Supplementary Dataset 2:

This dataset contains the significant hits from different viral genomes identified with a threshold E-value ≤ 0.1 using tBlastn. The viral genome database (ref_viruses_rep_genomes.tar.gz,ftp://ftp.ncbi.nlm.nih.gov/blast/db/) was downloaded from NCBI and this database was searched for the hormone peptide sequences reported in **Extended Dataset 1.** The significant hits with a threshold E value ≤ 0.1 using tBlastn are reported below. The name of the human protein is reported at the top of every new hit set and the name of the viruses, scores and E-values are listed under the protein name for each hit. This is followed by the alignment figures comparing the human hormones (query) with the identified viral proteins (subject). The identical residues (Identities), conservatively sequences (Positives, +) and the gaps of the alignment (Gaps, -) are reported at the beginning of each alignment. **PART A** reports the results obtained using the precursor sequences of the proteins for the database search. **PART B** (p. 27) reports the hits obtained using processed sequences of the hormones. All these processed sequences were collected from Uniprot database. Because there are many hits identified for adiponectin, mainly based on the collagen domain, we share the adiponectin hits at the end of the document (p. 47). The list of the proteins are organized according to the database search as shown below. Endothelin 1 was only identified when we make the search using the processed active form of the hormone.

A) The precursor sequences of human proteins that have significant sequences in viral genomes.

1. Insulin
2. Insulin-like growth factor-1
3. Insulin-like growth factor-2
4. Tumor necrosis factor
5. Transforming growth factor beta-1
6. Transforming growth factor beta-2
7. Endothelin-2
8. Inhibin beta A-chain
9. Complement factor D (Adipsin)
10. Resistin
11. Interleukin-6
12. Fibronectin type III domain-containing protein 5
13. Fibroblast growth factor 21
14. Fibroblast growth factor 19
15. Adiponectin (p.47)

B) The processed sequences of the human proteins that have significant sequences in viral genomes. Endothelin-1 is the only hormone that was not identified with whole sequence (and not reported above) but identified with the processed hormone sequence search.

1. Endothelin-2|49-69
2. Endothelin-1|53-90
3. Endothelin-1|53-73
4. Fibroblast growth factor 21|29-209
5. Fibroblast growth factor 19|25-216
6. Fibronectin type III domain-containing protein 5|32-212
7. Fibronectin type III domain-containing protein 5 (Irisin)|32-143
8. Transforming growth factor beta-2|303-414
9. Transforming growth factor beta-1|279-390

10. Tumor necrosis factor|57-233
11. Insulin-like growth factor 1|49-118
12. Insulin-like growth factor 2|25-91
13. Inhibin beta A chain|311-426
14. Interleukin-6|30-212
15. Resistin|19-108

PART A: The results of the precursor sequence search of the human proteins

1. Human insulin

```
Query= sp|P01308|INS_HUMAN Insulin OS=Homo sapiens GN=INS PE=1 SV=1

Length=110
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_033423.1  Lymphocystis disease virus Sa isolate SA9, complete ...  39.7    0.001
NC_001824.1  Lymphocystis disease virus 1, complete genome            37.0    0.007


>NC_033423.1 Lymphocystis disease virus Sa isolate SA9, complete genome
Length=208501

 Score = 39.7 bits (91),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/84 (35%), Positives = 37/84 (44%), Gaps = 26/84 (31%)
 Frame = +2

Query  28      QHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEGSLQ  87
               Q LCGS LV+AL LVCGE G  Y P      +            P +G
Sbjct  203636  QTLCGSELVDALELVCGEYGGIYRPPKNANKK------------PQSG------------  203743

Query  88      KRGIVEQCCTSI-CSLYQLENYCN  110
                + IV+ CCT+  C+   L+ YCN
Sbjct  203744  -KKIVDVCCTTKGCNYMDLKQYCN  203812


>NC_001824.1 Lymphocystis disease virus 1, complete genome
Length=102653

 Score = 37.0 bits (84),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 16/30 (53%), Positives = 19/30 (63%), Gaps = 0/30 (0%)
 Frame = +1

Query  30     LCGSHLVEALYLVCGERGFFYTPKTRREAE  59
              LC +HLV AL  VCG RG +  P TRR +
Sbjct  57112  LCSAHLVAALQRVCGNRGVYRPPPTRRRST  57201


Lambda      K        H        a         alpha
   0.322    0.140    0.438    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
```

```
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 2144481100
```

2. Human Insulin-like growth factor I

```
Query= sp|P05019|IGF1_HUMAN Insulin-like growth factor I OS=Homo sapiens
GN=IGF1 PE=1 SV=1

Length=195
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006549.1  Singapore grouper iridovirus, complete genome             54.3    7e-08
NC_033423.1  Lymphocystis disease virus Sa isolate SA9, complete ...  52.0    5e-07
NC_001824.1  Lymphocystis disease virus 1, complete genome             40.0    0.004


>NC_006549.1 Singapore grouper iridovirus, complete genome
Length=140131

 Score = 54.3 bits (129),  Expect = 7e-08, Method: Compositional matrix adjust.
 Identities = 26/61 (43%), Positives = 31/61 (51%), Gaps = 5/61 (8%)
 Frame = +3

Query  53     LCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEMYCAPL  112
              +CG EL+DAL   CGDRG Y     G  + S      G+ D CC   CD   L+ YC P
Sbjct  58659  VCGGELIDALTEHCGDRGVYTPPRRGRRTRS-----VGLADACCKNECDENELDRYCNPK  58823

Query  113    K  113
              K
Sbjct  58824  K  58826


>NC_033423.1 Lymphocystis disease virus Sa isolate SA9, complete genome
Length=208501

 Score = 52.0 bits (123),  Expect = 5e-07, Method: Compositional matrix adjust.
 Identities = 29/74 (39%), Positives = 43/74 (58%), Gaps = 7/74 (9%)
 Frame = +2

Query  39      LLTFTSSATAGPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTG--IVDECC  96
               +L   S +    +TLCG+ELVDAL+ VCG+ G  +  P     ++ + PQ+G  IVD CC
Sbjct  203600  ILIVMSVSPILCQTLCGSELVDALELVCGEYGGIYRPP----KNANKKPQSGKKIVDVCC  203767

Query  97      -FRSCDLRRLEMYC  109
                 + C+   L+ YC
Sbjct  203768  TTKGCNYMDLKQYC  203809


>NC_001824.1 Lymphocystis disease virus 1, complete genome
Length=102653

 Score = 40.0 bits (92),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 19/43 (44%), Positives = 24/43 (56%), Gaps = 0/43 (0%)
 Frame = +1

Query  35     LALCLLTFTSSATAGPETLCGAELVDALQFVCGDRGFYFNKPT  77
```

```
              + +CL  +    +   E LC A LV ALQ VCG+RG Y   PT
Sbjct  57058  IIVCLFVYCLLYSITAEILCSAHLVAALQRVCGNRGVYRPPPT  57186



Lambda      K        H        a         alpha
   0.319    0.133    0.412    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 7443888780
```

3. Human Insulin-like growth factor II

```
Query= sp|P01344|IGF2_HUMAN Insulin-like growth factor II OS=Homo sapiens
GN=IGF2 PE=1 SV=1

Length=180
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006549.1  Singapore grouper iridovirus, complete genome            53.1    1e-07
NC_033423.1  Lymphocystis disease virus Sa isolate SA9, complete ...  37.7    0.018


>NC_006549.1 Singapore grouper iridovirus, complete genome
Length=140131

 Score = 53.1 bits (126),  Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 39/99 (39%), Positives = 48/99 (48%), Gaps = 5/99 (5%)
 Frame = +3

Query  7      KSMLVLLTFLAFASCCIAAYRPSETLCGGELVDTLQFVCGDRGFYFsrpasrvsrrsrGI  66
              + ML  L  L F +  I      + +CGGEL+D L   CGDRG Y   P      RS G+
Sbjct  58587  RKMLFKLMLLVFMTATIEETHQLQ-VCGGELIDALTEHCGDRGVYT-PPRRGRRTRSVGL  58760

Query  67     VEECCFRSCDLALLETYCATPAKSERDVST--PPTVLPD  103
               + CC   CD   L+ YC  P KS    ST  P TV P+
Sbjct  58761  ADACCKNECDENELDRYC-NPKKSTVAPSTVAPSTVAPE  58874


>NC_033423.1 Lymphocystis disease virus Sa isolate SA9, complete genome
Length=208501

 Score = 37.7 bits (86),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 23/60 (38%), Positives = 34/60 (57%), Gaps = 3/60 (5%)
 Frame = +2

Query  30      ETLCGGELVDTLQFVCGDRGFYFsrpasrvsrrsrG--IVEECC-FRSCDLALLETYCAT  86
               +TLCG ELVD L+ VCG+ G  +  P +    +   G  IV+ CC  + C+   L+ YC +
Sbjct  203636  QTLCGSELVDALELVCGEYGGIYRPPKNANKKPQSGKKIVDVCCTTKGCNYMDLKQYCNS  203815



Lambda      K        H        a         alpha
   0.324    0.139    0.446    0.792     4.96
```

```
Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 6246711324
```

4. Human Tumor necrosis factor

```
Query= sp|P01375|TNFA_HUMAN Tumor necrosis factor OS=Homo sapiens GN=TNF
PE=1 SV=1

Length=233
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_030656.1  Pteropox virus strain Australia, complete genome         52.8    5e-07


>NC_030656.1 Pteropox virus strain Australia, complete genome
Length=133492

 Score = 52.8 bits (125),  Expect = 5e-07, Method: Compositional matrix adjust.
 Identities = 38/151 (25%), Positives = 63/151 (42%), Gaps = 24/151 (16%)
 Frame = +1

Query  86     DKPVAHVVANPQAEGQL-------------QWLNRRANALLANGVELRDNQLVVPSEGLY  132
              +  VAHV  N     +L              W N   N +L+N    + D +++V   GLY
Sbjct  34069  NTSVAHVTGNNNWNERLYPNNYSFLGNKITSWSNTSNNVVLSNSYYI-DGEIIVTVSGLY  34245

Query  133    LIYSQVLFK-----GQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEA  187
               IY+Q  FK          S ++ +   I +   SY   + L+ + +S C  +T E
Sbjct  34246  YIYAQTYFKLIFGYNSKGNSKNIQMVQYIYKNTSSYGDPLMLMKSARSNCWDKTAEYGLY  34425

Query  188    KPWYEPIYLGGVFQLEKGDRLSAEINRPDYL  218
                    +Y GG+  L+KGD +   +   ++L
Sbjct  34426  -----SVYQGGIHYLKKGDSVFVTVTNKNFL  34503



Lambda      K        H        a         alpha
   0.318    0.135    0.396    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 10435098712
```

5. Human Transforming growth factor beta-1

```
Query= sp|P01137|TGFB1_HUMAN Transforming growth factor beta-1 OS=Homo
sapiens GN=TGFB1 PE=1 SV=2

Length=390
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value
```

```
NC_006966.1  Deerpox virus W-848-83, complete genome               100     8e-22
NC_002188.1  Fowlpox virus, complete genome                        68.2    4e-11
NC_024446.1  Penguinpox virus isolate PSan92, complete genome      66.2    1e-10
NC_024447.1  Pigeonpox virus isolate FeP2, complete genome         64.7    4e-10
NC_005309.1  Canarypox virus, complete genome                      61.2    5e-09
NC_028238.1  Turkeypox virus strain TKPV-HU1124/2011, complete ge...  50.4    1e-05


>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 100 bits (249),  Expect = 8e-22, Method: Compositional matrix adjust.
 Identities = 59/154 (38%), Positives = 88/154 (57%), Gaps = 31/154 (20%)
 Frame = +3

Query  243     RRGDLA--TIHGMNRPFLLLMATPLERAQHLQSSRHRRALDTNYC-FSSTEKNCCVRQLY  299
               R  D+A   I  +N P +LL+    ++  ++++ RH   +D+  C  SST   CC+   Y
Sbjct  155088  RIQDMAKLNISNINNPHILLLK---KKNNNIRTVRH--VMDS--CELSST---CCLVDFY  155237

Query  300     IDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAL-YN---QHNPGASAAPC  355
               IDF+KD+GW WI++P+GYHAN C+G C +         K++ + YN   +HN       C
Sbjct  155238  IDFKKDMGWNWIYKPEGYHANLCIGNCNH---------KLINMPYNYAFKHN-----VFC  155375

Query  356     CVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
               C P+ ++ L I YY GRK KV+ L NM + SC C
Sbjct  155376  CAPKKMKSLIIAYYEGRKYKVDNLKNMKIVSCGC  155477


>NC_002188.1 Fowlpox virus, complete genome
Length=288539

 Score = 68.2 bits (165),  Expect = 4e-11, Method: Compositional matrix adjust.
 Identities = 38/109 (35%), Positives = 55/109 (50%), Gaps = 3/109 (3%)
 Frame = -2

Query  281    DTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVL  340
              D+   +SS   NC V + YI+FR  +G KWI  P G    +C+G C      D+    +L
Sbjct  80251  DSGVDYSSPSDNCKVYRKYINFRS-IGLKWILHPPGIDYGYCMGECQSFVYTDSFLYSLL  80075

Query  341    ALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
              A    +  G     CC  Q+++ L + Y +GR PK   L  + V+SCKC
Sbjct  80074  AF--HYIDGIELKQCCSIQSMDDLVVHYRLGRTPKTAILRKVSVKSCKC  79934


>NC_024446.1 Penguinpox virus isolate PSan92, complete genome
Length=306862

 Score = 66.2 bits (160),  Expect = 1e-10, Method: Compositional matrix adjust.
 Identities = 39/115 (34%), Positives = 55/115 (48%), Gaps = 11/115 (10%)
 Frame = -2

Query  275    RHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT  334
              + R   D+NYC         + + YI+FR D+G KWI  P G    +C+G C      D+
Sbjct  88680  KKRSIQDSNYCK--------IYRKYINFR-DIGLKWILHPPGIDYGYCVGECTSFAYTDS  88528

Query  335    QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
                  +LA    +  G     CC  Q ++ L + Y VGR PK   L  + V+SCKC
```

```
Sbjct  88527  FLYSLLAF--HYIDGIELKQCCSIQDMDDLIVHYRVGRTPKTSVLYKVSVKSCKC  88369


 Score = 50.4 bits (119),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 26/85 (31%), Positives = 37/85 (44%), Gaps = 1/85 (1%)
 Frame = +1

Query  306     LGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLP  365
               LG+KWIHEP+G    +C G C  + S D        +   +        CC P+  E +
Sbjct  166063  LGYKWIHEPRGIQFTYCYGTCV-MGSYDESSVIYGTVVTNYISDKGIPSCCSPKRREDIT  166239

Query  366     IVYYVGRKPKVEQLSNMIVRSCKCS  390
               I YY GR  +   + N +   C C
Sbjct  166240  ISYYRGRNIEKHTIHNFMPTHCGCG  166314


>NC_024447.1 Pigeonpox virus isolate FeP2, complete genome
Length=282356

 Score = 64.7 bits (156),  Expect = 4e-10, Method: Compositional matrix adjust.
 Identities = 35/98 (36%), Positives = 50/98 (51%), Gaps = 3/98 (3%)
 Frame = -3

Query  292    NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS  351
              +C + + YI+FR D+G KWI  P G    +C+G C      D+    +LA    +  G
Sbjct  87537  DCRIYRKYINFR-DIGLKWILHPPGIDYGYCVGECTSFAYTDSFLYSLLAF--HYIDGIE  87367

Query  352    AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
                 CC  Q ++ L + Y VGR PK   L  + V+SCKC
Sbjct  87366  LKQCCSIQDMDDLIVHYRVGRTPKTSVLYKVSVKSCKC  87253


>NC_005309.1 Canarypox virus, complete genome
Length=359853

 Score = 61.2 bits (147),  Expect = 5e-09, Method: Compositional matrix adjust.
 Identities = 35/100 (35%), Positives = 50/100 (50%), Gaps = 8/100 (8%)
 Frame = +1

Query  293     CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQ---YSKVLALYNQHNPG  349
               C +  +Y+DF   LG+KWIHEPKG    +C G C  + S D     Y  ++  Y  +N
Sbjct  199456  CSLNSVYLDFSA-LGYKWIHEPKGIQFTYCHGTCI-LSSYDKSSVIYGTIVTNYLSNN--  199623

Query  350     ASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
                    CC P+  + + I YY+GR  K + + N I   C C
Sbjct  199624  -RIPLCCSPKERKDITITYYLGRNVKKQTIRNFIPTHCGC  199740


 Score = 50.8 bits (120),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 29/97 (30%), Positives = 47/97 (48%), Gaps = 3/97 (3%)
 Frame = -3

Query  293     CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA  352
               C +R  ++ F KDLG  WI  PK +   +C G C  I S  T+ S +      ++   +
Sbjct  194440  CLLRHKHMKF-KDLGCNWILRPKSFIFTYCKGTC--IISSFTRSSIIYGSMFINDIKKNI  194270

Query  353     APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
                 CC P     + I+Y +G+  KV ++ + +  SC C
```

```
Sbjct  194269  HICCAPVTRSNITIMYMLGKNVKVSEIKDFLPSSCGC  194159


 Score = 49.3 bits (116),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 31/108 (29%), Positives = 42/108 (39%), Gaps = 10/108 (9%)
 Frame = +3

Query  286     FSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY--  343
               F   +  C +R + I F  D G KWI  P      +C G C       + Y K   +Y
Sbjct  195411  FLDIDAICNIRSINIKF-ADYGMKWILSPLSTVLTYCYGICSI-----SSYQKTSLMYGT  195572

Query  344     --NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
                   H P  +   CC P       I Y VGR  K + ++N +   C C
Sbjct  195573  IITNHMPDNTIPQCCYPITRSNFTIRYKVGRNIKTDVINNFMPLECAC  195716


 Score = 45.4 bits (106),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 31/100 (31%), Positives = 46/100 (46%), Gaps = 8/100 (8%)
 Frame = -2

Query  293     CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQ---YSKVLALYNQHNPG  349
               C +R  YI F +D+G  W+  PKG   ++C G C  + S D     Y K+L L + H
Sbjct  198458  CSLRYQYITF-EDMGCNWVLSPKGIMFSYCTGTCV-VSSFDKSSVIYGKML-LNSIHKTK  198288

Query  350     ASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
                    CC P   + + I Y  G+  K  ++ N +   C C
Sbjct  198287  LHV--CCKPIRRQSVKITYMHGKNIKQSEIKNFMPSECGC  198174


>NC_028238.1 Turkeypox virus strain TKPV-HU1124/2011, complete genome
Length=188534

 Score = 50.4 bits (119),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 32/100 (32%), Positives = 48/100 (48%), Gaps = 4/100 (4%)
 Frame = +2

Query  291    KNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVL-ALYNQHNPG  349
              K C +   YI F KD+G  W+  PKG+   +C G C  I S  T+ S V  A+
Sbjct  64325  KECALHYKYISF-KDVGCNWVLSPKGFTFRYCKGEC--IVSSFTKSSIVYGAMLVNDAKS  64495

Query  350    ASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
              ++   CC P++   + I+Y VG   +   + N +  SC C
Sbjct  64496  SNIHICCSPKSRTSMRIMYAVGSNIRESTIHNFMPSSCGC  64615


 Score = 48.1 bits (113),  Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 29/97 (30%), Positives = 40/97 (41%), Gaps = 2/97 (2%)
 Frame = -3

Query  293    CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA  352
              C +    IDF   LG KWI  PK     +C G C  + S D        L N +    +
Sbjct  63210  CKLHHKRIDF-SSLGMKWITYPKSIDITYCSGICV-VGSYDKTSVIYGTLVNSYMASHNI  63037

Query  353    APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  389
                CC P+    L + Y  GRK   + + N +  +C C
Sbjct  63036  PQCCFPKTRSHLTVTYMSGRKQMNQTIKNFMPATCSC  62926
```

```
Lambda      K        H        a         alpha
   0.320    0.135    0.426    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 23335195884
```

6. Human Transforming growth factor beta-2

```
Query= sp|P61812|TGFB2_HUMAN Transforming growth factor beta-2 OS=Homo
sapiens GN=TGFB2 PE=1 SV=1

Length=414
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006966.1  Deerpox virus W-848-83, complete genome                  83.2    7e-16
NC_024447.1  Pigeonpox virus isolate FeP2, complete genome            67.8    5e-11
NC_024446.1  Penguinpox virus isolate PSan92, complete genome         67.4    7e-11
NC_002188.1  Fowlpox virus, complete genome                           65.9    2e-10
NC_005309.1  Canarypox virus, complete genome                         62.4    3e-09
NC_028238.1  Turkeypox virus strain TKPV-HU1124/2011, complete ge...  47.8    8e-05


>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 83.2 bits (204),  Expect = 7e-16, Method: Compositional matrix adjust.
 Identities = 47/137 (34%), Positives = 67/137 (49%), Gaps = 22/137 (16%)
 Frame = +3

Query  278     TPHLLLMLLPSYRLESQQTNRRKKR-ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIH  336
                PH+LL       L+ +  N R  R  +D+      +   CCL   YIDFK+D+GW WI+
Sbjct  155130  NPHILL-------LKKKNNNIRTVRHVMDSC----ELSSTCCLVDFYIDFKKDMGWNWIY  155276

Query  337     EPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYYIGK  396
               +P+GY+AN C G C         H  +   YN          CC  + ++ L I YY G+
Sbjct  155277  KPEGYHANLCIGNC--------NHKLINMPYNY--AFKHNVFCCAPKKMKSLIIAYYEGR  155426

Query  397     TPKIEQLSNMIVKSCKC  413
                  K++ L NM + SC C
Sbjct  155427  KYKVDNLKNMKIVSCGC  155477


>NC_024447.1 Pigeonpox virus isolate FeP2, complete genome
Length=282356

 Score = 67.8 bits (164),  Expect = 5e-11, Method: Compositional matrix adjust.
 Identities = 39/105 (37%), Positives = 57/105 (54%), Gaps = 5/105 (5%)
 Frame = -3

Query  311    RNVQD--NCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYN  368
              R+VQD  +C +   YI+F RD+G KWI  P G +  +C G C     +D+    +L+ +
Sbjct  87558  RSVQDSNDCRIYRKYINF-RDIGLKWILHPPGIDYGYCVGECTSFAYTDSFLYSLLAFHY  87382
```

```
Query  369    TINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  413
                  E     CC  QD++ L + Y +G+TPK   L  + VKSCKC
Sbjct  87381  IDGIELKQ--CCSIQDMDDLIVHYRVGRTPKTSVLYKVSVKSCKC  87253


>NC_024446.1 Penguinpox virus isolate PSan92, complete genome
Length=306862

 Score = 67.4 bits (163),  Expect = 7e-11, Method: Compositional matrix adjust.
 Identities = 38/105 (36%), Positives = 57/105 (54%), Gaps = 5/105 (5%)
 Frame = -2

Query  311    RNVQDN--CCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYN  368
              R++QD+  C +   YI+F RD+G KWI  P G +  +C G C     +D+    +L+ +
Sbjct  88674  RSIQDSNYCKIYRKYINF-RDIGLKWILHPPGIDYGYCVGECTSFAYTDSFLYSLLAFHY  88498

Query  369    TINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  413
                  E     CC  QD++ L + Y +G+TPK   L  + VKSCKC
Sbjct  88497  IDGIELKQ--CCSIQDMDDLIVHYRVGRTPKTSVLYKVSVKSCKC  88369


 Score = 48.1 bits (113),  Expect = 8e-05, Method: Compositional matrix adjust.
 Identities = 25/85 (29%), Positives = 38/85 (45%), Gaps = 1/85 (1%)
 Frame = +1

Query  330     LGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLT  389
               LG+KWIHEP+G    +C G C  + S D       ++      +     CC  +  E +T
Sbjct  166063  LGYKWIHEPRGIQFTYCYGTC-VMGSYDESSVIYGTVVTNYISDKGIPSCCSPKRREDIT  166239

Query  390     ILYYIGKTPKIEQLSNMIVKSCKCS  414
               I YY G+  +   + N +   C C
Sbjct  166240  ISYYRGRNIEKHTIHNFMPTHCGCG  166314


>NC_002188.1 Fowlpox virus, complete genome
Length=288539

 Score = 65.9 bits (159),  Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 39/128 (30%), Positives = 60/128 (47%), Gaps = 3/128 (2%)
 Frame = -2

Query  286    LPSYRLESQQTNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANF  345
              LP+          +K    D+   + +  DNC +   YI+F R +G KWI  P G +  +
Sbjct  80308  LPTESTNKMSVGSKKYVESDSGVDYSSPSDNCKVYRKYINF-RSIGLKWILHPPGIDYGY  80132

Query  346    CAGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSN  405
              C G C     +D+    +L+ +     E     CC  Q ++ L + Y +G+TPK   L
Sbjct  80131  CMGECQSFVYTDSFLYSLLAFHYIDGIELKQ--CCSIQSMDDLVVHYRLGRTPKTAILRK  79958

Query  406    MIVKSCKC  413
              + VKSCKC
Sbjct  79957  VSVKSCKC  79934


>NC_005309.1 Canarypox virus, complete genome
Length=359853

 Score = 62.4 bits (150),  Expect = 3e-09, Method: Compositional matrix adjust.
```

```
 Identities = 36/102 (35%), Positives = 52/102 (51%), Gaps = 4/102 (4%)
 Frame = +1

Query  314     QDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPE  373
               Q  C L  +Y+DF   LG+KWIHEPKG    +C G C  + SS  + S +     T
Sbjct  199447  QHVCSLNSVYLDFSA-LGYKWIHEPKGIQFTYCHGTC--ILSSYDKSSVIYGTIVTNYLS  199617

Query  374     ASASP-CCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  414
                +  P CC  ++ + +TI YY+G+  K + + N I   C C
Sbjct  199618  NNRIPLCCSPKERKDITITYYLGRNVKKQTIRNFIPTHCGCG  199743


 Score = 52.4 bits (124),  Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 30/97 (31%), Positives = 48/97 (49%), Gaps = 3/97 (3%)
 Frame = -3

Query  317     CCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASA  376
               C LR  ++ FK DLG  WI  PK +   +C G C  + SS T+ S +       + + +
Sbjct  194440  CLLRHKHMKFK-DLGCNWILRPKSFIFTYCKGTC--IISSFTRSSIIYGSMFINDIKKNI  194270

Query  377     SPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  413
                 CC       +TI+Y +GK  K+ ++ + +  SC C
Sbjct  194269  HICCAPVTRSNITIMYMLGKNVKVSEIKDFLPSSCGC  194159


 Score = 45.1 bits (105),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 32/101 (32%), Positives = 48/101 (48%), Gaps = 6/101 (6%)
 Frame = -2

Query  315     DNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLS--LYNTINP  372
               D C LR  YI F+ D+G  W+  PKG   ++C G C  + SS  + S +    L N+I+
Sbjct  198464  DICSLRYQYITFE-DMGCNWVLSPKGIMFSYCTGTC--VVSSFDKSSVIYGKMLLNSIH-  198297

Query  373     EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  413
               +     CC     + + I Y  GK  K  ++ N +   C C
Sbjct  198296  KTKLHVCCKPIRRQSVKITYMHGKNIKQSEIKNFMPSECGC  198174


 Score = 43.9 bits (102),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 35/129 (27%), Positives = 53/129 (41%), Gaps = 17/129 (13%)
 Frame = +3

Query  290     RLESQQTNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGA  349
               R ES+   R K+  LD       +   C +R + I F  D G KWI  P      +C G
Sbjct  195372  RSESELLPRVKRDFLD-------IDAICNIRSINIKFA-DYGMKWILSPLSTVLTYCYGI  195527

Query  350     CPYLWSSDTQHSRVLSLYNTI----NPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSN  405
               C     S + + +   +Y TI     P+ +   CC        TI Y +G+  K + ++N
Sbjct  195528  C-----SISSYQKTSLMYGTIITNHMPDNTIPQCCYPITRSNFTIRYKVGRNIKTDVINN  195692

Query  406     MIVKSCKCS  414
                +   C C
Sbjct  195693  FMPLECACG  195719


>NC_028238.1 Turkeypox virus strain TKPV-HU1124/2011, complete genome
Length=188534
```

```
 Score = 47.8 bits (112),  Expect = 8e-05, Method: Compositional matrix adjust.
 Identities = 31/99 (31%), Positives = 47/99 (47%), Gaps = 6/99 (6%)
 Frame = +2

Query  317    CCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASA  376
              C L   YI FK D+G  W+  PKG+   +C G C  + SS T+ S V      +N   S+
Sbjct  64331  CALHYKYISFK-DVGCNWVLSPKGFTFRYCKGEC--IVSSFTKSSIVYGAM-LVNDAKSS  64498

Query  377    S--PCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  413
              +   CC  +    + I+Y +G   +   + N +  SC C
Sbjct  64499  NIHICCSPKSRTSMRIMYAVGSNIRESTIHNFMPSSCGC  64615


 Score = 43.9 bits (102),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 28/97 (29%), Positives = 42/97 (43%), Gaps = 2/97 (2%)
 Frame = -3

Query  317    CCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASA  376
              C L    IDF   LG KWI  PK  +  +C+G C  + S D       +L N+     +
Sbjct  63210  CKLHHKRIDFS-SLGMKWITYPKSIDITYCSGICV-VGSYDKTSVIYGTLVNSYMASHNI  63037

Query  377    SPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  413
                CC  +    LT+ Y  G+    + + N +  +C C
Sbjct  63036  PQCCFPKTRSHLTVTYMSGRKQMNQTIKNFMPATCSC  62926



Lambda      K        H        a         alpha
   0.322    0.135    0.415    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 25386641676
```

7. Human Endothelin-2

```
Query= sp|P20800|EDN2_HUMAN Endothelin-2 OS=Homo sapiens GN=EDN2 PE=1 SV=2

Length=178
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006966.1  Deerpox virus W-848-83, complete genome                  42.7    4e-04


>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 42.7 bits (99),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 17/56 (30%), Positives = 30/56 (54%), Gaps = 0/56 (0%)
 Frame = -1

Query  14    ALLVALHEGKGQAAATLEQPASSSHAQGTHLRLRRCSCSSWLDKECVYFCHLDIIW  69
             ++++   E      ++++   +   +   H R +RC C +  DKEC+ FC LDIIW
Sbjct  5273  SIMLCCCENDESYISSIDDNINKPDSNIPHKRTKRCYCDTHDDKECMNFCELDIIW  5106
```

```
Lambda      K        H        a         alpha
   0.320    0.129    0.418    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 6075568548
```

8. Human Inhibin beta A chain

```
Query= sp|P08476|INHBA_HUMAN Inhibin beta A chain OS=Homo sapiens GN=INHBA
PE=1 SV=2

Length=426
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006966.1  Deerpox virus W-848-83, complete genome                  63.2    1e-09
NC_028238.1  Turkeypox virus strain TKPV-HU1124/2011, complete ge...  58.9    4e-08
NC_005309.1  Canarypox virus, complete genome                         53.5    2e-06
NC_024446.1  Penguinpox virus isolate PSan92, complete genome         45.4    5e-04
NC_024447.1  Pigeonpox virus isolate FeP2, complete genome            40.0    0.026


>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 63.2 bits (152),  Expect = 1e-09, Method: Compositional matrix adjust.
 Identities = 34/106 (32%), Positives = 50/106 (47%), Gaps = 20/106 (19%)
 Frame = +3

Query  321     CCKKQFFVSFK-DIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMR  379
               CC   F++ FK D+GWN WI  P GYHAN C G C   +                  M
Sbjct  155217  CCLVDFYIDFKKDMGWN-WIYKPEGYHANLCIGNCNHKLIN-----------------MP  155342

Query  380     GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  425
                +  F +   CC P K++ + + YY +G+     +++NM +  CGC
Sbjct  155343  YNYAFKHNVFCCAPKKMKSLIIAYY-EGRKYKVDNLKNMKIVSCGC  155477


>NC_028238.1 Turkeypox virus strain TKPV-HU1124/2011, complete genome
Length=188534

 Score = 58.9 bits (141),  Expect = 4e-08, Method: Compositional matrix adjust.
 Identities = 31/99 (31%), Positives = 54/99 (55%), Gaps = 10/99 (10%)
 Frame = +2

Query  327    FVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFAN  386
              ++SFKD+G N W+++P G+   YC+GEC   ++  + SS+ + + ++N  +       +N
Sbjct  64349  YISFKDVGCN-WVLSPKGFTFRYCKGECI--VSSFTKSSIVYGAMLVNDAKS------SN  64501

Query  387    LKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  425
              +  CC P     M ++ Y  G NI +  I N +   CGC
Sbjct  64502  IHICCSPKSRTSMRIM-YAVGSNIRESTIHNFMPSSCGC  64615
```

```
 Score = 40.8 bits (94),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 30/118 (25%), Positives = 49/118 (42%), Gaps = 10/118 (8%)
 Frame = -3

Query  308    RRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLS  367
              ++  L+ D +   C      + F  +G   WI  P      YC G C   + G+   +
Sbjct  63249  KKDYLKADDRNTTCKLHHKRIDFSSLGMK-WITYPKSIDITYCSGIC---VVGSYDKTSV  63082

Query  368    FHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  425
               + T++N Y M  H    N+  CC P K R    + Y  G+  + + I+N +   C C
Sbjct  63081  IYGTLVNSY-MASH----NIPQCCFP-KTRSHLTVTYMSGRKQMNQTIKNFMPATCSC  62926


>NC_005309.1 Canarypox virus, complete genome
Length=359853

 Score = 53.5 bits (127),  Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 30/105 (29%), Positives = 49/105 (47%), Gaps = 2/105 (2%)
 Frame = -3

Query  321    CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRG  380
              C  KQ ++  K +  +D IIAP G    YC G C  +      S+  +    +    ++
Sbjct  74056  CTTKQKYLDLKYLDMDDTIIAPRGITFKYCSGYCDINSMKNFYSNSLYGILAMKFISLKA  73877

Query  381    HSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  425
               +  +N K CC P  +  +S+LY D   NI K ++ N  + +C C
Sbjct  73876  IN--SNFKRCCYPESMENISILYIDPNGNIKKGELVNSTISKCVC  73748


 Score = 53.1 bits (126),  Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 30/107 (28%), Positives = 56/107 (52%), Gaps = 10/107 (9%)
 Frame = -2

Query  319     NICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRM  378
               +IC  +  +++F+D+G N W+++P G   +YC G C   ++    SS+ +   ++N
Sbjct  198464  DICSLRYQYITFEDMGCN-WVLSPKGIMFSYCTGTCV--VSSFDKSSVIYGKMLLNSIHK  198294

Query  379     RGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  425
                       L  CC P + + + + Y   G+NI + +I+N +  ECGC
Sbjct  198293  ------TKLHVCCKPIRRQSVKITYMH-GKNIKQSEIKNFMPSECGC  198174


 Score = 52.0 bits (123),  Expect = 5e-06, Method: Compositional matrix adjust.
 Identities = 30/106 (28%), Positives = 49/106 (46%), Gaps = 10/106 (9%)
 Frame = +1

Query  320     ICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMR  379
               +C     ++ F  +G+  WI  P G    YC G C   I  +   S   + T++ +Y
Sbjct  199453  VCSLNSVYLDFSALGY-KWIHEPKGIQFTYCHGTC---ILSSYDKSSVIYGTIVTNYLSN  199620

Query  380     GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  425
                  P      CC P + + +++ YY  G+N+ K+ I+N I   CGC
Sbjct  199621  NRIPL-----CCSPKERKDITITYYL-GRNVKKQTIRNFIPTHCGC  199740


 Score = 49.3 bits (116),  Expect = 3e-05, Method: Compositional matrix adjust.
```

```
 Identities = 29/98 (30%), Positives = 50/98 (51%), Gaps = 11/98 (11%)
 Frame = -3

Query  328     VSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANL  387
               + FKD+G N WI+ P  +   YC+G C   I+  + SS+ + S  IN  +        N+
Sbjct  194419  MKFKDLGCN-WILRPKSFIFTYCKGTCI--ISSFTRSSIIYGSMFINDIK-------KNI  194270

Query  388     KSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  425
                 CC P     ++++Y   G+N+   +I++ +   CGC
Sbjct  194269  HICCAPVTRSNITIMYM-LGKNVKVSEIKDFLPSSCGC  194159


 Score = 45.4 bits (106),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 38/127 (30%), Positives = 54/127 (43%), Gaps = 14/127 (11%)
 Frame = +3

Query  299     QSEDHPHRRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHI  358
               +SE  P R +R  L+ D   NI   +   + F D G   WI++P      YC G C   I
Sbjct  195378  ESELLP-RVKRDFLDIDAICNI---RSINIKFADYGM-KWILSPLSTVLTYCYGICS--I  195536

Query  359     AGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNM  418
               +    +SL + + + N      H P   +  CC P   R    + Y  G+NI    I N
Sbjct  195537  SSYQKTSLMYGTIITN------HMPDNTIPQCCYPIT-RSNFTIRYKVGRNIKTDVINNF  195695

Query  419     IVEECGC  425
               +  EC C
Sbjct  195696  MPLECAC  195716


>NC_024446.1 Penguinpox virus isolate PSan92, complete genome
Length=306862

 Score = 45.4 bits (106),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 30/97 (31%), Positives = 45/97 (46%), Gaps = 10/97 (10%)
 Frame = +1

Query  329     SFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLK  388
               S+  +G+  WI  P G    YC G C   + G+   S   + TV+ +Y          +
Sbjct  166051  SYVHLGYK-WIHEPRGIQFTYCYGTC---VMGSYDESSVIYGTVVTNYISD-----KGIP  166203

Query  389     SCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  425
               SCC P +   +++ YY  G+NI K  I N +   CGC
Sbjct  166204  SCCSPKRREDITISYYR-GRNIEKHTIHNFMPTHCGC  166311


 Score = 38.5 bits (88),  Expect = 0.069, Method: Compositional matrix adjust.
 Identities = 24/77 (31%), Positives = 38/77 (49%), Gaps = 6/77 (8%)
 Frame = -2

Query  295    LQARQSEDHPHRRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGEC  354
              L +  + D+    ++R ++     N C   + +++F+DIG   WI+ P G    YC GEC
Sbjct  88719  LYSDDNVDYSFDIKKRSIQ---DSNYCKIYRKYINFRDIGLK-WILHPPGIDYGYCVGEC  88552

Query  355    PSHIAGTS--GSSLSFH  369
               S     S   S L+FH
Sbjct  88551  TSFAYTDSFLYSLLAFH  88501
```

```
>NC_024447.1 Pigeonpox virus isolate FeP2, complete genome
Length=282356

 Score = 40.0 bits (92),  Expect = 0.026, Method: Compositional matrix adjust.
 Identities = 25/77 (32%), Positives = 39/77 (51%), Gaps = 6/77 (8%)
 Frame = -3

Query  295    LQARQSEDHPHRRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGEC  354
              L +  + D+P   ++R ++     N C   + +++F+DIG   WI+ P G    YC GEC
Sbjct  87603  LYSDDNVDYPLDIKKRSVQ---DSNDCRIYRKYINFRDIGLK-WILHPPGIDYGYCVGEC  87436

Query  355    PSHIAGTS--GSSLSFH  369
               S     S   S L+FH
Sbjct  87435  TSFAYTDSFLYSLLAFH  87385



Lambda      K        H        a         alpha
   0.319    0.134    0.408    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 26323977680
```

9. Human Complement factor D (Adipsin)

```
Query= sp|P00746|CFAD_HUMAN Complement factor D OS=Homo sapiens GN=CFD PE=1
SV=5

Length=253
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_005906.1  Neodiprion lecontei NPV, complete genome                 112     3e-27
NC_008252.1  Neodiprion abietis NPV, complete genome                  112     5e-27
NC_005905.1  Neodiprion sertifer NPV, complete genome                 105     1e-24
NC_007346.1  Emiliania huxleyi virus 86, complete genome              70.5    8e-13
NC_019495.1  Cyprinid herpesvirus 2 strain ST-J1, complete genome     65.5    4e-11
NC_033174.1  Hubei virga-like virus 23 strain mosHB236486 RdRp, h...  62.4    4e-10
NC_009127.1  Cyprinid herpesvirus 3, complete genome                  50.8    3e-06
NC_019491.1  Cyprinid herpesvirus 1 strain NG-J1, complete genome     48.9    1e-05
NC_033829.1  Kallithea virus isolate DrosEU46_Kharkiv_2014, compl...  40.4    0.006


>NC_005906.1 Neodiprion lecontei NPV, complete genome
Length=81755

 Score = 112 bits (281),  Expect = 3e-27, Method: Compositional matrix adjust.
 Identities = 67/229 (29%), Positives = 111/229 (48%), Gaps = 4/229 (2%)
 Frame = -2

Query  25    RILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDAADGKVQVLLGAHS  84
             RI+GG        PY  S+Q+   H+CG  ++++ W+L+AAHC+        ++  G+
Sbjct  4363  RIVGGSPTSIDEIPYQVSLQVYSTHICGASIISDSWILTAAHCITYPVT-LYRIRSGSTL  4187
```

```
Query  85    LSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLLLLQLSEKATLGPAVRPLPWQRVDRDVAP  144
                     R+        +  +      +D+ LL+L+    LG     +P    +  +
Sbjct  4186  SISGGVVTRVESAYVHHAYYTNNYGIPVNDIALLKLTNSLILGITSAAVPLYDKNEIIPD  4007

Query  145   GTLCDVAGWGIVNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMCAES--NRRD  202
              +   + GWG +   G  P  L  V +PV+  +TC +   + G + E  +CA S    +D
Sbjct  4006  ESTAXITGWGTLTENGNTPVVLYSVNIPVIPTSTCAQIFRNWGGLPENQICAASPGGGKD  3827

Query  203   SCKGDSGGPLVCGGVLEGVVTSGSRVCGNRKKPGIYTRVASYAAWIDSV  251
             +C+GDSGGP+V    L G+V+ G+  CG    PG+YT VA+Y  WI S+
Sbjct  3826  ACQGDSGGPMVVNDRLAGIVSWGNG-CGRNGWPGVYTEVAAYREWITSL  3683


>NC_008252.1 Neodiprion abietis NPV, complete genome
Length=84264

 Score = 112 bits (279),  Expect = 5e-27, Method: Compositional matrix adjust.
 Identities = 70/238 (29%), Positives = 113/238 (47%), Gaps = 22/238 (9%)
 Frame = +3

Query  25     RILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDAA------DGKVQV  78
              RI+GG        PY  S+Q+   H+CG  ++++ W+++AAHC+           G
Sbjct  25179  RIVGGSPTSIDEIPYQVSLQVYSTHICGASIISDSWIVTAAHCITYPVTLYRIRSGSTLS  25358

Query  79     LLGAHSLSQPEPSK---RLYDVLRAVPHPDSQPDTIDHDLLLLQLSEKATLGPAVRPLPW  135
              + G   ++Q E +      Y     +P          +D+ LL+L+    LG     +P
Sbjct  25359  ISGG-VVTQVESAYVHHAYYTNNYGIPV---------NDIALLKLTNSLILGITSAAVPL  25508

Query  136    QRVDRDVAPGTLCDVAGWGIVNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMC  195
                 +  +   +   + GWG +   G  P  L  V +PV+  +TC +     G + E  +C
Sbjct  25509  YNKNEIIPDESTAIITGWGTLTENGNTPVVLYSVNIPVIPTSTCAQIFRSWGGLPENQIC  25688

Query  196    AES--NRRDSCKGDSGGPLVCGGVLEGVVTSGSRVCGNRKKPGIYTRVASYAAWIDSV  251
              A S    +D+C+GDSGGP+V    L G+V+ G+  CG    PG+YT VA+Y  WI S+
Sbjct  25689  AASPGGGKDACQGDSGGPMVVNDRLAGIVSWGNG-CGRNGWPGVYTEVAAYREWITSL  25859


>NC_005905.1 Neodiprion sertifer NPV, complete genome
Length=86462

 Score = 105 bits (261),  Expect = 1e-24, Method: Compositional matrix adjust.
 Identities = 68/232 (29%), Positives = 107/232 (46%), Gaps = 10/232 (4%)
 Frame = +1

Query  25    RILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDAADGKVQVLLGAHS  84
             RI+GG        PY  S+Q+   H+CGG +++E+W+++AAHC+       +  +    +
Sbjct  5422  RIVGGNPTSIDDVPYQVSLQVFSTHICGGSIISEKWIVTAAHCITYPV--SLYKIRTGST  5595

Query  85    LSQPEPSKRLYDVLRAVPHPDSQPDTID---HDLLLLQLSEKATLGPAVRPLPWQRVDRD  141
             LS       + DV   + H     +      +D+ LLQL     LG     +
Sbjct  5596  LSTC--GGVVSDVESIIVHHKYATNNYGVPVNDIALLQLKNSLILGITSDAVGLYDYGES  5769

Query  142   VAPGTLCDVAGWGIVNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMCAES--N  199
             +   +   V GWG +   G  P  L  V +P++    C       G + E  +CA +
Sbjct  5770  IPSESFGLVTGWGTLTENGNTPVVLYSVSIPIIPTDVCANIFQSWGGLPENQICAAAPGG  5949

Query  200   RRDSCKGDSGGPLVCGGVLEGVVTSGSRVCGNRKKPGIYTRVASYAAWIDSV  251
              +D+C+GDSGGPLV    L G+V+ G+  CG    PG YT +A +  WI S+
```

```
Sbjct  5950  GKDACQGDSGGPLVVDNRLAGIVSWGNG-CGRTGWPGAYTEIAPFRHWILSL  6102


>NC_007346.1 Emiliania huxleyi virus 86, complete genome
Length=407339

 Score = 70.5 bits (171),  Expect = 8e-13, Method: Compositional matrix adjust.
 Identities = 64/270 (24%), Positives = 109/270 (40%), Gaps = 62/270 (23%)
 Frame = -3

Query  34      AHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCL-----EDAADGKVQVL-------LG  81
               +H+ P  A+   N  H CGG L+  +WVL+AAHC+     ED  +  ++ +       +G
Sbjct  303183  SHSDPDSAA---NSPHYCGGTLINNRWVLTAAHCIYGHGREDTLEDSIKYIKEYHHARIG  303013

Query  82      AHSLSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLLLLQLSEKATLGPAVRPLP------W  135
               A    +   S   + +   + +P+   +T+++D+ LL+L  +     A +P+       W
Sbjct  303012  AKKSHEENISGDEFGIRNVIVYPNYNKNTLENDIALLELDREVGTDIA-KPMKVNSSKSW  302836

Query  136     QRVDRDVAP------------------GTLCDVAGWGIVNHAGRRPDSL---QHVLLPVL  174
                    DV                     +    AGWG    +     ++     + L
Sbjct  302835  SSQTEDVVTDVQQPKSQIFTDGNIMIRNSSVIAAGWGKTKMSDTHAATVLKTTDLTLVAT  302656

Query  175     DRATC----------NRRTHHDGAITERLMCAE--SNRRDSCKGDSGGPLVC----GGVL  218
               D   C           R   H   +T++ +CA   ++ R  C+GDSGGPL        VL
Sbjct  302655  DAGQCVPISSFGAPGTRSGIH---LTDQCICASGGNSNRGICQGDSGGPLFVHDGDTNVL  302485

Query  219     EGVVTSGSRVCGNRKKPGIYTRVASYAAWI  248
                G+ +  +  CG    P ++TR  +Y  WI
Sbjct  302484  IGISSFVAMPCGMANTPDVFTRTDTYTDWI  302395


 Score = 70.5 bits (171),  Expect = 9e-13, Method: Compositional matrix adjust.
 Identities = 55/193 (28%), Positives = 83/193 (43%), Gaps = 22/193 (11%)
 Frame = -1

Query  25      RILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDAADGKVQVLLGAHS  84
                I+ G +A+    P   S+Q  G H CG VL+++ + LSAAHC  D  D    V+ G  +
Sbjct  389621  HIINGVDADISGYPSSLSMQAIGQHFCGAVLISDYYALSAAHCF-DTLDFTGIVMAGGKT  389445

Query  85      LSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLLLLQLSEKATLGPAVRPLPWQRVD---RD  141
                      K ++    A  H      +I +D+ +++L+          PLP+   D
Sbjct  389444  NLNSNGGKSVF-AESAYLHASYDSSSIMNDIAVIKLAS---------PLPFGFADFTATS  389295

Query  142     VAPGTLCDVAGWGIVNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMCAESNRR  201
               VA        GWG+ +  G+    LQ     V    TC      D A+   ++C +S
Sbjct  389294  VAENEDVTSVGWGLTSPNGKSSMILQSTEQRVYADNTC------DAALIGTVVCTKSPTL  389133

Query  202     D--SCKGDSGGPL  212
               D  +C GDSGG L
Sbjct  389132  DTTTCNGDSGGGL  389094


 Score = 62.0 bits (149),  Expect = 6e-10, Method: Compositional matrix adjust.
 Identities = 59/198 (30%), Positives = 88/198 (44%), Gaps = 24/198 (12%)
 Frame = -3

Query  25      RILGGREAEAHARPYMASVQLN---GAHLCGGVLVAEQWVLSAAHCLE-DAADGKVQVLL  80
               RI+GG +   H   Y A+V LN    AH+CGG L+  +WV++AAHC+  D + G   + L
```

```
Sbjct  140577  RIIGGDDI--HITEYPATVSLNVYKTAHICGGTLIGSRWVVTAAHCINPDNSPGFYSINL  140404

Query  81      GAHSLSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLLLLQLSEKATLGPAVRPLPWQRVDR  140
                +  +   + +   Y V + V HP+     I  D+ +L+L    T       L  + +
Sbjct  140403  NSTFIG--DDALVDYTVKQYVIHPEYDETKITSDIAILELDRDVTY------LAKKAILS  140248

Query  141     DVAPGTLCDV--AGWGIVNHAGRRPDSLQHVLLPVLDRATC--NRRTHHDGAITERLMCA  196
                  P    DV   GWG++ + G     L   L       T   N + H D      ++C
Sbjct  140247  TTQPTVGIDVHTVGWGVIAYDGGNNGYLSAKLQYTNGVVTSPLNCQIHED---RPGIVCM  140077

Query  197     ESNRRDS--CKGDSGGPL  212
               +  R DS  C GDSG  L
Sbjct  140076  DP-REDSTTCNGDSGTGL  140026


 Score = 59.3 bits (142),  Expect = 4e-09, Method: Compositional matrix adjust.
 Identities = 62/224 (28%), Positives = 93/224 (42%), Gaps = 25/224 (11%)
 Frame = +2

Query  48     AHLCGGVLVAEQWVLSAAHCLEDAADGKVQVLLGAHSLSQPEPSKRLYDVLRAVPHPDSQ  107
              +H CGG L+  ++VL+A HC     D      + ++  +  + +   Y V R++ HP
Sbjct  16208  SHYCGGTLIHPKYVLTAGHCPVRVDDSVRIGSIYSYGNNNNDNNSYDYSVKRSIRHPSYN  16387

Query  108    PDTIDHDLLLLQLSEKA---TLGPAVRPLPWQRVDRDVAPGT------LCDVAGWGIVNH  158
               +T  HDL+L++L E+       P +        D    P             GWG
Sbjct  16388  GNTAQHDLMLVELKEEVPAHIATPMIVNSDQGDDDPHFTPTNAAINHEYMTATGWGKTRD  16567

Query  159    AGRRPDSLQHVLLPV-LDRATC-NRRTHHD-----GAI--TERLMCAESNRRDS-CKGDS  208
                  P  L+   L V L+  TC N  + H      G I  +   +CA  N+ D+ C GDS
Sbjct  16568  G--NPLILKSAKLRVELNTNTCVNTSSMHSLDNFPGQIGLSYTNICATGNKNDAICNGDS  16741

Query  209    GGPLV----CGGVLEGVVTSGSRVCGNRKKPGIYTRVASYAAWI  248
              GGPL         + GV +     CG + +P  + RV  Y  WI
Sbjct  16742  GGPLFKTYDGKKTVVGVSSFVILPCGLKGEPDAFVRVGIYTDWI  16873


 Score = 57.4 bits (137),  Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 58/202 (29%), Positives = 89/202 (44%), Gaps = 28/202 (14%)
 Frame = -3

Query  45      LNGAHLCGGVLVAEQWVLSAAHC--LEDAADGKVQVLLGAHSLSQPEPSKRLYDVLRAVP  102
               LN    C GVLV++QWVL+AAHC     A+ G V       SLS+  P+     V +
Sbjct  148380  LNNTPYCTGVLVSDQWVLTAAHCSGANPASPGDVIRYGTQDSLSKKTPTTTAV-VKKVYT  148204

Query  103     HPDSQPDTIDH-DLLLLQLSEKATLGPAVRPLPWQRVDRDVAPGTLCDVAGWGIVNHAGR  161
               HP     T    DL LL+L ++ T    + P+ +         GT    AGWG  +   R
Sbjct  148203  HPGYMGITKGGIDLALLKLDKRIT---TISPMSFLDDQSGYVVGTTLKQAGWGSKDIDAR  148033

Query  162     RP--------DSLQHVL----LPVLDRATCNRRTHHDGAITERLMCAESNRRDSCKGDSG  209
                         ++ + +L     PV+ +   N    ++   T+ ++  E N + + KGDSG
Sbjct  148032  HNMFSITSGLNTYRKILRSNEAPVISQKQYNSINEYEN--TKYIVNFEEN-KGTNKGDSG  147862

Query  210     GPLVC------GGVLEGVVTSG  225
                PL          V+ G+++SG
Sbjct  147861  SPLFLTTADKNKNVVVGILSSG  147796


>NC_019495.1 Cyprinid herpesvirus 2 strain ST-J1, complete genome
```

```
Length=290304

 Score = 65.5 bits (158),  Expect = 4e-11, Method: Compositional matrix adjust.
 Identities = 67/225 (30%), Positives = 96/225 (43%), Gaps = 53/225 (24%)
 Frame = -2

Query  25      RILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDA---ADGKVQVLLG  81
               +I+GG  A A   PYM  +  N   LCGG L     VL+AAHC  +       K++V  G
Sbjct  164201  KIMGGMTAIA-IPPYMGMITSNANVLCGGTLFNSTHVLTAAHCCINGMVRTFDKLEVTFG  164025

Query  82      AHSLSQPEPSKRLYDV----LRAVPHPDSQPDTIDH-------------------DLLLL  118
                +S+      KRL++      R         PD + +                   D+ L+
Sbjct  164024  LYSV------KRLFEQGVVRYRVKACHFYAPDFLQYVKKVLLESPVDQLFNYHGWDITLM  163863

Query  119     QLSEKATLGPAVRPLPWQRVDRDVAPGT-LCDVAGWG----IVNHAGRRPDSLQHVLLPV  173
               +L E     P +   P +      A G   C VAG+G    + +  G     L+ V +P+
Sbjct  163862  ELHE-----PVLYREPVKLFKPTEAHGRGECLVAGYGSRGYLDDRGGDYGIPLKTVHVPL  163698

Query  174     LDRATCNRRTHHDGAIT----ERLMCAESNRRDSCKGDSGGPLVC  214
               +D+ATC      DG  T       +CA S   D+C GDSGGPL+C
Sbjct  163697  VDKATC------DGEFTVGSPPNTLCAGSLDHDACNGDSGGPLMC  163581


>NC_033174.1 Hubei virga-like virus 23 strain mosHB236486 RdRp, hypothetical
protein, putative glycoprotein, and hypothetical protein
genes, complete cds
Length=14639

 Score = 62.4 bits (150),  Expect = 4e-10, Method: Compositional matrix adjust.
 Identities = 63/227 (28%), Positives = 93/227 (41%), Gaps = 37/227 (16%)
 Frame = +2

Query  25     RILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDAADGKVQVLLGAHS  84
              RI+ G   E     Y   +   G  +C  V V+    ++AAHC               H
Sbjct  12677  RIVNG---EPSTDLYTHPLFYQGTFICTAVAVSPTTAITAAHC--------------THG  12805

Query  85     LSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLLLLQLSE-KATLGPAVRPLPWQRVDRDVA  143
               +       L  V R V HP  +P T+ +D+ LL  SE +  +G      P       V
Sbjct  12806  YTNQFYISDL-RVTRFVTHPSFEPLTLANDISLLFASEFQFYVGLYYSLPPLNSPVTVVG  12982

Query  144    PGTLCDVAGWGIVNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMCA--ESNRR  201
               G+ C    +  V  +G +  +       VL+   C +R      +    +CA  +   +
Sbjct  12983  YGSTC----YKCVGTSGVQRSA-------VLEIKICPQRF----TVAPNTLCAGLDDGSK  13117

Query  202    DSCKGDSGGPLVCGGVLEGVVTSGSRVCGNRKKPGIYTRVASYAAWI  248
              DSC+GDSGGPL   G L  +V+ G  +C     PG+YT V SY  +I
Sbjct  13118  DSCQGDSGGPLFYEGKLLAIVSWG-YMCAQPLTPGVYTVVESYQNFI  13255


>NC_009127.1 Cyprinid herpesvirus 3, complete genome
Length=295146

 Score = 50.8 bits (120),  Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 66/270 (24%), Positives = 100/270 (37%), Gaps = 74/270 (27%)
 Frame = -1

Query  25      RILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDAADGK---VQVLLG  81
               +++GG  A A   PY+  V  N    CG  L      L+A HC  +    K   V V  G
```

```
Sbjct  174237  KLMGGMVAIA-VPPYLGVVSDNLGLFCGATLYNATHALTAGHCCINGRTQKLDSVVVAFG  174061

Query  82      AHSLSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLL--------LLQLSEKATLGPAVRPL  133
                 S+++      LY           QP  + H ++         +  + +    P
Sbjct  174060  LFSITE------LY-----------QPGVVRHKVVACHFYAPDFMARARRILADPIAELF  173932

Query  134     PWQ-------RVDRDVAPG---------------TLCDVAGWGIVNHA---GRRPDSLQH  168
                W         +DR  AP                  C VAG+G+  +    G     L+H
Sbjct  173931  NWNGYDVALMELDRPAAPSKKPVELFERGEHEGEEECLVAGYGLRGYPVVLGANMAELEH  173752

Query  169     ----VLLPVLDRATCNRRTHHDGAITERL----MCAESNRRDSCKGDSGGPLVCGGVLE-  219
                   + +P++D+  C+R       + ER     +CA S   D C GDSGGPL+C    +
Sbjct  173751  PVKTIHVPLVDKFRCDRD------MPERTPPFTVCAGSFDHDVCLGDSGGPLMCESSRDH  173590

Query  220     -----GVVTSGSRVCGNRKKPGIYTRVASY  244
                    G+V+ G      R    +YT V +Y
Sbjct  173589  RPRQLGIVSYGRPCVRGRNGLSVYTDVRAY  173500


>NC_019491.1 Cyprinid herpesvirus 1 strain NG-J1, complete genome
Length=291144

 Score = 48.9 bits (115),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 62/239 (26%), Positives = 99/239 (41%), Gaps = 37/239 (15%)
 Frame = -2

Query  39      YMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDA---ADGKVQVLLGAHSL----SQPEPS  91
               Y+A + +NG  +CGG L     VL+A HC  +    A  ++QV LG +++    S+
Sbjct  156644  YIAMITVNGELICGGTLFNASHVLTAGHCCVNPRVRATSEMQVSLGLYNVLDLHSKGNRR  156465

Query  92      KRLYDVLRAVPHPDSQPDTI-----------DHDLLLLQLSE--------KATLGPAVRP  132
                R+       P+  ++  +I            +D+ LL+LS+           L  ++R
Sbjct  156464  HRVKACHFYAPNFINRTRSIYALNQELFNKNGYDIALLELSDPQANQDVSPVKLFESLRE  156285

Query  133     LP-WQRVDRDVAPGTLCDVAGWGIVNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITE  191
                P +QR    +  G      G          P    HV  P+   + CN        I
Sbjct  156284  SPAFQRECLVIGYGRHGVGGGGDAFLEDTYVPVKTVHV--PLRSPSVCN--IAFGKPIPS  156117

Query  192     RLMCAESNRRDSCKGDSGGPLVCGGVLEGV-----VTSGSRVCGNRKKP-GIYTRVASY  244
                 +CA S   D+C GDSGGPL C G  +G+     + S  + C +R +   +YT V  +
Sbjct  156116  NTLCAGSQGHDACTGDSGGPLFCEGQDDGIPRQVGIVSYGKPCESRDEGLSVYTDVRGF  155940


>NC_033829.1 Kallithea virus isolate DrosEU46_Kharkiv_2014, complete genome
Length=152388

 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 41/167 (25%), Positives = 70/167 (42%), Gaps = 14/167 (8%)
 Frame = +1

Query  51     CGGVLVAEQWVLSAAHCLEDAADGKVQVLLGAHSLSQPEPSKRLYDVLRAVPHP----DS  106
              C G L+  Q VL++A CL DAA+    + L    ++  +  + + + +  + HP
Sbjct  56677  CAGSLIDRQHVLTSASCL-DAANENRSIFLIMGVVNINDNRRVVSEAISKIVHPLYNNKD  56853

Query  107    QPDTIDHDLLLLQLSEKA-TLGPAVRPLPWQRVDRDVAPGTLCDVAGWGIVNHAGRRPDS  165
               P   D  LL ++  E +  L PA+  L  +             + G+G +N  G
Sbjct  56854  YPYAYDVALLRIKTVEYSRNLQPAI--LAGKSTTEQSMFELPLYILGYGDIN-LGPNNQV  57024
```

```
Query  166    LQHVLLPVLDRATCNRRTHHDGAITERLMCAESNRRDSCKGDSGGPL  212
              L++    +   + C+         TE  +CA +N    C GD GGP+
Sbjct  57025  LKYSSAKLRKMSECDEYNK-----TESTLCARANPGSPCLGDEGGPV  57150



Lambda      K        H        a         alpha
   0.319    0.136    0.431    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 12058904868
```

10. Human Resistin

```
Query= sp|Q9HD89|RETN_HUMAN Resistin OS=Homo sapiens GN=RETN PE=1 SV=1

Length=108
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_030901.1  Gordonia phage ClubL, complete genome                    37.0    0.008


>NC_030901.1 Gordonia phage ClubL, complete genome
Length=92618

 Score = 37.0 bits (84),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 25/77 (32%), Positives = 32/77 (42%), Gaps = 9/77 (12%)
 Frame = -2

Query  36     AGSLIF---RAISSIGLECQSVTSRGDLATCPRGFAVTGCTC-----GSACGSWDVRAET  87
              AG+L+    R +S + LE   V  RGD+A  P+G A           G    +W VR E
Sbjct  56569  AGALVLEFERQLSRL-LESGRVQDRGDVAEDPKGIARVRVRHWLHRRGEPAAAWRVRTER  56393

Query  88     TCHCQCAGMDWTGARCC  104
                    A   W G R C
Sbjct  56392  PRRSARAASRWAGRRSC  56342



Lambda      K        H        a         alpha
   0.323    0.131    0.439    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 2144953500
```

11. Human Interleukin-6

```
Query= sp|P05231|IL6_HUMAN Interleukin-6 OS=Homo sapiens GN=IL6 PE=1 SV=1

Length=212
                                                                      Score     E
```

```
Sequences producing significant alignments:                          (Bits)  Value

NC_009333.1  Human herpesvirus 8, complete genome                     77.4    1e-15


>NC_009333.1 Human herpesvirus 8, complete genome
Length=137969

 Score = 77.4 bits (189),  Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 41/158 (26%), Positives = 77/158 (49%), Gaps = 0/158 (0%)
 Frame = -3

Query  55     KQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVK  114
              +++ ++L  I    ++ C ++ +C+   E  A  +L LP + + D C   GFNE +CL K
Sbjct  17733  QRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKK  17554

Query  115    IITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNAS  174
              +  G  EFEV  ++L   F  S      +++ TK L   +Q++   L       P  +
Sbjct  17553  LADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRG  17374

Query  175    LLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRALRQM  212
              LL +LQ    W++   +  +L + ++F   ++R L  +
Sbjct  17373  LLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVLNSI  17260



Lambda      K        H        a         alpha
   0.315    0.127    0.349    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 8725390488
```

12. Human Fibronectin type III domain-containing protein 5

```
Query= sp|Q8NAU1|FNDC5_HUMAN Fibronectin type III domain-containing protein
5 OS=Homo sapiens GN=FNDC5 PE=1 SV=3

Length=212
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_004166.2  Bacteriophage SPP1 complete nucleotide sequence          38.9    0.012


>NC_004166.2 Bacteriophage SPP1 complete nucleotide sequence
Length=44010

 Score = 38.9 bits (89),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 29/95 (31%), Positives = 44/95 (46%), Gaps = 9/95 (9%)
 Frame = +3

Query  34     PSAPVNVTVRHLKANSAVVSWDVLEDEVVIGFAISQQKKDVRMLRFIQEVNTTTRSCALW  93
              P+AP N+T      +S  V WD +E           +KK         + N TT S  L
Sbjct  11010  PNAPQNLTYT-ATTDSVTVKWDAVEGADSYNVYRGAEKK--------LDANVTTTSHTLT  11162
```

```
Query  94     DLEEDTEYIVHVQAISIQGQSPASEPVLFKTPREA  128
               ++ DT+  V+V A++  G+SP S+ V    P E+
Sbjct  11163  GIQPDTQLTVNVAAVNAGGESPMSQIVTKTLPAES  11267



Lambda      K        H        a         alpha
   0.317    0.130    0.373    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 8725390488
```

13. Human Fibroblast growth factor 21

```
Query= sp|Q9NSA1|FGF21_HUMAN Fibroblast growth factor 21 OS=Homo sapiens
GN=FGF21 PE=1 SV=1

Length=209
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006549.1  Singapore grouper iridovirus, complete genome            46.2    5e-05
NC_001875.2  Orgyia pseudotsugata MNPV, complete genome               45.1    1e-04
NC_021924.1  Choristoneura rosaceana alphabaculovirus, complete g...  38.1    0.024
NC_013953.1  Lymantria xylina MNPV, complete genome                   37.0    0.059


>NC_006549.1 Singapore grouper iridovirus, complete genome
Length=140131

 Score = 46.2 bits (108),  Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 30/101 (30%), Positives = 46/101 (46%), Gaps = 6/101 (6%)
 Frame = +1

Query  56      QTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLH  115
               +T   LE+      GG   QS  + L LK+++ G I I G     ++C   +GA+
Sbjct  125050  KTNFMLEVNGTAVSGGTDKQSQTAKLTLKSVRAGQIVIKG-SIGGYVCMDRNGAVSAKTT  125226

Query  116     FDPEACSFRELLLEDGYNVYQSEAHGLP-----LHLPGNKS  151
               +    C F E LL + YN Y +  H  P     +HL  +K+
Sbjct  125227  YVQSDCVFNETLLPNNYNSYSAAEHLNPETRANMHLAIDKA  125349


>NC_001875.2 Orgyia pseudotsugata MNPV, complete genome
Length=131995

 Score = 45.1 bits (105),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 25/76 (33%), Positives = 41/76 (54%), Gaps = 2/76 (3%)
 Frame = +3

Query  60     HLEIREDGTVGGAA-DQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP  118
              +L +R DGTVGG      S +++LQ  A+  G I +    +  ++C    GA+Y S
Sbjct  22833  YLAVRSDGTVGGTTYASSLDTVLQRIAIAHGRILLRNAVSCMYVCLDRCGAMYASAALSS  23012
```

```
Query  119    EACSFRELLLEDGYNV  134
              + C   E++LE+ Y+V
Sbjct  23013  D-CILNEVMLENNYDV  23057


>NC_021924.1 Choristoneura rosaceana alphabaculovirus, complete genome
Length=129052

 Score = 38.1 bits (87),  Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 23/77 (30%), Positives = 39/77 (51%), Gaps = 5/77 (6%)
 Frame = -2

Query  60      HLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALY--GSLHFD  117
               +L +R DGTVGG    S +++LQ        + +    +   +C    GA+Y  G+L  D
Sbjct  108408  YLAVRPDGTVGGTTHASMDTILQRVGYHKSRVLLQNAFSCMHVCLDRCGAMYASGALSMD  108229

Query  118     PEACSFRELLLEDGYNV  134
                  C   E++L++ Y+V
Sbjct  108228  ---CILNEVILDNNYDV  108187


>NC_013953.1 Lymantria xylina MNPV, complete genome
Length=156344

 Score = 37.0 bits (84),  Expect = 0.059, Method: Compositional matrix adjust.
 Identities = 35/126 (28%), Positives = 55/126 (44%), Gaps = 15/126 (12%)
 Frame = -2

Query  9       EHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGT  68
                H+ + +  L  L LGA +A P+  S+  L   G  RQ              L    +GT
Sbjct  146662  RHAQIMLVFLVVLALGA-RAFPLTASTGRLVQIGINRQ-------------LLTCFSNGT  146525

Query  69      VGGAADQSPE-SLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELL  127
               VGG+ D+  + ++ +  A+ P  + I    T  F C    G LY +     + C+F E L
Sbjct  146524  VGGSTDERADGTVWRRWAVNPREVLIRSAATCAFACLDDCGFLYTAAETPNKECAFVEEL  146345

Query  128     LEDGYN  133
                E+ Y+
Sbjct  146344  SENHYS  146327



Lambda      K        H        a         alpha
   0.315    0.136    0.409    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 8555249200
```

14. Human Fibroblast growth factor 19

```
Query= sp|O95750|FGF19_HUMAN Fibroblast growth factor 19 OS=Homo sapiens
GN=FGF19 PE=1 SV=1

Length=216
```

```
                                                                   Score     E
Sequences producing significant alignments:                       (Bits)  Value

NC_006549.1  Singapore grouper iridovirus, complete genome          46.2    6e-05


>NC_006549.1 Singapore grouper iridovirus, complete genome
Length=140131

 Score = 46.2 bits (108),  Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 26/85 (31%), Positives = 40/85 (47%), Gaps = 3/85 (4%)
 Frame = +1

Query  59      FLRIRADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVR-YLCMGADGKMQGLLQYSE  117
                L +    V      QS   + L +K+V    + IKG  S+  Y+CM  +G +     Y +
Sbjct  125062  MLEVNGTAVSGGTDKQSQTAKLTLKSVRAGQIVIKG--SIGGYVCMDRNGAVSAKTTYVQ  125235

Query  118     EDCAFEEEIRPDGYNVYRSEKHRLP  142
                DC  F E + P+ YN Y + +H  P
Sbjct  125236  SDCVFNETLLPNNYNSYSAAEHLNP  125310


 Score = 38.9 bits (89),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 21/57 (37%), Positives = 27/57 (47%), Gaps = 2/57 (4%)
 Frame = +2

Query  89      TVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEEEI--RPDGYNVYRSEKHRLPV  143
               TV IK      Y+CM + G + G L     DC F E I  +  GY  Y S+ H+ P
Sbjct  125645  TVTIKSASDNYYVCMYSGGTVYGRLGSLAADCEFTEHIDQKKHGYKSYSSKHHKAPT  125815



Lambda      K        H        a         alpha
   0.323    0.138    0.432    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 9067562664
```

PART B: The results of the processed sequence search of the human proteins

1. Endothelin-2|49-69

```
Query= sp|P20800|49-69

Length=21
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006966.1  Deerpox virus W-848-83, complete genome                  30.0    0.055


>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 30.0 bits (66),  Expect = 0.055, Method: Compositional matrix adjust.
 Identities = 13/21 (62%), Positives = 15/21 (71%), Gaps = 0/21 (0%)
 Frame = -1

Query  1     CSCSSWLDKECVYFCHLDIIW  21
             C C +  DKEC+ FC LDIIW
Sbjct  5168  CYCDTHDDKECMNFCELDIIW  5106



Lambda      K        H        a         alpha
   0.334    0.144    0.645    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 1818228804
```

2. Endothelin-1|53-90

```
Query= sp|P05305|53-90

Length=38
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006966.1  Deerpox virus W-848-83, complete genome                  31.2    0.055


>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 31.2 bits (69),  Expect = 0.055, Method: Compositional matrix adjust.
 Identities = 13/21 (62%), Positives = 15/21 (71%), Gaps = 0/21 (0%)
 Frame = -1

Query  1     CSCSSLMDKECVYFCHLDIIW  21
             C C +  DKEC+ FC LDIIW
```

```
Sbjct  5168  CYCDTHDDKECMNFCELDIIW  5106



Lambda      K        H        a         alpha
   0.325    0.141    0.509    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 2161487500
```

3. Endothelin-1|53-73

```
Query= sp|P05305|53-73

Length=21
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006966.1  Deerpox virus W-848-83, complete genome                  30.0    0.059


>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 30.0 bits (66),  Expect = 0.059, Method: Compositional matrix adjust.
 Identities = 13/21 (62%), Positives = 15/21 (71%), Gaps = 0/21 (0%)
 Frame = -1

Query  1     CSCSSLMDKECVYFCHLDIIW  21
             C C +  DKEC+ FC LDIIW
Sbjct  5168  CYCDTHDDKECMNFCELDIIW  5106



Lambda      K        H        a         alpha
   0.336    0.143    0.587    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 1818228804
```

4. Fibroblast growth factor 21|29-209

```
Query= sp|Q9NSA1|29-209

Length=181
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006549.1  Singapore grouper iridovirus, complete genome            46.2    3e-05
NC_001875.2  Orgyia pseudotsugata MNPV, complete genome               45.8    4e-05
NC_021924.1  Choristoneura rosaceana alphabaculovirus, complete g...  38.5    0.011
NC_013953.1  Lymantria xylina MNPV, complete genome                   36.2    0.061
```

```
NC_001973.1  Lymantria dispar MNPV, complete genome                   35.8    0.087


>NC_006549.1 Singapore grouper iridovirus, complete genome
Length=140131

 Score = 46.2 bits (108),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 30/101 (30%), Positives = 46/101 (46%), Gaps = 6/101 (6%)
 Frame = +1

Query  28      QTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLH  87
               +T   LE+      GG   QS  + L LK+++ G I I G     ++C   +GA+
Sbjct  125050  KTNFMLEVNGTAVSGGTDKQSQTAKLTLKSVRAGQIVIKG-SIGGYVCMDRNGAVSAKTT  125226

Query  88      FDPEACSFRELLLEDGYNVYQSEAHGLP-----LHLPGNKS  123
               +    C F E LL + YN Y +  H  P     +HL  +K+
Sbjct  125227  YVQSDCVFNETLLPNNYNSYSAAEHLNPETRANMHLAIDKA  125349


>NC_001875.2 Orgyia pseudotsugata MNPV, complete genome
Length=131995

 Score = 45.8 bits (107),  Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 25/76 (33%), Positives = 41/76 (54%), Gaps = 2/76 (3%)
 Frame = +3

Query  32     HLEIREDGTVGGAA-DQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP  90
              +L +R DGTVGG     S +++LQ  A+  G I +    +  ++C    GA+Y S
Sbjct  22833  YLAVRSDGTVGGTTYASSLDTVLQRIAIAHGRILLRNAVSCMYVCLDRCGAMYASAALSS  23012

Query  91     EACSFRELLLEDGYNV  106
              + C   E++LE+ Y+V
Sbjct  23013  D-CILNEVMLENNYDV  23057


>NC_021924.1 Choristoneura rosaceana alphabaculovirus, complete genome
Length=129052

 Score = 38.5 bits (88),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 23/77 (30%), Positives = 39/77 (51%), Gaps = 5/77 (6%)
 Frame = -2

Query  32      HLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALY--GSLHFD  89
               +L +R DGTVGG    S +++LQ        + +    +   +C    GA+Y  G+L  D
Sbjct  108408  YLAVRPDGTVGGTTHASMDTILQRVGYHKSRVLLQNAFSCMHVCLDRCGAMYASGALSMD  108229

Query  90      PEACSFRELLLEDGYNV  106
                  C   E++L++ Y+V
Sbjct  108228  ---CILNEVILDNNYDV  108187


>NC_013953.1 Lymantria xylina MNPV, complete genome
Length=156344

 Score = 36.2 bits (82),  Expect = 0.061, Method: Compositional matrix adjust.
 Identities = 21/69 (30%), Positives = 35/69 (51%), Gaps = 1/69 (1%)
 Frame = -2
```

```
Query  38      DGTVGGAADQSPE-SLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFR  96
               +GTVGG+ D+  + ++ +  A+ P  + I    T  F C    G LY +     + C+F
Sbjct  146533  NGTVGGSTDERADGTVWRRWAVNPREVLIRSAATCAFACLDDCGFLYTAAETPNKECAFV  146354

Query  97      ELLLEDGYN  105
               E L E+ Y+
Sbjct  146353  EELSENHYS  146327


>NC_001973.1 Lymantria dispar MNPV, complete genome
Length=161046

 Score = 35.8 bits (81),  Expect = 0.087, Method: Compositional matrix adjust.
 Identities = 22/69 (32%), Positives = 34/69 (49%), Gaps = 1/69 (1%)
 Frame = -2

Query  38      DGTVGGAADQSPE-SLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFR  96
               +GTVGG+ D+  + +  +  A KP  + I    T  F+C    G LY +     + C F
Sbjct  152876  NGTVGGSTDERADGTAWRRWAAKPREVLIRSAATCAFVCLDDCGFLYTAAEAPNKECLFV  152697

Query  97      ELLLEDGYN  105
               E L E+ Y+
Sbjct  152696  EELSENHYS  152670



Lambda      K        H        a         alpha
   0.314    0.136    0.406    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 6332282712
```

5. Fibroblast growth factor 19|25-216

```
Query= sp|O95750|25-216

Length=192
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006549.1  Singapore grouper iridovirus, complete genome             46.2    4e-05


>NC_006549.1 Singapore grouper iridovirus, complete genome
Length=140131

 Score = 46.2 bits (108),  Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 25/84 (30%), Positives = 38/84 (45%), Gaps = 1/84 (1%)
 Frame = +1

Query  35      FLRIRADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEE  94
                L +    V      QS  + L +K+V    + IKG     Y+CM  +G +     Y +
Sbjct  125062  MLEVNGTAVSGGTDKQSQTAKLTLKSVRAGQIVIKGSIG-GYVCMDRNGAVSAKTTYVQS  125238
```

```
Query  95      DCAFEEEIRPDGYNVYRSEKHRLP  118
               DC F E + P+ YN Y + +H  P
Sbjct  125239  DCVFNETLLPNNYNSYSAAEHLNP  125310


 Score = 38.5 bits (88),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 21/57 (37%), Positives = 27/57 (47%), Gaps = 2/57 (4%)
 Frame = +2

Query  65      TVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEEEI--RPDGYNVYRSEKHRLPV  119
               TV IK      Y+CM + G + G L     DC F E I  +  GY  Y S+ H+ P
Sbjct  125645  TVTIKSASDNYYVCMYSGGTVYGRLGSLAADCEFTEHIDQKKHGYKSYSSKHHKAPT  125815



Lambda      K        H        a         alpha
   0.321    0.138    0.419    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 7187202960
```

6. Fibronectin type III domain-containing protein 5|32-212

```
Query= sp|Q8NAU1|32-212

Length=181
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_004166.2  Bacteriophage SPP1 complete nucleotide sequence          38.9    0.009


>NC_004166.2 Bacteriophage SPP1 complete nucleotide sequence
Length=44010

 Score = 38.9 bits (89),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 29/95 (31%), Positives = 44/95 (46%), Gaps = 9/95 (9%)
 Frame = +3

Query  3      PSAPVNVTVRHLKANSAVVSWDVLEDEVVIGFAISQQKKDVRMLRFIQEVNTTTRSCALW  62
              P+AP N+T      +S  V WD +E           +KK         + N TT S  L
Sbjct  11010  PNAPQNLTYT-ATTDSVTVKWDAVEGADSYNVYRGAEKK--------LDANVTTTSHTLT  11162

Query  63     DLEEDTEYIVHVQAISIQGQSPASEPVLFKTPREA  97
               ++ DT+  V+V A++  G+SP S+ V    P E+
Sbjct  11163  GIQPDTQLTVNVAAVNAGGESPMSQIVTKTLPAES  11267



Lambda      K        H        a         alpha
   0.314    0.129    0.364    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
```

```
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 6332282712
```

7. Fibronectin type III domain-containing protein 5 (Irisin)|32-143

```
Query= sp|Q8NAU1|32-143

Length=112
                                                                     Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_004166.2  Bacteriophage SPP1 complete nucleotide sequence          38.9    0.002


>NC_004166.2 Bacteriophage SPP1 complete nucleotide sequence
Length=44010

 Score = 38.9 bits (89),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 29/95 (31%), Positives = 44/95 (46%), Gaps = 9/95 (9%)
 Frame = +3

Query  3      PSAPVNVTVRHLKANSAVVSWDVLEDEVVIGFAISQQKKDVRMLRFIQEVNTTTRSCALW  62
              P+AP N+T      +S  V WD +E           +KK         + N TT S  L
Sbjct  11010  PNAPQNLTYT-ATTDSVTVKWDAVEGADSYNVYRGAEKK--------LDANVTTTSHTLT  11162

Query  63     DLEEDTEYIVHVQAISIQGQSPASEPVLFKTPREA  97
               ++ DT+  V+V A++  G+SP S+ V    P E+
Sbjct  11163  GIQPDTQLTVNVAAVNAGGESPMSQIVTKTLPAES  11267



Lambda      K        H        a         alpha
   0.312    0.126    0.349    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 2144008700
```

8. Transforming growth factor beta-2|303-414

```
Query= sp|P61812|303-414

Length=112
                                                                     Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006966.1  Deerpox virus W-848-83, complete genome                  76.3    2e-16
NC_024447.1  Pigeonpox virus isolate FeP2, complete genome            67.0    2e-13
NC_024446.1  Penguinpox virus isolate PSan92, complete genome         66.2    4e-13
NC_002188.1  Fowlpox virus, complete genome                           62.8    7e-12
NC_005309.1  Canarypox virus, complete genome                         61.2    2e-11
NC_028238.1  Turkeypox virus strain TKPV-HU1124/2011, complete ge...  46.6    4e-06
```

```
>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 76.3 bits (186),  Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 38/97 (39%), Positives = 52/97 (54%), Gaps = 10/97 (10%)
 Frame = +3

Query  15      CCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASA  74
               CCL   YIDFK+D+GW WI++P+GY+AN C G C         H  +   YN
Sbjct  155217  CCLVDFYIDFKKDMGWNWIYKPEGYHANLCIGNC--------NHKLINMPYNY--AFKHN  155366

Query  75      SPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
                 CC  + ++ L I YY G+  K++ L NM + SC C
Sbjct  155367  VFCCAPKKMKSLIIAYYEGRKYKVDNLKNMKIVSCGC  155477


>NC_024447.1 Pigeonpox virus isolate FeP2, complete genome
Length=282356

 Score = 67.0 bits (162),  Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 39/105 (37%), Positives = 57/105 (54%), Gaps = 5/105 (5%)
 Frame = -3

Query  9      RNVQD--NCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYN  66
              R+VQD  +C +   YI+F RD+G KWI  P G +  +C G C     +D+    +L+ +
Sbjct  87558  RSVQDSNDCRIYRKYINF-RDIGLKWILHPPGIDYGYCVGECTSFAYTDSFLYSLLAFHY  87382

Query  67     TINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
                  E     CC  QD++ L + Y +G+TPK   L  + VKSCKC
Sbjct  87381  IDGIELKQ--CCSIQDMDDLIVHYRVGRTPKTSVLYKVSVKSCKC  87253


>NC_024446.1 Penguinpox virus isolate PSan92, complete genome
Length=306862

 Score = 66.2 bits (160),  Expect = 4e-13, Method: Compositional matrix adjust.
 Identities = 38/105 (36%), Positives = 57/105 (54%), Gaps = 5/105 (5%)
 Frame = -2

Query  9      RNVQDN--CCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYN  66
              R++QD+  C +   YI+F RD+G KWI  P G +  +C G C     +D+    +L+ +
Sbjct  88674  RSIQDSNYCKIYRKYINF-RDIGLKWILHPPGIDYGYCVGECTSFAYTDSFLYSLLAFHY  88498

Query  67     TINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
                  E     CC  QD++ L + Y +G+TPK   L  + VKSCKC
Sbjct  88497  IDGIELKQ--CCSIQDMDDLIVHYRVGRTPKTSVLYKVSVKSCKC  88369


 Score = 45.8 bits (107),  Expect = 7e-06, Method: Composition-based stats.
 Identities = 25/84 (30%), Positives = 38/84 (45%), Gaps = 1/84 (1%)
 Frame = +1

Query  28      LGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLT  87
               LG+KWIHEP+G    +C G C  + S D       ++      +     CC  +  E +T
Sbjct  166063  LGYKWIHEPRGIQFTYCYGTC-VMGSYDESSVIYGTVVTNYISDKGIPSCCSPKRREDIT  166239

Query  88      ILYYIGKTPKIEQLSNMIVKSCKC  111
               I YY G+  +   + N +   C C
```

```
Sbjct  166240  ISYYRGRNIEKHTIHNFMPTHCGC  166311


>NC_002188.1 Fowlpox virus, complete genome
Length=288539

 Score = 62.8 bits (151),  Expect = 7e-12, Method: Compositional matrix adjust.
 Identities = 36/109 (33%), Positives = 55/109 (50%), Gaps = 3/109 (3%)
 Frame = -2

Query  3      DAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVL  62
              D+   + +  DNC +   YI+F R +G KWI  P G +  +C G C     +D+    +L
Sbjct  80251  DSGVDYSSPSDNCKVYRKYINF-RSIGLKWILHPPGIDYGYCMGECQSFVYTDSFLYSLL  80075

Query  63     SLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
              + +     E     CC  Q ++ L + Y +G+TPK   L  + VKSCKC
Sbjct  80074  AFHYIDGIELKQ--CCSIQSMDDLVVHYRLGRTPKTAILRKVSVKSCKC  79934


>NC_005309.1 Canarypox virus, complete genome
Length=359853

 Score = 61.2 bits (147),  Expect = 2e-11, Method: Compositional matrix adjust.
 Identities = 36/101 (36%), Positives = 52/101 (51%), Gaps = 4/101 (4%)
 Frame = +1

Query  12      QDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPE  71
               Q  C L  +Y+DF   LG+KWIHEPKG    +C G C  + SS   + S +     T
Sbjct  199447  QHVCSLNSVYLDFSA-LGYKWIHEPKGIQFTYCHGTC--ILSSYDKSSVIYGTIVTNYLS  199617

Query  72      ASASP-CCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
                +  P CC  ++ + +TI YY+G+  K + + N I   C C
Sbjct  199618  NNRIPLCCSPKERKDITITYYLGRNVKKQTIRNFIPTHCGC  199740


 Score = 51.2 bits (121),  Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 30/97 (31%), Positives = 48/97 (49%), Gaps = 3/97 (3%)
 Frame = -3

Query  15      CCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASA  74
               C LR  ++ FK DLG  WI  PK +   +C G C  + SS T+ S +       + + +
Sbjct  194440  CLLRHKHMKFK-DLGCNWILRPKSFIFTYCKGTC--IISSFTRSSIIYGSMFINDIKKNI  194270

Query  75      SPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
                 CC       +TI+Y +GK  K+ ++ + +  SC C
Sbjct  194269  HICCAPVTRSNITIMYMLGKNVKVSEIKDFLPSSCGC  194159


 Score = 43.9 bits (102),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 32/101 (32%), Positives = 48/101 (48%), Gaps = 6/101 (6%)
 Frame = -2

Query  13      DNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLS--LYNTINP  70
               D C LR  YI F+ D+G  W+  PKG   ++C G C  + SS  + S +    L N+I+
Sbjct  198464  DICSLRYQYITFE-DMGCNWVLSPKGIMFSYCTGTC--VVSSFDKSSVIYGKMLLNSIH-  198297

Query  71      EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
               +     CC     + + I Y  GK  K  ++ N +   C C
```

```
Sbjct  198296  KTKLHVCCKPIRRQSVKITYMHGKNIKQSEIKNFMPSECGC  198174


 Score = 42.0 bits (97),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 29/108 (27%), Positives = 46/108 (43%), Gaps = 10/108 (9%)
 Frame = +3

Query  8       FRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNT  67
               F ++   C +R + I F  D G KWI  P      +C G C     S + + +   +Y T
Sbjct  195411  FLDIDAICNIRSINIKFA-DYGMKWILSPLSTVLTYCYGIC-----SISSYQKTSLMYGT  195572

Query  68      I----NPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
               I     P+ +   CC        TI Y +G+  K + ++N +   C C
Sbjct  195573  IITNHMPDNTIPQCCYPITRSNFTIRYKVGRNIKTDVINNFMPLECAC  195716


>NC_028238.1 Turkeypox virus strain TKPV-HU1124/2011, complete genome
Length=188534

 Score = 46.6 bits (109),  Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 30/98 (31%), Positives = 46/98 (47%), Gaps = 4/98 (4%)
 Frame = +2

Query  15     CCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEAS-  73
              C L   YI FK D+G  W+  PKG+   +C G C  + SS T+ S V       + ++S
Sbjct  64331  CALHYKYISFK-DVGCNWVLSPKGFTFRYCKGEC--IVSSFTKSSIVYGAMLVNDAKSSN  64501

Query  74     ASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
                 CC  +    + I+Y +G   +   + N +  SC C
Sbjct  64502  IHICCSPKSRTSMRIMYAVGSNIRESTIHNFMPSSCGC  64615


 Score = 43.1 bits (100),  Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 28/97 (29%), Positives = 42/97 (43%), Gaps = 2/97 (2%)
 Frame = -3

Query  15     CCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASA  74
              C L    IDF   LG KWI  PK  +  +C+G C  + S D       +L N+     +
Sbjct  63210  CKLHHKRIDFS-SLGMKWITYPKSIDITYCSGICV-VGSYDKTSVIYGTLVNSYMASHNI  63037

Query  75     SPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKC  111
                CC  +    LT+ Y  G+    + + N +  +C C
Sbjct  63036  PQCCFPKTRSHLTVTYMSGRKQMNQTIKNFMPATCSC  62926



Lambda      K        H        a         alpha
   0.323    0.136    0.465    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 2144008700
```

9. Transforming growth factor beta-1|279-390

```
Query= sp|P01137|279-390
```

```
Length=112
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006966.1  Deerpox virus W-848-83, complete genome                  90.5    2e-21
NC_002188.1  Fowlpox virus, complete genome                           67.4    2e-13
NC_024447.1  Pigeonpox virus isolate FeP2, complete genome            63.9    3e-12
NC_024446.1  Penguinpox virus isolate PSan92, complete genome         63.2    5e-12
NC_005309.1  Canarypox virus, complete genome                         60.5    5e-11
NC_028238.1  Turkeypox virus strain TKPV-HU1124/2011, complete ge...  49.7    3e-07


>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 90.5 bits (223),  Expect = 2e-21, Method: Composition-based stats.
 Identities = 42/97 (43%), Positives = 59/97 (61%), Gaps = 10/97 (10%)
 Frame = +3

Query  15      CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA  74
               CC+   YIDF+KD+GW WI++P+GYHAN C+G C +   ++  Y+       +HN
Sbjct  155217  CCLVDFYIDFKKDMGWNWIYKPEGYHANLCIGNCNHKL-INMPYNYAF----KHN-----  155366

Query  75      APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
                 CC P+ ++ L I YY GRK KV+ L NM + SC C
Sbjct  155367  VFCCAPKKMKSLIIAYYEGRKYKVDNLKNMKIVSCGC  155477


>NC_002188.1 Fowlpox virus, complete genome
Length=288539

 Score = 67.4 bits (163),  Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 38/109 (35%), Positives = 56/109 (51%), Gaps = 3/109 (3%)
 Frame = -2

Query  3      DTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVL  62
              D+   +SS   NC V + YI+FR  +G KWI  P G    +C+G C      D+    +L
Sbjct  80251  DSGVDYSSPSDNCKVYRKYINFRS-IGLKWILHPPGIDYGYCMGECQSFVYTDSFLYSLL  80075

Query  63     ALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
              A +  +  G     CC  Q+++ L + Y +GR PK   L  + V+SCKC
Sbjct  80074  AFH--YIDGIELKQCCSIQSMDDLVVHYRLGRTPKTAILRKVSVKSCKC  79934


>NC_024447.1 Pigeonpox virus isolate FeP2, complete genome
Length=282356

 Score = 63.9 bits (154),  Expect = 3e-12, Method: Compositional matrix adjust.
 Identities = 35/98 (36%), Positives = 51/98 (52%), Gaps = 3/98 (3%)
 Frame = -3

Query  14     NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS  73
              +C + + YI+FR D+G KWI  P G    +C+G C      D+    +LA +  +  G
Sbjct  87537  DCRIYRKYINFR-DIGLKWILHPPGIDYGYCVGECTSFAYTDSFLYSLLAFH--YIDGIE  87367

Query  74     AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
                 CC  Q ++ L + Y VGR PK   L  + V+SCKC
```

```
Sbjct  87366  LKQCCSIQDMDDLIVHYRVGRTPKTSVLYKVSVKSCKC  87253


>NC_024446.1 Penguinpox virus isolate PSan92, complete genome
Length=306862

 Score = 63.2 bits (152),  Expect = 5e-12, Method: Compositional matrix adjust.
 Identities = 35/97 (36%), Positives = 50/97 (52%), Gaps = 3/97 (3%)
 Frame = -2

Query  15     CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA  74
              C + + YI+FR D+G KWI  P G    +C+G C      D+    +LA +  + G
Sbjct  88650  CKIYRKYINFR-DIGLKWILHPPGIDYGYCVGECTSFAYTDSFLYSLLAFH--YIDGIEL  88480

Query  75     APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
                CC  Q ++ L + Y VGR PK   L  + V+SCKC
Sbjct  88479  KQCCSIQDMDDLIVHYRVGRTPKTSVLYKVSVKSCKC  88369


 Score = 47.0 bits (110),  Expect = 2e-06, Method: Composition-based stats.
 Identities = 26/84 (31%), Positives = 37/84 (44%), Gaps = 1/84 (1%)
 Frame = +1

Query  28      LGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLP  87
               LG+KWIHEP+G    +C G C  + S D        +   +        CC P+  E +
Sbjct  166063  LGYKWIHEPRGIQFTYCYGTC-VMGSYDESSVIYGTVVTNYISDKGIPSCCSPKRREDIT  166239

Query  88      IVYYVGRKPKVEQLSNMIVRSCKC  111
               I YY GR  +   + N +   C C
Sbjct  166240  ISYYRGRNIEKHTIHNFMPTHCGC  166311


>NC_005309.1 Canarypox virus, complete genome
Length=359853

 Score = 60.5 bits (145),  Expect = 5e-11, Method: Compositional matrix adjust.
 Identities = 35/100 (35%), Positives = 50/100 (50%), Gaps = 8/100 (8%)
 Frame = +1

Query  15      CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQ---YSKVLALYNQHNPG  71
               C +  +Y+DF   LG+KWIHEPKG    +C G C  + S D     Y  ++  Y  +N
Sbjct  199456  CSLNSVYLDFSA-LGYKWIHEPKGIQFTYCHGTCI-LSSYDKSSVIYGTIVTNYLSNN--  199623

Query  72      ASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
                    CC P+  + + I YY+GR  K + + N I   C C
Sbjct  199624  -RIPLCCSPKERKDITITYYLGRNVKKQTIRNFIPTHCGC  199740


 Score = 47.4 bits (111),  Expect = 2e-06, Method: Composition-based stats.
 Identities = 29/97 (30%), Positives = 47/97 (48%), Gaps = 3/97 (3%)
 Frame = -3

Query  15      CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA  74
               C +R  ++ F KDLG  WI  PK +   +C G C  I S  T+ S +      ++   +
Sbjct  194440  CLLRHKHMKF-KDLGCNWILRPKSFIFTYCKGTC--IISSFTRSSIIYGSMFINDIKKNI  194270

Query  75      APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
                 CC P     + I+Y +G+  KV ++ + +  SC C
```

```
Sbjct  194269  HICCAPVTRSNITIMYMLGKNVKVSEIKDFLPSSCGC  194159


 Score = 45.8 bits (107),  Expect = 7e-06, Method: Composition-based stats.
 Identities = 31/108 (29%), Positives = 42/108 (39%), Gaps = 10/108 (9%)
 Frame = +3

Query  8       FSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY--  65
               F   +  C +R + I F  D G KWI  P      +C G C       + Y K   +Y
Sbjct  195411  FLDIDAICNIRSINIKF-ADYGMKWILSPLSTVLTYCYGICSI-----SSYQKTSLMYGT  195572

Query  66      --NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
                   H P  +   CC P       I Y VGR  K + ++N +   C C
Sbjct  195573  IITNHMPDNTIPQCCYPITRSNFTIRYKVGRNIKTDVINNFMPLECAC  195716


 Score = 43.5 bits (101),  Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 31/100 (31%), Positives = 46/100 (46%), Gaps = 8/100 (8%)
 Frame = -2

Query  15      CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQ---YSKVLALYNQHNPG  71
               C +R  YI F +D+G  W+  PKG   ++C G C  + S D     Y K+L L + H
Sbjct  198458  CSLRYQYITF-EDMGCNWVLSPKGIMFSYCTGTCV-VSSFDKSSVIYGKML-LNSIHKTK  198288

Query  72      ASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
                    CC P   + + I Y  G+  K  ++ N +   C C
Sbjct  198287  LHV--CCKPIRRQSVKITYMHGKNIKQSEIKNFMPSECGC  198174


>NC_028238.1 Turkeypox virus strain TKPV-HU1124/2011, complete genome
Length=188534

 Score = 49.7 bits (117),  Expect = 3e-07, Method: Compositional matrix adjust.
 Identities = 32/100 (32%), Positives = 48/100 (48%), Gaps = 4/100 (4%)
 Frame = +2

Query  13     KNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVL-ALYNQHNPG  71
              K C +   YI F KD+G  W+  PKG+   +C G C  I S  T+ S V  A+
Sbjct  64325  KECALHYKYISF-KDVGCNWVLSPKGFTFRYCKGEC--IVSSFTKSSIVYGAMLVNDAKS  64495

Query  72     ASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
              ++   CC P++   + I+Y VG   +   + N +  SC C
Sbjct  64496  SNIHICCSPKSRTSMRIMYAVGSNIRESTIHNFMPSSCGC  64615


 Score = 46.6 bits (109),  Expect = 3e-06, Method: Composition-based stats.
 Identities = 29/97 (30%), Positives = 40/97 (41%), Gaps = 2/97 (2%)
 Frame = -3

Query  15     CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA  74
              C +    IDF   LG KWI  PK     +C G C  + S D        L N +    +
Sbjct  63210  CKLHHKRIDF-SSLGMKWITYPKSIDITYCSGIC-VVGSYDKTSVIYGTLVNSYMASHNI  63037

Query  75     APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC  111
                CC P+    L + Y  GRK   + + N +  +C C
Sbjct  63036  PQCCFPKTRSHLTVTYMSGRKQMNQTIKNFMPATCSC  62926
```

```
Lambda      K        H        a         alpha
   0.323    0.138    0.482    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 2144008700
```

10. Tumor necrosis factor|57-233

```
Query= sp|P01375|57-233

Length=177
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_030656.1  Pteropox virus strain Australia, complete genome         52.4    2e-07


>NC_030656.1 Pteropox virus strain Australia, complete genome
Length=133492

 Score = 52.4 bits (124),  Expect = 2e-07, Method: Compositional matrix adjust.
 Identities = 38/151 (25%), Positives = 63/151 (42%), Gaps = 24/151 (16%)
 Frame = +1

Query  30     DKPVAHVVANPQAEGQL-------------QWLNRRANALLANGVELRDNQLVVPSEGLY  76
              +  VAHV  N     +L              W N   N +L+N   + D +++V   GLY
Sbjct  34069  NTSVAHVTGNNNWNERLYPNNYSFLGNKITSWSNTSNNVVLSNSYYI-DGEIIVTVSGLY  34245

Query  77     LIYSQVLFK-----GQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEA  131
               IY+Q  FK          S ++ +   I +   SY   + L+ + +S C  +T E
Sbjct  34246  YIYAQTYFKLIFGYNSKGNSKNIQMVQYIYKNTSSYGDPLMLMKSARSNCWDKTAEYGLY  34425

Query  132    KPWYEPIYLGGVFQLEKGDRLSAEINRPDYL  162
                    +Y GG+  L+KGD +   +   ++L
Sbjct  34426  -----SVYQGGIHYLKKGDSVFVTVTNKNFL  34503



Lambda      K        H        a         alpha
   0.317    0.134    0.394    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 5989997160
```

11. Insulin-like growth factor I|49-118

```
Query= sp|P05019|49-118

Length=70
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value
```

```
NC_033423.1  Lymphocystis disease virus Sa isolate SA9, complete ...  49.3    7e-08
NC_006549.1  Singapore grouper iridovirus, complete genome            45.8    1e-06
NC_001824.1  Lymphocystis disease virus 1, complete genome            36.6    0.003


>NC_033423.1 Lymphocystis disease virus Sa isolate SA9, complete genome
Length=208501

 Score = 49.3 bits (116),  Expect = 7e-08, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 39/62 (63%), Gaps = 7/62 (11%)
 Frame = +2

Query  3       ETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTG--IVDECC-FRSCDLRRLEM  59
               +TLCG+ELVDAL+ VCG+ G  +  P     ++ + PQ+G  IVD CC  + C+   L+
Sbjct  203636  QTLCGSELVDALELVCGEYGGIYRPP----KNANKKPQSGKKIVDVCCTTKGCNYMDLKQ  203803

Query  60      YC  61
               YC
Sbjct  203804  YC  203809


>NC_006549.1 Singapore grouper iridovirus, complete genome
Length=140131

 Score = 45.8 bits (107),  Expect = 1e-06, Method: Composition-based stats.
 Identities = 26/61 (43%), Positives = 31/61 (51%), Gaps = 5/61 (8%)
 Frame = +3

Query  5      LCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEMYCAPL  64
              +CG EL+DAL   CGDRG Y     G   + S      G+ D CC   CD   L+ YC P
Sbjct  58659  VCGGELIDALTEHCGDRGVYTPPRRGRRTRS-----VGLADACCKNECDENELDRYCNPK  58823

Query  65     K  65
              K
Sbjct  58824  K  58826


>NC_001824.1 Lymphocystis disease virus 1, complete genome
Length=102653

 Score = 36.6 bits (83),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 22/41 (54%), Positives = 24/41 (59%), Gaps = 2/41 (5%)
 Frame = +1

Query  3      ETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGI  43
              E LC A LV ALQ VCG+RG Y   PT   S+  R   TGI
Sbjct  57106  EILCSAHLVAALQRVCGNRGVYRPPPTRRRST--RNGTTGI  57222



Lambda      K        H        a         alpha
   0.324    0.141    0.462    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6
```

```
Effective search space used: 2153929100
```

12. Insulin-like growth factor II|25-91

```
Query= sp|P01344|25-91

Length=67
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_006549.1  Singapore grouper iridovirus, complete genome            43.9    7e-06
NC_033423.1  Lymphocystis disease virus Sa isolate SA9, complete ...  37.7    0.001


>NC_006549.1 Singapore grouper iridovirus, complete genome
Length=140131

 Score = 43.9 bits (102),  Expect = 7e-06, Method: Composition-based stats.
 Identities = 27/59 (46%), Positives = 33/59 (56%), Gaps = 2/59 (3%)
 Frame = +3

Query  8      LCGGELVDTLQFVCGDRGFYFsrpasrvsrrsrGIVEECCFRSCDLALLETYCATPAKS  66
              +CGGEL+D L   CGDRG Y + P      RS G+ + CC   CD   L+ YC  P KS
Sbjct  58659  VCGGELIDALTEHCGDRGVY-TPPRRGRRTRSVGLADACCKNECDENELDRYC-NPKKS  58829


>NC_033423.1 Lymphocystis disease virus Sa isolate SA9, complete genome
Length=208501

 Score = 37.7 bits (86),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 23/60 (38%), Positives = 34/60 (57%), Gaps = 3/60 (5%)
 Frame = +2

Query  6       ETLCGGELVDTLQFVCGDRGFYFsrpasrvsrrsrG--IVEECC-FRSCDLALLETYCAT  62
               +TLCG ELVD L+ VCG+ G  +  P +   +   G  IV+ CC  + C+   L+ YC +
Sbjct  203636  QTLCGSELVDALELVCGEYGGIYRPPKNANKKPQSGKKIVDVCCTTKGCNYMDLKQYCNS  203815



Lambda      K        H        a         alpha
   0.326    0.143    0.475    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 2154637700
```

13. Inhibin beta A chain|311-426

```
Query= sp|P08476|311-426

Length=116
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value
```

```
NC_006966.1  Deerpox virus W-848-83, complete genome                 57.8    4e-10
NC_028238.1  Turkeypox virus strain TKPV-HU1124/2011, complete ge...  56.2    2e-09
NC_005309.1  Canarypox virus, complete genome                        52.0    6e-08
NC_024446.1  Penguinpox virus isolate PSan92, complete genome        45.1    1e-05
NC_024447.1  Pigeonpox virus isolate FeP2, complete genome           35.4    0.030
NC_002188.1  Fowlpox virus, complete genome                          34.7    0.062


>NC_006966.1 Deerpox virus W-848-83, complete genome
Length=166259

 Score = 57.8 bits (138),  Expect = 4e-10, Method: Compositional matrix adjust.
 Identities = 34/106 (32%), Positives = 50/106 (47%), Gaps = 20/106 (19%)
 Frame = +3

Query  11      CCKKQFFVSFK-DIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMR  69
               CC   F++ FK D+GWN WI  P GYHAN C G C   +                   M
Sbjct  155217  CCLVDFYIDFKKDMGWN-WIYKPEGYHANLCIGNCNHKLIN-----------------MP  155342


Query  70      GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
                +  F +   CC P K++ + + YY +G+     +++NM +  CGC
Sbjct  155343  YNYAFKHNVFCCAPKKMKSLIIAYY-EGRKYKVDNLKNMKIVSCGC  155477


>NC_028238.1 Turkeypox virus strain TKPV-HU1124/2011, complete genome
Length=188534

 Score = 56.2 bits (134),  Expect = 2e-09, Method: Compositional matrix adjust.
 Identities = 31/99 (31%), Positives = 54/99 (55%), Gaps = 10/99 (10%)
 Frame = +2

Query  17     FVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFAN  76
              ++SFKD+G N W+++P G+   YC+GEC   ++  + SS+ + + ++N  +       +N
Sbjct  64349  YISFKDVGCN-WVLSPKGFTFRYCKGECI--VSSFTKSSIVYGAMLVNDAKS------SN  64501

Query  77     LKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
              +  CC P     M ++ Y  G NI +  I N +   CGC
Sbjct  64502  IHICCSPKSRTSMRIM-YAVGSNIRESTIHNFMPSSCGC  64615


 Score = 41.6 bits (96),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 30/114 (26%), Positives = 47/114 (41%), Gaps = 10/114 (9%)
 Frame = -3

Query  2      LECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHST  61
              L+ D +   C       + F  +G   WI  P       YC G C   + G+   +   + T
Sbjct  63237  LKADDRNTTCKLHHKRIDFSSLGMK-WITYPKSIDITYCSGIC---VVGSYDKTSVIYGT  63070

Query  62     VINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
              ++N Y M  H    N+  CC P K R    + Y  G+  + + I+N +   C C
Sbjct  63069  LVNSY-MASH----NIPQCCFP-KTRSHLTVTYMSGRKQMNQTIKNFMPATCSC  62926


>NC_005309.1 Canarypox virus, complete genome
Length=359853

 Score = 52.0 bits (123),  Expect = 6e-08, Method: Compositional matrix adjust.
```

```
 Identities = 30/107 (28%), Positives = 56/107 (52%), Gaps = 10/107 (9%)
 Frame = -2

Query  9       NICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRM  68
               +IC  +  +++F+D+G N W+++P G   +YC G C   ++    SS+ +   ++N
Sbjct  198464  DICSLRYQYITFEDMGCN-WVLSPKGIMFSYCTGTCV--VSSFDKSSVIYGKMLLNSIHK  198294

Query  69      RGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
                       L  CC P + + + + Y   G+NI + +I+N +  ECGC
Sbjct  198293  ------TKLHVCCKPIRRQSVKITYMH-GKNIKQSEIKNFMPSECGC  198174


 Score = 51.6 bits (122),  Expect = 6e-08, Method: Compositional matrix adjust.
 Identities = 30/107 (28%), Positives = 50/107 (47%), Gaps = 10/107 (9%)
 Frame = +1

Query  9       NICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRM  68
               ++C     ++ F  +G+  WI  P G    YC G C   I  +   S   + T++ +Y
Sbjct  199450  HVCSLNSVYLDFSALGYK-WIHEPKGIQFTYCHGTC---ILSSYDKSSVIYGTIVTNYLS  199617

Query  69      RGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
                   P      CC P + + +++ YY  G+N+ K+ I+N I   CGC
Sbjct  199618  NNRIPL-----CCSPKERKDITITYYL-GRNVKKQTIRNFIPTHCGC  199740


 Score = 51.6 bits (122),  Expect = 7e-08, Method: Compositional matrix adjust.
 Identities = 30/105 (29%), Positives = 49/105 (47%), Gaps = 2/105 (2%)
 Frame = -3

Query  11     CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRG  70
              C  KQ ++  K +  +D IIAP G    YC G C  +      S+  +    +    ++
Sbjct  74056  CTTKQKYLDLKYLDMDDTIIAPRGITFKYCSGYCDINSMKNFYSNSLYGILAMKFISLKA  73877

Query  71     HSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
               +  +N K CC P  +  +S+LY D   NI K ++ N  + +C C
Sbjct  73876  IN--SNFKRCCYPESMENISILYIDPNGNIKKGELVNSTISKCVC  73748


 Score = 47.4 bits (111),  Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 30/105 (29%), Positives = 52/105 (50%), Gaps = 11/105 (10%)
 Frame = -3

Query  11      CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRG  70
               C  +   + FKD+G N WI+ P  +   YC+G C   I+  + SS+ + S  IN  +
Sbjct  194440  CLLRHKHMKFKDLGCN-WILRPKSFIFTYCKGTCI--ISSFTRSSIIYGSMFINDIK---  194279

Query  71      HSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
                    N+  CC P     ++++Y   G+N+   +I++ +   CGC
Sbjct  194278  ----KNIHICCAPVTRSNITIMYM-LGKNVKVSEIKDFLPSSCGC  194159


 Score = 42.7 bits (99),  Expect = 9e-05, Method: Compositional matrix adjust.
 Identities = 31/106 (29%), Positives = 44/106 (42%), Gaps = 10/106 (9%)
 Frame = +3

Query  10      ICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMR  69
               IC  +   + F D G   WI++P      YC G C   I+    +SL + + + NH
Sbjct  195429  ICNIRSINIKFADYGM-KWILSPLSTVLTYCYGIC--SISSYQKTSLMYGTIITNHM---  195590
```

```
Query  70      GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
                  P   +  CC P   R    + Y  G+NI    I N +  EC C
Sbjct  195591  ---PDNTIPQCCYPIT-RSNFTIRYKVGRNIKTDVINNFMPLECAC  195716


>NC_024446.1 Penguinpox virus isolate PSan92, complete genome
Length=306862

 Score = 45.1 bits (105),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 30/97 (31%), Positives = 45/97 (46%), Gaps = 10/97 (10%)
 Frame = +1

Query  19      SFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLK  78
               S+  +G+  WI  P G    YC G C   + G+   S   + TV+ +Y          +
Sbjct  166051  SYVHLGYK-WIHEPRGIQFTYCYGTC---VMGSYDESSVIYGTVVTNYISD-----KGIP  166203

Query  79      SCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
               SCC P +   +++ YY  G+NI K  I N +   CGC
Sbjct  166204  SCCSPKRREDITISYYR-GRNIEKHTIHNFMPTHCGC  166311


 Score = 36.2 bits (82),  Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 21/53 (40%), Positives = 28/53 (53%), Gaps = 3/53 (6%)
 Frame = -2

Query  9      NICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSG--SSLSFH  59
              N C   + +++F+DIG   WI+ P G    YC GEC S     S   S L+FH
Sbjct  88656  NYCKIYRKYINFRDIGLK-WILHPPGIDYGYCVGECTSFAYTDSFLYSLLAFH  88501


>NC_024447.1 Pigeonpox virus isolate FeP2, complete genome
Length=282356

 Score = 35.4 bits (80),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 21/53 (40%), Positives = 28/53 (53%), Gaps = 3/53 (6%)
 Frame = -3

Query  9      NICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSG--SSLSFH  59
              N C   + +++F+DIG   WI+ P G    YC GEC S     S   S L+FH
Sbjct  87540  NDCRIYRKYINFRDIGLK-WILHPPGIDYGYCVGECTSFAYTDSFLYSLLAFH  87385


>NC_002188.1 Fowlpox virus, complete genome
Length=288539

 Score = 34.7 bits (78),  Expect = 0.062, Method: Compositional matrix adjust.
 Identities = 27/101 (27%), Positives = 45/101 (45%), Gaps = 15/101 (15%)
 Frame = -2

Query  17     FVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSG--SSLSFHSTVINHYRMRGHSPF  74
              +++F+ IG   WI+ P G    YC GEC S +   S   S L+FH           +
Sbjct  80197  YINFRSIGLK-WILHPPGIDYGYCMGECQSFVYTDSFLYSLLAFH-----------YIDG  80054

Query  75     ANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC  115
                LK CC    +  + +++Y  G+      ++ + V+ C C
Sbjct  80053  IELKQCCSIQSMDDL-VVHYRLGRTPKTAILRKVSVKSCKC  79934
```

```
Lambda      K        H        a         alpha
   0.323    0.138    0.467    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 2143063900
```

14. Interleukin-6|30-212

```
Query= sp|P05231|30-212

Length=183
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_009333.1  Human herpesvirus 8, complete genome                     74.7    5e-15


>NC_009333.1 Human herpesvirus 8, complete genome
Length=137969

 Score = 74.7 bits (182),  Expect = 5e-15, Method: Composition-based stats.
 Identities = 41/158 (26%), Positives = 77/158 (49%), Gaps = 0/158 (0%)
 Frame = -3

Query  26     KQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVK  85
              +++ ++L  I    ++ C ++ +C+   E  A  +L LP + + D C   GFNE +CL K
Sbjct  17733  QRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKK  17554

Query  86     IITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNAS  145
              +  G  EFEV  ++L   F  S      +++ TK L   +Q++   L       P  +
Sbjct  17553  LADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRG  17374

Query  146    LLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRALRQM  183
              LL +LQ    W++   +  +L + ++F   ++R L  +
Sbjct  17373  LLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVLNSI  17260



Lambda      K        H        a         alpha
   0.315    0.128    0.355    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 6503425488
```

15. Resistin|19-108

```
Query= sp|Q9HD89|19-108
```

```
Length=90
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_030901.1  Gordonia phage ClubL, complete genome                    37.0    0.004


>NC_030901.1 Gordonia phage ClubL, complete genome
Length=92618

 Score = 37.0 bits (84),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 25/77 (32%), Positives = 32/77 (42%), Gaps = 9/77 (12%)
 Frame = -2

Query  18     AGSLIF---RAISSIGLECQSVTSRGDLATCPRGFAVTGCTC-----GSACGSWDVRAET  69
              AG+L+    R +S + LE   V  RGD+A  P+G A           G    +W VR E
Sbjct  56569  AGALVLEFERQLSRL-LESGRVQDRGDVAEDPKGIARVRVRHWLHRRGEPAAAWRVRTER  56393

Query  70     TCHCQCAGMDWTGARCC  86
                    A   W G R C
Sbjct  56392  PRRSARAASRWAGRRSC  56342


Lambda      K        H        a         alpha
   0.324    0.133    0.456    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 2149205100
```

Adiponectin

15. HUMAN Adiponectin

```
Query= sp|Q15848|ADIPO_HUMAN Adiponectin OS=Homo sapiens GN=ADIPOQ PE=1
SV=1

Length=244
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

NC_003390.2  Synechococcus phage P60, complete genome                 55.5    7e-08
NC_031039.1  Bacillus phage AR9, complete genome                      54.7    1e-07
NC_016072.1  Megavirus chiliensis, complete genome                    53.1    5e-07
NC_020842.1  Cellulophaga phage phiST genomic sequence                52.8    6e-07
NC_010324.1  Enterobacteria phage phiEco32, complete genome           52.4    8e-07
NC_029120.1  Shigella phage 75/02 Stx, complete genome                52.4    9e-07
NC_031001.1  Gordonia phage Terapin, complete genome                  52.0    1e-06
NC_025416.1  Staphylococcus phage MCE-2014, complete genome           51.2    2e-06
NC_032108.1  Cedratvirus A11 genome assembly, complete genome: mo...  51.2    2e-06
NC_017972.1  Pseudomonas phage Lu11, complete genome                  50.4    3e-06
NC_021782.1  Salmonella phage FSL SP-076, complete genome             50.4    4e-06
NC_014649.1  Acanthamoeba polyphaga mimivirus, complete genome        50.1    4e-06
NC_021308.1  Mycobacterium phage HINdeR, complete genome              50.1    4e-06
NC_023607.1  Mycobacterium phage 40AC, complete genome                50.1    5e-06
NC_021772.1  Salmonella phage FSL SP-058, complete genome             49.3    7e-06
NC_011356.1  Enterobacteria phage YYZ-2008, complete prophage genome  49.3    9e-06
NC_022336.1  Propionibacterium phage PHL010M04, complete genome       48.5    1e-05
NC_000852.5  Paramecium bursaria Chlorella virus 1, complete genome   48.5    1e-05
NC_018285.1  Streptococcus phage YMC-2011, complete genome            48.5    1e-05
NC_023639.1  Mimivirus terra2 genome                                  48.5    1e-05
NC_031279.1  Mycobacterium phage Bactobuster, complete genome         48.1    2e-05
NC_018842.1  Propionibacterium phage P1.1, complete genome             47.8    2e-05
NC_016071.1  Salmonella phage PVP-SE1, complete genome                47.8    3e-05
NC_027351.1  Salmonella phage SSE-121, complete genome                47.8    3e-05
NC_027628.1  Propionibacterium phage Lauchelly, complete genome       47.4    3e-05
NC_018840.1  Propionibacterium phage P100_1, complete genome          47.0    4e-05
NC_022087.1  Mycobacterium phage AnnaL29, complete genome             47.0    5e-05
NC_021795.1  Cellulophaga phage phi17:1, complete genome              46.6    6e-05
NC_028965.1  Mycobacterium phage Pioneer, complete genome             45.8    1e-04
NC_020104.1  Acanthamoeba polyphaga moumouvirus, complete genome      45.8    1e-04
NC_027386.1  Propionibacterium phage PHL152M00, complete genome       45.8    1e-04
NC_028881.1  Enterobacteria phage vB_EcoM_VR5, complete genome        45.8    1e-04
NC_031238.1  Mycobacterium phage Catalina, complete genome            45.4    1e-04
NC_005902.1  Lymphocystis disease virus - isolate China, complete...  45.4    1e-04
NC_030394.2  Short-finned eel ranavirus isolate ANGA14001, comple...  45.4    1e-04
NC_027357.1  Propionibacterium phage PHL025M00, complete genome       45.4    1e-04
NC_027401.1  Propionibacterium phage PHL095N00, complete genome       45.4    2e-04
NC_004167.1  Bacteriophage phi-105 DNA, complete sequence             45.4    2e-04
NC_007056.1  Staphylococcus phage EW, complete genome                 45.4    2e-04
NC_021791.1  Cellulophaga phage phi12:1, complete genome              45.1    2e-04
NC_023423.1  Pithovirus sibericum isolate P1084-T, complete genome    45.1    2e-04
NC_027621.1  Propionibacterium phage Wizzo, complete genome           45.1    2e-04
NC_027630.1  Propionibacterium phage Ouroboros, complete genome       45.1    2e-04
NC_009015.1  Burkholderia ambifaria phage BcepF1, complete genome     45.1    2e-04
NC_029072.1  Salmonella phage 19, complete genome                     45.1    2e-04
NC_025434.1  Shigella phage POCJ13, complete genome                   45.1    2e-04
NC_011357.1  Stx2-converting phage 1717, complete prophage genome     45.1    2e-04
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NC_009514.1  Phage cdtI DNA, complete genome                          45.1    2e-04
NC_022098.1  Pandoravirus salinus, complete genome                    44.7    3e-04
NC_031003.1  Propionibacterium phage Moyashi, complete genome         44.7    3e-04
NC_004813.1  Enterobacteria phage BP-4795, complete genome            44.7    3e-04
NC_011132.1  Sputnik virophage, complete genome                       44.3    3e-04
NC_007055.1  Staphylococcus phage 37, complete genome                 44.3    3e-04
NC_027626.1  Propionibacterium phage Procrass1, complete genome       44.3    3e-04
NC_022340.1  Propionibacterium phage PHL114L00, complete genome       44.3    3e-04
NC_020197.1  Streptococcus phage TP-J34 complete genome               44.3    3e-04
NC_000871.1  Streptococcus phage Sfi19, complete genome               44.3    4e-04
NC_024210.1  Escherichia phage e4/1c, complete genome                 43.9    4e-04
NC_017974.1  Cronobacter phage CR3, complete genome                   43.9    5e-04
NC_031256.1  Mycobacterium phage Loser, complete genome               43.9    5e-04
NC_027400.1  Propionibacterium phage PHL055N00, complete genome       43.5    5e-04
NC_018083.1  Clostridium phage phiCPV4, complete genome               43.5    5e-04
NC_017980.1  Clostridium phage phiCP7R, complete genome               43.5    5e-04
NC_021858.1  Pandoravirus dulcis, complete genome                     43.5    6e-04
NC_014792.1  Enterobacteria phage vB_EcoM-VR7, complete genome        43.5    6e-04
NC_033423.1  Lymphocystis disease virus Sa isolate SA9, complete ...  43.5    6e-04
NC_022335.1  Propionibacterium phage PHL067M10, complete genome       43.5    7e-04
NC_028967.1  Propionibacterium phage PAC1, complete genome            43.1    7e-04
NC_031922.1  Synechococcus phage S-CAM9 isolate 1109NB16, complet...  43.1    7e-04
NC_027367.1  Propionibacterium phage PHL132N00, complete genome       43.1    7e-04
NC_018846.1  Escherichia phage P13374, complete genome                43.1    8e-04
NC_031065.1  Salmonella phage vB_SnwM_CGG4-1, complete genome         43.1    8e-04
NC_014260.1  Enterobacteria phage IME08, complete genome              43.1    8e-04
NC_008464.1  Stx2-converting phage 86, complete genome                43.1    8e-04
NC_027389.1  Propionibacterium phage PHL141N00, complete genome       43.1    8e-04
NC_022968.1  Enterobacteria phage 4MG, complete genome                43.1    8e-04
NC_018839.1  Propionibacterium phage P14.4, complete genome           43.1    9e-04
NC_027333.1  Propionibacterium phage PHL070N00, complete genome       43.1    9e-04
NC_023716.1  Mycobacterium phage Alma, complete genome                43.1    9e-04
NC_027370.1  Propionibacterium phage PHL179M00, complete genome       42.7    0.001
NC_028685.1  Shigella phage Ss-VASD, complete genome                  42.7    0.001
NC_027354.1  Propionibacterium phage PHL301M00, complete genome       42.7    0.001
NC_031005.1  Propionibacterium phage QueenBey, complete genome        42.7    0.001
NC_018852.1  Propionibacterium phage P100D, complete genome           42.7    0.001
NC_026440.1  Pandoravirus inopinatum isolate KlaHel, complete genome  42.7    0.001
NC_018841.1  Propionibacterium phage P101A, complete genome           42.4    0.001
NC_022337.1  Propionibacterium phage PHL071N05, complete genome       42.4    0.001
NC_027629.1  Propionibacterium phage Attacne, complete genome         42.4    0.001
NC_027385.1  Propionibacterium phage PHL092M00, complete genome       42.4    0.001
NC_003225.3  White spot syndrome virus strain CN01, complete genome   42.4    0.001
NC_023557.1  Erwinia phage Ea35-70, complete genome                   42.4    0.002
NC_027294.1  Propionibacterium phage PHL150M00, complete genome       42.4    0.002
NC_015453.1  Propionibacterium phage PAS50 endogenous virus, comp...  42.4    0.002
NC_028660.1  Escherichia phage phi191, complete genome                42.4    0.002
NC_029077.1  Mycobacterium phage VohminGhazi, complete genome         42.0    0.002
NC_022985.1  Mycobacterium phage Zaka, complete genome                42.0    0.002
NC_022965.1  Mycobacterium phage CloudWang3, complete genome          42.0    0.002
NC_022334.1  Propionibacterium phage PHL112N00, complete genome       42.0    0.002
NC_025444.1  Mycobacteriophage RedRock, complete genome               42.0    0.002
NC_023717.1  Cronobacter phage CR9, complete genome                   41.6    0.003
NC_023609.1  Mycobacterium phage RhynO, complete genome               41.6    0.003
NC_029018.1  Mycobacterium phage Anubis, complete genome              41.2    0.003
NC_027362.1  Propionibacterium phage PHL116M00, complete genome       41.2    0.003
NC_027624.1  Propionibacterium phage SKKY, complete genome            41.2    0.003
NC_019442.1  Escherichia phage TL-2011c, complete genome              41.2    0.004
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NC_027625.1  Propionibacterium phage Kubed, complete genome           41.2    0.004
NC_018084.1  Clostridium phage phiZP2, complete genome                41.2    0.004
NC_010353.1  Streptococcus phage 858, complete genome                 41.2    0.004
NC_031254.1  Arthrobacter phage Kitkat, complete genome               40.8    0.004
NC_027984.1  Stx2 converting phage vB_EcoP_24B, complete genome       40.8    0.004
NC_004913.3  Stx1 converting phage DNA, complete genome               40.8    0.004
NC_000902.1  Enterobacteria phage VT2-Sakai, complete genome          40.8    0.004
NC_000924.1  Enterobacteria phage 933W, complete genome               40.8    0.004
NC_004914.3  Stx2 converting phage II DNA, complete genome            40.8    0.004
NC_010237.1  Enterobacteria phage Min27, complete genome              40.8    0.004
NC_028449.1  Escherichia phage PA2, complete genome                   40.8    0.004
NC_028656.1  Enterobacteria phage VT2phi_272, complete sequence       40.8    0.004
NC_018838.1  Propionibacterium phage P100_A, complete genome          40.8    0.004
NC_019914.1  Staphylococcus phage StB27, complete genome              40.8    0.005
NC_002515.1  Mycoplasma phage P1, complete genome                     40.8    0.005
NC_009541.1  Propionibacterium phage PA6, complete genome             40.8    0.005
NC_027295.1  Propionibacterium phage PHL199M00, complete genome       40.4    0.006
NC_024789.1  Escherichia phage bV_EcoS_AKS96, complete genome         40.4    0.007
NC_031074.1  Gordonia phage Bantam, complete genome                   40.0    0.007
NC_031927.1  Synechococcus phage S-CAM7 isolate 0910CC49, complet...  40.0    0.007
NC_020490.2  Staphylococcus phage StB12, complete genome              40.0    0.008
NC_024354.1  Cronobacter phage CR8, complete genome                   40.0    0.008
NC_020205.1  Xanthomonas citri phage CP2 DNA, complete genome         40.0    0.008
NC_018270.1  Weissella phage phiYS61, complete genome                 40.0    0.008
NC_018851.1  Propionibacterium phage ATCC29399B_C, complete genome    40.0    0.009
NC_018847.1  Propionibacterium phage ATCC29399B_T, complete genome    40.0    0.009
NC_030901.1  Gordonia phage ClubL, complete genome                    40.0    0.009
NC_030696.1  Gordonia phage Smoothie, complete genome                 40.0    0.009
NC_031029.1  Gordonia phage Cucurbita, complete genome                40.0    0.009
NC_030936.1  Gordonia phage Bachita, complete genome                  40.0    0.009
NC_023731.1  Mycobacterium phage Trixie, complete genome              39.7    0.011
NC_007734.1  Bacillus phage WBeta, complete genome                    39.7    0.011
NC_027627.1  Propionibacterium phage Solid, complete genome           39.7    0.012
NC_027623.1  Propionibacterium phage Pirate, complete genome          39.3    0.013
NC_004682.1  Mycobacterium phage Bxz2, complete genome                39.3    0.013
NC_031084.1  Propionibacterium phage BruceLethal, complete genome     39.3    0.013
AC_000012.1  Murine adenovirus A, complete genome                     39.3    0.014
NC_000942.1  Murine adenovirus A, complete genome                     39.3    0.014
NC_027361.1  Propionibacterium phage PHL085N00, complete genome       39.3    0.016
NC_028798.1  Mycobacterium phage MarQuardt, complete genome           39.3    0.016
NC_015463.1  Synechococcus phage S-CBS2, complete genome              38.9    0.019
NC_027346.1  Propionibacterium phage PHL171M01, complete genome       38.9    0.021
NC_024793.1  Escherichia phage bV_EcoS_AHP42, complete genome         38.5    0.022
NC_020883.1  Bacillus phage PM1 DNA, complete genome                  38.5    0.022
NC_028957.1  Enterobacteria phage vB_EcoM_VR26, complete genome       38.5    0.023
NC_028774.1  Klebsiella phage Sushi, complete genome                  38.5    0.024
NC_019400.1  Cronobacter phage vB_CsaM_GAP31, complete genome         38.5    0.024
NC_024141.1  Mycobacterium phage Kampy, complete genome               38.5    0.027
NC_022990.1  Zamilon virophage complete genome                        38.5    0.027
NC_023562.1  Mycobacterium phage BellusTerra, complete genome         38.5    0.028
NC_018834.1  Propionibacterium phage P9.1, complete genome            38.5    0.029
NC_022096.1  Pseudomonas phage PaBG, complete genome                  38.5    0.029
NC_023719.1  Bacillus phage G, complete genome                        38.1    0.030
NC_023565.1  Mycobacterium phage Nyxis, complete genome               38.1    0.032
NC_028925.1  Enterobacteria phage vB_EcoM_VR25, complete genome       38.1    0.032
NC_022776.1  Streptococcus phage TP-778L complete genome              38.1    0.033
NC_015454.1  Propionibacterium phage PAD20 endogenous virus, comp...  37.7    0.042
NC_020201.1  Pectobacterium phage phiTE, complete genome              37.7    0.045
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NC_027371.1  Propionibacterium phage Pacnes 2012-15, complete genome  37.7    0.047
NC_028672.1  Cronobacter phage PBES 02, complete genome               37.7    0.047
NC_018853.1  Streptomyce phage TG1, complete genome                   37.7    0.052
NC_013645.1  Streptococcus phage Abc2, complete genome                37.4    0.056
NC_015569.1  Synechococcus phage S-CRM01, complete genome             37.4    0.058
NC_024148.1  Mycobacterium phage Phantastic, complete genome          37.4    0.064
NC_022341.1  Propionibacterium phage PHL113M01, complete genome       37.0    0.071
NC_018849.1  Propionibacterium phage P105, complete genome            37.0    0.078
NC_011023.1  Mycobacterium phage Pukovnik, complete genome            36.6    0.095


>NC_003390.2 Synechococcus phage P60, complete genome
Length=46675

 Score = 55.5 bits (132),  Expect = 7e-08, Method: Compositional matrix adjust.
 Identities = 34/66 (52%), Positives = 42/66 (64%), Gaps = 0/66 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G PG+ G +GA G +G  G  G  G  G  G  GPKGD G+TG PGA+GP+G PG QG
Sbjct  39178  LKGDPGNDGADGATGPEGPQGPQGNPGADGADGAQGPKGDKGDTGDPGAQGPQGNPGDQG  39357

Query  100    RKGEPG  105
               +G PG
Sbjct  39358  PQGNPG  39375


 Score = 43.5 bits (101),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 44/144 (31%), Positives = 64/144 (44%), Gaps = 11/144 (8%)
 Frame = +1

Query  48     GHNGAPGRDGRDGTPGEKGEKGDPGLIGPK---GDIGETGVPGAEGPRGF---PGIQGRK  101
              G+ GA G DG  G  G+KG+ GDPG  GP+   GD G  G PGA+G  G     G QG +
Sbjct  39247  GNPGADGADGAQGPKGDKGDTGDPGAQGPQGNPGDQGPQGNPGADGADGAIGPEGPQGPQ  39426

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQN-HYDGSTGKFHCN-IPGLYY  159
              G  G    +  +A +V + + +   +  I +      Q +  Y+GS   F  N + G
Sbjct  39427  GPEGPEGPMSTAALTVDINSDIASASRAIIYAPGSNGQASLKYNGS---FLINPLNGTLT  39597

Query  160    FAYHITVYMKDVKVSLFKKDKAML  183
                  I     DV V+      + +
Sbjct  39598  APTFIGDLTGDVSVATISSSGSNI  39669


 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 34/83 (41%), Positives = 42/83 (51%), Gaps = 16/83 (19%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGD-------------PGLIGPKGDIGETGVP  86
              + G  G PG +GA G  G  G  GE+G +G             PG  GPKGD G+TG
Sbjct  38950  LQGPQGLPGADGADGAQGPQGIQGEQGLQGPQGLPGADGADSTVPGPQGPKGDKGDTGDA  39129

Query  87     GAEGPR---GFPGIQGRKGEPGE  106
              G +GP+    G  G QG KG+PG
Sbjct  39130  GPQGPKGDTGDAGPQGLKGDPGN  39198


>NC_031039.1 Bacillus phage AR9, complete genome
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Length=251042

 Score = 54.7 bits (130),  Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  GEKGE+GDPG  G  G  G  G+PG +G +G  G QG +
Sbjct  10522  GETGEKGEQGERGEKGEQGKSGEKGERGDPGPRGEPGPAGMDGIPGEKGEQGEKGEQGER  10343

Query  102    GEPGE  106
              GE GE
Sbjct  10342  GEKGE  10328


 Score = 51.6 bits (122),  Expect = 1e-06, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  GE+GEKG+ G  G KG+ G+ G  G  GP G  GI G K
Sbjct  10558  GEKGEQGEKGEKGETGEKGEQGERGEKGEQGKSGEKGERGDPGPRGEPGPAGMDGIPGEK  10379

Query  102    GEPGE  106
              GE GE
Sbjct  10378  GEQGE  10364


 Score = 50.4 bits (119),  Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  GEKGE+G  G  G +GD G  G PG  G  G PG +G +
Sbjct  10549  GEQGEKGEKGETGEKGEQGERGEKGEQGKSGEKGERGDPGPRGEPGPAGMDGIPGEKGEQ  10370

Query  102    GEPGE  106
              GE GE
Sbjct  10369  GEKGE  10355


 Score = 50.1 bits (118),  Expect = 5e-06, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  GEKGE+G+ G  G +G  GE G  G  GPRG PG  G
Sbjct  10576  GKQGERGEKGEQGEKGEKGETGEKGEQGERGEKGEQGKSGEKGERGDPGPRGEPGPAGMD  10397

Query  102    GEPGE  106
              G PGE
Sbjct  10396  GIPGE  10382


 Score = 48.1 bits (113),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 27/50 (54%), Positives = 33/50 (66%), Gaps = 3/50 (6%)
 Frame = -2
```

```
Query  57     GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
              G+DG  GE+GEKG+    G KG+ GETG  G +G RG  G QG+ GE GE
Sbjct  10585  GKDGKQGERGEKGEQ---GEKGEKGETGEKGEQGERGEKGEQGKSGEKGE  10445


 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 27/58 (47%), Positives = 33/58 (57%), Gaps = 0/58 (0%)
 Frame = -2

Query  48     GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
              G +G  G  G  G  GEKGEKG+ G  G +G+ GE G  G  G +G  G  G +GEPG
Sbjct  10585  GKDGKQGERGEKGEQGEKGEKGETGEKGEQGERGEKGEQGKSGEKGERGDPGPRGEPG  10412


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 26/67 (39%), Positives = 35/67 (52%), Gaps = 3/67 (4%)
 Frame = -2

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGE---KGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
               G  G  G  G  G  G+ G  GE+G+   +G+PG  G  G  GE G  G +G +G  G
Sbjct  10516  TGEKGEQGERGEKGEQGKSGEKGERGDPGPRGEPGPAGMDGIPGEKGEQGEKGEQGERGE  10337

Query  98     QGRKGEP  104
              +G KG+P
Sbjct  10336  KGEKGDP  10316


>NC_016072.1 Megavirus chiliensis, complete genome
Length=1259197

 Score = 53.1 bits (126),  Expect = 5e-07, Method: Compositional matrix adjust.
 Identities = 27/60 (45%), Positives = 35/60 (58%), Gaps = 0/60 (0%)
 Frame = -3

Query  47      PGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
                G  G PG++G  G PG KG+KGD   I  KGD G+ G+ G  G +G  G  G KG+ G+
Sbjct  679361  KGDKGDPGKNGLKGDPGLKGQKGDGSTIMGKGDKGDIGIKGQNGSKGLKGRIGNKGQKGD  679182


 Score = 50.4 bits (119),  Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 40/97 (41%), Positives = 46/97 (47%), Gaps = 2/97 (2%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G  G  GEKGEKGD G  G KGD+GE G  G  G +G  G  G K
Sbjct  272875  GEKGDFGNKGEKGNSGEKGDLGEKGEKGDIGDKGEKGDLGEKGEKGERGYKGEKGDLGEK  273054

Query  102     GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYN  138
               GE G+      S  S  + TY+     P  FT    N
Sbjct  273055  GEKGDLGEKGESGTSSFISTYLNT--TPGAFTSTVPN  273159


 Score = 48.9 bits (115),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 30/62 (48%), Positives = 39/62 (63%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G+ G  G  G  G DG  GEKG+ GD GL G KGDIG+ G+ G +G  G  G++G KG+
```

```
Sbjct  275528  GNDGLKGEKGDIGDDGLKGEKGDIGDDGLKGEKGDIGDDGLKGEKGDLGNDGLKGEKGDI  275707

Query  105     GE  106
               G+
Sbjct  275708  GD  275713


 Score = 48.9 bits (115),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 32/62 (52%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKGEKGD G  G KGD+GE G  G  G +G  G  G KGE 
Sbjct  276658  GEKGEKGDSGEKGEKGDSGEKGEKGDLGEKGEKGDLGEKGEKGDVGDKGEKGETGDKGEK  276837

Query  105     GE  106
               GE
Sbjct  276838  GE  276843


 Score = 48.5 bits (114),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 32/69 (46%), Positives = 41/69 (59%), Gaps = 3/69 (4%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDG---RDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
               + G  G  G+NG  G  G    DG  GEKG+ GD GL G KGDIG+ G+ G +G  G  G
Sbjct  275468  LKGEKGDLGNNGLKGEKGDLGNDGLKGEKGDIGDDGLKGEKGDIGDDGLKGEKGDIGDDG  275647

Query  97      IQGRKGEPG  105
               ++G KG+ G
Sbjct  275648  LKGEKGDLG  275674


 Score = 48.1 bits (113),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 32/62 (52%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKGEKGD G  G KGD+GE G  G  G +G  G  G KGE 
Sbjct  276631  GEKGEKGDLGEKGEKGDSGEKGEKGDSGEKGEKGDLGEKGEKGDLGEKGEKGDVGDKGEK  276810

Query  105     GE  106
               GE
Sbjct  276811  GE  276816


 Score = 47.4 bits (111),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 31/62 (50%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKGEKGD G  G KGD+GE G  G  G +G  G  G KGE 
Sbjct  276550  GEKGEKGDLGEKGEKGDLGEKGEKGDLGEKGEKGDLGEKGEKGDSGEKGEKGDSGEKGEK  276729

Query  105     GE  106
               G+
Sbjct  276730  GD  276735
```

```
 Score = 47.4 bits (111),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 32/62 (52%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKGEKGD G  G KGDIG+ G  G  G +G  G  G KGE
Sbjct  276874  GDKGEKGETGDKGEKGDLGEKGEKGDLGEKGEKGDIGDKGEKGETGDKGEKGETGDKGEK  277053

Query  105     GE  106
               GE
Sbjct  277054  GE  277059


 Score = 47.4 bits (111),  Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G IG KGD G+ G  G +G +G  G +G K
Sbjct  272686  GEKGDSGDKGEKGDKGEKGNIGDKGEKGDMGDIGLKGDKGDVGDKGEKGDKGDSGEKGEK  272865

Query  102     GEPGE  106
               G+ GE
Sbjct  272866  GDIGE  272880


 Score = 47.0 bits (110),  Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKGEKGD G  G KGD+G+ G  G  G +G  G  G K
Sbjct  276676  GDSGEKGEKGDSGEKGEKGDLGEKGEKGDLGEKGEKGDVGDKGEKGETGDKGEKGETGDK  276855

Query  102     GEPGE  106
               GE G+
Sbjct  276856  GEKGD  276870


 Score = 46.6 bits (109),  Expect = 7e-05, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 39/65 (60%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+ GD GL G KGD+G+TG+ G +G  G  G++G K
Sbjct  873385  GEKGDIGDTGLKGEKGDIGDKGEKGDIGDTGLKGEKGDLGDTGLKGEKGDIGDTGLKGEK  873564

Query  102     GEPGE  106
               G+ G+
Sbjct  873565  GDIGD  873579


 Score = 46.2 bits (108),  Expect = 8e-05, Method: Compositional matrix adjust.
 Identities = 30/71 (42%), Positives = 34/71 (48%), Gaps = 6/71 (8%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
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               GI G  G  G  GR G  G  G+      KGE G  G IG KGDIG  G  G++G  G
Sbjct  679250  GIKGQNGSKGLKGRIGNKGQKGDSGSSNMKGETGSKGDIGSKGDIGSKGDIGSKGESGST  679071

Query  96      GIQGRKGEPGE  106
                 +G KG  G
Sbjct  679070  AEKGDKGNDGN  679038


 Score = 46.2 bits (108),  Expect = 9e-05, Method: Compositional matrix adjust.
 Identities = 27/69 (39%), Positives = 39/69 (57%), Gaps = 0/69 (0%)
 Frame = +2

Query  48      GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEG  107
               G  G  G  G DG+ G+KG+ G+ GL G KGDIG  G+ G +G  G  G++G+KG+ G+
Sbjct  274934  GSKGEKGNIGNDGSKGQKGDIGNNGLKGQKGDIGNNGLKGQKGDIGNNGLKGQKGDLGDK  275113

Query  108     AYVYRSAFS  116
                 +
Sbjct  275114  GNIGNDGLK  275140


 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 39/65 (60%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G  G KGDIG+TG+ G +G  G  G++G K
Sbjct  873601  GDKGEKGDIGDTGLKGDKGDLGDKGEKGDIGDKGEKGDIGDTGLKGDKGDLGDTGLKGDK  873780

Query  102     GEPGE  106
               G+ G+
Sbjct  873781  GDIGD  873795


 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 28/68 (41%), Positives = 32/68 (47%), Gaps = 3/68 (4%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---IGPKGDIGETGVPGAEGPRGFPGIQ  98
               G+ G  G+ G  G  G     GE G KGD G    IG KGDIG  G  G+   +G  G
Sbjct  679223  GLKGRIGNKGQKGDSGSSNMKGETGSKGDIGSKGDIGSKGDIGSKGESGSTAEKGDKGND  679044

Query  99      GRKGEPGE  106
               G KG  G
Sbjct  679043  GNKGNDGN  679020


 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 32/70 (46%), Positives = 39/70 (56%), Gaps = 3/70 (4%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRD---GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
               + G  G  G  G   RD   G  G PG KG KG+ G IG KG+ GE G  G +G +G PG
Sbjct  274241  IRGKHGTKGEKGESCRDLTKGEKGDPGNKGNKGEKGDIGNKGNKGEKGDIGNKGEKGDPG  274420

Query  97      IQGRKGEPGE  106
                +G KGE G+
Sbjct  274421  NKGEKGEKGD  274450
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```
 Score = 45.4 bits (106),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 38/62 (61%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G+ G  G  G  G DG  GEKG+ G+ GL G KGD+G  G+ G +G  G  G++G KG+
Sbjct  275384  GNDGLKGNKGDLGNDGLKGEKGDLGNDGLKGEKGDLGNNGLKGEKGDLGNDGLKGEKGDI  275563

Query  105     GE  106
               G+
Sbjct  275564  GD  275569


 Score = 45.4 bits (106),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 31/75 (41%), Positives = 40/75 (53%), Gaps = 0/75 (0%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
                G+ G  G  G  G  G  G  G+KGEKGD G  G KGDIG+TG+ G +G  G  G +G
Sbjct  873508  TGLKGEKGDIGDTGLKGEKGDIGDKGEKGDLGDKGEKGDIGDTGLKGDKGDLGDKGEKGD  873687

Query  101     KGEPGEGAYVYRSAF  115
                G+ GE   +  +
Sbjct  873688  IGDKGEKGDIGDTGL  873732


 Score = 45.4 bits (106),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 36/86 (42%), Positives = 42/86 (49%), Gaps = 1/86 (1%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G PG KGEKG+ G IG KGDIG  G  G +G  G  G +G
Sbjct  274355  GNKGNKGEKGDIGNKGEKGDPGNKGEKGEKGDIGNKGDIGNKGDIGNKGDIGNKGEKGDL  274534

Query  102     GEPGE-GAYVYRSAFSVGLETYVTIP  126
               G  GE G    +      + T V IP
Sbjct  274535  GNKGEKGDIGDKGVNGSQILTGVGIP  274612


 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 38/65 (58%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G KGEKGD G  G KGDIG+TG+ G +G  G  G++G K
Sbjct  873349  GDKGEKGDIGDKGEKGDIGDTGLKGEKGDIGDKGEKGDIGDTGLKGEKGDLGDTGLKGEK  873528

Query  102     GEPGE  106
               G+ G+
Sbjct  873529  GDIGD  873543


 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 32/65 (49%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G  G KGD+GE G  G  G +G  G  G K
Sbjct  276838  GETGDKGEKGDLGDKGEKGETGDKGEKGDLGEKGEKGDLGEKGEKGDIGDKGEKGETGDK  277017

Query  102     GEPGE  106
               GE GE
Sbjct  277018  GEKGE  277032


 Score = 44.7 bits (104),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 31/76 (41%), Positives = 40/76 (53%), Gaps = 0/76 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  GEKG+ GD GL G KGDIG+TG+ G +G  G  G +G
Sbjct  873415  LKGEKGDIGDKGEKGDIGDTGLKGEKGDLGDTGLKGEKGDIGDTGLKGEKGDIGDKGEKG  873594

Query  100     RKGEPGEGAYVYRSAF  115
                 G+ GE   +  +
Sbjct  873595  DLGDKGEKGDIGDTGL  873642


 Score = 44.7 bits (104),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 34/90 (38%), Positives = 42/90 (47%), Gaps = 4/90 (4%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G+KGEKG+ G  G KGD+G+ G  G  G +G  G  G KGE
Sbjct  276982  GDKGEKGETGDKGEKGETGDKGEKGETGDKGEKGDVGDKGEKGETGDKGEKGETGDKGEK  277161

Query  105     GE----GAYVYRSAFSVGLETYVTIPNMPI  130
               G+    G        +   ET V+  N  I
Sbjct  277162  GDIGDKGETATCEIVNTDGETRVSACNTGI  277251


 Score = 44.7 bits (104),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 31/62 (50%), Positives = 33/62 (53%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKGEKGD G  G KGD GE G  G  G +G  G  G KGE
Sbjct  276577  GEKGEKGDLGEKGEKGDLGEKGEKGDLGEKGEKGDSGEKGEKGDSGEKGEKGDLGEKGEK  276756

Query  105     GE  106
               G+
Sbjct  276757  GD  276762


 Score = 44.7 bits (104),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 39/62 (63%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G+ G  G  G  G +G  GEKG+ G+ GL G KGDIG+ G+ G +G  G  G++G KG+
Sbjct  275456  GNDGLKGEKGDLGNNGLKGEKGDLGNDGLKGEKGDIGDDGLKGEKGDIGDDGLKGEKGDI  275635

Query  105     GE  106
               G+
```

```
Sbjct  275636  GD  275641


 Score = 44.7 bits (104),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 38/62 (61%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G+ G  G  G  G DG  GEKG+ G+ GL G KGD+G  G+ G +G  G  G++G KG+
Sbjct  275420  GNDGLKGEKGDLGNDGLKGEKGDLGNNGLKGEKGDLGNDGLKGEKGDIGDDGLKGEKGDI  275599

Query  105     GE  106
               G+
Sbjct  275600  GD  275605


 Score = 44.7 bits (104),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 31/62 (50%), Positives = 33/62 (53%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKGEKGD G  G KGD GE G  G  G +G  G  G KGE
Sbjct  276604  GEKGEKGDLGEKGEKGDLGEKGEKGDSGEKGEKGDSGEKGEKGDLGEKGEKGDLGEKGEK  276783

Query  105     GE  106
               G+
Sbjct  276784  GD  276789


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 32/65 (49%), Positives = 38/65 (58%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G DG  GEKG+ GD GL G KGDIG+ G+ G +G +G  G  G K
Sbjct  336539  GEKGDIGDKGEKGDFGDDGLKGEKGDFGDDGLKGDKGDIGDNGLKGDKGEKGDIGDNGLK  336718

Query  102     GEPGE  106
               G+ GE
Sbjct  336719  GDKGE  336733


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 30/66 (45%), Positives = 38/66 (58%), Gaps = 0/66 (0%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
                G+ G  G  G  G  G  G  GEKG+ GD GL G KGD+G+TG+ G +G  G  G +G
Sbjct  873634  TGLKGDKGDLGDKGEKGDIGDKGEKGDIGDTGLKGDKGDLGDTGLKGDKGDIGDKGEKGD  873813

Query  101     KGEPGE  106
                G+ GE
Sbjct  873814  IGDKGE  873831


 Score = 44.3 bits (103),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 33/85 (39%), Positives = 44/85 (52%), Gaps = 18/85 (21%)
 Frame = +1
```

```
Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGE------------------KGDPGLIGPKGDIG  81
               + G  G  G  G  G +G DG+ G+KG+                  KGD G IG KGDIG
Sbjct  872875  LKGQKGDIGLKGETGDNGNDGSKGDKGDIGDNGLKGDKGDIGDDGLKGDKGDIGDKGDIG  873054

Query  82      ETGVPGAEGPRGFPGIQGRKGEPGE  106
               ETG+ G +G  G  G++G KG+ G+
Sbjct  873055  ETGLKGDKGDIGDNGLKGDKGDLGD  873129


 Score = 43.9 bits (102),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 31/67 (46%), Positives = 38/67 (57%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KGEKGD G  G KGDIG+ G  G +G +G  G +G
Sbjct  337145  LKGEKGDIGDKGNKGEKGDIGDKGDKGEKGDIGDKGQKGDIGDKGQKGDKGDKGDIGDKG  337324

Query  100     RKGEPGE  106
                KG+ GE
Sbjct  337325  EKGDAGE  337345


 Score = 43.9 bits (102),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 31/66 (47%), Positives = 36/66 (55%), Gaps = 0/66 (0%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
                G+ G  G  G  G  G  G   GEKG+ GD GL G KGDIG+ G  G  G +G  G  G
Sbjct  873967  TGLKGEKGDIGDKGEKGDFGDKGEKGDIGDTGLKGEKGDIGDKGEKGDIGDKGEKGDIGD  874146

Query  101     KGEPGE  106
               KGE G+
Sbjct  874147  KGEKGD  874164


 Score = 43.9 bits (102),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 29/62 (47%), Positives = 39/62 (63%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G +G  G+KG+ GD GL G KGDIG+TG+ G +G  G  G++G KG+
Sbjct  873160  GDNGLKGDKGDIGDNGLKGDKGDLGDLGLKGEKGDIGDTGLKGDKGNIGDTGLKGDKGDL  873339

Query  105     GE  106
               G+
Sbjct  873340  GD  873345


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 31/71 (44%), Positives = 35/71 (49%), Gaps = 0/71 (0%)
 Frame = +2

Query  35      ACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGF  94
               +C     G  G PG+ G  G  G  G  G KGEKGD G  G KGD G  G  G +G  G
Sbjct  274280  SCRDLTKGEKGDPGNKGNKGEKGDIGNKGNKGEKGDIGNKGEKGDPGNKGEKGEKGDIGN  274459

Query  95      PGIQGRKGEPG  105
```

```
                G  G KG+ G
Sbjct  274460  KGDIGNKGDIG  274492


 Score = 43.5 bits (101),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 31/67 (46%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KGEKGD G  G KGDIG+ G  G  G   F G +G
Sbjct  336713  LKGDKGEKGDIGDNGLKGDKGEKGDKGEKGDKGEKGDKGDIGDKGNKGESGSAVFKGDKG  336892

Query  100     RKGEPGE  106
                KG+ GE
Sbjct  336893  EKGDTGE  336913


 Score = 43.1 bits (100),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 30/61 (49%), Positives = 35/61 (57%), Gaps = 0/61 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G+KGEKGD    G KGDIGETG+ G +G +G  G +G  GE
Sbjct  339410  GDVGEKGDVGDKGEKGDVGDKGEKGDISDKGEKGDIGETGLKGDKGEKGDIGDKGDIGET  339589

Query  105     G  105
               G
Sbjct  339590  G  339592


 Score = 43.1 bits (100),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 32/65 (49%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+KGD G  G KGDIGE G  G +G +G  G +G
Sbjct  272758  GEKGDMGDIGLKGDKGDVGDKGEKGDKGDSGEKGEKGDIGEKGDFGNKGEKGNSGEKGDL  272937

Query  102     GEPGE  106
               GE GE
Sbjct  272938  GEKGE  272952


 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKGEKGD G  G KG+ G+ G  G  G +G  G  G K
Sbjct  276703  GDSGEKGEKGDLGEKGEKGDLGEKGEKGDVGDKGEKGETGDKGEKGETGDKGEKGDLGDK  276882

Query  102     GEPGE  106
               GE GE
Sbjct  276883  GEKGE  276897


 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
```

```
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKG+ G  G KGD+GE G  G  G +G  G  G K
Sbjct  276811  GETGDKGEKGETGDKGEKGDLGDKGEKGETGDKGEKGDLGEKGEKGDLGEKGEKGDIGDK  276990

Query  102     GEPGE  106
               GE GE
Sbjct  276991  GEKGE  277005


 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+ GD GL G KGD+G+ G  G +G  G  G +G
Sbjct  272695  GDSGDKGEKGDKGEKGNIGDKGEKGDMGDIGLKGDKGDVGDKGEKGDKGDSGEKGEKGDI  272874

Query  102     GEPGE  106
               GE G+
Sbjct  272875  GEKGD  272889


 Score = 43.1 bits (100),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 33/64 (52%), Gaps = 3/64 (5%)
 Frame = -3

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G NG+ G  GR    G KG+KGD G    KG+ G  G  G++G  G  G  G KGE
Sbjct  679250  GIKGQNGSKGLKGR---IGNKGQKGDSGSSNMKGETGSKGDIGSKGDIGSKGDIGSKGES  679080

Query  105     GEGA  108
               G  A
Sbjct  679079  GSTA  679068


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 36/97 (37%), Positives = 47/97 (48%), Gaps = 5/97 (5%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KGEKGD G  G KGD GE G  G +G +G  G +G
Sbjct  339593  LKGDKGDIGDKGDIGDKGDKGEKGDKGEKGDIGDKGEKGDKGEKGDIGDKGEKGDIGDKG  339772

Query  100     RKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIF  136
                 G+ GE      ++F   + T+  I   P  F+ I
Sbjct  339773  DIGDKGEKGDSVATSF---ISTF--IQTTPGVFSSIV  339868


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G  G KGDIG+TG+ G +G  G  G +G
Sbjct  873934  GDKGEKGDIGDTGLKGEKGDIGDKGEKGDFGDKGEKGDIGDTGLKGEKGDIGDKGEKGDI  874113
```

```
Query  102     GEPGE  106
               G+ GE
Sbjct  874114  GDKGE  874128


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/61 (48%), Positives = 35/61 (57%), Gaps = 0/61 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKG  GD GL G KGDIG+ G+ G +G  G  G++G KG+
Sbjct  276226  GEKGEKGDLGDKGEKGDLGEKGNIGDTGLKGDKGDIGDAGLKGDKGDLGDAGLKGDKGDI  276405

Query  105     G  105
               G
Sbjct  276406  G  276408


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 33/77 (43%), Positives = 41/77 (53%), Gaps = 3/77 (4%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGE---KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G NG  G  G  G  GE   KG+KG+ G IG KGDIGETG+ G +G  G  G +
Sbjct  336296  GEKGDIGENGLKGDKGEKGDIGETGLKGDKGEKGDIGEKGDIGETGLKGDKGDLGDKGDK  336475

Query  99      GRKGEPGEGAYVYRSAF  115
               G  G+ GE   +  +
Sbjct  336476  GDLGDKGEKGDIGETGL  336526


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 30/62 (48%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G+KGEKGD G  G KGD+G+ G  G  G +G  G  G KGE
Sbjct  874114  GDKGEKGDIGDKGEKGDIGDKGEKGDLGDKGEKGDLGDKGDKGDIGDKGEKGDLGDKGEK  874293

Query  105     GE  106
               GE
Sbjct  874294  GE  874299


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 28/63 (44%), Positives = 36/63 (57%), Gaps = 0/63 (0%)
 Frame = +1

Query  44      PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
                G  G  G  G  G  G  G+KGEKG+ G  G KGD+G+ G+ G +G  G  G +G KG+
Sbjct  272665  KGDLGDKGEKGDSGDKGEKGDKGEKGNIGDKGEKGDMGDIGLKGDKGDVGDKGEKGDKGD  272844

Query  104     PGE  106
                GE
Sbjct  272845  SGE  272853


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
```

```
 Identities = 34/80 (43%), Positives = 37/80 (46%), Gaps = 12/80 (15%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGD------------PGLIGPKGDIGETGVPGAE  89
               G+ G  G  G  G  G  G  GEKGEKGD             G  G KGD+GE G  G
Sbjct  272785  GLKGDKGDVGDKGEKGDKGDSGEKGEKGDIGEKGDFGNKGEKGNSGEKGDLGEKGEKGDI  272964

Query  90      GPRGFPGIQGRKGEPGEGAY  109
               G +G  G  G KGE GE  Y
Sbjct  272965  GDKGEKGDLGEKGEKGERGY  273024


 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 26/55 (47%), Positives = 33/55 (60%), Gaps = 4/55 (7%)
 Frame = +2

Query  35      ACT----GWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGV  85
               ACT    G ++G PG  G  G  G  G DG+ G+KG+ G+ GL G KGDIG  G+
Sbjct  338918  ACTWILVGNLSGSPGQQGEKGEKGDIGNDGSKGDKGDLGNDGLKGEKGDIGVKGI  339082


 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 29/61 (48%), Positives = 35/61 (57%), Gaps = 0/61 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G+KGEKGD G  G KGDIG+TG+ G +G  G  G +G  G+
Sbjct  873790  GDKGEKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDIGDTGLKGEKGDLGDKGEKGDIGDT  873969

Query  105     G  105
               G
Sbjct  873970  G  873972


 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/70 (43%), Positives = 41/70 (59%), Gaps = 3/70 (4%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGR---DGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
               + G  G  G NG  G  G    +G  G+KG+ GD GL G KGDIG+ G+ G +G  G  G
Sbjct  873064  LKGDKGDIGDNGLKGDKGDLGDNGLKGDKGDFGDNGLKGDKGDIGDNGLKGDKGDLGDLG  873243

Query  97      IQGRKGEPGE  106
               ++G KG+ G+
Sbjct  873244  LKGEKGDIGD  873273


 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/71 (42%), Positives = 38/71 (54%), Gaps = 6/71 (8%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               G  G  GH G  G DG  G  GE      KG+KG+ G  G KGD+G  G+ G +G  G
Sbjct  287501  GEKGDKGHKGDFGNDGIKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKGDKGESGSA  287680

Query  96      GIQGRKGEPGE  106
                ++G KGE G+
Sbjct  287681  VLKGDKGEKGD  287713
```

```
 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G+KGEKG+ G  G KGD+G+ G  G  G +G  G  G KGE
Sbjct  276766  GEKGEKGDVGDKGEKGETGDKGEKGETGDKGEKGDLGDKGEKGETGDKGEKGDLGEKGEK  276945

Query  105     GE  106
               G+
Sbjct  276946  GD  276951


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G     G  G  G  G KG+KG+ G IG KGDIGETG+ G +G  G  G  G K
Sbjct  339464  GDKGEKGDISDKGEKGDIGETGLKGDKGEKGDIGDKGDIGETGLKGDKGDIGDKGDIGDK  339643

Query  102     GEPGE  106
               G+ GE
Sbjct  339644  GDKGE  339658


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G  G KGDIG+ G  G  G +G  G  G K
Sbjct  874024  GDKGEKGDIGDTGLKGEKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDLGDK  874203

Query  102     GEPGE  106
               GE G+
Sbjct  874204  GEKGD  874218


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/62 (48%), Positives = 38/62 (61%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G+KG+KGD G  G KGDIGETG+ G +G +G  G +G KG+
Sbjct  336404  GEKGDIGETGLKGDKGDLGDKGDKGDLGDKGEKGDIGETGLKGDKGEKGDIGDKGEKGDF  336583

Query  105     GE  106
               G+
Sbjct  336584  GD  336589


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/66 (42%), Positives = 36/66 (55%), Gaps = 0/66 (0%)
 Frame = +2
```

```
Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G DG  G KG+ G+ GL G KGD G  G+ G +G  G  G++G
Sbjct  275135  LKGQKGDLGDKGDKGDLGNDGLKGNKGDLGNDGLKGEKGDFGNDGLKGEKGDFGNDGLKG  275314

Query  100     RKGEPG  105
                KG+ G
Sbjct  275315  EKGDLG  275332


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/66 (45%), Positives = 38/66 (58%), Gaps = 0/66 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G+ G  G  G  G  G  G+KGEKGD G  G KGDIG+TG+ G +G  G  G +G
Sbjct  873280  LKGDKGNIGDTGLKGDKGDLGDIGDKGEKGDIGDKGEKGDIGDTGLKGEKGDIGDKGEKG  873459

Query  100     RKGEPG  105
                 G+ G
Sbjct  873460  DIGDTG  873477


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  GEKGE GD G  G  GD GE G  G +G +G  G +G K
Sbjct  276955  GEKGEKGDIGDKGEKGETGDKGEKGETGDKGEKGETGDKGEKGDVGDKGEKGETGDKGEK  277134

Query  102     GEPGE  106
               GE G+
Sbjct  277135  GETGD  277149


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GE G KGD G IG KGDIG+ G  G +G +G  G  G K
Sbjct  339518  GETGLKGDKGEKGDIGDKGDIGETGLKGDKGDIGDKGDIGDKGDKGEKGDKGEKGDIGDK  339697

Query  102     GEPGE  106
               GE G+
Sbjct  339698  GEKGD  339712


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 38/103 (37%), Positives = 48/103 (47%), Gaps = 13/103 (13%)
 Frame = +2

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGD---PGLIGPKGDIGETGVPGAEGPRGFPGI  97
                G  G  G  G  G  G  G  GEKGEKGD    G IG KGDIG  G  G +G +G  G
Sbjct  274361  KGNKGEKGDIGNKGEKGDPGNKGEKGEKGDIGNKGDIGNKGDIGNKGDIGNKGEKGDLGN  274540

Query  98      QGRKGEPGE-GAYVYRSAFSVGL---------ETYVTIPNMPI  130
               +G KG+ G+ G    +    VG+         + Y+ I N  +
```

```
Sbjct  274541  KGEKGDIGDKGVNGSQILTGVGIPSDNLGNVGDIYIDITNNDL  274669


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 26/62 (42%), Positives = 39/62 (63%), Gaps = 0/62 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G++G  G+ G  G  G+KG+ G+ GL G KGD+G  G+ G +G  G  G++G K
Sbjct  275105  GDKGNIGNDGLKGQKGDLGDKGDKGDLGNDGLKGNKGDLGNDGLKGEKGDFGNDGLKGEK  275284

Query  102     GE  103
               G+
Sbjct  275285  GD  275290


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKGEKGD G  G KG+ G+ G  G  G +G  G  G K
Sbjct  276892  GETGDKGEKGDLGEKGEKGDLGEKGEKGDIGDKGEKGETGDKGEKGETGDKGEKGETGDK  277071

Query  102     GEPGE  106
               GE G+
Sbjct  277072  GEKGD  277086


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 30/69 (43%), Positives = 42/69 (61%), Gaps = 3/69 (4%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGE---KGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
               AG+ G  G  G  G  G  G  GEKG+   KG+ G +G KG+IG+TG+ G +G  G  G+
Sbjct  276169  AGLKGDKGDIGDKGEKGNLGEKGEKGDLGDKGEKGDLGEKGNIGDTGLKGDKGDIGDAGL  276348

Query  98      QGRKGEPGE  106
               +G KG+ G+
Sbjct  276349  KGDKGDLGD  276375


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 29/62 (47%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G+KGEKGD G  G KGD+G+ G  G  G +G  G  G KGE
Sbjct  874087  GDKGEKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDLGDKGEKGDLGDKGDKGDIGDKGEK  874266

Query  105     GE  106
               G+
Sbjct  874267  GD  874272


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +2
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G  G KGD+G+TG+ G +G  G  G +G
Sbjct  337331  GDAGEKGEKGDLGEKGDKGDIGDKGEKGDIGNKGEKGDLGDTGLKGDKGDLGDKGDKGDL  337510

Query  102     GEPGE  106
               G+ GE
Sbjct  337511  GDKGE  337525


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G  G KGD+GE G  G  G +G  G  G K
Sbjct  337250  GQKGDIGDKGQKGDKGDKGDIGDKGEKGDAGEKGEKGDLGEKGDKGDIGDKGEKGDIGNK  337429

Query  102     GEPGE  106
               GE G+
Sbjct  337430  GEKGD  337444


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 30/67 (45%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KG+ GD G IG KGD GE G  G +G  G  G +G
Sbjct  339530  LKGDKGEKGDIGDKGDIGETGLKGDKGDIGDKGDIGDKGDKGEKGDKGEKGDIGDKGEKG  339709

Query  100     RKGEPGE  106
                KGE G+
Sbjct  339710  DKGEKGD  339730


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 31/72 (43%), Positives = 41/72 (57%), Gaps = 1/72 (1%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G  G  G +G  G  GEKG+ GD GL G KG+ G+ G  G +G +G  G  G K
Sbjct  336665  GLKGDKGEKGDIGDNGLKGDKGEKGDIGDNGLKGDKGEKGDKGEKGDKGEKGDKGDIGDK  336844

Query  102     GEPGE-GAYVYR  112
               G  GE G+ V++
Sbjct  336845  GNKGESGSAVFK  336880


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 27/74 (36%), Positives = 35/74 (47%), Gaps = 1/74 (1%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G     G  G  G  G+ G+ G KGD G  G  G   E G  G +G +G  G +G K
Sbjct  679187  GDSGSSNMKGETGSKGDIGSKGDIGSKGDIGSKGESGSTAEKGDKGNDGNKGNDGNKGDK  679008

Query  102     GEPGEGAYVYRSAF  115
```

```
               G  G+G + YR  +
Sbjct  679007  GMQGKG-FKYRCNY  678969


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 38/64 (59%), Gaps = 0/64 (0%)
 Frame = +1

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               + G  G  G  G  G  G  G+KG+ GD GL G KGD+G+ G+ G +G  G  G++G KG
Sbjct  873010  LKGDKGDIGDKGDIGETGLKGDKGDIGDNGLKGDKGDLGDNGLKGDKGDFGDNGLKGDKG  873189

Query  103     EPGE  106
               + G+
Sbjct  873190  DIGD  873201


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 32/70 (46%), Positives = 40/70 (57%), Gaps = 3/70 (4%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEK---GDPGLIGPKGDIGETGVPGAEGPRGFPG  96
               + G  G  G NG  G  G  G  G KGEK   GD GL G KG+IG+TG+ G +G  G  G
Sbjct  873172  LKGDKGDIGDNGLKGDKGDLGDLGLKGEKGDIGDTGLKGDKGNIGDTGLKGDKGDLGDIG  873351

Query  97      IQGRKGEPGE  106
                +G KG+ G+
Sbjct  873352  DKGEKGDIGD  873381


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 31/74 (42%), Positives = 38/74 (51%), Gaps = 0/74 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G KGEKGD G  G KGDIG+TG+ G +G  G  G +G
Sbjct  873844  GDKGEKGDIGDKGEKGDIGDTGLKGEKGDLGDKGEKGDIGDTGLKGEKGDIGDKGEKGDF  874023

Query  102     GEPGEGAYVYRSAF  115
               G+ GE   +  +
Sbjct  874024  GDKGEKGDIGDTGL  874065


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 30/71 (42%), Positives = 37/71 (52%), Gaps = 6/71 (8%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               G  G  G  G DG  G  GE      KG+KGD G+ G KGD+G  G+ G +G  G
Sbjct  271336  GDVGEKGDKGDLGNDGDKGDKGESGSAVFKGDKGDVGIKGDKGDLGNDGIKGDKGESGSA  271515

Query  96      GIQGRKGEPGE  106
                 +G KG+ GE
Sbjct  271516  VFKGDKGDVGE  271548


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
```

```
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G  G KGDIG+ G  G  G +G  G  G K
Sbjct  874051  GDTGLKGEKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDLGDKGEKGDLGDK  874230

Query  102     GEPGE  106
               G+ G+
Sbjct  874231  GDKGD  874245


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 29/62 (47%), Positives = 36/62 (58%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKG+ GD GL G KGD G+ G+ G +G  G  G++G KGE
Sbjct  336512  GETGLKGDKGEKGDIGDKGEKGDFGDDGLKGEKGDFGDDGLKGDKGDIGDNGLKGDKGEK  336691

Query  105     GE  106
               G+
Sbjct  336692  GD  336697


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 22/60 (37%), Positives = 31/60 (52%), Gaps = 0/60 (0%)
 Frame = -3

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
               + + G  G  G  G  G  G+ G+ G KG+ G    KGD G  G  G +G +G  G+QG+
Sbjct  679172  SNMKGETGSKGDIGSKGDIGSKGDIGSKGESGSTAEKGDKGNDGNKGNDGNKGDKGMQGK  678993


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KG+ G+ GL G KGDIG+ G  G +G +G  G +G K
Sbjct  339500  GEKGDIGETGLKGDKGEKGDIGDKGDIGETGLKGDKGDIGDKGDIGDKGDKGEKGDKGEK  339679

Query  102     GEPGE  106
               G+ G+
Sbjct  339680  GDIGD  339694


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 30/66 (45%), Positives = 35/66 (53%), Gaps = 0/66 (0%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
               +G  G  G  G  G  G  G  G  GEKGD G  G KGDIG+ G  G  G +G  G +G
Sbjct  272845  SGEKGEKGDIGEKGDFGNKGEKGNSGEKGDLGEKGEKGDIGDKGEKGDLGEKGEKGERGY  273024

Query  101     KGEPGE  106
               KGE G+
Sbjct  273025  KGEKGD  273042
```

```
 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 37/62 (60%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G +G  G+KG+ GD GL G KGD G+ G+ G +G  G  G++G KG+
Sbjct  873052  GETGLKGDKGDIGDNGLKGDKGDLGDNGLKGDKGDFGDNGLKGDKGDIGDNGLKGDKGDL  873231

Query  105     GE  106
               G+
Sbjct  873232  GD  873237


 Score = 40.4 bits (93),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKGE GD G  G  GD GE G  G +G +G  G +G K
Sbjct  276928  GEKGEKGDLGEKGEKGDIGDKGEKGETGDKGEKGETGDKGEKGETGDKGEKGDVGDKGEK  277107

Query  102     GEPGE  106
               GE G+
Sbjct  277108  GETGD  277122


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KG+ GD GL G KGDIG+ G  G  G +G  G  G K
Sbjct  873673  GEKGDIGDKGEKGDIGDTGLKGDKGDLGDTGLKGDKGDIGDKGEKGDIGDKGEKGDIGDK  873852

Query  102     GEPGE  106
               GE G+
Sbjct  873853  GEKGD  873867


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 29/70 (41%), Positives = 40/70 (57%), Gaps = 3/70 (4%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGR---DGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
               + G  G  G NG  G  G    +G  G+KG+ GD GL G KGD+G+ G+ G +G  G  G
Sbjct  873100  LKGDKGDLGDNGLKGDKGDFGDNGLKGDKGDIGDNGLKGDKGDLGDLGLKGEKGDIGDTG  873279

Query  97      IQGRKGEPGE  106
               ++G KG  G+
Sbjct  873280  LKGDKGNIGD  873309


 Score = 40.4 bits (93),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 28/73 (38%), Positives = 33/73 (45%), Gaps = 6/73 (8%)
 Frame = -3

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
```

```
                 G  G PG NG  G  G  G  G+      KG+KGD G+ G  G  G  G  G +G +G
Sbjct  679364  CKGDKGDPGKNGLKGDPGLKGQKGDGSTIMGKGDKGDIGIKGQNGSKGLKGRIGNKGQKG  679185

Query  94      FPGIQGRKGEPGE  106
                 G    KGE G
Sbjct  679184  DSGSSNMKGETGS  679146


 Score = 40.0 bits (92),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+ GD GL G KGD+G+ G  G  G +G  G  G K
Sbjct  337367  GEKGDKGDIGDKGEKGDIGNKGEKGDLGDTGLKGDKGDLGDKGDKGDLGDKGEKGDLGDK  337546

Query  102     GEPGE  106
               GE GE
Sbjct  337547  GEKGE  337561


 Score = 40.0 bits (92),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 34/75 (45%), Positives = 38/75 (51%), Gaps = 9/75 (12%)
 Frame = +2

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKG------EKGDP---GLIGPKGDIGETGVPGAEGP  91
                G PG+ G+ G  G  G  G  GEKG      EKGDP   G  G KGDIG  G  G +G
Sbjct  274307  KGDPGNKGNKGEKGDIGNKGNKGEKGDIGNKGEKGDPGNKGEKGEKGDIGNKGDIGNKGD  274486

Query  92      RGFPGIQGRKGEPGE  106
                G  G  G KGE G+
Sbjct  274487  IGNKGDIGNKGEKGD  274531


 Score = 40.0 bits (92),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 32/76 (42%), Positives = 41/76 (54%), Gaps = 0/76 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G +G+    G  G  GEKG+KGD G  G KGD GE+G    +G +G  G +G K
Sbjct  271093  GIKGDKGESGSAVFKGDKGDVGEKGDKGDLGNDGIKGDKGESGSAVFKGDKGDIGEKGDK  271272

Query  102     GEPGEGAYVYRSAFSV  117
               G+ GE      S  +V
Sbjct  271273  GDIGEKGDKGESGSAV  271320


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 37/64 (58%), Gaps = 0/64 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KG+ GD GL G KGD+G+ G+ G +G  G  G++G K
Sbjct  276253  GDKGEKGDLGEKGNIGDTGLKGDKGDIGDAGLKGDKGDLGDAGLKGDKGDIGNDGLKGEK  276432

Query  102     GEPG  105
               G+ G
Sbjct  276433  GDLG  276444
```

```
 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 38/64 (59%), Gaps = 0/64 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G +G+    G  G  G+KG+KGD G  G KGD GE+G    +G +G  G +G+K
Sbjct  287546  GIKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKGDKGESGSAVLKGDKGEKGDKGQK  287725

Query  102     GEPG  105
               G+ G
Sbjct  287726  GDLG  287737


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 30/74 (41%), Positives = 36/74 (49%), Gaps = 0/74 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G+KGEKGD G  G KGDIG+ G  G  G  G  G +G
Sbjct  873754  GDTGLKGDKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDIGDTGLKGEKGDL  873933

Query  102     GEPGEGAYVYRSAF  115
               G+ GE   +  +
Sbjct  873934  GDKGEKGDIGDTGL  873975


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 26/56 (46%), Positives = 31/56 (55%), Gaps = 0/56 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
               G  G  G  G  G DG  GEKG+ GD GL G KGD+G  G+ G +G  G  G+ G
Sbjct  275564  GDDGLKGEKGDIGDDGLKGEKGDIGDDGLKGEKGDLGNDGLKGEKGDIGDDGLNGE  275731


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 38/64 (59%), Gaps = 0/64 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G +G+    G  G  G+KG+KGD G  G KGD GE+G    +G +G  G +G+K
Sbjct  287645  GIKGDKGESGSAVLKGDKGEKGDKGQKGDLGNDGIKGDKGESGSAVFKGDKGEKGDKGQK  287824

Query  102     GEPG  105
               G+ G
Sbjct  287825  GDLG  287836


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G  GEKG  GD GL G KGDIG+ G  G  G +G  G  G K
Sbjct  276082  GEKGNLGDAGLKGDKGDIGDKGEKGNLGDAGLKGDKGDIGDKGEKGNLGEKGEKGDLGDK  276261
```

```
Query  102     GEPGE  106
               GE G+
Sbjct  276262  GEKGD  276276


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 28/74 (38%), Positives = 40/74 (54%), Gaps = 1/74 (1%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G+ G  G+ G  G  G KG+KG+    G KGD+G  G  G +G  G    +G
Sbjct  287261  LEGEKGDKGYKGDKGQKGDLGNDGVKGDKGEKAEKGQKGDLGNDGTKGDKGESGSAVFKG  287440

Query  100     RKGEPGE-GAYVYR  112
                KG+ GE G+ V++
Sbjct  287441  DKGDKGESGSAVFK  287482


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 31/74 (42%), Positives = 38/74 (51%), Gaps = 9/74 (12%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRG--  93
               G  G  G  G  G DG  G  GE      KG+KGD G  G KGD+G  G+ G +G  G
Sbjct  271732  GDVGEKGDKGDLGNDGDKGDKGESGSAVFKGDKGDVGEKGDKGDLGNDGIKGDKGESGSS  271911

Query  94      -FPGIQGRKGEPGE  106
                F G +G KG+ G+
Sbjct  271912  VFKGDKGEKGDKGD  271953


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  GEKG+ GD GL G KGD+G+ G  G  G  G  G +G
Sbjct  873817  GDKGEKGDIGDKGEKGDIGDKGEKGDIGDTGLKGEKGDLGDKGEKGDIGDTGLKGEKGDI  873996

Query  102     GEPGE  106
               G+ GE
Sbjct  873997  GDKGE  874011


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  GEKGE GD G  G  GD GE G  G +G +G  G +G K
Sbjct  276766  GEKGEKGDVGDKGEKGETGDKGEKGETGDKGEKGDLGDKGEKGETGDKGEKGDLGEKGEK  276945

Query  102     GEPGE  106
               G+ GE
Sbjct  276946  GDLGE  276960


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
```

```
 Identities = 29/65 (45%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G +G KGD+G+ G  G  G +G  G    K
Sbjct  339320  GDKGDLGDLGEKGEKGDVGDVGDKGEKGDVGDVGEKGDVGDKGEKGDVGDKGEKGDISDK  339499

Query  102     GEPGE  106
               GE G+
Sbjct  339500  GEKGD  339514


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 37/64 (58%), Gaps = 0/64 (0%)
 Frame = -3

Query  43       IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
                I G  G +G+ G +GR G  G KG+KGD G  G KGD G+ G  G +G  G  G +G  G
Sbjct  1129874  IGGFKGGDGSKGENGRHGLRGLKGDKGDKGDQGDKGDQGQQGDKGDKGDLGDKGDKGDLG  1129695

Query  103      EPGE  106
                + G+
Sbjct  1129694  DQGQ  1129683


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEK D G +G KG+ G++G  G +G +G  G  G K
Sbjct  272578  GDKGDLGDKGDLGDKGEKGDLGDKGEKSDKGDLGDKGEKGDSGDKGEKGDKGEKGNIGDK  272757

Query  102     GEPGE  106
               GE G+
Sbjct  272758  GEKGD  272772


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 28/71 (39%), Positives = 35/71 (49%), Gaps = 0/71 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G+KGEKGD G  G KGDI + G  G  G  G  G +G KG+
Sbjct  339383  GDKGEKGDVGDVGEKGDVGDKGEKGDVGDKGEKGDISDKGEKGDIGETGLKGDKGEKGDI  339562

Query  105     GEGAYVYRSAF  115
               G+   +  +
Sbjct  339563  GDKGDIGETGL  339595


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 33/62 (53%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G+KGEKGD G  G KG+ G+ G  G  G +G  G  G KGE
Sbjct  276793  GDKGEKGETGDKGEKGETGDKGEKGDLGDKGEKGETGDKGEKGDLGEKGEKGDLGEKGEK  276972
```

```
Query  105     GE  106
               G+
Sbjct  276973  GD  276978


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 30/74 (41%), Positives = 38/74 (51%), Gaps = 9/74 (12%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRG--  93
               G  G  G  G  G DG  G  GE      KG+KG+ G  G KGD+G  G+ G +G  G
Sbjct  288122  GEKGDKGQKGDLGNDGLKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKGDKGESGSA  288301

Query  94      -FPGIQGRKGEPGE  106
                F G +G KG+ G+
Sbjct  288302  VFKGDKGEKGDKGQ  288343


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 36/65 (55%), Gaps = 3/65 (5%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGE---KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G DG  G  G+   KGEKGD G  GPKGD G  G  G +G  G  G++G K
Sbjct  275947  GEKGDKGGIGNDGLKGDKGDIGDKGEKGDIGDAGPKGDEGNIGDKGEKGNLGDAGLKGDK  276126

Query  102     GEPGE  106
               G+ G+
Sbjct  276127  GDIGD  276141


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 38/64 (59%), Gaps = 0/64 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G +G+    G  G  G+KG+KGD G  G KGD GE+G    +G +G  G +G+K
Sbjct  287969  GIKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGLKGDKGESGSAVFKGDKGEKGDKGQK  288148

Query  102     GEPG  105
               G+ G
Sbjct  288149  GDLG  288160


 Score = 39.7 bits (91),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 30/71 (42%), Positives = 40/71 (56%), Gaps = 6/71 (8%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGP------KGDIGETGVPGAEGPRGFP  95
               G  GH G  G  G +G  G+ G+ G+KGD G IG      KGD+G  G  G +G +G
Sbjct  289190  GDKGHKGDLGNKGDEGDKGSKGDLGDKGDKGHIGDTGDKGHKGDLGNKGDKGDKGDQGDI  289369

Query  96      GIQGRKGEPGE  106
               GI+G KG+ G+
Sbjct  289370  GIKGEKGDLGD  289402
```

```
 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G KGEKGD G  G KGDIG+ G  G  G +G  G  G K
Sbjct  873997  GDKGEKGDFGDKGEKGDIGDTGLKGEKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDIGDK  874176

Query  102     GEPGE  106
               GE G+
Sbjct  874177  GEKGD  874191


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 31/68 (46%), Positives = 39/68 (57%), Gaps = 3/68 (4%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIG---PKGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G  G  G +G  G  GEKG+ GD GL G    KGDIG+ G+ G +G +G  G +
Sbjct  336620  GDDGLKGDKGDIGDNGLKGDKGEKGDIGDNGLKGDKGEKGDIGDNGLKGDKGEKGDKGEK  336799

Query  99      GRKGEPGE  106
               G KGE G+
Sbjct  336800  GDKGEKGD  336823


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 35/67 (52%), Gaps = 0/67 (0%)
 Frame = +2

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               + G  G  G  G+ G  G  G KG+KG+ G    KGD GE G  G +G  G  GI+G KG
Sbjct  287684  LKGDKGEKGDKGQKGDLGNDGIKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKGDKG  287863

Query  103     EPGEGAY  109
               E G   +
Sbjct  287864  ESGSAVF  287884


 Score = 39.3 bits (90),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 30/70 (43%), Positives = 34/70 (49%), Gaps = 3/70 (4%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
                 G  G  G  G  G  G DG  G+KGE G   L   KGD GE G  G +G  G  GI+G
Sbjct  287585  FKGDKGEKGDKGQKGDLGNDGIKGDKGESGSAVL---KGDKGEKGDKGQKGDLGNDGIKG  287755

Query  100     RKGEPGEGAY  109
                KGE G   +
Sbjct  287756  DKGESGSAVF  287785


 Score = 39.3 bits (90),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 29/79 (37%), Positives = 37/79 (47%), Gaps = 9/79 (11%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGE---------KGDPGLIGPKGDIGETGVPGAEG  90
               + G  G  G  G  G  G DG  G+KGE         KG+ G  G KGD+G  G+ G +G
```

```
Sbjct  287684  LKGDKGEKGDKGQKGDLGNDGIKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKGDKG  287863

Query  91      PRGFPGIQGRKGEPGEGAY  109
                 G    +G KGE G   +
Sbjct  287864  ESGSAVFKGDKGESGSAVF  287920


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 30/69 (43%), Positives = 39/69 (57%), Gaps = 3/69 (4%)
 Frame = +2

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGD---PGLIGPKGDIGETGVPGAEGPRGFPGI  97
                G  G  G+NG  G+ G  G  G KG+KGD    GL G KGD+G+ G  G +G +G  G
Sbjct  274976  KGQKGDIGNNGLKGQKGDIGNNGLKGQKGDIGNNGLKGQKGDLGDKGNIGNDGLKGQKGD  275155

Query  98      QGRKGEPGE  106
                G KG+ G+
Sbjct  275156  LGDKGDKGD  275182


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKGE GD G  G  GD GE G  G +G +G  G +G K
Sbjct  276739  GEKGEKGDLGEKGEKGDVGDKGEKGETGDKGEKGETGDKGEKGDLGDKGEKGETGDKGEK  276918

Query  102     GEPGE  106
               G+ GE
Sbjct  276919  GDLGE  276933


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 32/92 (35%), Positives = 46/92 (50%), Gaps = 3/92 (3%)
 Frame = -3

Query  38       GWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
                G   G  G  G NG  G  G  G  G+KG++GD G  G +GD G+ G  G +G +G  G
Sbjct  1129871  GGFKGGDGSKGENGRHGLRGLKGDKGDKGDQGDKGDQGQQGDKGDKGDLGDKGDKGDLGD  1129692

Query  98       QGRKGE---PGEGAYVYRSAFSVGLETYVTIP  126
                QG+ GE    G+   ++   ++      VT+P
Sbjct  1129691  QGQVGEQGIKGDSNLIFTFEYTTPGNFSVTVP  1129596


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 30/74 (41%), Positives = 38/74 (51%), Gaps = 9/74 (12%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRG--  93
               G  G  G  G DG  G  GE      KG+KG+ G  G KGD+G  G+ G +G  G
Sbjct  287600  GEKGDKGQKGDLGNDGIKGDKGESGSAVLKGDKGEKGDKGQKGDLGNDGIKGDKGESGSA  287779

Query  94      -FPGIQGRKGEPGE  106
                F G +G KG+ G+
Sbjct  287780  VFKGDKGEKGDKGQ  287821
```

```
 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 36/62 (58%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G+KG+KG+ G  G KGDIG+ G  G +G +G  G +G KG+
Sbjct  339581  GETGLKGDKGDIGDKGDIGDKGDKGEKGDKGEKGDIGDKGEKGDKGEKGDIGDKGEKGDI  339760

Query  105     GE  106
               G+
Sbjct  339761  GD  339766


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 36/64 (56%), Gaps = 6/64 (9%)
 Frame = +2

Query  49      HNGAPGRDGRDGTPGEKGEKGD------PGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               +NG  G  G  G  GEKGEKGD       G  G KGDIGE G+ G +G +G  G  G KG
Sbjct  336200  NNGLKGDKGDLGDKGEKGEKGDIGENGLKGDKGEKGDIGENGLKGDKGEKGDIGETGLKG  336379

Query  103     EPGE  106
               + GE
Sbjct  336380  DKGE  336391


 Score = 39.3 bits (90),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 28/61 (46%), Positives = 35/61 (57%), Gaps = 0/61 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G+KG+ GD GL G KGDIG  G+ G +G  G  G++G KG+
Sbjct  276298  GDTGLKGDKGDIGDAGLKGDKGDLGDAGLKGDKGDIGNDGLKGEKGDLGNDGLKGEKGDL  276477

Query  105     G  105
               G
Sbjct  276478  G  276480


 Score = 39.3 bits (90),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 39/102 (38%), Positives = 50/102 (49%), Gaps = 8/102 (8%)
 Frame = +2

Query  42      GIPGHPGHN--GAPGRDGRDGTPGE--KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
               G+ G  G +   G  G  G  G  GE  KG+KGD G    KGDIGE G+ G EG +G  G
Sbjct  283478  GLKGDLGESIKGDSGEKGLKGDIGESIKGDKGDQGES-IKGDIGEKGLKGDEGEKGSKGD  283654

Query  98      QGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQ  139
               QG KG+   G++   S         YV+ PN  +     +Y Q
Sbjct  283655  QGLKGDA--GSFTATSWTPTLSNIYVS-PNASLAVGAAYYTQ  283771


 Score = 38.9 bits (89),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 31/68 (46%), Positives = 36/68 (53%), Gaps = 5/68 (7%)
 Frame = +2

Query  43      IPGHPGHNGAPGRDGRD--GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
```

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               I G  G  G  G  G    G  G+KGEKGD G  G KGD GE+ + G  G +G  G QG
Sbjct  282629  IKGDSGEKGLKGDQGESIKGDSGDKGEKGDDGEKGLKGDQGES-IKGDSGEKGLKGDQGE  282805

Query  101     --KGEPGE  106
                 KG+ GE
Sbjct  282806  SIKGDSGE  282829


 Score = 38.9 bits (89),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 32/69 (46%), Positives = 37/69 (54%), Gaps = 3/69 (4%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDI---GETGVPGAEGPRGFPGI  97
                G+ G  G  G  G  G  G  G+KGEKGD G  G KGDI   GE G  G +G +G  G
Sbjct  873724  TGLKGDKGDLGDTGLKGDKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDIGD  873903

Query  98      QGRKGEPGE  106
                G KGE G+
Sbjct  873904  TGLKGEKGD  873930


 Score = 38.9 bits (89),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 32/71 (45%), Positives = 35/71 (49%), Gaps = 6/71 (8%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               G  G  G  G  G DG  G  GE      KG+KGD G  G KGDIGE G  G  G   F
Sbjct  271147  GDVGEKGDKGDLGNDGIKGDKGESGSAVFKGDKGDIGEKGDKGDIGEKGDKGESGSAVFK  271326

Query  96      GIQGRKGEPGE  106
               G +G  GE G+
Sbjct  271327  GDKGDVGEKGD  271359


 Score = 38.9 bits (89),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 30/71 (42%), Positives = 36/71 (51%), Gaps = 6/71 (8%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               G  G  G  G  G DG  G  GE      KG+KGD G  G KGD+G  G+ G +G  G
Sbjct  271534  GDVGEKGDKGDLGNDGDKGDKGESGSAVFKGDKGDVGEKGDKGDLGNDGIKGDKGESGSA  271713

Query  96      GIQGRKGEPGE  106
                 +G KG+ GE
Sbjct  271714  VFKGDKGDVGE  271746


 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 31/67 (46%), Positives = 37/67 (55%), Gaps = 6/67 (9%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGD------PGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G  G +G  G+KGEKGD       G  G KGDIGETG+ G +G +G  G +
Sbjct  336233  GDKGEKGEKGDIGENGLKGDKGEKGDIGENGLKGDKGEKGDIGETGLKGDKGEKGDIGEK  336412

Query  99      GRKGEPG  105
               G  GE G
Sbjct  336413  GDIGETG  336433
```

```
 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GE G+KG+ G +G KG+ GETG  G +G  G  G +G
Sbjct  276775  GEKGDVGDKGEKGETGDKGEKGETGDKGEKGDLGDKGEKGETGDKGEKGDLGEKGEKGDL  276954

Query  102     GEPGE  106
               GE GE
Sbjct  276955  GEKGE  276969


 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G  G KGD G+ G+ G +G  G  G++G K
Sbjct  336467  GDKGDLGDKGEKGDIGETGLKGDKGEKGDIGDKGEKGDFGDDGLKGEKGDFGDDGLKGDK  336646

Query  102     GEPGE  106
               G+ G+
Sbjct  336647  GDIGD  336661


 Score = 38.9 bits (89),  Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 31/71 (44%), Positives = 36/71 (51%), Gaps = 6/71 (8%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGE------KGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               G  G  G  G  G  G DG  G+KGE      KGD G IG KGD G+ G  G +G  G
Sbjct  271138  GDKGDVGEKGDKGDLGNDGIKGDKGESGSAVFKGDKGDIGEKGDKGDIGEKGDKGESGSA  271317

Query  96      GIQGRKGEPGE  106
                 +G KG+ GE
Sbjct  271318  VFKGDKGDVGE  271350


 Score = 38.9 bits (89),  Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 31/71 (44%), Positives = 39/71 (55%), Gaps = 6/71 (8%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGE------KGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               GI G  G  G  G  G  G  GEKG+      KG+ G IG KGD GE G  G +G +G
Sbjct  337088  GIKGEKGEKGDKGEIGETGLKGEKGDIGDKGNKGEKGDIGDKGDKGEKGDIGDKGQKGDI  337267

Query  96      GIQGRKGEPGE  106
               G +G+KG+ G+
Sbjct  337268  GDKGQKGDKGD  337300


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 33/81 (41%), Positives = 43/81 (53%), Gaps = 10/81 (12%)
 Frame = +1
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVP---------GAEGPR  92
               GI G  G +G+    G  G  GEKG+KGD G  G KGD GE+G           G +G +
Sbjct  271678  GIKGDKGESGSAVFKGDKGDVGEKGDKGDLGNDGDKGDKGESGSAVFKGDKGDVGEKGDK  271857

Query  93      GFPGIQGRKGEPGE-GAYVYR  112
               G  G  G KG+ GE G+ V++
Sbjct  271858  GDLGNDGIKGDKGESGSSVFK  271920


 Score = 38.9 bits (89),  Expect = 0.021, Method: Compositional matrix adjust.
 Identities = 33/81 (41%), Positives = 43/81 (53%), Gaps = 10/81 (12%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVP---------GAEGPR  92
               GI G  G +G+    G  G  GEKG+KGD G  G KGD GE+G           G +G +
Sbjct  271480  GIKGDKGESGSAVFKGDKGDVGEKGDKGDLGNDGDKGDKGESGSAVFKGDKGDVGEKGDK  271659

Query  93      GFPGIQGRKGEPGE-GAYVYR  112
               G  G  G KG+ GE G+ V++
Sbjct  271660  GDLGNDGIKGDKGESGSAVFK  271722


 Score = 38.9 bits (89),  Expect = 0.021, Method: Compositional matrix adjust.
 Identities = 30/74 (41%), Positives = 38/74 (51%), Gaps = 9/74 (12%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRG--  93
               G  G  G  G  G DG  G  GE      KG+KG+ G  G KGD+G  G+ G +G  G
Sbjct  288023  GEKGDKGQKGDLGNDGLKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGLKGDKGESGSA  288202

Query  94      -FPGIQGRKGEPGE  106
                F G +G KG+ G+
Sbjct  288203  VFKGDKGEKGDKGQ  288244


 Score = 38.9 bits (89),  Expect = 0.022, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 37/67 (55%), Gaps = 0/67 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G KG+KGD G IG KG+ G+ G  G +G  G  G++G
Sbjct  873244  LKGEKGDIGDTGLKGDKGNIGDTGLKGDKGDLGDIGDKGEKGDIGDKGEKGDIGDTGLKG  873423

Query  100     RKGEPGE  106
                KG+ G+
Sbjct  873424  EKGDIGD  873444


 Score = 38.5 bits (88),  Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G  G  G  G  G  GEKG+ GD G    KGD+G+ G  G  G +G  G +G K
Sbjct  272560  GLKGDKGDKGDLGDKGDLGDKGEKGDLGDKGEKSDKGDLGDKGEKGDSGDKGEKGDKGEK  272739

Query  102     GEPGE  106
               G  G+
```

```
Sbjct  272740  GNIGD  272754


 Score = 38.5 bits (88),  Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 24/50 (48%), Positives = 31/50 (62%), Gaps = 3/50 (6%)
 Frame = +2

Query  60      GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG---FPGIQGRKGEPGE  106
               G  GEKG+KGD G  G KGD+G  G+ G +G  G   F G +G KG+ G+
Sbjct  288560  GDKGEKGDKGDSGDKGQKGDLGNDGLKGDKGESGSAVFKGDKGEKGDKGQ  288709


 Score = 38.5 bits (88),  Expect = 0.025, Method: Compositional matrix adjust.
 Identities = 30/76 (39%), Positives = 38/76 (50%), Gaps = 9/76 (12%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
                 G  G  G  G  G DG  G  GE      KG+KG+ G  G KGD+G  G+ G +G  G
Sbjct  287918  FKGDKGDKGQKGDLGNDGIKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGLKGDKGESG  288097

Query  94      ---FPGIQGRKGEPGE  106
                  F G +G KG+ G+
Sbjct  288098  SAVFKGDKGEKGDKGQ  288145


 Score = 38.5 bits (88),  Expect = 0.025, Method: Compositional matrix adjust.
 Identities = 28/66 (42%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = +2

Query  44      PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
                G  G  G  G+ G  G  G KG+KG+ G    KGD GE G  G +G  G  GI+G KGE
Sbjct  288110  KGDKGEKGDKGQKGDLGNDGLKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKGDKGE  288289

Query  104     PGEGAY  109
                G   +
Sbjct  288290  SGSAVF  288307


 Score = 38.5 bits (88),  Expect = 0.026, Method: Compositional matrix adjust.
 Identities = 28/70 (40%), Positives = 38/70 (54%), Gaps = 6/70 (9%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
               + G  G  G+NG  G+ G  G  G       KG+KGD G  G KGD+G  G+ G +G  G
Sbjct  275045  LKGQKGDIGNNGLKGQKGDLGDKGNIGNDGLKGQKGDLGDKGDKGDLGNDGLKGNKGDLG  275224

Query  94      FPGIQGRKGE  103
                 G++G KG+
Sbjct  275225  NDGLKGEKGD  275254


 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 38/64 (59%), Gaps = 0/64 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G +G+    G  G  G+KG+KGD G  G KGD GE+G    +G +G  G +G+K
Sbjct  288167  GLKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKGDKGESGSAVFKGDKGEKGDKGQK  288346
```

```
Query  102     GEPG  105
               G+ G
Sbjct  288347  GDLG  288358


 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 35/66 (53%), Gaps = 0/66 (0%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
               +G  G  G  G  G  G  GEKG+ GD G  G  GD GE G  G +G +G  G +G
Sbjct  276709  SGEKGEKGDLGEKGEKGDLGEKGEKGDVGDKGEKGETGDKGEKGETGDKGEKGDLGDKGE  276888

Query  101     KGEPGE  106
               KGE G+
Sbjct  276889  KGETGD  276906


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 34/67 (51%), Gaps = 0/67 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G KGEKGD G  G KGD+G+ G  G  G  G  G +G
Sbjct  873478  LKGEKGDLGDTGLKGEKGDIGDTGLKGEKGDIGDKGEKGDLGDKGEKGDIGDTGLKGDKG  873657

Query  100     RKGEPGE  106
                 G+ GE
Sbjct  873658  DLGDKGE  873678


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 38/64 (59%), Gaps = 0/64 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G +G+    G  G  G+KG+KGD G  G KGD GE+G    +G +G  G +G+K
Sbjct  288068  GLKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGLKGDKGESGSAVFKGDKGEKGDKGQK  288247

Query  102     GEPG  105
               G+ G
Sbjct  288248  GDLG  288259


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 29/59 (49%), Positives = 34/59 (58%), Gaps = 6/59 (10%)
 Frame = +2

Query  54      GRDGRDGTPGEKGEKGDP------GLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               G  G DG  GEKGEKGD       GL G KGDIG+ G  G +G  G  G +G KG+ G+
Sbjct  337070  GDKGDDGIKGEKGEKGDKGEIGETGLKGEKGDIGDKGNKGEKGDIGDKGDKGEKGDIGD  337246


 Score = 38.5 bits (88),  Expect = 0.029, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 37/67 (55%), Gaps = 0/67 (0%)
 Frame = +1
```

```
Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G++G  G  G  G+   KG+KGD G  G KGD+G  G+ G +G  G    +G
Sbjct  271060  IKGDKGDLGNDGIKGDKGESGSAVFKGDKGDVGEKGDKGDLGNDGIKGDKGESGSAVFKG  271239

Query  100     RKGEPGE  106
                KG+ GE
Sbjct  271240  DKGDIGE  271260


 Score = 38.1 bits (87),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 30/69 (43%), Positives = 38/69 (55%), Gaps = 3/69 (4%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEK---GEKGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
               +G  G  G +G  G  G  G  GEK   GEKG+ G +G KG+ GETG  G +G  G  G
Sbjct  276682  SGEKGEKGDSGEKGEKGDLGEKGEKGDLGEKGEKGDVGDKGEKGETGDKGEKGETGDKGE  276861

Query  98      QGRKGEPGE  106
               +G  G+ GE
Sbjct  276862  KGDLGDKGE  276888


 Score = 38.1 bits (87),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 31/68 (46%), Positives = 36/68 (53%), Gaps = 3/68 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVP---GAEGPRGFPGIQ  98
               G  G  G  G  G  G  GEKG+ GD GL G KGDIG+ G     G +G +G  G
Sbjct  873880  GEKGDIGDTGLKGEKGDLGDKGEKGDIGDTGLKGEKGDIGDKGEKGDFGDKGEKGDIGDT  874059

Query  99      GRKGEPGE  106
               G KGE G+
Sbjct  874060  GLKGEKGD  874083


 Score = 38.1 bits (87),  Expect = 0.031, Method: Compositional matrix adjust.
 Identities = 27/66 (41%), Positives = 35/66 (53%), Gaps = 0/66 (0%)
 Frame = +1

Query  44      PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
                G  G  G  G  G  G+KG+KG+ G    KGD G+ G+ G +G  G  GI+G KGE
Sbjct  271324  KGDKGDVGEKGDKGDLGNDGDKGDKGESGSAVFKGDKGDVGIKGDKGDLGNDGIKGDKGE  271503

Query  104     PGEGAY  109
                G   +
Sbjct  271504  SGSAVF  271521


 Score = 38.1 bits (87),  Expect = 0.031, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G +G  G  GEKG  GD GL G KGDIG+ G  G  G  G  G +G
Sbjct  276019  GEKGDIGDAGPKGDEGNIGDKGEKGNLGDAGLKGDKGDIGDKGEKGNLGDAGLKGDKGDI  276198

Query  102     GEPGE  106
               G+ GE
```

```
Sbjct  276199  GDKGE  276213


 Score = 38.1 bits (87),  Expect = 0.031, Method: Compositional matrix adjust.
 Identities = 24/56 (43%), Positives = 32/56 (57%), Gaps = 0/56 (0%)
 Frame = +2

Query  60      GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAF  115
               G  G+KG+ GD G  G KGDIGE G+ G +G +G  G  G KG+ GE   +  +
Sbjct  336206  GLKGDKGDLGDKGEKGEKGDIGENGLKGDKGEKGDIGENGLKGDKGEKGDIGETGL  336373


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 32/68 (47%), Positives = 37/68 (54%), Gaps = 5/68 (7%)
 Frame = +2

Query  43      IPGHPGHNGAPGRDGRD--GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGP--RGFPGIQ  98
               I G  G  G  G DG    G  G KGEKGD G    KGDIGE G+ G +G   +G  G +
Sbjct  282143  IKGDSGEKGLKGDDGESIKGDIGTKGEKGDQGES-IKGDIGEKGLKGDDGESIKGDIGTK  282319

Query  99      GRKGEPGE  106
               G KG+ GE
Sbjct  282320  GEKGDDGE  282343


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 32/68 (47%), Positives = 37/68 (54%), Gaps = 5/68 (7%)
 Frame = +2

Query  43      IPGHPGHNGAPGRDGRD--GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGP--RGFPGIQ  98
               I G  G  G  G DG    G  G KGEKGD G    KGDIGE G+ G +G   +G  G +
Sbjct  283250  IKGDSGEKGLKGDDGESIKGDIGTKGEKGDQGES-IKGDIGEKGLKGDDGESIKGDIGTK  283426

Query  99      GRKGEPGE  106
               G KG+ GE
Sbjct  283427  GEKGDDGE  283450


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 34/67 (51%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G     G  G  G DGT G+KGE G     G KGD GE+G    +G +G  G +G
Sbjct  287333  VKGDKGEKAEKGQKGDLGNDGTKGDKGESGSAVFKGDKGDKGESGSAVFKGDKGEKGEKG  287512

Query  100     RKGEPGE  106
                KG  G+
Sbjct  287513  DKGHKGD  287533


 Score = 38.1 bits (87),  Expect = 0.033, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 37/64 (58%), Gaps = 0/64 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G +G+    G  G  GEKG+KGD G  G KGD GE+G    +G +G  GI+G K
Sbjct  271282  GEKGDKGESGSAVFKGDKGDVGEKGDKGDLGNDGDKGDKGESGSAVFKGDKGDVGIKGDK  271461
```

```
Query  102     GEPG  105
               G+ G
Sbjct  271462  GDLG  271473


 Score = 38.1 bits (87),  Expect = 0.035, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 33/66 (50%), Gaps = 0/66 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
                 G  G  G  G  G  G  G  G KG+KG+ G    KGD GE G  G +G  G  GI+G
Sbjct  287477  FKGDKGEKGEKGDKGHKGDFGNDGIKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKG  287656

Query  100     RKGEPG  105
                KGE G
Sbjct  287657  DKGESG  287674


 Score = 38.1 bits (87),  Expect = 0.035, Method: Compositional matrix adjust.
 Identities = 30/69 (43%), Positives = 37/69 (54%), Gaps = 3/69 (4%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDI---GETGVPGAEGPRGFPGI  97
                G+ G  G  G  G  G  G  GEKG+ GD GL G KGD+   GE G  G +G +G  G
Sbjct  873544  TGLKGEKGDIGDKGEKGDLGDKGEKGDIGDTGLKGDKGDLGDKGEKGDIGDKGEKGDIGD  873723

Query  98      QGRKGEPGE  106
                G KG+ G+
Sbjct  873724  TGLKGDKGD  873750


 Score = 37.7 bits (86),  Expect = 0.041, Method: Compositional matrix adjust.
 Identities = 27/68 (40%), Positives = 39/68 (57%), Gaps = 6/68 (9%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPR------GFPGIQ  98
               G+ G  G  G  G +G  G+KG+ G+ GL G KGDIG  G+ G +G        G  G++
Sbjct  274961  GNDGSKGQKGDIGNNGLKGQKGDIGNNGLKGQKGDIGNNGLKGQKGDLGDKGNIGNDGLK  275140

Query  99      GRKGEPGE  106
               G+KG+ G+
Sbjct  275141  GQKGDLGD  275164


 Score = 37.7 bits (86),  Expect = 0.041, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 33/66 (50%), Gaps = 0/66 (0%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
                G+ G  G  G  G  G  G  G KGEKGD G  G KGD G+ G  G  G  G  G +G
Sbjct  873904  TGLKGEKGDLGDKGEKGDIGDTGLKGEKGDIGDKGEKGDFGDKGEKGDIGDTGLKGEKGD  874083

Query  101     KGEPGE  106
                G+ GE
Sbjct  874084  IGDKGE  874101
```

```
 Score = 37.7 bits (86),  Expect = 0.044, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 32/62 (52%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKG+KGD G  G KGDIG  G  G  G  G  G +G  G+
Sbjct  337313  GDKGEKGDAGEKGEKGDLGEKGDKGDIGDKGEKGDIGNKGEKGDLGDTGLKGDKGDLGDK  337492

Query  105     GE  106
               G+
Sbjct  337493  GD  337498


 Score = 37.7 bits (86),  Expect = 0.045, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G     G  G+KGEKGD G  G KGD GE G  G +G +G  G  G K
Sbjct  272614  GDKGEKGDLGDKGEKSDKGDLGDKGEKGDSGDKGEKGDKGEKGNIGDKGEKGDMGDIGLK  272793

Query  102     GEPGE  106
               G+ G+
Sbjct  272794  GDKGD  272808


 Score = 37.7 bits (86),  Expect = 0.046, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G KG+KGD G  G KGDIG+ G  G  G +G  G  G K
Sbjct  873700  GEKGDIGDTGLKGDKGDLGDTGLKGDKGDIGDKGEKGDIGDKGEKGDIGDKGEKGDIGDK  873879

Query  102     GEPGE  106
               GE G+
Sbjct  873880  GEKGD  873894


 Score = 37.7 bits (86),  Expect = 0.046, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 37/64 (58%), Gaps = 0/64 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G  G  G  G  G  G+KG+KGD G  G KGD GE+G    +G +G  G +G+K
Sbjct  288533  GLKGDKGDVGDKGEKGDKGDSGDKGQKGDLGNDGLKGDKGESGSAVFKGDKGEKGDKGQK  288712

Query  102     GEPG  105
               G+ G
Sbjct  288713  GDLG  288724


 Score = 37.7 bits (86),  Expect = 0.050, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KG+KGD G  G KGD G+ G  G +G +G  G +G K
```

```
Sbjct  337178  GNKGEKGDIGDKGDKGEKGDIGDKGQKGDIGDKGQKGDKGDKGDIGDKGEKGDAGEKGEK  337357

Query  102     GEPGE  106
               G+ GE
Sbjct  337358  GDLGE  337372


 Score = 37.4 bits (85),  Expect = 0.058, Method: Compositional matrix adjust.
 Identities = 27/66 (41%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = +2

Query  44      PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
                G  G  G  G+ G  G  G KG+KG+ G    KGD GE G  G +G  G  G++G KGE
Sbjct  288011  KGDKGEKGDKGQKGDLGNDGLKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGLKGDKGE  288190

Query  104     PGEGAY  109
                G   +
Sbjct  288191  SGSAVF  288208


 Score = 37.4 bits (85),  Expect = 0.060, Method: Compositional matrix adjust.
 Identities = 33/81 (41%), Positives = 43/81 (53%), Gaps = 13/81 (16%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVP---------GAEGPR  92
               GI G  G +G+    G  G  GEKG+KGD   IG KGD GE+G           G +G +
Sbjct  271192  GIKGDKGESGSAVFKGDKGDIGEKGDKGD---IGEKGDKGESGSAVFKGDKGDVGEKGDK  271362

Query  93      GFPGIQGRKGEPGE-GAYVYR  112
               G  G  G KG+ GE G+ V++
Sbjct  271363  GDLGNDGDKGDKGESGSAVFK  271425


 Score = 37.4 bits (85),  Expect = 0.060, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 37/65 (57%), Gaps = 3/65 (5%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIG---PKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G DG  G+KG+ GD GL G    KGDIG+ G+ G +G +G  G  G K
Sbjct  336584  GDDGLKGEKGDFGDDGLKGDKGDIGDNGLKGDKGEKGDIGDNGLKGDKGEKGDIGDNGLK  336763

Query  102     GEPGE  106
               G+ GE
Sbjct  336764  GDKGE  336778


 Score = 37.4 bits (85),  Expect = 0.061, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G+KG+KGD G  G KGD GE G  G  G +G  G  G K
Sbjct  337223  GEKGDIGDKGQKGDIGDKGQKGDKGDKGDIGDKGEKGDAGEKGEKGDLGEKGDKGDIGDK  337402

Query  102     GEPGE  106
               GE G+
Sbjct  337403  GEKGD  337417
```

```
 Score = 37.4 bits (85),  Expect = 0.062, Method: Compositional matrix adjust.
 Identities = 29/71 (41%), Positives = 39/71 (55%), Gaps = 6/71 (8%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG------FP  95
               GI G  G +G+    G  G  G+KG+KGD G  G KGD GE+G    +G +G      F
Sbjct  287744  GIKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKGDKGESGSAVFKGDKGESGSAVFK  287923

Query  96      GIQGRKGEPGE  106
               G +G KG+ G+
Sbjct  287924  GDKGDKGQKGD  287956


 Score = 37.4 bits (85),  Expect = 0.063, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+ GEKGD G IG KG+ G+ G  G +G  G  G++G K
Sbjct  337295  GDKGDIGDKGEKGDAGEKGEKGDLGEKGDKGDIGDKGEKGDIGNKGEKGDLGDTGLKGDK  337474

Query  102     GEPGE  106
               G+ G+
Sbjct  337475  GDLGD  337489


 Score = 37.4 bits (85),  Expect = 0.067, Method: Compositional matrix adjust.
 Identities = 30/71 (42%), Positives = 36/71 (51%), Gaps = 6/71 (8%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGE------KGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               G  G  G  G  G DG  G+KGE      KGD G  G KGD G+ G  G +G +G
Sbjct  271822  GDKGDVGEKGDKGDLGNDGIKGDKGESGSSVFKGDKGEKGDKGDKGDLGNDGIKGDKGES  272001

Query  96      GIQGRKGEPGE  106
               G  G KG+ G+
Sbjct  272002  GDDGLKGDIGD  272034


 Score = 37.0 bits (84),  Expect = 0.073, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  GEK +KGD G  G KGD G+ G  G +G +G  G +G KG+
Sbjct  272596  GDKGDLGDKGEKGDLGDKGEKSDKGDLGDKGEKGDSGDKGEKGDKGEKGNIGDKGEKGDM  272775

Query  105     GE  106
               G+
Sbjct  272776  GD  272781


 Score = 37.0 bits (84),  Expect = 0.073, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
```

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               G  G  G  G  G  G  G  GEKG+ GD G  G KGD+G+ G  G  G +G  G  G K
Sbjct  339293  GETGLKGDKGDKGDLGDLGEKGEKGDVGDVGDKGEKGDVGDVGEKGDVGDKGEKGDVGDK  339472

Query  102     GEPGE  106
               GE G+
Sbjct  339473  GEKGD  339487


 Score = 37.0 bits (84),  Expect = 0.075, Method: Compositional matrix adjust.
 Identities = 31/88 (35%), Positives = 38/88 (43%), Gaps = 21/88 (24%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGE------------------KGDPGLIGPKGDIG  81
                 G  G  G  G  G  G DG  G+KGE                  KGD G  G KGD+G
Sbjct  287783  FKGDKGEKGDKGQKGDLGNDGIKGDKGESGSAVFKGDKGESGSAVFKGDKGDKGQKGDLG  287962

Query  82      ETGVPGAEGPRG---FPGIQGRKGEPGE  106
                 G+ G +G  G   F G +G KG+ G+
Sbjct  287963  NDGIKGDKGESGSAVFKGDKGEKGDKGQ  288046


 Score = 37.0 bits (84),  Expect = 0.077, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 36/65 (55%), Gaps = 3/65 (5%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVP---GAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G+KGEKGD G IG KG+ GE+G     G +G +G  G  G K
Sbjct  336746  GDNGLKGDKGEKGDKGEKGDKGEKGDKGDIGDKGNKGESGSAVFKGDKGEKGDTGEIGLK  336925

Query  102     GEPGE  106
               GE G+
Sbjct  336926  GEKGD  336940


 Score = 37.0 bits (84),  Expect = 0.078, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 34/65 (52%), Gaps = 3/65 (5%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G+ G  G  G  G DG  G+KGE G     G KGD+GE    G +G  G  GI+G KGE
Sbjct  271048  GNDGIKGDKGDLGNDGIKGDKGESGSAVFKGDKGDVGE---KGDKGDLGNDGIKGDKGES  271218

Query  105     GEGAY  109
               G   +
Sbjct  271219  GSAVF  271233


 Score = 37.0 bits (84),  Expect = 0.081, Method: Compositional matrix adjust.
 Identities = 28/66 (42%), Positives = 35/66 (53%), Gaps = 0/66 (0%)
 Frame = +2

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
                G+ G  G  G  G  G  G  G KG+KGD G  G KGD+G+ G  G  G  G  G +G
Sbjct  336365  TGLKGDKGEKGDIGEKGDIGETGLKGDKGDLGDKGDKGDLGDKGEKGDIGETGLKGDKGE  336544

Query  101     KGEPGE  106
               KG+ G+
Sbjct  336545  KGDIGD  336562
```

```
 Score = 37.0 bits (84),  Expect = 0.083, Method: Compositional matrix adjust.
 Identities = 30/74 (41%), Positives = 38/74 (51%), Gaps = 9/74 (12%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRG--  93
               G  G  G  G  G DG  G  GE      KG+KG+ G  G KGD+G  G+ G +G  G
Sbjct  288587  GDSGDKGQKGDLGNDGLKGDKGESGSAVFKGDKGEKGDKGQKGDLGNDGIKGDKGESGSA  288766

Query  94      -FPGIQGRKGEPGE  106
                F G +G KG+ G+
Sbjct  288767  VFKGDKGEKGDKGQ  288808


 Score = 37.0 bits (84),  Expect = 0.090, Method: Compositional matrix adjust.
 Identities = 29/68 (43%), Positives = 38/68 (56%), Gaps = 3/68 (4%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGD---IGETGVPGAEGPRGFPGIQ  98
               G  GH G  G  G  G  G  G++G+KG  G +G KGD   IG+TG  G +G  G  G +
Sbjct  289163  GDKGHIGDTGDKGHKGDLGNKGDEGDKGSKGDLGDKGDKGHIGDTGDKGHKGDLGNKGDK  289342

Query  99      GRKGEPGE  106
               G KG+ G+
Sbjct  289343  GDKGDQGD  289366


>NC_020842.1 Cellulophaga phage phiST genomic sequence
Length=79114

 Score = 52.8 bits (125),  Expect = 6e-07, Method: Compositional matrix adjust.
 Identities = 34/73 (47%), Positives = 40/73 (55%), Gaps = 6/73 (8%)
 Frame = -3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGD------PGLIGPKGDIGETGVPGAEGPRG  93
              + G  G  G  G  G  G  G  GEKGEKGD       G+ G KGDIG TG+ GA+G  G
Sbjct  56144  LKGSDGLVGEKGEKGDVGEKGDVGEKGEKGDVGATGADGIQGEKGDIGPTGLTGAKGDIG  55965

Query  94     FPGIQGRKGEPGE  106
                G QG KG+ G+
Sbjct  55964  LTGAQGEKGDQGD  55926


 Score = 48.1 bits (113),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 35/89 (39%), Positives = 40/89 (45%), Gaps = 24/89 (27%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETG-----------------  84
              G  G  G  G  G  G DG  GEKG+ G  GL G KGDIG TG
Sbjct  56084  GDVGEKGEKGDVGATGADGIQGEKGDIGPTGLTGAKGDIGLTGAQGEKGDQGDVGEKGEK  55905

Query  85     -------VPGAEGPRGFPGIQGRKGEPGE  106
                     + GA+G +G  GIQG KGE G+
Sbjct  55904  GEKGDIGLTGAQGDQGIQGIQGEKGEKGD  55818


>NC_010324.1 Enterobacteria phage phiEco32, complete genome
```

```
Length=77554

 Score = 52.4 bits (124),  Expect = 8e-07, Method: Compositional matrix adjust.
 Identities = 38/120 (32%), Positives = 53/120 (44%), Gaps = 8/120 (7%)
 Frame = -2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  GA G DG+DG  G+ G +G+ G  G  G  GETG+ GA G  G  G+ G+
Sbjct  70242  GDQGEKGDTGANGIDGKDGIDGKDGAQGEKGDSGADGKKGETGLTGAAGLNGVDGLNGKN  70063

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFA  161
              G+  + + V  +A S        I  +     K F + Q   D +       I G+   A
Sbjct  70062  GKDADMSAVNANAKS--------IKALEQSTNKRFASLQKQVDRNRDHASAGISGVAAMA  69907


 Score = 38.1 bits (87),  Expect = 0.036, Method: Compositional matrix adjust.
 Identities = 22/46 (48%), Positives = 27/46 (59%), Gaps = 0/46 (0%)
 Frame = -2

Query  60     GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
              G  G++GEKGD G  G  G  G  GA+G +G  G  G+KGE G
Sbjct  70251  GEKGDQGEKGDTGANGIDGKDGIDGKDGAQGEKGDSGADGKKGETG  70114


>NC_029120.1 Shigella phage 75/02 Stx, complete genome
Length=60875

 Score = 52.4 bits (124),  Expect = 9e-07, Method: Compositional matrix adjust.
 Identities = 56/192 (29%), Positives = 76/192 (40%), Gaps = 22/192 (11%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  GE+G KGD G +GPKG+ G+ GV G  GP G  G +G
Sbjct  38282  GEKGEQGERGPQGIPGLKGDTGERGPKGDQGDMGPKGEKGDPGVAGPAGPEGPQGPKGDT  38461

Query  102    GEPGEGAYVYRSA--------FSVGLETYVTI------PNMPIRFTKIFYNQQNHYDGST  147
              G PG+G  +  +A        F+ G+   +T+       ++ IR  K         D +
Sbjct  38462  GAPGQGTELLTTANTWTQAQTFNGGINGNLTVNGNGSFNDVQIRSDKRNKRNLVKLDNAL  38641

Query  148    GKFHCNIPGLYYFAYHITVYMKDVKVSLFKKDKAM--LFTYDQYQENNVDQASGSVLLHL  205
               +       LY   Y    +   V +      KA+  L T D       D  SG   L L
Sbjct  38642  DRLEALTGYLYEIQYSADGWQTSVGLIAQDAQKALPELVTED------ADVISGEKRLRL  38803

Query  206    EVGDQVWLQVYG  217
                   + L V G
Sbjct  38804  NYNGIIALLVEG  38839


 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +2

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  38174  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  38353

Query  105    G  105
              G
```

```
Sbjct  38354  G  38356


>NC_031001.1 Gordonia phage Terapin, complete genome
Length=66611

 Score = 52.0 bits (123),  Expect = 1e-06, Method: Compositional matrix adjust.
 Identities = 34/71 (48%), Positives = 43/71 (61%), Gaps = 3/71 (4%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETG---VPGAEGPRGFPGIQ  98
              GI G  G  G  G DG +G  G +G KGD GL G KGD G+TG   + G +GP+G  GIQ
Sbjct  24750  GIQGIQGVQGIQGEDGPEGPQGPQGTKGDTGLKGDKGDKGDTGDQGIQGVQGPKGDQGIQ  24929

Query  99     GRKGEPGEGAY  109
              G +G PG  ++
Sbjct  24930  GVQGPPGTTSW  24962


 Score = 44.7 bits (104),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 27/51 (53%), Positives = 34/51 (67%), Gaps = 6/51 (12%)
 Frame = +2

Query  63     GEKGEKGDPGLIGPKGDIGET------GVPGAEGPRGFPGIQGRKGEPGEG  107
              GEKG++GDPG  GPKGD G+T      GVPG +GP+G  G +G  G+ G G
Sbjct  23930  GEKGDQGDPGPQGPKGDKGDTGSQGLQGVPGDQGPQGDRGEKGDTGDTGRG  24082


 Score = 37.7 bits (86),  Expect = 0.050, Method: Compositional matrix adjust.
 Identities = 21/42 (50%), Positives = 29/42 (69%), Gaps = 0/42 (0%)
 Frame = +2

Query  65     KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
              +GEKGD G  GP+G  G+ G  G++G +G PG QG +G+ GE
Sbjct  23927  RGEKGDQGDPGPQGPKGDKGDTGSQGLQGVPGDQGPQGDRGE  24052


>NC_025416.1 Staphylococcus phage MCE-2014, complete genome
Length=141907

 Score = 51.2 bits (121),  Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 37/94 (39%), Positives = 45/94 (48%), Gaps = 3/94 (3%)
 Frame = -2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGD---PGLIGPKGDIGETGVPGAEGPRGFPG  96
              + G  G  G  G  G  G  G PGEKGE+G+    G  GPKGDIG  G  G  GP+G  G
Sbjct  10917  LKGADGAQGEQGPQGPKGDKGEPGEKGEQGERGPEGSEGPKGDIGPQGPTGPMGPKGDKG  10738

Query  97     IQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPI  130
                G KGE G G+        +  E Y     +P+
Sbjct  10737  NTGEKGEKGNGSVNQTRLPQILREQYFENLEIPV  10636


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 33/91 (36%), Positives = 39/91 (43%), Gaps = 23/91 (25%)
 Frame = -2

Query  39     WMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGV------------  85
```

```
              W+  I G  G  G  G  G  G  G KG++G  G  GPKGD G  GV
Sbjct  11115  WVKSIKGEQGPQGIKGDRGLQGPQGPKGDRGLQGPQGPKGDRGADGVDGIDGTMTFEELT  10936

Query  86     ----------PGAEGPRGFPGIQGRKGEPGE  106
                         GA+G +G  G +G KGEPGE
Sbjct  10935  EEQKATLKGADGAQGEQGPQGPKGDKGEPGE  10843


 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 32/80 (40%), Positives = 38/80 (48%), Gaps = 14/80 (18%)
 Frame = -2

Query  40     MAGIPGHPGHNGAPGRDGRDGT--------------PGEKGEKGDPGLIGPKGDIGETGV  85
              + G  G  G  GA G DG DGT               G  G +G+ G  GPKGD GE G
Sbjct  11022  LQGPQGPKGDRGADGVDGIDGTMTFEELTEEQKATLKGADGAQGEQGPQGPKGDKGEPGE  10843

Query  86     PGAEGPRGFPGIQGRKGEPG  105
               G +G RG  G +G KG+ G
Sbjct  10842  KGEQGERGPEGSEGPKGDIG  10783


>NC_032108.1 Cedratvirus A11 genome assembly, complete genome: monopartite
Length=589068

 Score = 51.2 bits (121),  Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 36/83 (43%), Positives = 43/83 (52%), Gaps = 18/83 (22%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETG---------------VP  86
               G PG PG +G PG+DG+DG  G+ GEKGDPG  G  G  GE G                P
Sbjct  567682  GDPGEPGKDGEPGKDGKDGLNGKDGEKGDPGKDGLNGKDGEKGEKGDPGKDGKDGKDGEP  567503

Query  87      GAEGPRGF---PGIQGRKGEPGE  106
               G +G +G    PG  G+ GE GE
Sbjct  567502  GKDGEKGDQGPPGKDGKDGEKGE  567434


 Score = 49.7 bits (117),  Expect = 6e-06, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 38/65 (58%), Gaps = 6/65 (9%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G PG+DG +G  GEKGEKGDP      G+ G+ G PG +G  G  G  G K
Sbjct  567763  GEKGEKGDQGEPGKDGINGKDGEKGEKGDP------GEPGKDGEPGKDGKDGLNGKDGEK  567602

Query  102     GEPGE  106
               G+PG+
Sbjct  567601  GDPGK  567587


 Score = 49.3 bits (116),  Expect = 8e-06, Method: Compositional matrix adjust.
 Identities = 31/70 (44%), Positives = 42/70 (60%), Gaps = 6/70 (9%)
 Frame = -3

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGEKGDP------GLIGPKGDIGETGVPGAEGPRGFPG  96
               I G  G +G  G +G+DG  GEKG++G+P      G  G KG+ G+ G PG +G  G  G
Sbjct  567877  IAGEKGRDGKDGLNGKDGEKGEKGDQGEPGKDGINGKDGEKGEKGDQGEPGKDGINGKDG  567698
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Query  97      IQGRKGEPGE  106
                +G KG+PGE
Sbjct  567697  EKGEKGDPGE  567668


 Score = 48.1 bits (113),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 46/167 (28%), Positives = 63/167 (38%), Gaps = 33/167 (20%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G+ G  G  G  G  G+ G  GE+G  G  G  G TGV GA+G  G  G QG+
Sbjct  523470  GVTGNTGVTGQQGNTGVTGSQGNIGERGVTGADGVTGQQGNTGVTGADGVTGNTGSQGQT  523649

Query  102     GEPGE----------------GAYVYRSAFSVGLETYVTIPNMPIRFTKI---------F  136
               G  G                 G+     A S      +T  N+P     +
Sbjct  523650  GVTGSQGQTGVTGSQGQTGVTGSQGQTGALSSEFMDAITSTNIPYVIANVTPYEFDEVTL  523829

Query  137     YNQQNHYDGSTGKFHCNIPGLYYFAYHI--------TVYMKDVKVSL  175
                +  + Y+  T +F     G+YY+A+ I         VYM    V L
Sbjct  523830  ISPGSTYNAVTNEFVAGSTGVYYYAFKICGYNTSATNVYMLTNSVQL  523970


 Score = 45.4 bits (106),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 31/67 (46%), Positives = 36/67 (54%), Gaps = 6/67 (9%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDP------GLIGPKGDIGETGVPGAEGPRGFP  95
               G  G  G  G PG+DG +G  GEKGEKGD       G+ G  G+ GE G PG  G  G P
Sbjct  567826  GEKGEKGDQGEPGKDGINGKDGEKGEKGDQGEPGKDGINGKDGEKGEKGDPGEPGKDGEP  567647

Query  96      GIQGRKG  102
               G  G+ G
Sbjct  567646  GKDGKDG  567626


 Score = 44.3 bits (103),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 33/67 (49%), Gaps = 2/67 (3%)
 Frame = +3

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEK--GEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               A I G  G+ G  G  G  G  G    G  G+ G+ G  G+ GETGV G EG  G PG+
Sbjct  258429  ASITGETGNTGVTGAQGETGVTGVSVTGATGEVGVTGNNGNTGETGVTGEEGASGLPGLT  258608

Query  99      GRKGEPG  105
               G  G  G
Sbjct  258609  GEGGVTG  258629


 Score = 43.9 bits (102),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G  G  G  G DG  G  G +G+ G  G  GDIG TGV G++G  G  G+ G
Sbjct  258600  GLTGEGGVTGNTGSTGVDGLTGVTGAQGNTGNTGLTGDIGNTGVTGSQGNTGNTGLTGNT  258779

Query  102     GEPG  105
               G+ G
```

```
Sbjct  258780  GQTG  258791


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/68 (41%), Positives = 36/68 (53%), Gaps = 2/68 (3%)
 Frame = -2

Query  42      GIPGHPGHNGAPGRDGRDGT--PGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               G+ G+ G  G  G  G  G    G +G  G+ G+ GP+G++G TGV G  G  G  G QG
Sbjct  211040  GVTGNTGVTGQQGNTGVTGAGETGAQGVTGNTGVTGPQGEVGNTGVTGEVGVTGVTGSQG  210861

Query  100     RKGEPGEG  107
                 G  GEG
Sbjct  210860  NTGATGEG  210837


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 38/65 (58%), Gaps = 3/65 (5%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G PG +G    +G+DG  GEKG+ G+PG  G  G  G+ G+ G +G +G PG  G
Sbjct  567745  GDQGEPGKDGI---NGKDGEKGEKGDPGEPGKDGEPGKDGKDGLNGKDGEKGDPGKDGLN  567575

Query  102     GEPGE  106
               G+ GE
Sbjct  567574  GKDGE  567560


 Score = 40.0 bits (92),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 29/63 (46%), Positives = 34/63 (54%), Gaps = 3/63 (5%)
 Frame = +3

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK--G  102
               G+ G  GA G  G  G  G+ G  G+ G IG  GDIG TGV GA G +G  G+ G    G
Sbjct  258267  GNTGVTGAQGETGVTGADGDIGNTGETG-IGVTGDIGNTGVTGASGEQGETGVTGASITG  258443

Query  103     EPG  105
               E G
Sbjct  258444  ETG  258452


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 31/62 (50%), Gaps = 0/62 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G PG  G NG  G  G  G PGE G+ G+PG  G  G  G+ G  G  G  G  G  G K
Sbjct  567736  GEPGKDGINGKDGEKGEKGDPGEPGKDGEPGKDGKDGLNGKDGEKGDPGKDGLNGKDGEK  567557

Query  102     GE  103
               GE
Sbjct  567556  GE  567551


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 34/83 (41%), Positives = 41/83 (49%), Gaps = 15/83 (18%)
 Frame = -3
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGE------------KGDPGLIGPKGDIGETGVPGAE  89
               G+ G  G  G PG+DG +G  GEKGE             G+PG  G KGD    G PG +
Sbjct  567628  GLNGKDGEKGDPGKDGLNGKDGEKGEKGDPGKDGKDGKDGEPGKDGEKGD---QGPPGKD  567458

Query  90      GPRGFPGIQGRKGEPGEGAYVYR  112
               G  G  G +G  GEPG+ A   R
Sbjct  567457  GKDGEKGEKGDPGEPGKDAPRER  567389


 Score = 39.3 bits (90),  Expect = 0.016, Method: Compositional matrix adjust.
 Identities = 24/55 (44%), Positives = 28/55 (51%), Gaps = 0/55 (0%)
 Frame = +2

Query  52      APGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               A G  G  G  G  G +G+ G+ G  GD+G TGV G  G  G  G QG  G  GE
Sbjct  185036  AQGNTGVTGENGVTGAQGNTGVTGVTGDVGATGVTGVTGASGNTGSQGNTGVTGE  185200


 Score = 38.9 bits (89),  Expect = 0.022, Method: Compositional matrix adjust.
 Identities = 29/88 (33%), Positives = 39/88 (44%), Gaps = 7/88 (8%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG--  99
               G  G  G  G PG+DG+DG  GEKG+ G+PG   P+  + E G   +  P G
Sbjct  567502  GKDGEKGDQGPPGKDGKDGEKGEKGDPGEPGKDAPRERLEEQGKYLSLSPEGVLSTNSTL  567323

Query  100     -RKGEPGEGAYVYRSAFSVGLETYVTIP  126
                +  EP    +      SVG E   + P
Sbjct  567322  LKSEEP----FAINGNLSVGYENKTSAP  567251


>NC_017972.1 Pseudomonas phage Lu11, complete genome
Length=280538

 Score = 50.4 bits (119),  Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 37/77 (48%), Positives = 44/77 (57%), Gaps = 4/77 (5%)
 Frame = +1

Query  29      LPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIG---PKGDIGETGV  85
               LP+P     G   G  G PG +G  G+DGRDG PG  G +G  G+IG   PKG+ G TG
Sbjct  188590  LPVPSRIPVG-PTGPQGLPGLDGKNGKDGRDGAPGPAGCEGPQGVIGQTGPKGETGRTGQ  188766

Query  86      PGAEGPRGFPGIQGRKG  102
               PG  GP G  G QG +G
Sbjct  188767  PGPAGPTGPTGPQGLQG  188817


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G PG PG +   G+DG+DG  G  G +G  G  GP GD G  G  GA GP G  G  G +
Sbjct  185445  GDPGRPGRDAEDGKDGKDGQAGCAGPRGPEGRPGPMGDPGIEGEVGAPGPYGPLGPTGPR  185624

Query  102     GE  103
               G+
```

```
Sbjct  185625  GD  185630


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 25/43 (58%), Positives = 27/43 (63%), Gaps = 3/43 (7%)
 Frame = +1

Query  56      DGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               DGRDGT G  GE+G  G  GP G  G+T   G EGPRG  GIQ
Sbjct  189712  DGRDGTNGRDGEQGATGCQGPPGPRGDT---GPEGPRGPQGIQ  189831


 Score = 37.4 bits (85),  Expect = 0.056, Method: Compositional matrix adjust.
 Identities = 43/139 (31%), Positives = 56/139 (40%), Gaps = 8/139 (6%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGF---PGIQGRK  101
               G PG  G  G  G  G  G  G  G  GP+G IG TG  G  GP+G     G  G K
Sbjct  194126  GLPGEKGPIGPTGPAGPTGPSGGAGQIGPTGPQGIIGLTGATGPTGPQGEIGPIGPTGPK  194305

Query  102     GEPG-EGAYVYRSAFSVGLETYVTIPNMP---IRFTKIFYNQQNHYDGSTGKFHCNIPGL  157
               GE G EGA   +          V +P  P     FT  F+  +N   G  G        +
Sbjct  194306  GESGTEGATGLQGPPGEPGPAGVGLPGPPGASAIFTNDFWTHENPSVGRYGSIEVGDKTM  194485

Query  158     YYF-AYHITVYMKDVKVSL  175
                    Y  +  ++D+ ++L
Sbjct  194486  EIMGTYKSSSSVQDISLTL  194542


>NC_021782.1 Salmonella phage FSL SP-076, complete genome
Length=72098

 Score = 50.4 bits (119),  Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 37/119 (31%), Positives = 53/119 (45%), Gaps = 4/119 (3%)
 Frame = +3

Query  40    MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDI---GETGVPGAEGPRGFPG  96
              +G  G  G NG  G +GRDG  G+ G KGD G  G  G     GE G  G  G  G  G
Sbjct  7149  ASGKDGKDGLNGTNGTNGRDGVDGKDGAKGDTGAQGEAGKDGLNGENGKDGLNGTNGLDG  7328

Query  97    IQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIP  155
              +G KG+ G+      +  + G +  +T  N      K    +Q+ ++ ST +   N+
Sbjct  7329  AKGDKGDEGKQGIAGIAGLN-GKDADMTQVNANTEANKSISKRQDAFEKSTNQRFANMD  7502


 Score = 47.4 bits (111),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +3

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G +GA G+DG +G  G KG+KGD G  G  G  G+ G+ G  G  G  G+ G+
Sbjct  7047  GKDGIDGKDGANGKDGINGIDGAKGDKGDKGDTGASGKDGKDGLNGTNGTNGRDGVDGKD  7226

Query  102   GEPGE  106
             G  G+
Sbjct  7227  GAKGD  7241
```

```
 Score = 47.4 bits (111),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 33/64 (52%), Gaps = 0/64 (0%)
 Frame = +3

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             GI G  G NG  G +G DG  G+KG+KGD G  G  G  G  G  G  G  G  G  G K
Sbjct  7056  GIDGKDGANGKDGINGIDGAKGDKGDKGDTGASGKDGKDGLNGTNGTNGRDGVDGKDGAK  7235

Query  102   GEPG  105
             G+ G
Sbjct  7236  GDTG  7247


 Score = 46.6 bits (109),  Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 27/63 (43%), Positives = 32/63 (51%), Gaps = 0/63 (0%)
 Frame = +3

Query  43    IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
             I G  G +G  G DG+DG  G+ G  G  G  G KGD G+TG  G +G  G  G  G  G
Sbjct  7023  IKGQDGKDGKDGIDGKDGANGKDGINGIDGAKGDKGDKGDTGASGKDGKDGLNGTNGTNG  7202

Query  103   EPG  105
               G
Sbjct  7203  RDG  7211


>NC_014649.1 Acanthamoeba polyphaga mimivirus, complete genome
Length=1181549

 Score = 50.1 bits (118),  Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 33/80 (41%), Positives = 44/80 (55%), Gaps = 2/80 (3%)
 Frame = +3

Query  27      VLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVP  86
                L+   +GA      G+ G PG NG+ G  G  G  G+KG KGD G  G KGD G  G+
Sbjct  298362  TLVSNLRGAS--GAQGVKGDPGSNGSKGTKGEKGDKGDKGSKGDNGEKGEKGDAGLNGLD  298535

Query  87      GAEGPRGFPGIQGRKGEPGE  106
               G++G +G  G +G KG  G+
Sbjct  298536  GSKGDKGDDGSKGSKGNKGD  298595


 Score = 49.7 bits (117),  Expect = 6e-06, Method: Compositional matrix adjust.
 Identities = 32/67 (48%), Positives = 39/67 (58%), Gaps = 0/67 (0%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  GEKG+KGD G IG KGD G+TG  G +G +G  G +G
Sbjct  884876  IKGDKGDIGEKGDKGDIGEKGNKGEKGDKGDKGDIGEKGDKGDTGSKGDKGDKGEKGDKG  884697

Query  100     RKGEPGE  106
                KGE G+
Sbjct  884696  DKGEKGD  884676


 Score = 49.7 bits (117),  Expect = 6e-06, Method: Compositional matrix adjust.
 Identities = 32/66 (48%), Positives = 39/66 (59%), Gaps = 0/66 (0%)
 Frame = -1
```

```
Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
               AG+ G  G  G  G  G  G  G+KGEKGD GL G KGDIG  G  G +G RG  G +G
Sbjct  883829  AGLKGDKGDIGQKGDKGTKGDRGDKGEKGDAGLKGNKGDIGLKGDKGTKGDRGDKGTKGD  883650

Query  101     KGEPGE  106
               +G+ G+
Sbjct  883649  RGDKGD  883632


 Score = 48.9 bits (115),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 39/65 (60%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G+NG PG  G  G  G+KGE G+ G  G KGD G+ G  G +G +G  G +G K
Sbjct  885743  GLKGEKGNNGDPGEKGEKGAKGDKGESGEKGAKGDKGDKGDIGEKGEKGDKGDIGEKGEK  885564

Query  102     GEPGE  106
               G+ G+
Sbjct  885563  GDKGD  885549


 Score = 48.9 bits (115),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 41/65 (63%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G  G  G  G +GT G+KG+ GD G+ G KGDIG+ G+ G +G +G  G +G K
Sbjct  237829  GIKGDNGTKGDNGTKGDNGTKGDKGDIGDNGIKGDKGDIGDNGIKGDKGNKGDNGDKGNK  238008

Query  102     GEPGE  106
               G+ G+
Sbjct  238009  GDKGD  238023


 Score = 48.9 bits (115),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 32/67 (48%), Positives = 39/67 (58%), Gaps = 0/67 (0%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
                 G  G  G  GA G  G  G  GEKGEKGD G IG KG+ G+ G  G +G +G  G +G
Sbjct  885686  AKGDKGESGEKGAKGDKGDKGDIGEKGEKGDKGDIGEKGEKGDKGDIGEKGDKGDLGEKG  885507

Query  100     RKGEPGE  106
                KG+PG+
Sbjct  885506  EKGDPGQ  885486


 Score = 48.1 bits (113),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 39/64 (61%), Gaps = 0/64 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G+ G  G +G  G++G+KGD G  G KGD G  G  G++G +G  GI+G K
Sbjct  879108  GSKGYKGDKGSKGTKGNNGFKGDRGDKGDKGSKGDKGDNGIKGNKGSKGDKGDNGIKGEK  878929

Query  102     GEPG  105
```

```
               GE G
Sbjct  878928  GESG  878917


 Score = 47.0 bits (110),  Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 32/65 (49%), Positives = 37/65 (57%), Gaps = 6/65 (9%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G  G  G  G +G PGEKGEK      G KGD GE+G  GA+G +G  G  G K
Sbjct  885770  GIKGEKGDRGLKGEKGNNGDPGEKGEK------GAKGDKGESGEKGAKGDKGDKGDIGEK  885609

Query  102     GEPGE  106
               GE G+
Sbjct  885608  GEKGD  885594


 Score = 47.0 bits (110),  Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 31/67 (46%), Positives = 38/67 (57%), Gaps = 3/67 (4%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKG---DIGETGVPGAEGPRGFPGIQ  98
               G  G PG  G+ G  G  G  G KG+KGDPG+ G  G   D G+ G  G++G +G  GI
Sbjct  293147  GDKGDPGIKGSKGEKGSKGDKGSKGDKGDPGIKGESGADADKGDKGDKGSKGDKGDKGID  293326

Query  99      GRKGEPG  105
               G KGE G
Sbjct  293327  GNKGEKG  293347


 Score = 47.0 bits (110),  Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 39/65 (60%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G  G  G  G  G  G+KG+KG+ G+ G KGD G  GV G +G +G  G++G K
Sbjct  239917  GIKGESGSKGDKGEKGNKGYKGDKGDKGNLGIKGDKGDKGIKGVKGTKGDKGTKGVKGTK  240096

Query  102     GEPGE  106
               G+ G+
Sbjct  240097  GDKGD  240111


 Score = 46.2 bits (108),  Expect = 8e-05, Method: Compositional matrix adjust.
 Identities = 29/63 (46%), Positives = 34/63 (54%), Gaps = 0/63 (0%)
 Frame = -3

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               + G  G  G+ G  G DG  G KG KGD G  G KGD G+ G  G  G +G  G +G KG
Sbjct  879348  LKGEKGEIGSKGTKGDDGNKGNKGIKGDKGTTGDKGDKGDVGNKGDAGDKGDAGKKGEKG  879169

Query  103     EPG  105
               E G
Sbjct  879168  EMG  879160


 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
```

```
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G PG  G  GA G  G  G  G KG+KGD G IG KG+ G+ G  G +G +G  G  G K
Sbjct  885716  GDPGEKGEKGAKGDKGESGEKGAKGDKGDKGDIGEKGEKGDKGDIGEKGEKGDKGDIGEK  885537

Query  102     GEPGE  106
               G+ G+
Sbjct  885536  GDKGD  885522


 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G NG  G  G +G  G KG+KGD G  G KGD G+ G  G +G +G  G  G K
Sbjct  878127  GDNGDKGDNGDKGNKGDNGDKGNKGDKGDNGDKGNKGDKGDNGDKGNKGDKGDKGDNGDK  877948

Query  102     GEPGE  106
               G+ G+
Sbjct  877947  GDNGD  877933


 Score = 45.4 bits (106),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 30/64 (47%), Positives = 38/64 (59%), Gaps = 0/64 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G +G  G +G  G  G+KG KG+ GL G KGDIG+ G  G++G  G  G +G K
Sbjct  298884  GNKGDKGEDGLKGENGDIGDKGDKGSKGEDGLKGDKGDIGDKGDKGSKGEDGLKGSKGDK  299063

Query  102     GEPG  105
               GE G
Sbjct  299064  GEIG  299075


 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 32/76 (42%), Positives = 42/76 (55%), Gaps = 4/76 (5%)
 Frame = -3

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G+ G  G  G  G  G KG++GD G  G KGD G+ G+ G +G +G  G  G KGE
Sbjct  879108  GSKGYKGDKGSKGTKGNNGFKGDRGDKGDKGSKGDKGDNGIKGNKGSKGDKGDNGIKGEK  878929

Query  105     GE-GAYVYRSAFSVGL  119
               GE G+ +    F +GL
Sbjct  878928  GESGSSIL---FGMGL  878890


 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G NG  G  G  G  G+KG+KGD G  G KGD G+ G  G  G +G  G  G K
Sbjct  878244  GDKGDKGDNGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDNGDKGNKGDNGDK  878065
```

```
Query  102     GEPGE  106
               G  G+
Sbjct  878064  GNKGD  878050


 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 33/64 (52%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G DGT GEKGEKG  G  G KGD GE G+ G  G  G  G +G K
Sbjct  298785  GEKGNKGDKGDVGVKGDDGTKGEKGEKGTKGDKGNKGDKGEDGLKGENGDIGDKGDKGSK  298964

Query  102     GEPG  105
               GE G
Sbjct  298965  GEDG  298976


 Score = 44.7 bits (104),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 29/70 (41%), Positives = 40/70 (57%), Gaps = 6/70 (9%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDG------RDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               GI G+ G  G  G +G        G+ G+KGEKG+ G  G KGD G  G+ G +G +G
Sbjct  239863  GIKGNKGDKGIKGSEGDKGIKGESGSKGDKGEKGNKGYKGDKGDKGNLGIKGDKGDKGIK  240042

Query  96      GIQGRKGEPG  105
               G++G KG+ G
Sbjct  240043  GVKGTKGDKG  240072


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 28/69 (41%), Positives = 36/69 (52%), Gaps = 0/69 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G +G  G  G+KG+ GD G  G KGD G+ G  G  G +G  G +G K
Sbjct  878082  GDNGDKGNKGDKGDNGDKGNKGDKGDNGDKGNKGDKGDKGDNGDKGDNGDKGDNGDKGDK  877903

Query  102     GEPGEGAYV  110
               GE G    +
Sbjct  877902  GESGSSCQI  877876


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 32/71 (45%), Positives = 41/71 (58%), Gaps = 6/71 (8%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGE------KGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               GI G  G NG  G +G +GT G+KG+      KGD G  G KGD G  G  G +G +G
Sbjct  238198  GIKGDKGDNGTKGDNGDNGTKGDKGDNGIKGDKGDKGTKGDKGDKGTKGDNGDKGTKGDN  238377

Query  96      GIQGRKGEPGE  106
               GI+G KG+ G+
Sbjct  238378  GIKGYKGDIGD  238410


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
```

```
 Identities = 29/65 (45%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG +GD G  G KG+ G+ G+ G+EG +G  G  G K
Sbjct  239764  GDKGIKGDKGNEGDKGDKGNKGEKGNRGDEGDKGIKGNKGDKGIKGSEGDKGIKGESGSK  239943

Query  102     GEPGE  106
               G+ GE
Sbjct  239944  GDKGE  239958


 Score = 44.3 bits (103),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 40/65 (62%), Gaps = 3/65 (5%)
 Frame = +3

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDI---GETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G DG  G+ G+KGE G+ G  G KGDI   G+ G  G +G +G PG++G K
Sbjct  299001  GDKGDKGSKGEDGLKGSKGDKGEIGNKGDKGDKGDIGIKGDKGDIGDKGDKGDPGLKGEK  299180

Query  102     GEPGE  106
               GE G+
Sbjct  299181  GEKGD  299195


 Score = 43.9 bits (102),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G +G  G  G+KG KGD G  G KGD G+ G  G +G +G  G +G K
Sbjct  878163  GDNGDKGNKGDKGDNGDKGDNGDKGNKGDNGDKGNKGDKGDNGDKGNKGDKGDNGDKGNK  877984

Query  102     GEPGE  106
               G+ G+
Sbjct  877983  GDKGD  877969


 Score = 43.9 bits (102),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 30/64 (47%), Positives = 37/64 (58%), Gaps = 0/64 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G  G  G+KGEKG+ G +G KGDIG  G  G  G +G  GI+G K
Sbjct  878775  GEKGDRGNVGDKGEKGDIGLKGDKGEKGEKGNVGDKGDIGTKGDKGNVGDKGDIGIKGEK  878596

Query  102     GEPG  105
               G+ G
Sbjct  878595  GDIG  878584


 Score = 43.9 bits (102),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G NG  G  G +G  G KG+KGD G  G KGD G+ G  G +G  G  G  G K
Sbjct  878271  GNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDNGDK  878092
```

```
Query  102     GEPGE  106
               G  G+
Sbjct  878091  GNKGD  878077


 Score = 43.9 bits (102),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 31/68 (46%), Positives = 39/68 (57%), Gaps = 3/68 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDG---RDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               GI G  G  G  G +G    +GT G+ G KGD G  G KGDIG+ G+ G +G  G  GI+
Sbjct  237784  GIKGDKGSEGIKGDNGIKGDNGTKGDNGTKGDNGTKGDKGDIGDNGIKGDKGDIGDNGIK  237963

Query  99      GRKGEPGE  106
               G KG  G+
Sbjct  237964  GDKGNKGD  237987


 Score = 43.9 bits (102),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 29/70 (41%), Positives = 41/70 (59%), Gaps = 0/70 (0%)
 Frame = +1

Query  37      TGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
               T  + G+ G  G++G+ G DG  G  G KGE G  G +G KGD G  G  G++G +G  G
Sbjct  296380  TKGITGLKGTKGNSGSKGDDGDKGIQGLKGEFGTKGNVGDKGDTGINGEKGSDGDKGNKG  296559

Query  97      IQGRKGEPGE  106
               + G KG+ G+
Sbjct  296560  LDGIKGDLGD  296589


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 28/60 (47%), Positives = 36/60 (60%), Gaps = 0/60 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G+ G NG  G  G  G  G+KG KGD G IG KGDIG+ G+ G +G  G  G++G
Sbjct  237958  IKGDKGNKGDNGDKGNKGDKGDIGDKGMKGDKGDIGDKGDIGDKGMKGDKGDIGDKGMKG  238137


 Score = 43.5 bits (101),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 30/69 (43%), Positives = 39/69 (57%), Gaps = 0/69 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G NG+ G  G  G  G KG KGD G  G KGD+G+TG+ G++G +G  G +G
Sbjct  296701  GDKGSKGDNGSKGESGDKGIFGLKGSKGDIGDKGEKGDLGDTGLKGSKGLKGSKGDKGLV  296880

Query  102     GEPGEGAYV  110
                  GE  +V
Sbjct  296881  NVKGENGFV  296907


 Score = 43.5 bits (101),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 34/68 (50%), Positives = 38/68 (56%), Gaps = 3/68 (4%)
 Frame = -1
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGP---KGDIGETGVPGAEGPRGFPGIQ  98
               GI G  G  G  G  G  G  GEKG KGD G IG    KGDIG+ G  G +G  G  GI+
Sbjct  885050  GIKGDIGDKGEKGDIGEKGDKGEKGIKGDKGDIGEKGNKGDIGDKGEKGDKGIDGDKGIK  884871

Query  99      GRKGEPGE  106
               G KG+ GE
Sbjct  884870  GDKGDIGE  884847


 Score = 43.5 bits (101),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 23/46 (50%), Positives = 31/46 (67%), Gaps = 0/46 (0%)
 Frame = +2

Query  57      GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               G +G  G KG+KGDPG+ G KG+ G  G  G++G +G PGI+G  G
Sbjct  293120  GENGDKGNKGDKGDPGIKGSKGEKGSKGDKGSKGDKGDPGIKGESG  293257


 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 33/89 (37%), Positives = 41/89 (46%), Gaps = 6/89 (7%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G +G  G KG+KGD G  G KGD G+ G  G +G  G  G  G K
Sbjct  878091  GNKGDNGDKGNKGDKGDNGDKGNKGDKGDNGDKGNKGDKGDKGDNGDKGDNGDKGDNGDK  877912

Query  102     GEPGEGAYVYRSAFSVGLETYVTIPNMPI  130
               G+ GE      S  S  +E    +  M +
Sbjct  877911  GDKGE------SGSSCQIENNDGVTIMSV  877843


 Score = 43.1 bits (100),  Expect = 9e-04, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G  G  G+KG+KGD G  G KGD G+ G  G +G  G  G +G K
Sbjct  878307  GNKGDKGNKGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDKGDNGDKGNKGDK  878128

Query  102     GEPGE  106
               G+ G+
Sbjct  878127  GDNGD  878113


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/74 (43%), Positives = 41/74 (55%), Gaps = 9/74 (12%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGE---------KGDPGLIGPKGDIGETGVPGAEGPR  92
               GI G  G+ G  G  G DG+ G+KG+         KGD G+ G  GD GE G  G +G +
Sbjct  885167  GIDGEKGNKGDTGDKGIDGSKGDKGDTGNKGDIGDKGDQGIKGDIGDKGEKGDIGEKGDK  884988

Query  93      GFPGIQGRKGEPGE  106
               G  GI+G KG+ GE
Sbjct  884987  GEKGIKGDKGDIGE  884946


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
```

```
 Identities = 31/65 (48%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G DG  G KG+KGD G  G KGDIGE G  G +G +G  G  G K
Sbjct  884942  GNKGDIGDKGEKGDKGIDGDKGIKGDKGDIGEKGDKGDIGEKGNKGEKGDKGDKGDIGEK  884763

Query  102     GEPGE  106
               G+ G+
Sbjct  884762  GDKGD  884748


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 38/65 (58%), Gaps = 0/65 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G +G  G  G  G  G+KG KG+ GL G KGD GE G  G +G +G  GI+G K
Sbjct  298947  GDKGSKGEDGLKGDKGDIGDKGDKGSKGEDGLKGSKGDKGEIGNKGDKGDKGDIGIKGDK  299126

Query  102     GEPGE  106
               G+ G+
Sbjct  299127  GDIGD  299141


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/68 (47%), Positives = 39/68 (57%), Gaps = 3/68 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGD---PGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G+NG  G+ G +G  G+ GEKGD    G  G KGDIGE G  G +G  G  G +
Sbjct  238504  GSKGDKGYNGEIGQKGDNGEKGDNGEKGDNGEKGDKGEKGDIGEKGDNGEKGDIGEKGNK  238683

Query  99      GRKGEPGE  106
               G KG+ GE
Sbjct  238684  GSKGDKGE  238707


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/67 (46%), Positives = 37/67 (55%), Gaps = 3/67 (4%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
                 G  G  G  G  G  G  G  GEKGEKGD G IG KGD G+    G +G +G PG +G
Sbjct  885650  AKGDKGDKGDIGEKGEKGDKGDIGEKGEKGDKGDIGEKGDKGDL---GEKGEKGDPGQKG  885480

Query  100     RKGEPGE  106
                KG+ G+
Sbjct  885479  EKGDKGD  885459


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/68 (47%), Positives = 38/68 (56%), Gaps = 3/68 (4%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKG---DPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               GI G  G  G  G  G  G  GEKG+KG   D G+ G KGDIGE G  G  G +G  G +
Sbjct  884978  GIKGDKGDIGEKGNKGDIGDKGEKGDKGIDGDKGIKGDKGDIGEKGDKGDIGEKGNKGEK  884799
```

```
Query  99      GRKGEPGE  106
               G KG+ G+
Sbjct  884798  GDKGDKGD  884775


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 38/65 (58%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G +G+ G  G  G  G KG+KGD G +G KGD G+ G+ G +G +G  G +G K
Sbjct  239908  GDKGIKGESGSKGDKGEKGNKGYKGDKGDKGNLGIKGDKGDKGIKGVKGTKGDKGTKGVK  240087

Query  102     GEPGE  106
               G  G+
Sbjct  240088  GTKGD  240102


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/70 (46%), Positives = 39/70 (56%), Gaps = 6/70 (9%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGE---KGEKGDPGLIGPKGDIGETGVPGAEGP---RGFP  95
               GI G  G  G  G  GT G+   KG KGD G+ G KGDIG+ G+ G  G    +G
Sbjct  238279  GIKGDKGDKGTKGDKGDKGTKGDNGDKGTKGDNGIKGYKGDIGDKGIKGESGANADKGDK  238458

Query  96      GIQGRKGEPG  105
               GI+G KG+ G
Sbjct  238459  GIKGDKGDKG  238488


 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/62 (48%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = -1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G PG+KGEKGD G  G KGD G+ G  G +G  G  G  G KG+
Sbjct  885545  GEKGDKGDLGEKGEKGDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDIGDKGEIGNKGDV  885366

Query  105     GE  106
               GE
Sbjct  885365  GE  885360


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G PG+ G +G  G +G  G+ GE G KGD G  G  G  G  G  G++G  G  GIQG
Sbjct  296281  IKGDPGNKGEDGIKGTNGLKGSKGETGSKGDDGTKGITGLKGTKGNSGSKGDDGDKGIQG  296460

Query  100     RKGE  103
                KGE
Sbjct  296461  LKGE  296472
```

```
 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/66 (42%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + GI G  G  G PG  G DG  G  G KG  G  G KGD G  G+ G +G +G  G +G
Sbjct  296254  IKGIIGSKGIKGDPGNKGEDGIKGTNGLKGSKGETGSKGDDGTKGITGLKGTKGNSGSKG  296433

Query  100     RKGEPG  105
                 G+ G
Sbjct  296434  DDGDKG  296451


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 37/64 (58%), Gaps = 1/64 (2%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G NG+ G  G  GT G KG+KG     G KG  GETG  G +G +G  G +G K
Sbjct  295984  GIKGMNGFNGSKGIKGDKGTDGIKGDKGQDNF-GSKGQKGETGSKGDDGIKGITGSKGFK  296160

Query  102     GEPG  105
               G+PG
Sbjct  296161  GDPG  296172


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G +G  G+KG+ GD G  G KGD G+ G  G +G +G  G +G K
Sbjct  878235  GDKGDNGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDNGDKGNKGDNGDKGNK  878056

Query  102     GEPGE  106
               G+ G+
Sbjct  878055  GDKGD  878041


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/67 (45%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  GEKG KG+ G  G KGDIGE G  G  G +G  G +G
Sbjct  884894  IDGDKGIKGDKGDIGEKGDKGDIGEKGNKGEKGDKGDKGDIGEKGDKGDTGSKGDKGDKG  884715

Query  100     RKGEPGE  106
                KG+ G+
Sbjct  884714  EKGDKGD  884694


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G+ G  G  G  G KGEKG  G  G KGDIG  G  GA+  +G  G +G KG+
```

```
Sbjct  293273  GDKGDKGSKGDKGDKGIDGNKGEKGSKGDKGDKGDIGLKGESGADADKGDKGDKGSKGDK  293452

Query  105     GE  106
               G+
Sbjct  293453  GD  293458


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/66 (42%), Positives = 35/66 (53%), Gaps = 0/66 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G +GA    G  G  G KG+KGD G IGPKG+ G     G +G +G  G +G KG
Sbjct  293381  GLKGESGADADKGDKGDKGSKGDKGDKGDIGPKGESGADADKGDKGDKGSKGDKGDKGTK  293560

Query  105     GEGAYV  110
               GE   +
Sbjct  293561  GESGLI  293578


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/60 (47%), Positives = 34/60 (57%), Gaps = 0/60 (0%)
 Frame = -1

Query  47      PGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
                G  G  G  G DG  G KG+ GD G+ G KGD G+TG  G  G +G  GI+G  G+ GE
Sbjct  885197  KGEKGDKGNKGIDGEKGNKGDTGDKGIDGSKGDKGDTGNKGDIGDKGDQGIKGDIGDKGE  885018


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G +G  G +G  G  G+KG KGD G  G KGD G  G  G  G  G  GI+G K
Sbjct  239701  GVKGDKGDSGIKGENGLKGDVGDKGIKGDKGNEGDKGDKGNKGEKGNRGDEGDKGIKGNK  239880

Query  102     GEPG  105
               G+ G
Sbjct  239881  GDKG  239892


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 38/65 (58%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G+ G  G  G  G+KG++GD G +G KG+ G+TG  G  G +G  G +G K
Sbjct  88518  GDQGDKGDTGSKGDQGDKGDQGDKGDQGDKGDVGDKGNKGDTGSKGDVGDKGDVGDKGDK  88339

Query  102    GEPGE  106
              G+ G+
Sbjct  88338  GDTGD  88324


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = -3
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G NG  G  G +G  G KG+KGD G  G  GD G  G  G +G +G  G  G K
Sbjct  878208  GNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDNGDKGNKGDNGDKGNKGDKGDNGDK  878029

Query  102     GEPGE  106
               G  G+
Sbjct  878028  GNKGD  878014


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G +G  G+KG+ GD G  G KGD G+ G  G  G +G  G +G
Sbjct  878298  GDKGNKGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDN  878119

Query  102     GEPGE  106
               G+ G+
Sbjct  878118  GDKGD  878104


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G  G  G  G  G  G KG+KG+ GL G  GDIG+ G  G++G  G  G +G
Sbjct  298821  GVKGDDGTKGEKGEKGTKGDKGNKGDKGEDGLKGENGDIGDKGDKGSKGEDGLKGDKGDI  299000

Query  102     GEPGE  106
               G+ G+
Sbjct  299001  GDKGD  299015


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G+ G+KGD G +G KGD+G+ G  G +G +G  G +G K
Sbjct  88347  GDKGDTGDKGDKGDTGDKGDKGDVGDKGDKGDVGDKGDVGDKGDVGDKGDKGDTGDKGDK  88168

Query  102    GEPGE  106
              G+ G+
Sbjct  88167  GDIGD  88153


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G +G  G KG+ GD G  G KGD G+ G  G +G  G  G +G K
Sbjct  878154  GDKGNKGDKGDNGDKGDNGDKGNKGDNGDKGNKGDKGDNGDKGNKGDKGDNGDKGNKGDK  877975

Query  102     GEPGE  106
```

```
               G+ G+
Sbjct  877974  GDKGD  877960


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G +G  G  G+KG+ GD G  G KG+ G+ G  G +G +G  G +G K
Sbjct  878199  GDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDNGDKGNKGDNGDKGNKGDKGDNGDKGNK  878020

Query  102     GEPGE  106
               G+ G+
Sbjct  878019  GDKGD  878005


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 28/61 (46%), Positives = 35/61 (57%), Gaps = 0/61 (0%)
 Frame = -1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G PG+ G  G  G+ G+KGD G IG KGD G+ G  G  G +G  G +G KG+
Sbjct  885518  GEKGEKGDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDIGDKGEIGNKGDVGEKGSKGDK  885339

Query  105     G  105
               G
Sbjct  885338  G  885336


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G     G  G  G  G  G+KG KGD G  G KGD G+ G  G +G +G  G +G K
Sbjct  878343  GDKGDKSDKGDKGNKGDKGNKGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDK  878164

Query  102     GEPGE  106
               G+ G+
Sbjct  878163  GDNGD  878149


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G PG KGE G  G  G KG  GETG  G +G +G  G++G K
Sbjct  296233  GTKGDDGIKGIIGSKGIKGDPGNKGEDGIKGTNGLKGSKGETGSKGDDGTKGITGLKGTK  296412

Query  102     GEPGE  106
               G  G
Sbjct  296413  GNSGS  296427


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
```

```
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G  G+ G+KGD G  G KG+ G+ G  G +G +G  G +G K
Sbjct  878316  GDKGNKGDKGNKGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDKGDNGDKGNK  878137

Query  102     GEPGE  106
               G+ G+
Sbjct  878136  GDKGD  878122


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 31/79 (39%), Positives = 40/79 (51%), Gaps = 12/79 (15%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG---  96
               + GI G  G  G PG  G +G  G KG KG  G +G KGD G  G+ G++G +G PG
Sbjct  296128  IKGITGSKGFKGDPGTKGENGINGTKGLKGSQGDLGTKGDDGIKGIIGSKGIKGDPGNKG  296307

Query  97      ---------IQGRKGEPGE  106
                        ++G KGE G
Sbjct  296308  EDGIKGTNGLKGSKGETGS  296364


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 30/72 (42%), Positives = 41/72 (57%), Gaps = 1/72 (1%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G  G  G  G  G  G+KG++ D GL G KGD G+TG  G +G +G  G +G K
Sbjct  883574  GVKGDKGDKGNKGDKGNIGIKGDKGDRSDKGLKGDKGDKGDTGDIGLKGDKGDIGEKGIK  883395

Query  102     GEPG-EGAYVYR  112
               G+ G  G+  Y+
Sbjct  883394  GDKGINGSKGYK  883359


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 24/46 (52%), Positives = 30/46 (65%), Gaps = 0/46 (0%)
 Frame = -1

Query  60      GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
               G  G+KG+ GD GL G KGDIGE G+ G +G  G  G +G KG+ G
Sbjct  883475  GDKGDKGDTGDIGLKGDKGDIGEKGIKGDKGINGSKGYKGDKGDKG  883338


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 30/64 (47%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G  G  G  G  G  G KG KGD G IG KGD G+ G  G +G +G  G +G K
Sbjct  298974  GLKGDKGDIGDKGDKGSKGEDGLKGSKGDKGEIGNKGDKGDKGDIGIKGDKGDIGDKGDK  299153

Query  102     GEPG  105
               G+PG
Sbjct  299154  GDPG  299165
```

```
 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G D   G+KG+KG  G  G KGDIG  G  GA+  +G  G +G K
Sbjct  293354  GDKGDKGDIGLKGESGADADKGDKGDKGSKGDKGDKGDIGPKGESGADADKGDKGDKGSK  293533

Query  102     GEPGE  106
               G+ G+
Sbjct  293534  GDKGD  293548


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKGEKGDPG  G KGD G+ G  G +G  G  G +G
Sbjct  885581  GEKGEKGDKGDIGEKGDKGDLGEKGEKGDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDI  885402

Query  102     GEPGE  106
               G+ GE
Sbjct  885401  GDKGE  885387


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 28/58 (48%), Positives = 32/58 (55%), Gaps = 0/58 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               G PG  G  G  G  G  G+ GEKGD G IG KG+IG  G  G +G +G  GI G
Sbjct  885500  GDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDIGDKGEIGNKGDVGEKGSKGDKGIDG  885327


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KG KGD G  G KGDIG  G  G  G +G  G  G K
Sbjct  883997  GSKGEKGDTGEKGDKGNKGDRGDKGIKGDIGSKGDKGDIGNKGDKGDRGDKGIKGDAGLK  883818

Query  102     GEPGE  106
               G+ G+
Sbjct  883817  GDKGD  883803


 Score = 40.4 bits (93),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 29/63 (46%), Positives = 34/63 (54%), Gaps = 0/63 (0%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KG KGD GL G KGDIG+ G  G +G RG  G +G
Sbjct  883922  IKGDIGSKGDKGDIGNKGDKGDRGDKGIKGDAGLKGDKGDIGQKGDKGTKGDRGDKGEKG  883743

Query  100     RKG  102
```

```
                 G
Sbjct  883742  DAG  883734


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 29/69 (42%), Positives = 38/69 (55%), Gaps = 3/69 (4%)
 Frame = -1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEK---GEKGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
               AG+ G+ G  G  G  G  G  G+K   G++GD G IG KGD G+ G  G  G +G  G
Sbjct  883739  AGLKGNKGDIGLKGDKGTKGDRGDKGTKGDRGDKGDIGNKGDKGDKGTKGDRGDKGVKGD  883560

Query  98      QGRKGEPGE  106
               +G KG  G+
Sbjct  883559  KGDKGNKGD  883533


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G NG  G +G  G  G+ G+KG+ G  G  GD G  G  G  G +G  G +G K
Sbjct  878145  GNKGDKGDNGDKGDNGDKGNKGDNGDKGNKGDKGDNGDKGNKGDKGDNGDKGNKGDKGDK  877966

Query  102     GEPGE  106
               G+ G+
Sbjct  877965  GDNGD  877951


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+KG+ GD G +G KGD+G+ G  G +G +G  G +G K
Sbjct  87798  GDTGDKGDTGDKGDTGDKGDTGDKGDVGDKGDVGDKGDVGDKGDVGDKGDKGDIGDKGDK  87619

Query  102    GEPGE  106
              G+ G+
Sbjct  87618  GDLGD  87604


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G+ G+KG KGD G  G KG+ GE G  G +G +G  G +G K
Sbjct  239458  GSKGYKGDKGDKGIKGNTGSKGDKGSKGDKGEKGSKGNKGEKGEKGFKGEKGSKGEKGSK  239637

Query  102     GEPGE  106
               G  G+
Sbjct  239638  GNKGD  239652


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
```

```
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G  G  G+KG KGD G  G KGD G  G+ G +G R   G++G K
Sbjct  883646  GDKGDIGNKGDKGDKGTKGDRGDKGVKGDKGDKGNKGDKGNIGIKGDKGDRSDKGLKGDK  883467

Query  102     GEPGE  106
               G+ G+
Sbjct  883466  GDKGD  883452


 Score = 40.4 bits (93),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G+KG KGD G  G KGD G+ G  G +G +G  G +G
Sbjct  878280  GDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDN  878101

Query  102     GEPG  105
               G+ G
Sbjct  878100  GDKG  878089


 Score = 40.4 bits (93),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 36/67 (54%), Gaps = 3/67 (4%)
 Frame = +1

Query  42      GIPGHPGH---NGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               GI G  G     G  G  G  G  G+KG KGD G  G KG+ G+ G  G +G +G  GI+
Sbjct  239143  GIKGESGSAVFKGDKGTKGDKGNKGDKGNKGDKGTNGDKGNKGDKGSKGDKGTKGDKGIK  239322

Query  99      GRKGEPG  105
               G KG+ G
Sbjct  239323  GDKGDKG  239343


 Score = 40.4 bits (93),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 35/62 (56%), Gaps = 0/62 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G+ G  G  G  G+ GEKG KGD G  G KGD G  G  GA+  +G  G +G KG+
Sbjct  293129  GDKGNKGDKGDPGIKGSKGEKGSKGDKGSKGDKGDPGIKGESGADADKGDKGDKGSKGDK  293308

Query  105     GE  106
               G+
Sbjct  293309  GD  293314


 Score = 40.0 bits (92),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 37/67 (55%), Gaps = 3/67 (4%)
 Frame = +1

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGE---KGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
                 G  G NG  G  G +G  G+KG+   KGD G  G KGD G+ G+ G +G +G  G +G
Sbjct  238147  TKGDKGDNGTKGDKGDNGIKGDKGDNGTKGDNGDNGTKGDKGDNGIKGDKGDKGTKGDKG  238326
```

```
Query  100     RKGEPGE  106
                KG  G+
Sbjct  238327  DKGTKGD  238347


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG KG+ G  G KGD G+ G  G  G +G  G++G K
Sbjct  239539  GDKGEKGSKGNKGEKGEKGFKGEKGSKGEKGSKGNKGDKGDKGFKGDNGIKGNIGVKGDK  239718

Query  102     GEPG  105
               G+ G
Sbjct  239719  GDSG  239730


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 22/40 (55%), Positives = 28/40 (70%), Gaps = 0/40 (0%)
 Frame = +3

Query  63      GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               G KG KGD G  G KGD+G+TG+ G +G +G PGI+G  G
Sbjct  299757  GTKGVKGDKGSKGDKGDLGDTGIKGDKGEKGDPGIKGEAG  299876


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G KG+KG+ G  G KG+ GE G  G +G +G  G +G K
Sbjct  239467  GYKGDKGDKGIKGNTGSKGDKGSKGDKGEKGSKGNKGEKGEKGFKGEKGSKGEKGSKGNK  239646

Query  102     GEPGE  106
               G+ G+
Sbjct  239647  GDKGD  239661


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 29/68 (43%), Positives = 36/68 (53%), Gaps = 3/68 (4%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGD---IGETGVPGAEGPRGFPGIQ  98
               G  G  G  G  G  G D   G+KGEKGD G+ G KGD    G+TG+ G  G     G +
Sbjct  294137  GEKGEKGDVGIKGESGADADKGDKGEKGDKGVNGDKGDKGSKGDTGIKGEAGTAANKGDK  294316

Query  99      GRKGEPGE  106
               G KG+ G+
Sbjct  294317  GSKGDKGD  294340


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 33/64 (52%), Gaps = 0/64 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
```

```
               G  G+ G  G  G  G  G  G+KG KGD G  G KGD G+ G  G  G +G  G +G
Sbjct  878217  GDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDNGDKGNKGDNGDKGNKGDKGDN  878038

Query  102     GEPG  105
               G+ G
Sbjct  878037  GDKG  878026


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G KG+KGD G IG KG+IG  G  G +G +G  G +G K
Sbjct  878631  GDKGDIGIKGEKGDIGTKGDIGNKGDKGDKGDIGNKGNIGNKGEKGDKGVKGDIGEKGEK  878452

Query  102     GEPG  105
               G+ G
Sbjct  878451  GDKG  878440


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G  G  G  G  G  G++G KGD G  G KGDIGE G  G +G +G  G  G K
Sbjct  885122  GIDGSKGDKGDTGNKGDIGDKGDQGIKGDIGDKGEKGDIGEKGDKGEKGIKGDKGDIGEK  884943

Query  102     GEPGE  106
               G  G+
Sbjct  884942  GNKGD  884928


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G+ G  G  G  G  G+KG+KG  G+ G KGD G  GV G +G +G  G  G K
Sbjct  239953  GEKGNKGYKGDKGDKGNLGIKGDKGDKGIKGVKGTKGDKGTKGVKGTKGDKGDKGTNGDK  240132

Query  102     GEPG  105
               G+ G
Sbjct  240133  GDKG  240144


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 30/64 (47%), Positives = 33/64 (52%), Gaps = 3/64 (5%)
 Frame = -1

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               I G  G  G  G  G  GT    GEKGD G  G KGD GE G  G +G RG  GI+G  G
Sbjct  884075  IKGDKGEKGDKGNAGDKGTS---GEKGDLGSKGEKGDTGEKGDKGNKGDRGDKGIKGDIG  883905

Query  103     EPGE  106
                 G+
Sbjct  883904  SKGD  883893
```

```
 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+KG+ GD G +G KGD+G+ G  G  G +G  G  G K
Sbjct  88329  GDKGDKGDTGDKGDKGDVGDKGDKGDVGDKGDVGDKGDVGDKGDKGDTGDKGDKGDIGDK  88150

Query  102    GEPGE  106
              G+ G+
Sbjct  88149  GDKGD  88135


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G     G  G  G+KG KGD G  G KGD G+ G  G  G +G  G +G
Sbjct  878361  GDKGNKGDKGDKSDKGDKGNKGDKGNKGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDN  878182

Query  102     GEPGE  106
               G+ G+
Sbjct  878181  GDKGD  878167


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 26/64 (41%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = -3

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              I G  G  G  G  G  G  G+KG++GD G  G KGD+G+ G  G  G +G  G +G  G
Sbjct  88533  IKGEKGDQGDKGDTGSKGDQGDKGDQGDKGDQGDKGDVGDKGNKGDTGSKGDVGDKGDVG  88354

Query  103    EPGE  106
              + G+
Sbjct  88353  DKGD  88342


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 36/62 (58%), Gaps = 0/62 (0%)
 Frame = -3

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G++G  G  G  G  G+KG KG  G  G KGD G+ G  G++G +G  GI+G KG
Sbjct  879144  GDKGNDGIKGDFGSKGYKGDKGSKGTKGNNGFKGDRGDKGDKGSKGDKGDNGIKGNKGSK  878965

Query  105     GE  106
               G+
Sbjct  878964  GD  878959


 Score = 39.7 bits (91),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 33/67 (49%), Gaps = 0/67 (0%)
 Frame = -3
```

```
Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G DG  G  G KG+KG  G  G KGD+G  G  G +G  G  G +G
Sbjct  879348  LKGEKGEIGSKGTKGDDGNKGNKGIKGDKGTTGDKGDKGDVGNKGDAGDKGDAGKKGEKG  879169

Query  100     RKGEPGE  106
                 G  G+
Sbjct  879168  EMGNKGD  879148


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G +G  G  G+KG+ GD G  G  GD G  G  G  G +G  G +G K
Sbjct  878262  GDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDNGDKGNK  878083

Query  102     GEPGE  106
               G+ G+
Sbjct  878082  GDNGD  878068


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+ G+KGD G  G KGD G+ G  G +G  G  G +G K
Sbjct  878190  GDNGDKGDKGDNGDKGNKGDKGDNGDKGDNGDKGNKGDNGDKGNKGDKGDNGDKGNKGDK  878011

Query  102     GEPGE  106
               G+ G+
Sbjct  878010  GDNGD  877996


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G NG  G  G  G+ GE G KGD G IG KGD G  G  G +G +G  G  G K
Sbjct  298902  GEDGLKGENGDIGDKGDKGSKGEDGLKGDKGDIGDKGDKGSKGEDGLKGSKGDKGEIGNK  299081

Query  102     GEPGE  106
               G+ G+
Sbjct  299082  GDKGD  299096


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G  G+KG KGD G IG KGD G+ G  G +G +G  G +G
Sbjct  884951  GEKGNKGDIGDKGEKGDKGIDGDKGIKGDKGDIGEKGDKGDIGEKGNKGEKGDKGDKGDI  884772

Query  102     GEPGE  106
               GE G+
```

```
Sbjct  884771  GEKGD  884757


 Score = 39.3 bits (90),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 26/63 (41%), Positives = 33/63 (52%), Gaps = 0/63 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G+ G  G  G+ G KGEKG+ G  G KG  GE G  G +G +G  G +G
Sbjct  239497  IKGNTGSKGDKGSKGDKGEKGSKGNKGEKGEKGFKGEKGSKGEKGSKGNKGDKGDKGFKG  239676

Query  100     RKG  102
                 G
Sbjct  239677  DNG  239685


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 33/64 (52%), Gaps = 0/64 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G  GT G+KG+KGD G  G  GD G+ G  G +G  G  G  G K
Sbjct  879315  GTKGDDGNKGNKGIKGDKGTTGDKGDKGDVGNKGDAGDKGDAGKKGEKGEMGNKGDIGDK  879136

Query  102     GEPG  105
               G  G
Sbjct  879135  GNDG  879124


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+ G+KG+ G +G KGDIG+ G  G +G  G  G +G K
Sbjct  879261  GTTGDKGDKGDVGNKGDAGDKGDAGKKGEKGEMGNKGDIGDKGNDGIKGDFGSKGYKGDK  879082

Query  102     GEPG  105
               G  G
Sbjct  879081  GSKG  879070


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 30/67 (45%), Positives = 37/67 (55%), Gaps = 3/67 (4%)
 Frame = +1

Query  47      PGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGV---PGAEGPRGFPGIQGRKGE  103
                G NG  G  G  G+ G+KGE GD G IG KGD G  GV    G +G +GF G  G KG+
Sbjct  296887  KGENGFVGDLGSKGSKGDKGESGDKGDIGIKGDKGAKGVTGDKGDKGTKGFIGNVGFKGD  297066

Query  104     PGEGAYV  110
                G+   +
Sbjct  297067  TGDKGII  297087


 Score = 39.3 bits (90),  Expect = 0.016, Method: Compositional matrix adjust.
 Identities = 32/68 (47%), Positives = 36/68 (53%), Gaps = 3/68 (4%)
 Frame = -1
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGD---PGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G  G  G  G  G  GEKG+KGD    G  G KGDIGE G  G  G +G  G
Sbjct  885671  GESGEKGAKGDKGDKGDIGEKGEKGDKGDIGEKGEKGDKGDIGEKGDKGDLGEKGEKGDP  885492

Query  99      GRKGEPGE  106
               G+KGE G+
Sbjct  885491  GQKGEKGD  885468


 Score = 39.3 bits (90),  Expect = 0.016, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G+ G  G  G  G KG+KG+ G  G KGDIG  G+ G  G   F G +G K
Sbjct  239017  GDKGSKGDKGSKGDKGDKGDEGIKGDKGNKGDKGDKGDIGSQGIKGESGSAVFKGDKGTK  239196

Query  102     GEPG  105
               G+ G
Sbjct  239197  GDKG  239208


 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+KG+ GD G +G KGD+G+ G  G  G +G  G  G K
Sbjct  87780  GDTGDKGDTGDKGDTGDKGDVGDKGDVGDKGDVGDKGDVGDKGDKGDIGDKGDKGDLGDK  87601

Query  102    GEPGE  106
              G+ G+
Sbjct  87600  GDKGD  87586


 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 24/56 (43%), Positives = 33/56 (59%), Gaps = 6/56 (11%)
 Frame = +1

Query  60      GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAF  115
               GT G KGEKG  G +GPKG+ G+ G  G++G R      G KGEP    + Y +++
Sbjct  291823  GTGGCKGEKGIKGELGPKGNTGQKGDIGSKGDR------GDKGEPTISMFSYINSY  291972


 Score = 38.9 bits (89),  Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+ G+KGD G +G KGD G+ G  G  G +G  G +G K
Sbjct  88374  GDKGDVGDKGDKGDTGDKGDKGDTGDKGDKGDVGDKGDKGDVGDKGDVGDKGDVGDKGDK  88195

Query  102    GEPGE  106
              G+ G+
Sbjct  88194  GDTGD  88180
```

```
 Score = 38.9 bits (89),  Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 29/70 (41%), Positives = 37/70 (53%), Gaps = 3/70 (4%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---IGPKGDIGETGVPGAEGPRGFPG  96
                +G  G  G  G  G  G  G  G KG++GD G+   IG KGD G+ G  G +G RG  G
Sbjct  884021  TSGEKGDLGSKGEKGDTGEKGDKGNKGDRGDKGIKGDIGSKGDKGDIGNKGDKGDRGDKG  883842

Query  97      IQGRKGEPGE  106
               I+G  G  G+
Sbjct  883841  IKGDAGLKGD  883812


 Score = 38.9 bits (89),  Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GE G KG+ G IG KGD G  G  G +G +G  G +G K
Sbjct  298839  GTKGEKGEKGTKGDKGNKGDKGEDGLKGENGDIGDKGDKGSKGEDGLKGDKGDIGDKGDK  299018

Query  102     GEPGE  106
               G  GE
Sbjct  299019  GSKGE  299033


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 31/68 (46%), Positives = 37/68 (54%), Gaps = 3/68 (4%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVP---GAEGPRGFPGIQ  98
               G  G  G  G  G  G  G  GEKG+KG+ G+ G KGDIGE G     G +G +G  GI
Sbjct  885068  GDKGDQGIKGDIGDKGEKGDIGEKGDKGEKGIKGDKGDIGEKGNKGDIGDKGEKGDKGID  884889

Query  99      GRKGEPGE  106
               G KG  G+
Sbjct  884888  GDKGIKGD  884865


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G DG  G  G KG+KGD G IG KG+ G     G +G +G  G +G K
Sbjct  293282  GDKGSKGDKGDKGIDGNKGEKGSKGDKGDKGDIGLKGESGADADKGDKGDKGSKGDKGDK  293461

Query  102     GEPG  105
               G+ G
Sbjct  293462  GDIG  293473


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+KG+KGD G  G KGD+G+ G  G +G +G  G +G K
```

```
Sbjct  87699  GDKGDVGDKGDVGDKGDKGDIGDKGDKGDLGDKGDKGDVGDKGDVGDKGDKGDIGDKGDK  87520

Query  102    GEPGE  106
              G+ G+
Sbjct  87519  GDLGD  87505


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G+ G  G+ G  G  G  G+KG+KGD G  G KGD G+ G  G  G +G  G  G K
Sbjct  88419  GDKGNKGDTGSKGDVGDKGDVGDKGDKGDTGDKGDKGDTGDKGDKGDVGDKGDKGDVGDK  88240

Query  102    GEPGE  106
              G+ G+
Sbjct  88239  GDVGD  88225


 Score = 38.9 bits (89),  Expect = 0.021, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+ G+KG+ G  G KGD+G+ G  G +G +G  G +G K
Sbjct  88491  GSKGDQGDKGDQGDKGDQGDKGDVGDKGNKGDTGSKGDVGDKGDVGDKGDKGDTGDKGDK  88312

Query  102    GEPGE  106
              G+ G+
Sbjct  88311  GDTGD  88297


 Score = 38.9 bits (89),  Expect = 0.022, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 32/64 (50%), Gaps = 0/64 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G  G KGD G  G KG+ G  G  G +G +GF G +G K
Sbjct  239440  GDKGDKGSKGYKGDKGDKGIKGNTGSKGDKGSKGDKGEKGSKGNKGEKGEKGFKGEKGSK  239619

Query  102     GEPG  105
               GE G
Sbjct  239620  GEKG  239631


 Score = 38.5 bits (88),  Expect = 0.023, Method: Compositional matrix adjust.
 Identities = 28/58 (48%), Positives = 32/58 (55%), Gaps = 0/58 (0%)
 Frame = +3

Query  48      GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
               G  G  G  G  G  GEKG KGD G +G KGD G  G  G +G +G  G +G KGE G
Sbjct  298740  GDKGITGDKGDKGEIGEKGNKGDKGDVGVKGDDGTKGEKGEKGTKGDKGNKGDKGEDG  298913


 Score = 38.5 bits (88),  Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 29/68 (43%), Positives = 36/68 (53%), Gaps = 3/68 (4%)
 Frame = +1
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGE---KGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G N   G  G +GT G+KG+   KGD G  G KGD G+ G  G +G  G  G +
Sbjct  238117  GDKGMKGDNSTKGDKGDNGTKGDKGDNGIKGDKGDNGTKGDNGDNGTKGDKGDNGIKGDK  238296

Query  99      GRKGEPGE  106
               G KG  G+
Sbjct  238297  GDKGTKGD  238320


 Score = 38.5 bits (88),  Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G +G  G KG KGD G+ G +GD G  G  G++G +G  G +G K
Sbjct  239800  GDKGDKGNKGEKGNRGDEGDKGIKGNKGDKGIKGSEGDKGIKGESGSKGDKGEKGNKGYK  239979

Query  102     GEPGE  106
               G+ G+
Sbjct  239980  GDKGD  239994


 Score = 38.5 bits (88),  Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 35/64 (55%), Gaps = 3/64 (5%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G PG  G  G   +KG+KGD    G KGD G+ G+ G +G +G  G +G K
Sbjct  293201  GDKGSKGDKGDPGIKGESGADADKGDKGDK---GSKGDKGDKGIDGNKGEKGSKGDKGDK  293371

Query  102     GEPG  105
               G+ G
Sbjct  293372  GDIG  293383


 Score = 38.5 bits (88),  Expect = 0.025, Method: Compositional matrix adjust.
 Identities = 22/44 (50%), Positives = 29/44 (66%), Gaps = 0/44 (0%)
 Frame = +2

Query  60      GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
               G  G+KG+KGD GL G KGD G+ G  G +G +G  G +G KG+
Sbjct  294527  GLKGDKGDKGDVGLKGDKGDKGDVGSKGDKGDKGSKGDKGSKGD  294658


 Score = 38.5 bits (88),  Expect = 0.026, Method: Compositional matrix adjust.
 Identities = 22/55 (40%), Positives = 30/55 (55%), Gaps = 0/55 (0%)
 Frame = -3

Query  63      GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSV  117
               G+KG KGD G+ G KGD G+ G  G  G +G  G +G KG+ G+      S   +
Sbjct  879612  GDKGSKGDIGVKGSKGDNGDKGSKGDIGVKGSKGDKGNKGDKGDNGLSILSGLDI  879448


 Score = 38.5 bits (88),  Expect = 0.026, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 38/67 (57%), Gaps = 3/67 (4%)
 Frame = -1
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDI---GETGVPGAEGPRGFPGIQ  98
               G  G  G+ G  G  G  GT G++G+KG  G  G KGDI   G+ G  G +G RG  G++
Sbjct  883745  GDAGLKGNKGDIGLKGDKGTKGDRGDKGTKGDRGDKGDIGNKGDKGDKGTKGDRGDKGVK  883566

Query  99      GRKGEPG  105
               G KG+ G
Sbjct  883565  GDKGDKG  883545


 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 30/68 (44%), Positives = 36/68 (53%), Gaps = 3/68 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGE---KGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G NG  G  G +G  G+KG+   KGD G  G KGD G+ G  G  G +G+ G
Sbjct  238225  GTKGDNGDNGTKGDKGDNGIKGDKGDKGTKGDKGDKGTKGDNGDKGTKGDNGIKGYKGDI  238404

Query  99      GRKGEPGE  106
               G KG  GE
Sbjct  238405  GDKGIKGE  238428


 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 35/67 (52%), Gaps = 0/67 (0%)
 Frame = -3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G  G  G  G  G  G  G  G+KG+ GD G  G KGD+G+ G  G +G  G  G  G
Sbjct  87840  IKGEKGDKGDTGDKGDTGDKGDTGDKGDTGDKGDTGDKGDVGDKGDVGDKGDVGDKGDVG  87661

Query  100    RKGEPGE  106
               KG+ G+
Sbjct  87660  DKGDKGD  87640


 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 37/67 (55%), Gaps = 3/67 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGP---KGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G  G  G +G  G  G KG+KGD G+ G    KGD+G+ G+ G +G  G  G +
Sbjct  239638  GNKGDKGDKGFKGDNGIKGNIGVKGDKGDSGIKGENGLKGDVGDKGIKGDKGNEGDKGDK  239817

Query  99      GRKGEPG  105
               G KGE G
Sbjct  239818  GNKGEKG  239838


 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G+ G KG  G+ G  G +G +G  G +G K
Sbjct  884987  GEKGIKGDKGDIGEKGNKGDIGDKGEKGDKGIDGDKGIKGDKGDIGEKGDKGDIGEKGNK  884808

Query  102     GEPGE  106
               GE G+
```

```
Sbjct  884807  GEKGD  884793


 Score = 38.5 bits (88),  Expect = 0.029, Method: Compositional matrix adjust.
 Identities = 30/69 (43%), Positives = 36/69 (52%), Gaps = 3/69 (4%)
 Frame = -3

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKG---EKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
               + G  G  G  G  G  G  GT G+KG   +KGD G+ G KGDIG  G  G +G +G  G
Sbjct  878718  LKGDKGEKGEKGNVGDKGDIGTKGDKGNVGDKGDIGIKGEKGDIGTKGDIGNKGDKGDKG  878539

Query  97      IQGRKGEPG  105
                 G KG  G
Sbjct  878538  DIGNKGNIG  878512


 Score = 38.5 bits (88),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 23/47 (49%), Positives = 31/47 (66%), Gaps = 0/47 (0%)
 Frame = -1

Query  60      GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               G  G+KG+KGD G IG KGD G+ G  G +G +G  G +G KG+ G+
Sbjct  883484  GLKGDKGDKGDTGDIGLKGDKGDIGEKGIKGDKGINGSKGYKGDKGD  883344


 Score = 38.1 bits (87),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G+ GEKG+ G+ G  G KGD G+ G+ G  G +G  G  G K
Sbjct  884051  GDKGNAGDKGTSGEKGDLGSKGEKGDTGEKGDKGNKGDRGDKGIKGDIGSKGDKGDIGNK  883872

Query  102     GEPGE  106
               G+ G+
Sbjct  883871  GDKGD  883857


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G+ G  G  G KG+ GD G  G KGD G  G  G +G +G  G  G K
Sbjct  879225  GNKGDAGDKGDAGKKGEKGEMGNKGDIGDKGNDGIKGDFGSKGYKGDKGSKGTKGNNGFK  879046

Query  102     GEPGE  106
               G+ G+
Sbjct  879045  GDRGD  879031


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 37/67 (55%), Gaps = 3/67 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---IGPKGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G  G  G  G  G  G+KG KGD G+   IG KGD G++G+ G  G +G  G +
Sbjct  239593  GFKGEKGSKGEKGSKGNKGDKGDKGFKGDNGIKGNIGVKGDKGDSGIKGENGLKGDVGDK  239772
```

```
Query  99      GRKGEPG  105
               G KG+ G
Sbjct  239773  GIKGDKG  239793


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+ G+KGD G +G KGD+G+ G  G  G +G  G  G K
Sbjct  87681  GDKGDVGDKGDKGDIGDKGDKGDLGDKGDKGDVGDKGDVGDKGDKGDIGDKGDKGDLGDK  87502

Query  102    GEPGE  106
              G+ G+
Sbjct  87501  GDKGD  87487


 Score = 38.1 bits (87),  Expect = 0.035, Method: Compositional matrix adjust.
 Identities = 29/70 (41%), Positives = 38/70 (54%), Gaps = 3/70 (4%)
 Frame = +1

Query  39      WM--AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
               W+   G+ G  G  G  G  G  G+KGE G  G  G KGD+G+ G  GA+G +G  G
Sbjct  237538  WIPQVGLKGSQGDQGYKGDQGSKGDKGQKGEFGSAGFKGDKGDMGQKGETGAKGDKGDKG  237717

Query  97      IQGRKGEPGE  106
                +G KG  G+
Sbjct  237718  -EGSKGSKGD  237744


 Score = 38.1 bits (87),  Expect = 0.035, Method: Compositional matrix adjust.
 Identities = 25/65 (38%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G +G  G  G+ G+KG+ G  G  GD G+ G  G +G  G  G +G K
Sbjct  878226  GDNGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDNGDKGNKGDNGDKGNKGDK  878047

Query  102     GEPGE  106
               G+ G+
Sbjct  878046  GDNGD  878032


 Score = 38.1 bits (87),  Expect = 0.035, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 32/64 (50%), Gaps = 0/64 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  GEKGEKG  G  G KG+ G  G  G +G +GF G  G K
Sbjct  239512  GSKGDKGSKGDKGEKGSKGNKGEKGEKGFKGEKGSKGEKGSKGNKGDKGDKGFKGDNGIK  239691

Query  102     GEPG  105
               G  G
Sbjct  239692  GNIG  239703
```

```
 Score = 38.1 bits (87),  Expect = 0.037, Method: Compositional matrix adjust.
 Identities = 25/65 (38%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G +G  G  G+ G+KG+ G  G  GD G+ G  G +G +G  G  G K
Sbjct  878289  GNKGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGDNGDK  878110

Query  102     GEPGE  106
               G+ G+
Sbjct  878109  GDNGD  878095


 Score = 38.1 bits (87),  Expect = 0.038, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+KG+KGD G  G KGD+G+ G  G  G +G  G  G K
Sbjct  87600  GDKGDVGDKGDVGDKGDKGDIGDKGDKGDLGDKGDKGDVGDKGDKGDVGDKGDKGDIGDK  87421

Query  102    GEPGE  106
              G+ G+
Sbjct  87420  GDKGD  87406


 Score = 37.7 bits (86),  Expect = 0.041, Method: Compositional matrix adjust.
 Identities = 24/55 (44%), Positives = 30/55 (55%), Gaps = 0/55 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
               G  G  G+ G  G  G  GT G+KG KGD G  G KG  G+ G+ G +G +G  G
Sbjct  239188  GTKGDKGNKGDKGNKGDKGTNGDKGNKGDKGSKGDKGTKGDKGIKGDKGDKGSKG  239352


 Score = 37.7 bits (86),  Expect = 0.041, Method: Compositional matrix adjust.
 Identities = 26/58 (45%), Positives = 31/58 (53%), Gaps = 0/58 (0%)
 Frame = +2

Query  48      GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
               G NG  G  G  G PG KG KG+ G  G KG  G+ G PG +G  G    +G KG+ G
Sbjct  293120  GENGDKGNKGDKGDPGIKGSKGEKGSKGDKGSKGDKGDPGIKGESGADADKGDKGDKG  293293


 Score = 37.7 bits (86),  Expect = 0.041, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 37/67 (55%), Gaps = 0/67 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G NG  G  G  G  G+KG KGD G IG KG  G+ G  G +G  G  G++G
Sbjct  237922  IKGDKGDIGDNGIKGDKGNKGDNGDKGNKGDKGDIGDKGMKGDKGDIGDKGDIGDKGMKG  238101

Query  100     RKGEPGE  106
                KG+ G+
Sbjct  238102  DKGDIGD  238122


 Score = 37.7 bits (86),  Expect = 0.041, Method: Compositional matrix adjust.
```

```
 Identities = 28/67 (42%), Positives = 37/67 (55%), Gaps = 0/67 (0%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  GEKG KGD G+ G KG  G+ G  G++G +G  G +G
Sbjct  883481  LKGDKGDKGDTGDIGLKGDKGDIGEKGIKGDKGINGSKGYKGDKGDKGSKGDKGNKGDKG  883302

Query  100     RKGEPGE  106
                KG+ G+
Sbjct  883301  SKGDKGD  883281


 Score = 37.7 bits (86),  Expect = 0.043, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+KG+KGD G  G KGD+G+ G  G  G +G  G +G
Sbjct  88392  GSKGDVGDKGDVGDKGDKGDTGDKGDKGDTGDKGDKGDVGDKGDKGDVGDKGDVGDKGDV  88213

Query  102    GEPGE  106
              G+ G+
Sbjct  88212  GDKGD  88198


 Score = 37.7 bits (86),  Expect = 0.043, Method: Compositional matrix adjust.
 Identities = 26/62 (42%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = -3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G+KG+KGD G  G KGD+G+ G  G +G  G  G +G  G+
Sbjct  88356  GDKGDKGDTGDKGDKGDTGDKGDKGDVGDKGDKGDVGDKGDVGDKGDVGDKGDKGDTGDK  88177

Query  105    GE  106
              G+
Sbjct  88176  GD  88171


 Score = 37.7 bits (86),  Expect = 0.043, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G  G KG+ G+ G  G KGDIG  G  G +G +G  G++G
Sbjct  878649  GDKGNVGDKGDIGIKGEKGDIGTKGDIGNKGDKGDKGDIGNKGNIGNKGEKGDKGVKGDI  878470

Query  102     GEPGE  106
               GE GE
Sbjct  878469  GEKGE  878455


 Score = 37.7 bits (86),  Expect = 0.044, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G  G  G DG  G  G  GE G  G  G KGD GE G  G +G +G  G  G K
Sbjct  238459  GIKGDKGDKGIKGDDGSKGDKGYNGEIGQKGDNGEKGDNGEKGDKGEKGDIGEK  238638
```

```
Query  102     GEPGE  106
               G+ GE
Sbjct  238639  GDNGE  238653


 Score = 37.7 bits (86),  Expect = 0.047, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G  G  G+ G KGD G IG KGD G  G  G +G +G  G++G K
Sbjct  883898  GDKGDIGNKGDKGDRGDKGIKGDAGLKGDKGDIGQKGDKGTKGDRGDKGEKGDAGLKGNK  883719

Query  102     GEPG  105
               G+ G
Sbjct  883718  GDIG  883707


 Score = 37.7 bits (86),  Expect = 0.047, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G  G KG KG+ G  G +GD G+ G  G +G  G  G +G K
Sbjct  879144  GDKGNDGIKGDFGSKGYKGDKGSKGTKGNNGFKGDRGDKGDKGSKGDKGDNGIKGNKGSK  878965

Query  102     GEPGE  106
               G+ G+
Sbjct  878964  GDKGD  878950


 Score = 37.7 bits (86),  Expect = 0.048, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G  G  G  G  G  G KG+KGD G  G KG  GE G+ G++G +G  G +G K
Sbjct  298911  GLKGENGDIGDKGDKGSKGEDGLKGDKGDIGDKGDKGSKGEDGLKGSKGDKGEIGNKGDK  299090

Query  102     GEPGE  106
               G+ G+
Sbjct  299091  GDKGD  299105


 Score = 37.7 bits (86),  Expect = 0.048, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KG KGD G  G KG+ G+ G  G +G +G  G +G
Sbjct  878136  GDKGDNGDKGDNGDKGNKGDNGDKGNKGDKGDNGDKGNKGDKGDNGDKGNKGDKGDKGDN  877957

Query  102     GEPGE  106
               G+ G+
Sbjct  877956  GDKGD  877942
```

```
 Score = 37.7 bits (86),  Expect = 0.048, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+ GEKGD G +G KG+ G+ G  G +G +G  G +G K
Sbjct  885617  GEKGEKGDKGDIGEKGEKGDKGDIGEKGDKGDLGEKGEKGDPGQKGEKGDKGDFGDKGDK  885438

Query  102     GEPGE  106
               G+ GE
Sbjct  885437  GDIGE  885423


 Score = 37.7 bits (86),  Expect = 0.049, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+KG+ GD G +G KGD+G+ G  G +G  G  G +G
Sbjct  87816  GDTGDKGDTGDKGDTGDKGDTGDKGDTGDKGDVGDKGDVGDKGDVGDKGDVGDKGDKGDI  87637

Query  102    GEPGE  106
              G+ G+
Sbjct  87636  GDKGD  87622


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 36/67 (54%), Gaps = 3/67 (4%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKG---DIGETGVPGAEGPRGFPGIQ  98
               G  G  G  G  G  G  G+ G+KG+KGD GL G  G   D G+ G  G++G +G  G
Sbjct  293291  GSKGDKGDKGIDGNKGEKGSKGDKGDKGDIGLKGESGADADKGDKGDKGSKGDKGDKGDI  293470

Query  99      GRKGEPG  105
               G KGE G
Sbjct  293471  GPKGESG  293491


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 28/68 (41%), Positives = 35/68 (51%), Gaps = 3/68 (4%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---IGPKGDIGETGVPGAEGPRGFPGIQ  98
              G  G  G  G  G  G  G  G+KG KGD G    +G KGD+G+ G  G  G +G  G
Sbjct  88482  GDQGDKGDQGDKGDQGDKGDVGDKGNKGDTGSKGDVGDKGDVGDKGDKGDTGDKGDKGDT  88303

Query  99     GRKGEPGE  106
              G KG+ G+
Sbjct  88302  GDKGDKGD  88279


 Score = 37.7 bits (86),  Expect = 0.052, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+KGD G  G KGDIGE G  G  G +G  G +G
```

```
Sbjct  885545  GEKGDKGDLGEKGEKGDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDIGDKGEIGNKGDV  885366

Query  102     GEPG  105
               GE G
Sbjct  885365  GEKG  885354


 Score = 37.7 bits (86),  Expect = 0.052, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 33/64 (52%), Gaps = 0/64 (0%)
 Frame = -1

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               + G  G  G  G DG  G  G+ G+KG  G  G KGD G  G  G +G +G  G  G KG
Sbjct  885200  LKGEKGDKGNKGIDGEKGNKGDTGDKGIDGSKGDKGDTGNKGDIGDKGDQGIKGDIGDKG  885021

Query  103     EPGE  106
               E G+
Sbjct  885020  EKGD  885009


 Score = 37.4 bits (85),  Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 37/67 (55%), Gaps = 0/67 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KG+KG+ G  G +GD G+ G+ G +G +G  G +G
Sbjct  239731  IKGENGLKGDVGDKGIKGDKGNEGDKGDKGNKGEKGNRGDEGDKGIKGNKGDKGIKGSEG  239910

Query  100     RKGEPGE  106
                KG  GE
Sbjct  239911  DKGIKGE  239931


 Score = 37.4 bits (85),  Expect = 0.055, Method: Compositional matrix adjust.
 Identities = 29/68 (43%), Positives = 35/68 (51%), Gaps = 3/68 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEK---GEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G NG  G  G +GT G+    G KGD G  G KGD G+ G  G +G +G  G
Sbjct  238171  GTKGDKGDNGIKGDKGDNGTKGDNGDNGTKGDKGDNGIKGDKGDKGTKGDKGDKGTKGDN  238350

Query  99      GRKGEPGE  106
               G KG  G+
Sbjct  238351  GDKGTKGD  238374


 Score = 37.4 bits (85),  Expect = 0.055, Method: Compositional matrix adjust.
 Identities = 25/63 (40%), Positives = 33/63 (52%), Gaps = 0/63 (0%)
 Frame = -3

Query  44      PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
                G  G+ G  G     G  G KG+KG+ G  G KGD G+ G  G +G  G  G +G KG+
Sbjct  878364  KGDKGNKGDKGDKSDKGDKGNKGDKGNKGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKGD  878185

Query  104     PGE  106
                G+
Sbjct  878184  NGD  878176
```

```
 Score = 37.4 bits (85),  Expect = 0.057, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G  G  G+ G+KG+ G IG KGD GE G+ G +G  G  G +G
Sbjct  885104  GDKGDTGNKGDIGDKGDQGIKGDIGDKGEKGDIGEKGDKGEKGIKGDKGDIGEKGNKGDI  884925

Query  102     GEPGE  106
               G+ GE
Sbjct  884924  GDKGE  884910


 Score = 37.4 bits (85),  Expect = 0.061, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G KG+ GD G +G KGD G+TG  G +G  G  G +G
Sbjct  88455  GDKGDQGDKGDVGDKGNKGDTGSKGDVGDKGDVGDKGDKGDTGDKGDKGDTGDKGDKGDV  88276

Query  102    GEPGE  106
              G+ G+
Sbjct  88275  GDKGD  88261


 Score = 37.4 bits (85),  Expect = 0.062, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 33/62 (53%), Gaps = 0/62 (0%)
 Frame = -3

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G+ G KGD G +G KGDIG  G  G  G +G  G +G KG+
Sbjct  878721  GLKGDKGEKGEKGNVGDKGDIGTKGDKGNVGDKGDIGIKGEKGDIGTKGDIGNKGDKGDK  878542

Query  105     GE  106
               G+
Sbjct  878541  GD  878536


 Score = 37.4 bits (85),  Expect = 0.064, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  G+KG+KGD G  G KGD+G+ G  G  G +G  G  G K
Sbjct  87627  GDKGDLGDKGDKGDVGDKGDVGDKGDKGDIGDKGDKGDLGDKGDKGDVGDKGDKGDVGDK  87448

Query  102    GEPGE  106
              G+ G+
Sbjct  87447  GDKGD  87433


 Score = 37.4 bits (85),  Expect = 0.065, Method: Compositional matrix adjust.
 Identities = 29/70 (41%), Positives = 35/70 (50%), Gaps = 5/70 (7%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRD-----GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
```

```
               GI G  G +G  G  G+D     G  GE G KGD G+ G  G  G  G PG +G  G  G
Sbjct  296020  GIKGDKGTDGIKGDKGQDNFGSKGQKGETGSKGDDGIKGITGSKGFKGDPGTKGENGING  296199

Query  97      IQGRKGEPGE  106
                +G KG  G+
Sbjct  296200  TKGLKGSQGD  296229


 Score = 37.0 bits (84),  Expect = 0.070, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KG+ GD G+ G KGDIG+ G+ G    +G  G  G K
Sbjct  238000  GNKGDKGDIGDKGMKGDKGDIGDKGDIGDKGMKGDKGDIGDKGMKGDNSTKGDKGDNGTK  238179

Query  102     GEPGE  106
               G+ G+
Sbjct  238180  GDKGD  238194


 Score = 37.0 bits (84),  Expect = 0.072, Method: Compositional matrix adjust.
 Identities = 24/61 (39%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = -3

Query  46      HPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
               + G  G  G  G     G+KG KGD G  G KG+ G+ G  G +G +G  G +G KG+ G
Sbjct  878367  NKGDKGNKGDKGDKSDKGDKGNKGDKGNKGDKGNKGDKGDNGDKGDKGDNGDKGNKGDKG  878188

Query  106     E  106
               +
Sbjct  878187  D  878185


 Score = 37.0 bits (84),  Expect = 0.072, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G KG KGD GL G KG  G+ G  G +G RG  G  G K
Sbjct  883799  GQKGDKGTKGDRGDKGEKGDAGLKGNKGDIGLKGDKGTKGDRGDKGTKGDRGDKGDIGNK  883620

Query  102     GEPGE  106
               G+ G+
Sbjct  883619  GDKGD  883605


 Score = 37.0 bits (84),  Expect = 0.074, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+ GEKG+ G IG KG+ G+ G+ G +G +G  G  G K
Sbjct  885023  GEKGDIGEKGDKGEKGIKGDKGDIGEKGNKGDIGDKGEKGDKGIDGDKGIKGDKGDIGEK  884844

Query  102     GEPGE  106
               G+ G+
Sbjct  884843  GDKGD  884829
```

```
 Score = 37.0 bits (84),  Expect = 0.074, Method: Compositional matrix adjust.
 Identities = 27/70 (39%), Positives = 34/70 (49%), Gaps = 0/70 (0%)
 Frame = -3

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
                 G  G  G  G  G  G  G  G+KGEKG+ G  G  GD G  G+ G  G +G+ G +G
Sbjct  879258  TTGDKGDKGDVGNKGDAGDKGDAGKKGEKGEMGNKGDIGDKGNDGIKGDFGSKGYKGDKG  879079

Query  100     RKGEPGEGAY  109
                KG  G   +
Sbjct  879078  SKGTKGNNGF  879049


 Score = 37.0 bits (84),  Expect = 0.077, Method: Compositional matrix adjust.
 Identities = 32/74 (43%), Positives = 36/74 (49%), Gaps = 9/74 (12%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---------IGPKGDIGETGVPGAEGPR  92
               GI G  G N   G  G  G  G+KG KGD G          IG KGD GE G  G +G
Sbjct  238414  GIKGESGANADKGDKGIKGDKGDKGIKGDDGSKGDKGYNGEIGQKGDNGEKGDNGEKGDN  238593

Query  93      GFPGIQGRKGEPGE  106
               G  G +G KG+ GE
Sbjct  238594  GEKGDKGEKGDIGE  238635


 Score = 37.0 bits (84),  Expect = 0.089, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G  G  G KG+KGD G  G KGD G+ G+ G  G +G  G  G+K
Sbjct  883970  GEKGDKGNKGDRGDKGIKGDIGSKGDKGDIGNKGDKGDRGDKGIKGDAGLKGDKGDIGQK  883791

Query  102     GEPG  105
               G+ G
Sbjct  883790  GDKG  883779


 Score = 36.6 bits (83),  Expect = 0.098, Method: Compositional matrix adjust.
 Identities = 27/68 (40%), Positives = 34/68 (50%), Gaps = 3/68 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGP---KGDIGETGVPGAEGPRGFPGIQ  98
               G  G  G  G  G  G  G  G+KG+KG  G IG    KGD G+ G+ G  G +G  G
Sbjct  296944  GESGDKGDIGIKGDKGAKGVTGDKGDKGTKGFIGNVGFKGDTGDKGIIGDNGSKGIKGSS  297123

Query  99      GRKGEPGE  106
                 KG+ G+
Sbjct  297124  NNKGDKGD  297147


 Score = 36.6 bits (83),  Expect = 0.098, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -1
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+ G+KGD G  G +GD GE G  G +G +G  G++G K
Sbjct  883871  GDKGDRGDKGIKGDAGLKGDKGDIGQKGDKGTKGDRGDKGEKGDAGLKGNKGDIGLKGDK  883692

Query  102     GEPGE  106
               G  G+
Sbjct  883691  GTKGD  883677


 Score = 36.6 bits (83),  Expect = 0.099, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
                G  G  G  G  G  G  G PG KGE G  G  G KG  G+ G  G +G +G  G +G
Sbjct  296104  TGSKGDDGIKGITGSKGFKGDPGTKGENGINGTKGLKGSQGDLGTKGDDGIKGIIGSKGI  296283

Query  101     KGEPG  105
               KG+PG
Sbjct  296284  KGDPG  296298


>NC_021308.1 Mycobacterium phage HINdeR, complete genome
Length=52617

 Score = 50.1 bits (118),  Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 33/59 (56%), Positives = 40/59 (68%), Gaps = 0/59 (0%)
 Frame = +3

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
             G PG  GAPG DG DG  G +G+ G  G+ GPKGD G+TG  G +GP+G  GIQG KG+
Sbjct  4083  GDPGDPGAPGADGADGAQGPQGDPGPQGIQGPKGDKGDTGDTGPQGPKGDQGIQGPKGD  4259


>NC_023607.1 Mycobacterium phage 40AC, complete genome
Length=53396

 Score = 50.1 bits (118),  Expect = 5e-06, Method: Compositional matrix adjust.
 Identities = 33/67 (49%), Positives = 42/67 (63%), Gaps = 0/67 (0%)
 Frame = +3

Query  40    MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
             + G  G  G  GA G  G+ G  G+KG+KGD GL GP+GD G  G  GA GP+G  G+QG
Sbjct  4944  LKGADGEQGPAGADGAQGQQGPKGDKGDKGDTGLQGPQGDPGPKGDTGATGPKGDTGLQG  5123

Query  100   RKGEPGE  106
              KG+ G+
Sbjct  5124  PKGDKGD  5144


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 34/76 (45%), Positives = 41/76 (54%), Gaps = 9/76 (12%)
 Frame = +3

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G  G  G  G +G DG  G KG+KGD G +GP+      G+ GA GPRG  G +G  GE
Sbjct  4704  GDTGATGPAGTNGVDGAQGPKGDKGDQGEMGPQ------GLTGATGPRGLEGPKGDTGER  4865
```

```
Query  105   GEGAYVYRSAFSVGLE  120
             G   Y   SA+ V LE
Sbjct  4866  GPLGY---SAYQVALE  4904


>NC_021772.1 Salmonella phage FSL SP-058, complete genome
Length=72394

 Score = 49.3 bits (116),  Expect = 7e-06, Method: Compositional matrix adjust.
 Identities = 32/73 (44%), Positives = 38/73 (52%), Gaps = 9/73 (12%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDP---------GLIGPKGDIGETGVPGAEGPR  92
              GI G  G NG  G +G DG  G+KG+KGD          GL G  G  G  GV G +G +
Sbjct  11471  GIDGKDGANGKDGINGIDGAKGDKGDKGDTGASGKDGKDGLNGTNGTNGRDGVDGKDGAK  11650

Query  93     GFPGIQGRKGEPG  105
              G  G QG +GE G
Sbjct  11651  GDTGAQGERGEQG  11689


 Score = 48.5 bits (114),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 37/128 (29%), Positives = 55/128 (43%), Gaps = 13/128 (10%)
 Frame = +2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDI------------GETGVPG  87
               +G  G  G NG  G +GRDG  G+ G KGD G  G +G+             GE G  G
Sbjct  11564  ASGKDGKDGLNGTNGTNGRDGVDGKDGAKGDTGAQGERGEQGIQGEAGKDGLNGENGKDG  11743

Query  88     AEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGST  147
                G  G  G +G KG+ G+      +  + G +  +T  N      K    +Q+ ++ ST
Sbjct  11744  LNGTNGLDGAKGDKGDEGKQGIAGIAGLN-GKDADMTQVNANTEANKSISKRQDAFEKST  11920

Query  148    GKFHCNIP  155
               +   N+
Sbjct  11921  NQRFANMD  11944


 Score = 47.0 bits (110),  Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G +GA G+DG +G  G KG+KGD G  G  G  G+ G+ G  G  G  G+ G+
Sbjct  11462  GKDGIDGKDGANGKDGINGIDGAKGDKGDKGDTGASGKDGKDGLNGTNGTNGRDGVDGKD  11641

Query  102    GEPGE  106
              G  G+
Sbjct  11642  GAKGD  11656


 Score = 46.2 bits (108),  Expect = 9e-05, Method: Compositional matrix adjust.
 Identities = 27/63 (43%), Positives = 32/63 (51%), Gaps = 0/63 (0%)
 Frame = +2

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              I G  G +G  G DG+DG  G+ G  G  G  G KGD G+TG  G +G  G  G  G  G
Sbjct  11438  IKGQNGKDGKDGIDGKDGANGKDGINGIDGAKGDKGDKGDTGASGKDGKDGLNGTNGTNG  11617
```

```
Query  103    EPG  105
                G
Sbjct  11618  RDG  11626


 Score = 45.4 bits (106),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 35/64 (55%), Gaps = 3/64 (5%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  GA G+DG+DG  G  G  G  G+ G  G  G+T   GA+G RG  GIQG
Sbjct  11534  GDKGDKGDTGASGKDGKDGLNGTNGTNGRDGVDGKDGAKGDT---GAQGERGEQGIQGEA  11704

Query  102    GEPG  105
              G+ G
Sbjct  11705  GKDG  11716


>NC_011356.1 Enterobacteria phage YYZ-2008, complete prophage genome
Length=54896

 Score = 49.3 bits (116),  Expect = 9e-06, Method: Compositional matrix adjust.
 Identities = 32/70 (46%), Positives = 39/70 (56%), Gaps = 0/70 (0%)
 Frame = +1

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              + G PG  G  G  G  G  G+KGE+GD G +G  G+ G  G  GA GP G  G QG KG
Sbjct  50290  VVGPPGPKGEQGPAGPQGPKGDKGERGDTGPVGATGERGPKGETGAAGPVGATGPQGPKG  50469

Query  103    EPGEGAYVYR  112
              +PGE    +R
Sbjct  50470  DPGETQIRFR  50499


>NC_022336.1 Propionibacterium phage PHL010M04, complete genome
Length=29511

 Score = 48.5 bits (114),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 32/76 (42%), Positives = 43/76 (57%), Gaps = 6/76 (8%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+ GE+G+ G  G  GP+G+ GE       GP+G  G+ G
Sbjct  15015  GVPGRAGDDGVNGADGRDGSAGERGDVGPSGSAGPQGERGE------RGPQGPAGVNGSD  15176

Query  102    GEPGEGAYVYRSAFSV  117
              G+ G+     RS  SV
Sbjct  15177  GKDGKDGRDGRSVVSV  15224


>NC_000852.5 Paramecium bursaria Chlorella virus 1, complete genome
Length=330611

 Score = 48.5 bits (114),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 30/88 (34%), Positives = 43/88 (49%), Gaps = 0/88 (0%)
 Frame = -3
```

```
Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GEKGEKGD G  G +G+ G+ G  G +G +G  G +G +GE
Sbjct  315729  GEKGDQGEKGDQGEKGDQGEKGEKGDQGEKGDQGEKGDQGEKGDQGEKGDQGEKGDQGEK  315550

Query  105     GEGAYVYRSAFSVGLETYVTIPNMPIRF  132
               G+   ++         T   + +M +R
Sbjct  315549  GDTTALFGFFRRKNASTPKNMEDMALRL  315466


 Score = 45.4 bits (106),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG++G+ G  G KGD GE G  G +G +G  G QG K
Sbjct  315729  GEKGDQGEKGDQGEKGDQGEKGEKGDQGEKGDQGEKGDQGEKGDQGEKGDQGEKGDQGEK  315550

Query  102     GE  103
               G+
Sbjct  315549  GD  315544


 Score = 37.4 bits (85),  Expect = 0.061, Method: Compositional matrix adjust.
 Identities = 21/42 (50%), Positives = 27/42 (64%), Gaps = 0/42 (0%)
 Frame = -3

Query  65      KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               KGEKGD G  G +G+ G+ G  G +G +G  G QG KG+ GE
Sbjct  315732  KGEKGDQGEKGDQGEKGDQGEKGEKGDQGEKGDQGEKGDQGE  315607


>NC_018285.1 Streptococcus phage YMC-2011, complete genome
Length=40758

 Score = 48.5 bits (114),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 30/59 (51%), Positives = 37/59 (63%), Gaps = 6/59 (10%)
 Frame = +2

Query  56    DGRDGTPGEKGEKGDPGLIGPKGDI---GETGVPGAEGPRGFPGIQGRKGEPGEGAYVY  111
             DGR+G    KG+KGDPG  GPKGD    GE G+ G +GP+G  GI G KG  G+  Y +
Sbjct  1409  DGRNGV---KGDKGDPGPAGPKGDRGLQGERGLQGLQGPKGDQGIPGVKGADGKTQYTH  1576


 Score = 38.9 bits (89),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 26/56 (46%), Positives = 30/56 (54%), Gaps = 0/56 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
             G  G  G  G PG  G  G  G +GE+G  GL GPKGD G  GV GA+G   +  I
Sbjct  1412  GRNGVKGDKGDPGPAGPKGDRGLQGERGLQGLQGPKGDQGIPGVKGADGKTQYTHI  1579


>NC_023639.1 Mimivirus terra2 genome
Length=1168989

 Score = 48.5 bits (114),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 38/65 (58%), Gaps = 0/65 (0%)
 Frame = -1
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G+KGEKGD GL G KGDIG+ G  G +G RG  G +G +
Sbjct  645750  GSKGDKGDIGQKGDKGTKGDRGDKGEKGDAGLKGDKGDIGQKGDKGIKGDRGDKGTKGDR  645571

Query  102     GEPGE  106
               G+ G+
Sbjct  645570  GDKGD  645556


 Score = 48.5 bits (114),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 32/65 (49%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  GEKGEKGD G  G KGD GE G+ G  G  G  G +G K
Sbjct  58972  GDNGEKGEKGDNGEKGEKGNNGEKGEKGDNGEKGEKGDNGEKGIKGDPGSNGSKGTKGEK  59151

Query  102    GEPGE  106
              GE G+
Sbjct  59152  GEKGD  59166


 Score = 47.8 bits (112),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 28/61 (46%), Positives = 37/61 (61%), Gaps = 0/61 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G+ G  G +G  G KG+KGDPG+ G KG+ G  G  G++G +G PGI+G
Sbjct  57982  GEKGDKGDKGSKGTKGENGDKGNKGDKGDPGIKGSKGEKGSKGDKGSKGDKGDPGIKGES  58161

Query  102    G  102
              G
Sbjct  58162  G  58164


 Score = 47.0 bits (110),  Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 32/80 (40%), Positives = 44/80 (55%), Gaps = 2/80 (3%)
 Frame = +2

Query  27     VLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVP  86
               L+   +GA      G+ G PG NG+ G  G  G  G+KG KG  G  G KGD G  G+
Sbjct  63305  TLVSNLRGAS--GAQGVKGDPGSNGSKGTKGEKGDKGDKGSKGVNGEKGEKGDAGLNGLD  63478

Query  87     GAEGPRGFPGIQGRKGEPGE  106
              G++G +G  G +G KG+ G+
Sbjct  63479  GSKGDKGDDGSKGSKGDKGD  63538


 Score = 46.6 bits (109),  Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 34/79 (43%), Positives = 39/79 (49%), Gaps = 3/79 (4%)
 Frame = +1

Query  40    MAGIPGHPGHNGAPGRDGRDGTP---GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
             + G  G  G NG  G  G  G+    G+KG KGD G  G KGD GETG+ G  G   F G
Sbjct  3082  LKGSQGEKGENGQKGLKGESGSSAFKGDKGSKGDKGNNGDKGDKGETGIKGESGSAVFKG  3261

Query  97    IQGRKGEPGEGAYVYRSAF  115
```

```
              +G KGE G       S F
Sbjct  3262  DKGDKGETGTKGESGSSVF  3318


 Score = 46.2 bits (108),  Expect = 7e-05, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             GI G  G  G  G  GR G  G+KG+ GD G  G KGDIG  G  G  G +G  G +G K
Sbjct  1373  GIKGDKGSKGDKGDKGRKGDKGDKGDIGDKGSKGDKGDIGAKGSKGDIGSKGSKGDKGSK  1552

Query  102   GEPGE  106
             G+ G+
Sbjct  1553  GDKGD  1567


 Score = 46.2 bits (108),  Expect = 9e-05, Method: Compositional matrix adjust.
 Identities = 31/67 (46%), Positives = 38/67 (57%), Gaps = 3/67 (4%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKG---DIGETGVPGAEGPRGFPGIQ  98
              G  G PG  G+ G  G  G  G KG+KGDPG+ G  G   D G+ G  G++G +G  GI
Sbjct  58054  GDKGDPGIKGSKGEKGSKGDKGSKGDKGDPGIKGESGADADKGDKGDKGSKGDKGDKGID  58233

Query  99     GRKGEPG  105
              G KGE G
Sbjct  58234  GNKGEKG  58254


 Score = 45.4 bits (106),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 30/64 (47%), Positives = 38/64 (59%), Gaps = 0/64 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G +G  G +G  G  G+KG KG+ GL G KGDIG+ G  G++G  G  G +G K
Sbjct  63827  GNKGDKGEDGLKGENGDIGDKGDKGSKGEDGLKGDKGDIGDKGDKGSKGEDGLKGSKGDK  64006

Query  102    GEPG  105
              GE G
Sbjct  64007  GEIG  64018


 Score = 45.4 bits (106),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 32/68 (47%), Positives = 39/68 (57%), Gaps = 3/68 (4%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGD---IGETGVPGAEGPRGFPGIQ  98
              G  G  G  G PG +G  GT GEKGEKGD G+ G KGD    G+TG+ G  G     G +
Sbjct  59080  GDNGEKGIKGDPGSNGSKGTKGEKGEKGDKGVNGDKGDKGSKGDTGIKGEAGTAANKGDK  59259

Query  99     GRKGEPGE  106
              G KG+ G+
Sbjct  59260  GSKGDKGD  59283


 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 33/64 (52%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
```

```
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G+ G  G  G  G DGT GEKGEKG  G  G KGD GE G+ G  G  G  G +G K
Sbjct  63728  GEKGNKGDKGDVGVKGDDGTKGEKGEKGTKGDKGNKGDKGEDGLKGENGDIGDKGDKGSK  63907

Query  102    GEPG  105
              GE G
Sbjct  63908  GEDG  63919


 Score = 44.7 bits (104),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 37/64 (58%), Gaps = 0/64 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G PG  G  G DG +G  G+ GEKGD G  G  G+ G TG  G +G +G  G++G K
Sbjct  3508  GDKGDPGIKGDKGSDGINGVKGDNGEKGDKGSKGDNGEKGSTGYNGEKGSKGDNGLKGSK  3687

Query  102   GEPG  105
             G+ G
Sbjct  3688  GDNG  3699


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 40/65 (62%), Gaps = 3/65 (5%)
 Frame = +2

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDI---GETGVPGAEGPRGFPGIQGRK  101
              G  G  G+ G DG  G+ G+KGE G+ G  G KGDI   G+ G  G +G +G PG++G K
Sbjct  63944  GDKGDKGSKGEDGLKGSKGDKGEIGNKGDKGDKGDIGIKGDKGDIGDKGDKGDPGLKGEK  64123

Query  102    GEPGE  106
              GE G+
Sbjct  64124  GEKGD  64138


 Score = 44.3 bits (103),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G   +KGEKGD G  G KG  GE G  G +G +G PGI+G K
Sbjct  57910  GDKGDKGEIGIQGLKGESGADADKGEKGDKGDKGSKGTKGENGDKGNKGDKGDPGIKGSK  58089

Query  102    GEPG  105
              GE G
Sbjct  58090  GEKG  58101


 Score = 43.9 bits (102),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = -3

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               I G  G  G  G  G  G  G+KG++GD G +G KGD G+TG  G  G +G  G  G KG
Sbjct  801097  IKGEKGDQGDKGDTGSKGDQGDKGDQGDKGDVGDKGDKGDTGSKGDVGDKGDKGDVGDKG  800918
```

```
Query  103     EPGE  106
               + G+
Sbjct  800917  DTGD  800906


 Score = 43.5 bits (101),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 30/69 (43%), Positives = 39/69 (57%), Gaps = 0/69 (0%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G NG+ G  G  G  G KG KGD G  G KGD+G+TG+ G++G +G  G +G
Sbjct  61644  GDKGSKGDNGSKGESGDKGIFGLKGSKGDIGDKGEKGDLGDTGLKGSKGLKGSKGDKGLV  61823

Query  102    GEPGEGAYV  110
                 GE  +V
Sbjct  61824  NVKGENGFV  61850


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 30/62 (48%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = -1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G PG+KGEKGD G  G KGD G+ G  G +G  G  G  G KG+
Sbjct  647424  GEKGDKGDLGEKGEKGDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDIGDKGESGDKGDV  647245

Query  105     GE  106
               GE
Sbjct  647244  GE  647239


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 31/71 (44%), Positives = 38/71 (54%), Gaps = 6/71 (8%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKG------DIGETGVPGAEGPRGFP  95
             GI G+ G  G  G  G  G    KG+KGD G+ G KG      D GETG+ G  G +G
Sbjct  4369  GIKGNKGDKGTQGIKGESGQAANKGDKGDKGIKGDKGNKGNKGDKGETGIKGNIGEKGLN  4548

Query  96    GIQGRKGEPGE  106
             G +G KG+ GE
Sbjct  4549  GDKGIKGDKGE  4581


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G  G+ G  G  G  G+KG KGD G+ G KGD G  G  G +G +G  G +G K
Sbjct  4819  GSKGDKGEKGSKGDKGNKGDNGDKGVKGDKGMKGDKGDKGNIGFKGDKGSKGDKGDKGIK  4998

Query  102   GEPG  105
             GE G
Sbjct  4999  GEKG  5010


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
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```
 Identities = 32/70 (46%), Positives = 39/70 (56%), Gaps = 3/70 (4%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGE---KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
             G  G  G  G+ G +G  G+ G+    KG KGD GL G KGD G  G  G +G +G  G +
Sbjct  3598  GSKGDNGEKGSTGYNGEKGSKGDNGLKGSKGDNGLKGSKGDNGLKGNKGVKGNKGDKGSK  3777

Query  99    GRKGEPGEGA  108
             G KG  GEGA
Sbjct  3778  GDKGNSGEGA  3807


 Score = 43.1 bits (100),  Expect = 9e-04, Method: Compositional matrix adjust.
 Identities = 28/61 (46%), Positives = 35/61 (57%), Gaps = 0/61 (0%)
 Frame = -1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G PG+ G  G  G+ G+KGD G IG KGD G+ G  G  G +G  G +G KG+
Sbjct  647397  GEKGEKGDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDIGDKGESGDKGDVGEKGDKGDK  647218

Query  105     G  105
               G
Sbjct  647217  G  647215


 Score = 43.1 bits (100),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 30/64 (47%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G  G  G  G  G  GEKG KGD GL G KGD G  G  G  G +G  G++G K
Sbjct  3580  GEKGDKGSKGDNGEKGSTGYNGEKGSKGDNGLKGSKGDNGLKGSKGDNGLKGNKGVKGNK  3759

Query  102   GEPG  105
             G+ G
Sbjct  3760  GDKG  3771


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 38/65 (58%), Gaps = 0/65 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G +G  G  G  G  G+KG KG+ GL G KGD GE G  G +G +G  GI+G K
Sbjct  63890  GDKGSKGEDGLKGDKGDIGDKGDKGSKGEDGLKGSKGDKGEIGNKGDKGDKGDIGIKGDK  64069

Query  102    GEPGE  106
              G+ G+
Sbjct  64070  GDIGD  64084


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G+ G+ G  G  G+ G+KG KGD G  G KGD G  G  G +G  GF G +G K
Sbjct  4792  GNKGDKGNKGSKGDKGEKGSKGDKGNKGDNGDKGVKGDKGMKGDKGDKGNIGFKGDKGSK  4971
```

```
Query  102   GEPGE  106
             G+ G+
Sbjct  4972  GDKGD  4986


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/62 (47%), Positives = 35/62 (56%), Gaps = 0/62 (0%)
 Frame = +2

Query  44    PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
              G  G+ G+ G  G  G  GEKG KG+ G  G KGD G  G  G +G +GF G +G KGE
Sbjct  1136  KGIKGNTGSKGDKGSKGDKGEKGSKGNKGDKGEKGDKGSKGEKGFKGEKGFKGEKGIKGE  1315

Query  104   PG  105
              G
Sbjct  1316  KG  1321


 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G  G  G  G  G  G+KGEKGD G  G KG  GE G  G +G +G  G +G K
Sbjct  1157  GSKGDKGSKGDKGEKGSKGNKGDKGEKGDKGSKGEKGFKGEKGFKGEKGIKGEKGSKGSK  1336

Query  102   GEPGE  106
             G+ G+
Sbjct  1337  GDKGD  1351


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 30/68 (44%), Positives = 35/68 (51%), Gaps = 0/68 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKGEKGD G IG KGD G+T   G +G +G  G +G
Sbjct  646713  GEKGEKGDKGDIGEKGNKGDIGEKGEKGDKGDIGEKGDKGDTSSKGDKGDKGEKGDKGDT  646534

Query  102     GEPGEGAY  109
                  G+  Y
Sbjct  646533  SSKGDKGY  646510


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G PG+ G +G  G +G  G+ GE G KGD G  G  G  G  G  G++G  G  GIQG
Sbjct  61224  IKGDPGNKGEDGIKGTNGLKGSKGETGSKGDDGTKGITGLKGTKGNSGSKGDDGDKGIQG  61403

Query  100    RKGE  103
               KGE
Sbjct  61404  LKGE  61415
```

```
 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 28/66 (42%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + GI G  G  G PG  G DG  G  G KG  G  G KGD G  G+ G +G +G  G +G
Sbjct  61197  IKGIIGSKGIKGDPGNKGEDGIKGTNGLKGSKGETGSKGDDGTKGITGLKGTKGNSGSKG  61376

Query  100    RKGEPG  105
                G+ G
Sbjct  61377  DDGDKG  61394


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 37/64 (58%), Gaps = 1/64 (2%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              GI G  G NG+ G  G  GT G KG+KG     G KG  GETG  G +G +G  G +G K
Sbjct  60927  GIKGMNGFNGSKGIKGDKGTDGIKGDKGQDNF-GSKGQKGETGSKGDDGIKGITGSKGFK  61103

Query  102    GEPG  105
              G+PG
Sbjct  61104  GDPG  61115


 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 27/57 (47%), Positives = 34/57 (60%), Gaps = 0/57 (0%)
 Frame = +2

Query  49    HNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
             + G  G  G  G  G KG+KG+ G  G KGD GE G  G++G +GF G +G KGE G
Sbjct  1133  NKGIKGNTGSKGDKGSKGDKGEKGSKGNKGDKGEKGDKGSKGEKGFKGEKGFKGEKG  1303


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 33/83 (40%), Positives = 40/83 (48%), Gaps = 18/83 (22%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTP------------------GEKGEKGDPGLIGPKGDIGET  83
               G PG  G  GA G  G  G                    GEKGEKGD G IG KG+ G+
Sbjct  647613  GDPGEKGEKGAKGDKGESGEKGAKGDKGDKGDKGDKGDIGEKGEKGDKGDIGEKGEKGDK  647434

Query  84      GVPGAEGPRGFPGIQGRKGEPGE  106
               G  G +G +G  G +G KG+PG+
Sbjct  647433  GDIGEKGDKGDLGEKGEKGDPGQ  647365


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/63 (48%), Positives = 35/63 (56%), Gaps = 0/63 (0%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G  G  G     G +G  G  G KG KGD G+IG KGDIG  G  GA+G  G  GI+G
Sbjct  61791  LKGSKGDKGLVNVKGENGFVGDLGSKGSKGDKGVIGDKGDIGIKGDKGAKGSIGDKGIKG  61970

Query  100    RKG  102
               KG
```

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Sbjct  61971  TKG  61979


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 25/53 (47%), Positives = 30/53 (57%), Gaps = 0/53 (0%)
 Frame = +2

Query  47    PGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              G  G  G  G  G  G KG+KGD G+ G KGDIG  G  G +G +G  GI+G
Sbjct  866   KGDKGTKGDKGNKGDKGNKGDKGDKGIKGDKGDIGAKGSKGDKGTKGDKGIKG  1024


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+ G  G  G  G  G  G  G KG+KG+ GL G  GDIG+ G  G++G  G  G +G
Sbjct  63764  GVKGDDGTKGEKGEKGTKGDKGNKGDKGEDGLKGENGDIGDKGDKGSKGEDGLKGDKGDI  63943

Query  102    GEPGE  106
              G+ G+
Sbjct  63944  GDKGD  63958


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 28/70 (40%), Positives = 40/70 (57%), Gaps = 0/70 (0%)
 Frame = +3

Query  37     TGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              T  + G+ G  G++G+ G DG  G  G KGE    G +G KGD G  G  G++G +G  G
Sbjct  61323  TKGITGLKGTKGNSGSKGDDGDKGIQGLKGEFSTKGNVGDKGDTGINGEKGSDGDKGNKG  61502

Query  97     IQGRKGEPGE  106
              + G KG+ G+
Sbjct  61503  LDGIKGDLGD  61532


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G  G  G  G  G  G KG+KGD G IG KG  G+ G  GA+G +G  G +G K
Sbjct  1355  GFKGDKGIKGDKGSKGDKGDKGRKGDKGDKGDIGDKGSKGDKGDIGAKGSKGDIGSKGSK  1534

Query  102   GEPG  105
             G+ G
Sbjct  1535  GDKG  1546


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G+ G  G  G  G+KG+KGD G  G KGDIG  G  G  G +G  G +G +
Sbjct  645867  GTSGEKGDLGSKGEKGDIGQKGDKGDKGDRGDRGIKGDIGSKGDKGDIGQKGDKGTKGDR  645688
```

```
Query  102     GEPGE  106
               G+ GE
Sbjct  645687  GDKGE  645673


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G+ G  G  G  G  G KG+KGD G IG KGD G  G  G +G +G  GI+G K
Sbjct  4846  GSKGDKGNKGDNGDKGVKGDKGMKGDKGDKGNIGFKGDKGSKGDKGDKGIKGEKGIKGDK  5025

Query  102   GEPGE  106
             G  G+
Sbjct  5026  GTKGD  5040


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G PG KGE G  G  G KG  GETG  G +G +G  G++G K
Sbjct  61176  GTKGDDGIKGIIGSKGIKGDPGNKGEDGIKGTNGLKGSKGETGSKGDDGTKGITGLKGTK  61355

Query  102    GEPGE  106
              G  G
Sbjct  61356  GNSGS  61370


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 33/65 (51%), Gaps = 3/65 (5%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGF---PGIQGRK  101
              G  G  G  G  G  G  GEKGEKG+ G  G KGD GE G  G  G +G    PG  G K
Sbjct  58954  GDKGEKGDNGEKGEKGDNGEKGEKGNNGEKGEKGDNGEKGEKGDNGEKGIKGDPGSNGSK  59133

Query  102    GEPGE  106
              G  GE
Sbjct  59134  GTKGE  59148


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 31/79 (39%), Positives = 40/79 (51%), Gaps = 12/79 (15%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG---  96
              + GI G  G  G PG  G +G  G KG KG  G +G KGD G  G+ G++G +G PG
Sbjct  61071  IKGITGSKGFKGDPGTKGENGINGTKGLKGSQGDLGTKGDDGIKGIIGSKGIKGDPGNKG  61250

Query  97     ---------IQGRKGEPGE  106
                       ++G KGE G
Sbjct  61251  EDGIKGTNGLKGSKGETGS  61307
```

```
 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G+ G NG  G  G  G  G+KG+KG+ G  G KG  G+ G  G +G +G  G +G K
Sbjct  4855  GDKGNKGDNGDKGVKGDKGMKGDKGDKGNIGFKGDKGSKGDKGDKGIKGEKGIKGDKGTK  5034

Query  102   GEPGE  106
             G+ G+
Sbjct  5035  GDKGD  5049


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKGEKGDPG  G KGD G+ G  G +G  G  G +G
Sbjct  647460  GEKGEKGDKGDIGEKGDKGDLGEKGEKGDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDI  647281

Query  102     GEPGE  106
               G+ GE
Sbjct  647280  GDKGE  647266


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 30/64 (47%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+ G  G  G  G  G  G  G KG KGD G IG KGD G+ G  G +G +G  G +G K
Sbjct  63917  GLKGDKGDIGDKGDKGSKGEDGLKGSKGDKGEIGNKGDKGDKGDIGIKGDKGDIGDKGDK  64096

Query  102    GEPG  105
              G+PG
Sbjct  64097  GDPG  64108


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 26/64 (41%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G+NG  G  G +G  GEKG+ G+ G+ G  G  G  G  G +G +G  G+ G K
Sbjct  59008  GEKGEKGNNGEKGEKGDNGEKGEKGDNGEKGIKGDPGSNGSKGTKGEKGEKGDKGVNGDK  59187

Query  102    GEPG  105
              G+ G
Sbjct  59188  GDKG  59199


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 28/56 (50%), Positives = 34/56 (61%), Gaps = 3/56 (5%)
 Frame = -1

Query  51      GAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               G  G  G  G  GEKGEKGD G IG KGD G+    G +G +G PG +G KG+ G+
```

```
Sbjct  647496  GEKGEKGDKGDIGEKGEKGDKGDIGEKGDKGDL---GEKGEKGDPGQKGEKGDKGD  647338


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +2

Query  44   PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
             G  G  G  G  G +G  G+KG+KG+ G  G KGDIG  G+ G  G   F G +G KG+
Sbjct  713  KGEKGSKGDKGYKGDEGIKGDKGDKGNKGDKGDKGDIGSQGIKGESGSAVFKGDKGTKGD  892

Query  104  PG  105
             G
Sbjct  893  KG  898


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 26/67 (39%), Positives = 38/67 (57%), Gaps = 0/67 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G +   G  G  G  G KG KG+ G  G KGD G+ G+ G++G +G  G +G
Sbjct  57940  IQGLKGESGADADKGEKGDKGDKGSKGTKGENGDKGNKGDKGDPGIKGSKGEKGSKGDKG  58119

Query  100    RKGEPGE  106
               KG+ G+
Sbjct  58120  SKGDKGD  58140


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = +1

Query  40    MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
             + G  G   + G  G  G  G  G KG KGD G  G KG+IGE G+ G +G +G  G  G
Sbjct  4408  IKGESGQAANKGDKGDKGIKGDKGNKGNKGDKGETGIKGNIGEKGLNGDKGIKGDKGETG  4587

Query  100   RKGEPGE  106
              KG+ GE
Sbjct  4588  TKGDIGE  4608


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G  G  G  G  G  GEKG KGD G  G KGD G+ G  G +G     G +G K
Sbjct  646740  GIKGDKGDIGEKGEKGDKGDIGEKGNKGDIGEKGEKGDKGDIGEKGDKGDTSSKGDKGDK  646561

Query  102     GEPGE  106
               GE G+
Sbjct  646560  GEKGD  646546


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 30/67 (45%), Positives = 35/67 (52%), Gaps = 3/67 (4%)
 Frame = +1
```

```
Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---IGPKGDIGETGVPGAEGPRGFPGIQG  99
              I G  G  G  G  G  G   +KGEKGDPG     G KGD G+TG+ G  G     G +G
Sbjct  58678  IKGDKGSKGDTGLKGESGADADKGEKGDPGNKGDKGSKGDKGDTGLKGESGADADKGDKG  58857

Query  100    RKGEPGE  106
               KGE G+
Sbjct  58858  DKGEKGD  58878


 Score = 40.0 bits (92),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 22/40 (55%), Positives = 28/40 (70%), Gaps = 0/40 (0%)
 Frame = +2

Query  63     GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              G KG KGD G  G KGD+G+TG+ G +G +G PGI+G  G
Sbjct  64700  GTKGVKGDKGSKGDKGDLGDTGIKGDKGEKGDPGIKGEAG  64819


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G  G  G  G  G  GEKG KG  G  G KG  G+ G+ G +G +G  G +GRK
Sbjct  1247  GSKGEKGFKGEKGFKGEKGIKGEKGSKGSKGDKGDKGFKGDKGIKGDKGSKGDKGDKGRK  1426

Query  102   GEPGE  106
             G+ G+
Sbjct  1427  GDKGD  1441


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  GEKGEKGD G  G KGD G  G  G +G +G  G +G
Sbjct  58999  GDNGEKGEKGNNGEKGEKGDNGEKGEKGDNGEKGIKGDPGSNGSKGTKGEKGEKGDKGVN  59178

Query  102    GEPGE  106
              G+ G+
Sbjct  59179  GDKGD  59193


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 30/64 (47%), Positives = 34/64 (53%), Gaps = 3/64 (5%)
 Frame = -1

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               I G  G  G  G  G  GT    GEKGD G  G KGDIG+ G  G +G RG  GI+G  G
Sbjct  645918  IKGDKGEKGDKGNTGDKGTS---GEKGDLGSKGEKGDIGQKGDKGDKGDRGDRGIKGDIG  645748

Query  103     EPGE  106
                 G+
Sbjct  645747  SKGD  645736
```

```
 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 27/50 (54%), Positives = 31/50 (62%), Gaps = 0/50 (0%)
 Frame = -1

Query  57      GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               G  G  GEKG KGD G  G KGDIG+ G  G +G  G  GI+G KG+ GE
Sbjct  646857  GNKGDIGEKGNKGDIGEKGNKGDIGDKGEKGDKGIDGDKGIKGDKGDIGE  646708


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 28/61 (46%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G+ G  G  G  G KGEKG  G  G KGDIG  G  GA+  +G  G +G KG+
Sbjct  58180  GDKGDKGSKGDKGDKGIDGNKGEKGSKGDKGDKGDIGLKGESGADADKGDKGDKGSKGDK  58359

Query  105    G  105
              G
Sbjct  58360  G  58362


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 29/62 (47%), Positives = 36/62 (58%), Gaps = 0/62 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G +G  G  G  G  GEKGEKGD G IG KG+ G+ G  G +G +G  G +G K
Sbjct  646776  GEKGDKGIDGDKGIKGDKGDIGEKGEKGDKGDIGEKGNKGDIGEKGEKGDKGDIGEKGDK  646597

Query  102     GE  103
               G+
Sbjct  646596  GD  646591


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G  G+ G  G  G  G+KG KG+ G  G KG  GE G+ G +G +G  G +G K
Sbjct  1175  GSKGDKGEKGSKGNKGDKGEKGDKGSKGEKGFKGEKGFKGEKGIKGEKGSKGSKGDKGDK  1354

Query  102   GEPGE  106
             G  G+
Sbjct  1355  GFKGD  1369


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+KGD G  G KGDIGE G  G  G +G  G +G
Sbjct  647424  GEKGDKGDLGEKGEKGDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDIGDKGESGDKGDV  647245

Query  102     GEPGE  106
               GE G+
```

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Sbjct  647244  GEKGD  647230


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G NG  G  G  G+ GE G KGD G IG KGD G  G  G +G +G  G  G K
Sbjct  63845  GEDGLKGENGDIGDKGDKGSKGEDGLKGDKGDIGDKGDKGSKGEDGLKGSKGDKGEIGNK  64024

Query  102    GEPGE  106
              G+ G+
Sbjct  64025  GDKGD  64039


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G  G  G  G  G  G KG+KGD G  G KGD G+ G  G++G +G  G +G K
Sbjct  1328  GSKGDKGDKGFKGDKGIKGDKGSKGDKGDKGRKGDKGDKGDIGDKGSKGDKGDIGAKGSK  1507

Query  102   GEPG  105
             G+ G
Sbjct  1508  GDIG  1519


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 24/56 (43%), Positives = 33/56 (59%), Gaps = 6/56 (11%)
 Frame = +3

Query  60     GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAF  115
              GT G KGEKG  G +GPKG+ G+ G  G++G R      G KGEP    + Y +++
Sbjct  56730  GTGGCKGEKGIKGELGPKGNTGQKGDTGSKGDR------GDKGEPTISMFSYINSY  56879


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 31/71 (44%), Positives = 36/71 (51%), Gaps = 6/71 (8%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPG------EKGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
              G  G  G NG  G  G  G PG      EKG KGD G  G KGD G  G  GA+  +G
Sbjct  58009  GSKGTKGENGDKGNKGDKGDPGIKGSKGEKGSKGDKGSKGDKGDPGIKGESGADADKGDK  58188

Query  96     GIQGRKGEPGE  106
              G +G KG+ G+
Sbjct  58189  GDKGSKGDKGD  58221


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 32/68 (47%), Positives = 37/68 (54%), Gaps = 3/68 (4%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKG---DPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               G  G+ G  G  G  G  G  GEKG+KG   D G+ G KGDIGE G  G +G  G  G +
Sbjct  646839  GEKGNKGDIGEKGNKGDIGDKGEKGDKGIDGDKGIKGDKGDIGEKGEKGDKGDIGEKGNK  646660
```

```
Query  99      GRKGEPGE  106
               G  GE GE
Sbjct  646659  GDIGEKGE  646636


 Score = 39.3 bits (90),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 30/70 (43%), Positives = 35/70 (50%), Gaps = 3/70 (4%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEK---GEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              + G  G  G  G  G  G D   GEK   G KGD G  G KGD G  G  GA+  +G  G
Sbjct  58678  IKGDKGSKGDTGLKGESGADADKGEKGDPGNKGDKGSKGDKGDTGLKGESGADADKGDKG  58857

Query  97     IQGRKGEPGE  106
               +G KG+ GE
Sbjct  58858  DKGEKGDKGE  58887


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G+ G  G  G  G+ GEKG KG+ G  G KG  GE G  G++G +G  G +G K
Sbjct  1193  GEKGSKGNKGDKGEKGDKGSKGEKGFKGEKGFKGEKGIKGEKGSKGSKGDKGDKGFKGDK  1372

Query  102   GEPGE  106
             G  G+
Sbjct  1373  GIKGD  1387


 Score = 39.3 bits (90),  Expect = 0.016, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G  GE G KG+ G IG KGD G  G  G +G +G  G +G K
Sbjct  63782  GTKGEKGEKGTKGDKGNKGDKGEDGLKGENGDIGDKGDKGSKGEDGLKGDKGDIGDKGDK  63961

Query  102    GEPGE  106
              G  GE
Sbjct  63962  GSKGE  63976


 Score = 39.3 bits (90),  Expect = 0.016, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G D   G+KG+KG  G  G KGDIG  G  GA+  +G  G +G K
Sbjct  58261  GDKGDKGDIGLKGESGADADKGDKGDKGSKGDKGNKGDIGPKGESGADADKGDKGDKGSK  58440

Query  102    GEPGE  106
              G+ G+
Sbjct  58441  GDKGD  58455
```

```
 Score = 39.3 bits (90),  Expect = 0.016, Method: Compositional matrix adjust.
 Identities = 28/60 (47%), Positives = 32/60 (53%), Gaps = 0/60 (0%)
 Frame = +2

Query  46     HPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
                G  G  G  G  G  GEKG KGD G +G KGD G  G  G +G +G  G +G KGE G
Sbjct  63677  SKGDKGITGDKGDKGEIGEKGNKGDKGDVGVKGDDGTKGEKGEKGTKGDKGNKGDKGEDG  63856


 Score = 39.3 bits (90),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G  G  G  G  G+ G KG+KGD G  G KG  G+ G  G +G +G  G +G K
Sbjct  1265  GFKGEKGFKGEKGIKGEKGSKGSKGDKGDKGFKGDKGIKGDKGSKGDKGDKGRKGDKGDK  1444

Query  102   GEPGE  106
             G+ G+
Sbjct  1445  GDIGD  1459


 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 34/66 (52%), Gaps = 1/66 (2%)
 Frame = +1

Query  44    PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
              G  G  G  G +G  G  G KG+KGDPG+ G KG  G  GV G  G +G  G +G  GE
Sbjct  3445  KGDKGDKGNSG-EGDKGDKGTKGDKGDPGIKGDKGSDGINGVKGDNGEKGDKGSKGDNGE  3621

Query  104   PGEGAY  109
              G   Y
Sbjct  3622  KGSTGY  3639


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 28/66 (42%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G  G     G  G  G  G+ G KGE GD G  G KGD G  G  G +G +G  G +G
Sbjct  57949  LKGESGADADKGEKGDKGDKGSKGTKGENGDKGNKGDKGDPGIKGSKGEKGSKGDKGSKG  58128

Query  100    RKGEPG  105
               KG+PG
Sbjct  58129  DKGDPG  58146


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 25/66 (38%), Positives = 33/66 (50%), Gaps = 0/66 (0%)
 Frame = -1

Query  65      KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVT  124
               KG+KGD G+ G KGD GE G  G +G +G PG    KGE G+      +  S+
Sbjct  646194  KGDKGDKGINGNKGDKGEKGDKGEKGDKGNPGTNAGKGEKGDKGDKGDAGTSILFGQGAP  646015

Query  125     IPNMPI  130
                PN  +
```

```
Sbjct  646014  DPNQGV  645997


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G D   G  G+KG KGD G  G KG+ G  G  G +G +G  GI+G K
Sbjct  58360  GNKGDIGPKGESGADADKGDKGDKGSKGDKGDKGTKGESGLIGTKGDKGDKGDEGIKGDK  58539

Query  102    GEPG  105
              GE G
Sbjct  58540  GEAG  58551


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 28/69 (41%), Positives = 39/69 (57%), Gaps = 3/69 (4%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---IGPKGDIGETGVPGAEGPRGFPG  96
                +G  G  G  G  G  G+ G  G+KG++GD G+   IG KGD G+ G  G +G +G  G
Sbjct  645864  TSGEKGDLGSKGEKGDIGQKGDKGDKGDRGDRGIKGDIGSKGDKGDIGQKGDKGTKGDRG  645685

Query  97      IQGRKGEPG  105
                +G KG+ G
Sbjct  645684  DKGEKGDAG  645658


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G+ G+KG+KG+ G  G KGD G+ G  G  G  GF G +G KGE
Sbjct  950218  GLKGSQGDQGYKGDQGSKGDKGQKGEFGNAGFKGDKGDMGQKGESGNVGFKGDKGDKGEG  950397

Query  105     GEGA  108
                +G+
Sbjct  950398  SKGS  950409


 Score = 38.9 bits (89),  Expect = 0.021, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G+ G  G  G  G D   G+KG+KG  G  G KG  GE+G+ G +G +G  G +G K
Sbjct  58351  GDKGNKGDIGPKGESGADADKGDKGDKGSKGDKGDKGTKGESGLIGTKGDKGDKGDEGIK  58530

Query  102    GEPGE  106
              G+ GE
Sbjct  58531  GDKGE  58545


 Score = 38.5 bits (88),  Expect = 0.023, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = -1
```

```
Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G DG  G  G+KG+ G+ G  G KGDIGE G  G  G +G  G +G  GE
Sbjct  646785  GDKGEKGDKGIDGDKGIKGDKGDIGEKGEKGDKGDIGEKGNKGDIGEKGEKGDKGDIGEK  646606

Query  105     GE  106
               G+
Sbjct  646605  GD  646600


 Score = 38.5 bits (88),  Expect = 0.023, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             GI G  G  G+ G  G  G  G+KG KGD G  G KGD G  G  G +G  G  G +G K
Sbjct  1301  GIKGEKGSKGSKGDKGDKGFKGDKGIKGDKGSKGDKGDKGRKGDKGDKGDIGDKGSKGDK  1480

Query  102   GEPG  105
             G+ G
Sbjct  1481  GDIG  1492


 Score = 38.5 bits (88),  Expect = 0.023, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G  G  G  G +G  G+KG KGD G  G  G  G+ G  G  G +G  G +G K
Sbjct  950485  GIKGDNGTKGDNGTKGDNGIKGDKGIKGDNGTKGDNGTKGDNGIKGDKGTKGDK  950664

Query  102     GEPGE  106
               G  G+
Sbjct  950665  GSKGD  950679


 Score = 38.5 bits (88),  Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 1/61 (2%)
 Frame = -1

Query  39      WMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               W+  I    G  G  G  G DG  G KG+ GD G+ G KGD G+TG  G  G +G  GI+
Sbjct  647097  WIP-ITNLKGEKGDKGNKGIDGEKGNKGDTGDKGIDGSKGDKGDTGNKGDIGDKGDQGIK  646921

Query  99      G  99
               G
Sbjct  646920  G  646918


 Score = 38.5 bits (88),  Expect = 0.026, Method: Compositional matrix adjust.
 Identities = 28/68 (41%), Positives = 35/68 (51%), Gaps = 3/68 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGE---KGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               GI G  G  G  G +G  G  G KG+   KGD G+ G  G  G+ G  G  G +G  GI+
Sbjct  950458  GIKGDKGSEGIKGDNGTKGDNGTKGDNGIKGDKGIKGDNGTKGDNGTKGDNGTKGDNGIK  950637

Query  99      GRKGEPGE  106
```

```
               G KG  G+
Sbjct  950638  GDKGTKGD  950661


 Score = 38.5 bits (88),  Expect = 0.026, Method: Compositional matrix adjust.
 Identities = 31/76 (41%), Positives = 37/76 (49%), Gaps = 8/76 (11%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPG-----LIGPKGDIGETGVPGAEGP---RG  93
             G+ G  G NG  G  G  G  G+KG KGD G       G KG+ GETG  G  G    +G
Sbjct  3697  GLKGSKGDNGLKGNKGVKGNKGDKGSKGDKGNSGEGAKGEKGEKGETGQKGESGSAVFKG  3876

Query  94    FPGIQGRKGEPGEGAY  109
               G +G KGE G   +
Sbjct  3877  DKGDKGSKGESGSAVF  3924


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = +1

Query  40    MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
             M G  G  G+ G  G  G  G  G+KG KG+ G+ G KG  G+ G  G +G +G  G +G
Sbjct  4912  MKGDKGDKGNIGFKGDKGSKGDKGDKGIKGEKGIKGDKGTKGDKGDKGVKGDKGIKGDKG  5091

Query  100   RKGEPGE  106
              KG  G+
Sbjct  5092  DKGNKGD  5112


 Score = 38.5 bits (88),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = -1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G+ G KGD G IG KGD G  G  G +G +G  G++G KG+
Sbjct  645813  GQKGDKGDKGDRGDRGIKGDIGSKGDKGDIGQKGDKGTKGDRGDKGEKGDAGLKGDKGDI  645634

Query  105     GE  106
               G+
Sbjct  645633  GQ  645628


 Score = 38.1 bits (87),  Expect = 0.031, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = +1

Query  40    MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
             + G  G  G  G  G  G  G  G KG+KGD G+ G KG  G+ G  G +G +G  G +G
Sbjct  4894  VKGDKGMKGDKGDKGNIGFKGDKGSKGDKGDKGIKGEKGIKGDKGTKGDKGDKGVKGDKG  5073

Query  100   RKGEPGE  106
              KG+ G+
Sbjct  5074  IKGDKGD  5094


 Score = 38.1 bits (87),  Expect = 0.031, Method: Compositional matrix adjust.
 Identities = 23/43 (53%), Positives = 27/43 (63%), Gaps = 0/43 (0%)
```

```
 Frame = -1

Query  60      GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               G  G+KG  GD GL G KGDIGE G+ G +G  G  G +G KG
Sbjct  645399  GDKGDKGNTGDIGLKGDKGDIGEKGIKGDKGINGSKGSKGDKG  645271


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 27/66 (41%), Positives = 35/66 (53%), Gaps = 0/66 (0%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G +GA    G  G  G KG+KG+ G IGPKG+ G     G +G +G  G +G KG
Sbjct  58288  GLKGESGADADKGDKGDKGSKGDKGNKGDIGPKGESGADADKGDKGDKGSKGDKGDKGTK  58467

Query  105    GEGAYV  110
              GE   +
Sbjct  58468  GESGLI  58485


 Score = 38.1 bits (87),  Expect = 0.034, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G DG  G  G KG+KGD G IG KG+ G     G +G +G  G +G K
Sbjct  58189  GDKGSKGDKGDKGIDGNKGEKGSKGDKGDKGDIGLKGESGADADKGDKGDKGSKGDKGNK  58368

Query  102    GEPG  105
              G+ G
Sbjct  58369  GDIG  58380


 Score = 38.1 bits (87),  Expect = 0.035, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 35/65 (54%), Gaps = 3/65 (5%)
 Frame = +2

Query  42    GIPGHPGH---NGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
             GI G  G     G  G  G  G  G+KG KGD G  G KGD G+ G  G++G +G  G +
Sbjct  833   GIKGESGSAVFKGDKGTKGDKGNKGDKGNKGDKGDKGIKGDKGDIGAKGSKGDKGTKGDK  1012

Query  99    GRKGE  103
             G KG+
Sbjct  1013  GIKGD  1027


 Score = 38.1 bits (87),  Expect = 0.036, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G+ G  G  G  G  G  G+ G+KG+KG  G  G KGD G  G  G +G +G  GI+G K
Sbjct  4909  GMKGDKGDKGNIGFKGDKGSKGDKGDKGIKGEKGIKGDKGTKGDKGDKGVKGDKGIKGDK  5088

Query  102   GEPG  105
             G+ G
Sbjct  5089  GDKG  5100
```

```
 Score = 38.1 bits (87),  Expect = 0.036, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G  G+KG KGD G IG KG+ G+ G  G +G +G  G +G K
Sbjct  646812  GEKGNKGDIGDKGEKGDKGIDGDKGIKGDKGDIGEKGEKGDKGDIGEKGNKGDIGEKGEK  646633

Query  102     GEPGE  106
               G+ G+
Sbjct  646632  GDKGD  646618


 Score = 38.1 bits (87),  Expect = 0.037, Method: Compositional matrix adjust.
 Identities = 26/62 (42%), Positives = 35/62 (56%), Gaps = 0/62 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G+ G+ G+KGD G +G KGD G+ G  G +G +G  G +G K
Sbjct  801028  GDQGDKGDVGDKGDKGDTGSKGDVGDKGDKGDVGDKGDTGDKGDIGDKGDKGDVGDKGDK  800849

Query  102     GE  103
               G+
Sbjct  800848  GD  800843


 Score = 38.1 bits (87),  Expect = 0.038, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+ GEKGD G +G KG+ G+ G  G +G +G  G +G K
Sbjct  647496  GEKGEKGDKGDIGEKGEKGDKGDIGEKGDKGDLGEKGEKGDPGQKGEKGDKGDFGDKGDK  647317

Query  102     GEPGE  106
               G+ GE
Sbjct  647316  GDIGE  647302


 Score = 38.1 bits (87),  Expect = 0.039, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G+ G  G  G  G  G  G KGEKG  G  G KGD G+ GV G +G +G  G +G K
Sbjct  4927  GDKGNIGFKGDKGSKGDKGDKGIKGEKGIKGDKGTKGDKGDKGVKGDKGIKGDKGDKGNK  5106

Query  102   GEPG  105
             G+ G
Sbjct  5107  GDKG  5118


 Score = 38.1 bits (87),  Expect = 0.039, Method: Compositional matrix adjust.
 Identities = 22/44 (50%), Positives = 29/44 (66%), Gaps = 0/44 (0%)
 Frame = +1

Query  60     GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
```

```
              G  G+KG+KGD GL G KGD G+ G  G +G +G  G +G KG+
Sbjct  59470  GLKGDKGDKGDVGLKGDKGDKGDVGSKGDKGDKGSKGDKGSKGD  59601


 Score = 37.7 bits (86),  Expect = 0.041, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G DG  G KG+KGD G  G KGD G+ G  G +G  G  G +G K
Sbjct  646803  GNKGDIGDKGEKGDKGIDGDKGIKGDKGDIGEKGEKGDKGDIGEKGNKGDIGEKGEKGDK  646624

Query  102     GEPGE  106
               G+ GE
Sbjct  646623  GDIGE  646609


 Score = 37.7 bits (86),  Expect = 0.041, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+ G  G  G  G  G  G  G KG+KGD G  G KG  GE G+ G++G +G  G +G K
Sbjct  63854  GLKGENGDIGDKGDKGSKGEDGLKGDKGDIGDKGDKGSKGEDGLKGSKGDKGEIGNKGDK  64033

Query  102    GEPGE  106
              G+ G+
Sbjct  64034  GDKGD  64048


 Score = 37.7 bits (86),  Expect = 0.042, Method: Compositional matrix adjust.
 Identities = 32/86 (37%), Positives = 38/86 (44%), Gaps = 21/86 (24%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGD---------------------PGLIGPKGDI  80
               G+ G  G+NG PG  G  G  G+KGE G+                      G  G KGDI
Sbjct  647640  GLKGEKGNNGDPGEKGEKGAKGDKGESGEKGAKGDKGDKGDKGDKGDIGEKGEKGDKGDI  647461

Query  81      GETGVPGAEGPRGFPGIQGRKGEPGE  106
               GE G  G +G  G  G +G  GE GE
Sbjct  647460  GEKGEKGDKGDIGEKGDKGDLGEKGE  647383


 Score = 37.7 bits (86),  Expect = 0.046, Method: Compositional matrix adjust.
 Identities = 37/112 (33%), Positives = 48/112 (43%), Gaps = 7/112 (6%)
 Frame = +1

Query  44    PGHPGHNGAPGRDGRDGTPGEKGEKGDPG---LIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              G  G  G  G +G  G  GE G KG+ G     G KGD GETG  G  G   F G +G
Sbjct  3157  KGDKGSKGDKGNNGDKGDKGETGIKGESGSAVFKGDKGDKGETGTKGESGSSVFKGDKGD  3336

Query  101   KGEPG----EGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTG  148
             KGE G     G+ V++       ET +   +    F     ++  N  +G  G
Sbjct  3337  KGETGTKGESGSAVFKGDKGDKGETGIKGESGSAVFKGDKGDKGNSGEGDKG  3492


 Score = 37.7 bits (86),  Expect = 0.052, Method: Compositional matrix adjust.
 Identities = 29/70 (41%), Positives = 35/70 (50%), Gaps = 5/70 (7%)
```

```
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRD-----GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              GI G  G +G  G  G+D     G  GE G KGD G+ G  G  G  G PG +G  G  G
Sbjct  60963  GIKGDKGTDGIKGDKGQDNFGSKGQKGETGSKGDDGIKGITGSKGFKGDPGTKGENGING  61142

Query  97     IQGRKGEPGE  106
               +G KG  G+
Sbjct  61143  TKGLKGSQGD  61172


 Score = 37.4 bits (85),  Expect = 0.053, Method: Compositional matrix adjust.
 Identities = 24/43 (56%), Positives = 26/43 (60%), Gaps = 0/43 (0%)
 Frame = +2

Query  45   GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPG  87
            G  G NG  G  G+ G  GEKGEKG+ G IG KGD GE G  G
Sbjct  203  GQKGDNGEKGEIGQKGDNGEKGEKGNNGEIGQKGDNGEKGDKG  331


 Score = 37.4 bits (85),  Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G  G  G  G  G  GEKG KG+ G+ G KG  G  G  G +G +G  GI+G K
Sbjct  1211  GNKGDKGEKGDKGSKGEKGFKGEKGFKGEKGIKGEKGSKGSKGDKGDKGFKGDKGIKGDK  1390

Query  102   GEPGE  106
             G  G+
Sbjct  1391  GSKGD  1405


 Score = 37.4 bits (85),  Expect = 0.055, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+ G+KGD G  G KGD+G+ G  G  G +G  G +G
Sbjct  801073  GDKGDTGSKGDQGDKGDQGDKGDVGDKGDKGDTGSKGDVGDKGDKGDVGDKGDTGDKGDI  800894

Query  102     GEPGE  106
               G+ G+
Sbjct  800893  GDKGD  800879


 Score = 37.4 bits (85),  Expect = 0.057, Method: Compositional matrix adjust.
 Identities = 26/63 (41%), Positives = 32/63 (51%), Gaps = 0/63 (0%)
 Frame = +1

Query  44    PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
              G  G  G  G  G  GT G KG KGD G  G KG+ G+    G +G +G  G +G KG
Sbjct  4312  KGDKGDKGNKGNKGDKGTQGIKGNKGDKGTQGIKGESGQAANKGDKGDKGIKGDKGNKGN  4491

Query  104   PGE  106
              G+
Sbjct  4492  KGD  4500
```

```
 Score = 37.4 bits (85),  Expect = 0.059, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 32/66 (48%), Gaps = 0/66 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G  G  G +   G  G  G  G KGE G     G KGD GETG+ G  G   F G +G K
Sbjct  3286  GTKGESGSSVFKGDKGDKGETGTKGESGSAVFKGDKGDKGETGIKGESGSAVFKGDKGDK  3465

Query  102   GEPGEG  107
             G  GEG
Sbjct  3466  GNSGEG  3483


 Score = 37.4 bits (85),  Expect = 0.062, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 35/64 (55%), Gaps = 3/64 (5%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G PG  G  G   +KG+KGD    G KGD G+ G+ G +G +G  G +G K
Sbjct  58108  GDKGSKGDKGDPGIKGESGADADKGDKGDK---GSKGDKGDKGIDGNKGEKGSKGDKGDK  58278

Query  102    GEPG  105
              G+ G
Sbjct  58279  GDIG  58290


 Score = 37.4 bits (85),  Expect = 0.063, Method: Compositional matrix adjust.
 Identities = 25/56 (45%), Positives = 31/56 (55%), Gaps = 0/56 (0%)
 Frame = +3

Query  44     PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               G  G  G  G  G  G+ GEKGEKG  G +G KG+ G  G+ G +G  G  GI+G
Sbjct  62127  KGIKGDKGIKGSKGDLGSVGEKGEKGTKGDVGTKGETGSKGIIGDKGELGSKGIKG  62294


 Score = 37.0 bits (84),  Expect = 0.070, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 33/64 (52%), Gaps = 0/64 (0%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G NG  G +G  G  G KG+KG  G  G KGD G  G  G +G  G  G +G K
Sbjct  950476  GSEGIKGDNGTKGDNGTKGDNGIKGDKGIKGDNGTKGDNGTKGDNGTKGDNGIKGDKGTK  950655

Query  102     GEPG  105
               G+ G
Sbjct  950656  GDKG  950667


 Score = 37.0 bits (84),  Expect = 0.071, Method: Compositional matrix adjust.
 Identities = 23/44 (52%), Positives = 27/44 (61%), Gaps = 0/44 (0%)
 Frame = +1

Query  62    PGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
              GEKG KGD G  G KGD GE G  G +G +G  G +G KG+ G
Sbjct  4780  KGEKGNKGDKGNKGSKGDKGEKGSKGDKGNKGDNGDKGVKGDKG  4911
```

```
 Score = 37.0 bits (84),  Expect = 0.081, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +3

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
               G  G  G  G  G  G  G PG KGE G  G  G KG  G+ G  G +G +G  G +G 
Sbjct  61047  TGSKGDDGIKGITGSKGFKGDPGTKGENGINGTKGLKGSQGDLGTKGDDGIKGIIGSKGI  61226

Query  101    KGEPG  105
              KG+PG
Sbjct  61227  KGDPG  61241


 Score = 37.0 bits (84),  Expect = 0.081, Method: Compositional matrix adjust.
 Identities = 22/46 (48%), Positives = 30/46 (65%), Gaps = 0/46 (0%)
 Frame = -1

Query  60      GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
               G  G+KG+KG+ G IG KGD G+ G  G +G +G  G +G KG+ G
Sbjct  645408  GLKGDKGDKGNTGDIGLKGDKGDIGEKGIKGDKGINGSKGSKGDKG  645271


 Score = 37.0 bits (84),  Expect = 0.085, Method: Compositional matrix adjust.
 Identities = 26/58 (45%), Positives = 31/58 (53%), Gaps = 0/58 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               G PG  G  G  G  G  G+ GEKGD G IG KG+ G+ G  G +G +G  G  G
Sbjct  647379  GDPGQKGEKGDKGDFGDKGDKGDIGEKGDKGDIGDKGESGDKGDVGEKGDKGDKGTDG  647206


 Score = 37.0 bits (84),  Expect = 0.086, Method: Compositional matrix adjust.
 Identities = 25/61 (41%), Positives = 32/61 (52%), Gaps = 0/61 (0%)
 Frame = +1

Query  44    PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
              G  G  G  G  G  G+   KG+KGD G  G KGD G  G+ G +G +G  GI+G  G+
Sbjct  4249  KGDKGDKGETGTKGESGSAVFKGDKGDKGNKGNKGDKGTQGIKGNKGDKGTQGIKGESGQ  4428

Query  104   P  104
             
Sbjct  4429  A  4431


 Score = 37.0 bits (84),  Expect = 0.087, Method: Compositional matrix adjust.
 Identities = 31/90 (34%), Positives = 44/90 (49%), Gaps = 14/90 (16%)
 Frame = -3

Query  31      LPKGACTG--WMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPG------------LIGP  76
               +P+G+  G   ++G  G  G  G+ G  G  G  G KGE+GD G             +G 
Sbjct  801589  VPQGSLKGDPGVSGSKGEKGDKGSSGEAGLKGEQGTKGEQGDQGEQGDKGDKGDKGDVGA  801410

Query  77      KGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               KGD G+ G  G  G +G  G +G KG+ G+
Sbjct  801409  KGDQGDKGDQGDVGAKGDQGDKGDKGDQGD  801320


 Score = 37.0 bits (84),  Expect = 0.092, Method: Compositional matrix adjust.
```

```
 Identities = 25/53 (47%), Positives = 31/53 (58%), Gaps = 0/53 (0%)
 Frame = -3

Query  54      GRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               G  G  G  G+KG+KGD G  G KGD+GE G  G  G +G  G  G KG+ G+
Sbjct  800182  GDKGDKGDLGDKGDKGDVGDKGDKGDVGEKGDKGDVGEKGDKGDIGDKGDKGD  800024


 Score = 36.6 bits (83),  Expect = 0.094, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 31/62 (50%), Gaps = 0/62 (0%)
 Frame = +1

Query  44      PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
                G  G  G  G  G  G  G+KG KGD G  G KGD G  G  G +G  G  G +G KG+
Sbjct  950392  EGSKGSKGDVGNKGDKGNKGDKGIKGDKGSEGIKGDNGTKGDNGTKGDNGIKGDKGIKGD  950571

Query  104     PG  105
                G
Sbjct  950572  NG  950577


 Score = 36.6 bits (83),  Expect = 0.095, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G++G KGD G  G KGDIG+ G  G +G RG  G +G
Sbjct  645840  GSKGEKGDIGQKGDKGDKGDRGDRGIKGDIGSKGDKGDIGQKGDKGTKGDRGDKGEKGDA  645661

Query  102     GEPGE  106
               G  G+
Sbjct  645660  GLKGD  645646


 Score = 36.6 bits (83),  Expect = 0.099, Method: Compositional matrix adjust.
 Identities = 35/93 (38%), Positives = 41/93 (44%), Gaps = 22/93 (24%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPG------------LIGPKGDIGET  83
             G  G  G+NG  G  G  G  GE      KG+KGD G              G KGD GET
Sbjct  3169  GSKGDKGNNGDKGDKGETGIKGESGSAVFKGDKGDKGETGTKGESGSSVFKGDKGDKGET  3348

Query  84    GVPGAEGPRGFPGIQGRKGEPG----EGAYVYR  112
             G  G  G   F G +G KGE G     G+ V++
Sbjct  3349  GTKGESGSAVFKGDKGDKGETGIKGESGSAVFK  3447


 Score = 36.6 bits (83),  Expect = 0.099, Method: Compositional matrix adjust.
 Identities = 24/53 (45%), Positives = 29/53 (55%), Gaps = 0/53 (0%)
 Frame = +1

Query  53    PGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
              G  G  G  G KG KGD G  G KGD G  G  G +G +G  G++G KG+ G
Sbjct  4780  KGEKGNKGDKGNKGSKGDKGEKGSKGDKGNKGDNGDKGVKGDKGMKGDKGDKG  4938


>NC_031279.1 Mycobacterium phage Bactobuster, complete genome
Length=52129
```

```
 Score = 48.1 bits (113),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 32/62 (52%), Positives = 36/62 (58%), Gaps = 0/62 (0%)
 Frame = +1

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G PG  G PG  G  G  G  G KGD G  GP+G IG+TG  GA G  G PG QG KG+
Sbjct  4408  GEPGPQGVPGLQGPQGIQGPAGPKGDKGDTGPQGPIGDTGATGAPGTPGAPGAQGPKGDK  4587

Query  105   GE  106
             G+
Sbjct  4588  GD  4593


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 35/76 (46%), Positives = 43/76 (57%), Gaps = 9/76 (12%)
 Frame = +1

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G  G  GAPG  G  G  G KG+KGD G +GP+      G+ G +GPRGF G QG +G+
Sbjct  4516  GDTGATGAPGTPGAPGAQGPKGDKGDQGEMGPQ------GLTGPQGPRGFEGPQGIEGQR  4677

Query  105   GEGAYVYRSAFSVGLE  120
             G   Y   SA+ V LE
Sbjct  4678  GPLGY---SAYGVALE  4716


>NC_018842.1 Propionibacterium phage P1.1, complete genome
Length=29348

 Score = 47.8 bits (112),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 37/95 (39%), Positives = 51/95 (54%), Gaps = 10/95 (11%)
 Frame = +2

Query  42     GIPGHPGH---NGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
              G+PG  G    NG  G DGRDG+ GE+G+ G  G  GP+G  GE G  G  GP+G PG
Sbjct  15026  GVPGRAGADGVNGVDGADGRDGSAGERGDVGPSGPAGPQGAQGERGPAGPVGPQGSPGAD  15205

Query  99     GRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              G  G+ G+     RS  SV    Y +   + ++++
Sbjct  15206  GTNGKDGKDG---RSVVSV----YCSGGRLAVKYS  15289


>NC_016071.1 Salmonella phage PVP-SE1, complete genome
Length=145964

 Score = 47.8 bits (112),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 34/92 (37%), Positives = 49/92 (53%), Gaps = 8/92 (9%)
 Frame = -3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G +G  G +G +G  G IGPKGD G+TG+ G  GP+G  G +G +GE
Sbjct  52494  GQKGDQGPEGPAGAEGPAGAEGPQGIQGPIGPKGDKGDTGLTGPVGPQGPQGPKGDRGET  52315

Query  105    GEGAYVYRSAFSVGL--------ETYVTIPNM  128
              G GA V  +  +V          + ++ +PN+
Sbjct  52314  GYGARVLGTKGAVSDLPATGTPGDAWIIVPNL  52219
```

```
>NC_027351.1 Salmonella phage SSE-121, complete genome
Length=147745

 Score = 47.8 bits (112),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 34/92 (37%), Positives = 49/92 (53%), Gaps = 8/92 (9%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G +G  G +G +G  G IGPKGD G+TG+ G  GP+G  G +G +GE
Sbjct  14841  GQKGDQGPEGPAGAEGPAGAEGPQGIQGPIGPKGDKGDTGLTGPVGPQGPQGPKGDRGET  15020

Query  105    GEGAYVVYRSAFSVGL--------ETYVTIPNM  128
              G GA V  +  +V           + ++ +PN+
Sbjct  15021  GYGARVLGTKGAVSDLPATGTPGDAWIIVPNL  15116


>NC_027628.1 Propionibacterium phage Lauchelly, complete genome
Length=29517

 Score = 47.4 bits (111),  Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 31/82 (38%), Positives = 41/82 (50%), Gaps = 3/82 (4%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG+DG  G  GE+GD   +GP G +G  G  G  G RG  G+ G
Sbjct  15036  GVPGRAGADGVNGSDGKDGANGADGERGD---VGPSGPVGPQGAQGERGERGPDGVNGSD  15206

Query  102    GEPGEGAYVYRSAFSVGLETYV  123
              G+ G       S +  G   +V
Sbjct  15207  GKDGANGRSVVSVYCSGGRLFV  15272


>NC_018840.1 Propionibacterium phage P100_1, complete genome
Length=29612

 Score = 47.0 bits (110),  Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 36/94 (38%), Positives = 49/94 (52%), Gaps = 7/94 (7%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              ++G  G  G NGA G+DGRDG+ GE+GE G  G  GP+G  GE    G  GP G  G  G
Sbjct  15042  VSGRAGVDGVNGADGKDGRDGSAGERGEVGPSGPAGPQGAQGER---GERGPAGVNGSDG  15212

Query  100    RKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              + G  G      RS  SV    Y +   + ++++
Sbjct  15213  KDGTDGADGRDGRSVISV----YCSGGRLVVKYS  15302


>NC_022087.1 Mycobacterium phage AnnaL29, complete genome
Length=53253

 Score = 47.0 bits (110),  Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 32/62 (52%), Positives = 35/62 (56%), Gaps = 0/62 (0%)
 Frame = +2

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G PG  G  G  G  G  G KG+KGD G  GPKGD G  G PGA G  G  G +G KG+
```

```
Sbjct  4586  GEPGPQGLQGPKGDTGPAGPKGDKGDTGEQGPKGDTGAAGTPGAPGATGAQGPKGDKGDQ  4765

Query  105   GE  106
             GE
Sbjct  4766  GE  4771


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 33/73 (45%), Positives = 39/73 (53%), Gaps = 9/73 (12%)
 Frame = +2

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEG  107
             G  G PG  G  G  G KG+KGD G +GP+      G+ GA GPRG  G +G  GE G
Sbjct  4694  GAAGTPGAPGATGAQGPKGDKGDQGEMGPQ------GLTGATGPRGLEGPKGDTGERGPL  4855

Query  108   AYVYRSAFSVGLE  120
              Y   SA+ V LE
Sbjct  4856  GY---SAYQVALE  4885


>NC_021795.1 Cellulophaga phage phi17:1, complete genome
Length=38776

 Score = 46.6 bits (109),  Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 39/99 (39%), Positives = 49/99 (49%), Gaps = 10/99 (10%)
 Frame = +3

Query  18     QETTTQGP-------GVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGD  70
              ++ TTQG        G+L+ L      G   G  G  G  G  G  G  G  G KG+ GD
Sbjct  26205  RDETTQGANTAERVGGILVDLSTALEEGGAVGPAGPQGEQGIQGEQGIQGEQGVKGDTGD  26384

Query  71     PG---LIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               G   + G +G+ GETG  G +G  G  GIQG +GEPGE
Sbjct  26385  TGPQGIQGIQGEPGETGPQGIQGETGPQGIQGIQGEPGE  26501


 Score = 43.9 bits (102),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 31/73 (42%), Positives = 38/73 (52%), Gaps = 6/73 (8%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGR------DGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
              + GI G PG  G  G  G        G  GE GE G  G+ G KGD G+TG  G +G +G
Sbjct  26400  IQGIQGEPGETGPQGIQGETGPQGIQGIQGEPGEDGAQGIQGIKGDTGDTGPQGLQGIQG  26579

Query  94     FPGIQGRKGEPGE  106
                G+QG +G  GE
Sbjct  26580  AAGLQGEQGIQGE  26618


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+ G  G  G  G  G  G PGE G +G  G  GP+G  G  G PG +G +G  GI+G
Sbjct  26361  GVKGDTGDTGPQGIQGIQGEPGETGPQGIQGETGPQGIQGIQGEPGEDGAQGIQGIKGDT  26540

Query  102    GEPG  105
```

```
              G+ G
Sbjct  26541  GDTG  26552


>NC_028965.1 Mycobacterium phage Pioneer, complete genome
Length=53219

 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 31/59 (53%), Positives = 37/59 (63%), Gaps = 3/59 (5%)
 Frame = +1

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
             G PG  GA G  G  G PGE G +GDPG  GP+G  G+T   GA+GP+G  G QG KG+
Sbjct  4873  GDPGTAGATGLTGSAGAPGEPGPQGDPGPTGPQGPKGDT---GAQGPKGDTGAQGPKGD  5040


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 33/64 (52%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             GI G  G  G  G  G  G  GEKG+KGD G  GPKGD G+ G PG  G  G  G  G
Sbjct  4747  GIQGATGPQGLQGPKGDQGIQGEKGDKGDLGPQGPKGDKGDKGDPGTAGATGLTGSAGAP  4926

Query  102   GEPG  105
             GEPG
Sbjct  4927  GEPG  4938


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 35/96 (36%), Positives = 45/96 (47%), Gaps = 12/96 (13%)
 Frame = +1

Query  41    AGIPGHPGHNGAPGRDGRDGTPGE------------KGEKGDPGLIGPKGDIGETGVPGA  88
             AG PG PG  G PG  G  G  G+            +G KGD G  GPKGD G TG  G+
Sbjct  4915  AGAPGEPGPQGDPGPTGPQGPKGDTGAQGPKGDTGAQGPKGDTGAQGPKGDTGATGATGS  5094

Query  89    EGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVT  124
             +GP+G  G         +   V ++A+  G +T  T
Sbjct  5095  QGPQGPSGTPSSTNTVLDFVKVTQAAYDAGPKTATT  5202


 Score = 39.3 bits (90),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 30/62 (48%), Positives = 35/62 (56%), Gaps = 0/62 (0%)
 Frame = +1

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G PG  G  G  G  G  G  G KGD G  GP+G  G TG  G +GP+G  GIQG KG+
Sbjct  4648  GDPGDTGPTGATGPAGPQGATGPKGDTGAQGPQGIQGATGPQGLQGPKGDQGIQGEKGDK  4827

Query  105   GE  106
             G+
Sbjct  4828  GD  4833


 Score = 37.4 bits (85),  Expect = 0.059, Method: Compositional matrix adjust.
 Identities = 27/59 (46%), Positives = 32/59 (54%), Gaps = 0/59 (0%)
 Frame = +1
```

```
Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
             G  G  G  G  G  G+KG+KGDPG  G  G  G  G PG  GP+G PG  G +G  G+
Sbjct  4810  GEKGDKGDLGPQGPKGDKGDKGDPGTAGATGLTGSAGAPGEPGPQGDPGPTGPQGPKGD  4986


>NC_020104.1 Acanthamoeba polyphaga moumouvirus, complete genome
Length=1021348

 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 31/68 (46%), Positives = 39/68 (57%), Gaps = 0/68 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G     G+KG++GD G  G KGD G+ G+ G +G +G  GIQG K
Sbjct  211289  GQKGAKGEQGIKGESGEVAFKGDKGDQGDQGTKGDKGDKGDQGINGEKGEKGDRGIQGIK  211468

Query  102     GEPGEGAY  109
               GE GE A+
Sbjct  211469  GESGEVAF  211492


 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 30/75 (40%), Positives = 41/75 (55%), Gaps = 9/75 (12%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPR-------  92
               + G  G  G NG  G  G  G  G+KG+KGD G+ G KGD G+ G+ G +G +
Sbjct  218327  VNGQKGDKGQNGVKGLKGNKGEKGDKGDKGDLGVNGQKGDKGQNGIKGLKGNKGEKGDKG  218506

Query  93      --GFPGIQGRKGEPG  105
                 GF G++G KG+ G
Sbjct  218507  ELGFRGLKGDKGDKG  218551


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 37/67 (55%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
                 G  G  G NG  G  G++G  G KG KG+ G  G KGD+G  G  G +G  G  G++G
Sbjct  218300  QKGDKGDLGVNGQKGDKGQNGVKGLKGNKGEKGDKGDKGDLGVNGQKGDKGQNGIKGLKG  218479

Query  100     RKGEPGE  106
                KGE G+
Sbjct  218480  NKGEKGD  218500


 Score = 44.3 bits (103),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 31/68 (46%), Positives = 38/68 (56%), Gaps = 3/68 (4%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGD---PGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
               GI G  G  G  G  G  G  G+KG KGD    G+ G KGD+G+ G+ G  G +G  G +
Sbjct  219278  GIKGDLGDKGIKGDKGDKGDLGDKGIKGDLGDKGIKGDKGDLGDKGIKGDLGDKGIKGDK  219457

Query  99      GRKGEPGE  106
               G KGE GE
```

```
Sbjct  219458  GDKGEKGE  219481


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 37/131 (28%), Positives = 57/131 (44%), Gaps = 21/131 (16%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KG+ GD GL G KGD+G+ G+ G +G  G  G++G K
Sbjct  212651  GEKGDKGEKGNLGEIGLKGDKGDKGDLGDEGLKGDKGDLGDEGLKGDKGDLGDEGLKGDK  212830

Query  102     GEPGE-------GAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNI  154
               G  G+       G+ ++         T V  P+  +      Y   N+     G  +
Sbjct  212831  GNKGDLGDKGDNGSRIF---------TGVGTPSSFLGVNGDIYIDNNN-----GNLYIKT  212968

Query  155     PGLYYFAYHIT  165
                G++    ++T
Sbjct  212969  SGIWVLQTNLT  213001


 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+KGD G  G KGD G+ G  G +G +G  G +G K
Sbjct  214586  GDKGEKGDLGEKGDKGEKGDLGEKGDKGDLGDKGEKGDKGDLGEKGEKGDKGEKGDKGEK  214765

Query  102     GEPGE  106
               G+ GE
Sbjct  214766  GDLGE  214780


 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+KG+ G +G KGD G+ G  G +G +G  G +G K
Sbjct  214550  GEKGEKGDLGDKGDKGEKGDLGEKGDKGEKGDLGEKGDKGDLGDKGEKGDKGDLGEKGEK  214729

Query  102     GEPGE  106
               G+ GE
Sbjct  214730  GDKGE  214744


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 39/66 (59%), Gaps = 5/66 (8%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGT-----PGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               G+PG+ G  G  G  G       G+KG+KGD G+ G KGD G+ GV G +G +G  G +G
Sbjct  218228  GYPGYRGIKGEKGNSGNINNDIKGQKGDKGDLGVNGQKGDKGQNGVKGLKGNKGEKGDKG  218407

Query  100     RKGEPG  105
                KG+ G
Sbjct  218408  DKGDLG  218425
```

```
 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 38/65 (58%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G+ G  G  G  G  G  G KG KGD G +G KGD+G+ G+ G +G +G  G +G K
Sbjct  218567  GSKGNKGDKGNLGDKGDLGDKGIKGNKGDKGDLGDKGDLGDKGIKGNKGDKGDLGDKGDK  218746

Query  102     GEPGE  106
               G+ G+
Sbjct  218747  GDLGD  218761


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G +G KG+ G+ G  G +G +G  G +G K
Sbjct  214613  GEKGDKGEKGDLGEKGDKGDLGDKGEKGDKGDLGEKGEKGDKGEKGDKGEKGDLGEKGEK  214792

Query  102     GEPGE  106
               G+ G+
Sbjct  214793  GDKGD  214807


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KGEKGD G  G KGD+G+ G  G +G  G  G +G K
Sbjct  214559  GEKGDLGDKGDKGEKGDLGEKGDKGEKGDLGEKGDKGDLGDKGEKGDKGDLGEKGEKGDK  214738

Query  102     GEPGE  106
               GE G+
Sbjct  214739  GEKGD  214753


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 31/71 (44%), Positives = 40/71 (56%), Gaps = 6/71 (8%)
 Frame = +2

Query  42      GIPGHPGH---NGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG---FP  95
               GI G  G     G  G  G  GT G+KG+KGD G+ G KG+ G+ G+ G +G  G   F
Sbjct  211316  GIKGESGEVAFKGDKGDQGDQGTKGDKGDKGDQGINGEKGEKGDRGIQGIKGESGEVAFK  211495

Query  96      GIQGRKGEPGE  106
               G +G KG+ GE
Sbjct  211496  GEKGDKGDLGE  211528


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
```

```
               G  G  G  G  G  G  G  G+KG+KG+ G +G KGD GE G  G +G +G  G +G K
Sbjct  214514  GEKGDKGDKGDLGEKGEKGDLGDKGDKGEKGDLGEKGDKGEKGDLGEKGDKGDLGDKGEK  214693

Query  102     GEPGE  106
               G+ G+
Sbjct  214694  GDKGD  214708


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKGEKGD G  G KG+ G+ G  G +G +G  G +G K
Sbjct  214649  GEKGDKGDLGDKGEKGDKGDLGEKGEKGDKGEKGDKGEKGDLGEKGEKGDKGDLGDKGEK  214828

Query  102     GEPGE  106
               G+ GE
Sbjct  214829  GDLGE  214843


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 28/63 (44%), Positives = 36/63 (57%), Gaps = 0/63 (0%)
 Frame = +2

Query  43      IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               I G  G  G  G  G  G  G+KG+KGD G  G KGD+G+ G+ G +G  G  GI+G  G
Sbjct  219254  IKGDLGDKGIKGDLGDKGIKGDKGDKGDLGDKGIKGDLGDKGIKGDKGDLGDKGIKGDLG  219433

Query  103     EPG  105
               + G
Sbjct  219434  DKG  219442


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G  G  G  G  G  GEKG+KG+ G  G KGD G+ G+ G  G +G  G +G
Sbjct  218423  GVNGQKGDKGQNGIKGLKGNKGEKGDKGELGFRGLKGDKGDKGIKGDLGSKGNKGDKGNL  218602

Query  102     GEPGE  106
               G+ G+
Sbjct  218603  GDKGD  218617


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 28/65 (43%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+ GEKGD G +G KG+ G+ G  G +G +G  G +G K
Sbjct  214577  GDKGDKGEKGDLGEKGDKGEKGDLGEKGDKGDLGDKGEKGDKGDLGEKGEKGDKGEKGDK  214756

Query  102     GEPGE  106
               GE G+
Sbjct  214757  GEKGD  214771
```

```
 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 26/58 (45%), Positives = 32/58 (55%), Gaps = 0/58 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               G  G  G  G  G  G  G+KG KGD G +G KGD+G+ G+ G  G +G  G  G KG
Sbjct  157475  GDKGDKGNLGDKGDKGDLGDKGIKGDKGDLGDKGDLGDKGIKGDLGDKGIKGDLGDKG  157648


 Score = 40.4 bits (93),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 38/67 (57%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G +   G  G  G  GEKG+KGD G +G KG+ G+ G  G +G +G  G +G
Sbjct  214445  IKGEKGEAGVDAEQGDKGDKGDLGEKGDKGDKGDLGEKGEKGDLGDKGDKGEKGDLGEKG  214624

Query  100     RKGEPGE  106
                KGE G+
Sbjct  214625  DKGEKGD  214645


 Score = 40.0 bits (92),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  G+KG+ GD G  G KGD+GE G  G +G +G  G +G
Sbjct  214595  GEKGDLGEKGDKGEKGDLGEKGDKGDLGDKGEKGDKGDLGEKGEKGDKGEKGDKGEKGDL  214774

Query  102     GEPGE  106
               GE GE
Sbjct  214775  GEKGE  214789


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 30/72 (42%), Positives = 41/72 (57%), Gaps = 5/72 (7%)
 Frame = +2

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
               +G  G  G  G  G  G  G+ G KG+KG+ G  G KGD+G+ G  G+ G +G  GI
Sbjct  212027  SGDKGDSGDKGDLGNKGDKGSIGNKGDKGNKGDSGDKGDLGDKGDKGSLGDKGDKGI---  212197

Query  101     KGEPGEGAYVYR  112
               KGEP  G+ V++
Sbjct  212198  KGEP--GSAVFK  212227


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 37/92 (40%), Positives = 46/92 (50%), Gaps = 2/92 (2%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G  G  G  G  G  G+KG KGD G +G KG  G+ G  G +G +G  G +G K
Sbjct  219305  GIKGDKGDKGDLGDKGIKGDLGDKGIKGDKGDLGDKGIKGDLGDKGIKGDKGDKGEKGEK  219484
```

```
Query  102     GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
               GE G  A Y S +  G+      P +PI  T
Sbjct  219485  GESGISAN-YISTYYNGVPGSFVAP-VPIGAT  219574


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G+ G  G  G  G  G  G KG KGD G +G KGD G+ G  G +G  G  GI+G
Sbjct  218630  GIKGNKGDKGDLGDKGDLGDKGIKGNKGDKGDLGDKGDKGDLGDKGTKGNLGDKGIKGDL  218809

Query  102     GEPGE  106
               G+ G+
Sbjct  218810  GDKGD  218824


 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 39/67 (58%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G+ G+ G  G  G  G  G  G+KG+KG  G +G KG+ G+ G  G +G  G  GI+G
Sbjct  218462  IKGLKGNKGEKGDKGELGFRGLKGDKGDKGIKGDLGSKGNKGDKGNLGDKGDLGDKGIKG  218641

Query  100     RKGEPGE  106
                KG+ G+
Sbjct  218642  NKGDKGD  218662


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 22/45 (49%), Positives = 28/45 (62%), Gaps = 0/45 (0%)
 Frame = +3

Query  65      KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAY  109
               KG KGDPG+ G KGD G     G +G +G  G +G KG+PG  A+
Sbjct  261474  KGSKGDPGIKGSKGDPGTAAFKGEKGDKGEKGDKGSKGDPGTAAF  261608


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 37/67 (55%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G+ G+ G  G  G  G  G  G+KG+KG  G+ G KG+ GE G  G  G RG  G +G
Sbjct  218363  VKGLKGNKGEKGDKGDKGDLGVNGQKGDKGQNGIKGLKGNKGEKGDKGELGFRGLKGDKG  218542

Query  100     RKGEPGE  106
                KG  G+
Sbjct  218543  DKGIKGD  218563


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 27/63 (43%), Positives = 35/63 (56%), Gaps = 0/63 (0%)
 Frame = +2

Query  44      PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
```

```
                G  G  G  G  G  G   E+G+KGD G +G KGD G+ G  G +G +G  G +G KGE
Sbjct  214421  KGEKGDIGIKGEKGEAGVDAEQGDKGDKGDLGEKGDKGDKGDLGEKGEKGDLGDKGDKGE  214600

Query  104     PGE  106
                G+
Sbjct  214601  KGD  214609


 Score = 39.3 bits (90),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 38/65 (58%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G+ G  G  G  G  G+KG+ GD G+ G KGD+G+ G  G +G +G  G +G K
Sbjct  157448  GDKGDKGNLGDKGDKGNLGDKGDKGDLGDKGIKGDKGDLGDKGDLGDKGIKGDLGDKGIK  157627

Query  102     GEPGE  106
               G+ G+
Sbjct  157628  GDLGD  157642


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 29/69 (42%), Positives = 38/69 (55%), Gaps = 2/69 (3%)
 Frame = +2

Query  44      PGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
                G  G  G  G  G+   KG+KGDPG  G KG++GE G  G +G  G  G +G KGE
Sbjct  213503  KGDKGDKGNEGLKGESGSAVFKGDKGDPGDKGDKGNLGEKGDKGDKGDLGVKGNKGDKGE  213682

Query  104     PGEGAYVYR  112
                  G+ V++
Sbjct  213683  S--GSAVFK  213703


 Score = 39.3 bits (90),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KG KGD G  G KGD+G+ G+ G  G +G  G  G
Sbjct  156560  IIGKNGPKGDKGDLGDKGIKGGLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLG  156739

Query  100     RKGEPGE  106
                KG+ G+
Sbjct  156740  DKGDKGD  156760


 Score = 38.9 bits (89),  Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+KGD G  G KGD GE G  G +G  G  G +G K
Sbjct  214622  GDKGEKGDLGEKGDKGDLGDKGEKGDKGDLGEKGEKGDKGEKGDKGEKGDLGEKGEKGDK  214801

Query  102     GEPGE  106
               G+ G+
Sbjct  214802  GDLGD  214816
```

```
 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 28/66 (42%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G KG+KGD G  G KGD+G+ G  G  G +G  G  G
Sbjct  218633  IKGNKGDKGDLGDKGDLGDKGIKGNKGDKGDLGDKGDKGDLGDKGTKGNLGDKGIKGDLG  218812

Query  100     RKGEPG  105
                KG+ G
Sbjct  218813  DKGDKG  218830


 Score = 38.5 bits (88),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 31/72 (43%), Positives = 41/72 (57%), Gaps = 4/72 (6%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G PG  G  G  G     G+KG+KGD G+ G KGD GE+G    +G +G    +G K
Sbjct  213569  GDKGDPGDKGDKGNLGE---KGDKGDKGDLGVKGNKGDKGESGSAVFKGDKGDLAEKGDK  213739

Query  102     GEPGE-GAYVYR  112
               GE GE G+ V++
Sbjct  213740  GEKGESGSAVFK  213775


 Score = 38.1 bits (87),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+KG+ G  G KGD+GE G  G +G  G  G +G
Sbjct  214658  GDKGDLGDKGEKGDKGDLGEKGEKGDKGEKGDKGEKGDLGEKGEKGDKGDLGDKGEKGDL  214837

Query  102     GEPGE  106
               GE G+
Sbjct  214838  GEKGD  214852


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G+ G  G  G  G  G  G+KG KG+ G  G KGD+G+ G  G  G +G  G  G K
Sbjct  218693  GIKGNKGDKGDLGDKGDKGDLGDKGTKGNLGDKGIKGDLGDKGDKGNLGDKGIKGDLGDK  218872

Query  102     GEPG  105
               G+ G
Sbjct  218873  GDKG  218884


 Score = 38.1 bits (87),  Expect = 0.034, Method: Compositional matrix adjust.
 Identities = 29/69 (42%), Positives = 37/69 (54%), Gaps = 3/69 (4%)
 Frame = +2
```

```
Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKG---EKGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
               AG+    G  G  G  G  G  G+KG   EKG+ G +G KGD GE G  G +G +G  G
Sbjct  214466  AGVDAEQGDKGDKGDLGEKGDKGDKGDLGEKGEKGDLGDKGDKGEKGDLGEKGDKGEKGD  214645

Query  98      QGRKGEPGE  106
                G KG+ G+
Sbjct  214646  LGEKGDKGD  214672


 Score = 38.1 bits (87),  Expect = 0.034, Method: Compositional matrix adjust.
 Identities = 28/71 (39%), Positives = 37/71 (52%), Gaps = 9/71 (13%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGF---------P  95
               G  G  G  G  G  G  G KG KGD G +G KGD+G+ G+ G +G +G
Sbjct  218513  GFRGLKGDKGDKGIKGDLGSKGNKGDKGNLGDKGDLGDKGIKGNKGDKGDLGDKGDLGDK  218692

Query  96      GIQGRKGEPGE  106
               GI+G KG+ G+
Sbjct  218693  GIKGNKGDKGD  218725


 Score = 37.7 bits (86),  Expect = 0.040, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  GEKG+KG+ G +G KG+ G+ G  G +G +G  G +G K
Sbjct  214676  GDKGEKGDKGDLGEKGEKGDKGEKGDKGEKGDLGEKGEKGDKGDLGDKGEKGDLGEKGDK  214855

Query  102     GEPGE  106
               G+ G+
Sbjct  214856  GDLGK  214870


 Score = 37.7 bits (86),  Expect = 0.044, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G+ G  G  G  G+KG+ GD G+ G KGD G+ G  G  G +G  G +G K
Sbjct  218540  GDKGIKGDLGSKGNKGDKGNLGDKGDLGDKGIKGNKGDKGDLGDKGDLGDKGIKGNKGDK  218719

Query  102     GEPGE  106
               G+ G+
Sbjct  218720  GDLGD  218734


 Score = 37.7 bits (86),  Expect = 0.045, Method: Compositional matrix adjust.
 Identities = 30/71 (42%), Positives = 37/71 (52%), Gaps = 6/71 (8%)
 Frame = +2

Query  42      GIPGHPGH------NGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
               GI G  G        G  G  G  G  G+KG+KGD G  G KGD+G+ G  G +G  G
Sbjct  214442  GIKGEKGEAGVDAEQGDKGDKGDLGEKGDKGDKGDLGEKGEKGDLGDKGDKGEKGDLGEK  214621

Query  96      GIQGRKGEPGE  106
               G +G KG+ GE
```

```
Sbjct  214622  GDKGEKGDLGE  214654


 Score = 37.7 bits (86),  Expect = 0.046, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 35/65 (54%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G D   G+KG+KGD G  G KGD G+ G  G +G  G  G +G K
Sbjct  214424  GEKGDIGIKGEKGEAGVDAEQGDKGDKGDLGEKGDKGDKGDLGEKGEKGDLGDKGDKGEK  214603

Query  102     GEPGE  106
               G+ GE
Sbjct  214604  GDLGE  214618


 Score = 37.4 bits (85),  Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 35/67 (52%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KG KGD G  G KGD+G+ G+ G  G +G  G  G
Sbjct  157046  IKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLG  157225

Query  100     RKGEPGE  106
                KG  G+
Sbjct  157226  DKGIKGD  157246


 Score = 37.4 bits (85),  Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 35/67 (52%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KG KGD G  G KGD+G+ G+ G  G +G  G  G
Sbjct  157073  IKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLG  157252

Query  100     RKGEPGE  106
                KG  G+
Sbjct  157253  DKGIKGD  157273


 Score = 37.4 bits (85),  Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 28/67 (42%), Positives = 35/67 (52%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G+KG KGD G  G KGD+G+ G+ G  G +G  G  G
Sbjct  157100  IKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLGDKGIKGDLG  157279

Query  100     RKGEPGE  106
                KG  G+
Sbjct  157280  DKGIKGD  157300


 Score = 37.4 bits (85),  Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +2
```

```
Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+ GD G  G KGD+GE G  G +G  G  G +G  
Sbjct  214496  GDKGDLGEKGDKGDKGDLGEKGEKGDLGDKGDKGEKGDLGEKGDKGEKGDLGEKGDKGDL  214675

Query  102     GEPGE  106
               G+ GE
Sbjct  214676  GDKGE  214690


 Score = 37.4 bits (85),  Expect = 0.064, Method: Compositional matrix adjust.
 Identities = 22/42 (52%), Positives = 26/42 (62%), Gaps = 0/42 (0%)
 Frame = +2

Query  65      KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               KG+KGD G  G KGD+GE G  G  G +G  GI   KGE G+
Sbjct  212540  KGDKGDLGEKGTKGDLGEKGTKGDLGEKGEAGIDAEKGEKGD  212665


 Score = 37.4 bits (85),  Expect = 0.065, Method: Compositional matrix adjust.
 Identities = 26/59 (44%), Positives = 36/59 (61%), Gaps = 0/59 (0%)
 Frame = +3

Query  48      GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               G  G  G  G  G  G+KG+ GD GL G KGD+G+ G+ G +G +G  G +G KG+ G+
Sbjct  261837  GLKGDKGDLGDIGLKGDKGDLGDIGLKGDKGDLGDIGLKGDKGDKGDLGTKGDKGDLGD  262013


 Score = 37.4 bits (85),  Expect = 0.067, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 34/65 (52%), Gaps = 0/65 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G  G  G  GEKG+ G+ G  G KGD+GE G  G  G +G  G +G
Sbjct  214532  GDKGDLGEKGEKGDLGDKGDKGEKGDLGEKGDKGEKGDLGEKGDKGDLGDKGEKGDKGDL  214711

Query  102     GEPGE  106
               GE GE
Sbjct  214712  GEKGE  214726


 Score = 37.0 bits (84),  Expect = 0.072, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G NG  G  G  G+KGE G  GL G KGD G  G  G++G +G  G  G
Sbjct  218426  VNGQKGDKGQNGIKGLKGNKGEKGDKGELGFRGLKGDKGDKGIKGDLGSKGNKGDKGNLG  218605

Query  100     RKGEPGE  106
                KG+ G+
Sbjct  218606  DKGDLGD  218626


 Score = 37.0 bits (84),  Expect = 0.075, Method: Compositional matrix adjust.
 Identities = 44/146 (30%), Positives = 57/146 (39%), Gaps = 44/146 (30%)
 Frame = +1
```

```
Query  35      ACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGD------------------------  70
                  G + G PG  G  G  G  G  G  GEKG+KGD
Sbjct  263623  VLVGNLTGPPGPSGSQGIKGDPGIQGIKGEKGDKGDTTNIGIKGDKGDKGDKGDIGNTGL  263802

Query  71      ---PGLIGPKGDIGETGVPGAEGPRGFPGIQ---------GRKGEPGEGAYVYRSAFSVG  118
                   G +G KGDIG+TG+ G +G +G  G Q            GEPG+  Y+  +   V
Sbjct  263803  KGEKGDLGEKGDIGDTGLKGDKGDKGEIGSQIFTGFGAPPDDLGEPGD-IYIDLNTGDV-  263976

Query  119     LETYVTIPNMPIRFT---KIFYNQQN  141
                  Y  I ++P+       IF  QQN
Sbjct  263977  ---YYKIQDVPLTINNSPNIFSVQQN  264045


 Score = 37.0 bits (84),  Expect = 0.090, Method: Compositional matrix adjust.
 Identities = 28/69 (41%), Positives = 37/69 (54%), Gaps = 3/69 (4%)
 Frame = +2

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG---I  97
               +G  G  G+ G  G  G  G  G KG+ GD G +G KGD G  G  G +G +G PG
Sbjct  212045  SGDKGDLGNKGDKGSIGNKGDKGNKGDSGDKGDLGDKGDKGSLGDKGDKGIKGEPGSAVF  212224

Query  98      QGRKGEPGE  106
               +G KG+ G+
Sbjct  212225  KGEKGDKGD  212251


>NC_027386.1 Propionibacterium phage PHL152M00, complete genome
Length=29247

 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 32/78 (41%), Positives = 41/78 (53%), Gaps = 0/78 (0%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  GH+G PGR G DG  G  G+ G  G+ G +GD G  G  G +GP+G  G  G
Sbjct  14973  LPGVNGSDGHDGVPGRAGADGVAGVDGKDGANGVDGERGDQGPAGSAGPQGPQGERGPAG  15152

Query  100    RKGEPGEGAYVYRSAFSV  117
                G  G+     RS  SV
Sbjct  15153  ANGSDGKDGKDGRSVVSV  15206


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 34/84 (40%), Positives = 40/84 (48%), Gaps = 4/84 (5%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG+DG  G  GE+GD    GP G  G  G  G  GP G  G  G+
Sbjct  15006  GVPGRAGADGVAGVDGKDGANGVDGERGDQ---GPAGSAGPQGPQGERGPAGANGSDGKD  15176

Query  102    GEPGEGAY-VYRSAFSVGLETYVT  124
              G+ G     VY S     L   VT
Sbjct  15177  GKDGRSVVSVYCSGGGACL*NIVT  15248


>NC_028881.1 Enterobacteria phage vB_EcoM_VR5, complete genome
Length=170473
```

```
 Score = 45.8 bits (107),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 36/85 (42%), Positives = 43/85 (51%), Gaps = 18/85 (21%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---------IGPKGDIGETGVPGAEG  90
               + GI G PG NG  G  G  G  G +G +GD GL         IGPKG  GETG  G +G
Sbjct  107854  LTGIKGEPGENGDIGPQGNQGPVGPQGIQGDTGLQGVPGENGAIGPKGIQGETGAQGIQG  108033

Query  91      PRGF---------PGIQGRKGEPGE  106
               P+G           GIQG KG+ G+
Sbjct  108034  PQGLQGDPGTQGPQGIQGLKGDKGD  108108


 Score = 44.7 bits (104),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 32/71 (45%), Positives = 40/71 (56%), Gaps = 6/71 (8%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGP------KGDIGETGVPGAEGPRGFP  95
               GI G  G  G  G  G  G  G KG+KG+ GL GP      +G+ GETG PG +G +G
Sbjct  108400  GIQGPQGIQGPKGDTGETGLQGLKGDKGETGLTGPQGLQGIRGEQGETGAPGIQGIQGIA  108579

Query  96      GIQGRKGEPGE  106
               G QG KG+ G+
Sbjct  108580  GDQGPKGDTGD  108612


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 38/64 (59%), Gaps = 3/64 (5%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               GI G  G  G PG +G  G  G +GE G  G+ GP+G  G+   PG +GP+G  G++G K
Sbjct  107932  GIQGDTGLQGVPGENGAIGPKGIQGETGAQGIQGPQGLQGD---PGTQGPQGIQGLKGDK  108102

Query  102     GEPG  105
               G+ G
Sbjct  108103  GDQG  108114


 Score = 41.6 bits (96),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 29/61 (48%), Positives = 34/61 (56%), Gaps = 0/61 (0%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  G KG+ G+ GL G KGD GETG+ G +G +G  G QG  G P
Sbjct  108373  GVEGAQGPQGIQGPQGIQGPKGDTGETGLQGLKGDKGETGLTGPQGLQGIRGEQGETGAP  108552

Query  105     G  105
               G
Sbjct  108553  G  108555


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 30/79 (38%), Positives = 41/79 (52%), Gaps = 3/79 (4%)
 Frame = +1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGD---IGETGVPGAEGPRGFPGIQ  98
               GI G  G  G  G  G  G PG +G +G  GL G KGD    GETG  G +G +G PG +
```

```
Sbjct  107995  GIQGETGAQGIQGPQGLQGDPGTQGPQGIQGLKGDKGDQGIQGETGAQGIQGIQGVPGAK  108174

Query  99      GRKGEPGEGAYVYRSAFSV  117
               G  G  G     ++ ++++
Sbjct  108175  GDIGPVGPAGLTWKGSWNI  108231


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 32/77 (42%), Positives = 39/77 (51%), Gaps = 12/77 (16%)
 Frame = +1

Query  42      GIPGHPGHNGA------PGRDGRDGTPGEKGEKGDPGLIGP------KGDIGETGVPGAE  89
               G+ G PG NGA       G  G  G  G +G +GDPG  GP      KGD G+ G+ G
Sbjct  107950  GLQGVPGENGAIGPKGIQGETGAQGIQGPQGLQGDPGTQGPQGIQGLKGDKGDQGIQGET  108129

Query  90      GPRGFPGIQGRKGEPGE  106
               G +G  GIQG  G  G+
Sbjct  108130  GAQGIQGIQGVPGAKGD  108180


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 37/62 (60%), Gaps = 6/62 (10%)
 Frame = +1

Query  51      GAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGI------QGRKGEP  104
               G  GR G +G  G +G +G  G+ GPKGD GETG+ G +G +G  G+      QG +GE
Sbjct  108355  GPEGRQGVEGAQGPQGIQGPQGIQGPKGDTGETGLQGLKGDKGETGLTGPQGLQGIRGEQ  108534

Query  105     GE  106
               GE
Sbjct  108535  GE  108540


>NC_031238.1 Mycobacterium phage Catalina, complete genome
Length=53411

 Score = 45.4 bits (106),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 40/99 (40%), Positives = 48/99 (48%), Gaps = 15/99 (15%)
 Frame = +2

Query  41    AGIPGHPGHNGAPGRDGRDGTPGE---KGEKGDPGLIGPKGDI------GETGVPGAEGP  91
             AG PG PG  GA G  G  G  G+   +G KGD G  GPKGD       G+TG  GA+GP
Sbjct  4919  AGAPGEPGPTGATGATGPQGPKGDTGPQGPKGDTGAQGPKGDTGAQGPKGDTGATGAQGP  5098

Query  92    RGFPGIQGRKGEPGEG------AYVYRSAFSVGLETYVT  124
              G  G QG  G P           V ++A+  G +T  T
Sbjct  5099  TGATGPQGPSGTPSSTNTVLDFVKVTQAAYDAGPKTATT  5215


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 27/49 (55%), Positives = 29/49 (59%), Gaps = 0/49 (0%)
 Frame = +2

Query  54    GRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
             G  G  G  G  G KGDPG  GPKGD G TG  GA GP+G  G QG +G
Sbjct  4607  GPAGPQGAVGPLGPKGDPGDTGPKGDTGATGPQGATGPKGDTGAQGPQG  4753
```

```
 Score = 37.4 bits (85),  Expect = 0.061, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             GI G  G  G  G  G  G  G+KG+ GD G  GPKGD G+ G PG  G  G  G  G
Sbjct  4751  GIQGATGPQGLQGPKGDTGPKGDKGDTGDLGPQGPKGDKGDKGDPGTAGLTGLQGPAGAP  4930

Query  102   GEPG  105
             GEPG
Sbjct  4931  GEPG  4942


>NC_005902.1 Lymphocystis disease virus - isolate China, complete genome
Length=186250

 Score = 45.4 bits (106),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 35/72 (49%), Positives = 41/72 (57%), Gaps = 10/72 (14%)
 Frame = +3

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPG-------LIGPKGDIGETGVPGAEGPRGF  94
               G PG PG  G  GRDG+ G PG KG++G+ G       +IGP G  GE G+P   GPRG
Sbjct  112869  GAPGMPGDPGRDGRDGQKGLPGFKGDRGERGFSCNESKVIGPSGPQGEQGLP---GPRGL  113039

Query  95      PGIQGRKGEPGE  106
               PG  G KG  G
Sbjct  113040  PGSDGLKGSAGS  113075


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 34/73 (47%), Positives = 40/73 (55%), Gaps = 6/73 (8%)
 Frame = -3

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGP------KGDIGETGVPGAEGPRG  93
               + G+ G  G +G PG+ G  G  G  G KGD GL GP      KGDIG  G  G+EG  G
Sbjct  168275  LPGVRGFTGESGEPGKKGDSGQKGYPGSKGDIGLHGPKGEIGLKGDIGYQGFKGSEGELG  168096

Query  94      FPGIQGRKGEPGE  106
                 G QG KG+ GE
Sbjct  168095  KQGDQGDKGDKGE  168057


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 36/98 (37%), Positives = 53/98 (54%), Gaps = 9/98 (9%)
 Frame = -3

Query  27      VLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGD---IGET  83
               + L  PKG     + G  G+ G  G+ G  G+ G  G+KG+KG+ GL G KG    +G+T
Sbjct  168182  IGLHGPKGEIG--LKGDIGYQGFKGSEGELGKQGDQGDKGDKGENGLRGYKGHKGYLGDT  168009

Query  84      GVPGAEGPR---GFPGIQGRKGEPG-EGAYVYRSAFSV  117
               G+PG  G +   G+ G  G KG+PG EG +  +    +
Sbjct  168008  GIPGKRGEKGESGWSGTPGEKGDPGTEGTFGEKGEKGI  167895


 Score = 37.0 bits (84),  Expect = 0.078, Method: Compositional matrix adjust.
 Identities = 29/60 (48%), Positives = 32/60 (53%), Gaps = 0/60 (0%)
 Frame = -3
```

```
Query  46      HPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
                PG  G  G DG  G  GEKG KGD G  G KG+ G  GV G  G  G PG +G  G+ G
Sbjct  168383  EPGDTGNHGIDGEKGKAGEKGSKGDKGARGIKGNKGLPGVRGFTGESGEPGKKGDSGQKG  168204


>NC_030394.2 Short-finned eel ranavirus isolate ANGA14001, complete genome
Length=126965

 Score = 45.4 bits (106),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 30/61 (49%), Positives = 35/61 (57%), Gaps = 0/61 (0%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G PG+DG DG  G KG+ G  G  GP+G  G+ G  G  GP+G  G  G KGEP
Sbjct  15117  GDAGERGYPGKDGADGPKGPKGDPGPRGEKGPRGPKGDVGARGLVGPKGDAGPAGAKGEP  15296

Query  105    G  105
              G
Sbjct  15297  G  15299


>NC_027357.1 Propionibacterium phage PHL025M00, complete genome
Length=29496

 Score = 45.4 bits (106),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 36/94 (38%), Positives = 49/94 (52%), Gaps = 13/94 (14%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              +AG  G  G NG  G DGRDG+ GE+GE+G  G  GP+G  GE    G  GP G  G  G
Sbjct  15063  VAGRAGADGVNGVDGADGRDGSAGERGEQGPSGPAGPQGAQGER---GERGPAGVNGSDG  15233

Query  100    RKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              + G+ G      RS  SV    Y +   + ++++
Sbjct  15234  KDGKDG------RSVVSV----YCSDGRLVVKYS  15305


 Score = 37.0 bits (84),  Expect = 0.072, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 35/67 (52%), Gaps = 0/67 (0%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G+DG DG  G  G  G  G+ G  G  G  G  G +GP G  G QG
Sbjct  15000  LNGVKGPDGLPGANGKDGVDGVAGRAGADGVNGVDGADGRDGSAGERGEQGPSGPAGPQG  15179

Query  100    RKGEPGE  106
               +GE GE
Sbjct  15180  AQGERGE  15200


>NC_027401.1 Propionibacterium phage PHL095N00, complete genome
Length=29751

 Score = 45.4 bits (106),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 28/60 (47%), Positives = 35/60 (58%), Gaps = 0/60 (0%)
 Frame = +3
```

```
Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+ GE+G+ G  G  GP+G+ GE G  G  G  G  G  GR
Sbjct  15045  GVPGRAGADGVNGADGRDGSAGERGDVGPSGPAGPQGERGERGPAGTNGSDGKDGKDGRS  15224


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 32/94 (34%), Positives = 46/94 (49%), Gaps = 7/94 (7%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  GH+G PGR G DG  G  G  G     G +GD+G +G  G +G RG  G  G
Sbjct  15012  LPGVNGSDGHDGVPGRAGADGVNGADGRDGS---AGERGDVGPSGPAGPQGERGERGPAG  15182

Query  100    RKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
                G  G+     RS  SV    Y +   + ++++
Sbjct  15183  TNGSDGKDGKDGRSVVSV----YCSDGRLVVKYS  15272


>NC_004167.1 Bacteriophage phi-105 DNA, complete sequence
Length=39325

 Score = 45.4 bits (106),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 26/53 (49%), Positives = 32/53 (60%), Gaps = 0/53 (0%)
 Frame = +1

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
             G PG  G  G  G  G PGE+G +G+PG  GPKGD GE G  G +G +G P +
Sbjct  6154  GEPGEPGPQGPKGDKGEPGEQGPQGEPGPAGPKGDTGEQGPQGEKGDKGDPAV  6312


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 37/64 (58%), Gaps = 3/64 (5%)
 Frame = +1

Query  43    IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
             + G  G  G  G  G  G  G +GE G+PG  GPKGD GE   PG +GP+G PG  G KG
Sbjct  6085  VKGLQGEKGEKGNKGDTGKQGPQGEPGEPGPQGPKGDKGE---PGEQGPQGEPGPAGPKG  6255

Query  103   EPGE  106
             + GE
Sbjct  6256  DTGE  6267


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 32/91 (35%), Positives = 43/91 (47%), Gaps = 5/91 (5%)
 Frame = +1

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G+ G  G  G  G  G PG +G KGD G  G +G  GE G  G +G  G  G QG KG+
Sbjct  6118  GNKGDTGKQGPQGEPGEPGPQGPKGDKGEPGEQGPQGEPGPAGPKGDTGEQGPQGEKGDK  6297

Query  105   GEGAYVYRSAFSVGLETYVTIPNMPIRFTKI  135
             G+ A +  S+      T+  +    +R   I
Sbjct  6298  GDPAVIEESSI-----TFEMLAEKSVRSKNI  6375


>NC_007056.1 Staphylococcus phage EW, complete genome
Length=45286
```

```
 Score = 45.4 bits (106),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 38/112 (34%), Positives = 48/112 (43%), Gaps = 23/112 (21%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGD---IGETGVPGAEGPRGFPGIQGRK  101
              G  G  G  G  G  G  G++GE+G  G +GPKGD   IG  G  GA GP+G  G QG +
Sbjct  21684  GARGETGLTGAKGAKGDKGDRGEQGFQGPVGPKGDKGDIGPVGATGAIGPKGDRGEQGPQ  21863

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCN  153
              G  G+                       IRF  +   QQN   G+ G+   N
Sbjct  21864  GPKGDEGV--------------------IRFENLTQEQQNLLKGAPGESIIN  21959


>NC_021791.1 Cellulophaga phage phi12:1, complete genome
Length=39148

 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G PG  G  G  G  G  G  G +GE G  G+ G KGD G+TG  G +G +G  G QG +
Sbjct  26566  GEPGEQGIQGETGPQGLQGEQGLQGEDGAQGIQGIKGDTGDTGPQGIQGEQGLQGEQGLQ  26745

Query  102    GEPG  105
              GE G
Sbjct  26746  GEQG  26757


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 29/67 (43%), Positives = 37/67 (55%), Gaps = 0/67 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G  G  G  G  G  G DG  G +G KGD G  GP+G  GE G+ G +G +G  G+QG
Sbjct  26587  IQGETGPQGLQGEQGLQGEDGAQGIQGIKGDTGDTGPQGIQGEQGLQGEQGLQGEQGLQG  26766

Query  100    RKGEPGE  106
               +G  GE
Sbjct  26767  EQGLQGE  26787


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 42/156 (27%), Positives = 61/156 (39%), Gaps = 8/156 (5%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G PG  G  G  G  G  GE+G +G+ G  G +G  G+TG  G +G +G  G+QG +G
Sbjct  26566  GEPGEQGIQGETGPQGLQGEQGLQGEDGAQGIQGIKGDTGDTGPQGIQGEQGLQGEQGLQ  26745

Query  105    GEGAYVYRSAF--SVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGK---FHCNIPGLYY  159
              GE             G  T  TI +  I   K+    Q   + S         N
Sbjct  26746  GEQGLQGEQGLQGEAGPSTPQTIDDGSIVEAKLSTEVQTKINDSATTQELEEANALNRKN  26925

Query  160    FAYHITVYMKDVKVSLFKKDKAMLFTYDQYQENNVD  195
               +    +   D    L K + +++    Q   N+VD
Sbjct  26926  ISVDFLISSDDSGAILKKSNSSIIRATVQ---NDVD  27024
```

```
 Score = 37.4 bits (85),  Expect = 0.057, Method: Compositional matrix adjust.
 Identities = 28/70 (40%), Positives = 38/70 (54%), Gaps = 3/70 (4%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG---FPG  96
              +A I G  G  G  G  G  G  GE G +G+PG  G +G+ G  G+ G +G +G     G
Sbjct  26479  LATIVGEGGAIGPAGPQGEQGIQGEPGPQGEPGEQGIQGETGPQGLQGEQGLQGEDGAQG  26658

Query  97     IQGRKGEPGE  106
              IQG KG+ G+
Sbjct  26659  IQGIKGDTGD  26688


>NC_023423.1 Pithovirus sibericum isolate P1084-T, complete genome
Length=610033

 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 29/100 (29%), Positives = 45/100 (45%), Gaps = 0/100 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G +G  G+DG+DG  G+ G+ G  G  G  G  G+ G  G +G  G  G+ G+
Sbjct  155077  GVDGVDGKDGVDGKDGKDGVDGKDGKDGVDGKDGKDGVDGKDGKDGVDGKDGKDGVDGKD  154898

Query  102     GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQN  141
                EP E         S+  E  +      + F ++    +N
Sbjct  154897  AEPCEKIVSNEKFLSLNDEGEIATNCHKVIFEQLSLTGKN  154778


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 46/190 (24%), Positives = 74/190 (39%), Gaps = 18/190 (9%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G+ G  G  G+ G  G  G IGE G  GA G  G  G  G  G
Sbjct  399637  GATGPTGEQGETGFTGSIGPIGPTGNIGFTGSTGTIGEVGAIGATGAIGSTGATGVTGAT  399816

Query  105     GEG------AYVYRSAFS--------VGLETYVTIPNM-PIRFTKIFYNQQNHYDGSTGK  149
               GEG      + +  S+F+        +GL ++V  PN    ++T    + QN Y  ++
Sbjct  399817  GEGVPPEVFSGIRSSSFTQSTTPTVVIGLTSFVPNPNFSSSQYTVPVSSSQNQYFLTS--  399990

Query  150     FHCNIPGLYYFAYHITVYMKDVKVSLFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGD  209
                   I G+       T+ + D    +   ++   + ++            S    L+ G+
Sbjct  399991  -LIQIAGVMTEGQIQTLQIYDQTAGIVLAEENFYWPFNSISITTETLVEASCFCQLQTGN  400167

Query  210     QVWLQVYGEG  219
                  ++V+  G
Sbjct  400168  SYVIRVFNTG  400197


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 26/64 (41%), Positives = 34/64 (53%), Gaps = 0/64 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G+ G  G NG  G+DGRDG  G  G+ G  G+ G  G  G  G  G +G  G  G+ G+
```

```
Sbjct  155185  GVDGVDGINGKDGKDGRDGVDGINGKDGKDGVDGKDGVDGVDGKDGVDGKDGKDGVDGKD  155006

Query  102     GEPG  105
               G+ G
Sbjct  155005  GKDG  154994


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 45/175 (26%), Positives = 71/175 (41%), Gaps = 5/175 (3%)
 Frame = -2

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
               AG+ G  G  G  G  G  G  GE G  G  GLIGP G +G TG+ G  GP G  G  G
Sbjct  446229  AGLVGPTGIAGEVGPTGLVGPTGEVGATGPTGLIGPTGLVGPTGIAGEVGPTGPVGATGD  446050

Query  101     KGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYF  160
                G  G G   Y   +++G +      ++      +      H  G++     N     Y
Sbjct  446049  AGATGAGLASYAYIYNLGAQVVPLEADITYDTNGVILGPITHAPGTSTITLGNA--GNYA  445876

Query  161     AYHITVYMKDVKVSLFKKDKAML-FTYDQYQENNVDQASGSVLLHLEVGDQVWLQ  214
                +     ++  + +L++    +   TY       ++  SG V+L    GD + ++
Sbjct  445875  VWFSESGVEPNQFTLYQNGAPVAGSTYGSGAGTQIN--SGMVILTASAGDVLTVR  445717


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/75 (44%), Positives = 37/75 (49%), Gaps = 5/75 (7%)
 Frame = -1

Query  32      PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGP  91
               PKG C     G  G  G  GA G+DG  G  G KG+ G  G  GPKG  G+ G  G  GP
Sbjct  308353  PKGDC-----GKDGCTGPKGADGKDGCTGPTGPKGDCGKDGCTGPKGADGKDGCTGPTGP  308189

Query  92      RGFPGIQGRKGEPGE  106
               +G  G  G  G  GE
Sbjct  308188  KGDCGKDGCTGPAGE  308144


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 26/66 (39%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G +G  G+DG+DG  G+ G  G  G  G  G  G  GV G +G  G  GI G
Sbjct  155335  VDGKDGVDGRDGVDGKDGKDGVDGKDGRDGVDGKDGVDGKDGVDGVDGKDGVDGVDGING  155156

Query  100     RKGEPG  105
               + G+ G
Sbjct  155155  KDGKDG  155138


 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 58/215 (27%), Positives = 89/215 (41%), Gaps = 22/215 (10%)
 Frame = -1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G  GE G  G+ G IGP G +G TG  G +GP+G  G  G  G
Sbjct  555805  GVTGEIGPTGSVGLTGPVGETGANGNVGTIGPTGIMGATGQTGPDGPQGPVGPTGATGIE  555626
```

```
Query  105      GEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQ-------QNHYDGSTGKFHC-NIPG  156
                G         FS+G   +   P +  + + I +          +++D ++G F   +IPG
Sbjct  555625  GPTGPSGIDFFSIGFSAFREDPIVLTQASNIVFVTDYQTTIPNSNFDPASGIFLVPSIPG  555446

Query  157      L--YYF---AYHITVYMKDVKVSLFKKDKAMLF-TYDQ----YQENNVDQASGSV--LLH  204
                    YF   +Y  +  +   +V+   +    L  T  Q    ++  NV +  G V  L
Sbjct  555445  TQGSYFLVSSYEASAVIGTGQVNFIVELAENLNPTLGQNRIVFRSANVTETEGQVFYLGP  555266

Query  205      LEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLL  239
                L  G  + ++V      N   +   N  +F GFL+
Sbjct  555265  LTPGTNISVRV--SVVLNAGASCTINRISFQGFLV  555167


 Score = 40.4 bits (93),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 27/70 (39%), Positives = 35/70 (50%), Gaps = 6/70 (9%)
 Frame = -1

Query  42       GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGV------PGAEGPRGFP  95
                G+ G  G +G  G+DGRDG  G+ G  G  G+ G  G  G  GV       G +G  G
Sbjct  155302  GVDGKDGKDGVDGKDGRDGVDGKDGVDGKDGVDGVDGKDGVDGVDGINGKDGKDGRDGVD  155123

Query  96       GIQGRKGEPG  105
                GI G+ G+ G
Sbjct  155122  GINGKDGKDG  155093


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 31/75 (41%), Positives = 36/75 (48%), Gaps = 1/75 (1%)
 Frame = -1

Query  32       PKGAC-TGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEG  90
                PKG C      G  G+ G NG  G  G  G  G+ G+ G  G  GPKGD G+ G  G  G
Sbjct  308668  PKGDCGRNGCTGPKGNDGKNGKDGCTGPKGNDGKNGKDGCTGATGPKGDCGKDGCTGPTG  308489

Query  91       PRGFPGIQGRKGEPG  105
                P+G  G  G  G  G
Sbjct  308488  PKGDCGKDGCTGPKG  308444


 Score = 38.5 bits (88),  Expect = 0.023, Method: Compositional matrix adjust.
 Identities = 25/61 (41%), Positives = 32/61 (52%), Gaps = 0/61 (0%)
 Frame = -1

Query  42       GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
                G  G  G++G  G+DG  G  G KG+ G  G  GP G  G+ G  G  GP+G  G  G+
Sbjct  308599  GCTGPKGNDGKNGKDGCTGATGPKGDCGKDGCTGPTGPKGDCGKDGCTGPKGADGKNGKD  308420

Query  102      G  102
                G
Sbjct  308419  G  308417


 Score = 37.7 bits (86),  Expect = 0.047, Method: Compositional matrix adjust.
 Identities = 35/84 (42%), Positives = 44/84 (52%), Gaps = 14/84 (17%)
 Frame = -1

Query  32       PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL------IGPKGDIGE---  82
                PKG C     G  G  G  GA G++G+DG  G KG++G  G        GPKGD G+
```

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Sbjct  308488  PKGDC-----GKDGCTGPKGADGKNGKDGCTGPKGDQGLIGCTGLKGDTGPKGDCGKDGC  308324

Query  83      TGVPGAEGPRGFPGIQGRKGEPGE  106
               TG  GA+G  G  G  G KG+ G+
Sbjct  308323  TGPKGADGKDGCTGPTGPKGDCGK  308252


 Score = 37.4 bits (85),  Expect = 0.053, Method: Compositional matrix adjust.
 Identities = 33/77 (43%), Positives = 37/77 (48%), Gaps = 5/77 (6%)
 Frame = -1

Query  32      PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGD---IGETGVPGA  88
               PKG C     G  G  G  G  G+DG  G  G  G+ G  G  GPKGD   IG TG+ G
Sbjct  308533  PKGDC--GKDGCTGPTGPKGDCGKDGCTGPKGADGKNGKDGCTGPKGDQGLIGCTGLKGD  308360

Query  89      EGPRGFPGIQGRKGEPG  105
                GP+G  G  G  G  G
Sbjct  308359  TGPKGDCGKDGCTGPKG  308309


 Score = 37.0 bits (84),  Expect = 0.089, Method: Compositional matrix adjust.
 Identities = 25/65 (38%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G +G  G+DG+DG  G+ G  G  G  G  G  G+ GV G +G  G  G  G+
Sbjct  155149  GKDGRDGVDGINGKDGKDGVDGKDGVDGVDGKDGVDGKDGKDGVDGKDGKDGVDGKDGKD  154970

Query  102     GEPGE  106
               G  G+
Sbjct  154969  GVDGK  154955


 Score = 37.0 bits (84),  Expect = 0.090, Method: Compositional matrix adjust.
 Identities = 24/66 (36%), Positives = 33/66 (50%), Gaps = 0/66 (0%)
 Frame = -1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G +G  G+DG+DG  G+ G  G  G+ G  G  G  G  G +G  G  G+ G
Sbjct  155398  VDGKDGVDGRDGVDGKDGKDGVDGKDGVDGRDGVDGKDGKDGVDGKDGRDGVDGKDGVDG  155219

Query  100     RKGEPG  105
               + G  G
Sbjct  155218  KDGVDG  155201


 Score = 36.6 bits (83),  Expect = 0.097, Method: Compositional matrix adjust.
 Identities = 27/65 (42%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = -1

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
               G  G  G  G  G+DG  G  G KG+ G  G  GPKG  G+ G  G  GP+G  G+ G
Sbjct  308554  GCTGATGPKGDCGKDGCTGPTGPKGDCGKDGCTGPKGADGKNGKDGCTGPKGDQGLIGCT  308375

Query  102     GEPGE  106
               G  G+
Sbjct  308374  GLKGD  308360
```

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>NC_027621.1 Propionibacterium phage Wizzo, complete genome
Length=29463

 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 32/76 (42%), Positives = 41/76 (54%), Gaps = 0/76 (0%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+ GE+G+ G  G  G +G  G  G  G +GP+G  G  G
Sbjct  15036  GVPGRAGADGVNGADGRDGSAGERGDVGPSGPAGLQGAQGARGPIGPQGPQGSAGADGTN  15215

Query  102    GEPGEGAYVYRSAFSV  117
              G  G+      RS  SV
Sbjct  15216  GRDGKDGKDGRSVVSV  15263


 Score = 37.0 bits (84),  Expect = 0.072, Method: Compositional matrix adjust.
 Identities = 28/63 (44%), Positives = 32/63 (51%), Gaps = 0/63 (0%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G+DG DG PG  G  G  G  G  GE G  G  GP G  G QG
Sbjct  14976  LNGVKGPDGLPGANGKDGVDGVPGRAGADGVNGADGRDGSAGERGDVGPSGPAGLQGAQG  15155

Query  100    RKG  102
               +G
Sbjct  15156  ARG  15164


>NC_027630.1 Propionibacterium phage Ouroboros, complete genome
Length=29506

 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 33/76 (43%), Positives = 39/76 (51%), Gaps = 6/76 (8%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG+DG  G  GE+GD G  GP G  G  G  G  GP G  G  G+
Sbjct  15010  GVPGRAGADGVNGADGKDGANGADGERGDVGPSGPAGPQGAQGEQGGRGPAGANGSDGKD  15189

Query  102    GEPGEGAYVYRSAFSV  117
              G+ G      RS  SV
Sbjct  15190  GKDG------RSVVSV  15219


>NC_009015.1 Burkholderia ambifaria phage BcepF1, complete genome
Length=72415

 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 37/65 (57%), Gaps = 0/65 (0%)
 Frame = -1

Query  38     GWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGI  97
              G +AG+    G  G  G  G+DG PG KG+KGD G  G KGD G+ GV G +G +G  G
Sbjct  65614  GAVAGLGTGTGPMGPQGPAGKDGAPGAKGDKGDAGTPGVKGDDGDQGVKGDKGDKGDTGE  65435

Query  98     QGRKG  102
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              G  G
Sbjct  65434  TGPAG  65420


>NC_029072.1 Salmonella phage 19, complete genome
Length=94766

 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 33/92 (36%), Positives = 48/92 (52%), Gaps = 8/92 (9%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G +G  G +G +G  G +GPKGD G+TG  G  GP+G  G +G +GE
Sbjct  10263  GQKGDQGPEGPAGAEGPAGAEGPQGIQGPVGPKGDKGDTGSTGPIGPQGPQGPRGDRGET  10442

Query  105    GEGAYVYRSAFSVGL--------ETYVTIPNM  128
              G GA V  +  +V          + ++ +PN+
Sbjct  10443  GYGARVLGTKGAVSDLPATGTPGDAWIIVPNL  10538


>NC_025434.1 Shigella phage POCJ13, complete genome
Length=62699

 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 52/185 (28%), Positives = 75/185 (41%), Gaps = 19/185 (10%)
 Frame = +1

Query  48     GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGE------TGVPGAEGPRGFPGIQGRK  101
              G  G PG  G  G  G KG++G+PG  GP+G  GE       GV G  GP G PG +G K
Sbjct  39337  GPAGEPGPRGEPGPQGLKGDRGEPGPTGPQGPAGERGPQGPQGVAGPVGPAGEPGAKGDK  39516

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFA  161
              G+PG G  +  SA +   +      N+ +     F + Q   D    +    I
Sbjct  39517  GDPG-GTELLASANTW-TQPQTINGNLTVTGNGSFNDVQIRSDKRNKRNAIRIDNCLEKL  39690

Query  162    YHITVYMKDVK---------VSLFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVW  212
                +T Y+ +++         V LF +D   L     +   ++ D  SG     L     +
Sbjct  39691  DLLTGYLYEIQNADGSWQQSVGLFAQD--ALKAQPELVTSDTDIISGEERFRLNYNGVIA  39864

Query  213    LQVYG  217
              L V G
Sbjct  39865  LLVEG  39879


 Score = 37.4 bits (85),  Expect = 0.061, Method: Compositional matrix adjust.
 Identities = 29/62 (47%), Positives = 31/62 (50%), Gaps = 0/62 (0%)
 Frame = +1

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  GE GE+G  G+ GP G  G TG  G  G RG  GIQG
Sbjct  38692  AGPRGEKGEQGERGPQGLQGLKGETGERGPQGVQGPAGPTGATGPAGPRGERGEQGIQGP  38871

Query  101    KG  102
               G
Sbjct  38872  AG  38877


>NC_011357.1 Stx2-converting phage 1717, complete prophage genome
```

```
Length=62147

 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +1

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  56872  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  57051

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
Sbjct  57052  KGDPGETQIRFR  57087


>NC_009514.1 Phage cdtI DNA, complete genome
Length=47021

 Score = 45.1 bits (105),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +1

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  20257  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  20436

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
Sbjct  20437  KGDPGETQIRFR  20472


>NC_022098.1 Pandoravirus salinus, complete genome
Length=2473870

 Score = 44.7 bits (104),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 28/55 (51%), Positives = 34/55 (62%), Gaps = 0/55 (0%)
 Frame = -2

Query  48      GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               G  G  G+DG+DG  G +G KG+ G  GP+G  GE G PGA GP+G  G QG  G
Sbjct  240984  GPKGPKGKDGKDGCDGARGPKGEKGDKGPRGAKGEDGCPGARGPKGPKGDQGECG  240820


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 28/55 (51%), Positives = 33/55 (60%), Gaps = 0/55 (0%)
 Frame = -2

Query  48      GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
               G  G  G+DG DG  G KGEKGD G  GPKG+ G  G  G +G +G PG  G+ G
Sbjct  241272  GPKGKDGKDGCDGARGPKGEKGDKGPRGPKGEDGCHGPRGPKGEKGAPGPCGKCG  241108


 Score = 37.7 bits (86),  Expect = 0.047, Method: Compositional matrix adjust.
 Identities = 29/59 (49%), Positives = 32/59 (54%), Gaps = 0/59 (0%)
 Frame = -2

Query  48      GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
               G  G PG  G  G  GEKGEKGD G  GP G  G  G  G +G  G  G +G KGE G+
```

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Sbjct  241083  GPKGEPGCHGPRGPKGEKGEKGDCGKCGPCGPCGPKGPKGKDGKDGCDGARGPKGEKGD  240907


 Score = 37.0 bits (84),  Expect = 0.074, Method: Compositional matrix adjust.
 Identities = 52/208 (25%), Positives = 75/208 (36%), Gaps = 43/208 (21%)
 Frame = -1

Query  59       DGTPGE---KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAF  115
                 GTPG     G++G  G +GP G  GETG  G  GP   PG+QG              +A
Sbjct  1627075  QGTPGTSGPSGQQGPAGAMGPLGPRGETGPSGDAGP---PGVQGPPA----------TAT  1626935

Query  116      SVGLETYVTIPNMPIR---FTKIFYNQQ----------NHYDGSTGKFHCNIPGLYYFAY  162
                +V        P  P+       + + Q+          ++YD +T  F   + G+Y F
Sbjct  1626934  TVAFRAVKNAPQGPLSGGVTVTVAFEQEVFDLADGAAADNYDPATSVFTAPLDGVYRFEV  1626755

Query  163      HITVYM-----KDVKVSLFKKDKA------MLFTYDQYQENNVDQASGSVLLHLEVGDQV  211
                 IT+        +V   L     A      +  T     +      SG  L  L  G  V
Sbjct  1626754  PITLIRFLASSSNVACRLVSDSGAPPIERWLALTTVSSVDLFASTLSGDFL--LAAGQTV  1626581

Query  212      WLQVYGEGERNGLYADNDNDSTFTGFLL  239
                 ++V        L +      TFTG L+
Sbjct  1626580  RVEVTSSAA-GVLISGTSPTPTFTGALV  1626500


 Score = 37.0 bits (84),  Expect = 0.077, Method: Compositional matrix adjust.
 Identities = 37/84 (44%), Positives = 43/84 (51%), Gaps = 11/84 (13%)
 Frame = -2

Query  32      PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGE---KGEKGDPGL------IGPKGDIGE  82
               PKG C     G  G  G  G  G+DG+DG  GE   KG KGD G        GPKG  G+
Sbjct  241422  PKGDCG--KCGPCGPRGPRGPKGKDGKDGCDGERGPKGAKGDCGKCGPCGPCGPKGKDGK  241249

Query  83      TGVPGAEGPRGFPGIQGRKGEPGE  106
                G  GA GP+G  G +G +G  GE
Sbjct  241248  DGCDGARGPKGEKGDKGPRGPKGE  241177


>NC_031003.1 Propionibacterium phage Moyashi, complete genome
Length=29254

 Score = 44.7 bits (104),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 33/92 (36%), Positives = 45/92 (49%), Gaps = 4/92 (4%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+ G  G +G  G DG+DG  G  GE+GD G  GP G  G  G  G  GP G  G  G+
Sbjct  15067  GVSGRAGVDGVNGADGKDGRDGSAGERGDVGPSGPAGPQGAQGERGERGPAGVNGSDGKD  15246

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              G+ G      RS  SV    Y +   + ++++
Sbjct  15247  GKDGADGRDGRSVISV----YCSGGRLVVKYS  15330


>NC_004813.1 Enterobacteria phage BP-4795, complete genome
Length=57930

 Score = 44.7 bits (104),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
```

```
 Frame = +3

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  48711  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  48890

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
Sbjct  48891  KGDPGETQIRFR  48926


>NC_011132.1 Sputnik virophage, complete genome
Length=18343

 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 34/96 (35%), Positives = 48/96 (50%), Gaps = 11/96 (11%)
 Frame = +3

Query  41    AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
             AG  G  G +G  G  G+ G  G KG+ G+ G+ G KG+ G  G+ G  G +G  G  G
Sbjct  3510  AGTDGLKGDSGTDGLKGQTGNDGLKGQAGNDGIKGDKGEPGNDGLKGQTGTQGIKGDPGA  3689

Query  101   KGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIF  136
             KG+PG          SV L + +  P+  + F+ IF
Sbjct  3690  KGDPGT---------SVVLSSGIWTPS--VTFSTIF  3764


 Score = 40.4 bits (93),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 30/69 (43%), Positives = 37/69 (54%), Gaps = 3/69 (4%)
 Frame = +3

Query  41    AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGD---IGETGVPGAEGPRGFPGI  97
             +G  G  G +G  G  G+ GT G KG+ G  GL G  G     G+TG  G +G  G  GI
Sbjct  3429  SGDKGDKGDSGTDGLKGQAGTDGLKGQAGTDGLKGDSGTDGLKGQTGNDGLKGQAGNDGI  3608

Query  98    QGRKGEPGE  106
             +G KGEPG
Sbjct  3609  KGDKGEPGN  3635


 Score = 37.7 bits (86),  Expect = 0.042, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 31/65 (48%), Gaps = 4/65 (6%)
 Frame = +3

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G+ G  G NG  G  G     G+KG+KGD G  G KG  G  G+ G  G  G  G  G
Sbjct  3381  GLKGETGSNGLKGETGS----GDKGDKGDSGTDGLKGQAGTDGLKGQAGTDGLKGDSGTD  3548

Query  102   GEPGE  106
             G  G+
Sbjct  3549  GLKGQ  3563


>NC_007055.1 Staphylococcus phage 37, complete genome
Length=43681

 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 27/54 (50%), Positives = 32/54 (59%), Gaps = 0/54 (0%)
```

```
 Frame = +2

Query  50     NGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
              N   G  G  G  G +G KGD G +GP+G  GE G  G +GP+GF G QG KGE
Sbjct  22283  NEFKGPKGDTGEQGIQGIKGDTGPVGPQGYKGEKGDTGEQGPQGFVGPQGMKGE  22444


>NC_027626.1 Propionibacterium phage Procrass1, complete genome
Length=29347

 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 35/92 (38%), Positives = 47/92 (51%), Gaps = 13/92 (14%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+    GE+GD GL GP G  G  G  G  GP G  G  G+
Sbjct  15021  GVPGRAGVDGVNGADGRDGS---AGERGDVGLSGPAGPQGAQGERGERGPAGVNGSDGQD  15191

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              G+ G      RS  SV    Y +   + ++++
Sbjct  15192  GKDG------RSVVSV----YCSEGRLVVKYS  15257


 Score = 38.1 bits (87),  Expect = 0.033, Method: Compositional matrix adjust.
 Identities = 30/66 (45%), Positives = 33/66 (50%), Gaps = 0/66 (0%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DG DG PG  G  G  G  G  GE G  G  GP G  G QG
Sbjct  14961  LNGVKGPDGLPGANGSDGHDGVPGRAGVDGVNGADGRDGSAGERGDVGLSGPAGPQGAQG  15140

Query  100    RKGEPG  105
               +GE G
Sbjct  15141  ERGERG  15158


>NC_022340.1 Propionibacterium phage PHL114L00, complete genome
Length=29464

 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 32/67 (48%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = +2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DGRDG  G  G  G  G+ G  GD G  G PGA G  G  G QG
Sbjct  14954  LNGVNGPDGLPGANGSDGRDGVRGLAGADGKDGVKGDLGDTGPAGEPGAPGSAGSAGTQG  15133

Query  100    RKGEPGE  106
               +GE GE
Sbjct  15134  AQGERGE  15154


 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 29/61 (48%), Positives = 34/61 (56%), Gaps = 0/61 (0%)
 Frame = +2

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G PG NG+ GRDG  G  G  G+ G  G +G  G  GE G PG+ G  G  G QG +GE
```

```
Sbjct  14978  GLPGANGSDGRDGVRGLAGADGKDGVKGDLGDTGPAGEPGAPGSAGSAGTQGAQGERGER  15157

Query  105    G  105
              G
Sbjct  15158  G  15160


>NC_020197.1 Streptococcus phage TP-J34 complete genome
Length=45606

 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 28/55 (51%), Positives = 34/55 (62%), Gaps = 3/55 (5%)
 Frame = +2

Query  57     GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVY  111
              G DG  G +GE+G  G  GPKGD GE G+   +GPRG  GI G KGE G+  Y +
Sbjct  34445  GNDGKQGPQGERGLTGPQGPKGDRGERGL---QGPRGDQGIPGPKGEDGKTQYTH  34600


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 28/55 (51%), Positives = 34/55 (62%), Gaps = 3/55 (5%)
 Frame = +2

Query  57     GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVY  111
              G DG  G +GE+G  G  GPKGD GE G+   +GPRG  GI G KGE G+  Y +
Sbjct  35357  GNDGKQGPQGERGLTGPQGPKGDRGERGL---QGPRGDQGIPGPKGEDGKTQYTH  35512


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 28/55 (51%), Positives = 34/55 (62%), Gaps = 3/55 (5%)
 Frame = +2

Query  57     GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVY  111
              G DG  G +GE+G  G  GPKGD GE G+   +GPRG  GI G KGE G+  Y +
Sbjct  36269  GNDGKQGPQGERGLTGPQGPKGDRGERGL---QGPRGDQGIPGPKGEDGKTQYTH  36424


 Score = 44.3 bits (103),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 28/55 (51%), Positives = 34/55 (62%), Gaps = 3/55 (5%)
 Frame = +2

Query  57     GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVY  111
              G DG  G +GE+G  G  GPKGD GE G+   +GPRG  GI G KGE G+  Y +
Sbjct  37181  GNDGKQGPQGERGLTGPQGPKGDRGERGL---QGPRGDQGIPGPKGEDGKTQYTH  37336


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +2

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              I G+ G  G  G  G  G  G KG++G+ GL GP+GD G  G  G +G   +  I
Sbjct  34439  IRGNDGKQGPQGERGLTGPQGPKGDRGERGLQGPRGDQGIPGPKGEDGKTQYTHIAYADT  34618

Query  103    EPGEG  107
              E GEG
Sbjct  34619  ESGEG  34633
```

```
 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +2

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              I G+ G  G  G  G  G  G KG++G+ GL GP+GD G  G  G +G   +  I
Sbjct  35351  IRGNDGKQGPQGERGLTGPQGPKGDRGERGLQGPRGDQGIPGPKGEDGKTQYTHIAYADT  35530

Query  103    EPGEG  107
              E GEG
Sbjct  35531  ESGEG  35545


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +2

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              I G+ G  G  G  G  G  G KG++G+ GL GP+GD G  G  G +G   +  I
Sbjct  36263  IRGNDGKQGPQGERGLTGPQGPKGDRGERGLQGPRGDQGIPGPKGEDGKTQYTHIAYADT  36442

Query  103    EPGEG  107
              E GEG
Sbjct  36443  ESGEG  36457


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 26/65 (40%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +2

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              I G+ G  G  G  G  G  G KG++G+ GL GP+GD G  G  G +G   +  I
Sbjct  37175  IRGNDGKQGPQGERGLTGPQGPKGDRGERGLQGPRGDQGIPGPKGEDGKTQYTHIAYADT  37354

Query  103    EPGEG  107
              E GEG
Sbjct  37355  ESGEG  37369


>NC_000871.1 Streptococcus phage Sfi19, complete genome
Length=37370

 Score = 44.3 bits (103),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 28/55 (51%), Positives = 34/55 (62%), Gaps = 3/55 (5%)
 Frame = +1

Query  57     GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVY  111
              G DG  G +GE+G  G  GPKGD GE G+   +GPRG  GI G KGE G+  Y +
Sbjct  18736  GNDGKQGPQGERGLTGPQGPKGDRGERGL---QGPRGDQGIPGPKGEDGKTHYTH  18891


>NC_024210.1 Escherichia phage e4/1c, complete genome
Length=47112

 Score = 43.9 bits (102),  Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 34/80 (43%), Positives = 40/80 (50%), Gaps = 18/80 (23%)
 Frame = +3
```

```
Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGD---PGLIGP---------------KGDIGETGVP  86
             G  G  G  G  G DGTPGEKGE+G     G +GP               KGD G+ G
Sbjct  7428  GEVGPEGPQGPKGDDGTPGEKGERGAVGPQGTVGPQGIQGPQGIQGPAGLKGDKGDRGDT  7607

Query  87    GAEGPRGFPGIQGRKGEPGE  106
             G +GP+G  G  G KG+PGE
Sbjct  7608  GPQGPQGLKGDTGEKGDPGE  7667


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 35/61 (57%), Gaps = 15/61 (25%)
 Frame = +3

Query  60    GTPGEKGEKGDPGLIGPKGDIGETG---------------VPGAEGPRGFPGIQGRKGEP  104
             GT G+KGEKGDPG  GP+G+ G+TG               +PG +GP+G  G+QG  G
Sbjct  7833  GTKGDKGEKGDPGDTGPQGEKGDTGPQGPRGIQGQQGIQGLPGDQGPKGDQGLQGIAGPT  8012

Query  105   G  105
             G
Sbjct  8013  G  8015


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 26/58 (45%), Positives = 32/58 (55%), Gaps = 0/58 (0%)
 Frame = +3

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
             G  G  GRDG  G  G +G +G+ G  GP+G  G+ G PG +G RG  G QG  G  G
Sbjct  7365  GFQGTSGRDGMAGPQGPQGPRGEVGPEGPQGPKGDDGTPGEKGERGAVGPQGTVGPQG  7538


>NC_017974.1 Cronobacter phage CR3, complete genome
Length=149273

 Score = 43.9 bits (102),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 27/47 (57%), Positives = 31/47 (66%), Gaps = 0/47 (0%)
 Frame = +3

Query  57     GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
              G  G  GEKG+KGDPG  GP+G  GE G PG +GP+G  G QG  GE
Sbjct  11517  GPQGPQGEKGDKGDPGPQGPQGVQGEPGNPGEKGPQGEQGPQGEAGE  11657


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/62 (50%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G PG  GEKG  G  GP+G+ GE G  G +GP G  G QG KGE
Sbjct  11544  GDKGDPGPQGPQGVQGEPGNPGEKGPQGEQGPQGEAGEIGPQGPQGPVGPTGPQGEKGER  11723

Query  105    GE  106
              GE
Sbjct  11724  GE  11729


 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
```

```
 Identities = 30/69 (43%), Positives = 38/69 (55%), Gaps = 3/69 (4%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLI---GPKGDIGETGVPGAEGPRGFPG  96
              + G PG+PG  G  G  G  G  GE G +G  G +   GP+G+ GE G PG +GP G  G
Sbjct  11583  VQGEPGNPGEKGPQGEQGPQGEAGEIGPQGPQGPVGPTGPQGEKGERGEPGPQGPEGPAG  11762

Query  97     IQGRKGEPG  105
               QG +G  G
Sbjct  11763  PQGEQGPAG  11789


 Score = 39.3 bits (90),  Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 37/64 (58%), Gaps = 3/64 (5%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+ G PG+   PG  G  G  G +GE G+ G  GP+G +G TG  G +G RG PG QG +
Sbjct  11580  GVQGEPGN---PGEKGPQGEQGPQGEAGEIGPQGPQGPVGPTGPQGEKGERGEPGPQGPE  11750

Query  102    GEPG  105
              G  G
Sbjct  11751  GPAG  11762


 Score = 37.7 bits (86),  Expect = 0.040, Method: Compositional matrix adjust.
 Identities = 45/185 (24%), Positives = 77/185 (42%), Gaps = 21/185 (11%)
 Frame = +3

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G+ G  G +GEKG+ G  GP G  G  G  G +GP   PG  G
Sbjct  12093  AGPQGEQGPQGLQGPQGQRGIQGVQGEKGEKGDQGPVGPAGPAGPQGEQGP---PGETGP  12263

Query  101    KGEPGEGAY-----VYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIP  155
              KG+ G+ A      +Y S  +    +++ +P   +   ++  +  N+   +   F
Sbjct  12264  KGDKGDNALPTISGIYASPINK-TNSWIQLPGNNLGNVRLILSANNNVSQTRVGFSAGTS  12440

Query  156    GLYY---FAYHITVYMKDV-KVSLFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQV  211
               +     F+Y +T    DV ++   +     +     Y  ++         +++  GD+V
Sbjct  12441  SVAKRIGFSYALTTTYTDVNRIKTGRTGPTSISNTVVYPSDST--------INVGFGDKV  12596

Query  212    WLQVY  216
               L V+
Sbjct  12597  VLVVF  12611


>NC_031256.1 Mycobacterium phage Loser, complete genome
Length=53486

 Score = 43.9 bits (102),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 34/74 (46%), Positives = 41/74 (55%), Gaps = 9/74 (12%)
 Frame = +3

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEG  107
             G  G  G +G DG  G KG+KGD G +GP+      G+ GA GPRG  G QG KG+ G
Sbjct  4698  GQTGPAGLNGVDGAQGPKGDKGDQGEMGPQ------GLTGATGPRGLEGPQGPKGDQGPL  4859

Query  108   AYVYRSAFSVGLET  121
```

```
              Y   SA+ V LE
Sbjct  4860  GY---SAYQVALEA  4892


>NC_027400.1 Propionibacterium phage PHL055N00, complete genome
Length=29264

 Score = 43.5 bits (101),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 33/76 (43%), Positives = 38/76 (50%), Gaps = 6/76 (8%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG DG  G  GE+GD G  GP G  G  G  G  GP G  G  G+
Sbjct  15039  GVPGRAGADGVNGVDGADGRDGSAGERGDVGPSGPAGPQGAQGERGERGPAGVNGSDGKD  15218

Query  102    GEPGEGAYVYRSAFSV  117
              G+ G      RS  SV
Sbjct  15219  GKDG------RSVVSV  15248


 Score = 38.5 bits (88),  Expect = 0.029, Method: Compositional matrix adjust.
 Identities = 29/79 (37%), Positives = 36/79 (46%), Gaps = 0/79 (0%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G PG  GA G +G DG  G  G  G+ G +GP G  G  G  G  G RG  G+ G  G+
Sbjct  15039  GVPGRAGADGVNGVDGADGRDGSAGERGDVGPSGPAGPQGAQGERGERGPAGVNGSDGKD  15218

Query  105    GEGAYVYRSAFSVGLETYV  123
              G+      S +  G    V
Sbjct  15219  GKDGRSVVSVYCSGGRLVV  15275


 Score = 38.1 bits (87),  Expect = 0.035, Method: Compositional matrix adjust.
 Identities = 31/67 (46%), Positives = 35/67 (52%), Gaps = 3/67 (4%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              +AG  G PG NG+   DG DG PG  G  G  G+ G  G  G  G  G  GP G  G QG
Sbjct  14988  VAGSDGLPGANGS---DGHDGVPGRAGADGVNGVDGADGRDGSAGERGDVGPSGPAGPQG  15158

Query  100    RKGEPGE  106
               +GE GE
Sbjct  15159  AQGERGE  15179


>NC_018083.1 Clostridium phage phiCPV4, complete genome
Length=17972

 Score = 43.5 bits (101),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 26/55 (47%), Positives = 33/55 (60%), Gaps = 0/55 (0%)
 Frame = -3

Query  63    GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSV  117
             G KGEKGDPG  G KG+ G  G+PGA+G +G PG  G +G PG+     R    +
Sbjct  9129  GAKGEKGDPGAPGAKGEQGIQGLPGAKGEKGDPGATGAQGAPGKNGQTPRITMRI  8965
```

```
>NC_017980.1 Clostridium phage phiCP7R, complete genome
Length=18397

 Score = 43.5 bits (101),  Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 26/55 (47%), Positives = 33/55 (60%), Gaps = 0/55 (0%)
 Frame = -3

Query  63    GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSV  117
             G KGEKGDPG  G KG+ G  G+PGA+G +G PG  G +G PG+     R    +
Sbjct  9413  GAKGEKGDPGAPGAKGEQGIQGLPGAKGEKGDPGATGAQGAPGKNGQTPRITMRI  9249


>NC_021858.1 Pandoravirus dulcis, complete genome
Length=1908524

 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 30/52 (58%), Positives = 32/52 (62%), Gaps = 3/52 (6%)
 Frame = -1

Query  48      GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               G  G  G+DG DG  G KGEKGD G  GPK   GE G PGA GP+G  G QG
Sbjct  302030  GPKGPKGKDGCDGARGPKGEKGDKGPRGPK---GEDGCPGARGPKGPKGDQG  301884


 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 35/81 (43%), Positives = 38/81 (47%), Gaps = 1/81 (1%)
 Frame = -1

Query  26      GVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGV  85
               G   P  K  C G   G  G  G  GA G  G DG  G +G KGD G  GP G  G  G
Sbjct  302363  GPRGPKGKDGCDGER-GPKGEKGDKGARGPKGEDGCQGPRGPKGDKGAPGPCGKCGPCGP  302187

Query  86      PGAEGPRGFPGIQGRKGEPGE  106
                G  GP+G PG  G +G  GE
Sbjct  302186  CGPRGPKGEPGCHGPRGPKGE  302124


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 34/71 (48%), Positives = 39/71 (55%), Gaps = 2/71 (3%)
 Frame = -1

Query  32      PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGP  91
               PKG C     G  G  G  G  G+DG DG  G KGEKGD G  GPKG+ G  G  G +G
Sbjct  302405  PKGDCG--KCGPCGPRGPRGPKGKDGCDGERGPKGEKGDKGARGPKGEDGCQGPRGPKGD  302232

Query  92      RGFPGIQGRKG  102
               +G PG  G+ G
Sbjct  302231  KGAPGPCGKCG  302199


>NC_014792.1 Enterobacteria phage vB_EcoM-VR7, complete genome
Length=169285

 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 39/64 (61%), Gaps = 0/64 (0%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
```

```
               GI G  G  G PG +G  G  G++G +GD GL G +G  G  G PG +GP+G  G++G K
Sbjct  108077  GIQGDTGLQGVPGENGAIGPKGDQGIQGDTGLQGIQGPQGLQGDPGTQGPQGIQGLKGDK  108256

Query  102     GEPG  105
               G+ G
Sbjct  108257  GDQG  108268


 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/71 (45%), Positives = 40/71 (56%), Gaps = 6/71 (8%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGP------KGDIGETGVPGAEGPRGFP  95
               GI G  G  G  G  G  G  G KG+KG+ GL GP      +G+ GETG PG +G +G
Sbjct  108554  GIQGPQGIQGPKGDTGETGLQGLKGDKGEAGLTGPQGLQGIRGEQGETGAPGIQGIQGIA  108733

Query  96      GIQGRKGEPGE  106
               G QG KG+ G+
Sbjct  108734  GDQGPKGDTGD  108766


 Score = 38.9 bits (89),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 34/76 (45%), Positives = 42/76 (55%), Gaps = 15/76 (20%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---------IGPKGD---IGETGVPGAE  89
               G+ G PG NGA G  G  G  G +G +GD GL         IGPKGD    G+TG+ G +
Sbjct  108005  GLQGVPGENGAIGPKGDQGPVGPQGIQGDTGLQGVPGENGAIGPKGDQGIQGDTGLQGIQ  108184

Query  90      GPRGF---PGIQGRKG  102
               GP+G    PG QG +G
Sbjct  108185  GPQGLQGDPGTQGPQG  108232


 Score = 38.9 bits (89),  Expect = 0.021, Method: Compositional matrix adjust.
 Identities = 28/63 (44%), Positives = 37/63 (59%), Gaps = 6/63 (10%)
 Frame = +2

Query  50      NGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGI------QGRKGE  103
                G  GR G +G  G +G +G  G+ GPKGD GETG+ G +G +G  G+      QG +GE
Sbjct  108506  EGPEGRQGVEGAQGPQGIQGPQGIQGPKGDTGETGLQGLKGDKGEAGLTGPQGLQGIRGE  108685

Query  104     PGE  106
                GE
Sbjct  108686  QGE  108694


 Score = 38.5 bits (88),  Expect = 0.023, Method: Compositional matrix adjust.
 Identities = 32/74 (43%), Positives = 39/74 (53%), Gaps = 3/74 (4%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + GI G PG NG  G  G  G  G +G +GD GL G  G+ G  G  G +GP G  GIQG
Sbjct  107909  LTGIQGEPGENGDIGPKGDQGPVGPQGIQGDTGLQGVPGENGAIGPKGDQGPVGPQGIQG  108088

Query  100     R---KGEPGEGAYV  110
                   +G PGE   +
Sbjct  108089  DTGLQGVPGENGAI  108130
```

```
 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 30/79 (38%), Positives = 41/79 (52%), Gaps = 3/79 (4%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGD---IGETGVPGAEGPRGFPGIQ  98
               GI G  G  G  G  G  G PG +G +G  GL G KGD    GETG  G +G +G PG +
Sbjct  108149  GIQGDTGLQGIQGPQGLQGDPGTQGPQGIQGLKGDKGDQGIQGETGAQGIQGIQGVPGAK  108328

Query  99      GRKGEPGEGAYVYRSAFSV  117
               G  G  G     ++ ++++
Sbjct  108329  GDIGPVGPAGLTWKGSWNI  108385


 Score = 37.7 bits (86),  Expect = 0.042, Method: Compositional matrix adjust.
 Identities = 28/61 (46%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G  G KG+ G+ GL G KGD GE G+ G +G +G  G QG  G P
Sbjct  108527  GVEGAQGPQGIQGPQGIQGPKGDTGETGLQGLKGDKGEAGLTGPQGLQGIRGEQGETGAP  108706

Query  105     G  105
               G
Sbjct  108707  G  108709


 Score = 37.0 bits (84),  Expect = 0.074, Method: Compositional matrix adjust.
 Identities = 32/80 (40%), Positives = 40/80 (50%), Gaps = 15/80 (19%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGE---------KGEKGDPGLIGP------KGDIGETGVP  86
               G+ G PG NGA G  G  G  G+         +G +GDPG  GP      KGD G+ G+
Sbjct  108095  GLQGVPGENGAIGPKGDQGIQGDTGLQGIQGPQGLQGDPGTQGPQGIQGLKGDKGDQGIQ  108274

Query  87      GAEGPRGFPGIQGRKGEPGE  106
               G  G +G  GIQG  G  G+
Sbjct  108275  GETGAQGIQGIQGVPGAKGD  108334


>NC_033423.1 Lymphocystis disease virus Sa isolate SA9, complete genome
Length=208501

 Score = 43.5 bits (101),  Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 27/50 (54%), Positives = 31/50 (62%), Gaps = 0/50 (0%)
 Frame = +3

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEG  90
               +G PG PG  G PG DG  G PGEKG  G  G  GPKG++G  G PG +G
Sbjct  136002  SGEPGQPGIEGPPGNDGLPGPPGEKGSPGMHGTPGPKGELGARGTPGPKG  136151


 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 35/75 (47%), Positives = 37/75 (49%), Gaps = 12/75 (16%)
 Frame = +3

Query  43      IPGHPGHNGAPGRDGRDGTPG---------EKGEKGDPGLIGPKGDIGETGVPGAEGPR-  92
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               I G+PG  G PG  G+ GT G           G KGD G  GP G  GE G PG EGP
Sbjct  135864  INGNPGSRGHPGSRGKTGTAGPIGLPGLTGSPGTKGDRGKCGPAGPSGEPGQPGIEGPPG  136043

Query  93      --GFPGIQGRKGEPG  105
                 G PG  G KG PG
Sbjct  136044  NDGLPGPPGEKGSPG  136088


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 27/68 (40%), Positives = 37/68 (54%), Gaps = 0/68 (0%)
 Frame = -2

Query  35      ACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGF  94
               +C     G+ G  G  G  G  G  G  G KG+KG PG+ G  G++GE G  G +G +GF
Sbjct  151761  SCISNEMGVTGDKGEVGIKGSKGERGHRGNKGDKGLPGVRGFTGEVGEPGKKGEQGQKGF  151582

Query  95      PGIQGRKG  102
                G +G +G
Sbjct  151581  SGSKGDQG  151558


 Score = 37.4 bits (85),  Expect = 0.061, Method: Compositional matrix adjust.
 Identities = 34/73 (47%), Positives = 38/73 (52%), Gaps = 6/73 (8%)
 Frame = +3

Query  36      CTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEK-----GDPGLIGPKGDIGETGVPGAEG  90
               C G    I GHPG  G  G  G+ G PG KGEK     G PG  G  G  GE G  G  G
Sbjct  135561  CKGDQGDI-GHPGVQGPQGPPGQTGKPGLKGEKGRSCIGKPGKDGQPGHPGEPGRDGHSG  135737

Query  91      PRGFPGIQGRKGE  103
                RG PG++G +GE
Sbjct  135738  QRGIPGMKGDRGE  135776


 Score = 36.6 bits (83),  Expect = 0.097, Method: Compositional matrix adjust.
 Identities = 32/83 (39%), Positives = 39/83 (47%), Gaps = 18/83 (22%)
 Frame = -2

Query  42      GIPGHPGHNGAPGRDGRDGT------------------PGEKGEKGDPGLIGPKGDIGET  83
               G  GHPG  GA G  G  G                    G KG  GD G+ G KG+ GE+
Sbjct  151524  GDTGHPGFKGAQGELGEQGPQGKKGNKGDKGVSGLRGYKGLKGYSGDNGITGRKGEKGES  151345

Query  84      GVPGAEGPRGFPGIQGRKGEPGE  106
               G+PG +G +G PG+ G  G  GE
Sbjct  151344  GLPGFQGEKGDPGVDGVTGGKGE  151276


>NC_022335.1 Propionibacterium phage PHL067M10, complete genome
Length=29377

 Score = 43.5 bits (101),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 35/79 (44%), Positives = 39/79 (49%), Gaps = 9/79 (11%)
 Frame = +1

Query  42     GIPGHPGH---NGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
              G+PG  G    NG  G DGRDG  G  GE+GD G  GP G  G  G  G  GP G  G
Sbjct  14998  GVPGRAGVDGVNGVDGADGRDGVNGSAGERGDVGPSGPAGPQGAQGERGERGPAGANGSD  15177
```

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Query  99     GRKGEPGEGAYVYRSAFSV  117
              G+ G+ G      RS  SV
Sbjct  15178  GKDGKDG------RSVVSV  15216


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 28/63 (44%), Positives = 36/63 (57%), Gaps = 0/63 (0%)
 Frame = +1

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG+ G  G +GA GRDG +G+ GE+G+ G  G  GP+G  GE G  G  G  G  G  G+
Sbjct  15013  AGVDGVNGVDGADGRDGVNGSAGERGDVGPSGPAGPQGAQGERGERGPAGANGSDGKDGK  15192

Query  101    KGE  103
               G
Sbjct  15193  DGR  15201


>NC_028967.1 Propionibacterium phage PAC1, complete genome
Length=29605

 Score = 43.1 bits (100),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 30/82 (37%), Positives = 40/82 (49%), Gaps = 6/82 (7%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+ GE+      G +GP G  G  G  G  G RG  G+ G
Sbjct  15140  GVPGRAGADGVNGADGRDGSAGER------GYVGPSGPAGPQGAQGERGERGPAGVNGSD  15301

Query  102    GEPGEGAYVYRSAFSVGLETYV  123
              G+ G+      S +  G   +V
Sbjct  15302  GKDGKDGRSVVSVYCSGGRLFV  15367


 Score = 38.1 bits (87),  Expect = 0.038, Method: Compositional matrix adjust.
 Identities = 30/66 (45%), Positives = 33/66 (50%), Gaps = 0/66 (0%)
 Frame = +2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DG DG PG  G  G  G  G  G  GE G  G  GP G  G QG
Sbjct  15080  LNGVKGPDGLPGANGLDGHDGVPGRAGADGVNGADGRDGSAGERGYVGPSGPAGPQGAQG  15259

Query  100    RKGEPG  105
               +GE G
Sbjct  15260  ERGERG  15277


 Score = 37.4 bits (85),  Expect = 0.059, Method: Compositional matrix adjust.
 Identities = 35/82 (43%), Positives = 38/82 (46%), Gaps = 12/82 (15%)
 Frame = +2

Query  41     AGIPGHPGHNGAPGRDGRDGT------------PGEKGEKGDPGLIGPKGDIGETGVPGA  88
              AG+ G  G  GA GRDG +G+            PG  G KG  GL G  G  G  GVPG
Sbjct  14975  AGVRGPQGPAGADGRDGVNGSAGLVGPVGPQGSPGLNGVKGPDGLPGANGLDGHDGVPGR  15154

Query  89     EGPRGFPGIQGRKGEPGEGAYV  110
               G  G  G  GR G  GE  YV
Sbjct  15155  AGADGVNGADGRDGSAGERGYV  15220
```

```
>NC_031922.1 Synechococcus phage S-CAM9 isolate 1109NB16, complete genome
Length=174830

 Score = 43.1 bits (100),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 24/50 (48%), Positives = 31/50 (62%), Gaps = 0/50 (0%)
 Frame = +2

Query  57     GRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
              G  G  GEKG+KG+ G  G KGD G+ G  G  GP+G  G  G+KG+ G+
Sbjct  31559  GEKGQKGEKGQKGEIGQKGQKGDKGQKGELGPTGPKGQKGEIGQKGQKGQ  31708


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 23/51 (45%), Positives = 28/51 (55%), Gaps = 0/51 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPR  92
              G  G  G  G  G  G+ G  G+KG+KG+ G  GPKG  GE G  G +G R
Sbjct  31559  GEKGQKGEKGQKGEIGQKGQKGDKGQKGELGPTGPKGQKGEIGQKGQKGQR  31711


 Score = 37.4 bits (85),  Expect = 0.056, Method: Compositional matrix adjust.
 Identities = 23/53 (43%), Positives = 30/53 (57%), Gaps = 0/53 (0%)
 Frame = +2

Query  51     GAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
              G  G  G+ G  G+KGE G  G  G KG  GE G  G +G +G  G +G+KG+
Sbjct  31550  GPKGEKGQKGEKGQKGEIGQKGQKGDKGQKGELGPTGPKGQKGEIGQKGQKGQ  31708


>NC_027367.1 Propionibacterium phage PHL132N00, complete genome
Length=29003

 Score = 43.1 bits (100),  Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 33/76 (43%), Positives = 41/76 (54%), Gaps = 9/76 (12%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+ GE+G+ G  G  GP+G  GE    G  GP G  G  G+
Sbjct  14999  GVPGRAGADGVNGVDGRDGSAGERGDVGPSGPAGPQGAQGER---GERGPAGANGSDGKD  15169

Query  102    GEPGEGAYVYRSAFSV  117
              G+ G      RS  SV
Sbjct  15170  GKDG------RSVVSV  15199


 Score = 40.4 bits (93),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 35/81 (43%), Positives = 43/81 (53%), Gaps = 3/81 (4%)
 Frame = +2

Query  26     GVLLPL-PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETG  84
              GV+ P+ P+G+    + G+ G  G  G  G DGRDG PG  G  G  G+ G  G  GE G
Sbjct  14900  GVVGPVGPQGSP--GLNGVKGPDGLPGVNGSDGRDGVPGRAGADGVNGVDGRDGSAGERG  15073

Query  85     VPGAEGPRGFPGIQGRKGEPG  105
                G  GP G  G QG +GE G
```

```
Sbjct  15074  DVGPSGPAGPQGAQGERGERG  15136


>NC_018846.1 Escherichia phage P13374, complete genome
Length=60894

 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G  G +G KGDPG  GPKGD G  G  G +G  G  G QG K
Sbjct  42064  GVPGPKGDKGDSGPAGPAGPRGVQGPKGDPGPQGPKGDTGAAGAKGEKGATGATGPQGPK  42243

Query  102    GEPG  105
              G+ G
Sbjct  42244  GDTG  42255


 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  41473  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  41652

Query  105    G  105
              G
Sbjct  41653  G  41655


>NC_031065.1 Salmonella phage vB_SnwM_CGG4-1, complete genome
Length=159878

 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 39/102 (38%), Positives = 46/102 (45%), Gaps = 21/102 (21%)
 Frame = +1

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL-----------------IGPKGDIGE-  82
              AG  G PG  G  G  G  G PG  GE G  GL                 IGPKGD G+
Sbjct  98305  AGPKGDPGPQGLQGIQGPKGDPGADGEPGPQGLQGPAGPQGPIGPGGEGSIGPKGDKGDP  98484

Query  83     --TGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETY  122
                 G+ G +GP G PGIQG  G  G    V+R  ++  +E Y
Sbjct  98485  GPQGLQGIQGPAGEPGIQGPIGPIGPAGLVWRGQWN-SIENY  98607


 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 42/136 (31%), Positives = 59/136 (43%), Gaps = 14/136 (10%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ---GRK  101
              G  G  G  G+ G  G  G KGD G+ GP+G  GE G+ G +GP G  G Q   G K
Sbjct  98974  GEEGPQGIQGPTGQRGATGPAGPKGDTGIAGPQGVQGERGIQGIQGPAGPTGAQGPVGPK  99153

Query  102    GEPGEGA-YVYRSAFSVGLETYVT--IPNMPIRFTKIFYNQQNHYDGSTGK--------F  150
              G+ GE A +   S     L+T     +   P R+ +        YD +  K        F
```

```
Sbjct  99154  GDKGEDAVFDVESLTQSQLQTLYNKLLAFHPTRYWRDSVKFPFPYDTTVEKILPLWAFNF  99333

Query  151    HCNIPGLYYFAYHITV  166
                +   + Y+++ I V
Sbjct  99334  KLHFKMISYYSFEIRV  99381


>NC_014260.1 Enterobacteria phage IME08, complete genome
Length=172253

 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 31/65 (48%), Positives = 36/65 (55%), Gaps = 0/65 (0%)
 Frame = +1

Query  41      AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
               +G  G  G  G  G  G  G  G KG+KGD GL GP G IG  G  G +G RG  GIQG
Sbjct  108829  SGAQGLQGPKGDKGDTGLQGIQGPKGDKGDTGLQGPIGPIGPKGDQGPQGSRGIQGIQGP  109008

Query  101     KGEPG  105
               +G+ G
Sbjct  109009  QGDQG  109023


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 30/60 (50%), Positives = 34/60 (57%), Gaps = 3/60 (5%)
 Frame = +1

Query  49      HNGAPGRDGRDGTPGEKGEKGDPGLIG---PKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
                 GA G  G  G  G KG+KGD GL G   PKGD G+TG+ G  GP G  G QG +G  G
Sbjct  108808  SQGARGESGAQGLQGPKGDKGDTGLQGIQGPKGDKGDTGLQGPIGPIGPKGDQGPQGSRG  108987


>NC_008464.1 Stx2-converting phage 86, complete genome
Length=60238

 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 51/185 (28%), Positives = 75/185 (41%), Gaps = 19/185 (10%)
 Frame = +1

Query  48     GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGE------TGVPGAEGPRGFPGIQGRK  101
              G  G PG  G  G  G KG++G+PG  GP+G  GE       GV G  GP G PG +G K
Sbjct  18607  GPAGEPGPRGEPGPQGLKGDRGEPGPTGPQGPAGERGPQGPQGVAGPVGPAGEPGAKGDK  18786

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFA  161
              G+PG G  +  SA +   +      ++ +     F + Q   D    +    I
Sbjct  18787  GDPG-GTELLASANTW-TQPQTINGDLTVTGNGSFNDVQIRSDKRNKRNAIRIDNCLEKL  18960

Query  162    YHITVYMKDVK---------VSLFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVW  212
                +T Y+ +++         V LF +D   L    +   ++ D  SG     L     +
Sbjct  18961  DLLTGYLYEIQNADGSWQQSVGLFAQD--ALKAQPELVTSDTDIISGEERFRLNYNGVIA  19134

Query  213    LQVYG  217
              L V G
Sbjct  19135  LLVEG  19149


 Score = 37.4 bits (85),  Expect = 0.062, Method: Compositional matrix adjust.
 Identities = 29/62 (47%), Positives = 31/62 (50%), Gaps = 0/62 (0%)
```

```
 Frame = +1

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  GE GE+G  G+ GP G  G TG  G  G RG  GIQG
Sbjct  17962  AGPRGEKGEQGERGPQGLQGLKGETGERGPQGVQGPAGPTGATGPAGPRGERGEQGIQGP  18141

Query  101    KG  102
               G
Sbjct  18142  AG  18147


>NC_027389.1 Propionibacterium phage PHL141N00, complete genome
Length=29494

 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 34/92 (37%), Positives = 45/92 (49%), Gaps = 10/92 (11%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG DG  G  GE+GD G  GP G  G  G  G  GP G  G  G+
Sbjct  15019  GVPGRAGADGVNGVDGADGRDGSAGERGDVGPSGPAGPQGAQGERGERGPAGANGSDGKD  15198

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              G+ G      RS  SV    Y +   + ++++
Sbjct  15199  GKDG------RSVVSV----YCSDGRLVVKYS  15264


>NC_022968.1 Enterobacteria phage 4MG, complete genome
Length=148567

 Score = 43.1 bits (100),  Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 32/92 (35%), Positives = 45/92 (49%), Gaps = 8/92 (9%)
 Frame = -1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  G  G +G  G +GPKGD G+TG+ G  GP+G  G +G +GE
Sbjct  49852  GQKGDQGPTGPTGPQGPQGNDGAQGIQGPVGPKGDKGDTGLTGPVGPQGPVGPKGDRGET  49673

Query  105    G--------EGAYVYRSAFSVGLETYVTIPNM  128
              G        +GA     A     + ++ +PN+
Sbjct  49672  GYSARVLGTKGATSELPATGTSGDAWIIVPNL  49577


>NC_018839.1 Propionibacterium phage P14.4, complete genome
Length=29729

 Score = 43.1 bits (100),  Expect = 9e-04, Method: Compositional matrix adjust.
 Identities = 28/60 (47%), Positives = 34/60 (57%), Gaps = 0/60 (0%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+ GE+G+ G  G  GP+G  GE G  G  G  G  G  GR
Sbjct  15024  GVPGRVGVDGVNGADGRDGSAGERGDVGPSGPAGPQGAQGERGERGPAGADGSDGKDGRS  15203


>NC_027333.1 Propionibacterium phage PHL070N00, complete genome
Length=29421
```

```
 Score = 43.1 bits (100),  Expect = 9e-04, Method: Compositional matrix adjust.
 Identities = 34/76 (45%), Positives = 42/76 (55%), Gaps = 3/76 (4%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+ GE G+ G  G  GP+G  GE G  G  GP+G  G  G
Sbjct  15017  GVPGRAGVDGVNGVDGRDGSAGELGDVGPAGPAGPQGAQGERGERGPIGPQGPAGADGTN  15196

Query  102    GEPGEGAYVYRSAFSV  117
              G+ G+     RS  SV
Sbjct  15197  GKDGKDG---RSVVSV  15235


 Score = 37.0 bits (84),  Expect = 0.090, Method: Compositional matrix adjust.
 Identities = 33/78 (42%), Positives = 37/78 (47%), Gaps = 12/78 (15%)
 Frame = +2

Query  41     AGIPGHPGHNGAPGRDGRD------------GTPGEKGEKGDPGLIGPKGDIGETGVPGA  88
              AG+ G  G  GA GRDG +            G+PG  G KG  GL G  G  G  GVPG
Sbjct  14852  AGVRGPQGPAGADGRDGVNGSAGLVGPVGPQGSPGLNGVKGPDGLPGANGSDGHDGVPGR  15031

Query  89     EGPRGFPGIQGRKGEPGE  106
               G  G  G+ GR G  GE
Sbjct  15032  AGVDGVNGVDGRDGSAGE  15085


>NC_023716.1 Mycobacterium phage Alma, complete genome
Length=53177

 Score = 43.1 bits (100),  Expect = 9e-04, Method: Compositional matrix adjust.
 Identities = 28/58 (48%), Positives = 34/58 (59%), Gaps = 0/58 (0%)
 Frame = +2

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
             G PG  GA G  G  G PG  G +G+PG  GP+G  G+TG  G +GP+G  G QG  G
Sbjct  4871  GDPGTAGATGLTGSAGAPGAPGPQGEPGPTGPQGPKGDTGATGPQGPKGDTGAQGPAG  5044


 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 37/96 (39%), Positives = 44/96 (46%), Gaps = 12/96 (13%)
 Frame = +2

Query  41    AGIPGHPGHNGAPGRDGRDGTPGE------KGEKGDPGLIGPKGDIGETGVPGAEGPRGF  94
             AG PG PG  G PG  G  G  G+      +G KGD G  GP G  G  G  GA+GP G
Sbjct  4913  AGAPGAPGPQGEPGPTGPQGPKGDTGATGPQGPKGDTGAQGPAGATGPKGDTGAQGPTGA  5092

Query  95    PGIQGRKGEPGEG------AYVYRSAFSVGLETYVT  124
              G QG  G P           V ++A+  G +T  T
Sbjct  5093  TGAQGPSGTPSSTNTVLDFVKVTQAAYDAGPKTATT  5200


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 28/59 (47%), Positives = 33/59 (56%), Gaps = 0/59 (0%)
 Frame = +2

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
             G  G  G  G  G  G+KG+KGDPG  G  G  G  G PGA GP+G PG  G +G  G+
Sbjct  4808  GEKGDKGDLGPQGPKGDKGDKGDPGTAGATGLTGSAGAPGAPGPQGEPGPTGPQGPKGD  4984
```

```
 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 34/70 (49%), Positives = 37/70 (53%), Gaps = 6/70 (9%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGF------P  95
             GI G  G  G  G  G  G  GEKG+KGD G  GPKGD G+ G PG  G  G       P
Sbjct  4745  GIQGATGPQGLQGPKGDQGIQGEKGDKGDLGPQGPKGDKGDKGDPGTAGATGLTGSAGAP  4924

Query  96    GIQGRKGEPG  105
             G  G +GEPG
Sbjct  4925  GAPGPQGEPG  4954


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 30/62 (48%), Positives = 35/62 (56%), Gaps = 0/62 (0%)
 Frame = +2

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G PG  G  G  G  G  G KGD G  GP+G  G TG  G +GP+G  GIQG KG+
Sbjct  4646  GDPGDTGPTGATGPAGPQGATGPKGDTGAQGPQGIQGATGPQGLQGPKGDQGIQGEKGDK  4825

Query  105   GE  106
             G+
Sbjct  4826  GD  4831


>NC_027370.1 Propionibacterium phage PHL179M00, complete genome
Length=29428

 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/76 (42%), Positives = 40/76 (53%), Gaps = 9/76 (12%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+ GE+G+      +GP G  G  GV G  G RG  G+ G
Sbjct  15032  GVPGRAGADGVNGVDGRDGSAGERGD------VGPSGPAGPQGVRGERGERGPAGVNGSD  15193

Query  102    GEPGEGAYVYRSAFSV  117
              G  G+     RS  SV
Sbjct  15194  GHDGKDG---RSVVSV  15232


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 36/66 (55%), Gaps = 0/66 (0%)
 Frame = +2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DGR+G PG  G  G  G+ G  G  GE G  G  GP G  G++G
Sbjct  14972  LNGVKGPDGLPGANGLDGRNGVPGRAGADGVNGVDGRDGSAGERGDVGPSGPAGPQGVRG  15151

Query  100    RKGEPG  105
               +GE G
Sbjct  15152  ERGERG  15169


 Score = 37.0 bits (84),  Expect = 0.072, Method: Compositional matrix adjust.
```

```
 Identities = 31/73 (42%), Positives = 37/73 (51%), Gaps = 12/73 (16%)
 Frame = +2

Query  40     MAGIPGHPG---HNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              +AG+PG  G     G  G DGRDG        G  GL+GP G  G  G+ G +GP G PG
Sbjct  14846  VAGVPGPAGVRGPQGPAGVDGRDGV------NGSAGLVGPVGPQGSPGLNGVKGPDGLPG  15007

Query  97     ---IQGRKGEPGE  106
                 + GR G PG
Sbjct  15008  ANGLDGRNGVPGR  15046


>NC_028685.1 Shigella phage Ss-VASD, complete genome
Length=62851

 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G +G KGDPG  GPKGD G  G  G +G  G  G QG K
Sbjct  43981  GVPGPKGDKGDSGPAGPAGPRGVQGPKGDPGPQGPKGDTGAAGAKGEKGATGATGPQGPK  44160

Query  102    GEPG  105
              G+ G
Sbjct  44161  GDTG  44172


 Score = 38.5 bits (88),  Expect = 0.023, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  43390  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  43569

Query  105    G  105
              G
Sbjct  43570  G  43572


 Score = 37.4 bits (85),  Expect = 0.062, Method: Compositional matrix adjust.
 Identities = 27/58 (47%), Positives = 29/58 (50%), Gaps = 0/58 (0%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              G PG  G  G  G  GEKG  G  G  GPKGD G  G  G +GP+G  G  G  G
Sbjct  44062  GDPGPQGPKGDTGAAGAKGEKGATGATGPQGPKGDTGAVGPAGPQGPKGDTGAAGPAG  44235


>NC_027354.1 Propionibacterium phage PHL301M00, complete genome
Length=29323

 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 33/76 (43%), Positives = 38/76 (50%), Gaps = 6/76 (8%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
```

```
              G+PG  G +G  G DG DG  G  GE+GD G  GP G  G  G  G  GP G  G  G+
Sbjct  15002  GVPGRAGADGVNGVDGADGRDGSAGERGDVGPSGPAGPQGAQGERGERGPAGANGSDGKD  15181

Query  102    GEPGEGAYVYRSAFSV  117
              G+ G      RS  SV
Sbjct  15182  GKDG------RSVVSV  15211


 Score = 38.1 bits (87),  Expect = 0.036, Method: Compositional matrix adjust.
 Identities = 30/67 (45%), Positives = 34/67 (51%), Gaps = 0/67 (0%)
 Frame = +2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  G  G DGRDG PG  G  G  G+ G  G  G  G  G  GP G  G QG
Sbjct  14942  LNGVKGPDGLPGVNGSDGRDGVPGRAGADGVNGVDGADGRDGSAGERGDVGPSGPAGPQG  15121

Query  100    RKGEPGE  106
               +GE GE
Sbjct  15122  AQGERGE  15142


 Score = 37.4 bits (85),  Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 29/69 (42%), Positives = 35/69 (51%), Gaps = 9/69 (13%)
 Frame = +2

Query  40     MAGIPGHPG---HNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              +AG+PG  G     G  G DGRDG        G  GL+GP G  G  G+ G +GP G PG
Sbjct  14816  VAGVPGPAGVRGPQGPAGVDGRDGV------NGSAGLVGPVGPQGSPGLNGVKGPDGLPG  14977

Query  97     IQGRKGEPG  105
              + G  G  G
Sbjct  14978  VNGSDGRDG  15004


>NC_031005.1 Propionibacterium phage QueenBey, complete genome
Length=29338

 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/76 (42%), Positives = 38/76 (50%), Gaps = 6/76 (8%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG+DG  G  GE+G  G  GP G  G  G  G  GP G  G  G+
Sbjct  15015  GVPGRAGADGVNGSDGKDGANGADGERGAVGPSGPAGPQGAQGERGERGPAGVNGADGKD  15194

Query  102    GEPGEGAYVYRSAFSV  117
              G+ G      RS  SV
Sbjct  15195  GKDG------RSVVSV  15224


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 32/67 (48%), Positives = 35/67 (52%), Gaps = 0/67 (0%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DGRDG PG  G  G  G  G  G  G  GA GP G  G QG
Sbjct  14955  LNGVNGPDGLPGANGSDGRDGVPGRAGADGVNGSDGKDGANGADGERGAVGPSGPAGPQG  15134
```

```
Query  100    RKGEPGE  106
               +GE GE
Sbjct  15135  AQGERGE  15155


 Score = 38.5 bits (88),  Expect = 0.025, Method: Compositional matrix adjust.
 Identities = 29/61 (48%), Positives = 31/61 (51%), Gaps = 0/61 (0%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G PG NG+ GRDG  G  G  G  G  G  G  GE G  G  GP G  G QG +GE
Sbjct  14979  GLPGANGSDGRDGVPGRAGADGVNGSDGKDGANGADGERGAVGPSGPAGPQGAQGERGER  15158

Query  105    G  105
              G
Sbjct  15159  G  15161


>NC_018852.1 Propionibacterium phage P100D, complete genome
Length=29506

 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/76 (41%), Positives = 39/76 (51%), Gaps = 12/76 (16%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DGRDG+ GE+G+      +GP G  G  G  G  GP G  G  G+
Sbjct  15025  GVPGRAGADGVNGVDGRDGSAGERGD------VGPSGPSGPAGAQGERGPAGVNGSDGKD  15186

Query  102    GEPGEGAYVYRSAFSV  117
              G+ G      RS  SV
Sbjct  15187  GKDG------RSVVSV  15216


 Score = 38.1 bits (87),  Expect = 0.037, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 33/66 (50%), Gaps = 0/66 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DG DG PG  G  G  G+ G  G  GE G  G  GP G  G QG
Sbjct  14965  LNGVKGPDGLPGANGSDGHDGVPGRAGADGVNGVDGRDGSAGERGDVGPSGPSGPAGAQG  15144

Query  100    RKGEPG  105
               +G  G
Sbjct  15145  ERGPAG  15162


>NC_026440.1 Pandoravirus inopinatum isolate KlaHel, complete genome
Length=2243109

 Score = 42.7 bits (99),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/62 (52%), Positives = 39/62 (63%), Gaps = 3/62 (5%)
 Frame = +2

Query  52       APGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPR---GFPGIQGRKGEPGEGA  108
                A G+DG+DG  G KGEKGD G  GPKG+ G  G  GA+GP+   G  G +G +G  GE A
Sbjct  2017676  AQGKDGKDGARGPKGEKGDKGPRGPKGEDGCPGARGAKGPKGDQGECGPRGPRGPKGEDA  2017855
```

```
Query  109      YV  110
                 V
Sbjct  2017856  VV  2017861


 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 37/122 (30%), Positives = 56/122 (46%), Gaps = 7/122 (6%)
 Frame = +3

Query  48       GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEG  107
                G  G  G  G +G  G++G +G  G  GP+G  G+ G  G EG +G  G QG+ GEP
Sbjct  1931964  GPQGPQGLMGPEGPQGQQGPEGPEGQQGPEGPEGQQGPEGPEGQQGPEGPQGQPGEP-RN  1932140

Query  108      AYVYRSAFSVGLETYVTIPNMPIRFTKIFYN-----QQNHYDGSTGKFHCNIPGLYYFAY  162
                   +R A  + L  Y      P+ +    Y+       N+YD +T  F   +  +Y F
Sbjct  1932141  TVAFR-ADGIVLSGYQGPVTDPVVYESEVYDLVNGAPANNYDPTTWTFTAPLAAVYRFTA  1932317

Query  163      HI  164
                ++
Sbjct  1932318  NL  1932323


 Score = 39.3 bits (90),  Expect = 0.016, Method: Compositional matrix adjust.
 Identities = 34/71 (48%), Positives = 39/71 (55%), Gaps = 2/71 (3%)
 Frame = +2

Query  32       PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGP  91
                PKG C     G  G  G  G  G+DG DG  G KGEKGD G  GPKG+ G  G  G +G
Sbjct  2017301  PKGDC--GKCGPCGPRGPRGPKGKDGCDGERGPKGEKGDKGPRGPKGEDGCHGPRGPKGE  2017474

Query  92       RGFPGIQGRKG  102
                +G PG  G+ G
Sbjct  2017475  KGAPGPCGKCG  2017507


 Score = 37.4 bits (85),  Expect = 0.066, Method: Compositional matrix adjust.
 Identities = 31/98 (32%), Positives = 40/98 (41%), Gaps = 10/98 (10%)
 Frame = -2

Query  68       KGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPN  127
                +G PG +GP G  G  G PG  GP G PG+      P      +      GL    TI
Sbjct  1627973  QGPPGQVGPIGSTGAMGAPGDTGPTGPPGVAAIV--PMVAFRAVKDTTQTGLGPGTTI--  1627806

Query  128      MPIRFTKIFYNQQN-----HYDGSTGKFHCNIPGLYYF  160
                  I F +  Y+  N     +YD +T  F     G+Y F
Sbjct  1627805  -TITFRQEIYDLVNGTTADNYDPTTSTFTAPADGVYRF  1627695


>NC_018841.1 Propionibacterium phage P101A, complete genome
Length=29574

 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 34/92 (37%), Positives = 45/92 (49%), Gaps = 10/92 (11%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG DG  G  GE+GD G  GP G  G  G  G  GP G  G  G+
Sbjct  15031  GVPGRAGADGVNGVDGADGRDGSAGERGDVGPSGPAGPQGAQGERGERGPAGANGSDGKD  15210
```

```
Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              G+ G      RS  SV    Y +   + ++++
Sbjct  15211  GKDG------RSVVSV----YCSGGRLVVKYS  15276


 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 31/67 (46%), Positives = 35/67 (52%), Gaps = 0/67 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DGRDG PG  G  G  G+ G  G  G  G  G  GP G  G QG
Sbjct  14971  LNGVKGPDGLPGANGSDGRDGVPGRAGADGVNGVDGADGRDGSAGERGDVGPSGPAGPQG  15150

Query  100    RKGEPGE  106
               +GE GE
Sbjct  15151  AQGERGE  15171


>NC_022337.1 Propionibacterium phage PHL071N05, complete genome
Length=29467

 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 33/92 (36%), Positives = 46/92 (50%), Gaps = 10/92 (11%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG+DG  G  GE+GD G  GP G  G  G  G  G  G  G +G+
Sbjct  15023  GVPGRAGVDGVAGVDGKDGANGADGERGDVGPSGPAGPQGAQGERGERGNAGANGSEGKD  15202

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              G+ G      RS  SV    Y +   + ++++
Sbjct  15203  GKDG------RSVVSV----YCSEGRLVVKYS  15268


 Score = 38.1 bits (87),  Expect = 0.031, Method: Compositional matrix adjust.
 Identities = 35/82 (43%), Positives = 44/82 (54%), Gaps = 3/82 (4%)
 Frame = +2

Query  26     GVLLPL-PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETG  84
              GV+ P+ P+G+    + G+ G  G  GA G+DG DG PG  G  G  G+ G  G  G  G
Sbjct  14924  GVVGPVGPQGSP--GLNGVKGPDGLPGASGKDGHDGVPGRAGVDGVAGVDGKDGANGADG  15097

Query  85     VPGAEGPRGFPGIQGRKGEPGE  106
                G  GP G  G QG +GE GE
Sbjct  15098  ERGDVGPSGPAGPQGAQGERGE  15163


 Score = 37.4 bits (85),  Expect = 0.062, Method: Compositional matrix adjust.
 Identities = 25/63 (40%), Positives = 32/63 (51%), Gaps = 0/63 (0%)
 Frame = +2

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              + G PG  G  G+ G  G  G  G  G  G++GP G  G  G+ G +GP G PG  G+ G
Sbjct  14837  VQGVPGPAGVRGQQGPAGADGRDGSNGSAGVVGPVGPQGSPGLNGVKGPDGLPGASGKDG  15016

Query  103    EPG  105
                G
```

```
Sbjct  15017  HDG  15025


>NC_027629.1 Propionibacterium phage Attacne, complete genome
Length=28876

 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 34/92 (37%), Positives = 46/92 (50%), Gaps = 10/92 (11%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG DG  G  GE+GD G  GP G  G  G  G  GP G  G  G+
Sbjct  15015  GVPGRAGADGVNGVDGADGRDGSAGERGDMGPSGPAGPQGAQGERGERGPAGANGSDGKD  15194

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              G+ G      RS  SV    Y +  ++ ++++
Sbjct  15195  GKDG------RSIVSV----YCSGGSLMVKYS  15260


>NC_027385.1 Propionibacterium phage PHL092M00, complete genome
Length=29261

 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 27/62 (44%), Positives = 36/62 (58%), Gaps = 0/62 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+ G  G +G  G DGRDG+ GE+G+ G  G  GP+G  GE G  G++G  G  G  G+
Sbjct  15023  GVAGRAGADGVNGADGRDGSAGERGDVGPSGPAGPQGAQGERGERGSDGVNGSDGKDGKD  15202

Query  102    GE  103
              G
Sbjct  15203  GR  15208


>NC_003225.3 White spot syndrome virus strain CN01, complete genome
Length=309286

 Score = 42.4 bits (98),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 38/75 (51%), Positives = 42/75 (56%), Gaps = 12/75 (16%)
 Frame = +1

Query  41    AGIPGHPGHNGAPGRDGRDGT---PGEKGEKGDPGL------IGPKGDIGETGVP---GA  88
             AG PG  G  G PGRDG DG+   PGE+GE G  G        GP+G+ GE G P   GA
Sbjct  1558  AGPPGERGATGIPGRDGVDGSVGPPGERGETGPAGRDGSVGPAGPQGERGENGRPGRDGA  1737

Query  89    EGPRGFPGIQGRKGE  103
              GP G  G QG KGE
Sbjct  1738  TGPIGPAGPQGEKGE  1782


 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 29/58 (50%), Positives = 36/58 (62%), Gaps = 0/58 (0%)
 Frame = +1

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
             G  G NG PG+DG  G  G  GE+G+ G IGP G  G TG+PG +G  G  G QG++G
Sbjct  2533  GEKGENGRPGKDGATGPMGPPGERGETGPIGPAGPQGATGLPGRDGVDGSVGPQGKRG  2706
```

```
 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 35/74 (47%), Positives = 40/74 (54%), Gaps = 12/74 (16%)
 Frame = +1

Query  41    AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL---------IGPKGDIGETGVP---GA  88
             AG PG  G NG PGRDG  G  G  G +G+ GL         IGP+G+ GE G P   GA
Sbjct  2395  AGPPGERGENGRPGRDGATGPIGPAGPQGETGLAGLPGRDGAIGPQGEKGENGRPGKDGA  2574

Query  89    EGPRGFPGIQGRKG  102
              GP G PG +G  G
Sbjct  2575  TGPMGPPGERGETG  2616


 Score = 38.9 bits (89),  Expect = 0.021, Method: Compositional matrix adjust.
 Identities = 44/106 (42%), Positives = 51/106 (48%), Gaps = 14/106 (13%)
 Frame = +1

Query  14    PGHDQETTTQGP----GVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGT---PGEKG  66
             PG D      GP    G + P  +    G  AG PG  G  G PGRDG DG+    GE+G
Sbjct  865   PGRDGAVGPAGPPGERGAIGPAGRDGAVGP-AGPPGERGATGIPGRDGVDGSVGPQGERG  1041

Query  67    EKGDPGL------IGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
             E G PG        GP+G  G TG  G +G  G  G QG KGE G+
Sbjct  1042  EIGRPGRDGAVGPAGPQGRRGATGRAGKDGAVGPAGPQGEKGEAGK  1179


 Score = 37.7 bits (86),  Expect = 0.042, Method: Compositional matrix adjust.
 Identities = 31/69 (45%), Positives = 37/69 (54%), Gaps = 3/69 (4%)
 Frame = +1

Query  41    AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFP---GI  97
             AG PG  G  G PGR+G DG+ G +G +G  G  G  G +G  G PG  G  G P   G+
Sbjct  1432  AGPPGERGATGLPGRNGVDGSIGPQGRRGATGRAGKDGAVGPAGPPGERGATGIPGRDGV  1611

Query  98    QGRKGEPGE  106
              G  G PGE
Sbjct  1612  DGSVGPPGE  1638


 Score = 37.7 bits (86),  Expect = 0.044, Method: Compositional matrix adjust.
 Identities = 38/92 (41%), Positives = 47/92 (51%), Gaps = 9/92 (10%)
 Frame = +1

Query  14    PGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGL  73
             PG D E  + GP     L +GA      G PG  G  G  GR G+DG  G  G +G  G+
Sbjct  2881  PGRDGEDGSTGPMGPQGL-RGAT-----GAPGPQGERGLKGRPGKDGETGPPGRQGRDGI  3042

Query  74    IGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
             +GP+G  GE G PG +   G  G +GR G PG
Sbjct  3043  MGPRGLRGEKGAPGND---GLEGPEGRDGAPG  3129


 Score = 37.4 bits (85),  Expect = 0.066, Method: Compositional matrix adjust.
 Identities = 33/70 (47%), Positives = 41/70 (59%), Gaps = 9/70 (13%)
 Frame = +1
```

```
Query  40    MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAE---GPRGFPG  96
             + GI G  G  G  G++GR G  G +GEKGD      KGD GE G+ GA+   GPRG  G
Sbjct  3544  LTGIEGPRGPRGIQGKEGRMGKIGHRGEKGD------KGDRGEQGIAGADGEKGPRGLRG  3705

Query  97    IQGRKGEPGE  106
             I+G  G PG+
Sbjct  3706  IRGPIGAPGK  3735


>NC_023557.1 Erwinia phage Ea35-70, complete genome
Length=271084

 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 36/103 (35%), Positives = 46/103 (45%), Gaps = 15/103 (15%)
 Frame = -1

Query  51      GAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGET------GVPGAEGPRGFPGIQGRKGEP  104
               G  G  G  G  G KG+KGD G +GPKGD G        GV GA+G  G  G +G KG+
Sbjct  254125  GPKGDQGLKGDTGAKGDKGDQGDVGPKGDAGAAGKDGTNGVDGAKGDTGAKGDKGDKGDT  253946

Query  105     GEG---------AYVYRSAFSVGLETYVTIPNMPIRFTKIFYN  138
               G G         A    +  S   + YV   N+ +  T  F +
Sbjct  253945  GAGLTIKGTVADASALPTTGSAEGDAYVVGENLYVYITGSFQD  253817


>NC_027294.1 Propionibacterium phage PHL150M00, complete genome
Length=29438

 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 33/92 (36%), Positives = 46/92 (50%), Gaps = 10/92 (11%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +G  G DG DG  G  GE+G+ G  GP G  G  G  G  GP G  G  G+
Sbjct  15026  GVPGRAGADGVNGVDGADGRDGSAGERGEQGPSGPAGPQGAQGERGERGPAGVNGSDGKD  15205

Query  102    GEPGEGAYVYRSAFSVGLETYVTIPNMPIRFT  133
              G+ G      RS  SV    Y +  ++ ++++
Sbjct  15206  GKDG------RSVVSV----YCSGGSLVVKYS  15271


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 30/67 (45%), Positives = 36/67 (54%), Gaps = 0/67 (0%)
 Frame = +2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G+DG DG PG  G  G  G+ G  G  G  G  G +GP G  G QG
Sbjct  14966  LNGVKGPDGLPGANGKDGVDGVPGRAGADGVNGVDGADGRDGSAGERGEQGPSGPAGPQG  15145

Query  100    RKGEPGE  106
               +GE GE
Sbjct  15146  AQGERGE  15166


>NC_015453.1 Propionibacterium phage PAS50 endogenous virus, complete genome
Length=29017

 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
```

```
 Identities = 26/52 (50%), Positives = 32/52 (62%), Gaps = 3/52 (6%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGT---PGEKGEKGDPGLIGPKGDIGETGVPGAEG  90
              G+PG  G +G  G DGRDG      GE+GE+G  G  GP+G+ GE G  GA G
Sbjct  14997  GVPGRAGADGVNGVDGRDGVNGSAGERGEQGPSGPAGPQGERGERGPAGANG  15152


 Score = 39.3 bits (90),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  G  G DGRDG PG  G  G  G+ G  G  G  G  G +GP G  G QG
Sbjct  14937  LNGVKGPDGLPGVNGSDGRDGVPGRAGADGVNGVDGRDGVNGSAGERGEQGPSGPAGPQG  15116

Query  100    RKGEPG  105
               +GE G
Sbjct  15117  ERGERG  15134


 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 26/63 (41%), Positives = 33/63 (52%), Gaps = 9/63 (14%)
 Frame = +3

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              + G PG  GA GRDG +G+          GL+GP G  G  G+ G +GP G PG+ G  G
Sbjct  14838  VQGVPGPAGADGRDGVNGS---------AGLVGPVGPQGSPGLNGVKGPDGLPGVNGSDG  14990

Query  103    EPG  105
                G
Sbjct  14991  RDG  14999


>NC_028660.1 Escherichia phage phi191, complete genome
Length=61035

 Score = 42.4 bits (98),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/64 (48%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = -2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G  G +G KGDPG  GPKGD G  G  G +G  G  G QG K
Sbjct  52787  GVPGPKGDKGDSGPAGPAGPRGVQGPKGDPGPQGPKGDTGAAGAKGEKGATGATGPQGPK  52608

Query  102    GEPG  105
              G+ G
Sbjct  52607  GDTG  52596


 Score = 37.7 bits (86),  Expect = 0.042, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = -2

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  53378  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  53199
```

```
Query  105    G  105
              G
Sbjct  53198  G  53196


 Score = 37.0 bits (84),  Expect = 0.084, Method: Compositional matrix adjust.
 Identities = 27/58 (47%), Positives = 29/58 (50%), Gaps = 0/58 (0%)
 Frame = -2

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              G PG  G  G  G  G  GEKG  G  G  GPKGD G  G  G +GP+G  G  G  G
Sbjct  52706  GDPGPQGPKGDTGAAGAKGEKGATGATGPQGPKGDTGAAGPAGPQGPKGDTGAAGPAG  52533


>NC_029077.1 Mycobacterium phage VohminGhazi, complete genome
Length=52155

 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/70 (43%), Positives = 37/70 (53%), Gaps = 2/70 (3%)
 Frame = +3

Query  60    GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGL  119
             G  G KGEKGD G  GP+G  GE G  G +GP+G  G+QG +G  GE         +V
Sbjct  4116  GARGPKGEKGDTGPQGPQGAKGEQGAQGIQGPQGEQGVQGEQGPQGEAGLNLDIQGTV--  4289

Query  120   ETYVTIPNMP  129
              TY  +P  P
Sbjct  4290  ATYADLPTDP  4319


>NC_022985.1 Mycobacterium phage Zaka, complete genome
Length=52122

 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/70 (43%), Positives = 37/70 (53%), Gaps = 2/70 (3%)
 Frame = +3

Query  60    GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGL  119
             G  G KGEKGD G  GP+G  GE G  G +GP+G  G+QG +G  GE         +V
Sbjct  4116  GARGPKGEKGDTGPQGPQGAKGEQGAQGIQGPQGEQGVQGEQGPQGEAGLNLDIQGTV--  4289

Query  120   ETYVTIPNMP  129
              TY  +P  P
Sbjct  4290  ATYADLPTDP  4319


>NC_022965.1 Mycobacterium phage CloudWang3, complete genome
Length=52873

 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/70 (43%), Positives = 37/70 (53%), Gaps = 2/70 (3%)
 Frame = +3

Query  60    GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGL  119
             G  G KGEKGD G  GP+G  GE G  G +GP+G  G+QG +G  GE         +V
Sbjct  4116  GARGPKGEKGDTGPQGPQGAKGEQGAQGIQGPQGEQGVQGEQGPQGEAGLNLDIQGTV--  4289

Query  120   ETYVTIPNMP  129
```

```
              TY  +P  P
Sbjct  4290  ATYADLPTDP  4319


>NC_022334.1 Propionibacterium phage PHL112N00, complete genome
Length=29266

 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 32/78 (41%), Positives = 42/78 (54%), Gaps = 6/78 (8%)
 Frame = +2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              +AG  G  G NG+ G+DGRDG+ GE+G+      +GP G  G  G  G  G RG  G+ G
Sbjct  15023  VAGRAGVAGVNGSDGKDGRDGSAGERGD------VGPSGPAGPQGAQGERGERGPAGVNG  15184

Query  100    RKGEPGEGAYVYRSAFSV  117
                G+ G+      RS  SV
Sbjct  15185  SDGKDGKDGKDGRSVVSV  15238


 Score = 37.7 bits (86),  Expect = 0.040, Method: Compositional matrix adjust.
 Identities = 25/55 (45%), Positives = 28/55 (51%), Gaps = 0/55 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              G+ G  G  G  G DG+DG  G  GE+GD G  GP G  G  G  G  GP G  G
Sbjct  15020  GVAGRAGVAGVNGSDGKDGRDGSAGERGDVGPSGPAGPQGAQGERGERGPAGVNG  15184


>NC_025444.1 Mycobacteriophage RedRock, complete genome
Length=53332

 Score = 42.0 bits (97),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 34/74 (46%), Positives = 41/74 (55%), Gaps = 9/74 (12%)
 Frame = +2

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEG  107
             G  G  G +G DG  G KG+KGD G +GP+      G+ GA GPRG  G QG KG+ G
Sbjct  4700  GQTGPAGLNGVDGAQGPKGDKGDQGEMGPQ------GLTGATGPRGPEGPQGPKGDQGPL  4861

Query  108   AYVYRSAFSVGLET  121
              Y   SA+ V LE
Sbjct  4862  GY---SAYQVALEA  4894


 Score = 38.1 bits (87),  Expect = 0.034, Method: Compositional matrix adjust.
 Identities = 30/61 (49%), Positives = 34/61 (56%), Gaps = 6/61 (10%)
 Frame = +2

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGET------GVPGAEGPRGFPGIQGRK  101
             G  G  G  G  G  G KG+KGD G  GPKGD G+T      GV GA+GP+G  G QG
Sbjct  4601  GPQGIQGPQGITGLQGPKGDKGDTGAQGPKGDTGQTGPAGLNGVDGAQGPKGDKGDQGEM  4780

Query  102   G  102
             G
Sbjct  4781  G  4783
```

```
>NC_023717.1 Cronobacter phage CR9, complete genome
Length=151924

 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 30/63 (48%), Positives = 34/63 (54%), Gaps = 0/63 (0%)
 Frame = +1

Query  43    IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
             I G  G  GA G  G  G  G +G +G  GL GP+G  GETG  GA GP G  G QG +G
Sbjct  7681  IKGDKGDTGATGPQGPIGPTGPQGPEGPEGLTGPQGPQGETGPQGATGPAGPAGAQGARG  7860

Query  103   EPG  105
               G
Sbjct  7861  PEG  7869


>NC_023609.1 Mycobacterium phage RhynO, complete genome
Length=46739

 Score = 41.6 bits (96),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 32/71 (45%), Positives = 42/71 (59%), Gaps = 3/71 (4%)
 Frame = +2

Query  39    WMAGIPGHPGHNGAPGRDGRDGTPG---EKGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
             W+A + G  G  G PG +G +G  G    KG+KGD G  GP+G  G  G  GA GP+G
Sbjct  2489  WLASLVGPQGPKGDPGPEGPEGPQGLQGPKGDKGDTGDRGPQGLQGPKGDTGATGPKGDT  2668

Query  96    GIQGRKGEPGE  106
             G+QG KG+ G+
Sbjct  2669  GLQGPKGDKGD  2701


>NC_029018.1 Mycobacterium phage Anubis, complete genome
Length=50856

 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 32/78 (41%), Positives = 36/78 (46%), Gaps = 0/78 (0%)
 Frame = +2

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEG  107
             G  G PG  G  G  G  G +GDPG  GPKGD G TG  G +GP+G  G  G  G  G
Sbjct  2345  GDTGNPGPTGPQGDIGPAGPQGDPGPQGPKGDTGATGPQGLQGPKGDKGDTGATGATGPA  2524

Query  108   AYVYRSAFSVGLETYVTI  125
               +     S G     TI
Sbjct  2525  NSLSIGTVSGGTSAAATI  2578


>NC_027362.1 Propionibacterium phage PHL116M00, complete genome
Length=29394

 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 29/64 (45%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              ++G  G  G NGA G+DG +GT GE+G+ G  G  GP+G  GE G  GA G  G  G  G
Sbjct  15035  VSGSAGAAGVNGADGKDGANGTDGERGDVGPSGPAGPQGAQGERGERGAAGVNGADGKDG  15214
```

```
Query  100    RKGE  103
                G
Sbjct  15215  ANGR  15226


 Score = 38.9 bits (89),  Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 30/82 (37%), Positives = 36/82 (44%), Gaps = 3/82 (4%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+ G  G  G  G DG+DG  G  GE+GD    GP G  G  G  G  G RG  G+ G
Sbjct  15032  GVSGSAGAAGVNGADGKDGANGTDGERGDV---GPSGPAGPQGAQGERGERGAAGVNGAD  15202

Query  102    GEPGEGAYVYRSAFSVGLETYV  123
              G+ G       S +  G    V
Sbjct  15203  GKDGANGRSVVSVYCSGGRLMV  15268


 Score = 37.4 bits (85),  Expect = 0.066, Method: Compositional matrix adjust.
 Identities = 31/77 (40%), Positives = 37/77 (48%), Gaps = 4/77 (5%)
 Frame = +2

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              + G PG  G  G  G  G  G  G PGL+GP G  G  G+ G +GP G PG  G  G
Sbjct  14846  VQGVPGPTGVRGPQGPAGVDGRDGVNGLPGLVGPVGPQGSPGLNGVKGPDGLPGTNGSDG  15025

Query  103    EPGEGAYVYRSAFSVGL  119
                G    V  SA + G+
Sbjct  15026  HDG----VSGSAGAAGV  15064


 Score = 37.0 bits (84),  Expect = 0.080, Method: Compositional matrix adjust.
 Identities = 34/83 (41%), Positives = 43/83 (52%), Gaps = 2/83 (2%)
 Frame = +2

Query  25     PGVLLPL-PKGA-CTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGE  82
              PG++ P+ P+G+     + G  G PG NG+ G DG  G+ G  G  G  G  G  G  GE
Sbjct  14930  PGLVGPVGPQGSPGLNGVKGPDGLPGTNGSDGHDGVSGSAGAAGVNGADGKDGANGTDGE  15109

Query  83     TGVPGAEGPRGFPGIQGRKGEPG  105
               G  G  GP G  G QG +GE G
Sbjct  15110  RGDVGPSGPAGPQGAQGERGERG  15178


>NC_027624.1 Propionibacterium phage SKKY, complete genome
Length=29594

 Score = 41.2 bits (95),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 32/67 (48%), Positives = 37/67 (55%), Gaps = 3/67 (4%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G +GA G DGRDG PG  G     G+ G  G  GE GV G  GP G  G QG
Sbjct  15012  LNGVKGPDGLSGANGSDGRDGVPGRAGVD---GVDGRDGSAGEQGVQGPVGPSGAAGPQG  15182

Query  100    RKGEPGE  106
               +GE GE
```

```
Sbjct  15183  AQGERGE  15203


 Score = 38.1 bits (87),  Expect = 0.036, Method: Compositional matrix adjust.
 Identities = 32/84 (38%), Positives = 41/84 (49%), Gaps = 9/84 (11%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGR------DGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
              ++G  G  G +G PGR      DGRDG+ GE+G +   G +GP G  G  G  G  G RG
Sbjct  15039  LSGANGSDGRDGVPGRAGVDGVDGRDGSAGEQGVQ---GPVGPSGAAGPQGAQGERGERG  15209

Query  94     FPGIQGRKGEPGEGAYVYRSAFSV  117
                G     G+ G+     RS  SV
Sbjct  15210  PTGAN*SDGKDGKDGRDGRSVVSV  15281


>NC_019442.1 Escherichia phage TL-2011c, complete genome
Length=60523

 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +2

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  41924  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  42103

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
Sbjct  42104  KGDPGETQIRFR  42139


 Score = 38.5 bits (88),  Expect = 0.026, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G  G+KGE+GD G +G  G+ G  G  G  GP+G  G +G +
Sbjct  41783  GVPGPKGDKGDTGPAGPAGPKGDKGERGDTGPVGATGERGPAGDAGPAGPQGPKGDRGER  41962

Query  102    GEPG  105
              GE G
Sbjct  41963  GETG  41974


 Score = 37.7 bits (86),  Expect = 0.049, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +2

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  41192  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  41371

Query  105    G  105
              G
Sbjct  41372  G  41374
```

```
>NC_027625.1 Propionibacterium phage Kubed, complete genome
Length=29461

 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 32/64 (50%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G DG +G  G  G  G  GL+GP G  G  G  G  GP G PG+ G
Sbjct  14848  GVPGERGPQGPTGADGVNGVNGRDGVNGSTGLVGPVGPQGSPGWNGVPGPSGLPGVDGSN  15027

Query  102    GEPG  105
              G  G
Sbjct  15028  GADG  15039


 Score = 38.1 bits (87),  Expect = 0.036, Method: Compositional matrix adjust.
 Identities = 29/76 (38%), Positives = 39/76 (51%), Gaps = 8/76 (11%)
 Frame = +1

Query  26     GVLLPLPKGACTGWM-----AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDI  80
              G++ P+      GW      +G+PG  G NGA G +G+DG    +G  G+PG +GP G
Sbjct  14938  GLVGPVGPQGSPGWNGVPGPSGLPGVDGSNGADGVNGKDGA---QGAAGEPGRVGPSGAA  15108

Query  81     GETGVPGAEGPRGFPG  96
              G  G  G  GP G  G
Sbjct  15109  GPQGEQGERGPAGSNG  15156


>NC_018084.1 Clostridium phage phiZP2, complete genome
Length=18078

 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 30/61 (49%), Positives = 34/61 (56%), Gaps = 3/61 (5%)
 Frame = -2

Query  40    MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
             + G  G PG  GA G  G  G PG KGEKGDPG+ G  G   + G PGA    G PGI G
Sbjct  9542  LKGAKGDPGAPGAKGERGEQGAPGAKGEKGDPGIPGVPGVKRDKGDPGAP---GTPGING  9372

Query  100   R  100
             +
Sbjct  9371  Q  9369


>NC_010353.1 Streptococcus phage 858, complete genome
Length=35543

 Score = 41.2 bits (95),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 28/87 (32%), Positives = 40/87 (46%), Gaps = 9/87 (10%)
 Frame = +3

Query  75     GPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTK  134
              GPKGD GE G+ G  G +G PG +G  G      +V    +S G + Y+ +   P  F +
Sbjct  18531  GPKGDRGERGLQGPRGDQGIPGPKGIDGTDAPTIFVKSYTYSAGSKAYIKLTG-PNAFEQ  18707

Query  135    IFYNQQNH----YDGSTGKF----HCN  153
                Y  + H     D +T K     HC+
```

```
Sbjct  18708  TLYYSRGHNVWVLDATTHKLKEFVHCD  18788


>NC_031254.1 Arthrobacter phage Kitkat, complete genome
Length=58560

 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 38/62 (61%), Gaps = 3/62 (5%)
 Frame = +2

Query  48     GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDI---GETGVPGAEGPRGFPGIQGRKGEP  104
              G +GAPG+DG  GTPG+ GE G+ G  G  G     G+ G+ G +G  G PG+ G+ G P
Sbjct  29792  GKDGAPGKDGAPGTPGKDGEPGNDGAPGATGAGGKDGQVGLAGTDGQDGAPGVPGKDGAP  29971

Query  105    GE  106
              G+
Sbjct  29972  GK  29977


>NC_027984.1 Stx2 converting phage vB_EcoP_24B, complete genome
Length=57677

 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +2

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  39596  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  39775

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
Sbjct  39776  KGDPGETQIRFR  39811


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G+KGE+GD G +G  G+ G  G  G  GP+G  G +G +
Sbjct  39455  GVPGPKGDKGDTGPAGPAGPKGDKGERGDTGPVGATGERGPAGDAGPAGPQGPKGDRGER  39634

Query  102    GEPG  105
              GE G
Sbjct  39635  GETG  39646


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +2

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  38864  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  39043

Query  105    G  105
              G
```

```
Sbjct  39044  G  39046


>NC_004913.3 Stx1 converting phage DNA, complete genome
Length=59866

 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +1

Query  41    AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
             AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  9457  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  9636

Query  101   KGEPGEGAYVYR  112
             KG+PGE    +R
Sbjct  9637  KGDPGETQIRFR  9672


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +1

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G+PG  G  G  G  G  G+KGE+GD G +G  G+ G  G  G  GP+G  G +G +
Sbjct  9316  GVPGPKGDKGDTGPAGPAGPKGDKGERGDTGPVGATGERGPAGDAGPAGPQGPKGDRGER  9495

Query  102   GEPG  105
             GE G
Sbjct  9496  GETG  9507


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +1

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  8725  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  8904

Query  105   G  105
             G
Sbjct  8905  G  8907


>NC_000902.1 Enterobacteria phage VT2-Sakai, complete genome
Length=60942

 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +1

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  38512  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  38691

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
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Sbjct  38692  KGDPGETQIRFR  38727


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G  G+KGE+GD G +G  G+ G  G  G  GP+G  G +G +
Sbjct  38371  GVPGPKGDKGDTGPAGPAGPKGDKGERGDTGPVGATGERGPAGDAGPAGPQGPKGDRGER  38550

Query  102    GEPG  105
              GE G
Sbjct  38551  GETG  38562


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  37780  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  37959

Query  105    G  105
              G
Sbjct  37960  G  37962


>NC_000924.1 Enterobacteria phage 933W, complete genome
Length=61670

 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +3

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  39471  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  39650

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
Sbjct  39651  KGDPGETQIRFR  39686


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G  G+KGE+GD G +G  G+ G  G  G  GP+G  G +G +
Sbjct  39330  GVPGPKGDKGDTGPAGPAGPKGDKGERGDTGPVGATGERGPAGDAGPAGPQGPKGDRGER  39509

Query  102    GEPG  105
              GE G
Sbjct  39510  GETG  39521
```

```
 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  38739  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  38918

Query  105    G  105
              G
Sbjct  38919  G  38921


>NC_004914.3 Stx2 converting phage II DNA, complete genome
Length=62706

 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +2

Query  41    AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
             AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  9458  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  9637

Query  101   KGEPGEGAYVYR  112
             KG+PGE    +R
Sbjct  9638  KGDPGETQIRFR  9673


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +2

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             G+PG  G  G  G  G  G  G+KGE+GD G +G  G+ G  G  G  GP+G  G +G +
Sbjct  9317  GVPGPKGDKGDTGPAGPAGPKGDKGERGDTGPVGATGERGPAGDAGPAGPQGPKGDRGER  9496

Query  102   GEPG  105
             GE G
Sbjct  9497  GETG  9508


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +2

Query  45    GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  8726  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  8905

Query  105   G  105
             G
Sbjct  8906  G  8908


>NC_010237.1 Enterobacteria phage Min27, complete genome
Length=63395
```

```
 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +2

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  41150  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  41329

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
Sbjct  41330  KGDPGETQIRFR  41365


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G  G+KGE+GD G +G  G+ G  G  G  GP+G  G +G +
Sbjct  41009  GVPGPKGDKGDTGPAGPAGPKGDKGERGDTGPVGATGERGPAGDAGPAGPQGPKGDRGER  41188

Query  102    GEPG  105
              GE G
Sbjct  41189  GETG  41200


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +2

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  40418  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  40597

Query  105    G  105
              G
Sbjct  40598  G  40600


>NC_028449.1 Escherichia phage PA2, complete genome
Length=63569

 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +1

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  45448  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  45627

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
Sbjct  45628  KGDPGETQIRFR  45663


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +1
```

```
Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G  G+KGE+GD G +G  G+ G  G  G  GP+G  G +G +
Sbjct  45307  GVPGPKGDKGDTGPAGPAGPKGDKGERGDTGPVGATGERGPAGDAGPAGPQGPKGDRGER  45486

Query  102    GEPG  105
              GE G
Sbjct  45487  GETG  45498


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
Sbjct  44716  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  44895

Query  105    G  105
              G
Sbjct  44896  G  44898


>NC_028656.1 Enterobacteria phage VT2phi_272, complete sequence
Length=65955

 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 33/72 (46%), Positives = 36/72 (50%), Gaps = 0/72 (0%)
 Frame = +3

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG  G  G  G  G  G  G  G +G KGD G  GP G  G  G  GA GP G  G QG
Sbjct  46827  AGPQGPKGDRGERGETGLTGNAGPQGPKGDTGAAGPAGPQGPKGETGAAGPVGATGPQGP  47006

Query  101    KGEPGEGAYVYR  112
              KG+PGE    +R
Sbjct  47007  KGDPGETQIRFR  47042


 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 36/64 (56%), Gaps = 0/64 (0%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G  G  G+KGE+GD G +G  G+ G  G  G  GP+G  G +G +
Sbjct  46686  GVPGPKGDKGDTGPAGPAGPKGDKGERGDTGPVGATGERGPAGDAGPAGPQGPKGDRGER  46865

Query  102    GEPG  105
              GE G
Sbjct  46866  GETG  46877


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 27/61 (44%), Positives = 33/61 (54%), Gaps = 0/61 (0%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G  G  G  G  G  G  GE+G+ G  G +GP G  GE G  G  GP+G PG++G  GE
```

```
Sbjct  46095  GPKGETGPVGPQGPAGPKGERGDVGAQGAVGPAGPRGEKGEQGERGPQGIPGLKGDTGER  46274

Query  105    G  105
              G
Sbjct  46275  G  46277


>NC_018838.1 Propionibacterium phage P100_A, complete genome
Length=29505

 Score = 40.8 bits (94),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 32/67 (48%), Positives = 36/67 (54%), Gaps = 3/67 (4%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DGRDG PG  G     G+ G  G  GE GV G  GP G  G QG
Sbjct  14979  LNGVKGPDGLPGANGSDGRDGVPGRAGVD---GVDGRDGSAGEQGVQGPVGPSGAAGPQG  15149

Query  100    RKGEPGE  106
               +GE GE
Sbjct  15150  AQGERGE  15170


 Score = 38.1 bits (87),  Expect = 0.037, Method: Compositional matrix adjust.
 Identities = 30/79 (38%), Positives = 38/79 (48%), Gaps = 3/79 (4%)
 Frame = +3

Query  45     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
              G PG  G  G DGRDG+ GE+G +G    +GP G  G  G  G  G RG  G  G  G+
Sbjct  15039  GVPGRAGVDGVDGRDGSAGEQGVQGP---VGPSGAAGPQGAQGERGERGPAGANGSDGKD  15209

Query  105    GEGAYVYRSAFSVGLETYV  123
              G+      S +  G   +V
Sbjct  15210  GKDGRSVVSMYCSGGRLFV  15266


 Score = 35.0 bits (79),  Expect(2) = 0.096, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 31/64 (48%), Gaps = 3/64 (5%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G  G  G  G DG     G  G  GL+GP G  G  G+ G +GP G PG  G
Sbjct  14859  GVPGPAGERGPQGPAGADG---RNGVNGSAGLVGPVGPQGSPGLNGVKGPDGLPGANGSD  15029

Query  102    GEPG  105
              G  G
Sbjct  15030  GRDG  15041


 Score = 20.4 bits (41),  Expect(2) = 0.096, Method: Compositional matrix adjust.
 Identities = 8/16 (50%), Positives = 8/16 (50%), Gaps = 0/16 (0%)
 Frame = +2

Query  24     GPGVLLPLPKGACTGW  39
              G GV  P   G C GW
Sbjct  14741  GEGVSQPCSAGVCAGW  14788
```

```
>NC_019914.1 Staphylococcus phage StB27, complete genome
Length=40071

 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 24/44 (55%), Positives = 27/44 (61%), Gaps = 0/44 (0%)
 Frame = +2

Query  63     GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
              G KG+KGD G  GPKGD G  G+ G  GP G  G  G KG+ GE
Sbjct  36500  GPKGDKGDTGPQGPKGDKGADGINGEMGPAGPTGPMGPKGDTGE  36631


>NC_002515.1 Mycoplasma phage P1, complete genome
Length=11660

 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 25/69 (36%), Positives = 35/69 (51%), Gaps = 0/69 (0%)
 Frame = -3

Query  34    GACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
                + ++  + G  G  G  G  G  G  G  G +G  G+ GPKGD G TG  G +GP+G
Sbjct  8451  NTISSYIEALRGPQGVQGPKGDRGERGPQGTTGLQGAQGVQGPKGDRGATGPQGLQGPKG  8272

Query  94    FPGIQGRKG  102
                G +G +G
Sbjct  8271  DRGERGPQG  8245


 Score = 37.4 bits (85),  Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 32/89 (36%), Positives = 43/89 (48%), Gaps = 3/89 (3%)
 Frame = -3

Query  51    GAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYV  110
             G  G  G  G  GE+G +G  GL G +G  G  G  GA GP+G  G +G +GE G    +
Sbjct  8418  GPQGVQGPKGDRGERGPQGTTGLQGAQGVQGPKGDRGATGPQGLQGPKGDRGERGPQGPM  8239

Query  111   YRSAFSVGLETYVTIPNMPIRFTKIFYNQ  139
                 FS   E   TI N+   + ++  NQ
Sbjct  8238  PSLTFSHNKE---TIDNVKYAYIRVGSNQ  8161


>NC_009541.1 Propionibacterium phage PA6, complete genome
Length=29739

 Score = 40.8 bits (94),  Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 40/102 (39%), Positives = 44/102 (43%), Gaps = 20/102 (20%)
 Frame = +2

Query  45     GHPGHNGAPGRDG---------RDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
              G PG NG+ GRDG          DG  G  GE+GD G  GP G  G  G  G  GP G
Sbjct  15011  GLPGANGSDGRDGVDGVNGNDGADGRDGSAGERGDVGPSGPAGPQGAQGERGERGPAGAN  15190

Query  96     GIQGRKGEPGEGAYVYRSAFSV-------GLET----YVTIP  126
              G  G+ G+ G      RS  SV       G ET    Y  IP
Sbjct  15191  GTNGKDGKDGADGRDGRSVVSVYCFGGLPGCETITCGYRVIP  15316


>NC_027295.1 Propionibacterium phage PHL199M00, complete genome
```

```
Length=29806

 Score = 40.4 bits (93),  Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 30/66 (45%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DGRDG PG  G  G+ G  G  G  G  G PG  G  G  G QG
Sbjct  14950  LNGVKGPDGLPGANGSDGRDGVPGVAGADGVNGVDGANGKDGANGEPGRMGHSGLAGPQG  15129

Query  100    RKGEPG  105
               +GE G
Sbjct  15130  ERGERG  15147


 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 29/76 (38%), Positives = 36/76 (47%), Gaps = 0/76 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+ G  G NG  G +G+DG  GE G  G  GL GP+G+ GE G  G  G  G  G  G+
Sbjct  15019  GVAGADGVNGVDGANGKDGANGEPGRMGHSGLAGPQGERGERGPAGVNGSDGKNGKDGKD  15198

Query  102    GEPGEGAYVYRSAFSV  117
              G      Y +     V
Sbjct  15199  GRSVVSVYCFEGRLVV  15246


>NC_024789.1 Escherichia phage bV_EcoS_AKS96, complete genome
Length=45746

 Score = 40.4 bits (93),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 25/58 (43%), Positives = 34/58 (59%), Gaps = 6/58 (10%)
 Frame = +2

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
             G  G  GRDG  G  G +G +G+ G  GP+G+ G+T      GP+G  G +G KG+PG
Sbjct  6695  GFKGTTGRDGMAGPQGPQGPRGEVGPQGPQGEKGDT------GPQGLKGDKGDKGDPG  6850


>NC_031074.1 Gordonia phage Bantam, complete genome
Length=92580

 Score = 40.0 bits (92),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 21/43 (49%), Positives = 27/43 (63%), Gaps = 0/43 (0%)
 Frame = +2

Query  51     GAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
              G  G  G  G  G+KG++GD G +GPKGD G+ G  G +GP G
Sbjct  35669  GTKGDTGERGAKGDKGDRGDKGDLGPKGDKGDKGDQGIQGPAG  35797


 Score = 38.1 bits (87),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 26/72 (36%), Positives = 33/72 (46%), Gaps = 0/72 (0%)
 Frame = +2

Query  47     PGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
              PG  G  G  G  G  G++G+KGD G  G KGD G+ G+ G  GP      Q       E
```

```
Sbjct  35666  PGTKGDTGERGAKGDKGDRGDKGDLGPKGDKGDKGDQGIQGPAGPAVSEADQVAIALRPE  35845

Query  107    GAYVYRSAFSVG  118
              G Y +    + G
Sbjct  35846  GVYAWHDHLAFG  35881


>NC_031927.1 Synechococcus phage S-CAM7 isolate 0910CC49, complete genome
Length=216121

 Score = 40.0 bits (92),  Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 37/87 (43%), Positives = 42/87 (48%), Gaps = 3/87 (3%)
 Frame = +2

Query  36      CTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFP  95
                TG  + IPG  G  GA G  G  G  G  G  G  GL G  G  G TG  G +GP G
Sbjct  171083  ATGPQSVIPGATGPVGATGL-GATGATGVFGSTGATGLTGSTGVFGSTGATGIDGPVGST  171259

Query  96      GIQGRKGEPG-EGAY-VYRSAFSVGLE  120
               GIQG  G  G  G+  V+ S  + GLE
Sbjct  171260  GIQGPTGATGLTGSTGVFGSTGATGLE  171340


 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 33/95 (35%), Positives = 42/95 (44%), Gaps = 11/95 (12%)
 Frame = +3

Query  32      PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDP--GLIGPKGDIGETGV----  85
               PKG     + G  G  G  G  G  G  G  G KG++GD   G  GP+GDIG +G
Sbjct  179703  PKGDQGDAIIGATGATGDQGDEGPVGASGATGPKGDQGDAVIGATGPQGDIGASGATGPQ  179882

Query  86      -----PGAEGPRGFPGIQGRKGEPGEGAYVYRSAF  115
                     GA GP+G PG  G       G Y+   ++
Sbjct  179883  GDIGASGATGPKGDPGSAGVSATLTAGTYLSGDSY  179987


 Score = 37.7 bits (86),  Expect = 0.051, Method: Compositional matrix adjust.
 Identities = 31/83 (37%), Positives = 40/83 (48%), Gaps = 12/83 (14%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG-FPGIQGR  100
               G+PG PG +         G+ G  G +G  G  GP+G  G TG+ GA GP+   PG  G
Sbjct  170966  GVPGGPGGS-------LRGSTGATGPRGPQGFEGPRGSTGSTGLTGATGPQSVIPGATGP  171124

Query  101     KGEPGEGAY----VYRSAFSVGL  119
                G  G GA     V+ S  + GL
Sbjct  171125  VGATGLGATGATGVFGSTGATGL  171193


 Score = 37.0 bits (84),  Expect = 0.076, Method: Compositional matrix adjust.
 Identities = 36/104 (35%), Positives = 46/104 (44%), Gaps = 3/104 (3%)
 Frame = +2

Query  32     PKGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGP  91
              P+GA      G+ G  G  G  G  G  G  G  G  G  G IG  G IG TG  G +GP
Sbjct  13430  PQGATGSGATGVRGATGEQGLTGPQGDPG--GATGATGPQGFIGATG-IGATGATGIQGP  13600

Query  92     RGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKI  135
```

```
              +G  G+QG +G+   GA        +   T +T P  P   T +
Sbjct  13601  QGATGVQGPQGDSITGATGPFGPGGLPGATGLTGPTGPQGATGV  13732


>NC_020490.2 Staphylococcus phage StB12, complete genome
Length=44714

 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 26/55 (47%), Positives = 29/55 (53%), Gaps = 0/55 (0%)
 Frame = +3

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              G  G  G  G  G  G DG  GE G  G  G +GPKGD GE G+ G +GP G  G
Sbjct  39999  GDKGDIGPQGPKGDRGADGVDGEIGPAGPAGPMGPKGDTGEKGLQGEQGPPGKDG  40163


 Score = 39.7 bits (91),  Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 25/44 (57%), Positives = 27/44 (61%), Gaps = 0/44 (0%)
 Frame = +3

Query  63     GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
              G KG+KGD G  GPKGD G  GV G  GP G  G  G KG+ GE
Sbjct  39990  GPKGDKGDIGPQGPKGDRGADGVDGEIGPAGPAGPMGPKGDTGE  40121


>NC_024354.1 Cronobacter phage CR8, complete genome
Length=149162

 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 37/132 (28%), Positives = 57/132 (43%), Gaps = 15/132 (11%)
 Frame = +2

Query  48     GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEG  107
              G  G  G+ G  G  GEKGEKGD G +GP G  G       +G +G PG  G KG+ G+
Sbjct  12125  GLQGPQGQRGIQGVQGEKGEKGDQGPVGPAGPAGP------QGEQGPPGETGPKGDKGDN  12286

Query  108    AY-----VYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYY---  159
              A      +Y S  +    +++ +P   +   ++  +  N    +   F      +
Sbjct  12287  ALPTISGIYASPINK-TNSWIQLPGNNLGNVRLILSANNKVSQTRVGFSAGTSSVAKRIG  12463

Query  160    FAYHITVYMKDV  171
              F+Y +T    DV
Sbjct  12464  FSYALTTTYTDV  12499


 Score = 37.7 bits (86),  Expect = 0.044, Method: Compositional matrix adjust.
 Identities = 30/71 (42%), Positives = 35/71 (49%), Gaps = 21/71 (30%)
 Frame = +2

Query  57     GRDGTPGEKGEKGDPGLIGPKG---------------------DIGETGVPGAEGPRGFP  95
              G  G  GEKG+KGDPG  GP+G                     ++GETG  G +GP G
Sbjct  11519  GPQGPQGEKGDKGDPGPQGPQGVQGAPGNPGEKGPQGGQGPQGEVGETGPQGPQGPVGPT  11698

Query  96     GIQGRKGEPGE  106
              G QG KGE GE
Sbjct  11699  GPQGEKGERGE  11731
```

```
 Score = 37.0 bits (84),  Expect = 0.082, Method: Compositional matrix adjust.
 Identities = 30/65 (46%), Positives = 33/65 (51%), Gaps = 0/65 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G PG  G  G  G  G  G  G  G  G  GP G  GE G  G +GP+G  GIQG +
Sbjct  11990  GAPGPVGPAGPTGPQGLQGPVGPAGPSGATGPAGPAGPQGEQGPQGLQGPQGQRGIQGVQ  12169

Query  102    GEPGE  106
              GE GE
Sbjct  12170  GEKGE  12184


>NC_020205.1 Xanthomonas citri phage CP2 DNA, complete genome
Length=42963

 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 29/68 (43%), Positives = 34/68 (50%), Gaps = 0/68 (0%)
 Frame = -1

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEG  107
             G  G PG  G  G  G +G KGD G  GP G  G TG  GA+G +G  G QG KG+ G
Sbjct  3258  GERGFPGVAGPQGVEGPQGPKGDTGATGPAGAKGATGATGAQGAQGTQGPQGAKGDTGAT  3079

Query  108   AYVYRSAF  115
                 + A
Sbjct  3078  GPSAKVAL  3055


>NC_018270.1 Weissella phage phiYS61, complete genome
Length=33594

 Score = 40.0 bits (92),  Expect = 0.008, Method: Compositional matrix adjust.
 Identities = 23/44 (52%), Positives = 29/44 (66%), Gaps = 0/44 (0%)
 Frame = +2

Query  60     GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
              G  G KG+KGD G  GPKGD G+TG  G +G +G  G QG +G+
Sbjct  20621  GPQGSKGDKGDTGPQGPKGDKGDTGPQGPKGDKGDTGPQGERGK  20752


>NC_018851.1 Propionibacterium phage ATCC29399B_C, complete genome
Length=29516

 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 34/78 (44%), Positives = 41/78 (53%), Gaps = 9/78 (12%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              +AG  G  G NG  G DGRDG+ GE+G  G  G  GP+G  GE    G +GP G  G  G
Sbjct  15012  VAGRAGADGVNGVDGADGRDGSAGERGAVGPSGPEGPQGTQGER---GEQGPAGANGSDG  15182

Query  100    RKGEPGEGAYVYRSAFSV  117
              + G+ G      RS  SV
Sbjct  15183  KDGKDG------RSVVSV  15218


>NC_018847.1 Propionibacterium phage ATCC29399B_T, complete genome
```

```
Length=29516

 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 34/78 (44%), Positives = 41/78 (53%), Gaps = 9/78 (12%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              +AG  G  G NG  G DGRDG+ GE+G  G  G  GP+G  GE    G +GP G  G  G
Sbjct  15012  VAGRAGADGVNGVDGADGRDGSAGERGAVGPSGPEGPQGTQGER---GEQGPAGANGSDG  15182

Query  100    RKGEPGEGAYVYRSAFSV  117
              + G+ G      RS  SV
Sbjct  15183  KDGKDG------RSVVSV  15218


>NC_030901.1 Gordonia phage ClubL, complete genome
Length=92618

 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 33/87 (38%), Positives = 44/87 (51%), Gaps = 15/87 (17%)
 Frame = +1

Query  37     TGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              T     +PG PG  G+   DG  G  G+KG+ G+ GL G KGD         +G +G  G
Sbjct  37960  TALFVPVPGMPGPRGS---DGDQGPKGDKGDPGERGLQGLKGD---------QGTKGDKG  38103

Query  97     IQGRKGEPGEGAYVYRSAFSVGLETYV  123
               QG +G PGE   V  +  + GL+T V
Sbjct  38104  DQGNQGPPGE---VSLAQLNSGLDTKV  38175


>NC_030696.1 Gordonia phage Smoothie, complete genome
Length=93139

 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 33/87 (38%), Positives = 44/87 (51%), Gaps = 15/87 (17%)
 Frame = +3

Query  37     TGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              T     +PG PG  G+   DG  G  G+KG+ G+ GL G KGD         +G +G  G
Sbjct  38499  TALFVPVPGMPGPRGS---DGDQGPKGDKGDPGERGLQGLKGD---------QGTKGDKG  38642

Query  97     IQGRKGEPGEGAYVYRSAFSVGLETYV  123
               QG +G PGE   V  +  + GL+T V
Sbjct  38643  DQGNQGPPGE---VSLAQLNSGLDTKV  38714


>NC_031029.1 Gordonia phage Cucurbita, complete genome
Length=93686

 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 33/87 (38%), Positives = 44/87 (51%), Gaps = 15/87 (17%)
 Frame = +3

Query  37     TGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              T     +PG PG  G+   DG  G  G+KG+ G+ GL G KGD         +G +G  G
Sbjct  39330  TALFVPVPGMPGPRGS---DGDQGPKGDKGDPGERGLQGLKGD---------QGTKGDKG  39473
```

```
Query  97     IQGRKGEPGEGAYVYRSAFSVGLETYV  123
               QG +G PGE   V  +  + GL+T V
Sbjct  39474  DQGNQGPPGE---VSLAQLNSGLDTKV  39545


>NC_030936.1 Gordonia phage Bachita, complete genome
Length=93843

 Score = 40.0 bits (92),  Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 33/87 (38%), Positives = 44/87 (51%), Gaps = 15/87 (17%)
 Frame = +2

Query  37     TGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPG  96
              T     +PG PG  G+   DG  G  G+KG+ G+ GL G KGD         +G +G  G
Sbjct  38471  TALFVPVPGMPGPRGS---DGDQGPKGDKGDPGERGLQGLKGD---------QGTKGDKG  38614

Query  97     IQGRKGEPGEGAYVYRSAFSVGLETYV  123
               QG +G PGE   V  +  + GL+T V
Sbjct  38615  DQGNQGPPGE---VSLAQLNSGLDTKV  38686


>NC_023731.1 Mycobacterium phage Trixie, complete genome
Length=53526

 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 30/61 (49%), Positives = 34/61 (56%), Gaps = 6/61 (10%)
 Frame = +3

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGET------GVPGAEGPRGFPGIQGRK  101
             G  G  G  G  G  G KG+KGD G  GPKGD G T      GV GA+GP+G  G QG +
Sbjct  4740  GPQGVQGPKGDTGATGAKGDKGDTGAQGPKGDTGATGPAGRDGVDGAQGPKGDTGPQGDE  4919

Query  102   G  102
             G
Sbjct  4920  G  4922


 Score = 38.9 bits (89),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 41/97 (42%), Positives = 45/97 (46%), Gaps = 6/97 (6%)
 Frame = +3

Query  19    ETTTQGP-GVLLPLPKGACTGWMA-----GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPG  72
             ET  QGP GV  P      TG        G  G  G  GA G  GRDG  G +G KGD G
Sbjct  4725  ETGLQGPQGVQGPKGDTGATGAKGDKGDTGAQGPKGDTGATGPAGRDGVDGAQGPKGDTG  4904

Query  73    LIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAY  109
               G +G  G TG  G+ GP G  G  G +G  G  AY
Sbjct  4905  PQGDEGPQGPTGATGSRGPEGPQGPTGERGPMGYSAY  5015


>NC_007734.1 Bacillus phage WBeta, complete genome
Length=40867

 Score = 39.7 bits (91),  Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 26/56 (46%), Positives = 32/56 (57%), Gaps = 0/56 (0%)
 Frame = +1

Query  48     GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGE  103
```

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              G  G  G  G  G  G +G +G PG+ GP G IG TG+ G +G +GFPGI G  G
Sbjct  33670  GIQGVQGNPGTTGPQGIQGIQGIPGVSGPIGPIGPTGIQGVQGIQGFPGIPGPMGP  33837


 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 28/64 (44%), Positives = 35/64 (55%), Gaps = 0/64 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + GIPG PG  G  G  G  G  G +G +G+PG  GP G  G TG+ G +G +G  GI G
Sbjct  34231  LQGIPGIPGSMGPTGLTGPTGLQGIQGIQGNPGPTGPFGPTGPTGLQGIQGLQGIQGIPG  34410

Query  100    RKGE  103
                G
Sbjct  34411  PTGP  34422


>NC_027627.1 Propionibacterium phage Solid, complete genome
Length=29440

 Score = 39.7 bits (91),  Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 35/87 (40%), Positives = 40/87 (46%), Gaps = 15/87 (17%)
 Frame = +3

Query  40     MAGIPGHPGHNGAPGR---------DGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEG  90
              + G+ G  GHNG PGR         DG DG  G  GE+GD G  GP G  G     G  G
Sbjct  14976  LPGVNGSDGHNGVPGRAGADGVNGVDGADGRNGSAGERGDVGPSGPAGPQGAQCERGERG  15155

Query  91     PRGFPGIQGRKGEPGEGAYVYRSAFSV  117
              P G  G  G+ G+ G      RS  SV
Sbjct  15156  PVGANGSDGKDGKDG------RSVVSV  15218


>NC_027623.1 Propionibacterium phage Pirate, complete genome
Length=29328

 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 26/64 (41%), Positives = 33/64 (52%), Gaps = 0/64 (0%)
 Frame = +1

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              + G PG  G  G  G  G  G+ G  G  G++GP G  G  G+ G +GP G PG  G  G
Sbjct  14833  VQGVPGPAGVRGPQGPAGADGKDGSNGSAGVVGPVGPQGSPGLNGVKGPDGLPGANGSDG  15012

Query  103    EPGE  106
              E G+
Sbjct  15013  ERGD  15024


 Score = 38.1 bits (87),  Expect = 0.035, Method: Compositional matrix adjust.
 Identities = 32/77 (42%), Positives = 37/77 (48%), Gaps = 12/77 (16%)
 Frame = +1

Query  41     AGIPGHPGHNGAPGRDGRDGT------------PGEKGEKGDPGLIGPKGDIGETGVPGA  88
              AG+ G  G  GA G+DG +G+            PG  G KG  GL G  G  GE G  G
Sbjct  14854  AGVRGPQGPAGADGKDGSNGSAGVVGPVGPQGSPGLNGVKGPDGLPGANGSDGERGDVGP  15033

Query  89     EGPRGFPGIQGRKGEPG  105
```

```
               GP G  G QG +GE G
Sbjct  15034  SGPAGLQGAQGERGERG  15084


>NC_004682.1 Mycobacterium phage Bxz2, complete genome
Length=50913

 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 29/57 (51%), Positives = 34/57 (60%), Gaps = 0/57 (0%)
 Frame = +3

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP  104
             G  G  G  G  G  G+KG+KGD G  GPKGD G+ G  GA+GP+G  G QG  G P
Sbjct  2454  GPKGDTGATGAQGPKGDKGDKGDTGDTGPKGDKGDKGDTGAQGPQGIQGPQGPAGVP  2624


>NC_031084.1 Propionibacterium phage BruceLethal, complete genome
Length=29249

 Score = 39.3 bits (90),  Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 31/85 (36%), Positives = 40/85 (47%), Gaps = 9/85 (11%)
 Frame = +1

Query  45     GHPGHNGAPGRDGRDG------TPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
              G  GH+G PGR G DG      T G  G  G+ G +GP G  G  GV   +G RG  G+
Sbjct  14980  GKDGHDGVPGRAGADGVKGVDGTDGRDGSAGERGAVGPSGPAGPQGV---QGERGAAGVN  15150

Query  99     GRKGEPGEGAYVYRSAFSVGLETYV  123
              G  G+ G+      S +  G   +V
Sbjct  15151  GSDGKDGKDGRSVVSVYCSGGRLFV  15225


 Score = 37.4 bits (85),  Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 28/66 (42%), Positives = 34/66 (52%), Gaps = 0/66 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              +AG+PG  G  G  G  G DG  G  G  G  G +GP+G  G  GV G +G  G  G+ G
Sbjct  14830  VAGVPGPAGERGPQGPAGADGRAGHDGSAGLVGPVGPQGSPGLNGVKGPDGKDGHDGVPG  15009

Query  100    RKGEPG  105
              R G  G
Sbjct  15010  RAGADG  15027


>AC_000012.1 Murine adenovirus A, complete genome
Length=30944

 Score = 39.3 bits (90),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 35/115 (30%), Positives = 49/115 (43%), Gaps = 9/115 (8%)
 Frame = -2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+PG  G  G PG  G  G PG+ G  G P      GD+G  GVPG  G  G PG  G
Sbjct  30055  LGGVPGDMGLGGVPGDMGLGGVPGDMGLGGVP------GDMGLGGVPGDMGLGGVPGNIG  29894

Query  100    RKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNI  154
               +  PG      R  +    E + +     +   + F++ Q+ Y    G   C +
```

```
Sbjct  29893  SR--PGNTWRCAREHWQSSREHWQS-SRKHLAACQGFFHLQSLYIKLCGLLKCIL  29738


>NC_000942.1 Murine adenovirus A, complete genome
Length=30944

 Score = 39.3 bits (90),  Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 35/115 (30%), Positives = 49/115 (43%), Gaps = 9/115 (8%)
 Frame = -2

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+PG  G  G PG  G  G PG+ G  G P      GD+G  GVPG  G  G PG  G
Sbjct  30055  LGGVPGDMGLGGVPGDMGLGGVPGDMGLGGVP------GDMGLGGVPGDMGLGGVPGNIG  29894

Query  100    RKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNI  154
               +  PG      R  +    E + +     +   + F++ Q+ Y    G   C +
Sbjct  29893  SR--PGNTWRCAREHWQSSREHWQS-SRKHLAACQGFFHLQSLYIKLCGLLKCIL  29738


>NC_027361.1 Propionibacterium phage PHL085N00, complete genome
Length=29454

 Score = 39.3 bits (90),  Expect = 0.016, Method: Compositional matrix adjust.
 Identities = 33/76 (43%), Positives = 41/76 (54%), Gaps = 12/76 (16%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G+PG  G +GA   DGRDG+ GE+G+ G  G  GP+G  GE    G  GP G  G  G+
Sbjct  15028  GVPGRAGVDGA---DGRDGSAGERGDVGPSGPAGPQGAQGER---GERGPVGANGSDGKD  15189

Query  102    GEPGEGAYVYRSAFSV  117
              G+ G      RS  SV
Sbjct  15190  GKDG------RSVVSV  15219


 Score = 37.7 bits (86),  Expect = 0.040, Method: Compositional matrix adjust.
 Identities = 27/63 (43%), Positives = 34/63 (54%), Gaps = 0/63 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+ G  G  GA G DGRDG PG  G  G  G  G+ G+ G  G  GP+G  G +G
Sbjct  14968  LNGVKGPDGLPGANGSDGRDGVPGRAGVDGADGRDGSAGERGDVGPSGPAGPQGAQGERG  15147

Query  100    RKG  102
               +G
Sbjct  15148  ERG  15156


>NC_028798.1 Mycobacterium phage MarQuardt, complete genome
Length=50882

 Score = 39.3 bits (90),  Expect = 0.016, Method: Compositional matrix adjust.
 Identities = 29/59 (49%), Positives = 34/59 (58%), Gaps = 0/59 (0%)
 Frame = +1

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGE  106
             G  G PG  G  G  G  G +GDPG  GPKGD G+TG  G +G  G  G QG KG+ G+
Sbjct  2335  GDAGNPGPTGPQGDIGPAGPQGDPGPQGPKGDTGDTGPQGPKGDTGATGAQGPKGDKGD  2511
```

```
 Score = 38.5 bits (88),  Expect = 0.023, Method: Compositional matrix adjust.
 Identities = 30/62 (48%), Positives = 36/62 (58%), Gaps = 0/62 (0%)
 Frame = +1

Query  41    AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
             AG PG  G  G  G  G  G PG +G KGD G  GP+G  G+TG  GA+GP+G  G +G
Sbjct  2341  AGNPGPTGPQGDIGPAGPQGDPGPQGPKGDTGDTGPQGPKGDTGATGAQGPKGDKGDKGD  2520

Query  101   KG  102
              G
Sbjct  2521  TG  2526


 Score = 37.7 bits (86),  Expect = 0.041, Method: Compositional matrix adjust.
 Identities = 34/79 (43%), Positives = 42/79 (53%), Gaps = 1/79 (1%)
 Frame = +1

Query  41    AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
             AG  G PG  G  G  G  G KG+ G  G  GPKGD G+ G  G  GP+G  G +G
Sbjct  2386  AGPQGDPGPQGPKGDTGDTGPQGPKGDTGATGAQGPKGDKGDKGDTGNTGPQGLQGPKGD  2565

Query  101   KGEPGE-GAYVYRSAFSVG  118
             KG+ G  GA    ++ S+G
Sbjct  2566  KGDTGATGATGPANSLSIG  2622


>NC_015463.1 Synechococcus phage S-CBS2, complete genome
Length=72332

 Score = 38.9 bits (89),  Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 25/58 (43%), Positives = 32/58 (55%), Gaps = 0/58 (0%)
 Frame = +2

Query  48     GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
              G  G  G  G  G  GE G +G+ G+ GP+G  GE G+ G +G +G  GIQG  G  G
Sbjct  39422  GPQGEQGIQGPQGIQGEPGIQGEQGIQGPQGIQGEPGIQGEQGIQGEQGIQGETGPAG  39595


 Score = 37.4 bits (85),  Expect = 0.064, Method: Compositional matrix adjust.
 Identities = 24/52 (46%), Positives = 28/52 (54%), Gaps = 0/52 (0%)
 Frame = +2

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
              GI G PG  G  G  G  G  GE G +G+ G+ G +G  GETG  G  GP G
Sbjct  39458  GIQGEPGIQGEQGIQGPQGIQGEPGIQGEQGIQGEQGIQGETGPAGPTGPAG  39613


>NC_027346.1 Propionibacterium phage PHL171M01, complete genome
Length=29327

 Score = 38.9 bits (89),  Expect = 0.021, Method: Compositional matrix adjust.
 Identities = 30/67 (45%), Positives = 34/67 (51%), Gaps = 0/67 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+PG  G  G  G  G DG  G  G  G  G +GP+G  G  GV G EG  G  GI G
```

```
Sbjct  14848  VQGVPGPAGERGPQGPAGADGRDGVNGSAGIVGPVGPQGSPGLNGVKGPEGLPGSDGING  15027

Query  100    RKGEPGE  106
              R G PG
Sbjct  15028  RDGVPGR  15048


>NC_024793.1 Escherichia phage bV_EcoS_AHP42, complete genome
Length=46847

 Score = 38.5 bits (88),  Expect = 0.022, Method: Compositional matrix adjust.
 Identities = 25/58 (43%), Positives = 34/58 (59%), Gaps = 6/58 (10%)
 Frame = +2

Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
             G  G  GRDG  G  G +G +G+ G  GP+G+ G+T      GP+G  G +G KG+PG
Sbjct  6695  GFKGTTGRDGMAGPQGPQGPRGEVGPQGPQGEKGDT------GPQGLKGDKGDKGDPG  6850


>NC_020883.1 Bacillus phage PM1 DNA, complete genome
Length=50861

 Score = 38.5 bits (88),  Expect = 0.022, Method: Compositional matrix adjust.
 Identities = 26/64 (41%), Positives = 34/64 (53%), Gaps = 6/64 (9%)
 Frame = +1

Query  34     GACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
              G  T W+A + G  G  G+ G  G       KG+KGD G  GP+G  G+ G  G +GP G
Sbjct  34039  GTETEWLASLKGPKGDTGSTGPQG------PKGDKGDTGATGPQGPKGDKGDTGPQGPAG  34200

Query  94     FPGI  97
               PG+
Sbjct  34201  KPGV  34212


>NC_028957.1 Enterobacteria phage vB_EcoM_VR26, complete genome
Length=171541

 Score = 38.5 bits (88),  Expect = 0.023, Method: Compositional matrix adjust.
 Identities = 30/66 (45%), Positives = 36/66 (55%), Gaps = 3/66 (5%)
 Frame = +3

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGV---PGAEGPRGFPG  96
               + GI G PG NG  G  G  G  G +G KGD G  G KGD G  G+    G +GP+G  G
Sbjct  109581  LTGIQGEPGENGDIGPKGPIGLTGPQGPKGDIGSKGIKGDTGPQGIQGPAGPQGPQGEKG  109760

Query  97      IQGRKG  102
               +QG  G
Sbjct  109761  VQGLAG  109778


 Score = 37.4 bits (85),  Expect = 0.063, Method: Compositional matrix adjust.
 Identities = 25/54 (46%), Positives = 30/54 (56%), Gaps = 0/54 (0%)
 Frame = +3

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
               + G+ G  G  G  G  G  G  G +G  G PGL GP+G  G TG  GA+GPRG
Sbjct  110223  IQGLKGETGPAGPQGIQGLKGEVGAQGPSGSPGLTGPEGPRGLTGEAGAQGPRG  110384
```

```
>NC_028774.1 Klebsiella phage Sushi, complete genome
Length=48754

 Score = 38.5 bits (88),  Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 23/44 (52%), Positives = 28/44 (64%), Gaps = 6/44 (14%)
 Frame = +2

Query  65    KGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGA  108
             KG+KGDPG  GPKGD G+ G  G +GP+      G KG+PG  A
Sbjct  6056  KGDKGDPGPQGPKGDKGDPGPQGQQGPK------GDKGDPGTSA  6169


>NC_019400.1 Cronobacter phage vB_CsaM_GAP31, complete genome
Length=147940

 Score = 38.5 bits (88),  Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 26/56 (46%), Positives = 32/56 (57%), Gaps = 2/56 (4%)
 Frame = +1

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGF--PGIQ  98
               G  G  G  G DG  G  G  G +G  G IGPKGD G+TG+ G  GP+G   PG++
Sbjct  100777  GQKGDQGPIGPDGATGPAGADGPQGIQGPIGPKGDKGDTGLTGPVGPQGEMGPGVE  100944


>NC_024141.1 Mycobacterium phage Kampy, complete genome
Length=51378

 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 35/118 (30%), Positives = 52/118 (44%), Gaps = 23/118 (19%)
 Frame = +2

Query  63    GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETY  122
             G+ G +G  GL GPKGD G+ G  G++GP+G  G QG +G   +G Y Y S+ +  L+
Sbjct  2471  GDLGPQGPQGLQGPKGDKGDKGDTGSQGPQGIQGPQGIQGP--QGPYGYLSSDATVLDFR  2644

Query  123   VTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY---HITVYMKDVKVSLFK  177
                     R T+  YN                P   ++     H+ V + D   S F+
Sbjct  2645  --------RMTQAQYN----------ALGAGRPATTFYVIVG*HMPVRIGDATPSGFR  2764


>NC_022990.1 Zamilon virophage complete genome
Length=17276

 Score = 38.5 bits (88),  Expect = 0.027, Method: Compositional matrix adjust.
 Identities = 34/96 (35%), Positives = 48/96 (50%), Gaps = 7/96 (7%)
 Frame = -2

Query  41     AGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR  100
              AG+ G  G  G+ G  G  G+ G+KG KGD G+ G KG+ G     G +G +G  G  G
Sbjct  13942  AGLDGLKGDIGSNGLKGDPGS-GDKGLKGDAGINGLKGETGS----GDKGLKGDTGTNGL  13778

Query  101    KGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIF  136
              KG  G+         +V L + +  P   + FT+IF
Sbjct  13777  KGNLGDKGLKGDVGSAVVLSSGIWTP--TVSFTQIF  13676
```

```
 Score = 37.0 bits (84),  Expect = 0.075, Method: Compositional matrix adjust.
 Identities = 50/180 (28%), Positives = 72/180 (40%), Gaps = 33/180 (18%)
 Frame = -3

Query  60     GTPGEKGEKGDPGLIGPKGDIGETGV--PGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSV  117
              G+ G KG+KGDPG  G KGD G+ GV   G  GP+G  G     G  G G Y     FS
Sbjct  13143  GSSGPKGDKGDPGTNGLKGDKGDIGVGIKGEMGPKGNTG-----GTVGSGTY-----FSG  12994

Query  118    GLETYVT-------IPNMP---IRF-TKIFYNQQNHYDG-----STGKFHCNIPGLYYFA  161
               L TY T       IP +    + F TK      ++ DG      T  F+  +    Y
Sbjct  12993  DLPTYETSGGTQASIPEVSTGTVAFTTKTLGGNCSYVDGVFTTTETAPFYVAVT---YIG  12823

Query  162    YHITVYMKDVKVSLFKKDKAMLFTYDQYQENNVDQASGSV--LLHLEVGDQVWLQVYGEG  219
                I      + +S+FK     ++           Q S S+  ++ +   D +++     G
Sbjct  12822  TSIGTLDGSLIISIFKNGGTAVYNTAVIYSGAGIQMSASLNGIIDMTPSDNIFIAFANSG  12643


>NC_023562.1 Mycobacterium phage BellusTerra, complete genome
Length=51236

 Score = 38.5 bits (88),  Expect = 0.028, Method: Compositional matrix adjust.
 Identities = 35/118 (30%), Positives = 52/118 (44%), Gaps = 23/118 (19%)
 Frame = +1

Query  63    GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETY  122
             G+ G +G  GL GPKGD G+ G  G++GP+G  G QG +G   +G Y Y S+ +  L+
Sbjct  2470  GDLGPQGPQGLQGPKGDKGDKGDTGSQGPQGIQGPQGIQGP--QGPYGYLSSDATVLDFR  2643

Query  123   VTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY---HITVYMKDVKVSLFK  177
                     R T+  YN                P   ++     H+ V + D   S F+
Sbjct  2644  --------RMTQAQYN----------ALGAGRPATTFYVIVG*HMPVRIGDATPSGFR  2763


>NC_018834.1 Propionibacterium phage P9.1, complete genome
Length=29214

 Score = 38.5 bits (88),  Expect = 0.029, Method: Compositional matrix adjust.
 Identities = 29/65 (45%), Positives = 33/65 (51%), Gaps = 3/65 (5%)
 Frame = +1

Query  42     GIPGHPGH---NGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQ  98
              G+PG  G    NG  G DG+DG  G  GE+G  G  GP G  GE G  GA G  G  G
Sbjct  15019  GVPGRTGADGVNGVAGADGKDGANGADGERGAVGPSGPAGPQGERGERGAAGVNGSDGKD  15198

Query  99     GRKGE  103
              G+ G
Sbjct  15199  GKDGR  15213


 Score = 37.0 bits (84),  Expect = 0.078, Method: Compositional matrix adjust.
 Identities = 26/63 (41%), Positives = 31/63 (49%), Gaps = 0/63 (0%)
 Frame = +1

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              + G PG  G  G  G  G  G  G  GL+GP G  G  G+ G +GP G PG+ G  G
Sbjct  14833  VQGVPGPAGVRGPQGPAGVDGRDGVNGSAGLVGPVGPQGSPGLNGVKGPDGLPGVNGSDG  15012

Query  103    EPG  105
```

```
                G
Sbjct  15013  RDG  15021


>NC_022096.1 Pseudomonas phage PaBG, complete genome
Length=258139

 Score = 38.5 bits (88),  Expect = 0.029, Method: Compositional matrix adjust.
 Identities = 29/79 (37%), Positives = 38/79 (48%), Gaps = 15/79 (19%)
 Frame = +2

Query  42      GIPGHPGHNGAPGRDGR---------------DGTPGEKGEKGDPGLIGPKGDIGETGVP  86
               G PG  G +G  GRDG                +G PG +G  G  G+ GP+G  G +G
Sbjct  197042  GNPGKDGQDGRDGRDGADGDPGCPGDPGPPGDEGYPGAEGNPGLIGIQGPEGCEGASGDR  197221

Query  87      GAEGPRGFPGIQGRKGEPG  105
               G  GP+G PG +G +G  G
Sbjct  197222  GLVGPQGRPGFEGSRGLTG  197278


>NC_023719.1 Bacillus phage G, complete genome
Length=497513

 Score = 38.1 bits (87),  Expect = 0.030, Method: Compositional matrix adjust.
 Identities = 26/56 (46%), Positives = 32/56 (57%), Gaps = 3/56 (5%)
 Frame = +2

Query  45      GHPGHNGAPGRDGRDGTPGEKGEKGDPG---LIGPKGDIGETGVPGAEGPRGFPGI  97
               G  G  GA G  G  G  G +G KGDPG   + G KGD G+ G  GA+G +G PG+
Sbjct  135008  GPKGDTGAQGIQGPKGDTGSQGLKGDPGAQGIQGVKGDKGDQGTAGAKGDKGDPGV  135175


 Score = 37.0 bits (84),  Expect = 0.080, Method: Compositional matrix adjust.
 Identities = 28/77 (36%), Positives = 33/77 (43%), Gaps = 5/77 (6%)
 Frame = +2

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
               + G  G  G  G  G  G  G  G KG+KGD G  G KGD G+ GVP   G  G
Sbjct  135038  IQGPKGDTGSQGLKGDPGAQGIQGVKGDKGDQGTAGAKGDKGDPGVPMLAGATG-----A  135202

Query  100     RKGEPGEGAYVYRSAFS  116
               R   P +G   Y    +
Sbjct  135203  RPSSPAKGQMFYDETLA  135253


>NC_023565.1 Mycobacterium phage Nyxis, complete genome
Length=51250

 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 35/118 (30%), Positives = 52/118 (44%), Gaps = 23/118 (19%)
 Frame = +1

Query  63    GEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETY  122
             G+ G +G  GL GPKGD G+ G  G++GP+G  G QG +G   +G Y Y S+ +  L+
Sbjct  2473  GDLGPQGPQGLQGPKGDKGDKGDTGSQGPQGIQGPQGIQGP--QGPYGYLSSDATVLDFR  2646

Query  123   VTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY---HITVYMKDVKVSLFK  177
                     R T+  YN                P   ++     H+ V + D   S F+
```

```
Sbjct  2647  --------RMTQAQYN----------ALGAGRPATTFYVIVG*HMPVRIGDATPSGFR  2766


>NC_028925.1 Enterobacteria phage vB_EcoM_VR25, complete genome
Length=170822

 Score = 38.1 bits (87),  Expect = 0.032, Method: Compositional matrix adjust.
 Identities = 29/66 (44%), Positives = 36/66 (55%), Gaps = 3/66 (5%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGV---PGAEGPRGFPG  96
               + G+ G PG NG  G  G  G  G +G KGD G  G KGD G  G+    G +GP+G  G
Sbjct  109441  LTGVQGEPGENGDIGPKGPIGLTGPQGPKGDTGSKGIKGDTGPQGIQGPAGPQGPQGEKG  109620

Query  97      IQGRKG  102
               +QG  G
Sbjct  109621  VQGLAG  109638


 Score = 37.0 bits (84),  Expect = 0.081, Method: Compositional matrix adjust.
 Identities = 25/54 (46%), Positives = 30/54 (56%), Gaps = 0/54 (0%)
 Frame = +1

Query  40      MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
               + G+ G  G  G  G  G  G +G  G PGL GP+G  G TG  GA+GPRG
Sbjct  110083  IQGLKGETGPAGPQGIQGLKGEVGAQGPSGSPGLTGPEGPRGLTGEAGAQGPRG  110244


>NC_022776.1 Streptococcus phage TP-778L complete genome
Length=41757

 Score = 38.1 bits (87),  Expect = 0.033, Method: Compositional matrix adjust.
 Identities = 35/129 (27%), Positives = 52/129 (40%), Gaps = 12/129 (9%)
 Frame = +1

Query  36     CTGWMAGIPGHPGHNGAPGR---DGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPR  92
               +GW + +P  P  N    +   +  D T          G  GPKGD G  G+ G  G +
Sbjct  32134  TSGWSSQVPNVPESNYLWTKTVWEYTDNTNETGYSVAKMGEQGPKGDRGIQGLQGPRGDQ  32313

Query  93     GFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNH----YDGSTG  148
              G PG +G  G      +V    +S G + Y+ +   P  F +  Y  + H     D +T
Sbjct  32314  GIPGPKGIDGTDAPTIFVKSYTYSAGSKAYIKLTG-PNAFEQTLYYSRGHNVWVLDATTH  32490

Query  149    KF----HCN  153
              K     HC+
Sbjct  32491  KLKEFVHCD  32517


>NC_015454.1 Propionibacterium phage PAD20 endogenous virus, complete genome
Length=29074

 Score = 37.7 bits (86),  Expect = 0.042, Method: Compositional matrix adjust.
 Identities = 25/60 (42%), Positives = 30/60 (50%), Gaps = 0/60 (0%)
 Frame = +1

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              + G PG  G  G  G  G  G  G  GL+GP G  G  G+ G +GP G PG+ G  G
Sbjct  14830  VRGVPGPAGVRGPQGPAGVDGRDGVDGSAGLVGPVGPQGSPGLNGVKGPDGLPGVNGSDG  15009
```

```
>NC_020201.1 Pectobacterium phage phiTE, complete genome
Length=142349

 Score = 37.7 bits (86),  Expect = 0.045, Method: Compositional matrix adjust.
 Identities = 30/72 (42%), Positives = 37/72 (51%), Gaps = 0/72 (0%)
 Frame = +3

Query  34      GACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRG  93
               G   G + G  G  G  GA G  G +G  G +G +G  G  G KGD G+TG  GA GP G
Sbjct  116997  GIFVGTVKGDKGDTGATGATGPAGPEGPIGPQGPEGPQGPQGEKGDTGDTGAVGATGPAG  117176

Query  94      FPGIQGRKGEPG  105
                 G +G +G  G
Sbjct  117177  AQGARGPEGPKG  117212


>NC_027371.1 Propionibacterium phage Pacnes 2012-15, complete genome
Length=29741

 Score = 37.7 bits (86),  Expect = 0.047, Method: Compositional matrix adjust.
 Identities = 27/66 (41%), Positives = 33/66 (50%), Gaps = 0/66 (0%)
 Frame = -1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              + G+PG  G  G  G  G  G  G  G  GL+GP G  G  G+ G +GP G PG  G
Sbjct  14831  VQGVPGPAGVRGPQGPAGVAGVDGRNGVDGSAGLVGPVGPQGSPGLNGVKGPDGLPGSDG  14652

Query  100    RKGEPG  105
              + G  G
Sbjct  14651  KDGRDG  14634


>NC_028672.1 Cronobacter phage PBES 02, complete genome
Length=149732

 Score = 37.7 bits (86),  Expect = 0.047, Method: Compositional matrix adjust.
 Identities = 30/71 (42%), Positives = 35/71 (49%), Gaps = 21/71 (30%)
 Frame = +2

Query  57     GRDGTPGEKGEKGDPGLIGPKG---------------------DIGETGVPGAEGPRGFP  95
              G  G  GEKG+KGDPG  GP+G                     ++GETG  G +GP G
Sbjct  65696  GPQGPQGEKGDKGDPGPQGPQGVQGEPGNPGEKGPQGGQGPQGEVGETGPQGPQGPVGPT  65875

Query  96     GIQGRKGEPGE  106
              G QG KGE GE
Sbjct  65876  GPQGEKGERGE  65908


>NC_018853.1 Streptomyce phage TG1, complete genome
Length=40474

 Score = 37.7 bits (86),  Expect = 0.052, Method: Compositional matrix adjust.
 Identities = 29/70 (41%), Positives = 35/70 (50%), Gaps = 3/70 (4%)
 Frame = +3

Query  33     KGACTGWMAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPR  92
```

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              +G+   W+A + G  G  G     G  G  G +G KGD G IGP+G  G  G  G EGP
Sbjct  14730  EGSEADWVASLEGDVGPVG---PQGPKGDTGPQGPKGDTGAIGPQGPEGAQGPAGPEGPM  14900

Query  93     GFPGIQGRKG  102
              G  G QG  G
Sbjct  14901  GPEGPQGPAG  14930


>NC_013645.1 Streptococcus phage Abc2, complete genome
Length=34882

 Score = 37.4 bits (85),  Expect = 0.056, Method: Compositional matrix adjust.
 Identities = 22/53 (42%), Positives = 31/53 (58%), Gaps = 0/53 (0%)
 Frame = +1

Query  59     DGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVY  111
              DG  G KG++G  G  G +G+ G  G+ G +GP+G  GI G KG  G+  Y +
Sbjct  16423  DGKQGPKGDRGPQGPKGDRGERGLQGLRGIQGPKGDQGIPGPKGADGKTQYTH  16581


>NC_015569.1 Synechococcus phage S-CRM01, complete genome
Length=178563

 Score = 37.4 bits (85),  Expect = 0.058, Method: Compositional matrix adjust.
 Identities = 27/64 (42%), Positives = 31/64 (48%), Gaps = 0/64 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              G  G  G NG  G  G  G  G +G  G  G  GP+G  G  G  G +GP+GF G QG
Sbjct  29047  GFQGVAGSNGTQGPQGFQGNQGSQGIAGSNGTQGPQGFQGVAGSNGTQGPQGFQGSQGIA  29226

Query  102    GEPG  105
              G  G
Sbjct  29227  GSNG  29238


 Score = 37.0 bits (84),  Expect = 0.088, Method: Compositional matrix adjust.
 Identities = 27/66 (41%), Positives = 36/66 (55%), Gaps = 0/66 (0%)
 Frame = +1

Query  40     MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQG  99
              +AG  G  G  G  G  G +GT G +G +G+ G  GP+G  G  G  G +GP+GF G+ G
Sbjct  26311  VAGSNGTQGPQGFQGNAGSNGTQGPQGFQGNAGSQGPQGFQGNAGSNGTQGPQGFQGVAG  26490

Query  100    RKGEPG  105
                G  G
Sbjct  26491  SNGTQG  26508


 Score = 37.0 bits (84),  Expect = 0.091, Method: Compositional matrix adjust.
 Identities = 28/61 (46%), Positives = 35/61 (57%), Gaps = 0/61 (0%)
 Frame = +1

Query  42     GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
              GI G  G  G  G +G DGT G +G  G  G  GP+G  G  G  G++GP+GF G QG +
Sbjct  25582  GINGTQGPQGFQGANGIDGTQGPQGNAGSNGTQGPQGFQGVGGNNGSQGPQGFQGNQGLR  25761

Query  102    G  102
```

```
              G
Sbjct  25762  G  25764


>NC_024148.1 Mycobacterium phage Phantastic, complete genome
Length=50101

 Score = 37.4 bits (85),  Expect = 0.064, Method: Compositional matrix adjust.
 Identities = 28/62 (45%), Positives = 34/62 (55%), Gaps = 0/62 (0%)
 Frame = +3

Query  42    GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK  101
             GI G  G  G  G  G +G  G  G +G  G IGP+G  GE G  G +GP+G  G QG +
Sbjct  2100  GIQGPQGLQGPQGEQGPEGPQGPVGPQGPQGEIGPQGPQGEQGPQGIQGPQGAQGPQGPQ  2279

Query  102   GE  103
             GE
Sbjct  2280  GE  2285


>NC_022341.1 Propionibacterium phage PHL113M01, complete genome
Length=29200

 Score = 37.0 bits (84),  Expect = 0.071, Method: Compositional matrix adjust.
 Identities = 26/63 (41%), Positives = 31/63 (49%), Gaps = 0/63 (0%)
 Frame = +2

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              + G PG  G  G  G  G  G  G  GL+GP G  G  G+ G +GP G PG  G+ G
Sbjct  14867  VQGVPGPAGVRGPQGPAGVDGRDGVNGSAGLVGPVGPQGSPGLNGVKGPDGLPGANGKDG  15046

Query  103    EPG  105
                G
Sbjct  15047  VAG  15055


>NC_018849.1 Propionibacterium phage P105, complete genome
Length=29202

 Score = 37.0 bits (84),  Expect = 0.078, Method: Compositional matrix adjust.
 Identities = 26/63 (41%), Positives = 31/63 (49%), Gaps = 0/63 (0%)
 Frame = +3

Query  43     IPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG  102
              + G PG  G  G  G  G  G  G  GL+GP G  G  G+ G +GP G PG  G+ G
Sbjct  14763  VQGVPGPAGVRGPQGPAGVDGRDGVNGSAGLVGPVGPQGSPGLNGVKGPDGLPGANGKDG  14942

Query  103    EPG  105
                G
Sbjct  14943  VAG  14951


>NC_011023.1 Mycobacterium phage Pukovnik, complete genome
Length=52892

 Score = 36.6 bits (83),  Expect = 0.095, Method: Compositional matrix adjust.
 Identities = 28/58 (48%), Positives = 35/58 (60%), Gaps = 0/58 (0%)
 Frame = +1
```

```
Query  48    GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPG  105
             G  G  G +G  G  G KG+KGD G  G KGD G+TG  G +G +G  G +G KG+PG
Sbjct  4705  GPTGPEGPEGPQGIQGPKGDKGDTGATGAKGDKGDTGSQGLQGIQGPAGPKGDKGDPG  4878



Lambda      K        H        a         alpha
   0.316    0.141    0.446    0.792     4.96

Gapped
Lambda      K        H        a         alpha    sigma
   0.267   0.0410    0.140     1.90     42.6     43.6

Effective search space used: 11375968268


Effective search space used: 865823240

--------------------------------------------------------------
```

Database: Refseq viruses representative genomes
Posted date: Sep 18, 2017 10:25 PM
Number of letters in database: 259,746,973
Number of sequences in database: 9,448

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Neighboring words threshold: 13
Window for multiple hits: 40

```
TBLASTN 2.6.0+

Reference: Stephen F. Altschul, 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.

Database: Refseq viruses representative genomes
           9,448 sequences; 259,746,973 total letters
```