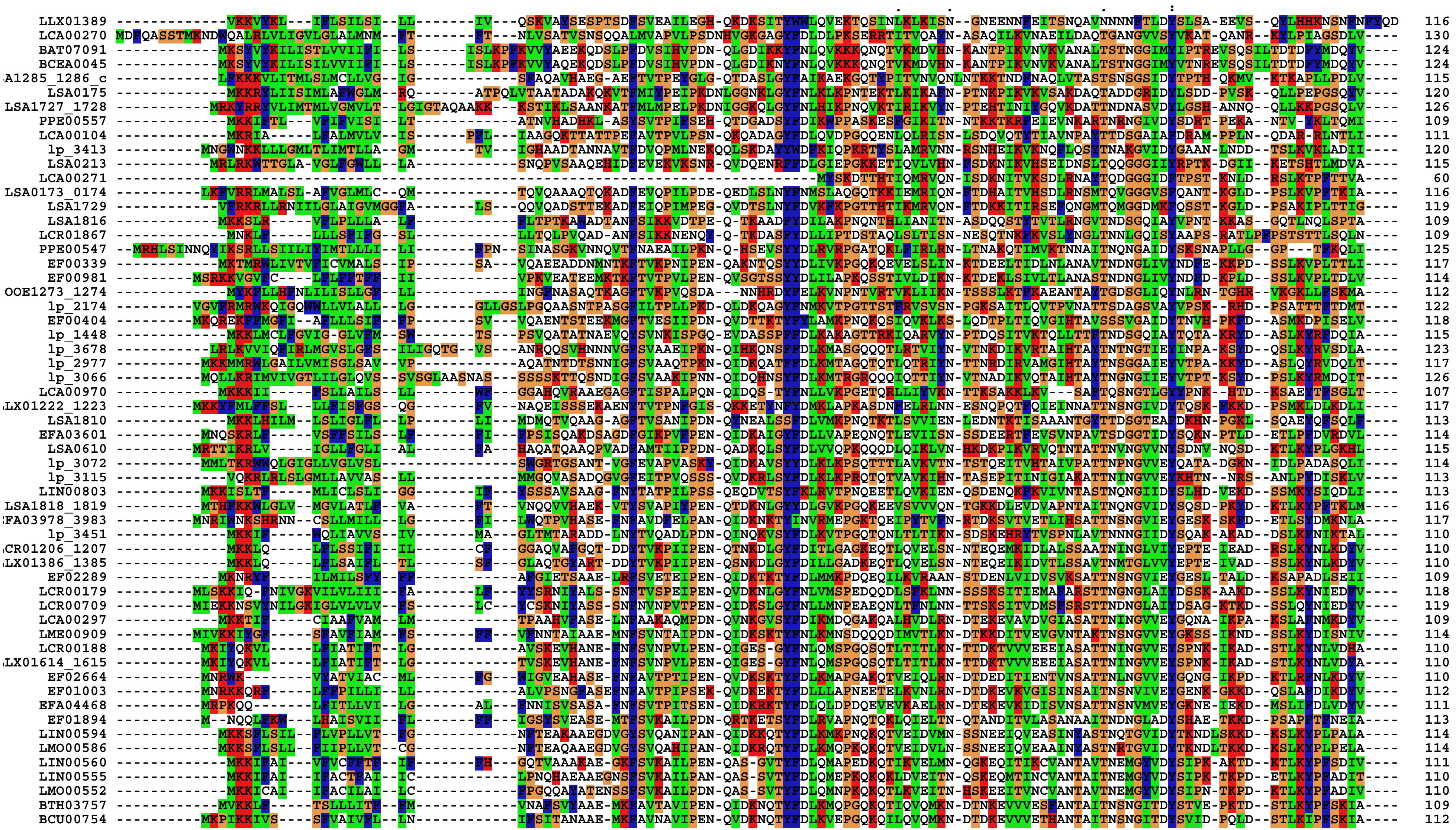

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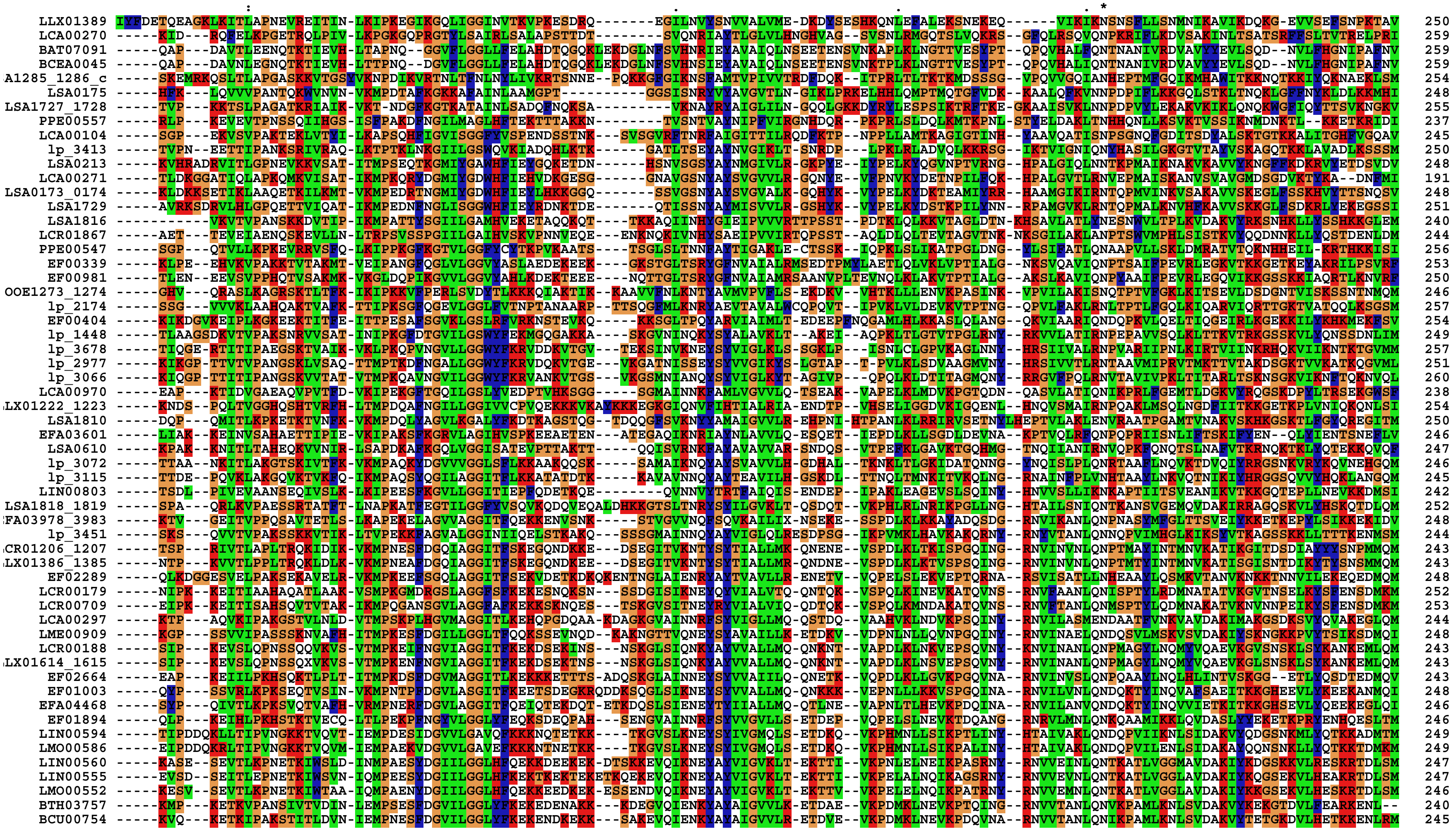

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    PPE00547 -----SGP---QTVLLKPKEVRRVSFQ-LKIPPKGFKGTVLGGFYCYTKPVKAATS----TSGLSLTNNFAYTIGAKLE-CTSSK--IQPKLSLIKATPGLDNG--YLSIFATLQNAAPVLLSKLDMRATVTQKNHHEIL-KRTHKKISI   256
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     EF00404 -----KIKDGVKEIPLKGKEEKTITFE-ITTPESAFSGVKLGSLRFVRKNSTEVKQ-----KKSGLTPQYARVIAIMLT-EDEEPFNQGAMLHLKKASLQLANG--QKVIAARIQNDQPKVLQELTIQGEIRLKGEKKILYKHKMEKFSV   254
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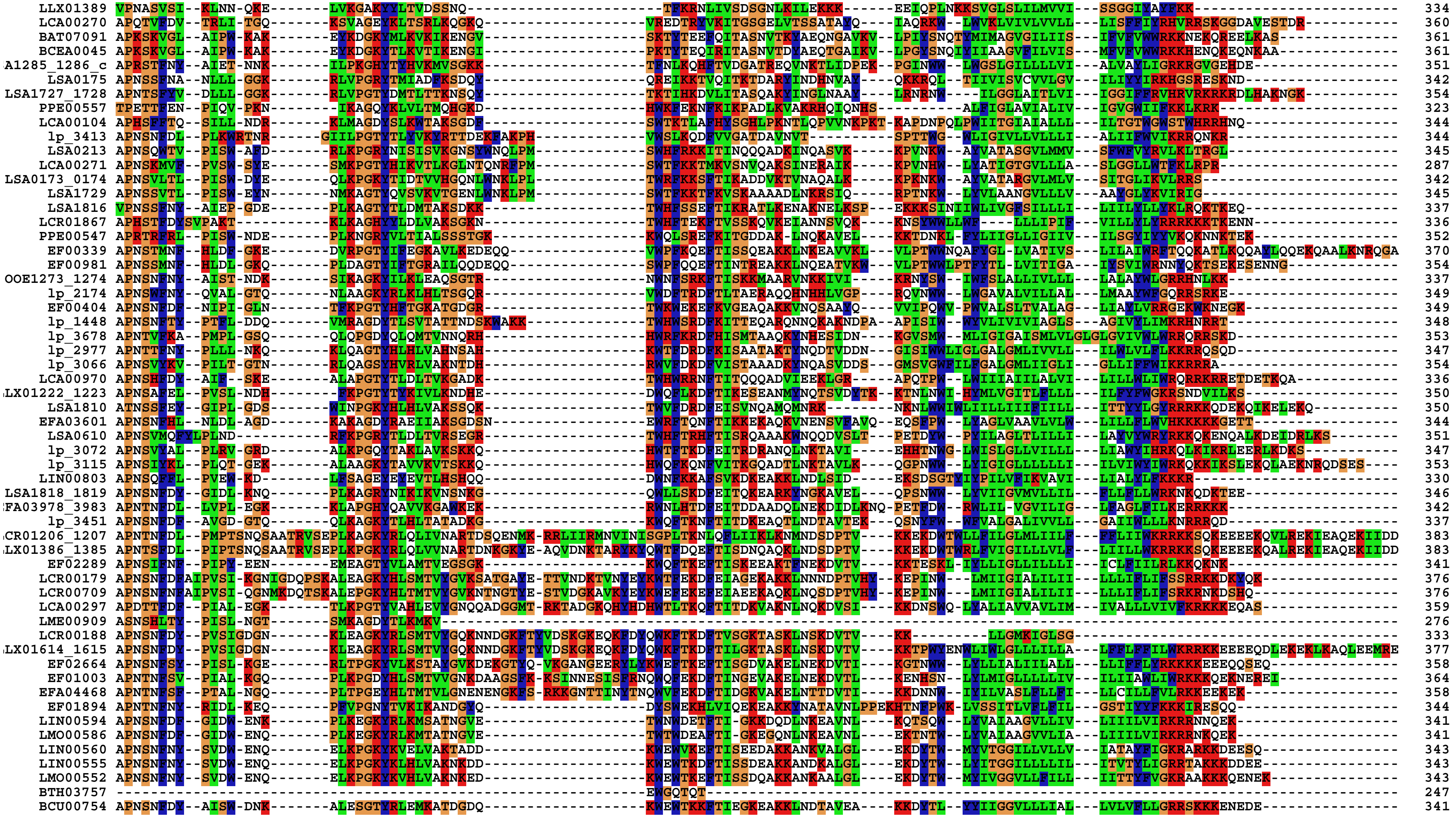

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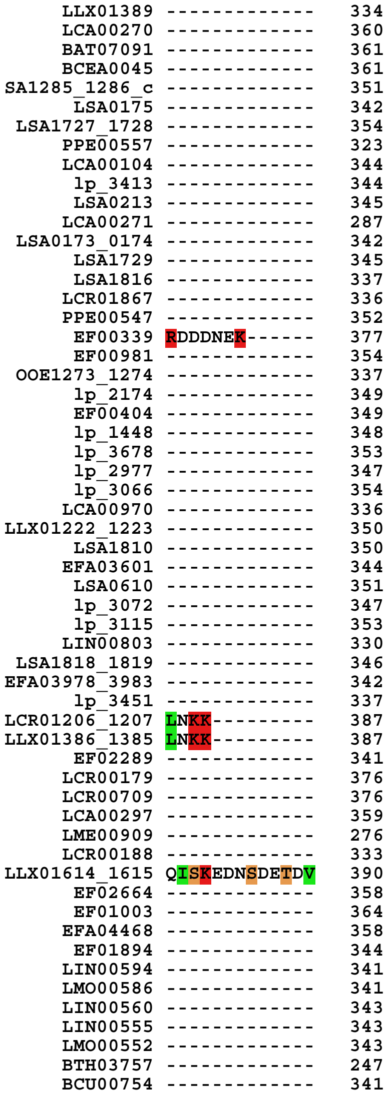

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Figure 4:
Multiple sequence alignment of CscA proteins. Proteins IDs can be found in additional file Table 5. Colour coding of highly conserved residues: green, hydrophobic (L, M, I, V); blue, aromatic (W, F. Y); red, basic (R, K, H); light brown, neutral and small (P, G, S, T).