

A

Identities = 237/528 (44%), Positives = 316/528 (59%), Gaps = 27/528 (5%)
 Query 63

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Hpa2c      LDVSTKNPVRTVNEFSLQLDPSIIHDG-WLDFLS SKRLVTLARGLSPAFILRFGGKRTD 121
           LD T+ P+ V+ +FLS+ +D ++ D +L L S +L TLARGLSPA+LRFGG +TD
Hpa1      41 LDFFTQEPLHLVSPSFLSVTIDANLATDPRFLILLGSPKLRRTLARGLSPAYLRFGGTKTD 100

Hpa2c     122 FLQFQNLNRNPAKSRGGPGPDYYLKNYEDDIVRSDVALDKQKGCKIAQHPDVMLELQREKA 181
           FL F +P K Y+ DI CK P + E R +
Hpa1     101 FLIF----DPKKESTFEERSYWQSQVNQDI-----CKYGSIPPDVEEKLRLEW 144

Hpa2c     182 AQMHLVLLKEQFSNTYSNLILTARSLDKLYNFADCSGLHLIFALNAXXXXXXXXXXXXXXXXXX 241
           +LL+E + + N + S+D LY FA+CSGL LIF LNAL R + WNSS+A
Hpa1     145 PYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCSGLDLIFGLNALLRATADLQWNSNA 204

Hpa2c     242 XXXXXXXXXXXXXNISWELGNEPNNYRTMHGRAVNGSQLGKDYIQLKSLLOPIRIYSRASL 301
           LL Y +SK YNISWELGNEPN++ +NGSQLG+D+IQL LL+ + A L
Hpa1     205 QLLLDYCS SKGYNISWELGNEPNSFLKKADIFINGSQLGEDFIQLHKLLRK-STFKNAKL 263

Hpa2c     302 YGPNIGRPRKNVIALLDGFMKVAGSTVDAVTWQHICYIDGRVVKVMDFLKTRLLDITLSDQI 361
           YGP++G+PR+ + L F+K G +D+VTW H Y++GR DFL +LD +
Hpa1     264 YGPDVGGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYILNGRTATREDFLNPVDVLDIFISSV 323

Hpa2c     362 RKIQKVVNTYTPGKKIWLEGVVVTSAGGTNNLSDSYAAGFLWLNTLGMLANQGIDVVIRH 421
           +K+ +VV + PGKK+WL + GG LSD++AAGF+WL+ LG+ A GI+VV+R
Hpa1     324 QKVFQVVESTRPGKKWLGETSSAYGGGAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQ 383

Hpa2c     422 SFFDHGYNHLVDQNFNPLPDYWLSLLYKRLIGPKVLAVHVAGLQKRPGRVIRDKLRIV 481
           FF G HLVD+NF+PLPDYWLSLL+K+L+G KVL V G +R+ KLR+Y
Hpa1     384 VFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLMASVQGSKRR-----KLRVY 434

Hpa2c     482 AHCTNHHHHNYVRGSITLFIINLHRSRKKIKLAGTLRDKLVHQYLLQPYGQEGLSKSVQ 541
           HCTN N Y G +TL+ INLH K ++L +K V +YLL+P G GL SKSVQ
Hpa1     435 LHCTNTDNPRYKEGDLTLYAINLHNVTKYLRPLPYPFSNKQVDKYLLRPLGPHGLLSKSVQ 494

Hpa2c     542 LNGQPLVMVDDGTLPELKPRPIRAGRTLVI PPVIMGFFVVKVNALAC 589
           LNG L MVDD TLP L +PIR G +L +P + FFV++N AC
Hpa1     495 LNGLTLKMVDDQTLPLMEKPLRPGSSSLGLPAFSYSFFVIRNAKVAAC 542
  
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