Supplementary Data

Section 1. Sequence Alignments.

ICAM 1 Protein Alignment. The deduced mature peptide sequence is shown in the one letter IUPAC code. Periods (**.**) indicate identities with respect to human sequence #1. Species: Hs, Human; Pt, Common Chimpanzee; Ppan, Bonobo (Pygmy Chimpanzee); Gg, Gorilla; Pp, Orangutan; Mm, Rhesus macaque. There are two human sequences from different individuals (that differ by a single amino acid residue). Our Hs1 sequence is identical to GenBank J03132. Our Pt sequence is identical to GenBank M86848.

```
Hs1   QTSVSPSKVI LPRGGSVLVT CSTSCDQPKL LGIETPLPKK ELLLPGNNRK VYELSNVQED
Hs2   .......... .......... .......... .......... .......... ..........
Pt    ......P... .......Q.. ........D. .......... ....G...W. ..........
Ppan  ......P... .......Q.. ........D. .......... ....G...W. ..........
Gg    ......P... .......... ........T. .......... ....L...Q. ..........
Pp    H....SAN.F .........N ........T. .......... ...PG...W. M.........
Mm    ....F.PE.. .......K.N ..A.....IS ..M....... .I.PG...W. M.........

Hs1   SQPMCYSNCP DGQSTAKTFL TVYWTPERVE LAPLPSWQPV GKNLTLRCQV EGGAPRANLT
Hs2   .......... .......... .......... .......... .......... ..........
Pt    .......... .......... .......... .......... ..D....... ..........
Ppan  .......... .......... .......... .......... ..D....... ..........
Gg    .......... .......... .......... .......... ..D....... .........I
Pp    .......... ....A..... .......... .......... .......... ..........
Mm    .......... ....S...L. .......... .....P.... .......... ..........

Hs1   VVLLRGEKEL KREPAVGEPA EVTTTVLVRR DHHGANFSCR TELDLRPQGL ELFENTSAPY
Hs2   .......... .......... .......... .......... .......... ..........
Pt    .......... .......... ........E. .......... .......... Q........H
Ppan  .......... .......... ........E. .......... .......... Q........H
Gg    .......E.. .......... ......P.EK .......L.. .......... K.........
Pp    .......E.. S.Q....... ...A...A.K .D........ .......... .........H
Mm    .M........ S.QS...... ......P.G. .D........ .......YV. K........H

Hs1   QLQTFVLPAT PPQLVSPRVL EVDTQGTVVC SLDGLFPVSE AQVHLALGDQ RLNPTVTYGN
Hs2   .......... .......... .......... .......... .......... ..........
Pt    .......... .......... .......... ........L. .......... ..........
Ppan  .......... .......... .......... ........L. .......... ..........
Gg    .......... .......... .......... .......... .......... ..........
Pp    .......... .......... .......... .......... .......... .........V
Mm    .....D.... .......Q.. .......... .......... ...S...... K....I....
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```
Hs1   DSFSAKASVS VTAEDEGTQR LTCAVILGNQ SQETLQTVTI YSFPAPNVIL TKPEVSEGTE
Hs2   .......... .......... .......... .......... .......... ..........
Pt    .......... .......... .......... .R........ .......... ..........
Ppan  .......... .......... .M........ .R........ .......... ..........
Gg    .......... .........W ........T. .......... .......... ..........
Pp    ..L....... ....E....W .W.....R.. ....R..... ........T. M.........
Mm    N.L......K ....E....Q .L.G.M.... T...R..... ........N. ..........

Hs1   VTVKCEAHPR AKVTLNGVPA QPLGPRAQLL LKATPEDNGR SFSCSATLEV AGQLIHKNQT
Hs2   .......... .......... .......... .......... .......... ..........
Pt    .......... .......... ..V...V... .......... .......... ..........
Ppan  .......... .......... ..V...V... .......... .......... ..........
Gg    .......... .......... ..P...T.F. .......... .......... ..........
Pp    .I.......A .N........ ..P.....F. .......... .......... ..........
Mm    .I.E...... ...M...... ..P.....F. .......... .......... ....V.....

Hs1   RELRVLYGPR LDERDCPGNW TWPENSQQTP MCQAWGNPLP ELKCLKDGTF PLPIGESVTV
Hs2   .......... .......... .......... .......... .......... ..........
Pt    .......... .......... .......... ....S..... .......... ...V......
Ppan  .......... .......... .......... ....S..... .......... ...V......
Gg    .......... .......... .......... .......... .......... ...V......
Pp    .......... .......... .......... .......... .......... ..........
Mm    .......... ...K...... .......... .......... Q......... .....Q....

Hs1   TRDLEGTYLC RARSTQGEVT REVTVNVLSP RYEIVIITVV AAAVIMGTAG LSTYLYNRQR
Hs2   .......... .......... .K........ .......... .......... ..........
Pt    .......... .......... .K........ .......... .......... ..........
Ppan  .......... .......... .K........ .......... .......... ..........
Gg    .......... .......... .......... ...F...A.. .......... ..........
Pp    .......... .......... .......... .......... ...A.L.... ..........
Mm    .......... Q....R.... .......... ...V...P.. .....L.... VA........

Hs1   KIKKYRLQQA QKGTPMKPNT QATPP
Hs2   .......... .......... .....
Pt    ..R....... .......... .....
Ppan  ..R....... .......... .....
Gg    ..R....... .......... .....
Pp    ..RI...... .......... .T...
Mm    ..R....... .N........ .....
```

ICAM 2 Protein Alignment. The deduced mature peptide sequence is shown in the one letter IUPAC code. Periods (.) indicate identities with respect to human sequence #1. Species: Hs, Human; Pt, Common Chimpanzee; Gg, Gorilla; Mm, Rhesus macaque. There are two human sequences from different individuals (that differ by a single amino acid residue). Our Hs1 sequence is identical to GenBank BC003097.

```
Hs1   SDEKVFEVHV RPKKLAVEPK GSLEVNCSTT CNQPEVGGLE TSLDKILLDE QAQWKHYLVS
Hs2   .......... .......... .......... .......... ...N...... ..........
Pt    .......... .......... ...K...... .......... .......... ..........
Gg    .......... .......... A......... .......... .......... ..........
Mm    ....A....M .LE..I.K.. E.F....... .......... ...N....L. .T......I.

Hs1   NISHDTVLQC HFTCSGKQES MNSNVSVYQP PRQVILTLQP TLVAVGKSFT IECRVPTVEP
Hs2   .......... .......... .......... .......... .......... ..........
Pt    .......... .......... .......... .......... .......... ..........
Gg    .......... .......... .......... .......... .......... ..........
Mm    ........W. ........K. .S........ ....F..... .W........ ......A...

Hs1   LDSLTLFLFR GNETLHYETF GKAAPAPQEA TATFNSTADR EDGHRNFSCL AVLDLMSRGG
Hs2   .......... .......... .......... .......... .......... ..........
Pt    .......... .......... .......... .V........ D......... ..........
Gg    .......... ......NQ.. ......L... .......... .......... .....I....
Mm    ......S.L. .S....SQ.. ......L... ....S.M.H. ....H..... ..........

Hs1   NIFHKHSAPK MLEIYEPVSD SQMVIIVTVV SVLLSLFVTS VLLCFIFGQH LRQQRMGTYG
Hs2   .......... .......... .......... .......... .......... ..........
Pt    .......... .......... .......... .......... .......... ..........
Gg    ...QE..... .......... .......... .......... .......... ..........
Mm    EV.CT..... ........P. .......... ....F..... .......S.. W..R......

Hs1   VRAAWRRLPQ AFRP
Hs2   .......... ....
Pt    .......... ....
Gg    .......... ....
Mm    .......... ....
```

ICAM 3 Protein Alignment. The deduced mature peptide sequence is shown in the one letter IUPAC code. Periods (**.**) indicate identities with respect to human sequence #1. Species: Hs, Human; Pt, Common Chimpanzee; Gg, Gorilla; Pp, Orangutan; Mm, Rhesus macaque. There are two human sequences from different individuals (that differ by a single amino acid residue). Our Hs1 sequence is identical to GenBank X69819. There are two chimpanzee sequences that also differ by a single amino acid residue.

```
Hs1   QEFLLRVEPQ NPVLSAGGSL FVNCSTDCPS SEKIALETSL SKELVASGMG WAAFNLSNVT
Hs2   .......... .......... .......... F......... .......... ..........
Pt1/2 .......... .......... .......... .......... .......... ..........
Pt3   .......... .......... .......... .......... .......... ..........
Gg    .......... .......... .......... .......... .......... ..........
Pp    .......... ....P..... L......... .K........ .....DN... ....Y.....
Mm    .......... ...FP..... L......... .K..I..... .....DN.T. ....Q.....

Hs1   GNSRILCSVY CNGSQITGSS NITVYGLPER VELAPLPPWQ PVGQNFTLRC QVEGGSPRTS
Hs2   .......... .......... .......... .......... .......... ..........
Pt1/2 .......... .......... .....R.... .......... R......... ..........
Pt3   .......... .......... .....R.... .......... R......... ..........
Gg    .......... .......... .....R.... .......... .......... ..........
Pp    .......... ......I... .....R.... .......L.. .......... ..........
Mm    ........G. ........F. D....S.... .......... .....LI... ..........

Hs1   LTVVLLRWEE ELSRQPAVEE PAEVTATVLA SRDDHGAPFS CRTELDMQPQ GLGLFVNTSA
Hs2   .......... .......... .......... .......... .......... ..........
Pt1/2 .......... .......... .......... .......... .......... ..........
Pt3   .......... .......... .......... .......... .......... ..........
Gg    .......... .......... ......P... ..G....... .......... ..........
Pp    .......... .......... .......... ..GH...H.. .......... ..........
Mm    .........K ..T.....G. ....NT...T ..E....H.. .......K.. ..E..R....

Hs1   PRQLRTFVLP VTPPRLVAPR FLEVETSWPV DCTLDGLFPA SEAQVYLALG DQMLNATVMN
Hs2   .......... .......... .......... .......... .......... ..........
Pt1/2 .......... .......... .......... .......... .......... ..........
Pt3   .......... .......... .......... .......... .......... ..........
Gg    .......... M......... .......... .......... .......... ..........
Pp    .......... .......... ...A...... .......... .......... ........V.
Mm    .......A.. .......... .....K.... N......... .......... ..........
```

```
Hs1   HGDTLTATAT ATARADQEGA REIVCNVTLG GERREARENL TVFSFLGPIV NLSEPTAHEG
Hs2   .......... .......... .......... .......... .......... ..........
Pt1/2 .......... .......... .......... .......... .........T. .......P..
Pt3   .......... .......... .......... .......... .........T. .......P..
Gg    .......... ...L...... .......... .......... .I........ .......P..
Pp    .......... .M........ Q......... .......... .........L .....S.P..
Mm    ...M...... .......... .......I.. ...L.T.... .........L .....S.P..

Hs1   STVTVSCMAG ARVQVTLDGV PAAAPGQPAQ LQLNATESDD GRSFFCSATL EVDGEFLHRN
Hs2   .......... .......... .......... .......... .......... ..........
Pt1/2 .......... .......... .......... .......... R......... ..........
Pt3   .......... .......... .......... .......... R......... ..........
Gg    .......... .......... .......... .......... .......... ..........
Pp    .......... .......... .......... .......... .......... ......F...
Mm    .......... .......... .......... .......... ..N....... .......C..

Hs1   SSVQLRVLYG PKIDRATCPQ HLKWKDKTRH VLQCQARGNP YPELRCLKEG SSREVPVGIP
Hs2   .......... .......... .......... .......... .......... ..........
Pt1/2 .......... .......... ........T. .......... .......... ..........
Pt3   .......... .......... ........T. .......... .......... ..........
Gg    .......... .......... ........T. .......... .......... ..........
Pp    .......... .......... .......... .......... H......... ..........
Mm    .......... .......... .......... .......... ..Q....... .N........

Hs1   FFVNVTHNGT YQCQASSSRG KYTLVVVMDI EAGSSHFVPV FVAVLLTLGV VTIVLALMYV
Hs2   .......... .......... .......... .......... .......... ..........
Pt1/2 .......... .......... .......... .......... .......... ..........
Pt3   .......... .......... .......... .......... .......... ..........
Gg    .......... .......... .......... .......... .......... ..........
Pp    .......... .......... R......... ...N....L. .L...V.... ..V.V.....
Mm    .......... .......... .......... ..PK...... .L...V.... ..V.V.....

Hs1   FREHQRSGSY HVREESTYLP LTSMQPTEAM GEEPSRAE
Hs2   .......... .......... .......... ........
Pt1/2 ....K..... .......... .......Q.. ........
Pt3   ....K..... .......... .......... ........
Gg    ....K..... .......... .......... ........
Pp    ....K...R. ...Q...S.. .......... .....T..
Mm    .K..K...R. ...Q...S.. .......... ........
```

ICAM 4 Protein Alignment. The deduced mature peptide sequence is shown in the one letter IUPAC code. Periods (**.**) indicate identities with respect to Hs sequence. Species: Hs, Human; Pt, Common Chimpanzee. Human sequence is from GenBank NM_001544.

```
Hs ALGRRTKRAQ SPKGSPLAPS GTSVPFWVRM SPEFVAVQPG KSVQLNCSNS CPQPQNSSLR
Pt .......... .......... .......... .......... .......... ..........

Hs TPLRQGKTLR GPGWVSYQLL DVRAWSSLAH CLVTCAGKTR WATSRITAYK PPHSVILEPP
Pt .......... .......... .......... .......... .......... ..........

Hs VLKGRKYTLR CHVTQVFPVG YLVVTLRHGS RVIYSESLER FTGLDLANVT LTYEFAAGPR
Pt .......... .......... .......... .......... .......... ..........

Hs DFWQPVICHA RLNLDGLVVR NSSAPITLML AWSPAPTALA SGSIAALVGI LLTVGAAYLC
Pt .......... .......... .......... ...S...... .V........ ..........

Hs KCLAMKSQA
Pt .........
```

ICAM 5 Protein Alignment. The deduced mature peptide sequence is shown in the one letter IUPAC code. Periods (**.**) indicate identities with respect to human sequence. Species: Hs, Human; Pt, Common Chimpanzee. There are two human sequences from different individuals (that differ by a single amino acid residue). Hs1: GenBank BC026338, Hs2: GenBank U72671.

```
Hs1 AVSQEPFWAD LQPRVAFVER GGSLWLNCST NCPRPERGGL ETSLRRNGTQ RGLRWLARQL
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 VDIREPETQP VCFFRCARRT LQARGLIRTF QRPDRVELMP LPPWQPVGEN FTLSCRVPGA
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 GPRASLTLTL LRGAQELIRR SFAGEPPRAR GAVLTATVLA RREDHGANFS CRAELDLRPH
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 GLGLFENSSA PRELRTFSLS PDAPRLAAPR LLEVGSERPV SCTLDGLFPA SEARVYLALG
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... ..P....... .......... .......... ..........
```

```
Hs1 DQNLSPDVTL EGDAFVATAT ATASAEQEGA RQLICNVTLG GENRETRENV TIYSFPAPLL
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... ...V...... .......... ..........

Hs1 TLSEPSVSEG QMVTVTCAAG TQALVTLEGV PAAVPGQPAQ LQLNATENDD RRSFFCDATL
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......S.. A......... .......... .......... ..........

Hs1 DVDGETLIKN RSAELRVLYA PRLDDSDCPR SWTWPEGPEQ TLRCEARGNP EPSVHCARSD
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 GGAVLALGLL GPVTRALSGT YRCKAANDQG EAVKDVTLTV EYAPALDSVG CPERITWLEG
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 TEASLSCVAH GVPPPDVICV RSGELGAVIE GLLRVAREHA GTYRCEATNP RGSAAKNVAV
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 TVEYGPRFEE PSCPSNWTWV EGSGRLFSCE VDGKPQPSVK CVGSGGATEG VLLPLAPPDP
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 SPRAPRIPRV LAPGIYVCNA TNRHGSVAKT VVVSAESPPE MDESTCPSHQ TWLEGAEASA
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 LACAARGRPS PGVRCSREGI PWPEQQRVSR EDAGTYHCVA TNAHGTDSRT VTVGVEYRPV
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 VAELAASPPG GVRPGGNFTL TCRAEAWPPA QISWRAPPGA LNIGLSSNNS TL
Hs2 .......... .......... .......... .......... .......... ..
Pt  .......... .......... .......... .......... .......... ..
```

LFA-1 α Protein Alignment. The deduced mature peptide sequence is shown in the one letter IUPAC code. Periods (.) indicate identities with respect to Hs sequence. Species: Hs, Human; Pt, Common Chimpanzee. Human sequence is from GenBank Y00796.

```
Hs YNLDVRGARS FSPPRAGRHF GYRVLQVGNG VIVGAPGEGN STGSLYQCQS GTGHCLPVTL
Pt .......... .......... .......... .......... .......... ..........

Hs RGSNYTSKYL GMTLATDPTD GSILACDPGL SRTCDQNTYL SGLCYLFRQN LQGPMLQGRP
Pt .......... .......... .......... .......... .......... ..........

Hs GFQECIKGNV DLVFLFDGSM SLQPDEFQKI LDFMKDVMKK LSNTSYQFAA VQFSTSYKTE
Pt .......... .......... .......... .......... .......... ..........

Hs FDFSDYVKWK DPDALLKHVK HMLLLTNTFG AINYVATEVF REELGARPDA TKVLIIITDG
Pt ........R. .......... .......... .......... .......... ..........

Hs EATDSGNIDA AKDIIRYIIG IGKHFQTKES QETLHKFASK PASEFVKILD TFEKLKDLFT
Pt .......... .......... .......... .......... .......... ..........

Hs ELQKKIYVIE GTSKQDLTSF NMELSSSGIS ADLSRGHAVV GAVGAKDWAG GFLDLKADLQ
Pt .......... .......... .......... .......... .......... ..........

Hs DDTFIGNEPL TPEVRAGYLG YTVTWLPSRQ KTSLLASGAP RYQHMGRVLL FQEPQGGGHW
Pt .......... .......... .........E .......... ....V..... ..........

Hs SQVQTIHGTQ IGSYFGGELC GVDVDQDGET ELLLIGAPLF YGEQRGGRVF IYQRRQLGFE
Pt .......... .......... ...M...... .......... .......... ..........

Hs EVSELQGDPG YPLGRFGEAI TALTDINGDG LVDVAVGAPL EEQGAVYIFN GRHGGLSPQP
Pt .......... ....Q..... .......... .......... .......... ..........

Hs SQRIEGTQVL SGIQWFGRSI HGVKDLEGDG LADVAVGAES QMIVLSSRPV VDMVTLMSFS
Pt .......... .......... .......... .......... .......... ..V.......

Hs PAEIPVHEVE CSYSTSNKMK EGVNITICFQ IKSLYPQFQG RLVANLTYTL QLDGHRTRRR
Pt .......... .......... .......... ....I..... .......... ..........

Hs GLFPGGRHEL RRNIAVTTSM SCTDFSFHFP VCVQDLISPI NVSLNFSLWE EEGTPRDQRA
Pt .......... .......... .......... .......... .......... ..........

Hs QGKDIPPILR PSLHSETWEI PFEKNCGEDK KCEANLRVSF SPARSRALRL TAFASLSVEL
Pt .......... .......... .......... .......... .......... ..........

Hs SLSNLEEDAY WVQLDLHFPP GLSFRKVEML KPHSQIPVSC EELPEESRLL SRALSCNVSS
Pt .......... .......... .......... .......... .......... ..........

Hs PIFKAGHSVA LQMMFNTLVN SSWGDSVELH ANVTCNNEDS DLLEDNSATT IIPILYPINI
Pt .......... .......... .........R .......... .......... ..........
```

```
Hs LIQDQEDSTL YVSFTPKGPK IHQVKHMYQV RIQPSIHDHN IPTLEAVVGV PQPPSEGPIT
Pt ......N... .......... .......... .......... .......... .....Q....

Hs HQWSVQMEPP VPCHYEDLER LPDAAEPCLP GALFRCPVVF RQEILVQVIG TLELVGEIEA
Pt .......... .......... .......... ...L...... .......... ..........

Hs SSMFSLCSSL SISFNSSKHF HLYGSNASLA QVVMKVDVVY EKQMLYLYVL SGIGGLLLLL
Pt .......... .......... .......... .......... .......... ..........

Hs LIFIVLYKVG FFKRNLKEKM EAGRGVPNGI PAEDSEQLAS GQEAGDPGCL KPLHEKDSES
Pt .......... .......... .......... .......... .......... ..........

Hs GGGKD
Pt .....
```

Mac-1 α Protein Alignment. The deduced mature peptide sequence is shown in the one letter IUPAC code. Periods (.) indicate identities with respect to human sequence. Species: Hs, Human; Pt, Common Chimpanzee. There are two slightly different human sequences from different individuals. Hs1: GenBank J04145, Hs2: GenBank M18044.

```
Hs1 FNLDTENAMT FQENARGFGQ SVVQLQGSRV VVGAPQEIVA ANQRGSLYQC DYSTGSCEPI
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... T......... .......... .......... ..........

Hs1 RLQVPVEAVN MSLGLSLAAT TSPPQLLACG PTVHQTCSEN TYVKGLCFLF GSNLRQQPQK
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 FPEALRGCPQ EDSDIAFLID GSGSIIPHDF RRMKEFVSTV MEQLKKSKTL FSLMQYSEEF
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .....N.Y.. .......... .......... ..........

Hs1 RIHFTFKEFQ NNPNPRSLVK PITQLLGRTH TATGIRKVVR ELFNITNGAR KNAFKILVVI
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 TDGEKFGDPL GYEDVIPEAD REGVIRYVIG VGDAFRSEKS RQELNTIASK PPRDHVFQVN
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .....H.... .......... ..........

Hs1 NFEALKTIQN QLREKIFAIE GTQTGSSSSF EHEMSQEGFS AAITSNGPLL STVGSYDWAG
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... ......G... .......... .......... ..........
```

```
Hs1 GVFLYTSKEK STFINMTRVD SDMNDAYLGY AAAIILRNRV QSLVLGAPRY QHIGLVAMFR
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 QNTGMWESNA NVKGTQIGAY FGASLCSVDV DSNGSTDLVL IGAPHYYEQT RGGQVSVCPL
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 PRGQRARWQC DAVLYGEQGQ PWGRFGAALT VLGDVNGDKL TDVAIGAPGE EDNRGAVYLF
Hs2 ...-...... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 HGTSGSGISP SHSQRIAGSK LSPRLQYFGQ SLSGGQDLTM DGLVDLTVGA QGHVLLLRSQ
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .....I.... .......... .......... .......... .......... ..........

Hs1 PVLRVKAIME FNPREVARNV FECNDQVVKG KEAGEVRVCL HVQKSTRDRL REGQIQSVVT
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 YDLALDSGRP HSRAVFNETK NSTRRQTQVL GLTQTCETLK LQLPNCIEDP VSPIVLRLNF
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... R......... .......... .......... .......... ..........

Hs1 SLVGTPLSAF GNLRPVLAED AQRLFTALFP FEKNCGNDNI CQDDLSITFS FMSLDCLVVG
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 GPREFNVTVT VRNDGEDSYR TQVTFFFPLD LSYRKVSTLQ NQRSQRSWRL ACESASSTEV
Hs2 .......... .......... .......... .......... .......... ..........
Pt  ........M. .......... .........G .......... .......... ....V.....

Hs1 SGALKSTSCS INHPIFPENS EVTFNITFDV DSKASLGNKL LLKANVTSEN NMPRTNKTEF
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 QLELPVKYAV YMVVTSHGVS TKYLNFTASE NTSRVMQHQY QVSNLGQRSL PISLVFLVPV
Hs2 .......... .......... .......... .......... .........P ..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 RLNQTVIWDR PQVTFSENLS STCHTKERLP SHSDFLAELR KAPVVNCSIA VCQRIQCDIP
Hs2 .......... .......... .......... .......... .......... ..........
..........
Pt  .......... .......... .......... .......... .......... ..........

Hs1 FFGIQEEFNA TLKGNLSFDW YIKTSHNHLL IVSTAEILFN DSVFTLLPGQ GAFVRSQTET
Hs2 .......... .......... .......... .......... .......... ..........
Pt  .......V.. .......... .......... .......... .......... ..........

Hs1 KVEPFEVPNP LPLIVGSSVG GLLLLALITA ALYKLGFFKR QYKDMMSEGG PPGAEPQ
Hs2 .......... .......... .......... .......... .......... .......
Pt  .......... .......... .......... .......... .......... .......
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Section 2. Important Amino Acid Residues: ICAMs, LFA-1.

ICAM 1 amino acid residues known or implicated to be important for LFA-1 binding. All of these residues are identical between human ICAM 1 and our chimpanzee ICAM 1 sequences. In fact, most of these residues are identical (or at least very well conserved) in all the primate sequences we have examined (see ICAM 1 protein alignment in Section 1). Residues that are identical in all primate ICAM 1 sequences are underlined; residues that are identical in all but one sequence are in *italics*.

Human	Chimpanzee	Reference
Asp-26	Asp-26	12
Leu-30	*Leu-30*	4
Leu-31	Leu-31	4
Ile-33	*Ile-33*	4
Glu-34	Glu-34	1, 4, 5, 6
Thr-35	Thr-35	5
Pro-36	Pro-36	5
Lys-39	Lys-39	5, 6
Gly-46	Gly-46	12
Gln-62	Gln-62	5
Met-64	Met-64	5, 6
Tyr-66	Tyr-66	5, 6
Asn-68	Asn-68	5, 6
Gln-62	Gln-62	5
Gln-73	Gln-73	5, 6

ICAM 1 amino acid residues known or implicated to be important for Mac-1 binding. All of these residues are identical between human ICAM 1 and our chimpanzee ICAM 1 sequences. In fact, most of these residues are identical (or at least very well conserved) in all the primate sequences we have examined (see ICAM 1 protein alignment in Section 1). Residues that are identical in all primate ICAM 1 sequences are underlined; residues that are identical in all but one sequence are in *italics*.

Human	Chimpanzee	Reference
Asp-229	Asp-229	12
Asn-240	Asn-240	12
Glu-254	Glu-254	12
Asn-269	*Asn-269*	12

ICAM 1 amino acid residues known or implicated to be important for ICAM 1 dimerization. All of these residues are identical (except residue 18: see text) between human ICAM and our chimpanzee ICAM 1 sequences, and most of these are identical or at least very well conserved in all the primate sequences we have examined (see ICAM 1 protein alignment in Section 1). Residues that are identical in all primate ICAM 1 sequences are underlined; residues that are identical in all but one sequence are in *italics*. The residue that differs between human and chimpanzee ICAM 1 is in **bold**.

Human	Chimpanzee	Reference
Leu-18	**Gln-18**	3
Leu-42	*Leu-42*	3
Leu-43	Leu-43	3
Leu-44	Leu-44	3
Val-51	Val-51	7

ICAM 1 amino acid residues known or implicated to be important for rhinovirus binding. All these of these residues are identical (except residues 29 and 49: see text) between human ICAM 1 and our chimpanzee ICAM 1 sequences. In fact, most of these residues are identical (or at least very well conserved) in all the primate sequences we have examined (see ICAM 1 protein alignment in Section 1). Residues that are identical in all primate ICAM 1 sequences are underlined; residues that are identical in all but one sequence are in *italics*. The two residues that differ between human and chimpanzee ICAM 1 are in **bold**.

Human	Chimpanzee	Reference
Gln-1	*Gln-1*	1
Thr-2	Thr-2	10
Asp-26	Asp-26	1
Gln-27	Gln-27	10
Pro-28	Pro-28	2
Lys-29	**Asp-29**	2, 9
Leu-30	*Leu-30*	2
Glu-34	Glu-34	1
Leu-37	Leu-37	2
Lys-40	Lys-40	2
Leu-43	Leu-43	10
Gly-46	Gly-46	1
Asn-47	Asn-47	10
Asn-48	Asn-48	10
Arg-49	**Trp-49**	1
Gln-58	*Gln-58*	1
Ser-67	Ser-67	2
Pro-70	Pro-70	2
Asp-71	Asp-71	1
Gly-72	Gly-72	10
Thr-75	Thr-75	10
Ala-76	Ala-76	10
Lys-77	Lys-77	1
Arg-166	Arg-166	1

ICAM 2 amino acid residues known or implicated to be important for LFA-1 binding. All but one of these residues are identical between human ICAM 1 and our chimpanzee ICAM 1 sequences, and most of these residues are identical, or at least very well conserved in all the primate sequences we have examined (see ICAM 2 protein alignment in Section 1). Residues that are identical in all primate ICAM 2 sequences are underlined; residues that are identical in all but one sequence are in *italics*. The one residue that differs between human and chimpanzee ICAM 2 is in **bold**. Our human sequences (from different individuals) differ at residue 41: one sequence is identical to chimpanzee (Asp), while the other shows Asn, which is identical to published human ICAM 2 sequences.

Human	**Chimpanzee**	**Reference**
Val-33	Val-33	13
Gly-35	Gly-35	13
Glu-37	Glu-37	4, 13
Leu-40	Leu-40	13
Asp-41/**Asn-41**	Asp-41	13
Lys-42	Lys-42	13
Leu-44	Leu-44	13
Leu-45	Leu-45	13
Glu-47	Glu-47	4
Lys-52	Lys-52	13
Tyr-54	Tyr-54	13
Gln-66	*Gln-66*	4
His-68	His-68	4
Thr-70	Thr-70	4
Gln-75	Gln-75	4

ICAM 3 amino acid residues known or implicated to be important for LFA-1 binding. All of these are identical between human ICAM 1 and our chimpanzee ICAM 1 sequences, or at least very well conserved in all the primate sequences we have examined (see ICAM 3 protein alignment in Section 1). Residues that are identical in all primate ICAM 3 sequences are underlined; residues that are identical in all but one sequence are in *italics*.

Human	Chimpanzee	Reference
Glu-2	Glu-2	18
Arg-6	Arg-6	18
Glu-8	Glu-8	18
Asn-23	Asn-23	14
Ser-25	Ser-25	14
Glu-32	Glu-32	16, 18
Lys-33	Lys-33	18
Glu-37	Glu-37	14, 15, 18
Thr-38	Thr-38	16
Lys-42	Lys-42	18
Phe-54	Phe-54	14
Arg-64	Arg-64	18
Leu-66	Leu-66	15, 18
Ser-68	Ser-68	15, 18
Gln-75	Gln-75	14, 15, 18
Arg-127	Arg-127	15
His-155	His-155	18
Asp-166	Asp-166	15

LFA-1 amino acid residues known or implicated to be important for binding to ICAM 1. All of these residues are identical between human LFA-1 and our chimpanzee LFA-1 sequence.

Human	Chimpanzee	Reference
Met-140	Met-140	5
Ser-141	Ser-141	4
Leu-142	Leu-142	5
Gln-143	Gln-143	5
Glu-146	Glu-146	4, 5
Ile-150	Ile-150	5
Phe-153	Phe-153	5
Thr-175	Thr-175	4
Leu-204	Leu-204	5
Leu-205	Leu-205	4, 5
Thr-206	Thr-206	4, 5
Lys-232	Lys-232	8
Ile-237	Ile-237	5
Asp-239	Asp-239	5
Gly-240	Gly-240	5
Glu-241	Glu-241	4, 5
Thr-243	Thr-243	4, 5
Ile-259	Ile-259	5
Ile-261	Ile-261	5
His-264	His-264	4
Phe-265	Phe-265	5
Ser-270	Ser-270	4
Lys-287	Lys-287	8
Phe-292	Phe-292	5
Glu-293	Glu-293	4
Gln-303	Gln-303	8
Lys-304	Lys-304	8
Lys-305	Lys-305	8
Tyr-307	Tyr-307	8
Glu-310	Glu-310	8

LFA-1 amino acid residues known or implicated to be important for binding to ICAM 2. All are identical between human LFA-1 and our chimpanzee LFA-1 sequence.

Human	Chimpanzee	Reference
Glu-146	Glu-146	4
Thr-175	Thr-175	4
Leu-205	Leu-205	4, 5
Glu-241	Glu-241	4, 5
Thr-243	Thr-243	4, 5
His-264	His-264	4
Lys-263	Lys-263	4
Glu-293	Glu-293	4

LFA-1 amino acid residues known or implicated to be important for binding to ICAM 3. All are identical between human LFA-1 and our chimpanzee LFA-1 sequence.

Human	Chimpanzee	Reference
Ile-126	Ile-126	17
Asn-129	Asn-129	17
Asp-182	Asp-182	17
Ser-184	Ser-184	17

Section 3. Experimental Procedures: Details.

PCR

The PCR reactions were carried out using HotStar Master Mix (Qiagen cat #203443) or Taq PCR Core Kit (Qiagen cat #201223). Each reaction contained 100 ng of each primer and variable amounts of cDNA or genomic template depending on the individual used. Cycling conditions were optimized for each template and gene: these are available upon request. Each 20 µl PCR reaction was run on a nuclease free agarose gel and purified using gel extraction spin columns (Qiagen cat #28706). The purified PCR products were concentrated and then sequenced.

Cloning

The AdvanTAge PCR Cloning kit (Clontech cat # K1901-1) was used for PCR cloning of ICAM 3 in chimp and human to search for potential new subunit. This is a standard TA cloning protocol for PCR products. The PCR products were gel purified using a nuclease free agarose gel and Qiagen gel extraction columns (cat # 28706). These cleaned up PCR products were ligated into the pT-Adv vector: 6 (l of fresh PCR product, 1 (l of 10x ligation buffer, 2 (l of pT-Adv Vector (25 ng/(l), and 1 (l of T4 DNA ligase (4.0 Weiss units). The approximate ratio of vector to PCR insert was 1:1. The ligation reaction was allowed to proceed at 14(C for fifteen hours on a thermal cycler. The ligation was then transformed into TOP10F *E. coli* competent cells as per Clontech's recommended protocol. White colonies were picked and grown in 3 ml overnights of Terrific Broth/Amp. Plasmid DNA was isolated from these overnights using the Qiagen Turbo prep protocol on the Qiagen BioRobot 9600.

Sequencing

For dye terminator sequencing, each reaction contained 2 µl of Perkin-Elmer's Big Dye Terminator mix (PE cat #430151), 1 µl of sequencing primer (5 pmol/µl), 1 µl of Perkin-Elmer sequencing reaction buffer (5x) (PE cat #4305605), 1-6 µl of template DNA, and 1-5 µl of water for a final reaction volume of 10 µl.

Cycling conditions were followed as recommended for Perkin-Elmer's Big Dye Terminators on a Perkin-Elmer 9700 Thermal Cycler. A standard NaOAc/Ethanol precipitation method was used to clean up the terminators and to concentrate the samples. The samples were resuspended in a formamide/EDTA solution and loaded onto a Perkin-Elmer ABI 373A sequencer. The sequencer was run as per Perkin Elmer's standard conditions with FMC Long Ranger gels (FMC cat #50693 or #50692) for either 34 cm or 48 cm well-to-read gels.

Section 4. Sequencing Summary: Genes, species, number of individuals from which sequences were obtained. We sequenced *ICAM* genes 1-3 from several individuals from several species whenever possible (number of individuals appears in parentheses after the species name. *ICAM*s 4 and 5 were sequenced from chimpanzee only.

ICAM 1

Species	Our Sequence	Length (nt)	GenBank	
Human (3)	Hs1	1807	AF340038	(Hs1 ≡ GenBank J03132)
	Hs2	1690	AF340039	
	Hs3	1723		(Hs3 ≡ Hs1 ≡ GenBank J03132)
Chimp (3)	Pt1	1813	AF340033	(Pt1 ≡ GenBank M86848)
	Pt2	1812	AF340034	(Pt2 ≡ Pt1 ≡ GenBank M86848)
	Pt3	1811	AF340035	(Pt3 ≡ Pt2 ≡ Pt1)
Bonobo (1)	Ppan exon1	217	AF340042	
	Ppan exon2	297	AF340043	
	Ppan exon3	428	AF340044	
	Ppan exon4	405	AF340045	
	Ppan exon5	376	AF340046	
	Ppan exon6	308	AF340047	
	Ppan exon7	208	AF340048	
Gorilla (2)	Gg1	1794	AF340036	
	Gg2	1793	AF340037	(Gg2 ≡ Gg1)
Orang (1)	Pp	1770	AF340041	
Rhesus (1)	Mm	1605	AF340040	

ICAM 2

Species	Our Sequence	Length (nt)	GenBank	
Human (2)	Hs1	1011	AF340052	(Hs1 ≡ GenBank BC003097)
	Hs2	1020	AF340053	
Chimp (2)	Pt1	997	AF340050	
	Pt2	990	AF340049	(Pt2 ≡ Pt1)
Gorilla (1)	Gg	970	AF340051	
Rhesus (1)	Mm	793	AF340054	

ICAM 3

Species	Our Sequence	Length (nt)	GenBank	
Human (2)	Hs1	1641	AF340060	(Hs ≡ GenBank X68711)
	Hs2	1630	AF340061	
Chimp (3)	Pt1	1638	AF340055	
	Pt2	1674	AF340056	(Pt2 ≡ Pt1)
	Pt3	1639	AF340057	
Gorilla (2)	Gg1	1649	AF340058	
	Gg2	1676	AF340059	(Gg2 ≡ Gg1)
Orang (1)	Pp	1650	AF340062	
Rhesus (1)	Mm	1607	AF340063	

ICAM 4

Species	Our Sequence	Length (nt)	GenBank
Chimp		826	AF340064

ICAM 5

Species	Our Sequence	Length (nt)	GenBank
Chimp		2316	AF340065

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