S9. Candidate coproantigen sequences

Sequences corresponding to the candidate coproantigens described in file S8.

# SCP/TAPS

### >SSTP\_0001008900\_23-256

QSISYSYRYENGKLIYTYNGNDYDTKEAMEDAIQRDYPDKIFTFGGDNNNGKKRKIDISKWKGNNTFSNKIFDEIWEGYNYDNDKAKNFKVMKTKLFNEQNKYRIAHGAKKLIKSKDLEKKAQAYAEVIARLGRLEHDPKNRIEGTGENLAYGTTFIGHLAVKGWYDEIALYNFKKPGFSPATGHFTQLVWKGTTHAGFGVVEKGDRVYVVCKYSPPGNYPRQFEANVLQHAAT

### >SSTP\_0001008900\_257-396

QNREDRTEYNENIARKPSLISTNNAPGKKPLNSKTTPRSQKPVRPASKSTKRPIKTTRKTPKTTKRPVKPTRKTPKTTKRPVKTTKPTLKTTKRPVTTTKSASVTTKAPKTPAKPSSVATKESTTSKVVTVSTAKPVVTE

### >SSTP\_0001008900\_397-480

KPPNNRIDPKYIPSAAEVDKLYTFDVNKEKVKNSGPFSIKVYDEVWKGYDYKKDFKTGYLDMRDRILKETNRYRQAHGVGPLTY

### >SSTP\_0000511800\_23-255

QSISYSLRSENGKLIYTYNGNDYDTKEKLEDAIQKDYPDTIISFGGDNDNGKKRKIDISKWKGNNTFSNKIFDEIWETYNYDNDKAKNFRVMKNKFFNEQNKYRVAHGVKKLIKSQDLEDKAQVYANVIAELGDLEHDPNNEIEGTGENLAYGTTFIGHLAVKGWYDEIDLYDFSKQGHSAETGHFTQLVWKDTTHAGFGVVEKDDVVYVVCKYSPPGNYPGEFEANVFQRKQ

### >SSTP\_0000511800\_41-61

NGNDYDTKEKLEDAIQKDYPD

### >SSTP\_0000511800\_156-166

DLEHDPNNEIE

### >SSTP\_0000511800\_193-204

LYDFSKQGHSAE

### >SSTP\_0000990000\_363-743

KRKFLSLNYLNIRQRKVSNSKGVNCVTHVFEYYVRFMRGKYFMVFGGTTYPNEKDLIYDLIRQYPELKNQEVYLRGLGEITSTYMLYKVYEPAYAKVCLSDPYDKENKKSKVKGISDNEVIKHSSLKKVTFVCNKTTVPSLTHLAKCALYGQPSEVGANCERYFSKHDPPNCVEKVSFKLPNSKRCSNSEDVVLEALYSKLGTNKFTDSVWKAIWLSSINFACFSYKKYLLLKQRYLRELNSYRTAHEAPSLVESSELSKIAQSYAANLNQIKQKYRDDGKEFELIVDSTDFLTAPLLIKKWYEESSYYDYRFGRINSKCQNFAKLIWKNTAIIGIGVAKNSCKLNVVLLLYPKRRFASSNLWNIKKRRVSNLKRSRSLSE

### >SSTP\_0000513400\_24-154

FTYHIRQMSYNGKFFFIYNGKHYDTFQEVMAQVEKDKEKYYRRLERAWSTRKTITYWERPLYLKTTPYPPQPVDTVSRFIKQPGPIDRPFSRTPRPPKIIGMPSTRLPTTGKVISTSTAQPIVATQTPPEN

### >SSTP\_0000513400\_155-234

RIPRKYIPNPRAVDKLYTFDVDEEKLKDSSGPFSEKVYDDVWKDYDYKKDYKTGYLDMRDRILEETNRYREAHRVDPLTY

### >SSTP\_0001008700\_24-139

FSYQIKQVIRNGESYFIYNNKRYGTFQEAMDQVNKDMTEYFNKMTGGSSVIWITRTPKIQPLPVMTTPRPNKPVWPALKTTRPSRPRPSSRIPPKTVKPGTKSTTKSVVTQKPPKS

### >SSTP\_0001008700\_140-219

RIDPKYIPSAAEVDKLYTFDVNQEKKKKSSGPFSERVYDEVWNGYNYKNDYKTGYLDMRDRILKETNRYRQAHGVPALTY

### >SSTP\_0001008500\_1-215

MEDAIQRDYPDKIFTFGGDNNNNGKKRKIDISRWKGNNTFSNKIFDEIWANYNYDKDKAKNFKVMKNKFFNEQNKYRVAHRVKKLKKSEELERKAQAYAEVIARLGRLEHDPKNREEGTGENLAYGTTFIGHLAVKGWYDEIGLYNFNKPGFSPATGHFTQLVWKGTTHAGFGVVEKGDRVYVVCKYSPPGNYPGEYETNVLQRRHYRTFSDVMA

### >SSTP\_0001008500\_291-375

RPPSNRIDPKYIPSAAEVDKLYPFDVNKEKLKDSSGPFSEKVYDEVWKGYDFRSDFKTGYIDMRNRILEETNRYRRAHNVQPLTY

# TTL

### >SSTP\_0000700800\_1-177

MVYAQGHITCDGEPLNDIVVKLINEKKKAFDVVKDTVRTHNDGRFYLQGDFKDFYKINPQVKFWHKCFVKSWNFFKNICYYEYTLLFNAEHCTRVEPKKPEKPKKSKKHRKSKRSKKHRKSKKSKKSKKSENSEKSENSEKSEEFEDFKPYLFCDYKEIKLKKNNVSGHKNCFAWGK

### >SSTP\_0000700800\_134-177

EKSENSEKSEEFEDFKPYLFCDYKEIKLKKNNVSGHKNCFAWGK

### >SSTP\_0000700900\_81-171

YEYTLFFNADHCIKVEPKKPKKPKKSKRSKKYRKSKKSKKSKKSKKSKKSENSEKSEEFEDFKPYFFCDYKEVKLKRNDVAGRRNCFAWGK

### >SSTP\_0000485800\_71-106

FQDDMKNFTGYNIKVKLWHKCYNKQFFEKHCYYKFT

### >SSTP\_0001133200\_21-151

TTPTRVTVRGRVTCDGKPLKFIFIKLVEFIEHARDRVLEEGYTTSKGAFYFQDEMQNFTGYNIKVKLWHKCYNKQFFEKRCYYKFTPDLPFGKITQKPGKDLIYFDLKEIKLSTKGRSGERDCSNIGNLFS

### >SSTP\_0001133200\_40-106

KFIFIKLVEFIEHARDRVLEEGYTTSKGAFYFQDEMQNFTGYNIKVKLWHKCYNKQFFEKRCYYKFT

### >SSTP\_0001133200\_109-123

LPFGKITQKPGKDLI

### > SSTP\_0001222000\_22-50

FKKKPSSKPKPTPKPKPIPIYISAYGHIT

### > SSTP\_0001222000\_87-116

FIRGKVKYPPNYEPKLKFTYKCHKKAPKKT

### > SSTP\_0001222000\_51-60

CNGKDMKFIT

### > SSTP\_0001222000\_51-86

CNGKDMKFITVTLLDVRQRKKTYVMGKKKTRRTGDF

### > SSTP\_0001222000\_125-160

KFPVVDEIKRKNDTIHIYFFNEIKVDDNFKNGMNKC

### > SSTP\_0001222000\_65-159

DVRQRKKTYVMGKKKTRRTGDFFIRGKVKYPPNYEPKLKFTYKCHKKAPKKTYCLKKNDSKFPVVDEIKRKNDTIHIYFFNEIKVDDNFKNGMNK

# AChE

### >SSTP\_0000509400\_85-103

PKEYNFSGLKSWYPEKHKM

### >SSTP\_0000509400\_390-411

MINEELTNQSFIPIRKLYNKFG

### >SSTP\_0000274700\_AChE\_1-43

MMILFFLTFLIAFASCYDEPNITTYYGNITGTKITVLGQKMTE

### >SSTP\_0000274700\_AChE\_63-104

REINKDHFKTTYHAVHLANSCPQIIRLMNFSGYNDSNPTNNI

### >SSTP\_0000274700\_AChE\_187-207

QMVLKWINRTIESFNGNKSEV

### >SSTP\_0000274700\_AChE\_243-266

THFMNTVSPIIAEINTLNVSVMVN

### >SSTP\_0000274700\_AChE\_268-306

TKDTIFNKTTIRLDSKNLNYYYQNIINKEEKNNTAILEC

### >SSTP\_0000274700\_AChE\_308-328

RTKNVSELLEAANKVRAKGQM

### >SSTP\_0000274700\_AChE\_372-451

ATFFMATSFTNNTNLNCSFYPQLPTNDTKNQCDMTKKNFKHLVDYVATLLKFSKNETLKLRRIYNKYGSTYTNRTIRLLS

### >SSTP\_0000274700\_AChE\_551-607

VSNPEAIVFNETLIKKSEPLYTNVELLTCKKLLKLIQQSKEKKQISKDLFNQLRPSN

# POP

### >SSTP\_0000289100\_101-127

KPPYCKPPPCKPIPPPTCEPVPPPTCE

### >SSTP\_0000289100\_143-175

LKPSKPSKPPKPSTPQKPSTPQKPKTTPKGTTT

### >SSTP\_0001108800\_211-266

KYLSDKLENIKLTNLAFAYNGKGFFYSTYGKKKDQNNPIDNGEYMH

### >SSTP\_0001108800\_384-421

KGEKVWKELIKTDSKRKIKSVTAAGGRYLIVNYLEDLE

### >SSTP\_0001108800\_422-507

DKVYIHDKWTGKMITKLDLEPGSIVSITASTHQSRFFIKVSSQVTPQTMYTGNLLELKHNKKINMKVIIKPIISGVKKSDYVIKKI

### >SSTP\_0001108800\_741-779

VSDARERNGVVTFRSNIDETIDIFAFIKETLNIKWKYDV

# Aspartic peptidase

### >SSTP\_0000164500\_107-140

GGSVDCPKYCSNAALCPFLCQLICCDKNKETKSN

# ColQ / SsIR

### >SSTP\_0001226800\_174-266

PKPKTTTQAPEEPEGPEEPEGPEEPEGPEGPEEPEGPEEPEGPEEPEGPAGPEEPEGPAGPEEPEGPEEPEGPAGPEEPRDDDDGVDEEDERD

# Collagen

### >SSTP\_0001040300\_1-123

MEKNNKNLLNTNFENQNKFSISSRQKRQARPRQRKRLLQALRRRRQERRRRQREQQKKRAERAKKQKAYLKSMEEKAKERRRIFIQNERARLEKFRQEREQRQTTTTTTTTTTTTSTTTSTTA