Rhodopseudomonas palustris operon predictions
50bp maximum intergenic space

>operons_50:RPA0007-kaiC 9442..12875 r
RPA0007:possible sensory transduction histidine kinase
kaiB:circadian clock protein
kaiC:circadian clock protein

>operons_50:RPA0011-fixG,rdxB 14266..18902 r
RPA0011:conserved hypothetical protein
rdxS,fixS:possible fixS
rdxI,fixI:putative cation (heavy metal) transporting
rdxH,fixH:conserved hypothetical protein
fixG,rdxB:4Fe-4S ferredoxin, iron-sulfur binding domain

>operons_50:ccoP,fixP-ccoN,fixN 19019..22475 r
ccoP,fixP:cytochrome-c oxidase fixP chain
ccoQ,fixQ:cytochrome oxidase subunit, small membrane
ccoO,fixO:cytochrome-c oxidase fixO chain
ccoN,fixN:cytochrome-c oxidase fixN chain, heme and copper

>operons_50:RPA0042-RPA0043 48211..50060 r
RPA0042:possible iron-sulfur cluster binding protein
RPA0043:possible glutathione S-transferase

>operons_50:RPA0047-RPA0048 53339..54753 f
RPA0047:conserved hypothetical protein
RPA0048:conserved hypothetical protein

>operons_50:ugpC-ugpA 60587..63410 r
ugpC:ATP-binding component of sn-glycerol 3-phosphate
ugpE:sn-glycerol 3-phosphate transport system,
ugpA:sn-glycerol-3-phosphate transport system

>operons_50:ihfB-RPA0067 73388..74126 f
ihfB:integration host factor beta chain
RPA0067:conserved unknown protein

>operons_50:trpF-trpA 74185..76890 f
trpF:putative N-(5'-phosphoribosyl)anthranilate
trpB:tryptophan synthase beta chain
trpA:tryptophan synthase alpha subunit

>operons_50:accD-folC 77000..79308 f
accD:acetyl-CoA carboxylase carboxyltransferase beta
folC:putative folylpolyglutamate synthase /

>operons_50:RPA0074-RPA0075 79901..86532 r
RPA0074:Possible exonuclease V and helicase activity
RPA0075:conserved hypothetical protein

>operons_50:RPA0078-RPA0079 87900..91963 r
RPA0078:Protein of unknown function UPF0079
RPA0079:possible two-component sensor histidine kinase

>operons_50:dut-coaBC 92150..93951 r

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dut:putative deoxyuridine 5'triphosphate
coaBC:pantothenate metabolism flavoprotein

>operons_50:ubiB-ubiE 94104..96439 r
ubiB:ubiquinone biosynthesis protein AarF, a gene
ubiE:ubiquinone/menaquinone biosynthesis

>operons_50:RPA0093-RPA0094 104575..106136 f
RPA0093:putative transcriptional regulator (TetR family)
RPA0094:hypothetical protein

>operons_50:RPA0095-RPA0096 106266..110564 f
RPA0095:putative multidrug efflux membrane fusion
RPA0096:putative multidrug-efflux transport protein

>operons_50:oppF-oppA 111260..116831 r
oppF:oligopeptide ABC transporter (ATP-binding
oppD:putative oligopeptide ABC transporter
oppC:putative ABC transporter permease protein
oppB:putative dipeptide transport system permease
oppA:putative ABC transporter oligopeptide-binding

>operons_50:RPA0103-RPA0104 116921..119517 r
RPA0103:Cobalamin synthesis protein/P47K
RPA0104:Amidohydrolase

>operons_50:RPA0106-RPA0109 121313..126188 r
RPA0106:possible branched-chain amino acid transport
RPA0107:putative Zn-binding dehydrogenase
RPA0108:Possible benzaldehyde lyase
RPA0109:putative 3-oxoacyl-(acyl carrier ptn) reductase

>operons_50:RPA0111-betB 127104..129412 r
RPA0111:DUF81
betB:putative betaine aldehyde dehydrogenase

>operons_50:rfbC-rmlA 133329..135661 f
rfbC:dTDP-6-deoxy-D-glucose-3,5-epimerase
rmlD:putative dTDP-6-deoxy-L-mannose-dehydrogenase
rmlA:glucose-1-phosphate thymidylyltransferase

>operons_50:cph1-RPA0123 136734..140646 f
cph1:putative cyanobacterial phytochrome 1
RPA0123:possible KTN NAD-binding domain involved with K+

>operons_50:RPA0124-RPA0125 140653..142298 r
RPA0124:possible 3',5'-cyclic-nucleotide
RPA0125:possible 3',5'-cyclic-nucleotide

>operons_50:RPA0126-RPA0129 142363..146605 r
RPA0126:possible sugar binding protein of ABC
RPA0127:putative permease protein of sugar ABC
RPA0128:possible permease protein of sugar ABC
RPA0129:putative sugar binding protein of ABC

>operons_50:RPA0131-RPA0135 147617..153960 r
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RPA0131:ABC sulfate transport system, ATP-binding
RPA0132:ABC sulfonate transport system, permease protein
RPA0133:ABC sulfate transport system, periplasmic
hydC:hydrogenase gamma-fused hydrogenase large and
RPA0135:possible oxidoreductase

>operons_50:RPA0136-cheR2 154100..157768 r
RPA0136:possible methyl accepting chemotaxis protein
cheB2:protein-glutamate methylesterase
cheR2:putative chemotaxis protein methyltransferase

>operons_50:cheW2-RPA0144 160747..163968 r
cheW2:putative chemotaxis signal transduction protein
cheA:putative chemotaxis histidine kinase
cheY2:putative chemotaxis response regulator
RPA0144:Sulfate transporter/antisigma-factor antagonist

>operons_50:RPA0145-RPA0146 164246..165883 f
RPA0145:putative two-component system, response
RPA0146:hypothetical protein

>operons_50:RPA0148-RPA0152 166873..170797 r
RPA0148:conserved hypothetical protein
RPA0149:possible ABC-type iron-siderophore transport
RPA0150:putative ABC transporter, iron, hemin permease
RPA0151:possible iron ABC transporter periplasmic
RPA0152:Protein of unknown function, UPF0066

>operons_50:RPA0154-RPA0156 173675..175608 f
RPA0154:possible MotA/TolQ/ExbB proton channel family
RPA0155:putative tolR/exbD protein
RPA0156:tonB like protein

>operons_50:proA-RPA0165 183222..185168 f
proA:gamma-glutamyl phosphate reductase
RPA0165:possible nicotinate-nucleotide

>operons_50:RPA0167-ctpA 185925..189191 f
RPA0167:DUF163
RPA0168:putative filament-A precursor
ctpA:putative periplasmic carboxyl-terminal

>operons_50:RPA0170-invA1 189342..191125 f
RPA0170:conserved hypothetical protein
invA1:putative dinucleoside polyphosphate hydrolase

>operons_50:RPA0173-invA2 192604..194069 f
RPA0173:putative sugar nucleotide dehydratase
invA2:putative dinucleoside polyphosphate hydrolase

>operons_50:atpA-atpH 197295..199387 r
atpA:putative H+-transporting ATP synthase alpha
atpH:putative H+-transporting ATP synthase delta

>operons_50:RPA0184-sucB 204891..209376 r
RPA0184:hypothetical protein

dldH:dihydrolipoamide dehydrogenase, E3 component of
RPA0186:putative short-chain dehydrogenase/reductase
RPA0187:conserved hypothetical protein
sucB:dihydrolipoamide succinyl transferase

>operons_50:RPA0196-RPA0197 218627..221944 f
RPA0196:putative ABC transporter, ATP-binding protein
RPA0197:possible ABC transporter permeases

>operons_50:RPA0201-acnA 224593..228232 r
RPA0201:conserved hypothetical protein
acnA:aconitate hydratase

>operons_50:cycV,ccmA-cycW,ccmB 228448..229715 f
cycV,ccmA:heme exporter protein A (heme ABC transporter
cycW,ccmB:putative heme exporter protein B (heme ABC

>operons_50:ispZ-ftsY 231999..233560 r
ispZ:possible intracellular septation protein (ispZ
ftsY:putative cell division protein FtsY

>operons_50:RPA0214-RPA0215 240179..240924 r
RPA0214:hypothetical protein
RPA0215:possible general stress protein 26

>operons_50:sdhA-sdhC 242052..244687 r
sdhA:succinate dehydrogenase flavoprotein subunit
sdhD:succinate dehydrogenase cytochrome b small
sdhC:succinate dehydrogenase membrane

>operons_50:rimM-rpsP,S16 268124..268987 r
rimM:putative 16S rRNA processing protein.
rpsP,S16:ribosomal protein S16

>operons_50:RPA0246-romA 271220..272657 f
RPA0246:PilT protein, N-terminal
romA:putative outer membrane protein

>operons_50:bp26-RPA0249 272667..274144 r
bp26:DUF541
RPA0249:hypothetical protein

>operons_50:dapF-RPA0251 274381..276533 f
dapF:diaminopimelate epimerase
RPA0251:MiaB-like tRNA modifying enzyme

>operons_50:RPA0253-gcp 277390..280000 r
RPA0253:DUF589
gpdA:putative glycerol-3-phosphate dehydrogenase
gcp:putative o-sialoglycoprotein endopeptidase (gcp)

>operons_50:RPA0257-RPA0258 280945..284060 f
RPA0257:conserved unknown protein
RPA0258:unknown protein

>operons_50:algJ-RPA0266 292504..295085 r

algJ:possible AlgJ protein, required for
RPA0266:putative alginate o-acetyltransferase AlgI

>operons_50:trx-RPA0268 295679..297303 f
trx:possible thioredoxin
RPA0268:putative Lon family ATP-dependent protease

>operons_50:glnK2-amtB2 302307..304125 f
glnK2:GlnK, nitrogen regulatory protein P-II
amtB2:putative ammonium transporter AmtB

>operons_50:RPA0278-RPA0280 304991..309727 f
RPA0278:putative N-succinyldiaminopimelate
RPA0279:possible FtsK/SpoIIIE family
RPA0280:unknown protein

>operons_50:RPA0282-RPA0283 310879..312054 r
RPA0282:possible transcriptional regulator
RPA0283:putative two-component response regulator

>operons_50:leuS-RPA0288 315572..318752 f
leuS:leucyl-tRNA synthetase
RPA0288:conserved unknown protein

>operons_50:RPA0290-parB 320082..321235 r
RPA0290:hypothetical protein
parB:chromosome partitioning protein, ParB

>operons_50:parA-gidB 321408..322961 r
parA:chromosome partitioning protein, ParA
gidB:putative glucose inhibited division protein B

>operons_50:RPA0298-maf 329001..330445 f
RPA0298:DUF299
maf:putative maf protein

>operons_50:coaE-dnaQ,mutD 330542..331875 f
coaE:putative dephospho-CoA kinase CoaE
dnaQ,mutD:putative DNA polymerase III epsilon chain

>operons_50:RPA0303-RPA0305 332729..335659 f
RPA0303:conserved unknown protein
RPA0304:possible outer membrane lipoprotein GNA33,
RPA0305:possible DNA mismatch repair protein (MutS)

>operons_50:hslU-hslV 335995..338515 r
hslU:heat shock protein HslU, proteasome-related
RPA0307:conserved hypothetical protein
hslV:heat shock protein HslV, proteasome-related

>operons_50:hisB-hisF 338703..342004 f
hisB:imidazoleglycerol-phosphate dehydratase
RPA0310:conserved hypothetical protein
hisH:imidazoleglycerol-phosphate synthase,
hisA:phosphoribosylformimino-5-aminoimidazole
hisF:imidazoleglycerol-phosphate synthase, cyclase

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>operons_50:RPA0319-RPA0320 348387..349264 r
RPA0319:hypothetical protein
RPA0320:autoinducer (acylhomoserine lactone) synthase

>operons_50:RPA0323-RPA0324 351332..352673 r
RPA0323:Protein of unknown function UPF0102
RPA0324:Uroporphyrin-III C/tetrapyrrole

>operons_50:hemN-RPA0328 354870..356649 r
hemN:possible oxygen-independent coproporphyrinogen
RPA0328:Ham1-like protein

>operons_50:RPA0336-RPA0338 364804..366440 f
RPA0336:NADPH-dependent FMN reductase
pyrF:orotidine 5`-phosphate decarboxylase
RPA0338:conserved unknown protein

>operons_50:ogt-RPA0342 369039..370502 r
ogt:possible Ada polyprotein (O6-methylguanine-DNA
RPA0342:conserved hypothetical protein

>operons_50:dcm-RPA0351 378721..381132 f
dcm:possible site-specific DNA-methyltransferase
vsr:putative patch repair protein
RPA0351:hypothetical protein

>operons_50:RPA0354-RPA0355 384654..385384 r
RPA0354:putative pts system phosphocarrier protein HPr
RPA0355:putative pts system permease (IIAMan)

>operons_50:RPA0356-exoS,chvG 385572..387781 r
RPA0356:conserved hypothetical protein
exoS,chvG:two-component sensor histidine kinase

>operons_50:glgC-glgA 416649..419359 f
glgC:glucose-1-phosphate adenylyltransferase
glgA:putative glycogen synthase

>operons_50:RPA0383-RPA0384 419505..420874 f
RPA0383:probable enoyl CoA-hydratase/isomerase
RPA0384:conserved unknown protein

>operons_50:RPA0393-RPA0396 433170..436318 r
RPA0393:PA-phosphatase related phosphoesterase
RPA0394:conserved hypothetical protein
RPA0395:Metal dependent phosphohydrolase, HD region
RPA0396:Cfr family protein

>operons_50:RPA0406-RPA0407 445859..449585 r
RPA0406:conserved unknown protein
RPA0407:possible TonB-dependent receptor (outer membrane

>operons_50:ppa-CPS1,CPS 454277..456330 f
ppa:inorganic pyrophosphatase
CPS1,CPS:putative Gly-X carboxypeptidase YSCS precursor
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>operons_50:RPA0414-RPA0415 457514..458363 r
RPA0414:DUF167
RPA0415:Family of unknown function YGGT

>operons_50:RPA0420-RPA0421 462010..464059 r
RPA0420:conserved hypothetical protein
RPA0421:possible cytochrome P450 hydroxylase superfamily

>operons_50:rpsO-rbfA 478426..480211 r
rpsO:ribosomal protein S15
truB:putative tRNA pseudouridine 55 synthase
rbfA:putative ribosome-binding factor A

>operons_50:infB-RPA0437 480385..483808 r
infB:putative translation initiation factor if-2
RPA0437:DUF448

>operons_50:nusA-RPA0439 483870..486265 r
nusA:putative NusA protein, transcriptional
RPA0439:DUF150

>operons_50:lnt-RPA0447 490161..494368 r
lnt:putative apolipoprotein n-acyltransferase
RPA0445:possible HlyC/CorC family of transporters with
RPA0446:Protein of unknown function UPF0054
RPA0447:possible phoH-like protein

>operons_50:rimI-RPA0452 497301..498504 r
rimI:putative RimI protein, peptide
RPA0452:Glycoprotease (M22) metalloprotease

>operons_50:RPA0458-RPA0459 504322..506015 r
RPA0458:possible fatty acid-CoA ligases.
RPA0459:possible fatty acid-CoA ligases

>operons_50:RPA0463-RPA0464 510757..513036 f
RPA0463:Bacterial regulatory protein TetR, HTH motif
RPA0464:putative long-chain fatty-acid-CoA ligase

>operons_50:RPA0466-RPA0470 514700..519174 r
RPA0466:conserved hypothetical protein
RPA0467:putative glycerate dehydrogenase
RPA0468:putative ATP-binding protein of ABC transporter
AtsC:putative sulfate ester transporter; ATP-binding
RPA0470:perplasmic binding protein of ABC transporter

>operons_50:RPA0480-RPA0482 530389..533480 f
RPA0480:possible acyl-CoA dehydrogenase
RPA0481:putative acyl-CoA dehydrogenase
RPA0482:probable short chain 3-hydroxyacyl-CoA

>operons_50:RPA0483-paaG2 533625..535180 r
RPA0483:unknown protein
paaG2:putative enoyl-CoA hydratase

>operons_50:RPA0486-RPA0487 536979..539233 f
RPA0486:Staphylococcus nuclease (SNase-like)
RPA0487:conserved unknown protein

>operons_50:RPA0495-cobS 550066..554550 r
RPA0495:conserved hypothetical protein
cobT:cobT protein
RPA0497:GCN5-related N-acetyltransferase
cobS:cobS protein

>operons_50:RPA0502-aroK 556564..559740 r
RPA0502:probable HlyC/CorC family of transporters with 2
aroB:putative 3-dehydroquinate synthase
aroK:putative shikimate kinase

>operons_50:RPA0505-RPA0506 559870..561049 f
RPA0505:conserved hypothetical protein
RPA0506:site-specific integrase/recombinase XerD

>operons_50:FarB-RPA0516 573372..576585 r
FarB:putative efflux pump protein FarB
RPA0515:possible efflux pump protein FarA
RPA0516:putative transcriptional regulator

>operons_50:RPA0518-gcpE 577437..579669 f
RPA0518:Permeases of the drug/metabolite transporter
gcpE:gcpE, Essential bacterial protein, involved in

>operons_50:RPA0521-RPA0522 581747..583917 f
RPA0521:Diguanylate cyclase/phosphodiesterase domain 2
RPA0522:possible activator of photopigment and puc

>operons_50:RPA0523-RPA0524 583928..585548 r
RPA0523:conserved hypothetical protein
RPA0524:putative geranyltranstransferase

>operons_50:RPA0544-RPA0545 607333..608435 f
RPA0544:LrgA family holin protein
RPA0545:conserved hypothetical protein

>operons_50:ChrR-RPA0550 611414..612660 r
ChrR:putative transcriptional regulator
RPA0550:putative sigma-70 factor, ECF subfamily

>operons_50:dctA-RPA0554 614276..616969 f
dctA:dicarboxylate transport protein
RPA0553:conserved hypothetical protein
RPA0554:putative ureidoglycolate hydrolase

>operons_50:RPA0573-RPA0574 635655..637279 f
RPA0573:putative ABC transporter (ATP-binding protein)
RPA0574:possible ABC transporter

>operons_50:RPA0586-RPA0588 652210..655335 r
RPA0586:putative PAN2 protein ; short shain alcohol
RPA0587:putative cationic amino acid transporter

RPA0588:Bacterial regulatory protein TetR, HTH motif

>operons_50:argJ-mutT 661788..663932 f
argJ:putative glutamate
RPA0593:hypothetical protein
mutT:putative mutator protein mutT

>operons_50:RPA0595-RPA0596 664109..665259 r
RPA0595:conserved hypothetical protein
RPA0596:conserved hypothetical protein

>operons_50:RPA0597-RPA0600 665365..667861 f
RPA0597:possible competence protein F (COMF)
RPA0598:putative glutaredoxin
RPA0599:possible nitrilase
RPA0600:conserved hypothetical protein

>operons_50:prfA-hemK 674416..676367 f
prfA:peptide chain release factor 1
hemK:putative protoporphyrinogen oxidase, hemK

>operons_50:RPA0610-RPA0611 678565..679766 f
RPA0610:putative glyoxalase II
RPA0611:conserved unknown protein

>operons_50:RPA0612-RPA0614 679887..682256 r
RPA0612:possible sugar kinase
RPA0613:NUDIX hydrolase
RPA0614:conserved unknown protein

>operons_50:dnaX-RPA0616 682649..684862 f
dnaX:possible DNA polymerase III tau subunit
RPA0616:Uncharacterized BCR

>operons_50:recR-RPA0618 684958..686008 f
recR:putative recombination protein recR
RPA0618:unknown protein

>operons_50:dapE-dapD 691642..694142 r
dapE:putative succinyl-diaminopimelate desuccinylase
RPA0625:conserved hypothetical protein
dapD:2,3,4,5-tetrahydropyridine-2-carboxylate

>operons_50:RPA0627-argB 694327..697042 r
RPA0627:putative haloacid dehalogenase superfamily
RPA0628:conserved unknown protein
argB:putative acetylglutamate kinase

>operons_50:RPA0630-RPA0631 697167..698185 r
RPA0630:DUF423
RPA0631:possible GTPases

>operons_50:RPA0632-rpmH,L34 698337..700721 r
RPA0632:60 kDa inner membrane protein
rnpA:probable ribonuclease p protein component
rpmH,L34:possible ribosomal protein L34

>operons_50:RPA0636-RPA0637 702970..704834 r
RPA0636:hypothetical protein
RPA0637:hypothetical protein

>operons_50:fliD-RPA0643 709543..712045 f
fliD:possible flagellar hook-associated protein 2
RPA0642:conserved hypothetical protein
RPA0643:conserved hypothetical protein

>operons_50:flgD-flgL 712294..717828 f
flgD:possible basal-body rod modification protein
flgE:possible flagellar hook protein FlgE
RPA0646:conserved hypothetical protein
RPA0647:hypothetical protein
flgK:possible flagellar hook-associated protein 1
flgL:possible flagellin and hook associated protein.

>operons_50:badK-aliA 717848..720295 r
badK:cyclohex-1-ene-1-carboxyl-CoA hydratase
aliA:cyclohexanecarboxylate-CoA ligase

>operons_50:badI-badH 721568..723148 r
badI:2-ketocyclohexanecarboxyl-CoA hydrolase
badH:2-hydroxycyclohexanecarboxyl-CoA dehydrogenase

>operons_50:badD-badF 725062..728878 f
badD:benzoyl-CoA reductase subunit
badE:benzoyl-CoA reductase subunit
badF:benzoyl-CoA reductase subunit

>operons_50:badA-badB 729921..731757 f
badA:benzoate-CoA ligase
badB:ferredoxin

>operons_50:hbaH-hbaF 732909..736278 r
hbaH:putative ABC transporter subunit, ATP-binding
hbaG:putative ABC transporter subunit, membrane
hbaF:putative membrane spanning subunit of ABC

>operons_50:hbaB-hbaD 739505..743306 f
hbaB:4-hydroxybenzoyl-CoA reductase, first of three
hbaC:4-hydroxybenzoyl-CoA reductase,second of three
hbaD:4-hydroxybenzoyl-CoA reductase, third of three

>operons_50:RPA0674-RPA0675 744248..746217 f
RPA0674:possible alcohol dehydrogenase class III family
RPA0675:possible hydrolases (alpha/beta hydrolase

>operons_50:RPA0681-RPA0683 755856..760731 f
RPA0681:membrane permeases, predicted cation efflux
RPA0682:possible ABC transporter ATP-binding component,
RPA0683:possible ABC transporter permease component

>operons_50:RPA0687-phnG 763121..770080 r
RPA0687:conserved hypothetical protein

phnN:ATP-binding component, PhnN protein, possible
phnM1:possible phosphonate utilization (C-P lyase)
phnL:phosphonate ABC transporter, ATP-binding
phnK:phosphonate ABC transporter, ATP-binding
phnJ:PhnJ protein, phosphonate metabolism, function
phnI:PhnI protein, phosphonate metabolism, function
phnH:putative PhnH protein, phosphonate metabolism,
phnG:PhnG protein, phosphonate metabolism, function

>operons_50:phnE1-phnE2 771245..772989 r
phnE1:putative PhnE protein, phosphonate ABC
phnE2:possible PhnE protein, phosphonate ABC

>operons_50:RPA0701-RPA0703 775029..777665 f
RPA0701:putative acetyltransferase (virginiamycin,
phnM2:possible phosphonate ABC transporter, permease
RPA0703:conserved hypothetical protein

>operons_50:RPA0709-RPA0710 781403..782251 f
RPA0709:conserved unknown protein
RPA0710:hypothetical protein

>operons_50:RPA0711-cobT,cobU 782498..784251 r
RPA0711:Nitroreductase family
cobT,cobU:putative

>operons_50:RPA0713-cobW 784566..786622 f
RPA0713:conserved unknown protein
cobU:bifunctional cobinamide kinase, cobinamide
cobW:putative cobalamin synthesis protein cobW

>operons_50:cobN-cobO,cobA,btuR 786757..791129 f
cobN:putative cobaltochelatase subunit CobN.
cobO,cobA,btuR:putative cob(I)alamin adenosyltransferase

>operons_50:cobD,cbiB-RPA0720 792734..794519 r
cobD,cbiB:putative cobalamin biosynthetic protein cobD
RPA0720:putative ABC-type cobalamin/Fe3+-siderophores

>operons_50:fecE-nxiA,nixA,hoxN,hupN 795584..798451 r
fecE:putative iron(III) dicitrate ABC transporter,
RPA0723:possible hemin ABC transporter, permease
nxiA,nixA,hoxN,hupN:putative high-affinity nickel-transport protein

>operons_50:sugE-btaB 798784..799841 r
sugE:possible chaperone
btaB:putative BtaB protein,

>operons_50:RPA0728-RPA0730 801773..804470 f
RPA0728:conserved unknown protein
RPA0729:conserved hypothetical protein
RPA0730:conserved hypothetical protein

>operons_50:fdsG-RPA0737 806161..813791 f
fdsG:putative NAD-dependent formate dehydrogenase
fdsB:NAD-dependent formate dehydrogenase beta subunit

fdsA:NAD-dependent formate dehydrogenase alpha
fdsC:putative FdsC protein, formate dehydrogenase
fdsD:possible NAD-dependent formate dehydrogenase
RPA0737:putative oxalate/formate Major Facilitator

>operons_50:RPA0740-RPA0742 816117..819561 f
RPA0740:possible Acyl-CoA dehydrogenase
RPA0741:conserved unknown protein
RPA0742:conserved hypothetical protein

>operons_50:cysA-cysT 826776..829567 r
cysA:putative sulfate ABC transporter, ATP-binding
cysW:possible sulfate ABC transporter, permease
cysT:putative sulfate ABC transporter, permease

>operons_50:cysD-cysN 832014..834815 f
cysD:putative ATP sulfurylase small subunit
cysN:putative CysN/CysC bifunctional enzyme,

>operons_50:oppD-nikB,dppB,appB 836321..841842 r
oppD:putative oligopeptide ABC transporter,
RPA0756:putative amidase
RPA0757:hypothetical protein
oppF,appF:putative oligopeptide ABC transporter,
dppC,oppC:putative oligopeptide ABC transporter, permease
nikB,dppB,appB:putative oligopeptide ABC transporter, permease

>operons_50:RPA0764-RPA0765 846490..849308 r
RPA0764:conserved hypothetical protein
RPA0765:putative outer membrane receptor for iron

>operons_50:RPA0770-RPA0771 853839..855022 r
RPA0770:Integrase, catalytic domain
RPA0771:possible protein commonly found in insertion

>operons_50:RPA0781-RPA0782 866150..866937 r
RPA0781:putative cytochrome c552 precursor
RPA0782:conserved unknown protein

>operons_50:RPA0790-RPA0792 876924..880396 r
RPA0790:conserved hypothetical protein
exoI:similar to Staphylococcus nuclease (SNase-like)
RPA0792:conserved unknown protein

>operons_50:RPA0796-uraI 883368..885049 f
RPA0796:conserved unknown protein
uraI:dihydroorotate dehydrogenase

>operons_50:matE-RPA0803 886913..891536 r
matE:putative cation efflux pump,
RPA0801:conserved hypothetical protein
RPA0802:possible DNA ligase
RPA0803:hypothetical protein

>operons_50:RPA0812-RPA0813 902897..904656 r
RPA0812:putative transmembrane protein

RPA0813:possible permease

>operons_50:RPA0821-gshA 918366..920396 f
RPA0821:possible transcriptional regulator
gshA:gamma-glutamylcysteine synthetase

>operons_50:lepB-RPA0825 921127..923321 r
lepB:signal peptidase I
RPA0825:TldD protein, suppresses inhibitory activity of

>operons_50:RPA0826-RPA0827 923443..923993 f
RPA0826:DUF433
RPA0827:conserved hypothetical protein

>operons_50:coxA-coxG 927249..930705 f
coxA:cytochrome c oxidase subunit I
coxE:heme O synthase
CoxF:putative CoxF
coxG:possible cytochrome-c oxidase assembly protein

>operons_50:RPA0837-RPA0838 931794..932989 f
RPA0837:conserved hypothetical protein in cyt c oxidase
RPA0838:possible surfeit 1

>operons_50:thrC-mpp 933049..935840 f
thrC:threonine synthase
mpp:putative protease

>operons_50:atpF1-atpF2 937373..938427 r
atpF1:putative Fo ATP synthase B chain
atpF2:putative FoF1 ATP synthase, subunit B'

>operons_50:atpE-atpB 938485..939507 r
atpE:probable ATP synthase subunit C TRANSMEMBRANE
atpB:Fo ATP synthase subunit A

>operons_50:RPA0848-RPA0850 940266..942016 f
RPA0848:conserved unknown protein
RPA0849:conserved hypothetical protein
RPA0850:Protein of unknown function UPF0047

>operons_50:RPA0858-RPA0860 955056..957605 f
RPA0858:ABC transporter, ATP-binding protein
RPA0859:ABC transporter, permease protein
RPA0860:ABC transporter, periplasmic binding protein

>operons_50:RPA0861-RPA0863 957713..960574 f
RPA0861:possible CobW protein involved in cobalamin
RPA0862:G-protein beta WD-40 repeat
RPA0863:possible MgtC - magnesium transport

>operons_50:RPA0868-RPA0869 964063..964819 r
RPA0868:hypothetical protein
RPA0869:GCN5-related N-acetyltransferase

>operons_50:RPA0872-RPA0874 967238..971296 f

RPA0872:putative peptidyl-dipeptidase
RPA0873:conserved hypothetical protein
RPA0874:conserved hypothetical protein

>operons_50:RPA0876-RPA0877 972666..974127 f
RPA0876:conserved unknown protein
RPA0877:conserved hypothetical protein

>operons_50:RPA0901-RPA0902 1004276..1005507 r
RPA0901:DUF81
RPA0902:Glyoxalase/Bleomycin resistance

>operons_50:RPA0921-RPA0922 1023394..1025438 r
RPA0921:possible flagellar motor protein MotB
RPA0922:conserved hypothetical protein

>operons_50:RPA0923-RPA0924 1025618..1027467 f
RPA0923:conserved hypothetical protein
RPA0924:possible cyclopropane-fatty-acyl-phospholipid

>operons_50:RPA0927-RPA0928 1028320..1029108 r
RPA0927:probable transcriptional regulator
RPA0928:conserved hypothetical protein

>operons_50:RPA0930-ubiD 1029992..1032129 r
RPA0930:possible 3-octaprenyl-4-hydroxybenzoate
ubiD:Carboxylyase-related protein

>operons_50:RPA0932-RPA0933 1032245..1033771 f
RPA0932:conserved unknown protein
RPA0933:putative protease, putative

>operons_50:RPA0938-RPA0940 1038125..1040932 r
RPA0938:conserved unknown protein
RPA0939:possible thiamine-phosphate pyrophosphorylase
RPA0940:fructose-bisphosphate aldolase

>operons_50:RPA0941-RPA0942 1040987..1041591 r
RPA0941:conserved hypothetical protein
RPA0942:conserved hypothetical protein

>operons_50:RPA0946-RPA0947 1046611..1047395 f
RPA0946:hypothetical protein
RPA0947:conserved hypothetical protein

>operons_50:RPA0948-matE 1047902..1050611 r
RPA0948:possible hypothetical RNA methyltransferase
matE:putative multidrug efflux protein (NorM)

>operons_50:tly-RPA0951 1050674..1051980 r
tly:putative hemolysin
RPA0951:Nucleoside 2-deoxyribosyltransferase

>operons_50:hupS-hupC 1064173..1067842 f
hupS:hydrogenase small chain
hupL:hydrogenase large chain

hupC:Ni/Fe-hydrogenase 1 B-type cytochrome subunit

>operons_50:hupD-hupF 1067904..1069487 f
hupD:hydrogenase maturation protein hupD
hupE:putative membrane-bound hydrogenase component
hupF:hydrogenase expression/formation protein hupF

>operons_50:hupG-RPA0980 1069708..1081615 f
hupG:putative hydrogenase expression/formation
hupH:hydrogenase expression/formation protein hupH
hupI:putative rubredoxin hupI
hupJ:putative hydrogenase expression/formation
hupK:putative hydrogenase expression/formation
hypA:hydrogenase formation/expression protein hypA
hypB:hydrogenase expression/formation protein hypB
hypF:hydrogenase maturation protein hypF
hypC:putative hypC
hypD:hydrogenase expression/formation protein hypD
hypE:hydrogenase expression/formation protein hypE
hoxA:transcriptional regulatory protein hoxA
RPA0980:putative histidine protein kinase

>operons_50:RPA0983-RPA0985 1085284..1089318 f
RPA0983:possible phthalate dioxygenase
glnA4:putative glutamine synthetase-like protein
RPA0985:putative branched-chain amino acid transport

>operons_50:RPA0986-RPA0989 1089530..1092852 f
RPA0986:possible urea/short-chain amide transport system
RPA0987:possible branched-chain amino acid ABC
RPA0988:putative branched-chain amino acid ABC
RPA0989:putative ATP-binding component of ABC

>operons_50:RPA1000-RPA1001 1102982..1103981 r
RPA1000:Nitrogenase-associated protein:Arsenate
RPA1001:conserved hypothetical protein

>operons_50:RPA1006-mhpB 1108128..1109402 f
RPA1006:possible protocatechuate 4,5-dioxygenase small
mhpB:possible 2,3-dihydroxyphenylpropionate

>operons_50:RPA1019-RPA1021 1119897..1124456 f
RPA1019:possible transcriptional activator HlyU
RPA1020:possible membrane fusion protein precursor;
RPA1021:putative transporter, AcrB/D/F family; Cation

>operons_50:RPA1023-RPA1025 1125380..1127320 f
RPA1023:hypothetical protein
RPA1024:putative oxidoreductase
RPA1025:possible Ectothiorhodospira Vacuolata

>operons_50:RPA1029-RPA1030 1130697..1132213 f
RPA1029:possible CoA transferase, subunit A
RPA1030:possible CoA transferase, subunit B

>operons_50:rnh2-RPA1035 1135479..1137973 f

rnh2:possible ribonuclease HII
RPA1035:conserved hypothetical protein

>operons_50:RPA1041-RPA1042 1145132..1146131 f
RPA1041:conserved hypothetical protein
RPA1042:conserved unknown protein

>operons_50:RPA1046-sygB 1149072..1151836 f
RPA1046:conserved hypothetical protein
sygB:putative glycyl-tRNA synthetase, beta chain

>operons_50:nadC-nadB 1161049..1163557 r
nadC:nicotinate-mononucleotide pyrophosphorylase
nadB:putative L-aspartate oxidase

>operons_50:RPA1059-tcmP 1168419..1171933 f
RPA1059:probable outer membrane protein, TonB-dependent
RPA1060:hypothetical protein
tcmP:possible polyketide synthesis protein

>operons_50:RPA1063-RPA1064 1174654..1176152 r
RPA1063:conserved hypothetical protein
RPA1064:conserved hypothetical protein

>operons_50:tag-RPA1068 1177191..1178725 r
tag:possible 3-methyladenine DNA glycosylase I
RPA1068:Glycine cleavage T protein (aminomethyl

>operons_50:RPA1072-RPA1074 1181286..1182522 r
RPA1072:conserved hypothetical protein
RPA1073:possible ADP-RIBOSE PHOSPHOHYDROLASE
RPA1074:conserved hypothetical protein

>operons_50:RPA1079-RPA1080 1187407..1189588 f
RPA1079:probable 4-methylmuconolactone Major Facilitator
RPA1080:possible 2-pyrone-4,6-dicarboxylate hydrolase

>operons_50:RPA1083-RPA1087 1192349..1195360 f
RPA1083:conserved hypothetical protein
csgB,agfB:possible minor curlin subunit precursor (fimbrin
RPA1085:hypothetical protein
csgG:possible curli production assembly/transport
RPA1087:possible transglycosylase SLT domain

>operons_50:ruvA-RPA1101 1205358..1206397 f
ruvA:RuvA; Holliday branch migration protein
RPA1101:putative cytidine deaminase

>operons_50:ruvB-RPA1103 1206575..1208096 f
ruvB:RuvB; Holliday branch migration protein
RPA1103:Thioesterase superfamily:4-hydroxybenzoyl-CoA

>operons_50:RPA1106-RPA1107 1210924..1211956 f
RPA1106:conserved hypothetical protein
RPA1107:possible transcriptional regulator

>operons_50:RPA1108-RPA1109 1212076..1213745 f
RPA1108:Myb DNA-binding domain:DGPF domain
RPA1109:possible sigma-70 factor, ECF subfamily

>operons_50:RPA1115-RPA1116 1217494..1218850 f
RPA1115:conserved hypothetical protein
RPA1116:putative RNA polymerase sigma factor

>operons_50:TolQ-TolA 1219157..1221404 f
TolQ:TolQ protein, inner membrane protein, tolerance
TolR:putative tolR protein, uptake of enterochelin;
TolA:putative TolA

>operons_50:RPA1127-RPA1128 1231651..1232714 f
RPA1127:probable branched-chain amino acid transport
RPA1128:conserved hypothetical protein

>operons_50:RPA1131-glcF 1235355..1237906 f
RPA1131:putative glycolate oxidase subunit GlcE
glcF:glycolate oxidase subunit, (Fe-S)protein, GlcF

>operons_50:groEL-groES 1247853..1249832 r
groEL:chaperonin GroEL1, cpn60
groES:chaperonin GroES1, cpn10

>operons_50:RPA1142-RPA1143 1250132..1251899 f
RPA1142:unknown protein
RPA1143:possible Major Facilitator Family (MFS)

>operons_50:RPA1147-RPA1148 1254853..1256786 r
RPA1147:conserved hypothetical protein
RPA1148:putative sugar transferase

>operons_50:hisG-RPA1150 1256880..1259002 r
hisG:ATP phosphoribosyltransferase
RPA1150:putative histidyl-tRNA synthetase

>operons_50:RPA1152-ubiA 1260277..1261757 f
RPA1152:hypothetical protein
ubiA:putative 4-hydroxybenzoate-octaprenyl

>operons_50:RPA1156-RPA1157 1264072..1265101 f
RPA1156:putative myo-inositol monophosphatase 2 family
RPA1157:conserved unknown protein

>operons_50:RPA1158-lpxK 1265171..1267490 f
RPA1158:putative 3-deoxy-D-manno-octulosonic-acid
lpxK:putative tetraacyldisaccharide 4'-kinase

>operons_50:RPA1160-xseA 1267500..1269489 r
RPA1160:conserved unknown protein
xseA:putative exonuclease VII, large subunit OB-fold

>operons_50:yfcB-pgsA 1275882..1278271 r
yfcB:possible adenine-specific methylase
moaE:molybdopterin converting factor, subunit 2

moaD:molybdopterin converting factor, subunit 1
pgsA:possible CDP-diacylglycerol-glycerol-3-phosphate

>operons_50:RPA1180-RPA1181 1288180..1290612 f
RPA1180:conserved hypothetical protein
RPA1181:Haloacid dehalogenase-like hydrolase

>operons_50:RPA1183-RPA1185 1292874..1297731 r
RPA1183:conserved unknown protein
RPA1184:DUF58
RPA1185:putative methanol dehydrogenase regulator

>operons_50:RPA1186-RPA1187 1297866..1299151 f
RPA1186:conserved hypothetical protein
RPA1187:NUDIX hydrolase

>operons_50:RPA1190-RPA1191 1301099..1302197 r
RPA1190:conserved hypothetical protein
RPA1191:putative RNA methyltransferase

>operons_50:RPA1192-RPA1193 1302375..1305108 f
RPA1192:cytochrome b6-F complex iron-sulfur subunit
RPA1193:cytochrome b/c1 precursor

>operons_50:fixR-pdxH 1306424..1307835 r
fixR:short-chain dehydrogenase
pdxH:pyridoxamine 5'-phosphate oxidase

>operons_50:RPA1208-RPA1211 1320610..1325616 r
RPA1208:putative dioxygenase
RPA1209:conserved hypothetical protein
RPA1210:conserved hypothetical protein
RPA1211:hypothetical protein

>operons_50:RPA1215-RPA1216 1330400..1332245 r
RPA1215:putative ABC transporter, permease protein
RPA1216:putative ABC transporter, permease protein

>operons_50:RPA1221-RPA1223 1338132..1340314 r
RPA1221:hypothetical protein
RPA1222:conserved hypothetical protein
RPA1223:hypothetical protein

>operons_50:iorA-RPA1229 1340580..1347272 f
iorA:putative indolepyruvate ferredoxin
RPA1225:possible pyruvate ferredoxin/flavodoxin
RPA1226:putative 2-oxoglutarate ferredoxin
oorB:putative 2-oxoglutarate ferredoxin
RPA1228:putative 2-oxoglutarate ferredoxin
RPA1229:probable aerobic phenylacetate-CoA ligase

>operons_50:RPA1230-RPA1235 1347482..1353942 f
RPA1230:putative ABC transporter, permease protein
RPA1231:possible ABC transporter, permease protein
RPA1232:putative branched-chain amino acid transport
RPA1233:putative branched-chain amino acid transport

RPA1234:possible long-chain-fatty-acid--CoA ligase
RPA1235:possible Leucine-Binding Protein (LBP)

>operons_50:RPA1236-RPA1238 1354133..1357336 r
RPA1236:putative acyl-CoA dehydrogenase
RPA1237:possible acyl-CoA dehydrogenase
RPA1238:putative enoyl-CoA hydratase/isomerase

>operons_50:exbB-RPA1241 1357474..1359771 f
exbB:putative biopolymer transport protein ExbB
exbD:biopolymer transport protein ExbD
RPA1241:possible tonB transport protein

>operons_50:RPA1243-RPA1246 1361637..1364501 f
RPA1243:hypothetical protein
RPA1244:conserved unknown protein
RPA1245:conserved hypothetical protein
RPA1246:conserved unknown protein

>operons_50:RPA1248-RPA1249 1365644..1369928 r
RPA1248:possible response regulator receiver domain
RPA1249:putative histidine kinase

>operons_50:RPA1251-fmdA 1371614..1376438 f
RPA1251:putative branched-chain amino acid transport
RPA1252:putative high-affinity branched-chain amino acid
RPA1253:branched-chain amino acid transport system
RPA1254:putative ATP-binding component of ABC
fmdA:formamide amidohydrolase

>operons_50:fliF-flbD 1385366..1390447 f
fliF:putative flagellar M-ring protein
fliG:putative flagellar motor switch protein
RPA1266:possible FlbE protein
fliY:putative flagellar motor switch protein
flbD:flagellar transcription activator

>operons_50:RPA1270-RPA1271 1391021..1391768 r
RPA1270:conserved hypothetical protein
RPA1271:conserved hypothetical protein

>operons_50:RPA1281-RPA1282 1400728..1401508 r
RPA1281:conserved hypothetical protein
RPA1282:putative transcriptional regulator

>operons_50:RPA1288-RPA1289 1406728..1409175 f
RPA1288:RNA polymerase sigma subunit
RPA1289:hypothetical protein

>operons_50:RPA1290-RPA1291 1409572..1410195 r
RPA1290:possible proteic killer active protein
RPA1291:putative proteic killer suppression protein

>operons_50:RPA1292-RPA1293 1410470..1411431 r
RPA1292:hypothetical protein
RPA1293:putative IS5 transposase

>operons_50:RPA1304-RPA1305 1423276..1425594 r
RPA1304:possible flagellar basal-body rod modification
RPA1305:possible flagellar hook length determination

>operons_50:trmU-RPA1307 1425895..1427758 f
trmU:tRNA
RPA1307:putative

>operons_50:RPA1314-RPA1315 1435192..1436306 f
RPA1314:putative two-component signaling protein
RPA1315:putative response regulator

>operons_50:RPA1324-RPA1325 1441783..1444992 f
RPA1324:possible FusB/FusC fusaric acid resistance pump
RPA4837:conserved hypothetical membrane protein
RPA1325:putative FusE - MFP/HlyD family membrane fusion

>operons_50:RPA1327-RPA1328 1446214..1451350 f
RPA1327:possible Protein kinase domain
RPA1328:possible histidine kinase

>operons_50:fumC-RPA1330 1451481..1454220 f
fumC:fumarate hydratase
RPA1330:conserved hypothetical protein

>operons_50:mqoB-RPA1332 1454615..1457000 f
mqoB:malate quinone oxidoreductase
RPA1332:possible phage integrase/recombinase

>operons_50:RPA1333-RPA1335 1457225..1459430 f
RPA1333:conserved hypothetical protein
RPA1334:probable sigma-70 factor, ECF subfamily
RPA1335:putative transmembrane sensor

>operons_50:RPA1336-RPA1337 1459664..1471704 f
RPA1336:conserved hypothetical protein
RPA1337:conserved hypothetical protein

>operons_50:RPA1338-RPA1339 1472806..1474103 f
RPA1338:conserved hypothetical protein
RPA1339:putative sigma-70 factor, ECF subfamily

>operons_50:RPA1343-RPA1344 1489054..1490317 f
RPA1343:conserved hypothetical protein
RPA1344:hypothetical protein

>operons_50:RPA1345-RPA1346 1490469..1491948 f
RPA1345:conserved hypothetical protein
RPA1346:possible TonB protein, possible colicin J

>operons_50:RPA1349-RPA1360 1494203..1505711 f
RPA1349:Hemolysin activation/secretion protein
exbB2:putative transport protein ExbB2
exbD:transport protein ExbD
RPA1352:hypothetical protein

RPA1353:conserved hypothetical protein
RPA1354:conserved hypothetical protein
RPA1355:conserved hypothetical protein
RPA1356:PpiC-type peptidyl-prolyl cis-trans isomerase
RPA1357:conserved hypothetical protein
RPA1358:hypothetical protein
RPA1359:possible transglycosylase
RPA1360:hypothetical protein

>operons_50:RPA1362-RPA1365 1506856..1512045 f
RPA1362:putative sulfate ester transport system
RPA1363:sulfate ester transport system permease protein
RPA1364:sulfate ester transport system ATP-binding
RPA1365:putative sulfatase

>operons_50:soxZ-soxY 1512100..1512902 r
soxZ:putative sulfur oxidation protein
soxY:putative sulfur oxidation protein

>operons_50:RPA1370-vnfE 1515576..1519905 r
RPA1370:Nitrogen-fixing NifU, C-terminal
vnfX:putative vanadium nitrogenase protein
vnfN:putative nitrogenase cofactor synthesis protein
vnfE:putative nitrogenase cofactor synthesis protein

>operons_50:vnfA-RPA1375 1520222..1522259 f
vnfA:putative transcriptional regulator (NifA family)
RPA1375:hypothetical protein

>operons_50:vnfD-vnfG 1524697..1526453 f
vnfD:nitrogenase vanadium-iron protein alpha chain
vnfG:vanadium dinitrogenase delta subunit

>operons_50:vnfK-RPA1382 1526517..1529356 f
vnfK:nitrogenase vanadium-iron protein, VnfK subunit
RPA1381:hypothetical protein
RPA1382:Nitrogen fixation-related protein

>operons_50:ptxC-ptxA 1529885..1532432 r
ptxC:putative phosphate permease component of
ptxB:putative phosphonate transport system
ptxA:putative ATP-binding component of ABC

>operons_50:RPA1388-RPA1392 1534069..1538441 f
RPA1388:hypothetical protein
RPA1389:conserved hypothetical protein
RPA1390:conserved hypothetical protein
RPA1391:possible ABC transporter ATP-binding protein
RPA1392:nitroreductase family proteins

>operons_50:RPA1395-RPA1403 1541222..1551406 f
RPA1395:possible trehalose/maltose binding protein
RPA1396:possible multiple sugar transport system
RPA1397:putative sugar ABC transporter, permease protein
RPA1398:putative sugar ABC transporter, ATP-binding
RPA1399:putative transport system ATP-binding protein

RPA1400:possible Glutamine amidotransferase
glnAIII:putative glutamine synthetase III
RPA1402:putative Glu-tRNA amidotransferase, subunit A
RPA1403:possible Glutamine amidotransferase

>operons_50:RPA1404-RPA1410 1551670..1561271 r
RPA1404:glutamyl-tRNA(Gln) amidotransferase subunit A
RPA1405:putative urea amidolyase
RPA1406:conserved hypothetical protein
RPA1407:conserved hypothetical protein
RPA1408:putative ABC transporter protein
RPA1409:possible taurine transport system permease
RPA1410:possible taurine transport system protein

>operons_50:RPA1415-RPA1419 1566319..1570871 f
RPA1415:possible branched-chain amino acid transport
RPA1416:putative branched-chain amino acid transport
RPA1417:putative branched-chain amino acid transport
RPA1418:possible transport system permease protein
RPA1419:possible transport system permease protein

>operons_50:ybdE-RPA1421 1570899..1575457 r
ybdE:putative inner membrane component for iron
RPA1421:possible efflux protein

>operons_50:RPA1423-RPA1424 1576971..1579875 f
RPA1423:putative membrane protein
RPA1424:possible selenocysteine lyase

>operons_50:RPA1426-RPA1428 1581162..1583743 f
RPA1426:ABC transporter, ATP-binding protein
RPA1427:putative ABC transporter, permease protein
RPA1428:possible lipoprotein

>operons_50:RPA1429-RPA1430 1584105..1586323 r
RPA1429:putative coenzyme F390 synthetase
RPA1430:putative outer membrane protein

>operons_50:RPA1433-RPA1434 1589047..1590326 r
RPA1433:conserved hypothetical protein
RPA1434:conserved hypothetical protein

>operons_50:anfK-anfH 1590406..1594702 r
anfK:alternative nitrogenase 3 beta chain
anfG:dinitrogenase 3 delta subunit
anfD:putative nitrogenase molybdenum-iron protein
anfH:nitrogenase iron protein (nitrogenase component

>operons_50:RPA1441-RPA1442 1597783..1599426 r
RPA1441:possible uridylate kinase
RPA1442:possible uridine monophosphate kinase

>operons_50:RPA1444-RPA1449 1600910..1608133 f
RPA1444:putative oligopeptide binding protein precursor
RPA1445:putative oligopeptide transport ATP-binding
RPA1446:possible dipeptide ABC transporter

RPA1447:putative oligopeptide ABC transporter (permease)
RPA1448:putative oligopeptide ABC transporter (permease)
RPA1449:putative long-chain fatty acid--CoA ligase

>operons_50:RPA1450-RPA1451 1608197..1612492 f
RPA1450:putative pyruvate carboxylase
RPA1451:unknown protein

>operons_50:norE-RPA1454 1612792..1613674 f
norE:putative denitrification protein NorE
RPA1454:hypothetical protein

>operons_50:norC-norB 1613786..1615622 f
norC:nitric-oxide reductase subunit C
norB:nitric-oxide reductase subunit B

>operons_50:RPA1461-RPA1462 1619349..1621665 r
RPA1461:conserved hypothetical protein
RPA1462:conserved hypothetical protein

>operons_50:RPA1466-RPA1467 1626850..1629317 r
RPA1466:putative glutamyl-tRNA(Gln) amidotransferase
RPA1467:possible transcriptional regulator

>operons_50:RPA1468-gatA 1629395..1631250 r
RPA1468:conserved hypothetical protein
gatA:possible glutamyl-tRNA (Gln) amidotransferase

>operons_50:RPA1471-RPA1472 1633461..1635393 r
RPA1471:putative dipeptide ABC transporter (permease)
RPA1472:putative dipeptide transport permease protein

>operons_50:RPA1476-cpdA 1638835..1643407 f
RPA1476:putative periplasmic solute-binding protein
RPA1477:putative permease protein
RPA1478:putative permease protein
RPA1479:putative transport system ATP-binding protein
cpdA:putative ICC protein

>operons_50:RPA1486-RPA1487 1649216..1650729 f
RPA1486:conserved hypothetical protein
RPA1487:conserved hypothetical protein

>operons_50:RPA1489-RPA1490 1652068..1655071 r
RPA1489:putative DNA-binding response regulator
RPA1490:possible phytochrome-like protein (AB034952)

>operons_50:pucBe-pucAe 1655417..1655764 f
pucBe:light harvesting protein B-800-850, beta chain E
pucAe:light harvesting protein B-800-850, alpha chain

>operons_50:pucC-RPA1495 1655951..1658365 f
pucC:PucC, possible chlorophyll Major Facilitator
RPA1494:unknown protein
RPA1495:unknown protein

>operons_50:mexC-mexD 1660402..1664779 f
mexC:putative RND multidrug efflux membrane fusion
mexD:RND multidrug efflux transporter MexD

>operons_50:RPA1500-RPA1501 1665626..1667417 r
RPA1500:unknown protein
RPA1501:possible coenzyme F420 hydrogenase beta subunit

>operons_50:RPA1502-RPA1504 1667478..1670889 r
RPA1502:conserved hypothetical protein
RPA1503:hypothetical protein
RPA1504:conserved unknown protein

>operons_50:RPA1505-bchD 1671137..1674917 f
RPA1505:putative porphobilinogen deaminase
bchI:putative Mg chelatase subunit BchI
bchD:putative magnesium chelatase subunit BchD

>operons_50:RPA1510-RPA1511 1677230..1679081 f
RPA1510:conserved unknown protein
RPA1511:Alpha/beta hydrolase fold

>operons_50:crtI-crtB 1679157..1681756 f
crtI:phytoene dehydrogenase CrtI
crtB:CrtB phytoene synthase

>operons_50:crtC-crtD 1684504..1687021 r
crtC:hydroxyneurosporene dehydrogenase
crtD:methoxyneurosporene dehydrogenase

>operons_50:crtE-crtF 1687143..1689180 f
crtE:geranylgeranyl pyrophosphate synthase
crtF:hydroxyneurosporene methyltransferase CrtF

>operons_50:bchC-bchZ 1689269..1694263 f
bchC:2-desacetyl-2-hydroxyethyl
bchX:bacteriochlorophyllide reductase subunit BchX
bchY:bacteriochlorophyllide reductase subunit BchY
bchZ:bacteriochlorophyllide reductase subunit

>operons_50:pufB-pufA 1694719..1695123 f
pufB:light-harvesting complex 1 beta chain
pufA:light-harvesting complex 1 alpha chain

>operons_50:pufL-pufM 1695255..1697039 f
pufL:photosynthetic reaction center L subunit
pufM:photosynthetic reaction center M protein

>operons_50:ppsR1-RPA1534 1697302..1702961 f
ppsR1:putative PPSR protein; crtJ protein
bchG:geranylgeranyl bacteriochlorophyll synthase
RPA1531:possible Bch2, light harvesting pigment Major
bchP:geranylgeranyl reductase
tspO:tryptophan-rich sensory protein
RPA1534:hypothetical protein

>operons_50:bchF-hemA 1709486..1725322 f
bchF:possible 2-vinyl bacteriochlorophillide
bchN:protochlorophyllide reductase subunit BchN
bchB:protochlorophyllide reductase BchB subunit
bchH:magnesium-protoporphyrin O-methyltransferase
bchL:protochlorophyllide reductase iron-sulfur
bchM:Mg-protoporphyrin IX methyl transferase
lhaA:photosynthetic complex (LH1) assembly protein
puhA:H subunit of photosynthetic reaction center
RPA1549:possible photosynthetic complex assembly
RPA1550:possible photosynthetic complex assembly
RPA1551:hypothetical protein
RPA1552:conserved unknown protein
RPA1553:conserved hypothetical protein
hemA:5-aminolevulinic acid synthase (ALAS)

>operons_50:RPA1556-RPA1558 1727226..1731500 f
RPA1556:possible response regulator
RPA1557:possible response regulator
RPA1558:possible histidine kinase

>operons_50:cbbL-cbbX 1731700..1734522 f
cbbL:ribulose-bisphosphate carboxylase large chain
cbbS:ribulose-bisphosphate carboxylase small chain
cbbX:cbbX protein homolog

>operons_50:RPA1564-RPA1567 1736816..1741569 f
RPA1564:possible urea/short-chain amide transport system
RPA1565:putative urea/short-chain amide transport system
RPA1566:possible branched-chain amino acid transport
RPA1567:putative branched-chain amino acid transport

>operons_50:RPA1568-RPA1569 1741619..1743700 r
RPA1568:possible carboxylesterase
RPA1569:O-acetylhomoserine sulfhydrylase

>operons_50:RPA1573-RPA1575 1749613..1751666 f
RPA1573:LemA family
RPA1574:DUF477
RPA1575:conserved hypothetical protein

>operons_50:RPA1583-RPA1584 1761958..1764533 r
RPA1583:conserved hypothetical protein
RPA1584:conserved hypothetical protein

>operons_50:RPA1590-RPA1591 1769020..1770191 r
RPA1590:conserved hypothetical protein
RPA1591:conserved unknown protein

>operons_50:RPA1604-RPA1605 1783527..1785812 r
RPA1604:conserved hypothetical protein
RPA1605:conserved hypothetical protein

>operons_50:RPA1606-RPA1607 1786040..1786962 f
RPA1606:conserved unknown protein
RPA1607:Appr-1''-p processing enzyme family protein

>operons_50:RPA1610-RPA1611 1790211..1792175 r
RPA1610:conserved unknown protein
RPA1611:putative dehydratase

>operons_50:RPA1612-RPA1613 1792376..1794847 r
RPA1612:putative acyl-CoA dehydrogenase
RPA1613:putative cytochrome P-450

>operons_50:cheAY1-cheW1 1807250..1810560 f
cheAY1:chemotaxis histidine kinase CheAY
cheW1:purine-binding chemotaxis protein CheW

>operons_50:cheB1-cheR1 1811072..1813122 f
cheB1:putative protein-glutamate methylesterase
cheR1:chemotaxis protein methyltransferase CheR

>operons_50:RPA1635-RPA1636 1816522..1818017 f
RPA1635:putative RNA polymerase sigma factor
RPA1636:conserved unknown protein

>operons_50:RPA1644-RPA1645 1828955..1829921 r
RPA1644:conserved unknown protein
RPA1645:unknown protein

>operons_50:RPA1648-RPA1650 1831520..1834678 f
RPA1648:membrane permeases, predicted cation efflux
RPA1649:predicted ABC-type transport systems, involved
RPA1650:putative ABC transporter, ATP-binding protein

>operons_50:hpaD-RPA1664 1848482..1849903 r
hpaD:putative 3,4-dihydroxyphenylacetate
RPA1664:Glyoxalase/Bleomycin resistance

>operons_50:hemN-bchE 1850616..1854373 r
hemN:putative coproporphyrinogen oxidase III
bchJ:putative 4-vinyl protochlorophyllide reductase
bchE:Mg-protoporphyrin IX monomethyl ester oxidative

>operons_50:RPA1670-RPA1671 1855181..1857364 f
RPA1670:Metallo-phosphoesterase
RPA1671:putative serine/threonine protein kinase

>operons_50:cheAY2-cheW4 1864447..1867757 f
cheAY2:chemotaxis protein histidine kinase CheAY
cheW4:putative purine-binding chemotaxis protein

>operons_50:cheR3-RPA1679 1867811..1869012 f
cheR3:chemotaxis protein methyltransferase
RPA1679:unknown protein

>operons_50:RPA1721-alkB 1921022..1922586 f
RPA1721:putative transcriptional regulator
alkB:alkylated DNA repair protein

>operons_50:paaK-paaI 1922593..1924412 r

paaK:phenylacetyl-CoA ligase
paaI:putative phenylacetic acid degredation protein

>operons_50:RPA1731-RPA1732 1936665..1938552 r
RPA1731:similar to eukaryotic molybdopterin
RPA1732:possible cytochrome P450

>operons_50:RPA1737-RPA1740 1943207..1947313 r
RPA1737:possible dehydrogenase
RPA1738:putative branched-chain amino acid transport
RPA1739:putative branched-chain amino acid transport
RPA1740:possible branched-chain amino acid transport

>operons_50:serA-RPA1745 1951061..1953260 r
serA:possible phosphoglycerate dehydrogenase (serA),
RPA1745:N-carbamoyl-beta-alanine amidohydrolase

>operons_50:RPA1749-RPA1752 1956692..1959930 f
RPA1749:putative branched-chain amino acid transport
RPA1750:putative branched-chain amino acid transport
RPA1751:putative branched-chain amino acid transport
RPA1752:branched-chain amino acid transport system

>operons_50:ragC-ragD 1961116..1965502 f
ragC:putative cation efflux system protein
ragD:possible cation/heavy metal efflux pump, HlyD

>operons_50:RPA1756-RPA1757 1965670..1968003 r
RPA1756:possible acetyl-CoA acetyltransferase
RPA1757:possible oxoacyl carrier protein reductase

>operons_50:RPA1758-RPA1760 1968171..1970367 f
RPA1758:putative enoyl-CoA hydratase paaG
RPA1759:Tyrosine protein kinase:Aminoglycoside
RPA1760:conserved unknown protein

>operons_50:RPA1769-RPA1770 1981608..1983559 r
RPA1769:putative transcriptional regulator
RPA1770:conserved hypothetical membrane protein

>operons_50:RPA1776-RPA1777 1991177..1992735 r
RPA1776:possible lipid transfer protein
RPA1777:DUF35

>operons_50:RPA1778-RPA1779 1993022..1995059 f
RPA1778:putative Glu-tRNA amidotransferase
RPA1779:conserved hypothetical protein

>operons_50:RPA1783-RPA1784 1998472..2000439 f
RPA1783:possible TrapT family, dctQ subunit,
RPA1784:TrapT family, dctM subunit, C4-dicarboxylate

>operons_50:RPA1786-fcs2 2001366..2004079 f
RPA1786:putative 3-hydroxybutyryl-CoA dehydratase
fcs2:putative feruloyl-CoA synthetase

>operons_50:RPA1791-RPA1793 2007080..2010614 r
RPA1791:branched-chain amino acid transport system
RPA1792:putative branched-chain amino acid transport
RPA1793:branched-chain amino acid transport system

>operons_50:RPA1805-RPA1806 2028745..2031139 f
RPA1805:possible transcriptional regulator
RPA1806:L-carnitine dehydratase/bile acid-inducible

>operons_50:RPA1813-RPA1814 2039897..2041146 f
RPA1813:putative SigD protein
RPA1814:conserved hypothetical protein

>operons_50:RPA1817-RPA1818 2043919..2046355 r
RPA1817:conserved hypothetical protein
RPA1818:possible GGDEF family protein

>operons_50:RPA1819-RPA1820 2046600..2047999 f
RPA1819:putative RNA polymerase sigma-E factor
RPA1820:hypothetical protein

>operons_50:RPA1828-argK 2057481..2059117 r
RPA1828:Pyrrolidone-carboxylate/pyroglutamyl peptidase I
argK:LAO/AO transport system kinase

>operons_50:RPA1830-RPA1831 2059204..2059796 r
RPA1830:hypothetical protein
RPA1831:conserved hypothetical protein

>operons_50:RPA1833-RPA1834 2060841..2061505 r
RPA1833:PilT protein, N-terminal
RPA1834:hypothetical protein

>operons_50:RPA1836-RPA1837 2063791..2066123 r
RPA1836:DUF636
RPA1837:possible methylmalonyl-CoA small subunit

>operons_50:folK-folP 2066281..2067993 r
folK:putative
folB:putative dihydroneopterin aldolase
folP:dihydropteroate synthase

>operons_50:RPA1841-RPA1842 2068059..2068852 r
RPA1841:conserved unknown protein
RPA1842:conserved unknown protein

>operons_50:RPA1846-RPA1847 2075163..2076175 f
RPA1846:unknown protein
RPA1847:conserved hypothetical protein

>operons_50:RPA1848-RPA1849 2076237..2078095 f
RPA1848:Uncharacterized iron-regulated membrane protein
RPA1849:conserved hypothetical protein

>operons_50:RPA1858-RPA1859 2086715..2089325 f
RPA1858:putative two component histidine sensor kinase

RPA1859:conserved hypothetical protein

>operons_50:RPA1865-RPA1867 2093990..2097448 r
RPA1865:conserved hypothetical protein
RPA1866:conserved hypothetical protein
RPA1867:putative penicillin-binding protein

>operons_50:RPA1871-thcC 2099919..2101487 f
RPA1871:putative cytochrome P450
thcC:Rhodocoxin

>operons_50:RPA1874-RPA1876 2102977..2106625 r
RPA1874:hypothetical protein
RPA1875:possible uncharacterized iron-regulated membrane
RPA1876:putative TonB-dependent iron siderophore

>operons_50:RPA1885-RPA1886 2118601..2120014 f
RPA1885:putative portal protein, R. capsulatus GTA orfg3
RPA1886:hypothetical protein

>operons_50:GTAorfg6-GTAorfg11 2131110..2133931 f
GTAorfg6:homologue of Rhodobacter capsulatus gene
GTAorfg7:homologue of Rhodobacter capsulatus gene
GTAorfg8:homologue of Rhodobacter capsulatus gene
GTAorfg9:homologue of Rhodobacter capsulatus gene
GTAorfg10:homologue of Rhodobacter capsulatus gene
GTAorfg10.1:homologue of Rhodobacter capsulatus gene
GTAorfg11:homologue of Rhodobacter capsulatus gene

>operons_50:GTAorfg13-GTAofrg14 2136963..2138366 f
GTAorfg13:homologue of Rhodobacter capsulatus gene
GTAofrg14:homologue of Rhodobacter capsulatus gene

>operons_50:RPA1909-RPA1911 2139516..2141014 f
RPA1909:putative transcriptional regulator, MarR family
RPA1910:conserved hypothetical protein
RPA1911:Nickel-dependent hydrogenase b-type cytochrome

>operons_50:RPA1912-RPA1913 2141169..2146418 f
RPA1912:homologue of Rhodobacter capsulatus gene
RPA1913:conserved hypothetical protein

>operons_50:feuP-feuQ 2147990..2150071 f
feuP:FeuP two-component system, regulatory protein
feuQ:FeuQ two-component system, sensor histidine

>operons_50:cycJ-cycL 2153641..2156634 f
cycJ:CycJ cytochrome-c biosynthesis protein
cycK:CycK cytochrome c-type synthesis protein
cycL:CycL cytochrome C-type biogenesis protein

>operons_50:RPA1927-RPA1928 2161591..2163041 r
RPA1927:hypothetical protein
RPA1928:ferredoxin-like protein [2Fe-2S]

>operons_50:RPA1932-glnE 2167673..2172090 f

RPA1932:sensor histidine kinase
glnE:putative glutamate-ammonia-ligase

>operons_50:RPA1940-RPA1941 2182941..2184950 r
RPA1940:putative quinone oxidoreductase
RPA1941:possible 2-nitropropane dioxygenase

>operons_50:pqqB-pqqE 2191349..2194524 f
pqqB:pyrroloquinoline quinone biosynthesis protein B
pqqC:pyrroloquinoline quinone biosynthesis protein C
pqqD:pyrroloquinoline quinone biosynthesis protein D
pqqE:putative pyrroloquinoline quinone biosynthesis

>operons_50:RPA1951-RPA1953 2194774..2197882 r
RPA1951:possible FusE - MFP/HlyD family membrane fusion
RPA1952:conserved hypothetical membrane protein
RPA1953:possible FusB/FusC Fusaric Acid resistance pump

>operons_50:RPA1959-RPA1963 2203559..2210269 f
RPA1959:putative RND efflux membrane protein
RPA1960:putative RND efflux membrane protein
RPA1961:RND efflux transporter
RPA1962:unknown protein
RPA1963:Patatin-like phospholipase domain

>operons_50:RPA1967-RPA1968 2213962..2218232 f
RPA1967:putative component of multidrug efflux system
RPA1968:RND efflux transporter

>operons_50:RPA1970-RPA1972 2219352..2221778 r
RPA1970:conserved hypothetical protein
RPA1971:hypothetical protein
RPA1972:histidine kinase sensor protein

>operons_50:RPA1976-RPA1977 2225766..2228241 r
RPA1976:possible TrapT family, dctM subunit, glutamate
RPA1977:possible TrapT family, dctQ subunit, glutamate

>operons_50:cbbI,rpiA,ppi-gor 2230997..2233634 f
cbbI,rpiA,ppi:ribose 5-phosphate isomerase
RPA1982:conserved unknown protein
gor:putative glutathione reductase

>operons_50:RPA1985-nadE 2235342..2237493 f
RPA1985:probable diacylglycerol kinase
nadE:NH3-dependent NAD synthetase

>operons_50:RPA1990-RPA1991 2240367..2243230 f
RPA1990:possible sulfatase
RPA1991:conserved hypothetical protein

>operons_50:RPA1992-RPA1993 2243485..2244155 r
RPA1992:possible NtrR protein
RPA1993:possible virulence-associated protein

>operons_50:RPA1998-RPA2000 2248843..2251069 f

RPA1998:hypothetical protein
RPA1999:GCN5-related
RPA2000:putative isopropyl malate synthase

>operons_50:leuA-RPA2002 2251263..2254228 f
leuA:putative acetolactate synthase large subunit
RPA2002:FAD linked oxidase, C-terminal:FAD linked

>operons_50:RPA2005-pssA 2257299..2260945 f
RPA2005:ABC transporter, fused ATPase and permease
psd:putative phosphatidylserine decarboxylase
pssA:possible phosphatidylserine synthase

>operons_50:RPA2009-motB1 2262032..2263660 f
RPA2009:possible chemotaxis protein motA
motB1:putative chemotaxis protein motB1

>operons_50:RPA2012-RPA2014 2265975..2268604 f
RPA2012:conserved unknown protein
RPA2013:possible aminotransferase
RPA2014:ABC transporter, polyamine transport protein

>operons_50:RPA2017-RPA2018 2272117..2274071 r
RPA2017:putative lipid A biosynthesis lauroyl
RPA2018:alcohol dehydrogenase

>operons_50:RPA2019-RPA2022 2274168..2277437 r
RPA2019:3-oxoacyl-acyl carrier protein synthase II
RPA2020:3-oxoacyl-acyl carrier protein synthase
RPA2021:3-hydroxymyristoyl-acyl carrier protein
RPA2022:specialized acyl carrier protein

>operons_50:RPA2039-RPA2040 2295590..2297742 r
RPA2039:possible choline ABC transporter permease and
RPA2040:possible choline ABC transporter ATP-binding

>operons_50:RPA2043-RPA2044 2299917..2301663 f
RPA2043:putative ABC transporter, periplasmic
RPA2044:conserved unknown protein

>operons_50:dctQ-dctM 2306192..2308098 f
dctQ:possible TrapT family, dctQ subunit,
dctM:TrapT family, dctM subunit, C4-dicarboxylate

>operons_50:RPA2051-RPA2052 2309647..2312569 f
RPA2051:putative ornithine decarboxylase
RPA2052:putative phophinothricin N-acetyltransferase

>operons_50:RPA2054-RPA2057 2313105..2318978 f
RPA2054:possible outer membrane protein precursor CzcC
RPA2055:possible RND divalent metal cation efflux
czcA:RND divalent metal cation efflux transporter
RPA2057:hypothetical protein

>operons_50:nosR-RPA2067 2320449..2329830 f
nosR:regulatory protein NosR

nosZ:nitrous-oxide reductase precursor NosZ
nosD:putative periplasmic ABC transport copper
nosF:putative NosF protein (an ABC transporter)
nosY:putative NosY protein, possible ABC permease
nosL:putative nosL (possibly a disulfide isomerase)
nosX:putative nosX
RPA2067:hypothetical protein

>operons_50:RPA2068-RPA2070 2329917..2332005 f
RPA2068:conserved unknown protein
RPA2069:conserved hypothetical protein
RPA2070:hypothetical protein

>operons_50:RPA2074-RPA2075 2333431..2335697 r
RPA2074:possible response regulator
RPA2075:possible sensor histidine kinase

>operons_50:RPA2076-RPA2077 2336125..2337734 r
RPA2076:possible sensory transduction histidine kinase
RPA2077:possible transcriptional regulator, Fnr-type

>operons_50:cobA-cobL 2341120..2345605 r
cobA:putative uroporphyrin III methylase
cobB:putative cobyrinic acid a,c-diamide synthase
cobM:precorrin 3 or 4 methylase
CbiG:cobalamin biosynthesis protein G; CbiG
cobL:putative precorrin 6y methylase

>operons_50:cobJ-RPA2091 2346353..2349025 r
cobJ:precorrin 3 methylase
cobI:precorrin 2 methylase
cobH:precorrin isomerase CobH
RPA2091:hypothetical protein

>operons_50:RPA2092-RPA2093 2349426..2351847 r
RPA2092:conserved hypothetical protein
RPA2093:conserved hypothetical protein

>operons_50:cobT-RPA2095 2352419..2354250 f
cobT:putative
RPA2095:possible cobalamin (5`-phosphate) synthase

>operons_50:cobQ-cobF 2354337..2356707 f
cobQ:cobyric acid synthase
cobF:putative cobF protein

>operons_50:RPA2101-RPA2104 2360535..2365212 f
RPA2101:conserved hypothetical protein
RPA2102:conserved hypothetical protein
RPA2103:conserved hypothetical protein
RPA2104:conserved hypothetical protein

>operons_50:RPA2107-RPA2108 2367208..2372719 r
RPA2107:possible histidine kinase
RPA2108:putative transcriptional activator

>operons_50:nrtB-cynS 2377950..2380213 f
nrtB:possible nitrate transport system permease
nrtC:putative nitrate transport system ATP-binding
cynS:putative cyanate lyase

>operons_50:RPA2116-RPA2117 2380320..2381197 r
RPA2116:hypothetical protein
RPA2117:putative flavodoxin

>operons_50:RPA2118-RPA2121 2381400..2384453 r
RPA2118:putative ATP-binding protein of ABC transporter
RPA2119:putative permease protein of ABC transporter
RPA2120:putative hemin binding protein
RPA2121:conserved unknown protein

>operons_50:RPA2122-RPA2123 2384786..2386905 f
RPA2122:putative oxygen independent coproporphyrinogen
RPA2123:conserved unknown protein

>operons_50:RPA2125-RPA2129 2389539..2392511 f
RPA2125:conserved unknown protein
RPA2126:conserved unknown protein
exbB:putative exbB, uptake of enterochelin;
exbD:biopolymer transport protein ExbD/TolR
RPA2129:possible energy transducer TonB, C-terminal

>operons_50:RPA2132-RPA2133 2396132..2398313 f
RPA2132:hypothetical protein
RPA2133:conserved hypothetical protein

>operons_50:RPA2143-RPA2144 2409057..2412658 f
RPA2143:putative acetyl/propionyl-CoA carboxylase
RPA2144:possible biotin carboxylase

>operons_50:RPA2149-RPA2150 2418328..2420184 f
RPA2149:putative hydroxyquinol 1,2-dioxygenase
RPA2150:putative oxidoreductase

>operons_50:RPA2169-RPA2170 2443567..2445160 f
RPA2169:possible ribulose-bisphosphate carboxylase large
RPA2170:hypothetical protein

>operons_50:RPA2172-RPA2174 2446500..2448556 r
RPA2172:putative oxidoreductase
RPA2173:GCN5-related N-acetyltransferase
RPA2174:conserved hypothetical protein

>operons_50:RPA2175-RPA2176 2448770..2450591 r
RPA2175:Transglutaminase-like domain
RPA2176:DUF403

>operons_50:RPA2183-RPA2184 2457284..2458878 f
RPA2183:DSBA oxidoreductase
RPA2184:putative oxidoreductase

>operons_50:RPA2185-RPA2186 2458970..2460373 f

RPA2185:nodN-like protein
RPA2186:possible 3-oxo-(acyl) acyl carrier protein

>operons_50:RPA2188-RPA2189 2461819..2462798 r
RPA2188:hypothetical protein
RPA2189:possible regulatory proteins, tetR family

>operons_50:RPA2190-RPA2191 2462902..2465206 r
RPA2190:ABC transporter, with duplicated ATPase domains
RPA2191:DUF188

>operons_50:RPA2207-RPA2209 2484202..2487543 f
RPA2207:putative recombinase
parB:possible ParB-like partioning protein
RPA2209:ParB-like nuclease

>operons_50:RPA2211-RPA2213 2489714..2495862 r
RPA2211:DEAD/DEAH box helicase:Helicase, C-terminal
RPA2212:hypothetical protein
RPA2213:hypothetical protein

>operons_50:RPA2214-RPA2216 2495915..2505340 r
RPA2214:possible helicase
RPA2215:possible ATP-dependent exodeoxyribonuclease
RPA2216:hypothetical protein

>operons_50:RPA2217-RPA2221 2505626..2520431 f
RPA2217:conserved unknown protein
RPA2218:possible ATP-dependent RNA helicase
RPA2219:Possible ATPase
RPA2220:conserved unknown protein
RPA2221:conserved unknown protein

>operons_50:RPA2223-trbB 2521433..2531018 r
RPA2223:conserved hypothetical protein
trbI:possible trbI, a component on a type IV
trbG:probable conjugal transfer protein trbG
trbF:putative conjugal transfer protein trbF
trbL:putative CONJUGAL TRANSFER protein trbL
trbK:probable trbK
trbJ:putative conjugal transfer protein trbJ
trbE:conjugal transfer protein trbE
trbD:conjugal transfer protein trbD
trbC:putative conjugal transfer protein; TrbC
trbB:conjugal transfer protein trbB

>operons_50:RPA2234-traG 2531155..2533598 r
RPA2234:conserved hypothetical protein
traG:plasmid transfer factor, traG protein

>operons_50:RPA2247-RPA2249 2543965..2550634 r
RPA2247:conserved hypothetical protein
RPA2248:conserved hypothetical protein
RPA2249:putative methylase/helicase

>operons_50:RPA2250-RPA2251 2550722..2553156 r

RPA2250:hypothetical protein
RPA2251:putative plasmid stabilization protein

>operons_50:RPA2254-RPA2255 2555371..2556767 r
RPA2254:hypothetical protein
RPA2255:hypothetical protein

>operons_50:RPA2256-arsH 2557368..2560178 f
RPA2256:putative ArsR regulatory protein
arsC:arsenate reductase pump modifier
arsB:arsenical pump membrane protein
arsH:possible arsH protein

>operons_50:RPA2263-RPA2265 2566820..2568734 r
RPA2263:possible plasmid stabilization protein
RPA2264:conserved hypothetical protein
RPA2265:conserved hypothetical protein

>operons_50:RPA2273-RPA2274 2576083..2576729 f
RPA2273:hypothetical protein
RPA2274:hypothetical protein

>operons_50:RPA2275-RPA2278 2576915..2580296 f
RPA2275:putative branched-chain amino acid transport
RPA2276:putative branched-chain amino acid transport
RPA2277:possible ABC transporter, permease protein
RPA2278:possible ABC transporter, permease protein

>operons_50:RPA2280-RPA2281 2583631..2585306 f
RPA2280:putative low-affinity phosphate transport
RPA2281:putative low-affinity phosphate transport

>operons_50:RPA2282-RPA2283 2585324..2585953 r
RPA2282:conserved hypothetical protein
RPA2283:putative proteic killer suppression protein

>operons_50:RPA2289-RPA2290 2592184..2595245 f
RPA2289:hypothetical protein
RPA2290:conserved hypothetical protein

>operons_50:RPA2295-RPA2296 2601286..2602415 f
RPA2295:unknown protein
RPA2296:conserved hypothetical protein

>operons_50:RPA2302-RPA2303 2609019..2611496 f
RPA2302:acyl-CoA synthetase
RPA2303:putative 3-hydroxyacyl-CoA dehydrogenase

>operons_50:RPA2304-RPA2305 2611555..2613877 f
RPA2304:putative acyl-CoA thiolase
RPA2305:acyl-CoA dehydrogenase

>operons_50:RPA2308-RPA2310 2617418..2620451 f
RPA2308:possible periplasmic iron siderophore binding
RPA2309:putative iron chelatin ABC transporter, permease
RPA2310:putative iron ABC transporter ATP-binding

>operons_50:RPA2311-RPA2313 2620446..2622218 r
RPA2311:hypothetical protein
RPA2312:hypothetical protein
RPA2313:unknown protein

>operons_50:RPA2314-RPA2315 2622816..2623934 f
RPA2314:cytochrome c556
RPA2315:putative nickel-dependent hydrogenase, b-type

>operons_50:RPA2316-gctA 2623966..2626562 r
RPA2316:enoyl-CoA hydratase
gctB:putative CoA transferase, small subunit B
gctA:possible glutaconate CoA-transferase, subunit A

>operons_50:RPA2320-RPA2321 2627760..2629738 r
RPA2320:possible TctA subunit of the Tripartite
RPA2321:possible TctB subunit of the Tripartite

>operons_50:goaT-RPA2326 2631514..2637214 f
goaT:4-aminobutyrate aminotransferase
gabD:succinate-semialdehyde dehydrogenase
RPA2325:possible acetylornithine deacetylase
RPA2326:acetolactate synthase I

>operons_50:RPA2327-RPA2330 2637293..2642408 f
RPA2327:putative ABC transporter oligopeptide-binding
RPA2328:putative ABC transporter permease protein
RPA2329:putative ABC transporter permease protein
RPA2330:putative ABC transporter ATP-binding protein

>operons_50:ctpC-RPA2338 2645744..2649677 r
ctpC:putative cation transport ATPase, possible
RPA2334:unknown protein
RPA2335:unknown protein
RPA2336:unknown protein
RPA2337:hypothetical protein
RPA2338:unknown protein

>operons_50:RPA2344-RPA2345 2656394..2658025 r
RPA2344:conserved unknown protein
RPA2345:unknown protein

>operons_50:RPA2346-RPA2348 2658270..2662416 r
RPA2346:hypothetical protein
RPA2347:possible vanadium nitrogenase associated protein
RPA2348:possible nitrogenase molybdenum-iron protein

>operons_50:RPA2352-RPA2355 2666343..2669107 r
RPA2352:conserved hypothetical protein
nifH:putative nitrogenase NifH subunit
nifB:putative nitrogenase iron-molybdenum cofactor
RPA2355:possible nitrogenase NifB

>operons_50:RPA2356-RPA2357 2669577..2672148 f
RPA2356:putative cystathionine beta-synthase

RPA2357:cystathionine gamma-lyase

>operons_50:RPA2359-RPA2364 2673702..2680643 f
RPA2359:putative periplasmic protein
RPA2360:ABC transporter, ATP-binding protein
RPA2361:putative ABC transporter, permease protein
RPA2362:putative O-acetylhomoserine sulfhydrylase
NifD:possible nitrogenase molybdenum-iron protein
RPA2364:possible nitrogenase iron-molybdenum cofactor

>operons_50:RPA2367-RPA2370 2682429..2684612 r
RPA2367:possible sensor protein (for BaeR)
RPA2368:possible transcriptional regulatory protein
RPA2369:possible two-component response regulator
RPA4839:hypothetical protein
RPA2370:hypothetical protein

>operons_50:mexA-RPA2374 2684924..2691043 f
mexA:putative RND multidrug efflux membrane fusion
mexB:RND multidrug efflux transporter MexB
RPA2373:possible outer membrane protein
RPA2374:hypothetical protein

>operons_50:RPA2379-RPA2380 2696546..2699288 r
RPA2379:probable acetyltransferase
RPA2380:probable tonB dependent iron siderophore

>operons_50:RPA2382-RPA2390 2700496..2711051 r
RPA2382:putative iron(III) ABC transporter, ATP-binding
RPA2383:putative iron(III) ABC transporter, permease
RPA2384:putative ironIII transport permease protein
RPA2385:putative ABC transporter, periplasmic Fe+3
RPA2386:conserved hypothetical protein
RPA2387:conserved hypothetical protein
RPA2388:possible acyl-CoA ligase for activation during
RPA2389:possible Rhizobactin siderophore biosynthesis
RPA2390:possible Rhizobactin siderophore biosynthesis

>operons_50:prpC-RPA2396 2713351..2715783 f
prpC:putative 2-methylcitrate synthase
prpB:putative carboxyphosphonoenolpyruvate
RPA2396:DUF208

>operons_50:RPA2398-RPA2401 2719364..2726476 f
RPA2398:iron siderophore uptake receptor family,
RPA2399:CobN/Magnesium chelatase family
RPA2400:conserved hypothetical protein
RPA2401:conserved unknown protein

>operons_50:draT-draG 2729949..2731723 f
draT:NAD+ ADP-ribosyltransferase
draG:dinitrogenase reductase activating

>operons_50:amiC-RPA2410 2732949..2736018 f
amiC:putative aliphatic amidase expression-regulating
RPA2409:possible AmiR antitermination protein

RPA2410:putative urea/short-chain amide transport system

>operons_50:RPA2411-RPA2417 2736137..2743059 f
RPA2411:putative permease of ABC transporter
RPA2412:possible permease of ABC transporter
RPA2413:putative urea/short-chain amide transport system
RPA2414:putative urea/short-chain amide transport system
RPA2415:Acetamidase/Formamidase
RPA2416:Nitrilase/cyanide hydratase and apolipoprotein
RPA2417:putative 3-ketoacyl-CoA reductase

>operons_50:RPA2424-RPA2425 2752915..2755300 r
RPA2424:conserved unknown protein
RPA2425:putative lipase/esterase

>operons_50:RPA2430-RPA2431 2759213..2761344 r
RPA2430:conserved hypothetical protein
RPA2431:conserved hypothetical protein

>operons_50:RPA2432-RPA2434 2761477..2764537 r
RPA2432:putative combined two-component sensor/response
RPA2433:possible two-component response regulator
RPA2434:putative sensor protein of two-component

>operons_50:accB-aroQ2 2766195..2767183 r
accB:putative biotin carboxyl carrier protein of
aroQ2:3-dehydroquinate dehydratase type 2

>operons_50:RPA2440-RPA2441 2768965..2770598 f
RPA2440:Cation efflux protein
RPA2441:possible transcription regulator

>operons_50:prfB-RPA2454 2787334..2789202 f
prfB:translation peptide releasing factor RF-2
RPA2454:putative dehydrogenase

>operons_50:sufC-RPA2469 2803960..2808088 f
sufC:sufC, related to ABC transporter ATP-binding
sufD:sufD, needed for fhuF Fe-S center
sufS:sufS, putative selenosysteine lyase
RPA2468:DUF59
RPA2469:putative lactoylglutathione lyase

>operons_50:RPA2471-RPA2473 2808744..2812284 f
RPA2471:unknown protein
RPA2472:hypothetical protein
RPA2473:possible translation initiation inhibitor

>operons_50:RPA2474-RPA2475 2812370..2814661 f
RPA2474:possible o-linked GlcNac transferase
RPA2475:TfoX, N-terminal

>operons_50:RPA2483-RPA2484 2824175..2825053 r
RPA2483:hypothetical protein
RPA2484:conserved hypothetical protein

>operons_50:RPA2490-argC 2831398..2833073 f
RPA2490:conserved hypothetical protein
argC:N-acetylglutamate semialdehyde dehydrogenase

>operons_50:RPA2497-RPA2498 2838147..2839813 f
RPA2497:putative anion ABC transporter, ATP-binding
RPA2498:possible ABC transporter, permease protein

>operons_50:RPA2507-recJ 2849176..2851867 f
RPA2507:possible haloacid dehalogenase
recJ:putative single-strand DNA-specific exonuclease

>operons_50:RPA2510-RPA2511 2852406..2854771 r
RPA2510:conserved hypothetical protein
RPA2511:possible membrane-bound lytic transglycosylase

>operons_50:RPA2514-kamA 2856757..2858900 f
RPA2514:putative lysyl-tRNA synthetase
kamA:putative L-lysine 2,3-aminomutase

>operons_50:RPA2528-RPA2530 2869057..2870819 f
RPA2528:hypothetical protein
RPA2529:hypothetical protein
RPA2530:hypothetical protein

>operons_50:RPA2533-RPA2534 2872381..2873579 f
RPA2533:unknown protein
RPA2534:hypothetical protein

>operons_50:RPA2538-RPA2539 2877195..2880879 f
RPA2538:putative acyl-CoA carboxylase, beta chain
RPA2539:putative acyl-CoA carboxylase biotin-carrying

>operons_50:RPA2541-RPA2543 2882000..2884922 r
RPA2541:TrapT family, dctM subunit, C4-dicarboxylate
RPA2542:possible TrapT family, dctQ subunit,
RPA2543:TrapT family, dctP subunit, C4-dicarboxylate

>operons_50:RPA2548-RPA2549 2890202..2891484 f
RPA2548:conserved hypothetical protein
RPA2549:conserved hypothetical protein

>operons_50:RPA2553-RPA2554 2894171..2901576 f
RPA2553:conserved unknown protein
RPA2554:penicillin binding protein

>operons_50:RPA2555-RPA2556 2901627..2904222 f
RPA2555:Glycosyl transferase, family 39
RPA2556:PA-phosphatase related phosphoesterase

>operons_50:RPA2557-RPA2558 2904286..2905376 f
RPA2557:Glycosyl transferase, family 2
RPA2558:conserved hypothetical protein

>operons_50:aapJ-1-aapP-1 2907057..2911557 f
aapJ-1:ABC transporter, periplasmic amino acid binding

aapQ-1:polar amino acid ABC transport permease protein
aapM-1:polar amino acid ABC transport permease protein
aapP-1:amino acid ABC transporter, ATP-binding protein

>operons_50:RPA2566-RPA2567 2912351..2914782 f
RPA2566:putative EA59 gene protein, phage lambda
RPA2567:possible EA31 gene protein, phage lambda

>operons_50:RPA2570-RPA2571 2917359..2919519 r
RPA2570:conserved hypothetical protein
RPA2571:possible NADPH-dependent oxidoreductase

>operons_50:RPA2572-RPA2573 2919954..2922762 f
RPA2572:possible outer membrane efflux protein.
RPA2573:possible membrane protein, permease.

>operons_50:RPA2574-RPA2576 2922833..2929810 f
RPA2574:possible RND efflux transporter
RPA2575:possible RND efflux transporter
RPA2576:conserved hypothetical protein

>operons_50:RPA2577-RPA2578 2930223..2932828 f
RPA2577:putative alginate o-acetyltransferase AlgI
RPA2578:possible alginate o-acetyltransferase AlgJ

>operons_50:RPA2580-RPA2581 2934119..2936386 f
RPA2580:possible protein-L-isoaspartate
RPA2581:putative outer membrane protein

>operons_50:valS-RPA2584 2937609..2940872 f
valS:valyl-tRNA synthetase
RPA2584:possible glyoxalase

>operons_50:lipA-RPA2588 2942590..2944049 f
lipA:lipoic acid synthetase
RPA2588:Protein of unknown function UPF0083

>operons_50:cinA-ispD 2944131..2945950 r
cinA:possible competence-damaged protein
ispD:4-diphosphocytidyl-2C-methyl-D-erythritol

>operons_50:nifR3-ntrC 2946224..2949846 f
nifR3:putative nitrogen regulation protein nifR3
ntrB:nitrogen regulation protein ntrB protein,
ntrC:nitrogen assimilation regulatory protein ntrC

>operons_50:ntrY-RPA2596 2950006..2954579 f
ntrY:nitrogen regulation protein ntrY, Sensory
ntrX:nitrogen assimilation regulatory protein ntrX -
RPA2596:D-alanine aminotransferase

>operons_50:kdtB-RPA2604 2960110..2962095 f
kdtB:phosphopantetheine adenylyltransferase
RPA2602:peptidyl prolyl cis-trans isomerase
RPA2603:conserved hypothetical protein
RPA2604:peptidyl prolyl cis-trans isomerase

>operons_50:queA-tgt 2962252..2964476 f
queA:S-adenosylmethionine tRNA ribosyltransferase
tgt:tRNA guanine transglycosylase

>operons_50:RPA2609-RPA2613 2967856..2972256 r
RPA2609:possible monooxygenase
ssuB:aliphatic sulfonate transport ATP-binding
RPA2611:putative aliphatic sulfonate transport membrane
msuD:methanesulfonate sulfonatase MsuD
RPA2613:putative aliphatic sulfonate binding protein,

>operons_50:RPA2614-RPA2617 2972643..2977439 f
RPA2614:conserved hypothetical protein
nifH:putative nitrogenase iron protein (nitrogenase
RPA2616:possible nitrogenase iron-molybdenum cofactor
RPA2617:possible vanadium nitrogenase associated protein

>operons_50:RPA2620-RPA2623 2980614..2983131 r
RPA2620:unknown protein
RPA2621:conserved unknown protein
RPA2622:putative sulfonate transport system, ATP-binding
RPA2623:possible sulfonate transport system permease

>operons_50:RPA2627-aapM-2 2987649..2992668 f
RPA2627:putative carboxylesterase
aapJ-2:polar amino acid ABC transport substrate-binding
aapQ-2:polar amino acid ABC transpor permease protein,
aapM-2:polar amino acid ABC transport system protein,

>operons_50:RPA2631-RPA2633 2993216..2996065 f
RPA2631:possible ABC transport substrate-binding
RPA2632:ABC transport permease protein, possibly for
RPA2633:putative ATP-binding protein of ABC transporter,

>operons_50:nifB-nifH 2996908..2998712 f
nifB:putative nitrogenase iron-molybdenum cofactor
nifH:putative nitrogenase reductase NifH subunit

>operons_50:NifD-RPA2637 2998778..3001680 f
NifD:possible nitrogenase molybdenum-iron protein
RPA2637:possible nitrogenase iron-molybdenum protein

>operons_50:RPA2639-RPA2641 3003327..3006129 r
RPA2639:probable L-2-amino-thiazoline-4-carboxylic acid
RPA2640:Isochorismatase hydrolase family
RPA2641:putative ABC transporter oligopeptide-binding

>operons_50:RPA2643-RPA2646 3007305..3012377 r
RPA2643:putative ABC transporter ATP-binding protein
RPA2644:putative ABC transporter permease protein
RPA2645:putative ABC transporter permease protein
RPA2646:putative ABC transporter oligopeptide-binding

>operons_50:RPA2647-RPA2648 3012547..3014525 r
RPA2647:putative hydrolase

RPA2648:unknown protein

>operons_50:pucAa-pucBa 3017745..3018093 r
pucAa:light harvesting protein B-800-850, alpha chain
pucBa:light harvesting protein B-800-850, beta chain A

>operons_50:RPA2664-RPA2666 3036761..3041462 r
RPA2664:hypothetical protein
RPA2665:possible acid-CoA ligase
RPA2666:possible binding protein component of ABC

>operons_50:RPA2668-RPA2669 3042513..3043561 r
RPA2668:unknown protein
RPA2669:conserved hypothetical protein

>operons_50:RPA2672-RPA2673 3045976..3047429 f
RPA2672:possible phosphatidylcholine synthase
RPA2673:possibly involved in transport

>operons_50:RPA2677-RPA2680 3051410..3054922 f
RPA2677:putative substrate-binding protein, subunit of
RPA2678:putative permease protein, subunit of ABC
RPA2679:putative transport system ATP-binding protein
RPA2680:conserved hypothetical protein

>operons_50:RPA2681-dur1 3054938..3057465 r
RPA2681:possible lactam utilization protein.
uahA:Urea amidolyase-related
dur1:DUF213

>operons_50:RPA2684-RPA2685 3057686..3058819 f
RPA2684:conserved unknown protein
RPA2685:conserved hypothetical protein

>operons_50:dapA-RPA2689 3058948..3061443 f
dapA:dihydrodipicolinate synthase
mscL:large-conductance mechanosensitive channel
SmpB:small protein B
RPA2689:possible thiol-specific antioxidant related

>operons_50:RPA2690-RPA2691 3061557..3062887 r
RPA2690:possible uracil-DNA glycosylase
RPA2691:DUF88

>operons_50:pdxJ-acpS 3066324..3067525 f
pdxJ:pyridoxal phosphate biosynthetic protein pdxJ
acpS:acyl carrier protein synthase

>operons_50:lepB-RPA2700 3067767..3071449 f
lepB:putative signal peptidase I
RPA2697:putative ribonuclease III
era:possible GTP-binding protein Era
RPA2699:hypothetical protein
RPA2700:putative DNA repair protein RecO

>operons_50:RPA2702-parC 3072441..3075224 f

RPA2702:DUF24, predicted transcriptional regulator,
parC:DNA topoisomerase IV subunitA

>operons_50:RPA2708-RPA2709 3079565..3082762 f
RPA2708:possible fusaric acid resistance pump
RPA4838:hypothetical membrane protein
RPA2709:possible FusE - MFP/HlyD family membrane fusion

>operons_50:RPA2716-RPA2719 3088824..3090321 f
RPA2716:conserved hypothetical protein
RPA2717:conserved hypothetical protein
RPA2718:hypothetical protein
RPA2719:conserved hypothetical protein

>operons_50:RPA2725-ribC 3095345..3097612 f
RPA2725:DUF193:ATP cone domain
ribD:putative riboflavin-specific deaminase /
ribC:riboflavin synthase alpha chain

>operons_50:ribE-RPA2729 3097743..3098764 f
ribE:riboflavin synthase, beta chain
RPA2729:putative N-utilization substance protein B

>operons_50:RPA2733-RPA2734 3103016..3104075 f
RPA2733:unknown protein
RPA2734:possible epoxide hydrolase-related protein

>operons_50:mexC-mexD 3104271..3108614 f
mexC:putative RND multidrug efflux membrane fusion
mexD:RND multidrug efflux transporter MexD

>operons_50:RPA2738-RPA2739 3109261..3110381 f
RPA2738:conserved hypothetical protein
RPA2739:conserved unknown protein

>operons_50:plsX-fabH 3110622..3112657 f
plsX:fatty acid/phospholipid synthesis protein
fabH:3-oxoacyl-acyl carrier protein synthase III

>operons_50:himA-RPA2743 3112791..3113914 f
himA:integration host factor alpha subunit
RPA2743:bacterial regulatory protein, MerR family

>operons_50:RPA2748-RPA2749 3118557..3120349 f
RPA2748:possible short-chain dehydrogenase
RPA2749:conserved unknown protein

>operons_50:RPA2759-RPA2760 3131802..3134283 r
RPA2759:possible transcriptional regulatory proteins,
RPA2760:possible benzaldehyde lyase

>operons_50:RPA2762-RPA2763 3134810..3136690 r
RPA2762:conserved hypothetical protein
RPA2763:putative O-acetylhomoserine sulfhydrylase

>operons_50:RPA2766-rpsI,S9 3138437..3139969 f

RPA2766:Phenylacetic acid degradation-related
rplM,L13:ribosomal protein L13
rpsI,S9:ribosomal protein S9

>operons_50:RPA2774-RPA2776 3145328..3148316 f
RPA2774:penicillin binding protein
RPA2775:thymidylate kinase
RPA2776:probable DNA polymerase III, delta prime

>operons_50:metG-RPA2779 3148397..3151562 f
metG:methionyl-tRNA synthetase
RPA2778:possible deoxyribonuclease
RPA2779:possible hydrolase

>operons_50:dctQ-dctP 3153461..3156376 r
dctQ:TrapT dctQ-M fusion permease, dicarboxylate
dctP:TrapT family, dctP subunit, C4-dicarboxylate

>operons_50:phaA-phaG 3163151..3169172 f
phaA:pH adaptation potassium efflux system components
phaC:pH adaptation K efflux system component
phaD:putative component of pH adaptation K-efflux
phaE:putative component of pH adaptation K-efflux
phaF:pH adaptation potassium efflux system phaF
phaG:putative pH adaptation potassium efflux system

>operons_50:RPA2795-glyA 3169197..3171304 r
RPA2795:Protein of unknown function UPF0001
glyA:glycine hydroxymethyltransferase

>operons_50:BenE-pdxK 3173005..3175151 f
BenE:probable Benzoate membrane transport protein
pdxK:putative pyridoxamine kinase

>operons_50:nthA-RPA2807 3180266..3181982 f
nthA:nitrile hydratase alpha subunit
nthB:putative nitrile hydratase beta subunit
RPA2807:conserved hypothetical protein

>operons_50:RPA2812-RPA2813 3186319..3187973 f
RPA2812:probable HlyC/CorC family of transporters with 2
RPA2813:hypothetical protein

>operons_50:RPA2819-RPA2820 3194789..3195492 r
RPA2819:conserved hypothetical protein
RPA2820:DUF433

>operons_50:RPA2821-RPA2822 3195528..3196896 f
RPA2821:possible ion transporter
RPA2822:conserved unknown protein

>operons_50:RPA2828-RPA2829 3202230..3203482 r
RPA2828:conserved hypothetical protein
RPA2829:conserved hypothetical protein

>operons_50:secF-yajC 3203644..3206871 r

secF:putative protein-export membrane protein secF
secD:protein-export membrane protein secD
yajC:putative membrane protein, possible preprotein

>operons_50:RPA2844-serS 3219531..3221512 r
RPA2844:SCP-like extracellular protein
serS:seryl-tRNA synthetase

>operons_50:tatC-tatB 3222083..3223404 r
tatC:putative sec-independent protein translocase
tatB:possible sec-independent protein secretion

>operons_50:RPA2850-RPA2853 3224004..3228849 r
RPA2850:conserved unknown protein
RPA2851:DUF173
RPA2852:putative sugar hydrolase
RPA2853:Proline-rich region

>operons_50:RPA2857-RPA2858 3232645..3234755 f
RPA2857:unknown protein
RPA2858:Gated ion-channel ligand binding domain

>operons_50:RPA2864-RPA2866 3241258..3244372 r
RPA2864:dihydrolipoamide acetyltransferase
RPA2865:conserved unknown protein
RPA2866:pyruvate dehydrogenase E1 beta subunit

>operons_50:RPA2876-RPA2877 3253245..3256903 f
RPA2876:periplasmic glucans biosynthesis protein OpgG
RPA2877:putative glycosyltransferase family protein

>operons_50:RPA2878-RPA2880 3256900..3259906 r
RPA2878:possible MDR related permease
kdsA:2-dehydro-3-deoxyphosphooctonate aldolase
RPA2880:conserved hypothetical protein

>operons_50:RPA2889-trpD 3266039..3268993 f
RPA2889:putative peptidyl-prolyl cis-trans isomerse D
trpD:anthranilate phosphoribosyltransferase

>operons_50:trpC-RPA2893 3269058..3273058 f
trpC:indole-3-glycerol phosphate synthase
moaC:molybdenum cofactor biosynthesis protein C
RPA2893:putative cation-transporting ATPase

>operons_50:RPA2898-RPA2899 3275975..3277120 f
RPA2898:Haloacid dehalogenase-like hydrolase
RPA2899:conserved hypothetical protein

>operons_50:lpxB-RPA2914 3288404..3295401 r
lpxB:lipid-A-disaccharide synthase
RPA2910:conserved hypothetical protein
lpxA:acyl-acyl carrier
RPA2912:possible (3R)-hydroxymyristoyl-acyl carrier
lpxD:UDP-3-o-[3-hydroxymyristoyl] glucosamine
RPA2914:putative outer membrane protein

>operons_50:RPA2915-uppS 3295574..3299611 r
RPA2915:Zinc metalloprotease
dxr:1-deoxy-d-xylulose 5-phosphate reductoisomerase
cdsA:Phosphatidate cytidylyltransferase
uppS:undecaprenyl pyrophosphate synthetase

>operons_50:RPA2926-RPA2927 3310911..3312901 r
RPA2926:ATP-binding protein of ABC transporter, possibly
RPA2927:possible ABC type permease; lipoprotein

>operons_50:RPA2929-RPA2931 3314473..3317137 r
RPA2929:conserved hypothetical protein
RPA2930:conserved unknown protein
RPA2931:DUF461

>operons_50:RPA2933-nuoL 3318298..3326576 r
RPA2933:conserved hypothetical protein
RPA2934:conserved unknown protein
RPA2935:Beta-lactamase-like
birA:putative biotin-protein ligase birA
nuoN:NADH-ubiquinone dehydrogenase chain N
nuoM:NADH-ubiquinone dehydrogenase chain M
nuoL:NADH-ubiquinone dehydrogenase chain L

>operons_50:nuoK-nuoD 3326636..3335688 r
nuoK:NADH-ubiquinone dehydrogenase chain K
nuoJ:NADH-ubiquinone dehydrogenase chain J
nuoI:NADH-ubiquinone dehydrogenase chain I
nuoH:NADH-ubiquinone dehydrogenase chain H
nuoG:NADH-ubiquinone dehydrogenase chain G
nuoF:NADH-ubiquinone dehydrogenase chain F
RPA2946:conserved hypothetical protein
nuoE:NADH-ubiquinone dehydrogenase chain E
fkbM:possible methyltransferase, FkbM family
nuoD:NADH-ubiquinone dehydrogenase chain D

>operons_50:nuoC-nuoA 3335740..3337341 r
nuoC:NADH-ubiquinone dehydrogenase chain C
nuoB:NADH-ubiquinone dehydrogenase chain B
nuoA:NADH-ubiquinone dehydrogenase chain A

>operons_50:mex-mexF 3340667..3345080 f
mex:possible RND efflux membrane fusion protein
mexF:putative RND multidrug efflux transporter MexF

>operons_50:ybiH-RPA2969 3362578..3363951 f
ybiH:putative transcriptional regulator, tetR family
RPA2969:unknown protein

>operons_50:bioA-bioF 3364094..3367133 r
bioA:adenosylmethionine-8-amino-7-oxononanoate
bioD:dethiobiotin synthetase
bioF:8-amino-7-oxononanoate synthase

>operons_50:RPA2980-RPA2982 3377728..3378907 r

RPA2980:integrase
RPA2981:P2 ISBm2
RPA2982:possible insertion element ISR1 hypothetical 10

>operons_50:yrkN-RPA2989 3384525..3386145 f
yrkN:GCN5-related N-acetyltransferase
RPA2989:putative quinone oxidoreductase

>operons_50:RPA2992-RPA2993 3387497..3388863 r
RPA2992:conserved hypothetical protein
RPA2993:Domain of unknown function UPF0126

>operons_50:nuoL-RPA2996 3389982..3394001 f
nuoL:possible NADH-Ubiquinone/plastoquinone (complex
RPA2996:conserved hypothetical protein

>operons_50:RPA2997-dapA 3394158..3395372 f
RPA2997:hypothetical protein
dapA:putative dihydrodipicolinate synthase

>operons_50:ptsN2-kdpA 3395404..3403792 r
ptsN2:possible phosphotransferase system enzyme IIA,
kdpE:two-component response regulator
kdpD:two-component sensor KdpD
kdpC:potassium-transporting atpase c chain, KdpC
kdpB:potassium-transporting atpase b chain, KdpB
kdpA:potassium-transporting ATPase, A chain, KdpA

>operons_50:RPA3006-RPA3007 3404723..3406031 f
RPA3006:hypothetical protein
RPA3007:hypothetical protein

>operons_50:pucAd-pucBd 3410110..3410457 r
pucAd:light harvesting protein B-800-850, alpha chain
pucBd:light harvesting protein B-800-850, beta chain D

>operons_50:phyB1-RPA3018 3411808..3418013 f
phyB1:putative cyanobacterial phytochrome B
phyB2:putative cyanobacterial phytochrome B
rphyB:putative response regulator
RPA3018:possible histidine kinase-, DNA gyrase B-,

>operons_50:RPA3025-RPA3026 3426447..3427469 f
RPA3025:hypothetical protein
RPA3026:similar to abortive infection protein

>operons_50:RPA3039-RPA3040 3438785..3440324 f
RPA3039:possible polysaccharide deacetylase
RPA3040:unknown protein

>operons_50:mao-aspS 3440872..3445002 r
mao:malate oxidoreductase
aspS:aspartate-tRNA ligase

>operons_50:rnd-RPA3046 3446844..3448942 f
rnd:ribonuclease D

RPA3046:conserved hypothetical protein

>operons_50:RPA3047-RPA3048 3448964..3452773 r
RPA3047:putative exopolyphosphatase
RPA3048:putative polyphosphate kinase

>operons_50:RPA3049-RPA3050 3452843..3454192 r
RPA3049:conserved hypothetical protein
RPA3050:CDP-alcohol phosphatidyltransferase

>operons_50:purM-purN 3454375..3456110 f
purM:5'-phosphoribosyl-5-aminoimidazole synthetase
purN:phosphoribosylglycinamide formyltransferase

>operons_50:RPA3059-RPA3060 3461736..3463701 r
RPA3059:hypothetical protein
RPA3060:leucine aminopeptidase

>operons_50:RPA3061-RPA3063 3464110..3468888 f
RPA3061:possible permease
RPA3062:predicted permease
RPA3063:organic solvent tolerance protein homolog

>operons_50:pdxA-RPA3068 3469954..3474239 f
pdxA:pyridoxal phosphate biosynthetic protein PdxA
ksgA:dimethyladenosine transferase
RPA3067:putative NAD-dependent alcohol dehydrogenase
RPA3068:conserved hypothetical protein

>operons_50:kguA-RPA3070 3474243..3475795 r
kguA:putative guanylate kinase
RPA3070:conserved unknown protein

>operons_50:fabG-fabD 3479262..3480978 r
fabG:3-oxoacyl-acyl carrier protein reductase fabG
fabD:putative malonyl CoA-acyl carrier protein

>operons_50:RPS6-RPS18 3482765..3483486 f
RPS6:possible 30S ribosomal protein S6
RPS18:30S ribosomal protein S18

>operons_50:RPA3079-RPL9 3483613..3485186 f
RPA3079:hypothetical protein
RPL9:putative 50S ribosomal protein L9, cultivar

>operons_50:RPA3086-RPA3087 3491385..3493276 r
RPA3086:hypothetical protein
RPA3087:conserved hypothetical protein

>operons_50:RPA3090-purF 3495947..3498135 f
RPA3090:putative colicin V production protein
purF:amidophosphoribosyltransferase

>operons_50:RPA3094-RPA3095 3500339..3503001 r
RPA3094:putative tetracycline-efflux transporter
RPA3095:GTP-binding protein

>operons_50:RPA3096-RPA3097 3503075..3504361 r
RPA3096:conserved unknown protein
RPA3097:conserved unknown protein

>operons_50:panB-RPA3099 3504491..3505902 r
panB:3-methyl-2-oxobutanoate hydroxymethyltransferase
RPA3099:conserved hypothetical protein

>operons_50:RPA3108-RPA3109 3515232..3515751 f
RPA3108:conserved hypothetical protein
RPA3109:conserved hypothetical protein

>operons_50:RPA3110-gatC 3515755..3516260 r
RPA3110:hypothetical protein
gatC:Glu-tRNA(Gln) amidotransferase subunit C

>operons_50:RPA3113-RPA3114 3517583..3518473 f
RPA3113:conserved hypothetical protein
RPA3114:SEC-C motif

>operons_50:RPA3115-ipdC 3518600..3521962 r
RPA3115:probable acyl-CoA dehydrogenase
ipdC:indole-3-pyruvate decarboxylase

>operons_50:pyrB-pyr 3522153..3524436 f
pyrB:aspartate carbamoyltransferase
pyr:putative noncatalytic chain of dihydroorotase

>operons_50:RPA3121-RPA3122 3526551..3529158 f
RPA3121:putative alginate o-acetyltransferase AlgI
RPA3122:hypothetical protein

>operons_50:TopA-RPA3126 3529873..3535384 f
TopA:DNA topoisomerase I
RNR:ribonuclease R
RPA3126:conserved hypothetical protein

>operons_50:RPA3130-RPA3133 3538223..3540719 r
RPA3130:Helix-turn-helix motif
RPA3131:conserved hypothetical protein
RPA3132:response regulator protein
RPA3133:response regulator

>operons_50:RPA3134-dinP 3540845..3542436 f
RPA3134:conserved unknown protein
dinP:DNA damage inducible protein P

>operons_50:RPA3137-RPA3140 3543689..3546733 f
RPA3137:Endoribonuclease L-PSP
RPA3138:putative glycerophosphoryl diester
RPA3139:DUF482
RPA3140:probable Hit-like protein involved in cell-cycle

>operons_50:RPA3141-RPA3143 3546739..3548333 r
RPA3141:possible VirR protein

RPA3142:conserved hypothetical protein
RPA3143:conserved hypothetical protein

>operons_50:RPA3156-RPA3157 3564418..3565910 r
RPA3156:conserved hypothetical protein
RPA3157:hypothetical protein

>operons_50:RPA3162-mgtE 3569316..3571147 r
RPA3162:possible helix-turn-helix
mgtE:putative magnesium transporter

>operons_50:RPA3166-RPA3167 3573642..3574546 f
RPA3166:conserved hypothetical protein
RPA3167:conserved hypothetical protein

>operons_50:RPA3173-RPA3175 3580184..3583371 r
RPA3173:putative protein
RPA3174:conserved unknown protein
RPA3175:propionyl-CoA carboxylase precursor, biotin

>operons_50:RPA3189-RPA3190 3601644..3603393 r
RPA3189:NUDIX hydrolase
RPA3190:possible dihydrodipicoline synthase related

>operons_50:RPA3193-RPA3194 3605568..3607108 r
RPA3193:DUF35
RPA3194:conserved hypothetical protein

>operons_50:RPA3200-RPA3201 3613758..3616398 r
RPA3200:putative serine/threonine-protein kinase
RPA3201:formate/nitrate transporter

>operons_50:RPA3205-RPA3206 3620427..3622498 r
RPA3205:Type III secretion proteins, related to
RPA3206:conserved hypothetical protein

>operons_50:RPA3209-RPA3210 3625343..3626662 r
RPA3209:hypothetical protein
RPA3210:possible prolyl oligopeptidase family

>operons_50:RPA3211-RPA3214 3626787..3631649 f
RPA3211:TPR repeat
RPA3212:unknown protein
RPA3213:hypothetical protein
RPA3214:hypothetical protein

>operons_50:adk-secY 3647585..3650028 r
adk:Adenylate kinase
secY:secretion protein SecY

>operons_50:rplO-rpmD 3650181..3650873 r
rplO:50S ribosomal protein L15
rpmD:ribosomal protein L30

>operons_50:rplR-rplF 3651568..3652475 r
rplR:50S ribosomal protein L18

rplF:50S ribosomal protein L6

>operons_50:rpsH-rplN 3652588..3654583 r
rpsH:30S ribosomal protein S8
rpsN:30S ribosomal protein S14
rplE:50S ribosomal protein L5
rplX:50S ribosomal protein L24
rplN:50S ribosomal protein L14

>operons_50:rpsQ-rplC 3654647..3659479 r
rpsQ:30S ribosomal protein S17
rpmC:50S ribosomal protein L29
rplP:50S ribosomal protein L16
rpsC:30S ribosomal protein S3
rplV:50S ribosomal protein L22
rpsS:30S ribosomal protein S19
rplB:50S ribosomal protein L2
rplW:50S ribosomal protein L23
rplD:50S ribosomal protein L4
rplC:50S ribosomal protein L3

>operons_50:tufA,EF-Tu-rpsL 3659926..3664115 r
tufA,EF-Tu:elongation factor Tu
fusA,EF-G:elongation factor G
rpsG:30S ribosomal protein S7
rpsL:30S ribosomal protein S12

>operons_50:rplA-rplK 3690510..3691635 r
rplA:50S ribosomal protein L1
rplK:50S ribosomal protein L11

>operons_50:nusG-secE 3691858..3692656 r
nusG:transcription antitermination protein
secE:preprotein translocase, SecE subunit

>operons_50:RPA3276-pigA 3692921..3695845 r
RPA3276:possible tonB protein
exbD:putative exbD, uptake of enterochelin;
exbB:putative exbB, uptake of enterochelin;
pigA:possible iron-starvation protein

>operons_50:RPA3293-RPA3296 3713619..3717370 r
RPA3293:putative branched-chain amino acid transport
RPA3294:putative branched-chain amino acid transport
RPA3295:possible branched-chain amino acid ABC
RPA3296:possible ABC transporter subunit (U75364)

>operons_50:RPA3299-RPA3300 3720964..3723184 r
RPA3299:putative long-chain-fatty-acid CoA ligase
RPA3300:possible transcriptional regulator, TetR family

>operons_50:RPA3301-paaG 3723347..3727052 f
RPA3301:putative lipid transfer protein
RPA3302:conserved hypothetical protein
RPA3303:MaoC-like dehydratase
fabG:putative 3-oxoacyl-acyl carrier protein

paaG:enoyl-CoA hydratase/isomerase family

>operons_50:RPA3308-RPA3309 3729714..3730804 f
RPA3308:ycfI, putative structural proteins
RPA3309:conserved unknown protein

>operons_50:RPA3317-RPA3318 3743574..3744712 r
RPA3317:hypothetical protein
RPA3318:putative transcriptional regulator, Fnr-type

>operons_50:algC-manC,cpsB,rfbM 3746647..3749626 r
algC:possible phosphomannomutase AlgC
manC,cpsB,rfbM:putative mannose-1-phosphate guanylyltransferase

>operons_50:RPA3330-RPA3332 3758733..3759948 f
RPA3330:conserved hypothetical protein
RPA3331:hypothetical protein
RPA3332:hypothetical protein

>operons_50:RPA3336-RPA3337 3762564..3764387 r
RPA3336:possible lipopeptide antibiotics iturin a
RPA3337:hypothetical protein

>operons_50:RPA3338-RPA3340 3764459..3776749 r
RPA3338:possible Condensation domain, peptide
mcyE:possible McyE polykeitde synthase and peptide
RPA3340:peptide synthetase (fragment)

>operons_50:RPA3346-RPA3347 3785284..3787297 f
RPA3346:possible mannosyltransferase
RPA3347:putative glycosyltransferase

>operons_50:RPA3351-RPA3352 3792003..3793958 f
RPA3351:possible glycosyl transferase
RPA3352:glycosyltransferase

>operons_50:RPA3359-pssN 3801814..3804464 r
RPA3359:O-antigen polymerase
pssN:putative capsule polysaccharide export outer

>operons_50:RPA3375-RPA3376 3815306..3819017 r
RPA3375:unknown protein
RPA3376:possible DNA methyltransferase

>operons_50:cheY3-RPA3381 3821616..3822769 f
cheY3:putative chemotaxis protein cheY3
RPA3381:Hpt domain

>operons_50:RPA3383-nrtC 3824681..3827327 f
RPA3383:possible taurine transport system permease
RPA3384:possible ABC related periplasmic binding
nrtC:putative nitrate transport system ATP-binding

>operons_50:RPA3386-RPA3387 3827388..3830087 f
RPA3386:possible amidohydrolase
RPA3387:putative transcriptional regulator

>operons_50:his3-gch1 3832039..3833212 r
his3:phosphoribosyl c-AMP cyclohydrolase
gch1:possible GTP cyclohydrolase I

>operons_50:RPA3396-RPA3397 3836526..3838113 r
RPA3396:hypothetical protein
RPA3397:hypothetical protein

>operons_50:RPA3400-RPA3401 3840107..3840596 f
RPA3400:hypothetical protein
RPA3401:hypothetical protein

>operons_50:RPA3402-RPA3403 3840586..3841645 r
RPA3402:conserved hypothetical protein
RPA3403:probable transcriptional regulator, TetR family

>operons_50:RPA3413-RPA3414 3855126..3858531 r
RPA3413:Uncharacterized iron-regulated membrane protein
RPA3414:putative hydroxamate-type ferrisiderophore

>operons_50:RPA3432-RPA3433 3873487..3874944 f
RPA3432:conserved hypothetical protein
RPA3433:possible salicylate hydroxylase

>operons_50:RPA3435-RPA3436 3876078..3877473 f
RPA3435:Glycosyl transferase, family 2
RPA3436:GCN5-related N-acetyltransferase

>operons_50:RPA3439-RPA3440 3880205..3882800 f
RPA3439:putative hydrolase
RPA3440:probable amidase

>operons_50:RPA3442-RPA3443 3883848..3885640 r
RPA3442:Putative cyclase
RPA3443:possible isomerase/decarboxylase

>operons_50:RPA3446-RPA3449 3888385..3891949 r
RPA3446:3-hydroxyisobutyrate dehydrogenase
RPA3447:putative enoyl-CoA hydratase/isomerase
RPA3448:acyl-CoA dehydrogenase
RPA3449:PilT protein, N-terminal

>operons_50:RPA3458-RPA3459 3900691..3903945 f
RPA3458:possible TrapT family, dctP subunit,
RPA3459:possible TrapT family, fused dctM-Q subunits,

>operons_50:RPA3461-RPA3462 3904676..3906252 r
RPA3461:conserved hypothetical protein
RPA3462:Thiolase

>operons_50:RPA3465-RPA3466 3908870..3911586 r
RPA3465:putative long-chain-fatty-acid CoA ligase
RPA3466:3-ketoacyl-CoA thiolase

>operons_50:RPA3468-RPA3469 3913033..3914905 r

RPA3468:putative permease protein of sugar ABC
RPA3469:probable permease protein of sugar ABC

>operons_50:exbD-exbB 3923696..3924853 r
exbD:exbD, uptake of enterochelin; tonB-dependent
exbB:possible exbB, uptake of enterochelin;

>operons_50:RPA3479-fiu 3925057..3927973 r
RPA3479:2OG-Fe(II) oxygenase superfamily:Prolyl
fiu:putative outer membrane receptor for iron

>operons_50:RPA3482-RPA3483 3929016..3933379 f
RPA3482:putative membrane protein
RPA3483:RND efflux transporter

>operons_50:RPA3487-RPA3488 3937437..3939562 r
RPA3487:conserved hypothetical protein
RPA3488:probable serine protease

>operons_50:hflC-hflK 3940220..3942294 r
hflC:putative hflC protein
hflK:putative protease subunit hflK

>operons_50:dyr-thyA 3942439..3943772 r
dyr:dihydrofolate reductase
thyA:thymidylate synthase

>operons_50:RPA3495-RPA3496 3945053..3947078 r
RPA3495:possible TctA subunit of the Tripartite
RPA3496:possible TctB subunit of the Tripartite

>operons_50:RPA3497-RPA3498 3947151..3948274 r
RPA3497:possible Chromate transporter related to ChrA
RPA3498:possible chromate transport protein similar to

>operons_50:uvrD-RPA3507 3958287..3961117 f
uvrD:DNA helicase II
RPA3507:Protein of unknown function UPF0150

>operons_50:RPA3508-RPA3509 3961413..3963097 f
RPA3508:ATP-binding component of ABC transporter
RPA3509:permease, ABC-2-type transport system

>operons_50:recN-RPA3520 3977199..3979805 r
recN:putative DNA repair protein RecN
RPA3520:Protein of unknown function UPF0169

>operons_50:ftsA-ftsQ 3983213..3985521 r
ftsA:putative cell division protein FtsA
ftsQ:putative cell division protein FtsQ

>operons_50:murB-murC 3989368..3991786 r
murB:UDP-N-acetylenolpyruvoylglucosamine reductase
murC:UDP-N-acetylmuramate-alanine ligase

>operons_50:murG-ftsW 3991923..3994170 r

murG:UDP-N-acetylglucosamine:N-acetylmuramyl-(pentapeptide)
ftsW:putative cell division protein ftsW

>operons_50:mraY-murE 3996009..3999998 r
mraY:phospho-N-acetylmuramoyl-pentapeptide-transferase
murF:putative
murE:UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate

>operons_50:RPA3536-RPA3538 4000111..4003240 r
RPA3536:putative penicillin-binding protein
RPA3537:conserved hypothetical protein
RPA3538:Bacterial methyltransferase

>operons_50:RPA3540-emrB 4005202..4007614 r
RPA3540:putative cell filamentation protein
RPA3541:hypothetical protein
emrB:putative multidrug resistance protein B (drug

>operons_50:RPA3547-RPA3548 4013379..4016911 r
RPA3547:hypothetical protein
RPA3548:possible serine protease/outer membrane

>operons_50:RPA3550-RPA3552 4018092..4021392 f
RPA3550:Coenzyme B12-binding:Elongator protein
RPA3551:putative oxidoreductase, short-chain
RPA3552:putative short-chain dehydrogenase/reductase

>operons_50:arsC-RPA3556 4022698..4023999 r
arsC:arsenate reductase
arsC:arsenate reductase
RPA3556:putative transcriptional regulator. ArsR

>operons_50:RPA3557-arsR 4024054..4025647 r
RPA3557:Thiol-disulfide isomerase and thioredoxins
RPA3558:possible permease
arsR:possible ArsR protein

>operons_50:RPA3561-RPA3562 4026812..4028009 f
RPA3561:possible arsenate reduction regulatory protein
RPA3562:UbiE/COQ5 methyltransferase

>operons_50:RPA3570-RPA3571 4035633..4037686 f
RPA3570:probable two-component response regulator
RPA3571:possible two-component regulatory system sensor

>operons_50:thiO-thiG 4039635..4040800 f
thiO:thiamine biosynthesis oxidoreductase thiO
thiG:putative thiamin biosynthesis ThiG

>operons_50:thiG-thiE 4041053..4042430 f
thiG:thiamin biosynthesis ThiG
thiE:thiamin phosphate pyrophosphorylase

>operons_50:RPA3579-RPA3580 4045969..4047152 f
RPA3579:possible insertion element ISR1 hypothetical 10
RPA3580:Integrase, catalytic domain

>operons_50:RPA3582-RPA3583 4047439..4048295 r
RPA3582:conserved hypothetical protein
RPA3583:conserved hypothetical protein

>operons_50:RPA3596-RPA3597 4058884..4061734 r
RPA3596:hypothetical protein
RPA3597:conserved hypothetical protein

>operons_50:RPA3603-RPA3604 4066589..4068423 r
RPA3603:possible transglycosylase
RPA3604:Uncharacterized protein family UPF0114

>operons_50:RPA3607-RPA3608 4069978..4070630 f
RPA3607:Transcriptional regulator AbrB
RPA3608:PilT protein, N-terminal

>operons_50:vanA-vanB 4082101..4084926 f
vanA:putative vanillate O-demethylase oxygenase,
vanR:putative transcriptional regulator VanR
vanB:putative vanillate O-demethylase oxidoreductase

>operons_50:RPA3626-RPA3628 4088910..4091053 r
RPA3626:conserved unknown protein
RPA3627:putative glutathione peroxidase
RPA3628:possible amidase

>operons_50:RPA3632-RPA3633 4093389..4094565 f
RPA3632:DUF24, predicted transcriptional regulator,
RPA3633:conserved hypothetical protein

>operons_50:gnd-RPA3638 4097820..4101643 f
gnd:6-phosphogluconate dehydrogenase
zwf:putative glucose-6-phosphate 1-dehydrogenase
pgl:putative 6-phosphogluconolactonase
RPA3638:thermoresistant gluconokinase

>operons_50:RPA3640-malQ 4102582..4106347 r
RPA3640:Glycoside hydrolase, family 15
malQ:putative 4-alpha-glucanotransferase

>operons_50:RPA3642-glgB 4106445..4113971 f
RPA3642:putative alpha-amylase
RPA3643:putative trehalose synthase
glgB:1,4-alpha-glucan branching enzyme (glycogen

>operons_50:glgX-RPA3647 4114210..4120840 f
glgX:probable glycosyl hydrolase
RPA3646:putative maltooligosyltrehalose trehalohydrolase
RPA3647:putative glycosyl hydrolase

>operons_50:ureC-ureB 4133317..4135867 r
ureC:urease alpha subunit
RPA3661:Metal dependent phosphohydrolase, HD region
ureB:urease beta subunit

>operons_50:ureA-ureD 4136029..4137295 r
ureA:urease gamma subunit
ureD:possible urease accessory protein D

>operons_50:RPA3666-RPA3667 4138409..4140369 r
RPA3666:possible ATP-binding component of ABC
RPA3667:possible permease of ABC transporter

>operons_50:RPA3670-infA 4143976..4145703 f
RPA3670:putative ATP-dependent RNA helicase
infA:translation initiation factor if-1 (infA)

>operons_50:RPA3673-RPA3674 4146311..4147483 r
RPA3673:conserved unknown protein
RPA3674:conserved hypothetical protein

>operons_50:RPA3677-RPA3680 4149514..4153568 f
RPA3677:conserved hypothetical protein
RPA3678:putative exporter protein, cpaC
RPA3679:possible pilus assembly protein cpaD
RPA3680:possible pilus assembly protein cpaE

>operons_50:RPA3681-RPA3683 4153661..4157013 f
RPA3681:secretory protein kinase, cpaF
RPA3682:conserved unknown protein
RPA3683:conserved hypothetical protein

>operons_50:RPA3685-RPA3686 4157949..4160169 f
RPA3685:leucine aminopeptidase
RPA3686:NLP/P60

>operons_50:RPA3687-RPA3692 4160153..4168470 r
RPA3687:putative MutT/ADP-ribose pyrophosphatase
RPA3688:peptide ABC transporter, ATP-binding protein
RPA3689:peptide ABC transporter, permease protein
RPA3690:peptide ABC transporter, permease protein
RPA3691:putative ABC transporter, solute-binding protein
RPA3692:putative peptide ABC transporter, periplasmic

>operons_50:emrA-RPA3699 4171914..4175366 f
emrA:putative multidrug resistance protein
emrB:putative drug efflux pump, Major Facilitator
RPA3699:possible iron-chelator utilization protein

>operons_50:metF-metH 4176861..4181642 f
metF:putative 5,10-methylenetetrahydrofolate
metH:methionine synthase

>operons_50:nasT-RPA3708 4185092..4187292 f
nasT:putative two-component response regulator NasT
RPA3707:possible nitrate transporter component, nrtA
RPA3708:Globin-like protein

>operons_50:RPA3709-RPA3711 4187646..4191502 f
RPA3709:possible hemoprotein
nirA:possible ferredoxin-nitrite reductase

RPA3711:possible sulfite reductase (NADPH)

>operons_50:pimB-pimA 4195279..4198156 r
pimB:acetyl-CoA acetyltransferase
pimA:pimeloyl-CoA ligase

>operons_50:RPA3718-livM 4200567..4204885 f
RPA3718:putative transcriptional regulator
livG:putative high-affinity branched-chain amino acid
livF:putative branched-chain amino acid transport
RPA3721:possible ABC transporter, permease protein
livM:putative branched-chain amino acid transport

>operons_50:RPA3730-RPA3731 4214978..4217499 f
RPA3730:GMC-type oxidoreductase
RPA3731:Alpha/beta hydrolase

>operons_50:lytB-RPA3735 4222189..4224309 f
lytB:penicillin tolerance protein
RPA3735:conserved unknown protein

>operons_50:pstS-RPA3737 4224384..4226666 r
pstS:putative phosphate transport system
RPA3737:putative phosphonoacetate hydrolase

>operons_50:RPA3739-RPA3743 4227805..4233510 r
RPA3739:unknown protein
sqhC:squalene-hopene-cyclase
RPA3741:putative oxidoreductase
RPA3742:putative poly-isoprenyl transferase
RPA3743:possible phytoene synthase-related protein

>operons_50:eutC-RPA3748 4237519..4239877 r
eutC:putative ethanolamine ammonia-lyase light chain
RPA3748:Elongator protein 3/MiaB/NifB

>operons_50:RPA3752-RPA3754 4243965..4250762 r
RPA3752:Transglutaminase-like domain
RPA3753:DUF404
RPA3754:Transglutaminase-like domain

>operons_50:RPA3756-RPA3757 4251974..4253639 r
RPA3756:malate dehydrogenase-like protein
RPA3757:possible MarR family transcriptional regulator

>operons_50:hpcG-hpcC 4253885..4256644 f
hpcG:2-oxo-hepta-3-ene-1,7-dioate hydratase
hpcD:putative 5-carboxymethyl-2-hydroxymuconate
hpcC:5-carboxy-2-hydroxymuconate semialdehyde

>operons_50:RPA3762-ilvB 4257949..4260475 f
RPA3762:putative 2-oxo-3-ene-1,7-dioic acid hydratase
ilvB:putative acetolactate synthase large subunit

>operons_50:RPA3764-paaC 4260666..4263036 r
RPA3764:putative 2Fe:2S ferredoxin

paaD:putative phenylacetic acid degradation protein
paaC:phenylacetic acid degradation protein paaC

>operons_50:RPA3771-RPA3773 4266349..4267782 r
RPA3771:unknown protein
RPA3772:conserved hypothetical protein
RPA3773:conserved unknown protein

>operons_50:RPA3776-RPA3777 4272651..4274547 r
RPA3776:possible RND efflux membrane fusion protein
RPA3777:putative transcriptional regulator, TetR family

>operons_50:RPA3783-RPA3784 4281276..4283916 r
RPA3783:Glycosyl transferase, family 39
RPA3784:putative dolichol-phosphate mannosyltransferase

>operons_50:RPA3788-RPA3791 4286411..4290046 r
RPA3788:putative ABC transporter, ATP-binding protein
RPA3789:putative ATP-binding component of a transport
RPA3790:putative efflux protein
RPA3791:putative transcriptional regulator TetR/AcrR

>operons_50:RPA3797-RPA3800 4294303..4298212 r
RPA3797:conserved hypothetical protein
RPA3798:conserved unknown protein
RPA3799:DUF182
RPA3800:conserved hypothetical protein

>operons_50:RPA3801-RPA3802 4298538..4300266 r
RPA3801:MoxR-like ATPases
RPA3802:carbon monoxide dehydrogenase medium subunit

>operons_50:RPA3806-RPA3808 4303024..4306118 f
RPA3806:permease of ABC transporter,putatively for
RPA3807:putative permease of ABC transporter
RPA3808:ATP-binding component of ABC transporter

>operons_50:RPA3819-RPA3820 4315777..4316285 r
RPA3819:hypothetical protein
RPA3820:Protein of unknown function UPF0062

>operons_50:RPA3826-RPA3827 4321678..4322361 f
RPA3826:conserved hypothetical protein
RPA3827:conserved hypothetical protein

>operons_50:RPA3829-RPA3831 4323708..4325186 r
RPA3829:putative transcription elongation factor greA
RPA3830:possible G/U mismatch-specific DNA glycosylase
RPA3831:conserved unknown protein

>operons_50:RPA3836-RPA3837 4331612..4332795 r
RPA3836:Integrase, catalytic domain
RPA3837:possible insertion element ISR1

>operons_50:RPA3840-RPA3842 4334584..4338550 f
RPA3840:putative hydroxamate-type ferrisiderophore

RPA3841:hypothetical protein
RPA3842:Uncharacterized iron-regulated membrane protein

>operons_50:RPA3846-alaS 4344559..4347991 r
RPA3846:GCN5-related N-acetyltransferase
alaS:alanyl-tRNA synthetase

>operons_50:gcvT2-RPA3849 4348444..4349967 f
gcvT2:glycine cleavage system protein T2
RPA3849:glycine cleavage system protein H

>operons_50:RPA3855-RPA3856 4357821..4359098 f
RPA3855:conserved hypothetical protein
RPA3856:hypothetical protein

>operons_50:RPA3862-RPA3863 4363538..4364614 r
RPA3862:hypothetical protein
RPA3863:possible Crp/Fnr-family transcriptional

>operons_50:flhB-fliR 4384623..4386490 r
flhB:putative flagellar biosynthetic protein flhB
fliR:putative flagellar biosynthetic protein FliR

>operons_50:RPA3886-RPA3888 4387018..4388312 r
RPA3886:Flagellar hook-basal body complex protein FliE
flgC:flagellar basal-body rod protein flgC
RPA3888:possible flagellar basal-body rod protein FlgB

>operons_50:RPA3889-fliP 4388533..4390448 f
RPA3889:unknown protein
fliP:putative flagellar biosynthesis protein fliP

>operons_50:RPA3893-RPA3894 4395182..4397354 r
RPA3893:putative carboxylesterase
RPA3894:possible transcriptional regulator

>operons_50:RPA3895-fliL 4397532..4400427 r
RPA3895:conserved hypothetical protein
RPA3896:hypothetical protein
fliM:possible flagellar motor switch protein FliM
fliL:Flagellar basal body-associated protein FliL

>operons_50:flgF-flgH 4400792..4404159 f
flgF:putative flagellar basal-body rod protein flgF
flgG:putative flagellar basal-body rod protein flgg
RPA3901:Flageller protein FlgA
flgH:putative flagellar L-ring protein FlgH

>operons_50:mexD-mexC 4404420..4408778 r
mexD:RND multidrug efflux transporter MexD
mexC:putative RND multidrug efflux membrane fusion

>operons_50:flgI-RPA3911 4411334..4413299 f
flgI:flagellar P-ring protein FlgI
RPA3910:conserved hypothetical protein
RPA3911:hypothetical protein

>operons_50:RPA3913-RPA3914 4413967..4414719 r
RPA3913:conserved hypothetical protein
RPA3914:putative flbT protein

>operons_50:RPA3917-RPA3921 4420277..4426368 r
RPA3917:possible acetolactate synthase large subunit
RPA3918:conserved hypothetical protein
RPA3919:possible mannose-1-phosphate guanyltransferase
RPA3920:possible ADP-heptose synthase
RPA3921:possible acetoin dehydrogenase (TPP-dependent)

>operons_50:RPA3922-RPA3926 4426519..4431196 r
RPA3922:putative acetoin dehydrogenase (TPP-dependent)
RPA3923:putative acetoin dehydrogenase (TPP-dependent)
RPA3924:conserved hypothetical protein
RPA3925:putative dTDP-glucose 4,6-dehydratase
RPA3926:putative sugar-nucleotide epimerase/dehydratase

>operons_50:RPA3930-RPA3932 4436179..4441501 r
RPA3930:unknown protein
flgK:possible flagellar hook-associated protein 1
RPA3932:probable flagellar hook protein flgE

>operons_50:RPA3933-RPA3934 4441771..4446011 f
RPA3933:possible response regulator receiver domain, PAS
RPA3934:putative sensor kinase

>operons_50:RPA3939-RPA3940 4450387..4451392 f
RPA3939:conserved unknown protein
RPA3940:Universal stress protein (Usp)

>operons_50:RPA3948-wbpX 4459023..4461624 r
RPA3948:hypothetical protein
wbpX:possible glycosyltransferase WbpX

>operons_50:gmd-RPA3952 4462907..4464876 f
gmd:GDP-mannose 4,6-dehydratase
RPA3952:possible oxidoreductase Rmd

>operons_50:RPA3962-RPA3963 4479631..4481558 r
RPA3962:ATP-binding component of ABC transporter
RPA3963:putative permease of ABC transporter

>operons_50:RPA3967-RPA3969 4485400..4488297 r
RPA3967:putative threonine dehydratase
RPA3968:putative glycosyl transferase 1
RPA3969:Metallo-phosphoesterase

>operons_50:RPA3972-RPA3973 4490291..4491703 r
RPA3972:putative diheme cytochrome c-553
RPA3973:cytochrome c556

>operons_50:RPA3983-RPA3985 4504132..4508569 r
RPA3983:putative nucleotide sugar epimerase/dehydratase
rfaE:putative ADP-heptose synthase

RPA3985:ADP-L-glycero-D-mannoheptose-6-epimerase

>operons_50:lpcA-RPA3988 4509900..4511026 f
lpcA:possible phosphoheptose isomerase
RPA3988:putative phosphatase

>operons_50:RPA3997-RPA3999 4519740..4521560 r
RPA3997:unknown protein
RPA3998:hypothetical protein
RPA3999:possible coenzyme PQQ synthesis protein E

>operons_50:RPA4009-RPA4010 4532346..4534768 f
RPA4009:GAF domain
RPA4010:putative response regulator

>operons_50:RPA4020-RPA4023 4550491..4553787 f
RPA4020:possible branched-chain amino acid transport
RPA4021:putative branched-chain amino acid ABC transport
RPA4022:putative branched-chain amino acid ABC transport
RPA4023:putative branched-chain amino acid ABC transport

>operons_50:RPA4024-RPA4026 4554023..4556514 r
RPA4024:Methionine synthase, vitamin-B12 independent
RPA4025:putative branched-chain amino acid ABC transport
RPA4026:possible ABC transporter,ATP binding protein

>operons_50:RPA4027-RPA4028 4556646..4558537 r
RPA4027:possible branched-chain amino acid ABC transport
RPA4028:possible ABC transport system permease protein

>operons_50:RPA4035-RPA4038 4564600..4568289 f
RPA4035:possible ABC transport system permease protein
RPA4036:possible branched-chain amino acid ABC
RPA4037:putative ABC transport system ATP-binding
RPA4038:possible ABC transport system ATP-binding

>operons_50:RPA4041-RPA4042 4571291..4574145 f
RPA4041:putative branched-chain amino acid ABC transport
RPA4042:putative long-chain-fatty-acid--CoA ligase

>operons_50:rfbF-RPA4057 4580288..4589979 f
rfbF:alpha-D-glucose-1-phosphate
rfbG:cdp-glucose 4,6-dehydratase
RPA4050:unknown protein
RPA4051:possible oxo-acyl acyl carrier protein
RPA4052:possible 3-dehydroquinate synthase
RPA4053:possible dTDPglucose 4,6-dehydratase
RPA4054:possible acetolactate synthase large subunit
RPA4055:hypothetical protein
RPA4056:unknown protein
RPA4057:possible dolichol phosphate mannose synthase

>operons_50:RPA4059-RPA4060 4591214..4593444 r
RPA4059:conserved unknown protein
RPA4060:hypothetical protein

>operons_50:RPA4069-msrA 4606983..4608041 r
RPA4069:DUF25
msrA:possible peptide methionine sulfoxide reductase

>operons_50:trxB-RPA4076 4614093..4615990 f
trxB:thioredoxin reductase
RPA4076:putative transcriptional regulator, lysR family

>operons_50:RPA4083-RPA4084 4621775..4624481 f
RPA4083:hypothetical protein
RPA4084:AAA ATPase

>operons_50:RPA4086-RPA4089 4625458..4631675 r
RPA4086:probable permease of ABC transporter
RPA4087:ABC-2 type transport system permease and double
RPA4088:probable membrane fusion protein (HlyD family of
RPA4089:Patatin-like phospholipase domain

>operons_50:RPA4094-RPA4096 4634535..4639741 r
RPA4094:conserved hypothetical protein
RPA4095:putative multidrug-efflux transport protein
RPA4096:possible multidrug efflux membrane fusion

>operons_50:RPA4098-RPA4100 4640831..4642200 f
RPA4098:unknown protein
RPA4099:hypothetical protein
RPA4100:hypothetical protein

>operons_50:RPA4101-RPA4103 4642335..4643931 f
RPA4101:putative organic hydroperoxide resistance
RPA4102:putative transcriptional regulator
RPA4103:possible glutathione S-transferase

>operons_50:rmrA-rmrB 4645025..4647786 f
rmrA:putative hlyD family multidrug secretion protein
rmrB:putative multidrug efflux pump, Major

>operons_50:oprN-RPA4108 4647970..4649986 f
oprN:putative outer membrane efflux protein OprN
RPA4108:possible transcriptional regulator

>operons_50:trbI-trbB 4658541..4667939 r
trbI:putative conjugal transfer protein trbI
trbG:conjugal transfer protein trbG
trbF:conjugal transfer protein trbF
RPA4118:conjugal transfer protein trbL
RPA4119:hypothetical protein, possible TrbK
RPA4120:possible conjugal transfer protein trbJ
trbE:conjugal transfer protein trbE
RPA4122:Conjugal transfer protein TrbD
trbC:conjugal transfer protein trbC
trbB:conjugal transfer protein trbB

>operons_50:RPA4125-RPA4128 4668297..4670845 r
RPA4125:conserved hypothetical protein
RPA4126:hypothetical protein

RPA4127:conserved hypothetical protein
RPA4128:conserved hypothetical protein

>operons_50:RPA4129-RPA4130 4670965..4672205 f
RPA4129:putative transcriptional regulator
RPA4130:unknown protein

>operons_50:RPA4131-traG 4672420..4674888 r
RPA4131:Helix-turn-helix protein, CopG family
traG:plasmid transfer factor, traG

>operons_50:RPA4141-RPA4142 4684624..4685276 f
RPA4141:conserved hypothetical protein
RPA4142:PilT protein, N-terminal

>operons_50:RPA4147-RPA4149 4688895..4692894 f
RPA4147:putative nucleoside phosphorylase
prsA:putative ribose-phosphate pyrophosphokinase
RPA4149:Beta-lactamase-like

>operons_50:RPA4155-RPA4156 4698521..4699899 r
RPA4155:3-oxoadipate CoA-transferase subunit B
RPA4156:3-oxoadipate CoA-transferase subunit A

>operons_50:potH-RPA4160 4703319..4705372 r
potH:polyamine ABC transporter permease protein
RPA4160:polyamine ABC transporter, ATP-binding protein

>operons_50:RPA4162-RPA4163 4706510..4708209 f
RPA4162:putative taurine ABC transport system permease
RPA4163:putative taurine transport system ATP-binding

>operons_50:RPA4165-RPA4166 4709325..4710985 f
RPA4165:conserved hypothetical protein
RPA4166:putative nitrilase

>operons_50:RPA4172-RPA4173 4718090..4719182 r
RPA4172:hypothetical protein
RPA4173:GGDEF

>operons_50:purE-purK 4719311..4720896 f
purE:phosphoribosylaminoimidazole carboxylase
purK:phosphoribosylaminoimidazole carboxylase ATPase

>operons_50:pntB-pntAalpha 4723562..4726455 r
pntB:nicotinamide nucleotide transhydrogenase,
pntAbeta:nicotinamide nucleotide transhydrogenase,
pntAalpha:nicotinamide nucleotide transhydrogenase,

>operons_50:RPA4192-pyk 4737334..4739348 f
RPA4192:conserved hypothetical protein
pyk:pyruvate kinase

>operons_50:osmC-RPA4195 4739575..4741004 r
osmC:osmotically inducible protein OsmC
RPA4195:putative hydrolase

>operons_50:RPA4202-RPA4203 4745124..4746945 r
RPA4202:putative MCP-domain signal transduction protein
RPA4203:putative signal-transduction sensor protein

>operons_50:RPA4206-RPA4207 4749468..4751444 r
RPA4206:D-beta-hydroxybutyrate dehydrogenase
RPA4207:Patatin-like phospholipase domain

>operons_50:RPA4212-cysG 4755200..4759109 r
RPA4212:conserved hypothetical protein
RPA4213:sulfite reductase hemoprotein subunit
RPA4214:conserved hypothetical protein
cysG:putative siroheme synthase

>operons_50:RPA4219-RPA4220 4762529..4763981 r
RPA4219:conserved hypothetical protein
RPA4220:ErfK/YbiS/YcfS/YnhG

>operons_50:RPA4224-RPA4225 4767160..4767989 f
RPA4224:unknown protein
RPA4225:putative RNA polymerase sigma factor

>operons_50:RPA4228-RPA4229 4770919..4771632 f
RPA4228:hypothetical protein
RPA4229:hypothetical protein

>operons_50:RPA4236-RPA4238 4777519..4780646 r
RPA4236:Mce4/Rv3499c/MTV023.06c protein
RPA4237:ATP-binding component of ABC transporter
RPA4238:putative permease of ABC transporter

>operons_50:fixL-fixJ 4791190..4793320 f
fixL:two-component, low oxygen sensor protein fixL
fixJ:two-component, nitrogen fixation regulatory

>operons_50:nuoN-nuoA 4796479..4810793 r
nuoN:NADH-ubiquinone dehydrogenase chain N
nuoM:NADH-ubiquinone dehydrogenase chain M
nuoL:NADH-ubiquinone dehydrogenase chain L
nuoK:NADH-ubiquinone dehydrogenase chain K
nuoJ:NADH-ubiquinone dehydrogenase chain J
nuoI:NADH-ubiquinone dehydrogenase chain I
nuoH:NADH-ubiquinone dehydrogenase chain H
nuoG:NADH-ubiquinone dehydrogenase chain G
nuoF:NADH-ubiquinone dehydrogenase chain F
nuoE:NADH-ubiquinone dehydrogenase chain E
nuoCD:NADH-ubiquinone dehydrogenase chain C,D
nuoB:NADH-ubiquinone dehydrogenase chain B
nuoA:NADH-ubiquinone dehydrogenase chain A

>operons_50:RPA4269-thrB 4817500..4818947 r
RPA4269:ribonuclease H
thrB:homoserine kinase

>operons_50:RPA4285-RPA4286 4833734..4835170 f

RPA4285:Nitroreductase family
RPA4286:Catalytic LigB subunit of aromatic ring-opening

>operons_50:RPA4288-RPA4289 4836310..4837640 f
RPA4288:conserved hypothetical protein
RPA4289:putative protein-tyrosine phosphatase

>operons_50:pucBb-pucAb 4838558..4838926 f
pucBb:light harvesting protein B-800-850, beta chain B
pucAb:light harvesting protein B-800-850, alpha chain

>operons_50:RPA4294-purA 4840036..4842967 r
RPA4294:unknown protein
purA:adenylosuccinate synthetase

>operons_50:RPA4310-RPA4312 4861265..4863556 r
RPA4310:hypothetical protein
RPA4311:possible methyl-accepting chemotaxis protein
RPA4312:putative signal-transduction sensor protein

>operons_50:RPA4313-gstA 4863729..4864804 r
RPA4313:putative transcriptional regulator
gstA:possible glutathione S-transferase

>operons_50:RPA4323-RPA4324 4873169..4874490 f
RPA4323:hypothetical protein
RPA4324:hypothetical protein

>operons_50:sulP-RPA4327 4875560..4877622 r
sulP:sulfate transporter family protein
RPA4327:Helix-turn-helix motif

>operons_50:RPA4351-RPA4352 4903498..4904468 r
RPA4351:conserved unknown protein
RPA4352:conserved unknown protein

>operons_50:pth-ctc,rplY,L25 4906232..4907566 r
pth:putative peptidyl-tRNA hydrolase
ctc,rplY,L25:putative 50S ribosomal protein L25

>operons_50:lgt-RPA4360 4908396..4911162 f
lgt:prolipoprotein diacylglyceryl transferase
RPA4359:DUF185
RPA4360:DUF152

>operons_50:RPA4364-RPA4365 4914215..4915140 f
RPA4364:conserved hypothetical protein
RPA4365:GCN5-related N-acetyltransferase

>operons_50:RPA4368-RPA4369 4918006..4919276 r
RPA4368:possible response regulator receiver domain
RPA4369:putative transcriptional regulator

>operons_50:RPA4373-RPA4374 4923703..4926614 r
RPA4373:possible protease
RPA4374:putative protease

>operons_50:RPA4378-ribF 4931347..4932884 r
RPA4378:maltose O-acetyltransferase
ribF:putative riboflavin kinase ribF

>operons_50:RPA4382-RPA4383 4934435..4935268 f
RPA4382:conserved hypothetical protein
RPA4383:conserved unknown protein

>operons_50:RPA4384-PA0781 4935410..4938261 f
RPA4384:hypothetical protein
PA0781:putative outer membrane hemin/siderophore

>operons_50:RPA4388-RPA4389 4941280..4943701 r
RPA4388:GCN5-related N-acetyltransferase
RPA4389:Small Conductance Mechanosensitive (MscS) Ion

>operons_50:RPA4393-aceA 4946115..4947989 r
RPA4393:unknown protein
aceA:isocitrate lyase

>operons_50:RPA4399-RPA4401 4954639..4957717 f
RPA4399:possible branched-chain amino acid transport
RPA4400:possible branched-chain amino acid ABC transport
RPA4401:possible branched-chain amino acid ABC

>operons_50:RPA4405-glpD 4962078..4967847 r
RPA4405:conserved hypothetical protein
RPA4406:sugar ABC transport system, permease component
RPA4407:permease protein of sugar ABC transporter
RPA4408:ATP-binding protein of sugar ABC transporter
RPA4409:ATP-binding protein of sugar ABC transporter
glpD:glycerol-3-phosphate dehydrogenase

>operons_50:RPA4412-RPA4415 4969028..4974557 r
RPA4412:conserved unknown protein
RPA4413:probable transcriptional regulator
RPA4414:putative RND efflux transporter
RPA4415:putative component of multidrug efflux system

>operons_50:ogt-RPA4428 4986620..4987754 r
ogt:putative methylated-DNA-protein-cystein
RPA4428:putative glucosyltransferase I;

>operons_50:RPA4429-RPA4430 4987875..4991355 r
RPA4429:Uncharacterized iron-regulated membrane protein
RPA4430:putative TonB-dependent receptor

>operons_50:RPA4436-metX 5007582..5009482 r
RPA4436:conserved hypothetical protein
metX:homoserine O-acetyltransferase

>operons_50:aro-tyrC 5009734..5012759 f
aro:Chorismate mutase
hisC:putative histidinol-phosphate aminotransferase
tyrC:putative cyclohexadienyl dehydrogenase

>operons_50:RPA4446-RPA4448 5020355..5021945 r
RPA4446:hypothetical protein
RPA4447:conserved hypothetical protein
RPA4448:possible RNA polymerase ECF-type sigma factor

>operons_50:RPA4450-RPA4452 5024628..5028905 f
RPA4450:hypothetical protein
RPA4451:unknown protein
RPA4452:putative aromatic-L-amino-acid decarboxylase

>operons_50:RPA4453-RPA4454 5029184..5030606 r
RPA4453:Metallo-phosphoesterase:Conserved hypothetical
RPA4454:Antifreeze protein, type

>operons_50:RPA4457-RPA4462 5032374..5037511 r
RPA4457:putative sulfide dehydrogenase
RPA4458:hypothetical protein
dhsU:putative flavocytochrome C sulfide
dhsU:putative flavocytochrome C sulfide
RPA4461:possible cytochrome subunit of sulfide
RPA4462:Lipocalin-related protein and Bos/Can/Equ

>operons_50:RPA4463-soxC 5037696..5039730 r
RPA4463:possible cytochrome
soxC:sulfite dehydrogenase

>operons_50:soxZ-soxY 5041640..5042472 r
soxZ:putative sulfur oxidation protein soxZ
soxY:putative sulfur oxidation protein soxY

>operons_50:RPA4468-RPA4469 5042658..5044236 f
RPA4468:conserved unknown protein
RPA4469:conserved unknown protein

>operons_50:RPA4471-RPA4472 5045047..5046412 r
RPA4471:conserved hypothetical protein
RPA4472:putative c-type cytochrome biogenesis protein

>operons_50:RPA4473-RPA4474 5046561..5047270 f
RPA4473:conserved hypothetical protein
RPA4474:possible transcriptional activator

>operons_50:RPA4478-czcB 5050403..5054907 r
RPA4478:conserved hypothetical protein
czcA:putative heavy metal cation efflux system
czcB:possible RND divalent metal cation efflux

>operons_50:RPA4481-RPA4482 5055101..5056922 r
RPA4481:possible methyl-accepting chemotaxis protein
RPA4482:putative signal-transduction sensor protein

>operons_50:RPA4483-RPA4484 5057092..5058910 r
RPA4483:possible signal transducer
RPA4484:putative signal-transduction sensor protein

>operons_50:RPA4508-RPA4509 5088621..5091109 r
RPA4508:conserved hypothetical protein
RPA4509:possible TrapT family, fused dctQ-M subunits,

>operons_50:maf-RPA4528 5108324..5110210 r
maf:putative septum formation maf protein
RPA4528:conserved hypothetical protein

>operons_50:RPA4530-hisD 5111319..5113102 r
RPA4530:conserved hypothetical protein
hisD:histidinol dehydrogenase

>operons_50:RPA4532-murA 5113226..5114990 r
RPA4532:conserved hypothetical protein
murA:UDP-N-acetylglucosamine

>operons_50:RPA4538-RPA4539 5118975..5120303 r
RPA4538:conserved unknown protein
RPA4539:hypothetical protein

>operons_50:RPA4543-RPA4546 5122780..5126418 r
RPA4543:conserved hypothetical protein
RPA4544:conserved unknown protein
RPA4545:hypothetical protein
RPA4546:conserved hypothetical protein

>operons_50:RPA4547-RPA4548 5126565..5127577 r
RPA4547:hypothetical protein
RPA4548:hypothetical protein

>operons_50:RPA4552-RPA4553 5131650..5134084 r
RPA4552:possible 4-hydroxybutyrate-CoA
RPA4553:putative acyl-CoA dehydrogenase

>operons_50:dctM-RPA4556 5134138..5137049 r
dctM:TrapT family, dctM subunit, C4-dicarboxylate
RPA4555:possible TrapT family, dctQ subunit,
RPA4556:possible TrapT family, dctP subunit,

>operons_50:RPA4557-iclR 5137253..5140566 f
RPA4557:conserved hypothetical protein
RPA4558:putative monoamine oxidase regulatory protein
RPA4559:putative citrate lyase beta chain
iclR:possible acetate operon repressor.

>operons_50:ackA-RPA4568 5145907..5149300 r
ackA:putative acetate kinase
pta:putative phosphate acetyltransferase
RPA4568:putative enoyl-acyl carrier protein reductase

>operons_50:RPA4575-RPA4577 5155586..5159130 f
RPA4575:putative ATP-binding protein of sugar ABC
RPA4576:putative permease protein of sugar ABC
RPA4577:putative permease protein of sugar ABC

>operons_50:RPA4579-RPA4580 5160505..5162597 r

RPA4579:possible serine protease, htrA-like
RPA4580:Uncharacterized protein family UPF0065:Tat

>operons_50:RPA4581-galE 5162843..5165116 f
RPA4581:conserved hypothetical protein
galE:UDP-galactose 4-epimerase

>operons_50:RPA4584-RPA4585 5166277..5169585 r
RPA4584:possible endoglucanase
RPA4585:Lipopolysaccharide biosynthesis

>operons_50:RPA4586-RPA4587 5169889..5172639 f
RPA4586:possible Glycosyl transferases group 1
RPA4587:conserved unknown protein

>operons_50:RPA4590-metY 5174703..5177021 r
RPA4590:possible homoserine O-succinyltransferase
metY:homocysteine synthase

>operons_50:RPA4592-RPA4593 5177281..5179988 f
RPA4592:putative fatty acid metabolism AMP-binding
RPA4593:possible branched-chain amino acid

>operons_50:RPA4595-fabG 5181226..5183329 f
RPA4595:conserved unknown protein
fabG:putative 3-oxoacyl-acyl carrier protein

>operons_50:RPA4597-RPA4598 5183551..5185756 r
RPA4597:possible seryl-tRNA synthetase
RPA4598:possible acyl-CoA dehydrogenase

>operons_50:fixX-fixA 5188040..5191666 r
fixX:ferredoxin like protein, fixX
fixC:nitrogen fixation protein,fixC
fixB:electron transfer flavoprotein alpha chain
fixA:electron trnasfer flavoprotein beta chain fixA

>operons_50:nifW-RPA4610 5191999..5196127 r
nifW:nitrogenase stabilizer NifW
nifV:putative homocitrate synthase
nifS:nitrogenase cofactor synthesis protein nifS
nifU:putative nifU protein
RPA4610:Protein of unknown function, HesB/YadR/YfhF

>operons_50:nifQ-fdxB 5196535..5197574 r
nifQ:putative nitrogen fixation protein nifQ
fdxB:ferredoxin 2[4Fe-4S] III, fdxB

>operons_50:RPA4613-nifX 5197635..5198724 r
RPA4613:DUF683
RPA4614:DUF269
nifX:nitrogenase molybdenum-iron protein nifX

>operons_50:nifN-nifK 5198780..5203226 r
nifN:nitrogenase reductase-associated ferredoxin,
nifE:nitrogenase molybdenum-cofactor synthesis

nifK:nitrogenase molybdenum-iron protein beta chain,

>operons_50:RPA4621-nifB 5206323..5211775 r
RPA4621:conserved hypothetical protein
RPA4622:hypothetical protein
fixU,nifT:conserved hypothetical protein
RPA4624:hypothetical protein
nifZ:NifZ domain
RPA4626:Protein of unknown function from Deinococcus and
RPA4627:conserved hypothetical protein
hesB:Protein of unknown function, HesB/YadR/YfhF
ferN:ferredoxin 2[4Fe-4S], fdxN
nifB:nitrogen fixation protein nifB

>operons_50:feoB-RPA4636 5216625..5218839 r
feoB:ferrous iron transport protein B
RPA4636:FeoA family

>operons_50:cbbP-cbbF 5228833..5230777 r
cbbP:phosphoribulokinase (phosphopentokinase) (PRK)
cbbF:fructose-1,6-bisphosphatase

>operons_50:RPA4648-potA 5232963..5237020 r
RPA4648:possible ABC transporter binding protein
RPA4649:probable ABC transporter permease protein
potA:putative spermidine/putrescine transport system

>operons_50:RPA4651-RPA4654 5237135..5241777 f
RPA4651:possible glutaconate CoA-transferase, subunit A
RPA4652:possible CoA transferase, subunit B
bisC:biotin sulfoxide reductase
RPA4654:conserved unknown protein

>operons_50:fucA-RPA4658 5241859..5245347 f
fucA:L-fuculose phosphate aldolase
RPA4656:possible sugar kinase
kduD:putative 2-keto-3-deoxygluconate dehydrogenase
RPA4658:zinc-binding dehydrogenases (related to alcohol

>operons_50:otsB-RPA4662 5254267..5256548 r
otsB:putative trehalose-6-phosphate phophatase,
RPA4662:putative suar transport protein

>operons_50:maiA-hmgA 5268784..5270783 r
maiA:putative maleylacetoacetate isomerase
hmgA:homogentisate 1,2-dioxygenase

>operons_50:RPA4679-RPA4682 5277277..5284153 f
RPA4679:possible component of multidrug efflux system
RPA4680:putative efflux transporter
RPA4681:possible asmA protein
RPA4682:possible RND efflux membrane fusion protein

>operons_50:lysS-RPA4686 5286747..5289173 r
lysS:lysyl tRNA synthetase
RPA4686:possible ABC transporter, periplasmic amino

>operons_50:RPA4694-ligR 5297448..5299370 f
RPA4694:Uncharacterized protein family UPF0065:Tat
ligR:putative lysR-type transcriptional regulator

>operons_50:ligJ-FldX 5300785..5303440 f
ligJ:4-oxalomesaconate hydratase
FldZ:possible acyl transferase
FldX:possible dehydrogenase

>operons_50:ligA-ligC 5304715..5306919 f
ligA:Protocatechuate 4,5-dioxygenase, alpha chain
ligB:Protocatechuate 4,5-dioxygenase, beta chain
ligC:4-carboxy-2-hydroxymuconate-6-semialdehyde

>operons_50:modC-modB 5316493..5318297 r
modC:putative molybdate transport system ATP-binding
modB:molybdate transport system permease protein

>operons_50:RPA4721-RPA4722 5321423..5329467 f
RPA4721:possible+E2677 pyruvate-flavodoxin
RPA4722:possible glutamate synthase, small subunit

>operons_50:plsC-RPA4734 5344975..5346565 r
plsC:putative 1-acyl-SN-glycerol-3-phosphate
RPA4734:conserved hypothetical protein

>operons_50:lysA-RPA4742 5353332..5354887 r
lysA:diaminopimelate decarboxylase
RPA4742:conserved hypothetical protein

>operons_50:etfA-etfB 5360445..5362138 r
etfA:electron transfer flavoprotein alpha-subunit,
etfB:electron transfer flavoprotein beta chain,

>operons_50:RPA4767-opgC 5382282..5385291 r
RPA4767:Lipolytic enzyme, G-D-S-L family
RPA4768:conserved hypothetical protein
opgC:putative opgC protein

>operons_50:argF-argD 5387283..5389474 r
argF:ornithine carbamoyltransferase
argD:putative acetylornithine aminotransferase

>operons_50:phoU-pstC 5391441..5394865 r
phoU:phosphate regulon transcriptional regulator,
pstB:phosphate ABC transporter ATP-binding protein,
pstA:phosphate transport system permease protein
pstC:phosphate ABC transporter, permease protein,

>operons_50:phoR-RPA4782 5396238..5398625 r
phoR:possible phosphate regulon, two-component sensor
RPA4782:conserved hypothetical protein

>operons_50:RPA4783-RPA4784 5398873..5400567 r
RPA4783:conserved hypothetical protein

RPA4784:OmpA/MotB domain

>operons_50:RPA4790-RPA4791 5407468..5409857 f
RPA4790:possible histidine kinase response regulator
RPA4791:putative two-component response regulator

>operons_50:QxtA-RPA4797 5411181..5415455 f
QxtA:cytochrome bd-quinol oxidase subunit I
qxtB:putative cytochrome bd-quinol oxidase subunit
RPA4795:conserved hypothetical protein
RPA4796:ErfK/YbiS/YcfS/YnhG
RPA4797:ABC transporter, amino acid binding protein

>operons_50:RPA4809-RPA4811 5430178..5434368 f
RPA4809:putative ABC transporter, ATP-binding protein
RPA4810:predicted permease
RPA4811:conserved hypothetical protein

>operons_50:RPA4816-RPA4818 5440041..5442417 r
RPA4816:putative two-component sensor protein
RPA4817:two-component system, response regulator
RPA4818:conserved hypothetical protein