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OspG<sub>SFLEX</sub> VTEPILGKLIIGQGSTAEIFEDVNDSSALYKKYDLIGNQYNEILEMAWQ-ESELFNAFYGDEASVVIQYGG

NleH1-1<sub>SAKAI</sub> NRLSVPGNVIIGKGNNAVVEYEDAEATKVLKMF~~TT~~---SQS---NEEVTSEVRCFNQYYGAGSAEKIYGNN

NleH1-2<sub>SAKAI</sub> NKSPVPGNVIIGKGNNAVVEYEDMEDTTKVLKMF~~TI~~---SQS---HEEVTSEVRCFNQYYGSGSAEKIYNDN

NleH1<sub>CIROD</sub> NKSPVPGNVIIGKGNNAVVEYEDMDDTTKVLKMF~~TT~~---SQN---PEEVTNEVSCFNQYYGSGSAEKIYDAN

NleH2<sub>YINT</sub> NPAIKLGKLIIGSGLTAEIYLDANNPGFVLKK---ISTRD~~T~~FLIDKVF~~FKKEVEFFNRY~~YYGEGSAELINQDN

Consens/100% s.....Gp.IGpG.st.labDhpsss.lbKb.....p.s....b.hp.Esphas.aaG..tt..l..ss

OspG<sub>SFLEX</sub> DVY--LRMLRVPGTP~~LS~~DI~~D~~TADIPDNI~~ES~~LYLQ~~L~~ICK~~L~~NELSIIHYDL~~NT~~GNM~~LY~~DKES~~ES~~LF~~P~~IDFRN

NleH1-1<sub>SAKAI</sub> GDIIGIRMDKINGES~~LN~~ISS--LPAQAEHAIYDMF~~DR~~LEQK~~G~~ILFVD~~TT~~ET~~N~~VLY~~D~~RAKNEFN~~P~~IDISS

NleH1-2<sub>SAKAI</sub> GNVIIGIRMNKINGES~~LD~~IPS--LPAQAEQAIYDMF~~DR~~LEKKG~~G~~ILFVD~~TT~~ET~~N~~VLY~~D~~DRMRNEFN~~P~~IDISS

NleH1<sub>CIROD</sub> GDIIGIRMNKINGES~~LF~~NIQS--LPTQAEQAIYDMF~~DR~~LEQKR~~R~~ILFVD~~TT~~ET~~N~~VLY~~D~~DRVRNEFN~~P~~IDISS

NleH3<sub>YINT</sub> QHY--IRMYRVP~~G~~KVLTEINTKI~~F~~PPGA~~K~~NSFL~~R~~MM~~D~~LAY~~N~~IIHND~~L~~NFNN~~V~~LY~~D~~DKKTNT~~F~~Y~~P~~IDFGD

Consens/100% ..h..lRM.+lsGpsL.pI.p..bPs.Acp.bbpbbbscl.bb.lla.Dhs.sshlad+.pppb.sldb.s

OspG<sub>SFLEX</sub> IYAEYYAATK~~K~~DKEI~~I~~DRRLQ~~M~~-RTNDFYSL~~I~~NRKY-L 24-196

NleH1-1<sub>SAKAI</sub> YNVSDRSWSE~~S~~QIMQSYHGGK~~Q~~DLISV~~V~~LSKI----- 130-293

NleH1-2<sub>SAKAI</sub> YNVSDI~~S~~WSE~~H~~QVMQSYHGGK~~L~~DLISV~~V~~LSKI----- 140-293

NleH1<sub>CIROD</sub> YNISDVSWREG~~Q~~IMQSYHGGK~~Q~~DLIRV~~V~~LSRI----- 130-293

NleH3<sub>YINT</sub> AVDGYYSLSE~~P~~NSGKQHWGI~~K~~M-RVGF~~I~~L~~E~~H~~I~~EEYART 829-999

Consens/100% h.....thpc.p..b..b.hpb.bh..hpb1.....