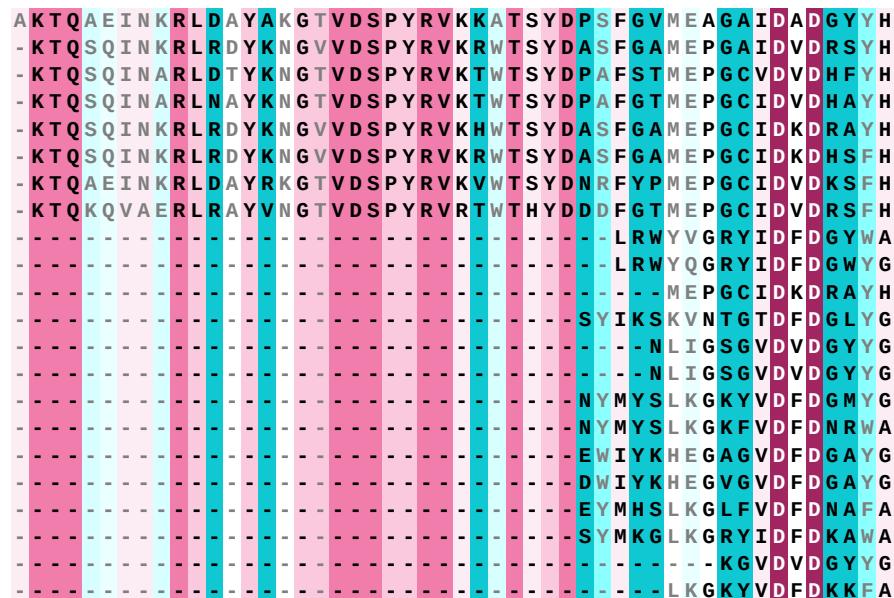# ConSurf Color-Coded MSA

CHAPk

UniRef90_U6FYE9. Autolysin. Staphylococcus capitis CR01
UniRef90_D3QFD1. Phage N-acetylmuramoyl-L-alanine amidase. Staphylococcus lugdunensis
UniRef90_UPI0002FAEBEA. Amidase. Staphylococcus capitis
UniRef90_H9A139. Lysin. Staphylococcus phage StB20
UniRef90_B9CV69. SH3 domain protein. Staphylococcus capitis SK14
UniRef90_Q4L3Y5. N-acetylmuramoyl-L-alanine amidase. Staphylococcus haemolyticus
UniRef90_D1GQI6. Phage amidase. Staphylococcus aureus
UniRef90_E8SE62. Autolysin. Staphylococcus pseudintermedius
UniRef90_Q8SDJ9. Amidase. Staphylococcus phage phi13
UniRef90_UPI00035CC3BA. Amidase. Staphylococcus epidermidis
UniRef90_Q4Z8Y9. ORF015. Staphylococcus phage Twort
UniRef90_E8SE60. Bifunctional autolysin Atl. Staphylococcus pseudintermedius
UniRef90_O56785. Cell wall hydrolase Ply187. Staphylococcus phage 187
UniRef90_H9A0Q2. Lysine. Staphylococcus phage StB27
UniRef90_I6T7G5. Amidase. Staphylococcus phage vB_SepiS-phiIPLA5
UniRef90_Q859K9. Amidase. Staphylococcus phage 44AHJD
UniRef90_A8D3S8. Amidase. Staphylococcus phage SAP-2
UniRef90_I7KMZ0. Possible N-acetylmuramoyl-L-alanine amidase.Staphylococcus equorum
UniRef90_K8N672. Uncharacterized protein. Staphylococcus simulans
UniRef90_UPI00036FC933. Hypothetical protein. Staphylococcus intermedius
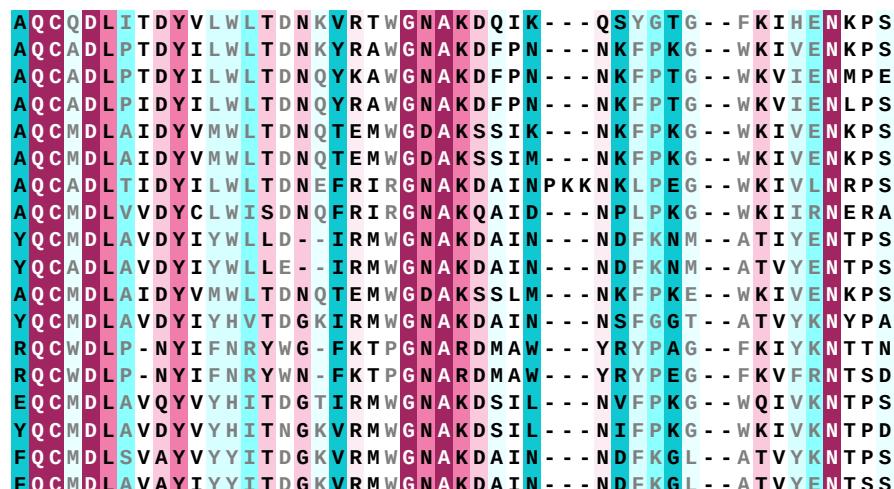UniRef90_K0U7Q5.Autolysin. Staphylococcus arlettae CVD059

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Input_pdb_ATOM_A               AKTQAEINKRLDAYAKGTVDSPYRVKKATSYDPSFGVMEAGAIDADGYYH
UniRef90_U6FYE9_2_161          -KTQSQINKRLRDYKNGVVDSPYRVKRWTSYDASFGAMEPGAIDVDRSYH
UniRef90_D3QFD1_2_162          -KTQSQINARLDTYKNGTVDSPYRVKTWTSYDPAFSTMEPGCVDVDHFYH
UniRef90_UPI0002FAEBEA_2_162   -KTQSQINARLNAYKNGTVDSPYRVKTWTSYDPAFGTMEPGCIDVDHAYH
UniRef90_H9A139_2_162          -KTQSQINKRLRDYKNGVVDSPYRVKHWTSYDASFGAMEPGCIDKDRAYH
UniRef90_B9CV69_2_162          -KTQSQINKRLRDYKNGVVDSPYRVKRWTSYDASFGAMEPGCIDKDHSFH
UniRef90_Q4L3Y5_3_166          -KTQAEINKRLDAYRKGTVDSPYRVKVWTSYDNRFYPMEPGCIDVDKSFH
UniRef90_D1GQI6_2_161          -KTQKQVAERLRAYVNGTVDSPYRVRTWTHYDDDFGTMEPGCIDVDRSFH
UniRef90_E8SE62_11_138         ---------------------------------LRWYVGRYIDFDGYWA
UniRef90_Q8SDJ9_11_138         ---------------------------------LRWYQGRYIDFDGWYG
UniRef90_UPI00035CC3BA_1_125   ------------------------------MEPGCIDKDRAYH
UniRef90_Q4Z8Y9_9_144          ----------------------------SYIKSKVNTGTDFDGLYG
UniRef90_E8SE60_20_150         -----------------------------NLIGSGVDVDGYYG
UniRef90_O56785_20_150         -----------------------------NLIGSGVDVDGYYG
UniRef90_H9A0Q2_224_354        ----------------------------NYMYSLKGKYVDFDGMYG
UniRef90_I6T7G5_224_354        ----------------------------NYMYSLKGKFVDFDNRWA
UniRef90_Q859K9_9_139          ----------------------------EWIYKHEGAGVDFDGAYG
UniRef90_A8D3S8_9_138          ----------------------------DWIYKHEGVGVDFDGAYG
UniRef90_I7KMZ0_224_353        ----------------------------EYMHSLKGLFVDFDNAFA
UniRef90_K8N672_224_351        ----------------------------SYMKGLKGRYIDFDKAWA
UniRef90_UPI00036FC933_26_147  ---------------------------------KGVDVDGYYG
UniRef90_K0U7Q5_4_128          ----------------------------LKGKYVDFDKKFA
```

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Input_pdb_ATOM_A               AQCQDLITDYVLWLTDNKVRTWGNAKDQIK---QSYGTG--FKIHENKPS
UniRef90_U6FYE9_2_161          AQCADLPTDYILWLTDNKYRAWGNAKDFPN---NKFPKG--WKIVENKPS
UniRef90_D3QFD1_2_162          AQCADLPTDYILWLTDNQYKAWGNAKDFPN---NKFPTG--WKVIENMPE
UniRef90_UPI0002FAEBEA_2_162   AQCADLPIDYILWLTDNQYRAWGNAKDFPN---NKFPTG--WKVIENLPS
UniRef90_H9A139_2_162          AQCMDLAIDYVMWLTDNQTEMWGDAKSSIK---NKFPKG--WKIVENKPS
UniRef90_B9CV69_2_162          AQCMDLAIDYVMWLTDNQTEMWGDAKSSIM---NKFPKG--WKIVENKPS
UniRef90_Q4L3Y5_3_166          AQCADLTIDYILWLTDNEFRIRGNAKDAINPKKNKLPEG--WKIVLNRPS
UniRef90_D1GQI6_2_161          AQCMDLVVDYCLWISDNQFRIRGNAKQAID--NPLPKG--WKIIRNERA
UniRef90_E8SE62_11_138         YQCMDLAVDYIYWLLD--IRMWGNAKDAIN---NDFKNM--ATIYENTPS
UniRef90_Q8SDJ9_11_138         YQCADLAVDYIYWLLE--IRMWGNAKDAIN---NDFKNM--ATVYENTPS
UniRef90_UPI00035CC3BA_1_125   AQCMDLAIDYVMWLTDNQTEMWGDAKSSLM---NKFPKE--WKIVENKPS
UniRef90_Q4Z8Y9_9_144          YQCMDLAVDYIYHVTDGKIRMWGNAKDAIN---NSFGGT--ATVYKNYPA
UniRef90_E8SE60_20_150         RQCWDLP-NYIFNRYWG-FKTPGNARDMAW---YRYPAG--FKIYKNTTN
UniRef90_O56785_20_150         RQCWDLP-NYIFNRYWN-FKTPGNARDMAW---YRYPEG--FKVFRNTSD
UniRef90_H9A0Q2_224_354        EQCMDLAVQYVYHITDGTIRMWGNAKDSIL---NVFPKG--WQIVKNTPS
UniRef90_I6T7G5_224_354        YQCMDLAVDYVYHITNGKVRMWGNAKDSIL---NIFPKG--WKIVKNTPD
UniRef90_Q859K9_9_139          FQCMDLSVAYVYYITDGKVRMWGNAKDAIN---NDFKGL--ATVYKNTPS
UniRef90_A8D3S8_9_138          FQCMDLAVAYIYYITDGKVRMWGNAKDAIN---NDFKGL--ATVYENTSS
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UniRef90_I7KMZ0_224_353         YQCMDLIVDFADHVTNG-YRIWGNAKDLTW---VALPKG--WKLVENTPD
UniRef90_K8N672_224_351         FQCMDVAVDYVYHVTKGKVRMWGDAKDSIR---NVFPTG--WKVIENTPD
UniRef90_UPI00036FC933_26_147   MQCWDLP-NYILKKYWG-FTTWGNANAMAQ---KSNYRGNDFKIYRNTPS
UniRef90_K0U7Q5_4_128           FQCMDLIVDYADHVTNG-YRIWGNAKDLTW---VALPKG--WKLVENTPD


Input_pdb_ATOM_A                TVPKKGWIAVFTSGSY--EQWGHIGIVY-DG---GNTSFTILEQNWNGY
UniRef90_U6FYE9_2_161           TIPKKGWIAVFTSGTY--AQYGHIGIVY-NG---GNTTSFQILEQNWNGW
UniRef90_D3QFD1_2_162           TVPQKGWIAVFTSGTY--AQYGHIGIVY-NG---GNTNSFQILEQNWNGY
UniRef90_UPI0002FAEBEA_2_162    TVPQKGWIAVFSSGTY--AQYGHIGLVY-DG---GNTNSFEILEQNWNGY
UniRef90_H9A139_2_162           TIPKKGWIAVYTAGTY--SRYGHIGIVY-NG---GNTNSFQILEQNWNGW
UniRef90_B9CV69_2_162           TIPKKGWIAVFTSGTY--DKYGHIGIVY-NG---GNTTSFQILEQNWNGW
UniRef90_Q4L3Y5_3_166           TVPRKGWIAVFTDGTY--WEYGHIGMVY-DG---GNTSRFQILEQNWNGW
UniRef90_D1GQI6_2_161           TVPKQGWIGVNTS-----TYYGHIWLVD-KG---ATQMTMPVIEQNWNSL
UniRef90_E8SE62_11_138          FVPQVGDVAVFRNGIY--KQYGHIGIVY-NS---GNTNQFLILEQNFDGN
UniRef90_Q8SDJ9_11_138          FVPQIGDVAVFTKGIY--KQYGHIGLVF-NG---GNTNQFLILEQNYDGN
UniRef90_UPI00035CC3BA_1_125    TVPKKGWIAVYTSGIY--SRYGHIGIVY-EG---GNTNSFQILEQNWNGW
UniRef90_Q4Z8Y9_9_144           FRPKYGDVVVWTTGNF--ATYGHIAIVT-NPDPYGDLQYVTVLEQNWNGN
UniRef90_E8SE60_20_150          FVPKPGDMAIWTGGNYNWNTWGHTGIVV-GP---STKDYFYSVDQNWNNA
UniRef90_O56785_20_150          FVPKPGDIAVWTGGNYNWNTWGHTGIVV-GP---STKSYFYSVDQNWNNS
UniRef90_H9A0Q2_224_354         YIPPVGAIGVCTTGIY--QEYGHIYLVWDNS---GGTNTQTVLEQNFDGN
UniRef90_I6T7G5_224_354         YVPPVGAIGVCTYGIY--QRYGHIYLVWDNS---GGTNTQTVLEQNFDGN
UniRef90_Q859K9_9_139           FKPQLGDVAVYTNG-----QYGHIQCVL--S---GNLDYYTCLEQNLGG
UniRef90_A8D3S8_9_138           FKPQLGDVAVYTNS-----QYGHIQCVT--S---GNLDYYTCLEQNLNG
UniRef90_I7KMZ0_224_353         YVPPIGTIAVFTKGIY--KKWGHTGLVWDNS---GGTESFVILEQNYDTL
UniRef90_K8N672_224_351         YIPPVASIAVNAAG-----EFGHIGLVWSNE---GGTEWFTIIEQNWDNQ
UniRef90_UPI00036FC933_26_147   FVPLPGDWAVWAGSNP----GHVSIVV-GP---ASTSYFYSCDQNWYTA
UniRef90_K0U7Q5_4_128           YVPPIASIAVFTKGIY--KKWGHTGLVWDNS---GGTETFVILEQNYDTL


Input_pdb_ATOM_A                ---ANKKPTKRVDNYYGLTHFIEIPVKA
UniRef90_U6FYE9_2_161           ---ANKKPSLRWDNYYGLTHFIVPP---
UniRef90_D3QFD1_2_162           ---ANKKPTLRWDNYYGLTHFIVPPV--
UniRef90_UPI0002FAEBEA_2_162    ---ANKKPTLRWDNYYGLTHFIVPPV--
UniRef90_H9A139_2_162           ---ANKKPSLRWDNYYGLTHFIVPPV--
UniRef90_B9CV69_2_162           ---ANKKPSLRWDNYYGLTHFIVPPV--
UniRef90_Q4L3Y5_3_166           ---ANKKPSLRWDNYYGLTHFIVPPV--
UniRef90_D1GQI6_2_161           ---ANLKPKRRLDYYYGCTHFIVPPISS
UniRef90_E8SE62_11_138          ---ANTPASLRWDNYYGCTHFIRPHYKS
UniRef90_Q8SDJ9_11_138          ---ANTPAKLRWDNYYGCTHFIRPKYKS
UniRef90_UPI00035CC3BA_1_125    ---ANKKPSLRWDNYYGLTHFIVPPV--
UniRef90_Q4Z8Y9_9_144           GIYKTELATIRTHDYTGITHFIRPNF--
UniRef90_E8SE60_20_150          NSYVGSPAAKIKHSYFGVTHFVRPAYKS
UniRef90_O56785_20_150          NSYVGSPAAKIKHSYFGVTHFVRPAYKA
UniRef90_H9A0Q2_224_354         ---HNTPAKLRVDNFYGTTHYIVPSF--
UniRef90_I6T7G5_224_354         ---ADTPAKLRVDNFYGTTHYIVPSF--
UniRef90_Q859K9_9_139           GFDGWEKATIRTHYYDGVTHFIRPKFSG
UniRef90_A8D3S8_9_138           GYDGWEKATIRTHYYDGVTHFIRPKFS-
UniRef90_I7KMZ0_224_353         ---ANSPAKLRTDNFEGLTHFIVPDF--
UniRef90_K8N672_224_351         ---ADTPAKLRKNDYSQITHFIVPDF--
UniRef90_UPI00036FC933_26_147   N-WTGSPAYKIKHNYNGVTHFVRPPYK-
UniRef90_K0U7Q5_4_128           ---ANSPAKLRTDNFEGLTHFIVPDF--
```

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1  2  3  4  5  6  7  8  9
Variable   Average   Conserved
```

X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.