

OspD1_SFLEX
OspD2_SFLEX MSVNRDNR (17) FKNKTAP (10) NINGVAK--DIYG---RQIVCRHLIASYWEMNFME T--NGKVNY-QLLSTP-D
OspD3_SFLEX NLIPSRKI (17) SLLHSKQ (12) NLNCQVT--DHSG---RLIVCRHLIASYWIAQFNKS--SGHVDY-HHFAFP-D
EspL1_SAKAI PIKANHLR (17) HCMKLSK (12) NLNGSAFFSQSPS---DAIFCRHLISLOYALDSLRLN-GKGVNLIKHYSSV-E
EspL2_SAKAI PIIKNSASNYVEYISKNNP (11) NLNGKVS--DCNG---EITWCRHLIASYWEFFCSN--SGKIDY-ETFSSP-Q
EspL3'_SAKAI PVLIKFLD (14) FTKKQIK (7) VDYNCLLHFTGKPK---SLIECRHFALQYCIDSMNE-HTGKVP LKAY YSSP-E
EspL4_SAKAI PIFEEYLM (14) LNLNSDR (7) VKLNGQCYFPGRPQ---NRIVCRHIAAOYINDIYQN-VDYKPHQ-DDYSSA-E
EspL4_EAEC PARIKFLD (14) FTKKQIK (7) IKYNCKLFFNEKPE---NKIECRHLISLOYCIDSMNE-HSGKVPLKAY YSSP-E
EspL5_RRSL --MERE GP---AASKETP (10) DLNGQIL--LTPD (5) DRILWCRHLIARAYQRAAEDD-DNGKEDF-SRFAMVGE
ESPL6_YPSE PTFDKSKPYISELKSREEK---NLNGEVNFKDNVD---KLIMCRHLISSQYILDSLSDDEDTKGVLDL-DKFSK-D
01003153_YPSE PVYDKNNG---DSTL KETE (10) RLGEQAY--EYSG---GDISNYHLSIQYIMDV LADQAKGVLDL-SHFSSE-E
Q66EA0_YPSE PVIYDKNS---DNLT KETE (10) RLGEQAY--EYSG---GDISNYHLSIQYIMDV LADQAKGVLDL-SHFSSE-E
Ent_STEC PIIKNSASNYVEYISKNNP (11) NLNGKVS--DCNG---EITWCRHLIASYWEFFCSN--SGKIDY-ETFSSP-Q
Consensus/80% .b.p.....cp.....pbs..h.....s.....l.sbHlt.ba.....p.pt+hsb...at...p

OspD1_SFLEX
OspD2_SFLEX AIAKNVCLKTEDFS---KS---PAYIYFVENKKGTVITNFFYNMKNKNGDFVRTLSACTLN---HQMALGLKI
OspD3_SFLEX EIKNYVSVSEEEKAI---NV---PAIYFVENGSWGDIFIFYIFNEMIFHSEKSRALISTSN---HNMALGLKI
EspL1_SAKAI SIQQHVPLVRDAEFR---AL (4) PAGSRVIASKDFGFALDIFCRMMANNVSHMSAILYIDN---HTLSVRLRI
EspL2_SAKAI LLSKAIIVIQENKGTN---NI---KGDVYFVENESWGSVIYNLFLQLEKENKSHTSLEVHSPG---HAMALGLKI
EspL3'_SAKAI DIQKHIPFELEQQFN---NL (4) PPGTCVVASDKFGEALSVFFHRMEKEKLTHTMTAIVQSQT---HAMAVRLRI
EspL4_SAKAI KFLTHEFNKCKNQTL---AL (4) PEGRCVAACGDFGLVMKAYFDKMESNDLSVMAAILLVDN---HALTVRLRI
EspL4_EAEC DIQKHIPFELEQQFH---NL (4) PPGTCVVASDKFGEALSVFFORMEKEKLTHTMAAIVQSQT---HAMAVRLRI
EspL5_RRSL PHYDNFVDRARDNY (6) NL (4) AMQRTVIDGDRFGVFLGEAFKELASTGKNHATAILVTAN (13) HALSVSMRI
ESPL6_YPSE IIANRITSNVEELYE---QLQLQAKEIYFIPNNEFGICLSKIFKSMERKSENTQSILLESFN---HAMAVRLRI
01003153_YPSE TLSSHVSLEKNEHNY---HC (4) ASTVYHINNDNFGRITLVDLFEQMNNSENGVRLKIDSSQ---HSMARLYI
Q66EA0_YPSE TLSSHVSLEKNEHNY---HC (4) ASTVYHINNDNFGRITLVDLFEQMNNSENGVRLKIDSSQ---HSMARLYI
Ent_STEC LLSKAIIVIQENKGTN---NI---KGDVYFVENESWGSVIYNLFLQLEKENKSHTSLEVHSPG---HAMALGLKI
Consensus/80% .b.p.hs.p.pp.....h.....hhl.s.pat.hl.ba.pb.p.ph.shbl.s.....+sbth.lbI

OspD1_SFLEX
OspD2_SFLEX KRVOESEK--WVVFQFDPNRTVTHKR (4) CDSHFELSQLSAKDFDFD-YWKIYGL-EQPGQVIFEDRHNSPLTN
OspD3_SFLEX KETKNGGD--FVIQLYDPNHTATHLR (4) KFNLAIKKLTVDNDFLEK-HQKCYGL-ISDGMISFVDRHTPTSMS
EspL1_SAKAI QQSAYQLN-YVVSVDPNNTNVAVR---GTHRTARGFLSLDKFISGGPDAQTWAD (7) IAILPLLEPGVPGAIF
EspL2_SAKAI KNDKENK---FVINFYDPNQATATHKR (4) TNNICDIINLTAYDFLSEQ-CLKCYGL-KEDTSLSFVDKTKSNDNN
EspL3'_SAKAI KKT PAGE TE-YVVSFYDPNATNTAVRYK-ANNCDSEFG--SLQSFINIQQAKQKVI (7) VGITPYLPREQAHLLS
EspL4_SAKAI KNTTEGCIH-YVVSVDPNVNTDKIRIM-SESKEDIKHYSLMDFMNVDYSLKWSN (7) VAIIPALPKEQLMLLK
EspL4_EAEC KKT PAGE KE-YVVSFYDPNATNTAVRYK-ANNYDSFG--TLQSEFMNINQETQKVV (7) VGITPYLPREQAHLLS
EspL5_RRSL KQDGESRDV-YVARVYDPNRTVTHKRVR-VTDLQLLERLTFHDFLTD---VDYGR---PSVLTVVS PSLSLHED
ESPL6_YPSE KENENNNTKR YVISVDPNMNTVVRCE-VDDLKLVKRDVQVDFINHHLFGNFYKS (7) EISTLYICKK PANESV
01003153_YPSE KNT EQQR--FVVNFYDPNITDKTVRCE-VDDALKLNGYSLRNFI SNQTYLSSYVD-AEIS IIVCDQADIHQH
Q66EA0_YPSE KDTEQQR--FVVNFYDPNITDKTVRCE-VDDALKLNDYSLRNFI SNQTYLSSYVD-AEIS IIVCDQADIHQH
Ent_STEC KNDKENK---FVINFYDPNQATATHKR (4) TNNICDIINLTAYDFLSEQ-CLKCYGL-KEDTSLSFVDKTKSNDNN
Consensus/80% +ps..sp...aVlphaDPN.Ts.h.+...sps...b...ph.sabs.....as.....s...hhsp.....

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OspD1_SFLEX
OspD2_SFLEX TVK---LLPDELINSRVYHAIKTNL TEVLFILMEKYKN-G---EISQSKLVNLLATRS SDGTPAFYIALQNGYS
OspD3_SFLEX SII---RWPDNLLHPKVIYHAMRGLTELIQKVT RVVQL-S---DLSDNTELELLA AKNDDGLSGILLALQNGHS
EspL1_SAKAI TGIAT-RMPFAPIHPSAMLLIMATGQTQQLITLFRQLPILP---EK---EIEIITAQNSIGTPALFLAMNGHT
EspL2_SAKAI NVFIK-KLPDNIQGVVINFAMGAGLREI IKKVNDRTRF-T---DLTKSQMKILCESKNVNNVPGLLALQNGHD
EspL3'_SAKAI GIENE-LQP--PLSPALFLLMRGIIKYNIVLFFDKLKNQSQ---EMTASKALDLA AKSPGEGYGLCVLLYHNTI
EspL4_SAKAI GTVDE-ITP--PLSPATMNLMLAIGQNHQLKQMLIQLKMP---EL---HRTEMLTAYNSINLPGLYLAINYGNA
EspL4_EAEC GINNE-LQP--PLTPSALFLLMRGITHENIVLFFDKLKKSQ---EMTASKALETLA AKSMTGT YGLYVLLYHNNT
EspL5_RRSL PAL (1) RTGDATLKG-RLHLAMQANMPWEVRAVARQLRN-P (4) NLSDEERIALLAGKDTSGATALGAAMLWGYV
ESPL6_YPSE PEC (8) DWIALPASSINLYTFLIEGFSQEIKNLKNQLEIY---KKNPEKLMELTAKSPDGMGFEQALLNDHA
01003153_YPSE KVK (9) QSSPLPLS AARLDLLLTDNFAVGIQKMAEEVKNLS-ESERKV-FFNQLLQ PRAKDDVPGLQCAFHQCF
Q66EA0_YPSE KVK (9) QSSPLPLS VARLDLLLTDNFAAGIQTMAEEVKNLS-ESERN-FFNQLLQ PRAENDLSGLQCAFNYQCF
Ent_STEC NVFIK-KLPDNIQGVVINFAMGAGLREI IKKVNDRTRF-T---DLTKSQMKILCESKNVNNVPGLLALQNGHD
Consensus/80% .h....b.s...lps..b.bhb..sb...l..hhpph.....cb...b...lh.sps..sh.tlhbhb..sp.

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OspD1_SFLEX DAARYGESLL---AAEIPKEEKLEVI AARNNAG-ESALFIALQEGHSAAIQAYGDFIKTFDLSPK 84-156
OspD2_SFLEX DIIQVYGIKLN---MCNLSQETITLLAAVANN-VPLGCMSEFMNGHVDTIKAYGEIVFKTPLTSD 25-376
OspD3_SFLEX DTLIAYGELLE---TSGLNLDKTVELLTAEGMGGRI SGLSQALONGHAETIKAYGRLLKRAINIE 5-359
EspL1_SAKAI DNVKIFMQEIQ (4) NHIHEDNLVKLLQTKSANE-TPGLYISMLYGFDEIIDIFLNALTTPIAQEL 110-478
EspL2_SAKAI NVIDEYGTLIK---KSNLNKEELIHILSARTLDGTPGLYQALQNGHAQAIKSYGNLVLDITINKNI 2-343
EspL3'_SAKAI DKFNDYITNLK (4) KYNFSQEDLETLLAKDNLG-VSWIPRALKNNQNKIVKAWLLAIDDFEKEFG 106-468
EspL4_SAKAI DIVETIENSLS (4) EGLLSKKNLMMHILEAKDKNG-FSGLFLAISRKDNVVTSLNALPKLAATHH 101-461
EspL4_EAEC YKFNEYIINLK (4) KYNFSYGDLENILLAQDKHG-VSWIPAALENNQKEI IKAWLLAIDDFEKEFG 105-467
EspL5_RRSL DAMAMYGLTLR---ESDLKPAQAELLA AKDAEG-VPALQLAVQNGHEDTVSEYKLVFCSGLDPE 1-362
ESPL6_YPSE DAINAFGELLQ---LV---PENKRELLVNNKTK-YTLFDIVCSREKNTTMAFKNIVLSIKNER 22-370
01003153_YPSE EALEAYGELLA---LA---PPEQRADLLTAESENG-YITMPWVIVSSGNPELVDFEFTLSRLLPLNDM 9-358
Q66EA0_YPSE DALEAYSALLV---LA---PPEQRADLLTGKSENG-WSSLAQAMSSGNSDMVSVCFYLLQWPLDDM 9-358
Ent_STEC NVIDEYGTLIK---KSNLNKEELIHILSARTLDGTPGLYQALQNGHAQAIKSYGNLVLDITINKNI 2-343
Consensus/80% s.hp.ah..l.....s.cpb.pll.tps..s.hshl.btbpssp.phlpsah.hl.....p..