

Fig. S1. Analysis of APEX2 modifiable targets of Inc proteins.

-APEX2 targeted amino acids in **red** (Y, W, H, C (Rhee et al 2013 Science))
-Transmembrane domains (TOPCONS predicted topologies) are **underlined**

> CT223 WP_010725128.1 hypothetical protein [Chlamydia trachomatis]
MVSLALGTSNGVEANNGINDLSPAPEAKKTGSGLCYKisavaalvlgllaaaggavvlALFCTFAPPLff
agvalvalgavilgvqvsNT**CSCCL**RSRKIEAHKQLILQQKEEISQLEQQLAYPASLLERRDLRENKA
WQ**SCCL**NLEKEVRDLLTKLGGYQERLKVLPAAKEKQIEELKAMLE**HYSRICH**ERGELINLLKTAN
KKLSKESEKLLFN**YKAHRDVCL**GEKVLVKSVDLIDLPKSDSSDGDGDDDDGFNYGSRV
14 APEX2

> CT119 IncA WP_009871466.1 inclusion membrane protein A [Chlamydia trachomatis]
MTTPTLIVTPPSPAPSYSANRVPQPSLMDKIKKIaaia*sliligtigflalghl*VGFLiapqitivil
alfiislagnAL**YL**QKTANL**HLY**QDLQREVGSLKEINFMLSVLQKEFL**HLS**KEFATTSKDL SAVSQDF
YSCLQGFRDNYKGFESLLDE**YKN**STEEMRKLFSQEIADLKGSVASLREEIRFLTPLAEEVRRLA
HNQQSLTVVIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESDL**CS**QIRETLSSPRKSASPS
TKSS
11 APEX2

>CT117 IncF
MGDVMIQSVKTESGLVEG**H**RGI**C**DSLGRVVGALAKVAKIvvalaalvlnгалcvlsivaLCVGATPVGP
avlvattlasflcaacvfiAAKDRG**W**IASTNK**C**
4 APEX2

> CT115 IncD WP_009871462.1 inclusion membrane protein D [Chlamydia trachomatis]
MTKV**Y**ANSIQQERVVDRIALLER**C**LDPNSNLPTAKRLvavavatilavallvvaqlifsgvLCSPV**Sv**laaslf
fgvgafllggalvgGVLTTEAVTRERL**H**RSQTL**MW**NNL**CCK**TAEVEQKISTASANAKSNDKTRKLGE
6 APEX2

> CT118 IncG WP_009871465.1 inclusion membrane protein G [Chlamydia trachomatis]
MI**CC**DKVLSSVQSMPVIDK**CS**VT**KCL**QTAQAAvlaalsifavfasgsilsaavifsGTAAVLPy*liltallgf*
vcavivlrnlSAVVQ**SC**KKRSPEEIEGAARPSDQQESGGRLSEESASPQASPTSSTFGLESALRSI
GDSVSGAFDDINKDNSRSR**HSF**
6 APEX2

> IncE tr|B7SCH9|B7SCH9_CHLTH IncE OS=Chlamydia trachomatis
ME**C**VKQL**CRNHL**RLDNLTDPVRSVLTKGTTAEKVQLAACCLGVVCSIICLALGIAAAAVGV**SC**
G
GFALGLGIIALLGIVLFATSALDVLEN**H**GLVGC**PF**KLP**C**KSSPANEPAVQFFKGKNGSADQVIL
VTQ
7 APEX2

>CT226 L2
LRNRGAMFNISF**CC**NSSKPLRAD**H**TETIGAQTTTSRKEQLLAIGALVGLVAVLGGALLLLFSG
SVLSLFAPIL**SLLAMTLGSACIGGSLVYMY**GFSLKPTRLPESSGLAPEAVTPGLVLS**YQELLYE**
AEEDLKEVEGLLAQKSKDLELAQKKIEQLQSGLK**C**VLEESLR
6 APEX2

>OmcB YP_001654774.1 outer membrane protein OmcB [Chlamydia trachomatis 434/Bu]
MRIGDPMNKLIRRAVTIFAVTSVASLFASGVLETSMAEFISTNVISLADTKAKDNTSHKSKKARKN
HSKETPVNRKKVAPVHESKATGPKQDSCFGRMYTVKVNDDRNVEITQAVPKYATVGSPPVEI
TATGKRDCVDVIITQQLPCEAEFVRSDPATTPTADGKLVWKIDRLGQGEKSKITVWVKPLKEGC
CFTAATVCAACPEIRSVTKCGQPAICVKQEGPENACLRCPVVYKINVVNQGATARNVVENPV
PDSYAHSSGQRVLTFTLGDMPGEHRTITVEFCPLKRGRATNIAMVSYCGGHKNTASVTTVIN
EPCVQVSIAGADWSYVCKPVEYVISVSNPGDLVLRDVVVKDTLSPGVTVLEAAGAQAISCNKVV
WTVKELNPGESLQYKVLVRAQTPGQFTNNVVVKS CSDCGTCTSCAEATTYWKGVAAATHMCMV
VDTCDPVCVGENTVYRIVCTNRGSAEDTNVSLMLKFSKELQPVSFSGPTKGTITGNTVVFDSL
RLGSKETVEFSVTLKAVSAGDARGEAILSSDTLTPVSDTENTHIY
49 APEX2

>MOMP YP_001654141.1 major outer membrane porin [Chlamydia trachomatis 434/Bu]
MKKLLKSVLVFAALSSASSLQALPVGNPAPESLMIDGILWEGFGGDP CDPCTTWCD AISM RMG
YYGDFVDFDRVLQTDVNKEFQMGAKPTTATGNAAAPSTCTARENPAYGRHMQDAEMFTNAAY
MALNIWDRFDVFC TLGATSGY LKGN SASFNLVGLFGDNENHATVSDSKLVPNMSLDQSVVELY
TDTTFAWSAGARAALWECGCATLGASFQYAQSKPKVEELNVL CNAAEFTINKPKGYVVGQEFPL
DLKAGTDGVTGTKDASIDYHEWQASLALS YRLNMFTPYIGVKWSRASFDADTIRIAQPKSATTV
FDVTTLNPTIAGAGDVKASAEQQLGDTMQIVSLQLNKMKS RKS CGIAVGT TIVDADKYAVTVET
RLIDERA AHVNAQFRF
26 APEX2

CT228 >tr|O84231|O84231_CHLTR Uncharacterized protein OS=Chlamydia trachomatis (strain
D/UW-3/Cx) OX=272561 GN=CT_228 PE=4 SV=1
MSTTISGDASSLPLPTASCVEIKSTSSSTKGNTCSKIL dialaivgalvvvaglalv |CASNV iftaigiaalii
gsacvqagi SRLMCRSSYASLEAKNVLAEQRLRNLSEEKDALVSVSFINKMFLRGLTDDLQALEA
KAIEVEIDCLDRLEKNEQALLSDVRLVLSSYTRWLD SAEKEKAALKASIDANQAS
APEX2

> CT850 WP_009872976.1 hypothetical protein [Chlamydia trachomatis]
MGFGTVRGK GKAVKSFFLRP lqnlevqlfslpivlllqeig CVSSIS svslvavlsivqvfvalvsffRswqyqlsvv
gaiffglalcnn FPVSV vwgqlltvsfiisylls VSLVEGHIKEKAVSLSELTASHNSLQDSYNREVQERK
EKELLAQSKITALEQELSVSHEQLQEVSRYTHASEDLQILIDQRDSWLKDYMTLHQEYVRVVA
GDEENVIFPWKVVFQGNSEKDSGYQQRVQDAEHKIAHLEKLC EEENSGKRYAEECLDKALADLL
ESTRLREILEKEIFQKDEEIASLKQEIAAEKLLSSSVSDDRAAYKGGKYLQLREQFTVKDSFLKKAR
RERFLAQEQLLVLKRAKEEEASNLSTTDSFSIIQNLLLQIEALEEEVTYLEELVLHNQNR
21 APEX2

> CT005 WP_009871351.1 hypothetical protein [Chlamydia trachomatis]
MTPVTPVPPQSPQQVKLLSRFLTAPDRHPKLRV vdialiaisilcivsiilwtg GSG lalfaiapalaigalqv
tliv SDLAESQKSKEIADTVAAVSL pfiltgtaaglmfsaiavgggavilanplfmgsmtlqfalmsL HRVYQYL
SNREQWKQKKLEQVELAAWESHLPKESKSSALEEVRYSPRLMKRGKTWRKRAIRRKNYTP
PLVDKTLQTMQPDALFSSTTTHTSDSEQILTSVSPQSSDTESSSSSFHTPPNSDKELSDSNSS
DSSSSSEYMDALETVAAGDVSGITPPSKPSSSPKTRRVVKLRSERNAQHHRNKDQEQRQD
SSESSEEDSSSDSSQKKKPSRK
16 APEX2

> CT249 WP_010725138.1 hypothetical protein [Chlamydia trachomatis]
MGIKPHDHGCWGSRGNI FTLDLTDQQANQSAASSSSVLKSECTAKVARY algflfglqfilsivtfia
aaATLplgtvtilimvtqaafaala FKL YDLFKHDVPTCSITSKA
9 APEX2

> CT058 WP_010725013.1 hypothetical protein [Chlamydia trachomatis]
MFTSLSAIQNAIRPS**C**QLPVLTPRRalitslasgiilqlagcvvqvLASFPAliavsavilqvsifasgl
flcR**YV**CPPKIVSRRPSTELPAEPTPELPEIKRPKPIAPPPDFIPPRPLRRTIGEMLF**GW****C**IGSIR
QMPFFLANDKTPLSFRNPSARFRA**W**NIPST**H**TIFVSTSGQFSSLRMQSNLPAAIANATQSAFA
KRGQGGLGVNDAFPAVLTDK**CW**EESKPDGILLPGE**C**SSAT**W**EDKN**HLVP****CW**DEETK**T**Y**N**KP
LLFIQMLAPKAS**Y**QDDSK**S****C**YEITLRA**Y**T**A****C**FEEAIR**C****G**CRIIQIPLIAAFGDFVPRALSKQP**K****W**I
ESAKLSLL**H**AVEKTAK**H**ASKDLVIVLTNIPQPVNL
25 APEX2

> IncB (AM884176.1:577850-578194 Chlamydia trachomatis strain L2/434/Bu)
MV**H**SV**Y**NSLAPEGFSQVSIQPSQIPTSKKVMIAIMTLFALTAIAAIVLSIVTVCGGFPFLAALNTV
TIG**A****C****V****S****L****P****I****F****T****C****I****A****T****T****L****L****L****L****C**L**R**NIELLARPQVLT**L**STQFSPTKPQE
6 APEX2 residues

>CT101 (CTL0356)
MISMIP**R****F****S****I****A****C****I****P****L****A****V****W****L****F****S****G****A****K****L****L****V****K****S****L****Y****L****A****L****H****Y****Q****F****S****L****V****L****S****A****E****L****F****A****I****A****W****I****L****A****S****I****K****H****R****F****I****L****R****K****S****M****L**
KQ**H**ELDAQLLIKEISP**W**T**F**IKRSF**L****S****K****R****M****F****V****I****S****M****S****V****I****S****S****L****H****R****S****T****T****I****P****L****L****S****F****L****M****C****S****S****V****S****Y****A****L****F****K****T****S**
L**A****H****W****K****S****L****K****E****L****K****S****K****Y****S****V****Y****Y****Y**
18 APEX2 residues

>CT222 (CTL0475)
MR**C****C****C**VRTN**C**EEVRSSSTGDQVVS**A**VKERK**C**DSSLRRK**I****A****S****V****A****F****T****L****I****G****A****L****L****L****G****I****G****M****V****L****S****F****A****L**
GSSAG**L****I****G****V****G****V****L****S****A****L****G****A****V****C****L****S****L****G****L****Y****K**LFLRMKRVSLDKAEQKMLEDQVELLRQENQELKAISV
F**H**
8 APEX2 residues