

Abbildung 1

Alignment der in Tab. 1 aufgeführten Aminosäuresequenzen
5 der LysE und ArgO Proteine. Alignmentlücken (gaps) sind
durch „-“ gekennzeichnet. Identische Aminosäuren sind durch
einen „*“ gekennzeichnet.

10	YP_225551.1 ZP_05749209.1 NP_939452.1 ZP_03933958.1 YP_002834652.1 ZP_03711883.1 15 ZP_03922319.1 ZP_03931790.1 ZP_03918361.1 YP_002958101.1 ZP_05365683.1 20 ZP_04835056.1	-----MEIFITGLLLGLSLLSIGPQNVLVIKQGIKREGLIAVLLV -----MEIFVTGLLLGLSLLAIGPQNVLVIKQGIKREGITAVIIV -----MSIAIAGFLMGLSLIVAIGPQNALIIRQGIKREGLIPILVV -----MSVLLAGFLLGLSLIVAIGPQNAYI IKMGVKRDHIGAILLA MRRLEA-----MSVLLAGFALGLSLIIAIGPQNAYI IKMGIKRDHVGPIIIA -----MSIAVAGFLLGLSLIVAIGPQNALVIRQGVKREGLIVVLAI -----MSIVLAGFFLGLSLIVAVGPQNAMLKYGIRRDHIGLIIVV -----MSIVLAGFVLGLSLIVAVGPQNAMLKYGIRRDHIGLIIVV MVPENLSFYLCVLLTHNKYVNVFFAGLLFNLSLILALGPQNALILKYGLRRQAITLVISV M-----WTLACTGLLTGLALIVAIGAQNAFVLRQGVRRHVGAIVVLV -----MSIVLAGFFLGLSLIVAVGPQNAMLKYGIRRDHIGLIIVV -----MSIAVAGFLLGLSLIVAIGPQNALVIRQGVKREGLIVVLAI * * * * *
25	YP_225551.1 ZP_05749209.1 NP_939452.1 ZP_03933958.1 YP_002834652.1 ZP_03711883.1 30 ZP_03922319.1 ZP_03931790.1 ZP_03918361.1 YP_002958101.1 ZP_05365683.1 35 ZP_04835056.1	CLISDVFLFIAGTLGVDLLSNAAPIVLDIRWGGIAYLLWFVAVMAAKDAMTNKVEA---- CLISDVVLFITLGTGVLISDTAPIILDILRWCGIAYLLWFVAVMAARDALRARTEV---- CILSDVILIFGGTAGVGALVDRAPIALVVLKWLGVAYLLYFGFTCFKEAFKRHGQA---- CLISDVILINAGVGGMGVLVEKFPTGLIIMKYLGAAYLIYFGFTCFRDAFKKEQEA---- CLISDVILITGGTAGVGVLFVERFPTALVVVKYLGAAYLIYFGFTCFRDAFKKQQDA---- CILSDIFLIFGGTAGVGVIIEKAPLALVALKWFGAAYLAWFAVSCFRDMV--KPR----- CALSDVILITSGTAGVGYLVEKFPNALQVLKYVGAAYLAYFTFTCFRDAFKTKGEA---- CALSDVILITSGTAGVGYLVERFPNALEALKYIGAAYLAFFFTCFRDAFKTKGEAIDVE CALCDITLIALSGVGVILQKAPIVLEILRYAGFLYLLWFAYTCFRDAIHPTLA---- CMASDAVLILAGTAGVGALVQAVPWLLVLRWGGALYLLWFVAVSSLRAL--R----- CALSDVILITSGTAGVGYLVEKFPNALQVLKYVGAAYLAYFTFTCFRDAFKTKGEA---- CMLSDIFLIFGGTAGVGVIIEKAPLALVALKWFGAAYLAWFAVSCFKDMVKPRALD---- * * * * *
40	YP_225551.1 ZP_05749209.1 NP_939452.1 ZP_03933958.1 YP_002834652.1 ZP_03711883.1 45 ZP_03922319.1 ZP_03931790.1 ZP_03918361.1 YP_002958101.1 ZP_05365683.1 50 ZP_04835056.1	---PQ-IIE-----ETEP---T--VP-----D-DTP-LG-----G-----SAVAT ---T--FVE-----HSEP---V--AA-----A-SAS-GG-----G-----V ---L-AVE-----QSEP---V--AY-----E-PVA-DA-----S-----SGVIT ---L-VVS-----STPP---S--AP-----N-ETE-LG-----G-----ATTV ---L-VIE-----ETTP---VAQVV-----D-ENS-GN-----A-----GAPGT ---LD-SSA-----TDDG---T--SL-----D-DAP-TAAHVSNDVTTSG-----NGGQV ---IE-V-E-----STQP---K--AP-----Q-EVASFD-----G-----SQARS STSPN-STE-----EVAT---F--DG-----D-GDS-TG-----G-VGTEHGSVAT ---TE-TVS-----ETKPHEEE--LP-----DVSST-TA-----G-----TTMAT ---PQGLMA-----EQAP---R--T-----A-----G-----SVIAT ---IE-V-E-----STQP---K--VP-----Q-EVASFD-----G-----SQARN ---SS-ATDNGTSLDDAP---T--VAHISNVD-STG-GN-----G-----GQVQT
55	YP_225551.1 ZP_05749209.1 NP_939452.1 ZP_03933958.1 YP_002834652.1 ZP_03711883.1 60 ZP_03922319.1 ZP_03931790.1 ZP_03918361.1 YP_002958101.1	DTRNRVRVEVS--VDKQ----RVWVK-----PMLMAIVLTWLNPNAYLDAFVFIGGVG TTKQRPRLRIT--SGTR---QVWVR-----PMLMAIVLTWLNPNAYLDAFVFIGGVG KTRTKAQPK----SAQ---RTWVK-----PVLAAALFTWLNPAAYIDVLVMLGGIA MTKQRT-----KS---RTWVK-----PVMGAMALTWLNPLAYVDVLVMLGGIA SVLTKIRPRV-----RS---KSWVK-----PVLGALALTWLNPLAYVDALVMLGSLA QTKTRPITTTA--PTRQAHPARPWVK-----PALAALFTWLNPSAYIDTLVMLGGIA TTKTAARVEIK---RS---PSWVK-----PLLTALALTWLNPGAYVDVLVMLGGIA ATATQ-RQEIK---RS---PSWVK-----PLLTALALTWLNPGAYVDVLVMLGGIA ATVMETATTVK--EKTH---RRTFHIPQEIKGPAVAAFVVSVINPAAWVDLFVVISIS -----TLALTWLNPHVYLDTVVLLGSLA

Abbildung 2

- Einstellung des Programmes Clone Manager 9 der Firma Scientific and Educational Software zur Bestimmung der
- 5 Identität zweier Aminosäuresequenzen durch ein globales Sequenzalignment.

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

< Zurück Weiter > Abbrechen Hilfe