

Supplementary Table 1: Light, Oxygen, Voltage (LOV) domain-containing proteins<sup>§</sup>

**Bacteria:  $\alpha$ -Proteobacteria**

| Species  | ssu Tree-ID              | Accession Number of LOV protein      | LOV protein Tree-ID                          | LOV protein domain content <sup>†</sup>           |
|--|--------------------------|--------------------------------------|--|---|
| <i>Rhodobacter sphaeroides</i> 2.4.1                               | Alpha1                   | Q3J4A0                               | Alpha1                                       | LOV   |
| <i>Dinoroseobacter shibae</i> DFL 12                               | (1)<br>(2)<br>(3)        | A0VR44<br>A0VVI8                     | Alpha2_1<br>Alpha2_2<br>Alpha2_3             | LOV+Kinase<br>LOV+PAS+PAS+Kinase+RR<br>LOV        |
| <i>Fulvimarina pelagi</i> HTCC2506                                 | Alpha3                   | Q0G496                               | Alpha3                                       | LOV+Kinase  |
| <i>Aurantimonas</i> sp. SI85-9A1                                   | (1)<br>(2)               | Q1YFS4<br>Q1YEU2                     | Alpha4_1<br>Alpha4_2                         | LOV+Kinase<br>LOV+Kinase                          |
| <i>Oceanicola granulosa</i> HTCC2516                               | Alpha5                   | Q2CIF5                               | Alpha5                                       | LOV+Kinase  |
| <i>Roseobacter denitrificans</i> OCh 114                           | Alpha6                   | Q167W8                               | Alpha6                                       | LOV+Kinase  |
| <i>Parvularcula bermudensis</i> HTCC2503                           | (1)<br>(2)               | A3VPU8<br>A3VTS2                     | Alpha7_1<br>Alpha7_2                         | LOV+Kinase<br>LOV+Kinase                          |
| <i>Erythrobacter litoralis</i> HTCC2594                            | (1)<br>(2)<br>(3)<br>(4) | Q2NB98<br>Q2NB77<br>Q2N9L9<br>Q2NCA3 | Alpha8_1<br>Alpha8_2<br>Alpha8_3<br>Alpha8_4 | LOV+HTH<br>LOV+Kinase<br>LOV+Kinase<br>LOV+Kinase |
| <i>Novosphingobium aromaticivorans</i> DSM12444                    | (1)<br>(2)               | Q2G5U0<br>Q2G8Z7                     | Alpha9_1<br>Alpha9_2                         | LOV+Kinase<br>LOV+HTH                             |
| <i>Brucella melitensis</i> 16M                                     | Alpha10                  | Q8YC53                               | Alpha10                                      | LOV+PAS+Kinase                                    |
| <i>Brucella abortus biovar 1</i> str. 9-941                        | Alpha11                  | Q577Y7                               | Alpha11                                      | LOV+PAS+Kinase                                    |
| <i>Brucella suis</i>   | Alpha12                  | Q8FW73                               | Alpha12                                      | LOV+PAS+Kinase                                    |
| <i>Caulobacter crescentus</i> CB15                                 | Alpha13                  | Q9ABE3                               | Alpha13                                      | LOV+Kinase  |
| <i>Caulobacter</i> sp. K31   | (1)<br>(2)               | Q0LTE1<br>Q0M3Z0                     | Alpha14_1<br>Alpha14_2                       | LOV+Kinase<br>LOV+Kinase                          |
| <i>Magnetospirillum magnetotacticum</i> MS-1                       | (1)<br>(2)               | ZP_00051334<br>ZP_00052303           | Alpha15_1<br>Alpha15_2                       | LOV+Kinase<br>LOV+Kinase                          |
| <i>Sphingopyxis alaskensis</i> RB2256                              | Alpha16                  | Q1GUF5                               | Alpha16                                      | LOV+HTH   |
| <i>Sphingomonas</i> sp. SKA58                                      | (1)<br>(2)               | Q1N7J1<br>Q1NI33                     | Alpha17_1<br>Alpha17_2                       | LOV+HTH<br>LOV+LOV+Kinase+RR                      |
| <i>Bradyrhizobium</i> sp. BTAi1                                    | Alpha18                  | Q35E64                               | Alpha18                                      | LOV+Kinase+RR                                     |
| <i>Rhizobium leguminosarum</i> bv <i>viciae</i> 3841 plasmid pRL11 | Alpha19                  | Q1M667                               | Alpha19                                      | LOV+Kinase  |
| <i>Rhodobacter sphaeroides</i> ATCC 17029                          | Alpha20                  | A3PI49                               | Alpha20                                      | LOV   |
| <i>Roseobacter</i> sp. CCS2  | (1)<br>(2)               | A4EHF4<br>A4EIJ8                     | Alpha21_1<br>Alpha21_2                       | LOV<br>LOV  |
| <i>Roseobacter litoralis</i> OCh 149                               | Alpha22                  | A9HBJ6                               | Alpha22                                      | LOV+Kinase  |
| <i>Roseovarius</i> sp. HTCC2601                                    | Alpha23                  | Q0FR10                               | Alpha23                                      | LOV   |
| <i>Sagittula stellata</i> E-37                                     | Alpha24                  | A3K7K8                               | Alpha24                                      | LOV   |
| <i>Oceanibulbus indolifex</i> HEL-45                               | Alpha25                  | A9DXF0                               | Alpha25                                      | LOV+Kinase  |
| <i>Granulobacter bethesdensis</i>                                  | Alpha26                  | Q0BT22                               | Alpha26                                      | LOV   |
| <i>Erythrobacter</i> sp. SD-21                                     | Alpha27                  | A5PBU7                               | Alpha27                                      | LOV+Kinase  |

|  |  |         |  |  |  |
|--|--|---------|--|--|--|
| <i>Erythrobacter</i> sp. NAP1                              |  | Alpha28 | A3WAQ8   | Alpha28  | LOV+Kinase   |
| <i>Bradyrhizobium</i> sp. ORS278                           |  | Alpha29 | A4Z279   | Alpha29  | LOV+Kinase+RR  |
| <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM1325 | (1)<br>(2)   | Alpha30 | B0JC21<br>B0JAE2   | Alpha30_1<br>Alpha30_2   | LOV+Kinase<br>LOV+Kinase   |
| <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM2304 |  | Alpha31 | B1CL99   | Alpha31  | LOV+Kinase   |
| <i>Brucella melitensis</i> biovar <i>Abortus</i> 2308      |  | Alpha32 | Q2YKK7   | Alpha32  | LOV+PAS+Kinase   |
| <i>Brucella suis</i> ATCC 23445                            |  | Alpha33 | A9WYQ7   | Alpha33  | LOV+PAS+Kinase   |
| <i>Brucella canis</i> ATCC 23365                           |  | Alpha34 | A9MBM8   | Alpha34  | LOV+PAS+Kinase   |
| <i>Brucella ovis</i> ATCC 25840                            |  | Alpha35 | A5VUS1   | Alpha35  | LOV+PAS+Kinase   |
| <i>Methylobacterium</i> sp. 4-46                           | (1)<br>(2)   | Alpha36 | B0UAI7<br>B0UDT0   | Alpha36_1<br>Alpha36_2   | LOV+PAS+PAS+Kinase+RR<br>LOV+Kinase+RR   |
| <i>Methylobacterium extorquens</i> PA1                     | (1)<br>(2)<br>(3)<br>(4)<br>(5)                      | Alpha37 | A9VYT5<br>A9W705<br>A9W8Q8<br>A9W392<br>A9W124                               | Alpha37_1<br>Alpha37_2<br>Alpha37_3<br>Alpha37_4<br>Alpha37_5  | LOV+Kinase+RR<br>LOV+Kinase<br>LOV+Kinase<br>LOV+Kinase+RR<br>LOV+Kinase   |
| <i>Methylobacterium chloromethanicum</i> CM4               | (1)<br>(2)<br>(3)<br>(4)<br>(5)<br>(6)               | Alpha38 | A7WBJ1<br>A7W6D6<br>A7W1J2<br>A7WCI5<br>A7W0I4<br>A7W7Z9                     | Alpha38_1<br>Alpha38_2<br>Alpha38_3<br>Alpha38_4<br>Alpha38_5<br>Alpha38_6                           | LOV+Kinase+RR<br>LOV+Kinase<br>LOV+Kinase<br>LOV+PAS+GAF+Kinase+RR<br>LOV+Kinase+RR<br>LOV+PAS+Kinase                                      |
| <i>Methylobacterium populi</i> BJ001                       | (1)<br>(2)<br>(3)<br>(4)<br>(5)<br>(6)<br>(7)<br>(8) | Alpha39 | B1Z812<br>B1ZJK1<br>B1ZCH2<br>B1ZG87<br>B1ZKQ8<br>B1ZGT9<br>B1ZH86<br>B1ZI10 | Alpha39_1<br>Alpha39_2<br>Alpha39_3<br>Alpha39_4<br>Alpha39_5<br>Alpha39_6<br>Alpha39_7<br>Alpha39_8 | LOV+PAS+Kinase<br>LOV+Kinase+RR<br>LOV+PAS+GAF+Kinase+RR<br>LOV+Kinase+RR<br>LOV+Kinase<br>LOV+Kinase<br>LOV<br>LOV+PAS+PAS+PAS+GAF+Kinase |
| <i>Methylobacterium radiotolerans</i> JCM 2831             | (1)<br>(2)<br>(3)<br>(4)<br>(5)<br>(6)               | Alpha40 | B1M4A2<br>B1LWD2<br>B1LUV7<br>B1M516<br>B1LSK7<br>B1M4V9                     | Alpha40_1<br>Alpha40_2<br>Alpha40_3<br>Alpha40_4<br>Alpha40_5<br>Alpha40_6                           | LOV<br>LOV+Kinase<br>LOV+Kinase+RR<br>LOV<br>LOV+PAS+Kinase<br>LOV+PAS+PAS+Kinase+RR   |
| <i>Methylobacterium nodulans</i> ORS 2060                  | (2)<br>(3)   | Alpha41 | A9G4X2<br>A9HHP8   | Alpha41_2<br>Alpha41_3   | LOV+Kinase+RR<br>LOV+PAS+PAS+Kinase+RR   |
| <i>Ochrobactrum anthropi</i> ATCC 49188                    |  | Alpha42 | A6X554   | Alpha42  | LOV+PAS+Kinase   |

<sup>S</sup>: It should be noted that the rapidly growing number of sequenced bacterial genomes as well as the huge amount of metagenome sequences deliver novel LOV sequences almost monthly. Therefore, a sequence analysis can *de facto* never be complete but merely represents a snapshot of the sequence and species data available at the given moment.

## Bacteria: $\beta$ -Proteobacteria

| Species   | ssu Tree-ID | Accession Number of LOV protein | LOV protein Tree-ID | LOV protein domain content            |
|---|-------------|---------------------------------|---------------------|---------------------------------------|
| <i>Burkholderia phymatum</i> STM815                   | Beta1       | A0FWN5                          | Beta1               | LOV+Kinase+RR                         |
| <i>Acidovorax avenae</i> sub. <i>citrulli</i> AAC00-1 | Beta2       | Q0XDC0                          | Beta2               | LOV+Kinase+RR                         |
| <i>Nitrospira multififormis</i> ATCC 25196            | Beta3       | Q2Y837                          | Beta3               | LOV                                   |
| <i>Ralstonia solanacearum</i> UW551                   | Beta4       | A3RWI2                          | Beta4               | HAMP+PAS+PAS+LOV+GGDEF+EAL            |
| <i>Ralstonia solanacearum</i> GMI1000                 | Beta5       | Q8XT61                          | Beta5               | HAMP+PAS+PAS+LOV+GGDEF+EAL            |
| <i>Rubrivivax gelatinosus</i> PM1                     | Beta6       | ZP_00244844                     | Beta6               | GAF+PAS+PAS+PAS+LOV+PAS+PAS+Kinase+RR |
| <i>Polaromonas naphthalenivorans</i>                  | Beta7       | A1VS30                          | Beta7               | LOV+Kinase                            |
| <i>Burkholderia xenovorans</i> LB400                  | Beta8       | Q145M2                          | Beta8               | PAS+PAS+LOV+GGDEF+EAL                 |
| <i>Methylibium petroleiphilum</i> PM1                 | Beta9       | A2SIR0                          | Beta9               | GAF+PAS+PAS+PAS+LOV+PAS+PAS+Kinase+RR |
| <i>Burkholderia graminis</i> C4D1M                    | Beta10      | B1FWL0                          | Beta10              | PAS+PAS+LOV+GGDEF+EAL                 |
| <i>Hermiimonas arsenicoxydans</i>                     | (1) Beta11  | A4G7R2                          | Beta11_1            | LOV+GGDEF                             |
|   | (2)         | A4G3M6                          | Beta11_2            | RR+PAS+LOV+GGDEF+EAL                  |

## Bacteria: $\gamma$ -Proteobacteria

| Species  | ssu Tree-ID | Accession Number of LOV protein | LOV protein Tree-ID | LOV protein domain content |
|--|-------------|---------------------------------|---------------------|----------------------------|
| <i>Xanthomonas axonopodis</i> pv. <i>citri</i> str.306         | Gamma1      | Q8PJH6                          | Gamma1              | LOV+Kinase+RR              |
| <i>Xanthomonas campestris</i> pv. <i>campestris</i> ATCC 33913 | Gamma2      | Q8P827                          | Gamma2              | LOV+Kinase+RR              |
| <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> MAFF 311018        | Gamma3      | Q2P134                          | Gamma3              | LOV+Kinase+RR              |
| <i>Xanthomonas campestris</i> pv. <i>Vesicatoria</i> str.85-10 | Gamma4      | Q3BRX8                          | Gamma4              | LOV+Kinase+RR              |
| <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a          | Gamma5      | Q4ZSY3                          | Gamma5              | LOV+Kinase+RR              |
| <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000           | Gamma6      | Q881J7                          | Gamma6              | LOV+Kinase+RR              |
| <i>Pseudomonas syringae</i> pv. <i>Phaseolicola</i> 1448A      | Gamma7      | Q48IV1                          | Gamma7              | LOV+Kinase+RR              |
| <i>Nitrosococcus oceani</i> ATCC 19707                         | Gamma8      | Q3J6W8                          | Gamma8              | LOV                        |
| <i>Thiomicrospira denitrificans</i> ATCC 33889                 | Gamma9      | Q30NS0                          | Gamma9              | HTH+LOV                    |
| <i>Alteromonas macleodii</i> 'Deep ecotype'                    | Gamma10     | A4AZT0                          | Gamma10             | LOV+Kinase+RR              |
| <i>Pseudomonas fluorescens</i> PF0-1                           | Gamma11     | Q3KHW7                          | Gamma11             | LOV                        |
| <i>Pseudomonas fluorescens</i> PF-5                            | Gamma12     | Q4BW45                          | Gamma12             | LOV                        |
| <i>Pseudomonas putida</i> KT2440                               | (1) Gamma13 | Q88E39                          | Gamma13_1           | LOV                        |
|  | (2)         | Q88JB0                          | Gamma13_2           | LOV                        |
| <i>Pseudomonas putida</i> F1                                   | (1) Gamma14 | A5W8Z9                          | Gamma14_1           | LOV                        |
|  | (2)         | A5W4T2                          | Gamma14_2           | LOV                        |
| <i>Pseudomonas putida</i> W619                                 | (1) Gamma15 | A1FD29                          | Gamma15_1           | LOV                        |
|  | (2)         | A1FFK5                          | Gamma15_2           | LOV                        |
| <i>Chromohalobacter salexigens</i> DSM 3043                    | Gamma16     | Q1QU87                          | Gamm16              | LOV                        |
| <i>Xanthomonas campestris</i> pv. <i>campestris</i> str. 8004  | Gamma17     | Q4UW16                          | Gamma17             | LOV+Kinase+RR              |
| <i>Xanthomonas campestris</i> pv. <i>campestris</i>            | Gamma18     | B0RRL1                          | Gamma18             | LOV+Kinase+RR              |
| <i>Pseudomonas stutzeri</i> A1501                              | Gamm19      | A4VKZ3                          | Gamm19              | LOV                        |

|                                      |     |         |                  |                        |                                    |
|--------------------------------------|-----|---------|------------------|------------------------|------------------------------------|
| <i>Pseudomonas mendocina ymp</i>     | (1) | Gamma20 | A4XP68<br>A4XXH1 | Gamma20_1<br>Gamma20_2 | MASE1+LOV+PAS+PAS+GGDEF+EAL<br>LOV |
| (2)                                  |     |         |                  |                        |                                    |
| <i>Oceanobacter sp. RED65</i>        |     | Gamma21 | Q1N482           | Gamma21                | LOV+Kinase+RR+RR                   |
| <i>Shewanella sp. ANA-3</i>          |     | Gamma22 | A0L2H7           | Gamma22                | MASE1+CHASE+PAS+LOV+GGDEF+EAL      |
| <i>Shewanella sp. W3-18-1</i>        |     | Gamma23 | A1RE55           | Gamma23                | MASE1+CHASE+PAS+LOV+GGDEF+EAL      |
| <i>Shewanella putrefaciens CN-32</i> |     | Gamma24 | A4YC79           | Gamma24                | MASE1+CHASE+PAS+LOV+GGDEF+EAL      |
| <i>Shewanella putrefaciens 200</i>   |     | Gamma25 | A2V2K2           | Gamma25                | PAS+LOV+GGDEF+EAL                  |
| <i>Shewanella baltica OS195</i>      |     | Gamma26 | A9KV07           | Gamma26                | MASE1+CHASE+PAS+LOV+GGDEF+EAL      |
| <i>Shewanella baltica OS185</i>      |     | Gamma27 | A6WU43           | Gamma27                | MASE1+CHASE+PAS+LOV+GGDEF+EAL      |
| <i>Shewanella baltica OS223</i>      |     | Gamma28 | A5NDX2           | Gamma28                | MASE1+CHASE+PAS+LOV+GGDEF+EAL      |
| <i>Shewanella sp. MR-7</i>           |     | Gamma29 | Q0HPR6           | Gamma29                | MASE1+CHASE+PAS+LOV+GGDEF+EAL      |
| <i>Shewanella sp. MR-4</i>           |     | Gamma30 | Q0HDI3           | Gamma30                | MASE1+CHASE+PAS+LOV+GGDEF+EAL      |
| <i>Marinobacter algicola DG893</i>   |     | Gamma31 | A6EZP7           | Gamma31                | GAF+PAS+LOV+GGDEF+EAL              |

## Bacteria: Chloroflexi

| Species                                     | ssu Tree-ID | Accession Number of LOV protein | LOV protein Tree-ID | LOV protein domain content              |
|---|-------------|---------------------------------|---------------------|---|
| <i>Chloroflexus aurantiacus</i>             | Chloro1     | Q3DVF5                          | Chloro1             | LOV+PAS+PAS+Kinase                      |
| <i>Chloroflexus aggregans DSM 9485</i>      | Chloro2     | A0H5C8                          | Chloro2             | LOV+PAS+PAS+Kinase+RR                   |
| <i>Herpetosiphon aurantiacus ATCC 23779</i> | Chloro3     | Q0LGE0                          | Chloro3             | HAMP+GAF+LOV+PAS+PAS+PAS+PAS+GAF+Kinase |

## Bacteria: Actinobacteria

| Species                                      | ssu Tree-ID | Accession Number of LOV protein | LOV protein Tree-ID | LOV protein domain content |
|--|-------------|---------------------------------|---------------------|----------------------------|
| <i>Kineococcus radiotolerans</i>             | (1)         | Q40X75                          | Actino1_1           | GGDEF+LOV+EAL              |
| (2)  | Actino1     | Q40XK1                          | Actino1_2           | LOV+GAF+PP2C               |
| (3)  |             | A6W4X7                          | Actino1_3           | LOV+PP2C                   |
| <i>Rubrobacter xylanophilus</i>              | Actino2     | Q1ARZ9                          | Actino2             | LOV+GAF+PP2C               |
| <i>Arthrobacter aurescens TC plasmid TC2</i> | Actino3     | A1RDS2                          | Actino3             | LOV+GGDEF+EAL              |

## Bacteria: Firmicutes

| Species   | ssu Tree-ID          | Accession Number of LOV protein | LOV protein Tree-ID  | LOV protein domain content |
|---|----------------------|---------------------------------|----------------------|----------------------------|
| <i>Listeria monocytogenes</i> EGD-e                 | Firmi1               | P58724                          | Firmi1               | LOV+STAS                   |
| <i>Listeria monocytogenes</i> F2365                 | Firmi2               | Q722B8                          | Firmi2               | LOV+STAS                   |
| <i>Listeria innocua</i> CLIP 11262                  | Firmi3               | Q92DM1                          | Firmi3               | LOV+STAS                   |
| <i>B.subtilis</i> 168                               | Firmi4               | Q34627                          | Firmi4               | LOV+STAS                   |
| <i>Oceanobacillus iheyensis</i> HTE831              | Firmi5               | Q8ESN8                          | Firmi5               | LOV+STAS                   |
| <i>Listeria monocytogenes</i> str. 1/2a F6854       | Firmi6               | Q4EN15                          | Firmi6               | LOV+STAS                   |
| <i>Bacillus amyloliquefaciens</i> FZB42             | Firmi7               | YP_001422316                    | Firmi7               | LOV+STAS                   |
| <i>Listeria welshimeri</i> serovar 6b str. SLCC5334 | Firmi8               | A0AGP3                          | Firmi8               | LOV+STAS                   |
| <i>Bacillus pumilus</i> SAFR-032                    | (1)<br>(2)<br>Firmi9 | A8FGG2<br>A8FI66                | Firmi9_1<br>Firmi9_2 | LOV+STAS<br>LOV+STAS       |
| <i>Bacillus selenitireducens</i> MLS10              | Firmi10              | A8W065                          | Firmi10              | LOV+STAS                   |

## Bacteria: Cyanobacteria

| Species                                     | ssu Tree-ID                                   | Accession Number of LOV protein                          | LOV protein Tree-ID  | LOV protein domain content   |
|---|---|--|--|--|
| <i>Thermosynechococcus elongatus</i> BP-1   | Cyano1  | Q8DJE3   | Cyano1   | GAF+PAS+LOV+GAF+GAF+Kinase+RR  |
| <i>Anabaena variabilis</i> ATCC 29413       | (1) Cyano2<br>(2)                             | Q3M6B3<br>Q3MED3   | Cyano2_1<br>Cyano2_2   | LOV+PAS+PAS+GGDEF+EAL<br>PAS+LOV+PAS+PAS+GAF+Kinase+RR+RR+HPT  |
| <i>Synechococcus</i> sp. PCC 6301           | (1) Cyano3<br>(2)                             | Q5N2F7<br>Q5N5M8   | Cyano3_1<br>Cyano3_2   | LOV+GGDEF+EAL<br>RR+PAS+PAS+LOV+GGDEF+EAL  |
| <i>Nostoc punctiforme</i> PCC 73102         | (1) Cyano4<br>(2)                             | ZP_00111211<br>ZP_00105980                               | Cyano4_1<br>Cyano4_2   | LOV+PAS+PAS+GGDEF+EAL<br>PAS+LOV+PAS+GAF+Kinase+RR+RR+HPT  |
| <i>Crocospaera watsonii</i>                 | Cyano5  | Q4BW45   | Cyano5   | RR+LOV   |
| <i>Lyngbya</i> sp. PCC 8106                 | (1) Cyano6<br>(2)<br>(3)<br>(4)<br>(5)<br>(6) | A0YVI7<br>A0YYE1<br>A0YS28<br>A0YI13<br>A0YJV6<br>A0YYE8 | Cyano6_1<br>Cyano6_2<br>Cyano6_3<br>Cyano6_4<br>Cyano6_5<br>Cyano6_6 | RR+LOV+GGDEF<br>PAS+LOV+PAS+GGDEF+EAL<br>RR+RR+LOV+PAS+GAF+Kinase+RR<br>PAS+LOV+PAS+PAS+PAS+GAF+GGDEF<br>GAF+PAS+LOV+PAS+GAF+Kinase<br>PAS+GAF+LOV+GGDEF+EAL |
| <i>Cyanothece</i> sp. CCY 0110              | Cyano7  | A3IMW4   | Cyano7   | RR+LOV+DUF   |
| <i>Anabaena</i> sp PCC7120( <i>Nostoc</i> ) | (1) Cyano8<br>(2)                             | Q8YT51<br>Q8YSB9   | Cyano8_1<br>Cyano8_2   | LOV+PAS+PAS+DUF1+DUF2<br>PAS+LOV+PAS+PAS+PAS+GAF+Kinase+RR   |
| <i>Synechocystis</i> sp. PCC 6803           | Cyano9  | Q55576   | Cyano9   | GAF+LOV+PAS+PAS+PAS+GGDEF+EAL  |
| <i>Synechococcus elongatus</i> PCC 7942     | (1) Cyano10<br>(2)                            | Q31RU9<br>Q31NI4   | Cyano10_1<br>Cyano10_2   | LOV+GGDEF+EAL<br>RR+PAS+PAS+LOV+GGDEF+EAL  |
| <i>Synechococcus</i> sp. PCC 7002           | Cyano11                                       | B1XLQ8   | Cyano11  | GAF+LOV+PAS+GGDEF  |
| <i>Cyanothece</i> sp. ATCC 51142            | Cyano12                                       | B1WPX1   | Cyano12  | RR+LOV+GGDEF   |
| <i>Cyanothece</i> sp. PCC 8801              | Cyano13                                       | B1U402   | Cyano13  | RR+LOV+GGDEF   |
| <i>Acaryochloris marina</i> MBIC11017       | Cyano14                                       | B0C6M6   | Cyano14  | PAS+LOV+PAS+PAS+GGDEF+EAL  |

## Eukaryota: Viridiplantae

| Species                              |  | ssu Tree-ID           | Accession Number of LOV protein   | LOV protein Tree-ID <sup>‡</sup>   | LOV protein domain content   |
|--------------------------------------|--|-----------------------|---|--|--|
| <i>Physcomitrella patens</i>         | (1)<br>(2)<br>(3)                      | Plant1_g,<br>_mt, _cp | BAD32622<br>BAD32623<br>BAD32624  | Plant1_1L1 / Plant1_1L2 (phot1)<br>Plant1_2L1 / Plant1_2L2 (phot2)<br>Plant1_3L1 / Plant1_3L2 (phot3)              | LOV1+LOV2+Kinase<br>LOV1+LOV2+Kinase<br>LOV1+LOV2+Kinase   |
| <i>Oryza sativa</i>                  | (1)<br>(2)<br>(3)                      | Plant2_g,<br>_mt, _cp | XP_471720<br>Q5Z8K3<br>Q67UX0   | Plant2L1 / Plant2L2 (phot)<br>Plant2_3 (ZTL)<br>Plant2_4 (ZTL)   | LOV1+LOV2+Kinase<br>LOV+Fbox+Kelch <sub>5</sub><br>LOV+Fbox+Kelch <sub>5</sub>   |
| <i>Chlamydomonas reinhardtii</i>     |  | Plant3_g,<br>_cp      | CAC94940  | Plant3L1 / Plant3L2 (phot)   | LOV1+LOV2+Kinase   |
| <i>Arabidopsis thaliana</i>          | (1)<br>(2)<br>(3)<br>(4)<br>(5)<br>(6) | Plant4_g,<br>_mt, _cp | NP_849983<br>Q94BT6<br>AAK27435<br>Q9C9W9<br>NM_114447.3<br>NM_180881.2 | Plant4_1<br>Plant4_2<br>Plant4_3<br>Plant4_4<br>Plant4P1L1 / Plant4P1L2 (phot1)<br>Plant4P2L1 / Plant4P2L2 (phot2) | LOV+Fbox+Kelch <sub>5</sub><br>LOV+Fbox+Kelch <sub>5</sub><br>LOV+Fbox+Kelch <sub>5</sub><br>LOV+Fbox+Kelch <sub>5</sub><br>LOV1+LOV2+Kinase<br>LOV1+LOV2+Kinase |
| <i>Mesembryanthemum crystallinum</i> | (1)<br>(2)                             | missing               | Q6UEI5<br>Q6UEI4  | Plant5_1<br>Plant5_2   | LOV+Fbox+Kelch <sub>5</sub><br>LOV+Fbox+Kelch <sub>5</sub>   |
| <i>Prototheca wickerhamii</i> *      |  | Plant6_mt             | no LOV  | -  | -  |
| <i>Vaucheria frigida</i>             | (1)<br>(2)                             | missing               | BAF91488<br>BAF91491  | Plant7aur1) (aureo)<br>Plant7aur2) (aureo)   | BZIP-LOV<br>BZIP-LOV   |
| <i>Adiantum capillus-veneris</i>     |  | Plant8                | BAA36192  | Plant8NL1 /Plant8NL2 (neo)   | PAS+GAF+Phy+LOV1+LOV1+Kinase   |
| <i>Mougeotia scalaris</i>            | (1)<br>(2)                             | Plant9_g              | BAE20165<br>BAE20166  | Plant9P1L1 /Plant9P1L2 (photA)<br>Plant9P2L1 / Plant9P2L2 (photB)  | LOV1+LOV2+Kinase<br>LOV1+LOV2+Kinase   |
| <i>Dryopteris filix-mas</i>          |  | missing               | BAC55265  | Plant10NL1 /Plant10NL2 (neo)   | Partial (...Phy-LOV1-LOV2 ...)   |
| <i>Hypolepis punctata</i>            |  | missing               | BAC55266  | Plant11NL1 /Plant11NL2 (neo)   | Partial (...Phy-LOV1-LOV2 ...)   |

<sup>‡</sup>: In the seed-alignment which was used for our phylogenetic analysis phototropin LOV sequences were split into LOV1 and LOV2 and included separately in the alignment (indicated by the abbreviations L1 and L2 in the respective sequence ID. For the ssu-rRNA IDs, the sufficies g, mt, and cp are added to the ssu rRNA sequences from nuclear, mitochondrial and chloroplast regions, respectively. Plant3\_mt is not included due to the scrambled rRNA gene regions over the mitochondrial DNA.

## Eukaryota: Fungi

| Species                                 | ssu Tree-ID                                 | Accession Number of LOV protein <sup>†</sup> | LOV protein Tree-ID              | LOV protein domain content        |
|---|---|--|----------------------------------|-----------------------------------|
| <i>Botrytis cinerea</i> B05.10          | (1)<br>(2)<br>(3)<br>Fungi1_g,<br>Fungi1_mt | BC1G_13505.1<br>BC1G_08584.1<br>BC1G_15404.1 | Fungi1_1<br>Fungi1_2<br>Fungi1_3 | LOV+PAS+PAS+ZnF<br>RGS+LOV<br>LOV |
| <i>Sclerotinia sclerotiorum</i>         | (1)<br>(2)<br>(3)<br>Fungi2_g,<br>Fungi2_mt | SS1G_02240<br>SS1G_11953<br>SS1G_12563       | Fungi2_1<br>Fungi2_2<br>Fungi2_3 | LOV<br>LOV+PAS+PAS+ZnF<br>LOV     |
| <i>Magnaporthe grisea</i> 70-15         | (1)<br>(2)<br>(3)<br>Fungi3_g,<br>Fungi3_mt | MGG_03538.5<br>MGG_01041.5<br>MGG_08735.5    | Fungi3_1<br>Fungi3_2<br>Fungi3_3 | LOV+PAS+PAS+ZnF<br>LOV<br>RGS+LOV |
| <i>Aspergillus nidulans</i>             | (1)<br>(2)<br>Fungi4_g,<br>Fungi4_mt        | AN3436.1<br>AN3435                           | Fungi4_1<br>Fungi4_2             | LOV+PAS+PAS+ZnF<br>LOV            |
| <i>Neurospora crassa</i>                | Fungi5_g,<br>Fungi5_mt                      | NCU02356                                     | Fungi5                           | LOV+PAS+PAS+ZnF                   |
| <i>Cryptococcus neoformans</i>          | Fungi6_g                                    | Q6DMM2                                       | Fungi6                           | LOV+PAS                           |
| <i>Schizosaccharomyces octosporus</i> * | Fungi7_mt                                   | no LOV                                       | -                                | -                                 |
| <i>Cryphonectria parasitica</i> *       | Fungi8_mt                                   | no LOV                                       | -                                | -                                 |

<sup>†</sup>: All fungal LOV protein, sequences with the exception of the *Neurospora crassa* and the *Cryptococcus neoformans* sequence, were obtained directly from the respective fungal genome database accessible at the Munich Information Center for Protein Sequences (<http://mips.gsf.de>). For the ssu IDs, the suffices g and mt are added to the ssu rRNA sequences from nuclear and mitochondrial regions, respectively. Fungi6\_mt is excluded due to too short sequence length.

\*: Additional mitochondrial ssu rRNA sequences of plants and fungi which help to bridge between genetically diverse taxa to better resolve the rRNA tree. For these species, the accession number of the rRNA sequences are used as ID.

## Eukaryota: Metazoa

| Species                          | ssu Tree-ID | Accession Number of LOV protein | LOV protein Tree-ID | LOV protein domain content |
|----------------------------------|-------------|---------------------------------|---------------------|----------------------------|
| <i>Homo sapiens</i> (primates)   | Human       | Q9ULD8                          | Human               | LOV?+Ion+cNMP              |
| <i>Mus musculus</i> (rodents)    | Mouse       | Q9WVJ0                          | Mouse               | LOV?+Ion+cNMP              |
| <i>Danio rerio</i> (bony fishes) | Danio       | A8WHX9                          | Danio               | LOV?+Ion+cNMP              |
| <i>Manduca sexta</i> (moths)     | Manduca     | Q7YW98                          | Manduca             | LOV?+Ion+cNMP              |
|                                  |             |                                 |                     |                            |



## Archaea: Euryarcheota

| Species  |                   | ssu Tree-ID | Accession Number of LOV protein | LOV protein Tree-ID           | LOV protein domain content   |
|--|-------------------|-------------|---------------------------------|-------------------------------|--|
| <i>Haloarcula marismortui</i> ATCC 43049                       | (1)<br>(2)<br>(3) | Arch1       | Q5V5P7<br>Q5V3S3<br>Q5UWI7      | Arch1_1<br>Arch1_2<br>Arch1_3 | RR+PAS+LOV+PAS+Kinase<br>RR+PAS+LOV+GAF+Kinase<br>PAS+GAF+PAS <sub>4</sub> +GAF+PAS <sub>4</sub> +LOV+PAS <sub>3</sub> +Kinase |
| <i>Natronomonas pharaonis</i> DSM 2160<br><i>plasmid PL131</i> | (1)<br>(2)        | Arch2       | Q3ITW5<br>Q3IM51                | Arch2_1<br>Arch2_2            | RR+LOV+GAF+HTH<br>PAS+LOV+PAS+Kinase   |
| <i>Halorubrum lacusprofundi</i> ATCC 49239                     | (1)<br>(2)        | Arch3       | ZP_02014689.1<br>EDN50126.1     | Arch3_1<br>Arch3_2            | PAS+LOV+Kinase<br>PAS+LOV+Kinase   |
| <i>Methanoculleus marisnigri</i> JR1                           | (1)<br>(2)<br>(3) | Arch6       | A3CUN9<br>A3CV78<br>A3CS54      | Arch6_1<br>Arch6_2<br>Arch6_3 | PAS+PAS+LOV+H-DimKinase<br>PAS+PAS+PAS+LOV+H-DimKinase<br>PAS+Pas+GAF+LOV+H-DimKinase  |
|  |                   |             |                                 |                               |  |

†: LOV: light, oxygen, voltage domain; S/T Kin: serine/threonine kinase; Kelch: Kelch repeats; Fbox : receptor domain for ubiquitination targets ; PAS: Per, Arndt, Sim domain; ZnF: zinc-finger motif; STAS: sulphate-transporter antisigma-factor antagonist domain; HisKin: histidine kinase; RR: response regulator; HTH: helix-turn-helix DNA binding domain; GGDEF: diguanylate cyclase; EAL: phosphodiesterase; GAF: domain present in phytochromes and cGMP-specific phosphodiesterases ; RGS : GTPase-activating protein domains ; HPT : Histidine phosphotransfer domain ; DUF(1/2) : domain of unknown function ; HAMP : Histidine kinases, Adenylyl cyclases, Methyl binding proteins, Phosphatases domains; PP2C: protein phosphatase 2C signature domain, NMT1 : ABC transporter, MASE1 : unknown function, CHASE : Cyclases/Histidine kinases Associated Sensory Extracellular, cNMP : Cyclic nucleotide-monophosphate binding domain, Ion : sodium, potassium, and calcium ion channels proteins, consisting of 6 transmembrane helices