List of PP-Clusters

Comments. This file contains the list of clusters of functionally related COGs, found using NJ algorithm and anticorrelation distance measure (see main text for more details). Every PP-cluster includes >=2 COGs. In several cases, when there is evidence that PP-cluster includes displacements of orthologous genes (DOGs), the complimentary phyletic patterns of presumably displaced genes (COGs) are included for illustrative purpose. Each pattern is a binary vector of 0s and 1s that indicate presence or absence of given COG in a particular genome. Thus, for convenience, three lines above two complementary patterns list three-letters codes of 66 microbial genomes (see http://www.ncbi.nlm.nih.gov/COG/new/orgs.html for full names of organisms) horizontally. For example,

Tma is listed as .
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T
m
a
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This way presence/absence is easily referred to a genome.

I. Functional Predictions and Gene Displacements

1) Specialized system consists of divalent cations transporter and cognate enzyme:

P_COG0053 Predicted_Co/Zn/Cd_cation_transporters
R_COG2220 Predicted_Zn-dependent hydrolases

2) New: Repair or Recombination

R_COG1019 Predicted_nucleotidyltransferase
L_COG1111 ERCC4-like_helicases
L_COG1311 Archaeal_DNA_polymerase_II,_small_subuni

3) DOG example: 1189 vs 0293 is a DOG

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TCBBSLSSLCASBMHPVYSEEEPRXNNCMMMFDSNRRBCCTBMUMMACHjHMPPAMMMTTSAPSSE
mashalppictmmlimcptcccasfmmglttnryopcutppbpupgajpHbahaftjkavspycpc
acuauaynnrueeonuheyoZseoaeAleuCuansrocrnauurneeeypscobuhaacooeaeou
111101111111110000000000000111110111100001110011110100100000000000: COG1189
000000000111111111111111111000000001110011000000001100111111000111: COG0293
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J_COG1189 Predicted_rRNA_methylase
J_COG0293 23S_rRNA_methylase
K_COG1420 Transcriptional_regulator_of_heat_shock
K_COG2740 Predicted_nucleic-acid-binding_protein

4) DOG example: 0207 vs 1351 is a DOG

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TCBBSLSSLCASBMHPVYSEEEPRXNNCMMMFDSNRRBCCTBMUMMACHjHMPPAMMMTTSAPSSE
mashalppictmmlimcptcccasfmmglttnryopcutppbpupgajpHbahaftjkavspycpc
acuauaynnrueeonuheyoZseoaeAleuCuansrocrnauurneeeypscobuhaacooeaeou
011111111111111111111111111111110000100001011000001001111100000111: COG0207
110000000000000000000000000011110011110111100001111011000011111000: COG1351
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F_COG0207 ThyA_Thymidylate_synthase
F_COG1351 ThyX_thymidylate_syntha

5) New system presumably involved in rRNA maturation.

S_COG0585 Novel pseudouridylate synthase distantly related to TruB
R_COG1444 Predicted_P-loop_ATPase_fused_to_an_acetyltransferase
A_COG0430 RNA_3'-terminal_phosphate_cyclase

6) Specialized system consists of divalent cations transporter and cognate enzyme (medline 12123839 and 12093726)
F_COG0213_Thymidine_phosphorylase   COG0213
P_COG0619_ABC-type_cobalt_transport_system
P_COG1122_ABC-type_cobalt_transport_system ATPase

7) Energy production and conversion and multiple DOGs event
C_COG0055_F0F1-type_ATP_synthase_beta_subunit
C_COG0056_F0F1-type_ATP_synthase_alpha_subunit
C_COG0224_F0F1-type_ATP_synthase_gamma_subunit
C_COG0355_F0F1-type_ATP_synthase_epsilon_subunit
C_COG0356_F0F1-type_ATP_synthase_subunit_a
C_COG0711_F0F1-type_ATP_synthase_subunit_b
C_COG0712_F0F1-type_ATP_synthase_delta_subunit
C_COG1155_Archaeal/vacuolar-type_H+-ATPase_subunit
C_COG1156_Archaeal/vacuolar-type_H+-ATPase_subunit
C_COG1269_Archaeal/vacuolar-type_H+-ATPase_subunit
C_COG1394_Archaeal/vacuolar-type_H+-ATPase_subunit
C_COG1390_Archaeal/vacuolar-type_H+-ATPase_subunit

8) Known and new DOGs (0764 is presumably artifact but close distance)
J_COG0423_Glycyl-tRNA_synthetase_(class_II)
J_COG0751_Glycyl-tRNA_synthetase_beta_subunit
J_COG0752_Glycyl-tRNA_synthetase_alpha_subunit
I_COG0764_3-hydroxymyristoyl/3- hydroxydecanoyl-dehydratases

9) *Known and new DOGs*
```
TCBBSLSSLCASBMHPVYSEEEPRXNNCMMMFDSNRRBCCTBMUMMACHjHMPPAMMMTTSAPSSE
mashalppictmmlimcptcccasfmmglttnryopcutppbpupgajpHbahaftjkavspycpc
acuauaynnrueeonuheyoZseoaeAleuCuansrocrnauurneeeypscobuhaacooeaeou
111111111111111111111111111111111111111100111111110000000000000111:COG0194
000000000000000000000000000000000000000011000000001111111111111000:COG1102
111111111111111111111111111111111111101111111110000000000000000001:COG0283
```
F_COG0194_Guanylate_kinase
F_COG1102_Cytidylate_kinase
F_COG0283_Cytidylate_kinase

10) *Known DOGs*
J_COG1190_Lysyl-tRNA_synthetase_(class_II)
J_COG1384_Lysyl-tRNA_synthetase_(class_I)

11) *New DOG*
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TCBBSLSSLCASBMHPVYSEEEPRXNNCMMMFDSNRRBCCTBMUMMACHjHMPPAMMMTTSAPSSE
mashalppictmmlimcptcccasfmmglttnryopcutppbpupgajpHbahaftjkavspycpc
acuauaynnrueeonuheyoZseoaeAleuCuansrocrnauurneeeypscobuhaacooeaeou
111111111111111111111111111111111111111111111111111111100000000111 COG0563
000000000000100000000000000000000000000000000000000011011111111000 COG2019
```
F_COG0563_Adenylate_kinase
F_COG2019_Archaeal_ad.kinase

12) Presumably new degradation/processing/chaperone system
E_COG0339_Zn-dependent_oligopeptidases
O_COG2377_Predicted_molecular_chaperone_distantly_related to HSP70
O_COG2360_Leu/Phe-tRNA-protein_transferase

13) *Presumably new DOG*
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TCBBSLSSLCASBMHPVYSEEEPRXNNCMMMFDSNRRBCCTBMUMMACHjHMPPAMMMTTSAPSSE
mashalppictmmlimcptcccasfmmglttnryopcutppbpupgajpHbahaftjkavspycpc
acuauaynnrueeonuheyoZseoaeAleuCuansrocrnauurneeeypscobuhaacooeaeou
111111111000001111111111111000010000011110011101111111111011000000:COG0551
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001100000111110000000000000111101001100011000000000000000000000000:COG1329
000000000111110000000000100111101111100001000000000000000000000000:COG1754
L_COG0551_Zn-f_dom_assoc w/topois I
K_COG1329_Transcriptional_regs/CarD
R_COG1754_Unchar_C-term_dom-topIA

14) *Presumably new DOG*
TCBBSLSSLCASBMHPVYSEEEPRXNNCMMMFDSNRRBCCTBMUMMACHjHMPPAMMMTTSAPSSE
mashalppictmmlimcptcccasfmmglttnryopcutppbpupgajpHbahaftjkavspycpc
acuauaynnrueeonuheyoZseoaeAleuCuansrocrnauurneeeypscobuhaacooeaeou
010011111111111111111111111000001110011111000000001111111111111111:COG0120
111110111001110101110000000111110101100000111111110000000000000000:COG0698
G_COG0120_Ribose_5-P_isomerase
G_COG0698_Ribose_5-P_isom_RpiB

15) DXPS pathway of isoprenoid biosynthesis; new: link with cell wall
I_COG0245_2C-methyl-D-erythritol_2,4-cyclodiphosph
I_COG1211_4-diphosphocytidyl-2-methyl-D-erithritol
I_COG0743_1-deoxy-D-xylulose_5-phosphate_reductois
IM_COG0761_Penicillin_tolerance_protein
I_COG0821_Enzyme_involved_in_the_deoxyxylulose_path.
HI_COG1154_Deoxyxylulose-5-phosphate_synthase   COG1154
M_COG0860_N-acetylmuramoyl-L-alanine_amidase
I_COG1947_4-diphosphocytidyl-2C-methyl-D-erythr.
M_COG0791_Cell_wall-associated_hydrolases
S_COG1496_Uncharacterized_conserved_protein
H_COG2022_Uncharacterized_enzyme_of_thiazole_bios.

16) *Presumably new DOG*
TCBBSLSSLCASBMHPVYSEEEPRXNNCMMMFDSNRRBCCTBMUMMACHjHMPPAMMMTTSAPSSE
mashalppictmmlimcptcccasfmmglttnryopcutppbpupgajpHbahaftjkavspycpc
acuauaynnrueeonuheyoZseoaeAleuCuansrocrnauurneeeypscobuhaacooeaeou
100000000111111111111111111111111111101110000001110000000000000000:COG0817
101111111000000000000000000000010000000000011110001111111111111001:COG1078
L_COG0817_Holliday_j_resolvase RuvC
R_COG1078_HD_sf_phosphohydrolases

17) *Presumably new DOG*
TCBBSLSSLCASBMHPVYSEEEPRXNNCMMMFDSNRRBCCTBMUMMACHjHMPPAMMMTTSAPSSE
mashalppictmmlimcptcccasfmmglttnryopcutppbpupgajpHbahaftjkavspycpc
acuauaynnrueeonuheyoZseoaeAleuCuansrocrnauurneeeypscobuhaacooeaeou
010100000111111101111111111111100111111100000011111111111111111000:COG0717
001011101000000000000000001000000000100000000111110000000000000000:COG1428
F_COG0717_Deoxycytidine_deaminase
F_COG1428_Deoxynucleoside_kinases

18) *Presumably new RNA processing system*
J_COG1514_2'-5'_RNA_ligase
S_COG1801_Uncharacterized_conserved_protein

19) *Presumably new functional link: nitrate reductase plus protection against NO/nitrosative stress*
C_COG1140_Nitrate_reductase_beta_subunit
C_COG5013_Nitrate_reductase_alpha_subunit
C_COG2180_Nitrate_reductase_delta_subunit
C_COG2181_Nitrate_reductase_gamma_subunit
P_COG2223_Nitrate/nitrite_transporter
C_COG1251_NAD(P)H-nitrite_reductase
S_COG1742_Uncharacterized_conserved_protein

Q_COG2162_Arylamine_N-acetyltransferase
S_COG2764_Uncharacterized_protein_conserved_in_bac.

20) *Presumably new functional link: 3931 utilizes histidine*
E_COG3931_Predicted_N-formylglutamate_amidohydrolase
E_COG3938_Proline_racemase

21) *New iron-dependent enzyme complex*
P_COG2703_Hemerythrin
S_COG3016_Uncharacterized_iron-regulated_protein
R_COG3019_Predicted_metal-binding_protein

22) *Presumably new RNA processing complex*
J_COG1096_Predicted_RNA-binding_protein
J_COG1097_RNA-binding_protein_Rrp4_and_related_pr
J_COG2123_RNase_PH-related_exoribonuclease

23) *New: connection between flagellae and cell shape: medline 12055288 (flagella vs cell division better studied: from medline 8071236 to 12471245)*
D_COG0455_ATPases_involved_in_chromosome_partition
N_COG1334_Uncharacterized_flagellar_protein_FlaG
N_COG1419_Flagellar_GTP-binding_protein
S_COG1699_Uncharacterized_protein_conserved_in_bac.
S_COG2257_Uncharacterized_homolog_of_the_cytoplasmic domain of FhlB
NT_COG1776_Chemotaxis_protein_CheC,_inhibitor
NT_COG0643_Chemotaxis_protein_histidine_kinase
NT_COG0840_Methyl-accepting_chemotaxis_protein
NT_COG0835_Chemotaxis_signal_transduction_protein
NT_COG1352_Methylase_of_chemotaxis_methyl-acceptin
NT_COG2201_Chemotaxis_response_regulator_containin
T_COG0784_FOG:_CheY-like_receiver
NT_COG1871_Chemotaxis_protein;_stimulates_methylat
D_COG1077_Actin-like_ATPase_involved_in_cell_shape determination MreB
M_COG1792_Cell_shape-determining_protein MreC
M_COG1664_Integral_memb.pr.CcmA_involved_in cell shape determination
K_COG1191_DNA-directed_RNA_polymerase_specialized_sigma subunit FliA
NU_COG1317_Flagellar_biosynthesis/type_III_secret.
N_COG1345_Flagellar_capping_protein
K_COG1510_Predicted_transcriptional_regulators
N_COG1580_Flagellar_basal_body-associated_protein
T_COG1551_Carbon_storage_regulator_(could_also_regulate swarming and quorum sensing)

II. Functionally linked clusters of genes, PP-Clusters

1) *Biosynthesis of amino acids: nearly complete pathways to arginine, proline, and histidine*
E_COG0002_Acetylglutamate_semialdehyde_dehydrogena
E_COG4992_Ornithine/acetylornithine_aminotransfera
E_COG0548_Acetylglutamate_kinase
CE_COG0473_Isocitrate/isopropylmalate_dehydrogenas
E_COG0066_3-isopropylmalate_dehydratase_small_subu
E_COG0119_Isopropylmalate/homocitrate/citramalate_
E_COG0040_ATP_phosphoribosyltransferase
E_COG0106_Phosphoribosylformimino-5-aminoimidazole

E_COG0107_Imidazoleglycerol-phosphate_synthase
E_COG0118_Glutamine_amidotransferase
E_COG0131_Imidazoleglycerol-phosphate_dehydratase
E_COG0139_Phosphoribosyl-AMP_cyclohydrolase
E_COG0141_Histidinol_dehydrogenase
E_COG0140_Phosphoribosyl-ATP_pyrophosphohydrolase
E_COG0065_3-isopropylmalate_dehydratase_large_subu
EH_COG0028_Thiamine_pyrophosphate-requiring_enzyme
E_COG0077_Prephenate_dehydratase
E_COG0137_Argininosuccinate_synthase
E_COG0165_Argininosuccinate_lyase
E_COG0079_Histidinol-phosphate/aromatic_aminotrans
E_COG0078_Ornithine_carbamoyltransferase

2) Middle portion of purine biosynthesis from phosphoribosylglycinamide
F_COG0041_Phosphoribosylcarboxyaminoimidazole_(NCA
F_COG0046_Phosphoribosylformylglycinamidine_(FGAM)
F_COG0047_Phosphoribosylformylglycinamidine_(FGAM)
F_COG0150_Phosphoribosylaminoimidazole_(AIR)_synth
F_COG0152_Phosphoribosylaminoimidazolesuccinocarbo

3) *Two adjoining genes/domains in heme biosynthesis (CobA/CysG)*
H_COG0007_Uroporphyrinogen-III_methylase
H_COG1648_Siroheme_synthase_(precorrin-2_oxidase)

4) Subunits of glutamate synthase
E_COG0067_Glutamate_synthase_domain_1
E_COG0069_Glutamate_synthase_domain_2
E_COG0070_Glutamate_synthase_domain_3

5) SbcC/D repair complex
L_COG0419_ATPase_involved_in_DNA_repair
L_COG0420_DNA_repair_exonuclease

6) Multicomponent trasport system
EP_COG0444_ABC-type_dipeptide/oligopeptide/nickel
E_COG4608_ABC-type_oligopeptide_transport_system
EP_COG0601_ABC-type_dipeptide/oligopeptide/nickel
EP_COG1173_ABC-type_dipeptide/oligopeptide/nickel
E_COG0747_ABC-type_dipeptide_transport_system

7) Transport, amidase may be required
P_COG0609_ABC-type_Fe3+-siderophore_transport_syst.
PH_COG1120_ABC-type_cobalamin/Fe3+-siderophores_tr.
P_COG0614_ABC-type_Fe3+-hydroxamate_transport_syst.
R_COG1473_Metal-dependent_amidase/aminoacylase/car.

8) Branched-chain amino acid transport system
E_COG0410_ABC-type_branched-chain_amino_acid_trans.
E_COG0559_Branched-chain_amino_acid_ABC-type_trans.
E_COG4177_ABC-type_branched-chain_amino_acid_trans.
E_COG0683_ABC-type_branched-chain_amino_acid_trans.
E_COG0411_ABC-type_branched-chain_amino_acid_trans.

9) Transketolase two-domain complex
G_COG3958_Transketolase_C-terminal_subunit
G_COG3959_Transketolase_N-terminal_subunit

10) FixA/B electron transfer complex
C_COG2025_Electron_transfer_flavoprotein,_alpha_sub.
C_COG2086_Electron_transfer_flavoprotein,_beta_sub.

11) Glycine cleavage system
E_COG0403_Glycine_cleavage_system_protein_P
E_COG1003_Glycine_cleavage_system_protein_P
E_COG0404_Glycine_cleavage_system_T_protein
E_COG0509_Glycine_cleavage_system_H_protein

12) CO dehydrogenase and its maturation factor
C_COG1319_Aerobic-type_carbon_monoxide_dehydrogen.
C_COG2080_Aerobic-type_carbon_monoxide_dehydrogen.
C_COG1529_Aerobic-type_carbon_monoxide_dehydrogen.
O_COG1975_Xanthine_and_CO_dehydrogenases_maturat.

13) *Histidine catabolism pathway, Q should probably be changed to E*
Q_COG1228_Imidazolonepropionase
E_COG2986_Histidine_ammonia-lyase
E_COG2987_Urocanate_hydratase

14) *Two adjoining steps in glyoxylate metabolism. COG2897 possibly also involved*
C_COG2224_Isocitrate_lyase
C_COG2225_Malate_synthase
P_COG2897_Rhodanese-related_sulfurtransferase

15) K+ transport and K+-dependent signal transduction. COG2353 role is unclear
P_COG2060_K+-transporting_ATPase_A_chain
P_COG2156_K+-transporting_ATPase_c_chain
P_COG2216_High-affinity_K+_transport_system_ATPase
T_COG2205_Osmosensitive_K+_channel_histidine_kinas.
S_COG2353_Uncharacterized_conserved_protein

16) Molybdopterin biosynthesis, including three new components (1280, 1526, 2050)
H_COG0303_Molybdopterin_biosynthesis_enzyme
H_COG0521_Molybdopterin_biosynthesis_enzymes
H_COG0315_Molybdenum_cofactor_biosynthesis_enzyme
P_COG0725_ABC-type_molybdate_transport_system
H_COG2896_Molybdenum_cofactor_biosynthesis_enzyme
H_COG0314_Molybdopterin_converting_factor,_large_sub.
H_COG0746_Molybdopterin-guanine_dinucleotide_bios.
H_COG1977_Molybdopterin_converting_factor,_small_sub.
Q_COG2050_Uncharacterized_protein,_possibly_putative thioesterase
E_COG1280_Putative_threonine_efflux_protein #transporter, not threonine
R_COG2005_N-terminal_domain_of_molybdenum-binding
C_COG1526_Uncharacterized_protein_required_for_formate_dehydrogenase_activity

17) *Cytochrome*
C_COG1271_Cytochrome_bd-type_quinol_oxidase_subun
C_COG1294_Cytochrome_bd-type_quinol_oxidase_subun

18)

G_COG0380_Trehalose-6-phosphate_synthase COG0380
G_COG1877_Trehalose-6-phosphatase   COG1877

19) Two pyrophosphatases (IPPI is related to the nudix family) involved in lipid metabolism
I_COG1443_Isopentenyldiphosphate_isomerase
I_COG2134_CDP-diacylglycerol_pyrophosphatase

20) Two prophage-encoded late proteins
L_COG3747_Phage_terminase,_small_subunit
R_COG5562_Phage_envelope_protein

21)
S_COG0011_Uncharacterized_conserved_protein
H_COG0214_Pyridoxine_biosynthesis_enzyme
H_COG0311_Predicted_glutamine_amidotransferase

22)
O_COG0396_ABC-type_transport_system_involved_in_Fe
O_COG0719_ABC-type_transport_system_involved_in_Fe

23) Presumably succinate to propionate conversion (medline 10769117)
E_COG1703_Putative_periplasmic_protein_kinase_ArgK
I_COG1884_Methylmalonyl-CoA_mutase,_N-terminal_dom.
I_COG2185_Methylmalonyl-CoA_mutase,_C-terminal_dom.

24)
H_COG1239_Mg-chelatase_subunit_ChlI COG1239
H_COG1240_Mg-chelatase_subunit_ChlD COG1240

25) Hydantoinases are themselves amidases
EQ_COG0145_N-methylhydantoinase_A/acetone_carboxyl.
EQ_COG0146_N-methylhydantoinase_B/acetone_carboxyl.
R_COG1402_Uncharacterized_protein,_putative_amidase.

26)
NU_COG2064_Flp_pilus_assembly_protein_TadC.
U_COG4962_Flp_pilus_assembly_protein,_ATPase_CpaF.

27) Almost full aerobic branch of cobalamin (vitamin B12) biosynthesis (medline 11007789)
H_COG0368_Cobalamin-5-phosphate_synthase
H_COG2038_NaMN:DMB_phosphoribosyltransferase
H_COG1010_Precorrin-3B_methylase
H_COG2082_Precorrin_isomerase
H_COG2243_Precorrin-2_methylase
H_COG2875_Precorrin-4_methylase
H_COG2241_Precorrin-6B_methylase_1
H_COG2242_Precorrin-6B_methylase_2
H_COG1797_Cobyrinic_acid_a,c-diamide_synthase
H_COG1492_Cobyric_acid_synthase
H_COG1270_Cobalamin_biosynthesis_protein_CobD/CbiB
H_COG1903_Cobalamin_biosynthesis_protein_CbiD
H_COG2073_Cobalamin_biosynthesis_protein_CbiG
H_COG1429_Cobalamin_biosynthesis_protein_CobN_
H_COG2099_Precorrin-6x_reductase

28) Urease and its Ni++ dependent maturation
OK_COG0378_Ni2+-binding_GTPase_involved_in_regulat.
E_COG0804_Urea_amidohydrolase_(urease)_alpha_subun.
E_COG0831_Urea_amidohydrolase_(urease)_gamma_subun.
E_COG0832_Urea_amidohydrolase_(urease)_beta_subun.
O_COG0830_Urease_accessory_protein_UreF
O_COG0829_Urease_accessory_protein_UreH
O_COG2371_Urease_accessory_protein_UreE
R_COG1123_ATPase_components_of_various_ABC-type
P_COG3376_High-affinity_nickel_permease

29) Two components of siderophore synthase
Q_COG3486_Lysine/ornithine_N-monooxygenase
Q_COG4264_Siderophore_synthetase_component

30) Spermidine biosynthesis
E_COG0421_Spermidine_synthase
E_COG1586_S-adenosylmethionine_decarboxylase

31) Two enzymes of tRNA processing
J_COG1859_RNA:NAD_2'-phosphotransferase
R_COG2110_Predicted_phosphatase_homologous_to_the_histone 2A/X domain

32) Hydrogenase and its maturation (0675 is most likely false positive)
O_COG0068_Hydrogenase_maturation_factor
O_COG0409_Hydrogenase_maturation_factor
C_COG0680_Ni,Fe-hydrogenase_maturation_factor
O_COG0298_Hydrogenase_maturation_factor
R_COG0375_Zn_finger_protein_HypA/HybF_(possibly_re
O_COG0309_Hydrogenase_maturation_factor
L_COG0675_Transposase_and_inactivated_derivatives
C_COG0650_Formate_hydrogenlyase_subunit_4
C_COG3260_Ni,Fe-hydrogenase_III_small_subunit
C_COG3261_Ni,Fe-hydrogenase_III_large_subunit

33)
C_COG0674_Pyruvate:ferredoxin_oxidoreductase
C_COG1013_Pyruvate:ferredoxin_oxidoreductase
C_COG1014_Pyruvate:ferredoxin_oxidoreductase

34) Pfl and NrdD have a similar glycyl radical, apparently produced by 1180;
O_COG1180_Pyruvate-formate_lyase-activating_enzyme
F_COG1328_Oxygen-sensitive_ribonucleoside-triphosp.

35) Benzoyl-CoA_reductase complex
C_COG0426_Uncharacterized_flavoproteins
C_COG1142_Fe-S-cluster-containing_hydrogenase_comp.
C_COG1151_6Fe-6S_prismane_cluster-containing_prot.
E_COG1775_Benzoyl-CoA_reductase/2-hydroxyglutaryl
I_COG1924_Activator_of_2-hydroxyglutaryl-CoA_dehyd.

36) Disparate functions in ubiquinone biosynthesis plus two or three (1520, 1765, maybe 1819) false positives
H_COG0684_Demethylmenaquinone_methyltransferase
H_COG3161_4-hydroxybenzoate_synthetase_(chorismate
GC_COG1819_Glycosyl_transferases_related_to_UDP-g

S_COG1520_FOG:_WD40-like_repeat
HC_COG0543_2-polyprenylphenol_hydroxylase_and_rela
O_COG1765_Predicted_redox_protein,_regulator_of_di

37) Known complex
CP_COG0651_Formate_hydrogenlyase_subunit_3/Multisub.
P_COG1006_Multisubunit_Na+/H+_antiporter,_MnhC_sub.
P_COG2111_Multisubunit_Na+/H+_antiporter,_MnhB_sub.
P_COG1320_Multisubunit_Na+/H+_antiporter,_MnhG_sub.
P_COG1863_Multisubunit_Na+/H+_antiporter,_MnhE_sub.
P_COG2212_Multisubunit_Na+/H+_antiporter,_MnhF_sub.

38) Transport complex for biotin (medline 12368242)
P_COG0803_ABC-type_metal_ion_transport_system
P_COG1108_ABC-type_Mn2+/Zn2+_transport_systems
P_COG1121_ABC-type_Mn/Zn_transport_systems_ATPase
R_COG1268_Uncharacterized_conserved_protein

39)
P_COG0600_ABC-type_nitrate/sulfonate/bicarbonate_t
P_COG0715_ABC-type_nitrate/sulfonate/bicarbonate_t
P_COG1116_ABC-type_nitrate/sulfonate/bicarbonate_t

40)
C_COG1148_Heterodisulfide_reductase_subunit_A
C_COG1150_Heterodisulfide_reductase_subunit_C

41)
H_COG4054_Methyl_coenzyme_M_reductase_beta_subun.
H_COG4055_Methyl_coenzyme_M_reductase_subunit_D
H_COG4056_Methyl_coenzyme_M_reductase_subunit_C
H_COG4057_Methyl_coenzyme_M_reductase_gamma_subun.
H_COG4058_Methyl_coenzyme_M_reductase_alpha_subun.
H_COG4059_Tetrahydromethanopterin_S-methyltransfer.
H_COG4060_Tetrahydromethanopterin_S-methyltransfer.
H_COG4061_Tetrahydromethanopterin_S-methyltransfer.
H_COG4062_Tetrahydromethanopterin_S-methyltransfer.
H_COG4063_Tetrahydromethanopterin_S-methyltransfer.
H_COG4064_Tetrahydromethanopterin_S-methyltransfer.

42)
P_COG0310_ABC-type_Co2+_transport_system_permease
P_COG1930_ABC-type_cobalt_transport_system_peripl

43)
C_COG1625_Fe-S_oxidoreductase,_related_to_NifB/Moa
C_COG1941_Coenzyme_F420-reducing_hydrogenase_gam.
C_COG3259_Coenzyme_F420-reducing_hydrogenase_alph.

44) Only part of type IV system
U_COG3701_Type_IV_secretory_pathway,_TrbF_componen.
OU_COG4959_Type_IV_secretory_pathway,_protease_TraF
NU_COG5268_Type_IV_secretory_pathway,_TrbD_component/VirB3
U_COG5314_Conjugal_transfer/entry_exclusion_protein TrbJ/K

45)
O_COG3175_Cytochrome_oxidase_assembly_factor

C_COG3474_Cytochrome_c2

46) New connection w/4321
E_COG4311_Sarcosine_oxidase_delta_subunit
R_COG4321_Uncharacterized_protein_related_to_aryls.
E_COG4583_Sarcosine_oxidase_gamma_subunit

47)
F_COG4630_Xanthine_dehydrogenase_iron-sulfur_clus.
F_COG4631_Xanthine_dehydrogenase_molybdopterin-bi.

48)
N_COG5442_Flagellar_biosynthesis_regulator_FlaF
N_COG5443_Flagellar_biosynthesis_regulator_FlbT

49)
H_COG5598_Trimethylamine:corrinoid_methyltransferase
R_COG5012_Predicted_cobalamin_binding_protein

50)
P_COG1348_Nitrogenase_subunit_NifH_(ATPase)
C_COG2710_Nitrogenase_molybdenum-iron_protein

51)
Q_COG4663_TRAP-type_mannitol/chloroaromatic
Q_COG4664_TRAP-type_mannitol/chloroaromatic
Q_COG4665_TRAP-type_mannitol/chloroaromatic

52)
H_COG2998_ABC-type_tungstate_transport_system
H_COG4662_ABC-type_tungstate_transport_system

53)

V_COG1401_GTPase_subunit_of_restriction_endonuclea	COG1401
V_COG4268_McrBC_5-methylcytosine_restriction_syste	COG4268

54) Both in folate biosynthesis (should be category H maybe)
E_COG3404_Methenyl_tetrahydrofolate_cyclohydrolase
E_COG3643_Glutamate_formiminotransferase

55) Polysaccharide hydrolysis system
G_COG3669_Alpha-L-fucosidase
G_COG3934_Endo-beta-mannanase

56) 1479 is anticorrelation artifact; 0531 is probably not AA transporter
C_COG0022_Pyruvate/2-oxoglutarate_dehydrogenase
C_COG1071_Pyruvate/2-oxoglutarate_dehydrogenase
S_COG1479_Uncharacterized_conserved_protein
C_COG0039_Malate/lactate_dehydrogenases
E_COG0531_Amino_acid_transporters
C_COG0508_Pyruvate/2-oxoglutarate_dehydrogenase
C_COG1249_Pyruvate/2-oxoglutarate_dehydrogenase

57)
C_COG1883_Na+-transporting_methylmalonyl-CoA
C_COG3630_Na+-transporting_methylmalonyl-CoA

C_COG5016_Pyruvate/oxaloacetate_carboxyltransf.

58) Funcster 65
U_COG3031_Type_II_secretory_pathway
U_COG3149_Type_II_secretory_pathway
U_COG3156_Type_II_secretory_pathway
U_COG3297_Type_II_secretory_pathway

59) Prophage late proteins
R_COG3628_Phage_baseplate_assembly_protein_W
R_COG3948_Phage-related_baseplate_assembly_protein
R_COG5004_P2-like_prophage_tail_protein_X
R_COG4540_Phage_P2_baseplate_assembly_protein_gpV
R_COG5301_Phage-related_tail_fibre_protein
R_COG4287_PhoPQ-activated_pathogenicity-related_pr
S_COG4727_Uncharacterized_protein_conserved_in_bac
R_COG3654_Prophage_maintenance_system_killer_prote
S_COG4893_Uncharacterized_protein_conserved_in_bac
N_COG5567_Predicted_small_periplasmic_lipoprotein

60
R_COG2358_TRAP-type_uncharacterized_transport_syst.
R_COG4666_TRAP-type_uncharacterized_transport_syst.

61) Pili synthesis and assembly
U_COG3745_Flp_pilus_assembly_protein_CpaB
S_COG3795_Uncharacterized_protein_conserved_in_bacteria
S_COG3813_Uncharacterized_protein_conserved_in_bac
K_COG4941_Predicted_RNA_polymerase_sigma_factor_co
U_COG3847_Flp_pilus_assembly_protein,_pilin_Flp
U_COG4964_Flp_pilus_assembly_protein,_secretin_Cpa
OU_COG4960_Flp_pilus_assembly_protein,_protease_Cp
U_COG4961_Flp_pilus_assembly_protein_TadG
U_COG4963_Flp_pilus_assembly_protein,_ATPase_CpaE
U_COG5010_Flp_pilus_assembly_protein_TadD,_contain

62)
M_COG1861_Spore_coat_polysaccharide_biosynthesis
M_COG2089_Sialic_acid_synthase
M_COG3980_Spore_coat_polysaccharide_biosynthesis

63)
H_COG0611_Thiamine_monophosphate_kinase
H_COG1564_Thiamine_pyrophosphokinase

64)
R_COG1079_Uncharacterized_ABC-type_transport_system
R_COG3845_ABC-type_uncharacterized_transport_syste
R_COG4603_ABC-type_uncharacterized_transport_syste
R_COG1744_Uncharacterized_ABC-type_transport_syste
R_COG1277_ABC-type_transport_system

65) G_COG3936_Protein_involved_in_polysaccharide
S_COG4502_Uncharacterized_protein_conserved_in_bac.
S_COG4640_Predicted_membrane_protein
G_COG4193_Beta-_N-acetylglucosaminidase (phosphate binding site?)
M_COG3944_Capsular_polysaccharide_biosynthesis

GM_COG4464_Capsular_polysaccharide_biosynthesis
R_COG3956_Protein_containing_tetrapyrrole_methyltr.
M_COG5577_Spore_coat_protein

66)
Q_COG4542_Protein_involved_in_propanediol_utilizat
Q_COG4909_Propanediol_dehydratase,_large_subunit
Q_COG4910_Propanediol_dehydratase,_small_subunit
Q_COG4869_Propanediol_utilization_protein

67) Other part of type IV secretory pathway
U_COG2948_Type_IV_secretory_pathway_VirB10_compon
U_COG3504_Type_IV_secretory_pathway_VirB9_compone
U_COG3736_Type_IV_secretory_pathway_component_VirB8
U_COG3451_Type_IV_secretory_pathway_VirB4_compone
U_COG3505_Type_IV_secretory_pathway_VirD4_compone

68)
R_COG1101_ABC-type_uncharacterized_transport_syst.
R_COG4120_ABC-type_uncharacterized_transport_syst.
R_COG2984_ABC-type_uncharacterized_transport_syst.

69) More of type IV and a false discovery (4553 unclear)
U_COG3838_Type_IV_secretory_pathway_VirB2_compon.
I_COG4553_Poly-beta-hydroxyalkanoate_depolymerase
U_COG3702_Type_IV_secretory_pathway_VirB3_compon.
U_COG3704_Type_IV_secretory_pathway_VirB6_compon.

70) Fatty acid transfer. Good cluster despite Hamming dist 12 between 2057 and 2031
I_COG1788_Acyl_CoA:acetate/3-ketoacid_CoA_transfer
I_COG2057_Acyl_CoA:acetate/3-ketoacid_CoA_transfer
I_COG2031_Short_chain_fatty_acids_transporter

71) More of Type IV
S_COG2958_Uncharacterized_protein_conserved_in_bact.
S_COG4694_Uncharacterized_protein_conserved_in_bac.
U_COG3843_Type_IV_secretory_pathway,_VirD2_compon.
U_COG3846_Type_IV_secretory_pathway,_TrbL_componen.

72) Bottom part of glycolysis minus dog'ged pgm
G_COG0057_Glyceraldehyde-3-phosphate_dehydrogenase
G_COG0126_3-phosphoglycerate_kinase
G_COG0148_Enolase
G_COG0149_Triosephosphate_isomerase

73)
G_COG0362_6-phosphogluconate_dehydrogenase
G_COG0364_Glucose-6-phosphate_1-dehydrogenase

74)
NU_COG1459_Type_II_secretory_pathway_component_Pu
NU_COG2804_Type_II_secretory_pathway_ATPase_PulE/
NU_COG2165_Type_II_secretory_pathway_pseudopilin

75)
P_COG4604_ABC-type_enterochelin_transport_system

P_COG4605_ABC-type_enterochelin_transport_system
P_COG4606_ABC-type_enterochelin_transport_system
P_COG4607_ABC-type_enterochelin_transport_system

76) Downstream portion of lysine biosynthesis, 0861 maybe false
E_COG0253_Diaminopimelate_epimerase
E_COG0289_Dihydrodipicolinate_reductase
P_COG0861_Membrane_protein_TerC
E_COG2171_Tetrahydrodipicolinate_N-succinyltransfe

77)
GM_COG1134_ABC-type_polysaccharide/polyol_phosphat.
GM_COG1682_ABC-type_polysaccharide/polyol_phosphat.

78)
R_COG1999_Uncharacterized_protein_SCO1/SenC/PrrC
C_COG2857_Cytochrome_c1

79)
P_COG3420_Nitrous_oxidase_accessory_protein
K_COG3901_Regulator_of_nitric_oxide_reductase_tran
C_COG4314_Predicted_lipoprotein_involved_in_nitrou
P_COG3256_Nitric_oxide_reductase_large_subunit

80)
C_COG3245_Cytochrome_c5
C_COG3658_Cytochrome_b

81) Pili (azurin is probably false, 3310, 4255)
NU_COG3167_Tfp_pilus_assembly_protein_PilO
NU_COG3168_Tfp_pilus_assembly_protein_PilP
NU_COG3170_Tfp_pilus_assembly_protein_FimV
NU_COG4968_Tfp_pilus_assembly_protein_PilE
NU_COG5008_Tfp_pilus_assembly_protein,_ATPase_PilU
NU_COG4970_Tfp_pilus_assembly_protein_FimT
S_COG3310_Uncharacterized_protein_conserved_in_bac
S_COG4255_Uncharacterized_protein_conserved_in_bac
NU_COG3215_Tfp_pilus_assembly_protein_PilZ
NU_COG4726_Tfp_pilus_assembly_protein_PilX
NU_COG4966_Tfp_pilus_assembly_protein_PilW
C_COG3241_Azurin
NU_COG3419_Tfp_pilus_assembly_protein,_tip-associa
NU_COG4972_Tfp_pilus_assembly_protein,_ATPase_PilM

82)
M_COG1083_CMP-N-acetylneuraminic_acid_synthetase
S_COG2830_Uncharacterized_protein_conserved_in_bac
M_COG3524_Capsule_polysaccharide_export_protein
M_COG3562_Capsule_polysaccharide_export_protein
M_COG3563_Capsule_polysaccharide_export_protein
S_COG2833_Uncharacterized_protein_conserved_in_bac
M_COG4092_Predicted_glycosyltransferase_involved_i
S_COG3512_Uncharacterized_protein_conserved_in_bac
S_COG3513_Uncharacterized_protein_conserved_in_bac

83)
C_COG1347_Na+-transporting_NADH:ubiquinone_oxidore

C_COG1726_Na+-transporting_NADH:ubiquinone_oxidore
C_COG2209_Na+-transporting_NADH:ubiquinone_oxidore
C_COG2869_Na+-transporting_NADH:ubiquinone_oxidore
C_COG2871_Na+-transporting_NADH:ubiquinone_oxidore

84)
S_COG3778_Uncharacterized_protein_conserved_in_bac
R_COG4228_Mu-like_prophage_DNA_circulation_protein
R_COG4379_Mu-like_prophage_tail_protein_gpP
S_COG4381_Mu-like_prophage_protein_gp46
S_COG4384_Mu-like_prophage_protein_gp45
R_COG4386_Mu-like_prophage_tail_sheath_protein_gpL
S_COG4382_Mu-like_prophage_protein_gp16
S_COG4383_Mu-like_prophage_protein_gp29
S_COG4387_Mu-like_prophage_protein_gp36
R_COG4388_Mu-like_prophage_I_protein
R_COG5003_Mu-like_prophage_protein_gp37
R_COG4396_Mu-like_prophage_host-nuclease_inhibitor
R_COG4397_Mu-like_prophage_major_head_subunit_gpT
R_COG5005_Mu-like_prophage_protein_gpG

85)
G_COG0021_Transketolase
H_COG0196_FAD_synthase
G_COG0036_Pentose-5-phosphate-3-epimerase
G_COG0191_Fructose/tagatose_bisphosphate_aldolase
H_COG0192_S-adenosylmethionine_synthetase
H_COG1057_Nicotinic_acid_mononucleotide_adenylyltr

86)
L_COG0178_Excinuclease_ATPase_subunit
L_COG0322_Nuclease_subunit_of_the_excinuclease_com
L_COG0556_Helicase_subunit_of_the_DNA_excision_rep

87) Mostly phylogenetic but distinguishable by a few discordants
J_COG1369_RNase_P/RNase_MRP_subunit_POP5
J_COG1603_RNase_P/RNase_MRP_subunit_p30

88)
C_COG0280_Phosphotransacetylase   COG0280
C_COG0282_Acetate_kinase   COG0282

89)
L_COG0632_Holliday_junction_resolvasome_DNA-bind.
L_COG2255_Holliday_junction_resolvasome_helicase

90)
IQ_COG0304_3-oxoacyl-(acyl-carrier-protein)_syntha
I_COG0331_(acyl-carrier-protein)_S-malonyltransfer

91)
L_COG1570_Exonuclease_VII_large_subunit
L_COG1722_Exonuclease_VII_small_subunit

92) 0816 is anticorr.artifact but closer to 1436 than 1436 is to 1527
L_COG0816_Predicted_endonuclease_involved_in_recom.
C_COG1436_Archaeal/vacuolar-type_H+-ATPase_subunit

C_COG1527_Archaeal/vacuolar-type_H+-ATPase_subunit

93)
IQ_COG0304_3-oxoacyl-(acyl-carrier-protein)_syntha
I_COG0331_(acyl-carrier-protein)_S-malonyltransfer

94)
L_COG1570_Exonuclease_VII_large_subunit
L_COG1722_Exonuclease_VII_small_subunit

95)
I_COG0332_3-oxoacyl-acyl-carrier-protein_synthase
I_COG0777_Acetyl-CoA_carboxylase_beta_subunit
I_COG0825_Acetyl-CoA_carboxylase_alpha_subunit

96) 1219 and 0740; Hamming distance 1 sets 0740 apart from 1219 and closer to 0766
O_COG1219_ATP-dependent_protease_Clp,_ATPase_subun.
OU_COG0740_Protease_subunit_of_ATP-dependent_Clp_p

97) 0772/FtsW facilitates septal peptidoglycan synthesis by the transpeptidase FtsI medline 11807049.
M_COG0766_UDP-N-acetylglucosamine_enolpyruvyl_tran.
M_COG0768_Cell_division_protein_FtsI/penicillin
D_COG0772_Bacterial_cell_division_membrane_protein
M_COG0773_UDP-N-acetylmuramate-alanine_ligase
M_COG0812_UDP-N-acetylmuramate_dehydrogenase

98)
M_COG0707_UDP-N-acetylglucosamine:LPS_N-acetylgluc
M_COG0769_UDP-N-acetylmuramyl_tripeptide_synthase
M_COG0771_UDP-N-acetylmuramoylalanine-D-glutamate_
M_COG0770_UDP-N-acetylmuramyl_pentapeptide_synthas

99)
G_COG1080_Phosphoenolpyruvate-protein_kinase
GT_COG1762_Phosphotransferase_system_mannitol
G_COG1925_Phosphotransferase_system,_HPr-related

100) In fact, discrete (few discordant points make it specific)
J_COG0227_Ribosomal_protein_L28
J_COG0230_Ribosomal_protein_L34
J_COG0257_Ribosomal_protein_L36
J_COG0238_Ribosomal_protein_S18
J_COG0267_Ribosomal_protein_L33
J_COG0360_Ribosomal_protein_S6

101)
R_COG0220_Predicted_S-adenosylmethionine-dependent
J_COG0564_Pseudouridylate_synthases,_23S_RNA-spec.

102)
N_COG1681_Archaeal_flagellins
NU_COG1955_Archaeal_flagella_assembly_protein_J
NU_COG2874_Predicted_ATPases_involved_in_biogenesi

103)

N_COG3351_Putative_archaeal_flagellar_protein_D/E
N_COG3352_Putative_archaeal_flagellar_protein_C
N_COG3354_Putative_archaeal_flagellar_protein_G
N_COG3353_Putative_archaeal_flagellar_protein_F

104)
G_COG0058_Glucan_phosphorylase
G_COG0296_1,4-alpha-glucan_branching_enzyme
G_COG0448_ADP-glucose_pyrophosphorylase
G_COG1523_Type_II_secretory_pathway_pullulanase_P
G_COG0297_Glycogen_synthase
G_COG1640_4-alpha-glucanotransferase

105)
E_COG0687_Spermidine/putrescine-binding_periplasmi
E_COG1176_ABC-type_spermidine/putrescine_transport
E_COG1177_ABC-type_spermidine/putrescine_transport
E_COG3842_ABC-type_spermidine/putrescine_transport

106)
F_COG0274_Deoxyribose-phosphate_aldolase
F_COG0295_Cytidine_deaminase
F_COG1435_Thymidine_kinase

107)
P_COG0168_Trk-type_K+_transport_systems,_membrane_
P_COG0569_K+_transport_systems,_NAD-binding_compon

108) NAD synthesis 3202 may be anticorr artifact
H_COG0171_NAD_synthase
FE_COG0462_Phosphoribosylpyrophosphate_synthetase
C_COG3202_ATP/ADP_translocase
H_COG1488_Nicotinic_acid_phosphoribosyltransferase

109)
G_COG0395_ABC-type_sugar_transport_system_permeas
G_COG1175_ABC-type_sugar_transport_systems_permea
G_COG1653_ABC-type_sugar_transport_system_peripla
G_COG3839_ABC-type_sugar_transport_systems_ATPase

110)
P_COG0226_ABC-type_phosphate_transport_system
P_COG0581_ABC-type_phosphate_transport_system
P_COG1117_ABC-type_phosphate_transport_syste_ATP
P_COG0573_ABC-type_phosphate_transport_system
P_COG0704_Phosphate_uptake_regulator
R_COG0714_MoxR-like_ATPases

111)
H_COG0262_Dihydrofolate_reductase
F_COG0634_Hypoxanth-guanine

112)
O_COG0109_Polyprenyltransferase
C_COG0843_Heme/copper-type_cytochrome/quinol_oxida
C_COG1845_Heme/copper-type_cytochrome/quinol_oxida
C_COG1622_Heme/copper-type_cytochrome/quinol_oxida

O_COG1612_Uncharacterized_protein_required_for_cyt

113)
I_COG2030_Acyl_dehydratase
I_COG4799_Acetyl-CoA_carboxylase_carboxyltransfer

114)
I_COG4770_Acetyl/propionyl-CoA_carboxylase_alpha
I_COG3243_Poly(3-hydroxyalkanoate)_synthetase

115)
G_COG2273_Beta-glucanase/Beta-glucan_synthetase
G_COG3534_Alpha-L-arabinofuranosidase
M_COG3773_Cell_wall_hydrolyses_involved_in_spore

116)
I_COG4981_Enoyl_reductase_domain_of_yeast-type_FAS
I_COG4982_3-oxoacyl-acyl-carrier_protein_reductase

117)
G_COG4282_Protein_involved_in_beta-1,3-glucan_synt.
M_COG5597_Alpha-N-acetylglucosamine_transferase

118) cf f. 3 and 40; system in pieces
H_COG0276_Protoheme_ferro-lyase_(ferrochelatase)
H_COG0407_Uroporphyrinogen-III_decarboxylase
H_COG2226_Methylase_involved_in_ubiquinone/menaqui

119) Discontinuous steps of pantothenate biosynthesis
H_COG0413_Ketopantoate_hydroxymethyltransferase
H_COG0414_Panthothenate_synthetase
H_COG0853_Aspartate_1-decarboxylase

120)
D_COG0850_Septum_formation_inhibitor
D_COG2894_Septum_formation_inhibitor-activating_AT

121)
Q_COG0767_ABC-type_transport_system_involved
Q_COG1127_ABC-type_transport_system_involved
Q_COG1463_ABC-type_transport_system_involved

122)
C_COG1282_NAD/NADP_transhydrogenase_beta_subunit
C_COG3288_NAD/NADP_transhydrogenase_alpha_subunit

123)
OT_COG1391_Glutamine_synthetase_adenylyltransferas
O_COG2844_UTP:GlnB_(protein_PII)_uridylyltransfera

124) Conserved part of mevalonate pathway
I_COG1257_Hydroxymethylglutaryl-CoA_reductase
I_COG1577_Mevalonate_kinase
I_COG3425_3-hydroxy-3-methylglutaryl_CoA_synthase

125)
O_COG1220_ATP-dependent_protease_HslVU_(ClpYQ)

O_COG5405_ATP-dependent_protease_HslVU_(ClpYQ)

126) Lipid A biosynthesis
M_COG3307_Lipid_A_core_-_O-antigen_ligase
M_COG0793_Periplasmic_protease
M_COG0763_Lipid_A_disaccharide_synthetase
M_COG0774_UDP-3-O-acyl-N-acetylglucosamine
M_COG1043_Acyl-acyl_carrier_protein
M_COG1044_UDP-3-O-3-hydroxymyristoyl_glucosamine
U_COG0848_Biopolymer_transport_protein
M_COG1212_CMP-2-keto-3-deoxyoctulosonic_acid_synth.
M_COG1519_3-deoxy-D-manno-octulosonic-acid_transf.
M_COG1663_Tetraacyldisaccharide-1-P_4'-kinase
M_COG2877_3-deoxy-D-manno-octulosonic_acid_(KDO)

127) =
M_COG1596_Periplasmic_protein_involved_in_polysacc.
M_COG3206_Uncharacterized_protein_involved_in_exop.

128)
H_COG0854_Pyridoxal_phosphate_biosynthesis_protein
H_COG1995_Pyridoxal_phosphate_biosynthesis_protein

129)
P_COG1118_ABC-type_sulfate/molybdate_transport_sys.
P_COG1613_ABC-type_sulfate_transport_system
P_COG2193_Bacterioferritin_(cytochrome_b1)
P_COG4208_ABC-type_sulfate_transport_system

130)
M_COG1462_Uncharacterized_protein_involved_in_form
NU_COG2805_Tfp_pilus_assembly_protein_pilus_retra
U_COG4796_Type_II_secretory_pathway_component_Hof

131)
U_COG2831_Hemolysin_activation/secretion_protein
U_COG3210_Large_exoproteins_involved_in_heme_utili

132)
S_COG0316_Uncharacterized_conserved_protein
H_COG0321_Lipoate-protein_ligase_B
R_COG0354_Predicted_aminomethyltransferase_related
HC_COG0654_2-polyprenyl-6-methoxyphenol_hydroxylas
H_COG0320_Lipoate_synthase
C_COG0567_2-oxoglutarate_dehydrogenase_complex

133)
C_COG2142_Succinate_dehydrogenase,_hydrophobic_anc
C_COG2009_Succinate_dehydrogenase/fumarate_reducta

134)
T_COG1366_Anti-anti-sigma_regulatory_factor
TK_COG2208_Serine_phosphatase_RsbU_regulator
T_COG2172_Anti-sigma_regulatory_factor

135) Carbohydrate metabolism
R_COG1480_Predicted_membrane-associated_HD_superf

G_COG3866_Pectate_lyase
G_COG3867_Arabinogalactan_endo-1,4-beta-galactosid.
R_COG3872_Predicted_metal-dependent_enzyme

136)
R_COG3694_ABC-type_uncharacterized_transport_syst.
R_COG4587_ABC-type_uncharacterized_transport_syst.
R_COG4586_ABC-type_uncharacterized_transport_syst.

137)
J_COG0064_Asp-tRNAAsn/Glu-tRNAGln_amidotransferase
J_COG0154_Asp-tRNAAsn/Glu-tRNAGln_amidotransferase
J_COG0721_Asp-tRNAAsn/Glu-tRNAGln_amidotransferase

138)
C_COG3051_Citrate_lyase_alpha
C_COG3052_Citrate_lyase_gamma
C_COG3053_Citrate_lyase_synthetasE

139) Start of mesaconate pathway;
E_COG3033_Tryptophanase
E_COG3799_Methylaspartate_ammonia-lyase
E_COG4865_Glutamate_mutase_epsilon_subunit

140)
C_COG0437_Fe-S-cluster-containing_hydrogenase_comp
C_COG2864_Cytochrome_b_subunit_of_formate_dehydrog

141)
D_COG3115_Cell_division_protein
R_COG2916_DNA-binding_protein_H-NS
L_COG2925_Exonuclease_I
D_COG3116_Cell_division_protein

142)
C_COG4656_Predicted_NADH:ubiquinone_oxidoreductase
C_COG4657_Predicted_NADH:ubiquinone_oxidoreductase
C_COG4659_Predicted_NADH:ubiquinone_oxidoreductase
C_COG4660_Predicted_NADH:ubiquinone_oxidoreductase
C_COG4658_Predicted_NADH:ubiquinone_oxidoreductase

143)
O_COG3058_Uncharacterized_protein_involved_in_formate_dehydrogenase_formation
R_COG3302_DMSO_reductase_anchor_subunit
P_COG3303_Formate-dependent_nitrite_reductase
S_COG3787_Uncharacterized_protein_conserved_in_bact distantly to flavin-dep oxidases

144)
E_COG0709_Selenophosphate_synthase
J_COG3276_Selenocysteine-specific_translation_elonG.
E_COG1921_Selenocysteine_synthase_seryl-tRNASer

145)
O_COG1138_Cytochrome_c_biogenesis_factor
O_COG2332_Cytochrome_c-type_biogenesis_protein_Ccm

O_COG4133_ABC-type_transport_system
O_COG2386_ABC-type_transport_system

146) cf medline 12874385
E_COG1509_Lysine_2,3-aminomutase
J_COG2269_Truncated,_possibly_inactive,_lysyl-tRNA

147)
E_COG2981_Uncharacterized_protein_involved_in_cyst
P_COG4148_ABC-type_molybdate_transport_system,_ATP
P_COG4531_ABC-type_Zn2+_transport_system,_periplas
E_COG4160_ABC-type_arginine/histidine_transport_sy
E_COG4215_ABC-type_arginine_transport_system,_perm

148)
C_COG3005_Nitrate/TMAO_reductases_membrane-bound
C_COG3043_Nitrate_reductase_cytochrome_c-type_sub.
P_COG3062_Uncharacterized_protein_involved_in_form

149)
M_COG3040_Bacterial_lipocalin
P_COG4771_Outer_membrane_receptor_for_ferrienteroc
P_COG4779_ABC-type_enterobactin_transport_system

150)
T_COG3456_Uncharacterized_conserved_protein
P_COG4558_ABC-type_hemin_transport_system
P_COG4559_ABC-type_hemin_transport_system_ATPase
P_COG3721_Putative_heme_iron_utilization_protein

151) slightly different patterns in different groups of genes
NU_COG1157_Flagellar_biosynthesis/type_III_secreto
NU_COG1298_Flagellar_biosynthesis_pathway,_compone
NU_COG1338_Flagellar_biosynthesis_pathway,_compone
NU_COG1377_Flagellar_biosynthesis_pathway,_compone
N_COG1536_Flagellar_motor_switch_protein
NU_COG1886_Flagellar_motor_switch/type_III_secreto
N_COG1256_Flagellar_hook-associated_protein
N_COG1558_Flagellar_basal_body_rod_protein
NU_COG1677_Flagellar_hook-basal_body_protein
NU_COG1684_Flagellar_biosynthesis_pathway,_compone
NU_COG1766_Flagellar_biosynthesis/type_III_secreto
N_COG1815_Flagellar_basal_body_protein
N_COG1843_Flagellar_hook_capping_protein
NU_COG1987_Flagellar_biosynthesis_pathway
N_COG4786_Flagellar_basal_body_rod_protein
N_COG1868_Flagellar_motor_switch_protein
N_COG1291_Flagellar_motor_component
N_COG1344_Flagellin_and_related_hook-associated
N_COG1360_Flagellar_motor_protein
N_COG1749_Flagellar_hook_protein_FlgE
NO_COG1261_Flagellar_basal_body_P-ring_biosyn.
N_COG2063_Flagellar_basal_body_L-ring_protein
N_COG1706_Flagellar_basal-body_P-ring_protein

152)
R_COG4174_ABC-type_uncharacterized_transport

R_COG4239_ABC-type_uncharacterized_transport

153)
E_COG3138_Arginine/ornithine_N-succinyltransferase
E_COG3724_Succinylarginine_dihydrolase

154)
S_COG4672_Phage-related_protein
S_COG4718_Phage-related_protein
S_COG4723_Phage-related_protein_tail_component
S_COG4733_Phage-related_protein_tail_component
S_COG5435_Uncharacterized_conserved_protein

155)
H_COG4138_ABC-type_cobalamin_transport_system_ATP
H_COG4139_ABC-type_cobalamin_transport_system

156) =
U_COG4790_Type_III_secretory_pathway_component_Es
U_COG4669_Type_III_secretory_pathway_lipoprotein
U_COG4789_Type_III_secretory_pathway_component_Es
U_COG4791_Type_III_secretory_pathway_component_Es
U_COG4794_Type_III_secretory_pathway_component_Es

157)
R_COG3822_ABC-type_sugar_transport_system
R_COG4158_Predicted_ABC-type_sugar_transport

158)
NU_COG3121_P_pilus_assembly_protein,_chaperone_Pap
NU_COG3188_P_pilus_assembly_protein,_porin_PapC
R_COG3497_Phage_tail_sheath_protein_FI
R_COG3500_Phage_protein_D
R_COG3498_Phage_tail_tube_protein_FII
R_COG3499_Phage_protein_U

159)
R_COG4135_ABC-type_uncharacterized_transport
R_COG4136_ABC-type_uncharacterized_transport
R_COG4588_Accessory_colonization_factor_AcfC

160) rRNA modification in 0116
L_COG0116_Predicted_N6-adenine-specific_DNA_methyl
J_COG1534_Predicted_RNA-binding_protein_containing

161)
G_COG1105_Fructose-1-phosphate_kinase_and_related
G_COG1263_Phosphotransferase_system_IIC_components
G_COG1264_Phosphotransferase_system_IIB_components
G_COG2190_Phosphotransferase_system_IIA_components
G_COG1299_Phosphotransferase_system,_fructose-spec.
G_COG1445_Phosphotransferase_system_fructose-spec.
G_COG4668_Mannitol/fructose-specific_phosphotransf.
G_COG2213_Phosphotransferase_system,_mannitol-spec.
S_COG3037_Uncharacterized_protein_conserved_in_bac.
G_COG3414_Phosphotransferase_system,_galactitol-sp.

162)
G_COG1869_ABC-type_ribose_transport_system,_auxili
CO_COG4987_ABC-type_transport_system
CO_COG4988_ABC-type_transport_system
F_COG1972_Nucleoside_permease

163)
G_COG2160_L-arabinose_isomerase
M_COG5581_Predicted_glycosyltransferase
G_COG1440_Phosphotransferase_system_cellobiose-spe
G_COG1447_Phosphotransferase_system_cellobiose-spe
G_COG1455_Phosphotransferase_system_cellobiose-spe
G_COG3444_Phosphotransferase_system,_mannose/fruct
G_COG3715_Phosphotransferase_system,_mannose/fruct
G_COG3716_Phosphotransferase_system,_mannose/fruct
K_COG3711_Transcriptional_antiterminator

164)
E_COG4166_ABC-type_oligopeptide_transport_system
E_COG0765_ABC-type_amino_acid_transport_system
E_COG1126_ABC-type_polar_amino_acid_transport
ET_COG0834_ABC-type_amino_acid_transport/signal

165) MenBCDEF part of ubiquinone biosysnthesis
H_COG0447_Dihydroxynaphthoic_acid_synthase
H_COG1165_2-succinyl-6-hydroxy-2,4-cyclohexadiene
H_COG1575_1,4-dihydroxy-2-naphthoate_octaprenyltr.
HQ_COG1169_Isochorismate_synthase
R_COG1090_Predicted_nucleoside-diphosphate_sugar

166)
Q_COG1021_Peptide_arylation_enzymes
Q_COG3433_Aryl_carrier_domain

167)
C_COG3029_Fumarate_reductase_subunit_C
C_COG3080_Fumarate_reductase_subunit_D

168)
G_COG3001_Fructosamine-3-kinase
R_COG2103_Predicted_sugar_phosphate_isomerase
G_COG2211_Na+/melibiose_symporter

169)
G_COG0246_Mannitol-1-phosphate/altronate_dehydrog.
G_COG1129_ABC-type_sugar_transport_system,_ATPase
G_COG1172_Ribose/xylose/arabinose/galactoside_ABC
G_COG1879_ABC-type_sugar_transport_system
G_COG1593_TRAP-type_C4-dicarboxylate_transport_sys.
G_COG3090_TRAP-type_C4-dicarboxylate_transport_sys.
G_COG1638_TRAP-type_C4-dicarboxylate_transport_sys.

170)
P_COG1135_ABC-type_metal_ion_transport_system_ATP
P_COG1464_ABC-type_metal_ion_transport_system
P_COG2011_ABC-type_metal_ion_transport_system

171)
S_COG3698_Predicted_periplasmic_protein
E_COG4597_ABC-type_amino_acid_transport_system
R_COG4134_ABC-type_uncharacterized_transport

172)
O_COG3088_Uncharacterized_protein_involved_in_bios.
O_COG4235_Cytochrome_c_biogenesis_factor

173) taurine vs phosphonate, medline 10582129
P_COG3454_Metal-dependent_hydrolase_involved_in_ph
P_COG3624_Uncharacterized_enzyme_of_phosphonate_me
P_COG3625_Uncharacterized_enzyme_of_phosphonate_me
P_COG3626_Uncharacterized_enzyme_of_phosphonate_me
P_COG3627_Uncharacterized_enzyme_of_phosphonate_me
P_COG4107_ABC-type_phosphonate_transport_system,_A
P_COG4778_ABC-type_phosphonate_transport_system,_A
P_COG3709_Uncharacterized_component_of_phosphonate
P_COG4525_ABC-type_taurine_transport_system,_ATPas
P_COG4521_ABC-type_taurine_transport_system,_perip
P_COG3720_Putative_heme_degradation_protein

174)
G_COG4213_ABC-type_xylose_transport_system
G_COG4214_ABC-type_xylose_transport_system

175)
G_COG2942_N-acyl-D-glucosamine_2-epimerase
G_COG3734_2-keto-3-deoxy-galactonokinase

176)
E_COG2113_ABC-type_proline/glycine_betaine_transp.
E_COG4175_ABC-type_proline/glycine_betaine_transp.
E_COG4176_ABC-type_proline/glycine_betaine_transp.

177)
P_COG4651_Kef-type_K+_transport_system
P_COG3158_K+_transporter

178) Sugar metabolism
G_COG1312_D-mannonate_dehydratase
G_COG2115_Xylose_isomerase
G_COG1904_Glucuronate_isomerase
E_COG1897_Homoserine_trans-succinylase
G_COG2721_Altronate_dehydratase
S_COG3254_Uncharacterized_conserved_protein

179)
P_COG1276_Putative_copper_export_protein
R_COG2372_Uncharacterized_protein_homolog_of_CopC

180)
P_COG1178_ABC-type_Fe3+_transport_system
H_COG4143_ABC-type_thiamine_transport_system
P_COG1840_ABC-type_Fe3+_transport_system

181)

R_COG2215_ABC-type_uncharacterized_transport_syste
R_COG3683_ABC-type_uncharacterized_transport_syste

182)
G_COG3730_Phosphotransferase_system_sorbitol-speci
G_COG3731_Phosphotransferase_system_sorbitol-speci
G_COG3732_Phosphotransferase_system_sorbitol-speci

183)
G_COG3684_Tagatose-1,6-bisphosphate_aldolase
G_COG3775_Phosphotransferase_system

184) ml 12554704
E_COG3192_Ethanolamine_utilization_protein
E_COG4302_Ethanolamine_ammonia-lyase_small_sub.
E_COG4303_Ethanolamine_ammonia-lyase_large_sub.
QC_COG4576_Carbon_dioxide_concentrating_mechanism
QC_COG4577_Carbon_dioxide_concentrating_mechanism
E_COG4766_Ethanolamine_utilization_protein
E_COG4810_Ethanolamine_utilization_protein
E_COG4812_Ethanolamine_utilization_cobalamin
E_COG4816_Ethanolamine_utilization_protein
E_COG4819_Ethanolamine_utilization_protein
E_COG4820_Ethanolamine_utilization_protein
E_COG4917_Ethanolamine_utilization_protein

185)
E_COG1125_ABC-type_proline/glycine_betaine_transp.
E_COG1174_ABC-type_proline/glycine_betaine_transp.
M_COG1732_Periplasmic_glycine_betaine/choline-bind

186)
P_COG3221_ABC-type_phosphate/phosphonate_transport
P_COG3638_ABC-type_phosphate/phosphonate_transport
P_COG3639_ABC-type_phosphate/phosphonate_transport

187)
R_COG3740_Phage_head_maturation_protease
R_COG4653_Predicted_phage_phi-C31_gp36_major_capsid

188) Early phage genes
S_COG2369_Uncharacterized_protein_homolog_of_phage_pr
R_COG2842_Uncharacterized_ATPase_putative_transp.
S_COG2852_Uncharacterized_protein_conserved_in_bac.
R_COG3378_Predicted_ATPase
K_COG3617_Prophage_antirepressor
S_COG5283_Phage-related_tail_protein
S_COG3477_Predicted_periplasmic/secreted_protein
S_COG3645_Uncharacterized_phage-encoded_protein
L_COG3728_Phage_terminase_small_subunit
L_COG3723_Recombinational_DNA_repair_protein
L_COG4570_Holliday_junction_resolvase
K_COG3561_Phage_anti-repressor_protein
M_COG3955_Exopolysaccharide_biosynthesis_protein
R_COG4416_Mu-like_prophage_protein_Com
R_COG4373_Mu-like_prophage_FluMu_protein_gp28
S_COG4518_Mu-like_prophage_FluMu_protein_gp41

S_COG5566_Uncharacterized_conserved_protein

189)
G_COG0153_Galactokinase
C_COG1085_Galactose-1-phosphate_uridylyltransferas

190)
P_COG0471_Di-_and_tricarboxylate_transporters
R_COG0733_Na+-dependent_transporters
E_COG1115_Na+/alanine_symporter
E_COG0786_Na+/glutamate_symporter

191)
M_COG1346_Putative_effector_of_murein_hydrolase
R_COG1380_Putative_effector_of_murein_hydrolase_Lr

192)
E_COG1984_Allophanate_hydrolase_subunit_2
E_COG2049_Allophanate_hydrolase_subunit_1

193)
S_COG2836_Uncharacterized_conserved_protein related to COG0785 cyt c biogenesis prot
C_COG2863_Cytochrome_c553
C_COG2993_Cbb3-type_cytochrome_oxidase_cytochrome
O_COG3278_Cbb3-type_cytochrome_oxidase_subunit_1
P_COG3197_Uncharacterized_protein
O_COG4736_Cbb3-type_cytochrome_oxidase_subunit_3

194)
P_COG0370_Fe2+_transport_system_protein_B
P_COG1918_Fe2+_transport_system_protein_A
R_COG0727_Predicted_Fe-S-cluster_oxidoreductase

195)
C_COG1838_Tartrate_dehydratase_beta_subunit
C_COG1951_Tartrate_dehydratase_alpha_subunit

196)
H_COG0043_3-polyprenyl-4-hydroxyben
H_COG0163_3-polyprenyl-4-hydroxybenzoate_decarbox.

197) 223 *1143 and 1894 have Hamming distance 15*
C_COG0377_NADH:ubiquinone_oxidoreductase_20_kD_sub
C_COG0649_NADH:ubiquinone_oxidoreductase_49_kD_sub.
C_COG0852_NADH:ubiquinone_oxidoreductase_27_kD_sub.
C_COG1143_Formate_hydrogenlyase_subunit_6/NADH:ub.
C_COG0713_NADH:ubiquinone_oxidoreductase_subunit_1
C_COG1008_NADH:ubiquinone_oxidoreductase_subunit_4
C_COG0838_NADH:ubiquinone_oxidoreductase_subunit_3
C_COG1005_NADH:ubiquinone_oxidoreductase_subunit_1
C_COG1007_NADH:ubiquinone_oxidoreductase_subunit_2
C_COG0839_NADH:ubiquinone_oxidoreductase_subunit_6
C_COG1034_NADH_dehydrogenase/NADH:ubiquinone_oxido
C_COG1894_NADH:ubiquinone_oxidoreductase_NADH-bin.
C_COG1905_NADH:ubiquinone_oxidoreductase_24_kD_sub.

198)
M_COG0836_Mannose-1-phosphate_guanylyltransferase
M_COG1089_GDP-D-mannose_dehydratase

199)
M_COG1088_dTDP-D-glucose_4,6-dehydratase
M_COG1209_dTDP-glucose_pyrophosphorylase
M_COG1091_dTDP-4-dehydrorhamnose_reductase
M_COG1898_dTDP-4-dehydrorhamnose_3,5-epimerase
R_COG1216_Predicted_glycosyltransferases

200)
H_COG0157_Nicotinate-nucleotide_pyrophosphorylase
H_COG0379_Quinolinate_synthase
H_COG0422_Thiamine_biosynthesis_protein_ThiC

201)
M_COG0859_ADP-heptose:LPS_heptosyltransferase
R_COG1778_Low_specificity_phosphatase_(HAD_superfa
M_COG2870_ADP-heptose_synthase,_bifunctional_sugar

202)
C_COG0374_Ni,Fe-hydrogenase_I_large_subunit
C_COG1740_Ni,Fe-hydrogenase_I_small_subunit
C_COG1969_Ni,Fe-hydrogenase_I_cytochrome_b_subunit

203) Crux of proline/purine/folate cofactor biosynthesis
E_COG0014_Gamma-glutamyl_phosphate_reductase
E_COG0263_Glutamate_5-kinase
F_COG0138_AICAR_transformylase/IMP_cyclohydrolase_
F_COG0299_Folate-dependent_phosphoribosylglycinami
H_COG0285_Folylpolyglutamate_synthase
F_COG0026_Phosphoribosylaminoimidazole_carboxylase

204)
L_COG1195_Recombinational_DNA_repair_ATPase
L_COG1381_Recombinational_DNA_repair_protein

205)
M_COG1589_Cell_division_septal_protein
M_COG1686_D-alanyl-D-alanine_carboxypeptidase
D_COG2919_Septum_formation_initiator
L_COG4974_Site-specific_recombinase_XerD

206)
D_COG2177_Cell_division_protein
D_COG2884_Predicted_ATPase_involved_in_cell_div.

207)
P_COG0155_Sulfite_reductase_beta_subunit
EH_COG0175_3'-phosphoadenosine_5'-phosphosulfate

208) Mix of enzymes involved in different aa biosynthesis
E_COG0019_Diaminopimelate_decarboxylase
EH_COG0059_Ketol-acid_reductoisomerase
EG_COG0129_Dihydroxyacid_dehydratase/phosphoglucon
E_COG0133_Tryptophan_synthase_beta_chain

E_COG0440_Acetolactate_synthase_small

209)
H_COG0340_Biotin-(acetyl-CoA_carboxylase)_ligase
I_COG0511_Biotin_carboxyl_carrier_protein
I_COG0439_Biotin_carboxylase

210) Repair of protein oxidative damage
O_COG0225_Peptide_methionine_sulfoxide_reductase
O_COG0229_Conserved_domain_frequently_associated_w
O_COG0652_Peptidyl-prolyl_cis-trans_isomerase_(rot

211) First steps in riboflavin biosynthesis
H_COG0117_Pyrimidine_deaminase
H_COG0307_Riboflavin_synthase_alpha_chain
H_COG0807_GTP_cyclohydrolase_II

212) Biotin synthesis
H_COG0132_Dethiobiotin_synthetase
H_COG0502_Biotin_synthase_and_related_enzymes
H_COG0161_Adenosylmethionine-8-amino-7-oxononanoat.

214)
U_COG0805_Sec-independent_protein_secretion_pathwa
U_COG1826_Sec-independent_protein_secretion_pathwa

215)
C_COG0723_Rieske_Fe-S_protein
C_COG1290_Cytochrome_b_subunit_of_the_bc_complex

216) Pyrimidine biosynthesis plus introgressed tryptophan
F_COG0015_Adenylosuccinate_lyase
F_COG0104_Adenylosuccinate_synthase
F_COG0151_Phosphoribosylamine-glycine_ligase
EH_COG0147_Anthranilate/para-aminobenzoate_synthas
EH_COG0512_Anthranilate/para-aminobenzoate_synthas
F_COG0167_Dihydroorotate_dehydrogenase
F_COG0284_Orotidine-5'-phosphate_decarboxylase
R_COG0491_Zn-dependent_hydrolases,_including_glyox
F_COG0461_Orotate_phosphoribosyltransferase

217) Pyrimidine biosynthesis
F_COG0540_Aspartate_carbamoyltransferase,_catalyti
EF_COG0458_Carbamoylphosphate_synthase_large_subun
EF_COG0505_Carbamoylphosphate_synthase_small_subun.

218)
E_COG1605_Chorismate_mutase
F_COG0518_GMP_synthase_-_Glutamine_amidotransferase
F_COG0519_GMP_synthase_PP-ATPase_domain/subunit

219) More tryptophane biosynthesis plus other amino acids
HE_COG0111_Phosphoglycerate_dehydrogenase_and_rela
E_COG0134_Indole-3-glycerol_phosphate_synthase
E_COG0547_Anthranilate_phosphoribosyltransferase
E_COG0159_Tryptophan_synthase_alpha_chain
E_COG0460_Homoserine_dehydrogenase

E_COG0498_Threonine_synthase
E_COG0287_Prephenate_dehydrogenase

220) Mix of: later steps in riboflavin biosynthesis, trunk of aromatic amino acid biosynthesis
H_COG0054_Riboflavin_synthase_beta-chain
H_COG0108_3,4-dihydroxy-2-butanone_4-phosphate_syn.
H_COG1985_Pyrimidine_reductase,_riboflavin_biosynt.
E_COG0082_Chorismate_synthase
E_COG0128_5-enolpyruvylshikimate-3-phosphate_synth.
E_COG0169_Shikimate_5-dehydrogenase
E_COG0136_Aspartate-semialdehyde_dehydrogenase
E_COG0527_Aspartokinases

221) Isoprenoid derivatives biosynthesis
I_COG0020_Undecaprenyl_pyrophosphate_synthase
H_COG0142_Geranylgeranyl_pyrophosphate_synthase

222) Amino acid biosynthesis; 0251 annotation is most likely spurious, it should be an (aa)
E_COG0031_Cysteine_synthase
J_COG0251_Putative_translation_initiation_inhibito
E_COG0626_Cystathionine_beta-lyases/cystathionine_
E_COG0337_3-dehydroquinate_synthetase
E_COG0345_Pyrroline-5-carboxylate_reductase

223)
J_COG2163_Ribosomal_protein_L14E/L6E/L27E
J_COG2174_Ribosomal_protein_L34E