

## Supplementary data

# Draft Genome Sequence of the Urinary Catheter Isolate *Enterobacter ludwigii* CEB04 with High Biofilm Forming Capacity

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Figure S1: Alignment of GGDEF domains in *E. ludwigii* CEB04. EL= *E. ludwigii*, ST= *S. typhimurium* and CC= *Caulobacter crescentus*.

|            |     |                                                                                                        |     |
|------------|-----|--------------------------------------------------------------------------------------------------------|-----|
| EL-1899    | 320 | IYQRSEWLKQDWQDRALTDPLTGLPNIRALEDFLQDHPD-----AKVCLLRMDNLEFLSRHYGILMRVHCKRMVTSLOPFL-QK-DERLFL            | 405 |
| EL-1965    | 315 | LATCQRAANKRRRLALLDPPVHMPRLALSRDLAKNPW-----SALCLLRIPLEVLGRNYGLLRILYKQQLAQWNGTL-QH-SERVYHL               | 400 |
| ST-STM2503 | 315 | LATRQRVYSRRARRLAYLDPVVHLPRLALNRALQNPW-----STICFLHVPGLLELLKNYGYMLRIQYKQKLSHWITPML-AS-NECVYQM            | 400 |
| EL-2988    | 227 | NOQMRQRQDELNSSATRFPPVELPNKAFLLMAMLEQTVARQQT-----TALMVIACTELDTACVLKENQRMLLTLVEKVKSVL-AP-RMVLTV          | 316 |
| EL-2734    | 210 | ADQRSRMDTLIRSYAAQDNKGLNRRLLFFDNQATLLDDPEKVGTH-----GVMMIRLPDFDRLRDTWGORVAEENLFTLINLLSTFIMRYPGALLAR      | 305 |
| EL-841     | 286 | SVAAINSILIRQVSLRADYDFLTHVYSRGLYEALKQEEAHRHSRF-----LTVMLLDIDYFKSINDNYGHECGDRTLAFAARQVQVV-GE-DMVMAR      | 377 |
| EL-842     | 149 | DGLALAEDEFAAVSAATDELGLFNRRGFNQLVRFILSVARRAEPP-----LTGLWLDLDRFKEINDRYGHEEGDKALNVMAQLMRSF-RE-ADLLVF      | 242 |
| EL-406     | 308 | DLSRKTRDNRAKLIASEDALGLFNRII FDEKILSEIAACAASDAP-----ISVLIYDVVDYFKKYNDNYGHEGDCRCLTLGNLSLRELNRD-NQVVAR    | 402 |
| EL-3489    | 284 | DITERKKAQQLEVKATTDLTGCFNRSTILQQLESALANARQDADSHFCVLMFDDFFKQINDRWGHQVGDRAIHFCQAIRESL-PE-NAALGRV          | 379 |
| EL-3421    | 441 | TIQSNKEREMAYVRQATHDALTCCKNRRAFDTDVEELMAAQPP-----FALALVDIDNFKSIINDTWGHLSCDIVLRNVAREGIOIM-QPHHISVYRY     | 531 |
| EL-4124    | 191 | TAIRLAEKRRRLMLSTRDGMTGVFNRRHWEVLLRNEFEHCRNRHCT-----ATILLIDIDHFKSINDTWGHDVGEAIIALTRQLQLTV-RS-GDAIGRF    | 284 |
| ST-Adra    | 194 | TAIKLAEKRRRLQAMSSRDGMTGVFNRRHWEILLRNEFDHSSRRHRE-----ATLLIIRIDHFKSINDTWGHDVGEAIIALTRQLQLTV-RG-SDIIGRF   | 287 |
| EL-1543    | 366 | MYSNMYTLQHSLLQQAWHDPILRLNRRGALFERAKMLSEKCRQSLP-----FSVIQIDIDHFKSINDRFHQAQDKVLSHAAGLISAL-RK-NDVAGRV     | 459 |
| EL-577     | 275 | LYRDSHIKYQSSYQNSIRDPILRLYNSYFYDTLNQALSI SKTNHP-----VSVIYSLDRFKRINDCYGHLQGDQKVLQFVANLLMDSV-RP-QDIAARI   | 367 |
| EL-3812    | 166 | LISRLLEERETLTDLSMMDPLTGLYNRRLGQSRLENLP AVEGE-----HFVLLMDIDHFKAYNDHYGHMMGDQALIRVSAARIDAV-RS-RDIAVAR     | 256 |
| EL-703     | 195 | RNQNNQLLISRLLEALAHQDPLTQIANRRKMEVVLLENAAVEQKKA-----FSLIMLIDIDHFKLYNDTYGHAQGECLTRVAQVLRQSV-RT-PDDVVSRY  | 285 |
| EL-1065    | 238 | DITEQKRLEQELEHAALRDSMTGLLNRQRFYIIDQANTHHLPAQQQ-----FSLLLVDIDHFKSINDLFGHLKGDEVLISLSRTLEACS-RK-EDLVFRW   | 331 |
| CC-PleD    | 274 | YDYLRNNLDHSLLEAVTDQLTGLHNRMYMTGLDLSLVKRAITLGGDP-----VSALLIDIDHFKSINDTFGHDIGDEVLRFAIRLASNV-RA-IDLPCTRY  | 367 |
| EL-4100    | 412 | LALANQRRLDALLEKALFDPGLTGLNRNHHLEDTLHTQMTQAIRNGEP-----LSCMMIDIDHFKSINDRFHQAQDKVLSHAAGLISAL-RK-NDVAGRV   | 505 |
| EL-1102    | 269 | LLLVHVSLLRFFGDRVNRDPLTQIFNRKYFFEALQRLRLMLRTEKG-----TSMIMLIDIDHFKSINDTFGHDIGDEVLRFAIRLASNV-RA-IDLPCTRY  | 360 |
| EL-2072    | 233 | WQLKLQAKNAQLLRTAMHDPGLTGLANRAAFRNSIAALMNDPAAKTN-----SALLFLDGDNFKSINDTWGHAAGDQVLEVARRMVEFG-DK-RHQSRL    | 325 |
| ST-STM2672 | 232 | WQLRLQAKNAQLLRTALHDPGLTGLANRAAFRNSIALMKNDSARSS-----SALLFLDGDNFKSINDTWGHAAGDQVLEVARRMVEFG-DK-RHQSRL     | 324 |
| EL-408     | 159 | LIQLREANAALIAHSYTDALGLPNRRAI FEELTLFLSLAKHLKRN-----AIIAFIDLDLDFKSLINDRYGHEGDRFLIEVKRLTEEK-QA-DEIIGRL   | 252 |
| EL-4362    | 211 | SKEILQQQNKKLAYDVYHDSLTGLKNRILFWDDLINNISIASRIHRP-----VTVMFLDLDRFKEVNSDFGHADGDLLEVAHRLSSMS-NE-TNIFYRL    | 304 |
| EL-1647    | 367 | DVTESRKMLRQLSYSSASHDALTHLANRVSFENHKLRLQLTVQETQR-----HALVFLDLDRFKAIVNDTGAHAAGDALLRELSLMLTML-RS-SDVLARL  | 460 |
| EL-1108    | 222 | DI TEERRAQERLRLANTDTITGLPNRAIHELI SDIASRGETQ-----GVVYLDLDRFKKVNDAIGHMFGDQLQAVAI LLSCL-DD-QVLARL        | 313 |
| ST-YcIR    | 219 | DI TEERRAQERLRLANTDTITGLPNRAIHELI FINHAISAGESQ-----GVVYLDLDRFKKINDAYGHMFGDQLQAVAI LLSCL-EE-DQLLARL     | 310 |
| EL-640     | 285 | DLYKLARGESQARLVARTDWLSHLPNRRALIEDLRVSLRGDIDV-----KSVYFLDLDGFKKVDNDIYGHVSGVDLIVTIAKTLNECV-PP-CGMLARM    | 376 |
| EL-1064    | 245 | LNDLRQLNRQLELQARFDALGLANRHQMDIRMQDCLRSALLSKPP-----FAVIFLNVDFHFKRINDTWGHNITGEDELLISLAQRITARL-TR-EMTLARL | 338 |
| EL-2748    | 246 | LASSLAEANRELAQLALQDGLTGLRPNRVLLIEDRLQDAISKADREGTH-----FALMFMDLDGFKTINDAYGHVGDQRLLVAVTQRLLTFL-KG-QFLARL | 339 |
| EL-1899    | 406 | PGSELVLVL-----LPGGTAE---RL-----GHMVDQLNSRKIVWNNTGLDI--EFGASWGMVENGKELHH-TLGLQLWLAEQSCGA-----HNVLAL     | 483 |
| EL-1965    | 401 | TGCDLAVRL-----NAESHQQ---RI-----FALDEHIKQRFVFDWGMP LQP---PVGVSVCYVRSVPVTHLYLVGLGEVIAADLSITNHPENLQQRGAV- | 484 |
| ST-STM2503 | 401 | SGHDLVRL-----NTEAHQQ---RI-----FALDKHIKQRFVFDWGL LQP---PVGVSVCYVRSVPVSHLYLLGLGSLTSDDLSTTAPEDLQRRGAMH    | 485 |
| EL-2988    | 317 | SGYDLVIA-----NGVKEPW---HAILTGLQVLTVINE-RLP LQIQL---RPSASIGIAMYYGDL---TAEGLYRRAFSAATARRKCKNOIQFFD       | 399 |
| EL-2734    | 306 | HRSDFAVLL-----PHRTLKE---SE-SIASQLLKAVDALPQSKMLDR-----DDMVHMGICAWRGGQ---SEGLVMEHAEEAATRNVAVLOGANGWAVYD  | 387 |
| EL-841     | 378 | GGEEFAVVV-----NSGDAQH---GF-ELAEIRITTVAAHPTWRQQTLYLTVSIGLGSCKSESQWLTE--VFNKLMAEADDDHLYRKKACGRNR         | 465 |
| EL-842     | 243 | GGEEFAVLF-----ADTDEQGAWIMQYLAEQVENYNARKLHPW-----SLLFSWGLSEFDHNGH--DLOGLWKEADEKMYAMKQQRHRR-----         | 321 |
| EL-406     | 403 | GGEEFALLL-----PDTDIQE---AL-RLGLTIRINVSLSLIEHAFSPFG---RVTVSVGLSTARAVDIAGSQQNI IIAADQALYQAKRACGRNR       | 489 |
| EL-3489    | 380 | GGEEFLLLL-----ARTDCNA---GA-LFSARLRTALKTNPLVVGDKKL---VLSFSAGAVEVCGQR--DTSGLLMRADKALYDAKRTGRGKTIVVAA     | 463 |
| EL-3421    | 532 | GGEEFAVVF-----EATQIAD---AI-SLLEAWRTTIEK--RVWREENL---QRTFSAGLGEWHFE---PLEGFVGSVDNALYSAKQQGNRI LQGS      | 611 |
| EL-4124    | 285 | GGEEFAVIM-----SRTAADS---AI-AVMSRVHERLETLSLPCAPKE-----SLRISVGVAPWGPQFG--HYREWKLKAADVVALYKAKNAGRGR       | 367 |
| ST-Adra    | 288 | GGEEFAVIM-----CPTADS---AI-TAMSRVHERLNTLRLPGAQPV---MLRISVGVAPLTPQIG--HYREWKLKSADMALYKAKNAGRGR           | 370 |
| EL-1543    | 460 | GGEEFCVVL-----PGSGLEE---AR-GIAERIRSRINSKEILVKKSTIV---RISASLGVSAQEKDNY-DFEQLQSVADARLYQAKQCGRNR          | 545 |
| EL-577     | 368 | GGEEFVLM-----TNTSSEA---AY-QVAERIRLKLSSFDKVS GGQLPE---SITISMGVFTATSPTT--TAEACVENADKAMYEAKE              | 453 |
| EL-3812    | 257 | GGEEFMVLL-----TNISLEH---AR-QIAERIRQKYVDLAKTPHMFNEIVAT-NVTISIGIAI FEDE----DAEGALEKADKALYEAHKMGRRN       | 341 |
| EL-703     | 286 | GGEEFVVL-----FDCPEENT---VE-KVAMRIQDGLRAEIAHDAASKISD---RVTYSMGIAGMAEGL---AGTIIARADEALYAKAAGRDRWSR--     | 368 |
| EL-1065    | 332 | GGEEFVILL-----PRTPLDT---AL-QIAETVRDAVAR---ITIPGLP---RFTVISIGVARNHPEGE--SMDLFKRVDDALYRAKSDGRNKVLA       | 410 |
| CC-PleD    | 368 | GGEEFVIM-----PDTALAD---AL-RIAEIRRMHVS GSPFTVAHGREML---NVTISIGVSAAGEGD--TPEALLKRADEGVYQAKASGRNAVVGKA    | 453 |
| EL-4100    | 506 | GGEEFLVLL-----SGADEEE---AH-DCAQIYNGVQGLSLRYGLTEIG--PVDVSIIGIASYPQHA--QSDNLLRAADVVALYRAKELGRSRI         | 589 |
| EL-1102    | 361 | GGEEFGLLL-----PDTDRSM---AV-VVAERIRKNVEQRTGQGNLYAVPL---TMTLSIGVCSATQENV--NSDIIRDVDEALYEAHKGGK           | 446 |
| EL-2072    | 326 | GGEEFAMVL-----YGVHSEP---EVQYLCAALSQQFIR--PFEHLNGQKA---SVLSIGFALAWENG---SVEALLKADRNNHVLKNQRTKTIN--      | 406 |
| ST-STM2672 | 325 | GGEEFAMVL-----YDVHSEY---EVQRI CAALSQAQFNR--PFEHLNGQRI---TMTLSIGFALWEHA---TAEKLELADRNMYQAKHRAER         | 406 |
| EL-408     | 253 | GGEEFLVASLSQTNSTGEST---QINLLKTRLDARLAGE-EYWLQGSVNII---YPLGASFGVIEVDPTVT--DPSALRAADVAMYQHKK-GKSK        | 340 |
| EL-4362    | 305 | GGEEFALLS-----HELTSES---AV-NLAMEICECKKK--PYIIGNSNY---TIGICVGIIVVSELER--RDYLYKFADLALYEAKRAGLNM          | 386 |
| EL-1647    | 461 | GGEEFGLLL-----PDCNIES---AR-YITGLRINTINDYHFWEGRLH---RIGASAGITLIDENNHH--QASEIMSQADIAICYAGK               | 544 |
| EL-1108    | 314 | GGEEFIVMA-----TDTSQGS---LE-AMASRILTRLRQ--PFRIGLIEI---YTGCSLGIALAPQHGN--DRESVIRNADTAMYAKENGRGK          | 396 |
| ST-YcIR    | 311 | GGEEFIVLA-----AHTSQAA---LE-AVASRILTRLRQ--PFRIGLIEI---YTGCAIGISLAPRHGQ--DRESLIRADTAMYNAGEGRG            | 393 |
| EL-640     | 377 | GGEEFAMTI-----GGEGAEA---LATTFAEVSVDLFLNT--PIRLGERTI---HIGASIGIASGTLIEC--TSELFRRADIAMYSKISGKGRV         | 460 |
| EL-1064    | 339 | GGDAFILLV-----PCDDDR---LN-ALLTTLLEDMMRR--PFSLCGHTL---STTISAGVSLYPODGE--TLHEKLLKADAALNRVKEDGRNG         | 421 |
| EL-2748    | 340 | GGDEFVLLA-----EGEGPDD---AA-SLANSLVRAIDS--PFLNDPYEL---VVTLSIGVSLYALPHDGK--TERELMFNDAAMYH                | 422 |



Figure S2: Alignment of EAL domains in *E. ludwigii* CEB04. EL= *E. ludwigii*, ST= *S. typhimurium* and PA= *Pseudomona aeruginosa*.

|            |     |                                                                 |                                                                                    |                                                          |      |     |
|------------|-----|-----------------------------------------------------------------|------------------------------------------------------------------------------------|----------------------------------------------------------|------|-----|
| EL-1647    | 859 | LDEQWHMIKDNH--LM--MI                                            | ARSVASPRIPESCENFWLILRLWTSQGE--VQEEHAFRSGLAEPPELLHALDRRIFFNEFFRTSAA--QVAHKCMGVA--LP | SEAGLAS-VTLVDELVDLLEKSPMPGR--LH                          | 978  |     |
| ST-STM1697 | 1   | -----MRY-----                                                   | FFMAEPIRAMEGDLLGVETTHFASSPARP--LHPEFVTSWDN--SQKRRFLDLRLTIAAKHGWFLRHGLFCI--VNI      | D-----RGMALVLQDKDIRAILHAMLFE                             | 102  |     |
| EL-2734    | 401 | -TLLEQMLSRGG-PR--                                               | IYQKPAV-MKNGNVHHRELMCRIFDGTTEEV--ISAE-YLPMVLQFGLSEEDRQQITRLMPFLSFW--P              | ENLA-LQVTVESLIR-PRFQRWLRRLMQCEKSQR-KHI                   | 514  |     |
| EL-2984    | 15  | EASLENLQEHRYWLQCERAYTYQPIY-RTDGRLMAIELTVVTHRNPSSQRIAPDRYFA----  | EVAVRQLDLVLEEQLRLMATKQAFFEQHAIIASVNDGPTLLA----                                     | LRQNAKLQELIALPW--MR                                      | 133  |     |
| ST-YhjH    | 13  | DAGLENLQEHRYWLQCERAYTYQPIY-QTDGRLMAVELLTVVTHRNPSSRRIAPDRYFA---- | ELAVRHRIDVVKELHQLLEQKADFFTRHLLASVNDGPTLLA----                                      | MRRQPDILAAMERLPW--LR                                     | 131  |     |
| EL-4271    | 9   | TPPRQLYLSQDI-VG--                                               | IKLEPIVALSSLRVGVVLSVLSEVQHS--EAFFR--HQ                                             | SADWSITLLEAQLTALKNTPHCNFF--INLPITVLTE-PDAFQRLSRIKCP--    | PLN  | 110 |
| EL-769     | 241 | ETALYNALLKRK-IF--                                               | PAYQIITDRYKKG-VGEILIRW-NNNGKI--IKPVNFLTDTSSQELWLKITALVIHAASGINKY--                 | NKYYFS-VNIPPRLASG-NALPDMAKKAVAMLLNPQWADKL                | V    | 357 |
| EL-524     | 170 | -SAQPEVVAAGADCS--                                               | FAFQPIVDFPMQVQVSWALIR--TGTGE--SGPTYFAQIPR--EEVYASDLKSKQVALSMASALGLQDOTLS--         | INLLPMTLVNVPGAVDFLLTAIDANGVPE--QIV                       | 283  |     |
| EL-905     | 160 | -FGESLGLDKQT-CQ--                                               | FALQPIVEPLEKISSLEALIR--GNDGG--SPEHFFSRLLDQ--DKIYEVDLQTKAWAFALADKLGI                | SHKIA-VNLLPMSLVKKVPGAVEFLVEQIKQHGLQPE--QVV               | 272  |     |
| EL-404     | 252 | ERTLVNAVKA--IS--                                                | VNYQPIRIRIDKKMGVGVLSRWRDNNHGE--VSPLEFIPLIKKIGLYQKYINIEKLAELIASLAIKHQ--LVIS-LN      | GRTEIED-GQFIKILCRECLVNSIPLS--LIK                         | 370  |     |
| PA-RocR    | 145 | -ADVVRGLDNGE-FE--                                               | AYYQPKVALDGGGLGAEVLARWNHPLHGV--LPPSHFLYVMETYNLVDKLFWQLFSQGLATRRKLAQLGQR--INLA-FNV  | VHPSQLGS-RALAENISALLTEFHLPPS--SVM                        | 263  |     |
| EL-1899    | 501 | -ARIKHALDAG-FH--                                                | LYAQPIQKADGSGY--EILTRM-ESEGEI--ITPDRFPLIAQTNLSHRFDMCMVEKLLVWLRDH-PATHAGVRFS-VN     | LMPLTLMQ-KEVAIEICSLFERYGAPQ--AVV                         | 616  |     |
| EL-1965    | 495 | MSRLQSALDSNA--FT--                                              | LLVQPVC-GVRGDCYH-EVLLRMSDANGAL--LSPLOFLPVAQEFGLSSRVLDVWVLENLIRFLAEH-RVHL           | PGORFA-INLGPSTVCR-AQPAEVSRLAKYAVEPW--QLI                 | 612  |     |
| EL-4205    | 273 | -NRLLDAINNRE-FV--                                               | VHYQPIELSSGKIVGAELTRWPQDGS--LSPDIFVPLAQTGILISQLTHLVIKVFEDMGYV-LHLHAGQHS--IN        | LAPADLTS-GKLPPLLSHLMNKWVHPQ--QIA                         | 391  |     |
| EL-3490    | 273 | -RLLQRALNKRK-LC--                                               | VHYQPIIDIKNNQCVGAELLRWPGFNGPV--MSPAEFPLAEKEGMSERITDYVVEEVFSDLGTF-LATHPHLYIS--IN    | SATDFHS-SRLIAMISDKARHYAVRAQ--QIK                         | 391  |     |
| ST-YjC     | 273 | -RLLQRAITRHL-LC--                                               | LHYQPIIDIRNCTCVGAELLRWPGYHGPV--MSPCEFPLAEKEGMIEQITDYVVEEVFNDLGGF-LAAHRLHYVS--IN    | LAAADFLS-SRLIVMIEHQRHSLAQ--QIK                           | 391  |     |
| EL-1108    | 416 | DTRLRKALDNRG-LL--                                               | IHYQPKI-TWRGEIRSLAEALRWQSPERGL--IPPLEFISYAESGLIVPLGRWVMDVVRQIAKWRDKIN-LRVA-VN      | FSARQLAD-QTIFSDLKQALKDLDFEYC--PID                        | 534  |     |
| ST-YciR    | 407 | DTRLRKALDNRG-LL--                                               | IHYQPKI-TWRGEVRSLEALRWQSPERGL--IPPLEFISYAESGLIVPLGRWVMDVVRQIAKWRDKIN-LRVA-VN       | FSARQLAD-QTIFSDLKQALKDLDFEYC--PID                        | 525  |     |
| EL-640     | 474 | ENQIRNGLERDGE-FE--                                              | VWYQPIIDARSOQMSVVALRWRRRPEGE-LGPDTFISIAETSGLIYKLCQFVLQRAQDLEPY--SELKLS-VN          | ISPAQFRD-PEFEKVAWVLESTRFAR--RLQ                          | 589  |     |
| EL-2988    | 413 | ESDILTALDNRG-FA--                                               | LWLPQVNLTKKVISAEALLRVQPDGWS--ELPEGLIERIESCGLMVTGYWVLEEQRQLAAWQERGV--LPLS-VN        | LSALQLMH-PTMVSEMLEIHRIRIKPD--TIT                         | 532  |     |
| EL-1383    | 271 | -WEINLGLAARE-FE--                                               | LFCQPLLNARTQKCVGEILLRWNNRQGW--ISPDVFIPLAEHNLIPLTRYVINEVVSQIGYE--PAT                | GFHIG-INAAASHFRH-GTILQDLNRYW-FSAHBTQ--QLI                | 387  |     |
| EL-1650    | 225 | -GRSLALKNDE-IL--                                                | PYYQPVV-GAGGELCGEILARWPLGHNYT--ISQREFIPLAESCGLINELTSYLMHKVASDLKQKSNGLNTP           | LFVA-FNVSPITLSN-PVFWECLNLELLELPV--KLM                    | 343  |     |
| EL-1742    | 265 | GKEILSAIKRG-FY--                                                | VVYQPVVDAETLQMRGEVLMRWKHPTMGE--IPPDAFINFAEAQKLIVPLTLHLFDLLIRDAVPLQTLPPGAKLG-INI    | APGHLHA-ESFKEDMRTFLDLMPDPH--QIV                          | 385  |     |
| EL-405     | 250 | EDDLRKAIIHGE-IV--                                               | PYYQPIVNGDTGGLYGVVALRWKHPKSGF--IPPDVFIPLAERSGLIPLTKGLMAKVTLEKLPPLKPLDGFHIG-VN      | SARHINA-PSFIADCRVFGKGFYKCEV--KLV                         | 370  |     |
| EL-4362    | 400 | ERDLISAVANKEL-LV--                                              | VYQPIVDSYTTIEIYGYEALLRWNNHVPKGI--IAPDDFISVAEKTGFHIEHGAALAEIACKETATW--KV            | PARIS-VNVSFVQLSS-MNFVDTRVAVLALGLAT--RLE                  | 516  |     |
| EL-1064    | 436 | -QELTQALERDGE-FE--                                              | LWYQPIWHAKDTTHGFEALLRWRRPEQGV--LLPNLFLPSLEQTGLIPVGNWAI                             | EACRQLHFWEQGFQSWTLS-FNLSPVQFEQ-PDIFHIISSMLHKYNLSPS--RLI  | 555  |     |
| EL-2748    | 436 | MNDLWLALIDRNGE-LR--                                             | LLYQPKFHAPAGPVVLFGEALLRWQHPKQGL--LTPDLFLPLAETKGLIPIGNWV                            | LNEACRQLREWHLQGHQNSMA-VNLSLQFEQ-PSLVKTVLDCLTRHNVPPE--MEI | 556  |     |
| EL-1647    | 979 | LVLIADVVCC----NPDKNLQQGLQKL RHAGCRVVL SQVGRDMNV--               | FSHLSANMADYLMLDTEMVTNMYGNLMDMMVTVIQGHAQRGMKTIAGPCNQPI                              | MMDTLSGIGIDFI-YGDTIAEPQLDLL                              | 1100 |     |
| ST-STM1697 | 103 | LQVAIEHFC----QDNALIDPLIHALHKKNPWLGLDQGNAT--                     | AAPLVCCGFSCKLDRSFF--VSIQIEKMPLLVKHIRRYCDKIVVGGQENTRYL                              | PVLKTAGIWA--GTLFLSVALEEV-                                | 219  |     |
| EL-2734    | 515 | FELAEADVCG--QHISRLRPVRLINALGRVAVTQAGLTLVS--                     | TNWIKVEDCFLKLHLPGLVRNIEKRTENQLLVGLVEACKGRQVFATGVR                                  | SRSEWQMLTEKVTGG-QGDFFAQPLD-                              | 635  |     |
| EL-2984    | 134 | FELVEHVRLL-----PQDSSFASMCFCG-PLWLDDFGTGMAN--                    | FSALSEVRDYIKVARDLFIMLRQTPEGRNLTLLQLLMNRYCQGVIVEGVET                                | LDWRDVQNSPAAAA-QGYFLSRPVPMDLT-                           | 250  |     |
| ST-YhjH    | 132 | FELVEHVRLL-----PKDSSFASMCFCG-PLWLDDFGTGMAN--                    | FSALSEVRDYIKVARDLFIMLRQTPEGRNLTLLQLLMNRYCQGVIVEGVET                                | LDWRDVQNSPAAAA-QGYFLSRPVPPLISL                           | 248  |     |
| EL-4271    | 111 | IELVDPSAFLTLSSAAQRQTVTRSLQLLIRQCHGIWLDIDETLIP--                 | PFLSCQLPLSCVKKIDDAFWRLRATPALRQLVSRCEQLAG--KVLI                                     | EGIETEEDCTWALQACAEFG-QGYWPSWTPED-                        | 232  |     |
| EL-769     | 358 | FEFAEDIDV--TKDRTIPETMRRLRNCGRLFLDDCFNHTQ--                      | MFPVRQVHFDGKLDRDIVEHFVANDNDYNIKAQIYSDMGTDICIAEGVDS                                 | EKFELVALGVKSF-QGYLLSAVKEDE-                              | 478  |     |
| EL-524     | 284 | VEFESEAI--SRFEETHSVRLKKSAGISVTIDHFGAGFAG--                      | LQLLAQFQPDRIKIRDLVANVHNSGPRQAIQAAITCCSSLEIQFCAGVGEK                                | PEWMWLESAGISQF-QGYLLSRPHGGIP-                            | 405  |     |
| EL-905     | 273 | IEVENEMI--SGFNKFNSAIKHLRAEGILGLAIDFGSGYAG--                     | LSLLTRFQPKIKIDREIVSNHLSGPKQAIVRISVSCCTDLIELTVAEGI                                  | EKLLEWCWLESAGIRRF-QGFLFARPALNGV-                         | 393  |     |
| EL-404     | 371 | VELSEKA-V--STADVLEGFCQALKSLGVRIISIDDFGVQNN--                    | LARISLLEYDEIKIDKSLVDGII-NEHYKQNI FVIFDALARLNKT                                     | LVFEGVESETYRFIADRYPDALIGWYFSLTIDE-                       | 490  |     |
| PA-RocR    | 264 | FEITEGLI--SAPASLENLVRRLIMCGGLAMDDFAGYSS--                       | LDRLCEFPFSQIKLDRTFVQMKMTQPRSCAVISVVALAQA                                           | LGISLVVEGVSEDEQRVRLIELGCSIA-QGYLFARMPPEQH-               | 384  |     |
| EL-1899    | 617 | IEFEQA--SNSGSSIKNIQQLRDCGFRIADDFGTGYAN--                        | YERLRLRLQADIKIDGCFVKDICTDDMDAMIVQSI CNLAKTKSLSVVA                                  | YVETPEERKELLHFGVDYL-QGYLIGKPKPLNE-                       | 737  |     |
| EL-1965    | 613 | FEVTECSTF--GSGEQALHTLRQLQKMCVRIAIDFGTGYAS--                     | YARLKSVDADILKIDGSIIRNIVNNSLDQIVASICH LARMKKMLVVA                                   | YVETTEEIRSAVHALGIDYV-QGYLIGRPVALE--                      | 732  |     |
| EL-4205    | 392 | LELTERG-F--ADPKISAPAI AAFRHSGCHAIYIDDFGTGYSS--                  | LSYLQDLVDVTLKIDAFVDAL--EYKNVTPIHIEMAKSLKAMVAEGV                                    | ETEGCLAWLRRHGVQYG-QGWYYSKALPKAD-                         | 507  |     |
| EL-3490    | 392 | IEVTERG-F--IDVPKTPVIAQFRQAGYEVAIDDFGTGYAN--                     | LHNLYSLNVDIKIDKSFIDTLTNTSHLIAEHIEMAQSRLKIIAEGVTA                                   | EQVSWLLKRGVQFC-QWHFAKAMPPE-                              | 511  |     |
| ST-YjC     | 392 | VEVTERG-F--IDVPKMTPIIAQFRQAGYEVAIDDFGTGYAN--                    | LHNLYSLNVDIKIDKSFIDTLTNTSASHLIVEHIIEMAQSRLKIIAEGVTA                                | EQVSWLLKRGVQFC-QWHFAKAMPPE-                              | 511  |     |
| EL-1108    | 535 | VELTESCLI--ENEELALSVIQQFSKLCAQIHLDDFGTGYSS--                    | LSQLARFPIDAKLDDSFVRDIHQKISQSLVRAIYAVAAQLNLQVIAEGV                                  | SAKEDAFLTKNGVNER-QGFLFAKMPMAA-                           | 655  |     |
| ST-YciR    | 526 | VELTESCLI--ENDTLALSVIQQFSKLCAQIHLDDFGTGYSS--                    | LSQLARFPIDAKLDDSFVRDIHQKIPLSQSLVRAIYAVAAQLNLQVIAEGV                                | ENAKEDAFLTKNGVNER-QGFLFAKMPMAA--                         | 644  |     |
| EL-640     | 590 | LEVTEYVVL--ENPERARTAIANLKA LGTAVALLDDFGTGYSS--                  | IGYLRFFNFDTIKIDKSLAGLVNDNEQAALVSGVRIANALGM                                         | AVVAEGVNEKOMKLLRLACDQL-QGFWFSQMPPIE--                    | 709  |     |
| EL-2988    | 533 | LEVESRRI--DDNEAVAILKPLRNAGIRIALDDFGMGYAGLRQ                     | LQHMKTLPVVDVLIKIDAFVEGL--PEDSSMVQAIQLARSLKLQLIAEGI                                 | ETDARTWLAEEAGVEGG-QGFLFAPAVPSD-                          | 652  |     |
| EL-1383    | 388 | VELTERDAL--QDVY--RIYRELHRQCVKLAIDDFGTGNS--                      | LSWLEKLHPDLVKIDKSFVTAITGDVANSVTDIILGQLRSI                                          | GLVAEGVTEQARYLRHGEVLEL-QGFLFAPMPLE-                      | 506  |     |
| EL-1650    | 344 | IEITENQTL--AVTAKELIRSLRNRGVMFALDDFGTGYAN--                      | LCYLINELELDVKKIDKTFINAIQADNQPLPMLSEINILAMI                                         | GLRTVAEGVEYAYRREWLSKQVDYL-QGYHFLPPVPFAD-                 | 464  |     |
| EL-1742    | 386 | LEITERD-M--VNHREANNLFEWLHNEGFEIADDFGTGHS--                      | LILYERFTMDYIKIDKSFVNAITETVTSVLDVAVTLARRLNMS                                        | VAEGVTEPEQAAWLREGVVFL-QGYWISRPMPLEQ-                     | 505  |     |
| EL-405     | 371 | LEITERPL--IDNPHLVENLHNA GFVIALDDFGTGYSG--                       | LSCLHALAIDYIKIDKSFVNRVS EAKDSTILLDCVIDLAKKLS                                       | LHIVAEGETKEQLDYLNRNQITLL-QGYFCKPVSQAQI                   | 492  |     |
| EL-4362    | 517 | LEVTESSLF--TDSETPIEILMALRVLGKISIDDFGTGYSS--                     | LSRLIQLGFDKIKIDKSFVRTISTDEETQIATKLMYGM                                             | AKMDMVI AEGVETNDQLLCLQRLGCDLA-QGYLFGKPPAF--              | 635  |     |
| EL-1064    | 556 | LEVTESSLF--KNLDRSIELLANFNQAGITVSIIDDFGTGYAN--                   | LLMLSVLPKELKIDKSFVHSMVLNNEKSRKLTVINI                                               | INARTMENVVAEGIETQEQVVLDTLDCGYL-QGFLFGRPLAEQ-             | 676  |     |
| EL-2748    | 557 | LEVTESSLF--SNPDESVRVLTETDAGVKASIDDFGTGYSS--                     | LLYLKRLPACELKIDKAFVKELSGESEDATIVSAI                                                | VALAKTLNLKVVAEGVTEAQTFLTALCNTL-QGYLLCKPVSQAQ-            | 677  |     |