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001 MFKLFEGFTD PFPKGEPQRP SNTLWAFCRH YTHGFEEKPLI VMALLSTAIA 050
051 IIEVSLFGFM GQLVDWLSTS SPDTFLVENQ STLIGLGLLV LVGMPLLIAF 100
101 YSLLIHQSLL GNYPMISIRWL AHRYLLKQSV SFYQDEFAGR ISTKVMQTAL 150
151 AVRETVMKSL DVFVYVMVYF TAIVVILAQA DWRLMIPMLI WLAIYVTVQM 200
201 YYVPKLKKVA SEQADARSLM SGRIVDSYTN IMTVKLFSSHS QRETQYAEEG 250
251 MQDFLGTVHR QMR LVTGFNI WVEMANYLLV FTIAALSIYL WTTSAISVGA 300
301 IAVAVSLSLC INGMSKWIMW EVSALFENIG TVVDGMTMLG KPITVTDKPD 350
351 AKPLVVKHGG ITFDDVSFHY GENKSVINHL NLNIKPGKEV GLVGRSGAGK 400
401 STLVNLLLR F HDVESGRILI DGQPISEVTQ ESLRSKIGMV TQDTSLLHRS 450
451 IRDNILYGNP NATEEQLLKA TAQAHAEFI LGLTDPHGNS GYDAQVGERG 500
501 VKLSGGQRQR IAISRVLLKD APLLVLDEAT SALDSEVEAA IQESLNELMQ 550
551 GKTVIAIAHR LSTIAAMDRL IVLDKGQIVE QGSHQELIAQ NGIYAH LWAH 600
601 QTGGFIGCDE DEVEEAILA 619

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S1 Figure. The predicted transmembrane regions of VcaM from *V. cholerae* (Genbank, Q93GU0). The estimated transmembrane helices amino acid residues: 39–61, 83–105, 162–180, 184–203, 264–286, 290–312 amino acid residues, predicted by TMHMM.