

Supplementary Dataset 2. Comparison of sequence coverage of predicted cell wall proteins that were identified in this study with that previously published for “surfomic” analysis (Prados de la Torre et al, Vaccines 2020, 8(2):188. doi: 10.3390/vaccines8020188). For such a comparison, peptides found in both proteomics datasets were mapped on the sequences of cell wall proteins. For each protein sequence, those highlighted in yellow represent the peptides found in the exoproteomes; those represented in green, the peptides found in the “surfomes”.

A0A0H3MXC9-Exoproteome

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>tr|A0A0H3MXC9|A0A0H3MXC9_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0180 PE=4
SV=1
METANKKFRYSIRKFKVGVGSVLIATCLLGAGVSTPTAFATTETSTATQVEAMAKVEEVQ
KLVKELEKELGELDKVPSYGDAQDYSYQKALWEEFLRIGKDNMDYASKMKADDKFFHKVK
GDLNDFKYQIKVENYIRQVAELRKKYPGDNTIEEEYNAHLKQDEGKSIASQEGATLRDYV
DREASEAMGRIKQRVAELEKSKQPQPSPADEPAPAPKEEDTPAPTPKVEDETQEPKTEEK
APETKEETPTPTPKKEGIPAPKEDEVPAPEEETPAPKEEDTPAPDAAPAPAPTPEVDPA
PTPIPDTPKAEKEEAPTVPDTPAPKEDEVPAPIPDAPTTPKVEEETQEPKTEEKAPETKEE
TPTPAPDAEPAPTVPDTPAPDTPAPKEDEVPAPEEETPAPKEEDTPAPDAAPAPAPTPEVDPA
PKTDKVESDKQMPEAKQPEMEQPKAEDMPKEEMPKSEQPKAEDSAPKTAVPEVAPKTAEK
PKLDFTTKERKVEEALPIKEEIRYDASLPLGKSYLLQEGKAGKKVSVYQDVIVDGKVVAT
NLLSETVVEGQNRILVKGSLEMKKKEEVKTTPSVQSNPTLSHKGAPSANKATLPATGEQRN
NLALVGLGLAGISLAVVATAINKKSKDQI
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A0A0H3MXC9-Surfome

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>tr|A0A0H3MXC9|A0A0H3MXC9_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0180 PE=4
SV=1
METANKKFRYSIRKFKVGVGSVLIATCLLGAGVSTPTAFATTETSTATQVEAMAKVEEVQ
KLVKELEKELGELDKVPSYGDAQDYSYQKALWEEFLRIGKDNMDYASKMKADDKFFHKVK
GDLNDFKYQIKVENYIRQVAELRKKYPGDNTIEEEYNAHLKQDEGKSIASQEGATLRDYV
DREASEAMGRIKQRVAELEKSKQPQPSPADEPAPAPKEEDTPAPTPKVEDETQEPKTEEK
APETKEETPTPTPKKEGIPAPKEDEVPAPEEETPAPKEEDTPAPDAAPAPAPTPEVDPA
PTPIPDTPKAEKEEAPTVPDTPAPKEDEVPAPIPDAPTTPKVEEETQEPKTEEKAPETKEE
TPTPAPDAEPAPTVPDTPAPDTPAPKEDEVPAPEEETPAPKEEDTPAPDAAPAPAPTPEVDPA
PKTDKVESDKQMPEAKQPEMEQPKAEDMPKEEMPKSEQPKAEDSAPKTAVPEVAPKTAEK
PKLDFTTKERKVEEALPIKEEIRYDASLPLGKSYLLQEGKAGKKVSVYQDVIVDGKVVAT
NLLSETVVEGQNRILVKGSLEMKKKEEVKTTPSVQSNPTLSHKGAPSANKATLPATGEQRN
NLALVGLGLAGISLAVVATAINKKSKDQI
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A0A0H3MTA4-Exoproteome

>tr|A0A0H3MTA4|A0A0H3MTA4_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0194 PE=4
SV=1

MNKKIFLKSAIILLSVTCLINAIKALDSSGVSSSTGEIVNQDRIYNITLKVKTDGVYNDL
GGNVISENNVLSGISGTKINLKVSTNSGYRFVGYQSFLESGNSTDGLLP IENDSFEISDK
TGNVTVVAMFEKIPIDETIYFSDEFSTENINNYLLSENLI GKI AVSNGKLN I HAPGVSSI
KPILSRQIDESS TLGYEIQFSIQQIGEVKQWNTFRVVF KENS DGSVYALEFTGKA VSIKK
LSSIDAPNQ TGEK YAETGHN LGSEEHRIRLVVRGDTVTVSDNEIPLLSYSSPENWEGATA
SIVFTPISNRSVSLDDIIIRQTRALRSLLVVSRI DGQEVTDIQPGSIR GNTSQVFVGDSL
PLEVIEKPGYQFIGFKDEF GNVVDLSTFSVPNDES DLVIYADFQTAEVVNRET KTFYIDS
IEGNDTNSGESETNAWK TLEQLRKNTLIAGDRVLLKRGSR FVGEDAALTFKGS GLEDAP I
LISSYGE GELPLLEAQGK IESVIKLYNQEYIT IENLEITNLDPNFSTSFELNSNNRSKI
LRGVHVIAEDYGVVHDIVLRNMYLHDINGNLNSKWN GGIFFDVYGTTPVKYDGILIENN
YLERVDRSGIKLVGSTWANQN LKNKNIPLNWYPSTNVVVRGNRIE KAGGDSITVRDTDG
ALIEYNISADARYQDTGYNAGIWP FQASNTVIQYNESFR THGVQDGGQLDL DHVSNN SVM
QYNYSHDNEGGFMLIMNWYEQTSP TVRYNISQNDKDKIFELARGGAQGTAIYNN TIFSDS
KLTGRAGVIDMPSTSGGTGVKDIFLFNNIFYFTDGEKMFVEASDAGKYKDSIHFYNNAYV
GVEVPDDPKAITEGITLKG VGTGPTENKSMIANAGKFLTGQLDGYRLPENSSLAKLG VSK
EEAISYFYK KLGVQPTIDFQDNGSLTMSPT EAFALARQ TNSVDAIARVYPAIEGV TYDTD
FFGETLSS ENLSVGAAQEKKSVFEEKISDIEISDVKTGIGMRYKRSNQLADV NLSIRLIN
KDELQYTINANNPTFSYEIQ LQKNFGEYMDLSESVTIT IPIEADKKILNVLKINKNEQTE
SVKELPYRIENNKI ILETDELGSFII EYQMEKIKKENNTNATISESGKSSLGLQNKENS D
VQAVGDKDYFSGLELSNKGEELSREDSKLMGNSINN LQTIKESESI FEGNLGRNKELSDM
YQKSLPKTGESNQAYIVLIGLFSLFVVLICQIFKKSID

A0A0H3MTA4-Surfome

>tr|A0A0H3MTA4|A0A0H3MTA4_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0194 PE=4
SV=1

MNKKIFLKSAIILLSVTCLINAIKALDSSGVSSSTGEIVNQDR IYNITLKVKTDGVYNDL
CGNVISENNVLSGISGTK INLK VSTNSGYR FVGYQSFLESGNSTDGLLP IENDSFEISDK
TGNVTVVAMFEKIPIDETIYFSDEFSTENINNYLLSENLI GKI AVSNGK LNIHAPGVSSI
KPILSRQIDESS TLGYEIQFSIQQIGEVKQWNTFRVVF KENS DGSVYALEFTGKA VSIKK
LSSIDAPNQ TGEK YAETGHN LGSEEHR IRLVVRGDTVTVSDNEIPLLSYSSPENWEGATA
SIVFTPISNRSVSLDDIIIRQTRALRS LLVVSRI DGQEVTDIQPGSIR GNTSQVFVGDSL
PLEVIEKPGYQFIGFKDEF GNVVDLSTFSVPNDES DLVIYADFQTAEVVNRET KTFYIDS
IEGNDTNSGESETNAWK TLEQLRKNTLIAGDR VLLKRGSRFVGEDAALTFKGS GLEDAP I
LISSYGE GELPLLEAQGK IESVIKLYNQEYIT IENLEITNLDPNFSTSFELNSNNRSKI
LRGVHVIAEDYGVVHDIVLRN MYLHDINGNLNSK WNGGIFFDVYGTTPVKYDGILIENN
YLERVDRSGIKLVGSTWANQN LKNKNIPLNWYPSTNVVVRGNRIE KAGGDSITVRDTDG
ALIEYNISADARYQDTGYNAGIWP FQASNTVIQYNESFR THGVQDGGQLDL DHVSNN SVM
QYNYSHDNEGGFMLIMNWYEQTSP TVRYNISQNDKDKIFELARGGAQGTAIYNN TIFSDS
KLTGRAGVIDMPSTSGGTGVKDIFLFNNIFYFTDGEKMFVEASDAGKYKDSIHFYNNAYV
GVEVPDDPKAITEGITLKG VGTGPTENKSMIANAGK FLTGQLDGYRLPENSSLAKLG VSK
EEAISYFYK KLGVQPTIDFQDNGSLTMSPT EAFALARQ TNSVDAIARVYPAIEGV TYDTD
FFGETLSS ENLSVGAAQEKKSVFEEKISDIEISDVKTGIGMRYKR SNQLADV NLSIRLIN
KDELQYTINANNPTFSYEIQ LQKNFGEYMDLSESVTIT IPIEADKKILNVLKINKNEQTE
SVKELPYRIENNKI ILETDELGSFII EYQMEK IKKENNTNATISESGK SSLGLQNKENS D
VQAVGDKDYFSGLELSNKGEELSREDSK LMGNSINN LQTIKESESI FEGNLGRNKELSDM
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A0A0H3MTC5-Exoproteome

>tr|A0A0H3MTC5|A0A0H3MTC5_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0244 PE=4
SV=1
MSKQKVVSSLLLSTVVLGGLAFYSTTTVKAESLEPDVTSVNASDATNKPVPNEEGGDFLAELEELEDDDT
LEELNEKAEVTEPSSPEALLQPRAMMSDSETSGMEEIPMNDEPSDNTEEKVEKQQSPLIQTSNADYKS
GKDQEKLRTSVSINLLKAEEGQIQWKVTFDTSSEWSFNVKHGGVYFILPNGLDLTKIVDNNQHDITASFPT
DINDYRNSGQEKYRFFSSKQGLDNENGFN SQWNWSAGQANPSETVNSWKSGNRLSKIYFINQITDTELT
YTTLAKVTEPNQQSFPLLAVMKSFTYTNKSTEVTSLGAREITLEKEKTLPPKENPKPEPEAPKPDAPQA
PSAPESPTTEEPKKEDAPQTPQAPSTPEKQPEVPESPNPETPDAPSTPKDEPQAPSIPEEKPVPEEPKQE
APSAPSTPEKQPEAPESTTEEPKKEDAPAPSTPEKQPEVPESPNPETPDAPSTPKDEPQVPSIPEEQPKE
TPAPEEPKKEDTPQTPQAPSTPKKEAPKEEVPTPPAPSVPEEQPKETPTPEVPKQEDVQPEAPKSDKVES
DKQMPETKKPDMKQPKADDMPKEQKPKADEPKAEQPQMDKPQMEAPKDKSEAPKSDKVETDKQLPETKQP
DMKQPKADDMPKEQKPKADEPKAEQPQMDKPQMEAPKDKSEAPKSDKVETDKMPMPETKQPDMDKQPKADKP
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A0A0H3MTC5-Surfome

>tr|A0A0H3MTC5|A0A0H3MTC5_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0244 PE=4
SV=1
MSKQKVVSSLLLSTVVLGGLAFYSTTTVKAESLEPDVTSVNASDATNKPVPNEEGGDFLAELEELEDDDT
LEELNEKAEVTEPSSPEALLQPRAMMSDSETSGMEEIPMNDEPSDNTEEKVEKQQSPLIQTSNADYKS
GKDQEKLRTSVSINLLKAEEGQIQWKVTFDTSSEWSFNVKHGGVYFILPNGLDLTKIVDNNQHDITASFPT
DINDYRNSGQEKYRFFSSKQGLDNENGFN SQWNWSAGQANPSETVNSWKSGNRLSKIYFINQITDTELT
YTTLAKVTEPNQQSFPLLAVMKSFTYTNKSTEVTSLGAREITLEKEKTLPPKENPKPEPEAPKPDAPQA
PSAPESPTTEEPKKEDAPQTPQAPSTPEKQPEVPESPNPETPDAPSTPKDEPQAPSIPEEKPVPEEPKQE
APSAPSTPEKQPEAPESTTEEPKKEDAPAPSTPEKQPEVPESPNPETPDAPSTPKDEPQVPSIPEEQPKE
TPAPEEPKKEDTPQTPQAPSTPKKEAPKEEVPTPPAPSVPEEQPKETPTPEVPKQEDVQPEAPKSDKVES
DKQMPETKKPDMKQPKADDMPKEQKPKADEPKAEQPQMDKPQMEAPKDKSEAPKSDKVETDKQLPETKQP
DMKQPKADDMPKEQKPKADEPKAEQPQMDKPQMEAPKDKSEAPKSDKVETDKMPMPETKQPDMDKQPKADKP
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A0A0H3MTL3-Exoproteome

>tr|A0A0H3MTL3|A0A0H3MTL3_STRS4 Major pilus subunit OS=Streptococcus
suis (strain BM407) OX=568814 GN=SSUBM407_0414 PE=4 SV=1
MKKLQQFFTSLSVAVLTVFAFGSTALAQTVDSGKSGAGTITVSNASQGQTYTAYKLFDATVTTDGSGISYK
LPAGKTATNFGGDTWFEVDKGNITAKEGATVSSEAFAAWAKNFGTEVTSATANDNSLVFTHLTFGYFV
TSSLGAVLTVDSTTPNATVIDKNTTNPTIPDSNNGGKKILSNGATTSETTAKIGDTINFQIKFNATNYV
TKDRQTKQIVSYTIEDSPTALAIQNSVNVKVDGVDITAKISKTFDATGKMNLVITWADAAASNKTIYNS
PAEVIITYSAVVTKDAKEGEATNSATIGYNTIDNPTTPPTPVDPKPTETTKVTTHRFTLKKTNNVGETL
TGAEFKLYDAANNNGTEIKVVKESDGVYRVAQADEQGVVIEAGEVVIKGLKHSTTYYLEEMKAPNGYNILT
ERQSIEVKENNTAQANIVNKKGGVLPSTGAIGTTLFYLVGSILLVALVYTISKRRMNNI

A0A0H3MTL3-Surfome

>tr|A0A0H3MTL3|A0A0H3MTL3_STRS4 Major pilus subunit OS=Streptococcus
suis (strain BM407) OX=568814 GN=SSUBM407_0414 PE=4 SV=1
MKKLQQFFTSLSVAVLTVFAFGSTALAQTVDSGKSGAGTITVSNASQGQTYTAYKLFDATVTTDGSGISYK
LPAGKTATNFGGDTWFEVDKGNITAKEGATVSSEAFAAWAKNFGTEVTSATANDNSLVFTHLTFGYFV
TSSLGAVLTVDSTTPNATVIDKNTTNPTIPDSNNGGKKILSNGATTSETTAKIGDTINFQIKFNATNYV
TKDRQTKQIVSYTIEDSPTALAIQNSVNVKVDGVDITAKISKTFDATGKMNLVITWADAAASNKTIYNS
PAEVIITYSAVVTKDAKEGEATNSATIGYNTIDNPTTPPTPVDPKPTETTKVTTHRFTLKKTNNVGETL
TGAEFKLYDAANNNGTEIKVVKESDGVYRVAQADEQGVVIEAGEVVIKGLKHSTTYYLEEMKAPNGYNILT
ERQSIEVKENNTAQANIVNKKGGVLPSTGAIGTTLFYLVGSILLVALVYTISKRRMNNI

A0A0H3N2T0-Exoproteome

>tr|A0A0H3N2T0|A0A0H3N2T0_STRS4 Membrane dipeptidase OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407 0574 PE=3 SV=1
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AKGDMLVDESFGFTAPHLANEFKYTSTPDAARGDGSNGNFGAHGFNEKGVSMTATVTAIPNKKVLAVDPL
VTAGGLGEAILIDYVLPVTSAREGIELIAKTIDEKGS AEGNIIVIADKNEVWYMEILSGHQYVAIKFPE
DKY AIFANTYYLGHVDFDTENVIASAKVEEVAKQAENYMMVDGKFHIAKSYG PENYADGDRSRTYAGIK
LLDPASSVTYEDAVYDLLRQPTDPSRRFSLQDTFALQNRNFEHLPEFRPDDEAGKVKQGDNGANDQAADA
TYKYALGNENVIDAHVYQINSSLPSAFGGTVWLGLAQTRNTPYVPFYGIVTDTYEAFKNRSASYDTNSWY
WTVQNIDKMAISHPELFGTSIQEKWIALEKEWIASQAALDAQYAGLSEDA AVALAPT VTEATLARS AEI F
AQLKAVEAEMMAKIEAATTPSSSSSTEPSTSTEPSSSGTETSTSTSQSTSDSNTGGATDTSSSSRTVVPSPD
KKVTPTNKKGKSSLPSTGEQVSLLLVALGVAGILTAIFLHRKKSSKE

A0A0H3N2T0-Surfome

>tr|A0A0H3N2T0|A0A0H3N2T0_STRS4 Membrane dipeptidase OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407 0574 PE=3 SV=1
MKKTFVRIATFLMLVCLFPVQLVQACSGFIIGKGLTTDGSILYGRTE DYPPPPNNGAHNKNYIVVPATAY
AKGDMLVDESFGFTAPHLANEFKYTSTPDAARGDGSNGNFGAHGFNEKGVSMTATVTAIPNKKVLAVDPL
VTAGGLGEAILIDYVLPVTSAREGIELIAKTIDEKGS AEGNIIVIADKNEVWYMEILSGHQYVAIKFPE
DKY AIFANTYYLGHVDFDTENVIASAKVEEVAKQAENYMMVDGKFHIAKSYG PENYADGDRSRTYAGIK
LLDPASSVTYEDAVYDLLRQPTDPSRRFSLQDTFALQNRNFEHLPEFRPDDEAGKVKQGDNGANDQAADA
TYKYALGNENVIDAHVYQINSSLPSAFGGTVWLGLAQTRNTPYVPFYGIVTDTYEAFKNRSASYDTNSWY
WTVQNIDKMAISHPELFGTSIQEKWIALEKEWIASQAALDAQYAGLSEDA AVALAPT VTEATLARS AEI F
AQLKAVEAEMMAKIEAATTPSSSSSTEPSTSTEPSSSGTETSTSTSQSTSDSNTGGATDTSSSSRTVVPSPD
KKVTPTNKKGKSSLPSTGEQVSLLLVALGVAGILTAIFLHRKKSSKE

A0A0H3MU32-Exoproteome

>tr|A0A0H3MU32|A0A0H3MU32_STRS4 Putative surface-anchored protein OS=Streptococcus suis (strain BM407) OX=568814 GN=sao PE=4 SV=1
MNTKKWRTSL LIPGIVLFGTVALVNNVSAQEVKNTIISAKQPDGGQATSKAVNVKIPAVVRLFGRELLEN
EFKFELREANGEELPVLDTAQNTKEGQVRFKNLSFDKPGKYWYTISEVKDELGGIEYDSKYIVAKITVED
RNGQLQAMIEFIDNDNVFN NFYTPAPAAASLSIKKVLEGR TLNTGEFEFVLKNEKGDEIEKVS NQADGSV
NFSALTFTTKEGTYTYTVSEVDGGLGDI IYDKSDIKATVTVKDNNHGQLVSTV TYENS DQIFENILNPGKL
IAPT TDSVITDNEVSK EAMTGKEKGNI EPPKEQIANEEKDNIEASEKQMP SIVNDMVVTPPEKQMTNKEND
KVVISEKQMP SVVNENAVTPEKQMTNKENDNIETSEKQMP SVVNENAVTPEKQMTNKEKDNIETSEKQMP
SIVNDMVVTPQEQMANKENDKV VISEKQMP SIVNDMVVTPQEQMANKENDKV VISEKQMP SIVNDMVVTP
QEQMANKENDKV VISEKQMP SIVNDMVVTPQEQMANKENDKVETSEKQMPVNEKDNAVTPEKQMANKEKE
NIETSKKQIPVNENNQNGTVEENSNTKPTTEKTDKQETSTFKTETAKQILPVTGEKGS LWLLTSGIIGLA
IALFTRKRK

A0A0H3MU32-Surfome

>tr|A0A0H3MU32|A0A0H3MU32_STRS4 Putative surface-anchored protein OS=Streptococcus suis (strain BM407) OX=568814 GN=sao PE=4 SV=1
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EFKFELREANGEELPVLDTAQNTKEGQVRFKNLSFDKPGKYWYTISEVKDELGGIEYDSKYIVAKITVED
RNGQLQAMIEFIDNDNVFN NFYTPAPAAASLSIKKVLEGR TLNTGEFEFVLKNEKGDEIEKVS NQADGSV
NFSALTFTTKEGTYTYTVSEVDGGLGDI IYDKSDIKATVTVKDNNHGQLVSTV TYENS DQIFENILNPGKL
IAPT TDSVITDNEVSK EAMTGKEKGNI EPPKEQIANEEKDNIEASEKQMP SIVNDMVVTPPEKQMTNKEND
KVVISEKQMP SVVNENAVTPEKQMTNKENDNIETSEKQMP SVVNENAVTPEKQMTNKEKDNIETSEKQMP
SIVNDMVVTPQEQMANKENDKV VISEKQMP SIVNDMVVTPQEQMANKENDKV VISEKQMP SIVNDMVVTP
QEQMANKENDKV VISEKQMP SIVNDMVVTPQEQMANKENDKVETSEKQMPVNEKDNAVTPEKQMANKEKE
NIETSKKQIPVNENNQNGTVEENSNTKPTTEKTDKQETSTFKTETAKQILPVTGEKGS LWLLTSGIIGLA
IALFTRKRK

A0A0H3MU94-Exoproteome

>tr|A0A0H3MU94|A0A0H3MU94_STRS4 Putative surface-anchored zinc carboxypeptidase OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0646 PE=4 SV=1
MKLSYKKRLLNQVLLASTVLLAASLAQGTVFANTEEIPTTNETVTPLPEETPITK**TSTSEATDNLVEGK**
ETEKQTEEIADTSPASVSTEEETTSSEPNAEETTLRTANNDNQNTTEEKPAVPTIDTITLETCTVYLSEA
VTITESVTLPDTEKIEWILDGKPISEWKTWNLKEGDFTGDTFITVEESRQDNQLHLNIQLAALFGEDLS
KRTPSNIRRTYRHFIDKMLLEGTSADGNLIISKTLHFRPYEAYRTHEEMLTEIEETKNNAATDRLVR**IES**
IGQSAEGRDIKMAVVAKNQASIDK**YLTETTPMLMLTQPDQMLK**QLQAGTFDYRLPILINNTHADEQPGIDV
VTSLFKEFAQKDTITFPSTDADGNPVTLLHLKVTDLLDKFIFLNFNFTENPDGDVKNLRSVLNGLDPNRDTG
FQVNPETQAIVRQIHKWNPISVLDIHGFVSGFLIEPATPPHDPNFEYDLLADIMLEKAHEMGRAGIANSK
YERYTIPKVHWGDGWDSDSGYTAVYAMYHGILGHTIEIPEGNQESFKAGFFAVLGGVHNMATKPDLSME
MRLKYYSRQVNVKVEDPK**AESSELVGPDGAVVGR**VKKDQPKFFPDYYVIPMTLDKHNDMQEAFKMIIEYFNRRN
GVVV**KELTEDVGNFR**KGDLVVDMAQAKRGFANHVLYAGSDESAWGAMYAELVVNFPDMKGFSK**AVFEEN**
TFSGKLGSITWTKAPR**TTEIDFK**APYYVVANTSESQVAINQAIKSGAKVYLTDDGYIMETNQFSHLLDT
YALYGEPLYKKPLGQELKAMKVYAPSHSYSWAGDFAILANAALAVERMGFIVNSADEADAIILESQDFD
ASVFGKKPIIIVGGVAMQKLEELGILAGFNAEQFTDGGDYEGLMQAIIDDKDPLTSGYAMNGLFYNSNGN
WIEGIPEGFKTLVKIADKDYYIAGWWPGHDKLANKIVAIAGNYQDQPVFIYAGNPNTKVHPVHFFRWVSN
ALFGSQLASLEDLPAVEILVPQPEMPKNILDEAPKTTTVVHTTKSTEAKQLPQTGEKTNIAIALGSLLL
GSIALRRKERS

A0A0H3MU94-Surfome

>tr|A0A0H3MU94|A0A0H3MU94_STRS4 Putative surface-anchored zinc carboxypeptidase OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0646 PE=4 SV=1
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ETEKQTEEIADTSPASVSTEEETTSSEPNAEETTLRTANNDNQNTTEEKPAVPTIDTITLETCTVYLSEA
VTITESVTLPDTEKIEWILDGKPISEWKTWNLKEGDFTGDTFITVEESRQDNQLHLNIQLAALFGEDLS
KRTPSNIRRTYRHFIDKMLLEGTSADGNLIISKTLHFRPYEAYRTHEEMLTEIEETKNNAATDRLVRIES
IGQSAEGRDIKMAVVAKNQASIDKYLTETTPMLMLTQPDQMLKQLQAGTFDYRLPILINNTHADEQPGIDV
VTSLFKEFAQKDTITFPSTDADGNPVTLLHLKVTDLLDKFIFLNFNFTENPDGDVKNLRSVLNGLDPNRDTG
FQVNPETQAIVRQIHKWNPISVLDIHGFVSGFLIEPATPPHDPNFEYDLLADIMLEKAHEMGRAGIANSK
YERYTIPKVHWGDGWDSDSGYTAVYAMYHGILGHTIEIPEGNQESFKAGFFAVLGGVHNMATKPDLSME
MRLKYYSRQVNVKVEDPKAESSELVGPDGAVVGRVKKDQPKFFPDYYVIPMTLDKHNDMQEAFKMIIEYFNRRN
GVVVKELTEDVGNFRKGDLVVDMAQAKRGFANHVLYAGSDESAWGAMYAELVVNFPDMKGFSKAVFEEN
TFSGKLGSITWTKAPRTTEIDFKAPYYVVANTSESQVAINQAIKSGAKVYLTDDGYIMETNQFSHLLDT
YALYGEPLYKKPLGQELKAMKVYAPSHSYSWAGDFAILANAALAVERMGFIVNSADEADAIILESQDFD
ASVFGKKPIIIVGGVAMQKLEELGILAGFNAEQFTDGGDYEGLMQAIIDDKDPLTSGYAMNGLFYNSNGN
WIEGIPEGFKTLVKIADKDYYIAGWWPGHDKLANKIVAIAGNYQDQPVFIYAGNPNTKVHPVHFFRWVSN
ALFGSQLASLEDLPAVEILVPQPEMP**KNILDEAPKTTTVVHTTKS**TEAKQLPQTGEKTNIAIALGSLLL
GSIALRRKERS

A0A0H3MUB3-Exoproteome

>tr|A0A0H3MUB3|A0A0H3MUB3_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0661 PE=4
SV=1
MKKKAIVKPLLMSGIFLALLGGATLPSGAVPVVAAETSQSTTYHLTDDEKVAVR**EYIQAKMTIDMQEYRL**
AFLEGMMEEMASGSAEAAWDEEADLKANLTAEQVVVLDELEANLIGSIAQHYHYLFETLTVAGKSGR**EE**
AAAIIVSKYESEDDASTPEAELAALKYAREVIVVELLNKESAAIDNYIAYAEATGQELAGLLESNGNSNLESI
TSATIGYGQALATASQPK**F**FPYDFSEMDRQIAELTASLQSKVEDKSTAK**TENTGVQTSQS**SATNGSNDLQTV
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A0A0H3MUB3-Surfome

>tr|A0A0H3MUB3|A0A0H3MUB3_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_0661 PE=4
SV=1
MKKKAIVKPLLMSGIFLALLGGATLPSGAVPVVAAETSQSTTYHLTDDEKVAV**REYIQAKMTIDMQEYRL**
AFLEGMMEEMASGSAEAAWDEEADLKANLTAEQVVVLDELEANLIGSIAQHYHYLFETLTVAG**KSGREE**
AAAIIVSKYESEDDASTPEAELAALKYAREVIVVELLNKESAAIDNYIAYAEATGQELAGLLESNGNSNLESI
TSATIGYGQALATASQPK**F**FPYDFSEMDRQIAELTASLQSKVEDK**STAKTENTGVQTSQS**SATNGSNDLQTV
PDQGGGQISDVATGKGNISEAGQKKVIPNDNAKVLPKTSGKSSLPLTVLGLITIFAGWLLTNKQEEK

A0A0H3MV17-Exoproteome

>tr|A0A0H3MV17|A0A0H3MV17_STRS4 Putative 5'-nucleotidase
OS=Streptococcus suis (strain BM407) OX=568814 GN=sntC PE=3 SV=1
MPKKGLFMKKKKILLPVMSTLLLAPFVLAQQVQAAETTTAATTTNQPATTDATATVPATTDATATVPATS
VENVATEETVVPAAEETVEAVIIHTNDVHGRILEEKNVIGDAK**AAAVIEEERAKVENTIVVDAGDAFQGL**
PISNSTKGEDRANIMNQVGYDAMAVGNHEFDFGMDQAIKYKETLNFPLLSANTYVNGARVFEASTIVDKT
PTVVGDEFVVGVTTPETATKTHPKNVEGVTFDTPVTEVNKVIDEVEARALADNRVYKNYIILAHLGVDS
TTPVEWRGSTLAEALS**SKNSKLAGKRVIVIDGHSHTVEATTYGDNVTYNQTSYLN**NIGKVTLKSDKLLGE
ASLISAADTKNVTPNAK**IAALVDEIKAKYEAENAQVVIENN**PVELNGDRSNVRVRETNLGNAVTDAIYAY
GQTGF**SNKTS**SLAVTNGGGLRATI**AKDQPVTKGDII**AVLPFGNIVSQITVTGQQIYDMFTKSL**SSTLQVNP**
ETGEMLLDENGMP**LFEASGGFLHISGANVFYDPTLPVEER**VLLIGILNPETGEYDALDLEKTYYLATNDF
LAAGGDGYTMLGGAREEGPSMDSVFAEYLYKTADLSAYEVVNPYSR**IIPVN**SSIDTDEDGYPDFIEILLDT
DPENPASNPETVPAENTD**SPSNQVQNTSATDKKAPVDS**SPKVGDKKTEVASPAKTTKAGVLPNTGDQMNLT
LSLFLGLGLAGLAVAVGRRKEN

A0A0H3MV17-Surfome

>tr|A0A0H3MV17|A0A0H3MV17_STRS4 Putative 5'-nucleotidase
OS=Streptococcus suis (strain BM407) OX=568814 GN=sntC PE=3 SV=1
MPKKGLFMKKKKILLPVMSTLLLAPFVLAQQVQAAETTTAATTTNQPATTDATATVPATTDATATVPATS
VENVATEETVVPAAEETVEAVIIHTNDVHG**RILEEKNVIGDAKAAAVIEEERAKVENTIVVDAGDAFQGL**
PISNSTKGEDRANIMNQVGYDAMAVGNHEFDFGMDQAIKYKETLNFPLLSANTYVNGARVFEASTIVDKT
PTVVGDEFVVGVTTPETATKTHPKNVEGVTFDTPVTEVNKVIDEVEARALADNRVYKNYIILAHLGVDS
TTPVEWRGSTLAEALS**SKNSKLAGKRVIVIDGHSHTVEATTYGDNVTYNQTSYLN**NIGKVTLKSDKLLGE
ASLISAADTKNVTPNAK**IAALVDEIKAKYEAENAQVVIENN**PVELNGDRSNVRVRETNLGNAVTDAIYAY
GQTGF**SNKTS**SLAVTNGGGLRATI**AKDQPVTKGDII**AVLPFGNIVSQITVTGQQIYDMFTKSL**SSTLQVNP**
ETGEMLLDENGMP**LFEASGGFLHISGANVFYDPTLPVEE**RVLLIGILNPETGEYDALDLEKTYYLATNDF
LAAGGDGYTMLGGAREEGPSMDSVFAEYLYKTADLSAYEVVNPYSR**IIPVN**SSIDTDEDGYPDFIEILLDT
DPENPASNPETVPAENTD**SPSNQVQNTSATDKKAPVDS**SPKVGDKKTEVASPAKTTKAGVLPNTGDQMNLT
LSLFLGLGLAGLAVAVGRRKEN

A0A0H3MV42-Exoproteome

>tr|A0A0H3MV42|A0A0H3MV42_STRS4 Putative glucan-binding surface-anchored protein OS=Streptococcus suis (strain BM407) OX=568814
GN=SSUBM407_0949 PE=4 SV=1
MTKTCNHHFLVNQEKGEKHVFRKSKKYRTLCSVALGTMVTAVVAWGGTVAHADEVVLSVDSTIQRTENPA
TNLPEAQPNPVSEQTESLGSTGKSNGAIAVTPHETVTQTVEQAKAEGVSTVEDSPMDLGNTTSAETNQ
QISKAEADAQNQVVAINEVTETYKADKAAYVDEKARIEQENKELSQAYEGANQTGKETNAWVDSKVNDLK
SQYADADVTVKEQVVSSEGKTSVLDTDYGKAVETIQSTNEQAVADYLTKKTKADDIVAKNQAIQKENE
GLAKAKADNEAIERRNQAGQAAVDAENRAGQAAVDQANQEKQQLVSDRAVEIEVITKRNQAKEVAARKEN
EAI DAYNAKEMERYQRDLAEISKGEEGYISEALAQAALNLNNGEPQAQHGAITRNPQIISTGDAMLGGYS
RILDSTGFFVYDSFKTGETLSFNYQNLQHARFDGKKISRVTYDITNLVSPAGTDAVKLVVPNDPTEGFIA
YRNDGNGDWR

TDKMEFRVVAKYFLEDGSQVTFKSKEKPGVFTHSSLNHNNDIGLEYVKDSSGKFVPINGSTV
QVTNEGLARSLGSNRASDLNLPPEWDTTSSRYAYKGAIVSTVTSNGNTYTVTFGQGDMPQNVGLSYWFALN
TLPVARTVTPYSPKPHVTVELEPVPEPITVTPDVYTPKFTTPEKPVFTTPKPLEEVVQPSLTTLTKVTLPV
KPIPKELPTPPQVPTIHYHAYRLTTTPEIMKEVINSDQANLHDKTVAKDSTVIYPLTVDALSPKRTQTTS
LIFEDYLPAGYLFDKETTQKENGNYALSFDKSNFVTLTAKETLLQEVNQDLTKSYQLTAPKLYGTQND
GATYSNSYKLLVNKGTANSYTVTSNIVTVRTPGDGETTTLITPDKNNENADGVLINDTVVALGTTNHYRL
TWDLDQYKEDRSaketIARGFFVDDYPEEVLDVVENGTSVTTLDGQKVSGITVKTYASLNEAPKYLQDK
FARAKITPTGAFQVFPDDNQAFYDQYVKTGTSLALLTKMTVKDSLYGQTKTYTNKGYQVDFGNGYETKE
VTNTLVSPPEPKQNLNKDKVDINGKPMVLGTQNHYTLSWDLQYRGIKADNSQIAQGFFVDDYPEEALL
PDEAAIQFVTS DGKTVSGITVKAYSQ LSEAPKTLQAALSKQKI QPKGAFQVFPEDPQAFYNSYVTKGEN
ITIVTPMTVLETMINSGKSYENVAYQVDFGQAYETNTVTNFPKVPKPHKSNTNQEGISIDGKTVPNTVN
YYKIVLDYSQYKDMVVTDDVLAKGFYMVDDYPEEALTLNPDGIQVLDKDGNRVSGISVSTYDSLSEAPKV
VEDAMAKRQFTPKGAIQVLSSDDPKTFYETYVKTGQTLVVTLPMTVKNELTKTGGQYENTAYQIDFGLAY
VTETVNNVNPKLDPQKDVVVDLSHKNNSLDGKEVALNQI INYRLVGAMIPSNRATDLFEYGFEDNYDEKH
DEYNGVYRSYLMTDITLKDGSILKEGTEVTKYTLQQVDTENGLVSI SFDKSFLETVSDDSAFQADVYLHM
KRIAAGQVENTYLHTVNGYVISSNTVVTHTPQPEEPSNPQPTPPQPPIETIEPPVPASILPNTGEQESLL
GLIGAGILLGTAYGLKKKEEK

A0A0H3MV42-Surfome

>tr|A0A0H3MV42|A0A0H3MV42_STRS4 Putative glucan-binding surface-anchored protein OS=Streptococcus suis (strain BM407) OX=568814
GN=SSUBM407_0949 PE=4 SV=1
MTKTCNHHFLVNQEKGEKHVFRKSKKYRTLCSVALGTMVTAVVAWGGTVAHADEVVLSVDSTIQRTENPA
TNLPEAQPNPVSEQTESLGSTGKSNGAIAVTPHETVTQTVEQAKAEGVSTVEDSPMDLGNTTSAETNQ
QISKAEADAQNQVVAINEVTETYKADKAAYVDEKARIEQENKELSQAYEGANQTGKETNAWVDSKVNDLK
SQYADADVTVKEQVVSSEGKTSVLDTDYGKAVETIQSTNEQAVADYLTKKTKADDIVAKNQAIQKENE
GLAKAKADNEAIERRNQAGQAAVDAENRAGQAAVDQANQEKQQLVSDRAVEIEVITKRNQAKEVAARKEN
EAI DAYNAKEMERYQRDLAEISKGEEGYISEALAQAALNLNNGEPQAQHGAITRNPQIISTGDAMLGGYS
RILDSTGFFVYDSFKTGETLSFNYQNLQHARFDGKKISRVTYDITNLVSPAGTDAVKLVVPNDPTEGFIA
YRNDGNGDWR

YTDKMEFRVVAKYFLEDGSQVTFKSKEKPGVFTHSSLNHNNDIGLEYVKDSSGKFVPINGSTV
QVTNEGLARSLGSNRASDLNLPPEWDTTSSRYAYKGAIVSTVTSNGNTYTVTFGQGDMPQNVGLSYWFALN
TLPVARTVTPYSPKPHVTVELEPVPEPITVTPDVYTPKFTTPEKPVFTTPKPLEEVVQPSLTTLTKVTLPV
KPIPKELPTPPQVPTIHYHAYRLTTTPEIMKEVINSDQANLHDKTVAKDSTVIYPLTVDALSPKRTQTTS
LIFEDYLPAGYLFDKETTQKENGNYALSFDKSNFVTLTAKETLLQEVNQDLTKSYQLTAPKLYGTQND
GATYSNSYKLLVNKGTANSYTVTSNIVTVRTPGDGETTTLITPDKNNENADGVLINDTVVALGTTNHYRL
TWDLDQYKEDRSaketIARGFFVDDYPEEVLDVVENGTSVTTLDGQKVSGITVKTYASLNEAPKYLQDK
FARAKITPTGAFQVFPDDNQAFYDQYVKTGTSLALLTKMTVKDSLYGQTKTYTNKGYQVDFGNGYETKE
VTNTLVSPPEPKQNLNKDKVDINGKPMVLGTQNHYTLSWDLQYRGIKADNSQIAQGFFVDDYPEEALL
PDEAAIQFVTS DGKTVSGITVKAYSQ LSEAPKTLQAALSKQKI QPKGAFQVFPEDPQAFYNSYVTKGEN
ITIVTPMTVLETMINSGKSYENVAYQVDFGQAYETNTVTNFPKVPKPHKSNTNQEGISIDGKTVPNTVN
YYKIVLDYSQYKDMVVTDDVLAKGFYMVDDYPEEALTLNPDGIQVLDKDGNRVSGISVSTYDSLSEAPKV
VEDAMAKRQFTPKGAIQVLSSDDPKTFYETYVKTGQTLVVTLPMTVKNELTKTGGQYENTAYQIDFGLAY
VTETVNNVNPKLDPQKDVVVDLSHKNNSLDGKEVALNQI INYRLVGAMIPSNRATDLFEYGFEDNYDEKH
DEYNGVYRSYLMTDITLKDGSILKEGTEVTKYTLQQVDTENGLVSI SFDKSFLETVSDDSAFQADVYLHM
KRIAAGQVENTYLHTVNGYVISSNTVVTHTPQPEEPSNPQPTPPQPPIETIEPPVPASILPNTGEQESLL
GLIGAGILLGTAYGLKKKEEK

A0A0H3MVU2-Exoproteome

>tr|A0A0H3MVU2|A0A0H3MVU2_STRS4 Beta-N-acetylhexosaminidase
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1236 PE=3
SV=1
MKKETSKFTKKVILGQLLICTSFLVWAGQTVAAEEVSQGEPVAINNETPPVIEAKPLVEATPSTETEPST
PEEKQEEPQVAGKNVVEGK**KPVTNSQHQMVSELSTVPSVSIKNPDAATDGSAYGSSDDANSNTKIIAGKE**
TGEPDNGYSKWDHVYVQYDFEKEVPVHTVKIHRNTYDNAVSTFKDVK**VELSTSADFSPETTEVIFKQADV**
EETIANKGQPQVIQLPAPINARYIRIWGRGHYIQNTNSSWKGYSGVLFNEIEVLAQVEADAGTNEEPQT
ELVNLAKLKKPYFYGKAPTNPPEAINDGKFDENYTTQESIGDKAYLQYEFRNVYTIEEIKVQLAPGEYRNF
RIDLDDDYNDGNNTIYKNENFTIDKEQIITIKTPKNSKARYVRFRGTRVDDTPLRYSEIQIMGRGKSY
DESAPEYVPPKSEYDTLVWSDEFNGDKIDESKWQIIDGMWNHAAIYNRKAVSIKKDGDKSYLSIRSTNHK
DKKTLVEAVGHDRYDDKELPDKVTWSSGRLESKDYSFQFGRMAVRAKVNDKSGIWPPIWMLAQDETGH
EIDVLEYLGNPQWYAWTTNHFILAKNKKSDGSAYKNYEAWSQEFHVYEVEWTPDVIKWIYIDGKVFVQTD
RGKDRDGMHTRPMFPFILETQVGDGWVGVDYKRNMTKQDSEYLVWVRIYQKADQSKVRFDNLDDAKPND
YVIKPPQQLGHLVTVSNGKAAHENKNNFYGGQPRYETSRLYADGDGENALVYKIANPEALHLLTTYKTL
EDYSVYNKEAGANEGKSVRKHLINAKDGEIDFTVYSSVDGKSWNKENVTVVDNFVEATPAYARTTFDIRN
IRKGTGKFVKIVFPTVKGISYKLEDGTEKGLQASDVQLAKVTFVATHPEAEPEKPIVDQEKLLSKVFSLD
AGRKYFSVNQIKEIIDLISSYGYTDMNLLLGNDGLRFLDDMNLTVGDKVYDSEAVRKAIINGNKHYDD
PNGTTLSQSEMDDILAYAKEKNISIPTINSPGHMDAIVEAMEELGIKSPKFSYNGKTSARTVDLKNQDA
VAFTKALIDKYASYFAGKSKIFNIGLDEYANDATNASGWHILQTQGDYGKFIQYANDLAAIVKKHGLEPM
AFNDGIYYNHDTSSGTFDKDIIASFWTGGWGGYDVASSKFLHEKGHKILNTNDAWYYYVIGREAEGLGWYN
LDQGLRGTKSTRFDQVPKSENTKVPIIGSMVAVWADDPSKPYSDSIKKLLHSFTENNSDYFLAEYRDLR
EEVGKIPTDLNSYTPESVATLKEVLNKIDWKLSRNNQAFVDGYLAEVKAAR**EALVPVTAK**GDSVKAELP
EGKLPLITAKGKSVQAEPRPAFKGYLTSNYGPSVTPLSLVSKPSSEQSNSKQAASQKKELPNTGVVDGLG
FSLGMIGLAFASRRRKKE

A0A0H3MVU2-Surfome

>tr|A0A0H3MVU2|A0A0H3MVU2_STRS4 Beta-N-acetylhexosaminidase
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1236 PE=3
SV=1
MKKETSKFTKKVILGQLLICTSFLVWAGQTVAAEEVSQGEPVAINNETPPVIEAKPLVEATPSTETEPST
PEEKQEEPQVAGKNVVEGKKPVTNSQHQMVSELSTVPSVSIKNPDAATDGSAYGSSDDANSNTKIIAGKE
TGEPDNGYSKWDHVYVQYDFEKEVPVHTVKIHRNTYDNAVSTFKDVK**VELSTSADFSPETTEVIFKQADV**
EETIANKGQPQVIQLPAPINARYIRIWGRGHYIQNTNSSWKGYSGVLFNEIEVLAQVEADAGTNEEPQT
ELVNLAKLKKPYFYGKAPTNPPEAINDGKFDENYTTQESIGDKAYLQYEFRNVYTIEEIKVQLAPGEYRNF
RIDLDDDYNDGNNTIYKNENFTIDKEQIITIKTPKNSKARYVRFRGTRVDDTPLRYSEIQIMGRGKSY
DESAPEYVPPKSEYDTLVWSDEFNGDKIDESKWQIIDGMWNHAAIYNRKAVSIKKDGDKSYLSIRSTNHK
DKKTLVEAVGHDRYDDKELPDKVTWSSGRLESKDYSFQFGRMAVRAKVNDKSGIWPPIWMLAQDETGH
EIDVLEYLGNPQWYAWTTNHFILAKNKKSDGSAYKNYEAWSQEFHVYEVEWTPDVIKWIYIDGKVFVQTD
RGKDRDGMHTRPMFPFILETQVGDGWVGVDYKRNMTKQDSEYLVWVRIYQKADQSKVRFDNLDDAKPND
YVIKPPQQLGHLVTVSNGKAAHENKNNFYGGQPRYETSRLYADGDGENALVYKIANPEALHLLTTYKTL
EDYSVYNKEAGANEGKSVRKHLINAKDGEIDFTVYSSVDGKSWNKENVTVVDNFVEATPAYARTTFDIRN
IRKGTGKFVKIVFPTVKGISYKLEDGTEKGLQASDVQLAKVTFVATHPEAEPEKPIVDQEKLLSKVFSLD
AGRKYFSVNQIKEIIDLISSYGYTDMNLLLGNDGLRFLDDMNLTVGDKVYDSEAVRKAIINGNKHYDD
PNGTTLSQSEMDDILAYAKEKNISIPTINSPGHMDAIVEAMEELGIKSPKFSYNGKTSARTVDLKNQDA
VAFTKALIDKYASYFAGKSKIFNIGLDEYANDATNASGWHILQTQGDYGKFIQYANDLAAIVKKHGLEPM
AFNDGIYYNHDTSSGTFDKDIIASFWTGGWGGYDVASSKFLHEKGHKILNTNDAWYYYVIGREAEGLGWYN
LDQGLRGTKSTRFDQVPKSENTKVPIIGSMVAVWADDPSKPYSDSIKKLLHSFTENNSDYFLAEYRDLR
EEVGKIPTDLNSYTPESVATLKEVLNKIDWKLSRNNQAFVDGYLAEVKAAREALVPVTAKGDSVKAELP
EGKLPLITAKGKSVQAEPRPAFKGYLTSNYGPSVTPLSLVSKPSSEQSNSKQAASQKKELPNTGVVDGLG
FSLGMIGLAFASRRRKKE

This protein was not found in the surfome analysis

A0A0H3N5E4-Exoproteome

>tr|A0A0H3N5E4|A0A0H3N5E4_STRS4 Putative surface-anchored 5'-nucleotidase OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1432 PE=3 SV=1
MKKNIRLKSSI~~L~~ALVAGFSVIATQAVLADELAVQIMGVNDFHGALDMTG~~T~~ARLEGETVRNAGTAALLDAY
MDDSQA~~E~~FEETA~~A~~ETETPAESIRVQAGDMVGASPSNSGLLQDEPTVKVFNKMDVEYGT~~L~~GNHEFDEGLDE
YNRIMTGEAPKKGQFNEIVDNYTREAAKQEIVIANVIDKETGEIPYGWKPYA~~I~~KTIPVNDKEAKIGFIGV
VTTEIPNLVLKKNYEQY~~T~~FLNEAETIAKYARELAEKGVNAIVVLAHVPATSKDGVAA~~G~~EAA~~D~~MI~~A~~KLNEI
YPEHSVDLVFAGHNH~~V~~YTNGTTGKTLIVQATSQGKAYADVR~~A~~VYD~~T~~DIADFKAVPTAKIIAVAPGQKT~~P~~S
PEIQAI~~V~~DEANTIVK~~K~~VT~~E~~QKIATASQATDISREVN~~E~~FKESAVGNLV~~T~~SAQLAIAKKSGYD~~V~~DFAMTNDG
GIRADLK~~V~~QEDGTVTWGAAQAVQPFGNILQVVQMTGEQIYTALNQQYDEGEKYFLQMSGIKYIYTKADNP
TEENPYKV~~V~~KAFKEDGTEIVPTET~~Y~~TLVINDFLFGGGDGFSIFKEAKLIGAINPDTEVFVEY~~L~~TDLEKAG
QTISATIPGRKAFVEKYVEEPKAE~~E~~KEDNAGTTT~~D~~VKTPEKANDGGDSVTN~~Q~~KATEQPAPSGSMAPISNK
KTEKASGNQTL~~P~~NTGQEALGSL~~L~~ISLGGIVSLGMAVSVRRKEGE

A0A0H3N5E4-Surfome

>tr|A0A0H3N5E4|A0A0H3N5E4_STRS4 Putative surface-anchored 5'-nucleotidase OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1432 PE=3 SV=1
MKKNIRLKSSI~~L~~ALVAGFSVIATQAVLADELAVQIMGVNDFHGALDMTGTA~~R~~LEGETVRNAGTAALLDAY
MDDSQA~~E~~FEETA~~A~~ETETPAESIRVQAGDMVGASPSNSGLLQDEPTVKVFNKMDVEYGT~~L~~GNHEFDEGLDE
YNRIMTGEAPKKGQFNEIVDNYTREAAKQEIVIANVIDKETGEIPYGWKPYA~~I~~KTIPVNDKEAKIGFIGV
VTTEIPNLVLKKNYEQY~~T~~FLNEAETIAKYARELAEKGVNAIVVLAHVPATSKDGVAA~~G~~EAA~~D~~MI~~A~~KLNEI
YPEHSVDLVFAGHNH~~V~~YTNGTTGKTLIVQATSQGKAYADVR~~A~~VYD~~T~~DIADFKAVPTAKIIAVAPGQKT~~P~~S
PEIQAI~~V~~DEANTIVK~~K~~VT~~E~~QKIATASQATDISREVN~~E~~FKESAVGNLV~~T~~SAQLAIAKKSGYD~~V~~DFAMTNDG
GIRADLK~~V~~QEDGTVTWGAAQAVQPFGNILQVVQMTGEQIYTALNQQYDEGEKYFLQMSGIKYIYTKADNP
TEENPYKV~~V~~KAFKEDGTEIVPTET~~Y~~TLVINDFLFGGGDGFSIFKEAKLIGAINPDTEVFVEY~~L~~TDLEKAG
QTISATIPGRKAFVEKYVEEPKAE~~E~~KEDNAGTTT~~D~~VKTPEKANDGGDSVTN~~Q~~KATEQPAPSGSMAPISNK
KTEKASGNQTL~~P~~NTGQEALGSL~~L~~ISLGGIVSLGMAVSVRRKEGE

A0A0H3N5P5-Exoproteome

>tr|A0A0H3N5P5|A0A0H3N5P5_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1550 PE=4
SV=1
MNSKIFSLRKSKMGLVSVIAIAFLWIGTGMMNETAMAEETDATALETQLESTESSLTNTVSENAAEEVTD
EVPSEEKKSEEMEDMEEELSFIEHLEVAPIQAGDQTISGNTTPGGYVAITIDGEAITSIENILEADDKG
DFSyrLSKPLAHSQTVEISALPKQFWTLEADSEERKVVVRNTHPEAYEIPAKRLEKTSNGMHQVFIEPV
FEHTSKVIGHTSVKGSVYLSINGSFVSDKTLIDPKDGRFEVTFSESLAGSKFKADDRLVLSFVSEDGQPV
ITNTIVKPLVKEKVSSQMTVKPLSSATSVLEGTTFPLGRVHLYNADTSEFIMEAIADETGHYKIALPALQ
SEDKYYRLTHNQEDLVSVHLDTVDGSSILLDKSVMASLATYLQDADMDEATDEDPIIVPKLHNKKDYIV
GRTIHLNAYVRMVSSIIGKQYPPVQVDELGFFGFQIQDLQLPFEKGERIRFEIIDPVTNNIIASKEEVVG
QYLEDEDVMDLPFQVEKVTTDHGYISGKTAPDVMIELVSTQNGEEIIGKTSTDSTGRFEFDLGSRLKNG
ETLSFRAFDKEGEQVAWEVVTQKGNHGRINKPKDKDEKEEQPSKEITKNIEQSNLTLEQTTLPPVRQTLT
DKKVEQNAEPSKEETVSIFFDSKKDMPTKQEKMARTVRDKGTGNVSVHDSGENTQVQSLPKTGEKTSLV
ANIMLSIILFLFALFIGKKKITESE

A0A0H3N5P5- Surfome

>tr|A0A0H3N5P5|A0A0H3N5P5_STRS4 Putative surface-anchored protein
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1550 PE=4
SV=1
MNSKIFSLRKSKMGLVSVIAIAFLWIGTGMMNETAMAEETDATALETQLESTESSLTNTVSENAAEEVTD
EVPSEEKKSEEMEDMEEELSFIEHLEVAPIQAGDQTISGNTTPGGYVAITIDGEAITSIENILEADDKG
DFSyrLSKPLAHSQTVEISALPKQFWTLEADSEERKVVVRNTHPEAYEIPAKRLEKTSNGMHQVFIEPV
FEHTSKVIGHTSVKGSVYLSINGSFVSDKTLIDPKDGRFEVTFSESLAGSKFKADDRLVLSFVSEDGQPV
ITNTIVKPLVKEKVSSQMTVKPLSSATSVLEGTTFPLGRVHLYNADTSEFIMEAIADETGHYKIALPALQ
SEDKYYRLTHNQEDLVSVHLDTVDGSSILLDKSVMASLATYLQDADMDEATDEDPIIVPKLHNKKDYIV
GRTIHLNAYVRMVSSIIGKQYPPVQVDELGFFGFQIQDLQLPFEKGERIRFEIIDPVTNNIIASKEEVVG
QYLEDEDVMDLPFQVEKVTTDHGYISGKTAPDVMIELVSTQNGEEIIGKTSTDSTGRFEFDLGSRLKNG
ETLSFRAFDKEGEQVAWEVVTQKGNHGRINKPKDKDEKEEQPSKEITKNIEQSNLTLEQTTLPPVRQTLT
DKKVEQNAEPSKEETVSIFFDSKKDMPTKQEKMARTVRDKGTGNVSVHDSGENTQVQSLPKTGEKTSLV
ANIMLSIILFLFALFIGKKKITESE

A0A0H3MXZ4-Exoproteome

>tr|A0A0H3MXZ4|A0A0H3MXZ4_STRS4 Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1786 PE=3 SV=1
MTKCDFDKRQRFGIRKFTIGACSVLIGATLFGTQVSADQLENVDSLSEPAVELSSVVNEHVEKTEAEEGM
SPISADEKAVTEELNGEASVSDSREEKLPSAPSDNPENKLEDTEEAEDKEVDSSDGLLLSDFPQVEDQG
IRPKEIKFDNWDQVLAWEPGARPDDDLNRASVELVERFRGHVVNERANENAKVEALSNTNSKAKDHASVG
GEEFKAYAFDYWQYIDSMVFW EGLIPSPDVIDAGHRNGVPVLGTIFYNWSSSIEDQEKFVSSMRQDPDGS
FPVARKLVDMAKYYGFDGYFINQETTGGVLVQPLGETMRNFMLYTKEYAESIGYPITYSWYDAMTYEYGRY
HEDGLGEYNYPFMEKEGDKVPADHFFANFNWTRAKNNYSIEVAKRIGRNPFDIFAGFELQRGGSYKTQIN
WDALFDENGKLLKLSLGLFAPDTITSLGATGEDYHENENIFFTGYQGDPKQKPSDKNWKYGLANLIADKTA
ITSSNFNSSFNTGHGKKWFVDGKVAKDGEWNYRSVSGILPTWRWWIEASGEKLAAAYDFDDAYNGGNSLR
FTGDLEKDGKQEI KLYSTKIPLSETSRRLVAHKGGQGANISLALALEPDYQFANKEAWRLKLSGDWQDQ
TFDLSSLAGKTVYGIQVVVENEAAALSDFDFRLGQLAIYDQENSPTAPKDGQVLAKRLKNAQDAEAVISFT
GTDDADYYEVYAQVDGQWKLLTGSSNTRIYLPQLVRSQAEGRTQALKVHAVGKNGLRSEAGEFIFDWEM
TVKDTSLPKPSAENIVLGAEVIGSSFAKKEGEGEGIEGMLNGTITSLSDKWSSHQLSGHVDIRLTQPRTVV
RWAMDHAGAGGESVNDGLMNTKDFDLYYKNENGDWVLAKEVRGNRDHVTDIVLDKPIRAQEWRLDVLTS
DNGTPWKAIRIYNWRMYEELDMETPNIPMTHAVARHLGNHQIQVGFKDVPANRKIALYSSPDVAVKPLAELE
TTESGNLIFDPIRFESLPEFIYYRTLEEGKDWSNLLAIRVPQGEKVVKAMEWIAPLEKKVYRQGSPLSLA
GAQFRVVFEGDWPAERVNTTNPAVTVRGFDPQKLGEQTLTVSYLGETLAQPLMVYVVEDIAQGEKKAVGL
EIQQLPKVQYVVGDDLDVTNGRFAIYDDESTQSFSLTEAGVEIVGFDSRKEGRQSLGLRYAGLET SFDV
LVSPKPIVND EYLKQKIAEIEALQTQTAYLYSSEQTQLALQTALEEA KSVVADTNRTVEQVEAAQTLL EK
QLGELDGEKLYQADLGRNLNQLIQEVKGIDRPINSELSSLLEKTEKILGSDSIRPDEM KELLSEWTDLFE
QSSLVTHVGT RDSMESKNLLAPEKPRMDLTIELVPRQIIITRTSTDPLGKERIVQEGADGQMMIAHLVYS
DGRRELYSRIVADESQPKIVEVGSGLP IQQEKTLMVENS LQVEKQIRDASLQKSGLPQTGD TYQEKYVFL
GLIGVALAGLSQLAKLRKQGE

A0A0H3MXZ4-Surfome

>tr|A0A0H3MXZ4|A0A0H3MXZ4_STRS4 Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1786 PE=3 SV=1
MTKCDFDKRQRFGIRKFTIGACSVLIGATLFGTQVSADQLENVDSLSEPAVELSSVVNEHVEKTEAEEGM
SPISADEKAVTEELNGEASVSDSREEKLPSAPSDNPENKLEDTEEAEDKEVDSSDGLLLSDFPQVEDQG
IRPKEIKFDNWDQVLAWEPGARPDDDLNRASVELVERFRGHVVNERANENAKVEALSNTNSKAKDHASVG
GEEFKAYAFDYWQYIDSMVFW EGLIPSPDVIDAGHRNGVPVLGTIFYNWSSSIEDQEKFVSSMRQDPDGS
FPVARKLVDMAKYYGFDGYFINQETTGGVLVQPLGETMRNFMLYTKEYAESIGYPITYSWYDAMTYEYGRY
HEDGLGEYNYPFMEKEGDKVPADHFFANFNWTRAKNNYSIEVAKRIGRNPFDIFAGFELQRGGSYKTQIN
WDALFDENGKLLKLSLGLFAPDTITSLGATGEDYHENENIFFTGYQGDPKQKPSDKNWKYGLANLIADKTA
ITSSNFNSSFNTGHGKKWFVDGKVAKDGEWNYRSVSGILPTWRWWIEASGEKLAAAYDFDDAYNGGNSLR
FTGDLEKDGKQEI KLYSTKIPLSETSRRLVAHKGGQGANISLALALEPDYQFANKEAWRLKLSGDWQDQ
TFDLSSLAGKTVYGIQVVVENEAAALSDFDFRLGQLAIYDQENSPTAPKDGQVLAKRLKNAQDAEAVISFT
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RWAMDHAGAGGESVNDGLMNTKDFDLYYKNENGDWVLAKEVRGNRDHVTDIVLDKPIRAQEWRLDVLTS
DNGTPWKAIRIYNWRMYEELDMETPNIPMTHAVARHLGNHQIQVGFKDVPANRKIALYSSPDVAVKPLAELE
TTESGNLIFDPIRFESLPEFIYYRTLEEGKDWSNLLAIRVPQGEKVVKAMEWIAPLEKKVYRQGSPLSLA
GAQFRVVFEGDWPAERVNTTNPAVTVRGFDPQKLGEQTLTVSYLGETLAQPLMVYVVEDIAQGEKKAVGL
EIQQLPKVQYVVGDDLDVTNGRFAIYDDESTQSFSLTEAGVEIVGFDSRKEGRQSLGLRYAGLET SFDV
LVSPKPIVND EYLKQKIAEIEALQTQTAYLYSSEQTQLALQTALEEA KSVVADTNRTVEQVEAAQTLL EK
QLGELDGEKLYQADLGRNLNQLIQEVKGIDRPINSELSSLLEKTEKILGSDSIRPDEM KELLSEWTDLFE
QSSLVTHVGT RDSMESKNLLAPEKPRMDLTIELVPRQIIITRTSTDPLGKERIVQEGADGQMMIAHLVYS
DGRRELYSRIVADESQPKIVEVGSGLP IQQEKTLMVENS LQVEKQIRDASLQKSGLPQTGD TYQEKYVFL
GLIGVALAGLSQLAKLRKQGE

This protein was not found in the surfome analysis

A0A0H3MXF6-Exoproteome

>tr|A0A0H3MXF6|A0A0H3MXF6_STRS4 Surface-anchored DNA nuclease
OS=Streptococcus suis (strain BM407) OX=568814 GN=ssnA PE=4 SV=1
MKIRNRSIFYTVGSVAVTAGLLLSLATSPIPSVHATEVAIENYPSLAITKSEVTIQGYLIAPLNSSGTAF
DATNKTNLALGASMDTAAADTIPIQLKEPLRSQFNLVNHPPELVGKLVRITGTSDTYMKRAGIKPATAIEI
VDSSSTNVQPPTSSENTATKPSDLVSTPIATVRSGAQGTEYTVSGKIIISLVNGWGGNGFYLQGSAGAGIYI
YPGAALGYQLGDTVQLTGTGLGEYKGELQLTTVSNHKAISENFNTPIETNIAQLATQAQATLVSLKNLTV
GDIQSDSYQNSTFTVTVDSEGQTVDVRLDSRTGIKTADLLNRINKGDKINLTAILSTYNGKIQLKPFDLSH
FEVIEKATTEAGLGKTEAVTVGRIQGASHQSPLVNQSVMLKNVVVTVTSANNFYVQDVTDPDGTCTKSDG
INIFTDKLKTNVKVGDVLVTIAGRVEEYQGRGYAERDKTDLTITQIRATEVTVDGTAPVPSPIVLGLDRTI
PADIIDNDGLAQFDPEQDALDFWESVEGMVVAVDDAKILGPLKNKEIYVTPATSQLPLNNVGGVNLRRPEG
NNTNIIPLLLKNGKQIVKSGDYFIGRIAGPVTYSYTNKYVYVDDSTLPTLHEGATKPETTTTIIPNDDKLT
IASYNIENFSANSKSTSDAKVQRIAKSFVSDLHSPDVIGLIEVQDNNGATNDGTTDASKSAERLIAAIQA
AGGPTYTYVDIAPENNKDGGQEGGNIRVGFYLYNSKRVSLSKPIGTATQAVAWENGELNLSLGRIDPTNP
AWAAVRKTAAEFVFKGEKVVLNHLNSKRGDNGLYGKIQPVSEFKSEKRRHILAQTIADFTKAGLAQNP
NANIVMLGDFNDYEFKTIETILEAGGMANLVSRRHSDRFSYFYNGNNSLDNMLVSTNLFERYAFDMVH
VNSAFMEEHGRASDHDPLLVQLDVTKAQEPTQPEPSDKQTDDSGTVNNSDDNGTTNNKPTNLSTSNQTA
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A0A0H3MXF6-Surfome

>tr|A0A0H3MXF6|A0A0H3MXF6_STRS4 Surface-anchored DNA nuclease
OS=Streptococcus suis (strain BM407) OX=568814 GN=ssnA PE=4 SV=1
MKIRNRSIFYTVGSVAVTAGLLLSLATSPIPSVHATEVAIENYPSLAITKSEVTIQGYLIAPLNSSGTAF
DATNKTNLALGASMDTAAADTIPIQLKEPLRSQFNLVNHPPELVGKLVRITGTSDTYMKRAGIKPATAIEI
VDSSSTNVQPPTSSENTATKPSDLVSTPIATVRSGAQGTEYTVSGKIIISLVNGWGGNGFYLQGSAGAGIYI
YPGAALGYQLGDTVQLTGTGLGEYKGELQLTTVSNHKAISENFNTPIETNIAQLATQAQATLVSLKNLTV
GDIQSDSYQNSTFTVTVDSEGQTVDVRLDSRTGIKTADLLNRINKGDKINLTAILSTYNGKIQLKPFDLSH
FEVIEKATTEAGLGKTEAVTVGRIQGASHQSPLVNQSVMLKNVVVTVTSANNFYVQDVTDPDGTCTKSDG
INIFTDKLKTNVKVGDVLVTIAGRVEEYQGRGYAERDKTDLTITQIRATEVTVDGTAPVPSPIVLGLDRTI
PADIIDNDGLAQFDPEQDALDFWESVEGMVVAVDDAKILGPLKNKEIYVTPATSQLPLNNVGGVNLRRPEG
NNTNIIPLLLKNGKQIVKSGDYFIGRIAGPVTYSYTNKYVYVDDSTLPTLHEGATKPETTTTIIPNDDKLT
IASYNIENFSANSKSTSDAKVQRIAKSFVSDLHSPDVIGLIEVQDNNGATNDGTTDASKSAERLIAAIQA
AGGPTYTYVDIAPENNKDGGQEGGNIRVGFYLYNSKRVSLSKPIGTATQAVAWENGELNLSLGRIDPTNP
AWAAVRKTAAEFVFKGEKVVLNHLNSKRGDNGLYGKIQPVSEFKSEKRRHILAQTIADFTKAGLAQNP
NANIVMLGDFNDYEFKTIETILEAGGMANLVSRRHSDRFSYFYNGNNSLDNMLVSTNLFERYAFDMVH
VNSAFMEEHGRASDHDPLLVQLDVTKAQEPTQPEPSDKQTDDSGTVNNSDDNGTTNNKPTNLSTSNQTA
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A0A0H3N6J4-Exoproteome

>tr|A0A0H3N6J4|A0A0H3N6J4_STRS4 Putative surface-anchored serine protease OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1843 PE=3 SV=1

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GPLSDDPVKTEQVDEPVAEEGVVEEVVDTEAGEESGLLTDQAATEIETTAGKTDESKEKEDISGKEASA
PQTIPQESQLEPEEVTTGRYILQFSEENRNVLVDKLLKIDGVKIVHEYKEVLTGASVEVGKESLSDVKAI
TELTSLEESRRIRPTLHTAKQLVGALKASSKYQTDGRGMVIAVIDSGLDIKHKDMRLDDGVIPIKIDITP
STTGTYTLKVPHGYNVYVSGNDNLYDDTHEPHGMHIAAGTLAGNATDEEVASKKGVDDGIAPNAQLLVYKIF
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SDTSFDLHTNNALGAVDTATTVGVAATPAVIAVGSARNTHLVQREFMLNGQSFYGYPIGYTTLTTEGKYEF
VDAGNGHWEEVQGLDLAGKVAVIKKDKFDLKDAVRNLKFKDVAGIIVINTDQGWNKDYYRTHQLLVDDKT
LLSYSSIWGISLSGEDGRRLLEVANQSQGNTGLVLKPTIGMKKLIEVPTVSGFSSWGPTVNLELKPEIVA
PGEDVYATLNDNRYGSMGTSMA SPIVAGASALLLPRIRQMTPEGMTRMDLLRIILMNTATPLVDVLDS
SGHALENSPRQQAGLLQIDRAFETDVILHHRLLKGGVELKEIGRETEFEVTLENLGNQQRSAISAGKVL
TSQDVPVDRIGRSGKVVKELHATEIKGSSIHLSQSIQLGPKEKRTIRLKL DAGEAKDQFAEGYIYFKSL
TEGQSDISIPYFGFVGWDSKERIVDAPAWETSSKLLKLT SVLSSYKHNSGRYIELGREKIQDNQSPLNPD
NIAIQNQHSDSQIGNAFVRFALLRDITNYDLDIVKEATEDAPVLRRIDTGTMLSRVRYVDYFESLSEYSK
LRTPIELHRWDGKVYDASNDENIPAPEGQYFFRLRVKNKENGAYQYTYLPVKIDNQKPEIVAIDTNRLLSS
HRELVVTA KDNNKVWEVRANLNGEDLLVEKVVDAGQLHYHLKEVELPLDAKNHLRVEVMDIAGNVVAVE
KDLMAPVIQFKNLEDLMAIRSKKTVEIKANVSAQVSDVQANLDAQAVNYSLENGQLSLQIPEQSDGRHSF
ELILKDKDGNLIYTKTLNLYVDNEKPTIDLDIEKDEEDEEVIQIGKNGRFTLKGKVSDNVSLPKDIKLYY
SNLDIGKGERKIIDVKEDGSFEQDFFKSDFPRAIMLTAVDEKGNKLDLRINTSPESLDEEEETEVPITV
NNWLIDPIRFNKESLGRELD SGLVDFKKQEDGTYLFTFEIEAE TEQAHSVRINGGEKRYFEDGKLTYPVT
LIEEGNVVDISVYNEADELTYTKKYQMLVDTENPVLQLENEVLP LERQVVDSEDEDEENQYAGVLLADA
DGHLTLTGSAKDNGIYWSLKINEDFVARGGFWRQYGNNEKAFRYELHSLKDGD TVKLDLSDSFGNAVVKK
YKVRINDKEVSEQVPEKDLHVERSDKDQTPSIPILKSEAHI PMPKEENSLAPQTGST EIALLTGDTREDG
VEHLGKLTKEEPLGISDERIEVSVPHREFFERSGIGETGALAADTS GKLPQTGDSLGSVFISTLLGLFG
GAMALGNLKRKE

A0A0H3N6J4-Surfome

>tr|A0A0H3N6J4|A0A0H3N6J4_STRS4 Putative surface-anchored serine protease
OS=Streptococcus suis (strain BM407) OX=568814 GN=SSUBM407_1843 PE=3 SV=1

MKQKWSQIENKQRFSIKKLSVGVASVSI GFFITGVPMVQADTS GEGLESTVAVATDMDSRQNSAVEKKED
GPLSDDPVKTEQVDEPVAEEGVVEEVVDTEAGEESGLLTDQAATEIETTAGKTDESKEKEDISGKEASA
PQTIPQESQLEPEEVTTGRYILQFSEENRNVLVDKLLKIDGVKIVHEYKEVLTGASVEVGKESLSDVKAI
TELTSLEESRRIRPTLHTAKQLVGALKASSKYQTDGRGMVIAVIDSGLDIKHKDMRLDDGVIPIKIDITP
STTGTYTLKVPHGYNVYVSGNDNLYDDTHEPHGMHIAAGTLAGNATDEEVASKKGVDDGIAPNAQLLVYKIF
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SDTSFDLHTNNALGAVDTATTVGVAATPAVIAVGSARNTHLVQREFMLNGQSFYGYPIGYTTLTTEGKYEF
VDAGNGHWEEVQGLDLAGKVAVIKKDKFDLKDAVRNLKFKDVAGIIVINTDQGWNKDYYRTHQLLVDDKT
LLSYSSIWGISLSGEDGRRLLEVANQSQGNTGLVLKPTIGMKKLIEVPTVSGFSSWGPTVNLELKPEIVA
PGEDVYATLNDNRYGSMGTSMA SPIVAGASALLLPRIRQMTPEGMTRMDLLRIILMNTATPLVDVLDS
SGHALENSPRQQAGLLQIDRAFETDVILHHRLLKGGVELKEIGRETEFEVTLENLGNQQRSAISAGKVL
TSQDVPVDRIGRSGKVVKELHATEIKGSSIHLSQSIQLGPKEKRTIRLKL DAGEAKDQFAEGYIYFKSL
TEGQSDISIPYFGFVGWDSKERIVDAPAWETSSKLLKLT SVLSSYKHNSGRYIELGREKIQDNQSPLNPD
NIAIQNQHSDSQIGNAFVRFALLRDITNYDLDIVKEATEDAPVLRRIDTGTMLSRVRYVDYFESLSEYSK
LRTPIELHRWDGKVYDASNDENIPAPEGQYFFRLRVKNKENGAYQYTYLPVKIDNQKPEIVAIDTNRLLSS
HRELVVTA KDNNKVWEVRANLNGEDLLVEKVVDAGQLHYHLKEVELPLDAKNHLRVEVMDIAGNVVAVE
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NNWLIDPIRFNKESLGRELD SGLVDFKKQEDGTYLFTFEIEAE TEQAHSVRINGGEKRYFEDGKLTYPVT
LIEEGNVVDISVYNEADELTYTKKYQMLVDTENPVLQLENEVLP LERQVVDSEDEDEENQYAGVLLADA
DGHLTLTGSAKDNGIYWSLKINEDFVARGGFWRQYGNNEKAFRYELHSLKDGD TVKLDLSDSFGNAVVKK
YKVRINDKEVSEQVPEKDLHVERSDKDQTPSIPILKSEAHI PMPKEENSLAPQTGST EIALLTGDTREDG
VEHLGKLTKEEPLGISDERIEVSVPHREFFERSGIGETGALAADTS GKLPQTGDSLGSVFISTLLGLFG
GAMALGNLKRKE

A0A0H3MYG2-Exoproteome

>tr|A0A0H3MYG2|A0A0H3MYG2_STRS4 Putative surface-anchored
amylopullulanase OS=Streptococcus suis (strain BM407) OX=568814
GN=SSUBM407_1919 PE=3 SV=1
MKRTGMLEKKQIFGIRKLNVGVASVGIAAALFLSGAGQLVQAEEVVLPASTSSTTLSEQDGGAVEATTTA
IEATDSMVAEATAVTETADATAPEEAPIEEGSIRLHFENVDETAPESQGLWTWGGVAEPSDGNQWPTDTA
NFSSSQVDDYGHYVDIKKSETPGTIGYLVLKNGEKITESDQKVELLVPEQNEAWIASDYSVSSYEPLKDE
NVLRIINYTREDDNNEGWSVWGTWGTTEASSGWPAGAVDFKLGKYGAYVDIPLSNGLDSKLGFLINQNNP
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DVTITERIKADGEKDWDEQVIYFMMTDRFYNGDTGNDKLVEGTASNPRGLYQGGDFKGVTAKLDYLKELG
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ETVLPPIAEVRYDATLAKGQSYVLQEGKAGKRVLVYQDVLVDGKVVATNLLSETVVDGEARIVVKGSMEA
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A0A0H3MYG2-Surfome

>tr|A0A0H3MYG2|A0A0H3MYG2_STRS4 Putative surface-anchored
amylopullulanase OS=Streptococcus suis (strain BM407) OX=568814
GN=SSUBM407_1919 PE=3 SV=1
MKRTGMLEKKQIFGIRKLNVGVASVGIAAALFLSGAGQLVQAEEVVLPASTSSTTLSEQDGGAVEATTTA
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NFSSSQVDDYGHYVDIKKSETPGTIGYLVLKNGEKITESDQKVELLVPEQNEAWIASDYSVSSYEPLKDE
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GLVSVTVTNPENAEIVKMEVDTSAGGGGLVPISTELNRVTIKATSSSTAPGTYSPLPVKVDKNGYYETKL
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A0A0H3MXR4-Exoproteome

>tr|A0A0H3MXR4|A0A0H3MXR4_STRS4 2',3'-cyclic-nucleotide 2'-
phosphodiesterase/3'-nucleotidase OS=Streptococcus suis (strain BM407)
OX=568814 GN=SSUBM407_1949 PE=3 SV=1
MNFRRFSKCAVALTLALLAASNPKLAQAEEILNTTPASSTEASQAVPVESDTTEEADNTESPVPATTEAEN
PSSSETAETS DPTSETTDTTTSEAR TVTPAATETSQPV EGQTV DVRI LATTDLHTNLVNYDYYQDKPVET
LGLAKTAVLIEEAKKENPNVVLVDNGDTIQGTPLGNYKSIVDPIEEGEQHMPYAALETLGFDVGT LGNHE
FNYGLAYLEKVIR TANMPLVNANVLDPTTKDFLYTPYTIVKKKTFTDTEGKKVTLNVGVTGIVPPQILNWD
KAYLEGKVIVRDAVEAVRDIIP TMRENGADIVLVLSHSGIGDDQYEVGEENVGYQIASLSGVD AVITGHS
HAEFPGTAEKPSFYAKYSGVDDTNGKINGTPVTMAGKYGDHLGVIDLNLVFKD GKWTTTSSKAAIRKIDT
KSSVADGRIIDLAKEAHNETIKYVRQQVGETTAPINSFFALVQDDPSVQIVNNAQIWIYAKQQLAGTSEAN
LPILSAAAPFKAGTRGDASAYTDIPAGPIAIK NVADLYLYDNVVAILKVNGAQLKEWLEMSAGQFNQVDL
SSTEPQNLVNTDFRTYNFDVIDGVTYQYDITQPNKYDRDGKIVNETASRVRNLQYNGQDVTADQEFIVVT
NNYRANGTFPGVREASINRLNLENRQAIINYIIAEKVINPTADNNWTF TDSIKGLDLRFLTADRAKSLV
TDQECIVYLQASTASEGFGEFKFVYTESKV VTPDEQQSDQGNTGQDIVLES GQRITLPAVNPPAPAPQHK
LASPHSQASTKTLPATGEATSMLSLLGLTLIGFVGAWTKKKEH

A0A0H3MXR4-Surfome

>tr|A0A0H3MXR4|A0A0H3MXR4_STRS4 2',3'-cyclic-nucleotide 2'-
phosphodiesterase/3'-nucleotidase OS=Streptococcus suis (strain BM407)
OX=568814 GN=SSUBM407_1949 PE=3 SV=1
MNFRRFSKCAVALTLALLAASNPKLAQAEEILNTTPASSTEASQAVPVESDTTEEADNTESPVPATTEAEN
PSSSETAETS DPTSETTDTTTSEAR TVTPAATETSQPV EGQTV DVRI LATTDLHTNLVNYDYYQDKPVET
LGLAKTAVLIEEAKKENPNVVLVDNGDTIQGTPLGNYKSIVDPIEEGEQHMPYAALETLGFDVGT LGNHE
FNYGLAYLEKVIR TANMPLVNANVLDPTTKDFLYTPYTIVKKKTFTDTEGKKVTLNVGVTGIVPPQILNWD
KAYLEGKVIVRDAVEAVRDIIP TMRENGADIVLVLSHSGIGDDQYEVGEENVGYQIASLSGVD AVITGHS
HAEFPGTAEKPSFYAKYSGVDDTNGKINGTPVTMAGKYGDHLGVIDLNLVFKD GKWTTTSSKAAIRKIDT
KSSVADGRIIDLAKEAHNETIKYVRQQVGETTAPINSFFALVQDDPSVQIVNNAQIWIYAKQQLAGTSEAN
LPILSAAAPFKAGTRGDASAYTDIPAGPIAIK NVADLYLYDNVVAILKVNGAQLKEWLEMSAGQFNQVDL
SSTEPQNLVNTDFRTYNFDVIDGVTYQYDITQPNKYDRDGKIVNETASRVRNLQYNGQDVTADQEFIVVT
NNYRANGTFPGVREASINRLNLENRQAIINYIIAEKVINPTADNNWTF TDSIKGLDLRFLTADRAKSLV
TDQECIVYLQASTASEGFGEFKFVYTESKV VTPDEQQSDQGNTGQDIVLES GQRITLPAVNPPAPAPQHK
LASPHSQASTKTLPATGEATSMLSLLGLTLIGFVGAWTKKKEH

A0A0H3MV01-Exoproteome

>tr|A0A0H3MV01|A0A0H3MV01_STRS4 Putative IgA-specific zinc metalloproteinase OS=Streptococcus suis (strain BM407) OX=568814 GN=zmpC PE=4 SV=1

MKRSLGEKRQRFGRKMSVGLVSAAVTSLFFVSSVATAPTASAQSIYNSYVTEQELTDGEKELIIRDLPGLAQETDVNYLIYRPATGTTSTPSTSTSQVLPNTGVSVESELLVAGGVSLLLAVRFGKKGKKELAGVILLTATGASFFGPTSSALTSQILARYNHAIEISAGQALPAPAEIDGYVYVGYLKDSKAIEQTTSEEEKTAEFFASEGIRTTETIVNKTAEIPFEIQTVENPQLSAGTERVVQEGQDGERIVTIKQVHSGQIIISEEEISSTVTKTAVPKIVEVGTQATDDIVTEVPDTEPSYENSTNSLTEETVTHTEVFADFVQEIYDVNLAEGSREVEQKGQDGVRTIETRNYYADGVLIKSEQVSDVVTKEPVTETVVRVGTKTDDVIGSETIVTTEELPFETTVTETEELVVGEEKFITEGKVGSKVETTTTYQTINGVSQPNPTVTEKVLLEPTTKVLEKGTKPIEGTEIETNQVEITFEYVYVDDPTLLEGGTKVVVTAGVNGSKTVTTTYQTIKGVVQENSTVTEETITKQPVKQVIARGTKVEKVPQVITDLDLVENDDAKSATISYKLTDETANFQRAVALLYDNTGALVQEQTITDPNGQLTLENLDFYTDYTVKTKI FYTMAEQEQSSEQEAILES MRKFDLVYKKIEIKDIDAVTVYRRKNGSYIGQEFLEELPASTDELFIKVTSDRFKEVYLPVSSIEETTLNGKAVFKLVSSSFDELVDQDKDAQYVANREFYIPKMATDANTYTSFKALLDAMKANPSGTFKLGAHLDASEVPVGDVASVYTNFSGTLDGLNDGYAFSISNLKAPLFFNLGGKVQNLDIKNASLNTSSKNPLATIAINANGATITNVAVEASIKGPQNVSGLVHSATNTTIKGVSFKGSIEVTGTNASLTGGIILGNGTMAVGNNAKVDATITLPGTENQVAGGIVGRITMLVYDVPGSVYNSYAAGSIVTTESAAIVGGIAGANQVTGAYAPHSGNVNNVSDMTGTSIIGQPANPTGKIKGDFTTTSDSLTNVTVITDEEAQAKVEAMAIQATIDDSVPLNPNHYSVDYLTLDKAQADHETAYYNMEKILPFYNKELLVYYGNKIATDDKLNKVRLLDVVPMKDNAVVDVYAEKANINKIMLHYADGTVDYKTVSYLEDYFKNNHVVEYITISGTDLIYTPESFLNDRSALVNDLVSSLSVVLDSDAMKAVINYPTTLNADTQTGTAKDFYFGESYDQVMTNLESNVRKILVASLNGQGQASEDYIKDKIINNKAAPVFLGLTYLNRWYDINFGEMNTKDLTIFEPDFFGNDAAALDMLAIGNGGYDVLRAHNNVTTFASIIIGKQNNQTKLFDMLEDYRQLFLPEMTNNEWFKQTTKAYVVEGKSLIPEVAAKQETTTDTYSKYNVGAYSKIVNDTVSNPTWKYNHMLPLTLPLQENIFITNMNTIAIGSYEHYVDDVSTVENRDKVRQMVDLAAERQDNDADFVYKILDETNRDKLFRSVLNNEGYVMYGKDGTYSYRNLTAADVDAIQDFYGPINKWYREHPSIKTAFADGSETYYITYDMLTDYGTALYTHEMVHNQDGDIIYLGKGRRIGQGMEVYAQGLLQNVFNVT EMNLGFNAVYNSDDANRVHVGDPVARENSEADFNEYHNQFDVLYLLDYLEGTNILAQSDANKKAWLRKIENYYVQNNGVDTTHAGNSARALTDAEVASLKSFNLDLIDQSIIVQRQYVNNPTNTSKKWDNRNSYVSPMFAAFNFSALSNSNGSPGDIMFRRMAFELIAAKGYTDGFVPYASGQLSDLAMEKGSIIYDTWNKKNKTGLITDDHVL EYVVFQGGYTSWTEFFKAMFTERLEKAATGQLKPFTMQYELGVADSTKEVTITTSFEQLQNLMEAMEADI QANSLNLNNSRVHALKVKVYQALMNSTNDFRTSIFN

A0A0H3MV01-Surfome

>tr|A0A0H3MV01|A0A0H3MV01_STRS4 Putative IgA-specific zinc metalloproteinase OS=Streptococcus suis (strain BM407) OX=568814 GN=zmpC PE=4 SV=1

MKRSLGEKRQRFGRKMSVGLVSAAVTSLFFVSSVATAPTASAQSIYNSYVTEQELTDGEKELIIRDLPGLAQETDVNYLIYRPATGTTSTPSTSTSQVLPNTGVSVESELLVAGGVSLLLAVRFGKKGKKELAGVILLTATGASFFGPTSSALTSQILARYNHAIEISAGQALPAPAEIDGYVYVGYLKDSKAIEQTTSEEEKTAEFFASEGIRTTETIVNKTAEIPFEIQTVENPQLSAGTERVVQEGQDGERIVTIKQVHSGQIIISEEEISSTVTKTAVPKIVEVGTQATDDIVTEVPDTEPSYENSTNSLTEETVTHTEVFADFVQEIYDVNLAEGSREVEQKGQDGVRTIETRNYYADGVLIKSEQVSDVVTKEPVTETVVRVGTKTDDVIGSETIVTTEELPFETTVTETEELVVGEEKFITEGKVGSKVETTTTYQTINGVSQPNPTVTEKVLLEPTTKVLEKGTKPIEGTEIETNQVEITFEYVYVDDPTLLEGGTKVVVTAGVNGSKTVTTTYQTIKGVVQENSTVTEETITKQPVKQVIARGTKVEKVPQVITDLDLVENDDAKSATISYKLTDETANFQRAVALLYDNTGALVQEQTITDPNGQLTLENLDFYTDYTVKTKI FYTMAEQEQSSEQEAILES MRKFDLVYKKIEIKDIDAVTVYRRKNGSYIGQEFLEELPASTDELFIKVTSDRFKEVYLPVSSIEETTLNGKAVFKLVSSSFDELVDQDKDAQYVANREFYIPKMATDANTYTSFKALLDAMKANPSGTFKLGAHLDASEVPVGDVASVYTNFSGTLDGLNDGYAFSISNLKAPLFFNLGGKVQNLDIKNASLNTSSKNPLATIAINANGATITNVAVEASIKGPQNVSGLVHSATNTTIKGVSFKGSIEVTGTNASLTGGIILGNGTMAVGNNAKVDATITLPGTENQVAGGIVGRITMLVYDVPGSVYNSYAAGSIVTTESAAIVGGIAGANQVTGAYAPHSGNVNNVSDMTGTKSIIIGQPANPTGKIKGDFTTTSDSLTNVTVITDEEAQAKVEAMAIQATIDDSVPLNPNHYSVDYLTLDKAQADHETAYYNMEKILPFYNKELLVYYGNKIATDDKLNKVRLLDVVPMKDNAVVDVYAEKANINKIMLHYADGTVDYKTVSYLEDYFKNNHVVEYITISGTDLIYTPESFLNDRSALVNDLVSSLSVVLDSDAMKAVINYPTTLNADTQTGTAKDFYFGESYDQVMTNLESNVRKILVASLNGQGQASE

DYIKEKIINNKAAFVLGLTYLNRWYDINFGEMNTKDLTIFEPDFFGNDAASALDMILAIGNGGYDVLRAH
NNVTTFASIIIGKQNNQTKLFDMLEDYRQLFLPEMTNNEWFKQTTKAYVVEGKS LIPEVAAKQETTDITYSK
YNVGAYSKIIVNDTVSNPTWKYNHMLLP LLTLPQENIFIITNMNTIAIGSYEHYVDDYSTVENRDKV RQMV
DLAAERQRDNADFWYKILDETNRDKLFRSVLNNEGYVMYGKDGTKSYRNLTA DVDAIQDFYGPINKWYRE
HPSIKTAFADGSETYYITYDMLTDYGTALYTHEMVHNQDGDIIYLKGYGRRIGQGMEVYAQGLLQNVFNVT
EMNLGFNAVYNSDDANRVHVGD PVARENSEADFNEYHNQFDVLYLLDYLEG TNILAQSDANKKAWLRKI
ENYYVQNNGV DTHAGNSARAL TDAEVASLKSFN DLIDQSIIVQRQYVNNPTNTSKK WDRNSYVSVPMFAA
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LEYVFGQYTSWTEFKKAMF TERLEKAATGQLKPFTMQYELGVADSTKEVTITSFEQLQNL MKEAMEADI
QANSLN LNNSRV HALKV K VYQALMNSTNDFRTSIFN
