MexN Mutant

Gene	**Reguliert**		**Zähler**	**Descriptions**
	hoch	**herab**		
AFFX-Athal_actin_at	4,4		1	U37281 Arabidopsis thaliana actin-2 mRNA
AFFX-Athal_GAPDH_at	9,1		3	M64116 Arabidopsis thaliana glyceraldehyde 3-phosphate dehydrogenase C subunit (GapC) gene
AFFX-YEL002C_WPB1_at	24,6		3	X61388 SGD:YEL002C S.cerevisiae WBP1 Oligosaccharyl transferase beta glycoprotein comples, beta subunit
ig_2116265_2117030_at	4,0		1	Intergenic region between PA1978 and PA1979, 2116265-2117030, (+) strand
ig_224101_223454_at	5,9		1	Intergenic region between PA0263 and PA0264, 223454-224101, (-) strand
ig_2450765_2451707_at	10,5		4	Intergenic region between PA2319 and PA2320, 2450765-2451707, (+) strand
ig_2902217_2901558_at	7,6		2	Intergenic region between PA2570 and PA2571, 2901558-2902217, (-) strand
ig_2923366_2922568_at	5,3		1	Intergenic region between PA2587 and PA2588, 2922568-2923366, (-) strand
ig_3129070_3129728_at	4,5		1	Intergenic region between PA2852 and PA2853, 3129070-3129728, (+) strand
ig_3475955_3475169_at	5,1		1	Intergenic region between PA3133 and PA3134, 3475169-3475955, (-) strand
ig_4240578_4241341_at	4,5		1	Intergenic region between PA3835 and PA3836, 4240578-4241341, (+) strand
ig_4297249_4294604_at	4,8		1	Intergenic region between PA3860 and PA3861, 4294604-4297249, (-) strand
ig_517462_518083_at		9,3	2	Intergenic region between PA0484 and PA0485, 517462-518083, (+) strand
ig_5207621_5208463_at		3,0	1	Intergenic region between PA4674 and PA4675, 5207621-5208463, (+) strand
ig_546334_545644_at	13,1		4	Intergenic region between PA0574 and PA0575, 545644-546334, (-) strand
ig_785174_785969_at	10,0		2	Intergenic region between PA0716 and PA0717, 785174-785969, (+) strand
ig_863300_864095_at	7,8		2	Intergenic region between PA0806 and PA0807, 863300-864095, (+) strand
ig_991198_991830_at	17,8		3	Intergenic region between PA0961 and PA0962, 991198-991830, (+) strand
PA0001_dnaA_at		5,4	2	PA0001 /GENE=dnaA /DEF=chromosomal replication initiator protein DnaA /FUNCTION=DNA replication, recombination, modification and repair
PA0009_glyQ_at		8,2	2	PA0009 /GENE=glyQ /DEF=glycyl-tRNA synthetase alpha chain /FUNCTION=Amino acid biosynthesis and metabolism; Translation, post-translational modification, degradation
PA0022_at	7,2		2	PA0022 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0131_at	9,4		2	PA0131 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0132_at	7,8		2	PA0132 /DEF=beta-alanine--pyruvate transaminase /FUNCTION=Amino acid biosynthesis and metabolism
PA0150_at		5,0	1	PA0150 /DEF=probable transmembrane sensor /FUNCTION=Membrane proteins; Transcriptional regulators
PA0172_at		3,0	1	PA0172 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0177_at	5,2		1	PA0177 /DEF=probable purine-binding chemotaxis protein /FUNCTION=Adaptation,

				protection; Chemotaxis
PA0200_i_at		11,0	4	PA0200 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0219_at	6,8		2	PA0219 /DEF=probable aldehyde dehydrogenase /FUNCTION=Putative enzymes
PA0220_at	3,9		1	PA0220 /DEF=probable amino acid permease /FUNCTION=Transport of small molecules
PA0256_at	4,7		1	PA0256 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0258_at		4,0	1	PA0258 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0263_hcpC_s_at		14,3	3	PA0263 /GENE=hcpC /DEF=secreted protein Hcp /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA0286_at		3,4	2	PA0286 /DEF=probable fatty acid desaturase /FUNCTION=Fatty acid and phospholipid metabolism
PA0289_at	4,6		1	PA0289 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA0372_at		3,4	1	PA0372 /DEF=probable zinc protease /FUNCTION=Putative enzymes
PA0452_at	7,4		2	PA0452 /DEF=probable stomatin-like protein /FUNCTION=Membrane proteins
PA0492_at	3,9		1	PA0492 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0497_at	6,8		2	PA0497 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0508_at		2,7	1	PA0508 /DEF=probable acyl-CoA dehydrogenase /FUNCTION=Putative enzymes
PA0527_dnr_at		7,3	2	PA0527 /GENE=dnr /DEF=transcriptional regulator Dnr /FUNCTION=Transcriptional regulators
PA0546_metK_at		6,6	1	PA0546 /GENE=metK /DEF=methionine adenosyltransferase /FUNCTION=Amino acid biosynthesis and metabolism; Central intermediary metabolism
PA0547_at		4,8	1	PA0547 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA0552_pgk_at		6,3	2	PA0552 /GENE=pgk /DEF=phosphoglycerate kinase /FUNCTION=Carbon compound catabolism; Energy metabolism
PA0555_fda_at		6,0	2	PA0555 /GENE=fda /DEF=fructose-1,6-bisphosphate aldolase /FUNCTION=Carbon compound catabolism; Central intermediary metabolism
PA0587_at	4,8		1	PA0587 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0593_pdxA_at		4,4	1	PA0593 /GENE=pdxA /DEF=pyridoxal phosphate biosynthetic protein PdxA /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA0594_surA_at		10,9	4	PA0594 /GENE=surA /DEF=peptidyl-prolyl cis-trans isomerase SurA /FUNCTION=Adaptation, protection; Chaperones & heat shock proteins; Translation, post-translational modification, degradation
PA0595_ostA_at		6,9	2	PA0595 /GENE=ostA /DEF=organic solvent tolerance protein OstA precursor /FUNCTION=Adaptation, protection
PA0602_at	7,8		2	PA0602 /DEF=probable binding protein component of ABC transporter /FUNCTION=Transport of small molecules
PA0613_at	20,2		4	PA0613 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0625_at	5,2		1	PA0625 /DEF=hypothetical protein /FUNCTION=Related to phage, transposon, or plasmid

PA0628_at	4,8		1	PA0628 /DEF=conserved hypothetical protein /FUNCTION=Related to phage, transposon, or plasmid
PA0658_at		7,1	2	PA0658 /DEF=probable short-chain dehydrogenase /FUNCTION=Putative enzymes
PA0673_at	5,8		1	PA0673 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0675_at	5,3		1	PA0675 /DEF=probable sigma-70 factor, ECF subfamily /FUNCTION=Transcriptional regulators
PA0696_at	4,0		1	PA0696 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0713_at		7,9	3	PA0713 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0716_at	32,9		4	PA0716 /DEF=hypothetical protein /FUNCTION=Related to phage, transposon, or plasmid
PA0767_lepA_at		7,0	1	PA0767 /GENE=lepA /DEF=GTP-binding protein LepA /FUNCTION=Protein secretion/export apparatus; Translation, post-translational modification, degradation
PA0786_at	8,3		2	PA0786 /DEF=probable transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA0802_i_at	6,3		2	PA0802 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA0842_at	13,6		3	PA0842 /DEF=probable glycosyl transferase /FUNCTION=Putative enzymes
PA0843_plcR_at	7,4		2	PA0843 /GENE=plcR /DEF=phospholipase accessory protein PlcR precursor /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA0852_cpbD_at		23,2	4	PA0852 /GENE=cpbD /DEF=chitin-binding protein CbpD precursor /FUNCTION=Hypothetical, unclassified, unknown
PA0860_at	4,3		1	PA0860 /DEF=probable ATP-binding/permease fusion ABC transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA0878_at	6,2		1	PA0878 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0903_alaS_at		9,3	3	PA0903 /GENE=alaS /DEF=alanyl-tRNA synthetase /FUNCTION=Transcription, RNA processing and degradation
PA0911_at	4,9		1	PA0911 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0922_at	6,0		1	PA0922 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0948_at		7,0	2	PA0948 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0963_aspS_at		12,1	4	PA0963 /GENE=aspS /DEF=aspartyl-tRNA synthetase /FUNCTION=Transcription, RNA processing and degradation
PA0964_at		5,2	2	PA0964 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0969_tolQ_at		5,4	1	PA0969 /GENE=tolQ /DEF=TolQ protein /FUNCTION=Membrane proteins; Transport of small molecules
PA0977_at	5,7		1	PA0977 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0996_at		21,8	4	PA0996 /DEF=probable coenzyme A ligase /FUNCTION=Putative enzymes
PA0997_at		27,1	4	PA0997 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0998_at		7,8	2	PA0998 /DEF=hypothetical protein /FUNCTION=Putative enzymes

PA1008_bcp_at		10,5	4	PA1008 /GENE=bcp /DEF=bacterioferritin comigratory protein /FUNCTION=Adaptation, protection
PA1011_at		8,2	2	PA1011 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1013_purC_at		10,3	3	PA1013 /GENE=purC /DEF=phosphoribosylaminoimidazole-succinocarboxamide synthase /FUNCTION=Nucleotide biosynthesis and metabolism
PA1047_at		2,3	1	PA1047 /DEF=probable esterase /FUNCTION=Putative enzymes
PA1062_at		4,1	1	PA1062 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Putative enzymes
PA1089_at	5,5		2	PA1089 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1133_at	7,9		2	PA1133 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1136_at	7,0		2	PA1136 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA1144_at	7,9		2	PA1144 /DEF=probable MFS transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA1168_at		14,1	3	PA1168 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1169_at		37,4	4	PA1169 /DEF=probable lipoxygenase /FUNCTION=Putative enzymes
PA1171_at		3,3	1	PA1171 /DEF=probable transglycolase /FUNCTION=Cell wall / LPS / capsule; Putative enzymes
PA1190_at	9,6		2	PA1190 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA1219_at	9,5		2	PA1219 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1225_at	5,0		1	PA1225 /DEF=probable NAD(P)H dehydrogenase /FUNCTION=Putative enzymes
PA1250_aprI_at		5,5	1	PA1250 /GENE=aprI /DEF=alkaline proteinase inhibitor AprI /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA1264_at	18,7		4	PA1264 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA1298_i_at	9,8		2	PA1298 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1302_at	9,5		2	PA1302 /DEF=probable heme utilization protein precursor /FUNCTION=Membrane proteins; Transport of small molecules
PA1318_cyoB_at		5,0	1	PA1318 /GENE=cyoB /DEF=cytochrome o ubiquinol oxidase subunit I /FUNCTION=Energy metabolism
PA1352_at	4,3		1	PA1352 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA1365_at	6,4		1	PA1365 /DEF=probable siderophore receptor /FUNCTION=Transport of small molecules
PA1418_at	4,4		1	PA1418 /DEF=probable sodium:solute symport protein /FUNCTION=Transport of small molecules
PA1424_at	5,0		1	PA1424 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1431_rsaL_at		33,0	4	PA1431 /GENE=rsaL /DEF=regulatory protein RsaL /FUNCTION=Adaptation, protection; Transcriptional regulators; Secreted Factors (toxins, enzymes, alginate)

PA1434_at	4,9		1	PA1434 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1500_at	14,6		2	PA1500 /DEF=probable oxidoreductase /FUNCTION=Putative enzymes
PA1502_gcl_at	8,6		3	PA1502 /GENE=gcl /DEF=glyoxylate carboligase /FUNCTION=Central intermediary metabolism
PA1509_at		5,0	2	PA1509 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1510_at		8,2	2	PA1510 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1546_hemN_at		18,2	4	PA1546 /GENE=hemN /DEF=oxygen-independent coproporphyrinogen III oxidase /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA1554_at		12,7	3	PA1554 /DEF=probable cytochrome oxidase subunit (cbb3-type) /FUNCTION=Energy metabolism
PA1556_at		86,1	4	PA1556 /DEF=probable cytochrome c oxidase subunit /FUNCTION=Energy metabolism
PA1557_at		8,0	2	PA1557 /DEF=probable cytochrome oxidase subunit (cbb3-type) /FUNCTION=Energy metabolism
PA1581_sdhC_at		16,4	4	PA1581 /GENE=sdhC /DEF=succinate dehydrogenase (C subunit) /FUNCTION=Energy metabolism
PA1583_sdhA_at		13,3	4	PA1583 /GENE=sdhA /DEF=succinate dehydrogenase (A subunit) /FUNCTION=Energy metabolism
PA1588_sucC_at		6,3	2	PA1588 /GENE=sucC /DEF=succinyl-CoA synthetase beta chain /FUNCTION=Energy metabolism
PA1589_sucD_at		6,7	1	PA1589 /GENE=sucD /DEF=succinyl-CoA synthetase alpha chain /FUNCTION=Energy metabolism
PA1605_at	11,5		2	PA1605 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1626_at	9,9		2	PA1626 /DEF=probable MFS transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA1632_kdpF_at	11,9		3	PA1632 /GENE=kdpF /DEF=KdpF protein /FUNCTION=Transport of small molecules
PA1642_selD_at		3,6	1	PA1642 /GENE=selD /DEF=selenophosphate synthetase /FUNCTION=Translation, post-translational modification, degradation
PA1656_at		17,9	4	PA1656 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1657_at		13,9	3	PA1657 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1658_at		39,8	4	PA1658 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1659_at		7,6	2	PA1659 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1660_at		4,4	2	PA1660 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1664_at		20,7	4	PA1664 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1667_at		25,8	4	PA1667 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1673_at		13,9	4	PA1673 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1691_pscT_at	6,7		2	PA1691 /GENE=pscT /DEF=translocation protein in type III secretion /FUNCTION=Protein secretion/export apparatus

PA1693_pscR_at	4,3		1	PA1693 /GENE=pscR /DEF=translocation protein in type III secretion /FUNCTION=Protein secretion/export apparatus
PA1737_at	8,2		2	PA1737 /DEF=probable 3-hydroxyacyl-CoA dehydrogenase /FUNCTION=Putative enzymes
PA1756_cysH_at		5,2	1	PA1756 /GENE=cysH /DEF=3 -phosphoadenosine-5 -phosphosulfate reductase /FUNCTION=Amino acid biosynthesis and metabolism
PA1760_at	6,7		1	PA1760 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA1761_at	10,4		3	PA1761 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1762_at	24,2		3	PA1762 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1764_at	8,0		2	PA1764 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1770_ppsA_at		4,2	1	PA1770 /GENE=ppsA /DEF=phosphoenolpyruvate synthase /FUNCTION=Carbon compound catabolism; Central intermediary metabolism; Energy metabolism
PA1776_at		4,8	1	PA1776 /DEF=probable sigma-70 factor, ECF subfamily /FUNCTION=Transcriptional regulators
PA1779_at	11,6		2	PA1779 /DEF=assimilatory nitrate reductase /FUNCTION=Central intermediary metabolism
PA1785_at	6,3		1	PA1785 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1786_at	5,5		1	PA1786 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1789_at		44,1	4	PA1789 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1794_glnS_at		5,0	1	PA1794 /GENE=glnS /DEF=glutaminyl-tRNA synthetase /FUNCTION=Amino acid biosynthesis and metabolism
PA1817_at	4,8		1	PA1817 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1819_at	6,8		2	PA1819 /DEF=probable amino acid permease /FUNCTION=Membrane proteins; Transport of small molecules
PA1840_at		6,0	1	PA1840 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1869_at		20,7	4	PA1869 /DEF=probable acyl carrier protein /FUNCTION=Fatty acid and phospholipid metabolism
PA1901_s_at		10,0	2	PA1901 /DEF=phenazine biosynthesis protein PhzC /FUNCTION=Hypothetical, unclassified, unknown; Secreted Factors (toxins, enzymes, alginate)
PA1902_s_at		29,3	4	PA1902 /DEF=phenazine biosynthesis protein PhzD /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA1903_s_at		11,2	2	PA1903 /DEF=phenazine biosynthesis protein PhzE /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA1905_s_at		20,5	4	PA1905 /DEF=probable pyridoxamine 5 -phosphate oxidase /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA1907_at	11,2		2	PA1907 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1930_at	5,6		1	PA1930 /DEF=probable chemotaxis transducer /FUNCTION=Adaptation, protection; Chemotaxis
PA1947_rbsA_at	4,7		1	PA1947 /GENE=rbsA /DEF=ribose transport protein RbsA /FUNCTION=Transport of small molecules

PA1968_at	9,9		2	PA1968 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1972_at	7,2		2	PA1972 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2005_at	5,6		1	PA2005 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2030_at		7,3	1	PA2030 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2035_at	8,2		1	PA2035 /DEF=probable decarboxylase /FUNCTION=Putative enzymes
PA2046_at	4,7		1	PA2046 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2069_at		5,4	1	PA2069 /DEF=probable carbamoyl transferase /FUNCTION=Putative enzymes
PA2070_at	4,6		1	PA2070 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2098_at	5,2		1	PA2098 /DEF=probable esterase/deacetylase /FUNCTION=Carbon compound catabolism
PA2099_at	6,6		1	PA2099 /DEF=probable short-chain dehydrogenase /FUNCTION=Putative enzymes
PA2100_at	5,4		1	PA2100 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2119_at		18,6	4	PA2119 /DEF=alcohol dehydrogenase (Zn-dependent) /FUNCTION=Putative enzymes
PA2121_at	6,2		2	PA2121 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2147_katE_at	5,6		1	PA2147 /GENE=katE /DEF=catalase HPII /FUNCTION=Adaptation, protection
PA2163_at	4,5		1	PA2163 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2185_at	4,6		1	PA2185 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2191_exoY_at	5,0		1	PA2191 /GENE=exoY /DEF=adenylate cyclase ExoY /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA2193_hcnA_at		63,4	4	PA2193 /GENE=hcnA /DEF=hydrogen cyanide synthase HcnA /FUNCTION=Central intermediary metabolism
PA2194_hcnB_at		8,9	2	PA2194 /GENE=hcnB /DEF=hydrogen cyanide synthase HcnB /FUNCTION=Central intermediary metabolism
PA2195_hcnC_at		13,5	4	PA2195 /GENE=hcnC /DEF=hydrogen cyanide synthase HcnC /FUNCTION=Central intermediary metabolism
PA2201_at		3,7	1	PA2201 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2204_at		35,5	4	PA2204 /DEF=probable binding protein component of ABC transporter /FUNCTION=Transport of small molecules
PA2238_at		4,9	1	PA2238 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2255_pvcB_at	4,1		1	PA2255 /GENE=pvcB /DEF=pyoverdine biosynthesis protein PvcB /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA2266_at	6,3		1	PA2266 /DEF=probable cytochrome c precursor /FUNCTION=Carbon compound catabolism; Energy metabolism
PA2300_chiC_at		8,2	2	PA2300 /GENE=chiC /DEF=chitinase /FUNCTION=Carbon compound catabolism
PA2331_at		10,8	4	PA2331 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2404_at	7,0		2	PA2404 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown;

				Membrane proteins
PA2430_at	5,7		1	PA2430 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2441_at		7,9	2	PA2441 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2447_at	17,3		4	PA2447 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2458_at	4,8		1	PA2458 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2493_mexE_at	6,2		1	PA2493 /GENE=mexE /DEF=RND multidrug efflux membrane fusion protein MexE precursor /FUNCTION=Antibiotic resistance and susceptibility; Transport of small molecules
PA2501_at		48,1	4	PA2501 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2505_at	3,3		1	PA2505 /DEF=probable porin /FUNCTION=Transport of small molecules
PA2509_catB_at	5,3		1	PA2509 /GENE=catB /DEF=muconate cycloisomerase I /FUNCTION=Carbon compound catabolism
PA2512_antA_at	5,6		1	PA2512 /GENE=antA /DEF=anthranilate dioxygenase large subunit /FUNCTION=Carbon compound catabolism
PA2551_at	8,1		2	PA2551 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2570_pa1L_at	9,2		2	PA2570 /GENE=pa1L /DEF=PA-I galactophilic lectin /FUNCTION=Adaptation, protection; Motility & Attachment
PA2587_at		3,9	1	PA2587 /DEF=probable FAD-dependent monooxygenase /FUNCTION=Putative enzymes
PA2594_at	7,5		2	PA2594 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2637_nuoA_at		10,3	2	PA2637 /GENE=nuoA /DEF=NADH dehydrogenase I chain A /FUNCTION=Energy metabolism
PA2639_nuoD_at		7,3	2	PA2639 /GENE=nuoD /DEF=NADH dehydrogenase I chain C,D /FUNCTION=Energy metabolism
PA2647_nuoL_at		10,3	4	PA2647 /GENE=nuoL /DEF=NADH dehydrogenase I chain L /FUNCTION=Energy metabolism
PA2648_nuoM_at		4,2	2	PA2648 /GENE=nuoM /DEF=NADH dehydrogenase I chain M /FUNCTION=Energy metabolism
PA2666_at		7,0	1	PA2666 /DEF=probable 6-pyruvoyl tetrahydrobiopterin synthase /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA2706_at	5,4		1	PA2706 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2716_at	5,3		1	PA2716 /DEF=probable FMN oxidoreductase /FUNCTION=Energy metabolism
PA2753_at		15,3	4	PA2753 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2766_at	8,5		2	PA2766 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2774_at	5,0		1	PA2774 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2789_at	4,9		1	PA2789 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2800_at		9,4	3	PA2800 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified,

				unknown
PA2807_at	4,0		1	PA2807 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2810_at	5,4		1	PA2810 /DEF=probable two-component sensor /FUNCTION=Two-component regulatory systems
PA2814_at	12,5		4	PA2814 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2844_at	5,7		1	PA2844 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2845_at	5,3		1	PA2845 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2854_at		5,3	1	PA2854 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2862_lipA_at	13,4		4	PA2862 /GENE=lipA /DEF=lactonizing lipase precursor /FUNCTION=Carbon compound catabolism; Secreted Factors (toxins, enzymes, alginate)
PA2872_at		2,8	1	PA2872 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2908_cbiD_at		3,0	1	PA2908 /GENE=cbiD /DEF=cobalamin biosynthetic protein CbiD /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA2920_at	9,8		2	PA2920 /DEF=probable chemotaxis transducer /FUNCTION=Adaptation, protection; Chemotaxis
PA2928_at		4,2	2	PA2928 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2935_at		3,0	1	PA2935 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2939_at		11,0	3	PA2939 /DEF=probable aminopeptidase /FUNCTION=Putative enzymes
PA2946_at		8,4	2	PA2946 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2950_at		7,5	1	PA2950 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2951_etfA_at		4,8	2	PA2951 /GENE=etfA /DEF=electron transfer flavoprotein alpha-subunit /FUNCTION=Energy metabolism
PA2952_etfB_at		9,2	2	PA2952 /GENE=etfB /DEF=electron transfer flavoprotein beta-subunit /FUNCTION=Energy metabolism
PA2967_fabG_at		18,6	4	PA2967 /GENE=fabG /DEF=3-oxoacyl-[acyl-carrier-protein] reductase /FUNCTION=Fatty acid and phospholipid metabolism
PA2968_fabD_at		5,6	2	PA2968 /GENE=fabD /DEF=malonyl-CoA-[acyl-carrier-protein] transacylase /FUNCTION=Fatty acid and phospholipid metabolism
PA2974_at		5,3	1	PA2974 /DEF=probable hydrolase /FUNCTION=Putative enzymes
PA2984_at	8,2		2	PA2984 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2999_nqrA_at		9,4	4	PA2999 /GENE=nqrA /DEF=Na+-translocating NADH:ubiquinone oxidoreductase subunit Nrq1 /FUNCTION=Energy metabolism
PA3001_at		6,7	2	PA3001 /DEF=probable glyceraldehyde-3-phosphate dehydrogenase /FUNCTION=Putative enzymes
PA3044_at	5,1		1	PA3044 /DEF=probable two-component sensor /FUNCTION=Two-component regulatory systems

PA3049_rmf_at	9,7		2	PA3049 /GENE=rmf /DEF=ribosome modulation factor /FUNCTION=Translation, post-translational modification, degradation
PA3080_at	13,1		3	PA3080 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3087_at		5,3	1	PA3087 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3094_at		3,5	1	PA3094 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA3105_xcpQ_at		9,9	2	PA3105 /GENE=xcpQ /DEF=general secretion pathway protein D /FUNCTION=Protein secretion/export apparatus
PA3148_wbpI_at	6,1		2	PA3148 /GENE=wbpI /DEF=probable UDP-N-acetylglucosamine 2-epimerase WbpI /FUNCTION=Cell wall / LPS / capsule; Putative enzymes
PA3154_wzy_at	8,9		2	PA3154 /GENE=wzy /DEF=B-band O-antigen polymerase /FUNCTION=Cell wall / LPS / capsule; Membrane proteins
PA3162_rpsA_at		16,9	4	PA3162 /GENE=rpsA /DEF=30S ribosomal protein S1 /FUNCTION=Translation, post-translational modification, degradation
PA3188_at	9,1		2	PA3188 /DEF=probable permease of ABC sugar transporter /FUNCTION=Transport of small molecules
PA3217_at	7,6		1	PA3217 /DEF=probable adenylate cyclase /FUNCTION=Putative enzymes
PA3244_minD_at		10,5	3	PA3244 /GENE=minD /DEF=cell division inhibitor MinD /FUNCTION=Cell division
PA3252_at	13,1		3	PA3252 /DEF=probable permease of ABC transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA3264_at	7,8		2	PA3264 /DEF=probable transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA3309_at		11,0	3	PA3309 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3313_at		6,7	2	PA3313 /DEF=hypothetical protein /FUNCTION=Transport of small molecules
PA3325_at	5,8		1	PA3325 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3329_at		5,6	2	PA3329 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3330_at		17,5	4	PA3330 /DEF=probable short chain dehydrogenase /FUNCTION=Putative enzymes
PA3334_at		11,7	3	PA3334 /DEF=probable acyl carrier protein /FUNCTION=Fatty acid and phospholipid metabolism
PA3337_rfaD_at		32,2	4	PA3337 /GENE=rfaD /DEF=ADP-L-glycero-D-mannoheptose 6-epimerase /FUNCTION=Cell wall / LPS / capsule
PA3369_at	5,8		1	PA3369 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA3397_fpr_at		15,0	4	PA3397 /GENE=fpr /DEF=ferredoxin--NADP+ reductase /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers; Energy metabolism
PA3427_at	5,4		1	PA3427 /DEF=probable short-chain dehydrogenases /FUNCTION=Putative enzymes
PA3431_at	8,0		2	PA3431 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA3446_at		6,2	1	PA3446 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified,

				unknown
PA3464_at	5,3		1	PA3464 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3471_at		4,4	1	PA3471 /DEF=probable malic enzyme /FUNCTION=Central intermediary metabolism
PA3476_rhlL_at		5,7	2	PA3476 /GENE=rhlL /DEF=autoinducer synthesis protein RhlL /FUNCTION=Adaptation, protection
PA3482_metG_at		7,1	1	PA3482 /GENE=metG /DEF=methionyl-tRNA synthetase /FUNCTION=Amino acid biosynthesis and metabolism; Translation, post-translational modification, degradation
PA3486_at	6,2		2	PA3486 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3493_at	4,5		1	PA3493 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3502_at		4,8	2	PA3502 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3509_at	5,0		1	PA3509 /DEF=probable hydrolase /FUNCTION=Putative enzymes
PA3525_argG_at		10,4	3	PA3525 /GENE=argG /DEF=argininosuccinate synthase /FUNCTION=Amino acid biosynthesis and metabolism
PA3541_at	3,8		1	PA3541 /DEF=alginate biosynthesis protein Alg8 /FUNCTION=Adaptation, protection; Cell wall / LPS / capsule; Secreted Factors (toxins, enzymes, alginate)
PA3556_at	4,9		1	PA3556 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Adaptation, protection
PA3565_at	6,7		2	PA3565 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA3581_glpF_at	13,5		4	PA3581 /GENE=glpF /DEF=glycerol uptake facilitator protein /FUNCTION=Transport of small molecules
PA3582_glpK_at	8,8		2	PA3582 /GENE=glpK /DEF=glycerol kinase /FUNCTION=Central intermediary metabolism
PA3584_glpD_at	17,2		4	PA3584 /GENE=glpD /DEF=glycerol-3-phosphate dehydrogenase /FUNCTION=Central intermediary metabolism; Energy metabolism
PA3613_at		10,9	3	PA3613 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3621_fdxA_at		11,2	2	PA3621 /GENE=fdxA /DEF=ferredoxin I /FUNCTION=Energy metabolism
PA3626_at		3,9	1	PA3626 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3635_eno_at		5,5	2	PA3635 /GENE=eno /DEF=enolase /FUNCTION=Energy metabolism; Translation, post-translational modification, degradation; Carbon compound catabolism
PA3653_frr_at		15,2	4	PA3653 /GENE=frr /DEF=ribosome recycling factor /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers; Cell wall / LPS / capsule
PA3678_at		1,4	1	PA3678 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA3686_adk_at		3,4	1	PA3686 /GENE=adk /DEF=adenylate kinase /FUNCTION=Nucleotide biosynthesis and metabolism
PA3701_prfB_at		9,4	2	PA3701 /GENE=prfB /DEF=peptide chain release factor 2 /FUNCTION=Translation, post-translational modification, degradation
PA3705_at	3,8		1	PA3705 /DEF=hypothetical protein /FUNCTION=Chemotaxis; Hypothetical, unclassified, unknown

PA3716_at		11,0	3	PA3716 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3724_lasB_at		6,7	2	PA3724 /GENE=lasB /DEF=elastase LasB /FUNCTION=Translation, post-translational modification, degradation; Secreted Factors (toxins, enzymes, alginate)
PA3736_hom_at		5,5	2	PA3736 /GENE=hom /DEF=homoserine dehydrogenase /FUNCTION=Amino acid biosynthesis and metabolism
PA3743_trmD_at		9,3	3	PA3743 /GENE=trmD /DEF=tRNA (guanine-N1)-methyltransferase /FUNCTION=Transcription, RNA processing and degradation
PA3744_rimM_at		14,2	4	PA3744 /GENE=rimM /DEF=16S rRNA processing protein /FUNCTION=Transcription, RNA processing and degradation
PA3745_rpsP_at		29,1	4	PA3745 /GENE=rpsP /DEF=30S ribosomal protein S16 /FUNCTION=Translation, post-translational modification, degradation; DNA replication, recombination, modification and repair
PA3770_guaB_at		17,4	4	PA3770 /GENE=guaB /DEF=inosine-5 -monophosphate dehydrogenase /FUNCTION=Nucleotide biosynthesis and metabolism
PA3785_at	5,3		1	PA3785 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3801_at		4,2	1	PA3801 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3806_at		9,2	2	PA3806 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3814_iscS_at		3,7	2	PA3814 /GENE=iscS /DEF=L-cysteine desulfurase (pyridoxal phosphate-dependent) /FUNCTION=Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers
PA3815_at		9,8	4	PA3815 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3834_valS_at		15,6	4	PA3834 /GENE=valS /DEF=valyl-tRNA synthetase /FUNCTION=Amino acid biosynthesis and metabolism; Translation, post-translational modification, degradation
PA3859_at		4,6	1	PA3859 /DEF=probable carboxylesterase /FUNCTION=Putative enzymes
PA3871_at	4,6		1	PA3871 /DEF=probable peptidyl-prolyl cis-trans isomerase, PpiC-type /FUNCTION=Chaperones & heat shock proteins; Translation, post-translational modification, degradation
PA3890_at		3,3	2	PA3890 /DEF=probable permease of ABC transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA3904_i_at		21,1	4	PA3904 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3907_at		9,2	3	PA3907 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3913_at	6,1		1	PA3913 /DEF=probable protease /FUNCTION=Putative enzymes
PA3919_at	36,8		4	PA3919 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3931_at		6,6	2	PA3931 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3944_at	6,4		2	PA3944 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified,

				unknown
PA3967_at	4,7		1	PA3967 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3972_at	7,2		1	PA3972 /DEF=probable acyl-CoA dehydrogenase /FUNCTION=Putative enzymes
PA3973_at	12,1		4	PA3973 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA3980_at		7,7	2	PA3980 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3990_at	6,4		1	PA3990 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4002_rodA_at	4,8		1	PA4002 /GENE=rodA /DEF=rod shape-determining protein /FUNCTION=Cell wall / LPS / capsule
PA4004_at		10,0	3	PA4004 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4008_at	4,1		1	PA4008 /DEF=probable hydrolase /FUNCTION=Membrane proteins; Putative enzymes
PA4024_eutB_at	5,0		1	PA4024 /GENE=eutB /DEF=ethanolamine ammonia-lyase large subunit /FUNCTION=Central intermediary metabolism
PA4026_at	5,3		1	PA4026 /DEF=probable acetyltransferase /FUNCTION=Putative enzymes
PA4029_at		7,2	2	PA4029 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4064_at		6,1	2	PA4064 /DEF=probable ATP-binding component of ABC transporter /FUNCTION=Transport of small molecules
PA4067_oprG_at		18,7	4	PA4067 /GENE=oprG /DEF=outer membrane protein OprG precursor /FUNCTION=Hypothetical, unclassified, unknown
PA4107_at		3,7	1	PA4107 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4115_at	5,2		1	PA4115 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4130_at		4,4	1	PA4130 /DEF=probable sulfite or nitrite reductase /FUNCTION=Central intermediary metabolism
PA4131_at		10,9	2	PA4131 /DEF=probable iron-sulfur protein /FUNCTION=Putative enzymes
PA4134_i_at		22,1	4	PA4134 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4139_at		25,4	4	PA4139 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4140_at		13,6	4	PA4140 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4141_at		34,7	4	PA4141 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4142_at		6,6	2	PA4142 /DEF=probable secretion protein /FUNCTION=Protein secretion/export apparatus
PA4175_at		14,0	4	PA4175 /DEF=probable endoproteinase Arg-C precursor /FUNCTION=Putative enzymes
PA4182_at	6,9		1	PA4182 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4209_at		8,6	2	PA4209 /DEF=probable O-methyltransferase /FUNCTION=Putative enzymes
PA4210_s_at		14,1	4	PA4210 /DEF=probable phenazine biosynthesis protein /FUNCTION=Secreted Factors (toxins, enzymes, alginate)

PA4222_at	4,7		1	PA4222 /DEF=probable ATP-binding component of ABC transporter /FUNCTION=Transport of small molecules
PA4235_bfrA_at		19,2	4	PA4235 /GENE=bfrA /DEF=bacterioferritin /FUNCTION=Adaptation, protection; Transport of small molecules
PA4238_rpoA_at		13,7	4	PA4238 /GENE=rpoA /DEF=DNA-directed RNA polymerase alpha chain /FUNCTION=Transcription, RNA processing and degradation
PA4239_rpsD_at		8,6	2	PA4239 /GENE=rpsD /DEF=30S ribosomal protein S4 /FUNCTION=Translation, post-translational modification, degradation
PA4241_rpsM_at		12,5	4	PA4241 /GENE=rpsM /DEF=30S ribosomal protein S13 /FUNCTION=Translation, post-translational modification, degradation
PA4242_rpmJ_at		9,9	2	PA4242 /GENE=rpmJ /DEF=50S ribosomal protein L36 /FUNCTION=Translation, post-translational modification, degradation
PA4243_secY_at		6,7	2	PA4243 /GENE=secY /DEF=secretion protein SecY /FUNCTION=Membrane proteins; Protein secretion/export apparatus
PA4245_rpmD_at		16,9	4	PA4245 /GENE=rpmD /DEF=50S ribosomal protein L30 /FUNCTION=Translation, post-translational modification, degradation
PA4246_rpsE_at		79,6	4	PA4246 /GENE=rpsE /DEF=30S ribosomal protein S5 /FUNCTION=Translation, post-translational modification, degradation
PA4247_rplR_at		12,9	4	PA4247 /GENE=rplR /DEF=50S ribosomal protein L18 /FUNCTION=Translation, post-translational modification, degradation
PA4249_rpsH_at		9,4	2	PA4249 /GENE=rpsH /DEF=30S ribosomal protein S8 /FUNCTION=Translation, post-translational modification, degradation
PA4251_rplE_at		8,4	1	PA4251 /GENE=rplE /DEF=50S ribosomal protein L5 /FUNCTION=Translation, post-translational modification, degradation
PA4253_rplN_at		9,6	3	PA4253 /GENE=rplN /DEF=50S ribosomal protein L14 /FUNCTION=Translation, post-translational modification, degradation
PA4254_rpsQ_at		15,0	4	PA4254 /GENE=rpsQ /DEF=30S ribosomal protein S17 /FUNCTION=Translation, post-translational modification, degradation
PA4256_rplP_at		12,6	4	PA4256 /GENE=rplP /DEF=50S ribosomal protein L16 /FUNCTION=Translation, post-translational modification, degradation
PA4258_rplV_at		38,9	4	PA4258 /GENE=rplV /DEF=50S ribosomal protein L22 /FUNCTION=Translation, post-translational modification, degradation
PA4260_rplB_at		9,4	3	PA4260 /GENE=rplB /DEF=50S ribosomal protein L2 /FUNCTION=Translation, post-translational modification, degradation
PA4261_rplW_at		12,8	3	PA4261 /GENE=rplW /DEF=50S ribosomal protein L23 /FUNCTION=Translation, post-translational modification, degradation
PA4262_rplD_at		34,0	4	PA4262 /GENE=rplD /DEF=50S ribosomal protein L4 /FUNCTION=Transcription, RNA processing and degradation; Translation, post-translational modification, degradation
PA4263_rplC_at		60,2	4	PA4263 /GENE=rplC /DEF=50S ribosomal protein L3 /FUNCTION=Translation, post-translational modification, degradation
PA4264_rpsJ_at		11,9	4	PA4264 /GENE=rpsJ /DEF=30S ribosomal protein S10 /FUNCTION=Translation, post-translational modification, degradation; Transcription, RNA processing and degradation

PA4268_rpsL_at		15,4	4	PA4268 /GENE=rpsL /DEF=30S ribosomal protein S12 /FUNCTION=Translation, post-translational modification, degradation
PA4273_rplA_at		17,2	4	PA4273 /GENE=rplA /DEF=50S ribosomal protein L1 /FUNCTION=Translation, post-translational modification, degradation
PA4274_rplK_at		6,5	2	PA4274 /GENE=rplK /DEF=50S ribosomal protein L11 /FUNCTION=Translation, post-translational modification, degradation
PA4321_at		5,5	2	PA4321 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4328_at		11,3	4	PA4328 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4348_at		18,6	4	PA4348 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4368_at	9,4		2	PA4368 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4376_pncB2_at		4,2	1	PA4376 /GENE=pncB2 /DEF=nicotinate phosphoribosyltransferase /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA4379_at	6,8		1	PA4379 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4430_at		24,9	4	PA4430 /DEF=probable cytochrome b /FUNCTION=Energy metabolism
PA4432_rpsI_at		27,2	4	PA4432 /GENE=rpsI /DEF=30S ribosomal protein S9 /FUNCTION=Translation, post-translational modification, degradation
PA4433_rplM_at		12,1	3	PA4433 /GENE=rplM /DEF=50S ribosomal protein L13 /FUNCTION=Translation, post-translational modification, degradation
PA4434_at		7,1	2	PA4434 /DEF=probable oxidoreductase /FUNCTION=Putative enzymes
PA4442_cysN_at		3,2	1	PA4442 /GENE=cysN /DEF=ATP sulfurylase GTP-binding subunit/APS kinase /FUNCTION=Amino acid biosynthesis and metabolism; Central intermediary metabolism
PA4443_cysD_at		7,6	2	PA4443 /GENE=cysD /DEF=ATP sulfurylase small subunit /FUNCTION=Amino acid biosynthesis and metabolism; Central intermediary metabolism
PA4449_hisG_at		7,4	2	PA4449 /GENE=hisG /DEF=ATP-phosphoribosyltransferase /FUNCTION=Amino acid biosynthesis and metabolism
PA4453_at		3,4	1	PA4453 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4457_at		8,5	2	PA4457 /DEF=conserved hypothetical protein /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA4479_mreD_at		7,0	2	PA4479 /GENE=mreD /DEF=rod shape-determining protein MreD /FUNCTION=Cell division; Cell wall / LPS / capsule
PA4482_gatC_at		8,9	3	PA4482 /GENE=gatC /DEF=Glu-tRNA(Gln) amidotransferase subunit C /FUNCTION=Translation, post-translational modification, degradation
PA4483_gatA_at		7,4	2	PA4483 /GENE=gatA /DEF=Glu-tRNA(Gln) amidotransferase subunit A /FUNCTION=Translation, post-translational modification, degradation
PA4499_at		4,2	1	PA4499 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA4553_pilX_at	8,0		1	PA4553 /GENE=pilX /DEF=type 4 fimbrial biogenesis protein PilX /FUNCTION=Motility & Attachment

PA4556_pilE_at	4,4		1	PA4556 /GENE=pilE /DEF=type 4 fimbrial biogenesis protein PilE /FUNCTION=Motility & Attachment
PA4560_ileS_at		7,9	2	PA4560 /GENE=ileS /DEF=isoleucyl-tRNA synthetase /FUNCTION=Amino acid biosynthesis and metabolism; Translation, post-translational modification, degradation
PA4568_rplU_at		8,8	2	PA4568 /GENE=rplU /DEF=50S ribosomal protein L21 /FUNCTION=Translation, post-translational modification, degradation
PA4572_fklB_at		17,5	4	PA4572 /GENE=fklB /DEF=peptidyl-prolyl cis-trans isomerase FklB /FUNCTION=Chaperones & heat shock proteins; Translation, post-translational modification, degradation
PA4583_at		2,1	1	PA4583 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4611_at		2,8	1	PA4611 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4621_at	6,0		1	PA4621 /DEF=probable oxidoreductase /FUNCTION=Putative enzymes
PA4636_at		7,9	2	PA4636 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4637_i_at	5,4		1	PA4637 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4638_at	5,3		1	PA4638 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4665_prfA_at		6,6	1	PA4665 /GENE=prfA /DEF=peptide chain release factor 1 /FUNCTION=Translation, post-translational modification, degradation
PA4682_at	11,0		2	PA4682 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4685_at		3,6	1	PA4685 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4690_at	6,8		1	PA4690 /DEF=still frameshift hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA4691_at	4,1		1	PA4691 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4694_ilvC_at		8,4	2	PA4694 /GENE=ilvC /DEF=ketol-acid reductoisomerase /FUNCTION=Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers
PA4696_ilvI_at		29,2	4	PA4696 /GENE=ilvI /DEF=acetolactate synthase large subunit /FUNCTION=Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers
PA4698_at		3,1	1	PA4698 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4710_at	5,8		1	PA4710 /DEF=probable outer membrane hemin receptor /FUNCTION=Transport of small molecules
PA4743_rbfA_at		6,6	1	PA4743 /GENE=rbfA /DEF=ribosome-binding factor A /FUNCTION=Adaptation, protection; Translation, post-translational modification, degradation
PA4756_carB_at		9,8	3	PA4756 /GENE=carB /DEF=carbamoylphosphate synthetase large subunit /FUNCTION=Nucleotide biosynthesis and metabolism; Amino acid biosynthesis and metabolism
PA4757_at		9,5	2	PA4757 /DEF=conserved hypothetical protein /FUNCTION=Membrane proteins
PA4758_carA_at		9,0	2	PA4758 /GENE=carA /DEF=carbamoyl-phosphate synthase small chain /FUNCTION=Nucleotide biosynthesis and metabolism; Amino acid biosynthesis and metabolism

PA4765_omlA_at		8,8	3	PA4765 /GENE=omlA /DEF=outer membrane lipoprotein OmlA /FUNCTION=Membrane proteins
PA4770_lldP_at		12,5	4	PA4770 /GENE=lldP /DEF=L-lactate permease /FUNCTION=Transport of small molecules
PA4777_at	5,4		1	PA4777 /DEF=probable two-component sensor /FUNCTION=Two-component regulatory systems
PA4778_at		5,8	1	PA4778 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA4787_at	6,1		1	PA4787 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA4846_aroQ1_at		8,6	2	PA4846 /GENE=aroQ1 /DEF=3-dehydroquinate dehydratase /FUNCTION=Amino acid biosynthesis and metabolism
PA4857_at		6,4	1	PA4857 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA4871_at	19,0		4	PA4871 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4872_at		4,0	1	PA4872 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4898_at	8,3		1	PA4898 /DEF=probable porin /FUNCTION=Membrane proteins
PA4909_at	4,1		1	PA4909 /DEF=probable ATP-binding component of ABC transporter /FUNCTION=Transport of small molecules
PA4916_at		9,7	2	PA4916 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4917_at		4,9	1	PA4917 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4933_at		10,8	4	PA4933 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA4957_psd_at		2,9	1	PA4957 /GENE=psd /DEF=phosphatidylserine decarboxylase /FUNCTION=Amino acid biosynthesis and metabolism; Fatty acid and phospholipid metabolism
PA4958_at	3,8		1	PA4958 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4989_at	5,6		1	PA4989 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA5019_at	5,0		1	PA5019 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5024_at		3,9	1	PA5024 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5047_at	9,1		2	PA5047 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5109_at		3,8	1	PA5109 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5114_at	8,6		2	PA5114 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA5128_secB_at		8,9	2	PA5128 /GENE=secB /DEF=secretion protein SecB /FUNCTION=Protein secretion/export apparatus
PA5149_at	3,5		1	PA5149 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5161_rmlB_at		6,2	2	PA5161 /GENE=rmlB /DEF=dTDP-D-glucose 4,6-dehydratase /FUNCTION=Carbon compound catabolism; Cell wall / LPS / capsule
PA5170_arcD_at		7,2	2	PA5170 /GENE=arcD /DEF=arginine/ornithine antiporter /FUNCTION=Amino acid

				biosynthesis and metabolism; Membrane proteins; Transport of small molecules
PA5211_at	14,7		3	PA5211 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA5220_at		5,3	2	PA5220 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5223_ubiH_at		3,8	1	PA5223 /GENE=ubiH /DEF=ubiH protein /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers; Energy metabolism
PA5224_pepP_at		7,4	1	PA5224 /GENE=pepP /DEF=aminopeptidase P /FUNCTION=Translation, post-translational modification, degradation
PA5232_at		7,2	2	PA5232 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5239_rho_at		4,2	1	PA5239 /GENE=rho /DEF=transcription termination factor Rho /FUNCTION=Transcription, RNA processing and degradation
PA5257_at		8,7	2	PA5257 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5274_rnk_at		4,5	2	PA5274 /GENE=rnk /DEF=nucleoside diphosphate kinase regulator /FUNCTION=Transcriptional regulators
PA5297_poxB_at		4,5	1	PA5297 /GENE=poxB /DEF=pyruvate dehydrogenase (cytochrome) /FUNCTION=Central intermediary metabolism; Energy metabolism
PA5311_at	5,2		1	PA5311 /DEF=probable MFS transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA5316_rpmB_at		8,4	2	PA5316 /GENE=rpmB /DEF=50S ribosomal protein L28 /FUNCTION=Translation, post-translational modification, degradation
PA5322_algC_at		10,3	2	PA5322 /GENE=algC /DEF=phosphomannomutase AlgC /FUNCTION=Amino acid biosynthesis and metabolism; Cell wall / LPS / capsule; Secreted Factors (toxins, enzymes, alginate)
PA5351_at		8,5	3	PA5351 /DEF=rubredoxin /FUNCTION=Carbon compound catabolism
PA5352_at	10,9		2	PA5352 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5380_at	7,7		1	PA5380 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA5384_at	7,1		2	PA5384 /DEF=probable lipolytic enzyme /FUNCTION=Putative enzymes
PA5444_at	5,3		1	PA5444 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA5446_i_at		37,0	4	PA5446 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5468_at		26,5	4	PA5468 /DEF=probable citrate transporter /FUNCTION=Transport of small molecules
PA5525_at	7,1		2	PA5525 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA5528_at		8,5	2	PA5528 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA5534_at		11,1	3	PA5534 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5549_glmS_at		6,1	2	PA5549 /GENE=glmS /DEF=glucosamine--fructose-6-phosphate aminotransferase /FUNCTION=Central intermediary metabolism

PA5553_atpC_at		9,1	2	PA5553 /GENE=atpC /DEF=ATP synthase epsilon chain /FUNCTION=Energy metabolism
PA5556_atpA_at		28,3	4	PA5556 /GENE=atpA /DEF=ATP synthase alpha chain /FUNCTION=Energy metabolism
PA5557_atpH_at		11,4	4	PA5557 /GENE=atpH /DEF=ATP synthase delta chain /FUNCTION=Energy metabolism
PA5558_atpF_at		27,5	4	PA5558 /GENE=atpF /DEF=ATP synthase B chain /FUNCTION=Energy metabolism
PA5564_gidB_at		7,3	2	PA5564 /GENE=gidB /DEF=glucose inhibited division protein B /FUNCTION=Cell division
PA5568_at		5,8	2	PA5568 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA5569_rnpA_at		8,1	2	PA5569 /GENE=rnpA /DEF=ribonuclease P protein component /FUNCTION=Translation, post-translational modification, degradation
PA5570_rpmH_at		139,4	4	PA5570 /GENE=rpmH /DEF=50S ribosomal protein L34 /FUNCTION=Central intermediary metabolism; Translation, post-translational modification, degradation
Pae_AF147795cds3_at	6,9		1	AF147795 /GENE=wzx /PROD=putative O-antigen transporter /FEATURE=cds3 /DEFINITION=Pseudomonas aeruginosa integration host factor beta-subunit (himD), complete cds; O-antigen biosynthesis locus, tRNA-Asn gene, complete sequence; and aromatic-amino-acid aminotransferase (tyrB) gene, complete cds.
Pae_AF147795cds4_at	4,2		1	AF147795 /GENE=wbjA /PROD=putative glucosyl transferase /FEATURE=cds4 /DEFINITION=Pseudomonas aeruginosa integration host factor beta-subunit (himD), complete cds; O-antigen biosynthesis locus, tRNA-Asn gene, complete sequence; and aromatic-amino-acid aminotransferase (tyrB) gene, complete cds.
Pae_AF241171cds16_at	8,9		2	AF241171 /GENE= /PROD= /FEATURE=cds16 /DEFINITION=putative aldehyde dehydrogenase [Escherichia coli]
Pae_AF241171cds21_at	3,8		1	AF241171 /GENE= /PROD= /FEATURE=cds21 /DEFINITION=No significant similarity
Pae_AF241171cds22_at	16,6		4	AF241171 /GENE= /PROD= /FEATURE=cds22 /DEFINITION=Conserved hypothetical protein [Mycobacterium tuberculosis]
Pae_AF241171cds40_at	13,6		2	AF241171 /GENE= /PROD= /FEATURE=cds40 /DEFINITION=No significant similarity
Pae_AF241171cds45_at	6,5		1	AF241171 /GENE= /PROD= /FEATURE=cds45 /DEFINITION=TAT motifIII
Pae_AF241171cds49_i_at	7,2		2	AF241171 /GENE= /PROD= /FEATURE=cds49 /DEFINITION=No significant similarity
Pae_L37109cds2_at		5,0	2	L37109 /GENE= /PROD= /FEATURE=cds2 /DEFINITION=Pseudomonas aeruginosa type IV pilin (pilA) gene, complete cds.
Pae_M21652cds_at	6,5		1	M21652 /GENE= /PROD=type IV pilin precursor /FEATURE=cds /DEFINITION=Pseudomonas aeruginosa strain P1 type IV pilin precursor, gene, complete cds.
Pae_tRNA_Gly_s_at		6,1	2	tRNA_Glycine, 4785688-4785761 (-) strand

RrR Mutant

Gene	**Reguliert**		**Zähler**	**Descriptions**
	hoch	**herab**		
AFFX-Athal_actin_at	14,1		3	U37281 Arabidopsis thaliana actin-2 mRNA
ig_1064555_1063544_at	8,0		1	Intergenic region between PA1003 and PA1004, 1063544-1064555, (-) strand
ig_224101_223454_at	11,6		2	Intergenic region between PA0263 and PA0264, 223454-224101, (-) strand
ig_2902217_2901558_at	11,2		2	Intergenic region between PA2570 and PA2571, 2901558-2902217, (-) strand
ig_3961922_3962824_at	9,9		1	Intergenic region between PA3781 and PA3782, 3961922-3962824, (+) strand
ig_4240578_4241341_at	4,7		1	Intergenic region between PA3835 and PA3836, 4240578-4241341, (+) strand
ig_4241341_4240578_at	5,3		1	Intergenic region between PA3835 and PA3836, 4240578-4241341, (-) strand
ig_4297249_4294604_at	7,3		1	Intergenic region between PA3860 and PA3861, 4294604-4297249, (-) strand
ig_5086695_5087407_at	5,1		1	Intergenic region between PA4581 and PA4582, 5086695-5087407, (+) strand
ig_546334_545644_at	11,1		3	Intergenic region between PA0574 and PA0575, 545644-546334, (-) strand
ig_5775619_5774806_at	5,8		1	Intergenic region between PA5169 and PA5170, 5774806-5775619, (-) strand
ig_64729_65339_at	5,5		1	Intergenic region between PA0050 and PA0051, 64729-65339, (+) strand
ig_785174_785969_at	19,2		4	Intergenic region between PA0716 and PA0717, 785174-785969, (+) strand
PA0021_at	4,6		1	PA0021 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA0022_at	13,4		2	PA0022 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0082_at	5,8		1	PA0082 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0109_at	11,7		4	PA0109 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA0131_at	19,8		4	PA0131 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0132_at	8,0		2	PA0132 /DEF=beta-alanine--pyruvate transaminase /FUNCTION=Amino acid biosynthesis and metabolism
PA0157_at		6,9	2	PA0157 /DEF=probable RND efflux membrane fusion protein precursor /FUNCTION=Transport of small molecules
PA0188_at	6,3		1	PA0188 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA0195_pntA_at		8,9	2	PA0195 /GENE=pntA /DEF=still frameshift pyridine nucleotide transhydrogenase alpha subunit /FUNCTION=Energy metabolism; Transport of small molecules
PA0200_i_at		7,5	2	PA0200 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0203_at	7,3		1	PA0203 /DEF=probable binding protein component of ABC transporter /FUNCTION=Transport of small molecules
PA0254_at	6,0		1	PA0254 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown

PA0263_hcpC_s_at		24,9	4	PA0263 /GENE=hcpC /DEF=secreted protein Hcp /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA0283_sbp_at		7,9	2	PA0283 /GENE=sbp /DEF=sulfate-binding protein precursor /FUNCTION=Transport of small molecules
PA0285_at		5,9	1	PA0285 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA0288_speB1_at	6,0		1	PA0288 /GENE=speB1 /DEF=agmatinase /FUNCTION=Amino acid biosynthesis and metabolism
PA0293_at		7,9	2	PA0293 /DEF=probable hydratase /FUNCTION=Putative enzymes
PA0311_at	6,7		1	PA0311 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0323_at	14,2		3	PA0323 /DEF=probable binding protein component of ABC transporter /FUNCTION=Transport of small molecules
PA0339_at	8,4		2	PA0339 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0372_at		5,3	2	PA0372 /DEF=probable zinc protease /FUNCTION=Putative enzymes
PA0399_at		7,2	2	PA0399 /DEF=cystathionine beta-synthase /FUNCTION=Amino acid biosynthesis and metabolism
PA0409_pilH_at		6,0	2	PA0409 /GENE=pilH /DEF=twitching motility protein PilH /FUNCTION=Chemotaxis; Two-component regulatory systems; Motility & Attachment
PA0422_at		5,0	1	PA0422 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0441_at	18,6		3	PA0441 /DEF=dihydropyrimidinase /FUNCTION=Nucleotide biosynthesis and metabolism
PA0476_at	13,7		4	PA0476 /DEF=probable permease /FUNCTION=Transport of small molecules
PA0531_at	4,7		1	PA0531 /DEF=probable glutamine amidotransferase /FUNCTION=Putative enzymes
PA0542_at		3,8	1	PA0542 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0547_at		12,2	4	PA0547 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA0548_tktA_at		13,9	4	PA0548 /GENE=tktA /DEF=transketolase /FUNCTION=Energy metabolism
PA0577_dnaG_at		3,2	1	PA0577 /GENE=dnaG /DEF=DNA primase /FUNCTION=DNA replication, recombination, modification and repair
PA0587_at	6,5		2	PA0587 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0595_ostA_at		14,3	3	PA0595 /GENE=ostA /DEF=organic solvent tolerance protein OstA precursor /FUNCTION=Adaptation, protection
PA0598_at	9,5		2	PA0598 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0615_at	4,8		1	PA0615 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0621_at	5,1		1	PA0621 /DEF=conserved hypothetical protein /FUNCTION=Related to phage, transposon, or plasmid
PA0627_at	12,0		2	PA0627 /DEF=conserved hypothetical protein /FUNCTION=Related to phage, transposon, or plasmid

PA0628_at	6,7		1	PA0628 /DEF=conserved hypothetical protein /FUNCTION=Related to phage, transposon, or plasmid
PA0645_at	8,8		2	PA0645 /DEF=hypothetical protein /FUNCTION=Related to phage, transposon, or plasmid
PA0649_trpG_at		8,9	2	PA0649 /GENE=trpG /DEF=anthranilate synthase component II /FUNCTION=Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers; Energy metabolism
PA0654_speD_at		6,8	1	PA0654 /GENE=speD /DEF=S-adenosylmethionine decarboxylase proenzyme /FUNCTION=Central intermediary metabolism
PA0657_at	8,1		2	PA0657 /DEF=probable ATPase /FUNCTION=Putative enzymes
PA0658_at		7,3	2	PA0658 /DEF=probable short-chain dehydrogenase /FUNCTION=Putative enzymes
PA0671_at	6,3		1	PA0671 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0672_at	4,3		1	PA0672 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0673_at	6,8		1	PA0673 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0674_at	3,8		1	PA0674 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0683_at	6,1		1	PA0683 /DEF=probable type II secretion system protein /FUNCTION=Protein secretion/export apparatus
PA0684_at	5,7		1	PA0684 /DEF=probable type II secretion system protein /FUNCTION=Protein secretion/export apparatus
PA0686_at		6,5	1	PA0686 /DEF=probable type II secretion system protein /FUNCTION=Protein secretion/export apparatus
PA0687_at	5,5		1	PA0687 /DEF=probable type II secretion system protein /FUNCTION=Protein secretion/export apparatus
PA0757_at		6,7	2	PA0757 /DEF=probable two-component sensor /FUNCTION=Two-component regulatory systems
PA0767_lepA_at		3,8	1	PA0767 /GENE=lepA /DEF=GTP-binding protein LepA /FUNCTION=Protein secretion/export apparatus; Translation, post-translational modification, degradation
PA0773_pdxJ_at		5,2	1	PA0773 /GENE=pdxJ /DEF=pyridoxal phosphate biosynthetic protein PdxJ /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA0806_i_at	7,9		1	PA0806 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA0827_at	5,3		1	PA0827 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0837_slyD_at		11,9	3	PA0837 /GENE=slyD /DEF=peptidyl-prolyl cis-trans isomerase SlyD /FUNCTION=Chaperones & heat shock proteins; Translation, post-translational modification, degradation
PA0842_at	11,0		2	PA0842 /DEF=probable glycosyl transferase /FUNCTION=Putative enzymes
PA0850_at	18,8		3	PA0850 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0852_cpbD_at		21,0	4	PA0852 /GENE=cpbD /DEF=chitin-binding protein CbpD precursor /FUNCTION=Hypothetical, unclassified, unknown
PA0865_hpd_at	28,5		4	PA0865 /GENE=hpd /DEF=4-hydroxyphenylpyruvate dioxygenase /FUNCTION=Amino acid biosynthesis and metabolism

PA0903_alaS_at		26,1	4	PA0903 /GENE=alaS /DEF=alanyl-tRNA synthetase /FUNCTION=Transcription, RNA processing and degradation
PA0911_at	10,5		2	PA0911 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0921_at	7,9		1	PA0921 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA0922_at	9,4		2	PA0922 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0943_at		10,7	4	PA0943 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0973_oprL_at		7,4	2	PA0973 /GENE=oprL /DEF=outer membrane protein OprL precursor /FUNCTION=Membrane proteins; Transport of small molecules
PA0977_at	4,3		1	PA0977 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0990_at	8,7		2	PA0990 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0991_at		3,3	1	PA0991 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0996_at		14,7	4	PA0996 /DEF=probable coenzyme A ligase /FUNCTION=Putative enzymes
PA0997_at		13,9	3	PA0997 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA0998_at		11,4	4	PA0998 /DEF=hypothetical protein /FUNCTION=Putative enzymes
PA1000_at		38,1	4	PA1000 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1002_phnB_at		17,8	4	PA1002 /GENE=phnB /DEF=anthranilate synthase component II /FUNCTION=Adaptation, protection; Amino acid biosynthesis and metabolism
PA1008_bcp_at		4,3	1	PA1008 /GENE=bcp /DEF=bacterioferritin comigratory protein /FUNCTION=Adaptation, protection
PA1011_at		11,9	3	PA1011 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1013_purC_at		4,0	1	PA1013 /GENE=purC /DEF=phosphoribosylaminoimidazole-succinocarboxamide synthase /FUNCTION=Nucleotide biosynthesis and metabolism
PA1014_at	9,4		2	PA1014 /DEF=probable glycosyl transferase /FUNCTION=Putative enzymes
PA1045_at		7,6	1	PA1045 /DEF=hypothetical protein /FUNCTION=Putative enzymes
PA1052_at	5,8		1	PA1052 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1062_at		2,9	1	PA1062 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Putative enzymes
PA1076_at		10,1	2	PA1076 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1077_flgB_at	11,1		2	PA1077 /GENE=flgB /DEF=flagellar basal-body rod protein FlgB /FUNCTION=Motility & Attachment; Cell wall / LPS / capsule
PA1084_flgI_at		5,4	2	PA1084 /GENE=flgI /DEF=flagellar P-ring protein precursor FlgI /FUNCTION=Motility & Attachment; Cell wall / LPS / capsule
PA1086_flgK_at	4,6		1	PA1086 /GENE=flgK /DEF=flagellar hook-associated protein 1 FlgK /FUNCTION=Motility & Attachment; Cell wall / LPS / capsule
PA1105_fliJ_at	8,0		1	PA1105 /GENE=fliJ /DEF=flagellar protein FliJ /FUNCTION=Motility & Attachment; Cell wall / LPS / capsule

PA1133_at	7,2		1	PA1133 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1136_at	11,4		3	PA1136 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA1152_at	6,4		1	PA1152 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1157_at		4,6	1	PA1157 /DEF=probable two-component response regulator /FUNCTION=Nucleotide biosynthesis and metabolism
PA1169_at		40,4	4	PA1169 /DEF=probable lipoxygenase /FUNCTION=Putative enzymes
PA1190_at	8,4		2	PA1190 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA1192_at	7,1		1	PA1192 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1208_at		6,2	1	PA1208 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1225_at	11,2		3	PA1225 /DEF=probable NAD(P)H dehydrogenase /FUNCTION=Putative enzymes
PA1249_aprA_at		4,7	1	PA1249 /GENE=aprA /DEF=alkaline metalloproteinase precursor /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA1259_at	4,7		1	PA1259 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1264_at	14,8		3	PA1264 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA1278_cobP_at		9,2	2	PA1278 /GENE=cobP /DEF=cobinamide kinase /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA1285_at	6,7		1	PA1285 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA1293_at		8,2	2	PA1293 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1298_i_at	8,3		2	PA1298 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1302_at	16,3		4	PA1302 /DEF=probable heme utilization protein precursor /FUNCTION=Membrane proteins; Transport of small molecules
PA1303_at	5,7		1	PA1303 /DEF=probable signal peptidase /FUNCTION=Putative enzymes
PA1380_at	5,7		1	PA1380 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA1381_at	5,3		1	PA1381 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1397_at	7,5		1	PA1397 /DEF=probable two-component response regulator /FUNCTION=Transcriptional regulators; Two-component regulatory systems
PA1403_at	5,5		1	PA1403 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA1431_rsaL_at		62,5	4	PA1431 /GENE=rsaL /DEF=regulatory protein RsaL /FUNCTION=Adaptation, protection; Transcriptional regulators; Secreted Factors (toxins, enzymes, alginate)
PA1432_lasI_at		10,2	3	PA1432 /GENE=lasI /DEF=autoinducer synthesis protein LasI /FUNCTION=Adaptation, protection
PA1434_at	7,4		1	PA1434 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1438_at	11,3		1	PA1438 /DEF=probable two-component sensor /FUNCTION=Two-component regulatory systems

PA1500_at	17,4		4	PA1500 /DEF=probable oxidoreductase /FUNCTION=Putative enzymes
PA1510_at		5,1	1	PA1510 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1511_at		3,5	1	PA1511 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1514_at	13,3		3	PA1514 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1537_at	8,1		2	PA1537 /DEF=probable short-chain dehydrogenase /FUNCTION=Putative enzymes
PA1546_hemN_at		49,2	4	PA1546 /GENE=hemN /DEF=oxygen-independent coproporphyrinogen III oxidase /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA1552_at		25,8	4	PA1552 /DEF=probable cytochrome c /FUNCTION=Energy metabolism
PA1553_at		5,0	1	PA1553 /DEF=probable cytochrome c oxidase subunit /FUNCTION=Energy metabolism
PA1554_at		3,3	1	PA1554 /DEF=probable cytochrome oxidase subunit (cbb3-type) /FUNCTION=Energy metabolism
PA1555_at		5,5	1	PA1555 /DEF=probable cytochrome c /FUNCTION=Energy metabolism
PA1557_at		4,7	1	PA1557 /DEF=probable cytochrome oxidase subunit (cbb3-type) /FUNCTION=Energy metabolism
PA1581_sdhC_at		13,0	4	PA1581 /GENE=sdhC /DEF=succinate dehydrogenase (C subunit) /FUNCTION=Energy metabolism
PA1582_sdhD_at		9,8	2	PA1582 /GENE=sdhD /DEF=succinate dehydrogenase (D subunit) /FUNCTION=Energy metabolism
PA1583_sdhA_at		26,0	4	PA1583 /GENE=sdhA /DEF=succinate dehydrogenase (A subunit) /FUNCTION=Energy metabolism
PA1588_sucC_at		10,6	4	PA1588 /GENE=sucC /DEF=succinyl-CoA synthetase beta chain /FUNCTION=Energy metabolism
PA1595_at	7,5		2	PA1595 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA1598_at		9,5	3	PA1598 /DEF=conserved hypothetical protein /FUNCTION=Putative enzymes
PA1626_at	10,1		2	PA1626 /DEF=probable MFS transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA1656_at		3,7	1	PA1656 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1657_at		61,1	4	PA1657 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1658_at		34,9	4	PA1658 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1660_at		8,2	2	PA1660 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1663_at		5,4	2	PA1663 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA1665_at		13,6	4	PA1665 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1666_at		5,7	2	PA1666 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1667_at		18,9	4	PA1667 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown

PA1669_at		13,5	4	PA1669 /DEF=hypothetical protein /FUNCTION=Membrane proteins; Hypothetical, unclassified, unknown
PA1707_pcrH_at		3,6	1	PA1707 /GENE=pcrH /DEF=regulatory protein PcrH /FUNCTION=Protein secretion/export apparatus; Secreted Factors (toxins, enzymes, alginate)
PA1734_at	7,1		1	PA1734 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1737_at	6,3		1	PA1737 /DEF=probable 3-hydroxyacyl-CoA dehydrogenase /FUNCTION=Putative enzymes
PA1757_thrH_at		10,6	3	PA1757 /GENE=thrH /DEF=homoserine kinase /FUNCTION=Amino acid biosynthesis and metabolism
PA1761_at	13,7		4	PA1761 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1762_at	19,9		4	PA1762 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1800_tig_at		28,9	4	PA1800 /GENE=tig /DEF=trigger factor /FUNCTION=Cell division; Chaperones & heat shock proteins
PA1812_mltD_at		19,0	4	PA1812 /GENE=mltD /DEF=membrane-bound lytic murein transglycosylase D precursor /FUNCTION=Amino acid biosynthesis and metabolism; Cell wall / LPS / capsule
PA1829_at	6,9		1	PA1829 /DEF=hypothetical protein /FUNCTION=Putative enzymes
PA1837_at		9,3	2	PA1837 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1848_at	4,9		1	PA1848 /DEF=probable MFS transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA1868_xqhA_at		2,6	1	PA1868 /GENE=xqhA /DEF=secretion protein XqhA /FUNCTION=Protein secretion/export apparatus
PA1869_at		11,8	2	PA1869 /DEF=probable acyl carrier protein /FUNCTION=Fatty acid and phospholipid metabolism
PA1873_at		9,1	3	PA1873 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA1901_s_at		47,0	4	PA1901 /DEF=phenazine biosynthesis protein PhzC /FUNCTION=Hypothetical, unclassified, unknown; Secreted Factors (toxins, enzymes, alginate)
PA1902_s_at		18,8	4	PA1902 /DEF=phenazine biosynthesis protein PhzD /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA1903_s_at		35,0	4	PA1903 /DEF=phenazine biosynthesis protein PhzE /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA1904_s_at		8,2	2	PA1904 /DEF=probable phenazine biosynthesis protein /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA1905_s_at		47,6	4	PA1905 /DEF=probable pyridoxamine 5 -phosphate oxidase /FUNCTION=Secreted Factors (toxins, enzymes, alginate)
PA1907_at	8,9		2	PA1907 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1918_at	6,4		1	PA1918 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1955_at	6,8		2	PA1955 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA1984_s_at	10,9		3	PA1984 /DEF=probable aldehyde dehydrogenase /FUNCTION=Putative enzymes
PA1988_pqqD_at	6,2		1	PA1988 /GENE=pqqD /DEF=pyrroloquinoline quinone biosynthesis protein D /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers

PA2035_at	9,5		1	PA2035 /DEF=probable decarboxylase /FUNCTION=Putative enzymes
PA2036_at	4,8		1	PA2036 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2038_at	4,7		1	PA2038 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2046_at	10,3		2	PA2046 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2065_pcoA_at		5,7	1	PA2065 /GENE=pcoA /DEF=copper resistance protein A precursor /FUNCTION=Adaptation, protection
PA2067_at		14,9	4	PA2067 /DEF=probable hydrolase /FUNCTION=Putative enzymes
PA2069_at		10,8	2	PA2069 /DEF=probable carbamoyl transferase /FUNCTION=Putative enzymes
PA2074_at	9,7		2	PA2074 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2087_at		4,7	1	PA2087 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2100_at	17,2		3	PA2100 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2119_at		18,0	4	PA2119 /DEF=alcohol dehydrogenase (Zn-dependent) /FUNCTION=Putative enzymes
PA2158_at	4,4		1	PA2158 /DEF=probable alcohol dehydrogenase (Zn-dependent) /FUNCTION=Putative enzymes
PA2188_at	10,7		2	PA2188 /DEF=probable alcohol dehydrogenase (Zn-dependent) /FUNCTION=Putative enzymes
PA2195_hcnC_at		4,6	2	PA2195 /GENE=hcnC /DEF=hydrogen cyanide synthase HcnC /FUNCTION=Central intermediary metabolism
PA2204_at		76,2	4	PA2204 /DEF=probable binding protein component of ABC transporter /FUNCTION=Transport of small molecules
PA2219_opdE_at	12,9		3	PA2219 /GENE=opdE /DEF=membrane protein OpdE /FUNCTION=Membrane proteins
PA2221_at	9,4		3	PA2221 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2247_bkdA1_at	5,6		1	PA2247 /GENE=bkdA1 /DEF=2-oxoisovalerate dehydrogenase (alpha subunit) /FUNCTION=Amino acid biosynthesis and metabolism
PA2288_r_at	6,5		1	PA2288 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2295_at		2,2	1	PA2295 /DEF=probable permease of ABC transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA2331_at		6,9	1	PA2331 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2379_at	7,9		1	PA2379 /DEF=probable oxidoreductase /FUNCTION=Putative enzymes
PA2400_at	7,6		1	PA2400 /DEF=probable non-ribosomal peptide synthetase /FUNCTION=Adaptation, protection
PA2404_at	9,6		2	PA2404 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2413_at	5,4		1	PA2413 /DEF=probable class III aminotransferase /FUNCTION=Putative enzymes
PA2415_at	5,4		1	PA2415 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2457_at	14,5		3	PA2457 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown

PA2469_at		4,0	2	PA2469 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2501_at		9,0	2	PA2501 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2509_catB_at	4,9		1	PA2509 /GENE=catB /DEF=muconate cycloisomerase I /FUNCTION=Carbon compound catabolism
PA2545_xthA_at		5,7	1	PA2545 /GENE=xthA /DEF=exodeoxyribonuclease III /FUNCTION=DNA replication, recombination, modification and repair
PA2547_at		4,0	1	PA2547 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2551_at	6,4		1	PA2551 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2598_at	5,1		1	PA2598 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2601_at		5,8	1	PA2601 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA2624_idh_at		6,0	1	PA2624 /GENE=idh /DEF=isocitrate dehydrogenase /FUNCTION=Energy metabolism
PA2629_purB_at		4,6	1	PA2629 /GENE=purB /DEF=adenylosuccinate lyase /FUNCTION=Amino acid biosynthesis and metabolism; Nucleotide biosynthesis and metabolism
PA2634_at		23,8	4	PA2634 /DEF=probable isocitrate lyase /FUNCTION=Putative enzymes
PA2661_at		3,2	1	PA2661 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2674_at	5,5		1	PA2674 /DEF=probable type II secretion system protein /FUNCTION=Protein secretion/export apparatus
PA2687_pfeS_at		5,1	1	PA2687 /GENE=pfeS /DEF=two-component sensor PfeS /FUNCTION=Two-component regulatory systems
PA2695_at	5,8		1	PA2695 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2700_at	4,8		1	PA2700 /DEF=probable porin /FUNCTION=Membrane proteins; Transport of small molecules
PA2714_at	7,9		1	PA2714 /DEF=probable molybdopterin oxidoreductase /FUNCTION=Energy metabolism
PA2716_at	9,5		2	PA2716 /DEF=probable FMN oxidoreductase /FUNCTION=Energy metabolism
PA2721_at	4,8		1	PA2721 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2723_at	5,8		1	PA2723 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2800_at		5,4	1	PA2800 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2858_at	5,5		1	PA2858 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2862_lipA_at	14,1		4	PA2862 /GENE=lipA /DEF=lactonizing lipase precursor /FUNCTION=Carbon compound catabolism; Secreted Factors (toxins, enzymes, alginate)
PA2901_at		7,1	2	PA2901 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2911_at		5,9	1	PA2911 /DEF=probable TonB-dependent receptor /FUNCTION=Membrane proteins; Transport of small molecules
PA2920_at	14,5		3	PA2920 /DEF=probable chemotaxis transducer /FUNCTION=Adaptation, protection; Chemotaxis

PA2937_at	6,9		1	PA2937 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2938_at	6,8		1	PA2938 /DEF=probable transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA2944_cobN_at	8,3		2	PA2944 /GENE=cobN /DEF=cobalamin biosynthetic protein CobN /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA2946_at		5,0	1	PA2946 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA2950_at		9,9	3	PA2950 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2956_at		8,2	2	PA2956 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA2967_fabG_at		9,2	2	PA2967 /GENE=fabG /DEF=3-oxoacyl-[acyl-carrier-protein] reductase /FUNCTION=Fatty acid and phospholipid metabolism
PA2968_fabD_at		12,4	4	PA2968 /GENE=fabD /DEF=malonyl-CoA-[acyl-carrier-protein] transacylase /FUNCTION=Fatty acid and phospholipid metabolism
PA2970_rpmF_at		13,3	3	PA2970 /GENE=rpmF /DEF=50S ribosomal protein L32 /FUNCTION=Translation, post-translational modification, degradation
PA2999_nqrA_at		10,4	2	PA2999 /GENE=nqrA /DEF=Na+-translocating NADH:ubiquinone oxidoreductase subunit Nrq1 /FUNCTION=Energy metabolism
PA3001_at		28,3	4	PA3001 /DEF=probable glyceraldehyde-3-phosphate dehydrogenase /FUNCTION=Putative enzymes
PA3014_faoA_at		6,0	2	PA3014 /GENE=faoA /DEF=fatty-acid oxidation complex alpha-subunit /FUNCTION=Amino acid biosynthesis and metabolism; Fatty acid and phospholipid metabolism
PA3049_rmf_at	16,0		4	PA3049 /GENE=rmf /DEF=ribosome modulation factor /FUNCTION=Translation, post-translational modification, degradation
PA3077_at		5,5	1	PA3077 /DEF=probable two-component response regulator /FUNCTION=Transcriptional regulators; Two-component regulatory systems
PA3080_at	11,6		2	PA3080 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3090_at	5,1		1	PA3090 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3133_at	9,1		2	PA3133 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA3139_at		5,8	2	PA3139 /DEF=probable amino acid aminotransferase /FUNCTION=Amino acid biosynthesis and metabolism; Putative enzymes
PA3145_wbpL_at	25,8		4	PA3145 /GENE=wbpL /DEF=glycosyltransferase WbpL /FUNCTION=Cell wall / LPS / capsule; Membrane proteins
PA3149_wbpH_at	7,6		1	PA3149 /GENE=wbpH /DEF=probable glycosyltransferase WbpH /FUNCTION=Cell wall / LPS / capsule; Putative enzymes
PA3162_rpsA_at		17,8	4	PA3162 /GENE=rpsA /DEF=30S ribosomal protein S1 /FUNCTION=Translation, post-translational modification, degradation
PA3166_pheA_at		7,9	2	PA3166 /GENE=pheA /DEF=chorismate mutase /FUNCTION=Amino acid biosynthesis and metabolism
PA3181_at	19,5		2	PA3181 /DEF=2-keto-3-deoxy-6-phosphogluconate aldolase /FUNCTION=Carbon compound catabolism; Central intermediary metabolism

PA3190_at	8,7		1	PA3190 /DEF=probable binding protein component of ABC sugar transporter /FUNCTION=Transport of small molecules
PA3204_at		11,4	4	PA3204 /DEF=probable two-component response regulator /FUNCTION=Transcriptional regulators; Two-component regulatory systems
PA3206_at	4,8		1	PA3206 /DEF=probable two-component sensor /FUNCTION=Two-component regulatory systems
PA3217_at	11,9		2	PA3217 /DEF=probable adenylate cyclase /FUNCTION=Putative enzymes
PA3246_rluA_at		2,8	1	PA3246 /GENE=rluA /DEF=pseudouridine synthase RluA /FUNCTION=Transcription, RNA processing and degradation
PA3252_at	11,7		2	PA3252 /DEF=probable permease of ABC transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA3262_at		4,9	2	PA3262 /DEF=probable peptidyl-prolyl cis-trans isomerase, FkbP-type /FUNCTION=Translation, post-translational modification, degradation; Chaperones & heat shock proteins
PA3291_at		4,5	1	PA3291 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3298_at	6,2		1	PA3298 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3313_at		9,0	2	PA3313 /DEF=hypothetical protein /FUNCTION=Transport of small molecules
PA3326_at		20,8	4	PA3326 /DEF=probable Clp-family ATP-dependent protease /FUNCTION=Translation, post-translational modification, degradation
PA3330_at		26,0	4	PA3330 /DEF=probable short chain dehydrogenase /FUNCTION=Putative enzymes
PA3331_at		9,6	2	PA3331 /DEF=cytochrome P450 /FUNCTION=Adaptation, protection; Carbon compound catabolism
PA3334_at		5,6	1	PA3334 /DEF=probable acyl carrier protein /FUNCTION=Fatty acid and phospholipid metabolism
PA3337_rfaD_at		25,9	4	PA3337 /GENE=rfaD /DEF=ADP-L-glycero-D-mannoheptose 6-epimerase /FUNCTION=Cell wall / LPS / capsule
PA3369_at	9,9		2	PA3369 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA3397_fpr_at		37,3	4	PA3397 /GENE=fpr /DEF=ferredoxin--NADP+ reductase /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers; Energy metabolism
PA3405_hasE_at		2,0	1	PA3405 /GENE=hasE /DEF=metalloprotease secretion protein /FUNCTION=Protein secretion/export apparatus
PA3416_at	40,8		4	PA3416 /DEF=probable pyruvate dehydrogenase E1 component, beta chain /FUNCTION=Energy metabolism
PA3427_at	8,7		2	PA3427 /DEF=probable short-chain dehydrogenases /FUNCTION=Putative enzymes
PA3431_at	7,3		1	PA3431 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA3441_at		10,2	3	PA3441 /DEF=probable molybdopterin-binding protein /FUNCTION=Transport of small molecules
PA3446_at		8,6	2	PA3446 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown

PA3450_at		4,3	1	PA3450 /DEF=probable antioxidant protein /FUNCTION=Adaptation, protection
PA3465_at		3,1	1	PA3465 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA3477_rhlR_at		5,9	2	PA3477 /GENE=rhlR /DEF=transcriptional regulator RhlR /FUNCTION=Adaptation, protection; Transcriptional regulators
PA3509_at	10,1		2	PA3509 /DEF=probable hydrolase /FUNCTION=Putative enzymes
PA3525_argG_at		17,1	4	PA3525 /GENE=argG /DEF=argininosuccinate synthase /FUNCTION=Amino acid biosynthesis and metabolism
PA3541_at	9,6		2	PA3541 /DEF=alginate biosynthesis protein Alg8 /FUNCTION=Adaptation, protection; Cell wall / LPS / capsule; Secreted Factors (toxins, enzymes, alginate)
PA3558_at	6,7		1	PA3558 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA3581_glpF_at	10,1		4	PA3581 /GENE=glpF /DEF=glycerol uptake facilitator protein /FUNCTION=Transport of small molecules
PA3582_glpK_at	9,1		2	PA3582 /GENE=glpK /DEF=glycerol kinase /FUNCTION=Central intermediary metabolism
PA3584_glpD_at	16,2		4	PA3584 /GENE=glpD /DEF=glycerol-3-phosphate dehydrogenase /FUNCTION=Central intermediary metabolism; Energy metabolism
PA3621_fdxA_at		20,3	4	PA3621 /GENE=fdxA /DEF=ferredoxin I /FUNCTION=Energy metabolism
PA3625_surE_at		10,8	4	PA3625 /GENE=surE /DEF=survival protein SurE /FUNCTION=Adaptation, protection
PA3635_eno_at		10,7	2	PA3635 /GENE=eno /DEF=enolase /FUNCTION=Energy metabolism; Translation, post-translational modification, degradation; Carbon compound catabolism
PA3637_pyrG_at		3,4	1	PA3637 /GENE=pyrG /DEF=CTP synthase /FUNCTION=Nucleotide biosynthesis and metabolism
PA3644_lpxA_at		7,0	2	PA3644 /GENE=lpxA /DEF=UDP-N-acetylglucosamine acyltransferase /FUNCTION=Cell wall / LPS / capsule
PA3653_frr_at		7,4	2	PA3653 /GENE=frr /DEF=ribosome recycling factor /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers; Cell wall / LPS / capsule
PA3655_tsf_at		5,5	1	PA3655 /GENE=tsf /DEF=elongation factor Ts /FUNCTION=Translation, post-translational modification, degradation
PA3656_rpsB_at		6,2	2	PA3656 /GENE=rpsB /DEF=30S ribosomal protein S2 /FUNCTION=Translation, post-translational modification, degradation
PA3675_at		6,6	1	PA3675 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3702_at	6,5		1	PA3702 /DEF=probable two-component response regulator /FUNCTION=Chemotaxis; Two-component regulatory systems
PA3743_trmD_at		18,6	4	PA3743 /GENE=trmD /DEF=tRNA (guanine-N1)-methyltransferase /FUNCTION=Transcription, RNA processing and degradation
PA3745_rpsP_at		32,7	4	PA3745 /GENE=rpsP /DEF=30S ribosomal protein S16 /FUNCTION=Translation, post-translational modification, degradation; DNA replication, recombination, modification and repair
PA3749_at		6,9	1	PA3749 /DEF=probable MFS transporter /FUNCTION=Membrane proteins; Transport of small molecules

PA3768_at		3,7	1	PA3768 /DEF=probable metallo-oxidoreductase /FUNCTION=Putative enzymes
PA3770_guaB_at		8,1	2	PA3770 /GENE=guaB /DEF=inosine-5 -monophosphate dehydrogenase /FUNCTION=Nucleotide biosynthesis and metabolism
PA3785_at	5,6		1	PA3785 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3803_at		4,9	1	PA3803 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3806_at		8,3	1	PA3806 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3807_ndk_at		11,2	2	PA3807 /GENE=ndk /DEF=nucleoside diphosphate kinase /FUNCTION=Nucleotide biosynthesis and metabolism
PA3815_at		16,0	4	PA3815 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3834_valS_at		23,1	4	PA3834 /GENE=valS /DEF=valyl-tRNA synthetase /FUNCTION=Amino acid biosynthesis and metabolism; Translation, post-translational modification, degradation
PA3871_at	6,7		1	PA3871 /DEF=probable peptidyl-prolyl cis-trans isomerase, PpiC-type /FUNCTION=Chaperones & heat shock proteins; Translation, post-translational modification, degradation
PA3879_narL_at		5,4	1	PA3879 /GENE=narL /DEF=two-component response regulator NarL /FUNCTION=Energy metabolism; Two-component regulatory systems
PA3887_nhaP_at		6,3	1	PA3887 /GENE=nhaP /DEF=Na+/H+ antiporter NhaP /FUNCTION=Membrane proteins; Transport of small molecules
PA3898_at		5,9	2	PA3898 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA3904_i_at		13,7	4	PA3904 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3906_at		8,1	2	PA3906 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3907_at		9,2	2	PA3907 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3908_at		4,4	1	PA3908 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3919_at	64,9		4	PA3919 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3928_r_at	4,0		1	PA3928 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3935_tauD_at		4,9	1	PA3935 /GENE=tauD /DEF=taurine dioxygenase /FUNCTION=Carbon compound catabolism
PA3972_at	8,7		1	PA3972 /DEF=probable acyl-CoA dehydrogenase /FUNCTION=Putative enzymes
PA3973_at	9,7		2	PA3973 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA3990_at	5,3		1	PA3990 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA3998_at		4,2	2	PA3998 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4002_rodA_at	5,4		1	PA4002 /GENE=rodA /DEF=rod shape-determining protein /FUNCTION=Cell wall / LPS / capsule

PA4023_at	29,8		4	PA4023 /DEF=probable transport protein /FUNCTION=Transport of small molecules
PA4026_at	6,7		1	PA4026 /DEF=probable acetyltransferase /FUNCTION=Putative enzymes
PA4031_ppa_at		8,1	2	PA4031 /GENE=ppa /DEF=inorganic pyrophosphatase /FUNCTION=Central intermediary metabolism
PA4064_at		10,5	4	PA4064 /DEF=probable ATP-binding component of ABC transporter /FUNCTION=Transport of small molecules
PA4067_oprG_at		16,1	4	PA4067 /GENE=oprG /DEF=outer membrane protein OprG precursor /FUNCTION=Hypothetical, unclassified, unknown
PA4075_at	5,6		1	PA4075 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4091_hpaA_at	6,5		1	PA4091 /GENE=hpaA /DEF=4-hydroxyphenylacetate 3-monooxygenase large chain /FUNCTION=Carbon compound catabolism
PA4115_at	6,0		1	PA4115 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4131_at		36,6	4	PA4131 /DEF=probable iron-sulfur protein /FUNCTION=Putative enzymes
PA4133_at		12,0	3	PA4133 /DEF=cytochrome c oxidase subunit (cbb3-type) /FUNCTION=Energy metabolism
PA4134_i_at		25,9	4	PA4134 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4139_at		70,2	4	PA4139 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4140_at		34,0	4	PA4140 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4147_acoR_at	6,5		2	PA4147 /GENE=acoR /DEF=transcriptional regulator AcoR /FUNCTION=Hypothetical, unclassified, unknown
PA4182_at	7,8		1	PA4182 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4190_at		4,5	2	PA4190 /DEF=probable FAD-dependent monooxygenase /FUNCTION=Putative enzymes
PA4207_at	6,8		1	PA4207 /DEF=probable RND efflux transporter /FUNCTION=Membrane proteins; Transport of small molecules
PA4209_at		6,4	2	PA4209 /DEF=probable O-methyltransferase /FUNCTION=Putative enzymes
PA4229_pchC_at	5,1		1	PA4229 /GENE=pchC /DEF=pyochelin biosynthetic protein PchC /FUNCTION=Transport of small molecules; Secreted Factors (toxins, enzymes, alginate)
PA4234_uvrA_at		8,3	1	PA4234 /GENE=uvrA /DEF=excinuclease ABC subunit A /FUNCTION=DNA replication, recombination, modification and repair
PA4235_bfrA_at		23,1	4	PA4235 /GENE=bfrA /DEF=bacterioferritin /FUNCTION=Adaptation, protection; Transport of small molecules
PA4238_rpoA_at		18,2	4	PA4238 /GENE=rpoA /DEF=DNA-directed RNA polymerase alpha chain /FUNCTION=Transcription, RNA processing and degradation
PA4242_rpmJ_at		10,1	2	PA4242 /GENE=rpmJ /DEF=50S ribosomal protein L36 /FUNCTION=Translation, post-translational modification, degradation
PA4243_secY_at		5,8	2	PA4243 /GENE=secY /DEF=secretion protein SecY /FUNCTION=Membrane proteins; Protein secretion/export apparatus
PA4244_rplO_at		17,6	4	PA4244 /GENE=rplO /DEF=50S ribosomal protein L15 /FUNCTION=Translation, post-translational modification, degradation

PA4246_rpsE_at	84,0	4	PA4246 /GENE=rpsE /DEF=30S ribosomal protein S5 /FUNCTION=Translation, post-translational modification, degradation
PA4247_rplR_at	11,5	4	PA4247 /GENE=rplR /DEF=50S ribosomal protein L18 /FUNCTION=Translation, post-translational modification, degradation
PA4248_rplF_at	8,7	1	PA4248 /GENE=rplF /DEF=50S ribosomal protein L6 /FUNCTION=Translation, post-translational modification, degradation
PA4249_rpsH_at	9,5	2	PA4249 /GENE=rpsH /DEF=30S ribosomal protein S8 /FUNCTION=Translation, post-translational modification, degradation
PA4253_rplN_at	9,3	2	PA4253 /GENE=rplN /DEF=50S ribosomal protein L14 /FUNCTION=Translation, post-translational modification, degradation
PA4254_rpsQ_at	14,1	4	PA4254 /GENE=rpsQ /DEF=30S ribosomal protein S17 /FUNCTION=Translation, post-translational modification, degradation
PA4255_rpmC_at	7,2	2	PA4255 /GENE=rpmC /DEF=50S ribosomal protein L29 /FUNCTION=Translation, post-translational modification, degradation
PA4256_rplP_at	12,8	4	PA4256 /GENE=rplP /DEF=50S ribosomal protein L16 /FUNCTION=Translation, post-translational modification, degradation
PA4257_rpsC_at	11,3	4	PA4257 /GENE=rpsC /DEF=30S ribosomal protein S3 /FUNCTION=Translation, post-translational modification, degradation
PA4258_rplV_at	25,6	4	PA4258 /GENE=rplV /DEF=50S ribosomal protein L22 /FUNCTION=Translation, post-translational modification, degradation
PA4259_rpsS_at	28,7	4	PA4259 /GENE=rpsS /DEF=30S ribosomal protein S19 /FUNCTION=Translation, post-translational modification, degradation
PA4260_rplB_at	12,4	4	PA4260 /GENE=rplB /DEF=50S ribosomal protein L2 /FUNCTION=Translation, post-translational modification, degradation
PA4261_rplW_at	17,4	4	PA4261 /GENE=rplW /DEF=50S ribosomal protein L23 /FUNCTION=Translation, post-translational modification, degradation
PA4262_rplD_at	47,0	4	PA4262 /GENE=rplD /DEF=50S ribosomal protein L4 /FUNCTION=Transcription, RNA processing and degradation; Translation, post-translational modification, degradation
PA4263_rplC_at	54,4	4	PA4263 /GENE=rplC /DEF=50S ribosomal protein L3 /FUNCTION=Translation, post-translational modification, degradation
PA4267_rpsG_at	7,3	1	PA4267 /GENE=rpsG /DEF=30S ribosomal protein S7 /FUNCTION=Translation, post-translational modification, degradation
PA4268_rpsL_at	32,5	4	PA4268 /GENE=rpsL /DEF=30S ribosomal protein S12 /FUNCTION=Translation, post-translational modification, degradation
PA4271_rplL_at	11,1	3	PA4271 /GENE=rplL /DEF=50S ribosomal protein L7 / L12 /FUNCTION=Translation, post-translational modification, degradation
PA4272_rplJ_at	11,4	3	PA4272 /GENE=rplJ /DEF=50S ribosomal protein L10 /FUNCTION=Translation, post-translational modification, degradation
PA4274_rplK_at	8,3	2	PA4274 /GENE=rplK /DEF=50S ribosomal protein L11 /FUNCTION=Translation, post-translational modification, degradation
PA4321_at	6,9	2	PA4321 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown

PA4326_at	9,9		2	PA4326 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4328_at		15,6	4	PA4328 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4338_at		7,8	2	PA4338 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA4368_at	9,2		2	PA4368 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4369_at	6,6		1	PA4369 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4383_at	5,7		1	PA4383 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA4403_secA_at		6,7	2	PA4403 /GENE=secA /DEF=secretion protein SecA /FUNCTION=Protein secretion/export apparatus
PA4429_at		18,4	4	PA4429 /DEF=probable cytochrome c1 precursor /FUNCTION=Energy metabolism
PA4431_at		4,8	1	PA4431 /DEF=probable iron-sulfur protein /FUNCTION=Putative enzymes
PA4432_rpsI_at		13,0	4	PA4432 /GENE=rpsI /DEF=30S ribosomal protein S9 /FUNCTION=Translation, post-translational modification, degradation
PA4433_rplM_at		15,5	4	PA4433 /GENE=rplM /DEF=50S ribosomal protein L13 /FUNCTION=Translation, post-translational modification, degradation
PA4453_at		4,1	1	PA4453 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4459_at		24,1	4	PA4459 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4468_sodM_at	5,3		1	PA4468 /GENE=sodM /DEF=superoxide dismutase /FUNCTION=Adaptation, protection
PA4479_mreD_at		5,6	1	PA4479 /GENE=mreD /DEF=rod shape-determining protein MreD /FUNCTION=Cell division; Cell wall / LPS / capsule
PA4483_gatA_at		7,2	1	PA4483 /GENE=gatA /DEF=Glu-tRNA(Gln) amidotransferase subunit A /FUNCTION=Translation, post-translational modification, degradation
PA4516_at		2,8	1	PA4516 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4539_at	7,4		2	PA4539 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4553_pilX_at	7,6		2	PA4553 /GENE=pilX /DEF=type 4 fimbrial biogenesis protein PilX /FUNCTION=Motility & Attachment
PA4560_ileS_at		6,6	1	PA4560 /GENE=ileS /DEF=isoleucyl-tRNA synthetase /FUNCTION=Amino acid biosynthesis and metabolism; Translation, post-translational modification, degradation
PA4563_rpsT_at		35,6	4	PA4563 /GENE=rpsT /DEF=30S ribosomal protein S20 /FUNCTION=Translation, post-translational modification, degradation; Central intermediary metabolism
PA4568_rplU_at		6,4	1	PA4568 /GENE=rplU /DEF=50S ribosomal protein L21 /FUNCTION=Translation, post-translational modification, degradation
PA4569_ispB_at		11,9	4	PA4569 /GENE=ispB /DEF=octaprenyl-diphosphate synthase /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers; Energy metabolism
PA4572_fklB_at		19,7	4	PA4572 /GENE=fklB /DEF=peptidyl-prolyl cis-trans isomerase FklB /FUNCTION=Chaperones & heat shock proteins; Translation, post-translational modification, degradation
PA4575_at	7,3		2	PA4575 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown

PA4610_at		13,9	4	PA4610 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4636_at		6,5	1	PA4636 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4642_at		8,9	2	PA4642 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4662_murI_at		4,7	1	PA4662 /GENE=murI /DEF=glutamate racemase /FUNCTION=Cell wall / LPS / capsule
PA4665_prfA_at		11,4	3	PA4665 /GENE=prfA /DEF=peptide chain release factor 1 /FUNCTION=Translation, post-translational modification, degradation
PA4671_at		4,4	1	PA4671 /DEF=probable ribosomal protein L25 /FUNCTION=Adaptation, protection; Translation, post-translational modification, degradation
PA4672_at		4,7	1	PA4672 /DEF=peptidyl-tRNA hydrolase /FUNCTION=Translation, post-translational modification, degradation
PA4682_at	12,3		2	PA4682 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4686_at		3,3	1	PA4686 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4690_at	8,9		2	PA4690 /DEF=still frameshift hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA4694_ilvC_at		40,5	4	PA4694 /GENE=ilvC /DEF=ketol-acid reductoisomerase /FUNCTION=Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers
PA4696_ilvI_at		17,4	4	PA4696 /GENE=ilvI /DEF=acetolactate synthase large subunit /FUNCTION=Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers
PA4705_at		8,1	2	PA4705 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4715_at		9,9	3	PA4715 /DEF=probable aminotransferase /FUNCTION=Putative enzymes
PA4737_at		2,3	1	PA4737 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4740_pnp_at		13,1	3	PA4740 /GENE=pnp /DEF=polyribonucleotide nucleotidyltransferase /FUNCTION=Transcription, RNA processing and degradation
PA4741_rpsO_at		14,4	4	PA4741 /GENE=rpsO /DEF=30S ribosomal protein S15 /FUNCTION=Translation, post-translational modification, degradation
PA4744_infB_at		11,6	3	PA4744 /GENE=infB /DEF=translation initiation factor IF-2 /FUNCTION=Translation, post-translational modification, degradation
PA4746_at		3,8	1	PA4746 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4757_at		10,3	2	PA4757 /DEF=conserved hypothetical protein /FUNCTION=Membrane proteins
PA4770_lldP_at		10,2	2	PA4770 /GENE=lldP /DEF=L-lactate permease /FUNCTION=Transport of small molecules
PA4813_lipC_at	12,6		2	PA4813 /GENE=lipC /DEF=lipase LipC /FUNCTION=Fatty acid and phospholipid metabolism
PA4823_at	5,1		1	PA4823 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4846_aroQ1_at		6,6	1	PA4846 /GENE=aroQ1 /DEF=3-dehydroquinate dehydratase /FUNCTION=Amino acid biosynthesis and metabolism
PA4847_accB_at		5,5	2	PA4847 /GENE=accB /DEF=biotin carboxyl carrier protein (BCCP) /FUNCTION=Fatty acid and phospholipid metabolism
PA4871_at	6,1		1	PA4871 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown

PA4872_at		3,8	1	PA4872 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4893_ureG_at		5,3	2	PA4893 /GENE=ureG /DEF=urease accessory protein UreG /FUNCTION=Biosynthesis of cofactors, prosthetic groups and carriers
PA4916_at		4,7	1	PA4916 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4917_at		5,3	1	PA4917 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4926_at	7,5		1	PA4926 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4958_at	5,7		1	PA4958 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA4962_at	5,4		1	PA4962 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA4976_aspC_at	5,6		1	PA4976 /GENE=aspC /DEF=aspartate transaminase /FUNCTION=Amino acid biosynthesis and metabolism
PA4989_at	5,7		1	PA4989 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA5001_at		6,1	1	PA5001 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5004_at		6,3	1	PA5004 /DEF=probable glycosyl transferase /FUNCTION=Putative enzymes
PA5024_at		6,4	2	PA5024 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5026_at		5,3	1	PA5026 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5051_argS_at		6,9	2	PA5051 /GENE=argS /DEF=arginyl-tRNA synthetase /FUNCTION=Translation, post-translational modification, degradation
PA5091_hutG_at	8,9		2	PA5091 /GENE=hutG /DEF=N-formylglutamate amidohydrolase /FUNCTION=Hypothetical, unclassified, unknown
PA5128_secB_at		12,2	2	PA5128 /GENE=secB /DEF=secretion protein SecB /FUNCTION=Protein secretion/export apparatus
PA5146_at		1,9	1	PA5146 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5161_rmlB_at		9,8	3	PA5161 /GENE=rmlB /DEF=dTDP-D-glucose 4,6-dehydratase /FUNCTION=Carbon compound catabolism; Cell wall / LPS / capsule
PA5162_rmlD_at		3,1	1	PA5162 /GENE=rmlD /DEF=dTDP-4-dehydrorhamnose reductase /FUNCTION=Cell wall / LPS / capsule
PA5211_at	6,3		1	PA5211 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA5263_argH_at		4,3	2	PA5263 /GENE=argH /DEF=argininosuccinate lyase /FUNCTION=Amino acid biosynthesis and metabolism
PA5268_corA_at		3,0	1	PA5268 /GENE=corA /DEF=magnesium/cobalt transport protein /FUNCTION=Membrane proteins; Transport of small molecules
PA5274_rnk_at		11,5	3	PA5274 /GENE=rnk /DEF=nucleoside diphosphate kinase regulator /FUNCTION=Transcriptional regulators
PA5287_amtB_at	8,1		2	PA5287 /GENE=amtB /DEF=ammonium transporter AmtB /FUNCTION=Membrane proteins; Transport of small molecules
PA5322_algC_at		10,5	4	PA5322 /GENE=algC /DEF=phosphomannomutase AlgC /FUNCTION=Amino acid

				biosynthesis and metabolism; Cell wall / LPS / capsule; Secreted Factors (toxins, enzymes, alginate)
PA5325_at	10,3		4	PA5325 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5349_at	9,6		1	PA5349 /DEF=probable rubredoxin reductase /FUNCTION=Carbon compound catabolism
PA5352_at	11,9		2	PA5352 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5365_phoU_at		4,8	1	PA5365 /GENE=phoU /DEF=phosphate uptake regulatory protein PhoU /FUNCTION=Membrane proteins; Transcriptional regulators
PA5380_at	9,1		2	PA5380 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA5395_at		6,4	1	PA5395 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5438_at		6,5	2	PA5438 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulators
PA5444_at	12,3		2	PA5444 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown; Membrane proteins
PA5446_i_at		51,2	4	PA5446 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5455_at		7,1	1	PA5455 /DEF=hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5468_at		12,9	3	PA5468 /DEF=probable citrate transporter /FUNCTION=Transport of small molecules
PA5491_at		5,9	1	PA5491 /DEF=probable cytochrome /FUNCTION=Energy metabolism
PA5535_at		5,6	1	PA5535 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical, unclassified, unknown
PA5553_atpC_at		10,9	2	PA5553 /GENE=atpC /DEF=ATP synthase epsilon chain /FUNCTION=Energy metabolism
PA5555_atpG_at		10,8	2	PA5555 /GENE=atpG /DEF=ATP synthase gamma chain /FUNCTION=Energy metabolism
PA5556_atpA_at		7,7	1	PA5556 /GENE=atpA /DEF=ATP synthase alpha chain /FUNCTION=Energy metabolism
PA5557_atpH_at		54,2	4	PA5557 /GENE=atpH /DEF=ATP synthase delta chain /FUNCTION=Energy metabolism
PA5558_atpF_at		13,7	4	PA5558 /GENE=atpF /DEF=ATP synthase B chain /FUNCTION=Energy metabolism
PA5559_atpE_at		9,1	2	PA5559 /GENE=atpE /DEF=atp synthase C chain /FUNCTION=Energy metabolism
PA5560_atpB_at		3,6	2	PA5560 /GENE=atpB /DEF=ATP synthase A chain /FUNCTION=Energy metabolism
PA5569_rnpA_at		7,1	1	PA5569 /GENE=rnpA /DEF=ribonuclease P protein component /FUNCTION=Translation, post-translational modification, degradation
PA5570_rpmH_at		137,3	4	PA5570 /GENE=rpmH /DEF=50S ribosomal protein L34 /FUNCTION=Central intermediary metabolism; Translation, post-translational modification, degradation
Pae_AF035937cds12_at	5,3		1	AF035937 /GENE=wbpV /PROD=WbpV /FEATURE=cds12 /DEFINITION=Pseudomonas aeruginosa strain IATS O6 RpsA (rpsA) gene, partial cds; Ihf-Beta, Wzz (wzz), and Wzx (wzx) genes, complete cds; and wbp gene cluster for O-antigen biosynthesis, complete sequence.
Pae_AF133699cds4_at	12,3		3	AF133699 /GENE=aadB /PROD=amonoglycoside adenylyltransferase /FEATURE=cds4 /DEFINITION=Pseudomonas aeruginosa integron In50 integrase (int1), IS2000 transposase (IS2000 tnpA), extended spectrum beta-lactamase (blaVEB-1), amonoglycoside adenylyltransferase (aadB), quaternary ammonium compound-resistance protein (qacEdelta1),

				and dihydropteroate synthase (sul1) genes, complete cds.
Pae_AF147795cds2_at	26,5		4	AF147795 /GENE=wzz /PROD=O-antigen chain length determinant /FEATURE=cds2 /DEFINITION=Pseudomonas aeruginosa integration host factor beta-subunit (himD), complete cds; O-antigen biosynthesis locus, tRNA-Asn gene, complete sequence; and aromatic-amino-acid aminotransferase (tyrB) gene, complete cds.
Pae_AF147795cds8_at	6,2		1	AF147795 /GENE=wbjD /PROD=WbjD /FEATURE=cds8 /DEFINITION=Pseudomonas aeruginosa integration host factor beta-subunit (himD), complete cds; O-antigen biosynthesis locus, tRNA-Asn gene, complete sequence; and aromatic-amino-acid aminotransferase (tyrB) gene, complete cds.
Pae_AF241171cds16_at	11,3		2	AF241171 /GENE= /PROD= /FEATURE=cds16 /DEFINITION=putative aldehyde dehydrogenase [Escherichia coli]
Pae_AF241171cds21_at	3,9		1	AF241171 /GENE= /PROD= /FEATURE=cds21 /DEFINITION=No significant similarity
Pae_AF241171cds40_at	10,3		2	AF241171 /GENE= /PROD= /FEATURE=cds40 /DEFINITION=No significant similarity
Pae_AF241171cds45_at	6,5		1	AF241171 /GENE= /PROD= /FEATURE=cds45 /DEFINITION=TAT motifIII
Pae_J05162cds_at	6,8		1	J05162 /GENE= /PROD= /FEATURE=cds /DEFINITION=P.aeruginosa carbenicillinase gene, complete cds.
Pae_M21652cds_at	8,0		1	M21652 /GENE= /PROD=type IV pilin precursor /FEATURE=cds /DEFINITION=Pseudomonas aeruginosa strain P1 type IV pilin precursor, gene, complete cds.
Pae_M98270cds3_at	8,1		1	M98270 /GENE= /PROD=ORF3 /FEATURE=cds3 /DEFINITION=Pseudomonas aeruginosa aminoglycoside-4 -adenyltransferase (ant(4)-IIa) gene, complete cds.
Pae_tRNA_Lys_f_at	7,6		2	tRNA_Lysine, 1060356-1060431 (+) strand
Pae_tRNA_Val_f_at		5,9	2	tRNA_Valine , 3650815-3650890 (-) strand

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Query: 5521  ctcaagctcgatgggggacagcacatagtcggccgcgaagagggcggccgccaggccgac 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10853 ctcaagctcgatgggggacagcacatagtcggccgcgaagagggcggccgccaggccgac 10912


Query: 5581  gccaagggtcggggccgtgtcgatcaggcacacgtcgaagccttggttcgccagggcctt 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10913 gccaagggtcggggccgtgtcgatcaggcacacgtcgaagccttggttcgccagggcctt 10972


Query: 5641  gatgttcgccccgaacagctcgcgggcgtcgtccagcgacagccgttcggcgttcgccag 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10973 gatgttcgccccgaacagctcgcgggcgtcgtccagcgacagccgttcggcgttcgccag 11032


Query: 5701  taccgggttggactcgatgagggcgaggcgcgcggcctggccgtcgccggctgcgggtgc 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11033 taccgggttggactcgatgagggcgaggcgcgcggcctggccgtcgccggctgcgggtgc 11092


Query: 5761  ggtttcggtccagccgccggcagggacagcgccgaacagcttgcttgcatgcaggccggt 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11093 ggtttcggtccagccgccggcagggacagcgccgaacagcttgcttgcatgcaggccggt 11152


Query: 5821  agcaaagtccttgagcgtgtaggacgcattgccctggggggtccaggtcgatcacggcaac 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11153 agcaaagtccttgagcgtgtaggacgcattgccctggggggtccaggtcgatcacggcaac 11212


Query: 5881  ccgcaagccgcgctcgaaaaagtcgaaggcaagatgcacaagggtcgaagtcttgccgac 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11213 ccgcaagccgcgctcgaaaaagtcgaaggcaagatgcacaagggtcgaagtcttgccgac 11272


Query: 5941  gccgcctttctggttggccgtgaccaaagttttcatcgtttggtttcctgtttttttcttg 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11273 gccgcctttctggttggccgtgaccaaagttttcatcgtttggtttcctgtttttttcttg 11332


Query: 6001  gcgtccgcttcccacttccggacgatgtacgcctgatgttccggcagaaccgccgttacc 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11333 gcgtccgcttcccacttccggacgatgtacgcctgatgttccggcagaaccgccgttacc 11392


Query: 6061  cgcgcgtacccctcgggcaagttcttgtcctcgaacgcggcccacacgcgatgcaccgct 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11393 cgcgcgtacccctcgggcaagttcttgtcctcgaacgcggcccacacgcgatgcaccgct 11452


Query: 6121  tgcgacactgcgcccctggtcagtcccagcgacgttgcgaacgtcgcctgtggcttccca 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11453 tgcgacactgcgcccctggtcagtcccagcgacgttgcgaacgtcgcctgtggcttccca 11512


Query: 6181  tcgactaagacgccccgcgctatctcgatggtctgctgccccacttccagcccctggatc 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11513 tcgactaagacgccccgcgctatctcgatggtctgctgccccacttccagcccctggatc 11572


Query: 6241  gcctcctggaactggctttcggtaagccgtttcttcatggataacacccataatttgctc 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11573 gcctcctggaactggctttcggtaagccgtttcttcatggataacacccataatttgctc 11632
```

oriT-plafr1

```
Score =  692 bits (360), Expect = 0.0
Identities = 360/360 (100%)
 Strand = Plus / Minus


Query: 8635 cgtctctcgcctgtcccctcagttcagtaatttcctgcatttgcctgtttccagtcggta 8694
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 360  cgtctctcgcctgtcccctcagttcagtaatttcctgcatttgcctgtttccagtcggta 301


Query: 8695 gatattccacaaaacagcagggaagcagcgcttttccgctgcataaccctgcttcggggt 8754
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 300  gatattccacaaaacagcagggaagcagcgcttttccgctgcataaccctgcttcggggt 241


Query: 8755 cattatagcgattttttcggtatatccatcctttttcgcacgatatacaggattttgcca 8814
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 240  cattatagcgattttttcggtatatccatcctttttcgcacgatatacaggattttgcca 181


Query: 8815 aagggttcgtgtagactttccttggtgtatccaacggcgtcagccgggcaggataggtga 8874
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 180  aagggttcgtgtagactttccttggtgtatccaacggcgtcagccgggcaggataggtga 121


Query: 8875 agtaggcccacccgcgagcgggtgttccttcttcactgtcccttattcgcacctggcggt 8934
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 120  agtaggcccacccgcgagcgggtgttccttcttcactgtcccttattcgcacctggcggt 61


Query: 8935 gctcaacgggaatcctgctctgcgaggctggccggctaccgccggcgtaacagatgaggg 8994
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60   gctcaacgggaatcctgctctgcgaggctggccggctaccgccggcgtaacagatgaggg 1
```

OriT-plafr3

```
Score =  692 bits (360), Expect = 0.0
Identities = 360/360 (100%)
 Strand = Plus / Plus


Query: 1    ccctcatctgttacgccggcggtagccggccagcctcgcagagcaggattcccgttgagc 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3377 ccctcatctgttacgccggcggtagccggccagcctcgcagagcaggattcccgttgagc 3436


Query: 61   accgccaggtgcgaataagggacagtgaagaaggaacacccgctcgcgggtgggcctact 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3437 accgccaggtgcgaataagggacagtgaagaaggaacacccgctcgcgggtgggcctact 3496


Query: 121  tcacctatcctgcccggctgacgccgttggatacaccaaggaaagtctacacgaaccctt 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3497 tcacctatcctgcccggctgacgccgttggatacaccaaggaaagtctacacgaaccctt 3556


Query: 181  tggcaaaatcctgtatatcgtgcgaaaaaggatggatataccgaaaaaatcgctataatg 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3557 tggcaaaatcctgtatatcgtgcgaaaaaggatggatataccgaaaaaatcgctataatg 3616


Query: 241  accccgaagcagggttatgcagcggaaaagcgctgcttccctgctgttttgtggaatatc 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3617 accccgaagcagggttatgcagcggaaaagcgctgcttccctgctgttttgtggaatatc 3676


Query: 301  taccgactggaaacaggcaaatgcaggaaattactgaactgaggggacaggcgagagacg 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3677 taccgactggaaacaggcaaatgcaggaaattactgaactgaggggacaggcgagagacg 3736
```

```
Oriv-plafr1

Score = 1346 bits (700), Expect = 0.0
Identities = 711/720 (98%)
 Strand = Plus / Minus


Query: 19365 cttccagcgcctttccgacgctcaccgggctggttgccctcgccgctgggctggcggccg 19424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 720   cttccagcgcctttccgacgctcaccgggctggttgccctcgccgctgggctggcggccg 661


Query: 19425 tctatggccctgcaaacgcgccagaaacgccgtcgaagccgtgtgcgagacaccgcggcc 19484
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 660   tctatggccctgcaaacgcgccagaaacgccgtcgaagccgtgtgcgagacaccgcggcc 601


Query: 19485 gccggcgttgtggatacctcgcggaaaacttggccctcactgacagatgaggggcggacg 19544
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct: 600   gccggcgttgtggataccacgcggaaaacttggccctcactgacagatgaggggcggacg 541


Query: 19545 ttgacacttgaggggccgactcacccggcgcggcgttgacagatgaggggcaggctcgat 19604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 540   ttgacacttgaggggccgactcacccggcgcggcgttgacagatgaggggcaggctcgat 481


Query: 19605 ttcggccggcgacgtggagctggccagcctcgcaaatcggcgaaaacgcctgattttacg 19664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 480   ttcggccggcgacgtggagctggccagcctcgcaaatcggcgaaaacgcctgattttacg 421


Query: 19665 cgagtttcccacagatgatgtggacaagcctggggataagtgccctgcggtattgacact 19724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 420   cgagtttcccacagatgatgtggacaagcctggggataagtgccctgcggtattgacact 361


Query: 19725 tgaggggcgcgactactgacagatgaggggcgcgatccttgacacttgaggggcagagtg 19784
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 360   tgaggggcgcgactactgacagatgaggggcgcgatccttgacacttgaggggcagagtg 301


Query: 19785 ctgacagatgaggggcgcacctattgacatttgaggggctgtccacaggcagaaaatcca 19844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 300   atgacagatgaggggcgcacctattgacatttgaggggctgtccacaggcagaaaatcca 241


Query: 19845 gcatttgcaagggtttccgcccgtttttcggccaccgctaacctgtcttttaacctgctt 19904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 240   gcatttgcaagggtttccgcccgtttttcggccaccgctaacctgtcttttaacctgctt 181


Query: 19905 ttaaaccaatatttataaaccttgtttttaaccagggctgcgccctgtgcgcgtgaccgc 19964
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 180   ttaaaccaatatttataaaccttgtttttaaccagggctgcgccctgtgcgcgtgaccgc 121


Query: 19965 gcacgccgaaggggggtgnnnnnnnttctcgaaccctcccggcccgctaacgcgggcctc 20024
             ||||||||||||||||||       |||||||||||||||||||||||||||||||||||
Sbjct: 120   gcacgccgaaggggggtgcccccccttctcgaaccctcccggcccgctaacgcgggcctc 61


Query: 20025 ccatcccccccaggggctgcgcccctcggccgcgaacggcctcaccccaaaaatggcagcg 20084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60    ccatcccccccaggggctgcgcccctcggccgcgaacggcctcaccccaaaaatggcagcg 1
```

```
Oriv-plafr3

Score = 1346 bits (700), Expect = 0.0
Identities = 711/720 (98%)
 Strand = Plus / Plus


Query: 1     cgctgccattttttggggtgaggccgttcgcggccgaggggcgcagcccctgggggatgg 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13009 cgctgccattttttggggtgaggccgttcgcggccgaggggcgcagcccctgggggatgg 13068


Query: 61    gaggcccgcgttagcgggccgggagggttcgagaannnnnnncaccccccttcggcgtgc 120
             |||||||||||||||||||||||||||||||||||       ||||||||||||||||||
Sbjct: 13069 gaggcccgcgttagcgggccgggagggttcgagaagggggggcaccccccttcggcgtgc 13128


Query: 121   gcggtcacgcgcacagggcgcagccctggttaaaaacaaggtttataaatattggtttaa 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13129 gcggtcacgcgcacagggcgcagccctggttaaaaacaaggtttataaatattggtttaa 13188


Query: 181   aagcaggttaaaagacaggttagcggtggccgaaaaacgggcggaaacccttgcaaatgc 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13189 aagcaggttaaaagacaggttagcggtggccgaaaaacgggcggaaacccttgcaaatgc 13248


Query: 241   tggattttctgcctgtggacagcccctcaaatgtcaataggtgcgcccctcatctgtcat 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct: 13249 tggattttctgcctgtggacagcccctcaaatgtcaataggtgcgcccctcatctgtcag 13308


Query: 301   cactctgcccctcaagtgtcaaggatcgcgcccctcatctgtcagtagtcgcgcccctca 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13309 cactctgcccctcaagtgtcaaggatcgcgcccctcatctgtcagtagtcgcgcccctca 13368


Query: 361   agtgtcaataccgcagggcacttatccccaggcttgtccacatcatctgtgggaaactcg 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13369 agtgtcaataccgcagggcacttatccccaggcttgtccacatcatctgtgggaaactcg 13428


Query: 421   cgtaaaatcaggcgttttcgccgatttgcgaggctggccagctccacgtcgccggccgaa 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13429 cgtaaaatcaggcgttttcgccgatttgcgaggctggccagctccacgtcgccggccgaa 13488


Query: 481   atcgagcctgcccctcatctgtcaacgccgcgccgggtgagtcggcccctcaagtgtcaa 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13489 atcgagcctgcccctcatctgtcaacgccgcgccgggtgagtcggcccctcaagtgtcaa 13548


Query: 541   cgtccgcccctcatctgtcagtgagggccaagttttccgcgtggtatccacaacgccggc 600
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct: 13549 cgtccgcccctcatctgtcagtgagggccaagttttccgcgaggtatccacaacgccggc 13608


Query: 601   ggccgcggtgtctcgcacacggcttcgacggcgtttctggcgcgtttgcagggccataga 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13609 ggccgcggtgtctcgcacacggcttcgacggcgtttctggcgcgtttgcagggccataga 13668


Query: 661   cggccgccagcccagcggcgagggcaaccagcccggtgagcgtcggaaaggcgctggaag 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13669 cggccgccagcccagcggcgagggcaaccagcccggtgagcgtcggaaaggcgctggaag 13728
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Plafr1-plafr3

Score = 2.370e+04 bits (12324), Expect = 0.0
Identities = 12346/12363 (99%), Gaps = 1/12363 (0%)
 Strand = Plus / Minus

Query: 9     gggttcgtgcgatccgtctgcatgatggtgatagccgtcagcatgattttcgtgtcgtcg 68
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12362 gggttcgtgcgatccgtctgcatgatggtgatagccgtcagcatgattttcgtgtcgtcg 12303


Query: 69    aacttggtgaagggcattctcggcggcgatcacgacgccggccctgcggagccttcgccg 128
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12302 aacttggtgaagggcattctcggcggcgatcacgacgccggccctgcggagccttcgccg 12243


Query: 129   cgtgcgcgattcatggcggccgtggaggccaaggatttcgcgcgagtgcaagagctgatc 188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12242 cgtgcgcgattcatggcggccgtggaggccaaggatttcgcgcgagtgcaagagctgatc 12183


Query: 189   gaggcgcgtggagccaagtcggcggctgattatgtccttgcgcagctcgccgtggccgaa 248
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12182 gaggcgcgtggagccaagtcggcggctgattatgtccttgcgcagctcgccgtggccgaa 12123


Query: 249   ggtctggaccgcaagcctggtgcgcgcgtcgtggtcgggaaagcggcgggcagcatggca 308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12122 ggtctggaccgcaagcctggtgcgcgcgtcgtggtcgggaaagcggcgggcagcatggca 12063


Query: 309   atgccgcctgcggcgctgggttttacgccaaggggagaagcggcatacgccatcgagcgg 368
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12062 atgccgcctgcggcgctgggttttacgccaaggggagaagcggcatacgccatcgagcgg 12003


Query: 369   tcagcctatggtgagccgaggtccagcattgcgaagcagtaccagcaggaatggaaccgg 428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12002 tcagcctatggtgagccgaggtccagcattgcgaagcagtaccagcaggaatggaaccgg 11943


Query: 429   aaggcggcgacctggtgggcgatggccggtgtggccggcatcatcggcgcgatcctggcg 488
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11942 aaggcggcgacctggtgggcgatggccggtgtggccggcatcatcggcgcgatcctggcg 11883


Query: 489   gcggcggcaaccggctttgttgggctggcagtgtcgatccgcaaccgagtgaagcgcgtg 548
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11882 gcggcggcaaccggctttgttgggctggcagtgtcgatccgcaaccgagtgaagcgcgtg 11823


Query: 549   cgcgacctgttggtgatggagccgggtgcagagccataagcggcaagagacgaaagcccg 608
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11822 cgcgacctgttggtgatggagccgggtgcagagccataagcggcaagagacgaaagcccg 11763


Query: 609   gtttccgggcttttgttttgttacgccaaggacgagttttagcggctaaaggtgttgacg 668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11762 gtttccgggcttttgttttgttacgccaaggacgagttttagcggctaaaggtgttgacg 11703


Query: 669   tgcgagaaatgtttagctaaacttctctcatgtgctggcggctgtcaccgctatgttcaa 728
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11702 tgcgagaaatgtttagctaaacttctctcatgtgctggcggctgtcaccgctatgttcaa 11643


Query: 729   ccaaggcgcggagcaaattatgggtgttatccatgaagaaacggcttaccgaaagccagt 788
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11642 ccaaggcgcggagcaaattatgggtgttatccatgaagaaacggcttaccgaaagccagt 11583


Query: 789   tccaggaggcgatccaggggctggaagtggggcagcagaccatcgagatagcgcggggcg 848
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11582 tccaggaggcgatccaggggctggaagtggggcagcagaccatcgagatagcgcggggcg 11523
```

```
Query: 849   tcttagtcgatgggaagccacaggcgacgttcgcaacgtcgctgggactgaccaggggcg 908
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11522 tcttagtcgatgggaagccacaggcgacgttcgcaacgtcgctgggactgaccaggggcg 11463


Query: 909   cagtgtcgcaagcggtgcatcgcgtgtgggccgcgttcgaggacaagaacttgcccgagg 968
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11462 cagtgtcgcaagcggtgcatcgcgtgtgggccgcgttcgaggacaagaacttgcccgagg 11403


Query: 969   ggtacgcgcgggtaacggcggttctgccggaacatcaggcgtacatcgtccggaagtggg 1028
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11402 ggtacgcgcgggtaacggcggttctgccggaacatcaggcgtacatcgtccggaagtggg 11343


Query: 1029  aagcggacgccaagaaaaaacaggaaaccaaacgatgaaaactttggtcacggccaacca 1088
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11342 aagcggacgccaagaaaaaacaggaaaccaaacgatgaaaactttggtcacggccaacca 11283


Query: 1089  gaaaggcggcgtcggcaagacttcgacccttgtgcatcttgccttcgactttttcgagcg 1148
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11282 gaaaggcggcgtcggcaagacttcgacccttgtgcatcttgccttcgactttttcgagcg 11223


Query: 1149  cggcttgcgggttgccgtgatcgacctggacccccagggcaatgcgtcctacacgctcaa 1208
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11222 cggcttgcgggttgccgtgatcgacctggacccccagggcaatgcgtcctacacgctcaa 11163


Query: 1209  ggactttgctaccggcctgcatgcaagcaagctgttcggcgctgtccctgccggcggctg 1268
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Sbjct: 14975 cttggttttgctgaaaccagacacacagcaactgaataccagaaagaaaatcactttacc 14916


Query: 18178 tttctgacatcagaagggcagaaatttgccgttgaacacctggtcaatacgcgttttggt 18237
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Sbjct: 14915 tttctgacatcagaagggcagaaatttgccgttgaacacctggtcaatacgcgttttggt 14856


Query: 18238 gagcagcaatattgcgcttcgatgacgcttggcgttgagattgatacctctgctgcacaa 18297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14855 gagcagcaatattgcgcttcgatgacgcttggcgttgagattgatacctctgctgcacaa 14796


Query: 18298 aaggcaatcgacgagctggaccagcgcattcgtgacaccgtctccttcgaacttattcgc 18357
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Sbjct: 14795 aaggcaatcgacgagctggaccagcgcattcgtgacaccgtctccttcgaacttattcgc 14736
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Sbjct: 14735 aatggagtgtcattcatcaaggacgccgctatcgcaaatggtgctatccacgcagcggca 14676


Query: 18418 atcgaaacacctcagccggtgaccaatatctacaacatcagccttggtatccagcgtgat 18477
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Sbjct: 14675 atcgaaacacctcagccggtgaccaatatctacaacatcagccttggtatccagcgtgat 14616


Query: 18478 gagccagcgcagaacaaggtaaccgtcagtgccgataagttcaaagttaaacctggtgtt 18537
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Sbjct: 14615 gagccagcgcagaacaaggtaaccgtcagtgccgataagttcaaagttaaacctggtgtt 14556


Query: 18538 gataccaacattgaaacgttgatcgaaaacgcgctgaaaaacgctgctgaatgtgcggcg 18597
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Sbjct: 14555 gataccaacattgaaacgttgatcgaaaacgcgctgaaaaacgctgctgaatgtgcggcg 14496


Query: 18598 ctggatgtcacaaagcaaatggcagcagacaagaaagcgatggatgaactggcttcctat 18657
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Sbjct: 14495 ctggatgtcacaaagcaaatggcagcagacaagaaagcgatggatgaactggcttcctat 14436


Query: 18658 gtccgcacggccatcatgatggaatgtttccccggtggtgttatctggcagcagtgccgt 18717
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Sbjct: 14435 gtccgcacggccatcatgatggaatgtttccccggtggtgttatctggcagcagtgccgt 14376


Query: 18718 cgatagtatgcaattgataattattatcatttgcgggtcctttccggcgatccgccttgt 18777
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Sbjct: 14375 cgatagtatgcaattgataattattatcatttgcgggtcctttccggcgatccgccttgt 14316


Query: 18778 tacggggcggcgacctcgcgggttttcgctatttatgaaaattttccggtttaaggcgtt 18837
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Sbjct: 14315 tacggggcggcgacctcgcgggttttcgctatttatgaaaattttccggtttaaggcgtt 14256


Query: 18838 tccgttcttcttcgtcataacttaatgtttttatttaaaataccctctgaaaagaaagga 18897
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Sbjct: 14255 tccgttcttcttcgtcataacttaatgtttttatttaaaataccctctgaaaagaaagga 14196


Query: 18898 aacgacaggtgctgaaagcgagctttttggcctctgtcgtttcctttctctgtttttgtc 18957
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Query: 18958 cgtggaatgaacaatggaagtcaacaaaaagcagctggctgacattttcggtgcgagtat 19017
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Query: 19018 ccgtaccattcagaactggcaggaacagggaatgcccgttctgcgaggcggtggcaaggg 19077
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Sbjct: 14075 ccgtaccattcagaactggcaggaacagggaatgcccgttctgcgaggcggtggcaaggg 14016


Query: 19078 taatgaggtgctttatgactctgccgccgtcataaaatggtatgccgaaagggatgctga 19137
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Sbjct: 13955 aattgagaacgaaaagctgcgccgggaggttgaagaactgcggcaggccagcgaggcaga 13896


Query: 19198 tctagcgtggaytcaagrmtctcgcgaatggctcgcgtyggaractttcattgwcacttg 19257
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Query: 19318 agcctgcgcccttggcttgtctcgcccctctccgcgtcgctacggggcttccagcgcctt 19377
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Sbjct: 13715 tccgacgctcaccgggctggttgccctcgccgctgggctggcggccgtctatggccctgc 13656


Query: 19438 aaacgcgccagaaacgccgtcgaagccgtgtgcgagacaccgcggccgccggcgttgtgg 19497
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Sbjct: 13655 aaacgcgccagaaacgccgtcgaagccgtgtgcgagacaccgcggccgccggcgttgtgg 13596


Query: 19498 atacctcgcggaaaacttggccctcactgacagatgaggggcggacgttgacacttgagg 19557
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Sbjct: 13595 atacctcgcggaaaacttggccctcactgacagatgaggggcggacgttgacacttgagg 13536


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Sbjct: 13535 ggccgactcacccggcgcggcgttgacagatgaggggcaggctcgatttcggccggcgac 13476


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Sbjct: 13475 gtggagctggccagcctcgcaaatcggcgaaaacgcctgattttacgcgagtttcccaca 13416


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Sbjct: 13055 ggctgcgcccctcggccgcgaacggcctcaccccaaaaatggcagcgctggcagtccttg 12996


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Query: 20158 gcattgacgtgccgcaggtgctggcatcgacattcagcgaccaggtgccgggcagtgagg 20217
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Sbjct: 12935 gcattgacgtgccgcaggtgctggcatcgacattcagcgaccaggtgccgggcagtgagg 12876


Query: 20218 gcggcggcctgggtggcggcctgcccttcacttcggccgtcggggcattcacggacttca 20277
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Sbjct: 12875 gcggcggcctgggtggcggcctgcccttcacttcggccgtcggggcattcacggacttca 12816
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Query: 20278 tggcggggccggcaatttttaccttgggcattcttggcatagtggtcgcgggtgccgtgc 20337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12815 tggcggggccggcaatttttaccttgggcattcttggcatagtggtcgcgggtgccgtgc 12756


Query: 20338 tcgtgttcgggg 20349
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Sbjct: 12755 tcgtgttcgggg 12744
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Puc8-plafr3

```
Score =  738 bits (384), Expect = 0.0
Identities = 384/384 (100%)
 Strand = Plus / Plus

Query: 8     atacgcaaaccgcctctccccgcgcgttggccgattcattaatgcagctggcacgacagg 67
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12363 atacgcaaaccgcctctccccgcgcgttggccgattcattaatgcagctggcacgacagg 12422


Query: 68    tttcccgactggaaagcgggcagtgagcgcaacgcaattaatgtgagttagctcactcat 127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12423 tttcccgactggaaagcgggcagtgagcgcaacgcaattaatgtgagttagctcactcat 12482


Query: 128   taggcaccccaggctttacactttatgcttccggctcgtatgttgtgtggaattgtgagc 187
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Sbjct: 12483 taggcaccccaggctttacactttatgcttccggctcgtatgttgtgtggaattgtgagc 12542


Query: 188   ggataacaatttcacacaggaaacagctatgaccatgattacgaattcccggggatccgt 247
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Sbjct: 12543 ggataacaatttcacacaggaaacagctatgaccatgattacgaattcccggggatccgt 12602


Query: 248   cgacctgcagccaagcttggcactggccgtcgttttacaacgtcgtgactgggaaaaccc 307
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Sbjct: 12603 cgacctgcagccaagcttggcactggccgtcgttttacaacgtcgtgactgggaaaaccc 12662


Query: 308   tggcgttacccaacttaatcgccttgcagcacatccccctttcgccagctggcgtaatag 367
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Sbjct: 12663 tggcgttacccaacttaatcgccttgcagcacatccccctttcgccagctggcgtaatag 12722


Query: 368   cgaagaggcccgcaccgatcgccc 391
             ||||||||||||||||||||||||
Sbjct: 12723 cgaagaggcccgcaccgatcgccc 12746
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Rk2a-plafr3

Score = 9764 bits (5078), Expect = 0.0
Identities = 5101/5105 (99%), Gaps = 3/5105 (0%)
 Strand = Plus / Plus

Query: 12991 agatctatctcatctgcgcaaggcagaacgtgaagacggccgccctggacctcgcccgcg 13050
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15632 agatctatctcatctgcgcaaggcagaacgtgaagacggccgccctggacctcgcccgcg 15691


Query: 13051 agcgccaggcgcacgaggccggcgcgcggacccgcgccacggcccacgagcggacgccgc 13110
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15692 agcgccaggcgcacgaggccggcgcgcggacccgcgccacggcccacgagcggacgccgc 15751


Query: 13111 agcaggagcgccagaaggccgccagagaggccgagcgcggccgtgaggcttggacgctag 13170
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15752 agcaggagcgccagaaggccgccagagaggccgagcgcggccgtgaggcttggacgctag 15811


Query: 13171 ggcagggcatgaaaaagcccgtagcgggctgctacgggcgtctgacgcggtggaaagggg 13230
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15812 ggcagggcatgaaaaagcccgtagcgggctgctacgggcgtctgacgcggtggaaagggg 15871


Query: 13231 gaggggatgttgtctacatggctctgctgtagtgagtgggttgcgctccggcagcggtcc 13290
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Sbjct: 15872 gaggggatgttgtctacatggctctgctgtagtgagtgggttgcgctccggcagcggtcc 15931


Query: 13291 tgatcaatcgtcaccctttctcggtccttcaacgttcctgacaacgagcctccttttcgc 13350
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Sbjct: 15932 tgatcaatcgtcaccctttctcggtccttcaacgttcctgacaacgagcctccttttcgc 15991


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Sbjct: 15992 caatccatcgacaatcaccgcgagtccctgctcgaacgctgcgtccggaccggcttcgtc 16051


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Sbjct: 16052 gaaggcgtctatcgcggcccgcaacagcggcgagagcggagcctgttcaacggtgccgcc 16111


Query: 13471 gcgctcgccggcatcgctgtcgccggcctgctcctcaagcacggccccaacagtgaagta 13530
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Query: 13531 gctgattgtcatcagcgcattgacggcgtccccggccgaaaaacccgcctcgcagaggaa 13590
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Sbjct: 16172 gctgattgtcatcagcgcattgacggcgtccccggccgaaaaacccgcctcgcagaggaa 16231


Query: 13591 gcgaagctgcgcgtcggccgtttccatctgcggtgcgcccggtcgcgtgccggcatggat 13650
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Sbjct: 16232 gcgaagctgcgcgtcggccgtttccatctgcggtgcgcccggtcgcgtgccggcatggat 16291


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Query: 13711 aaatgagcgccagtcgtcgtcggctctcggcaccgaatgcgtatgattctccgccagcat 13770
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Query: 13771 ggcttcggccagtgcgtcgagcagcgcccgcttgttcctgaagtgccagtaaagcgccgg 13830
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Query: 13831 ctgctgaacccccaaccgttccgccagtttgcgtgtcgtcagaccgtctacgccgacctc 13890
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Query: 13891 gttcaacaggtccagggcggcacggatcactgtattcggctgcaactttgtcatgcttga 13950
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Sbjct: 16532 gttcaacaggtccagggcggcacggatcactgtattcggctgcaactttgtcatgcttga 16591


Query: 13951 cactttatcactgataaacataatatgtccaccaacttatcagtgataaagaatccgcgc 14010
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Sbjct: 16592 cactttatcactgataaacataatatgtccaccaacttatcagtgataaagaatccgcgc 16651


Query: 14011 gttcaatcggaccagcggaggctggtccggaggccagacgtgaaacccaacatacccctg 14070
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Sbjct: 16652 gttcaatcggaccagcggaggctggtccggaggccagacgtgaaacccaacatacccctg 16711


Query: 14071 atcgtaattctgagcactgtcgcgctcgacgctgtcggcatcggcctgattatgccggtg 14130
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Sbjct: 16712 atcgtaattctgagcactgtcgcgctcgacgctgtcggcatcggcctgattatgccggtg 16771


Query: 14131 ctgccgggcctcctgcgcgatctggttcactcgaacgacgtcaccgcccactatggcatt 14190
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Sbjct: 16772 ctgccgggcctcctgcgcgatctggttcactcgaacgacgtcaccgcccactatggcatt 16831


Query: 14191 ctgctggcgctgtatgcgttggtgcaatttgcctgcgcacctgtgctgggcgcgctgtcg 14250
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Sbjct: 16832 ctgctggcgctgtatgcgttggtgcaatttgcctgcgcacctgtgctgggcgcgctgtcg 16891


Query: 14251 gatcgtttcgggcggcggccaatcttgctcgtctcgctggccggcgccactgtcgactac 14310
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Sbjct: 16892 gatcgtttcgggcggcggccaatcttgctcgtctcgctggccggcgccactgtcgactac 16951


Query: 14311 gccatcatggcgacagcgcctttcctttgggttctctatatcgggcggatcgtggccggc 14370
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Sbjct: 16952 gccatcatggcgacagcgcctttcctttgggttctctatatcgggcggatcgtggccggc 17011


Query: 14371 atcaccggggcgactggggcggtagccggcgcttatattgccgatatcactgatggcgat 14430
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Query: 14431 gagcgcgcgcggcacttcggcttcatgagcgcctgtttcgggttcgggatggtcgcggga 14490
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Sbjct: 661   gtcttgcaggctaa-cactttcggtatatcgtttgcctgtgcgataatgttgctaatgat 719


Query: 18801 ttgttgcgtaggggttactgaaaagtgagcgggaaagaagagtttcagaccatcaaggag 18860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 720   ttgttgcgtaggggttactgaaaagtgagcgggaaagaagagtttcagaccatcaaggag 779


Query: 18861 cgggccaagcgcaagctggaacgcgacatgggtgcggacctgttggccgcgctcaacgac 18920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 780   cgggccaagcgcaagctggaacgcgacatgggtgcggacctgttggccgcgctcaacgac 839


Query: 18921 ccgaaaaccgttgaagtcatgctcaacgcggacggcaaggtgtggcacgaacgccttggc 18980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 840   ccgaaaaccgttgaagtcatgctcaacgcggacggcaaggtgtggcacgaacgccttggc 899


Query: 18981 gagccgatgcggtacatctgcgacatgcggcccagccagtcgcaggcgattatagaaacg 19040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 900   gagccgatgcggtacatctgcgacatgcggcccagccagtcgcaggcgattatagaaacg 959


Query: 19041 gtggccggattccacggcaaagaggtcacgcggcattcgcccatcctggaaggcgagttc 19100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 960   gtggccggattccacggcaaagaggtcacgcggcattcgcccatcctggaaggcgagttc 1019


Query: 19101 cccttggatggcagccgctttgccggccaattgccgccggtcgtggccgcgccaaccttt 19160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1020  cccttggatggcagccgctttgccggccaattgccgccggtcgtggccgcgccaaccttt 1079


Query: 19161 gcgatccgcaagcgcgcggtcgccatcttcacgctggaacagtacgtcgaggcgggcatc 19220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1080  gcgatccgcaagcgcgcggtcgccatcttcacgctggaacagtacgtcgaggcgggcatc 1139


Query: 19221 atgacccgcgagcaatacgaggtcattaaaagcgccgtcgcggcgcatcgaaacatcctc 19280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1140  atgacccgcgagcaatacgaggtcattaaaagcgccgtcgcggcgcatcgaaacatcctc 1199


Query: 19281 gtcattggcggtactggctcgggcaagaccacgctcgtcaacgcgatcatcaatgaaatg 19340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1200  gtcattggcggtactggctcgggcaagaccacgctcgtcaacgcgatcatcaatgaaatg 1259


Query: 19341 gtcgccttcaacccgtctgagcgcgtcgtcatcatcgaggacaccggcgaaatccagtgc 19400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1260  gtcgccttcaacccgtctgagcgcgtcgtcatcatcgaggacaccggcgaaatccagtgc 1319


Query: 19401 gccgcagagaacgccgtccaataccacaccagcatcgacgtctcgatgacgctgctgctc 19460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1320  gccgcagagaacgccgtccaataccacaccagcatcgacgtctcgatgacgctgctgctc 1379
```

```
Query: 19461 aagacaacgctgcgtatgcgccccgaccgcatcctggtcggtgaggtacgtggccccgaa 19520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1380  aagacaacgctgcgtatgcgccccgaccgcatcctggtcggtgaggtacgtggccccgaa 1439


Query: 19521 gcccttgatctgttgatggcctggaacaccgggcatgaaggaggtgccgccaccctgcac 19580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1440  gcccttgatctgttgatggcctggaacaccgggcatgaaggaggtgccgccaccctgcac 1499


Query: 19581 gcaaacaaccccaaagcgggcctgagccggctcgccatgcttatcagcatgcacccggat 19640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1500  gcaaacaaccccaaagcgggcctgagccggctcgccatgcttatcagcatgcacccggat 1559


Query: 19641 tcaccgaaacccattgagccgctgattggcgaggcggttcatgtggtcgtccatatcgcc 19700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1560  tcaccgaaacccattgagccgctgattggcgaggcggttcatgtggtcgtccatatcgcc 1619


Query: 19701 aggacccctagcggccgtcgagtgcaagaaattctcgaagttcttggttacgagaacggc 19760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1620  aggacccctagcggccgtcgagtgcaagaaattctcgaagttcttggttacgagaacggc 1679


Query: 19761 cagtacatcaccaaaaccctgtaaggagtatttccaatgacaacggctgttccgttccgt 19820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1680  cagtacatcaccaaaaccctgtaaggagtatttccaatgacaacggctgttccgttccgt 1739


Query: 19821 ctgaccatgaatcgcggcattttgttctaccttgccgtgttcttcgttctcgctctcgcg 19880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1740  ctgaccatgaatcgcggcattttgttctaccttgccgtgttcttcgttctcgctctcgcg 1799


Query: 19881 ttatccgcgcatccggcgatggcctcggaaggcaccggcggcagcttgccatatgagagc 19940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1800  ttatccgcgcatccggcgatggcctcggaaggcaccggcggcagcttgccatatgagagc 1859


Query: 19941 tggctgacgaacctgcgcaactccgtaaccggcccggtggccttcgcgctgtccatcatc 20000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1860  tggctgacgaacctgcgcaactccgtaaccggcccggtggccttcgcgctgtccatcatc 1919

Score = 1659 bits (863), Expect = 0.0
Identities = 881/891 (98%), Gaps = 1/891 (0%)
 Strand = Plus / Plus

Query: 12107 gcgctgccatttttggggtgaggccgttcgcggccgaggggcgcagcccctggggggatg 12166
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13008 gcgctgccatttttggggtgaggccgttcgcggccgaggggcgcagcccctggggggatg 13067


Query: 12167 ggaggcccgcgttagcgggccgggagggttcgagaannnnnnncaccccccttcggcgtg 12226
             ||||||||||||||||||||||||||||||||||||       |||||||||||||||||
Sbjct: 13068 ggaggcccgcgttagcgggccgggagggttcgagaagggggggcaccccccttcggcgtg 13127


Query: 12227 cgcggtcacgcgc-cagggcgcagccctggttaaaaacaaggtttataaatattggttta 12285
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13128 cgcggtcacgcgcacagggcgcagccctggttaaaaacaaggtttataaatattggttta 13187


Query: 12286 aaagcaggttaaaagacaggttagcggtggccgaaaaacgggcggaaacccttgcaaatg 12345
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13188 aaagcaggttaaaagacaggttagcggtggccgaaaaacgggcggaaacccttgcaaatg 13247


Query: 12346 ctggattttctgcctgtggacagcccctcaaatgtcaataggtgcgcccctcatctgtca 12405
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13248 ctggattttctgcctgtggacagcccctcaaatgtcaataggtgcgcccctcatctgtca 13307


Query: 12406 tcactctgcccctcaagtgtcaaggatcgcgcccctcatctgtcagtagtcgcgcccctc 12465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13308 gcactctgcccctcaagtgtcaaggatcgcgcccctcatctgtcagtagtcgcgcccctc 13367
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Query: 12466 aagtgtcaataccgcagggcacttatccccaggcttgtccacatcatctgtgggaaactc 12525
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13368 aagtgtcaataccgcagggcacttatccccaggcttgtccacatcatctgtgggaaactc 13427


Query: 12526 gcgtaaaatcaggcgttttcgccgatttgcgaggctggccagctccacgtcgccggccga 12585
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13428 gcgtaaaatcaggcgttttcgccgatttgcgaggctggccagctccacgtcgccggccga 13487


Query: 12586 aatcgagcctgcccctcatctgtcaacgccgcgccgggtgagtcggcccctcaagtgtca 12645
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13488 aatcgagcctgcccctcatctgtcaacgccgcgccgggtgagtcggcccctcaagtgtca 13547


Query: 12646 acgtccgcccctcatctgtcagtgagggccaagttttccgcgtggtatccacaacgccgg 12705
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct: 13548 acgtccgcccctcatctgtcagtgagggccaagttttccgcgaggtatccacaacgccgg 13607


Query: 12706 cggccgcggtgtctcgcacacggcttcgacggcgtttctggcgcgtttgcagggccatag 12765
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13608 cggccgcggtgtctcgcacacggcttcgacggcgtttctggcgcgtttgcagggccatag 13667


Query: 12766 acggccgccagcccagcggcgagggcaaccagcccggtgagcgtcggaaaggcgctggaa 12825
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13668 acggccgccagcccagcggcgagggcaaccagcccggtgagcgtcggaaaggcgctggaa 13727


Query: 12826 gccccgtagcgacgcggagaggggcgagacaagccaagggcgcaggctcgatgcgcagca 12885
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13728 gccccgtagcgacgcggagaggggcgagacaagccaagggcgcaggctcgatgcgcagca 13787


Query: 12886 cgacatagccggttctcgcaaggacgagaatttccctgcggtgcccctcaagtgtcaatg 12945
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13788 cgacatagccggttctcgcaaggacgagaatttccctgcggtgcccctcaagtgtcaatg 13847


Query: 12946 aaagtttccaacgcgagccattcgcgagagccttgagtccacgctagatct 12996
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13848 aaagtttccaacgcgagccattcgcgagagccttgagtccacgctagatct 13898

Score =  515 bits (268), Expect = e-141
Identities = 268/268 (100%)
 Strand = Plus / Plus

Query: 6     ccccgaacacgagcacggcacccgcgaccactatgccaagaatgcccaaggtaaaaattg 65
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12744 ccccgaacacgagcacggcacccgcgaccactatgccaagaatgcccaaggtaaaaattg 12803


Query: 66    ccggccccgccatgaagtccgtgaatgccccgacggccgaagtgaagggcaggccgccac 125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12804 ccggccccgccatgaagtccgtgaatgccccgacggccgaagtgaagggcaggccgccac 12863


Query: 126   ccaggccgccgccctcactgcccggcacctggtcgctgaatgtcgatgccagcacctgcg 185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12864 ccaggccgccgccctcactgcccggcacctggtcgctgaatgtcgatgccagcacctgcg 12923


Query: 186   gcacgtcaatgcttccgggcgtcgcgctcgggctgatcgcccatcccgttactgccccga 245
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12924 gcacgtcaatgcttccgggcgtcgcgctcgggctgatcgcccatcccgttactgccccga 12983


Query: 246   tcccggcaatggcaaggactgccagcgc 273
             ||||||||||||||||||||||||||||
Sbjct: 12984 tcccggcaatggcaaggactgccagcgc 13011
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Score =  108 bits (56), Expect = 6e-19
Identities = 64/68 (94%)
 Strand = Plus / Plus

Query: 13781 agtgcgtcgagcagcgcccgcttgttcctgaagtgccagtaaagcgccggctgctgaacc 13840
             |||||||||||||| ||||||||||||||||| |||||||||||||| ||||||||||||
Sbjct: 19076 agtgcgtcgagcagtgcccgcttgttcctgaaatgccagtaaagcgctggctgctgaacc 19135


Query: 13841 cccaaccg 13848
             |||| |||
Sbjct: 19136 cccagccg 19143


Score =  108 bits (56), Expect = 6e-19
Identities = 64/68 (94%)
 Strand = Plus / Plus

Query: 16434 agtgcgtcgagcagtgcccgcttgttcctgaaatgccagtaaagcgctggctgctgaacc 16493
             |||||||||||||| ||||||||||||||||| |||||||||||||| ||||||||||||
Sbjct: 16422 agtgcgtcgagcagcgcccgcttgttcctgaagtgccagtaaagcgccggctgctgaacc 16481


Query: 16494 cccagccg 16501
             |||| |||
Sbjct: 16482 cccaaccg 16489


Score = 60.3 bits (31), Expect = 2e-04
Identities = 46/51 (90%), Gaps = 1/51 (1%)
 Strand = Plus / Plus

Query: 2334  agaagtttagctaaactttctatccctcgtcaacacctttagccgctaaaa 2384
             |||||||||||||||| || | || | ||||||||||||||||||||||||
Sbjct: 11677 agaagtttagctaaacatt-tctcgcacgtcaacacctttagccgctaaaa 11726


Rk2b-plafr3

Score = 1831 bits (952), Expect = 0.0
Identities = 952/952 (100%)
 Strand = Plus / Plus

Query: 1    ggcatcgtcgtcgccggcggcgtgctgatcttcggcggcgaactcaacgccttcttccga 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1920 ggcatcgtcgtcgccggcggcgtgctgatcttcggcggcgaactcaacgccttcttccga 1979


Query: 61   accctgatcttcctggttctggtgatggcgctgctggtcggcgcgcagaacgtgatgagc 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1980 accctgatcttcctggttctggtgatggcgctgctggtcggcgcgcagaacgtgatgagc 2039


Query: 121  accttcttcggtcgtggtgccgaaatcgcggccctcggcaacggggcgctgcaccaggtg 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2040 accttcttcggtcgtggtgccgaaatcgcggccctcggcaacggggcgctgcaccaggtg 2099


Query: 181  caagtcgcggcggcggatgccgtgcgtgcggtagcggctggacggctcgcctaatcatgg 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2100 caagtcgcggcggcggatgccgtgcgtgcggtagcggctggacggctcgcctaatcatgg 2159


Query: 241  ctctgcgcacgatccccatccgtcgcgcaggcaaccgagaaaacctgttcatgggtggtg 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2160 ctctgcgcacgatccccatccgtcgcgcaggcaaccgagaaaacctgttcatgggtggtg 2219


Query: 301  atcgtgaactggtgatgttctcgggcctgatggcgtttgcgctgattttcagcgcccaag 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2220 atcgtgaactggtgatgttctcgggcctgatggcgtttgcgctgattttcagcgcccaag 2279


Query: 361  agctgcgggccaccgtggtcggtctgatcctgtggttcggggcgctctatgcgttccgaa 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2280 agctgcgggccaccgtggtcggtctgatcctgtggttcggggcgctctatgcgttccgaa 2339
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Query: 421  tcatggcgaaggccgatccgaagatgcggttcgtgtacctgcgtcaccgccggtacaagc 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2340 tcatggcgaaggccgatccgaagatgcggttcgtgtacctgcgtcaccgccggtacaagc 2399


Query: 481  cgtattacccggcccgctcgaccccgttccgcgagaacaccaatagccaagggaagcaat 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2400 cgtattacccggcccgctcgaccccgttccgcgagaacaccaatagccaagggaagcaat 2459


Query: 541  accgatgatccaagcaattgcgattgcaatcgcgggcctcggcgcgcttctgttgttcat 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2460 accgatgatccaagcaattgcgattgcaatcgcgggcctcggcgcgcttctgttgttcat 2519


Query: 601  cctctttgcccgcatccgcgcggtcgatgccgaactgaaactgaaaaagcatcgttccaa 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2520 cctctttgcccgcatccgcgcggtcgatgccgaactgaaactgaaaaagcatcgttccaa 2579


Query: 661  ggacgccggcctggccgatctgctcaactacgccgctgtcgtcgatgacggcgtaatcgt 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2580 ggacgccggcctggccgatctgctcaactacgccgctgtcgtcgatgacggcgtaatcgt 2639


Query: 721  gggcaagaacggcagctttatggctgcctggctgtacaagggcgatgacaacgcaagcag 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2640 gggcaagaacggcagctttatggctgcctggctgtacaagggcgatgacaacgcaagcag 2699


Query: 781  caccgaccagcagcgcgaagtagtgtccgcccgcatcaaccaggccctcgcgggcctggg 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2700 caccgaccagcagcgcgaagtagtgtccgcccgcatcaaccaggccctcgcgggcctggg 2759


Query: 841  aagtgggtggatgatccatgtggacgccgtgcggcgtcctgctccgaactacgcggagcg 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2760 aagtgggtggatgatccatgtggacgccgtgcggcgtcctgctccgaactacgcggagcg 2819


Query: 901  gggcctgtcggcgttccctgaccgtctgacggcagcgattgaagaagagcgc 952
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2820 gggcctgtcggcgttccctgaccgtctgacggcagcgattgaagaagagcgc 2871



Rk2c-plafr3

Score = 1.810e+04 bits (9413), Expect = 0.0
Identities = 9476/9500 (99%), Gaps = 6/9500 (0%)
 Strand = Plus / Plus

Query: 10595 gcgctcggtcttgccttgctcgtcggtgatgtacttcaccagctccgcgaagtcgctctt 10654
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2868  gcgctcggtcttgccttgctcgtcggtgatgtacttcaccagctccgcgaagtcgctctt 2927


Query: 10655 cttgatggagcgcatggggacgtgcttggcaatcacgcgcacccccggccgttttagcg 10714
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2928  cttgatggagcgcatggggacgtgcttggcaatcacgcgcacccccggccgttttagcg 2987


Query: 10715 gctaaaaaagtcatggctctgccctcgggcggaccacgcccatcatgaccttgccaagct 10774
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2988  gctaaaaaagtcatggctctgccctcgggcggaccacgcccatcatgaccttgccaagct 3047


Query: 10775 cgtcctgcttctcttcgatcttcgccagcagggcgaggatcgtggcatcaccgaaccgcg 10834
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3048  cgtcctgcttctcttcgatcttcgccagcagggcgaggatcgtggcatcaccgaaccgcg 3107


Query: 10835 ccgtgcgcgggtcgtcggtgagccagagtttcagcaggccgcccaggcggcccaggtcgc 10894
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3108  ccgtgcgcgggtcgtcggtgagccagagtttcagcaggccgcccaggcggcccaggtcgc 3167
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Query: 10895 cattgatgcgggccagctcgcggacgtgctcatagtccacgacgcccgtgattttgtagc 10954
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3168  cattgatgcgggccagctcgcggacgtgctcatagtccacgacgcccgtgattttgtagc 3227


Query: 10955 cctggccgacggccagcaggtaggccgacaggctcatgccggccgccgccgccttttcct 11014
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3228  cctggccgacggccagcaggtaggccgacaggctcatgccggccgccgccgccttttcct 3287


Query: 11015 caatcgctcttcgttcgtctggaaggcagtacaccttgataggtgggctgcccttcctgg 11074
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3288  caatcgctcttcgttcgtctggaaggcagtacaccttgataggtgggctgcccttcctgg 3347


Query: 11075 ttggcttggtttcatcagccatccgcttgccctcatctgttacgccggcggtagccggcc 11134
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3348  ttggcttggtttcatcagccatccgcttgccctcatctgttacgccggcggtagccggcc 3407


Query: 11135 agcctcgcagagcaggattcccgttgagcaccgccaggtgcgaataagggacagtgaaga 11194
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query: 11195 aggaacacccgctcgcgggtgggcctacttcacctatcctgcccggctgacgccgttgga 11254
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Rk2a-prk310


Score = 1.514e+04 bits (7873), Expect = 0.0
Identities = 7887/7895 (99%), Gaps = 1/7895 (0%)
 Strand = Plus / Plus


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Sbjct: 9541 gccacccaggccgccgccctcactgcccggcacctggtcgctgaatgtcgatgccagcac 9600


Query: 181  ctgcggcacgtcaatgcttccgggcgtcgcgctcgggctgatcgcccatcccgttactgc 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9601 ctgcggcacgtcaatgcttccgggcgtcgcgctcgggctgatcgcccatcccgttactgc 9660


Query: 241  cccgatcccggcaatggcaaggactgccagcgc 273
            |||||||||||||||||||||||||||||||||
Sbjct: 9661 cccgatcccggcaatggcaaggactgccagcgc 9693
```

```
Score =  108 bits (56), Expect = 6e-19
Identities = 64/68 (94%)
 Strand = Plus / Plus

Query: 13781 agtgcgtcgagcagcgcccgcttgttcctgaagtgccagtaaagcgccggctgctgaacc 13840
             |||||||||||||| ||||||||||||||||| |||||||||||||| ||||||||||||
Sbjct: 14018 agtgcgtcgagcagtgcccgcttgttcctgaaatgccagtaaagcgctggctgctgaacc 14077


Query: 13841 cccaaccg 13848
             |||| |||
Sbjct: 14078 cccagccg 14085

Score =  108 bits (56), Expect = 6e-19
Identities = 64/68 (94%)
 Strand = Plus / Plus

Query: 16434 agtgcgtcgagcagtgcccgcttgttcctgaaatgccagtaaagcgctggctgctgaacc 16493
             |||||||||||||| ||||||||||||||||| |||||||||||||| ||||||||||||
Sbjct: 11365 agtgcgtcgagcagcgcccgcttgttcctgaagtgccagtaaagcgccggctgctgaacc 11424


Query: 16494 cccagccg 16501
             |||| |||
Sbjct: 11425 cccaaccg 11432

Score = 60.3 bits (31), Expect = 2e-04
Identities = 46/51 (90%), Gaps = 1/51 (1%)
 Strand = Plus / Plus

Query: 2334 agaagtttagctaaactttctatccctcgtcaacacctttagccgctaaaa 2384
            |||||||||||||||| || | || | ||||||||||||||||||||||||
Sbjct: 8729 agaagtttagctaaacatt-tctcgcacgtcaacacctttagccgctaaaa 8778
```

Rk2b-prk310

```
Score = 1831 bits (952), Expect = 0.0
Identities = 952/952 (100%)
 Strand = Plus / Plus

Query: 1     ggcatcgtcgtcgccggcggcgtgctgatcttcggcggcgaactcaacgccttcttccga 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17585 ggcatcgtcgtcgccggcggcgtgctgatcttcggcggcgaactcaacgccttcttccga 17644


Query: 61    accctgatcttcctggttctggtgatggcgctgctggtcggcgcgcagaacgtgatgagc 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17645 accctgatcttcctggttctggtgatggcgctgctggtcggcgcgcagaacgtgatgagc 17704


Query: 121   accttcttcggtcgtggtgccgaaatcgcggccctcggcaacggggcgctgcaccaggtg 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17705 accttcttcggtcgtggtgccgaaatcgcggccctcggcaacggggcgctgcaccaggtg 17764


Query: 181   caagtcgcggcggcggatgccgtgcgtgcggtagcggctggacggctcgcctaatcatgg 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17765 caagtcgcggcggcggatgccgtgcgtgcggtagcggctggacggctcgcctaatcatgg 17824


Query: 241   ctctgcgcacgatccccatccgtcgcgcaggcaaccgagaaaacctgttcatgggtggtg 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17825 ctctgcgcacgatccccatccgtcgcgcaggcaaccgagaaaacctgttcatgggtggtg 17884


Query: 301   atcgtgaactggtgatgttctcgggcctgatggcgtttgcgctgattttcagcgcccaag 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17885 atcgtgaactggtgatgttctcgggcctgatggcgtttgcgctgattttcagcgcccaag 17944
```

```
Query: 361   agctgcgggccaccgtggtcggtctgatcctgtggttcggggcgctctatgcgttccgaa 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17945 agctgcgggccaccgtggtcggtctgatcctgtggttcggggcgctctatgcgttccgaa 18004


Query: 421   tcatggcgaaggccgatccgaagatgcggttcgtgtacctgcgtcaccgccggtacaagc 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18005 tcatggcgaaggccgatccgaagatgcggttcgtgtacctgcgtcaccgccggtacaagc 18064


Query: 481   cgtattacccggcccgctcgaccccgttccgcgagaacaccaatagccaagggaagcaat 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18065 cgtattacccggcccgctcgaccccgttccgcgagaacaccaatagccaagggaagcaat 18124


Query: 541   accgatgatccaagcaattgcgattgcaatcgcgggcctcggcgcgcttctgttgttcat 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18125 accgatgatccaagcaattgcgattgcaatcgcgggcctcggcgcgcttctgttgttcat 18184


Query: 601   cctctttgcccgcatccgcgcggtcgatgccgaactgaaactgaaaaagcatcgttccaa 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18185 cctctttgcccgcatccgcgcggtcgatgccgaactgaaactgaaaaagcatcgttccaa 18244


Query: 661   ggacgccggcctggccgatctgctcaactacgccgctgtcgtcgatgacggcgtaatcgt 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18245 ggacgccggcctggccgatctgctcaactacgccgctgtcgtcgatgacggcgtaatcgt 18304


Query: 721   gggcaagaacggcagctttatggctgcctggctgtacaagggcgatgacaacgcaagcag 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18305 gggcaagaacggcagctttatggctgcctggctgtacaagggcgatgacaacgcaagcag 18364


Query: 781   caccgaccagcagcgcgaagtagtgtccgcccgcatcaaccaggccctcgcgggcctggg 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18365 caccgaccagcagcgcgaagtagtgtccgcccgcatcaaccaggccctcgcgggcctggg 18424


Query: 841   aagtgggtggatgatccatgtggacgccgtgcggcgtcctgctccgaactacgcggagcg 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18425 aagtgggtggatgatccatgtggacgccgtgcggcgtcctgctccgaactacgcggagcg 18484


Query: 901   gggcctgtcggcgttccctgaccgtctgacggcagcgattgaagaagagcgc 952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18485 gggcctgtcggcgttccctgaccgtctgacggcagcgattgaagaagagcgc 18536
```

Rk2c-prk310

```
Score = 1.493e+04 bits (7767), Expect = 0.0
Identities = 7782/7797 (99%)
 Strand = Plus / Plus

Query: 12303 gcgcttttcgtggtctggctgaacccgtattgggggcctatcgagcatgagggcaagagc 12362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1624  gcgcttttcgtggtctggctgaacccgtattgggggcctatcgagcatgagggcaagagc 1683


Query: 12363 tttgagcagatgaaggcgtacacggccaacaaggcccgcgtgtcgtccatcatccagatt 12422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1684  tttgagcagatgaaggcgtacacggccaacaaggcccgcgtgtcgtccatcatccagatt 1743


Query: 12423 ccggccctcaaggaagaaacctacggccgcgatttcagcgacatgctgcaagagcggctg 12482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1744  ccggccctcaaggaagaaacctacggccgcgatttcagcgacatgctgcaagagcggctg 1803


Query: 12483 acgttcgaccaggcgctggccgatgaatcgctcacgatcatgacgcggcaacgcctcaag 12542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1804  acgttcgaccaggcgctggccgatgaatcgctcacgatcatgacgcggcaacgcctcaag 1863
```

```
Query: 12543 atcgtgcggcgcggcctgtttgaacagctcgacgcggcggccgtgctatgagcgaccaga 12602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1864  atcgtgcggcgcggcctgtttgaacagctcgacgcggcggccgtgctatgagcgaccaga 1923


Query: 12603 ttgaagagctgatccgggagattgcggccaagcacggcatcgccgtcggccgcgacgacc 12662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1924  ttgaagagctgatccgggagattgcggccaagcacggcatcgccgtcggccgcgacgacc 1983


Query: 12663 cggtgctgatcctgcataccatcaacgcccggctcatggccgacagtgcggccaagcaag 12722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1984  cggtgctgatcctgcataccatcaacgcccggctcatggccgacagtgcggccaagcaag 2043


Query: 12723 aggaaatccttgccgcgttcaaggaagagctggaagggatcgcccatcgttggggcgagg 12782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2044  aggaaatccttgccgcgttcaaggaagagctggaagggatcgcccatcgttggggcgagg 2103


Query: 12783 acgccaaggccaaagcggagcggatgctgaacgcggccctggcggccagcaaggacgcaa 12842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2104  acgccaaggccaaagcggagcggatgctgaacgcggccctggcggccagcaaggacgcaa 2163


Query: 12843 tggcgaaggtaatgaaggacagcgccgcgcaggcggccgaagcgatccgcagggaaatcg 12902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2164  tggcgaaggtaatgaaggacagcgccgcgcaggcggccgaagcgatccgcagggaaatcg 2223


Query: 12903 acgacggccttggccgccagctcgcggccaaggtcgcggacgcgcggcgcgtggcgatga 12962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2224  acgacggccttggccgccagctcgcggccaaggtcgcggacgcgcggcgcgtggcgatga 2283


Query: 12963 tgaacatgatcgccggcggcatggtgttgttcgcggccgccctggtggtgtgggcctcgt 13022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2284  tgaacatgatcgccggcggcatggtgttgttcgcggccgccctggtggtgtgggcctcgt 2343


Query: 13023 tatgaatcgcagaggcgcagatgaaaaagcccggcgttgccgggcttgtttttgcgttag 13082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2344  tatgaatcgcagaggcgcagatgaaaaagcccggcgttgccgggcttgtttttgcgttag 2403


Query: 13083 ctgggcttgtttgacaggcccaagctctgactgcgcccgcgctcgcgctcctgggcctgt 13142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2404  ctgggcttgtttgacaggcccaagctctgactgcgcccgcgctcgcgctcctgggcctgt 2463


Query: 13143 ttcttctcctgctcctgcttgcgcatcagggcctggtgccgtcgggctgcttcacgcatc 13202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2464  ttcttctcctgctcctgcttgcgcatcagggcctggtgccgtcgggctgcttcacgcatc 2523


Query: 13203 gaatcccagtcgccggccagctcgggatcgtccgcgcgcatcttgcgcgtcgccagttcc 13262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2524  gaatcccagtcgccggccagctcgggatcgtccgcgcgcatcttgcgcgtcgccagttcc 2583


Query: 13263 tcgatcttgggcgcgtgaatgcccatgccttccttgatttcgcgcaccatgtccagccgc 13322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2584  tcgatcttgggcgcgtgaatgcccatgccttccttgatttcgcgcaccatgtccagccgc 2643


Query: 13323 gtgtgcagggtctgcaagcgggcttgctgttgggcctgctgctgctgccaggcggccttt 13382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2644  gtgtgcagggtctgcaagcgggcttgctgttgggcctgctgctgctgccaggcggccttt 2703


Query: 13383 gtacgcggcagggacagcaagccgggggcattggactgtagctgctgcaaacgcgcctgc 13442
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2704  gtacgcggcagggacagcaagccgggggcattggactgtagctgctgcaaacgcgcctgc 2763


Query: 13443 tgacggtctacgagctgttctaggcggtcctcgatgcgctccacctggtcatgctttgcc 13502
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2764  tgacggtctacgagctgttctaggcggtcctcgatgcgctccacctggtcatgctttgcc 2823
```

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Query: 13503 tgcacgtagagcgcaagggtctgctggtaggtctgctcgatgggcgcggattctaagagg 13562
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Sbjct: 2824  tgcacgtagagcgcaagggtctgctggtaggtctgctcgatgggcgcggattctaagagg 2883


Query: 13563 gcctgctgttccgtctcggcctcctgggccgcctgtagcaaatcctcgccgctgttgccg 13622
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2884  gcctgctgttccgtctcggcctcctgggccgcctgtagcaaatcctcgccgctgttgccg 2943


Query: 13623 ctggactgctttactgccggggactgctgttgccctgctcgcgccgtcgtcgcagttcgg 13682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2944  ctggactgctttactgccggggactgctgttgccctgctcgcgccgtcgtcgcagttcgg 3003


Query: 13683 cttgcccccactcgattgactgcttcatttcgagccgcagcgatgcgatctcggattgcg 13742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3004  cttgcccccactcgattgactgcttcatttcgagccgcagcgatgcgatctcggattgcg 3063


Query: 13743 tcaacggacggggcagcgcggaggtgtccggcttctccttgggtgagtcggtcgatgcca 13802
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3064  tcaacggacggggcagcgcggaggtgtccggcttctccttgggtgagtcggtcgatgcca 3123


Query: 13803 tagccaaaggtttccttccaaaatgcgtccattgctggaccgtgtttctcattgatgccc 13862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3124  tagccaaaggtttccttccaaaatgcgtccattgctggaccgtgtttctcattgatgccc 3183


Query: 13863 gcaagcatcttcggcttgaccgccaggtcaagcgcgccttcatgggcggtcatgacggac 13922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3184  gcaagcatcttcggcttgaccgccaggtcaagcgcgccttcatgggcggtcatgacggac 3243


Query: 13923 gccgccatgaccttgccgccgttgttctcgatgtagccgcgtaatgaggcaatggtgccg 13982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3244  gccgccatgaccttgccgccgttgttctcgatgtagccgcgtaatgaggcaatggtgccg 3303


Query: 13983 cccatcgtcagcgtgtcatcgacaacgatgtacttctggccggggatcacctccccctcg 14042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3304  cccatcgtcagcgtgtcatcgacaacgatgtacttctggccggggatcacctccccctcg 3363


Query: 14043 aaagtcgggttgaacgccaggcgatgatctgaaccggctccggttcgggcgaccttctcc 14102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3364  aaagtcgggttgaacgccaggcgatgatctgaaccggctccggttcgggcgaccttctcc 3423


Query: 14103 cgctgcacaatgtccgtttcgacctcaaggccaaggcggtcggccagaacgaccgccatc 14162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3424  cgctgcacaatgtccgtttcgacctcaaggccaaggcggtcggccagaacgaccgccatc 3483


Query: 14163 atggccggaatcttgttgttccccgccgcctcgacggcgaggactggaacgatgcggggc 14222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3484  atggccggaatcttgttgttccccgccgcctcgacggcgaggactggaacgatgcggggc 3543


Query: 14223 ttgtcgtcgccgatcagcgtcttgagctgggcaacagtgtcgtccgaaatcaggcgctcg 14282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3544  ttgtcgtcgccgatcagcgtcttgagctgggcaacagtgtcgtccgaaatcaggcgctcg 3603


Query: 14283 accaaattaagcgccgcttccgcgtcgccctgcttcgcagcctggtattcaggctcgttg 14342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3604  accaaattaagcgccgcttccgcgtcgccctgcttcgcagcctggtattcaggctcgttg 3663


Query: 14343 gtcaaagaaccaaggtcgccgttgcgaaccaccttcgggaagtctccccacggtgcgcgc 14402
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Sbjct: 3664  gtcaaagaaccaaggtcgccgttgcgaaccaccttcgggaagtctccccacggtgcgcgc 3723


Query: 14403 tcggctctgctgtagctgctcaagacgcctccctttttagccgctaaaactctaacgagt 14462
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```

```
Query: 14463 gcgcccgcgactcaacttgacgctttcggcacttacctgtgccttgccacttgcgtcata 14522
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Sbjct: 3784  gcgcccgcgactcaacttgacgctttcggcacttacctgtgccttgccacttgcgtcata 3843


Query: 14523 ggtgatgcttttcgcactcccgatttcaggtactttatcgaaatctgaccgggcgtgcat 14582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3844  ggtgatgcttttcgcactcccgatttcaggtactttatcgaaatctgaccgggcgtgcat 3903


Query: 14583 tacaaagttcttccccacctgttggtaaatgctgccgctatctgcgtggacgatgctgcc 14642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3904  tacaaagttcttccccacctgttggtaaatgctgccgctatctgcgtggacgatgctgcc 3963


Query: 14643 gtcgtggcgctgcgacttatcggccttttgggccatatagatgttgtaaatgccaggttt 14702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3964  gtcgtggcgctgcgacttatcggccttttgggccatatagatgttgtaaatgccaggttt 4023


Query: 14703 cagggccccggctttatctaccttcgtggttcgtccatgcgccttggttctcggtctcgg 14762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4024  cagggccccggctttatctaccttcgtggttcgtccatgcgccttggttctcggtctcgg 4083


Query: 14763 acaattctttcgcccattcatgaccaggaggcggtgtttcattgggtgactcctgacggt 14822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4084  acaattctttcgcccattcatgaccaggaggcggtgtttcattgggtgactcctgacggt 4143


Query: 14823 tgcctctggtgttcaaacgtgtcctggtcgcttgccggctnnnnnnnngccgacctcggc 14882
             ||||||||||||||||||||||||||||||||||||||||        ||||||||||||
Sbjct: 4144  tgcctctggtgttcaaacgtgtcctggtcgcttgccggctaaaaaaaagccgacctcggc 4203


Query: 14883 agttcgaggccggctttccctagagccgggcgcgtcaaggttgttccatctattttagtg 14942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4204  agttcgaggccggctttccctagagccgggcgcgtcaaggttgttccatctattttagtg 4263


Query: 14943 aactgcgttcgatttatcagttactttcctcccgctttgtgtttcctcccactcgtttcc 15002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4264  aactgcgttcgatttatcagttactttcctcccgctttgtgtttcctcccactcgtttcc 4323


Query: 15003 gcgtctagccgacccctcaacatagcggcctcttcttgggctgcctttgcctcttgccgc 15062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4324  gcgtctagccgacccctcaacatagcggcctcttcttgggctgcctttgcctcttgccgc 4383


Query: 15063 gcttcgtcacgctcggcttgcaccgtcgtaaagcgctcggcctgcctggccgcctcttgc 15122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8644  cggtaagccgtttcttcatggataacacccataatttgctccgcgccttggttgaacata 8703


Query: 19383 gcggtgacagccgccagcacatgagagaagtttagctaaacatttctcgcacgtcaacac 19442
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8704  gcggtgacagccgccagcacatgagagaagtttagctaaacatttctcgcacgtcaacac 8763


Query: 19443 ctttagccgctaaaactcgtccttggcgtaacaaaacaaaagcccggaaaccgggctttc 19502
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8764  ctttagccgctaaaactcgtccttggcgtaacaaaacaaaagcccggaaaccgggctttc 8823


Query: 19503 gtctcttgccgcttatggctctgcacccggctccatcaccaacaggtcgcgcacgcgctt 19562
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8824  gtctcttgccgcttatggctctgcacccggctccatcaccaacaggtcgcgcacgcgctt 8883


Query: 19563 cactcggttgcggatcgacactgccagcccaacaaagccggttgccgccgccgccaggat 19622
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8884  cactcggttgcggatcgacactgccagcccaacaaagccggttgccgccgccgccaggat 8943


Query: 19623 cgcgccgatgatgccggccacaccggccatcgcccaccaggtcgccgccttccggttcca 19682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8944  cgcgccgatgatgccggccacaccggccatcgcccaccaggtcgccgccttccggttcca 9003


Query: 19683 ttcctgctggtactgcttcgcaatgctggacctcggctcaccataggctgaccgctcgat 19742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9004  ttcctgctggtactgcttcgcaatgctggacctcggctcaccataggctgaccgctcgat 9063


Query: 19743 ggcgtatgccgcttctccccttggcgtaaaacccagcgccgcaggcggcattgccatgct 19802
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9064  ggcgtatgccgcttctccccttggcgtaaaacccagcgccgcaggcggcattgccatgct 9123


Query: 19803 gcccgccgctttcccgaccacgacgcgcgcaccaggcttgcggtccagaccttcggccac 19862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9124  gcccgccgctttcccgaccacgacgcgcgcaccaggcttgcggtccagaccttcggccac 9183


Query: 19863 ggcgagctgcgcaaggacataatcagccgccgacttggctccacgcgcctcgatcagctc 19922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9184  ggcgagctgcgcaaggacataatcagccgccgacttggctccacgcgcctcgatcagctc 9243


Query: 19923 ttgcactcgcgcgaaatccttggcctccacggccgccatgaatcgcgcacgcggcgaagg 19982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9244  ttgcactcgcgcgaaatccttggcctccacggccgccatgaatcgcgcacgcggcgaagg 9303


Query: 19983 ctccgcagggccggcgtcgtgatcgccgccgagaatgcccttcaccaagttcgacgacac 20042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9304  ctccgcagggccggcgtcgtgatcgccgccgagaatgcccttcaccaagttcgacgacac 9363


Query: 20043 gaaaatcatgctgacggctatcaccatcatgcagacggatcgcacgaacccgctgaa 20099
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9364  gaaaatcatgctgacggctatcaccatcatgcagacggatcgcacgaacccgctgaa 9420
```

```
Score = 2313 bits (1203), Expect = 0.0
Identities = 1203/1203 (100%)
 Strand = Plus / Plus

Query: 11104 ccctcatctgttacgccggcggtagccggccagcctcgcagagcaggattcccgttgagc 11163
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1     ccctcatctgttacgccggcggtagccggccagcctcgcagagcaggattcccgttgagc 60


Query: 11164 accgccaggtgcgaataagggacagtgaagaaggaacacccgctcgcgggtgggcctact 11223
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61    accgccaggtgcgaataagggacagtgaagaaggaacacccgctcgcgggtgggcctact 120


Query: 11224 tcacctatcctgcccggctgacgccgttggatacaccaaggaaagtctacacgaacccttt 11283
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   tcacctatcctgcccggctgacgccgttggatacaccaaggaaagtctacacgaacccttt 180


Query: 11284 tggcaaaatcctgtatatcgtgcgaaaaaggatggatataccgaaaaaatcgctataatg 11343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181   tggcaaaatcctgtatatcgtgcgaaaaaggatggatataccgaaaaaatcgctataatg 240


Query: 11344 accccgaagcagggttatgcagcggaaaagcgctgcttccctgctgttttgtggaatatc 11403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241   accccgaagcagggttatgcagcggaaaagcgctgcttccctgctgttttgtggaatatc 300


Query: 11404 taccgactggaaacaggcaaatgcaggaaattactgaactgaggggacaggcgagagacg 11463
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301   taccgactggaaacaggcaaatgcaggaaattactgaactgaggggacaggcgagagacg 360


Query: 11464 atgccaaagagctacaccgacgagctggccgagtgggttgaatcccgcgcggccaagaag 11523
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361   atgccaaagagctacaccgacgagctggccgagtgggttgaatcccgcgcggccaagaag 420


Query: 11524 cgccggcgtgatgaggctgcggttgcgttcctggcggtgagggcggatgtcgaggcggcg 11583
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421   cgccggcgtgatgaggctgcggttgcgttcctggcggtgagggcggatgtcgaggcggcg 480


Query: 11584 ttagcgtccggctatgcgctcgtcaccatttgggagcacatgcgggaaacggggaaggtc 11643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481   ttagcgtccggctatgcgctcgtcaccatttgggagcacatgcgggaaacggggaaggtc 540


Query: 11644 aagttctcctacgagacgttccgctcgcacgccaggcggcacatcaaggccaagcccgcc 11703
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541   aagttctcctacgagacgttccgctcgcacgccaggcggcacatcaaggccaagcccgcc 600


Query: 11704 gatgtgcccgcaccgcaggccaaggctgcggaacccgcgccggcacccaagacgccggag 11763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601   gatgtgcccgcaccgcaggccaaggctgcggaacccgcgccggcacccaagacgccggag 660


Query: 11764 ccacggcggccgaagcagggggcaaggctgaaaagccggcccccgctgcggccccgacc 11823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661   ccacggcggccgaagcagggggcaaggctgaaaagccggcccccgctgcggccccgacc 720


Query: 11824 ggcttcaccttcaacccaacaccggacaaaaaggatctactgtaatggcgaaaattcaca 11883
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721   ggcttcaccttcaacccaacaccggacaaaaaggatctactgtaatggcgaaaattcaca 780


Query: 11884 tggttttgcagggcaagggcggggtcggcaagtcggccatcgccgcgatcattgcgcagt 11943
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781   tggttttgcagggcaagggcggggtcggcaagtcggccatcgccgcgatcattgcgcagt 840
```

```
Query: 11944 acaagatggacaaggggcagacacccttgtgcatcgacaccgacccggtgaacgcgacgt 12003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841   acaagatggacaaggggcagacacccttgtgcatcgacaccgacccggtgaacgcgacgt 900


Query: 12004 tcgagggctacaaggccctgaacgtccgccggctgaacatcatggccggcgacgaaatta 12063
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901   tcgagggctacaaggccctgaacgtccgccggctgaacatcatggccggcgacgaaatta 960


Query: 12064 actcgcgcaacttcgacaccctggtcgagctgattgcgccgaccaaggatgacgtggtga 12123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961   actcgcgcaacttcgacaccctggtcgagctgattgcgccgaccaaggatgacgtggtga 1020


Query: 12124 tcgacaacggtgccagctcgttcgtgcctctgtcgcattacctcatcagcaaccaggtgc 12183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1021  tcgacaacggtgccagctcgttcgtgcctctgtcgcattacctcatcagcaaccaggtgc 1080


Query: 12184 cggctctgctgcaagaaatggggcatgagctggtcatccataccgtcgtcaccggcggcc 12243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1081  cggctctgctgcaagaaatggggcatgagctggtcatccataccgtcgtcaccggcggcc 1140


Query: 12244 aggctctcctggacacggtgagcggcttcgcccagctcgccagccagttcccggccgaag 12303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141  aggctctcctggacacggtgagcggcttcgcccagctcgccagccagttcccggccgaag 1200


Query: 12304 cgc 12306
             |||
Sbjct: 1201  cgc 1203

Score =  979 bits (509), Expect = 0.0
Identities = 509/509 (100%)
 Strand = Plus / Plus

Query: 10595 gcgctcggtcttgccttgctcgtcggtgatgtacttcaccagctccgcgaagtcgctctt 10654
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18533 gcgctcggtcttgccttgctcgtcggtgatgtacttcaccagctccgcgaagtcgctctt 18592


Query: 10655 cttgatggagcgcatggggacgtgcttggcaatcacgcgcacccccggccgttttagcg 10714
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18593 cttgatggagcgcatggggacgtgcttggcaatcacgcgcacccccggccgttttagcg 18652


Query: 10715 gctaaaaaagtcatggctctgccctcgggcggaccacgcccatcatgaccttgccaagct 10774
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18653 gctaaaaaagtcatggctctgccctcgggcggaccacgcccatcatgaccttgccaagct 18712


Query: 10775 cgtcctgcttctcttcgatcttcgccagcagggcgaggatcgtggcatcaccgaaccgcg 10834
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18713 cgtcctgcttctcttcgatcttcgccagcagggcgaggatcgtggcatcaccgaaccgcg 18772


Query: 10835 ccgtgcgcgggtcgtcggtgagccagagtttcagcaggccgcccaggcggcccaggtcgc 10894
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18773 ccgtgcgcgggtcgtcggtgagccagagtttcagcaggccgcccaggcggcccaggtcgc 18832


Query: 10895 cattgatgcgggccagctcgcggacgtgctcatagtccacgacgcccgtgattttgtagc 10954
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18833 cattgatgcgggccagctcgcggacgtgctcatagtccacgacgcccgtgattttgtagc 18892


Query: 10955 cctggccgacggccagcaggtaggccgacaggctcatgccggccgccgccgccttttcct 11014
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18893 cctggccgacggccagcaggtaggccgacaggctcatgccggccgccgccgccttttcct 18952


Query: 11015 caatcgctcttcgttcgtctggaaggcagtacaccttgataggtgggctgcccttcctgg 11074
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18953 caatcgctcttcgttcgtctggaaggcagtacaccttgataggtgggctgcccttcctgg 19012
```

```
Query: 11075 ttggcttggtttcatcagccatccgcttg 11103
             |||||||||||||||||||||||||||||
Sbjct: 19013 ttggcttggtttcatcagccatccgcttg 19041
```

Plcd-plafr3

```
Score = 2.369e+04 bits (12322), Expect = 0.0
Identities = 12346/12363 (99%), Gaps = 1/12363 (0%)
 Strand = Plus / Minus


Query: 6778  gggttcgtgcgatccgtctgcatgatggtgatagccgtcagcatgattttcgtgtcgtcg 6837
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12362 gggttcgtgcgatccgtctgcatgatggtgatagccgtcagcatgattttcgtgtcgtcg 12303


Query: 6838  aacttggtgaagggcattctcggcggcgatcacgacgccggccctgcggagccttcgccg 6897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12302 aacttggtgaagggcattctcggcggcgatcacgacgccggccctgcggagccttcgccg 12243


Query: 6898  cgtgcgcgattcatggcggccgtggaggccaaggatttcgcgcgagtgcaagagctgatc 6957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12242 cgtgcgcgattcatggcggccgtggaggccaaggatttcgcgcgagtgcaagagctgatc 12183


Query: 6958  gaggcgcgtggagccaagtcggcggctgattatgtccttgcgcagctcgccgtggccgaa 7017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12182 gaggcgcgtggagccaagtcggcggctgattatgtccttgcgcagctcgccgtggccgaa 12123


Query: 7018  ggtctggaccgcaagcctggtgcgcgcgtcgtggtcgggaaagcggcgggcagcatggca 7077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12122 ggtctggaccgcaagcctggtgcgcgcgtcgtggtcgggaaagcggcgggcagcatggca 12063


Query: 7078  atgccgcctgcggcgctgggttttacgccaaggggagaagcggcatacgccatcgagcgg 7137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12062 atgccgcctgcggcgctgggttttacgccaaggggagaagcggcatacgccatcgagcgg 12003


Query: 7138  tcagcctatggtgagccgaggtccagcattgcgaagcagtaccagcaggaatggaaccgg 7197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12002 tcagcctatggtgagccgaggtccagcattgcgaagcagtaccagcaggaatggaaccgg 11943


Query: 7198  aaggcggcgacctggtgggcgatggccggtgtggccggcatcatcggcgcgatcctggcg 7257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11942 aaggcggcgacctggtgggcgatggccggtgtggccggcatcatcggcgcgatcctggcg 11883


Query: 7258  gcggcggcaaccggctttgttgggctggcagtgtcgatccgcaaccgagtgaagcgcgtg 7317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11882 gcggcggcaaccggctttgttgggctggcagtgtcgatccgcaaccgagtgaagcgcgtg 11823


Query: 7318  cgcgacctgttggtgatggagccgggtgcagagccataagcggcaagagacgaaagcccg 7377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11822 cgcgacctgttggtgatggagccgggtgcagagccataagcggcaagagacgaaagcccg 11763


Query: 7378  gtttccgggcttttgttttgttacgccaaggacgagttttagcggctaaaggtgttgacg 7437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11762 gtttccgggcttttgttttgttacgccaaggacgagttttagcggctaaaggtgttgacg 11703


Query: 7438  tgcgagaaatgtttagctaaacttctctcatgtgctggcggctgtcaccgctatgttcaa 7497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11702 tgcgagaaatgtttagctaaacttctctcatgtgctggcggctgtcaccgctatgttcaa 11643
```

```
Query: 7498  ccaaggcgcggagcaaattatgggtgttatccatgaagaaacggcttaccgaaagccagt 7557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11642 ccaaggcgcggagcaaattatgggtgttatccatgaagaaacggcttaccgaaagccagt 11583


Query: 7558  tccaggaggcgatccaggggctggaagtggggcagcagaccatcgagatagcgcggggcg 7617
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11582 tccaggaggcgatccaggggctggaagtggggcagcagaccatcgagatagcgcggggcg 11523


Query: 7618  tcttagtcgatgggaagccacaggcgacgttcgcaacgtcgctgggactgaccaggggcg 7677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11522 tcttagtcgatgggaagccacaggcgacgttcgcaacgtcgctgggactgaccaggggcg 11463


Query: 7678  cagtgtcgcaagcggtgcatcgcgtgtgggccgcgttcgaggacaagaacttgcccgagg 7737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11462 cagtgtcgcaagcggtgcatcgcgtgtgggccgcgttcgaggacaagaacttgcccgagg 11403


Query: 7738  ggtacgcgcgggtaacggcggttctgccggaacatcaggcgtacatcgtccggaagtggg 7797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11402 ggtacgcgcgggtaacggcggttctgccggaacatcaggcgtacatcgtccggaagtggg 11343


Query: 7798  aagcggacgccaagaaaaaacaggaaaccaaacgatgaaaactttggtcacggccaacca 7857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11342 aagcggacgccaagaaaaaacaggaaaccaaacgatgaaaactttggtcacggccaacca 11283


Query: 7858  gaaaggcggcgtcggcaagacttcgacccttgtgcatcttgccttcgactttttcgagcg 7917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11282 gaaaggcggcgtcggcaagacttcgacccttgtgcatcttgccttcgactttttcgagcg 11223


Query: 7918  cggcttgcgggttgccgtgatcgacctggacccccagggcaatgcgtcctacacgctcaa 7977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11222 cggcttgcgggttgccgtgatcgacctggacccccagggcaatgcgtcctacacgctcaa 11163


Query: 7978  ggactttgctaccggcctgcatgcaagcaagctgttcggcgctgtccctgccggcggctg 8037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11162 ggactttgctaccggcctgcatgcaagcaagctgttcggcgctgtccctgccggcggctg 11103


Query: 8038  gaccgaaaccgcacccgcagccggcgacggccaggccgcgcgcctcgccctcatcgagtc 8097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 11102 gaccgaaaccgcacccgcagccggcgacggccaggccgcgcgcctcgccctcatcgagtc 11043


Query: 8098  caacccggtactggcgaatgccgaacggctgtcgctggacgacgcccgcgagctgttcgg 8157
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct: 11042 caacccggtactggcgaacgccgaacggctgtcgctggacgacgcccgcgagctgttcgg 10983


Query: 8158  ggcgaacatcaaggccctggcgaaccaaggcttcgacgtgtgcctgatcgacacggcccc 8217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10982 ggcgaacatcaaggccctggcgaaccaaggcttcgacgtgtgcctgatcgacacggcccc 10923


Query: 8218  gacccttggcgtcggcctggcggccgccctcttcgcggccgactatgtgctgtcccccat 8277
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10922 gacccttggcgtcggcctggcggccgccctcttcgcggccgactatgtgctgtcccccat 10863


Query: 8278  cgagcttgaggcgtacagcatccagggcatcaagaagatggtcacgaccattgcgaacgt 8337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10862 cgagcttgaggcgtacagcatccagggcatcaagaagatggtcacgaccattgcgaacgt 10803


Query: 8338  gcgccagaagaacgccaagctgcaattccttggcatggtgcccagcaaggtcgatgcgcg 8397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10802 gcgccagaagaacgccaagctgcaattccttggcatggtgcccagcaaggtcgatgcgcg 10743


Query: 8398  gaatccgcgccacgcgcgccaccaagccgagctgctggccgcgtaccccaagatgatgat 8457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10742 gaatccgcgccacgcgcgccaccaagccgagctgctggccgcgtaccccaagatgatgat 10683
```

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Query: 4578  gctggatgtcacaaagcaaatggcagcagacaagaaagcgatggatgaactggcttccta 4637
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Sbjct: 14496 gctggatgtcacaaagcaaatggcagcagacaagaaagcgatggatgaactggcttccta 14437


Query: 4638  tgtccgcacggccatcatgatggaatgtttccccggtggtgttatctggcagcagtgccg 4697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14436 tgtccgcacggccatcatgatggaatgtttccccggtggtgttatctggcagcagtgccg 14377


Query: 4698  tcgatagtatgcaattgataattattatcatttgcgggtcctttccggcgatccgccttg 4757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14376 tcgatagtatgcaattgataattattatcatttgcgggtcctttccggcgatccgccttg 14317


Query: 4758  ttacggggcggcgacctcgcgggttttcgctatttatgaaaattttccggtttaaggcgt 4817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14316 ttacggggcggcgacctcgcgggttttcgctatttatgaaaattttccggtttaaggcgt 14257


Query: 4818  ttccgttcttcttcgtcataacttaatgtttttatttaaaataccctctgaaaagaaagg 4877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14256 ttccgttcttcttcgtcataacttaatgtttttatttaaaataccctctgaaaagaaagg 14197


Query: 4878  aaacgacaggtgctgaaagcgagctttttggcctctgtcgtttcctttctctgtttttgt 4937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14196 aaacgacaggtgctgaaagcgagctttttggcctctgtcgtttcctttctctgtttttgt 14137


Query: 4938  ccgtggaatgaacaatggaagtcaacaaaaagcagctggctgacattttcggtgcgagta 4997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14136 ccgtggaatgaacaatggaagtcaacaaaaagcagctggctgacattttcggtgcgagta 14077


Query: 4998  tccgtaccattcagaactggcaggaacagggaatgcccgttctgcgaggcggtggcaagg 5057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14076 tccgtaccattcagaactggcaggaacagggaatgcccgttctgcgaggcggtggcaagg 14017
```

```
Query: 5058  gtaatgaggtgctttatgactctgccgccgtcataaaatggtatgccgaaagggatgctg 5117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14016 gtaatgaggtgctttatgactctgccgccgtcataaaatggtatgccgaaagggatgctg 13957


Query: 5118  aaattgagaacgaaaagctgcgccgggaggttgaagaactgcggcaggccagcgaggcag 5177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13956 aaattgagaacgaaaagctgcgccgggaggttgaagaactgcggcaggccagcgaggcag 13897


Query: 5178  atc 5180
             |||
Sbjct: 13896 atc 13894

Score = 2194 bits (1141), Expect = 0.0
Identities = 1148/1155 (99%)
 Strand = Plus / Minus


Query: 24225 agatctagcgtggactcaaggctctcgcgaatggctcgcgttggaaactttcattgacac 24284
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13898 agatctagcgtggactcaaggctctcgcgaatggctcgcgttggaaactttcattgacac 13839


Query: 24285 ttgaggggcaccgcagggaaattctcgtccttgcgagaaccggctatgtcgtgctgcgca 24344
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13838 ttgaggggcaccgcagggaaattctcgtccttgcgagaaccggctatgtcgtgctgcgca 13779


Query: 24345 tcgagcctgcgcccttggcttgtctcgcccctctccgcgtcgctacggggcttccagcgc 24404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13778 tcgagcctgcgcccttggcttgtctcgcccctctccgcgtcgctacggggcttccagcgc 13719


Query: 24405 ctttccgacgctcaccgggctggttgccctcgccgctgggctggcggccgtctatggccc 24464
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13718 ctttccgacgctcaccgggctggttgccctcgccgctgggctggcggccgtctatggccc 13659


Query: 24465 tgcaaacgcgccagaaacgccgtcgaagccgtgtgcgagacaccgcggccgccggcgttg 24524
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13658 tgcaaacgcgccagaaacgccgtcgaagccgtgtgcgagacaccgcggccgccggcgttg 13599


Query: 24525 tggatacctcgcggaaaacttggccctcactgacagatgaggggcggacgttgacacttg 24584
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13598 tggatacctcgcggaaaacttggccctcactgacagatgaggggcggacgttgacacttg 13539


Query: 24585 aggggccgactcacccggcgcggcgttgacagatgaggggcaggctcgatttcggccggc 24644
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13538 aggggccgactcacccggcgcggcgttgacagatgaggggcaggctcgatttcggccggc 13479


Query: 24645 gacgtggagctggccagcctcgcaaatcggcgaaaacgcctgattttacgcgagtttccc 24704
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13478 gacgtggagctggccagcctcgcaaatcggcgaaaacgcctgattttacgcgagtttccc 13419


Query: 24705 acagatgatgtggacaagcctggggataagtgccctgcggtattgacacttgaggggcgc 24764
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13418 acagatgatgtggacaagcctggggataagtgccctgcggtattgacacttgaggggcgc 13359


Query: 24765 gactactgacagatgaggggcgcgatccttgacacttgaggggcagagtgctgacagatg 24824
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13358 gactactgacagatgaggggcgcgatccttgacacttgaggggcagagtgctgacagatg 13299


Query: 24825 aggggcgcacctattgacatttgaggggctgtccacaggcagaaaatccagcatttgcaa 24884
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13298 aggggcgcacctattgacatttgaggggctgtccacaggcagaaaatccagcatttgcaa 13239


Query: 24885 gggtttccgcccgtttttcggccaccgctaacctgtcttttaacctgcttttaaaccaat 24944
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13238 gggtttccgcccgtttttcggccaccgctaacctgtcttttaacctgcttttaaaccaat 13179
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Query: 24945 atttataaaccttgtttttaaccagggctgcgccctgtgcgcgtgaccgcgcacgccgaa 25004
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13178 atttataaaccttgtttttaaccagggctgcgccctgtgcgcgtgaccgcgcacgccgaa 13119


Query: 25005 ggggggtgnnnnnnnttctcgaaccctcccggcccgctaacgcgggcctcccatcccccc 25064
             ||||||||       |||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13118 ggggggtgcccccccttctcgaaccctcccggcccgctaacgcgggcctcccatcccccc 13059


Query: 25065 aggggctgcgcccctcggccgcgaacggcctcaccccaaaaatggcagcgctggcagtcc 25124
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13058 aggggctgcgcccctcggccgcgaacggcctcaccccaaaaatggcagcgctggcagtcc 12999


Query: 25125 ttgccattgccgggatcggggcagtaacgggatgggcgatcagcccgagcgcgacgcccg 25184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12998 ttgccattgccgggatcggggcagtaacgggatgggcgatcagcccgagcgcgacgcccg 12939


Query: 25185 gaagcattgacgtgccgcaggtgctggcatcgacattcagcgaccaggtgccgggcagtg 25244
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12938 gaagcattgacgtgccgcaggtgctggcatcgacattcagcgaccaggtgccgggcagtg 12879


Query: 25245 agggcggcggcctgggtggcggcctgcccttcacttcggccgtcggggcattcacggact 25304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12878 agggcggcggcctgggtggcggcctgcccttcacttcggccgtcggggcattcacggact 12819


Query: 25305 tcatggcggggccggcaatttttaccttgggcattcttggcatagtggtcgcgggtgccg 25364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12818 tcatggcggggccggcaatttttaccttgggcattcttggcatagtggtcgcgggtgccg 12759


Query: 25365 tgctcgtgttcgggg 25379
             |||||||||||||||
Sbjct: 12758 tgctcgtgttcgggg 12744

Score =  429 bits (223), Expect = e-115
Identities = 223/223 (100%)
 Strand = Plus / Minus


Query: 77    cgtaatcatggtcatagctgtttcctgtgtgaaattgttatccgctcacaattccacaca 136
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12585 cgtaatcatggtcatagctgtttcctgtgtgaaattgttatccgctcacaattccacaca 12526


Query: 137   acatacgagccggaagcataaagtgtaaagcctggggtgcctaatgagtgagctaactca 196
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12525 acatacgagccggaagcataaagtgtaaagcctggggtgcctaatgagtgagctaactca 12466


Query: 197   cattaattgcgttgcgctcactgcccgctttccagtcgggaaacctgtcgtgccagctgc 256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12465 cattaattgcgttgcgctcactgcccgctttccagtcgggaaacctgtcgtgccagctgc 12406


Query: 257   attaatgaatcggccaacgcgcggggagaggcggtttgcgtat 299
             |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12405 attaatgaatcggccaacgcgcggggagaggcggtttgcgtat 12363
```

```
Score =  239 bits (124), Expect = 3e-58
Identities = 124/124 (100%)
 Strand = Plus / Minus


Query: 27377 gggcgatcggtgcgggcctcttcgctattacgccagctggcgaaagggggatgtgctgca 27436
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12746 gggcgatcggtgcgggcctcttcgctattacgccagctggcgaaagggggatgtgctgca 12687


Query: 27437 aggcgattaagttgggtaacgccagggttttcccagtcacgacgttgtaaaacgacggcc 27496
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12686 aggcgattaagttgggtaacgccagggttttcccagtcacgacgttgtaaaacgacggcc 12627


Query: 27497 agtg 27500
             ||||
Sbjct: 12626 agtg 12623

Score =  108 bits (56), Expect = 8e-19
Identities = 64/68 (94%)
 Strand = Plus / Minus


Query: 23373 cggttggggggttcagcagccggcgctttactggcacttcaggaacaagcgggcgctgctc 23432
             ||| |||||||||||||||| |||||||||||||| ||||||||||||||||| ||||||
Sbjct: 19143 cggctgggggttcagcagccagcgctttactggcatttcaggaacaagcgggcactgctc 19084


Query: 23433 gacgcact 23440
             ||||||||
Sbjct: 19083 gacgcact 19076

Score =  108 bits (56), Expect = 8e-19
Identities = 64/68 (94%)
 Strand = Plus / Minus


Query: 20720 cggctgggggttcagcagccagcgctttactggcatttcaggaacaagcgggcactgctc 20779
             ||| |||||||||||||||| |||||||||||||| ||||||||||||||||| ||||||
Sbjct: 16489 cggttgggggttcagcagccggcgctttactggcacttcaggaacaagcgggcgctgctc 16430

Query: 20780 gacgcact 20787
             ||||||||
Sbjct: 16429 gacgcact 16422
```