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Figure 1

Alignment of the amino acid sequences of the LysE and ArgO proteins listed in Table 1. Alignment gaps are indicated by "-". Identical amino acids are indicated by "*".

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YP_225551.1      -----MEIFITGLLLGASLLLSIGPQNVLVKQGIKREGLIAVLLV
ZP_05749209.1    -----MEIFVTGLLLGASLLLAIGPQNVLVKQGIKREGITAVIIV
NP_939452.1      -----MSIAIAGFLMGLSLIVAIGPQNALIIRQGIKREGLIPILVV
ZP_03933958.1    -----MSVLLAGFLLGLSLIVAIGPQNAVYIIKMGVKRDHIGAITLA
YP_002834652.1    MRRLEA-----MSVLLAGFALGLSLIIAIGPQNAVYIIKMGVKRDHIGAITLA
ZP_03711883.1    -----MSIIVAGFLLGLSLIVAIGPQNALVIRQGVKREGLIVVLAI
ZP_03922319.1    -----MSIVLAGFLLGLSLIVAVGPQNAMLLKYGIRRDHIGLIIVV
ZP_03931790.1    -----MSIVLAGFVLGLSLIVAVGPQNAMLLKYGIRRDHIGLIIVV
ZP_03918361.1    MYPENLSFYLCVLLTHNKYVNVFPAGLLFNLSLILALGPQNALILKYGLRRQAITLVISV
YP_002958101.1    M-----WTLAGTGLTGLALIVAIGQNAFVLRQGVRRHVGAVVLV
ZP_05365683.1    -----MSIVLAGFLLGLSLIVAVGPQNAMLLKYGIRRDHIGLIIVV
ZP_04835056.1    -----MSIIVAGFLLGLSLIVAIGPQNALVIRQGVKREGLIVVLAI

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YP_225551.1      CLISDVFLFIAGTLGVDDLSSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEA---
ZP_05749209.1    CLISDVVLFTLGLTGLVGLISDTAPIILDILRWCGIAYLLWFAVMAARDALRARTEV---
NP_939452.1      CILSDVILIFGGTAGVGALVDRAPIALVVLKWLGVAYLLYFGFTCFKEAFKRHGQA---
ZP_03933958.1    CLISDVILINAGVGGMGVLVEKFPTGLIIMKYLGAAYLIYFGFTCFRDAFKKEQEA---
YP_002834652.1    CLISDVILITGGTAGVGVLVERFPTALVVKYLGAAYLIYFGFTCFRDAFKKQQA---
ZP_03711883.1    CILSDIFLIFGGTAGVGVIIEKAPLALVALKWFGAAYLAWFAVSCFRDMV--KPR---
ZP_03922319.1    CALSDVILITSGTAGVGVLVEKFPNALQVLKYVGAAYLAYFTFTCFRDAFKTKGEA---
ZP_03931790.1    CALSDVILITSGTAGVGVLVERFPNLEALKYIGAYLAFFFTFTCFRDAFKTKGEAIDVE
ZP_03918361.1    CALCDITLIALSGVGVGVILQKAPIVLEILRYAGFLYLLWFAYTTCFRDAIHPKTLA---
YP_002958101.1    CMASDAVLILAGTAGVGALVQAVFWLLEVLWGGALYLLWFAVSSSLRAAL---R---
ZP_05365683.1    CALSDVILITSGTAGVGVLVEKFPNALQVLKYVGAAYLAYFTFTCFRDAFKTKGEA---
ZP_04835056.1    CMLSDIFLIFGGTAGVGVIIEKAPLALVALKWFGAAYLAWFAVSCFKDMVKPRALD---

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YP_225551.1      ---PQ-IIE---ETEP---T---VP-----D-DTP-LG-----G-----SAVAT
ZP_05749209.1    ---T---FVE---HSEP---V---AA-----A-SAS-GG-----G-----V
NP_939452.1      ---L-AVE---QSEP---V---AY-----E-PVA-DA-----S-----SGVIT
ZP_03933958.1    ---L-VVS---STPP---S---AP-----N-ETE-LG-----G-----ATTV
YP_002834652.1    ---L-VIE---ETTP---VAQVV-----D-ENS-GN-----A-----GAPGT
ZP_03711883.1    ---LD-SSA---TDDG---T---SL-----D-DAP-TAAHVSNDVTTSG---NGGQV
ZP_03922319.1    ---IE-V-E---STQP---K---AP-----Q-EVASFD-----G-----SQARS
ZP_03931790.1    STSPN-STE---EVAT---F---DG-----D-GDS-TG-----G---GVGTEHGSVAT
ZP_03918361.1    ---TE-TVS---ETKPHEEE---LP-----DVSST-TA-----G-----TIMAT
YP_002958101.1    ---PQGLMA---EQAP---R---T-----A-----G-----SVIAT
ZP_05365683.1    ---IE-V-E---STQP---K---VP-----Q-EVASFD-----G-----SQARN
ZP_04835056.1    ---SS-ATDNGTSLDDAP---T---VAHISNVD-STG-GN-----G-----GQVQT

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YP_225551.1      DTRNRVRVEVS--VDKQ---RVWVK-----PMLMAIVLTWLNPNAYLDAFVFIGGVG
ZP_05749209.1    TTKQRPRLRIT--SGTR---QVWVR-----PMLMAIVLTWLNPNAYLDAFVFIGGVG
NP_939452.1      KTRTKAQPK----SAQ---RTWVK-----PVLAAALFTWLNPNAYIDVLVMLGGIA
ZP_03933958.1    MTKQRT-----KS---RTWVK-----PVMGAMALTWLNPLAYVDVLVMLGGIA
YP_002834652.1    SVLTKIRPRV---RS---KSWVK-----PVLGALALTWLNPLAYVDALVMLGSLA
ZP_03711883.1    QTKTRPITTTA--PTRQAHPARPWVK-----PALAALFTWLNPNAYIDTLVMLGGIA
ZP_03922319.1    TTKTAARVEIK---RS---PSWVK-----PLLTALALTWLNPNAYVDVVMLGSLA
ZP_03931790.1    ATATQ-RQEIK---RS---PSWVK-----PLLTALALTWLNPNAYVDVLVMLGGIA
ZP_03918361.1    ATVMETATTVK--EKTH---RRTFHIPQEIKGPAVAFAFVSVINPAAWDLFVVIGSIS
YP_002958101.1    -----TLALTWLNPNHVLDTTVVLLGSLA

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ZP_05365683.1
ZP_04835056.1

TTKTATRVEIK----RS----PSWVK-----PLLALALTWLNPGAYVDVVVMLGSIA
KTRPITTTAPTRQAHBA----RPWVK-----PALAALFTWLNPSAYIDTLVMLGGIA
* * * *

YP_225551.1
ZP_05749209.1
NP_939452.1
ZP_03933958.1
YP_002834652.1
ZP_03711883.1
ZP_03922319.1
ZP_03931790.1
ZP_03918361.1
YP_002958101.1
ZP_05365683.1
ZP_04835056.1

AQYGDTGRWIFAAGAFASLIWFPLVGFAGAAALSRPLSSPKVWRWINVVAVVMTALAIAK
AQYGETGRWIFAAGAFASLWFFPLVGYGAAALSRPLSSPRVWRWINIGVAVVLTGLAVK
NQHGPDGRWVFALGALCASLTWFFFIGYTSRSTVLSRPVAVRYINIAIGIIMMIMCAR
QHYGDQ-RWVFAAGAIMASAVWFFTVGYGAFKLSHVLAKPTTWRYVNFAGCVMMLLTAK
NQYGDQ-RWVFAAGAILASAVWFFSLGFGAYKLSHVLAKPTTWRYVNVIVIGCVMLALTAK
NQHGESGRWVFAAGALMASAVWFFLLGFFSTRFSRVLSRPQAWRVINGVIGCIMVVMCIR
NQYGESGRWLFVAVGAICASFVWFFFIGFGAARFSHVLSRPTVWRWINFGIGVIMIGLTLK
NQYGDGPGRWLFAGGATAASFVWFFVIGFGAARFSHVLSRPEVWRWINVIGVIMIGLTLK
SSYGP-DKWAFLLGTMAASLVWFFPAFGYGAAALSRPLSSPKVWRWINVIGVIMIGLTLK
NQHGPDARWVFAAGAVAASVLWFTALGYGARLLARVLADPKAWRVVDVVIIVVMVAVLAVR
NQYGESGRWLFVAVGAICASFVWFFFIGFGAARFSHVLSRPTVWRWINFGIGVIMIGLTLK
NQHGESGRWVFAAGALMASAVWFFLLGFFSTRFSRVLSRPQAWRVINGVIGCIMVVMCIR
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YP_225551.1
ZP_05749209.1
NP_939452.1
ZP_03933958.1
YP_002834652.1
ZP_03711883.1
ZP_03922319.1
ZP_03931790.1
ZP_03918361.1
YP_002958101.1
ZP_05365683.1
ZP_04835056.1

LMLMG----
LILMG----
LIMH-----
LLLH-----
LLFL-----
LVMH-----
LLLL-----
LLLL-----
VLFM-----
LIAGSDVWG
LLLL-----
LIMH-----

Figure 2

Setting of the Clone Manager 9 program from Scientific and Educational Software for determining the identity of two amino acid sequences by global sequence alignment.

Compare Two Sequences

Comparison type

☐ Local Find regions of local similarity between two molecules. Param

Method: Report:

☐ Assembled Progressively assemble an alignment using local similarities. Use for sequences with some similar and some different regions.

☒ Global Maximize alignment of bases along full length of both molecules. Use for sequences that are very similar overall.

Compare sequences as ...

☐ DNA bases ☒ Compare both strands

☒ Amino acids (translate in frame, as needed)

☐ Translation, display as DNA

Scoring matrix

☐ Standard Linear

☒ BLOSUM 62

☐ PAM 250

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