Supplementary Information

Mechanisms of Polyethylene Terephthalate Pellet Fragmentation into Nanoplastics and Assimilable Carbons by Wastewater *Comamonas*

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Content Summary:

Total pages: 125

SI Appendix (13 pages) :

Number of figures: 10

Number of tables: 2

Supplemental Dataset:

-Protein sequence of PETases used for alignment (12 pages)

-Percent identify matrix of the alignment result (13 pages)

-Extracellular proteomics data (15 pages)

-Intracellular proteomics data (68 pages)

-Plasmid sequences used for the construction of the mutants (4 pages)

SI APPENDIX

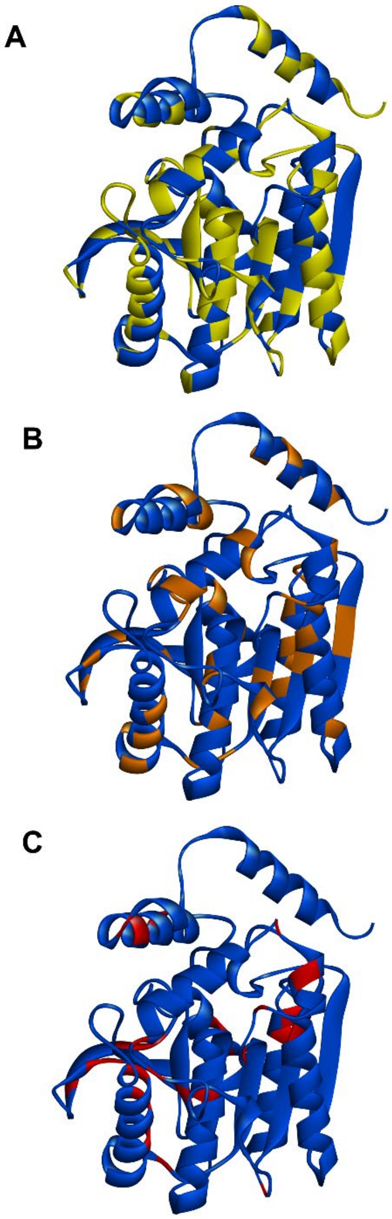

Figure S1. Illustration of sequence motifs that are identical (**A**, yellow), strongly similar (**B**, orange), or weakly similar (**C**, red) between the two esterases.

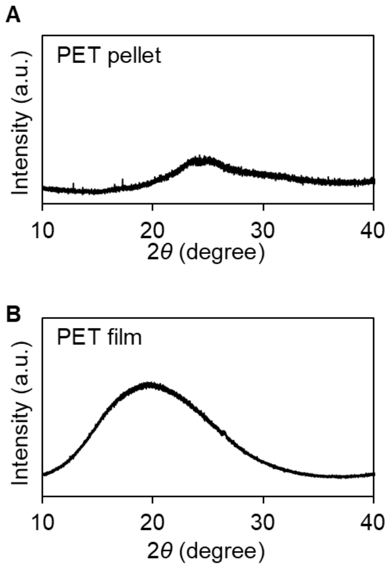

Figure S2. X-ray diffraction characterization of (A) PET pellets, and (B) PET films.

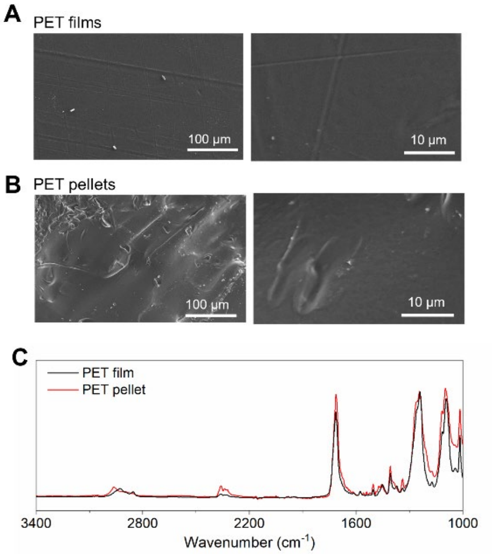

Figure S3. Shown are SEM images of the reference (A) PET films and (B) PET pellets; scale bars specify the magnification for each image. (C) superimposed FTIR spectra for the reference PET pellet (red) and a reference PET film (back).

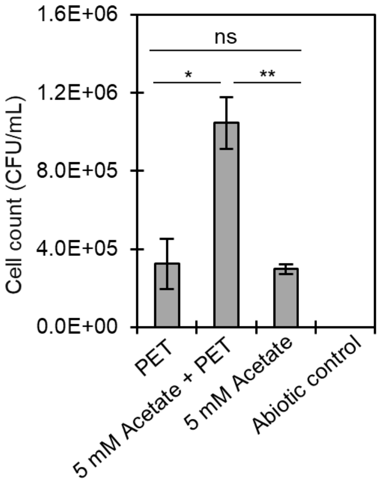

Figure S4. Colony-forming unit counting at the end of incubation (42 days).

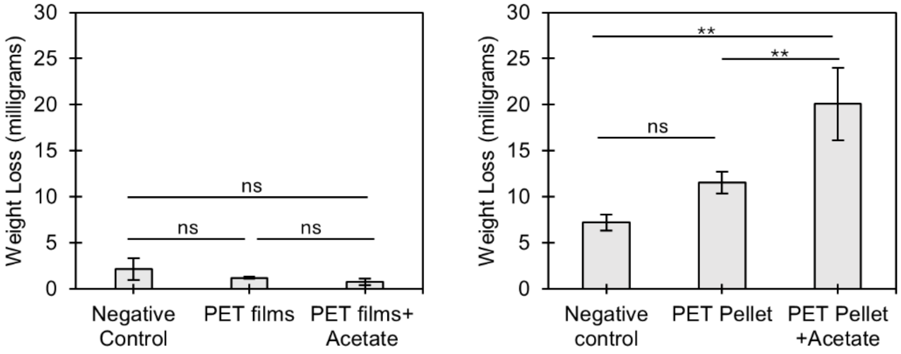

Figure S5. Weight loss of PET films and pellets after incubating with *C. testosteroni* KF-1. One-way ANOVA analysis with post hoc Tukey's test was performed: *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$. ns: not significant.

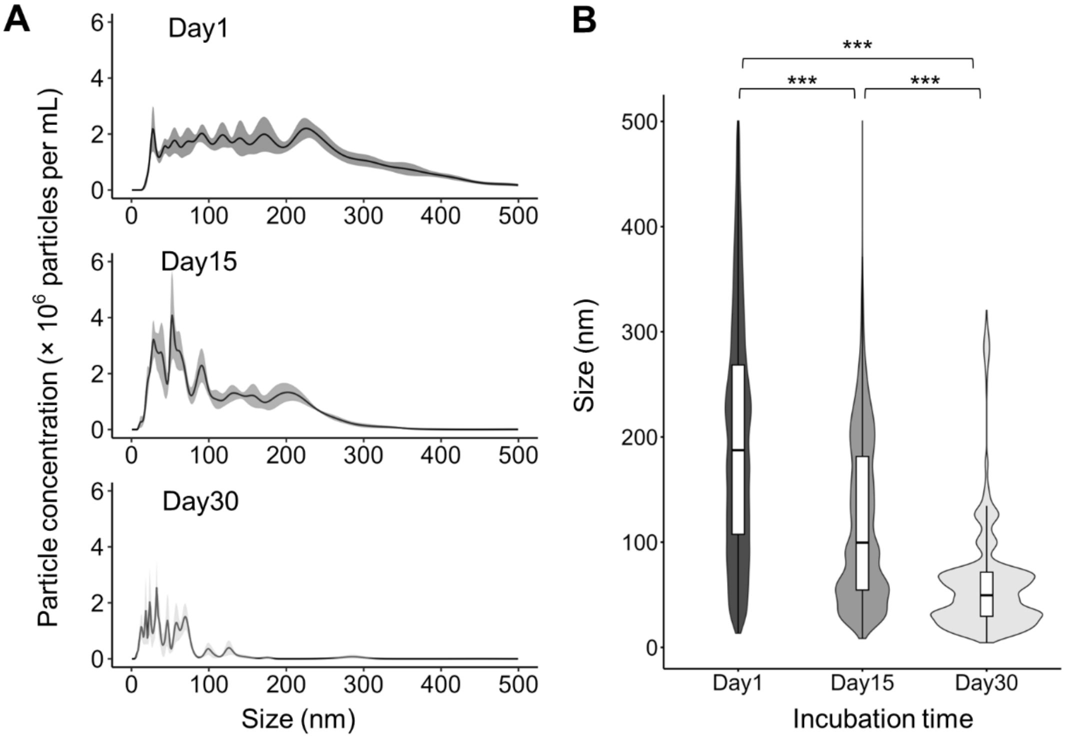

Figure S6. (A) Nanoparticle size concentration and (B) violin plot with inserted box plot of particle size distribution following 1 d, 15 d, and 30 d of PET pellets incubated with cells and 5 mM Ac. In A, the solid lines represent the mean value of the particle concentration, and the shades represent the 95% confidential intervals. In B, the top and bottom edges of the box plot represent the first and third quartiles, respectively, the line inside represents the median value, and the whiskers represent the upper and lower extremes in the data. The width of the violin plot illustrates the concentration of different particle sizes. In (B), Welch's *t*-test was performed for pairwise comparison due to the unequal sample sizes and variances in different conditions (*$P < 0.05$, **$P < 0.01$, ***$P < 0.001$). Data was collected from one biological replicate at each incubation time.

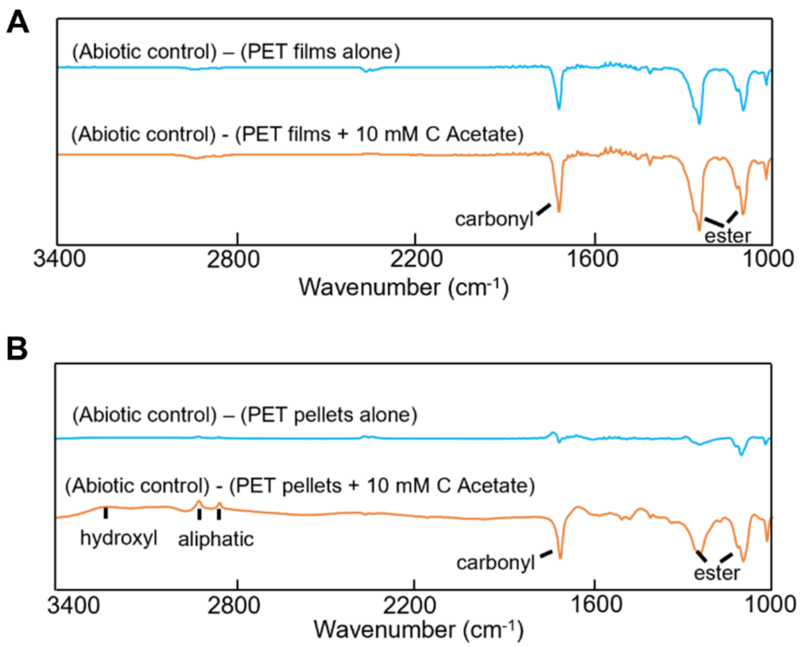

Figure S7. FTIR spectra revealed functional group change on the surface of PET films (A) and pellets (B) after incubating with *C. testosteroni* KF-1.

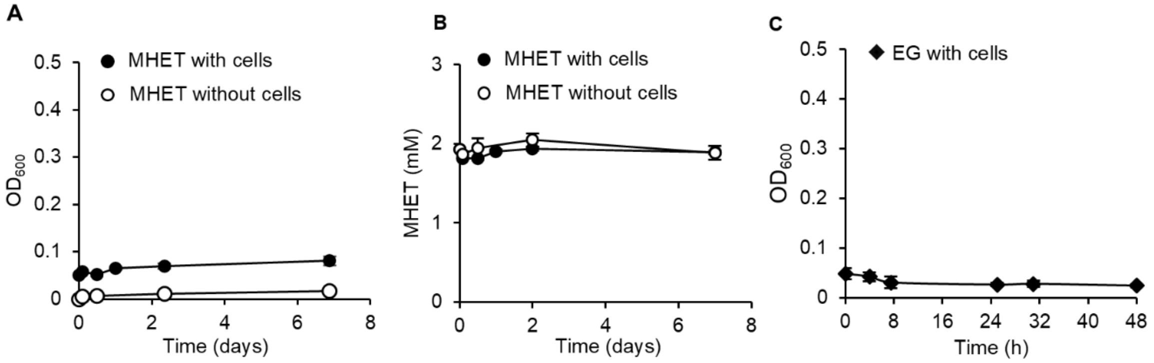

Figure S8. (A) Cell growth of *C. testosteroni* KF-1 on MHET. (B) MHET consumption during the incubation. (C) Cell growth of *C. testosteroni* KF-1 on ethylene glycol (EG).

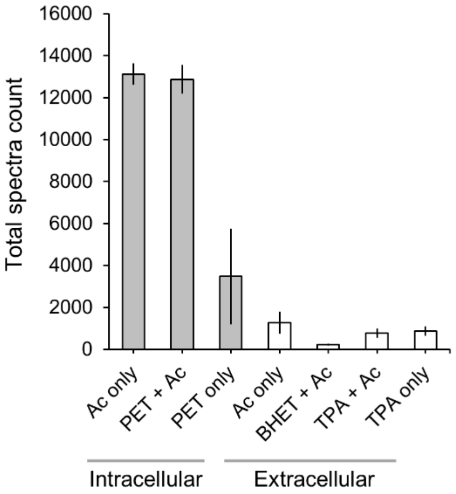

Figure S9. Total spectra identified from intracellular and extracellular proteomics of *C. testosteroni* KF-1.

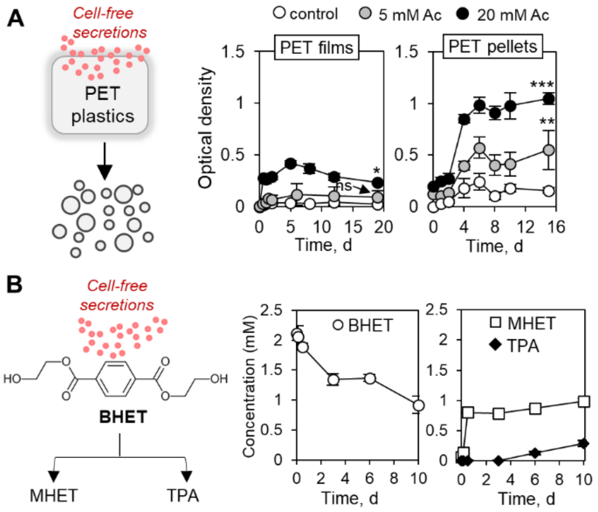

Figure S10. (A) Schematic illustration (left) and release of MPs from PET films (middle) and PET pellets (right) incubated with cell-free spent media obtained after growth of *C. testosteroni* KF-1 on 5 mM or 20 mM of acetate. (B) Schematic illustration (left) and depletion of BHET (middle) and associated production of MHET and TPA (right) during reaction of BHET with cell-free spent media of 5 mM acetate-grown *C. testosteroni* KF-1.

Table S1. Enzymes uniquely identified in PET only condition relative to acetate only condition

Locus tag	**Function**
CtesDRAFT_PD0030	Transcriptional_regulator,_LysR_family
CtesDRAFT_PD0333	TonB dependent receptor
CtesDRAFT_PD1318	TolA_protein
CtesDRAFT_PD1422	SSU_ribosomal_protein_S2p
CtesDRAFT_PD2655	Formate_dehydrogenase_O_beta_subunit
CtesDRAFT_PD3077	DnaJ-class_molecular_chaperone_CbpA
CtesDRAFT_PD3217	DNA-binding_protein_HU-beta
CtesDRAFT_PD4753	LemA_family_protein
CtesDRAFT_PD5366	Urease_alpha_subunit

Table S2. Enzymes uniquely identified in PET with acetate condition relative to acetate only condition

Locus tag	Function
CtesDRAFT_PD0163	SSU_ribosomal_protein_S13p_(S18e)
CtesDRAFT_PD0167	LSU_ribosomal_protein_L17p
CtesDRAFT_PD0184	2-hydroxy-3-oxopropionate_reductase_(EC_1.1.1.60)
CtesDRAFT_PD0289	Acetylornithine_deacetylase
CtesDRAFT_PD0333	TonB-dependent_receptor;_Outer_membrane_receptor_for_ferrienterochelin_and_colicins
CtesDRAFT_PD0361	dTDP-glucose_4,6-dehydratase_(EC_4.2.1.46)
CtesDRAFT_PD0367	Putative_virion_core_protein_(lumpy_skin_disease_virus)
CtesDRAFT_PD0408	TRAP-type_C4-dicarboxylate_transport_system,_small_permease_component
CtesDRAFT_PD0435	CzcABC_family_efflux_RND_transporter,_membrane_fusion_protein
CtesDRAFT_PD0492	TldD_protein,_part_of_TldE/TldD_proteolytic_complex
CtesDRAFT_PD0530	Thiol:disulfide_interchange_protein_DsbC
CtesDRAFT_PD0550	Hydroxymethylpyrimidine_phosphate_kinase_ThiD_(EC_2.7.4.7)
CtesDRAFT_PD0654	Putative_transmembrane_protein
CtesDRAFT_PD0688	Zinc_protease
CtesDRAFT_PD0738	Methionyl-tRNA_synthetase_(EC_6.1.1.10)
CtesDRAFT_PD0800	Fumarylacetoacetase_(EC_3.7.1.2)
CtesDRAFT_PD0801	3-hydroxybutyrate_dehydrogenase_(EC_1.1.1.30)
CtesDRAFT_PD0836	L-carnitine_dehydratase/bile_acid-inducible_protein_F
CtesDRAFT_PD0868	Transaldolase_(EC_2.2.1.2)
CtesDRAFT_PD1016	SSU_ribosomal_protein_S20p
CtesDRAFT_PD1034	Rrf2-linked_NADH-flavin_reductase
CtesDRAFT_PD1103	Aerobic_carbon_monoxide_dehydrogenase_(quinone),_small_chain_(EC_1.2.5.3)
CtesDRAFT_PD1362	Murein_hydrolase_activator_NlpD
CtesDRAFT_PD1411	Chorismate_synthase_(EC_4.2.3.5)
CtesDRAFT_PD1415	Soluble_lytic_murein_transglycosylase_and_related_regulatory_proteins
CtesDRAFT_PD1422	SSU_ribosomal_protein_S2p_(SAe)
CtesDRAFT_PD1482	Phosphoadenylyl-sulfate_reductase_[thioredoxin]_(EC_1.8.4.8)
CtesDRAFT_PD1527	SWIB/MDM2_domain-containing_proteins
CtesDRAFT_PD1534	LSU_ribosomal_protein_L20p
CtesDRAFT_PD1620	Fructose-1,6-bisphosphatase,_type_I_(EC_3.1.3.11)
CtesDRAFT_PD1628	Thiamin-phosphate_pyrophosphorylase_(EC_2.5.1.3)
CtesDRAFT_PD1639	Peptidyl-prolyl_cis-trans_isomerase_(EC_5.2.1.8)
CtesDRAFT_PD1782	Prolidase_(EC_3.4.13.9)
CtesDRAFT_PD1871	UDP-glucose_6-dehydrogenase_(EC_1.1.1.22)
CtesDRAFT_PD1908	Iron-sulfur_cluster_regulator_IscR
CtesDRAFT_PD1958	RND_efflux_system,_inner_membrane_transporter
CtesDRAFT_PD2492	Protein-L-isoaspartate_O-methyltransferase_(EC_2.1.1.77)
CtesDRAFT_PD2496	Phosphoglucomutase_(EC_5.4.2.2)_@_Phosphomannomutase_(EC_5.4.2.8)
CtesDRAFT_PD2504	Predicted_metal-dependent_hydrolase_with_the_TIM-barrel_fold
CtesDRAFT_PD2537	Ribose-5-phosphate_isomerase_A_(EC_5.3.1.6)
CtesDRAFT_PD2588	Succinyl-CoA:3-ketoacid-coenzyme_A_transferase_subunit_B_(EC_2.8.3.5)
CtesDRAFT_PD3077	DnaJ-class_molecular_chaperone_CbpA
CtesDRAFT_PD3169	MoxR-like_ATPases
CtesDRAFT_PD3217	DNA-binding_protein_HU-beta
CtesDRAFT_PD3230	2-isopropylmalate_synthase_(EC_2.3.3.13)
CtesDRAFT_PD3261	Nucleoid-associated_protein_YaaK
CtesDRAFT_PD3322	Phage_recombination_protein_Bet
CtesDRAFT_PD3595	Amidophosphoribosyltransferase_(EC_2.4.2.14)
CtesDRAFT_PD3738	CoA-transferase_subunit_alpha,_IpdA
CtesDRAFT_PD3877	Deoxyuridine_5'-triphosphate_nucleotidohydrolase_(EC_3.6.1.23)
CtesDRAFT_PD4127	LSU_ribosomal_protein_L28p_@_LSU_ribosomal_protein_L28p,_zinc-independent
CtesDRAFT_PD4324	Ubiquinol-cytochrome_C_reductase_iron-sulfur_subunit_(EC_1.10.2.2)
CtesDRAFT_PD4402	Type_IV_pilus_biogenesis_protein_PilM
CtesDRAFT_PD4510	Lactam_utilization_protein_LamB
CtesDRAFT_PD4563	Excinuclease_ABC_subunit_A,_dimeric_form
CtesDRAFT_PD4568	Acetate_permease_ActP_(cation/acetate_symporter)
CtesDRAFT_PD4621	Chemotaxis_regulator_-_transmits_chemoreceptor_signals_to_flagellar_motor_components_CheY
CtesDRAFT_PD4644	Flagellin_protein_FlaA
CtesDRAFT_PD4645	Flagellar_cap_protein_FliD

CtesDRAFT_PD4654	Flagellar_hook-associated_protein_FlgL
CtesDRAFT_PD4678	Ferric_iron_ABC_transporter,_iron-binding_protein
CtesDRAFT_PD4741	LSU_ribosomal_protein_L11p_(L12e)
CtesDRAFT_PD4743	Protein_translocase_subunit_SecE
CtesDRAFT_PD4753	LemA_family_protein
CtesDRAFT_PD4905	Glycolate_dehydrogenase_(EC_1.1.99.14),_iron-sulfur_subunit_GlcF
CtesDRAFT_PD5013	Pyrimidine_permease
CtesDRAFT_PD5112	N-acetyl-gamma-glutamyl-phosphate_reductase_(EC_1.2.1.38)
CtesDRAFT_PD5157	Protein_translocase_subunit_SecD
CtesDRAFT_PD5209	Barstar,_ribonuclease_(Barnase)_inhibitor
CtesDRAFT_PD5249	PTS_IIA-like_nitrogen-regulatory_protein_PtsN
CtesDRAFT_PD5310	N5-carboxyaminoimidazole_ribonucleotide_synthase_(EC_6.3.4.18)
CtesDRAFT_PD5427	Ribulose-phosphate_3-epimerase_(EC_5.1.3.1)
CtesDRAFT_PD5443	NADPH_dependent_aldo-keto_reductase_YajO

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LAPEHPFPAGIEDAVAAARWVVANAHALGGSATVAVAGDSAGGNFCAVVTQQLRDAG
IALAAQFLIYPAVDHAAAEYASAEQNAKGYFLEAETMAWFYNHYAGTFPDALDPRLAP
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SPGAQAVITHSIERFAALLTTRAR
>00057 | Cutinase | Thermobifida fusca | 2011.0 | PET
MANPYERGPNPTDALLEARSGPFSVSEENVSRLSASGFGGGTIYYPRENNTYGAVAISPG
YTGTEASIAWLGERIASHGFVVITIDTITTLDQPDSRAEQLNAALNHMINRASSTVRSRID
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>00058 | Cutinase | Thermobifida cellulosilytica | 2011.0 | PET
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FLCPGPRDGLFGEVEEYRSTCPF
>00059 | Cutinase | Thermobifida cellulosilytica | 2011.0 | PET
MANPYERGPNPTDALLEASSGPFSVSEENVSRLSASGFGGGTIYYPRENNTYGAVAISPG
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CPGPRDGLFGEVEEYRSTCPF
>00073 | Cutinase | Thermobifida fusca | 2014.0 | PET
MRGVWRYMPVYYYKCMLIPLLTFTKISIISKPQESRISLIICRTMPTVATFLGLAISGAAM
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>00074 | Cutinase | Saccharomonospora viridis | 2014.0 | PBAT PBS PBSA PCL PET PHB PLA
PHA
MRIRRQAGTGARASMARAIGVMTTALAVLVGAVGGVAGAEVSTAQDNPYERGPDPTE
DSIEAIRGPFSVATERVSSFASGFGGGTIYYPRETDEGTFGAVAVAPGFTASQGSMSWYG
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ESLPSSLPKAYMELDGATHFAPNIPNTTIAKYVISWLKRFVDEDTRYSQFLCPNPTDRAIE
EYRSTCPY
>00075 | Cutinase | Fusarium oxysporum | 2015.0 | PCL PET
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MRIRRQAGTGARASMARAIGVMTTALAVLVGAVGGVAGAEVSTAQDNPYERGPDPTE
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ESLPSSLPKAYMELDGATHFAPNIPNTTIAKYVISWLKRFVDEDTRYSQFLCPNPTDRAIE
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>00083 | PETase | Ideonella sakaiensis | 2016.0 | PET PEF
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>00084 | MHETase | Ideonella sakaiensis | 2016.0 | PET
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DMVWPNAATVVEVAAWRDAAPATASAAALPEHCEVSGAIAKRTGIDGYPYEIKFRLR
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FARLFLVPGMNHCSGGPGTDRFDMLTPLVAWVERGEAPDQISAWSGTPGYFGVAARTR
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>00095 | PETase | Vibrio gazogenes | 2018.0 | PCL PET
MMNVLTKCKLALGIIAIFFSLPSFAVPCSDCSNGFERGQVPRVDQLESSRGPYSVKTINVS
RLARGFGGGTIHYSTESGGQQGIIAVVPGYVSLEGSIKWWGPRLASWGFTVITIDTNTIY
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>00097 | PETase | Oleispira antarctica | 2018.0 | PCL PET
MNKSILKKLSFGTSVLLVSMNALSWTPSPTPNPDPIPDPTPCQDDCDFTRGPNPTPSSLEA
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>00098 | PETase | Uncultured bacterium | 2018.0 | PCL PET
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CPY
>00105 | Polyester hydrolase | Pseudomonas aestusnigri | 2020.0 | PET PU
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>00106 | Cutinase | Thermobifida fusca | 2018.0 | PET
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ATHAKPFYNSLPSSISKAYLELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQFLC
PGPRDGLFGEVEEYRSTCPF
>00107 | Cutinase | Thermobifida alba | 2018.0 | PET
MANPYERGPNPTDALLEASSGPFSVSEENVSRLSASGFGGGTIYYPRENNTYGAVAISPG
YTGTEASIAWLGGRIASHGFVVITIDTITTLDQPDSRAEQLNAALNHMINRASSTVRSRID
SSRLAVMGHSMGGGGTPRLASQRPDLKAAIPLTPWHLNKNRSSVTVPTLIIGADLDTIAP
VATHAKPFYNSLPSSISKAYLELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQFL
CPGPRDGLFGEVEEYCSTCPF
>00108 | Serine hydrolase | Thermobifida halotolerans | 2018.0 | PET
MANPYERGPNPTNSSIEALRGPFRVDEERVSRLQARGFGGGTIYYPTDNNTFGAVAISPG
YTGTQSSISWLGERLASHGFVVMTIDTNTTLDQPDSRASQLDAALDYMVEDSSYSVRNR
IDSSRLAAMGHSMGGGGTLRLAERRPDLQAAIPLTPWHTDKTWGSVRVPTLIIGAENDTI
ASVRSHSEPFYNSLPGSLDKAYLELDGASHFAPNLSNTTIAKYSISWLKRFVDDDTRYTQ
FLCPGPSTGWGSDVEEYRSTCPF
>00109 | Triacylglycerol lipase | Polyangium brachysporum | 2018.0 | PET
MPPDCVLPRRLAAAALLASATLVPLSAAAQTNPYQRGPDPTTRDLEDSRGPFRYASTNV
RSPSGYGAGTIYYPTDVSGSVGAVAVVPGYLARQSSIRWWGPRLASHGFVVITLDTRST
SDQPASRSAQQMAALRQVVALSETRSSPIYGKVDPNRLAVMGWSMGGGGTLISARDNP
SLKAAVPFAPWHNTANFSGVQVPTLVIACENDTVAPISRHASSFYNSFSSSLAKAYLEIN
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NGSHTCANTGNSNQALIGKYGVAWIKRFVDNDTRYSPFLCGAPHQADLRSSRLSEYRES
CPY
>00110 | Triacylglycerol lipase | Thermomonospora curvata | 2018.0 | PET
MSLRKSFGLLSATAALVAGLVAAPPAQAAANPYQRGPDPTESLLRAARGPFAVSEQSVS
RLSVSGFGGGRIYYPTTTSQGTFGAIAISPGFTASWSSLAWLGPRLASHGFVVIGIETNTR
LDQPDSRGRQLLAALDYLTQRSSVRNRVDASRLAVAGHSMGGGGTLEAAKSRTSLKA
AIPIAPWNLDKTWPEVRTPTLIIGGELDSIAPVATHSIPFYNSLTNAREKAYLELNNASHFF
PQFSNDTMAKFMISWMKRFIDDDTRYDQFLCPPPRAIGDISDYRDTCPHT
>00113 | Cutinase | Moniliophthora roreri | 2021.0 | PES PCL PET
MVRVFGLTLLALLVPALAAPVPEDLEARQSGCADVMVVYARGTDQDSPIGDPASVGVL
FRDNIKSLLGSRTFSFQGVNYAANVIGFLQGGDPAGSRQMTTDLTNVANSCPNAKIVSA
GYSQGGQLVHNSAAQLTAAVRNRINAVVIFGDPKSDQAVTGIPSSNVKIICHDGDNICEG
GFIVTSQHTNYQQDAPAAAQFVLSKV
>00118 | Cutinase | Pseudomonas oleovorans | 2011.0 | PCL PET
MINRTLPNSLLSMLAAGALLLSTSVMATNPPVDEPTDPGDSYARGPDPTVAFLEASSGP
YSTRTSRVSGLVSGFGGGTIHYPTGTTGTMAAIVVIPGFVSAESSIDWWGPKLASHGFVV
MTIDTNTGFDQPPSRARQINNALDYLVDQNSRRTSPVNGMIDTDRLGVIGWSMGGGGT
LRVASQGRIKAAIPLAPWDTTNARSVQAPTLIFACQADIIAPVGVHASPFYNQLPNDIEK
AYVEISGGSHYCANGGGLNNDVLSRLGVSWMKRFLDNDTRYSQFLCGPNHTSDRRVSE
YRGNCPY
>00119 | Lipase | Halopseudomonas pelagia | 2017.0 | PET
MKNTLIPKSLSTLFAASALMLSATVMAANPAPPQDPVEPGGFARGPDPSVSFLEADRGP
YSVNTSRVSGLVSGFGGGTIHYPSGTTGTMAAIVVIPGYVSAESSIEWWGPKLASHGFV
VMTIDTNTSFDQPPSRARQINSALDYLIDQNTATRSAVRGMIDTNRLGVVGWSMGGGG
TLRVATEGRISAAIPLAPWDTSSLQFRNVQAPTLIFACESDIIAPVGSHASPFYNRLPGDLN
KAFVEIDGGNHYCANGAASFGRYDSVLSRMGVSWMKLHLDQDERYKQFLCGPNHTAD
NRISEYRGNCPY
>00120 | Cutinase | Pseudomonas mendocina | 2009.0 | PET
APLPDTPGAPFPAVANFDRSGPYTVSSQSEGPSCRIYRPRDLGQGGVRHPVILWGNGTG
AGPSTYAGLLSHWASHGFVVAAAETSNAGTGREMLACLDYLVRENDTPYGTYSGKLN
TGRVGTSGHSQGGGGSIMAGQDTRVRTTAPIQPYTLGLGHDSASQRRQQGPMFLMSGG
GDTIAFPYLNAQPVYRRANVPVFWGERRYVSHFEPVGSGGAYRGPSTAWFRFQLMDDQ
DARATFYGAQCSLCTSLLWSVERRGL
>00121 | Cutinase | Humicola insolens | 2009.0 | PET
QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGP
YDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG
AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIE
ARGEAARFLRDRIRA
>00122 | Cutinase | Fusarium solani | 2009.0 | PET
MKFFALTTLLAATASALPTSNPAQELEARQLGRTTRDDLINGNSASCADVIFIYARGSTE
TGNLGTLGPSIASNLESAFGKDGVWIQGVGGAYAATLGDNALPRGTSSAAIREMLGLFQ
QANTKCPDATLIAGGYSQGAALAAASIEDLDSAIRDKIAGTVLFGYTKNLQNRGRIPNYP
ADRTKVFCNTGDLVCTGSLIVAAPHLAYGPDARGPAPEFLIEKVRAVRGSA
>00123 | Lipase | Moesziomyces antarcticus | 2009.0 | PET
MKLLSLTGVAGVLATCVAATPLVKRLPSGSDPAFSQPKSVLDAGLTCQGASPSSVSKPIL
LVPGTGTTGPQSFDSNWIPLSTQLGYTPCWISPPPFMLNDTQVNTEYMVNAITALYAGS
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GNNKLPVLTWSQGGLVAQWGLTFFPSIRSKVDRLMAFAPDYKGTVLAGPLDALAVSAP
SVWQQTTGSALTTALRNAGGLTQIVPTTNLYSATDEIVQPQVSNSPLDSSYLFNGKNVQ
AQAVCGPLFVIDHAGSLTSQFSYVVGRSALRSTTGQARSADYGITDCNPLPANDLTPEQ
KVAAAALLAPAAAAIVAGPKQNCEPDLMPYARPFAVGKRTCSGIVTP
>00125 | PETase | Uncultured bacterium | 2021.0 | PET
MQVVLGRVRSAGLLAALLALAAWALVWASPSAEAQSNPYQRGPNPTRSALTTDGPFSV
ATYSVSRLSVSGFGGGVIYYPTGTTLTFGGIAMSPGYTADASSLAWLGRRLASHGFVVI
VINTNSRLDFPDSRASQLSAALNYLRTSSPSAVRARLDANRLAVAGHSMGGGATLRISE
QIPTLKAGVPLTPWHTDKTFNTPVPQLIVGAEADTVAPVSQHAIPFYQNLPSTTPKVYVE
LDNATHFAPNSPNAAISVYTISWMKLWVDNDTRYRQFLCNVNDPALSDFRSNNRHCQ
>00126 | Hydrolase | Thermobifida fusca | 2006.0 | PET
MAVMTPRRERSSLLSRALQVTAAAATALVTAVSLAAPAHAANPYERGPNPTDALLEAS
SGPFSVSEENVSRLSASGFGGGTIYYPRENNTYGAVAISPGYTGTEASIAWLGERIASHGF
VVITIDTITTLDQPDSRAEQLNAALNHMINRASSTVRSRIDSSRLAVMGHSMGGGGTLRL
ASQRPDLKAAIPLTPWHLNKNWSSVTVPTLIIGADLDTIAPVATHAKPFYNSLPSSISKAY
LELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQFLCPGPRDGLFGEVEEYRSTCP
F
>00127 | Hydrolase | Thermobifida fusca | 2006.0 | PET
MAVMTPRRERSSLLSRALRFTAAAATALVTAVSLAAPAHAANPYERGPNPTDALLEAR
SGPFSVSEERASRFGADGFGGGTIYYPRENNTYGAVAISPGYTGTQASVAWLGKRIASH
GFVVITIDTNTTLDQPDSRARQLNAALDYMINDASSAVRSRIDSSRLAVMGHSMGGGGS
LRLASQRPDLKAAIPLTPWHLNKNWSSVRVPTLIIGADLDTIAPVLTHARPFYNSLPTSIS
KAYLELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQFLCPGPRDGLFGEVEEYR
STCPF
>00128 | Cutinase | Thermobifida fusca | 2008.0 | PET
MAVMTPRRERSSLLSRALQVTAAAATALVTAVSLAAPAHAANPYERGPNPTDALLEAS
SGPFSVSEENVSRLSASGFGGGTIYYPRENNTYGAVAISPGYTGTEASIAWLGERIASHGF
VVITIDTITTLDQPDSRAEQLNAALNHMINRASSTVRSRIDSSRLAVMGHSMGGGGTLRL
ASQRPDLKAAIPLTPWHLNKNWSSVTVPTLIIGADLDTIAPVATHAKPFYNSLPSSISKAY
LELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQFLCPGPRDGLFGEVEEYRSTCP
F
>00129 | Cutinase | Thermobifida fusca | 2008.0 | PET
MPPHAARPGPAQNRRGRAMAVITPRRERSSLLSRALRFTAAAATALVTAVSLAAPAHA
ANPYERGPNPTDALLEARSGPFSVSEERASRFGADGFGGGTIYYPRENNTYGAVAISPGY
TGTQASVAWLGERIASHGFVVITIDTNTTLDQPDSRARQLNAALDYMINDASSAVRSRID
SSRLAVMGHSMGGGGTLRLASQRPDLKAAIPLTPWHLNKNWSSVRVPTLIIGADLDTIA
PVLTHARPFYNSLPTSISKAYLELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQF
LCPGPRDGLFGEVEEYRSTCPF
>00131 | Cutinase | Thermobifida fusca | 2013.0 | PET
MAVMTPRRERSSLLSRALQVTAAAATALVTAVSLAAPAHAANPYERGPNPTDALLEAS
SGPFSVSEENVSRLSASGFGGGTIYYPRENNTYGAVAISPGYTGTEASIAWLGERIASHGF
VVITIDTITTLDQPDSRAEQLNAALNHMINRASSTVRSRIDSSRLAVMGHSMGGGGTLRL
ASQRPDLKAAIPLTPWHLNKNWSSVTVPTLIIGADLDTIAPVATHAKPFYNSLPSSISKAY
LELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQFLCPGPRDGLFGEVEEYRSTCP
F
>00132 | Cutinase | Thermobifida cellulosilytica | 2011.0 | PET PLA
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MANPYERGPNPTDALLEASSGPFSVSEENVSRLSASGFGGGTIYYPRENNTYGAVAISPG
YTGTEASIAWLGERIASHGFVVITIDTITTLDQPDSRAEQLNAALNHMINRASSTVRSRID
SSRLAVMGHSMGGGGTLRLASQRPDLKAAIPLTPWHLNKNWSSVTVPTLIIGADLDTIA
PVATHAKPFYNSLPSSISKAYLELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQF
LCPGPRDGLFGEVEEYRSTCPF
>00133 | Cutinase | Thermobifida cellulosilytica | 2011.0 | PET PLA
MANPYERGPNPTDALLEARSGPFSVSEERASRFGADGFGGGTIYYPRENNTYGAVAISP
GYTGTQASVAWLGERIASHGFVVITIDTNTTLDQPDSRARQLNAALDYMINDASSAVRS
RIDSSRLAVMGHSMGGGGTLRLASQRPDLKAAIPLTPWHLNKNWSSVRVPTLIIGADLD
TIAPVLTHARPFYNSLPTSISKAYLELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYT
QFLCPGPRDGLFGEVEEYRSTCPF
>00134 | P-nitrobenzylesterase | Bacillus subtilis | 2011.0 | PET
MTHQIVTTQYGKVKGTTENGVHKWKGIPYAKPPVGQWRFKAPEPPEVWEDVLDATAY
GPICPQPSDLLSLSYTELPRQSEDCLYVNVFAPDTPSQNLPVMVWIHGGAFYLGAGSEPL
YDGSKLAAQGEVIVVTLNYRLGPFGFLHLSSFNEAYSDNLGLLDQAAALKWVRENISAF
GGDPDNVTVFGESAGGMSIAALLAMPAAKGLFQKAIMESGASRTMTKEQAASTSAAFL
QVLGINEGQLDKLHTVSAEDSLKAADQLRIAEKENIFQLFFQPALDPKTLPEEPEKAIAEG
AASGIPLLIGTTRDEGYLFFTPDSDVHSQETLDAALEYLLGKPLAEKAADLYPRSLESQIH
MMTDLLFWRPAVAYASAQSHYAPVWMYRFDWHPKKPPYNKAFHALELPFVFGNLDG
LERMAKAEITDEVKQLSHTIQSAWITFAKTGNPSTEAVNWPAYHEETRETLILDSEITIEN
DPESEKRQKLFPSKGE
>00135 | Hydrolase | Thermomonospora curvata | 2014.0 | PET PCL
MKRTLKRALSLLPAAALAASALVAASPAQAAANPYQRGPNPTEASITAARGPFNTAEIT
VSRLSVSGFGGGKIYYPTTTSEGTFGAIAISPGFTAYWSSLEWLGHRLASQGFVVIGIETN
TTLDQPDQRGQQLLAALDYLTQRSAVRDRVDASRLAVAGHSMGGGGSLEAAKARTSL
KAAIPLAPWNLDKTWPEVRTPTLIIGGELDAVAPVATHSIPFYNSLSNAPEKAYLELDNA
SHFFPNITNTQMAKYMIAWMKRFIDDDTRYTQFLCPPPSTGLLSDFSDARFTCPM
>00136 | Hydrolase | Uncultured bacterium | nan | PET
ANPYERGPDPTESSIEAVRGPFAVAQTTVSRLQADGFGGGTIYYPTDTSQGTFGAVAISP
GFTAGQESIAWLGPRIASQGFVVITIDTITRLDQPDSRGRQLQAALDHLRTNSVVRNRIDP
NRMAVMGHSMGGGGALSAAANNTSLEAAIPLQGWHTRKNWSSVRTPTLVVGAQLDTI
APVSSHSEAFYNSLPSDLDKAYMELRGASHLVSNTPDTTTAKYSIAWLKRFVDDDLRYE
QFLCPAPDDFAISEYRSTCPF
>00137 | Polyester hydrolase | Uncultured bacterium | 2021.0 | PET PCL
MANPYERGPDPTESSIEAVRGPFAVAQTTVSRLQADGFGGGTIYYPTDTSQGTFGAVAIS
PGFTAGQESIAWLGPRIASQGFVVITIDTITRLDQPDSRGRQLQAALDHLRTNSVVRNRID
PNRMAVMGHSMGGGGALSAAANNTSLEAAIPLQGWHTRKNWSSVRTPTLVVGAQLD
TIAPVSSHSEAFYNSLPSDLDKAYMELRGASHLVSNTPDTTTAKYSIAWLKRFVDDDLR
YEQFLCPAPDDFAISEYRSTCPFLEHHHHHH
>00138 | Polyester hydrolase | Uncultured bacterium | 2021.0 | PET
MANPYERGPDPTVQSIEAVRGPFSVSETNVSRLVVTGFGGGTIYYPRDTSQGTFGAVAIA
PGFTASEGSMAWYGPRIASQGFVVFTIDTLTRLDQPDSRGRQLLAALDYLTQRSSVRSRI
DSSRLAVMGHSMGGGGSLEASESRPSLKASIPLTPWNLKKNWRNNRVPTLIVGAENDSI
ASVRTHAEPFYESIPSTTNKAYLELNNATHFAPNISNTTIAKYSISWLKRFVDNDTRYEQF
LCPPPRPDRDIEEYRCTCPY
>00139 | Polyester hydrolase | Uncultured bacterium | 2021.0 | PET
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MANPYERGPAPTTSSIEASRGPFAIASVTVSRSSVSGFGGGTIYYPRDTSEGTFGAVAIAP
GFTADEGSMAWYGPRIASQGFVVFTIDTITRLDQPDSRGRQLLAALDYLTQRSSVRSRID
SSRLAVMGHSMGGGGSLEASVSRPSLKAAIPLTPWNLKKNWRDVRVPTLIVGAESDSIA
SVRTHAEPFYESIPSTTNKAYLELNNATHFAPNISNTTIAKYSISWLKRFVDNDTRYEQFL
CPPPRPDRDIEEYRSTCPH
>00140 | Polyester hydrolase | Uncultured bacterium | 2021.0 | PET
MENPYERGPDPTESSIEAVRGPFAVAQTTVSRLQADGFGGGTIYYPTDTSQGTFGAVAIS
PGFTAGQESIAWLGPRIASQGFVVITIDTITRLDQPDSRGRQLQAALDHLRTNSVVRNRID
PNRMAVMGHSMGGGGALSAAANNTSLEAAIPLQGWHTRKNWSSVRTPTLVVGAQLD
TIAPVSSHSEAFYNSLPSDLDKAYMELRGASHFVSNTPDTTTAKYSIAWLKRFVDNDLR
YEQFLCPAPDDFAISEYRATCPF
>00141 | Polyester hydrolase | Uncultured bacterium | 2021.0 | PET
MENPYERGPDPTTQSVEAARGPYAVSQITVGGQFGSYSGGTIYYPTSTADGKFGAVAIA
PGFLSFQSSVAWLGPRIASQGFVVMTIDTGTIFDQPAQRGDQLLDALDFLTQRSSVKDRI
DPNRLAVAGWSWGGGGSLEAAADRPSLKAAIPMAGWNLNTNWSRLTTPVLVVGVQN
DLIAPVAMHSEPFYNSIRSEKAYLELAGGSHFTVTSANTPQAKLMISWLKRFVDNDTRY
EQFICPGPSRGFSVSEYRSTCPY
>00142 | Polyester hydrolase | Uncultured bacterium | 2021.0 | PET
MDNPYERGPDPTTQSVEAARGPYAVSQITVGGQFGSYSGGTIYYPTSTADGKFGAVAIA
PGFLSFQSSVAWLGPRLASQGFVVMTIDTGTIFDQPAQRGDQLLDALDFLTQRSSVKDRI
DPNRLAVAGWSMGGGGSLEAAADRPSLKAAIPMAGWNLNTNWSRLTTPVLVVGVQN
DLIAPVGSHSEPFYNSIRSEKAYLELAGGSHFTVTSANTPQAKLMISWLKRFVDNDTRYE
QFICPGPSRGFSVSEYRSTCPF
>00143 | Polyester hydrolase | Uncultured bacterium | 2021.0 | PET
MDNPYERGPDPTTQSVEAARGPYAVSQITVGGQFGSYSGGTIYYPTSTTDGKFGAVAIA
PGFLSFQSSVAWLGPRIASQGFVVMTIDTGTIFDQPAQRGDQLLDALDFLTQRSSVKDRI
DPNRLAVAGWSMGGGGSLEAAADRPSLKAAIPMAGWNLNTNWSRLTTPVLVVGVQN
DLIAPVAMHSEPFYNSIRSEKAYLELAGGSHFTVTSANTPQAKLMISWLKRFVDNDTRY
EQFICPGPSRGFSVSEYRSTCPF
>00144 | Esterase | Aequorivita sp. | 2022.0 | PET PU PCL
MKKIYAVALFFLATSFAPNIIFAQCGDVTIESLTNPGPYEVATLTEADGLRNGPDYQGAT
VYYPTNATPPFASIAIVPGFTALPSSVEEWGPFYASHGIVTIIIGTNSLFDFPEERAVALIDA
LETMRQENTRSSSPLENQLDVDKFAVSGWSMGGGGAQRAAVLDNTIKGVVALCPWLP
NASLNHDSPVLIFSGENDPTAPPAQHADLHYAATPNTTNKLLFEIENGNHSVANTPNGG
NGAVGKIALSWLKLYVDENDCYCPLLTESLLVDPPAASKVLSSFECELLSVPDNSFAISV
YPNPTHDFVNINSTNPVHFEVYSALGQRLLSGELTQSEKQIDFSNFAKGLYYVRLGNETV
KIVRN
>00145 | Esterase | Kaistella jeonii | 2022.0 | PET PU PCL
MRKLYLFLFLTLISPISISIFHAQCTGATVESLTNPGPYTVATLSEADGVRNGPKYAGSTIY
YPTNATPPYASIAIVPGFTAAPSSVQEWGPFYASHGIVAIIIGTNSLYDQPEARALALLDA
LETIKQENGRATSPLIGKLDVTKLAVSGWSMGGGGAQRAAVLDNTISAVVALCPYLTSP
QLNHTVPVLIFSGQSDPTAPPSQHANVHYNTTPGTTNKLLFEVKNGNHSVANSPTGGGG
AVGKLALSWLKIYLEKNDCYCSVLATAIVNSTTVSSKISQSYQCNNALGVVDSKTRFNL
YPNPTKDFVQVNVREMASYQLSSSTGQIVLKGIVTSSKNQIDLSKLPAGVYYLQINGETI
KVIKKQ
>00062 | Cutinase | Uncultured bacterium | 2012.0 | PCL PET
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MDGVLWRVRTAALMAALLALAAWALVWASPSVEAQSNPYQRGPNPTRSALTADGPFS
VATYTVSRLSVSGFGGGVIYYPTGTSLTFGGIAMSPGYTADASSLAWLGRRLASHGFVV
LVINTNSRFDYPDSRASQLSAALNYLRTSSPSAVRARLDANRLAVAGHSMGGGGTLRIA
EQNPSLKAAVPLTPWHTDKTFNTSVPVLIVGAEADTVAPVSQHAIPFYQNLPSTTPKVY
VELDNASHFAPNSNNAAISVYTISWMKLWVDNDTRYRQFLCNVNDPALSDFRTNNRHC
Q
>00124 | Polyester hydrolase | Moraxella sp. | 2021.0 | PET PCL PU PHB PBS PLA PHA
MFIMIKKSELAKAIIVTGALVFSIPTLAEVTLSETTVSSIKSEATVSSTKKALPATPSDCIAD
SKITAVALSDTRDNGPFSIRTKRISRQSAKGFGGGTIHYPTNASGCGLLGAIAVVPGYVSY
ENSIKWWGPRLASWGFVVITINTNSIYDDPDSRAAQLNAALDNMIADDTVGSMIDPKRL
GAIGWSMGGGGALKLATERSTVRAIMPLAPYHDKSYGEVKTPTLVIACEDDRIAETKKY
ANAFYKNAIGPKMKVEVNNGSHFCPSYRFNEILLSKPGIAWMQRYINNDTRFDKFLCAN
ENYSKSPRISAYDYKDCP
>00173 | Esterase | Pseudomonas sp. | 2022.0 | PET
MTEPLILQPVKPADACVIWLHGLGADRYDFLPVAEALQESLLSTRFVLPQAPTRPVTING
GYAMPSWYDIKAMSPARAIDRDELEASADRIIELIEEQRSSGIDASRIFLAGFSQGGAVVY
HTAFLKWQGPLGGVLALSTYAPTFSDELELSASQQRIPVLSLHGQFDNVVQNSMGRTAY
EYLKAHGVTVTWQEYPMEHEVLPEEIRDIGTWLSERLR
>00175 | Hydrolase | Uncultured bacterium | 2022.0 | PET
MKALTFSKSFLSAIAAGALMLSASAMANNPPPPDDPGAPSPYQRGPDPTVSFVEASRGN
YRVATSNVSSLVSGFGGGTIHYPSNATGTMGAIVVIPGYVSGEGSIDWWGPKLASYGFV
VMTIGTNSGFDQPPSRARQINNALDYLVEQNTRTGSPVRGMIDPSRLGVIGWSMGGGGT
IRVAGEGRIKAAIPLAPWDTSSIPSRGVQAPTLIFACQSDVVAPVRSHASPFYNALPGSISK
AFVNLNNGNHFCANGGSSFGRYDAALGRLGVSWMKRFLDEDRRYSQFLCGPNHTGDR
QITEYRGNCPY
>00176 | Hydrolase | Rhizobacter gummiphilus | 2021.0 | PET
MFGKLPFARASLAVGALLLSAAAVAQTNPYQRGPDPTVSSLEATRGPFSTSSFTVSRPSG
YGAGTVYYPTNAGGKVGAIAVVPGYTARQSSINWWGPRLASHGFVVITIDTNSTLDQPS
SRSSQQMAALRQVVSLAGTSSSPIYNKVDTARLGVMGWSMGGGGSLISAKNNPSLRAA
APQAPWAQESFSSVTVPTLIVSCENDSIAPNSSHSFPFYNQMTRNKKANLVINGGSHSCA
NSGNSDAGLIGKYGVAWMKRFMDDDTRYSKFLCGAEHQADLSKRAVEAYKENCPY
>00183 | PETase | Marinobacter sp. | 2022.0 | PET PBSeT PBAT Ecovio-FT
MFRTIAKNPVRSLIAAGSLLLSASAFAAGGGGDGGDGGCTSDCGFQRGPDPTVSFLEASS
GPYSVRTDNVSSLVGGFGGGTVHYPTGTTGTMAAVVVIPGFVSAESSIEWWGPKLASY
GFVVMTIDTNSGFDQPPSRATQINNALDYLLEENDSSSSPYSGMIDPNRLGVIGWSMGG
GGTLRVAAEGRIQAAIPLAPWDTSSLRFRNIETPTLIFACESDVIAPVGSHADPFYEAIPDS
TDKAFFELNNGSHYCGNGGNSYNNELGRLGVSWMKLHLDQDQRYNQFLCGPDHEDEY
RISEYRGTCPY
>00184 | PETase | Marinobacter sp. | 2022.0 | PET PBSeT PBAT Ecovio-FT
MFNQIGKKSALSLMAAGSLMFSATALAIGGGGSGGGNNGGGGGCEADCGYERGPDPS
VSLLEASTGPFSVRTSNVSSSVRGFGGGTIHYPTNTTGTMAAIVVIPGFVSPESSIAWWGP
KLASHGFVVMTIGTNSGFDQPASRASQLNNALDYLIEQNGSSRSPINGMIDTDRLGVMG
WSMGGGGTLRVATEGRVSAAIPLAPWDSSSSQFRSIDTPTLIFACENDSTAPVRSHADPF
YDAIPDSTAKAFVELDGGGHTCANGSSGFGGSYNDVLSRLGVSWMKLHLDKDQRYNQ
FVCGPNHESDRSISEYRGTCPY
>00185 | PETase | Uncultured bacterium | 2022.0 | PET
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MQSPAQSSAPTVELDSGAIAGSTADGVVSFKGIPYAAPPVGNLRWRAPQPVASWTGVR
AATEYGYDCIQLPLEGDAAASGGEMSEDCLVLNVWRPAEIAPGERLPVLVWIHGGGFL
NGSAAAPIYDGTAFAQQGLVVVSFNYRLGRLGFFAHPALTAANEGPLGNYGLMDQIAA
LEWVQRNIAAFGGDPARITLMGQSAGGISVMYHLTAPESQGLFHQAAVLSGGGRTYLL
GLRNLRESTDALPSAEQSGLAFGRRFGIRGRGRAALRSLRSLSAEEVNGDLSMAALVEK
PADYAGLEHHHHHH
>00186 | PETase | Uncultured bacterium | 2022.0 | PET
MVDITGNGMAATAPTDERIVDKPLPQPQIRSGNVRAMPAARKLAQEHGIDLSTLTGSGP
GGVIVKEDVERAITARAVPVSPLQRVNFYSAGYRLDGLLYTPRHLPAGERRPGVVLLVG
YTYLKTMVMPDIAKVLNAAGYVALVFDYRGFGESEGPRGRLIPLEQVADARAALTFLA
EQSMVDPDRLAVIGISLGGAHAITTAALDQRVRAVVALEPPGHGARWLRSLRRHWEWR
QFLSRLAEDRRQRVLSGGSTMVDPLEIVLPDPESQAFLDQVAAEFPQMKVTLPLESAEA
LIEYVSEDLAGRIAPRPLLIIHSDADQLVPVAEAQAIAERAGSSAQLEIIPGMSHFNWVMP
GSPGFTRVTDSIVKFLRNTLPVSADNLEHHHHHH
>00187 | PETase | Uncultured bacterium | 2022.0 | PET
MVPSAGVGLSGVLHLPAGVSRPVLFLHGFTGNKTESGRLYTDMARVLCSAGYAALRFD
FRGHGDSPLPFEEFRISLAVEDARNAAGFLKNVPEVDGTRFGVVGLSMGGGVAVSLAA
GREDVGALVLLSPALDWPELFQRARGFFRAEEGYVVYWGPHRMRDVYAMETMNFSVM
GLAEEIQAPTLIIHSVDDMVVPISQAKRFYEKLKVEKKFIEIEHGGHVFDDYNVRRRIEQE
VLDWVKRHLLEHHHHHH
>00188 | PETase | Uncultured bacterium | 2022.0 | PET
MLIRPVTFRNMNQQIIGILHTPDNIRLNEKVPGILMFHGFTGNKTEAHRLFVHVARSLSE
HGFIVLRFDFRGSGDSDGEFEDMTLPGEVSDAERALTFLLRQRNVDKNRIGVIGLSMGG
RVAAILASKDRRVKFAVLYSPALGPLRDRSLSFMSKEKIERLNSGEAVEFFAEGWYIKK
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HTFSKKEHTLEVIKKTLDWIRSLGILEHHHHHH
>00189 | PETase | Uncultured bacterium | 2022.0 | PET
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IGISLGGAHAITTAALDQRVRAVVAIEPPGHGAHWLRSLRRHWEWSQFLSRLTEDRRQR
VLSGVSSTVDPLEIVLPDPESQAFLDQVAAEFPQMKVTLPLESAEALIEYVPEDLAGRIAP
RPLLLEHHHHHH
>00190 | PETase | Uncultured bacterium | 2022.0 | PET
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SADCITPPAQHQVPMYNALPDCKAYGGSSRVDLQACKLEHHHHHH
>00191 | PETase | Uncultured bacterium | 2022.0 | PET
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QHLASHGFLVAVPQHIGSDLQYRQELIKGTLSSALSPVEFLARPTDLSTIIDYLQATQNTG
SWQKRANLQQIGVIGDSLGGTTALTIGGAPLDIPRLQTKCTSDNVIVNVALILQCQASFLP
PSEYNLADSRVKAVIATHPLISGIFSPDSLAKIQIPVMITAGNFDIITPLEHHHHHH
>00192 | PETase | Uncultured bacterium | 2022.0 | PET
MQTVTSMLKDLDAVITQVSEKFPQIDNKRVCLIGHSQGAYVSFLHATKDERIKCLVSW
MGRLSDLKEFWSKLWFDEIERKGYIYEWDYKITKKYVRDSLKYNLSKAAWRIKVPTLLI

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YGELDDIVPPSEGMKFYRNIKSPKKIVIVKDLNHTFSGEKAKKSVIRITLKWLSKWLKRL
DLEHHHHHH
>00193 | PETase | Uncultured bacterium | 2022.0 | PET
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TNAGGGKMAGIVVIPGYLSFESSIEWWGPRLASHGFVVMTIDTNTIYDQPSQRRDQIEAA
LQYLVNQSNSSSSPISGMVDSSRLAAVGWSMGGGGTLQLAADGGIKAAIALAPWNSSIN
DFNRIQVPTLIFACQLDAIAPVALHASPFYNRIPNTTPKAFFEMTGGDHWCANGGNIYSA
LLGKYGVSWMKLHLDQDTRYAPFLCGPNHAAQTLISEYRGNCPYLEHHHHHH
>00194 | PETase | Ketobacter sp. | 2022.0 | PET
MTTPTPTPEPEPEPPGGCGDCYQRGPDPTVAALEADRGPYSVRTINVSSWVSGFGGGTIH
YPVGTQGTMGAIAVIPGYVSYENSIEWWGGRLASWGFVVITIDTNSIYDQPDSRANQLS
AALDYVIAQSNSSRSAIQGMVDPNRLGAIGWSMGGGGTLKLSTDRYLKAAIPQAPWYS
GFNPFDEITTPTLIIACQLDAVAPVAQHASPFYNEIPNSTAKAFLEIRNGDHFCANSGYPD
EDILGKYGVAWMKRFIDDDRRYDAFLCGPNHEAEWDISEYRDTCNYLEHHHHHH
>00195 | PETase | Actinomycetota bacterium | 2022.0 | PET
MQADTDTTAVAPAAANPYERGPAPTEASVTAARGPFAIAQVNVPSGSGAGFNDGTIYY
PTDTSQGTFGAVAVIPGFISPQAVIQWFGPRLASQGFVVFTLDSNGLADLPDARGRQLLA
ALDYLTTQSTVRTRIDPNRLAVMGHSMGGGGTLLAAENRPTLKAAIPLAPWEPDTSWE
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LSWLKRFVDDDTRYDQFLCPGPTPDTDISQYLDTCPNGSLEHHHHHH
>00196 | PETase | Micromonosporaceae bacterium | 2022.0 | PET
MADNPYQRGPDPTRDSVAASRGTFATASTTVGSGNGFGAGFIYYPTDTSQGTFGAVAIV
PGYTATWAAEGAWMGHWLASFGFVVIGIDTINRNDWDTARGTQLLAALDYLTQRSTV
RDRVDASRLAVMGHSMGGGGAMYAALQRPSLKAAVGLAPFSPSQNLNGMRVPTMLL
AGQHDTTTTPASITSLYNGIPAATEKAYLELSGAGHGFPTSNNSVMMRKVIPWLKIFVDS
DVRYTQFLCPLMDNTGIRSYQSTCPLLPGTPTPPNRYEAETSPAVCTGTIASNHTGYSGT
GFCDGNNATNAYAQFTVNASAAGSMTLRVRFANGTTTARPASLIVNGSTVQTPSFEGT
GAWTTWATKTLTVTLNAGNNTIRFNPTTANGLPNLDYIEIAAPLEHHHHHH
>00197 | PETase | Ketobacter sp. | 2022.0 | PET
MGDCPATAICRSESPGAYSGNGPYGSRSYTLSRFQTPGGATVYYPANAEPPYAGMVFTP
PYTGTQAMFAAWGPFFASHGFVLVTMDTSTTLDSVDQRAAQQKEVLNALKSENTRSGS
PLRGKLDTARLGAVGWSMGGGATWINSAEYSGLKTAMSLAGHNLTAVDIDSKGYNTR
VPTLLFNGAQDLTYLGGLGQSDGVYNNIPAGIPKVFYEVSSAGHFDWGSPTAANRSVAS
LALAFHKAYLDGDTRWLQYITRPSSDVTTWRTANIRLEHHHHHH
>00198 | PETase | Ketobacter alkanivorans | 2022.0 | PET
MSQVPPTPPTDDPMGDCPSTAICRGEAPGSYSGNGPYGSRSYTLSRFQTPGGATVYYPSN
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DVLKQENTRSGSPLRGKLDTSRLGAVGWSMGGGATWINSAEYNGLKTAMSLAGHNMT
AIDLDSKGGNTRVPTLLFNGALDLTMLGGLGQSIGVYNAIPRGIPKVIYEVASAGHFDW
GSPTAANRSVAGIALAFHKTFLDGDTRWVSYIKRPSSDVATWRTENLPQLEHHHHHH
>00199 | PETase | Nocardioidaceae bacterium | 2022.0 | PET
MESPYERGPDPTSASVLDNGTFSLSSTSVSSLVTGFGGGTIYYPTSTTQGTFGGVVLAPG
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DETRIAVSGHSMGGGGTLAAANQDSSIKAAVALQPWHTDKTWPGIQIPTMIIGAENDSV
APVASHSIPFYTSMTGAREKAYGEINNGDHFIANTDDDWQGRLFVTWLKRYVDDDTRY
SQFLCPAPSSIYLSDYRNTCPDLEHHHHHH
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>00200 | PETase | Caldimonas taiwanensis | 2022.0 | PET
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TGTSSTMTFWGERLASHGFVVLVIDTITLYDQPDSRARQLKAALDYLATQNGRSSSPIYR
KVDTSRRAVAGHSMGGGGSLLAARDNPSYKAAIPMAPWNTSSTAFRTVSVPTMIFGCQ
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DNDTRYSPFVCGAEYNRVVSSYEVSRSYNNCPYLEHHHHHH
>00201 | PETase | Marinactinospora thermotolerans | 2022.0 | PET
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GYTASQSSMAWMGHRIASQGFVVFTIDTITRYDQPDSRGRQIEAALDYLVEDSDVADRV
DGNRLAVMGHSMGGGGTLAAAENRPELRAAIPLTPWHLQKNWSDVEVPTMIIGAEND
TVASVRTHSIPFYESLDEDLERAYLELDGASHFAPNISNTVIAKYSISWLKRFVDEDERYE
QFLCPPPDTGLFSDFSDYRDSCPHTTLEHHHHHH
>00202 | PETase | Saccharopolyspora flava | 2022.0 | PET
MAEPADVHGPDPTEESITAPRGPFEVDEESVSRLSVSGFGGGTIYYPTDTTDGLFSAVSIS
PGFTGTQETMAWYGPRLASQGFVVFTIDTITTTDQPDSRARQLQASLDYLVNDSDVKDII
DPARLGVMGHSMGGGGSLKAALDNPALKAAIPLTPWHTTKDFSGVQTPTLIIGAQNDT
VAPVSQHAKPFYESLPDDPGKAYLELAGASHLAPNTDNTTIAKFSIAWLKRFLDDDTRY
DQFLCPPPENDDSISDYQSTCPYLEHHHHHH
>00203 | PETase | Thermobifida fusca | 2022.0 | PET
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YTGTEASIAWLGKRIASHGFVVITIDTITTLDQPDSRAEQLNAALNHMINRASSTVRSRID
SSRLAVMGHSMGGGGSLRLASQRPDLKAAIPLTPWHLNKNWSSVRVPTLIIGADLDTIA
PVLTHARPFYNSLPTSISKAYLELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQF
LCPGPRDGLFGEVEEYRSTCPFLEHHHHHH
>00204 | PETase | Thermobifida fusca | 2022.0 | PET
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GYTGTEASIAWLGERIASHGFVVITIDTITTLDQPDSRAEQLNAALNHMINRASSTVRSRI
DSSRLAVMGHSMGGGGTLRLASQRPDLKAAIPLTPWHLNKNWSSVTVPTLIIGADLDTI
APVATHAKPFYNSLPSSISKAYLELDGATHFAPNIPNKIIGKYSVAWLKWFVDNDTRYT
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>00205 | PETase | Thermobifida alba | 2022.0 | PET
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YTGTQSSIAWLGERIASHGFVVIAIDTNTTLDQPDSRARQLNAALDYMLTDASSSVRNRI
DASRLAVMGHSMGGGGTLRLASQRPDLKAAIPLTPWHLNKSWRDITVPTLIIGADLDTI
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>00206 | PETase | Thermobifida cellulosilytica | 2022.0 | PET
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TATQSSVAWLGERIASHGFVVITIDTNTTLDQPDSRADQLEAALDHMVDGASSTVRSRID
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>00207 | PETase | Thermobifida halotolerans | 2022.0 | PET
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>00208 | PETase | Thermobifida cellulosilytica | 2022.0 | PET
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>00213 | Lipase | Moraxella sp. | 2022.0 | PET
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GFVVITISANSGFDQPASRATQLGRALDYVINQSNGSNSPISGMVDTTRLGVVGWSMGG
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RSVSEYRDTCNY
>00214 | Lipase | Oleispira antarctica | 2022.0 | PET
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GAIGWSMGGGGALKLATERSTVRAIMPLAPYHDKSYGEVKTPTLVIACEDDRIAETKKY
ANAFYKNAIGPKMKVEVNNGSHFCPSYRFNEILLSKPGIAWMQRYINNDTRFDKFLCAN
ENYSKSPRISAYDYKDCP
>00216 | Cutinase | Marinactinospora thermotolerans | 2022.0 | PET
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TESSVTAVRGYFDTDTDTVSSLVSGFGGGTIYYPTDTSEGTFGGVVIAPGYTASQSSMA
WMGHRIASQGFVVFTIDTITRYDQPDSRGRQIEAALDYLVEDSDVADRVDGNRLAVMG
HSMGGGGTLAAAENRPELRAAIPLTPWHLQKNWSDVEVPTMIIGAENDTVASVRTHSIP
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73	100	11.86	15.76	15.74	15.45	10.43	11.63	9.66	8.67	9.09	5.41	8.2
	7.73	6.57	4.69	4.03	5.42	6.47	8.28	5.65	6.09	7.34	5.65	6.19
	6.19	8.6	8.38	6.28	7.33	7.98	7.94	11.76	11.76	7.57	7.02	9.42
	9.94	9.09	9.09	8.89	8.89	8.24	8.72	12.14	10.65	8.95	10	7.6
	8.88	9.47	8.88	8.93	8.28	5.64	5.92	5.95	5.64	5.92	6.51	6.51
	8.28	8.28	8.28	8.93	7.69	7.69	7.69	8.28	6.51	3.23	8.19	11.35
	9.57	7.65	7.06	7.06	10	9.42	9.47	9.47	9.36	9.36		
113	11.86	100	27.72	27	29.65	7.91	12.57	10.78	12	11.25	5.17	9.09
	9.09	7.69	6.87	9.72	10.58	9.38	8.33	5.63	4.23	8.82	7.35	10
	10	7.25	7.25	8.7	7.25	8.7	8.7	10.14	10.14	13.04	11.59	8.7
	8.7	8.96	8.96	10.45	10.45	10.45	8.96	11.59	5.8	10.29	10.29	8.7
	8.7	7.25	7.25	7.46	8.96	7.46	7.46	7.46	7.46	7.46	7.46	7.46
	7.46	7.46	7.46	7.46	7.46	7.46	7.46	7.46	8.96	7.41	10.14	10.14
	10.14	5.8	5.8	5.8	7.25	7.25	7.25	7.25	7.25	7.25		
121	15.76	27.72	100	52.85	54.69	12.4	12.57	9.03	9.04	10.98	9.38	7.41
	6.67	7.27	3.31	9.86	7.53	10.77	6.25	4.69	4.69	4.69	6.25	7.69
	7.69	6.25	6.25	4.69	6.25	6.25	6.25	9.38	9.38	7.81	12.5	12.5
	12.5	12.7	12.7	7.94	7.94	9.52	9.68	7.69	4.69	7.94	7.94	6.25
	10.94	12.5	12.5	8.06	8.06	8.06	8.06	8.06	8.06	8.06	8.06	8.06
	8.06	8.06	8.06	8.06	8.06	8.06	8.06	8.06	8.06	6	6.25	9.38
	9.38	9.38	9.38	9.38	9.38	9.38	6.25	6.25	7.81	7.81		
75	15.74	27	52.85	100	75.81	12.5	15.18	14.44	13.11	13.27	10.67	11.31
	11.9	10.57	8.57	8.43	7.94	9.46	10.71	9.64	7.23	6.33	5.06	9.76
	9.76	10.13	10.13	11.39	10.13	11.39	8.86	11.39	11.39	11.39	11.39	11.39
	11.39	12.82	12.82	11.54	11.54	11.54	13.92	12.5	11.25	10	10	11.11
	11.25	11.25	10	8.97	8.86	8.86	8.86	8.86	8.86	8.86	8.86	8.86
	8.86	8.86	8.86	8.86	8.86	8.86	8.86	8.86	11.39	8.47	8.64	11.11
	12.35	11.11	11.11	11.11	13.75	13.75	10	10	9.88	9.88		
122	15.45	29.65	54.69	75.81	100	13.64	17.07	14.84	12.77	19.32	10.77	9.09
	9.82	9.84	6.52	9.33	9.57	14.93	11.84	12.66	10.13	8.45	5.63	10.84
	10.84	10	11.25	10	12.5	10	11.25	12.35	12.35	12.82	12.5	13.75
	13.89	14.86	14.86	13.51	13.51	13.51	15.49	13.89	11.11	10.67	10.67	12.33
	11.11	11.11	11.11	10	9.86	9.21	9.86	9.86	9.21	9.86	9.86	9.86
	9.86	9.86	9.86	9.86	9.21	9.21	9.21	9.86	12.68	8.62	9.59	14.1
	14.1	12.33	12.33	12.33	13.89	13.58	11.11	11.11	10.96	10.96		
CtesDRAFT_PD1902			10.43	7.91	12.4	12.5	13.64	100	17.15	11.62	10.31	9.43
	5.56	11.22	10.53	6.3	5.8	9.09	9.01	8.55	10.81	8.96	8.21	10.17
	11.38	9.21	9.21	9.03	6.04	7.38	8.05	6.8	9.4	8.22	8.22	9.29
	11.81	9.4	9.52	7.19	7.19	8.03	8.03	7.41	10.92	11.48	6.67	10.34
	9.66	11.11	13.22	13.22	13.22	6.72	9.17	8	8.33	8.4	8.33	8.33
	8.33	8.33	8.33	9.09	8.4	8.4	8.67	8.67	8.67	8.33	9.17	8.86
	8.13	10.64	10.49	11.48	12.4	12.3	6.61	6.88	10.26	10.26	9.02	9.84
84	11.63	12.57	12.57	15.18	17.07	17.15	100	11.86	14.72	8.65	6.62	12.25
	11.64	13.07	11.31	10.14	12.5	15.03	11.45	14.23	12.36	10.58	10.91	14.29
	14.29	13.39	11.2	15.68	15.68	13.5	14.96	11.98	11.98	16.81	14.16	14.29
	12.39	15.49	15.49	14.16	14.16	11.95	14.29	15.38	15.66	15.74	15.28	12.92

	13.78	13.27	13.27	16.75	16.16	15.32	16.16	16.24	15.32	16.16	17.17	17.17
	17.68	17.59	17.77	17.77	16.67	16.67	16.67	17.68	13.64	14.15	13.57	13.51
	11.71	15.66	15.23	15.15	13.71	13.78	15.49	15.49	14.14	13.64		
134	9.66	10.78	9.03	14.44	14.84	11.62	11.86	100	39.43	10.23	9.32	14.2
	14.09	10.92	11.84	11.92	13.24	11.82	11	9.56	9.93	14.22	12.5	12.99
	12.99	14.54	13.42	14.72	12.12	12.72	12.66	11.89	11.89	14.54	14.98	13.42
	13.16	12.55	12.55	12.28	12.28	13.22	14.04	10.14	12	13.08	15.19	11.4
	13.78	13.33	13.33	12.44	11.95	11.76	12.39	12.44	11.76	12.39	12.39	12.39
	12.83	13.27	12.83	13.33	12.18	12.18	12.18	12.83	12.39	12.04	14.04	12.72
	12.55	13.22	12.78	12.78	14.1	14.4	12.97	12.97	11.4	12.28		
185	8.67	12	9.04	13.11	12.77	10.31	14.72	39.43	100	11.21	15.94	14.75
	15.43	13.01	12.2	18.52	12.08	17.39	12.12	13.49	12.7	13.11	12.3	17.83
	17.83	16.94	17.32	18.11	15.75	16	15.75	13.71	13.71	18.55	19.35	17.97
	17.6	19.84	19.84	19.35	19.35	18.7	15.45	16.13	16.94	14.71	16.18	16.67
	16.8	16	16	16.26	15.32	14.71	16.13	16.26	13.64	16.13	15.32	15.32
	15.32	15.32	15.32	15.32	13.97	13.97	13.97	15.32	16.94	13.51	16.67	14.96
	14.73	16.67	16.67	16.67	16.8	14.79	16.67	16.67	15.87	15.87		
123	9.09	11.25	10.98	13.27	19.32	9.43	8.65	10.23	11.21	100	15.08	11.4
	12.99	12.99	11.61	13.38	11.66	12.44	11.72	14.62	14.57	13.24	12.38	15.28
	15.28	16.83	16.83	17.16	18.14	18.05	18.23	16.27	16.27	17.31	14.42	17.39
	16.74	15.79	15.79	15.69	15.69	17.22	15.38	17.65	13.3	12.87	12.38	15.09
	14.36	14.36	14.36	13.53	14.01	14.56	13.81	14.65	14.56	14.57	13.57	13.04
	13.57	12.98	13.64	13.57	13.59	13.59	13.59	13.57	14.07	13.46	14.22	16.26
	14.22	14.43	14.51	13.86	15.46	15.53	14.78	14.78	14.36	14.36		
192	5.41	5.17	9.38	10.67	10.77	5.56	6.62	9.32	15.94	15.08	100	17.84
	14.75	24.68	25.3	23.62	14.55	17.02	18.97	17.02	17.73	17.02	17.73	20.9
	20.9	18.57	18.44	15.6	18.44	18.57	17.27	15	15	18.57	16.43	17.14
	17.14	17.02	17.02	15	15	17.86	16.31	17.04	16.06	16.91	17.65	20
	16.42	16.42	16.42	17.52	21.9	18.98	18.25	18.25	18.25	18.25	18.98	18.98
	18.98	18.98	19.71	19.12	18.98	18.98	18.98	18.98	16.06	12.9	17.78	17.04
	17.04	17.78	17.78	17.78	14.81	14.81	16.79	16.79	17.78	17.04		
186	8.2	9.09	7.41	11.31	9.09	11.22	12.25	14.2	14.75	11.4	17.84	100
	92.74	28.34	27.82	20.74	16.43	17.11	15	15.66	14.46	16.46	14.9	15.85
	15.85	19.77	16.98	18.85	20	20.31	20.16	17.74	17.74	17.65	19.53	19.08
	19.69	20.08	20.08	18.97	18.97	17.39	19.25	17.09	20.51	17.6	18.4	19.43
	21.98	21.98	21.98	21.89	21.37	25.1	23.08	23.18	24.32	23.08	22.65	23.08
	23.5	23.4	23.61	23.18	25.1	25.1	25.1	23.5	19.23	16.13	21.28	19.28
	19.28	21.79	21.46	21.37	21.03	20.63	21.65	21.65	21.79	21.79		
189	7.73	9.09	6.67	11.9	9.82	10.53	11.64	14.09	15.43	12.99	14.75	92.74
	100	30.32	28.64	22.54	16.32	17.04	16	14.86	14.86	17.36	15.28	19.01
	19.01	22.22	18.06	22.22	21.53	20.83	20.98	17.36	17.36	17.36	19.44	20.69
	20.69	20.83	20.83	19.44	19.44	19.44	22.07	22.7	21.68	19.01	20.42	20.42
	21.99	21.28	21.28	20.57	21.13	23.24	22.54	22.7	22.54	22.54	21.83	22.54
	21.83	21.83	21.83	21.83	21.83	21.83	21.83	21.83	19.01	15.79	19.72	21.13
	21.13	21.83	21.83	21.83	23.4	23.4	22.38	22.38	23.24	23.94		

187	6.57	7.69	7.27	10.57	9.84	6.3	13.07	10.92	13.01	12.99	24.68	28.34
	30.32	100	33.6	17.68	15.2	13.66	19.08	19.27	18.75	16.84	16.32	21.74
	21.74	23.16	20.42	21.47	23.04	23.68	22.75	22.63	22.63	23.16	22.11	21.47
	21.47	23.04	23.04	20.53	20.53	20	21.47	18.82	21.93	18.82	20.43	21.62
	19.02	17.93	18.48	19.79	20.32	20.32	20.32	20.43	20.32	20.32	21.39	21.39
	21.93	21.39	21.93	22.04	21.93	21.93	21.93	21.93	19.25	14.29	25.41	20.54
	21.08	20.54	20.54	20.54	21.08	21.08	22.46	22.46	18.92	18.92		
188	4.69	6.87	3.31	8.57	6.52	5.8	11.31	11.84	12.2	11.61	25.3	27.82
	28.64	33.6	100	17.65	23.2	15.34	18.48	20.69	21.67	18.09	17.59	20.1
	20.1	21.5	20.4	18.91	20.9	19	21.61	23	23	21.5	22.5	22.89
	22.89	20.6	20.6	23.23	23.23	22.73	22.5	20	21.32	19.9	21.43	22.96
	21.24	19.69	20.21	20.51	20.41	20.92	20.92	21.03	20.92	20.92	20.92	20.92
	20.92	20.41	20.92	21.03	20.92	20.92	20.92	20.92	19.39	14.58	19.39	20.92
	19.9	18.37	18.37	18.37	18.97	18.97	18.27	18.27	18.37	18.37		
173	4.03	9.72	9.86	8.43	9.33	9.09	10.14	11.92	18.52	13.38	23.62	20.74
	22.54	17.68	17.65	100	17.44	18.33	13.64	14.44	17.11	14.66	14.66	17.03
	17.03	18.72	18.18	18.18	17.65	17.65	17.74	14.97	14.97	15.51	16.58	17.65
	17.65	17.11	17.11	15.05	15.05	16.13	14.89	19.35	17.11	17.74	18.82	18.38
	18.03	18.03	18.03	18.18	17.11	18.72	19.25	19.35	19.25	19.25	19.25	18.72
	17.65	18.18	18.18	18.18	18.18	18.18	18.18	18.18	18.72	15.56	20	18.92
	20	18.38	18.38	18.38	16.76	16.76	16.58	16.58	16.76	17.3		
191	5.42	10.58	7.53	7.94	9.57	9.01	12.5	13.24	12.08	11.66	14.55	16.43
	16.32	15.2	23.2	17.44	100	25.16	21.71	21.3	20.71	12.94	13.53	20.12
	20.12	24.1	24.7	24.1	24.7	24.7	25.61	24.1	24.1	25.3	25.3	24.1
	24.1	19.88	19.88	21.69	21.69	20	23.95	24.69	25.61	23.78	25	24.24
	25.61	25	25	22.7	24.39	21.95	22.56	21.47	21.95	21.95	21.95	21.95
	21.34	21.95	21.95	21.95	21.95	21.95	21.95	21.95	22.56	23.08	24.85	27.27
	25.45	24.24	24.24	24.24	21.34	21.34	21.95	21.95	22.42	23.03		
120	6.47	9.38	10.77	9.46	14.93	8.55	15.03	11.82	17.39	12.44	17.02	17.11
	17.04	13.66	15.34	18.33	25.16	100	20.62	18.52	22.22	20.16	19.35	19.25
	19.25	22.76	22.76	22.36	22.76	22.76	24.59	22.76	22.76	19.92	21.54	23.89
	23.89	20.97	20.97	23.46	23.46	24.8	25	20.68	23.11	22.18	22.59	21.34
	21.52	21.52	21.52	23.75	24.17	23.65	23.33	23.43	23.24	23.33	22.92	22.92
	22.08	22.41	23.01	22.18	21.99	21.99	21.99	22.08	21.67	23.08	24.69	26.78
	23.24	22.36	22.46	22.36	22.08	21.99	23.75	23.75	24.79	23.95		
190	8.28	8.33	6.25	10.71	11.84	10.81	11.45	11	12.12	11.72	18.97	15
	16	19.08	18.48	13.64	21.71	20.62	100	26.6	24.63	22.06	21.08	20.51
	20.51	27.5	25.5	25	26	27.5	26.26	22.5	22.5	21.5	21.5	23.88
	23.88	22.5	22.5	23.12	23.12	23.23	27.86	22.16	19.19	23.86	25.89	22.84
	23.71	23.2	23.2	21.94	20.3	21.83	22.34	22.45	22.34	22.34	21.83	21.83
	22.84	22.84	22.34	22.96	22.84	22.84	22.84	22.84	21.83	19.27	23.35	23.86
	22.84	24.37	24.37	24.37	21.43	21.43	21.21	21.21	19.29	19.29		
144	5.65	5.63	4.69	9.64	12.66	8.96	14.23	9.56	13.49	14.62	17.02	15.66
	14.86	19.27	20.69	14.44	21.3	18.52	26.6	100	60.99	28.09	27.68	26.91
	26.91	35.94	34.16	32.86	32.5	32.03	32.97	34.88	34.88	30.25	29.14	34.52
	34.53	31.05	31.05	34.69	34.69	33.7	31.73	26.15	32.58	35.34	35.71	29.41

	32.81	32.81	33.6	33.59	31.56	31	30.83	31.37	31	31.64	30.86	30.04
	31.25	30.3	31.37	30.98	30.63	30.63	30.63	31.25	30.86	33.07	30.68	31.37
	31	31.64	32.16	31.18	27.65	27.11	30.04	30.04	32.03	32.03		
145	6.09	4.23	4.69	7.23	10.13	8.21	12.36	9.93	12.7	14.57	17.73	14.46
	14.86	18.75	21.67	17.11	20.71	22.22	24.63	60.99	100	28.73	29.04	28.73
	28.73	33.81	34.52	34.64	34.29	32.38	34.41	35.59	35.59	31.56	30.82	34.88
	34.41	30.69	30.69	34.32	34.32	33.33	32.72	25.69	32.45	35.34	34.96	30.04
	31.62	31.23	32.02	31.18	31.44	31	30.71	30.98	31	31.25	30.47	29.55
	30.86	29.81	30.98	30.59	30.63	30.63	30.63	30.86	29.69	31.5	29.81	29.41
	30.26	30.86	30.98	29.92	26.42	26.64	27.47	27.47	31.25	30.86		
197	7.34	8.82	4.69	6.33	8.45	10.17	10.58	14.22	13.11	13.24	17.02	16.46
	17.36	16.84	18.09	14.66	12.94	20.16	22.06	28.09	28.73	100	84.48	26.46
	26.46	31.09	30.34	29.21	29.96	31.09	31.7	24.72	24.72	24.63	27.41	32.21
	32.22	26.59	26.59	33.33	33.33	29.43	29.66	27.73	25.68	30.47	29.69	25.67
	30.56	29.76	30.16	30.74	31.52	32.17	32.68	33.2	32.56	33.07	32.68	32.68
	32.28	32.56	32.41	32.41	32.17	32.17	32.17	32.68	31.1	33.87	29.46	29.07
	29.46	29.25	29.37	29.3	26.85	26.54	26.64	26.64	29.92	31.1		
198	5.65	7.35	6.25	5.06	5.63	11.38	10.91	12.5	12.3	12.38	17.73	14.9
	15.28	16.32	17.59	14.66	13.53	19.35	21.08	27.68	29.04	84.48	100	24.07
	24.07	28.57	27.5	30.55	29.82	29.96	30.77	26.43	26.43	24.82	27.76	31.77
	32.38	26.3	26.3	31.82	31.82	29.48	31.06	27.24	25.19	29.73	29.34	26.04
	30.16	29.37	29.76	30.23	31.01	31.42	32.56	32.81	31.8	32.68	31.5	31.78
	31.5	31.66	31.23	31.23	30.65	30.65	30.65	31.5	31.89	33.87	30.12	29.12
	29.5	28.85	28.57	28.79	27.52	26.62	26.72	26.72	29.53	31.1		
124	6.19	10	7.69	9.76	10.84	9.21	14.29	12.99	17.83	15.28	20.9	15.85
	19.01	21.74	20.1	17.03	20.12	19.25	20.51	26.91	28.73	26.46	24.07	100
	100	39.66	42.14	40.89	41.92	41.78	42.07	42.28	42.28	44.56	48.9	37.97
	41.11	40.85	40.85	40.71	40.71	40.93	39.84	31.47	36.25	36	36.36	37.83
	36.36	35.18	35.97	41.43	41.27	38.08	41.67	42.23	38.08	42.06	42.06	42.06
	41.67	41.5	42.23	42.23	38.08	38.08	38.08	42.06	42.86	43.65	40.78	39.86
	39.58	40.32	39.68	39.53	37.15	34.97	35.44	35.44	39.37	40.16		
214	6.19	10	7.69	9.76	10.84	9.21	14.29	12.99	17.83	15.28	20.9	15.85
	19.01	21.74	20.1	17.03	20.12	19.25	20.51	26.91	28.73	26.46	24.07	100
	100	39.66	42.14	40.89	41.92	41.78	42.07	42.28	42.28	44.56	48.9	37.97
	41.11	40.85	40.85	40.71	40.71	40.93	39.84	31.47	36.25	36	36.36	37.83
	36.36	35.18	35.97	41.43	41.27	38.08	41.67	42.23	38.08	42.06	42.06	42.06
	41.67	41.5	42.23	42.23	38.08	38.08	38.08	42.06	42.86	43.65	40.78	39.86
	39.58	40.32	39.68	39.53	37.15	34.97	35.44	35.44	39.37	40.16		
183	8.6	7.25	6.25	10.13	10	9.03	13.39	14.54	16.94	16.83	18.57	19.77
	22.22	23.16	21.5	18.72	24.1	22.76	27.5	35.94	33.81	31.09	28.57	39.66
	39.66	100	70.36	64.55	66.22	67.44	64.31	55.23	55.23	49.66	57.39	60.13
	62.99	46.15	46.15	46.79	46.79	47.54	50	38.04	45.53	42.49	44.69	42.54
	48.03	46.46	47.24	48.83	50	43.37	47.66	47.06	43.73	46.88	46.88	46.88
	46.88	47.08	47.06	47.84	44.44	44.44	44.44	47.66	48.83	54.33	48.25	44.44
	42.29	46.48	46.67	46.48	46.09	43.11	44.37	44.37	49.61	48.44		

184	8.38	7.25	6.25	10.13	11.25	6.04	11.2	13.42	17.32	16.83	18.44	16.98
	18.06	20.42	20.4	18.18	24.7	22.76	25.5	34.16	34.52	30.34	27.5	42.14
	42.14	70.36	100	66.45	68.4	67.11	66.56	57.65	57.65	49.32	57.75	56.54
	59.79	45.7	45.7	49.47	49.47	48.42	51.53	40	44.75	43.53	44.96	44.24
	46.85	45.67	46.46	49.61	50	43.66	49.22	48.63	44.01	48.44	48.83	48.83
	48.83	49.42	49.02	49.8	45.07	45.07	45.07	49.61	51.56	52.76	48.25	46.45
	43.31	45.7	45.88	45.7	47.27	44.79	42.91	42.91	50.78	49.61		
175	6.28	8.7	4.69	11.39	10	7.38	15.68	14.72	18.11	17.16	15.6	18.85
	22.22	21.47	18.91	18.18	24.1	22.36	25	32.86	34.64	29.21	30.55	40.89
	40.89	64.55	66.45	100	72.64	73.18	71.52	53.85	53.85	49.15	58.36	56.11
	60.43	49.31	49.31	46.45	46.45	47.54	51.53	40	47.47	42.6	44.4	46.27
	44.49	43.7	44.09	50.78	50.39	45.94	50	49.41	46.29	49.22	49.22	49.22
	49.61	49.42	49.41	50.2	47	47	47	50	50.78	53.54	47.47	46.26
	45.23	46.88	46.67	46.48	48.05	44.95	44.79	44.79	49.22	50		
119	7.33	7.25	6.25	10.13	12.5	8.05	15.68	12.12	15.75	18.14	18.44	20
	21.53	23.04	20.9	17.65	24.7	22.76	26	32.5	34.29	29.96	29.82	41.92
	41.92	66.22	68.4	72.64	100	73.18	74.17	53.18	53.18	49.49	57.65	59.41
	62.59	45.17	45.17	45.04	45.04	45.77	48.47	36.08	44.75	43.68	44.77	43.28
	44.88	43.7	44.09	49.61	48.83	45.58	48.83	49.02	45.94	48.83	47.66	47.66
	47.27	47.86	47.84	48.24	45.23	45.23	45.23	48.05	50.39	54.33	47.08	45.2
	44.52	46.88	47.06	46.88	48.05	44.25	42.36	42.36	47.66	47.27		
105	7.98	8.7	6.25	11.39	10	6.8	13.5	12.72	16	18.05	18.57	20.31
	20.83	23.68	19	17.65	24.7	22.76	27.5	32.03	32.38	31.09	29.96	41.78
	41.78	67.44	67.11	73.18	73.18	100	75.33	55.48	55.48	48.3	57.09	56.95
	60.57	49.13	49.13	48.76	48.76	48.42	51.15	38.82	47.86	44.2	46.01	45.72
	48.03	47.64	48.03	53.12	51.56	46.1	50.78	50.98	46.45	50.78	50	50
	49.61	50.19	50.2	50.59	46.1	46.1	46.1	50.39	52.34	59.84	51.75	49.65
	45.39	48.83	49.02	48.83	51.17	47.9	45.3	45.3	50	50		
118	7.94	8.7	6.25	8.86	11.25	9.4	14.96	12.66	15.75	18.23	17.27	20.16
	20.98	22.75	21.61	17.74	25.61	24.59	26.26	32.97	34.41	31.7	30.77	42.07
	42.07	64.31	66.56	71.52	74.17	75.33	100	56.57	56.57	53.26	57.71	58.8
	62.32	49.31	49.31	50.36	50.36	49.12	54.23	39.13	47.84	43.27	45.09	44.36
	49.21	48.41	48.81	52.36	51.97	49.11	52.76	52.96	49.47	52.76	51.97	51.97
	51.97	51.76	52.17	52.96	49.47	49.47	49.47	52.76	51.57	53.54	51.37	48.75
	47.33	48.43	48.22	48.03	50	46.32	44.41	44.41	49.61	49.61		
97	11.76	10.14	9.38	11.39	12.35	8.22	11.98	11.89	13.71	16.27	15	17.74
	17.36	22.63	23	14.97	24.1	22.76	22.5	34.88	35.59	24.72	26.43	42.28
	42.28	55.23	57.65	53.85	53.18	55.48	56.57	100	100	53.04	61.97	54.97
	57.65	51.74	51.74	50	50	51.4	50.38	38.43	43.19	41.97	43.07	42.75
	47.64	46.46	47.24	49.22	48.83	43.42	47.66	47.45	43.42	47.27	48.05	48.05
	48.05	47.86	48.63	49.02	44.84	44.84	44.84	48.83	48.44	52.76	46.69	48.4
	45.2	47.27	46.67	46.48	45.31	42.81	43.01	43.01	48.44	49.22		
213	11.76	10.14	9.38	11.39	12.35	8.22	11.98	11.89	13.71	16.27	15	17.74
	17.36	22.63	23	14.97	24.1	22.76	22.5	34.88	35.59	24.72	26.43	42.28
	42.28	55.23	57.65	53.85	53.18	55.48	56.57	100	100	53.04	61.97	54.97
	57.65	51.74	51.74	50	50	51.4	50.38	38.43	43.19	41.97	43.07	42.75

	47.64	46.46	47.24	49.22	48.83	43.42	47.66	47.45	43.42	47.27	48.05	48.05
	48.05	47.86	48.63	49.02	44.84	44.84	44.84	48.83	48.44	52.76	46.69	48.4
	45.2	47.27	46.67	46.48	45.31	42.81	43.01	43.01	48.44	49.22		
95	7.57	13.04	7.81	11.39	12.82	9.29	16.81	14.54	18.55	17.31	18.57	17.65
	17.36	23.16	21.5	15.51	25.3	19.92	21.5	30.25	31.56	24.63	24.82	44.56
	44.56	49.66	49.32	49.15	49.49	48.3	53.26	53.04	53.04	100	62.32	50.51
	51.77	48.58	48.58	47.46	47.46	48.93	47.15	35.16	42.64	41.04	42.16	39.85
	44.49	44.09	44.09	48.25	49.03	46.18	49.42	49.02	45.82	48.83	49.61	49.42
	49.22	48.84	50.2	50.2	46.91	46.91	46.91	50	46.48	49.61	44.57	42.03
	42.55	45.7	45.49	45.14	43.58	40.36	42.86	42.86	44.92	43.36		
194	7.02	11.59	12.5	11.39	12.5	11.81	14.16	14.98	19.35	14.42	16.43	19.53
	19.44	22.11	22.5	16.58	25.3	21.54	21.5	29.14	30.82	27.41	27.76	48.9
	48.9	57.39	57.75	58.36	57.65	57.09	57.71	61.97	61.97	62.32	100	61.97
	63.67	54.01	54.01	50	50	51.47	52.96	38.4	47.17	46.59	46.59	47.08
	47.24	47.24	47.24	54.17	53.41	50.38	52.65	52.55	50.75	52.34	52.34	53.26
	53.12	53.82	53.33	53.73	51.88	51.88	51.88	53.52	48.83	55.91	50.57	51.69
	52.26	47.27	47.45	48.86	46.21	44.78	46.82	46.82	50	48.44		
98	9.42	8.7	12.5	11.39	13.75	9.4	14.29	13.42	17.97	17.39	17.14	19.08
	20.69	21.47	22.89	17.65	24.1	23.89	23.88	34.52	34.88	32.21	31.77	37.97
	37.97	60.13	56.54	56.11	59.41	56.95	58.8	54.97	54.97	50.51	61.97	100
	99.65	49.49	49.49	48.07	48.07	49.13	51.71	37.89	46.12	40.86	42.29	40.74
	48.63	48.24	48.63	50.19	48.25	45.1	49.03	49.22	45.45	49.03	48.64	48.64
	48.64	49.22	49.22	49.61	45.8	45.8	45.8	49.42	47.86	51.56	44.57	45.77
	45.1	42.8	42.97	42.8	45.14	40.69	41.92	41.92	46.69	45.53		
193	9.94	8.7	12.5	11.39	13.89	9.52	12.39	13.16	17.6	16.74	17.14	19.69
	20.69	21.47	22.89	17.65	24.1	23.89	23.88	34.53	34.41	32.22	32.38	41.11
	41.11	62.99	59.79	60.43	62.59	60.57	62.32	57.65	57.65	51.77	63.67	99.65
	100	51.47	51.47	50.75	50.75	51.11	53.14	37.12	47.74	42.75	44.27	41.91
	48.63	48.24	48.63	51.7	49.81	47.35	48.68	49.22	47.73	49.03	48.64	49.62
	48.64	50.19	49.22	49.61	48.11	48.11	48.11	49.42	47.86	51.56	46.24	47.55
	46.59	42.8	42.97	44.53	45.28	43.61	45.28	45.28	46.69	45.53		
99	9.09	8.96	12.7	12.82	14.86	7.19	15.49	12.55	19.84	15.79	17.02	20.08
	20.83	23.04	20.6	17.11	19.88	20.97	22.5	31.05	30.69	26.59	26.3	40.85
	40.85	46.15	45.7	49.31	45.17	49.13	49.31	51.74	51.74	48.58	54.01	49.49
	51.47	100	100	63.45	63.45	65.41	50.94	43.75	48.25	43.26	45.04	48.15
	50.2	49.8	49.8	55.77	50.77	47.4	51.92	51.35	47.75	51.15	51.92	51.92
	52.31	52.49	52.51	53.28	49.13	49.13	49.13	53.08	51.15	49.22	50.39	45.77
	46.88	53.12	52.94	52.73	49.81	47.22	45.99	45.99	49.81	50.58		
109	9.09	8.96	12.7	12.82	14.86	7.19	15.49	12.55	19.84	15.79	17.02	20.08
	20.83	23.04	20.6	17.11	19.88	20.97	22.5	31.05	30.69	26.59	26.3	40.85
	40.85	46.15	45.7	49.31	45.17	49.13	49.31	51.74	51.74	48.58	54.01	49.49
	51.47	100	100	63.45	63.45	65.41	50.94	43.75	48.25	43.26	45.04	48.15
	50.2	49.8	49.8	55.77	50.77	47.4	51.92	51.35	47.75	51.15	51.92	51.92
	52.31	52.49	52.51	53.28	49.13	49.13	49.13	53.08	51.15	49.22	50.39	45.77
	46.88	53.12	52.94	52.73	49.81	47.22	45.99	45.99	49.81	50.58		

83	8.89	10.45	7.94	11.54	13.51	8.03	14.16	12.28	19.35	15.69	15	18.97
	19.44	20.53	23.23	15.05	21.69	23.46	23.12	34.69	34.32	33.33	31.82	40.71
	40.71	46.79	49.47	46.45	45.04	48.76	50.36	50	50	47.46	50	48.07
	50.75	63.45	63.45	100	100	73.52	54.05	41.2	45.02	44.36	45.82	43.94
	47.6	46.4	46.8	53.54	50.39	49.11	51.57	50.99	48.75	51.18	51.97	51.97
	51.97	51.37	52.57	52.57	49.47	49.47	49.47	52.36	51.18	55.47	46.83	46.76
	47.86	50	49.8	49.6	47.04	45.36	44.44	44.44	48.61	50.2		
96	8.89	10.45	7.94	11.54	13.51	8.03	14.16	12.28	19.35	15.69	15	18.97
	19.44	20.53	23.23	15.05	21.69	23.46	23.12	34.69	34.32	33.33	31.82	40.71
	40.71	46.79	49.47	46.45	45.04	48.76	50.36	50	50	47.46	50	48.07
	50.75	63.45	63.45	100	100	73.52	54.05	41.2	45.02	44.36	45.82	43.94
	47.6	46.4	46.8	53.54	50.39	49.11	51.57	50.99	48.75	51.18	51.97	51.97
	51.97	51.37	52.57	52.57	49.47	49.47	49.47	52.36	51.18	55.47	46.83	46.76
	47.86	50	49.8	49.6	47.04	45.36	44.44	44.44	48.61	50.2		
176	8.24	10.45	9.52	11.54	13.51	7.41	11.95	13.22	18.7	17.22	17.86	17.39
	19.44	20	22.73	16.13	20	24.8	23.23	33.7	33.33	29.43	29.48	40.93
	40.93	47.54	48.42	47.54	45.77	48.42	49.12	51.4	51.4	48.93	51.47	49.13
	51.11	65.41	65.41	73.52	73.52	100	52.47	40.94	46.27	44.93	46.38	43.66
	47.64	46.85	46.85	52.71	52.33	48.06	50.39	50.19	47.7	50	50.78	50.78
	50.39	50.19	51.36	50.97	48.06	48.06	48.06	50.78	53.1	57.03	48.05	48.93
	48.94	51.18	51.78	51.57	48.25	46.1	45.55	45.55	49.41	49.41		
200	8.72	8.96	9.68	13.92	15.49	10.92	14.29	14.04	15.45	15.38	16.31	19.25
	22.07	21.47	22.5	14.89	23.95	25	27.86	31.73	32.72	29.66	31.06	39.84
	39.84	50	51.53	51.53	48.47	51.15	54.23	50.38	50.38	47.15	52.96	51.71
	53.14	50.94	50.94	54.05	54.05	52.47	100	41.76	49.43	49.22	51.94	46.79
	48.03	47.24	47.24	52.24	53.9	49.81	50.19	50.38	49.81	50.19	50.96	51.5
	49.04	51.13	50.77	50.38	49.81	49.81	49.81	50.19	50.57	51.97	52.83	55.04
	50.58	50.78	50.2	51.89	46.24	45.38	49.42	49.42	52.14	54.86		
196	12.14	11.59	7.69	12.5	13.89	11.48	15.38	10.14	16.13	17.65	17.04	17.09
	22.7	18.82	20	19.35	24.69	20.68	22.16	26.15	25.69	27.73	27.24	31.47
	31.47	38.04	40	40	36.08	38.82	39.13	38.43	38.43	35.16	38.4	37.89
	37.12	43.75	43.75	41.2	41.2	40.94	41.76	100	44.11	44.66	46.25	51.69
	49.61	48.43	49.21	48.09	46.56	48.24	46.42	47.83	48.24	48.03	48.82	47.71
	49.21	48.29	49.01	49.41	49.41	49.41	49.41	49.21	49.21	50.79	46.79	54.65
	55.25	52.34	52.94	51.52	50.38	52.12	50.39	50.39	53.12	55.08		
199	10.65	5.8	4.69	11.25	11.11	6.67	15.66	12	16.94	13.3	16.06	20.51
	21.68	21.93	21.32	17.11	25.61	23.11	19.19	32.58	32.45	25.68	25.19	36.25
	36.25	45.53	44.75	47.47	44.75	47.86	47.84	43.19	43.19	42.64	47.17	46.12
	47.74	48.25	48.25	45.02	45.02	46.27	49.43	44.11	100	49.22	50.39	50.57
	47.45	47.45	47.84	55.85	53.96	50.58	51.32	51.56	50.97	51.36	50.97	51.91
	50.58	51.91	51.17	51.95	51.36	51.36	51.36	51.75	52.92	55.12	50.94	56.59
	53.31	52.14	51.56	53.21	57.36	56.76	52.71	52.71	54.47	52.14		
125	8.95	10.29	7.94	10	10.67	10.34	15.74	13.08	14.71	12.87	16.91	17.6
	19.01	18.82	19.9	17.74	23.78	22.18	23.86	35.34	35.34	30.47	29.73	36
	36	42.49	43.53	42.6	43.68	44.2	43.27	41.97	41.97	41.04	46.59	40.86
	42.75	43.26	43.26	44.36	44.36	44.93	49.22	44.66	49.22	100	92.15	47.58

	42.69	41.9	42.29	56.03	58.53	52.05	56.59	56.42	52.4	56.2	56.59	56.59
	56.98	57.14	57.2	57.2	53.42	53.42	53.42	57.36	57.36	60.16	50.19	55.76
	55.67	52.94	52.36	52.16	55.47	51.6	51.96	51.96	57.03	57.03		
62	10	10.29	7.94	10	10.67	9.66	15.28	15.19	16.18	12.38	17.65	18.4
	20.42	20.43	21.43	18.82	25	22.59	25.89	35.71	34.96	29.69	29.34	36.36
	36.36	44.69	44.96	44.4	44.77	46.01	45.09	43.07	43.07	42.16	46.59	42.29
	44.27	45.04	45.04	45.82	45.82	46.38	51.94	46.25	50.39	92.15	100	48.33
	46.25	45.45	45.85	56.81	58.53	51.03	56.2	56.03	51.37	55.81	56.2	56.2
	56.59	57.14	56.81	57.2	52.4	52.4	52.4	56.98	58.53	58.59	51.75	56.12
	56.74	54.51	53.94	53.73	57.42	53.02	52.31	52.31	56.64	57.42		
195	7.6	8.7	6.25	11.11	12.33	11.11	12.92	11.4	16.67	15.09	20	19.43
	20.42	21.62	22.96	18.38	24.24	21.34	22.84	29.41	30.04	25.67	26.04	37.83
	37.83	42.54	44.24	46.27	43.28	45.72	44.36	42.75	42.75	39.85	47.08	40.74
	41.91	48.15	48.15	43.94	43.94	43.66	46.79	51.69	50.57	47.58	48.33	100
	55.64	54.47	54.86	55.47	54.14	51.29	54.1	53.7	51.66	53.49	53.1	53.21
	53.1	53.76	53.7	54.09	52.03	52.03	52.03	53.88	57.75	55.12	56.13	58.61
	57.88	58.3	59.69	59.18	59.85	56.57	57.56	57.56	59.62	61.92		
142	8.88	8.7	10.94	11.25	11.11	13.22	13.78	13.78	16.8	14.36	16.42	21.98
	21.99	19.02	21.24	18.03	25.61	21.52	23.71	32.81	31.62	30.56	30.16	36.36
	36.36	48.03	46.85	44.49	44.88	48.03	49.21	47.64	47.64	44.49	47.24	48.63
	48.63	50.2	50.2	47.6	47.6	47.64	48.03	49.61	47.45	42.69	46.25	55.64
	100	97.67	98.44	57.65	55.69	55.69	56.08	55.51	55.29	55.69	55.69	55.69
	54.9	55.29	56.3	56.3	55.69	55.69	55.69	56.08	59.61	58.73	54.86	60.16
	59.92	64.45	63.92	64.06	56.42	56.03	58.2	58.2	63.04	63.04		
141	9.47	7.25	12.5	11.25	11.11	13.22	13.27	13.33	16	14.36	16.42	21.98
	21.28	17.93	19.69	18.03	25	21.52	23.2	32.81	31.23	29.76	29.37	35.18
	35.18	46.46	45.67	43.7	43.7	47.64	48.41	46.46	46.46	44.09	47.24	48.24
	48.24	49.8	49.8	46.4	46.4	46.85	47.24	48.43	47.45	41.9	45.45	54.47
	97.67	100	98.44	57.65	54.9	55.29	55.69	55.12	54.9	55.29	55.29	55.29
	54.9	55.29	56.3	56.3	55.69	55.69	55.69	56.08	58.04	57.94	54.86	59.77
	59.53	64.06	63.14	63.28	56.42	56.03	57.81	57.81	63.42	63.04		
143	8.88	7.25	12.5	10	11.11	13.22	13.27	13.33	16	14.36	16.42	21.98
	21.28	18.48	20.21	18.03	25	21.52	23.2	33.6	32.02	30.16	29.76	35.97
	35.97	47.24	46.46	44.09	44.09	48.03	48.81	47.24	47.24	44.09	47.24	48.63
	48.63	49.8	49.8	46.8	46.8	46.85	47.24	49.21	47.84	42.29	45.85	54.86
	98.44	98.44	100	58.43	55.69	56.08	56.47	55.91	55.69	56.08	56.08	56.08
	55.69	56.08	57.09	57.09	56.47	56.47	56.47	56.86	58.82	57.94	54.86	60.16
	59.92	64.45	63.92	64.06	56.81	56.42	58.2	58.2	63.42	63.42		
206	8.93	7.46	8.06	8.97	10	6.72	16.75	12.44	16.26	13.53	17.52	21.89
	20.57	19.79	20.51	18.18	22.7	23.75	21.94	33.59	31.18	30.74	30.23	41.43
	41.43	48.83	49.61	50.78	49.61	53.12	52.36	49.22	49.22	48.25	54.17	50.19
	51.7	55.77	55.77	53.54	53.54	52.71	52.24	48.09	55.85	56.03	56.81	55.47
	57.65	57.65	58.43	100	80.67	78.93	78.81	80	79.69	80.08	79.31	79.32
	78.54	78.95	79.23	80.38	79.69	79.69	79.69	80.08	75.1	72.44	61.51	60.85
	60.62	61.72	61.96	63.26	64.04	63.6	64.73	64.73	66.93	66.54		

205	8.28	8.96	8.06	8.86	9.86	9.17	16.16	11.95	15.32	14.01	21.9	21.37
	21.13	20.32	20.41	17.11	24.39	24.17	20.3	31.56	31.44	31.52	31.01	41.27
	41.27	50	50	50.39	48.83	51.56	51.97	48.83	48.83	49.03	53.41	48.25
	49.81	50.77	50.77	50.39	50.39	52.33	53.9	46.56	53.96	58.53	58.53	54.14
	55.69	54.9	55.69	80.67	100	84.73	83.7	85.82	85.5	85.88	82.44	82.4
	81.68	82.77	83.14	83.14	82.82	82.82	82.82	83.21	77.86	70.31	59.4	63.71
	62.69	64.98	65.23	66.42	61.05	60.54	63.57	63.57	68.22	67.83		
127	5.64	7.46	8.06	8.86	9.21	8	15.32	11.76	14.71	14.56	18.98	25.1
	23.24	20.32	20.92	18.72	21.95	23.65	21.83	31	31	32.17	31.42	38.08
	38.08	43.37	43.66	45.94	45.58	46.1	49.11	43.42	43.42	46.18	50.38	45.1
	47.35	47.4	47.4	49.11	49.11	48.06	49.81	48.24	50.58	52.05	51.03	51.29
	55.69	55.29	56.08	78.93	84.73	100	98.09	98.85	99	98.85	94.27	94.66
	90.84	91.63	93.1	91.57	92.69	92.69	92.69	91.98	75.57	67.97	60.62	56.99
	58.62	64.59	64.84	64.59	61.39	59.17	60.42	60.42	68.22	67.83		
208	5.92	7.46	8.06	8.86	9.86	8.33	16.16	12.39	16.13	13.81	18.25	23.08
	22.54	20.32	20.92	19.25	22.56	23.33	22.34	30.83	30.71	32.68	32.56	41.67
	41.67	47.66	49.22	50	48.83	50.78	52.76	47.66	47.66	49.42	52.65	49.03
	48.68	51.92	51.92	51.57	51.57	50.39	50.19	46.42	51.32	56.59	56.2	54.1
	56.08	55.69	56.47	78.81	83.7	98.09	100	99.23	98.85	99.24	95.42	94.07
	92.37	92.22	93.87	93.49	93.51	93.51	93.51	93.89	76.72	69.53	59.77	61.78
	61.54	65.37	65.23	64.53	62.08	61.69	66.28	66.28	68.99	68.22		
58	5.95	7.46	8.06	8.86	9.86	8.4	16.24	12.44	16.26	14.65	18.25	23.18
	22.7	20.43	21.03	19.35	21.47	23.43	22.45	31.37	30.98	33.2	32.81	42.23
	42.23	47.06	48.63	49.41	49.02	50.98	52.96	47.45	47.45	49.02	52.55	49.22
	49.22	51.35	51.35	50.99	50.99	50.19	50.38	47.83	51.56	56.42	56.03	53.7
	55.51	55.12	55.91	80	85.82	98.85	99.23	100	99.62	100	94.64	94.25
	91.57	92.34	93.08	92.69	92.72	92.72	92.72	93.1	76.63	68.5	59.92	61.48
	61	64.84	64.71	64.84	62.02	61.63	66.54	66.54	68.09	67.7		
129	5.64	7.46	8.06	8.86	9.21	8.33	15.32	11.76	13.64	14.56	18.25	24.32
	22.54	20.32	20.92	19.25	21.95	23.24	22.34	31	31	32.56	31.8	38.08
	38.08	43.73	44.01	46.29	45.94	46.45	49.47	43.42	43.42	45.82	50.75	45.45
	47.73	47.75	47.75	48.75	48.75	47.7	49.81	48.24	50.97	52.4	51.37	51.66
	55.29	54.9	55.69	79.69	85.5	99	98.85	99.62	100	99.62	94.27	93.89
	91.22	92.4	93.1	92.34	93.02	93.02	93.02	92.75	76.34	67.97	60.23	57.34
	58.28	64.59	64.84	64.59	61.78	57.76	58.72	58.72	67.83	67.44		
133	5.92	7.46	8.06	8.86	9.86	8.33	16.16	12.39	16.13	14.57	18.25	23.08
	22.54	20.32	20.92	19.25	21.95	23.33	22.34	31.64	31.25	33.07	32.68	42.06
	42.06	46.88	48.44	49.22	48.83	50.78	52.76	47.27	47.27	48.83	52.34	49.03
	49.03	51.15	51.15	51.18	51.18	50	50.19	48.03	51.36	56.2	55.81	53.49
	55.69	55.29	56.08	80.08	85.88	98.85	99.24	100	99.62	100	94.66	94.27
	91.6	92.37	93.1	92.72	92.75	92.75	92.75	93.13	76.72	68.75	60.08	61.63
	61.15	64.98	64.84	64.98	62.16	61.78	66.28	66.28	68.22	67.83		
57	6.51	7.46	8.06	8.86	9.86	8.33	17.17	12.39	15.32	13.57	18.98	22.65
	21.83	21.39	20.92	19.25	21.95	22.92	21.83	30.86	30.47	32.68	31.5	42.06
	42.06	46.88	48.83	49.22	47.66	50	51.97	48.05	48.05	49.61	52.34	48.64
	48.64	51.92	51.92	51.97	51.97	50.78	50.96	48.82	50.97	56.59	56.2	53.1

	55.69	55.29	56.08	79.31	82.44	94.27	95.42	94.64	94.27	94.66	100	99.62
	96.18	96.95	98.47	97.32	97.33	97.33	97.33	97.71	75.19	70.31	60.47	61.63
	61.92	65.37	65.23	65.37	61	60.62	65.5	65.5	69.38	69.38		
203	6.51	7.46	8.06	8.86	9.86	8.33	17.17	12.39	15.32	13.04	18.98	23.08
	22.54	21.39	20.92	18.72	21.95	22.92	21.83	30.04	29.55	32.68	31.78	42.06
	42.06	46.88	48.83	49.22	47.66	50	51.97	48.05	48.05	49.42	53.26	48.64
	49.62	51.92	51.92	51.97	51.97	50.78	51.5	47.71	51.91	56.59	56.2	53.21
	55.69	55.29	56.08	79.32	82.4	94.66	94.07	94.25	93.89	94.27	99.62	100
	96.18	96.67	98.08	96.93	96.95	96.95	96.95	97.33	74.81	70.31	61.22	61.39
	61.92	65.37	65.23	66.03	60.9	60.15	65.12	65.12	69.38	69.38		
107	8.28	7.46	8.06	8.86	9.86	8.33	17.68	12.83	15.32	13.57	18.98	23.5
	21.83	21.93	20.92	17.65	21.34	22.08	22.84	31.25	30.86	32.28	31.5	41.67
	41.67	46.88	48.83	49.61	47.27	49.61	51.97	48.05	48.05	49.22	53.12	48.64
	48.64	52.31	52.31	51.97	51.97	50.39	49.04	49.21	50.58	56.98	56.59	53.1
	54.9	54.9	55.69	78.54	81.68	90.84	92.37	91.57	91.22	91.6	96.18	96.18
	100	96.95	97.7	98.08	98.09	98.09	98.09	98.47	73.66	70.31	60.08	60.85
	60.38	64.2	64.06	64.2	60.23	59.85	64.34	64.34	67.83	68.22		
204	8.28	7.46	8.06	8.86	9.86	9.09	17.59	13.27	15.32	12.98	18.98	23.4
	21.83	21.39	20.41	18.18	21.95	22.41	22.84	30.3	29.81	32.56	31.66	41.5
	41.5	47.08	49.42	49.42	47.86	50.19	51.76	47.86	47.86	48.84	53.82	49.22
	50.19	52.49	52.49	51.37	51.37	50.19	51.13	48.29	51.91	57.14	57.14	53.76
	55.29	55.29	56.08	78.95	82.77	91.63	92.22	92.34	92.4	92.37	96.95	96.67
	96.95	100	98.85	98.08	98.48	98.48	98.48	98.47	74.05	68.75	61.36	61.54
	61.3	64.59	64.84	65.27	60.53	60.31	65.25	65.25	68.22	68.22		
106	8.28	7.46	8.06	8.86	9.86	8.4	17.77	12.83	15.32	13.64	19.71	23.61
	21.83	21.93	20.92	18.18	21.95	23.01	22.34	31.37	30.98	32.41	31.23	42.23
	42.23	47.06	49.02	49.41	47.84	50.2	52.17	48.63	48.63	50.2	53.33	49.22
	49.22	52.51	52.51	52.57	52.57	51.36	50.77	49.01	51.17	57.2	56.81	53.7
	56.3	56.3	57.09	79.23	83.14	93.1	93.87	93.08	93.1	93.1	98.47	98.08
	97.7	98.85	100	98.85	99.23	99.23	99.23	99.23	74.71	70.08	61.09	61.87
	62.16	65.23	65.23	65.23	60.85	60.85	66.54	66.54	69.26	69.26		
59	8.93	7.46	8.06	8.86	9.86	8.4	17.77	13.33	15.32	13.57	19.12	23.18
	21.83	22.04	21.03	18.18	21.95	22.18	22.96	30.98	30.59	32.41	31.23	42.23
	42.23	47.84	49.8	50.2	48.24	50.59	52.96	49.02	49.02	50.2	53.73	49.61
	49.61	53.28	53.28	52.57	52.57	50.97	50.38	49.41	51.95	57.2	57.2	54.09
	56.3	56.3	57.09	80.38	83.14	91.57	93.49	92.69	92.34	92.72	97.32	96.93
	98.08	98.08	98.85	100	99.23	99.23	99.23	99.62	75.48	70.31	60.7	62.26
	61.39	65.23	65.1	65.23	61.24	60.85	65.37	65.37	68.87	69.26		
126	7.69	7.46	8.06	8.86	9.21	8.67	16.67	12.18	13.97	13.59	18.98	25.1
	21.83	21.93	20.92	18.18	21.95	21.99	22.84	30.63	30.63	32.17	30.65	38.08
	38.08	44.44	45.07	47	45.23	46.1	49.47	44.84	44.84	46.91	51.88	45.8
	48.11	49.13	49.13	49.47	49.47	48.06	49.81	49.41	51.36	53.42	52.4	52.03
	55.69	55.69	56.47	79.69	82.82	92.69	93.51	92.72	93.02	92.75	97.33	96.95
	98.09	98.48	99.23	99.23	100	100	100	99.62	74.81	69.53	60.62	57.69
	58.62	64.98	65.23	64.98	61	58.48	60.42	60.42	68.6	68.99		

128	7.69	7.46	8.06	8.86	9.21	8.67	16.67	12.18	13.97	13.59	18.98	25.1
	21.83	21.93	20.92	18.18	21.95	21.99	22.84	30.63	30.63	32.17	30.65	38.08
	38.08	44.44	45.07	47	45.23	46.1	49.47	44.84	44.84	46.91	51.88	45.8
	48.11	49.13	49.13	49.47	49.47	48.06	49.81	49.41	51.36	53.42	52.4	52.03
	55.69	55.69	56.47	79.69	82.82	92.69	93.51	92.72	93.02	92.75	97.33	96.95
	98.09	98.48	99.23	99.23	100	100	100	99.62	74.81	69.53	60.62	57.69
	58.62	64.98	65.23	64.98	61	58.48	60.42	60.42	68.6	68.99		
131	7.69	7.46	8.06	8.86	9.21	8.67	16.67	12.18	13.97	13.59	18.98	25.1
	21.83	21.93	20.92	18.18	21.95	21.99	22.84	30.63	30.63	32.17	30.65	38.08
	38.08	44.44	45.07	47	45.23	46.1	49.47	44.84	44.84	46.91	51.88	45.8
	48.11	49.13	49.13	49.47	49.47	48.06	49.81	49.41	51.36	53.42	52.4	52.03
	55.69	55.69	56.47	79.69	82.82	92.69	93.51	92.72	93.02	92.75	97.33	96.95
	98.09	98.48	99.23	99.23	100	100	100	99.62	74.81	69.53	60.62	57.69
	58.62	64.98	65.23	64.98	61	58.48	60.42	60.42	68.6	68.99		
132	8.28	7.46	8.06	8.86	9.86	8.33	17.68	12.83	15.32	13.57	18.98	23.5
	21.83	21.93	20.92	18.18	21.95	22.08	22.84	31.25	30.86	32.68	31.5	42.06
	42.06	47.66	49.61	50	48.05	50.39	52.76	48.83	48.83	50	53.52	49.42
	49.42	53.08	53.08	52.36	52.36	50.78	50.19	49.21	51.75	57.36	56.98	53.88
	56.08	56.08	56.86	80.08	83.21	91.98	93.89	93.1	92.75	93.13	97.71	97.33
	98.47	98.47	99.23	99.62	99.62	99.62	99.62	100	75.19	70.31	60.47	62.02
	61.54	65.37	65.23	65.37	61.39	61	65.89	65.89	68.99	69.38		
108	6.51	8.96	8.06	11.39	12.68	9.17	13.64	12.39	16.94	14.07	16.06	19.23
	19.01	19.25	19.39	18.72	22.56	21.67	21.83	30.86	29.69	31.1	31.89	42.86
	42.86	48.83	51.56	50.78	50.39	52.34	51.57	48.44	48.44	46.48	48.83	47.86
	47.86	51.15	51.15	51.18	51.18	53.1	50.57	49.21	52.92	57.36	58.53	57.75
	59.61	58.04	58.82	75.1	77.86	75.57	76.72	76.63	76.34	76.72	75.19	74.81
	73.66	74.05	74.71	75.48	74.81	74.81	74.81	75.19	100	81.25	64.34	65.12
	65.38	68.87	69.53	69.65	68.73	68.34	69.38	69.38	70.16	69.77		
207	3.23	7.41	6	8.47	8.62	8.86	14.15	12.04	13.51	13.46	12.9	16.13
	15.79	14.29	14.58	15.56	23.08	23.08	19.27	33.07	31.5	33.87	33.87	43.65
	43.65	54.33	52.76	53.54	54.33	59.84	53.54	52.76	52.76	49.61	55.91	51.56
	51.56	49.22	49.22	55.47	55.47	57.03	51.97	50.79	55.12	60.16	58.59	55.12
	58.73	57.94	57.94	72.44	70.31	67.97	69.53	68.5	67.97	68.75	70.31	70.31
	70.31	68.75	70.08	70.31	69.53	69.53	69.53	70.31	81.25	100	61.42	65.35
	63.78	66.93	67.46	67.72	61.11	60.32	61.72	61.72	66.93	64.57		
202	8.19	10.14	6.25	8.64	9.59	8.13	13.57	14.04	16.67	14.22	17.78	21.28
	19.72	25.41	19.39	20	24.85	24.69	23.35	30.68	29.81	29.46	30.12	40.78
	40.78	48.25	48.25	47.47	47.08	51.75	51.37	46.69	46.69	44.57	50.57	44.57
	46.24	50.39	50.39	46.83	46.83	48.05	52.83	46.79	50.94	50.19	51.75	56.13
	54.86	54.86	54.86	61.51	59.4	60.62	59.77	59.92	60.23	60.08	60.47	61.22
	60.08	61.36	61.09	60.7	60.62	60.62	60.62	60.47	64.34	61.42	100	59.77
	60.15	64.48	65.5	66.29	63.3	63.36	62.55	62.55	63.46	63.46		
110	11.35	10.14	9.38	11.11	14.1	10.64	13.51	12.72	14.96	16.26	17.04	19.28
	21.13	20.54	20.92	18.92	27.27	26.78	23.86	31.37	29.41	29.07	29.12	39.86
	39.86	44.44	46.45	46.26	45.2	49.65	48.75	48.4	48.4	42.03	51.69	45.77
	47.55	45.77	45.77	46.76	46.76	48.93	55.04	54.65	56.59	55.76	56.12	58.61

	60.16	59.77	60.16	60.85	63.71	56.99	61.78	61.48	57.34	61.63	61.63	61.39
	60.85	61.54	61.87	62.26	57.69	57.69	57.69	62.02	65.12	65.35	59.77	100
	79.17	64.09	64.73	64.23	63.08	57.99	58.95	58.95	70.27	70.27		
135	9.57	10.14	9.38	12.35	14.1	10.49	11.71	12.55	14.73	14.22	17.04	19.28
	21.13	21.08	19.9	20	25.45	23.24	22.84	31	30.26	29.46	29.5	39.58
	39.58	42.29	43.31	45.23	44.52	45.39	47.33	45.2	45.2	42.55	52.26	45.1
	46.59	46.88	46.88	47.86	47.86	48.94	50.58	55.25	53.31	55.67	56.74	57.88
	59.92	59.53	59.92	60.62	62.69	58.62	61.54	61	58.28	61.15	61.92	61.92
	60.38	61.3	62.16	61.39	58.62	58.62	58.62	61.54	65.38	63.78	60.15	79.17
	100	62.16	62.79	62.55	65.52	61.17	59.03	59.03	65.38	67.31		
140	7.65	5.8	9.38	11.11	12.33	11.48	15.66	13.22	16.67	14.43	17.78	21.79
	21.83	20.54	18.37	18.38	24.24	22.36	24.37	31.64	30.86	29.25	28.85	40.32
	40.32	46.48	45.7	46.88	46.88	48.83	48.43	47.27	47.27	45.7	47.27	42.8
	42.8	53.12	53.12	50	50	51.18	50.78	52.34	52.14	52.94	54.51	58.3
	64.45	64.06	64.45	61.72	64.98	64.59	65.37	64.84	64.59	64.98	65.37	65.37
	64.2	64.59	65.23	65.23	64.98	64.98	64.98	65.37	68.87	66.93	64.48	64.09
	62.16	100	98.45	98.46	65.5	65.12	65.76	65.76	68.73	69.11		
136	7.06	5.8	9.38	11.11	12.33	12.4	15.23	12.78	16.67	14.51	17.78	21.46
	21.83	20.54	18.37	18.38	24.24	22.46	24.37	32.16	30.98	29.37	28.57	39.68
	39.68	46.67	45.88	46.67	47.06	49.02	48.22	46.67	46.67	45.49	47.45	42.97
	42.97	52.94	52.94	49.8	49.8	51.78	50.2	52.94	51.56	52.36	53.94	59.69
	63.92	63.14	63.92	61.96	65.23	64.84	65.23	64.71	64.84	64.84	65.23	65.23
	64.06	64.84	65.23	65.1	65.23	65.23	65.23	65.23	69.53	67.46	65.5	64.73
	62.79	98.45	100	100	64.98	64.98	66.02	66.02	68.22	68.99		
137	7.06	5.8	9.38	11.11	12.33	12.3	15.15	12.78	16.67	13.86	17.78	21.37
	21.83	20.54	18.37	18.38	24.24	22.36	24.37	31.18	29.92	29.3	28.79	39.53
	39.53	46.48	45.7	46.48	46.88	48.83	48.03	46.48	46.48	45.14	48.86	42.8
	44.53	52.73	52.73	49.6	49.6	51.57	51.89	51.52	53.21	52.16	53.73	59.18
	64.06	63.28	64.06	63.26	66.42	64.59	64.53	64.84	64.59	64.98	65.37	66.03
	64.2	65.27	65.23	65.23	64.98	64.98	64.98	65.37	69.65	67.72	66.29	64.23
	62.55	98.46	100	100	64.66	64.23	65.76	65.76	68.34	69.11		
201	10	7.25	9.38	13.75	13.89	6.61	13.71	14.1	16.8	15.46	14.81	21.03
	23.4	21.08	18.97	16.76	21.34	22.08	21.43	27.65	26.42	26.85	27.52	37.15
	37.15	46.09	47.27	48.05	48.05	51.17	50	45.31	45.31	43.58	46.21	45.14
	45.28	49.81	49.81	47.04	47.04	48.25	46.24	50.38	57.36	55.47	57.42	59.85
	56.42	56.42	56.81	64.04	61.05	61.39	62.08	62.02	61.78	62.16	61	60.9
	60.23	60.53	60.85	61.24	61	61	61	61.39	68.73	61.11	63.3	63.08
	65.52	65.5	64.98	64.66	100	99.62	68.22	68.22	69.11	71.43		
216	9.42	7.25	9.38	13.75	13.58	6.88	13.78	14.4	14.79	15.53	14.81	20.63
	23.4	21.08	18.97	16.76	21.34	21.99	21.43	27.11	26.64	26.54	26.62	34.97
	34.97	43.11	44.79	44.95	44.25	47.9	46.32	42.81	42.81	40.36	44.78	40.69
	43.61	47.22	47.22	45.36	45.36	46.1	45.38	52.12	56.76	51.6	53.02	56.57
	56.03	56.03	56.42	63.6	60.54	59.17	61.69	61.63	57.76	61.78	60.62	60.15
	59.85	60.31	60.85	60.85	58.48	58.48	58.48	61	68.34	60.32	63.36	57.99
	61.17	65.12	64.98	64.23	99.62	100	60.93	60.93	68.73	71.04		

74	9.47	7.25	6.25	10	11.11	10.26	15.49	12.97	16.67	14.78	16.79	21.65
	22.38	22.46	18.27	16.58	21.95	23.75	21.21	30.04	27.47	26.64	26.72	35.44
	35.44	44.37	42.91	44.79	42.36	45.3	44.41	43.01	43.01	42.86	46.82	41.92
	45.28	45.99	45.99	44.44	44.44	45.55	49.42	50.39	52.71	51.96	52.31	57.56
	58.2	57.81	58.2	64.73	63.57	60.42	66.28	66.54	58.72	66.28	65.5	65.12
	64.34	65.25	66.54	65.37	60.42	60.42	60.42	65.89	69.38	61.72	62.55	58.95
	59.03	65.76	66.02	65.76	68.22	60.93	100	100	76.36	76.36		
76	9.47	7.25	6.25	10	11.11	10.26	15.49	12.97	16.67	14.78	16.79	21.65
	22.38	22.46	18.27	16.58	21.95	23.75	21.21	30.04	27.47	26.64	26.72	35.44
	35.44	44.37	42.91	44.79	42.36	45.3	44.41	43.01	43.01	42.86	46.82	41.92
	45.28	45.99	45.99	44.44	44.44	45.55	49.42	50.39	52.71	51.96	52.31	57.56
	58.2	57.81	58.2	64.73	63.57	60.42	66.28	66.54	58.72	66.28	65.5	65.12
	64.34	65.25	66.54	65.37	60.42	60.42	60.42	65.89	69.38	61.72	62.55	58.95
	59.03	65.76	66.02	65.76	68.22	60.93	100	100	76.36	76.36		
138	9.36	7.25	7.81	9.88	10.96	9.02	14.14	11.4	15.87	14.36	17.78	21.79
	23.24	18.92	18.37	16.76	22.42	24.79	19.29	32.03	31.25	29.92	29.53	39.37
	39.37	49.61	50.78	49.22	47.66	50	49.61	48.44	48.44	44.92	50	46.69
	46.69	49.81	49.81	48.61	48.61	49.41	52.14	53.12	54.47	57.03	56.64	59.62
	63.04	63.42	63.42	66.93	68.22	68.22	68.99	68.09	67.83	68.22	69.38	69.38
	67.83	68.22	69.26	68.87	68.6	68.6	68.6	68.99	70.16	66.93	63.46	70.27
	65.38	68.73	68.22	68.34	69.11	68.73	76.36	76.36	100	91.15		
139	9.36	7.25	7.81	9.88	10.96	9.84	13.64	12.28	15.87	14.36	17.04	21.79
	23.94	18.92	18.37	17.3	23.03	23.95	19.29	32.03	30.86	31.1	31.1	40.16
	40.16	48.44	49.61	50	47.27	50	49.61	49.22	49.22	43.36	48.44	45.53
	45.53	50.58	50.58	50.2	50.2	49.41	54.86	55.08	52.14	57.03	57.42	61.92
	63.04	63.04	63.42	66.54	67.83	67.83	68.22	67.7	67.44	67.83	69.38	69.38
	68.22	68.22	69.26	69.26	68.99	68.99	68.99	69.38	69.77	64.57	63.46	70.27
	67.31	69.11	68.99	69.11	71.43	71.04	76.36	76.36	91.15	100		

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6023561_6024535-hypothetical_protein_CDS
3581727_3582743-hypothetical_protein_CDS
5595442_5596419-hypothetical_protein_CDS
3581247_3581720-hypothetical_protein_CDS
3583240_3583998-hypothetical_protein_CDS
3579296_3579763-hypothetical_protein_CDS
2850509_2851507-hypothetical_protein_CDS
711395_712393-hypothetical_protein_CDS
4742676_4744310-hypothetical_protein_CDS
3598998_3599294-hypothetical_protein_CDS
631500_631844-hypothetical_protein_CDS
3088735_3089250-hypothetical_protein_CDS
4854754_4855101-hypothetical_protein_CDS
736780_737322-hypothetical_protein_CDS
922204_923166-hypothetical_protein_CDS
5987864_5988655-Oxidoreductase,_short-chain_dehydrogenase/reductase_family_CDS
146245_146784-LSU_ribosomal_protein_L5p_(L11e)_CDS
146793_147098-SSU_ribosomal_protein_S14p_(S29e)_@_SSU_ribosomal_protein_S14p_(S29e),_zinc-indepe
147119_147514-SSU_ribosomal_protein_S8p_(S15Ae)_CDS
147539_148072-LSU_ribosomal_protein_L6p_(L9e)_CDS
148084_148449-LSU_ribosomal_protein_L18p_(L5e)_CDS
149195_149626-LSU_ribosomal_protein_L15p_(L27Ae)_CDS
151219_151584-SSU_ribosomal_protein_S13p_(S18e)_CDS
151602_152006-SSU_ribosomal_protein_S11p_(S14e)_CDS
152097_152720-SSU_ribosomal_protein_S4p_(S9e)_@_SSU_ribosomal_protein_S4p_(S9e),_zinc-independen
153967_154350-LSU_ribosomal_protein_L17p_CDS
169465_170118-Uncharacterized_protein_YraP_CDS
4237272_4238252-BUG/TctC_family_periplasmic_protein_CDS
262673_263662-BUG/TctC_family_periplasmic_protein_CDS
2842892_2843875-BUG/TctC_family_periplasmic_protein_CDS
5167542_5168552-BUG/TctC_family_periplasmic_protein_CDS
4232203_4233207-BUG/TctC_family_periplasmic_protein_CDS
1124415_1125383-BUG/TctC_family_periplasmic_protein_CDS
3807012_3808049-Outer_membrane_porin_CDS
5384218_5385213-Outer_membrane_porin_CDS
5978809_5979603-Enoyl-CoA_hydratase_(EC_4.2.1.17)_CDS
6020513_6021304-Enoyl-CoA_hydratase_(EC_4.2.1.17)_CDS
288211_289059-3-hydroxybutyryl-CoA_dehydrogenase_(EC_1.1.1.157)_CDS
427819_428856-TRAP-type_transport_system,_periplasmic_component,_predicted_N-acetylneuraminate-bin
4981133_4982119-TRAP-type_transport_system,_periplasmic_component,_predicted_N-acetylneuraminate-
432603_433502-Glutamate/aspartate_ABC_transporter,_substrate-binding_protein_GltI_(TC_3.A.1.3.4)_CDS
1898170_1899990-3-methylmercaptopropionyl-CoA_dehydrogenase_(DmdC)_CDS
526827_527987-2-keto-3-deoxy-D-arabino-heptulosonate-7-_phosphate_synthase_I_alpha_(EC_2.5.1.54)_CD
4019815_4020681-Putative_transmembrane_protein_CDS
895644_896393-Electron_transfer_flavoprotein,_beta_subunit_CDS
896548_897480-Electron_transfer_flavoprotein,_alpha_subunit_CDS
5123763_5124749-ABC_transporter,_substrate-binding_protein_(cluster_7,_di-/tri-carboxylate)_CDS
1814991_1815497-transport-associated_CDS
2606013_2606399-Copper_resistance_protein_CopC_CDS
961647_962033-Copper_resistance_protein_CopC_CDS
2070006_2071202-Aromatic-amino-acid_aminotransferase_(EC_2.6.1.57)_CDS

1103047_1103340-SSU_ribosomal_protein_S20p_CDS
2836663_2837784-Branched-chain_amino_acid_ABC_transporter,_substrate-binding_protein_LivJ_(TC_3.A.1
1118259_1119395-Branched-chain_amino_acid_ABC_transporter,_substrate-binding_protein_LivJ_(TC_3.A.1
1161403_1161978-Protein_yceI_precursor_CDS
1185839_1186921-TRAP_transporter_solute_receptor,_unknown_substrate_6_CDS
1276051_1276263-SSU_ribosomal_protein_S21p_CDS
1385313_1386623-Citrate_synthase_(si)_(EC_2.3.3.1)_CDS
1386947_1387651-Succinate_dehydrogenase_iron-sulfur_protein_(EC_1.3.5.1)_CDS
1391518_1392507-Malate_dehydrogenase_(EC_1.1.1.37)_CDS
1395034_1397619-Aconitate_hydratase_2_(EC_4.2.1.3)_@_2-methylisocitrate_dehydratase_(EC_4.2.1.99)_C
1480091_1480957-Murein_hydrolase_activator_NlpD_CDS
1553658_1554410-SSU_ribosomal_protein_S2p_(SAe)_CDS
1554519_1555412-Translation_elongation_factor_Ts_CDS
1590025_1591056-Phosphate_ABC_transporter,_substrate-binding_protein_PstS_(TC_3.A.1.7.1)_CDS
1635100_1636131-Sulfate_and_thiosulfate_binding_protein_CysP_CDS
2975996_2977168-Sulfate_and_thiosulfate_binding_protein_CysP_CDS
1637017_1638039-Alkanesulfonate_ABC_transporter_substrate-binding_protein_SsuA_CDS
1659299_1659706-Protein_GlcG_CDS
1675144_1676475-Isocitrate_lyase_(EC_4.1.3.1)_CDS
1679854_1680213-LSU_ribosomal_protein_L20p_CDS
1692552_1703069-RTX_toxins_and_related_Ca2+-binding_proteins_CDS
1767716_1768807-Outer_membrane_porin_protein_32_precursor;_putative_3-hydroxyphenylpropionic_aci
3098787_3099572-Methionine_ABC_transporter_substrate-binding_protein_CDS
3822492_3823328-Methionine_ABC_transporter_substrate-binding_protein_CDS
3037836_3038636-Methionine_ABC_transporter_substrate-binding_protein_CDS
1953741_1954397-Adenylate_kinase_(EC_2.7.4.3)_CDS
1967318_1967905-Superoxide_dismutase_[Fe]_(EC_1.15.1.1)_CDS
1974589_1976820-Isocitrate_dehydrogenase_[NADP]_(EC_1.1.1.42);_Monomeric_isocitrate_dehydrogenase_
2102539_2103420-ABC_transporter,_substrate-binding_protein_(cluster_12,_methionine/phosphonates)_CD
4764425_4765234-ABC_transporter,_substrate-binding_protein_(cluster_3,_basic_aa/glutamine/opines)_CD
2406186_2407154-ABC_transporter,_substrate-binding_protein_PA3836_CDS
4827227_4828297-Outer_membrane_porin_protein_32_precursor_CDS
3359466_3359987-Superoxide_dismutase_[Cu-Zn]_precursor_(EC_1.15.1.1)_CDS
2746996_2747307-ElaB_protein_CDS
2767612_2769372-Hypothetical_protein,_restriction_endonuclease-like_VRR-NUC_domain_CDS
2875541_2876779-Dihydrolipoamide_succinyltransferase_component_(E2)_of_2-oxoglutarate_dehydrogenas
2876843_2879722-2-oxoglutarate_dehydrogenase_E1_component_(EC_1.2.4.2)_CDS
2122591_2123925-RND_efflux_system,_membrane_fusion_protein_CDS
3112715_3114856-Outer_membrane_(iron.B12.siderophore.hemin)_receptor_CDS
3116778_3117833-CobW_GTPase_involved_in_cobalt_insertion_for_B12_biosynthesis_CDS
3163269_3164177-Phage_major_capsid_protein_CDS
3365976_3368561-Arginine_decarboxylase_(EC_4.1.1.19);_Ornithine_decarboxylase_(EC_4.1.1.17);_Lysine_d
5244624_5246732-Translation_elongation_factor_G_CDS
3415794_3416735-esterase/lipase/thioesterase_CDS
6016818_6018371-Acetyl-CoA_acetyltransferase_CDS
3507908_3508180-DNA-binding_protein_HU-beta_CDS
3517045_3517599-Translation_elongation_factor_P_CDS
3526323_3527339-Ketol-acid_reductoisomerase_(NADP(+))_(EC_1.1.1.86)_CDS
3541262_3541789-Inorganic_pyrophosphatase_(EC_3.6.1.1)_CDS
3601658_3602725-Phage_recombination_protein_Bet_CDS
3781517_3783076-photolyase_protein_family_CDS
3850341_3850988-Outer_membrane_protein_A_precursor_CDS

3859649_3861331-SSU_ribosomal_protein_S1p_CDS
4075906_4077216-Cell_division_trigger_factor_(EC_5.2.1.8)_CDS
4118444_4119409-Tripartite_tricarboxylate_transporter_TctC_family_CDS
5316957_5318159-ABC_transporter,_substrate-binding_protein_(cluster_4,_leucine/isoleucine/valine/benzoa
4173178_4173753-Alkyl_hydroperoxide_reductase_protein_C_(EC_1.11.1.15)_CDS
4224685_4225971-Enolase_(EC_4.2.1.11)_CDS
4241025_4242515-N-acetylmuramoyl-L-alanine_amidase_(EC_3.5.1.28)_CDS
4340397_4340849-LSU_ribosomal_protein_L9p_CDS
4340861_4341142-SSU_ribosomal_protein_S18p_@_SSU_ribosomal_protein_S18p,_zinc-independent_CDS
4410019_4411293-DNA_polymerase_IV_(EC_2.7.7.7)_CDS
4484875_4485129-SSU_ribosomal_protein_S16p_CDS
4645988_4646611-LSU_ribosomal_protein_L25p_CDS
4822517_4822807-Heat_shock_protein_10_kDa_family_chaperone_GroES_CDS
4822901_4824544-Heat_shock_protein_60_kDa_family_chaperone_GroEL_CDS
4960442_4960834-SSU_ribosomal_protein_S9p_(S16e)_CDS
4965832_4967262-Adenosylhomocysteinase_(EC_3.3.1.1)_CDS
5016806_5017888-FIG00536973:_hypothetical_protein_CDS
5083945_5085354-Flagellin_FliC_CDS
5085649_5087211-Flagellin_protein_FlaA_CDS
5087368_5088780-Flagellar_cap_protein_FliD_CDS
5097812_5099026-Flagellar_hook-associated_protein_FlgL_CDS
5099050_5100996-Flagellar_hook-associated_protein_FlgK_CDS
5100993_5102015-Flagellar_protein_FlgJ_[peptidoglycan_hydrolase]_CDS
5105708_5106976-Flagellar_hook_protein_FlgE_CDS
5109584_5109898-Negative_regulator_of_flagellin_synthesis_FlgM_(anti-sigma28)_CDS
5201172_5201696-LSU_ribosomal_protein_L10p_(P0)_CDS
5201923_5202618-LSU_ribosomal_protein_L1p_(L10Ae)_CDS
5202619_5203050-LSU_ribosomal_protein_L11p_(L12e)_CDS
5204320_5205510-Translation_elongation_factor_Tu_CDS
5220471_5221880-ATP_synthase_beta_chain_(EC_3.6.3.14)_CDS
5222800_5224359-ATP_synthase_alpha_chain_(EC_3.6.3.14)_CDS
5237236_5237742-Peroxiredoxin_CDS
5238138_5238335-LSU_ribosomal_protein_L29p_(L35e)_CDS
5238346_5238762-LSU_ribosomal_protein_L16p_(L10e)_CDS
5238765_5239634-SSU_ribosomal_protein_S3p_(S3e)_CDS
5239651_5239983-LSU_ribosomal_protein_L22p_(L17e)_CDS
5240280_5241104-LSU_ribosomal_protein_L2p_(L8e)_CDS
5241107_5241421-LSU_ribosomal_protein_L23p_(L23Ae)_CDS
5241418_5242041-LSU_ribosomal_protein_L4p_(L1e)_CDS
5242041_5242715-LSU_ribosomal_protein_L3p_(L3e)_CDS
5242916_5243227-SSU_ribosomal_protein_S10p_(S20e)_CDS
5599605_5600714-RecA_protein_CDS
5607104_5608264-Succinyl-CoA_ligase_[ADP-forming]_beta_chain_(EC_6.2.1.5)_CDS
5608285_5609184-Succinyl-CoA_ligase_[ADP-forming]_alpha_chain_(EC_6.2.1.5)_CDS
5768577_5769575-NAD-dependent_glyceraldehyde-3-phosphate_dehydrogenase_(EC_1.2.1.12)_CDS
5782381_5783445-Fructose-bisphosphate_aldolase_class_II_(EC_4.1.2.13)_CDS
5850317_5852509-Malate_synthase_G_(EC_2.3.3.9)_CDS
5864257_5864907-Periplasmic_thiol:disulfide_interchange_protein_DsbA_CDS

mean_30T	mean_30T-	mean_30B-	mean_40A	se_30T	se_30T-10	se_30B-10	se_40A
-0.5604	-0.57584	-0.81785	0.600564575	0.288331	0.511157	0.396969	0.204059
0.237298	-0.24982	0.352519	-0.055008183	0.171424	0.510857	0.266896	0.248421
-0.39786	0.482129	-0.57315	0.241164495	0.380023	0.306204		0.31674
0.249905	0.222088	-1.11039	-0.029186151	0.299691	0.537023	0.761697	0.18925
-0.70375	-0.27789	0.642123	-0.038952128	0.771606	0.988449	0.40286	0.569217
0.009606	-0.5856	0.320212	-0.370625176	0.318444	0.345723	0.607312	0.24949
1.352477	0.730802	0.855957	-0.58793512	0.785119	0.676707		1.070369
0.483553	0.532817	1.709611	0.049688195	0.512948	0.362982		0.722291
-0.09937			0.310635158				0.405109
-0.29455	0.244906		-0.015889426	0.393184	0.114974		0.148343
-0.02721			0.077394808				0.098933
			1.151457766				0.2806
0.114636	-1.13993		0.457865236	0.800923	1.425027		0.485077
-2.39529	-2.6387	-1.77202	-2.993116828	0.698546	0.139791		0.345172
-6.54647	-7.53084	-5.31599	-8.084131645	0.353479	0.459622		0.929978
-0.21153	0.284397		0.34522933	0.151184	0.413627		0.820018
-0.10721	0.025891		-0.24885759		0.296443		0.306955
	-0.63335		0.059507852				0.129536
0.272158	0.637099		-0.106164843	0.502152	0.170152		0.116503
-0.06223	0.446012		0.003479843				0.202955
-0.70642	0.204275	-0.60836	-0.052882091	0.198469	0.199844	0.315095	0.188278
-0.51106			0.035091066				0.892319
	-0.56602		-0.812876696				0.500376
0.409141	0.699287	0.032663	0.469101838	0.28769	0.305348		0.188229
			-0.518889636				0.231387
0.180866	0.60995		0.429946103				0.157269
0.063018	-0.21173	0.34864	-0.089221269	0.332802	0.640596		0.413184
-0.09677	-0.16583	-1.10599	0.488028453	0.292565	0.492165	0.455581	0.273955
-0.60719	-0.65992	-0.9894	-0.173368518	0.326963	0.344981	0.392779	0.866291
	0.324427		0.595286582		1.147281		0.458706
	-0.53755		0.078635198				0.157106
			0.289612358				0.100677
			0.204614546				0.208534
0.011355	-0.35268	0.181199	-0.5006691	0.243353	0.196255		0.260878
0.821366	0.690599	1.679156	0.869618026	0.469054	0.443728		0.184925
0.911893	0.38652		0.510246946				0.166291
0.684329	0.237415	0.137686	0.185356904	0.263524			0.266988
1.147137	1.924509	3.496379	0.808505462	1.05263	0.938872		1.212771
-1.24123	-0.11353	-0.45835	0.095563577	0.414329	0.6208		0.281753
	-0.54747		-0.843292931		0.15195		0.693962
-0.82635	-0.33684	-0.27728	0.381586965	0.443413	0.462487	0.270811	0.222061
			0.231329417				0.19571
	-0.1273		-0.03824676				0.179368
0.325469	0.561836		0.940993927				0.326609
-0.04243	-0.42051	0.640797	-0.274074221	0.265336	0.106073		0.224615
0.494292	-0.29318	0.118861	0.054722996	0.6901	0.618347	0.572306	0.547555
0.810856	0.694748		-1.192671079	0.17244	0.508385		0.189096
0.319645	0.388242	0.52712	-0.380162292	0.183662	0.422471	0.346088	0.240981
-2.11553	-1.51544		0.364981865	0.492496	0.56925		0.347158
			0.894935184				0.252363
0.193767	0.282344		0.058183036	0.217729	0.349064		0.321832

-0.17831	0.356772	0.154934	0.101403999	0.303896	0.407019		0.197403
0.204267	-0.35228		0.813766289	0.297657	0.309147		0.289003
-0.60105			-0.308452556	0.353017			0.264039
-0.3836	-0.18782		0.89674523	0.36902			0.351949
-1.02358	-0.21463		-0.143258908	0.456041	0.283095		0.222709
0.444959			0.410717193				0.527604
	0.439437		-0.037823334		0.447335		0.145692
-0.53263	-0.73438		-1.077147719				0.113578
-1.09363	-0.34581	-0.95667	0.162002904	0.606345	0.467823		0.371064
-0.77357	-0.06349		-0.144001673	0.315278	0.426873		0.166614
-0.40519	0.32762		0.094220757	0.161735			0.313801
	5.778472		3.77253731				3.426131
0.462629	0.107279		-0.415431784	0.24401			0.690806
-0.42112			0.186834033				0.35986
-0.78787	-1.14894		0.416298178		0.962116		0.568364
-1.19949	-0.57507	-1.12857	0.645583341	0.325075	0.362756		0.317698
			0.165030967				0.367557
-1.19912	-0.79004	0.667153	0.179405871	0.105494	0.350614	0.261627	0.362456
-2.86129	-1.4489	-0.82214	0.213816104		0.189557	0.417605	0.410023
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392696_393826-WbjC_CDS
411411_412607-3-ketoacyl-CoA_thiolase_[fadN-fadA-fadE_operon]_(EC_2.3.1.16)_CDS
851660_852394-Transcriptional_regulator,_GntR_family_CDS
434371_435042-Glutamate/aspartate_ABC_transporter,_permease_protein_GltK_(TC_3.A.1.3.4)_CD
3874384_3877473-CzcABC_family_efflux_RND_transporter,_transmembrane_protein_CDS
494654_495973-ATP-dependent_hsl_protease_ATP-binding_subunit_HslU_CDS
549108_550496-Signal_recognition_particle_protein_Ffh_CDS
558719_559804-Molybdenum_ABC_transporter_ATP-binding_protein_ModC_CDS
572031_573167-2-polyprenyl-3-methyl-6-methoxy-1,4-benzoquinol_hydroxylase_CDS
606831_607793-Aspartate_carbamoyltransferase_(EC_2.1.3.2)_CDS
668882_670780-Phage_terminase,_ATPase_subunit_GpP_CDS
820515_821480-Phosphate_acetyltransferase_(EC_2.3.1.8)_CDS
839069_841324-Guanosine-3',5'-bis(diphosphate)_3'-pyrophosphohydrolase_(EC_3.1.7.2)_/_GTP_py
4039390_4040544-Acyl-CoA_dehydrogenase,_long-chain_specific_(EC_1.3.8.8)_CDS
2608986_2611436-Lead,_cadmium,_zinc_and_mercury_transporting_ATPase_(EC_3.6.3.3)_(EC_3.6.
2474778_2475206-Transcriptional_regulator,_MerR_family_CDS
1051114_1052088-Hypothetical_protein_with_Rieske_(2Fe-2S)_region_CDS
1065472_1066998-L-aspartate_oxidase_(EC_1.4.3.16)_CDS
1126992_1128185-Glutaryl-CoA_dehydrogenase_(EC_1.3.8.6)_CDS
1187331_1189160-TRAP_dicarboxylate_transporter,_DctM_subunit,_unknown_substrate_6_CDS
973029_974978-Methyl-accepting_chemotaxis_protein_I_(serine_chemoreceptor_protein)_CDS
1356064_1357176-S-(hydroxymethyl)glutathione_dehydrogenase_(EC_1.1.1.284)_CDS

1506519_1507364-Polysaccharide_deacetylase_CDS
1512862_1514412-Nitrogen_regulation_protein_NR(I),_GlnG_(=NtrC)_CDS
1518006_1518509-Dihydrofolate_reductase_(EC_1.5.1.3)_CDS
1547686_1550298-3'-to-5'_exoribonuclease_RNase_R_CDS
1600007_1600252-LSU_ribosomal_protein_L31p_@_LSU_ribosomal_protein_L31p,_zinc-independen
1651261_1652145-NAD-dependent_epimerase/dehydratase_CDS
2235301_2235483-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
1837047_1837925-Uncharacterized_protein_YcgL_CDS
2016530_2017624-Selenide,water_dikinase_(EC_2.7.9.3)_CDS
2079005_2079343-Ferredoxin,_2Fe-2S_CDS
2248739_2250124-sigma-54-dependent_transcriptional_regulator_CDS
2282474_2284987-Sensory_box_histidine_kinase/response_regulator_CDS
2358214_2359323-Prophage_Lp2_protein_6_CDS
2360112_2360273-conserved_hypothetical_protein_CDS
2451414_2452352-Ribosomal_protein_L3_N(5)-glutamine_methyltransferase_(EC_2.1.1.298)_CDS
2495032_2496015-Tn4651_auxiliary_cointegrate_resolution_protein_T_CDS
2571765_2572811-Outer_membrane_porin_protein_32_precursor_CDS
2761186_2762259-Choloylglycine_hydrolase_(EC_3.5.1.24)_CDS
4467283_4468779-Outer_membrane_factor_(OMF)_lipoprotein_associated_wth_EmrAB-OMF_efflu
4490159_4490923-Branched-chain_amino_acid_ABC_transporter,_ATP-binding_protein_LivF_(TC_3.
5174047_5174562-Copper_metallochaperone_PCu(A)C,_inserts_Cu(I)_into_cytochrome_oxidase_su
3237282_3238331-Conjugative_transfer_protein_TrbB_CDS
3323623_3324255-Cytochrome_c_oxidase_(cbb3-type)_subunit_CcoO_(EC_1.9.3.1)_CDS
3447793_3448407-Outer_membrane_protein_W_precursor_CDS
3448621_3449634-Inner_membrane_protein_YedI_CDS
4815453_4817156-NAD_synthetase_(EC_6.3.1.5)_/_Glutamine_amidotransferase_chain_of_NAD_sy
3687696_3690149-Hemophore_HasA_outer_membrane_receptor_HasR_/_Iron_siderophore_recept
3923033_3926008-Na(+)_H(+)_antiporter_subunit_A_/_Na(+)_H(+)_antiporter_subunit_B_CDS
3984280_3985704-Aldehyde_dehydrogenase_(EC_1.2.1.3);_Probable_coniferyl_aldehyde_dehydrog
4114366_4115997-Two-component_transcriptional_response_regulator,_AtoC_family_CDS
4124143_4124889-SSU_rRNA_pseudouridine(516)_synthase_(EC_5.4.99.19)_CDS
4139093_4140070-Acetyl-coenzyme_A_carboxyl_transferase_alpha_chain_(EC_6.4.1.2)_CDS
4161625_4162446-Phosphoenolpyruvate_synthase_regulatory_protein_CDS
4183578_4185989-DNA_topoisomerase_IV_subunit_A_(EC_5.99.1.3)_CDS
4211330_4211950-Outer_membrane_lipoprotein_CDS
4223393_4224250-2-Keto-3-deoxy-D-manno-octulosonate-8-phosphate_synthase_(EC_2.5.1.55)_CD
4226048_4226326-Cell_division_protein_DivIC_(FtsB),_stabilizes_FtsL_against_RasP_cleavage_CDS
4287825_4288505-NADH-ubiquinone_oxidoreductase_chain_J_(EC_1.6.5.3)_CDS
4305273_4309706-Type_IV_fimbrial_biogenesis_protein_PilY1_CDS
4797211_4799550-Multimodular_transpeptidase-transglycosylase_(EC_2.4.1.129)_(EC_3.4.-.-)_CDS
4459649_4461655-Alkaline_phosphatase_(EC_3.1.3.1)_CDS
4660721_4661365-Uncharacterized_membrane_anchored_protein_Mext_4159_CDS
4729961_4730329-FIG146285:_Diadenosine_tetraphosphate_(Ap4A)_hydrolase_and_other_HIT_fa
4757666_4758610-Efflux_ABC_transporter,_ATP-binding_protein_CDS
4759731_4760528-Outer-membrane-phospholipid-binding_lipoprotein_MlaA_CDS
4855885_4858056-Efflux_ABC_transporter,_permease/ATP-binding_protein_Reut_A2584_CDS
4884492_4885763-Nitrate_ABC_transporter,_substrate-binding_protein_CDS
4941361_4942791-N-acetylglucosamine-1-phosphate_uridyltransferase_(EC_2.7.7.23)_/_Glucosami
5287669_5289084-NAD(P)_transhydrogenase_subunit_beta_(EC_1.6.1.2)_CDS
5358450_5358788-Nitrogen_regulatory_protein_P-II,_GlnK_CDS
5410639_5411607-Histidine_ABC_transporter,_substrate-binding_protein_CDS
5470950_5472170-Two-component_system_sensor_histidine_kinase_Dtpsy_0212_CDS

5729370_5729744-Lactoylglutathione_lyase_and_related_lyases_CDS
5758821_5759654-4-hydroxy-tetrahydrodipicolinate_reductase_(EC_1.17.1.8)_CDS
5816428_5817426-Threonylcarbamoyl-AMP_synthase_(EC_2.7.7.87)_/_SUA5_domain_with_internal
5881220_5882962-Urease_alpha_subunit_(EC_3.5.1.5)_CDS
5896991_5898259-Urea_ABC_transporter,_substrate-binding_protein_UrtA_CDS
2736860_2739361-Probable_two-component_transmembrane_sensor_histidine_kinase_transcriptio
3360230_3361069-DNA_ligase_(ATP)_(EC_6.5.1.1)_CDS
5133847_5134980-Uroporphyrinogen_III_decarboxylase_(EC_4.1.1.37)_CDS
5171709_5172959-hypothetical_protein_CDS
2635861_2636307-hypothetical_protein_CDS
5028977_5029588-Resolvase,_N-terminal_domain_CDS
4240507_4241028-tRNA_threonylcarbamoyladenosine_biosynthesis_protein_TsaE_CDS
3562314_3562487-micrococcal_nuclease-like_protein_CDS
4487989_4488999-Probable_low-affinity_inorganic_phosphate_transporter_CDS
4096937_4099219-Xanthine_dehydrogenase,_molybdenum_binding_subunit_(EC_1.17.1.4)_CDS
5087368_5088780-Flagellar_cap_protein_FliD_CDS
5510224_5512080-Phosphoenolpyruvate_carboxykinase_[GTP]_(EC_4.1.1.32)_CDS
5203763_5204146-Protein_translocase_subunit_SecE_CDS
378961_379851-Glucose-1-phosphate_thymidylyltransferase_(EC_2.7.7.24)_CDS
4251891_4253711-Cation_transporting_ATPase,_N-terminal:Haloacid_dehalogenase-like_hydrolase:
4142631_4143182-Uncharacterized_protein_Tbd_1903_CDS
5358813_5360180-Ammonium_transporter_CDS
5219478_5219747-FIG00537936:_hypothetical_protein_CDS
5063350_5065542-Signal_transduction_histidine_kinase_CheA_CDS
5202619_5203050-LSU_ribosomal_protein_L11p_(L12e)_CDS
729482_730660-Signal_recognition_particle_receptor_FtsY_CDS
1433407_1434552-TolA_protein_CDS
1161403_1161978-Protein_yceI_precursor_CDS
1839912_1841489-Putative_ribonucleoprotein_related-protein_TROVE_Domain_CDS
4154971_4155276-hypothetical_protein_CDS
4911602_4912255-FIG00538201:_hypothetical_protein_CDS
5097812_5099026-Flagellar_hook-associated_protein_FlgL_CDS
4143948_4144475-Peptidyl-prolyl_cis-trans_isomerase_PpiB_(EC_5.2.1.8)_CDS
2457279_2458772-Methyl-accepting_chemotaxis_protein_I_(serine_chemoreceptor_protein)_CDS
961647_962033-Copper_resistance_protein_CopC_CDS
1616670_1616999-Thioredoxin_CDS
3552408_3552740-Nucleoid-associated_protein_YaaK_CDS
5678232_5678630-RNA-binding_protein_CDS
5852986_5853345-hypothetical_protein_CDS
5483216_5484379-Benzoate_ABC_transporter,_substrate-binding_protein_CDS
170180_171091-2-hydroxy-3-oxopropionate_reductase_(EC_1.1.1.60)_CDS
1301627_1302559-Electron_transfer_flavoprotein,_alpha_subunit_CDS
3933607_3935343-3-oxo-5-alpha-steroid_4-dehydrogenase_(EC_1.3.99.5)_CDS
5149508_5150671-Acyl-CoA_dehydrogenase_CDS
4822517_4822807-Heat_shock_protein_10_kDa_family_chaperone_GroES_CDS
706559_707497-hypothetical_protein_CDS
3202471_3204018-hypothetical_protein_CDS
1668346_1668882-Uncharacterized_protein_CC_3060_CDS
3768676_3769254-hypothetical_protein_CDS
5085649_5087211-Flagellin_protein_FlaA_CDS
4936745_4938661-Glutamine--fructose-6-phosphate_aminotransferase_[isomerizing]_(EC_2.6.1.16)
151219_151584-SSU_ribosomal_protein_S13p_(S18e)_CDS

984669_985169-FIG00799023:_hypothetical_protein_CDS
739990_740370-Two-component_transcriptional_response_regulator_receiver_domain_CDS
1487842_1488267-Nucleoside_diphosphate_kinase_(EC_2.7.4.6)_CDS
5216505_5217122-LemA_family_protein_CDS
4181712_4183373-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
2600543_2601946-Heavy_metal_sensor_histidine_kinase_CDS
1103047_1103340-SSU_ribosomal_protein_S20p_CDS
5083945_5085354-Flagellin_FliC_CDS
1074797_1075087-DNA-binding_protein_H-NS_CDS
2001674_2002570-3-hydroxyisobutyrate_dehydrogenase_(EC_1.1.1.31)_CDS
1321263_1321670-Regulator_of_nucleoside_diphosphate_kinase_CDS
5140465_5140824-hypothetical_protein_CDS
4960442_4960834-SSU_ribosomal_protein_S9p_(S16e)_CDS
4277480_4278199-Broad-specificity_amino_acid_ABC_transporter,_ATP-binding_protein_2_CDS
147539_148072-LSU_ribosomal_protein_L6p_(L9e)_CDS
1971806_1972165-DNA-binding_protein_H-NS_CDS
5254821_5255513-Dienelactone_hydrolase_family_protein_CDS
4944045_4945277-Tyrosyl-tRNA_synthetase_(EC_6.1.1.1)_CDS
3385093_3385578-UPF0234_protein_Yitk_CDS
2028726_2029373-Galactoside_O-acetyltransferase_(EC_2.3.1.18)_CDS
3665031_3665792-Cell_division_coordinator_CpoB_CDS
4529048_4529845-Oxidoreductase,_short-chain_dehydrogenase/reductase_family_CDS
1300723_1301472-Electron_transfer_flavoprotein,_beta_subunit_CDS
3517045_3517599-Translation_elongation_factor_P_CDS
5065575_5065937-Chemotaxis_regulator_-_transmits_chemoreceptor_signals_to_flagellar_motor_c
4717554_4718156-Ubiquinol-cytochrome_C_reductase_iron-sulfur_subunit_(EC_1.10.2.2)_CDS
4645988_4646611-LSU_ribosomal_protein_L25p_CDS
4340861_4341142-SSU_ribosomal_protein_S18p_@_SSU_ribosomal_protein_S18p,_zinc-independe
1409813_1411519-Acyl-CoA_dehydrogenase_CDS
3284230_3285237-L-threonine_3-O-phosphate_decarboxylase_(EC_4.1.1.81)_CDS
5006888_5007670-Methylglutaconyl-CoA_hydratase_(EC_4.2.1.18)_CDS
2840866_2841579-Branched-chain_amino_acid_ABC_transporter,_ATP-binding_protein_LivF_(TC_3
644441_644752-hypothetical_protein_CDS
734712_735206-Phosphopantetheine_adenylyltransferase_(EC_2.7.7.3)_CDS
375464_375934-Uncharacterized_LysM_domain_protein_YgaU_CDS
2431693_2434167-diguanylate_cyclase/phosphodiesterase_(GGDEF_&_EAL_domains)_with_PAS/PA
1799870_1801105-ABC_transporter,_substrate-binding_protein_RSc1750_CDS
152097_152720-SSU_ribosomal_protein_S4p_(S9e)_@_SSU_ribosomal_protein_S4p_(S9e),_zinc-ind
237626_239236-Diguanylate_cyclase_CDS
266362_267678-ABC-type_branched-chain_amino_acid_transport_systems,_periplasmic_componen
3507908_3508180-DNA-binding_protein_HU-beta_CDS
4342148_4342693-Heat_shock_protein_GrpE_CDS
4501814_4502047-LSU_ribosomal_protein_L28p_@_LSU_ribosomal_protein_L28p,_zinc-independen
5242916_5243227-SSU_ribosomal_protein_S10p_(S20e)_CDS
2518732_2519028-DNA-binding_protein_H-NS_CDS
5677515_5677991-RNA-binding_protein_CDS
369622_370146-3-hydroxyacyl-[acyl-carrier-protein]_dehydratase,_FabA_form_(EC_4.2.1.59)_@_Tr
2844585_2845028-Universal_stress_protein_family_CDS
1692552_1703069-RTX_toxins_and_related_Ca2+-binding_proteins_CDS
4587607_4588851-Ferredoxin_reductase_CDS
1553658_1554410-SSU_ribosomal_protein_S2p_(SAe)_CDS
5977665_5978792-putative_oxidoreductase,_nitronate_monooxygenase_family_CDS

5237236_5237742-Peroxiredoxin_CDS
4354112_4357039-Probable_type_iv_pilus_assembly_fimv-related_transmembrane_protein_CDS
284891_285307-Organic_hydroperoxide_resistance_protein_CDS
1953741_1954397-Adenylate_kinase_(EC_2.7.4.3)_CDS
4500583_4501536-Thioredoxin_reductase_(EC_1.8.1.9)_CDS
5855702_5856637-Transcriptional_regulator,_LysR_family_CDS
1322005_1322667-Two-component_transcriptional_response_regulator,_LuxR_family_CDS
739299_739931-Two-component_transcriptional_response_regulator,_LuxR_family_CDS
5242041_5242715-LSU_ribosomal_protein_L3p_(L3e)_CDS
2606013_2606399-Copper_resistance_protein_CopC_CDS
4665565_4666563-Uncharacterized_membrane_protein_Bcep18194_A6058_CDS
2829218_2829592-Glycine_cleavage_system_H_protein_CDS
6023561_6024535-hypothetical_protein_CDS
4288540_4289049-NADH-ubiquinone_oxidoreductase_chain_I_(EC_1.6.5.3)_CDS
146245_146784-LSU_ribosomal_protein_L5p_(L11e)_CDS
1794776_1795432-Intracellular_septation_protein_IspA_CDS
4389892_4390635-3-oxoacyl-[acyl-carrier_protein]_reductase_(EC_1.1.1.100),_FadG_CDS
2268872_2269384-Tol-Pal_system_peptidoglycan-associated_lipoprotein_PAL_CDS
5612752_5613621-Orotidine_5'-phosphate_decarboxylase_(EC_4.1.1.23)_CDS
1118259_1119395-Branched-chain_amino_acid_ABC_transporter,_substrate-binding_protein_LivJ_(
1555506_1556228-Uridylate_kinase_(EC_2.7.4.22)_CDS
491414_492157-DksA_family_protein_PA5536_(no_Zn-finger)_CDS
4216237_4216686-Deoxyuridine_5'-triphosphate_nucleotidohydrolase_(EC_3.6.1.23)_CDS
1497541_1497795-RNA-binding_protein_Hfq_CDS
780093_781184-[4Fe-4S]_cluster_assembly_scaffold_protein_Mrp_(=ApbC)_CDS
1676797_1678716-Threonyl-tRNA_synthetase_(EC_6.1.1.3)_CDS
4352627_4353739-Aspartate-semialdehyde_dehydrogenase_(EC_1.2.1.11)_CDS
1801336_1802571-ABC_transporter,_substrate-binding_protein_RSc1750_CDS
4358756_4359955-Tryptophan_synthase_beta_chain_(EC_4.2.1.20)_CDS
5316957_5318159-ABC_transporter,_substrate-binding_protein_(cluster_4,_leucine/isoleucine/valin
5246878_5247351-SSU_ribosomal_protein_S7p_(S5e)_CDS
5864257_5864907-Periplasmic_thiol:disulfide_interchange_protein_DsbA_CDS
1793634_1794425-Peptidyl-prolyl_cis-trans_isomerase_(EC_5.2.1.8)_CDS
3280987_3281415-FIG00348236:_hypothetical_protein_CDS
3350573_3351718-DnaJ-class_molecular_chaperone_CbpA_CDS
4217377_4218603-Phosphopantothenoylcysteine_decarboxylase_(EC_4.1.1.36)_/_Phosphopantothe
5986509_5987777-L-carnitine_dehydratase/bile_acid-inducible_protein_F_CDS
2102539_2103420-ABC_transporter,_substrate-binding_protein_(cluster_12,_methionine/phosphon
2441534_2442271-Acetoacetyl-CoA_reductase_(EC_1.1.1.36)_CDS
4232203_4233207-BUG/TctC_family_periplasmic_protein_CDS
1679854_1680213-LSU_ribosomal_protein_L20p_CDS
4991922_4992935-Outer_membrane_porin_CDS
5776257_5777693-Pyruvate_kinase_(EC_2.7.1.40)_CDS
4145582_4147228-3-methylmercaptopropionyl-CoA_ligase_(EC_6.2.1.44)_of_DmdB1_type_CDS
2507664_2509154-hypothetical_protein_CDS
895644_896393-Electron_transfer_flavoprotein,_beta_subunit_CDS
4421360_4423018-L-lactate_permease_CDS
2476320_2476766-Universal_stress_protein_family_CDS
1389925_1390350-Succinate_dehydrogenase_cytochrome_b-556_subunit_CDS
1501858_1503006-ATP_phosphoribosyltransferase_regulatory_subunit_(EC_2.4.2.17)_CDS
2840099_2840866-Branched-chain_amino_acid_ABC_transporter,_ATP-binding_protein_LivG_(TC_3
148084_148449-LSU_ribosomal_protein_L18p_(L5e)_CDS

5081139_5081525-Chemotaxis_regulator_-_transmits_chemoreceptor_signals_to_flagellar_motor_c
2986944_2987444-(Y14336)_putative_extracellular_protein_containing_predicted_35aa_signal_pept
5865691_5866473-Lipopolysaccharide_ABC_transporter,_ATP-binding_protein_LptB_CDS
1168637_1169947-Uncharacterized_protein_EC-HemY_in_Proteobacteria_(unrelated_to_HemY-type
147119_147514-SSU_ribosomal_protein_S8p_(S15Ae)_CDS
1787072_1787944-Hydroxymethylpyrimidine_phosphate_kinase_ThiD_(EC_2.7.4.7)_CDS
1590025_1591056-Phosphate_ABC_transporter,_substrate-binding_protein_PstS_(TC_3.A.1.7.1)_CD
3891457_3891807-hypothetical_protein_CDS
5817604_5818761-N5-carboxyaminoimidazole_ribonucleotide_synthase_(EC_6.3.4.18)_CDS
1572209_1573381-Carbamoyl-phosphate_synthase_small_chain_(EC_6.3.5.5)_CDS
2739358_2740011-Two-component_transcriptional_response_regulator,_LuxR_family_CDS
4340397_4340849-LSU_ribosomal_protein_L9p_CDS
2668440_2668865-Lactoylglutathione_lyase_(EC_4.4.1.5)_CDS
432603_433502-Glutamate/aspartate_ABC_transporter,_substrate-binding_protein_GltI_(TC_3.A.1.3
1112263_1113201-BUG/TctC_family_periplasmic_protein_CDS
3453988_3455070-MoxR-like_ATPases_CDS
5715211_5715600-Barstar,_ribonuclease_(Barnase)_inhibitor_CDS
3527412_3527903-Acetolactate_synthase_small_subunit_(EC_2.2.1.6)_CDS
5291835_5292197-Probable_ALANIN-rich_signal_peptide_protein_CDS
5499633_5499899-Cell_division_topological_specificity_factor_MinE_CDS
4118444_4119409-Tripartite_tricarboxylate_transporter_TctC_family_CDS
196899_198194-Cobalt/zinc/cadmium_efflux_RND_transporter,_membrane_fusion_protein_CzcB_C
4551741_4552997-Methyl-accepting_chemotaxis_protein_I_(serine_chemoreceptor_protein)_CDS
4384356_4385858-HtrA_protease/chaperone_protein_CDS
262673_263662-BUG/TctC_family_periplasmic_protein_CDS
5248134_5249306-D-alanyl-D-alanine_carboxypeptidase_(EC_3.4.16.4)_CDS
528852_529169-hypothetical_protein_CDS
2930206_2930862-hypothetical_protein_CDS
5173032_5173919-hypothetical_protein_CDS
391646_392692-UDP-N-acetylglucosamine_4,6-dehydratase_(EC_4.2.1.135)_CDS
5861584_5863299-Arginyl-tRNA_synthetase_(EC_6.1.1.19)_CDS
1536570_1537403-FIG016425:_Soluble_lytic_murein_transglycosylase_and_related_regulatory_prot
5587772_5589016-ABC_transporter,_substrate-binding_protein_RSc1750_CDS
1635100_1636131-Sulfate_and_thiosulfate_binding_protein_CysP_CDS
1386947_1387651-Succinate_dehydrogenase_iron-sulfur_protein_(EC_1.3.5.1)_CDS
2827959_2829095-Aminomethyltransferase_(glycine_cleavage_system_T_protein)_(EC_2.1.2.10)_CD
5062827_5063315-Positive_regulator_of_CheA_protein_activity_(CheW)_CDS
773824_775983-Methionyl-tRNA_synthetase_(EC_6.1.1.10)_CDS
5809547_5810737-Phospholipase/lecithinase/hemolysin_CDS
1554519_1555412-Translation_elongation_factor_Ts_CDS
5622511_5623059-Single-stranded_DNA-binding_protein_CDS
3193707_3196013-Xanthine_dehydrogenase,_molybdenum_binding_subunit_(EC_1.17.1.4)_CDS
1503044_1504420-Adenylosuccinate_synthetase_(EC_6.3.4.4)_CDS
4382119_4383975-Translation_elongation_factor_LepA_CDS
4795171_4795782-Type_IV_pilus_biogenesis_protein_PilN_CDS
1032941_1034218-CzcABC_family_efflux_RND_transporter,_membrane_fusion_protein_CDS
5206990_5208306-RND_efflux_system,_membrane_fusion_protein_CDS
2406186_2407154-ABC_transporter,_substrate-binding_protein_PA3836_CDS
4269100_4269540-PhnB_protein;_putative_DNA_binding_3-demethylubiquinone-9_3-methyltransfe
5231107_5232882-Phosphoenolpyruvate-protein_phosphotransferase_of_PTS_system_(EC_2.7.3.9)_
1963115_1964035-TyrA_protein_CDS
5666222_5667409-Uncharacterized_protein_with_LysM_domain,_COG1652_CDS

2732066_2733751-Dihydrolipoamide_acetyltransferase_component_of_pyruvate_dehydrogenase_c
5201923_5202618-LSU_ribosomal_protein_L1p_(L10Ae)_CDS
5605387_5606382-N-acetyl-gamma-glutamyl-phosphate_reductase_(EC_1.2.1.38)_CDS
427819_428856-TRAP-type_transport_system,_periplasmic_component,_predicted_N-acetylneuram
4221546_4223243-CTP_synthase_(EC_6.3.4.2)_CDS
3678914_3679771-4-hydroxybenzoyl-CoA_thioesterase_family_active_site_CDS
400940_401860-N-acetylglutamate_kinase_(EC_2.7.2.8)_CDS
2360868_2361548-hypothetical_protein_CDS
2277146_2278813-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
4694118_4695860-Prolyl-tRNA_synthetase_(EC_6.1.1.15),_bacterial_type_CDS
5830281_5830793-LPS-assembly_lipoprotein_LptE_CDS
3822492_3823328-Methionine_ABC_transporter_substrate-binding_protein_CDS
4298351_4299394-Quinone_oxidoreductase_(EC_1.6.5.5)_CDS
4794491_4795171-Type_IV_pilus_biogenesis_protein_PilO_CDS
524831_526291-TldD_protein,_part_of_TldE/TldD_proteolytic_complex_CDS
5614752_5615735-hypothetical_protein_CDS
5670961_5672154-Phosphoglycerate_kinase_(EC_2.7.2.3)_CDS
2563491_2564909-Cobalt/zinc/cadmium_efflux_RND_transporter,_membrane_fusion_protein_CzcB_
5531410_5532162-hypothetical_protein_CDS
2746569_2746964-Phage_holin_CDS
4283961_4285436-NADH-ubiquinone_oxidoreductase_chain_M_(EC_1.6.5.3)_CDS
4237272_4238252-BUG/TctC_family_periplasmic_protein_CDS
1287779_1288234-CBS_domain_protein_CDS
1882092_1882724-Uracil_phosphoribosyltransferase_(EC_2.4.2.9)_CDS
711395_712393-hypothetical_protein_CDS
3430657_3432300-Geranyl-CoA_carboxylase_carboxyl_transferase_subunit_(EC_6.4.1.5)_CDS
3358493_3359293-Enoyl-[acyl-carrier-protein]_reductase_[NADH]_(EC_1.3.1.9)_CDS
2842892_2843875-BUG/TctC_family_periplasmic_protein_CDS
4673045_4674358-Glycerol-3-phosphate_ABC_transporter,_substrate-binding_protein_UgpB_CDS
3893957_3895951-Acetyl-CoA_synthetase_(EC_6.2.1.1)_CDS
4924821_4926461-Allophanate_hydrolase_2_subunit_1_(EC_3.5.1.54)_/_Allophanate_hydrolase_2_
1675144_1676475-Isocitrate_lyase_(EC_4.1.3.1)_CDS
1945905_1946351-Universal_stress_protein_family_CDS
4173178_4173753-Alkyl_hydroperoxide_reductase_protein_C_(EC_1.11.1.15)_CDS
3807012_3808049-Outer_membrane_porin_CDS
4799973_4800227-Diaminopimelate_decarboxylase_and/or_diaminopimelate_epimerase_leader_pe
4250440_4251786-NADP-specific_glutamate_dehydrogenase_(EC_1.4.1.4)_CDS
5608285_5609184-Succinyl-CoA_ligase_[ADP-forming]_alpha_chain_(EC_6.2.1.5)_CDS
1185839_1186921-TRAP_transporter_solute_receptor,_unknown_substrate_6_CDS
464839_465759-Cysteine_synthase_(EC_2.5.1.47)_CDS
1492872_1494176-Histidyl-tRNA_synthetase_(EC_6.1.1.21)_CDS
5239651_5239983-LSU_ribosomal_protein_L22p_(L17e)_CDS
2769499_2769828-Possible_carboxymuconolactone_decarboxylase_family_protein_(EC_4.1.1.44)_C
3694926_3695642-hypothetical_protein_CDS
45956_46417-hypothetical_protein_CDS
5635953_5637359-Adenylosuccinate_lyase_(EC_4.3.2.2)_@_SAICAR_lyase_(EC_4.3.2.2)_CDS
1243822_1245042-Broad-specificity_amino_acid_ABC_transporter,_substrate-binding_protein_CDS
1891719_1892396-Ribosomal_silencing_factor_RsfA_CDS
1289506_1290108-NAD(P)H_dehydrogenase_(quinone),_Type_IV_(EC_1.6.5.2)_CDS
5456438_5457808-NAD-specific_glutamate_dehydrogenase_(EC_1.4.1.2);_NADP-specific_glutamate_
5121172_5122200-Ferric_iron_ABC_transporter,_iron-binding_protein_CDS
1518633_1519517-Thymidylate_synthase_(EC_2.1.1.45)_CDS

406306_408102-Long_chain_acyl-CoA_dehydrogenase_[fadN-fadA-fadE_operon]_(EC_1.3.8.8)_CDS
1240005_1240925-Inositol-1-monophosphatase_(EC_3.1.3.25)_CDS
4691051_4691371-Glutaredoxin-related_protein_CDS
1107215_1108267-Phosphoribosylformylglycinamidine_cyclo-ligase_(EC_6.3.3.1)_CDS
3528062_3529849-Acetolactate_synthase_large_subunit_(EC_2.2.1.6)_CDS
5541482_5542252-Chromosome_(plasmid)_partitioning_protein_ParA_CDS
3098787_3099572-Methionine_ABC_transporter_substrate-binding_protein_CDS
4075164_4075772-ATP-dependent_Clp_protease_proteolytic_subunit_ClpP_(EC_3.4.21.92)_CDS
2744994_2746088-Dihydroorotate_dehydrogenase_(quinone)_(EC_1.3.5.2)_CDS
4186929_4188899-DNA_topoisomerase_IV_subunit_B_(EC_5.99.1.3)_CDS
5138053_5139174-L-asparaginase_(EC_3.5.1.1)_CDS
3075775_3076533-hypothetical_protein_CDS
5247520_5247897-SSU_ribosomal_protein_S12p_(S23e)_CDS
847388_847714-hypothetical_protein_CDS
526827_527987-2-keto-3-deoxy-D-arabino-heptulosonate-7-_phosphate_synthase_I_alpha_(EC_2.5.
145536_145904-LSU_ribosomal_protein_L14p_(L23e)_CDS
5595442_5596419-hypothetical_protein_CDS
5818773_5819327-N5-carboxyaminoimidazole_ribonucleotide_mutase_(EC_5.4.99.18)_CDS
2468017_2468718-Transcriptional_regulator,_GntR_family_CDS
5960683_5961615-Esterase/lipase_CDS
3666387_3667640-Tol-Pal_system_beta_propeller_repeat_protein_TolB_CDS
1120556_1121215-Rrf2-linked_NADH-flavin_reductase_CDS
5012288_5014051-Acetoacetyl-CoA_synthetase_[leucine]_(EC_6.2.1.16)_CDS
4555315_4556025-Two-component_transcriptional_response_regulator,_OmpR_family_CDS
5724664_5725671-Alcohol_dehydrogenase_(EC_1.1.1.1)_CDS
5850317_5852509-Malate_synthase_G_(EC_2.3.3.9)_CDS
1974589_1976820-Isocitrate_dehydrogenase_[NADP]_(EC_1.1.1.42);_Monomeric_isocitrate_dehydr
5076165_5076992-Flagellar_assembly_protein_FliH_CDS
3463205_3467215-Phosphoribosylformylglycinamidine_synthase,_synthetase_subunit_(EC_6.3.5.3)_
5167542_5168552-BUG/TctC_family_periplasmic_protein_CDS
5607104_5608264-Succinyl-CoA_ligase_[ADP-forming]_beta_chain_(EC_6.2.1.5)_CDS
5252319_5253329-Porphobilinogen_synthase_(EC_4.2.1.24)_CDS
4294124_4295377-NADH-ubiquinone_oxidoreductase_chain_D_(EC_1.6.5.3)_CDS
5283978_5284697-Orotate_phosphoribosyltransferase_(EC_2.4.2.10)_CDS
5200758_5201135-LSU_ribosomal_protein_L7p/L12p_(P1/P2)_CDS
3039964_3041010-Methionine_ABC_transporter_ATP-binding_protein_CDS
2436020_2436685-Maleylacetoacetate_isomerase_(EC_5.2.1.2)_@_Glutathione_S-transferase,_zeta
2746996_2747307-ElaB_protein_CDS
511392_512621-Cell_division_protein_FtsA_CDS
435186_435923-Glutamate/aspartate_ABC_transporter,_ATP-binding_protein_GltL_(TC_3.A.1.3.4)_
5987864_5988655-Oxidoreductase,_short-chain_dehydrogenase/reductase_family_CDS
2454971_2455819-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate_N-succinyltransferase_(EC_2.3.1.11
5768577_5769575-NAD-dependent_glyceraldehyde-3-phosphate_dehydrogenase_(EC_1.2.1.12)_CD
3830850_3832586-putative_carboxypeptidase_CDS
5529707_5530534-hypothetical_protein_CDS
1500535_1501425-HflC_protein_CDS
5201172_5201696-LSU_ribosomal_protein_L10p_(P0)_CDS
1659299_1659706-Protein_GlcG_CDS
3912835_3914388-Fumarate_hydratase_class_I,_aerobic_(EC_4.2.1.2)_CDS
4775721_4776932-Acetyl-CoA_acetyltransferase_(EC_2.3.1.9)_@_3-oxoadipyl-CoA_thiolase_(EC_2.3
896548_897480-Electron_transfer_flavoprotein,_alpha_subunit_CDS
5659218_5659550-Protein_translocase_subunit_YajC_CDS

760444_760809-Probable_5-carboxymethyl-2-hydroxymuconate_delta_isomerase_CDS
5268133_5269176-Rod_shape-determining_protein_MreB_CDS
2669619_2670143-Cytochrome_c_oxidase_polypeptide_II_(EC_1.9.3.1)_CDS
4873885_4875327-2,5-dioxovalerate_dehydrogenase_(EC_1.2.1.26)_CDS
396992_397666-Acetyltransferase_(isoleucine_patch_superfamily)_CDS
1049775_1050932-Nucleoside_ABC_transporter,_substrate-binding_protein_CDS
5650389_5651048-Probable_lipoprotein_YiaD_CDS
1191477_1191947-Aerobic_carbon_monoxide_dehydrogenase_(quinone),_small_chain_(EC_1.2.5.3)
124685_125485-Indole-3-glycerol_phosphate_synthase_(EC_4.1.1.48)_CDS
2990400_2992340-hypothetical_protein_CDS
4795779_4796861-Type_IV_pilus_biogenesis_protein_PilM_CDS
5241418_5242041-LSU_ribosomal_protein_L4p_(L1e)_CDS
2836663_2837784-Branched-chain_amino_acid_ABC_transporter,_substrate-binding_protein_LivJ_(
3365976_3368561-Arginine_decarboxylase_(EC_4.1.1.19);_Ornithine_decarboxylase_(EC_4.1.1.17);_
736780_737322-hypothetical_protein_CDS
4981133_4982119-TRAP-type_transport_system,_periplasmic_component,_predicted_N-acetylneura
4378926_4380029-GTP-binding_protein_Era_CDS
3828795_3830636-ATP-dependent_RNA_helicase_RhlE_(EC_3.6.4.13)_CDS
4714639_4715250-Stringent_starvation_protein_A_CDS
2741208_2743259-Oligopeptidase_A_(EC_3.4.24.70)_CDS
1023805_1024716-2-hydroxy-3-oxopropionate_reductase_(EC_1.1.1.60)_CDS
1665021_1667312-Ferrichrome-iron_receptor_CDS
3815830_3817236-Multicopper_oxidase_CDS
260995_262266-Cyclopropane-fatty-acyl-phospholipid_synthase_(EC_2.1.1.79)_CDS
4226936_4227943-33_kDa_chaperonin_HslO_CDS
1097698_1098894-N-acetylornithine_aminotransferase_(EC_2.6.1.11)_CDS
6018377_6020500-hypothetical_protein_CDS
3908879_3910270-Fumarate_hydratase_class_II_(EC_4.2.1.2)_CDS
4963383_4964210-5,10-methylenetetrahydrofolate_reductase_(EC_1.5.1.20)_CDS
2137869_2139215-Cell_division_protein_CDS
337786_338220-Thioredoxin_2_CDS
3335741_3337600-Dihydroxy-acid_dehydratase_(EC_4.2.1.9)_CDS
5757598_5758023-Ferric_uptake_regulation_protein_FUR_CDS
736386_736706-Osmotically_inducible_protein_Y_CDS
3400373_3402496-Translation_elongation_factor_G_CDS
5221915_5222781-ATP_synthase_gamma_chain_(EC_3.6.3.14)_CDS
4290134_4292251-NADH-ubiquinone_oxidoreductase_chain_G_(EC_1.6.5.3)_CDS
3539369_3541123-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
744920_745381-Protein-export_protein_SecB_(maintains_pre-export_unfolded_state)_CDS
1814991_1815497-transport-associated_CDS
4746229_4746972-Phosphoribosylformimino-5-aminoimidazole_carboxamide_ribotide_isomerase_(
5530581_5531204-FOG:_TPR_repeat,_SEL1_subfamily_CDS
5822074_5823024-FIG000875:_Thioredoxin_domain-containing_protein_EC-YbbN_CDS
3328483_3328926-Universal_stress_protein_family_CDS
4926458_4927225-Lactam_utilization_protein_LamB_CDS
5782381_5783445-Fructose-bisphosphate_aldolase_class_II_(EC_4.1.2.13)_CDS
4296027_4296506-NADH-ubiquinone_oxidoreductase_chain_B_(EC_1.6.5.3)_CDS
45220_45966-Acetoacetyl-CoA_reductase_(EC_1.1.1.36)_CDS
3665792_3666319-Tol-Pal_system_peptidoglycan-associated_lipoprotein_PAL_CDS
4991564_4991701-hypothetical_protein_CDS
2744297_2744995-Ribose-5-phosphate_isomerase_A_(EC_5.3.1.6)_CDS
1194403_1195188-Aerobic_carbon_monoxide_dehydrogenase_(quinone),_medium_chain_(EC_1.2.5

4194635_4195531-4-hydroxy-tetrahydrodipicolinate_synthase_(EC_4.3.3.7)_CDS
1889223_1890515-Phosphoribosylamine--glycine_ligase_(EC_6.3.4.13)_CDS
1457804_1458637-protein_of_unknown_function_DUF306,_Meta_and_HslJ_CDS
743983_744390-Rhodanese-related_sulfurtransferase_YibN_CDS
3872515_3873465-3-hydroxyacyl-CoA_dehydrogenase_CDS
1480091_1480957-Murein_hydrolase_activator_NlpD_CDS
1680415_1681467-Phenylalanyl-tRNA_synthetase_alpha_chain_(EC_6.1.1.20)_CDS
151602_152006-SSU_ribosomal_protein_S11p_(S14e)_CDS
5507026_5507448-universal_stress_protein,_UspA_family_CDS
5220471_5221880-ATP_synthase_beta_chain_(EC_3.6.3.14)_CDS
590572_591876-Glutamate-1-semialdehyde_2,1-aminomutase_(EC_5.4.3.8)_CDS
1169965_1171080-Uncharacterized_protein_EC-HemX_CDS
4292275_4293639-NADH-ubiquinone_oxidoreductase_chain_F_(EC_1.6.5.3)_CDS
1626893_1627540-Phosphoadenylyl-sulfate_reductase_[thioredoxin]_(EC_1.8.4.8)_CDS
1561140_1563455-Outer_membrane_protein_assembly_factor_YaeT_CDS
5238346_5238762-LSU_ribosomal_protein_L16p_(L10e)_CDS
3781517_3783076-photolyase_protein_family_CDS
2299849_2300772-Transcriptional_regulator,_LysR_family_CDS
4360948_4361823-Acetyl-coenzyme_A_carboxyl_transferase_beta_chain_(EC_6.4.1.2)_CDS
1979005_1980267-Isocitrate_dehydrogenase_[NADP]_(EC_1.1.1.42)_CDS
1391518_1392507-Malate_dehydrogenase_(EC_1.1.1.37)_CDS
4985490_4991426-Excinuclease_ABC_subunit_A,_dimeric_form_CDS
5985694_5986500-Ribulose-5-phosphate_4-epimerase_and_related_epimerases_and_aldolases_CD
1494226_1494903-UPF0070_protein_YfgM_CDS
2375470_2376945-Inosine-5'-monophosphate_dehydrogenase_(EC_1.1.1.205)_/_CBS_domain_CDS
5783659_5785335-Long-chain-fatty-acid--CoA_ligase_(EC_6.2.1.3)_CDS
153967_154350-LSU_ribosomal_protein_L17p_CDS
2005905_2007428-Methylmalonate-semialdehyde_dehydrogenase_(EC_1.2.1.27)_CDS
5241107_5241421-LSU_ribosomal_protein_L23p_(L23Ae)_CDS
2881992_2884418-Formate_dehydrogenase_O_alpha_subunit_(EC_1.2.1.2)_@_selenocysteine-cont
5573088_5574209-DNA_polymerase_III_beta_subunit_(EC_2.7.7.7)_CDS
1581156_1583078-Cell_division-associated,_ATP-dependent_zinc_metalloprotease_FtsH_CDS
29576_30934-Metallo-beta-lactamase_family_protein,_RNA-specific_CDS
1767716_1768807-Outer_membrane_porin_protein_32_precursor;_putative_3-hydroxyphenylpropi
5551778_5552965-3-ketoacyl-CoA_thiolase_(EC_2.3.1.16)_@_Acetyl-CoA_acetyltransferase_(EC_2.3
1191981_1194368-Aerobic_carbon_monoxide_dehydrogenase_(quinone),_large_chain_(EC_1.2.5.3)
4764425_4765234-ABC_transporter,_substrate-binding_protein_(cluster_3,_basic_aa/glutamine/opi
5225463_5225714-ATP_synthase_F0_sector_subunit_c_(EC_3.6.3.14)_CDS
2440093_2441274-Acetyl-CoA_acetyltransferase_(EC_2.3.1.9)_CDS
4329525_4330949-Threonine_synthase_(EC_4.2.3.1)_CDS
5978809_5979603-Enoyl-CoA_hydratase_(EC_4.2.1.17)_CDS
2975996_2977168-Sulfate_and_thiosulfate_binding_protein_CysP_CDS
1967318_1967905-Superoxide_dismutase_[Fe]_(EC_1.15.1.1)_CDS
402018_402737-Two-component_transcriptional_response_regulator,_LuxR_family_CDS
3112715_3114856-Outer_membrane_(iron.B12.siderophore.hemin)_receptor_CDS
1302700_1303830-ABC-type_branched-chain_amino_acid_transport_systems,_periplasmic_compon
744462_744719-Glutaredoxin_3_(Grx3)_CDS
4860683_4863253-Cyanophycin_synthase_(EC_6.3.2.29)(EC_6.3.2.30)_CDS
732492_733844-FIG015287:_Zinc_protease_CDS
1509562_1510977-Glutamine_synthetase_type_I_(EC_6.3.1.2)_CDS
1110078_1111643-Poly(A)_polymerase_(EC_2.7.7.19)_CDS
284229_284894-FIG00350035:_hypothetical_protein_CDS

693437_695011-Cytochrome_c_oxidase_polypeptide_II_(EC_1.9.3.1)_CDS
2694693_2696585-Propionate--CoA_ligase_(EC_6.2.1.17)_CDS
5758169_5758714-Outer_membrane_beta-barrel_assembly_protein_BamE_CDS
5967089_5968069-NADPH_dependent_aldo-keto_reductase_=>_YajO_CDS
4075906_4077216-Cell_division_trigger_factor_(EC_5.2.1.8)_CDS
2910239_2912449-TonB-dependent_receptor_CDS
5548874_5550562-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
1898170_1899990-3-methylmercaptopropionyl-CoA_dehydrogenase_(DmdC)_CDS
3698906_3699202-ElaB_protein_CDS
5225760_5226623-ATP_synthase_F0_sector_subunit_a_(EC_3.6.3.14)_CDS
1531392_1532489-Chorismate_synthase_(EC_4.2.3.5)_CDS
338266_339300-Alcohol_dehydrogenase_(EC_1.1.1.1)_CDS
1623889_1624218-4Fe-4S_dicluster_fused_with_DUF3470_CDS
4398464_4399504-LSU_rRNA_pseudouridine(955/2504/2580)_synthase_(EC_5.4.99.24)_CDS
1395034_1397619-Aconitate_hydratase_2_(EC_4.2.1.3)_@_2-methylisocitrate_dehydratase_(EC_4.2
133735_134703-Hydrogen_peroxide-inducible_genes_activator_=>_OxyR_CDS
4391628_4392608-3-oxoacyl-[acyl-carrier-protein]_synthase,_KASIII_(EC_2.3.1.180)_CDS
1416469_1419372-Aconitate_hydratase_(EC_4.2.1.3)_@_2-methylisocitrate_dehydratase_(EC_4.2.1
5930292_5931281-Flp_pilus_assembly_protein_RcpC/CpaB_CDS
1681634_1684087-Phenylalanyl-tRNA_synthetase_beta_chain_(EC_6.1.1.20)_CDS
3369217_3370137-Protein_QmcA_(possibly_involved_in_integral_membrane_quality_control)_CDS
1113352_1114398-2-polyprenylphenol_hydroxylase_and_related_flavodoxin_oxidoreductases_/_CD
5865014_5865694-Lipopolysaccharide_export_system_protein_LptA_CDS
148465_148986-SSU_ribosomal_protein_S5p_(S2e)_CDS
1304112_1305068-putative_oxidoreductase,_nitronate_monooxygenase_family_CDS
172520_173563-Twitching_motility_protein_PilT_CDS
2353518_2354996-Prolidase_(EC_3.4.13.9)_CDS
3819204_3820181-hypothetical_protein_CDS
4718306_4718740-Large-conductance_mechanosensitive_channel_CDS
2070006_2071202-Aromatic-amino-acid_aminotransferase_(EC_2.6.1.57)_CDS
5856722_5857168-Putative_inner_membrane_protein_CDS
4438729_4444740-Large_extracellular_alpha-helical_protein_CDS
3071525_3073756-Inactive_(p)ppGpp_3'-pyrophosphohydrolase_domain_/_GTP_pyrophosphokinas
2684419_2685705-CzcABC_family_efflux_RND_transporter,_membrane_fusion_protein_CDS
5240280_5241104-LSU_ribosomal_protein_L2p_(L8e)_CDS
2729142_2730980-Dihydrolipoamide_dehydrogenase_of_pyruvate_dehydrogenase_complex_(EC_1.
2888678_2890603-Selenocysteine-specific_translation_elongation_factor_CDS
376927_377997-dTDP-glucose_4,6-dehydratase_(EC_4.2.1.46)_CDS
3038841_3039149-hypothetical_protein_CDS
671860_672813-hypothetical_protein_CDS
1197530_1198177-Carbon_monoxide_oxidation_accessory_protein_CoxG_CDS
169465_170118-Uncharacterized_protein_YraP_CDS
2850509_2851507-hypothetical_protein_CDS
1771516_1772538-Fructose-1,6-bisphosphatase,_type_I_(EC_3.1.3.11)_CDS
2884431_2885360-Formate_dehydrogenase_O_beta_subunit_(EC_1.2.1.2)_CDS
568409_569188-3-methylthioacryloyl-CoA_hydratase_2_(DmdD2)_CDS
5947340_5948020-Ribulose-phosphate_3-epimerase_(EC_5.1.3.1)_CDS
584821_586419-IMP_cyclohydrolase_(EC_3.5.4.10)_/_Phosphoribosylaminoimidazolecarboxamide_f
5361481_5362734-Glycolate_dehydrogenase_(EC_1.1.99.14),_iron-sulfur_subunit_GlcF_CDS
4791835_4793946-Type_IV_pilus_biogenesis_protein_PilQ_CDS
2671177_2671788-Superoxide_dismutase_[Cu-Zn]_precursor_(EC_1.15.1.1)_CDS
4708805_4710034-Glutamate_N-acetyltransferase_(EC_2.3.1.35)_@_N-acetylglutamate_synthase_(

1444049_1445728-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
3322528_3323439-Cytochrome_c_oxidase_(cbb3-type)_subunit_CcoP_(EC_1.9.3.1)_CDS
5315785_5316558-Ferredoxin--NADP(+)_reductase_(EC_1.18.1.2)_@_Flavodoxin--NADP(+)_reductas
4174134_4174610-Bacterioferritin_(EC_1.16.3.1)_CDS
4336470_4338248-Predicted_ATPase_related_to_phosphate_starvation-inducible_protein_PhoH_CD
3578138_3578692-hypothetical_protein_CDS
4658897_4660702-Aspartyl-tRNA_synthetase_(EC_6.1.1.12)_@_Aspartyl-tRNA(Asn)_synthetase_(EC
1390497_1391288-Transcriptional_regulator,_GntR_family_CDS
4276228_4277424-Broad-specificity_amino_acid_ABC_transporter,_substrate-binding_protein_CDS
1818807_1819463-ABC-type_antimicrobial_peptide_transport_system,_ATPase_component_CDS
4927246_4927908-Pyrrolidone-carboxylate_peptidase_(EC_3.4.19.3)_CDS
3859649_3861331-SSU_ribosomal_protein_S1p_CDS
5224405_5224944-ATP_synthase_delta_chain_(EC_3.6.3.14)_CDS
2373013_2374629-GMP_synthase_[glutamine-hydrolyzing],_amidotransferase_subunit_(EC_6.3.5.2)
4578687_4579445-Transcriptional_regulator,_GntR_family_CDS
5222800_5224359-ATP_synthase_alpha_chain_(EC_3.6.3.14)_CDS
4351177_4352253-3-isopropylmalate_dehydrogenase_(EC_1.1.1.85)_CDS
1494906_1496081-Outer_membrane_beta-barrel_assembly_protein_BamB_CDS
4827227_4828297-Outer_membrane_porin_protein_32_precursor_CDS
3541262_3541789-Inorganic_pyrophosphatase_(EC_3.6.1.1)_CDS
5810771_5811442-Outer_membrane_protein_W_precursor_CDS
3341648_3343474-GTP-binding_protein_TypA/BipA_CDS
5170315_5171469-Alkylhydroperoxidase_AhpD_domain_protein_CDS
5003980_5006016-Methylcrotonyl-CoA_carboxylase_biotin-containing_subunit_(EC_6.4.1.4)_CDS
737816_739165-Two-component_system_sensor_histidine_kinase_CDS
5633610_5634365-Membrane_protein_TerC,_possibly_involved_in_tellurium_resistance_CDS
4556106_4557806-putative_peptidoglycan_binding_protein_CDS
4332394_4333776-Homoserine_dehydrogenase_(EC_1.1.1.3)_CDS
4509283_4509969-Virulence_factor_mviM_CDS
3011777_3012352-hypothetical_protein_CDS
574908_576002-GTP-binding_and_nucleic_acid-binding_protein_YchF_CDS
2097657_2099036-Gluconate_2-dehydrogenase_(EC_1.1.99.3),_membrane-bound,_cytochrome_c_C
4586345_4587523-Benzoate_ABC_transporter,_substrate-binding_protein_CDS
4784452_4785417-Transaldolase_(EC_2.2.1.2)_CDS
2688983_2689693-Protein-L-isoaspartate_O-methyltransferase_(EC_2.1.1.77)_CDS
4342817_4344760-Chaperone_protein_DnaK_CDS
5219902_5220318-ATP_synthase_epsilon_chain_(EC_3.6.3.14)_CDS
532297_532746-Biotin_carboxyl_carrier_protein_of_acetyl-CoA_carboxylase_CDS
5674437_5675438-D-arabinose-5-phosphate_isomerase_(EC_5.3.1.13)_CDS
1048435_1049580-Nucleoside_ABC_transporter,_substrate-binding_protein_CDS
5213124_5213990-Cytochrome_c5_CDS
3521707_3523245-2-isopropylmalate_synthase_(EC_2.3.3.13)_CDS
4394277_4394831-FIG01269488:_protein,_clustered_with_ribosomal_protein_L32p_CDS
4136585_4137850-Aspartokinase_(EC_2.7.2.4)_CDS
5037227_5038414-Isovaleryl-CoA_dehydrogenase_(EC_1.3.8.4)_CDS
2972774_2973901-Sulfate_and_thiosulfate_import_ATP-binding_protein_CysA_(EC_3.6.3.25)_CDS
5753150_5753623-PTS_IIA-like_nitrogen-regulatory_protein_PtsN_CDS
4520947_4523802-Isoleucyl-tRNA_synthetase_(EC_6.1.1.5)_CDS
4590641_4591966-InterPro_IPR005806_COGs_COG2146_CDS
1256694_1258115-TldE_protein,_part_of_TldE/TldD_proteolytic_complex_CDS
1535018_1536265-Serine_hydroxymethyltransferase_(EC_2.1.2.1)_CDS
1678874_1679431-Translation_initiation_factor_3_CDS

842342_843250-UPF0701_protein_YicC_CDS
195625_196887-Cobalt/zinc/cadmium_efflux_RND_transporter,_outer_membrane_protein_CzcC_CD
1941526_1941723-hypothetical_protein_CDS
1435212_1435916-Tol-Pal_system_protein_TolQ_CDS
5931285_5932649-Type_II/IV_secretion_system_secretin_RcpA/CpaC,_associated_with_Flp_pilus_as
5384218_5385213-Outer_membrane_porin_CDS
496767_497696-16S_rRNA_(cytosine(1402)-N(4))-methyltransferase_(EC_2.1.1.199)_CDS
3076837_3077568-Two-component_system_response_regulator_OmpR_CDS
5203176_5203763-Transcription_antitermination_protein_NusG_CDS
571197_571961-Thiol:disulfide_interchange_protein_DsbC_CDS
2969255_2970160-Class_A_beta-lactamase_(EC_3.5.2.6)_CDS
5033337_5034521-3-ketoacyl-CoA_thiolase_(EC_2.3.1.16)_CDS
5224957_5225427-ATP_synthase_F0_sector_subunit_b_(EC_3.6.3.14)_CDS
3475119_3477017-Peptidyl-prolyl_cis-trans_isomerase_PpiD_(EC_5.2.1.8)_CDS
4158982_4161372-Phosphoenolpyruvate_synthase_(EC_2.7.9.2)_CDS
2701468_2703213-Predicted_metal-dependent_hydrolase_with_the_TIM-barrel_fold_CDS
4344861_4345991-Chaperone_protein_DnaJ_CDS
4822901_4824544-Heat_shock_protein_60_kDa_family_chaperone_GroEL_CDS
2604930_2605901-Copper_resistance_protein_B_CDS
215874_216722-Formyltetrahydrofolate_deformylase_(EC_3.5.1.10)_CDS
5570372_5572939-DNA_gyrase_subunit_B_(EC_5.99.1.3)_CDS
1669047_1669847-Uncharacterized_protein_CC_3061_CDS
4109928_4111115-ABC_transporter,_substrate-binding_protein_(cluster_4,_leucine/isoleucine/valin
2407692_2409470-Electron_transfer_flavoprotein-ubiquinone_oxidoreductase_(EC_1.5.5.1)_CDS
1672608_1672916-SWIB/MDM2_domain-containing_proteins_CDS
2807269_2809470-Catalase-peroxidase_KatG_(EC_1.11.1.21)_CDS
985763_986917-Peptidase_S1,_chymotrypsin:PDZ/DHR/GLGF_domain_precursor_CDS
4699508_4699819-LSU_ribosomal_protein_L21p_CDS
4716124_4717539-Ubiquinol-cytochrome_C_reductase,_cytochrome_B_subunit_(EC_1.10.2.2)_CDS
3102745_3104667-Uncharacterized_protein_YeaG_CDS
384807_386921-Glycyl-tRNA_synthetase_beta_chain_(EC_6.1.1.14)_CDS
50366_51445-HlyD-like_membrane_fusion_protein_YhiI_CDS
2345855_2347297-hypothetical_protein_CDS
1253770_1254978-Broad-specificity_amino_acid_ABC_transporter,_substrate-binding_protein_CDS
1387679_1389484-Succinate_dehydrogenase_flavoprotein_subunit_(EC_1.3.5.1)_CDS
3565936_3573498-Phage_tail_tip,_host_specificity_protein_J_CDS
5008621_5010228-Methylcrotonyl-CoA_carboxylase_carboxyl_transferase_subunit_(EC_6.4.1.4)_CD
5979600_5981171-Acetyl-CoA_acetyltransferase_CDS
127871_128725-lipopolysaccharide_biosynthesis_CDS
3116778_3117833-CobW_GTPase_involved_in_cobalt_insertion_for_B12_biosynthesis_CDS
6016818_6018371-Acetyl-CoA_acetyltransferase_CDS
3347799_3349286-Transcription_termination_protein_NusA_CDS
493947_494576-ATP-dependent_protease_subunit_HslV_(EC_3.4.25.2)_CDS
2030674_2031843-UDP-glucose_6-dehydrogenase_(EC_1.1.1.22)_CDS
2868025_2868840-Outer_membrane_beta-barrel_assembly_protein_BamD_CDS
4547856_4549601-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
1028178_1028762-Uncharacterized_lipoprotein_Bmul_4930_CDS
5460383_5461321-Branched-chain_amino_acid_aminotransferase_(EC_2.6.1.42)_CDS
47597_50362-Ribosome-associated_ATPase_RbbA_CDS
1688020_1690158-Type_I_secretion_system_ATPase_CDS
3526323_3527339-Ketol-acid_reductoisomerase_(NADP(+))_(EC_1.1.1.86)_CDS
4959864_4960229-Iron-sulfur_cluster_insertion_protein_ErpA_CDS

2073672_2074208-Iron-sulfur_cluster_regulator_IscR_CDS
1773596_1776298-Membrane_alanine_aminopeptidase_N_(EC_3.4.11.2)_CDS
2562260_2563537-Cobalt/zinc/cadmium_efflux_RND_transporter,_outer_membrane_protein_CzcC_
4790022_4791113-3-dehydroquinate_synthase_(EC_4.2.3.4)_CDS
3552768_3554975-DNA_polymerase_III_subunits_gamma_and_tau_(EC_2.7.7.7)_CDS
3882365_3883771-Glutamyl-tRNA_synthetase_(EC_6.1.1.17)_CDS
4195595_4196707-FIG002207:_Probable_transmembrane_protein_CDS
276033_277982-Chaperone_protein_HtpG_CDS
4930731_4931714-TRAP_transporter_solute_receptor,_unknown_substrate_5_CDS
5761604_5763004-Aspartate_ammonia-lyase_(EC_4.3.1.1)_CDS
134767_135303-DNA_protection_during_starvation_protein_CDS
5769718_5771766-Transketolase_(EC_2.2.1.1)_CDS
297286_299067-Acetylornithine_deacetylase/Succinyl-diaminopimelate_desuccinylase_and_related_
5408979_5409758-Histidine_ABC_transporter,_ATP-binding_protein_CDS
5537567_5538853-Glutamate_carboxypeptidase_(EC_3.4.17.11)_CDS
4562071_4563204-CzcABC_family_efflux_RND_transporter,_membrane_fusion_protein_CDS
5204320_5205510-Translation_elongation_factor_Tu_CDS
6021301_6023514-Acyl-CoA_dehydrogenase_CDS
3405470_3406519-Muramoyltetrapeptide_carboxypeptidase_(EC_3.4.17.13)_CDS
977740_978312-Small_HspC2_heat_shock_protein_CDS
3850341_3850988-Outer_membrane_protein_A_precursor_CDS
2232569_2233993-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
5761109_5761486-Ribosome-associated_inhibitor_A_CDS
2733770_2736484-Pyruvate_dehydrogenase_E1_component_(EC_1.2.4.1)_CDS
5211491_5212924-Efflux_transport_system,_outer_membrane_factor_(OMF)_lipoprotein_CDS
2693102_2694490-Phosphoglucomutase_(EC_5.4.2.2)_@_Phosphomannomutase_(EC_5.4.2.8)_CDS
4282443_4283936-NADH-ubiquinone_oxidoreductase_chain_N_(EC_1.6.5.3)_CDS
2881353_2881943-Formate_dehydrogenase_O_alpha_subunit_(EC_1.2.1.2)_@_selenocysteine-cont
4319613_4322225-Chaperone_protein_ClpB_(ATP-dependent_unfoldase)_CDS
5289112_5290761-NAD(P)_transhydrogenase_N-domain_of_subunit_alpha_(EC_1.6.1.2)_/_NAD(P)_
2498125_2499726-L-aspartate_beta-decarboxylase_(EC_4.1.1.12)_CDS
3537168_3538937-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
6020513_6021304-Enoyl-CoA_hydratase_(EC_4.2.1.17)_CDS
4044126_4045004-CoA-transferase_subunit_alpha,_IpdA_CDS
1530524_1530976-CBS_domain_protein_CDS
5927269_5928117-YecA-like_protein_CDS
363848_364969-4-hydroxyphenylpyruvate_dioxygenase_(EC_1.13.11.27)_CDS
1928710_1930269-Cytosol_aminopeptidase_PepA_(EC_3.4.11.1)_CDS
849332_850645-Fumarylacetoacetase_(EC_3.7.1.2)_CDS
3359466_3359987-Superoxide_dismutase_[Cu-Zn]_precursor_(EC_1.15.1.1)_CDS
1006568_1008865-NADP-dependent_malic_enzyme_(EC_1.1.1.40)_CDS
2387727_2388842-Renalase_(EC_1.6.3.5),_oxidases_1,2-dihydro-_and_1,6-dihydro-_beta-NAD(P)H_i
4380719_4381069-Putative_transmembrane_protein_CDS
3851218_3853914-DNA_gyrase_subunit_A_(EC_5.99.1.3)_CDS
1686040_1687563-Type_I_secretion_outer_membrane_protein,_TolC_family_CDS
1172947_1175796-Phosphoenolpyruvate_carboxylase_(EC_4.1.1.31)_CDS
3862201_3863358-Lipopolysaccharide_assembly_protein_LapB_CDS
288211_289059-3-hydroxybutyryl-CoA_dehydrogenase_(EC_1.1.1.157)_CDS
4995171_4995479-Inner_membrane_protein_YjcH,_clustering_with_ActP_CDS
397704_398879-4-keto-6-deoxy-N-Acetyl-D-hexosaminyl-(Lipid_carrier)_aminotransferase_CDS
5577364_5579076-Inner_membrane_protein_translocase_and_chaperone_YidC,_long_form_CDS
2585401_2585745-hypothetical_protein_CDS

3443798_3445075-O-acetylhomoserine_sulfhydrylase_(EC_2.5.1.49)_@_O-succinylhomoserine_sulfh
152832_153830-DNA-directed_RNA_polymerase_alpha_subunit_(EC_2.7.7.6)_CDS
5961612_5963717-hypothetical_protein_CDS
2868893_2870977-DinG_family_ATP-dependent_helicase_YoaA_CDS
4299490_4301733-Polyribonucleotide_nucleotidyltransferase_(EC_2.7.7.8)_CDS
5599605_5600714-RecA_protein_CDS
2482759_2484933-Methylmalonyl-CoA_mutase_(EC_5.4.99.2)_/_B12_binding_domain_of_Methylm
4830138_4831691-Threonine_dehydratase_biosynthetic_(EC_4.3.1.19)_CDS
968107_968451-hypothetical_protein_CDS
5690005_5691432-Periplasmic_chaperone_and_peptidyl-prolyl_cis-trans_isomerase_of_outer_mem
5244624_5246732-Translation_elongation_factor_G_CDS
1385313_1386623-Citrate_synthase_(si)_(EC_2.3.3.1)_CDS
1499132_1500523-HflK_protein_CDS
1882836_1883810-L-threo-3-hydroxyaspartate_ammonia-lyase_(EC_4.3.1.16)_CDS
3891914_3893251-Argininosuccinate_synthase_(EC_6.3.4.5)_CDS
4644872_4645831-Ribose-phosphate_pyrophosphokinase_(EC_2.7.6.1)_CDS
3074839_3075627-3-hydroxybutyrate_dehydrogenase_(EC_1.1.1.30)_CDS
4553934_4555235-Tryptophanyl-tRNA_synthetase_(EC_6.1.1.2)_CDS
188756_190777-TonB-dependent_receptor;_Outer_membrane_receptor_for_ferrienterochelin_and_
5580874_5583183-NADP-dependent_malic_enzyme_(EC_1.1.1.40)_CDS
3344941_3347775-Translation_initiation_factor_2_CDS
4389493_4389732-Acyl_carrier_protein_CDS
608001_609293-Dihydroorotase_(EC_3.5.2.3)_CDS
3292525_3294438-Outer_membrane_vitamin_B12_receptor_BtuB_CDS
41350_42771-Enoyl-CoA_hydratase_/_Phosphate_acetyltransferase_(EC_2.3.1.8)_CDS
2853310_2854365-Cytochrome_O_ubiquinol_oxidase_subunit_II_(EC_1.10.3.-)_CDS
3885432_3886940-Amidophosphoribosyltransferase_(EC_2.4.2.14)_CDS
4710413_4713172-Protein_translocase_subunit_SecA_CDS
2874032_2875459-Dihydrolipoamide_dehydrogenase_of_2-oxoglutarate_dehydrogenase_(EC_1.8.1.
5659639_5661537-Protein_translocase_subunit_SecD_CDS
5192026_5196249-DNA-directed_RNA_polymerase_beta'_subunit_(EC_2.7.7.6)_CDS
4715351_4716106-Ubiquinol-cytochrome_C_reductase,_cytochrome_C1_subunit_CDS
4400054_4403044-Ribonuclease_E_(EC_3.1.26.12)_CDS
1783493_1784434-Thiamin-phosphate_pyrophosphorylase_(EC_2.5.1.3)_CDS
2602997_2604904-Multicopper_oxidase_CDS
5564722_5566002-CzcABC_family_efflux_RND_transporter,_outer_membrane_protein_CDS
5196371_5200483-DNA-directed_RNA_polymerase_beta_subunit_(EC_2.7.7.6)_CDS
2875541_2876779-Dihydrolipoamide_succinyltransferase_component_(E2)_of_2-oxoglutarate_dehy
1189180_1189800-TRAP_dicarboxylate_transporter,_DctQ_subunit,_unknown_substrate_6_CDS
2804461_2805099-Succinyl-CoA:3-ketoacid-coenzyme_A_transferase_subunit_B_(EC_2.8.3.5)_CDS
1871449_1873059-Methyl-accepting_chemotaxis_sensor/transducer_protein_CDS
4274290_4275282-Broad-specificity_amino_acid_ABC_transporter,_permease_protein_2_CDS
304691_305704-Phosphate_starvation-inducible_protein_PhoH,_predicted_ATPase_CDS
4445974_4447422-Argininosuccinate_lyase_(EC_4.3.2.1)_CDS
40554_41306-Oxidoreductase,_short-chain_dehydrogenase/reductase_family_CDS
5278123_5279370-D-3-phosphoglycerate_dehydrogenase_(EC_1.1.1.95)_CDS
51460_52947-Efflux_transport_system,_outer_membrane_factor_(OMF)_lipoprotein_CDS
1893730_1895217-Ribonuclease_G_CDS
1615131_1616393-Transcription_termination_factor_Rho_CDS
5269710_5271200-Aspartyl-tRNA(Asn)_amidotransferase_subunit_A_(EC_6.3.5.6)_@_Glutamyl-tRN
331788_332519-Putative_transmembrane_lipoprotein_CDS
2486056_2487591-Propionyl-CoA_carboxylase_carboxyl_transferase_subunit_(EC_6.4.1.3)_CDS

4150061_4152508-RNA_polymerase_sigma_factor_RpoD_CDS
6015685_6016809-putative_oxidoreductase,_nitronate_monooxygenase_family_CDS
5827420_5830128-Leucyl-tRNA_synthetase_(EC_6.1.1.4)_CDS
4224685_4225971-Enolase_(EC_4.2.1.11)_CDS
3826870_3828531-Energy-dependent_translational_throttle_protein_EttA_CDS
4858341_4860587-Cyanophycin_synthase_(EC_6.3.2.29)(EC_6.3.2.30)_CDS
2496395_2498080-Putative_transport_protein_CDS
2355192_2355641-Universal_stress_protein_family_CDS
3703840_3704391-DNA_protection_during_starvation_protein_CDS
4678560_4679543-BUG/TctC_family_periplasmic_protein_CDS
2851631_2852971-Uncharacterized_MFS-type_transporter_CDS
532871_534229-Biotin_carboxylase_of_acetyl-CoA_carboxylase_(EC_6.3.4.14)_CDS
5238765_5239634-SSU_ribosomal_protein_S3p_(S3e)_CDS
2696852_2697454-Isochorismatase_(EC_3.3.2.1)_CDS
4922420_4924147-Urea_carboxylase_(EC_6.3.4.6)_without_Allophanate_hydrolase_2_domains_CD
2767612_2769372-Hypothetical_protein,_restriction_endonuclease-like_VRR-NUC_domain_CDS
5982335_5984557-Acyl-CoA_dehydrogenase_CDS
4810880_4812067-S-adenosylmethionine_synthetase_(EC_2.5.1.6)_CDS
3254765_3256108-Oxidoreductase_FAD/NAD(P)-binding:Oxidoreductase_FAD-binding_region_precu
1573374_1576625-Carbamoyl-phosphate_synthase_large_chain_(EC_6.3.5.5)_CDS
3893360_3893815-hypothetical_protein_CDS
4071157_4073571-ATP-dependent_protease_La_(EC_3.4.21.53)_Type_I_CDS
2564923_2568096-Cobalt/zinc/cadmium_efflux_RND_transporter,_transmembrane_protein_CzcA_C
5661549_5662505-Protein_translocase_subunit_SecF_CDS
1815582_1816805-Cystathionine_beta-lyase_(EC_4.4.1.8)_CDS
978413_981268-ATP-dependent_Clp_protease_ATP-binding_subunit_PA0459,_ClpC_family_CDS
2383007_2385631-Alanyl-tRNA_synthetase_(EC_6.1.1.7)_CDS
4363516_4365060-Lysyl-tRNA_synthetase_(class_II)_(EC_6.1.1.6)_CDS
80211_81113-hypothetical_protein_APECO1_2271_CDS
5249458_5250096-Hydrolase_PA4440,_alpha/beta_fold_family_CDS
5773727_5775136-Xaa-Pro_aminopeptidase_(EC_3.4.11.9)_CDS
5786998_5787804-Transcriptional_regulator,_IclR_family_CDS
2020794_2022569-Capsular_polysaccharide_export_system_periplasmic_protein_KpsD_CDS
4965832_4967262-Adenosylhomocysteinase_(EC_3.3.1.1)_CDS
1470028_1470720-Serine_esterase_CDS
4550761_4551405-YciO_protein,_TsaC/YrdC_paralog_CDS
2876843_2879722-2-oxoglutarate_dehydrogenase_E1_component_(EC_1.2.4.2)_CDS
594477_596720-twitching_motility_protein_PilJ_CDS
382271_383380-Putative_virion_core_protein_(lumpy_skin_disease_virus)_CDS
631500_631844-hypothetical_protein_CDS
5498815_5499627-Septum_site-determining_protein_MinD_CDS
5465893_5466909-Glycosyl_transferase,_family_2_CDS
5624088_5624801-Type_IV_pilin_PilA_CDS
1214339_1216510-Ferrichrome-iron_receptor_CDS
1156925_1159828-Valyl-tRNA_synthetase_(EC_6.1.1.9)_CDS
2487619_2489667-Propionyl-CoA_carboxylase_biotin-containing_subunit_(EC_6.4.1.3)_CDS
4531392_4532903-Tripartite_tricarboxylate_transporter_TctA_family_CDS
5271351_5272808-Aspartyl-tRNA(Asn)_amidotransferase_subunit_B_(EC_6.3.5.6)_@_Glutamyl-tRN
730725_732158-FIG015547:_peptidase,_M16_family_CDS
5036514_5037176-Carbonic_anhydrase,_beta_class_(EC_4.2.1.1)_CDS
5208319_5211498-RND_efflux_system,_inner_membrane_transporter_CDS
5491212_5492534-Pyrimidine_permease_CDS

2740159_2741013-Methenyltetrahydrofolate_cyclohydrolase_(EC_3.5.4.9)_/_Methylenetetrahydrof
471057_471956-FIG01289198:_hypothetical_protein_CDS
430234_430797-TRAP-type_C4-dicarboxylate_transport_system,_small_permease_component_CDS
771435_772712-Flavocytochrome_c:sulfide_dehydrogenase_CDS
3246710_3249805-CzcABC_family_efflux_RND_transporter,_transmembrane_protein_CDS
4995476_4997209-Acetate_permease_ActP_(cation/acetate_symporter)_CDS
2784468_2786681-hypothetical_protein_CDS
4993195_4994877-Uncharacterized_MFS-type_transporter_CDS
1308794_1310383-Cytochrome_d_ubiquinol_oxidase_subunit_I_(EC_1.10.3.-)_CDS
4295406_4296017-NADH-ubiquinone_oxidoreductase_chain_C_(EC_1.6.5.3)_CDS
3601658_3602725-Phage_recombination_protein_Bet_CDS
4289061_4290137-NADH-ubiquinone_oxidoreductase_chain_H_(EC_1.6.5.3)_CDS
370143_371366-3-oxoacyl-[acyl-carrier-protein]_synthase,_KASI_(EC_2.3.1.41)_CDS
2854428_2856434-Cytochrome_O_ubiquinol_oxidase_subunit_I_(EC_1.10.3.-)_CDS
5589843_5592779-DNA_topoisomerase_III,_Burkholderia_type_(EC_5.99.1.2)_CDS
841651_842292-Guanylate_kinase_(EC_2.7.4.8)_CDS
2599577_2599921-hypothetical_protein_CDS
1124415_1125383-BUG/TctC_family_periplasmic_protein_CDS
433617_434369-Glutamate/aspartate_ABC_transporter,_permease_protein_GltJ_(TC_3.A.1.3.4)_CD
2504603_2505574-BUG/TctC_family_periplasmic_protein_CDS
4960845_4961273-LSU_ribosomal_protein_L13p_(L13Ae)_CDS
5704777_5706222-Tricarballylate_dehydrogenase,_TcuA_CDS
1585503_1587911-Polyphosphate_kinase_(EC_2.7.4.1)_CDS
2223454_2224437-BUG/TctC_family_periplasmic_protein_CDS
873180_874697-Lignostilbene-alpha,beta-dioxygenase_and_related_enzymes_CDS

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0.378696759	0.330147672	NA	0.596537	0.186023	NA	-0.04855	-0.06204
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-1.23128

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0.001842	0.972074	2.492157	0.006348
4.45E-06	2.137716		
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9.36E-05	2.029619	5.028694	2.47E-07
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0.093346			
0.159054			
0.000518	0.139331	0.317552	0.375413

0.079581	0.962758		
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4.64E-06	3.009741	3.744331	9.04E-05
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0.207416	-0.92677		
0.168036	-0.9624	-1.86651	0.030985
0.105822			
0.015512	4.164542	3.60676	0.000155
0.160757			
0.020651	-1.77367	-4.96801	3.38E-07
0.468116			
0.258003	0.003606		
0.010873	-2.30876		
0.105854	-1.51431	-2.45384	0.007067
0.25026			
0.024761	-0.08727	-0.18354	0.427189
0.252692	-0.64449	-1.10921	0.133669
0.15583	-0.7475	-1.82326	0.034132
0.24366			
0.165465			
0.344003			
0.072443			
0.084969	-0.83541	-1.01759	0.154435
0.005117	-0.07366	-0.17804	0.429345
0.261532			
0.355687	1.199866	1.86506	0.031086
0.275909			
0.329785			
0.085351			
0.4506			
0.081502			
	-1.57972		

0.227208			
0.185747			
0.038839	-2.84508	-2.55787	0.005266
6.11E-15			
0.370937	-0.19679	-0.26712	0.394689
0.208988	-0.42879		
0.037929			
0.029296	-1.19242		
0.407419			
0.316272	0.502958	0.446209	0.327723
0.23167	-1.11185		
0.055123			
	0.577044		

Synthesized fragment for construction of pALC1026 (**Bold – RE sites EcoRI, NotI, and HindIII**, *Italics – upstream and downstream homology regions for* CtesDRAFT_PD1902)

GAATT*C*_TGGATTACGAGGGCAAGCGCATCGTGGTCATAGGCTCGGGTGCCACGGCGGCCACGCTGATCCCCAGC_
CTGGCACCGGATGCGGGCCATGTGACCATGCTGCAGCGCTCGCCCACCTTTTTCCTGCCCGCGTCCGAGCATCCG
CTGGTGCCGCTGCTCAAGCCTCTGAATCTGCCCGAGGACTGGTACCACGAAATCATGCGCCGCGCCTTTATCGCAC
GCACCGACGAGATCGTGCAGACCTCCAGGCAGCACCCCGAAGCGATGCGCGCCTTCCTGCTTGGCGAGATCCGCT
CCCATCTGCCAGAGGGCTTCGACATCGATAGGCACTTCAACCCCGGCTACCGCCCCTGGCAGCAGCGCATTGCCG
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TCGATGGCAGCGGCATACAGCTGACCGGCGGCGGGCATCTGGACGCCGACATCATCGTTACTGCCACGGGCTTCA
ATCTCAAGCGGTTCGGCGGCATCGCGTTCAGCGTGGATGACGCGCCGGTGGATTTTCGCGAGCGCATCTCCTACC
GCGGCGTGATGATCGAGGGCTTGCCCAATATGGCCTACACCCAGGGCTACTTCCGCTCCAGCTGGACGCTGCGCT
GCGACCTGGTGTGCGACTGGGTGTGCCGCCTGCTTGCCCATATGCGCGAGCAAGGCCATGCCGAGGTACGGCCC
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CTGCGTGCGCAGGATGCCATGTTCGGCCAGGGCGACCGCCAGCCCTGGAGGCATGACCTGGAGTACGCCGAAGA
GCGCGTGGTTCTGCCTGCCGCATCGCTGCAGGACGATGCCTTGGCCTATCGCTAGGTCCGCCCCCGTATCCGTTC
CCTCACTCTTTGTAACGACAGGAGACTACAAGC**GCGGCCGC**_GTCAACCAACGGGACCTCGTGGGCATGAAGACTT_
GCTTGATGAGCAACGAGTCTCCGTCGGCCTGATGGCAGTAGAAGGTGCGCTGGGCAAACGAACTGCTTGATTGATT
TGCAGAGGGCTGGGCGGCCCCGGCGGGTCTAGGCCCGCCAGCCGACCTACTTTCTTGCGCCGGTGTGCCTGACC
ACCAGAAAGGAGGCAAAGAGCCGGCCCCTACTGCCACGACTCCTTCGCTGCGCTACGGGGTAACCTAAGCCCCAA
GAGCTTGCCGTCACAGGCGTGGGCACAAGGGGCAATACCAGAGCTTCTTTGTCTTTTTGATGGCTGTTATCGCTTTC
TGGATGGGCATTTGAGATTGATTTCGCCATAACTCTTGCTGGCAGCATGAGTTCACCCGTGTGTCAGCGCCTGCGG
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TCGACACCGCTGCTCTCTATGGCTTTGGCGCCAGCGAATCGCTGATCGGCCCTGTGCTCAAGCCAAGCTTGGCACT
GGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTT
TCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAAT
GGCGATAA**GCTAGC**

pALC1026 sequence
CCGGATGAATGTCAGCTACTGGGCTATCTGGACAAGGGAAAACGCAAGCGCAAAGAGAAAGCAGGTAGCT
TGCAGTGGGCTTACATGGCGATAGCTAGACTGGGCGGTTTTATGGACAGCAAGCGAACCGGAATTGCCAGC
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TTCACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAGCGGAACACGTAGAAAGCCAGTCCGC
AGAAACGGTGCTGACC

Synthesized fragment for construction of pALC1022 (**Bold – RE sites EcoRV and XbaI**, *Italics – Ptac promoter + lacO operator*, Underlined – RBS, CAPITAL – PD1902 SEQUENCE)

atatc*a**gtctctatggaggtcaggtatgattactattgacaattaatcatcggctcgtataatgtgatcagacctggaattgtgagcggataacaatt*gttctacgggtaaggggg
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GTTGACAACTAGGGCTCGATAA**tctaga**

pALC1022 sequence
CCAATGATACTGATTTTTAAGGCGACTGATGAGTCGCCTTTTTTTTGTCTAAGAATTCATCAGAAGAACTCGT
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