```
   LCA00972 -------------------FGMVLGPLQSVAAAEATW--PSGTYPAPATGSFTRSN-GLFDRVSTD-SSPIKSGTDEVGFEL--------NADQASKVGSVWSKT-----PFVDLNKDKF-------TLD-----MQIYLGNKT--GGAD  100
    LSA0172 -------------------------------------------------------------------TVTYAKDEQVITYRYE-------ESHIGIIADKRWDFG-----K-HDTTGTDRNYYLKAKTKDNQKQPYAVSVEDYY---TSK   67
SA1730_1731 -----------------------------------------------------------------D-DPVFTDKVRTITYGYY-------KRMLSVEAPSYWDFG-----T-HNRTQTDSTYYLEDRKTP-----QAVKVTDHY---GVD   63
SA0211_0212 -------------------------------------------------------------KAYRD-DPQIGDQDRIITYGYK-------KAMLSIDAPSSWEFG-----DYNNKPMDRTYYLNHNQGTP-----QAVTVTDNY---GVQ   68
    LSA1283 ------------------AKDSLFMKQAAAATAIGKR--YQAQLTLTTSVDSEEES-SKKAEKVVV-VSNKAELQVEPSL----------GKLTLDQVPN-FRFG--NVLAKDVYTGTNTQNQPY--EVN-----DTLKITDTR---VNP  105
   LME00911 -----------------------SNAILSPEGIVTLS--GIGTFNGNIVAHKYVGN-NTFPTSSTF-PDLELPIDRNNDVSPK-----------LISAPD-VDFG-----S-HKINSETSLIGN-----------WKGNCQVSG--EKSK   92
T07092_7093 ------------------------------VGGVQFT--NQTSIQFPTDYAKP----QYVHIRTVD-KAGNKSTTKHISTTQK-------GRVDMLTVPKSVEFT-----P-IQLNGEKQNSFG---TLG------KLMIHDSR--NQAD   89
   BCEA0044 ------------------------------VGGVQFT--NQTSIQFPTDYAKP----QYVHIRTVD-KAGNKSTTKHISTTQK-------GRVDMLTVPKSVEFT-----P-IQLNGEKQNSFG---TLG------KLMIHDSR--NQAD   89
   LCR00181 --------------------------AQNWLNDWITN--NASGWSIKNFLSPYHQV-NYGSLKDAV-AGAGGVAFSEVNIYQANLVYN--GKIDFSSVPTKIDFG-----E-NAISSVEKSYQG---VLD-----NSVIVSDTRATNLAT  104
  LCR00710A ---------------------------QKWLNDWITN--NAAGWSVKDFLDPNLVSYVNSGLSSAV-TGAGGVAFSKNNVYQVNLIYS--GSIGFSSVPSQIDFG-----K-NPVVPVDKSYQG---MLD-----NSVVVSDTRAPNLAT  104
    EF02660 --------------ELAQWTQATVIFADGRANQTPSL--DAATFQAIQQAKPEELA-KTVPANYQF-TEAGETLNKKVNVSIS-------GELTLEKVPKTIDFG-----K-QKISAKPEVYWP---TLS-----DDLVVQDTR-GSEST  110
   LCA00293 -------------------WQLNGKKVERTPTKLDKS--AANRIQKSTALRFTRNGSPFKATSPDV-KPPDQPKPDEKDKQS--------GALKLVEVPD-FDFG-----T-LLISGETQVVRP---QMR-----GKLLIEDSR-KIAKK  104
   LCR00187 --------------------FKADGTIEEPVISSPSD--LVTTLQTIQANNPIIDG-DGNIRPVTY-TYNGLSKDITLNLTF--------GAISLST-PNSYDFG-----T-LDVSPKPLISWAT--SPA-----SDVVVTDTRTGSALK  104
   LLX01616 --------------------FKADGTIEEPVISSPSN--LVTTLQTIQANNPIIDG-DGNIRPVTY-TYNGLSKDITLNLTF--------GSISLST-PNSYDFG-----T-LDVSPKPLISWAT--SPA-----SDVVVTDTRTGSALK  104
    EF01001 ----------------EKTVTVFYKDAEGKDIAPPKS--VTGKIGAPYQEKPLDIS-GYVFTKDSG-NAEGTMTEETKDIYFYYRL----GELYFKEAPKQITFG-----T-EKIRNQPLIKLG---HPT-----EGLKVVDER---NAN  109
   EFA03340 -----------------DIHVYYKDKDSQIDIAEMKT--ITGKIGEKYKETPIDIE-GYVFDSDSA-NTEGIFSENTEDIYFY-YRK---GKLYLSTAPQYVNFG-----K-HKISSRPLSEFG---QFS-----GGLKIIDER---AFG  108
   LCA00329 ------------------------------YDLKTPA--GKDFLAYILDPETGELVLEKVPSFVFE-LKNGQTGYRNPTVMEM-------VKGLPTPTTTNWDQA-----NADQWLTNQQGREPTNSTGK------VLSVKDTR--PTKQ   97
SA0613_0614 --------------------SLLKGPAKAAAANQAFD--YQFESDLPTQPNQIVVE-ANYPAPYAL-TTPVRKVLKDIPA----------GKLGFLAAPTHLDFG-----S-LPLTNSQSPLYPYTKTAD-----TSLIVSDPR-ATTRG  104
   PPE00545 ----------SKLTVSFTHEDGAKVRLVGNCAGEKRI--LKEYSNAAHQVDDEIIC-QFPKSWINK-KVDFYLEDDQHQMSNKETRIIKQERGPELSLPSKIDFG-----S-HEIPLEITVCSL---TRA-----EWVHVKDRS-ELDHY  121
   LIN00557 ----------------------ATLTGPGSVPNDLKD-------DFASKVDLNKAG-DYFVELSTPDWPPLTDAAKPVTILVRV------REGLEMKISDDFRMDVDENTDPIPISNNKQTLKCFAQEGD-----AEIEVLDRR--RAKQ  107
   LIN00552 ------------------------VNATLTGVGSLVD-------DFESVVDLTKAG-DYVVTLSS--PGNPPASQTAIPVTVVVHV----RESMELQIPNDFRMGIDENSESVPILNRKQTLKCYGADGK-----VDLKVTDRR--RSKQ  105
   LMO00549 ------------------------VNATLTGEGTLRD-------DFIYKVRLNTAG-DYVVTLTS--PKSGYYEQDAIPVTVIVHV----KELLELQIPDEFRMDIDANADSVPISDKKQTLKCYGSSGK-----AELEVIDRR--TVRQ  105
    lp_2173 -------------TALNVTDTSYTVKVPTNADDDGTA--YYASLSYPVNGKPQTV--TTNAALLTV-KSGGRLSLSAVPNFNF-------GTLNLQRLAQGTDLA-----TDPTAVKANDGYDG---NND-----YRLAVVDDR--TVGA  110
   EFA03594 --------------------GDTIHLTYNYQLNTVDT--SVQSVSILTKAAVLSSN-ITLADGAKL-PNPVVQTSAKTILVPK-------QELTLVNVPDDFTFG-----NDLPKPLKTSYYEA---KGD-----FSFDVRDTR-LPSTS  105
   EFA03967 ----------------NQLFAGDVLEIVLNDQAGEAT--AKGVQNKPSTNDEIGNH-NPSDTPVVY-HDAPPFA-PATKIVVE-------GGLSFLA-PSKLDFG-----Q-IKATGLTQEAFGQM-DIQ-----EKLWIYDQR--ETKN  107
   LLX01219 ------------VLTVGDSLDISKGFLSATDNAGNPLKFDKVSVLGADKVDTHKVG-DYSLTYSLK-PISPIEKVVHVHVKS--------GALTLSSLPS-IDFN-----N-IILNGSSQTSKPK--IED-----ISLNLRDRR--GLSD  112
   LBR00959 --------------DSSSHYIPVTFNGGSMAQGFLKP--SAPSTTDDYTGLEPADS-KFNAAGSTV-NSNDLTNANNKGLLISAELL---GTDLGAVDQYKWDYN-------IADLSEQPTLLPRTTGND-----LYFRVIDTR--SATP  115
    lp_3075 -------------------------DAAGKYLAPDTK--ISGATGDAYHIKPIEIQ-GYVPDQPDGVQGNFTDKDETITLMYNP------GGLMFVSAPQTINFG-----Q-NPITGKSENYGA---SYD-----TGLVIQDGR--SIGS  100
    lp_3117 ---------------------VKYVDGDGVEIADEET--SSGTSGDAYQTTAKTID-GYTLHATPT-NATGTYDASTITVTYVYD-----GNLFFNSSPTMLDFG-----S-HTISGTTETYAP---TLD-----KTLAVQNNG--QISS  104
    EF02286 -----------------------GQEIQKLADETTTN--SKTFKEKALLLPELTYGKQQLVVEEVY-DKGYKIDELALTVTVV-------GSVRFKTVPTAISFG-----NELQIASSTTQYPIV--SMD-----QPLNIRDTR--QTGN  103
    EF01892 -----------------------YHNSLPADNFTEAN--TQFTLQYTATVTEEWIN-QFLLFSSTV-TGNDGGGTPITPITKEQSLPIKNGTLRFVQMPTTVSFK-----N-LPFPSKRTIYSPS--TIS-----APFLIADGR--VAKT  108
    lp_3676 ----------------AHADGTPIANYKANGSVNEPD--KAGYFHLKLPTESLKQGPNDVKVWVSD-QHGQRSNIDTLTVNVN-------SGLMFGQINAQMRFR-----S-NTIPQSERLLSP---TNQ-----WQIEVHDTR--SVAS  108
    lp_3064 ---------------WLVKQAGIVATNPDSATDTITY--AANETSLASKLSSLAVG-SSTTINIYG-KGSSGLKSDAKAITVT-MRD---GTLSLGTLPASLTFG-----T-LTIPFKETLYQP---TNA-----WNITVNDTR--KTGS  111
    lp_2975 -------------------QAGVVATNPSNANDTMTY--HASESGLVALFKGLADN-QSTAVHIYA-TSASGLTSDKIALQVT-KLA---GTLSFGQLTTNMSFG-----D-LKVPLTPQVYQP---TNP-----LAISVTDTR--ATGA  107
   LBR01269 ----------------ANLNGQPWPTFTLNGTAASPN--EVGAFTLTLSADKVISGTNSVTVYVTD-SRGNRSATIATTVMVA-------GKLAFSQFAKTSSFT-----T-TILSGQQMLINR---NPD-----WQVQVQNSL--GTGT  108
    LSA1820 --------------------GTLHYAIDDGAEKTIAQ--NNVGPKLVSGIPTVGLSLNDTHKLTLY-MTNAGYNEKSAVVTVYFKLKG--GTLLLGKVKNEIGFE-----P-VTVGKNTINKRD---NTD-----WAPTVADTR--GTGS  109
    lp_0297 --------------DGMRIEYRVNGEAGEDYQLSMDD--PVGYVEFEVDAEELQIGENQITLRAHS-KDNAYSEPVTVTVTVIG------GELQLKKVSTESVFA-----P-IKLTGTAQVSRPEG---------LEVVVNDDT--GSKA  110
   LBR00331 -----------------PIWVHVTINGKVQKEPIKVA--EDGTFKVTLQANQLQKG-DNVIEVVAT-SGELRSNAEEVTISCS-------GCLEL-TAPSDVSFE-----S-KQLTGQRQELKR---GDG-----WELSVQDTR--GAGS  105
    lp_3450 ----------------VTLHPTLNGKEMPTVQMSDDD--EQGYFYYKVKAEDLHVGDDNEIELWASDRYENVSPVDKAQIIVTA------GELGFKTVAKSSTFK-----T-ITLDGSAQTTDR---EDD-----WQLVVRDSR--GKGS  110
BR1027_1028 ----------------ITVKSTLNGRAQADFKIPESDDNESGRFDYTVKPNQLTAGDNTLIITVAD-PYGNESNPLKVTITLT-------GQVLFNGVAEASSFQ-----S-TTLTGSQQQVKR---GND-----WQVNVLDTR--TAGA  110
   LBR00625 ----------------PRVTIQPVLNGTRLTVITPAT---DGTFSLPLKASDLQAGTNTLTLVATA-DTGDTSNTVTVPITVA-------GDLKFSDVAAASHFQ-----T-ATLTGQDQLAKR---GDD-----WRLAVSDTR--GTGR  107
   LIN00595 ----------------NLNDEEVKQFILDKSEAKAFN--IVTGKDLTPDVKVTSTNLKKETGTYTA-TIQIGTLTKEITIQVT-------GELKFNHVPATMSFE-----S-IELNNQKSIAKR---NTD-----FDLSVLDSR--GAGS  108
   LMO00587 ----------------ELNDAELEQFILTKSGAKAFQ--IETGEDLTTDVKVASTNLKKETGTYTA-TIQIGGLTKEIAIQVT-------GELKFNHVPETISFE-----T-MGLNQQKNIAKR---NAD-----FDLSVLDSR--GAGD  108
   BCU00750 MGEAVPQTVKVGTDLSKIDISNFVTNLSVDTNAEIDK--PISVVRLEDIPKTDALG-DYTVTAIIK-TNQGVEAKVKVPIKIVE-------GTLKLVDVPKVISFN-----N-LVIASKPTIYNPS--FID-----GKVTVVDGR--AKKQ  125
   BTH03761 -----------------MDISKFVTDLSVDTNLDVDK--PISVMKLINIPDTKTIG-NHTVTVVIE-TKQGVQAEIQVPVTVVD------GTLKLVDVPKEITFG-----D-VTIPSKTTTYTPK--AIS-----NSLKVTDNR--VKKQ  108
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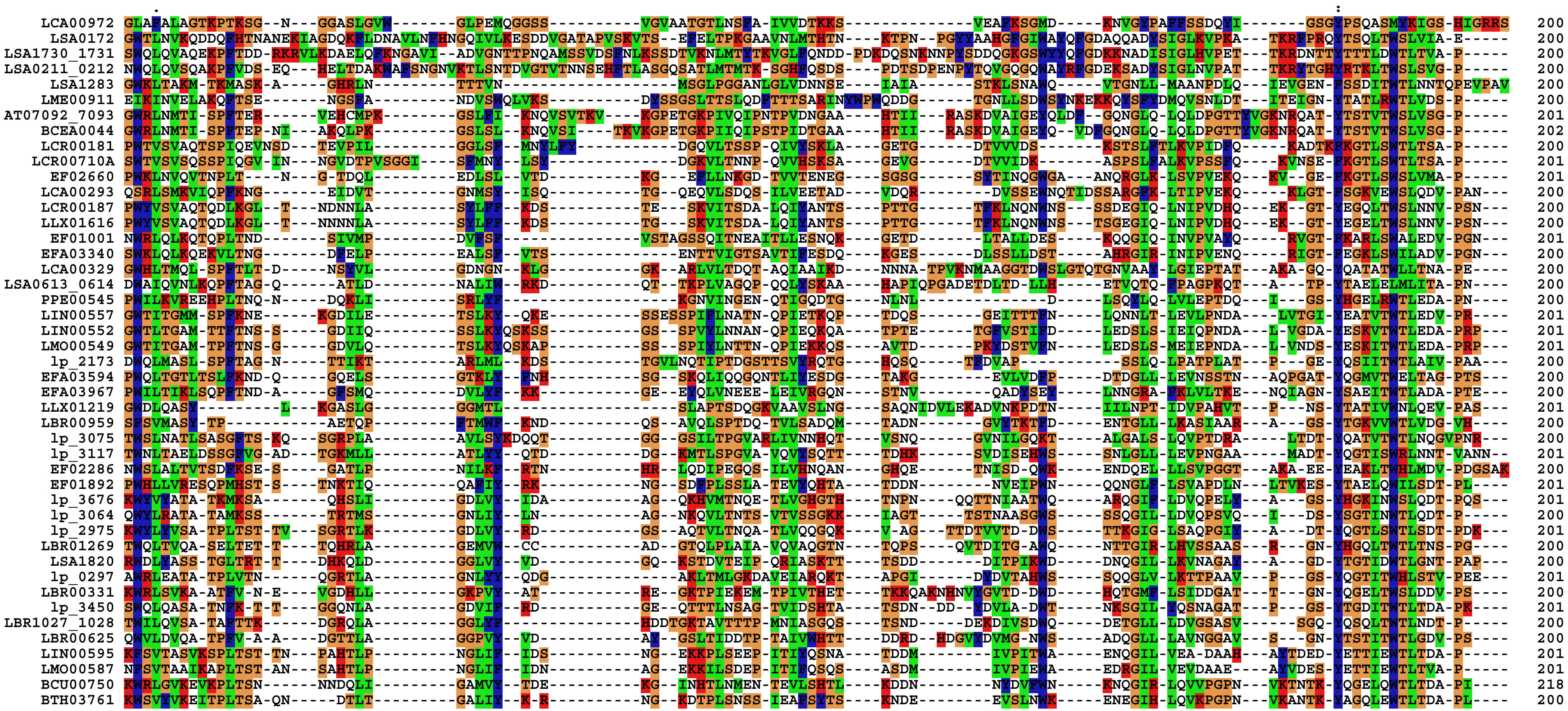

Figure 6:

Multiple sequence alignment of CscC proteins. Only the last 200 residues are shown. Proteins IDs can be found in additional file Table 5. Colour coding of highly conserved residues: green, hydrophobic (L, M, I, V); blue, aromatic (W, F. Y); red, basic (R, K, H); light brown, neutral and small (P, G, S, T).