**Highly expressed and alien gene**

**IMG number IMG annotation Eg number**

**2600256191** Protein-export membrane protein, SecD/SecF family 1.05

**Highly expressed genes**

**IMG number IMG annotation Eg number**

**2600254915** ATP synthase F1 subcomplex beta subunit 1.50

**2600254966** Superfamily II DNA and RNA helicases 1.10

**2600254993** Parvulin-like peptidyl-prolyl isomerase 1.17

**2600255027** DNA-binding protein, YbaB/EbfC family 1.20

**2600255064** Pyruvate:ferredoxin oxidoreductase and related 1.70

2-oxoacid:ferredoxin oxidoreductases, beta subunit

**2600255065** Pyruvate:ferredoxin oxidoreductase and related 1.32

2-oxoacid:ferredoxin oxidoreductases, alpha subunit

**2600255172** Thioredoxin-like proteins and domains 1.10

**2600255235** 5'-deoxy-5'-methylthioadenosine phosphorylase 1.45

**2600255249** Sugar transferases involved in lipopolysaccharide synthesis 1.05

**2600255283** P22 coat protein - gene protein 5 1.12

**2600255291** Vacuolar-type H(+)-translocating pyrophosphatase 1.69

**2600255297** Aspartyl-tRNA synthetase, bacterial type 1.35

**2600255302** Hypothetical protein 1.10

**2600255315** S-adenosylmethionine decarboxylase 1.28

**2600255327** Predicted P-loop-containing kinase 1.01

**2600255352** Chaperone protein DnaK 1.62

**2600255416** NADH dehydrogenase subunit A (EC 1.6.5.3) 1.11

**2600255450** Malate dehydrogenase (NAD) (EC 1.1.1.37) 1.13

**2600255470** Membrane protein insertase, YidC/Oxa1 family, 1.18

C-terminal domain

**2600255524** YtxH-like protein 1.02

**2600255533** Signal peptide peptidase SppA, 36K type 1.05

**2600255566** Outer membrane protein 1.16

**2600255576** Glyceraldehyde-3-phosphate dehydrogenase (NAD+) 1.32

(EC 1.2.1.12)

**2600255586** RNA polymerase sigma factor, sigma-70 family 1.41

**2600255592** Chaperonin GroL 1.86

**2600255626** Ribosomal protein L7/L12 1.43

**2600255627** DNA-directed RNA polymerase subunit beta (EC 2.7.7.6) 1.41

**2600255628** DNA-directed RNA polymerase gamma chain (EC 2.7.7.6) 1.49

**2600255637** Two component transcriptional regulator, LuxR family 1.10

**2600255664** Ribonucleotide reductase, beta subunit 1.14

**2600255681** ATPases with chaperone activity, ATP-binding subunit 1.21

**2600255723** Cbb3-type cytochrome oxidase, subunit 1 1.07

**2600255734** Hypothetical protein 1.08

**2600255835** Flagellar basal body L-ring protein 1.14

**2600255847** Superoxide dismutase 1.30

**2600255852** Ribosomal protein L9 1.41

**2600255862** Protein of unknown function (DUF561) 1.38

**2600255880** Septum site-determining protein MinD 1.07

**2600255892** Ribosomal protein S3, bacterial type 1.52

**2600255895** LSU ribosomal protein L2P 1.40

**2600255900**  Translation elongation factor 1A (EF-1A/EF-Tu) 1.41

**2600255911** Translation elongation factor EF-G 2.00

**2600255941** Rare lipoprotein A 1.24

**2600255966** Ribosomal protein L17 1.31

**2600255967** DNA-directed RNA polymerase, alpha subunit, bacterial 1.23

and chloroplast-type

**2600255975** LSU ribosomal protein L15P 1.34

**2600255977** Ribosomal protein S5, bacterial/organelle type 1.59

**2600256085** Polyribonucleotide nucleotidyltransferase 1.71

**2600256086** SSU ribosomal protein S15P 1.07

**2600256099** Translation elongation factor P 1.21

**2600256132** Phosphopentomutase 1.21

**2600256134** Uncharacterized protein conserved in bacteria 1.04

**2600256170** Uncharacterized conserved protein 1.05

**2600256171** 6-pyruvoyl-tetrahydropterin synthase 1.11

**2600256173** Bacterial regulatory proteins, gntR family 1.23

**2600256207** Enoyl-[acyl-carrier-protein] reductase [NADH] 1.30

(EC 1.3.1.9)

**2600256221** Hypothetical protein 1.16

**2600256238** Ribose-phosphate pyrophosphokinase 1.15

**2600256248** Hypothetical protein 1.28

**2600256265** Aconitase (EC 4.2.1.3) 1.11

**2600256266** Isocitrate dehydrogenase (NADP) (EC 1.1.1.42) 1.34

**2600256282** Peroxiredoxin 1.53

**2600256283**  Ribosomal protein L1, bacterial/chloroplast 1.47

**2600256284** LSU ribosomal protein L11P 1.19

**2600256314** S1 RNA binding domain 1.67

**2600256336** S1 RNA binding domain 1.38

**2600256348** Adenosylhomocysteinase (EC 3.3.1.1) 1.38

**2600256354** Carbon storage regulator, CsrA 1.18

**2600256361** NusA antitermination factor 1.15

**2600256362** Translation initiation factor IF-2 1.24

**2600256385** Bacterial SH3 domain 1.28

**2600256386** Hypothetical protein 1.84

**2600256388** Thioredoxin 1.36

**2600256401** Hypothetical protein 1.08

**2600256411** FKBP-type peptidyl-prolyl cis-trans isomerases 2 1.14

**2600256417** Inosine-5'-monophosphate dehydrogenase 1.06

(EC 1.1.1.205)

**2600256436** Glycosyl hydrolases family 8 1.10

**2600256437** Threonyl-tRNA synthetase (EC 6.1.1.3) 1.02

**2600256466** 6-phosphofructokinase 1.10

**2600256529** LL-diaminopimelate aminotransferase apoenzyme 1.27

(EC 2.6.1.83)

**2600256549** Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase 1.12

subunit C (EC 6.3.5.-)

**2600256550** CTP synthase (EC 6.3.4.2) 1.10

**2600256560** Fe2+/Zn2+ uptake regulation proteins 1.11

**2600256561** Rubrerythrin 1.09

**2600256583** Two component transcriptional regulator, LuxR family 1.12

**2600256588** Nucleoside diphosphate kinase (EC 2.7.4.6) 1.41

**2600256597** Cyanobacterial porin (TC 1.B.23) 1.67

**2600256623** 2-oxoacid:acceptor oxidoreductase, alpha subunit 1.79

**2600256624** 2-oxoacid:acceptor oxidoreductase, beta subunit, 1.41

pyruvate/2-ketoisovalerate family

**2600256651** Flagellar hook-basal body protein 1.17

**2600256660** Biopolymer transport proteins 1.08

**2600256663** Hypothetical protein 1.09

**2600256675** 3-deoxy-D-arabinoheptulosonate-7-phosphate 1.03

synthase (EC 2.5.1.54)

**2600256710** GTP-binding protein TypA/BipA 1.46

**2600256731** Hypothetical protein 1.13

**2600256733** Adenine phosphoribosyltransferase (EC 2.4.2.7) 1.18

**2600256757** ATP synthase F1 subcomplex alpha subunit 1.31

**2600256779** Hemolysin activation/secretion protein 1.23

**2600256821** Phosphate transport regulator 1.05

**2600256833**  Hypothetical protein 1.06

**2600256897** YlqD protein 1.18

**2600256918** Exodeoxyribonuclease VII small subunit (EC 3.1.11.6) 1.06

**2600256944** S-layer homology domain 1.07

**2600256966** RNA polymerase, sigma 28 subunit, SigD/FliA/WhiG 1.38

**2600256998**  Glutaredoxin-related protein 1.14

**2600257077** Cell division protein FtsZ 1.28

**2600257160** Alpha-glucan phosphorylases 1.38

**2600257195** Peroxiredoxin, OsmC subfamily 1.43

**2600257223** Type III secretion system ATPase, FliI/YscN 1.08

**2600257249** Hypothetical protein 1.13

**2600257292** Protein of unknown function (DUF1292) 1.33

**2600257293** Succinyl-CoA synthetase (ADP-forming) beta subun 1.28

(EC 6.2.1.5)

**2600257294** Succinyl-CoA synthetase, alpha subunit 1.27

**2600257316** Ribosomal protein S2, bacterial type 1.79

**2600257317** Translation elongation factor Ts (EF-Ts) 1.15

**2600257354** Hypothetical protein 1.12

**2600257355** Hypothetical protein 1.10

**2600257409** ATP-dependent Clp protease ATP-binding subunit 1.00

ClpX (EC 3.4.21.92)

**2600257410** ATP-dependent Clp protease proteolytic subunit 1.10

ClpP (EC 3.4.21.92)

**2600257411**  Trigger factor 1.48

**2600257427** Succinate dehydrogenase/fumarate reductase, flavoprotein 1.30

subunit

**2600257445** Flagellar basal body rod protein 1.07

**2600257449** Flagellar basal-body rod protein FlgC 1.06

**Alien genes**

**IMG number IMG annotation Eg number**

**2600256772** Hypothetical protein 0.99

**2600255126** Hypothetical protein 0.98

**2600256735** Hypothetical protein 0.92

**2600255443** Hypothetical protein 0.88

**2600257671** Periplasmic protein involved in polysaccharide export 0.88

**2600257031** Hypothetical protein 0.86

**2600257567** Imidazoleglycerol-phosphate synthase 0.86

**2600256774** Beta-lactamase class C and other penicillin binding 0.85

proteins

**2600257020** Hypothetical protein 0.85

**2600257499** Hypothetical protein 0.85

**2600257685** Hypothetical protein 0.85

**2600255194** Hypothetical protein 0.84

**2600255922** FOG: CheY-like receiver 0.84

**2600256485** prepilin-type N-terminal cleavage/methylation domain 0.84

**2600257568** Imidazole glycerol phosphate synthase, glutamine 0.84

amidotransferase subunit

**2600256419** Hypothetical protein 0.83

**2600256973** Hypothetical protein 0.82

**2600257103** Outer membrane protein 0.82

**2600257113** Hypothetical protein 0.82

**2600257585** Transposase and inactivated derivatives 0.82

**2600257699** Conjugal transfer protein TrbH 0.82

**2600257732** AAA ATPase domain/AAA domain 0.82

**2600255868** Hypothetical protein 0.81

**2600257187** Twin arginine targeting (Tat) protein translocase TatC 0.81

**2600257497** Diadenosine tetraphosphate (Ap4A) hydrolase and other 0.81

HIT family hydrolases

**2600257527** Nucleotidyl transferase of unknown function (DUF1814) 0.81

**2600257529** Nucleotidyl transferase of unknown function (DUF1814) 0.81

**2600257563** Methyltransferase domain 0.81

**2600255144** Hypothetical protein 0.80

**2600255224** Hypothetical protein 0.80

**2600255777** TIR domain 0.80

**2600257632** Uncharacterized protein conserved in bacteria 0.80

**2600257676** Glycosyl transferase family 2 0.80

**2600254951** Hypothetical protein 0.79

**2600255590** Hypothetical protein 0.79

**2600255756** Hypothetical protein 0.79

**2600255862** Protein of unknown function (DUF561) 0.79

**2600256409** Domain of unknown function (DUF4145) 0.79

**2600256512** Alginate lyase 0.79

**2600257109** RHS repeat-associated core domain 0.79

**2600257362** Hypothetical protein 0.79

**2600257480** Plasmid encoded RepA protein 0.79

**2600257489** TaqI-like C-terminal specificity domain/ 0.79

Methyltransferase domain

**2600257491** Hypothetical protein 0.79

**2600257570** Hypothetical protein 0.79

**2600257594** Plasmid encoded RepA protein 0.79

**2600257630** Predicted ATP-dependent endonuclease of the OLD family 0.79

**2600257665** Hypothetical protein 0.79

**2600257691** Trypsin-like peptidase domain/PDZ domain 0.79

**2600255719** Hypothetical protein 0.78

**2600257105** RND family efflux transporter, MFP subunit 0.78

**2600257230** Dehydrogenases (flavoproteins) 0.78

**2600257492** Predicted ATPase (AAA+ superfamily) 0.78

**2600257669** Teichoic acid biosynthesis proteins 0.78

**2600255978** Predicted phosphohydrolases 0.77

**2600256525** Hypothetical protein 0.77

**2600256642** Hypothetical protein 0.77

**2600257225** Protein of unknown function (DUF2971) 0.77

**2600257562** Predicted pyridoxal phosphate-dependent enzyme 0.77

apparently involved in regulation of cell wall biogenesis

**2600257599** Domain of unknown function (DUF389) 0.77

**2600257674** Hypothetical protein 0.77

**2600257711** DnaA N-terminal domain 0.77

**2600256983** Peptidase M15 0.76

**2600257091** Hypothetical protein 0.76

**2600257561** Nucleoside-diphosphate-sugar epimerases 0.76

**2600257610** Uncharacterized conserved protein (COG2071) 0.76

**2600257667** Nucleoside-diphosphate-sugar pyrophosphorylase 0.76

involved in lipopolysaccharide biosynthesis/translation

initiation factor 2B

**2600257680** Endoglucanase 0.76

**2600255374** Hypothetical protein 0.75

**2600255506** Predicted phosphohydrolases 0.75

**2600257104** The (Largely Gram-negative Bacterial) 0.75

Hydrophobe/Amphiphile Efflux-1 (HAE1) Family

**2600257228** Predicted naringenin-chalcone synthase 0.75

**2600257508** Hypothetical protein 0.75

**2600257517** Hypothetical protein 0.75

**2600257663** Hypothetical protein 0.75

**2600257672** Uncharacterized protein involved in exopolysaccharide 0.75

biosynthesis

**2600257678** Glycosyltransferase 0.75

**2600255258** Dihydrofolate reductase 0.74

**2600255507** Type II secretion system (T2SS), protein F 0.74

**2600256033** Sugar transferases involved in lipopolysaccharide synthesis 0.74

**2600256720** Hypothetical protein 0.74

**2600257493** Adenine-specific DNA methylase containing a Zn-ribbon 0.74

**2600257537** RND family efflux transporter, MFP subunit 0.74

**2600257646** P-type conjugative transfer protein TrbL 0.74

**2600255269** Hypothetical protein 0.73

**2600257541** HipA-like C-terminal domain/HipA N-terminal domain/ 0.73

HipA-like N-terminal domain

**2600257572** ABC-type multidrug transport system, ATPase and 0.73

permease components

**2600257666** UDP-galactose 4-epimerase (EC 5.1.3.2) 0.73

**2600257677** Glycosyltransferase 0.73

**2600254929** Ankyrin repeats (3 copies) 0.72

**2600255090** Restriction endonuclease S subunits 0.72

**2600255508** Flp pilus assembly protein TadB 0.72

**2600256159** Glycosyltransferase 0.72

**2600257232** Ankyrin repeats (3 copies)/Ankyrin repeats 0.72

**2600255059** Hypothetical protein 0.71

**2600256873** Hypothetical protein 0.71

**2600257088** UvrD-like helicase C-terminal domain/UvrD/REP 0.71

helicase N-terminal domain

**2600257494** Hypothetical protein 0.71

**2600257607** DoxX-like family 0.71

**2600257673** Lipid A core - O-antigen ligase and related enzymes 0.71

**2600257675** Glycosyltransferases involved in cell wall biogenesis 0.71

**2600257686** Predicted ATPase (AAA+ superfamily) 0.71

**2600255060** Hypothetical protein 0.70

**2600255674** Translation factor SUA5 0.70

**2600257601** Trehalose-6-phosphate synthase 0.70

**2600255536** Hypothetical protein 0.68

**2600256155** Hypothetical protein 0.67

**2600256156** Glycosyltransferase 0.69

**2600257209** Ammonium transporter (TC 1.A.11) 0.69

**2600257275** Hypothetical protein 0.69

**2600257516** Type IV secretory pathway, VirB10 components 0.68

**2600256157** Coenzyme F390 synthetase 0.68

**2600256158** Coenzyme F390 synthetase 0.68

**2600256160** Membrane protein involved in the export of O-antigen 0.68

and teichoic acid

**2600256524** Hypothetical protein 0.68

**2600257575** Predicted dehydrogenase 0.68

**2600257231** Predicted membrane protein 0.67

**2600257569** Hypothetical protein 0.67

**2600257369** Hypothetical protein 0.66

**2600257564** Asparagine synthase 0.66

**2600257017** Dolichyl-phosphate-mannose-protein mannosyltransferase 0.64