# **Supplementary Information**

BacEffluxPred: A two-tier system to predict and categorize bacterial efflux mediated antibiotic resistance proteins

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## **Tier-II dataset**

The complete dataset of efflux families which is used in building of models for Tier-II (family predictions) are attached below in the form of protein sequences.

# 1. ATP-binding cassette (ABC): 41 protein sequences

>1071078.3.peg.1866 ABC

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>1156433.3.peg.1263 ABC

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>1156433.3.peg.1264 ABC

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>1158608.3.peg.145 ABC

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>1232427.4.peg.1332 ABC

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>1234876.3.peg.1456 ABC

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>1413510.3.peg.681 ABC

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VLLPAFVWISRRVGNERKKITTQRQKQMAAMAATVTESLSVSGILLGRTMGRADSLTESF
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>1460652.3.peg.5862 ABC

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>1638.4.peg.885 ABC

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>226185.9.peg.2536 ABC

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>226185.9.peg.2721 ABC

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>29379.8.peg.680 ABC

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>315749.8.peg.286 ABC

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>33009.3.peg.2745 ABC

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>333849.13.peg.130 ABC

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>66692.6.peg.3722 ABC

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>66692.6.peg.3723 ABC

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>73044.3.peg.968 ABC

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>904314.5.peg.208 ABC

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LIASGTPDDLKAQSANDEQPDPTMEQAFIQLIHDWDKEHSNE
>P0AFP9 ABC

MFHRLWTLIRKELQSLLREPQTRAILILPVLIQVILFPFAATLEVTNATIAIYDEDNGEHSVE LTQRFARASAFTHVLLLKSPQEIRPTIDTQKALLLVRFPADFSRKLDTFQTAPLQLILDGRN SNSAQIAANYLQQIVKNYQQELLEGKPKPNNSELVVRNWYNPNLDYKWFVVPSLIAMITT IGVMIVTSLSVAREREQGTLDQLLVSPLTTWQIFIGKAVPALIVATFQATIVLAIGIWAYQIP FAGSLALFYFTMVIYGLSLVGFGLLISSLCSTQQQAFIGVFVFMMPAILLSGYVSPVENMPV WLQNLTWINPIRHFTDITKQIYLKDASLDIVWNSLWPLLVITATTGSAAYAMFRRKVM >P0AFO2 ABC

MSNPILSWRRVRALCVKETRQIVRDPSSWLIAVVIPLLLLFIFGYGINLDSSKLRVGILLEQR SEAALDFTHTMTGSPYIDATISDNRQELIAKMQAGKIRGLVVIPVDFAEQMERANATAPIQ VITDGSEPNTANFVQGYVEGIWQIWQMQRAEDNGQTFEPLIDVQTRYWFNPAAISQHFIIP GAVTIIMTVIGAILTSLVVAREWERGTMEALLSTEITRTELLLCKLIPYYFLGMLAMLLCM LVSVFILGVPYRGSLLILFFISSLFLLSTLGMGLLISTITRNQFNAAQVALNAAFLPSIMLSGFI FQIDSMPAVIRAVTYIIPARYFVSTLQSLFLAGNIPVVLVVNVLFLIASAVMFIGLTWLKTK RRLD

>A0LM36\_ABC

MDLIELQDIRKTYRLGEIDVPVLRGISLKVSPGDFVALMGTSGSGKTTLMNILGCLDRPTS
GHYRFDGQDVVDLTPDQRAALRNRKIGFVFQNFNLLPRMSAVENVMMPLSYAGGGVSD
QNGRERAGALLTRMGLGEHLDNEPSQLSGGQQQRVAIARALINNPSLLFADEPTGNLDSA
TSEEVLRVFQRLNEEEGVTIILVTHDPSVAQCARRIVRIRDGVIEPESGAVGDMPQVSKAAP
AQSKPVHSAMRRGDLDKFRRSLHTALSSLRRNVLRAALTTLGIIIGVAAVIAMMEIGRGSS
TAIQRTIASMGAHTLALLPGTAASGGVSFGGGSVMTMTPQDSEAIVNECPAVLAAAPIVR
ARTQVVHGSRNWVPAGIYGTTPTFLEIREWPLAEGDVFTERDVRNASKVCVLGQRLVDE
LFQGENPIGLEVRIKNVAFKVIGVLSPKGANMMGMDQDDLLLAPWTAIKYRVTGSSLAN
VNQSAASTSSASITDQVNSLSNLYPTEKVVLYPEISTTQAFDTPLPVRFTNVDQILVGIRSTS
GTRAAIRQIGEVLRERHRLRPGEPDDFSVRDMTEMTKTLASTATMMTKLLLAVALISLIVG
GVGIMNIMMVSVTERTREIGLRMAVGARAKNILQQFLFEAVLLCFLGGAVGILVGRGISH
LVTVLLNWPTELSLDAILAAVGVSATVGIVFGYYPAWKASRLDPIVALRYE
>P75830 ABC

MKKRKTVKKRYVIALVIVIAGLITLWRILNAPVPTYQTLIVRPGDLQQSVLATGKLDALRK VDVGAQVSGQLKTLSVAIGDKVKKDQLLGVIDPEQAENQIKEVEATLMELRAQRQQAEA ELKLARVTYSRQQRLAQTKAVSQQDLDTAATEMAVKQAQIGTIDAQIKRNQASLDTAKT NLDYTRIVAPMAGEVTQITTLQGQTVIAAQQAPNILTLADMSAMLVKAQVSEADVIHLKP GQKAWFTVLGDPLTRYEGQIKDVLPTPEKVNDAIFYYARFEVPNPNGLLRLDMTAQVHIQ LTDVKNVLTIPLSALGDPVGDNRYKVKLLRNGETREREVTIGARNDTDVEIVKGLEAGDE VVIGEAKPGAAQ

>P9WG20 ABC

MITTTSQEIELAPTRLPGSQNAARLFVAQTLLQTNRLLTRWARDYITVIGAIVLPILFMVVL NIVLGNLAYVVTHDSGLYSIVPLIALGAAITGSTFVAIDLMRERSFGLLARLWVLPVHRAS GLISRILANAIRTLVTTLVMLGTGVVLGFRFRQGLIPSLMWISVPVILGIAIAAMVTTVALY TAQTVVVEGVELVQAIAIFFSTGLVPLNSYPGWIQPFVAHQPVSYAIAAMRGFAMGGPVL SPMIGMLVWTAGICVVCAVPLAIGYRRASTH

>P9WG22 ABC

MSGPAIDASPALTFNQSSASIQQRRLSTGRQMWVLYRRFAAPSLLNGEVLTTVGAPIIFMV GFYIPFAIPWNQFVGGASSGVASNLGQYITPLVTLQAVSFAAIGSGFRAATDSLLGVNRRF QSMPMAPLTPLLARVWVAVDRCFTGLVISLVCGYVIGFRFHRGALYIVGFCLLVIAIGAVL SFAADLVGTVTRNPDAMLPLLSLPILIFGLLSIGLMPLKLFPHWIHPFVRNQPISQFVAALRA LAGDTTKTASQVSWPVMAPTLTWLFAFVVILALSSTIVLARRP

>P9WOL7 ABC

MTALNRAVASARVGTEVIRVRGLTFRYPKAAEPAVRGMEFTVGRGEIFGLLGPSGAGKST TQKLLIGLLRDHGGQATVWDKEPAEWGPDYYERIGVSFELPNHYQKLTGYENLRFFASLY AGATADPMQLLAAVGLADDAHTLVGKYSKGMQMRLPFARSLINDPELLFLDEPTSGLDP VNARKIKDIIVDLKARGRTIFLTTHDMATADELCDRVAFVVDGRIVALDSPTELKIARSRR RVRVEYRGDGGGLETAEFGMDGLADDPAFHSVLRNHHVETIHSREASLDDVFVEVTGRQ LT

>Q1C5W7 ABC

MTGPQQGKILLRLENVSREFITGEQTVRVLNNINLTLHSGEMVAIVGTSGSGKSTLMNILG CLDKPSAGEYWVAGRIPQYLGSDALAELRREHFGFIFQRYHLLNDLSARENVEIPAIYAGI DREERRKRAVNLLSRIGLAERLDYRPSQLSGGQQQRVSIARALMNGGDVILADEPTGALD THSGNEVLNILKDLHQQGHTVVIVTHDMSIAEHAQRIIELKDGEIIADRPRDHAQEKPKMV DIPSVIDIPSMDEKISTGAQQETEIARKPLLTRWKVQYDRLHEAFKMAILAMAAQRLRTAL TMLGIIIGIASVVSVVALGKGSQQQVLANINAMGTSTLEIFPGKDFGDMRSAAIHTLRDTD ADVLAQQGYIHSVTPTVSTSVTLRYGNKSVSGTVNGVGEQYFLVRGYTIAQGMAFTRTSV NDLMQDAVIDENTRDKLFPNGETPLGKVILLGSLPCRVIGVAAKKQSGFGSDENLNVWIP YTTAMKRMLGQSYLKSITVRVNDDIDLANAEQGVIKLLSQRHGTQDFFVMNTDSIRQTIQ ATTSTMTLLVSMIAVISLIVGGIGVMNIMLVSVTERTKEIGVRMAVGARASDIMQQFLIEA

VLVCLLGGSLGVALSLGIGLLFSLFSSNFSMVYSAASIITAFVCSSLIGVIFGFFPAKRAAEM DPIRALERE

>O3B5J7 ABC

MAPTTPLLELVDVHRTYPVGESTVNALRGVSLEIREGEFVAIMGSSGSGKSSLLHILGLLD
NPDRGEYRILGRNVNALPEDGQAGLRNHVAGFVFQQFHLLKRMSIVDNVRLPHIYSGLKG
DFRHEALESLKKVGLMHRLDHTPGQLSGGEQQRVAIARALIGNPMILFADEPTGNLDSRN
SLEIMKILEELHREGRTIVMVTHEDEIAAYADRVITMRDGLVVSDQRRDRVCLPAGPSVPL
TLDPHAMMDASRNLSVWQDGRFIGFVQQAFQSIFANKVRSLLSVLGILVGVASVIAMMA
LGEGAKVSIEEELKSMGSNLISVRGGSARVRGAAQGDGAVARFTFKDVKDISRMHSLVKG
AAGTVNGSGQIVFGNRNWSTTLDGVGYEYGSMRAFVPSIGRWFTRDEIRKREKVAVIGVT
VARELFGNNNPIGHTVKINRINFKVIGIAPAKGFSTHRDQDDVVLVPVTTAMYRVLGRDY
LNSIYVEVRSAEGIDGAKEAVSDLIVKNHRLREGDDSFNIRDMTEIQEMLSSTTRTMSMLL
GAIAAISLLVGGIGIMNIMLVSVTERTREIGLRKAIGARREDIMLQFLVESVGLTLSGGIIGII
AGIGISALLAVFAGWAVKTSIVSIVLATFFSAITGIFFGLWPARKAAELRPVEALRYE
>07ULB5 ABC

MIQLYGLRKDYRVGDHDLPVLKGITLNIEAGEYVALMGSSGSGKTTLMNLLGSLDHPTD GDYHLAGIDVSSLTPLELAAFRSQHIGFVFQNFNLLPRATALDNVMLPTIYASDGRSRRECI EDATKLLESVGLGGRLDHMPNQLSGGERQRIAIARALMNRPKLLLADEPTGNLDTVTEQE ILALFRQLNQEHGITLVVVTHDAEVAHEADRVVRMKDGLVAEDVRQRASTVDRSRLANS RAEPLREPASAWSLPATWNAIVVAVLALRRNALRTVLTMLGVIIGVASVISTMELSAGAST AIEETVASMGASMLTISPGKASSTSGRQRPIQIIPDDVVAVAEQCSAVKVAAPLVYSQVQL VRQNRRWSPNLALGTTSQYLAARNWDQLELGTPFTQEQVLDAAKVCILGKTVAHELFDS EYPIGEEIRVNGVPLRVVGVLTEKGGDVIGNDQDDIIIGPWTTFKLRVNSSTGATAQFSTFA DQMPPMQLASTRRSTQREEIHQIYVEAESPDHVELARQQITQVLSRRHNVEPAGAYRINDI TEVSKVVGQVVGGVSALGLVIAGVSLMVGGVGIMNIMLVSVTERTREIGLRMAVGANRS AILRQFLIEATVLCVVGGFIGIFAGHMWSVLVGRVIGWPTAMSIWAPIVAVTVAATVGIVF GYYPARTASRLNPIDALRYE

>O7VMF9 ABC

MKQPLIELKNIERYHTNGDTLTTVLKSINLKIYSGEMVAIVGASGSGKSTLMNIIGALDVPN SGEYFIYGRNIADLSGDELAELRCRHFGFVFQRYHLLSHLTAVKNVEVPAIYAMADKILRN QRANALLCQLGLEKQLENKPAQLSGGQQQRVSIARALMNGGDIILADEPTGALDSQSSQD VLKILKDLNRKGHTVILITHDLAIAEHADRVICIQDGKIVSDTANALESMIKPQNKRTFIDD AVIEVCQQHNTEKLNRPNEKNNIDNDNKENNNGYNRNDNSFLNNPKKKLNSSILRSFNSY AESFFMAFNMMMAHKIRTFLTMLGIIIGIIAVVFVIALGEGTKKKVLDEFSSLGNNTIDIFPG KWGDESDNVHTLNMEDLELLYQQPYVQRATPVLLHIAKARYLNKTMRSLINGVSHDFFM LKNYQLVTGRLFDQNDLTLSQPVGVIDKKSAKLLFDMDDPINKIIFIDDIPLSIIGVVESSSL QQNSGKEILIWIPHSTMATRILNQSYIQQISVQLQPNVSPLKSDKAIIDLLTIKHGQKDFYTF SSSRFLQSLNKTTQALTLMISSIAFISLIVGGIGIMNIMLVSVIERTKEIGIRIAVGAKERDIRF QFLIESTMVSLIGGCIGVGCALLFGGLFSLAETSIKIQFTLSSFLIAFLCSSMIGIVFGYFPARN AAKLRPVDALSRE

>088101 ABC

MNQKVDIEALHETSINSDQPLLRLQQVSRSFMAGDREFQVLKHIDLAIHTGELVAIIGASGS GKSTLMNILGCLDHASAGSYQVNGQETRELDDDALAALRRDHFGFIFQRYHLLPHLDAV RNVEIPAIYAGTAQTTRHERAQALLTRLGLGGHLQHRPSQMSGGQQQRVSIARALMNGG QVILADEPTGALDTASGKEVMRTLLELHAAGHTVILVTHDPKVAANAERIIEVSDGEIISDR RTAQTTQPAPEAQPATPPGPAPRRLLASLGLFREAFNMAWIALISHRMRTLLTMLGIIIGITS VVSISAIGEGAKRYVLKDIQSIGSNTIDIYAGANFGDSRAKSIETLLPSDVAALNQLYYIDSA TPVVGRSMLVRYRNVDVDAQLNGVSSRYFQVRNIQLAAGITFSDQDARRQAQVVVLDH NTAQRLFGPGVNPLGQVILVGKLPCTVIGVTSDHKNLFIAGNTLNLWMPYETAAGRVLGQ RHLDSISVRVKDGMPSKAVEEQIKALMLQRHGTKDFFTNNLDSVMQTVQKTSRSLTLLLS

LIAVISLVVGGIGVMNIMLVSVTERTREIGIRMAVGARQSDIRQQFLVEAVMVCLMGGVIG IGLSYAIGYLFTLFVQQWEMVFSLASVVTAFACSTLIGVLFGFVPARNAARLDPIEALARD >P9WJB1 ABC

MTRLVPALRLELTLQVRQKFLHAAVFSGLIWLAVLLPMPVSLRPVAEPYVLVGDIAIIGFF FVGGTVFFEKQERTIGAIVSTPLRFWEYLAAKLTVLLAISLFVAVVVATIVHGLGYHLLPL VAGIVLGTLLMLLVGFSSSLPFASVTDWFLAAVIPLAIMLAPPVVHYSGLWPNPVLYLIPT QGPLLLLGAAFDQVSLAPWQVGYAVVYPIVCAAGLCRAAKALFGRYVVQRSGVL >P9WJB3 ABC

MRAISSLAGPRALAAFGRNDIRGTYRDPLLVMLVIAPVIWTTGVALLTPLFTEMLARRYGF DLVGYYPLILTAFLLLTSIIVAGALAAFLVLDDVDAGTMTALRVTPVPLSVFFGYRAATVM VVTTIYVVATMSCSGILEPGLVSSLIPIGLVAGLSAVVTLLLILAVANNKIQGLAMVRALG MLIAGLPCLPWFISSNWNLAFGVLPPYWAAKAFWVASDHGTWWPYLVGGAVYNLAIVW VLFRRFRAKHA

>P0C068 ABC

MVRRTKEEAQETPAQIIEAAERAFYKRGVARTTLADIAELAGVTRGAIYWHFNNKAELVQ ALLDSLHETHDHLARASESEDELDPLGCMRKLLLQVFNELVLDARTRRINEILHHKCEFTD DMCEIRQQRQSAVLDCHKGITLALANAVRRGQLPGELDVERAAVAMFAYVDGLIGRWLL LPDSVDLLGDVEKWVDTGLDMLRLSPALRK

## 2. Multidrug and toxic compound extrusion (MATE): 23 protein sequences

>1638.4.peg.962 MATE

MKQTDEFYLTKASIPKAIAHLSIPMMLGMSVGVIYNIINAFFIGMLHDTSMLTAVTLGLPM FTILMAIGNMFGVGGGAYISRLLGKKENSQAKQVSAFVLYGSLALGIICASILGLMINPVTH FLGADAASFLHTRNYTLALLICSPFIIANFALEQVVRAEGASKISMNGMFISTIVNLIFDPLLI LYFDFNVVGAAVSVGLASAFSLVYYAWYLEKKSAYLSIHFKWFRVTKGTISNVFKIGVSE LLLSLFLIVTTLILNYYSISYGEGVVAGFGVALRVVQLPEFICMGLYMGIIPLLAYNYSAGNI ARFEKAIRFTAISIGLIVLVISSLVFLFRFQVMHLFSESPSVIMLGVHIMVAMLISSLFSGFTG LFTSTFQAIGKAIPATIMSVSQGIIFIPVIMLGQYYFGLVGVIWSLTATEILTCIIGVTLFTIYNI KIASSTKAKDLAV

>182217.3.peg.1605 MATE

MEKVFKRIGAYSMLKAKIDLHKDSIRKLFFYYFIPLAFSMISLSTYSMIDGMFVGKKLGKE AIAAVNIAWPIFPSLVAYELLFGFGAASIVGYFLGRGKTHRAKLVFSSVFYFVALSTFILSM ALLPFSETIARLFGSNDALLAMSSRYIEIILMGAVFMVLHPLADVFVVNDKRPILAMVAML IGSLTNVFFNYLFIFVLEVGVQGSAYATIIGHGVGFLVLMQHFLFKKGQLSFIKRFSFPAVIS SAKSGVPQSTAELSFALMILIFNATIMHTAGERFLSMYGIIMYNAIIFWTTLFSISQGIQPIAS FSYGARNLERVKGVFLFGLKVAFLVGVVLYGIYYFLDEFLIKMYLQANEQDLDFIQETKQ AMNVYYLGYIFLGMSILCAVFFQSIQCTRSSFIITLSHTLIFIVVLLPLMSHFYGIKGIWATYP IAQFLAFLSAMGVTYYEIKKGVFTTYREQSLINGAKK

>272563.8.peg.1578 MATE

MENLFTRKFTTFEFLKFVSPAIISMIFISLYTIIDGIFVSTLVGSDALASINIVLPIINLVCGFGI MMATGGGAIVSIRMGENRQDEANSTFSFIVLFSLIVGILFTVISYFFIKEISILLGATDKLLPY CITYGKVMILCTPFYILKFIFEYFARTDGNSKFSLFLSVIGGVTNIILDYVFIKYFGMGLLGA AVATAIGIILTCVLGIIYFLSNKSTLKLRKPKTDFRLIRDTMINGSSEMVTELSTGITTFLFNV VALKLAGENGLAALTIVLYAHFLMTSVYLGFAAGVSPLISYNFGAENSDKLKETFKHSLK FIFISSLLVFIIALVFAPFIVRVFVNPDNTVFKLALQGLKIFAFAFLFVGINIFASGFFTAFHNG KISAIISFSRAFVFIIIGIIILPPMLNMTGLWLTVPFAEVITIFISILFIKKYKGRYKY >1028805.3.peg.567 MATE

 $MNFRLLSQYHADIKKLIKISLPILLAQIAQNSMGLADTIMAGRVSSTDMAAISVGASIWMP\\ LVLFGQGLLLALPPTISYLNGSGQRHRIAHQVRQGIWLVLGMSIPLGLLIYFCEIPLQYMQ$ 

MESKMSDLARDYLHAMLWGLPAYLMLINFRCLNDGIAKTKPAMVITFLGLLLNIPLNYIFI
YGKFGMPAFGAVGCGIATSIVNWAMCLMMMFYSYTNAQERSLKVFSQLIEMPNPKTLKK
LLRLGLPIAIALCCEVALFALTSLMLSPLGSTIVASHQITLNTSSFIFMFPLSIGMATTILVGQ
ALGAGSPQNAKKMSYAALLLGLTVTIITALITIFFRYEIASIFVTDEIVIAMAANLLLFAALY
QFSDTVQMVVGGILRGYKDTKVILYITLFSYWVIGVPLGYTLGRTDWLVPHIDAKGFWIA
FVVSLTFAAILLALRMKKMQAMSDNAILQRLEKLK
>O4L8N9 MATE

MKDEQLFYFEESSIFKAMMHFSLPMMIGSLLSVIYGILNIYFIGFLDNSHMISAISLTLPIFAV LMAFGNLFGVGGGTYISRLLGAKDYIKSHYVSSFSIYSSLVLGLIIAVITLPFTDQIASILCAS GETLNYTSDYLKIEFLSTPFVILFFVLEQFARAIGKPIISMIGMLSSVGINIILDPILIFGLHLDV VGAALGTAISNAIAGLFFIIYFSRKNETLSFNVKHAKPTKAMMQEIFKIGIPAFLMVVLMGV TGLVVNLFLATYGNYAIASYGISFRLVQFPELIIMGLSEGVVPLIAYNFVSNKTRMKDTIKV VIVSIAVIFAVCMTVVLVAGHSIVQLFSTDPQIVVLATFILKVTMTSLLLNGIGFLFTGMLQ ATGQGRGATIMAIAQGTVIIPVLFVLNSLFGLTGVIWSLLIAETVCAFLAMFIVYSLRNRLT VDKASLIEVE

>Q5MZD9 MATE

MNLRTIRAELQQFLQLAIPLAAAQVAQAAVGFVDTVMMGRLGPEPLAAGGLASALFQFIL ATASGVVMAVSPLVAEAQGAGKDYKIAAIARQGLWLSVLLGLPVMLIISQLARLMPVLG QSATTIALARDYWMAVLWGIIPGLGFAMLRGYVAALEQARIILPLVLFGTLVNGLGNYLL GYGQLGFPRLELTGLGLSSALGLWVMFLGLLAYTAWQPKLRRYPFWQDWRRLQPSICRQ ILQLGWAIAVTVAVEFGLFTIITILMGAIGVEALAAHQTVSQTIILIFMVPLGCSFAVTVRVG WWLGRQDGLGARRAGLVGVGAIALWMLLLAIPLALFPRAIVGIYVDLNNPVNAGLLNLA LPMLRVASLALVLDGVQRVAMGALHGLQDTRIPLLLSLLAFWMVGVGSSAMLGFQLGW GSTGLWIGQSLGVAIAGGLFLQRFLKLTQNRTFKQRLQPQPLATHP >O5NYX9 MATE

MSAPILFPLSAPESSFTIAGRLFHHAWPVLVAQLLSMSMLIADTVITGRYGTLDLAAVAVG SGVYISIVMLLVGVLQAVAPTVAHHFGARRVDAIGPALQQGFWLALMLALPGIALLAFPG FLLELSSVPADVAGKTRDYLLATAFGLPAVLLYRTFYAFNNALGRPRALMMISFIVTSTHI PLAWALVHGAFGLPPLGAIGCGISTAIVNWIAFACGAGYLAHNRDYRPYRLFANWQPPRR RDLLALLKLGIPMGLSTFIEVSSFTLIALFAARLGAEAVAGHRVVANLAALIYMLPLAISIAI LVLVGQAAGAREPARARATVRVGMGLTVGLVALIGVLLWVGREPVVALFSADPAVRAV ALGLVFYICIYQIFDAVQTVAAHALRGYKVTFMPMLLHALCFWGIALAGGYWLAFHAPG REQSPTVAGFWEASVVATILASVLFGWLLRVVMRRPQNVQT >Q62LW6 MATE

MSPTGFTRAAAAPPPTLSRHAADTARLAAPLAIAQLSQMAMSVTDTVLLGSLGPDALAAG
GLGANLFFVVVTLLQGVLTSVSVSVAHARGAMAEDRVPHIYWTGFALSLLLAVPAFALLS
FAQPLLLAFGEPAALARNVGEYAAVLRFAAPGSLIGVGLMRSFLPAIGAAKRLLWVSLAG
VGVNAFLNYGLIHGAFGLPRLGFLGSATATTITIWLTAITLVALLHGRSTFRHFVAATRPRL
PLMGELFGIGWPVAITYGVESTLFLATGLTVGVLGESSLAAHQIALNVASVAFMVPLAIGQ
AANVRVGYWAGAGAPVAARHAGFVALGLGVAFMSLSGLVLIVAPHAIVGLYLKLDDPA
NARTVVLATSLLGIAAVFQIVDGMQTVGSGCLRGLKDTRVPMLAATLGYWGIGFPTGYW
FAFHAGLGARGLWWGLAAGLASVAMLMTWRFHRKSAALGVRADARGQA
>Q6FEY7 MATE

MAKVAGFRFELKQLFHLMWPILITQFAQAGLGLIDTIMAGHLSANDLAAIAVGVGLWMP VMLLFSAIMIATTPLVAEAKGARTPEHIPVIVRQSLWVAVSLGVIAMLILQLMPFLLPILGV PESLQPKAGLFLHAIGFGMPAVTMYAALRGYSEALGYPRPVTVISLLALVVLVPLNYIFMY GIGPVPHLGSAGCGFATAILQWLMLITLASYIYRAKAYQSTQVFSHWERINLTLVKRILKL GLPIGLAVFFEVSIFSTGAIVLSPLGDTLVAAHQIAMSVTSQLFMIPMSLAIALTIRVGMYY GEKNWVSMRLVQKLGLATATFFAMCTMSLIWFARPQIVAIYTQDPAVFDIALYLLLFAM AYQLMDAWQVGAAGCLRGMQDTKGPMWITLIAYWVVAFPVGTYLARVAKMGPAGVW

LGLITGLSIACVLLLMRLYRNNHKLAQQS >Q6NB79 MATE

MVRAMTAPGSNIAAGALAPAKSSAWRTELIETLWLAWPMALTQLGQIAMMTTDLALIGR LGDAAVAAAALAHFVLFSTFTMGLGLVSAVTPLAAQAFGARAPRQVRASLRVGLWAGVI AGVPLTLGQLYGEELLVALGQNPATSRLAGDYLDGLAWSLVPGWLFIALRGLMGAVNRP EPALWIMLTAIPINLGLAYVLIHGSFGLPRLEIFGAGLATSIVSWAMCIAAAVVCVTMRPFR KYQVFGELFRFDGELMRRLLQLGLPISGASVLEYGVFGAAALLMGKFGTTALAAHQIALQ VAAIMFMVPMGISVAATVRVGHAVGRGDPPSARRAGFAAIGLGFVFMAAMTLLVALTRH QIPQLFLGDSDTSIETATLTAALLIVGASFFIADGLQVVANGALRGRNDTKVPLLFAVLGF WVIGFPFCWVLGFHTDLGPFGVWIGLAVGLVVYAALLVWRFHRLTRDAMAAAVAA >07N1G0 MATE

MAKFSNWRELKQLLFFSFPIIVSQIARTAMSFVDIVMSGHYATADLAAVTLGSSIWFPIFVL GYGTIIMLAADVAKQKAQHDDEGIKDSLKNYLFLAVILSIPIIILLMLVSWLLSFIGIDEHILE ITQGYVIALACGVPSVMIFNVFRSFLQGLEDTKIAMYLSAGALLLNIPLNYILIYGKLGLPE MGGIGAGITTAIINNLIAVCLIIYFLLKKEYRRYRPDFSLPKYNSLIRTFYIGMPSGLALFVE MVFLDVIAITAAPLGAQVIAAHNIMLNITSIIYTITGGIAAAVTVRVGSYIGKRDKISLTGTIK ISIALILSISAVIGVLIYYFAGSFISLYTNDNGVIIIALNIIFLLCLFQFFDSCQAALSGILRGFHD TRSVFYAPLFGYWLVGLPLGFILALTDWVTERMGIIGFWYGLVLGLFVNAILLFIILKVRQ RGMISRLISY

>0879Z5 MATE

MFLPRPDFRIALSICFMAVSFVISRFGSEVRPTLLLALPLVLGHVSTGLIGFVLNVIAGHHST VTLAASTIGTALLWLPMLVPMGTLISLTVLVSQLHGAERERDIGPLFRQALWLAMLLGLV MFTFLSVVPALLPLFGIVPDIVPGAAKFLHVVRWGSLAFPLYFCMRYFCEGMHCTFPTML LGFGGLLVLVPLSYALTYGRFGFAEYGVEGLGIATVTVMWLQAVVFALYLWRSRRFAHL QLFAHLELPCWARIRDLLNIGLPIGISILMEGGLFIVTTLLIGRFGTDEIAAHQIALSVAQLCF MIPMGVAEATTVRIGHAVGRCDLLVMRRVAWAGYAIVIGTQTLSASVLLLGYDVIVAAY TDDLVVASLASKLLLFAAIFQFPDGLQMLSSGVLRGMKDTRVPMLLAMISYWGLGMPLG LGLGFALEWNSRGMWIGLIIGLTAAALLLGWRFRVVSERMFAGIP >Q89AX2 MATE

MKKHLHEIKMLLKITIPIFLAQISQTSMSLINSIMIGHLKENNIAAISVGISIWSPIILFGHGLLL SLVPTVSRIHGSGKINKIPEQINNAYWLATLISLVIMIVLWNSDVIIHTISQVNPIIEQESIKYI RILLWSTPGYLYFQVIQNQCEGLLKPKPAMVIGLIGLLFNIVVSYTLISEKFHCFNYGSTGC GISAIIVYWFMFIAMKKITKNDILINYNIKNKNISNLEMYLPNYKIIWNLFKMGFPIALSLFC EITLFTLITLLIASMETFQIIAHQIALNISSTIFILPLSIATAASIRLGFYLGKKSFSKISTIILSSQII GLIISTTISTFIILFHYQIITLYTKNANIIKLTKQMLFITASYQIFDFFQIIGNGILRSYKDTNIIFII TCTSYWIVGFPFGYFLALTNYIVPHMGAIGFWYGILIALITSSIMILFRIYILQKK >08G2I1 MATE

MDGTFDAGFREPTISKANRWGREMVVALKLGWPLIFTNLSQAALTATDVIFIGRLGADTL ASALLATSFYHTLMIFSMGLVSAVMPMIAIALGKNRHSVRDVRRTVRQGFWSAIMIVIPL WVVLWHCEEIFLFLGQRPDIAARSTDFMHTLQWALLPYLFYIVLRSFFAAMEKPMWTLLV AALAIGFNALAGWTLIFGHFGFAPMGLHGAGMATTASSTMMFLGLAFITLRHPRFRRYHL FGRFWRPDWPRLIELWRIGLPMALTFVFETSIFYAAVVMMGRIGPTAMAAHAVAIQIASLS FMVPLGFGQVATVRVGRAYGRGDPKAIAYAGWSAYALGVGFMALMGILMVLMPRVFIG IFLNLNDPQNLPVMELAVTFLALAALFQIVDGAQAVAAGMLRGLRDTRIPMLLALFGYW GVGLPLGAVLAFQFGMGGVGIWLGLAAGLGMVAVLMTIRWRRHLAHVSAVAAA >Q8UDF5 MATE

MSSSVVAETVPSGSGSWFSHFKATLVLGIPLIGAQLAQLGIHTTDMVIVGQLGAEKLAAM VLAGQFFFVVFIFGSGFSVAVVPMVAQAYGQGDATSARRSLRMGMWVAIAYWLLALPIF FNAERILVYLGQNPNVAALTGHYLAIAKFGLLPALLFYVLRGLVSAIGRAGIILYVTIIMLV MNGLMAYVLVFGHFGLPAMGMNGAAVVAVIVNAFSFIFIVAYVQTREETKKYELFVRFW

RPDWHALFEVLRLGLPISITILAEVTLFAAASILMGQIGTVQLAAHGIALQLASIAFMIPLGL SQAATVRVGVARGQGDFKNLIRASIMIYAIACGIALCGGILFAAVPEFLAKWFLDPKLPEA AEVLAYASSLVVIAGIFQLVDGIQAVTAGLLRGLKDARIPAMLALISYWPIGLALAWTMA FPLGFGGRGVWFGFVIGLSTAAVLLTVRFVLLVKREMKTAR >O9HTR0 MATE

MSSPSLVELKAILRLAGPLIAAQLAYVAMVFTDTVMMGKLGPDALAAGGLGAVSYAFVS TFCVGVVAAVGNLVAIRHGCDDAAGAAAAARSGLWVGAALALAAGLLLWNLRPLLLVF GQAPQTVDGAMQFLHSLTFALPGYMAFMVLRGFTSAIDRAGPVMAISVLGALANLALNY SFIEGLFGLPRLGLAGIGLVTALVMNCMPLLLALYIRLQPAYAEYSLLRGLGRPQRAMVEE ILRLGLPIGGTYAVESGMFTVATLCMGIIGDHALAAHQIAIQAVYVAFMVPVGLSYATTYR IGQHFGAGRLLEARRAGRVGIGFGALCMLLFAGLFWWMPEAIIGLFLDRDAPANREVAA MAVSLLAIAAWFELFDGTQNVAMGAIRGLKDARTTFLVGLACYWLVGVPLACLLAFAA GWGAAGVWWGLAGGLACAAIGLTLAFEWKTARLLPKATASEASALNCRAAGRGAPSAR LCPGNAPVPPTAAAD

>O9JV27 MATE

MLLDLNRFSFSVFLKEVRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALG SSAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGLFLGVFGMVLMWAA ITPFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYASSLNRPRLIMLVSFAAF VLNVPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFG KPDWAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMLAVITVLSLVLFRSPLVSMYNNDPAVLSI AATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFDM GIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAV

>Q9KEJ2 MATE

MKPTETLQEKGKLFLVVMMPILITQIGLYAMNFFDTVMSGQAGANDLAGVAIGSSLWVP VFTGLNGVLLALTPIIAQSIGAEKRDDVPYVFLQGLYLSIAISIAVILIGAVVLDPILSAMSLE DEVGRIAKEYLIGLAFGIVPLFIYTTIRCLIDSLGETRVTMFITLLSLPINIFFNYVLIFGKLGFP RLGGVGAGYASAITYWFILAVAIVVVVKVRPFTDFQLFKKLYHVSLKKWKEILLLGLPIGF TIFFETSIFAAVTLLMSTFDTATIAAHQAAVNFASFLYMIPLSIAFTLTIAVGYEVGAKRVED ARQYSRLGITFALIMGLVAGVIIYVLRAPVASLYTNDSQVAWLIQQFLIYSIFFQLSDALAT PIQGVLRGHKDVNVPFVMALVSFWIIGLPTGYLLANFSPLGPYGYWIGLITGLASCAIALS WRLKQMQRKFERAARLSQNGNS

>O9RY44 MATE

MTTLPAPTISTTAELRALLRLAGPVVVSQFAANALALIATAVIGRLGERELAAAAYANAA YYLVFIMVVGVMLSVAPRVAQAHGAGDARGVARALGGGLRLALLLSAVMLPLMWALS FVLPNFAPAGVSRDLVAAYLRVYSLGMLPNLAFIALRGTLEGTGKPGAVTGVALTGVVW ALLVAPALAFGWGPLPRLGLAGAAGASASAAWIMAALLWPLARRRVAYAGPLGPLGDE VRALFRLGWPIGLTLGAEGGMFSVTTLLMARFGPEVLAAHNVTMQTITAFFMVPLGIASA TGVRVGTEAGAGRLAQARRAGLVGLGLSSAVMLTFAVIELAAPRTVFSVFVNVNDPANA GLIAAATGFLSIAALFQLMDGLQVTANGALRGLQDTRVPLLVSLVAYWVVGLGLGSVLSS VAGLGARGLWFGLTAGLTLAGLSLVGRFLYRTRAGRAA

>O9WZS2 MATE

MRYSLFKNYLPKEEVPEIRKELIKLALPAMGENVLQMLFGMADTAFLGHYSWKAMSGVG LSNQVFWVVQVVLIAASMGATVTIANAIGAGNRKAVRSLAWNSVFLAIFTGVILTALTPL SDVLINIFPNLEGEIESSAKEYLKVILSGSMGFSIMAVFSAMLRGAGDTRTPMIVTGLTNFL NIFLDYAMIFGKFGFPEMGVRGAAVATILSRFVGAGILTYVIFKREEFQLRKGLVPPKWSS QKEILRVGFPTAIENFVFSTGVLMFANILLIAGAEAYAGHRIGINVESLSFMPAFGISVAITT LVGRYNGMGNKEHVLGVIRQGWILSLLFQVTVGIIIFLFPEPLIRIFTSDPQIIEISKLPVKIIG LFQFFLAIDSTMNGALRGTGNTLPPMIITFISIWTARLPVAFVMVKYFQLGLLGAWIGMIA DIIFRSTLKLLFFLSGKWEKRAVLTRERVKELG

>P58163 MATE

MTVVTTMPRDAAGTALLPERPRGPIMTDLIELLRLAGPVVLSRLGIMVMGLTDAIVVGHF SAQQLGYHAMAWAPSSVFVTATVGLLVGVQVMTARAMGAGNPHETGAVLRRGLVYAG WLGFGSMALLALFGPMFLQAMGLKDGLAEGATLPLIVFSLSLPVYAISVVLTFWLEGLSR PGPGAAMMWLANVVNLGANLLLVPGVLGPPALGAVGGAWATFIARTALALALAIFVIR MKEARELGVFDKPARDRPAEIEQRRIGYGAGASNFFEVSAFAGMNLICGWISAVAVAAYT VVLNVSAIIFMVPLGVASATAVMVGRAYGARDPAGMTRAGWIAFAVIGVIGVLFGLLLYP TKHWVALAYTTDPAALALILPALVLACLFFAPDAVQVVAAQALRARGEVWVPTITHLISY ALVMGPLAWWLAIPKGMGLNGVLVSIIVTSFLAAGFLLMRFRMLDWRDRKAAQEAA >P45272 MATE

MNFRLLSQYHADIKKLIKISLPILLAQIAQNSMGLADTIMAGRVSSTDMAAISIGASIWMPL MFFGQGLLLALPPTISYLNGSGQHHRIAHQVRQGIWLVLGVSIPLGLLIYFCEIPLQYMQM ESKMSDLARDYLHAMLWGLPAYLMLINFRCLNDGIEKTKPAMVITFLGLLINIPLNYIFIY GKFGMPAFGAVGCGIATAIVNWAMCLMMIFYSYTNTQERSLKVFSQLIEMPNPKTLKKLL RLGLPIAIAICCEVALYALTSLMLSPLGATIVASHQITLNTSSFIFMFPMSIGMATTILVGQAL GAGSPQNAKKIGYAALLLGLTVTIVTALITIFFRYEIASIFVTDEIVIAMAANLLLFAALYQF SDTIQMVVGGILRGYKDTKVILYITLFSYWVIGVPLGYTLGRTDWLVPHIDAKGFWIAFVV SLTFAAFLLSLRMKKMQAMNDNAILQRLEKLK

>O9I3Y3 MATE

MNSPALPLSRGLRIRAELKELLTLAAPIMIAQLATTAMGFVDAVMAGRASPHDLAAVALG NSIWIPMFLLMTGTLLATTAKVAQRHGAGDQPGTGPLVRQALWLALLIGPLSGAVLWWL SEPILGLMKVRPELIGPSLLYLKGIALGFPAAALYHVLRCYTNGLGRTRPSMVLGIGGLLL NIPINYALIYGHFGMPKMGGPGCGWATGSVMWFMFLGMLFWVNKASIYRASQLFSRWE WPDRATIGPLVAVGLPIGIAVFAESSIFSVIALLIGGLDENVVAGHQIALNFSALVFMIPYSL GMAVTVRVGHNLGAGLPRDARFAAGVGMAAALGYACVSASLMLLLREQIAAMYSPDPA VIAIAASLIVFSALFQFSDALQVTAAGALRGYQDTRVTMIMTLFAYWGIGLPVGYSLGLTD WFQEPTGPRGLWQGLVVGLTGAAIMLCIRLARSARRFIRQHERLQREDAEAASVLGR

# 3. Major facilitator superfamily (MFS): 95 protein sequences

>757424.7.peg.2755 MFS

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>757424.7.peg.3311 MFS

MIIMSHSDSQAAHTLAEEAKQRNEAASAAAAAQKRKKLFSIFGGVVAIAAIGYGAYWYLIGSR YVETDNAYTATEIATVTPAINGIVAAVDVVDTQAVKKGDVLVRIDDADARLAVDQAAADLDR TERKVKGFFANDAGLAAQVLAREAEQKRASAQLLSAQADLKRAEIDLQRREALAKSGSVSGE ELSNARTALLTAQANLKAAEAAEVQSRANIKATQGAQKASTVLTANTTVDDNPEVVLARAKL EQAKLDLERTVLRAPVDGVIARRQVQVGQRVQSGATLLSVVPLQQMHVDANFKEGQLTKVRI GQPVTMKADLYGGSVEYHGVVTGLSGGTGSAFAVIPAQNATGNWIKVVQRLPVRISLDPKEL AQRPLSVGLSMVVEIDTRGQIQAGDAQRKSARNDNAQAAAL

>1006000.3.peg.2818 MFS

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TLINWRACYGFLLVLCAGVTFSMARWMPETRPTGAPKTRLISNYKTLFGNSGFNCYLLMLIGG LAGIAVFEASSGVLMGGVLGLSSMTVSILFILPIPAAFFGAWFAGRPKKRFPTLMWQSVVCCLA AGVMMWIPGLLGVMNIWTLLVPAALFFFGAGMLFPLATSGAMEPFPFLAGTAGALVGGLQNI GSGVLAWLSAMMPQTGQASIGLLMTLMGLLIFLCWLPLASRFAHQGQAV >1007096.3.peg.27 MFS

MNRIKNWKKQFVVIYTGQAFSILGSAAVQFAVIWWLTIQTESAITLTIASLVAFLPNMLIGPFAG VWIDRYNRRTVMILADGLVAVSSIILGAAFLLVETPPIWFIYIVLFLRGLGNTFHGPAMQAAIPM FVPADMLTKAGGWGNMIQSISNMMGPVLGAALMSFLPISSIMIVDILGAAFAIVCLLFVIIPDIPQ TNEKMSVLSDMKQGFIAMKANKPLMAVFFPMLLMTILYMPLGSLFPLLVRSHFMGEAWHNSI VEFVFATGLLLSSLVIGVWGGMKRRFFMASLAIGLMGLATLISGALPTSGFWIFAICCFFLGASG TFMNVPVMAYVQESIAPEMMGKVFSLLMTAMTLSMPIGLLVAGPVVEVIGVNTWFFWSGVV LMADAILCRLLTRRYDKETMRPQAD

>1041522.3.peg.1113 MFS

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>1042163.3.peg.2341 MFS

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>1089544.3.peg.284 MFS

MTTVAAPIDRATWRICWVIVFGAFASGLDASVVTIGLDSISRDLHADLSVTQWVASGYLLALA LSLPLTGWLSRRFGAGRVWLVALAAFTVASGLCALAPEVGLLIVFRLLQGLAGGMLIPAGQTV LGQQVGAARLGRVMATLGIAVSVAPALGPLVGGVLLQSLSWPWLFAINLPIGAIGLALGLRYV PRGTPTETHRIDFAGLALVAAGLPLALFAVTSWGESGQLPWPILLPALGLLAWFVLRCRRHPHP LLDFSLYRNRLYRAASLAAAFNGALIFGSGIVVTLYFQIGRQLSFVGTGLSLLGFAGATAAAAP FTGRAVDRYGTAPVALAGAVLAVASTMPFAFLPANAPMAVVQLLLAGYGASVALVSMPMGI AAYKTVSPAKLPDAAAQVTILLRLGGSLGGAAFTVLIANHLPDVAAAFRLGFLAVSVGAGGAL AAAWLVARAARNPGRAETMAG

>1095552.3.peg.572 MFS

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>1104996.3.peg.2243 MFS

MAEGDFIPRDRVITMVREIMLFKTLPTQTIIGLCALFACTFTALTSEVAPVGLLIDMAQAFHIAE GQAGLAVSAFALMVALGAVPLTILTVAVDRKKLMLLSLGGYILSNLIVALAPTFLILCAGRAV GGVAHALLMSIVSAYAARLAPANMTGRAISFVYGGTSLGAILGVPGAAAIGHFASWRIAMFV MTGLAVLLAICIAFFLPPVAPTGTGSAQLPSIGSRKAMRVFLVVVAIDALFFVAHNLLYTYVTPL LLLHGLPKAVLSLALLLTGVVSISGLWAAGQVVDRWPAAGLLGGGLAMLVGMGLMSGHIVT GWVAVASVGLWCTGYSAIIPFVMSGAIRARATRPDVAGAAINGASNLGILLGSALGGQILTWS GFNILTPLAVGVALAAILLAVFSPDAFPRILHPHEDEASS

>1120960.3.peg.3781\_MFS

MSTPRALRPLRNPAYRWLAAALVASMVGSGIWMVALVWQIVAIGGGAAELSLVAGASAVGM LLTTLLGGALADRIPQKRILLVVEVVRAASVGVVALLSLTGGLAAWQLAAVAFVGGVMAGLY YPAYSALLPSVLPEDELLAANGFEGMARPILMQAGGPALASGLIAISSPGAALAVAALTGVVA AVCILRLPETSVRGAEASTGDTGYTGAASDTDVAVDTAPRHPALALLVDVRDGFTYMVRTPW LFGTLVFASLLILLIMGPFEVLVPFVIKDVAGGGPDDHALILAAFGIGGAAGSMAVASLELPKRY LTVMNLLWAFGCLPLAVFGLTDQIWVMAIAAFLVGAAFNGGVVIWGTLLQRRVPPHMLGRV SSLDFFVSLAFMPVSMAFAGPAGEAVGLPTVFLIAGAAPLLIGVVAIFAARMRRDEIAHPLDAV DEPTDVADTADVPDAAAVAEITSDDTDAAELSRSSAREFAASVA

>1121096.3.peg.137 MFS

MNHWKSTLAVIGIGQLISILTSTIVGFSIIFWISNEFKSPTALSLAILAGFLPQFVLGLFTGVYVDR WNRKKTMFYSDLFIAFCTLCLFIVITKGYKDLSFFYLLTACRSIGSTFHAPALQASIPLLVPKHHL VRVSGLYHSIQSFSEVIAPVVGASLVVWLPIQYILLIDVIGAVAACLTLLCVQIPSLQKTKVLPDF KKELTECWHTLRRTMGILPLFVCFTLVTFVLMPVFTLFPFMTLLHFNGNILQMGVVEMGWGSG ALLGGLVLACKALKSKQTLVMHTAYVILGLYLISASYLPSSAFIGFVCLTFTGGIAYSIYHALFI AIIQQNLASDMLGRTFSLIFSLSTFPSMLGIVASGYWVEAWGITSVFMISGWVIFLIGVGANFISSI KOLDNYA

>1122999.3.peg.2079\_MFS

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>1123032.3.peg.1828 MFS

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>1123308.3.peg.229 MFS

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MSQSQEFQPANMALCVFAIALGVFMQVLDTTIANVSLPTIAGNMGVSLNQGTWVITSFTVSNA IGLPITAWLSRRIGEVHLYVGALIAFSVTSFLCGISQTMGELVIFRTLQGLAAAPLFPMSQVLLM SVFPKEKRSMALALIGMVAVVGPIVGPILGGWLTYDYSWPWIFFINIPIGIFSVTVILSQLKDRPH QPMKTKLDIVGLATMALGVGALQIVLDKGNELDWFANNWIVGGAVFSVIMLIFMVIWELTDE

NPIINLRLFANRNFCIGTIILTLGFAGFFSINLILPQWLQSQMDYTALWAGLAAAPMGIIPLFMTPI LGRFGSHLDMRKLASLSFVVIGLSCYARARFNSDVDFATIALVQLFMGIGISLFFMPMTTILLSD LHGPEIADATSLSTFIRTIGASFASSLTSWIWSRNAGVHHSIMAEQISPYNPQIAPSLQHGDPVSF LAQWNGIITSQSFMMSTIDLFSILTLLFAALVPLIFLTRKAVKEA

>1128399.3.peg.2447 MFS

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>1134055.3.peg.2323 MFS

MKPEIVLRGWRFWTIQFVLPLEFVLALYGSSSYAAFNLYSVGDLGQSPSHASWSSAIFFAGRGF GMFLAPLVSRRFRSIPSLLASCFGLSAVSFFCGLIGDFYLFLVLRLLLGFLSGTAMILAQFITLRL HPVERWPNVITGFGLLLGSTFAFGPNVGAILEEAVGWRAFFLIAALLHLFFGSLLWAVLVRRQE EPVAFRFDWVGLGLMLLSMLFLQAVVVRGQDEDWYNSTFVIVLAAVSVLSLIAFVIWELGQK EPLIDVRLFLQPHYTTAVLASSVLLMLAFGMLSLILLNLQAVGGYTPDLAARSFLPVFLLMPAG WILATYLNRHVDPRWPSALYLLGFAAFAYWVSTYDYFGRRSWYTNLLGSQVLEGFCLGAIAT LTAVALQRTPRHRESTASQTLMLVRTYGMSWGPGILGTFLTHRTAFQQTRLVETAPWGDPAF GLALDRLLQAGASSLQGVRLLGRYASSHAVMLATEDVFRFCFWCFLGLAILVCTPLARKREPT RANQSPE

>1138383.4.peg.3759\_MFS

MAGQAMTSNGTRPAAKFPGGMQAWGMQTDSTDTPEIGAGVRWSIMVVSLLATASSFLFINGV AFLIPSLRVRGVRLDEAALLASMPSWGMVVTLVLWGYVLDRVGERVVMATGSALTAAAAYA AASAHSLVLMSVYLFLGGMAAASCNTAGGRLVSAWFPPQQRGLAMGIRQTAQPLGIALGAM VIPELAEHGPQHGLRFAALACAVGAIASVIGIVDPPRKPRASASHQELASPYRKSLTLWRIHAV AGLMMMPQTVTVTFMLVWLIRNLHWSVTAAGGLVTLSQLLGALGRVAVGRLSDRVGSRMR PVRYIAAVAVLALLLLAWADYMNSRWQAGLMVVIAVISVLDNGLEATAITEFAGPYWSGRAL GIQNTTQRMMAAAGPPLFGALIAAAKYPPAWLLCALFPLAAVPLVPTRLLPPGLETRARRQTV RRVRWWRAIRSHAMPNRPERRLPQRSGENY

>1154756.4.peg.1911 MFS

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>1156937.4.peg.1301 MFS

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### >1193181.3.peg.769 MFS

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### >1195763.3.peg.611 MFS

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MALESKKELKPALLVVLQGLFSIEFLLGTYSPPAYATFNLYPAGDLGVSPSHASWISTIYFAGQA FGLFIGPWFDRAFGRVKSLLLSIGFFALFDFLVAISSDYYLSLFFRLLLGISGGSTMTLCQLNLLD YYPISRWPFVTTYFGFLQVSVFGFGPVVGGFINESFGWRAYFLTSCSLHIICGLIISWILLVLTEK RQEDTPVPHPFDWIGFMLLLFAALCFQTLVTRGQDEDWYNSTFIDLLFLFGGISLLYFVVWEM GEKNPFINLKLFFKPTFLISSIITPISFAIVYGLFSTLVFTLQVLKNHTNFSSFQAGLAMAPLLFFLPI IYPLSVFLSPRINPKIVASILLILLGIFCYWTGYYDFFNKRAFFDQFFNQYILFTQVLNGAYVGLV PALNAIAINGLSKKNQESAVNTSILLRTYFLTWGGGLLGTMLMEHRRDFQQTRLVETFTGQNS ESLSFIASLQHLGLNNLQIQSKMVEQAASHSIILALDDTYRLCSWIFFLMAILVWIPAMKKKEYN FLKIFYNVCRKEKNDPKIILALAKYYHGMLFIYGALDKRQILQRSFSAISVNAYWHDGCRLCYS AKRHTCCSSP

#### >1206730.4.peg.6049 MFS

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### >1212819.3.peg.2871 MFS

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TLNRVVMQQAYMMATGDMFWMASMTCVALAAMMWLTRPKRGAAASFGH >1235279.3.peg.2664 MFS

MIERTGIKGENFMKKNIMLTTVLINLFIAFMGIGLVIPVLPALINELGLSGSAAANLVAAFALTQ LIVSPIAGKWTDKYGRKRMIVVGLILFSLSELLFGLAQSISLLFVSRLLGGISAAFIMPAVTAFIA DITTIDERPKALGYMSAAISTGFIVGPGFGGFLAEIGTRVPFFAAFGLAFIAALFSMAALREPKRQ KAEAEEMVPGTTGIRKIFAPVFFIAFVIIFILSFGLAAFESLFALYTDHKYGFTPKDIAIMVTGGG VVGAVAQVFLFDRLNKWLGEIRLVRWCLIVSAVLVYCVTLVSSYFMILLVTMTVFVGFDLVRP AVTTYLSKVAGNEQGFAGGMNSMFTSLGNVFGPVIGGILFDMQLDYPFYFATATLAAGVILSY FWKKPKALAAGPS

>1235795.3.peg.2132\_MFS

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>1242245.3.peg.4106 MFS

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>1243664.3.peg.3878 MFS

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>1378168.3.peg.1312 MFS

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>1410653.3.peg.3382 MFS

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>1429438.4.peg.3523 MFS

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>1432558.3.peg.787 MFS

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>1432558.3.peg.3586 MFS

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>1432561.3.peg.1625 MFS

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>1463858.3.peg.4357 MFS

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>1505605.3.peg.2079 MFS

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>1522311.4.peg.159 MFS

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>1536652.3.peg.3452\_MFS

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>1560354.3.peg.1457 MFS

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>1590596.3.peg.2139 MFS

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>1678637.3.peg.358 MFS

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>1682204.3.peg.5478 MFS

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#### **GGSSDAAAAAH**

>1688405.3.peg.76\_MFS

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>169963.11.peg.2889 MFS

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>1736316.3.peg.4820 MFS

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>1778.10.peg.4006 MFS

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>1791.3.peg.3532 MFS

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>225992.4.peg.2582 MFS

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>333849.13.peg.1278 MFS

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>339854.8.peg.2484 MFS

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>381666.6.peg.5563 MFS

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>382638.14.peg.388 MFS

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>388357.3.peg.2216\_MFS

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>439375.7.peg.2032 MFS

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>557599.3.peg.5424\_MFS

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>575.7.peg.222 MFS

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>637389.3.peg.233 MFS

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#### **DADTSSVHA**

>637389.3.peg.799 MFS

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>637390.5.peg.2638 MFS

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>637905.5.peg.2019 MFS

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>661478.3.peg.216 MFS

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>66429.3.peg.1684 MFS

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>754436.4.peg.3313 MFS

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>83332.12.peg.2605 MFS

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>926569.3.peg.1825 MFS

MIKKTSARLVYLILSGGNTLADTIMFTVNMVYFVEIIGLSPLQLVLVGTVLEGAILLFEIPTGVLA DTIGRKVSIVTGWFIMAGGFLLVGIVPELWAVFIGQVLWGLGYTFTSGATEAWLADEIGEDLV GKINIESGQINRILGLIGSAISVAIASVALNLPIVIGGLMYLFLAVFLLFTMPETQFTPRYKSSKSLE TPFQSFIQTFQEGVKAVGKSPILLALLLVELFIGAASEGYDRLSSAHLLKNFQIPPIGALQPVVWF GILNITGSLASFSTTAMFRKKLEVISQSYQLAARYLVLLHSLGIAMVVMLALTGNFYAAIAAILV KGVMGALIFPLYNAWLVQNILPTTRATVISIVGQANAFGQVVGGPGIGAVGNRSLRLAILLTAL LSIPALPLYTSAQKKQTVFSPESTR

>95606.3.peg.1781\_MFS

MLTSYLVANAVIVPISGWLSDVIGRKRFYMISVLLFSIASLMCGLAPSLGFLVISRILQGIGGGGL APSEQSFLADTFPPSKRGMAFAAYGVVVVIAPVLGPSIGGWITDNISWHWIFLINVPVGAISLVL VHFLVVEPKALEKERKKKLRKGLNVDAIGFALVALGLGCLEVFMDRGQRDDWFGSGFITSMA IIAVISLVLLVVWELNQKEPIVDLKLLGVPNFAICFVMMLGVGVIIYGSTQLIPQLLQEVFGYTA TDAGLALTLGGAAALLAMPLVGALSGEIQGRWFLGWAFFMQAASMWYFTGINADVSFDHIA VGRLIQAIAIPALFVPINAQAYAGLQPNRYNHASALMNVARNLGGSIGISTAQALLLQREQFHQ SRIVESLNPLDPNYVEGLKQIGASLGGAKGGDADQSQLAALYQMATKQAAMISYIDVFHVLA VVMILMVPLSILLKPAKGEH

>P76242 MFS

MTCSTSLSGKNRIVLIAGILMIATTLRVTFTGAAPLLDTIRSAYSLTTAQTGLLTTLPLLAFALISP LAAPVARRFGMERSLFAALLLICAGIAIRSLPSPYLLFGGTAVIGGGIALGNVLLPGLIKRDFPHS VARLTGAYSLTMGAAAALGSAMVVPLALNGFGWQGALLMLMCFPLLALFLWLPQWRSQQH ANLSTSRALHTRGIWRSPLAWQVTLFLGINSLVYYVIIGWLPAILISHGYSEAQAGSLHGLLQLA TAAPGLLIPLFLHHVKDQRGIAAFVALMCAVGAVGLCFMPAHAITWTLLFGFGSGATMILGLT FIGLRASSAHQAAALSGMAQSVGYLLAACGPPLMGKIHDANGNWSVPLMGVAILSLLMAIFG LCAGRDKEIR

>P46104 MFS

MSVFARATSLFSRAARTRAADEAARSRSRWVTLVFLAVLQLLIAVDVTVVNIALPAIRDSFHV DTRQLTWVVTGYTVVGGGLLMVGGRIADLFGRRRTLLFGAFLFGASSLAAGLAPNLELLVLA RFGQGAGEALSLPAAMSLIACSSRTAPFQGVERLASVASVGLVLGFLLSGVITQLFSWRWIFLIN IPLVSLVLVAVLLLVKKDETTARNPVDLPGALLFTAAPLLLIFGVNELGEDEPRLPLAVGSLLAA AVCAAAFVAVERRTAHPLVPLTFFGNRVRLVANGATVLLSAALSTSFFLLTMHLQEERDLSPIE AGLSFLPLGLSLILACVLVRGLIERIGTTGAAVLGMALAGPRHRLFALLPSDNSLLTSVFPGMIL LLRMATGLVALQNAALHAVTEADAGVASGVQRCADQLGGASGIAVYVSIGFSPHLGGDWDP FTVAYSLAGIGLIAAVLAVLALSPDRRLAAPREQED

>P46105 MFS

MSSVEADEPDRATAPPSALLPEDGPGPDGTAAGPPPYARRWAALGVILGAEIMDLLDGTVMN VAAPAVRADLGGSLSVIQWITVGYTLAFAVLLVVGGRLGDIYGRKRMFVVGAVGFTAASVLC SVAAGPEMLTAARFLQGGLGALMIPQGLGLIKQMFPPKETAAAFGAFGPAIGLGAVLGPIVAG FLVDADLFGTGWRSVFLINLPIGVAVIVGAVLLLPEGKAPVRPKFDVVGMALVTSGLTLLIFPL VQGRERGWPAWAFVLMLAGAAVLVGFVAHELRQERRGGATLIELSLLRRSRYAAGLAVALV FFTGVSGMSLLLALHLQIGLGFSPTRAALTMTPWSVFLVVGAILTGAVLGSKFGRKALHGGLV VLALGVLIMLLTIGDQAGGLTSWELVPGIAVAGLGMGIMIGLLFDIALADVDKQEAGTASGVL TAVQQLGFTVGVAVLGTLFFGLLGSQATASVDDGASRARTELAAAGASTTEQDRLLADLRVC LRESASQQDSERTPDSCRNLQQARPAVAEATARAWRTAHTENFSTAMVRTLWVVIALLAVSF ALAFRLPPKPREEEGF

>D0ZXO3 MFS

MFRQWLTLVIIVLVYIPVAIDATVLHVAAPTLSMTLGASGNELLWIIDIYSLVMAGMVLPMGA LGDRIGFKRLLMLGGTLFGLASLAAAFSHTASWLIATRVLLAIGAAMIVPATLAGIRATFCEEK HRNMALGVWAAVGSGGAAFGPLIGGILLEHFYWGSVFLINVPIVLVVMGLTARYVPRQAGRR DQPLNLGHAVMLIIAILLLVYSAKTALKGHLSLWVISFTLLTGALLLGLFIRTQLATSRPMIDMR LFTHRIILSGVVMAMTAMITLVGFELLMAQELQFVHGLSPYEAGVFMLPVMVASGFSGPIAGV LVSRLGLRLVATGGMALSALSFYGLAMTDFSTQQWQAWGLMALLGFSAASALLASTSAIMA AAPAEKAAAAGAIETMAYELGAGLGIAIFGLLLSRSFSASIRLPAGLEAQEIARASSSMGEAVQL ANSLPPTQGQAILDAARHAFIWSHSVALSSAGSMLLLLAVGMWFSLAKAQRR >Q99S97 MFS

MRLKSIITVIALILIMFMSAIESSIISLALPTIKQDLNAGNLISLIFTAYFIALVIANPIVGELLSRFKII YVAIAGLLLFSIGSFMCGLSTNFTMLIISRVIQGFGSGVLMSLSQIVPKLAFEIPLRYKIMGIVGSV WGISSIIGPLLGGGILEFATWHWLFYINIPIAIIAIILVIWTFHFPEEETVAKSKFDTKGLTLFYVFIG LIMFALLNQQLLLLNFLSFILAIVVAMCLFKVEKHVSSPFLPVVEFNRSITLVFITDLLTAICLMG FNLYIPVYLQEQLGLSPLQSGLVIFPLSVAWITLNFNLHRIEAKLSRKVIYLLSFTLLLVSSIIISFGI KLPVLIAFVLILAGLSFGYIYTKDSVIVQEETSPLQMKKMMSFYGLTKNLGASIGSTIMGYLYAI QSGIFGPNLHNVLSAVAVISIGLIVLWVVFFKEQSSQSKE

>P96712 MFS

MDTTTAKQASTKFVVLGLLLGILMSAMDNTIVATAMGNIVADLGSFDKFAWVTASYMVAVM
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PPEKRGKMSGMFGAVFGLSSVLGPLLGAIITDSISWHWVFYINVPIGALSLFFIIRYYKESLEHRK
QKIDWGGAITLVVSIVCLMFALELGGKTYDWNSIQIIGLFIVFAVFFIAFFIVERKAEEPIISFWMF
KNRLFATAQILAFLYGGTFIILAVFIPIFVQAVYGSSATSAGFILTPMMIGSVIGSMIGGIFQTKAS
FRNLMLISVIAFFIGMLLLSNMTPDTARVWLTVFMMISGFGVGFNFSLLPAASMNDLEPRFRGT
ANSTNSFLRSFGMTLGVTIFGTVQTNVFTNKLNDAFSGMKGSAGSGAAQNIGDPQEIFQAGTRS
QIPDAILNRIIDAMSSSITYVFLLALIPIVLAAVTILFMGKARVKTTAEMTKKAN
>P11545 MFS

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GAGAALFMPSSLSLLVFSFPEKRQRTRMLGLWSAIVATSSGLGPTVGGLMVSAFGWESIFLLNL
PIGAIGMAMTYRYIAATESRATRLAVPGHLLWIVALAAVSFALIEGPQLGWTAGPVLTAYAVA
VTAAALLALREHRVTNPVMPWQLFRGPGFTGANLVGFLFNFALFGSTFMLGLYFQHARGATP
FQAGLELLPMTIFFPVANIVYARISARFSNGTLLTAFLLLAGAASLSMVTITASTPYWVVAVAV
GVANIGAGIISPGMTAALVDAAGPENANVAGSVLNANRQIGSLVGIAAMGVVLHSTSDWDHG
AAISFLAVGLAYLLGGLSAWRLIARPERRSAVTAAT
>P39642 MFS

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MARKPDISAVPVESAACQGPDPRRWWGLVVILAAQLLVVLDGTVVNIALPSVQRDLGMSDTS RQWVITAYTLAFGGLLLLGGRVADAFGRRRIFAVGILGFGLASLLGGAAPDPGTLFLARALQG VFAAALAPAALALINTLFTEPGERGKAFGVYGAVSGGGAAVGLLAGGLLTEYLDWRWCLYV NAPVALLALLGCRLLPRDRRTGRAVRLDLPGTLLGCGGLVAIVYAFAEAESGWGDPLVVRLL VLGVLMLVAFALVERRVQDPLLPPGVVAHRVRGGSFLVVGLPQIGLFGLFLFLTYYLQGILDY SPVLTGVAFLPLGLGIAVGSSLIAARLLPRTRPRTLIVGALLAAAAGMALLTRLEPDTPQVYLTH LLPAQILIGLGIGCMMMPAMHTATARVAPHEAGAAAAVVNSAQQVGGALGVALLNTVSTGA TAAYLADHGTSPAATVDGTVHGYTVAIAFAVGVLLLTAVLAWVLIDSRTEAADETGSASVTP ARPR

>A0QYL8 MFS

MSAPQAAIDTDHADRHGPRRAWAAVGVLALVGTLNYVDRFLPSVLAEPIKHDLELSDTAIGVI

NGFGFLIVYAVMGIAVARVADRGAFGAVVAGCLTLWGTMTMLGGAVQSGFQLALTRVGVAI GEAGSTPAAHAYVARNFVPQRRSAPLAVITIAIPLASTASLLGGGLLAQSLGWRTAFVIMGAVS VVLAPLVLLVVGVRQSLPAAPAVVDKTAGGWWNLLRKPSFLIVVAGTAFISAAGYSLTTFSPA FLMRTRGMSLGEVGVEYGLATGAIGVLGLLIVGRLADRLAERDPRWLLWIVVTLTLVLLPASV LAFVVEDRMLCVLFLALSYAIGTSYLAPSIAAIQRLVLPEQRATASAMFLFFNAVFGSVGPFVV GMLSDSLTDDLGAQALGRALLLLVAAMQLVGAICYWLASARYRRDIIEEAR >A0OWU7 MFS

MSSRGNRNIAISAGSLAVLLGALDTYVVITIIVDIMADVGIAINQIQQVTPIITGYLLGYIAAMPL
LGRASDRFGRKMLIQVGLAGFAVGSVVTALSSDLTMLVIGRIIQGSASGALLPVTLALAADLW
SARSRASVLGGVGAAQELGAVLGPMYGIALVWLFNHWQAVFWVNVPLAVIAMVMIHFSLPA
RQQVDEPERVDVIGGVLLAIALGLTVVGLYNPEPDGKQVLPSWGLPVLAGALVAAVAFFAWE
KVAKTRLIDPAGVRFRPFLAALAASLCAGAALMVTLVNVELFGQGVLGQDQDHAAFLLLRFLI
ALPIGALIGGWLATRIGDRLVVLIGLLIAAGGFVLISHWSVDVLADRHNLGLFTLPVLDTDLAIV
GLGLGLVIGPLTSATLRAVPAAEHGIASAAVVVARMIGMLIGIAALGAWGFYRFNQHLATLAA
RAAGDAGSPMSLAERLTAQAVRYREAYVMMYGDIFLSAAVVCVIGALLGLLISGKHEHAEEF
EPAYAPTYGGGGAIDPYDAGDADDAPTEMLDLPTQVLSAPPSDPGDERPGRHRAP
>A9MWE8 MFS

MNENIAEKFRADGVARPNWSAVFAVAFCVACLITVEFLPVSLLTPMAQDLGISEGVAGQSVTV TAFVAMFSSLFITQIIQATDRRYIVILFAVLLTASCLMVSFANSFTLLLLGRACLGLALGGFWAM SASLTMRLVPARTVPKALSVIFGAVSIALVIAAPLGSFLGGIIGWRNVFNAAAVMGVLCVIWVV KSLPSLPGEPSHQKQNMFSLLQRPGVMAGMIAIFMSFAGQFAFFTYIRPVYMNLAGFDVDGLT LVLLSFGIASFVGTSFSSYVLKRSVKLALAGAPLLLALSALTLIVWGSDKTVAAVIAIIWGLAFA LVPVGWSTWITRSLADQAEKAGSIQVAVIQLANTCGAAVGGYALDNFGLLSPLALSGGLMLLT ALVVAAKVRITPMS

>P45123 MFS

MNQQKSTFIFILTLGILSMLPPFGVDMYLPSFLEIAKDLDVSPEQVQHTLTSFAYGMAFGQLFW GPFGDSFGRKPIILLGVIVGALTALVLTEINSVGNFTALRFVQGFFGAAPVVLSGALLRDLFSKD QLSKVMSTITLVFMLAPLVAPIIGGYIVKFFHWHAIFYVISLVGLLAAALVFFIIPETHKKENRIPL RLNIIARNFLLLWKQKEVLGYMFAASFSFGGLFAFVTAGSIVYIGIYGVPVDQFGYFFMMNIVT MIFASFLNSRFVTKVGAETMLRIALAIQFLSGMWLILTALLDLGFWPMAIGVAFFVGPNPVISSN AMASALERCPQMAGTANSLIGSVRFAVGAIMGSLVASMKMDTAAPMLFTMGACVVISVLAY YFLTSRNLKSRG

>C5BC70 MFS

MQNHLSSTRRLGRRALLFPLCLVLYEFATYIGNDMIQPGMLSVVQTFGVDESWVPTSMTAYLA GGMFLQWLLGPLSDRIGRRPVMLIGTLYFAATCLAILLTNSIEQFTLMRFLQGISLCFIGAVGYA AIQESFEESVCIKITALMANVALIAPLLGPLAGAAWVHLFPWEGMFILFAALSLLAFLGLYKAM PETATRRGEKLSLSALGRDYTLVLKNRRFLCGSLACGFASLPLLAWIAQSPVIIISGEGLSSYDY GMLQVPIFGMLILGNLTLARLSGRRPVRRLIQLGAWPMVGGLAIAAASTLYSAHAYLWMTAG LSLYAFGIGLANAGLYRLTLFSSTMSKGTVSAAMGMISMFIYTLGIEVGKYAWLLGGNGAFNL FNLISGLLWLALIARMLRDQLVGRMAGR

# 4. Resistance-nodulation and cell division (RND): 47 protein sequences

>757424.7.peg.1547 RND

MTNTPNPHPPSPSNASARGSILRRWWFWVLVAALAAGGGYKMWSKKKAEQEQMAAMG GPGGRPGPGAAGARRPGGPGAFGPQTMPVGVAKARLQDVNVFLNGLGAVTPTATATVR ARVDGOLMKLHYKEGOVVKAGDLLAEIDPRSLOAALTOAEGOLARDRALLASARLDLK RYQTLLAQDSIASQQVDTQVALVKQYEGTVKADEGNVASARLQLSFTRVTAPISGRLGLR QADVGNNVTTSDTNGLVIITQLQPITAIFSIPEDNIPKVLQQLQSGRKLPAQAWDREQKNK LADGVLLTIDNVVDATTGTVKLKAQFPNTDYALFPSQFVNIRLQLNTEQGATVIPTAAIQR GSKGLFVYVVKDDSSVTVRPVKTGPVQDDLTVITDGVSAGETVVIDGIDRLREGAKVEAV ARGGADDPANKLTTENPERRHGKRGQGNPGAQAGAGGDAGQGAQGGMSPEERQKRWA ELNKRIDAGEFGEEIKKLPEDQRRQKMMELRRQREAAGNGNGNAAK >757424.7.peg.2067 RND

MKLAQLRRPKFIFLALLVLLIAAWIIRSVLTPPAPPTYLSATARVADIQDVVLASGTVKAY KQVSVGAQVSGQIKSLKVALGDQVKKGQLVAEIDSLTQANALASAEFSLQNLQAQLRAK EASLKQAQLAYARQKMMLAGDASSRENFESAEATLNTTQADIAALQAQIKDGAIKVDTA RLNLGYTRISSPIEGQVVAIVAQEGQTVNANQSTPTIIKVARMDTVTIKAQISEADVVRVKP GQPVFFTILGDPDHRYRTTLRAIEPAPDSILQDDTSSSTTSITSSSSASSTAIYYNGLLDVPNP DGKLRISMTTQVNIVLSEASNALVLPSTALGAKAADGSYTVRVLDDQGQAHERKVRIGIN TNALVQIVEGVKAGERVVTGTVLPGAAASSSAHDGPPPHM

>757424.7.peg.2754\_RND

MNRINSSAFRLRAIAAVAALAGVLGLSGCASFAGIGSDRQVAQAGDFATQRSLSDPNPGA PNGQWPGSDWVRQFGDAQLVALVEQALTSSPSLQQARARIAAASALAESRGAPLLPSVN AEASVTRNQFSSTTIYPPPYGGNWYNEKKAGLNVGYELDLWNKNQAALAQAISSEKAAQ ASEQEARLALTASIVTVYSQLAAQYALHDILQSTVDQRTSLEKITAERLRTGLDSQIERDQS RTSSADARAQLAQSEGQIVLLRQQLGALAGKGPDYGLQLAPPALQGLATPGLPAELPLNL MGRRPDIVAARWQVEAASRGVDVAKARFYPDINLSAMIGFDTLLDSNPFTAASKSIAFGP AITLPIFEGGALRAGLKGEYASYELAVATYNKTLNDAYADVARQIAAIHATERQLPIRSEA LQAAERAYALARERYRLGLVSQLTLLSAQTGVLAQRQAMVALQAQRRDQQVALYKALG GGFDAQRDGLAYGAQP

>757424.7.peg.3310 RND

MAGCASFSDLGERAQPKSIDRYQSQQSLAASAVQAAWPSDQWWRVYGDAQLNALIDEA LQSAPSMAVAKARLMKAEGAAQQQGAALYPQVSANASLDRMKQSYNNGVPPDFVPKD YNNATRATLDFSYEIDFWGKNRAALAAATSELEASRADAAQARITLATSIASAYAELAQL YAQRDTNEAALKVRVESLDLFNQRFTNGLETRGSVKQMEARRAIAQADLKATDESIGLQ RNKLAALLGAGPDRGLQLTRPQIDLSRPFALPAQLPVELLGRRPDIVAARLRAEAAGKQIK VARAAFYPNVNLTAYFGFQSLGIDMLTRAGSDIGSIGPAISLPIFNGGRLRGQFRSASASYD EAVANYDQAVTQALQDVADVGVSEKALAGRLADVQAAADAAEEAYRIVSNRYNGGLA TYLDVLNAQDTLISNLRQLSDLRSRMFTLDVALVRALGGGYRAADDSSSQNSADAPLHD TQAKG

>1006551.4.peg.3864 RND

MSSAASCPAATNTGIKIMSLQKYWGNFHLTVPGVMLLSALLVGCDEGVAQNAAPQAPAV SAADVVVKSISQWDSFNGRIEAVESVQLRPRVSGYIDKVNYTDGQEVKKGEVLFTIDDRT YRAALEQAQATLARAKTQASLARSEANRTDKLVNTNLVSREEWEQRRAAATQAQADIR AAQAAVDAAQLNLDFTKVTAPIDGRASRALITSGNLVTAGDSASVLTTLVSQKTVYVYFD VDESTYLHYQNLARSGQGASSNHLALPVEIGLVGEEGYPHQGKVDFLDNQLTPSTGTIRM RALLDNAQRQFTPGLFARVRLPGSAEFNATLIDDKAVLTDQDRKYVYVVDKEGKAQRRD ITPGRLADGLRIVQQGLKPGDRVIVDGLQKVFMPGMPVNAKTVAMTASTALH >1069631.3.peg.2211 RND

MLFSLFVTIGLNVYLYAVVPKGLFPQQDTGQLMGFFRVDRGTSFQSMVPKLEYFRSILNQ DPDIRSVAVFAGGRSGSTSSFILVELKPMDERKASTTDVVNRLREPLSTTPGARMFMVPQQ DIPVGSGGGGRSGSYDYSLLGSDLELLKTWLPKVQQAMAELPELVDVDTGTDDKAGLVQ LEIDRDMATRLGIDMSMVAGTLNNSFSQRQVSTIFGRLNQYYVVMEVEPRFAQDLESLKE IEVVAKDGTRVPLSAFTRFTTGTAPRSINHMGLLVAESVSFGLAEGVTLSQATAAIEQAMA RIQLPTREIQAGFEGNTAQMLDALAKQPMMFLAAWWLCISCWGCCTRAICTRSPFCPLCL RPGLGHCWL

>1120928.3.peg.3378 RND

MSISRKQLTLSAVIVAIFATGGSFILFQEKADAKATPTASAAPAATVDVANVISQTITDWQE YSGRLEAIDQVDVRPQVSGKLIAVHFKDGSLVNKGDLLFTIDPRPFEAELNRAKAQLASAE AQVTYSSANLGRNQRLIQSNAIAHQELDQAENEARSANANLQAAKAAVETARLNLEYTRI TAPVSGRISRAEVTVGNVVSAGNGAQVLTSLVSVSRLYASFDVDEQTYLKYISNQRNSAQ VPVYLGLANESGFSREGFISSIDNNLNTTSGTIRVRATFDNPKGVMLPGLYARIRLGGGQPR AAILISPTAIGVDQDKRFVVVVDAKNQTAYREVKLGAQQDGLQIINSGLQVGDRIVVNGL QRIRPGDPVSPHLVSMPNPQIITDNTAQQPQPTEKTPTSAKG

>1154758.3.peg.1457 RND

MIVATVGLFVLSVVMFKFVPQQFFPASGRLELMIDLKLAEGASLTNTAEQVKRLEQMLKD HQGIDNYVAYVGTGSPRFYLPLDQQLPAPSFAQFVVLARSIEDREAIRGWLISSLNEQFPTL RSRVTRLENGPPVGYPVQFRVTGEHIEVVRALARKVQDRVRENPHVANVHLDWEEPSKV VHLNIDQDRARALGVTTADLSAFLRNSLTGSSVSQFRDDDELIDILLRGTRNEREQLGALS SLAIPTQNGTSVALSQVATLDYGFEEGVIWHRNRLPSVTVRADIYGKGQPATLVKQILPTL DSVRAELPDGYLLEVGGTVEDSARGQNSVNAGMPLFIVVVLTLLMIQLRSFSRMLMVFIT APLAADRRHAVPADLQSAVRLCGHAGHHRAVRNDHAQFGDSGRSDRAGHHRRAGPMA RDHRCHRAPLPPDRADCSGRSAGDDTAVTQPVFRPDGRGYHGWSDRRHGADPAVPARA VCRVVOGETGG

>1161913.3.peg.4313 RND

MALGTLVLTVVLYIFIPKGFFPVQDTGVIQGISEATQSVSFGAMAERQQALAKVVLEDPAV ESLSSFIGVDGINATLNSGRMLINLKPHESRDISASDVIRRLQPRLNEKVPGITLYMQPVQD LTIEDSVSRTQYQFTLEDADAAELSTWVPKIVDRLRQLPELADVATLHVLDVLDDAVALV VHQHDDHVGLFLHGGRQLTQVEDEAAVAGQREGLLARGGHRCADGGADAHRQALADA AAECMHAGQRIENAQIAIAPGAVRHGDVAHPVELAAGGLLYLLNQRAVGTETVDQAGD GGIARLFQVGHEGRIDVDCALAFFEAIRQAFQRQCSIAADEVVAVVAAAFRRWIGVDAIQ RTRQLQFVLQGFVAAQARADHDDGVAGLVEVLDRLVQVE

>1194405.4.peg.3028 RND

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SARAELAGTRALLAPLETQRRLAQYRIAVLAAMRPAELGELRQEQPLAPLAAQLPIGDVA MLLQRRPDVRAAERLLAATNADVGAITAELYPRIDLGGFLGFIALRGGDLGQASSKAFAL APTISWPALHLGSVQAQLRAGQARHDAARARYEQVALQAIEEVEGALTRYGQNQQRLRD LLDSATQSQRAADLAQTRYREGAAPYLTVLDAQRTLLRAQDAVAQSESESYTSLVALYK ALGGGWNTDAAAPARSARTAALPASP

>1218169.3.peg.6920\_RND

MRRYNFLSAAGEVKGEYVVTSINASTELKSAEAFAALPVKTSGDSRVLLGDVARVEMGA ENYDTVSSFDGTPIGVHRHQGHTSRQPAGRHQGSAAHHARAGKPAALGAEGIDRL >1224163.3.peg.561 RND

 $MFRTEADVMRAAAGNVDDTNTSVQGELKRLQNVVDTVRGSWAGTAQVSFDNLMIRYN\\ ESARDLHEALASIADNIRSNAVGFEDMEATNAQSFDRVGAQGLAL$ 

>1231351.3.peg.1176 RND

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>1267562.4.peg.5000 RND

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PPAVMELGNATGFDVYLQDRAGVGRGVLMQARDRFLQLAAQRPELQRVRMNGLNDEP QYRLEIDDEKARALGVSLAEINSTVSIAWGSSYVNDFIDQGRVKRVYLQGRPDARMHPDD LAKWFVRNDRGAMVPFTAFASGSWGHGSPKLQRYNGVAAIQILGEPAPGHSSGEAMAA VEAIMAQMPAGVGHSWSGLSYEERLSGAQAPALYALSLLVVFLCLAALYESWTIPFSVML IVPLGIVGALAATLLRGLPNDVFFQVGLLTTMGLSAKNAILIVEFAKALHDQGKGIVEAAI EASRMRLRPIVMTSLAFVLGVVPLATSVGAGSGSQHAIGTGVIGGVITATVLAIFWVPLFY VAVHRWFGGRRGTPASEISTRTA

>1343158.3.peg.407 RND

MVFCRLFIDRPVATTLLALAIFLSGMIALPFLPISTMPDMTATSIMVIANQPGSDPQQMATS VSTPLERRLATIADIOTLESVTTRGOTSIFLDFSSSRNINGALRDVQAALHAARSDLPTSTLE ADPQAFKLDGDKPIYLLHLTSDQLPRAQLYDLATIRVRPILAQIAGVGRVELFGASNPAVR VELNPYPLYRWGLNPEDVRAALASANAFTPKGFITSGNQRIQLQTNDQATEAAHYRDLIV AYRNGKNPIYLKDIATVRDDVQDVYQNSTLNGKTAITIAVIPQPHANAVEIVNDIVRRLPR LQQALPASAELRTGLDLSLTIRASLADAKQTLVISIFLVVLVIALFFRHMASTLIPAITIPVAL SGTLTAMAWFNFSLNILSLMALTIAVGFVIDDAIVVLENIARHMENGMNRYQASIVGTSEI AFTIISISLSLIAVFIPLLCIPGTLGSALHEFALTMAATIAISMVLSLTLTPMLCAHFLTIEPAG GTPAIPERPRYSPLADPVSWLLYGAMRTVRAVETGLYHLTSLYDRSMHWSLRHPIIIGLTL PGSFLLMVGIIILMPKTAIPSMDLAILOGSINGEPSLSFKALTRRMHOVESIIOKDPAVOTVV TFNRTSHTGRIFVTLKAKSMRDSIPVILARLRKAIPQQAGAEAFFWALNNGRQGGGDSNTT GNYRYVLQSDSNGPLYATMPPLLAQLRASGKFRNLSTDAEDLSFFANVLIHRDLEARYNI TPQLVQNALFDAYGQSIVSTIHLPLTNHRVVMVVAEPFREYSNTLHHLWLSTSAGTAAGG IASNLIRVRTKGTLSTQASLSRDSVTNSLANKLSGNSSNGAAVSSSQETMIPLDNVASIVKT PMPLSITHHNGYYATTLSFDLAEGTSYDDAISLIHRALVNLHASDSIHGEFTGTTGETTDLM LNALLAFLAAITIMYIALGVLYESLLHPITILSTLPSAGVGGVLGLWASGEQFSLVAIIGVIL LTGLVKKNAILVIDFALHIHHHHPDMTAEETIRHASVTRFRPILMTTLAAALGGIPLLMSQG YGCELRRPLGVAILGGMAISQLLTFYTTPAVYLLMEKLKHHSLSLMRRVRAAL

>1385369.3.peg.6651 RND

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>1439940.3.peg.2461 RND

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>1469502.3.peg.806 RND

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>1500894.3.peg.2187 RND

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>1502724.3.peg.3508 RND

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>1736280.3.peg.4105 RND

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MIKTAINRPITTLMIFLSLVVFGIYSLKTMNVNLYPQVNIPIVKITTYANGDMNYIKTKITQK IEDEISSIEGIKKIYSTSFDNLSVVSIEFELNKDLESATNDVRDKMQKARVGANYEIEKLNGL SSSVFSLFITRLDGNETKLMQEIDDVAKPFLERISGVSKVKTNGFLEPAVKILLDRFKLDKN ALSANEVANLIKVENLKAPLGKIENEQIQMAIKSNFSAKSIDEIRNLTIKQGVFLKDIASVDL SYKDANEAAIMDKKSGVLLGLELAPDANALTVIALAKSKLDQFKSLLGSEYDVKIAYDKS EVIQKHIDQTAFDMILGILLTIVIVYLFLRNFSITIISVVAIPTSIVATFFIINALGYDINRLSLIA LTLGIGIFIDDAIVVTENIASKLKDEPNALKASFAGIKEIAFSVFAISLVLLCVFVPIAFMSGIV GKYFNSFAMSVAAGIVISFFVSIFLVPTLSARFVNAKQSGFFLKSEPFFEALENFYEKILALA LKFKLIFLAITLVVVVCSFTLAKFVGGDFMPSEDNSEFNIYFKLDPSLSLQASKDKLKDKIS LINADPOVAYAYFILGYTDAKQPYLVKAYVRLKELKDRVNHERQNAIMQSFRDRLKSDD MSVIVADLPVVEGGDVQPVKLTITSENGKELEKFVPKISKMLKEINDATDVNSPEEDLLKR VOISIDEDKAKRLILDKASVASAVYSAFSONEVSVFENENGKEYELYMRLDDKFRSDTDDI LKTKIRSKEGFFVTLGDVATISFEQKPASISRFNRADEIKFLANTKNNAPLNSVANEISKKL DEILPANFKYKFLGFVELMDDTNASFIFTVSASAVLIYMVLAALYESFLLPFLIMLAMPLAF CGVVIGLFISGNPFSLFVMVGVILLFGMVGKNAILVVDFANHFANNGIEANEAVKMAAKK RLRAVLMTTFAMIFAMLPLALGRGAGFEANSPMAISIIFGLISSTLLSLLVVPVLFAWVYNL **DKFIRKFYERERI** 

>208964.12.peg.1484 RND

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>244582.5.peg.1519 RND

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MYLCGFSLDNLSLMAMTIATGFVVDDAVVVLENISRHIEAGLKPIQAAILGAKEVGFTVLS MSASLIAVFIPILLMGGIVGRLFREFALTLSIAILMSMVVSLTVTPMMSAYILKPEKKGHHQ GRVMNFMMRHYROSLGWALRRPKFMLTLTAATIASDIFLFVIIPKGFFPOODVGRIVASIO AQQDISFQALKQKLNDYVKIVKDDPAVETVVGFIGGNSASGNAGTMYISLKPLEERKLPID DIMGRLRGKLAAIPGASVYMRATODLVIGGROSNALYOYTLTSYDLNELNTWAPRVLEK LATLPGIVDVNSDQLSNGKEVFVTIDRDAASRLGVSPQTIDNTLYDAFGQRQIAIMYTALN OYHVVMELAPOYWORPETLDLIYAPSATNNOIPLSVVTKSKISNTLLLVNHOGOFPAATIS FNLLPGYSLGQAVEMINEATTEIGMPKATMHGSFQGTAQAFQDSLSSQPLLILAALIAVYI VLGILYESTIHPITILSTLPSAGIGAMIALLLTGTELSIIAIIGMILLIGIVKKNAIMMIDFALEK EROOHKSAIASIYEACLLRFRPIMMTTMAAILSAVPLAFGSGVGSELRKPLGISIIGGLIFSO MLTLYTTPVIYLSMERVSSWWKRRHKQTSVVVLPLLLLLLNACEVGPDYVRPVIETPAQF KEPPAGWKFATPQDTVDRGTWWDMFNDPLLSNLVAEVELTNQNLALAEAQHRQSQALV DQARAGFFPTINATTSATRQKSFSTGSTNLASAPTNLYNVGLNATWELDVWGSVRRSVES SEAGAEAAAANVALTKLSSEASLTQFYYELRAVDATQKLLDETVGSYQKLLVLTQNRHR MGVSTGLDIAOAESOLKTAEVKAIDNKVTRAOYEHAIAVLVGKAASDFSIPVDSSALPEPP TLPSALPATLMERRPDIAQAERQMAQANATIGVNIAAYFPNLTLNGSGGYESTLWHKLFT APSQIWSMAGQMAQLVFDGGLVSGKVEAARAAYDQSVANYRQVVLTAFQETEDNLAAL RILESEIKSOVEAVKAAKKOLNLTINEYKSGTIYFSDVMTAEINYFTARSNYIAIAARRLTA TASLVKSLGGGWCSSDLIREGNWEHKPSPTQQENNR

>318161.16.peg.3236\_RND

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>343509.12.peg.4097 RND

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>360107.7.peg.546 RND

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RRDMAKKPKISQWFNKIFDISTNIYAAGVAKILKHIIPSLIVVAILCFCTWRLFTMVPASLVP EEDKGVSIAVSQLPPASTITRTENVIKKQSDELLKNPLIDAVGAMMGYDLFAGGLRENATV IFLKFKDWSERKEKDQSSFAINKKYNILFSQDRNSTTFVLNPPPINGLSLTGGFELFAQNTT GKSFAEIEKDMKVVAAKANARGDLVRVRTTLDTNFPQYKLIVNTQKAKMLNVNIKNLY MTINTMLGQYYVNDFNFLGKTFKVNVKAAGEYRNSVDDLRAIFVKSNDGKSIPVNSLIKL ENALGPDTVNRFNGFPAAKIMGDPAEGYTSGQAIDAIAQVFKEEFPNEYTLGWSGTSYQE VQSSGKGATAFIFGLIFVYLILAAQYERWLMPAAVMTAVPFSVFGAILFTYLRGLTNDIYF QIGLILLIGLGAKNAILIVEFAMTEHKKGKNIIEASIAAARLRFRPIVMTSLAFAFGVLPMVIS SGAGSASRHSLGTGVIGGMIAASTIAIFFVPLFFYLLETFNNWQAKLSRTKEIKRIRKIRREE NA

>401053.4.peg.383 RND

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>436717.3.peg.1877 RND

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>547045.3.peg.622 RND

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LESSRAQLAGAQATLAKANADLARYKPLVAADAISKQDYDAAVTAKRSAEASVKAAQA
AIKSAGINLNRARITAPISGFIGQSKVSEGTLLNAGDTTVLATIRQTNPMYVNITQSATEVM
KLRQQVAEGKLSSVDGAIEVGIKFDNGEVYPHKGRLLFSDPSVNETTGQITLRASVPNDKN
ILMSGLYVRVLMEQVAADNAFVVPQQAVTRGTKDTVMIVNAKGEMEPREVTVAQQQGT
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VQTTSEAKPASAAK

>575.7.peg.976 RND

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PTSFLPQEDRGMFLTSVQLPSGATQQQTLKVVQKVEDYFFNHEQANVASIFATVGSGPGG NGQNVARMFIRLKDWDERDAKTGTSFAIIERATKAFNSINEARVFATNPPAISGLGSSAGLI WSLKTTPATGTRRSWOPAIRCSIWRRKMSG

>648757.4.peg.592 RND

MSGPTAEEPGGVGAQGADAAGEDTYSGISAPFIARPIATSLLAVAILLASLLAYSLLPISSLP QVDFPVVQVTTRLPGANADTMARLVTAPLERQLGQIPSLENMSSTSSEGLSQITLRFMLSR DINAAGODVOSAISAAGGSLPONLPYPPVYAKVNPSDPPIVTIALTSOSVSLERLSDFADTL LAPRLSQVAGVGRVTVQGNIRPAIRIQANPLQLASLGIALETVRSAIANANVTGSKGLISGP EKSYIVGANDQLETAGAYEDVVVAYRNKAPVLLRDVATVVAGLENERVAARYNGTPAV VIDVOROPSANIVGTVDELKKILPKLVDALPAGVKLDIVADRTGTIRASVEEVOFTLVLSV ALVIMVVLLFLRTLSATIVAGITLPLSLMAAFGVMYYAGFSLNNLSLMALTIATGFVVDDA IVMIENVMRYIEKGEKPLVAAYKGAGEIGFTIVSLTLSLIAVFIPLLFMEGIVGRLFREFALT LTAAVVTSMIVALTLTPMMAARLLRAPRHGETAPWYSRAFEAPFNALLSVYRVTLDWAL NARRFMLLVAAATFVLTVVLYIAIPKGFLPDQDTGFLTAETEAAPGVSFERINALQAEVER IIRRDPDVLGVVSVIGVGTTNATPNAAHLALTLKPKTERKATATEILORLTEATADFPGLRT TFQIVQDIQIGTARSRTQYQYVIVGLDREGFSGWAQKLEAELSRDRRLIHVASDLQEDGNA VLIKTDRVIAGRLGVTMQALNDTLYDAFGQRQISTIYGQSNQYRVVLEVAPAFQTDTAAL GSIYVPGTAISNSTSGNASTGNATASGATNSSITATSASGTGVGSQVPLSSFSVIERATAPLS VNHVQQYPAATISFDVAPGFSLDAAVQAVTDAQSRIALPSSIVGSYTGAAAEFNASLANQP LLILAAVVTIYIILGVLYESFIHPFTILTTLPSAGIGALLALEILGMEFSFIALIGIILLMGIVKK NAIIMIDFALDAERTRGLAPFDAIREACLLRFRPIMMTTVAALLGALPLVIGSGPGSELRMP LGVTIIGGLLLSQLLTLYTTPVIYLAMDGLKRRIERRFGIDEPNYPPPALRPEPGLPDPGPRG GSPRGTGGGGAAGLLPIFGTPSLPMLPPRADWLLLPSPEGNAALPSPNEPLALPPPDKPAS >679897.3.peg.488 RND

MYKFAIQRPITTLMFAIAVMFFGILGIKKIPVALFPNIDFPIIVISTTYPGGSPEIIESKVTDKVE EAVMGIDGVKKITSNSARNVSIVVVEFYLEKPVEQAMTDVIGKISSIKFDDSNIQQPSIRKF DTSGQAIISLFMSSKQKGPTEIMRHADLIVKPILQSILGVGGVQLNGYRERQIRIYADSTLM NKYGITYDNLFGMLGKENLEANGGRIESATKDFSITVDANSTSIKDIANIRIGKDNVRLSDV AVVEDGLQEETTYAAFNNEPGVIFEVMKVSGANELEVADGVYKALPKIQVASHGYEIVPF LDTTOYIRHSIKDVOFDLMLGGVLAVLIVFLFLRSVTITLVAAISLPISILGTFALIEMLGHTL NMMTMMALTLAIGIIIDDAIVVIENIHKKLELGMSKKQAAYEGVNEIAFAIIAISAMLLSVF VPIANMSGIIGKFFASFGVTVALAIVISYVVVITVIPMVSSLIVSSKQSRFYHFTEPFFNGME NFYLKILRLGLSHKLLFSALTFLIFGFSIYVAKGLGMEFMLKEDKSOFYVWLETSPGISIHE MKVRTLALQEAIAKHEEIEYTTLQVGYGSIQSIFKAKIYAKMKPIEERKISQFDMMKSITDE LKKMPQAKGLNVFSSEVPVLGGGDSTPFQVTIYGMTQQAVDKSVAKLKKMLDEDPRFQG KITNYHTSTSDIQPEYKITVLRQNADKYGVRTQEIANVVSAAFSGVNQAAYFKQGGKEYK ITMRVPDDERVSVDDIRKLOVMNSSGKLMFLDGLVEITRSOSPSLINRYGRORSVTVYAAP LKNSGLSLGSMISIVOTNSKDWLEEGVNFAFSGESNNAAESAASFMTAIITAFILIYLILAAL YESLLEPFIIMITMPLSFAGVFFSLKLAHQPFSMFSFMGLILLIGIVGKNATLLIDVANEYRK KFKAGVHEAIIFAGKSRLRPILMTTIAMVFGMLPLAVATGSGYAMKSPIGISMIGGLLISMF LSLLMVPILYVIVAPIDDKLKRFYQSEDGEGILQSVVKKIKPGKKEKEKQEEDKDSKKKKK **KKDKKKD** 

>754502.3.peg.2425 RND

MNISRLFILRPVATLLLMIALVLVGLIAMRVLPVSSLPNVDYPTIQVQTFYPGASPTVMATT VTAPLEVQLGEIPGLQQMTSYSSDGASVITLQFDLSLNLDIAEQNVQQAINAANSYLPSGLP APPTYAKVNPADQPILTLAVTSKSMSLTQLEDVANNRLGTKISEVSGVGVVTTSGGNVPAI RVEADPHKLAAYGLNIDDLRTLLSYVNVSQPKGNFDGPDLDYTINGNDQITDPKDYLDTV IAYQNGSPVFMRDVARVSQAAQDVERGAWYNGSPAIVLNVQRQPGANVIKTVNQIMKEL PQLESTLPAGMKVTVVSDSTGVIRASVADAAFELILAIVLVVAVIFVFLRNVPATLIPSISVP VSLIGTLAVMYQLNYSIDNLSLMALIIATGFVVDDSIVMIENIVRYLEEGMSPLEAALEGAG

QIGFTILSLTVSLIAVLIPLLFMGGVIGRLFSEFAVTLAVTIVISAVVSLTVVPMLCARMLRA QAERHPSRFERISEGLFDKTLAAYERGLRWVLDHQTLTLMVAIATVVLTGILYVVIPKGLF PVODVGVIEGISVADNSVSYAAMVOROSALADAVLKDPDVVSLTSYVGIDGTNATLNNG RFLINLRERDKRSDNAQEIARRLAQEVAHVPGVKLFMQPEQDLTLDTTVSPNQYSFALRG PSQQAFQKYVPELVARLKRIPSLSDVQSDLNSDGLSVNVEVNRQLAARFGITPATIDNALY DALGQRIVSTIFEQSAQYRVILVAKPETMPTLQSIGDLYLPSQTSSTGQVPLSGIAKIEIRKA PLVISHLAOFPAVTVSFNLAKGASLSTAVKEIHOAEOAIDLPPSITSSLOGATAAFEDSLSSE VYLLIAALVAVYIVLGVLYESFIHPVTILSTLPSAGIGALLSLMLAGMDLDVIGIIGIVLLIGI VKKNAIMMVDFALDAERNHGKAPRDAIFEASLLRFRPILMTTLAAMLGALPMLLGTGTG SELRRPLGLAIIGGLTLSOMLTLFTTPVIYLFFDRMAARVNRWRAARAERNGGDEPGGRPP EGGAGGTRVNIPAIFIRRPVATTLLAIAILISGTLAYFRMPVAPLPNIAFPVIVVQANMAGAS PSVMASTVAEPLERRLATIADVEELTSISYVGSSMIIVEFGLKRDINGAARDVEAAIQAARA DLPTTLRSNPSYRQYNPADAPIMVLSLTSDTLTKAQLYDSADSVIQQQLSQVRGVGQITLG GGALPSVRVELOPGKLNSYGIGMEDVRAAISAANADSAKGHLDVGDORYVVTSNDOITH AAPYRDLVVAYRDGAPVQLRDVAQVRDSNENIRNAGLFNGKSAILVIVYPMPGSNVVST VRQIRNVLPSIQATLPSSVHVDVAIDRSQSVTSSVSDTERTLFIAVLLVVGVVFIFLQSPRAT LVPAVALPLSIVGTFGPMYLLGYSIDNLSLMALTIGTGFVVDDAVVVLENVVRYIEQGLSP KEAALKGAGEVGFTVISMSLSLIAVFLPIILFPGIVGLMFHEFAITLSIAILISLVISLTVTPAM CAYVLSRDHAGHSRARWAQWIERQFDRFKGVYARSLTAVLDHSLLVILLLFALLVGNVF LLKLVPATFFPEQDTGILIGQIIADQSISFSAMQKKLAQLQSIVQRDPAVQSVAGFTGGRAL NTANVFIELKPLSQRHATAAQIVNRLRPKLNQVSGARLFLQAQQDLRIGGRQSAAEYQYT LTSDDSAALFTWTPKLVAALSKERGRLLDVNSDLQQNGLQTYVSINRATAARYGFAPNQ VDNVLYDAFGQRTVSTIYNPLNQYFVVMEVAPEYWQYPQTLNQIYLSKSAGNPSGTAAT QMPHGTVSALSSTNASTSSTSSTTNSRNSDAQSNATNNSIANSKGGSSTGSADSTAAETMV PLAVMASYASSHTSTQVNHQSGLVAATISFNLPAGGSLSQAGAAINDTIREIGMPASIHGSF AGAAAAYSQSMGVVPLLILAALAVVYIVLGVLYESSIHPLTILSTLPSAGIGATLALLIFGTP FSVIAMIGIILLIGIVKKNGIMMVDVAIQLQRQQQMTARDAIHEAALIRLRPIMMTTFAAVL GAVPLAIGIGQGGSLRQPLGITVMGGLILSQMFTLYTTPVIYLYLDRLRARLVRWSAGLRW NRDAKPGQPDTMA

>887898.3.peg.390 RND

MNLSRPFIRRPIGSTMLALAILLAGWLAWRQLPVAPLPQIDTPMVVVSASLPGASPTSMAA TVAGPLERALGAIAGLSSISSSSSTGTTEVRLFFDIDRDLNEASREVQAAINGVIDQLPPGMP GRPTFRKLNSSTSPILALALSSATLPPSQLYDLADNIVLQKISRVQGVGEVSLGGASLPAVRI RFEPSALAALGMSLEDARQVVVAASAEAPEGFLEDEGNRWLVATGHKLKNAADFSDLVL RWKNGQAVRLSDVAEVSDSVENRYSSGFHNHQPAIIALVTRQPDANVVATIDAIKATLPQ LQAILPPQASLTVVMDRSLGIRGSLAEAQWTLVFSCLIVAAVVWLFVARLRTALIPVAVIP VSLIGTFAVIWLAGFSLNNLSIMALVVAAGLVVDDAIVVLENITRHTERGLSPYRAAMRG AGEVSFTLLALNVALVVVFVAVLFMGGIIERLFREFSLTLAAAIVISLVVSISLTPALCAHGL PRERROKAAEHGAAQAAALPGGMPDVTHDAGQGMPGSVSLQDDAEVARAPWHRRLLG LHASYFHHLQAAYEQSLAWMLRYAWYGVVALVGLIAASVWLFANLPRSDLPEQDTGVI GAFIRGDDGFSFOIMOPRIERYRRWILSDPAVODVAGISGGNGGLTNARLVITLKPLAERK VSARQVIDRLRRNAPQMAGTMFFGRVEQDLQLSPPKFGDDADHVIVLKSGDRDLLRTWN QRLGVALSKRPELENVRYSLGEDTRQIVLDIDRNTASRLGVQLTDISAALSNSFAQRQVAT LYQDRNQYRVVMEVSERFTENPLALDRVQIITSEGKSVALAEVARWHFGMVQDRERHVD QFSASTISFSVAADVTDTAALEAVRKVIDAERMPVTVIADIDGDDGRPKSLVKADGQGWL ILGVVLAVYLVLGILYENLLHPITVLSTIPSAGVGALLALWASNTPFSLIALLGLFLLIGVVM KNGILMIDVALKKQLHEGLAPQVAILQAAGQRLRPILMTNVAALAGAIPLAMGLGDGGEL RRPMGLVIIGGLAVSQLITLYTTPALYLLLERLQQRLRRGRG

>P9WJV1 RND

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VFDTLDGIDVMTEDINNLLPLMQRLDTLMPQLTAMMPEMIQTMKSMKAQMLSMHSTQE
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SHEGDPMSQAGIARIAKIKTAAKEAIKGTPLEGSAIYLGGTAAMFKDLSDGNTYDLMIAGI
SALCLIFIIMLITTRSVVAAAVIVGTVVLSLGASFGLSVLIWQHILGIELHWLVLAMAVIILL
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QVGTTIGMGLLFDTLIVRSFMTPSIAALLGKWFWWPQVVRQRPIPQPWPSPASARTFALV
>P32714 RND

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>Q2EHL7 RND

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>Q83KF5 RND

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>O8FWV8 RND

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PNPNNVLIDGQYVQVTAASKHPVEALLVPQKAIMTDQSGNYVLAVGEDNKVIQRQITQGS TFGSNVVVKSGLAVGDQVVVDGLQRIRPGQKVDPQIVDATTPAQKAMSVGN >O8FWV9 RND

MLSSVFINRPRLAIVIAIVITLAGLIAVTRIPVAQFPDIVPPQVSVTATYPGASAETVEAAIAQ PIEAOVNGVDDMIYMSSTSGNNGTYTLTVTFKVGSDPNLNTVNVONRVRLAEANLPOEV TRLGVTVKKQSSSFLQIITLLSPDSRYDELFLNNYGVINVVDRLARVPGVGQAQSFGTFNY SMRIWFNTDALTSLNLTPNDIVNAISSONVOAAVGRLGAPPMTDOOOIOLTLTTOGRLTD AKQFENIIIRANPDGSSVRLKDVARVELAAQSYDTIGRLNGKPASVIAVYQAPGSNAVAAA EGVRNVMEQLKQSFPAGLDYKITYDTTVFVSSTIHEVIKTLLEAFVLVVVVVFIFLGNFRA TLIPTLAVPVSLIGTFAVLLVLGFSANTISLFAMILAIGIVVDDAIVVVENVERVMAETGLPP KEAAKQAMQEITAPIIAITLVLLSVFVPVAFIPGITGALYAQFALTVSVAMLISAINALTLSP ALCGVFLKPHQGRKKSLYGRTMDKLSSGIEKISDGYAHIVRRLVRMAFLSIVLVAGLGAG AYFLNTIVPTGFLPEEDQGLFFVQVNLPPAASQSRTAAVVSEIEADITKMAGVADVTSVTG FSFIDGLAVSNAGLMIVTLKPLEERLKDNITVFDVIAEVNRRTAAIPSAVAITMNLPPILGLG SSGGFQYQLEDQEGQSPQQLASVAQGLVMAANQNPKLSRVFTTFATDTPQLNLNIDRQK ALSLGVSPNNIIQALQSTLGGYFVNNFNTLGRTWQVIIQGEQQDRKTVEDIYRINVRSSHG DMVPLRSLVSVEERLGPLYITRYNNYRSASIQGNAAPGVSSGEALAAMAQVSKTTLPSGY GYEWTGTALQELQAAGQTSMILALAVLFAYLFLVALYESWTIPVGVLLSVTAGLAGAML ALWITGLSNDIYAQIGIVVLIALASKNGILIVEFAKERREEGVPLEQAAIIGARQRFRPVMM TSFAFILGLVPLVIAVGAAAASRRAVGTSVFGGMIAASAVGIFLIPMLYVVLERVREWGHA RILRKPLYEEEKQEKADGDASGPTVPPTQPEDRGLS

>O8G2M7 RND

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>A0A0P7CXJ9 RND

MGFNLSAWALRNRQIVLFLMILLAAIGAMSYTKLGQSEDPPFTFKAMVIRTLWPGATAEE VSRQVTERIEKKLMETGEYERIVSFSRPGESQVTFMARDSLHSKDIPELWYQIRKKVADIR HTLPPEIQGPFFNDEFGTTFGNIYALTGEGFDYAVLKDYADRIQIQLQRVKDVGKVELIGL QDEKIWIELSNVKLATLGVPLEAVQQALQEQNAVSTAGFFETPSERLQLRVSGRFDSVEQI RQFPIRIAERTFRIGDVAEVHRGFNDPPAPRMRFMGEDAIGLAVSMKDGGDILVLGKALES EFERLARSLPAGMELRKVSDQPAAVKAGVGEFVQVLVEALVIVLLVSFFSLGLRTGLVVA LAIPLVLAMTFAAMHYFGIGLHKISLGALVLALGLLVDDAIIAVEMMAIKMEOGYDRLKA ASYAWSSTAFPMLTGTLITAAGFLPIATAASSTGEYTRSIFOVVTIALLTSWVAAVVFVPYL GERLLPDLAKLHASRHGKDGHAPDPYATPFYQRVRRVVEWCVRRRKTVILLTIAAFVGSI LLFRFVPQQFFPASGRPELMVDLKLAEGASLANTAERVKQLEALLKQQEGIDNYVAYVGT GSPRFYLPLDQQLPAASFAQFVVLAKSMEDRERLRSWLISTMDQQFPDLRARVTRLENGP PVGYPVOFRVTGEHIEKARALAREVADKVRONPHVVNVHLDWEEPSKAVFLEIDODRAR ALGVSTAHLSSFLQSSLTGTTVSQYREDNELIEILLRGTRQERSELGNLGSLALPTDNGQSV ALSQVATLEYGFEEGIIWHRNRLPTVTVRADIYDKEQPATLVKQIEPTLRDIRAKLPDGYL LEVGGTVEDSERGOKSVNAGMPLFVVVVLSLLMIOLRSFSRTVMVFLTAPLGLIGVTLFLL VFRQPFGFVAMLGTIALAGMIMRNSVILVDQIEQDIAAGLDRWQAIIEATVRRFRPIVLTAL AAVLAMIPLSRSVFYGPMAVAIMGGLIVATVLTLLFLPALYAAWFRVKKA >W0HU59 RND

MNISRLFIFRPVATLLLTLAILLLGLLGYRLLPVAPLPQVDFPTIMVSASLSGASPETMAATV ATPLERSLGQIAGVTEMTSSSSTGSTRIILQFELDRDINGAARDVQAAINAARSLLPSSMPSL

PTYRKANPSDAPIVMLALTSNTRASGELYDLASSTIQQKIAQVQGVGQVSLLGSALPAVRI DLQPQMLNHLGISLDTVRSAIANSTTNLPKGMLQGATTSFVVDGNGQLDKARDYRSLIIT YINGTAIRLSDVATVTDSVEDKYNIGFYNQTPSVMIGVTRQAGANMLETIDAINAALPALQ AELPGDVELHKVVDRSPTIRASLYDTEETLLIAIFLVIAVVFIFLRNLQAVIIPALALPVSLIG TCAVMYLLDYSLDNLSLMALIICTGFVVDDAIVVLENITRYIEEGLGPVRASIKGAQEVGF TVLAMTLSLVAVFIPILLMGSIVGRLFREFAVTLTVSLLISMVVSLSLTPMLCSRLLRRKPPV SKRPNRLYLLIESGLARLLAGYALALGWVMRHQRLTLFSLVLTIMLNLFLYGVVQKGFFP NQDTGLLMGMVRADQNISFQAMKPKVEAIAKLIQQDSAVDGVMSSIGGGAFGSRNSGTF FVRLKDYDKRSDSATVVANRLTNKFRNEAGMQLFLMAAQDLHIGGRSANASYQYSLQA DDLNLLRVWTPKVKAALEKLPELTSVDADSENGGQEIMLNIDRDKATRLGVNADMLDA MLNNSFSQRQVATIYKTLNQYHVIMGLNEAYTGDAEVLKKLFVVNDNGESIPLSAFITFSS ANAALSVAHQGQSATSTVAFNLADGVSLEQAQAAIKDAMVKIALPSTIQAGFQGTAKAF AALAASMPWLILAALAAVYIVLGVLYESYIHPLTILSTLPSAGLGALLLMLVTGTQLTVIA LIGILLLIGIVKKNAIMMIDFALAAERNQGLTPQQAITQACLMRFRPIMMTTLAAFFGALPL ALGSGGDADLRSPLGMAIAGGLALSQLLTLFTTPVVYLYLDRLSRNSQRAWHRLRKTGT A

## 5. **Small Multidrug Resistance (SMR)**: 4 protein sequences

>sp|Q65JB2|EBRB\_BACLD Multidrug resistance protein EbrB OS=Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46) OX=279010 GN=ebrB PE=3 SV=1

MKGMIFLAAAILSEVFGSTMLKLSEGFSAPLPAAGVIIGFAASFTFLSFSLKTLPLSAAY ATWAGTGTALTAAIGHFIFQEPFNLKTLIGLTLIIGGVFLLNSKRTEAADQKAQLTIEI >502347.3.peg.3992\_SMR

MPFVFSAIVTKVIVEIPLPPGKISVQLPALRDDLQTRLFIGDGPNSSEPDMSWIILVIAGLLEV VWAVGVMTPTY

>56780.15.peg.233 SMR

MLSPFRALAAVACPPAISEQKTGASRIFPEIGLASSSSSSRSLVFTISFRTQIGRYIMKGWLFL VIAIVGEVIATSALKSSEGFTKLAPSAVVIIGYGIAFYFLSLVLKSIPVGVAYAVWSGLGVVI ITAIAWLLHGQKLDAWGFVGMGLIIAAFLLARSPSWKSLRRPTPW >214092.21.peg.591 SMR

MAVFCYLGLAILPLIIEHDNVSRLSLCWLGRPSYASVFRGRPRLSEVVTMAWIILVIAGLLE VIWAIGLKYSHGFSRLTPSIITLVAMAASVFLLAYAMKSLPAGTAYAVWTGIGAVGTAILG IVLLGESASLARILSLGLILAGIIGLKLAS