

Table S6: Alignment of *Peptonophilus* genomes. Black lines indicate genome rearrangements in *P. harei* relative to *Pepto. Carrol*. Gray blocks indicate missing genes. Red highlights indicate mobile element-like genes. Bold text indicates gene content differences; purple indicates differences involving regulators, orange indicates those involving transporters.

Best hit from <i>Peptoniphilus harei</i> ACS-146-V-Sch2b	Pepto001	Best hit in <i>Pepto. Carrol</i>
650262399 HMPREF9286_0438 site-specific recombinase, phage integrase family		Size Start End
650262398 HMPREF9286_0437 conserved hypothetical protein		
650262397 HMPREF9286_0436 phage holin, LL-H family		
650262396 HMPREF9286_0435 copper amine oxidase N-terminal domain protein		
650262395 HMPREF9286_0434 conserved hypothetical protein		
650262392 HMPREF9286_0431 conserved hypothetical protein	Pepto001_1	912 1214 2125 + C BLAST: predicted exonuclease; K07502 hypothetical protein (db=KEGG eval=9.0e-08 bit_score=121.4 identity=92.27)
650262391 HMPREF9286_0430 putative cysteine desulfurase	Pepto001_2	1146 2248 3393 + B RBH: toc:Toce_1465 aminotransferase class V; K04487 cysteine desulfurase [EC:2.8.1.7] (db=K04487)
650262390 HMPREF9286_0429 thiamine biosynthesis/tRNA modification protein ThiI	Pepto001_3	1188 3402 4589 + B RBH: aoe:Clos_1813 thiamine biosynthesis protein ThiI; K03151 thiamine biosynthesis protein ThiI (db=KEGG eval=4.0e-49 bit_score=73.2 identity=55.5)
650262389 HMPREF9286_0428 LemA family protein	Pepto001_4	570 4573 5142 + C BLAST: cytoplasmic membrane protein; K03744 LemA protein (db=KEGG eval=4.0e-49 bit_score=73.2 identity=55.5)
650262388 HMPREF9286_0427 conserved hypothetical protein	Pepto001_5	810 5152 5961 + C BLAST: putative transmembrane protein; K06872 (db=KEGG eval=2.0e-11 bit_score=73.2 identity=55.5)
650262387 HMPREF9286_0426 putative membrane protein	Pepto001_6	702 5963 6664 + C BLAST: hypothetical protein (db=KEGG eval=3.0e-26 bit_score=121.0 identity=39.29 coverage=100.0)
650262386 HMPREF9286_0425 DNA-binding helix-turn-helix protein	Pepto001_7	540 6865 7404 + C BLAST: DNA-binding protein, putative (db=KEGG eval=2.0e-57 bit_score=224.0 identity=55.5)
650262385 HMPREF9286_0424 polyamine ABC transporter, ATP-binding protein	Pepto001_8	1035 7415 8449 + B RBH: cpe:CPE1968 potA; spermidine/putrescine ABC transporter; K11072 spermidine/putrescine ABC transporter (db=KEGG eval=2.0e-11 bit_score=224.0 identity=55.5)
650262384 HMPREF9286_0423 putative spermidine/putrescine ABC transporter, permease	Pepto001_9	837 8446 9282 + B RBH: UniRef90_D1VUI2 Spermidine/putrescine transport system permease protein PotB n=1
650262383 HMPREF9286_0422 putative spermidine/putrescine ABC transporter, permease	Pepto001_10	786 9279 10064 + B RBH: UniRef90_D1VUI1 Spermidine/putrescine transport system permease protein PotC n=1
650262382 HMPREF9286_0421 ABC transporter, solute-binding protein	Pepto001_11	1044 10061 11104 + B RBH: cno:NT01CX_1229 extracellular solute-binding protein, putative; K11069 spermidine/putrescine ABC transporter (db=KEGG eval=2.0e-11 bit_score=224.0 identity=55.5)
650262381 HMPREF9286_0420 conserved hypothetical protein		
650262380 HMPREF9286_0419 conserved hypothetical protein	Pepto001_12	1029 11188 12216 + C BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650262379 HMPREF9286_0418 conserved hypothetical protein		
650262378 HMPREF9286_0417 basic membrane protein	Pepto001_13	1098 12356 13453 + B RBH: UniRef90_D1VUH8 CD4+ T-cell-stimulating antigen n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650262377 HMPREF9286_0416 ABC transporter, ATP-binding protein	Pepto001_14	1533 13573 15105 + B RBH: UniRef90_D1VTG9 Putative carbohydrate transport ATP-binding protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650262376 HMPREF9286_0415 conserved hypothetical protein TIGR03982	Pepto001_15	1128 15092 16219 + B RBH: UniRef90_D1VTH0 Ribose/galactoside ABC transporter permease protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650262375 HMPREF9286_0414 branched-chain amino acid ABC transporter, permease protein	Pepto001_16	960 16212 11711 + B RBH: cst:CLOST_1121 nucleoside transport system permease protein; K02057 simple sugar tri
650261074 HMPREF9286_0081 electron transport complex, RnfABCDGE type, C subunit	Pepto001_17	1335 17488 18822 + B RBH: UniRef90_D1VUL2 Electron transport complex protein RnfC n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650261073 HMPREF9286_0080 electron transport complex, RnfABCDGE type, D subunit	Pepto001_18	984 18835 19818 + B RBH: thx:Thet_0116 electron transport complex, RnfABCDGE type subunit D (db=KEGG eval=2.0e-11 bit_score=73.2 identity=55.5)
650261072 HMPREF9286_0079 electron transport complex, RnfABCDGE type, G subunit	Pepto001_19	585 19819 20403 + C BLAST: electron transport complex, RnfABCDGE type, G subunit; K20362 electron transport complex, RnfABCDGE type, G subunit (db=KEGG eval=2.0e-11 bit_score=73.2 identity=55.5)
650261071 HMPREF9286_0078 electron transport complex, RnfABCDGE type, E subunit	Pepto001_20	597 20414 21010 + C BLAST: electron transport complex, RnfABCDGE type, E subunit; K03613 electron transport complex, RnfABCDGE type, E subunit (db=KEGG eval=2.0e-11 bit_score=73.2 identity=55.5)
650261070 HMPREF9286_0077 electron transport complex, RnfABCDGE type, A subunit	Pepto001_21	579 21010 21588 + C BLAST: rnfA; inner membrane subunit of an electron transport system, putative; K10669 electron transport complex, RnfABCDGE type, A subunit (db=KEGG eval=2.0e-11 bit_score=73.2 identity=55.5)
650261069 HMPREF9286_0076 electron transport complex, RnfABCDGE type, B subunit	Pepto001_22	918 21598 22515 + B RBH: UniRef90_D1VUK7 Electron transport complex, rnfABcdge type, b subunit n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650261068 HMPREF9286_0074 branched-chain amino acid transport system II carrier protein		
650261067 HMPREF9286_0073 ABC transporter, ATP-binding protein	Pepto001_23	414 22689 23102 + C BLAST: integrase catalytic region (db=KEGG eval=1.0e-39 bit_score=165.0 identity=55.4 coverage=100.0)
650261066 HMPREF9286_0072 ABC transporter, ATP-binding protein	Pepto001_24	459 23125 23583 + C BLAST: putative transposase (db=KEGG eval=3.0e-20 bit_score=100.0 identity=47.92 coverage=100.0)
	Pepto001_25	6648 24015 30662 + B RBH: spv:SPH_0733 serine protease (db=KEGG)
	Pepto001_26	993 31492 32484 + B RBH: fma:FMG_1404 transcriptional regulator (db=KEGG)
	Pepto001_27	1755 32645 34399 + B RBH: snm:SP70585_1475 ABC transporter, ATP-binding/permease protein (db=KEGG)
	Pepto001_28	1722 34383 36104 + B RBH: apr:Apr_0708 ABC transporter related; K06147 ATP-binding cassette, subfamily B, bact
	Pepto001_29	1344 36116 37459 + B RBH: fma:FMG_1401 hypothetical protein (db=KEGG)
	Pepto001_30	585 37518 38102 + C BLAST: hypothetical protein (db=KEGG eval=2.0e-68 bit_score=261.0 identity=92.27 coverage=100.0)
	Pepto001_31	696 38102 38797 + B RBH: snt:SPT_0838 hypothetical protein; K02008 cobalt/nickel transport system permease I
	Pepto001_32	1365 38785 40149 + B RBH: spr:spr1293 ABC-NBD; ABC transporter ATP-binding protein; K02006 cobalt/nickel tra
	Pepto001_33	891 40410 41300 + C BLAST: IS4 family transposase (db=KEGG eval=4.0e-63 bit_score=244.0 identity=43.38 coverage=100.0)
	Pepto001_34	1521 42074 43594 + B RBH: vpr:Vpr_0181 GMP synthase, large subunit; K01951 GMP synthase [glutamine-hydro
	Pepto001_35	2739 43814 46552 + B RBH: tmt:Tmath_0586 preprotein translocase, SecA subunit; K03070 preprotein translocase
650262024 HMPREF9286_0600 conserved hypothetical protein	Pepto001_36	1740 47360 49099 + C BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650262023 HMPREF9286_0599 putative lipoprotein	Pepto001_37	300 49266 49565 + D IPSCAN: PROKAR_LIPOPROTEIN (db=ProfileScan db_id=PS51257 from=1 to=23 eval=7.0)
650262022 HMPREF9286_0598 DNA polymerase III, subunit gamma and tau	Pepto001_38	1674 49772 51445 + B RBH: ccb:Clocel_0050 DNA polymerase III, subunits gamma and tau; K02343 DNA polymerase
650262021 HMPREF9286_0597 DNA-binding protein, YbaB/EbfC family	Pepto001_39	342 51454 51795 + C BLAST: hypothetical protein; K09747 hypothetical protein (db=KEGG eval=4.0e-21 bit_score=73.2 identity=55.5)
650262020 HMPREF9286_0596 recombination protein RecR	Pepto001_40	603 51797 52399 + C BLAST: recR; recombination protein RecR; K06187 recombination protein RecR (db=KEGG eval=2.0e-11 bit_score=73.2 identity=55.5)
650262019 HMPREF9286_0595 cell division protease FtsH	Pepto001_41	1890 52445 54334 + B RBH: aoe:Clos_2310 ATP-dependent metalloprotease FtsH [EC:3.6.4.3]; K03798 cell division p
650262018 HMPREF9286_0594 Na ⁺ /H ⁺ antiporter family protein	Pepto001_42	1302 54525 55826 + B RBH: fnu:FN1403 histidine permease; K07084 (db=KEGG)
650262017 HMPREF9286_0593 transcriptional regulator, Fur family	Pepto001_43	423 56039 56461 + C BLAST: ferric uptake regulator, Fur family; K03711 Fur family transcriptional regulator, ferric u
650262016 HMPREF9286_0592 ABC transporter, substrate-binding protein	Pepto001_44	1065 56580 57644 + C BLAST: periplasmic solute binding protein; K09815 zinc transport system substrate-binding pr
650262015 HMPREF9286_0591 ABC transporter, ATP-binding protein	Pepto001_45	660 57644 58303 + C BLAST: ABC transporter related protein; K09817 zinc transport system ATP-binding protein [E
650262014 HMPREF9286_0590 ABC 3 transport family protein	Pepto001_46	792 58303 59094 + B RBH: UniRef90_D1VUE1 Zinc ABC transporter permease protein n=1 Tax=Peptoniphilus lacrim
650262004 HMPREF9286_0580 YbaK/EbcS protein	Pepto001_47	471 59357 59827 + C BLAST: putative transcriptional regulator; K03976 putative transcriptional regulator (db=KEGG
650262003 HMPREF9286_0579 putative phosphoglucomutase	Pepto001_48	1662 59830 61491 + B RBH: fma:FMG_1032 putative phosphoglucomutase (db=KEGG)
650262002 HMPREF9286_0578 conserved hypothetical protein	Pepto001_49	909 61496 62404 + C BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650262001 HMPREF9286_0577 isochorismatase family protein	Pepto001_50	552 62413 62964 + C BLAST: isochorismatase hydrolase (db=KEGG eval=3.0e-41 bit_score=170.0 identity=45.6 coverage=100.0)
650262000 HMPREF9286_0576 Ser/Thr phosphatase family protein	Pepto001_51	1026 63042 64067 + C BLAST: putative phosphoesterase (db=KEGG eval=3.0e-34 bit_score=149.0 identity=35.13 coverage=100.0)
650261999 HMPREF9286_0575 conserved hypothetical protein	Pepto001_52	2250 64057 66306 + C BLAST: hypothetical protein (db=KEGG eval=1.0e-19 bit_score=102.0 identity=32.61 coverage=100.0)
650261998 HMPREF9286_0574 Ser/Thr phosphatase family protein	Pepto001_53	684 66314 66997 + B RBH: UniRef90_D1VUF4 Ser/Thr protein phosphatase family protein n=1 Tax=Peptoniphilus lacrim
650261997 HMPREF9286_0573 putative adenyl cyclase CyaB	Pepto001_54	534 66997 67530 + C BLAST: adenylate cyclase; K05873 adenylate cyclase, class 2 [EC:4.6.1.1] (db=KEGG eval=2.2e-11 bit_score=73.2 identity=55.5)
650261995 HMPREF9286_0571 putative pyruvate, water dikinase	Pepto001_55	2352 67585 69396 + B RBH: aco:Amico_0764 phosphoenolpyruvate synthase; K01007 pyruvate, water dikinase [EC:2.7.1.30]
650261996 HMPREF9286_0572 pyruvate phosphate dikinase, PEP/pyruvate binding domain protein		
	Pepto001_56	303 69994 70296 + E GENE: 70120..70422 - (rbs_motif=AGGA rbs_spacer=5-10bp)
650261499 HMPREF9286_1722 repeat protein		
650261498 HMPREF9286_0682 transposase		
650261497 HMPREF9286_1379 conserved hypothetical protein		
650261496 HMPREF9286_1378 conserved hypothetical protein		
650261495 HMPREF9286_1377 DNA binding domain protein, excisionase family		
650261494 HMPREF9286_1376 site-specific recombinase, phage integrase family		
650261493 HMPREF9286_1375 putative methionine-tRNA ligase, beta subunit		
650261492 HMPREF9286_1374 conserved hypothetical protein		
650261491 HMPREF9286_1373 putative bacitracin ABC transporter, ATP-binding protein BcrA		
650261490 HMPREF9286_1372 putative membrane protein		
650261489 HMPREF9286_1371 DNA-binding helix-turn-helix protein		
650261488 HMPREF9286_1370 putative lipoprotein		
650261487 HMPREF9286_1369 conserved hypothetical protein		
650261486 HMPREF9286_1368 conserved hypothetical protein		
650261485 HMPREF9286_1087 conserved hypothetical protein	Pepto001_57	288 70298 70585 + C BLAST: hypothetical protein (db=KEGG eval=3.0e-13 bit_score=77.4 identity=41.94 coverage=100.0)
650261484 HMPREF9286_1086 siroheme synthase domain protein	Pepto001_58	798 70601 71398 + C BLAST: siroheme synthase [EC:4.99.1.4]; K02304 precorrin-2 dehydrogenase / sirohydrochlori
650261483 HMPREF9286_1085 conserved hypothetical protein	Pepto001_59	2022 71610 73631 + B RBH: UniRef90_D1VUE8 Putative S-layer domain-containing protein n=1 Tax=Peptoniphilus lacrim
650261482 HMPREF9286_1084 conserved hypothetical protein	Pepto001_60	1059 73713 74771 + C BLAST: exported protein of unknown function (db=KEGG eval=1.0e-13 bit_score=81.3 identity=55.5)
650261481 HMPREF9286_1083 ThiF family protein	Pepto001_61	681 74815 75495 + C BLAST: UBA/ThiF-type NAD/FAD-binding protein (db=KEGG eval=2.0e-51 bit_score=205.0 identity=55.5)
650261480 HMPREF9286_1082 putative ATP-dependent DNA helicase PcrA	Pepto001_62	2196 75542 77737 + B RBH: UniRef90_D1VUE5 ATP-dependent DNA helicase PcrA n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650261479 HMPREF9286_1081 DNA ligase (NAD ⁺)	Pepto001_63	1995 77749 79743 + B RBH: UniRef90_D1VUE4 DNA ligase (NAD ⁺) n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650261478 HMPREF9286_1080 aspartyl-glutamyl-tRNA(Asn/Gln) amidotransferase, C subunit	Pepto001_64	282 79736 80017 + C BLAST: gatC; aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit C [EC:6.3.5.6]
650261477 HMPREF9286_1079 aspartyl-glutamyl-tRNA(Asn/Gln) amidotransferase, A subunit	Pepto001_65	1452 80026 81477 + B RBH: UniRef90_D1VUE2 Glutamyl-tRNA(Gln) amidotransferase subunit A n=1 Tax=Peptoniphilus lacrim
650261476 HMPREF9286_1078 aspartyl-glutamyl-tRNA(Asn/Gln) amidotransferase, B subunit	Pepto001_66	1431 81474 82904 + B RBH: apr:Apr_0978 glutamyl-tRNA(Gln) amidotransferase, B subunit; K02434 aspartyl-tRNA[Asp]
650261616 HMPREF9286_0735 alkaline phosphatase synthesis transcriptional regulatory protein	Pepto001_67	672 83124 83795 + B RBH: UniRef90_D1VUD8 Transcriptional regulatory protein ResD n=1 Tax=Peptoniphilus lacrim
650261615 HMPREF9286_0734 ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	Pepto001_68	1437 83779 85215 + B RBH: UniRef90_D1VUD7 Sensor protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VUI
650261614 HMPREF9286_0733 protein MraZ	Pepto001_69	429 85515 85943 + C BLAST: cell division protein MraZ; K03925 MraZ protein (db=KEGG eval=2.0e-40 bit_score=73.2 identity=55.5)
650261613 HMPREF9286_0732 5'-adenosyl-methyltransferase MraW	Pepto001_70	939 85943 86881 + B RBH: cpe:CPE1865 mraW; 5'-adenosyl-methyltransferase MraW; K03438 5'-adenosyl-methyltr
650261612 HMPREF9286_0731 septum formation initiator	Pepto001_71	408 86883 87290 + C BLAST: Putative cell division protein FtsL n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650261611 HMPREF9286_0730 penicillin-binding protein, transpeptidase domain protein	Pepto001_72	2412 87301 89712 + B RBH: aoe:Clos_1373 peptidoglycan glycosyltransferase [EC:2.4.1.129]; K08384 stage V sporu
650261610 HMPREF9286_0729 phospho-N-acetylmuramoyl-pentapeptide-transferase	Pepto001_73	951 89728 90678 + B RBH: UniRef90_D1VUD2 Phospho-N-acetylmuramoyl-pentapeptide-transferase n=1 Tax=Pept
650261609 HMPREF9286_0728 UDP-N-acetylmuramoyl-L-alanine-D-glutamate ligase	Pepto001_74	1320 90688 92007 + C RBH: ttm:The_1768 UDP-N-acetylmuramoylalanine/D-glutamate ligase; K01925 UDP-N-acety
650261608 HMPREF9286_0727 putative stage V sporulation protein E	Pepto001_75	1113 92008 93120 + B RBH: UniRef90_D1VUD0 Stage V sporulation protein E n=1 Tax=Peptoniphilus lacrimalis 315-B

650261607	HMPREF9286_0726 undecaprenyldiphospho-muramoylpentapeptide beta-N-ace	Pepto001_76	1080	93117	94196	+	B	RBH: UniRef90_D1VUC9 UDP-N-acetylglucosamine--N-acetylmuramyl-(Pentapeptide) pyroph
650261606	HMPREF9286_0725 POTRA domain protein, FtsQ-type	Pepto001_77	825	94212	95036	+	C	BLAST: divl8; cell division septal protein DivlB/FtsQ; K03589 cell division protein FtsQ (db=KE
650261605	HMPREF9286_0724 cell division protein FtsZ	Pepto001_78	1092	95153	96244	+	B	RBH: cth:Cthe_0445 cell division protein FtsZ; K03531 cell division protein FtsZ (db=KEGG)
650262101	HMPREF9286_0677 conserved hypothetical protein							
650262100	HMPREF9286_0676 conserved hypothetical protein							
650262099	HMPREF9286_0675 cysteine protease domain, YopT-type							
650262098	HMPREF9286_0674 conserved hypothetical protein							
650262097	HMPREF9286_0673 conserved hypothetical protein							
650262096	HMPREF9286_0672 conserved hypothetical protein							
650262095	HMPREF9286_0671 conserved hypothetical protein							
650262094	HMPREF9286_0670 conserved hypothetical protein	Pepto001_79	1140	96281	97420	+	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-48 bit_score=196.0 identity=37.63 covera
650262093	HMPREF9286_0669 acetate kinase	Pepto001_80	1197	97522	98718	+	B	RBH: cst:CLOST_1354 ackA; acetate kinase A and propionate kinase 2 [EC:2.7.2.- 2.7.2.1]; K00
650262092	HMPREF9286_0668 conserved hypothetical protein	Pepto001_81	540	98790	99329	+	C	BLAST: protein of unknown function DUF177; K07040 (db=KEGG eval=1.0e-16 bit_score=85
650262091	HMPREF9286_0667 ribosomal protein L32	Pepto001_82	183	99332	99514	+	C	BLAST: ribosomal protein L32; K02911 large subunit ribosomal protein L32 (db=KEGG eval=
650262090	HMPREF9286_0666 transposase-like protein							
650262088	HMPREF9286_0664 conserved hypothetical protein	Pepto001_83	573	99633	100205	+	C	BLAST: hypothetical protein (db=KEGG eval=5.0e-22 bit_score=107.0 identity=35.42 covera
650262087	HMPREF9286_0663 hemerythrin HHE cation binding domain protein	Pepto001_84	552	100214	100765	+	C	BLAST: hemerythrin HHE cation binding domain protein (db=KEGG eval=9.0e-42 bit_score=
650262086	HMPREF9286_0662 conserved hypothetical protein	Pepto001_85	870	100846	101715	+	C	BLAST: S-layer-like domain-containing protein (db=KEGG eval=1.0e-11 bit_score=73.6 ident
650262085	HMPREF9286_0661 conserved domain protein	Pepto001_86	351	101790	102140	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT
		Pepto001_87	1263	102377	103639	+	B	RBH: UniRef90_D4CGM6 Sodium/glutamate symport carrier protein n=3 Tax=Clostridiales F
650262084	HMPREF9286_0660 conserved hypothetical protein	Pepto001_88	1248	103743	104990	+	B	RBH: UniRef90_D1VTC9 Integral membrane protein n=1 Tax=Peptoniphilus lacrimalis 315-B R
650262083	HMPREF9286_0659 glutamine-fructose-6-phosphate transaminase (isomerizing)	Pepto001_89	1827	105077	106903	+	B	RBH: UniRef90_D1VTC8 Glutamine-fructose-6-phosphate transaminase (Isomerizing) n=1 Tax
650262081	HMPREF9286_0657 Acyl-ACP thioesterase	Pepto001_90	720	107196	107915	+	C	BLAST: acyl-ACP thioesterase (db=KEGG eval=2.0e-25 bit_score=119.0 identity=32.88 cover
650262080	HMPREF9286_0656 putative peptidylprolyl isomerase PrsA1	Pepto001_91	750	107993	108742	+	C	BLAST: PpiC-type peptidyl-prolyl cis-trans isomerase; K03769 peptidyl-prolyl cis-trans isomera
650262079	HMPREF9286_0655 RelA/SpoT domain protein	Pepto001_92	1332	108750	110081	+	B	RBH: UniRef90_D1VTC5 RelA/SpoT domain protein n=1 Tax=Peptoniphilus lacrimalis 315-B Re
650262078	HMPREF9286_0654 Xaa-His dipeptidase	Pepto001_93	1455	110130	111584	+	B	RBH: cbe:CbeI_0486 aminoacyl-histidine dipeptidase [EC:3.4.13.3]; K01270 aminoacylhistidin
650262077	HMPREF9286_0653 conserved hypothetical protein	Pepto001_94	333	111599	111931	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT
650262076	HMPREF9286_0652 radical SAM protein, TIGR01212 family	Pepto001_95	909	111943	112851	+	B	RBH: UniRef90_D1VTC2 Radical SAM protein, family n=1 Tax=Peptoniphilus lacrimalis 315-B R
650262075	HMPREF9286_0651 conserved hypothetical protein	Pepto001_96	426	112848	113273	+	C	BLAST: hypothetical protein (db=KEGG eval=6.0e-29 bit_score=129.0 identity=39.13 covera
650262074	HMPREF9286_0650 conserved hypothetical protein	Pepto001_97	492	113440	113931	+	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-29 bit_score=130.0 identity=43.83 covera
650262073	HMPREF9286_0649 conserved hypothetical protein							
650262072	HMPREF9286_0648 conserved hypothetical protein							
650261162	HMPREF9286_1192 copper amine oxidase N-terminal domain protein							
650261161	HMPREF9286_1191 hydrolase, alpha/beta domain protein							
650261160	HMPREF9286_1190 conserved hypothetical protein							
650261159	HMPREF9286_1189 conserved hypothetical protein	Pepto001_98	258	113991	114248	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650261158	HMPREF9286_1188 Sodium:neurotransmitter symporter family protein	Pepto001_99	1305	114407	115711	+	C	BLAST: sodium:neurotransmitter symporter; K0368 neurotransmitter-Na+ symporter, NSS fa
		Pepto001_100	294	115829	116122	+	E	GENE: 115955..116248 + (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp)
650261157	HMPREF9286_1187 ribosomal protein S4	Pepto001_101	597	116176	116772	+	B	RBH: UniRef90_D1VVU0 30S ribosomal protein S4 n=1 Tax=Peptoniphilus lacrimalis 315-B Re
650261156	HMPREF9286_1186 pyruvate carboxylase subunit B	Pepto001_102	1344	117003	118346	+	B	RBH: UniRef90_A8UAD0 Oxaloacetate decarboxylase n=1 Tax=Carnobacterium sp. AT7 RepID
650260747	HMPREF9286_1540 oligopeptide ABC transporter, ATP-binding protein OppF	Pepto001_103	966	118454	119419	+	C	BLAST: oligopeptide ABC transporter ATP-binding protein; K02032 peptide/nickel transport sy
650260748	HMPREF9286_1541 oligopeptide ABC transporter, ATP-binding protein OppD	Pepto001_104	1032	119416	120447	+	C	BLAST: oligopeptide ABC transporter ATP-binding protein; K02031 peptide/nickel transport sy
650260749	HMPREF9286_1542 oligopeptide ABC transporter, permease protein AppC	Pepto001_105	930	120458	121387	+	B	RBH: fma:FMG_1249 oligopeptide ABC transporter permease protein; K02034 peptide/nickel
650260750	HMPREF9286_1543 dipeptide ABC transporter, permease protein DppB	Pepto001_106	900	121392	122291	+	B	RBH: fma:FMG_1250 oligopeptide ABC transporter permease protein; K02033 peptide/nickel
650260751	HMPREF9286_1544 ABC transporter, substrate-binding protein, family 5	Pepto001_107	1686	122385	124070	+	B	RBH: fma:FMG_1251 oligopeptide ABC transporter substrate-binding protein; K02035 peptide
650261155	HMPREF9286_1185 putative aminopeptidase II	Pepto001_108	1248	124314	125561	+	B	RBH: fma:FMG_0040 aminopeptidase II; K01269 aminopeptidase [EC:3.4.11.-] (db=KEGG)
650261154	HMPREF9286_1184 copper amine oxidase N-terminal domain protein							
650261153	HMPREF9286_1183 Mg chelatase-like protein	Pepto001_109	1521	125712	127232	+	B	RBH: fma:FMG_0068 putative ATPase ComM with chaperone activity; K07391 magnesium chi
650261152	HMPREF9286_1182 DNA protecting protein DprA	Pepto001_110	1080	127233	128312	+	B	RBH: UniRef90_D1VVV2 DNA protecting protein DprA n=1 Tax=Peptoniphilus lacrimalis 315-B
650261151	HMPREF9286_1181 DNA topoisomerase I	Pepto001_111	2082	128338	130419	+	B	RBH: tex:TethS14_1700 DNA topoisomerase I [EC:5.99.1.2]; K03168 DNA topoisomerase I [EC
650261150	HMPREF9286_1180 putative general secretion pathway protein E	Pepto001_112	1443	130412	131854	+	B	RBH: aoe:Clos_1638 type II secretion system protein E; K02652 type IV pilus assembly protei
650261149	HMPREF9286_1179 type II secretion system F domain protein	Pepto001_113	1170	131851	133020	+	C	BLAST: Tfp pilus biogenesis protein PilC; K02653 type IV pilus assembly protein PilC (db=KEGG
650261148	HMPREF9286_1178 prelin-type cleavage/methylation N-terminal domain prot	Pepto001_114	378	133032	133409	+	C	BLAST: Putative type IV pilin n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VVU8_9FRIM (
650261147	HMPREF9286_1177 bacterial peptidase A24, N-terminal domain protein	Pepto001_115	720	133411	134130	+	C	BLAST: hypothetical protein; K02654 leader peptidase (prelin peptidase) / N-methyltransfer
650261146	HMPREF9286_1176 conserved hypothetical protein	Pepto001_116	1275	134134	135408	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650261145	HMPREF9286_1175 conserved hypothetical protein	Pepto001_117	987	135435	136421	+	B	RBH: UniRef90_D1VUU5 Hydrogenase maturation factor n=1 Tax=Peptoniphilus lacrimalis 31:
650261144	HMPREF9286_1174 N-acetylmuramoyl-L-alanine amidase	Pepto001_118	1347	136491	137837	+	C	BLAST: N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]; K01448 N-acetylmuramoyl-L-alani
650261143	HMPREF9286_1173 tRNA nucleotidyltransferase	Pepto001_119	717	137849	138565	+	B	RBH: UniRef90_D1VUU3 tRNA nucleotidyltransferase n=1 Tax=Peptoniphilus lacrimalis 315-B
650261142	HMPREF9286_1172 non-canonical purine NTP pyrophosphatase RdgB	Pepto001_120	585	138562	139146	+	C	BLAST: non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family; K01516 nucleoside-t
650261139	HMPREF9286_1169 conserved hypothetical protein	Pepto001_121	393	139562	139954	+	C	BLAST: protein of unknown function DUF1312 (db=KEGG eval=2.0e-14 bit_score=80.5 identi
650261138	HMPREF9286_1168 heptaprenyl diphosphate synthase component I	Pepto001_122	501	139951	140451	+	C	BLAST: heptaprenyl diphosphate synthase component I; K00805 heptaprenyl diphosphate syr
650261137	HMPREF9286_1167 septum formation protein Maf	Pepto001_123	576	140462	141037	+	C	BLAST: maf; Maf-like protein; K06287 septum formation protein (db=KEGG eval=1.0e-42 bi
650261136	HMPREF9286_1166 DNA repair protein RadC	Pepto001_124	717	141042	141758	+	C	BLAST: DNA replication and repair protein RADC; K03630 DNA repair protein RadC (db=KEGG
650261135	HMPREF9286_1165 GDSL-like protein	Pepto001_125	549	141777	142325	+	C	BLAST: Putative esterase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VVJ6_9FRIM (db=
650261134	HMPREF9286_1164 conserved hypothetical protein	Pepto001_126	1143	142312	143454	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650261133	HMPREF9286_1163 prelin-type cleavage/methylation N-terminal domain prot	Pepto001_127	444	143441	143884	+	C	BLAST: Prokaryotic N-methylation domain protein n=1 Tax=Peptoniphilus lacrimalis 315-B R
650261132	HMPREF9286_1162 conserved hypothetical protein	Pepto001_128	384	143868	144521	+	D	IPRSCAN: iv_pilin_GFxxxE: prelin-type N-term (db=HMMTigr db_id=TIGR02532 from=7 to=3
650261131	HMPREF9286_1161 conserved domain protein	Pepto001_129	504	144196	144699	+	D	IPRSCAN: PROKAR_NTER_METHYL (db=PatternScan db_id=PS00409 from=13 to=33 eval=0.e-
650261130	HMPREF9286_1160 conserved hypothetical protein	Pepto001_130	948	144696	145643	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650261129	HMPREF9286_1159 translation elongation factor P	Pepto001_131	558	145672	146229	+	B	RBH: UniRef90_D1VVJ0 Elongation factor P n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1
650261128	HMPREF9286_1158 conserved hypothetical protein	Pepto001_132	309	146242	146550	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650261127	HMPREF9286_1157 dihydroorotase	Pepto001_133	1269	146611	147879	+	B	RBH: ctc:CTC00927 pyrC; dihydroorotase [EC:3.5.2.3]; K01465 dihydroorotase [EC:3.5.2.3] (db
650261126	HMPREF9286_1156 conserved hypothetical protein							
650261125	HMPREF9286_1155 putative membrane protein	Pepto001_134	1755	147973	149727	+	B	RBH: UniRef90_D1VV77 Putative membrane protein n=1 Tax=Peptoniphilus lacrimalis 315-B F
650261124	HMPREF9286_1154 conserved hypothetical protein	Pepto001_135	501	149742	150242	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650261123	HMPREF9286_1153 inorganic diphosphatase PpaC	Pepto001_136	1635	150305	151939	+	B	RBH: fma:FMG_1581 putative manganese-dependent inorganic pyrophosphatase; K01507 inc
650261122	HMPREF9286_1152 flavoprotein family protein	Pepto001_137	1209	152030	153238	+	B	RBH: UniRef90_D1VTV2 Flavoprotein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VTV2
650261121	HMPREF9286_1151 SAF domain protein	Pepto001_138	1278	153309	154586	+	B	RBH: UniRef90_D1VTV1 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 31
		Pepto001_139	405	154622	155026	+	C	BLAST: rrf2 family protein (db=KEGG eval=2.0e-24 bit_score=114.0 identity=50.41 covera
650261120	HMPREF9286_1149 isoleucine--tRNA ligase	Pepto001_140	3102	155265	158366	+	B	RBH: aoe:Clos_2197 ileS; isoleucyl-tRNA synthetase; K01870 isoleucyl-tRNA synthetase [EC:6.
650261119	HMPREF9286_1148 conserved hypothetical protein	Pepto001_141	363	158613	158975	+	C	BLAST: hypothetical protein; K09790 hypothetical protein (db=KEGG eval=5.0e-10 bit_score
650261118	HMPREF9286_1147 ABC transporter, ATP-binding protein	Pepto001_142	1719	158978	160696	+	B	RBH: elm:ELI_2760 ABC transporter (db=KEGG)
650261117	HMPREF9286_1146 ABC transporter, ATP-binding protein	Pepto001_143	1659	160680	162338	+	B	RBH: ols:Olsu_1658 ABC transporter, CydCD cysteine exporter (CydDC-E) family, permease/AT
650261116	HMPREF9286_1145 conserved hypothetical protein	Pepto001_144	834	162344	163177	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT
650261115	HMPREF9286_1144 iron transport-associated domain protein	Pepto001_145	1431	163386	164816	+	B	RBH: UniRef90_D1VTB5 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 31
650261114	HMPREF9286_1143 conserved hypothetical protein	Pepto001_146	957	164806	165762	+	B	RBH: UniRef90_D1VTB4 Putative ABC transporter n=1 Tax=Peptoniphilus lacrimalis 315-B Rep
650261113	HMPREF9286_1142 heme ABC transporter, heme-binding protein isDE	Pepto001_147	927	165755	166681	+	B	RBH: sez:Sez_0373 ferrichrome ABC transporter heme substrate-binding lipoprotein; K02016
650261112	HMPREF9286_1141 iron chelate uptake ABC transporter, FeCT family, permease	Pepto001_148	990	166668	167657	+	B	RBH: UniRef90_D1VTB1 Iron(3+)-hydroxamate import system permease protein FluB n=1 Tax
650261111	HMPREF9286_1140 putative ferrichrome ABC transporter, ATP-binding protein	Pepto001_149	762	167647	168408	+	B	RBH: UniRef90_D1VTB0 Ferrichrome transporter ATP-binding protein FluC n=1 Tax=Peptoniph
650261110	HMPREF9286_1139 conserved hypothetical protein	Pepto001_150	522	168433	168954	+	C	BLAST: flavodoxin family protein (db=KEGG eval=2.0e-19 bit_score=98.2 identity=33.53 cov
		Pepto001_151	3936	168993	172928	+	C	BLAST: peptidoglycan-binding lysin domain protein (db=KEGG eval=4.0e-41 bit_score=17.
650261109	HMPREF9286_1138 conserved hypothetical protein	Pepto001_152	603	173185	173787	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT
650261108	HMPREF9286_1137 conserved hypothetical protein	Pepto001_153	4173	173838	178010	+	B	RBH: UniRef90_D1VSL7 Amylopullulanase (Fragment) n=1 Tax=Peptoniphilus lacrimalis 315-B
650261107	HMPREF9286_1136 copper amine oxidase N-terminal domain protein	Pepto001_154	870	178091	178960	+	B	RBH: UniRef90_D1VV56 Copper amine oxidase N-domain superfamily n=1 Tax=Peptoniphilus
		Pepto001_155	723	179068	179790	+	C	BLAST: amino acid ABC transporter, ATP-binding protein; K02028 polar amino acid transpor
		Pepto001_156	798	179777	180574	+	C	BLAST: amino acid ABC transporter, ATP-binding protein; K02029 polar amino acid transpor
		Pepto001_157	807	180583	181389	+	C	BLAST: polar amino acid ABC transporter amino acid-binding protein (db=KEGG eval=2.0e
		Pepto001_158	1221	182074	183294	+	B	RBH: cbe:CbeI_4515 argininosuccinate synthase [EC:6.3.4.5]; K01940 argininosuccinate synt
		Pepto001_159	1371	183296	184666	+	C	BLAST: argininosuccinate lyase; K01755 argininosuccinate lyase [EC:4.3.3.21] (db=KEGG eval
650261106	HMP							

650261583 HMPREF9286_0702 radical SAM protein, TIGR01212 family	Pepto001_164	963	190872	191834	B	RBH: UniRef90_D1VTU6 Iron-sulfur protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1
650261582 HMPREF9286_0701 tetratricopeptide repeat protein	Pepto001_165	891	191933	192823	C	BLAST: TPR repeat-containing protein (db=KEGG eval=3.0e-32 bit_score=142.0 identity=37.37)
650261581 HMPREF9286_0700 methionine aminopeptidase, type I	Pepto001_166	756	192820	193575	B	RBH: clj:CLIU_c35780 map; methionine aminopeptidase [EC:3.4.11.18]; K01265 methionyl am
650261580 HMPREF9286_0699 MATE efflux family protein						
650261579 HMPREF9286_0698 peptidyl-prolyl cis-trans isomerase, cyclophilin-type	Pepto001_167	606	193796	194401	C	BLAST: ppiB; peptidyl-prolyl cis-trans isomerase; K03768 peptidyl-prolyl cis-trans isomerase B
650261578 HMPREF9286_0697 thymidine kinase	Pepto001_168	603	194410	195012	C	BLAST: thymidine kinase; K00857 thymidine kinase [EC:2.7.1.21] (db=KEGG eval=2.0e-59 bit
650261577 HMPREF9286_0696 HTH domain protein	Pepto001_169	1071	195073	196143	B	RBH: UniRef90_D1VTT7 PfkB family kinase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1\
650261576 HMPREF9286_0695 indigoldine synthase A-like protein	Pepto001_170	921	196136	197056	B	RBH: ipo:lyop_2663 indigoldine synthase A family protein (db=KEGG)
650261575 HMPREF9286_0694 thioesterase family protein	Pepto001_171	504	197037	197540	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-19 bit_score=98.2 identity=38.81 coverag
650260747 HMPREF9286_1540 oligopeptide ABC transporter, ATP-binding protein OppF	Pepto001_172	780	197586	198365	B	RBH: apr:Apr_0391 ABC transporter related (db=KEGG)
650260748 HMPREF9286_1541 oligopeptide ABC transporter, ATP-binding protein OppD	Pepto001_173	990	198343	199332	B	RBH: apr:Apr_0390 oligopeptide/dipeptide ABC transporter, ATPase subunit (db=KEGG)
650260749 HMPREF9286_1542 oligopeptide ABC transporter, permease protein AppC	Pepto001_174	816	199329	200144	B	RBH: apr:Apr_0389 binding-protein-dependent transport systems inner membrane compon
650260750 HMPREF9286_1543 dipeptide ABC transporter, permease protein DppB	Pepto001_175	942	200146	201087	B	RBH: apr:Apr_0388 binding-protein-dependent transport systems inner membrane compon
650260751 HMPREF9286_1544 ABC transporter, substrate-binding protein, family 5	Pepto001_176	1521	201080	202600	B	RBH: apr:Apr_0387 extracellular solute-binding protein family 5; K02035 peptide/nickel tran
650261574 HMPREF9286_0693 conserved hypothetical protein	Pepto001_177	282	202784	203065	C	BLAST: hypothetical protein; K09764 hypothetical protein (db=KEGG eval=2.0e-14 bit_sco
650261573 HMPREF9286_0692 endonuclease III	Pepto001_178	645	203077	203721	C	BLAST: nth; endonuclease III [EC:4.2.99.18]; K10773 endonuclease III [EC:4.2.99.18] (db=KEGG
650261572 HMPREF9286_0691 VanW-like protein	Pepto001_179	1383	203726	205108	B	RBH: UniRef90_D1VTT3 Vancomycin B-type resistance protein VanW n=1 Tax=Peptoniphilus
	Pepto001_180	573	205175	205747	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1\
650261571 HMPREF9286_0690 S1 RNA binding domain protein	Pepto001_181	828	205738	206565	C	BLAST: RNA-binding domain-containing protein; K00243 hypothetical protein (db=KEGG eval
650261570 HMPREF9286_0689 23S rRNA (uracil-5-)-methyltransferase RumaA	Pepto001_182	1278	206552	207829	B	RBH: UniRef90_D1VTT0 23S rRNA (Uracil-5-)-methyltransferase RumA n=1 Tax=Peptoniphilus
650261569 HMPREF9286_0688 conserved hypothetical protein						
650261568 HMPREF9286_0687 conserved hypothetical protein						
	Pepto001_183	117	208154	208270	E	GENE: 208280..208396 - (rbs_motif=AGGAGG rbs_spacer=5-10bp)
	Pepto001_184	213	208295	208507	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-12 bit_score=74.7 identity=58.73 coveri
	Pepto001_185	1818	208520	210337	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-74 bit_score=284.0 identity=33.17 cove
	Pepto001_186	444	210341	210784	C	BLAST: hypothetical protein (db=KEGG eval=6.0e-11 bit_score=69.7 identity=35.25 coveri
	Pepto001_187	963	210777	211739	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-19 bit_score=99.0 identity=32.08 coveri
	Pepto001_188	600	212120	212719	C	BLAST: hypothetical protein (db=KEGG eval=5.0e-23 bit_score=110.0 identity=53.85 cove
	Pepto001_189	252	212813	213064	C	BLAST: hypothetical protein (db=KEGG eval=6.0e-09 bit_score=62.8 identity=41.94 coveri
	Pepto001_190	297	213006	213302	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-13 bit_score=77.4 identity=48.57 coveri
	Pepto001_191	1113	213302	214414	B	RBH: det:DET1102 hypothetical protein (db=KEGG)
	Pepto001_192	549	214416	214964	B	RBH: UniRef90_C2HHU4 Phage-associated protein n=1 Tax=Finogoldia magna ATCC 53516 R
	Pepto001_193	201	214974	215174	C	BLAST: Putative uncharacterized protein n=1 Tax=Finogoldia magna ATCC 53516 RepID=C2H
	Pepto001_194	1932	215149	217080	B	RBH: clj:CLIU_c03390 phage related DNA polymerase [EC:2.7.7.7]; K02334 DNA polymerase
	Pepto001_195	675	217162	217836	B	RBH: hmo:HM1_2938 hypothetical protein (db=KEGG)
	Pepto001_196	201	217823	218023	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-13 bit_score=77.4 identity=57.14 coveri
	Pepto001_197	387	218016	218402	C	BLAST: hypothetical protein (db=KEGG eval=7.0e-36 bit_score=152.0 identity=56.1 coveri
	Pepto001_198	2229	218403	220631	B	RBH: mcu:HMPREF0573_11256 phage-associated protein (db=KEGG)
	Pepto001_199	282	220764	221045	C	BLAST: phage associated protein (db=KEGG eval=8.0e-23 bit_score=108.0 identity=55.56
	Pepto001_200	1347	221046	222392	B	RBH: cce:Ccel_2848 SNF2-related protein (db=KEGG)
	Pepto001_201	408	222486	222893	C	BLAST: hypothetical protein (db=KEGG eval=5.0e-44 bit_score=179.0 identity=64.18 cove
	Pepto001_202	1365	223279	224643	B	RBH: pgi:PG0827 MATE efflux family protein (db=KEGG)
	Pepto001_203	360	224777	225136	C	BLAST: HNH endonuclease (db=KEGG eval=2.0e-35 bit_score=150.0 identity=64.1 coverag
	Pepto001_204	648	225187	225834	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-79 bit_score=297.0 identity=92.67 cove
	Pepto001_205	783	225845	226627	B	RBH: apr:Apr_0832 hypothetical protein (db=KEGG)
	Pepto001_206	1248	226624	227871	B	RBH: afn:Acfcr_1080 DNA methylase N-4/N-6 domain protein (db=KEGG)
	Pepto001_207	216	227915	228130	C	BLAST: hypothetical protein (db=KEGG eval=5.0e-18 bit_score=93.2 identity=61.19 coveri
	Pepto001_208	369	228202	228570	C	BLAST: Putative uncharacterized protein n=1 Tax=Finogoldia magna ATCC 53516 RepID=C2H
	Pepto001_209	288	228663	228950	C	BLAST: Putative uncharacterized protein n=1 Tax=Finogoldia magna ATCC 53516 RepID=C2H
	Pepto001_210	1590	229048	230637	B	RBH: ckr:CKR_2343 hypothetical protein (db=KEGG)
	Pepto001_211	420	230682	231101	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-46 bit_score=187.0 identity=61.87 cove
	Pepto001_212	1278	231141	232418	B	RBH: det:DET1087 HK97 family portal protein, putative (db=KEGG)
	Pepto001_213	687	232405	233091	B	RBH: UniRef90_C2HHW7 ATP-dependent Clp protease proteolytic subunit n=1 Tax=Finogold
	Pepto001_214	1191	233096	234286	B	RBH: UniRef90_C2HHW8 HK97 family phage major capsid protein n=1 Tax=Finogoldia magn
	Pepto001_215	273	234297	234569	C	BLAST: DNA packaging protein, putative (db=KEGG eval=3.0e-19 bit_score=97.1 identity=
	Pepto001_216	333	234569	234901	C	BLAST: head-tail adaptor, putative (db=KEGG eval=1.0e-10 bit_score=68.2 identity=34.69
	Pepto001_217	381	234898	235278	C	BLAST: hypothetical protein (db=KEGG eval=6.0e-33 bit_score=142.0 identity=56.0 coveri
	Pepto001_218	345	235271	235615	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-16 bit_score=87.4 identity=57.58 coveri
	Pepto001_219	597	235608	236204	C	BLAST: phage major tail protein, phi13 family (db=KEGG eval=6.0e-60 bit_score=233.0 id
	Pepto001_220	357	236204	236560	C	BLAST: hypothetical protein (db=KEGG eval=6.0e-41 bit_score=169.0 identity=66.67 cove
	Pepto001_221	330	236739	237068	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-25 bit_score=117.0 identity=54.46 covera
	Pepto001_222	324	237065	237388	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-13 bit_score=78.2 identity=43.02 covera
	Pepto001_223	129	237478	237606	C	BLAST: TP901 family tail tape measure protein (db=KEGG eval=2.0e-10 bit_score=67.8 ide
	Pepto002					
	Pepto002_1	150	2159	+	B	RBH: bse:Bsel_2996 TP901 family phage tail tape measure protein (db=KEGG)
	Pepto003					
	Pepto003_1	342	223	564	C	BLAST: mdlB9; ABC-type multidrug/protein/lipid transport system, ATPase component; K06
650261213 HMPREF9286_1714 conserved hypothetical protein						
650261214 HMPREF9286_1715 relaxase/mobilization nuclease domain protein	Pepto003_2	762	1084	1845	B	RBH: fma:FMG_0943 hypothetical protein (db=KEGG)
650261214 HMPREF9286_1715 relaxase/mobilization nuclease domain protein	Pepto003_3	393	2023	2415	C	BLAST: relaxase/mobilization nuclease family protein (db=KEGG eval=5.0e-64 bit_score=24
650261215 HMPREF9286_1716 conserved hypothetical protein	Pepto003_4	357	2417	2773	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-49 bit_score=196.0 identity=96.61 covera
650261216 HMPREF9286_1380 conserved hypothetical protein						
650261217 HMPREF9286_1381 conserved hypothetical protein						
650261218 HMPREF9286_1382 Abi-like protein						
	Pepto003_5	1083	2941	4023	B	RBH: spi:MGAS10750_Spy1712 RhuM (db=KEGG)
	Pepto003_6	483	4016	4498	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-68 bit_score=260.0 identity=92.5 coveri
	Pepto003_7	549	4507	5055	B	RBH: spi:MGAS10750_Spy1713 hypothetical protein (db=KEGG)
	Pepto003_8	402	5064	5465	C	BLAST: transcriptional regulator, Cro/Ci family (db=KEGG eval=5.0e-63 bit_score=242.0 id
	Pepto003_9	408	5768	6175	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-72 bit_score=272.0 identity=98.52 cove
	Pepto003_10	411	6445	6855	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-54 bit_score=214.0 identity=97.79 cove
	Pepto003_11	156	7397	7552	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-10 bit_score=67.4 identity=96.08 coveri
	Pepto003_12	1671	7653	9323	B	RBH: spi:MGAS10750_Spy1717 site-specific recombinase (db=KEGG)
	Pepto003_13	168	9323	9490	E	GENE: 10425..10592 + (rbs_motif=GGAGG rbs_spacer=5-10bp)
	Pepto003_14	687	9661	10347	B	RBH: spi:MGAS10750_Spy1718 site-specific recombinase (db=KEGG)
	Pepto003_15	498	10495	10992	C	BLAST: site-specific recombinase (db=KEGG eval=1.0e-72 bit_score=274.0 identity=97.58
	Pepto003_16	1494	10985	12478	B	RBH: spi:MGAS10750_Spy1719 site-specific recombinase (db=KEGG)
	Pepto003_17	699	12607	13305	C	BLAST: hypothetical protein (db=KEGG eval=6.0e-13 bit_score=77.4 identity=28.31 coveri
	Pepto003_18	1164	13320	14483	B	RBH: dae:Dtox_2224 protein of unknown function DUF955 (db=KEGG)
	Pepto003_19	135	14618	14752	C	BLAST: DNA methylase n=1 Tax=Finogoldia magna ATCC 53516 RepID=C2HHW0_PEPMA (db
	Pepto003_20	225	14796	15020	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-16 bit_score=88.2 identity=57.14 coveri
	Pepto003_21	306	15108	15413	E	GENE: 16210..16515 + (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp)
	Pepto003_22	288	15512	15799	C	BLAST: Putative uncharacterized protein n=1 Tax=Finogoldia magna ATCC 53516 RepID=C2H
	Pepto003_23	1590	15898	17487	B	RBH: UniRef90_C2HHW4 Phage terminase n=1 Tax=Finogoldia magna ATCC 53516 RepID=C2
	Pepto003_24	621	17537	18157	B	RBH: smc:SmuNN2025_0027 hypothetical protein (db=KEGG)
	Pepto003_25	1278	18203	19480	B	RBH: UniRef90_C2HHW6 HK97 family portal protein n=1 Tax=Finogoldia magna ATCC 53516
	Pepto003_26	684	19715	20398	C	BLAST: peptidase S14, ClpP; K01358 ATP-dependent Clp protease, protease subunit [EC:3.4.
	Pepto003_27	1191	20401	21591	B	RBH: ccb:Clocel_3975 phage major capsid protein, HK97 family (db=KEGG)
	Pepto003_28	273	21602	21874	C	BLAST: DNA packaging protein, putative (db=KEGG eval=3.0e-19 bit_score=97.1 identity=
	Pepto003_29	333	21874	22206	C	BLAST: head-tail adaptor, putative (db=KEGG eval=2.0e-10 bit_score=67.8 identity=33.67
	Pepto003_30	390	22203	22592	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-32 bit_score=140.0 identity=56.1 coveri
	Pepto003_31	597	23182	23778	B	RBH: UniRef90_C2HHX3 Prophage pi2 protein 39 n=1 Tax=Finogoldia magna ATCC 53516 R
	Pepto003_32	357	23778	24134	C	BLAST: hypothetical protein (db=KEGG eval=6.0e-41 bit_score=169.0 identity=66.67 cove
	Pepto003_33	165	24152	24316	C	BLAST: phage-like protein (db=KEGG eval=2.0e-13 bit_score=77.8 identity=62.96 covera

		Pepto003_34	849	24396	25244	+	B	RBH: apr:Apr_1790 transcriptional regulator, AraC family; K13653 AraC family transcriptio
		Pepto003_35	129	25317	25445	+	C	BLAST: TP901 family tail tape measure protein (db=KEGG eval=2.0e-10 bit_score=67.8 ide
		Pepto004						
		Pepto004_1	1947	550	2496	+	D	IPRSCAN: FtsX (db=HMMPfam db_id=PF02687 from=63 to=197 eval=8.4e-09 interpo_id=I
		Pepto005						
650262199	HMPREF9286_1105 pyruvate carboxylase	Pepto005_1	3426	1032	4457	+	B	RBH: cbl:CLK_2728 pyc; pyruvate carboxylase [EC:6.4.1.1]; K01958 pyruvate carboxylase [EC:6
650262198	HMPREF9286_1104 PspC domain protein	Pepto005_2	294	4529	4822	+	C	BLAST: phage shock protein C, PspC; K03973 phage shock protein C (db=KEGG eval=2.0e-10
650262197	HMPREF9286_1103 helicase, RecD/TraA family	Pepto005_3	2184	4973	7156	+	B	RBH: aoe:Clos_2526 RecD/TraA family helicase [EC:3.1.11.5]; K03581 exodeoxyribonuclease V
650262196	HMPREF9286_1102 comF family protein	Pepto005_4	603	7137	7739	+	C	BLAST: competence protein F; K02242 competence protein ComF (db=KEGG eval=2.0e-17
650262195	HMPREF9286_1101 YihY family protein	Pepto005_5	924	7736	8659	+	C	BLAST: ribonuclease BN, putative [EC:3.1.-.-]; K07058 (db=KEGG eval=9.0e-32 bit_score=14
650262194	HMPREF9286_1100 putative alkaline phosphatase synthesis transcriptional regu	Pepto005_6	693	8743	9435	+	C	BLAST: two-component response regulator (db=KEGG eval=3.0e-73 bit_score=277.0 identit
650262193	HMPREF9286_1099 histidine kinase A domain protein	Pepto005_7	1218	9435	10652	+	C	BLAST: two-component sensor histidine kinase (db=KEGG eval=3.0e-46 bit_score=189.0 ide
650262192	HMPREF9286_1098 glutamate-ammonia ligase, catalytic domain protein	Pepto005_8	2073	10774	12846	+	B	RBH: apr:Apr_0442 glutamine synthetase catalytic region; K01915 glutamine synthetase [EC
650262191	HMPREF9286_1097 CTP synthase	Pepto005_9	1599	12855	14453	+	B	RBH: fma:FMG_0991 CTP synthetase; K01937 CTP synthase [EC:6.3.4.2] (db=KEGG)
650262190	HMPREF9286_1096 NAD(+)/NADH kinase	Pepto005_10	804	14612	15415	+	B	RBH: UniRef90_D1VV87 Probable inorganic polyphosphate/ATP-NAD kinase n=1 Tax=Peptoni
650262189	HMPREF9286_1095 pseudouridine synthase, RluA family	Pepto005_11	903	15491	16393	+	C	BLAST: pseudouridine synthase, RluA family [EC:5.4.99.-]; K06180 ribosomal large subunit pse
650262187	HMPREF9286_1093 conserved hypothetical protein	Pepto005_12	561	16696	17256	+	C	BLAST: Putative general stress protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV85
650262186	HMPREF9286_1092 conserved domain protein	Pepto005_13	495	17272	17766	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650262185	HMPREF9286_1091 lipid kinase, YegS/Rv2252/BmrU family	Pepto005_14	951	17783	18733	+	B	RBH: UniRef90_D1VV83 Diacylglycerol kinase catalytic region n=1 Tax=Peptoniphilus lacrimali
650262184	HMPREF9286_1090 putative glucose-resistance amylase regulator	Pepto005_15	1014	18744	19757	+	B	RBH: fma:FMG_1021 catabolite control protein; K02529 LacI family transcriptional regulator (
650262183	HMPREF9286_1089 transcriptional regulator, LuxR family	Pepto005_16	540	19750	20289	+	C	BLAST: LuxR family DNA-binding response regulator (db=KEGG eval=4.0e-10 bit_score=249.0 id
650262182	HMPREF9286_1088 conserved hypothetical protein	Pepto005_17	816	20341	21156	+	C	BLAST: protein of unknown function DUF1113 (db=KEGG eval=2.0e-64 bit_score=249.0 id
		Pepto005_18	117	21177	21293	+	D	IPRSCAN: DUF1706 (db=HMMPfam db_id=PF08020 from=1 to=38 eval=1.6e-08 interpo_id
		Pepto005_19	279	21423	21701	+	C	BLAST: protein of unknown function DUF1706 (db=KEGG eval=9.0e-31 bit_score=135.0 id
		Pepto006						
		Pepto006_1	363	890	1252	+	C	BLAST: hypothetical protein (db=KEGG eval=9.0e-32 bit_score=138.0 identity=55.83 cove
		Pepto006_2	1872	1252	3123	+	B	RBH: det:DET1076 hypothetical protein (db=KEGG)
		Pepto006_3	1380	3110	4489	+	B	RBH: UniRef90_C2HHY1 Putative uncharacterized protein n=1 Tax=Finnegoldia magna ATCC !
		Pepto006_4	337	4491	4827	+	C	BLAST: toxin secretion/phage lysis holin (db=KEGG eval=1.0e-24 bit_score=114.0 identity
		Pepto006_5	810	4893	5702	+	C	RBH: UniRef90_C2HHY3 Putative uncharacterized protein n=1 Tax=Finnegoldia magna ATCC !
		Pepto006_6	549	5753	6301	+	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-12 bit_score=73.9 identity=28.31 cover
		Pepto006_7	609	6882	7490	+	C	BLAST: TetR family transcriptional regulator (db=KEGG eval=1.0e-35 bit_score=152.0 ider
650261544	HMPREF9286_1770 conserved hypothetical protein							
650261543	HMPREF9286_1769 thioesterase domain protein							
650261542	HMPREF9286_1768 4'-phosphopantetheinyl transferase family protein							
650261541	HMPREF9286_1767 putative (2,3-dihydroxybenzoyl)adenylate synthase							
650261540	HMPREF9286_1766 condensation domain protein							
650261539	HMPREF9286_1765 AMP-binding enzyme							
650261538	HMPREF9286_1764 saccharopine dehydrogenase							
650261537	HMPREF9286_1763 conserved hypothetical protein							
650261536	HMPREF9286_1762 transcriptional regulator, TetR family							
650261535	HMPREF9286_1761 putative membrane protein	Pepto006_8	582	7661	8242	+	C	BLAST: hypothetical protein (db=KEGG eval=6.0e-62 bit_score=239.0 identity=75.42 covera
650261534	HMPREF9286_1760 cobalt transport protein	Pepto006_9	687	8239	8925	+	C	BLAST: ABC transporter, permease protein, putative (db=KEGG eval=5.0e-54 bit_score=214
650261533	HMPREF9286_1759 ABC transporter, ATP-binding protein	Pepto006_10	1461	8922	10382	+	B	RBH: tde:TDE1603 ABC transporter, ATP-binding protein; K02006 cobalt/nickel transport syst
650261531	HMPREF9286_1757 ABC transporter, ATP-binding protein	Pepto006_11	1716	10383	12098	+	C	BLAST: multidrug ABC transporter (db=KEGG eval=0.0 bit_score=892.0 identity=76.88 cove
650261530	HMPREF9286_1756 ABC transporter, ATP-binding protein	Pepto006_12	1737	12098	13834	+	C	BLAST: multidrug ABC transporter; K06147 ATP-binding cassette, subfamily B, bacterial (db=K
650261529	HMPREF9286_1755 conserved hypothetical protein							
650261528	HMPREF9286_1754 conserved hypothetical protein							
650261532	HMPREF9286_1758 MATE efflux family protein	Pepto006_13	1338	13847	15184	+	B	RBH: UniRef90_A8SKT1 Putative uncharacterized protein n=1 Tax=Parvimonas micra ATCC 33
		Pepto006_14	99	15205	15303	+	E	GENE: 15259..15357 + (rbs_motif=AGGAGG rbs_spacer=5-10bp)
		Pepto006_15	264	15555	15818	+	C	BLAST: putative transposase (db=KEGG eval=2.0e-19 bit_score=97.4 identity=76.36 cover
		Pepto006_16	210	16183	16392	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Finnegoldia magna ATCC 53516 RepID=C2H
		Pepto006_17	1560	16452	18011	+	C	BLAST: resolvase domain protein (db=KEGG eval=2.0e-139 bit_score=499.0 identity=53.51
		Pepto006_18	417	18004	18420	+	C	BLAST: recombinase (db=KEGG eval=3.0e-23 bit_score=110.0 identity=42.96 coverage=94
		Pepto006_19	1566	18410	19975	+	B	RBH: UniRef90_C2HHZ0 DNA recombinase n=1 Tax=Finnegoldia magna ATCC 53516 RepID=C
		Pepto006_20	945	20166	21110	+	C	BLAST: Abi family protein (db=KEGG eval=2.0e-57 bit_score=226.0 identity=42.36 covera
		Pepto006_21	312	21338	21649	+	C	BLAST: rumA1; 23S rRNA (uracil-5)-methyltransferase RumA [EC:2.1.1.-]; K00599 [EC:2.1.1.-
		Pepto006_22	156	21859	22014	+	C	BLAST: hsdM2; type I restriction-modification system methylation subunit [EC:2.1.1.-] (db=
		Pepto006_23	309	22148	22456	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-13 bit_score=77.4 identity=62.75 cover
		Pepto006_24	195	22706	22900	+	C	BLAST: hypothetical protein; K07727 putative transcriptional regulator (db=KEGG eval=4.0
		Pepto006_25	414	23059	23472	+	C	BLAST: transcriptional repressor, copy family (db=KEGG eval=1.0e-10 bit_score=68.2 ider
		Pepto006_26	1374	23453	24826	+	B	RBH: UniRef90_C2BH72 Possible peptidase M56, BlaR1 n=1 Tax=Anaerococcus lactolyticus +
		Pepto006_27	1236	24995	26230	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-08 bit_score=63.5 identity=33.0e cove
		Pepto006_28	789	26510	27298	+	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-26 bit_score=123.0 identity=44.89 cove
		Pepto006_29	201	27314	27514	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=5 to=24)
		Pepto006_30	474	27750	28223	+	C	BLAST: transposase IS200-family protein (db=KEGG eval=3.0e-70 bit_score=266.0 identity
		Pepto006_31	291	28375	28665	+	C	BLAST: hypothetical protein (db=KEGG eval=8.0e-29 bit_score=129.0 identity=90.62 cove
		Pepto006_32	1635	29000	30634	+	B	RBH: apr:Apr_1788 MobA/MobL protein (db=KEGG)
		Pepto006_33	174	30708	30881	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-24 bit_score=114.0 identity=100.0 cove
		Pepto006_34	528	31065	31592	+	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-59 bit_score=229.0 identity=95.43 cove
650261547	HMPREF9286_1773 conserved hypothetical protein	Pepto006_35	1143	31838	32980	+	B	RBH: seu:SEQ_1252 conjugative transposon single-strand binding protein (db=KEGG)
650261546	HMPREF9286_1772 relaxase/mobilization nuclease domain protein	Pepto006_36	1371	33169	34539	+	B	RBH: seu:SEQ_1250 conjugative transposon mobilization protein (db=KEGG)
650261545	HMPREF9286_1771 conserved hypothetical protein	Pepto006_37	369	34539	34907	+	C	BLAST: conjugative transposon mobilization protein (db=KEGG eval=1.0e-36 bit_score=155
		Pepto006_38	645	35399	36043	+	C	BLAST: 4'-phosphopantetheinyl transferase; K06133 4'-phosphopantetheinyl transferase [E
		Pepto006_39	465	36058	36522	+	C	BLAST: GCN5-related N-acetyltransferase (db=KEGG eval=1.0e-12 bit_score=75.5 identity
		Pepto006_40	1194	36583	37776	+	B	RBH: cbb:CLD_1974 putative seryl-tRNA synthetase (db=KEGG)
		Pepto006_41	1005	37785	38789	+	B	RBH: cbl:CLK_1970 putative 3-oxoacyl-(acyl-carrier-protein) synthase III (db=KEGG)
		Pepto006_42	1026	38801	39826	+	B	RBH: UniRef90_D0WF94 Putative uncharacterized protein n=1 Tax=Slackia exigua ATCC 700
		Pepto006_43	255	39850	40104	+	D	IPRSCAN: ACP-like (db=superfamily db_id=SSF47336 from=1 to=79 eval=1.9e-09 interpo
		Pepto006_44	1554	40097	41650	+	C	BLAST: putative acyl-CoA synthetase (db=KEGG eval=1.0e-32 bit_score=144.0 identity=28
		Pepto006_45	267	41662	41928	+	D	IPRSCAN: ACP-like (db=superfamily db_id=SSF47336 from=1 to=80 eval=6.8e-11 interpo
		Pepto006_46	612	41925	42536	+	C	RBH: UniRef90_C2BCW3 TetR family transcriptional regulator n=2 Tax=Clostridiales RepID=
		Pepto006_47	1767	42647	44413	+	C	RBH: ckl:CKL_3734 transport protein, ATPase and permease component (db=KEGG)
		Pepto006_48	1722	44413	46134	+	B	RBH: bfr:BF2112 ABC transporter ATP-binding protein; K06147 ATP-binding cassette, subfa
650262244	HMPREF9286_0286 transcriptional regulator, TetR family							
650262243	HMPREF9286_0285 putative membrane protein	Pepto006_49	591	46165	46755	+	B	RBH: UniRef90_D6GPM7 Membrane protein n=2 Tax=Clostridiales RepID=D6GPM7_9FIRM (d
650262242	HMPREF9286_0284 cobalt transport protein	Pepto006_50	729	46755	47483	+	B	RBH: UniRef90_C2BCW7 Transporter n=2 Tax=Clostridiales RepID=C2BCW7_9FIRM (db=UNIR
		Pepto006_51	1386	47480	48865	+	B	RBH: ols:Olsu_0223 ABC transporter related protein; K02006 cobalt/nickel transport system
		Pepto006_52	402	49139	49540	+	C	BLAST: DNA-binding protein (db=KEGG eval=1.0e-22 bit_score=108.0 identity=52.31 cove
		Pepto006_53	195	50012	50206	+	E	GENE: 50066..50260 + (rbs_motif=AGGAGG rbs_spacer=5-10bp)
		Pepto006_54	1626	50312	51937	+	C	RBH: UniRef90_C7HT51 TnpX site-specific recombinase n=1 Tax=Anaerococcus vaginalis ATCC
650261527	HMPREF9286_1753 resolvase, N-terminal domain protein	Pepto006_55	1629	51938	53566	+	B	RBH: UniRef90_C7HT52 Site-specific recombinase n=2 Tax=Anaerococcus RepID=C7HT52_9FI
650261526	HMPREF9286_1752 resolvase, N-terminal domain protein	Pepto006_56	1458	53585	55042	+	C	BLAST: site-specific recombinase (db=KEGG eval=1.0e-82 bit_score=310.0 identity=39.96 c
650261525	HMPREF9286_1751 resolvase, N-terminal domain protein							
		Pepto007						
		Pepto007_1	363	879	1241	+	C	BLAST: hypothetical protein (db=KEGG eval=9.0e-32 bit_score=138.0 identity=54.17 cove
		Pepto007_2	666	1348	2013	+	C	BLAST: hypothetical protein (db=KEGG eval=9.0e-65 bit_score=249.0 identity=54.81 cove
		Pepto007_3	1386	3213	4598	+	C	BLAST: hypothetical protein (db=KEGG eval=9.0e-51 bit_score=204.0 identity=32.46 cove
		Pepto007_4	411	4600	5010	+	C	BLAST: toxin secretion/phage lysis holin (db=KEGG eval=2.0e-38 bit_score=160.0 identity
		Pepto007_5	810	5000	5809	+	C	BLAST: sporulation domain-containing protein (db=KEGG eval=3.0e-55 bit_score=218.0 id
		Pepto007_6	192	5896	6087	+	C	BLAST: putative transcriptional regulator; K07729 putative transcriptional regulator (db=KE
		Pepto007_7	795	6642	7436	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=12 to=34)
		Pepto007_8	663	7433	8095	+	C	BLAST: radical SAM domain protein; K06871 (db=KEGG eval=1.0e-14 bit_score=83.2 ident
		Pepto007_9	717	8096	8812	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Collinsella intestinalis DSM 13280 RepID=

	Pepto007_10	888	8816	9703	C	BLAST: ABC transporter, ATP-binding protein; K09687 antibiotic transport system ATP-bind
	Pepto007_11	765	9693	10457	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=12 to=31)
	Pepto007_12	699	10447	11145	C	BLAST: radical SAM domain-containing protein (db=KEGG eval=1.0e-23 bit_score=113.0 i
	Pepto007_13	1299	11314	12612	C	BLAST: arylsulfatase regulator (Fe-S oxidoreductase); K06871 (db=KEGG eval=5.0e-43 bi
	Pepto007_14	1080	12629	13708	C	BLAST: ABC superfamily ATP binding cassette transporter, membrane protein n=1 Tax=Ana
	Pepto007_15	537	13705	14241	C	BLAST: hypothetical protein; K02003 (db=KEGG eval=7.0e-14 bit_score=79.7 identity=31.1
	Pepto007_16	210	14676	14885	C	BLAST: Putative uncharacterized protein n=1 Tax=Finigoldia magna ATCC 53516 RepID=C2H
	Pepto007_17	1563	14945	16507	B	RBH: cce:Ccel_2816 resolvase domain protein (db=KEGG)
	Pepto007_18	417	16500	16916	C	BLAST: recombinase (db=KEGG eval=8.0e-23 bit_score=108.0 identity=42.96 coverage=94
	Pepto007_19	1563	16909	18471	B	RBH: thx:Thet_1635 resolvase domain-containing protein (db=KEGG)
650261086 HMPREF9286_0093 response regulator receiver domain protein	Pepto007_20	663	18553	19215	B	RBH: UniRef90_C2BEN4 Possible response regulator n=3 Tax=Anaerococcus RepID=C2BEN4_5
650261085 HMPREF9286_0092 ATPase/histidine kinase/DNA gyrase B/HSP90 domain prote	Pepto007_21	978	19208	20185	B	RBH: UniRef90_B6W6F0 Sensor protein n=3 Tax=Anaerococcus RepID=B6W6F0_9FIRM (db=U
650261084 HMPREF9286_0091 ABC transporter, ATP-binding protein	Pepto007_22	690	20286	20975	B	RBH: UniRef90_C2BEN6 ABC superfamily ATP binding cassette transporter, ABC protein n=3 T
650261083 HMPREF9286_0090 efflux ABC transporter, permease protein	Pepto007_23	2496	20962	23457	B	RBH: UniRef90_C2BEN7 Putative uncharacterized protein n=1 Tax=Anaerococcus lactolytic
	Pepto007_24	423	23777	24199	C	BLAST: Putative uncharacterized protein n=1 Tax=Anaerococcus hydrogenalis DSM 7454 Rej
	Pepto007_25	300	24318	24617	C	BLAST: TrmA family tRNA (uracil-5-)-methyltransferase; K00599 [EC:2.1.1.-] (db=KEGG eval
	Pepto007_26	111	24651	24761	E	GENE: 27704..27814 - (rbs_motif=GGA/GAG/AGG rbs_spacer=5-10bp)
	Pepto007_27	3366	24877	28242	D	IPRSCAN: P-loop containing nucleoside triphosphate hydrolases (db=superfamily db_id=SSF
	Pepto007_28	258	29465	29722	C	IPRSCAN: AtrB family transcriptional regulator (db=KEGG eval=4.0e-15 bit_score=83.6 iden
	Pepto007_29	1128	29719	30846	B	RBH: tde:TDE0343 alpha/beta fold family hydrolase (db=KEGG)
	Pepto007_30	444	31251	31694	C	BLAST: putative flavodoxin (db=KEGG eval=5.0e-78 bit_score=292.0 identity=96.6 covera
	Pepto007_31	657	31970	32626	B	RBH: fma:FMG_0952 hypothetical protein (db=KEGG)
	Pepto007_32	5574	33471	39044	C	BLAST: collagen adhesin precursor (db=KEGG eval=9.0e-26 bit_score=124.0 identity=28.5
	Pepto007_33	300	40157	40456	C	BLAST: resolvase domain-containing protein (db=KEGG eval=7.0e-12 bit_score=72.8 iden
	Pepto007_34	249	40582	40830	C	BLAST: Abi-alpha protein n=1 Tax=Anaerococcus vaginalis ATCC 51170 RepID=C7HTF7_9FIRI
	Pepto007_35	369	40688	41236	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-38 bit_score=160.0 identity=75.76 cove
	Pepto007_36	201	41674	41874	C	BLAST: DNA recombinase n=1 Tax=Finigoldia magna ATCC 53516 RepID=C2HH20_PEPMA (d
	Pepto007_37	651	42124	42774	B	RBH: fma:FMG_0948 two-component response regulator (db=KEGG)
	Pepto007_38	861	42776	43636	B	RBH: fma:FMG_0947 two-component sensor histidine kinase (db=KEGG)
	Pepto007_39	681	43689	44369	B	RBH: fma:FMG_0946 ABC transporter ATP-binding protein; K02003 (db=KEGG)
	Pepto007_40	2436	44362	46797	B	RBH: apr:Apr_0744 protein of unknown function DUF214 (db=KEGG)
650261082 HMPREF9286_0089 conserved hypothetical protein	Pepto007_41	258	46820	47077	C	BLAST: hypothetical protein (db=KEGG eval=9.0e-09 bit_score=62.4 identity=80.0 coverage
	Pepto007_42	330	47602	47931	C	BLAST: hypothetical protein (db=KEGG eval=9.0e-39 bit_score=164.0 identity=76.24 cove
	Pepto007_43	189	48658	48846	D	IPRSCAN: seg (db=Seg db_id=seg from=1 to=15)
	Pepto007_44	696	48870	49565	B	RBH: cbl:CLK_0108 ABC transporter, ATP-binding protein (db=KEGG)
	Pepto007_45	1812	49549	51360	B	RBH: cby:CLM_0928 ABC transporter, permease protein (db=KEGG)
	Pepto007_46	591	51715	52305	C	BLAST: tetR family transcriptional regulator (db=KEGG eval=1.0e-75 bit_score=285.0 iden
	Pepto007_47	129	52334	52462	E	GENE: 3..131 - (rbs_motif=None rbs_spacer=None)
	Pepto008					
650261281 HMPREF9286_1447 ABC transporter, ATP-binding protein	Pepto008_1	1746	468	2213	B	RBH: fma:FMG_0248 multidrug ABC transporter (db=KEGG)
650261282 HMPREF9286_1448 integral membrane protein MvIN	Pepto008_2	1602	2362	3963	B	RBH: UniRef90_D1VTZ3 Integral membrane protein MvIN n=1 Tax=Peptoniphilus lacrimalis 31
650261283 HMPREF9286_1449 conserved hypothetical protein	Pepto008_3	813	4085	4897	D	IPRSCAN: seg (db=Seg db_id=seg from=2 to=16)
650261284 HMPREF9286_1450 HD domain protein	Pepto008_4	471	5024	5494	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-41 bit_score=171.0 identity=50.66 covera
650261285 HMPREF9286_1451 conserved hypothetical protein	Pepto008_5	702	5491	6192	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-32 bit_score=142.0 identity=30.97 cove
	Pepto008_6	1764	6234	7997	C	BLAST: antibiotic ABC transporter ATP-binding protein (db=KEGG eval=5.0e-66 bit_score
	Pepto008_7	1785	8020	9804	C	BLAST: ABC transporter related (db=KEGG eval=3.0e-71 bit_score=273.0 identity=30.23 ci
	Pepto008_8	1734	9917	11650	B	RBH: UniRef90_D1VTY5 Pyruvate kinase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT
650261287 HMPREF9286_1453 6-phosphofructokinase	Pepto008_9	954	11659	12612	B	RBH: fma:FMG_1002 6-phosphofructokinase; K00850 6-phosphofructokinase [EC:2.7.1.11] (d
650261288 HMPREF9286_1454 DNA polymerase III, alpha subunit	Pepto008_10	3429	12628	16056	B	RBH: aoe:Clos_0583 dnaE; DNA polymerase III DnaE [EC:2.7.7.7]; K02337 DNA polymerase III :
650261289 HMPREF9286_1455 HPr-like protein crh	Pepto008_11	267	16229	16495	C	BLAST: phosphocarrier protein Chr; K11184 catabolite repression HPr-like protein (db=KEGG e
650261290 HMPREF9286_1456 conserved hypothetical protein	Pepto008_12	936	16497	17432	B	RBH: UniRef90_D1VTY1 YvcL n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VTY1_9FIRM (d
650261291 HMPREF9286_1457 putative foldase protein PrsA	Pepto008_13	1083	17641	18723	B	RBH: UniRef90_D1VSM7 Foldase protein PrsA n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=
650261292 HMPREF9286_1458 transcription-repair coupling factor	Pepto008_14	3480	18773	22252	B	RBH: tte:TTE2565 mfd; transcription-repair coupling factor; K03723 transcription-repair coupl
650261293 HMPREF9286_1459 aminoacyl-tRNA hydrolase	Pepto008_15	570	22261	22830	C	BLAST: peptidyl-tRNA hydrolase; K01056 peptidyl-tRNA hydrolase, PTH1 family [EC:3.1.1.29] (
650261294 HMPREF9286_1460 ribose-phosphate diphosphokinase	Pepto008_16	951	22840	23790	B	RBH: aoe:Clos_2645 ribose-phosphate pyrophosphokinase [EC:2.7.6.1]; K00948 ribose-phosph
650261295 HMPREF9286_1461 UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-γ	Pepto008_17	1380	23800	25179	B	RBH: UniRef90_D1VSM3 Bifunctional protein glmU n=1 Tax=Peptoniphilus lacrimalis 315-B Re
650261296 HMPREF9286_1462 cysteine synthase A	Pepto008_18	891	25662	26552	C	RBH: UniRef90_C2HF35 Cysteine synthase n=1 Tax=Finigoldia magna ATCC 53516 RepID=C2H
650261297 HMPREF9286_1463 putative serine O-acetyltransferase	Pepto008_19	552	26545	27096	C	BLAST: serine O-acetyltransferase; K00640 serine O-acetyltransferase [EC:2.3.1.30] (db=KEGG e
	Pepto008_20	831	27116	27946	B	RBH: cbt:CLH_0676 AP endonuclease, family 2; K01151 deoxyribonuclease IV [EC:3.1.21.2] {
	Pepto008_21	1131	28146	29276	C	BLAST: hypothetical protein; K07085 (db=KEGG eval=1.0e-23 bit_score=114.0 identity=33
	Pepto008_22	1161	29386	30546	C	BLAST: 8-amino-7-oxononanoate synthase; K00652 8-amino-7-oxononanoate synthase [EC:
	Pepto008_23	714	30539	31252	C	BLAST: 6-carboxyhexanoate-CoA ligase [EC:6.2.1.14]; K01906 6-carboxyhexanoate-CoA lig
	Pepto008_24	483	31249	31731	C	BLAST: rplI; S05 ribosomal protein L7/L12; K02935 large subunit ribosomal protein L7/L12 (d
650261298 HMPREF9286_1464 ribosomal protein L7/L12	Pepto008_25	384	31825	32208	C	BLAST: rplI; S05 ribosomal protein L7/L12; K02935 large subunit ribosomal protein L7/L12 (d
650261299 HMPREF9286_1465 ribosomal protein L10	Pepto008_26	591	32234	32844	C	BLAST: ribosomal protein L10; K02864 large subunit ribosomal protein L10 (db=KEGG eval=
650261300 HMPREF9286_1467 conserved hypothetical protein						
	Pepto008_27	555	33161	33715	C	BLAST: proton-coupled thiamine transporter YuaJ (db=KEGG eval=4.0e-51 bit_score=203.
650261301 HMPREF9286_1468 ribosomal protein L1	Pepto008_28	702	33805	34506	B	RBH: UniRef90_D1VTJ9 S05 ribosomal protein L1 n=1 Tax=Peptoniphilus lacrimalis 315-B Repl
650261302 HMPREF9286_1469 ribosomal protein L11	Pepto008_29	468	34543	35013	C	BLAST: S05 ribosomal protein L11; K02867 large subunit ribosomal protein L11 (db=KEGG eva
650261303 HMPREF9286_1470 transcription termination/antitermination factor NusG	Pepto008_30	543	35019	35561	C	BLAST: NusG antitermination factor; K02601 transcriptional antiterminator NusG (db=KEGG e
650261304 HMPREF9286_1471 preprotein translocase, SecE subunit	Pepto008_31	216	35576	35791	D	IPRSCAN: SecE (db=HMM Pfam db_id=PF00584 from=17 to=71 eval=4.2e-17 interpo_id=IP
	Pepto008_32	186	35801	35986	C	BLAST: ribosomal protein L33; K02913 large subunit ribosomal protein L33 (db=KEGG eval
650261305 HMPREF9286_1472 CAAX amino terminal protease family protein	Pepto008_33	882	36146	37027	D	IPRSCAN: Abi (db=HMM Pfam db_id=PF02517 from=120 to=201 eval=2.2e-08 interpo_id=II
650261306 HMPREF9286_1473 DEAD2 domain protein	Pepto008_34	2298	37060	39357	B	RBH: fma:FMG_1294 ATP dependent helicase (db=KEGG)
650261307 HMPREF9286_1474 RNA methyltransferase, TrmH family, group 2	Pepto008_35	465	39407	39871	C	BLAST: RNA methyltransferase, TrmH family, group 2; K03216 RNA methyltransferase, TrmH f
650261308 HMPREF9286_1475 pyridine nucleotide-disulfide oxidoreductase	Pepto008_36	1557	39865	41421	B	RBH: apr:Apr_1079 FAD dependent oxidoreductase; K07137 (db=KEGG)
	Pepto008_37	519	41515	42033	C	BLAST: signal peptidase I; K03100 signal peptidase I [EC:3.4.21.89] (db=KEGG eval=4.0e-2
	Pepto008_38	240	42039	42278	D	IPRSCAN: seg (db=Seg db_id=seg from=6 to=17)
650261309 HMPREF9286_1476 ATPase/histidine kinase/DNA gyrase B/HSP90 domain prote	Pepto008_39	1155	42455	43609	C	BLAST: histidine kinase (db=KEGG eval=5.0e-50 bit_score=201.0 identity=35.99 coverage=9
650261310 HMPREF9286_1477 response regulator receiver domain protein	Pepto008_40	666	43606	44271	C	BLAST: transcriptional activator protein (db=KEGG eval=1.0e-73 bit_score=278.0 identity=6
650261311 HMPREF9286_1478 dihydrofolate reductase	Pepto008_41	477	44268	44744	C	BLAST: folA; dihydrofolate reductase type III; K00287 dihydrofolate reductase [EC:1.5.1.3] (d
	Pepto008_42	729	45119	45847	C	BLAST: hypothetical protein CLOSPO_03515 n=1 Tax=Clostridium sporogenes ATCC 15579 R
650262265 HMPREF9286_0307 conserved domain protein	Pepto008_43	942	46516	47457	B	RBH: UniRef90_D1VR29 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 31
650262266 HMPREF9286_0308 methionine adenosyltransferase	Pepto008_44	1173	47578	48750	B	RBH: tva:TVAG_243700 methionine adenosyltransferase (db=KEGG)
650262267 HMPREF9286_0310 transporter, auxin efflux carrier (AEC) family protein	Pepto008_45	954	49076	50029	B	RBH: tva:TVAG_243690 Auxin Efflux Carrier family protein; K07088 (db=KEGG)
650262268 HMPREF9286_0311 conserved hypothetical protein	Pepto008_46	909	50116	51024	B	RBH: tva:TVAG_243680 hypothetical protein (db=KEGG)
650262269 HMPREF9286_0312 hydrid cluster protein-associated redox disulfide domain pr	Pepto008_47	231	51036	51266	C	BLAST: hypothetical protein (db=KEGG eval=9.0e-28 bit_score=125.0 identity=88.41 covera
650262270 HMPREF9286_0313 peptidase propeptide and YPEB domain protein	Pepto008_48	2010	51327	53336	C	BLAST: S-layer domain protein (db=KEGG eval=6.0e-09 bit_score=68.2 identity=30.67 cover
650262271 HMPREF9286_0314 conserved hypothetical protein						
650262272 HMPREF9286_0315 polysaccharide deacetylase	Pepto008_49	1005	53393	54397	B	RBH: tva:TVAG_243660 Polysaccharide deacetylase family protein (db=KEGG)
650262273 HMPREF9286_0316 conserved hypothetical protein						
650261313 HMPREF9286_1480 glyoxalase family protein						
650261314 HMPREF9286_1481 glutamate dehydrogenase, NAD-specific	Pepto008_50	1266	54681	55946	B	RBH: cby:CLM_1968 gluD; glutamate dehydrogenase, NAD-specific [EC:1.4.1.2]; K00260 gluta
650261315 HMPREF9286_1482 putative membrane protein	Pepto008_51	885	56346	57230	C	BLAST: hypothetical protein (db=KEGG eval=7.0e-36 bit_score=154.0 identity=38.36 covera
650261316 HMPREF9286_1483 CAAX amino terminal protease family protein	Pepto008_52	720	57276	57995	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-08 bit_score=62.4 identity=30.72 coverag
650261317 HMPREF9286_1484 5-formyltetrahydrofolate cyclo-ligase	Pepto008_53	543	57967	58509	C	BLAST: 5-formyltetrahydrofolate cyclo-ligase; K01934 5-formyltetrahydrofolate cyclo-ligase [E
650261318 HMPREF9286_1485 conserved hypothetical protein	Pepto008_54	2592	58511	61102	C	BLAST: ATP-dependent nucleic acid subunit B-like protein (db=KEGG eval=2.0e-12 bit_score=7
650261319 HMPREF9286_1486 putative rRNA pseudouridylation synthase C	Pepto008_55	990	61083	62072	B	RBH: UniRef90_D1VR23 Pseudouridylation synthase n=1 Tax=Peptoniphilus lacrimalis 315-B Repl
650261320 HMPREF9286_1487 conserved hypothetical protein	Pepto008_56	726	62147	62872	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VR
650261321 HMPREF9286_1488 Creatinase						
650260649 HMPREF9286_0480 iron-only hydrogenase maturation rSAM protein HydG	Pepto008_57	1176	62896	64071	B	RBH: elm:ELI_3378 hypothetical protein (db=KEGG)
650260650 HMPREF9286_0481 iron-only hydrogenase maturation rSAM protein HydE	Pepto008_58	1440	64071	65510	B	RBH: cpy:Cphy_2082 thiH; thiamine biosynthesis protein ThiH; K03150 thiamine biosynthes
	Pepto008_59	1041	65507	66547	B	RBH: cth:Cthe_1839 biotin synthase [EC:2.8.1.6]; K01012 biotin synthetase [EC:2.8.1.6] (db=K

650260651	HMPREF9286_0482	MATE efflux family protein	Pepto008_60	1356	66763	68118	+ B	RBH: csh:Closa_2499 MATE efflux family protein (db=KEGG)
650260652	HMPREF9286_0483	thioredoxin-disulfide reductase	Pepto008_61	954	68197	69150	+ B	RBH: aoe:Clos_0954 thioredoxin reductase; K00384 thioredoxin reductase (NADPH) [EC:1.8.1.1]
650260653	HMPREF9286_0484	conserved hypothetical protein	Pepto008_62	813	69294	70106	+ D	IPRSCAN: DUF2207 (db=HMMPfam db_id=PF09972 from=36 to=206 eval=2.7e-11 interpro, BLAST: hypothetical protein (db=KEGG eval=7.0e-21 bit_score=102.0 identity=42.42 covera
650260654	HMPREF9286_0485	conserved hypothetical protein	Pepto008_63	522	70176	70697	+ C	RBH: UniRef90_D1VSU6 isopentenyl-diphosphate delta-isomerase, type 2 n=1 Tax=Peptoniph
650260655	HMPREF9286_0486	isopentenyl-diphosphate delta-isomerase, type 2	Pepto008_64	1017	70698	71714	+ B	RBH: UniRef90_D1VSU5 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 31
650260656	HMPREF9286_0487	conserved hypothetical protein	Pepto008_65	969	71762	72730	+ B	RBH: UniRef90_D1VSU4 UPF0042 nucleotide-binding protein HMPREF0628_1009 n=1 Tax=Pe
650260657	HMPREF9286_0488	conserved hypothetical protein	Pepto008_66	867	72715	73581	+ B	RBH: UniRef90_D1VSU3 UDP-N-acetylenolpyruvoylglucosamine reductase n=1 Tax=Peptonip
650260658	HMPREF9286_0489	UDP-N-acetylmuramate dehydrogenase	Pepto008_67	903	73600	74502	+ D	IPRSCAN: seg (db=Seg db_id=seg from=5 to=21)
650260672	HMPREF9286_0503	ferritin-like protein	Pepto008_68	678	74964	75641	+ D	IPRSCAN: PROKAR_LIPOPROTEIN (db=ProfileScan db_id=PS51257 from=1 to=25 eval=5.0)
650260673	HMPREF9286_0504	conserved domain protein	Pepto008_69	477	75722	77160	+ C	BLAST: ferritin Dps family protein; K02217 ferritin [EC:1.16.3.1] (db=KEGG eval=3.0e-36 bit
650260674	HMPREF9286_0505	PSP1 C-terminal domain protein	Pepto008_70	483	76678	79085	+ B	RBH: tva:TVAG_208700 hypothetical protein (db=KEGG)
650260675	HMPREF9286_0506	conserved domain protein	Pepto008_71	1830	77256	80280	+ B	RBH: tva:TVAG_208710 signal peptidase-like protein (db=KEGG)
650260676	HMPREF9286_0507	conserved hypothetical protein	Pepto008_72	894	79387	81214	+ C	BLAST: DNA polymerase III, delta prime subunit (EC:2.7.7.7); K02341 DNA polymerase III subu
650260677	HMPREF9286_0508	conserved hypothetical protein	Pepto008_73	933	80282	81504	+ C	BLAST: protein of unknown function DUF970 (db=KEGG eval=1.0e-13 bit_score=79.0 identi
650260678	HMPREF9286_0509	dTMP kinase	Pepto008_74	291	81214	81839	+ C	BLAST: hypothetical protein (db=KEGG eval=2.0e-22 bit_score=107.0 identity=48.62 covera
650260679	HMPREF9286_0510	Orn/Lys/Arg decarboxylase, major domain protein	Pepto008_75	327	81513	82444	+ B	RBH: tva:TVAG_134830 thymidylate kinase family protein; K00943 dTMP kinase [EC:2.7.4.9] (i
650260680	HMPREF9286_0511	biotin-[acetyl-CoA-carboxylase] ligase	Pepto008_76	609	81836	83793	+ B	RBH: UniRef90_D1VST6 Arginine/lysine/ornithine decarboxylase n=1 Tax=Peptoniphilus lacrim
650260683	HMPREF9286_0514	conserved hypothetical protein	Pepto008_77	1353	82441	84835	+ B	RBH: UniRef90_D1VV73 Biotin-[Acetyl-CoA-carboxylase] ligase n=1 Tax=Peptoniphilus lacrima
650260684	HMPREF9286_0515	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	Pepto008_78	981	83855	85996	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650260664	HMPREF9286_0495	conserved hypothetical protein	Pepto008_79	744	85253	86828	+ C	BLAST: 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [EC:2.7.1.148]; K00919 4-diphosph
650260665	HMPREF9286_0496	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Pepto008_81	267	87051	87317	+ C	BLAST: veg; veg (db=KEGG eval=4.0e-14 bit_score=80.1 identity=48.75 coverage=87.64044)
650260666	HMPREF9286_0497	ribosomal protein L25, Ctc-form	Pepto008_82	1062	87608	88669	+ B	RBH: UniRef90_D1VRR9 tRNA-specific 2-thiouridylase mmmA n=1 Tax=Peptoniphilus lacrima
650260667	HMPREF9286_0498	haloacid dehalogenase-like hydrolase	Pepto008_83	639	88692	89330	+ C	BLAST: 50S ribosomal protein L25; K02897 large subunit ribosomal protein L25 (db=KEGG eva
650261917	HMPREF9286_0188	SsrA-binding protein	Pepto008_84	681	89383	90063	+ C	BLAST: phosphoglycolate phosphatase (EC:3.1.3.18); K01091 phosphoglycolate phosphatase [
650261918	HMPREF9286_0189	ribonuclease R	Pepto008_85	1335	90041	91375	+ C	BLAST: hypothetical protein (db=KEGG eval=2.0e-36 bit_score=157.0 identity=34.17 cove
650261919	HMPREF9286_0190	D-ala D-ala ligase R N-terminal domain protein	Pepto008_86	1308	91436	92743	+ B	RBH: cbk:CLL_A3192 putative glycerol-3-phosphate ABC transporter, glycerol-3-phosphate-l
650261920	HMPREF9286_0191	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase	Pepto008_87	822	92785	93606	+ B	RBH: UniRef90_C2HG00 ABC superfamily ATP binding cassette transporter, membrane prot
650261921	HMPREF9286_0192	hydrolase, alpha/beta domain protein	Pepto008_88	894	93603	94496	+ B	RBH: UniRef90_C2HGC9 ABC superfamily ATP binding cassette transporter, membrane prot
650261922	HMPREF9286_0193	conserved hypothetical protein	Pepto008_89	1077	94486	95562	+ C	BLAST: msmX; sugar ABC transporter ATPase; K10112 maltose/maltodextrin transport syste
650261923	HMPREF9286_0194	glutaredoxin	Pepto008_90	456	96196	96651	+ C	BLAST: smpB; SsrA-binding protein; K03664 SsrA-binding protein (db=KEGG eval=9.0e-48 bi
650260668	HMPREF9286_0499	adenosylmethionine-8-amino-7-oxononanoate transaminase	Pepto008_91	2103	96644	98746	+ B	RBH: UniRef90_D1VT23 Ribonuclease R n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT2
650260669	HMPREF9286_0500	dethiobiotin synthase	Pepto008_92	1173	98746	99818	+ B	RBH: tte:TTE2545 dIdA2; D-alanine-D-alanine ligase and related ATP-grasp enzyme; K01921 D
650260670	HMPREF9286_0501	BioY family protein	Pepto008_93	1554	99924	101477	+ B	RBH: tte:TTE2546 murF; UDP-N-acetylmuramyl pentapeptide synthase; K01929 UDP-N-acetyl
650260671	HMPREF9286_0502	transcriptional regulator, MerR family	Pepto008_94	771	101487	102257	+ B	RBH: UniRef90_D1VT20 Alpha/beta superfamily hydrolase/acetyltransferase n=1 Tax=Peptonip
650260685	HMPREF9286_0516	putative membrane protein	Pepto008_95	432	102244	102675	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT
650260686	HMPREF9286_0517	ABC transporter, ATP-binding protein	Pepto008_96	240	102782	103021	+ C	BLAST: glutaredoxin (db=KEGG eval=1.0e-18 bit_score=95.1 identity=61.64 coverage=88.75
650260687	HMPREF9286_0518	transcriptional regulator, GntR family	Pepto008_97	1200	103526	104725	+ B	RBH: tva:TVAG_258770 adenosylmethionine-8-amino-7-oxononanoate aminotransferase fam
650260670	HMPREF9286_0501	BioY family protein	Pepto008_98	684	104734	105417	+ B	RBH: UniRef90_D1VTK1 Dethiobiotin biosynthe n=1 Tax=Peptoniphilus lacrimalis 315-B Rep
650260671	HMPREF9286_0502	transcriptional regulator, MerR family	Pepto008_99	555	105434	105988	+ C	BLAST: BioY protein; K03523 putative biotin biosynthesis protein BioY (db=KEGG eval=2.0e-
650261334	HMPREF9286_1500	aminotransferase, class V	Pepto008_100	768	106142	106909	+ D	IPRSCAN: seg (db=Seg db_id=seg from=152 to=169)
650261335	HMPREF9286_1501	conserved hypothetical protein	Pepto008_101	687	106909	107595	+ C	BLAST: ABC transporter related; K01990 ABC-2 type transport system ATP-binding protein (db
650261336	HMPREF9286_1504	Fic family protein	Pepto008_102	360	107592	107951	+ C	BLAST: transcriptional regulator, GntR family (db=KEGG eval=2.0e-38 bit_score=160.0 identi
650261337	HMPREF9286_1505	valine--tRNA ligase	Pepto008_103	1125	108162	109286	+ B	RBH: lla:L86881 yeiG; YeiG; K00839 aminotransferase [EC:2.6.1.1] (db=KEGG)
650261338	HMPREF9286_1506	L-lactate dehydrogenase	Pepto008_104	606	109380	109985	+ C	BLAST: hypothetical protein (db=KEGG eval=5.0e-43 bit_score=177.0 identity=49.75 covera
650261339	HMPREF9286_1507	conserved domain protein	Pepto008_105	1377	110231	111607	+ B	RBH: UniRef90_D1VRS2 Putative Erk family protein n=1 Tax=Peptoniphilus lacrimalis 315-B R
650261340	HMPREF9286_1508	amidohydrolase	Pepto008_106	402	112137	112538	+ C	BLAST: hypothetical protein (db=KEGG eval=3.0e-23 bit_score=110.0 identity=43.08 covera
650261341	HMPREF9286_1509	C4-dicarboxylate anaerobic carrier	Pepto008_107	1164	112633	113796	+ B	RBH: ctc:CTC02464 amidohydrolase [EC:3.5.1.1]; K01463 [EC:3.5.1.1] (db=KEGG)
650261342	HMPREF9286_1510	LysR substrate binding domain protein	Pepto008_108	1398	113806	115203	+ B	RBH: afn:ArfR_1810 C4-dicarboxylate anaerobic carrier-like protein (db=KEGG)
650261343	HMPREF9286_1511	conserved hypothetical protein	Pepto008_109	900	115386	116285	+ C	BLAST: LysR family transcriptional regulator (db=KEGG eval=5.0e-21 bit_score=105.0 identi
650261344	HMPREF9286_1512	conserved hypothetical protein	Pepto008_110	1176	116747	117922	+ C	BLAST: hypothetical protein (db=KEGG eval=6.0e-18 bit_score=95.5 identity=40.91 coverag
650261345	HMPREF9286_1513	conserved hypothetical protein	Pepto008_111	840	118004	118843	+ C	BLAST: hypothetical protein (db=KEGG eval=1.0e-29 bit_score=133.0 identity=36.79 cove
650261346	HMPREF9286_1514	bifunctional protein FolC	Pepto008_112	1296	118879	120174	+ B	RBH: UniRef90_D1VVT1 Bifunctional protein FolC n=1 Tax=Peptoniphilus lacrimalis 315-B Rep
650261347	HMPREF9286_1515	valine--tRNA ligase	Pepto008_113	2652	120171	122822	+ B	RBH: fma:FMG_0807 valyl-tRNA synthetase; K01873 valyl-tRNA synthetase [EC:6.1.1.9] (db=K
650261348	HMPREF9286_1517	tryptophan--tRNA ligase	Pepto008_114	345	123100	123444	+ D	IPRSCAN: seg (db=Seg db_id=seg from=62 to=78)
650261349	HMPREF9286_1518	CAAX amino terminal protease family protein	Pepto008_115	993	123389	124381	+ B	RBH: cst:CLOST_1872 trpS; tryptophanyl-tRNA synthetase [EC:6.1.1.2]; K01867 tryptophanyl-t
650261350	HMPREF9286_1519	amidohydrolase family protein	Pepto008_116	1284	124386	125669	+ B	RBH: tit:Thit_1438 amidohydrolase (db=KEGG)
650261351	HMPREF9286_1520	putative membrane protein	Pepto008_117	657	125767	126423	+ C	BLAST: protein of unknown function UPF0126 (db=KEGG eval=2.0e-30 bit_score=135.0 ider
650261352	HMPREF9286_1521	conserved hypothetical protein	Pepto008_118	315	126425	126739	+ C	BLAST: protein of unknown function DUF77 (db=KEGG eval=3.0e-25 bit_score=117.0 identi
650261353	HMPREF9286_1522	peptidase family T4	Pepto008_119	963	126816	127778	+ B	RBH: tte:TTE1796 dmpA2; L-aminopeptidase/D-esterase (db=KEGG)
650261354	HMPREF9286_1523	putative membrane protein	Pepto008_120	756	127822	128577	+ B	RBH: apr:Apr_0579 hypothetical protein (db=KEGG)
650261355	HMPREF9286_1524	putative pantothene kinase, type III	Pepto008_121	783	128579	129361	+ C	BLAST: putative transcriptional activator, Baf family (db=KEGG eval=4.0e-56 bit_score=221.
650261356	HMPREF9286_1525	glutamate racemase	Pepto008_122	867	129371	130237	+ C	BLAST: glutamate racemase [EC:5.1.1.3]; K01776 glutamate racemase [EC:5.1.1.3] (db=KEGG
650262106	HMPREF9286_0784	transcriptional regulator, GntR family	Pepto008_123	669	130545	131213	+ C	BLAST: gntR; transcriptional regulator (db=KEGG eval=1.0e-27 bit_score=126.0 identity=35.
650262107	HMPREF9286_0785	putative lipoprotein	Pepto008_124	687	131372	132058	+ D	IPRSCAN: PepSY (db=HMMPfam db_id=PF03413 from=91 to=147 eval=4.4e-05 interpro_id:
650262108	HMPREF9286_0786	conserved hypothetical protein						
650262109	HMPREF9286_0787	conserved hypothetical protein						
650262110	HMPREF9286_0788	putative membrane protein						
650262111	HMPREF9286_0789	putative o-succinylbenzoate synthase						
650262113	HMPREF9286_0791	GMP synthase (glutamine-hydrolyzing), C-terminal domain protein						
650262112	HMPREF9286_0790	preprotein translocase, SecA subunit						
650262114	HMPREF9286_0792	conserved hypothetical protein						
650262115	HMPREF9286_0793	conserved hypothetical protein						
650262116	HMPREF9286_0794	conserved hypothetical protein						
650262117	HMPREF9286_0795	conserved hypothetical protein						
650262118	HMPREF9286_0796	copper transport repressor, CopY/TcrY family						
650262119	HMPREF9286_0797	copper-exporting ATPase						
650262120	HMPREF9286_0798	conserved hypothetical protein						
650262121	HMPREF9286_0799	conserved hypothetical protein						
650262122	HMPREF9286_0800	transcriptional regulator, MarR family						
650262123	HMPREF9286_0801	conserved hypothetical protein						
650262124	HMPREF9286_0802	E1-E2 ATPase						
650262125	HMPREF9286_0803	magnesium-transporting ATPase, P-type 1 domain protein						
650262126	HMPREF9286_0804	aspartate kinase	Pepto008_125	411	132252	132662	+ C	BLAST: flavodoxin (db=KEGG eval=1.0e-35 bit_score=151.0 identity=51.85 coverage=97.0
650262127	HMPREF9286_0805	aspartate-semialdehyde dehydrogenase	Pepto008_126	1134	132678	133811	+ B	RBH: fsu:Fisuc_2457 cation diffusion facilitator family transporter (db=KEGG)
650262128	HMPREF9286_0806	homoserine dehydrogenase	Pepto008_127	1323	134047	135369	+ B	RBH: fma:FMG_0317 aspartate kinase; K00928 aspartate kinase [EC:2.7.2.4] (db=KEGG)
650262129	HMPREF9286_0807	homoserine kinase	Pepto008_128	978	135359	136336	+ B	RBH: fma:FMG_0318 aspartate-semialdehyde dehydrogenase; K00133 aspartate-semialdehy
650262130	HMPREF9286_0808	aldehyde dehydrogenase (NAD) family protein	Pepto008_129	1182	136338	137519	+ B	RBH: fma:FMG_0319 homoserine dehydrogenase; K00003 homoserine dehydrogenase [EC:1.
650262131	HMPREF9286_0809	ethanolamine utilization protein EutJ	Pepto008_130	2295	137516	139810	+ B	RBH: fma:FMG_0320 threonine synthase; K01733 threonine synthase [EC:4.2.3.1] (db=KEGG)
650262132	HMPREF9286_0810	propanediol utilization protein PduL						
650262133	HMPREF9286_0811	putative membrane protein						
650262134	HMPREF9286_0812	methionine adenosyltransferase						
650262135	HMPREF9286_0813	transcriptional regulator, AraC family						
650262136	HMPREF9286_0814	conserved hypothetical protein						
650262137	HMPREF9286_0815	putative NADPH-dependent butanol dehydrogenase						

650262138	HMPREF9286_0816 aldehyde dehydrogenase (NAD) family protein				
650262139	HMPREF9286_0817 carbon dioxide concentrating mechanism protein CcmL				
650262140	HMPREF9286_0818 BMC domain protein				
650262141	HMPREF9286_0819 conserved hypothetical protein				
650262142	HMPREF9286_0820 major carboxysome shell protein 1A				
650262143	HMPREF9286_0821 propanediol utilization protein PduB				
650262144	HMPREF9286_0822 putative pyruvate formate-lyase 1-activating enzyme				
650262145	HMPREF9286_0823 formate C-acetyltransferase				
650262146	HMPREF9286_0824 BMC domain protein				
650262147	HMPREF9286_0825 tetratricopeptide repeat protein				
650262148	HMPREF9286_0826 conserved hypothetical protein				
650262149	HMPREF9286_0827 conserved hypothetical protein	Pepto008_131	507	139909	140415 + C BLAST: hypothetical protein (db=KEGG eval=2.0e-28 bit_score=127.0 identity=45.58 covera
650262150	HMPREF9286_0828 Fic family protein				
650262151	HMPREF9286_0829 chaperonin HsIc	Pepto008_132	924	140472	141395 + B RBH: UniRef90_D1VWV8 33 kDa chaperonin n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D
650262152	HMPREF9286_0830 methyltransferase domain protein	Pepto008_133	726	141559	142284 + C BLAST: methyltransferase type 11 (db=KEGG eval=7.0e-38 bit_score=160.0 identity=33.74 c
650262153	HMPREF9286_0831 putative NAD-dependent deacetylase	Pepto008_134	738	142281	143018 + B RBH: UniRef90_D1VWV6 NAD-dependent deacetylase 2 n=1 Tax=Peptoniphilus lacrimalis 315
650262154	HMPREF9286_0832 CAAX amino terminal protease family protein	Pepto008_135	915	143028	143942 + C BLAST: abortive infection protein; K07052 (db=KEGG eval=6.0e-15 bit_score=85.1 identit
650262155	HMPREF9286_0833 hypoxanthine phosphoribosyltransferase				
650262156	HMPREF9286_0834 conserved hypothetical protein	Pepto008_136	516	144072	144587 + C BLAST: hypothetical protein (db=KEGG eval=7.0e-17 bit_score=89.4 identity=31.71 coverag
650262157	HMPREF9286_0835 heavy metal translocating P-type ATPase				
650262158	HMPREF9286_0836 conserved hypothetical protein				
650261691	HMPREF9286_1299 CAAX amino terminal protease family protein				
650261692	HMPREF9286_1300 sodium/glutamate symporter				
650261693	HMPREF9286_1301 glutamate 5-semialdehyde dehydrogenase	Pepto008_137	1257	144623	145879 + B RBH: UniRef90_D1VRN9 Gamma-glutamyl phosphate reductase n=1 Tax=Peptoniphilus lacrim
650261694	HMPREF9286_1302 glutamate 5-kinase	Pepto008_138	783	145857	146639 + B RBH: UniRef90_D1VRN8 Glutamate 5-kinase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D
650261695	HMPREF9286_1303 glutamate synthase (NADPH), homotetrameric	Pepto008_139	2322	146798	149119 + B RBH: clj:CLJU_c37240 glutamate synthase (EC:1.4.1.13); K00266 glutamate synthase (NADPH/
650261730	HMPREF9286_0886 conserved hypothetical protein	Pepto008_140	1353	149460	150812 + B RBH: ccb:ClcJ_2608 hypothetical protein; K03699 putative hemolysin (db=KEGG)
650261731	HMPREF9286_0887 conserved hypothetical protein	Pepto008_141	621	150965	151585 + C BLAST: hypothetical protein (db=KEGG eval=1.0e-38 bit_score=162.0 identity=54.32 covera
650261732	HMPREF9286_0888 enoyl-CoA hydratase/isomerase family protein	Pepto008_142	1116	151774	152889 + B RBH: apr:Apr_1099 enoyl-CoA hydratase/isomerase; K01692 enoyl-CoA hydratase [EC:4.2.1.
		Pepto008_143	471	152940	153410 + C BLAST: nitroimidazole resistance protein, putative; K07005 (db=KEGG eval=8.0e-33 bit_sc
650261733	HMPREF9286_0889 conserved domain protein	Pepto008_144	627	153506	154132 + C BLAST: hypothetical protein (db=KEGG eval=2.0e-33 bit_score=145.0 identity=36.36 covera
650261734	HMPREF9286_0890 putative membrane protein	Pepto008_145	900	154216	155115 + B RBH: UniRef90_D1VU00 Permease n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU00_9i
		Pepto008_146	585	155584	156168 + D IPSCAN: PR-1-like (db=superfamily db_id=SSF55797 from=59 to=187 eval=2.3e-06 inter
650261735	HMPREF9286_0891 cytosol aminopeptidase family, catalytic domain protein	Pepto008_147	1428	156324	157751 + B RBH: smf:Smon_1500 leucyl aminopeptidase (EC:3.4.11.1); K01255 leucyl aminopeptidase [EC
650261548	HMPREF9286_1774 helicase C-terminal domain protein				
650261549	HMPREF9286_1775 conserved hypothetical protein				
650261550	HMPREF9286_1776 conserved hypothetical protein				
650261551	HMPREF9286_1777 conserved hypothetical protein				
650261552	HMPREF9286_1778 DNA topoisomerase	Pepto008_148	264	157874	158137 + C BLAST: putative DNA topoisomerase; K03169 DNA topoisomerase III [EC:5.99.1.2] (db=KEGG e
650261553	HMPREF9286_1779 conserved hypothetical protein	Pepto008_149	837	158340	159176 + C BLAST: hypothetical protein (db=KEGG eval=6.0e-44 bit_score=181.0 identity=44.87 covera
650261554	HMPREF9286_1780 abortive infection protein AbiG1	Pepto008_150	597	159173	159769 + C BLAST: hypothetical protein (db=KEGG eval=9.0e-28 bit_score=126.0 identity=30.57 covera
650261555	HMPREF9286_1781 conserved hypothetical protein				
650261556	HMPREF9286_1782 copper amine oxidase N-terminal domain protein				
650261557	HMPREF9286_1783 conserved hypothetical protein				
650261558	HMPREF9286_1784 putative phage tail component, N-terminal domain protein				
650261559	HMPREF9286_1785 DNA (cytosine-5-)-methyltransferase				
650261560	HMPREF9286_1786 putative TraE protein				
650261561	HMPREF9286_1787 conserved hypothetical protein				
650261562	HMPREF9286_1788 ribosome-binding factor A domain protein				
650261563	HMPREF9286_1789 conserved hypothetical protein				
650261564	HMPREF9286_0683 conserved domain protein				
650261565	HMPREF9286_0684 conserved hypothetical protein				
650261566	HMPREF9286_0685 conserved hypothetical protein				
650261567	HMPREF9286_0686 methyltransferase domain protein				
		Pepto008_151	795	160177	160971 + C BLAST: helix-turn-helix domain protein (db=KEGG eval=4.0e-37 bit_score=158.0 identity=
		Pepto008_152	2436	161008	163443 + D IPSCAN: FtsX (db=HMMPfam db_id=PF02687 from=204 to=367 eval=6.5e-18 interpo_id
		Pepto008_153	669	164340	164408 + B RBH: putative oligopeptide ABC transporter, ATP-binding protein; K02003 (db=KEGG eval
		Pepto008_154	327	164884	165210 + C BLAST: Transposase family protein (db=KEGG eval=1.0e-40 bit_score=168.0 identity=79.6
		Pepto008_155	2004	165398	167401 + B RBH: ctc:CTC00383 hppA; membrane-bound proton-translocating pyrophosphatase [EC:3.6.1.
		Pepto008_156	225	167430	167654 + C BLAST: Preprotein translocase, SecE subunit n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D
650261736	HMPREF9286_0892 V-type H(+)-translocating pyrophosphatase				
650261737	HMPREF9286_0893 putative preprotein translocase, SecG subunit				
650261738	HMPREF9286_0894 HDIG domain protein				
650261739	HMPREF9286_0895 glyceraldehyde-3-phosphate dehydrogenase, type I	Pepto008_157	1020	167889	168908 + B RBH: UniRef90_D1VSM2 Glyceraldehyde-3-phosphate dehydrogenase, type I n=1 Tax=Pepton
650261740	HMPREF9286_0896 amino acid kinase family				
650261741	HMPREF9286_0897 homoserine O-succinyltransferase	Pepto008_158	1797	168997	170793 + B RBH: cst:CLOST_2148 homoserine O-succinyltransferase (homoserine O-transsuccinylase) (ht
650261742	HMPREF9286_0898 copper amine oxidase N-terminal domain protein				
650261743	HMPREF9286_0899 conserved hypothetical protein				
650261744	HMPREF9286_0900 citrate lyase, alpha subunit	Pepto008_159	1548	171251	172798 + B RBH: fnu:FN1380 citrate lyase beta chain (EC:4.1.3.6); K01643 citrate lyase subunit alpha / cit
650261745	HMPREF9286_0901 citrate (pro-3S)-lyase, beta subunit	Pepto008_160	900	172788	173687 + B RBH: fnu:FN1379 citrate lyase beta chain (EC:4.1.3.34 4.1.3.6); K01644 citrate lyase subunit b
650261746	HMPREF9286_0902 citrate lyase acyl carrier protein	Pepto008_161	282	173692	173973 + C BLAST: citG; putative citrate lyase gamma-subunit; K01646 citrate lyase subunit gamma [EC:4.
650261747	HMPREF9286_0903 citrate-sodium symporter	Pepto008_162	1290	173992	175281 + B RBH: amt:Amet_3226 citrate carrier protein (db=KEGG)
650261748	HMPREF9286_0904 SCP-like protein				
650261749	HMPREF9286_0905 holo-ACP synthase CitX	Pepto008_163	513	175554	176066 + C BLAST: citX; putative apo-citrate lyase phosphoribosyl-dephospho-CoA transferase; K05964 h
650261750	HMPREF9286_0906 [citrate (pro-3S)-lyase] ligase	Pepto008_164	993	176053	177045 + C BLAST: citC1; citrate (pro-3S)-lyase ligase (EC:6.2.1.22); K01910 [citrate (pro-3S)-lyase] ligase [
650261751	HMPREF9286_0907 triphosphoribosyl-dephospho-CoA synthase	Pepto008_165	825	177038	177862 + C BLAST: 2-(5'-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase (EC:2.7.8.25); K05966 tri
650261752	HMPREF9286_0908 threonine ammonia-lyase	Pepto008_166	1209	177996	179204 + B RBH: apr:Apr_1062 threonine dehydratase; K01754 threonine dehydratase [EC:4.3.1.19] (db
650261753	HMPREF9286_0909 conserved hypothetical protein	Pepto008_167	225	179206	179430 + C BLAST: hypothetical protein (db=KEGG eval=1.0e-21 bit_score=105.0 identity=65.28 covera
650261754	HMPREF9286_0910 transporter, small conductance mechanosensitive ion chann	Pepto008_168	879	179417	180295 + C BLAST: MscS mechanosensitive ion channel; K03442 small conductance mechanosensitive ch
650261755	HMPREF9286_0911 conserved hypothetical protein	Pepto008_169	1164	180292	181455 + B RBH: UniRef90_D1VUS9 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 31
650261756	HMPREF9286_0912 putative membrane protein				
650261757	HMPREF9286_0913 transketolase	Pepto008_170	1950	181474	183423 + B RBH: UniRef90_D1VUT1 Transketolase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VUT
650261758	HMPREF9286_0914 glycosyltransferase, WecB/TagA/CpsF family	Pepto008_171	753	183435	184187 + B RBH: UniRef90_D1VUT2 Teichoic acid biosynthesis protein n=1 Tax=Peptoniphilus lacrimalis 3
		Pepto008_172	1560	184349	185908 + B RBH: cpy:Cphy_1439 transposase IS4 family protein (db=KEGG)
		Pepto008_173	123	186657	186779 + C BLAST: Toxin-antitoxin system, antitoxin component, ribbon-helix-helix fold n=2 Tax=Mobil
		Pepto008_174	318	187191	187508 + E GENE: 187193..187510 + (rbs_motif=AGGAGG rbs_spacer=5-10bp)
		Pepto008_175	219	187518	187736 + D IPSCAN: DUF2599 (db=HMMPfam db_id=PF10783 from=18 to=65 eval=8.8e-11 interpro,
		Pepto008_176	270	187759	188028 + D IPSCAN: seg (db=Seg db_id=seg from=37 to=47)
		Pepto008_177	1125	188170	189294 + B RBH: fma:FMG_P0155 putative transposase (db=KEGG)
		Pepto008_178	438	189257	189694 + C BLAST: putative transposase (db=KEGG eval=5.0e-54 bit_score=212.0 identity=70.42 cove
650261759	HMPREF9286_0915 toxin-antitoxin system, toxin component, MazF family	Pepto008_179	348	189885	190232 + C BLAST: transcriptional modulator of MazE/toxin, MazF; K07171 (db=KEGG eval=2.0e-44 bit
		Pepto008_180	273	190354	190626 + D IPSCAN: seg (db=Seg db_id=seg from=7 to=18)
		Pepto008_181	258	190675	190932 + D IPSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=24)
		Pepto008_182	678	190945	191622 + D IPSCAN: seg (db=Seg db_id=seg from=8 to=20)
650261760	HMPREF9286_0916 holo-[acyl-carrier-protein] synthase	Pepto008_183	1188	191702	192889 + B RBH: UniRef90_D1VUT4 YjeF domain protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=C
650261761	HMPREF9286_0917 tyrosine-tRNA ligase	Pepto008_184	1227	193092	194318 + B RBH: fma:FMG_1451 tyrosyl-tRNA synthetase; K01866 tyrosyl-tRNA synthetase [EC:6.1.1.1] (c
650261762	HMPREF9286_0918 Xaa-His dipeptidase	Pepto008_185	1392	194326	195717 + B RBH: fnu:FN1277 aminoacyl-histidine dipeptidase (EC:3.4.13.3); K01270 aminoacylhistidine di
650261763	HMPREF9286_0919 conserved hypothetical protein	Pepto008_186	411	195912	196322 + C BLAST: hypothetical protein; K04757 anti-sigma B factor [EC:2.7.11.1] (db=KEGG eval=9.0e-
650261764	HMPREF9286_0920 rubredoxin	Pepto008_187	162	196475	196636 + C BLAST: rubredoxin (db=KEGG eval=2.0e-16 bit_score=87.4 identity=78.0 coverage=90.7407
650261765	HMPREF9286_0921 phospholipase/carboxylesterase				
		Pepto008_188	1110	196714	197823 + B RBH: cst:CLOST_0671 yjeE (EC:3.4.11.4) (db=KEGG)
		Pepto008_189	669	197832	198500 + C BLAST: hypothetical protein (db=KEGG eval=6.0e-30 bit_score=134.0 identity=36.02 cove
		Pepto008_190	687	198526	199212 + C BLAST: hypothetical protein (db=KEGG eval=3.0e-42 bit_score=175.0 identity=39.47 cove
		Pepto008_191	861	199383	200243 + B RBH: fma:FMG_1546 hypothetical protein (db=KEGG)
		Pepto008_192	216	200243	200458 + D IPSCAN: seg (db=Seg db_id=seg from=3 to=17)

650261766	HMPREF9286_0922 uracil-DNA glycosylase	Pepto008_193	672	200492	201163	+	B	RBH: UniRef90_D1VRU4 Uracil-DNA glycosylase n=1 Tax=Peptoniphilus lacrimalis 315-B RepIC
650261767	HMPREF9286_0923 TrkA C-terminal domain protein	Pepto008_194	1368	201168	202535	+	B	RBH: UniRef90_D1VRU3 Putative potassium transporter peripheral membrane component n=
650261768	HMPREF9286_0924 potassium uptake protein, TrkH family	Pepto008_195	1455	202535	203989	+	B	RBH: aoe:Clos_0674 cation transporter; K03498 trk system potassium uptake protein TrkH (dl
650261769	HMPREF9286_0925 TrkA N-terminal domain protein	Pepto008_196	1401	203979	205379	+	B	RBH: aoe:Clos_0673 trkA; potassium transporter peripheral membrane component; K03499 t
650261770	HMPREF9286_0926 cation diffusion facilitator family transporter	Pepto008_197	1149	205389	206537	+	B	RBH: UniRef90_D1VRU0 Cobalt-zinc-cadmium resistance protein Czcd n=1 Tax=Peptoniphilus
650261771	HMPREF9286_0927 conserved hypothetical protein							
650261772	HMPREF9286_0928 DJ-1 family protein	Pepto008_198	567	206767	207333	+	C	BLAST: DJ-1 family protein; K03152 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate bios
650261773	HMPREF9286_0929 pyrroline-5-carboxylate reductase	Pepto008_199	765	207353	208117	+	C	BLAST: proC; pyrroline-5-carboxylate reductase (EC:1.5.1.2); K00286 pyrroline-5-carboxylate r
650261774	HMPREF9286_0930 chromate transport protein	Pepto008_200	561	208196	208756	+	C	BLAST: chromate transport protein; K07240 chromate transporter (db=KEGG eval=1.0e-39
650261775	HMPREF9286_0931 chromate transport protein	Pepto008_201	558	208749	209306	+	C	BLAST: chromate transport protein; K07240 chromate transporter (db=KEGG eval=5.0e-45
650261776	HMPREF9286_0932 copper amine oxidase N-terminal domain protein							
650261777	HMPREF9286_0933 toxin-antitoxin system, toxin component, RelE family							
650261778	HMPREF9286_0934 toxin-antitoxin system, antitoxin component, ribbon-helix-helix domain protein							
650261779	HMPREF9286_0936 erythromycin esterase							
650260741	HMPREF9286_1534 4-phosphoerythronate dehydrogenase	Pepto008_202	939	209345	210283	+	C	BLAST: D-isomer specific 2-hydroxyacid dehydrogenase, nad-binding (db=KEGG eval=1.0e-6
		Pepto008_203	903	210284	211186	+	C	BLAST: alpha/beta hydrolase fold (db=KEGG eval=5.0e-25 bit_score=118.0 identity=28.57
650260742	HMPREF9286_1535 tetratricopeptide repeat protein	Pepto008_204	1566	211322	212887	+	B	RBH: UniRef90_D1VV21 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 31
650260743	HMPREF9286_1536 Sigma-70 region 2	Pepto008_205	570	212993	213562	+	C	BLAST: ECF subfamily RNA polymerase sigma-24 factor; K03088 RNA polymerase sigma-70 fac
650260744	HMPREF9286_1537 conserved hypothetical protein	Pepto008_206	762	213555	214316	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Oribacterium sp. oral taxon 078 str. F0262 f
650260745	HMPREF9286_1538 DnaI domain protein	Pepto008_207	846	214408	215253	+	C	BLAST: heat shock protein DnaI domain protein (db=KEGG eval=8.0e-21 bit_score=104.0 id
650260746	HMPREF9286_1539 conserved hypothetical protein	Pepto008_208	465	215246	215710	+	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-08 bit_score=62.0 identity=53.33 covera
650260747	HMPREF9286_1540 oligopeptide ABC transporter, ATP-binding protein OppF	Pepto008_209	834	215788	216621	+	B	RBH: UniRef90_D1VVB0 Oligopeptide transport ATP-binding protein OppF n=1 Tax=Peptonipil
650260748	HMPREF9286_1541 oligopeptide ABC transporter, ATP-binding protein OppD	Pepto008_210	957	216587	217543	+	B	RBH: tit:Thit_2211 oligopeptide/dipeptide ABC transporter, ATPase subunit; K02031 peptide/
650260749	HMPREF9286_1542 oligopeptide ABC transporter, permease protein AppC	Pepto008_211	843	217545	218387	+	C	BLAST: binding-protein-dependent transport systems inner membrane component; K02034 p
650260750	HMPREF9286_1543 dipeptide ABC transporter, permease protein DppB	Pepto008_212	930	218395	219324	+	B	RBH: aoe:Clos_1348 binding-protein-dependent transport systems inner membrane compone
650260751	HMPREF9286_1544 ABC transporter, substrate-binding protein, family 5	Pepto008_213	1527	219393	220919	+	B	RBH: aoe:Clos_1347 extracellular solute-binding protein; K02035 peptide/nickel transport sy
650260752	HMPREF9286_1545 UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Pepto008_214	1263	220919	222181	+	B	RBH: amt:Amet_0358 UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC:2.5.1.7); K007
650260753	HMPREF9286_1546 aminotransferase, class I/II							
650260754	HMPREF9286_1547 8-oxoguanine DNA-glycosylase (ogg)	Pepto008_215	876	222417	223292	+	B	RBH: UniRef90_D1VVZ7 8-oxoguanine DNA glycosylase domain-containing protein n=1 Tax=P
650260755	HMPREF9286_1548 putative redox-sensing transcriptional repressor Rex	Pepto008_216	630	223334	223963	+	C	BLAST: redox-sensing transcriptional repressor REX; K01926 AT-rich DNA-binding protein (db-
		Pepto008_217	1467	224272	225738	+	C	BLAST: amino acid permease-associated region (db=KEGG eval=1.0e-61 bit_score=241.0 i
650260756	HMPREF9286_1549 conserved hypothetical protein							
650260757	HMPREF9286_1550 sortase, SrtB family							
650260758	HMPREF9286_1551 conserved hypothetical protein							
650260759	HMPREF9286_1552 Amidinotransferase	Pepto008_218	888	225797	226684	+	C	BLAST: putative amidinotransferase (db=KEGG eval=6.0e-57 bit_score=224.0 identity=40.7.
650260760	HMPREF9286_1553 tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-bi	Pepto008_219	828	226779	227606	+	C	BLAST: folD; methylenetetrahydrofolate dehydrogenase (EC:1.5.1.5); K01491 methylenetetra
		Pepto008_220	891	227607	228497	+	C	BLAST: hypothetical protein; K07029 (db=KEGG eval=6.0e-50 bit_score=201.0 identity=40
650260761	HMPREF9286_1554 oxidoreductase, short chain dehydrogenase/reductase fami	Pepto008_221	735	228537	229271	+	C	BLAST: 3-oxoacyl-[acyl-carrier protein] reductase; K00059 3-oxoacyl-[acyl-carrier protein] redi
650260762	HMPREF9286_1556 serine/threonine transporter family protein	Pepto008_222	1239	229402	230640	+	B	RBH: fma:FMG_0902 serine/threonine sodium symporter (db=KEGG)
650260763	HMPREF9286_1557 L-serine dehydratase, iron-sulfur-dependent, alpha subunit	Pepto008_223	882	230646	231527	+	B	RBH: UniRef90_D1VRW1 L-serine dehydratase, iron-sulfur-dependent, alpha subunit n=1 Tax:
650260764	HMPREF9286_1558 L-serine dehydratase, iron-sulfur-dependent, beta subunit	Pepto008_224	669	231528	232196	+	C	BLAST: L-serine dehydratase beta subunit; K01752 L-serine dehydratase [EC:4.3.1.17] (db=KE
650260765	HMPREF9286_1559 AbgT transporter family	Pepto008_225	1572	232437	234008	+	B	RBH: afn:Acf_1863 AbgT putative transporter; K12942 aminobenzoate-glutamate transport p
650260766	HMPREF9286_1560 conserved hypothetical protein							
650260767	HMPREF9286_1561 conserved hypothetical protein	Pepto008_226	699	234093	234791	+	C	BLAST: radical SAM-superfamily protein (db=KEGG eval=3.0e-84 bit_score=314.0 identity=6
650260768	HMPREF9286_1562 transcriptional regulator, MarR family							
650260769	HMPREF9286_1563 EDD domain protein, DegV family	Pepto008_227	843	235016	235858	+	C	BLAST: DegV family protein (db=KEGG eval=3.0e-58 bit_score=228.0 identity=41.07 covera
650260770	HMPREF9286_1564 putative membrane protein	Pepto008_228	918	235986	236903	+	C	BLAST: Putative membrane protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV24_5
650260771	HMPREF9286_1565 DHHA1 domain protein	Pepto008_229	1998	236915	238912	+	B	RBH: amt:Amet_4770 phosphoesterase domain-containing protein (db=KEGG)
650260772	HMPREF9286_1566 ribosomal protein L9	Pepto008_230	450	238915	239364	+	C	BLAST: rplI; 50S ribosomal protein L9; K02939 large subunit ribosomal protein L9 (db=KEG e
650260773	HMPREF9286_1567 replicative DNA helicase	Pepto008_231	1362	239369	240730	+	B	RBH: aoe:Clos_2797 replicative DNA helicase; K02314 replicative DNA helicase [EC:3.6.1.-] (dt
650260774	HMPREF9286_1568 undecaprenyl-diphosphatase UppP	Pepto008_232	876	240826	241701	+	B	RBH: apr:Apr_0234 undecaprenol kinase (EC:3.6.1.27); K06153 undecaprenyl-diphosphatase
650260775	HMPREF9286_1569 hydrolase, carbon-nitrogen family	Pepto008_233	798	241712	242520	+	B	RBH: UniRef90_D1VW19 Hydrolase C26A3.11 n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=
650260776	HMPREF9286_1570 transposase-like protein							
650260777	HMPREF9286_1571 putative membrane protein	Pepto008_234	642	242585	243226	+	C	BLAST: protein of unknown function DUF1648 (db=KEGG eval=1.0e-32 bit_score=142.0 ide
650260778	HMPREF9286_1572 putative arsenical resistance operon repressor	Pepto008_235	276	243216	243491	+	C	BLAST: transcriptional regulator, ArsR family (db=KEGG eval=3.0e-26 bit_score=120.0 ident
		Pepto008_236	390	243673	244062	+	C	BLAST: XRE family transcriptional regulator (db=KEGG eval=2.0e-10 bit_score=67.8 identi
		Pepto008_237	1356	244265	245620	+	B	RBH: UniRef90_D6BCY8 Putative uncharacterized protein n=2 Tax=Fusobacterium sp. D11 R
		Pepto008_238	1074	245629	246702	+	C	BLAST: D-lactate dehydrogenase; K03778 D-lactate dehydrogenase [EC:1.1.1.28] (db=KEGG
		Pepto008_239	552	246692	247243	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=29)
		Pepto008_240	750	247312	248061	+	B	RBH: UniRef90_D1VV56 Putative transcriptional regulator n=1 Tax=Peptoniphilus lacrimalis 3
650260779	HMPREF9286_1573 lclR helix-turn-helix domain protein							
650260780	HMPREF9286_1574 Fic family protein							
650260781	HMPREF9286_1575 conserved domain protein							
650260782	HMPREF9286_1576 ABC transporter, ATP-binding protein	Pepto008_241	1890	248498	250387	+	B	RBH: apr:Apr_1467 ABC transporter related; K06158 ATP-binding cassette, sub-family F, mer
		Pepto008_242	228	250393	250620	+	E	GENE: 250395..250622 - (rbs_motif=None rbs_spacer=None)
650260783	HMPREF9286_1577 XkdX family protein	Pepto008_243	645	250755	251399	+	C	BLAST: racemase (db=KEGG eval=1.0e-32 bit_score=142.0 identity=45.37 coverage=93.023
650260784	HMPREF9286_1578 lipid kinase, YegS/Rv252/BmrU family							
650260785	HMPREF9286_1579 conserved hypothetical protein							
650260786	HMPREF9286_1580 arylsulfatase							
650260787	HMPREF9286_1581 putative membrane protein							
650260788	HMPREF9286_1582 conserved hypothetical protein							
650260789	HMPREF9286_1583 hemerythrin HHE cation binding domain protein							
650260790	HMPREF9286_1584 tRNA 2-selenouridine synthase							
650260791	HMPREF9286_1585 selenide, water dikinase							
650260792	HMPREF9286_1586 selenium metabolism protein YedF							
650260793	HMPREF9286_1587 conserved hypothetical protein							
650260794	HMPREF9286_1588 cysteine desulfurase family protein							
		Pepto008_244	834	251527	252360	+	C	BLAST: protein of unknown function zinc metallopeptidase putative; K07054 (db=KEGG eval
650260795	HMPREF9286_1589 putative membrane protein	Pepto008_245	570	252592	253161	+	D	IPRSCAN: seg (db=Seg db_id=seg from=119 to=133)
		Pepto008_246	138	253204	253341	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=26)
650260796	HMPREF9286_1590 glutaminase A	Pepto008_247	930	253486	254415	+	B	RBH: tva:TVAG_134820 Glutaminase family protein; K01425 glutaminase [EC:3.5.1.2] (db=KE
650260797	HMPREF9286_1591 amino acid carrier protein	Pepto008_248	1467	254425	255891	+	B	RBH: ctc:CTC01187 alst; amino acid carrier protein Alst; K03310 alanine or glycine:cation sym
650260800	HMPREF9286_1594 [(+)-tartarate dehydratase subunit beta							
650260801	HMPREF9286_1595 tartrate dehydratase subunit alpha							
650260802	HMPREF9286_1596 transporter, DASS family							
650260803	HMPREF9286_1597 transcriptional regulator, AraC family							
650261989	HMPREF9286_0260 sortase family protein	Pepto008_249	822	256015	256836	+	C	BLAST: sortase family protein (db=KEGG eval=4.0e-43 bit_score=178.0 identity=35.46 cove
650261990	HMPREF9286_0261 sortase family protein	Pepto008_250	828	256826	257553	+	C	BLAST: sortase family protein (db=KEGG eval=1.0e-81 bit_score=306.0 identity=62.34 cove
650261991	HMPREF9286_0262 sortase family protein	Pepto008_251	921	257637	258557	+	C	BLAST: sortase; K07284 sortase A (db=KEGG eval=1.0e-78 bit_score=296.0 identity=60.37 c
650261992	HMPREF9286_0263 LPXTG-motif cell wall anchor domain protein	Pepto008_252	1182	258599	259780	+	C	BLAST: cell wall surface anchor family protein (db=KEGG eval=3.0e-24 bit_score=116.0 ider
650261993	HMPREF9286_0264 LPXTG-motif cell wall anchor domain protein	Pepto008_253	2187	259673	262149	+	B	RBH: sag:SAG1407 cell wall surface anchor family protein (db=KEGG)
650261994	HMPREF9286_0265 putative flagellar protein Fls	Pepto008_254	13419	262358	275776	+	B	RBH: apr:Apr_1579 Cna B domain protein (db=KEGG)
650260798	HMPREF9286_1592 conserved hypothetical protein	Pepto008_255	354	276293	276645	+	C	BLAST: yvId; YvId; K08972 putative membrane protein (db=KEGG eval=1.0e-14 bit_score=8
650260799	HMPREF9286_1593 conserved hypothetical protein	Pepto008_256	306	276716	277021	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-17 bit_score=90.9 identity=42.86 covera
		Pepto008_257	2016	277174	279189	+	C	BLAST: S-layer domain protein (db=KEGG eval=7.0e-23 bit_score=112.0 identity=37.75 co
650260804	HMPREF9286_1598 amidohydrolase							
650260805	HMPREF9286_1599 phosphoribosylformylglycinamide synthase	Pepto008_258	3672	279365	283036	+	B	RBH: fma:FMG_1359 phosphoribosylformylglycinamide synthase; K01952 phosphoribosylfo
650260806	HMPREF9286_1600 amidophosphoribosyltransferase	Pepto008_259	1362	280326	284387	+	C	BLAST: phosphoribosylpyrophosphate amidotransferase; K00764 amidophosphoribosyltransf
650260807	HMPREF9286_1601 putative membrane protein	Pepto008_260	2520	284674	287193	+	B	RBH: UniRef90_D1VW15 Lysine-tRNA ligase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D
650260808	HMPREF9286_1602 hydrolase, alpha/beta domain protein							
650260809	HMPREF9286_1603 conserved hypothetical protein							
		Pepto008_261	2667	287392	290058	+	B	RBH: bin:Blon_2122 metallophosphoesterase (db=KEGG)
650260810	HMPREF9286_1604 putative aspartyl aminopeptidase	Pepto008_262	1323	290226	291548	+	B	RBH: shi:Shel_04970 putative aminopeptidase 2 (db=KEGG)
650260811	HMPREF9286_1605 amino acid permease	Pepto008_263	1437	291566	293002	+	B	RBH: lac:LBA0696 amino acid permease (db=KEGG)

650260812 HMPREF9286_1606 methionine synthase, vitamin-B12 independent
650260813 HMPREF9286_1607 methionine synthase, vitamin-B12 independent
650260814 HMPREF9286_1609 conserved hypothetical protein

	Pepto008_264	240	293934	294173	+ C	BLAST: hypothetical protein (db=KEGG eval=3.0e-10 bit_score=67.4 identity=50.85 cover
	Pepto008_265	267	294299	294565	+ E	GENE: 294301..294567 - (rbs_motif=GGAG/GAG/AGG rbs_spacer=5-10bp)
	Pepto008_266	1140	294562	295701	+ C	BLAST: putative phage related amidase (db=KEGG eval=5.0e-41 bit_score=172.0 identity=
	Pepto008_267	393	295698	296900	+ C	BLAST: holin (db=KEGG eval=6.0e-09 bit_score=63.2 identity=32.54 coverage=94.6564885
	Pepto008_268	600	296113	296712	+ E	GENE: 296115..296714 - (rbs_motif=AGGAGG rbs_spacer=5-10bp)
	Pepto008_269	1830	296712	298541	+ D	IPRSCAN: coiled-coil (db=Coil db_id=coil from=133 to=154 eval=NA)
	Pepto008_270	273	298553	298825	+ D	IPRSCAN: coiled-coil (db=Coil db_id=coil from=21 to=49 eval=NA)
	Pepto008_271	2418	298828	301245	+ C	BLAST: ps140; hypothetical protein (db=KEGG eval=6.0e-59 bit_score=233.0 identity=33.!
	Pepto008_272	810	301242	302051	+ C	BLAST: ps139; hypothetical protein (db=KEGG eval=3.0e-09 bit_score=65.5 identity=26.4!
	Pepto008_273	2802	302063	304864	+ B	RBH: lmm:LM5578_0704 hypothetical protein (db=KEGG)
	Pepto008_274	258	304867	305124	+ E	GENE: 304869..305126 - (rbs_motif=None rbs_spacer=None)
	Pepto008_275	414	305217	305630	+ D	IPRSCAN: DUF3647 (db=HMMPfam db_id=PF12363 from=11 to=122 eval=3.8e-22)
	Pepto008_276	543	305703	306245	+ C	BLAST: hypothetical protein (db=KEGG eval=1.0e-23 bit_score=112.0 identity=45.57 cove
	Pepto008_277	417	306258	306674	+ C	BLAST: Predicted protein n=1 Tax=Mollicutes bacterium D7 RepID=C3RHH7_9MOLU (db=UN
	Pepto008_278	333	306674	307006	+ C	BLAST: hypothetical protein (db=KEGG eval=7.0e-19 bit_score=95.9 identity=44.76 cover
	Pepto008_279	300	307003	307302	+ E	GENE: 307005..307304 - (rbs_motif=AGxAGG/AGGxGG rbs_spacer=11-12bp)
	Pepto008_280	339	307299	307637	+ C	BLAST: ps131; hypothetical protein (db=KEGG eval=6.0e-13 bit_score=76.3 identity=43.0!
	Pepto008_281	198	307649	307846	+ E	GENE: 307651..307848 - (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp)
	Pepto008_282	867	307860	308726	+ C	BLAST: phage protein (db=KEGG eval=1.0e-56 bit_score=223.0 identity=44.78 coverage=9
	Pepto008_283	636	308743	309378	+ C	BLAST: phage scaffold protein (db=KEGG eval=4.0e-26 bit_score=120.0 identity=42.86 co
	Pepto008_284	933	309472	310404	+ C	BLAST: phage Mu protein F like protein (db=KEGG eval=3.0e-35 bit_score=152.0 identity=
	Pepto008_285	1350	310391	311740	+ B	RBH: sds:SDEG_1632 portal protein (db=KEGG)
	Pepto008_286	1296	311753	313048	+ B	RBH: ipo:lyop_2057 phage terminase, large subunit, PBX family (db=KEGG)
	Pepto008_287	477	313005	313481	+ C	BLAST: phage terminase small subunit (db=KEGG eval=8.0e-19 bit_score=95.5 identity=3!
	Pepto008_288	633	313640	314272	+ D	IPRSCAN: seg (db=Seg db_id=seg from=64 to=78)
	Pepto008_289	402	314265	314666	+ C	BLAST: hypothetical protein (db=KEGG eval=2.0e-08 bit_score=61.6 identity=40.58 cover
	Pepto008_290	408	314798	315205	+ C	BLAST: hypothetical protein (db=KEGG eval=7.0e-30 bit_score=132.0 identity=59.5 cover
	Pepto008_291	243	315220	315462	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Anaerococcus lactolyticus ATCC 51172 Re
	Pepto008_292	204	315476	315679	+ E	GENE: 315478..315681 - (rbs_motif=GGxGG rbs_spacer=3-4bp)
	Pepto008_293	216	315676	315891	+ E	GENE: 315678..315893 - (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp)
	Pepto008_294	297	315888	316184	+ E	GENE: 315890..316186 - (rbs_motif=GGxGG rbs_spacer=3-4bp)
	Pepto008_295	192	316195	316386	+ E	GENE: 316197..316388 - (rbs_motif=AGxAGG/AGGxGG rbs_spacer=5-10bp)
	Pepto008_296	177	316408	316584	+ D	IPRSCAN: coiled-coil (db=Coil db_id=coil from=1 to=22 eval=NA)
	Pepto008_297	615	316584	317198	+ D	IPRSCAN: NAD(P)-binding Rossmann-fold domains (db=superfamily db_id=SSF51735 from=
	Pepto008_298	372	317242	317613	+ C	BLAST: endodeoxyribonuclease RusA (db=KEGG eval=2.0e-28 bit_score=127.0 identity=5!
	Pepto008_299	849	317613	318461	+ C	BLAST: putative Asp-tRNAAsn/Glu-tRNAArg amidotransferase B subunit (db=KEGG eval=!
	Pepto008_300	756	318487	319242	+ C	BLAST: hypothetical protein (db=KEGG eval=2.0e-32 bit_score=142.0 identity=42.02 cove
	Pepto008_301	471	319253	319723	+ C	BLAST: GP157 family protein (db=KEGG eval=1.0e-22 bit_score=108.0 identity=47.44 cove
	Pepto008_302	213	319710	319922	+ E	GENE: 319712..319924 - (rbs_motif=AGxAGG/AGGxGG rbs_spacer=5-10bp)
	Pepto008_303	750	319977	320726	+ D	IPRSCAN: seg (db=Seg db_id=seg from=39 to=47)
	Pepto008_304	186	320704	320889	+ E	GENE: 320706..320891 - (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp)
	Pepto008_305	246	321092	321337	+ D	IPRSCAN: excise: DNA binding domain, excisionase fami (db=HMMTigr db_id=TIGR01764 fr
	Pepto008_306	183	321371	321553	+ D	IPRSCAN: HTH_3 (db=HMMPfam db_id=PF01381 from=15 to=58 eval=4.6e-07 interpro_id
	Pepto008_307	312	321811	322122	+ C	BLAST: XRE family transcriptional regulator (db=KEGG eval=5.0e-09 bit_score=63.2 identi
	Pepto008_308	513	322167	322679	+ D	IPRSCAN: DUF955 (db=HMMPfam db_id=PF06114 from=42 to=146 eval=1.1e-13 interpro
	Pepto008_309	501	322730	323230	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Ruminococcus sp. SR1/5 RepID=D4LPN9_!
	Pepto008_310	1170	323329	324498	+ C	BLAST: integrase family protein (db=KEGG eval=8.0e-23 bit_score=111.0 identity=29.44 c
650261784 HMPREF9286_0942 VanZ-like protein	Pepto008_311	609	325125	325733	+ C	BLAST: hypothetical protein (db=KEGG eval=8.0e-08 bit_score=60.1 identity=49.0 coverage
650261785 HMPREF9286_0943 HAD hydrolase, family IA, variant 3	Pepto008_312	639	325730	326368	+ C	BLAST: haloacid dehalogenase, IA family protein (db=KEGG eval=3.0e-21 bit_score=104.0 ic
650261788 HMPREF9286_0946 carbon starvation protein CstA	Pepto008_313	1455	326852	328306	+ B	RBH: apr:Apr_0605 carbon starvation protein CstA (db=KEGG)
650261787 HMPREF9286_0945 conserved hypothetical protein	Pepto008_314	318	328361	328678	+ C	BLAST: hypothetical protein (db=KEGG eval=1.0e-15 bit_score=85.5 identity=44.76 coverage
	Pepto008_315	1617	328835	330451	+ B	RBH: ppm:PPSC2_c3050 alkaline phosphatase III; K01077 alkaline phosphatase [EC:3.1.3.1]
650261789 HMPREF9286_0947 ribosomal subunit interface protein	Pepto008_316	528	330627	331154	+ C	BLAST: SSU ribosomal protein S30P; K05808 putative sigma-54 modulation protein (db=KEGG
650261790 HMPREF9286_0948 conserved hypothetical protein	Pepto008_317	900	331308	332207	+ C	BLAST: hypothetical protein (db=KEGG eval=2.0e-29 bit_score=132.0 identity=34.34 covera
650261791 HMPREF9286_0949 conserved hypothetical protein	Pepto008_318	1665	332216	333880	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650261792 HMPREF9286_0950 transporter gate domain protein	Pepto008_319	1308	334072	335379	+ B	RBH: fnu:FN0340 hypothetical protein (db=KEGG)
650261793 HMPREF9286_0951 conserved hypothetical protein						
650261797 HMPREF9286_0955 copper amine oxidase N-terminal domain protein						
650261798 HMPREF9286_0956 ribosomal protein S18	Pepto008_320	225	335739	335963	+ C	BLAST: 30S ribosomal protein S18; K02963 small subunit ribosomal protein S18 (db=KEGG eva
650261799 HMPREF9286_0957 single-strand binding family protein	Pepto008_321	501	335975	336475	+ C	BLAST: single-strand binding protein (db=KEGG eval=7.0e-33 bit_score=142.0 identity=60.3
650261800 HMPREF9286_0958 ribosomal protein S6	Pepto008_322	285	336485	336769	+ C	BLAST: 30S ribosomal protein S6; K02990 small subunit ribosomal protein S6 (db=KEGG evalua
650261801 HMPREF9286_0959 methylglyoxal synthase	Pepto008_323	471	336888	337358	+ C	BLAST: mgsA; methylglyoxal synthase (EC:4.2.3.3); K01734 methylglyoxal synthase [EC:4.2.3.3
	Pepto008_324	423	337444	337866	+ C	BLAST: hypothetical protein; K06934 (db=KEGG eval=2.0e-37 bit_score=157.0 identity=50
650261802 HMPREF9286_0960 peptidase T	Pepto008_325	1200	337985	339184	+ B	RBH: fma:FMG_0500 peptidase T; K01258 tripeptide aminopeptidase [EC:3.4.11.4] (db=KEGG
650261803 HMPREF9286_0961 cell envelope-like function transcriptional attenuator comm	Pepto008_326	1128	339311	340438	+ B	RBH: UniRef90_D1VRV0 Membrane-bound protein n=1 Tax=Peptoniphilus lacrimalis 315-B Re
650261804 HMPREF9286_0962 Yai/Yqx family protein	Pepto008_327	690	340538	341227	+ C	BLAST: hypothetical protein; K09768 hypothetical protein (db=KEGG eval=8.0e-24 bit_scor
650261805 HMPREF9286_0963 nitroreductase family protein	Pepto008_328	555	341232	341786	+ C	BLAST: nitroreductase (db=KEGG eval=3.0e-37 bit_score=157.0 identity=43.18 coverage=9;
650261806 HMPREF9286_0964 response regulator receiver domain protein						
650261807 HMPREF9286_0965 putative membrane protein						
650261808 HMPREF9286_0966 putative membrane protein						
650261809 HMPREF9286_0967 putative membrane protein						
650261810 HMPREF9286_0968 ABC transporter, ATP-binding protein						
650261811 HMPREF9286_0969 conserved hypothetical protein						
650261812 HMPREF9286_0970 putative lipoprotein						
650261813 HMPREF9286_0971 GAF domain protein						
650261814 HMPREF9286_0972 amidohydrolase family protein						
650261815 HMPREF9286_0973 amino acid permease						
650261816 HMPREF9286_0974 conserved hypothetical protein	Pepto008_329	1356	341906	343261	+ B	RBH: elm:ELI_2536 hypothetical protein; K09157 hypothetical protein (db=KEGG)
650261817 HMPREF9286_0975 ACT domain protein	Pepto008_330	270	343271	343540	+ C	BLAST: hypothetical protein; K07166 ACT domain-containing protein (db=KEGG eval=1.0e-2
650261818 HMPREF9286_0976 putative lipoprotein						
650261819 HMPREF9286_0977 peptidase C26						
650261820 HMPREF9286_0978 MATE efflux family protein	Pepto008_331	1311	343770	345080	+ C	BLAST: putative drug/sodium antiporter (db=KEGG eval=2.0e-65 bit_score=253.0 identity=;
650261821 HMPREF9286_1313 G5 domain protein						
650261822 HMPREF9286_1314 conserved hypothetical protein						
650261823 HMPREF9286_1315 branched-chain-amino-acid transaminase						
650260920 HMPREF9286_0106 conserved hypothetical protein						
650260919 HMPREF9286_1127 conserved hypothetical protein						
650260918 HMPREF9286_1126 radical SAM domain protein						
650260917 HMPREF9286_1713 conserved hypothetical protein						
650260916 HMPREF9286_1712 G5 domain protein						
650260915 HMPREF9286_1711 copper amine oxidase N-terminal domain protein						
650260914 HMPREF9286_1710 copper amine oxidase N-terminal domain protein						
650260913 HMPREF9286_1709 conserved hypothetical protein						
650260912 HMPREF9286_1708 EDD domain protein, DegV family	Pepto008_332	885	345165	346049	+ C	BLAST: DegV family protein (db=KEGG eval=2.0e-46 bit_score=189.0 identity=36.11 covera
650260911 HMPREF9286_1707 cytidine and deoxycytidylate deaminase zinc-binding region	Pepto008_333	438	346212	346649	+ C	BLAST: cytidine and deoxycytidylate deaminase family protein (db=KEGG eval=5.0e-33 bit_
650260910 HMPREF9286_1706 PAP2 family protein	Pepto008_334	546	346629	347174	+ C	BLAST: phosphatase (db=KEGG eval=5.0e-19 bit_score=97.1 identity=43.41 coverage=69.2;
650260909 HMPREF9286_1705 conserved hypothetical protein	Pepto008_335	240	347221	347460	+ E	GENE: 347223..347462 - (rbs_motif=GGAGG rbs_spacer=5-10bp)
650260908 HMPREF9286_1704 ABC transporter, ATP-binding protein	Pepto008_336	1737	347637	349373	+ B	RBH: cst:CLOST_0790 ABC transporter, ATP-binding/permease protein (db=KEGG)
650260907 HMPREF9286_1703 ABC transporter, ATP-binding protein	Pepto008_337	1875	349330	351204	+ B	RBH: clj:CLJU_c15180 putative ABC transporter ATPase/permease (db=KEGG)
650260898 HMPREF9286_1694 putative lipoprotein	Pepto008_338	456	351393	351848	+ D	IPRSCAN: PROKAR_LIPOPROTEIN (db=ProfileScan db_id=PS51257 from=1 to=17 eval=6.0)

650260906	HMPREF9286_1702 conserved hypothetical protein				
650260905	HMPREF9286_1701 conserved hypothetical protein				
650260904	HMPREF9286_1700 ABC transporter, ATP-binding protein				
650260903	HMPREF9286_1699 transcriptional regulator, GntR family				
650260902	HMPREF9286_1698 conserved hypothetical protein				
650260901	HMPREF9286_1697 conserved hypothetical protein				
650260900	HMPREF9286_1696 DNA-binding helix-turn-helix protein				
650260899	HMPREF9286_1695 conserved hypothetical protein				
650260897	HMPREF9286_1693 putative copper-sensing transcriptional repressor CsoR	Pepto008_339	270	351856	352125 + C BLAST: protein of unknown function DUF156 (db=KEGG evalue=7.0e-21 bit_score=102.0 ident
650260896	HMPREF9286_1692 copper-exporting ATPase	Pepto008_340	2742	352122	354863 + B RBH: apr:Apr_0987 heavy metal translocating P-type ATPase; K01533 Cu2+-exporting ATPas
650260895	HMPREF9286_1691 Fic family protein				
650260894	HMPREF9286_1690 hemerythrin HHE cation binding domain protein	Pepto008_341	636	355068	355703 + C BLAST: protein of unknown function DUF542 ScdA domain protein; K07322 regulator of cell r
650260893	HMPREF9286_1689 Beta-eliminating lyase	Pepto008_342	999	355713	356711 + B RBH: UniRef90_D1VTV4 Putative threonine aldolase, B subunit n=1 Tax=Peptoniphilus lacrim
		Pepto008_343	648	356889	357536 + C BLAST: sortase; K07284 sortase A (db=KEGG evalue=4.0e-17 bit_score=91.3 identity=38.46 c
		Pepto008_344	5145	357526	362670 + B RBH: UniRef90_ABSINO Putative uncharacterized protein n=1 Tax=Parvimonas micra ATCC 3
650260892	HMPREF9286_1688 putative histidinol-phosphate transaminase	Pepto008_345	1068	362941	364008 + B RBH: cst:CLOST_1921 hisC; histidinol-phosphate aminotransferase; K04720 threonine-phosph
650260891	HMPREF9286_1687 GumN protein	Pepto008_346	1431	364019	365449 + B RBH: UniRef90_D1VRJ8 GumN protein (Fragment) n=1 Tax=Peptoniphilus lacrimalis 315-B Rej
650260889	HMPREF9286_1685 conserved hypothetical protein	Pepto008_347	1245	365506	366750 + B RBH: apr:Apr_1231 protein of unknown function DUF1063 (db=KEGG)
650261932	HMPREF9286_0203 C4-dicarboxylate anaerobic carrier	Pepto008_348	1410	367042	368451 + B RBH: aar:Acear_1936 C4-dicarboxylate anaerobic carrier (db=KEGG)
650261931	HMPREF9286_0202 Xaa-His dipeptidase	Pepto008_349	1449	368461	369909 + B RBH: fnu:FN1804 aminoacyl-histidine dipeptidase (EC:3.4.13.3); K01270 aminoacylhistidine di
650260890	HMPREF9286_1686 conserved hypothetical protein				
650260888	HMPREF9286_1684 conserved hypothetical protein				
650260887	HMPREF9286_1683 conserved hypothetical protein				
650260886	HMPREF9286_1682 putative membrane protein				
650260885	HMPREF9286_1681 3-dehydroquinase synthase				
650260884	HMPREF9286_1680 putative membrane protein				
650260883	HMPREF9286_1679 putative membrane protein				
650260882	HMPREF9286_1677 glycerol kinase	Pepto008_350	1476	369982	371457 + B RBH: UniRef90_D1VVX3 Glycerol kinase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650260881	HMPREF9286_1676 conserved hypothetical protein	Pepto008_351	642	371667	372308 + C BLAST: hypothetical protein (db=KEGG evalue=8.0e-22 bit_score=106.0 identity=35.35 covera
650260880	HMPREF9286_1675 putative RNA polymerase sigma-B factor	Pepto008_352	786	372308	373093 + B RBH: amt:Amet_0010 RlnA family phage transcriptional regulator; K03090 RNA polymerase si
650260879	HMPREF9286_1674 conserved hypothetical protein	Pepto008_353	351	373103	373453 + D IPSCAN: colled-coil (db=Coil db_id=coil from=26 to=47 evalue=NA)
650260878	HMPREF9286_1673 STAS domain protein	Pepto008_354	312	373455	373766 + C BLAST: anti-sigma-factor antagonist; K04749 anti-sigma B factor antagonist (db=KEGG evalue=
650260877	HMPREF9286_1672 DNA gyrase, A subunit	Pepto008_355	2430	373775	376204 + B RBH: apr:Apr_0006 DNA gyrase, A subunit [EC:5.99.1.3]; K02469 DNA gyrase subunit A [EC:5
650260876	HMPREF9286_1671 DNA gyrase, B subunit	Pepto008_356	1914	376124	378127 + B RBH: fma:FMG_0005 DNA gyrase B subunit; K02470 DNA gyrase subunit B [EC:5.99.1.3] (db=k
650260875	HMPREF9286_1670 DNA replication and repair protein RecF	Pepto008_357	1077	378141	379217 + B RBH: UniRef90_D1VRK7 DNA replication and repair protein recF n=1 Tax=Peptoniphilus lacrir
650260874	HMPREF9286_1669 S4 domain protein YaaA	Pepto008_358	213	379214	379426 + C BLAST: RNA-binding S4 domain-containing protein (db=KEGG evalue=8.0e-13 bit_score=75.9 i
650260873	HMPREF9286_1668 DNA polymerase III, beta subunit	Pepto008_359	1095	379429	380523 + B RBH: fma:FMG_0002 DNA polymerase III beta subunit; K02338 DNA polymerase III subunit be
650260872	HMPREF9286_1667 chromosomal replication initiator protein DnaA	Pepto008_360	1350	380672	382021 + B RBH: UniRef90_D1VRL0 Chromosomal replication initiator protein dnaA n=1 Tax=Peptoniphil
650260871	HMPREF9286_1666 ribosomal protein L34				
650260870	HMPREF9286_1665 ribonuclease P protein component	Pepto008_361	336	382609	382944 + C BLAST: rnpA; ribonuclease P; K03536 ribonuclease P protein component [EC:3.1.26.5] (db=KE
650260869	HMPREF9286_1664 conserved hypothetical protein	Pepto008_362	216	382941	383156 + C BLAST: alpha-hemolysin; K08998 hypothetical protein (db=KEGG evalue=5.0e-19 bit_score=9e
650260868	HMPREF9286_1663 membrane protein insertase, YidC/Oxa1 family	Pepto008_363	747	383175	383921 + C BLAST: hypothetical protein; K03217 preprotein translocase subunit YidC (db=KEGG evalue=6
650260867	HMPREF9286_1662 putative protein jag	Pepto008_364	828	383918	384745 + C BLAST: single stranded nucleic acid binding protein; K06346 spoIII-associated protein (db=KE
650260866	HMPREF9286_1661 tRNA modification GTPase TrmE	Pepto008_365	1380	384829	386208 + B RBH: UniRef90_D1VRL6 tRNA modification GTPase mnmE n=1 Tax=Peptoniphilus lacrimalis 31
650260865	HMPREF9286_1660 tRNA uridine 5-carboxymethylaminomethyl modification en	Pepto008_366	1908	386215	388122 + B RBH: aoe:Clos_2871 tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA; K
650260864	HMPREF9286_1659 16S rRNA methyltransferase GidB	Pepto008_367	696	388109	388804 + C BLAST: gidB; 16S rRNA methyltransferase GidB; K03501 glucose inhibited division protein B [E
650260863	HMPREF9286_1658 sporulation initiation inhibitor protein Soj	Pepto008_368	765	388949	389713 + B RBH: UniRef90_D1VSW0 Sporulation initiation inhibitor protein Soj n=1 Tax=Peptoniphilus lac
650260862	HMPREF9286_1657 stage 0 sporulation protein J	Pepto008_369	846	389697	390542 + C BLAST: spoJ; stage 0 sporulation protein J; K03497 chromosome partitioning protein, ParB f
650260861	HMPREF9286_1656 phenazine biosynthesis protein, PhzF family	Pepto008_370	891	390547	391437 + B RBH: UniRef90_D1VSW2 PhzF family phenazine biosynthesis protein n=1 Tax=Peptoniphilus i
650260860	HMPREF9286_1655 conserved hypothetical protein	Pepto008_371	417	391437	391853 + D IPSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=13 to=32)
650260859	HMPREF9286_1654 conserved hypothetical protein	Pepto008_372	333	392146	392478 + C BLAST: hypothetical protein (db=KEGG evalue=5.0e-10 bit_score=66.6 identity=43.0 coverage
650260858	HMPREF9286_1653 conserved hypothetical protein	Pepto008_373	312	392566	392877 + C BLAST: hypothetical protein (db=KEGG evalue=3.0e-18 bit_score=94.0 identity=47.06 coverag
650260856	HMPREF9286_1651 serine-type D-Ala-D-Ala carboxypeptidase	Pepto008_374	1362	393099	394460 + B RBH: UniRef90_D1VVS0 Putative D-alanyl-D-alanine carboxypeptidase n=1 Tax=Peptoniphilus
650260855	HMPREF9286_1650 GTP cyclohydrolase I	Pepto008_375	555	394642	395196 + C BLAST: foIE; GTP cyclohydrolase I [EC:3.5.4.16]; K01495 GTP cyclohydrolase I [EC:3.5.4.16] (
650260854	HMPREF9286_1649 HDG domain protein	Pepto008_376	480	395196	395675 + C BLAST: HD superfamily hydrolase (db=KEGG evalue=1.0e-47 bit_score=191.0 identity=57.86 c
650260853	HMPREF9286_1648 2-amino-4-hydroxy-6- hydroxymethylidihydropteridine diph	Pepto008_377	819	395686	396504 + B RBH: fma:FMG_0080 bifunctional aldolase-pyrophosphokinase; K13940 dihydronopterin ald
650260852	HMPREF9286_1647 exo-glucosaminidase LytG family protein	Pepto008_378	576	396494	397059 + C BLAST: N-acetylmuramoyl-L-alanine amidase (db=KEGG evalue=4.0e-28 bit_score=120.0 identi
650260851	HMPREF9286_1646 conserved hypothetical protein				
650260850	HMPREF9286_1645 conserved hypothetical protein	Pepto008_379	702	397086	397787 + C BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650260849	HMPREF9286_1644 copper amine oxidase N-terminal domain protein	Pepto008_380	1737	398203	399939 + B RBH: UniRef90_D1VVS4 Maltose ABC transporter, periplasmic maltose-binding protein n=1 Tr
650260848	HMPREF9286_1643 ribonucleoside-diphosphate reductase, alpha subunit	Pepto008_381	2529	400145	402673 + B RBH: fma:FMG_1316 ribonucleotide-diphosphate reductase subunit alpha; K00525 ribonucle
650260847	HMPREF9286_1641 conserved hypothetical protein				
650260846	HMPREF9286_1642 ribonucleoside-diphosphate reductase, beta subunit	Pepto008_382	1041	402688	403728 + C BLAST: ribonucleotide-diphosphate reductase subunit beta; K00526 ribonucleoside-diphosph
650260845	HMPREF9286_1640 cell division protease FtsH	Pepto008_383	1842	403820	405661 + C BLAST: hypothetical protein; K03798 cell division protease FtsH [EC:3.4.24.-] (db=KEGG evalue
650260844	HMPREF9286_1639 glutathione S-transferase, C-terminal domain protein				
650260843	HMPREF9286_1638 conserved hypothetical protein	Pepto008_384	2004	405778	407781 + B RBH: ssa:SSA_1593 dipeptidase, putative (EC:3.4.4.-) (db=KEGG)
650260842	HMPREF9286_1637 ABC 3 transport family protein	Pepto008_385	810	408055	408864 + C BLAST: zinc ABC transporter permease protein; K09816 zinc transport system permease prote
650260841	HMPREF9286_1636 ABC transporter, ATP-binding protein	Pepto008_386	675	408851	409525 + C BLAST: zinc ABC transporter ATP-binding protein; K09817 zinc transport system ATP-binding p
650260840	HMPREF9286_1635 ABC transporter, substrate-binding protein	Pepto008_387	1296	409528	410823 + C BLAST: periplasmic solute binding protein; K09815 zinc transport system substrate-binding pr
650260839	HMPREF9286_1634 putative lipoprotein	Pepto008_388	648	410897	411544 + C BLAST: putative zinc-binding lipoprotein; K09815 zinc transport system substrate-binding prot
650260838	HMPREF9286_1633 methionine-S-sulfoxide reductase	Pepto008_389	942	411850	412791 + B RBH: ccv:CCV52592_1839 peptide methionine sulfoxide reductase MsrA/MsrB; K12267 pepti
650260837	HMPREF9286_1632 glutaminase A				
650260836	HMPREF9286_1631 amino acid carrier protein				
650260835	HMPREF9286_1630 conserved hypothetical protein	Pepto008_390	672	412876	413547 + B RBH: UniRef90_ASTXQ1 Putative uncharacterized protein n=2 Tax=Fusobacterium RepID=AST
650260834	HMPREF9286_1629 transporter gate domain protein	Pepto008_391	1383	413575	414957 + C BLAST: hypothetical protein (db=KEGG evalue=3.0e-105 bit_score=385.0 identity=44.21 cover
650260833	HMPREF9286_1628 transcriptional regulator, AraC family	Pepto008_392	1203	415049	416251 + C BLAST: two component transcriptional regulator, AraC family; K07720 two-component system
650260832	HMPREF9286_1627 conserved hypothetical protein				
650260831	HMPREF9286_1626 DNA-binding helix-turn-helix protein				
650260830	HMPREF9286_1625 magnesium transporter	Pepto008_393	1329	416477	417805 + B RBH: apr:Apr_1068 magnesium transporter (db=KEGG)
650260829	HMPREF9286_1624 conserved hypothetical protein				
650260828	HMPREF9286_1623 putative lipoprotein	Pepto008_394	441	417877	418317 + C BLAST: hypothetical protein (db=KEGG evalue=1.0e-12 bit_score=75.1 identity=41.18 coverage
650260827	HMPREF9286_1622 5'/3'-nucleotidase SurE	Pepto008_395	747	418478	419224 + B RBH: UniRef90_D1VSZ7 5'-nucleotidase surE n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D
650260826	HMPREF9286_1621 metallo-beta-lactamase domain protein	Pepto008_396	786	419238	420023 + B RBH: UniRef90_D1VSZ6 Metallo-beta-lactamase superfamily hydrolase n=1 Tax=Peptoniphilu
650260825	HMPREF9286_1620 YchC protein	Pepto008_397	849	420071	420919 + C BLAST: protein of unknown function YchC (db=KEGG evalue=1.0e-15 bit_score=87.0 identity=
650260824	HMPREF9286_1619 conserved hypothetical protein	Pepto008_398	1344	420925	422268 + B RBH: UniRef90_D1VSZ4 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 31
650260823	HMPREF9286_1618 ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	Pepto008_399	1797	422249	424045 + B RBH: aoe:Clos_2783 multi-sensor signal transduction histidine kinase [EC:2.7.13.3]; K07652 tv
650260822	HMPREF9286_1617 alkaline phosphatase synthesis transcriptional regulatory pr	Pepto008_400	708	424042	424749 + B RBH: UniRef90_D1VSZ2 Transcriptional regulatory protein WalR n=1 Tax=Peptoniphilus lacrir
650260821	HMPREF9286_1616 putative HTH-type transcriptional regulator Ptr2	Pepto008_401	486	424764	425249 + C BLAST: transcriptional regulator (db=KEGG evalue=4.0e-26 bit_score=120.0 identity=39.42 c
650260820	HMPREF9286_1615 acetyltransferase, GNAT family	Pepto008_402	573	425485	426057 + C BLAST: gcn5-related N-acetyltransferase (db=KEGG evalue=4.0e-22 bit_score=107.0 identity=
650260819	HMPREF9286_1614 DnaD domain protein	Pepto008_403	1011	426061	427071 + B RBH: UniRef90_D1VSY9 Primosome, DnaD subunit n=1 Tax=Peptoniphilus lacrimalis 315-B Re
650260818	HMPREF9286_1613 DNA replication protein DnaC	Pepto008_404	975	427046	428020 + B RBH: UniRef90_D1VSY8 DNA replication protein DnaC n=1 Tax=Peptoniphilus lacrimalis 315-B
650260817	HMPREF9286_1612 aminotransferase, class I/II	Pepto008_405	1215	428028	429242 + B RBH: amt:Amet_2618 aspartate aminotransferase [EC:2.6.1.1]; K00811 aspartate aminotransf
650260816	HMPREF9286_1611 conserved hypothetical protein	Pepto008_406	282	429235	429516 + D IPSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=13 to=31)
650260815	HMPREF9286_1610 potassium/proton antiporter	Pepto008_407	1590	429624	431213 + B RBH: cth:Cthe_2757 cvrA, nhaP2, ycgO; potassium/proton antiporter; K11105 cell volume reg
650261783	HMPREF9286_0940 conserved hypothetical protein	Pepto008_408	417	432186	432602 + C BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650261782	HMPREF9286_0939 metallo-beta-lactamase domain protein	Pepto008_409	996	432650	433645 + B RBH: UniRef90_C2B61 Zn-dependent hydrolase n=1 Tax=Anaerococcus lactolyticus ATCC 511
650261781	HMPREF9286_0938 dihydropteroate synthase	Pepto008_410	975	433705	434679 + B RBH: snt:SPT_0335 folP; dihydropteroate synthase [EC:2.5.1.15]; K00796 dihydropteroate syn
650261780	HMPREF9286_0937 phosphate acetyltransferase	Pepto008_411	972	434732	435703 + B RBH: UniRef90_D1VUX8 Phosphate acetyltransferase n=1 Tax=Peptoniphilus lacrimalis 315-B
650260740	HMPREF9286_1533 CRISPR-associated endonuclease Cas3-HD	Pepto008_412	2568	435852	438419 + B RBH: smu:SMU_1764c hypothetical protein; K07012 (db=KEGG)
650260739	HMPREF9286_1532 CRISPR-associated protein Cas5, Dvulg subtype	Pepto008_413	705	438617	439321 + B RBH: UniRef90_D1VVR8 Crisp-associated protein Cas5, dvulg subtype n=1 Tax=Peptoniphilus
650260738	HMPREF9286_1531 CRISPR-associated protein, Csd1 family	Pepto008_414	1944	439335	441278 + B RBH: seq:SZO_14410 CRISPR-associated protein (db=KEGG)
650260737	HMPREF9286_1530 conserved hypothetical protein	Pepto008_415	855	441271	442125 + B RBH: seq:SZO_14400 CRISPR-associated protein (db=KEGG)
650260736	HMPREF9286_1529 CRISPR-associated protein Cas4	Pepto008_416	654	442127	442780 + B RBH: UniRef90_D1VVR5 Crisp-associated reb family exonuclease cas4b n=1 Tax=Peptoniphi

650260735	HMPREF9286_1528 CRISPR-associated endonuclease Cas1	Pepto008_417	1032	442777	443808	+ B	RBH: seq:SZO_14380 CRISPR-associated protein Cas1 (db=KEGG)
650260734	HMPREF9286_1527 CRISPR-associated protein Cas2	Pepto008_418	294	443810	444103	+ C	BLAST: hypothetical protein (db=KEGG eval=1.0e-25 bit_score=118.0 identity=62.89 coverage=100%)
		Pepto008_419	213	445753	445965	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Coprococcus eutactus ATCC 27759 RepID=AA010000
		Pepto008_420	354	445922	446275	+ C	BLAST: putative cytoplasmic protein (db=KEGG eval=1.0e-11 bit_score=71.6 identity=45.0 coverage=100%)
		Pepto008_421	135	446217	446351	+ E	GENE: 3.137 + (rbs_motif=None rbs_spacer=None)
		Pepto008_422	72	446537	446608	+ E	GENE: 3.74 - (rbs_motif=GGTG rbs_spacer=6bp)
		Pepto008_423	192	446618	446809	+ E	GENE: 505.696 - (rbs_motif=None rbs_spacer=None)
		Pepto008_424	159	446860	447018	+ E	GENE: 296.454 - (rbs_motif=None rbs_spacer=None)
		Pepto008_425	150	447356	447505	+ E	GENE: 1.150 + (rbs_motif=None rbs_spacer=None)
		Pepto008_426	162	447604	447765	+ E	GENE: 249.410 + (rbs_motif=None rbs_spacer=None)
		Pepto008_427	63	447872	447934	+ D	IPRSCAN: seg (db=Seg db_id=seg from=8 to=19)
		Pepto008_428	150	447876	448025	+ D	IPRSCAN: seg (db=Seg db_id=seg from=38 to=45)
		Pepto008_429	63	448678	448740	+ E	GENE: 3.65 - (rbs_motif=TTATA rbs_spacer=13bp)
650260994	HMPREF9286_0180 conserved hypothetical protein						
650260993	HMPREF9286_0179 conserved hypothetical protein						
650260992	HMPREF9286_0178 conserved hypothetical protein						
650260991	HMPREF9286_0177 conserved hypothetical protein						
650260990	HMPREF9286_0176 conserved hypothetical protein						
650260989	HMPREF9286_0175 proline-tRNA ligase	Pepto008_430	1704	449057	450760	+ B	RBH: UniRef90_D1VV63 Proline-tRNA ligase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V542
650260988	HMPREF9286_0174 conserved hypothetical protein	Pepto008_431	222	450762	450983	+ C	BLAST: hypothetical protein (db=KEGG eval=4.0e-19 bit_score=96.7 identity=58.57 coverage=100%)
650260987	HMPREF9286_0173 trigger factor	Pepto008_432	1359	451053	452411	+ B	RBH: fma:FMG_1209 FKBP-type peptidyl-prolyl cis-transisomerase; K03545 trigger factor (db=KEGG)
650260986	HMPREF9286_0172 ATP-dependent Clp endopeptidase, proteolytic subunit ClpP	Pepto008_433	585	452429	453013	+ B	RBH: UniRef90_D1VV60 ATP-dependent Clp protease proteolytic subunit n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V542
650260985	HMPREF9286_0171 ATP-dependent Clp protease, ATP-binding subunit ClpX	Pepto008_434	1218	453022	454239	+ B	RBH: aoe:Clos_2173 clpX; ATP-dependent protease ATP-binding subunit ClpX; K03544 ATP-dependent Clp protease
650260984	HMPREF9286_0170 endopeptidase La	Pepto008_435	2334	454286	456619	+ B	RBH: aoe:Clos_2171 ATP-dependent protease La [EC:3.4.21.53]; K01338 ATP-dependent Lon protease
650260983	HMPREF9286_0169 ribosome biogenesis GTP-binding protein YsxC	Pepto008_436	597	456606	457202	+ C	BLAST: engB; ribosome biogenesis GTP-binding protein YsxC; K03978 GTP-binding protein (db=KEGG)
650260982	HMPREF9286_0168 copper amine oxidase N-terminal domain protein						
650260981	HMPREF9286_0167 conserved hypothetical protein	Pepto008_437	867	457349	458215	+ C	BLAST: hypothetical protein (db=KEGG eval=2.0e-62 bit_score=243.0 identity=46.74 coverage=100%)
		Pepto008_438	672	458301	458972	+ C	BLAST: putative transcriptional regulator (db=KEGG eval=1.0e-48 bit_score=196.0 identity=58.95 coverage=100%)
		Pepto008_439	1215	459193	460407	+ B	RBH: dhb:DhaF_2963 diaminopropionate ammonia-lyase; K01751 diaminopropionate ammonia-lyase
		Pepto008_440	1173	460404	461576	+ B	RBH: cpy:Cpy_1500 peptidase (db=KEGG)
		Pepto008_441	1587	461587	463173	+ B	RBH: dsy:DSY1804 hypothetical protein; K06015 [EC:3.5.1.81] (db=KEGG)
		Pepto008_442	1482	463176	464657	+ B	RBH: afn:AcfR_1992 Na+/solute symporter; K03307 solute:Na+ symporter, SSS family (db=KEGG)
		Pepto008_443	519	464772	465290	+ C	BLAST: nitroreductase (db=KEGG eval=1.0e-19 bit_score=99.0 identity=38.15 coverage=98.0%)
650260980	HMPREF9286_0166 nitroreductase family protein						
650260979	HMPREF9286_0165 conserved hypothetical protein						
650260978	HMPREF9286_0164 conserved hypothetical protein	Pepto008_444	663	465723	466385	+ C	BLAST: S-layer domain protein (db=KEGG eval=1.0e-30 bit_score=136.0 identity=37.06 coverage=100%)
650260977	HMPREF9286_0163 5'-nucleotidase, C-terminal domain protein						
650260976	HMPREF9286_0162 phosphonate ABC transporter, permease protein PhnE						
650260975	HMPREF9286_0161 phosphonate ABC transporter, permease protein PhnE						
650260974	HMPREF9286_0160 phosphonate ABC transporter, ATP-binding protein						
650260973	HMPREF9286_0159 phosphate/phosphite/phosphonate ABC transporter, periplasmic binding protein						
650260972	HMPREF9286_0158 23S rRNA (uracil-5-)-methyltransferase RumA	Pepto008_445	1605	466544	468148	+ B	RBH: aoe:Clos_0725 RNA methyltransferase (db=KEGG)
		Pepto008_446	480	469853	470332	+ B	RBH: apr:AprE_1780 BFD domain protein (2Fe-2S)-binding domain protein (db=KEGG)
		Pepto008_447	1833	470333	472165	+ B	RBH: apr:AprE_0693 resolvase domain protein (db=KEGG)
		Pepto008_448	138	472221	472358	+ C	BLAST: hypothetical protein (db=KEGG eval=2.0e-13 bit_score=77.8 identity=91.11 coverage=100%)
		Pepto008_449	1737	472666	474402	+ B	RBH: apr:AprE_0691 ABC transporter related; K06147 ATP-binding cassette, subfamily B, member 1
		Pepto008_450	1722	474395	476116	+ B	RBH: apr:AprE_0690 ABC transporter related; K06147 ATP-binding cassette, subfamily B, member 1
650260644	HMPREF9286_1267 ABC transporter, ATP-binding protein	Pepto008_451	1452	476128	477579	+ B	RBH: UniRef90_C2HI16 ABC superfamily ATP binding cassette transporter, ABC protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V542
650260645	HMPREF9286_1268 cobalt transport protein	Pepto008_452	672	477581	478252	+ B	RBH: UniRef90_C2HI15 ABC superfamily ATP binding cassette transporter permease protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V542
650260646	HMPREF9286_1269 putative membrane protein	Pepto008_453	591	478249	478839	+ B	RBH: UniRef90_C2HI14 Putative uncharacterized protein n=1 Tax=Finexigolia magna ATCC 5357
650260647	HMPREF9286_1270 transcriptional regulator, AraC family	Pepto008_454	978	478906	479883	+ B	RBH: UniRef90_C2HI13 AraC family transcriptional regulator n=1 Tax=Finexigolia magna ATCC 5357
650260648	HMPREF9286_0479 conserved hypothetical protein						
		Pepto008_455	585	479893	480477	+ B	RBH: apr:AprE_0684 transcriptional regulator, TetR family (db=KEGG)
		Pepto008_456	357	480826	481182	+ C	BLAST: hypothetical protein (db=KEGG eval=8.0e-49 bit_score=195.0 identity=88.95 coverage=100%)
		Pepto008_457	306	481972	482277	+ C	BLAST: relaxase/mobilisation protein (db=KEGG eval=7.0e-39 bit_score=162.0 identity=71.0 coverage=100%)
		Pepto008_458	831	482517	483347	+ D	IPRSCAN: seg (db=Seg db_id=seg from=30 to=45)
		Pepto008_459	111	483573	483683	+ E	GENE: 348711.34981 - (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp)
		Pepto008_460	2235	483769	486003	+ B	RBH: lwe:lwe0773 AAA - ATPase, putative (db=KEGG)
		Pepto008_461	1068	485996	487063	+ B	RBH: mco:MCI_004930 AAA family ATPase (db=KEGG)
		Pepto008_462	339	487502	487840	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Anaerococcus hydrogenalis DSM 7454 RepID=D1V542
		Pepto008_463	1299	488480	489778	+ B	RBH: bin:Blon_0026 ATPase (AAA+ superfamily)-like protein; K07133 (db=KEGG)
		Pepto008_464	1359	490360	491718	+ B	RBH: apr:AprE_1095 radical SAM domain protein (db=KEGG)
		Pepto008_465	123	491863	491985	+ E	GENE: 431611.43283 + (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp)
		Pepto008_466	351	492610	492360	+ C	BLAST: acetyltransferase (db=KEGG eval=4.0e-22 bit_score=106.0 identity=46.55 coverage=100%)
		Pepto008_467	735	492731	493465	+ B	RBH: smf:Smon_0573 ABC transporter related protein; K05847 osmoprotectant transport system
		Pepto008_468	1521	493462	494982	+ B	RBH: smf:Smon_0574 substrate-binding region of ABC-type glycine betaine transport system
650260971	HMPREF9286_0157 conserved hypothetical protein						
650260970	HMPREF9286_0156 transcriptional regulator, AbrB family						
650260969	HMPREF9286_0155 conserved domain protein						
650260968	HMPREF9286_0154 Mg2+ transporter-C family protein						
650260967	HMPREF9286_0153 conserved hypothetical protein						
650260966	HMPREF9286_0152 methyltransferase domain protein						
650260965	HMPREF9286_0151 conserved hypothetical protein						
650260964	HMPREF9286_0150 transcriptional regulator, PadR family						
650260963	HMPREF9286_0149 oxidoreductase, short chain dehydrogenase/reductase family protein						
650260962	HMPREF9286_0148 conserved hypothetical protein						
650260961	HMPREF9286_0147 thioesterase family protein	Pepto008_469	483	495111	495593	+ C	BLAST: thioesterase superfamily protein (db=KEGG eval=3.0e-61 bit_score=236.0 identity=52.0 coverage=100%)
650260960	HMPREF9286_0146 conserved hypothetical protein						
650260959	HMPREF9286_0145 putative manganese ABC transporter substrate-binding lipoprotein						
650260958	HMPREF9286_0144 manganese transport system ATP-binding protein MntA						
650260957	HMPREF9286_0143 ABC 3 transport family protein						
650260956	HMPREF9286_0142 ABC 3 transport family protein						
650260955	HMPREF9286_0141 transcriptional regulator MntR family protein						
650260954	HMPREF9286_0140 DNA-binding helix-turn-helix protein						
650260953	HMPREF9286_0139 conserved hypothetical protein						
650260952	HMPREF9286_0138 acetyltransferase, GNAT family						
650260951	HMPREF9286_0137 conserved hypothetical protein						
650260950	HMPREF9286_0136 transporter, major facilitator family protein	Pepto008_470	1197	495775	496971	+ B	RBH: bpb:bpr_III138 MFS transporter (db=KEGG)
		Pepto008_471	555	497498	498052	+ C	BLAST: Transposase family protein (db=KEGG eval=9.0e-39 bit_score=162.0 identity=43.6 coverage=100%)
650260949	HMPREF9286_0135 Na+/Pi-cotransporter II-like protein	Pepto008_472	1599	498504	500102	+ B	RBH: elm:ELI_3014 Na+/Pi-cotransporter (db=KEGG)
		Pepto008_473	1224	500265	501488	+ B	RBH: fma:FMG_0106 biotin synthase related domain-containing protein (db=KEGG)
650260948	HMPREF9286_0134 putative DNA metabolism protein	Pepto008_474	726	501497	502222	+ C	BLAST: hypothetical protein (db=KEGG eval=2.0e-48 bit_score=195.0 identity=45.68 coverage=100%)
650260947	HMPREF9286_0133 conserved domain protein	Pepto008_475	597	502257	502853	+ C	BLAST: hypothetical protein (db=KEGG eval=8.0e-26 bit_score=119.0 identity=36.6 coverage=100%)
650260946	HMPREF9286_0132 conserved hypothetical protein	Pepto008_476	687	502893	503579	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V542
650260945	HMPREF9286_0131 PAP2 family protein	Pepto008_477	525	503609	504133	+ C	BLAST: PAP2 family protein (db=KEGG eval=3.0e-25 bit_score=117.0 identity=52.71 coverage=100%)
650260944	HMPREF9286_0130 LysR substrate binding domain protein	Pepto008_478	870	504135	505004	+ C	BLAST: LysR substrate binding domain family protein (db=KEGG eval=2.0e-23 bit_score=11.7 coverage=100%)
650260943	HMPREF9286_0129 putative lipoprotein	Pepto008_479	1026	505165	506190	+ B	RBH: UniRef90_D1VS42 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V542
650260942	HMPREF9286_0128 putative alginate O-acetyltransferase AlgI	Pepto008_480	1434	506199	507632	+ B	RBH: bhy:BHWAI_02519 algI; alginate O-acetyltransferase (db=KEGG)
650260941	HMPREF9286_0127 transcriptional regulator, AraC family	Pepto008_481	639	507684	508322	+ C	BLAST: response regulator receiver protein (db=KEGG eval=5.0e-11 bit_score=70.9 identity=52.0 coverage=100%)
650260940	HMPREF9286_0126 Yjef-like protein	Pepto008_482	624	508578	509201	+ C	BLAST: carbohydrate kinase, Yjef related protein (db=KEGG eval=4.0e-32 bit_score=140.0 identity=52.0 coverage=100%)
650260939	HMPREF9286_0125 MATE efflux family protein	Pepto008_483	1350	509194	510543	+ B	RBH: UniRef90_D1VVX9 MATE efflux family protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V542
650260938	HMPREF9286_0124 conserved hypothetical protein	Pepto008_484	1200	510636	511835	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V542
650260937	HMPREF9286_0123 putative ATP synthase FO, A subunit	Pepto008_485	1527	511825	513351	+ C	BLAST: chloride channel protein (db=KEGG eval=3.0e-65 bit_score=253.0 identity=37.57 coverage=100%)
650260936	HMPREF9286_0122 transcriptional regulator, Spx/MgsR family	Pepto008_486	351	513478	513828	+ C	BLAST: arsenate reductase and related (db=KEGG eval=4.0e-28 bit_score=126.0 identity=50.0 coverage=100%)

650260935	HMPREF9286_0121 metallo-beta-lactamase domain protein	Pepto008_487	1206	514467	515672	+ B	RBH: cst:CLOST_0656 beta-lactamase domain protein (db=KEGG)
		Pepto008_488	765	515691	516455	+ C	BLAST: exodeoxyribonuclease III (EC:3.1.11.2); K01142 exodeoxyribonuclease III (EC:3.1.11.1;
650260934	HMPREF9286_0120 PP-loop family protein	Pepto008_489	819	516464	517282	+ B	RBH: cbt:CLH_0722 PP-loop family protein (db=KEGG)
650260933	HMPREF9286_0119 nicotinate phosphoribosyltransferase	Pepto008_490	1455	517573	519027	+ B	RBH: cth:Cthe_1177 nicotinate phosphoribosyltransferase (EC:2.4.2.11); K00763 nicotinate pl
650260932	HMPREF9286_0118 radical SAM domain protein	Pepto008_491	867	519058	519924	+ B	RBH: UniRef90_D1VRT6 Radical SAM domain protein n=1 Tax=Peptoniphilus lacrimalis 315-B
650260931	HMPREF9286_0117 conserved hypothetical protein	Pepto008_492	909	519945	520853	+ D	IPRSCAN: seg (db=Seg db_id=seg from=56 to=76)
650260930	HMPREF9286_0116 putative membrane protein	Pepto008_493	1215	520866	522080	+ B	RBH: UniRef90_D1VRT9 Putative permease n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1
		Pepto008_494	345	522149	522493	+ C	BLAST: hypothetical protein; K09700 hypothetical protein (db=KEGG eval=5.0e-31 bit_scc
650260929	HMPREF9286_0115 choline ABC transporter, ATP-binding protein OpuBA	Pepto008_495	1221	522639	523859	+ C	BLAST: opuCa; glycine betaine/L-proline ABC transporter ATPase; K05847 osmoprotectant tra
650260928	HMPREF9286_0114 choline transport system permease protein opuB8	Pepto008_496	636	523852	524487	+ C	BLAST: putative glycine/betaine/carnitine/choline ABC transporter, membrane-spanning sub
650260927	HMPREF9286_0113 glycine betaine/carnitine/choline-binding protein	Pepto008_497	975	524487	525461	+ B	RBH: UniRef90_A8U9U5 Glycine betaine/carnitine/choline ABC transporter, glycine betaine/c
650260926	HMPREF9286_0112 glycine betaine/carnitine/choline transport system permeas	Pepto008_498	645	525454	526098	+ C	BLAST: opuD; glycine betaine/carnitine/choline ABC transporter, ATP-binding protein; K05846
		Pepto008_499	1350	526147	527496	+ C	BLAST: hypothetical protein; K03315 Na ⁺ /H ⁺ antiporter, NhaC family (db=KEGG eval=4.0e-5
650260924	HMPREF9286_0110 putative Na ⁺ /H ⁺ antiporter NhaC	Pepto008_500	2031	527759	529789	+ B	RBH: UniRef90_D1VU12 Putative Hyd family protein n=1 Tax=Peptoniphilus lacrimalis 315-B
650260923	HMPREF9286_0109 efflux transporter, RND family, MFP subunit	Pepto008_501	684	529779	530462	+ B	RBH: UniRef90_D1VU13 Macrolide export ATP-binding/permease protein MacB n=1 Tax=Pepti
650260922	HMPREF9286_0108 ABC transporter, ATP-binding protein	Pepto008_502	1254	530462	531715	+ B	RBH: UniRef90_D1VU14 Macrolide export ATP-binding/permease protein MacB n=1 Tax=Pepti
650260921	HMPREF9286_0107 efflux ABC transporter, permease protein	Pepto008_503	1140	531874	533013	+ C	BLAST: hypothetical protein (db=KEGG eval=2.0e-64 bit_score=249.0 identity=44.86 cove
		Pepto008_504	1356	533106	534461	+ B	RBH: fma:FMG_1259 N-acetylmuramoyl-L-alanine amidase (db=KEGG)
		Pepto008_505	1248	534087	535334	+ C	BLAST: N-acetylmuramoyl-L-alanine amidase (db=KEGG eval=4.0e-64 bit_score=249.0 ide
		Pepto008_506	849	535641	536489	+ C	BLAST: S-layer domain protein (db=KEGG eval=2.0e-25 bit_score=119.0 identity=38.33 co
650261876	HMPREF9286_1720 HNH endonuclease domain protein						
650261874	HMPREF9286_1367 putative membrane protein						
650261873	HMPREF9286_1366 ornithine cyclodeaminase						
650261872	HMPREF9286_1365 conserved hypothetical protein						
650261871	HMPREF9286_1364 conserved hypothetical protein						
650261870	HMPREF9286_1363 conserved hypothetical protein	Pepto008_507	471	536621	537091	+ D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=6 to=28)
650261869	HMPREF9286_1362 DNA-binding protein	Pepto008_508	222	537100	537321	+ C	BLAST: transcriptional regulator; K07727 putative transcriptional regulator (db=KEGG eval=
650261868	HMPREF9286_1361 conserved hypothetical protein	Pepto008_509	480	537311	537790	+ D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=10 to=27)
650261867	HMPREF9286_1360 aldehyde dehydrogenase B	Pepto008_510	1485	537957	539441	+ B	RBH: cpy:Cphy_0958 aldehyde dehydrogenase (db=KEGG)
650261866	HMPREF9286_1359 sodium/glutamate symporter						
650261865	HMPREF9286_1358 histidine-tRNA ligase	Pepto008_511	1308	539598	540905	+ B	RBH: ctc:CTC01958 hisS; histidyl-tRNA synthetase (EC:6.1.1.21); K01892 histidyl-tRNA synthet
650261864	HMPREF9286_1357 GTP-binding protein TypA	Pepto008_512	1824	541234	543057	+ B	RBH: fma:FMG_1042 putative GTP-binding elongation factor; K06207 GTP-binding protein (db
650261863	HMPREF9286_1356 putative cardiolipin synthetase	Pepto008_513	1464	543076	544539	+ B	RBH: UniRef90_D1VRV6 Cardiolipin synthetase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID
650261862	HMPREF9286_1355 conserved hypothetical protein	Pepto008_514	540	544541	545080	+ C	BLAST: zinc metalloprotease; K07043 (db=KEGG eval=2.0e-18 bit_score=94.7 identity=34.1)
650261861	HMPREF9286_1354 conserved hypothetical protein	Pepto008_515	216	545089	545304	+ D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=29)
650261860	HMPREF9286_1353 metal cation transporter, ZIP family	Pepto008_516	756	545430	546185	+ C	BLAST: GufA protein; K07238 zinc transporter, ZIP family (db=KEGG eval=4.0e-72 bit_score=
		Pepto008_517	381	546262	546642	+ D	IPRSCAN: seg (db=Seg db_id=seg from=52 to=62)
650261859	HMPREF9286_1352 conserved hypothetical protein	Pepto008_518	483	546651	547133	+ C	BLAST: rRNA large subunit methyltransferase; K00783 hypothetical protein (db=KEGG eval=
650261858	HMPREF9286_1351 rRNA large subunit m3Psi methyltransferase RimH	Pepto008_519	501	547130	547630	+ C	BLAST: redoxin domain protein; K11065 thiol peroxidase, atypical 2-Cys peroxidoredoxin [EC:1.1
		Pepto008_520	414	547787	548200	+ D	IPRSCAN: PROKAR_LIPOPROTEIN (db=ProfileScan db_id=P551257 from=1 to=21 eval=7.0)
650261857	HMPREF9286_1350 redoxin family protein						
650261856	HMPREF9286_1349 putative phage DNA packaging protein						
650261855	HMPREF9286_1348 putative lipoprotein						
650261854	HMPREF9286_1347 conserved hypothetical protein						
650261853	HMPREF9286_1346 glutacnyl-CoA decarboxylase subunit beta						
650261852	HMPREF9286_1345 pyridine nucleotide-disulfide oxidoreductase						
		Pepto008_521	396	548219	548614	+ D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=25)
		Pepto008_522	666	548659	549324	+ D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=9 to=28)
		Pepto008_523	1854	549670	551523	+ B	RBH: nth:Nther_0856 heat shock protein 90; K04079 molecular chaperone HtpG (db=KEGG)
650261851	HMPREF9286_1344 chaperone protein HtpG						
650261850	HMPREF9286_1342 ABC transporter substrate binding protein						
650261849	HMPREF9286_1341 branched-chain amino acid ABC transporter, permease protein						
650261848	HMPREF9286_1340 ABC transporter, ATP-binding protein						
		Pepto008_524	693	551786	552478	+ C	BLAST: putative ATP/GTP-binding protein (db=KEGG eval=5.0e-54 bit_score=213.0 identit
		Pepto008_525	219	552489	552707	+ C	BLAST: ferredoxin; K00176 2-oxoglutarate ferredoxin oxidoreductase subunit delta [EC:1.2.7
		Pepto008_526	1065	552719	553783	+ B	RBH: cst:CLOST_0491 vorB; ketoisovalerate oxidoreductase subunit vorB (vor) [2-oxoisovaler
		Pepto008_527	753	553783	554535	+ B	RBH: amt:Amet_4304 thiamine pyrophosphate binding domain-containing protein; K00175
		Pepto008_528	1203	554535	555737	+ C	BLAST: subunit of oxidoreductase [EC:1.2.7.1]; K00177 2-oxoglutarate ferredoxin oxidoredu
650261847	HMPREF9286_1339 formimidoylglutamate	Pepto008_529	1032	555861	556892	+ B	RBH: clj:CLJU_c21420 formiminoglutamate [EC:3.5.3.8]; K01479 formiminoglutamate [EC:3.5.
650261846	HMPREF9286_1338 glyoxylate reductase	Pepto008_530	954	556901	557854	+ B	RBH: fma:FMG_0407 putative dehydrogenase (db=KEGG)
650261845	HMPREF9286_1337 conserved hypothetical protein						
		Pepto008_531	636	558113	558748	+ D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=24)
		Pepto008_532	300	558773	559072	+ D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=29)
		Pepto008_533	1344	559496	560839	+ B	RBH: cpy:Cphy_2060 MATE efflux family protein (db=KEGG)
650261844	HMPREF9286_1336 MATE efflux family protein						
650261843	HMPREF9286_1335 translation elongation factor Tu						
650261842	HMPREF9286_1334 endoribonuclease L-PSP						
650261841	HMPREF9286_1333 ABC transporter transmembrane region						
		Pepto008_534	186	560922	561107	+ C	BLAST: elongation factor Tu; K02358 elongation factor EF-Tu [EC:3.6.5.3] (db=KEGG eval=
		Pepto008_535	75	562041	562115	+ D	IPRSCAN: GTP_EFTU_D3 (db=HMM Pfam db_id=PF03143 from=1 to=23 eval=1.3e-07 inter
650261840	HMPREF9286_1332 ABC transporter, ATP-binding protein	Pepto008_536	1707	562304	564010	+ C	BLAST: ABC transporter, ATP-binding protein (db=KEGG eval=1.0e-128 bit_score=463.0 ide
650261839	HMPREF9286_1331 ABC transporter, ATP-binding protein	Pepto008_537	1746	564003	565748	+ C	BLAST: yfiC; YfiC; K11085 ATP-binding cassette, subfamily B, bacterial MsbA [EC:3.6.3.-] (db=K
650261838	HMPREF9286_1330 NADH-dependent butanol dehydrogenase A	Pepto008_538	1173	565757	566929	+ B	RBH: cbb:CLD_3130 NADH-dependent butanol dehydrogenase (EC:1.1.1.-); K00100 [EC:1.1.1.-
650261837	HMPREF9286_1329 ABC transporter, permease protein						
650261836	HMPREF9286_1328 ABC transporter, ATP-binding protein						
650261835	HMPREF9286_1327 NMT1/THI5-like protein						
650261834	HMPREF9286_1326 superoxide reductase	Pepto008_539	354	567015	567368	+ C	BLAST: superoxide reductase; K05919 superoxide reductase [EC:1.15.1.2] (db=KEGG eval=5
650261833	HMPREF9286_1325 conserved hypothetical protein	Pepto008_540	1131	567496	568626	+ B	RBH: UniRef90_D1VVQ9 Protein YpsC n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VVQ9
650261832	HMPREF9286_1324 stage II sporulation protein E	Pepto008_541	1119	568668	569786	+ B	RBH: UniRef90_D1VVR0 Putative PAS/PAC sensor protein n=1 Tax=Peptoniphilus lacrimalis 31
650261831	HMPREF9286_1323 repeat protein	Pepto008_542	1962	570033	571994	+ B	RBH: UniRef90_D1VVL9 Cell surface glycoprotein 1 n=1 Tax=Peptoniphilus lacrimalis 315-B Re
650261830	HMPREF9286_1322 conserved hypothetical protein						
650261829	HMPREF9286_1321 putative membrane protein						
650261828	HMPREF9286_1320 transcriptional regulator, Tetr family						
650261827	HMPREF9286_1319 universal stress family protein	Pepto008_543	435	572456	572890	+ C	BLAST: UspA domain protein (db=KEGG eval=1.0e-14 bit_score=81.6 identity=39.16 covera
650261826	HMPREF9286_1318 butyryl-CoA dehydrogenase	Pepto008_544	1143	573281	574423	+ B	RBH: aoe:Clos_0091 acyl-CoA dehydrogenase domain-containing protein (db=KEGG)
650261825	HMPREF9286_1317 electron transfer flavoprotein subunit beta	Pepto008_545	801	574442	575242	+ B	RBH: elm:ELU_0541 hypothetical protein; K03521 electron transfer flavoprotein beta subunit (
650261824	HMPREF9286_1316 electron transfer flavoprotein subunit alpha	Pepto008_546	1008	575257	576264	+ B	RBH: aoe:Clos_0638 electron transfer flavoprotein alpha/beta-subunit; K03522 electron trans
650262241	HMPREF9286_0283 ABC transporter, ATP-binding protein						
650262240	HMPREF9286_0282 MATE efflux family protein						
650262239	HMPREF9286_0281 conserved hypothetical protein						
650262238	HMPREF9286_0280 conserved hypothetical protein						
650262237	HMPREF9286_0279 MobA/MobI family protein						
650262236	HMPREF9286_0278 phage replisome organizer N-terminal domain protein						
650262235	HMPREF9286_0277 conserved hypothetical protein						
650262234	HMPREF9286_0276 conserved hypothetical protein						
650262233	HMPREF9286_0275 conserved hypothetical protein						
650262232	HMPREF9286_0274 conserved hypothetical protein						
650262231	HMPREF9286_0273 conserved hypothetical protein						
650262230	HMPREF9286_0272 conserved domain protein						
650262229	HMPREF9286_0271 conserved hypothetical protein						
650262228	HMPREF9286_0270 conserved hypothetical protein						
650262227	HMPREF9286_0269 conserved hypothetical protein						
650262226	HMPREF9286_0268 conserved hypothetical protein						
650262225	HMPREF9286_0267 conserved hypothetical protein						
650262224	HMPREF9286_0266 conserved hypothetical protein						

[illegible]

650262347	HMPREF9286_0385 modification methylase DpnIIA				
650262346	HMPREF9286_0384 conserved hypothetical protein				
650262345	HMPREF9286_0383 methyltransferase domain protein				
650262344	HMPREF9286_0382 carbamoyl-phosphate synthase, large subunit	Pepto009_54	3204	59854	63057 + B RBH: cdc:CD196_3382 carB; carbamoyl phosphate synthase large subunit; K01955 carbamoyl-
650262343	HMPREF9286_0381 glycosyltransferase, group 1 family protein				
650262342	HMPREF9286_0380 conserved hypothetical protein				
650262341	HMPREF9286_0379 conserved hypothetical protein				
650262339	HMPREF9286_0377 glycosyltransferase, group 1 family protein	Pepto009_55	1137	63334	64470 + B RBH: csc:Csc_1346 glycosyl transferase, group 1; K00754 [EC:2.4.1.-] (db=KEGG)
		Pepto009_56	489	64457	64945 + C BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V
		Pepto009_57	549	64947	65495 + C BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V
650262340	HMPREF9286_0378 O-antigen polymerase	Pepto009_58	1392	65489	66880 + B RBH: UniRef90_D1VV2 Putative O-antigen polymerase n=1 Tax=Peptoniphilus lacrimalis 315
650262338	HMPREF9286_0376 polysaccharide pyruvyl transferase CsaB	Pepto009_59	1104	66884	67987 + B RBH: UniRef90_D1VVC1 Polysaccharide pyruvyl transferase CsaB n=1 Tax=Peptoniphilus lacrir
		Pepto009_60	1290	68068	69357 + C BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VV
650262070	HMPREF9286_0646 DNA internalization competence protein ComEC/Rec2-like p	Pepto009_61	2271	69433	71703 + B RBH: UniRef90_D1VVK4 DNA internalization-related competence protein ComEC/Rec2 n=1 Ta
650262069	HMPREF9286_0645 DNA polymerase III, delta subunit	Pepto009_62	1029	71675	72703 + C BLAST: DNA polymerase III, delta subunit; K02340 DNA polymerase III subunit delta [EC:2.7.7.
650262068	HMPREF9286_0644 ribosomal protein S20	Pepto009_63	279	72771	73049 + C BLAST: 30S ribosomal protein S20 n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VVK2_9FI
650262067	HMPREF9286_0643 putative oxygen-independent coproporphyrinogen III oxidase	Pepto009_64	1143	73129	74271 + B RBH: ccc:Ccel_1980 oxygen-independent coproporphyrinogen III oxidase; K02495 oxygen-ind
650262066	HMPREF9286_0642 GTP-binding protein LepA	Pepto009_65	1812	74255	76066 + B RBH: fma:FMG_0784 GTP-binding protein LepA; K03596 GTP-binding protein LepA (db=KEGG)
650262065	HMPREF9286_0641 signal peptidase I	Pepto009_66	534	76122	76655 + C BLAST: signal peptidase I; K03100 signal peptidase I [EC:3.4.21.89] (db=KEGG eval=5.0e-33)
650262064	HMPREF9286_0640 heat-inducible transcription repressor HrcA	Pepto009_67	1023	76903	77925 + B RBH: UniRef90_D1VV6 Heat-inducible transcription repressor HrcA n=1 Tax=Peptoniphilus la
650262063	HMPREF9286_0639 co-chaperone GrpE	Pepto009_68	543	77934	78476 + C BLAST: GrpE protein; K03687 molecular chaperone GrpE (db=KEGG eval=8.0e-31 bit_score=
650262062	HMPREF9286_0638 chaperone protein DnaK	Pepto009_69	1830	78503	80332 + B RBH: elm:ELI_3543 hypothetical protein; K04043 molecular chaperone DnaK (db=KEGG)
650262061	HMPREF9286_0637 chaperone protein DnaJ	Pepto009_70	1128	80474	81601 + B RBH: UniRef90_D1VVE3 Chaperone protein DnaJ n=1 Tax=Peptoniphilus lacrimalis 315-B Repl
650262060	HMPREF9286_0636 ribosomal protein L11 methyltransferase	Pepto009_71	909	81675	82583 + B RBH: UniRef90_D1VVE1 Ribosomal protein L11 methyltransferase n=1 Tax=Peptoniphilus lac
650262059	HMPREF9286_0635 RNA methyltransferase, RsmE family	Pepto009_72	690	82576	83265 + C BLAST: protein of unknown function DUF558; K09761 ribosomal RNA small subunit methyltra
650262058	HMPREF9286_0634 RNA methylthiotransferase YqeY	Pepto009_73	1299	83265	84563 + B RBH: fma:FMG_0776 Fe-S oxidoreductase (db=KEGG)
650262057	HMPREF9286_0633 conserved hypothetical protein	Pepto009_74	357	84591	84947 + C BLAST: hypothetical protein; K09706 hypothetical protein (db=KEGG eval=1.0e-10 bit_score
650262056	HMPREF9286_0632 histidine triad domain protein	Pepto009_75	339	84949	85287 + C BLAST: HIT family protein; K02503 Hit-like protein involved in cell-cycle regulation (db=KEGG
650262055	HMPREF9286_0631 phospholipase, patatin family	Pepto009_76	852	85467	86318 + B RBH: UniRef90_C6LB9 Phospholipase, patatin family n=1 Tax=Bryantella fortameigenis DSM
650262054	HMPREF9286_0630 SNARE-like domain protein	Pepto009_77	756	86345	87100 + C BLAST: DedA family protein (db=KEGG eval=6.0e-09 bit_score=64.7 identity=25.57 coverage
650262053	HMPREF9286_0629 ribosomal protein S21	Pepto009_78	180	87189	87368 + C BLAST: ribosomal protein S21; K02970 small subunit ribosomal protein S21 (db=KEGG eval=
650262052	HMPREF9286_0628 YqeY-like protein	Pepto009_79	444	87834	87827 + C BLAST: GatB/YqeY domain protein; K09117 hypothetical protein (db=KEGG eval=3.0e-38 bit
650262051	HMPREF9286_0627 conserved hypothetical protein				
650262050	HMPREF9286_0626 modulation efficiency protein D	Pepto009_80	720	88011	88730 + C BLAST: hypothetical protein (db=KEGG eval=2.0e-12 bit_score=75.9 identity=37.7 coverage
650262049	HMPREF9286_0625 conserved hypothetical protein	Pepto009_81	993	88739	89731 + B RBH: fma:FMG_0772 hypothetical protein (db=KEGG)
650262048	HMPREF9286_0624 conserved hypothetical protein	Pepto009_82	582	89731	90312 + D IPSCAN: coiled-coil (db=Coil db_id=coil from=65 to=92 eval=NA)
650262047	HMPREF9286_0623 PhoH-like protein	Pepto009_83	1035	90394	91428 + B RBH: cth:Cthe_1071 PhoH-like protein; K06217 phosphate starvation-inducible protein PhoH
650262046	HMPREF9286_0622 translation metalloprotein YbeY	Pepto009_84	447	91412	91858 + C BLAST: putative metal-dependent hydrolase; K07042 (db=KEGG eval=4.0e-24 bit_score=11.
650262045	HMPREF9286_0621 prokaryotic diacylglycerol kinase	Pepto009_85	708	91863	92570 + B RBH: UniRef90_D1VTF5 Diacylglycerol kinase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=C
650262044	HMPREF9286_0620 cytidine deaminase	Pepto009_86	414	92571	92984 + C BLAST: cdd; cytidine deaminase (EC:3.5.4.5); K01489 cytidine deaminase [EC:3.5.4.5] (db=KEG
650262043	HMPREF9286_0619 ribosome biogenesis GTPase Era	Pepto009_87	906	92971	93876 + B RBH: elm:ELI_2843 hypothetical protein; K03595 GTP-binding protein Era (db=KEGG)
650262042	HMPREF9286_0618 DNA repair protein RecO	Pepto009_88	705	93860	94564 + C BLAST: recO; DNA repair protein RecO; K03584 DNA repair protein RecO (recombination prot
650262041	HMPREF9286_0617 glycine-tRNA ligase, alpha subunit	Pepto009_89	885	94576	95460 + B RBH: cdl:CDR20291_2325 glyO; glycyL-tRNA synthetase subunit alpha; K01878 glycyL-tRNA syr
650262040	HMPREF9286_0616 conserved domain protein				
650262039	HMPREF9286_0615 glycine-tRNA ligase, beta subunit	Pepto009_90	2073	95453	97525 + B RBH: cdc:CD196_2277 glyS; glycyL-tRNA synthetase beta chain; K01879 glycyL-tRNA synthetasi
650262038	HMPREF9286_0614 transcriptional repressor CcpN	Pepto009_91	630	97538	98167 + C BLAST: putative signal transduction protein with CBS domains (db=KEGG eval=2.0e-56 bit_s
650262037	HMPREF9286_0613 conserved hypothetical protein	Pepto009_92	822	98184	99005 + B RBH: UniRef90_D1VTG2 Putative phosphotransferase HMPREF0628_0242 n=1 Tax=Peptonip
650262036	HMPREF9286_0612 putative dGTPase	Pepto009_93	1014	99001	100023 + B RBH: toc:Toce_0930 deoxyguanosinotriphosphate triphosphohydrolase; K01129 dGTPase [EC
650262035	HMPREF9286_0611 DNA primase	Pepto009_94	1794	100024	101817 + B RBH: cac:CA_C1299 dnaG; DNA primase; K02316 DNA primase [EC:2.7.7.-] (db=KEGG)
650262034	HMPREF9286_0610 RNA polymerase sigma factor RpoD	Pepto009_95	1089	101807	102895 + B RBH: cth:Cthe_0895 RNA polymerase sigma factor RpoD; K03086 RNA polymerase primary sig
650262033	HMPREF9286_0609 conserved hypothetical protein	Pepto009_96	693	102892	103584 + C BLAST: hypothetical protein; K06967 (db=KEGG eval=1.0e-16 bit_score=90.1 identity=35.68
650262032	HMPREF9286_0608 dinuclear metal center protein, YbgI family	Pepto009_97	777	103565	104341 + C BLAST: hypothetical protein (db=KEGG eval=1.0e-34 bit_score=149.0 identity=39.91 covera
650262030	HMPREF9286_0606 NlpC/P60 family protein	Pepto009_98	1125	104860	105984 + B RBH: UniRef90_D1VTG8 Cell wall-associated hydrolase n=1 Tax=Peptoniphilus lacrimalis 315-I
650261604	HMPREF9286_0723 sodium/glutamate symporter	Pepto009_99	1257	106430	107686 + B RBH: cbi:CLJ_00733 gltS; sodium/glutamate symporter; K03312 glutamate:Na+ symporter, ES
650261603	HMPREF9286_0722 transcriptional regulator NrdR	Pepto009_100	459	107848	108306 + C BLAST: nrdR; transcriptional regulator of nrd genes; K07738 transcriptional repressor NrdR [d
650261602	HMPREF9286_0721 ATPase, AAA family	Pepto009_101	1302	108308	109069 + B RBH: tjr:TherJR_1916 AAA ATPase central domain protein; K07478 putative ATPase (db=KEGG
650261601	HMPREF9286_0720 asparagine-tRNA ligase	Pepto009_102	1389	109685	111073 + B RBH: ctc:CTC00143 asnC; asparaginyl-tRNA synthetase [EC:6.1.1.22]; K01893 asparaginyl-tRN
650261600	HMPREF9286_0719 leucine-tRNA ligase	Pepto009_103	2412	111082	113493 + B RBH: fma:FMG_0623 leuS; leucyl-tRNA synthetase; K01869 leucyl-tRNA synthetase [EC:6.1.1.4
650261599	HMPREF9286_0718 TIGR00255 family protein	Pepto009_104	876	113544	114419 + C BLAST: hypothetical protein (db=KEGG eval=9.0e-54 bit_score=213.0 identity=42.37 covera
650261598	HMPREF9286_0717 guanylate kinase	Pepto009_105	621	114448	115068 + B RBH: UniRef90_D1VSF0 Guanylate kinase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V
650261597	HMPREF9286_0716 DNA-directed RNA polymerase, omega subunit	Pepto009_106	303	115065	115367 + C BLAST: DNA-directed RNA polymerase, omega subunit; K03060 DNA-directed RNA polymeras
650261596	HMPREF9286_0715 phosphoantithenocysteine decarboxylase/phosphopant	Pepto009_107	1194	115369	116562 + B RBH: clo:HMPREF0868_0650 coaB; phosphoantithenocysteine decarboxylase/phosphopant
650261595	HMPREF9286_0714 phospholipase protein N'	Pepto009_108	2340	116592	118391 + B RBH: UniRef90_D1VSE7 Primosomal protein N' n=1 Tax=Peptoniphilus lacrimalis 315-B RepID
650261594	HMPREF9286_0713 peptide deformylase	Pepto009_109	480	118940	119419 + C BLAST: peptide deformylase [EC:3.5.1.88]; K01462 [EC:3.5.1.88] (db=KEGG eval=5.0e-41 bit
650261593	HMPREF9286_0712 methionyl-tRNA formyltransferase	Pepto009_110	924	119149	120342 + C BLAST: fmt; methionyl-tRNA formyltransferase [EC:2.1.2.9]; K00604 methionyl-tRNA formyltr
650261592	HMPREF9286_0711 putative neutral zinc metallopeptidase	Pepto009_111	690	120342	121031 + C BLAST: hypothetical protein; K06973 (db=KEGG eval=2.0e-50 bit_score=202.0 identity=50.7
650261591	HMPREF9286_0710 ribosomal RNA small subunit methyltransferase B	Pepto009_112	1299	121031	122329 + B RBH: cth:Cthe_0571 snr protein; K03500 ribosomal RNA small subunit methyltransferase B [E
650261590	HMPREF9286_0709 23S rRNA m2A2503 methyltransferase	Pepto009_113	1020	122424	123443 + B RBH: UniRef90_D1VSE2 Radical SAM enzyme, Cfr family n=1 Tax=Peptoniphilus lacrimalis 315
650261589	HMPREF9286_0708 putative serine/threonine phosphatase stp	Pepto009_114	717	123443	124159 + C BLAST: protein serine/threonine phosphatase, putative; K01090 protein phosphatase [EC:3.1.
650261588	HMPREF9286_0707 putative serine/threonine-protein kinase PrkC	Pepto009_115	1977	124167	126143 + B RBH: UniRef90_D1VSE0 Serine/threonine-protein kinase PrkC n=1 Tax=Peptoniphilus lacrima
650261587	HMPREF9286_0706 ribosome small subunit-dependent GTPase A	Pepto009_116	855	126143	126997 + B RBH: UniRef90_D1VSD9 Ribosome small subunit-dependent GTPase A n=1 Tax=Peptoniphilus
650261586	HMPREF9286_0705 ribulose-phosphate 3-epimerase	Pepto009_117	645	126997	127641 + C BLAST: ribulose-phosphate 3-epimerase (EC:5.1.3.1); K01783 ribulose-phosphate 3-epimerase
650261585	HMPREF9286_0704 thiamine diphosphokinase	Pepto009_118	639	127638	128276 + B BLAST: thiamine pyrophosphokinase; K00949 thiamine pyrophosphokinase [EC:2.7.6.2] (db=K
650261020	HMPREF9286_0026 ribosomal protein L28	Pepto009_119	192	128454	128645 + C BLAST: rpmB; 50S ribosomal protein L28; K02902 large subunit ribosomal protein L28 (db=KE
650261019	HMPREF9286_0025 conserved hypothetical protein	Pepto009_120	354	128825	129178 + C BLAST: hypothetical protein (db=KEGG eval=1.0e-28 bit_score=128.0 identity=52.14 covera
650261018	HMPREF9286_0024 DAK2 domain fusion protein YloV	Pepto009_121	1665	129192	130856 + B RBH: amt:Amet_2771 Dak phosphatase; K07030 (db=KEGG)
650261017	HMPREF9286_0023 ATP-dependent DNA helicase RecG	Pepto009_122	2034	130904	132937 + B RBH: ttm:Tthe_1511 ATP-dependent DNA helicase RecG; K03655 ATP-dependent DNA helicas
650261016	HMPREF9286_0022 RNA methyltransferase, RsmD family	Pepto009_123	567	132991	133557 + C BLAST: hypothetical protein (db=KEGG eval=5.0e-32 bit_score=140.0 identity=43.09 covera
650261015	HMPREF9286_0021 pantetheine-phosphate adenylyltransferase	Pepto009_124	486	133535	134020 + C BLAST: pantetheine-phosphate adenylyltransferase [EC:2.7.7.3]; K00954 pantetheine-phosph
650261014	HMPREF9286_0020 conserved hypothetical protein	Pepto009_125	441	134017	134457 + C BLAST: vacuolar-type H+-ATPase subunit H (db=KEGG eval=2.0e-21 bit_score=104.0 identit
650261067	HMPREF9286_0073 ABC transporter, ATP-binding protein	Pepto009_126	1746	134796	136541 + B RBH: UniRef90_D1VU16 ABC transporter, ATP-binding/permease protein n=1 Tax=Peptonip
650261066	HMPREF9286_0072 ABC transporter, ATP-binding protein	Pepto009_127	1722	136538	138259 + B RBH: UniRef90_D1VU17 ABC transporter, ATP-binding protein n=1 Tax=Peptoniphilus lacrima
		Pepto009_128	582	138689	139270 + C BLAST: alkaline shock protein (db=KEGG eval=8.0e-37 bit_score=156.0 identity=70.16 cov
		Pepto009_129	336	139299	139634 + D IPSCAN: DUF2273 (db=HMMFam db_id=PF10031 from=60 to=95 eval=1.5e-10 interpro
		Pepto009_130	549	139644	140192 + C BLAST: hypothetical protein (db=KEGG eval=1.0e-27 bit_score=125.0 identity=36.81 cove
650262029	HMPREF9286_0605 transporter, dicarboxylate/amino acid:cation Na+/H+ sympe	Pepto009_131	1206	140570	141775 + B RBH: apr:Apr_1230 sodium:dicarboxylate symporter (db=KEGG)
650262028	HMPREF9286_0604 sodium/glutamate symporter	Pepto009_132	1230	141884	143113 + B RBH: fnu:FN1801 sodium/glutamate symport carrier protein; K03312 glutamate:Na+ symport
650262027	HMPREF9286_0603 flavodoxin	Pepto009_133	429	143366	143794 + C BLAST: flavodoxin (db=KEGG eval=3.0e-37 bit_score=156.0 identity=50.0 coverage=98.601:
650262026	HMPREF9286_0602 conserved hypothetical protein	Pepto009_134	588	143803	144390 + C BLAST: hypothetical protein (db=KEGG eval=9.0e-26 bit_score=119.0 identity=38.34 covera
650262025	HMPREF9286_0601 conserved hypothetical protein	Pepto009_135	666	144648	145313 + C BLAST: hypothetical protein (db=KEGG eval=6.7e-09 bit_score=63.9 identity=27.09 coverag
650261077	HMPREF9286_0084 poly(R)-hydroxyalkanoic acid synthase, class III, PhaE subunit	Pepto009_136	1062	145433	146494 + C BLAST: hypothetical protein (db=KEGG eval=5.0e-41 bit_score=171.0 identity=30.12 covera
650261076	HMPREF9286_0083 poly(R)-hydroxyalkanoic acid synthase, class III, PhaC subunit	Pepto009_137	1071	146510	147580 + B RBH: apr:Apr_0114 poly(R)-hydroxyalkanoic acid synthase, class III, PhaC subunit; K03821 pc
650261075	HMPREF9286_0082 MaoC-like protein				
		Pepto009_138	588	147680	148267 + C BLAST: class II aldolase/adducin family protein; K01628 L-fuculose-phosphate aldolase [EC:4
		Pepto009_139	831	148370	149200 + C BLAST: purine nucleoside phosphorylase I, inosine and guanosine-specific [EC:2.4.2.1]; K037
		Pepto009_140	1050	149193	150242 + B RBH: bpo:BP951000_2178 hypothetical protein; K08963 methylthioribose-1-phosphate ison
650261065	HMPREF9286_0071 putative membrane protein				
650261064	HMPREF9286_0070 cobalt transport protein				
650261063	HMPREF9286_0069 ABC transporter, ATP-binding protein				
650261062	HMPREF9286_0068 conserved hypothetical protein				
650261061	HMPREF9286_0067 transcriptional regulator, AraC family				
650261060	HMPREF9286_0066 conserved hypothetical protein	Pepto009_141	795	150787	151581 + B RBH: UniRef90_D1VUK6 Putative nitroreductase n=1 Tax=Peptoniphilus lacrimalis 315-B Repl
650261059	HMPREF9286_0065 UvrD/REP helicase	Pepto009_142	1857	151692	153548 + B RBH: fma:FMG_0647 DNA helicase II; K03657 DNA helicase II / ATP-dependent DNA helicase f

650261058 HMPREF9286_0064 magnesium transporter	Pepto009_143	1338	153535	154872	+	B	RBH: afn:Acerf_1271 magnesium transporter; K06213 magnesium transporter (db=KEGG)
650261057 HMPREF9286_0063 conserved hypothetical protein							
650261056 HMPREF9286_0062 acetyltransferase, GNAT family	Pepto009_144	504	154993	155496	+	C	BLAST: acetyltransferase (db=KEGG eval=4.0e-20 bit_score=100.0 identity=36.9 coverage=5
650261055 HMPREF9286_0061 sugar fermentation stimulation protein	Pepto009_145	717	155469	156185	+	C	BLAST: sugar fermentation stimulation protein; K06206 sugar fermentation stimulation protei
650261054 HMPREF9286_0060 pyrazinamidase/nicotinamidase family protein	Pepto009_146	525	156266	156790	+	C	BLAST: isochorismatase hydrolase (db=KEGG eval=1.0e-38 bit_score=162.0 identity=46.2 c
650261050 HMPREF9286_0056 cadmium-exporting ATPase	Pepto009_147	2076	157355	159430	+	B	RBH: UniRef90_D1VVW1 Cadmium-exporting ATPase n=1 Tax=Peptoniphilus lacrimalis 315-B
650261049 HMPREF9286_0055 ferredoxin	Pepto009_148	171	159697	159867	+	C	BLAST: ferredoxin (db=KEGG eval=1.0e-14 bit_score=82.0 identity=74.55 coverage=94.736f
650261048 HMPREF9286_0054 putative CoA-substrate-specific enzyme activase	Pepto009_149	4278	160187	164464	+	B	RBH: fma:FMG_1146 hypothetical protein (db=KEGG)
650261047 HMPREF9286_0053 copper amine oxidase N-terminal domain protein	Pepto009_150	939	164515	165453	+	C	BLAST: copper amine oxidase domain protein (db=KEGG eval=2.0e-21 bit_score=106.0 iden
650261046 HMPREF9286_0052 putative lipoprotein	Pepto009_151	507	165465	165971	+	C	BLAST: Ferlin, putative n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT33_9FIRM (db=UN
650261045 HMPREF9286_0051 putative tRNA adenyllyltransferase	Pepto009_152	1323	166072	167394	+	B	RBH: cst:CLOST_0552 poly a polymerase family protein (db=KEGG)
650261044 HMPREF9286_0050 phosphoglucosamine mutase	Pepto009_153	1347	167399	168745	+	B	RBH: aoe:Clos_2382 glmM; phosphoglucosamine mutase (EC:5.4.2.10); K03431 phosphoglucc
650261043 HMPREF9286_0049 EDD domain protein, DegV family	Pepto009_154	834	168750	169583	+	B	RBH: UniRef90_D1VT36 DegV family protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D
650261042 HMPREF9286_0048 conserved hypothetical protein	Pepto009_155	1134	169592	170725	+	B	RBH: UniRef90_D1VT37 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 31
650261041 HMPREF9286_0047 toxic anion resistance protein TelA	Pepto009_156	1122	170728	171849	+	B	RBH: apr:Apr_0195 toxic anion resistance family protein (db=KEGG)
650261040 HMPREF9286_0046 xanthine phosphoribosyltransferase	Pepto009_157	573	171901	172473	+	C	BLAST: xpt; xanthine phosphoribosyltransferase (EC:2.4.2.22); K03816 xanthine phosphorib
650261180 HMPREF9286_1210 conserved hypothetical protein	Pepto009_158	543	172628	173170	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Clostridium asparagiforme DSM 15981 Repl
650261179 HMPREF9286_1209 putative lipoprotein	Pepto009_159	2244	173161	175404	+	B	RBH: rci:RCIX2261 hypothetical protein (db=KEGG)
650261178 HMPREF9286_1208 nitroreductase family protein	Pepto009_160	534	174877	176020	+	C	BLAST: probable nitroreductase (db=KEGG eval=4.0e-29 bit_score=130.0 identity=40.12 co
650261177 HMPREF9286_1207 hydrolase, P-loop family	Pepto009_161	459	176004	176462	+	C	BLAST: hypothetical protein; K06925 (db=KEGG eval=3.0e-37 bit_score=156.0 identity=47.5
650261176 HMPREF9286_1206 universal bacterial protein YeaZ	Pepto009_162	675	176443	177117	+	C	BLAST: putative O-sialoglycoprotein endopeptidase (db=KEGG eval=4.0e-26 bit_score=121.
650261175 HMPREF9286_1205 ribosomal-protein-alanine acetyltransferase	Pepto009_163	435	177089	177523	+	C	BLAST: ribosomal-protein-alanine acetyltransferase; K03789 ribosomal-protein-alanine N-ace
650261174 HMPREF9286_1204 putative glycoprotease GCP	Pepto009_164	999	177528	178526	+	B	RBH: UniRef90_D1VV12 Putative glycoprotease GCP n=1 Tax=Peptoniphilus lacrimalis 315-B R
650261173 HMPREF9286_1203 conserved hypothetical protein	Pepto009_165	1539	178570	180108	+	D	IPRSCAN: seg (db=Seg db_id=seg from 8-to 26)
650261172 HMPREF9286_1202 peptidase M16 inactive domain protein	Pepto009_166	2892	180224	183115	+	B	RBH: ctc:CTC00810 zinc-dependent peptidase; K06972 (db=KEGG)
650261171 HMPREF9286_1201 inositol monophosphatase family protein							
650261170 HMPREF9286_1200 Ppx/GppA phosphatase family protein	Pepto009_167	918	183289	184206	+	C	BLAST: Ppx/GppA phosphatase family protein (db=KEGG eval=2.0e-34 bit_score=149.0 ider
650261169 HMPREF9286_1199 polyphosphate kinase 1	Pepto009_168	2142	184184	186325	+	B	RBH: sub:SUB0262 ppx; polyphosphate kinase (EC:2.7.4.1); K00937 polyphosphate kinase [EC
	Pepto009_169	1233	186508	187140	+	B	RBH: apr:Apr_0570 sugar-binding domain protein (db=KEGG)
650261168 HMPREF9286_1198 phosphoribosylaminoimidazole succinocarboxamide synthas	Pepto009_170	681	188201	188881	+	B	RBH: UniRef90_C7HSM9 Phosphoribosylaminoimidazole-succinocarboxamide synthase n=2 T
650261167 HMPREF9286_1197 phosphoribosylaminoimidazole carboxylase, catalytic subun	Pepto009_171	477	188967	189371	+	C	BLAST: purE_2; phosphoribosylaminoimidazole carboxylase, catalytic subunit (EC:4.1.1.21); K
650261166 HMPREF9286_1196 phosphoribosylformylglycinamidine cyclo-ligase	Pepto009_172	1032	189379	190410	+	B	RBH: aoe:Clos_0539 phosphoribosylaminoimidazole synthetase (EC:6.3.3.1); K01933 phospho
650261165 HMPREF9286_1195 phosphoribosylglycinamide formyltransferase	Pepto009_173	603	190394	190996	+	C	BLAST: purN; phosphoribosylglycinamide formyltransferase; K11175 phosphoribosylglyciami
650261164 HMPREF9286_1194 phosphoribosylaminoimidazolecarboxamide formyltransfer	Pepto009_174	1512	190998	192509	+	B	RBH: UniRef90_D1VVH5 Phosphoribosylaminoimidazolecarboxamide formyltransferase/JMP
650261163 HMPREF9286_1193 phosphoribosylamine-glycine ligase	Pepto009_175	1245	192518	193762	+	B	RBH: aoe:Clos_0542 phosphoribosylamine-glycine ligase (EC:6.3.4.13); K01945 phosphorib
650262337 HMPREF9286_0375 conserved hypothetical protein	Pepto009_176	669	193844	194512	+	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-45 bit_score=184.0 identity=45.79 cove
650262336 HMPREF9286_0374 putative lipoprotein							
650262335 HMPREF9286_0373 putative sugar ABC transporter, ATP binding protein							
650262334 HMPREF9286_0372 branched-chain amino acid ABC transporter, permease protein							
650262333 HMPREF9286_0371 branched-chain amino acid ABC transporter, permease protein							
650262332 HMPREF9286_0370 putative lipoprotein	Pepto009_177	747	194602	195348	+	C	BLAST: putative glutamine amidotransferase; K07010 putative glutamine amidotransferase
650262331 HMPREF9286_0369 transcriptional regulator, TetR family	Pepto009_178	867	195469	196335	+	C	BLAST: putative lipoprotein (db=KEGG eval=6.0e-56 bit_score=221.0 identity=46.96 covera
650262330 HMPREF9286_0368 intracellular growth attenuator protein IgaA	Pepto009_179	600	196644	197243	+	C	BLAST: transcriptional regulator, TetR family (db=KEGG eval=1.0e-55 bit_score=219.0 ident
650262329 HMPREF9286_0367 Gram-positive signal peptide protein, YSIRK family	Pepto009_180	2055	197240	199294	+	B	RBH: fma:FMG_0143 hypothetical protein (db=KEGG)
650262328 HMPREF9286_0366 acetyltransferase, GNAT family	Pepto009_181	2427	199309	201735	+	B	RBH: fma:FMG_0144 hypothetical protein; K01421 putative membrane protein (db=KEGG)
650262105 HMPREF9286_0681 putative membrane protein	Pepto009_183	1020	202491	203510	+	B	RBH: UniRef90_C7HWR7 Membrane protein n=2 Tax=Anaerococcus RepID=C7HWR7_9FIRM (
650262104 HMPREF9286_0680 nitroreductase family protein	Pepto009_184	582	203501	204091	+	C	BLAST: ubiquinone/menaquinone biosynthesis methylase (db=KEGG eval=9.0e-25 bit_scor
650262103 HMPREF9286_0679 rubredoxin	Pepto009_185	1938	204402	206339	+	B	RBH: cbt:CLH_1350 acyl-coA dehydrogenase (db=KEGG)
650262102 HMPREF9286_0678 metallo-beta-lactamase domain protein	Pepto009_186	1242	206351	207592	+	B	RBH: elm:ELI_1519 uncharacterized flavoprotein (db=KEGG)
650261209 HMPREF9286_1239 copper amine oxidase N-terminal domain protein							
650261208 HMPREF9286_1238 peptide chain release factor 2	Pepto009_187	1116	207791	208906	+	B	RBH: UniRef90_D1VSK7 Peptide chain release factor 2 n=1 Tax=Peptoniphilus lacrimalis 315-E
650261207 HMPREF9286_1237 orotidine 5'-phosphate decarboxylase	Pepto009_188	705	208914	209810	+	B	RBH: UniRef90_D1VSK6 Orotidine 5'-phosphate decarboxylase n=1 Tax=Peptoniphilus lacrima
650261206 HMPREF9286_1236 orotate phosphoribosyltransferase	Pepto009_189	630	209618	210247	+	C	BLAST: pyrE; orotate phosphoribosyltransferase (EC:2.4.2.10); K00762 orotate phosphoribos
	Pepto009_190	216	210298	210513	+	E	GENE: 164942..165157 + (rbs_motif=AGAGG/AGGAGG rbs_spacer=5-10bp)
650261205 HMPREF9286_1235 conserved hypothetical protein	Pepto009_191	168	210513	210680	+	D	IPRSCAN: DUF1232 (db=HMM)Pfam db_id=PF06803 from=1 to=34 eval=3.7e-11 interpro_id
650261204 HMPREF9286_1234 3-methyladenine DNA glycosylase	Pepto009_192	603	210667	211269	+	C	BLAST: 3-methyladenine DNA glycosylase (EC:3.2.2.-); K03652 DNA-3-methyladenine glycosyl
650261203 HMPREF9286_1233 cobalt ABC transporter, ATP-binding protein	Pepto009_193	825	211325	212146	+	B	RBH: cbe:CbeJ_0182 cobalt transporter ATP-binding subunit; K02006 cobalt/nickel transport s
650261202 HMPREF9286_1232 cobalt ABC transporter, ATP-binding protein	Pepto009_194	867	212140	213006	+	B	RBH: ctc:CTC02575 cbiO; cobalt transporter ATP-binding subunit; K02006 cobalt/nickel transp
650261201 HMPREF9286_1231 cobalt transport protein	Pepto009_195	798	212999	213796	+	B	RBH: UniRef90_D1VSK2 Putative ABC transporter, ATP-binding protein n=1 Tax=Peptoniphilus
650261200 HMPREF9286_1230 tRNA pseudouridine synthase A	Pepto009_196	732	213793	214524	+	B	RBH: UniRef90_D1VSK1 tRNA pseudouridine synthase A n=1 Tax=Peptoniphilus lacrimalis 315
	Pepto009_197	693	215078	215770	+	E	GENE: 169722..170414 + (rbs_motif=None rbs_spacer=None)
	Pepto009_198	195	215770	215964	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Anaerococcus lactolyticus ATCC 51172 Re
	Pepto009_199	369	216546	216914	+	C	BLAST: Transposase IS116/IS110/IS902 family protein (db=KEGG eval=7.0e-43 bit_score=
650261199 HMPREF9286_1229 conserved hypothetical protein	Pepto009_200	387	217189	217575	+	C	BLAST: hypothetical protein (db=KEGG eval=7.0e-18 bit_score=92.8 identity=45.3 coverage
650261198 HMPREF9286_1228 transcription antitermination factor NusB	Pepto009_201	399	217572	217970	+	C	BLAST: NusB antitermination factor; K03625 N utilization substance protein B (db=KEGG eval
650261197 HMPREF9286_1227 exodeoxyribonuclease VII, large subunit	Pepto009_202	1452	217972	219423	+	B	RBH: UniRef90_D1VSJ5 Exodeoxyribonuclease 7 large subunit n=1 Tax=Peptoniphilus lacrima
650261196 HMPREF9286_1226 exodeoxyribonuclease VII, small subunit	Pepto009_203	225	219424	219648	+	C	BLAST: Exodeoxyribonuclease VII, small subunit n=1 Tax=Peptoniphilus lacrimalis 315-B Repl
650261195 HMPREF9286_1225 putative geranyltransferase	Pepto009_204	858	219632	220489	+	C	BLAST: geranyltransferase (EC:2.5.1.10); K13789 geranylgeranyl diphosphate synthase, t
650261194 HMPREF9286_1224 ribosomal RNA large subunit methyltransferase J	Pepto009_205	801	220489	221289	+	C	BLAST: hemolysin A; K06442 putative hemolysin (db=KEGG eval=1.0e-72 bit_score=276.0 ic
650261193 HMPREF9286_1223 DNA repair protein RecN	Pepto009_206	1662	221297	222958	+	B	RBH: UniRef90_D1VSJ1 DNA repair protein RecN n=1 Tax=Peptoniphilus lacrimalis 315-B Repl
650261192 HMPREF9286_1222 hydrolase, NUDIX family	Pepto009_207	546	222959	223504	+	C	BLAST: NUDIX hydrolase; K01515 ADP-ribose pyrophosphatase (EC:3.6.1.13) (db=KEGG eval
650261191 HMPREF9286_1221 purine nucleoside phosphorylase 1	Pepto009_208	858	223443	224300	+	B	RBH: UniRef90_D1VSJ9 Purine nucleoside phosphorylase I, inosine and guanosine-specific n=
650261190 HMPREF9286_1220 pyrimidine nucleoside phosphorylase	Pepto009_209	1302	224297	225598	+	C	BLAST: pyrimidine nucleoside phosphorylase; K00756 pyrimidine-nucleoside phosphorylase [E
650261189 HMPREF9286_1219 peptidase, M50 family	Pepto009_210	633	225600	226232	+	C	BLAST: zinc-dependent metalloprotease (db=KEGG eval=5.0e-33 bit_score=144.0 identity=
650261188 HMPREF9286_1218 ScpA/B protein	Pepto009_211	747	226211	226957	+	C	BLAST: scpA; segregation and condensation protein A; K05896 segregation and condensation
650261187 HMPREF9286_1217 segregation and condensation protein B	Pepto009_212	528	226926	227453	+	C	BLAST: putative transcriptional regulator; K06024 segregation and condensation protein B (dt
650261186 HMPREF9286_1216 pseudouridine synthase B, ribosomal large subunit	Pepto009_213	708	227450	228157	+	B	RBH: UniRef90_D1VSI5 Pseudouridine synthase n=1 Tax=Peptoniphilus lacrimalis 315-B Repl
650261185 HMPREF9286_1215 putative rRNA methylase	Pepto009_214	546	228154	228699	+	C	BLAST: putative rRNA methylase (db=KEGG eval=1.0e-32 bit_score=142.0 identity=45.78 cc
650261184 HMPREF9286_1214 flavoprotein family protein	Pepto009_215	1191	228704	229894	+	B	RBH: cno:NT01CX_2094 NAD(FAD)-utilizing dehydrogenase; K07007 (db=KEGG)
650261183 HMPREF9286_1213 cytidylate kinase	Pepto009_216	621	229978	230598	+	C	BLAST: cytidylate kinase; K00945 cytidylate kinase [EC:2.7.4.14] (db=KEGG eval=5.0e-49 bit
650261182 HMPREF9286_1212 Acyltransferase	Pepto009_217	588	230605	231192	+	C	BLAST: 1-acyl-sn-glycerol-3-phosphate acyltransferase; K00655 1-acyl-sn-glycerol-3-phosphat
650261181 HMPREF9286_1211 4-hydroxy-3-methylbut-2-enyl diphosphate reductase	Pepto009_218	2112	231177	233288	+	B	RBH: apr:Apr_1019 hydroxymethylbutenyl pyrophosphate reductase; K02945 small subunit I
	Pepto009_219	87	233409	233495	+	D	IPRSCAN: seg (db=Seg db_id=seg from 13 to 29)
650261039 HMPREF9286_0045 NlpC/P60 family protein							
650261038 HMPREF9286_0044 putative alkaliphosphonate utilization operon protein PhnA							
650261037 HMPREF9286_0043 conserved hypothetical protein	Pepto009_220	516	233448	233963	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VSI
650261036 HMPREF9286_0042 TGR00159 family protein	Pepto009_221	831	233965	234795	+	B	RBH: UniRef90_D1VSH8 YbbP n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VSH8_9FIRM
650261035 HMPREF9286_0041 YbbR-like protein	Pepto009_222	942	234746	235717	+	C	BLAST: YbbR family protein (db=KEGG eval=4.0e-24 bit_score=115.0 identity=26.91 covera
650261034 HMPREF9286_0040 inosine-5'-monophosphate dehydrogenase	Pepto009_223	1446	235745	237190	+	B	RBH: UniRef90_D1VSH6 Inosine-5'-monophosphate dehydrogenase n=1 Tax=Peptoniphilus lacra
650261033 HMPREF9286_0039 alkaline phosphatase synthesis transcriptional regulatory pr	Pepto009_224	684	237257	237940	+	B	RBH: UniRef90_D1VSH5 Alkaline phosphatase synthesis transcriptional regulatory protein Phx
650261032 HMPREF9286_0038 ATPase/histidine kinase/DNA gyrase B/HS90 domain prot	Pepto009_225	1422	237954	239375	+	B	RBH: cbi:CLJ_B0409 sensor histidine kinase (EC:2.7.3.-) (db=KEGG)
650261031 HMPREF9286_0037 putative lipoprotein	Pepto009_226	1425	239368	240792	+	B	RBH: UniRef90_D1VSH3 Putative lipoprotein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D
650261030 HMPREF9286_0036 conserved hypothetical protein	Pepto009_227	336	240805	241140	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VSI
650261029 HMPREF9286_0035 comEa protein	Pepto009_228	645	241220	241864	+	C	BLAST: competence protein ComEa helix-hairpin-helix repeat protein; K02237 competence pr
650261028 HMPREF9286_0034 translation elongation factor G	Pepto009_229	2061	242013	244073	+	B	RBH: fma:FMG_1310 translation elongation factor G; K02355 elongation factor EF-G [EC:3.6.5
650261027 HMPREF9286_0033 transcriptional regulator CtsR	Pepto009_230	453	244355	244807	+	C	BLAST: transcriptional regulator CtsR; K03708 transcriptional regulator CtsR (db=KEGG eval
650261026 HMPREF9286_0032 conserved hypothetical protein	Pepto009_231	507	244819	245325	+	C	BLAST: putative UvrR/UvrC domain-containing protein (db=KEGG eval=3.0e-28 bit_score=1
650261025 HMPREF9286_0031 ATP:guanine phosphotransferase, C-terminal catalytic doma	Pepto009_232	981	245318	246298	+	C	BLAST: mcsB; ATP:guanine phosphotransferase (EC:2.7.3.3); K00936 [EC:2.7.3.-] (db=KEGG ev
650261024 HMPREF9286_0030 negative regulator of genetic competence CtpC/MecB	Pepto009_233						

	Pepto009_237	1230	252969	254198 +	B	RBH: fma:FMG_1434 hypothetical protein (db=KEGG)
	Pepto009_238	1281	254385	255665 +	B	RBH: bth:BT_1923 O-acetylthioserine (thiol)-lyase; K01740 O-acetylthioserine (thiol)-lyase
	Pepto009_239	516	256268	256783 +	C	BLAST: two component transcriptional regulator (db=KEGG eval=1.0e-33 bit_score=145.0)
650262173 HMPREF9286_0851 ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	Pepto009_240	873	256771	257643 +	C	BLAST: histidine kinase (db=KEGG eval=2.0e-39 bit_score=166.0 identity=40.16 coverage=8)
650262172 HMPREF9286_0850 ABC transporter, ATP-binding protein	Pepto009_241	657	257277	258383 +	C	BLAST: ABC transporter, ATP-binding protein (db=KEGG eval=2.0e-71 bit_score=271.0 identity=29.1)
650262171 HMPREF9286_0849 efflux ABC transporter, permease protein	Pepto009_242	2484	258380	260863 +	C	BLAST: hypothetical protein; K02004 (db=KEGG eval=5.0e-54 bit_score=216.0 identity=29.1)
650261103 HMPREF9286_1132 CarD-like protein	Pepto009_243	483	261122	261604 +	C	BLAST: transcriptional regulator, CarD family; K07736 CarD family transcriptional regulator (db=KEGG eval=1.0e-33 bit_score=145.0)
650261102 HMPREF9286_1131 PIN domain protein	Pepto009_244	1092	261638	262729 +	B	RBH: UniRef90_D1VW17 PIIT domain-containing protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V17
650261101 HMPREF9286_1130 aminotransferase, class V						
650261100 HMPREF9286_1129 copper amine oxidase N-terminal domain protein	Pepto009_245	2274	262893	265166 +	B	RBH: UniRef90_D1VTW3 Copper amine oxidase N-domain superfamily n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VTW3
650261099 HMPREF9286_1128 UDP-N-acetylmuramate-L-alanine ligase	Pepto009_246	1383	265301	266683 +	B	RBH: cth:Cthe_2626 murC; UDP-N-acetylmuramate-L-alanine ligase (EC:6.3.2.8); K01924 UDF
650261664 HMPREF9286_0783 putative negative regulator of asymmetric septation	Pepto009_247	321	266847	267167 +	C	BLAST: regulatory protein SpoVG; K06412 stage V sporulation protein G (db=KEGG eval=1.0e-33 bit_score=145.0)
650261663 HMPREF9286_0782 alanine racemase	Pepto009_248	1158	267273	268430 +	B	RBH: chd:Calhy_0881 alanine racemase (EC:5.1.1.1); K01775 alanine racemase [EC:5.1.1.1] (db=KEGG eval=1.0e-33 bit_score=145.0)
650261662 HMPREF9286_0781 putative permease	Pepto009_249	123	268533	268655 +	D	IPRSCAN: seg (db=Seg db_id=seg from=11 to=27)
650261661 HMPREF9286_0780 protein CrcB	Pepto009_250	363	268973	269335 +	C	BLAST: Camphor resistance protein CrcB n=1 Tax=Selenomonas flueggei ATCC 43531 RepID=D1V17
650261660 HMPREF9286_0779 response regulator receiver domain protein	Pepto009_251	699	269413	270111 +	B	RBH: UniRef90_D1VT63 Regulatory protein VanR n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT63
650261659 HMPREF9286_0778 histidine kinase A domain protein	Pepto009_252	2082	270108	272189 +	B	RBH: UniRef90_D1VT62 Sensor protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT62
	Pepto009_253	384	272340	272723 +	C	BLAST: putative penicillin-binding protein repressor (db=KEGG eval=1.0e-12 bit_score=75)
	Pepto009_254	1374	272720	274093 +	C	BLAST: peptidase M56, BlaI (db=KEGG eval=2.0e-20 bit_score=104.0 identity=29.85 cov
	Pepto009_255	345	274525	274869 +	D	IPRSCAN: Thioredoxin-like (db=superfamily db_id=SF52833 from=19 to=110 eval=2.3e-0
	Pepto009_256	525	274887	275411 +	C	BLAST: phospholipase A2 family enzyme (db=KEGG eval=7.0e-16 bit_score=86.3 identity=
	Pepto009_257	174	275465	275638 +	D	IPRSCAN: seg (db=Seg db_id=seg from=4 to=14)
	Pepto009_258	225	275740	275964 +	E	GENE: 151825..152049 - (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp)
	Pepto009_259	399	275988	276386 +	D	IPRSCAN: seg (db=Seg db_id=seg from=6 to=23)
	Pepto009_260	231	276458	276688 +	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V17
650261658 HMPREF9286_0777 Creatinase	Pepto009_261	1761	276794	278554 +	B	RBH: cbt:CLH_0088 Xaa-Pro aminopeptidase 1 (EC:3.4.11.9); K01262 Xaa-Pro aminopeptidase
650261657 HMPREF9286_0776 excinuclease ABC, C subunit	Pepto009_262	1863	278555	280417 +	B	RBH: aoe:Clos_2255 uvrC; excinuclease ABC subunit C; K03703 excinuclease ABC subunit C (db=KEGG eval=1.0e-33 bit_score=145.0)
650261656 HMPREF9286_0775 Hpr(Ser) kinase/phosphatase	Pepto009_263	924	280407	281330 +	B	RBH: UniRef90_D1VT50 HPr(Ser) kinase/phosphatase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT50
650261655 HMPREF9286_0774 pyruvate synthase	Pepto009_264	3534	281536	285069 +	B	RBH: fma:FMG_0385 pyruvate/ferredoxin oxidoreductase; K03737 putative pyruvate-flavodoxin
650261654 HMPREF9286_0773 fatty acyl-phospholipid synthesis protein PlsX	Pepto009_265	993	285252	286244 +	B	RBH: UniRef90_D1VT47 Phosphate acyltransferase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT47
650261653 HMPREF9286_0772 acyl carrier protein	Pepto009_266	228	286234	286461 +	C	BLAST: acpP; acyl carrier protein; K02078 acyl carrier protein (db=KEGG eval=2.0e-12 bit_score=75)
650261652 HMPREF9286_0771 ribonuclease III	Pepto009_267	699	286466	287164 +	C	BLAST: rnc; ribonuclease III [EC:3.1.26.3]; K03685 ribonuclease III [EC:3.1.26.3] (db=KEGG eval=1.0e-33 bit_score=145.0)
650261651 HMPREF9286_0770 radical SAM protein, TIGR01212 family	Pepto009_268	1050	287157	288206 +	B	RBH: UniRef90_D1VT44 Radical SAM domain protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT44
650261650 HMPREF9286_0769 chromosome segregation protein SMC	Pepto009_269	3522	288118	291732 +	B	RBH: cfb:CLL_2508 smc; chromosome segregation protein SMC; K03529 chromosome segregation protein SMC
650261649 HMPREF9286_0768 signal recognition particle-docking protein FtsY	Pepto009_270	1497	291742	293238 +	B	RBH: aoe:Clos_1461 signal recognition particle-docking protein FtsY; K01914 fused signal recognition particle
650261648 HMPREF9286_0767 helix-turn-helix protein, YlmM/p13 family	Pepto009_271	357	293418	293774 +	C	BLAST: putative helix-turn-helix protein YlmM/p13 family protein; K09787 hypothetical protein
650261647 HMPREF9286_0766 signal recognition particle protein	Pepto009_272	1338	293786	295123 +	C	RBH: amt:Amet_2747 signal recognition particle protein; K03106 signal recognition particle S
650261646 HMPREF9286_0765 ribosomal protein S16	Pepto009_273	300	295173	295472 +	C	BLAST: 30S ribosomal protein S16; K02959 small subunit ribosomal protein S16 (db=KEGG eval=1.0e-33 bit_score=145.0)
650261645 HMPREF9286_0764 conserved hypothetical protein	Pepto009_274	234	295494	295727 +	C	BLAST: hypothetical protein; K06960 (db=KEGG eval=4.0e-09 bit_score=63.5 identity=43.84)
650261644 HMPREF9286_0763 16S rRNA processing protein RimM	Pepto009_275	504	295714	296217 +	C	BLAST: rimM; 16S rRNA-processing protein RimM; K02860 16S rRNA processing protein RimM
650261643 HMPREF9286_0762 tRNA (guanine-N(1))-methyltransferase	Pepto009_276	744	296214	296957 +	B	RBH: UniRef90_D1VUW9 tRNA (guanine-N(1))-methyltransferase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VUW9
650261642 HMPREF9286_0761 ribosomal protein L19	Pepto009_277	348	296944	297291 +	C	BLAST: rplS; 50S ribosomal protein L19; K02884 large subunit ribosomal protein L19 (db=KEGG eval=1.0e-33 bit_score=145.0)
650261641 HMPREF9286_0760 SH3 domain protein	Pepto009_278	1641	297363	299003 +	B	RBH: pjd:PjdR_1095 glycoside hydrolase family 18 (db=KEGG)
650261640 HMPREF9286_0759 conserved hypothetical protein	Pepto009_279	651	299001	299711 +	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-27 bit_score=125.0 identity=36.62 coverage=8)
650261639 HMPREF9286_0758 aspartate-ammmonia ligase	Pepto009_280	996	299768	300763 +	B	RBH: cpr:CPR_1945 asnA; asparagine synthetase AsnA (EC:6.3.1.1); K01914 aspartate-ammmonia
650261638 HMPREF9286_0757 conserved hypothetical protein	Pepto009_281	762	300847	301608 +	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VUW9
650261637 HMPREF9286_0756 crossover junction endonuclease RuvC	Pepto009_282	486	301656	302141 +	C	BLAST: ruvC; Holliday junction resolvase (EC:3.1.2.2.4); K01159 crossover junction endonuclease
650261636 HMPREF9286_0755 Holliday junction DNA helicase RuvA	Pepto009_283	585	302141	302725 +	C	BLAST: ruvA; Holliday junction DNA helicase RuvA; K03550 Holliday junction DNA helicase RuvA
650261635 HMPREF9286_0754 Holliday junction DNA helicase RuvB	Pepto009_284	1002	302730	303731 +	B	RBH: fma:FMG_0815 Holliday junction DNA helicase; K03551 Holliday junction DNA helicase R
650261634 HMPREF9286_0753 putative amidase enhancer	Pepto009_285	1122	303733	304854 +	B	RBH: UniRef90_D1VUW0 Amidase enhancer n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VUW0
650261633 HMPREF9286_0752 S-adenosylmethionine:tRNA ribosyltransferase-isomerase	Pepto009_286	1020	304867	305886 +	B	RBH: cbe:CbeI_1532 queA; S-adenosylmethionine:tRNA ribosyltransferase-isomerase; K07568
650261632 HMPREF9286_0751 tRNA-guanine transglycosylase	Pepto009_287	1113	305892	307004 +	C	RBH: fma:FMG_0813 queA; tRNA-guanine transglycosylase; K07073 queA; tRNA-guanine transglycosylase
650261631 HMPREF9286_0750 preprotein translocase, YajC subunit	Pepto009_288	300	307074	307373 +	C	BLAST: Preprotein translocase, YajC subunit n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VUW9
650261630 HMPREF9286_0749 SAM-modified six-cysteine peptide	Pepto009_289	147	307382	307528 +	C	BLAST: hypothetical protein (db=KEGG eval=8.0e-09 bit_score=62.4 identity=78.26 coverage=8)
650261629 HMPREF9286_0748 six-cys-in-45 modification radical SAM protein	Pepto009_290	1353	307579	308931 +	B	RBH: aoe:Clos_1718 radical SAM domain-containing protein; K06871 (db=KEGG)
	Pepto009_291	267	309071	309337 +	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=29)
	Pepto009_292	276	309344	309619 +	E	GENE: 118170..118445 - (rbs_motif=None rbs_spacer=None)
	Pepto009_293	231	309649	309879 +	D	IPRSCAN: seg (db=Seg db_id=seg from=23 to=53)
	Pepto009_294	4140	310160	314299 +	C	BLAST: cpy:Cpy_1155 nucleic acid binding O646 tRNA/helicase-type (db=KEGG)
650261628 HMPREF9286_0747 single-stranded-DNA-specific exonuclease RecJ	Pepto009_295	1791	314846	316276 +	B	RBH: cbe:CbeI_4321 single-stranded-DNA-specific exonuclease RecJ; K07462 single-stranded-DNA-specific exonuclease RecJ
650261627 HMPREF9286_0746 GTP diphosphokinase	Pepto009_296	2148	316260	318407 +	B	RBH: toc:TocC_1364 (p)ppGpp synthetase I, SpoV/RelA (EC:2.7.6.5); K00951 GTP pyrophosphatase
650261626 HMPREF9286_0745 Act domain protein						
650261625 HMPREF9286_0744 D-tyrosyl-tRNA(Tyr) deacylase	Pepto009_297	450	318412	318861 +	C	BLAST: D-tyrosyl-tRNA(Tyr) deacylase; K07560 D-tyrosyl-tRNA(Tyr) deacylase [EC:3.1.1.-] (db=KEGG eval=1.0e-33 bit_score=145.0)
650261624 HMPREF9286_0743 metallo-beta-lactamase domain protein	Pepto009_298	627	318869	319495 +	C	BLAST: beta-lactamase domain protein (db=KEGG eval=1.0e-46 bit_score=189.0 identity=4.4)
650261623 HMPREF9286_0742 coproporphyrinogen dehydrogenase HemZ	Pepto009_299	1329	319492	320820 +	B	RBH: UniRef90_D1V556 Oxygen-independent coproporphyrinogen III oxidase 2 n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V556
650261622 HMPREF9286_0741 UDP-N-acetylmuramyl-L-alanyl-D-glutamate-2-, 6-diaminop	Pepto009_300	1536	320823	322358 +	B	RBH: aoe:Clos_0298 UDP-N-acetylmuramyl-tripeptide synthetase (db=KEGG)
650261621 HMPREF9286_0740 aspartate-tRNA ligase	Pepto009_301	1782	322507	324288 +	B	RBH: aoe:Clos_1709 aspartyl-tRNA synthetase; K01876 aspartyl-tRNA synthetase [EC:6.1.1.12]
650261620 HMPREF9286_0739 positive regulator of sigma(E), RseC/MucC	Pepto009_302	423	324300	324722 +	C	BLAST: hypothetical protein; K03803 sigma-E factor negative regulatory protein RseC (db=KEGG eval=1.0e-33 bit_score=145.0)
650261619 HMPREF9286_0738 conserved hypothetical protein	Pepto009_303	828	324730	325557 +	C	BLAST: Putative DNA double-strand break repair Rad50 ATPase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VUW9
650261618 HMPREF9286_0737 conserved hypothetical protein	Pepto009_304	972	325541	326512 +	C	BLAST: Putative hemagglutination activity domain-containing protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VUW9
650261617 HMPREF9286_0736 TraB family protein	Pepto009_305	1182	326509	327690 +	B	RBH: amt:Amet_1699 TraB family protein (db=KEGG)
650261475 HMPREF9286_1077 conserved hypothetical protein	Pepto009_306	447	327734	328180 +	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-17 bit_score=91.3 identity=33.56 coverage=8)
650261474 HMPREF9286_1076 conserved hypothetical protein	Pepto009_307	780	328177	328956 +	C	BLAST: membrane protein (db=KEGG eval=3.0e-40 bit_score=168.0 identity=38.74 coverage=8)
650261473 HMPREF9286_1075 ribosome biogenesis GTPase Der	Pepto009_308	1341	329064	330404 +	B	RBH: fma:FMG_0854 GTP-binding protein; K03977 GTP-binding protein (db=KEGG)
650261472 HMPREF9286_1074 acyl-phosphate glycerol 3-phosphate acyltransferase	Pepto009_309	591	330401	330991 +	C	BLAST: hypothetical protein; K08591 glycerol-3-phosphate acyltransferase PlsY [EC:2.3.1.15] (db=KEGG eval=1.0e-33 bit_score=145.0)
650261471 HMPREF9286_1073 glycerol-3-phosphate dehydrogenase [NAD(P)+]	Pepto009_310	1008	330988	331995 +	B	RBH: cdc:CD196_2471 glyC; glycerol-3-phosphate dehydrogenase [NAD(P)+]; K00057 glycerol-3-phosphate dehydrogenase [NAD(P)+]
650261470 HMPREF9286_1072 putative membrane fusion protein	Pepto009_311	1266	332047	333312 +	B	RBH: UniRef90_D1V568 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V568
650261469 HMPREF9286_1071 pyridoxal phosphate enzyme, YggS family	Pepto009_312	711	333322	334032 +	C	BLAST: proline synthetase aspartate phosphohydrolase (EC:3.1.4.16); K06950 (db=KEGG eval=1.0e-33 bit_score=145.0)
650261468 HMPREF9286_1070 conserved hypothetical protein	Pepto009_313	450	334042	334491 +	C	BLAST: hypothetical protein; K09772 cell division inhibitor SepF (db=KEGG eval=1.0e-22 bit_score=75)
650261467 HMPREF9286_1069 S4 domain protein	Pepto009_314	783	334485	335267 +	C	BLAST: putative RNA-binding cell division protein (db=KEGG eval=5.0e-34 bit_score=148.0 identity=38.74 coverage=8)
650261466 HMPREF9286_1068 signal peptidase II	Pepto009_315	456	335277	335732 +	C	BLAST: LspA; signal peptidase II [EC:3.4.23.36]; K03101 signal peptidase II [EC:3.4.23.36] (db=KEGG eval=1.0e-33 bit_score=145.0)
650261465 HMPREF9286_1067 ribosomal large subunit pseudouridine synthase D	Pepto009_316	903	335736	336638 +	B	RBH: UniRef90_D1V573 Pseudouridine synthase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V573
650261464 HMPREF9286_1066 pyridine nucleotide-disulfide oxidoreductase	Pepto009_317	1377	336640	338016 +	B	RBH: cfb:CLL_3862 pyridine nucleotide-disulfide oxidoreductase family protein; K07137 (db=KEGG eval=1.0e-33 bit_score=145.0)
650261463 HMPREF9286_1065 tRNA-i(G)A37 thiotransferase enzyme MiaB	Pepto009_318	1401	338097	339497 +	B	RBH: tex:TethS14_1610 (dimethylallyl)adenosine tRNA methylthiotransferase (EC:1.3.1.74); K
650261462 HMPREF9286_1064 DNA mismatch repair protein MutS	Pepto009_319	2610	339487	342096 +	B	RBH: UniRef90_D1V585 DNA mismatch repair protein mutS n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V585
650261461 HMPREF9286_1063 DNA mismatch repair protein, C-terminal domain protein	Pepto009_320	1875	342093	343967 +	B	RBH: cdf:CD1976 mutL; DNA mismatch repair protein; K03572 DNA mismatch repair protein h
650261460 HMPREF9286_1062 tRNA dimethylallyltransferase	Pepto009_321	912	343969	344880 +	C	BLAST: miaA; tRNA delta(2)-isopentenylpyrophosphate transferase (EC:2.5.1.75); K00791 tRNA delta(2)-isopentenylpyrophosphate transferase
650261459 HMPREF9286_1061 aluminum resistance protein	Pepto009_322	1287	344725	346261 +	B	RBH: fma:FMG_0746 putative aluminum resistance protein (db=KEGG)
650261458 HMPREF9286_1060 cytosine deaminase						
650261457 HMPREF9286_1059 repressor LexA	Pepto009_323	621	346412	347032 +	B	RBH: UniRef90_D1V589 LexA repressor n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V589
650261456 HMPREF9286_1058 LysM domain protein	Pepto009_324	297	347423	347539 +	C	BLAST: Peptidoglycan-binding LysM n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V590_9
650261455 HMPREF9286_1057 YmdA/YtgF family protein	Pepto009_325	1536	347663	349198 +	B	RBH: tjr:TherJR_1279 metal dependent phosphohydrolase (EC:3.1.4.16); K06950 (db=KEGG eval=1.0e-33 bit_score=145.0)
650261454 HMPREF9286_1056 phosphate integrase, N-terminal SAM domain protein	Pepto009_326	972	349251	350222 +	C	RBH: cth:Cthe_0728 xerC; site-specific tyrosine recombinase XerC (db=KEGG)
650261453 HMPREF9286_1055 copper amine oxidase N-terminal domain protein	Pepto009_327	639	350241	350879 +	C	BLAST: copper amine oxidase domain-containing protein (db=KEGG eval=6.0e-15 bit_score=75)
650261452 HMPREF9286_1054 putative fibronectin-binding protein	Pepto009_328	1719	351373	353091 +	B	RBH: aoe:Clos_1419 fibronectin-binding A domain-containing protein (db=KEGG)
650261451 HMPREF9286_1053 TrpA family protein YecY/YecD	Pepto009_329	312	353113	353424 +	C	BLAST: TrpA like protein, YecY/YecD (db=KEGG eval=7.0e-31 bit_score=135.

650261443	HMPREF9286_1045 ribosomal protein S12 methylthiotransferase RimO	Pepto009_337	1317	359696	361012	+	B	RBH: thx:Thet_1270 MiaB-like tRNA modifying enzyme YliG (db=KEGG)
650261442	HMPREF9286_1044 stage III sporulation protein E	Pepto009_338	2355	361005	363359	+	B	RBH: toc:Toce_1223 DNA translocase FtsK; K03466 DNA segregation ATPase FtsK/SpolIIE, S-D
650261441	HMPREF9286_1043 dUTP diphosphatase	Pepto009_339	432	363399	363830	+	C	BLAST: dut; deoxyuridine 5'-triphosphate nucleotidohydrolase [EC:3.6.1.23]; K01520 dUTP py
650261440	HMPREF9286_1042 polyribonucleotide nucleotidyltransferase	Pepto009_340	2109	363888	365996	+	B	RBH: UniRef90_D1VSA7 Polyribonucleotide nucleotidyltransferase n=1 Tax=Peptoniphilus laci
650261439	HMPREF9286_1041 ribosomal protein S15	Pepto009_341	267	366040	366306	+	C	BLAST: rpsO; 30S ribosomal protein S15; K02956 small subunit ribosomal protein S15 (db=KEG
650261438	HMPREF9286_1040 riboflavin biosynthesis protein RibF	Pepto009_342	909	366420	367328	+	B	RBH: UniRef90_D1VSA9 Riboflavin biosynthesis protein RibF n=1 Tax=Peptoniphilus lacrimalis
650261437	HMPREF9286_1039 tRNA pseudouridine synthase B	Pepto009_343	888	367325	368125	+	B	RBH: UniRef90_D1VSB0 tRNA pseudouridine synthase B n=1 Tax=Peptoniphilus lacrimalis S15
650261436	HMPREF9286_1038 DHHA1 domain protein	Pepto009_344	984	368209	369192	+	B	RBH: UniRef90_D1VSB1 Phosphoesterase domain-containing protein n=1 Tax=Peptoniphilus l
650261435	HMPREF9286_1037 ribosome-binding factor A	Pepto009_345	354	369179	369532	+	C	BLAST: rbfA; ribosome-binding factor A; K02834 ribosome-binding factor A (db=KEGG evalu
650261434	HMPREF9286_1036 translation initiation factor IF-2	Pepto009_346	2244	369532	371775	+	B	RBH: UniRef90_D1VSB3 Translation initiation factor IF-2 n=1 Tax=Peptoniphilus lacrimalis 315
650261433	HMPREF9286_1035 conserved hypothetical protein	Pepto009_347	264	371801	372064	+	C	BLAST: hypothetical protein; K07742 hypothetical protein (db=KEGG evalu=8.0e-24 bit_scor
650261432	HMPREF9286_1034 transcription termination factor NusA	Pepto009_348	1236	372090	373325	+	B	RBH: tjr:TherJR_1374 transcription termination factor NusA; K02600 N utilization substance p
650261431	HMPREF9286_1033 conserved hypothetical protein	Pepto009_349	462	373337	373798	+	C	BLAST: protein of unknown function DUF150; K09748 hypothetical protein (db=KEGG evalu
650261430	HMPREF9286_1032 DNA polymerase III, alpha subunit, Gram-positive type	Pepto009_350	4248	373901	378148	+	B	RBH: tex:TethS14_1650 polC; DNA polymerase III PolC [EC:2.7.7.7]; K03763 DNA polymerase I
650261429	HMPREF9286_1031 nucleic acid-binding domain protein							
650261428	HMPREF9286_1030 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Pepto009_351	1056	378153	379208	+	B	RBH: fma:FMG_0730 1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate synthase; K03526 (E-4
650261427	HMPREF9286_1029 RIP metalloprotease RseP	Pepto009_352	1011	379205	380215	+	B	RBH: UniRef90_D1VSB9 RIP metalloprotease RseP n=1 Tax=Peptoniphilus lacrimalis 315-B Rej
650261426	HMPREF9286_1028 phosphatidate cytidyllyltransferase	Pepto009_353	783	380226	381008	+	C	BLAST: cdsA; phosphatidate cytidyllyltransferase [EC:2.7.7.41]; K00981 phosphatidate cytidyl
650261425	HMPREF9286_1027 di-trans,poly-cis-decaprenylcistransferase	Pepto009_354	726	381010	381735	+	B	RBH: UniRef90_D1VSC1 Di-trans,poly-cis-decaprenylcistransferase n=1 Tax=Peptoniphilus laci
650261424	HMPREF9286_1026 ribosome recycling factor	Pepto009_355	558	381782	382339	+	C	BLAST: frr; ribosome recycling factor; K02838 ribosome recycling factor (db=KEGG evalu=6.0
650261423	HMPREF9286_1025 UMP kinase	Pepto009_356	705	382349	383053	+	B	RBH: UniRef90_D1VSC3 UMP kinase n=1 Tax=Peptoniphilus lacrimalis 315-B ReplD=D1VSC3_5
650261422	HMPREF9286_1024 translation elongation factor Ts	Pepto009_357	645	383071	383715	+	B	RBH: UniRef90_D1VSC4 Elongation factor Ts n=1 Tax=Peptoniphilus lacrimalis 315-B ReplD=D
650261421	HMPREF9286_1023 ribosomal protein S2	Pepto009_358	789	383787	384575	+	B	RBH: fma:FMG_0706 30S ribosomal protein S2; K02967 small subunit ribosomal protein S2 (d
650261420	HMPREF9286_1022 rubredoxin	Pepto009_359	543	385020	385562	+	C	BLAST: ruberythrin (db=KEGG evalu=4.0e-75 bit_score=283.0 identity=73.89 coverage=98.8
650261419	HMPREF9286_1021 peptide chain release factor 1	Pepto009_360	1068	385673	386740	+	B	RBH: cdf:CD3484 prfA; peptide chain release factor 1; K02835 peptide chain release factor RF
650261418	HMPREF9286_1020 protein-(glutamine-N5) methyltransferase, release factor-sp	Pepto009_361	831	386749	387579	+	C	BLAST: modification methylase, HemK family; K02493 methyltransferase [EC:2.1.1.-] (db=KEG
650261417	HMPREF9286_1019 ribosomal protein L31	Pepto009_362	204	387622	387825	+	C	BLAST: ribosomal protein L31; K02909 large subunit ribosomal protein L31 (db=KEGG evalu
650261416	HMPREF9286_1018 transcription termination factor Rho	Pepto009_363	1395	387974	389368	+	B	RBH: aoe:Clos_2591 rho; transcription termination factor Rho; K03628 transcription terminat
650261415	HMPREF9286_1017 fructose-1,6-bisphosphatase, class II	Pepto009_364	966	389365	390330	+	B	RBH: aoe:Clos_2595 glpX; fructose 1,6-bisphosphatase II; K02446 fructose-1,6-bisphosphatasi
650261414	HMPREF9286_1016 fructose-6-phosphate aldolase	Pepto009_365	654	390332	390985	+	C	BLAST: putative transaldolase [EC:2.2.1.2]; K00616 transaldolase [EC:2.2.1.2] (db=KEGG evalu
650261413	HMPREF9286_1015 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Pepto009_366	477	390986	391462	+	C	BLAST: ispF; 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase; K01770 2-C-methyl-D-en
650261412	HMPREF9286_1014 2-C-methyl-D-erythritol 4-phosphate cytidyllyltransferase	Pepto009_367	702	391459	392160	+	B	RBH: UniRef90_D1VSG6 2-C-methyl-D-erythritol 4-phosphate cytidyllyltransferase n=1 Tax=Pe
650261411	HMPREF9286_1013 penicillin-binding protein, transpeptidase domain protein	Pepto009_368	1443	392165	393607	+	B	RBH: apr:Apr_0876 peptidoglycan glycosyltransferase [EC:2.4.1.129]; K05364 peptidoglycan
650261410	HMPREF9286_1012 cell cycle protein, FtsW/RodA/SpoVE family	Pepto009_369	1269	393597	394865	+	B	RBH: UniRef90_D1VSG8 Cell division membrane protein n=1 Tax=Peptoniphilus lacrimalis 315
650261409	HMPREF9286_1011 FHA domain protein	Pepto009_370	441	394870	395310	+	C	BLAST: hypothetical protein (db=KEGG evalu=3.0e-19 bit_score=97.1 identity=46.67 covera
650261408	HMPREF9286_1010 regulatory protein RecX	Pepto009_371	606	395428	396033	+	C	BLAST: recX; recombination regulator RecX; K03565 regulatory protein (db=KEGG evalu=3.0e
650261407	HMPREF9286_1009 GII-YIG catalytic domain protein	Pepto009_372	300	396035	396334	+	C	RBH: excinuclease ABC C subunit domain protein; K07461 putative endonuclease (db=KEGG
650261406	HMPREF9286_1008 conserved hypothetical protein	Pepto009_373	1833	396384	398216	+	B	RBH: aar:Acear_0052 protein of unknown function DUF87; K06915 (db=KEGG)
650261405	HMPREF9286_1007 NurA domain protein	Pepto009_374	945	398225	399169	+	B	RBH: UniRef90_D1VVU9 NurA domain superfamily n=1 Tax=Peptoniphilus lacrimalis 315-B Re
650261404	HMPREF9286_1006 S-adenosylmethionine-dependent methyltransferase, YraL f	Pepto009_375	795	399166	399960	+	B	RBH: UniRef90_D1VVU8 Protein YabC n=1 Tax=Peptoniphilus lacrimalis 315-B ReplD=D1VVU8
650261403	HMPREF9286_1005 conserved hypothetical protein							
650261402	HMPREF9286_1004 methyltransferase small domain protein	Pepto009_376	690	399957	400646	+	C	BLAST: methyltransferase [EC:2.1.1.-]; K00599 [EC:2.1.1.-] (db=KEGG evalu=1.0e-11 bit_scor
650261401	HMPREF9286_1003 bacterial capsule synthesis protein	Pepto009_377	1185	400643	401827	+	B	RBH: UniRef90_D1VVU6 Poly-gamma-glutamate biosynthesis protein n=1 Tax=Peptoniphilus l
650261400	HMPREF9286_1002 conserved hypothetical protein	Pepto009_378	612	401824	402435	+	C	BLAST: protein of unknown function DUF208; K09765 hypothetical protein (db=KEGG evalu
650261399	HMPREF9286_1001 prolipoprotein diacylglycerol transferase	Pepto009_379	762	402476	403237	+	C	BLAST: prolipoprotein diacylglycerol transferase; K13292 phosphatidylglycerol:prolipoprotei
650261398	HMPREF9286_1000 deoxyribose-phosphate aldolase	Pepto009_380	660	403234	403893	+	C	BLAST: deoxyribose-phosphate aldolase [EC:4.1.2.4]; K01619 deoxyribose-phosphate aldolase
650261397	HMPREF9286_0999 DNA-binding regulatory protein, YebC/PmpR family	Pepto009_381	726	403893	404618	+	B	RBH: UniRef90_D1VVU1 UPF0082 protein HMPREF0628_0871 n=1 Tax=Peptoniphilus lacrim
		Pepto009_382	531	405091	405621	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Anaerococcus lactolyticus ATCC 51172 Re
650261396	HMPREF9286_0998 ATPase/histidine kinase/DNA gyrase B/HSP90 domain protei	Pepto009_383	1296	405742	407037	+	B	RBH: apr:Apr_0644 histidine kinase (db=KEGG)
650261395	HMPREF9286_0997 putative sensory transduction protein RegX3	Pepto009_384	696	407042	407737	+	C	BLAST: two-component response regulator (db=KEGG evalu=2.0e-77 bit_score=291.0 identit
650261394	HMPREF9286_0996 putative bacitracin ABC transporter, ATP-binding protein Bcr	Pepto009_385	894	407874	408767	+	B	RBH: apr:Apr_0642 ABC transporter related; K09687 antibiotic transport system ATP-binding
650261393	HMPREF9286_0995 putative membrane protein	Pepto009_386	756	408775	409530	+	C	BLAST: hypothetical protein (db=KEGG evalu=5.0e-35 bit_score=150.0 identity=47.6 covera
650261392	HMPREF9286_0994 conserved hypothetical protein	Pepto009_387	717	409541	410257	+	C	BLAST: hypothetical protein (db=KEGG evalu=6.0e-30 bit_score=134.0 identity=68.97 covera
650261391	HMPREF9286_0993 O-acetylhomoserine aminocarboxypropyltransferase/cysteine synthase							
		Pepto009_388	1437	410389	411825	+	B	RBH: dsy:DSY1102 hypothetical protein; K00128 aldehyde dehydrogenase (NAD+) [EC:1.2.1.1.
		Pepto009_389	162	412537	412698	+	E	GENE: 15091.15252 + (rbs_motif=GGAG/GAG/AGG rbs_spacer=11-12bp)
		Pepto009_390	519	412686	413204	+	B	RBH: UniRef90_C2HHU0 Putative uncharacterized protein n=1 Tax=Finnegoldia magna ATCC
		Pepto009_391	165	413539	413703	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Finnegoldia magna ATCC 53516 ReplD=C2H
		Pepto009_392	450	413776	414225	+	B	RBH: UniRef90_C2HHT8 Putative uncharacterized protein n=1 Tax=Finnegoldia magna ATCC 1
		Pepto009_393	285	414277	414561	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Finnegoldia magna ATCC 53516 ReplD=C2H
		Pepto009_394	372	414564	414935	+	C	BLAST: XRE family transcriptional regulator (db=KEGG evalu=7.0e-18 bit_score=92.4 identi
		Pepto009_395	462	415225	415686	+	B	RBH: apr:Apr_0423 putative flavodoxin (db=KEGG)
650261794	HMPREF9286_0952 low molecular weight phosphotyrosine protein phosphatase	Pepto009_396	423	416676	417098	+	C	BLAST: arsC; arsenate reductase [EC:1.20.4.1]; K03741 arsenate reductase [EC:1.20.4.1] (db=B
		Pepto009_397	402	417100	417501	+	C	BLAST: hypothetical protein (db=KEGG evalu=1.0e-51 bit_score=204.0 identity=90.23 cov
		Pepto009_398	996	417586	418581	+	B	RBH: cha:CHAB381_0335 permease; K07089 (db=KEGG)
650261795	HMPREF9286_0953 arsenical-resistance protein	Pepto009_399	1059	418599	419657	+	B	RBH: cha:CHAB381_0334 arsB; arsenical-resistance protein; K03325 arsenite transporter, ACP
650261796	HMPREF9286_0954 arsenical resistance operon repressor	Pepto009_400	312	419720	420031	+	C	BLAST: transcriptional regulator, ArsR family; K03892 ArsR family transcriptional regulator (db
		Pepto009_401	102	421167	421268	+	E	GENE: 6521.6622 + (rbs_motif=GGAGG rbs_spacer=5-10bp)
		Pepto009_402	606	421431	422036	+	B	RBH: apr:Apr_0699 cadmium resistance transporter, CadJ family (db=KEGG)
		Pepto009_403	1839	422538	424376	+	B	RBH: cbi:CLJ_82256 hypothetical protein (db=KEGG)
		Pepto009_404	1218	424376	425593	+	C	BLAST: hypothetical protein (db=KEGG evalu=3.0e-42 bit_score=176.0 identity=34.72 cov
		Pepto009_405	2070	425590	427659	+	B	RBH: chb:CLC_1988 hypothetical protein (db=KEGG)
		Pepto010						
		Pepto011						
650262306	HMPREF9286_1240 biotin synthase	Pepto011_1	966	189	1154	+	B	RBH: bhy:BHWA1_02062 bioB; biotin synthase; K01012 biotin synthetase [EC:2.8.1.6] (db=KE
650262307	HMPREF9286_1241 tRNA [guanine-N(7)]-methyltransferase	Pepto011_2	642	1217	1858	+	C	BLAST: trmB, yggH; tRNA [guanine-N(7)]-methyltransferase [EC:2.1.1.33]; K03439 tRNA (guar
650262308	HMPREF9286_1242 conserved hypothetical protein	Pepto011_3	741	1998	2738	+	C	BLAST: endonuclease (db=KEGG evalu=7.0e-50 bit_score=200.0 identity=53.01 coverage=73
650261696	HMPREF9286_1304 cupin domain protein	Pepto011_4	330	2725	3054	+	C	BLAST: cupin 2 conserved barrel domain protein; K11312 cupin 2 domain-containing protein (
650262309	HMPREF9286_1243 Na+/H+ antiporter family protein	Pepto011_5	1386	3356	4741	+	B	RBH: apr:Apr_1578 Na+/H+ antiporter NhaC (db=KEGG)
650262310	HMPREF9286_1244 conserved hypothetical protein							
650262311	HMPREF9286_1245 GTP diphosphokinase family protein							
650262312	HMPREF9286_1246 conserved hypothetical protein							
650262313	HMPREF9286_1247 hydrogenase maturation GTPase HydF							
650262314	HMPREF9286_0352 transcriptional regulator, MarR family							
650262315	HMPREF9286_0353 putative beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ							
650262316	HMPREF9286_0354 beta-ketoacyl-acyl-carrier-protein synthase II							
650262317	HMPREF9286_0355 3-oxoacyl-[acyl-carrier-protein] reductase							
650262318	HMPREF9286_0356 acyl transferase domain protein							
650262319	HMPREF9286_0357 oxidoreductase, 2-nitropropane dioxigenase family protein							
650262320	HMPREF9286_0358 putative enoyl-[acyl-carrier-protein] reductase II							
650262321	HMPREF9286_0359 beta-ketoacyl-acyl-carrier-protein synthase III							
650262322	HMPREF9286_0360 Acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit							
650262323	HMPREF9286_0361 putative acetyl-CoA carboxylase, carboxyl transferase, beta subunit							
650262324	HMPREF9286_0362 putative acetyl-CoA carboxylase, biotin carboxylase subunit							
650262325	HMPREF9286_0363 Biotin-requiring enzyme							
650262326	HMPREF9286_0364 putative acyl carrier protein							
650262327	HMPREF9286_0365 channel protein, hemolysin III family							
		Pepto011_6	1203	4769	5971	+	B	RBH: cbi:CLK_3163 megL; methionine gamma-lyase [EC:4.4.1.11]; K01761 methionine-gamm
650262013	HMPREF9286_0589 conserved hypothetical protein							
650262012	HMPREF9286_0588 putative 3-dehydroquininate synthase	Pepto011_7	1053	6108	7160	+	C	BLAST: aroB; 3-dehydroquininate synthase; K01735 3-dehydroquininate synthase [EC:4.2.3.4] (db
650262011	HMPREF9286_0587 putative 3-phosphoshikimate 1-carboxyvinyltransferase	Pepto011_8	1236	7144	8379	+	C	BLAST: aroA; 3-phosphoshikimate 1-carboxyvinyltransferase [EC:2.5.1.19]; K00800 3-phospho
650262010	HMPREF9286_0586 chorismate synthase	Pepto011_9	1095	8369	9463	+	B	RBH: cpr:CPR_0691 aroC; chorismate synthase [EC:4.2.3.5]; K01736 chorismate synthase [EC:
650262009	HMPREF9286_0585 shikimate kinase	Pepto011_10	1512	9451	10962	+	B	RBH: UniRef90_C7HV14 Shikimate dehydrogenase n=1 Tax=Anaerococcus vaginalis ATCC 511

650262008 HMPREF9286_0584 3-dehydroquinate dehydratase, type II	Pepto011_11	441	10943	11383	C	BLAST: dehydroquinase class II; K03786 3-dehydroquinate dehydratase II [EC:4.2.1.10] (db=KEGG)
650262007 HMPREF9286_0583 aminodeoxychorismate synthase, component I	Pepto011_12	2022	11380	13401	B	RBH: naz:Aazo_0310 para-aminobenzoate synthase subunit I; K13950 para-aminobenzoate synthase subunit I
650262006 HMPREF9286_0582 3-deoxy-7-phosphoheptulonate synthase	Pepto011_13	789	13398	14186	C	BLAST: 3-deoxy-7-phosphoheptulonate synthase; K03856 3-deoxy-7-phosphoheptulonate synthase
650262005 HMPREF9286_0581 aminotransferase, class IV	Pepto011_14	726	14170	14895	C	BLAST: putative branched-chain-amino-acid aminotransferase; K02619 4-amino-4-deoxychorismate synthase
650261696 HMPREF9286_1304 cupin domain protein						
650261697 HMPREF9286_1305 pyridoxamine S'-phosphate oxidase family protein						
650261698 HMPREF9286_1306 bile acid transporter	Pepto011_15	957	14956	15912	C	BLAST: bile acid:sodium symporter; K03453 bile acid:Na ⁺ symporter, BASS family (db=KEGG e
650261699 HMPREF9286_1307 pantoate-β-alanine ligase	Pepto011_16	834	15914	16747	B	RBH: cth:Cthe_0901 panC; pantoate-β-alanine ligase [EC:6.3.2.1]; K01918 pantoate-β-al
	Pepto011_17	1179	17159	18337	B	RBH: UniRef90_D4MR69 Amidohydrolase n=2 Tax=Clostridiales RepID=D4MR69_9FIRM (db
	Pepto011_18	1401	18339	19739	B	RBH: afn:Acerf_2084 amidohydrolase; K12941 aminobenzoyl-glutamate utilization protein I
	Pepto011_19	1374	19758	21131	B	RBH: UniRef90_D4MR67 Na ⁺ /glutamate symporter n=2 Tax=Clostridiales RepID=D4MR67_5
	Pepto011_20	918	21167	22084	C	BLAST: glutaminase [EC:3.5.1.2]; K01425 glutaminase [EC:3.5.1.2] (db=KEGG evalue=7.0e-55
	Pepto011_21	711	22096	22806	C	BLAST: hypothetical protein (db=KEGG evalue=3.0e-10 bit_score=68.9 identity=33.62 covera
	Pepto011_22	726	22809	23534	C	BLAST: hypothetical protein (db=KEGG evalue=8.0e-20 bit_score=100.0 identity=33.33 cove
	Pepto011_23	1119	23734	24852	D	IPRSCAN: coiled-coil (db=Coil db_id=coil from=305 to=333 evalue=NA)
650262296 HMPREF9286_0341 dihydroorotate oxidase, catalytic subunit	Pepto011_24	906	24937	25842	C	RBH: ctc:CTC00930 dihydroorotate dehydrogenase 1B [EC:1.3.3.1]; K00226 dihydroorotate ox
650262297 HMPREF9286_0342 putative dihydroorotate oxidase, electron transfer subunit	Pepto011_25	702	25832	26533	C	BLAST: dihydroorotate dehydrogenase electron transfer subunit [EC:1.3.5.2]; K02823 dihydro
650262298 HMPREF9286_0343 aspartate carbamoyltransferase regulatory chain, allosteric	Pepto011_26	432	26536	26967	C	BLAST: hypothetical protein; K00610 aspartate carbamoyltransferase regulatory subunit (db=
650262299 HMPREF9286_0344 aspartate carbamoyltransferase	Pepto011_27	912	26964	27875	B	RBH: cno:NT01CX_0395 pyrB; aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]; K
650262300 HMPREF9286_0345 guanylate kinase	Pepto011_28	540	27987	28526	C	BLAST: gmK: guanylate kinase [EC:2.7.4.8]; K00942 guanylate kinase [EC:2.7.4.8] (db=KEGG ev
650262301 HMPREF9286_0347 riboflavin biosynthesis protein RibD	Pepto011_29	1083	28771	29853	B	RBH: UniRef90_D1VVV6 Riboflavin biosynthesis protein RibD n=1 Tax=Peptoniphilus lacrima
650262302 HMPREF9286_0348 riboflavin synthase, alpha subunit	Pepto011_30	645	29846	30490	C	BLAST: ribE; riboflavin synthase subunit alpha; K00793 riboflavin synthase alpha chain [EC:2.5
650262303 HMPREF9286_0349 GTP cyclohydrolase II	Pepto011_31	1206	30503	31708	B	RBH: ere:EUBREC_3130 riboflavin biosynthesis; GTP-cyclohydrolase II; K01497 GTP cyclohydr
650262304 HMPREF9286_0350 6,7-dimethyl-8-ribityllumazine synthase	Pepto011_32	468	31777	32244	C	BLAST: ribH; 6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.9]; K00794 riboflavin synthase
650262305 HMPREF9286_0351 haloacid dehalogenase-like hydrolase	Pepto011_33	648	32237	32884	C	BLAST: haloacid dehalogenase domain protein hydrolase; K01091 phosphoglycolate phosphat
	Pepto011_34	1404	33019	34422	C	RBH: UniRef90_C0B7K1 Putative uncharacterized protein n=1 Tax=Coprococcus genes ATCC
650261877 HMPREF9286_0445 3-hydroxybutyryl-CoA dehydrogenase	Pepto011_35	846	35111	35956	B	RBH: cpr:CPR_2283 hbd; 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.17]; K00074 3-hydr
650261878 HMPREF9286_0446 3-hydroxybutyryl-CoA dehydratase	Pepto011_36	777	35958	36734	C	RBH: UniRef90_D1VRM9 3-hydroxybutyryl-CoA dehydratase n=1 Tax=Peptoniphilus lacrima
650261879 HMPREF9286_0447 acetyl-CoA C-acetyltransferase	Pepto011_37	1188	36741	37928	B	RBH: apr:Apr_1351 acetyl-CoA acetyltransferase; K00626 acetyl-CoA C-acetyltransferase [EC
	Pepto011_38	414	37943	38356	C	BLAST: dehydratase (db=KEGG evalue=8.0e-49 bit_score=195.0 identity=73.72 coverage=97
650261880 HMPREF9286_0448 UDP-N-acetylglucosamine 2-epimerase	Pepto011_39	1104	38426	39529	B	RBH: amt:Amet_0343 UDP-N-acetylglucosamine 2-epimerase [EC:5.1.3.14]; K01791 UDP-N-ac
650261881 HMPREF9286_0449 glycosyltransferase, group 4 family	Pepto011_40	1029	39531	40559	B	RBH: UniRef90_D1VRM5 Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transfe
650261882 HMPREF9286_0450 uracil phosphoribosyltransferase	Pepto011_41	627	40569	41195	C	RBH: UniRef90_D1VRM4 Uracil phosphoribosyltransferase n=1 Tax=Peptoniphilus lacrima
650261883 HMPREF9286_0451 ribose-5-phosphate isomerase B	Pepto011_42	432	41197	41628	C	BLAST: rpiB; ribose-5-phosphate isomerase B [EC:5.3.1.6]; K01808 ribose 5-phosphate isom
650261884 HMPREF9286_0452 Sua5/YciO/YrdC/YwIC family protein	Pepto011_43	1056	41638	42693	B	RBH: cbl:CLK_3317 SUA5/YciO/YrdC/YwIC family protein; K07566 putative translation factor (
650261885 HMPREF9286_0453 amidohydrolase						
650261886 HMPREF9286_0454 arylsulfatase	Pepto011_44	1923	42856	44778	B	RBH: UniRef90_D1VRM1 Putative sulfatase n=1 Tax=Peptoniphilus lacrima
650261887 HMPREF9286_0455 LysR substrate binding domain protein						
	Pepto011_45	906	44854	45759	B	RBH: Isa:LSA0444 putative malate dehydrogenase [EC:1.1.1.37] (db=KEGG)
650261888 HMPREF9286_0456 serine protease do-like protein	Pepto011_46	1275	46141	47415	B	RBH: UniRef90_D1VTZ8 Peptidase Do n=1 Tax=Peptoniphilus lacrima
650261889 HMPREF9286_0457 conserved hypothetical protein						
650261271 HMPREF9286_1436 conserved hypothetical protein	Pepto011_47	798	47547	48344	B	RBH: par:Psc_1103 hypothetical protein (db=KEGG)
650261272 HMPREF9286_1437 biotin-dependent carboxylase domain protein	Pepto011_48	945	48341	49285	C	RBH: fnu:FNO436 UreA carboxylase [EC:6.3.4.6] (db=KEGG)
650261273 HMPREF9286_1438 TIGR00370 family protein	Pepto011_49	747	49278	50024	B	RBH: UniRef90_D1VTZ6 Kinase A inhibitor n=1 Tax=Peptoniphilus lacrima
650261274 HMPREF9286_1439 transporter, branched chain amino acid:cation symporter (U	Pepto011_50	1197	50041	51237	B	RBH: fnu:FNO438 branched chain amino acid ABC transporter (db=KEGG)
650261275 HMPREF9286_1440 LamB/YcsF family protein	Pepto011_51	774	51248	52021	B	RBH: fnu:FNO439 LamB/YcsF family protein; K07160 (db=KEGG)
	Pepto011_52	1761	52514	54274	B	RBH: cbl:CLJ_82234 putative lantibiotic ABC transporter,ATP-binding protein (db=KEGG)
	Pepto011_53	867	54284	55150	D	IPRSCAN: Abi (db=HMMpfam db_id=PF05127 from=143 to=231 evalue=5.9e-15 interpre_id=
	Pepto011_54	273	55209	55481	E	GENE: 13077..13349 + (rbs_motif=AGGAG rbs_spacer=5-10bp)
	Pepto011_55	1182	55643	56824	D	IPRSCAN: LANC_like (db=HMMpfam db_id=PF05147 from=162 to=387 evalue=8.2e-14)
	Pepto011_56	303	56984	57286	E	GENE: 11272..11574 + (rbs_motif=GGAG/GAG/AGG rbs_spacer=5-10bp)
	Pepto011_57	882	57317	58198	C	BLAST: CAAX amino terminal protease family protein (db=KEGG evalue=6.0e-10 bit_score=6
	Pepto011_58	1284	58422	59705	C	BLAST: lantionine synthetase C-like protein (db=KEGG evalue=4.0e-16 bit_score=89.7 iden
	Pepto011_59	3012	59708	62719	C	BLAST: lantibiotic dehydratase domain-containing protein (db=KEGG evalue=1.0e-73 bit_sc
	Pepto011_60	108	63225	63332	E	GENE: 5226..5333 + (rbs_motif=AGGA rbs_spacer=5-10bp)
	Pepto011_61	933	63366	64298	C	BLAST: CAAX amino terminal protease family protein (db=KEGG evalue=4.0e-18 bit_score=5
650261276 HMPREF9286_1441 ABC transporter, ATP-binding protein	Pepto011_62	750	64556	65305	C	BLAST: ABC transporter related; K02049 sulfonate/nitrate/taurine transport system ATP-bind
650261277 HMPREF9286_1442 NMT1/THIS-like protein	Pepto011_63	1032	65302	66333	B	RBH: csh:Closa_0970 NMT1/THIS-like domain-containing protein; K02051 sulfonate/nitrate/t
650261278 HMPREF9286_1443 ABC transporter, permease protein	Pepto011_64	765	66300	67094	C	BLAST: binding-protein-dependent transport systems inner membrane component; K02050 s
650261279 HMPREF9286_1444 conserved hypothetical protein	Pepto011_65	300	67063	67362	C	BLAST: hypothetical protein (db=KEGG evalue=1.0e-12 bit_score=75.5 identity=49.0 coverage
650261280 HMPREF9286_1446 nitroreductase family protein						
	Pepto011_66	591	67809	68399	C	BLAST: TetR family transcriptional regulator (db=KEGG evalue=1.0e-74 bit_score=281.0 iden
	Pepto012					
650261211 HMPREF9286_1124 conserved hypothetical protein	Pepto012_1	279	1384	1662	C	BLAST: hypothetical protein (db=KEGG evalue=6.0e-27 bit_score=122.0 identity=68.54 cove
650261210 HMPREF9286_1721 transposase-like protein						
	Pepto013					
	Pepto013_1	252	2	253	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=12 to=31)
	Pepto013_2	276	261	536	D	IPRSCAN: seg (db=Seg db_id=seg from=12 to=30)
	Pepto013_3	249	565	813	D	IPRSCAN: seg (db=Seg db_id=seg from=3 to=15)
	Pepto014					
	Pepto015					
650261278 HMPREF9286_0884 peptidase C26	Pepto015_1	459	190	648	C	BLAST: Putative uncharacterized protein n=1 Tax=Anaerococcus tetradius ATCC 35098 Repl
650261702 HMPREF9286_1310 anaerobic ribonucleoside-triphosphate reductase activating	Pepto015_2	654	1229	1882	C	BLAST: Putative uncharacterized protein n=1 Tax=Parvimonas micra ATCC 33370 ReplD=A85
650261701 HMPREF9286_1309 anaerobic ribonucleoside-triphosphate reductase	Pepto015_3	261	2208	2468	C	BLAST: hypothetical protein (db=KEGG evalue=2.0e-08 bit_score=61.2 identity=76.19 cover
650261700 HMPREF9286_1308 conserved hypothetical protein	Pepto015_4	177	2454	2630	C	BLAST: hypothetical protein (db=KEGG evalue=3.0e-26 bit_score=120.0 identity=98.28 cove
	Pepto016					
	Pepto016_1	918	498	1415	C	BLAST: LysR-family transcriptional regulator (db=KEGG evalue=7.0e-16 bit_score=88.2 iden
	Pepto016_2	672	1549	2220	C	BLAST: ctfA; butyrate-acetoacetate CoA-transferase subunit A; K01034 acetate CoA-transfe
	Pepto016_3	675	2220	2894	C	BLAST: butyryl-CoA:acetoacetate CoA-transferase beta subunit [EC:2.8.3.9]; K01029 3-oxoa
650261879 HMPREF9286_0447 acetyl-CoA C-acetyltransferase	Pepto016_4	1245	2908	4152	B	RBH: sub:SUB1804 thIA; acetyl-CoA acetyltransferase [EC:2.3.1.9] (db=KEGG)
	Pepto016_5	1467	4161	5627	C	BLAST: sodium/sulphate symporter (db=KEGG evalue=2.0e-48 bit_score=197.0 identity=29.9
650261704 HMPREF9286_1312 conserved hypothetical protein						
650261703 HMPREF9286_1311 conserved hypothetical protein						
650261702 HMPREF9286_1310 anaerobic ribonucleoside-triphosphate reductase activating	Pepto016_6	495	5701	6195	C	BLAST: anaerobic ribonucleoside-triphosphate reductase activator; K04068 anaerobic ribonuc
650261701 HMPREF9286_1309 anaerobic ribonucleoside-triphosphate reductase	Pepto016_7	2124	6195	8318	B	RBH: fma:FMG_1178 anaerobic ribonucleoside triphosphate reductase; K00527 ribonucleosid
650261700 HMPREF9286_1308 conserved hypothetical protein	Pepto016_8	810	8515	9324	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrima
	Pepto016_9	840	9600	10439	C	BLAST: peptidase C26; K07010 putative glutamine amidotransferase (db=KEGG evalue=2.0e-3
650261728 HMPREF9286_0882 ATP-dependent chaperone protein CnpB	Pepto016_10	921	10773	11693	C	BLAST: heat shock protein; K05516 curved DNA-binding protein (db=KEGG evalue=4.0e-53 bi
650261726 HMPREF9286_0882 ATP-dependent chaperone protein CnpB	Pepto016_11	2583	11703	12485	B	RBH: cst:CLOST_1982 cnpB; protein disaggregation chaperone; K03695 ATP-dependent Cnp pr
650261725 HMPREF9286_0881 conserved hypothetical protein	Pepto016_12	1773	14467	16239	C	BLAST: cellulosome anchoring protein, cohesin region (db=KEGG evalue=1.0e-33 bit_score=14
650261724 HMPREF9286_0879 ABC transporter, substrate-binding protein, family 3						
650261723 HMPREF9286_0878 ABC transporter, permease protein						
650261722 HMPREF9286_0877 arginine ABC transporter, ATP-binding protein ArtM						
650261721 HMPREF9286_0876 putative membrane protein						
650261720 HMPREF9286_0875 methionine-tRNA ligase	Pepto016_13	1956	16583	18538	B	RBH: aoe:Clos_2662 methionyl-tRNA synthetase; K01874 methionyl-tRNA synthetase [EC:6.1.
650261719 HMPREF9286_0874 hydrolase, TatD family	Pepto016_14	765	18547	19311	B	RBH: UniRef90_D1VVP7 TatD family hydrolase n=1 Tax=Peptoniphilus lacrima
650261718 HMPREF9286_0873 ribonuclease M5	Pepto016_15	552	19308	19859	C	BLAST: putative DNA-binding protein; K05985 ribonuclease M5 [EC:3.1.26.8] (db=KEGG eval
650261717 HMPREF9286_0872 putative dimethyladenosine transferase	Pepto016_16	780	19924	20703	B	RBH: UniRef90_D1VVP9 Ribosomal RNA small subunit methyltransferase A n=1 Tax=Peptonip
650261716 HMPREF9286_0871 putative HTH-type transcriptional repressor CsrA	Pepto016_17	351	20711	21061	C	BLAST: transcriptional regulator, ArsR family (db=KEGG evalue=9.0e-24 bit_score=112.0 iden
650261715 HMPREF9286_0870 glutaredoxin	Pepto016_18	228	21133	21360	C	BLAST: glutaredoxin (db=KEGG evalue=7.0e-18 bit_score=92.8 identity=55.56 coverage=93.42
650261714 HMPREF9286_0869 conserved hypothetical protein	Pepto016_19	597	21383	21979	C	BLAST: hypothetical protein (db=KEGG evalue=2.0e-47 bit_score=191.0 identity=55.38 covera
650261713 HMPREF9286_0868 sodium pump decarboxylase, gamma subunit	Pepto016_20	318	22543	22860	C	BLAST: Oxaloacetate decarboxylase gamma chain n=1 Tax=Peptoniphilus lacrima

650261712	HMPREF9286_0867	glutaconyl-CoA decarboxylase subunit gamma	Pepto016_21	432	22907	23338	+ C	BLAST: biotin/lipoyl attachment domain-containing protein (db=KEGG eval=1.0e-16 bit_sco
650261711	HMPREF9286_0866	glutaconyl-CoA decarboxylase subunit beta	Pepto016_22	1137	23354	24490	+ B	RBH: fnu:FN0201 glutaconyl-CoA decarboxylase beta subunit (EC:4.1.1.70) (db=KEGG
650261710	HMPREF9286_0865	glutaconate CoA-transferase subunit A	Pepto016_23	960	24573	25532	+ B	RBH: afn:Acerf_1819 coenzyme A transferase; K01039 glutaconate CoA-transferase, subunit A
650261709	HMPREF9286_0864	glutaconate CoA-transferase subunit B	Pepto016_24	798	25532	26329	+ B	RBH: afn:Acerf_1818 coenzyme A transferase; K01040 glutaconate CoA-transferase, subunit B
650261708	HMPREF9286_0863	glutaconyl-CoA decarboxylase subunit alpha	Pepto016_25	1770	26341	28110	+ B	RBH: afn:Acerf_1817 carboxyl transferase; K01615 glutaconyl-CoA decarboxylase [EC:4.1.1.70
650261707	HMPREF9286_0862	(R)-2-hydroxyglutaryl-CoA dehydratase activator	Pepto016_26	819	28350	29168	+ B	RBH: fnu:FN0206 (R)-2-hydroxyglutaryl-CoA dehydratase activator protein (db=KEGG
650261706	HMPREF9286_0861	(R)-2-hydroxyglutaryl-CoA dehydratase D-component	Pepto016_27	1323	29189	30511	+ B	RBH: fnu:FN0207 (R)-2-hydroxyglutaryl-CoA dehydratase alpha-subunit [EC:4.2.1.-] (db=KEGG
650261705	HMPREF9286_0860	(R)-2-hydroxyglutaryl-CoA dehydratase D-component	Pepto016_28	1149	30524	31672	+ B	RBH: fnu:FN0208 (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit [EC:4.2.1.-]; K01726 [E
			Pepto016_29	276	31885	32160	+ C	BLAST: predicted ATPase (AAA+ superfamily); K07133 (db=KEGG eval=2.0e-24 bit_score=
			Pepto016_30	1107	32106	33212	+ B	RBH: ere:EUBREC_0502 hypothetical protein (db=KEGG eval=2.0e-24 bit_score=
			Pepto016_31	594	33269	33862	+ C	BLAST: putative cytoplasmic protein (db=KEGG eval=3.0e-51 bit_score=204.0 identity=51
			Pepto016_32	1296	34264	35559	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V
650261942	HMPREF9286_0213	6-O-methylguanine DNA methyltransferase, DNA binding do	Pepto016_33	519	35717	36235	+ C	BLAST: ogt1; methylated-DNA-protein-cysteine methyltransferase 1; K00567 methylated-DN
650261941	HMPREF9286_0212	chaperonin GroS	Pepto016_34	282	36359	36640	+ C	BLAST: heat shock protein; K04078 chaperonin GroES (db=KEGG eval=3.0e-16 bit_score=87
650261940	HMPREF9286_0211	chaperonin GroL	Pepto016_35	1623	36652	38274	+ B	RBH: fma:FMG_0886 heat shock protein; K04077 chaperonin GroEL (db=KEGG
650261939	HMPREF9286_0210	hydroxyacylglutathione hydrolase	Pepto016_36	690	38735	39424	+ C	BLAST: gloB; hydroxyacylglutathione hydrolase; K01069 hydroxyacylglutathione hydrolase [E
650261938	HMPREF9286_0209	Sodium:neurotransmitter symporter family protein	Pepto016_37	1341	39496	40836	+ B	RBH: fnu:FN1944 sodium-dependent tryptophan transporter; K03308 neurotransmitter-Na+ s
650261937	HMPREF9286_0208	tryptophan 2,3-dioxygenase	Pepto016_38	1644	40959	42602	+ C	RBH: fnu:FN1943 tnaA; tryptophanase (EC:4.1.99.1); K01667 tryptophanase [EC:4.1.99.1] (db
650261936	HMPREF9286_0207	fructose-bisphosphate aldolase class 1	Pepto016_39	891	42966	43856	+ B	RBH: cac:CA_P0064 alf; fructose-1,6-bisphosphate aldolase (EC:4.1.2.13); K01623 fructose-bis
650261935	HMPREF9286_0206	ribonuclease HI	Pepto016_40	579	43946	44524	+ C	BLAST: putative ribonuclease; K03469 ribonuclease HI [EC:3.1.26.4] (db=KEGG eval=2.0e-36
650261934	HMPREF9286_0205	putative ComE operon protein 2	Pepto016_41	420	44521	44940	+ C	BLAST: putative late competence protein required for DNA binding; K01493 dCMP deaminase
650261933	HMPREF9286_0204	transcriptional regulator, TetR family						
650261930	HMPREF9286_0201	conserved hypothetical protein						
650261929	HMPREF9286_0200	putative membrane protein						
650261928	HMPREF9286_0199	large conductance mechanosensitive channel protein	Pepto016_42	417	44960	45376	+ C	BLAST: large conductance mechanosensitive channel protein; K03282 large conductance mec
650261927	HMPREF9286_0198	phospholipase, patatin family	Pepto016_43	1035	45373	46407	+ B	RBH: UniRef90_D1VW11 Phospholipase, patatin family n=1 Tax=Peptoniphilus lacrimalis 315-
650261926	HMPREF9286_0197	hydrolase, NUDIX family	Pepto016_44	630	46397	47026	+ C	BLAST: putative hydrolase (db=KEGG eval=1.0e-40 bit_score=169.0 identity=46.46 coverage
650261925	HMPREF9286_0196	3D domain protein	Pepto016_45	987	47329	48315	+ C	BLAST: 3D domain-containing protein (db=KEGG eval=2.0e-43 bit_score=179.0 identity=41.
650261924	HMPREF9286_0195	putative membrane protein	Pepto016_46	891	48473	49363	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V
650261330	HMPREF9286_1497	conserved hypothetical protein						
650261329	HMPREF9286_1496	conserved hypothetical protein	Pepto016_47	2640	49842	52481	+ B	RBH: UniRef90_D1VWV9 Putative middle cell wall protein n=1 Tax=Peptoniphilus lacrimalis 3:
650261328	HMPREF9286_1495	conserved hypothetical protein						
650261327	HMPREF9286_1494	sigma-70, region 4	Pepto016_48	597	52847	53443	+ C	BLAST: ECF subfamily RNA polymerase sigma-24 factor; K03091 RNA polymerase sporulation-
650261325	HMPREF9286_1492	conserved hypothetical protein	Pepto016_49	477	53458	53934	+ C	BLAST: putative phage related amidase (db=KEGG eval=1.0e-52 bit_score=207.0 identity=6
650261324	HMPREF9286_1491	conserved domain protein	Pepto016_50	222	54017	54238	+ E	GENE: 112883..113104 - (rbs_motif=AGGAGG rbs_spacer=5-10bp)
650261323	HMPREF9286_1490	conserved domain protein						
			Pepto016_51	216	54285	54500	+ D	IPRSCAN: DUF2922 (db=HMM Pfam db_id=PF11148 from=6 to=71 eval=1.2e-10 interpro_ID
650261322	HMPREF9286_1489	conserved hypothetical protein	Pepto016_52	153	54497	54649	+ C	BLAST: Conserved domain protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VTE3_9FI
650262170	HMPREF9286_0848	glycine cleavage T-protein						
650262169	HMPREF9286_0847	quinolinate synthetase complex, A subunit	Pepto016_53	918	55722	56639	+ B	RBH: fnu:FN0008 quinolinate synthetase (EC:4.1.99.-); K03517 quinolinate synthase [EC:2.5.1.
650262168	HMPREF9286_0846	FAD binding domain protein	Pepto016_54	1263	56641	57903	+ B	RBH: fnu:FN0009 L-aspartate oxidase (EC:1.4.3.16); K00278 L-aspartate oxidase [EC:1.4.3.16]
650262167	HMPREF9286_0845	nicotinate-nucleotide diphosphorylase (carboxylating)	Pepto016_55	846	57875	58720	+ B	RBH: UniRef90_D1VT87 Nicotinate-nucleotide diphosphorylase (Carboxylating) n=1 Tax=Pept
650262166	HMPREF9286_0844	HTH domain protein	Pepto016_56	510	58728	59237	+ C	BLAST: hypothetical protein; K07105 (db=KEGG eval=4.0e-35 bit_score=150.0 identity=50.5
			Pepto016_57	192	59324	59515	+ E	GENE: 107606..107797 - (rbs_motif=GGAG/GAG/AGG rbs_spacer=5-10bp)
650262165	HMPREF9286_0843	phosphate ABC transporter, phosphate-binding protein	Pepto016_58	927	59717	60643	+ B	RBH: UniRef90_D1VWN3 Phosphate-binding protein PstS 2 n=1 Tax=Peptoniphilus lacrimalis 3
650262164	HMPREF9286_0842	phosphate ABC transporter, permease protein PstC	Pepto016_59	909	60663	61571	+ B	RBH: UniRef90_D1VWN4 Phosphate ABC transporter, permease protein PstC n=1 Tax=Peptoni
650262163	HMPREF9286_0841	phosphate ABC transporter, permease protein PstA	Pepto016_60	682	61564	62445	+ B	RBH: UniRef90_D1VWN5 Phosphate ABC transporter, permease protein PstA n=1 Tax=Peptoni
650262162	HMPREF9286_0840	phosphate ABC transporter, ATP-binding protein	Pepto016_61	756	62247	63202	+ B	RBH: fma:FMG_0593 phosphate ABC transporter ATP-binding protein; K02036 phosphate tra
650262161	HMPREF9286_0839	phosphate transport system regulatory protein PhoU	Pepto016_62	630	63202	63831	+ C	BLAST: phosphate transport system protein; K02039 phosphate transport system protein (db
650262160	HMPREF9286_0838	putative response regulator ArlR	Pepto016_63	681	63836	64516	+ B	RBH: UniRef90_D1VWN8 Alkaline phosphatase synthesis transcriptional regulatory protein Ph
650262159	HMPREF9286_0837	ATPase/histidine kinase/DNA gyrase B/HSP90 domain prote	Pepto016_64	1689	64519	66207	+ B	RBH: cth:Cthe_1599 PAS/PAC sensor signal transduction histidine kinase (EC:2.7.3.-); K07636
			Pepto016_65	372	66408	66779	+ D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=24)
			Pepto016_66	1545	66815	68359	+ D	BLAST: hypothetical protein (db=KEGG eval=2.0e-07 bit_score=61.6 identity=26.57 cover
			Pepto016_67	630	68356	68985	+ C	BLAST: ABC transporter ATP-binding protein; K01990 ABC-2 type transport system ATP-bind
			Pepto016_68	681	68978	69658	+ D	IPRSCAN: seg (db=Seg db_id=seg from=17 to=30)
650261690	HMPREF9286_1298	conserved hypothetical protein						
650261689	HMPREF9286_1297	protein TraX						
650261688	HMPREF9286_1296	4-phosphorylthronate dehydrogenase	Pepto016_69	942	69870	70811	+ B	RBH: UniRef90_D1VVP3 Phosphoglycerate dehydrogenase n=1 Tax=Peptoniphilus lacrimalis 3
650261687	HMPREF9286_1295	MutS domain V protein	Pepto016_70	1605	70929	72533	+ C	BLAST: DNA mismatch repair protein MutS domain-containing protein (db=KEGG eval=2.0e
650261686	HMPREF9286_1294	phosphoglycerate mutase family protein	Pepto016_71	606	72671	73276	+ C	BLAST: hypothetical protein; K01834 phosphoglycerate mutase [EC:5.4.2.1] (db=KEGG eval=
650261685	HMPREF9286_1293	putative thioredoxin-disulfide reductase 2	Pepto016_72	936	73287	74222	+ B	RBH: UniRef90_D1VU46 Thioredoxin-disulfide reductase n=1 Tax=Peptoniphilus lacrimalis 31:
650261684	HMPREF9286_1292	thioredoxin	Pepto016_73	1788	74219	76006	+ B	RBH: str:Sterm_0484 thioredoxin domain protein (db=KEGG
650261683	HMPREF9286_1291	conserved hypothetical protein	Pepto016_74	627	76025	76651	+ C	BLAST: HAD family hydrolase n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU51_9FIRM (
650261682	HMPREF9286_1290	ImpB/MucB/SamB family protein	Pepto016_75	1035	76725	77759	+ B	RBH: tte:TTE0254 dinP; DNA polymerase IV; K02346 DNA polymerase IV [EC:2.7.7.7] (db=KEG
650261681	HMPREF9286_1289	TIGR02206 family protein						
650261680	HMPREF9286_1288	conserved hypothetical protein						
			Pepto016_76	426	77772	78197	+ C	BLAST: thioesterase superfamily protein (db=KEGG eval=1.0e-11 bit_score=72.0 identity=
			Pepto016_77	459	78241	78699	+ C	BLAST: hypothetical protein (db=KEGG eval=8.0e-19 bit_score=95.9 identity=41.01 cover
			Pepto016_78	795	78699	79493	+ C	BLAST: hypothetical protein (db=KEGG eval=5.0e-34 bit_score=147.0 identity=47.04 cove
			Pepto016_79	1179	79502	80680	+ B	RBH: fnu:FN1063 N-acyl-L-amino acid amidohydrolase (EC:3.5.1.14); K01436 aminocyclase [
650261679	HMPREF9286_1287	formate/nitrite transporter	Pepto016_80	762	80866	81627	+ C	BLAST: formate/nitrite transporter; K02598 nitrite transporter NirC (db=KEGG eval=3.0e-4C
650261678	HMPREF9286_1286	Na+/H+ antiporter NhaC	Pepto016_81	1425	81685	83109	+ B	RBH: aoe:Clos_2497 Na+/H+ antiporter NhaC; K03315 Na+/H+ antiporter, NhaC family (db=KE
650261677	HMPREF9286_1285	adenine phosphoribosyltransferase	Pepto016_82	543	83208	83750	+ C	BLAST: adenine phosphoribosyltransferase [EC:2.4.2.7]; K00759 adenine phosphoribosyltra
650261676	HMPREF9286_1283	thiamine biosynthesis protein ThiC	Pepto016_83	1302	83930	85231	+ B	RBH: apr:Apr_1114 thiamine biosynthesis protein ThiC; K03147 thiamine biosynthesis protei
650261675	HMPREF9286_1281	protein ThiW	Pepto016_84	516	85457	85972	+ C	BLAST: ThiW protein (db=KEGG eval=2.0e-38 bit_score=161.0 identity=56.93 coverage=79.1
650261674	HMPREF9286_1280	phosphomethylpyrimidine kinase	Pepto016_85	813	85962	86774	+ C	BLAST: thiK; hydroxyethylthiazole kinase ThiM/ThiK; K00941 hydroxymethylpyrimidine/phosp
650261673	HMPREF9286_1279	putative hydroxyethylthiazole kinase	Pepto016_86	1389	86758	88146	+ C	BLAST: hydroxyethylthiazole kinase; K00878 hydroxyethylthiazole kinase [EC:2.7.1.50] (db=KE
650261672	HMPREF9286_1278	conserved hypothetical protein						
650261671	HMPREF9286_1277	uracinate hydratase	Pepto016_87	2028	88213	90240	+ B	RBH: sgo:SGO_1805 hutU; uracinate hydratase (EC:4.2.1.49); K01712 uracinate hydratase [E
			Pepto016_88	411	90749	91159	+ E	GENE: 75874..76284 - (rbs_motif=None rbs_spacer=None)
			Pepto016_89	213	91170	91382	+ D	IPRSCAN: seg (db=Seg db_id=seg from=8 to=27)
650261670	HMPREF9286_1276	imidazolonepropionase	Pepto016_90	1266	91589	92854	+ B	RBH: ssa:SSA_0436 hutI; imidazolonepropionase (EC:3.5.2.7); K01468 imidazolonepropionase
650261669	HMPREF9286_1275	Na+/H+ antiporter family protein						
650261668	HMPREF9286_1274	Na+/H+ antiporter NhaC	Pepto016_91	1536	93318	94853	+ B	RBH: apr:Apr_1400 Na+/H+ antiporter NhaC; K03315 Na+/H+ antiporter, NhaC family (db=KE
650261667	HMPREF9286_1273	conserved hypothetical protein	Pepto016_92	516	94908	95423	+ C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650261666	HMPREF9286_1272	putative gamma-glutamyltransferase	Pepto016_93	1626	95634	97259	+ B	RBH: nth:Nther_2809 Gamma-glutamyltransferase 2. Threonine peptidase. MEROPS family TC
650261665	HMPREF9286_1271	excinuclease ABC, B subunit	Pepto016_94	1992	97271	99262	+ B	RBH: fma:FMG_0901 UvrABC system protein B; K03702 excinuclease ABC subunit B (db=KEGG
650260733	HMPREF9286_0564	excinuclease ABC, A subunit	Pepto016_95	2817	99275	102091	+ B	RBH: aoe:Clos_2257 excinuclease ABC, A subunit; K03701 excinuclease ABC subunit A (db=KE
650260732	HMPREF9286_0563	Erk/YbiS/Ycfs/YnhG	Pepto016_96	795	102093	102887	+ B	RBH: UniRef90_D1VNS3 Erk/YbiS/Ycfs/YnhG family protein n=1 Tax=Peptoniphilus lacrimalis
650260731	HMPREF9286_0562	ABC transporter, substrate-binding protein, family 3	Pepto016_97	855	102996	103850	+ B	UniRef90_D1VU37 Amino acid ABC ABC transporter n=1 Tax=Peptoniphilus lacrimalis 315-B
650260730	HMPREF9286_0561	putative arginine ABC transporter, permease protein ArtQ	Pepto016_98	678	103908	104585	+ B	RBH: UniRef90_D1VU38 Arginine transport system permease protein ArtQ n=1 Tax=Peptonipl
650260729	HMPREF9286_0560	arginine ABC transporter, ATP-binding protein ArtM	Pepto016_99	723	104578	105300	+ B	RBH: cpe:CP0602 amino acid ABC ABC transporter; K02028 polar amino acid transport system AT
650260728	HMPREF9286_0559	conserved hypothetical protein						
650260727	HMPREF9286_0558	conserved hypothetical protein						
650260726	HMPREF9286_0557	histidine ammonia-lyase	Pepto016_100	1539	105749	107287	+ B	RBH: sgo:SGO_1811 hutH; histidine ammonia-lyase (EC:4.3.1.3); K01745 histidine ammonia-ly
650260725	HMPREF9286_0556	glutamate formimidoyltransferase	Pepto016_101	894	107355	108248	+ B	RBH: ctc:CTC02305 glutamate formimidoyltransferase (EC:2.1.2.5); K00603 glutamate formimr
650260724	HMPREF9286_0555	formate-tetrahydrofolate ligase	Pepto016_102	1680	108254	109933	+ B	RBH: ctc:CTC02304 formate-tetrahydrofolate ligase (EC:6.3.4.3); K01938 formate-tetrahydr
650260723	HMPREF9286_0554	putative methenyltetrahydrofolate cyclohydrolase	Pepto016_103	627	109942	110568	+ C	BLAST: formiminetetrahydrofolate cyclodeaminase (EC:4.3.1.4); K01746 formiminetetrahydr
650260722	HMPREF9286_0553	conserved hypothetical protein	Pepto016_104	1344	110565	111908	+ B	RBH: ctc:CTC02567 mutL; glutamate mutase, MutL (db=KEGG
650260721	HMPREF9286_0552	conserved hypothetical protein						
650260720	HMPREF9286_0551	conserved hypothetical protein						
			Pepto016_105	462	111948	112409		

650260718	HMPREF9286_0549	cysteine--tRNA ligase	Pepto016_107	1398	113014	114411	+	B	RBH: fma:FMG_0415 cysteinyl-tRNA synthetase; K01883 cysteinyl-tRNA synthetase [EC:6.1.1.
650260717	HMPREF9286_0548	RNase3 domain protein	Pepto016_108	408	114396	114803	+	C	BLAST: hypothetical protein; K11145 ribonuclease III family protein (db=KEGG eval=3.0e-30
650260716	HMPREF9286_0547	thymidylate synthase, flavin-dependent	Pepto016_109	762	114800	115561	+	B	RBH: cdf:CD0054 thx; FAD-dependent thymidylate synthase [EC:2.1.1.148]; K03465 thymidyl
650260715	HMPREF9286_0546	RNA methyltransferase, TrmH family, group 3	Pepto016_110	708	115558	116265	+	C	BLAST: RNA methyltransferase, TrmH family, group 3; K03218 RNA methyltransferase, TrmH f
650260714	HMPREF9286_0545	conserved hypothetical protein	Pepto016_111	582	116274	116855	+	C	BLAST: protein of unknown function DUF901; K06962 (db=KEGG eval=3.0e-28 bit_score=12
650260713	HMPREF9286_0544	SH3 domain protein	Pepto016_112	207	116839	117045	+	D	IPRSCAN: seg (db=Seg db_id=seg from=47 to=64)
650260712	HMPREF9286_0543	FeoA domain protein	Pepto016_113	273	117258	117530	+	C	BLAST: hypothetical protein; K04758 ferrous iron transport protein A (db=KEGG eval=8.0e-
650260711	HMPREF9286_0542	FeoA domain protein	Pepto016_114	243	117533	117775	+	C	BLAST: hypothetical protein; K04758 ferrous iron transport protein A (db=KEGG eval=6.0e-
650260710	HMPREF9286_0541	ferrous iron transport protein B	Pepto016_115	2163	117776	119938	+	B	RBH: fma:FMG_1213 ferrous iron transport protein B; K04759 ferrous iron transport protein f
650260709	HMPREF9286_0540	conserved hypothetical protein							
650260708	HMPREF9286_0539	conserved hypothetical protein							
650260707	HMPREF9286_0538	ABC transporter, ATP-binding protein							
650260706	HMPREF9286_0537	iron permease FTR1 family							
650260705	HMPREF9286_0536	putative pathogen-specific surface antigen							
650260704	HMPREF9286_0535	putative membrane protein							
650260703	HMPREF9286_0534	efflux ABC transporter, permease protein							
650260702	HMPREF9286_0533	efflux ABC transporter, permease protein							
650260701	HMPREF9286_0532	ABC transporter, ATP-binding protein							
650260700	HMPREF9286_0531	putative lipoprotein							
650260699	HMPREF9286_0530	efflux ABC transporter, permease protein							
650261988	HMPREF9286_0259	addiction module antitoxin, RelB/DinJ family	Pepto016_116	147	119925	120071	+	D	IPRSCAN: seg (db=Seg db_id=seg from=25 to=41)
650261987	HMPREF9286_0258	conserved hypothetical protein							
650261986	HMPREF9286_0257	beta-aspartyl peptidase							
650261985	HMPREF9286_0256	C4-dicarboxylate anaerobic carrier							
650261984	HMPREF9286_0255	conserved hypothetical protein							
650261983	HMPREF9286_0254	conserved hypothetical protein	Pepto016_117	1440	120202	121641	+	C	BLAST: hypothetical protein (db=KEGG eval=5.0e-29 bit_score=132.0 identity=28.68 covera
650261982	HMPREF9286_0253	putative glycolate oxidase, subunit GlcD	Pepto016_118	1413	121822	123234	+	B	RBH: fnu:FN1536 (S)-2-hydroxy-acid oxidase chain D (EC:1.1.3.15); K00104 glycolate oxidase [
650261981	HMPREF9286_0252	acyl-CoA dehydrogenase	Pepto016_119	1137	123250	124386	+	B	RBH: fnu:FN1535 acyl-CoA dehydrogenase, short-chain specific [EC:1.3.99.2]; K00248 butyryl
650261980	HMPREF9286_0251	electron transfer flavoprotein domain protein	Pepto016_120	768	124390	125157	+	C	BLAST: electron transfer flavoprotein subunit beta; K03521 electron transfer flavoprotein be
650261979	HMPREF9286_0250	electron transfer flavoprotein FAD-binding domain protein	Pepto016_121	969	125167	126135	+	C	BLAST: electron transfer flavoprotein subunit alpha; K03522 electron transfer flavoprotein al
650261978	HMPREF9286_0249	conserved hypothetical protein	Pepto016_122	354	126154	126507	+	C	BLAST: LrgA family protein; K06518 holin-like protein (db=KEGG eval=1.0e-42 bit_score=17
650261977	HMPREF9286_0248	TIGR00659 family protein	Pepto016_123	693	126497	127189	+	C	BLAST: LrgB family protein (db=KEGG eval=4.0e-73 bit_score=277.0 identity=65.94 coverag
650260698	HMPREF9286_0529	transposase							
650260697	HMPREF9286_0528	conserved hypothetical protein	Pepto016_124	324	127592	127915	+	C	BLAST: Viral A-type inclusion protein repeat protein n=1 Tax=Peptoniphilus lacrimalis 315-B R
650260696	HMPREF9286_0527	ATP synthase, subunit C	Pepto016_125	1008	127908	128915	+	C	BLAST: v-type sodium ATP synthase subunit C [EC:3.6.3.14]; K02119 V-type H+-transporting A
650260695	HMPREF9286_0526	putative ATP synthase F0, A subunit	Pepto016_126	1929	128905	130833	+	B	RBH: fma:FMG_1170 V-type sodium ATP synthase subunit I; K02123 V-type H+-transporting A
650260694	HMPREF9286_0525	ATP synthase subunit C	Pepto016_127	423	130848	131270	+	C	BLAST: V-type sodium ATP synthase subunit K; K02124 V-type H+-transporting ATPase subun
650260693	HMPREF9286_0524	putative ATP synthase (F/14-kDa) subunit	Pepto016_128	315	131270	131584	+	C	BLAST: V-type sodium ATP synthase subunit F; K02122 V-type H+-transporting ATPase subuni
650260692	HMPREF9286_0523	conserved hypothetical protein	Pepto016_129	642	131585	132226	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650260691	HMPREF9286_0522	ATP synthase ab C terminal domain protein	Pepto016_130	1773	132207	133979	+	B	RBH: fma:FMG_1166 V-type ATP synthase subunit A; K02117 V-type H+-transporting ATPase ;
650260690	HMPREF9286_0521	ATP synthase ab C terminal domain protein	Pepto016_131	1392	133976	135367	+	B	RBH: fma:FMG_1165 V-type ATP synthase subunit B; K02118 V-type H+-transporting ATPase ;
650260689	HMPREF9286_0520	V-type ATPase, D subunit	Pepto016_132	627	135357	135983	+	C	BLAST: V-type sodium ATP synthase subunit D; K02120 V-type H+-transporting ATPase subuni
650260688	HMPREF9286_0519	AspT/YidE/YjI antiporter duplication domain protein							
650260663	HMPREF9286_0494	conserved hypothetical protein	Pepto016_133	1185	136174	137358	+	B	RBH: ctc:CTC01949 hypothetical protein (db=KEGG)
650260662	HMPREF9286_0493	putative cell division ATP-binding protein FtsE	Pepto016_134	699	137597	138295	+	B	RBH: UniRef90_D1VTW5 Cell division ATP-binding protein FtsE n=1 Tax=Peptoniphilus lacrima
650260661	HMPREF9286_0492	efflux ABC transporter, permease protein	Pepto016_135	903	138270	139172	+	B	RBH: UniRef90_D1VTW6 Cell division protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=
650260660	HMPREF9286_0491	peptidase, M23 family	Pepto016_136	1233	139181	140413	+	B	RBH: UniRef90_D1VTW7 Peptidase M23B n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V
650260659	HMPREF9286_0490	peptidase, S41 family	Pepto016_137	1167	140413	141579	+	B	RBH: UniRef90_D1VTW8 Carboxyl-protease n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1
650261976	HMPREF9286_0247	electron transfer flavoprotein FAD-binding domain protein	Pepto016_138	996	141802	142797	+	B	RBH: UniRef90_D1VTK5 Electron transfer flavoprotein subunit alpha n=1 Tax=Peptoniphilus tr
650261975	HMPREF9286_0246	electron transfer flavoprotein domain protein	Pepto016_139	798	142806	143603	+	C	BLAST: electron transfer flavoprotein, beta subunit/FixA family protein; K03521 electron tra
650261974	HMPREF9286_0245	peroxidoredoxin							
650261973	HMPREF9286_0244	alkyl hydroperoxide reductase, F subunit							
650261972	HMPREF9286_0243	ribosomal protein S10	Pepto016_140	318	144151	144468	+	C	BLAST: ribosomal protein S10; K02946 small subunit ribosomal protein S10 (db=KEGG eval=
650261971	HMPREF9286_0242	S05 ribosomal protein L3	Pepto016_141	633	144527	145159	+	B	RBH: UniRef90_D1VTX8 S05 ribosomal protein L3 n=1 Tax=Peptoniphilus lacrimalis 315-B Rep
650261970	HMPREF9286_0241	S05 ribosomal protein L4	Pepto016_142	624	145177	145800	+	B	RBH: UniRef90_D1VTX9 S05 ribosomal protein L4 n=1 Tax=Peptoniphilus lacrimalis 315-B Rep
650261969	HMPREF9286_0240	ribosomal protein L23	Pepto016_143	288	145800	146087	+	C	BLAST: LSU ribosomal protein L23P; K02892 large subunit ribosomal protein L23 (db=KEGG ev
650261968	HMPREF9286_0239	ribosomal protein L2	Pepto016_144	831	146105	146935	+	B	RBH: fma:FMG_0158 rplB; S05 ribosomal protein L2; K02886 large subunit ribosomal protein
650261967	HMPREF9286_0238	ribosomal protein S19	Pepto016_145	285	146948	147232	+	C	BLAST: ribosomal protein S19; K02965 small subunit ribosomal protein S19 (db=KEGG eval=
650261966	HMPREF9286_0237	ribosomal protein L22	Pepto016_146	336	147244	147579	+	C	BLAST: S05 ribosomal protein L22; K02890 large subunit ribosomal protein L22 (db=KEGG eva
650261965	HMPREF9286_0236	ribosomal protein S3	Pepto016_147	747	147591	148337	+	B	RBH: UniRef90_D1VTL4 S05 ribosomal protein S3 n=1 Tax=Peptoniphilus lacrimalis 315-B Rep
650261964	HMPREF9286_0235	ribosomal protein L16	Pepto016_148	432	148355	148786	+	C	BLAST: rplP; S05 ribosomal protein L16; K02878 large subunit ribosomal protein L16 (db=KEG
650261963	HMPREF9286_0234	ribosomal protein L29	Pepto016_149	219	148764	148982	+	C	BLAST: S05 ribosomal protein L29; K02904 large subunit ribosomal protein L29 (db=KEGG ev
650261962	HMPREF9286_0233	S05 ribosomal protein S17	Pepto016_150	255	148987	149241	+	C	BLAST: hypothetical protein; K02961 small subunit ribosomal protein S17 (db=KEGG eval=6
650261961	HMPREF9286_0232	ribosomal protein L14	Pepto016_151	369	149265	149633	+	C	BLAST: ribosomal protein L14; K02874 large subunit ribosomal protein L14 (db=KEGG eval=
650261960	HMPREF9286_0231	ribosomal protein L24	Pepto016_152	309	149648	149956	+	C	BLAST: S05 ribosomal protein L24; K02895 large subunit ribosomal protein L24 (db=KEGG eva
650261959	HMPREF9286_0230	ribosomal protein L5	Pepto016_153	546	149668	150513	+	B	RBH: UniRef90_D1VTM0 S05 ribosomal protein L5 n=1 Tax=Peptoniphilus lacrimalis 315-B Rej
650261958	HMPREF9286_0229	ribosomal protein S14p/S29e	Pepto016_154	186	150525	150710	+	C	BLAST: S05 ribosomal protein S14; K02954 small subunit ribosomal protein S14 (db=KEGG eva
650261957	HMPREF9286_0228	ribosomal protein S8	Pepto016_155	396	150740	151135	+	C	BLAST: S05 ribosomal protein S8; K02994 small subunit ribosomal protein S8 (db=KEGG eva
650261956	HMPREF9286_0227	ribosomal protein L6	Pepto016_156	537	151150	151686	+	C	BLAST: rplF; S05 ribosomal subunit protein L6; K02933 large subunit ribosomal protein L6 (db
650261955	HMPREF9286_0226	ribosomal protein L18	Pepto016_157	363	151702	152064	+	C	BLAST: rplR; S05 ribosomal protein L18; K02881 large subunit ribosomal protein L18 (db=KEG
650261954	HMPREF9286_0225	ribosomal protein S5	Pepto016_158	507	152078	152584	+	C	BLAST: S05 ribosomal protein S5; K02988 small subunit ribosomal protein S5 (db=KEGG eval
650261953	HMPREF9286_0224	ribosomal protein L30	Pepto016_159	177	152596	152772	+	C	BLAST: ribosomal protein L30; K02907 large subunit ribosomal protein L30 (db=KEGG eval=
650261952	HMPREF9286_0223	ribosomal protein L15	Pepto016_160	450	152786	153235	+	C	BLAST: LSU ribosomal protein L15P; K02876 large subunit ribosomal protein L15 (db=KEGG ev
650261951	HMPREF9286_0222	preprotein translocase, SecY subunit	Pepto016_161	1281	153235	154515	+	B	RBH: aoe:Clos_0512 preprotein translocase, SecY subunit; K03076 preprotein translocase sub
650261950	HMPREF9286_0221	adenylate kinase	Pepto016_162	642	154526	155167	+	B	RBH: cst:CLOST_2177 adk; adenylate kinase [EC:2.7.4.3]; K00939 adenylate kinase [EC:2.7.4.3
650261949	HMPREF9286_0220	conserved hypothetical protein	Pepto016_163	255	155171	155425	+	C	BLAST: Putative S05 ribosomal protein L14e n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1
650261948	HMPREF9286_0219	translation initiation factor IF-1	Pepto016_164	219	155444	155662	+	C	BLAST: translation initiation factor IF-1; K02518 translation initiation factor IF-1 (db=KEGG ev
650261947	HMPREF9286_0218	ribosomal protein L36	Pepto016_165	114	155686	155799	+	C	BLAST: ribosomal protein L36; K02919 large subunit ribosomal protein L36 (db=KEGG eval=
650261946	HMPREF9286_0217	S05 ribosomal protein S13	Pepto016_166	363	155811	156173	+	C	BLAST: rpsM; S05 ribosomal protein S13; K02952 small subunit ribosomal protein S13 (db=KEI
650261945	HMPREF9286_0216	S05 ribosomal protein S11	Pepto016_167	396	156186	156581	+	C	BLAST: ribosomal protein S11; K02948 small subunit ribosomal protein S11 (db=KEGG eval=
650261944	HMPREF9286_0215	DNA-directed RNA polymerase, alpha subunit	Pepto016_168	948	156608	157555	+	B	RBH: UniRef90_D1VTN5 DNA-directed RNA polymerase, alpha subunit n=1 Tax=Peptoniphilus
650261943	HMPREF9286_0214	ribosomal protein L17	Pepto016_169	342	157566	157907	+	C	BLAST: ribosomal protein L17; K02879 large subunit ribosomal protein L17 (db=KEGG eval=
650262264	HMPREF9286_0306	tetrapyrrole methylase	Pepto016_170	918	157967	158884	+	C	BLAST: hypothetical protein; K02499 tetrapyrrole methylase family protein / MazG family pr
650262263	HMPREF9286_0305	DNA-binding protein HU	Pepto016_171	279	159019	159297	+	C	BLAST: DNA-binding protein HU (db=KEGG eval=1.0e-44 bit_score=181.0 identity=98.91 co
650262262	HMPREF9286_0304	S4 domain protein	Pepto016_172	243	159393	159635	+	C	BLAST: S4 domain-containing protein (db=KEGG eval=4.0e-17 bit_score=90.1 identity=56.9
650262261	HMPREF9286_0303	septum formation initiator	Pepto016_173	315	159668	159982	+	C	BLAST: Cell division protein FtsB n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VTP1_9FIRI
650262260	HMPREF9286_0302	S1 RNA binding domain protein	Pepto016_174	378	159999	160376	+	C	BLAST: S1 RNA binding domain containing protein (db=KEGG eval=7.0e-51 bit_score=202.0
650262259	HMPREF9286_0301	tRNA(Ile)-lysidine synthetase	Pepto016_175	1332	160422	161753	+	B	RBH: tva:TVAG_243760 PP-loop family protein (db=KEGG)
650262258	HMPREF9286_0300	hypoxanthine phosphoribosyltransferase	Pepto016_176	546	161743	162288	+	C	BLAST: hypoxanthine phosphoribosyltransferase; K00760 hypoxanthine phosphoribosyltransf
650262257	HMPREF9286_0299	cell division protease FtsH	Pepto016_177	1950	162294	164243	+	B	RBH: tva:TVAG_243780 Clan MA, family M41, FtsH endopeptidase-like metalloprotease (db=
650262256	HMPREF9286_0298	transglycosylase	Pepto016_178	2400	164480	166879	+	B	RBH: tva:TVAG_243790 penicillin binding protein transpeptidase (db=KEGG)
650262255	HMPREF9286_0297	BioY family protein	Pepto016_179	537	167045	167581	+	C	BLAST: BioY family protein (db=KEGG eval=5.0e-31 bit_score=136.0 identity=76.64 coverage
650262254	HMPREF9286_0296	pantothenate kinase, type III	Pepto016_180	783	167822	168604	+	B	RBH: UniRef90_D1VTQ1 Type III pantothenate kinase n=1 Tax=Peptoniphilus lacrimalis 315-B
650262253	HMPREF9286_0295	TIM-barrel protein, nifR3 family	Pepto016_181	933	168615	169547	+	B	RBH: tva:TVAG_243820 TIM-barrel protein, nifR3 family protein (db=KEGG)
			Pepto016_182	261	169596	169856	+	D	IPRSCAN: seg (db=Seg db_id=seg from=76 to=86)
			Pepto016_183	963	169923	170885	+	C	BLAST: transposase IS1239 (db=KEGG eval=7.0e-74 bit_score=280.0 identity=50.95 coveri
			Pepto016_184	627	171142	171768	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=5 to=24)
			Pepto016_185</						

650262249 HMPREF9286_0291 conserved hypothetical protein	Pepto016_190	828	175814	176641	+	B	RBH: spi:MGAS10750_Spy1680 hypothetical protein (db=KEGG)
650262248 HMPREF9286_0290 conserved hypothetical protein	Pepto016_191	486	176634	177119	+	B	RBH: spi:MGAS10750_Spy1681 hypothetical protein (db=KEGG)
650262247 HMPREF9286_0289 BRO family, N-terminal domain protein	Pepto016_192	735	177116	177850	+	B	RBH: snp:SPAP_0868 hypothetical protein (db=KEGG)
650262246 HMPREF9286_0288 TraG family protein							
	Pepto016_193	1797	177843	179639	+	B	RBH: apr:Apr_1805 TraG family protein; K03205 type IV secretion system protein VirD4 (db=KEGG)
	Pepto016_194	276	179658	179933	+	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-42 bit_score=174.0 identity=96.7 coverage=100.0)
	Pepto016_195	201	180201	180401	+	C	BLAST: type IV secretory pathway protein VirD4; K03205 type IV secretion system protein V
	Pepto016_196	381	180454	180834	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-66 bit_score=253.0 identity=100.0 coverage=100.0)
	Pepto016_197	339	180834	181172	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-49 bit_score=196.0 identity=100.0 coverage=100.0)
	Pepto016_198	312	181365	181676	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-43 bit_score=176.0 identity=98.9 coverage=100.0)
	Pepto016_199	159	181678	181836	+	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-20 bit_score=101.0 identity=98.04 coverage=100.0)
	Pepto016_200	219	181954	182172	+	C	BLAST: hypothetical protein (db=KEGG eval=8.0e-33 bit_score=142.0 identity=95.77 coverage=100.0)
	Pepto016_201	519	182428	182946	+	B	RBH: fma:FMG_0967 hypothetical protein (db=KEGG)
	Pepto016_202	303	183198	183500	+	C	BLAST: gntR; GntR family transcriptional regulator; K07979 GntR family transcriptional regul
	Pepto016_203	879	183500	184378	+	B	RBH: UniRef90_C2BCM9 ABC superfamily ATP binding cassette transporter, ABC protein n=
	Pepto016_204	591	184436	185026	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Anaerococcus lactolyticus ATCC 51172 Re
	Pepto016_205	2211	185037	187247	+	B	RBH: cbh:CLC_0497 radical SAM domain-containing protein (db=KEGG)
	Pepto016_206	291	187264	187554	+	E	GENE: 12262..12552 - (rbs_motif=AGxAGG/AGxGG rbs_spacer=5-10bp)
	Pepto016_207	150	187600	187749	+	D	IPRSCAN: seg (db=Seg db_id=seg from=32 to=45)
	Pepto016_208	249	187829	188077	+	D	IPRSCAN: seg (db=Seg db_id=seg from=2 to=18)
	Pepto016_209	315	188401	188715	+	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-54 bit_score=214.0 identity=100.0 coverage=100.0)
	Pepto016_210	384	188734	189117	+	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-68 bit_score=259.0 identity=100.0 coverage=100.0)
650262174 HMPREF9286_0852 FtsK/SpoIIIE family protein	Pepto016_211	1092	189440	190531	+	B	RBH: sag:SAG0933 Tn916, FtsK/SpoIIIE family protein (db=KEGG)
650262175 HMPREF9286_0853 replication initiation factor	Pepto016_212	1206	190709	191914	+	B	RBH: spx:SPG_1242 Tn5251 transcriptional regulator Cro/Ci family (db=KEGG)
	Pepto016_213	222	191957	192178	+	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-31 bit_score=137.0 identity=100.0 coverage=100.0)
650262176 HMPREF9286_0854 antirestriction protein ArdA	Pepto016_214	498	192295	192792	+	B	RBH: snb:SP670_1163 conjugative transposon protein (db=KEGG)
650262177 HMPREF9286_0855 conserved hypothetical protein	Pepto016_215	507	192767	193273	+	B	RBH: sag:SAG0929 Tn916 hypothetical protein (db=KEGG)
650262178 HMPREF9286_0856 putative ATP/GTP-binding protein	Pepto016_216	2448	193257	195704	+	B	RBH: ssb:SSUBM407_0977 hypothetical protein (db=KEGG)
650262179 HMPREF9286_0857 putative membrane protein	Pepto016_217	2112	195773	197884	+	B	RBH: sag:SAG0927 hypothetical protein (db=KEGG)
650262180 HMPREF9286_0858 NlpC/P60 family protein	Pepto016_218	1002	197881	198882	+	B	RBH: spp:SPP_1158 NLP/P60 family protein (db=KEGG)
650262181 HMPREF9286_0859 conserved hypothetical protein	Pepto016_219	936	198879	199814	+	B	RBH: spw:SPCG_0169 hypothetical protein (db=KEGG)
	Pepto016_220	354	202456	202809	+	C	BLAST: putative DNA-binding protein (db=KEGG eval=5.0e-62 bit_score=239.0 identity=100.0)
650261910 HMPREF9286_0181 GTP-binding domain protein							
650261911 HMPREF9286_0182 elongation factor G C-terminal domain protein							
650261912 HMPREF9286_0183 RNA polymerase sigma factor, sigma-70 family	Pepto016_221	423	203314	203736	+	C	BLAST: putative DNA-binding protein (db=KEGG eval=4.0e-76 bit_score=285.0 identity=100.0)
	Pepto016_222	231	203733	203963	+	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-37 bit_score=158.0 identity=100.0 coverage=100.0)
	Pepto016_223	204	204424	204627	+	C	BLAST: excisionase (db=KEGG eval=6.0e-31 bit_score=135.0 identity=100.0 coverage=97.1)
	Pepto016_224	1218	204709	205926	+	B	RBH: svv:SSU98_0923 Tn916, transposase (db=KEGG)
650261913 HMPREF9286_0184 site-specific recombinase, phage integrase family							
650261914 HMPREF9286_0185 putative response regulator ArlR							
650261915 HMPREF9286_0186 efflux ABC transporter, permease protein							
650261916 HMPREF9286_0187 ABC transporter, ATP-binding protein							
	Pepto016_225	1500	206155	207654	+	C	BLAST: ABC transporter related (db=KEGG eval=8.0e-64 bit_score=248.0 identity=30.37 coverage=100.0)
	Pepto016_226	291	207895	208185	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-29 bit_score=130.0 identity=92.71 coverage=100.0)
	Pepto016_227	1641	208519	210159	+	B	RBH: snc:HMPREF0837_11442 nic; nickase [EC:3.1.21.-] (db=KEGG)
	Pepto016_228	174	210233	210406	+	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-23 bit_score=111.0 identity=96.49 coverage=100.0)
	Pepto016_229	1071	211561	212631	+	B	RBH: ere:EUBREC_3364 hypothetical protein (db=KEGG)
	Pepto016_230	714	212714	213427	+	B	RBH: fma:FMG_0972 putative replisome organizer (db=KEGG)
	Pepto016_231	225	213582	213806	+	C	BLAST: Putative uncharacterized protein n=2 Tax=Clostridiales Family XI. Incertae Sedis Rep
650262245 HMPREF9286_0287 putative TnpX site-specific recombinase	Pepto016_232	1647	213810	215456	+	B	RBH: cdi:CDR20291_1788 hypothetical protein (db=KEGG)
650261390 HMPREF9286_0992 copper amine oxidase N-terminal domain protein							
650261389 HMPREF9286_0991 RecF/RecN/SMC N-terminal domain protein							
650261388 HMPREF9286_0990 conserved hypothetical protein							
650261387 HMPREF9286_0989 putative membrane protein							
650261386 HMPREF9286_0988 conserved domain protein							
650261385 HMPREF9286_0987 conserved hypothetical protein							
650261384 HMPREF9286_0986 conserved hypothetical protein							
650261383 HMPREF9286_0985 TrkA N-terminal domain protein							
650261382 HMPREF9286_0984 putative membrane protein							
650261381 HMPREF9286_0983 conserved hypothetical protein							
650261380 HMPREF9286_0982 conserved hypothetical protein							
650261379 HMPREF9286_0981 methyltransferase domain protein							
650261378 HMPREF9286_0980 BAAT/acyl-CoA thioester hydrolase C-terminal domain protein							
650261377 HMPREF9286_0979 conserved hypothetical protein							
650261376 HMPREF9286_1264 conserved hypothetical protein	Pepto016_233	864	215554	216417	+	B	RBH: apr:Apr_1812 hypothetical protein (db=KEGG)
650261375 HMPREF9286_1263 conserved hypothetical protein	Pepto016_234	291	216427	216717	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-28 bit_score=127.0 identity=98.96 coverage=100.0)
650261374 HMPREF9286_1262 conserved hypothetical protein							
650261373 HMPREF9286_1261 putative TraE protein	Pepto016_235	2424	217020	219443	+	B	RBH: snp:SPAP_0880 type IV secretory pathway, VirB4 component (db=KEGG)
650261372 HMPREF9286_1260 NlpC/P60 family protein	Pepto016_236	2580	219451	222030	+	B	RBH: spi:MGAS10750_Spy1692 NlpC/P60 family protein (db=KEGG)
650261371 HMPREF9286_1259 conserved hypothetical protein	Pepto016_237	240	222045	222284	+	C	BLAST: hypothetical protein (db=KEGG eval=4.0e-10 bit_score=66.6 identity=100.0 coverage=100.0)
650261370 HMPREF9286_1258 copper amine oxidase N-terminal domain protein							
	Pepto016_238	2352	222271	224622	+	B	RBH: fma:FMG_0958 putative chimeric erythrocyte-binding protein (db=KEGG)
650261369 HMPREF9286_1257 conserved hypothetical protein	Pepto016_239	864	224637	225500	+	B	RBH: apr:Apr_1819 hypothetical protein (db=KEGG)
650261368 HMPREF9286_1256 conserved hypothetical protein	Pepto016_240	612	225574	226185	+	B	RBH: apr:Apr_1820 hypothetical protein (db=KEGG)
650261367 HMPREF9286_1255 conserved hypothetical protein	Pepto016_241	780	226178	226957	+	B	RBH: apr:Apr_1821 hypothetical protein (db=KEGG)
650261367 HMPREF9286_1255 conserved hypothetical protein	Pepto016_242	213	226950	227162	+	C	BLAST: hypothetical protein (db=KEGG eval=6.0e-30 bit_score=132.0 identity=91.43 coverage=100.0)
650261366 HMPREF9286_1254 DNA topoisomerase							
650261365 HMPREF9286_1253 DNA (cytosine-5-)-methyltransferase							
650261364 HMPREF9286_1252 helicase C-terminal domain protein							
650261363 HMPREF9286_1251 conserved hypothetical protein							
650261362 HMPREF9286_1250 transcriptional regulator, ArsR family							
650261361 HMPREF9286_1249 heavy metal-associated domain protein							
650261360 HMPREF9286_1248 cadmium-exporting ATPase							
	Pepto016_243	1038	227942	228979	+	B	RBH: apr:Apr_0109 peptidase M42 family protein (db=KEGG)
650261897 HMPREF9286_0466 conserved hypothetical protein	Pepto016_244	492	228991	229482	+	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-32 bit_score=141.0 identity=42.94 coverage=100.0)
650261896 HMPREF9286_0465 4Fe-4S binding domain protein	Pepto016_245	147	229807	229953	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=9 to=26)
650261895 HMPREF9286_0464 redoxin family protein	Pepto016_246	885	229946	230830	+	B	RBH: ols:Olsu_1771 4Fe-4S ferredoxin iron-sulfur binding domain protein (db=KEGG)
650261894 HMPREF9286_0463 hydroxylamine reductase	Pepto016_247	561	230802	231362	+	C	BLAST: tlpA; hypothetical protein (db=KEGG eval=2.0e-32 bit_score=141.0 identity=40.57 coverage=100.0)
650261893 HMPREF9286_0461 ABC transporter, ATP-binding protein	Pepto016_248	1614	231555	233168	+	B	RBH: cpr:CPR_1120 hydroxylamine reductase; K00378 hydroxylamine reductase [EC:1.7.-.-] (db=KEGG)
650261892 HMPREF9286_0460 putative D-methionine transport system permease protein	Pepto016_249	1005	233482	234486	+	B	RBH: UniRef90_D1VTI5 Methionine import ATP-binding protein MetN 2 n=1 Tax=Peptoniphil
650261891 HMPREF9286_0459 D-methionine-binding lipoprotein MetQ	Pepto016_250	651	234487	235137	+	C	BLAST: ABC transporter permease; K02072 D-methionine transport system permease protein
650261890 HMPREF9286_0458 lipoprotein, YaeC family	Pepto016_251	849	235196	236044	+	B	RBH: UniRef90_D1VTI7 Oligopeptide/amino acid ABC transporter substrate-binding protein n
	Pepto016_252	1089	236248	237336	+	B	RBH: mcl:MCCL_0340 ABC transporter, substrate-binding protein; K02055 putative spermid
	Pepto016_253	840	237346	238185	+	C	BLAST: ABC transporter, permease protein; K02054 putative spermidine/putrescine transp
	Pepto016_254	780	238185	238964	+	C	BLAST: hypothetical protein; K02053 putative spermidine/putrescine transport system per
	Pepto016_255	1005	238961	239965	+	B	RBH: mcl:MCCL_0343 hypothetical protein; K02052 putative spermidine/putrescine transp
	Pepto016_256	912	239974	240885	+	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-53 bit_score=213.0 identity=40.26 coverage=100.0)
650261270 HMPREF9286_1435 putative lipoprotein	Pepto016_257	453	241036	241488	+	D	IPRSCAN: coiled-coil (db=Coil db_id=coil from=120 to=141 eval=NA)
650261269 HMPREF9286_1434 conserved hypothetical protein							
650261268 HMPREF9286_1433 conserved hypothetical protein	Pepto016_258	903	241796	242698	+	B	RBH: UniRef90_D1VVK8 Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 31
650261267 HMPREF9286_1432 conserved hypothetical protein	Pepto016_259	711	243062	243772	+	B	RBH: UniRef90_D1VVA8 TIM-barrel fold family protein n=1 Tax=Peptoniphilus lacrimalis 315-1
650261266 HMPREF9286_1431 Na+/H+ antiporter family protein	Pepto016_260	1509	243797	245305	+	B	RBH: elm:ELI_2146 Na+/H+ antiporter NhaC-like protein (db=KEGG)
	Pepto016_261	426	245428	245853	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=4 to=21)

650261265	HMPREF9286_1430 macro domain protein	Pepto016_262	513	245990	246502	+	C	BLAST: Appr-1-p processing domain protein (db=KEGG eval=4.0e-38 bit_score=160.0 identity
650261264	HMPREF9286_1429 conserved hypothetical protein							
650261263	HMPREF9286_1428 penicillin-binding protein, transpeptidase domain protein	Pepto016_263	198	246548	246745	+	D	IPRSCAN: seg (db=Seg db_id=seg from=18 to=43)
650261262	HMPREF9286_1427 transglycosylase	Pepto016_264	2892	246759	249650	+	B	RBH: apr:Apr_1213 glycosyl transferase family 51; K05366 penicillin-binding protein 1A [EC:2
650261261	HMPREF9286_1426 GTP-binding protein HflX	Pepto016_265	1290	249843	251132	+	B	RBH: UniRef90_D1VRR0 GTP-binding protein HflX n=1 Tax=Peptoniphilus lacrimalis 315-B Rep
650261260	HMPREF9286_1425 YigZ family protein	Pepto016_266	633	251125	251757	+	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-44 bit_score=182.0 identity=48.7 coverage
650261259	HMPREF9286_1424 NAD+ synthase	Pepto016_267	720	251775	252494	+	B	RBH: UniRef90_D1VRQ7 NH(3)-dependent NAD(+) synthetase n=1 Tax=Peptoniphilus lacrim
		Pepto016_268	432	253062	253493	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Filifactor aloeis ATCC 35896 RepID=D6G58
		Pepto016_269	1947	254112	256058	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-32 bit_score=144.0 identity=27.74 cov
		Pepto016_270	660	256060	256719	+	C	BLAST: ABC transporter related; K02003 (db=KEGG eval=4.0e-51 bit_score=204.0 identity
650261258	HMPREF9286_1423 conserved hypothetical protein							
650261257	HMPREF9286_1422 conserved hypothetical protein							
650261256	HMPREF9286_1421 conserved hypothetical protein							
650261255	HMPREF9286_1420 conserved hypothetical protein							
650261254	HMPREF9286_1419 ABC transporter substrate binding protein							
650261253	HMPREF9286_1417 ABC transporter substrate binding protein	Pepto016_271	999	257136	258134	+	B	RBH: UniRef90_D1VV79 ABC transporter, substrate-binding lipoprotein n=1 Tax=Peptoniphil
650261252	HMPREF9286_1416 branched-chain amino acid ABC transporter, permease prot	Pepto016_272	885	258162	259046	+	B	RBH: UniRef90_D1VV78 Inner-membrane translocator n=1 Tax=Peptoniphilus lacrimalis 315-F
650261251	HMPREF9286_1415 ABC transporter, ATP-binding protein	Pepto016_273	750	259033	259782	+	B	RBH: UniRef90_D1VV77 Spermidine/putrescine import ATP-binding protein PotA n=1 Tax=Pej
650261250	HMPREF9286_1414 conserved hypothetical protein							
650261249	HMPREF9286_1413 RNA polymerase sigma factor, sigma-70 family							
		Pepto016_274	489	259865	260353	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=7 to=29)
		Pepto016_275	267	260363	260629	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=30 to=47)
650261248	HMPREF9286_1412 putative ATP synthase F0, A subunit	Pepto016_276	840	260761	261600	+	C	BLAST: ABC transporter, permease protein, putative (db=KEGG eval=1.0e-21 bit_score=107
650261247	HMPREF9286_1411 ABC transporter, ATP-binding protein	Pepto016_277	1254	261590	262843	+	B	RBH: UniRef90_D1VVL7 Putative ABC transporter, ATP-binding protein n=1 Tax=Peptoniphilus
650261246	HMPREF9286_1410 acetolactate synthase 3 regulatory subunit domain protein							
650261245	HMPREF9286_1409 GTP-binding protein YchF	Pepto016_278	1089	263093	264181	+	B	RBH: cst:CLOST_1906 ychF; gtp-binding protein; K06942 (db=KEGG
650261244	HMPREF9286_1408 HAD hydrolase, family IIB	Pepto016_279	825	264190	265014	+	C	BLAST: HAD hydrolase, IIB family; K07024 (db=KEGG eval=3.0e-21 bit_score=105.0 identity
650261243	HMPREF9286_1407 ribosome biogenesis GTP-binding protein YlqF	Pepto016_280	849	265015	265863	+	B	RBH: UniRef90_D1VVL4 Ribosome biogenesis GTP-binding protein YlqF n=1 Tax=Peptoniphil
650261242	HMPREF9286_1406 ribonuclease HII	Pepto016_281	618	265853	266470	+	B	RBH: UniRef90_D1VVL3 Ribonuclease HII n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1V
650261241	HMPREF9286_1405 TIGR00252 family protein	Pepto016_282	360	266464	266823	+	C	BLAST: hypothetical protein; K07460 putative endonuclease (db=KEGG eval=2.8e-23 bit_sc
650261240	HMPREF9286_1404 FeS assembly ATPase SufC	Pepto016_283	747	266949	267695	+	B	RBH: fma:FMG_0469 putative iron-regulated ABC transporter ATP-binding protein; K09013 Fe
650261239	HMPREF9286_1403 FeS assembly protein SufB	Pepto016_284	1413	267696	268108	+	B	RBH: fma:FMG_0470 putative iron-regulated ABC transporter ATP-binding protein; K09014 Fe
650261238	HMPREF9286_1402 SufB/sufD domain protein	Pepto016_285	1050	269116	270165	+	B	RBH: UniRef90_D1VU65 FeS assembly protein SufD n=1 Tax=Peptoniphilus lacrimalis 315-B Ri
650261237	HMPREF9286_1401 cysteine desulfurase, SufS family	Pepto016_286	1242	270167	271408	+	C	RBH: fma:FMG_0472 selenocysteine lyase; K11717 cysteine desulfurase / selenocysteine lyasi
650261236	HMPREF9286_1400 Suf system FeS assembly protein, NifU family	Pepto016_287	456	271398	271853	+	C	BLAST: iron-sulfur cofactor synthesis protein NifU-like protein; K04488 nitrogen fixation pro
650261235	HMPREF9286_1399 putative HTH-type transcriptional regulator IscR	Pepto016_288	396	271865	272260	+	C	BLAST: transcriptional regulator, BadM/Rrf2 family (db=KEGG eval=7.0e-34 bit_score=145.1
650261234	HMPREF9286_1398 putative cysteine desulfurase NifS	Pepto016_289	1128	272268	273395	+	B	RBH: cce:CceL_1932 cysteine desulfurase NifS; K04487 cysteine desulfurase [EC:2.8.1.7] (db=k
650261233	HMPREF9286_1397 putative membrane protein	Pepto016_290	1284	273400	274683	+	B	RBH: UniRef90_D1VU70 Putative permease n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1
650261232	HMPREF9286_1396 alanine--tRNA ligase	Pepto016_291	2613	274761	277373	+	B	RBH: cst:CLOST_1491 alaS; alanyl-tRNA synthetase (EC:6.1.1.7); K01872 alanyl-tRNA synthet
650261231	HMPREF9286_1395 conserved hypothetical protein	Pepto016_292	255	277421	277675	+	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-21 bit_score=104.0 identity=57.83 covera
650261230	HMPREF9286_1394 RNase H domain protein, YqgF family	Pepto016_293	417	277733	278149	+	C	BLAST: Holliday junction resolvase YqgF; K07447 putative holliday junction resolvase [EC:3.1.-
650261229	HMPREF9286_1393 conserved hypothetical protein	Pepto016_294	243	278159	278401	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VU
650261228	HMPREF9286_1392 putative ferric uptake regulator	Pepto016_295	471	278398	278866	+	C	BLAST: ferric uptake regulator family protein; K03711 Fur family transcriptional regulator, fer
650261227	HMPREF9286_1391 ribonuclease J1	Pepto016_296	1662	278868	280529	+	B	RBH: cst:CLOST_1482 rnjA; ribonuclease J1; K12574 ribonuclease J [EC:3.1.-.] (db=KEGG
650261226	HMPREF9286_1390 O-methyltransferase	Pepto016_297	657	280572	281228	+	C	BLAST: O-methyltransferase family protein (db=KEGG eval=1.0e-54 bit_score=215.0 identit
650261225	HMPREF9286_1389 peptidase, U32 family	Pepto016_298	1230	281215	282444	+	B	RBH: fma:FMG_0634 collagenase family protease; K08303 putative protease [EC:3.4.-.] (db=k
650261224	HMPREF9286_1388 conserved hypothetical protein							
650261223	HMPREF9286_1387 replication initiator protein A, N-terminal domain protein							
650261222	HMPREF9286_1386 DNA replication protein DnaC family protein							
650261221	HMPREF9286_1385 conserved hypothetical protein							
650261220	HMPREF9286_1384 conserved hypothetical protein							
650261219	HMPREF9286_1383 TraG/TraD family protein							
650261218	HMPREF9286_1382 conserved hypothetical protein							
650261217	HMPREF9286_1381 conserved hypothetical protein							
650261216	HMPREF9286_1380 conserved hypothetical protein							
650261215	HMPREF9286_1749 phosphoribulokinase/uridine kinase family protein	Pepto016_299	618	282434	283051	+	C	BLAST: udK; uridine kinase [EC:2.7.1.48]; K00876 uridine kinase [EC:2.7.1.48] (db=KEGG eval
650261214	HMPREF9286_1748 translation initiation factor IF-3	Pepto016_300	567	283176	283742	+	C	BLAST: translation initiation factor IF-3; K02520 translation initiation factor IF-3 (db=KEGG ev
650261213	HMPREF9286_1746 ribosomal protein L35	Pepto016_301	192	283754	283945	+	C	BLAST: 50S ribosomal protein L35 n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VTH9_9FI
650261212	HMPREF9286_1745 ribosomal protein L20	Pepto016_302	351	283958	284308	+	C	BLAST: ribosomal protein L20; K02887 large subunit ribosomal protein L20 (db=KEGG eval=
650261211	HMPREF9286_1744 Ktr system potassium uptake protein B	Pepto016_303	1329	284372	285700	+	B	RBH: cpf:CPF_2143 TrkH family potassium uptake protein; K03498 trk system potassium upta
650261210	HMPREF9286_1743 TrkA N-terminal domain protein	Pepto016_304	651	285703	286353	+	C	BLAST: TrkA domain-containing protein; K03499 trk system potassium uptake protein TrkA [d
650261209	HMPREF9286_1742 conserved hypothetical protein							
650261208	HMPREF9286_1741 conserved hypothetical protein							
650261207	HMPREF9286_1740 putative lipoprotein	Pepto016_305	1089	286512	287600	+	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-41 bit_score=173.0 identity=33.33 covera
650261206	HMPREF9286_1739 UBA7/TS-N domain protein	Pepto016_306	519	287645	288163	+	C	BLAST: ubiquitin-associated-domain-containing protein (db=KEGG eval=2.0e-15 bit_score=1
650261205	HMPREF9286_1738 RNA methyltransferase, TrmH family	Pepto016_307	747	288217	288963	+	C	BLAST: RNA methyltransferase; K03437 RNA methyltransferase, TrmH family (db=KEGG eval
650261204	HMPREF9286_1737 conserved hypothetical protein	Pepto016_308	687	288960	289646	+	C	BLAST: hypothetical protein (db=KEGG eval=3.0e-25 bit_score=118.0 identity=39.61 covera
650261203	HMPREF9286_1736 conserved hypothetical protein	Pepto016_309	504	289760	290263	+	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-10 bit_score=68.6 identity=32.12 cover
650261202	HMPREF9286_1735 threonine--tRNA ligase	Pepto016_310	1911	291048	292958	+	B	RBH: apr:Apr_1664 threonyl-tRNA synthetase; K01868 threonyl-tRNA synthetase [EC:6.1.1.3
650261201	HMPREF9286_1733 ribosomal protein L21	Pepto016_311	306	293186	293491	+	C	BLAST: rplJ; 50S ribosomal protein L21; K02888 large subunit ribosomal protein L21 (db=KEG
650261200	HMPREF9286_1732 conserved hypothetical protein	Pepto016_312	339	293491	293829	+	C	BLAST: Putative ribosomal protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VUN7_9F
650261199	HMPREF9286_1731 ribosomal protein L27	Pepto016_313	297	293822	294118	+	C	BLAST: rpmA; 50S ribosomal protein L27; K02889 large subunit ribosomal protein L27 (db=KE
650261198	HMPREF9286_1730 Olg family GTPase CgtA	Pepto016_314	1269	294258	295526	+	B	RBH: aoe:CloS_1750 GTP-binding protein Olg/CgtA; K03979 GTP-binding protein (db=KEGG)
650261197	HMPREF9286_1729 RNA-binding protein, YhbY family	Pepto016_315	288	295535	295822	+	C	BLAST: hypothetical protein; K07574 putative RNA-binding protein containing KH domain (db
650261196	HMPREF9286_1728 nicotinate-nucleotide adenyllyltransferase	Pepto016_316	609	295822	296430	+	C	BLAST: nicotinate (nicotinamide) nucleotide adenyllyltransferase [EC:2.7.7.18]; K00969 nicotin
650261195	HMPREF9286_1727 hydrolase, HD family	Pepto016_317	573	296420	296992	+	C	BLAST: hydrolase (db=KEGG eval=1.0e-42 bit_score=175.0 identity=50.89 coverage=87.958
650261194	HMPREF9286_1726 cell envelope-like function transcriptional attenuator comm	Pepto016_318	879	296989	297867	+	B	RBH: UniRef90_D1VUN1 Transcriptional regulator n=1 Tax=Peptoniphilus lacrimalis 315-B Rep
650261193	HMPREF9286_1725 iojap-like protein	Pepto016_319	351	297876	298226	+	C	BLAST: iojap-like protein; K09710 hypothetical protein (db=KEGG eval=1.0e-26 bit_score=1
650261192	HMPREF9286_1724 putative endoribonuclease L-PSP	Pepto016_320	378	298229	298606	+	C	BLAST: putative endoribonuclease L-PSP; K07567 TdcF protein (db=KEGG eval=1.0e-41 bit_
650261191	HMPREF9286_1723 rhodanese-like protein	Pepto016_321	300	298658	298957	+	C	BLAST: YtwF protein (db=KEGG eval=1.0e-10 bit_score=68.6 identity=45.68 coverage=79.0)
650261012	HMPREF9286_0018 DEAD-box ATP-dependent RNA helicase CshA							
650261013	HMPREF9286_0019 conserved hypothetical protein							
650261011	HMPREF9286_0017 DNA-directed DNA polymerase	Pepto016_322	2658	299065	301722	+	B	RBH: apr:Apr_1330 DNA polymerase I [EC:2.7.7.7]; K02335 DNA polymerase I [EC:2.7.7.7] (dl
650261010	HMPREF9286_0016 dephospho-CoA kinase domain protein							
650261009	HMPREF9286_0015 putative dephospho-CoA kinase	Pepto016_323	594	301709	302302	+	C	BLAST: coaE; dephospho-CoA kinase (EC:2.7.1.24); K00859 dephospho-CoA kinase [EC:2.7.1.2
650261007	HMPREF9286_0013 toxin-antitoxin system, antitoxin component, HicB family							
650261006	HMPREF9286_0012 copper amine oxidase N-terminal domain protein							
650261005	HMPREF9286_0011 conserved domain protein							
		Pepto016_324	243	302346	302588	+	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm from=10 to=28)
650261004	HMPREF9286_0010 phenylalanine--tRNA ligase, alpha subunit	Pepto016_325	654	302590	303243	+	C	BLAST: Putative uncharacterized protein n=1 Tax=Anaerococcus vaginalis ATCC 51170 RepIC
650261003	HMPREF9286_0009 phenylalanine--tRNA ligase, beta subunit	Pepto016_326	1023	303615	304637	+	B	RBH: fma:FMG_0868 phenylalanyl-tRNA synthetase alpha subunit; K01889 phenylalanyl-tRNA
650261002	HMPREF9286_0008 M protein repeat protein	Pepto016_327	2376	304648	307023	+	B	RBH: amt:Amet_1640 phenylalanyl-tRNA synthetase subunit beta (EC:6.1.1.20); K01890 phen
650261001	HMPREF9286_0007 peptidase, U32 family	Pepto016_328	552	307034	307585	+	C	BLAST: Cell division protein ZapA n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VSY1_9FIR
650261000	HMPREF9286_0006 recombination and DNA strand exchange inhibitor protein	Pepto016_329	2343	307572	309914	+	B	RBH: aoe:CloS_1969 peptidase U32; K08303 putative protease [EC:3.4.-.] (db=KEGG)
650260999	HMPREF9286_0005 arginine--tRNA ligase	Pepto016_330	2373	309907	312279	+	B	RBH: cce:CceL_1470 MutS2 family protein; K07456 DNA mismatch repair protein MutS2 (db=k
650260998	HMPREF9286_0004 putative membrane protein	Pepto016_331	1710	312289	313998	+	B	RBH: cst:CLOST_1149 argS; arginyl-tRNA synthetase 2 (arginine--tRNA ligase 2) [ArgRS 2] (EC:6
650260997	HMPREF9286_0003 exodeoxyribonuclease III	Pepto016_332	762	314003	314764	+	C	BLAST: Putative membrane protein n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VSX7_9I
650260996	HMPREF9286_0002 conserved hypothetical protein, YfiH family							
650260995	HMPREF9286_0001 tetratricopeptide repeat protein	Pepto016_333	1101	314765	315865	+	C	BLAST: hypothetical protein (db=KEGG eval=1.0e-12 bit_score=77.4 identity=27.7 coverage
	Pepto017							
	Pepto017_1	939	368	1306	+	B	RBH: fma:FMG_0239 antibiotic ABC transporter ATP-binding protein; K09687 antibiotic tran	
	Pepto017_2	1098	1308	2405	+	B	RBH: fma:FMG_0240 antibiotic ABC transporter permease protein; K09686 antibiotic transp	
	Pepto017_3	1116	2392	3507	+	B	RBH: fma:FMG_0241 putative ABC transporter; K09686 antibiotic transporter system permea	

	Pepto017_4	393	3711	4103 +	C	BLAST: IS200 family transposase; K07491 putative transposase (db=KEGG eval=4.0e-64 bit_score=87.8 identity=38.06 coverage=100%)
	Pepto017_5	540	4239	4778 +	C	BLAST: transposase, putative (db=KEGG eval=3.0e-16 bit_score=87.8 identity=38.06 coverage=100%)
	Misc					
	308144_2565_2	147	135	281 -	C	BLAST: Kinase A inhibitor n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VT26_9FIRM (dt
	308222_40_3	270	746	1015 -	C	BLAST: DNA-cytosine methyltransferase (EC:2.1.1.37); K00558 DNA (cytosine-5-)-methyltr
	309019_1476_1	519	2	520 -	C	BLAST: ABC transporter, ATP-binding/permease protein; K06147 ATP-binding cassette, subf
	309796_1477_1	333	2	334 -	C	BLAST: potC; spermidine/putrescine ABC transporter, permease protein 2; K11070 spermid
	309856_2493_1	177	784	960 -	C	BLAST: LamB/YcsF family protein; K07160 (db=KEGG eval=3.0e-18 bit_score=94.0 identity
	309988_2630_1	240	1	240 -	C	BLAST: ESS family glutamate:sodium n=1 Tax=Peptoniphilus lacrimalis 315-B RepID=D1VSV
	310415_1471_1	726	1225	1950 -	C	BLAST: (R)-2-hydroxyglutaryl-CoA dehydratase alpha-subunit (EC:4.2.1.-) (db=KEGG eval=
	310908_946_3	291	982	1272 +	C	BLAST: hypothetical protein (db=KEGG eval=2.0e-38 bit_score=160.0 identity=88.51 cove
650260641	HMPREF9286_1790 MATE efflux family protein					
650260642	HMPREF9286_1265 ABC transporter, ATP-binding protein					
650260643	HMPREF9286_1266 ABC transporter, ATP-binding protein					