

PROTEOMICS

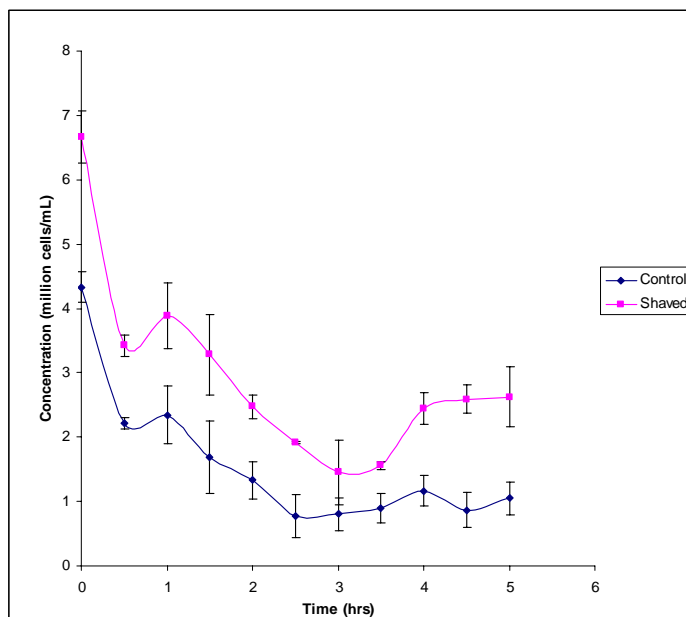
Supporting Information for Proteomics

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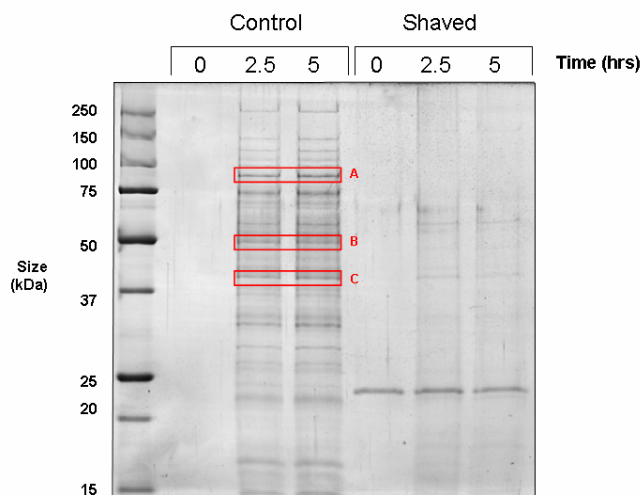
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Improved accuracy of cell surface shaving proteomics in *Staphylococcus aureus* using a false-positive control

Supplementary Figure 1A.

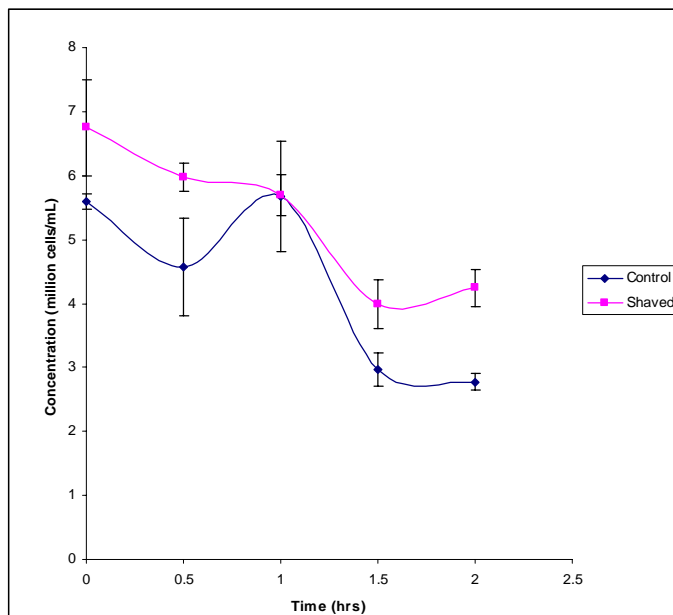


***S. aureus* COL total cell integrity assay with and without proteolytic treatment.** Counts were taken in triplicate on a hemocytometer using phase-contrast microscopy. The x-axis shows time versus the y-axis (concentration in millions of cells/mL). Cell numbers are reduced in both trypsin treated and control experiments.

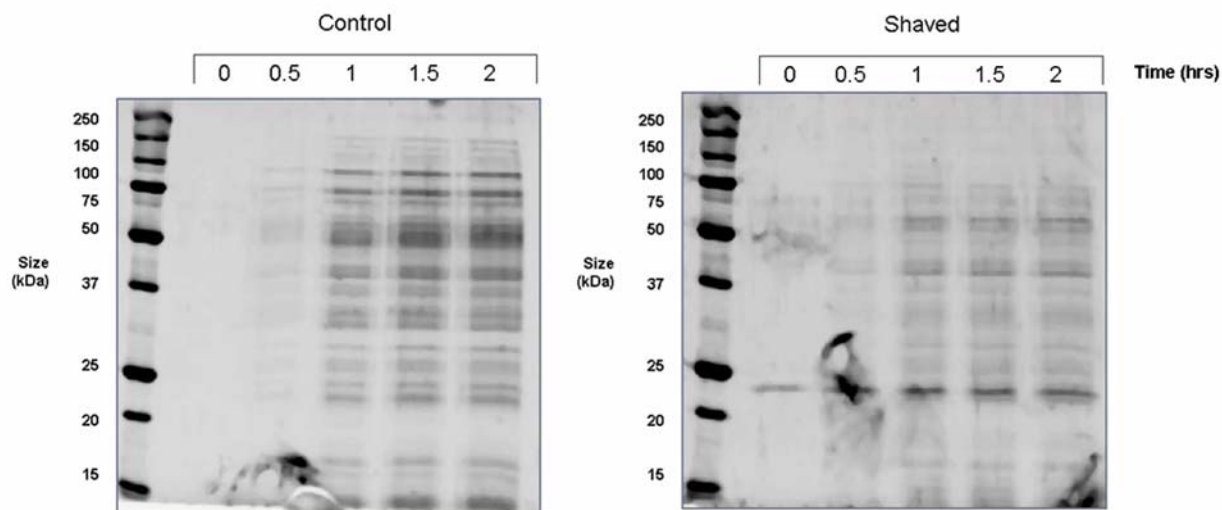


SDS-PAGE of *S. aureus* COL supernatants from cell shaving experiments conducted with (Shaved) and without (Control) trypsin. The most intense bands were excised and identified by MS. Typical cytoplasmic proteins were identified in the control treatment after 2.5 hrs (A = Elongation Factor G; B= Elongation Factor Tu; C = GAPDH; identification data not shown). At time 0 there were no proteins present in the supernatants, except for trypsin (23 kDa) in the treated sample. No major bands were seen in the Shaved samples, as the contaminating cytoplasmic proteins have been trypsin digested.

Supplementary Figure 1B.

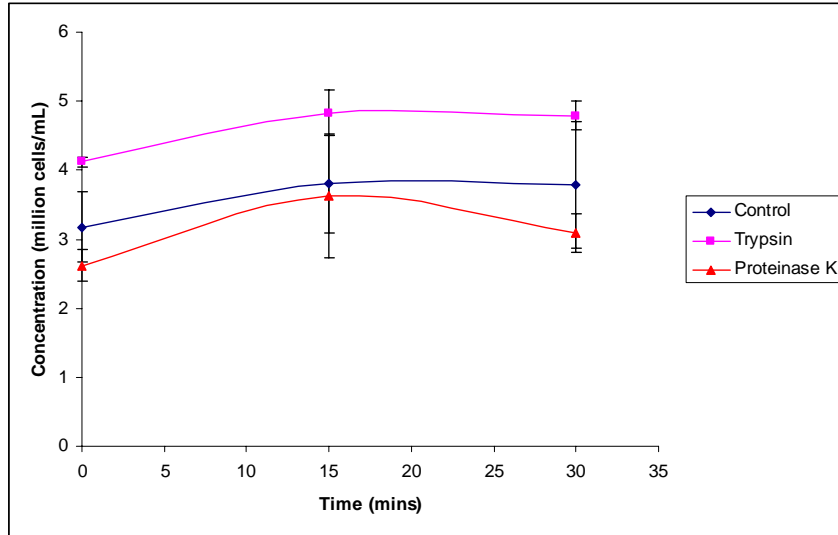


***S. aureus* COL total cell integrity assay with and without proteolytic treatment.** Counts were taken in triplicate on a hemocytometer using phase-contrast microscopy. The x-axis shows time versus the y-axis (concentration in millions of cells/mL). Cell numbers are reduced in both trypsin treated and control experiments approximately 0.5-1.5 hours after resuspension, indicating cell lysis.

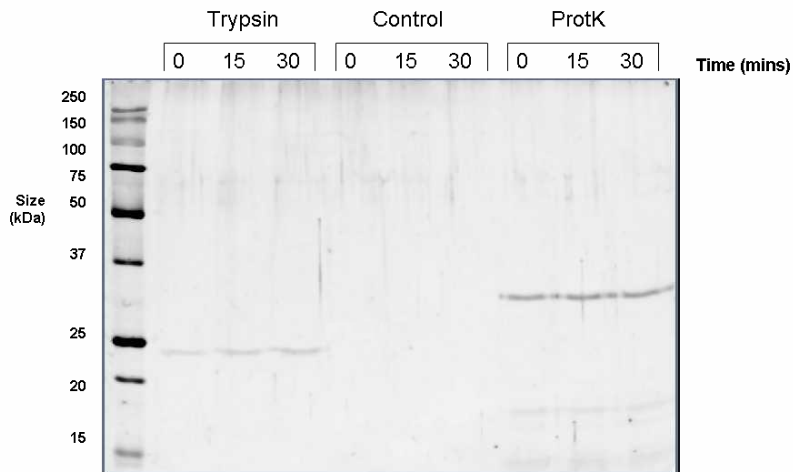


SDS-PAGE of *S. aureus* COL supernatants from cell shaving experiments conducted with (Shaved) and without (Control) trypsin. A low concentration of cytoplasmic proteins could be identified as early as 0.5 hrs post-resuspension.

Supplementary Figure 1C.



***S. aureus* COL total cell integrity assay with and without proteolytic treatment (20 μ g trypsin or 8 μ g proteinase K).** Counts were taken in triplicate on a hemocytometer using phase-contrast microscopy. The x-axis shows time versus concentration in 10^6 cells/mL. No significant drop in cell numbers is observed after 15 min treatment.



SDS-PAGE of *S. aureus* COL supernatants from cell shaving experiments conducted with trypsin and proteinase K. No visible proteins other than the enzymes used for cell shaving are present in the supernatants.

Supplementary Table 1. Peptide sequences identified by trypsin and proteinase-K cell shaving and trypsin false positive control. Peptide sequences were identified at least twice from replicate datasets and verified by manual interpretation of the MS/MS data. Sequences highlighted in grey were identified in the false positive control set and were removed to create the trypsin ‘corrected’ dataset.

<i>Protein name – Accession code</i>	<i>Peptide sequence</i>
TRYPSIN CELL SHAVED DATASET	
30S ribosomal protein S10 - [RS10_STAAC]	SGADVSGPIPLPTEK
30S ribosomal protein S12 - [RS12_STAAC]	GALDTSGVDGR
30S ribosomal protein S16 - [RS16_STAAC]	IVVADARSPR
30S ribosomal protein S17 - [RS17_STAAC]	IQETRPLSATKR
30S ribosomal protein S18 - [RS18_STAAC]	DTELLKR
	MLTTAIKR
	SRHMALLPYVK
30S ribosomal protein S19 - [RS19_STAAC]	KGPFVDEHLMK
30S ribosomal protein S20 - [RS20_STAAC]	AAQSNLIHSNKADR
	IKSQLMTANK
30S ribosomal protein S3 - [RS3_STAAC]	LGGADIAR
30S ribosomal protein S4 - [RS4_STAAC]	RPYAPGQHGPNQK
	YLYGMTER
30S ribosomal protein S5 - [RS5_STAAC]	AVLELAGITDILSK
	DLVVVPR
30S ribosomal protein S9 - [RS9_STAAC]	AGLLTRDPR
50S ribosomal protein L11 - [RL11_STAAC]	TQDQAGLIIPVEISVYEDR
50S ribosomal protein L14 - [RL14_STAAC]	EGNFMKIVSLAPEVL
50S ribosomal protein L15 - [RL15_STAAC]	AHKFSASAAEAIDAK
	SGGGVVRPGFEGGQLPLFR
50S ribosomal protein L18 - [RL18_STAAC]	DSDIATTATKVELATK
	GGYLYHGRVK
	VRTNLSGTAEKPR
50S ribosomal protein L2 - [RL2_STAAC]	ATIGQVGNLQHELNVNMGK
	GSVMNPNDHPHGGGEGR
50S ribosomal protein L24 - [RL24_STAAC]	VVVEGVNIMK
50S ribosomal protein L27 - [RL27_STAAC]	GTKIYPGENVGR
50S ribosomal protein L30 - [RL30_STAAC]	KTNSSVVVEDNPAIR
	SVIGRPETQR
	TNSSVVVEDNPAIR
	VKHLVTVEEK
50S ribosomal protein L5 - [RL5_STAAC]	FNTEVTENLMK
50S ribosomal protein L7/L12 - [RL7_STAAC]	EATGLGLKDAK
	EMSVLELNDLVK
	TEFDVELTSAGSSK
Adenylate kinase - [KAD_STAAC]	TIEQAEALNIMSELDR
Asparaginyl-tRNA synthetase - [SYN_STAAC]	VDDLELLEQR
Bifunctional autolysin - [ATL_STAAC]	AEVKNPTQNISGTQVYQDPAIVQPK
	AFNEQPFVVK
	ANQSATTNNTQPVAK
	DLTAPTAVKPTTSAAK
	DVYLYGTINNR
	DYNYTYVIK
	EQVINGQTWYYGK
	GVLENQGAAFNK
	IAQVKPNNTGIR
	IEEDYTSYFPKYAYR
	IGEVGKYFDIPQYK
	IITAPTIDYLSWVGAVGNPR
	LDQPQNISIDKINQFLK
	LTVAANNGVAQIKPTNSGLYTTVYDK
	NGNGYYYVTPNSDTAK

	NGVGRPEGIVVHDTANDR
	NNGLFTTVYDK
	NPTQNISGTQVYQDPAIVQPK
	NQVILTGNNIAQGTFNATK
	SAAKPAALETQYK
	SNNGLSMVPWGK
	TNTNVTNAGYSLVDEDDNSENQINPELIK
	VTTFSASAQPR
	WTGANFNDVK
Clumping factor B fibrinogen-binding protein [CLFB_STAAC]	NSQTLDPQSSPQTISNAQGTSKPSVR
Dihydrolipoyl dehydrogenase - [DLDH_STAAC]	NAIATGSRPIEIPNFK
Dihydrolipoyllysine-residue acetyltransferase [ODP2_STAAC]	SIFQISDEINELAVK
DNA-binding protein HU - [DBH_STAAC]	EAGSAVDVAFESIQNSLAK
	TDLINAVAEQADLTKK
	VQLIGFGNFEVR
Elastin-binding protein ebpS - [EBPS_STAAC]	IAIQYYGSGSPENVEK
Elongation factor G - [EFG_STAAC]	ASLIEVAETSDELMEK
	YLGDEEISVSELK
Elongation factor Tu - [EFTU_STAAC]	AEVYVLSKDEGGR
	EHILLSR
	NGDSVAQSYDMIDNAPEEK
	TTLTAAIATVLAK
	VGEEVEIIGLHDTSK
Enolase - [ENO_STAAC]	GIENGIGNSILIK
	GNPTVEVEVLTESGAFGR
	SGETEDTTIADIAVATNAGQIK
	VNQIGTLTETFDAIEMAQK
	VQLVGDDLFVTNTEILAK
Foldase protein prsA - [PRSA_STAAC]	AGDVTVADTMKK
Fructose-bisphosphate aldolase class 1 - [ALF1_STAAC]	ALGDVAVESIYDASVNK
Glyceraldehyde-3-phosphate dehydrogenase 1 - [G3P1_STAAC]	AAAENIIPNSTGAAK
	FTGEVEVVDGGFR
	VPVATGSLTELTVVLEK
Glycerol phosphate lipoteichoic acid synthase [LTAS_STAAC]	DLEMSDNVNLNGDLFR
	EVTPLNK
	FYKNPDFK
	GDNTYQSLPAILDQK
	GHNQVVPFR
	IYSNKNNELITTQPADFEK
	NNELITTQPADFEK
	NYLMFGTDLFSK
	SNTGDATVDGYIQTAR
Glycyl-glycine endopeptidase lytM - [LYTM_STAAC]	AGDQIAYSGSTGNSTAPHVHFQR
	DASWLTSR
	MSGGIGNQYAVDPTSYLQSR
Immunodominant staphylococcal antigen B - [ISAB_STAAC]	EADSGIFYYQNAK
	GNEASQLQFVVK
	NNISLKDIQK
Immunoglobulin G binding protein A - [Q5HIQ8_STAAC]	EDGNGVHVVKPGDVTNDIAKANGTTADK
	NGFIQSLK
	DDPSQSANVLGEAQK
<i>N</i> -acetylmuramoyl- <i>L</i> -alanine amidase sle1 - [SLE1_STAAC]	SLNNLTSNLIFPNQVLK
Probable cell wall hydrolase lytN - [LYTN_STAAC]	EAPKTQIYTVK
Probable quinol oxidase subunit 2 - [QOX2_STAAC]	DVSDKPLIPAR
Probable thiol peroxidase - [TPX_STAAC]	AVFVLDADNK
Probable transglycosylase isaA - [ISAA_STAAC]	AQGLGAWGF
	DGAYDIHFVK
	ESNGQVNAYNPSGASGLFQTMPGWGPTNTVDQQINAQVK
	LSNGNTAGATGSSAAQIMAQR
	TGVSASTWAAIAR
Probable transglycosylase sceD - [SCED_STAAC]	GVSPANAPESVQDAAAVK
	YQFLQSTWDSVAPAK
Putative branched-chain amino acid carrier protein - [BRNQL_STAAC]	INFIESLPLR

Putative surface protein SACOL0050 - [PLS_STAAC]	AATEEAPKAEETEK	
	AATEEAPKAEETSK	
	AATEETPAVEDTNAK	
	ADTTEQATTEEAPK	
	ADTTEQATTEEAPKAEGTDK	
	AEETDKATTEEAPK	
	AEETKATTEEAPK	
	AEETNKVETEEAPAAEETNK	
	AEGTDK VETEEAPK	
	AEIEKVLPK	
	AGEPEVTKEEIPFEK	
	ANTTEQASTEELKADTTEQATTEEAPK	
	ATTEEAPAAEETSK	
	ATTEEAPKAETDK	
	DGLKDPETGEIIEEPQDEVIHGAK	
	DISNLSNEEIK	
	DISNLSNEEIKK	
	EEFPNEGTLTAFNTNFPNTGTK	
	EFDPTLEPGSPDVIVQK	
	EFNPDLKPGEEK	
	EFNPDLKPGEEKVTQEGQTGEK	
	GNVQTIEQSSANSNESDIPEQVDVTK	
	GNVQTIEQSSANSNESDIPEQVDVTKDTTEQASTEELK	
	HGPKAGEPEVTK	
	IALSEVLK	
	IALSEVLKETANK	
	LNDVVLNYDAATSTITATYAGKTKW	
	NGADGVTNQVGQNALNTK	
	NPETGEVVTTPVDDVTK	
	SEVTEAEKAEIEK	
	SQKYNFLITSSHMQR	
	TEETDKATTEEAPAAEETSK	
	TEETDKATTEEAPK	
	TNLEGVTITTPQADLIDDVEVTK	
	TQVVDTVAK	
	TQVVDTVAKDLYK	
	TTNVNYSATALR	
	TTTTPTKVDPTGDVVER	
	TTTTPTTINPLTGEK	
	VETEEAPAAEETNK	
	VETEEAPKAETSK	
	VGYGTFVK	
	VGYGTFVKNQADGVTNQVGQNALNTK	
	VKGNVQTIEQSSANSNESDIPEQVDVTK	
	VTQEGQTGEKTTTTPTTINPLTGEK	
	YNFLITSSHMQR	
	YSNGIMR	
	Pyruvate dehydrogenase E1 component subunit beta - [ODPB_STAAC]	TVQPIDVDTIVASVEK
	Ribonuclease J 1 - [RNJ1_STAAC]	KPMILPVIMK
	Ribosome-recycling factor - [RRF_STAAC]	AIIAANLGVNPTSDGEVIR
	Serine-aspartate repeat-containing protein E - [SDRE_STAAC]	ENVKPSTDKTATEDTSVILEEK NDSNTDHSKPVATAPTSVAPK TATEDTSVILEEK
	Staphylococcal secretory antigen ssaA2 - [SSAA2_STAAC]	AGAIMQTTQGAYGHVAYVESVNSNGSVR IGSTWGNASNWANAAAR TGGLGASYSTSSNNVQVTTTMAPSSNGR TISASQAAGYNFIH VSEMNYGYGPGVVTSR
	Superoxide dismutase [Mn/Fe] 1 - [SODM1_STAAC]	LNAAVEGTDLESK SIEEIVANLDSVPANIQTAVR VDELYNATK
	Trigger factor - [TIG_STAAC]	ATDNTTIDIPEAMVNTELDR
	Virulence factor esxA - [ESXA_STAAC]	AQGEIAANWEGQAFSR FAQLLEEIK FEEQFQLSPK

	MSPEIR
	QILSDLTR
	SQSYGQGSDQIR
	SQSYGQGSDQIRQILSDLTR
5'-nucleotidase family protein - [Q5HJX2_STAAC]	EAATNVSASAQGTADDTNSK
Amino acid ABC transporter, amino acid-binding protein - [Q5HDE2_STAAC]	DIKDFDDVK
	TINVGTEGTYAPFSFHDK
Cell wall surface anchor family protein - [Q5HF18_STAAC]	RVETNGIATLK
Competence/damage-inducible protein CinA - [Q5HGE7_STAAC]	QTNPTIAPLAGSHEVYIR
Iron compound ABC transporter, iron compound-binding protein - [Q5HDS3_STAAC]	GGEVLYQAFGLK
	LGANIVAVNQVDQSK
LPXTG cell wall surface anchor family protein - [Q5HCQ1_STAAC]	SDLMSEVNK
Penicillin-binding protein 2 - [Q5HFX3_STAAC]	ANLVNRTPEER
	TGGLVAISGGR
Penicillin-binding protein 2' - [Q5HJW3_STAAC]	ATSHLLGYVGPINSEELK
	DINIQR
	DIQLTIDAK
	DKEINNTIDAIEDK
	DQSIHIENLK
	EDGMWK
	EINNTIDAIEDK
	ELSISEDIYIK
	ENINLLTDGMQQVVNK
	IKTNYGNIDR
	KFHLLTNETESR
	KMDEYLSDFAK
	LDWDHVSIIIPGMQK
	LGVGEDIPSDYPFYNAQISNK
	MDEYLSDFAK
	NNVELANTGTAYEIGIVPK
	NVQFNFKEDGMWK
QAISSDNIFAR	
QQMDQNWVQDDTFVPLK	
SDNGEVEMTERPIK	
VTIVDDNSNTIAHTLIEK	
VYDELYENGNK	
YEVVNGNIDLK	
Protein-export membrane protein SecDF - [Q5HFC6_STAAC]	VQLAGVTDQNEAR
Putative uncharacterized protein - [Q5HGC5_STAAC]	EPIECGADLIAGSLIK
Putative uncharacterized protein - [Q5HH06_STAAC]	TEDINQTKQDIQDTLN
Putative uncharacterized protein - [Q5HJ81_STAAC]	DIDNLVAQSK
	VEYEINGER
FALSE POSITIVE CONTROL DATASET	
30S ribosomal protein S10 - [RS10_STAAC]	LIDIVNPTPK
	SGADVSGPIPLPEK
	SVYTIIR
30S ribosomal protein S11 - [RS11_STAAC]	ALQSAGLEVTAIR
	STPFAAQMASSETASK
30S ribosomal protein S12 - [RS12_STAAC]	FTDLNSPQK
	GALDTSGVDGR
30S ribosomal protein S13 - [RS13_STAAC]	LMEISSYR
30S ribosomal protein S16 - [RS16_STAAC]	IIEQIGTYNPTSANAPEIK
	IVVADARSPR
30S ribosomal protein S2 - [RS2_STAAC]	KVDEAYNFLK
30S ribosomal protein S20 - [RS20_STAAC]	TAVSNNADNKNELVSLAVK
	AAQSNLIHSNKADR
	IKSQLMTANK
30S ribosomal protein S21 - [RS21_STAAC]	EFYEKPSVK
	KNESLEDALR
	NESLEDALR
30S ribosomal protein S3 - [RS3_STAAC]	AEQYSEGTVPLHTLR
	DFASLLHEDLK

	INPIGLR
	LGGADIAR
30S ribosomal protein S4 - [RS4_STAAC]	LDAVVVYSLGLAR
	LGISLSGTGK
	LSEYGLQLR
	RPYAPGQHGPNQK
	YLYGMTER
30S ribosomal protein S5 - [RS5_STAAC]	AVLELAGITDILSK
	DLVVVPR
	SLGSNTPINMVR
30S ribosomal protein S6 - [RS6_STAAC]	LAYEINDFK
30S ribosomal protein S7 - [RS7_STAAC]	LANEILDAANNTGGAVK
	TTLGLR
	VGGSNYQVPVEVRPER
30S ribosomal protein S9 - [RS9_STAAC]	AGLLTR
	ALLEADPEYR
50S ribosomal protein L1 - [RL1_STAAC]	AGIVHASIGK
	SQSVLVFAK
	TGTVTMDVK
50S ribosomal protein L10 - [RL10_STAAC]	SGVMEGNVITAEVVK
50S ribosomal protein L15 - [RL15_STAAC]	AHKFSASAAEIDAK
	EYAIVNLDQLNK
	SGGGVVRPGFEGGQLPLFR
50S ribosomal protein L17 - [RL17_STAAC]	LFGEIAER
	NVEILNEDETTQTALQK
50S ribosomal protein L19 - [RL19_STAAC]	ISSGVGVER
	LYYLR
50S ribosomal protein L2 - [RL2_STAAC]	ATIGQVGNLQHELVNVGK
	GSVMNPNDDHPHGGGEGR
	NMTSLDFAEITK
	SAGASAQVLGK
	VDSIQYDPNR
50S ribosomal protein L20 - [RL20_STAAC]	AFAQLVTK
	INAAARQHEMSYSR
	MLSEIAISDEK
50S ribosomal protein L21 - [RL21_STAAC]	ITVFTYK
	VEEGQEIVFEK
	VLFVGGDSVK
50S ribosomal protein L22 - [RL22_STAAC]	EAYANEGPTLK
	NAAEAIAILK
50S ribosomal protein L23 - [RL23_STAAC]	MAVEEIFNVK
50S ribosomal protein L24 - [RL24_STAAC]	VVVEGVNIMK
50S ribosomal protein L25 - [RL25_STAAC]	TVEVPVQLVGEAVGAK
	VDEVEFIK
	VPAVVYGYGTK
50S ribosomal protein L27 - [RL27_STAAC]	ADGQFVTGGSILYR
	IYPGENVGR
50S ribosomal protein L28 - [RL28_STAAC]	KVWVSAR
50S ribosomal protein L29 - [RL29_STAAC]	DLTSEIEEIQK
	FQLATGQLEETAR
50S ribosomal protein L3 - [RL3_STAAC]	APGSVGMASDASR
	KGLVEIR
50S ribosomal protein L30 - [RL30_STAAC]	HLVTVEEK
	KTVEALGLK
	LQITLTR
	SVIGRPETQR
	TNSSVVVEDNPAIR
	TVEALGLK
50S ribosomal protein L31 type B - [RL31B_STAAC]	LDISSDHPFYTGR
50S ribosomal protein L35 - [RL35_STAAC]	AFTSHLFANK
50S ribosomal protein L4 - [RL4_STAAC]	GGGIVFGPTPR
	NVLSTLEQPK
50S ribosomal protein L5 - [RL5_STAAC]	FNTEVTENLMK
	MYEFLDK
50S ribosomal protein L6 - [RL6_STAAC]	AEENITFSVEK
	EQVGALASNIR

	VLELVGVGYR
50S ribosomal protein L7/L12 - [RL7_STAAC]	EATGLGLK
	ELVDGAPK
	EMSVLELNDLVK
	TEFDVELTSAGSSK
6-phosphogluconate dehydrogenase, decarboxylating - [6PGD_STAAC]	AADLPANLIQAQR NLAWNIESR
77 kDa membrane protein - [OMP7_STAAC]	IDIDVK
Acyl carrier protein - [ACP_STAAC]	FINSLEK
	INTVGDAVK
	LGVDADKVTEDASFK
	VKDIIIVDR
Alkaline shock protein 23 - [ASP23_STAAC]	GILDMK
	IAGIAAR
	LTFSEDEVVEK
	VILEYGESAPK
Alkyl hydroperoxide reductase subunit C - [AHPC_STAAC]	TLQPGLDLVGKI
Amidophosphoribosyltransferase - [PUR1_STAAC]	GLGLLTEAIKDDQMER
ATP synthase subunit alpha - [ATPA_STAAC]	IMEVPVGEELIGR
ATP synthase subunit beta - [ATPB_STAAC]	IGLFGGAGVGK
	LVGSMDDVIK
	VTQVMGPVIDVR
ATP-dependent Clp protease ATP-binding subunit - [CLPX_STAAC]	DVSGEGVQQALLK
Bifunctional autolysin - [ATL_STAAC]	NPTQNISGTQVYQDPAIVQPK
Cell division protein ftsZ - [FTSZ_STAAC]	VIGVGGGGNNAVNR
Chaperone protein dnaK - [DNAK_STAAC]	IINEPTAAALAYGLDK
Cold shock protein cspA - [CSPA_STAAC]	GPQAANVVK
Dihydrolipoyl dehydrogenase - [DLDH_STAAC]	ALSLDDTNGFVK
	LTGGVEGLLK
	NAIATGSRPIEIPNFK
	RPNTDELGLEELGVK
Dihydrolipoyllysine-residue acetyltransferase [ODP2_STAAC]	GLLVPVVK
	IDAPDAEDMQFK
	SIFQISDEINELAVK
DNA-binding protein HU - [DBH_STAAC]	EAGSAVDAVFESIQNSLAK
	TDLINAVAEQADLTK
	TDLINAVAEQADLTCK
	VQLIGFGNFEVR
DNA-directed RNA polymerase subunit alpha - [RPOA_STAAC]	FVVEPLER
	ILLSSLPGAAVK
DNA-directed RNA polymerase subunit beta' - [RPOC_STAAC]	IIVEIGQPVQR
DNA-directed RNA polymerase subunit omega - [RPOZ_STAAC]	ALEEIADGK
Elongation factor G - [EFG_STAAC]	ADDSAEFAALAFK
	ASLIEAVAETSDELMEK
	ASNPEEEVIK
	EYIPSVEAGLK
	LTFFR
	MTQALVK
	VYSGTMTSGSYVK
YLGDEEISVSELK	
Elongation factor Ts - [EFTS_STAAC]	LVDFVR
	NEGFQELVK
Elongation factor Tu - [EFTU_STAAC]	AEVYVLSK
	ALEGDAQYEEK
	EHILLSR
	GQVLAAPGSITPHTEFK
	NGDSVAQSYDMIDNAPEEK
	TTLTAAIATVLAK
	TTVTGVEMFR
	TVGSGVVTEIHK
VGEEVEIIGLHDTSK	
Enolase - [ENO_STAAC]	AAADLLGQPLYK
	GIENGIGNSILIK

	GLETAVGDEGGFAPK
	IEDEFETAK
	MMIALDGTPNK
	VNQIGTLTETFDAIEMAQK
Foldase protein prsA - [PRSA_STAAC]	AGDVTVADTMK
Fructose-bisphosphate aldolase class 1 - [ALF1_STAAC]	ALGDAVESIYDASVNKN
Fructose-bisphosphate aldolase - [ALF2_STAAC]	GFIAALDQSGGSTPK
	INVNTENQIASAK
Glyceraldehyde-3-phosphate dehydrogenase 1 - [G3P1_STAAC]	FTGEVEVVDGGFR
	TLAYLAELSK
	VLISAPATGDLK
Immunodominant staphylococcal antigen B - [ISAB_STAAC]	EADSGIFYYQNAK
	GNEASQLQFVVK
	NFINAIK
Molybdenum cofactor biosynthesis protein A - [MOAA_STAAC]	INVSLDAIDDTLQFQSIINRNK
Naphthoate synthase - [MENB_STAAC]	LNVLDLQR
Phosphoenolpyruvate-protein phosphotransferase - [PT1_STAAC]	EFVQGFATNIGGR
Phosphoglucosamine mutase - [GLMM_STAAC]	DMGAELGVMISASHNPVADNGIK
Phosphoglycerate kinase - [PGK_STAAC]	ADFNVPLKDGIEITNDNR
Probable malate:quinone oxidoreductase 2 - [MQO2_STAAC]	NEDWQLYTAGK
Probable thiol peroxidase - [TPX_STAAC]	AVFVLADANK
Probable transglycosylase isaA - [ISAA_STAAC]	DGAYDIHFVK
Putative dipeptidase SACOL1801 - [PEPVL_STAAC]	ASEDAPVGPGR
Putative surface protein SACOL0050 - [PLS_STAAC]	AATEETPAVEDTNAK
	ADTTEQATTEEAPK
	AEETDKATEEAPK
	AEETNKVETEEAPAAEETNK
	AEGTDKVEEAPK
	AGEPEVTKEEIPFEK
	DGLKDPETGEIIEEPQDEVIHGA
	EFDPTLEPGSPDVIVQK
	GNVQTEIQSSANSNESDIPEQVDVTK
	IALSEVLK
	NPETGEVVTPVDDVTK
	TQVVDTVAK
	TTNVNYSATALR
	TTTTPTTINPLTGEK
VDPDTGDVVER	
Pyridoxal biosynthesis lyase pdxS - [PDXS_STAAC]	GLDINQLSLEER
Pyruvate dehydrogenase E1 component subunit alpha - [ODPA_STAAC]	AVAGEGPTLIETMTYR
	GLWNEDKENEVIER
Pyruvate dehydrogenase E1 component subunit beta - [ODPB_STAAC]	AILSLEAPIGR
	AVVVQEAQR
	TVQPIDVDIVASVEK
Pyruvate kinase - [KPYK_STAAC]	DGIIELEER
	GSVVGTTLVAETVK
	STDALLNNAVATAVETGR
Ribose-phosphate pyrophosphokinase - [KPRS_STAAC]	LVANLIETAGATR
S-adenosylmethionine:tRNA ribosyltransferase-isomerase - [QUEA_STAAC]	LDELGEMPLPPYIK
Staphylococcal secretory antigen ssaA2 - [SSAA2_STAAC]	TISASQAAGYNFIH
	VSEMNYGYGPGVVTSR
Transcriptional regulator sarA - [SARA_STAAC]	ILSQEDYFDK
Translation initiation factor IF-1 - [IF1_STAAC]	VTVEMSPYDLTR
Trigger factor - [TIG_STAAC]	EGNEGLLTVTVPAEK
	ATDNTTIDIPEAMVNTELDLDR
Triosephosphate isomerase - [TPIS_STAAC]	TPIIAGNWK
Tyrosyl-tRNA synthetase - [SYT_STAAC]	ISQALFSGDLKSLSAK
UPF0337 protein SACOL0912 - [Y912_STAAC]	ATDFIDK
	EFVENAK
	EFVENAKEK
UPF0337 protein SACOL1680 - [Y1680_STAAC]	ETVGNVTDNK
	FDQFK

UPF0478 protein SACOL1789 - [Y1789_STAAC]	TLDGVEGQVQGITR
Virulence factor esxA - [ESXA_STAAC]	FAQLLEEIK FEEQFQQLSPK
Amino acid ABC transporter, amino acid-binding protein - [Q5HDE2_STAAC]	FDVIANQVGINPDR LTGYDIDVIK
GTP pyrophosphokinase - [Q5HFC9_STAAC]	ETLEIYAPLAHRLGINTIK
Immunoglobulin G binding protein A - [Q5HJQ8_STAAC]	EDGNGVHVVKPGDVTNNDIAKANGTTADK
Penicillin-binding protein 2' - [Q5HJW3_STAAC]	DINIQR DKEINNTIDAIEDK EINNTIDAIEDK SDNGEVEMTERPIK
Putative uncharacterized protein - [Q5HHK7_STAAC]	EMQEEITLNQSKIGGMPFLK
Putative uncharacterized protein - [Q5HIE1_STAAC]	FDVENNYLNK
Putative uncharacterized protein - [Q5HJ97_STAAC]	LFMTFIYALAMGIVYLIIFM
Tetracenomycin polyketide synthesis O-methyltransferase TemP, putative - [Q5HEH8_STAAC]	EKISWIDLDPESIEIR
Threonine synthase - [Q5HG91_STAAC]	ESNGLIDSVTDDEILEAYQLMTTK IVICASTGNTSASAAAAYAARAGLK
Transcriptional regulator, putative - [Q5HGE9_STAAC]	REMLVHIENNEFDQLPNK
Transferrin receptor - [Q5HHT4_STAAC]	ENPDVILAMDR
PROTEINASE-K SHAVED DATASET	
50S ribosomal protein L15 - [RL15_STAAC]	EGSRKERNRVGRGVA KPAEGSRKERNRVGRGV
50S ribosomal protein L24 - [RL24_STAAC]	TLPKKDRVV
50S ribosomal protein L33 1 - [RL331_STAAC]	MRVNVTL
50S ribosomal protein L7/L12 - [RL7_STAAC]	GLKDAKEL
6-phosphogluconate dehydrogenase, decarboxylating - [6PGD_STAAC]	NASKELNGPKA
Alanine dehydrogenase 1 - [DHA1_STAAC]	ACTPENVRKL
Aminoacyltransferase femB - [FEMB_STAAC]	NDKENRRDQMMAKENKSDKQMKKI
Arginine deiminase - [ARCA_STAAC]	WLDRDCPF WLDRDCPFNI
Bifunctional autolysin - [ATL_STAAC]	DNDPLREGIKY IKMGKV KMRWNPAPHPGTHQYA NVQNLGKEV RLDQPONISI
Cell wall-related protein scdA - [SCDA_STAAC]	DTFKNGMLEHMQKEDDV KETYDTFKNGML NELLQRL
Choline dehydrogenase - [BETA_STAAC]	KRMPFI LHPSCSAKMGPA
Exodeoxyribonuclease 7 large subunit - [EX7L_STAAC]	KNDLKNKVENL LIKGEL RAATPTQA
Extracellular matrix-binding protein ebh - [EBH_STAAC]	AHMQNATGL DEQPAVNEI DGQQNLQRAKTEA DSPVQNGPFEI DQLPNLNQA EGVNTVKA EQINTNTSTANQA EVSQGNVQTKKV GGNTPKADVERA GQTTSPSMNAQEINQA GVNTVKQQTDL IGETTNPMTDV INGQKPAESPGV ISGTPNATL ITPSDVNNA KDALRQMTHL KDAVSGMTHL KDNEHSPL KGQNLNNGTDAMNY KNTTITLTPNGWTSNL KQDAKTTL

	KQSVKF
	KTNATNTINNA
	KTPSNKVL
	LTQLNTPQKA
	MGNLKNSL
	NNAQKDAL
	RTRNPIRLMI
	TELNSAMTA
Glycerol phosphate lipoteichoic acid synthase - [LTAS_STAAC]	AETDRPEL
	FAETDRPEL
	KFTDL
	KGDNTYQSLPA
	KKKGLY
	KYVNGKI
	LGEKITPA
	MNPYSLV
Histidyl-tRNA synthetase - [SYH_STAAC]	KGQMKQADRL
Immunodominant staphylococcal antigen B - [ISAB_STAAC]	DQTFKGV
	KFNGIKL
Iron-regulated surface determinant protein H - [ISDH_STAAC]	EGQYHVRI
	KDAIKDPA
	YELEKL
Leucyl-tRNA synthetase - [SYL_STAAC]	KTNDNLGQKKFY
Lipase 1 - [LIP1_STAAC]	DQTSQREI
	EKQVNMGNSQEDTV
	GKATEKEWRENDGL
	KNQDPIV
Na(+)/H(+) antiporter subunit B1 - [MNHB1_STAAC]	ETMRKI
	MNRQQNDLIL
NADH dehydrogenase-like protein SACOL0944 - [Y944_STAAC]	QAEVTKI
	QDRKKVL
Phenylalanyl-tRNA synthetase beta chain - [SYFB_STAAC]	FDKVTSGQL
	IDYTKDI
Probable quinol oxidase subunit 2 - [QOX2_STAAC]	KDPNFTSEENMF
	KDPNFTSEENMFKDV
	KEmKKI
	TIPKDRPVV
Protein translocase subunit secA 1 - [SECA1_STAAC]	DTMDQLRQGIHL
	EAKEGVQI
	ERMILL
	HLTEQGADKA
	LSLQDEL
	RGRSGRQGDGDSRFYL
Putative surface protein SACOL0050 - [PLS_STAAC]	DPNLPIDGTEEV
	DTTEQATTEEAPKA
	EEPQDEVI
	ETEEAPKA
	KDPETGEII
	LNTKDKPVNKI
	NDKIDF
	NTKDKPVNKII
	PGKPGIKNPETGEV
	PKTEETDKATTEEA
	QNNGTLFGSL
	SNEEIKKI
	SNEEIKKIA
Response regulator arlR - [ARLR_STAAC]	ENKNHVMQREQIL
Ribulokinase - [ARAB_STAAC]	MKDIQSL
Staphylococcal secretory antigen ssaA2 - [SSAA2_STAAC]	GYNPNDPTSY
Thioredoxin - [THIO_STAAC]	KDQQPVDKVV
Transcriptional repressor nrdR - [NRDR_STAAC]	RDEGHTEVSSRDI
UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2 - [MURA2_STAAC]	NNIVPKHV
Uncharacterized epimerase/dehydratase SACOL059 - [Y599_STAAC]	ASMTKLML
Uncharacterized protein SACOL1240 - [Y1240_STAAC]	INTEDII

	IPTKSIQGI
	KANESLENTPNL
	LMGARGNSGV
UPF0342 protein SACOL1902 - [Y1902_STAAC]	KANEESKKL
UvrABC system protein C - [UVR_C_STAAC]	FIRQGNMI
	LMKDRNDQVI
	PYRKCDKMPDKLCL
5'-nucleotidase family protein - [Q5HJX2_STAAC]	DDTNSKVTSNA
	DKATTDKQQVPPTKEA
	GYDAMA
	KGKVTRYDL
	KTVKEQEKPDL
ABC transporter, ATP-binding protein - [Q5HEF4_STAAC]	DEPTNHLDIDSKEML
	DFEVKTGERI
	GDVKRYV
	KEETDWLSKHANDY
	KTGERIGIV
	KTHMSRYESL
	PLMNEKDIRA
ABC transporter, ATP-binding/permease protein - [Q5HDC4_STAAC]	KDIESKQLNDL
	NLTFKENI
ABC transporter, substrate-binding protein - [Q5HI37_STAAC]	KMMKSNL
	KMMKSNLTVHGSMK
	KNVGGDNVDI
	NDIPKEQRAMI
Acetyl-CoA carboxylase, biotin carboxylase - [Q5HFP5_STAAC]	LNIPNI
AcrB/AcrD/AcrF family protein - [Q5HDU7_STAAC]	DQNKAAENGI
	ISAGDDKF
	KHPGEWKNQDLGTGA
	MSKINNLDKPNNV
Amino acid ABC transporter, amino acid-binding protein - [Q5HDE2_STAAC]	KFSKPY
	LDYKKQKPNNA
Capsular polysaccharide biosynthesis protein C - [Q5HJK7_STAAC]	ANELTKI
Cchloylglycine hydrolase family protein - [Q5HJA0_STAAC]	KLTDDL
	KYYGSNEL
	LKLTDDL
Exonuclease RexB - [Q5HHB8_STAAC]	GMNDGTMPQPV
	RKPSEVL
FeS assembly ATPase SufC - [Q5HHH2_STAAC]	DKNMDFL
	EDKEIL
	IMGPNGTGKSTL
	KREEGQEINL
Gramicidin S synthetase 2 related protein - [Q5HJJ4_STAAC]	ANHIMSQQHDV
	DREQLLAMI
	EKSIEMII
	EVIPETI
	FFKQEL
	IMQGERRCVGI
	KDSNINQLMY
	KTNRFSMVMNDL
	KTTNGAMMSFTMNQMRQL
	LDFHV
	LLNGGKL
	LWRLSSEL
	MLDNEMY
	MMSFTMNQMRQLL
	RGNTVINNTRQHA
	RTQYI
Heat shock protein, Hsp20 family - [Q5HDG8_STAAC]	NGNPSDTFKDL
ImpB/MucB/SamB family protein - [Q5HG55_STAAC]	AKTIDQL
	DTKRQGSVI
	INEDERQLSL
Iojap-related protein - [Q5HFG9_STAAC]	NEQNIEVKRMEGY
Iron compound ABC transporter, iron compound-binding	DIPKDPKRIA

protein - [Q5HDS3_STAAC]	DYNKHKY
	FDEFDKKL
	GDNWGRGGEVL
	KEKPDLII
Leukotoxin LukD - [Q5HEV0_STAAC]	KMDDGKTVDI
	KDKSYDKDTL
	LLSNTV
Lipoprotein, putative - [Q5HD92_STAAC]	QREMDRYTNQWNRL
	IEHLDI
Na/Pi cotransporter family protein - [Q5HJR4_STAAC]	ELTEEYV
	FKRSKINNI
	IQSSSGTTV
	MLDMSTNPIL
	NNIGRI
Pathogenicity island protein - [Q5HHI7_STAAC]	SLDGFQQL
	QIMPAPENL
Penicillin-binding protein 2 - [Q5HFX3_STAAC]	AEDRKNTV
	DKNGELVKTL
	EGDIGPSEVL
	GGSASEFSPTQL
	LDSKTGGL
Penicillin-binding protein 2' - [Q5HJW3_STAAC]	NYEGDI
	DDNSNTIAHTL
	DKKLQHEDGYRV
	DRNNVEL
	DRNNVELA
	EDKNFKQVY
	GVKDINI
	INPVQI
	KDVQDKGMASY
	MIGLNNKTL
NAPHLL	
Penicillin-binding protein 4 - [Q5HI26_STAAC]	SNKNLDNEIL
	DTKWNPASMTKLMTRY
	GDYKNLGGEKQRNMMGNA
	KETPKIL
Peptide ABC transporter, ATP-binding protein - [Q5HD88_STAAC]	KNLGGEKQRNMMGNA
	KSMWEEHPL
Peptide ABC transporter, peptide-binding protein - [Q5HD84_STAAC]	KNGKIEEQI
	NDQPMHKKKV
Prophage L54a, major capsid protein, putative - [Q5HIZ5_STAAC]	KNGTTKDGVKKF
	LDEAGWKKGKDSDV
	TKMSAMLL
Putative uncharacterized protein - [Q5HD08_STAAC]	KDKGEAYQSL
	QDIEEKEKAKV
Putative uncharacterized protein - [Q5HEC8_STAAC]	SKEIVSEPF
	FNQFTNV
Putative uncharacterized protein - [Q5HF62_STAAC]	NEGMPLSGFHRHF
	EEGHSY
	EQQTIMERL
Putative uncharacterized protein - [Q5HFK0_STAAC]	IMPLPL
	LQSNIQTENL
Putative uncharacterized protein - [Q5HHF7_STAAC]	FVDKDKL
	ITKETQQAI
	KDVIDI
Putative uncharacterized protein - [Q5HHN2_STAAC]	AFKMEI
	ARFTEPY
Putative uncharacterized protein - [Q5HI14_STAAC]	GGDTEKRTVSGA
	MMMNKEATKI
	EKNKRVI
Putative uncharacterized protein - [Q5HI71_STAAC]	LNMTSIGNEKV
	ENEMLLEV
Putative uncharacterized protein - [Q5HJ11_STAAC]	KSFNEVKL
	DKLELI
Putative uncharacterized protein - [Q5HJH5_STAAC]	PFQYL

Putative uncharacterized protein - [Q5HJV8_STAAC]	KEDENILSI
S1 RNA binding domain protein - [Q5HED8_STAAC]	KGAQDII
	KLNSLDMDEL
	KNPMDIVSV
SasB protein - [Q5HE44_STAAC]	ENITDSTQTKMDA
	EQDVITPTV
	KEKMTSTNL
	KNEEISKI
	KNEEISKIENI
	KQQVQTEKTTA
Staphylococcus aureus sex pheromone - [Q5HEL9_STAAC]	EQDFYGGGDTKGKNI
	GLNPSHEGETDPEKIA
	SKKLDDSEVKKQGKQMA
Sua5/YciO/YrdC/YwIC family protein - [Q5HHA7_STAAC]	KFEEIKERL
	RSQNKTNYKTSSII
Transcriptional regulator, putative - [Q5HH28_STAAC]	NDKNDFL
Transporter, putative - [Q5HD89_STAAC]	EQEPDTSKDI
	PKVGRNMLL
Type I restriction-modification enzyme, S subunit, EcoA family - [Q5HEW8_STAAC]	NLNQHVCII