Supplementary Information for

RubyACRs, non-algal anion channelrhodopsins with highly red-shifted absorption

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Fig. S1. Protein sequence alignment of the rhodopsin domains of Laby channelrhodopsins. Residues are color-coded according to their chemical properties. The arrows point to the positions of the residues known to be functionally important in GtACR1.


Fig. S2. Protein sequence alignment of the rhodopsin domains of Hapto channelrhodopsins. Residues are color-coded according to their chemical properties. The arrows point to the positions of the residues known to be functionally important in GtACR1.


Fig. S3. Photocurrent traces recorded in response to the first 1-s light pulse at -60 mV at the amplifier output, normalized at their peak value. The duration of illumination is showed as a colored bar on top.


Fig. S4. (A and B) The magnitude of desensitization during continuous illumination (A) and halfdecay of photocurrent after switching the light off ( $B$ ). The black lines show the mean values and s.e.m. ( $n=5-10$ cells for each variant); colored circles, the individual data points. (C) The ratio of the peak amplitude to that of the stationary current (measured at the end of a $1-\mathrm{s}$ light pulse) in a series of pulses applied with $30-\mathrm{s}$ time interval. The lines are single exponential fits.


Fig. S5. (A, B and D) The action spectra of photocurrents generated by indicated proteins reconstituted with A1 (black) and A2 (red) retinal. (C) The difference spectra (A2-A1 retinal).


Fig. S6. The absorption spectrum of HfACR1 detergent-purified from Pichia (red solid line) compared to the action spectrum of photocurrents generated upon its expression in HEK293 cells from Fig. 1B (black dashed line).

Table S1. A list of Laby ACR homologs (in bold - synthesized and tested by patch clamp in this study)

|  | GenBank accession number | Abbreviate d protein name | Source organism | JGI gene model name | Total CDS <br> lengt <br> h | $\begin{aligned} & \lambda_{\max } \\ & (\mathrm{nm}) \end{aligned}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1. | QDJC01000532 | AaACR1 | Aurantiochytrium acetophilum HS399 | identical to AIACR1 | 691 |  |
| 2. | QDJC01003161 | AaACR2 |  | identical to AIACR2 | 635 |  |
| 3. | QDJC01000037 | AaACR3 |  | only two <br> mismatches <br> with <br> AIACR3 | 683 |  |
| 4. | MT002467 | AIACR1 | Aurantiochytrium limacinum ATCC MYA-1381 | $\begin{aligned} & \text { fgenesh1_p } \\ & \text { g. } 12 \text { \# } 284 \end{aligned}$ | 696 | 590 |
| 5. | MT002473 | AIACR2 |  | $\begin{aligned} & \mathrm{gm1.7690} \\ & \mathrm{~g} \end{aligned}$ | 635 | 545 |
| 6. | MT002476 | AIACR3 |  | estExt Gen emark1.C <br> 1_t20010 | 678 | 485 |
| 7. | $\begin{array}{\|l\|} \hline \text { MT002468, } \\ \text { BGKB01000037 } \\ \hline \end{array}$ | A1ACR1 | Aurantiochytrium sp. KH105 |  | 646 | 610 |
| 8. | BGKB01000105 | A1ACR1 |  |  | 645 |  |
| 9. | BGKB01000099 | A1ACR3 |  |  | 680 |  |
| 10. | BGKB01000102 | A1ACR3 |  |  | 680 |  |
| 11. | LNGJ01004228 | A2ACR1 | Aurantiochytrium sp. T66 | identical to T1ACR1 | 649 |  |
| 12. | LNGJ01002066 | A2ACR3 |  |  | 759 |  |
| 13. | $\begin{aligned} & \text { MT002469, } \\ & \text { GBG24568 } \end{aligned}$ | HfACR1 | Hondaea fermentalgiana FCC1311 |  | 646 | 610 |
| 14. | GBG24569 | HfACR2 |  |  | 663 |  |
| 15. | GBG23965 | HfACR3 |  |  | 680 |  |
| 16. | MT002463 | SaACR | Schizochytrium aggregatum ATCC 28209 | $\begin{aligned} & \text { fgenesh1_p } \\ & \text { g.3_\#_476 } \end{aligned}$ | 546 | 520 |
| 17. | JTFK01000019 | S1ACR1 | Schizochytrium sp. CCTCC M209059 |  | 645 |  |
| 18. | JTFK01000324 | S1ACR3 |  |  | 680 |  |
| 19. | SMSO01000032 | S2ACR1 | $\begin{aligned} & \text { Schizochytrium sp. } \\ & \text { TIO01 } \end{aligned}$ | Identical to AIACR1 | 696 |  |
| 20. | SMSO01000014 | S2ACR3 |  |  | 583 |  |
| 21. | MT002470, MUFY01006470 | T1ACR1 | Thraustochytrium sp. ATCC 26185 |  | 649 | 590 |
| 22. | MUFY01006469 | T1ACR2 |  |  | 666 |  |
| 23. | MUFY01009420 | T1ACR3 |  |  | 682 |  |

Table S2. A list of Hapto ACR homologs tested in this study

|  | GenBank accession number | Abbreviated protein name | Source organism | JGI gene model name | Total CDS <br> length | $\begin{aligned} & \lambda_{\max } \\ & (\mathrm{nm}) \end{aligned}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1. | MT002471 | PaACR1 | Phaeocystis antarctica CCMP1374 | Phant.0066s0015.1 | 1682 | 520 |
| 2. | MT002474 | PaACR2 |  | Phant.0011s0329.1 | 647 | 505 |
| 3. | MT002477 | PaACR3 |  | Phant.0016s0461.1, <br> Phant.0016s0462.1, <br> Phant.0016s0464.1 | 427 | 475 |
| 4. | MT002464 | PaACR4 |  | Phant.0060s0074.1 | 469 | 475 |
| 5. | MT002465 | PaACR5 |  | Phant.0086s0086.1 | 312 | N.A. |
| 6. | MT002466 | PaACR6 |  | Phant.0001s0932.1 | 471 | N.A. |
| 7. | MT002472 | PgACR1 | Phaeocystis globosa PgG | Phglo.0395s0005.1 | 327 | 480 |
| 8. | MT002475 | PgACR2 |  | Phglo.0149s0014.1 | 435 | 480 |
| 9. | MT002478 | PgACR3 |  | Phglo.0128s0040.1 | 505 | N.A. |

