

SUPPLEMENTAL MATERIAL

Phylogenetic and Kinetic Characterization of a Suite of Dehydrogenases from a Newly Isolated Bacterium, strain SG61-1L, that Catalyze the Turnover of Guaiacylglycerol- β -guaiacyl Ether Stereoisomers

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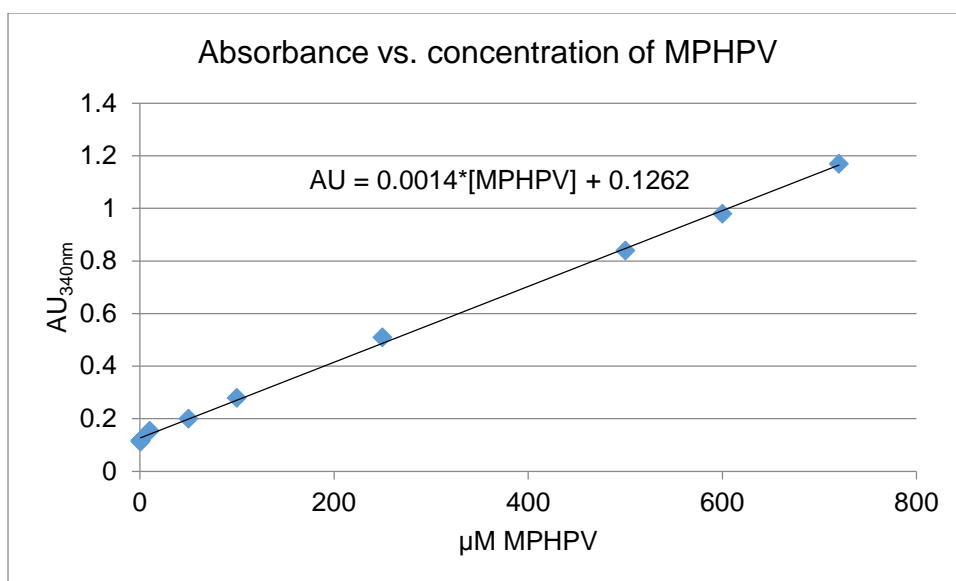
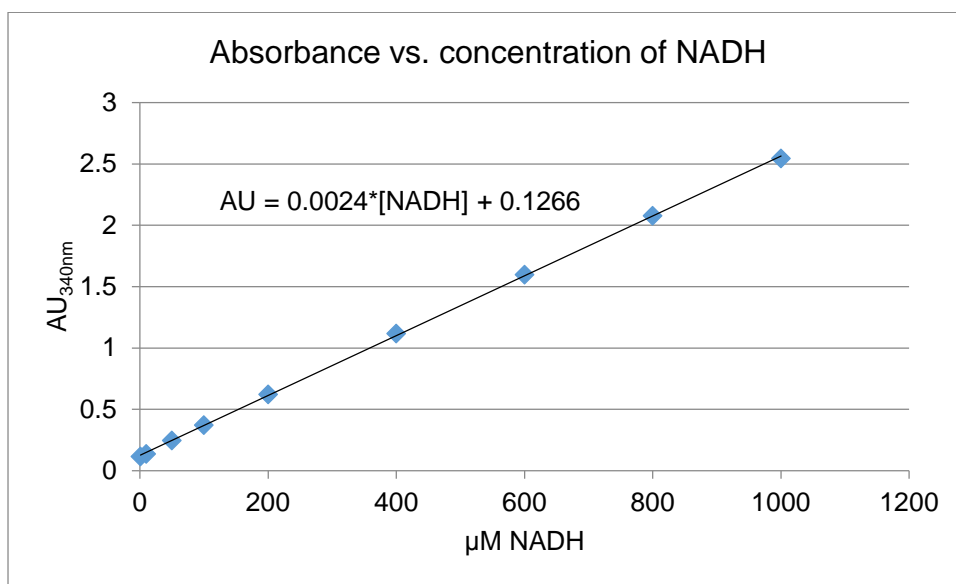
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Running Head: Characterization of GGE dehydrogenases

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S.P and N.D. contributed equally to this work

Construction of NADH and MPHPV standard curves. The NADH standard curve (shown below) was constructed by adding varying amounts of NADH to wells simulating kinetic assay reaction conditions (50mM Tris pH 8.0 at 28 °C). The MPHPV standard curve was constructed as follows: a GGE dehydrogenase reaction was set up to convert the GGE substrate to MPHPV. The peak corresponding to MPHPV was extracted from the LC-MS and any remaining GGE was quantified. The amount of biosynthetic MPHPV was quantified by subtracting the remaining GGE from the amount of GGE added to the initial reaction. The MPHPV fraction from the LC-MS was then evaporated to dryness and resuspended in 50mM Tris pH 8.0. The standard curve for MPHPV (shown below) was then constructed similarly as for the NADH standard curve.



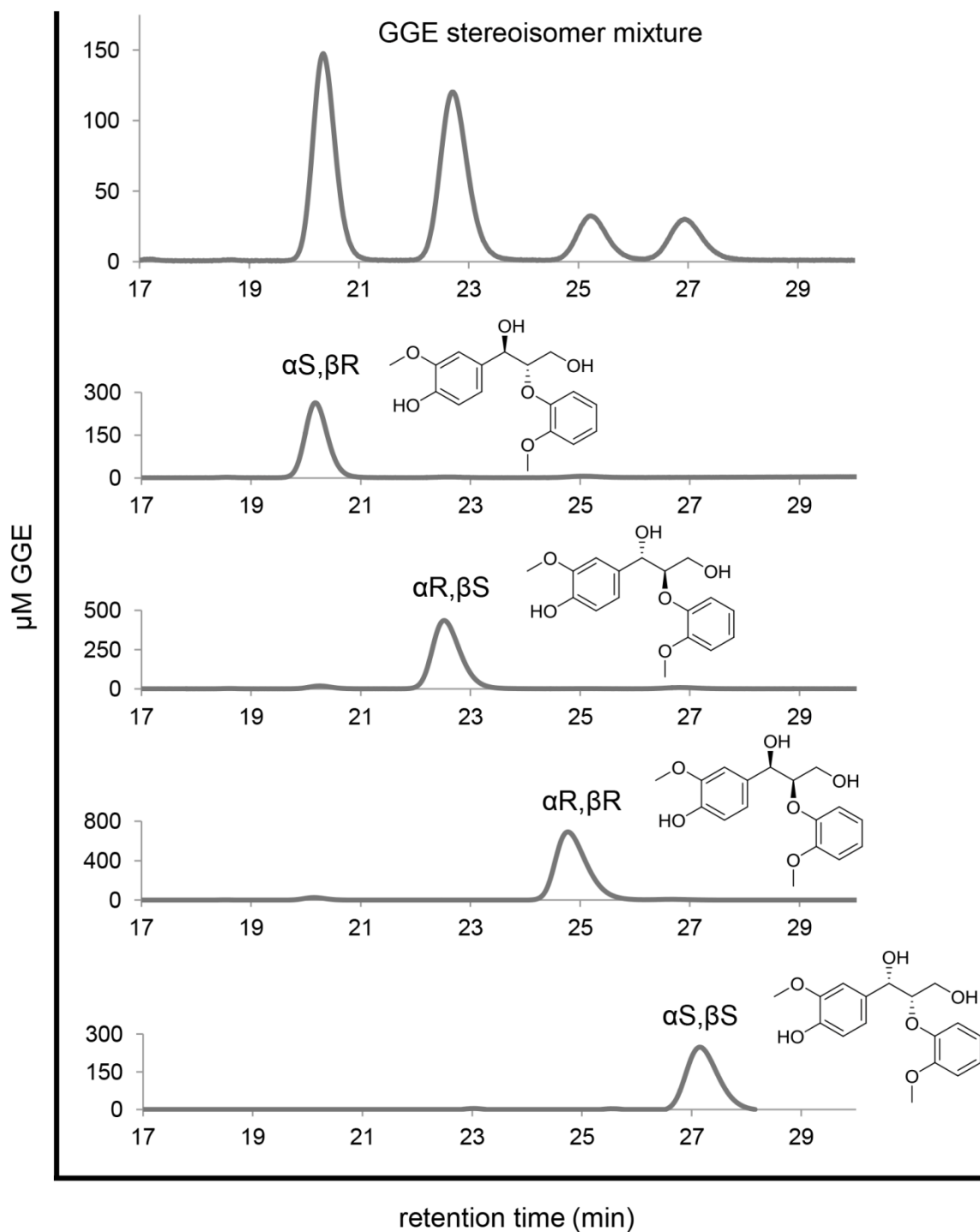


FIG. S1. Chiral column separation of GGE stereoisomers. The GGE mixture (top panel) and each individual stereoisomer (bottom four panels) was run separately through the chiral column on the TOF LC-MS.

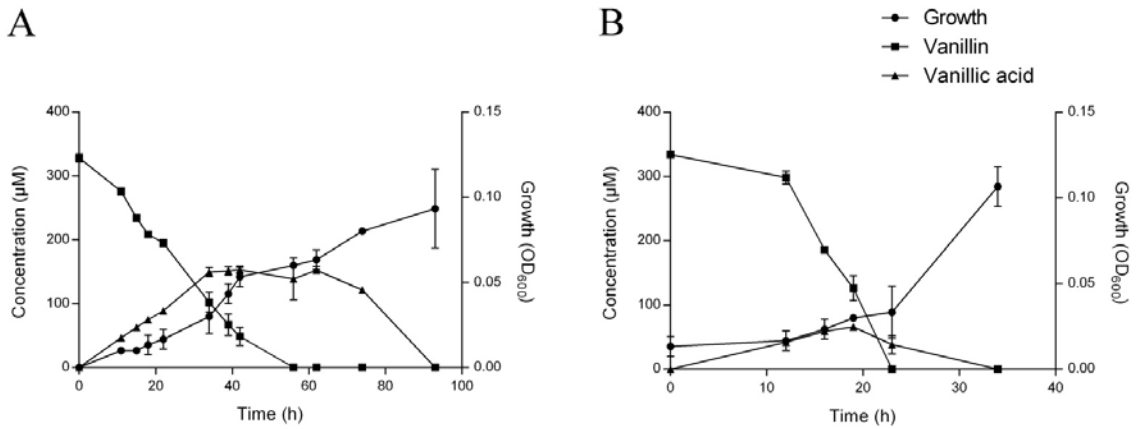
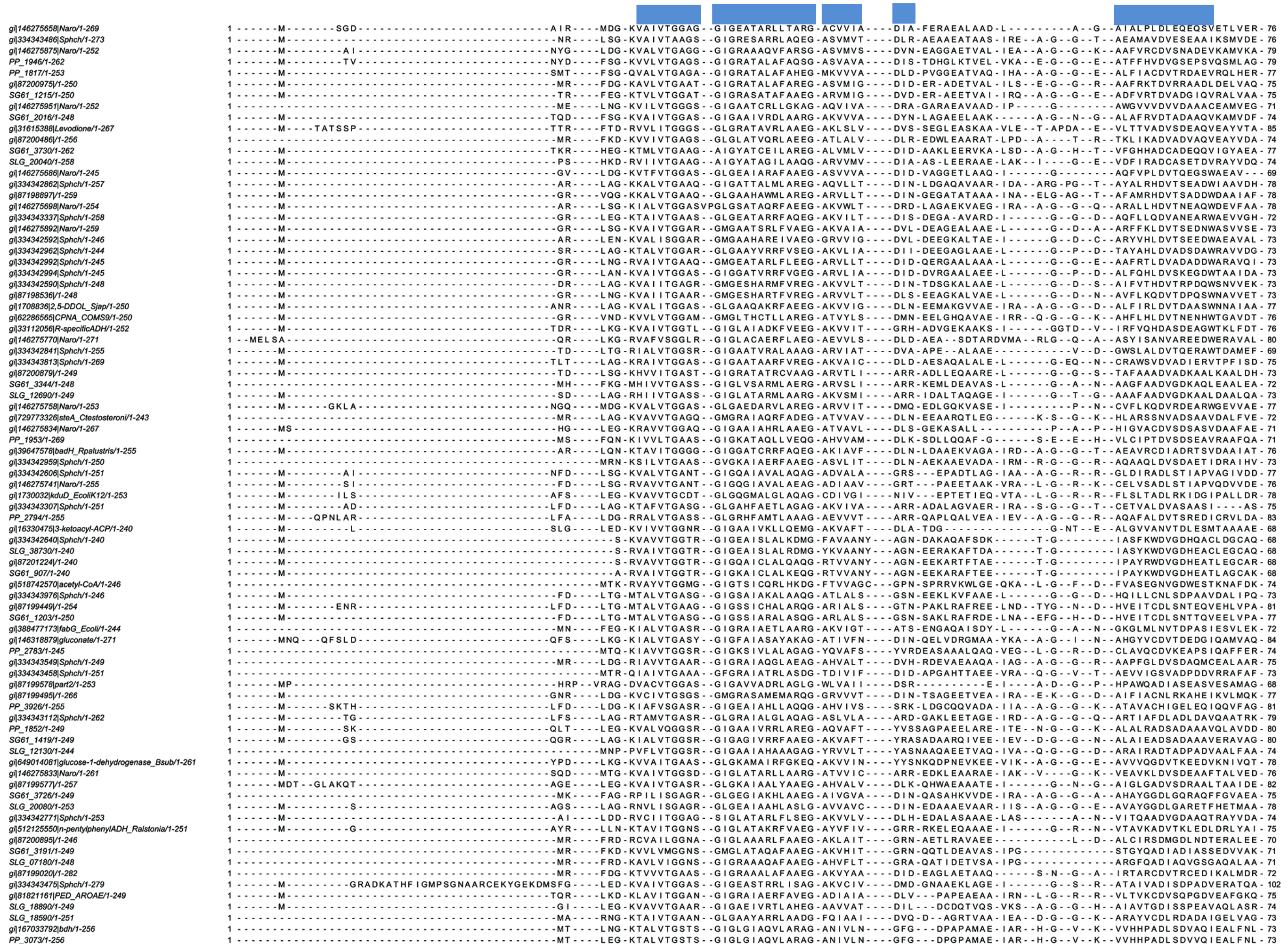


Fig. S2. Growth of SG61 (panel A) and SYK-6 (panel B) on monoaryl compounds over time. For each graph, the left y-axis shows the concentration of metabolite and the right y-axis shows the OD₆₀₀ values for either bacteria. Both bacteria were monitored for growth using vanillin as a sole carbon source. The experiments were monitored for disappearance of vanillin and formation / disappearance of the transient metabolite, vanillic acid.

FIG. S3. Alignment of dehydrogenase genes. Blue blocks are regions of the alignment that were used as input for IQtree.



g|84570596|bdh2_Rpicketti/1-256 1 --- -M-----LQG-KTALVTGSTC--GIGLGAQALAAQG--ANIIVN---GFR--RADGARQQ-IAA--A-GQVI--R--LGYHGADMSKASEIEDMMRY-74
g|33434517|Sphch/1-263 1 --- -M-----LSG-KTALITGSTS--GIGLAYAKALAGEG--ANVVIN---GFGDADAIEKERVG-LEA-LS-G--G--K--ALYSGHDLTKADQIEAMMQE-79
SLG_32730/1-261 1 --- -M-----MT-----LKG-RTALVTGSTS--GIGLAYAKAFAAQG--ANIVIN---GFGDAGAEQERLA-LEA-AS-G--G--K--AIYSAHDLTRADEIEMMAQ-77
g|87199767|1-261 1 --- -M-----MF-----LKD-KCALVTGSTS--GIGLAYARALAAEG--AHIVLN---GFGDPAEIEALCRE-LAD-AS-G--G--R--AIFAAGDLTRREGTEAMMAT-77
SG61_1243/1-257 1 --- -M-----MF-----LKG-KRAVVTGSTS--GIGLIARALAGEG--ASVVLN---GFGDAEIASAILHE-LSA-MS-G--A--D--AMHVPADLMQRSGVEALMEA-77
g|84570594|bdh1_Rpicketti/1-260 1 --- -M-----MQ-----LKG-KSAIVTGAAS--GIGKIAEELLAKEG--AAVAIA---DLN-LEAARAAAG-IEA--A-G--G--K--AIYAVAMDVTSEASVNSQATDE-75
g|334342462|Sphch/1-265 1 --- -M-----TD-----ARR-----LTG-RNALITGSVG--GLGQAMARKLASAG--ANVMLH---GLEEPEEAACLTEA-IER--EFG--V--R--AFYCRADLRQTAARELVDR-81
g|334343092|Sphch/1-255 1 --- -M-----SD-----RRR-----FEG-RSVFITGAGS--GIGEATAHFAEAG--AKVTIA---ELD-PAKGEAVRDA-IRA--K-G--G--T--AIFVATDATDEASVKAIAA-79
g|334343456|Sphch/1-245 1 --- -M-----YD-----FEG-KTLLTGAAG--GIGREVARLFAAHG--ANLVLV---DLN-LLVLAASLADLEI--P-P--E--R--VAVIAFDASSEQAQAQAAVL-76
g|334343408|Sphch/1-258 1 --- -MTF---PLPNA-----SQD-----LSG-QIALVTGATS--GLGYRFARILAHAG--ARVAVA---GRR-KDRLDKVVD-IRA--A-G--G--Q--ACAIIIDVGDAGSLADAVAQ-84
g|146275993|Naro/1-256 1 --- -M-----AGT-----FEG-KVALVTGAAS--GIGRAAIRFAEAG--ARVFCA---DLN-LAGAEVAAG--I-----G--K--G--ASAVQVVDVSNASNAQMVDA-74
g|146275997|Naro/1-246 1 --- -M-----ML-----FEG-KNVIPTGAAS--GIGRATAIRFAEAG--ARVTIG---DKN-VAGLEETAAM-MAS--A-----PVIQPFDVADNASCRLKLEVE-72
g|87199890|1-279 1 --- -M-----GTL-----RFD-----IKG-RSALVTGAAS--GIGLAYAEAMAEAG--AAVTLT---DID-AEGAEREAAAR-LRA--E-G--Y--E--VRAEKL DVSDWDNVAADFDA-81
SG61_474/1-283 1 --- -M-----KTL-----QFD-----IRG-RSALVTGAAS--GIGLAYAECEMAEG--ARVTLT---DID-GEAAEREAAAR-LRE--A-G--Y--E--ARAAKCDVSKLEDVAAAFDD-81
SLG_24920/1-278 1 --- -MVSHP-----KALE-----QFD-----IAG-RSAIVTGAAS--GIGLAYAETMAEAG--ARVTLT---DID-DVAGAAEREAAAR-LRA--E-G--Y--D--ARAQDLVSDRARTQVDFE-86
PP_1951/1-275 1 --- -M-----KLD-----VFS-----VEG-ARVIVTGAAS--GLGLAFTEAMAESG--AQVAML---DLN-REALDAQFR-LRS--L-G--Y--S--VRSHVLDVTRDRAVDVDFNA-81
PP_2002/1-257 1 --- -MI-----EISG-----TPG-----HNG-RVALVTGAAR--GIGLGAIAAWLICEG--WQVVLV---DLN-RQRGTQVAKA-L---G--D--N--AWFIMTDVADEAQVAGVSE-80
SLG_15310/1-259 1 --- -M-----ADD-----LFN-----VAG-KVALVTGGS--GIGRMAIEGYAERG--VRTYIT---GRD-FDRLGQIAAD-LSA--STG--G--T--CLPLVADLADPEGPARLVEA-81
g|146275988|Naro/1-261 1 --- -M-----LGM-----LKG-KTUVVTAAGT--GIGFVAKRAEAG--ARLLIS---DFH-ERRLGAAADR-IAA--E-VG-CE--R--PATVVCDVTNEAQQVQLRDA-90
SG61_609/1-245 1 --- -M-----TALVTGTAS--GIGGAASARWLDAQGIERLILV---DRD-ADGLNALELS-----C--V--VERHAGDVSDPAFWQA-----62
g|146275674|Naro/1-255 1 --- -M-----IQG-LAAIVTGGAS--GLGAATAELLAAR--AKVTLF---DLN-ADLGNAAKAAE--I-----G-----GRFAAVNVDDEDVANAIAE-70
g|334343001|Sphch/1-254 1 --- -M-----FRG-LAAIVTGGAS--GLGGATAERLARGG--AKVTVF---DLN-ADLGEAHAKA--I-----G-----GHF1KVDVTDNEAAYDAALDE-70
g|334343319|Sphch/1-259 1 --- -M-----MK-----LEG-LSAVVTGGAS--GLGAATARALSAHG--VEVALF---DLN-EESGEAVARE--I-----G-----GIFCKADVSSEESI EAAFAK-70
g|87199092|1-261 1 --- -M-----MK-----LDNTVAAVVTGGAS--GLGAATARALAAKG--VKVAF---DLQ-KEKGEAVAAE--I-----G-----GVFCEVNVTSDESVDAGFAK-71
SG61_354/1-260 1 --- -M-----MK-----IDNTVSAVITGGAS--GLGEATARALAAKG--AKVAF---DLQ-KEKGEVAAE--I-----G-----GIFCQVDVTSDESVDAGFAK-71
PP_2214/1-255 1 --- -M-----MH-----IAN-KHFIVSGAAS--GLGAATAQMLVEAG--AKVMLV---DLN-AQAVEAKARE--L-----G--D--N--ARFAVADISDEQAQASVDA-72
SG61_3175/1-254 1 --- -M-----MD-----PAG-KIAIVSGGAS--GLGEGGVKCLLAAG--AEVVSF---DVS-GDAPQ-----G-----AEFIRCDVSDVESVKAADVQ-64
g|146276032|Naro/1-246 1 --- -M-----MM-----EAVLITGGAR--GLGEVLVRAFHAAG--WRVAVS---DID-GDAAHLAIS-LDA--S-G--K--T--ALGLALDVRMGTDFEAARDV-72
g|334342802|Sphch/1-249 1 --- -M-----M-KSALIGGAS--GVGAATARAFAAEG--WRVAVA---DLA-VEPAQAL---VDE--L-G--P--D--HRYRCDITSETDILSLFDK-68
PP_1708/1-252 1 --- -M-----MS-----QNK-KVALVTGAGS--GIGRAVALALLEDN--FSLVLA---GRR-AEPLQAVVEQ-AL-A--G--G--E--ALAVPTDVRDEQSVAHLFAT-75
SLG_05090/1-250 1 --- -M-----MTG-RVAVITGAGS--GIGRAVTLTAAR--YRLVLA---GRR-ADALDETAAL--ASG--S-P--E--P--ILCVPTDVSDEGSAVALFKD-73
SG61_2863/1-244 1 --- -MN---L-----LKG-RVAVVTGASS--GIGACALGYAAAG--AKVVLA---ARR-VDREGLVKK--IED--A-G--G--E--ALAVATDVTSEAVANL FKQ-78
SLG_35070/1-243 1 --- -M-----QD-----LSR-HTAITGASS--GIGAGIARCFAAAG--ARLILA---ARR-ADRLDALAE-LSA--S-G--A--Q--VLPRPTDVTIEEDVIGLFAD-76
g|146275941|Naro/1-266 1 --- -M-----T-----GNR-----LDN-RAAVVTGAAD--GIGEGIARRFAAG--AAVVVA---DYD-DERGPAVARD-LRG--L-G--A--R--AEFIRCDVSRREDVIGAVDL-78
g|334343077|Sphch/1-254 1 --- -M-----ERP-----LEG-KVALITGSGS--GMGVGIALAVAKAG--AAVLVA---GRT-AQTLERTRAQ-IEA--A-G--G--R--AIVAPCDITDRAQVAAVAR-77
g|334342781|Sphch/1-260 1 --- -M-----SK-----IAG-KRVIITGGAR--GIGADTARYFAHHG--AKVVTF---DIR-DEEGDALAKE--ASS--Q-G-PG--S--VVYRRVDITSIPEINAGVEF-77
SLG_31530/1-250 1 --- -M-----KRVLTGGA--GIGLAIKRFIEDG--ARVLTC---DVD-ETALNALEA-VPG-----L-LGLHCDVTSREADLDALFGA-67
SG61_2583/1-255 1 --- -M-----TEQ-RTLLVTGASS--GIGAACARRLAAPG--VRLMLHASGRDEHKRAALEAAE-LAE--G-G--A--Q--TATCFDLAEPGAGTALASA-79
PP_2175/1-234 1 --- -M-----SVE-----KVAITAGGS--GMGAAAARLAADG--FKVGIL---SSS--GKGEALAAE--L-----G-----GIGVTGSNQSVEDL KRLVDA-68
PP_0488/1-253 1 --- -M-----KTAFTVGTASS--GFGRAICTLIGKG--YRVI G---ARR-MDKLKALEAE-L-----G--V--N--FIPALDVTDSVSLDKAVEQ-68
g|2506152|YDFG_ECOLI/1-248 1 --- -M-----MIVLVTGATA--GFGECTRFRICQ--HKVIAT---GRR-QERLQELKDE-L-----G--D--N--LYIAQLDVRNRAIIEEMLAS-67
g|334345036|Sphch/1-249 1 --- -M---A-----GTALITGATA--GIGAAAARRFTAAG--WKVIVT---GRR-AERLDALVAE-L-----G--A--D--KVHAFSDVDMRDEAIDAAALAA-70
PP_4862/1-254 1 --- -M---T-----STVITGATS--GFGEATARRFAEAG--WKLVLT---GRR-KERLDALCAE-L-----S--A--KTEVHGLVLDVRDRKAMEQAIAN-71
g|334346119|Sphch/1-241 1 --- -M-----TR-----TID-KVVLITGASS--GIGETTRELVAAG--ARLFIG---ARR-TERLKALADE-L-----G--E--N--VAWQELDVTGDAAFADADA-73
SLG_33310/1-241 1 --- -M-----TG-----VTD-KIILVTGASS--GIGETVRELVTGAG--AKLVIG---ARR-QDLQALAAEE-L-----G--E--Q--VAWQVLDVTDSDSVEAFVAA-73
g|334342779|Sphch/1-273 1 --- -M-----KN-----FSN-RVAVVTGAGS--GIGFGLAERFLAEG--MKVVLG---DIE-AAALDKAVGA--LSE--N--G--E--VLGVQTDVSDFRSLQSLADA-75
g|334342815|Sphch/1-290 1 --- -M-----TE-----VQG-RTAFITGAH--GIGLIARALAADG--VKVALA---DLN-ANALSLCKAE--LAS--I--T-----E--VETVRLDVRDRQGFVEAIDH-75
g|87198230|1-306 1 --- -M-----QS-----FEN-EIAFITGAS--GAGFGQAQVFGAG--AKIVVA---DVR-AEAVEKAVAE--LEG--L-G--I--T--AHGIVLDMIDREAYARAAD-76
SLG_08640/1-305 1 --- -M-----KD-----FQD-QVAFITGAS--GAGFGQAQVFGAG--AKIVVA---DVR-AEAVEKAVAE--LEG--L-G--I--T--AHGIVLDMIDREAYARAAD-76
SLG_35880/1-297 1 --- -M-----QD-----LEG-KVAFVTGGGS--GVALGQAKVLAEEAQMVAIA---DIR-QDHLDEAMGY--FSQ--K-N--V--A--VHPVRLDVTDRDQVAAAAD-77
g|87198815|1-310 1 --- -M-----KD-----FAG-RTAFVTGGAN--GVGIGLVRQLLNEG--CKVAIA---DIR-QDHDIDKALAT-LEA--E-G--SGPE--VMGVQLDVASREGFKAAAD-78
SG61_724/1-305 1 --- -M-----KD-----FAG-RTAFVTGGAN--GVGIGLVRQLLNEG--CKVAIA---DIR-QDHDIDKALAT-LDN--R-----E--VMGVQLDVASREGFKAAAD-74
g|87199892|1-280 1 --- -M-----G-----IET-----FAG-RTAFVTGGAS--GIGLIVKALARR--AFVVIA---DMR-TDHSRALKALAS--A-GLGE--S--VAAVELDVTDRAYASMAAR-80
SG61_2550/1-291 1 --- -M-----P-----IGS-----FEG-KVAFVTGGAS--GIGLISKVLIERG--AQVVA---DLR-QDHIDHALAL--FAG--G-GQS--N--A--VSAQLDVTNREKYREAAER-80
SLG_33660/1-289 1 --- -M-----MD-----IAG-TTAFITGAS--GIGFGIAQRLLANG--ARLVLA---DIR-QDHLDEARQF--FEERQ-G--R--N--VHTIRLDVSDRMAQEAARE-77
SLG_07240/1-277 1 --- -M-----MSFVTGGGS--GIGLIARALAAQG--ARVAIC---DLR-EDHLAQARDV--AAR--E-GWAD--R--FAAFLDVTDRPFGFAALDE-71
g|87198816|1-310 1 --- -M-----MQN-----LPG-KTAFTVGTASS--GIGLIIKALLGAG--MNVVIA---DIR-QDHLDSA---VAE--L-GGG--R--VLAVKLDVTDNRDQFKAADA-75
SG61_2705/1-303 1 --- -M-----MQD-----VAG-KGAFITGAS--GIGLGMVIFARAG--MNVVIA---DVR-QDHLDTAQAE--LAE--A-GLAG--K--VHGLLDVTDTRDQVAAAAD-78
SG61_1498/1-309 1 --- -M-----MKE-----VRG-KTAFITGAS--GMGLGMAKAFAEAG--MKVVIA---DIR-QQALDEAMAE--FAH--T-NF---A--VHPIRLDVTDTRDQVAAAAD-76
SLG_35900/1-311 1 --- -M-----MLD-----VSG-KTAFITGAS--GMGWMAKAFAG--MKVIA---DIR-QDLDQAMEG--FSK--T-NL---A--VHSILLDVTSDRQVAAAAD-76
g|87198727|1-305 1 --- -M-----TRD-----FTG-KTAFITGVN--GIGFIAARAFALAG--MDLILT---YRK-DEDRDAARW--LAD--N-G-LA--P--ARFVRLDVTDRARFAQVAAE-81
SG61_3329/1-309 1 --- -M-----STA-----DRP-----WEG-RVAFITGAVT--GIGLVQAQAFADAG--MRLALS---YRN-EDDKNRVAEW--FKA--K-G-YE--Q--PLFLKLDVTDRAVFAQVAAE-81
SLG_12640/1-304 1 --- -M-----D-----WTG-KVAFITGAGT--GIGFGIARAFSDAG--MRLALS---YRN-EAQARCDAA--FAQ--R-G-RE--A--PLWIRLDVTDRAVFAQVAAE-81
SG61_2549/1-315 1 --- -M-----QE-----LTG-KVAFITGGAN--GIGFGMVRFLAEG--MKVVVA---DWS-TSHIENAKA--LKG--N--N--A--AHFIRTDVADRANLKAADVE-76
SLG_28340/1-294 1 --- -M-----RN-----FAG-KVAFVTGGAS--GIGLGMVRNFLAEG--MKVVIA---DYN-EDHLDQAREI--LRG--N--N--A--THLIRVDVADRANLKAADVE-75
SG61_2706/1-296 1 --- -M-----RE-----FRG-KTAFITGGS--GIGLGMARAVLDRG--MNVVVA---DLL-DSHLTEAREL--LGS--T--N--R--LHCLDVTSDRAAMKAAEE-75
PP_1745/1-269 1 --- -M-----Q-----KRIMITGAGS--GLGREIAQRWARG--WRLALA---DVN-EAGLRETLEQ--VRQ--A-G--G--D--GFVQRCDVDRDYSQTLAQA-72
g|334342965|Sphch/1-259 1 --- -M-----M-----VER-KAIFITGGGS--GIGRAVARRFAAG--WLVGIA---DIH-PAGMAETAA--LPP-----G--S--ASLHQLDVTDRDQVAAAAD-73
g|87199139|1-266 1 --- -M-----MG-KTIFITGAS--GIGRAVARRFAAG--WLVGIA---DIH-PAGMAETAA--LPP-----G--S--ASLHQLDVTDRDQVAAAAD-73
SG61_504/1-269 1 --- -M-----MTQ-RAIFITGGGS--GIGRAVARRFAAG--WLVGIA---DIH-PAGMAETAA--LPP-----G--S--ASLHQLDVTDRDQVAAAAD-73
SG61_782/1-273 1 MMP -M-----LGG-QVALVSGAGR--GFGRAIAERLASEG--ARVALL---ARS-LEQLEEVAGT--IRA--S-G--G--E--ALPLACDVTDRASIEAAVEA-79
SLG_38070/1-265 1 --- -M-----PA-----LAG-EIAIVTGAGR--GFGRAIAERLASEG--AAVALI---ARN-KAQLDEAVAG--IRQ--A-G--G--E--AIALCADVTDPADVDRASVQ-76
SLG_27950/1-266 1 --- -M-----SA-R-LTE--TVAFVTGGRR--GLGAGIATALAEAG--ASVVVA---ART-LPQVEETVQA--ITR--A-G--G--R--AIVRCDVTDRAVFAQVAAE-77
g|87200928|1-272 1 --- -M-----MA-----FAG-QVVWITGASS--GIGAMARALAAQG--AKLVLS---GRN-EAALAEARNC-----G--D--ALVLPFEATDYAAAASAAK-71
g|146275769|Naro/1-259 1 --- -M-----TIA-----LNN-VVAVVTGAAG--GIGRELVKAMKAA--AIVIAT---DMA-----PSAD--VE---G---A--DHYLQHDVTSEAGWKAVAAL-68
g|146275845|Naro/1-289 1 --- -M-----ARET-----DNRDRDAFAG--GVAVITGAGS--GIGAGLARRAGELG--MTVVV---DIN-QEGAARTVGE--IEA--A-G--G--K--AEALRVDVSPPEELDRLEAET-85
4BMV:A|PDBID|n-pentyl/1-262 1 --- -M-----TTL-PTVLITGASS--GIGATYAEERFARR--HDLVLV---ARD-KVRLDALAAR--LRD--ESG--V--A--VEALQADLTRPADLAAVEIR-75
PP_2989/1-264 1 --- -M-----TTR-PTVLITGASS--GIGATYAEERFARR--HDLVLV---ARD-KVRLDALAAR--LRD--ESG--V--A--VEALQADLTRPADLAAVEIR-75
SLG_18780/1-267 1 --- -M-----VTM--KKALVTGSSS--GIGAFAAHLARRG--SDLVLV---ARR-QDRETLAER--LRG--ETG--V--S--VEVLKADLADPTDLHRIER-75
PP_0429/1-260 1 --- -M-----MT-RYAMITGASS--GLGLALAEALARRG--RNLILV---ARQ-RETLEPVAIE--LQ--RFG--V--E--VLFACDLSPQLRLSGFVLE-73
g|334343146|Sphch/1-268 1 --- -M-----GR-----LAG-KVAVIMGATREGNMQQA--ARRFLDEG--AHVVVS---GRG-KEGLDVFAAA---T-G-----ATAMACDIGSRAQLQSLADA-73
g|334343373|Sphch/1-250 1 --- -M-----QTILITGASS--GYGLETARHFLEAG--WNVIAT---MRS-PDRS-----VLP--P-S--E--N--LRVLPLDVTSEASIAATLVEA-65
SG61_417/1-252 1 --- -M-----KTVLITGCS--GYGLETARHFHANG--WNVIAT---MRH-PRAD-----ILP--A-D--D--R--MRIVPLDVTRTESIAEIAE-65

g|146275658|Nara/1-269 77 T V A H F - G R L - D V L H N - - - - - N A A L - L G - P E I A Q A - - - - - D G D V E R - - - - - M G T A L W D R T F A V N V R G T M I A - - C R A A L P H L - - - - - R E - - - - - T - - - - - R - - - - - G C I V N T V S N 148
g|334343486|Sphch/1-273 77 S V A R F - G R L - D I L H N - - - - - N A A L - L D - P D I T P L - - - - - D L S V V T - - - - - I P A D L W D R V M A V N V R S V M L G - - C K Y A I P V M - - - - - L E - - - - - N G - - - - - G - - - - - G S I I N T G S T 149
g|146275875|Nara/1-252 80 T V D T F - G G L - D C A F N - - - - - N A G I - N R - - - - - - - - - - - V T D - - - - - D Q Y D D A I W E R D I A I N L S G V M R C - - M R E E S A V M - - - - - L E - - - - - R G - - - - - G - - - - - G A I V N T A S I 145
P P _ 1 9 4 6 / 1 - 2 6 2 80 V V A H Y - G G L - D I A H N - - - - - N A G I - E A - N - - - - - I V P L A E - - - - - L D S D N W R R V I D V N L S S V F Y C - - L K G E I P L M - - - - - L K - - - - - R G - - - - - G - - - - - G A I V N T A S A 147
P P _ 1 8 1 7 / 1 - 2 5 3 78 L M A A Y - G R L - D Y A F N - - - - - N A G I - E I - E - - - - - Q H R L A E - - - - - G S E A E F D A I M G V N V K G V W L C - - M K Y Q L P L L - - - - - L A - - - - - Q Q - - - - - G - - - - - G A I V N T A S V 145
g|87200975|1-250 76 C L D R F - G R M - D A A F N - - - - - N A G V - L P - P - - - - - Q R P I H E - - - - - V P E D E L D L A I D V D F K G V F F A - - M Q A E I R H F - - - - - L K - - - - - V G - - - - - G - - - - - G A I V N T A S V 143
S G 6 1 _ 1 2 1 5 / 1 - 2 5 0 76 C L K R F - G S M - D A A F N - - - - - N A G I - L P - P - - - - - Q R P I H E - - - - - V P D E E L N A A I D V D F K G V W Y C - - V Q A Q V R H F - - - - - L N - - - - - V G - - - - - G - - - - - G A I V N T A S V 143
g|146275951|Nara/1-252 72 I R E R F - G R L - D G A F N - - - - - N A G I - T E - V T A L G - - - - - G A P I P E T - - - - - H A L P L E V W R K V L S V D L D G V F N C - - L R A E I P L M - - - - - L A - - - - - S G - - - - - G - - - - - G A I V N T T S L 146
S G 6 1 _ 2 0 1 6 / 1 - 2 4 8 75 A V A Q F - G R L - D L A V N - - - - - N A G I - A G - A - - - - - D K P V G E - - - - - I D L D D W H R V I D V N L H G V F Y G - - M R Y Q I P A M - - - - - L E - - - - - T G - - - - - G - - - - - G S I V N M A S I 142
g|31615388|Levodione/1-267 86 T T E R F - G R I - D G F F N - - - - - N A G I - E G - K - - - - - Q N P T E S - - - - - F T A A E F D K V V S I N L R G V F L G - - L E K V L K I M - - - - - R E - - - - - Q G - - - - - S - - - - - G M V V N T A S V 153
g|87200486|1-256 75 T V A Q F - G R I - D G F F N - - - - - N A G I - E G - R - - - - - Q N L T E N - - - - - F G A E E F H R V I S I N L D G V F Y G - - M A A V L K V M - - - - - R E - - - - - Q G - - - - - F - - - - - G A I V N T A S V 142
S G 6 1 _ 3 7 3 0 / 1 - 2 6 2 78 A L K A M - G R V - D G F F N - - - - - N A G I - E G - H - - - - - L A P T H E - - - - - Y E V A E F D R V L H V N L R G M F L G - - L R Y V L P D M - - - - - V K - - - - - R G - - - - - A - - - - - G A V V N T A S I 145
S L G _ 2 0 0 4 0 / 1 - 2 5 8 75 T V A K H - G R I - D G F F N - - - - - N A G V - E G - V - - - - - I T P I H E - - - - - Y P I D E Y D R I L A V N L R G V F L G - - L R F V L V Q M - - - - - V A - - - - - Q G - - - - - S - - - - - G A V V N T A S I 142
g|146275686|Nara/1-245 70 - - A P F - E R I - D V L V N - - - - - N A G I - T T - - - - - L G S V E E - - - - - I T L D Q F R H E L D I D V L G V F M G - - I Q A T L P R M - - - - - K T - - - - - H - - - - - G - - - - - G S I I N M S S L 133
g|334342862|Sphch/1-257 79 A R E T M - G G L - S V L V N - - - - - N A G I - V V - - - - - T G S V E E - - - - - L S L D D W H R G M A I N N D S V F L G - - S K Y A L P L L - - - - - R E - - - - - N Q - - - - - P - - - - - A S I V N L S S I 145
g|87198897|1-259 79 A A E K L - G G L - S V L V N - - - - - N A G V - G V - - - - - R G N I E T - - - - - C T L E W H R G F A I N V D S V F L G - - G Q A L P L L - - - - - R D - - - - - S Q - - - - - P - - - - - A S I V N I S S I 145
g|146275698|Nara/1-254 79 I E A E D - G K L - D V L V N - - - - - N A G I - A V - - - - - L R P I A E - - - - - M T T A D W N L Q N S V N L D S V F Q G - - T K R A V V L M - - - - - R K - - - - - T G - - - - - T - - - - - K - - - - - G S I I N I S S I 146
g|334343337|Sphch/1-258 73 A E E S W - G R L - D I L I N - - - - - N A G I - S M - - - - - F G L V T D - - - - - L T Y A Q W R R C I E V D L D S V F L G - - T R A A I P L M - - - - - R R - - - - - S G - - - - - G - - - - - G A I V N I S S M 139
g|146275892|Nara/1-259 74 V E A A L - G P V - D V L V N - - - - - N A G I - L M - - - - - F K S L L E - - - - - T T K A D E Y K V L G V N L V G E F L G - - I K A V A P G M - - - - - I A - - - - - R G - - - - - K - - - - - G S I V N I S S V 140
g|334342592|Sphch/1-246 74 A I A E F - G R L - N V L V N - - - - - N A G I - C T - - - - - M G S I E E - - - - - F T L A D W N R I I N I N L T G Q F L G - - I R A A T A A L - - - - - V Q - - - - - S A - - - - - P - - - - - S S I I N I S S T 140
g|334342962|Sphch/1-244 74 C I D R F - G R L - D I L V N - - - - - N A G V - G G - - - - - G A E L A D - - - - - T S D Q Q W E R Q I A V N L G G V F L G - - M R A C I P H M - - - - - A K - - - - - N G - - - - - G - - - - - G S V I N I S S I 140
g|334342992|Sphch/1-245 74 A A E L F - G G V - D I L V N - - - - - N A G Y - Y K - - - - - P L S L L D - - - - - S H S E E F G R H V E I N D K G T F L G - - M Q A V V A P M - - - - - R A - - - - - A G - - - - - G - - - - - G A V V N I A S V 140
g|334342994|Sphch/1-245 74 A M R A F - G R I - D I L V N - - - - - D A G Y - Y R - - - - - A T P L Q D - - - - - A T V E E F Q R H V E V N Q L G V F L G - - M Q A V V A P M - - - - - R A - - - - - A G - - - - - G - - - - - G A I V N I S S T 140
g|334342590|Sphch/1-248 74 A L A A F - G K I - D I L V N - - - - - N A G I - L G - P - - - - - M A N T V D - - - - - L T E E G Y H L V C A I N Q H A V F Y G - - M Q A V L P A M - - - - - V K - - - - - A N - - - - - K - - - - - G S I V N I S S I 141
g|87198536|1-248 74 A V R E F - G T I - D I L V N - - - - - N A G I - L G - P - - - - - M A P T D S - - - - - L D D E G Y R K V C A V N Q D S V F F G - - M R A V L P V M - - - - - V K - - - - - A R - - - - - R - - - - - G S I V N I S S I 141
g|1708836|2,5-DDOL_Sjap/1-250 78 A V D G F - G G L - T T L S N - - - - - T A G I - I H - - - - - P G G F E E - - - - - E S I E G W N K M V A V N Q T A I F L G - - I K A A I P E L - - - - - V K - - - - - S G - - - - - N - - - - - G S I I N I S S L 144
g|62286565|CPNA_COMS9/1-250 77 I L A E S - D R L - D A L V N - - - - - N A G I - L T - - - - - L K P V Q D - - - - - T S N E E W D R I F E I N V R S V F L G - - T R A V I E P M - - - - - R K - - - - - A H - - - - - K - - - - - G C I V N V S S I 143
g|33112056|R-specificADH/1-252 77 T E E A F - G P V - T T V V N - - - - - N A G I - A V - - - - - S K S V D - - - - - T T T E E W R K L L S V N L D G V F F G - - T R L G I Q R M - - - - - K N - - - - - K G - - - - - L - - - - - A S I I N M S S I 144
g|146275770|Nara/1-271 81 V K E R H - G K C - H V L V N - - - - - N A G I - D L - - - - - T G P V E T - - - - - L S M E G W R R I M S I N V D G V F L G - - T K H F V P L M - - - - - A E - - - - - S G - - - - - K D F R G G - - - - - S S I I N V S S I 152
g|334342841|Sphch/1-255 70 A Q E E A - G G L - D I L V N - - - - - N A G I - L I - - - - - T S P L K E - - - - - T S L E D W R R V Q S V N V E G V F L G - - C K Y A V P L I - - - - - A E - - - - - R A - - - - - A R W A G G - - - - - G S I I N M S S I 141
g|334343813|Sphch/1-269 76 A A A W L - G G I - D I L V N - - - - - N A G I - A I - - - - - P G T V I Q - - - - - L D P A N W R K I F A V D V D S I F Y A - - S R I A I P I M - - - - - I A - - - - - A G - - - - - G - - - - - G A V V N I A S I 142
g|87200879|1-249 74 A V A A N - G P I - D G L F L - - - - - N A G I - G G - M - - - - - F A P V E D - - - - - Y G D E A F D A V L A V N L K S V F W A - - I Q H A L P A M - - - - - K E - - - - - R G - - - - - Q - - - - - G A I L V T G S L 141
S G 6 1 _ 3 3 4 4 / 1 - 2 4 8 73 A A A H F - G P I - E G L F A - - - - - N A G L - T G - G - - - - - F T P A V S - - - - - F D P D V F E Q T I K V N L T S V F W A - - I Q K V L P A M - - - - - I E - - - - - A N - - - - - K - - - - - G A I L V T G S M 140
S L G _ 1 2 6 9 0 / 1 - 2 4 9 74 A A D R F - G P A - Y G L F A - - - - - N A G L - A G - N - - - - - F A P A L D - - - - - Y P G E L F E D V L R V N L T S V F W A - - M Q A V L P A M - - - - - I A - - - - - A G - - - - - E - - - - - G S I L V T G S M 141
g|146275758|Nara/1-253 78 T L R L F - G R L - D T L V N - - - - - N A G L - V R - - - - - F G T V E D - - - - - L S W D D Y K L T D V M A G G T F L G - - C K A A I P H M - - - - - S K - - - - - D G - - - - - S - - - - - G S I I N M A S V 144
g|729773326|steA_Ctestosteroni/1-243 73 I R E K L - G T V - D V L V N - - - - - N A G V - G S - - - - - V D Q F A D - - - - - I P D A T W E R V I G V N L N G A F Y C - - A R A A V K Q M - - - - - Q E - - - - - G K - - - - - G - - - - - G A I V N I S S T 139
g|146275834|Nara/1-267 72 V A A R L - G G V - D I L V N - - - - - N A G I - G S A P G D G M A E Y Y A G Q A A Q A G G D A S A - - Y A D Q T I H - - - - - C T D D G W S R V L S V T L D G A F R C - - S R A A V R I M - - - - - A E - - - - - Q G T - - - - - G - - - - - G A I V N I G S T 163
P P _ 1 9 5 3 / 1 - 2 6 9 72 V D A K F - G R V - D V I I N - - - - - A A G I - N A P T R E A N Q K M V D A N V A A L D A M K S G R A P T F D F L A D - - - - - T S D Q D F R R V M E V N L F S Q F Y C - - I R E G V P L M - - - - - R R - - - - - A G - - - - - G - - - - - G S I V N I S S V 165
g|39647578|badH_Rpalustris/1-255 77 T T T T L - G P V - D I L V N - - - - - N A G W - D I - - - - - F K P F T K - - - - - T E P G E W E R L I A I N L T G A L H M - - H H A V L P G M - - - - - V E - - - - - R R - - - - - H - - - - - G R I V N I A S D 143
g|334342959|Sphch/1-250 74 M I D W T - G Q L - D T V V N - - - - - A A G M - W F - - - - - G G T V L D - - - - - V D P D Q W R R V L E V N T T G A Y L L - - A R A A L P R L - - - - - K E - - - - - T - - - - - N - - - - - G S I I N I A S V 139
g|334342606|Sphch/1-251 78 T V A A L - G R I - D I L V N - - - - - N A G I - I R - - - - - R A D L P V - - - - - F S E E D W D A V V D T N L K T L F F L - - S Q A A A R P M - - - - - A A - - - - - Q G - - - - - A - - - - - G K I V N I A S L 144
g|146275741|Nara/1-255 77 V L S S L - G G L - D I L V N - - - - - N A G I - I R - - - - - R A D A V D - - - - - F T E E D W D A V V D T N L K S V F F L - - S Q A A G R H M - - - - - I A - - - - - N R - - - - - E A T G R R G K I I N I A S M 148
g|1730032|kduD_Ecolik12/1-253 79 A V A E F - G H I - D I L V N - - - - - N A G L - I R - - - - - R E D A L E - - - - - F S E K D W D D V M N L I K S V F F M - - S Q A A A K H F - - - - - I A - - - - - Q G - - - - - N - - - - - G - - - - - G K I I N I A S M 146
g|334343307|Sphch/1-251 76 V E P L L - A E V - D I L V N - - - - - N A G V - A A - - - - - D K P F L L - - - - - Q S E E D W D R V L D T N A K G M F L L - - S Q S A A R A M - - - - - K A - - - - - H G - - - - - R - - - - - G - - - - - G S I I N I A S I 143
P P _ 2 7 9 4 / 1 - 2 5 5 84 A - - - - - G P L - D V L V N - - - - - N A G V - S D - - - - - S Q P L L A - - - - - C Q D D T W D H V L D T N L K G A W A V - - A Q E S A R R M - - - - - V V - - - - - A G - - - - - K - - - - - G - - - - - G S I I N V T S I 147
g|16330475|3-ketoacyl-ACP/1-240 69 I T D K L - G P V - Y G V V A - - - - - N A G I - T K - - - - - D N F F P K - - - - - L T P A D W D A V L N V N L K G V A Y S - - I K P F I E G M - - - - - Y E - - - - - R K - - - - - A - - - - - G S I V A I S S I 135
g|334342640|Sphch/1-240 69 V A E A L - G P I - D V V V N - - - - - N A G I - T R - - - - - D G V L A K - - - - - M S F D D W N E V M R I N L G G C F N M - - A K A T F G G M - - - - - R E - - - - - R G - - - - - W - - - - - G R F V N I G S I 135
S L G _ 3 8 7 3 0 / 1 - 2 4 0 69 V A E D L - G P I - D V L V N - - - - - N A G I - T R - - - - - D N V M L K - - - - - M S F E E W N E V I R I N L G G C F N M - - A K A V F P G M - - - - - R E - - - - - R G - - - - - W - - - - - G R I V N I G S I 135
g|87201224|1-240 69 V A A E V - G P I - D I V V N - - - - - N A G I - T R - - - - - D G V L H K - - - - - M S F D D W N E V M R I N L G G C F N M - - A K A T F S G M - - - - - R E - - - - - R G - - - - - W - - - - - G R I V N I G S I 135
S G 6 1 _ 9 0 7 / 1 - 2 4 0 69 V A A E V - G P I - E I V V N - - - - - N A G I - T R - - - - - D A T L H K - - - - - M S F D D W N E V M R I N L G G C F N M - - A K A C F P G M - - - - - R E - - - - - R G - - - - - W - - - - - G R I V N I G S I 135
g|518742570|acetyl-CoA/1-246 75 V K A E V - G E V - D V L V N - - - - - N A G I - T R - - - - - D V V F R K - - - - - M T H E D W T A V I D T N L T S L F N V - - T K Q V I D G M - - - - - V E - - - - - R G - - - - - F - - - - - G R I I N I S S V 141
g|334343976|Sphch/1-246 74 A V E A L G G K I - D I L V N - - - - - N A G I - T R - - - - - D N L I L R - - - - - M K D E E W S D V I S V N L E A A F R L - - A R A A A K P M - - - - - M K - - - - - A R - - - - - F - - - - - G R I I S I T S V 141
g|87199449|1-254 82 A L D T L - G K L - D I L V N - - - - - N A G I - T R - - - - - D N L A M R - - - - - M K D E E W D A V I R V N L E A A F R L - - M R A A T K P M - - - - - M K - - - - - A R - - - - - F - - - - - G R I V T I T S V 148
S G 6 1 _ 1 2 0 3 / 1 - 2 5 0 78 T V D T L - G K I - D I L V N - - - - - N A G I - T R - - - - - D N L A M R - - - - - M K D E E W D Q V I R I N L E A A F R L - - M R A S C K P M - - - - - M K - - - - - A R - - - - - F - - - - - G R I I T I T S V 144
g|388477173|fabG_Ecolik1-244 73 I R A E F - G E V - D I L V N - - - - - N A G I - T R - - - - - D N L L M R - - - - - M K D E E W N D I I E T N L S S V F R L - - S K A V M R A M - - - - - M K - - - - - K R - - - - - H - - - - - G R I I T I G S V 139
g|146318879|gluconate/1-271 85 I E S E V - G I I - D I L V N - - - - - N A G I - I R - - - - - R V P M I E - - - - - M T A A Q F R Q V I D I D L N A P F I V - - S K A V I P S M - - - - - I K - - - - - K G - - - - - H - - - - - G K I I N I C S M 151
P P _ 2 7 8 3 / 1 - 2 4 5 75 V E Q R F - E R I - D L L V N - - - - - N A G I - T R - - - - - G L L A T - - - - - Q S L N D I T E V I Q T N L V G T L L C - - C Q Q V L P C M - - - - - M R - - - - - Q R - - - - - S - - - - - G C I V N L S S V 141
g|334343549|Sphch/1-249 76 L E R E I - G P V - S I L V N - - - - - N A G V - I F - - - - - P G R I D D - - - - - P G A R E K W D R T L A I N V G G P F N M - - C R A F Y P Q L - - - - - R A - - - - - T - - - - - R - - - - - G A V I N L A S I 142
g|334343458|Sphch/1-251 74 V D D R F - G G V - D I L I N - - - - - N A G V - T G - - - - - N R P T V D - - - - - I T D E E W R T M S I D L D G V F Y C - - S R E A G R A M - - - - - I G - - - - - R R - - - - - P - - - - - G V I V N I G S I 140
g|87199578|part2/1-253 69 I A G Q L - G P V - T L L V N - - - - - N A G I - V E - P - - - - - M A K S A D - - - - - Q A L A D F R R T I D V N V K G T I H A - - S R A A A R Q M - - - - - I G - - - - - A G - - - - - G - - - - - G A I V N L S S I 136
g|87199495|1-266 78 T A D H F - G G I - D V L H N - - - - - N A A I - H E - T D L T D - - - - - K T S I E D - - - - - L P E E I W D A V Y E V N L K A L W L T - - T R Y A V P W L - - - - - K L - - - - - S K - - - - - G - - - - - A A I V N V A S T 149
P P _ 3 9 2 6 / 1 - 2 5 5 82 I R E Q F - G R L - D V L V N - - - - - N A A T - N P - Q - - - - - F C N V L D - - - - - T D P G A F Q K T V D V N I R G Y F F M - - S V E A G K L M - - - - - R E - - - - - N G - - - - - G - - - - - G S I I N V A S I 149
g|334343112|Sphch/1-262 80 L N A E G - P A I - D I L V N - - - - - N G A I - G G - - - - - W G P L H D - - - - - S T L G Q W E N M F D V N V S S M Y L L - - C R D L S K G M - - - - - A A - - - - - R K - - - - - W - - - - - G R I I N F A S Y 146
P P _ 1 8 5 2 / 1 - 2 4 9 81 T E K A L - G R L - D I L V N - - - - - N A G V - L A - - - - - V A P V T E - - - - - F D L A D F D H M L A V N V R S V F V A - - S Q A A A R Y M - - - - - G Q - - - - - G - - - - - G R I I N I G S T 145
S G 6 1 _ 1 4 1 9 / 1 - 2 4 9 81 T A D H F - G G L - D I L V N - - - - - N A G G - G T - - - - - P E L I G E - - - - - A T L A N Y E H I F A V H V R A A F V A - - M N E A A K I M - - - - - P A - - - - - G - - - - - G R I I T I G S I 145
S L G _ 1 2 1 3 0 / 1 - 2 4 4 75 V E E A - G P L - R V L V Y - - - - - N G G I T G A - - - - - A S R L A D - - - - - A D P E T L A R V V A V N L T G A M L C - - A R A A I P L M S T R T G G Q - - - - - G - - - - - G - - - - - G A I V F M S S R 144
g|649014081|glucose-1-dehydrogenase_Bsub/1-261 79 A I K E F - G T L - D I M I N - - - - - N A G L - E N - - - - - P V P S H E - - - - - M P L K D W D K V I G T N L T G A F L G - - S R E A I K Y F - - - - - V E - - - - - N D - - - - - I - - - - - K - - - - - G N V I N M S S V 146
g|146275833|Nara/1-261 77 V A A R H - G R L - D M L V N - - - - - N A M S - V H - - - - - Y A P I A K - - - - - L R L D H W R K D F A V N A D A V F V G - - T K A A M K V M - - - - - A A - - - - - Q E - - - - - Q R G R Q R - - - - - G A I V N I A S T 148
g|87199577|1-257 83 A A A R F - G K I - D V L V N - - - - - N A M W - N S - - - - - Y D L I A D - - - - - I T P E I F A R M T G V G L G G I V W G - - I Q A V L P H M - - - - - P E - - - - - S - - - - - G - - - - - G A I V N I G S M 148
S G 6 1 _ 3 7 2 6 / 1 - 2 4 9 76 F R Y D A - G P L - R A V I N - - - - - N A S V - L V - - - - - Y E P I E D - - - - - V T E E T L E L M S A G L K S V F W G - - V Q A F L A Y R - - - - - D E - - - - - E A - - - - - S - - - - - G N I L N Y S S P 142
S L G _ 2 0 0 8 0 / 1 - 2 5 3 79 F A R A Y - G P V - D T L I N - - - - - N A S Y - L V - - - - - Y E P I E R - - - - - V T E E T L D R M I S S G L K S V F W G - - V Q A F L A H R - - - - - D - P E - - - - - A G - - - - - K - - - - - G W I N Y S S P 146
g|33434277|Sphch/1-253 75 A V A K W - G R I - D V L F C - - - - - N A G N - S G - P - - - - - I G G I E D - - - - - Y P E D A M D A Y R V H V R G S F L G - - A K H A L P H M - - - - - D K - - - - - G - - - - - G S I I V M S S V 140
g|512125550|n-pentylphenylADH_Ralstonia/1-251 76 V R E Q R - G S I - D V L F A - - - - - N S G A - I E - - - - - Q K T L E E - - - - - I T P E H Y D R T F D V N V R G L I F T - - V Q K A L P L L - - - - - R D - - - - - G - - - - - G S V I L T S S V 140
g|87200895|1-246 71 I E D A L - G G I - D V L F V - - - - - N A G V - G G - - - - - F A M V P D - - - - - V T P E F W D Q I H S V N L R G A F F A - - I Q R A L P L M - - - - - R D - - - - - G - - - - - G S I V I T G S I 135
S G 6 1 _ 3 1 9 1 / 1 - 2 4 9 72 I G A S D - G R I - D V L Y I - - - - - N A G V - G G - - - - - F A P L R D - - - - - I T S E A W D H T S I N L K G C V F A - - L Q A V R I M - - - - - G K - - - - - G - - - - - G S V V T G S I 136
S L G _ 0 7 1 8 0 / 1 - 2 4 8 72 I R E A H - G R L - D I L F V - - - - - N A G I - G T - - - - - F A P V A E - - - - - V T P A Q W D E V H N V N L R G C F F A - - V Q E A L P L M - - - - - G K - - - - - G - - - - - G A I V I T G S I 136
g|87199020|1-282 73 A G T E T - G G I - D T V F N - - - - - N A G A - G G - D - - - - - R A P I D E - - - - - I E P E G W D R T M D L L L R S V A F G - - I R Y A V P H M - - - - - K G - - - - - R H - - - - - G - - - - - A S F V N T S S V 140
g|334343475|Sphch/1-279 103 A L S A F - G R I - D L L H S - - - - - N A G I - I G - E - - - - - P G P I A G - - - - - A S A A N F D R V F S V N V R S A V L M - - I G A V P E M - - - - - R R - - - - - Q G - - - - - G - - - - - G S I V I T A S V 170
g|81821161|PED_AROAE/1-249 76 V I S T F - G R C - D I L V N - - - - - N A G I - Y P - - - - - L I P F D E - - - - - L T F E Q W K K T F E I N V D S G F L M - - A K A F V P G M - - - - - K R - - - - - N G - - - - - W - - - - - G R I I N L T S T 142
S L G _ 1 8 8 9 0 / 1 - 2 4 9 75 T A E A F - G P A - H I L V N - - - - - N A G L - H P - S - - - - - P M P F E E - - - - - L G F D Y W R R T M S V N L D A M F L T - - I Q A F L P Q L - - - - - K Q - - - - - N S - - - - - W - - - - - G R I V N F S A 142
S L G _ 1 8 5 9 0 / 1 - 2 5 1 74 L D K E M - G G V - D V L V N - - - - - N A G V - Y S - - - - - F T P H E T - - - - - V T I D V W R K I M S L N L D G M F L L - - T Q A V L P G M - - - - - K A - - - - - K G - - - - - W - - - - - G R I I N V A S N 140
g|167033792|bdh/1-256 74 A E G Q F - G G V - D I L V N - - - - - N A G I - Q H - - - - - V A P V E Q - - - - - F P T E S W D K I I A L N L S A V F H G - - T R L A L P G M - - - - - R T - - - - - R N - - - - - W - - - - - G R I I N I A S V 140
P P _ 3 0 7 3 / 1 - 2 5 6 74 A E R E F - G G V - D I L V N - - - - - N A G I - Q H - - - - - V A P V E Q - - - - - F P P E S W D K I I A L N L S A V F H G - - T R L A L P G M - - - - - R T - - - - - R N - - - - - W - - - - - G R I I N I A S V 140

gj|84570596|bdh2_Rpickett/1-256
 gj|33434517|1|Sphch/1-263
 SLG_32730/1-261
 gj|87199767/1-261
 SG61_1243/1-257
 gj|84570594|bdh1_Rpickett/1-260
 gj|33434246|1|Sphch/1-265
 gj|334343092|1|Sphch/1-255
 gj|334343456|1|Sphch/1-245
 gj|334343408|1|Sphch/1-258
 gj|146275993|Nara/1-256
 gj|146275997|Nara/1-246
 gj|87199890/1-279
 SG61_474/1-283
 SLG_24920/1-278
 PP_1951/1-275
 PP_2002/1-257
 SLG_15310/1-259
 gj|146275988|Nara/1-261
 SG61_609/1-245
 gj|146275674|Nara/1-255
 gj|334343001|1|Sphch/1-254
 gj|334343319|1|Sphch/1-259
 gj|87199902/1-261
 SG61_354/1-260
 PP_2214/1-255
 SG61_3175/1-254
 gj|146276032|Nara/1-246
 gj|334342802|1|Sphch/1-249
 PP_1708/1-252
 SLG_05090/1-250
 SG61_2863/1-244
 SLG_35070/1-243
 gj|146275941|Nara/1-266
 gj|334343077|1|Sphch/1-254
 gj|334342781|1|Sphch/1-260
 SLG_31530/1-250
 SG61_2583/1-255
 PP_2175/1-234
 PP_0488/1-253
 gj|2506152|YDFG_ECOLI/1-248
 gj|334345036|1|Sphch/1-249
 PP_4862/1-254
 gj|334346119|1|Sphch/1-241
 SLG_33310/1-241
 gj|334342779|1|Sphch/1-273
 gj|334342815|1|Sphch/1-290
 gj|87198230/1-306
 SLG_08640/1-305
 SLG_35880/1-297
 gj|87198815/1-310
 SG61_724/1-305
 gj|8719892/1-280
 SG61_2550/1-291
 SLG_33660/1-289
 SLG_07240/1-277
 gj|87198816/1-310
 SG61_2705/1-303
 SG61_1498/1-309
 SLG_35900/1-311
 gj|87198727/1-305
 SG61_3329/1-309
 SLG_12640/1-304
 SG61_2549/1-315
 SLG_28340/1-294
 SG61_2706/1-296
 PP_1745/1-269
 gj|334342965|1|Sphch/1-259
 gj|87199139/1-266
 SG61_504/1-269
 SG61_782/1-273
 SLG_38070/1-265
 SLG_27950/1-266
 gj|87200928/1-272
 gj|146275769|Nara/1-259
 gj|146275845|Nara/1-289
 4BMV:AlPDBID|n-pentyl/1-262
 PP_2989/1-264
 SLG_18780/1-267
 PP_0429/1-260
 gj|334343146|1|Sphch/1-268
 gj|334343373|1|Sphch/1-250
 SG61_417/1-252

75	AEAEF	-AA	-DILVN	-NAGI	-QH	VASIED	FPPERWDA	IA	AINLTS	SAFHT	-TRLAL	PGM	-RQ	-KN	-W	-GRVINI	AST	140																																																				
80	AADF	-GGV	-DILIN	-NAGM	-QH	VAPVEE	FPVDKWNL	IA	ALNLNS	SAFHT	-SRLA	IPYM	-KQ	-KK	-W	-GRI	IQTASA	146																																																				
78	AAETF	-GGV	-DILVN	-NAGT	-QH	VAPVES	FPVDKWNL	IA	ALNLTS	SAFHT	-TRLA	VPYM	-KE	-KK	-W	-GRI	IQTASA	144																																																				
78	ALAEF	-GAV	-DILIN	-NAGM	-QH	VAPVEE	FPVEKWDA	IA	ALNLTS	AFDA	-CRLA	IPGM	-KA	-KG	-W	-GRI	IFTASA	144																																																				
78	A	-GPV	-DILVN	-NAGM	-QH	VSPVDE	FPPEKWDA	IA	ALNLTA	AFDT	-SRLA	IPHM	-KA	-AG	-W	-GRI	INTASA	140																																																				
76	VAQAF	-GNI	-DILVS	-NAGI	-QI	VNP IQN	YAFSDWKMQA	I	HVDGAF	FLT	-TKAAL	KYM	-Y	-RD	-G	-GTV	IYMGSV	143																																																				
82	TEEAL	-GPV	-HILIN	-NAVV	-RH	FARIED	FPIEKWTEAL	AVNVT	AFLA	-TQMV	LPGM	-RA	-AH	-Y	-G	-GRV	NMTSV	148																																																				
80	ANEAH	-GPI	-AHAFN	-NIGM	-SR	PGSIEE	MSLEDWNWT	IG	ISLT	STFLA	-MKYE	IPVM	-KA	-NG	-G	-GT	VNTASM	146																																																				
77	CQDRF	-GGL	-DFLVP	-SAGI	-YV	DQSFD	MRFDQWRQ	TMSV	NLDG	IFLI	-TRAA	I PAL	-RK	-G	-GA	I	VLSSM	141																																																				
85	VEEAM	-GMV	-TILVN	-NAGM	-PD	AQLATR	MPLDL	IDQV	IGVNL	RGFIL	-AREV	AKRL	-I	-EA	-P	-GRI	INVASM	152																																																				
75	VMANA	-GQL	-DVAF	-NAGF	-YG	AEGLD	VDEAL	FDRLVA	INL	KGAF	NG	-IKAV	QAVI	-A	-T	-G	-GAV	VNTASA	140																																																			
73	GAR	-NGL	-DVLN	-ISGV	-LK	WGRSD	FSLED	DFL	VMRV	NTHS	VFTL	-CQAAL	PHL	-VE	-S	-K	-GRI	VNTASA	136																																																			
82	HDKAY	-GGL	-DICFA	-NAGI	-DTGAG	F-W	NPAGHRNPE	GGVDT	YDHR	KR	WDRS	IQ	INL	NGV	FYT	-V	SN	VR	IM	-K	KE	GRA	-NG	R	T	-G	-GS	V	T	ASN	167																																							
82	HAAAY	-NGC	-DIAFA	-NAGL	-DVGNG	F-W	TPEGKRN	PDGQ	IDV	YE	PER	WYK	IG	INL	NGV	FHT	-V	RE	AAR	VM	-K	NEAL	-S	GR	-G	-GS	I	V	T	SSN	167																																							
87	HEAAY	-GGL	-DIAFA	-NAGV	-DIPG	PFAAL	DPNGHRA	PDGQ	VD	YEP	EY	WDR	IA	INL	TG	AYNT	-M	R	DA	VR	LM	-K	K	-G	-GS	I	A	T	SSN	167																																								
82	VAGG	-GGL	-DIVFA	-NAGI	-DIPG	PFAAL	NAAGERE	PAN	MLEE	Y	SD	HR	WR	KV	IV	S	LD	DA	V	FYS	-I	R	A	AR	H	M	-S	-GS	I	V	T	TSV	163																																					
81	VLGQF	-GRL	-DALVC	-NAAI	-AN	-PH	NQTLES	LSL	AQ	WN	RV	L	GV	N	L	S	G	P	M	L	-A	K	H	C	A	P	Y	-N	-G	-G	A	I	V	N	L	T	ST	148																																
82	FGERE	-GKL	-DILVN	-NAGT	-GG	NGPIET	VDI	PD	WNA	AME	VNL	R	APF	LL	-VQ	QAL	P	L	-R	-A	A	A	P	G	-T	-Y	-AS	V	I	N	L	G	S	I	152																																			
91	ALEKL	-GKV	-DVLIN	-NAGL	-GG	EVDVDD	MTDDQ	WSR	V	DV	T	L	T	S	L	F	R	M	-T	R	A	F	L	P	A	M	-Y	-N	-S	-G	-G	V	M	V	N	N	A	S	157																															
63	LEPQI	-GRL	-DHAVV	-NAGI	-AA	GAPIAE	ESFE	Q	W	R	I	M	S	V	N	L	D	G	A	F	L	T	-L	A	T	A	L	R	L	-A	-K	-N	-G	-G	V	V	L	L	S	V	130																													
71	AEAVN	-GKA	-RILVN	-CAGI	-GP	PAKVL	N	R	D	G	S	P	-L	P	A	D	F	A	R	I	I	N	L	L	G	T	F	N	V	-L	S	K	F	A	S	R	-H	D	A	E	P	L	N	E	D	G	E	-R	-G	V	I	V	N	T	A	S	V	149												
71	AEALN	-GKA	-RILVN	-CAGI	-GP	PAKVI	I	R	D	G	S	P	-L	P	N	D	F	S	K	I	V	I	N	L	I	G	S	F	N	V	-L	S	K	F	A	A	R	L	-H	D	A	E	P	V	G	G	E	-R	-G	V	I	V	N	T	A	S	V	148												
71	AREAH	-GQE	-RILIN	-CAGT	-GN	A	I	K	T	A	S	R	S	K	T	T	G	E	I	Q	H	F	L	D	A	F	E	R	I	Q	I	N	L	I	G	T	F	R	C	-I	A	K	S	A	A	G	M	-L	T	L	D	P	M	E	D	-G	A	-R	-G	V	I	V	N	T	A	S	V	153		
72	ARAAH	-GQE	-RILVN	-CAGT	-GN	A	I	K	T	A	S	R	S	K	E	T	G	E	I	K	H	F	P	M	D	A	F	N	W	I	Q	I	N	L	V	G	T	F	R	C	-I	A	K	S	A	A	G	M	-M	T	L	D	P	C	D	E	F	G	E	-R	-G	A	I	V	N	T	A	S	V	155
72	ARAAH	-GQE	-RILVN	-CAGI	-GT	IGK	T	R	R	D	R	E	T	G	A	I	S	H	F	P	I	A	A	F	A	K	T	E	N	V	T	G	T	F	R	C	-I	A	K	A	A	A	G	M	-M	T	L	E	P	L	N	E	-R	-G	A	I	V	N	T	A	S	V	154							
73	AVSAF	-GSL	-HGLVN	-CAGI	-VG	AEK	V	L	G	K	Q	G	P	H	G	-L	A	S	F	A	K	I	V	N	V	N	L	I	G	S	F	N	L	-L	R	L	A	A	A	A	M	-A	E	G	A	A	D	E	S	-G	E	-R	-G	V	I	N	T	A	S	I	149									
65	VIERH	-GRI	-DILLN	-NAGI	-GG	L	G	P	V	A	T	P	E	G	P	G	D	-M	A	A	F	R	I	I	G	V	N	L	L	G	A	T	Q	-V	A	H	V	A	H	R	M	-M	A	N	E	P	S	G	P	D	G	E	-R	-G	V	I	V	N	T	C	S	I	142							
73	MLDRW	-GVV	-HALVN	-NAVV	-TR	A	P	D	D	F	S	A	V	E	N	L	R	G	T	F	V	G	-S	Q	V	F	R	L	F	-K	T	-Y	-G	-R	I	V	N	I	A	S	L	139																												
69	VEQDL	-GDL	-TILV	TAA	G	T	A	G	T	A	G	F	L	N	G	T	M	-P	R	-L	Q	-D	-P	S	D	H	W	D	Q	Y	M	N	I	N	L	R	G	G	F	L	A	R	E	M	L	R	R	R	M	A	-K	P	-H	-A	R	I	V	T	I	S	S	M	142							
76	IEEVH	-GRL	-DVMFN	-NAGI	-NA	-P	A	V	P	V	D	-L	P	E	N	W	R	N	V	I	A	T	N	V	D	G	V	F	L	C	-A	R	A	A	F	G	L	M	-R	-R	-Q	-Q	-P	-Q	-G	-G	R	I	N	N	G	S	I	145																
74	AVARF	-GRV	-DLLFN	-NAGL	-NG	-G	R	F	P	I	E	D	-M	V	A	L	F	R	E	V	D	V	N	L	T	G	A	F	L	C	-L	Q	A	A	F	R	V	M	-K	A	-Q	-Q	-P	-R	-G	-G	R	I	N	N	G	S	I	143																
79	AVDRF	-GTV	-DILIN	-NAGI	-AD	STP	VY	E	-L	S	E	M	W	H	R	V	I	E	T	N	L	S	A	F	L	C	-S	R	E	A	F	R	I	M	-K	D	-K	-G	-H	-G	R	I	N	V	G	S	I	145																						
77	A	-EAF	-SPV	-TLLVA	-NAGM	-AI	H	R	P	T	V	D	-V	T	L	E	Q	W	R	A	V	I	D	V	N	L	T	A	A	F	L	C	-G	R	E	A	L	R	V	M	-Q	P	-R	-G	-G	R	I	N	V	G	S	L	142																	
79	CVERF	-GSV	-DILVN	-NAYR	-GE	-G	P	V	R	I	E	D	-K	T	D	E	R	F	D	E	A	L	R	M	C	L	F	A	T	K	W	A	-M	E	R	A	L	P	H	M	-K	A	-K	-G	-W	-G	R	V	I	N	M	A	S	L	146															
78	TQAL	-GPV	-WLLVN	-NAVS	-TD	N	R	P	I	E	E	-V	D	D	A	N	L	L	R	S	S	I	H	G	S	L	Y	M	-M	Q	A	C	F	P	T	M	-K	E	-R	-G	-G	-G	-R	I	V	A	I	M	S	S	143																			
78	AAEQL	-GGL	-DGVPN	-IAGA	-YP	Y	A	P	A	D	A	-I	P	E	A	D	W	L	L	A	V	N	V	K	G	L	H	Y	V	-C	A	A	F	P	H	L	-K	E	-A	-G	-G	-G	-G	-V	I	V	N	M	A	S	D	144																		
68	VDHQL	-GGL	-DVLVS	-NVGI	-GG	-P	T	L	P	A	D	-L	P	S	E	D	W	R	R	V	I	D	I	N	L	T	A	S	F	L	C	-T	Q	R	A	I	P	L	L	-K	G	-S	-A	-G	-T	I	-I	M	S	S	134																			
80	TLAHF	-GEL	-DGIVS	-NAGF	-AD	R	P	F	L	N	-V	P	R	E	R	L	D	S	S	F	S	V	M	T	G	L	F	D	-A	R	A	A	A	P	A	L	-A	A	-S	G	-R	-G	-R	I	V	A	I	S	S	146																				
69	VVEKW	-GRI	-DVLLN	-SAGH	-GP	R	A	P	I	L	E	-I	S	D	E	D	W	H	K	G	M	D	T	Y	L	L	N	V	I	R	P	-T	R	L	V	T	P	Y	M	-Q	R	-Q	-G	-G	-V	I	N	I	S	T	A	135																		
69	MREAS	-LQI	-DLLVN	-NAGL	-AL	-G	V	D	R	A	Q	-S	S	A	N	W	Q	M	I	D	T	N	I	T	G	L	A	M	V	-T	H	K	I	L	P	Q	M	-V	E	-A	-D	-S	-G	-M	I	N	I	G	S	136																				
68	LPAEW	-CNI	-DILVN	-NAGL	-AL	-G	M	E	P	A	H	-A	S	V	D	E	W	E	T	M	I	D	T	N	N	K	L	V	Y	M	-T	R	A	V	L	P	G	M	-V	E	-R	-N	-H	-G	H	I	N	I	G	S	T	135																		
71	LPADF	-AQI	-DILIN	-NAGL	-AL	-G	T	A	P	A	Q	W	-A	D	L	Q	W	R	Q	M	I	N	T	N	I	T	G	L	V	T	I	-T	Q	K	L	L	P	R	L	-I	E	-R	-K	-G	-A	I	N	L	S	S	137																			
72	LPAGF	-EKI	-RGLVN	-NAGL	-AL	-G	V	D	A	A	Q	-C	S	L	D	D	W	E	T	M	V	D	T	N	I	K	L	M	Y	T	-T	R	L	L	P	R	L	-I	A	-H	-G																													

g|146275658|Naro/1-269
g|334343486|Sphch/1-273
g|146275875|Naro/1-252
PP_1946/1-262
PP_1871/1-253
g|87200975/1-250
SG61_1215/1-250
g|146275951|Naro/1-252
SG61_2016/1-248
g|31615398|Levodione/1-267
g|87200486/1-256
SG61_3730/1-262
SLG_20040/1-258
g|146275686|Naro/1-245
g|334342862|Sphch/1-257
g|87198897/1-259
g|146275698|Naro/1-254
g|334343337|Sphch/1-258
g|146275892|Naro/1-259
g|334342592|Sphch/1-246
g|334342962|Sphch/1-244
g|334342992|Sphch/1-245
g|334342994|Sphch/1-245
g|334342590|Sphch/1-248
g|87198536/1-248
g|1708836|2,5-DDOL_Sjap/1-250
g|62286565|CPNA_COMS9/1-250
g|33112056|R-specificADH/1-252
g|146275770|Naro/1-271
g|334342841|Sphch/1-255
g|334343813|Sphch/1-269
g|87200879/1-249
SG61_3344/1-248
SLG_12690/1-249
g|146275758|Naro/1-253
g|729773326|steA_Ctestosteroni/1-243
g|146275834|Naro/1-267
PP_1953/1-269
g|39647578|badH_Rpalustris/1-255
g|334342959|Sphch/1-250
g|334342606|Sphch/1-251
g|146275741|Naro/1-255
g|1730032|kduD_EcoliK12/1-253
g|334343307|Sphch/1-251
PP_2794/1-255
g|16330475|3-ketoacyl-ACP/1-240
g|334342640|Sphch/1-240
SLG_38730/1-240
g|87201224/1-240
SG61_907/1-240
g|518742570|acetyl-CoA/1-246
g|334343976|Sphch/1-246
g|87199449/1-254
SG61_1203/1-250
g|388477173|fabG_Ecoli/1-244
g|146318879|gluconate/1-271
PP_2783/1-245
g|334343549|Sphch/1-249
g|334343458|Sphch/1-251
g|87199578|part2/1-253
g|87199495/1-266
PP_3926/1-255
g|334343112|Sphch/1-262
PP_1852/1-249
SG61_1419/1-249
SLG_12130/1-244
g|64901408|glucose-1-dehydrogenase_Bsub/1-261
g|146275833|Naro/1-261
g|87199577/1-257
SG61_3726/1-249
SLG_20080/1-253
g|334342771|Sphch/1-253
g|512125550|n-pentylphenylADH_Ralstonia/1-251
g|87200895/1-246
SG61_3191/1-249
SLG_07180/1-248
g|87199020/1-282
g|334343475|Sphch/1-279
g|81821161|PED_AROAE/1-249
SLG_18890/1-249
SLG_18590/1-251
g|167033792|bdh/1-256
PP_3073/1-256

149 LALQ-GHLI-Q--AAYSSSKAAV IQMTRA I AASHGKA -G--VRCNAVAPGMTMTPI--L-REAF-----PPALRQV-----VE-D-ET--LR-DRLGD---P-RDIAEAIAFLAS--D-AAR---NVT 241
150 MGLG-GEAW-Q--VSYGTSKAAV IQLTKRYVATHFGKQ -G--IRCNAIAPALVMTPI--V-ETAM-----HPQLQA-----HE-E-NC--LT-PYLGD---P-EDIAAAVAFLAS--D-DAR---YVT 242
146 NGLV-GNGS-Q--PAYTAAKHGTVGLTRKHAALRWAKN -G--IRVNAVCPGV IETPM--T-APLV-----QNPRIKAL-----MD-S-MT--PM-GRMGS---A-MEIAEAVVWVLS--P-AAS---FVT 239
148 SGLI-GGYR-L--SGYTATKHGVVGLTKAAAIDYANQ -N--IRINAVCPGPVDSFP--L-ADMP-----QPMRDR-----LL-F-GT--PI-GRLAT---A-EEIARSVLWLCS--D-DAK---YVY 239
146 AGLG-AAPK-M--SIYSASKHAV IGLTKSAAIEYAKK -G--IRVNAVCPAV IETDM--F-RRAY-----QADPRKAEF-----AA-A-MH--PV-GRIGK---V-EEIASAVLYLCS--D-GAA---FTT 240
144 GALI-ADPN-M--SAYCAMKHAVSGLTKAAAVEYAQA -G--IRVNAIAPGVVTPM--T-QHWA-----DSNEFTQM-----FF-A-QN--IS-GRAAR---P-EEIAPTVLHLCS--D-GAS---FIN 237
144 GGLI-ADPN-M--AAYCAMKHAV IGLTKGAAVEYARH -N--IRVNAIAPGVVTPM--T-QHWA-----DSPEFTSA-----FF-Q-HN--VS-GRCAQ---P-EEIAGTVLHLCS--D-AAS---FVN 237
147 QAH I-SYPR-T--AAYTAAKHGVLG LTKAI AKEYGEQ -G--IRCNVSPGVVDTP L--T-AGVI-----HSPQYKDM-----LL-A-PI--PL-KRFAT---P-EDIAKAALWVLS--D-ESA---YIN 240
143 LGSV-GWRG-A--AAYVAKHGVCGMTKSAALEYSQA -G--IRVNAVGPFIETPL--I-ENAM-----TDEARAA-----LV-G-MH--PI-GRLGQ---P-EEVAALTNFLS--D-AAS---FVT 235
154 GGI R-GIGN-Q--SGYAAAKHGTVGLTRNSAVEYGRY -G--IRINAIAPGA IETPM--V-ENSMKQL----DP----ENPRKAAEE-----FI-Q-VN--PS-KRYGE---A-PEIAAVVAFLLS--D-DAS---YVN 253
143 GGI R-GVGN-Q--SGYAAAKHGTVGLTRNSAVEYGGY -G--VQINAIAPGA IETAM--V-EGSLRQI----GG----ENWEEAGRQ-----FV-S-VN--PM-KRFRG---P-EEVAALVAFLLS--G-EAI---FIN 242
146 GSER-GLAG-A--CAYNAAKHGAVGLTRTAASEVAQK -G--VRVNCVMPGV IETPL--L-VGML EQMF-----DDVAAGMRK-----LG-E-VA--TL-NRVGQ---P-AEVGNVVSFLLS--D-EAS---YVN 244
143 GSER-GLAG-G--AAYNAAKHGTVGLTRTAADLGP K -G--IRVNCVMPGV IETPL--L-NEVLVQM---FD----GDQLKGLD-----LG-W-VS--VM-NRCGK---P-AEVGHVVVFLS--D-EAS---FVT 242
134 SGVK-ASAN-L--VAYNAAKAAVT LMTKSCALHFADKGYG -G--IRCN IHPGA IHTPI--I-DKVL AQS-----DDPDALYRS-----FV-D-VH--PV-KRLGK---P-EEIAAIAVYLAS--D-ASA---FAT 233
146 AGL I-AAHN-L--ANYNASKAAVWVLSK IALHCARN -GWD I RCNSVHPT I RTPI--L-DDL IADR-----DEATMMAK-----LA-R-QV--PL-GRLGD---P-EEVAHAVVYLAS--D-ESR---FMT 244
146 AGL I-ASDT-M--PGYNASKAAVWMLTKSVYALCAKR -G--IRVNAVCPGV IETPL--L-DG I SANAN-----LEKSVVMGK-----LA-R-QI--PL-GRVGE---P-DDIAAGVLYLAS--D-ESR---FMT 246
147 AGL I-GVPA-C--GAYAAAKGGVRLFSKT IAVETAKD -G--IRVNSVHPGM I LTN I--Q-GVAQ-----EDNAANYDA-----TL-A-LV--PM-GYMGD---P-LDIANMNLFLAS--D-ESR---YVT 241
140 AGIT-GQRA-L--SAYCAAKGGVRFSSKAAHL ECASARDN -IRVNSVHPG I IDTP I--F-HATEADERRA-----PVGQAAMDVGP-----MA-AFAV--PM-GVPGK---A-EDIAAACLYLAS--D-DGR---FMT 245
141 DGMK-GANS-L--VAYASSKVGVRGLTKVAAAMELGHK -G--IRVNSVHPGGVDVTM--S-NHSG-----AAREDVDK-----GY-A-NV--PL-QRIGG---P-EEVAASLFLAS--D-DAS---YH 234
141 QGIE-GIPG-L--HGYTASKFVRGLTRCIA IELAGR -G--VRANTICPGT IATPM--N-EGLD-----DPLQKGLD-----VS-G-FN--PM-NRKAD---P-REVAKLVVFLAS--D-ESP---FIS 226
141 NGIR-GNRN-R--YGYVASKFVGLTKTAAALDFAPA -G--VRVNAVLPGM I STPM--T-AGLK-----V-----DT-S-LI--PL-GRPGN---M-EEIAQVVAFLAS--D-EAS---YIT 227
141 AGLR-GGPG-M--FSYGAAKWA VRGMT RSAAHDLAPF -H--IRVNAVLPGP I DTM--I-NTGN-----DPALNAA-----IT-E-RT--LL-KRMGQ---P-REVAMATLFLAS--D-EAS---YVT 233
141 GGMR-GGPS-L--FHYRTKWA VRGMT RSAAHDLASL -N--IRVNTVLPGP IETPM--M-KAGN-----SQDRIDA-----MK-G-RT--LL-QRLGQ---P-SELAAVLFLAS--D-EAS---YIT 233
142 AGMA-ANYG-FPSLAYVASKFAVRGMTKATAMEYGYK -N--IRVNSVHPGF I QTPM--M-VEAT-----DEVGGD-----AL-A-EI--PL-GR IAD---P-SEVSNLVLFLAS--D-ESS---YIT 235
142 AGMA-ANYG-FPSLAYVASKFAVRGMTKATAVEFVKH -N--IRVNSVHPGF I QTPM--M-VEAT-----DEVGGE-----AL-A-QI--PL-GR IAD---P-SEVSNLVLFLAS--D-ESS---YIT 235
145 IGMF-PTAG-G--AAYNAAKKAVRIMS KAAAL EFDVDR -G--VRVNT I VPGGMNTPI--T-ANVP-----DVLKQK-----QT-S-QI--PM-KGLGD---P-IDIANGALFLAS--D-EAK---YIT 236
144 YGLV-GAPG-A--AAYEASKGAVRLFTKACAVDLAPF -N--IRVNSVHPGV IATPM--T-QQIL-----DAPQSARA-----LL-G-PT--LL-GRAAQ---P-MEVSQAVLFLVS--D-EAS---FVH 237
145 EGFV-GDPT-L--GAYNASKGAVRIMS KSAALDCAL KDYD -VRVNTVHPG I K TPL--V-DDLE-----GAEEMMS-----QR-T-KT--PM-GHIGE---P-NDIAWICYVYLAS--D-ESK---FAT 239
153 MGLV-GMNE-V--SAYNASKGAVRLFTKGI AIEFAQK -KTP I RANSLHPGFVETPLLKAG -FQRVWDQGF A-----DKPDDL VAG-----VVT-G-AT--PI-GR LAQ---P-SELASAFFLAS--D-DSS---YMT 258
142 AGLR-GTAA-F--TAYSASKGAVRLMTKSLAHELAGR -R--IRVNSVHPGLVETEM--G-RQLVSEIALR-----DRGDPTCPS-----DT-A-AV--QPL-DSAGA---P-HDIAHAVVFLAS--D-KAA---FMN 243
143 SGLR-GDHA-L--VGYNAAKGAVVNLTRAMAVDHADP -N--VRVNAVCPGL IETPL--T-QAAK-----DAGLWYA-----WT-S-TI--PM-RRAGT---A-EEMASVVAFLAS--D-EAS---YVS 235
142 ASER-GLPM-N--AGYVASKHAVLGLSRVAENAAEA -G--VRCNCLPGL IETPM--L-DGLP-----PEASQ-----MA-R-AV--PQ-GR TGS---S-DEVAQVAFFLS--D-AAS---HVT 233
141 GSKR-GMAM-N--PAYVASKHGVLGLTR IAVEMAPH -S--IRANCI I PGFIRTEA--L-DRIP-----PEQADR-----IA-A-RV--PQ-RRMGS---P-EELAEVACFLS--D-AAS---HVT 232
142 ASKR-GMAM-N--PAYVASKHGVLGLSR IAVEMAPH -G--VRCNCV I PGF I DTPA--F-DLIP-----PDQAAR-----IN-Q-RV--PQ-RRMGS---A-DELAEVACFLS--P-AAS---HVT 233
145 GGIK-GISA-I--PAYAAAKAG IGMTRS IAVHCREQ -GYR I RCNS I APG I VTPM--T-AQAL-----AELPADNA-----GL-D-QA--HN-HGMGQ---P-IDIANMVLVYAC--D-DGR---HIT 240
140 SAVS-GD-G-P--AHYCAASKAALMTRGMADELASK -K--IRVNTLVPGPTNTPM--M-QGIP-----QEWADA-----I-I-A-GV--PM-GRMAE---P-EDIAKVAVFLAS--D-DGS---FVT 230
164 AALA-GN-G-P--VPYVAKAAV LGMTRAMARELAPR -G--IRVNAVNP GATETPI--Y-APLP-----DEVKAA-----VA-A-DS--VM-KRLAH---P-DEIAGAVVFLAG--N-DAS---FAT 254
166 AALL-GV-AMP--LYYPASKAAV LGRTRAAAALAPY -N--IRVNAIAPGSVDTP L--M-HEQP-----PEVVQF-----LV-S-MQ--PI-KRLAQ---P-EELAQSLFLAG--E-HSS---FIT 257
144 AARV-GSSG-E--AVYAAACKGLVAFS KTLAREHARH -G--ITVNVVCPGPTD T L--L-ADVTSGA-----ANPEKLEA-----FT-K-AI--PL-KRLGK---P-DDLAGAIAFFGS--D-DAG---FIT 241
140 AGLK-GTAG-T--VVYNTSKTAVVGLTKCMALDFAAA -G--VRVNC ICPG I IDTPM--V-DTVLGHF-----GEAFTREA-----LA-R-RH--PL-GRLGK---P-EDIAGAFFLAS--D-DAS---WIT 236
145 LSFQ-GGIR-V--PSYAAAKSGVAVG TKAMANELAPQ -G--VQVNA I APG I ATNN--T-AALQ-----ADETRDRQ-----IM-E-RI--PT-GRWGR---P-EDIAGAFFLAS--P-ASD---YVT 238
149 LSFQ-GGIR-V--PSYTASKSGVAGLTKLLACEWAAR -G--VNVNA I APG I ATNN--T-SALQ-----ADETRDRQ-----IM-E-RI--PE-GRWGD---P-ADIGAAVFLAS--G-AAD---YVQ 242
147 LSFQ-GGIR-V--PSYTASKSGVMTLRMANEWAKH -N--INVNA I APG I MATNN--T-QQLR-----ADEQRSAE-----IL-D-RI--PA-GRWGL---P-SDLMGPIVFLAS--S-ASD---YVN 240
144 LGLR-QGSR-V--ATYAVSKAAT IQLTKVAALELARF -G--VRVNC ICPG I IATDI--N-RDFW-----ETEAGD-----ML-R-RV--PQ-RRLGE---P-RELDGPLL L L L AS--D-ASS---FMT 236
148 LASR-VAGA-V--GPYLAAGKAGLH LTRAMALELARH -G--IRVNAIAPGVMTDL--N-EAFL-----ASEAGDK-----LR-S-RI--PS-RRFSV---P-SDLDGAL L L L AS--D-AGR---AMS 240
136 SGER-GNVG-Q--TNYSATKAGV I GMMKSLGAREGARY -G--VRANAVAPG I DTEM--T-LAIR-----EDIREK-----IT-K-EI--PF-RRFGK---P-EEIAWAVAFLLS--PVASS---YVT 228
136 NGQA-GQYG-Q--VNYAAAKSG I HGFTKALAQEGAKY -G--VTVNA I APG I IDTM--V-AAVP-----PAVLEK-----IV-A-KI--PV-GRLGH---A-DEIARGVAFCS--E-DGG---FVT 227
136 NGQA-GQYG-Q--VNYAAAKSG I HGFTKALAQEGARA -G--VTVNA I APG I IDTM--V-AAVP-----QAVLEK-----IV-A-RI--PV-GRLGH---A-EEIARGVAFCS--E-DAG---FVT 227
136 NGQA-GQYG-Q--VNYAAAKSG I HGFTKALAQEGARV -G--VTVNA I APG I IDTM--V-AAVP-----EPVLEK-----IV-A-KI--PV-GRLGH---A-EEIARGVAFCS--E-EAG---FVT 227
142 NGQK-GQFG-Q--TNYSTAKAG I HGFTMALAQEVATK -G--VTVNTVSPG I DTM--V-KSIR-----PEVLEK-----IV-A-TI--PV-RRLGT---P-DEIGSIVAWLAS--D-ESG---FST 233
142 VGVT-GNPG-Q--ALYASAKAG I GMSKSLGQELASR -G--ITVNCVAPG I RTAM--T-DALN-----DAQKGA-----IL-A-RI--PA-GDLGS---G-EDIGA AVVY LAS--K-EAG---YVT 233
149 VGAT-GNPG-Q--VNYAAAKAGL VGMSKSLGQELASR -G--VTVNCVAPG I RTAM--T-DVLP-----DGQKDA-----LN-A-RI--PM-GRMGE---G-SDIGA AVVY LAS--K-EAG---YVT 240
145 VGAT-GNPG-Q--VNYAAAKAGL VGMSKSLGQEVASR -G--ITVNCVAPG I RTAM--T-DVLP-----DAQKDA-----LN-A-RI--PM-GRMGE---G-EDIGA AVVY LAS--K-EAG---YVT 236
140 VGTM-GNGG-Q--ANYAAAKAGL IGFSKSLAREVASR -G--ITVNVVAPG I DTM--T-RALS-----DDQDRAG-----IL-A-QV--PA-GRLGG---A-QEIANAVAF LAS--D-EAA---YIT 231
152 MSEL-GRET-V--SAYAAAKGGLKMLTKN IASEYGEA -N--IQCNIGPGY IATPQ--T-APLRELQK---D---GSRHPFDQF-----I-I-A-KT--PA-ARWGE---A-EDLMGPAVFLAS--D-ASN---FVN 251
142 AAQK-PGKQ-Q--SNYAAAKGGVEALTRALAVELAPR -N--IRVNAVAPG I VSTDM--S-QALV-----GAHEQE-----IQ-S-RL--LI-KRFAR---P-EEIADAVLYLAE--RGL---YIT 232
143 RSFV-AAPN-A--AAYAASKGAVMQLTRALAVEWGGD -G--IRVNAIAPGFIETTL--V-PDHE-----KTAEREA-----IL-A-RT--PL-RRQR---P-DEIAGTAVY LAS--D-AAC---YVS 236
141 YSLV-AAPE-R--ASYCASKAGVAML TRSLAVEWAPH -G--IRVNCVAPG I DTEM--M-RELA-----AVG IALEP-----LL-R-RT--PQ-GRLTQ---M-EDVAQVAFCD--P-RSV---HIT 235
137 TASL-GLPG-R--NAYCASKSAVTMLTRSLACEWAAH -G--IRVNAVAPG I LTPA--V-QALL-----ASGERDMNS-----VV-R-RI--PV-ARLQ---P-DEVADIAFLAS--D-AAS---YVT 231
150 GSFV-SYPQ-A--GAYCATKGGVLL LTKATAVDLAKY -G--IRCNVCPGA IETPM--L-QKYLDA-----EDKKA IMSV-----LT-G-AH--LI-PRLGK---P-EEVAKLACFLAS--D-DSS---FIN 247
150 NGVS-PGLF-Q--GIYSVTKAAV INMTKVAFKECAPF -G--IRCNALLPGLTDTKF--A-SALV-----KNEAL I LNA-----L-T-Q-I--PL-KRVAD---P-KEMAGAVLYLAS--D-ASS---YTT 243
147 VSDT-GRPN-L--SAYVASKHAVLGLTR I AADLAPH -G--VTCNA IAPGF FDTDM--A-APT V-----GHPERAKI-----FR-S-AI--AL-DRFGD---P-KEMVGPVQFLAS--D-ASA---YIT 240
146 NAERMPFAG-G--APYAMS KSAALVGLTRGMARDLGPQ -G--ITVNVVCPGVDTPM--N-PA-----SGEFAES-----L-I-P-LM--AI-GRYGE---P-EEIASFVAYLAG--P-EAG---YIT 237
146 NARRLPFTY-G--ALYSATKAAV LGLTKGAARDLGP K -G--ITVNV IEPG I DTDL--N-PA-----DGPWAAAP-----AL-A-AL--AT-GKFG---A-SDVAGLA AVY LAS--E-EGR---FIT 237
145 ATAYGSPNE-W--VWYAASKGG I DSLTLGLAREVGI E -G--IRVNAVSPGPIGTEML--S-PE-----KVKMATS-----LS-P-----V-GRIGT---P-QEAAA AVMFLAS--D-EAS---FIT 234
147 HEVI-PWPL-F--VHYAASKGG I KLMTETLAL EYAPK -G--IRVNNIGPGA I NTP I--N-AEFK-----ADPKQKAD-----VE-S-MI--PM-GYIGE---P-EEIAAVAALWVLS--K-EAS---YVT 240
149 CGIR-AAPN-M--ASYASASKAAVHFTAAAAMEGAPL -G--IRVNAI VPGQVMTAA--T-QEFA-----DRAPEVAAR-----TT-G-AI--PM-QRGE---P-EELAEA I V F M L S--E-AAS---YVT 243
149 AGR L-GSAG-A--LLYAAVKAGVDGLTRSAAMELGPR -S--IRVNAIAPSTVATEG--V-KAIL-----TPEQFES-----RV-G-QT--PL-GRLGE---I-DDIAQAALWVLAG--A-RSG---FVT 241
143 VAYR-GRPN-T--GAYTT I KAG IAGLTKVLAGELGPR -G--IRVNAIAPGSVPTPA--T-DGFV-----TPEQYAQ-----RA-N-NI--PL-RRNGT---P-EDVARAAAF ILS--D-EAD---FVN 235
147 VAYR-GRPN-T--GAYT I KGAVALTNVLAGELGPR -G--IRVNAIAPGSVPTPA--T-AGFV-----SAEDYER-----RA-A-GI--PL-RRNGR---P-EDVARAVAF I G--E-DAD---FIN 239
141 AGLG-GSPG-V--YAYCTAKHAG IGLMRS LAKELVAGR -G--IRVNSLHPGPI DNSF--Q-TA I ED AF SPL-----IGGDATAM-----LN-S-MI--PM-GRHQ---P-AEIAQSALFLAS--S-MDA---FTT 241
141 AGVL-GLQA-H--DTYSAAKAAVRSLARTWTELKGR -S--IRVNAVSPG I DTP I--I-ENQVSTQ-----EEADELRK-----FA-A-AT--PL-GRVGR---P-EELAAAVLFLAS--D-DSS---YVA 238
136 GSMA-AVPG-N--VAYAAAKAGL RAMAR I V GKELLPR -R--IRVNMVSPGPTDTE I--F-KRDASA-----EEIQGMKDM-----LS-S-VV--PI-GRMGT---S-EEVARAVLFLAS--A-EAS---FIN 232
137 GAHA-SLPG-N--AVYAAAKGGLYAAAMKVFAGELVSE -G--IRLNMVSPGPI DTP L--L-YRNPGMTD-----EA I AALKEK-----MI-E-NV--PM-HRMGQ---S-EEVAKAVLFLAS--D-EAS---FIT 235
137 GSVA-TVPG-N--VIYATAKAGLRAAARTLAAELVGR -G--IRVNMVSPGPTETPI--I-NRTGGVPA-----EAVPGLREI-----MT-Q-AV--PM-KRMGT---P-EEIARPVLF LAS--E-EAS---FIT 235
141 AAVG-PGYS-P--TAYAVAKAGV LHLTKVAAADLAKH -Q--IRVNAVQPGF I NTP I--F-TSSLMEPELEA-----QAKGA I AAM-----SQ-Q-AQ--PV-ARGGQ---P-EDIAQAVLFLAS--E-AAG---FVT 243
171 GGI R-PSPG-L--GIYAAKALVALAKTAAVELGVD -N--IRVNAIAPGLDTPA--F-RATRQIPA-----GEDEG I FD-----N-V-AL--PL-GRVGS---P-AEVANMVAVLFG--D-EAS---YVT 267
143 TYWL-KIEA-Y--THYISTKAAN I GFTRALASDLGKD -G--ITVNA IAPSLVRTAT--T-EASA-----LSAMFDVLP-----NML-Q-----A-I-PRLQV---P-LDLTGAAAF LAS--D-DAS---FIT 236
143 AANT-APPN-G--APYVASKAGV VGLTRAAATEFGKY -N--ITVNS I APNPVTPG--A-DDA I-----NEDMFQA-----IA-Q-LQ--PV-PKVME---P-RHLTGAILFLCT--D-GAE---FIT 235
141 SCFI-PPPG-L--TAYVASKAS I GYVRSLAGELGQY -G--ITVNAVAPGPTVTEG--T-RGGFPDEA-----FV-E-SQ--SV-KKVS L--P-EYSAPVVVFFAS--E-EAG---FVT 238
141 HGLV-GSTG-K--AAYVAAKHGTVGLTKVVGLETATS -K--VTCNA ICPGWVLTPL--V-QKQ I DDRA--ANGG-----DPLQAMHDL-----LA-E-KQ--PS-LAFVT---P-EHLGELVFLCS--E-AGS---QVR 243
141 HGLV-GSIG-K--AAYVAAKHGTVGLTKVVGLETATS -H--VTCNA ICPGWVLTPL--V-QKQ I DDRA--AKGG-----DRLQAQHD L-----LA-E-KQ--PS-LAFVT---P-EHLGELVFLCS--E-AGS---QVR 243

g|84570596|bdh2_Rpickettii/1-256
 g|33434517|Sphch/1-263
 SLG_32730/1-261
 g|87199767/1-261
 SG61_1243/1-257
 g|84570594|bdh1_Rpickettii/1-260
 g|334342462|Sphch/1-265
 g|334343092|Sphch/1-255
 g|334343456|Sphch/1-245
 g|334343408|Sphch/1-258
 g|146275993|Naro/1-256
 g|146275997|Naro/1-246
 g|87199890/1-279
 SG61_474/1-283
 SLG_24920/1-278
 PP_1951/1-275
 PP_2002/1-257
 SLG_15310/1-259
 g|146275988|Naro/1-261
 SG61_609/1-245
 g|146275674|Naro/1-255
 g|334343007|Sphch/1-254
 g|334343319|Sphch/1-259
 g|87199902/1-261
 SG61_354/1-260
 PP_2214/1-255
 SG61_3175/1-254
 g|146276032|Naro/1-246
 SLG_24920/1-278
 g|334342802|Sphch/1-249
 PP_1708/1-252
 SLG_05090/1-250
 SG61_2863/1-244
 SLG_35070/1-243
 g|146275941|Naro/1-266
 g|334343077|Sphch/1-254
 g|334342781|Sphch/1-260
 SLG_31530/1-250
 SG61_2583/1-255
 PP_2175/1-234
 PP_0488/1-253
 g|2506152|YDFG_ECOLI/1-248
 g|334345036|Sphch/1-249
 PP_4862/1-254
 g|3343446119|Sphch/1-241
 SLG_33310/1-241
 g|334342779|Sphch/1-273
 g|334342815|Sphch/1-290
 g|87198230/1-306
 SLG_08640/1-305
 SLG_35880/1-297
 g|87198815/1-310
 SG61_724/1-305
 g|87198992/1-280
 SG61_2550/1-291
 SLG_33660/1-289
 SLG_07240/1-277
 g|87198816/1-310
 SG61_2705/1-303
 SG61_1498/1-309
 SLG_35900/1-311
 g|87198727/1-305
 SG61_3329/1-309
 SLG_12640/1-304
 SG61_2549/1-315
 SLG_28340/1-294
 SG61_2706/1-296
 PP_1745/1-269
 g|334342965|Sphch/1-259
 g|87199139/1-266
 SG61_504/1-269
 SG61_782/1-273
 SLG_38070/1-265
 SLG_27950/1-266
 g|87200928/1-272
 g|146275769|Naro/1-259
 g|146275845|Naro/1-289
 4BMV:A|PDB|n-pentyl/1-262
 PP_2989/1-264
 SLG_18780/1-267
 PP_0429/1-260
 g|334343146|Sphch/1-268
 g|334343373|Sphch/1-250
 SG61_4171/1-252

141 HGLV-ASAP-K--SAYVAAKHGIVGLTKVTALETAQN--R--VTANAICPGWVLTPL--V-QKQVQARP-AHG I---SVEQAKREL-----VI-E-KQ--PS-GQFVT---P-DELGALAVFLAS--E-AGR---QVR 243
 147 HSLT-ASPY-K--SAYVTAKHGLAGLTKTLALELATF--G--ITANCI SPGYVWTP L--V-ENQIPDTMKARGM---TREQVMNDV-----LL-A-GQ--PT-KQFVT---V-EQVASMALYLCS--D-AA--NIT 250
 145 HSLV-ASPF-K--SAYVTAKHGLAGFTKTIALELATF--G--VTANCI SPGYVWTP L--V-ENQIPDTMKARNM---TREQVINDV-----LL-A-GQ--PT-KQFVT---A-EQVAEIALFLGS--D-AAS--NIT 248
 145 HSLT-ASPF-K--AAYVSAKHGIAGLTKTLALELATH--G--VTANCI SPGYVWTP L--V-ENQIPDTMKARGM---TREQVINDV-----LL-T-RQ--PT-KQFVQ---P-EDVAALALFLCR--H-EAR--NIT 248
 141 HSLV-ASPF-K--AAYVAAKHG IAGLTKTLALELAQF--G--TTVNCI SPGYVWTP L--V-ENQIPDTMKARGM---TREQVMHDV-----LL-A-KQ--PT-KKFFVQ---V-EEVAALALFLCR--D-EAQ--NIN 244
 144 HSHE-ASPL-K--SAYVAAKHALLGLARVLAKEGAEF--N--VRSHVICPGFVRTPL--V-DKQIPEQAKELGI---SEEEVRRV-----ML-G-GT--VD-GVFTT---V-DDVARTALFLCA--F-PSA--ALT 247
 149 YGYR-GTVN-R--VDYVTTKTAIQGLTRATALETAGG--P--ITCHALMPGSLVTP L--W-SDRLERMMIEEGL---TRPEAEIRF-----LD-G-KQ--PS-GRFVD---A-DSVAEVL L L LCG--P-AGT---DMN 252
 147 AARL-YTPS-AP-CSYAAKAGVIHL SHHASCAYADD--N--IRVNAVLPGLTAPQ---I-ASMF-----TAEQAEI-----AG-E-NQ--VI-RRAVD---P-REIANAVLFLSS--D-DAS--MIT 241
 142 AAHR-GSAQ-H--AHYAATKGA INSLVRSLAKEIGPD---IRVNAVAPGLIATPM--T-VALL-----QGRGVT-----DL-E-ST--PL-KRHGQ---P-AEVASVIGFLCS--S-SAS--YVT 232
 153 AAFHYPGKG-A--SLYAITKSAVVRMTEVLAWEWATA--N--INVNCIAPGAFSSEM---M-DGMR-----SRIGDG-----FI-E-KF--PR-KRLGD---P-AQLDSTL LYLAS--P-ASE--AVT 245
 141 AGIV-GHPA-N--PAYSAAKHG VVGLVKSCVDFAFAAR--G--ARINALCPGGVETPL--I-GAPD-----VAIVPA---DL-P-RV--PA-RGMGR---A-QHVAEVALW LSS--P-AAG--FIT 233
 137 AALQ-GIAY-T--VAYVASKHAVAGMTKSLAVEFASR--G--VRVNAICPGDVKTPT--T-QQTA-----VPENVDWA-----LVMR-NAP-KLL-DGSCF---P-EDIAELFAFLS--E-RAR--KIT 233
 168 AGLV-TEPI-VG-LPYMPAKAGVLMHVRALGLELAEF--G--IRINAIAPGPFVTNI--G-GGWL-----KKDPVARAA---WD-A-IV--PL-GSVAE---T-DQIKPLALLLAS--D-ASD--YMT 263
 168 AAEV-NEAI-VG-VPYMAAKAGVKKHMRHAAFELAA Y--G--IRVNAIAPGPFVTNI--G-DGWV-----KKNPAAKA---WD-E-LC--PL-GRMAE---T-YQIKPLALLLAS--D-AGS--YMT 263
 168 AAVI-CEAI-VP-LPYMPAKAGVSHMVKHLFAFELAEY--H--IRVNAI L PGPFDLNI--A-DGSL-----KDPVVREA---WD-K-ST--PM-GRIAE---P-YQIKPLALYLAS--D-AAS--YVT 262
 164 SALR-PAVT-LG-AAYAAAKAGAAQVRATALEL ASD--G--VRVNAIAPGPFETDI--G-GGFM-----HNSEVRAK---MA-A-GV--PM-GRIAE---V-EEIKPLALYLAS--K-ASS--FVT 258
 149 RARQ-SEPD-T--EAYAASKGGLVALTHALAMSLGPE--G--IRVNAVSPGVIDARD--P-SQRRL-----AEPLSEA---DH-A-QH--PT-GRVGT---V-EDVAAMVAWL L S--R-QAA--FVT 240
 153 GGLHVPNEW-A--HAYGASKAALHHLTRLSAKRLGRD--G--IRVNAIAPGPFHSRM--T-DTTS-----EAVKAS---VA-A-HI--PL-GRPGE---A-DDVKGLCLFLAS--R-AGA--YVH 245
 158 LGWR-AQKG-Q--AHYAAKAGVMAFTRCAAL EAADH--G--VRINAVAPSLAMHPF--L-AKVT-----TEERLAE---LV-K-TE--AY-GRP AE---V-WEVANVMFLAS--D-LSS--YMT 250
 131 TGVK-PMAG-T--GAYGSSKAAL AHLAKIAALENAGA--G--IRVNAIAPGGVDTP I--W-DSANFRAMAAD---MGDRAA IAG-----FA-S-GT--PL-KRFAT---P-DEIAATIGFLLS--A-QAA--NIT 233
 150 AAFE-GQIG-Q--PAYAASKG VVGMALPIAREFARY--G--IRVNTIAPGIFWRTL--L-GSLP-----QEAQDS-----LG-R-QVP--FP-SRLGK---P-AEYAKMVEAIV---TNP--MLN 249
 149 AAFD-GQIG-Q--AAYAASKG VVGMTP LPIAREFARY--G--IRVMTIAPGLFLTP L--L-ASLP-----QEAQDS-----LG-R-QVP--FP-SRLGH---P-DEYALMVEQIV---ANP--MLN 239
 154 AAEV-GQMG-Q--AAYAASKG VVGLTLPVARDL MSE--G--IRVNTI L P G I FNTPL--M-NRAP-----EEVKAA---LA-A-SVP--FP-KRLGN---P-EEYASLAVEMC---RNS--YFN 244
 156 AAEV-GQMG-Q--AAYSASKG VVGMTP LPIARDL MSE--G--IRVNTI L P G I FNTPL--L-QGAP-----DNUKAS---LA-A-SVP--FP-KRLGQ---P-EEYANLALCM I---ETG--YFN 246
 155 AAVD-GQMG-Q--AAYSASKG VGMTP LPIARDL MSE--G--IRVNTI L P G I FRTPL--L-AGLP-----EAAQAS---LA-A-QVP--FP-KRLGH---P-EEYANLALVMTMI---EIG--YFN 245
 150 AAYD-GQIG-Q--AAYAASKGAIASLTLP AARELARF--G--IRVMTIAPGIFETPM--M-AGMS-----DEVRAS---LA-A-GVP--FP-PRLGR---P-QEYAAARH I---ENS--MLN 240
 143 ASFE-GQEG-M--GAYTASKSALAALTLVWARDLSH--A--IRVNVAPGFMPTPM--V-AMLP-----PDFVAE---LL-A-DNE--FP-KRAGR---A-EEYGQVAFEL I---RTP--L I N 233
 140 AGQN-GQIG-T--AHYAASKG IITLTKYFARDLAPF--G--VAVSAIAPGFLD LPS--V-REL V-----PAELTA---LT-E-TI--PV-RQLGD---P-GFIARTAVHLAG--R-DAA--FAN 233
 143 APQK-IPSV-AG-AAYVVS K GALLTLTKVAAGEA P F--G--MTVNTVAPGAI DTPM--L-RERT-----PVEQFEQ-----LF-G-PT--LA-GRPAR---P-DEIASAVLYLAS--E-QAA--FVN 236
 146 SAHT-PRPF-T--APYTASHAVLGLTKALALDGRPY--H--IVCSQVDIGNAL TEL--S-ERMT-----RGVRQANG---EIA-A-----EPMLD---V-RHVADAVRYI AALPL--DAN--VLN 238
 144 SAYS-PRPD-T--PAYCASKHVLGLTRLSAKSLGRRH--D--IAVGQIDIGNAASAF--S-EAFA-----RGVPAQD G---RLV-P-----EPYMD---A-SVVGETVAYMDSLPP--DAN--AQF 236
 146 SARV-PRAD-S--PAYAASKWGLDGLTRSLAIDGREF--N--IAASMFNP GIVATEI--A-PGAV-----KLDKDF-----AAM---P-EDIAADAIHMTALPD--HLN--FYE 230
 143 SAQM-PRAD-S--IAYTASKFLEGLTRALALEGRPH--G--ITASIH P GATISEL--I-GER S-----LRAS-AS-----PTTME---A-RHVAELVATMAAVPD--EIN--VLS 229
 147 NGVN-AHMG-S--ADYNVAKEAVRAYSRTAAREWAPY--G--ICVNVICPAAVSAAY--R-RFAE-----MAPQVAAA---LA-A-AN--PM-GRMGD---PESDIGGVAFLAS--E-DAR--YLT 241
 144 GATM-GLPE-V--GAYAIAKEGVRLTKTAAATGWGRY--G--ITVNTVCP-MVATPL--F-DTWVQ-----SLSEAEREH---QL-S-MI--PM-RRMGD---GEQDVGGLIVFLGS--E-AG--YIT 239
 145 AGLI-DDPI-HS-CAYSASKGAVHSYRSLAK EWAKY--N--IRVNSVNTMATNAE--I-DTLAKMTP-----EEQQFRAK-----IQ-D-AI--PLGGKMG E---TYRDLAPVLAF L AS--D-DSR--FIT 246
 135 AGRY-GYPN-R--IAYATSKWGLVGF AKTLAIELGPH--D--ISVNAI L P GAVGGER--F-DRVIEGRARASG---RSFEFVAAL-----GL-G-SQ--SL-KRIVA---P-AHVADLALFLTT--P-AGR--SIS 237
 147 VAHR-FAPDGL-R--AVTAAAKAGLEALRSLA L E L G P Q--G--VTVNCVAPGVT RKEA--S-GHRA-----IPEAMEAL E---MA-S-RA--PT-GRIAE---P-DDIAAAVAFLMG--P-DAR--QIT 242
 136 WAFE-PSEL-F--PTSAVFRSGLAAFTKIFADQFAGD--N--VRINNVLPGWIDSLP--AT-EQRR-----D-SV--PL-KRYGT---C-EEIAATIAFLAS--E-GAA--YIT 220
 137 AGTY-PYPG-G--NVYGASKAFVRFSLNLRADLAGT--R--VRVNSI EPGLCSGTD--F-SVVR-----NGDMDAVQA-----LYRD-----VEALL---P-EDIAATVAWVAE---QPA--HVN 228
 136 AGSW-PYAG-G--NVYGATKAFVRQFSLNLRDLHGT--A--VRVDI EPGLVGGTE--F-SNRF-----KGDDGKA EK-----TYQN-----VTALT---P-EDVSEAVVWVST---LPA--HVN 227
 138 AATY-PYAG-G--NVYGGTKAFVRSQFSLGLRSDLHGT--G--VRVTSI EPGMV-ETE--F-TLVR-----TGSQTASDA---LYHA-----ANPMT---A-EDIAETLFWVAT---QPA--HLN 227
 141 AGNY-PYPG-S--NVYGGTKAFVRSQFSLRCDLRTGT--G--VRVNSI EPGLC-ESE--F-SLVRF-----GGDAQYDA-----TYAG-----AEP IQ---P-QDIAETIFWILN---QPA--HIN 231
 141 AARI-VTPA-S--SVYSATKHAVRVIDGLRQ EHN--N--IRATILSPGPTSEL--G-HDVS-----DPNIAAW-----IK-Q-----GL-TAQS---P-FAIAQAIRYALE---QPD--NVD 228
 141 AAHF-VMPT-A--AVYCATKHAVWAITDGLRQ EHD--D--IRATV I S P G V V A T E L--G-HDIT-----DQNVAAA-----LQ-E-----WR-RKSLT---P-DAIARAIRFAL E---QPE--GVD 228
 143 AAIM-HPPF-L--QPYNVAKTAVVALSSGLRQEFQEE--GAPIGVSVLYPFFTQTRI--A-DDERNL PASMGR---EEADPTLAA---LR-E-EVR-AGL-ATGQT---P-AEVAEAVMAGIR--A-DRL--HIF 250
 144 SGLV-GGTA-T--MAYCTAKAGVVGLSESLRTELKGS--G--IGVSVLCPGPVATS I--L-THSAENLASVSV---SRPVSAER-----RD-A-QMS-NVL-EKAIQ---P-DEVGRVLAAR I--A-NQF---YIH 248
 146 GGLM-GSAL-A--APYSAAKAAVINLMESYRQGLDKH--G--IGVSVLCPGANIKSNI--A-EASRLRPAQFGK---SGYVNEES-----IA--SLH-SIH-QHGM D---P-VELAEHVKAGIV--A-NQL--YI 249
 146 GGF M-GSAL-A--GPYSAAKAASINLMEGYRQGLEKY--G--IGVSVCTPANIKSNI--A-EASRLRPAKYGT---SGYVNEES-----IA--SLH-SIH-QHGLE---P-EKLAEAIKKGV--D-NAL--YI 249
 146 SAFV-ALPT-T--GIYCTTKYAVRGLAESLRVEMP KY--N--IGVSVLCPGGVNTNI--H-RSVEARPEKYGN---TGYGRDEA-----VF-A-GLK-RVI-EHGF D---P-VDLGRVLD A VR--N-DRF--WV 250
 152 AAF L-AAGS-P--GIYNTTKFAVRGLSESLRHSYLLKY--E--IGVSVLCPGLVKS YI--Y-ASDDIRPDAL KG---EMKPVDKTA-----VE--RLA-GVH-EFGME---P-DVIGARVIEAMK--A-NRL--HIF 255
 148 ASFI-AGGA-P--GIYNTAKFAVRGMSYSLRHSMYKY--G--IGVSVVHPGLVKS YI--Y-ASDDVRPDAL KG---AMKPVDT EA-----VK--RLE-GLH-EFGME---P-DIIGARILDGVR--E-NRA--NIF 251
 149 AATV-VMPG-HL-AIYAAGKA AVLNTENMRADLAGR--G--IGSVLCPG F VRSNI--H-EAARNRPAHLREG---SGFAASEQA---LS-M-RE--TG-SEWMD---P-DAVGEVADAIL--A-DQL--YV 253
 149 AAEV-VMPG-QM-AIYAASKA AVNCHCEAAKGLAQH--D--IGVSI L P G P V K S NI--H-ETIDNRPEHLREG---SGFKAASEK---LS-M-RI--VG-DNWM E---P-EDVGNLVAAIL--N-NTT--YV 253
 146 AGLT-PMPS-FM-AIYATAKA AVITLTETIRDSMAED--N--IGVTVLMPGPIKSR I--H-ESGQNRPERFRAG---SGLAETEQQ---LA-K-RV--VA-DNWM E---P-TEVGD MIVDAIV--H-NKL--YVS 250
 140 GAVM-SARL-TR-GIYAPTAAV I S T E H L R L E L E A K--G L A I G A S V V C P G P V A T N I--A-DQTEENRPAARFVE---SFRGAREP---HG-ALP-A-DTG-GA-PFWDL---P-LDVGHMTLHAIR--A-NKL--YV 250
 144 SALV-PVAG-T--TIYSAGKAAVAMMCEMRPELEGR--G--VICSAFCPGAVQSN I--A-DAAKTRPAELAD---VTYAEADK-----R-RA--AG-GNFMHLYQTK-EQVGERVLEGI L--N-DEL--YI 247
 147 AGVL-QY-S-QA-GMYVATKFAVVVGLSEALRAELAPQ--G--IGVSAFCPG F VRSNI--R-EYEKTRPARFAAQ---DEAPKGGPPP---RF-NLS-D-EDRERLS-KLTAS---P-EEAGEI VLQGI R--D-NAL--YI 256
 145 GGFS-AV-G-TA-GLYCTAKFAISGMMEALATELEGT--P--IGVSCFYPPGPVQTNL--GATTGEVRPEHLQNE---PQPEVGP---DG-RPP-R-NFTF-DP-SVFMS---K-EEVGKRVLRGIR--R-GDL--FIM 252
 145 GGFS-AV-G-GA-GLYCAAKYCVAGMFESLARTDLRGT--A--LGASVFFCPGPVQTNL--GISTQATRPEHLRNEAPP P P P P S V G A Q Q---DK-RPA-P-G-F-DP-SLFMT---S-EEVGQRVLRGIR--R-RDL--FIM 256
 146 AAYL-SGPQ-A--GIYTASKFAVRGLTESLRYNLAPH--G--IGVSLMCPGLTRTNA--W-TSALKRPDGFAE---SGFKPADAT---EL-E-QFG-TAF-ELGMD---P-FEVGQKTLAGMI--E-NRG--LIL 250
 150 AAF L-PGPQ-A--GIYTASKFAVRGLTESLRYNLAPH--K--IGCSLCCPALTRTNA--W-TSALKRPDGFGT---SGFPDVAKG---EL-E-QFG-TAF-EEGMD---P-YEVGTKILAGMT--E-QKG--LIL 254
 145 AAYL-SGPQ-A--GIYTASKFAVRGLTESLRYNLAPH--G--IGVSLVCPALVATDA--G-LSALKRPARLGE---SGFAPVDEA---EL-R-HFA-SAF-SNGMD---P-L EAGEKILRGMS--E-NRG--LIF 249
 144 AGIV-PLPG-F--AAYTSKYAVRGLYAESLRYNLAPH--G--IGVSVLCPGATRTGM--L-HPPEDEPRTDFNE---EAAGTFQKA---LW-D-----AA-RAAID---P-LDTGRAVDAIK--E-NRF--LIF 245
 144 AGVV-PLPG-M--GAYSAGKYAVRGLTQALRLDLAPH--G--IGVSVLCPGAVKAL--M-AIPEDDASAPPGE---E--GDFIRN-----LW-A-----AM-RVAVD---P-MDMGRVVDAIR--E-NRF--HIL 243
 144 AGMI-PVPP-FM-GVNYAASKFAVRGLSDSLRRLALAPY--N--IGVSVLCPGMVKTNA--M-TAGDVYRQAHEG---AGADEKRD-----TI-EGGMD---P-FDLGNEVDAIE--N-NRP--YIF 241
 139 AALM-QPPP-M--SNYNAKAGV LALSESLVELRQV--E--VAVHVVCPSPFFQTRN L--L-DSFRGPNPAMKAQ---VGKLLLEGSP-----IS---A-ADIADYIHQQVA--A-GEF--LIL 232
 141 SALY-GSPG-L--AVYSATKYAIRGLSEALDVEWRSS--G--VKVRCLFPTFVDTPM--L-AAAPGSSEDSK--RD-----RVL-KSGATLTS--V-EEVADHAWKAVH--D-DRL--HVL 234
 140 AGIY-GSPG-A--SVYSATKFGVRAIT E S L DGEWAED--G--IRVRDLMPGFIETPL--L-DHAPNRASNDI RS-----RVR-GAGLEITP--V-SEVAEAAWAVH--G-ERL--HTL 234
 140 AALY-GMPS-Q--SIYGTAKAGVRSLETLDGEWQAD--G--IRVRS L M P S F I D T P L--L-SHPNSRSNVP I RQ-----RVA-EAGLEFTP--V-EEVADNAWDAVH--G-DRV--HYL 234
 148 ASRM-VAPN-L--SAYCTGKI AQNRVVAEAAAELAGT--G--VSVFAIDPGFVFTQL--A-RETMESPEAQKYL---GGMVDR LRA-----ASG-DPAAQ--TDL-ARCAQRVLDLAS--G-RY-----245
 145 AARK-VAPY-L--SAYCTGKI AQNRIVEAAAELADT--G--VKIFAIDPGFVFTSL--A-RDTMNAPAAQKWL---PGMVARLKE-----VSD-GSETA--AGL-ARCAQRCLD LVS--G-RY-----242
 146 AGTF-VAPP-A--SAYAVAKASIRLTHELDRAEQAA--G--VRAFAIQPQTIMTAM--A-QETLKSPEAHFA---KPLVALLES-----TTA-EESAQ--GM-ARLRRFVVALAA--G-EH-----242
 139 AGKV-GSPM-R--TGYSAAKFGFLGYS DALRAEFVAGL--G--IKVHV I A P G S I R T D V--S-RNAI-----TADGSRRG-----V-S-DK--AI-ENGLD---PADAVDQMLSAI--A-D-ERE--IM 232
 141 GGLR-GAAF-N--AAYCTSKAAVKMLSKCLGA EFAAL--GYNIRVNSVH P G G I D T P M--L-GS I M D K Y V E L G A A---PSREVAQAA---ME-M-RH--PI-GRMGR---P-AEMGGGVVY LCS--D-AAS--FVT 246
 154 GAFG-AMPA-Q--TAYVVTKHAVQSFTECLYEMQL--GLPIHVSAIVPGMIRTNI--F-NAEAGDGEP AHSQ---AHRRAMFEMMRDYGMDLDEGRL--FL-----EQMAEKKFVAHSQPDQSEQ---I I A 265
 142 VGFA-PEFG-M--SIYGATKAFVFLSQGLNLELSPS--G--IYVQAVLPAATRTEI--W-GRAG-----ID-V-NTL-PE---VME---V-DELVDAALVGF D---RRE--LVT 225
 142 VGFA-PEFG-M--SIYGATKAFVFLSQGLSQELSPK--G--VYVQAVLPAATRTEI--W-ARAG-----ID-V-NTL-PE---VME---V-GELVDAALVGF D---RRE--LVT 225
 142 FAFD-YMPG-A--SVYAATKSYVAQLTHVLDAELREK--G--MRFQALVPLTRTEL--G-GDAE-----FF-D-MFP--PE--HVMS---P-EVLVEVSLASLE---LGE---RVC 226
 141 AGVA-PGPW-M--AAYAASKAYVLSFSQALREELKRT--G--IKVSVLCPGPVRSAR--R-RIAR-----LDG-K---PR---CLS---P-EEVALYTVRALD---KNR--AL I 222
 145 VADI-MSND-H--CSYMGAKAALNQMTRFVAYEYGHK--G--IRAN I L A P G L T I T P M--L-GGFN-----VPLGVEA---YA-K-EY--PL-GRITT---V-EDIAANAALFMAS---DEC--FMT 236
 129 VTLG-DFPL-A--AAYTGSKQAVEGFTASLAIELAYF--G--VRAKLVEPGYAPTR--F-GANSIVPVDQLLP---GDYAAFAQP-----IL-E-AF--ANPMTTR---E-SDVAEAVWNAVH--D-DSGRLRFP A 236
 129 VTLA-PMPL-V--AAYTASKTAVAGFTASLAL E L A A F--G--IGAKLVEPGYGPTR--F-AQNTDLRL E D T I P--EAYADFA RP-----FL-E-AF--AQPALVTT---P-QDVAETVWRAAT--D-SGERLHYPA 236

gj|146275658|Nara/1-269
gj|334343486|Sphch/1-273
gj|146275875|Nara/1-252
PP_1946/1-262
PP_1817/1-253
gj|87200975/1-250
SG61_1215/1-250
gj|146275951|Nara/1-252
SG61_2016/1-248
gj|31615388|Levodione/1-267
gj|87200486/1-256
SG61_3730/1-262
SLG_20040/1-258
gj|146275686|Nara/1-245
gj|334342862|Sphch/1-257
gj|87198897/1-259
gj|146275698|Nara/1-254
gj|334343337|Sphch/1-258
gj|146275892|Nara/1-259
gj|334342592|Sphch/1-246
gj|334342962|Sphch/1-244
gj|334342992|Sphch/1-245
gj|334342994|Sphch/1-245
gj|334342590|Sphch/1-248
gj|87198536/1-248
gj|1708836|2,5-DDOL_Sjap/1-250
gj|62286565|CPNA_COMS9/1-250
gj|33112056|R-specificADH/1-252
gj|146275770|Nara/1-271
gj|334342841|Sphch/1-255
gj|334343813|Sphch/1-269
gj|87200879/1-249
SG61_3344/1-248
SLG_12690/1-249
gj|146275758|Nara/1-253
gj|729773326|steA_Ctestosteroni/1-243
gj|146275834|Nara/1-267
PP_1953/1-269
gj|39647578|badH_Rpalustris/1-255
gj|334342959|Sphch/1-250
gj|334342606|Sphch/1-251
gj|146275741|Nara/1-255
gj|1730032|kduD_EcolliK12/1-253
gj|334343307|Sphch/1-251
PP_2794/1-255
gj|16330475|3-ketoacyl-ACP/1-240
gj|334342640|Sphch/1-240
SLG_38730/1-240
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SG61_907/1-240
gj|518742570|acetyl-CoA/1-246
gj|334343976|Sphch/1-246
gj|87199449/1-254
SG61_1203/1-250
gj|388477173|fabG_Ecoli/1-244
gj|146318879|gluconate/1-271
PP_2783/1-245
gj|334343549|Sphch/1-249
gj|334343458|Sphch/1-251
gj|87199578|part2/1-253
gj|87199495/1-266
PP_3926/1-255
gj|334343112|Sphch/1-262
PP_1852/1-249
SG61_1419/1-249
SLG_12130/1-244
gj|649014081|glucose-1-dehydrogenase_Bsub/1-261
gj|146275833|Nara/1-261
gj|87199577/1-257
SG61_3726/1-249
SLG_20080/1-253
gj|334342771|Sphch/1-253
gj|512125550|n-pentylphenylADH_Ralstonia/1-251
gj|87200895/1-246
SG61_3191/1-249
SLG_07180/1-248
gj|87199020/1-282
gj|334343475|Sphch/1-279
gj|81821161|PED_AROAE/1-249
SLG_18890/1-249
SLG_18590/1-251
gj|167033792|bdh/1-256
PP_3073/1-256

242 GQV L V C D G G G A S H V P - - - - G L A G F R S - - - - - F F A G - - E Q
243 G H C L P V D G G T M A H L P - - - - T S P A A H G - - - - - W - - - - L R R N M G I D - - - - -
240 G H A M V V D G G A T A F - - - - -
240 G H S M S V D G G V A V T A V - - - - G T R M D D L F - - - - -
241 G H C L T V D G G A T A I - - - - -
238 G A T F T I D G G Q T A H - - - - -
238 G A T F V I D G G Q T A H - - - - -
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245 G A K W E I D G G A L A T I R - - - - N D - - - - -
243 G A A W P V D G G A L C T I K - - - - H - - - -
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247 G A E L K L D G G I S A M - - - - -
242 G T E L V V D G G M T A L - - - - -
246 G T E V I V D G G F C A A - - - - -
235 G A E I V V D G G M T V G T Y - - - - Y M G F P G S - - - - P G M - - - - -
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234 G I D L P V D G G T M A - - - - -
236 A S E H L V D A G M L A H - - - - -
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238 G S E L V V D G G Y T A N - - - - -
240 G A E F V V D G G Y T A Q - - - - -
259 G A E L V I D G G W T A Q - - - - -
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233 G Q D W A V D G G V L E S I E - - - - V - - - -
234 A Q G W A V D G G V L E T L E - - - - V - - - -
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231 G Q N V A V N G G S A F L - - - - -
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236 G Q V I A V D G G W T A N G - - - - - Y I - - - - -
232 G A T L Q V D G G Y L A S G H - - - - P P D G P M P - - - - -
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238 G A E L A I D G G Y S I - - - - -
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SG61_417/1-252

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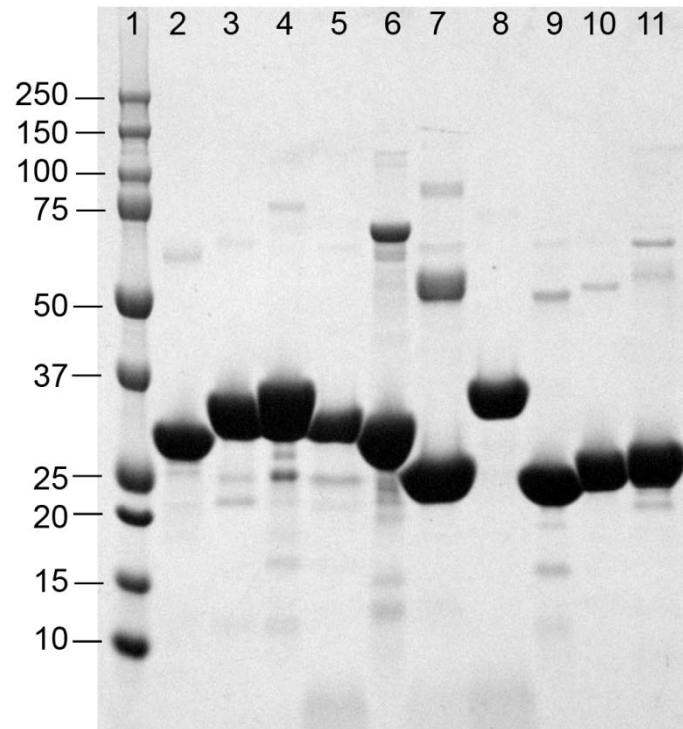


Fig. S4. SDS-PAGE Gel of purified GGE dehydrogenase enzymes. lane 1.

Precision Plus Protein™ Prestained Standards; lane 2. SG61-1L 474; lane 3. SG61-1L 724; lane 4. SG61-1L 1498; lane 5. SG61-1L 2705; lane 6. SG61-1L 2550; lane 7. SG61-1L 3175; lane 8. SG61-1L 3329; lane 9. SG61-1L 3344; lane 10. SG61-1L 3726; lane 11. SG61-1L 3730.

Table S1. Retention times and m/z values for metabolites observed during GGE degradation

Compound	Molecular weight	Authentic standard		SYK-6		SG61-1L	
		Rt (min)	m/z [molecular ion]	Rt (min)	m/z [molecular ion]	Rt (min)	m/z [molecular ion]
GGE	320.34	5.10	303.12 [M-H ₂ O+H] ⁺	5.12	303.12 [M-H ₂ O+H] ⁺	5.10	303.13 [M-H ₂ O+H] ⁺
MPHPV	318.32	-	-	6.78	319.10 [M+H] ⁺	6.77	319.12 [M+H] ⁺
HPV	196.20	-	-	3.78	197.06 [M+H] ⁺	3.79	197.03 [M+H] ⁺
Vanillin	152.15	5.52	153.05 [M+H] ⁺	5.53	153.05 [M+H] ⁺	5.52	153.05 [M+H] ⁺
Vanillic acid	168.15	4.16	169.05 [M+H] ⁺	4.16	169.08 [M+H] ⁺	4.16	169.04 [M+H] ⁺
Guaiacol	124.14	7.50	n/a	7.54	n/a	7.52	n/a

Table S2. Protein names and corresponding accession numbers for genes encoding proteins included in the phylogenetic analysis.

Gene name	gene identification (GI) number or accession ID	Reference
ADH_Syanoikuyae	4BMV (pdb ID)	(1)
Ga5DH_Ssuis	146318879	(2)
phaB_Synechocystis	16330475	(3)
bdh_Pputida	167033792	(4, 5)
2,5-DDOL_Spaucimobilis	1708836	(6)
kduD_Ecoli	1730032	(7)
ydfG_Ecoli	2506152	(8)
LVR_Caquaticum	31615388	(9)
(R)-ADH_Lkefiri	33112056	(10)
fabG_Ecoli	388477173	(11)
badH_Rpalustris	39647578	(12)
ADH_Ralstonia	512125550	(1)
phaB_Burkholderia	518742570	(13)
CPNA_Comamonas	62286565	(14)
Gluc-DH_Bsubtilis	649014081	(15)
steA_Ctestosteroni	729773326	(16)
(S)-PED_Aaro	81821161	(17)
bdh1_Rpickettii	84570594	(18)
bdh2_Rpickettii	84570596	(18)
SG61_1203	SZ64_06710	
SG61_1215	SZ64_06655	
SG61_1243	SZ64_06525	
SG61_1419	SZ64_05615	
SG61_1498	SZ64_05225	this work
SG61_2016	SZ64_08220	
SG61_2549	SZ64_00035	this work
SG61_2550	SZ64_00030	this work
SG61_2583	SZ64_09815	
SG61_2705	SZ64_01645	this work
SG61_2706	SZ64_01650	this work
SG61_2863	SZ64_11380	
SG61_3175	SZ64_16025	this work
SG61_3191	SZ64_15940	this work
SG61_3329	SZ64_12360	this work
SG61_3344	SZ64_12435	this work
SG61_354	SZ64_16980	
SG61_3726	SZ64_14315	this work
SG61_3730	SZ64_14335	this work
SG61_417	SZ64_16655	this work
SG61_474	SZ64_16365	
SG61_504	SZ64_17190	
SG61_609	SZ64_02580	
SG61_724	SZ64_15290	this work
SG61_782	SZ64_15575	
SG61_907	SZ64_14565	

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