## SUPPLEMENTARY DATA

### *Data in the Relational Database*

**Table B.1. Amino Acid Information**

| Amino ID | Amino Acid | Mass |
|---|---|---|
| 1 | A | 71.03711 |
| 2 | C | 103.0092 |
| 3 | E | 129.0426 |
| 4 | D | 115.0269 |
| 5 | G | 57.02146 |
| 6 | F | 147.0684 |
| 7 | I | 113.0841 |
| 8 | H | 137.0589 |
| 9 | K | 128.095 |
| 10 | M | 131.0405 |
| 11 | L | 113.0841 |
| 12 | N | 114.0429 |
| 13 | Q | 128.0586 |
| 14 | P | 97.05276 |
| 15 | S | 87.03203 |
| 16 | R | 156.1011 |
| 17 | T | 101.0477 |
| 18 | W | 186.0793 |
| 19 | V | 99.06841 |
| 20 | Y | 163.0633 |

**Table B.2. Enzyme Information**

| EnzID | EnzName | CutPosition | AA_Postion | Exception | Comment |
|---|---|---|---|---|---|
| 1 | Trypsin | C-Terminal | K, R | P | K, R not follow by P |

**Table B.3. Post-Translational Modification Information**

| ModID | Category | TypeMod | Condition1 | Condition2 | Added Mass | Comment |
|---|---|---|---|---|---|---|
| 1 | 0 | Acetyl (K) | K | 0 | 42.01057 | modify K |
| 2 | 0 | Acetyl (N-term) | NT | 0 | 42.01057 | every fragment(1) |
| 3 | 0 | Acetyl (Protein N-term) | PNT | 0 | 42.01057 | 1st fragment of each protein(0) |
| 4 | 0 | Carbamidomethyl (C) | C | 0 | 57.02146 | modify C |
| 5 | 0 | Carbamyl (K) | K | 0 | 43.00581 | modify K |
| 6 | 0 | Carbamyl (N-term) | NT | 0 | 43.00581 | every fragment |
| 7 | 0 | Carboxymethyl (C) | C | 0 | 58.00548 | modify C |
| 8 | 0 | Guanidinyl (K) | K | 0 | 42.0218 | modify K |
| 9 | 1 | ICAT-C (C) | C | 0 | 227.127 | modify C |
| 10 | 1 | ICAT-C:13C (9) (C) | C | 0 | 236.1572 | modify C |
| 11 | 1 | ICPL (K) | K | 0 | 105.0215 | modify K |
| 12 | 1 | ICPL (Protein N-term) | PNT | 0 | 105.0215 | 1st fragment of each protein |
| 13 | 1 | ICPL:13C (6) (K) | K | 0 | 111.0416 | modify K |
| 14 | 1 | ICPL:13C (6) (Protein N-term) | PNT | 0 | 111.0416 | 1st fragment of each protein |
| 15 | 1 | ICPL:2H (4) (K) | K | 0 | 109.0466 | modify K |
| 16 | 1 | ICPL:2H (4) (Protein N-term) | PNT | 0 | 109.0466 | 1st fragment of each protein |
| 17 | 1 | iTRAQ4plex (K) | K | 0 | 144.1021 | modify K |
| 18 | 1 | iTRAQ4plex (N-term) | NT | 0 | 144.1021 | every fragment |
| 19 | 1 | iTRAQ4plex (Y) | Y | 0 | 144.1021 | modify Y |
| 20 | 1 | iTRAQ8plex (K) | K | 0 | 304.2054 | modify K |
| 21 | 1 | iTRAQ8plex (N-term) | NT | 0 | 304.2054 | every fragment |
| 22 | 1 | iTRAQ8plex (Y) | Y | 0 | 304.2054 | modify Y |
| 23 | 0 | Methyl (C-term) | CT | 0 | 14.01565 | every fragment |
| 24 | 0 | Methyl (DE) | D | E | 14.01565 | modify D and E |
| 25 | 0 | Methylthio (C) | C | 0 | 45.98772 | modify C |
| 26 | 0 | Oxidation (HW) | H | W | 15.99492 | modify H and W |
| 27 | 0 | Oxidation (M) | M | 0 | 31.98983 | modify M |
| 28 | 0 | Phospho (ST) | S | T | 97.9769 | modify S and T |
| 29 | 0 | Phospho (Y) | Y | 0 | 79.96633 | modify Y |
| 30 | 0 | Sulfo (S) | S | 0 | 79.95682 | modify S |
| 31 | 0 | Sulfo (T) | T | 0 | 79.95682 | modify T |
| 32 | 0 | Sulfo (Y) | Y | 0 | 79.95682 | modify Y |
| 33 | 1 | TMT(K) | K | 0 | 224.1525 | modify K |
| 34 | 1 | TMT (N-term) | NT | 0 | 224.1525 | every fragment |
| 35 | 1 | TMT2plex (K) | K | 0 | 225.1558 | modify K |
| 36 | 1 | TMT2plex (N-term) | NT | 0 | 225.1558 | every fragment |
| 37 | 1 | TMT6plex (K) | K | 0 | 229.1629 | modify K |
| 38 | 1 | TMT6plex (N-term) | NT | 0 | 229.1629 | every fragment |

## Table B.4. Protein Information of *E. coli*

| ProtID | Orf_name | Computer annotation | Sequences | length | protMass | pI_wiki | pI_EMB | pI_DTA | pI_Sol | pI_Sil | pI_Rod |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | YP_001728984.1 | thr operon leader peptide [*Escherichia coli* str. K-12 *substr*. DH10B] | MKRISTTITTTITITTGNGAG | 21 | 2119.130708 | 11.513428 | 11.652588 | 11.000732 | 11.528076 | 11.198486 | 11.498779 |
| 2 | YP_001728985.1 | fused aspartokinase I and homoserine dehydrogenase I [*Escherichia coli* str. K-12 *substr*. DH10B] | MRVLKFGGTSVANAERFLRVADILESNARQGQVATVLSAPAKITNHLVAMIEKTISGQDALPNISDAERIFAELLTGLAAAQPGFPLAQLKTFVDQEFAQIKHVLHGISLLGQCPDSINAALICRGEKMSIAIMAGVLEARGHNVTVIDPVEKLLAVGHYLESTVDIAESTRRIAASRIPADHMVLMAGFTAGNEKGELVVLGRNGSDYSAAVLAACLRADCCEIWTDVDGVYTCDPRQVPDARLLKSMSYQEAMELSYFGAKVLHPRTITPIAQFQIPCLIKNTGNPQAPGTLIGASRDEDELPVKGISNLNNMAMFSVSGPGMKGMVGMAARVFAAMSRARISVVLITQSSSEYSISFCVPQSDCVRAERAMQEEFYLELKEGLLEPLAVTERLAIISVVGDGMRTLRGISAKFFAALARANINIVAIAQGSSERSISVVVNNDDATTGVRVTHQMLFNTDQVIEVFVIGVGGVGGALLEQLKRQQSWLKNKHIDLRVCGVANSKALLTNVHGLNLENWQEELAQAKEPFNLGRLIRLVKEYHLLNPVIVDCTSSQAVADQYADFLREGFHVVTPNKKANTSSMDYYHQLRYAAEKSRRKFLYDTNVGAGLPVIENLQNLLNAGDELMKFSGILSGSLSYIFGKLDEGMSFSEATTLAREMGYTEPDPRDDLSGMDVARKLLILARETGRELELADIEIEPVLPAEFNAEGDVAAFMANLSQLDDLFAARVAKARDEGKVLRYVGNIDEDGVCRVKIAEVDGNDPLFKVKNGENALAFYSHYYQPLPLVLRGYGAGNDVTAAGVFADLLRTLSWKLGV | 820 | 89045.79721 | 5.265381 | 5.385986 | 5.677979 | 5.366943 | 5.601807 | 5.303467 |
| 3 | YP_001728986.1 | homoserine kinase [*Escherichia coli* str. K-12 *substr*. DH10B] | MVKVYAPASSANMSVGFDVLGAAVTPVDGALLGDVVTVEAAETFSLNNLGRFADKLPSEPRENIVYQCWERFCQELGKQIPVAMTLEKNMPIGSGLGSSACSVVAALMAMNEHCGKPLNDTRLLALMGELEGRISGSIHYDNVAPCFLGGMQLMIEENDIISQQVPGFDEWLWVLAYPGIKVSTAEARAILPAQYRRQDCIAHGRHLAGFIHACYSRQPELAAKLMKDVIAEPYRERLLPGFRQARQAVAEIGAVASGISGSGPTLFALCDKPETAQRVADWLGKNYLQNQEGFVHICRLDTAGARVLEN | 310 | 33583.89254 | 5.252686 | 5.392334 | 5.658936 | 5.360596 | 5.608154 | 5.303467 |
| 4 | YP_001728987.1 | threonine synthase [*Escherichia coli* str. K-12 *substr*. DH10B] | MKLYNLKDHNEQVSFAQAVTQGLGKNQGLFFPHDLPEFSLTEIDEMLKLDFVTRSAKILSAFIGDEIPQEILEERVRAAFAFPAPVANVESDVGCLELFHGPTLAFKDFGGRFMAQMLTHIAGDKPVTILTATSGDTGAAVAHAFYGLPNVKVVILYPRGKISPLQEKLFCTLGGNIETVAIDGDFDACQALVKQAFDDEELKVALGLNSANSINISRLLAQICYYFEAVAQLPQETRNQLVVSVPSGNFGDLTAGLLAKSLGLPVKRFIAATNVNDTVPRFLHDGQWSPKATQATLSNAMDVSQPNNWPRVEELFRRKIWQLKELGYAAVDDETTQQTMRELKELGYTSEPHAAVAYRALRDQLNPGEYGLFLGTAHPAKFKESVEAILGETLDLPKELAERADLPLLSHNLPADFAALRKLMMNHQ | 428 | 47066.21502 | 4.998779 | 5.068604 | 5.405029 | 5.119385 | 5.335205 | 5.043213 |
| 5 | YP_001728988.1 | hypothetical protein ECDH10B_0005 [*Escherichia coli* str. K-12 *substr*. DH10B] | MKKMQSIVLALSLVLVAPMAAQAAEITLVPSVKLQIGDRDNRGYYWDGGHWRDHGWWKQHYEWRGNRWHLHGPPPPPRHHKKAPHDHHGGHGPGKHHR | 98 | 11329.76301 | 10.671143 | 10.773682 | 10.158447 | 10.568604 | 10.429443 | 10.993408 |
| 6 | YP_001728989.1 | hypothetical protein ECDH10B_0006 [*Escherichia coli* str. K-12 *substr*. DH10B] | MLILISPAKTLDYQSPLTTTRYTLPELLDNSQQLIHEARKLTPPQISTLMRISDKLAGINAARFHDWQPDFTPANARQAILAFKGDVYTGLQAETFSEDDFDFAQQHLRMLSGLYGVLRPLDLMQPYRLEMGIRLENARGKDLYQFWGDIITNKLNEALAAQGDNVVINLASDEYFKSVKPKKLNAEIIKPVFLDEKNGKFKIISFYAKKARGLMSRFIIENRLTKPEQLTGFNSEGYFFDEDSSSNGELVFKRYEQR | 258 | 29549.30289 | 7.36792 | 7.726807 | 7.477783 | 7.660889 | 7.521729 | 7.265381 |
| 7 | YP_001728990.1 | transporter [*Escherichia coli* str. K-12 *substr*. DH10B] | MPDFFSFINSVLWGSVMIYLLFGAGCWFTFRTGFVQFRYIRQFGKSLKNSIHPQPGGLTSFQSLCTSLAARVGSGNLAGVALAITAGGPGAVFWMWVAAFIGMATSFAECSLAQLYKERDVNGQFRGGPAWYMARGLGMRWMGVLFAVFLLIAYGIIFSGVQANAVARALSFSFDFPPLVTGIILAVFTLLAITRGLHGVARLMQGFVPLMAIIWVLTSLVICVMNIGQLPHVIWSIFESAFGWQEAAGGAAGYTLSQAITNGFQRSMFSNEAGMGSTPNAAAAAASWPPHPAAQGIVQMIGIFIDTLVICTASAMLILLAGNGTTYMPLEGIQLIQKAMRVLMGSWGAEFVTLVVILFAFSSIVANYIYAENNLFFLRLNNPKAIWCLRICTFATVIGGTLLSLPLMWQLADIIMACMAITNLTAILLLSPVVHTIASDYLRQRKLGVRPVFDPLRYPDIGRQLSPDAWDDVSQE | 476 | 51610.72194 | 8.451904 | 8.715576 | 8.620361 | 8.63501 | 8.986572 | 8.532471 |
| 8 | YP_001728991.1 | transaldolase B [*Escherichia coli* str. K-12 *substr*. DH10B] | MTDKLTSLRQYTTVVADTGDIAAMKLYQPQDATTNPSLILNAAQIPEYRKLIDDAVAWAKQQSNDRAQQIVDATDKLAVNIGLEILKLVPGRISTEVDARLSYDTEASIAKAKRLIKLYNDAGISNDRILIKLASTWQGIRAAEQLEKEGINCNLTLLFSFAQARACAEAGVFLISPFVGRILDWYKANTDKKEYAPAEDPGVVSVSEIYQYYKEHGYETVVMGASFRNIGEILELAGCDRLTIAPALLKELAESEGAIERKLSYTGEVKARPARITESEFLWQHNQDPMAVDKLAEGIRKFAIDQEKLEKMIGDLL | 317 | 35179.30972 | 4.821045 | 4.840088 | 5.2146 | 4.960693 | 5.138428 | 4.871826 |

**(Table B4). Contd…..**

| ProtID | Orf_name | Computer annotation | Sequences | length | protMass | pI_wiki | pI_EMB | pI_DTA | pI_Sol | pI_Sil | pI_Rod |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 9 | YP_001728992.1 | molybdochelatase [*Escherichia coli* str. K-12 *substr*. DH10B] | MNTLRIGLVSISDRASSGVYQDKGIPALEEWLTSALTTPFELETRLIPDEQAIIEQTLCELVDEMSCHLVLTTGGTGPARRDVTPDATLAVADREMPGFGEQMRQISLHFVPTAILSRQVGVIRKQALILNLPGQPKSIKETLEGVKDAEGNVVVHGIFASVPYCIQLLEGPYVETAPEVVAAFRPKSARRDVSE | 195 | 21191.02092 | 4.636963 | 4.662354 | 5.011475 | 4.789307 | 4.979736 | 4.713135 |
| 10 | YP_001728993.1 | inner membrane protein associated with acetate transport [*Escherichia coli* str. K-12 *substr*. DH10B] | MGNTKLANPAPLGLMGFGMTTILLNLHNVGYFALDGIILAMGIFYGGIAQIFAGLLEYKKGNTFGLTAFTSYGSFWLTLVAILLMPKLGLTDAPNAQFLGVYLGLWGVFTLFMFFGTLKGARVLQFVFFSLTVLFALLAIGNIAGNAAIIHFAGWIGLICGASAIYLAMGEVLNEQFGRTVLPIGESH | 188 | 20039.64122 | 8.16626 | 8.44458 | 8.158936 | 8.605713 | 8.415283 | 8.122314 |
| 11 | YP_001728994.1 | hypothetical protein ECDH10B_0011 [*Escherichia coli* str. K-12 *substr*. DH10B] | MNVNYLNDSDLDFLQHCSEEQLANFARLLTHNEKGKTRLSSVLMRNELFKSMEGHPEQHRRNWQLIAGELQHFGGDSIANKLRGHGKLYRAILLDVSKRLKLKADKEMSTFEIEQQLLEQFLRNTWKKMDEEHKQEFLHAVDARVNELEELLPLLMKDKLLAKGVSHLLSSQLTRILRTHAAMSVLGHGLLRGAGLGGPVGAALNGVKAVSGSAYRVTIPAVLQIACLRRMVSATQV | 237 | 26630.06438 | 9.806885 | 9.924072 | 9.323486 | 9.762939 | 9.645752 | 10.158447 |
| 12 | YP_001728995.1 | hypothetical protein ECDH10B_0012 [*Escherichia coli* str. K-12 *substr*. DH10B] | MRVSWLESKCDTPFANNLSFISSGSSSSSSFTLASTACRNSCLCSSSIFFQVLRRNCSSNCCSISNVDISLSAFSFNRFETSSKMARYNLPCPRSLLAILSPPKCCNSPAISCQLRRCCSGCPSIDLNSSLRISTLERRVLPFSLWVSNRAKFANCSSLQC | 161 | 17607.42598 | 8.437256 | 8.759521 | 8.708252 | 8.620361 | 9.19165 | 8.569092 |
| 13 | YP_001728996.1 | hypothetical protein ECDH10B_0013 [*Escherichia coli* str. K-12 *substr*. DH10B] | MKSVFTISASLAISLMLCCTAQANDHKLLGAIAMPRNETNDLALKLPVCRIVKRIQLSADHGDLQLSGASVYFKAARSASQSLNIPSEIKEGQTTDWININSDNDNKRCVSKITFSGHTVNSSDMATLKIIGDD | 134 | 14454.33549 | 7.616943 | 7.961182 | 7.814697 | 7.829346 | 8.158936 | 7.682861 |
| 14 | YP_001728997.1 | chaperone Hsp70, co-chaperone with DnaJ [*Escherichia coli* str. K-12 *substr*. DH10B] | MGKIIGIDLGTTNSCVAIMDGTTPRVLENAEGDRTTPSIIAYTQDGETLVGQPAKRQAVTNPQNTLFAIKRLIGRRFQDEEVQRDVSIMPFKIIAADNGDAWVEVKGQKMAPPQISAEVLKKMKKTAEDYLGEPVTEAVITVPAYFNDAQRQATKDAGRIAGLEVKRIINEPTAAALAYGLDKGTGNRTIAVYDLGGGTFDISIIEIDEVDGEKTFEVLATNGDTHLGGEDFDSRLINYLVEEFKKDQGIDLRNDPLAMQRLKEAAEKAKIELSSAQQTDVNLPYITADATGPKHMNIKVTRAKLESLVEDLVNRSIEPLKVALQDAGLSVSDIDDVILVGGQTRMPMVQKKVAEFFGKEPRKDVNPDEAVAIGAAVQGGVLTGDVKDVLLLDVTPLSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSAKDKNSGKEQKITIKASSGLNEDEIQKMVRDAEANAEADRKFEELVQTRNQGDHLLHSTRKQVEEAGDKLPADDKTAIESALTALETALKGEDKAAIEAKMQELAQVSQKLMEIAQQQHAQQQTAGADASANNAKDDDVVDAEFEEVKDKK | 638 | 69054.47579 | 4.560791 | 4.579834 | 4.973389 | 4.681396 | 4.852783 | 4.573486 |
| 15 | YP_001728998.1 | chaperone Hsp40, co-chaperone with DnaK [*Escherichia coli* str. K-12 *substr*. DH10B] | MAKQDYYEILGVSKTAEEREIRKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEAYEVLTDSQKRAAYDQYGHAAFEQGGMGGGGFGGGADFSDIFGDVFGDIFGGGRGRQRAARGADLRYNMELTLEEAVRGVTKEIRIPTLEECDVCHGSGAKPGTQPQTCPTCHGSGQVQMRQGFFAVQQTCPHCQGRGTLIKDPCNKCHGHGRVERSKTLSVKIPAGVDTGDRIRLAGEGEAGEHGAPAGDLYVQVQVKQHPIFEREGNNLYCEVPINFAMAALGGEIEVPTLDGRVKLKVPGETQTGKLFRMRGKGVKSVRGGAQGDLLCRVVVETPVGLNERQKQLLQELQESFGGPTGEHNSPRSKSFFDGVKKFFDDLTR | 376 | 41056.47279 | 7.587646 | 7.924561 | 7.843994 | 7.726807 | 8.195557 | 7.682861 |
| 16 | YP_001728999.1 | IS186/IS421 transposase [*Escherichia coli* str. K-12 *substr*. DH10B] | MNYSHDNWSAILAHIGKPEELDTSARNAGALTRRREIRDAATLLRLGLAYGPGGMSLREVTAWAQLHDVATLSDVALLKRLRNAADWFGILAAQTLAVRAAVTGCTSGKRLRLVDGTAISAPGGGSAEWRLHMGYDPHTCQFTDFELTDSRDAERLDRFAQTADEIRIADRGFGSRPECIRSLAFGEADYIVRVHWRGLRWLTAEGMRFDMMGFLRGLDCGKNGETTVMIGNSGNKKAGAPFPARLIAVSLPPEKALISKTRLLSENRRKGRVVQAETLEAAGHVLLLTSLPEDEYSAEQVADCYRLRWQIELAFKRLKSLLHLDALRAKEPELAKAWIFANLLAAFLIDDIIQPSLDFPPRSAGSEKKN | 370 | 40865.22403 | 8.437256 | 8.715576 | 8.532471 | 8.664307 | 8.906006 | 8.517822 |
| 17 | YP_001729000.1 | regulatory protein for HokC, overlaps CDS of hokC [*Escherichia coli* str. K-12 *substr*. DH10B] | MLNTCRVPLTDRKVKEKRAMKQHKAMIVALIVICITAVVAALVTRKDLCEVHIRTGQTEVAVFTAYESE | 69 | 7719.162545 | 9.228271 | 9.440674 | 9.059814 | 9.491943 | 9.447998 | 9.411377 |
| 18 | YP_001729001.1 | toxic membrane protein, small [*Escherichia coli* str. K-12 *substr*. DH10B] | MKQHKAMIVALIVICITAVVAALVTRKDLCEVHIRTGQTEVAVFTAYESE | 50 | 5479.921998 | 7.023682 | 7.419189 | 7.287354 | 7.148193 | 7.397217 | 7.009033 |
| 19 | YP_001729002.1 | sodium-proton antiporter [*Escherichia coli* str. K-12 *substr*. DH10B] | MKHLHRFFSSDASGGIILIIAAILAMIMANSGATSGWYHDFLETPVQLRVGSLEINKNMLLWINDALMAVFFLLVGLEVKRELMQGSLASLRQAAFPVIAAIGGMIVPALLYLAFNYADPITREGWAIPAATDIAFALGVLALLGSRVPLALKIFLMALAIIDDLGAIIIIALFYTNDLSMASLGVAAVAIAVLAVLNLCGARRTGVYILVGVVLWTAVLKSGVHATLAGVIVGFFIPLKEKHGRSPAKRLEHVLHPWVAYLILPLFAFANAGVSLQGVTLDGLTSILPLGIIAGLLIGKPLGISLFCWLALRLKLAHLPEGTTYQQIMVVGILCGIGFTMSIFIASLAFGSVDPELINWAKLGILVGSISSAVIGYSWLRVRLRPSV | 388 | 41310.87065 | 9.609131 | 9.550537 | 9.19165 | 9.52124 | 9.440674 | 9.565186 |

**(Table B4). Contd…..**

| **ProtID** | **Orf_name** | **Computer annotation** | **Sequences** | **length** | **protMass** | **pI_wiki** | **pI_EMB** | **pI_DTA** | **pI_Sol** | **pI_Sil** | **pI_Rod** |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 20 | YP_001729003.1 | DNA-binding transcriptional activator [*Escherichia coli* str. K-12 *substr.* DH10B] | MSMSHINYNHLYYFWHVYKEGSVVGAAEALYLTPQTITGQIRALEERLQGKLFKRKGRGLEPSELGELVYRYADKMFTLSQEMLDIVNYRKESNLLFDVGVADALSKRLVSSVLNAAVVEGEPIHLRCFESTHEMLLEQLSQHKLDMIISDCPIDSTQQEGLFSVRIGECGVSFWCTNPPPEKPFPACLEERRLLIPGRRSMLGRKLLNWFNSQGLNVEILGEFDDAALMKAFGAMHNAIFVAPTLYAYDFYADKTVVEIGRVENVMEEYHAIFAERMIQHPAVQRICNTDYSALFSPAVR | 301 | 34244.23491 | 5.531982 | 5.83667 | 5.957275 | 5.589111 | 5.893799 | 5.557373 |
| 21 | YP_001729004.1 | IS1 transposase InsAB' [*Escherichia coli* str. K-12 *substr*. DH10B] | MPGNSPHYGRWPQHDFTSLKKLRPQSVTSRIQPGSDVIVCAEMDEQWGYVGAKSRQRWLFYAYDSLRKTVVAHVFGERTMATLGRLMSLLSPFDVVIWMTDGWPLYESRLKGKLHVISKRYTQRIERHNLNLRQHLARLGRKSLSFSKSVELHDKVIGHYLNIKHYQ | 167 | 19534.19771 | 10.627197 | 10.64917 | 10.121826 | 10.473389 | 10.348877 | 10.795654 |
| 22 | YP_001729005.1 | IS1 repressor protein InsA [*Escherichia coli* str. K-12 *substr*. DH10B] | MASVSISCPSCSATDGVVRNGKSTAGHQRYLCSHCRKTWQLQFTYTASQPGTHQKIIDMAMNGVGCRATARIMGVGLNTILRHLKNSGRSR | 91 | 9843.868046 | 10.773682 | 10.861572 | 10.282959 | 10.678467 | 10.539307 | 10.868896 |
| 23 | YP_001729006.1 | 30S ribosomal subunit protein S20 [*Escherichia coli* str. K-12 *substr.* DH10B] | MANIKSAKKRAIQSEKARKHNASRRSMMRTFIKKVYAAIEAGDKAAAQKAFNEMQPIVDRQAAKGLIHKNKAARHKANLTAQINKLA | 87 | 9660.310005 | 11.689209 | 11.828369 | 11.183838 | 11.674561 | 11.381592 | 11.806396 |
| 24 | YP_001729007.1 | hypothetical protein ECDH10B_0025 [*Escherichia coli* str. K-12 *substr.* DH10B] | MCRHSLRSDGAGFYQLAGCEYSFSAIKIAAGGQFLPVICAMAMKSHFFLISVLNRRLTLTAVQGILGRFSLF | 72 | 7867.057684 | 10.04126 | 9.975342 | 9.638428 | 9.982666 | 9.880127 | 9.968018 |
| 25 | YP_001729008.1 | bifunctional riboflavin kinase and FAD synthetase [*Escherichia coli* str. K-12 *substr*. DH10B] | MKLIRGIHNLSQAPQEGCVLTIGNFDGVHRGHRALLQGLQEEGRKRNLPVMVMLFEPQPLELFATDKAPARLTRLREKLRYLAECGVDYVLCVRFDRRFAALTAQNFISDLLVKHLRVKFLAVGDDFRFGAGREGDFLLLQKAGMEYGFDITSTQTFCEGGVRISSTAVRQALADDNLALAESLLGHPFAISGRVVHGDELGRTIGFPTANVPLRRQVSPVKGVYAVEVLGLGEKPLPGVANIGTRPTVAGIRQQLEVHLLDVAMDLYGRHIQVVLRKKIRNEQRFASLDELKAQIARDELTAREFFGLTKPA | 313 | 34694.52495 | 9.645752 | 9.675049 | 9.235596 | 9.601807 | 9.535889 | 9.704346 |
| 26 | YP_001729009.1 | isoleucyl-tRNA synthetase [*Escherichia coli* str. K-12 *substr*. DH10B] | MSDYKSTLNLPETGFPMRGDLAKREPGMLARWTDDDLYGIIRAAKKGKKTFILHDGPPYANGSIHIGHSVNKILKDIIVKSKGLSGYDSPYVPGWDCHGLPIELKVEQEYGKPGEKFTAAEFRAKCREYAATQVDGQRKDFIRLGVLGDWSHPYLTMDFKTEANIIRALGKIIGNGHLHKGAKPVHWCVDCRSALAEAEVEYYDKTSPSIDVAFQAVDQDALKAKFAVSNVNGPISLVIWTTTPWTLPANRAISIAPDFDYALVQIDGQAVILAKDLVESVMQRIGVTDYTILGTVKGAELELLRFTHPFMGFDVPAILGDHVTLDAGTGAVHTAPGHGPDDYVIGQKYGLETANPVGPDGTYLPGTYPTLDGVNVFKANDIVVALLQEKGALLHVEKMQHSYPCCWRHKTPIIFRATPQWFVSMDQKGLRAQSLKEIKGVQWIPDWGQARIESMVANRPDWCISRQRTWGVPMSLFVHKDTEELHPRTLELMEEVAKRVEVDGIQAWWDLDAKEILGDEADQYVKVPDTLDVWFDSGSTHSSVVDVRPEFAGHAADMYLEGSDQHRGWFMSSLMISTAMKGKAPYRQVLTHGFTVDGQGRKMSKSIGNTVSPQDVMNKLGADILRLWVASTDYTGEMAVSDEILKRAADSYRRIRNTARFLLANLNGFDPAKDMVKPEEMVVLDRWAVGCAKAAQEDILKAYEAYDFHEVVQRLMRFCSVEMGSFYLDIIKDRQYTAKADSVARRSCQTALYHIAEALVRWMAPILSFTADEVWGYLPGEREKYVFTGEWYEGLFGLADSEAMNDAFWDELLKVRGEVNKVIEQARADKKVGGSLEAAVTLYAEPELSAKLTALGDELRFVLLTSGATVADYNDAPADAQQSEVLKGLKVALSKAEGEKCPRCWHYTQDVGKVAEHAEICGRCVSNVAGDGEKRKFA | 938 | 104212.5416 | 5.563721 | 5.868408 | 6.008057 | 5.601807 | 5.906494 | 5.557373 |
| 27 | YP_001729010.1 | prolipoprotein signal peptidase (signal peptidase II) [*Escherichia coli* str. K-12 *substr*. DH10B] | MSQSICSTGLRWLWLVVVVLIIDLGSKYLILQNFALGDTVPLFPSLNLHYARNYGAAFSFLADSGGWQRWFFAGIAIGISVILAVMMYRSKATQKLNNIAYALIIGGALGNLFDRLWHGFVVDMIDFYVGDWHFATFNLADTAICVGAALIVLEGFLPSRAKKQ | 164 | 18126.52111 | 8.437256 | 8.686279 | 8.473877 | 8.781494 | 8.781494 | 8.44458 |
| 28 | YP_001729011.1 | FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase) [*Escherichia coli* str. K-12 *substr*. DH10B] | MSESVQSNSAVLVHFTLKLDDGTTAESTRNNGKPALFRLGDASLSEGLEQHLLGLKVGDKTTFSLEPDAAFGVPSPDLIQYFSRREFMDAGEPEIGAIMLFTAMDGSEMPGVIREINGDSITVDFNHPLAGQTVHFDIEVLEIDPALEA | 149 | 16052.92173 | 4.040283 | 4.059326 | 4.433838 | 4.141846 | 4.300537 | 4.02124 |
| 29 | YP_001729012.1 | 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase, 4Fe-4S protein [*Escherichia coli* str. K-12 *substr.* DH10B] | MQILLANPRGFCAGVDRAISIVENALAIYGAPIYVRHEVVHNRYVVDSLRERGAIFIEQISEVPDGAILIFSAHGVSQAVRNEAKSRDLTVFDATCPLVTKVHMEVARASRRGEESILIGHAGHPEVEGTMGQYSNPEGGMYLVESPDDVWKLTVKNEEKLSFMTQTTLSVDDTSDVIDALRKRFPKIVGPRKDDICYATTNRQEAVRALAEQAEVVLVVGSKNSSNSNRLAELAQRMGKRAFLIDDAKDIQEEWVKEVKCVGVTAGASAPDILVQNVVARLQQLGGGEAIPLEGREENIVFEVPKELRVDIREVD | 316 | 34734.93683 | 4.909912 | 4.954346 | 5.303467 | 5.049561 | 5.252686 | 4.973389 |

**(Table B4). Contd…..**

| ProtID | Orf_name | Computer annotation | Sequences | length | protMass | pI_wiki | pI_EMB | pI_DTA | pI_Sol | pI_Sil | pI_Rod |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 30 | YP_001729013.1 | ribonucleoside hydrolase 3 [*Escherichia coli* str. K-12 *substr.* DH10B] | MRLPIFLDTDPGIDDAVAIAAAIFAPELDLQLMTTVAGNVSVEKTTRNALQLLHFWNAEIPLAQGAAVPLVRAPRDAASVHGESGMAGYDFVEHNRKPLGIPAFLAIRDALMRAPEPVTLVAIGPLTNIALLLSQCPECKPYIRRLVIMGGSAGRGNCTPNAEFNIAADPEAAACVFRSGIEIVMCGLDVTNQAILTPDYLSTLPQLNRTGKMLHALFSHYRSGSMQSGLRMHDLCAIAWLVRPDLFTLKPCFVAVETQGEFTSGTTVVDIDGCLGKPANVQVALDLDVKGFQQWVAEVLALAS | 304 | 32521.71241 | 5.02417 | 5.100342 | 5.443115 | 5.113037 | 5.32251 | 5.030518 |
| 31 | YP_001729014.1 | dihydrodipicolinate reductase [*Escherichia coli* str. K-12 *substr.* DH10B] | MHDANIRVAIAGAGGRMGRQLIQAALALEGVQLGAALEREGSSLLGSDAGELAGAGKTGVTVQSSLDAVKDDFDVFIDFTRPEGTLNHLAFCRQHGKGMVIGTTGFDEAGKQAIRDAAADIAIVFAANFSVGVNVMLKLLEKAAKVMGDYTDIEIIEAHHRHKVDAPSGTALAMGEAIAHALDKDLKDCAVYSREGHTGERVPGTIGFATVRAGDIVGEHTAMFADIGERLEITHKASSRMTFANGAVRSALWLSGKESGLFDMRDVLDLNNL | 273 | 28720.56185 | 5.32251 | 5.551025 | 5.760498 | 5.373291 | 5.652588 | 5.32251 |
| 32 | YP_001729015.1 | carbamoyl phosphate synthetase small subunit, glutamine amidotransferase [*Escherichia coli* str. K-12 *substr.* DH10B] | MIKSALLVLEDGTQFHGRAIGATGSAVGEVVFNTSMTGYQEILTDPSYSRQIVTLTYPHIGNVGTNDADEESSQVHAQGLVIRDLPLIASNFRNTEDLSSYLKRHNIVAIADIDTRKLTRLLREKGAQNGCIIAGDNPDAALALEKARAFPGLNGMDLAKEVTTAEAYSWTQGSWTLTGGLPEAKKEDELPFHVVAYDFGAKRNILRMLVDRGCRLTIVPAQTSAEDVLKMNPDGIFLSNGPGDPAPCDYAITAIQKFLETDIPVFGICLGHQLLALASGAKTVKMKFGHHGGNHPVKDVEKNVVMITAQNHGFAVDEATLPANLRVTHKSLFDGTLQGIHRTDKPAFSFQGHPEASPGPHDAAPLFDHFIELIEQYRKTAK | 382 | 41387.12127 | 5.919189 | 6.344482 | 6.376221 | 5.906494 | 6.274658 | 5.893799 |
| 33 | YP_001729016.1 | carbamoyl-phosphate synthase large subunit [*Escherichia coli* str. K-12 *substr.* DH10B] | MPKRTDIKSILILGAGPIVIGQACEFDYSGAQACKALREEGYRVILVNSNPATIMTDPEMADATYIEPIHWEVVRKIIEKERPDAVLPTMGGQTALNCALELERQGVLEEFGVTMIGATADAIDKAEDRRRFDVAMKKIGLETARSGIAHTMEEALAVAADVGFPCIIRPSFTMGGSGGGIAYNREEFEEICARGLDLSPTKELLIDESLIGWKEYEMEVVRDKNDNCIIVCSIENFDAMGIHTGDSITVAPAQTLTDKEYQIMRNASMAVLREIGVETGGSNVQFAVNPKNGRLIVIEMNPRVSRSSALASKATGFPIAKVAAKLAVGYTLDELMNDITGGRTPASFEPSIDYVVTKIPRFNFEKFAGANDRLTTQMKSVGEVMAIGRTQQESLQKALRGLEVGATGFDPKVSLDDPEALTKIRRELKDAGADRIWYIADAFRAGLSVDGVFNLTNIDRWFLVQIEELVRLEEKVAEVGITGLNADFLRQLKRKGFADARLAKLAGVREAEIRKLRDQYDLHPVYKRVDTCAAEFATDTAYMYSTYEEECEANPSTDREKIMVLGGGPNRIGQGIEFDYCCVHASLALREDGYETIMVNCNPETVSTDYDTSDRLYFEPVTLEDVLEIVRIEKPKGVIVQYGGQTPLKLARALEAAGVPVIGTSPDAIDRAEDRERFQHAVERLKLKQPANATVTAIEMAVEKAKEIGYPLVVRPSYVLGGRAMEIVYDEADLRRYFQTAVSVSNDAPVLLDHFLDDAVEVDVDAICDGEMVLIGGIMEHIEQAGVHSGDSACSLPAYTLSQEIQDVMRQQVQKLAFELQVRGLMNVQFAVKNNEVYLIEVNPRAARTVPFVSKATGVPLAKVAARVMAGKSLAEQGVTKEVIPPYYSVKEVVLPFNKFPGVDPLLGPEMRSTGEVMGVGRTFAEAFAKAQLGSNSTMKKHGRALLSVREGDKERVVDLAAKLLKQGFELDATHGTAIVLGEAGINPRLVNKVHEGRPHIQDRIKNGEYTYIINTTSGRRAIEDSRVIRRSALQYKVHYDTTLNGGFATAMALNADATEKVISVQEMHAQIK | 1073 | 117749.335 | 4.94165 | 4.986084 | 5.341553 | 5.087646 | 5.284424 | 5.011475 |
| 34 | YP_001729017.1 | DNA-binding transcriptional activator [*Escherichia coli* str. K-12 *substr.* DH10B] | MCEGYVEKPLYLLIAEWMMAENRWVIAREISIHFDIEHSKAVNTLTYILSEVTEISCEVKMIPNKLEGRGCQCQRLVKVVDIDEQIYARLRNNSREKLVGVRKTPRIPAVPLTELNREQKWQMMLSKSMRR | 131 | 15408.01419 | 8.686279 | 8.942627 | 8.7229 | 8.9646 | 9.096436 | 8.766846 |
| 35 | YP_001729018.1 | acyl transferase [*Escherichia coli* str. K-12 *substr.* DH10B] | MSYYAFEGLIPVVHPTAFVHPSAVLIGDVIVGAGVYIGPLASLRGDYGRLIVQAGANIQDGCIMHGYCDTDTIVGENGHIGHGAILHGCLIGRDALVGMNSVIMDGAVIGEESIVAAMSFVKAGFRGEKRQLLMGTPARAVRNVSDDELHWKRLNTKEYQDLVGRCHVSLHETQPLRQMEENRPRLQGTTDVTPKR | 196 | 21212.76353 | 6.344482 | 6.789307 | 6.789307 | 6.319092 | 6.70874 | 6.312744 |
| 36 | YP_001729019.1 | crotonobetainyl CoA hydratase [*Escherichia coli* str. K-12 *substr.* DH10B] | MKQQGTTLPANNHTLKQYAFFAGMLSSLKKQKWRKGMSESLHLTRNGSILEITLDRPKANAIDAKTSFEMGEVFLNFRDDPQLRVAIITGAGEKFFSAGWDLKAAAEGEAPDADFGPGGFAGLTEIFNLDKPVIAAVNGYAFGGGFELALAADFIVCADNASFALPEAKLGIVPDSGGVLRLPKILPPAIVNEMVMTGRRMGAEEALRWGIVNRVVSQAELMDNARELAQQLVNSAPLAIAALKEIYRTTSEMPVEEAYRYIRSGVLKHYPSVLHSEDAIEGPLAFAEKRDPVWKGR | 297 | 32272.66332 | 5.830322 | 6.1604 | 6.261963 | 5.874756 | 6.185791 | 5.843018 |

**(Table B4). Contd…..**

| ProtID | Orf_name | Computer annotation | Sequences | length | protMass | pI_wiki | pI_EMB | pI_DTA | pI_Sol | pI_Sil | pI_Rod |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 37 | YP_001729020.1 | crotonobetaine CoA ligase:carnitine CoA ligase [*Escherichia coli* str. K-12 *substr.* DH10B] | MDRGAMDIIGGQHLRQMWDDLADVYGHKTALICESSGGVVNRYSYLELNQEINRTANLFYTLGIRKGDKVALHLDNCPEFIFCWFGLAKIGAIMVPINARLLCEESAWILQNSQACLLVTSAQFYPMYQQIQQEDATQLRHICLTDVALPADDGVSSFTQLKNQQPATLCYAPPLSTDDTAEILFTSGTTSRPKGVVITHYNLRFAGYYSAWQCALRDDDVYLTVMPAFHIDCQCTAAMAAFSAGATFVLVEKYSARAFWGQVQKYRATVTECIPMMIRTLMVQPPSANDQQHRLREVMFYLNLSEQEKDAFCERFGVRLLTSYGMTETIVGIIGDRPGDKRRWPSIGRVGFCYEAEIRDDHNRPLPAGEIGEICIKGIPGKTIFKEYFLNPQATAKVLEADGWLHTGDTGYRDEEDFFYFVDRRCNMIKRGGENVSCVELENIIAAHPKIQDIVVVGIKDSIRDEAIKAFVVLNEGETLSEEEFFRFCEQNMAKFKVPSYLEIRKDLPRNCSGKIIRKNLK | 522 | 59033.40545 | 5.468506 | 5.690674 | 5.893799 | 5.53833 | 5.811279 | 5.487549 |
| 38 | YP_001729021.1 | crotonobetainyl CoA:carnitine CoA transferase [*Escherichia coli* str. K-12 *substr.* DH10B] | MDHLPMPKFGPLAGLRVVFSGIEIAGPFAGQMFAEWGAEVIWIENVAWADTIRVQPNYPQLSRRNLHALSLNIFKDEGREAFLKLMETTDIFIEASKGPAFARRGITDEVLWQHNPKLVIAHLSGFGQYGTEEYTNLPAYNTIAQAFSGYLIQNGDVDQPMPAFPYTADYFSGLTATTAALAALHKVRETGKGESIDIAMYEVMLRMGQYFMMDYFNGGEMCPRMSKGKDPYYAGCGLYKCADGYIVMELVGITQIEECFKDIGLAHLLGTPEIPEGTQLIHRIECPYGPLVEEKLDAWLATHTIAEVKERFAELNIACAKVLTVPELESNPQYVARESITQWQTMDGRTCKGPNIMPKFKNNPGQIWRGMPSHGMDTAAILKNIGYSENDIQELVSKGLAKVED | 405 | 45079.38695 | 4.840088 | 4.884521 | 5.227295 | 4.986084 | 5.189209 | 4.91626 |
| 39 | YP_001729022.1 | crotonobetaine reductase subunit II, FAD-binding [*Escherichia coli* str. K-12 *substr.* DH10B] | MDFNLNDEQELFVAGIRELMASENWEAYFAECDRDSVYPERFVKALADMGIDSLLIPEEHGGLDAGFVTLAAVWMELGRLGAPTYVLYQLPGGFNTFLREGTQEQIDKIMAFRGTGKQMWNSAITEPGAGSDVGSLKTTYTRRNGKIYLNGSKCFITSSAYTPYIVVMARDGASPDKPVYTEWFVDMSKPGIKVTKLEKLGLRMDSCCEITFDDVELDEKDMFGREGNGFNRVKEEFDHERFLVALTNYGTAMCAFEDAARYANQRVQFGEAIGRFQLIQEKFAHMAIKLNSMKNMLYEAAWKADNGTITSGDAAMCKYFCANAAFEVVDSAMQVLGGVGIAGNHRISRFWRDLRVDRVSGGSDEMQILTLGRAVLKQYR | 380 | 42512.81073 | 4.802002 | 4.827393 | 5.201904 | 4.94165 | 5.119385 | 4.846436 |
| 40 | YP_001729023.1 | transporter [*Escherichia coli* str. K-12 *substr.* DH10B] | MKNEKRKTGIEPKVFFPPLIIVGILCWLTVRDLDAANVVINAVFSYVTNVWGWAFEWYMVVMLFGWFWLVFGPYAKKRLGNEPPEFSTASWIFMMFASCTSAAVLFWGSIEIYYYISTPPFGLEPNSTGAKELGLAYSLFHWGPLPWATYSFLSVAFAYFFFVRKMEVIRPSSTLVPLVGEKHAKGLFGTIVDNFYLVALIFAMGTSLGLATPLVTECMQWLFGIPHTLQLDAIIITCWIILNAICVACGLQKGVRIASDVRSYLSFLMLGWVFIVSGASFIMNYFTDSVGMLLMYLPRMLFYTDPIAKGGFPQGWTVFYWAWWVIYAIQMSIFLARISRGRTVRELCFGMVLGLTASTWILWTVLGSNTLLLIDKNIINIPNLIEQYGVARAIIETWAALPLSTATMWGFFILCFIATVTLVNACSYTLAMSTCREVRDGEEPPLLVRIGWSILVGIIGIVLLALGGLKPIQTAIIAGGCPLFFVNIMVTLSFIKDAKQNWKD | 504 | 56531.51581 | 8.019775 | 8.320068 | 8.232178 | 8.173584 | 8.627686 | 8.129639 |
| 41 | YP_001729024.1 | electron transfer flavoprotein subunit [*Escherichia coli* str. K-12 *substr.* DH10B] | MKIITCYKCVPDEQDIAVNNADGSLDFSKADAKISQYDLNAIEAACQLKQQAAEAQVTALSVGGKALTNAKGRKDVLSRGPDELIVVIDDQFEQALPQQTASALAAAAQKAGFDLILCGDGSSDLYAQQVGLLVGEILNIPAVNGVSKIISLTADTLTVERELEDETETLSIPLPAVVAVSTDINSPQIPSMKAILGAAKKPVQVWSAADIGFNAEAAWSEQQVAAPKQRERQRIVIEGDGEEQIAAFAENLRKVI | 256 | 27109.01948 | 4.192627 | 4.21167 | 4.598877 | 4.306885 | 4.465576 | 4.186279 |
| 42 | YP_001729025.1 | electron transfer flavoprotein subunit [*Escherichia coli* str. K-12 *substr.* DH10B] | MNTFSQVWVFSDTPSRLPELMNGAQALANQINTFVLNDADGAQAIQLGANHVWKLNGKPDDRMIEDYAGVMADTIRQHGADGLVLLPNTRRGKLLAAKLGYRLKAAVSNDASTVSVQDGKATVKHMVYGGLAIGEERIATPYAVLTISSGTFDAAQPDASRTGETHTVEWQAPAVAITRTATQARQSNSVDLDKARLVVSVGRGIGSKENIALAEQLCKAIGAELACSRPVAENEKWMEHERYVGISNLMLKPELYLAVGISGQIQHMVGANASQTIFAINKDKNAPIFQYADYGIVGDAVKILPALTAALAR | 313 | 33474.24833 | 6.716064 | 7.148193 | 7.118896 | 6.70874 | 7.067627 | 6.686768 |
| 43 | YP_001729026.1 | oxidoreductase [*Escherichia coli* str. K-12 *substr.* DH10B] | MSEDIFDAIIVGAGLAGSVAALVLAREGAQVLVIERGNSAGAKNVTGGRLYAHSLEHIIPGFADSAPVERLITHEKLAFMTEKSAMTMDYCNGDETSPSQRSYSVLRSKFDAWLMEQAEEAGAQLITGIRVDNLVQRDGKVVGVEADGDVIEAKTVILADGVNSILAEKLGMAKRVKPTDVAVGVKELIELPKSVIEDRFQLQGNQGAACLFAGSPTDGLMGGGFLYTNENTLSLGLVCGLHHLHDAKKSVPQMLEDFKQHPAVAPLIAGGKLVEYSAHVVPEAGINMLPELVGDGVLIAGDAAGMCMNLGFTIRGMDLAIAAGEAAAKTVLSAMKSDDFSKQKLAEYRQHLESGPLRDMRMYQKLPAFLDNPRMFSGYPELAVGVARDLFTIDGSAPELMRKKILRHGKKVGFINLIKDGMKGVTVL | 428 | 45655.55285 | 5.551025 | 5.83667 | 5.982666 | 5.595459 | 5.893799 | 5.551025 |
| 44 | YP_001729027.1 | 4Fe-4S ferredoxin-type protein [*Escherichia coli* str. K-12 *substr.* DH10B] | MTSPVNVDVKLGVNKFNVDEEHPHIVVKADADKQALELLVKACPAGLYKKQDDGSVRFDYAGCLECGTCRILGLGSALEQWEYPRGTFGVEFRYG | 95 | 10454.19525 | 5.043213 | 5.100342 | 5.443115 | 5.144775 | 5.354248 | 5.068604 |

**(Table B4). Contd…..**

| ProtID | Orf_name | Computer annotation | Sequences | length | protMass | pI_wiki | pI_EMB | pI_DTA | pI_Sol | pI_Sil | pI_Rod |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 45 | YP_001729028.1 | transporter [*Escherichia coli* str. K-12 *substr*. DH10B] | MQPSRNFDDLKFSSIHRRILLWGSGGPFLDGYVLVMIGVALEQLTPALKLDADWIGLLGAGTLAGLFVGTSLFGYISDKVGRRKMFLIDIIAIGVISVATMFVSSPVELLVMRVLIGIVIGADYPIATSMITEFSSTRQRAFSISFIAAMWYVGATCADLVGYWLYDVEGGWRWMLGSAAIPCLLILIGRFELPESPRWLLRKGRVKECEEMMIKLFGEPVAFDEEQPQQTRFRDLFNRRHFPFVLFVAAIWTCQVIPMFAIYTFGPQIVGLLGLGVGKNAALGNVVISLFFMLGCIPPMLWLNTAGRRPLLIGSFAMMTLALAVLGLIPDMGIWLVVMAFAVYAFFSGGPGNLQWLYPNELFPTDIRASAVGVIMSLSRIGTIVSTWALPIFINNYGISNTMLMGAGISLFGLLISVAFAPETRGMSLAQTSNMTIRGQRMG | 443 | 48616.51875 | 8.437256 | 8.686279 | 8.547119 | 8.649658 | 8.891357 | 8.49585 |
| 46 | YP_001729029.1 | flavoprotein subunit for the KefC potassium efflux system [*Escherichia coli* str. K-12 *substr*. DH10B] | MILIIYAHPYPHHSHANKRMLEQARTLEGVEIRSLYQLYPDFNIDIAAEQEALSRADLIVWQHPMQWYSIPPLLKLWIDKVFSHGWAYGHGGTALHGKHLLWAVTTGGGESHFEIGAHPGFDVLSQPLQATAIYCGLNWLPPFAMHCTFICDDETLEGQARHYKQRLLEWQEAHHG | 176 | 20139.01068 | 6.109619 | 6.562256 | 6.562256 | 6.084229 | 6.471436 | 6.077881 |