



S1 Fig. Homology modeling of active sites of trans-sialidase candidates falling for criterion 1. Active site and aromatic sandwich of TcTS (grey) aligned to homology models of (putative) sialidases from (a) *Actinomyces* sp. oral taxon 849 str. F0330, (b) *Actinomyces odontolyticus*, (c) *Congregibacter litoralis*, (d) *Diplosphaera colitermitum*, (e) *Oceanobacter* sp., (f) *Opitutaceae* bacterium TAV1, (g) *Opitutaceae* bacterium TAV5, (h) *Pirellula staleyii*, (i) *Verrucomicrobium spinosum*, (j) *Pseudomonas mendocina*, (k) *Ruminococcus albus*, and (l) *Streptomyces griseoflavus*. None of these produced active sites with all nine sialyl interacting residues, thus falling for selection criterion 1.