SUPPLEMENTAL MATERIALS

Genome-based comparison of c-di-GMP signaling in pathogenic and commensal *Escherichia coli* strains

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Table S1. *E. coli* strains analyzed in this study.

Pathotype	**Strain Name/Serotype**	**GI Number**
Pathogenic *E. coli* (enteric)		
EAEC	042 (O44:H18)	387605479
	55989 (O104:H4)	218693476
	01-09591 (HUSEC41) (O104:H4)	417836893
	LB226692 (O104:H4)	417809159
	2009EL-2050 (O104:H4)	410480139
	2009EL-2071 (O104:H4)	407466711
	2011C-3493 (O104:H4)	407479587
ETEC	E24377A (O139:H28)	157154711
	ETEC H10407 (O7:H104)	387610477
EHEC	12009 (O103:H2)	260842239
	EC4115 (O157:H7)	209395693
	EDL933 (O157:H7)	749302083
	Sakai (O157:H7)	15829254
	TW14359 (O157:H7)	254791136
	Xuzhou21 (O157:H7)	387880559
	11368 (O26:H1)	260853213
STEC	11128 (O111:H-)	260866153
	RM13516 (O145:H28)	749302049
	RM13514 (O145:H28)	749302203
	RM12761 (O145:H28)	749304472
	RM12581 (O145:H28)	749302183
	JJ1886 (Subclone of ST131) (O25:H4)	556550243
EPEC	E2348/69 (O127:H6)	215485161
	CB9615 (O55:H7)	291280824
	RM12579 (O55:H7)	387504934
AIEC	LF82 (O83:H1)	222154829
	UM146	386602643
	NRG 857C (O83:H1)	387615344
Pathogenic *E. coli* (extraintestinal)		
NMEC	CE10 (O7:K1)	386622414
	IHE3034 (O18:K1:H7)	386597751
	S88 (O45:K1:H7)	218556939
ExPEC	IAI39 (O7:K1)	218698419
	PMV-1 (O18:K1)	693169392
	UMN026 (O7:K1:H18)	218703261
UPEC	536 (O6:K15:H31)	110640213
	CFT073 (O6:K2:H1)	26245917
	UTI89 (O18:K1:H7)	91209055
***E. coli* isolated outside the human host**		
Environmental Isolate	SMS-3-5 (O19:H34)	170679574

APEC	APEC O1 (O1:K1:H7)	117622295
	APEC O78 (O78:H19)	443615330
Porcine ETEC	UMNF18 (O147)	418300889
	UMNK88 (O149)	386612163
Commensal *E. coli*		
	ABU 83972 (probiotic) (OR:K5:H2)	386637352
	ATCC 8739 (O146)	170018061
	B str. REL606 (O7)	254160123
	BL21(DE3) (O7)	387825439
	'BL21-Gold(DE3)pLysS AG' (O7)	253771435
	BW2952 (K-12 derivative) (O16)	238899406
	DH1 (K-12 derivative) (O16)	386593590
	ED1a (O81)	218687878
	HS (O9)	157159467
	IAI1 (O8)	218552585
	KO11FL (O6:K-:H49)	378710836
	Nissle 1917 (probiotic) (O6:K5:H1)	749302377
	SE11 (O152:H28)	209917191
	SE15 (O150:H5)	387828053
	W (O6:K-:H49)	386707734
	K-12 substr. DH10B (O16)	170079663
	K-12 substr. MDS42 (O16)	471332236
	K-12 substr. MG1655 (O16)	749204315
	K-12 substr. W3110 (O16)	388476123

Table S2. Physiological functions, sensory domains and conserved motifs of the 35 GGDEF/EAL domain proteins found in 61 *E. coli* strains.

Name	**Physiological function**	**Number of TMSs**	**Sensory Domains**	**GGDEF Domain**	**EAL Domain**			
				I-Site **A-Site** RxxD GG[D/E]EF	**EALxR**	**C-di-GMP binding**	**Catalysis**	**Mg^{2+} binding**
I. Diguanylate cyclases								
DgcC (YaiC)	Cellulose synthesis	6	MASE2	**R**GS**D**VIGRF**GGDEF**				
DgcE (YegE)	Downregulates motility, activates *csgD* transcription	10	MASE1, PAS, PAS, PAS,	**R**SS**D**VLARL**GGDEF**	**EA**RNL	-/-/-/-	-/-	
DgcF (YneF)	Unknown	8	xMASE1	GDKGLVARM**GGEEF**				
DgcI (YliF)	Unknown	2	GAPES2	VDKGKVYRF**GGDEF**				
DgcJ (YeaJ)	Downregulates motility	2	GAPES1	**R**KS**D**YAIRL**GGDEF**				
DgcM (YdaM)	Co-activator for MlrA in *csgD* transcription	0	PAS, sensory box AtoS, PAS$_2$	**R**KG**D**LVFRW**GGEEF**				
DgcN (YfiN)	Unknown	2	CHASE8, HAMP	GLRHKAYRL**GGDEF**				
DgcO (DosC, YddV)	Regulates PNPase activity	0	Sensor globin	**R**SS**D**YVFRY**GGDEF**				
DgcP (YeaP)	Unknown	0	GAF	QNGEVIGRL**GGDEF**				
DgcQ (YedQ)	Cellulose synthesis	2	CHASE7	**R**AQ**D**VAGRV**GGEEF**				
DgcT (YcdT)	Regulates PGA production	8	MASE4	**R**PD**D**LLARV**GGEEF**				
DgcZ (YdeH)	Regulates PGA production	0	CZB	**R**DYETVYRY**GGEEF**				
DgcX	Unknown	8	MASE4	**R**KE**D**ILGRL**GGEEF**				
DgcY	Unknown	6	MASE5	QSE**D**VVVRY**GGEEF**				
II. c-di-GMP-specific phosphodiesterases								
PdeA (YfeA)	Unknown	8	MASE1,	QENEKLYQLP**G**SEL	**E**I**L**A**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeB (YlaB)	Unknown	2	CSS		**EAL**A**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeC (YjcC)	Unknown	2	CSS		**EAL**L**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeD (YoaD)	Unknown	2	CSS		**E**I**L**L**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeF (YfgF)	Unknown	9	MASE1,	EPGEDVYQLS**G**NDL	**E**I**L**L**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeG (YcgG)	Unknown	2	CSS		**E**V**L**A**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeH (YhjH)	Promotes motility	0			**E**L**L**TV	**Q**/V/**D**/A	L/**E**	**E/N**/P/R/**D/K/E/Q**
PdeI (YliE)	Unknown	2			**EAL**C**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeK (YhjK)	Unknown	2	GAPES3, HAMP	SPRMILAQIS**G**YD**F**	**E**V**L**L**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeL (YahA)	Unknown	0	LuxR		**EAL**V**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeN (Rtn)	Unknown	2	CSS		**E**V**L**L**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeO (DosP, YddU)	Regulates PNPase activity	0	PAS, PAS, xGAF	KPDQYLCRIE**G**TQ**F**	**EAL**A**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeR (YciR)	Inhibits YdaM and MlrA and thereby *csgD* transcription	0	PAS	EHDQVLARP**GGDEF**	**EAL**V**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeT (VmpA)	Promotes motility	2	CSS		**EAL**M**R**	**Q/R/D/D**	**T**/S	**E/N/E/E/D/K/E/Q**
PdeW	Unknown	0			**E**L**L**S**R**	E/**R/D/D**	S/**E**	**E**/L/**E/E/D/K/E/Q**
PdeX	Unknown	0			**E**L**L**V**R**	**Q/R/D/D**	**T/E**	**E/N/E/E/D/K/E/Q**
PdeY (SfaY)	Unknown	0			**E**M**L**SD	E/D/**D**/S	S/**E**	**E/N/E/E/D/K/E/Q**
III. Degenerate GGDEF/EAL domain proteins								
BluF (YcgF)	Blue light-controlled direct antagonist for the BluR (YcgE) repressor	0	BLUF		**EA**IVQ	N/Q/H/S	**T**/A	**E/N/E/E/D/K**/M/**Q**
CdgI (YeaI)	Unknown	8	MASE4	**R**PD**D**ILARLE**GEVF**				
CsrD (YhdA)	Turnover of RNAs CsrB/CsrC	2	GAPES4	YPGALLARYHRSD**F**	**E**LMC**R**	**Q/R**/Q/H	A/R	**E**/E/**E/E**/N/**K/E/Q**
RflP (YdiV)	Inhibitor and proteolytic targeting factor for FlhDC	0			**EVL**x**R**	F/H/N/**D**	N/D	**E**/-/L/**E**/G/M/G/**Q**

Figure S1. Alignment of nine MASE4-GGDEF proteins from *E. coli*, *Klebsiella pneumoniae* and *Enterobacter lignolyticus*. The alignment was generated using the CLUSTAL-W programme (Larkin et al. 2007. Bioinformatics 23:2947-2948). Hydrophobic putative transmembrane regions are underlied in grey, highly conserved amino acid residues in hydrophilic loop regions of the MASE4 domain are highlighted in yellow, the I-site and A-site of the GGDEF domain are marked in green and red, respectively.

```
YP_003036092.1 CdgI(YeaI)_E.coli
YP_003942334.1 DgcX-like_E.lignolyticus_1
ACT29591.1     DgcT(YcdT)_E.coli
YP_001461960.1 DgcX_E.coli
YP_002919757.1 DgcX-like_K.pneumoniae_1
YP_001335641.1 DgcX-like_K.pneumoniae_2
YP_003941726.1 DgcX-like_E.lignolyticus_2
YP_001176536.1 DgcX-like_E.lignolyticus_638
YP_003940930.1 DgcX-like_E.lignolyticus_3
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gi|253773261|ref|YP_003036092.      -------------------------MIQSTRISMGLFFKYFLSLTKIDLG 25
gi|311280103|ref|YP_003942334.      --------------------------------------MHPLFLSKNCLL 12
gi|253324989|gb|ACT29591.1|         ------------------------------------MEKDYLRISSTVLV 14
gi|157155149|ref|YP_001461960.      ----------------------------------MIINQVPIKIKIFIFL 16
gi|238895023|ref|YP_002919757.      MRLRNILSARPYYPQERKLALVTHRRCRCLLCGILPMPEHVHHIVKRLIL 50
gi|152970532|ref|YP_001335641.      --------------------------------------------------
gi|311279495|ref|YP_003941726.      ------------------------------------MPVPTLIPLRRLFF 14
gi|146311462|ref|YP_001176536.      ------------------------------------MITISPRLRNRYVA 14
gi|311278699|ref|YP_003940930.      ------------------------------MARKFKLTNIFNFPKHSLQK 20

gi|253773261|ref|YP_003036092.      QNYISLPSIKSSTHIALLFMVSMGTQKLKAQSFFIFSLLLTLILFCITTL 75
gi|311280103|ref|YP_003942334.      SLCVSLISLMAAS---------------------------TLIIY----- 30
gi|253324989|gb|ACT29591.1|         SLLFGLALVLVNS------------------------------WFN---- 30
gi|157155149|ref|YP_001461960.      FSCISIIFLLLHE------------------------------------- 29
gi|238895023|ref|YP_002919757.      YICICLLAGIGISGMT---------------------------------- 66
gi|152970532|ref|YP_001335641.      --------------------------------------------------
gi|311279495|ref|YP_003941726.      FLCICAVSIIALYSVS---------------------------------- 30
gi|146311462|ref|YP_001176536.      FTFFCLFFFVALHFLA---------------------------------- 30
gi|311278699|ref|YP_003940930.      FTAISILVFTILQTLA---------------------------------- 36

gi|253773261|ref|YP_003036092.      YNENTNVKLIPQMNYLMVVVALFFLNAVIFLFMLMKYFTNKQILPTLILS 125
gi|311280103|ref|YP_003942334.      --DDINITIIPQSTYQIVIVALFFIDAIAAIFMFTQYICNKKHYDILLLG 78
gi|253324989|gb|ACT29591.1|         --QPGVEEVVPRSTYLMVMIALFFIDTVAFIFMQLYFIYDRRQFSNCVLS 78
gi|157155149|ref|YP_001461960.      -NNGIYITQTTQISYSVFIIGLFFINLMIFIFLLLYYVSNQRQSYLLILS 78
gi|238895023|ref|YP_002919757.      AFFHTSFSSTSSILFPLLTSFLMVFHITIACFMGMKYWSSKRRLYLTPVS 116
gi|152970532|ref|YP_001335641.      --------------------------------MGMKYWSSKRRLYLTPVS 18
gi|311279495|ref|YP_003941726.      HVIVYHIPLTTTVLFPVMTIFLMVFHLMIAGFMVMKYLCDKSRLYHIAIA 80
gi|146311462|ref|YP_001176536.      IKLLNFAPAFSPLLFPLLTSFLAVFHLFIACFMVMKYWCDKKRIYHLAIA 80
gi|311278699|ref|YP_003940930.      ENTIQNTVSIAPVLLPIITITLLISYIIISILMILKYLSDKQCLFLVPVI 86
                                                                    :   :  .:       :

gi|253773261|ref|YP_003036092.      LAFLSGLIYLVETIVIIHKPI-NGSTLIQTKSNDVSIFYIFRQLSFICLT 174
gi|311280103|ref|YP_003942334.      FAFLSGLLYFAETIAVIQKPL-ETCTTIESKSNDIAIFYLFRQLSFLFLL 127
gi|253324989|gb|ACT29591.1|         LAFLSCLIYFVKTVIIIQQII-EERLTSSVVQNDIAIYYLFRQMSLCILI 127
gi|157155149|ref|YP_001461960.      FAFLSNTYYLLEVAIISLSPLGNDLSTIYQKSNDIAIYYLFRQFSFISII 128
gi|238895023|ref|YP_002919757.      FGFACSALLMLGTLSSYPDWLTCNPAPVVN-QNDAVIYYFFRNIMMAVLF 165
gi|152970532|ref|YP_001335641.      FGFACSALLMLGTLSSYPDWLTCNPAPVVN-QNDAVIYYFFRNIMMAVLF 67
gi|311279495|ref|YP_003941726.      CAFSGATLFMLGTLSSYPDWLTCSPAARIN-YNDALIYYFFRNVLMAVLF 129
gi|146311462|ref|YP_001176536.      FAFTGSTVLLLATLTCFPVWLMQPGMPHVN-YSGAMIFFMMRNVMMAVLF 129
gi|311278699|ref|YP_003940930.      CAFTGSVVLNMYYFSSYPEGFIYKIITISN-YNDYLIGYFYRNIMLMITI 135
                                     .*                 :           ..  * :: *:. :

gi|253773261|ref|YP_003036092.      SLALFCYGKDNILDNNKKK-TGILLLALIPFLVFPLLAHNLSSYNADYSL 223
gi|311280103|ref|YP_003942334.      LLSLFIHTPGHKTNKNRK--LLLLLLSLFPLLIFPILSHNLSSYNPEMAI 175
gi|253324989|gb|ACT29591.1|         FLALVNKVSENTKQRNLFSKKMTLCISLFFVFGGPIVAHILSSHYESYNL 177
gi|157155149|ref|YP_001461960.      FLAVYSTNVKNKSVLEDKRNIIIVVLSILILFITPYVAKNLSSDNIKYSL 178
gi|238895023|ref|YP_002919757.      MSSIILYYFRQRIMHSWKAHVLTFTACILFTLTIIVLSWLYSSHSPWLSV 215
gi|152970532|ref|YP_001335641.      MSSIILYYFRQRIMHSWKAHVLTFTACILFTLTIIVLSWLYSSHSPWLSV 117
gi|311279495|ref|YP_003941726.      LAAVILFKYRKHNMHTRSNHIIILSVIVSFTLAMLVLSWFVSSHYEGINV 179
gi|146311462|ref|YP_001176536.      TLAGVLFIFRHSPLTRLMRH-LIFAGLLVFTLTMVTVAWFYSGHSELFPL 178
gi|311278699|ref|YP_003940930.      LMSALLYGLRKHRLLSPENNIITVWVIINASIIMVALSWLSSSYYIKTNI 185
                                      :       :            .   :   :    ::   *.      :
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gi|253773261|ref|YP_003036092.      YVVDYCPDNHTATWGINYTKILVCLWAFLLFFIIMRTRLASELWPLIALL 273
gi|311280103|ref|YP_003942334.      TITYYHTGSKSQMWVMGYVYLLLALWALCLLLIIYRTKLHDDMWRSITVL 225
gi|253324989|gb|ACT29591.1|         HIAELTNENGQVVWKASYVTIMIFMWLTLLSVNLYFNGLRYDIWNGVTVI 227
gi|157155149|ref|YP_001461960.      NIIQYSLNRHLPTWNIVYTKIISVFWLVLLISSCISIRNYSKIWLCIILI 228
gi|238895023|ref|YP_002919757.      NFIDDLSHTFTPLWQSIIGWLLMAVWFITLILLISLSKLRNIFWFSGAFF 265
gi|152970532|ref|YP_001335641.      NFIDDLSHTFTPLWQSIIGWLLMAVWFITLILLISLSKLRNIFWFSGAFF 167
gi|311279495|ref|YP_003941726.      AFIDNMTLAFTPLWQKATGGLLITMWLVTLIAMLIITRLRNIFWFSGCFF 229
gi|146311462|ref|YP_001176536.      DLINNTTRQFTALWKQIINGALIILWLIALTTLLIITRLRNLFWASGTFL 228
gi|311278699|ref|YP_003940930.      DLTHQKISDFFPFWR---PGVMFVAWCVILIIAIITTRFRNMYWTGIYFV 232
                                     .           *       :   *   *             *    ..

gi|253773261|ref|YP_003036092.      CLASLCCNLLLLTLDEYNYTIWYISRGIEVSSKLFVVSFLIYNIFQELQL 323
gi|311280103|ref|YP_003942334.      CLSGFCCNLLLIALLRYDLSIWYICRMLEAISKMCIITTLMYSIFHTLNN 275
gi|253324989|gb|ACT29591.1|         AFCAVLYNISLLFMSRYSVSTWYISRTIEVVSKLTVMVIFMCHIFSALRV 277
gi|157155149|ref|YP_001461960.      SIVSVCNNLILLYFIDKSHPAWYMTKFLELISMIYIISTLMYYVFRKLNH 278
gi|238895023|ref|YP_002919757.      CSAYLFTLFQLLSTAGELDQTWYQARFFETLCTLFLILVLLVDVFILYRE 315
gi|152970532|ref|YP_001335641.      CSAYLFTLFQLLSTAGELDQTWYQARFFETLCTLFLILVLLVDVFILYRE 217
gi|311279495|ref|YP_003941726.      CVFYIFTLTILLLSPVGESNNWYQARMFETIATLFLIFVLLGDVFTLYKD 279
gi|146311462|ref|YP_001176536.      CTCYVIILITLLPADFIGGSVWYSARLFETTASLLIILTLLHDVFSLYRN 278
gi|311278699|ref|YP_003940930.      CISYMLMSFQLITSEYSTDNMLYRTRMLEVLSTLVFVFILFINSFILYKN 282
                                    .   .     *:          *  : :*  . : .:  ::   *   .

gi|253773261|ref|YP_003036092.      SS-------KLAVHDVLTNIYNRRYFFNSVESLLSRP-VVKDFCVMLVDI 365
gi|311280103|ref|YP_003942334.      IS-------EKAFHDPLTAIYNRRFFFTEFDRFLQEW-NFTPYCAMIVDI 317
gi|253324989|gb|ACT29591.1|         TK-------NIAHRDPLTNIFNRNYFFNELTVQSASA-QKTPYCVMIMDI 319
gi|157155149|ref|YP_001461960.      AN-------HMAIHDPLTNTYNRRYFIDSLKNIS----KHHDFSVIMLDI 317
gi|238895023|ref|YP_002919757.      SNHKYVHSYQNSIRDPLTRLYNRSFFYDTLNQQLAKVNAQHPLSVLISDL 365
gi|152970532|ref|YP_001335641.      SNHKYVHSYQNSIRDPLTRLYNRSFFYDTLNQQLAKVNAQHPLSVLISDL 267
gi|311279495|ref|YP_003941726.      SNNKYQNSYQNSIRDPMTQLYNRSYFYDSLTQTIARVTPQQPASVIVCDL 329
gi|146311462|ref|YP_001176536.      SHIKYQQSYQNSIRDALTRLYNRSYFYESLNQALGKITDSHPVSVIVCDL 328
gi|311278699|ref|YP_003940930.      SNTKYKNAYQNSIRDHLTMLYNRRYFYDALMKLIPCITVKNPLSIIVCDI 332
                                             . : :* :*  :** :*   .             . :: *:

gi|253773261|ref|YP_003036092.      NQFKRINAQWGHRVGDKVLVSIVDIIQQSIRPDDILARLEGEVFGLLFTE 415
gi|311280103|ref|YP_003942334.      DRFKRINDRYGHEVGDKTLIAVARIIADTLRNEDLFARIGGEEFGILSQN 367
gi|253324989|gb|ACT29591.1|         DHFKKVNDTWGHPVGDQVIKTVVNIIGKSIRPDDLLARVGGEEFGVLLTD 369
gi|157155149|ref|YP_001461960.      DSFKSINDKWGHHMGDQVIVMVTRIIKKSIRKEDILGRLGGEEFGIIIKG 367
gi|238895023|ref|YP_002919757.      DHFKRINDSYGHVAGDKVIQFAASVLESHSRVDDAAARIGGEEFALLLVN 415
gi|152970532|ref|YP_001335641.      DHFKRINDSYGHVAGDKVIQFAASVLESHSRVDDAAARIGGEEFALLLVN 317
gi|311279495|ref|YP_003941726.      DHFKRINDSYGHLQGDKVIQFVASILQDSVRENDLAARIGGEEFALLLVN 379
gi|146311462|ref|YP_001176536.      DYFKRINDNYGHLQGDKVLQFVANLLMDSVRPQDITARIGGEEFVLLLSN 378
gi|311278699|ref|YP_003940930.      DFFKSINDKYGHQHGDKVIQFIAIKIQSLLRQNDILARIGGEEFALLLPG 382
                                    : ** :*  :**  **:.:   .  : .  * :*  .*: ** * ::

gi|253773261|ref|YP_003036092.      LNS-AQAKIIAERMRKNVELLTGFSNRYDVPEQMTISIGTVFSTGDTRNI 464
gi|311280103|ref|YP_003942334.      INNREMAKNIAEKIRINIERNTSIDGYYNLPESMTVCIGVYFSTPIKHTS 417
gi|253324989|gb|ACT29591.1|         IDT-ERAKALAERIRENVERLTGDNPEYAIPQKVTISIGAVVTQENALNP 418
gi|157155149|ref|YP_001461960.      NTQ-KLLLSIAERIRKNIEEQCSEKLLSHGPEKITVSIGCFTSKENNLSP 416
gi|238895023|ref|YP_002919757.      TGE-KEAQAIAERIRLAVSAGES-----HLPERMTISMGVYTTYDNSVTA 459
gi|152970532|ref|YP_001335641.      TGE-KEAQAIAERIRLAVSAGES-----HLPERMTISMGVYTTYDNSVTA 361
gi|311279495|ref|YP_003941726.      TSS-EEAYRVAERIRLIISEHDAQSSSGSFPEKITISMGVFTTTSAGLGV 428
gi|146311462|ref|YP_001176536.      THS-EAARLVAERIRLSLSSFDRITTEGMLPESVTISMGIYTATTLPVTA 427
gi|311278699|ref|YP_003940930.      VNE-ENAKIIAERICHAVSQHDSKNTDIHQSERITISMGIYSATDNTMTE 431
                                             :**::   :.           .: :*:.:*   :

gi|253773261|ref|YP_003036092.      SLVMTEADKALREAKSEGGNKVIIHHI------------------- 491
gi|311280103|ref|YP_003942334.      SEAMRLADIALYQAKNSGRNKVIVYEPSFDAPPPARGEEH------ 457
gi|253324989|gb|ACT29591.1|         NEIYRLADNALYEAKETGRNKVVVRDVVNFCESP------------ 452
gi|157155149|ref|YP_001461960.      SEMLVNADKALYQAKRTGKNKVIIHSK------------------- 443
gi|238895023|ref|YP_002919757.      EACVQRADEAMYEAKNNGRNQVIVWHQQGG---------------- 489
gi|152970532|ref|YP_001335641.      EACVQRADEAMYEAKNNGRNQVIVWHQQGG---------------- 391
gi|311279495|ref|YP_003941726.      EVCVQRADEAMYQAKENGRNRVVTWQPER----------------- 457
gi|146311462|ref|YP_001176536.      EECVERADKAMYEAKETGRNRVVVYQENKALRGKAFHDVSRGFATR 473
gi|311278699|ref|YP_003940930.      DVYISRADDAMYKAKHAGRNCVKVWQQ------------------- 458
                                    .     ** *: :**  * * *
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