

Supporting Information S3

The benchmark dataset $S_{\xi=7}(\mathbf{R})$ used to train and test the model for predicting the possibility of carbonylation at Arg site. It contains 136 positive samples and 847 negative samples. None of the sequences included has $\geq 30\%$ pairwise sequence identity with any other in a same subset.

(1) List of the 136 peptide samples in the positive subset $S_{\xi=7}^+(\mathbf{R})$

ASKLSKIRVVRKSIA
 IIIQSYRMHVQKK
 HCKAFKIRKHYLHLR
 IHLELRNRTPAAVRE
 LEELDRERCFLNEI
 YEMHKMTRDPLNLAL
 RPPVSGLRRRKPRAT
 KTQRSPVRIPFMQRP
 KQFFKDWRDKDQSDG
 KSEYKSYRLRAQLYK
 KSRDEGPRLGDAKLL
 SLRKLPPRSEISSEK
 RKSTEFPRKIREQEP
 GSVTGTKRLRCMPAP
 ELQDMAARQQQIEN
 RKLANAPRPLKKRSS
 ASSRAHRRHRRQAVF
 RALLTAPRSLRRSSC
 TMLLPLLRRFPEQVR
 SIDSLKQRLNVAVKE
 EADEEKERILAQLRE
 VADLEKQRDCSQDLL
 EEEEEILRLHQKEQ
 IELLRKVREQVLKCP
 LLAEVERRIRRGHAR
 PDGENRARFLPGKDL
 WERKQNLRPMPKKYH
 RVLSGRWRLPLRALP
 VSWGKLRKRVKGWAP
 TLPKRVPRAGEARNL
 EGGHFKLRTISSNN
 TLVEKEMRVTLAKLL
 GDSRLKMRAELGEYI
 REQEPTEPLKGIQS
 ALAKHKERKMAVPMMP
 KDLGLHPRAVSTSFG
 CLEVVLCCRVEGMTEL
 IKGLTYLREKHKIMH
 MQKLNQKRAELKLVV
 RIPQLWKRVSWSST
 GYKRKVMRMLKRQVS
 ALVPPWTRVYRVQRD
 KCSEETFRFELGGGV
 GAGSGLGRLLALQFA
 SQDKMEIRSCLPKLL
 VDKSGVVRVVEGDN
 KERLQEVDRDKLGLQY

YVGKAATRLSILSLL
RSVFTVMRRQLEQA
QRGLTEKREELLSVP
RKQLIPRHKTREK
LLEAEKERNKLSLQ
STEPLPGRKQVRDTL
RQLAIETRKTAAQT
LSHPKIPRCQERLLR
RDRPGDPRRKRSSDG
FKDMDKRLSMEIEK
LKRSLMRERVLGPD
DRGHEELRKLESTLD
SGILRQLRQTVEATN
TAEDLRTRKSKLQEL
KAAAADGRGMLPKRA
PPSAASSRYSMRNRI
SRSYTRSRLASSHS
HIAQKLFRDGHFNPE
ETSLNKAREHSLRS
HVTKTRRRCKTVRVD
RLSSVFLRVRTNMGV
GQDGSRRGPQKRGV
PRVFPPRRPHTPAER
APYVTLRRGLNAESS
TSQGKLLRILFGVK
IYKPKRGRPKSKEMP
ENELTFLRSQIAAIV
IANVFQNRDYQCDTV
LMEFITSRKRGPLWN
VVRPKDRRVGTPSQG
RRSVRMKRPSSVKSL
PKTMPRVRKPKTTPT
HFHTVIARRAGMAAS
RIKNPKARVTEVMKA
LFTQELARRLKSGSV
WDATEDLRISRTDSF
ELIRLTQRLRFHKVK
LPLVSWRRLEFQGE
FLQVETRRAGERLGW
LSYRSLRRRVRLRR
VGLGLPNRLRFFRQS
GLAARLQRQFVVRAW
SLRKGIPRTKSVGED
ETRQRLLRVTKKEVK
AIVRQRERESHAAAL
ASPWKSARLMVHTVA
LGKRADQRKAKLGDS
IKSMAASRRAKLNES
QRMKALARALPLQPR
SASKASVRSISVEDK
EEELLNVRRELMVSF
AQLNIKERLIPPSFT
SDPIKACRPIKPPGP
HHVVSGLRENEYFF
VVESVLRRAKEVTWY
LKRTKKPRPPSLKKK

KESLLQDRRQEEDQR
 QEERLEQRLKREEVE
 PEKENAVRDNKVYCK
 EKLHLITRNLQEVLG
 HGKQPSLRAAKEHAM
 NCILDDKRPHVKKAT
 NRRLLVVRPISKQDP
 QADNPLGRSVLRKDI
 GPPTGAGRGPSQLQA
 KVLKNNIRFMNHMKH
 SRLSRHRAVHGPPE
 LAPLNDTRVVHAAKA
 YCDLPEPRKPLEKAV
 CALSHHERLKCDEWS
 VKVPMMKRLGMFNIQ
 YQLEGNKRITCRNGQ
 HKSEVAHRFKDLGEE
 LPKLDELREDEGKASS
 SLQKFGERAFKAWAV
 EKTPVSDRVTKCCTE
 CTLSEKERQIKKQTA
 PLPKEPPRKDPPPKD
 XXXXXXERIDGGITG
 RGGEGNARTHGTPDL
 VLGNDGHREVVKV
 RGADYSLRAVRMKIR
 QQARLHERGAAEMVL
 LPKIETMREKVLTS
 CTKPESERMPCTEDY
 YLSLILNRLCVLHEK
 TESLVNRRPCFSALT
 VGVNGFGRIGRLVTR
 AITIFQERDPANIKW

(2) List of the 847 peptide samples in the negative subset $S_{\xi=7}^-(R)$

VTPHTQCRLKLLKLE
 VLSFSETRAHQVVQQ
 ELSKANSRFATTFYQ
 EEAAGSDRASDLDSV
 GSNGVDHRSYRIIRG
 HSGASQHRIARPSRQ
 DSSLGKNRKALAKGL
 IVDEVHERDVNTDFL
 SDVEAHFRAAHENTK
 ELFVKGVREVDYYC
 HASCYGIRPELVNEG
 ASPATVSRMGMVYIS
 RVQRLGERVVDSGRS
 RSLSRFERSARFDIF
 PNTYDIHRLEKILKA
 EKPGGKERGSSASHP
 VTEASPWRATNPFLN

KKKKKKGRMKKEDNI
GEPKDVIRKDVRAIL
PHQLLLQRLQEEKDR
LSLSHFCSRSPFLCFG
TTEAPVKRASLLGDM
QEECGYLRRHHQEEV
VSNTLESRLDLIAQQ
KKKMTKARLERFKLR
VYTTKSPRERAILGL
PASPISQRLPPKVES
GAQMEAAARPLVQENP
TKDNEHKRSLTKTPA
LHVTDAGRKHIAIAW
INYVLESRLIGTEKF
SSASLIWRSEAEASV
KFTTEEKRFVESRDV
EGEQYLFRIRAQNEK
PPIYTAAREQTPFRH
IRGNEAGRFRDLITL
EWDKDVARKLGSTTV
TDDSGTYRAVCTNYK
ESKGPMTTRLLLHEV
LDLKETLRLRILSED
DELLRHHRDEQKPAT
ALNMLTWRAEQEGGM
PSSGLKKRPISRLQT
CVIQSYWRMRQDRVR
DVWIDVQRRWVYLEG
WLLAHCGRPQTECRH
AACVMPSRLKALGTL
HKQTKKRRILIPSDI
SIQDWAKRMKALVEQ
QENCILLRLDNELGG
SQFNLSGRNPQKQAR
KSMSIVLRENHQKPE
LPEEIALRASDGPQL
EIEKLEFRVRELEQA
EKQVELYRNGQRLLLE
AKKPAATRKSSENPK
EGQEYSFRVRAVNKA
SISGCKMRLSYLSSR
RFRTLMMRRRFLSLK
TYDSYYSRSRSRSRS
EKETLLQRLTEVEQE
HWGQQQIRPIKSVIP
AVPPAKGRTVLEEKV
DLSTIQERMEELKGQ
SECGFCLRQFPRSLL
TPSEAHSRIFESVTL
RIQVFLARYSYNPF
KREKEVARKLEFDGL
PLKTDIPRHPMPFAA
CYIFPGGRGDSALFA
RDMEKVERQAVPQAN
LDLDELKRGIVVRA
SNQSVLHRWERKQNL

ECSKTSFRVANLEEG
MSTIEPHRQVAWKRA
YKDKRELRSKGKYYKI
LEAQVLPRFQPRVLQ
SPQPPLSRAEAIKQV
ELEAHLCRMMKHSMD
EKKLEDARARCEGQE
TYSSAEERMQSEQIR
GLELSIDRFRLRKKKT
SEIRITHRSHHFIPR
CSKDELERALHYLKN
HFIPTIGRLRKRAGK
KQLPQVPRPLQLFSA
CEPLSNKRNSNSVTN
HVHEASSRSHAFIT
KNPASSKRRLKTSLG
GPKLEALRAEVSKLE
WICKCVRCKSCGST
NCVSGQERGRGLVLA
KLNETMERQRTEIAR
NYSESLYRQAMEEAK
LAMLAKERLQEVDRK
EEKQEEERSKVDDL
SEPGANMRHIRKPVI
HVEAVYSRRCVSFIL
QNQVGIGRPAELKEA
IHYLMLPRVREELID
YGLITHQRIHTGEKP
TGLETPDRKGKGTTE
KVVPSPMRRIRAQKG
RRELLELRKGREEK
PLGLILNRFSA DTNI
GNLSILSRQESSFFT
IQGKDVLR LPPSSIT
LNTSIDLRTNVLNDA
EKTINQQR IHARIGQ
KAKEQETRISEEITK
VLIPFKGRPPPTVTW
MALEETLRQYQA AKS
PGFKGEGREVDVNLP
RDLLLQTRLVNHVSS
DNKKKKQRTSSKKKA
WDDIITNRCFFLSKI
RKTRSARRRTTQIIN
YIRISPTRAYNRPTL
LEEELPKRVR SRLSL
QLKSFPARLRQYASY
STGLLPGRGPGTSAP
VKAGDSSRLECKIAG
ATEISTERDLGQCDR
CREVGLQRRSVQLFC
EFKQKLCRAEQAFQA
KVNGCLGRNCKLPIT
HQAAAATREASSED
GAQMLAMRGEQLGVV
TEGMDDFRYACQSPE

IKKANMKRENKAYSF
FSCQRRTRFISLGEA
NSIEASLRCSSVVPR
ALTDEESRKNWEEFG
EEKPEEERSAEESKP
SQELDVKRREAIYND
EKKSKKIRDKTSKKK
DVFLDSGRKTRSARR
KIDHELHRLQALLKH
LCPEGVHRFQWIRNL
QDQKVNIQVAVLPCS
GATTSTIRSSCLVGC
APMTPAARPEDEYEA
KNLVQKERELEEQEK
QFGGIDQRKIFTFAE
QERDRKFRLEEQKVR
VVLPLDERAFEKTLT
ALAVEGKRIGKVLDH
EFLELKYRLLSLLVL
AKWFKDGRELSADSK
RVRPLSKRETKEGGR
IDVNVIARPSAPKEL
EAYITATRQYVAQAN
AQSEAAGRTEPTGPK
CYFHSGPRGTHDLWD
VNLVSVGRVLWQWTK
ALHTEITRNKDSTLE
LQVNDHVRKVTDQIS
VTLQSA YRGMKVRKR
IVTEEHLRRAIGNIE
CPGMMLWRYPEPRVL
EDVHIKGRIIDTVAQ
ELVPPSFRGGKQIDS
KLQTAIHRVTLAQT
VHSPDIYRVVVEGER
DIANVMQRLQDEQEI
KFVGDATRLTDKLE
GLTNPSLRSPPESTE
KGNEIVLRQDIMPTT
RSRSGKGRGLPKKGG
SGAGCSSRDPGPPEP
LEKIKAKRSDSGKYC
KFSSKYLRTEHGSEM
SKSIEKKRGRPPTFP
RKVFSPIRSEPRSPS
WYNVENWRATAVTSPD
HRLIAKSRELYEKTE
GLLFYSLRTLTTMAP
ESDSFCLRNIMEAPL
VKEVAAWRERYEDSQ
KLGKVNDRWQHLLDL
LGYWLEKREVNSTHW
ERDYLLERRDLAVDF
IIDEGLKRFIIEITF
AEAAHNQRAGAPGIQ
TSVPTTPRATPILQP

PLDQTLPRQPGQSL
IKALADEREAVQKKT
LINGGSERKSCFWKL
VADLGNIRIRFIRKN
AKISDLHRESVDHLT
EDVTFNKRKMKLEED
KKQQQCRPSISISS
PKVLQDYRKLKNTAE
IKKLEPSRIVKQDEF
GKPKVLARTKGSMLV
AWIPVPARREAEKVP
SLDWLISRLEAS
RLKAQEHRAEMEEKG
DEAKTSARDAALAYH
PTTRSSARRSQAGVS
LYYYNFTRTVISSGG
DTQTIWARTGYLGFL
NELAYFKRENQELMI
ETQIDETRMGYKPVA
ALFPKGSRSVPRDT
EVFTYSVRGLYENHK
PRARPRERDPGRRPH
NAALDNLKVVPCYS
ESTSQIERPLSQEPA
YDGPKNVRSDISDQE
PFTPVPPRGEPVTY
MKKFEESRAELEKVL
GTIDGEVRLTGELDR
SETKDPLRVQPHLKK
LMVHVDKRITLAAFK
FFAKLNCRLYRKANK
QKVAEQERTAQQLR
SEILSNIRSCRLQCF
PLPTVNERDTENHTS
EQEQLYLRSGVVSSA
AVVDVSDRAVPPSFT
LEYCEVQRDPYSNYG
EDISKLNRAAKVVQE
QGETNKNRTKGGWQQ
EFITSRKRGPLWNHE
DMSMLEERIKRSAKR
AKQFRAVRTTEGEEE
VKERESERNQCNFKP
DKINKTYRSQLSSEE
EGVKYQFRAMAINAA
GPPASNLRKQKSLTN
DVLLGASRTLSLALD
EEVMHTPRTTPSCSAD
PGLPVEVRGSNGAFY
PGSTVLYRIFTVNHK
AQGALPERDASRGGL
PVWAAKQRVLCALNH
LEKRQMDRAEHKGEL
ITESDAQRTMYPGSC
ETPSYAKRRRLAGPS
EDEVQFLRTDDEVVL

AVVLTSYRSTAERKL
RSEGEKVRVGDDLIL
LHNSLLQRKSKLQSL
GWWVRNTRILRKCIE
LLANAPERVVERRRR
RNGPAQTRVSSSSSH
SVQLTEKRMDKVGKY
EDTWKLGRNWXQSVE
SWIWWQLRTGLARDG
HCFHMCDRMVYFFI
STPSLTSRKHGLSH
QSVAKMFRAVEEGLT
LSVKDAVRVDSGNYI
KIYNIEDRTRVPNKF
DADLEALRRKLANAP
NFLASKHRQPPEYNP
CEPNCYSRVINIDGQ
PPEPVDKRAKAPKAR
NKPIPALRVVEEKKK
SKLLKNWRDLARIT
IRNGVTKRGETLSWL
YTMESTDRNQTFEKE
CNGQNTLRNIVHLSK
PLPIDLYRYDDVSGK
LRGLLRSRGAWEQQI
EDELQLPRLPELFET
FKHIKDTRYMSSYFK
QRAAAMARTKVEIAN
QNSSVLDRLPQPAES
TSKSSDNRETPRNHS
KDTLMISRTPEVTCV
QLKNLKIRTNRIRF
HQWIQETRTRYLLDGS
QALLSKMRAIDLQIK
KKTWAKVRTAKFFIL
MSFKDAERGGDTSCE
VEEIMYLRQIYKQQL
TTAATVQRPGPGQTG
VGLWSMCRNTRGTVG
XXXXMSARTPLPTVN
PHPSPEARAPLASAS
DTPPSALRGSQSVSL
HCSLDALREFFSTIV
STSYMHRSPGGPTK
LLIQKYYRAYSIGRE
ESESNDHRSSDFFE
ARFDIFSRYESMCAA
TNYILEKRETMSKRW
KAPSESARGPPGPTD
RKKKSKDRPSKLEKK
KVELSQLRVAKVTGG
VTSQFTTRDDILRDW
GHDEDNTRISSAGCL
SGSFVSSRARREKKS
HLFYKIHRNRYPVCT
GLCIVFVRCRNDVAI

SLEKNLDRMKLDWVN
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AETVPEERARGDPDS
NEHCPSKRDPSKLYK
LQQEQLRALQGRQA
RLPTLPKRVPAGEA
PDSMFGDRGEIIDPF
EGQEYYEREEGYDEG
EVNAAWQRLKGLALQ
TFQTLERASDAKNQ
FLALILQRTFLQASY
EHQMYEFRVKAVNEI
QVWETWPRAQELCPE
IVNLLKMRQGEEVFQ
QIHMIQRDAMAHR
SLSEEIQRRELEATGM
VYTTAEQRPNAYIPE
RRVRETQRHISTVKY
AFYEKMGRMLGSAFP
PGAKVTIRASLGPLQ
TKLLKALRVRKKTGG
ITLMDVTRNSVLSW
LVAVLLSRTWHVRRQ
YLTVTLQRPTKELHG
AAMFQSERKNPAPQC
QDHFQVARQNHFPQR
SPRRRKSRSPPRRR
SSEKTQRMSLMRHH
KHKGTEKRESPPAP
FLDVFLPRVTEALALT
HFFFPSRIVRSLMP
AVQKTTFRVTRLHEG
GYTEVQFRPYRTDDF
DPVEHGQRHTATKRE
HEYEPYSRLKSDIKD
TKFQKLHRDMEEATL
PSAMPQSRSTESAHA
VWEPLIERVEGKRQW
PNVDYQFRVCARGDG
SWIADCARHHCSSTP
VLESTTGRENDSQHY
ELSLNKQRKLNKSES
AWYMHGERAHYSHTM
SATLKNFRYHISLKT
YIKSELDRELQDRYV
LGLDEHNRVKVYRFX
LDTYNVKREAAEQWL
KAWKKHCRGEGKISK
VFKHGYERYNAMRAD
QLSEEQGRNLELQVL
IKVLEKKRAMFECEV
GTPVFADRLPEKMKT
DPSAPQPRAETSGKD
KSLLDWLRQQADYSL
KAAQQHWRHELASAQ
LNKHTALRGEMSGRL

TCMKFYARVCRSGSG
PKKVEMQRSLPGSLL
AKCQVTPRRNVLQKR
FVELGVTRVGHMNI
IMEEAVTRKFBHEDS
EPIQFTKRIQNIVVS
LVIQKYWRRVLAQRK
LEAKQKARKKEERQS
LLEEALLRLLPAELP
YQTMLKGRCPVSAP
LTKEKVSRLDRIVAE
KELADLARLHPTSCA
FNELEALRAESVATK
YLVLQQLRCNGVLEG
QMVTPPPRLVVGTYD
VPYFEQCRRDACRCG
EQEIVQKRTFTKWIN
KNQGLFHRVLRREIS
AACCGSCRNVSCLFT
SLAKFAGRKLKDCGE
CSSLSPQRLCSKHMP
DAAAAGDRRPAPDTW
LDINVVIRQVYHLME
DDQEIQKRLAEQQDL
RYIRSALRQEKALSA
LEKAAAQRKAKLDEN
SGEAPGIRKEMKDVT
REEAEKQRVASENLR
VLQKCSHRLQELEKN
MEFAVNGRPLEPSQA
AREHSLLRSDRPAYV
SNYQSTTRVKPFICT
AVASAASRPDSTHMV
LKYQSLLRMFLSYCI
NSQVTFPRIQVTSLS
DALTDPSRKTQKCLQ
EVLFLSSRSKVFERA
DTIAHLERTRENMEQ
AEQKSLLRVSVASRGE
TSAEQDNRFSNKQKK
PANAGNMRYSHSTGK
MVAVLVSRTVGPTQR
NHHMEVLRELCEELP
LVNKDSTRRDSGAYT
AMVFMDVRMPKFKIY
LVSHVTLRLLKPECV
EKFGLEKRQGALELI
EGCEYEVRYAENAA
YACGVEDRKSARLF
QPDVTGIRLLSLGAG
EELHKEIRLIGNESK
SFLKLTTRAQLGAKS
LRVIEMEREGKGRIS
QIYGQKGRTEILLN
IYNTKSSRERAALS
VELLFNTRYAKAIGI

YGGSYGGRGRGRRTG
EDTQYQFRVYAVNKI
NSQPVAVRGGGGKQV
TPSPPPRRRSPSPRR
LEFDGGSRGKGEHFP
YLMGGTYRCTYTRKR
MAVGMGERPEVLHLT
EGGKGEKRKRETDDE
ITMWLSKRLPQFLQV
NIVWKYQRYHFIMAY
LTASPSSRPVASPGA
XXXXMAVRQALGRGL
QAMPYNCRNNLAFPA
LFGKMIARAGRAGNL
LIVCFIKRSRGGKYP
AHEKRKERLQMLQTN
ASLQPKGRRDPPLLP
LQRQHLYLRQRHSAVI
ELKALAQRGIGYHHS
QDEWEIPRQSLRLVR
AALESLNRAVLAAMD
QFLEEEGRTLEDVAR
KDDIKSTRKLIKESLI
YVRVKTERKNFLAVQ
VNSTHWSRVNKSLLN
VDTKYQIRIQIEKL
AGLSTDNRNVCLWDT
PRRASPLRTSRSRPH
MPSKFSCRQLREAGQ
GENQLLERRRLYHCA
TTIDDGSRCFFTKSK
AAKVFGLRSRKLKLF
ERLKEPTRQALQQL
VIFYDFLRGLEASWI
DEEASYLRFNRNSIWK
PKNDGGSRIKGYIVE
LQVITTLRTAAKEME
SGEGDLRHLGLLGL
NDQLEEQRQEALQR
QEGSLSARWPVAGQI
RQILRLLRLRCTEND
DPVDSTLRDFCGRCI
PVYKTSARRGTLSTT
KTIGSPKRIQSPLNN
TNSVTAVRIQPLEDI
LIPVIGPRKNIKKQQ
ILVNTNLRALINKHT
WGTATVGRPRGPPKA
WLEAQEERLKTQKP
GETPEACRQARSYLE
LRQCLAPRLPHSVTC
ADEIYELRVTGRTQD
NAEKYYGRKSPVGRD
LELESQKRLYEKNLT
KSEAKLSRKQVDSEH
SSLSSAGRPGPSEGG

KVFAKVLREEDSKDA
FIAKAFKRIKDSEFE
QHHRLESRYSSSSGG
LAVGKFTRTSGETTH
VKMCVGSRRMVDM
QRPSGEDRWQEKDQD
GSKKVTIRSPVQIRN
TSENTLKRVS LAGF
QPGTFLRFSESSRE
TDFWKTLRYLSLLYP
AEPGEGTRPATVGDS
PLSPPQHRYSEGERT
GCFLFISRSKPLKTL
VFLHQKPRLPKLFKQ
HSYSVLERFVEECFQ
TNDLTAKRLLHVKGR
KSLKAKFRKSDTNEW
LNELEILRNSAVSQE
EWKFKLFRVRSFEKT
KASAAMVRLRLYDIL
EYNAVKEREHFNQYR
MVTMGFARDEINDAL
INIDQFVRKYRAALG
DISALTLRISELESQ
SCFKDGV RQPIESI
PWAKYVVREGDNVNY
LSFLDAYRNYAQHQR
SESEDEQRPRTRSAK
IGSDSQGRATAANNK
EPPGSSRESVSKAG
GPIFTTARQLVHALA
GQSPFQQRKKKIKRE
DALEEQQRCISELKA
YKTLHDTRTHFLKTK
HSSEHAGRNGRNAAD
AAIGATPRAKGKAKH
SKRKVLGRRDSDDDH
INKEAQKRWTRREQA
SFMSLQLRELVIKSL
EHKTMASRAKVMADW
VKQKELSRIEEALQK
QYSFNSQRFAELLST
SLHYALARKGGAGGT
AHTKPLNRRSVLEKN
SLDAANARLMSALTQ
SGLDIFERINTSAFE
AVDSPAGRQQLLQRG
LVFHSITRSHAENLE
AEYTVVARNKYGEDS
NAQILSQRIEKAKCL
EDKGEPKRRGYLQVN
YGQIESVFRSLIPA
ENQQCLREETWLAS
HQVESFIRKKLESLL
MKFKQKPREEQLEAD
ASAADTSRSLWGIQ

LPKVTLSRDGVPLKA
ETLGVLARAVGEMPR
EPRRLSSRRSVLTSP
SVVWLKDRGEVIRE
ILTLAWDRVDIAKNH
VYNENSNRQKLEHVK
FKIAGDMRATCPAFN
PSHGLADRVINCREV
AQQEELERRKRLEQQ
MEDKIYDRQVTKQSL
EEQPTSQRDRLSQVL
TNYVIELRDKTSIRW
QKKSATRTVSPGSV
EVLNEVNRRSLKCLA
QTAGVIDRWELLQAQ
RSKVDDLRTGTPMSVG
REGITTKREQVQITQ
EASTSALRESCQAEH
PANGFLVRYLRRKLV
NNTDEMARLIRSVMQ
ASERKLNRRGMSYL
YSASTPVRKPRPGQQ
EMDISADRVKVEGEL
WDLKLLRIPASRL
SLALKNIRCRRGIHK
ALQAALARVVPSYMQ
GMYSEPLRQFRDSSV
MDGAAWDRRNGKLME
GSYLQFLRILFRMLI
LKHFIGQREEFETAR
LVSKDLIRKAGVGSV
GFKSHLIRLIGNLCY
AHEDISQRVAENQD
EIEEDKARRILELSG
SMLQHLLRRLVFDVP
ISPPSPDRPPHSQTS
RSRGKEQRKLARQRS
EEAEAAARALARFAQ
TLTIQKARVTEKAVT
EFTQDLFRFLQLLCE
GAHKATLRIGQDGIS
ANLKMELRDALCAII
ENSLETLRFSISNLS
MFKWLVARINRALDA
HKFLTIPRLEELYNT
RYNERKGRSELIVVE
SVDVKSVRMGSIQRK
KGGSKLLRMKLSDFN
TGTPSDPRRRLRSYE
PEVFKYNRFLNPDGS
ESVKASERPLPPGKI
AYPICEWRYDACASP
PETIDTARLHYRNSW
RSALFALRYNILTLM
EPLKELFRQQEAVRG
GDEEQKLRFAFSIYD

YMLDNRKRKEVVHKI
RLDPVSGRLSTISSL
KPQDYIPRAPTFMLN
NSHHECIRKLLQSKC
TSSLSPQRSKLRIMS
QGLKIHQRFHFASAL
SSKPIKIRGPHCAG
HANNVTIRESMQNDV
PGHFVGPGRPHPSQF
GLDPTQFRVHHYHKD
PSTNTESRKDVITIS
IDAIGTKRYDSNSGG
AESNSNMRCTCRIIE
VEVAATERTLLGFFL
YDYVHSVRGKVAPTT
SRALSHDRQLISQDA
GLPNNAERVLLTTQG
FDFPDLNRFLTRTLQ
GGKPVQNRELQGYES
LSLQVVNREIREENK
KAFVTLERFDQLYGS
EAVKYSERSLTKCIG
FGKKAANRSWQNVYC
TLRMRSHRVPCGQNT
QVSETLKRFBAGKVT
EAVNVCGRATAVVEV
EKALRSMRKAQVSPQ
EKVLSPLRSPLIGS
LDLVSHPRATQTHVE
LISQINKRYKTKDDI
SSEKVAERKETEFFS
TAKPINPRPSLPPNS
EAKAELERKLSEKDE
ITKVGEERKGPLPKS
LVEETEERLVERISF
QIYSTGLRKGNLHNV
KHFPNIDREKAMSRP
SMSKGGKRKDSVWGS
WADPTGTRKLTWTYA
AQIADGFRIRVDLAS
LRDWNLIRDAATLIL
AEAADNQREEAADNQ
VYQIKVHRKYTGEDF
ARLETLVRKAGEQQE
DASPGDKRLAAYLML
LSSYATARLMMNNEY
KLPVDFERSFQEEKP
GPLPYPERQKRARSM
DSAKELQRSVEFDRE
TGTLVSKREVELEKN
GLFNKNPRHSSSENN
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