

```
>gi|1684788|gb|AAB36530.1| 4-phosphoerythronate dehydrogenase [Escherichia coli str. K-12
substr. W3110]
MKILVDENMPYARDLFSRLGEVTA VPGRPPIVAQLADADALMVRSVTKVNESLLAGKPIKFVGTATAGTDHVDEAWLKQAGIGFSAAPGCNAIA
VVEYVFSSLLMLAERDGFSLYDRTVGIVGVGNVGRRLQARLEALGIKTLLCDPPRADRGDEGDFRSLDELVQRADILTFHTPLFKDGPYKTLHL
ADEKLIRSLKPGAILINACRGAVVDNTALLTCLNEGQKLSVVL DVWEGEPELNVELLKKVDIGTSHIAGYTLEGKARGTTQVFEAYSKFIGHEQ
HVALDITLLPAPEFGRITLHGPLDQPTLKRVLVHLVYDVRDDAPLRKVAGIPGEFDKLRKNYLERREWSSLYVICDDASAASLLCKLGFNAVHHP
AR
```

```
>gi|745997998|sp|P0DKH9.1|AREP1_ARATH RecName: Full=Auxin-responsive endogenous peptide 1
[Arabidopsis thaliana] (len=40)
Score = 20 (i=277, j=31)
Identities = 4/8 (50%), Positives = 4/8 (50%), Gaps = 0/8 (0%)
Query: 270 VFEAYSKF 277
      F Y KF
Sbjct: 24 PFYFYHKF 31
```

```
>gi|745997997|sp|P0DKH8.1|AMP2_FAGES RecName: Full=Antimicrobial peptide 2; Short=Fa-AMP2
[Fagopyrum esculentum] (len=40)
Score = 17 (i=88, j=13)
Identities = 2/7 (29%), Positives = 5/7 (71%), Gaps = 0/7 (0%)
Query: 82 IGFSAAP 88
      G +++P
Sbjct: 7 GGGATCP 13
```

```
>gi|745997996|sp|P0DKH7.1|AMP1_FAGES RecName: Full=Antimicrobial peptide 1; Short=Fa-AMP1
[Fagopyrum esculentum] (len=40)
Score = 17 (i=88, j=13)
Identities = 2/7 (29%), Positives = 5/7 (71%), Gaps = 0/7 (0%)
Query: 82 IGFSAAP 88
      G +++P
Sbjct: 7 GGGATCP 13
```

```
>gi|745755594|sp|Q29243.2|DAG1_PIG RecName: Full=Dystroglycan; AltName:
Full=Dystrophin-associated glycoprotein 1; Contains: RecName: Full=Alpha-dystroglycan;
Short=Alpha-DG; Contains: RecName: Full=Beta-dystroglycan; Short=Beta-DG; Flags: Precursor
[Sus scrofa] (len=877)
Score = 29 (i=332, j=797)
Identities = 9/39 (23%), Positives = 21/39 (54%), Gaps = 4/39 (10%)
Query: 294 FGRITLHGPLDQP-TLKRLVHLVYDVRDDAPLRKVAGI 332
      G++TL DQ +K+ V +++ + DD+ +++
Sbjct: 759 KGKLTTL---EDQATFIKKGVPPIIFADELDDSKPPSSSM 797
```

```
>gi|745755649|sp|P9WGI9.2|GLYA1_MYCTU RecName: Full=Serine hydroxymethyltransferase 1;
Short=SHM1; Short=SHMT 1; Short=Serine methylase 1 [Mycobacterium tuberculosis H37Rv]
(len=438)
Score = 36 (i=55, j=323)
Identities = 7/19 (37%), Positives = 15/19 (79%), Gaps = 0/19 (0%)
Query: 37 DADALMVRSVTKVNESLLA 55
      AD LM+ +V+K++ S+++
Sbjct: 305 IADRLMAPDVAKAGVSVVS 323
```

```
>gi|745755659|sp|Q5PR66.2|IFT56_DANRE RecName: Full=Intraflagellar transport protein 56;
AltName: Full=Tetratricopeptide repeat protein 26; Short=TPR repeat protein 26 [Danio rerio]
(len=557)
Score = 32 (i=118, j=387)
Identities = 16/73 (22%), Positives = 36/73 (49%), Gaps = 1/73 (1%)
Query: 46 VTKVNESLLAGKPIKFVGTATAGTDHVDEAWLKQAGIGFSAAPGCNAIAVVEYVFSSLLMLAERDGFSLYDRT 118
      T +E +L G +G ++ DH+ A +G SA+ C++I + + S +++L + + +Y ++
Sbjct: 315 PTTPEYILKGVVNAALGQEIGSRDHLKIAQQFFQLVGGSAS-ECDTIPGRQCMASCFLLKQFEDVLIYLS 387
```

```
>gi|728048777|sp|I1JLC8.1|SLE2_SOYBN RecName: Full=Protein SLE2; AltName: Full=Em protein;
AltName: Full=Protein Glycine max physiologically mature 11; AltName: Full=Protein GmD-19;
AltName: Full=Soybean group-1 late embryogenesis abundant protein 2; AltName: Full=Soybean
group-1 lea protein 2; Short=Sle2 [Glycine max] (len=105)
Score = 26 (i=286, j=84)
Identities = 9/42 (21%), Positives = 22/42 (52%), Gaps = 4/42 (10%)
Query: 245 LKKVDIGTSHIAGYTLEGKARGTTQVFEAYSKFIGHEQHVAL 286
      +K ++GT GY G+ G + E ++ ++E+ +++
Sbjct: 43 TRKEQLGT---EGYQEMGRKGGLST-VEKSGEERAQEEGIGI 84
```

```
>gi|728048695|sp|P0CT50.1|SDC_TRIMF RecName: Full=Salicylate decarboxylase; AltName:
```

Full=Salicylic acid decarboxylase [Trichosporon moniliiforme] (len=350)

Score = 30 (i=259, j=59)

Identities = 4/14 (29%), Positives = 12/14 (86%), Gaps = 0/14 (0%)

Query: 246 KKVDIGTSHIAGYT 259

++++++H GYT

Sbjct: 46 NRLELSNKHGIGYT 59

>gi|728048647|sp|F1QEG2.1|KL41B_DANRE RecName: Full=Kelch-like protein 41b; AltName:

Full=Kelch repeat and BTB domain-containing protein 10b [Danio rerio] (len=605)

Score = 35 (i=264, j=269)

Identities = 11/34 (32%), Positives = 19/34 (56%), Gaps = 4/34 (12%)

Query: 231 LDVWEGEPELNVELLKKVDIGTSHIAGYTLEGKA 264

D+ +G+PE LLKK+++ + + G E K

Sbjct: 236 DDIKGDPE----LLKKLQLVKDAFKGKLPEKKP 269

>gi|728048573|sp|C0HJB3.1|MANA_CANEN RecName: Full=Alpha-mannosidase; Short=JBM;

Short=Jbalpha-man; Contains: RecName: Full=Alpha-mannosidase, heavy subunit; Contains:

RecName: Full=Alpha-mannosidase, light subunit, partial [Canavalia ensiformis] (len=981)

Score = 48 (i=109, j=61)

Identities = 12/40 (30%), Positives = 24/40 (60%), Gaps = 0/40 (0%)

Query: 70 DHVDEAWLQKQAGIGFSAAPGCNAIAVVEYVFSSLLMLAER 109

+H D +WLK + + ++ + A VE V++S++M +R

Sbjct: 22 SHDDVGWLKTVDQYYVGSENYIQEACVENVLDSVMSLQR 61

>gi|728048514|sp|S4R3Y5.1|HMN11_HUMAN RecName: Full=Humanin-like 11; Short=HN11; AltName:

Full=MT-RNR2-like protein 11 [Homo sapiens] (len=24)

Score = 20 (i=113, j=19)

Identities = 5/15 (33%), Positives = 10/15 (67%), Gaps = 0/15 (0%)

Query: 99 VFSSLLMLAERDGF 113

FS LL++ ++ +S

Sbjct: 5 GFSCLLLVISEIDLS 19

>gi|727863585|sp|Q6ZM89.3|RH42A_DANRE RecName: Full=Rho GTPase-activating protein 42;

AltName: Full=Rho GTPase-activating protein 10-like; AltName: Full=Rho-type

GTPase-activating protein 42 [Danio rerio] (len=805)

Score = 33 (i=175, j=778)

Identities = 7/25 (28%), Positives = 17/25 (68%), Gaps = 0/25 (0%)

Query: 151 DRGDEGDFRSLDELVQRADILTFHT 175

R+ +G+++SL + QR ++ ++H

Sbjct: 754 FRSCHGSIQSLVSRSQRDSLKSLHM 778

>gi|728047640|sp|D6REC4.1|CFA99_HUMAN RecName: Full=Cilia- and flagella-associated protein

99 [Homo sapiens] (len=459)

Score = 33 (i=262, j=238)

Identities = 9/18 (50%), Positives = 11/18 (61%), Gaps = 2/18 (11%)

Query: 245 LKKVDIGTSHIAGYTLEG 262

K VD ++I GY LEG

Sbjct: 221 GKLVD--LTQIPGYGLEG 238

>gi|728047699|sp|P0DMQ6.1|DHSO_CHICK RecName: Full=Sorbitol dehydrogenase; AltName:

Full=L-iditol 2-dehydrogenase [Gallus gallus] (len=355)

Score = 30 (i=228, j=91)

Identities = 8/33 (24%), Positives = 20/33 (61%), Gaps = 0/33 (0%)

Query: 196 SLKPGAILINACRGAVVDNTALLTCLNEGQKLS 228

+K +L + + G+V+ A +T L+ G++++

Sbjct: 59 VVKDPMVLGHEASGTVIKVGAGVTHLKPGRVA 91

>gi|704045459|sp|G0SC29.2|NLE1_CHATD RecName: Full=Ribosome assembly protein 4; AltName:

Full=Notchless protein homolog 1; AltName: Full=Ribosome biogenesis factor RSA4 [Chaetomium thermophilum var. thermophilum DSM 1495] (len=517)

Score = 29 (i=242, j=185)

Identities = 8/40 (20%), Positives = 26/40 (65%), Gaps = 2/40 (5%)

Query: 203 LINACRGAVVDNTALLTCLNEGQKLSVVLVDVWEGEPELNV 242

I +C+ + V+++ L ++G++ + + D+ +G P++++

Sbjct: 146 PILSCQFSPVSSSRLA--TGSGDNTARIWDTDSGTPKFTL 185

>gi|704045435|sp|Q9SX54.2|SCRK8_ARATH RecName: Full=Putative fructokinase-8 [Arabidopsis thaliana] (len=210)

Score = 28 (i=232, j=175)

Identities = 12/53 (23%), Positives = 27/53 (51%), Gaps = 6/53 (11%)

Query: 180 DGPYKTLHLADEKLIIRSLKPGAILINACRGAVVDNTALLTCLNEGQKLSVVLVD 232

G +T+H + + G +++A + +VD+ ++ L+E ++L VL
 Sbjct: 123 HGSVETFH---VDAVDTTGAGDSFVGALLNQIVDDQSV---LEEEERLRKVL 175

>gi|704044129|sp|P0DMQ3.1|TO1D_HADMO RecName: Full=Omega-hexatoxin-Hmold; Flags: Precursor
 [Hadroryche modesta] (len=84)
 Score = 24 (i=115, j=36)
 Identities = 9/36 (25%), Positives = 18/36 (50%), Gaps = 4/36 (11%)
 Query: 80 FSAAPGCNAIAVVEYVFSS----LLMLAERDGFSLY 115
 +++A G A+ V+ V++ M + GF+ Y
 Sbjct: 1 MNTATGVIALLVLATVIGCIQAEDTMADLQGGFESY 36

>gi|704044123|sp|P0DMQ2.1|TO1C_HADMO RecName: Full=Omega-hexatoxin-Hmolc; Flags: Precursor
 [Hadroryche modesta] (len=84)
 Score = 25 (i=16, j=65)
 Identities = 4/12 (33%), Positives = 7/12 (58%), Gaps = 0/12 (0%)
 Query: 5 VDENMPYARDLF 16
 +D+ PY +D
 Sbjct: 54 TDQPCPYDQDCC 65

>gi|704044116|sp|P0DMQ1.1|TO1B_HADMO RecName: Full=Omega-hexatoxin-Hmolb; Flags: Precursor
 [Hadroryche modesta] (len=84)
 Score = 25 (i=16, j=65)
 Identities = 4/12 (33%), Positives = 7/12 (58%), Gaps = 0/12 (0%)
 Query: 5 VDENMPYARDLF 16
 +D+ PY +D
 Sbjct: 54 TDQPCPYDQDCC 65

>gi|704044110|sp|P0DMQ0.1|TO1A_HADMO RecName: Full=Omega-hexatoxin-Hmola; Flags: Precursor
 [Hadroryche modesta] (len=84)
 Score = 24 (i=171, j=51)
 Identities = 5/23 (22%), Positives = 12/23 (52%), Gaps = 5/23 (22%)
 Query: 149 DEGDFRSL-----DELVQRADIL 171
 +G F+S +++ +RA +
 Sbjct: 29 FQGGFESYDGEAAEKIFRRAPVC 51

>gi|704044094|sp|P0DMQ4.1|TK1A_HADMO RecName: Full=Kappa-hexatoxin-Hmold; Flags: Precursor
 [Hadroryche modesta] (len=73)
 Score = 23 (i=118, j=38)
 Identities = 4/11 (36%), Positives = 9/11 (82%), Gaps = 0/11 (0%)
 Query: 108 ERDGFSLYDRT 118
 ++D ++L+ RT
 Sbjct: 28 RKDVMGLFRRT 38

>gi|704043461|sp|C0HJD7.1|NXL4_DENPO RecName: Full=Alpha-elapitoxin-Dpp2d;
 Short=Alpha-EPTX-Dpp2d [Dendroaspis polylepis polylepis] (len=72)
 Score = 21 (i=252, j=42)
 Identities = 3/8 (38%), Positives = 6/8 (75%), Gaps = 0/8 (0%)
 Query: 245 LKKVDIGT 252
 K+V++G
 Sbjct: 35 GKRVELGC 42

>gi|704045556|sp|Q9SUC3.2|MS5_ARATH RecName: Full=Protein POLLENLESS 3; AltName:
 Full=Protein MALE STERILE 5; AltName: Full=Protein THREE-DIVISION MUTANT 1 [Arabidopsis
 thaliana] (len=434)
 Score = 32 (i=165, j=272)
 Identities = 7/20 (35%), Positives = 13/20 (65%), Gaps = 0/20 (0%)
 Query: 146 DPPRADRGDEGDFRSLDELV 165
 +P +++ GDE +S D+ V
 Sbjct: 253 SPAESECGDPEPFAKSYDRAV 272

>gi|704044187|sp|C0HJM7.1|TXL1_PHOPT RecName: Full=Toxin Tx1; Short=PpTx1, partial
 [Phoneutria pertyi] (len=10)
 Score = 15 (i=223, j=9)
 Identities = 2/8 (25%), Positives = 4/8 (50%), Gaps = 0/8 (0%)
 Query: 216 ALLTCLNE 223
 L +C+
 Sbjct: 2 ELTSCFPV 9

>gi|704000372|sp|E2RE76.2|APOA4_CANFA RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV;
 Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor [Canis lupus familiaris]
 (len=378)

Score = 38 (i=45, j=118)

Identities = 9/28 (32%), Positives = 19/28 (68%), Gaps = 1/28 (4%)

Query: 18 RLGEVTAVPGRPIPVQAQLADADALMVRS 45
+G+ +++ G+P+ VA L ++ L V+S

Sbjct: 91 IMGRQVGIFGQPLRVATLPNC-DLPVNS 118

>gi|704000369|sp|C9JSJ3.2|BHMGI_HUMAN RecName: Full=Basic helix-loop-helix and HMG box domain-containing protein 1 [Homo sapiens] (len=638)

Score = 36 (i=329, j=198)

Identities = 9/39 (23%), Positives = 21/39 (54%), Gaps = 0/39 (0%)

Query: 291 PAPEFGRITLHGPLDQPTLKRLVHLVYDVRDDAPLRKV 329
+P+ + L+G ++P K+L++ + R P R++

Sbjct: 160 SSPSSQKSCIQGACQKPRKKKLTQASESQTRTPKPRRSL 198

>gi|704000365|sp|B2NI93.2|GEDH_CARLC RecName: Full=Geraniol dehydrogenase; Short=GeDH; AltName: Full=Farnesol dehydrogenase; AltName: Full=NAD(+)-farnesol dehydrogenase [Carpoglyphus lactis] (len=378)

Score = 31 (i=98, j=83)

Identities = 7/19 (37%), Positives = 12/19 (63%), Gaps = 0/19 (0%)

Query: 80 AGIGFSAAPGCNAIAVVEY 98
+GIG A G ++ ++VE

Sbjct: 65 GGIGCPAIAAGHEGAGIVES 83

>gi|704000364|sp|K7N5M5.2|HBA1_ELEMC RecName: Full=Hemoglobin subunit alpha 1; AltName: Full=Alpha-1-globin; AltName: Full=Hemoglobin alpha-1 chain [Eleginops maclovinus] (len=142)

Score = 30 (i=289, j=129)

Identities = 5/10 (50%), Positives = 7/10 (70%), Gaps = 0/10 (0%)

Query: 280 HEQHVALDTL 289
E HV+LD +

Sbjct: 120 PEAHVSLDKF 129

>gi|704000363|sp|G0S616.2|MRT4_CHATD RecName: Full=Ribosome assembly factor mrt4; AltName: Full=mRNA turnover protein 4 [Chaetomium thermophilum var. thermophilum DSM 1495] (len=270)

Score = 31 (i=344, j=53)

Identities = 5/9 (56%), Positives = 8/9 (89%), Gaps = 0/9 (0%)

Query: 336 FDKLRKNYL 344
D++R+NYL

Sbjct: 45 VDNMRNNYL 53

>gi|704000358|sp|C0HJM8.1|LEC_ALLCE RecName: Full=Lectin, partial [Allium cepa] (len=10)

Score = 19 (i=52, j=9)

Identities = 4/10 (40%), Positives = 6/10 (60%), Gaps = 0/10 (0%)

Query: 43 VRSVTKVNES 52
R+V NE+

Sbjct: 0 RNVLLNNEG 9

>gi|704000357|sp|C0HJN0.1|KAX6V_HETLA RecName: Full=Potassium channel toxin alpha-KTx 6 hetlaxin [Heterometrus laoticus] (len=34)

Score = 23 (i=333, j=20)

Identities = 4/10 (40%), Positives = 6/10 (60%), Gaps = 0/10 (0%)

Query: 324 APLRKVAGIP 333
P +K +G P

Sbjct: 11 DPCKKKTGCP 20

>gi|704000346|sp|F1QDF8.1|FXJ1A_DANRE RecName: Full=Forkhead box protein J1-A [Danio rerio] (len=458)

Score = 28 (i=335, j=96)

Identities = 6/14 (43%), Positives = 10/14 (71%), Gaps = 0/14 (0%)

Query: 322 DDAPLRKVAGIPGE 335
+DAP +AG P++

Sbjct: 83 SDAPSSPLAGDPAS 96

>gi|704000341|sp|P0DKH4.1|F26G_SOLTO RecName: Full=Furostanol glycoside 26-O-beta-glucosidase; AltName: Full=Torvosidase, partial [Solanum torvum] (len=61)

Score = 27 (i=42, j=30)

Identities = 5/29 (17%), Positives = 19/29 (66%), Gaps = 0/29 (0%)

Query: 14 DLFSRLGEVTAVPGRPIPVQAQLADADALM 42
L +++G+++ + +R I +A ++ +++

Sbjct: 2 TLEEKIGQMSQIDARRIGAATALEVRGFL 30

>gi|704000316|sp|W5EP13.1|CA1P_WHEAT RecName: Full=2-carboxy-D-arabinitol-1-phosphatase;

Flags: Precursor [Triticum aestivum] (len=495)

Score = 32 (i=42, j=54)

Identities = 8/27 (30%), Positives = 15/27 (56%), Gaps = 1/27 (4%)

Query: 16 FSRLGEVTAVPGRPIPVQQLADADALM 42
S + E+ P+R P+ LA+A ++

Sbjct: 28 CSSVRELDLRSPSR-PPLPLAEAKRVV 54

>gi|746590800|sp|P0CT51.1|BLP1_CANAL RecName: Full=Blood-induced peptide 1 [Candida albicans SC5314] (len=77)

Score = 29 (i=197, j=66)

Identities = 6/15 (40%), Positives = 11/15 (73%), Gaps = 0/15 (0%)

Query: 183 YKTLHLADEKLIRSL 197
K+L++ +EKL + L

Sbjct: 52 LKNLEMENEKLNIL 66

>gi|704000362|sp|Q59PD6.2|MAD1_CANAL RecName: Full=Spindle assembly checkpoint component MAD1 [Candida albicans SC5314] (len=696)

Score = 35 (i=239, j=200)

Identities = 7/22 (32%), Positives = 15/22 (68%), Gaps = 0/22 (0%)

Query: 218 LTCLNEGQKLSVVDVWEGEPE 239
T++NE ++ S +LD +G+ +

Sbjct: 179 DTAINLEQYSKILDKKNGSDN 200

>gi|703556459|sp|A2BD09.3|OLM2A_PIG RecName: Full=Olfactomedin-like protein 2A; Flags: Precursor [Sus scrofa] (len=650)

Score = 30 (i=355, j=579)

Identities = 3/16 (19%), Positives = 13/16 (81%), Gaps = 0/16 (0%)

Query: 340 RKNYLERREWSSLYVI 355
K+ L+R+++++ +++

Sbjct: 564 WKTRLRRNSYGNCFVLV 579

>gi|703556453|sp|P84718.2|PSBO_PINST RecName: Full=Putative oxygen-evolving enhancer protein 1; Short=OEE1; AltName: Full=33 kDa subunit of oxygen evolving system of photosystem II; AltName: Full=33 kDa thylakoid membrane protein; AltName: Full=OEC 33 kDa subunit; AltName: Full=PS2, partial [Pinus strobus] (len=116)

Score = 30 (i=133, j=41)

Identities = 8/27 (30%), Positives = 18/27 (67%), Gaps = 0/27 (0%)

Query: 107 AERDGFSLYDRTVGIVGVGNVGRRLQA 133
+ER G + YD++V++ + G+ + L+

Sbjct: 15 GERGGSTGYDNAVALPAGGRGSSMLDP 41

>gi|703556448|sp|P81018.2|LADD_ONCMY RecName: Full=Ladderlectin; Flags: Precursor [Oncorhynchus mykiss] (len=190)

Score = 29 (i=112, j=110)

Identities = 7/28 (25%), Positives = 15/28 (54%), Gaps = 3/28 (11%)

Query: 85 PGCNAIA---VVEYVFSSLLMLAERDGF 112
G+N + +EY F + ++ ++ GF

Sbjct: 83 LGANLASVHSSAEYQFLQEYVASKTGGF 110

>gi|728048788|sp|C9J7I0.1|UMAD1_HUMAN RecName: Full=UBAP1-MVB12-associated (UMA)-domain containing protein 1; AltName: Full=RPA3 antisense RNA 1; AltName: Full=RPA3 opposite strand [Homo sapiens] (len=102)

Score = 27 (i=71, j=75)

Identities = 14/68 (21%), Positives = 34/68 (50%), Gaps = 1/68 (1%)

Query: 4 LVDENMPYARDLFSRLGEVTAVPGRPIPVQQLADADALMVRSVTKVNESLLAGKPIKFVGTATAGTDH 71
++ N+P + + + +++ P ++Q + ++LM++ ++ V + LA + GT T DH

Sbjct: 8 DIEANQPLETNKENSSSVTVSDPEMENKAGQTLNSSLMAELLSDPFT-LAPHVLAVQGTITDLPDH 75

>gi|694016595|sp|Q5TYJ0.4|OBP71_ANOGA RecName: Full=General odorant-binding protein 71; Flags: Precursor [Anopheles gambiae] (len=228)

Score = 26 (i=235, j=221)

Identities = 6/19 (32%), Positives = 14/19 (74%), Gaps = 2/19 (11%)

Query: 217 LLTCLNEGQKLSVVDVWE 235
++TCL+ +++++ D WE

Sbjct: 203 FVTCLS--DRFETNCDDWE 221

>gi|694016591|sp|U3KRG0.2|LECB1_CRATA RecName: Full=Bark lectin isoform 1; Short=CrataBL; Short=CrataBL-form I [Crateva tapia] (len=165)

Score = 38 (i=132, j=149)

Identities = 9/17 (53%), Positives = 10/17 (59%), Gaps = 0/17 (0%)

Query: 116 DRTVGIVGVGNVGRRLQ 132

R VGI VG+ GRR
 Sbjct: 133 CRDVGIEITVGGGGRRYL 149

>gi|694016588|sp|C0HJA4.1|LECB2_CRATA RecName: Full=Bark lectin isoform 2; Short=CrataBL;
 Short=CrataBL-form II [Crateva tapia] (len=165)
 Score = 38 (i=132, j=149)
 Identities = 9/17 (53%), Positives = 10/17 (59%), Gaps = 0/17 (0%)
 Query: 116 DRTVGIVGVGNVGRRLQ 132
 R VGI VG+ GRR
 Sbjct: 133 CRDVGIEITVGGGGRRYL 149

>gi|694016584|sp|C0HJL9.1|TAN_BACIU RecName: Full=Tannase; AltName: Full=Tannin
 acylhydrolase, partial [Bacillus subtilis] (len=15)
 Score = 15 (i=154, j=9)
 Identities = 4/9 (44%), Positives = 8/9 (89%), Gaps = 1/9 (11%)
 Query: 146 DPPRADRGD 154
 +PP+ ++GD
 Sbjct: 1 QPPH-SHGD 9

>gi|694016581|sp|P0DKH2.1|RI2BC_ARATH RecName: Full=Putative ribonucleoside-diphosphate
 reductase small chain B; AltName: Full=Ribonucleoside-diphosphate reductase R2B subunit;
 AltName: Full=Ribonucleotide reductase small subunit B [Arabidopsis thaliana] (len=158)
 Score = 25 (i=275, j=32)
 Identities = 3/8 (38%), Positives = 6/8 (75%), Gaps = 0/8 (0%)
 Query: 268 TQVFEAYS 275
 Q++E Y+
 Sbjct: 25 PQIWEMYK 32

>gi|694016580|sp|C0HJM0.1|PPO3_SARAR RecName: Full=Phenoloxidase 3; AltName: Full=Tyrosinase
 3, partial [Sarcophaga argyrostoma] (len=71)
 Score = 29 (i=325, j=14)
 Identities = 5/13 (38%), Positives = 7/13 (54%), Gaps = 0/13 (0%)
 Query: 313 VHLVYDVRRDDAP 325
 HLVY ++ D
 Sbjct: 2 WHLVYPIEAPDRS 14

>gi|694016558|sp|D4A693.2|AZIN2_RAT RecName: Full=Antizyme inhibitor 2; Short=Azi2; AltName:
 Full=Ornithine decarboxylase-like protein; Short=ODC-like protein; AltName: Full=ornithine
 decarboxylase paralog; Short=ODC-p [Rattus norvegicus] (len=457)
 Score = 36 (i=30, j=258)
 Identities = 7/14 (50%), Positives = 10/14 (71%), Gaps = 0/14 (0%)
 Query: 17 SRLGEVTAVPGRPI 30
 R+ EVT+V G+ I
 Sbjct: 245 VRFEEVTSVIGKNI 258

>gi|694016556|sp|F4I9R6.2|JA15S_ARATH RecName: Full=Jacalin-related lectin 15; AltName:
 Full=Protein JACALIN-TYPE LECTIN REQUIRED FOR POTEXVIRUS RESISTANCE1 [Arabidopsis thaliana]
 (len=131)
 Score = 37 (i=337, j=114)
 Identities = 5/12 (42%), Positives = 10/12 (83%), Gaps = 0/12 (0%)
 Query: 326 LRKVAGIPGEFD 337
 +K++G+ G+FD
 Sbjct: 103 GKKIVGFHGSFD 114

>gi|694016548|sp|S4R3P1.1|HMN13_HUMAN RecName: Full=Humanin-like 13; Short=HN13; AltName:
 Full=MT-RNR2-like protein 13 [Homo sapiens] (len=24)
 Score = 24 (i=116, j=22)
 Identities = 6/18 (33%), Positives = 11/18 (61%), Gaps = 0/18 (0%)
 Query: 99 VFSSLLMLAERDGFSLYD 116
 FS LL+L ++ +S+
 Sbjct: 5 GFSCLLLLISEIDLSVKR 22

>gi|694016547|sp|P0DMP1.1|HMN12_HUMAN RecName: Full=Humanin-like 12; Short=HN12; AltName:
 Full=MT-RNR2-like protein 12 [Homo sapiens] (len=27)
 Score = 19 (i=104, j=10)
 Identities = 4/6 (67%), Positives = 4/6 (67%), Gaps = 0/6 (0%)
 Query: 99 VFSSLL 104
 FS LL
 Sbjct: 5 GFSCLL 10

>gi|694016530|sp|C0HJM6.1|CHIT_TRISX RecName: Full=Endochitinase; AltName: Full=Chitinase;

```

AltName: Allergen=Trip s 1, partial [Triplochiton scleroxylon] (len=11)
Score = 15 (i=80, j=7)
Identities = 2/3 (67%), Positives = 3/3 (100%), Gaps = 0/3 (0%)
Query:      78 KQA 80
           +QA
Sbjct:      5 SQA 7

>gi|694016529|sp|P86977.1|CHIT_STRVO RecName: Full=Chitinase, partial [Streptomyces
violaceusniger] (len=10)
Score = 19 (i=88, j=8)
Identities = 3/9 (33%), Positives = 5/9 (56%), Gaps = 0/9 (0%)
Query:      80 AGIGFSAAP 88
           G G + +P
Sbjct:      0  GDGTGPGP 8

>gi|693586058|sp|Q6ZMS4.4|ZN852_HUMAN RecName: Full=Zinc finger protein 852 [Homo sapiens]
(len=543)
Score = 32 (i=244, j=510)
Identities = 13/44 (30%), Positives = 25/44 (57%), Gaps = 5/44 (11%)
Query:     201 INACRGAVVDNTALLT--CLNEGQ-KLSVVLDVWEGEPELNVEL 244
           N+C  A  D++ L +  ++ G+ +L  VL+  G+P ++V L
Sbjct:     467 CNSCGKAFSDSSQLTVHQRVHTGEKNLMNVLS--VGKPLVSVPL 510

>gi|694016571|sp|P0DL37.1|KAX6L_UROYA RecName: Full=Potassium channel toxin alpha-KTx 6.21;
AltName: Full=Urotoxin; Flags: Precursor [Urodacus yaschenkoi] (len=62)
Score = 22 (i=174, j=20)
Identities = 5/12 (42%), Positives = 7/12 (58%), Gaps = 0/12 (0%)
Query:     163 ELVQRADILTFH 174
           LV  + +LTF
Sbjct:      9 LLVVTTMMLTFD 20

>gi|75523137|sp|Q7M181.1|ACLR_ACHOB RecName: Full=2-aminohexano-6-lactam racemase; AltName:
Full=2-amino-hexano-6-lactam racemase; AltName: Full=Alpha-amino-epsilon-caprolactam
racemase [Achromobacter obae] (len=436)
Score = 35 (i=39, j=69)
Identities = 11/37 (30%), Positives = 19/37 (51%), Gaps = 0/37 (0%)
Query:      3 ILVDENMPYARDLFSRLGEVTAVPGRPIPVACLADAD 39
           L++EN  DL +  G ++  G+P  VA ++ A
Sbjct:     33 RLIEENGRELIDLSGAWGAASLGYGHPAIVAAVSAAA 69

>gi|678021173|sp|Q9C918.2|UBC38_ARATH RecName: Full=Putative ubiquitin-conjugating enzyme E2
38; AltName: Full=Ubiquitin carrier protein 38 [Arabidopsis thaliana] (len=326)
Score = 29 (i=212, j=261)
Identities = 7/22 (32%), Positives = 12/22 (55%), Gaps = 0/22 (0%)
Query:     191 EKLIRSLKPGAILINACRGAVV 212
           K  ++ K GA L +  +G+V
Sbjct:     240 VKACNAYKAGAPLGSMVKGGVQ 261

>gi|678019224|sp|C0HJK0.1|VP_DINQU RecName: Full=Venom peptides; Contains: RecName:
Full=Peptide Dq-1984; Contains: RecName: Full=Peptide Dq-1897; Contains: RecName:
Full=Peptide Dq-1839/Dq-1840/Dq-1856 [Dinoponera quadricaps] (len=20)
Score = 20 (i=63, j=8)
Identities = 3/9 (33%), Positives = 7/9 (78%), Gaps = 0/9 (0%)
Query:      55 AGKPIKFVG 63
           G+ +K+V+
Sbjct:      0  GSLVKLVS 8

>gi|678019209|sp|C0HJK2.1|VP987_DINQU RecName: Full=Peptide Dq-987; Contains: RecName:
Full=Peptide Dq-761 [Dinoponera quadricaps] (len=9)
Score = 19 (i=37, j=8)
Identities = 3/9 (33%), Positives = 7/9 (78%), Gaps = 0/9 (0%)
Query:      29 PIPVAQLAD 37
           +P+ +L+D
Sbjct:      0  LPLDDLSD 8

>gi|678019205|sp|C0HJK4.1|VP88_DINQU RecName: Full=Peptide Dq-1288; Contains: RecName:
Full=Peptide Dq-1061 [Dinoponera quadricaps] (len=11)
Score = 14 (i=147, j=6)
Identities = 1/2 (50%), Positives = 1/2 (50%), Gaps = 0/2 (0%)
Query:     146 DP 147
           P

```

Sbjct: 5 LP 6

>gi|678019201|sp|C0HJK3.1|VP32_DINQU RecName: Full=Peptide Dq-1132 [Dinoponera quadriceps] (len=9)
 Score = 14 (i=147, j=5)
 Identities = 1/2 (50%), Positives = 1/2 (50%), Gaps = 0/2 (0%)
 Query: 146 DP 147
 P
 Sbjct: 4 LP 5

>gi|678019198|sp|C0HJK1.1|VP30_DINQU RecName: Full=Peptide Dq-1030 [Dinoponera quadriceps] (len=9)
 Score = 16 (i=322, j=4)
 Identities = 2/5 (40%), Positives = 3/5 (60%), Gaps = 0/5 (0%)
 Query: 318 DVRRD 322
 +R D
 Sbjct: 0 LRPD 4

>gi|678019123|sp|C0HJK5.1|TXHM3_HERML RecName: Full=Neurotoxin Hm-3 [Heriaeus melloteei] (len=35)
 Score = 18 (i=321, j=29)
 Identities = 2/6 (33%), Positives = 5/6 (83%), Gaps = 0/6 (0%)
 Query: 316 VYDVRR 321
 Y+++R
 Sbjct: 24 KYSIKR 29

>gi|678019117|sp|C0HJH6.1|TX62_DINQU RecName: Full=Dinoponeratoxin Dq-3162/Dq-3163/Dq-3178 [Dinoponera quadriceps] (len=28)
 Score = 26 (i=247, j=19)
 Identities = 5/17 (29%), Positives = 11/17 (65%), Gaps = 0/17 (0%)
 Query: 231 LDVWEGEPELNVELLKK 247
 D W+ + + VE++K+
 Sbjct: 3 KDWWNKHKDKIVEVVKE 19

>gi|678019113|sp|C0HJH7.1|TX04_DINQU RecName: Full=Dinoponeratoxin Dq-3104 [Dinoponera quadriceps] (len=28)
 Score = 24 (i=245, j=17)
 Identities = 4/15 (27%), Positives = 9/15 (60%), Gaps = 0/15 (0%)
 Query: 231 LDVWEGEPELNVELL 245
 D W+ + + VE++
 Sbjct: 3 KDWWNKHKDKIVEVV 17

>gi|678000802|sp|I1N462.3|SBT1_SOYBN RecName: Full=Subtilisin-like protease Glyma18g48580; Contains: RecName: Full=Subtilase peptide GmSubPep; AltName: Full=Glycine max subtilase peptide; Short=GmSubPep; Flags: Precursor [Glycine max] (len=789)
 Score = 43 (i=113, j=568)
 Identities = 11/29 (38%), Positives = 21/29 (72%), Gaps = 1/29 (3%)
 Query: 85 AAPGCNAIAV-VEYVFSSLLMLAERDGF 113
 +APG N +A+ E++ +S L++ +R GF+
 Sbjct: 540 TAPGVNIIAAYSEFASASSLLVDNRRGFK 568

>gi|678000774|sp|Q0J0A4.3|LPAAT_ORYSJ RecName: Full=Probable 1-acylglycerol-3-phosphate O-acyltransferase; AltName: Full=Lipid droplet-binding protein CGI-58 homolog [Oryza sativa Japonica Group] (len=414)
 Score = 27 (i=172, j=147)
 Identities = 5/16 (31%), Positives = 12/16 (75%), Gaps = 0/16 (0%)
 Query: 157 DFRSLDELVQRADILT 172
 FR++D L++R +++
 Sbjct: 132 FFRNFDALASRFRVIA 147

>gi|678000753|sp|Q7XMI0.3|KCY2_ORYSJ RecName: Full=Probable UMP/CMP kinase 2 [Oryza sativa Japonica Group] (len=243)
 Score = 29 (i=247, j=129)
 Identities = 5/10 (50%), Positives = 9/10 (90%), Gaps = 0/10 (0%)
 Query: 238 PELNVELLKK 247
 E++VEL++K
 Sbjct: 120 SEITVELIRK 129

>gi|678000260|sp|Q9SGX9.2|ESFL1_ARATH RecName: Full=EMBRYO SURROUNDING FACTOR 1-like protein 1; Flags: Precursor [Arabidopsis thaliana] (len=80)
 Score = 27 (i=55, j=40)

Identities = 5/13 (38%), Positives = 7/13 (54%), Gaps = 0/13 (0%)

Query: 43 VRSVTKVNESLLA 55
R KVNE+ +

Sbjct: 28 QRHSQKVNEACVP 40

>gi|678000242|sp|A8MQP7.2|ESFL7_ARATH RecName: Full=EMBRYO SURROUNDING FACTOR 1-like protein 7; Flags: Precursor [Arabidopsis thaliana] (len=88)

Score = 23 (i=107, j=20)

Identities = 6/16 (38%), Positives = 10/16 (62%), Gaps = 0/16 (0%)

Query: 92 AIAVVEYVFSSLLMLA 107
IA++ V+ SL+ L

Sbjct: 5 HIALICIVMFSLFALH 20

>gi|678000229|sp|O82377.2|ESFL6_ARATH RecName: Full=EMBRYO SURROUNDING FACTOR 1-like protein 6; Flags: Precursor [Arabidopsis thaliana] (len=77)

Score = 22 (i=368, j=40)

Identities = 4/13 (31%), Positives = 7/13 (54%), Gaps = 0/13 (0%)

Query: 356 CDDASAASLLCKL 368
D + +S +C L

Sbjct: 28 FDANKLGSSVCHL 40

>gi|678000206|sp|Q0J6P7.2|KAD5_ORYSJ RecName: Full=Probable adenylate kinase 5, chloroplastic; AltName: Full=Adenylate monophosphate kinase 5; Flags: Precursor [Oryza sativa Japonica Group] (len=608)

Score = 31 (i=298, j=582)

Identities = 6/21 (29%), Positives = 13/21 (62%), Gaps = 0/21 (0%)

Query: 278 IGHEQHVALDTLLPAPEFGRI 298
G+E++V L+ ++ P +I

Sbjct: 562 NGQERYVLLLEEFVEKPTPDEI 582

>gi|678000108|sp|A2ZU80.2|NRT24_ORYSJ RecName: Full=Probable high-affinity nitrate transporter 2.4; Short=OsNRT2.4 [Oryza sativa Japonica Group] (len=485)

Score = 35 (i=376, j=322)

Identities = 7/20 (35%), Positives = 14/20 (70%), Gaps = 0/20 (0%)

Query: 357 DDASAASLLCKLGFNAVHHP 376
+A++A+ C ++NAV +P

Sbjct: 303 MEAAGAAAACFGAMNAVARP 322

>gi|678000080|sp|K7LFFJ0.2|PP890_SOYBN RecName: Full=Protein PROPEP890; Short=GmPROPEP890; Contains: RecName: Full=Peptide GmPep890; Flags: Precursor [Glycine max] (len=52)

Score = 23 (i=347, j=24)

Identities = 4/13 (31%), Positives = 9/13 (69%), Gaps = 0/13 (0%)

Query: 335 EFDKLRKNYLERR 347
+F K+ K+++ R

Sbjct: 12 NFGKMAKRFBVWRT 24

>gi|677995804|sp|P0DMM5.1|MCSB_GEOSE RecName: Full=Protein-arginine kinase [Geobacillus stearothermophilus] (len=363)

Score = 35 (i=291, j=132)

Identities = 7/21 (33%), Positives = 15/21 (71%), Gaps = 0/21 (0%)

Query: 271 FEAYSKFIGHEQHVALDTLLP 291
E S +I++E+H+ ++ L+P

Sbjct: 112 NEEISIMINEEDHIRIQCLFP 132

>gi|677995449|sp|P86907.1|PA2A_BOTAM RecName: Full=Acidic phospholipase A2; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase [Bothrops ammodytoides] (len=122)

Score = 24 (i=333, j=16)

Identities = 3/9 (33%), Positives = 6/9 (67%), Gaps = 0/9 (0%)

Query: 325 PLRKVAGIP 333
++K+AG

Sbjct: 8 LIKKIAGRS 16

>gi|677992918|sp|P0DMM7.1|SLB_TROWA RecName: Full=Snaclec trowaglerix subunit beta, partial [Tropidolaemus wagleri] (len=10)

Score = 17 (i=146, j=4)

Identities = 2/4 (50%), Positives = 2/4 (50%), Gaps = 0/4 (0%)

Query: 143 LLCD 146
LC

Sbjct: 1 ELCC 4

>gi|677992907|sp|P0DMM6.1|SLA_TROWA RecName: Full=Snaclec trowaglerix subunit alpha, partial

```
[Tropidolaemus wagleri] (len=9)
Score = 17 (i=222, j=5)
Identities = 1/4 (25%), Positives = 3/4 (75%), Gaps = 0/4 (0%)
Query: 219 TCLN 222
      C++
Sbjct: 2 KCMS 5

>gi|677991645|sp|C0HJF7.1|ITR1_JATCU RecName: Full=Trypsin inhibitor 1; Short=JcTI-I,
partial [Jatropha curcas] (len=27)
Score = 21 (i=350, j=15)
Identities = 4/11 (36%), Positives = 7/11 (64%), Gaps = 0/11 (0%)
Query: 340 RKNYLERREWS 350
      K+ ER++ S
Sbjct: 5 CKKEAERQDLS 15

>gi|677991295|sp|P0DKH1.1|ESFL2_ARATH RecName: Full=EMBRYO SURROUNDING FACTOR 1-like protein
2; Flags: Precursor [Arabidopsis thaliana] (len=86)
Score = 25 (i=347, j=75)
Identities = 6/28 (21%), Positives = 16/28 (57%), Gaps = 0/28 (0%)
Query: 320 RRDDAPLRKVAGIPGEFDKLRKNYLER 347
      +DD+ +AG ++ L+K++ + +
Sbjct: 48 FKDDCWCCLAAGTKKDWLEKDFPDAK 75

>gi|677286758|sp|Q8NCS7.4|CTL5_HUMAN RecName: Full=Choline transporter-like protein 5;
AltName: Full=Solute carrier family 44 member 5 [Homo sapiens] (len=719)
Score = 30 (i=127, j=284)
Identities = 7/40 (18%), Positives = 21/40 (52%), Gaps = 2/40 (5%)
Query: 88 PGCNAIAVVEYVFSSLLMLAERDGFSLYDRTVGIVGVGNV 127
      G + V++++ L++L G ++ +G++G+ +
Sbjct: 245 IGLTIAMVLSWI--FLILLRFIAGCLFWVFMIGVIGIIGY 284

>gi|677286751|sp|Q8IVT5.3|KSR1_HUMAN RecName: Full=Kinase suppressor of Ras 1 [Homo sapiens]
(len=923)
Score = 42 (i=362, j=196)
Identities = 12/38 (32%), Positives = 22/38 (58%), Gaps = 7/38 (18%)
Query: 325 PLRKVAGIPGEFDKLRKNYLERREWSSLYVICDDASAA 362
      LRKV+G+ G ++ E +WSSL + +++S+
Sbjct: 159 CLRKVTGLGG-----EHKEDSSWSSLDARRESGSGP 196

>gi|677286748|sp|P0CF96.3|MZT1_SCHPO RecName: Full=Mitotic-spindle organizing protein 1;
AltName: Full=Mitotic-spindle organizing protein associated with a ring of gamma-tubulin 1;
AltName: Full=Transcripts altered in meiosis protein 4 [Schizosaccharomyces pombe 972h-]
(len=64)
Score = 30 (i=221, j=32)
Identities = 6/19 (32%), Positives = 13/19 (68%), Gaps = 0/19 (0%)
Query: 203 LINACRGAVVDNTALLTCL 221
      I++ G+ +D+T+L C+
Sbjct: 14 EIGTLLGTELDKTTLSLCI 32

>gi|677286739|sp|A1UI62.2|RSMH_MYCSK RecName: Full=Ribosomal RNA small subunit
methyltransferase H; AltName: Full=16S rRNA m(4)C1402 methyltransferase; AltName: Full=rRNA
(cytosine-N(4)-)-methyltransferase RsmH [Mycobacterium sp.
KMS]
>gi|677286740|sp|Q1B6W3.2|RSMH_MYCSS RecName: Full=Ribosomal RNA small subunit
methyltransferase H; AltName: Full=16S rRNA m(4)C1402 methyltransferase; AltName: Full=rRNA
(cytosine-N(4)-)-methyltransferase RsmH [Mycobacterium sp. MCS] (len=370)
Score = 40 (i=339, j=258)
Identities = 13/35 (37%), Positives = 22/35 (63%), Gaps = 4/35 (11%)
Query: 305 PTLKRLVHLVYDVRDDAPLRKVAGIPG--EFDKL 339
      T +LV+L+YD+ AP R+++G P+ F+ L
Sbjct: 224 NTTGELVELLYDA--IPAPARRTGGHPAKRTFQAL 258

>gi|677286738|sp|A3Q1M6.2|RSMH_MYCSJ RecName: Full=Ribosomal RNA small subunit
methyltransferase H; AltName: Full=16S rRNA m(4)C1402 methyltransferase; AltName: Full=rRNA
(cytosine-N(4)-)-methyltransferase RsmH [Mycobacterium sp. JLS] (len=370)
Score = 40 (i=339, j=258)
Identities = 13/35 (37%), Positives = 22/35 (63%), Gaps = 4/35 (11%)
Query: 305 PTLKRLVHLVYDVRDDAPLRKVAGIPG--EFDKL 339
      T +LV+L+YD+ AP R+++G P+ F+ L
Sbjct: 224 NTTGELVELLYDA--IPAPARRTGGHPAKRTFQAL 258

>gi|677286737|sp|A0R024.2|RSMH_MYCS2 RecName: Full=Ribosomal RNA small subunit
```

methyltransferase H; AltName: Full=16S rRNA m(4)C1402 methyltransferase; AltName: Full=rRNA
 (cytosine-N(4)-)-methyltransferase RsmH [Mycobacterium smegmatis str. MC2 155] (len=373)
 Score = 38 (i=339, j=268)
 Identities = 12/35 (34%), Positives = 23/35 (66%), Gaps = 4/35 (11%)
 Query: 305 PTLKRLVHLVYDVRDDAPLRKVAGIPG--EFDKL 339
 T ++LV+L+Y++ AP R+++G P+ F+ L
 Sbjct: 234 TTTSELVELLYEA--IPAPARRTGGHPAKRTFQAL 268

>gi|677286735|sp|B2HGS5.2|RSMH_MYCMM RecName: Full=Ribosomal RNA small subunit
 methyltransferase H; AltName: Full=16S rRNA m(4)C1402 methyltransferase; AltName: Full=rRNA
 (cytosine-N(4)-)-methyltransferase RsmH [Mycobacterium marinum M] (len=395)
 Score = 34 (i=43, j=322)
 Identities = 9/44 (20%), Positives = 24/44 (55%), Gaps = 0/44 (0%)
 Query: 0 MKILVDENMPYARDLFSRLGEVTAVPGRPIPVQAQLADADALMV 43
 ++I V++++ R+ + ++ AV GR + +A + D ++
 Sbjct: 279 ALRIAVNDELGSLRSAIPAAMDALAVGGRIVVMAYQSLEDRIK 322

>gi|677286732|sp|B1MP29.2|RSMH_MYCA9 RecName: Full=Ribosomal RNA small subunit
 methyltransferase H; AltName: Full=16S rRNA m(4)C1402 methyltransferase; AltName: Full=rRNA
 (cytosine-N(4)-)-methyltransferase RsmH [Mycobacterium abscessus ATCC 19977] (len=384)
 Score = 34 (i=220, j=108)
 Identities = 8/22 (36%), Positives = 13/22 (59%), Gaps = 0/22 (0%)
 Query: 199 PGAILINACRGAVVDNTALLTC 220
 GA+L++A GA + +LT
 Sbjct: 87 SGAVLV DATL GAGGHT EHF LTM 108

>gi|677286731|sp|A0QF44.2|RSMH_MYCA1 RecName: Full=Ribosomal RNA small subunit
 methyltransferase H; AltName: Full=16S rRNA m(4)C1402 methyltransferase; AltName: Full=rRNA
 (cytosine-N(4)-)-methyltransferase RsmH [Mycobacterium avium 104] (len=386)
 Score = 32 (i=43, j=318)
 Identities = 9/44 (20%), Positives = 23/44 (52%), Gaps = 0/44 (0%)
 Query: 0 MKILVDENMPYARDLFSRLGEVTAVPGRPIPVQAQLADADALMV 43
 ++I V++++ R + ++ AV GR + +A + D ++
 Sbjct: 275 ALRIAVNDELDTLR CALPAALDALAVDGRIVVLAYQSLEDRIK 318

>gi|677286728|sp|Q8NH95.2|O13C6_HUMAN RecName: Full=Putative olfactory receptor 13C6;
 AltName: Full=Olfactory receptor, family 13, subfamily C, member 6 pseudogene; AltName:
 Full=Olfactory receptor, family 13, subfamily C, member 7 pseudogene; AltName: Full=Putative
 olfactory receptor 13C7 [Homo sapiens] (len=151)
 Score = 23 (i=376, j=148)
 Identities = 4/23 (17%), Positives = 12/23 (52%), Gaps = 0/23 (0%)
 Query: 354 VICDDASAASLLCKLGFNAVHHP 376
 +IC+ ++ K ++ ++ P
 Sbjct: 126 AICNPLRYPVMSKAAYMPIRLP 148

>gi|677286723|sp|P20303.2|GTR1_PIG RecName: Full=Solute carrier family 2, facilitated
 glucose transporter member 1; AltName: Full=Glucose transporter type 1, erythrocyte/brain;
 Short=GLUT-1 [Sus scrofa] (len=492)
 Score = 26 (i=97, j=408)
 Identities = 7/15 (47%), Positives = 9/15 (60%), Gaps = 0/15 (0%)
 Query: 83 GFSAAPGCNAIAVVE 97
 FS +P AIAV+
 Sbjct: 394 LFSQGPRPAAIAVAG 408

>gi|694016578|sp|C0HJE6.1|PORA_CORAY RecName: Full=Porin PorA; Flags: Precursor
 [Corynebacterium amycolatum] (len=386)
 Score = 29 (i=60, j=257)
 Identities = 5/18 (28%), Positives = 14/18 (78%), Gaps = 0/18 (0%)
 Query: 43 VRSVTKVNESLLAGKPIK 60
 R++T++++S LA+ ++
 Sbjct: 240 GRKLT EADKSS LASMRLS 257

>gi|667467199|sp|B3EWZ2.1|USOM8_ACRMI RecName: Full=Uncharacterized skeletal organic matrix
 protein 8; Short=Uncharacterized SOMP-8; Flags: Precursor [Acropora millepora] (len=214)
 Score = 34 (i=152, j=168)
 Identities = 6/14 (43%), Positives = 8/14 (57%), Gaps = 0/14 (0%)
 Query: 139 GIKTLLCDPPRADR 152
 I+ +LCD P D
 Sbjct: 155 FINEVLCDVPGLDC 168

>gi|667467198|sp|B8WI85.1|USOM7_ACRMI RecName: Full=Uncharacterized skeletal organic matrix

```

protein 7; Short=Uncharacterized SOMP-7; Flags: Precursor [Acropora millepora] (len=422)
Score = 36 (i=264, j=344)
Identities = 8/31 (26%), Positives = 16/31 (52%), Gaps = 0/31 (0%)
Query:   234 WEGEPELNVELLKKVDIGTSHIAGYTLEGKA 264
          E E + + ++ ++G +GY L+GK
Sbjct:   314 AEDEDNYDFVYFRPHSVGGCFQTGYLLKGKP 344

>gi|667467197|sp|B8VIX3.1|USOM6_ACRMI RecName: Full=Uncharacterized skeletal organic matrix
protein 6; Short=Uncharacterized SOMP-6; Flags: Precursor [Acropora millepora] (len=436)
Score = 30 (i=25, j=226)
Identities = 6/22 (27%), Positives = 13/22 (59%), Gaps = 0/22 (0%)
Query:    4 LVDENMPYARDLFSRLGEVTAV 25
          V+ENM R+++ +E+ +
Sbjct:   205 SVEENMQALRNFLPSQSEAMD 226

>gi|667467196|sp|B8VIU6.1|USOM5_ACRMI RecName: Full=Uncharacterized skeletal organic matrix
protein 5; Short=Uncharacterized SOMP-5; Flags: Precursor [Acropora millepora] (len=256)
Score = 35 (i=368, j=122)
Identities = 8/49 (16%), Positives = 27/49 (55%), Gaps = 6/49 (12%)
Query:   320 RRDDAPLRKVAGIPGEFDKLRKNYLERREWSSLYVICDDASAASLLCKL 368
          R +AP+ ++++ +FD ++ + S++Y + ++++ + C +
Sbjct:    74 PRHSAPVASISSCKEQFD-----KNNSSPSQVYELTFGSQVVPVYCHM 122

>gi|667467195|sp|B8UU74.1|USOM4_ACRMI RecName: Full=Uncharacterized skeletal organic matrix
protein 4; Short=Uncharacterized SOMP-4, partial [Acropora millepora] (len=204)
Score = 31 (i=55, j=66)
Identities = 9/37 (24%), Positives = 20/37 (54%), Gaps = 5/37 (14%)
Query:   19 LGEVTAVPGRPIPVAQLADADALMVRSVTKVNESLLA 55
          G VTA G + ++A+A + + +K++ ++ A
Sbjct:   30 TGPVTAPKG-----RHTVEAEAQALPQQAKMQATVAA 66

>gi|667467194|sp|B8RJM0.1|USOM3_ACRMI RecName: Full=Uncharacterized skeletal organic matrix
protein 3; Short=Uncharacterized SOMP-3; Flags: Precursor, partial [Acropora millepora]
(len=433)
Score = 32 (i=46, j=386)
Identities = 10/29 (34%), Positives = 16/29 (55%), Gaps = 1/29 (3%)
Query:   18 LGEVTA-VPGRPIPVAQLADADALMVRSV 46
          G+VT P P+P + A+ ++ RSV
Sbjct:   358 GGVTRMGPLPPLPGEESIYAEPMIKRSV 386

>gi|667467193|sp|B7WFQ1.1|USOM2_ACRMI RecName: Full=Uncharacterized skeletal organic matrix
protein 2; Short=Uncharacterized SOMP-2; Flags: Precursor [Acropora millepora] (len=505)
Score = 26 (i=374, j=218)
Identities = 5/22 (23%), Positives = 11/22 (50%), Gaps = 0/22 (0%)
Query:   353 YVICDDASAASLLCKLGFNAVH 374
          + C+D ++A L +F+
Sbjct:   197 CISCEDKKSACALLAGSFKFRK 218

>gi|667467192|sp|B3EX00.1|USOM1_ACRMI RecName: Full=Uncharacterized skeletal organic matrix
protein 1; Short=Uncharacterized SOMP-1, partial [Acropora millepora] (len=448)
Score = 29 (i=69, j=167)
Identities = 7/26 (27%), Positives = 16/26 (62%), Gaps = 0/26 (0%)
Query:   44 RSVTKVNESLLAGKPIKFVGTATAGT 69
          +V++VN +L A+ +++ G T+
Sbjct:   142 LNVNSVNLTLASVSVQIDGPHTSRI 167

>gi|667467190|sp|B3EWZ7.1|TRP_ACRMI RecName: Full=Threonine-rich protein; Flags: Precursor,
partial [Acropora millepora] (len=288)
Score = 36 (i=92, j=115)
Identities = 8/26 (31%), Positives = 18/26 (69%), Gaps = 0/26 (0%)
Query:   67 AGTDHVDEAWLKQAGIGFSAAPGCNA 92
          +GT V ++ ++ +G++ + PGC+A
Sbjct:   90 TGTTTVTRGCFNITGLNCGDNPGCGA 115

```