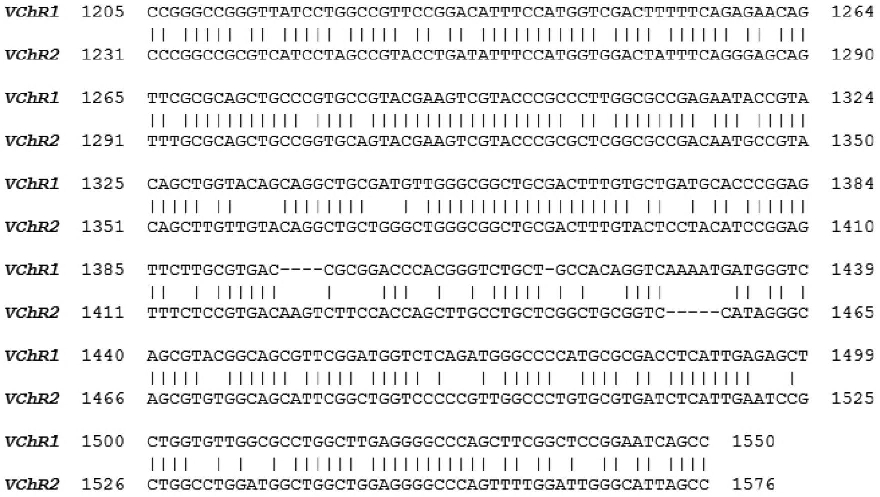
```
Identities: 577 of 817 nucleotides (71%), gaps: 8 of 817 nucleotides (1%).

VChR1  254    TATGCGTACCAGGCATGGCGAGCGACGTGCGGGTGGGAGGAGGTTTATGTGGCATTGATT  313
              ||||| |||  | | ||| || | || ||||| ||||||||||| ||||||   |   |
VChR2  238    TATGCATACGCGACCTGGAGAACCACCTGCGGCTGGGAGGAGGTATATGTGTGCTGCGTC  297

VChR1  314    GAGATGATGAAGAGTATTATCGAGGCCTTTCACGAATTCGATTCACCTGCGACTCTGTGG  373
              ||| |||  |||    | ||||||  ||| ||||| || ||    || |  |  ||||
VChR2  298    GAGTTGACCAAGGTCGTGATCGAGTTCTTCCACGAGTTTGACGAGCCCGGCATGCTGTAC  357

VChR1  374    CTATCTAGCGGAAACGGGGTTGTCTGGATGCGATACGGCGAATGGTTGCTTACATGCCCG  433
              ||  | | ||| ||| | ||  | ||| |||| |||||||| |||||||| || |||||
VChR2  358    CTTGCGAACGGCAACCGAGTGCTGTGGCTGCGGTACGGCGAGTGGTTGCTGACCTGCCCC  417

VChR1  434    GTGCTCCTGATCCACTTGTCAAATTTAACTGGGCTCAAAGATGATTACAGCAAGCGGACA  493
              ||  | || ||||||||||| ||||| ||||| ||||| || || |||| |||||||||
VChR2  418    GTCATTCTCATCCACTTGTCCAATTTGACTGGCCTCAAGGACGACTACAACAAGCGGACC  477

VChR1  494    ATGGGTTTGCTCGTCTCCGATGTCGGATGCATCGTATGGGGTGCCACATCCGCCATGTGT  553
              ||| | ||||| ||||||||||||||   |||||| |||||||| ||  | |||||||
VChR2  478    ATGCGGTTGCTTGTCTCCGATGTCGGCACCATCGTGTGGGGTGCTACTGCGGCCATGTCC  537

VChR1  554    ACGGGATGGACCAAGATCCTGTTCTTCCTTATCTCACTTTC--TTACGGCATGTACACGT  611
              || || |  |  ||  |  | ||||||||   |||  || |   ||||||    |||| |
VChR2  538    ACTGGCTACATAAAAGTGATTTTCTTCCT--CCTCGGTTGCATGTACGGCGCAAACACAT  595

VChR1  612    ACTTCCACGCCGCCAAGGTTTACATCGAGGCATTTCACACGGTGCCCAAGGGCATCTGCC  671
               |||||||||||||||||| || || ||| | |  ||||| || ||||||||  | || |
VChR2  596    TCTTCCACGCCGCCAAGGTGTATATTGAGTCGTACCACACCGTCCCCAAGGGTCTGTGTC  655

VChR1  672    GTGAGCTGGTGCGGGTCATGGCATGGACCTTTTTCGTCGCGTGGGGCATGTTCCCCGTGC  731
              || ||||||| || | |||||| |||   || |||||  | ||||| ||||| ||||| |
VChR2  656    GTCAGCTGGTCCGCGCCATGGCCTGGCTGTTCTTCGTGTCATGGGGGATGTTTCCCGTAC  715

VChR1  732    TCTTCTTACTGGGAACTGAGGGATTCGGCCACATTTCACC--TTATGGTTCGGCCATCGG  789
              | ||| |  ||||  | ||||| |||||  |||| | | |   || || ||  | |||||
VChR2  716    TGTTCCTGTTGGGGCCCGAGGGCTTCGG--ACATCTGAGCGTCTACGGGTCAACAATCGG  773

VChR1  790    CCATTCCATATTAGACTTGATCGCAAAGAACATGTGGGGTGTTCTCGGCAACTACCTGCG  849
               ||  ||||  | ||| |  || | ||||||   |||||| | || ||| ||| ||| ||
VChR2  774    TCACACCATTATCGACCTTCTCTCCAAGAACTGCTGGGGTCTGCTGGGCCACTTCCTCCG  833

VChR1  850    TGTCAAGATCCACGAGCACATCCTGTTGTACGGCGATATACGGAAGAAGCAGAAGATCAC  909
                | ||||| ||||||||||| ||| |||| |||||||| || |||   ||||||||||
VChR2  834    CCTGAAGATTCACGAGCACATTCTGCTGTATGGCGATATCCGCAAGGTTCAGAAGATCAG  893

VChR1  910    CATCGCAGGCCAGGAGATGGAGGTGGAGACTCTTGTGGCCGAAGAGGAGGACGACACGGT  969
                | || ||  ||||| ||||||||||||| ||  || | || ||||    |||||| ||
VChR2  894    GGTGGCCGGTGAGGAGCTGGAGGTGGAGACCCTCATGACGGAGGAGGCCCCCGACACCGT  953

VChR1  970    CAAACAGTCGACTGCCAAGTATGCATCTCGTGACTCGTTCATCACCATGCGCAATCGTAT  1029
              |||  |||| |||||  |||| ||     | || || ||| | ||||||||  ||    |
VChR2  954    CAAGAAGTCCACTGCGCAGTACGCCAACAGGGAGTCCTTCTTGACCATGCGTGATAAGCT  1013

VChR1  1030   GCGGGAGAAGGGCTTGGAGGTGCGGGCCTCACTGGAT  1066
                 ||||||||| || || ||||| || || ||||||
VChR2  1014   CAAGGAGAAGGGTTTCGAAGTGCGTGCTTCGCTGGAT  1050
```

`Identities: 259 of 351 nucleotides (74%), gaps: 10 of 351 nucleotides (3%).`



```
VChR1  1205  CCGGGCCGGGTTATCCTGGCCGTTCCGGACATTTCCATGGTCGACTTTTTCAGAGAACAG  1264
             || ||||| || ||||| ||||| || || ||||||||||| |||| |||||| || |||
VChR2  1231  CCCGGCCGCGTCATCCTAGCCGTACCTGATATTTCCATGGTGGACTATTTCAGGGAGCAG  1290

VChR1  1265  TTCGCGCAGCTGCCCGTGCCGTACGAAGTCGTACCCGCCCTTGGCGCCGAGAATACCGTA  1324
             || ||||||||||| |||| |||||||||||||||||| || |||||||| ||| |||||
VChR2  1291  TTTGCGCAGCTGCCGGTGCAGTACGAAGTCGTACCCGCGCTCGGCGCCGACAATGCCGTA  1350

VChR1  1325  CAGCTGGTACAGCAGGCTGCGATGTTGGGCGGCTGCGACTTTGTGCTGATGCACCCGGAG  1384
             ||||| ||    ||||||||   | ||||||||||||||||||| ||  | || ||||||
VChR2  1351  CAGCTTGTTGTACAGGCTGCTGGGCTGGGCGGCTGCGACTTTGTACTCCTACATCCGGAG  1410

VChR1  1385  TTCTTGCGTGAC----CGCGGACCCACGGGTCTGCT-GCCACAGGTCAAAATGATGGGTC  1439
             ||  | ||||||    |    |||  |  | ||||| | |   ||||      || || |
VChR2  1411  TTTCTCCGTGACAAGTCTTCCACCAGCTTGCCTGCTCGGCTGCGGTC-----CATAGGGC  1465

VChR1  1440  AGCGTACGGCAGCGTTCGGATGGTCTCAGATGGGCCCCATGCGCGACCTCATTGAGAGCT  1499
             |||||  |||||| ||||| ||||| |   | |||||  |||| || ||||||||   | 
VChR2  1466  AGCGTGTGGCAGCATTCGGCTGGTCCCCCGTTGGCCCTGTGCGTGATCTCATTGAATCCG  1525

VChR1  1500  CTGGTGTTGGCGCCTGGCTTGAGGGGCCCAGCTTCGGCTCCGGAATCAGCC  1550
             ||||  | |  | |||||| ||||||||||| || || |  || || ||||
VChR2  1526  CTGGCCTGGATGGCTGGCTGGAGGGGCCCAGTTTTGGATTGGGCATTAGCC  1576
```

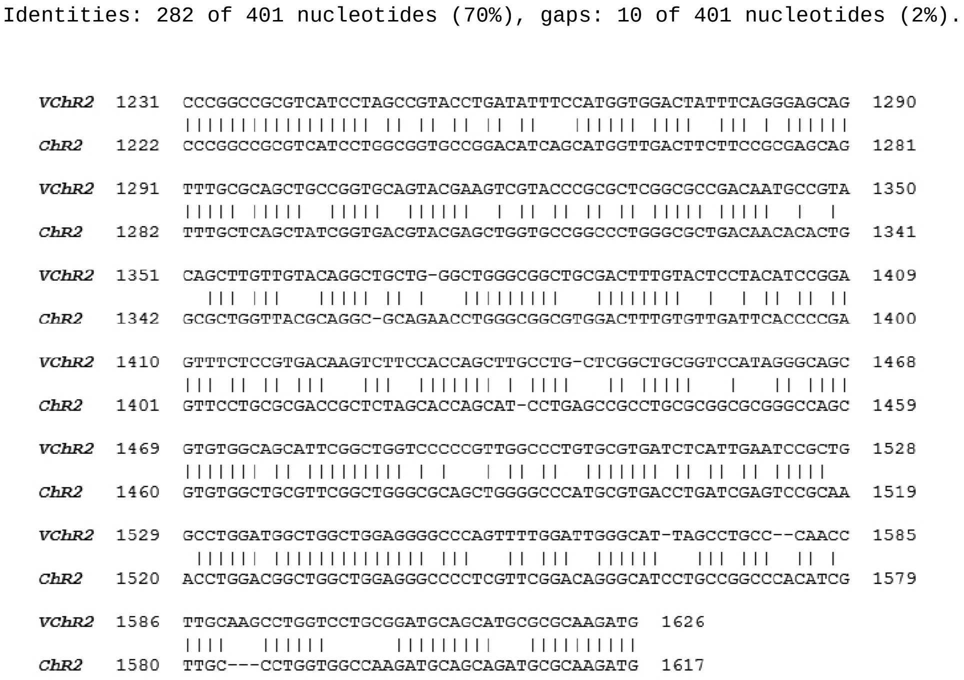
Supplemental Figure S1. Nucleotide sequence alignment of the *VChR1* and *VChR2* coding sequences. BLASTn result (basic local alignment search tool, nucleotide) using the National Center for Biotechnology Information (NCBI) databases. Numbers on both sides of the sequence alignment correspond to nucleotide numbering of *VChR1* (Acc. No. EU285658) and *VChR2* (Acc. No. EU285660) coding sequences.

```
Identities: 1004 of 1432 nucleotides (70%), gaps: 48 of 1432 nucleotides (3%).

VChR1   260    TACCAGGCATGGCGAGCGACGTGCGGGTGGGAGGAGGTTTATGTGGCATTGATTGAGATG   319
               |||||| | |||    | || ||||| ||||||||| |||| |||||   ||| ||||||
ChR1    419    TACCAGACCTGGAAGTCTACTTGCGGCTGGGAGGAGATTTACGTGGCCACGATCGAGATG   478

VChR1   320    ATGAAGAGTATTATCGAGGCCTTTCACGAATTCGATTCACCTGCGACTCTGTGGCTATCT   379
               || |||   || ||||||   || || || || ||   |||||||    | |    |||
ChR1    479    ATCAAGTTCATCATCGAGTATTTCCATGAGTTTGACGAACCTGCGGTGATCTACTCATCC   538

VChR1   380    AGCGGAAACGGGGTTGTCTGGATGCGATACGGCGAATGGTTGCTTACATGCCCGGTGCTC   439
               | ||| |||  |   || ||| | || ||||  || ||| |||| || ||||| ||  |
ChR1    539    AACGGCAACAAGACCGTGTGGCTTCGTTACGCGGAGTGGCTGCTGACCTGCCCTGTCATT   598

VChR1   440    CTGATCCACTTGTCAAATTTAACTGGGCTCAAAGATGATTACAGCAAGCGGACAATGGGT   499
               || |||||  ||   ||  | || || ||     | || || | |||||| || ||||||
ChR1    599    CTTATCCATCTGAGCAACCTTACGGGTCTGGCGAACGACTATAACAAGCGTACCATGGGT   658

VChR1   500    TTGCTCGTCTCCGATGTCGGATGCATCGTATGGGGTGCCACATCCGCCATGTGTACGGGA   559
                |||| || || ||| ||||    ||||| |||||  ||||  ||||  |||  | ||||
ChR1    659    CTGCTGGTGTCAGATATCGGCACGATCGTGTGGGGCACCACGGCCGCGCTGTCCAAGGGA   718

VChR1   560    TG-GACCAAGATCCTGTTCTTCCTTATCTCACTTTCTTACGGCATGTACACGTACTTCCA   618
               |  | ||  | || | |||||||| ||    || |  |||||||| ||||| | |||| |
ChR1    719    TACGTCCGTG-TCATTTTCTTCCTGATGGGCCTGTGCTACGGCATCTACACATTCTTCAA   777

VChR1   619    CGCCGCCAAGGTTTACATCGAGGCATTTCACACGGTGCCCAAGGGCATCTGCCGTGAGCT   678
               ||| |||||||| ||||| ||||| |  ||||| |||||||||||||| ||||| || ||
ChR1    778    CGCAGCCAAGGTCTACATTGAGGCGTACCACACCGTGCCCAAGGGCATTTGCCGCGACCT   837

VChR1   679    GGTGCGGGTCATGGCATGGACCTTTTTCGTCGCGTGGGGCATGTTCCCCGTGCTCTTCTT   738
               ||| ||   | | || |||  ||  |||    | ||||  |||||||| ||||| ||| |
ChR1    838    GGTCCGCTACCTTGCCTGGCTCTACTTCTGTTCATGGGCTATGTTCCCGGTGCTGTTCCT   897

VChR1   739    ACTGGGAACTGAGGGATTCGGCCACATTTCACCTTATGGT--TCGGCCATCGGCCATTCC   796
                |||||  | ||||| || ||||||||  || |  ||     || ||||||| |||  ||
ChR1    898    GCTGGGCCCCGAGGGCTTTGGCCACAT--CAACCAATTCAACTCTGCCATCGCCCACGCC   955

VChR1   797    ATATTAGACTTGATCGCAAAGAACATGTGGGGTGTTCTCGGCAACTACCTGCGTGTCAAG   856
               ||  | ||| |   | | ||||||   ||| || |  | ||  |||  ||||||||||||
ChR1    956    ATCCTGGACCTTGCCTCCAAGAACGCTTGGAGTATGATGGGTCACTTTCTGCGTGTCAAG   1015

VChR1   857    ATCCACGAGCACATCCTGTTGTACGGCGATATACGGAAGAAGCAGAAGATCACCATCGCA   916
               |||||||||||||||||| |||||||||| || || |||||||||||| ||| | | ||
ChR1    1016   ATCCACGAGCACATCCTGCTGTACGGCGACATCCGCAAGAAGCAGAAGGTCAACGTGGCT   1075

VChR1   917    GGCCAGGAGATGGAGGTGGAGACTCTTGTGGCCGAAGAGGAGGACGACACGGTCAAACAG   976
               |||||||||||||||||||||||  | |||  ||| ||||| ||||| |||   ||   |
ChR1    1076   GGCCAGGAGATGGAGGTGGAGACCATGGTGCACGAGGAGGACGACGAGACGCAGAAGGTG   1135

VChR1   977    TCGACTGCCAAGTATGCATCTCGTGACTCGTTCATCACCATGCGCAATCGTATGCGGGAG   1036
                | || || ||||| ||    || ||||||||||||| ||||||| | ||  |   ||||
ChR1    1136   CCCACGGCAAAGTACGCCAACCGCGACTCGTTCATCATCATGCGCGACCGCCTCAAGGAG   1195

VChR1   1037   AAGGGCTTGGAGGTGCGGGCCTCACTGGATGCCGGTGGTGGCGACAGCGGTATGGAGGCC   1096
               |||||||| |||   || ||||| |||||          ||||||  | | | ||  | |
ChR1    1196   AAGGGCTTCGAGACCCGCGCCTCGCTGGA---------CGGCGAC--CCGAACGG-CGAC   1243
```

```
VChR1  1097  GGCGGTGGCGGCGCCGCACACGCCCAACCACACATGGCAAAGCCCGGCACGGAACTGGGC  1156
             | ||  | |  ||| |||  || |           ||| |||||||| | |||  |||||
ChR1   1244  GCCGAGGCCAACGCTGCAGCCGGC-----------GGC-AAGCCCGGAATGGAGATGGGC  1291

VChR1  1157  AAGACGATGTCCGCCA---GCTTTACAAACGGAGCCGCCA---------CAAGCTTGGAG  1204
             ||   |||| ||| ||   || | |  |  || |||| ||         | | | | ||
ChR1   1292  AA---GATGACCGGCATGGGCATGAGCATGGGTGCCGGCATGGGCATGGCGAACATCGAT  1348

VChR1  1205  CCGGGCCGGGTTATCCTGGCCGTTCCGGACATTTCCATGGTCGACTTTTTCAGAGAACAG  1264
              ||||||| || ||||| ||||| |||||||| |||||||| ||||||||| | || |||
ChR1   1349  TCGGGCCGCGTCATCCTCGCCGTGCCGGACATCTCCATGGTGGACTTTTTCCGCGAGCAG  1408

VChR1  1265  TTCGCGCAGCTGCCCGTGCCGTACGAAGTCGTACCCGCCCTTGGCGCCGAGAATACCGTA  1324
             ||||||| |||||||||||| |||||| | || ||||| || ||||| ||||| ||| |
ChR1   1409  TTCGCGCGGCTGCCCGTGCCCTACGAACTGGTGCCCGCGCTGGGCGCGGAGAACACCCTC  1468

VChR1  1325  CAGCTGGTACAGCAGGCTGCGATGTTGGGCGGCTGCGACTTTGTGCTGATGCACCCGGAG  1384
             |||||||| ||||||||   |    |||| ||||||||||| || || |||||||| |||
ChR1   1469  CAGCTGGTGCAGCAGGCGCAGTCACTGGGAGGCTGCGACTTCGTCCTCATGCACCCCGAG  1528

VChR1  1385  TTCTTGCGTGACCGCGGACCCACGGGTCTGCTGCCACAGGTCAAAATGATGGGTCAGCGT  1444
             ||| |||| |||||| | ||||||||||||||||| |   |||| |||   || |||||
ChR1   1529  TTCCTGCGCGACCGCAGTCCCACGGGTCTGCTGCCCCGCCTCAAGATGGGCGGGCAGCGC  1588

VChR1  1445  ACGGCAGCGTTCGGATGGTCTCAGATGGGCCCCATGCGCGACCTCATTGAGAGCTCTGGT  1504
              | || || ||||| ||| |    || ||||||||||| ||| | || ||| | || ||
ChR1   1589  GCCGCGGCCTTCGGCTGGGCGGCAATCGGCCCCATGCGGGACTTGATCGAGGGTTCGGGC  1648

VChR1  1505  GTTGGCGCCTGGCTTGAGGGGCCCAGCTTCGGCTCCGGAATCAGCCAGGCTGCTCTCCAG  1564
             |||| || |||||| ||||| |||||||| ||| |||| |||| ||||   || ||   |
ChR1   1649  GTTGACGGCTGGCTGGAGGGCCCCAGCTTTGGCGCCGGCATCAACCAGCAGGCGCTGGTG  1708

VChR1  1565  CAGCTGGTGGTGAAGATGCAACAGGCCAAGCGCATGGCGGCCATGGGTAGCATGATGGGT  1624
               |||| |       ||||| |||||||||   | |  || ||||    ||   ||||||
ChR1   1709  GCGCTGATCAACCGCATGCAGCAGGCCAAG---AAGATGGGCATGATGGGCGGTATGGGT  1765

VChR1  1625  GGCGGCATGGGCAACGGCATGGGCATGGGCATGGGTATGGGCATGGGCATGG  1676
                |||||||||  ||||||||| ||||||||||||||||||||||||||||
ChR1   1766  ATGGGCATGGGCGGCGGCATGGGTATGGGCATGGGTATGGGCATGGGCATGG  1817
```

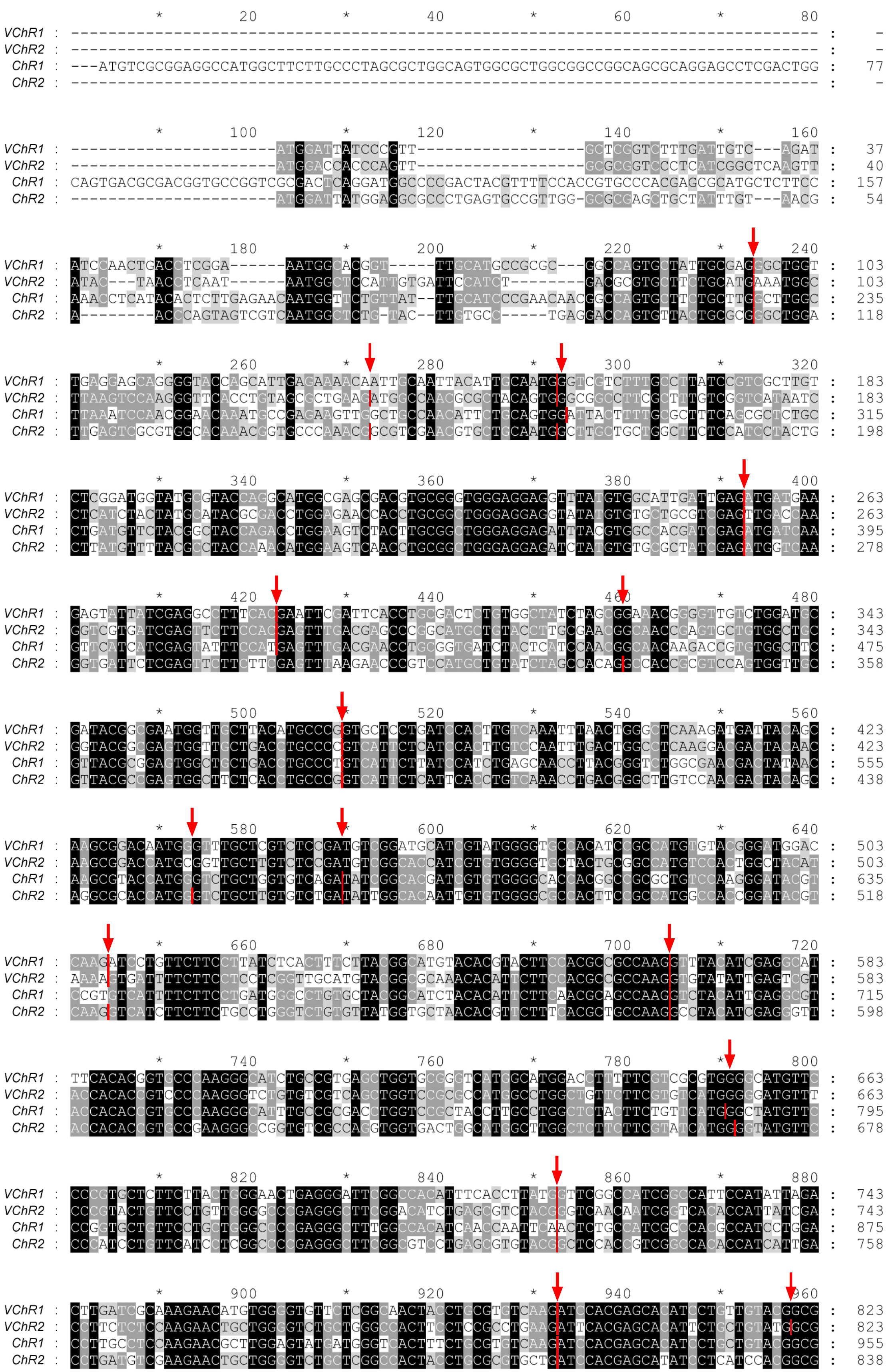
Supplemental Figure S2. Nucleotide sequence alignment of the *VChR1* and Chlamydomonas *ChR1* coding sequences. BLASTn result (basic local alignment search tool, nucleotide) using the National Center for Biotechnology Information (NCBI) databases. Numbers on both sides of the sequence alignment correspond to nucleotide numbering of *VChR1* (Acc. No. EU285658) and *ChR1* (Sineshchekov et al., 2002, Acc. No. AF508965) coding sequences.

```
Identities: 596 of 804 nucleotides (74%), gaps: 15 of 804 nucleotides (2%).

VChR2  262   ACCTGCGGCTGGGAGGAGGTATATGTGTGCTGCGTCGAGTTGACCAAGGTCGTGATCGAG  321
             |||||||||||||||||| | |||||||||    ||||| ||  ||||||  |  |||||
ChR2   262   ACCTGCGGCTGGGAGGAGATCTATGTGTGCGCTATCGAGATGGTCAAGGTGATTCTCGAG  321

VChR2  322   TTCTTCCACGAGTTTGACGAGCCCG-GCATGCTGTACCTTGCGAACGGCAACCGAGTGCT  380
             ||||||  ||||||| | || ||||  ||||||||| || || |  ||| |||| || | 
ChR2   322   TTCTTCTTCGAGTTT-AAGAACCCGTCCATGCTGTATCTAGCCACAGGCCACCGCGTCCA  380

VChR2  381   GTGGCTGCGGTACGGCGAGTGGTTGCTGACCTGCCCCGTCATTCTCATCCACTTGTCCAA  440
             |||| |||| |||| ||||||| | || |||||||| ||||||||||| ||| |||| ||
ChR2   381   GTGGTTGCGTTACGCCGAGTGGCTTCTCACCTGCCCGGTCATTCTCATTCACCTGTCAAA  440

VChR2  441   TTTGACTGGCCTCAAGGACGACTACAACAAGCGGACCATGCGGTTGCTTGTCTCCGATGT  500
               |||| ||| |     ||||||||| || ||| |||||| |  ||||||| || ||| |
ChR2   441   CCTGACGGGCTTGTCCAACGACTACAGCAGGCGCACCATGGGTCTGCTTGTGTCTGATAT  500

VChR2  501   CGGCACCATCGTGTGGGGTGCTACTGCGGCCATGTCCACTGGCTACATAAAAGTGATTTT  560
              ||||| || |||||||| || ||| | |||||| |||| || ||| | || || || ||
ChR2   501   TGGCACAATTGTGTGGGGCGCCACTTCCGCCATGGCCACCGGATACGTCAAGGTCATCTT  560

VChR2  561   CTTCCTCCTCGGT-TGCATGTACGGCGCAAACACATTCTTCCACGCCGCCAAGGTGTATA  619
             ||||  ||| ||| ||  | || || || ||||| ||||| ||||| |||||||  || |
ChR2   561   CTTCTGCCTGGGTCTGTGT-TATGGTGCTAACACGTTCTTTCACGCTGCCAAGGCCTACA  619

VChR2  620   TTGAGTCGTACCACACCGTCCCCAAGGGTCTGTGTCGTCAGCTGGTCCGCGCCATGGCCT  679
             | |||   ||||||||||| || ||||| | |||||| ||| ||||    | |||||| |
ChR2   620   TCGAGGGTTACCACACCGTGCCGAAGGGCCGGTGTCGCCAGGTGGTGACTGGCATGGCTT  679

VChR2  680   GGCTGTTCTTCGTGTCATGGGGGATGTTTCCCGTACTGTTCCTGTTGGGGCCCGAGGGCT  739
             |||| |||||||| |||||||| ||||| ||| | |||||| |  | || ||||||||||
ChR2   680   GGCTCTTCTTCGTATCATGGGGTATGTTCCCCATCCTGTTCATCCTCGGCCCCGAGGGCT  739

VChR2  740   TCGGACATCTGAGCGTCTACGGGTCAACAATCGGTCACACCATTATCGACCTTCTCTCCA  799
             ||||    |||||||| ||||| || ||  |||| |||||||| || |||||  | || |
ChR2   740   TCGGCGTCCTGAGCGTGTACGGCTCCACCGTCGGCCACACCATCATTGACCTGATGTCGA  799

VChR2  800   AGAACTGCTGGGGTCTGCTGGGCCACTTCCTCCGCCTGAAGATTCACGAGCACATTCTGC  859
             ||||||||||||||||||| ||||||| ||| ||| ||  ||| |||||||| || ||  
ChR2   800   AGAACTGCTGGGGTCTGCTCGGCCACTACCTGCGCGTGCTGATCCACGAGCATATCCTCA  859

VChR2  860   TGTATGGCGATATCCGCAAG--GTTCAGA-AGATCA-GGGTGGCCGGTGAGGAGCTGGAG  915
             |  | ||||| || ||||||     || |  || ||  ||||||       ||| | |||
ChR2   860   TCCACGGCGACATTCGCAAGACCACCAAATTGAACATTGGTGGC----ACTGAGATTGAG  915

VChR2  916   GTGGAGACCCTCATGACGGAGGAGGCC---CCCGACACCGTCAAGAAGTCCACTGCGCAG  972
             || ||||| ||  ||  ||| ||||||    | | | | ||||| |||  ||| |   ||
ChR2   916   GTCGAGACGCTGGTGGAGGACGAGGCCGAGGCTGGCGCGGTCAACAAGGGCACCGGCAAG  975

VChR2  973   TACGCCAACAGGGAGTCCTTCTTGACCATGCGTGATAAGCTCAAGGAGAAGGGTTTCGAA  1032
             ||||||  | | ||||||||| ||  |||||| || ||| | |||||||||||  | || 
ChR2   976   TACGCCTCCCGCGAGTCCTTCCTGGTCATGCGCGACAAGATGAAGGAGAAGGGCATTGAC  1035

VChR2  1033  GTGCGTGCTTCGCTGGATAACAGC  1056
             ||||| || || ||||| ||||||
ChR2   1036  GTGCGCGCCTCTCTGGACAACAGC  1059
```

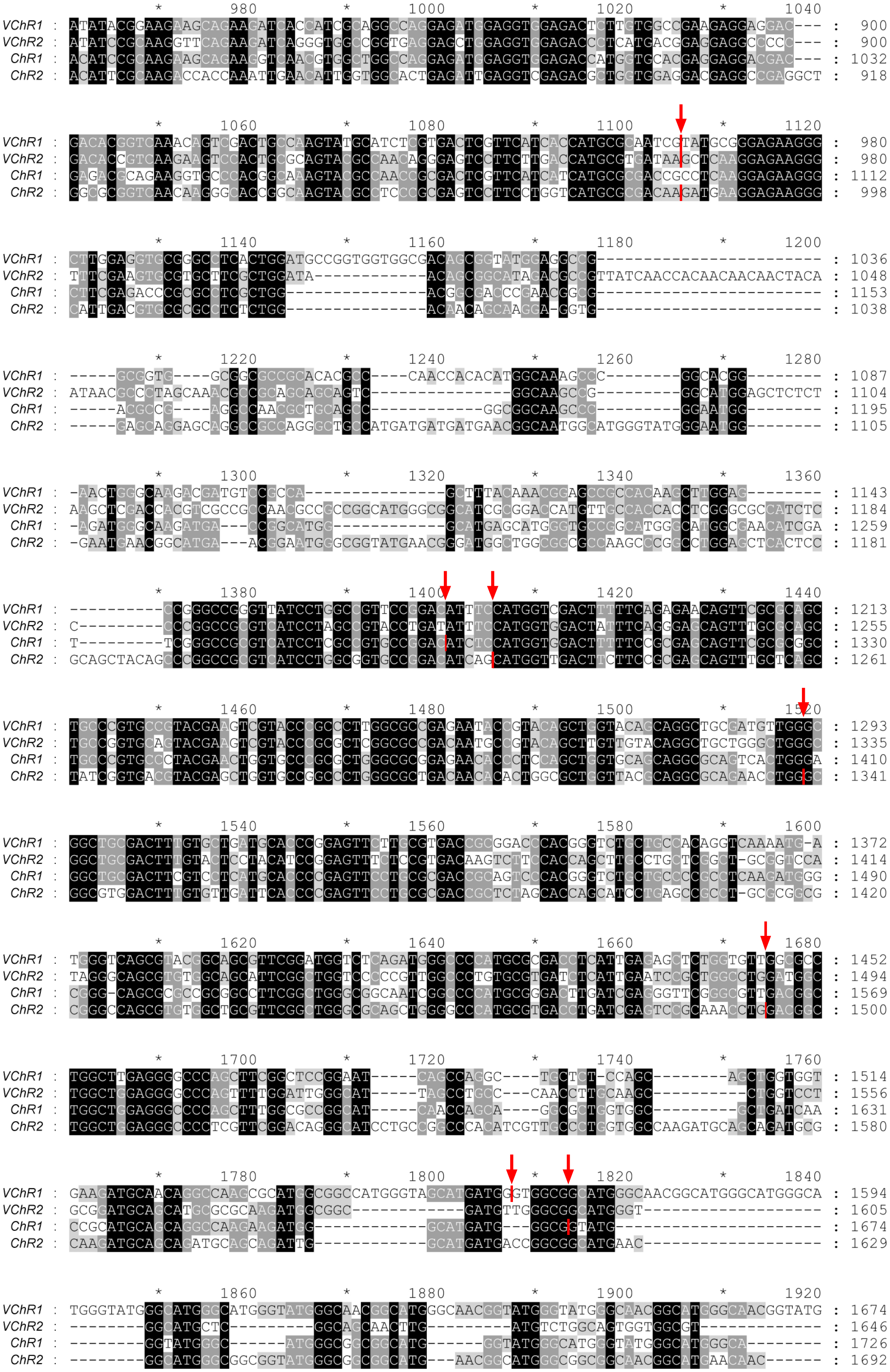


```
Identities: 282 of 401 nucleotides (70%), gaps: 10 of 401 nucleotides (2%).

VChR2  1231  CCCGGCCGCGTCATCCTAGCCGTACCTGATATTTCCATGGTGGACTATTTCAGGGAGCAG  1290
             ||||||||||||||||| || || || || ||   |||||| ||||  ||| | ||||||
ChR2   1222  CCCGGCCGCGTCATCCTGGCGGTGCCGGACATCAGCATGGTTGACTTCTTCCGCGAGCAG  1281

VChR2  1291  TTTGCGCAGCTGCCGGTGCAGTACGAAGTCGTACCCGCGCTCGGCGCCGACAATGCCGTA  1350
             ||||| |||||  |||||  ||||||  | || || || || ||||| |||||  |  |
ChR2   1282  TTTGCTCAGCTATCGGTGACGTACGAGCTGGTGCCGGCCCTGGGCGCTGACAACACACTG  1341

VChR2  1351  CAGCTTGTTGTACAGGCTGCTG-GGCTGGGCGGCTGCGACTTTGTACTCCTACATCCGGA  1409
               ||| |||   ||||| || |   |||||||||   ||||||||  |  | || || ||
ChR2   1342  GCGCTGGTTACGCAGGC-GCAGAACCTGGGCGGCGTGGACTTTGTGTTGATTCACCCCGA  1400

VChR2  1410  GTTTCTCCGTGACAAGTCTTCCACCAGCTTGCCTG-CTCGGCTGCGGTCCATAGGGCAGC  1468
             ||| || || |||   |||  ||||||| |  ||||   || |||||   |   || ||||
ChR2   1401  GTTCCTGCGCGACCGCTCTAGCACCAGCAT-CCTGAGCCGCCTGCGCGGCGCGGGCCAGC  1459

VChR2  1469  GTGTGGCAGCATTCGGCTGGTCCCCCGTTGGCCCTGTGCGTGATCTCATTGAATCCGCTG  1528
             ||||||| || ||||||||| | |   | || ||  ||||||| || || || |||||
ChR2   1460  GTGTGGCTGCGTTCGGCTGGGCGCAGCTGGGGCCCATGCGTGACCTGATCGAGTCCGCAA  1519

VChR2  1529  GCCTGGATGGCTGGCTGGAGGGGCCCAGTTTTGGATTGGGCAT-TAGCCTGCC--CAACC  1585
              |||||| ||||||||||||||| |||   || |||  ||||||   ||| |||  || |
ChR2   1520  ACCTGGACGGCTGGCTGGAGGGCCCCTCGTTCGGACAGGGCATCCTGCCGGCCCACATCG  1579

VChR2  1586  TTGCAAGCCTGGTCCTGCGGATGCAGCATGCGCGCAAGATG  1626
             ||||   ||||||      |||||||||   ||||||||||
ChR2   1580  TTGC---CCTGGTGGCCAAGATGCAGCAGATGCGCAAGATG  1617
```

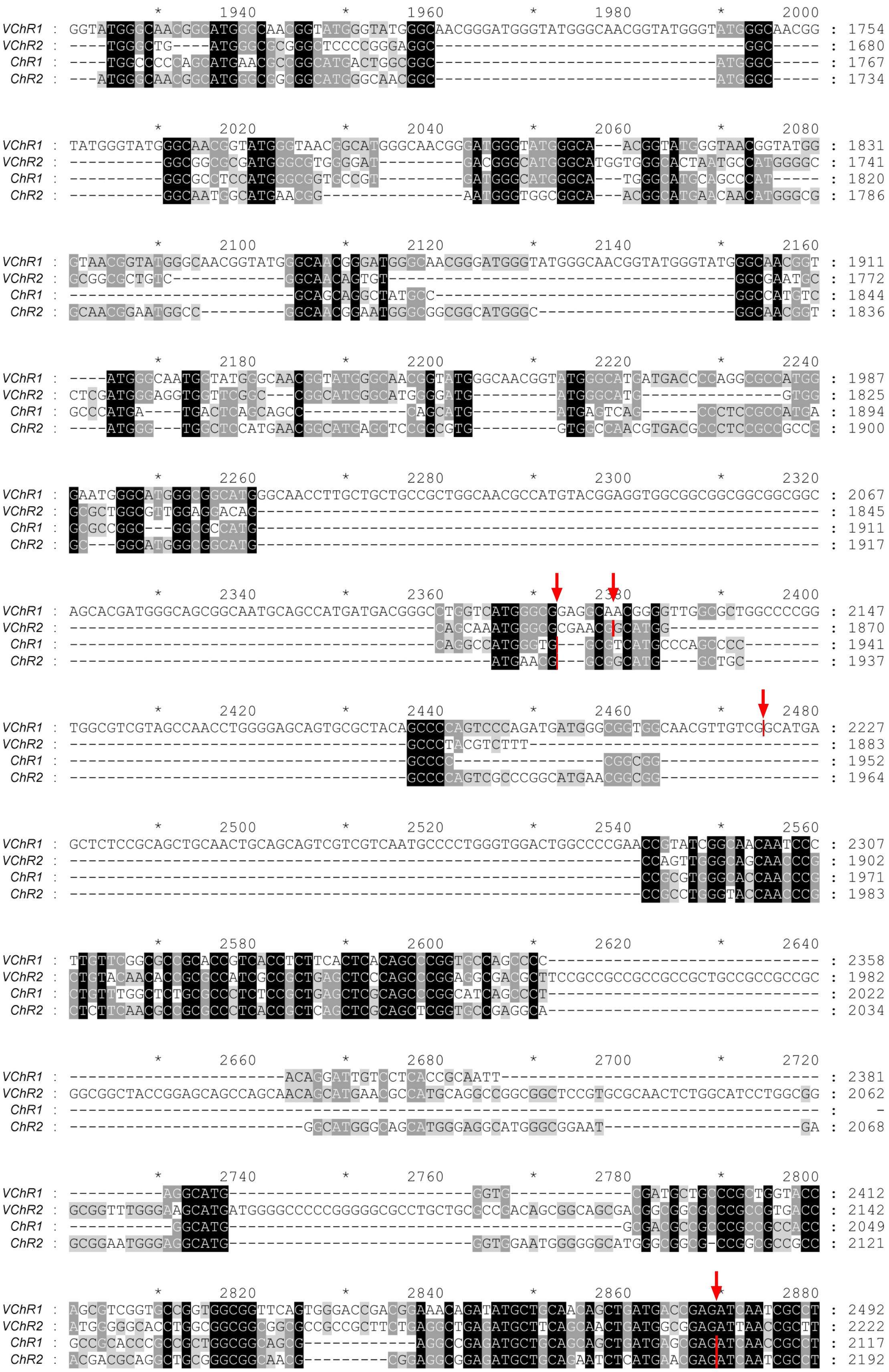
Supplemental Figure S3. Nucleotide sequence alignment of the *VChR2* and Chlamydomonas *ChR2* coding sequences. BLASTn result (basic local alignment search tool, nucleotide) using the National Center for Biotechnology Information (NCBI) databases. Numbers on both sides of the sequence alignment correspond to nucleotide numbering of *VChR2* (Acc. No. EU285660) and *ChR2* (Sineshchekov et al., 2002, Acc. No. AF508966) coding sequences.



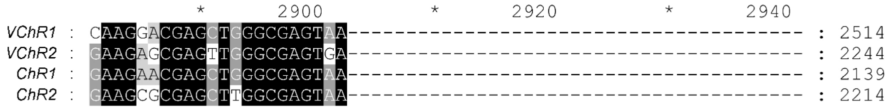
```
                 *        20         *        40         *        60         *        80
VChR1 : -------------------------------------------------------------------------------- :   -
VChR2 : -------------------------------------------------------------------------------- :   -
 ChR1 : ---ATGTCGCGGAGGCCATGGCTTCTTGCCCTAGCGCTGGCAGTGGCGCTGGCGGCCGGCAGCGCAGGAGCCTCGACTGG :  77
 ChR2 : -------------------------------------------------------------------------------- :   -

                 *       100         *       120         *       140         *       160
VChR1 : ----------------------ATGGATTATCCCGTT------------------GCTCGGTCTTTGATTGTC---AGAT :  37
VChR2 : ----------------------ATGGACCACCCAGTT------------------GCGCGGTCCCTCATCGGCTCAAGTT :  40
 ChR1 : CAGTGACGCGACGGTGCCGGTCGCGACTCAGGATGGCCCCGACTACGTTTTCCACCGTGCCCACGAGCGCATGCTCTTCC : 157
 ChR2 : ----------------------ATGGATTATGGAGGCGCCCTGAGTGCCGTTGG-GCGCCAGCTGCTATTTGT---AACG :  54

                 *       180         *       200         *       220         *       240
VChR1 : ATCCAACTGACCTCGGA------AATGGCACGGT-----TTGCATGCCGCGC---GGCCAGTGCTATTGCGAGGGCTGGT : 103
VChR2 : ATAC---TAACCTCAAT------AATGGCTCCATTGTGATTCCATCT--------GACGCGTGCTTCTGCATGAAATGGC : 103
 ChR1 : AAACCTCATACACTCTTGAGAACAATGGTTCTGTTAT--TTGCATCCCGAACAACGGCCAGTGCTTCTGCTTGGCTTGGC : 235
 ChR2 : A--------ACCCAGTAGTCGTCAATGGCTCTG-TAC--TTGTGCC-----TGAGGACCAGTGTTACTGCGCGGGCTGGA : 118

                 *       260         *       280         *       300         *       320
VChR1 : TGAGGAGCAGGGGTACCAGCATTGAGAAAACAATTGCAATTACATTGCAATGGGTCGTCTTTGCCTTATCCGTCGCTTGT : 183
VChR2 : TTAAGTCCAAGGGTTCACCTGTAGCGCTGAAGATGGCCAACGCGCTACAGTGGGCGGCCTTCGCTTTGTCGGTCATAATC : 183
 ChR1 : TTAAATCCAACGGAACAAATGCCGAGAAGTTGGCTGCCAACATTCTGCAGTGGATTACTTTTGCGCTTTCAGCGCTCTGC : 315
 ChR2 : TTGAGTCGCGTGGCACAAACGGTGCCCAAACGGCGTCGAACGTGCTGCAATGGCTTGCTGCTGGCTTCTCCATCCTACTG : 198

                 *       340         *       360         *       380         *       400
VChR1 : CTCGGATGGTATGCGTACCAGGCATGGCGAGCGACGTGCGGGTGGGAGGAGGTTTATGTGGCATTGATTGAGATGATGAA : 263
VChR2 : CTCATCTACTATGCATACGCGACCTGGAGAACCACCTGCGGCTGGGAGGAGGTATATGTGTGCTGCGTCGAGTTGACCAA : 263
 ChR1 : CTGATGTTCTACGGCTACCAGACCTGGAAGTCTACTTGCGGCTGGGAGGAGATTTACGTGGCCACGATCGAGATGATCAA : 395
 ChR2 : CTTATGTTTTACGCCTACCAAACATGGAAGTCAACCTGCGGCTGGGAGGAGATCTATGTGTGCGCTATCGAGATGGTCAA : 278

                 *       420         *       440         *       460         *       480
VChR1 : GAGTATTATCGAGGCCTTTCACGAATTCGATTCACCTGCGACTCTGTGGCTATCTAGCGGAAACGGGGTTGTCTGGATGC : 343
VChR2 : GGTCGTGATCGAGTTCTTCCACGAGTTTGACGAGCCCGGCATGCTGTACCTTGCGAACGGCAACCGAGTGCTGTGGCTGC : 343
 ChR1 : GTTCATCATCGAGTATTTCCATGAGTTTGACGAACCTGCGGTGATCTACTCATCCAACGGCAACAAGACCGTGTGGCTTC : 475
 ChR2 : GGTGATTCTCGAGTTCTTCTTCGAGTTTAAGAACCCGTCCATGCTGTATCTAGCCACAGGCCACCGCGTCCAGTGGTTGC : 358

                 *       500         *       520         *       540         *       560
VChR1 : GATACGGCGAATGGTTGCTTACATGCCCGGTGCTCCTGATCCACTTGTCAAATTTAACTGGGCTCAAAGATGATTACAGC : 423
VChR2 : GGTACGGCGAGTGGTTGCTGACCTGCCCCGTCATTCTCATCCACTTGTCCAATTTGACTGGCCTCAAGGACGACTACAAC : 423
 ChR1 : GTTACGCGGAGTGGCTGCTGACCTGCCCTGTCATTCTTATCCATCTGAGCAACCTTACGGGTCTGGCGAACGACTATAAC : 555
 ChR2 : GTTACGCCGAGTGGCTTCTCACCTGCCCGGTCATTCTCATTCACCTGTCAAACCTGACGGGCTTGTCCAACGACTACAGC : 438

                 *       580         *       600         *       620         *       640
VChR1 : AAGCGGACAATGGGTTTGCTCGTCTCCGATGTCGGATGCATCGTATGGGGTGCCACATCCGCCATGTGTACGGGATGGAC : 503
VChR2 : AAGCGGACCATGCGGTTGCTTGTCTCCGATGTCGGCACCATCGTGTGGGGTGCTACTGCGGCCATGTCCACTGGCTACAT : 503
 ChR1 : AAGCGTACCATGGGTCTGCTGGTGTCAGATATCGGCACGATCGTGTGGGGCACCACGGCCGCGCTGTCCAAGGGATACGT : 635
 ChR2 : AGGCGCACCATGGGTCTGCTTGTGTCTGATATTGGCACAATTGTGTGGGGCGCCACTTCCGCCATGGCCACCGGATACGT : 518

                 *       660         *       680         *       700         *       720
VChR1 : CAAGATCCTGTTCTTCCTTATCTCACTTTCTTACGGCATGTACACGTACTTCCACGCCGCCAAGGTTTACATCGAGGCAT : 583
VChR2 : AAAAGTGATTTTCTTCCTCCTCGGTTGCATGTACGGCGCAAACACATTCTTCCACGCCGCCAAGGTGTATATTGAGTCGT : 583
 ChR1 : CCGTGTCATTTTCTTCCTGATGGGCCTGTGCTACGGCATCTACACATTCTTCAACGCAGCCAAGGTCTACATTGAGGCGT : 715
 ChR2 : CAAGGTCATCTTCTTCTGCCTGGGTCTGTGTTATGGTGCTAACACGTTCTTTCACGCTGCCAAGGCCTACATCGAGGGTT : 598

                 *       740         *       760         *       780         *       800
VChR1 : TTCACACGGTGCCCAAGGGCATCTGCCGTGAGCTGGTGCGGGTCATGGCATGGACCTTTTTCGTCGCGTGGGGCATGTTC : 663
VChR2 : ACCACACCGTCCCCAAGGGTCTGTGTCGTCAGCTGGTCCGCGCCATGGCCTGGCTGTTCTTCGTGTCATGGGGGATGTTT : 663
 ChR1 : ACCACACCGTGCCCAAGGGCATTTGCCGCGACCTGGTCCGCTACCTTGCCTGGCTCTACTTCTGTTCATGGGCTATGTTC : 795
 ChR2 : ACCACACCGTGCCGAAGGGCCGGTGTCGCCAGGTGGTGACTGGCATGGCTTGGCTCTTCTTCGTATCATGGGGTATGTTC : 678

                 *       820         *       840         *       860         *       880
VChR1 : CCCGTGCTCTTCTTACTGGGAACTGAGGGATTCGGCCACATTTCACCTTATGGTTCGGCCATCGGCCATTCCATATTAGA : 743
VChR2 : CCCGTACTGTTCCTGTTGGGGCCCGAGGGCTTCGGACATCTGAGCGTCTACGGGTCAACAATCGGTCACACCATTATCGA : 743
 ChR1 : CCGGTGCTGTTCCTGCTGGGCCCCGAGGGCTTTGGCCACATCAACCAATTCAACTCTGCCATCGCCCACGCCATCCTGGA : 875
 ChR2 : CCCATCCTGTTCATCCTCGGCCCCGAGGGCTTCGGCGTCCTGAGCGTGTACGGCTCCACCGTCGGCCACACCATCATTGA : 758

                 *       900         *       920         *       940         *       960
VChR1 : CTTGATCGCAAAGAACATGTGGGGTGTTCTCGGCAACTACCTGCGTGTCAAGATCCACGAGCACATCCTGTTGTACGGCG : 823
VChR2 : CCTTCTCTCCAAGAACTGCTGGGGTCTGCTGGGCCACTTCCTCCGCCTGAAGATTCACGAGCACATTCTGCTGTATGGCG : 823
 ChR1 : CCTTGCCTCCAAGAACGCTTGGAGTATGATGGGTCACTTTCTGCGTGTCAAGATCCACGAGCACATCCTGCTGTACGGCG : 955
 ChR2 : CCTGATGTCGAAGAACTGCTGGGGTCTGCTCGGCCACTACCTGCGCGTGCTGATCCACGAGCATATCCTCATCCACGGCG : 838
```



```
                  *       980         *      1000         *      1020         *      1040
VChR1 : ATATACGGAAGAAGCAGAAGATCACCATCGCAGGCCAGGAGATGGAGGTGGAGACTCTTGTGGCCGAAGAGGAGGAC--- :  900
VChR2 : ATATCCGCAAGGTTCAGAAGATCAGGGTGGCCGGTGAGGAGCTGGAGGTGGAGACCCTCATGACGGAGGAGGCCCCC--- :  900
 ChR1 : ACATCCGCAAGAAGCAGAAGGTCAACGTGGCTGGCCAGGAGATGGAGGTGGAGACCATGGTGCACGAGGAGGACGAC--- : 1032
 ChR2 : ACATTCGCAAGACCACCAAATTGAACATTGGTGGCACTGAGATTGAGGTCGAGACGCTGGTGGAGGACGAGGCCGAGGCT :  918

                  *      1060         *      1080         *      1100         *      1120
VChR1 : GACACGGTCAAACAGTCGACTGCCAAGTATGCATCTCGTGACTCGTTCATCACCATGCGCAATCGTATGCGGGAGAAGGG :  980
VChR2 : GACACCGTCAAGAAGTCCACTGCGCAGTACGCCAACAGGGAGTCCTTCTTGACCATGCGTGATAAGCTCAAGGAGAAGGG :  980
 ChR1 : GAGACGCAGAAGGTGCCCACGGCAAAGTACGCCAACCGCGACTCGTTCATCATCATGCGCGACCGCCTCAAGGAGAAGGG : 1112
 ChR2 : GGCGCGGTCAACAAGGGCACCGGCAAGTACGCCTCCCGCGAGTCCTTCCTGGTCATGCGCGACAAGATGAAGGAGAAGGG :  998

                  *      1140         *      1160         *      1180         *      1200
VChR1 : CTTGGAGGTGCGGGCCTCACTGGATGCCGGTGGTGGCGACAGCGGTATGGAGGCCG------------------------ : 1036
VChR2 : TTTCGAAGTGCGTGCTTCGCTGGATA------------ACAGCGGCATAGACGCCGTTATCAACCACAACAACAACTACA : 1048
 ChR1 : CTTCGAGACCCGCGCCTCGCTGG---------------ACGGCGACCCGAACGGCG------------------------ : 1153
 ChR2 : CATTGACGTGCGCGCCTCTCTGG---------------ACAACAGCAAGGA-GGTG------------------------ : 1038

                  *      1220         *      1240         *      1260         *      1280
VChR1 : -----GCGGTG----GCGGCGCCGCACACGCC----CAACCACACATGGCAAAGCCC---------GGCACGG-------- : 1087
VChR2 : ATAACGCCCTAGCAAACGCCGCAGCAGCAGTC---------------GGCAAGCCG---------GGCATGGAGCTCTCT : 1104
 ChR1 : -----ACGCCG----AGGCCAACGCTGCAGCC------------GGCGGCAAGCCC---------GGAATGG-------- : 1195
 ChR2 : -----GAGCAGGAGCAGGCCGCCAGGGCTGCCATGATGATGATGAACGGCAATGGCATGGGTATGGGAATGG-------- : 1105

                  *      1300         *      1320         *      1340         *      1360
VChR1 : -AACTGGGCAAGACGATGTCCGCCA---------------GCTTTACAAACGGAGCCGCCACAAGCTTGGAG-------- : 1143
VChR2 : AAGCTCGACCACGTCGCCGCCAACGCCGCCGGCATGGGCGGCATCGCGGACCATGTTGCCACCACCTCGGCGCCATCTC : 1184
 ChR1 : -AGATGGGCAAGATGA---CCGGCATGG------------GCATGAGCATGGGTGCCGGCATGGGCATGGCGAACATCGA : 1259
 ChR2 : -GAATGAACGGCATGA---ACGGAATGGGCGGTATGAACGGGATGGCTGGCGGCGCCAAGCCCGGCCTGGAGCTCACTCC : 1181

                  *      1380         *      1400         *      1420         *      1440
VChR1 : ----------CCGGGCCGGGTTATCCTGGCCGTTCCGGACATTTCCATGGTCGACTTTTTCAGAGAACAGTTCGCGCAGC : 1213
VChR2 : C---------CCCGGCCGCGTCATCCTAGCCGTACCTGATATTTCCATGGTGGACTATTTCAGGGAGCAGTTTGCGCAGC : 1255
 ChR1 : T---------TCGGGCCGCGTCATCCTCGCCGTGCCGGACATCTCCATGGTGGACTTTTTCCGCGAGCAGTTCGCGCGGC : 1330
 ChR2 : GCAGCTACAGCCCGGCCGCGTCATCCTGGCGGTGCCGGACATCAGCATGGTTGACTTCTTCCGCGAGCAGTTTGCTCAGC : 1261

                  *      1460         *      1480         *      1500         *      1520
VChR1 : TGCCCGTGCCGTACGAAGTCGTACCCGCCCTTGGCGCCGAGAATACCGTACAGCTGGTACAGCAGGCTGCGATGTTGGGC : 1293
VChR2 : TGCCGGTGCAGTACGAAGTCGTACCCGCGCTCGGCGCCGACAATGCCGTACAGCTTGTTGTACAGGCTGCTGGGCTGGGC : 1335
 ChR1 : TGCCCGTGCCCTACGAACTGGTGCCCGCGCTGGGCGCGGAGAACACCCTCCAGCTGGTGCAGCAGGCGCAGTCACTGGGA : 1410
 ChR2 : TATCGGTGACGTACGAGCTGGTGCCGGCCCTGGGCGCTGACAACACACTGGCGCTGGTTACGCAGGCGCAGAACCTGGGC : 1341

                  *      1540         *      1560         *      1580         *      1600
VChR1 : GGCTGCGACTTTGTGCTGATGCACCCGGAGTTCTTGCGTGACCGCGGACCCACGGGTCTGCTGCCACAGGTCAAAATG-A : 1372
VChR2 : GGCTGCGACTTTGTACTCCTACATCCGGAGTTTCTCCGTGACAAGTCTTCCACCAGCTTGCCTGCTCGGCT-GCGGTCCA : 1414
 ChR1 : GGCTGCGACTTCGTCCTCATGCACCCCGAGTTCCTGCGCGACCGCAGTCCCACGGGTCTGCTGCCCCGCCTCAAGATGGG : 1490
 ChR2 : GGCGTGGACTTTGTGTTGATTCACCCCGAGTTCCTGCGCGACCGCTCTAGCACCAGCATCCTGAGCCGCCT-GCGCGGCG : 1420

                  *      1620         *      1640         *      1660         *      1680
VChR1 : TGGGTCAGCGTACGGCAGCGTTCGGATGGTCTCAGATGGGCCCATGCGCGACCTCATTGAGAGCTCTGGTGTTGGCGCC : 1452
VChR2 : TAGGGCAGCGTGTGGCAGCATTCGGCTGGTCCCCCGTTGGCCCTGTGCGTGATCTCATTGAATCCGCTGGCCTGGATGGC : 1494
 ChR1 : CGGG-CAGCGCGCCGCGGCCTTCGGCTGGGCGGCAATCGGCCCCATGCGGGACTTGATCGAGGGTTCGGGCGTTGACGGC : 1569
 ChR2 : CGGGCCAGCGTGTGGCTGCGTTCGGCTGGGCGCAGCTGGGGCCCATGCGTGACCTGATCGAGTCCGCAAACCTGGACGGC : 1500

                  *      1700         *      1720         *      1740         *      1760
VChR1 : TGGCTTGAGGGGCCCAGCTTCGGCTCCGGAAT-----CAGCCAGGC----TGCTCT-CCAGC--------AGCTGGTGGT : 1514
VChR2 : TGGCTGGAGGGGCCCAGTTTTGGATTGGGCAT-----TAGCCTGCC---CAACCTTGCAAGC----------CTGGTCCT : 1556
 ChR1 : TGGCTGGAGGGCCCCAGCTTTGGCGCCGGCAT-----CAACCAGCA----GGCGCTGGTGGC---------GCTGATCAA : 1631
 ChR2 : TGGCTGGAGGGCCCCTCGTTCGGACAGGGCATCCTGCCGGCCCACATCGTTGCCCTGGTGGCCAAGATGCAGCAGATGCG : 1580

                  *      1780         *      1800         *      1820         *      1840
VChR1 : GAAGATGCAACAGGCCAAGCGCATGGCGGCCATGGGTAGCATGATGGGTGGCGGCATGGGCAACGGCATGGGCATGGGCA : 1594
VChR2 : GCGGATGCAGCATGCGCGCAAGATGGCGGC------------GATGTTGGGCGGCATGGGT------------------- : 1605
 ChR1 : CCGCATGCAGCAGGCCAAGAAGATGG------------GCATGATG---GGCGGTATG---------------------- : 1674
 ChR2 : CAAGATGCAGCAGATGCAGCAGATTG------------GCATGATGACCGGCGGCATGAAC------------------- : 1629

                  *      1860         *      1880         *      1900         *      1920
VChR1 : TGGGTATGGGCATGGGCATGGGTATGGGCAACGGCATGGGCAACGGTATGGGTATGGGCAACGGCATGGGCAACGGTATG : 1674
VChR2 : --------GGCATGCTC----------GGCAGCAACTTG----------ATGTCTGGCAGTGGTGGCGT------------ : 1646
 ChR1 : --------GGTATGGGC------ATGGGCGGCGGCATG------GGTATGGGCATGGGTATGGGCATGGGCA--------- : 1726
 ChR2 : --------GGCATGGGCGGCGGTATGGGCGGCGGCATG---AACGGCATGGGCGGCGGCAACGGCATGAACAAC------ : 1692
```



```
                 *      1940         *      1960         *      1980         *      2000
VChR1 : GGTATGGGCAACGGCATGGGCAACGGTATGGGTATGGGCAACGGGATGGGTATGGGCAACGGTATGGGTATGGGCAACGG : 1754
VChR2 : ----TGGGCTG----ATGGGCGCGGGCTCCCCGGGAGGC---------------------------------GGC----- : 1680
 ChR1 : ----TGGCCCCCAGCATGAACGCCGGCATGACTGGCGGC------------------------------ATGGGC----- : 1767
 ChR2 : ---ATGGGCAACGGCATGGGCGGCGGCATGGGCAACGGC------------------------------ATGGGC----- : 1734

                 *      2020         *      2040         *      2060         *      2080
VChR1 : TATGGGTATGGGCAACGGTATGGGTAACGGCATGGGCAACGGGATGGGTATGGGCA---ACGGTATGGGTAACGGTATGG : 1831
VChR2 : ----------GGCGGCGCGATGGGCGTGGGAT----------GACGGGCATGGGCATGGTGGGCACTAATGCCATGGGGC : 1741
 ChR1 : ----------GGCGCCTCCATGGCGGTGCCGT----------GATGGGCATGGGCA---TGGGCATGCAGCCCAT----- : 1820
 ChR2 : ----------GGCAATGGCATGAACGG---------------AATGGGTGGCGGCA---ACGGCATGAACAACATGGGCG : 1786

                 *      2100         *      2120         *      2140         *      2160
VChR1 : GTAACGGTATGGGCAACGGTATGGGCAACGGGATGGGCAACGGGATGGGTATGGGCAACGGTATGGGTATGGGCAACGGT : 1911
VChR2 : GCGGCGCTGTC------------GGCAACAGTGT-------------------------------------GGCGAATGC : 1772
 ChR1 : ------------------------GCAGCAGGCTATGCC--------------------------------GGCCATGTC : 1844
 ChR2 : GCAACGGAATGGCC---------GGCAACGGAATGGGCGGCGGCATGGGC---------------------GGCAACGGT : 1836

                 *      2180         *      2200         *      2220         *      2240
VChR1 : ----ATGGGCAATGGTATGGGCAACGGTATGGGCAACGGTATGGGCAACGGTATGGGCATGATGACCCCAGGCGCCATGG : 1987
VChR2 : CTCGATGGGAGGTGGTTCGGC---CGGCATGGGCATGGGGATG---------ATGGGCATG---------------GTGG : 1825
 ChR1 : GCCCATGA----TGACTCAGCAGCC-----------CAGCATG---------ATGAGTCAG------CCCTCCGCCATGA : 1894
 ChR2 : ----ATGGG---TGGCTCCATGAACGGCATGAGCTCCGGCGTG---------GTGGCCAACGTGACGCCCTCCGCCGCCG : 1900

                 *      2260         *      2280         *      2300         *      2320
VChR1 : GAATGGGCATGGGCGGCATGGGCAACCTTGCTGCTGCCGCTGGCAACGCCATGTACGGAGGTGGCGGCGGCGGCGGCGGC : 2067
VChR2 : GCGCTGGCGTTGGAGGACAG------------------------------------------------------------ : 1845
 ChR1 : GCGCCGGC---GGCGCCATG------------------------------------------------------------ : 1911
 ChR2 : GC---GGCATGGGCGGCATG------------------------------------------------------------ : 1917

                 *      2340         *      2360         *      2380         *      2400
VChR1 : AGCACGATGGGCAGCGGCAATGCAGCCATGATGACGGGCCTGGTCATGGGCGGAGGCAACGGGGTTGGCGCTGGCCCCGG : 2147
VChR2 : ---------------------------------------CAGCAAATGGGCGCGAACGGCATGG---------------- : 1870
 ChR1 : ---------------------------------------CAGGCCATGGGTG---GCGTCATGCCCAGCCCC-------- : 1941
 ChR2 : ---------------------------------------------ATGAACG---GCGGCATG----GCTGC-------- : 1937

                 *      2420         *      2440         *      2460         *      2480
VChR1 : TGGCGTCGTAGCCAACCTGGGGAGCAGTGCGCTACAGCCCCAGTCCCAGATGATGGGCGGTGGCAACGTTGTCGGCATGA : 2227
VChR2 : ------------------------------------GCCCTACGTCTTT------------------------------- : 1883
 ChR1 : ------------------------------------GCCCC----------------CGGCGG----------------- : 1952
 ChR2 : ------------------------------------GCCCCAGTCGCCCGGCATGAACGGCGG----------------- : 1964

                 *      2500         *      2520         *      2540         *      2560
VChR1 : GCTCTCCGCAGCTGCAACTGCAGCAGTCGTCGTCAATGCCCCTGGGTGGACTGGCCCCGAACCGTATCGGCAACAATCCC : 2307
VChR2 : -------------------------------------------------------------CCAGTTGGGCAGCAACCCG : 1902
 ChR1 : -------------------------------------------------------------CCGCGTGGGCACCAACCCG : 1971
 ChR2 : -------------------------------------------------------------CCGCCTGGGTACCAACCCG : 1983

                 *      2580         *      2600         *      2620         *      2640
VChR1 : TTGTTCGGCGCCGCACCGTCACCTCTTCACTCACAGCCCGGTGCCAGCCCC----------------------------- : 2358
VChR2 : CTGTACAACACCGCGCCATCGCCGCTGAGCTCCCAGCCCGGAGGCGACGCTTCCGCCGCCGCCGCCGCTGCCGCCGCCGC : 1982
 ChR1 : CTGTTTGGCTCTGCGCCCTCTCCGCTGAGCTCGCAGCCCGGCATCAGCCCT----------------------------- : 2022
 ChR2 : CTCTTCAACGCCGCGCCCTCACCGCTCAGCTCGCAGCTCGGTGCCGAGGCA----------------------------- : 2034

                 *      2660         *      2680         *      2700         *      2720
VChR1 : -----------------------ACAGGATTGTCCTCACCGCAATT---------------------------------- : 2381
VChR2 : GGCGGCTACCGGAGCAGCCAGCAACAGCATGAACGCCATGCAGGCCGGCGGCTCCGTGCGCAACTCTGGCATCCTGGCGG : 2062
 ChR1 : -------------------------------------------------------------------------------- :    -
 ChR2 : -------------------------GGCATGGGCAGCATGGGAGGCATGGGCGGAAT---------------------GA : 2068

                 *      2740         *      2760         *      2780         *      2800
VChR1 : ----------AGGCATG--------------------------GGTG-------------CGATGCTGCCCGCTGGTACC : 2412
VChR2 : GCGGTTTGGGAAGCATGATGGGGCCCCCGGGGGCGCCTGCTGCGCCGACAGCGGCAGCGACGGCGGCGCCCGCCGTGACC : 2142
 ChR1 : -----------GGCATG------------------------------------------GCGACGCCGCCCGCCGCCACC : 2049
 ChR2 : GCGGAATGGGAGGCATG--------------------------GGTGGAATGGGGGGCATGGGCGGCG-CCGGCGCCGCC : 2121

                 *      2820         *      2840         *      2860         *      2880
VChR1 : AGCGTCGGTGCCGGTGGCGGTTCAGTGGGACCGACGGAAACAGATATGCTGCAACAGCTGATGACCGAGATCAATCGCCT : 2492
VChR2 : ATGGGGGCACCTGGCGGCGGCGGCGCCGCCGCTTCTGAGGCTGAGATGCTTCAGCAACTGATGGCGGAGATTAACCGCTT : 2222
 ChR1 : GCCGCACCCGCCGCTGGCGGCAGCG------------AGGCCGAGATGCTGCAGCAGCTGATGAGCGAGATCAACCGCCT : 2117
 ChR2 : ACGACGCAGGCTGCGGGCGGCAACG---------CGGAGGCGGAGATGCTGCAGAATCTCATGAACGAGATCAATCGCCT : 2192
```



```
                   *       2900         *       2920         *       2940
VChR1 : CAAGGACGAGCTGGGCGAGTAA--------------------------------------- : 2514
VChR2 : GAAGAGCGAGTTGGGCGAGTGA--------------------------------------- : 2244
 ChR1 : GAAGAACGAGCTGGGCGAGTAA--------------------------------------- : 2139
 ChR2 : GAAGCGCGAGCTTGGCGAGTAA--------------------------------------- : 2214
```

Supplemental Figure S4. Aligned coding sequences of *VChR1*, *VChR2*, *ChR1* and *ChR2* with highlighted intron positions. Alignment of nucleotide sequences was done using the MUltiple Sequence Comparison by Log-Expectation program (MUSCLE) . Alignments were illustrated using GeneDoc 2.6 . White letters on black background, conserved in 100% of the sequences at the corresponding position; white letters on dark gray background, conserved in 75% of the sequences at the corresponding position; black letters on light gray background, conserved in 50% of the sequences at the corresponding position. Intron positions are indicated within each coding sequence by vertical red bars. Sites with introns are highlighted with red arrows. Numbers at the right side of the sequence alignment correspond to nucleotide numbering of *VChR1* (Acc. No. EU285658), *VChR2* (Acc. No. EU285660), *ChR1* (Sineshchekov et al., 2002, Acc. No. AF508965), and *ChR2* (Sineshchekov et al., 2002, Acc. No. AF508966) coding sequences. The numbers above the alignment (marker line) are for orientation.

con1

```
Identities: 51 of 70 residues (73%), similarities: 64 of 70 residues (91%),
gaps: 0 of 70 residues (0%).

VChR1  266  IHEHILLYGDIRKKQKITIAGQEMEVETLVAEEEDDTVKQSTAKYASRDSFITMRNRMRE  325
            IHEHILLYGDIRK QKI +AG+E+EVETL+ EE  DTVK+STA+YA+R+SF+TMR++++E
VChR2  266  IHEHILLYGDIRKVQKIRVAGEELEVETLMTEEAPDTVKKSTAQYANRESFLTMRDKLKE  325

VChR1  326  KGLEVRASLD  335
            KG EVRASLD
VChR2  326  KGFEVRASLD  335
```

con2

```
Identities: 86 of 113 residues (76%), similarities: 98 of 113 residues (87%),
gaps: 0 of 113 residues (0%).

VChR1  383  GRVILAVPDISMVDFFREQFAQLPVPYEVVPALGAENTVQLVQQAAMLGGCDFVLMHPEF  442
            GRVILAVPDISMVD+FREQFAQLPV YEVVPALGA+N VQLV QAA LGGCDFVL+HPEF
VChR2  397  GRVILAVPDISMVDYFREQFAQLPVQYEVVPALGADNAVQLVVQAAGLGGCDFVLLHPEF  456

VChR1  443  LRDRGPTGLLPQVKMMGQRTAAFGWSQMGPMRDLIESSGVGAWLEGPSFGSGI  495
            LRD+  T L  +++ +GQR AAFGWS +GP+RDLIES+G+  WLEGPSFG GI
VChR2  457  LRDKSSTSLPARLRSIGQRVAAFGWSPVGPVRDLIESAGLDGWLEGPSFGLGI  509
```

con3

```
Identities: 17 of 21 residues (81%), similarities: 18 of 21 residues (86%),
gaps: 0 of 21 residues (0%).

VChR1  817  ETDMLQQLMTEINRLKDELGE  837
            E +MLQQLM EINRLK ELGE
VChR2  727  EAEMLQQLMAEINRLKSELGE  747
```

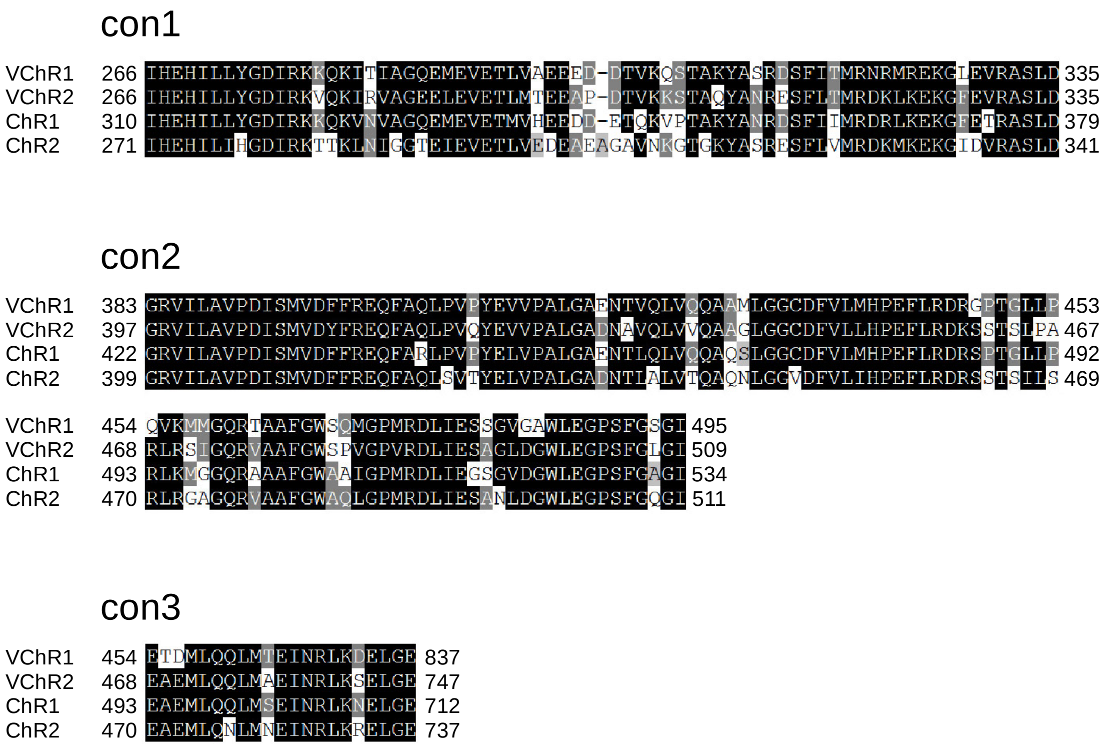
Supplemental Figure S5. Protein sequence alignment of the con1, con2 and con3 regions of VChR1 and VChR2. BLASTp result (basic local alignment search tool, protein) using the National Center for Biotechnology Information (NCBI) databases. Numbers on both sides of the sequence alignment correspond to amino acid residue numbering of VChR1 (Acc. No. EU285658) and VChR2 (Acc. No. EU285660). Identical and similar (“+”) amino acid residues are given between the sequences.

```
                        10        20        30        40        50        60        70        80        90       100
                ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
VChR1/V.c.      YCEGWLWVVFALSVACLGWYAYQAWRATCGWEEVYVALIEMMKSIIEAFHEFDSPATLWLSSGNGVVWMRYGEWLLTCPVLLIHLSNLTDYSKRTMGLLV
VChR2/V.c.      FCMKWLWAAFALSVIILIYYAYATWRTTCGWEEVYVCCVELTKVVIEFFHEFDEPGMLYLANGNRVLWLRYGEWLLTCPVILIHLSNLTDYNKRTMRLLV
ChR1/C.r.       FCLAWLWITFALSALCLMFYGYQTWKSTCGWEEIYVATIEMIKFIIEYFHEFDEPAVIYSSNGNKTVWLRYAEWLLTCPVILIHLSNLTDYNKRTMGLLV
ChR2/C.r.       YCAGWIWLAAGFSILLLMFYAYQTWKSTCGWEEIYVCAIEMVKVILEFFFEFKNPSMLYLATGHRVQWLRYAEWLLTCPVILIHLSNLTDYSRRTMGLLV
Br/G.v.         SVSDSLSFAIAAMFASALFFFS.AQALVGQRYRLALLVSAIVVSIYHYFRIFNSAAYVLENGVKFNDAYRYVDWLLTVPLLLVETVAVLKEARPLLKLTV
Ops2/G.t.       SGAIFDVLAWIALLFTALFMAFKAVNA.DPVVRKFYYINAFVCGVFSYFAMISGMGWETIMGCRQMFYVRYIDWFITTPLMILNIGLLAGEEQWMIAIMG
Ops1/G.t.       TGVGALTITFLILAVST..IIFITRVGPATSQKVYYYCNVFICGLMSYFAMLSGQGWTAVAGCRQFFYARYVDWTITTALIILELGLIAGAEPALIGVMG
Ops/Cry.sp.     TGIGGLTLGFLALTVTTVVMVAKAANA.DPERRKYYFCNTFICGIFAYFAMLSGQGWTAISGCRQFFYAHYVDWLLTTPLIILNLGLIAGQDYVTIAVCG
Nop-1/N.c.      PTPTEYWVTFALMVLSSGIFALLSWNVPTSK.RLFHVITTLITVVLSYFAMATG.HATTFNCDRQVFWGRYVDWALTTPLLLLELCLLAGVDGAHTMAIV
Hop/S.r.        ALASSIYVNIALAGLTIIVIAVMSRSIHDSRAKLITMSTLMISVVSSYMGLASGIDPLVMPEGVLSLWGRYLTWAFSTPFILLALGLLARSTTDKISAIV
ChoP3/Ha.v.     LLNSSLWVNIALAGVVILLFVAMGRELESSRAKLIWVATMLVPLVSSYAGLASGVGFLQMPPGVLSPWGRYLTWTFSTPMILLALGLLADTDMASLTAIT
Hop/H.m.        LLNSSIWVNIALAGVVILLFVAMGRDLESPRAKLIWVATMLVPLVSSYAGLASGVGFLQMPPGVLSPWGRYLTWTFSTPMILLALGLLADTDIASLTAIT
Hop/N.p.        LLASSLYINIALAGLSILLFVFMTRGLDDPRAKLIAVSTILVPVVASYTGLASGISVLEMPAGVVTMWGRYLTWALSTPMILLALGLLAGSNATKLTAIT
Hop/H.sp.       LLASSLWINIALAGLSILLFVYMGRNVEDPRAQLIFVATLMVPLVSSYTGLVSGVSFLEMPAGVLTPWGRYLTWALSTPMILIAVGLLAGSNTTKLTAVV
Hop/Hr.sod.     LLASSLWINIALAGLSILLFVYMGRNLEDPRAQLIFVATLMVPLVSSYTGLVSGVSFLEMPAGVLTPWGRYLTWALSTPMILVALGLLAGSNATKLTAVT
Hopa/Ht.sp.     LLHSSLWVNIALAGLSILVFLYMARTVRANRARLIVGATLMIPLVSSYLGLVTGAGPIEMPAAVLSQWGRYLTWTLSTPMILLALGWLAEVDTADLVVIA
Hopb/Ht.sp.     LLHSSLWVNIALAGLSILVFLYMARTVRANRARLIVGATLMIPLVSSYLGLVTGAGPIEMPAAVLSQWGRYLTWTLSTPMILLALGWLAEVDTADLVVIA
Hop/H.s.        LLSSSLWVNVALAGIAILVFVYMGRTIRPGRPRLIWGATLMIPLVSSYLGLLSGVGMIEMPAGVRSQWGRYLTWALSTPMILLALGLLADVDLGSLTVIA
Hop/H.w.        LLSSSLWVNIALAGLSILLFVYMGRNITSGRARLIWGATLMIPLVSSYLGLASGVGFIEMPAGVMSQWGRYLTWALSTPMILLALGVLADVDRGSLTVIA
Br/N.sp.        LESLLHWIYVAGMTIGALHFWSLSRNPRGVPQYEYLVA.MFIPIWLAYMAMAIDQGKVEAAGQ.IAHYARYIDWMVTTPLLLLSLSWTAKKDWTLIFLMS
Xop2/H.m.       QEIVWYGAGAGAFFVSAVVFVWFAATRGNIRSSFYYLPPIHTS.VAAYVAMAL.IAGGQLGDTVSITTLRFADWIVSTPIITYYLARLAGVDTQTRLAVA
Sop1/H.sp.      AVSAAYWIAAVAFLVGLGITAALYAKLGESEDRGRLAALAVIPGFLAYAGMALGIGTVTVNGA.ELVGLRYVDWIVTTPLLVGFIGYVAGASRRAIGVML
Sop/Hr.sod.     AVTSAYWLAAVAFLIGVGITAALYAKLEGSRARTRLAALAVIPGFLSYVGMALGIGTVTVNGA.ELVGLRYVDWVVTTPLLVGFIGYNAGASRRAIGVMI
Sop1/H.s.       AVATAYLGGAVALIVGVAFVWLLYRSLDGSPHQSALAPLAIIPVFLSYVGMAYDIGTVIVNGN.QIVGLRYIDWLVTTPILVGYVGYAAGASRRSIGVMV
Csr3/Ha.v.      AVAVVYGITAAGFAVGVAIVGYLYASLEGSEERSILAALALIPGFISYVAMAFGIGTVTIGET.TLVGFRYLDWVVTTPLLVGFVGYAAGASRRAIGVMV
Sria/S.r.       PITIVYIIGTLGMLVGI....PPALSLVGDEVGLDFDYVWAIPGIFMYLLMTFDVGSVQFQGY.HVPIPRYIDWALTTPLLVGYTAYIAGASRGMIGTAL
Srib/S.r.       ATTIVLMLGTAGMLFGI....PPCLRLLDMEADGHFGYLLLIPGFLMYALMTFGVGTQTFQGQ.TVPLLRYLDWLVTTPIMIGYAAYVAGTSKRGIGAAL
BopII/H.w.      SEATWLWIGTIGMVLGTVYFAVRGRGSTDPEQQTYYIITTLIPAIAAYLAMATGLGVISMPIRIDIYWARYADWLLTTPLLIIDLALVAGARKQTLKLII
BopI/H.w.       GEGIWLALGTIGMLLGMLYFIADGLDVQDPRQKEFYVITILIPAIASYLSMFFGFGLTEVSLAVDVYWARYADWLFTTPLLLLDIGLLAGASQRDIALVG
Xop1/H.m.       GEGIWLALGTVGMLLGMVYFMAKGWDVQDPEQEEFYVITILIAGISSYLSMFFGFGLTEVELVIDVYWARYADWLFTTPLLLLDIGLLAGASNRDMSLIT
Bop/H.s.        PEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAITMYLSMLLGYGLTMVPFGNPIYWARYADWLFTTPLLLLDLALLVDADQGTIALVG
Ar2/H.sp.       PETLWLGIGTLLMLIGTFYFIARGWGVTDKEAREYYAITILVPGIAAYLAMFFGIGVTEVELALDIYYARYADWLFTTPLLLLDLALLAKVDRVTITLIG
Ar3/Hr.sod.     PETLWLGIGTLLMLIGTFYFLVRGWGVTDKDAREYYAVTILVPGIAAYLSMFFGIGLTEVTVGLDIYYARYADWLFTTPLLLLDLALLAKVDRVTITLVG
Ar1/H.sp.       PETLWLGIGTLLMLIGTFYFIVKGWGVTDKEAREYYSITILVPGIAAYLSMFFGIGLTEVQVGLDIYYARYADWLFTTPLLLLDLALLAKVDRVSITLVG
Aop/H.x.        PETLWLGIGTLLMLIGTFYFIVKGWGVTDKEAREYYSITILVPGIAAYLSMFFGIGLTEVQVGLDIYYARYADWLFTTPLLLLDLALLAKVDRVSITLVG
Br/H.l.         PESLWLWVGTIGMTLGTLYFLGRGRGVRDPKMQQFYIITIFVTTIAMYFAMATGFGVTEVTVGLTIYWARYADWIFTTPLLLLDLALLAGANRNTITLLG
Bop/Ht.sp.      PESIWLWIGTIGMTLGTLYFVGRGRGVRDRKMQEFYIITIFITTIAMYFAMATGFGVTEVMVGLTIYWARYADWLFTTPLLLLDLSLLAGANRNTITLIG
Cop2/H.sp.      GESIFLWVGTAGMFLGMLYFIARGWSVSDQRRQKFYIATIMIAAIVNYLSMALGFGVTTIELGRAIYWARYTDWLFTTPLLLYDLALLAGADRNTISLVG
Bop/H.m.        SEGIWLWLGTAGMFLGMLYFIARGWGETDGRRQKFYIATILITAIVNYLAMALGFGLTFIEFGHPIYWARYTDWLFTTPLLLYDLGLLAGADRNTISLVS
Cop/H.j.        SEAIWLWLGTAGMFLGMLYFIGRGWGETDSRRQKFYIATILITAIVNYLAMALGFGLTIVEFAHPIYWARYSDWLFTTPLLLYDLGLLAGADRNTISLVS
Cop3/Ha.v.      GEAIWLWLGTAGMFLGMLYFIARGWGETDSRRQKFYIATILITAIVNYLAMALGFGLTIVEIARPIYWARYSDWLFTTPLLLYDLGLLAGADRNTISLVS
Sop2/H.s.       ALTTWFWVGAVGMLAGTVLPI..RDCIRHPSHRRYDLVLAGITGLIAYTTMGLGITATTVGDR.TVYLARYIDWLVTTPLIVLYLAMLARPGHRTSWLLA
Pr/H.sp.        DTTVWAWIGALAMGAGTLWAWLSGSSATDESHGVYYGTLAGVTGVLAYLAMALGVGTLSTAAG.ELEVVRYVDWLVTTPLILLYLGLLARPSRRVLGLIG
Sop2/Ha.v.      TITTWFTLGLLGELLGTAVLAY.GYTLVPEETRKRYLLLIAIPGIVAYALMALGFGSIQSEGH.AVYVVRYVDWLLTTPLNVWFLALLAGASREDTKLVV
Sop2/N.p.       GLTTLFWLGAIGMLVGTLAFAWAGRDAGSGERR.YYVTLVGISGIVAYVVMALGVGWVPVAER.TVFAPRYIDWILTTPLIVYFLGLLAGLDSREFIVIT
```

```
                        110       120       130       140       150       160       170       180       190
                ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|.
VChR1/V.c.      SDVGCIVWGATSAMCTGWTILFFLISLSYGMYTYFLVRVMAWTFFVAWGMFPVLFLLGTEGFGHISPYGSAIGHSILDLIAKNMWGVLYLR
VChR2/V.c.      SDVGTIVWGATAAMSTGYIVIFFLLGCMYGANTFFLVRAMAWLFFVSWGMFPVLFLLGPEGFGHLSVYGSTIGHTIIDLLSKNCWGLLFLR
ChR1/C.r.       SDIGTIVWGTTAALSKGYVVIFFLMGLCYGIYTFFLVRYLAWLYFCSWAMFPVLFLLGPEGFGHINQFNSAIAHAILDLASKNAWSMMFLR
ChR2/C.r.       SDIGTIVWGATSAMATGYVVIFFCLGLCYGANTFFVVTGMAWLFFVSWGMFPILFILGPEGFGVLSVYGSTVGHTIIDLMSKNCWGLLYLR
Br/G.v.         ASVLMIATGYPGEISDDITIIWGTVSTIPFAYILYLVRNMRWLLLLSWGVYPIAYLLPMLGSGTSAAVGVQVGYTIADVLAKPVFGLLVF.
Ops2/G.t.       ADMGMIFAGYMGSVALVPTWLWFVIGLVVYIPVVILYGKVSLLTVVSWSVYPFVWLLSV.GTGGLGVSAESILYALLDVTSKCFFSFM...
Ops1/G.t.       ADVIMIVGGYLGTVSIVTTWFWFVISMALFVVVLYVYGRLAWLTIVSWIFYPVVWLF.SDGFASFSVSFEVCAYSILDIASKAIFGFMVMS
Ops/Cry.sp.     ADVLMIISGYMASVSVVTTWFWYLFGIGMFLPIIYLYGKVAWLTIIIWCFYPIVWLF.SQGFASFSVSFETVAITIMDVIAKCVFSFMIIA
Nop-1/N.c.      ADVIMVLCGLFAALGEGGNWGWYTIGCFSYLFVIWLFTGLAVFALLLWTAYPIIW..GIAGARRTNVDTEILIYTVLDLLAKPVFGFWLLL
Hop/S.r.        LDVFMCLTGLAAALTTSSHWLWYALSTAFFVGVLYIFSTLQWMTIVLWIGYPVVWALGNEGLALLEVGATSWAYSGLDIFAKYAFTIILVL
ChoP3/Ha.v.     MDIGMCITGLAAALVTSSHWVFYGISCAFFIAVLYIFGTLKLLTVVLWLGYPILWALGSEGVALLSVGVTSWGYSGLDILAKYVFAFLLLR
Hop/H.m.        MDIGMCVTGLAAALITSSHWVFYGISCAFFVAVLYIFGTLKILTVVLWLGYPILWALGSEGVALLSVGVTSWGYSGLDILAKYVFAFLLLR
Hop/N.p.        FDIAMCVTGLAAALTTSSHWFWYAISCACFLVVLYMFNTLKLLTVVMWLGYPIVWALGVEGIAVLPVGVTSWGYSFLDIVAKYIFAFLLLN
Hop/H.sp.       ADIGMCVTGLAAALTTSSYWVWYAISCAFFVVVLYIFNTLKVLTVVLWLGYPIFWALGAEGLAVLDVAITSWAYSGMDIVAKYLFAFLLLR
Hop/Hr.sod.     ADIGMCVTGLAAALTTSSYWVWYVISCAFFVVVLYIFNTLKLLTVVLWLGYPIFWALGAEGLAVLDVAVTSWAYSGMDIVAKYLFAFLLLR
Hopa/Ht.sp.     ADIGMCLTGLAAALTTSSYWAFYLVSTAFFVVVLYIFGTLRWLTVILWLGYPILWALGVEGFALVSVGLTSWGYSLLDIGAKYLFAALLLR
Hopb/Ht.sp.     ADIGMCLTGLAAALTTSSYWAFYLVSTAFFVVVLYIFGTLRWLTVILWLGYPILWALGVEGFALVSVGLTSWGYSLLDIGAKYLFAALLLR
Hop/H.s.        ADIGMCVTGLAAAMTTSALWAFYAISCAFFVVVLSIFDTLRVLTVVLWLGYPIVWAVGVEGLALVSVGVTSWAYSVLDVFAKYVFAFILLR
Hop/H.w.        ADIGMCVTGLGAALITSSYWAFYIISCTFFVVVLFIFSTLRLLTVVLWIGYPVIWAAGVEGFALISVGLTSWGYSGLDILAKYAFSFLLLR
Br/N.sp.        TQIVVITSGLIADLSERDWYLWYICGVCAFLIILWLYDKLVTYFTVLWIGYPIVWIIGPSGFGWINQTIDTFLFCLLPFFSKVGFSFLDLH
Xop2/H.m.       ANVVMIGVGYGFVSMSGSLWIAFAVSTVAFIGLLYLFQSLRDLTVVTWSLYPVVYFLGPLGTGIIQAPDLNFLVAVLDTIAKVGFMSILLV
Sop1/H.sp.      ADALMIAFGAGAVVTGGTLWVLFGVSSIFHVTLFALFSLLKNHVGLLWLAYPFVWLMGPAGIGFTTGVGAALTYAFLDVLAKVPYVYFFYA
Sop/Hr.sod.     ADALMIVFGAAAVVSGGTLWALFGVSALFHVSLFALFSLLKNHVGLLWLAYPFVWLMGPAGIGFTGAVGAALTYAFLDVLAKVPYVYFFYA
Sop1/H.s.       ADALMIAVGAGAVVTDGTLWALFGVSSIFHLSLFALFNLLKNHIGLLWLAYPLVWLFGPAGIGEATAAGVALTYVFLDVLAKVPYVYFFYA
Csr3/Ha.v.      ADALMILTGVGAVVADGTLWVLFGVSTVFHVSLFALFSLLKNHIGLLWIAYPLVWLAGPEGLGLATYVGVSITYAFLDLLAKVPYVYFFYA
Sria/S.r.       ADFMMIVFGLGAVVFSSTAWVFFGLSSACHLTLLALARLLLNYVGLLWLAYPLVWLFGP.GLQWVDAAGIAVIISYLDVTAKVPFVYFIYR
Srib/S.r.       VDAVMIGLGTAAVVTAPPTWIFFGLAALCHLVLLGLARLLVNHTGLLWITYPVVWVFGP.GLQLISATGVSIMIMYMDVLAKVPFVYFVYR
BopII/H.w.      IDAIMILGGLAGSMMQQGAIVWWAVSTAAFIILLYVFNRLRNITLGLWALYPIVWILGTGGFGIIAVTTEIMLYVMLDIGTKIGFGAVLLE
BopI/H.w.       IDAFMIVTGLVATLTKVVVYAFWTISTISMVFLLYTFNALRNIILVTWAIYPVAWLVGTEGLALTGLYGETLLFMVLDLVAKVGFGFILLR
Xop1/H.m.       IDAFMIVTGLAATLMKVPVYAFWTISTIAMLFVLYTFNVLRNIILVAWAIYPVAWLVGTEGLGLVGLFGETLLFMILDLTAKIGFGFILLR
Bop/H.s.        ADGIMIGTGLVGALTKVYSFVWWAISTAAMLYILYTFKVLRNVTVVLWSAYPVVWLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGLILLR
Ar2/H.sp.       VDALMIVTGLIGALSKTPLYTWWLFSTIAFLFVLYTFNTLTALVAVLWTAYPILWIVGTEGAGVVGLGIETLAFMVLDVTAKVGFGFVLLR
Ar3/Hr.sod.     VDALMIVTGLIGALSHTAIYSWWLFSTICMIVVLYTFNTLTALVLVLWTAYPILWIIGTEGAGVVGLGIETLLFMVLDVTAKVGFGFILLR
Ar1/H.sp.       VDALMIVTGLVGALSHTPLYTWWLFSTICMIVVLYTFNTLTALVLVLWTAYPILWIIGTEGAGVVGLGIETLLFMVLDVTAKVGFGFILLR
Aop/H.x.        VDALMIVTGLIGALSHTPLYTWWLFSTICMIVVLYTFNTLTALVLVLWTAYPILWIVGTEGAGVVGLGIETLLFMVLDVTAKVGFGFILLR
Br/H.l.         LDVFMIGTGTIAAFAATPGIAWWGISTGALLVLLYLFSTLRNLLIVLWLLYPVVWILGTEGFGILPLYWETAAFMILDLSAKVGFGVLLLR
Bop/Ht.sp.      LDVFMIGTGAIAALSSTPGIAWWAISTGALLALLYLFGRLRNLVIALWFLYPVVWILGTEGFGILPLYWETAAFMVLDLSAKVGFGVILLQ
Cop2/H.sp.      LDVLMIGTGALATLSAGSGLVWWGISTGFLLVLLYKFSTLRNLVLVLWLVYPVLWLVGTEGLGLVGLPIETAAFMVLDLTAKIGFGIILLQ
Bop/H.m.        LDVLMIGTGVVATLSAGSGLVWWGISTAFLLVLLYTFKTLRNLVTVVWLVYPVWWLVGSEGLGLVGIGIETAGFMVIDLVAKVGFGIILLR
Cop/H.j.        LDVLMIGTGLVATLSAGSGLVWWGISTAFLLVLLYTFKTLRNLVTVVWLVYPVWWLIGTEGLGLVGIGIETAGFMVIDLTAKVGFGIILLR
Cop3/Ha.v.      LDVLMIGTGLVATLSAGSGLVWWGISTAFLLVLLYTFKTLRNLVTVVWLVYPVWWLVGTEGIGLVGIGIETAGFMVIDLVAKVGFGIILLR
Sop2/H.s.       ADVFVIAAGIAAALTTGVQWLFFAVGAAGYAALLYLFVTLRNITVVLWTLYPVVWLLSPAGIGILQTEMYTIVVVYLDFISKVAFVAFAVL
Pr/H.sp.        VDVVVIAGGVTGAATGGAVWAAFAVGGGAYLALVYVFGTLRNITVVLWTLYPVVRLLAPTGFGLLTSATEMLVFVYLDIVSKVGFVVIAVA
Sop2/Ha.v.      LQALTIVFGFAGAVTPSPVYALFAVGGALFGGVIYLYRTLRNFVVVLWLVYPVVWLLGAAGVGLMDVETATLVVVYLDVVTKVGFGVIALL
Sop2/N.p.       LNTVVMLAGFAGAMVPGIEYALFGMGAVAFLGLVYLYVRLRNLTVILWAIYPFIWLLGPPGVALLTPTVDVALIVYLDLVTKVGFGFIALD
```

Supplemental Figure S6. Trimmed alignment of 45 rhodopsin-related proteins from green algae, fungi, cyanobacteria, cryptomonads, and halobacteria.

Alignment of protein sequences was done using the MUltiple Sequence Comparison by Log-Expectation program (MUSCLE) (Edgar, 2004). Minor manual optimization of alignments, trimming, and management of multi-aligned data was done with BioEdit v7.0.9 (Hall, 1999). Investigated rhodopsins and source organisms are as follows: VChR1/V.c., channelrhodopsin-1, *Volvox carteri*; VChR2/V.c., channelrhodopsin-2, *Volvox carteri*; ChR1/C.r., channelrhodopsin-1, *Chlamydomonas reinhardtii*; ChR2/C.r., channelrhodopsin-2, *Chlamydomonas reinhardtii*; Br/G.v., bacterioopsin, *Gloeobacter violaceus*; Ops2/G.t., opsin-2, *Guillardia theta*; Ops1/G.t., opsin-1, *Guillardia theta*; Ops/Cry.sp., opsin, *Cryptomonas* sp.; Nop-1/N.c., opsin-1, *Neurospora crassa*; Hop/S.r., halorhodopsin, *Salinibacter ruber*; ChoP3/Ha.v., cruxhalorhodopsin-3, *Haloarcula vallismortis*; Hop/H.m., halorhodopsin, *Haloarcula marismortui*; Hop/N.p., halorhodopsin, *Natronomonas pharaonis*; Hop/H.sp., halorhodopsin, *Halobacterium* sp.; Hop/Hr.sod., halorhodopsin, *Halorubrum sodomense*; Hopa/Ht.sp., halorhodopsin, *Haloterrigena* sp.; Hopb/Ht.sp., halorhodopsin, *Haloterrigena* sp.; Hop/H.s., halorhodopsin, *Halobacterium salinarum*; Hop/H.w., halorhodopsin, *Haloquadratum walsbyi*; Br/N.sp., bacteriorhodopsin, *Nostoc* sp.; Xop2/H.m., opsin, *Haloarcula marismortui*; Sop1/H.sp., sensory rhodopsin-1, *Halobacterium* sp.; Sop/Hr.sod., rhodopsin, *Halorubrum sodomense*; Sop1/H.s., sensory rhodopsin-1, *Halobacterium salinarum*; Csr3/Ha.v., bacterial rhodopsin, *Haloarcula vallismortis*; Sria/S.r., sensory rhodopsin a, *Salinibacter ruber*; Srib/S.r., sensory rhodopsin b, *Salinibacter ruber*; BopII/H.w., bacteriorhodopsin II, *Haloquadratum walsbyi*; BopI/H.w., bacteriorhodopsin I, *Haloquadratum walsbyi*; Xop1/H.m., bacteriorhodopsin, *Haloarcula marismortui*; Bop/H.s., bacteriorhodopsin, *Halobacterium salinarum*; Ar2/H.sp., archaerhodopsin-2, *Halobacterium* sp.; Ar3/Hr.sod., archaerhodopsin-2, *Halorubrum sodomense*; Ar1/H.sp., archaerhodopsin-1, *Halobacterium* sp.; Aop/H.x., archaerhodopsin, *Halorubrum xinjiangense*; Br/H.l., bacteriorhodopsin, *Halobiforma lacisalsi*; Bop/Ht.sp., bacteriorhodopsin, *Haloterrigena* sp.; Cop2/H.sp., cruxrhodopsin-2, *Haloarcula* sp.; Bop/H.m., bacteriorhodopsin, *Haloarcula marismortui*; Cop/H.j., cruxrhodopsin, *Haloarcula japonica*; Cop3/Ha.v., cruxrhodopsin-3, *Haloarcula vallismortis*; Sop2/H.s., sensory rhodopsin-2, *Halobacterium salinarum*; Pr/H.sp., phoborhodopsin, *Halobacterium* sp.; Sop2/Ha.v., sensory rhodopsin-2, *Haloarcula vallismortis*; Sop2/N.p., sensory rhodopsin-2, *Natronomonas pharaonis*.



Supplemental Figure S7. Multiple alignment of the con1, con2 and con3 regions of the channelrhodopsins from Volvox and Chlamydomonas. Conserved amino acid residues were shaded with similarity groups enabled. White letters on black background represent residues conserved in 100% of the sequences at the corresponding position; residues seen in white letters on gray background are conserved in >60% of the sequences.

Supplemental Table S1. Sequence comparison of VChR1 and VChR2 to related rhodopsins.

				Comparison to VChR1			**Comparison to VChR2**		
Gene product	**Species**	**Group**	**Acc.No.**	**Percent identity***	**Percent similarity***	**E-value**	**Percent identity***	**Percent similarity***	**E-value**
channelrhodopsin-1	*Volvox carteri*	green algae	EU285658	100% (837/837)	100% (837/837)	0.0	63% (335/530)	77% (412/530)	0.0
channelrhodopsin-2	*Volvox carteri*	green algae	EU285660	62% (331/526)	77% (410/526)	0.0	100% (747/747)	100% (747/747)	0.0
channelrhodopsin-1	*Chlamydomonas reinhardtii*	green algae	AF508965	66% (328/496)	80% (397/496)	0.0	62% (328/522)	77% (403/522)	0.0
channelrhodopsin-2	*Chlamydomonas reinhardtii*	green algae	AF508966	56% (300/532)	70% (375/532)	1e-177	60% (325/534)	73% (393/534)	0.0
bacterioopsin	*Gloeobacter violaceus*	cyanobacteria	NP_923144	25% (42/164)	45% (75/164)	5e-10	30% (46/152)	49% (75/152)	4e-13
bacteriorhodopsin	*Nostoc* sp.	cyanobacteria	BAB74864	34% (16/47)	53% (25/47)	6e-05	30% (12/39)	56% (22/39)	6e-04
opsin-2	*Guillardia theta*	cryptomonads	ABA08438	22% (32/141)	48% (68/141)	6e-06	20% (33/163)	49% (81/163)	5e-05
opsin-1	*Guillardia theta*	cryptomonads	ABA08437	25% (38/148)	50% (74/148)	4e-08	25% (43/170)	44% (76/170)	4e-07
opsin	*Cryptomonas* sp.	cryptomonads	ABA08439	24% (34/141)	47% (67/141)	7e-09	25% (38/149)	48% (73/149)	1e-09
opsin-1	*Neurospora crassa*	fungi	AF135863	47% (9/19)	57% (11/19)	0.43	26% (42/158)	46% (74/158)	0.024
halorhodopsin	*Salinibacter ruber*	haloarch. (Cl$^-$)	YP_446872	23% (35/150)	42% (64/150)	4e-08	22% (33/149)	44% (67/149)	2e-06
cruxhalorhodopsin-3	*Haloarcula vallismortis*	haloarch. (Cl$^-$)	P94853	26% (40/151)	47% (72/151)	7e-07	27% (44/159)	47% (75/159)	8e-09
halorhodopsin	*Haloarcula marismortui*	haloarch. (Cl$^-$)	YP_136278	26% (40/151)	47% (71/151)	6e-08	28% (45/160)	45% (73/160)	7e-08
halorhodopsin	*Natronomonas pharaonis*	haloarch. (Cl$^-$)	P15647	38% (19/49)	65% (32/49)	9e-05	23% (38/160)	43% (70/160)	1e-04
halorhodopsin	*Halobacterium* sp.	haloarch. (Cl$^-$)	CAA49773	24% (38/157)	45% (72/157)	1e-05	22% (38/166)	43% (73/166)	5e-08
halorhodopsin	*Halorubrum sodomense*	haloarch. (Cl$^-$)	O93742	25% (40/157)	45% (72/157)	2e-06	23% (36/155)	45% (70/155)	1e-08
halorhodopsin	*Haloterrigena* sp.	haloarch. (Cl$^-$)	O93741	23% (36/152)	46% (71/152)	1e-07	23% (33/143)	46% (66/143)	3e-07
halorhodopsin	*Haloterrigena* sp.	haloarch. (Cl$^-$)	BAA75201	23% (36/152)	46% (71/152)	2e-07	23% (33/143)	46% (66/143)	5e-07
halorhodopsin	*Halobacterium salinarum*	haloarch. (Cl$^-$)	P16102	23% (43/181)	42% (77/181)	5e-07	22% (42/185)	42% (78/185)	3e-06

halorhodopsin	*Haloquadratum walsbyi*	haloarch. (Cl$^-$)	YP_658762	26% (40/153)	46% (71/153)	4e-06	24% (37/150)	47% (71/150)	3e-07
opsin	*Haloarcula marismortui*	haloarch. (SR)	YP_135281	21% (31/142)	45% (64/142)	5e-07	23% (36/156)	44% (69/156)	9e-09
sensory rhodopsin-1	*Halobacterium* sp.	haloarch. (SR)	P33743	25% (37/147)	53% (78/147)	1e-09	25% (39/154)	49% (76/154)	7e-11
rhodopsin	*Halorubrum sodomense*	haloarch. (SR)	O93743	26% (40/152)	48% (74/152)	6e-09	26% (41/155)	48% (75/155)	3e-11
sensory rhodopsin-1	*Halobacterium salinarum*	haloarch. (SR)	P25964	26% (39/147)	51% (75/147)	6e-12	26% (52/198)	46% (93/198)	3e-13
bacterial rhodopsin	*Haloarcula vallismortis*	haloarch. (SR)	Q48334	25% (38/148)	50% (74/148)	1e-09	28% (42/148)	47% (71/148)	6e-10
sensory rhodopsin a	*Salinibacter ruber*	haloarch. (SR)	YP_446609	26% (40/149)	44% (67/149)	6e-04	23% (29/124)	42% (53/124)	0.017
sensory rhodopsin b	*Salinibacter ruber*	haloarch. (SR)	YP_446677	40% (8/20)	70% (14/20)	0.007	25% (39/155)	42% (66/155)	1e-04
sensory rhodopsin-2	*Halobacterium salinarum*	haloarch. (SR)	P71411	27% (42/151)	48% (73/151)	3e-09	31% (48/151)	52% (79/151)	1e-12
phoborhodopsin	*Halobacterium* sp.	haloarch. (SR)	BAB86796	32% (12/37)	56% (21/37)	0.003	37% (14/37)	59% (22/37)	3e-05
sensory rhodopsin-2	*Haloarcula vallismortis*	haloarch. (SR)	P42197	27% (42/155)	45% (71/155)	9e-09	25% (40/155)	50% (79/155)	2e-10
sensory rhodopsin-2	*Natronomonas pharaonis*	haloarch. (SR)	P42196	25% (35/140)	46% (65/140)	9e-06	26% (38/146)	45% (67/146)	2e-07
bacteriorhodopsin II	*Haloquadratum walsbyi*	haloarch. (H$^+$)	YP_656804	25% (41/158)	43% (69/158)	4e-07	22% (37/162)	46% (75/162)	1e-07
bacteriorhodopsin I	*Haloquadratum walsbyi*	haloarch. (H$^+$)	YP_656801	31% (46/148)	47% (71/148)	4e-11	27% (43/158)	49% (78/158)	5e-11
bacteriorhodopsin	*Haloarcula marismortui*	haloarch. (H$^+$)	YP_136594	32% (47/144)	48% (70/144)	3e-09	28% (46/164)	43% (71/164)	3e-08
bacteriorhodopsin	*Halobacterium salinarum*	haloarch. (H$^+$)	P02945	20% (35/168)	35% (60/168)	2e-04	20% (36/174)	37% (65/174)	3e-05
archaerhodopsin-2	*Halobacterium* sp.	haloarch. (H$^+$)	P29563	26% (42/159)	45% (73/159)	8e-06	27% (12/43)	60% (26/43)	0.002
archaerhodopsin-2	*Halorubrum sodomense*	haloarch. (H$^+$)	P96787	27% (41/151)	46% (70/151)	3e-05	28% (13/46)	58% (27/46)	9e-04
archaerhodopsin-1	*Halobacterium* sp.	haloarch. (H$^+$)	J05165	26% (40/151)	46% (70/151)	5e-05	28% (13/46)	58% (27/46)	8e-04
archaerhodopsin	*Halorubrum xinjiangense*	haloarch. (H$^+$)	AAS15567	26% (40/151)	46% (70/151)	6e-05	28% (13/46)	58% (27/46)	0.001
bacteriorhodopsin	*Halobiforma lacisalsi*	haloarch. (H$^+$)	AAU04564	42% (6/14)	64% (9/14)	0.006	28% (45/156)	46% (73/156)	6e-05
bacteriorhodopsin	*Haloterrigena* sp.	haloarch. (H$^+$)	O93740	32% (50/156)	48% (76/156)	2e-07	29% (47/157)	49% (78/157)	2e-07

cruxrhodopsin-2	*Haloarcula* sp.	haloarch. (H$^+$)	AAB32951	38% (17/44)	59% (26/44)	3e-05	34% (16/46)	60% (28/46)	5e-05
bacteriorhodopsin	*Haloarcula marismortui*	haloarch. (H$^+$)	YP_137573	25% (38/152)	45% (69/152)	7e-05	22% (46/206)	44% (92/206)	1e-06
cruxrhodopsin	*Haloarcula japonica*	haloarch. (H$^+$)	BAA81816	37% (16/43)	60% (26/43)	1e-04	24% (37/152)	45% (69/152)	1e-05
cruxrhodopsin-3	*Haloarcula vallismortis*	haloarch. (H$^+$)	P94854	37% (16/43)	62% (27/43)	4e-05	24% (37/152)	46% (70/152)	7e-06

* The number of identical or similar amino acid residues as well as the total number of residues is given in parentheses.

haloarch., haloarchaea; SR, sensory rhodopsin; Cl$^-$, chloride pump; H$^+$, proton pump.

```
> VChR1/V.c.
YCEGWLWVVFALSVACLGWYAYQAWRATCGWEEVYVALIEMMKSIIEAFHEFDSPATLWL
SSGNGVVWMRYGEWLLTCPVLLIHLSNLTDYSKRTMGLLVSDVGCIVWGATSAMCTGWTI
LFFLISLSYGMYTYFLVRVMAWTFFVAWGMFPVLFLLGTEGFGHISPYGSAIGHSILDLI
AKNMWGVLYLR

> VChR2/V.c.
FCMKWLWAAFALSVIILIYYAYATWRTTCGWEEVYVCCVELTKVVIEFFHEFDEPGMLYL
ANGNRVLWLRYGEWLLTCPVILIHLSNLTDYNKRTMRLLVSDVGTIVWGATAAMSTGYIV
IFFLLGCMYGANTFFLVRAMAWLFFVSWGMFPVLFLLGPEGFGHLSVYGSTIGHTIIDLL
SKNCWGLLFLR

> ChR1/C.r.
FCLAWLWITFALSALCLMFYGYQTWKSTCGWEEIYVATIEMIKFIIEYFHEFDEPAVIYS
SNGNKTVWLRYAEWLLTCPVILIHLSNLTDYNKRTMGLLVSDIGTIVWGTTAALSKGYVV
IFFLMGLCYGIYTFFLVRYLAWLYFCSWAMFPVLFLLGPEGFGHINQFNSAIAHAILDLA
SKNAWSMMFLR

> ChR2/C.r.
YCAGWIWLAAGFSILLLMFYAYQTWKSTCGWEEIYVCAIEMVKVILEFFFEFKNPSMLYL
ATGHRVQWLRYAEWLLTCPVILIHLSNLTDYSRRTMGLLVSDIGTIVWGATSAMATGYVV
IFFCLGLCYGANTFFVVTGMAWLFFVSWGMFPILFILGPEGFGVLSVYGSTVGHTIIDLM
SKNCWGLLYLR

> Br/G.v.
SVSDSLSFAIAAMFASALFFFS-AQALVGQRYRLALLVSAIVVSIYHYFRIFNSAAYVLE
NGVKFNDAYRYVDWLLTVPLLLVETVAVLKEARPLLKLTVASVLMIATGYPGEISDDITI
IWGTVSTIPFAYILYLVRNMRWLLLLSWGVYPIAYLLPMLGSGTSAAVGVQVGYTIADVL
AKPVFGLLVF-

> Ops2/G.t.
SGAIFDVLAWIALLFTALFMAFKAVNA-DPVVRKFYYINAFVCGVFSYFAMISGMGWETI
MGCRQMFYVRYIDWFITTPLMILNIGLLAGEEQWMIAIMGADMGMIFAGYMGSVALVPTW
LWFVIGLVVYIPVVILYGKVSLLTVVSWSVYPFVWLLSV-GTGGLGVSAESILYALLDVT
SKCFFSFM---
```

```
> Ops1/G.t.
TGVGALTITFLILAVST--IIFITRVGPATSQKVYYYCNVFICGLMSYFAMLSGQGWTAV
AGCRQFFYARYVDWTITTALIILELGLIAGAEPALIGVMGADVIMIVGGYLGTVSIVTTW
FWFVISMALFVVVLYVYGRLAWLTIVSWIFYPVVWLF-SDGFASFSVSFEVCAYSILDIA
SKAIFGFMVMS

> Ops/Cry.sp.
TGIGGLTLGFLALTVTTVVMVAKAANA-DPERRKYYFCNTFICGIFAYFAMLSGQGWTAI
SGCRQFFYAHYVDWLLTTPLIILNLGLIAGQDYVTIAVCGADVLMIISGYMASVSVVTTW
FWYLFGIGMFLPIIYLYGKVAWLTIIIWCFYPIVWLF-SQGFASFSVSFETVAITIMDVI
AKCVFSFMIIA

> Nop-1/N.c.
PTPTEYWVTFALMVLSSGIFALLSWNVPTSK-RLFHVITTLITVVLSYFAMATG-HATTF
NCDRQVFWGRYVDWALTTPLLLLELCLLAGVDGAHTMAIVADVIMVLCGLFAALGEGGNW
GWYTIGCFSYLFVIWLFTGLAVFALLLWTAYPIIW--GIAGARRTNVDTEILIYTVLDLL
AKPVFGFWLLL

> Hop/S.r.
ALASSIYVNIALAGLTIIVIAVMSRSIHDSRAKLITMSTLMISVVSSYMGLASGIDPLVM
PEGVLSLWGRYLTWAFSTPFILLALGLLARSTTDKISAIVLDVFMCLTGLAAALTTSSHW
LWYALSTAFFVGVLYIFSTLQWMTIVLWIGYPVVWALGNEGLALLEVGATSWAYSGLDIF
AKYAFTIILVL

> ChoP3/Ha.v.
LLNSSLWVNIALAGVVILLFVAMGRELESSRAKLIWVATMLVPLVSSYAGLASGVGFLQM
PPGVLSPWGRYLTWTFSTPMILLALGLLADTDMASLTAITMDIGMCITGLAAALVTSSHW
VFYGISCAFFIAVLYIFGTLKLLTVVLWLGYPILWALGSEGVALLSVGVTSWGYSGLDIL
AKYVFAFLLLR

> Hop/H.m.
LLNSSIWVNIALAGVVILLFVAMGRDLESPRAKLIWVATMLVPLVSSYAGLASGVGFLQM
PPGVLSPWGRYLTWTFSTPMILLALGLLADTDIASLTAITMDIGMCVTGLAAALITSSHW
VFYGISCAFFVAVLYIFGTLKILTVVLWLGYPILWALGSEGVALLSVGVTSWGYSGLDIL
AKYVFAFLLLR
```

```
> Hop/N.p.
LLASSLYINIALAGLSILLFVFMTRGLDDPRAKLIAVSTILVPVVASYTGLASGISVLEM
PAGVVTMWGRYLTWALSTPMILLALGLLAGSNATKLTAITFDIAMCVTGLAAALTTSSHW
FWYAISCACFLVVLYMFNTLKLLTVVMWLGYPIVWALGVEGIAVLPVGVTSWGYSFLDIV
AKYIFAFLLLN

> Hop/H.sp.
LLASSLWINIALAGLSILLFVYMGRNVEDPRAQLIFVATLMVPLVSSYTGLVSGVSFLEM
PAGVLTPWGRYLTWALSTPMILIAVGLLAGSNTTKLTAVVADIGMCVTGLAAALTTSSYW
VWYAISCAFFVVVLYIFNTLKVLTVVLWLGYPIFWALGAEGLAVLDVAITSWAYSGMDIV
AKYLFAFLLLR

> Hop/Hr.sod.
LLASSLWINIALAGLSILLFVYMGRNLEDPRAQLIFVATLMVPLVSSYTGLVSGVSFLEM
PAGVLTPWGRYLTWALSTPMILVALGLLAGSNATKLTAVTADIGMCVTGLAAALTTSSYW
VWYVISCAFFVVVLYIFNTLKLLTVVLWLGYPIFWALGAEGLAVLDVAVTSWAYSGMDIV
AKYLFAFLLLR

> Hopa/Ht.sp.
LLHSSLWVNIALAGLSILVFLYMARTVRANRARLIVGATLMIPLVSSYLGLVTGAGPIEM
PAAVLSQWGRYLTWTLSTPMILLALGWLAEVDTADLVVIAADIGMCLTGLAAALTTSSYW
AFYLVSTAFFVVVLYIFGTLRWLTVILWLGYPILWALGVEGFALVSVGLTSWGYSLLDIG
AKYLFAALLLR

> Hopb/Ht.sp.
LLHSSLWVNIALAGLSILVFLYMARTVRANRARLIVGATLMIPLVSSYLGLVTGAGPIEM
PAAVLSQWGRYLTWTLSTPMILLALGWLAEVDTADLVVIAADIGMCLTGLAAALTTSSYW
AFYLVSTAFFVVVLYIFGTLRWLTVILWLGYPILWALGVEGFALVSVGLTSWGYSLLDIG
AKYLFAALLLR

> Hop/H.s.
LLSSSLWVNVALAGIAILVFVYMGRTIRPGRPRLIWGATLMIPLVSSYLGLLSGVGMIEM
PAGVRSQWGRYLTWALSTPMILLALGLLADVDLGSLTVIAADIGMCVTGLAAAMTTSALW
AFYAISCAFFVVVLSIFDTLRVLTVVLWLGYPIVWAVGVEGLALVSVGVTSWAYSVLDVF
AKYVFAFILLR
```

```
>Hop/H.w.
LLSSSLWVNIALAGLSILLFVYMGRNITSGRARLIWGATLMIPLVSSYLGLASGVGFIEM
PAGVMSQWGRYLTWALSTPMILLALGVLADVDRGSLTVIAADIGMCVTGLGAALITSSYW
AFYIISCTFFVVVLFIFSTLRLLTVVLWIGYPVIWAAGVEGFALISVGLTSWGYSGLDIL
AKYAFSFLLLR

> Br/N.sp.
LESLLHWIYVAGMTIGALHFWSLSRNPRGVPQYEYLVA-MFIPIWLAYMAMAIDQGKVEA
AGQ-IAHYARYIDWMVTTPLLLLSLSWTAKKDWTLIFLMSTQIVVITSGLIADLSERDWY
LWYICGVCAFLIILWLYDKLVTYFTVLWIGYPIVWIIGPSGFGWINQTIDTFLFCLLPFF
SKVGFSFLDLH

> Xop2/H.m.
QEIVWYGAGAGAFFVSAVVFVWFAATRGNIRSSFYYLPPIHTS-VAAYVAMAL-IAGGQL
GDTVSITTLRFADWIVSTPIITYYLARLAGVDTQTRLAVAANVVMIGVGYGFVSMSGSLW
IAFAVSTVAFIGLLYLFQSLRDLTVVTWSLYPVVYFLGPLGTGIIQAPDLNFLVAVLDTI
AKVGFMSILLV

> Sop1/H.sp.
AVSAAYWIAAVAFLVGLGITAALYAKLGESEDRGRLAALAVIPGFLAYAGMALGIGTVTV
NGA-ELVGLRYVDWIVTTPLLVGFIGYVAGASRRAIGVMLADALMIAFGAGAVVTGGTLW
VLFGVSSIFHVTLFALFSLLKNHVGLLWLAYPFVWLMGPAGIGFTTGVGAALTYAFLDVL
AKVPYVYFFYA

> Sop/Hr.sod.
AVTSAYWLAAVAFLIGVGITAALYAKLEGSRARTRLAALAVIPGFLSYVGMALGIGTVTV
NGA-ELVGLRYVDWVVTTPLLVGFIGYNAGASRRAIGVMIADALMIVFGAAAVVSGGTLW
ALFGVSALFHVSLFALFSLLKNHVGLLWLAYPFVWLMGPAGIGFTGAVGAALTYAFLDVL
AKVPYVYFFYA

> Sop1/H.s.
AVATAYLGGAVALIVGVAFVWLLYRSLDGSPHQSALAPLAIIPVFLSYVGMAYDIGTVIV
NGN-QIVGLRYIDWLVTTPILVGYVGYAAGASRRSIGVMVADALMIAVGAGAVVTDGTLW
ALFGVSSIFHLSLFALFNLLKNHIGLLWLAYPLVWLFGPAGIGEATAAGVALTYVFLDVL
AKVPYVYFFYA
```

```
> Csr3/Ha.v.
AVAVVYGITAAGFAVGVAIVGYLYASLEGSEERSILAALALIPGFISYVAMAFGIGTVTI
GET-TLVGFRYLDWVVTTPLLVGFVGYAAGASRRAIGVMVADALMILTGVGAVVADGTLW
VLFGVSTVFHVSLFALFSLLKNHIGLLWIAYPLVWLAGPEGLGLATYVGVSITYAFLDLL
AKVPYVYFFYA

> Sria/S.r.
PITIVYIIGTLGMLVGI----PPALSLVGDEVGLDFDYVWAIPGIFMYLLMTFDVGSVQF
QGY-HVPIPRYIDWALTTPLLVGYTAYIAGASRGMIGTALADFMMIVFGLGAVVFSSTAW
VFFGLSSACHLTLLALARLLLNYVGLLWLAYPLVWLFGP-GLQWVDAAGIAVIISYLDVT
AKVPFVYFIYR

> Srib/S.r.
ATTIVLMLGTAGMLFGI----PPCLRLLDMEADGHFGYLLLIPGFLMYALMTFGVGTQTF
QGQ-TVPLLRYLDWLVTTPIMIGYAAYVAGTSKRGIGAALVDAVMIGLGTAAVVTAPPTW
IFFGLAALCHLVLLGLARLLVNHTGLLWITYPVVWVFGP-GLQLISATGVSIMIMYMDVL
AKVPFVYFVYR

> BopII/H.w.
SEATWLWIGTIGMVLGTVYFAVRGRGSTDPEQQTYYIITTLIPAIAAYLAMATGLGVISM
PIRIDIYWARYADWLLTTPLLIIDLALVAGARKQTLKLIIIDAIMILGGLAGSMMQQGAI
VWWAVSTAAFIILLYVFNRLRNITLGLWALYPIVWILGTGGFGIIAVTTEIMLYVMLDIG
TKIGFGAVLLE

> BopI/H.w.
GEGIWLALGTIGMLLGMLYFIADGLDVQDPRQKEFYVITILIPAIASYLSMFFGFGLTEV
SLAVDVYWARYADWLFTTPLLLLDIGLLAGASQRDIALVGIDAFMIVTGLVATLTKVVVY
AFWTISTISMVFLLYTFNALRNIILVTWAIYPVAWLVGTEGLALTGLYGETLLFMVLDLV
AKVGFGFILLR

> Xop1/H.m.
GEGIWLALGTVGMLLGMVYFMAKGWDVQDPEQEEFYVITILIAGISSYLSMFFGFGLTEV
ELVIDVYWARYADWLFTTPLLLLDIGLLAGASNRDMSLITIDAFMIVTGLAATLMKVPVY
AFWTISTIAMLFVLYTFNVLRNIILVAWAIYPVAWLVGTEGLGLVGLFGETLLFMILDLT
AKIGFGFILLR
```

```
> Bop/H.s.
PEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAITMYLSMLLGYGLTMV
PFGNPIYWARYADWLFTTPLLLLDLALLVDADQGTIALVGADGIMIGTGLVGALTKVYSF
VWWAISTAAMLYILYTFKVLRNVTVVLWSAYPVVWLIGSEGAGIVPLNIETLLFMVLDVS
AKVGFGLILLR

> Ar2/H.sp.
PETLWLGIGTLLMLIGTFYFIARGWGVTDKEAREYYAITILVPGIAAYLAMFFGIGVTEV
ELALDIYYARYADWLFTTPLLLLDLALLAKVDRVTITLIGVDALMIVTGLIGALSKTPLY
TWWLFSTIAFLFVLYTFNTLTALVAVLWTAYPILWIVGTEGAGVVGLGIETLAFMVLDVT
AKVGFGFVLLR

> Ar3/Hr.sod.
PETLWLGIGTLLMLIGTFYFLVRGWGVTDKDAREYYAVTILVPGIAAYLSMFFGIGLTEV
TVGLDIYYARYADWLFTTPLLLLDLALLAKVDRVTITLVGVDALMIVTGLIGALSHTAIY
SWWLFSTICMIVVLYTFNTLTALVLVLWTAYPILWIIGTEGAGVVGLGIETLLFMVLDVT
AKVGFGFILLR

> Ar1/H.sp.
PETLWLGIGTLLMLIGTFYFIVKGWGVTDKEAREYYSITILVPGIAAYLSMFFGIGLTEV
QVGLDIYYARYADWLFTTPLLLLDLALLAKVDRVSITLVGVDALMIVTGLVGALSHTPLY
TWWLFSTICMIVVLYTFNTLTALVLVLWTAYPILWIIGTEGAGVVGLGIETLLFMVLDVT
AKVGFGFILLR

> Aop/H.x., Aopbd1_H.x.
PETLWLGIGTLLMLIGTFYFIVKGWGVTDKEAREYYSITILVPGIAAYLSMFFGIGLTEV
QVGLDIYYARYADWLFTTPLLLLDLALLAKVDRVSITLVGVDALMIVTGLIGALSHTPLY
TWWLFSTICMIVVLYTFNTLTALVLVLWTAYPILWIVGTEGAGVVGLGIETLLFMVLDVT
AKVGFGFILLR

> Br/H.l.
PESLWLWVGTIGMTLGTLYFLGRGRGVRDPKMQQFYIITIFVTTIAMYFAMATGFGVTEV
TVGLTIYWARYADWIFTTPLLLLDLALLAGANRNTITLLGLDVFMIGTGTIAAFAATPGI
AWWGISTGALLVLLYLFSTLRNLLIVLWLLYPVVWILGTEGFGILPLYWETAAFMILDLS
AKVGFGVLLLR
```

```
> Bop/Ht.sp.

PESIWLWIGTIGMTLGTLYFVGRGRGVRDRKMQEFYIITIFITTIAMYFAMATGFGVTEV

MVGLTIYWARYADWLFTTPLLLLDLSLLAGANRNTITLIGLDVFMIGTGAIAALSSTPGI

AWWAISTGALLALLYLFGRLRNLVIALWFLYPVVWILGTEGFGILPLYWETAAFMVLDLS

AKVGFGVILLQ

> Cop2/H.sp.

GESIFLWVGTAGMFLGMLYFIARGWSVSDQRRQKFYIATIMIAAIVNYLSMALGFGVTTI

ELGRAIYWARYTDWLFTTPLLLYDLALLAGADRNTISLVGLDVLMIGTGALATLSAGSGL

VWWGISTGFLLVLLYKFSTLRNLVLVLWLVYPVLWLVGTEGLGLVGLPIETAAFMVLDLT

AKIGFGIILLQ

> Bop/H.m.

SEGIWLWLGTAGMFLGMLYFIARGWGETDGRRQKFYIATILITAIVNYLAMALGFGLTFI

EFGHPIYWARYTDWLFTTPLLLYDLGLLAGADRNTISLVSLDVLMIGTGVVATLSAGSGL

VWWGISTAFLLVLLYTFKTLRNLVTVVWLVYPVWWLVGSEGLGLVGIGIETAGFMVIDLV

AKVGFGIILLR

> Cop/H.j.

SEAIWLWLGTAGMFLGMLYFIGRGWGETDSRRQKFYIATILITAIVNYLAMALGFGLTIV

EFAHPIYWARYSDWLFTTPLLLYDLGLLAGADRNTISLVSLDVLMIGTGLVATLSAGSGL

VWWGISTAFLLVLLYTFKTLRNLVTVVWLVYPVWWLIGTEGLGLVGIGIETAGFMVIDLT

AKVGFGIILLR

> Cop3/Ha.v.

GEAIWLWLGTAGMFLGMLYFIARGWGETDSRRQKFYIATILITAIVNYLAMALGFGLTIV

EIARPIYWARYSDWLFTTPLLLYDLGLLAGADRNTISLVSLDVLMIGTGLVATLSAGSGL

VWWGISTAFLLVLLYTFKTLRNLVTVVWLVYPVWWLVGTEGIGLVGIGIETAGFMVIDLV

AKVGFGIILLR

> Sop2/H.s.

ALTTWFWVGAVGMLAGTVLPI--RDCIRHPSHRRYDLVLAGITGLIAYTTMGLGITATTV

GDR-TVYLARYIDWLVTTPLIVLYLAMLARPGHRTSWLLAADVFVIAAGIAAALTTGVQW

LFFAVGAAGYAALLYLFVTLRNITVVLWTLYPVVWLLSPAGIGILQTEMYTIVVVYLDFI

SKVAFVAFAVL
```

```
> Pr/H.sp.
DTTVWAWIGALAMGAGTLWAWLSGSSATDESHGVYYGTLAGVTGVLAYLAMALGVGTLST
AAG-ELEVVRYVDWLVTTPLILLYLGLLARPSRRVLGLIGVDVVVIAGGVTGAATGGAVW
AAFAVGGGAYLALVYVFGTLRNITVVLWTLYPVVRLLAPTGFGLLTSATEMLVFVYLDIV
SKVGFVVIAVA

> Sop2/Ha.v.
TITTWFTLGLLGELLGTAVLAY-GYTLVPEETRKRYLLLIAIPGIVAYALMALGFGSIQS
EGH-AVYVVRYVDWLLTTPLNVWFLALLAGASREDTKLVVLQALTIVFGFAGAVTPSPVY
ALFAVGGALFGGVIYLYRTLRNFVVVLWLVYPVVWLLGAAGVGLMDVETATLVVVYLDVV
TKVGFGVIALL

> Sop2/N.p.
GLTTLFWLGAIGMLVGTLAFAWAGRDAGSGERR-YYVTLVGISGIVAYVVMALGVGWVPV
AER-TVFAPRYIDWILTTPLIVYFLGLLAGLDSREFIVITLNTVVMLAGFAGAMVPGIEY
ALFGMGAVAFLGLVYLYVRLRNLTVILWAIYPFIWLLGPPGVALLTPTVDVALIVYLDLV
TKVGFGFIALD
```

Supplemental Data Set S1. Trimmed sequences of 45 rhodopsin-related proteins from green algae, fungi, cyanobacteria, cryptomonads, and halobacteria corresponding to the alignment in Supplemental Figure S6.

Source organisms: VChR1/V.c., channelrhodopsin-1, *Volvox carteri*; VChR2/V.c., channelrhodopsin-2, *Volvox carteri*; ChR1/C.r., channelrhodopsin-1, *Chlamydomonas reinhardtii*; ChR2/C.r., channelrhodopsin-2, *Chlamydomonas reinhardtii*; Br/G.v., bacterioopsin, *Gloeobacter violaceus*; Ops2/G.t., opsin-2, *Guillardia theta*; Ops1/G.t., opsin-1, *Guillardia theta*; Ops/Cry.sp., opsin, *Cryptomonas* sp.; Nop-1/N.c., opsin-1, *Neurospora crassa*; Hop/S.r., halorhodopsin, *Salinibacter ruber*; ChoP3/Ha.v., cruxhalorhodopsin-3, *Haloarcula vallismortis*; Hop/H.m., halorhodopsin, *Haloarcula marismortui*; Hop/N.p., halorhodopsin, *Natronomonas pharaonis*; Hop/H.sp., halorhodopsin, *Halobacterium* sp.; Hop/Hr.sod., halorhodopsin, *Halorubrum sodomense*; Hopa/Ht.sp., halorhodopsin, *Haloterrigena* sp.; Hopb/Ht.sp., halorhodopsin, *Haloterrigena* sp.; Hop/H.s., halorhodopsin, *Halobacterium salinarum*; Hop/H.w., halorhodopsin, *Haloquadratum walsbyi*; Br/N.sp., bacteriorhodopsin, *Nostoc* sp.; Xop2/H.m., opsin, *Haloarcula marismortui*; Sop1/H.sp., sensory rhodopsin-1, *Halobacterium* sp.; Sop/Hr.sod., rhodopsin, *Halorubrum sodomense*; Sop1/H.s., sensory rhodopsin-1, *Halobacterium salinarum*; Csr3/Ha.v., bacterial rhodopsin, *Haloarcula vallismortis*; Sria/S.r., sensory rhodopsin a, *Salinibacter ruber*; Srib/S.r., sensory rhodopsin b, *Salinibacter ruber*; BopII/H.w., bacteriorhodopsin II, *Haloquadratum walsbyi*; BopI/H.w., bacteriorhodopsin I, *Haloquadratum walsbyi*; Xop1/H.m., bacteriorhodopsin, *Haloarcula marismortui*; Bop/H.s., bacteriorhodopsin, *Halobacterium salinarum*; Ar2/H.sp., archaerhodopsin-2, *Halobacterium* sp.; Ar3/Hr.sod., archaerhodopsin-2, *Halorubrum sodomense*; Ar1/H.sp., archaerhodopsin-1, *Halobacterium* sp.; Aop/H.x., archaerhodopsin, *Halorubrum xinjiangense*; Br/H.l., bacteriorhodopsin, *Halobiforma lacisalsi*; Bop/Ht.sp., bacteriorhodopsin, *Haloterrigena* sp.; Cop2/H.sp., cruxrhodopsin-2, *Haloarcula* sp.; Bop/H.m., bacteriorhodopsin, *Haloarcula marismortui*; Cop/H.j., cruxrhodopsin, *Haloarcula japonica*; Cop3/Ha.v., cruxrhodopsin-3, *Haloarcula vallismortis*; Sop2/H.s., sensory rhodopsin-2, *Halobacterium salinarum*; Pr/H.sp., phoborhodopsin, *Halobacterium* sp.; Sop2/Ha.v., sensory rhodopsin-2, *Haloarcula vallismortis*; Sop2/N.p., sensory rhodopsin-2, *Natronomonas pharaonis.*