

A

species	amino acid alignment	GenBank accession number
<i>human herpesvirus 1</i>	398 -PAR <b>PRAAVAPCVR</b> APP-----PGPGPRAPAPG--- 424	NC_001806
<i>human herpesvirus 2</i>	406 RAAR <b>PRAAVAPRVRS</b> SPPRAAAAPVVSASADAAG--- 438	NC_001798
<i>macacine herpesvirus 1</i>	298 ---- <b>PVVPVAPRPR</b> ---PAAEPPAPAPGAAPRQPAH 326	NC_004812
<i>cercopithecine herpesvirus 2</i>	254 ---- <b>PVAPVAPRPR</b> -----AAMPRPPAQARPP---A 277	NC_006560
<i>papiine herpesvirus 2</i>	323 VPVV <b>PVVPVAPRPR</b> VAAEAPAPPRPPAQARPPTTLT 358	NC_007653

B

HSV-2 ICP0

residues	alignment
311-322	<b>PAVAAVVPRVAS</b>
410-420	<b>PR-AAVAPRVRS</b>
consensus	<b>Px-AxVxPxxR</b>

Supplemental Figure S1. SIAH-1 binding motif in ICP0 homologs of primate simplexesviruses.

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HSV-1 MEPRPGASTRR---PEGRPQREP---APDVVWFPCDRDLPDSSDSEAEDEVGGRGDADH 53
HSV-2 MEPRPGTSSRADPGPERPPRQTPGTPAAPHAWGMLNDMQWLASSDSEEEDEVG-ISDDDL 59
*****:*:* ** *:: * **..* : * : ***** ***** .* *

HSV-1 HDDDSASEADSTDTELFETGLLGPQVDGG--AVSGGSPPREEDPGSCGGAPPRED--GG 109
HSV-2 HR-DSTSEAGSTDTEMFEAGLMDAATPPARPPAERQGSPTPADAQGGSCGGGPGVGEIEAEA 118
* **:*:**.*****:***:***:.. . * ***. : *****.* *: .

HSV-1 SDEGDVCAAVCTDEIAPHLRCDTFPCMHRFCIPCMKTWMQLRNTCPLCNAKLVYLIVGVTP 169
HSV-2 GGGGDVCAAVCTDEIAPPLRCQSFCLHPFCIPCMKTWIPLRNTCPLCNTPVAYLIVGVTA 178
.. ***** ***** **::***:* *****: *****: :.*****.

HSV-1 SGSFSTIPIVNDPQTRMEAEAEAVRAGTAVDFIWTGNQRFAAPRYLTLGGHTVRALSPTHPE 229
HSV-2 SGSFSTIPIVNDPRTVEAEAAVRAGTAVDFIWTGNPRTAPRSLSLGGHTVRALSPTPPW 238
*****:***:*** ***** ***** * *** *:***** *

HSV-1 PTTDEDDDDLDADYVPPAPRRTPRAPRRRGAAAPPVTGGASHAAPQPAARTAPPSAPI 289
HSV-2 PGTDEDDDLADVDYVPPAPRRAP----RRGGGG---AGATRGTSSQPAATRPAPPGAPR 290
* **::*** * .*****:* **.. . .**:::*****:*.***.*

HSV-1 GPHGSSNTNTTTNSSGGGSRQSRAAAPRGASGP--SGGVGVGVVVEAEAGRPRGRTP 347
HSV-2 SSSSGGAPLRAGVGSVGGGPAVAAVVPRVASLPPAAGGGRAQARRVGEDAAAAEGRTPP 350
.. . . . : .**.*. *..** ** * :** . . * :. .*** *

HSV-1 LVNRPAPLANNRDPIVIVSDSPASPFRPP-----AAPMPGSAPRPGPPASAAASG-P 398
HSV-2 AR---QPRAAQEPPIVIVSDSPPPSPRRPAGPGPLSFVSSSSAQVSSGPGGGGLPQSSGRA 407
* * :. *****.***:**. :. . :. ** . . :** .

HSV-1 ARPRAAVAPCVRAPP----PGPGPRAPAPGAEPAPARPADARRVPQSHSSLAQAANQEQS 453
HSV-2 ARPRAAVAPRVRSPPRAAAAPVVSASADAAGPAPPVVDHRAPRSRMTQAQTDTQAQS 467
***** **:* * .. * **.* ** *:**:*:*: : **:* * **

HSV-1 LCRARATVARGSGGPGVEGGHGPSRGAAPSGAAPLPSAASVEQEAAVRPRKRRGS----- 508
HSV-2 LGRAGATDARGSGGPGAEGGPGVPRGTNTPGAAPHAAEG----AAARPRKRRGSDSGPA 522
* * * * *****.*** * **:* ..***** :. . **.******

HSV-1 -GQENPSPQSTRPPLAP--AGAKRAATHPPSDSGPGGRGQG-----GPGTPLTS---- 554
HSV-2 ASSSASSAAPRSPLAPQGVGAKRAAPRRAPDSDSGDRGHGLAPASAGAAPPSPSSQ 582
... *. :.*.*** .*****: ..*****:** *...* :*

HSV-1 -----SAASASSSSASSSSAPTAGAASSAAG--AASSSASASSGGAVGALG-----GR 601
HSV-2 AAVAAAASSSSASSSSASSSSASSSSASSSSASSSSASSSSASSSAGGAGGSVASASGAGE 642
*:*:*****.:.:.*:**. *:*:**:*:** *:. *

HSV-1 QEETSLGPRAASGPRGPRKCARKTRHAETS---GAVPAGGLTRYLPISGVSSVVALSPY 657
HSV-2 RRETSLGPRAAA-PRGPRKCARKTRHAEGGPEPGARDPAPGLTRYLPVAGVSSVVALAPY 701
:.******: ***** . . ** *****:*****:**

HSV-1 VNKTITGDCLPILDMETGNIGAYVVLVDOTGNMATRLRAAVPGWSRRTLLPETAGNHVMP 717
HSV-2 VNKTITGDCLPVLDMETGHIGAYVVLVDQTNVADLLRAAAPAWSRRTLLPEHARNVVRP 761
****:*:**:*:**:*:**:*:**:*:**:* ***.***** * * * *

HSV-1 PEYPTAPASEWNSLWMTVPGNMLFDQGTLVGALDFRSLRSRHPWSGEQGASTRDEGKQ-- 775
HSV-2 PDYPTPPASEWNSLWMTVPGNMLFDQGTLVGALDFHGLRSRHPWSREQGAPAPAGDAPAG 821
*:*.*.*****:*****:*****.***** ***. : .

HSV-1 ---
HSV-2 HGE 824

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Supplemental Figure S2. Complete Alignment of ICP0 homologues of HSV-1 and HSV-2.

SIAH-1\_Hs\_ MSRQTATALPTGT--SKCPPSQ-----RVPALTGTTAS--- 31  
 SIAH-2\_Hs\_ MSRPSSTGPSANKPCSKQPPPQPQHTPSPAAPPAAATISAAGPGSSAVPAAAAVISGPGG 60  
 \*\*\* :\*: . :... \*\* \*\*.\* \*\*\* :.. :.

SIAH-1\_Hs\_ -----NNDLASLFECVPCFDYVLPPIILQCQSGHLVCSNCRPKLTCCPTCRGPLG- 80  
 SIAH-2\_Hs\_ GGGAGPVSPQHHELTSLFECVPCFDYVLPPIILQCQAGHLVCNQCRLKLSCCPTCRGALTP 120  
 :\*: :\*:\*\*\*\*\*:\*\*\*\*\*.:\*\* \*\*\*:\*\*\*\*\*.\*

SIAH-1\_Hs\_ SIRNLAMEKVANSVLFPCKYASSGCEITLPHTEKADHEELCEFRPYSCPCPGASCKWQGS 140  
 SIAH-2\_Hs\_ SIRNLAMEKVASAVLFPCKYATTGCSLTLHHTEKPEHEDICEYRPYSCPCPGASCKWQGS 180  
 \*\*\*\*\*.:\*\*\*\*\*:\*. :\*\* \*\*\*\*\*.:\*\* :\*:\*\*\*\*\*

SIAH-1\_Hs\_ **LD**AVMPHLMHQHKS**ITTL**QGEDIV**F**LATDINLPGAVDW**MM**QSCFGHFMLVLEKQEKYD 200  
 SIAH-2\_Hs\_ **LE**AVM**SH**LMHAHKS**ITTL**QGEDIV**F**LATDINLPGAVDW**MM**QSCF**G**H**H**FMLVLEKQEKYE 240  
 \* :\*\*\*.\*\*\* \*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*:

SIAH-1\_Hs\_ **GH**Q**Q**FFAIV**Q**LIGTRK**Q**AENFAYRLELNGHRRRLTWEATPRSIHEGIATAIMNSDCLVFD 260  
 SIAH-2\_Hs\_ **GH**Q**Q**FFAIV**L**LIGTRK**Q**AENFAYRLELNGNRRLTWEATPRSIHDGVAAAIMNSDCLVFD 300  
 \*\*\*\*\* \*\*\*\*\*:\*\*\*\*\*:\*. :\*:\*\*\*\*\*

SIAH-1\_Hs\_ **TS**IA**Q**LFAENGLGINVT**IS**MC-- 282  
 SIAH-2\_Hs\_ TAI**A**HL**F**ADNGNLGINVT**IS**TCCP 324  
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