

BLASTx Search Outputs of the DNA sequence at the Parental Locus of Maize Event DAS-40278-9 against GenBank Non-redundant Protein Sequences “nr”

BLASTX 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), “Gapped BLAST and PSI-BLAST: a new generation of protein database search programs”, *Nucleic Acids Res.* 25:3389-3402.

Query= DAS-40278-9\Original\Locus
(2212 letters)

Database: /usr/local/blast/db/blastlibs/nr
10,862,569 sequences; 3,701,345,023 total letters

Searching..... done

Sequences producing significant alignments:	Score	E
	(bits)	Value
gb AAP94585.1 putative gag-pol precursor [Zea mays]	304	4e-80
gb EEC72934.1 hypothetical protein OsI_06790 [Oryza sativa Indi...	47	0.010
ref NP_001046582.1 Os02g0288200 [Oryza sativa (japonica cultiva...	47	0.010
ref XP_001924431.1 PREDICTED: similar to Sister chromatid cohes...	44	0.085
ref XP_002720626.1 PREDICTED: PDS5, regulator of cohesion maint...	43	0.15
ref XP_001494417.2 PREDICTED: similar to KIAA0979 protein [Equu...	43	0.19
ref XP_613447.3 PREDICTED: similar to KIAA0979 protein [Bos tau...	42	0.25
ref XP_002147803.1 class III chitinase ChiA1 [Penicillium marne...	42	0.42
ref XP_001118201.1 PREDICTED: similar to androgen-induced prost...	41	0.55
ref XP_001690916.1 extracellular matrix protein [Chlamydomonas ...	41	0.72
gb AAB53953.1 amino acid feature: rod protein domain, aa 266	41	0.72
ref NP_518660.1 ATP-dependent RNA helicase protein [Ralstonia s...	40	0.94
ref ZP_00946209.1 UROPORPHYRINOGEN-III SYNTHASE / Uroporphyrin-...	40	1.2
ref XP_001703772.1 calcineurin-like phosphoesterase family prot...	40	1.2
ref NP_998607.1 serine/arginine repetitive matrix 1 [Danio reri...	40	1.6
ref ZP_06358420.1 methyl-accepting chemotaxis sensory transduce...	39	2.7
ref XP_002545229.1 hypothetical protein CTRG_00010 [Candida tro...	39	2.7
ref ZP_01731188.1 hypothetical protein CY0110_12282 [Cyanothece...	39	2.7
ref YP_001360075.1 response regulator receiver modulated CheB m...	39	2.7
ref XP_002440032.1 hypothetical protein SORBIDRAFT_09g024830 [S...	39	3.6
gb AAI66483.1 Tbc1d9b protein [Rattus norvegicus]	39	3.6
gb EDM04252.1 similar to TBC1 domain family, member 8; BUB2-lik...	39	3.6
ref NP_001101744.1 TBC1 domain family, member 9B [Rattus norveg...	39	3.6
emb CAF97873.1 unnamed protein product [Tetraodon nigroviridis]	39	3.6
tpe CBF69865.1 TPA: cytochrome c (Eurofung) [Aspergillus nidula...	38	4.7
ref ZP_04606890.1 NLP/P60 protein [Micromonospora sp. ATCC 3914...	38	4.7

ref XP_001513638.1	PREDICTED: similar to amyloid precursor-like...	38	4.7
ref XP_368121.2	hypothetical protein MGG_01123 [Magnaporthe gri...	38	4.7
ref XP_001470260.1	hypothetical protein [Leishmania infantum] >...	38	4.7
ref XP_001208907.1	hypothetical protein ATEG_01542 [Aspergillus...	38	4.7
ref NP_595234.1	RNAPII degradation factor (predicted) [Schizosa...	38	4.7
ref XP_001698611.1	hydroxyproline-rich cell wall protein [Chlam...	38	6.1
ref XP_001367617.1	PREDICTED: similar to KIAA0979 protein [Mono...	38	6.1
ref XP_001321923.1	hypothetical protein [Trichomonas vaginalis ...	38	6.1
ref XP_001291104.1	surface antigen BspA-like [Trichomonas vagin...	38	6.1
ref ZP_04365811.1	alanyl-tRNA synthetase [Cellulomonas flavigen...	37	8.0
gb EFE41315.1	hypothetical protein TRV_03963 [Trichophyton verr...	37	8.0
gb EFE33790.1	hypothetical protein ARB_07255 [Arthroderma benha...	37	8.0
emb CBA33079.1	hypothetical protein [Curvibacter putative symbi...	37	8.0
ref XP_001499099.2	PREDICTED: similar to Protein MCM10 homolog ...	37	8.0
gb EDL25622.1	mCG1547 [Mus musculus]	37	8.0
ref YP_001223207.1	hypothetical protein CMM_2463 [Clavibacter m...	37	8.0
sp P55200.2	MLL1_MOUSE RecName: Full=Histone-lysine N-methyltran...	37	8.0
ref XP_001263507.1	spindle-pole body protein (Pcp1), putative [...	37	8.0
ref XP_001272992.1	nuclear condensin complex subunit Smc4, puta...	37	8.0
ref YP_603300.1	Fibronectin-binding protein [Streptococcus pyog...	37	8.0
ref NP_001074518.1	myeloid/lymphoid or mixed-lineage leukemia 1...	37	8.0
ref YP_138567.1	glucan binding protein [Streptococcus thermophi...	37	8.0
dbj BAE24386.1	unnamed protein product [Mus musculus]	37	8.0
pir A48205	All-1 protein +GTE form - mouse (fragment)	37	8.0
gb AAA62593.1	All-1 protein [Mus musculus]	37	8.0
ref XP_754682.1	spindle-pole body protein (Pcp1) [Aspergillus f...	37	8.0
ref XP_659690.1	hypothetical protein AN2086.2 [Aspergillus nidu...	37	8.0
ref XP_958911.1	hypothetical protein NCU09139 [Neurospora crass...	37	8.0

>gb|AAP94585.1| putative gag-pol precursor [Zea mays]
Length = 1833

Score = 304 bits (778), Expect = 4e-80
Identities = 176/329 (53%), Positives = 200/329 (60%)
Frame = +1

Query: 1225 MTITSKCKIALRPGTMFCFGTISSEIADDEEGLHRIADLLEKKLSSEISRGARAEQRVAPS 1404
M +T KIA+RPG++FCFGTISS+ADEEG LH +ADL E+K S A
Sbjct: 1 MAVTFHSKIIVRPGSVFCFGTISSEIADDEEGLHRIADLLEKKLSSEISRGARAEQRVAPS 1404

Query: 1405 PAPQAKMTSYKPKVGSPPTRKTPPLSTPTKEWTRITRKKEASVPSQGTGTRQAIFFPTPSP 1584
PA + K+ S + SS TRK+PLSTSP+EWTR+ RKKE T RQ + P P
Sbjct: 57 PALRKKIVSGEAGARSSLTRKSPLSTPTREWTRVVRKKE-----TRERQIVLPVPPT 109

Query: 1585 SNEDGKKSALAPFYPDVLFIIRGRLELAPVFNDEPTMQGEXXXXXXXXXXXXXXXXXXXXXX 1764
S E+GKK A A PFYPDVLFI GR E V +DEPT GE
Sbjct: 110 SKENGKVVAAAIPFYPDVLFI--GRAESLAVSDDEPTAPGEEPPQRESRRRRRRRRNVRR 168

Query: 1765 HHEAGERDPAQPVSRDEALEVGKTPDEWVHXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 1944

HH AGE DP QPVS RDE EVG+TP+E V
Sbjct: 169 HHAAGEWDPEQPVS RDEVSEVGETPEERV----FRERRNSRRRDRRRTQEQA EQDARQRR 224

Query: 1945 XNALFARNLYPDFARAMNTPSEVGGVLAQIADGLPRTLDTGYRRL LTRAVNHLLPITNP 2124
N LF RNL PDFARAMNTPSEVGGVLA IADGLPRT D EGYRRL T+A NHLLP+ +P

Sbjct: 225 ENPLFGRNLPDFARAMNTPSEVGGVLAWIADGLPRT PDAEGYRRLFTQAANHLLPLAHP 284

Query: 2125 PSDLRHAINSRDRTRSSINASRDR*HESE 2211
P+DLRH INSRDR RSSINASR+R HE+E

Sbjct: 285 PNDLRHTINSRRDARSSINASRERRHENE 313

>gb|EEC72934.1| hypothetical protein OsI_06790 [Oryza sativa Indica Group]
Length = 556

Score = 47.0 bits (110), Expect = 0.010
Identities = 29/90 (32%), Positives = 46/90 (51%), Gaps = 4/90 (4%)
Frame = +1

Query: 1345 KKLSS EISRGARAEQRVAPSPAPQAKM TSYKPKV GSSPTRKTPL-STSP TKEWTRITRKK 1521
KK S++ ++ ++R AP PAP K KP+ SS P S+ +K+ + K

Sbjct: 87 KKESAKKAKAEAKKKRAAPEPAPSGKAKKAKPEKSSSAAAPEPAPSSGKSKKAAKAEAAK 146

Query: 1522 EAS---VPSQGTGTRQAI FPTSPS NEDGK 1602
A+ PS G ++ + P P S P S++ GK

Sbjct: 147 AAAAEPAPSTGKVS KYNLAPEPSPSSKSGK 176

>ref|NP_001046582.1| Os02g0288200 [Oryza sativa (japonica cultivar-group)]
dbj|BAD21720.1| putative Neurofilament triplet M protein [Oryza sativa Japonica
Group]
dbj|BAF08496.1| Os02g0288200 [Oryza sativa Japonica Group]
Length = 578

Score = 47.0 bits (110), Expect = 0.010
Identities = 29/90 (32%), Positives = 46/90 (51%), Gaps = 4/90 (4%)
Frame = +1

Query: 1345 KKLSS EISRGARAEQRVAPSPAPQAKM TSYKPKV GSSPTRKTPL-STSP TKEWTRITRKK 1521
KK S++ ++ ++R AP PAP K KP+ SS P S+ +K+ + K

Sbjct: 109 KKESAKKAKAEAKKKRAAPEPAPSGKAKKAKPEKSSSAAAPEPAPSSGKSKKAAKAEAAK 168

Query: 1522 EAS---VPSQGTGTRQAI FPTSPS NEDGK 1602
A+ PS G ++ + P P S P S++ GK

Sbjct: 169 AAAAEPAPSTGKVS KYNLAPEPSPSSKSGK 198

>ref|XP_001924431.1| PREDICTED: similar to Sister chromatid cohesion protein PDS5 homolog
B (Androgen-induced proliferation inhibitor)

(Androgen-induced prostate proliferative
shutoff-associated protein AS3) [Sus scrofa]
Length = 617

Score = 43.9 bits (102), Expect = 0.085
Identities = 32/102 (31%), Positives = 47/102 (46%), Gaps = 1/102 (0%)
Frame = +1

Query: 1294 SIADDEEGLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQA-KMTSYKPKVGSPPTRKT 1470
S A+EE R + E+K S+ R +R Q+ A SP A + T P+ G KT
Sbjct: 491 SAAEEEEEEERQSGNTEQKSKSKQHRTSRRRAQQRAESPETSVESTQSTPQKGRGRPSKT 550

Query: 1471 PLSTSPTKEWTRITRKKEASVPSQGTGTRQAIFFTPSPSNED 1596
P + P K R+ R K+A+ + +F SP N+D
Sbjct: 551 PSPSQPKN-VRLGRSKQAATKENDSSEEVDVFGSSPVNDD 591

>ref|XP_002720626.1| PREDICTED: PDS5, regulator of cohesion maintenance, homolog B-like
[Oryctolagus cuniculus]
Length = 1408

Score = 43.1 bits (100), Expect = 0.15
Identities = 31/100 (31%), Positives = 46/100 (46%), Gaps = 1/100 (1%)
Frame = +1

Query: 1300 ADEEGLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQA-KMTSYKPKVGSPPTRKTPL 1476
A+EE R + E+K S+ R +R Q+ A SP A + T P+ G KTP
Sbjct: 1284 AEEEEEEERQSVNAEQKSKSKQHRASRRRAQQRAESPETSVESTQSTPQKGRGRPSKTTPS 1343

Query: 1477 STSPTKEWTRITRKKEASVPSQGTGTRQAIFFTPSPSNED 1596
+ P K R+ R K+A+ + +F SP N+D
Sbjct: 1344 PSQPKN-VRVGRSKQAATKENDSSEEVEVFGNSPVNDD 1382

>ref|XP_001494417.2| PREDICTED: similar to KIAA0979 protein [Equus caballus]
Length = 1469

Score = 42.7 bits (99), Expect = 0.19
Identities = 31/102 (30%), Positives = 47/102 (46%), Gaps = 1/102 (0%)
Frame = +1

Query: 1294 SIADDEEGLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQA-KMTSYKPKVGSPPTRKT 1470
S A+EE + + E+K S+ R +R Q+ A SP A + T P+ G KT
Sbjct: 1343 SAAEEEEEEEKQSGNTEQKSKSKQHRMSRRRAQQRAESPETSVESTQSTPQKGRGRPSKT 1402

Query: 1471 PLSTSPTKEWTRITRKKEASVPSQGTGTRQAIFFTPSPSNED 1596
P + P K R+ R K+A+ + +F SP N+D
Sbjct: 1403 PSPSQPKN-VRVGRSKQAATKENDSSEEVDVFGSSPVNDD 1443

>ref|XP_613447.3| PREDICTED: similar to KIAA0979 protein [Bos taurus]
Length = 1463

Score = 42.4 bits (98), Expect = 0.25
Identities = 31/102 (30%), Positives = 48/102 (47%), Gaps = 1/102 (0%)
Frame = +1

Query: 1294 SIADEEGTLHRIADLLEKKLSSEISRGARAEQVAPSP-APQAKMTSYKPKVGSSPTRKT 1470
S A+EE R + E+K S+ R +R Q+ A SP A+ T P+ G KT
Sbjct: 1337 SAAEEEEEEERQSGNTEQKSKSKQHRTSRRAQQRAESPDTTAAEPTQSTPQKGRGGPSKT 1396

Query: 1471 PLSTSPTKEWTRITRKKEASVPSQGTGTRQAIFFPTSPSNED 1596
P + P K+ R+ R K+A+ + +F SP N++
Sbjct: 1397 PSPSQPPK-VRVGRSKQAATKENDSSEEIDVFGSSPVNDE 1437

>ref|XP_002147803.1| class III chitinase ChiA1 [Penicillium marneffei ATCC 18224]
gb|EEA24292.1| class III chitinase ChiA1 [Penicillium marneffei ATCC 18224]
Length = 854

Score = 41.6 bits (96), Expect = 0.42
Identities = 46/195 (23%), Positives = 74/195 (37%), Gaps = 3/195 (1%)
Frame = +1

Query: 1015 VVYYASLSGPNLQKTAYPSLVRPARTIELQSTAPSYPKAPQGVALGVRTDSKHRQLARQV 1194
+V+YA+ P+ T P+ P T S+A + + + S +
Sbjct: 329 LVHYATTIAPSPTPTPTPTPPSTASVSSAATSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 388

Query: 1195 GGVSLI*ASSMTITSCKIALRPGTMFCFGTISIADEEGTLHRIADLLEKKLSSEI--- 1365
+SS +T P + SS + + +D + SS
Sbjct: 389 -----SSSVVTPPTPTPTPSGSSSSSSSSSSSSSSAAVSSSDAVSSASSSAASS 441

Query: 1366 SRGARAEQVAPSPAPQAKMTSYKPKVGSSPTRKTPLSTSPTKEWTRITRKKEASVPSQG 1545
S A + A S +P A T+ +P SS TRKTP +SP T +V S
Sbjct: 442 SAAVSSSSSAVSSSPAASSTAVRPTRSSCTRKTPSPSSPAVIST--PSPSSPAVVSTP 499

Query: 1546 TGTRQAIFFPTSPSN 1590
+ + A+ TPSPS+
Sbjct: 500 SPSSPAVVSTPSPSS 514

>ref|XP_001118201.1| PREDICTED: similar to androgen-induced prostate proliferative shutoff
associated protein [Macaca mulatta]
Length = 1528

Score = 41.2 bits (95), Expect = 0.55
Identities = 30/99 (30%), Positives = 45/99 (45%), Gaps = 1/99 (1%)
Frame = +1

Query: 1303 DEEGTLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQA-KMTSYKPKVGSSPTRKTPLS 1479
+EE R + E+K S+ R +R Q+ A SP A + T P+ G KTP
Sbjct: 1405 EEEEEERQSGNTEQKSKSKQHRVSRRAQQRAESPESAIESTQSTPQKGRGRPSKTPSP 1464

Query: 1480 TSPTKEWTRITRKKEASVPSQGTGTRQAIFFTPSPSNED 1596
+ P K R+ R K+A+ + +F SP N+D
Sbjct: 1465 SQPKKN-VRVGRSKQAATKENDSSEEVDVFGSSPVNDD 1502

>ref|XP_001690916.1| extracellular matrix protein [Chlamydomonas reinhardtii]
gb|EDP05362.1| extracellular matrix protein [Chlamydomonas reinhardtii]
Length = 474

Score = 40.8 bits (94), Expect = 0.72
Identities = 31/117 (26%), Positives = 46/117 (39%), Gaps = 9/117 (7%)
Frame = +1

Query: 1264 GTMFCFGTISSIADEEGTLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQAKMT----- 1428
G+ F + D G +A+ S S A +V+PSP+P+A +
Sbjct: 236 GSSFAMPHLKGIEDMSGVAVTLANFNRTGASPSPSPKASPSPKVSPSPKASPSPSPKA 295

Query: 1429 ----SYKPKVGSSPTRKTPLSTSPKEWTRITRKKEASVPSQGTGTRQAIFFTPSPS 1587
S PK SP+ S SP+ + K + PS + A P+PSPS
Sbjct: 296 SPSPSPKASPSPSPKASPSPSPSPSPKASPSPSPSVQASKPSPSPS 352

>gb|AAB53953.1| amino acid feature: rod protein domain, aa 266 .. 468; amino acid
feature: globular protein domain, aa 32 .. 265
[Chlamydomonas reinhardtii]
Length = 473

Score = 40.8 bits (94), Expect = 0.72
Identities = 31/117 (26%), Positives = 46/117 (39%), Gaps = 9/117 (7%)
Frame = +1

Query: 1264 GTMFCFGTISSIADEEGTLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQAKMT----- 1428
G+ F + D G +A+ S S A +V+PSP+P+A +
Sbjct: 236 GSSFAMPHLKGIEDMSGVAVTLANFNRTGASPSPSPKASPSPKVSPSPKASPSPSPKA 295

Query: 1429 ----SYKPKVGSSPTRKTPLSTSPKEWTRITRKKEASVPSQGTGTRQAIFFTPSPS 1587
S PK SP+ S SP+ + K + PS + A P+PSPS
Sbjct: 296 SPSPSPKASPSPSPKASPSPSPSPSPKASPSPSPSVQASKPSPSPS 352

>ref|NP_518660.1| ATP-dependent RNA helicase protein [Ralstonia solanacearum GMI1000]
emb|CAD14067.1| probable atp-dependent rna helicase protein [Ralstonia solanacearum
GMI1000]
Length = 540

Score = 40.4 bits (93), Expect = 0.94
Identities = 23/89 (25%), Positives = 41/89 (46%), Gaps = 3/89 (3%)
Frame = +1

Query: 1303 DEEGLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQAKMTSYKPKVG---SSPTRKTP 1473
DE G L I L++++L + G + +AP P P + ++ P+ G S P R+
Sbjct: 357 DEHGLLRDIERLIKRELPRTVLAGFEPDPTIAPEPIPNGRNSARAPRQGGGRSQPPRQAA 416

Query: 1474 LSTSPTKEWTRITRKKEASVPSQGTGTRQ 1560
+ +P + ++E+ QG G Q
Sbjct: 417 GNAAPREPRAPREPREREGASGQGQGGQ 445

>ref|ZP_00946209.1| UROPORPHYRINOGEN-III SYNTHASE / Uroporphyrin-III C-methyltransferase
[Ralstonia solanacearum UW551]
gb|EAP71324.1| UROPORPHYRINOGEN-III SYNTHASE / Uroporphyrin-III C-methyltransferase
[Ralstonia solanacearum UW551]
Length = 1065

Score = 40.0 bits (92), Expect = 1.2
Identities = 37/121 (30%), Positives = 44/121 (36%), Gaps = 8/121 (6%)
Frame = +3

Query: 1608 RHRAGSFLPRRPLHQGEIGVSTRLQR*ANHARGRASP*AATTEE*KPERAATSRGW--- 1778
R R G PRRPL QG + R A H R R S +P RAA RG
Sbjct: 115 RARRGPRRPRRPLAQGRADGAPAGLRAAGHPRARARSARCLCLQPVRPRRAARGRGGGHV 174

Query: 1779 -----GTGSGATRIPGRSFRSRKNSRRVGTTPRKAELXXXXXXXXLGPTRASRARCKAAP 1943
G +GA PG +R++ G R L G R RA+ A
Sbjct: 175 EPAPRGVAAGAVSAPGHPAAARQSRHAPGQARPRRLR-----GHHPRGCRAQAAGAV 226

Query: 1944 R 1946
R
Sbjct: 227 R 227

>ref|XP_001703772.1| calcineurin-like phosphoesterase family protein [Chlamydomonas
reinhardtii]
gb|ED096298.1| calcineurin-like phosphoesterase family protein [Chlamydomonas
reinhardtii]
Length = 382

Score = 40.0 bits (92), Expect = 1.2
Identities = 29/77 (37%), Positives = 37/77 (48%), Gaps = 6/77 (7%)
Frame = -1

Query: 1894 LVGDHG----GESSAFLGVPTREFFLLKLRPGIR--VAPDPVPQPRDVAARSGFYSSV 1733
++GDH G + FLG T R+F L+K R G APDP+ + RD AAR+ SS

Sbjct: 120 VMGDHRYATPGANLEFLGFSTWRDFCALMKRRSGCNGAGAPDPLQERRDAAARAS--SSP 177

Query: 1732 VAPHAGEALPLAWLAHR 1682
P WL R

Sbjct: 178 HTASMARLAPYNWLRSR 194

>ref|NP_998607.1| serine/arginine repetitive matrix 1 [Danio rerio]
gb|AAH58068.1| Serine/arginine repetitive matrix 1 [Danio rerio]
Length = 896

Score = 39.7 bits (91), Expect = 1.6
Identities = 24/80 (30%), Positives = 35/80 (43%), Gaps = 4/80 (5%)
Frame = +1

Query: 1378 RAEQVRVAPSPAPQAKMTSYKPKVGSPTKTRKPLSTSPKTRITRKRKEASVPSQGTGTR 1557
R QR + SP P+ + S P P +K P S SP++ +R P
Sbjct: 772 RKSQRGSQSPPERRQVSRSPSASPPPAQKRPASVSPSRSTSR-----SPPPPAKKN 823

Query: 1558 QAIFPTSPSN----EDGKK 1605
++ P+PSP+ E GKK
Sbjct: 824 SSVSPSPSPNKNSDAEGGKK 843

>ref|ZP_06358420.1| methyl-accepting chemotaxis sensory transducer [Rhodopseudomonas
palustris DX-1]
gb|EFC25518.1| methyl-accepting chemotaxis sensory transducer [Rhodopseudomonas
palustris DX-1]
Length = 563

Score = 38.9 bits (89), Expect = 2.7
Identities = 42/168 (25%), Positives = 73/168 (43%), Gaps = 11/168 (6%)
Frame = +1

Query: 961 LHSGDLACNPPHIDPSQEVVYASLSGPNLQKTAYPSLVRPARTIELQSTAPSYPKAPQG 1140
L GDLA PH S E+ A + + A + + A + +A +
Sbjct: 230 LGRGDLA AEVPHRGESTEIGAMADAL-----QIFKEALIAKRDADAAAAREAEK 279

Query: 1141 VALGVRTDSKHRQLARQVGGV-----SLI*ASSMTITSKCKIALRPGTMFCFGTISS 1296
+A G R D+ RQ R +G + + + AS+ T+TS + + T +++++
Sbjct: 280 IARGQRVDAATRQFERAIGEIVETVSSASTELEASAGTLTSTADRSQQLAT-----SVAA 334

Query: 1297 IADEEGT-LHRIADLLEKKLSS--EISRGARAEQVRVAPSPAPQAKMTS 1431
++E T + +A E+ SS EISR + R+A QA+ T+
Sbjct: 335 ASEEASTNVQSVASATEEMSSSITEISRQVQESSRIASEAVEQARKTN 382

>ref|XP_002545229.1| hypothetical protein CTRG_00010 [Candida tropicalis MYA-3404]
gb|EER35271.1| hypothetical protein CTRG_00010 [Candida tropicalis MYA-3404]

Length = 1006

Score = 38.9 bits (89), Expect = 2.7
Identities = 34/125 (27%), Positives = 48/125 (38%), Gaps = 4/125 (3%)
Frame = +1

Query: 1279 FGTISSIADEEGLHRIADLLEKKLSSEISRGARAEQRV----APSPAPQAKMTSYKPKV 1446
+ T D E + HR + +K SS A +Q AP+P Q K++ V
Sbjct: 288 YATPGGSKDIEASKHRFQQQIVQKYSSNAPTPAPMQQSPMSSAPTPHQQRKLSRASNSV 347

Query: 1447 GSSPTRKTPLSTSPKTRITRKEASVPSQGTGTRQAIFFTPSPSNEDGKKSALALAP 1626
+SP +P T+P R+ +A VP A P P P + S AP
Sbjct: 348 HNSPNVNSPYQTTP-----RQSQAPVVPVNPAPASQTPVVPVVPAPTQNSVPPSAP 399

Query: 1627 FYPDV 1641
P V
Sbjct: 400 PQPVV 404

>ref|ZP_01731188.1| hypothetical protein CY0110_12282 [Cyanothecae sp. CCY0110]
gb|EAZ89412.1| hypothetical protein CY0110_12282 [Cyanothecae sp. CCY0110]
Length = 315

Score = 38.9 bits (89), Expect = 2.7
Identities = 38/123 (30%), Positives = 53/123 (43%), Gaps = 4/123 (3%)
Frame = +1

Query: 1231 ITSKCKIALRPGTMFCFGTSSIADEEGLHRIADLLEKKLSS--EISRGARAEQRVAPS 1404
+ SK ++ RP MF I I L L EKK EI + + PS
Sbjct: 10 LLSKFRVLRFP--MFFLSLIFHIGFLSLPLPSSPKLEEKKTEEQEEIQEKVEITRLIPPS 67

Query: 1405 PAPQAKMTSYKPKVGSPPTRKTPLSTSPKTRITRKEAS-VPSQGTGTRQAIFFTP 1578
P P + PKV S+PT + P+ PT ++ RIT ++ + + T I P P
Sbjct: 68 PQSPETPKTPPKVKSTPTPQ-PIQRPTVRQIPRITTPSPSTQITATPEKTPLQINPEP 126

Query: 1579 SPS 1587
SPS
Sbjct: 127 SPS 129

>ref|YP_001360075.1| response regulator receiver modulated CheB methyltransferase
[Kineococcus radiotolerans SRS30216]
gb|ABS01811.1| response regulator receiver modulated CheB methyltransferase
[Kineococcus radiotolerans SRS30216]
Length = 419

Score = 38.9 bits (89), Expect = 2.7
Identities = 30/87 (34%), Positives = 38/87 (43%)
Frame = +1

Query: 1285 TISSIADEEGTLHRIADLLEKKSSEISRGARAEQRVAPSPAPQAKMTSYKPKVGSSPTR 1464
T IADE L IAD ++++L GAR P A S +P V +SPTR
Sbjct: 340 TREGIADEVLPISAIADAIQRRLLGP----GARTASAPHPAARPPAAGSTRPTVSTSPTR 395

Query: 1465 KTPLSTSPTKEWTRITRKKEASVPSQG 1545
TP + P A+ PSQG
Sbjct: 396 STPPARPPASR-----PAAPAARPSQG 417

>ref|XP_002440032.1| hypothetical protein SORBIDRAFT_09g024830 [Sorghum bicolor]
gb|EES18462.1| hypothetical protein SORBIDRAFT_09g024830 [Sorghum bicolor]
Length = 305

Score = 38.5 bits (88), Expect = 3.6
Identities = 32/112 (28%), Positives = 49/112 (43%), Gaps = 15/112 (13%)
Frame = +1

Query: 1351 LSSEISRGARAEQ-----RVAPSPAPQAKMTSYKPKVGSSPTRKTPLSTSPT 1491
+S E+SRGAR E+ R +PSP P + G P R++P SP
Sbjct: 141 VSGEVSRGARRERGVPGGAGGRPGGGRASPPPPQQPRRRDVTGERPARRSP---SPA 197

Query: 1492 KEWTRITRKKEASVPSQGTGT-RQAIFFPTSP-SNEDGKKSALAPFYPDV 1641
+ T+ R+ A S +GT R+ P P ++ A AP +P++
Sbjct: 198 AKRTQEQRRTVAGAGSAASGTQRKPPVPMARPCGRASPRRQEAPAPAHPEL 249

>gb|AAI66483.1| Tbc1d9b protein [Rattus norvegicus]
Length = 730

Score = 38.5 bits (88), Expect = 3.6
Identities = 34/131 (25%), Positives = 55/131 (41%)
Frame = +1

Query: 1219 SSMTITSKCKIALRPGTMFCFGTISSIADEEGTLHRIADLLEKKSSEISRGARAEQRVA 1398
SS + S I+ + F F +++ D + + RI+D L+K S + A +
Sbjct: 357 SSSVLPSPSISTKSKMTFLF---ANLKDRDFLVQRISDFLQKTPSKQTGSIAGGTKASV 413

Query: 1399 PSPAPQAKMTSYKPKVGSSPTRKTPLSTSPTKEWTRITRKKEASVPSQGTGTRQAIFFPTP 1578
P PAP++ T P+ S P TSPT + +P+ G + +F
Sbjct: 414 PDPAPESLPT---PQEASEP-----PTSPTSPLSSPLSFSTQEIPTTSQGLLK-VFQKN 463

Query: 1579 SPSNEDGKKS A 1611
SP + G K A
Sbjct: 464 SPMEDLGAKGA 474

>gb|EDM04252.1| similar to TBC1 domain family, member 8; BUB2-like protein 1;
vascular Rab-GAP/TBC-containing (predicted), isoform

CRA_b [Rattus norvegicus]
Length = 1156

Score = 38.5 bits (88), Expect = 3.6
Identities = 34/131 (25%), Positives = 55/131 (41%)
Frame = +1

Query: 1219 SSMTITSKCKIALRPGTMFCFGTISSIADEEGLHRIADLLEKKLSSEISRGARAEQRVA 1398
SS + S I+ + F F +++ D + + RI+D L+K S + A +
Sbjct: 286 SSSVLPSPSISTKSKMTFLF---ANLKDRDFLVQRISDFLQKTPSKQTGSIAGGTKASV 342

Query: 1399 PSPAPQAKMTSYKPKVSSPTRKTPLSTSPTKEWTRITRKKEASVPSQGTGTRQAIPTP 1578
P PAP++ T P+ S P TSPT + +P+ G + +F
Sbjct: 343 PDPAPESLPT---PQEASEP-----PTSPTSPLSSPLSFSTQEIPTTSQGLLK-VFQKN 392

Query: 1579 SPSNEDGKKS A 1611
SP + G K A
Sbjct: 393 SPMEDLGAKGA 403

>ref|NP_001101744.1| TBC1 domain family, member 9B [Rattus norvegicus]
gb|EDM04251.1| similar to TBC1 domain family, member 8; BUB2-like protein 1;
vascular Rab-GAP/TBC-containing (predicted), isoform
CRA_a [Rattus norvegicus]
Length = 1262

Score = 38.5 bits (88), Expect = 3.6
Identities = 34/131 (25%), Positives = 55/131 (41%)
Frame = +1

Query: 1219 SSMTITSKCKIALRPGTMFCFGTISSIADEEGLHRIADLLEKKLSSEISRGARAEQRVA 1398
SS + S I+ + F F +++ D + + RI+D L+K S + A +
Sbjct: 357 SSSVLPSPSISTKSKMTFLF---ANLKDRDFLVQRISDFLQKTPSKQTGSIAGGTKASV 413

Query: 1399 PSPAPQAKMTSYKPKVSSPTRKTPLSTSPTKEWTRITRKKEASVPSQGTGTRQAIPTP 1578
P PAP++ T P+ S P TSPT + +P+ G + +F
Sbjct: 414 PDPAPESLPT---PQEASEP-----PTSPTSPLSSPLSFSTQEIPTTSQGLLK-VFQKN 463

Query: 1579 SPSNEDGKKS A 1611
SP + G K A
Sbjct: 464 SPMEDLGAKGA 474

>emb|CAF97873.1| unnamed protein product [Tetraodon nigroviridis]
Length = 1257

Score = 38.5 bits (88), Expect = 3.6
Identities = 33/105 (31%), Positives = 47/105 (44%), Gaps = 1/105 (0%)
Frame = +1

Query: 1330 ADLLEKLSSEISRGARAEQRVAPSPAPQAKMTSYKPKVGSSPTRKTPLSTSPTKEWTRI 1509
A++ EKKL+ + + R S P + TS P VG+SP + P S S + +
Sbjct: 423 ANMQEKLAGQ--QRTRPNMGALRSKGPVVQYTSDBGP-VGASPVKSPPTSPSQPPQTSPQ 479

Query: 1510 TRKKEASVPSQGTGTRQ-AIFPTSPSNEDGKKSALAPFYPDV 1641
T+ S P Q Q A P P ++ KKS +PF P V
Sbjct: 480 TQHPPPSEPQQAQAPQPAPLPRPEGKHQMAKKST---SPFVPGV 521

>tpe|CBF69865.1| TPA: cytochrome c (Eurofung) [Aspergillus nidulans FGSC A4]
Length = 130

Score = 38.1 bits (87), Expect = 4.7
Identities = 24/79 (30%), Positives = 37/79 (46%), Gaps = 1/79 (1%)
Frame = +1

Query: 1315 TLHRIADLLEKLSSEISRGARAEQ-RVAPSPAPQAKMTSYKPKVGSSPTRKTPLSTSPT 1491
TL R A +S +S R + R P+P P ++ TS + S T +TP S+SP
Sbjct: 26 TLSRTAAATRSAPTSTVSSAVRLVRLRATPTPMTSRPTSPGTRTLCSSTSRTPRSSSPV 85

Query: 1492 KEWTRITRKKEASVPSQGT 1548
W + ++ P +GT
Sbjct: 86 PRWLSVVSRR----PRRGT 100

>ref|ZP_04606890.1| NLP/P60 protein [Micromonospora sp. ATCC 39149]
gb|EEP72820.1| NLP/P60 protein [Micromonospora sp. ATCC 39149]
Length = 491

Score = 38.1 bits (87), Expect = 4.7
Identities = 29/74 (39%), Positives = 35/74 (47%)
Frame = +1

Query: 1366 SRGARAEQRVAPSPAPQAKMTSYKPKVGSSPTRKTPLSTSPTKEWTRITRKKEASVPSQG 1545
SR A + V PAP K T+ PK PT TP T+PT + T T K P
Sbjct: 390 SRLYAATRNVGAVPAP--KPTTPTPK----PTTPTPKPTTPTPKPTTPTPKPTTPTPKPT 443

Query: 1546 TGTRQAIPTSPSPS 1587
T T + P+PSPS
Sbjct: 444 TPTPKPTTSPSPS 457

>ref|XP_001513638.1| PREDICTED: similar to amyloid precursor-like protein 1
[Ornithorhynchus anatinus]
Length = 425

Score = 38.1 bits (87), Expect = 4.7
Identities = 33/121 (27%), Positives = 52/121 (42%), Gaps = 2/121 (1%)

Frame = +1

Query: 1279 FGTISSIADEEGLHRIADLLEKKSSEISRGARAEQRVAPSPAPQAKMTSYKPKVGSSP 1458
FG +A+ E + HR ++ + E+ R +R+ Q SPAP P+ S
Sbjct: 202 FGHQERMAECESSAHR-----QRQAQEV-RDSRSSQPGHLS PAPS GSPCLAPQRASPL 254

Query: 1459 TRKTPLSTSPTKEWTRITRKEASVPSQG--TGTRQAIPTSPSNEGKKSALALAPFY 1632
P + PT W + +R AS P+QG G + P+P P G +++ L
Sbjct: 255 PPTAPDLSVPTDSWNKESRPSLASNPAQGRWAGGPRWADPSPLPRTTPGGETSSPLPGMP 314

Query: 1633 P 1635
P
Sbjct: 315 P 315

>ref|XP_368121.2| hypothetical protein MGG_01123 [Magnaporthe grisea 70-15]
gb|EDK02191.1| hypothetical protein MGG_01123 [Magnaporthe grisea 70-15]
Length = 1179

Score = 38.1 bits (87), Expect = 4.7
Identities = 19/56 (33%), Positives = 30/56 (53%)
Frame = +2

Query: 50 KGREGEDRWHERGVDDHDDASEEERVATTQGRKERDARSVKGVGEGRVGGMKDD 217
KG G+ +W +++G DD DD+ + E + +RDA +G G GR G + D
Sbjct: 1084 KGLRGKWKWSNKKGRDDEDEMDGEEVAVALKGRDAGRGRGGGGGRGRGGRPD 1139

>ref|XP_001470260.1| hypothetical protein [Leishmania infantum]
emb|CAM69455.1| hypothetical protein, conserved [Leishmania infantum]
Length = 912

Score = 38.1 bits (87), Expect = 4.7
Identities = 40/135 (29%), Positives = 55/135 (40%), Gaps = 2/135 (1%)
Frame = +1

Query: 1066 PSLVRP-ARTIELQSTAPSYPKAPQGVALGVRTDSKHRQLARQVGGVSLI*ASSMTITSK 1242
P LV P A TI ST P++ +P+ + V S+ R A G S SS + TSK
Sbjct: 626 PPLVHPKALTITSASTVPAHLSLPRRRSTTVSMPSRSRGTAPFRAGSSTATRSSASFTSK 685

Query: 1243 CKIALRPGTMFCFGTSSIADEEGLHRIADLLEKKSSEISRGARAEQRVAPSPAPQAK 1422
+ +RPG ++AD + H+ LSS R A V P
Sbjct: 686 RRSVVRPG-----NVADSLVSSHQRTHTAAASLSAEPRPAITAAAVPRDSTPSPS 736

Query: 1423 MTSY-KPKVGSSPTR 1464
TS P+ G +R
Sbjct: 737 GTSVATPRPGREKSR 751

>ref|XP_001208907.1| hypothetical protein ATEG_01542 [Aspergillus terreus NIH2624]
gb|EAU38299.1| hypothetical protein ATEG_01542 [Aspergillus terreus NIH2624]
Length = 1229

Score = 38.1 bits (87), Expect = 4.7
Identities = 29/102 (28%), Positives = 50/102 (49%), Gaps = 3/102 (2%)
Frame = +1

Query: 1246 KIALRPGTMFCFGTISIADEEGTLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQAKM 1425
K+ LR T+ G + + DE+ TL + LE +L+SEI R E R++ A++
Sbjct: 817 KVELRKTTLRLEGELKRLKDEKSTLLEAKESLENQLNSEIERATAEENRLS-----AEV 870

Query: 1426 TSYKPKVGSSP---TRKTPLSTSPTKEWTRITRKKEASVPSQ 1542
+ K+ +S R+ LS S + + R ++ EA + Q
Sbjct: 871 DQLQDKLQASAGGRDRELTLKSKLQRYERRIQELEALLEQQ 912

>ref|NP_595234.1| RNAPII degradation factor (predicted) [Schizosaccharomyces pombe
972h-]
sp|043024.1|YGVA_SCHPO RecName: Full=CUE domain-containing protein C354.10
emb|CAA17810.1| RNAPII degradation factor (predicted) [Schizosaccharomyces pombe]
Length = 963

Score = 38.1 bits (87), Expect = 4.7
Identities = 50/193 (25%), Positives = 80/193 (41%), Gaps = 6/193 (3%)
Frame = +1

Query: 1069 SLVRPARTIELQSTAPSYPKAPQGVVALGVRTD--SKHRQLARQVGGVSLI*ASSMTITSK 1242
SL +PA T +L S+ S KAP + D + + + + S AS +T +
Sbjct: 191 SLEKPAGTGDLPSSSEIS-TKAPASTTVSSSVDPGTINEDSSMKDHTTSNEQASVLTSANT 249

Query: 1243 CKIALRPGTMFCFGTISIADEEGTLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQAK 1422
GT GT +S +A K + + A++++V P+PAP +
Sbjct: 250 AASTNTNGT--AGGTSASAKSTSAADQAVAS--SKPIKKAWASVAKSKKKVTPAPAPAPE 305

Query: 1423 MTSYKPKVGSSPTRKTPLSTSPTKEWTRITRKKEASVP----SQGTGTRQAIPTPSPSN 1590
KP + S KT +S + + + +SVP SQ + T + TPS +
Sbjct: 306 SEPSKPSIAPSQPSKTNVSA-----YEKPAELSSSSVFPFKSQDSATPANVETTPSTAT 361

Query: 1591 EDGKKSALALAPF 1629
KKS APF
Sbjct: 362 SAPKKST---APF 371

>ref|XP_001698611.1| hydroxyproline-rich cell wall protein [Chlamydomonas reinhardtii]
gb|EDP08104.1| hydroxyproline-rich cell wall protein [Chlamydomonas reinhardtii]
Length = 398

Score = 37.7 bits (86), Expect = 6.1

Identities = 24/71 (33%), Positives = 33/71 (46%), Gaps = 1/71 (1%)
Frame = +1

Query: 1378 RAEQRVAPSPAPQAKMT-SYKPKVGSSPTRKTPLSTSPKTRITRKKEASVPSQGTGT 1554
+A +P+P+P+A + S PK SPT S SPT K + PS T
Sbjct: 285 KASPSPTSPKASPSPSPKASPSPTSPKASPSPTPS-----PKASPSPSPSPT 338

Query: 1555 RQAIPTSPSPS 1587
+ PTPSP+
Sbjct: 339 SPKVSPSPSPA 349

>ref|XP_001367617.1| PREDICTED: similar to KIAA0979 protein [Monodelphis domestica]
Length = 1448

Score = 37.7 bits (86), Expect = 6.1
Identities = 29/100 (29%), Positives = 45/100 (45%), Gaps = 1/100 (1%)
Frame = +1

Query: 1300 ADEEGLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQA-KMTSYKPKVGSSPTRKTPL 1476
A+EE R ++ +E+K R +R Q+ SP A + T P+ KTP
Sbjct: 1323 AEEEEEDRQSENMEQKQKGRQHRTSRRRAQQRTESSPESSAVESTQSTPQKRRGRPPKTPP 1382

Query: 1477 STSPTKEWTRITRKKEASVPSQGTGTRQAIPTSPSPSNED 1596
+ P K+ R R K+AS + +F + SP N+D
Sbjct: 1383 PSQP-KKTVRTGRSKQASSKENESSEEMDVFHSSSPVND 1421

>ref|XP_001321923.1| hypothetical protein [Trichomonas vaginalis G3]
gb|EAY09700.1| hypothetical protein TVAG_098350 [Trichomonas vaginalis G3]
Length = 3352

Score = 37.7 bits (86), Expect = 6.1
Identities = 22/64 (34%), Positives = 33/64 (51%)
Frame = +1

Query: 1435 KPKVGSSPTRKTPLSTSPKTRITRKKEASVPSQGTGTRQAIPTSPSPSNEDGKKSAL 1614
+PK S P + P S + K +I KKE S S+ + +PSP+N++ K +
Sbjct: 2350 QPKKASKPQNE-PHSQTQEKPKQDKIAEKKENSGESKPDNKESPVSSSPSPTNQENKPLSS 2408

Query: 1615 ALAP 1626
ALAP
Sbjct: 2409 ALAP 2412

>ref|XP_001291104.1| surface antigen BspA-like [Trichomonas vaginalis G3]
gb|EAX78174.1| surface antigen BspA-like [Trichomonas vaginalis G3]
Length = 432

Score = 37.7 bits (86), Expect = 6.1
Identities = 24/102 (23%), Positives = 46/102 (45%)
Frame = +1

Query: 1330 ADLLEKKSSEISRGARAEQRVAPSPAPQAKMTSYKPKVGSPTKTRKTPPLSTPTKEWTRI 1509
++L+ SS +++ E V P+ + ++ +P P+ TP +S T E +
Sbjct: 200 SELVTNSSSSHVTKIETPEPTVQ-KPSSSELSSSTIEPTPEPSSSTPEPSSSTPEPSSS 258

Query: 1510 TRKKEASVPSQGTGTRQAIPTSPSPSNEDGKKSALALAPFYP 1635
T + + P T T + PTP PS+ + ++ + P P
Sbjct: 259 TPEPKTPTPEPKTPTPEPKTPTPEPSSSTPESNSSTIEPKTP 300

>ref|ZP_04365811.1| alanyl-tRNA synthetase [Cellulomonas flavigena DSM 20109]
gb|EEN39000.1| alanyl-tRNA synthetase [Cellulomonas flavigena DSM 20109]
Length = 897

Score = 37.4 bits (85), Expect = 8.0
Identities = 30/112 (26%), Positives = 45/112 (40%)
Frame = +3

Query: 1347 EAFLRNLEGSQGRTAGGTITRTSSEDDLQTESRELTYPKNSAVHFAHKGVDTDYSKEGS 1526
+A ++ L GR GT+T + + T R ++A H HK + + G
Sbjct: 542 QAPIKGLSVHHGRLVDGTLTLGDTGTATIDTARRRAIARAHTATHMVHKALREEL---GD 598

Query: 1527 ECPESGDGNTPSHLSDAFALK*GWKEERHRAGSFLPRRPLHQGEIGVSTRLQ 1682
++G N PS L F R+G +P L Q E V+ RLQ
Sbjct: 599 TATQAGSENAPSRLRFD-----RSGQSVPASSLSQIEGRVNERLQ 639

>gb|EFE41315.1| hypothetical protein TRV_03963 [Trichophyton verrucosum HKI 0517]
Length = 293

Score = 37.4 bits (85), Expect = 8.0
Identities = 33/111 (29%), Positives = 52/111 (46%), Gaps = 7/111 (6%)
Frame = +1

Query: 1324 RIADLLEKKSSEISRGARAEQR----VAPSPAPQAKMTSYKPK-VGSSPTKTRKTPPLSTSP 1488
R A LL++ L S + R + P+ AP + ++ P+ V ++ R P S SP
Sbjct: 15 RQASLLQQILVSRLLTHTKRKQSESPALFPPTSAPDPTILFTPRPVYTTGRRDLPASCSP 74

Query: 1489 TKEW--TRITRKKEASVPSQGTGTRQAIPTSPSPSNEDGKKSALALAPFYP 1635
E T T+ + S+P+ R + PT SP+N +A LA +YP
Sbjct: 75 NDESSNTFATKASDLSLPTLEPIRNILTPTSSPTN-----AAQHLEAYYP 120

>gb|EFE33790.1| hypothetical protein ARB_07255 [Arthroderma benhamiae CBS 112371]
Length = 293

Score = 37.4 bits (85), Expect = 8.0
Identities = 33/111 (29%), Positives = 52/111 (46%), Gaps = 7/111 (6%)
Frame = +1

Query: 1324 RIADLLEKKLSSEISRGARAEQR----VAPSPAPQAKMTSYKPK-VGSSPTRKTPLSTSP 1488
R A LL++ L S + R + P+ AP + ++ P+ V ++ R P S SP
Sbjct: 15 RQASLLQQILVSRLLTHTKRRKQSESPALFPPTSAPDPTILTFTPRPVYTTGRRDLPTSCSP 74

Query: 1489 TKEW--TRITRKEASVPSQGTGTRQAIFFPTSPSNEDGKKSAIALAPFYP 1635
E T T+ + S+P+ R + PT SP+N +A LA +YP
Sbjct: 75 NDESSNTFATKASDLSLPTLEPIRNILTPTSSPTN-----AAQHLEAYYP 120

>emb|CBA33079.1| hypothetical protein [Curvibacter putative symbiont of Hydra
magnipapillata]
Length = 469

Score = 37.4 bits (85), Expect = 8.0
Identities = 40/164 (24%), Positives = 64/164 (39%), Gaps = 3/164 (1%)
Frame = +1

Query: 1129 APQG--VALGVRTDSKHRQLARQVGGVSLI*ASSMTITSKCKIALRPGTMFCFGTISSIA 1302
AP+G VA G D+ A+ + +S+ S PGT + ++IA
Sbjct: 196 APEGRNVASGRAVDATAADSAKTPASAPSVASSAAAPASSTATPAAPGT-----SAAAIA 250

Query: 1303 DEEGTLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQAKMTSYKPKVGSSPTR-KTPLS 1479
+ T+ + S A+ Q A +PAP A + P +S T K P+S
Sbjct: 251 AKPPTV-----AASSPAKPGQTAASAPAPAASTPARLPAAAASATAAKAPVS 298

Query: 1480 TSPTKEWTRITRKEASVPSQGTGTRQAIFFPTSPSNEDGKKSA 1611
+ + A P + T A P P+P+ G+K+A
Sbjct: 299 AAAPAVANKPAASASAVNPLRPAPTAASAPAPTPAKSSGEKAA 342

>ref|XP_001499099.2| PREDICTED: similar to Protein MCM10 homolog (HsMCM10) [Equus
caballus]
Length = 996

Score = 37.4 bits (85), Expect = 8.0
Identities = 38/137 (27%), Positives = 53/137 (38%), Gaps = 18/137 (13%)
Frame = +1

Query: 1279 FGTISSIADEE-----GTLHRIAD---LLEKKLSSEISRGARAEQRVAPSPAPQAKMTS 1431
FG + + DEE T +R+ L + K + E+ R Q S Q KM +
Sbjct: 199 FGDMDLTDDEEDVPALQSTKNRVLSAPALSQKTNQELQDELRLKLEQMKSLLEEQLKMAT 258

Query: 1432 YK-----PKVGSSPTRKTPLSTSPKEWTRITRK----KEASVPSQGTGTRQAIFFPTSP 1584
K P + SP K+P K+ RI +E VP+ R A P SP
Sbjct: 259 IKQPASPPVLHKSPVEKSPRPPLKEKKIQRIQESTCFSEELDVPAPPKTKRVARTPKVSP 318

Score = 37.4 bits (85), Expect = 8.0
Identities = 26/82 (31%), Positives = 38/82 (46%), Gaps = 2/82 (2%)
Frame = +1

Query: 1396 APSAPQAKMTSYKPKVGSSTPRKTPPLSTSTKEWTRITRKKEA--SVPSQGTGTRQAIF 1569
AP+PAP+ K S SS P + P + + +KKEA +VPS+ ++
Sbjct: 1275 APAPAPEPKQVSAPASRKSSKQVSQPAAVVPPQPSTAPQKKEAPKAVPSE---PKKKQP 1331

Query: 1570 PTPSPSNEDGKKSALALAPFYF 1635
P P P E K+ +A P P
Sbjct: 1332 PPPEPGPEQSKQKKVAPRPSIP 1353

>ref|XP_001263507.1| spindle-pole body protein (Pcp1), putative [Neosartorya fischeri NRRL
181]
gb|EAW21610.1| spindle-pole body protein (Pcp1), putative [Neosartorya fischeri NRRL
181]
Length = 1229

Score = 37.4 bits (85), Expect = 8.0
Identities = 19/51 (37%), Positives = 30/51 (58%)
Frame = +1

Query: 1246 KIALRPGTMFCFGTISIADEEGTLHRIADLLEKKLSSEISRGARAEQRVA 1398
KI LR T+ G + + D++ +L + LEK+LSSEI R + E R++
Sbjct: 815 KIDLRKSTLRLEGEVKRLKDDKASLLEAKESLEKQLSSEIERATQEENRLS 865

>ref|XP_001272992.1| nuclear condensin complex subunit Smc4, putative [Aspergillus
clavatus NRRL 1]
gb|EAW11566.1| nuclear condensin complex subunit Smc4, putative [Aspergillus
clavatus NRRL 1]
Length = 1441

Score = 37.4 bits (85), Expect = 8.0
Identities = 39/140 (27%), Positives = 63/140 (45%), Gaps = 6/140 (4%)
Frame = +1

Query: 1294 SIADEEGTLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQAKMTSY-KPKVGSSTPRKT 1470
S A+EEG L E++ S A A+QR + + +++++S P+ S PT +
Sbjct: 101 SDANEEGDS---IVLKEEPEPESPSQNAAAAQQRKSMAPRKSRSVSTPNPEKSSLPTPEP 157

Query: 1471 PLSTSTKEWTRITRKKEASVPSQGTGTRQAIFPTSPSNEDGKKSALALAPFYFDPVL-- 1644
+S P R + ASVP T A+ TP+ ++D K S I++ VL
Sbjct: 158 SVSPQPQP-----RSQRASVPPLADITESAVNQTPAKPSDDAKPSQISVINPNSTVLER 211

Query: 1645 ---FIRGRLELAPVFNDEPT 1695
+ LAP +EP+

Sbjct: 212 PMDIVAKSRTLAPPVPEEPS 231

>ref|YP_603300.1| Fibronectin-binding protein [Streptococcus pyogenes MGAS10750]
gb|ABF38756.1| Fibronectin-binding protein [Streptococcus pyogenes MGAS10750]
Length = 281

Score = 37.4 bits (85), Expect = 8.0
Identities = 26/81 (32%), Positives = 37/81 (45%), Gaps = 5/81 (6%)
Frame = +1

Query: 1384 EQRVAPSPAPQAKMTSYKPKVGSSPTRKTP-----LSTSPTKEWTRITRKKEASVPSQGT 1548
E+ APSP+P+++ S +PT TP S SP E + E P+ T
Sbjct: 197 EEPAAPSPSESEEPSVAASSEETPTPSTPEEPAAPSPSESEEPSVAASSE-ETPTPST 255

Query: 1549 GTRQAIFPTSPSPSNEDGKKS A 1611
A P+PSP +ED +A
Sbjct: 256 PEEPAAPSPSESEEPSVAASSEETPTPSTPEEPAAPSPSESEEPSVAASSE-ETPTPST 275

>ref|NP_001074518.1| myeloid/lymphoid or mixed-lineage leukemia 1 [Mus musculus]
Length = 3963

Score = 37.4 bits (85), Expect = 8.0
Identities = 26/82 (31%), Positives = 38/82 (46%), Gaps = 2/82 (2%)
Frame = +1

Query: 1396 APSPAPQAKMTSYKPKVGSSPTRKTPPLSTSPKEWTRITRKKEA--SVPSQGTGTRQAIF 1569
AP+PAP+ K S SS P + P + + +KKEA +VPS+ ++
Sbjct: 1275 APAPAPEPKQVSAPASRKSSKQVSQPAAVVPPQPPSTAPQKKEAPKAVPSE---PKKKQP 1331

Query: 1570 PTPSPSNEDGKKSALALAPFYP 1635
P P P E K+ +A P P
Sbjct: 1332 PPPEPGPEQSKQKKVAPRPSIP 1353

>ref|YP_138567.1| glucan binding protein [Streptococcus thermophilus LMG 18311]
gb|AAV59752.1| glucan binding protein [Streptococcus thermophilus LMG 18311]
gb|AAW82375.1| PcsB [Streptococcus thermophilus LMG 18311]
Length = 474

Score = 37.4 bits (85), Expect = 8.0
Identities = 33/107 (30%), Positives = 44/107 (41%), Gaps = 1/107 (0%)
Frame = +1

Query: 1357 SEISRGARAEQRVAPSPAPQAKMTSYKPKVGSSPTRKTPPLSTSPKEWTRITRKKEASVP 1536
SE S + A Q A S + + S P V +P P++TS E T + ASV
Sbjct: 278 SETSTASEAAQEPASSETSEVQPESAAPAVSEAPASVAVPATS---EAAPATSEAPASVA 334

Query: 1537 SQGTG-TRQAIFFTPSPSNEDGKKSALAPFYDPVLFIRGRLELAP 1674
T A+ P+P+ E K SA + YP G LAP
Sbjct: 335 PVATSEAAPAVSEAPAPAAETHKVSAASTPNTYPVGGCTWGVKSLAP 381

>dbj|BAE24386.1| unnamed protein product [Mus musculus]
Length = 1082

Score = 37.4 bits (85), Expect = 8.0
Identities = 26/82 (31%), Positives = 38/82 (46%), Gaps = 2/82 (2%)
Frame = +1

Query: 1396 APSPAPQAKMTSYKPKVGSSTPRKTPLSTSPTEWTRITRKKEA--SVPSQGTGTRQAI 1569
AP+PAP+ K S SS P + P + + +KKEA +VPS+ ++
Sbjct: 840 APAPAPEPKQVSAPASRKSSKQVSQPAAVVPPQPPSTAPQKKEAPKAVPSE---PKKKQP 896

Query: 1570 PTPSPSNEDGKKSALAPFY 1635
P P P E K+ +A P P
Sbjct: 897 PPPEPGPEQSKQKKVAPRPSIP 918

>pir||A48205 All-1 protein +GTE form - mouse (fragment)
Length = 3869

Score = 37.4 bits (85), Expect = 8.0
Identities = 26/82 (31%), Positives = 38/82 (46%), Gaps = 2/82 (2%)
Frame = +1

Query: 1396 APSPAPQAKMTSYKPKVGSSTPRKTPLSTSPTEWTRITRKKEA--SVPSQGTGTRQAI 1569
AP+PAP+ K S SS P + P + + +KKEA +VPS+ ++
Sbjct: 1178 APAPAPEPKQVSAPASRKSSKQVSQPAAVVPPQPPSTAPQKKEAPKAVPSE---PKKKQP 1234

Query: 1570 PTPSPSNEDGKKSALAPFY 1635
P P P E K+ +A P P
Sbjct: 1235 PPPEPGPEQSKQKKVAPLPSIP 1256

>gb|AAA62593.1| All-1 protein [Mus musculus]
Length = 3866

Score = 37.4 bits (85), Expect = 8.0
Identities = 26/82 (31%), Positives = 38/82 (46%), Gaps = 2/82 (2%)
Frame = +1

Query: 1396 APSPAPQAKMTSYKPKVGSSTPRKTPLSTSPTEWTRITRKKEA--SVPSQGTGTRQAI 1569
AP+PAP+ K S SS P + P + + +KKEA +VPS+ ++
Sbjct: 1175 APAPAPEPKQVSAPASRKSSKQVSQPAAVVPPQPPSTAPQKKEAPKAVPSE---PKKKQP 1231

Query: 1570 PTPSPSNEDGKKSALAPFY 1635

PPPEK+ +A P P
Sbjct: 1232 PPPEPGPEQSKQKKVAPLPSIP 1253

>ref|XP_754682.1| spindle-pole body protein (Pcp1) [Aspergillus fumigatus Af293]
gb|EAL92644.1| spindle-pole body protein (Pcp1), putative [Aspergillus fumigatus Af293]
gb|EDP52807.1| spindle-pole body protein (Pcp1), putative [Aspergillus fumigatus A1163]
Length = 1271

Score = 37.4 bits (85), Expect = 8.0
Identities = 19/51 (37%), Positives = 30/51 (58%)
Frame = +1

Query: 1246 KIALRPGTMFCFGTISSIADEEGLHRIADLLEKKLSSEISRGARAEQRVA 1398
KI LR T+ G + + D++ +L + LEK+LSSEI R + E R++
Sbjct: 857 KIDLRKSTLRLEGEVKRLKDDKASLLEAKESLEKQLSSEIERATQEENRLS 907

>ref|XP_659690.1| hypothetical protein AN2086.2 [Aspergillus nidulans FGSC A4]
gb|EAA64918.1| hypothetical protein AN2086.2 [Aspergillus nidulans FGSC A4]
tpe|CBF86150.1| TPA: Nuclear pore complex protein An-Nup159 (Eurofung) [Aspergillus nidulans FGSC A4]
Length = 1394

Score = 37.4 bits (85), Expect = 8.0
Identities = 34/124 (27%), Positives = 49/124 (39%)
Frame = +1

Query: 1258 RPGTMFCFGTISSIADEEGLHRIADLLEKKLSSEISRGARAEQRVAPSPAPQAKMTSYK 1437
+P +F FG SS + T + + E E S A PAP S K
Sbjct: 637 KPSGLFSFG---SSFDEMSTPSKTSPPTEAMDDIEDSNATSQNLPAAKEPAPSLFGASSK 694

Query: 1438 PKVGSSPTRKTPLSTSPTKEWTRITRKEASVPSQGTGTRQAIFFPTSPSNEDGKKS AIA 1617
P GSS S T+ + + + P G ++A P SPS+ +K+A+A
Sbjct: 695 PSTGSSIFGSFG---SQTQNSPFGSAQTSKSPFLLGNKKADNQAPSPSSAPSEKTAVA 751

Query: 1618 LAPF 1629
PF
Sbjct: 752 SPPF 755

>ref|XP_958911.1| hypothetical protein NCU09139 [Neurospora crassa OR74A]
gb|EAA29675.1| conserved hypothetical protein [Neurospora crassa OR74A]
Length = 584

Score = 37.4 bits (85), Expect = 8.0
Identities = 18/45 (40%), Positives = 26/45 (57%), Gaps = 1/45 (2%)

Frame = +2

Query: 74 WHERGVDDHDDASEEERVATTQGRKERDARSVKGVG-EGRVGG 205
W G DDHD D+SE+E + + R++ DA S+ G G+ GG
Sbjct: 508 WDPVGGFDDHDGDSSEDEEIEAERERRQDDAASLAGTSIAGKKGG 552

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Apr 19, 2010 11:58 AM
Number of letters in database: 3,701,345,023
Number of sequences in database: 10,862,569

Lambda	K	H
0.318	0.134	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 10862569
Number of Hits to DB: 14,995,642,493
Number of extensions: 347914421
Number of successful extensions: 1011802
Number of sequences better than 10.0: 54
Number of HSP's gapped: 1007481
Number of HSP's successfully gapped: 55
Length of query: 737
Length of database: 3,701,345,023
Length adjustment: 145
Effective length of query: 592
Effective length of database: 2,126,272,518
Effective search space: 1258753330656
Effective search space used: 1258753330656
Neighboring words threshold: 12
Window for multiple hits: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 33 (17.3 bits)