

CLUSTAL O(1.2.4) multiple sequence alignment

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HlyA      ----- 0
sp|P09983| MPTITAAQIKSTLQSAKQSAANKLHSAQSTKDALKKAAEQTRNAGNRLILLIPKDYKGQ 60

HlyA      ----- 0
sp|P09983| GSSLNDLVRTADELGIQYDEKNGTAITKQVFGTAEKLIQLTERGVTFIFAPQLDKLLQK 120

HlyA      ----- 0
sp|P09983| YQKAGNKLGGSAENIGDNLGKAGSVLSTFQNLFGTALSSMKIDELIKKQKSGGNVSSSEL 180

HlyA      ----- 0
sp|P09983| AKASIELINQLVDTAASLNNVNSFSQQLNKLGSVLSNTKHLNGVGNKLQNLPLNDNIGAG 240

HlyA      ----- 0
sp|P09983| LDTVSGILSAISASFILSNADADTGTKAAAGVELTKVLGNVKGKISQYIIAQRAAQGLS 300

HlyA      ----- 0
sp|P09983| TSAAAAGLIASVVTLAISPLSFLSIADKFKRANKIEEYSQRFKKLGYDGDSSLAAAFHKET 360

HlyA      ----- 0
sp|P09983| GAIDASLTRISTVLASVSSGISAAATSLVGAPVSALVGAVTGIIISGILEASKQAMFEHV 420

HlyA      ----- 0
sp|P09983| ASKMADVIAEWKKGKKNYFENGYDARHAAFLDNFKILSQYNKEYSVERSVLITQQHWD 480

HlyA      ----- 0
sp|P09983| TLIGELAGVTRNGDKTSLGKSYIDIYEEGKRLEKPPDEFQKQVFDPLKGNIDLSDSKSST 540

HlyA      LLKFVTPLLTPGEEIRERRQSGKYEYITELLVKGVDKWTVKGVQDKGSDYDYNLIQHAS 60
sp|P09983| LLKFVTPLLTPGEEIRERRQSGKYEYITELLVKGVDKWTVKGVQDKGSDYDYNLIQHAS 600
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HlyA      VGNNQYREIRIESHLGDGDDKVFLSAGSANIYAGKGHDVVYYDKTDTGYLTIDGTKATEA 120
sp|P09983| VGNNQYREIRIESHLGDGDDKVFLSAGSANIYAGKGHDVVYYDKTDTGYLTIDGTKATEA 660
*****

HlyA      GNYTVTRVLGGDVKVLQEVVKEQEVSVGKRTEKTQYRSYEFTHINGKNLTETDNLYSVEE 180
sp|P09983| GNYTVTRVLGGDVKVLQEVVKEQEVSVGKRTEKTQYRSYEFTHINGKNLTETDNLYSVEE 720
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HlyA      LI----- 182
sp|P09983| LIGTTRADKFFGSKFADIFHGADGDDHIEGNDGNDRLYGDKGNDTLSGGNGDDQLYGGDG 780
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HlyA      ----- 182
sp|P09983| NDKLIGGAGNNYLNGGDGDELQVQGNLAKNVLSGGKGNDKLYGSEGADLLDGGEGNDL 840

HlyA      ----- 182
sp|P09983| LKGGYGNDIYRYSYGHHIIDDDGGKDDKLSLADIDFRDVAFRREGNDLIMYKAEGNVL 900

HlyA      ----- 182
sp|P09983| SIGHKNGITFKNWFEKESGDISNHQIEQIFDKDGRVITPDSLKKALEYQQSNNKASYVYG 960

HlyA      ----- 182
sp|P09983| NDALAYGSQGNLNLPLINEISKIISAAGNFDVKEERAAASLLQLSGNASDFSYGRNSITLT 1020

HlyA      --- 182
sp|P09983| ASA 1023

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Figure S1. Alignment between P09983 and alpha-hemolysin, indicating that the peptides matched to P09983 are between positions 543 and 717 of the whole hemolysin.