

315 GWV TGH SYVVY GPLALGATS IMFEGV P NYPTYSRFWQVVEKYKVT SFYTAPT AIRAIAKE
338 GWI TGH SYVVY GPLCNGATSVLFESTPVYPNAGRYWETVERL KINQFYGAPTAVRLL LKY
257 GWV TGT VYGI FAPWLN GATNVI VGGRF ---SPESWYGTIEQLGVNVWYSAPTA FRMLMGA
308 GWV TGH SYLLY GPLACGAT TLMFEGV P NWPTPARMAQVVDK HQVNILYTAPT AIRALMAE
326 GWI TGH TYVVY APLL LGCSTV VFE S TPAYPDFSRYW DVI EKHKVTQFYVAPTALRLLKRA
332 GWV TGH SYIVY APLI LGMTSLMYEGAADYPDFGRW WKNIQDHKVTVLYTAPTAVR MFMKQ
308 GWV TGH SYLLY GPLACGAT TLMFEGV P NWPTPARMCQVVDK HQVNILYTAPT AIRALMAE

374 WP_011418543 **Syntrophus aciditrophicus**
397 Q9NUB1 *Homo sapiens*
313 P39062 *Bacillus subtilis*
367 P27550 *Escherichia coli* K12
385 P16928 *Aspergillus nidulans*
391 P27095 *Methanosaeta concilii*
367 Q8ZKF6 *Salmonella typhimurium*

375 GDEWLK GIDLSSLRVLSSV GEPLNPEAWQWFYEKIGNSQCP IVDTWQ TETGGHMILPLP
398 GDAWVK KYDRSSLR TLG SV GEPINCEAWEWLHRVVGDSRCTLV DTTWQ TETGGICIA PRP
314 GDEMAA KYDLTSLRHVLSV GEPLNPEVIRWGHKVFNK ---RIH DTTWMT ETGSQLICNYP
368 GDKAIEG TDRSSLRILG SV GEPINPEAW EWYWK KIGNEKCPVV DTTWQ TETGGFMITPLP
386 GDH HHH-KMEHL RVLG SV GEP IAAEVWK WYFEKVGKEEAHIC DTYWQ TETGSNVITPLA
392 GAEPDKY DLSSLRLLG SV GEPINPEAW M WYREHIGRGELQIM DTTWQ TETGTFLNSPLP
368 GDKAIEG TDRSSLRILG SV GEPINPEAW EWYWK KIGKEKCPVV DTTWQ TETGGFMITPLP

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435 GA--IDIKPAK PALPIMGVIPTLVDDQTG EELKNMEANGALCFKTA WPGITRTIYGDH KR
458 SEEGAEILPAMAMR PFFGIVPVLMD EKGSV-VEGSNVSGALCISQAWPGMARTIYGDHQR
371 C---MDIKPGS MGKPIPGVEAAIVDNQGNELP--PYRMGN LAIKKGWPSMHTIWN NPEK
428 GA--TELKAGSATR PFFGVQPALVDNEG NP-L-EGATEGSLVITDSWPGQARTLFGDHER
445 GV--TPTKPGSASL PFFGIEPAI IDPVS GEEISGNDVEGVLAFKQPWPSMARTVWGAH KR
452 I---TPLKPGSCTF PPLPGYDISILDEEGNEVP--LGSGGNIVAL KPYP SMLRAFWDKER
428 GA--IELKAGSATR PFFGVQPALVDNEGHP-Q-EGATEGNLVITDSWPGQARTLFGDHER

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493 YEETYFEPY-----PGNYFSGD GALRDKDGYRITGR IDDVINVS GH R MGTA EIEATLN
517 FVDAYFKAY-----PGYYFTGD GAYRTEGGYYQITGR MDDVINI S GHRLGTAEIEDAIA
426 YESYFMP-----GGWYVSGD SAYMDEEGYFWFQGR VDDVIMT S GERVGPFEVESKLV
484 FEQTYFSTF-----KNMYFSGD GARRDEDGYYWITGR VDDVLNV S GHRLGTAEIESALV
503 YMDTYLNVY-----KGYFTGD GAGR DHEGYWIRGR VDDVVNV S GHRLSTAEIEAALI
507 FMKEYWQFYWDVPGRRGVYLAGD KAQRDKDGYFFIQGR IDDVLSVAGHR IANAEEVESALV
484 FEQTYFSTF-----KNMYFSGD GARRDEDGYYWITGR VDDVLNV S GHRLGTAEIESALV

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547 AHEKVAESA VVGYPHEVKGQSIYAYITLKTGFEPSEDLKKELTQYVRTIIGPIATPEKIQ
571 DHPAVPESA VIGYPHDIKGEAAFAFIVVKDSAGDSV VVQELKSMVATKI AKYAVPDEIL
478 EHPAIAEAGVIGKPD PVRGEI I KAFIALREGFEP S DKLKEEIRLFV KQGLAAHAAPREIE
538 AHPKIAEAAVVGIPHNI KGQAIYAYVTLNHGEEPSPELYAEVRNWVRKEIGPLATPDVLH
557 EHPMVAEAAVVGIADEL TGQAVNAFVSLKEGNETNDQVRKDLILQVRK SIGPFAAPKAVF
567 AHPKIAEAAVVGKPD E VKGESIVAFVILRVGNEPSPELAKDAIAFV RKTLPVAAPTEVH
538 AHPKIAEAAVVGIPHAIKGQAIYAYVTLNHGEEPSPELYAEVRNWVRKEIGPLATPDVLH

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