP6_HUMAN      SDPEDVDTWAISPRGAGWLFGAKVTNEFVHINNLKLICRAHQLVHEGYKF 246
***:* . *.*****: ** .:*** * * *.*.*:***** **:*

sp|P67775|PP2AA_HUMAN      CHDRNVVTIFSAPNYCYRCGNQAAIMELDDTLKYSFLQFDPAPRRGEPHV 300
sp|O00743|PPP6_HUMAN      MFDEKLVTVWSAPNYCYRCGNIASIMVFKDVNTREPKLFRAVPDSERVIP 296
.*.:***:*****:***** **:* :*. . . * ..* .

sp|P67775|PP2AA_HUMAN      TRRTPDYFL 309
sp|O00743|PPP6_HUMAN      PRTTTPYFL 305
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B



Legend

- missense mutation
- synonymous mutation
- nonsense mutation
- in-frame deletion
- frameshift insertion
- splice site mutation

