Fig. 25-7. Alignment of integrase proteins of phage P2 and some P2-like phages. The amino acids were aligned using the CLUSTAL X program (58). Amino acids present in at least 4 proteins are indicated by gray shades. The conserved boxes and patches among the integrase family of proteins are boxed (109).

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P2 Int      M....AIKKL DDGR...YEV DIRPTGRNGK RIRRKFDKKS EAVAFEKYTL
WΦInt       M....SIKKL DDGR...YEV DIRPRGRDGK RIRRKFERKA EAVAFERYTI
K139 Int    M....SVRNL KDGSKKPWLC ECYPQGREGK RVRKRFATKG EATAYENFIM
186 Int     M....TVRKN PAGG...WIC ELYPNGAKGK RIRKKFATKG EALAF.....
HP1 Int     M....AVRKD TKNGK..WLA EVYVN...GN ASRKWFLTKG DALRFYNQAK
HP2 Int     M....AVRKD TKNGK..WLA EVYVN...GK RLRKWFLTKG DALRFYNQAK
ΦCTX Int    MADGVEVRGK RIRIYFRYQG ELCRESIPGD ATPENIANAE RLAGIINYEI

P2 Int      YNHH...NKE WLSK.PTDKR RLSELTQIWW DLKGKHEEHG KSN...LGKI
WΦ Int      AYAS...QKE WAGQ.RADRR TLSELLDIWW KYHGQNHEHG TKE...FNYL
K139 Int    REVD...DKP WMGS.KPDNR RLSELLETWW QVHGHTIKSG KVV...YRKT
186 Int     EQYT..VQNP WQEE.KEDRR TLKELVDSWY SAHGITLKDG LKR...QLAM
HP1 Int     EQTTSAVDSV QVLE.SSDLP ALSFYVQEWF DLHGKTLSDG KAR...LAKL
HP2 Int     EQTTSAVDSV QVLE.SSDLP ALSFYVQEWF DLHGKTLSDG EAR...LAKL
ΦCTX Int    KQGVFSYSRH FPDSPRVKSN TLGHYIDLWL DIKRNQIAAS GFRGYTSRVE

P2 Int      EIFTKITNDP CAFQITKSLI SQYCATRR.. .......SQG IKPSSINRDL
WΦ Int      LKTISGIGDI PVSRMSKRAL MDYRSMRL.. .......RDG ISAATINRDM
K139 Int    ALTIKELGDP IASTFTSKQY LAFRASRVS. ..HFNKENKS LSPTYQNFQL
186 Int     HHAFECMGEP LARDFDAQMF SRYREKRLKG EYARSNRVKE VSPRTLNLEL
HP1 Int     KNLCSNLGDP PANEFNAKIF ADYRKRRLDG EFS.VNKNNP PKEATVNREH
HP2 Int     KNLCANLGDP PANEFNAEIF ADYRKRRLDG EFS.VNKNNP PKEATVNREH
ΦCTX Int    THIRPRWGDS QADSIDHLDI QDWVQNTLMP .........K LHNKTVREIV

P2 Int      TCISGMFTAL IEAELFFGEH PIRGTKRLKE EKPETGYLTQ EEIALLLAAL
WΦ Int      YRLSGMFTKL IQLDEFSGQH PIHGLPPLAE ANPEMTFLEK AEIEKLLNVL
K139 Int    NLLSGMFSRL IKYKQWNLPN PLDDIEPIKV NQRALAYLDK ADIQPFLQRL
186 Int     AYFRAVFNEL NRLGEWKGEN PLKNMRPFRT EEMEMTWLTH DQISQLLGEC
HP1 Int     AYLRAVFNEL KSLRKWTTEN PLDGVRLFKE RETELAFLYE RDIYRLLAEC
HP2 Int     AYLRAVFNEL KSLRKWTAEN PLDGVRLFKE RETELAFLYE RDIYRLLAEC
ΦCTX Int    SNLRQIFR.L YRTRNRSAHD PTDGIVITLP DADDPDPFTR EEIDLILGTE
                                                      Patch I

P2 Int      DGDN...... .....KKIAI LCLSTGARWG EAARLKAE.. .........N
WΦ Int      AGDD...... .....LLVAL LCLSTGGRWT EVATLKPA.. .........Q
K139 Int    GGFESDGRSV SIPEIVLIAK ICLATGARIS EALSLERS.. .........Q
186 Int     NRHDH..... ..PDLETVVR ICLATGARWS EAESLRKS.. .........Q
HP1 Int     DNSRN..... ..PDLGLIVR ICLATGARWS EAETLTQS.. .........Q
HP2 Int     DNSRN..... ..PDLGLIVR ICLATGARWS EAETLTQS.. .........Q
ΦCTX Int    TARIG..... ....ELNLAE FMIWSGPRVS EAIALAWEDV DLDTGTVVFR
                                             Box I

P2 Int      IIHNRVTFVK TKTNK..... .......... .......PRT VPISEAVAKM
WΦ Int      ITNCRVTFLK TKNGK..... .......... .......KRT VPISEELEKK
K139 Int    ISEFKLTFVE TKGKR..... .......... .......IRS VPISENLYKE
186 Int     LAKYKITYTN TKGRK..... .......... .......NRT VPISKELYES
HP1 Int     VMPYKITFTN TKSKK..... .......... .......NRT VPISKELFDM
HP2 Int     VMPYKITFVN TKSKK..... .......... .......NRT VPISKELFDM
ΦCTX Int    RARVRSQYKV TKTRRSTRKV QLLAPALRAL QQQAKLTRRL PPVQIEVIDR
                                      Patch II

P2 Int      IADNKRG... .FLFPDADYP RFRRTMKAIK PDLPMGQAT. ........HA
WΦ Int      VKEEASA... .KLF.KVDYE KFCGILRRVK PDIPPNQAT. ........HI
K139 Int    IMLASSSS.. TKIFSTTYGS AHRYIKKALP DYVPEGQAT. ........HV
186 Int     LPDDKKG... .RLFSDCYGA .FRSALERTG IELPAGQLT. ........HV
HP1 Int     LPK.KRG... .RLFNDAYES .FENAVLRAE IELPKGQLT. ........HV
HP2 Int     LPK.KRG... .RLFNDAYES .FENAVLRAE IELPKGQLT. ........HV
ΦCTX Int    DNRTRKPQRV RFVFHNSASG AAYSTSDTLR NGWWHGHLRN AGVRSRGPNQ
                   Patch III

P2 Int      LRHSFATHFM INGGSIITLQ RILGHT.RIE QTMVYAHFAP EYLQDAISLN
WΦ Int      LRHTFASHFM MNGGNIIALQ QILGHA.SIQ QTMAYAHLAP DYLQNAVALN
K139 Int    LRHTFATHFM MNRGDILILQ RILGHQ.KIE QTMAYAHFSP DHLIQAVQLN
186 Int     LRHTFASHFM MNGGNILVLQ RVLGHT.DIK MTMRYAHFAP DHLEDAVKLN
HP1 Int     LRHTFASHFM MNGGNILVLK EILGHS.TIE MTMRYAHFAP SHLESAVKFN
HP2 Int     LRHTFASHFM MNGGNILVLK EILGHS.TIE MTMRYAHFAP SHLESAVKFN
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ΦCTX Int   CRHTFASQML SSG..IATPE WIADQMGHTS TAMIFKHYAK WISKDGPDIV
                      Box II

P2 Int     PLRGGTEAES VHTVSTVE
WΦ Int     PLKGGVTL
K139 Int   PLEN
186 Int    PLVHITNSK
HP1 Int    PLSNPAQ
HP2 Int    PLSNPAQ
ΦCTX Int   GLLNQALKLS
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