

TAT.SABAEUS

1 21 41 61

MDQEQEARPQVWEEELQEELHRPLQACDNTCYCKVCCFHCILCFHRKALGICYYPVPRPRRASKKIQNNKVPVHN

MDQEQEARPQVWEEEL (15) [-1.55]

QEARPQVWEEELQEEL (15) [-1.43]

PQVWEEELQEELHRPL (15) [-1.15]

EELQEELHRPLQACD (15) [-1.21]

EELHRPLQACDNTCY (15) [-0.96]

RPLQACDNTCYCKVC (15) [-0.18]

ACDNTCYCKVCCFHC (15) [0.51]

TCYCKVCCFHCILCF (15) [1.60]

KVCCFHCILCFHRKA (15) [0.75]

FHCILCFHRKALGIC (15) [1.09]

LCFHRKALGICYYP (15) [0.65]

RKALGICYYPVPRR (15) [-0.75]

GICYYPVPRPRRASKK (15) [-1.02]

YVPRPRRASKKIQNN (15) [-1.77]

PRRASKKIQNNKVPV (15) [-1.37]

SKKIQNNKVPVHN (14) [-1.31]

ENV.SABAEUS

Word length: 15
 Overlap consecutive peptides by: 11
 Shorten by: 3
 Lengthen by: 2
 Number of peptides generated: 221 + 52 = 273

1 21 41 61 81
 MKLLTVLLWLSGCWSIVWLQYVTVFYGIPVWKNSSVQAFCKTPNTNLWASTNCIPDDEPEGTIAEVPIPNITEKFDWKNRNPLVG
 MKLLTVLLWLSGCWS (15) [1.28]
 TVLLWLSGCWSIVWL (15) [1.68]
 WLSGCWSIVWLQYV (15) [1.18]
 CWSIVWLQYVTVFY (15) [1.40]
 VWLVQYVTVFYGIPV (15) [1.49]
 QYVTVFYGIPVWKN (15) [0.13]
 VFYGIPVWKNSSVQA (15) [0.33]
 IPVWKNSSVQAFCKT (15) [0.03]
 KNSSVQAFCKTPNTN (15) [-1.01]
 VQAFCKTPNTNLWAS (15) [-0.15]
 CKTPNTNLWASTNCI (15) [-0.31]
 NTNLWASTNCIPDDE (15) [-0.87]
 WASTNCIPDDEPEGT (15) [-1.03]
 NCIPDDEPEGTIAEV (15) [-0.52]
 DDEPEGTIAEVPIPN (15) [-0.79]
 EGTIAEVPIPNITEK (15) [-0.23]
 AEVPIPNITEKFDW (15) [-0.21]
 IPNITEKFDWKNRN (15) [-1.29]
 TEKFDWKNRNPLVG (15) [-1.15]

81 101 121 141 161
 DAWKNRNPLVGQAESNIHLLFESTLKPCVKLTPMCICKMNCYRLEGGAATTKTPSTTTARPEVVSVDGYNDSVIEKEMEKEQAMNCSFAMAGY
 DAWKNRNPLVGQAES (15) [-1.20]
 NRNPLVGQAESNIHL (15) [-0.66]
 LVGQAESNIHLLFES (15) [0.37]
 AESNIHLLFESTLKP (15) [-0.07]
 IHLLFESTLKPCVKL (15) [0.77]
 FESTLKPCVKLTPMC (15) [0.32]
 LKPCVKLTPMCICKM (15) [0.40]
 VKLTPMCICKMNCYRL (15) [0.38]
 PMCIKMNCYRLEGGA (15) [-0.01]
 KMNCYRLEGGAATTK (15) [-0.73]
 YRLEGGAATTKTPST (15) [-0.79]
 GGAATTKTPSTTTAR (15) [-0.69]
 TTKTPSTTTARPEVV (15) [-0.66]
 PSTTTARPEVVSVDGY (15) [-0.15]
 TARPEVVSVDGYNSV (15) [-0.13]
 EVVSVGYNDSVIEKE (15) [-0.23]
 VGYNDSVIEKEMEKE (15) [-1.10]
 DSVIEKEMEKEQAMN (15) [-1.25]
 EKEMEKEQAMNCSFA (15) [-1.13]

EKEQAMNCSFAMAGY (15) [-0.39]

161 181 201 221 241
AMNCSFAMAGYRRDVKKNYSTVWDDQEVVCEEGRKSNATNTVGCYMIHCNDSVIKEACDKTYWDTFRLRYCAPAGYALLKCNDHDYRGHK
AMNCSFAMAGYRRDVKKNYSTVWDDQEVVCEEGRKSNATNTVGCYMIHCNDSVIKEACDKTYWDTFRLRYCAPAGYALLRCADTDYSGHK
AMNCSFAMAGYRRDV (15) [0.01]
SFAMAGYRRDVKKNY (15) [-1.01]
AGYRRDVKKNYSTVW (15) [-1.27]
RDVKKNYSTVWDDQE (15) [-1.91]
KNYSTVWDDQEVVCE (15) [-0.90]
TVWDDQEVVCEEGR (15) [-1.06]
DQEVVCEEGRKSNA (15) [-1.43]
VCEEGRKSNATNTV (15) [-1.05]
GREKSNATNTVGCYM (15) [-0.85]
SNATNTVGCYMIHCN (15) [-0.01]
NTVGCYMIHCNDSVI (15) [0.49]
CYMIHCNDSVIKEAC (15) [0.31]
HCNDSVIKEACDKTY (15) [-0.82]
SVIKEACDKTYWDTF (15) [-0.46]
EACDKTYWDTFRLRY (15) [-1.16]
KTYWDTFRLRYCAPA (15) [-0.68]
DTFRLRYCAPAGYAL (15) [0.03]
LRYCAPAGYALLKCN (15) [0.35]
LRYCAPAGYALLRCA (15) [0.67]
APAGYALLKCNDHDY (15) [-0.45]
APAGYALLRCADTDY (15) [0.03]
YALLKCNDHDYRGHK (15) [-1.35]
YALLRCADTDYSGHK (15) [-0.63]

241 261 281 301 321
 KCNDHDYRGHKNCQNVSVAACTGLMNTTISTGIGINGSRAENRTEIWQEDGDSNDTVIIKLNKYNNLTIRCRRPGNKTVPVTIMAGLVFH
 RCADTDYSGHKACQNVTVSACTRLINTTVSTGIGINGSYVANRTEIWQENGNSNDTVIIRLNRYNNLTIRCRRPGNKTVPVTIMAGLVFH
 KCNDHDYRGHKNCQN (15) [-2.43]
 RCADTDYSGHKACQN (15) [-1.35]
 HDYRGHKNCQNVSV (15) [-1.24]
 TDYSGHKACQNVTVS (15) [-0.64]
 GHKNCQNVSVAACTG (15) [-0.19]
 GHKACQNVTVSACTR (15) [-0.28]
 CQNVSVAACTGLMNT (15) [0.64]
 CQNVTVSACTRLINT (15) [0.37]
 SVAACTGLMNTTIST (15) [0.81]
 TVSACTRLINTTVST (15) [0.53]
 CTGLMNTTISTGIGI (15) [0.89]
 CTRLINTTVSTGIGI (15) [0.77]
 MNTTISTGIGINGSR (15) [-0.07]
 INTTVSTGIGINGSY (15) [0.30]
 ISTGIGINGSRAENR (15) [-0.51]
 VSTGIGINGSYVANR (15) [0.19]
 IGINGSRAENRTEIW (15) [-0.73]
 IGINGSYVANRTEIW (15) [-0.00]
 GSRAENRTEIWQEDG (15) [-1.79]
 GSYVANRTEIWQENG (15) [-1.07]
 ENRTEIWQEDGDSND (15) [-2.29]
 ANRTEIWQENGNSND (15) [-1.93]
 EIWQEDGDSNDTVII (15) [-0.64]
 EIWQENGNSNDTVII (15) [-0.64]
 EDGDSNDTVIIKLNK (15) [-0.91]
 ENGNSNDTVIIRLN (15) [-0.99]
 SNDTVIIKLNKYNNL (15) [-0.34]
 SNDTVIIRLNRYNNL (15) [-0.42]
 VIKLNKYNNLTIRC (15) [0.35]
 VIIRLNRYNNLTIRC (15) [0.27]
 LNKYNNLTIRCRRPG (15) [-1.01]
 LNRYNNLTIRCRRPG (15) [-1.05]
 YNLTIRCRRPGNKTVP (15) [-0.94]
 IRCRRPGNKTVPVT (15) [-0.45]
 RPGNKTVPVTIMAG (15) [0.21]
 KTVLPVTIMAGLVFH (15) [1.38]

321 341 361 381 401
 PVTIMAGLVFHSQKYNTRLKQAWCWFGGNWTQAWKEVRETIVKLPNTTYKGTRNISQIFLQRQWGDPEAENFFNCQGEFFYCKMDWFLNY
 PVTIMAGLVFHSQKYNTRLKQAWCWFGGNWRGAWQEVKETIVKLPPTRYSGTNDTSKIFLQRQWGDPEAEFFNCQGEFFYCKMDWFLNY
 PVTIMAGLVFHSQKY (15) [0.52]
 MAGLVFHSQKYNTRL (15) [-0.23]
 VFHSQKYNTRLKQAW (15) [-1.14]
 QKYNTRLKQAWCWFG (15) [-1.07]
 TRLKQAWCWFGGNWT (15) [-0.63]
 TRLKQAWCWFGGNWR (15) [-0.88]
 QAWCWFGGNWTQAWK (15) [-0.71]
 QAWCWFGGNWRGAWQ (15) [-0.73]
 WFGGNWTQAWKEVRE (15) [-1.19]
 WFGGNWRGAWQEVKE (15) [-1.17]
 NWTQAWKEVRETIVK (15) [-0.99]
 NWRGAWQEVKETIVK (15) [-0.97]
 AWKEVRETIVKLPPNT (15) [-0.55]
 AWQEVKETIVKLPPPT (15) [-0.35]
 VRETIVKLPPNTTYKG (15) [-0.53]
 VKETIVKLPPTRYSG (15) [-0.41]
 IVKLPPNTTYKGTRNI (15) [-0.51]
 IVKLPPTRYSGTNDT (15) [-0.71]
 PNTTYKGTRNISQIF (15) [-0.89]
 PPTRYSGTNDTSKIF (15) [-1.11]
 YKGTRNISQIFLQRQ (15) [-0.97]
 YSGTNDTSKIFLQRQ (15) [-1.07]
 RNISQIFLQRQWGD (15) [-0.97]
 NDTSKIFLQRQWGD (15) [-1.28]
 QIFLQRQWGDPEAEN (15) [-1.27]
 KIFLQRQWGDPEAEF (15) [-0.87]
 QRQWGDPEAENFFN (15) [-1.45]
 QRQWGDPEAEFFFN (15) [-1.03]
 GDPEAENFFNCQGE (15) [-0.95]
 GDPEAEFFNCQGE (15) [-0.53]
 AENFFNCQGEFFYC (15) [0.11]
 AEFFNCQGEFFYC (15) [0.53]
 FFNCQGEFFYCKMDW (15) [-0.16]
 QGEFFYCKMDWFLNY (15) [-0.35]

401 421 441 461 481
 FYCKMDWFLN~~YL~~NNQS~~VD~~PDHNP~~CN~~KTGDKK~~W~~QRTY~~VP~~CHIRQVVNV~~W~~Y~~TL~~AKKTYAPPREGHLECTSTATALY~~VEL~~NFDSN~~SR~~SN~~VT~~LS
 FYCKMDWFLN~~YL~~NNQS~~VD~~PDHNP~~CN~~K~~NN~~DKKCWQRTYVPCHIRQVVNDWY~~TL~~SKKTYAPPREGHLEC~~N~~STATALY~~VEL~~N~~YN~~S~~KN~~R~~T~~N~~VT~~LS
 FYCKMDWFLN~~YL~~NNQ (15) [-0.49]
 MDWFLN~~YL~~NNQS~~VD~~P (15) [-0.61]
 L~~N~~Y~~L~~NNQS~~VD~~PDHNP (15) [-1.41]
 NNQS~~VD~~PDHNP~~CN~~KT (15) [-1.97]
 NNQS~~VD~~PDHNP~~CN~~KN (15) [-2.16]
 VDPDHNP~~CN~~KTGDKK (15) [-2.00]
 VDPDHNP~~CN~~KNNDKK (15) [-2.39]
 HNP~~CN~~KTGDKK~~CW~~QR (15) [-2.13]
 HNP~~CN~~KNNDKK~~CW~~QR (15) [-2.53]
 NKTGDKK~~CW~~QRTYVP (15) [-1.71]
 NKNNDKK~~CW~~QRTYVP (15) [-2.10]
 DKK~~CW~~QRTYVPCHIR (15) [-1.19]
 WQRTYVPCHIRQVVN (15) [-0.51]
 YVPCHIRQVVNDWYT (15) [-0.29]
 HIRQVVNDWY~~TL~~AKK (15) [-0.69]
 HIRQVVNDWY~~TL~~SKK (15) [-0.87]
 VVNDWY~~TL~~AKKTYAP (15) [-0.37]
 VVNDWY~~TL~~SKKTYAP (15) [-0.54]
 WY~~TL~~AKKTYAPPREG (15) [-1.13]
 WY~~TL~~SKKTYAPPREG (15) [-1.30]
 AKKTYAPPREGHLEC (15) [-1.21]
 SKKTYAPPREGHLEC (15) [-1.39]
 YAPPREGHLECTSTA (15) [-0.79]
 YAPPREGHLECSTA (15) [-0.98]
 REGHLECTSTATALY (15) [-0.37]
 REGHLECSTAATALY (15) [-0.56]
 LECTSTATALY~~VEL~~N (15) [0.47]
 LECSTAATALY~~VEL~~N (15) [0.28]
 STATALY~~VEL~~NFDSN (15) [-0.01]
 STATALY~~VEL~~NYSK (15) [-0.31]
 ALY~~VEL~~NFDSN~~SR~~SN (15) [-0.62]
 ALY~~VEL~~NYSK~~R~~TN (15) [-1.09]
 ELNFDSN~~SR~~SN~~VT~~LS (15) [-0.75]
 ELNYSK~~R~~TN~~VT~~LS (15) [-1.23]

481 501 521 541 561
DSNSRSNVTLSPIRSIWSYELGDYKLVEIKPIGFAPTEVRRYTGPERQKRVPFVLGFLGFLGAAGAAMGAAATALTQVSQQLLAGILQQQ
NSKNRTNVTLSPIRSIWSANELGDYKLVEIKPIGFAPTEVRRYTGPERQKRVPFVLGFLGFLGAAGAAMGAAATALTQVSQQLLAGILQQQ
DSNSRSNVTLSPIR (15) [-1.07]
NSKNRTNVTLSPIR (15) [-1.27]
RSNVTLSPIRSIWS (15) [-0.36]
RTNVTLSPIRSIWA (15) [-0.18]
TLSPQIRSIWSYELG (15) [-0.15]
TLSPQIRSIWANELG (15) [-0.12]
QIRSIWSYELGDYKL (15) [-0.52]
QIRSIWANELGDYKL (15) [-0.49]
IWSYELGDYKLVEIK (15) [-0.15]
IWANELGDYKLVEIK (15) [-0.12]
ELGDYKLVEIKPIGF (15) [0.11]
YKLVEIKPIGFAPTE (15) [0.08]
EIKPIGFAPTEVRRY (15) [-0.51]
IGFAPTEVRRYTGPE (15) [-0.63]
PTEVRRYTGPERQKR (15) [-2.30]
RRYTGPERQKRVPFV (15) [-1.55]
GPERQKRVPFVLGFL (15) [-0.15]
QKRVPFVLGFLGFLG (15) [0.90]
PFVLGFLGFLGAAGA (15) [1.75]
GFLGFLGAAGAAMGA (15) [1.47]
FLGAAGAAMGAAATA (15) [1.40]
AGAAMGAAATALTQV (15) [1.12]
MGAAATALTQVSQQL (15) [0.52]
ATALTQVSQQLLAGI (15) [0.83]
TVQSQQLLAGILQQQ (15) [-0.07]

561 581 601 621 641
 QQLLAGILQQQKNLLAAVEQQQMLKLTIIWGVKNLNARVTALEKYLEDAQRLNIWGCAFRQVCHTTVPWKFNNTPDWDNMTWQEWERQIAK
 QQLLAGILQQQKNLL (15) [0.00]
 AGILQQQKNLLAAVE (15) [0.25]
 QQQKNLLAAVEQQQQ (15) [-1.33]
 NLLAAVEQQQMLKL (15) [-0.00]
 AVEQQQMLKLTIIWG (15) [-0.23]
 QQQMLKLTIIWGVKNL (15) [-0.12]
 LKLTIIWGVKNLNARV (15) [0.32]
 IWGVKNLNARVTALE (15) [0.21]
 KNLNARVTALEKYLE (15) [-0.61]
 ARVTALEKYLEDAQAR (15) [-0.78]
 ALEKYLEDAQRLNIW (15) [-0.57]
 YLEDAQRLNIWGCAF (15) [-0.01]
 QARLNIWGCAFRQVC (15) [0.21]
 NIWGCAFRQVCHTTV (15) [0.34]
 CAFRQVCHTTVPWKF (15) [0.12]
 QVCHTTVPWKFNNTP (15) [-0.67]
 TTVPWKFNNTPDWDN (15) [-1.43]
 WKFNNTPDWDNMTWQ (15) [-1.73]
 NTPDWDNMTWQEWER (15) [-2.19]
 WDNMTWQEWERQIAK (15) [-1.64]

641 661 681 701 721
 TWQEWERQIAKLEGNISRTLEQAHEQEKNLDSYQKLVSWSDFWSWFDLTKWFGWMKIAIMVIAGIIIIARILFVIISLLRKFRAGYAPLSS
 TWQEWERQIAKLEGN (15) [-1.48]
 WERQIAKLEGNISRT (15) [-1.01]
 IAKLEGNISRTLEQA (15) [-0.27]
 EGNISRTLEQAHEQE (15) [-1.60]
 SRTLEQAHEQEKNL (15) [-1.88]
 EQAHEQEKNLDSYQ (15) [-2.34]
 EQEKNLDSYQKLVS (15) [-1.56]
 KNLDSYQKLVSWSDF (15) [-0.79]
 SYQKLVSWSDFWSWF (15) [-0.30]
 LVSWSDFWSWFDLTK (15) [0.05]
 SDFWSWFDLTKWFGW (15) [-0.33]
 SWFDLTKWFGWMKIA (15) [0.11]
 LTKWFGWMKIAIMVI (15) [1.28]
 FGWMKIAIMVIAGII (15) [2.09]
 KIAIMVIAGIIIIARI (15) [2.28]
 MVIAGIIIIARILFVI (15) [2.84]
 GIIIIARILFVIISLL (15) [2.77]
 ARILFVIISLLRKFR (15) [1.22]
 FVIISLLRKFRAGYA (15) [0.97]

SLLRKFRAGYAPLSS (15) [-0.05]

721 741 761 781 801
KFRAGYAPLSSLPYNNQIIHLDKGQPDKEEEQSGGGLNSDSRSYTWQREFLRHLCHRLITWLRNLTNWFLTIFSNLHRCQLQVILQIRIQ
KFRAGYAPLSSLPY (15) [-0.20]
GYAPLSSLPYNNQII (15) [-0.35]
LSSLPYNNQIIHL (15) [-0.12]
PSYNNQIIHLDKGQ (15) [-1.27]
QQIIHLDKGQPDKE (15) [-1.63]
IHLDKGQPDKEEEQ (15) [-1.97]
KGQPDKEEEQSGGL (15) [-1.93]
DKEEEQSGGGLNSDS (15) [-1.88]
EQSGGGLNSDSRSY (15) [-1.41]
GGLNSDSRSYTWQRE (15) [-1.69]
SDRSYTWQREFLRH (15) [-1.73]
SYTWQREFLRHLCHR (15) [-1.18]
QREFLRHLCHRLITW (15) [-0.49]
LRHLCHRLITWLRNL (15) [0.07]
CHRLITWLRNLTNWF (15) [-0.08]
ITWLRNLTNWFLTIF (15) [0.71]
RNLTNWFLTIFSNLH (15) [0.01]
NWFLTIFSNLHRCQL (15) [0.23]
TIFSNLHRCQLQVILQ (15) [0.68]
NLHRCQLQVILQIRIQ (15) [-0.24]

801 821 841 861 881
CLQVILQIRIQLTAHLEYGWQEFKAAATSLAVAVVQAATSASDLIRHACRSIVRAVLAHPRMRQELERWFNARRLINRRRYKNETSRKSG
CLQVILQIRIQLTAH (15) [0.37]
ILQIRIQLTAHLEYG (15) [-0.19]
IRQLTAHLEYGWQEF (15) [-0.55]
TAHLEYGWQEFKAAA (15) [-0.47]
EYGWQEFKAAATSLA (15) [-0.31]
QEFKAAATSLAVAVV (15) [1.05]
AAATSLAVAVVQAAT (15) [1.55]
SLAVAVVQAATSASD (15) [1.02]
AVVQAATSASDLIRH (15) [0.46]
AATSASDLIRHACRS (15) [-0.05]
ASDLIRHACRSIVRA (15) [0.21]
IRHACRSIVRAVLAH (15) [0.56]
CRSIVRAVLAHPRMR (15) [0.07]
VRAVLAHPRMRQEL (15) [-0.55]
LAHPRMRQELERWF (15) [-1.34]
RRMRQELERWFNARR (15) [-2.11]
QELERWFNARRLINR (15) [-1.31]
RWFNARRLINRRRYK (15) [-1.81]
ARRLINRRRYKNETS (15) [-1.97]
INRRRYKNETSRKSG (15) [-2.39]

881
RYKNETSRKSGRVVGR
RYKNETSRKSGRVVG (15) [-1.62]

ETSRKSGRVVGR (13) [-1.20]

GAG.SABAEUS

Word length: 15
Overlap consecutive peptides by: 11
Shorten by: 3
Lengthen by: 2
Number of peptides generated: 136 + 39 = 175

1 21 41 61 81
MGASNSVLSGRKLDAFELVRLRPNGKKKYKLRHLVWASKELDRFGLSANLLETKEGVVKILSVLLPLVPTGSENLIALFNLCCVLAC
MGASNSVLSGRKLDAFESVRLRPNGKKKYKLRHLVWASKELDRFGLSANLLETKEGVVKILSVLLPLVPTGSENLIALFNLCCVLAC
MGASNSVLSGRKLDA (15) [-0.09]
NSVLSGRKLDAFELV (15) [0.23]
NSVLSGRKLDAFESV (15) [-0.07]
SGRKLDAFELVRLRP (15) [-0.47]
SGRKLDAFESVRLRP (15) [-0.77]
LDAFELVRLRPNGKK (15) [-0.61]
LDAFESVRLRPNGKK (15) [-0.91]
ELVRLRPNGKKKYKL (15) [-1.29]
ESVRLRPNGKKKYKL (15) [-1.59]
LRPNGKKKYKLRHLV (15) [-1.27]
GKKKYKLRHLVWASK (15) [-1.13]
YKLRHLVWASKELDR (15) [-0.84]
HLVWASKELDRFGLS (15) [-0.09]
ASKELDRFGLSANLL (15) [0.05]
LDRFGLSANLLETKE (15) [-0.30]
GLSANLLETKEGVVK (15) [0.07]
NLLETKEGVVKILSV (15) [0.55]
TKEGVVKILSVLLPL (15) [1.17]
VVKILSVLLPLVPTG (15) [1.83]
LSVLLPLVPTGSEN (15) [0.97]
LPLVPTGSENLIALF (15) [1.09]
PTGSENLIALFNLCC (15) [0.77]
ENLIALFNLCCVLAC (15) [1.82]

81 101 121 141 161
 ALFNLCCVLACIHAIEIKVKDTEEAkakIKQEVPLEMTESATVTSSGQKQELQQGKKNEAIAPSGGGSQNYPIVSVNNQWVHQPLSPRTLNA
 ALFNLCCVLACVHAEIKVKDTEEAkakVKQEVPAEMTESATATSSGQKQELQAKKKNEPTATSSGGSQNYPIVSVNNQWVHQPLSPRTLNA
 ALFNLCCVLACIHAIE (15) [1.71]
 ALFNLCCVLACVHAE (15) [1.69]
 LCCVLACIHAIEIKVK (15) [1.44]
 LCCVLACVHAEIKVK (15) [1.42]
 LACIHAIEIKVKDTEE (15) [-0.17]
 LACVHAEIKVKDTEE (15) [-0.19]
 HAEIKVKDTEEAkak (15) [-1.29]
 KVKDTEEAkakIKQE (15) [-1.69]
 KVKDTEEAkakIKQE (15) [-1.71]
 TEEAKAKIKQEVPLE (15) [-1.03]
 TEEAKAKVKQEVPAE (15) [-1.18]
 KAKIKQEVPLEMTES (15) [-0.84]
 KAKVKQEVPAEMTES (15) [-0.99]
 KQEVPLEMTESATVT (15) [-0.43]
 KQEVPAEMTESATAT (15) [-0.73]
 PLEMTESATVTSSGQ (15) [-0.35]
 PAEMTESATATSSGQ (15) [-0.65]
 TESATVTSSGQKQEL (15) [-0.87]
 TESATATSSGQKQEL (15) [-1.03]
 TVTSSGQKQELQQGK (15) [-1.41]
 TATSSGQKQELQAKK (15) [-1.45]
 SGQKQELQQGKKNEA (15) [-2.15]
 SGQKQELQAKKKNEP (15) [-2.25]
 QELQQGKKNEAIAPS (15) [-1.31]
 QELQAKKKNEPTATS (15) [-1.71]
 QGKKNEAIAPSGGGS (15) [-1.00]
 AKKKNEPTATSSGGS (15) [-1.42]
 NEAIAPSGGGSQNYPIVSV (15) [-0.88]
 NEPTATSSGGSQNYPIVSV (15) [-1.42]
 APSGGGSQNYPIVSV (15) [-0.03]
 ATSSGGSQNYPIVSV (15) [0.01]
 GGSQNYPIVSVNNQW (15) [-0.72]
 NYPIVSVNNQWVHQPLSPR (15) [-0.65]
 VSVNNQWVHQPLSPR (15) [-0.73]
 NQWVHQPLSPRTLNA (15) [-0.91]

161 181 201 221 241
HQPLSPRTLNAWVKVIEEKKFSAEVVPMFSALAEGAIPYDINQMLNAVGDHQGALQIVKDVINEEAADWDLRHPPPQPPAQGVLRDPQGS
HQPLSPRTLNAWVKVIEEKKFSAEVVPMFSALAEGAIPYDINQMLNAVGEHQGALQIVKDVINEEAADWDLRHPPPQPPAQGVLRDPQGS
HQPLSPRTLNAWVKV (15) [-0.43]
SPRTLNAWVKVIEEKK (15) [-0.55]
LNAWVKVIEEKKFSA (15) [-0.05]
VKVIEEKKFSAEVVP (15) [0.09]
EKKFSAEVVPMFSA (15) [-0.13]
FSAEVVPMFSALAEG (15) [0.97]
VVPFSAALAEGAIPY (15) [1.17]
FSALAEGAIPYDINQ (15) [0.19]
AEGAIPYDINQMLNA (15) [-0.05]
IPYDINQMLNAVGDH (15) [-0.22]
IPYDINQMLNAVGEH (15) [-0.22]
INQMLNAVGDHQGAL (15) [0.02]
INQMLNAVGEHQGAL (15) [0.02]
LNAVGDHQGALQIVK (15) [0.15]
LNAVGEHQGALQIVK (15) [0.15]
GDHQGALQIVKDVIN (15) [-0.16]
GEHQGALQIVKDVIN (15) [-0.16]
GALQIVKDVINEEAA (15) [0.32]
IVKDVINEEAADWDL (15) [-0.07]
VINEEAADWDLRHPP (15) [-0.88]
EAADWDLRHPPPQP (15) [-1.67]
WDLRHPPPQPPAQG (15) [-1.69]
HPPPQPPAQGVLR (15) [-1.35]
HPPPQPPAQGVLRD (15) [-1.35]
QPPAQGVLRDPQGS (15) [-1.24]
QPPAQGVLRDPQGS (15) [-1.24]

241 261 281 301 321
A Q G V L R E P Q G S D I A G T T S T I P E Q I E W T T R A Q N A I N V G N I Y K G W I I L G L Q K C V K M Y N P V N I L D I K Q G P K E P F K D Y V D R F Y K A L R A E Q T D P A V
A Q G V L R D P Q G S D I A G T T S T I A E Q I E W T T R A Q N A I N V G N I Y K G W I I L G L Q K C V K M Y N P V N I L D I K Q G P K E P F K D Y V D R F Y K A L R A E Q T D P A V
A Q G V L R E P Q G S D I A G (15) [-0.40]
A Q G V L R D P Q G S D I A G (15) [-0.40]
L R E P Q G S D I A G T T S T (15) [-0.73]
L R D P Q G S D I A G T T S T (15) [-0.73]
Q G S D I A G T T S T I P E Q (15) [-0.62]
Q G S D I A G T T S T I A E Q (15) [-0.39]
I A G T T S T I P E Q I E W T (15) [-0.11]
I A G T T S T I A E Q I E W T (15) [0.11]
T S T I P E Q I E W T T R A Q (15) [-0.92]
T S T I A E Q I E W T T R A Q (15) [-0.69]
P E Q I E W T T R A Q N A I N (15) [-1.12]
A E Q I E W T T R A Q N A I N (15) [-0.89]
E W T T R A Q N A I N V G N I (15) [-0.53]
R A Q N A I N V G N I Y K G W (15) [-0.57]
A I N V G N I Y K G W I I L G (15) [0.90]
G N I Y K G W I I L G L Q K C (15) [0.36]
K G W I I L G L Q K C V K M Y (15) [0.47]
I L G L Q K C V K M Y N P V N (15) [0.22]
Q K C V K M Y N P V N I L D I (15) [0.06]
K M Y N P V N I L D I K Q G P (15) [-0.52]
P V N I L D I K Q G P K E P F (15) [-0.48]
L D I K Q G P K E P F K D Y V (15) [-1.02]
G P K E P F K D Y V D R F Y K (15) [-1.54]
E P F K D Y V D R F Y K A L R (15) [-1.07]
D Y V D R F Y K A L R A E Q T (15) [-1.05]
R F Y K A L R A E Q T D P A V (15) [-0.72]

321 341 361 381 401
 ALRAEQTDPVAVKNWMTQSLLIQNANPDCKTVLRGLGMNPTLEEMLTACQGIGGAQHKARLMAKAMSAAFQQQTVGNIFVQQGARPRGPPGG
 ALRAEQTDPVAVKNWMTQSLLIQNANPDCKTVLRGLGMNPTLEEMLTACQGIGGAQHKARLMAEAMSAAFQQQTVGNIFVQQGARPRGPPGG
 ALRAEQTDPVAVKNWM (15) [-0.69]
 EQTDPVAVKNWMTQSL (15) [-0.96]
 PAVKNWMTQSLLIQN (15) [-0.13]
 NWMTQSLLIQNANPD (15) [-0.61]
 QSLLIQNANPDCKTV (15) [-0.26]
 IQNANPDCKTVLRGL (15) [-0.30]
 IQNANPDCKTVLRGL (15) [-0.26]
 NPDCKTVLRGLGMNP (15) [-0.49]
 NPDCKTVLRGLGMNP (15) [-0.45]
 KTVLRGLGMNPTLEE (15) [-0.35]
 KTVLRGLGMNPTLEE (15) [-0.31]
 RGLGMNPTLEEMLT (15) [-0.12]
 KGLGMNPTLEEMLT (15) [-0.08]
 MNPTLEEMLTACQGI (15) [0.19]
 LEEMLTACQGIGGAQ (15) [0.28]
 LTACQGIGGAQHKAR (15) [-0.29]
 QGIGGAQHKARLMAK (15) [-0.54]
 QGIGGAQHKARLMAE (15) [-0.51]
 GAQHKARLMAKAMSA (15) [-0.24]
 GAQHKARLMAEAMSA (15) [-0.21]
 KARLMAKAMSAAFQQ (15) [-0.05]
 KARLMAEAMSAAFQQ (15) [-0.02]
 MAKAMSAAFQQQTVG (15) [0.11]
 MAEAMSAAFQQQTVG (15) [0.14]
 MSAAFQQQTVGNIFV (15) [0.54]
 FQQQTVGNIFVQQGA (15) [-0.15]
 TVGNIFVQQGARPRG (15) [-0.37]
 IFVQQGARPRGPPGG (15) [-0.61]

401 421 441 461 481
QGAPRGPPGGRGRPMNPNIKCYNCGKPGHLARFCKAPRRQGCWKCGSPDHQMKDCQKQVNFLGFGPWGRGKPRNFPLTSIRPTAPPMERD
QGAPRGPPGGRGRP (15) [-1.87]
PRGPPGGRGRPMNPN (15) [-1.88]
PGGRGRPMNPNIKCY (15) [-1.22]
GRPMNPNIKCYNCGK (15) [-1.11]
NPNIKCYNCGKPGHL (15) [-0.90]
KCYNCGKPGHLARFC (15) [-0.45]
CGKPGHLARFCKAPR (15) [-0.59]
GHLARFCKAPRRQGC (15) [-0.75]
RFCKAPRRQGCWKCG (15) [-1.07]
APRRQGCWKCGSPDH (15) [-1.47]
QGCWKCGSPDHQMKD (15) [-1.48]
KCGSPDHQMKDCQKQ (15) [-1.89]
PDHQMDCQKQVNFL (15) [-1.23]
MKDCQKQVNFLGFGP (15) [-0.41]
QKQVNFLGFGPWGRG (15) [-0.63]
NFLGFGPWGRGKPRN (15) [-1.08]
FGPWGRGKPRNFPLT (15) [-0.97]
GRGKPRNFPLTSIRP (15) [-1.13]
PRNFPLTSIRPTAPP (15) [-0.65]
PLTSIRPTAPPMERD (15) [-0.84]

481 501 521 541
IRPTAPPMERDYSRPEENWYADRPPTRGPGPDDPATALLKQYAVQRRRQRRQSCPPQQSPYEEAYSSLRSLFGEDQ
IRPTAPPMERDYSRP (15) [-1.43]
APPMERDYSRPEENW (15) [-2.04]
ERDYSRPEENWYADR (15) [-2.57]
SRPEENWYADRPTR (15) [-2.28]
ENWYADRPTRGPGP (15) [-1.85]
ADRPTRGPGPDDPA (15) [-1.69]
PTRGPGPDDPATALL (15) [-0.59]
PGPDDPATALLKQYA (15) [-0.57]
DPATALLKQYAVQGR (15) [-0.38]
ALLKQYAVQRRRQ (15) [-1.18]
QYAVQRRRQRRQS (15) [-2.37]
QRRRQRRQSCPPQ (15) [-2.73]
QRQRQSCPPQQSPY (15) [-2.35]
RQSCPPQQSPYEEAY (15) [-1.78]
PPQQSPYEEAYSSLR (15) [-1.51]
SPYEEAYSSLRSLFG (15) [-0.47]
EAYSSLRSLFGEDQ (15) [-0.69]

GAG.VERVET

Word length: 15
 Overlap consecutive peptides by: 11
 Shorten by: 3
 Lengthen by: 2
 Number of peptides generated: 128 (-1) = 127

1 21 41 61 81
 MGAATSALNRRQLDQFEHIRLRPNGKKKYQIKHLIWAGKEMERFGLHERLLETEEGCKKIIEVLYPLEPTGSEGLKSLFNLVVCVLYC
 MGAATSALNRRQLDQ (15) [-0.67]
 TSALNRRQLDQFEHI (15) [-0.97]
 NRRQLDQFEHIRLRP (15) [-1.69]
 LDQFEHIRLRPNGKK (15) [-1.41]
 EHIRLRPNGKKKYQI (15) [-1.66]
 LRPNGKKKYQIKHLI (15) [-1.13]
 GKKKYQIKHLIWAGK (15) [-0.97]
 YQIKHLIWAGKEMER (15) [-0.81]
 HLIWAGKEMERFGLH (15) [-0.33]
 AGKEMERFGLHERLL (15) [-0.63]
 MERFGLHERLLETEE (15) [-0.98]
 GLHERLLETEEGCKK (15) [-1.14]
 RLLETEEGCKKIIEV (15) [-0.27]
 TEEGCKKIIEVLYPL (15) [0.07]
 CKKIIEVLYPLEPTG (15) [0.19]
 IEVLYPLEPTGSEGL (15) [0.19]
 YPLEPTGSEGLKSLF (15) [-0.29]
 PTGSEGLKSLFNLVC (15) [0.35]
 EGLKSLFNLVVCVLYC (15) [1.20]

81 101 121 141 161
 SLFNLVVCVLYCIHKEQKVVDTEEAVATVRQCCHLVEKEKNATENTTEPSSGQKKNKGTTAPPGGSQNFPAQQGNVWVHPLSPRTLNAW
 SLFNLVVCVLYCIHKE (15) [1.06]
 LVCVLYCIHKEQKV (15) [0.43]
 LYCIHKEQKVVDTEE (15) [-1.29]
 HKEQKVVDTEEAVAT (15) [-1.45]
 KVKDTEEAVATVRQC (15) [-0.60]
 TEEAVATVRQCCHLV (15) [0.36]
 VATVRQCCHLVEKEK (15) [-0.23]
 RQCCHLVEKEKNATE (15) [-1.26]
 HLVEKEKNATENTTE (15) [-1.62]
 KEKNATENTTEPSSG (15) [-1.95]
 ATENTTEPSSGQKKN (15) [-1.95]
 TTEPSSGQKKNKGTT (15) [-2.12]
 SSGQKKNKGTTAPP (15) [-1.83]
 KKNKGTTAPPGGSQ (15) [-1.80]
 KGTTAPPGGSQNFPA (15) [-0.85]
 APPGGSQNFPAQQG (15) [-1.19]
 GSQNFPAQQGNVW (15) [-0.97]

FPAQQQGNVHVPL (15) [-0.21]
 QQGNVHVPLSPRT (15) [-0.68]
 AVHVPLSPRTLNAV (15) [0.13]

161 181 201 221 241
 VPLSPRTLNAVVKAVEEKKFGAEIVPMFQALSEGCTPYDINQMLNVLGDHQQGALQIVKEIINEEAAQWDVTHPPPAGPLPAGQLRDPRGSD
 VPLSPRTLNAVVKAV (15) [0.42]
 PRTLNAVVKAVEEKK (15) [-0.94]
 NAVVKAVEEKKFGAE (15) [-0.69]
 KAVEEKKFGAEIVPM (15) [-0.20]
 EKKFGAEIVPMFQAL (15) [0.22]
 GAEIVPMFQALSEGC (15) [0.64]
 VPMFQALSEGCTPYD (15) [0.01]
 QALSEGCTPYDINQM (15) [-0.52]
 EGCTPYDINQMLNVL (15) [-0.05]
 PYDINQMLNVLGDH (15) [-0.62]
 NQMLNVLGDHQQGALQ (15) [-0.38]
 NVLGDHQQGALQIVKE (15) [-0.21]
 DHQGALQIVKEIINE (15) [-0.35]
 ALQIVKEIINEEAAQ (15) [0.13]
 VKEIINEEAAQWDVT (15) [-0.37]
 INEEAAQWDVTHPPP (15) [-0.99]
 AAQWDVTHPPPAGPL (15) [-0.35]
 DVTHPPPAGPLPAGQ (15) [-0.54]
 PPPAGPLPAGQLRDP (15) [-0.71]
 GPLPAGQLRDPRGSD (15) [-1.13]

241 261 281 301 321
 AGQLRDPRGSDIAGTTSTVQEQLEWIYTANPRVDVGAIYRRWIILGLQKCVKMYNPVSVLDIRQGPKEPFKDYVDRFYKAIRAEQASGEVK
 AGQLRDPRGSDIAGT (15) [-0.79]
 RDPRGSDIAGTTSTV (15) [-0.77]
 GSDIAGTTSTVQEQ (15) [-0.28]
 AGTTSTVQEQLEWIY (15) [-0.35]
 STVQEQLEWIYTANP (15) [-0.61]
 EQLEWIYTANPRVDV (15) [-0.53]
 WIYTANPRVDVGAIY (15) [0.22]
 ANPRVDVGAIYRRWI (15) [-0.25]
 VDVGAIYRRWIILGL (15) [1.05]
 AIYRRWIILGLQKCV (15) [0.71]
 RWIILGLQKCVKMYN (15) [0.22]
 LGLQKCVKMYNPVSV (15) [0.38]
 KCVKMYNPVSVLDIR (15) [0.15]
 MYNPVSVLDIRQGP (15) [-0.40]
 VSVLDIRQGPKEPFK (15) [-0.51]
 DIRQGPKEPFKDYVD (15) [-1.55]
 GPKEPFKDYVDRFYK (15) [-1.54]
 PFKDYVDRFYKAIRA (15) [-0.67]
 YVDRFYKAIRAEQAS (15) [-0.66]
 FYKAIRAEQASGEVK (15) [-0.56]

321 341 361 381 401
IRAEQASGEVKQWMTESLLIQNANPDCKVILKGLGMHPTLEEMLTACQGVGGPSYKAKVMAEMMQNMQTQNMVQQGGGRGRQRPLKCYNC
IRAEQASGEVKQWMT (15) [-0.73]
QASGEVKQWMTESLL (15) [-0.40]
EVKQWMTESLLIQNA (15) [-0.25]
WMTESLLIQNANPDC (15) [-0.21]
SLLIQNANPDCKVIL (15) [0.57]
QNANPDCKVILKGLG (15) [-0.24]
PDCKVILKGLGMHPT (15) [0.10]
VILKGLGMHPTLEEM (15) [0.45]
GLGMHPTLEEMLTAC (15) [0.37]
HPTLEEMLTACQGVG (15) [0.03]
EEMLTACQGVGGPSY (15) [-0.13]
TACQGVGGPSYKAKV (15) [-0.16]
GVGGPSYKAKVMAEM (15) [-0.03]
PSYKAKVMAEMMQNM (15) [-0.44]
AKVMAEMMQNMQTQN (15) [-0.68]
AEMMQNMQTQNMVQQ (15) [-1.01]
QNMQTQNMVQQGGGR (15) [-1.53]
TQNMVQQGGGRGRQR (15) [-1.81]
VQQGGGRGRQRPLK (15) [-1.65]
GGRGRQRPLKCYNC (15) [-1.42]

401 421 441 461 481
RQRPLKCYNCGKFGHMQRQCPEPRKIKCLKCGKPGHLAKDCRGQVNFLGYGRWMGAKPRNFPAATLGAEPSAPPPPTPYDPAKKLLQQYA
RQRPLKCYNCGKFG (15) [-1.17]
PLKCYNCGKFGHMQR (15) [-0.85]
YNCGKFGHMQRQCPE (15) [-1.31]
KFGHMQRQCPEPRKI (15) [-1.49]
MQRQCPEPRKIKCLK (15) [-1.28]
CPEPRKIKCLKCGKP (15) [-0.87]
RKIKCLKCGKPGHLA (15) [-0.45]
CLKCGKPGHLAKDCR (15) [-0.56]
GKPGHLAKDCRGQVN (15) [-1.10]
HLAKDCRGQVNFLGY (15) [-0.35]
DCRGQVNFLGYGRWM (15) [-0.51]
QVNFLGYGRWMGAKP (15) [-0.39]
LGYGRWMGAKPRNFP (15) [-0.85]
RWMGAKPRNFPAATL (15) [-0.51]
AKPRNFPAATLGAEP (15) [-0.50]
NFPATLGAEPSAPP (15) [-0.10]
ATLGAEPSAPPPPTP (15) [-0.43]
AEPSAPPPPTPYDPA (15) [-1.04]
APPPPTPYDPAKKLL (15) [-0.78]
PTYDPAKKLLQQYA (15) [-1.01]

481 501 521
DPAKKLLQQYAEKGKQLREQRKRPAPVNPDWTEGYSLNSLFGEDQ
DPAKKLLQQYAEKGK (15) [-1.45]
KLLQQYAEKGKQLRE (15) [-1.48]
QYAEKGKQLREQRK (15) [-2.59]
KGKQLREQRKRPAPV (15) [-1.97]
LREQRKRPAPVNPDW (15) [-1.82]
RKRPAPVNPDWTEGY (15) [-1.70]
PAVNPDWTEGYSLNS (15) [-0.82]
PDWTEGYSLNSLFG (15) [-0.70]
EGYSLNSLFGEDQ (14) [-0.77]