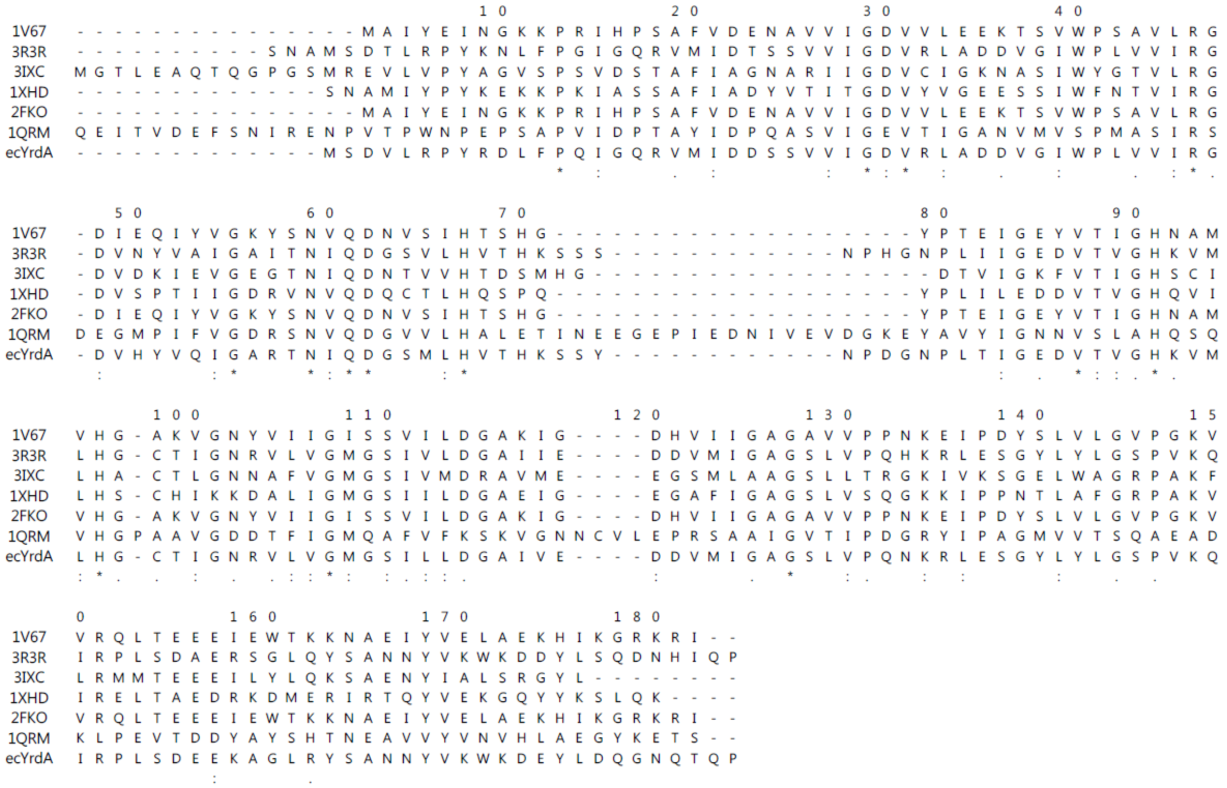
Supplementary Material



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                                                  1 0                 2 0                 3 0                 4 0
1V67    - - - - - - - - - - - - - - - M A I Y E I N G K K P R I H P S A F V D E N A V V I G D V V L E E K T S V W P S A V L R G
3R3R    - - - - - - - - - - S N A M S D T L R P Y K N L F P G I G Q R V M I D T S S V V I G D V R L A D D V G I W P L V V I R G
3IXC    M G T L E A Q T Q G P G S M R E V L V P Y A G V S P S V D S T A F I A G N A R I I G D V C I G K N A S I W Y G T V L R G
1XHD    - - - - - - - - - - - - - S N A M I Y P Y K E K K P K I A S S A F I A D Y V T I T G D V Y V G E E S S I W F N T V I R G
2FKO    - - - - - - - - - - - - - - - M A I Y E I N G K K P R I H P S A F V D E N A V V I G D V V L E E K T S V W P S A V L R G
1QRM    Q E I T V D E F S N I R E N P V T P W N P E P S A P V I D P T A Y I D P Q A S V I G E V T I G A N V M V S P M A S I R S
ecYrdA  - - - - - - - - - - - - - M S D V L R P Y R D L F P Q I G Q R V M I D D S S V V I G D V R L A D D V G I W P L V V I R G
                                                          *   :       .   :           :   * : *   :     .     :       .   : * .

            5 0                 6 0                 7 0                                         8 0                 9 0
1V67    - D I E Q I Y V G K Y S N V Q D N V S I H T S H G - - - - - - - - - - - - - - - - - - - Y P T E I G E Y V T I G H N A M
3R3R    - D V N Y V A I G A I T N I Q D G S V L H V T H K S S S - - - - - - - - - - - N P H G N P L I I G E D V T V G H K V M
3IXC    - D V D K I E V G E G T N I Q D N T V V H T D S M H G - - - - - - - - - - - - - - - - - - D T V I G K F V T I G H S C I
1XHD    - D V S P T I I G D R V N V Q D Q C T L H Q S P Q - - - - - - - - - - - - - - - - - - - Y P L I L E D D V T V G H Q V I
2FKO    - D I E Q I Y V G K Y S N V Q D N V S I H T S H G - - - - - - - - - - - - - - - - - - - Y P T E I G E Y V T I G H N A M
1QRM    D E G M P I F V G D R S N V Q D G V V L H A L E T I N E E G E P I E D N I V E V D G K E Y A V Y I G N N V S L A H Q S Q
ecYrdA  - D V H Y V Q I G A R T N I Q D G S M L H V T H K S S Y - - - - - - - - - - - N P D G N P L T I G E D V T V G H K V M
          :           : *       * : * *       : *                                                       :   .   * : : . * .

                1 0 0               1 1 0                       1 2 0               1 3 0               1 4 0               1 5
1V67    V H G - A K V G N Y V I I G I S S V I L D G A K I G - - - - D H V I I G A G A V V P P N K E I P D Y S L V L G V P G K V
3R3R    L H G - C T I G N R V L V G M G S I V L D G A I I E - - - - D D V M I G A G S L V P Q H K R L E S G Y L Y L G S P V K Q
3IXC    L H A - C T L G N N A F V G M G S I V M D R A V M E - - - - E G S M L A A G S L L T R G K I V K S G E L W A G R P A K F
1XHD    L H S - C H I K K D A L I G M G S I I L D G A E I G - - - - E G A F I G A G S L V S Q G K K I P P N T L A F G R P A K V
2FKO    V H G - A K V G N Y V I I G I S S V I L D G A K I G - - - - D H V I I G A G A V V P P N K E I P D Y S L V L G V P G K V
1QRM    V H G P A A V G D D T F I G M Q A F V F K S K V G N N C V L E P R S A A I G V T I P D G R Y I P A G M V V T S Q A E A D
ecYrdA  L H G - C T I G N R V L V G M G S I L L D G A I V E - - - - D D V M I G A G S L V P Q N K R L E S G Y L Y L G S P V K Q
        : * .   .   :   .   . : : * :   : . : : .                   :         .   *     : .     :   :         :     .   .

        0               1 6 0               1 7 0               1 8 0
1V67    V R Q L T E E E I E W T K K N A E I Y V E L A E K H I K G R K R I - -
3R3R    I R P L S D A E R S G L Q Y S A N N Y V K W K D D Y L S Q D N H I Q P
3IXC    L R M M T E E E I L Y L Q K S A E N Y I A L S R G Y L - - - - - - - -
1XHD    I R E L T A E D R K D M E R I R T Q Y V E K G Q Y Y K S L Q K - - - -
2FKO    V R Q L T E E E I E W T K K N A E I Y V E L A E K H I K G R K R I - -
1QRM    K L P E V T D D Y A Y S H T N E A V V Y V N V H L A E G Y K E T S - -
ecYrdA  I R P L S D E E K A G L R Y S A N N Y V K W K D E Y L D Q G N Q T Q P
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Supplementary Fig. S1. Sequence alignment of γ-CAs and their related proteins. Each protein was labeled as their PDB IDs (PDB ID 1QRM corresponds to the structure of γ-mtCA and 1V67 to that of γ-phCA), except for ecYrdA. The numbering follows the amino acid sequence of ecYrdA. Identical residues across all sequences are marked by "*". Conserved residues are labeled by ":" or ".".