

**File:** /media/morpheus/disk1/fst/pep\_msa/AGC01161.psf  
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**File:** /media/morpheus/disk1/fst/pep\_msa/AGC01161.psf  
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*:*****:*.* ***:~::~*****:~***** :*****:~*** :***
AAAEAAVSQTGFIIYDENTGLYYDHSTGFYYNSENQLYYDPATGIYYCDVESGRYQFHSR 234
AAAEAAVSQTGFIIYDENTGLYYDHSTGFYYNSENQLYYDPATGIYYCDVESGRYQFHSR 234
AAAEAAVSQTGFIIYDENTGLYYDHSTGFYYNSENQLYYDPATGIYYCDVESGRYQFHSR 234
AAAEAAVSQTGFIIYDENTGLYYDHSTGFYYNSENQLYYDPTTGIYYCDVESGRYQFHSR 241
AAAEAAVSQTGFYDESTGLYFDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 255
AAAEAAVSQTSFTYDESTGLYFDHSTGFYYDSENQLYYDASTGIYYCDVESGRYQFHSR 248
AAAEAAVSQTGFSYDENTGLYFDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 255
AAAEAAVSQTGFSYDENTGLYFDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 255
AAAEAAVSQTGFSYDENTGLYFDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 251
AAAEAAVSQTGFSYDENTGLYFDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 257
AAAEAAVSQTGFSYDENTGLYFDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 255
AAAEAAVSQTGFSYDENTGLYFDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 253
AAAEAAVSQTGFSYDESTGLYFDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 255
AAAEAAVSQTGFSYDESTGLYFDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 259
ATAEAAVSQTGFYIDESGLYYDHSTGFYYDSENQLYYDPSTGIYYCDVESGRYQFHSR 248
ATAEAAVITQTFVYDENTGMYYDHSTGFYYDSENQLYYDGTGIIYYCDVDSGRVLYHSR 280
.....250.....260.....270.....280.....290.....300

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	..** :	.	:::: **::** :	*	
Pavo_muticus	VDLQSY	--QASGSQHVKDKKGKKKRKE	PEWSTANEY	----	268
Pavo_cristatus	VDLQSY	--QASGSQHVKDKKGKKKRKE	PEWSTANEY	----	268
Gallus_gallus	VDLQSY	--QASGSQHAKDKKGKKKRK	OPEWSTANEY	----	268
Chelonia_mydas	VDLQSY	--QAS--TTQTKDKKGKKKRK	DPEWITANEY	KVHQLTETMANLKISSFELAASGE	298
Mus_musculus	VDLQPY	--QTSSTKPNRERRLLKKRRKE	PGFYTANEY	----	289
Rattus_norvegicus	VHLQPY	--QTSSTKPSKDKKLKKRRKE	PGFWIATEE	----	282
Homo_sapiens	VDLQPY	--PTSSTKQSKDKKLKKKRK	DPDSSATNEE	----	289
Pan_troglodytes	VDLQPY	--QTSSTKQSKDKKLKKKRK	DPDSSATNEE	----	289
Macaca_mulatta	VDLQPY	--QTSSTKQSKDKKLKKKRK	DPDSSATNEE	----	285
Callithrix_jacchus	VDLQPY	--QTSATKQSKDKKLKKKRK	DPDSSATNEE	----	291
Canis_lupus_familiaris	VDLQPY	--QTCGTQSKDKKLKKKRK	DPDSSLANEY	----	289
Bos_taurus	VDLQPY	--QTSGTKQSKDKKLKKKRK	DPASSTNEE	----	287
Equus_caballus	VDLQPY	--QTSGAKQSRDKSKKKRK	DPDSSSTNEE	----	289
Heterocephalus_glaber	IDLQPY	--QSATTKQSKNKKLKKRK	DPDCSSTNEE	----	293
Rhinatrema_bivittatum	VDLQCYHTE	TSGAOGKEKKGKKRRREP	----	CNEE	280
Xenopus_tropicalis	VDLQSF	--TDINPQPTKDKRSKKRRD	DPASMEKEE	----	314
	.....310.....	320.....	330.....	340.....350.....360	

## CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

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		*:	*:	:	
Pavo_muticus	-----	K	M	D	282
Pavo_cristatus	-----	K	M	D	282
Gallus_gallus	-----	K	M	D	282
Chelonia_mydas	GRVETPNICHKMPLYFKNELKSVSRFNITEHQSMKEGTFIPFKNEK	K	M	D	358
Mus_musculus	-----	K	L	S	298
Rattus_norvegicus	-----	K	L	S	291
Homo_sapiens	-----	K	L	N	298
Pan_troglodytes	-----	K	L	N	298
Macaca_mulatta	-----	K	L	N	294
Callithrix_jacchus	-----	K	L	N	300
Canis_lupus_familiaris	-----	K	L	N	298
Bos_taurus	-----	K	N	L	296
Equus_caballus	-----	K	L	T	298
Heterocephalus_glaber	-----	K	L	N	302
Rhinatrema_bivittatum	-----	K	L	N	294
Xenopus_tropicalis	-----	K	E	K	323
	.....370.....380.....390.....400.....410.....420				

Pavo_muticus	NCFSTTE-QVSS <del>TEEEES</del> SP-NARKKTKMDIKIRNN-LTAKESIS <del>TDSMNS</del> QSHKSTPDTIA	339
Pavo_cristatus	NCFSTTE-QVSS <del>TEEEES</del> SP-NARKKTKMDIKIRNN-LTAKESIS <del>TDSMNS</del> QSHKSTPDTIA	339
Gallus_gallus	NCFSTTE-QVSS <del>TEEEESI</del> -NARKKTKMDAKIRNN-LTAKESIATDSMN <del>SHSKST</del> PDTIA	339
Chelonia_mydas	NCLSTTE-QIS <del>SSEEEES</del> SP-NARKKAKVDIDVRNR-LTAKESVITDGIN <del>SHLNKRKT</del> QDTIA	415
Mus_musculus	--VCSVE-YINCSEDEHSG-INVKKKARTDTSHKSSPLQLTVAVSGDIVESPGDD---NSA	351
Rattus_norvegicus	--VCSIE-YINCSEDENSG-INVKKKARTDTSHKSSPLPLAGAVSGDMVESPGDE---ASA	344
Homo_sapiens	--AFSVE-HTSCNEEENFA-NMKKKAKIGIHHKNSPPKVIVPTSGNTIESPLHENISNST	354
Pan_troglodytes	--AFSVE-HTSCNEEENFA-NMKKKAKIGIHHKNSPPKVIVPTSGNTIESPLHENISNST	354
Macaca_mulatta	--AFSVE-HTSCNEEENIA-NMKKKAKIGIHHKN <del>SLPKFTVPASGNTIES</del> PLHEDISNST	350
Callithrix_jacchus	--AFSVE-HITSNEEENFNS-HMKKKAKIGIHHKNSPPKFTVPASGNTIESPLHENISYST	356
Canis_lupus_familiaris	--ASSVE-HISCNEGEGDFA-NMKKKAKIDVHYKNSPPKFTVS <del>VSGKTTESSLNESIYN</del> ST	354
Bos_taurus	--TSSIE-HISCSEGEDFA-INVKKKAKVDIHYKNSPPKYTVPVSAKTIVESPLNENIYNSA	352
Equus_caballus	--ASSVE-HINCKEGEGDFA-TVKKKAKIDIHYKNSPPKFTVPVSGKTIVES-LNENTYNLT	353
Heterocephalus_glaber	--ASSVE-YLNCSEGENFA-HVKKKVKIDS-----VESPVNENISNSA	341
Rhinatrema_bivittatum	SYQNIVNGQV <del>SCTKWKE</del> SAYNTKKKAKVAMEIENGLLHAERQTAIKNIDSQS <del>DTK</del> --ETV	352
Xenopus_tropicalis	-----HEPVSPPERELA-AERKKARMGS-----LVE	349
	.....430.....440.....450.....460.....470.....480	

	..:*****:..::*	
Pavo_muticus	AYTDDSRITVDTESEPEEGEITDSEREYPYSTDEVITSEETNDSSEDSENE-----	387
Pavo_cristatus	AYTDDSRITVDTESEPEEGEITDSEREYPYSTDEVITSEETNDSSEDSENE-----	387
Gallus_gallus	AYTDDNRIVDTSESEPEEGEITDSEREYPYSTDEVITSEETNDSSEDSENE-----	387
Chelonia_mydas	AFMDDSKIIETESEPEEGEITDSECEYSSSEDEVITSEESVNSSEDSENE-----	463
Mus_musculus	SSKDE-RIGESESEPEEGEITDSQSE-KSYDGDSSSGDRETSEESDDED-----	398
Rattus_norvegicus	SLKDE-RERASESEPEEGEITDSQSE-CSYDGDPSGDRQSSEESDDED-----	391
Homo_sapiens	SFKDE-KIMETDSEPEEGEITDSQTE-DSYDEAITSEGNVIAEDSEDE-----	400
Pan_troglodytes	SFKDE-KIMETDSEPEEGEITDSQTE-DSFDEDITSEGNVIAEDSEDE-----	400
Macaca_mulatta	SFKDE-KIMETDSEPEEGEITDSQTE-DSYDEDITSEGNVIAEDSEDE-----	396
Callithrix_jacchus	SFKDE-KIMETDSEPEEGEITDSQTE-DSYDEDITSEGNVIAEDSEDE-----	402
Canis_lupus_familiaris	SFKDE-KIMETDSEPEEGEITDSQTE-DSFDEDITSEDNVIAEDSEDEA-----	401
Bos_taurus	SFKDE-KIIDTDSEPEEGEITDSQTE-DSSDEDLTSEDNATAEDTEDE-----	398
Equus_caballus	SFKDE-KIVETDSEPEEGEITDSQTE-DSYDEDMTSEDSVIAEDTEDE-----	399
Heterocephalus_glaber	SFKDE-IIIESDSEPEEGEITDSQTE-GSYDEDITSEDNRTTEETEDE-----	387
Rhinatrema_bivittatum	PLEAESDVIMESESEPEEGEITDSENK-DYSDEDESCTDSTSGDSEQEDSEMIWPPSMRV	411
Xenopus_tropicalis	SYERE-SSSDESEPEEGEITDSENEKTSDDDRSSGLSVTSHTESEPE-----	396
	.....490.....500.....510.....520.....530.....540	

## CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

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Pavo_muticus	-----	387
Pavo_cristatus	-----	387
Gallus_gallus	-----	387
Chelonia_mydas	-----	463
Mus_musculus	-----	398
Rattus_norvegicus	-----	391
Homo_sapiens	-----	400
Pan_troglodytes	-----	400
Macaca_mulatta	-----	396
Callithrix_jacchus	-----	402
Canis_lupus_familiaris	-----	401
Bos_taurus	-----	398
Equus_caballus	-----	399
Heterocephalus_glaber	-----	387
Rhinatrema_bivittatum	IVIRSPVLOTGSLYMITATEHSTIGRKKGLEHTIVIP EAAVSKFHAEVFFSHDLQSYVIV	471
Xenopus_tropicalis	-----	396
	.....550.....560.....570.....580.....590.....600	

Pavo_muticus	-----	387
Pavo_cristatus	-----	387
Gallus_gallus	-----	387
Chelonia_mydas	-----	463
Mus_musculus	-----	398
Rattus_norvegicus	-----	391
Homo_sapiens	-----	400
Pan_troglodytes	-----	400
Macaca_mulatta	-----	396
Callithrix_jacchus	-----	402
Canis_lupus_familiaris	-----	401
Bos_taurus	-----	398
Equus_caballus	-----	399
Heterocephalus_glaber	-----	387
Rhinatrema_bivittatum	DOGSQTGTVINGNLILQPDIISEPYILEHGDEVKFGETVLSFHVHPGRGTCDCDPCQIR	531
Xenopus_tropicalis	.....610.....620.....630.....640.....650.....660	396

		***** *:***** *:*:**** .*****: :: **:	
Pavo_muticus	-----	DEEKIWPPCIRVIVIRSPVLQTGSLYIITAVKPATIGREKDVGHTLQ	434
Pavo_cristatus	-----	DEEKIWPPCIRVIVIRSPVLQTGSLYIITAVKPATIGREKDVGHTLQ	434
Gallus_gallus	-----	DEEKIWPPCIRVIVIRSPVLQTGSLYIITAVKPATIGREKDVGHTLQ	434
Chelonia_mydas	-----	DEERIWPPCIRVIVIRSPVLQTGSLYIITAVKTATIGREKDMOHTLQ	510
Mus_musculus	-----	EERIWPPCIRVIVIRSPVLQMGSFLIITAVSPATIGREKDMEHTVR	444
Rattus_norvegicus	-----	DEEKIWPPCIRVIVIRSPVLQMGSFLIITAVSPATIGREKDMEHTVR	438
Homo_sapiens	-----	DEDKIWPPCIRVIVIRSPVLQIGSLFIITAVNPATIGREKDMEHTLR	447
Pan_troglodytes	-----	DEDKIWPPCIRVIVIRSPVLQIGSLFIITAVNSATIGREKDMEHTLR	447
Macaca_mulatta	-----	DEDKIWPPCIRVIVIRSPVLQTGSLFIITAVNPATIGREKDMEHTLR	443
Callithrix_jacchus	-----	DEDKIWPPCIRVIVIRSPVLQTGSLFIITAVNPATIGREKDMEHTLR	449
Canis_lupus_familiaris	-----	DEEKIWPPCIRVIVIRSPVLQTGSLFIITAVNPATIGREKDMEHTLR	448
Bos_taurus	-----	DEEKIWPPCIRVIVIRSPVLQTGSLFIITAVNPATIGREKDMEHTLR	445
Equus_caballus	-----	DEEKIWPPCIRVIVIRSPVLQTGSLFIITAVNPATIGREKDMEHTLR	446
Heterocephalus_glaber	-----	DEEKIWPPCIRVIVIRSPVLQTGSLFIITAVKPATIGREKDMEHTLR	434
Rhinatrema_bivittatum	-----	THLCLNKESPTSSDTERIWPPCIRVIVIRSPVLQIGSLYIITATKHATIGRDGNLEHTVL	591
Xenopus_tropicalis	-----	DPERIWPPCIRVTVVRSPVLQKGLTFIITADKTATIGREKDLGHTIR	443
	.....670.....680.....690.....700.....710.....720		



## CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

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***  .:*****:***:*.**:***** **:**: ***  .:.*:*****:
IPEVGVSKFHAENVYFDHDLQNYVLVDQGSQNGTVVNGNQILQPKTKCDPYILEHGDEVKI 494
IPEVGVSKFHAENVYFDHDLQNYVLVDQGSQNGTVVNGNQILQPKTKCDPYILEHGDEVKI 494
IPEVGVSKFHAENVYFDHDLQNYVLVDQGSQNGTVVNGNQILQPKTKCDPYILEHGDEVKI 494
IPEVGVSKFHAENVYFDHDLQNYVLVDQGSQNGTVVNGNQILQPKTKCDPYVLEHGDEVKI 570
IPEVAVSKFHAENVYFDHDLQSYVLVDQGSQNGTIVNGKQILQPKTKCDPYVLEHGDEVKI 504
IPEVAVSKFHAENVYFDHDLQSYVLVDQGSQNGTIVNGKQILQPKTKCDPYILEHGDEVKI 498
IPEVGVSKFHAENVYFDHDLQSYVLVDQGSQNGTIVNGKQILQPKTKCDPYVLEHGDEVKI 507
IPEVGVSKFHAENVYFDHDLQSYVLVDQGSQNGTIVNGKQILQPKTKCDPYVLEHGDEVKI 507
IPEVGVSKFHAENVYFDHDLQSYVLVDQGSQNGTVVNGKQILQPKTKCDPYVLEHGDEVKI 503
IPEVGVSKFHAENVYFDHDLQSYVLVDQGSQNGTIVNGKQILQPKTKCDPYVLEHGDEVKI 509
IPEVGVSKFHAENVYFDHDLQSYVLVDQGSQNGTIVNGKQILQPKTKCDPYVLEHGDEVKI 508
IPEVGVSKFHAENVYFDHDLQSYVLVDQGSQNGTVVNGKQILQPKTKCDPYVLEHGDEVKI 505
IPEVGVSKFHAENVYFDHDLQSYVLVDQGSQNGTIVNGKQILQPKTKCDPYVLEHGDEVKI 506
IPEVGVSKFHAENVYFDHDLQSYVLVDQGSQNGTIVNGKHILQPKTKCDPYVLEHGDEVKI 494
IPEAAVSKFHAENVYFDHDLQSYVIVDQGSQIGTVINGNLILQPGVISEPCVLEHGDEVRF 651
IPELGISKFHAENVYFDHDLQSYVLVDQGSQNGTVINGNHILQPKVSEQPCVLEHGDEVKF 503
.....730.....740.....750.....760.....770.....780

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*****:*::*:*****:*****:::.* *::** : ** *: : **:***
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKK-ESSVCPALSKEERELVRRKALKQIR 553
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKK-ESSVCPALSKEERELVRRKALKQIR 553
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKK-ESSVCPALSKEERELVRRKALKQIR 553
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKK-EFSG-PALSKEERELVRRKALKKIR 628
GETVLSFHIHPGSETCDGCEPGQVRAHLRLDRKD-EPLVGPALSKEEKELERRKALKKIR 563
GETVLSFHIHPGSETCDGCEPGQVRAHLRLDKKD-EPLVGPALSKEEKELERRKALKKIR 557
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKD-ESFVGPTLSKEEKELERRKELKKIR 566
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKD-ESFVGPTLSKEEKELERRKELKKIR 566
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKD-ESFVGPTLSKEEKELERRKELKKIR 562
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKD-ESFVGPTLSKEEKELERRKELKKIR 568
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKD-ECFVGPALSKEEKELERRKELKKIR 567
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKD-ELFVGPALSKEEKELERRKELKKIR 564
GETVLSFHIHPGSETCDGCEPGQVRAHLRLDKKD-ESFVGPTLSKEEKELERRKELKKIR 565
GETVLSFHIHPGSDTCDGCEPGQVRAHLRLDKKD-ESFVGPALSKEEKELERRKELKKIR 553
GETVLSFHVHPGCETCNGCEPGQIRAHRLRNKESPTSSAGPILSKEEKELIRRKELKHIR 711
GETVLSFHVHPGSETCDGCEPGQVRAHLRLNKKE-EHSAGPVLTKEGKELLRKGLKKIR 562
.....790.....800.....810.....820.....830.....840
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*****.: ** *.:**:*:** :*: **:***: :*:.* **. *.**:*:  
VKYGLQNTHEYEDNKAVKNPKYKDRAGKRRETIGSEGTFORGDTPASVHIEISDSNKGHKM 613  
VKYGLQNTHEYEDNKAVKNPKYKDRAGKRRETIGSEGTFORGDTPASVHIEISDSNKGHKM 613  
VKYGLQNTHEYEDNKAVKNPKYKDRAGKRRETIGSEGTFORGDTPASVHIEISDSNKGHKM 613  
VKYGLQNTDYEDNKAVKNPKYKDRAGKRRETIGSEGTQRDDTPASVHVEISDSNKGGRKM 688  
VKYGLQNTDYEAEKALKNPKYKDRAGKRREQVGSEGTFORDDAPASVHSEITDSNKGGRKM 623  
VKYGLQNTDYEDEKALKNPKYKDRAGKRREQVGSEGTFORDDAPASVHSEITDSNKGGRKM 617  
VKYGLQNTYEYDEKTLKNPKYKDRAGKRREQVGSEGTFORDDAPASVHSEITDSNKGGRKM 626  
VKYGLQNTYEYDEKTLKNPKYKDRAGKRREQVGSEGTFORDDAPASVHSEITDSNKGGRKM 626  
VKYGLQNTYEYDEKTLKNPKYKDRAGKRREQIGSEGTFORDDAPASVHSEITDSNKGGRKM 622  
VKYGLQNTVYDEKTLKNPKYKDRAGKRREQIGSEGTFORDDAPASVHSEITDSNKGGRKM 628  
VKYGLQNTDYEDEKALKNPKYKDRAGKRREQIGSEGTFORDDAPASVHFEITDSNKGGRKM 627  
VKYGLQNTDYEDEKTLKNPKYKDRAGKRREQIGSEGTFORDDAPASVHSEITDSNKGGRKM 624  
VKYGLQNTYEYDEKALKNPKYKDRAGKRREQIGSEGTFORDDAPASVHSEITDSNKGGRKM 625  
VKYGLQNTDYEDEKALKNPKYKDRAGKRREQVGSEGTFORDDAPASIHSEITDSNKGGRKM 613  
VKYGLQNTDYEDCKALKNPKYRDRAEKRRKRVGSEAFPQRECAPASVHVEINDSNKGGRKM 771  
AKYGLQSADYEDNKVLTNPKYKDRAGRRRQVGS DGTFOKEEAPASVHVEINDNKGGRKM 622  
.....850.....860.....870.....880.....890.....900
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 LEKMGWKKGEGLGKDDGGGMDPIHLQLHKMHAGLGTSRPTSIEDIQIIPSKNKKKNWDKAR  
 LEKMGWKKGEGLGKDDGGGMDPIHLQLHKMHAGLGTSRPTSIEDIQIIPSKNKKKNWDKAR  
 LEKMGWKKGEGLGKDDGGGMDPIHLQLHKMHAGLGTSRPTSIEDIQIVPSKNKKKNWEKAR  
 LEKMGWKKGEGLGKDDGGGKNPIQLIHKMHAGLGTSRPASVEDVQIIKSKNKKKNWDKAR  
 LEKMGWKKRGEGLGKDDGGGMDPIQLQLRRTHAGLGTGKLSSIDDVHLLIQNKSKKHWWDKAR  
 LEKMGWKKGEGLGKDDGGGMDPIQLQLRRTHAGLGTGKPPSSIDDVHFLQNKSKKNWDKAR  
 LEKMGWKKGEGLGKDDGGGMDPIQLQLRRTHAGLGTGKPPSSFEDVHLLQNKKNKKKNWDKAR  
 LEKMGWKKGEGLGKDDGGGMDPIQLQLRRTHAGLGTGKPPSSIEDVHLLQNKKNKKKNWDKAR  
 LEKMGWKKGEGLGKDDGGGMDPIQLQLRRTHAGLGTGKPPSSIEDVHLLQNKKNKKKNWDKAR  
 LEKMGWKKGEGLGKDDGGGMDPIQLQLRRTHAGLGTGKPPSSIEDVHLLQNKKNKKKNWDKAR  
 LEKMGWKKGEGLGKDDGGGMDPIQLQLRRTHAGLGTGKPPSSIEDVHLLQNKSKKNWEKAR  
 LEKMGWKKGEGLGKDDGGGMDPIQLQLRRTHAGLGTGKPPSSIEDVQLLQNKSKKNWEKAR  
 LEKMGWKKGEGLGKDDGGGMDPIELQLRRTHAGLGTGKPPSVEDAHLLOSKSKKNWEKAR  
 LEKMGWKKGEGLGKDDGGGMDPIQLQLRRTHAGLGTGKTSSIEDVPLLQSKSKKNWDKAR  
 LERMGWKKGEGLGKDDGGGMDPIQLQLRKKQAGLGASMPSSIEDAPVR-SKNKNWEKAR  
 LEKMGWKKGEGLGKSSDGIKDPIQLQLRKKAGLGAQNPTSIEDIQPT-TQNKKNWEKAR  
 .....910.....920.....930.....940.....950.....960

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**::* * : * .: .*: *: *
ERFAENFQEPKSORDTPKNTPWVRGIVE 701
ERFAENFQEPKSORDTPKNTPWVRGIVE 701
ERFAENFQEPKSOKDTPKSTPWVRGIVE 701
ERFAESFQEAKTOKDAPKVMPPWVRGTAE 776
ERFAETFTENKPRKETPGAVPWTGTAE 711
ERFAENFTEKKACKEAPGPPIPWVTGTAE 705
ERFTENFPETKPOKDDPGTMPWVKGITLE 714
ERFTENFPETKPOKDDPGTMPWVKGITLE 714
ERFTENFPETKPOKDDPGTMPWVKGITLE 710
ERFTENFAETKPOKDDPVTIPWVKGITLE 716
ERFAENFTEAKSOKDVPGTVPWVKGITIE 715
ERFAENFPEAKSOKDAPGTVPWVKGAVE 712
ERFAENFPETKPOKADPGSAPWVKGITTE 713
ERFAESFPETKPPKADPGTTPWVKGIVE 701
ERFSETTFQNVKLKHDPSRPTPWVKGAME 858
ERYAEAFDPAKTKNETKTSVTWIKGSIE 709

          .970.....980.....

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