```
-msrC, Neisseria meningitidis, (Bacteria Proteobacteria)
                                 →N/A, (Response regulator receiver domain protein), Neisseria_meningitidis, (Bacteria_Proteobacteria)
                                 •N/A, (transcriptional regulator), Streptomyces_coelicolor, (Bacteria_Terrabacteria group)
                                  •N/A, (Phosphoenolpyruvate hydrolase-like), Bradyrhizobium_diazoefficiens, (Bacteria_Proteobacteria)

    VP0514, Thermodesulfovibrio yellowstonii, (Bacteria Nitrospirae)

                                 •N/A, (COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains), Leptospira_interrogans, (Bacteria_Spirochaetes)
                                    •N/A, (transcription factor binding), Thermotoga_maritima, (Bacteria_Thermotogae)
                                •pspF, Gloeobacter_violaceus, (Bacteria_Terrabacteria group)
                                pspF, Synechocystis sp., (Bacteria Terrabacteria group)
                                     •rsbU, Leptospira_interrogans, (Bacteria_Spirochaetes)
                                      •N/A, (PFAM metal-dependent phosphohydrolase, HD sub domain), Dictyoglomus_turgidum, (Bacteria_Dictyoglomi)
                                      •N/A, (ATP-binding region, ATPase domain protein), Chloroflexus_aurantiacus, (Bacteria_Terrabacteria group)
                                    •N/A, (histidine kinase, dimerisation and phosphoacceptor region), Chloroflexus_aurantiacus, (Bacteria_Terrabacteria group)
                            •dhaR, Escherichia_coli, (Bacteria_Proteobacteria)
                          dhaR, Chloroflexus_aurantiacus, (Bacteria_Terrabacteria group)
                               N/A, (HDOD domain), Thermodesulfovibrio_yellowstonii, (Bacteria_Nitrospirae)

    pspF, Bacillus subtilis, (Bacteria Terrabacteria group)

                                   •flgR, Helicobacter_pylori, (Bacteria_Proteobacteria)
                                  •atoC, Chlamydia_trachomatis, (Bacteria_PVC group)
                                 •fleR, Pseudomonas_aeruginosa, (Bacteria_Proteobacteria)
                                atoC, Thermodesulfovibrio_yellowstonii, (Bacteria_Nitrospirae)
                                N/A, (response regulator), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                                 N/A, (phosphorelay signal transduction system), Thermodesulfovibrio_yellowstonii, (Bacteria_Nitrospirae)
                                  •norR, Thermodesulfovibrio_yellowstonii, (Bacteria_Nitrospirae)
                                   nifA, Bradyrhizobium_diazoefficiens, (Bacteria_Proteobacteria)
                                   _norR, Aquifex_aeolicus, (Bacteria_Aquificae)
                                   NP_Unk02 - Aquifex aeolicus
                                  _enorR, Aquifex_aeolicus, (Bacteria_Aquificae)
                                   •norR, N/A, (N/A)

    norR, Leptospira interrogans, (Bacteria Spirochaetes)

                               N/A, (phosphorelay signal transduction system), Thermodesulfovibrio yellowstonii, (Bacteria Nitrospirae)

    N/A, (Bacterial regulatory protein, Fis family), Thermodesulfovibrio yellowstonii, (Bacteria Nitrospirae)

                               ⊸N/A, (Sigma-54-dependent sensor transcriptional response regulator, PAS domain-containing), Geobacter sulfurreducens, (Bacteria Proteobacteria)
                               └-N/A, (Sigma-54 factor interaction domain-containing protein), Geobacter sulfurreducens, (Bacteria Proteobacteria)
                               -N/A, (Bacterial regulatory protein, Fis family), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                                 •tacA, Bradyrhizobium_diazoefficiens, (Bacteria_Proteobacteria)
                               •N/A, (response regulator), Geobacter sulfurreducens, (Bacteria Proteobacteria)

    atoC, Geobacter sulfurreducens, (Bacteria Proteobacteria)

    stc, Geobacter sulfurreducens, (Bacteria Proteobacteria)

                              N/A, (Bacterial regulatory protein, Fis family), Geobacter_sulfurreducens, (Bacteria_Proteobacteria-

    atoC, Geobacter sulfurreducens, (Bacteria Proteobacteria)

                                    •N/A, (acetoacetate metabolism regulatory protein AtoC K07714), Bacteroides_thetaiotaomicron, (Bacteria_FCB group)
                                      -N/A, (COG2204 Response regulator containing CheY-like receiver AAA-type ATPase and DNA-binding domains), Bacteroides_thetaiotaomicron, (Bacteria_FCB group)
                                    <sup>1</sup> zraR, Bacteroides_thetaiotaomicron, (Bacteria_FCB group)
                                    ¬N/A, (Sigma-54 interaction domain protein), Bacteroides thetaiotaomicron, (Bacteria FCB group)

    algB, Pseudomonas aeruginosa, (Bacteria Proteobacteria)

    pspF, Escherichia coli, (Bacteria Proteobacteria)

    N/A, (two component, sigma54 specific, transcriptional regulator, Fis family), Geobacter sulfurreducens, (Bacteria Proteobacteria)

                                   •N/A, (Response regulator with CheY-like receiver, AAA-type ATPase, and DNA-binding domains), Rhodopirellula baltica, (Bacteria PVC group)
                                    -N/A, (COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains), Rhodopirellula baltica, (Bacteria PVC group)

    glnG, Geobacter sulfurreducens, (Bacteria Proteobacteria)

                                   glnG, Escherichia coli, (Bacteria Proteobacteria)
                                    └•glnG, Pseudomonas aeruginosa, (Bacteria Proteobacteria)
                                     •glnG, Bradyrhizobium diazoefficiens, (Bacteria Proteobacteria)
                                    •N/A, (COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains), Rhodopirellula_baltica, (Bacteria_PVC group)

    atoC, Escherichia coli, (Bacteria Proteobacteria)

                                 •ntrX, Geobacter sulfurreducens, (Bacteria Proteobacteria)
                                rtrX, Thermodesulfovibrio yellowstonii, (Bacteria Nitrospirae) −
                                    ntrX, Bradyrhizobium diazoefficiens, (Bacteria Proteobacteria)

    ntrX, Leptospira interrogans, (Bacteria Spirochaetes)

    fleQ, Pseudomonas aeruginosa, (Bacteria Proteobacteria)

    dctD, Pseudomonas aeruginosa, (Bacteria Proteobacteria)

    dctD, Pseudomonas aeruginosa, (Bacteria Proteobacteria)

                                  V02 08980, Pseudomonas aeruginosa, (Bacteria Proteobacteria)
                                    →N/A, (Bacterial regulatory protein, Fis family), Bradyrhizobium_diazoefficiens, (Bacteria_Proteobacteria)

    tyrR, Escherichia coli, (Bacteria Proteobacteria)

    tyrR, Pseudomonas aeruginosa, (Bacteria Proteobacteria)

    tyrR, Pseudomonas aeruginosa, (Bacteria Proteobacteria)

                                        •N/A, (Bacterial regulatory protein, Fis family), Pseudomonas_aeruginosa, (Bacteria_Proteobacteria)

    norR, Escherichia coli, (Bacteria Proteobacteria)

                                      -norR, Pseudomonas aeruginosa, (Bacteria Proteobacteria)

    nifA, Pseudomonas aeruginosa, (Bacteria Proteobacteria)

                                      •prpR, Escherichia_coli, (Bacteria_Proteobacteria)
                                         pspF, Pseudomonas_aeruginosa, (Bacteria_Proteobacteria)

    N/A, (Sigma-54 interaction domain), Pseudomonas aeruginosa, (Bacteria Proteobacteria)

                                      sfnR, Pseudomonas_aeruginosa, (Bacteria_Proteobacteria)

    flbD, Bradyrhizobium diazoefficiens, (Bacteria Proteobacteria)

    N/A, (GAF domain), Rhodopirellula baltica, (Bacteria PVC group)

    fhlA, Escherichia coli, (Bacteria Proteobacteria)

                                   fhIA, Escherichia coli, (Bacteria Proteobacteria)

    nifA, Rhodopirellula baltica, (Bacteria PVC group)

                                     N/A, (Sigma-54 interaction domain), Bradyrhizobium diazoefficiens, (Bacteria Proteobacteria)
                                     ygeV, Escherichia coli, (Bacteria Proteobacteria)
                                       -acoR, Pseudomonas aeruginosa, (Bacteria Proteobacteria)
                                       -acoR, Pseudomonas aeruginosa, (Bacteria Proteobacteria)

    MA20 04760, Bradyrhizobium diazoefficiens, (Bacteria Proteobacteria)

    acoR, Bacillus subtilis, (Bacteria Terrabacteria group)

    rocR, Bacillus subtilis, (Bacteria Terrabacteria group)

    bkdR, Bacillus subtilis, (Bacteria Terrabacteria group)

    N/A, (Bacterial regulatory protein, Fis family), Pseudomonas aeruginosa, (Bacteria Proteobacteria)

    N/A, (Sigma-54 interaction domain), Bradyrhizobium diazoefficiens, (Bacteria Proteobacteria)

    acxR, Bradyrhizobium diazoefficiens, (Bacteria Proteobacteria)

                                 •N/A, (Domains REC, sigma54 interaction, HTH8), Geobacter sulfurreducens, (Bacteria Proteobacteria)
                                  yfhA, Escherichia coli, (Bacteria Proteobacteria)
                                 N/A, (Bacterial regulatory protein, Fis family), Rhodopirellula baltica, (Bacteria PVC group)
                                •N/A, (CheY-like receiver AAA-type ATPase and DNA-binding domains), Rhodopirellula baltica, (Bacteria PVC group)
                                renla6, Rhodopirellula baltica, (Bacteria PVC group)
                                -nla6, Rhodopirellula baltica, (Bacteria PVC group)
                                •N/A, (COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains), Rhodopirellula baltica, (Bacteria PVC group)

    N/A, (Domains REC, sigma54 interaction, HTH8), Geobacter sulfurreducens, (Bacteria Proteobacteria)

                               •N/A, (Domains REC, sigma54 interaction, HTH8), Geobacter sulfurreducens, (Bacteria Proteobacteria)
                              →N/A, (response regulator), Geobacter sulfurreducens, (Bacteria Proteobacteria)
                              •atoC, Thermodesulfovibrio yellowstonii, (Bacteria Nitrospirae)
                             N/A, (response regulator), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                             pilR, Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                             →N/A, (two component, sigma54 specific, transcriptional regulator, Fis family), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                             →N/A, (Sigma-54 interaction domain), Thermodesulfovibrio_yellowstonii, (Bacteria_Nitrospirae)
                                  N/A, (response regulator), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)

¬N/A, (response regulator), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)

                                →N/A, (response regulator), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                               └─N/A, (phosphorelay signal transduction system), Thermodesulfovibrio_yellowstonii, (Bacteria_Nitrospirae)
                             •nla28, Thermodesulfovibrio yellowstonii, (Bacteria Nitrospirae)
                              N/A, (phosphorelay signal transduction system), Thermodesulfovibrio_yellowstonii, (Bacteria_Nitrospirae)
                             •N/A, (two component, sigma54 specific, transcriptional regulator, Fis family), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                             •N/A, (response regulator), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                              cbrB, Thermodesulfovibrio_yellowstonii, (Bacteria_Nitrospirae)
                            zraR, Escherichia_coli, (Bacteria_Proteobacteria)
                             •cbrB, Pseudomonas_aeruginosa, (Bacteria_Proteobacteria)
                             •N/A, (Bacterial regulatory protein, Fis family), Rhodopirellula_baltica, (Bacteria_PVC group)
                              -N/A, (COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains), Rhodopirellula_baltica, (Bacteria_PVC group)
                             •pilR, Pseudomonas_aeruginosa, (Bacteria_Proteobacteria)
                               zraR, Pseudomonas_aeruginosa, (Bacteria_Proteobacteria)
                             N/A, (Sigma-54 interaction domain), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                             •hsfA, Rhodopirellula_baltica, (Bacteria_PVC group)

    zraR, Geobacter sulfurreducens, (Bacteria Proteobacteria)

                             •N/A, (COG2204 Response regulator containing CheY-like receiver AAA-type ATPase and DNA-binding domains), Bacteroides_thetaiotaomicron, (Bacteria_FCB group)
                             _•N/A, (acetoacetate metabolism regulatory protein AtoC K07714), Bacteroides_thetaiotaomicron, (Bacteria_FCB group)
                             └•N/A, (acetoacetate metabolism regulatory protein AtoC K07714), Bacteroides_thetaiotaomicron, (Bacteria_FCB group)
                            _ntrX, Aquifex_aeolicus, (Bacteria_Aquificae)
                            ntrX. N/A. (N/A)
                           •N/A. (two component, sigma54 specific, transcriptional regulator, Fis family), Aguifex aeolicus, (Bacteria Aguificae)
                           N/A, (two component, sigma54 specific, transcriptional regulator, Fis family), N/A, (N/A)
                            N/A, (phosphorelay signal transduction system), Aquifex_aeolicus, (Bacteria_Aquificae)
                            N/A, (phosphorelay signal transduction system), N/A, (N/A)
                           •atoC, Bacteroides_thetaiotaomicron, (Bacteria_FCB group)
                           N/A, (Domains FehydlgC, FeS, sigma54 interaction, HTH8), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                            •hoxA, Bradyrhizobium_diazoefficiens, (Bacteria_Proteobacteria)
                            N/A, (Bacterial regulatory protein, Fis family), Rhodopirellula_baltica, (Bacteria_PVC group)
                            N/A, (Ornithine decarboxylase inhibitor-putative sigma54 transciptional regulator), Rhodopirellula_baltica, (Bacteria_PVC group)

    nifA, Bacteroides thetaiotaomicron, (Bacteria FCB group)

                         •N/A, (Acetoacetate metabolism regulatory protein atoC), Fusobacterium_nucleatum, (Bacteria_Fusobacteria)
                         •N/A, (Bacterial regulatory protein, Fis family), Fusobacterium_nucleatum, (Bacteria_Fusobacteria)
                     •bkdR, Aquifex_aeolicus, (Bacteria_Aquificae)
                      N/A, (transcription factor binding), Aquifex_aeolicus, (Bacteria_Aquificae)
                      N/A, (Sigma-54 interaction domain), N/A, (N/A)
                        N/A, (Sigma-54 interaction domain), Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
                     rtcR, Escherichia_coli, (Bacteria_Proteobacteria)
                      •rtcR, Pseudomonas_aeruginosa, (Bacteria_Proteobacteria)
                     rtcR, Rhodopirellula baltica, (Bacteria PVC group)
•levR, Bacillus_subtilis, (Bacteria_Terrabacteria group)
•nifA, Geobacter_sulfurreducens, (Bacteria_Proteobacteria)
•N/A, (histidine kinase A domain protein), Chloroflexus_aurantiacus, (Bacteria_Terrabacteria group)
•N/A, (SMART protein phosphatase 2C domain protein), Chloroflexus_aurantiacus, (Bacteria_Terrabacteria group)
•msrC, Bacteroides_thetaiotaomicron, (Bacteria_FCB group)
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