

## **Supplementary information**

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# **Near-atomic cryo-electron microscopy structures of varicella-zoster virus capsids**

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In the format provided by the authors and unedited

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### MCP

VZV 1 10 20 30 40 50 60 70 80  
VZV MTTVSCPANVITTTESDRIAGLFNIPAGLPTGNVSTIEVCAHRCHEDFKQIRSDNSLFSADQDLLLSYCNNTNFV  
HSV-1 .....MAAPNRDPPGYRYAAAVPTGSLSTIEVASHRRDFDFSRVRSDNSLYDVFSDALLSYCNNTSLV  
HSV-2 .....MAAPARDPPGYRYAAAVPTGSLSTIEVASHRRDFDFARVRSDNSLYDVFSDALLSYCNNTSLV  
PRV .....MERPAFLPSGQLSNI EVSHHRAFDIFKRFRSDNNLYGAFSDALLSYCNNTSLV  
HCMV .....MENWSALELLPKVGIPTDLDTHVKTSAAGEEESALRIYYGDDPERYNIHSAIFAFHCNRLWEV  
MCMV .....MGENWTATELLPKLDVPIDLDTHIKLSVGEEEMNNFRLYYGDPERYNIHSAIFAFHCNKLWEV  
EBV .....MASNEGVENRPPFYLVADADLSNLRQSAAGEEESFDLLVKGDKAREAGLFSVLLSNTYNAQYF  
KSHV .....MEATLEQRPPFYLVATEANLHQLKESAADGEGKSEQLLLGKDAREGFSVSEALLSNTYNYVFF  
acc

VZV h1 h2 bA h3 bB bC bD TT  
222 222 100 110 120 130 140 150 160  
VZV RFLDLGLS VACI CTK FPELAY VRD GVIQEPVQO PMLARDG PHFVDQPVHNYMVYRIHKRSLSAAFALASEALSLSNTIYV  
HSV-1 RFLDLGLS VACV CTK FPELAY MNEGRVQEVHQPLARDGPHLEQPTHNYMVIDRRRLNAAFSLATEAALLTGEAL  
HSV-2 RFLDLGLS VACV CTK FPELAY MNEGRVQEVHQPLARDGPHLEQPTHNYMVIDRRRLNAAFSLATEAALLTGEAL  
PRV RFLDLGLS VACV CTK FPELAY SYVAGCIQEPVQO PMLARDG PHFVDQPVHNYMVIDRRRLNAAFSLATEAALLTGEAL  
HCMV YFTLGSLLAAAHAIKFDHLDNKLDTCCKMLFVQVQVPRMAGSALPPTSROTTIMVYKSEKSPITIPFELSAACITLIRET.F  
MCMV TETGATLATAAAHAIKFDHLDNKMTDCKMLFVQVQVPRMAGSALPPTSROTTIMVYKSEKSPITIPFELSAACITLIRET.F  
EBV RFLDLGLS VACV CTK FPELAY VRD GVIQEPVQO PMLARDG PHFVDQPVHNYMVYRIHKRSLSAAFALASEALSLSNTIYV  
KSHV RFLDLGLS VACV CTK FPELAY VRD GVIQEPVQO PMLARDG PHFVDQPVHNYMVYRIHKRSLSAAFALASEALSLSNTIYV  
acc

VZV a1 a2 a3  
170 180 190 200 210 220 230  
VZV DCGEITDSSLRTRATQOMARNLRTVLDSEFERGTADQLLGVILEKAPPLSLLSPNKFQPE..GHLNRVARAALLSDLKRKY  
HSV-1 DCGEITDSSLRTRATQOMARNLRTVLDSEFERGTADQLLGVILEKAPPLSLLSPNKFQPE..GHLNRVARAALLSDLKRKY  
HSV-2 DCGEITDSSLRTRATQOMARNLRTVLDSEFERGTADQLLGVILEKAPPLSLLSPNKFQPE..GHLNRVARAALLSDLKRKY  
PRV DCGEITDSSLRTRATQOMARNLRTVLDSEFERGTADQLLGVILEKAPPLSLLSPNKFQPE..GHLNRVARAALLSDLKRKY  
HCMV DCGEITDSSLRTRATQOMARNLRTVLDSEFERGTADQLLGVILEKAPPLSLLSPNKFQPE..GHLNRVARAALLSDLKRKY  
MCMV DCGEITDSSLRTRATQOMARNLRTVLDSEFERGTADQLLGVILEKAPPLSLLSPNKFQPE..GHLNRVARAALLSDLKRKY  
EBV DCGEITDSSLRTRATQOMARNLRTVLDSEFERGTADQLLGVILEKAPPLSLLSPNKFQPE..GHLNRVARAALLSDLKRKY  
KSHV DCGEITDSSLRTRATQOMARNLRTVLDSEFERGTADQLLGVILEKAPPLSLLSPNKFQPE..GHLNRVARAALLSDLKRKY  
acc

VZV a4 bE bF a5 bG  
240 250 260 270 280 290 300 310  
VZV CADMFMTFRHARE...PRLISAYSLSMVSCTQPSVVMVSRIPTHNTRGRQVDSVVTATLKRQLLQGLLQFDDTAA  
HSV-1 CADMFMTFRHARE...REAVEAWLVDLTATQPSVAVPRLTHADTRGRQVDSVVTATLKRQLLQGLLQFDDTAA  
HSV-2 CADMFMTFRHARE...REAVEAWLVDLTATQPSVAVPRLTHADTRGRQVDSVVTATLKRQLLQGLLQFDDTAA  
PRV RDDTFPLTKHERN...KDAVLDRLDLVNCTAPSVAVARMTHADTRGRQVDSVVTATLKRQLLQGLLQFDDTAA  
HCMV LATLFLNLRTRDR...DYVLKFLTRIAEAATSIIDNPTTYTSSGAKVSVVSTANVMQIMSLSSHTRKTV  
MCMV LATLFLNLRTRDR...DYVLKFLTRIAEAATSIIDNPTTYTSSGAKVSVVSTANVMQIMSLSSHTRKTV  
EBV LEHSEFLDRSRDR...GQLTRYLDMDFDCVTSIIDNPTTYTSSGAKVSVVSTANVMQIMSLSSHTRKTV  
KSHV IEHSEFLDRSRDR...GQLTRYLDMDFDCVTSIIDNPTTYTSSGAKVSVVSTANVMQIMSLSSHTRKTV  
acc

VZV bH a6 a7 bI bJ  
320 330 340 350 360 370 380 390  
VZV DVEVYVGMVYVQGNVDTALVMGKAVRGMDDVARHLLDITDPNTLNIPSIIPQSNDSSTTAGLPVNARVPAADLVVPSKL  
HSV-1 DVEVYVGMVYVQGNVDTALVMGKAVRGMDDVARHLLDITDPNTLNIPSIIPQSNDSSTTAGLPVNARVPAADLVVPSKL  
HSV-2 DVEVYVGMVYVQGNVDTALVMGKAVRGMDDVARHLLDITDPNTLNIPSIIPQSNDSSTTAGLPVNARVPAADLVVPSKL  
PRV DVEVYVGMVYVQGNVDTALVMGKAVRGMDDVARHLLDITDPNTLNIPSIIPQSNDSSTTAGLPVNARVPAADLVVPSKL  
HCMV SAPAVYVGNVYVQGNVDTALVMGKAVRGMDDVARHLLDITDPNTLNIPSIIPQSNDSSTTAGLPVNARVPAADLVVPSKL  
MCMV KTPASVYVGNVYVQGNVDTALVMGKAVRGMDDVARHLLDITDPNTLNIPSIIPQSNDSSTTAGLPVNARVPAADLVVPSKL  
EBV MGSVYVGNVYVQGNVDTALVMGKAVRGMDDVARHLLDITDPNTLNIPSIIPQSNDSSTTAGLPVNARVPAADLVVPSKL  
KSHV SCGLAVYVGNVYVQGNVDTALVMGKAVRGMDDVARHLLDITDPNTLNIPSIIPQSNDSSTTAGLPVNARVPAADLVVPSKL  
acc

VZV bK bL h4 bM bN  
400 410 420 430 440 450 460 470  
VZV VFLDLGLS VACI CTK FPELAY VRD GVIQEPVQO PMLARDG PHFVDQPVHNYMVYRIHKRSLSAAFALASEALSLSNTIYV  
HSV-1 VFLDLGLS VACV CTK FPELAY MNEGRVQEVHQPLARDGPHLEQPTHNYMVIDRRRLNAAFSLATEAALLTGEAL  
HSV-2 VFLDLGLS VACV CTK FPELAY MNEGRVQEVHQPLARDGPHLEQPTHNYMVIDRRRLNAAFSLATEAALLTGEAL  
PRV VFLDLGLS VACV CTK FPELAY SYVAGCIQEPVQO PMLARDG PHFVDQPVHNYMVIDRRRLNAAFSLATEAALLTGEAL  
HCMV VFLDLGLS VACV CTK FPELAY MNEGRVQEVHQPLARDGPHLEQPTHNYMVIDRRRLNAAFSLATEAALLTGEAL  
MCMV VFLDLGLS VACV CTK FPELAY MNEGRVQEVHQPLARDGPHLEQPTHNYMVIDRRRLNAAFSLATEAALLTGEAL  
EBV VFLDLGLS VACV CTK FPELAY MNEGRVQEVHQPLARDGPHLEQPTHNYMVIDRRRLNAAFSLATEAALLTGEAL  
KSHV VFLDLGLS VACV CTK FPELAY MNEGRVQEVHQPLARDGPHLEQPTHNYMVIDRRRLNAAFSLATEAALLTGEAL  
acc

VZV h5 a8 a9 TT a10 a11 TT a12  
480 490 500 510 520 530 540  
VZV LRDAGTICHSLLDVEATLVAIRQOHLDR..QCYFGVYVLEGTEDTLDVQMGFRFMETADMMPH.FPHWVNEHETILO  
HSV-1 LEHAGTICHSLLMNVDAAGGNNRDFVEA..ANPYGAYVAAAP.AGPAADQQLFLNAGQRLAHGRVVRWVREGQVTEPEQ  
HSV-2 MENAGTICHSLLMNIDAAVGGVNRDFVEA..ANPYGAYVAAAP.AGPAADQQRFLNAGQRLAHGRVVRWVREGQVTEPEQ  
PRV FEHAGTICHSFLDLDVATLAAALRQEPVEV..QCAFQAYVADARPDALVLMQRFLEENPMMV.PRRLW..APAAADQ  
HCMV FVDAKICHSFVLEHAPAPCQAFTERPPS.EPAMQRLLECRFQOEPMGARRIPHFVVRREVPRTVNIKQDFVVT  
MCMV HAEAKICHSFVLEHAPAPCQAFTERPPS.EPAMQRLLECRFVREHMAHARRLVHFVQARFDPPRTANEAKHDFSTKE  
EBV LQNAKICHSFVLEHAPAPCQAFTERPPS.EPAMQRLLECRFVREHMAHARRLVHFVQARFDPPRTANEAKHDFSTKE  
KSHV YQNAKICHSFVLEHAPAPCQAFTERPPS.EPAMQRLLECRFVREHMAHARRLVHFVQARFDPPRTANEAKHDFSTKE  
acc

(Continued on next page)

ZSV h6 bO bp h7 h8 a13  
 550 560 570 580 590 600 610 620  
 ZSV FTAPS N P R R . F D L N P A F D F F V A P G D V L P G P Q R P P E A M P T V N A T L R I N G N P L P L C P A F S P D C R E L . . . T Q L G L G R H T  
 HSV-1 F M Q P P N A N L A . L E L H P A F D F F V G V A D V L P G G D V P P A G F G E I Q A T W R V V G N P L P L C P A F S P D A R G . . . L E L G V G R H A  
 HSV-2 F M Q P P N A N L A . L E L H P A F D F F A G V A D V L P G G E V P P A G F G A I Q A T W R V V G N P L P L C P A F S P D A R G . . . L E L G V G R H A  
 PRV L L A P P N A D L R . L E L H P A F D F F V A P . E V D V P G P F A V P Q V M G Q V R A M P R H I G N P L P L C P A F S P D A R G . . . F E L S V G R H R  
 HCMV F Y K V G N I T L Y . T E L H P F F D F T H C Q E N S E . . . . . T V A L C T P R H V G N P D G L A P F F H E I R T W E I M E H M R L R P P P  
 MCMV F A K V D N Y L D F . T E L H P F F D F C F H T E N G Q . . . . . V R P L C T P R I M V G N P E A L A P D F H D R A K A Q E L E T K V R A P E  
 EBV F L H P P N D L R L B L H P L Y I G R D A G E R . . . . . A R H R A V H R M V G N P P T L A P A F E A R S Q Q F E T A T S L A H V V  
 KSHV L L R P P S H R L R L B L H P F D F F V H F C P G A R . . . . . G S Y R A T H R M V G N P P T L A P A F E S S N A Q P F A V I N H R H V I  
 acc

ZSV a14 a15 a16 a17 a18  
 630 640 650 660 670 680 690 700  
 ZSV M T F A T I K A V R D T F E D R A V F T I F Y L E A V T H G N E R N F C A L L R L L T Q C I R G Y W E Q S H R V A F N N F H M L M Y I T L Y L G N G E L P E  
 HSV-1 M A F A T I A A V R G A F E D R R M P A V F L Q A A H G S E H V F C L A R L V Q C I T S Y W N T R C A F N D Y S L V S V V F V L G L S D L P E  
 HSV-2 M A F A T I A A V R G A F E D R R M P A V F L Q A A H G S E H V F C L A R L V Q C I T S Y W N T R C A F N D Y S L V S V V F V L G L S D L P E  
 PRV L A F A T V A A V R G A F R A N Y P M V F Y I E A V L H G S E R T F C L A R L V A Q C I Q S Y H R T H N A F N N F Y H V M V I V N Y L G N G E L P E  
 HCMV D Y E E T L R L F T T V T S P N Y P E L C V L V D V L H G S E N A D A F L I R A F I A R C I V N M F H T R L L V F H S Y A L V T L A E H L A D A L P P  
 MCMV G H E A T L Q V L R A S L T H O Y P E L F Y I E S L H G D P A A E T F I E L V T R C V N N Y W R D R G L A F N S Y D M V R L I A F R L G D A V P P  
 EBV D . Q A V I E V O D T A Y T A Y A F F Y V E A M I H G P E E R E V M N V P L S L C I N T Y W E R S G R L A F N S F S M I K F I C H L G N N A F S K  
 KSHV D . Q L T I D V I O E T A F P A Y P L F C Y I E A M I H G P E E R E V M N P L I A L V I Q T Y W N S G K L A F N S Y H M V R F I C H M G N S I P K  
 acc

ZSV a19 a20 bQ a21  
 710 720 730 740 750 760 770 780  
 ZSV V C I N I V R L L Q H V R L R Q T T I D F T I Q G E G H N G E T S E A L N N I L T D T F I A P L W D C D A L Y R D E A A R D R L P A F R V S G R N G Y  
 HSV-1 E C M A Y V R D L V A H V E A L A Q L V D D F T L T G P E L G G Q A Q A E L N H L M R D P A L L P P V W D C D A L M R R A A L D R H R D C R V S A G G . H D P  
 HSV-2 E C M A Y V R D L V A H V E A L A Q L V D D F T L T G P E L G G Q A Q A E L N H L M R D P A L L P P V W D C D G L M R H A A L D R H R D C R I D A G G . H E P  
 PRV D C A A Y V K D L L E H V H A L R R L L G E F T L P G D P L G N Q P Q E E L N H A L A D A T L L P P H W D C D P L Y R D G L A . E R L P E L R V N G . A H F  
 HCMV Q L L F H Y R D L V A V L R L V T R I S A L P G L A E E P L S A Y V N A L H D H R L W P P . . . . . F V T H L P R N M E G V Q V V A D V . . . . . P  
 MCMV A A Y T H Y R N L S I T R F V A R T C E L T G L N . G R L C D E P L A I V S A L H D P R L W P P . . . . . F V Q A L P R N A N L V R V V A D V . . . . . P  
 EBV E A Y S W R K Y I G E L L A L E Q A L M R L A S S . D V V S D E S V G Q Y V C A L L D N L L P V A V F D I F H L L T V S D R A P Q I T G N E V Y A D T  
 KSHV E A H G H R K L G E L L A L E Q A L K L A S H . E T V G R T P T H L V S A L L D P H L L P P F A I H D V F T D L M Q K S S R Q P I I M L S Q N Q D N P  
 acc

ZSV bR bS a22 a23 bT a24  
 790 800 810 820 830 840 850  
 ZSV Q A L H F V D M A G H N F Q R R D N V L T H G . . . . . R P V R G D T G Q G I P I T P H H D R E W G L S K I Y Y I V I F F S R G S C T M G Y R D R L Y  
 HSV-1 V V A A C N V A T A D F N R N D G Q L L H N . . . . . T Q A R A A D . . . . . R A D D R P H R G A D W T H H L V M V V F F R G R C T A V R F D R V Y  
 HSV-2 V V A A C N V A T A D F N R N D G R L L H N . . . . . T Q A R A A D . . . . . R A D D R P H R G A D W T H H L V M V V F F R G R C T A V R F D R V Y  
 PRV Q H I L W V E M A Q V N F R N V G G L V H N . . . . . R E V R N E N . . . . . O P L H P H D A E W S V L S L I Y Y A V V F F R G N C I D V R Y D R V Y  
 HCMV L N P A N I E A R H H G V S D V P R . . . . . L G A M D A D E P F V D D Y A T D D E W T L O K V P L C L I P M T N N R A . . . . . G L G N L K T L L  
 MCMV L D A H I E E R N P G T S D V A R . . . . . M I A M D Q A E P L F V D A R R F S D E E M V A O K V L L Q V L N N H A C A G S L K H R H L L  
 EBV L A A P Q F I E R V N M D E M A A Q F Y A L Y G Y R V N G D H D H F R L H L G P Y V D E G H A D V L R K I Y Y V F L P C T N A H M C G L G V D F H V A  
 KSHV Q N R A T F I N L R G M E D L V N N L V N I Y Q T R V N E D H D E R H V L D V A P L D E N D Y N P V L R K I Y Y V L M C E N G H M C G M S D Y Q N V A  
 acc

ZSV a25 a26 h9  
 860 870 880 890 900 910 920  
 ZSV P A T Q A V I V P E I P A D E E A P T T P E . . . . . D P R H P L H A H Q L V P N S L N V Y F H N A H L T V D G D A L L T D E L W G D M A E  
 HSV-1 A T L Q N M V P E I T P G E D C P S D P V T . . . . . D P A H P L H P A N L V A N T V N A M F H G R V V V D G P A M L T Q V L A H N N A E  
 HSV-2 A T L Q N M V P E I T P G E D C P S D P V T . . . . . D P A H P L H P A N L V A N T V N A M F H G R V V V D G P A M L T Q V L A H N N A E  
 PRV Q V I Q T M V V P E T . . . . . D E E V G T D . . . . . D P R H P L H P R N L V P N S L N V L F H V A C V A V D A D A M L I O E T V T N N A E  
 HCMV V D L F Y R P A F L L M P A A T A V S T S G T T S K E S T S G V T P E D S V A A Q R Q A V G E M T E L V E D V A T D A H T P L L Q A C R E L F L A Y Q F V G P  
 MCMV V K L F Y T K F L T A D P D S L T A G . . . . . E E A L T N N . . . . . P L A A L V R D V A T D E N V T A N Q A A E P H L V A H V P E  
 EBV Q T L A Y N G P A F S H H F T . . . . . R D E P I L D N L E N . . . . . G L R D L L E L S D L R F T V G M I R D S A S F M T C P F  
 KSHV L T L T Y N G V F A D V V N . . . . . A Q D D I L L H L E N . . . . . L G E L K D I L V Q G D L R F T V D M I R V T S E L T C P F  
 acc

ZSV bU h10 h11 bV bW bX h12  
 930 940 950 960 970 980 990 1000  
 ZSV R T A T L L V S S A P D A G A A T T R N M R I Y D G A L Y H G L I M A Y Q A Y D E T I A T G T F Y P V P V N P L F A C P E H L A S L R G M T N A R R . .  
 HSV-1 R T A T L L C S A A P D A G A N T S T N M R I E D G A L H A G I L L M A P Q H L D H T I Q N G D F P L P H A L F A G A D H A N A N F P P A I R . .  
 HSV-2 R T A T L L C S A A P D A G A N T S T A N M R I E D G A L H A G V L L M A P Q H L D H T I Q N G D F P L P H A L F A G A D H A N A N F P P A I R . .  
 PRV R T P T L L S A P D A G M A T V A T R D M T H D G S H H G L L M A Y Q P N D A T L L E G A F T Y P A P N A L F A C A D H L G A M R D V G A E V R . .  
 HCMV H V K V L E V R A P L D H A Q R O G L P . . . . . D F I S R Q H V L Y N G C C V T A P . . . . . K T L I E I S L V P H R F Y S N P T I C A A L S D D K R R V T E  
 MCMV N A Q M L E I R A A I D P A Q R H G A P S A G F E S L Q H V L Y N G F C M T V T P . . . . . K L L Q E Y L T V E P H R F Y S D P G L A A T A H D D I R V F L N D  
 EBV F T R A V R V S G D N D V T Q Q L A P N P A D K R T E Q T V L V N G L V A F A F S E R T R A V T Q C L F H A I P H M F Y G D P R V A A T M H Q D V A T F V M R  
 KSHV V T Q A A R V I T K R D P A Q S F A T H E Y G K D V A Q T V L V N G F G A F A V A D R S R E A A E T M F Y P V P F N K L Y A D P L V A A T L H P L L A N V V T R  
 acc

ZSV a27 h13 h14 a28 a29 a30 bY  
 1010 1020 1030 1040 1050 1060 1070  
 ZSV . . . . . V L A K M V P I P F F L G A N H A T I R Q P V A Y H V T H S K S D F N T L T Y S L L G G Y F K S T P I S L T H Q L R T G F H P G I A F T V R R D R  
 HSV-1 . . . . . D L S R Q V P L V P P A L G A N Y F S S I R Q P V V Q H R E S A A G E N A L T Y A L M A G Y F K S P V A L H H Q L K T G L H P G F G F T V R R D R  
 HSV-2 . . . . . D L A R H V P L V P P A L G A N Y F S S I R Q P V V Q H R E S A A G E N A L T Y A L M A G Y F K S P V A L Y H Q L K T G L H P G F G F T V R R D R  
 PRV . . . . . A A A Q H V P C V P H F L G A N Y Y A T V R Q P V A Q H A Q S R A D E N T L S Y A L M A G Y F K S P V A F T H L R Q L H P G F A L T V R R D R  
 HCMV F P H Y R H R D G C F F L P T A F A H E Y H N W L R S P F S R Y S A T C P N V L H S V M . T L A A M L Y K S P V S L V L Q T K A H H P G F A L T V R R D T  
 MCMV F P Q Y Q R C D G C F F L S P I F A H E Y H H W H T P F S C Y S A C A N T L E S V L . T L A I M H H K S P V S A A L S R M G L H P G F A L T V R R D P  
 EBV N F Q . Q R A V E H F N R P E Q L F A H R E W H S G M K Y A C L S L V S L S . G H T A M H T K S P M A I A D A K L K H P Q V A L T V R R D P  
 KSHV L F N . Q R N A V U F N V S N L M A E E B E W H S K P A A Y A S C Q A T P G A L E . A M V S M H Q L S A F S F I C Q A K H R M H P G A M T V R R D P  
 acc

(Continued on next page)

VZV → bZ → bA → TT → bB → bC → bD → bE → bF → bG → h15

1080 1090 1100 1110 1120 1130 1140 1150

VZV FATEQLVFAERASESYFVGGLOVHHHD.AIGGVNFTLTPRAHVVDLGVGYTAVCATALRCPLTDMGNTAQLFESRGGV  
 HSV-1 FVTENVLFSERASEAYFLGLOVARHE.TGGGVNFTLTPRGNVDLGVGYTAVVATATVRNPVTDMGNLPOIFYLGRGAP  
 HSV-2 FVTENVLFSERASEAYFLGLOVARHE.TGGGVNFTLTPRGNVDLGVGYTAVVATATVRNPVTDMGNLPOIFYLGRGAP  
 PRV FATEENVLFAERASESYFMGGMQVARTES.GGGGLHLQLTPRANVDLGVGYTAAAYAAALRAPVTDMLPATRGA  
 HCMV FEVDMLLVSGKSCTSVLIINNF.IVTKERDISITTYVTQININTVDMGLGYTSNTCVYVYVNRVTDMGVVRVDFLFRVFMN  
 MCMV FETDTLLSTKASTAVIINTF.IVTKERDRDINVFVHVSQININTVEMGLGYGATTCTAHLRVRVSDMGSRMDLQVFMH  
 EBV ILSENLVSSRASSTSMFIGTFVSRREARVDAITFEVHHEMASIDTGLSYSSTMTPARVAITDMGHDTDFSVFPAE  
 KSHV VLAEHLVCSRASSTSMFVGLFVYVRRVRSDAITFEVHHEMASIDTGLSYSSTMTPARVAITDMGHDTDFSVFPAE  
 acc

VZV → a31 → bH → bI → TT → h16 → TT → T

1160 1170 1180 1190 1200 1210 1220 1230 T

VZV PMLHNDVTESLRRITASGGR...LNPTPELPIFGGLRPATSAGITARQASVCEPVMVPVPTDQYFRTACPRGRASGM  
 HSV-1 PLLDNAAVYLRNAVVAGNR...LGPAQPFVFGCAQVFRASMDHGDVCEIATPVTDNFRFCPRGRAGGV  
 HSV-2 PLLDNAAVYLRNAVVAGNR...LGPAQPFVFGCAQVFRASMDHGDVCEIATPVTDNFRFCPRGRAGGV  
 PRV PMLDADDVYLRRTVNAENR...LAP...VYVFGQMLPOVPAALARGQVCEIATPVVDNFRACPRGRAGEV  
 HCMV VYRHDVDRWIRHAAGVERPQLDDETISMLTFGMSERNAAATVHGQKVVCEIATPVMDNFRKTNPRGRASCML  
 MCMV VYRHDVDRWIRHAAGVERPQLDDETISMLTFGMSERNAAATVHGQKVVCEIATPVMDNFRKTNPRGRASCML  
 EBV AFGNQVNDYIKAKVGAQRNGTLLRDRPT.YLAGMTNVNGAPGLCHGQATCEIATPVADNFRKSNPRGRASCML  
 KSHV AYQDRQLHDYIKMKRAGVQTGPPGNRMDHVYRACVPRCENLPLSHGQATCEIATPVADNFRKSNPRGRASCML  
 acc

VZV → a32 → a33 → a34 → h17

1240 1250 1260 1270 1280 1290 1300

VZV YMGDRDAEIEALIMFDHQSDDVAYTDRAIHPWASQKHSYEDRLYNGTYN...LTGASPLYSPCFKFTPAEIVNENCNTLD  
 HSV-1 YAGDKREGVITALMYDHSQSDPSRAFAAANPWASQKHSYEDRLYNGTYN...LNGASPLYSPCFKFTPAEDIAAKHRCLE  
 HSV-2 YAGDKREGVITALMYDHSQSDPSRAFAAANPWASQKHSYEDRLYNGTYN...LNGASPLYSPCFKFTPAEDIAAKHRCLE  
 PRV HGE...EGLMFDHSHADPAHPHRAANPWASQKHSYEDRLYNGTYN...MSG...PAYSPCFKFTPAEAVAKSRGLA  
 HCMV GVDPYDTEAATKAIYDHRADAQ.TFAAANPWASQACCLDQVLYNTRRRLGYNKFSYSPCAQVFNTEEIIANKTLF  
 MCMV GVDPYDTEAATKAIYDHRADAQ.TFAAANPWASQACCLDQVLYNTRRRLGYNKFSYSPCAQVFNTEEIIANKTLF  
 EBV SCENYQVVEGLIYDHSRPAAYEYRSNPNWASQKHSYEDRLYNGTYN...LYSPCRAFPKELLRNNRGLY  
 KSHV SCDAYSNSESERLLYDHSIPDAPYECRSNPNWASQKHSYEDRLYNGTYN...LYSPCRAFPKELLRNNRGLY  
 acc

VZV → h18 → TT → a35 → bJ → bK

1310 1320 1330 1340 1350 1360 1370 1380

VZV RLLMEAKAVAS...QSTDEYQFKRPPGSTEMTQDPCGLFOEAYPLCSDAAMLRTAHAG...ETGADENVLAQYLRID  
 HSV-1 RLIVETGSAV...TATAASDQFKRPPGCRELVEPCGLFOEAYPLCADDPALLRARNG...EAHARETHQYLVYD  
 HSV-2 RLIVETGSAV...TATAASDQFKRPPGCRELVEPCGLFOEAYPLCADDPALLRARNG...EAHARETHQYLVYD  
 PRV RLIIATGAAAS...PTSNGEYQFKRPPGAGELVEPCGLFOEAYPLCADDALLRPLG...AEPHAYLVYD  
 HCMV KTIIDVYLLRAKDCIRGDDTDOVVCVEGTEQLIENPCRLFOEAYPLSTTTLALMETKLGKGGAGAFATSEPHENYVJGE  
 MCMV KTIIDVYLLRAKDCIRGDDTDOVVCVEGTEQLIENPCRLFOEAYPLSTTTLALMETKLGKGGAGAFATSEPHENYVJGE  
 EBV NMVNYYSQRLLGGHPATSNTEVQVVIAGTDVLEPCGLFOEAYPLSASRRALIDEFMSV...KQTHAPVYGHYVIEE  
 KSHV TLVNEYSARLAGAPATSTDLQVYVNVGTDVLEPCGLFOEAYPLSASRRALIDEFMSV...KQTHAPVYGHYVIEE  
 acc

VZV → 1390

VZV ASFLRGCPLPR...  
 HSV-1 ASFLRGLAL...  
 HSV-2 ASFLRGLSL...  
 PRV ESFLRGCPOHASA...  
 HCMV IIFLQSSMLFNS...  
 MCMV IIFLQSSMLFNS...  
 EBV VAVVRIKFGNKVVV...  
 KSHV VAVVRIKFGNKVVV...  
 acc

(Continued on next page)

b

### SCP

```
VZV          1          TT 10          TT 20          η1 222          α1 300 30          40          50          000000
VZV          . . . . . MTQPASSR VVFDPSNITTFESVEATAAYTPVALTRDLNASG . . . . . PLOPG . . . . . HRVDIADARS
HSV-1        . . . . . MAVPQFHRPSTVTDSVRALGMRGLVLLATNNSQ . . . . . FIMDNNHPHQGTQGA VR
HSV-2        . . . . . MAAPQFHRPSTITADNVRALGMRGLVLLATNNAQ . . . . . FIMDNSYPHPHGTQGA VR
PRV          . . . . . MSFDPNRPRTITAQTLLEGALPVDILLRLNRAT . . . . . GLQMDAAEAHAIVEDARR
HCMV        . . . . . MSNTAPGPTVANKRDEKRRHVNVVLELPT . . . . . EISEATH
MCMV        . . . . . MSTNVSSASGGSSCGSSGASSGGGGGGSSGSKKEER . . . . . RKQFGANVLNLAPAMV AQ
EBV         . MARRLPKFTLQGRLEADFPDSPLLKPFQELMNNLPNDVFREAQRSYLVFLTSQFCYEEYVQRITFGVPRQRALDKRQR
KSHV        MSNFKVRDPVFIQERLDHDIYAHPLVLRMNTLDGQMSQAEYLVQKRHYLVFLIAHHYYEAYLRRMGGIQRRDHLQLTRD
acc
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```
VZV          α2 60          α3 70          TT 90          100          110          120          130
VZV          IYTVGAASAAARARANHNANTIRRTAMFAETDPTWLRPFVGLKRTFNPRRIIRFPQPPNPSMSLSGISGPTILPQKTQSADQ
HSV-1        EFLRQAAALITDGLAHANNFTFPQMFAGDAFAAWLRFAPGLRRITYSPPFVVRREPSTPGTP . . . . .
HSV-2        EFLRQAAALITDGLVTHANNFTFAPQMFAGDAFAAWLRFAPGLRRITYSPPFVVRREPSTPGTP . . . . .
PRV          TLFIGTSLALVNRHRAHDKHLVERQPMFATS DYSSAWLRFVGLKRTFPCP . . . . . RPPP . . . . .
HCMV        PVLATMISKYTRMS . . . . . SLENDKCAFK . . . . . LDLLR.MVAVSTRR . . . . .
MCMV        PVISTMIPKYMKG . . . . . HEDKLAYQ . . . . . LDLLR.MLSIAKKATVIQ . . . . .
EBV         ASVAGAGAAHHLGGSSATPVQQAQAASAGTGALASSAPSTAVASATPSVSSSISLRAATSG . . . . . A
KSHV        QKPREARADRVSAASAYDAGTFVPSRPGPASGTPGQDLSLGSSTITLSSGPHSLSP . . . . . A
acc
```

```
VZV          140          150          160          170          180          190          200          210
VZV          SALQQPAALAFSGSSPQHPPPTTSASVGGQQHVVS GSSGQQPQQGAQSSVQPTTGSPPPAAQGVFPQSTPPPTQNTFQGG
HSV-1        . . . . .
HSV-2        . . . . .
PRV          . . . . .
HCMV        . . . . .
MCMV        . . . . .
EBV         TAAASAAAAVDTGSGGGGQPHDTAPRGARKKQ . . . . .
KSHV        SDILITLSSSTTETAAPAVADARKFPSGKKK . . . . .
acc
```

```
VZV          220          230
VZV          KGQTL SHTGQSGNASRSRRV
HSV-1        . . . . .
HSV-2        . . . . .
PRV          . . . . .
HCMV        . . . . .
MCMV        . . . . .
EBV         . . . . .
KSHV        . . . . .
acc
```

(Continued on next page)

C

### Tri1

VZV 1 10 20 30 40 50 60 70 80  
VZV MGSQPTNSHFTLNEQTLNCGTINISLLGNRRFIOIENGGLHMTVAEPFFGNWSRDITIGPRFGGLNKQPIHVPPKRTTETASIQ  
HSV-1 MKTNP...LPATPSVWGGSTVELPPTTRDTAGQGLLRRVLRPFIARRDGPVILFRGSGPRRAASTLWLLGLDGDTPDAPPGA  
HSV-2 MKTKP...LPATPMAWAESAVENTTSPRELACHAPLRRVLRPFIARRDGPVILFRGDRAPRRSTASTMWWLLGLDPAESSFGT  
PRV MS...VOIENGGLLMVVAEPG...TLTVG...  
HCMV ...MDARAVAKRRFRD...  
MCMV ...MANVSSFGPKRRB...  
EBV ...MKVQGSVDRRRLRRIAGLRFPPARR...LN...SRGSEFTRDVRGLVEEHAQASSLS...  
KSHV ...MKVQAEAN.AARLRGRQVLLGLLRFPPTHR...VSLTRGFEPFARGVRDLSKYAASTRPT...  
acc

VZV 90 100 110 120 130 140 150 160  
VZV VTFRSIVINRMNNIQINFTSIGNPQVITIRLPLNNFKSTTQLIQQVSTLDFFRPDIEHAGSIILILRHPSPDMIGEANTLTQ  
HSV-1 LTPNDDTEQALDKILRGTM.R.GGAALIG...SPRHLLTRQVILLTDLCQPNADRAGTLLEALRHPADLPHLAHQRAP  
HSV-2 RATRDDTEQAVDKILRGARRAGGLTVFG...APRYHLTRQVILLTDLCQPNADRAGTLLEALRHPADLPHLAHQRAP  
PRV ...SARARLITRQVILLADFCQEPQAEPPGLVLEALRHPADLAGAAYAATP  
HCMV ...PADEDNE.LVTLAKAKREVNITISVRYIYHADHQALTAARFFVPEGL  
MCMV ...VMEFDPEDPYKVKSKMRKLESIKAGYVYGGADHQAITARFFVRESL  
EBV ...AAAVWRAGLILAPGEVAVAGGGSGGGSFSSGWRPFPVFGDFLIHAS  
KSHV ...VGSLEHALRQAP...L...FRQPTYGDFLIVYSQ  
acc

VZV 170 180 190 200 210 220 230 240  
VZV AGRDPDVLEGLRNFNACTAPWIVGEGGLRQVYVLSLFLAACRAEEYTDKQADANRTAVSAVGCSSRMETRIIRFSE  
HSV-1 PGRQTERLEAWGQLEMEATLGSRAESGCTRAGLVSFNFLVAACAASDARDADAVRAHTANVGRTRVGRLEDRFSE  
HSV-2 PGRQTERLEAWGQLEASALGSRAESGCTRAGLVSFNFLVAACAASDARDADAVRAHTANVGRTRVGRLEDRFSE  
PRV PGNHRDLAEAWLALDEGGG...LG.GDGIRASVVSFLNFLVA...AENADADLRAHTANVGRTRVGRLEDRFSE  
HCMV VEFPAQ.PGALLIRMETG...CDSPRHLYISLYLLGIR...ASNVSASTRCLLESVVTASARAAALQWLLD  
MCMV GEVEQKNGLVLMFRIDTG...IEMPSITVIVSLFLFSMV...AENVSAATRNTAAITGRGEGE.AITRWLDR  
EBV SFNNAEAGTGLPQFKQ...SDPFGVDVFTPLSLFLIMNHGRGVAAVAGGLTSMANLLYD.SPATLADLVP  
KSHV TFSPOQETGLPQFKQ...EDNGSSMDLLETSLFLMLSGMAAAKQVPHK...L...VAGVWYWG.SGSLADFI  
acc

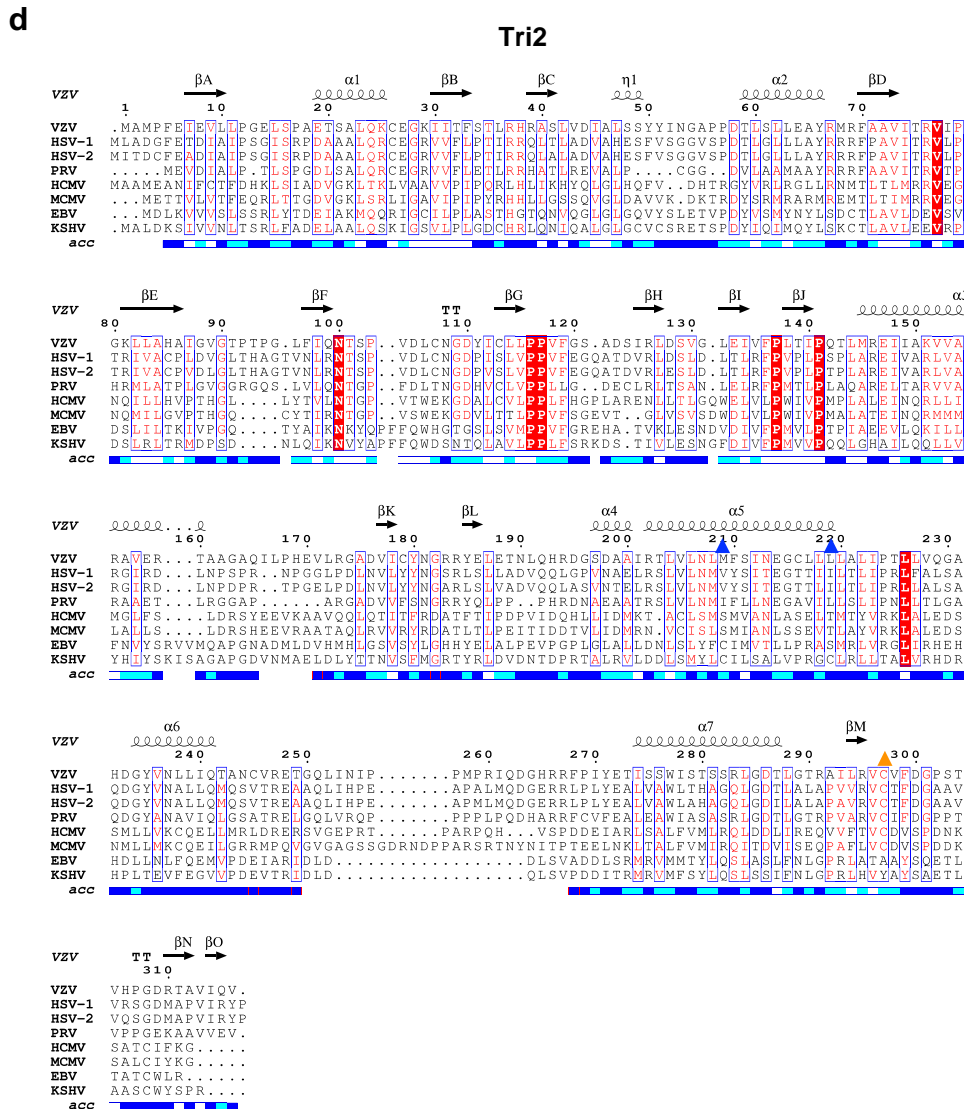
VZV 250 260 270 280 290 300 310  
VZV CTRAMVQCHVFFHRFISFFSGLLEYTIQDNLCNTHAVAKCPQEAARTDKISTRRVTAANRACVFWVDVKDLHLHS.ADGLK  
HSV-1 CTRAMVHHTVFFHEVYRFFGLVSMWTDDELASVAVCAQCEAAHTGHPGRPSAATLEACAFVDLDAELGLG.GPGAA  
HSV-2 CTRAMVHHTVFFHEVYRFFGLVSMWTDDELASVAVCAQCEAAHTGHPGRPSAATLEACAFVDLDAELGLG.GPGAA  
PRV VLRAMIRSHVFFHRAIHVLCGLLGHVTDORLASVAVCAQCEAAARTNDMAARRSQVHPCALMDVDRRLRGGDGLR  
HCMV GPBLL...HRRLETLGCVKTVSLGITSLNCSMRG...YLYNTLKTVEFALMFKDMLYLTWE...  
MCMV GAWRL...HRVVHPLGCTNSITPGATCLINCSMRG...HSYNTLKTVEFALMFKDMLYLTWE...  
EBV DFGRLVADRRR.HNFITPVGELVENIKSTYLNKIITVVHG...PVSKAIPRSTVKTVEQEFVVDLDAWLSGGAGGGGG  
KSHV NLSELMDTGEEHTLLTPVGMVQSVHSTFTVKVTSAMK...VGLARDEFRAHVGLTFCDFMLVDLDESCEPMVQRR...  
acc

VZV 320 330 340 350 360 370 380 390  
VZV HVFLVFVYTIQRQREGVIRHIALSQLNEQCFCGRGFGFLGRIRAENAAGTEGVANTHQOPYNTRALPLVQLSNDPTSPRC  
HSV-1 FLYLVFTYRQRDQELCCVYVYIKSQLPPRGLEPALERFGLRITNTIHGTEDMT.PPAPNRPDPFPLAGLAANPQTFRC  
HSV-2 FLYLVFTYRQRDQELCCVYVYIKSQLPPRGLEPALERFGLRITNTIHGTEDMT.PPPNRPDPFPLAVLAASSQSPRC  
PRV FAYLVFVYTIQRHREARLVHVAVSRLE.LGDALSFLLAGTRVDNAIHGTEDADAPAPAAAAAFP.AYLFNDPSPRC  
HCMV ...ETRGRLOQVYVITIVYDYDGP.ETRFPYVYVITS...SIAHWQ  
MCMV ...STDEIRFVYVITIVYDYSRDRGPRFVYVYVITS...RITHK  
EBV VCFVGGGLGFCPAD.HRLLVYALTYEAGPR...LFTFFQ...SSRGK  
KSHV ...EPAGLN.DTIVYASLVYLRVNRQPSMLETFFQ...SGKGEA  
acc

VZV 400 410 420 430 440 450 460 470 480  
VZV SLSGPTICVNWNLARQRYQITCDFRGLPTQLSCMVAAYTLCTIPSESVRYTRMERFGGYVPTIWLKCVVWGGTNTN  
HSV-1 SLSGQITN...PQADRLYRQPDLRGRPTARTCTAAFAE.CMMPEDSPRCLRTERFGAVSVVWVLEGVVWR.PCEWR  
HSV-2 SLSGQITN...PQVDRLYRQPDLRGRPTARTCTAAFAE.CMMPEDSPRCLRTERFGAVSVVWVLEGVVWR.PCEWR  
PRV FTGRNLN...TPAAEA.LPVAPDMRGRATRNCSMVAAYVRCVTE...RVVRAERCQSVLDPLAHMERFTWV.CAEW  
HCMV ...TIVDVAR...GKFAERERCSFVNRITRPRQIPLCTGVIQKGCWCLADD.IHISFLVHKELKLSVVRDLNFSVE.LDFR  
MCMV ...TILINVL...YRFVRSRFFLNNSISGYGPSTGCLGTLQR.GWFCSDR...SRSGIVASRAGQLSVVVKLEKPYVD.VGFLV  
EBV ...QIMNLLR...IYVSPSMMHRYAVV.QPLHIEELTFGAVAC.GTFSATD.GWRRSAPNYRGSLLPVVLEIDSPYSN.VSDWE  
KSHV ...EVVAMIK...DHFITDVIKTYIQLRHELVIINRLVCAVCTGTVPFDS.HPVHQSLNVKGTSLPVIVEANFEAA.CGFWT  
acc

VZV 480  
VZV ECYVY  
HSV-1 ACA.  
HSV-2 ACA.  
PRV ECVFF  
HCMV EFW.  
MCMV EFA.  
EBV VLL.  
KSHV VFL.  
acc

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**Supplementary Figure 1. Structure-based sequence alignment of representative herpesvirus capsid proteins MCP (a), SCP (b), Tri1 (c) and Tri2 (d).**

Esript<sup>1</sup> representation of a structure-based sequence alignment of the capsid proteins MCP, SCP, Tri1 and Tri2 of VZV, HSV-1, HSV-2, PRV, HCMV, MCMV, EBV and KSHV (GenBank accession no. AB097933.1, JQ780693.1, JN561323.2, JF797219.1, GU937742.2, GU305914.1, V01555.2 and GQ994935.1, respectively). Secondary structure elements and relative accessibility are indicated above and below the sequences, respectively. Positions forming intermolecular disulfide bonds in HSV (Tri1 C266 and Tri2B C298) and KSHV (Tri2A C212 and Tri2B C222) are highlighted as orange and blue triangles, respectively.

### **Supplementary reference**

1. Robert, X. & Gouet, P. Deciphering key features in protein structures with the new ENDscript server. *Nucleic Acids Res.* **42**, W320-324 (2014).