

| Nr.Org. | Species/strain                                        | Group | Uniprot | Gene name       | aa  | Architecture (Interpro) | Nr.Prot   |
|---------|-------------------------------------------------------|-------|---------|-----------------|-----|-------------------------|-----------|
| 1       | <i>Paenibacillus</i> sp. HGF5                         | F     | F3MK65  | HMPREF9412_5833 | 848 | PAS+GAF+PHY+PAS+GGDEF   | 1         |
|         |                                                       | F     | F5LIA9  | HMPREF9413_4279 | 851 | PAS+GAF+PHY+PAS+GGDEF   | 2         |
| 2       | <i>Actinosynnema mirum</i> ATCC 29888 / DSM 43827     | Ac    | C6WQH8  | Amir_2910       | 783 | PAS+GAF+PHY+Kinase      | 3         |
| 3       | <i>Blastococcus saxobidens</i> (strain DD2)           | Ac    | H6RWS6  | BLASA_1197      | 787 | PAS+GAF+PHY+SpoIIE      | 4         |
| 4       | <i>Cellulomonas fimi</i> DSM 20113                    | Ac    | F4H001  | Celf_0783       | 753 | PAS+GAF+PHY+SpoIIE      | 5         |
| 5       | <i>Cellulomonas flavigena</i> DSM 20109               | Ac    | D5UCU7  | Cfla_3458       | 760 | PAS+GAF+PHY+SpoIIE      | 6         |
| 6       | <i>Cellvibrio gilvus</i> ATCC 13127                   | Ac    | F8A6D9  | Celgi_2934      | 760 | PAS+GAF+PHY+SpoIIE      | 7         |
| 7       | <i>Frankia alni</i> (strain ACN14a)                   | Ac    | Q0REY5  | FRAL5334        | 783 | PAS+GAF+PHY+SpoIIE      | 8         |
| 8       | <i>Geodermatophilus obscurus</i> DSM 43160            | Ac    | D2SCC9  | Gobs_3673       | 738 | PAS+GAF+PHY+SpoIIE      | 9         |
|         |                                                       |       | D2SBY3  | Gobs_1419       | 770 | PAS+GAF+PHY+SpoIIE      | 10        |
| 9       | <i>Kineococcus radiotolerans</i> SRS30216             | Ac    | A6W9I3  | Krad_1986       | 798 | PAS+GAF+PHY+SpoIIE      | 11        |
| 10      | <i>Isoptericola variabilis</i> (strain 225)           | Ac    | F6FU87  | Isova_0486      | 753 | PAS+GAF+PHY+SpoIIE      | 12        |
| 11      | <i>Mycobacterium colombiense</i> CECT 3035            | Ac    | J4JW60  | MCOL_12233      | 761 | PAS+GAF+PHY+SpoIIE      | 13        |
| 12      | <i>Mycobacterium flavescens</i> ATCC 700033           | Ac    | A4TD79  | Mflv_4519       | 755 | PAS+GAF+PHY+SpoIIE      | 14        |
| 13      | <i>Mycobacterium parascrofulaceum</i> ATCC BAA-614    | Ac    | D5P4C5  | HMPREF0591_1019 | 752 | PAS+GAF+PHY+SpoIIE      | 15        |
| 14      | <i>Mycobacterium rhodesiae</i> (strain NBB3)          | Ac    | G8RPP6  | Mycrhn_2006     | 746 | PAS+GAF+PHY+SpoIIE      | 16        |
| 15      | <i>Mycobacterium</i> sp. Spyr1                        | Ac    | E6TMF3  | Mspyr1_39190    | 755 | PAS+GAF+PHY+SpoIIE      | 17        |
| 16      | <i>Mycobacterium tusciae</i> JS617                    | Ac    | H1JWC3  | MyctuDRAFT_1726 | 769 | PAS+GAF+PHY+SpoIIE      | 18        |
| 17      | <i>Sanguibacter keddieii</i> ATCC 51767/DSM 10542     | Ac    | D1BEH6  | Sked_13140      | 772 | PAS+GAF+PHY+SpoIIE      | 19        |
| 18      | <i>Streptomyces albus</i> J1074                       | Ac    | D6B7A6  | SSHG_00462      | 752 | PAS+GAF+PHY+Kinase      | 20        |
| 19      | <i>Streptomyces griseus</i> subsp. griseus JCM 4626   | Ac    | B1VL07  | SGR_3206        | 835 | PAS+GAF+PHY+Kinase      | 21        |
| 20      | <i>Streptomyces griseus</i> XylebKG-1                 | Ac    | G0Q372  | SACT1_3456      | 811 | PAS+GAF+PHY+Kinase      | 22        |
| 21      | <i>Streptomyces</i> sp. SirexAA-E                     | Ac    | G2NNR2  | SACTE_3158      | 776 | PAS+GAF+PHY+Kinase      | 23        |
| 22      | <i>Streptomyces venezuelae</i> ATCC 10712/ CBS 650.69 | Ac    | F2RG57  | SVEN_6491       | 787 | PAS+GAF+PHY+Kinase      | 24        |
| 23      | <i>Acetobacter tropicalis</i> NBRC 101654             | P (α) | F7VE10  | ATPR_1609       | 858 | PAS+GAF+PHY+Kinase+RR   | 25        |
| 24      | <i>Agrobacterium</i> sp. ATCC 31749                   | P (α) | F5J6F4  | AGRO_0709       | 850 | PAS+GAF+PHY+Kinase+RR   | 26        |
|         |                                                       |       | F5JJM0  | AGRO_5382       | 736 | PAS+GAF+PHY+Kinase      | 27        |
| 25      | <i>Agrobacterium</i> sp. ( strain H13-3)              | P (α) | F0L8D1  | AGROH133_07592  | 850 | PAS+GAF+PHY+Kinase+RR   | 28        |
| 26      | <i>Agrobacterium tumefaciens</i> 5A                   | P (α) | H0H7H1  | AT5A_08005      | 850 | PAS+GAF+PHY+Kinase+RR   | 29        |
| 27      | <i>Agrobacterium tumefaciens</i> C58                  | P (α) | A9CI81  | Atu2165         | 850 | PAS+GAF+PHY+Kinase+RR   | 30        |
|         |                                                       |       | Q7CY45  | Atu1990         | 736 | PAS+GAF+PHY+Kinase      | 31        |
| 28      | <i>Agrobacterium tumefaciens</i> CCNWS0286            | P (α) | G6XR11  | ATCR1_06661     | 850 | PAS+GAF+PHY+Kinase+RR   | 32        |
|         |                                                       |       | G6XXW4  | ATCR1_17507     | 736 | PAS+GAF+PHY+Kinase      | 33        |
| 29      | <i>Agrobacterium tumefaciens</i> F2                   | P (α) | F7U7Z1  | Agau_C200253    | 850 | PAS+GAF+PHY+Kinase+RR   | 34        |
|         |                                                       |       | F7UC55  | Agau_L101989    | 752 | PAS+GAF+PHY+Kinase      | 35 cph1   |
| 30      | <i>Agrobacterium vitis</i> (strain S4 / ATCC BAA-846) | P (α) | B9JR96  | Avi_3496        | 852 | PAS+GAF+PHY+Kinase+RR   | 36        |
|         |                                                       |       | B9K3G4  | Avi_9083        | 856 | PAS+GAF+PHY+Kinase+RR   | 37        |
| 31      | <i>Azorhizobium caulinodans</i> ATCC 43989/DSM 5975   | P (α) | A8HU76  | AZC_0915        | 850 | PAS+GAF+PHY+Kinase+RR   | 38        |
| 32      | <i>Azospirillum amazonense</i> Y2                     | P (α) | G1Y089  | AZA_33581       | 746 | PAS+GAF+PHY+Kinase      | 39        |
| 33      | <i>Azospirillum brasilense</i> Sp245                  | P (α) | G8AZK3  | AZOBR_p440075   | 763 | PAS+GAF+PHY+Kinase      | 40        |
|         |                                                       |       | G8AZ44  | AZOBR_p420015   | 853 | PAS+GAF+PHY+Kinase+RR   | 41        |
| 34      | <i>Azospirillum lipoferum</i> 4B                      | P (α) | G7ZDI9  | AZOLI_p20424    | 752 | PAS+GAF+PHY+Kinase      | 42        |
| 35      | <i>Azospirillum</i> sp. B510                          | P (α) | D3NW14  | AZL_019550      | 835 | PAS+GAF+PHY+Kinase+RR   | 43        |
|         |                                                       |       | D3P0D5  | AZL_a05830      | 751 | PAS+GAF+PHY+Kinase      | 44        |
| 36      | <i>Bradyrhizobium japonicum</i> USDA 6                | P (α) | G7D887  | BJ6T_73190      | 848 | PAS+GAF+PHY+Kinase+RR   | 45        |
| 37      | <i>Bradyrhizobium</i> sp. BTAi1                       | P (α) | A5EQ94  | BBta_6428       | 723 | PAS+GAF+PHY+PAS         | 46 bzbphP |
|         |                                                       |       | A5EEA8  | BBta_2330       | 842 | PAS+GAF+PHY+Kinase+RR   | 47        |
|         |                                                       |       | A5EGA4  | BBta_3080       | 783 | PAS+GAF+PHY+Kinase      | 48        |
| 38      | <i>Bradyrhizobium</i> sp. ORS 285                     | P (α) | H0S7K1  | BRAO285_950065  | 724 | PAS+GAF+PHY+PAS         | 49        |
|         |                                                       |       | H0RYP4  | BRAO285_220015  | 855 | PAS+GAF+PHY+Kinase+RR   | 50        |
| 39      | <i>Bradyrhizobium</i> sp. ORS 375                     | P (α) | H0SNP3  | BRAO375_4770021 | 754 | PAS+GAF+PHY+Kinase      | 51        |
|         |                                                       |       | H0SQA1  | BRAO375_590041  | 724 | PAS+GAF+PHY+PAS         | 52        |
|         |                                                       |       | H0SIV0  | BRAO375_3120007 | 854 | PAS+GAF+PHY+Kinase+RR   | 53        |
|         |                                                       |       | H0SQW2  | BRAO375_650013  | 781 | PAS+GAF+PHY+Kinase      | 54        |
| 40      | <i>Bradyrhizobium</i> sp. ORS278                      | P (α) | Q8VUB6  | BRAO1628        | 724 | PAS+GAF+PHY             | 55        |

|    |                                                    |        |           |                   |                       |                        |        |
|----|----------------------------------------------------|--------|-----------|-------------------|-----------------------|------------------------|--------|
|    |                                                    | A4YMN8 | BRADO1262 | 620               | PAS+GAF+PHY           | 56                     |        |
|    |                                                    | A4YPN9 | BRADO2008 | 853               | PAS+GAF+PHY+Kinase+RR | 57                     |        |
| 41 | Bradyrhizobium sp. STM 3809                        | P (α)  | H0T1C0    | BRAS3809_3280003  | 844                   | PAS+GAF+PHY+Kinase+RR  | 58     |
|    |                                                    |        | H0T0P2    | BRAS3809_3160004  | 718                   | PAS+GAF+PHY+PAS        | 59     |
|    |                                                    |        | H0T3R1    | BRAS3809_4200008  | 614                   | PAS+GAF+PHY            | 60     |
| 42 | Bradyrhizobium sp. STM 3843                        | P (α)  | H0TIK2    | BRAO3843_1660016  | 843                   | PAS+GAF+PHY+Kinase+RR  | 61     |
| 43 | Brevundimonas sp. BAL3                             | P (α)  | B4WDC8    | BBAL3_100         | 723                   | PAS+GAF+PHY+Kinase     | 62     |
| 44 | Caulobacter segnis DSM 7131                        | P (α)  | D5VPQ8    | Cseg_4069         | 844                   | PAS+GAF+PHY+Kinase+RR  | 63     |
| 45 | Citreicella sp. SE45                               | P (α)  | D0D2X2    | CSE45_2096        | 864                   | PAS+GAF+PHY+Kinase+RR  | 64     |
| 46 | Erythrobacter sp. NAP1                             | P (α)  | A3WKG7    | NAP1_15213        | 857                   | PAS+GAF+PHY+Kinase+RR  | 65     |
| 47 | Erythrobacter sp. SD-21                            | P (α)  | A5PCV2    | ED21_22988        | 855                   | PAS+GAF+PHY+Kinase+RR  | 66     |
| 48 | Fulvimarina pelagi HTCC2506                        | P (α)  | Q0G229    | FP2506_01340      | 888                   | PAS+GAF+PHY+Kinase+RR  | 67     |
| 49 | Gluconacetobacter sp.SXCC-1                        | P (α)  | F3S8W7    | SXCC_02493        | 831                   | PAS+GAF+PHY+Kinase+RR  | 68     |
| 50 | Gluconacetobacter xylinus NBRC 3288/BCRC 11682     | P (α)  | G2I3Y5    | GLX_04200         | 831                   | PAS+GAF+PHY+Kinase+RR  | 69     |
| 51 | Gluconobacter morbifer G707                        | P (α)  | G6XFS1    | GMO_03360         | 682                   | GAF+PHY+Kinase         | 70     |
| 52 | Gluconobacter oxydans 621H                         | P (α)  | Q5FQG4    | GOX1641           | 744                   | PAS+GAF+PHY+Kinase     | 71     |
| 53 | Granulibacter thesedensis CGDNIH1                  | P (α)  | Q0BS12    | GbCGDNIH1_1492    | 529                   | PAS+GAF+PHY            | 72     |
| 54 | Hyphomicrobium denitrificans ATCC 51888 / DSM 1869 | P (α)  | D8JTM6    | Hden_0770         | 851                   | PAS+GAF+PHY+Kinase+RR  | 73     |
| 55 | Labrenzia aggregata IAM                            | P (α)  | A0NNX8    | SIAM614_24607     | 848                   | PAS+GAF+PHY+Kinase+RR  | 74     |
| 56 | Magnetospirillum gryphiswaldense                   | P (α)  | A4TZU6    | MGR_1425          | 753                   | PAS+GAF+PHY+Kinase     | 75     |
| 57 | Manganese-oxidizing bacterium (strain SI85-9A1)    | P (α)  | Q1YI19    | SI859A1_01485     | 726                   | PAS+GAF+PHY+Kinase     | 76     |
| 58 | Maritimibacter alkaliphilus HTCC2654               | P (α)  | A3V9Y6    | RB2654_19128      | 857                   | PAS+GAF+PHY+Kinase+RR  | 77     |
| 59 | Methylobacterium chloromethanicum CM4              | P (α)  | B7KNA8    | MCHL_4449         | 875                   | PYP+PAS+GAF+PHY+Kinase | 78 Ppr |
| 60 | Methylobacterium extorquens AM1                    | P (α)  | C5AQ42    | MexAM1_METAlp4471 | 875                   | PYP+PAS+GAF+PHY+Kinase | 79 Ppr |
| 61 | Methylobacterium extorquens DM4                    | P (α)  | C7CJ18    | METDI5076         | 875                   | PYP+PAS+GAF+PHY+Kinase | 80 Ppr |
| 62 | Methylobacterium extorquens DSM 13060              | P (α)  | H1KM11    | MetexDRAFT_3673   | 875                   | PYP+PAS+GAF+PHY+Kinase | 81 Ppr |
| 63 | Methylobacterium extorquens PA1                    | P (α)  | A9W8V2    | Mext_4081         | 895                   | PYP+PAS+GAF+PHY+Kinase | 82 Ppr |
| 64 | Methylobacterium populi BJ001                      | P (α)  | B1ZK65    | Mpop_0539         | 751                   | PAS+GAF+PHY+Kinase     | 83     |
|    |                                                    |        | B1ZGY2    | Mpop_4562         | 874                   | PYP+PAS+GAF+PHY+Kinase | 84 Ppr |
| 65 | Methylobacterium radiotolerans ATCC 27329          | P (α)  | B1M9J3    | Mrad2831_6244     | 849                   | PAS+GAF+PHY+Kinase+RR  | 85     |
|    |                                                    |        | B1M2J7    | Mrad2831_4270     | 751                   | PAS+GAF+PHY+Kinase     | 86     |
|    |                                                    |        | B1LW23    | Mrad2831_3723     | 871                   | PYP+PAS+GAF+PHY+Kinase | 87 Ppr |
| 66 | Methylobacterium sp. 4-46                          | P (α)  | B0UDE6    | M446_2206         | 762                   | PAS+GAF+PHY+Kinase     | 88     |
|    |                                                    |        | B0UNZ0    | M446_3192         | 864                   | PYP+PAS+GAF+PHY+Kinase | 89 Ppr |
| 67 | Methylocella silvestris BL2 / DSM 15510            | P (α)  | B8EJ78    | Msil_3686         | 709                   | PAS+GAF+PHY+Kinase     | 90     |
|    |                                                    |        | B8EPV6    | Msil_2020         | 771                   | PAS+GAF+PHY+Kinase     | 91     |
| 68 | Novosphingobium pentaromativorans US6-1            | P (α)  | G6EE31    | NSU_2602          | 850                   | PAS+GAF+PHY+Kinase+RR  | 92     |
| 69 | Novosphingobium sp. PP1Y                           | P (α)  | F6IK49    | PP1Y_AT9272       | 864                   | PAS+GAF+PHY+Kinase+RR  | 93     |
| 70 | Oceanicola batsensis HTCC2597                      | P (α)  | A3TUU8    | OB2597_09129      | 866                   | PAS+GAF+PHY+Kinase+RR  | 94     |
| 71 | Oceanicola granulosus HTCC2516                     | P (α)  | Q2CCS8    | OG2516_08858      | 855                   | PAS+GAF+PHY+Kinase+RR  | 95     |
| 72 | Ochrobactrum anthropi ATCC 49188                   | P (α)  | A6X7F4    | Oant_4458         | 844                   | PAS+GAF+PHY+Kinase+RR  | 96     |
| 73 | Parvularcula bermudensis HTCC2503                  | P (α)  | E0TEY6    | PB2503_10134      | 867                   | PAS+GAF+PHY+Kinase+RR  | 97     |
| 74 | Phaeobacter gallaeciensis 2.10                     | P (α)  | I7EF73    | RG210_10397       | 858                   | PAS+GAF+PHY+Kinase+RR  | 98     |
| 75 | Phaeobacter gallaeciensis DSM 17395                | P (α)  | I7F2C9    | RGBS107_03018     | 858                   | PAS+GAF+PHY+Kinase+RR  | 99     |
| 76 | Phenylobacterium zucineum HLK1                     | P (α)  | B4RFA1    | PHZ_c2261         | 746                   | PAS+GAF+PHY+Kinase     | 100    |
| 77 | Phaeospirillum molischianum DSM 120                | P (α)  | H8FVX0    | PHAMO_40069       | 509                   | PAS+GAF+PHY            | 101    |
| 78 | Rhizobium etli CIAT 652                            | P (α)  | B3PX96    | RHECIAT_CH0003531 | 854                   | PAS+GAF+PHY+Kinase+RR  | 102    |
| 79 | Rhizobium etli CNPAF512                            | P (α)  | F2A7P5    | RHECNPAF_214007   | 854                   | PAS+GAF+PHY+Kinase+RR  | 103    |
| 80 | Rhizobium leguminosarum bv viciae 3841             | P (α)  | Q1MCK7    | RL3714            | 855                   | PAS+GAF+PHY+Kinase+RR  | 104    |
| 81 | Rhizobium leguminosarum bv. trifolii WSM1325       | P (α)  | C6AUG6    | Rleg_3289         | 855                   | PAS+GAF+PHY+Kinase+RR  | 105    |
| 82 | Rhizobium leguminosarum bv. trifolii WSM2304       | P (α)  | B5ZMM3    | Rleg2_3034        | 856                   | PAS+GAF+PHY+Kinase+RR  | 106    |
| 83 | Rhizobium sp. PDO-076                              | P (α)  | H4FBD4    | PDO_0469          | 859                   | PAS+GAF+PHY+Kinase+RR  | 107    |
| 84 | Rhodobacter sphaeroides ATCC 17023                 | P (α)  | Q3IUZ1    | RHOS4_40750       | 980                   | PAS+GAF+PHY+GGDEF+EAL  | 108    |
|    |                                                    |        | Q3IV48    | RHOS4_40180       | 931                   | PAS+GAF+PHY+GGDEF+EAL  | 109    |
| 85 | Rhodobacter sphaeroides ATCC 17025                 | P (α)  | A4X0G2    | Rsph17025_4279    | 936                   | PAS+GAF+PHY+GGDEF+EAL  | 110    |
| 86 | Rhodobacteraceae bacterium HTCC2083                | P (α)  | B6B3N3    | RB2083_1766       | 699                   | GAF+PHY+Kinase         | 111    |

|     |                                                        |       |                                                          |                                                                            |                                                                                                                                                          |                                                               |
|-----|--------------------------------------------------------|-------|----------------------------------------------------------|----------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|
| 87  | <i>Rhodobacterales bacterium Y4I</i>                   | P (α) | B6BFK0<br>B6BFX9                                         | RBY4I_4155<br>RBY4I_79                                                     | 741 PAS+GAF+PHY+Kinase<br>859 PAS+GAF+PHY+Kinase+RR                                                                                                      | 112<br>113                                                    |
| 88  | <i>Rhodomicrobium vannielii</i> ATCC 17100 / ATH 3.1.1 | P (α) | E317B2                                                   | Rvan_1511                                                                  | 789 PAS+GAF+PHY+GGDEF                                                                                                                                    | 114                                                           |
| 89  | <i>Rhodopseudomonas palustris</i> BisA53               | P (α) | Q07TZ5<br>Q07TZ4<br>Q07RY9                               | RPE_0631<br>RPE_0632<br>RPE_1343                                           | 765 PAS+GAF+PHY+Kinase<br>776 PAS+GAF+PHY+Kinase<br>726 PAS+GAF+PHY+PAS                                                                                  | 115<br>116<br>117                                             |
| 90  | <i>Rhodopseudomonas palustris</i> BisB5                | P (α) | Q137V7<br>Q137V6<br>Q137Y0<br>Q132I0<br>Q132M8           | RPD_2402<br>RPD_2403<br>RPD_2377<br>RPD_3788<br>RPD_3740                   | 762 PAS+GAF+PHY+Kinase<br>776 PAS+GAF+PHY+Kinase<br>759 PAS+GAF+PHY+Kinase<br>773 PAS+GAF+PHY+Kinase<br>732 PAS+GAF+PHY+PAS                              | 118<br>119<br>120<br>121<br>122                               |
| 91  | <i>Rhodopseudomonas palustris</i> BisB18               | P (α) | Q20ZX2<br>Q219R5                                         | RPC_3780<br>RPC_1309                                                       | 779 PAS+GAF+PHY+Kinase<br>722 PAS+GAF+PHY+PAS                                                                                                            | 123<br>124                                                    |
| 92  | <i>Rhodopseudomonas palustris</i> DX-1                 | P (α) | E6VJN7<br>E6VDD3<br>E6VJI8<br>E6VG36                     | Rpdx1_4031<br>Rpdx1_1142<br>Rpdx1_3982<br>Rpdx1_0116                       | 771 PAS+GAF+PHY+Kinase<br>845 PAS+GAF+PHY+Kinase<br>731 PAS+GAF+PHY+PAS<br>759 PAS+GAF+PHY+Kinase                                                        | 125<br>126<br>127<br>128                                      |
| 93  | <i>Rhodopseudomonas palustris</i> CGA009               | P (α) | Q6N5G3<br>Q6N5G2<br>Q6NDI6<br>Q6N9P8<br>Q6NB40           | RPA3015<br>RPA3016<br>RPA0122<br>RPA1490<br>RPA0990                        | 758 PAS+GAF+PHY+Kinase<br>775 PAS+GAF+PHY+Kinase<br>759 PAS+GAF+PHY+Kinase<br>770 PAS+GAF+PHY+Kinase<br>845 PAS+GAF+PHY+Kinase                           | 129 PhyB1<br>130 PhyB2<br>131 PhyB3<br>132 PhyB4<br>133 PhyB4 |
| 94  | <i>Rhodopseudomonas palustris</i> HaA2                 | P (α) | Q2IRM7<br>Q2IST3<br>Q2ISY2<br>Q2IRM6<br>Q2IY35           | RPB_4450<br>RPB_4034<br>RPB_3985<br>RPB_4451<br>RPB_2169                   | 758 PAS+GAF+PHY+Kinase<br>775 PAS+GAF+PHY+Kinase<br>732 PAS+GAF+PHY+PAS<br>775 PAS+GAF+PHY+Kinase<br>812 PAS+GAF+PHY+PAS+GGDEF                           | 134<br>135<br>136<br>137<br>138                               |
| 95  | <i>Rhodopseudomonas palustris</i> TIE-1                | P (α) | B3Q6C8<br>B3Q8U2<br>B3Q7C0<br>B3QGX4<br>B3Q8U3<br>B3Q6Z9 | Rpal_1677<br>Rpal_3424<br>Rpal_1726<br>Rpal_1182<br>Rpal_3425<br>Rpal_0125 | 770 PAS+GAF+PHY+Kinase<br>758 PAS+GAF+PHY+Kinase<br>731 PAS+GAF+PHY+PAS<br>846 PAS+GAF+PHY+Kinase+RR<br>775 PAS+GAF+PHY+Kinase<br>759 PAS+GAF+PHY+Kinase | 139<br>140<br>141<br>142<br>143<br>144                        |
| 96  | <i>Rhodospirillum centenum</i> ATCC 51521 / SW         | P (α) | B6IXX2<br>B6IWB2                                         | DivJ<br>ppR                                                                | 894 PAS+GAF+PHY+Kinase<br>883 PYP+PAS+GAF+PHY+Kinase                                                                                                     | 145<br>146 Ppr                                                |
| 97  | <i>Rhodospirillum photometricum</i> DSM 122            | P (α) | H6SJB3                                                   | RSPPHO_01452                                                               | 926 PAS+GAF+PHY+PAS+Kinase                                                                                                                               | 147                                                           |
| 98  | <i>Rhodospirillum rubrum</i> ATCC 11170                | P (α) | Q2RS60                                                   | Rru_A2235                                                                  | 865 PAS+GAF+PHY+PAS+Kinase                                                                                                                               | 148                                                           |
| 99  | <i>Rhodospirillum rubrum</i> F11                       | P (α) | G2TDU8                                                   | F11_11500                                                                  | 838 PAS+GAF+PHY+PAS+Kinase                                                                                                                               | 149                                                           |
| 100 | <i>Roseomonas cervicalis</i> ATCC 49957                | P (α) | D5RIE4                                                   | HMPREF0731_0854                                                            | 736 PAS+GAF+PHY+Kinase                                                                                                                                   | 150                                                           |
| 101 | <i>Ruegeria</i> sp. R11                                | P (α) | B7QYT9                                                   | RR11_1369                                                                  | 858 PAS+GAF+PHY+Kinase+RR                                                                                                                                | 151                                                           |
| 102 | <i>Sagittula stellata</i> E-37                         | P (α) | A3K9F1                                                   | SSE37_05552                                                                | 861 PAS+GAF+PHY+Kinase+RR                                                                                                                                | 152                                                           |
| 103 | <i>Silicibacter</i> sp. TM1040                         | P (α) | Q1GMQ3                                                   | TM1040_3089                                                                | 740 PAS+GAF+PHY+Kinase                                                                                                                                   | 153                                                           |
| 104 | <i>Sphingobium japonicum</i> NBRC 101211 / UT26S       | P (α) | D42653                                                   | SJA_C1-32510                                                               | 855 PAS+GAF+PHY+Kinase+RR                                                                                                                                | 154                                                           |
| 105 | <i>Sphingomonas</i> sp. SKA58                          | P (α) | Q1NF69                                                   | SKA58_15137                                                                | 858 PAS+GAF+PHY+Kinase+RR                                                                                                                                | 155 PhyB5                                                     |
| 106 | <i>Sphingomonas</i> sp.S17                             | P (α) | F3WYE4                                                   | SUS17_2206                                                                 | 718 PAS+GAF+PHY                                                                                                                                          | 156                                                           |
| 107 | <i>Xanthobacter autotrophicus</i> ATCC BAA-1158/Py2    | P (α) | A7II43                                                   | Xaut_2444                                                                  | 721 PAS+GAF+PHY+Kinase                                                                                                                                   | 157                                                           |
| 108 | <i>Achromobacter arsenitoxydans</i> SY8                | P (β) | H0F0I2                                                   | KYC_01425                                                                  | 688 GAF+PHY+Kinase                                                                                                                                       | 158                                                           |
| 109 | <i>Achromobacter piechaudii</i> ATCC 43553             | P (β) | D4XHI7                                                   | HMPREF0004_4934                                                            | 730 PAS+GAF+PHY+Kinase                                                                                                                                   | 159                                                           |
| 110 | <i>Achromobacter xylosoxidans</i> AXA-A                | P (β) | F7SVG1                                                   | AXXA_03279                                                                 | 730 PAS+GAF+PHY+Kinase                                                                                                                                   | 160                                                           |
| 111 | <i>Achromobacter xylosoxidans</i> C54                  | P (β) | E5U4B9                                                   | HMPREF0005_02653                                                           | 730 PAS+GAF+PHY+Kinase                                                                                                                                   | 161                                                           |
| 112 | <i>Acidovorax avenae</i> DSM 7227                      | P (β) | F0QCD9                                                   | Acav_2318                                                                  | 745 PAS+GAF+PHY+Kinase                                                                                                                                   | 162                                                           |
| 113 | <i>Acidovorax avenae</i> subsp. Citrulli AAC00-1       | P (β) | A1TRF7                                                   | Aave_2978                                                                  | 567 PAS+GAF+PHY                                                                                                                                          | 163                                                           |
| 114 | <i>Burkholderia gladioli</i> (strain BSR3)             | P (β) | F2LQM6                                                   | bg1s_2g24560                                                               | 785 PAS+GAF+PHY+Kinase                                                                                                                                   | 164                                                           |
| 115 | <i>Burkholderia glumae</i> (strain BGR1)               | P (β) | C5AJW1                                                   | bg1u_2g18650                                                               | 796 PAS+GAF+PHY+Kinase                                                                                                                                   | 165                                                           |
| 116 | <i>Burkholderia phytofirmans</i> PsJN                  | P (β) | B2T288                                                   | Bphyt_1284                                                                 | 791 PAS+GAF+PHY+Kinase                                                                                                                                   | 166                                                           |
| 117 | <i>Burkholderia</i> sp. CCGE1003                       | P (β) | E1TJN9                                                   | BC1003_3847                                                                | 786 PAS+GAF+PHY+Kinase                                                                                                                                   | 167                                                           |

|     |                                                                  |       |        |                   |      |                           |         |
|-----|------------------------------------------------------------------|-------|--------|-------------------|------|---------------------------|---------|
| 118 | <i>Burkholderia</i> sp.YI23                                      | P (β) | G8MJQ1 | BYI23_D011810     | 788  | PAS+GAF+PHY+Kinase        | 168     |
|     |                                                                  |       | G8M3M1 | BYI23_A015050     | 775  | PAS+GAF+PHY+Kinase        | 169     |
| 119 | <i>Candidatus Burkholderia kirkii</i> UZHbot1                    | P (β) | G4M3I9 | BKIR_c11_4469     | 795  | PAS+GAF+PHY+Kinase        | 170     |
| 120 | <i>Gallionella capsiferriiformans</i> (strain ES-2               | E (β) | D9SIA6 | GalF_0118         | 481  | GAF+PHY                   | 171     |
| 121 | <i>Herbaspirillum seropedicae</i> SmR1                           | P (β) | D81WH1 | Hsero_2492        | 732  | PAS+GAF+PHY+Kinase        | 172     |
| 122 | <i>Methyloversatilis universalis</i> FAM5                        | P (β) | F5RI34 | METUNv1_03984     | 721  | PAS+GAF+PHY+PAS           | 173     |
| 123 | <i>Methylovorus</i> sp. SIP3-4                                   | P (β) | C6XE59 | Msip34_1589       | 730  | PAS+GAF+PHY+Kinase        | 174     |
| 124 | <i>Methylovorus</i> sp. MP688                                    | P (β) | E4QIH3 | MPQ_1656          | 714  | PAS+GAF+PHY+Kinase        | 175     |
| 125 | <i>Oxalobacteraceae bacterium</i> IMCC9480                       | P (β) | F1WLW9 | IMCC9480_301      | 785  | PAS+GAF+PHY+Kinase        | 176     |
| 126 | <i>Ralstonia pickettii</i> (strain 12D)                          | P (β) | C6BF22 | Rpic12D_2793      | 763  | PAS+GAF+PHY+Kinase        | 177     |
| 127 | <i>Ralstonia pickettii</i> (strain 12J                           | P (β) | B2UDM2 | Rpic_3141         | 762  | PAS+GAF+PHY+Kinase        | 178     |
| 128 | <i>Ralstonia</i> sp. 5_7_47FAA                                   | P (β) | E2T4I4 | HMPREF1004_04309  | 762  | PAS+GAF+PHY+Kinase        | 179     |
| 129 | <i>Ramlibacter tataouinensis</i> ATCC BAA-407/DSM 14655          | P (β) | F5Y2U7 | Rta_25470         | 720  | PAS+GAF+PHY+Kinase        | 180     |
|     |                                                                  |       | F5Y6C4 | Rta_28950         | 736  | PAS+GAF+PHY+Kinase        | 181     |
|     |                                                                  |       | E6UYD5 | Varpa_3575        | 754  | PAS+GAF+PHY+Kinase        | 182     |
| 130 | <i>Variovorax paradoxus</i> (strain EPS)                         | P (β) | Q0A8J1 | Mlg_1497          | 689  | PAS+GAF+PHY+GGDEF         | 183     |
| 131 | <i>Alkalilimnicola ehrlichei</i> MLHE-1                          | P (γ) | D3RPS7 | Alvin_0710        | 1037 | PAS+GAF+PHY+PAS+Kinase+RR | 184     |
| 132 | <i>Allochromatium vinosum</i> ATCC 17899                         | P (γ) | D3RSX1 | Alvin_1343        | 526  | PAS+GAF+PHY               | 185     |
|     |                                                                  |       | D3RS29 | Alvin_3066        | 1114 | PYP+PAS+GAF+PHY+GGDEF+EAL | 186 Ppd |
| 133 | <i>Alteromonas macleodii</i> DSM 17117 Deep ecotype              | P (γ) | F2G740 | MAD_E_1017830     | 908  | PAS+GAF+PHY+Kinase+RR     | 187     |
|     |                                                                  |       | F2GBD7 | MAD_E_1014245     | 884  | PAS+GAF+PHY+Kinase+RR     | 188     |
|     |                                                                  |       | F2G8S9 | MAD_E_1013275     | 853  | PAS+GAF+PHY+Kinase+RR     | 189     |
| 134 | <i>Alteromonas</i> sp. (strain SN2)                              | P (γ) | F5Z4Z9 | ambt_15280        | 500  | PAS+GAF+PHY               | 190     |
| 135 | <i>gamma proteobacterium</i> NOR5-3                              | P (γ) | B8KJL6 | NOR53_936         | 535  | PAS+GAF+PHY               | 191     |
| 136 | <i>Halomonas boliviensis</i> LC1                                 | P (γ) | G9EAS1 | KUC_1078          | 668  | PAS+GAF+PHY+GGDEF         | 192     |
| 137 | <i>Halomonas</i> sp. GFAJ-1                                      | P (γ) | H0J0U2 | MOY_06240         | 667  | PAS+GAF+PHY+GGDEF         | 193     |
| 138 | <i>Halomonas</i> sp.TD01                                         | P (γ) | F7SQE3 | GME_13605         | 679  | PAS+GAF+PHY+GGDEF         | 194     |
| 139 | <i>Idiomarina baltica</i> OS145                                  | P (γ) | A3WMD3 | OS145_06937       | 689  | PAS+GAF+PHY+GGDEF         | 195     |
| 140 | <i>Idiomarina</i> sp.A28L                                        | P (γ) | F7RW09 | A28LD_0430        | 683  | PAS+GAF+PHY+GGDEF         | 196     |
| 141 | <i>Marichromatium purpuratum</i> 984                             | P (γ) | F9TX13 | MarpuDRAFT_0525   | 729  | PAS+GAF+PHY+PAS           | 197     |
|     |                                                                  |       | F9TWU6 | MarpuDRAFT_0436   | 521  | PAS+GAF+PHY               | 198     |
| 142 | <i>Marinobacter</i> sp. ELB17                                    | P (γ) | A3J9Q2 | MELB17_18219      | 1020 | PAS+GAF+PHY+PAS+GGDEF+EAL | 199     |
| 143 | <i>Methylomicrobium alcaliphilum</i> (strain DSM 19304)          | P (γ) | G4T394 | MEALZ_0892        | 492  | PAS+GAF+PHY               | 200     |
| 144 | <i>Pseudoalteromonas atlantica</i> T6c /ATCC BAA-1087            | P (γ) | Q15YT5 | Patl_0423         | 799  | PAS+GAF+PHY+Kinase        | 201     |
| 145 | <i>Pseudomonas aeruginosa</i> 2192                               | P (γ) | A3LFL2 | PA2G_03568        | 728  | PAS+GAF+PHY+Kinase        | 202     |
| 146 | <i>Pseudomonas aeruginosa</i> 138244                             | P (γ) | F5K3K8 | PA13_13257        | 728  | PAS+GAF+PHY+Kinase        | 203     |
| 147 | <i>Pseudomonas aeruginosa</i> 152504                             | P (γ) | F5KLX3 | PA15_14216        | 728  | PAS+GAF+PHY+Kinase        | 204     |
| 148 | <i>Pseudomonas aeruginosa</i> 39016                              | P (γ) | E2ZZM9 | PA39016_001870017 | 728  | PAS+GAF+PHY+Kinase        | 205     |
| 149 | <i>Pseudomonas aeruginosa</i> ATCC 15692/PAO1/1C/PRS 101/LMG 12. | P (γ) | Q9HWR3 | PA4117            | 728  | PAS+GAF+PHY+Kinase        | 206     |
| 150 | <i>Pseudomonas aeruginosa</i> C3719                              | P (γ) | A3KZ15 | PACG_03030        | 728  | PAS+GAF+PHY+Kinase        | 207     |
| 151 | <i>Pseudomonas aeruginosa</i> strain LESB58                      | P (γ) | B7V6N3 | PLES_08541        | 728  | PAS+GAF+PHY+Kinase        | 208     |
| 152 | <i>Pseudomonas aeruginosa</i> M18                                | P (γ) | G2LAG6 | PAML8_0822        | 728  | PAS+GAF+PHY+Kinase        | 209     |
| 153 | <i>Pseudomonas aeruginosa</i> MPA01/P1                           | P (γ) | H3SUH4 | O1O_07518         | 728  | PAS+GAF+PHY+Kinase        | 210     |
| 154 | <i>Pseudomonas aeruginosa</i> MPA01/P2                           | P (γ) | H3TJB5 | O1Q_22088         | 728  | PAS+GAF+PHY+Kinase        | 211     |
| 155 | <i>Pseudomonas aeruginosa</i> NCGM1179                           | P (γ) | G2U532 | NCGM1179_0139     | 728  | PAS+GAF+PHY+Kinase        | 212     |
| 156 | <i>Pseudomonas aeruginosa</i> NCGM2.S1                           | P (γ) | G4LD77 | NCGM2_5318        | 728  | PAS+GAF+PHY+Kinase        | 213     |
| 157 | <i>Pseudomonas aeruginosa</i> PA7                                | P (γ) | A6UZX6 | PSPA7_0975        | 728  | PAS+GAF+PHY+Kinase        | 214     |
| 158 | <i>Pseudomonas aeruginosa</i> UCBPP-PA14                         | P (γ) | Q02ST1 | PA14_10700        | 728  | PAS+GAF+PHY+Kinase        | 215     |
| 159 | <i>Pseudomonas brassicaearum</i> NFM421                          | P (γ) | F2KBD1 | PSEBR_a334        | 744  | PAS+GAF+PHY+Kinase        | 216     |
| 160 | <i>Pseudomonas entomophila</i> L48                               | P (γ) | Q1I877 | PSEEN3401         | 746  | PAS+GAF+PHY+Kinase        | 217     |
| 161 | <i>Pseudomonas fluorescens</i> PF0-1                             | P (γ) | Q3KEA1 | PF101_2162        | 745  | PAS+GAF+PHY+Kinase        | 218     |
| 162 | <i>Pseudomonas fluorescens</i> PF-5                              | P (γ) | Q4K656 | PFL_5200          | 746  | PAS+GAF+PHY+Kinase        | 219     |
| 163 | <i>Pseudomonas fluorescens</i> (strain SBW25)                    | P (γ) | C3K1S9 | PFLU_5120         | 747  | PAS+GAF+PHY+Kinase        | 220     |
| 164 | <i>Pseudomonas fluorescens</i> WH6                               | P (γ) | E2XXU5 | PFWH6_4867        | 747  | PAS+GAF+PHY+Kinase        | 221     |
| 165 | <i>Pseudomonas fulva</i> (strain 12-X)                           | P (γ) | F6AHN9 | Psefu_0523        | 752  | PAS+GAF+PHY+Kinase        | 222     |
| 166 | <i>Pseudomonas mendocina</i> (strain NK-01)                      | P (γ) | F4DXW2 | MDS_0283          | 749  | PAS+GAF+PHY+Kinase        | 223     |

|     |                                                                    |       |                   |                                                |                                                     |            |
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| 167 | <i>Pseudomonas psychrotolerans</i> L19                             | P (Y) | H0JD31<br>H0J927  | PPL19_11282<br>PPL19_04600                     | 740 PAS+GAF+PHY+Kinase<br>749 PAS+GAF+PHY+Kinase    | 224<br>225 |
| 168 | <i>Pseudomonas putida</i> ( <i>Arthrobacter siderocapsulatus</i> ) | P (Y) | Q8VRN7<br>Q8VRN6  | Bacteriophytochrome 1<br>Bacteriophytochrome 2 | 748 PAS+GAF+PHY+Kinase<br>847 PAS+GAF+PHY+Kinase+RR | 226<br>227 |
| 169 | <i>Pseudomonas putida</i> F1                                       | P (Y) | A5W5Q5<br>A5W323  | Pput_3339<br>Pput_2394                         | 748 PAS+GAF+PHY+Kinase<br>847 PAS+GAF+PHY+Kinase+RR | 228<br>229 |
| 170 | <i>Pseudomonas putida</i> GB-1                                     | P (Y) | B0KKF3<br>B0KSG0  | PputGB1_1956<br>PputGB1_2586                   | 748 PAS+GAF+PHY+Kinase<br>847 PAS+GAF+PHY+Kinase+RR | 230<br>231 |
| 171 | <i>Pseudomonas putida</i> KT2440                                   | P (Y) | Q88KD4<br>Q88HJ2  | PP_2356<br>PP_3364                             | 755 PAS+GAF+PHY+Kinase<br>847 PAS+GAF+PHY+Kinase+RR | 232<br>233 |
| 172 | <i>Pseudomonas putida</i> S16                                      | P (Y) | F8FYR7            | PPS_1937                                       | 749 PAS+GAF+PHY+Kinase                              | 234        |
| 173 | <i>Pseudomonas putida</i> (strain BIRD-1)                          | P (Y) | E4R796_<br>E4RCB0 | PPUBIRD1_3331<br>PPUBIRD1_2417                 | 748 PAS+GAF+PHY+Kinase<br>847 PAS+GAF+PHY+Kinase+RR | 235<br>236 |
| 174 | <i>Pseudomonas putida</i> (strain W619)                            | P (Y) | B1J6D2<br>B1J8C3  | PputW619_1796<br>PputW619_2574                 | 756 PAS+GAF+PHY+Kinase<br>844 PAS+GAF+PHY+Kinase+RR | 237<br>238 |
| 175 | <i>Pseudomonas savastanoi</i> pv. <i>savastanoi</i> NCPPB 3335     | P (Y) | D7I2E3<br>D7I067  | PSA3335_3356<br>PSA3335_2564                   | 745 PAS+GAF+PHY+Kinase<br>1003 PAS+GAF+PHY+2Kinase  | 239<br>240 |
| 176 | <i>Pseudomonas</i> sp. 2_1_26                                      | P (Y) | G5FKU2            | HMPREF1030_00095                               | 728 PAS+GAF+PHY+Kinase                              | 241        |
| 177 | <i>Pseudomonas</i> sp. TJI-51                                      | P (Y) | F0EBQ6            | G1E_25089                                      | 752 PAS+GAF+PHY+Kinase                              | 242        |
| 178 | <i>Pseudomonas stutzeri</i> DSM 4166                               | P (Y) | F2N3C1            | PSTAA_4337                                     | 445 PAS+GAF+PHY                                     | 243        |
| 179 | <i>Pseudomonas stutzeri</i> DSM 5190                               | P (Y) | F8H7L2            | PSTAB_4167                                     | 756 PAS+GAF+PHY+Kinase                              | 244        |
| 180 | <i>Pseudomonas stutzeri</i> ATCC 14405                             | P (Y) | H7EYN4            | PstZobell_15649                                | 756 PAS+GAF+PHY+Kinase                              | 245        |
| 181 | <i>Pseudomonas stutzeri</i> (strain A1501)                         | P (Y) | A4VS53            | PST_4182                                       | 756 PAS+GAF+PHY+Kinase                              | 246        |
| 182 | <i>Pseudomonas syringae</i> Cit 7                                  | P (Y) | F3H3N1            | PSYCIT7_20394                                  | 745 PAS+GAF+PHY+Kinase                              | 247        |
| 183 | <i>Pseudomonas syringae</i> pv. <i>aceris</i> str.M302273PT        | P (Y) | F3JP53<br>F3JN00  | PSYAR_24021<br>PSYAR_21982                     | 745 PAS+GAF+PHY+Kinase<br>803 PAS+GAF+PHY+Kinase    | 248<br>249 |
| 184 | <i>Pseudomonas syringae</i> pv. <i>Actinidiae</i> str.M302091      | P (Y) | F3I595<br>F3HXA6  | PSYAC_18035<br>PSYAC_03576                     | 745 PAS+GAF+PHY+Kinase<br>918 PAS+GAF+PHY+2Kinase   | 250<br>251 |
| 185 | <i>Pseudomonas syringae</i> pv. <i>aesculi</i> str. 0893_23        | P (Y) | F3DHN7<br>F3DGB4  | PSYAE_18180<br>PSYAE_15626                     | 745 PAS+GAF+PHY+Kinase<br>998 PAS+GAF+PHY+2Kinase   | 252<br>253 |
| 186 | <i>Pseudomonas syringae</i> pv. <i>aptata</i> str. DSM 50252       | P (Y) | F3IV44<br>F3J113  | PSYAP_04739<br>PSYAP_15628                     | 745 PAS+GAF+PHY+Kinase<br>1003 PAS+GAF+PHY+2Kinase  | 254<br>255 |
| 187 | <i>Pseudomonas syringae</i> pv. <i>glycinea</i> str. B076          | P (Y) | E7P372<br>E7P4T6  | PsgB076_08500<br>PsgB076_11380                 | 733 PAS+GAF+PHY+Kinase<br>973 PAS+GAF+PHY+2Kinase   | 256<br>257 |
| 188 | <i>Pseudomonas syringae</i> pv. <i>glycinea</i> str. race 4        | P (Y) | F3C4Z8<br>E7PNE5  | Pgy4_13721<br>PsgRace4_16464                   | 908 PAS+GAF+PHY+2Kinase<br>973 PAS+GAF+PHY+2Kinase  | 258<br>259 |
| 189 | <i>Pseudomonas syringae</i> pv. <i>japonica</i> str. M301072PT     | P (Y) | F3FEX0<br>F3FQH3  | PSYJA_07206<br>PSYJA_27284                     | 532 PAS+GAF+PHY<br>1003 PAS+GAF+PHY+2Kinase         | 260<br>261 |
| 190 | <i>Pseudomonas syringae</i> pv. <i>lachrymans</i> str. M301315     | P (Y) | F3EL04<br>F3EAZ4  | PLA107_27276<br>PLA107_09368                   | 745 PAS+GAF+PHY+Kinase<br>998 PAS+GAF+PHY+2Kinase   | 262<br>263 |
| 191 | <i>Pseudomonas syringae</i> pv. <i>lachrymans</i> str. M302278PT   | P (Y) | F3IKA7            | PLA106_15844                                   | 744 PAS+GAF+PHY+Kinase                              | 264        |
| 192 | <i>Pseudomonas syringae</i> pv. <i>maculicola</i> str. ES4326      | P (Y) | F3HET6            | PMA4326_03304                                  | 739 PAS+GAF+PHY+Kinase                              | 265        |
| 193 | <i>Pseudomonas syringae</i> pv. <i>mori</i> str. 301020            | P (Y) | F3EV10            | PSYMO_09914                                    | 531 PAS+GAF+PHY                                     | 266        |
| 194 | <i>Pseudomonas syringae</i> pv. <i>morsprunorum</i> str. M302280PT | P (Y) | F3DWD9<br>F3E2L2  | PSYMP_13059<br>PSYMP_24056                     | 673 PAS+GAF+PHY+Kinase<br>740 PAS+GAF+PHY+Kinase    | 267<br>268 |
| 195 | <i>Pseudomonas syringae</i> pv. <i>oryzae</i> str. 1_6             | P (Y) | F2Z147<br>F2ZMP6  | POR16_10111<br>POR16_18243                     | 577 GAF+PHY+Kinase<br>373 PAS+GAF                   | 269<br>270 |
| 196 | <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A          | P (Y) | Q48G81            | PSPPH_3446                                     | 745 PAS+GAF+PHY+Kinase                              | 271        |
| 197 | <i>Pseudomonas syringae</i> pv. <i>pisi</i> str. 1704B             | P (Y) | F3GHC7<br>F3GGR1  | PSYPI_30903<br>PSYPI_29724                     | 690 PAS+GAF+PHY+Kinase<br>909 PAS+GAF+PHY+2Kinase   | 272<br>273 |
| 198 | <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a              | P (Y) | Q4ZQN6<br>Q4ZTU8  | Psyr_3504<br>Psyr_2385                         | 745 PAS+GAF+PHY+Kinase<br>1003 PAS+GAF+PHY+2Kinase  | 274<br>275 |
| 199 | <i>Pseudomonas syringae</i> pv. <i>tabaci</i> ATCC 11528           | P (Y) | F3K5K8<br>F3JUV0  | PSYTB_22528<br>PSYTB_02804                     | 745 PAS+GAF+PHY+Kinase<br>998 PAS+GAF+PHY+2Kinase   | 276<br>277 |
| 200 | <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000               | P (Y) | Q885D3<br>Q882H5  | PSPTO_1902<br>PSPTO_2652                       | 745 PAS+GAF+PHY+Kinase<br>993 PAS+GAF+PHY+2Kinase   | 278<br>279 |

|     |                                                                |       |        |                   |      |                                                   |     |      |
|-----|----------------------------------------------------------------|-------|--------|-------------------|------|---------------------------------------------------|-----|------|
| 201 | <i>Pseudomonas syringae</i> pv. tomato T1                      | P (Y) | E2MD74 | PSPTOT1_0876      | 744  | PAS+GAF+PHY+Kinase                                | 280 |      |
|     |                                                                |       | E2MGQ1 | PSPTOT1_5204      | 998  | PAS+GAF+PHY+2Kinase                               | 281 |      |
| 202 | <i>Pseudoxanthomonas spadix</i> BD-a59                         | P (Y) | G7UVJ4 | DSC_02290         |      | PAS+GAF+PHY+PAS                                   | 282 |      |
| 203 | <i>Pseudoxanthomonas suwonensis</i> 11-1                       | P (Y) | E6WXH5 | Psesu_3018        | 631  | PAS+GAF+PHY                                       | 283 |      |
| 204 | <i>Salinisphaera shabanensis</i> E113A                         | P (Y) | F7Q4I6 | SSPSH_03007       | 649  | PAS+GAF+PHY+GGDEF                                 | 284 |      |
| 205 | <i>Shewanella denitrificans</i> OS217                          | P (Y) | Q12SQ8 | Sden_0221         | 710  | GAF+PHY+GGDEF+EAL                                 | 285 |      |
| 206 | <i>Stenotrophomonas maltophilia</i> K279a                      | P (Y) | B8LBD6 | SSKA14_2517       | 715  | PAS+GAF+PHY+Kinase                                | 286 |      |
|     |                                                                |       | B2FRG9 | Smlt2382          | 745  | PAS+GAF+PHY+Kinase                                | 287 |      |
| 207 | <i>Stenotrophomonas maltophilia</i> JV3                        | P (Y) | G0K0O9 | BurJV3_2024       | 745  | PAS+GAF+PHY+Kinase                                | 288 |      |
| 208 | <i>Stenotrophomonas</i> sp. SKA                                | P (Y) | B8LBD6 | DSC_02290         | 715  | GAF+PHY+Kinase                                    | 289 |      |
| 209 | <i>Thermochromatium tepidum</i>                                | P (Y) | E9M2C9 | ppD               | 1108 | PYP+PAS+GAF+PHY+GGDEF                             | 290 | Ppd  |
| 210 | <i>Thiocapsa marina</i> 5811                                   | P (Y) | F9U8K6 | ThimaDRAFT_1064   | 731  | PAS+GAF+PHY+PAS                                   | 291 |      |
| 211 | <i>Thiocystis violascens</i> DSM 198                           | P (Y) | I3YBF7 | ThiviDRAFT_0484   | 502  | PAS+GAF+PHY                                       | 292 |      |
|     |                                                                |       | I3YBD7 | ThiviDRAFT_0504   | 720  | PAS+GAF+PHY+PAS                                   | 293 |      |
|     |                                                                |       | I3YDQ8 | ThiviDRAFT_4045   | 524  | PAS+GAF                                           | 294 |      |
|     |                                                                |       | I3YGC8 | ThiviDRAFT_1693   | 1122 | PYP+PAS+GAF+PHY+GGDEF                             | 295 | Ppd  |
| 212 | <i>Thiorhodococcus dreswii</i> AZ1                             | P (Y) | G2E3H4 | ThidrDRAFT_2837   | 1287 | PAS+GAF+PHY+2PAS+Kinase+RR                        | 296 |      |
| 213 | <i>Thiorhodovibrio</i> sp. 970                                 | P (Y) | H8Z6X2 | Thi970DRAFT_03353 | 937  | PAS+GAF+PHY+Kinase+RR                             | 297 |      |
|     |                                                                |       | H8Z584 | Thi970DRAFT_04129 | 522  | PAS+GAF+PHY                                       | 298 |      |
|     |                                                                |       | H8Z583 | Thi970DRAFT_04128 | 1081 | PAS+GAF+PHY+Kinase+RR                             | 299 |      |
| 214 | <i>Xanthomonas albilineans</i> (strain GPE PC73)               | P (Y) | D2UGT7 | XALc_3119         | 636  | PAS+GAF+PHY+PAS                                   | 300 |      |
| 215 | <i>Xanthomonas axonopodis</i> pv. citri str.306                | P (Y) | Q8PEQ2 | aphB              | 634  | PAS+GAF+PHY+PAS                                   | 301 |      |
| 216 | <i>Xanthomonas axonopodis</i> pv. citrumelo F1                 | P (Y) | G2M0H7 | XACM_4165         | 634  | PAS+GAF+PHY+PAS                                   | 302 |      |
| 217 | <i>Xanthomonas axonopodis</i> pv. punicae str. LMG 859         | P (Y) | H1XJP7 | XAPC_3154         | 625  | PAS+GAF+PHY+PAS                                   | 303 |      |
| 218 | <i>Xanthomonas campestris</i> pv. campestris 8004              | P (Y) | Q4UNU4 | XC_4241           | 634  | PAS+GAF+PHY+PAS                                   | 304 |      |
| 219 | <i>Xanthomonas campestris</i> pv. campestris ATCC 33913        | P (Y) | Q8P3C2 | XCC4154           | 634  | PAS+GAF+PHY+PAS                                   | 305 |      |
| 220 | <i>Xanthomonas campestris</i> pv. campestris B100              | P (Y) | B0RZ52 | xcc-b100_4368     | 634  | PAS+GAF+PHY+PAS                                   | 306 |      |
| 221 | <i>Xanthomonas campestris</i> pv. raphani 756C                 | P (Y) | G0CAV9 | XCR_4489          | 634  | PAS+GAF+PHY+PAS                                   | 307 |      |
| 222 | <i>Xanthomonas campestris</i> pv. vesicatoria 85-10            | P (Y) | Q3BM90 | XCV4392           | 634  | PAS+GAF+PHY+PAS                                   | 308 |      |
| 223 | <i>Xanthomonas citri</i> pv. mangiferaeindicae LMG 94          | P (Y) | H8FJV4 | XMIN_3633         | 634  | PAS+GAF+PHY+PAS                                   | 309 |      |
| 224 | <i>Xanthomonas fuscans</i> subsp. aurantifolii str. ICPB 10535 | P (Y) | D4T663 | XAUC_18130        | 625  | PAS+GAF+PHY+PAS                                   | 310 |      |
| 225 | <i>Xanthomonas fuscans</i> subsp. aurantifolii str. ICPB 11122 | P (Y) | D4SUE0 | XAUB_17110        | 625  | PAS+GAF+PHY+PAS                                   | 311 |      |
| 226 | <i>Xanthomonas gardneri</i> ATCC 19865                         | P (Y) | F0C019 | XGA_0178          | 625  | PAS+GAF+PHY+PAS                                   | 312 |      |
| 227 | <i>Xanthomonas oryzae</i> pv. oryzae MAFF 311018               | P (Y) | Q2P8V8 | XOO0264           | 634  | PAS+GAF+PHY+PAS                                   | 313 |      |
| 228 | <i>Xanthomonas oryzae</i> pv. oryzae PXO99A                    | P (Y) | B2STV1 | PXO_03310         | 625  | PAS+GAF+PHY+PAS                                   | 314 |      |
| 229 | <i>Xanthomonas oryzae</i> pv. oryzicola BLS256                 | P (Y) | G7TJS3 | XOC_0228          | 634  | PAS+GAF+PHY+PAS                                   | 315 |      |
| 230 | <i>Xanthomonas perforans</i> 91-118                            | P (Y) | F0BT48 | XPE_2490          | 625  | PAS+GAF+PHY+PAS                                   | 316 |      |
| 231 | <i>Xanthomonas vesicatoria</i> ATCC 35937                      | P (Y) | F0BID9 | XVE_4041          | 625  | PAS+GAF+PHY+PAS                                   | 317 |      |
| 232 | <i>Corallococcus coralloides</i> DSM 2259                      | P (δ) | H8MLG4 | COCOR_00946       | 756  | PAS+GAF+PHY+Kinase                                | 318 |      |
| 233 | <i>Haliangium ochraceum</i> DSM 14365 / JCM 11303              | P (δ) | D0LR16 | Hoch_4724         | 774  | PAS+GAF+PHY+Kinase                                | 319 |      |
| 234 | <i>Stigmatella aurantiaca</i> DW4/3-1                          | P (δ) | E3FW41 | STAUR_7006        | 728  | PAS+GAF+PHY+Kinase                                | 320 |      |
|     |                                                                |       | Q09E27 | STIAU_8420        | 747  | PAS+GAF+PHY+Kinase                                | 321 |      |
|     |                                                                |       | Q097N3 | STAUR_8015        | 760  | PAS+GAF+PHY+Kinase                                | 322 |      |
| 235 | <i>OscilloCHLoris trichoides</i> DG-6                          | Ch1   | E11CD6 | OSCT_0987         | 765  | PAS+GAF+PHY+Kinase                                | 323 |      |
| 236 | <i>Acaryochloris marina</i> (strain MBIC 11017)                | Cya   | B0CLJ9 | AM1_5894          | 847  | PAS+GAF+PHY+Kinase+RR                             | 324 | bphP |
|     |                                                                |       | B0CDG5 | AM1_1870          | 1514 | GAF <sub>Ins</sub> +PHY+2GAF+Kinase+2RR           | 325 |      |
|     |                                                                |       | B0C6I8 | AM1_1378          | 665  | GAF <sub>Asp</sub> +MCP                           | 326 |      |
|     |                                                                |       | B0C524 | AM1_0048          | 810  | 2GAF <sub>Asp</sub>                               | 327 |      |
|     |                                                                |       | B0C2P1 | AM1_5997          | 1764 | 4C/Bsy+2GAF+PAS+GAF+GAF <sub>Asp</sub> +Kinase+RR | 328 |      |
|     |                                                                |       | B0C7F1 | AM1_6305          | 904  | GAF <sub>Asp</sub> +GAF+Kinase+RR                 | 329 |      |
|     |                                                                |       | B0BYI8 | AM1_0829          | 714  | GAF <sub>Asp</sub> +2PAS+Kinase                   | 330 |      |
|     |                                                                |       | B0CF10 | cikA              | 735  | GAF+Kinase+RR                                     | 331 |      |
| 237 | <i>Anabaena variabilis</i> ATCC 29413/PCC 7937                 | Cya   | Q3M6C9 | Ava_3852          | 765  | PAS+GAF+PHY+Kinase                                | 332 |      |
|     |                                                                |       | Q3MEF9 | Ava_1003          | 751  | PAS+GAF+PHY+Kinase                                | 333 |      |
|     |                                                                |       | Q3M570 | Ava_4267          | 920  | GAF+PHY+GAF+Kinase                                | 334 |      |
|     |                                                                |       | Q3M4Z3 | Ava_4345          | 890  | GAF+2PAS+GAF <sub>Asp</sub> +Kinase               | 335 |      |

cikA

|     |                                      |     |        |                   |                                                                    |     |      |  |
|-----|--------------------------------------|-----|--------|-------------------|--------------------------------------------------------------------|-----|------|--|
| 238 | <i>Arthrospira maxima</i> CS-328     | Cya | Q3M8S2 | Ava_3004          | 941 GAF+3PAS+GAF <sub>Asp</sub> +Kinase                            | 336 |      |  |
|     |                                      |     | Q3M6K3 | Ava_3778          | 1100 GAF+3GAF <sub>Asp</sub> +Hamp+MCP                             | 337 |      |  |
|     |                                      |     | Q3MEY4 | Ava_0828          | 734 EAL+GAF <sub>Asp</sub> +GGDEF                                  | 338 |      |  |
|     |                                      |     | Q3MH46 | Ava_0064          | 1714 RR+GAF <sub>Asp</sub> +9PAS+Kinase                            | 339 |      |  |
|     |                                      |     | Q3M734 | Ava_3596          | 2017 S/T_Kinase+GAF+GAF <sub>Asp</sub> +Kinase                     | 340 |      |  |
|     |                                      |     | Q3M874 | Ava_3204          | 179 Short-GAF <sub>Asp</sub>                                       | 341 |      |  |
|     |                                      |     | Q3MFU1 | Ava_0521          | 1072 3GAF+GAF <sub>Asp</sub> +Kinase                               | 342 |      |  |
|     |                                      |     | Q3M3Y8 | Ava_4701          | 1274 4C/Bsy+GAF <sub>Asp</sub> +PAS+GAF <sub>Asp</sub> +Kinase+RR  | 343 |      |  |
|     |                                      |     | Q3MA47 | Ava_2524          | 751 PAS+GAF <sub>Asp</sub> +GAF+Kinase                             | 344 |      |  |
|     |                                      |     | Q3MDV2 | Ava_1210          | 1036 GAF+GAF <sub>Ins</sub> +2GAF+Kinase                           | 345 |      |  |
| 239 | <i>Arthrospira platensis</i> NIES-39 | Cya | B5W221 | AmaxDRAFT_2819    | 1019 PAS+GAF+PHY+Kinase+RR                                         | 346 |      |  |
|     |                                      |     | B5VU87 | AmaxDRAFT_0128    | 1769 4C/Bsy+GAF <sub>Asp</sub> +5PAS+GAF <sub>Asp</sub> +Kinase+RR | 347 |      |  |
|     |                                      |     | B5W263 | AmaxDRAFT_2858    | 1487 PAS+GAF+2PAS+GAF+2PAS+GAF <sub>Asp</sub> +Kinase              | 348 |      |  |
|     |                                      |     | B5W9P3 | AmaxDRAFT_5493    | 1778 4C/Bsy+GAF <sub>Asp</sub> +4PAS+GAF+PAS+Kinase+RR             | 349 |      |  |
|     |                                      |     | B5W0L0 | AmaxDRAFT_2304    | 179 Short-GAF <sub>Asp</sub>                                       | 350 |      |  |
|     |                                      |     | B5W0Z7 | AmaxDRAFT_2437    | 104 Short-GAF <sub>Asp</sub>                                       | 351 |      |  |
|     |                                      |     | B5W0E3 | AmaxDRAFT_2237    | 1380 4C/Bsy+GAF <sub>Asp</sub> +4PAS+GAF <sub>Asp</sub> +GGDEF     | 352 |      |  |
|     |                                      |     | B5VW22 | AmaxDRAFT_0714    | 790 4C/Bsy+GAF <sub>Asp</sub> +Kinase                              | 353 |      |  |
|     |                                      |     | D5A3R8 | NIES39_C03450     | 770 GAF+PHY+Kinase                                                 | 354 |      |  |
|     |                                      |     | D4ZN51 | NIES39_D04330     | 1778 4C/Bsy+GAF <sub>Asp</sub> +5PAS+GAF+PAS+Kinase+RR             | 355 |      |  |
| 240 | <i>Arthrospira</i> sp. PCC 8005      | Cya | D4ZS74 | NIES39_E04120     | 1487 PAS+GAF+2PAS+GAF+2PAS+GAF <sub>Asp</sub> +Kinase              | 356 |      |  |
|     |                                      |     | D5A2W9 | NIES39_M02490     | 147 Short-GAF <sub>Asp</sub>                                       | 357 |      |  |
|     |                                      |     | D4ZR22 | NIES39_E01230     | 1384 4C/Bsy+GAF <sub>Asp</sub> +4PAS+GAF <sub>Asp</sub> +GGDEF     | 358 |      |  |
|     |                                      |     | D4ZUI1 | NIES39_J03990     | 1009 GAF+GAF <sub>Ins</sub> +Kinase+RR                             | 359 |      |  |
|     |                                      |     | D5A285 | NIES39_C00690     | 1062 2PAS+GAF <sub>Ins</sub> +Kinase+RR                            | 360 |      |  |
|     |                                      |     | H1WK68 | ARTHRO_740026     | 1019 PAS+GAF+PHY+Kinase+RR                                         | 361 |      |  |
|     |                                      |     | H1WBT6 | ARTHRO_1530024    | 767 GAF+PHY+Kinase                                                 | 362 |      |  |
|     |                                      |     | H1WLN2 | ARTHRO_840086     | 1769 4C/Bsy+GAF <sub>Asp</sub> +5PAS+GAF+Kinase+RR                 | 363 |      |  |
|     |                                      |     | H1W7R7 | ARTHRO_1160013    | 1487 PAS+GAF+2PAS+GAF+2PAS+GAF <sub>Asp</sub> +Kinase              | 364 |      |  |
|     |                                      |     | H1W6M5 | ARTHRO_1050008    | 1778 4C/Bsy+GAF <sub>Asp</sub> +5PAS+GAF+PAS+Kinase+RR             | 365 |      |  |
| 241 | <i>Crocospaera watsonii</i> WH 0003  | Cya | H1WA55 | ARTHRO_1430037    | 179 Short-GAF <sub>Asp</sub>                                       | 366 |      |  |
|     |                                      |     | H1WEQ8 | ARTHRO_300026     | 104 Short-GAF <sub>Asp</sub>                                       | 367 |      |  |
|     |                                      |     | H1WHX4 | ARTHRO_580008     | 1068 5PAS+GAF <sub>Asp</sub> +GGDEF                                | 368 |      |  |
|     |                                      |     | H1WLZ1 | ARTHRO_870005     | 1380 4C/Bsy+GAF <sub>Asp</sub> +4PAS+GAF+GGDEF                     | 369 |      |  |
|     |                                      |     | H1W9I0 | ARTHRO_1400062    | 578 GAF <sub>Asp</sub> +3PAS                                       | 370 |      |  |
|     |                                      |     | G5J7P5 | CWATWH0003_3481   | 760 PAS+GAF+PHY+Kinase                                             | 371 |      |  |
|     |                                      |     | G5JC40 | CWATWH0003_5001   | 916 GAF+PHY+Kinase+RR                                              | 372 |      |  |
|     |                                      |     | G5IY48 | CWATWH0003_0203   | 730 GAF <sub>Asp</sub> +Kinase+RR                                  | 373 |      |  |
|     |                                      |     | G5J3L5 | CWATWH0003_2091   | 1147 Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                         | 374 |      |  |
|     |                                      |     | G5J3L2 | CWATWH0003_2088   | 1131 Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                         | 375 |      |  |
| 242 | <i>Crocospaera watsonii</i> WH 8501  | Cya | G5J234 | CWATWH0003_1568a6 | 949 2GAF+GAF+GAF <sub>Asp</sub> +GAF                               | 376 |      |  |
|     |                                      |     | Q4C9H5 | CwatDRAFT_6440    | 422 PAS+GAF+PHY                                                    | 377 |      |  |
|     |                                      |     | Q4C1B2 | CwatDRAFT_2808    | 593 GAF+PHY+Kinase                                                 | 378 |      |  |
|     |                                      |     | Q4CAI6 | CwatDRAFT_6130    | 758 GAF <sub>Asp</sub> +Kinase+RR                                  | 379 |      |  |
|     |                                      |     | Q4C6M7 | CwatDRAFT_5100    | 1249 3GAF+GAF <sub>Asp</sub> +GAF+PAS+Kinase                       | 380 |      |  |
|     |                                      |     | Q4BZ88 | CwatDRAFT_2358    | 289 GAF+GAF <sub>Ins</sub>                                         | 381 |      |  |
|     |                                      |     | B1X1A4 | cce_1983          | 760 PAS+GAF+PHY+Kinase                                             | 382 | aphA |  |
|     |                                      |     | B1X1N1 | cce_3713          | 752 PAS+GAF+PHY+Kinase                                             | 383 |      |  |
|     |                                      |     | B1WRV0 | cce_4193          | 1146 Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                         | 384 |      |  |
|     |                                      |     | B1WRU8 | cce_4191          | 1081 Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                         | 385 |      |  |
| 243 | <i>Cyanothecce</i> sp. ATCC 51142    | Cya | B1WX33 | cce_4751          | 765 GAF <sub>Asp</sub> +Kinase+RR                                  | 386 |      |  |
|     |                                      |     | B1WWN9 | cce_1413          | 1317 GAF+GAF+GAF+GAF <sub>Asp</sub> +GAF+PAS+Kinase                | 387 |      |  |
|     |                                      |     | B1WSQ8 | cce_4289          | 864 GAF <sub>Ins</sub> +Kinase+RR                                  | 388 |      |  |
|     |                                      |     | B1WRU8 | cce_4191          | 1081 Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                         | 389 |      |  |
|     |                                      |     |        |                   |                                                                    |     |      |  |
|     |                                      |     |        |                   |                                                                    |     |      |  |
|     |                                      |     |        |                   |                                                                    |     |      |  |



|     |                                            |        |               |                  |                                                           |                                                                |     |              |
|-----|--------------------------------------------|--------|---------------|------------------|-----------------------------------------------------------|----------------------------------------------------------------|-----|--------------|
|     |                                            | E0UKI3 | Cyan7822_5181 | 729              | 4C/Bsy+PAS+GAF <sub>Asp</sub> +GGDEF                      | 444                                                            |     |              |
|     |                                            | E0U979 | Cyan7822_5462 | 944              | GAF <sub>Asp</sub> +3PAS+GAF+GGDEF                        | 445                                                            |     |              |
|     |                                            | E0UEY6 | Cyan7822_1109 | 1016             | RR+GAF <sub>Asp</sub> +2PAS+Kinase+RR                     | 446                                                            |     |              |
|     |                                            | E0UGH4 | Cyan7822_0015 | 610              | GAF <sub>Asp</sub> +GAF+Kinase                            | 447                                                            |     |              |
|     |                                            | E0U7N0 | Cyan7822_2884 | 1751             | 2GAF+GAF+2GAF <sub>Asp</sub> +2GAF+Kinase                 | 448                                                            |     |              |
|     |                                            | E0U8V6 | Cyan7822_3015 | 217              | Short-GAF <sub>Asp</sub>                                  | 449                                                            |     |              |
|     |                                            | E0U715 | Cyan7822_5290 | 1305             | GAF <sub>Asp</sub> +GAF+GAF <sub>Asp</sub> +GAF+Kinase+RR | 450                                                            |     |              |
|     |                                            | E0U6T9 | Cyan7822_4053 | 1486             | 4C/Bsy+2PAS+GAF+PAS+GAF <sub>Asp</sub> +GAF+Kinase+RR     | 451                                                            |     |              |
|     |                                            | E0U9V2 | Cyan7822_3067 | 1613             | 4C/Bsy+GAF <sub>Asp</sub> +3PAS+GAF+Kinase+RR             | 452                                                            |     |              |
|     |                                            | E0UJZ1 | Cyan7822_2659 | 1107             | 2PAS+GAF+PAS+GAF <sub>Asp</sub> +Kinase                   | 453                                                            |     |              |
|     |                                            | E0U998 | Cyan7822_5482 | 762              | GAF <sub>Asp</sub> +Kinase+RR                             | 454                                                            |     |              |
|     |                                            | E0UDA7 | Cyan7822_2118 | 933              | GAF+2GAF <sub>Asp</sub> +Hamp+MCP                         | 455                                                            |     |              |
|     |                                            | E0UEU2 | Cyan7822_1063 | 1297             | GAF+GAF+GGDEF+EAL+GAF <sub>Asp</sub> +GGDEF               | 456                                                            |     |              |
|     |                                            | E0ULR0 | Cyan7822_6043 | 1490             | 2PAS+GAF <sub>Asp</sub> +6PAS+Kinase                      | 457                                                            |     |              |
|     |                                            | E0U7N0 | Cyan7822_2884 | 1751             | GAF+GAF+GAF+4GAF+GAF+Kinase+RR                            | 458                                                            |     |              |
|     |                                            | E0U715 | Cyan7822_5290 | 1305             | GAF <sub>Asp</sub> +GAF+2GAF+Kinase+RR                    | 459                                                            |     |              |
| 249 | Cyanothece sp. strain PCC 8801             | Cya    | B7K5Z0        | PCC8801_4111     | 760                                                       | PAS+GAF+PHY+Kinase                                             | 460 |              |
|     |                                            |        | B7JUJ6        | PCC8801_1484     | 1002                                                      | PAS+GAF+PHY+Kinase+RR                                          | 461 |              |
|     |                                            |        | B7JZA0        | PCC8801_3341     | 1142                                                      | Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                          | 462 |              |
|     |                                            |        | B7JZ98        | PCC8801_3339     | 1153                                                      | Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                          | 463 | Tsr or; CheD |
|     |                                            |        | B7K0E1        | PCC8801_3457     | 1070                                                      | 3PAS+GAF <sub>Asp</sub> +PAS+Kinase+RR                         | 464 |              |
|     |                                            |        | B7K4M3        | PCC8801_1431     | 625                                                       | 2PAS+GAF <sub>Asp</sub> +GGDEF                                 | 465 |              |
|     |                                            |        | B7JZ62        | PCC8801_3302     | 763                                                       | GAF <sub>Asp</sub> +Kinase+RR                                  | 466 |              |
|     |                                            |        | B7JWR5        | PCC8801_1716     | 1099                                                      | GAF+GAF+GAF+GAF <sub>Asp</sub> +GAF+Kinase                     | 467 |              |
|     |                                            |        | B7K5D0        | PCC8801_4017     | 1781                                                      | GAF+4GAF <sub>Ins</sub> +2GAF+Hamp+MCP                         | 468 |              |
| 250 | Cyanothece sp. strain PCC 8802             | Cya    | C7QSV0        | Cyan8802_4151    | 760                                                       | PAS+GAF+PHY+Kinase                                             | 469 |              |
|     |                                            |        | C7QRB8        | Cyan8802_1511    | 1002                                                      | PAS+GAF+PHY+Kinase+RR                                          | 470 |              |
|     |                                            |        | C7QRG6        | Cyan8802_2776    | 1142                                                      | Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                          | 471 | Tsr or; CheD |
|     |                                            |        | C7QRG8        | Cyan8802_2778    | 1153                                                      | Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                          | 472 |              |
|     |                                            |        | C7QQC6        | Cyan8802_2659    | 1070                                                      | 3PAS+GAF <sub>Asp</sub> +PAS+Kinase+RR                         | 473 |              |
|     |                                            |        | C7QR66        | Cyan8802_1457    | 624                                                       | 2PAS+GAF <sub>Asp</sub> +GGDEF                                 | 474 |              |
|     |                                            |        | C7QRK2        | Cyan8802_2814    | 763                                                       | GAF <sub>Asp</sub> +Kinase+RR                                  | 475 |              |
|     |                                            |        | C7QUM9        | Cyan8802_1740    | 1319                                                      | GAF+GAF+GAF+GAF <sub>Asp</sub> +GAF+Kinase                     | 476 |              |
|     |                                            |        | C7QRV9        | Cyan8802_4055    | 1781                                                      | GAF+4GAF <sub>Ins</sub> +2GAF+Hamp+MCP                         | 477 |              |
| 252 | Fischerella sp. JSC-11                     | Cya    | G6FNF0        | FJSC11DRAFT_0397 | 767                                                       | PAS+GAF+PHY+Kinase                                             | 478 |              |
|     |                                            |        | G6FME7        | FJSC11DRAFT_0044 | 882                                                       | GAF+PHY+PAS+Kinase                                             | 479 |              |
|     |                                            |        | G6FTH6        | FJSC11DRAFT_2173 | 971                                                       | RR+GAF+2PAS+GAF <sub>Asp</sub> +Kinase                         | 480 |              |
|     |                                            |        | G6FW32        | FJSC11DRAFT_3123 | 2072                                                      | Tpr+GAF+7PAS+GAF <sub>Asp</sub> +3PAS+Kinase                   | 481 |              |
|     |                                            |        | G6FU46        | FJSC11DRAFT_2393 | 949                                                       | Hamp+GAF <sub>Asp</sub> +Hamp+MCP                              | 482 |              |
|     |                                            |        | G6FMM5        | FJSC11DRAFT_0122 | 1113                                                      | GAF+2GAF+GAF <sub>Asp</sub> +Kinase                            | 483 |              |
|     |                                            |        | G6FUQ0        | FJSC11DRAFT_2597 | 609                                                       | GAF <sub>Asp</sub> +GAF+Kinase                                 | 484 |              |
|     |                                            |        | G6FZM8        | FJSC11DRAFT_4327 | 866                                                       | GAF+2PAS+GAF <sub>Asp</sub> +Kinase                            | 485 |              |
|     |                                            |        | G6FVX         | FJSC11DRAFT_3062 | 179                                                       | Short-GAF <sub>Asp</sub>                                       | 486 |              |
|     |                                            |        | G6FXB2        | FJSC11DRAFT_3511 | 695                                                       | GAF <sub>Asp</sub> +Kinase                                     | 487 |              |
|     |                                            |        | G6FNB4        | FJSC11DRAFT_0361 | 2264                                                      | RR+2PAS+GAF+PAS+GAF+PAS+GAF+3PAS+GAF <sub>Ins</sub> +Kinase+RR | 488 |              |
|     |                                            |        | G6FWD8        | FJSC11DRAFT_2997 | 904                                                       | GAF+GAF <sub>Gap</sub> +Hamp+MCP                               | 489 |              |
|     |                                            |        | G6FTY1        | FJSC11DRAFT_2328 | 957                                                       | 2GAF+GAF <sub>Asp</sub> +Kinase                                | 490 |              |
|     |                                            |        | A0YIE9        | L8106_05116      | 1627                                                      | 2GAF+3PAS+GAF <sub>Ins</sub> +Kinase+RR                        | 491 |              |
|     |                                            |        | G6FVT6        | FJSC11DRAFT_3027 | 755                                                       | PAS+GAF <sub>Cc</sub> +PHY+Kinase                              | 492 |              |
| 253 | Fremyella diplosiphon (Calothrix PCC 7601) | Cya    | Q47897        | rcaE             | 655                                                       | GAF+PAS+Kinase                                                 | 493 | rcaE         |
| 254 | Gloeobacter violaceus (strain PCC 7421)    | Cya    | Q7NFU2        | glr3432          | 566                                                       | PAS+GAF <sub>Asp</sub> +Kinase                                 | 494 |              |
| 255 | Lyngbya sp. (strain PCC 8106)              | Cya    | A0YWS9        | L8106_03574      | 766                                                       | PAS+GAF+PHY+Kinase                                             | 495 |              |
|     |                                            |        | A0YVG7        | L8106_21634      | 1016                                                      | PAS+GAF+PHY+Kinase+RR                                          | 496 |              |
|     |                                            |        | A0YPG3        | L8106_19136      | 925                                                       | GAF+PHY+GAF <sub>Asp</sub> +Kinase                             | 497 | PECF         |

|                                                                                                     |     |        |                 |      |                                                           |     |  |
|-----------------------------------------------------------------------------------------------------|-----|--------|-----------------|------|-----------------------------------------------------------|-----|--|
| 256 <i>Microcoleus chthonoplastes</i> PCC 7420<br>( <i>Coleofasciculus chthonoplastes</i> PCC 7420) | Cya | A0YLL7 | L8106_24810     | 872  | GAF+PHY+GGDEF+EAL                                         | 498 |  |
|                                                                                                     |     | A0YM29 | L8106_05940     | 1311 | 4GAF+GAF <sub>Asp</sub> +Hamp+MCP                         | 499 |  |
|                                                                                                     |     | A0YP49 | L8106_11362     | 1291 | 5GAF <sub>Asp</sub> +MCP                                  | 500 |  |
|                                                                                                     |     | A0YMU5 | L8106_16674     | 1260 | GAF+GAF+GGDEF+EAL+GAF <sub>Asp</sub> +GGDEF               | 501 |  |
|                                                                                                     |     | A0YSU9 | L8106_07656     | 1295 | GAF+GAF <sub>Asp</sub> +3GAF+MCP                          | 502 |  |
|                                                                                                     |     | A0YVN1 | L8106_03989     | 1252 | GAF <sub>Asp</sub> +5PAS+GAF+GGDEF                        | 503 |  |
|                                                                                                     |     | A0YM62 | L8106_06105     | 1008 | 2C/Bsy+GAF <sub>Asp</sub> +2GAF+Kinase                    | 504 |  |
|                                                                                                     |     | A0YVU5 | L8106_18442     | 767  | GAF+GAF <sub>Asp</sub> +GAF+GGDEF                         | 505 |  |
|                                                                                                     |     | A0YPG2 | L8106_19131     | 703  | 2GAF <sub>Asp</sub> +Kinase                               | 506 |  |
|                                                                                                     |     | A0YK20 | L8106_15590     | 182  | Short-GAF <sub>Asp</sub>                                  | 507 |  |
|                                                                                                     |     | A0YIR3 | L8106_01327     | 1111 | GAF+2GAF+GAF <sub>Asp</sub> +Kinase                       | 508 |  |
|                                                                                                     |     | A0YLT4 | L8106_25145     | 1225 | 3MHYT+2PAS+GAF <sub>Ina</sub> +Kinase+RR                  | 509 |  |
|                                                                                                     |     | A0YXJ8 | L8106_24225     | 1027 | GAF+GAF <sub>Ina</sub> +Kinase+RR                         | 510 |  |
|                                                                                                     |     | B4VQA8 | MC7420_6262     | 949  | GAF+PHY+GAF+Kinase                                        | 511 |  |
|                                                                                                     |     | B4VWL9 | MC7420_6742     | 1193 | Hamp+GAF+GAF <sub>Asp</sub> +Hamp+Kinase+MCP              | 512 |  |
|                                                                                                     |     | B4WL10 | MC7420_5151     | 1474 | Mase1+3PAS+GAF <sub>Asp</sub> +Kinase+RR                  | 513 |  |
|                                                                                                     |     | B4W0J6 | MC7420_930      | 1218 | 4C/Bsy+GAF <sub>Asp</sub> +2PAS+Kinase                    | 514 |  |
|                                                                                                     |     | B4W4U2 | MC7420_1550     | 1028 | Hamp+2GAF+GAF <sub>Asp</sub> +Hamp+MCP                    | 515 |  |
|                                                                                                     |     | B4VZC7 | MC7420_4951     | 1432 | 3PAS+GAF+GAF <sub>Asp</sub> +2GAF+Kinase                  | 516 |  |
|                                                                                                     |     | B4VR49 | MC7420_1519     | 929  | PAS+GAF <sub>Asp</sub> +PAS+Kinase                        | 517 |  |
|                                                                                                     |     | B4VIH4 | MC7420_7722     | 1946 | 4C/Bsy+2PAS+2GAF <sub>Asp</sub> +GAF+Kinase+2RR+Hpt       | 518 |  |
|                                                                                                     |     | B4W057 | MC7420_3507     | 1659 | 4GAF+GAF <sub>Asp</sub> +GAF+GAF+Hamp+MCP                 | 519 |  |
|                                                                                                     |     | B4W4M8 | MC7420_107      | 1321 | GAF <sub>Asp</sub> +GAF+GAF+GAF <sub>Asp</sub> +Kinase+RR | 520 |  |
|                                                                                                     |     | B4VJ82 | MC7420_7724     | 981  | PAS+GAF+GAF <sub>Ina</sub> +Kinase                        | 521 |  |
| 257 <i>Microcoleus vaginatus</i> FGP-2                                                              | Cya | B4VUR2 | MC7420_3869     | 1022 | GAF+GAF <sub>Ina</sub> +Kinase+RR                         | 522 |  |
|                                                                                                     |     | B4VJW5 | MC7420_3017     | 164  | Short-GAF <sub>Asp</sub>                                  | 523 |  |
|                                                                                                     |     | F5UNP4 | MicvaDRAFT_5199 | 1148 | PAS+GAF+PHY+3PAS+Kinase                                   | 524 |  |
|                                                                                                     |     | F5UHX6 | MicvaDRAFT_2674 | 1031 | PAS+GAF+PHY+Kinase+RR                                     | 525 |  |
|                                                                                                     |     | F5UKJ2 | MicvaDRAFT_0709 | 840  | PAS+GAF+PHY+Kinase                                        | 526 |  |
|                                                                                                     |     | F5UFR8 | MicvaDRAFT_1510 | 886  | GAF+PHY+GGDEF+EAL                                         | 527 |  |
|                                                                                                     |     | F5UKT2 | MicvaDRAFT_0811 | 1232 | GAF+PAS+GAF <sub>Asp</sub> +Kinase+RR                     | 528 |  |
|                                                                                                     |     | F5UMI9 | MicvaDRAFT_5021 | 2165 | RR+7PAS+GAF+2PAS+GAF <sub>Asp</sub> +Kinase+RR            | 529 |  |
|                                                                                                     |     | F5UMI7 | MicvaDRAFT_5019 | 1678 | RR+8PAS+GAF <sub>Asp</sub> +Kinase                        | 530 |  |
|                                                                                                     |     | F5UFU7 | MicvaDRAFT_3059 | 2626 | 4C/Bsy+GAF <sub>Asp</sub> +10PAS+2GAF+Kinase              | 531 |  |
|                                                                                                     |     | F5UEP6 | MicvaDRAFT_1123 | 699  | GAF+GAF <sub>Asp</sub> +Kinase                            | 532 |  |
|                                                                                                     |     | F5UH75 | MicvaDRAFT_5302 | 1317 | PAS+GAF+4PAS+GAF <sub>Asp</sub> +GGDEF                    | 533 |  |
|                                                                                                     |     | F5UEX9 | MicvaDRAFT_1208 | 1731 | RR+7PAS+GAF <sub>Asp</sub> +Kinase+RR                     | 534 |  |
|                                                                                                     |     | F5UIS2 | MicvaDRAFT_3534 | 1285 | GAF+GAF+GAF <sub>Asp</sub> +2GAF+Kinase                   | 535 |  |
|                                                                                                     |     | F5UC70 | MicvaDRAFT_4634 | 1519 | GAF <sub>Asp</sub> +6PAS+GAF+Kinase+RR                    | 536 |  |
|                                                                                                     |     | F5UDJ4 | MicvaDRAFT_1642 | 164  | Short-GAF <sub>Asp</sub>                                  | 537 |  |
|                                                                                                     |     | F5UE76 | MicvaDRAFT_1902 | 1001 | 2GAF+GAF <sub>Asp</sub> +Kinase                           | 538 |  |
|                                                                                                     |     | F5UJV8 | MicvaDRAFT_1100 | 730  | 2PAS+GAF <sub>Asp</sub> +GGDEF                            | 539 |  |
|                                                                                                     |     | F5UE98 | MicvaDRAFT_1929 | 538  | PAS+GAF <sub>Asp</sub> +GGDEF                             | 540 |  |
|                                                                                                     |     | F5UFV7 | MicvaDRAFT_3072 | 1376 | Hamp+2PAS+GAF <sub>Ina</sub> +Kinase+RR                   | 541 |  |
|                                                                                                     |     | F5UPG3 | MicvaDRAFT_2184 | 1566 | RR+PAS+GAF+3PAS+GAF <sub>Ina</sub> +Kinase+RR             | 542 |  |
| 258 <i>Microcystis aeruginosa</i> NIES-843                                                          | Cya | B0JT05 | MAE_12270       | 760  | PAS+GAF+PHY+Kinase                                        | 543 |  |
|                                                                                                     |     | B0JT90 | MAE_43710       | 731  | GAF <sub>Asp</sub> +Kinase+RR                             | 544 |  |
|                                                                                                     |     | B0JVN6 | MAE_48070       | 742  | PAS+GAF <sub>Asp</sub> +GAF+Kinase                        | 545 |  |
|                                                                                                     |     | A8YK54 | IPF_1271        | 768  | PAS+GAF+PHY+Kinase                                        | 546 |  |
| 259 <i>Microcystis aeruginosa</i> PCC 7806                                                          | Cya | A8YCR2 | IPF_2820        | 733  | GAF <sub>Asp</sub> +Kinase+RR                             | 547 |  |
|                                                                                                     |     | A8YF79 | IPF_5486        | 742  | PAS+GAF <sub>Asp</sub> +GAF+Kinase                        | 548 |  |
|                                                                                                     |     | F4XI50 | LYNGBM3L_00300  | 760  | PAS+GAF+PHY+Kinase                                        | 549 |  |
| 260 <i>Moorea producta</i> 3L                                                                       | Cya | F4XU05 | LYNGBM3L_35680  | 998  | Hamp+GAF <sub>Asp</sub> +Hamp+MCP                         | 550 |  |
|                                                                                                     |     | F4XN10 | LYNGBM3L_23250  | 1140 | Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP                     | 551 |  |

|     |                                                           |     |        |                |      |                                                           |     |  |
|-----|-----------------------------------------------------------|-----|--------|----------------|------|-----------------------------------------------------------|-----|--|
| 261 | <i>Nodularia spumigena</i> CCY9414                        | Cya | F4XU88 | LYNGBM3L_32080 | 1522 | GAF+5PAS+GAF+PAS+GAF <sub>Asp</sub> +Kinase               | 552 |  |
|     |                                                           |     | F4XZC1 | LYNGBM3L_56870 | 1783 | 4GAF+GAF <sub>Asp</sub> +2GAF+Hamp+MCP                    | 553 |  |
|     |                                                           |     | F4XWC2 | LYNGBM3L_43800 | 1034 | GAF+2GAF <sub>Inn</sub> +Hamp+MCP                         | 554 |  |
|     |                                                           |     | A0ZGM2 | N9414_03251    | 765  | PAS+GAF+PHY+Kinase                                        | 555 |  |
|     |                                                           |     | A0ZC04 | N9414_21791    | 752  | PAS+GAF+PHY+Kinase                                        | 556 |  |
|     |                                                           |     | A0ZC81 | N9414_00370    | 162  | Short-GAF                                                 | 557 |  |
|     |                                                           |     | A0ZEH0 | N9414_12803    | 922  | GAF+2GAF <sub>Gap</sub> +Hamp+MCP                         | 558 |  |
|     |                                                           |     | A0ZA61 | N9414_04500    | 1045 | 4C/Bsy+GAF <sub>Asp</sub> +2PAS+Kinase                    | 559 |  |
|     |                                                           |     | A0ZJ29 | N9414_08909    | 472  | PAS+GAF <sub>Asp</sub> +Kinase                            | 560 |  |
|     |                                                           |     | A0ZEQ4 | N9414_23678    | 850  | GAF <sub>Asp</sub> +2PAS+GAF <sub>Asp</sub> +Kinase       | 561 |  |
| 262 | <i>Nostoc azollae</i> (strain 0708)                       | Cya | A0ZGP9 | N9414_11002    | 1613 | GAF <sub>Asp</sub> +8PAS+GAF+GGDEF                        | 562 |  |
|     |                                                           |     | A0ZB66 | N9414_24173    | 1508 | GAF+CHASE+PAS+GAF+GAF <sub>Asp</sub> +Kinase+2RR          | 563 |  |
|     |                                                           |     | D7DZ23 | Aazo_5067      | 1002 | PAS+GAF+PHY+Kinase+RR                                     | 564 |  |
|     |                                                           |     | D7DYK6 | Aazo_0203      | 928  | GAF <sub>Asp</sub> +GAF+GAF+Kinase                        | 565 |  |
|     |                                                           |     | D7DYK6 | Aazo_0203      | 928  | GAF <sub>Asp</sub> +GAF+GAF+Kinase                        | 566 |  |
|     |                                                           |     | D7DYO3 | Aazo_0288.     | 884  | GAF <sub>Gap</sub> +3PAS+Kinase                           | 567 |  |
|     |                                                           |     | D7DW48 | Aazo_4225      | 1322 | RR+GAF+PAS+GAF+GAF <sub>Inn</sub> +Kinase+RR              | 568 |  |
|     |                                                           |     | B2J2D1 | Npun_F0020     | 768  | PAS+GAF+PHY+Kinase                                        | 569 |  |
|     |                                                           |     | B2J2J0 | Npun_R1759     | 706  | GAF+PHY+Kinase                                            | 570 |  |
|     |                                                           |     | B2J4E4 | Npun_R5313     | 910  | GAF+PHY+GAF <sub>Asp</sub> +Kinase                        | 571 |  |
| 263 | <i>Nostoc punctiforme</i> (strain ATCC 29133 / PCC 73102) | Cya | B2IZ18 | Npun_R4776     | 1102 | GAF+PHY+2GAF+Kinase                                       | 572 |  |
|     |                                                           |     | B2J3R7 | Npun_F1883     | 858  | GAF+3GAF <sub>Asp</sub>                                   | 573 |  |
|     |                                                           |     | B2IY35 | Npun_F6362     | 853  | GAF+2PAS+GAF <sub>Asp</sub> +Kinase                       | 574 |  |
|     |                                                           |     | B2IWI2 | Npun_R2903     | 1116 | RR+PAS+GAF+2PAS+GAF <sub>Asp</sub> +Kinase                | 575 |  |
|     |                                                           |     | B2IU14 | Npun_R6012.    | 1102 | GAF+3GAF <sub>Gap</sub> +Hamp+MCP                         | 576 |  |
|     |                                                           |     | B2J186 | Npun_F4973     | 178  | Short-GAF <sub>Asp</sub>                                  | 577 |  |
|     |                                                           |     | B2IVK2 | Npun_F2854     | 1060 | 2GAF+GAF <sub>Gap</sub> +GAF+Kinase                       | 578 |  |
|     |                                                           |     | B2J469 | Npun_F3797     | 750  | GAF <sub>Gap</sub> +2PAS+Kinase                           | 579 |  |
|     |                                                           |     | B2J261 | Npun_R5113     | 1005 | 3GAF <sub>Asp</sub> +GAF+Kinase                           | 580 |  |
|     |                                                           |     | B2IU03 | Npun_F6001     | 651  | 2PAS+GAF <sub>Asp</sub> +Kinase                           | 581 |  |
| 264 | <i>Nostoc sp.</i> (strain PCC 7120 / UTEX 2576)           | Cya | B2IVB0 | Npun_R1060     | 742  | EAL+GAF <sub>Asp</sub> +GGDEF                             | 582 |  |
|     |                                                           |     | B2J1W6 | Npun_R3572     | 1504 | RR+GAF <sub>Asp</sub> +5PAS+Kinase+RR                     | 583 |  |
|     |                                                           |     | B2JQA4 | Npun_AF142     | 1204 | 3GAF3+GAF <sub>Asp</sub> +Kinase                          | 584 |  |
|     |                                                           |     | B2J186 | Npun_F4973     | 178  | Short-GAF <sub>Asp</sub>                                  | 585 |  |
|     |                                                           |     | B2J0R5 | Npun_R1597     | 1042 | GAF <sub>Asp</sub> +GAF+2GAF+Kinase                       | 586 |  |
|     |                                                           |     | B2IVK2 | Npun_F2854     | 1060 | 3GAF+GAF <sub>Asp</sub> +Kinase                           | 587 |  |
|     |                                                           |     | B2J668 | Npun_F2164     | 1737 | GAF+GAF <sub>Inn</sub> +GAF+4GAF+Hamp+MCP                 | 588 |  |
|     |                                                           |     | B2J0R5 | Npun_R1597     | 1042 | GAF <sub>Asp</sub> +GAF+2GAF+Kinase                       | 589 |  |
|     |                                                           |     | B2IV55 | Npun_F1000     | 683  | GAF <sub>Asp</sub> +Kinase                                | 590 |  |
|     |                                                           |     | B2IWG3 | Npun_F1183     | 775  | PAS+GAF <sub>CC</sub> +PHY+Kinase                         | 591 |  |
| 265 | <i>Oscillatoria sp.</i> PCC 6506                          | Cya | Q9LCC2 | alr3157        | 765  | PAS+GAF+PHY+Kinase                                        | 592 |  |
|     |                                                           |     | Q9R6X3 | al12899        | 751  | PAS+GAF+PHY+Kinase                                        | 593 |  |
|     |                                                           |     | Q8YTL8 | al12699        | 920  | GAF+PHY+GAF+Kinase                                        | 594 |  |
|     |                                                           |     | Q8YXY7 | al11069        | 1102 | GAF+GAF <sub>Gap</sub> +2GAF+Hamp+Kinase                  | 595 |  |
|     |                                                           |     | Q8YVK9 | alr1966        | 879  | GAF+2PAS+GAF <sub>Asp</sub> +Kinase                       | 596 |  |
|     |                                                           |     | Q8YSG5 | alr3120        | 1286 | 4C/Bsy+GAF <sub>Asp</sub> +PAS+GAF <sub>Asp</sub> +Kinase | 597 |  |
|     |                                                           |     | Q8YQX0 | al13691        | 2021 | S/T_Kinase+Tpr+GAF+GAF <sub>Asp</sub> +Kinase             | 598 |  |
|     |                                                           |     | Q8YU02 | al12239        | 1707 | RR+GAF <sub>Asp</sub> +8PAS+Kinase                        | 599 |  |
|     |                                                           |     | Q8YUQ6 | alr2279        | 1299 | 2HNOBA+2PAS+GAF <sub>Asp</sub> +Kinase+2RR+Hpt            | 600 |  |
|     |                                                           |     | Q8YRT7 | alr3356        | 179  | Short-GAF <sub>Asp</sub>                                  | 601 |  |

|     |                                                |        |              |                  |                                                       |                                                   |      |       |
|-----|------------------------------------------------|--------|--------------|------------------|-------------------------------------------------------|---------------------------------------------------|------|-------|
|     |                                                | D8G237 | OSCI_3130004 | 1017             | PAS+GAF+PHY+Kinase+RR                                 | 606                                               |      |       |
|     |                                                | D8FWG8 | OSCI_1020014 | 870              | GAF+PHY+GGDEF+EAL                                     | 607                                               |      |       |
|     |                                                | D8G6R0 | OSCI_3720019 | 1265             | GAF+PHY+GAF+2PAS+GAF+GGDEF                            | 608                                               |      |       |
|     |                                                | D8G3W0 | OSCI_3400003 | 1174             | GAF <sub>Asp</sub> +PAS+GAF <sub>Asp</sub> +Kinase+RR | 609                                               |      |       |
|     |                                                | D8G2H0 | OSCI_3180052 | 559              | 2RR+GAF <sub>Asp</sub> +GGDEF                         | 610                                               |      |       |
|     |                                                | D8FVN0 | OSCI_860033  | 666              | 2PAS+GAF <sub>Asp</sub> +GGDEF                        | 611                                               |      |       |
|     |                                                | D8G1M5 | OSCI_3040016 | 716              | GAF+GAF <sub>Asp</sub> +Kinase                        | 612                                               |      |       |
|     |                                                | D8G1S2 | OSCI_3060042 | 1199             | 2RR+GAF+GAF <sub>Asp</sub> +Kinase+RR                 | 613                                               |      |       |
|     |                                                | D8FX76 | OSCI_1410007 | 1629             | PAS+GAF <sub>Asp</sub> +4PAS+GAF+PAS+Kinase           | 614                                               |      |       |
|     |                                                | D8FY13 | OSCI_1600053 | 1693             | RR+3PAS+GAF+4PAS+GAF <sub>Asp</sub> +Kinase           | 615                                               |      |       |
|     |                                                | D8FY11 | OSCI_1600051 | 1581             | RR+2PAS+GAF+4PAS+GAF <sub>Asp</sub> +Kinase+RR        | 616                                               |      |       |
|     |                                                | D8G946 | OSCI_4030009 | 1504             | RR+GAF <sub>Asp</sub> +5PAS+Kinase+RR                 | 617                                               |      |       |
|     |                                                | D8FU12 | OSCI_310004  | 164              | Short-GAF <sub>Asp</sub>                              | 618                                               |      |       |
|     |                                                | D8G2H6 | OSCI_3190006 | 999              | 2GAF+GAF <sub>Asp</sub> +Kinase                       | 619                                               | ENCF |       |
|     |                                                | D8G2H0 | OSCI_3180052 | 559              | 2RR+GAF <sub>Ins</sub> +GGDEF                         | 620                                               |      |       |
|     |                                                | D8G3X0 | OSCI_3400013 | 1231             | 2GAF+GAF <sub>Ins</sub> +Kinase+RR                    | 621                                               |      |       |
| 266 | Planktothrix rubescens NIVA-CYA 18             | Cya    | Q9RF27       | cphA2            | 142                                                   | Short-GAF                                         | 622  |       |
| 267 | Synechococcus elongatus PCC 7942               | Cya    | Q31PY1       | Synpcc7942_0858  | 1406                                                  | Hamp+5GAF <sub>Asp</sub> +Hamp+MCP                | 623  | pixJ1 |
|     |                                                |        | Q31K55       | Synpcc7942_2534  | 421                                                   | GAF <sub>Asp</sub> +GGDEF                         | 624  |       |
|     |                                                |        | Q9KH15       | cikA             | 754                                                   | GAF+Kinase+RR                                     | 625  | cikA  |
| 268 | Synechococcus sp. ATCC 27264 / PCC 7002 / PR-6 | Cya    | B1XKU6       | SYNPCC7002_A0048 | 1490                                                  | 5GAF+GAF <sub>Asp</sub> +Hamp+MCP                 | 626  |       |
|     |                                                |        | B1XIW2       | SYNPCC7002_A0900 | 760                                                   | GAF <sub>Asp</sub> +Kinase+RR                     | 627  |       |
|     |                                                |        | P32039       | SYNPCC7002_A0852 | 162                                                   | Short-GAF <sub>Asp</sub>                          | 628  |       |
|     |                                                |        | B1XQF2       | SYNPCC7002_A0689 | 774                                                   | RR+GAF <sub>Ins</sub> +Kinase+RR                  | 629  |       |
| 269 | Synechococcus sp. JA-3-3Ab                     | Cya    | Q2JR82       | CYA_2779         | 835                                                   | GAF+PHY+GAF+Kinase                                | 630  |       |
|     |                                                |        | Q2JRS4       | CYA_2553         | 1151                                                  | 4PAS+GAF <sub>Asp</sub> +GAF+Kinase               | 631  |       |
|     |                                                |        | Q2JR31       | CYA_2836         | 1523                                                  | GAF+CHASE+2PAS+GAF <sub>Asp</sub> +Kinase+2RR+Hpt | 632  |       |
|     |                                                |        | Q2JXK5       | CYA_0253         | 1036                                                  | 2PAS+GAF <sub>Asp</sub> +GAF+Kinase               | 633  |       |
| 270 | Synechococcus sp. JA-2-3B'a (2-13)             | Cya    | Q2JI25       | CYB_2465         | 834                                                   | GAF+PHY+GAF+Kinase                                | 634  |       |
|     |                                                |        | Q2JP01       | CYB_0507         | 1526                                                  | GAF+CHASE+2PAS+GAF <sub>Asp</sub> +Kinase+2RR+Hpt | 635  |       |
|     |                                                |        | Q2JKQ1       | CYB_1773         | 1247                                                  | 4PAS+GAF <sub>Asp</sub> +GAF+Kinase               | 636  |       |
| 271 | Synechococcus sp. PCC 6301                     | Cya    | Q5N497       | syc0682_c        | 1406                                                  | Hamp+5GAF <sub>Asp</sub> +Hamp+MCP                | 637  | pixJ1 |
|     |                                                |        | Q5N1Q4       | syc1576_d        | 438                                                   | GAF <sub>Asp</sub> +GGDEF                         | 638  |       |
|     |                                                |        | Q5N3P8       | cikA             | 754                                                   | GAF+Kinase+RR                                     | 639  | cikA  |
| 272 | Synechococcus sp. PCC 7335                     | Cya    | B4WKH0       | S7335_4337       | 775                                                   | PAS+GAF+PHY+Kinase                                | 640  |       |
|     |                                                |        | B4WLJ5       | S7335_3716       | 1070                                                  | PAS+GAF+PHY+Kinase+RR                             | 641  |       |
|     |                                                |        | B4WP27       | S7335_1346       | 858                                                   | GAF+PHY+PAS+Kinase                                | 642  |       |
|     |                                                |        | B4WJU8       | S7335_2562       | 1232                                                  | Hamp+GAF+GAF <sub>Asp</sub> +Hamp+MCP             | 643  |       |
|     |                                                |        | B4WKG8       | S7335_1579       | 601                                                   | RR+GAF <sub>Asp</sub> +Kinase                     | 644  |       |
|     |                                                |        | B4WTP2       | S7335_394        | 708                                                   | GAF <sub>Asp</sub> +2PAS+Kinase                   | 645  |       |
|     |                                                |        | B4WTB3       | S7335_286        | 1097                                                  | RR+2PAS+GAF <sub>Asp</sub> +2PAS+Kinase           | 646  |       |
|     |                                                |        | B4WMF2       | S7335_4945       | 814                                                   | RR+PAS+GAF <sub>Asp</sub> +PAS+Kinase             | 647  |       |
|     |                                                |        | B4WLJ7       | S7335_4864       | 1052                                                  | 3GAF+GAF <sub>Asp</sub> +Kinase                   | 648  |       |
|     |                                                |        | B4WTM3       | S7335_249        | 831                                                   | 2PAS+GAF <sub>Asp</sub> +Kinase                   | 649  |       |
|     |                                                |        | B4WTQ0       | S7335_348        | 495                                                   | GAF <sub>Ins</sub> +Kinase                        | 650  |       |
| 273 | Synechocystis sp. PCC 6803 substr. GT-I        | Cya    | H0P166       | SYNGTI_2823      | 1000                                                  | GAF+GAF <sub>Asp</sub> +Hamp+MCP                  | 651  | pixJ1 |
|     |                                                |        | H0P008       | SYNGTI_2573      | 1276                                                  | GAF+GAF+GGDEF+EAL+GAF <sub>Asp</sub> +GGDEF       | 652  | cph2  |
|     |                                                |        | H0P3M2       | SYNGTI_0820      | 844                                                   | 2PAS+GAF <sub>Asp</sub> +Kinase                   | 653  | ETR1  |
|     |                                                |        | H0P2N8       | SYNGTI_3025      | 753                                                   | GAF <sub>Gsp</sub> +2PAS+Kinase                   | 654  | CcaS  |
|     |                                                |        | H0P5X4       | slr1969          | 750                                                   | GAF+Kinase+RR                                     | 655  | CikA  |
| 273 | Synechocystis sp. PCC 6803 / GT-S              | Cya    | F7USI0       | SYNGTS_2344      | 748                                                   | PAS+GAF+PHY+Kinase                                | 656  | cph1  |
|     |                                                |        | F7UKS4       | SYNGTS_2824      | 1000                                                  | GAF+GAF <sub>Asp</sub> +Hamp+MCP                  | 657  | pixJ1 |
|     |                                                |        | F7UTN7       | SYNGTS_2574      | 1276                                                  | GAF+PHY+GGDEF+EAL+GAF <sub>Asp</sub> +GGDEF       | 658  | cph2  |
|     |                                                |        | F7UN56       | SYNGTS_0820      | 844                                                   | 2PAS+GAF <sub>Asp</sub> +Kinase                   | 659  | ETR1  |

|     |                                                            |         |             |                  |                                 |                                                      |      |        |      |
|-----|------------------------------------------------------------|---------|-------------|------------------|---------------------------------|------------------------------------------------------|------|--------|------|
|     |                                                            | F7ULT7  | SYNGTS_3026 | 753              | GAF <sub>Gap</sub> +2PAS+Kinase | 660                                                  | CcaS |        |      |
|     |                                                            | F7UQF8  | slr1969     | 750              | GAF+Kinase+RR                   | 661                                                  | CikA | CikA   |      |
| 274 | <i>Synechocystis</i> sp. PCC 6803 / Kazusa                 | Cya     | Q55168      | slr0473          | 748                             | PAS+GAF+PHY+Kinase                                   | 662  | cph1   |      |
|     |                                                            |         | Q55445      | sl10041          | 1000                            | GAF+GAF <sub>Asp</sub> +Hamp+MCP                     | 663  | pixJ1  |      |
|     |                                                            |         | Q55434      | SYNGTS_2574      | 1276                            | GAF+GAF+GGDEF+EAL+GAF <sub>Asp</sub> +GGDEF          | 664  | cph2   |      |
|     |                                                            |         | P74111      | cikA             | 750                             | GAF+Kinase+RR                                        | 665  | CikA   | CikA |
|     |                                                            |         | P74623      | Sl11473          | 481                             | GAF <sub>Gap</sub> +2PAS                             | 666  |        |      |
|     |                                                            |         | P73363      | slr1212          | 844                             | 2PAS+GAF <sub>Asp</sub> +Kinase                      | 667  | ETR1   |      |
| 275 | <i>Synechocystis</i> sp. PCC 6803 substr. PCC-N            | Cya     | H0PBC7      | SYNPCCN_2342     | 748                             | PAS+GAF+PHY+Kinase                                   | 668  | cph1   |      |
|     |                                                            |         | H0PDI1      | SYNPCCN_2822     | 1000                            | GAF+GAF <sub>Asp</sub> +Hamp+MCP                     | 669  | pixJ1  |      |
|     |                                                            |         | H0PCC3      | SYNPCCN_2572     | 1276                            | GAF+GAF+GGDEF+EAL+GAF <sub>Asp</sub> +GGDEF          | 670  | cph2   |      |
|     |                                                            |         | H0P9A6      | slr1969          | 750                             | GAF+Kinase+RR                                        | 671  | CikA   | CikA |
|     |                                                            |         | H0PF02      | SYNPCCN_3024     | 753                             | GAF <sub>Gap</sub> +2PAS+Kinase                      | 672  | CcaS   |      |
|     |                                                            |         | H0P704      | SYNPCCN_0819     | 844                             | 2PAS+GAF <sub>Asp</sub> +Kinase                      | 673  | ETR1   |      |
| 276 | <i>Synechocystis</i> sp. PCC 6803 substr. PCC-P            | Cya     | H0PGB0      | SYNPCCP_2342     | 748                             | PAS+GAF+PHY+Kinase                                   | 674  | cph1   |      |
|     |                                                            |         | H0PID6      | SYNPCCP_2822     | 1000                            | GAF+GAF <sub>Asp</sub> +Hamp+MCP                     | 675  |        |      |
|     |                                                            |         | H0PGZ0      | SYNPCCP_2572     | 1276                            | GAF+GAF+GGDEF+EAL+GAF <sub>Asp</sub> +GGDEF          | 676  | cph2   |      |
|     |                                                            |         | H0PJE7      | SYNPCCP_3024     | 753                             | GAF <sub>Gap</sub> +2PAS+Kinase                      | 677  | CcaS   |      |
|     |                                                            |         | H0PL06      | SYNPCCP_0819     | 844                             | 2PAS+GAF <sub>Asp</sub> +Kinase                      | 678  | ETR1   |      |
|     |                                                            |         | H0PNA8      | slr1969          | 750                             | GAF+Kinase+RR                                        | 679  | CikA   | CikA |
| 277 | <i>Thermosynechococcus elongatus</i> strain BP-1           | Cya     | Q8DLC7      | tl10569          | 940                             | Hamp+GAF <sub>Asp</sub> +Hamp+MCP                    | 680  | TePixj |      |
|     |                                                            |         | Q8DHG0      | tlr1999          | 790                             | RR+GAF <sub>Asp</sub> +GGDEF+EAL                     | 681  |        |      |
|     |                                                            |         | Q8DKE8      | tlr0911          | 1240                            | 4PAS+GAF <sub>Asp</sub> +PAS+GGDEF+EAL               | 682  |        |      |
|     |                                                            |         | Q8DKD5      | tlr0924          | 773                             | 4C/Bsy+PAS+GAF <sub>Asp</sub> +GGDEF                 | 683  |        |      |
| 278 | <i>Tolypothrix</i> sp. PCC 7601                            | Cya     | Q8RTN1      | cphA             | 767                             | PAS+GAF+PHY+Kinase                                   | 684  | cphA   |      |
|     |                                                            |         | Q8RTM9      | cphB             | 765                             | PAS+GAF+PHY+Kinase                                   | 685  | cphB   |      |
| 279 | <i>Trichodesmium erythraeum</i> strain IMS101              | Cya     | Q118C6      | Tery_0715        | 1313                            | GAF <sub>Asp</sub> +GAF+GAF <sub>Asp</sub> +2GAF+MCP | 686  |        |      |
| 280 | <i>Leptospirillum ferrodiazotrophum</i>                    | Nit     | C6HVI4      | UBAL3_79160030   | 501                             | PAS+GAF+PHY                                          | 687  |        |      |
| 281 | <i>Acidobacterium</i> sp. (strain MP5ACTX9)                | Acido   | E8X537      | Acix9_0155       | 565                             | PAS+GAF+PHY                                          | 688  |        |      |
| 282 | <i>Chitinophaga pinensis</i> ATCC 43595 / DSM 2588         | Bact/Ch | C7PF81      | Cpin_4127        | 743                             | PAS+GAF+PHY+Kinase                                   | 689  |        |      |
|     |                                                            |         | C7PU12      | Cpin_7207        | 508                             | PAS+GAF+PHY                                          | 690  |        |      |
| 283 | <i>Chryseobacterium gleum</i> ATCC 35910                   | Bact/Ch | D7W641      | HMPREF0204_12346 | 732                             | PAS+GAF+PHY+Kinase                                   | 691  |        |      |
| 284 | <i>Cytophaga hutchinsonii</i> ATCC 33406/NCIMB 9469        | Bact/Ch | Q11YS3      | CHU_0150         | 752                             | PAS+GAF+PHY+Kinase                                   | 692  |        |      |
| 285 | <i>Dokdonia donghaensis</i> MED134                         | Bact/Ch | A2TTK4      | MED134_02440     | 735                             | PAS+GAF+PHY+Kinase                                   | 693  |        |      |
| 286 | <i>Dyadobacter fermentans</i> ATCC 700827/DSM 18053        | Bact/Ch | C6W7C0      | Dfer_3185        | 762                             | PAS+GAF+PHY+Kinase                                   | 694  |        |      |
| 287 | <i>Flavobacteriaceae bacterium</i> (strain 3519-10)        | Bact/Ch | C6X273      | FIC_02099        | 729                             | PAS+GAF+PHY+Kinase                                   | 695  |        |      |
| 288 | <i>Flavobacterium johnsoniae</i> ATCC 17061/DSM 2064/UW101 | Bact/Ch | A5FCX0      | Fjoh_3936        | 757                             | PAS+GAF+PHY+Kinase                                   | 696  |        |      |
|     |                                                            |         | A5FD80      | Fjoh_3820        | 755                             | PAS+GAF+PHY+Kinase                                   | 697  |        |      |
| 289 | <i>Flavobacterium</i> sp. (strain MED217)                  | Bact/Ch | A3XMS7      | MED217_07101     | 737                             | PAS+GAF+PHY+Kinase                                   | 698  |        |      |
| 290 | <i>Gramella forsetii</i> KT0803                            | Bact/Ch | A0M2S9      | GFO_1959         | 737                             | PAS+GAF+PHY+Kinase                                   | 699  |        |      |
| 291 | <i>Kordia algicida</i> OT-1                                | Bact/Ch | A9EBJ4      | KAOT1_01090      | 753                             | PAS+GAF+PHY+Kinase                                   | 700  |        |      |
| 292 | <i>Krokinobacter</i> sp. 4H-3-7-5                          | Bact/Ch | F4AY80      | Krodi_0361       | 735                             | PAS+GAF+PHY+Kinase                                   | 701  |        |      |
| 293 | <i>Mucilaginibacter paludis</i> DSM 18603                  | Bact/Ch | H1Y750      | Mucpa_4580       | 500                             | PAS+GAF+PHY                                          | 702  |        |      |
| 294 | <i>Niastella koreensis</i> DSM 17620 / KACC 11465          | Bact/Ch | G8TRP9      | Niako_5967       | 509                             | PAS+GAF+PHY                                          | 703  |        |      |
| 295 | <i>Pedobacter heparinus</i> DSM 2366                       | Bact/Ch | C6XVN0      | Phep_3914        | 509                             | PAS+GAF+PHY                                          | 704  |        |      |
| 296 | <i>Pedobacter</i> sp. BAL39                                | Bact/Ch | A6EDC8      | PBAL39_25550     | 737                             | PAS+GAF+PHY+Kinase                                   | 705  |        |      |
|     |                                                            |         | A6EEB3      | PBAL39_20029     | 509                             | PAS+GAF+PHY                                          | 706  |        |      |
| 297 | <i>Pedobacter saltans</i> DSM 12145                        | Bact/Ch | F0S4K6      | Pedsa_1432       | 718                             | PAS+GAF+PHY+Kinase                                   | 707  |        |      |
| 298 | <i>Polaribacter</i> sp.MED152                              | Bact/Ch | A2TX11      | MED152_00100     | 862                             | PAS+GAF+PHY+Kinase+RR                                | 708  |        |      |
| 299 | <i>Sphingobacterium</i> sp. (strain 21)                    | Bact/Ch | F4CCB9      | Sph21_2157       | 500                             | PAS+GAF+PHY                                          | 709  |        |      |
| 300 | <i>Sphingobacterium spiritivorum</i> ATCC 33300            | Bact/Ch | C2G147      | HMPREF0765_3303  | 731                             | PAS+GAF+PHY+Kinase                                   | 710  |        |      |
|     |                                                            |         | C2FUW2      | HMPREF0765_1118  | 723                             | PAS+GAF+PHY+Kinase                                   | 711  |        |      |
| 301 | <i>Sphingobacterium spiritivorum</i> ATCC 33861            | Bact/Ch | D7VIF7      | HMPREF0766_10776 | 731                             | PAS+GAF+PHY+Kinase                                   | 712  |        |      |
|     |                                                            |         | D7VQ30      | HMPREF0766_13084 | 722                             | PAS+GAF+PHY+Kinase                                   | 713  |        |      |
| 302 | <i>Spirosoma linguale</i> ATCC 33905/DSM 74                | Bact/Ch | D2QE92      | Slin_0383        | 746                             | PAS+GAF+PHY+Kinase                                   | 714  |        |      |

| Accession | Strain                          | Host                 | Accession | Strain | Host          | Accession | Strain             | Host     |
|-----------|---------------------------------|----------------------|-----------|--------|---------------|-----------|--------------------|----------|
| 303       | <i>Zunongwangia profunda</i>    | DSM 18752            | Bact/Ch   | D5BC06 | ZPR_2281      | 745       | PAS+GAF+PHY+Kinase | 715      |
| 304       | <i>Deinococcus deserti</i>      | VCD115               | DeTh      | C1D3W9 | Deide_3p02370 | 768       | PAS+GAF+PHY+Kinase | 716      |
|           |                                 |                      |           | C1D2Z0 | Deide_2p01130 | 764       | PAS+GAF+PHY+Kinase | 717      |
| 305       | <i>Deinococcus gobiensis</i>    | I-0                  | DeTh      | H8GTR9 | DGo_CA1470    | 759       | PAS+GAF+PHY+Kinase | 718      |
| 306       | <i>Deinococcus maricopensis</i> | DSM 21211            | DeTh      | E8U3T3 | Deima_3148    | 756       | PAS+GAF+PHY+Kinase | 719      |
| 307       | <i>Deinococcus radiodurans</i>  | ATCC 13939/DSM 20539 | DeTh      | Q9R2A4 | DR_A0050      | 755       | PAS+GAF+PHY+Kinase | 720 bphP |

**Color codes**

BphP-like GAF

Cph1-like GAF (Cys259)

Gapped bilin-GAF, Cys259

DXCF GAF-two cysteine (variations of the motifs are indicated)

β3-α3 Cys insert, two cysteine

TP1 (trichromatic phytochrome) CysCys motif