

GRAS family transcription factor family protein [Arabidopsis thaliana]

NCBI Reference Sequence: NP_178266.1

[GenPept](#) [Identical Proteins](#) [Graphics](#)

>NP_178266.1 GRAS family transcription factor family protein [Arabidopsis thaliana]

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MKRDHHQFQGRLSNHGTSSSSSSSISKDKMMVMKKEEDGGGNMDELLAVLGKVRSEMAEVALKLEQLE
TMMSNVQEDGLSHLATDTVHYNPSELYSWLDNMLSELNPPPLPASSNGLDPVLPSPEICGFPASDYDLKV
IPGNAIYQFPAIDSSSSSSNNQNKRLKSCSSPDSMVTSTSTGTQIGGVIGTTVTTTTTTTTTAAGESTRSVI
LVDSQENGVRVLVHALMACAEAIQQNNLTAEALVKQIGCLAVSQAGAMRKVATYFAEALARRIYRLSPPQ
NQIDHCLSDTLQMHFYETCPYLKFAHFTANQAILEAFEGKKRVHVIDFSMNQGLQWPALMQALALREGGP
PTFRLTGIGPPAPDNSDHLHEVGCKLAQLAEAIHVEFEYRGFVANSLADLDASMLELRPSDTEAVAVNSV
FELHKLLGRPGGIEKVLGVVKQIKPVIFTVVEQESNHNGPVFLDRFTESLHYYSTLFDSLEGVPNSQDKV
MSEVYLKGQICNLVACEGPD RVERHETLSQWGNRFGSSGLAPAHLGSAFKQASMLLSVFNSGQGYRVEE
SNGCLMLGWHTRPLITTS AWKLSTAAY
```

221-581 Motif Domain

<https://www.ebi.ac.uk/interpro/result/InterProScan/iprscan5-R20221027-080812-0001-93212281-p1m/>

Sequence							
> Sequence title 46							
0	MKRDHHQFQG	RLSNHGTSSS	SSSISKDKMM	MVKKEEDGGG	NMDELLAVL	GYKVRSEMA	EVALKLEQLE
70	TMMSNVQEDG	LSHLATDTVH	YNPSELYSWL	DNMLSELNPP	PLPASSNGLD	PVLPSPEICG	FPASDYDLKV
140	IPGNAIYQFP	AIDSSSSSNN	QNKRLKSCSS	PDSMVTSTST	GTQIGGVIGT	TVTTTTTTTT	AAGESTRSVI
210	LVDSQENGVR	LVHALMACAE	AIQQNNLTAE	EALVKQIGCL	AVSQAGAMRK	VATYFAEALA	RIYRLSPPQ
280	NQIDHCLSDT	LQMHFYETCP	YLKFAHFTAN	QAILEAFEGK	KRVHVIDFSM	NQGLQWPALM	QALALREGGP
350	PTFRLTGIGP	PAPDNSDHLH	EVGCKLAQLA	EAIHVEFEYR	GFVANSLADL	DASMLELRPS	DTEAVAVNSV
420	FELHKLLGRP	GGIEKVLGVV	KQIKPVIFTV	VEQESNHNGP	VFLDRFTESL	HYYSTLFDSL	EGVPNSQDKV
490	MSEVYLKGQI	CNLVACEGPD	RVERHETLSQ	WGNRFGSSGL	APAHLGSAFK	KQASMLLSVF	NSGQGYRVEE
560	SNGCLMLGWH	TRPLITTS AW	KLSTAAY				

GRAS Protein 221-581

LVHALMACAEAIQQNNLTAEALVKQIGCLAVSQAGAMRKVATYFAEALARRIYRLSPPQNQIDHCLSDTLQMHFYET
CPYLKFAHFTANQAILEAFEGKKRVHVIDFSMNQGLQWPALMQALALREGGPPTFRLTGIGPPAPDNSDHLHEVGCKL
AQLAEAIHVEFEYRGFVANSLADLDASMLELRPSDTEAVAVNSVFELHKLLGRPGGIEKVLGVVKQIKPVIFTVVEQESN
HNGPVFLDRFTESLHYYSTLFDSLEGVPNSQDKVMSEVYLKGQICNLVACEGPD RVERHETLSQWGNRFGSSGLAPAH
LGSAFKQASMLLSVFNSGQGYRVEESNGCLMLGWHTRPLITTS AWK

Description	Max score	Total score	Query cover	E value	Ident
chr10	564	564	100%	1e-179	75%
chr11	374	906	100%	5e-114	53%
chr03	369	562	100%	6e-112	53%
chr04	224	470	100%	4e-62	35%
chr01	221	969	100%	5e-61	40%
chr08	219	1723	100%	2e-60	53%
chr02	198	1125	100%	3e-53	35%
chr06	192	845	100%	3e-51	36%
chr05	175	822	100%	1e-48	48%
chr07	168	649	100%	6e-43	31%

1. AtPAT1 (119-490)

>AED95624.1 GRAS family transcription factor [Arabidopsis thaliana]
MYKQPRQELEYFEPNSVEKLRYPVNNSRKRFTLEFPDSPYPNALSTATYDDTCGSCVTDELNDFK
HKIREIETVMMGPDSLDDLVDCTDSFDSTASQEINGWRSTLEAISRRDLRADLVSCAKAMSENDLMMHS
MMEKLRQMVSVSGEPIQRLGAYLLEGLVAQLASSGSSIIKALNRCPEPASTELLSYMHILYEVCPYFKFG
YMSANGAIAEAMKEENRVHIIDFQIGQGSQWVTLIQAFARPGGPPRIRITGIDDMTSAYARGGGLSIVG
NRLAKLAKQFNVPFEFNSVSVSVSEVKPKNLGVRPGEALAVNFAFVLHHMPDESSTENHRDRLLRMVKS
LSPKVVTLVEQESNTNTAAFFPRFMETMNYAAMFESIDVTLPRDHKQRINVEQHCLARDVUNI IACEGA
DRVERHELLGKWRSRFGMAGFTPYPLSPLVNSTIKSLLRNYSDKYRLEERDGLYLGMHMRDLVASCWK

QEINGWRSTLEAISRRDLRADLVSCAKAMSENDLMMHSMMEKLRQMVSVSGEPIQRLGAYLLEGLVAQLASSGSSII
YKALNRCPEPASTELLSYMHILYEVCPYFKFGYMSANGAIAEAMKEENRVHIIDFQIGQGSQWVTLIQAFARPGGP
PRIRITGIDDMTSAYARGGGLSIVGNRLAKLAKQFNVPFEFNSVSVSVSEVKPKNLGVRPGEALAVNFAFVLHHMPD
ESSTENHRDRLLRMVKSLSPKVVTLVEQESNTNTAAFFPRFMETMNYAAMFESIDVTLPRDHKQRINVEQHCLAR
DVUNI IACEGADRVERHELLGKWRSRFGMAGFTPYPLSPLVNSTIKSLLRNYSDKYRLEERDGLYLGMHMRDLVA

AtGRAS (221-581)

MKRDHHQFQGRLSNHGTSSSSSSISKDKMMMVKKEEDGGGNMDELAVLGYKVRSSSEMAEVALKLEQLE
TMMSNVQEDGLSHLATDTVHYNPSELYSWLDNMLSELNPPPLPASSNGLDPVLPSPICGFPASDYDLKV
IPGNAIYQFPAIDSSSSSNQNKRLKSCSSPDMSMTSTSTGTQIGGVIGTTVT'TTTTTTTTAAGESTRSVI
LVDSQENGVRVLVHALMACAEAIQQNNLTAEALVKQIGCLAVSQAGAMRKVATYFAEALARRIYRLSPQP
NQIDHCLSDTLQMHFYETCPYLKFAHFTANQAILEAFEGKKRVHVIDFSMNQGLQWPALMQALALREGGP
PTFRLTGIGPPAPDNSDHLHEVGCKLAQLAEAIHVEFEYRGFVANSLADLDASMLELRPSDTEAVAVNSV
FELHKLLGRPGGIEKVLGVVKQIKPVIFTVVEQESNHNGPVFLDRFTESLHYYSTLFDSLEGVPNSQDKV
MSEVYLKGQICNLVACEGPDRVERHETLSQWGNRFGSSGLAPAHLGSNFAFKQASMLLSVFNSGQGYRVEE
SNGCLMLGWHTRPLITTSWKLSTAAAY

AtGRAS (221-581)

LVHALMACAEAIQQNNLTAEALVKQIGCLAVSQAGAMRKVATYFAEALARRIYRLSPQPQNQIDHCLSDTLQMHFYE
TCPYLKFAHFTANQAILEAFEGKKRVHVIDFSMNQGLQWPALMQALALREGGPPTFRLTGIGPPAPDNSDHLHEVGC
KLAQLAEAIHVEFEYRGFVANSLADLDASMLELRPSDTEAVAVNSVFELHKLLGRPGGIEKVLGVVKQIKPVIFTV
VEQESNHNGPVFLDRFTESLHYYSTLFDSLEGVPNSQDKVMSEVYLKGQICNLVACEGPDRVERHETLSQWGNRFGSS
GLAPAHLGSNFAFKQASMLLSVFNSGQGYRVEESNGCLMLGWHTRPLITTSWKL

AtLAS

MLTSFKSSSSSE DATATTTENPPPLCIASSSAATSASHHLRRLLF TAANFVSQSNFTAAQNLLSILSLN
SSPHGDSTERLVHLFTKALSVRINRQQDQTAETVATWTTNEMTMSNSTVFTSSVCKEQFLFRTKNNSD
FESCYYLWLNQLTPFIRFGHLTANQAILDATETNDNGALHILDLDISQGLQWPPLMQALAERSSNPSSPP
PSLRITGCGRDVTGLNRTGDRLTRFADSLGLQFQFHTLVIVEEDLAGLLLQIRLLALSAVQGETIAVNCV
HFLHKIFNDDGDMIGHFLSAIKSLNSRIVTMAEREANHGDSFLNRFSEAVDHYMAIFDSLEATLPPNSR
ERLTLEQRWFGKEILDVVAEEETERKQRHRRFEIWEEMMKRFGFVNVPISFALSQAKLLLRHYPSEGY
NLQFLNNSLFLGWQNRPLFSVSSWK

>AtLAS Pfam Domain

SSAATSASHHLRRLLF TAANFVSQSNFTAAQNLLSILSLNSSPHGDSTERLVHLFTKALSVRINRQQDQTAETVAT
WTTNEMTMSNSTVFTSSVCKEQFLFRTKNNSDFESCYYLWLNQLTPFIRFGHLTANQAILDATETNDNGALHILD
DISQGLQWPPLMQALAERSSNPSSPPPSLRITGCGRDVTGLNRTGDRLTRFADSLGLQFQFHTLVIVEEDLAGLLLQ
IRLLALSAVQGETIAVNCVHFLHKIFNDDGDMIGHFLSAIKSLNSRIVTMAEREANHGDSFLNRFSEAVDHYMAIF
DSLEATLPPNSRERLTLEQRWFGKEILDVVAEEETERKQRHRRFEIWEEMMKRFGFVNVPISFALSQAKLLLRHYP
SEGYNLQFLNNSLFLGWQNRPLFSVSSWK

AtSCL

>CAB10504.1 SCARECROW like protein [Arabidopsis thaliana]

MEATVKIFYYGTVGKSKIRELEVSLLSGDTKVEEFSGFSPAAGKSWNWDELLALTPQLDLKEVLVEAARA
VADGDFATAYGFLDVLEQMVSVSGSPIQRLGTYMAEGLRARLEGSGSNIYKSLKCNEPTGRELSYMSVL
YEICPYWKFAYYTANVEILEAIAGETRVHIIDFQIAQGSQYMFLIQELAKHPGGPPLLRVTGVDDSQSTY
ARGGGLSLVGERLATLAQSCGVPPFEFHDAIMSGCKVQREHLGLEPGFAVVVNFYVLHHPDESVSVENH
RDRLHLIKSLSPKLVTLVEQESNTNTSPFLSRFVETLDYYTAMFESIDAARPRDDKQRISAEQHCVAR
DIVNMIACEESERVERHEVLGNNGSE

Pfam >AtSCL

LKEVLVEAARAVADGDFATAYGFLDVLEQMVSVSGSPIQRLGTYMAEGLRARLEGSGSNIYKSLKCNEPTGRELSY
MSVLYEICPYWKFAYYTANVEILEAIAGETRVHIIDFQIAQGSQYMFLIQELAKHPGGPPLLRVTGVDDSQSTYARG
GGLSLVGERLATLAQSCGVPPFEFHDAIMSGCKVQREHLGLEPGFAVVVNFYVLHHPDESVSVENH
RDRLHLIKSLSPKLVTLVEQESNTNTSPFLSRFVETLDYYTAMFESIDAARPRDDKQRISAEQHCVAR
DIVNMIACEESERVERHEVL

AtSHR (Short Root Like Protein)

>NP_195480.1 GRAS family transcription factor [Arabidopsis thaliana]

MDTLFRLVSLQQQQSDSIITNQSSLRTSTTTTGSPQTAYHYNFPQNDVVEECFNFFMDEEDLSSSSSH
HNHHNNNPNTYYSPFTTPTQYHPATSSPTPSSTAAAAALASPYSSSGHHNDPSAFSIPQTTPPSDFDSANA
KWADSVLLEAARAFSDKDTARAQQILWTLNELSSPYGDTEQKLASYFLQALFNRMTGSGERCYRTMVTAA
ATEKTCSFESTRKTVLKFQEVSPWATFGHVAANGAILEAVDGEAKIHIVDISSTFCTQWPTLLEALATRS
DDTPHLRLTTVVVANKFVNDQTASHRMMKEIGNRMEKFARLMGVPPFKFNI IHHVGDLSFEDLNELDVKPD
EVLAINCVGAMHGIIASRGSPRAVISSFRRLRPRIVTVEEEADLVGEEEGGFDEFLLRFGFGECLRWFRV
CFESWEESFPRTSNERLMLERAAGRAIVDLVACEPSDSTERRETARKWSRRMRNSGFGAVGYSDEVADDV
RALLRRYKEGVWSMVQCPDAAGIFLCWRDQPVVWASAWRPT

SVLLEAARAFSDKDTARAQQILWTLNELSSPYGDTEQKLASYFLQALFNRMTGSGERCYRTMVTAA
ATEKTCSFESTRKTVLKFQEVSPWATFGHVAANGAILEAVDGEAKIHIVDISSTFCTQWPTLLEALATRS
DDTPHLRLTTVVVANKFVNDQTASHRMMKEIGNRMEKFARLMGVPPFKFNI IHHVGDLSFEDLNELDVKPD
EVLAINCVGAMHGIIASRGSPRAVISSFRRLRPRIVTVEEEADLVGEEEGGFDEFLLRFGFGECLRWFRV
CFESWEESFPRTSNERLMLERAAGRAIVDLVACEPSDSTERRETARKWSRRMRNSGFGAVGYSDEVADDV
RALLRRYKEGVWSMVQCPDAAGIFLCWRDQPVVWASAWR

OSRGA3 (RGL3)

>OAO92748.1 RGL3 [Arabidopsis thaliana]
MKRSHQETSVEEEEASSMVEKLENGCGGGGDDNMDEFLAVLGYKVRSSDMADVAQKLEQLEIVLSNDIASS
SNAFNDTVHYNPSDLGWAQSMLSDLNYYPDLDPNRICDLRPITDDDECCSSNSNSNKRIRLGPWCDSVT
SESTRSVVLIETGVRLVQALVACAEAVQLENLSLADALVKRVGLLAASQAGAMGKVATYFAEALARRIY
RIHPSAAAIDPSFEEILQMNIFYDSCPYLKFAHFTANQAILEAVTTSRVVHVIDLGLNQGMQWPALMQALA
LRPGGPPSFRLTGVGPNPSNREGIQELGWKLAQLAQAGVEFKFNGLTTERLSDLPEPDMFETRTESETLVV
NSVFELHPVLSQPGSIEKLLATVKAVKPGLVTVVEQEANHNGDVFLDRFNEALHYSSSLFDSLEDGVVIP
SQDRVMSEVYLGRQILNVVATEGSDRIERHETLAQWRKRMGSAGFDPVNLGSDAFKQASLLALSGGGDG
YRVEENDGSLMLAWQTKPLIAASAWKLAELRR

LVQALVACAEAVQLENLSLADALVKRVGLLAASQAGAMGKVATYFAEALARRIYRIHPSAAAIDPSFEEILQMNIFYD
SCPYLKFAHFTANQAILEAVTTSRVVHVIDLGLNQGMQWPALMQALALRPGGPPSFRLTGVGPNPSNREGIQELGWKL
AQLAQAGVEFKFNGLTTERLSDLPEPDMFETRTESETLVVNSVFELHPVLSQPGSIEKLLATVKAVKPGLVTVVEQ
ANHNGDVFLDRFNEALHYSSSLFDSLEDGVVIPSQDRVMSEVYLGRQILNVVATEGSDRIERHETLAQWRKRMGSAG
FDPVNLGSDAFKQASLLALSGGGDG YRVEENDGSLMLAWQTKPLIAASAWK

SlDELLA

>NP_001234365.1 DELLA protein GAI [Solanum lycopersicum]
MKRDRDRDREREKRAFSNGAVSSGKSKIWEDEEEKPDAGMDELLAVLGYKVKSSDMADVAQKLEQLEMA
MGTTMEDGITHLSTDTVHKNPSPDMAGWVQSMSSISTNFDMCNQENDVLVSGCGSSSSIIDFSQNHRTST
ISDDDLRAIPGGAVFNSDSNKRHRSTTSSFSSTSSSMVTDSATRPVVLVDSQETGVRLVHTLMACAEAV
QQENLTADQLVRHIGILAVSQSGAMRKVATYFAEALARRIYKIYPQDSMESSYTDVLQMHFYETCPYLK
FAHFTANQAILEAFTGCNKVHVIDFSLKQGMQWPALMQALALRPGGPPAFRLTGIGPPQPDNTDALQQVG
WKLAQLAETIGVEFEFRGFVANSLADLDATILDIRPSETEAVAINSVFELHRLLSRPGAIEKVLNSIKQI
NPKIVTLVEQEANHNAGVFIDRFNEALHYSTMFDSLESSGSSSSASPTGILPQPPVNNQDLVMSEVYLG
RQICNVVACEGSDRVERHETLNQWRVRMNSSGFDPVHLGSNAFKQASMLLALFAGGDGYRVEENDGCLML
GWHTRPLIATSAWKLLPDSGTGAGEVEL

VDSQETGVRLVHTLMACAEAVQQENLTADQLVRHIGILAVSQSGAMRKVATYFAEALARRIYKIYPQDSMESSYTD
VLQMHFYETCPYLKFAHFTANQAILEAFTGCNKVHVIDFSLKQGMQWPALMQALALRPGGPPAFRLTGIGPPQPDNT
DALQQVGWKLAQLAETIGVEFEFRGFVANSLADLDATILDIRPSETEAVAINSVFELHRLLSRPGAIEKVLNSIKQI
NPKIVTLVEQEANHNAGVFIDRFNEALHYSTMFDSLESSGSSSSASPTGILPQPPVNNQDLVMSEVYLG
RQICNVVACEGSDRVERHETLNQWRVRMNSSGFDPVHLGSNAFKQASMLLALFAGGDGYRVEENDGCLMLGWHTRPLIATSAWK

OsSLR1

DELLA protein SLR1, putative, expressed >LOC_Os06g03710.1

OsSLR1

MLAGCSFSSSRHQMSTAQRFDILPCGFSKRGSRGDGAAPRVAGDARSGATTCSFRTHPAP
PVTQSVSWGAKPEPGGNGGAHRAVKRAHDEDAVEEYGPVIRAKRTRMGGDGDEVWFHQ
IAGTMQATAAGEGEEAEKVFLLVPSAAAFPHGMAAAGPSLAAAKKEEYSKSPSDSSSS
GTDGGSSAMPPPPQPEFDARNGVPAPGQAREALELVRALTACADSLSAGNHEAANYL
ARLGEMASAPGPTPMHRVAAYFTEALALRVVRMWPBMFDIGPPRELTDDAFGGGDDDDAMA
LRILNAITPIPRFLHFTLNERLLREFEGHERVHVIDFDIKQGLQWPGLLQSLAARAVPPA
HVRITGVGESRQELQETGARLARVAAALGLAFEFHVVDRLEDVRLWMLHVKRGECAVAVN
CVLAMHRLLRDDAALTDFLGLARSTGATILLGEHEGGGLNSGRWEARFARALRYAAAF
DAVDAAGLPEASPARAKAEEMFAREIRNAVAFEGPERFERHESFAGWRRRMEDGGGFKNA
GIGEREAMQGRMIARMFGPKYTVQAHGGGGSGGGEALTLRWLDQPLYTVTAWTPAGDGA
GGSTVSASTTASHSQS

GQAEREALELVRALTACADSLSAGNHEAANYLARLGEMASAPGPTPMHRVAAYFTEALALRVVRMWPBMFDIG
PPRELTDDAFGGGDDDDAMALRLINAITPIPRFLHFTLNERLLREFEGHERVHVIDFDIKQGLQWPGLLQSLAAR
AVPPAHVRITGVGESRQELQETGARLARVAAALGLAFEFHVVDRLEDVRLWMLHVKRGECAVAVN CVLAMHRL

RDDAALTDFLGLARSTGATILLGHEGGGLNSGRWEARFARALRYAAAFDAVDAAGLPEASPARAKAEEMFA
REIRNAVAFEGPERFERHESFAGWRRRMEDGGGFKNAGIGEREAMQGRMIARMFGPDKYTVQAHGGGSGGGEA
LTLRWLDQPLYTVTAWT

Medicago Trunctula

> >MtrunA17_Chr1g0159461

MSLIISP ELADASYGNAKLYSLKGADVTPGLSSHDFAPDKHRSMYMNDSYSSSESYEKYFLDSPTEELIEPSSSGISGNSV
HADGDSSYQLRANS GGSMITDNPFDTYVSSTRQRDAYQSNFESDFLESESPDCFEFDGDMRLKIQELERALLGDNNDECD
DDEENMFRTVQSMEIDPDFAECANPIQNKSHHDSPKESLSSDSNLSSTSSTKEISQNFPRTPKQLLYECASALSEGNEVK
ASAMIDDLRQLVSIQGEPSDRIAAYMVEGLAARLASSGKCIYKALKCKEPPSSDRLAAMQILFEVCPCKFGFIAANGAI
SEAIKDDKKVHIIDFDINQGSQYITLIQTLASRPGKPPYVRLTGVD DPESVQRSVGGLSIIGQRLEKLAEVLGLPFEFRA
VASRSSIVTPSMLNCRPGEALVVNFAFQLHHMPDES VSTVN ERDQLLRMVKSLNPKLVTVVEQDVNTNTSPFLPRFVEAY
NYYS AVFESLDATLPRESQDRVNVERQCLARDIVNVIACEGEDRIERYEVAGKWRARMKMAGFTSSPMSTNVKEAIRELI
RQYCDKYKII EEMGGLHFGWEDKNLIVASAWK

>MtGRAS

LSSDSNLSSTSSTKEISQNFPRTPKQLLYECASALSEGNEVKASAMIDDLRQLVSIQGEPSDRIAAYMVEGLAA
RLASSGKCIYKALKCKEPPSSDRLAAMQILFEVCPCKFGFIAANGAISEAIKDDKKVHIIDFDINQGSQYITL
IQTLASRPGKPPYVRLTGVD DPESVQRSVGGLSIIGQRLEKLAEVLGLPFEFRAVASRSSIVTPSMLNCRPGEA
LVVNFAFQLHHMPDES VSTVN ERDQLLRMVKSLNPKLVTVVEQDVNTNTSPFLPRFVEAYNYYS AVFESLDATL
PRESQDRVNVERQCLARDIVNVIACEGEDRIERYEVAGKWRARMKMAGFTSSPMSTNVKEAIRELIRQYCDKYK
II EEMGGLHFGWEDKNLIV

>AFT82684.1 GRAS23 GRAS type transcription factor, partial [Zea mays subsp.
mays]

MVMDAGLHEPCALLPGSKRDSHMLVYPQIAAAAANGFTAQELLESLLFLSSDGITLAAGSGGGGGGSYLN
APT'TVPPAPTNRASPPRDVSAAPPSVGQPDDSEAFSDIVLGYINRMLMAEDIDDKFEHYEHPAVLAAE
KPFLEILAERPSSSGGSAVESPGGSSVGN SCYSARSCTCATATAASDAFGAVLTPALDFPSAAFLQPPQL
YQDLSPEGSVVDAGGAWPYDSTEFYQLHSNPSSFASSNGSCATISDGFESLLSSPGVMPDVGFTDFAVQS
QQAMQFCRGFEEASKFLPDESKLVIDLEKPASVTSLVANIKGENRFAEVKA EKADVQAEIHRGKKHFYGD
DLDAEEGRRSKHSAP AIDTDHLVREMMDKVLLCNGETCSKGVKELREALQHDVAKNSHG VHKGSGHGKG
RGKKQPKKEVV DLETL LVHCAQSVATDDRRGATELLKQIRQHASPNGDGDQRLAHCFANGLEARLAGNGS
QIYKSLIMTRFPCTDVLKAYQLYLAACPFFKKISHFFANQTIMNAVEKAKKVHIVDYGIIYGFQWPCLIQRL
LSTRPGGPRLRIT AIDTPHPGFRPAERIEETGRYLKDYAETFNVPFEFRAIPSRFEAVQIEDLHIAKDE
LLIVNSMFKFKTLMDES VVAESPRNMVLSTIRKMNPHLFIHGIINGSYNAPFFASRFREALYHYS AIFDM
LETNI PRDNEQRLLIESALFGREAINVISCEGLERMERPETYKQWQVRYQRAGFRQLPINQDIMKRAREK
VRCYHKDFLIDEDNRWLLQGWKGRIVLALSTWKPDHRSP

PAIDTDHLVREMMDKVLLCNGETCSKGVKELREALQHDVAKNSHG VHKGSGHGKGGRGKKQPKKEVV DLETL LV
HCAQSVATDDRRGATELLKQIRQHASPNGDGDQRLAHCFANGLEARLAGNGS QIYKSLIMTRFPCTDVLKAYQL
YLAACPFFKKISHFFANQTIMNAVEKAKKVHIVDYGIIYGFQWPCLIQRLSTRPGGPRLRIT AIDTPHPGFRPA
ERIEETGRYLKDYAETFNVPFEFRAIPSRFEAVQIEDLHIAKDELLIVNSMFKFKTLMDES VVAESPRNMVLST
IRKMNPHLFIHGIINGSYNAPFFASRFREALYHYS AIFDMLETNI PRDNEQRLLIESALFGREAINVISCEGLE
RMERPETYKQWQVRYQRAGFRQLPINQDIMKRAREKVRCYHKDFLIDEDNRWLLQGWKGRIVL

