results for 7096 residue sequence made from 1 records, starting "MESLVPGFNE"

Covid gen: je dlouhý 7096 znaků

výsledky pro sekvenci zbytků 4883 "YP\_009724389.1 ORF1ab [organismus = těžký akutní respirační syndrom koronavirus 2] [GeneID = 43740578]" počínaje "MSVGNKTHVS"

Sekvence s počtem zastoupení:

1 MSVGNKTHVS VVRDVVRGGD SVVSARHKDG TCGVVKGVYV KRSDARTAHG HVMVVAGYGR SGTGVVHVGV AYRKVRKNGN

81 KGAGGHSYGA DKSDGDGTDY DNWNTKHSSG VTRMRNGGAY TRYVDNNCGD GYCKDARAGK ASCTSDDTKR GVYCCRHHAW

161 YTRSKSYTKA KKDTNGCNVN SKTRVKKKDG MGRRSVYVAS NCNMCSTMKC DHCGTSWTGD VKATCCGTNT KGATTCGYNA

241 VVKYCACHNS VGHSAYHNSG KTRKGGRTAG GCVSYVGCHN KCAYWVRASA NGCNHTGVVG GSGNDNKKVN NVGDKNAASS

321 ASTSAVTVKG DYKAKVSCGN KVTKGKAKKG AWNGKSSYAA SAARVVRSSR TTANSVRVKA ATDGSYSRDA MMTSDATNNV

401 VMAYTGGVVT SWTNGTVYKK VDWKKGVRDG WVKSTCACVG GVTCAKKSVT KVNKACADSG GAKKANGTVT HSKGYRKCVK

481 SRTGMKAKGT TVTVVKTGDT SAVAVGTVCN GMKDTKYCAA NMMVTNNTTK GGATKVTGDD TVVGYKSVNT DRDKVNKCSA

561 YTVGTVNACV VADAVKTVST GDDWSMATYY DSGKASHMYC SYDDGDCSTY YGTDDYGKGA TSAADWDDDS TVGDGSDNTT

641 TTVVMTVVTV NSSGYKTDNV YKNADVAKKV KTVVVNAANV YKHGGGVAGA NKATNNAMVS DDYATNGKVG GSCVSGHNAK

721 HCHVVGNVNK GDKSAYNNHV ASAGGADHSR VCVDTVRTNV YAVDKNYDKV SSMKSKVKAK VKTSKSVRKD DKKKACVVTT

801 TTKTNYDNGN HDSATVSDDT KKDAYVGDVV GVTAVVTKKA GGTTMAKARK VTDNYTTYGG NGYTVAKTVK KCKSAYSSNK

881 GTVSWNRMAH ATRKMVCVTK AVSTRKYKGK GVVDYGARYY TSKTTVASNT NDNTVTMGYV THGNAARYMR SKVATVSVSS

961 DAVTAYNGYT SSSKTHTSAG SYKDWSYSGS TGKRGDKSVY YTSNTTHDGV TDNKTSRVRT KVTTVDNNHT VVDMSMTYGG

1041 TYDGADVTKK HNSHGKTYVN DDTRVAYYHT TDSGRYMSAN HTKKWKYVNG TSKWADNNCY ATATKNADAY YRARAGAANC

1121 AAYCNKTVGG DVRTMSYHAN DSCKRVNVVC KTCGTTKGVA VMYMGTSYKK GVCTCGKATK YVSVMMSAAY KHGTTCASYT

1201 GNYCGHYKHT SKTYCDGATK SSYKGTDVYK NSYTTTKVTY KDGVVCTDKD NYYKKDNSYT DVNYNASDNK VCDNKADDNT

1281 GYKKASRKVT DNGDVVADYK HYTSKKGAKH KVWHVNNATN KATYKNTWCR CWSTKVTSNS DVKSDAGMDN ACDKVSVVNT

1361 KDVCNVKTTV VGDKANNSKT VGHTDMAAYV DNSSTKKNSR VGKTATHGAA VNSVWDTANY AKNKVVSTTT NVTRCNRVCT

1441 NYMYTCTTRS TNSRKASMTT AKNTVKSVGK CASNYKSNSK NWSVCGSYST AAGVMSNGMS YCTGYRGYNS TNVTATYCTG

1521 SCSVCSGDSD TYSTTSSKWD TAGVAWAYTR YVGAAMSYAV HSNSWMWNVM ASAMVRMYAS YYVWKSYVHV VDGCNSSTCM

1601 MCYKRNRATR VCTTVNGVRR SYVYANGGKG CKHNWNCVNC DTCAGSTSDV ARDSKRNTDS SYVDSVTVKN GSHYDKAGKT

1681 YRHSSHVNDN RANNTKGSNV VDGKSKCSSA KSASVYYSMC DAVSDVGDSA VAVKMDAYVN TSSTNVMKKT VATAAAKNVS

1761 DNVSTSAARG VDSDVTKDVV CKSHSDVTGD SCNNYMTYNK VNMTRDGACD CSARHNAVAK SHNAWNVKDM SSRKRSAAKK

1841 NNKTCATTRV VNVVTTKAKG GKVNNWKKVT VVAAYTVHVM SKHTDSSGYK ADGGVTRDAS TDTCANKHAD DTWSRGGSYT

1921 NDKACAAVTR VGVVGGTRTT NGDHRVSAVG NCYTSKYTDA TSACVAACTK DASGKVYCYD TNVGSVAYSR DTRYVMDGSN

2001 TYGSVRVVTT DSYCRHGTCR SAGVCVSTSG RWVNNDYYRS GVCGVDAVNT NMTGADSASV AGGVAVVTCA YYMRRRAGYS

2081 HVVANTMSTV CTVYSGVYSV YYTYTNDVSA HWMVMTVWTA YCSTKHYWSN YKRRVVNGVS STAACTNKMY KRSDVTYNRY

2161 AYNKYKYSGA MDTTSYRAAC CHAKANDSNS GSDVYTSTSA VSGRKMASGK VGCMVVTCGT TTNGWDDVVY CRHVCTSDMN

2241 NYDRKSNHNV AGNVRVGHSM NCVKKVDTAN KTKYKVRGTS VACYNGSSGV YCAMRNTKGS NGSCGSVGND YDCVSCYMHH

2321 MTGVHAGTDG NYGVDRTAAA GTDTTTVNVA WYAAVNGDRW NRTTTNDNVA MKYNYTDHVD GSATGAVDMC ASKNGMNGRT

2401 GSADTDVVRC SGVTSAVKRT KGTHHWTTSV VSTWSYNAAM GAMSAAMMVK HKHACSATVA YNMVYMASWV MRMTWDMVDT

2481 SSGKKDCVMY ASAVVMTART VYDDGARRVW TMNVTVYKVY YGNADASMWA SVTSNYSGVV TTVMARGVMC VYCTGNTCMV

2561 YCGYCTCYGC NRYRTGVYDY VSTRYMNSGK NSDAKNKGVG GKCKVATVSK MSDVKCTSVV SVRVSSSKWA CVHNDAKDTT

2641 AKMVSSVSMG AVDNKCMDNR ATAASSSSYA AATAAYAVAN GDSVVKKKKS NVAKSDRDAA MRKKMADAMT MYKARSDKRA

2721 KVTSAMTMTM RKDNDANNNN ARDGCVNTTA AKMVVDYNTY KNTCDGTTTY ASAWVVDADS KVSSMDNSNA WVTARANSAV

2801 KNNSVARMSC AAGTTTACTD DNAAYYNTTK GGRVASDDKW ARKSDGTGTY TCRVTDTKGK VKYYKGNNNR GMVGSAATVR

2881 AGNATVANST VSCAAVDAAK AYKDYASGGT NCVKMCTHTG TGATVTANMD SGGASCCYCR CHDHNKGCDK GKYVTTCAND

2961 VGTKNTVCTV CGMWKGYGCS CDRMSADASN RVCGVSAART CGTGTSTDVV YRADYNDKVA GAKKTNCCRK DDDNDSYVVK

3041 RHTSNYHTYN KDCAVAKHDK RDGDMVHSRR TKYTMADVYA RHDGNCDTKV TYNCCDDDYN KKDWYDVNDR VYANGRVRAK

3121 TVCDAMRNAG VGVTDNDNGN WYDGDTTGSG VVVDSYYSMT TRATASHVDT DTKYKWDKYD TRKDRYKYWD TYHNCVNCDD

3201 RCHCANNVST VTSGVRKVDG VVVSTGYHRG VVHNDVNHSS RSKVYAADAM HAASGNDKRT TCSVAATNNV ATVKGNNKDY

3281 DAVSKGKGSS VKHADGNAAS DYDYYRYNTM CDRVVVVDKY DCYDGGCNAN VVNNDKSAGN KWGKARYYDS MSYDDAAYTK

3361 RNVTTMNKYA SAKNRARTVA GVSCSTMTNR HKKSAATRGA TVVGTSKYGG WHNMKTVYSD VNHMGWDYKC DRAMNMRMAS

3441 VARKHTTCCS SHRYRANCAV SMVMCGGSYV KGGTSSGDAT TAYANSVNCA VTANVNASTD GNKADKYVRN HRYCYRNRDV

3521 DTDVNYAYRK HSMMSDDAVV CNSTYASGVA SKNKSVYYNN VMSAKCWTTD TKGHCSHTMV KGDDYVYYDS RGAGCVDDVK

3601 TDGTMRVSAD AYTKHNYADV HYYRKHDTGH MDMYSVMTND NTSRYWYAMY THTVAVGACV CNSTSRCGAC RRCCKCCYDH

3681 VSTSHKVSVN YVCNAGCDVT DVTYGGMSYY CKSHKSCANG VGYKNTCVGS DNVTDNAATC DWTNAGDYAN TCTRKAATKA

3761 TTKSYGATVR VSDRHSWVGK RNRNYVTGYR VTKNSKVGYT KGDYGDAVVY RGTTTYKNVG DYVTSHTVMS ATVHYVRTGY

3841 TNSDSSNVAN YKVGMKYSTG GTGKSHAGAY YSARVYTACS HAAVDACKAK YDKCSRARAR VCDKKVNSTY VCTVNATTAD

3921 VVDSMATNYD SVVNARRAKH YVYGDAARTT KGTYNSVCRM KTGDMGTCRR CAVDTVSAVY DNKKAHKDKS ACKMYKGVTH

4001 DVSSANRGVV RTRNAWRKAV SYNSNAVASK GTTVDSSGSY DYVTTTTAHS CNVNRNVATR AKVGCMSDRD YDKTSRRNVA

4081 TANVTGKDCS KVTGHTATHS VDTKKTGCVD GKDMTYRRSM MGKMNYVNGY NMTRARHVRA WGDVGCHATR AVGTNGSTGV

4161 NVAVTGYVDT NNTDSRVSAK GDKHMYKGWN VVRKVMSDTK NSDRVVVWAH GTSMKYVKGR TCCCDRRATC STASDTYACW

4241 HHSGDYVYNM DVWGTGNSNH DYCVHGNAHV ASCDAMTRCA VHCVKRVDWT YGDKNAACRK VHMVVKAAAD KVHDGNKAKC

4321 VADVWKYDAC SDKAYKYSYA THSDKTDGVC WNCNVDRYAN SVCRDTRVSN NGCDGGSYVN KHAHTADKSA VNKYYSDSCS

4401 HGKVVSDDYV KSATCTRCNG GAVCRHHANY RYDAYNMMSA GSWVYKDTYN WNTTRSNVAN VVNKGHDGGV VSNNTVYTKV

4481 DGVDVNKTTV NVAWAKRNKV VKNNGVDAAN TVWDYKRDAA HSTGVCSMTD AKKTTCATVD GRVDGVDRNA RNGVTGSVKG

4561 SVGKASNGVT GAVKTNYYKK VDGVVTYTSR NKRSMDAMDR YKGYAHVYGD SHSGGHGAKR KSDMDSTVKN YTDATGSSKC

4641 VCSVDDDVKS DSVVSKVVKV TDYTSMWCKD GHVTYKSSAW GVAMNYKMRM KCDNYGDSAT KGMMNVAKYT CYNTTAVYNM

4721 RVHGAGSDKG VAGTAVRWTG TVDSDNDVSD ADSTGDCATV HTANKWDSDM YDKTKNVTKN DSKGTYCGKA GGSVAKTHSW

4801 NADYKMGHAW WTAVTNVNAS SSAGCNYGKR DGYVMHANYW RNTNSSYSDM SKKRGTAVMS KGNDMSSKGR RNNRVVSSDV

4881 VNN

Nějaký triplety:

**tcg, 31 to 33 (Ser)**

XXXXXXXXXXXXXXX 0.15

**gag, 82 to 84 (Glu)**

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 0.32

**atc, 223 to 225 (Ile)**

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 0.41

**cgt, 226 to 228 (Arg)**

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 0.37

**ntk, 229 to 231 (???)**

0.00

**gat, 232 to 234 (Asp)**

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 0.63

**cac, 436 to 438 (His)**

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 0.43

**gga, 460 to 462 (Gly)**

XXXXXXXXXXXX 0.12

**gat, 532 to 534 (Asp)**

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 0.63

A mnoho dalších

Počet zastoupených genu se zastoupení a procentu lení zastoupené:

|  |  |  |
| --- | --- | --- |
| **Pattern:** | **Times found:** | **Percentage:** |
| g | 412 | 8.44 |
| a | 487 | 9.97 |
| t | 527 | 10.79 |
| c | 226 | 4.63 |
| n | 384 | 7.86 |
| u | 0 | 0.00 |
| r | 244 | 5.00 |
| y | 335 | 6.86 |
| s | 456 | 9.34 |
| w | 78 | 1.60 |
| k | 434 | 8.89 |
| m | 168 | 3.44 |
| b | 0 | 0.00 |
| d | 389 | 7.97 |
| h | 145 | 2.97 |
| v | 598 | 12.25 |
| gg | 39 | 0.80 |
| ga | 37 | 0.76 |
| gt | 50 | 1.02 |
| gc | 19 | 0.39 |
| gn | 28 | 0.57 |
| ag | 35 | 0.72 |
| aa | 56 | 1.15 |
| at | 56 | 1.15 |
| ac | 24 | 0.49 |
| an | 40 | 0.82 |
| tg | 44 | 0.90 |
| ta | 40 | 0.82 |
| tt | 68 | 1.39 |
| tc | 33 | 0.68 |
| tn | 37 | 0.76 |
| cg | 20 | 0.41 |
| ca | 28 | 0.57 |
| ct | 21 | 0.43 |
| cc | 11 | 0.23 |
| cn | 18 | 0.37 |
| ng | 37 | 0.76 |
| na | 36 | 0.74 |
| nt | 35 | 0.72 |
| nc | 17 | 0.35 |
| nn | 33 | 0.68 |
| g,c | 638 | 13.07 |
| a,t | 1014 | 20.77 |
| r,y,s,w,k | 1547 | 31.68 |
| b,h,d,v,n | 1516 | 31.05 |
| r,y,s,w,k,m,b,d,h,v,n | 3231 | 66.17 |

Bráno z:

>YP\_009724389.1 ORF1ab [organism=Severe acute respiratory syndrome coronavirus 2] [GeneID=43740578]

MESLVPGFNEKTHVQLSLPVLQVRDVLVRGFGDSVEEVLSEARQHLKDGTCGLVEVEKGVLPQLEQPYVF

IKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPHVGEIPVAYRKVLLRKNGNKGAGGHSYGADL

KSFDLGDELGTDPYEDFQENWNTKHSSGVTRELMRELNGGAYTRYVDNNFCGPDGYPLECIKDLLARAGK

ASCTLSEQLDFIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVFPLNSI

IKTIQPRVEKKKLDGFMGRIRSVYPVASPNECNQMCLSTLMKCDHCGETSWQTGDFVKATCEFCGTENLT

KEGATTCGYLPQNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTILRKGGRTIAFGGCVFSYVGCHNKC

AYWVPRASANIGCNHTGVVGEGSEGLNDNLLEILQKEKVNINIVGDFKLNEEIAIILASFSASTSAFVET

VKGLDYKAFKQIVESCGNFKVTKGKAKKGAWNIGEQKSILSPLYAFASEAARVVRSIFSRTLETAQNSVR

VLQKAAITILDGISQYSLRLIDAMMFTSDLATNNLVVMAYITGGVVQLTSQWLTNIFGTVYEKLKPVLDW

LEEKFKEGVEFLRDGWEIVKFISTCACEIVGGQIVTCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKL

KALNLGETFVTHSKGLYRKCVKSREETGLLMPLKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT

SEAVEAPLVGTPVCINGLMLLEIKDTEKYCALAPNMMVTNNTFTLKGGAPTKVTFGDDTVIEVQGYKSVN

ITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVIKTLQPVSELLTPLGIDLDEWSMATYYLFDE

SGEFKLASHMYCSFYPPDEDEEEGDCEEEEFEPSTQYEYGTEDDYQGKPLEFGATSAALQPEEEQEEDWL

DDDSQQTVGQQDGSEDNQTTTIQTIVEVQPQLEMELTPVVQTIEVNSFSGYLKLTDNVYIKNADIVEEAK

KVKPTVVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVGGSCVLSGHNLAKHCLHVVGP

NVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSLRVCVDTVRTNVYLAVFDKNLYDKLVSSF

LEMKSEKQVEQKIAEIPKEEVKPFITESKPSVEQRKQDDKKIKACVEEVTTTLEETKFLTENLLLYIDIN

GNLHPDSATLVSDIDITFLKKDAPYIVGDVVQEGVLTAVVIPTKKAGGTTEMLAKALRKVPTDNYITTYP

GQGLNGYTVEEAKTVLKKCKSAFYILPSIISNEKQEILGTVSWNLREMLAHAEETRKLMPVCVETKAIVS

TIQRKYKGIKIQEGVVDYGARFYFYTSKTTVASLINTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLK

VPATVSVSSPDAVTAYNGYLTSSSKTPEEHFIETISLAGSYKDWSYSGQSTQLGIEFLKRGDKSVYYTSN

PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVDNINLHTQVVDMSMTYGQQFGPTYLDGADVTKIKPH

NSHEGKTFYVLPNDDTLRVEAFEYYHTTDPSFLGRYMSALNHTKKWKYPQVNGLTSIKWADNNCYLATAL

LTLQQIELKFNPPALQDAYYRARAGEAANFCALILAYCNKTVGELGDVRETMSYLFQHANLDSCKRVLNV

VCKTCGQQQTTLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQESPFVMMSAPPAQYELKHGT

FTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYKGPITDVFYKENSYTTTIKPVTYKLDGVVCT

EIDPKLDNYYKKDNSYFTEQPIDLVPNQPYPNASFDNFKFVCDNIKFADDLNQLTGYKKPASRELKVTFF

PDLNGDVVAIDYKHYTPSFKKGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKS

EDAQGMDNLACEDLKPVSEEVVENPTIQKDVLECNVKTTEVVGDIILKPANNSLKITEEVGHTDLMAAYV

DNSSLTIKKPNELSRVLGLKTLATHGLAAVNSVPWDTIANYAKPFLNKVVSTTTNIVTRCLNRVCTNYMP

YFFTLLLQLCTFTRSTNSRIKASMPTTIAKNTVKSVGKFCLEASFNYLKSPNFSKLINIIIWFLLLSVCL

GSLIYSTAALGVLMSNLGMPSYCTGYREGYLNSTNVTIATYCTGSIPCSVCLSGLDSLDTYPSLETIQIT

ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIINLVQMAPISAM

VRMYIFFASFYYVWKSYVHVVDGCNSSTCMMCYKRNRATRVECTTIVNGVRRSFYVYANGGKGFCKLHNW

NCVNCDTFCAGSTFISDEVARDLSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSH

FVNLDNLRANNTKGSLPINVIVFDGKSKCEESSAKSASVYYSQLMCQPILLLDQALVSDVGDSAEVAVKM

FDAYVNTFSSTFNVPMEKLKTLVATAEAELAKNVSLDNVLSTFISAARQGFVDSDVETKDVVECLKLSHQ

SDIEVTGDSCNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIR

SAAKKNNLPFKLTCATTRQVVNVVTTKIALKGGKIVNNWLKQLIKVTLVFLFVAAIFYLITPVHVMSKHT

DFSSEIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITREVGFVVPGLP

GTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEYTDFATSACVLAAECTIFKDASGKPVPYCYDTNVLE

GSVAYESLRPDTRYVLMDGSIIQFPNTYLEGSVRVVTTFDSEYCRHGTCERSEAGVCVSTSGRWVLNNDY

YRSLPGVFCGVDAVNLLTNMFTPLIQPIGALDISASIVAGGIVAIVVTCLAYYFMRFRRAFGEYSHVVAF

NTLLFLMSFTVLCLTPVYSFLPGVYSVIYLYLTFYLTNDVSFLAHIQWMVMFTPLVPFWITIAYIICIST

KHFYWFFSNYLKRRVVFNGVSFSTFEEAALCTFLLNKEMYLKLRSDVLLPLTQYNRYLALYNKYKYFSGA

MDTTSYREAACCHLAKALNDFSNSGSDVLYQPPQTSITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTTL

NGLWLDDVVYCPRHVICTSEDMLNPNYEDLLIRKSNHNFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPK

TPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGSVGFNIDYDCVSFCYMHHMEL

PTGVHAGTDLEGNFYGPFVDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFTTTLNDFNLVAMKY

NYEPLTQDHVDILGPLSAQTGIAVLDMCASLKELLQNGMNGRTILGSALLEDEFTPFDVVRQCSGVTFQS

AVKRTIKGTHHWLLLTILTSLLVLVQSTQWSLFFFLYENAFLPFAMGIIAMSAFAMMFVKHKHAFLCLFL

LPSLATVAYFNMVYMPASWVMRIMTWLDMVDTSLSGFKLKDCVMYASAVVLLILMTARTVYDDGARRVWT

LMNVLTLVYKVYYGNALDQAISMWALIISVTSNYSGVVTTVMFLARGIVFMCVEYCPIFFITGNTLQCIM

LVYCFLGYFCTCYFGLFCLLNRYFRLTLGVYDYLVSTQEFRYMNSQGLLPPKNSIDAFKLNIKLLGVGGK

PCIKVATVQSKMSDVKCTSVVLLSVLQQLRVESSSKLWAQCVQLHNDILLAKDTTEAFEKMVSLLSVLLS

MQGAVDINKLCEEMLDNRATLQAIASEFSSLPSYAAFATAQEAYEQAVANGDSEVVLKKLKKSLNVAKSE

FDRDAAMQRKLEKMADQAMTQMYKQARSEDKRAKVTSAMQTMLFTMLRKLDNDALNNIINNARDGCVPLN

IIPLTTAAKLMVVIPDYNTYKNTCDGTTFTYASALWEIQQVVDADSKIVQLSEISMDNSPNLAWPLIVTA

LRANSAVKLQNNELSPVALRQMSCAAGTTQTACTDDNALAYYNTTKGGRFVLALLSDLQDLKWARFPKSD

GTGTIYTELEPPCRFVTDTPKGPKVKYLYFIKGLNNLNRGMVLGSLAATVRLQAGNATEVPANSTVLSFC

AFAVDAAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQESFGGASCCLYCRCHIDHPNPK

GFCDLKGKYVQIPTTCANDPVGFTLKNTVCTVCGMWKGYGCSCDQLREPMLQSADAQSFLNRVCGVSAAR

LTPCGTGTSTDVVYRAFDIYNDKVAGFAKFLKTNCCRFQEKDEDDNLIDSYFVVKRHTFSNYQHEETIYN

LLKDCPAVAKHDFFKFRIDGDMVPHISRQRLTKYTMADLVYALRHFDEGNCDTLKEILVTYNCCDDDYFN

KKDWYDFVENPDILRVYANLGERVRQALLKTVQFCDAMRNAGIVGVLTLDNQDLNGNWYDFGDFIQTTPG

SGVPVVDSYYSLLMPILTLTRALTAESHVDTDLTKPYIKWDLLKYDFTEERLKLFDRYFKYWDQTYHPNC

VNCLDDRCILHCANFNVLFSTVFPPTSFGPLVRKIFVDGVPFVVSTGYHFRELGVVHNQDVNLHSSRLSF

KELLVYAADPAMHAASGNLLLDKRTTCFSVAALTNNVAFQTVKPGNFNKDFYDFAVSKGFFKEGSSVELK

HFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNK

WGKARLYYDSMSYEDQDALFAYTKRNVIPTITQMNLKYAISAKNRARTVAGVSICSTMTNRQFHQKLLKS

IAATRGATVVIGTSKFYGGWHNMLKTVYSDVENPHLMGWDYPKCDRAMPNMLRIMASLVLARKHTTCCSL

SHRFYRLANECAQVLSEMVMCGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGNKIADK

YVRNLQHRLYECLYRNRDVDTDFVNEFYAYLRKHFSMMILSDDAVVCFNSTYASQGLVASIKNFKSVLYY

QNNVFMSEAKCWTETDLTKGPHEFCSQHTMLVKQGDDYVYLPYPDPSRILGAGCFVDDIVKTDGTLMIER

FVSLAIDAYPLTKHPNQEYADVFHLYLQYIRKLHDELTGHMLDMYSVMLTNDNTSRYWEPEFYEAMYTPH

TVLQAVGACVLCNSQTSLRCGACIRRPFLCCKCCYDHVISTSHKLVLSVNPYVCNAPGCDVTDVTQLYLG

GMSYYCKSHKPPISFPLCANGQVFGLYKNTCVGSDNVTDFNAIATCDWTNAGDYILANTCTERLKLFAAE

TLKATEETFKLSYGIATVREVLSDRELHLSWEVGKPRPPLNRNYVFTGYRVTKNSKVQIGEYTFEKGDYG

DAVVYRGTTTYKLNVGDYFVLTSHTVMPLSAPTLVPQEHYVRITGLYPTLNISDEFSSNVANYQKVGMQK

YSTLQGPPGTGKSHFAIGLALYYPSARIVYTACSHAAVDALCEKALKYLPIDKCSRIIPARARVECFDKF

KVNSTLEQYVFCTVNALPETTADIVVFDEISMATNYDLSVVNARLRAKHYVYIGDPAQLPAPRTLLTKGT

LEPEYFNSVCRLMKTIGPDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYKGVITHDVSS

AINRPQIGVVREFLTRNPAWRKAVFISPYNSQNAVASKILGLPTQTVDSSQGSEYDYVIFTQTTETAHSC

NVNRFNVAITRAKVGILCIMSDRDLYDKLQFTSLEIPRRNVATLQAENVTGLFKDCSKVITGLHPTQAPT

HLSVDTKFKTEGLCVDIPGIPKDMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCH

ATREAVGTNLPLQLGFSTGVNLVAVPTGYVDTPNNTDFSRVSAKPPPGDQFKHLIPLMYKGLPWNVVRIK

IVQMLSDTLKNLSDRVVFVLWAHGFELTSMKYFVKIGPERTCCLCDRRATCFSTASDTYACWHHSIGFDY

VYNPFMIDVQQWGFTGNLQSNHDLYCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWTIEYPIIGDELKI

NAACRKVQHMVVKAALLADKFPVLHDIGNPKAIKCVPQADVEWKFYDAQPCSDKAYKIEELFYSYATHSD

KFTDGVCLFWNCNVDRYPANSIVCRFDTRVLSNLNLPGCDGGSLYVNKHAFHTPAFDKSAFVNLKQLPFF

YYSDSPCESHGKQVVSDIDYVPLKSATCITRCNLGGAVCRHHANEYRLYLDAYNMMISAGFSLWVYKQFD

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AKRNIKPVPEVKILNNLGVDIAANTVIWDYKRDAPAHISTIGVCSMTDIAKKPTETICAPLTVFFDGRVD

GQVDLFRNARNGVLITEGSVKGLQPSVGPKQASLNGVTLIGEAVKTQFNYYKKVDGVVQQLPETYFTQSR

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DPKTKNVTKENDSKEGFFTYICGFIQQKLALGGSVAIKITEHSWNADLYKLMGHFAWWTAFVTNVNASSS

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SLLSKGRLIIRENNRVVISSDVLVNN