

1/4

ALIGNMENT OF UvsX RELATIVES

```

t4      MS-----DLKSRLIKASTSKLTAELTASKFFNEKDV-VRTKIPMMNIALSGEI
t6      MS-----IADLKSRLIKASTSKMTAELTTSKFFNEKDV-IRTKIPMLNIAISGAI
Phage133 MS-----SLKERLIKASTSKMTAELTTSKFFNDKTV-VRTRIPMLNIALSGAL
Rb69    MS-----DLKSRLIKASTSKMTADLTSSKLFNNRDE-VPTRIPMLNIALGGAL
Aehl    MAKGIKTAKTGNLQSLMSKLAETSSNMSSVLADSKFFNDKDC-VRTRVPLNIALMSGEL
Ae65    MA---KKAKVVNSGDLLERLNGTSSNMKSAMLAESIFFNEKDT-IRTRVPIINLMMSGRL
Kvp40   MS-----DLMKSLKKSSTSGYAQVLSSESQFMFDKDH-TRTYVPAINIAFSGEV
Rb43    MS-----NKALLKKLIKNSNSQSAAILSESQVFNNTK-TRTRVPILNLALSGAF
PSSM2   M-----DFLXEIVKEIGDEYTOVAAD---IQENERFIDTGSYIFNGLVSGSI
PSSM4   M-----NFLKDIKEIGNDYASLVSEGVSAGDTAGFIDTGSYIFNALLSGSI
          *           : : : : : : : : : : : : * : * : * :

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recA GPESGKTTLT Walker A

```

t4      TGGMQSG-LLILAGPSKSFKSNFGLTMVSSYMRQYDPAVCLFYDSEFGITPAYLPMSGVD
t6      DGGMQSG-LTIFAGPSKHFKSNMGLTMVAAYLNKYDPAVCLFYDSEFGITPAYLPMSGVD
Phage133 MGGMQSG-LTIFAGPSKHFKSNMGLTMVAAYMKAFDPAVCMFYDSEFGITPAYLKAMGVD
Rb69    NAGLQSG-LTIFAGPSKHFKSLFGLTMVAAYMKKYDAICLPYDSEFGASESYFRSMGVD
Aehl    DGGITPG-LTVLAGPSKHFKSNLSLVFVAAYLRXYPDAVCIFDNEFGSTPGYFESQGV
Ae65    DGGITPG-LTICAGPSKHFKSNLSLVFVAAYLRXYPKAVCLFFDNEFGSTPDYFTSQGV
Kvp40   DGGITSG-LTVLAGPSKHFKSNLGLVGVAAYLKXYPDAVCVFIDTEFGITPSYLRSGVD
Rb43    DGGITSG-LTLFAGPSKHFKSNLGLVTVSAYLKANEDAVCLFYDSEKGVTKSYLKSMGVD
PSSM2   FGGVSSSRITAIAGESSTGKTYPSLAVVKNFLDNNPDGYCLYFDTEAAVNKGLLESRGID
PSSM4   YGGIPNNKITAIAGETSTGKTFFCLGMVQHFLESNPDAGVIYFESESATSKQMIEDRGID
          * : : : : * : : * : * : : : : : : : * : : : * :

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DNA binding loop1

```

t4      PERVIHTPVQSLEQLRIDMVNQDAI-----ERGEKVVFIDSLGHLASKKETED
t6      PERVIHTPIQSVEQLKIDMVNQLEAI-----ERGEKVIVFIDSIGNVASKKETED
Phage133 PDRVIHTPVQSVEQLKIDMTNQLEEV-----ERGEKVIVFIDSIGNVASKKETED
Rb69    LDRVHTPIQSVEQLKIDMTNQDAI-----ERGDKVIFIDSIGNVASKKETED
Aehl    ISRVHCPFKNIEELKFDIVKKLEAI-----ERGDVIVFVDSIGNVASKKEIDD
Ae65    ISRVHCPFDVVEELKFDIVKKLESI-----TRGDKVIIYIDSIGNVASKKELOD
Kvp40   PDRVLIHQCESVERMKFEMANQLKDLAERKRAKAGEEPDRVIFPIDSVGNVSAKEIDD
Rb43    PDRVVYTRITTVQELRNDVVSQDLAL-----ERGDKVIIFVDSVGNVASKKELAD
PSSM2   MNRLVVNVVTIEEFRRSKALRAVDIY----LKTSEERKPCMPVLDSLGNLSTEKEIRD
PSSM4   SNRMLLVVPTTVQSFRLQAIIKILDKY----NEQTASERKPLMPVLDSLGNLSTSKEVED
          * : : : : : : : : : : : : : : : : : : * : : * :

```

DNA binding loop2

```

t4      EIGDSHMG recA [NQIRMKIGVMFGNPETTTGG
t6      ALNEKVVSDMTRAKTKSLFRIVTPYPSTKNIPCIAMHT-YETQEMF-SKTVMTGGTGP
Phage133 ALNEKSVADMTRAKSLKSLFRIVTPYPSIKNIPCAVAMHT-IETIEMF-SKTVMTGGTGV
Rb69    ALNEKVVSDMSRAKALKSLFRIVTPYLTIKDIPCAVAMHTAMEIGGLY-PKEINGGGTGI
Aehl    AIDEKSVSDMTRAKQIKSLFRMMTPPYLTVMNDIPAINVAMHT-YDTQEMY-SKKVVSGGTGI
Ae65    AKDEKSAQDMTRAKQIKSLFRMVTPPYLTVDIPCAVAMHT-YETQEMF-SKTVMTGGTGP
Kvp40   AQNEKSVADMRAKQIKSLFRITPYFTMLDIPCAVAMHT-YQTQEIY-SKTVMTGGTGI
Rb43    ALSDNDKQDMTRAKALKGMFRMVTPPYLADLDIPMVCIMHT-YDTQEMY-SKKVVSGGTGL
PSSM2   ALDDKQVRDMTKSQLVKGAFRMLTLKLGQANIPLIVTNHT-YDVIGSYVPTKEMGGGSGL
PSSM4   SEAGKETRDMTRAQVVKSI PRVLTLKLGKANVPLIVTNHT-YDVVGAYIPTKEMGGGSGL
          ( : : : : * : : : : * : : : : : : : : : : : : : : : : : : * : : * :

```

FIG. 1A

ALIGNMENT OF U_vSX RELATIVES

[illegible]

$\frac{A}{B} = \frac{C}{D}$

Figure 1. The structure of the proposed model.

t4	NE-----
t6	NE-----
Phage133	ED-----
Rb69	DE-----
Aehl	DELFANLD
Ae65	-----
Kvp40	-----
Rb43	-----
PSSM2	-----
PSSM4	-----

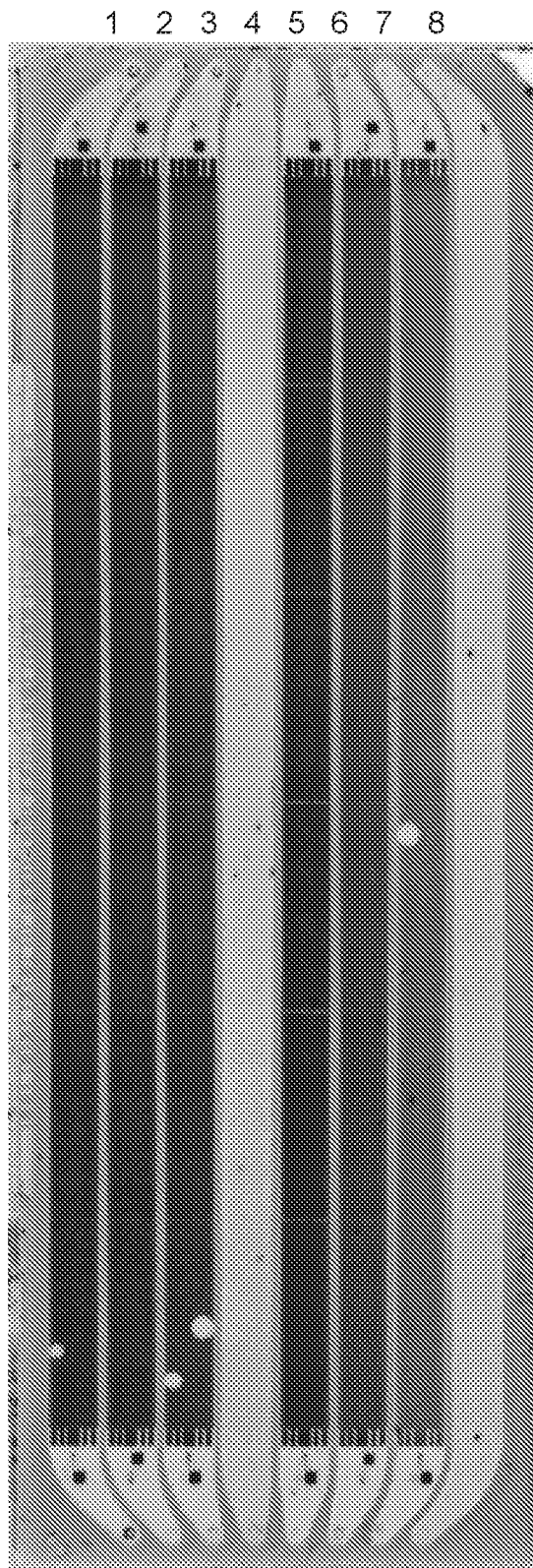
FIG. 1B

3/4

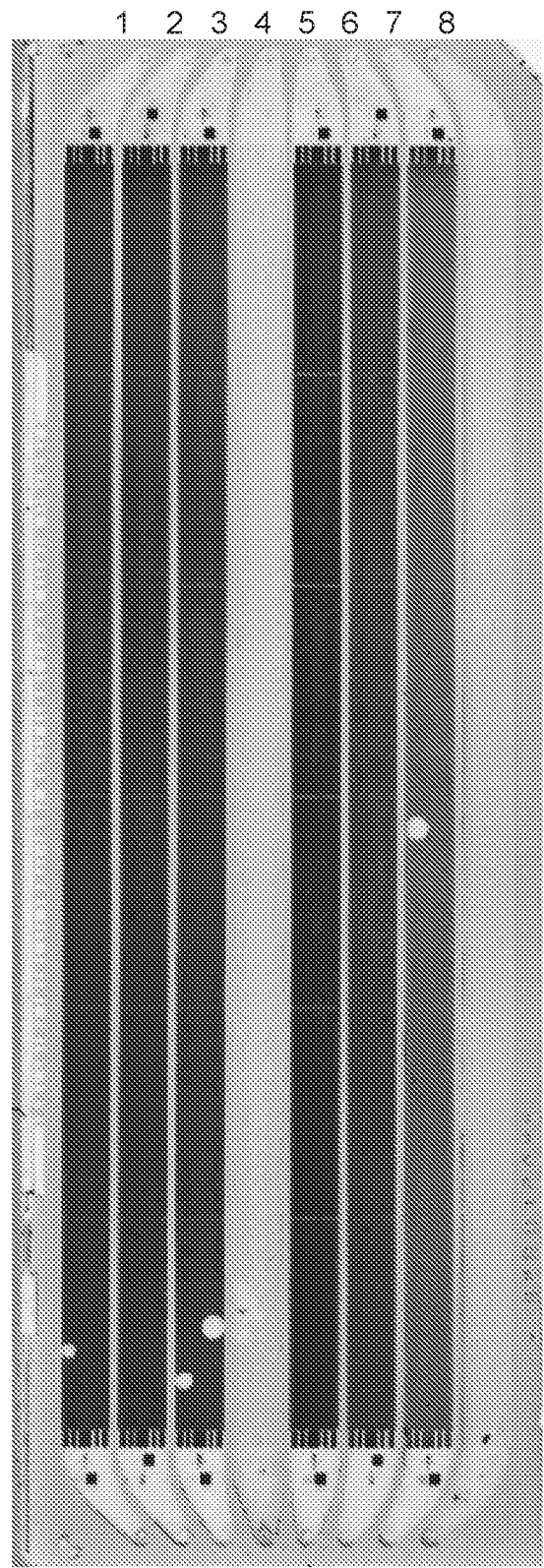
RB49	MS-VLEKLLKNSTLKTAVLSKSSFFNEKTNTRTKIPMLNIAFSGDLKKGFSGLIFFAGPSKHFK	65
T4	MSDLKSRLIKASTSKLTAELTASKFFNEKDVVRTKIPMMNIALSGEITGGMQSGLLILAGPSKSFK	66
RB49	SNMGLTCVSAYMKQNPDAACLFDFSEFGITSAYLESMGVDPDRVVHVPIKNIEELKFEIM	125
T4	SNFGLTMVSSYMRQYPDAVCLFYDSEFGITPAYLRSMGVDPERVIHTPVQSLEQLRIDMV	126
RB49	NQLEQITREDKVIIIFIDSIGNLASKKEVEDAINEKSAQDMTRAKALKGLFRMVTPYLTMN	185
T4	NQLDAIERGEKVVVFIDSLGNLASKKETEDALNEKVVSDMTRAKTMKSLFRIVTPYFSTK	186
RB49	DIPCIAINHTYETQEMFSKTVMSGGTGAMYSANEVFIIGRRQQKEGTEITGYDFILNAEK	245
T4	NIPCIAINHTYETQEMFSKTVMGGGTGPMYSADTVFIIGKRQIKDGSDDLQGYQFVLNVEK	246
RB49	SRTVKEKSKEFISVTFSGGIDPYSGLLELAVELGWVVKPSNGWYSRSILNTETGEMETEE	305
T4	SRTVKEKSKEFIDVKFDGGIDPYSGLLDMALELGFVVKPKNGWYAREFLDEETGEMIREE	306
RB49	RKFRACKETNSIEFWKPLLNDKFNENAINDHYKLGQVISDEAVDKEIEDML	355
T4	KSWRAKDTNCTTFWGPFLFKHQPFDAIKRAYQLGAIDSNEIVEAEVDELI	356

FIG. 2

4/4



Cy3-Green Channel



Cy3-Red Channel

FIG. 3