

*Supplementary information*

Non-specific signal peptidase processing during extracellular protein transport in *Staphylococcus aureus* N315

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**Supplementary Table S1. Signal peptide cleavage sites and middle cleavages in the protein sequence observed in top-down analysis agree with amidination bottom-up analysis.**

No.	Protein accession/Name	Protein sequence in red color observed in the top-down analysis (Signal peptide ↓ cleavage site)	*N-term amidinated peptide observed in bottom-up analysis
1	P99134 Immunoglobulin G binding protein A precursor/ Spa, SACOL0095	MKKKNIYSIRKLGVGIASVTLGTLISGGVTPAANA↓ <b>AQHDEAAQQNAFYQVLNMPNLNADQR</b> NGFIQSLKDDPSQSANVLGEAQKLND SQAPKADAQQNNFNK DQQSAFYEILNMPNLNEAQRNGFIQSLKDDPSQSTNVLGEAKKLNESQAPKADNNFNKEQQNAFYEILN MPNLNEEQRNNGFIQSLKDDPSQSANLLSEAKKLNESQAPKADNKFNKEQQNAFYEILHLPNLNEEQRNNGF IQSLKDDPSVSKEILAEAKKLND AQAPKEEDNKKPGKEDGNKPGKEDGNKPGKEDNKKPGKEDGNKPG KEDNNKPGKEDGNKPGKEDNKKPGKEDGNKPGKEDGNKPGKEDGNVHVVKPGDTVNDIAKANGTT ADKIAADNKLADKNMIKPGQELVVDKKQPANHADANKAQALPET↓ <b>GEENPFIGTTVFGLSLALGAALLAGRREL</b>	*AQHDEAAQQNAFYQVLNMPNLNADQR  *GEENPFIGTTVFGLSLALGAALLAGR R
2	Q99SU9 Staphylococcal complement inhibitor	MKIRKSILAGTLAIVLASPLVTNLDKNEAQA↓ <b>STSLPTSNEYQNEKLANELKSLLDDELNVNELATGSLNTYYKRTIKISGLKAMYALKSKDFKKMSEA</b> <b>KYQLQKIYNEIDEALKSKY</b>	*STSLPTSNEYQNEK
3	P99160 Probable transglycosylase IsaA	MKKTIMASSLAVALGVTGYAAGTGHQAHA↓ <b>AEVNVDQAHLVDLAHNHQDQLNAAPI</b> KDGAYDIHFVKDGFQYNFTSNGTTWSWSYEAANGQTAGFS NVAGADYTTSYNQGSQSDVQSVSYNAQSSNSNVEAVSPTYHNYSTSTTSSSVRLSNGNTAGATGSSAAQI MAQRTGVSASTWAAIIARESNQGVNAYNPSGASGLFQTMPGWGPTNTVDQQINAAVKAYKAQGLGAW GF	*KKTIMASSLAVALGVTGYAAGTGHQA HA *AEVNVDQAHLVDLAHNHQDQLNAAPI K
4		MKKTIMASSLAVALGVTGYAAGTGHQAHA AEVNVDQAHLVDLAHNHQDQLNAAPIKDGAYDIHFVKD GFQYNFTSNGTTWSWSYEAANGQTAGFSNVAGADYTTSYNQGSQSDVQSVSYNAQSSNSNVEAVS↓ <b>APTYHNYSTSTTSSSVRLSNGNTAGATGSSAAQIMAQRTGVSASTWAAIIARESNQGVNAYNPSGAS</b> <b>GLFQTMPGWGPTNTVDQQINAAVKAYKAQGLGAWGF</b>	*APTYHNYSTSTTSSSVR
5	A0A0H3JK15 Uncharacterized protein	MKKLLTASHIACSVVMGVGLVNTSAEA↓ <b>ASGNSIDTVKQLIKGDQSLNENKIGESIKDVLTKYKNPMYSYNEDGTEHYEYFHTKKGMILLVTTDG</b> <b>KKNNGKVTHISMMYNDANGPTYQAVKNYVGKAVTHTEYSKVAGNFGYIEKGKTTYQFASAPKDK</b> <b>NIKLYRIDLEK</b>	*ASGNSIDTVK
6	A0A0H3JPH2 Uncharacterized protein	MKKKFVSSCIASTILFGTLLGVTYKAEA↓ <b>ATVHVAGGVWSHGIGKHYVWSYSHNKRNHGSTAVGKYSSFSGVARPGVQSKASAPKAWGGNK</b> <b>TFYSLH</b>	*ATVHVAGGVWSHGIGK *ATVHVAGGVWSHGIGKHYVWSYSH NKR
7		MKKKFVSSCIASTILF↓ <b>GTLLGVTYKAEATVHVAGGVWSHGIGKHYVWSYSHNKRNHGSTAVGKYSSFSGVARPGVQSK</b> <b>ASAPKAWGGNKTFYSLH</b>	*GTLLGVTYK



14	Q99TJ8 SACOL1710 Valine-tRNA ligase valS	MEMKPKYDPREVEAGRYEEVVKNGYFKPSEDKSKETYTIVIPPNVTGKLHLGHAWDTTLQDIITRMKR MQGYDTLYLPGMDHAGIATQAKVEAKLNEQGITRYDLGREKFLEQAWDWKEEYASFIRAQWAKLGLG LDYSRERFTLDEGLSKAVKKVFVDLYNKGIYRGERIINWDPKARTALSDIEVIHEDVQGAFYHFKYPYA DGEGFIEIATTRPETMLGDTAIVVNPNDERYKDVIGKTVILPIVGRELPILADEYVDIDFGSGAMKVTPAH DPNDFEIGQRHQLENIIVMDENGKMNDKAGKYEGMDRFDCKQLVKDLKEQDLVIKIEDHVHVSUGHSE RSGAVVEPYLSTQWVRMEDLAKRSLDNQKTD DRIDFYQRFEFHTFNQWMENIRDWTISRQLWWGHQI PAWYHKETGEIYVGEEAPTDIENWQQDEVDLDTWFSSALWPFSTLGWPDLESEDFKRYYP TNALVTGY DIIFFWARMIFQGLEFTDRRPFNDVLLHGLVRAEDGRKMSKSLGNGVDPMDVIDEYGADSLRYFLATG SSPGHDLRYSTEKVESVWNFINKIWNGARFSLMNIGEDFKVEDIDLSGNLSLADKWILTRLNETIATVTDL SDKYEFGEVGRALYNFIWDDFCDWYIEMSKIPMNSNDEEQKVTRSVLSYTLDNIMRMLHPFMPFVTEK IWQLPHEGDTIVKASWPEVRESLIFEESKQTMQQLVEIISKVRSRVEVNTPLSKEIPILIQAKDKEIETTLS QNKDYLIKFCNPSTLNISTDVEIPEKAMTSVVIAGKVVLPLEGLIDMDKEISRLEK ↓ <b>ELAKLQSELDRVDK</b> KLSNENFVSKAPEKVINEEKRKKQDYQEKYDGVKARIEQLKA	* <b>ELAKLQSELDRVDK</b>
15	A0A0H3JM99 SA1477, Uncharacterized protein	MSILT ↓ <b>HLIALLVILL</b> FRVGLSILRFLIYVGLVLLCIYLYGLIWLDDFFQINSGFLPHFQFNN	* <b>HLIALLVILLFRVGLSILR</b>
16	A0A0H3JLW4 SA1235, conserved hypothetical protein	<b>MWTVTKIRADYEGWWLFSDW</b> ↓ <b>PENIVEKYQYQDFDDMFKHYQQLIN</b> QCKVQFDNYVTGKYNIAFYNNCDMNYCEDCEDLQIFYSFI VLQNNEVYYKLPIID	* <b>PENIVEKYQYQDFDDMFKHYQQLIN</b> <b>CKVQFDNYVTGK</b>
17	P65986 DNA repair protein RecO	MLMRQKGIIKAVDYGESDKIITILNEHGAKVPLMARRAKKVKTGLQAQTQLFVYGLFIYNQWRGMGTL NSVDVISQHYKLQMDLYVSSYASLAAETIERSMDEGDIAPYNYQLLQFVLEKIESGTSACLMSVVVMLK CMKRFGFTASFNRCAVSGNDTQADLIGYSFKFDGAISRQEASK ↓ <b>DVHAVILSNK</b> TLYLDDVLQKLPIDKMNSLNHQEIDEMSDIILMLYREYAGMFFKSQKLINQLKRLEQ	* <b>DVHAVILSNK</b>

**Supplementary Table S2: Alternate signal peptide cleavages occurred during the SPase processing.**

	Protein accession, name, and sequence
1	<p><b>Q7A5M1 Extracellular matrix-binding protein</b></p> <p>Additional cleavages at one or more residues (↓) on either side of AXA</p> <p>MNYRDKIQKFSIRKYTVGTFSTVIATLVFLGFNTSQAH↓A↓A↓E↓TNQPASVVVKQKQSSNNEQTENRESQVQNSQNSQNSQSLSATHENEQPNNSEQANL VNQVAQSSTTNDQ<sup>160</sup>...<sup>3870</sup>LGTLTHTTTAQRNDLTNQIS</p> <p>Known/predicted signal peptide cleavage (↓) follows AXA pattern</p>
2	<p><b>P99134 Immunoglobulin G binding protein A</b></p> <p>MKKKNIYSIRKLGVGIASVTLGTLISGGVTPAAN↓A↓A↓QHDEAQQNAFYQVLNMPNLNADQQRNGFIQSLKDDPSQSANVLGEAQKLND SQAPKADAQQ NNFNKDQQSAFYEILNMPNLNEAQQRNGFIQSLKDDPSQSTNVLGEAKKLNESQAPKADNNFNKEQQNAFYEILNMPNLNEEQQRNGFIQSLKDDPSQSANLL SEAKKLNESQAPKADNKFNKEQQNAFYEILHLPNLNEEQQRNGFIQSLKDDPSVSKEILAEAKKLNDAPKEEDNKKPGKEDGNKPGKEDGNKPGKEDNKK PGKEDGNKPGKEDNKKPGKEDGNKPGKEDNKKPGKEDGNKPGKEDGNKPGKEDGNKPGKEDGNKPGKEDGNKPGKEDGNKPGKEDGNKPGKEDGNKPGKEDGNK KKQPANHADANKAQA LPET↓GEENPFIGTTVFGGSLSLALGAALLAGRREL</p>
3	<p><b>P61598 Putative surface protein SA2285</b></p> <p>MRDKKGPVNKRVDFLSNKLNKYSIRKFTVGTASILIGSLMYLGTQQEAEA↓A↓ENNIENPTTLKDNVQSKEVKIEEVTNKDTAPQGVEAKSEVTSNKDTI EHEASVKAEDISKEDTPKEVANVAEVQPKSSVTHNAEAPKVRKARSVDEGSFDITRDSKNVVESTPITIQGKEHFEGYGSV<sup>180</sup>.....<sup>1281</sup>ENPEKPSRPTHPS GPVNPNNPGLSKDRAKPNGPVHSMKDNDKVKKSKIAKESVANQEKKRAELPKTGLESTQKGLIFSSIIIGIAGLMLLARRRKN</p>
4	<p><b>A0A0H3JNG8 Staphylocoagulase</b></p> <p>MKKQIISLGALAVASSLFTWDNKADA↓I↓VTKDYSKESRVNEKSKKGATVSDYYYWKIIDSLEAQFTGAIDLLEDYKYGDPIYKEAKDRLMTRVLGEDQY LLKKKID EYELYKKWKSSNKNTNMLTFHKYNLYNLTMNEYNDIFNSLKDAVYQFNKEVKEIEHKNVDLKQFDKDGEDKATKEVYDLVSEIDTLVVTTYAD KDYGEHAKELRAKLDLILGDTDNPHKITNERIKKEMIDDLNSIIDDFFMETKQNRPN SITKYDPTKHNFKESKSNKPNFDKLVEETKKAVKEADESWKNKT VKKYEETVTKSPVVKEEKKVEEPQLPKVGNQQEVKTTAGKAEETTQPVAQPLVKIPQETIYGETVKGPEYPTMENKTLQGEIVQGPDFLTMEQNRPSLSDN YTQPTTPNP ILEGLEGSSSKLEIKPQGTESTLKG IQGESSDIEVKPQATETTEASQYGRPRQFNKTPKYVKYRDAGTGIREYNDGTFGYEARPRFNKPSSET NAYNVTTNQDGTVSYGARPTQNKPSSETNAYNVTTTHANGQVSYGARPTQKKPSKTNAYNVTTTHANGQVSYGARPTQKKPSKTNAYNVTTTHANGQVSYGARPT YKKPSETNAYNVTTTHANGQVSYGARPTQKKPSETNAYNVTTTHADGTATYGPRVTK</p>
5	<p><b>Q7A4V3 UPF0342 protein SA1663</b></p> <p>MAVNLYDYANQLEQALRESEEYKAIKEAF↓AN↓VKANEESKKLFDEFRETQINFQQKMQGEEIEAEDLQKAQEQAQAIEKDENISALMNAEQKMSQVFQ EINQIIVKPLDEIYAD</p>

6	<b>Q99SU9 Staphylococcal complement inhibitor</b> MKIRKSILAGTLAIVLASPLVTNLDKNEAQA↓S↓TSLPTSNEYQNEKLANELKSLLDELNVNELATGSLNTYYKRTIKISGLKAMYALKSKDFKKMSEAK YQLQKIYNEIDEALKSKY
7	<b>Q7A6A6 Glutamyl endopeptidase</b> MKGKFLKVSSLFVATLTTATLVSSPAANA↓L↓SSKAMDNHPQQTQSSKQQTPIKKGGNLKPLEQREHANVILPNNDRHQITD TTNGHYAPVTYIQVEAP TGTFIASGVVVGKDTLLTNKHVV DATHGDPHALKAFPSAINQDNYPNGGFTAEQITKYSGEGDLAIVKFSPNEQNKHIGEVVKPATMSNNAETQVNQNITV TGYPGDKPVATMWESKGKIT YLKGEAMQYDLSTTGGNSGSPVFNEKNEVIGIHWGGVPNEFN GAVFINENVRNFLKQNI EDIHFANDDQPNNPDNPDNPNN PDNPNNPDNPNNPDEPNPDNPNNPDNPNGDNNNSDNPDA A

The Yellow highlighted sequence is the typical signal peptide with ↓ a SPase cleavage site. The red arrow ↓ indicates the new additional cleavages.

A<sup>160</sup> ... <sup>3870</sup>B- The superscript number denotes the residue number in the protein sequence. The longer protein sequence is omitted due to the limited space.

**Supplementary Table S3: The non-specific cleavages occurred middle of the protein sequence in addition to the signal peptide cleavage during the SPase processing.**

NO.	Protein accession, name and sequence
1	<p><b>A0A0H3JPH2, Uncharacterized protein</b></p> <p>MKKKFVSSCIAS↓TILF↓GTLLGVITYKAEA↓</p> <p>ATVHVAGGVWSHGIGKHYVWSYYSHNKRNHGSTAVGKYSSF↓SGVARPGVQSKASAPKAWGGNKTfYSLH</p>
2	<p><b>P99160, Probable transglycosylase IsaA</b></p> <p>MKKTIMASSLAVALGVTGYAAGTGHQAHA↓</p> <p>AEVNVDAQHLVDLAHNHQDQLNAAPIKDGAYDIHFVKDGFQYNFTSNGTTWSWSYEAANGQTAGFSNVAGADYTTSYNQSDVQSVSYNAQSSN</p> <p>SNVEAVS↓APTYHNYSTSTTSSSVRLSNGNTAGATGSSAAQIMAQRTGVSASTWAAIIARESNGQVNAYNPSGASGLFQTMPGWGPTNTVDQQ</p> <p>INAAVKAYKAQGLGAWGF</p>
3	<p><b>P68800, Fibrinogen-binding protein</b></p> <p>MKNKLIAKSLLTIAAIGITTTTIASTADA↓</p> <p>SEGYGPREKKPVSINHN↓IVEYNDGTFKYQSRPKFNSTPKYIKFKHDYNILEFNDGTFEYGARPQFNKPAAKTDATIKKEQKLIQAQNLVREF</p> <p>EKTHTVSAHRKAQKAVNLVSFEYKVKMMVLQERIDNV↓LKQGLVR</p>
4	<p><b>P65289, Lipase 1</b></p> <p>MKSQNKYSIRKFSVGASSILIATLLFLSGGQAQA↓</p> <p>AEKQVNMGNSQEDTVTAQSIGDQQTRENANYQRENGVDEQQHTENLTKNLHNDKTI SEENHRKTDDLNDQLKDDKNSSLNNKNIQRDTTKNNN</p> <p>ANPSDVNQGLEQAINDGKQSKVASQQQSKEVDNSQDSNANNLPSQSLTKEAPSLNKSDQTSQREIVNETEIEKVQPQQNNQANDKITNHNFN</p> <p>EQEVKPKQDEKTLVSDLKNNQKSPVEPTKDNDKKNGLNLLKSSAVATLPNKGTKELTAKAKDDQTNKVAKQGQYKNQDPIVLVHGFNGFTDDI</p> <p>NPSVLAHYWGGNKMNIRQDLEENGYKAYEASISAFGSNYDRAVELYIIKGGRVYDGAHAHAAYGHERYGKTYEGIKDWKPGQKVHLVGHSMG</p> <p>GQTIRQLEELLRNGNREEIEYQKKHGGEISPLFKGNNDNMISITTLGTPHNGTHASDLAGNEALVRQIVFDIGKMFNGKNRSRVDFGLAQWGLK</p> <p>QKPNEsyIDYVkrvKQSNLWkskdNGfyDLTREGATDLNRKtSL↓NPNIVYKTYTGEATHKALNSDRQKADLNMFFPFVITGNLIGKATEKEW</p> <p>RENDGLVSVISSQHFPNQAYTNATDKIQKGIWQVTPTKHDWDHVDVFGQDSSDTVRTREELQDFWHHLADDLVKTEKVTDTKQA</p>
5	<p><b>Q7A7P2, Lipase 2</b></p> <p>MLRGQEERKYSIRKYSIGVSVLAATMFVVSSEAQA↓</p> <p>SEKTPTSNAAAQKETLNQPGEQGNAITSHQMQSGKQLDDMHKENGKSGTVTEGKDTLQSSKHQSTQNSKTI RTQNDNQVKQDSErQGSKQSHQN</p> <p>NATNNTerQNDQVQNTHHAERNGSQSTTSQSNVDKsQPSIPaQKVLpNHDKAAPTSTTPPSNDKTAPKSTKAQDATTDKHPNQDTHQPAHQI</p> <p>IDAKQDDTVRQSEQKPQVGDLskHIDGQNSPEKPTDKNTDNKQLIKDALQAPKTRSTTNAADAKKVRPLKANQVQPLNKYPVVFVHGFLGLVG</p> <p>DNAPALYPNYWGGNKFKVIEELRKQGYNVHQASVSafGSNYDRAVELYIIKGGRVYDGAHAHAAYGHERYGKTYKGIMPNWEPGKKVHLVGHs</p> <p>MGGQTIrLMEEFLRNGNKEEIAyHKAHGGEISPLFTGGHNMVASITTLATPHNGSQAADKFGNTEAVRKIMFALNRFMGNKYSNIDLGLTQWG</p>





	HRDEFDPKLPTGEKEEVPGKPGIKNPETGDVVRPPVDSVTKYGPVKGDSIVEKEEIPFKKERKFNPDLAPGTEKVTREGQKGEKTITPTLKNPLTGEIISKGESKEEITKDPINELTEYGPETITPGHRDEFDPKLPTGEKEEVPGKPGIKNPETGDVVRPPVDSVTKYGPVKGDSIVEKEEIPFEKERKFNPDLAPGTEKVTREGQKGEKTITPTLKNPLTGEIISKGESKEEITKDPVNELTEFGGEKIPQGHKIDFDPNLPDQTEKVPKPGIKNPDTGKVIEEPVDDVIKHGPKTGTPETKTVEIPFETKREFNPQLQPGEEVRVQEGQPGSKTITPTITVNPLTGEKVGEQGPTEEITKQPVDKIVEFGGEKPKDPKGPENPEKPSRPTHPSGPVNPNNGLSKDRAPNGPVHSMKDNDKVKKSKIAKESVANQEKKRAELPKTGLESTQKGLIFSSIIGIAGLMLLARRRKN
10	<b>Q7A6P2, Thermonuclease</b> MTEYLLSAGICMAIVSILLIGMA↓ ISNVSKGQYAKRFFFFFATSCLVLTLLVVVSSLSSSANA↓ <b>SQTDNGVN</b> RSGSEDPTVYSATSTKKLHKEPATLIKAIDGDTVCLMYKGQPMTRLLLVDTPETKHPKKGVEKYGPEASAFKKMVENANKIEVEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAVVYKPNNTHEQLLRKSEAQAKKEKLNWSEDNADSGQ
11	<b>A0A0H3JNR9, Uncharacterized protein</b> <b>MRENFKLRKMKVGLVSVVAITMLYIMTNGQAEA</b> ↓ <b>SETNQKVSTNQES</b> KAVSQTEQNSKETKAAESSKNFVNLDPIKPGAQKVTGTTLPNHIILLNIDGKSADSVEGGYGDFITANDKGEFEYPLNNRKIVHNQEI EVSSSSPD LGDDEEDEEVEESSTEKAGAEESTDAKATYTTTRYEKAYEIPKEQLKEKDGHHQVFIEPITEGSGIIKGHTSVKGKVAL↓ <b>SINNKFINFEER</b> AKGGISKEDTKASSDGVWMPINEKGYFDFDFKKNPFDNLELKKND EISLTFAPDDEDEALKSLIFKTKVTSLEDIDKAETKYDHTKVEKVKVLKDVKEDIHVDEIYGSLYHTEKGKGI LDKQGTKEITGKTKFANAVVKVYSDLGDAQLFDPDIQVDENGKFSFDAEKAGFRLQNGETLNFVAVVKPITGDL LHQGFVSKYIDVYESPEEKKEREFEEKLENTPAYHKLHGDKIVGYDVQGNPSTWFYPLGEKKVERTTPKLEK
12	<b>A0A0H3JKR2, Penicillin binding protein 2 prime</b> MKKIKIVPLILIVVVVVGFIYFYASKDKEINNTIDAIEDKNFKQVYKDSSYISKSDNGEVEEMTERPIKIYNSLGVKDINIQRKIKKVSKNKKRVDAQYKIKTNYGNIDRNVQFNFKEDGMWKLWDHDSV IIPGMQKQDSIHIENLKSERGI LDRNNVELANTGTAYEIGIVPKNVSKKDYKAI AKELSI SEDYIKQQMDQNWVQDDTFVPLKTVKKMDEYLSDFAKKFHLTTNETESRNYPLGKATSHLLGYVGPINSEELKQKEYKGYKDDAVIGKKGL↓EKLYDKKLQHEDGYRVTIVDDNSNTIAHTLIEKKKKDGKDIQLTIDAKVQKSIYNNMKNDYSGGTAIHPQTGELLALVSTPSYDVYPFMYGMSNEEYNKLTEDKKEPLL NKFQITTS PGSTQKILTAMIGLNNKTLDDKTSYKIDGKGWQKDKSWGGYNVTRYEVVNGNIDLKQAI ESSDNIFFA RVALELGSKKFEKGMKKLGVGEDIPSDYPFYNAQISKNLNDNEILLADSGYGQGEILINPVQILSIYSALENNGNINAPHLLKDTKNKVWKKNIISKENINLLTDGMQOV↓ <b>VNKTHKEDI</b> YRSYANLIGKSGTAE↓ <b>LKMKQGETGR</b> QIGWFI SYDKDNPNNMMMAINVKDVQDKGMASYNAKISGKVYDELYENGNNKYDIDE
13	<b>A0A0H3JTB6, Uncharacterized protein</b> MTVKNLFLGFVAVILTVCLIGLLILATNEDALAKVHKTINTLNAINVSTEDTYKKKMDILNIHTAKA↓SEVNENVEKQNHFKHRVNANKSNSFNEQECQVIADRYADKHINDNYGLERISKTNHGYNYVYSNDNSTSKQHVSISNQGIITK
14	<b>A0A0H3JNE5, Putative long chain fatty acid-CoA ligase VraA</b> MIMGNLRQQEYFRIYKNNTSTTHRNAYWVKLAKNVEATKMMYALSTIVQQHASIRHFFDVTDDNLTMLHEFLPFIEIKQVPSSSANYDLEAFFKQELSTYHFNDSPFLFKVKLFQFADAAYILLDFHVSIFDDSQIDIFLDDL CNAYRGNTVINNTRQHAHINRNDKDNQDASHIALDSNYFRL

	<p>ENNSDIHIDSYFPIKHPFEQALYQTYLIDDMTSIDMASLAVSVYLANHIMSQQHDTVLTGIVHPSHLPNDLHGNIVPLTLTIDAKDVCQRFTTDF  NKCVLQNMSQLQCAKSSLSLETIFHCYHHMMSCCNDVIEDVHQIHDATSLADIEIFPHQHGFKI IYNSAAYDLLSIETLSDLVRNIYQLITEE  NGNKRRTTVDELNLMTERDIQLYDDINLSLPEIDDAQTVVTLFEQQVEATPNHVAVQFDGVFITYQTLNARANDLAHRLRNQYGVPEPNDRVAVIA  EKS IEMI IAMIGVLKAGGAYVPIDPNYPSDRQEYILKDATPKVVITYQALYENGKQNIHIDLNKIAWKNIDNLSKCNLTLEDHAYVIYTSGTTG  NPKGTLIPHGRIVRLVHRNHVPLNEETTILLSGTIAFDAATFEIYGALLNGGKLIVAKKEQLLNPIAVEQLINENDVNTMWLTSSLFNQIASE  RIEVLVPLKYLLIGGEVLNAKWVDLLNQKPKHPQI INGYGPTENTTFTTTYNI PNKVPNRIPIGKPI LGTHVYIMQGERRCGVGIPGELCTSGF  GLAAGYLNQPELTADKFIKDSNINQLMYRSGDIVRLLPDGNIDYLYRKDKQVKIRGFRIELSEVEHALERI QGINKAVVIVQNHDQDQYIVAYY  EAMHTLSHNKIKSQLRMTLPEYMI PVNFMHIEQIPITINGKLDKKALPIMDYVDTDAYVAPSTDTEHLLCQIFADILHVNQVGIHDNFFELGGH  SLKATLVVNRIEASTGKRLQIGDLLQKPTVFELAQAIKQVQEQNYEVIPEAIVKDDYVLSSAQKRMVLLWKSNNHKDTVYNVPFLWRLSSGLNVA  QLQQAVQH LIARHEILRTQYIVVDDEVQRIVADVADFEENVTHFTDEQEIMRQFVAPFNLEKPSQIRVRYIRSP L HAYLFIDTHHI INDGMS  NIQLMNDLNALYQHKL L LPLKLQYKDYSEWMSHRDMTKHRQYWLSQFKDEVPI LSLPTDYVRPNIKT TNGAMMSFTMNQMRQLLQKYVEKHQI  TDFMFFMSVVM TLLSRYARKDDVVVGSVMSARMHKGTEQMLGMF↓ANTLVYRGQPSPKMW TQFLQEVKEMSLEAYEHQEYPFEC LVNDLDQS  HDASRNPLFDVMLVLQNNETNHAHFGH SKLTHIQPKSVTAKFDLSFI I EEDRDDYTINIEYNTDLYHSETVRHMG NQCMIMIDYILKHQDTLQI  CDIPNGTEELLNWVNTHVNDRLNVPGNKSIISYFNEVVS RQGNHVALVMNDLTMTYETLRNYVDAIAHMLLSNGVGNQORVALFTERSFEMIA  AMLATVKVGASYIPIDIDFPNKRQGAILED AKVTAVMSYGV E IETTL PVIQLEN AKGFVESKE NEQYDDLHGNQLENTAMLDNEMYAIYTS GTT  GMPKGVAIRQRNLLNLVHAWSTELQLGDNEVFLQHANIVFDASVMEIYCCLLNGHTLVI PDREERVNPEQLQQLINKHRVTVASIPLQMC SIME  DFYIEKLITGGATSTASFVKYIEKHCGTYFNAYGPSESTVITSYWSHHCGDLIPETIPIGKPLSNIQVYIMSDGLLCGIGMPGELCIAGDSLAI  GYINRPELMADKWQNNPFGKGKLYHSGDLARYTSDGQIEFLGRIDKQVKVNGYRIELDEIENVILAIRGISDCVVTVSHFDTHDILNAYYVGEQ  QVEQDLKQYLNQDLPKYMI PKTITHIDCMPLTTNDKVDTRRLPNPSP IQQSNKVYSEPSNEIEQT FVDVFGEVLKQNDVGVD DDFELGGNSLE  AMLVVSHLKRFGHHISMQTLYQYKTVRQIVNYMYQNQSSLVALPDNLSELQKIVMSRYNLGILEDSLSHRPLGNTLLTGATGFLGAYLIEALQG  YSHRIYCFIRADNEEIAWYKLMTNLNDYFSEETVEMMLSNI EIVGVDFECMDDVVL PENMDTI IHAGARTDHF GDDDEF EKVN VQGTVDVIRLA  QQHHARLIYVSTISVGTYFDIDTEDVTFSEADVYKGQLLTSPYTRSKFYSELKVLEAVNNGLDGRIVRVGNLTSPYNGRWHMRNIKTNRFSMVM  NDLLQLDCIGV SMAEMPVDFS FVDTTARQIVALAQVNT PQI IYHVLSPNKMPVKSLLECVRKEIELVSEDSFNEILQKQDMYETIGLTSVDRE  QQLAMIDTTLTLKIMNHISEKWPTITNNWLYHWAQYIKTIFNK</p>
15	<p><b>P64416, Histidine ammonia-lyase</b></p> <p>MTLYLDGETLTIEDIKSFLQQQSKIEIIDDALERVKKSRAVVERI IENEETVYGITTGFGLFSDVRIDPTQYNE↓LQVNLIRSHACGLGEPFS  KEVALVMMILRLNLTLLKGHSGATLELVRQLQFFINERI IPII PQQGLGASGD LAPLSHLALALIGEGKVLYRGE EKSDDDVLRELNRQPLNLQ  AKEGLALINGTQAMTAQGVISYIEAEDLG YQSEWIAALTHQSLNGI IDAYRHDVH SVRN FQE QINVAARMRDWLEGSTLTTRQAEIRVQDAYTL  RCIPQIHGASFQVFNYVKQQL E FEMNAANDNPLIFEEANET FVISGGNFHGQPIAFALDHLKLG VSELANVSERRLERLVNPQLNGDLP AFLSP  EPGLQSGAMIMQYAAASLVSENKTLAHPASVDSITSSANQEDHVSMTTAARHGYQI IENARRVLAIECVIALQA AELKGVEGLSPKTRRKYEE  FRSIVPSITHDRQFHKDIEAVAQYLKQSIYQTTACH</p>
16	<p><b>A0A0H3JQ77, Penicillin-binding protein 3</b></p> <p>MLKRLKEKSNDEIVQNTINKRINFIFGVIVFIFAVLVLR LGLYQIAQGSHYKQI IKNDENITVNESVPRGRILDRNGKVLVDNASKMAITYTRG  RKTTQSEMLDTAEKLSKLIKMDTKKITERDKKDFWIQLHPKKAKAMMTKEQAMLADGSIKQDQYDKQLLSKIGKSQ LDELSSKDLQVLAIFREM  NAGTVLDPQMIKNEDVSEKEYAAVSQQLSKLPGVNTSMDWDRKYPYGDTLRGIFGDVSTPAEGIPKELTEHYLSKGYSRNDRVGKSYLEYQYED  VLRGKKKEMKYTTDKSGKVTSS EVLNPGARGQDLKLTIDIDLQKEVEALLDKQIKKLR SQGAKMDNAMMVVQNPKNGDILALAGKQINKSGKM  TDYDIGTFTSQFAVGSSVKG GTLLAGYQNKAIKV↓GETMVDEPLHFQGG LTKRSYFNKNGHVSINDKQALMHSSNVYMFKTALKLAGDPYYSG  MALPSDISSPAQKLRRGLNQVGLGVKTGIDL PNETRGQIEPLTNPN GNYLDLSIGQYDTYTPQLSQYVSTIANDGYRIQPHIGLTIHESTNKD</p>

	EVGPLKKKINGTVLNKVNTEKEIKQIQEGFKMAFNDKDGTYVSFKDTVVPVPTAGKTGTAEVFQNGEPRVNSTYIGYAPIDDPKLAFSIVYTNQ PVPPPWLTTGGDLGRDVINYFYKQLGKDDKNKDKDK
17	<b>A0A0H3JKY5, SA1224 protein</b> MLQVTDVSLRFGDRKLFEDVNIKFTEGNCYGLIGANGAGKSTF↓ <b>LKILSGELDSQTGHVSLGKNER</b> LAVLKQDHYAYEDERVLDVVIKgherL YEVMKEKDEIYMKPDFSDEDGIRAAEEGEFAEMNGWNAEADAANLLSGLGIDPTLHDKKMAELENQKI KVLLAQSLFGEPDVLLLLDEPTNGL DIPAI SWLEDFLINF DNTVIVVSHDRHFLNNVCTHIADLDFGKIKVYVGN YDFWYQSSQLAQKMAEQNKKKKEEKMKELQDFIARFSANASKSK QATSRKKQLEKIELDDIQSSRRYPFVKFTPEREIGNDLLIVQNLSKTIDGKVLDNVSFTMNPNDKAILIGDSEIAKTTLLKILAGEMEPEDEG SFKWGVTTSLSYFPKDNSEFFEGVNMNLVDWLRQYAPEDEQTETFLRGFLGRMLFSGEEVKKKASVLSGGGEKVR CMLSKMMLSSANVLLLDEPT NHLDESITAVNDGLKSFKGSIIFTSYDFEFINTIANRVIDLNKQGGVSKEIPYEEYLQEIGVLK
18	<b>Q7A600, Probable dual-specificity RNA methyltransferase RlmN</b> MITAEKKKKKNKFLPNFDKQSIYSLRFDEM QNWLVEQGGQKFRAKQIFEWLYQKRVD SIDEMTNLSKDLRQLLKDNFTVTTLTTVVKQESKDGTI KFLFELQDGYTIETVLMRHDYGN SVCVTTQVGCRIGCTFCA↓ <b>STLGGLKRN</b> LEAGEIVSQVLTVQKALDATEERSVQIVIMGIGEPFENYDEM MDFLRIVNDDNSLNIGARHITVSTSGIIPRIYDFADEDIQINFAVSLHAAKDEVRSRLMPINRAYNVEKLEIAIQYYQEKTNRRTFEYGLFGG VNDQLEHARELAHLIKGLNCHVNLIPVNHVPERNYVK TAKNDIFKFEKELKRLGINATIRREQSDIDAACGQLRAKERQVETR
19	<b>P99135, Phosphoglycerate kinase</b> MAKKIVSDLDLKGKTVLVRADFNVPLKDGEITNDNRIVQALPTIQYII EQGGKIVLFSHLGKVKEESDKAKLTLRPVAEDLSKKLDKEVVFVPE TRGEKLEAA↓ <b>IKDLKEGDVLLVENTRY</b> EDLDGKKESKNDPELGKYWASLGDFVND AFGTAHREHASNVGISTHLETAAGFLMDKEIKFIGGV VNDPHKPVVAILGGAKVSDKINVIKNLVNIADKIIIGGGMAYTFLKAQGKEIGISLLEEDKIDFAKD LLEKHGDKIVLPVDTKVAKEFSNDAKI TVVPSDSIPADQEGMDIGPNTVKLFADELEGAHTVVWNGPMGVFEFSNFAQGTIGVCKAIANLKDAITIIIGGDSAAAAISLGFENDFTHISTG GGASLEYLEGGKELPGIKAINNK
21	<b>A0A0H3JM99, Uncharacterized protein</b> MSILT↓ <b>IILIALLVILLFR</b> VGLSILRFLIYVGLVLLCIYLG YQGLIWLLDFFQINSGFLPHFQFN
22	<b>P99108, Cell division protein FtsZ</b> MLEFEQGFNHLATLKVIGVGGGGNNAVNRMIDHGMNNVEFIAINTDGQALNLSKAESKIQIGEKLTRGLGAGANPEIGKKA AEE SREQIEDAIQ GADMVFTVSGMGGGTGTGAAPVVA KIAKEMGALT VGVVTRPFSFEGRKRQTQAAAGVEAMKA AVDTLIVIPNDRLLDIVDKSTPMMEAFK EADN VLRQGVQGISDLIAVSGEVNLD FADVKTIMSNQGSALMGIGVSSGENRAVEAAKKAISSPLLET SIVGAQQVLMNITGGESLSLFEAQEAADIV QDAADEDVNMI FGTVINPELQDEIVVTVIATGFDDKPTSHGRKSGSTGFGTSVNTSSNATSKDESFT↓ <b>SNSSNAQATDSVSERT</b> HTTTKEDDIP SFIRNREERRSRRTTR
23	<b>A0A0H3JNV0, SA2202 protein</b> <b>MKRLLFVMI</b> AFVF <b>FILAACGNSSK</b> ↓ <b>DKEANKDSK</b> TINVGTETGYAPFSFHDKDGKLTGYDIDVIKAVAKEEGLKLKFNETSWDSMFAGLDAGR FDVIANQVGINPDREKKYKFSKPYTFSSAVLVIRENEKDIKDFDDVKGKKLAQTFTSNYGLAKADKGADITKVDGFNQSM DLLLSKRVDGTFND SLSYLDYKKQKPN↓ <b>AKIKA</b> KGNAEQSRSAFAFSKADDET VQKFNDGLKKIEENGELAKIGKKWFGQDVSKSK

24	<p><b>A0A0H3JMK9, SA1273 protein</b></p> <p>MPNKILLVDGMALLFRHFYATSLHKQFMYN SQGVPTNGIQGFVRHIFSAIHEIRPTHVAVCWDMGQSTFRNDMFDGYKQNR SAPPEELIPQFDY  VKEISEQFGFVNIGVKNYEADDVIGTLAQQYSTDNVDVYIITGDKDLLQCINDNVEVWLIKKGFNINYR YTLHRFN E EYALEPQQLIDIKAFMGD  TADGYAGVKGIGEKTAIKLIQQYQSVENVVENID↓<b>ALSAGQR</b>NKINDNLDELYLSKRLAEIHTQVPIDSEALFEKMSFATTLNHILSICNEHE  LHVSGKYISSHF</p>
25	<p><b>Q7A423, Staphylococcal secretory antigen ssaA2</b></p> <p><b>MKKIATATIATAGFATIAIASGNQAHA</b>↓SEQDNYGYNPNDPTSYSYTYTIDAQGNHYHTWKGNWHPSQLNQDNGYYSYYYNGYNNYNNYNNNG  YSYNNYSRYNNYSNNNQSYNNYNSYNTNSYRTGGLGASYSTSSNNVQVTTTMAPSSNGRSISSGYTSGRNLYTSGQCTYYVFDRVGGKIGST  WGNASNWANAAAAGYTVNNTPKAGAIMQTTQGAYGHVAYVESVNSNGSVRVSEMNYGY↓<b>GPGVVTSRT</b>ISASQAAGYNFIH</p>
26	<p><b>A0A0H3JK15, Uncharacterized protein</b></p> <p><b>MKKLLTASIIACSVVMGVGLVNTSAEA</b>↓ASGNSIDTVKQLIKGDQSL ENVKIGESIKDVLTKYKNPMYSYNEDGTEHYEYEFHTKKGMLLVTTD  GKKNNGVKVTTHISMMYNDANGPTYQAVKNYVGKAVTHTHEY↓<b>SKVAGNFGYIEKGK</b>TTYQFASAPKDKNIKLYRIDLEK</p>
27	<p><b>A0A0H3JM43, TPR_REGION domain-containing protein</b></p> <p>MNIDKQFWKTIYYWIRYLNFDIVSREKDDQEIWLAHKRKKQVVIKQHIKSTQEIRFDKAKVLEHKDEIANFISFEPQSFEFYFTESEFSEEQ  LNEVSPIRIKFNVIRHTKDLIKHMPNIFLARLISEDNDKKTMYFYKRKVLTDNFLDKYMQKFSPATYTIIFVNVLIWLCMILYLN NFSDVKLLD  VGGLVHFNVVHGEWYRIVTSMFLHFSFEHILMNMLSLFIFGKIVEAII GSWRMLTVYFIAGLFGNFVLSFN TTTISVGASGAIFGLIGSIFAM  MYVSKTFNKKMLGQLLIALVILVGVSLFMSNINIVAHIGGFIGGLLITLIGYYYKVN RNIFWILLIGMLVIFIALQIRIFTIKEDNIYNKLIKD  DMTSGNYDNAQNIVKQTINKNYADDQTYYS↓<b>GMIMATINSKSEGMTEWER</b>GLRMFPKSGLLNFELAIANRSLNDDEKALKYVRKALNADPKN  TDYINLEKELTKSNESKNK</p>
28	<p><b>A0A0H3JTW9, Cell division protein FtsL</b></p> <p>MAVEKVYQPYDEQVYNSIPKQQPQTKPEKKT VSRKV VVQLTKFEKVLYITLITVIAMLSIYMLS LKMDAYDTRGKIADLDYKIDKQSSENSALQ  SEIKKNSSYERIYEKAKKQGM↓<b>SLENDNVKVVR</b>SNGEAKN</p>
29	<p><b>A0A0H3JPQ1, SA1000 Fibrinogen-binding protein</b></p> <p><b>MKKNFIGKSILSIAAISLTVSTFAGESHA</b>↓<b>QTKNVEAAK</b>KYDQYQTNFKKQVNKKV VDAQAVNLFKRTRTVATHRKAQRAVNLIHFQHSYEK  KKLQRQIDL V↓<b>LKYNTLK</b></p>
30	<p><b>P60432, 50S ribosomal protein L2</b></p> <p>MAIKKYPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQKGLTVRHHGGG HKRQYRVIDFKRNKDGINAKVDSIQYDPNRSANIALV  VYADGEKRYIIAPKGLEVGQIVESGA EADIKVGNALPLQNI PVGTVVHNI ELKPGKGGQIARSAGASAQVLGKEGKYVLIRLSRSGEVRMILSTC  RATIGQVGNLQHEL VNVGKAGRSRWKGIRPTVRG↓<b>SVMNPNDHPHGGGEG</b>RAPIGRPSMPSPWGKPTLGKKTRRGKSSDKLIVRGRKKK</p>

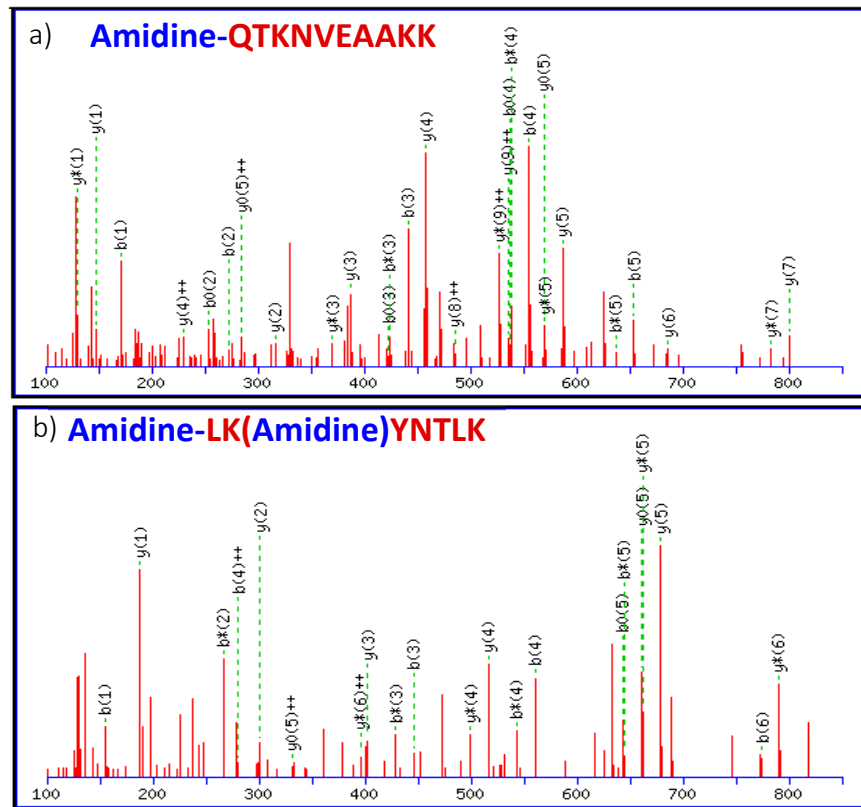
31	<p><b>P99152, Elongation factor Tu</b></p> <p>MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERGITINTSHIEYQTDKRHYAHVDCPGHADYVKNMIT  GAAQMDGGILVVSAADGPMPTREHILLSRNVGVPALVVFLNKVDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALEGDAQYEEK  ILELMEAVDTYIPTPERDSKPFMMPVEDVFSITGRGT VATGRVERGQIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGV  AREDVQRGQVLA↓<b>APGSITPHTEFKA</b>EVYVLSKDEGGRHTPFFSNYRPQFYFRTTDVTGVVHLPEGTEMVMPGDNVEMTVELIAPIAIEDGTR  FSIREGGRTVGSGVVTEIIK</p>
32	<p><b>P60185, Adapter protein Meca</b></p> <p>MRIERVDDTTVKLFITYSDIEARGFSREDLWTRKRGEFFWSMMDEINEEEDFVVEGPLWIQVHAFEKGVEVTISKSKNEDMMNMSDDDATDQ  <u>FDEQVQELLAQTLEGEDQLEELFEQRTKEKEAQGSKRQKSSARKNTRTIIVKFNDLEDVINYAYHSNPITTEFEDLLYMVDGTYYYAVHFDSHV</u>  DQEVINDSYSQLEFAYPTDRTEVYLNDYAKIIMSH↓<b><u>NVTAQVRRY</u></b>FPETTE</p>

**Figure S1**

**A0A0H3JPQ1 SA1000 Fibrinogen-binding protein**

**MKKNFIGKSILSIAAISLTVSTFAGESHA**<sup>29</sup>↓<sup>30</sup>**QTKNVEAAKK**YDQYQTNFKKQVNKKVVDAQK

AVNLFKRTRTVATHRKAQRAVNLIHFQHSYEKKKLQRQIDL↓<sup>103</sup>**LKYNTLK**

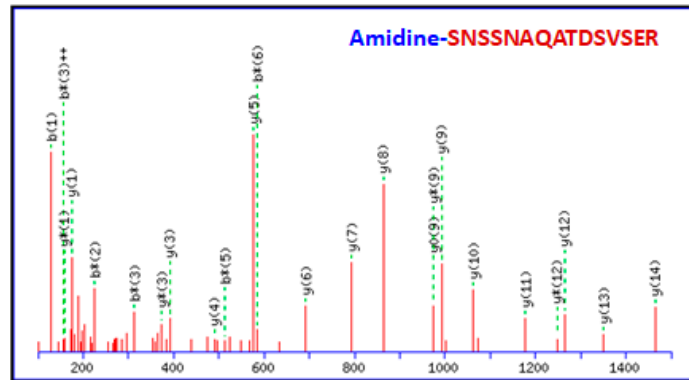


**Figure S1. MS/MS spectra of the normal SPase I cleavage and cleavage near to C-terminal.** a. MS/MS spectrum of the peptide <sup>30</sup>QTKNVEAAKK amidinated at the N-terminus confirms the signal peptide cleavage. b. MS/MS spectrum of the peptide <sup>103</sup>LKYNTLK amidinated at the N-terminus and lysine residue. This cleavage occurs near the C-terminus of the protein.

Figure S2.

a) **P99108 Cell division protein FtsZ**

MLEFEQGFNHLATLKVIGVGGGGNNAVNRMIDHGMNNVEFI AINTDGGQAL  
NLSKAESKIQIGELTRGLGAGANPEIGKAAEESREQIEDAIQGADMVFTS  
GMGGGTGTGAAPVVAKIAKEMGALTGVVTRPFSFEGRKRQTQAAAGVEA  
MKAAVDTLIVPNDRLLDIVDKSTPMMEAFK EADNVLRQGVQGISDLIAVSG  
EVNLDFAVDKTIMSNQGSALMGIGVSSGENRAVEAAKAISSPLLETSIVGAQ  
GVLNMITGGESLSLFEAQEAADIVQDAADEDVNMIFGTVINPELQDEIVVTVI  
ATGFDDKPTSHGRKSGSTGFGTSVNTSSNATSKDESFT↓**SNSSNAQATDSV**  
**SER**THTTKEDDIPSFIRNREERRSRRTTR



b) **P60432 Ribosomal protein L2**

MAIKKYPITNGRRNMTSLDFAEITKTTPEKSLKPLPKAGRNNQGKLTVR  
HHGGGHKRQYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRYI  
IAPKGLEVGQIVESGAEDIKVGNALPLQNIPVGTVVHNIELKPGKGGQIARS  
AGASAQVLGKEGKYVLIRLSGEVRMILSTCRATIGQVGNLQHELNVNGKAG  
RSRWKGIRPTVRG↓**SVMNPNDHPHGGGEGR**APIGRPSPMPSPWGKPTLG  
KKTRRGKKSSDKLIVGRKKK

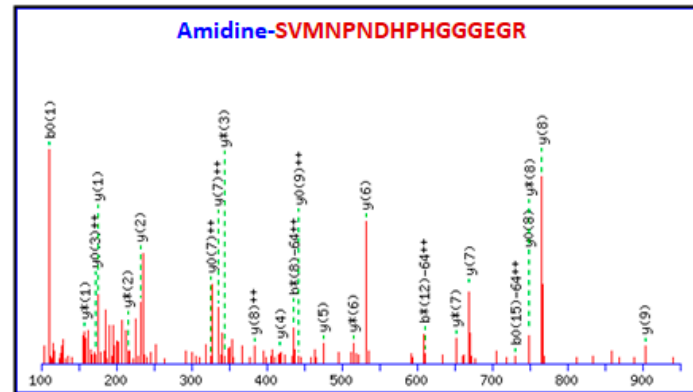


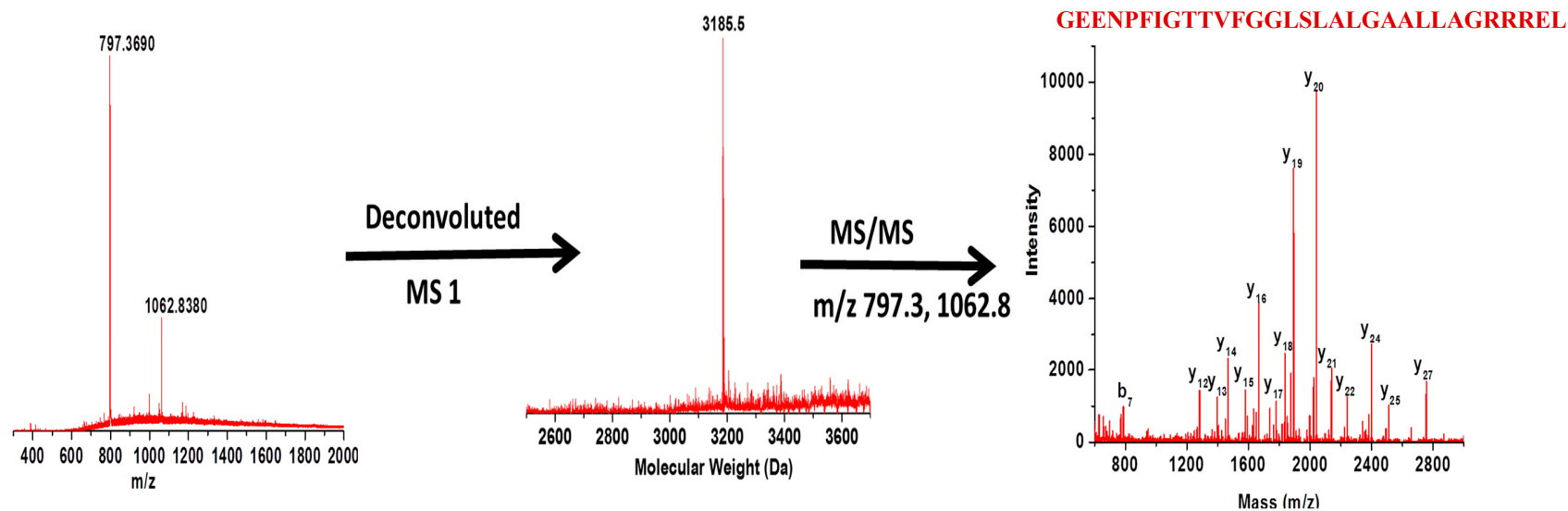
Figure S2. Cytoplasmic proteins are processed middle of their sequence and may be exported outside of the cell

- MS/MS spectrum of the peptide non-specifically cleaved middle of the proteins. Cell division protein FtsZ is not a secretory protein and does not have the signal peptide. It is present in the inner surface of the cell membrane and is involved in cell division.
- The MS/MS spectrum of a peptide from ribosomal protein L2. The protein is processed middle of the sequence and exported outside of the cell.

**Figure S3. Representative deconvoluted top-down mass spectra**

**a. P99134 Immunoglobulin G binding protein A**

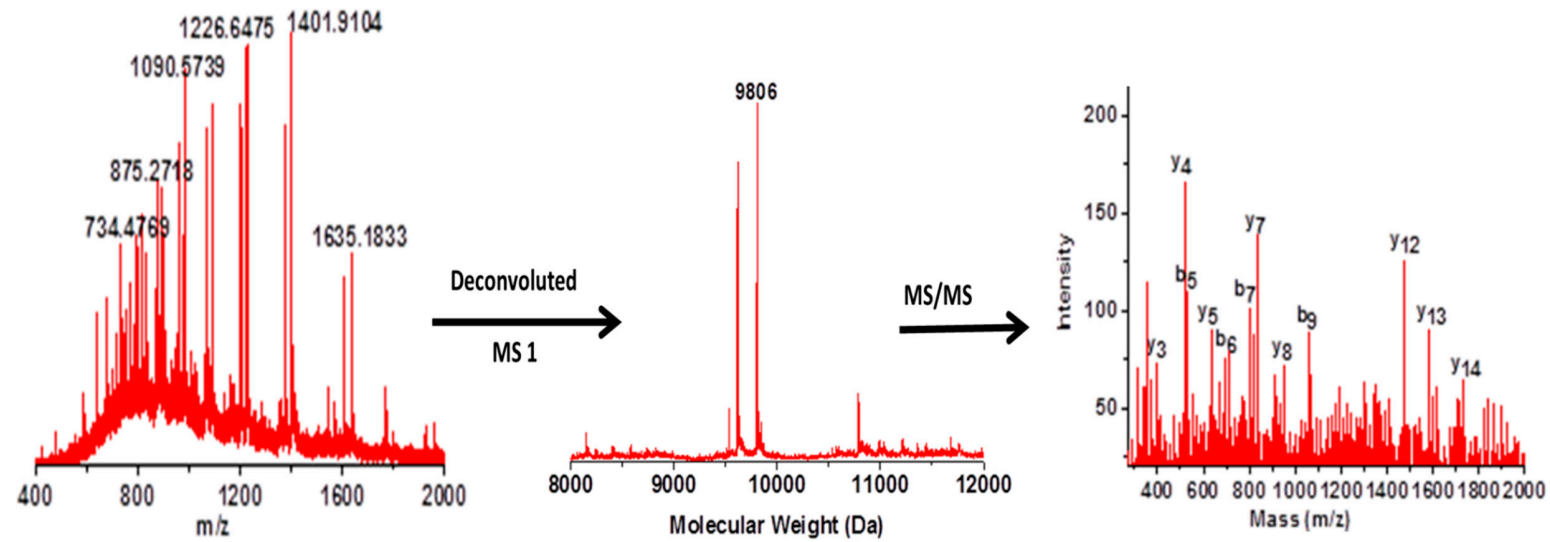
MKKKNIYSIRKLGVGIA SVTLGTLISGGVTPAANAAQHDEAQQNAFYQVLNMPNLNADQRNGFIQSLKDDPSQSANVLGE  
 AQLNDSQAPKADAQQNNFNKDQQSAFYEILNMPNLNEAQRNGFIQSLKDDPSQSTNVLGEAKKLNESQAPKADNNFNKE  
 QQNAFYEILNMPNLNEEQRNGFIQSLKDDPSQSANLLSEAKKLNESQAPKADNKFNKEQQNAFYEILHLPNLNEEQRNGFIQS  
 LKDDPSVSKEILAEAKKLNDAQAPKEEDNKKPGKEDGNKPGKEDGNKPGKEDNKKPGKEDGNKPGKEDNKKPGKEDGNK  
 PGKEDNNKPGKEDGNKPGKEDGNKPGKEDGNKVHVVKPGDTVNDIAKANGTTADKIAADNKLADKNMIKPGQELVVDKK  
 QPANHADANKA QALPET ↓ **GEENPFIGTTVFGGLSLALGAALLAGRRREL**





**b. Q99SU9 Staphylococcal complement inhibitor**

MKIRKSILAGTLAIVLASPLVTNLDKNEAQA↓**STSLPTSNEYQNEKLANELKSLLDELNVNELATGSLNTYYKRTIKISGLKAMYAL**  
**KSKDFKKMSEAKYQLQKIYNEIDEALKSKY**



**Supplementary Table S4. Proteins and their fragments observed in intact protein analysis. Red colored amino acid sequence is the best match to the observed mass.**

Sr. No	Protein Accession, name	Observed Mass (Da)	Protein Sequence
1	P99160, Probable transglycosylase IsaA	9189.4	MKKTIMASSLAVALGVTGYAAGTGHQAHA AEVNVDQAHLVDLAHNHQDQLNAAPIKDGAYD IHFVKDGFQYNFTSNGTTWSWSYEAANGQTAGFSNVAGADYTTSYNQGS DVQSVSYNAQSSN SNVEAVSAPTYHNYSTSTTSSSVRLSNGNTAGATGSSAAQIMAQRTGVSASTWAAIIARESNQ VNAYNPSGASGLFQTMPGWGPTNTVDQQINA AVKAYKAQGLGAWGF
2		9203(-17Da)	MKKTIMASSLAVALGVTGYAAGTGHQAHA AEVNVDQAHLVDLAHNHQDQLNAAPIKDGAYD IHFVKDGFQYNFTSNGTTWSWSYEAANGQTAGFSNVAGADYTTSYNQGS DVQSVSYNAQSSN SNVEAVSAPTYHNYSTSTTSSSVRLSNGNTAGATGSSAAQIMAQRTGVSASTWAAIIARESNQ VNAYNPSGASGLFQTMPGWGPTNTVDQQINA AVKAYKAQGLGAWGF
3		10602	MKKTIMASSLAVALGVTGYAAGTGHQAHA AEVNVDQAHLVDLAHNHQDQLNAAPIKDGAYD IHFVKDGFQYNFTSNGTTWSWSYEAANGQTAGFSNVAGADYTTSYNQGS DVQSVSYNAQSSN SNVEAVSAPTYHNYSTSTTSSSVRLSNGNTAGATGSSAAQIMAQRTGVSASTWAAIIARESNQ VNAYNPSGASGLFQTMPGWGPTNTVDQQINA AVKAYKAQGLGAWGF
4	P99134, Immunoglobulin G binding protein A precursor	3185.5	MKKKNIYSIRKLGVG IASVTLGTLISGGVTPAANAAQHDEAQQNAFYQVLNMPNLNADQRNG FIQSLKDDPSQSANVLGEAQKLND SQAPKADAQQNNFNKDQQSAFYEILNMPNLNEAQRNGFI QSLKDDPSQSTNVLGEAKKLNESQAPKADN FNKEQQNAFYEILNMPNLNEEQRNGFIQSLKD DPSQSANLLSEAKKLNESQAPKADN KFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSVSK EILAEAKKLND AQAPKEEDNKKPGKEDGNKPGKEDGNKPGKEDNKKPGKEDGNKPGKEDNN KPGKEDGNKPGKEDNNKPGKEDGNKPGKEDGNKPGKEDGNKVHVVKPGD TVNDIAKANGTT ADKIAADNKLADKNMIKPGQELVVDKKQP ANHADANKAQA LPETGEENPFIGTTVF GGLSLAL GAALLAGRRREL
5		17579	MKKKNIYSIRKLGVG IASVTLGTLISGGVTPAANAAQHDEAQQNAFYQVLNMPNLNADQRNG FIQSLKDDPSQSANVLGEAQKLND SQAPKADAQQNNFNKDQQSAFYEILNMPNLNEAQRNGFI QSLKDDPSQSTNVLGEAKKLNESQAPKADN FNKEQQNAFYEILNMPNLNEEQRNGFIQSLKD DPSQSANLLSEAKKLNESQAPKADN KFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSVSK EILAEAKKLND AQAPKEEDNKKPGKEDGNKPGKEDGNKPGKEDNKKPGKEDGNKPGKEDNN KPGKEDGNKPGKEDNNKPGKEDGNKPGKEDGNKPGKEDGNKVHVVKPGD TVNDIAKANGTT ADKIAADNKLADKNMIKPGQELVVDKKQP ANHADANKAQA LPETGEENPFIGTTVF GGLSLAL GAALLAGRRREL
6		28807	MKKKNIYSIRKLGVG IASVTLGTLISGGVTPAANAAQHDEAQQNAFYQVLNMPNLNADQRNG FIQSLKDDPSQSANVLGEAQKLND SQAPKADAQQNNFNKDQQSAFYEILNMPNLNEAQRNGFI QSLKDDPSQSTNVLGEAKKLNESQAPKADN FNKEQQNAFYEILNMPNLNEEQRNGFIQSLKD DPSQSANLLSEAKKLNESQAPKADN KFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSVSK EILAEAKKLND AQAPKEEDNKKPGKEDGNKPGKEDGNKPGKEDNKKPGKEDGNKPGKEDNN KPGKEDGNKPGKEDNNKPGKEDGNKPGKEDGNKPGKEDGNKVHVVKPGD TVNDIAKANGTT

			ADKIAADNKLADKNMIKPGQELVVDKKQPANHADANKAQALPETGEENPFIGTTVFGLSLAL GAALLAGRREL
7		12835	MKKKNIYSIRKLGVGIASVTLGTLISGGVTPAANAAQHDEAQQNAFYQVLNMPNLNADQRNG FIQSLKDDPSQSANVLGEAQKLNDQAPKADAQQNNFNKDQQSAFYEILNMPNLNEAQRNGFI QSLKDDPSQSTNVLGEAKKLNESQAPKADNNFNKEQQNAFYEILNMPNLNEEQRNGFIQSLKD DPSQSANLLSEAKKLNESQAPKADNKFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSVSK EILAEAKKLNDQAPKEEDNKKPGKEDGNKPGKEDGNKPGKEDNKKPGKEDGNKPGKEDNN KPGKEDGNKPGKEDNNKPGKEDGNKPGKEDGNKPGKEDGNVHVVKPGDTVNDIAKANGTT ADKIAADNKLADKNMIKPGQELVVDKKQPANHADANKAQALPETGEENPFIGTTVFGLSLAL GAALLAGRREL
8	A0A0H3JNG8, staphylocoagulase	13416	MKKQIISLGALAVASSLFTWDNKADAIVTKDYSKESRVNEKSKKGATVSDYYYWKIIDSLEAQF TGAIDLLEDYKYGDPIYKEAKDRLMTRVLGEDQYLLKKKIDEYELYKKWYKSSNKNTNMLTF HKYNLYNLTMNEYNDIFNSLKDAVYQFNKEVKEIEHKNVDLKQFDKDGEDKATKEVYDLVSEI DTLVVTTYADKDYGEHAKELRAKLDLILGDTDNPHKITNERIKKEMIDDLNSIIDFFMETKQN RPNSITKYDPTKHNFKESKNPNFDKLVEETKKA VKEADESWKNKTVKKYEETVTKSPVKE EKKVEEPQLPKVGNQQEVKTTAGKAEETTQPAQPLVKIPQETIYGETVKGPEYPTMENKTLQG EIVQGPDLTMEQNRPSLSDNYTQPTTPNPILEGLEGSSSKLEIKPQGTESTLKGIGESSDIEVKP QATETTEASQYGPRPQFNKTPKYVKYRDAGTGIREYNDGTFGYEARPRFNKPSETNAYNVTTN QDGTVSYGARPTQNKPSETNAYNVTTHANGQVSYGARPTQKKPSKTNAYNVTTHANGQVSYG ARPTQKKPSKTNAYNVTTHANGQVSYGARPTYKKPSETNAYNVTTHANGQVSYGARPTQKKP SETNAYNVTTHADGTATYGPRVTK
9	P67579, Methionine-- tRNA ligase	13176	MAKETFYITPIYPSGNLHIGHAYSTVAGDVIARYKRMQGYDVRYLTGTDEHGQKIQEKAKQ AGKTEIEYLDEMIAGIKQLWAKLEISNDDFIRTTEERHKHVVEQVFERLLKQGDIYLGEYEGWY SVPDETYTESQLVDPQYENGKIIGGKSPDSGHEVELVKEESYFFNISKYTDRLLEFYDQNPFDIQ PPSRKNEMINNFIKPGLADLAVSRTSFNWGVHVPSNPKHVYVWIDALVNYISALGYLSDDDSL FNKYWPADIHLMAKEIVRFHSIIWPILLMALDLPLPKKVFAHGWILMKDGKMSKSKGNVDPNI LIDRYGLDATRYYLMRELPGSDGVFTPEAFVERTNFDLANDLGNLVNRTISMVNKYFDGELPA YQGPLELDEEMEAMALETVKSYTESMESLQFSVALSTVWKFISRTNKYIDETTPWVLAKDDS QKMDLGNVMAHLVENIRYAAVLLRPFLTHAPKEIFEQLNINNPQFMEFSSLEQYGVLTESIMVT GQPKPIFPRLDSEAEIAYIKESMQPPATEEEKEEIPSKPQIDIKDFDKVEIKAATIIDAHVKKSDKL LKIQVDLDSEQRQIVSGIAKFYTPDDIIGKKVAVVTNLKPAKLMGQKSEG MILSAEKDGVLT LVS LPSAIPNGAVIK
10	Q7A7T0, Glycyl-glycine endopeptidase LytM	14901	MKKLTAAAIA TMGFATFTMAHQADAAETTNTQQAHTLMSTQSQDVSYGTYYTIDSNGDYHHT PDGNWNQAMFDNKEYSYTFVDAQGHTHYFYNCYPKNANANGSGQTYVNPATAGDNNDYTA SQSQQHINQYGYQSNVGPDASYSHSNNNQAYNSHDGNGKVNYPNGTSNQNGGSASKATASG HAKDASWLT SRKQLQPYGQYHGGGAHYGV DYAMPENSPVYSLTDGTVVQAGWSNYGGGNQ VTIKEANSNNYQWYMHNNRLTVSAGDKVKAGDQIAYS GSTGNSTAPHVHFQRMSSGIGNQYA VDPTS YLQSR
11		11669	MKKLTAAAIA TMGFATFTMAHQADAAETTNTQQAHTLMSTQSQDVSYGTYYTIDSNGDYHHT PDGNWNQAMFDNKEYSYTFVDAQGHTHYFYNCYPKNANANGSGQTYVNPATAGDNNDYTA

			SQSQQHINQYGYQSNVGPDASYSHSNNNQAYNSHDGNGKVNYPNGTSNQNGGSASKATASG HAKDASWLTSRKQLQPYGQYHGGGAHYGV DYAMPENSPVYSLTDGTVVQAGWSNYGGGNQ VTIKEANSNNYQWYMHNNRLTVSAGDKVKAGDQIAYSGSTGNSTAPHVHFQRMSSGIGNQYA VDPTS YLQSR
12		18495	MKKLTA AAIATMGFATFTMAHQADAAETTNTQQAHTLMSTQSQDVSYGTYYTIDSNGDYHHT PDGNWNQAMFDNKEYSYTFVDAQGH THYFYNCYPKNANANGSGQTYVNPATAGDNNDYTA SQSQQHINQYGYQSNVGPDASYSHSNNNQAYNSHDGNGKVNYPNGTSNQNGGSASKATASG HAKDASWLTSRKQLQPYGQYHGGGAHYGV DYAMPENSPVYSLTDGTVVQAGWSNYGGGNQ VTIKEANSNNYQWYMHNNRLTVSAGDKVKAGDQIAYSGSTGNSTAPHVHFQRMSSGIGNQYA VDPTS YLQSR
13	A0A0H3JLB5, SA0295 protein	12910	MNKISKYIAIASLSVAVTVSAPQTTNSTAFAKSSAEVQQTQQASIPASQKANLGNQNIMAVAWY QNSAEAKALYLQGYNSAKTQLDKEIKKNGKHKLAIALDLDET VLDNSPYQGYASIH NKPFPE GWHEWVQA AKAPVYGAK EFLKYADKKGV DIYYISDRDKEKDLKATQKNLKQQGIPQAKKS HILLKGKDDKSKESRRQMVQKDHKL VMLFGDNL LDFTDPKEATAESREALIEKH KDDFGKKYII FPNPMYGSWEATIYN NNYKASDKAKDKLRKNAIKQFDPKTGEVK
14		9626	MNKISKYIAIASLSVAVTVSAPQTTNSTAFAKSSAEVQQTQQASIPASQKANLGNQNIMAVAWY QNSAEAKALYLQGYNSAKTQLDKEIKKNGKHKLAIALDLDET VLDNSPYQGYASIH NKPFPE GWHEWVQA AKAPVYGAK EFLKYADKKGV DIYYISDRDKEKDLKATQKNLKQQGIPQAKKS HILLKGKDDKSKESRRQMVQKDHKL VMLFGDNL LDFTDPKEATAESREALIEKH KDDFGKKYII FPNPMYGSWEATIYN NNYKASDKAKDKLRKNAIKQFDPKTGEVK
15	A0A0H3J JV0, Exotoxin 15	11595	MKLKNI AKASLALGILTTGMITTTAQPVKASTLEVRSQATQDLSEYYKGRGFELTNVTGYKYG NKVTFIDNSQQIDVTLTGNEKLT VKDDDEVS NVDVFV VREGSDKSAITTSIGGITKTNGTQH KDT VQNVNLSVSKSTGQHTTSVTSEYYSIYKEEISLKELDFKLRKHLIDKHDLYKTEPKDSKIRITMK NGGYTFELNKKLQPHRMGDTIDSRNIEKIEVNL
16		13003	MKLKNI AKASLALGILTTGMITTTAQPVKASTLEVRSQATQDLSEYYKGRGFELTNVTGYKYG NKVTFIDNSQQIDVTLTGNEKLT VKDDDEVS NVDVFV VREGSDKSAITTSIGGITKTNGTQH KDT VQNVNLSVSKSTGQHTTSVTSEYYSIYKEEISLKELDFKLRKHLIDKHDLYKTEPKDSKIRITMK NGGYTFELNKKLQPHRMGDTIDSRNIEKIEVNL
17		8516	MKLKNI AKASLALGILTTGMITTTAQPVKASTLEVRSQATQDLSEYYKGRGFELTNVTGYKYG NKVTFIDNSQQIDVTLTGNEKLT VKDDDEVS NVDVFV VREGSDKSAITTSIGGITKTNGTQH KDT VQNVNLSVSKSTGQHTTSVTSEYYSIYKEEISLKELDFKLRKHLIDKHDLYKTEPKDSKIRITMK NGGYTFELNKKLQPHRMGDTIDSRNIEKIEVNL MKLKNI AKASLALGILTTGMITTTAQPVKAS TLEVRSQATQDLSEYYKGRGFELTNVTGYKYGNKVTFIDNSQQIDVTLTGNEKLT VKDDDEVS NVDVFV VREGSDKSAITTSIGGITKTNGTQH KDTVQNVNLSVSKSTGQHTTSVTSEYYSIYKEE ISLKELDFKLRKHLIDKHDLYKTEPKDSKIRITMK NGGYTFELNKKLQPHRMGDTIDSRNIEK IEVNL
18	A0A0H3J NR9, Uncharacterized protein	15445	MRENFKLRKMKVGLVSVAITMLYIMTNGQAEASETNQKVSTNQESKAVSQTEQNSKETKAAE SSKNFVNLDPIKPGAQKV TGTTLPNHIILLNIDGKSADSV EGGYGDFITANDKGEFEYPLNNRKIV HNQEIEVSSSPDLGDDEE DEEVEESSTEKAGAEESTDAKATYTTPRYEKAYEIPKEQLKEKDG HHQVFIEPITEGSGIIKGHTSVKGKVALSINNKF INFEERAKGGISKEDTKASSDGVWMPINEKGY

			FDFDFKKNPFDNLELKKNDEISLTFAPDDEDEALKSLIFKTKVTSLEDIDKAETKYDHTKVEKVK VLKDVKEDIHVDEIYGSLYHTEKGKGILDKQGTKEITGKTKFANAVVKVYSDLGDAQLFPDIQV DENGKFSFDAEKAGFRLQNGETLNFVVKPITGDLLHQGFVSKYIDVYESPEEKKEREFEEKLE NTPAYHKLHGDKIVGYDVQGNPSTWIFYPLGEKKVERTTPKLEK
19		10282	MRENFKLRKMKVGLVSVAITMLYIMTNGQAEASETNQKVSTNQESKAVSQTEQNSKETKAAE SSKNFVNLDPIKPGAQKVTGTTLPNHIILLNIDGKSADSVEGGYGDFITANDKGEFEYPLNNRKIV HNQEIEVSSSSPDLGDDEEDEEVEESSTEKAGAEESTDAKATYTTPRYEKAYEIPKEQLKEKDG HHQVFIPIPEGSGIIKGHTSVKGKVALSINNKFINFEEERAKGGISKEDTKASSDGVWMPINEKGY FDFDFKKNPFDNLELKKNDEISLTFAPDDEDEALKSLIFKTKVTSLEDIDKAETKYDHTKVEKVK VLKDVKEDIHVDEIYGSLYHTEKGKGILDKQGTKEITGKTKFANAVVKVYSDLGDAQLFPDIQV DENGKFSFDAEKAGFRLQNGETLNFVVKPITGDLLHQGFVSKYIDVYESPEEKKEREFEEKLE NTPAYHKLHGDKIVGYDVQGNPSTWIFYPLGEKKVERTTPKLEK
20		15604	MRENFKLRKMKVGLVSVAITMLYIMTNGQAEASETNQKVSTNQESKAVSQTEQNSKETKAAE SSKNFVNLDPIKPGAQKVTGTTLPNHIILLNIDGKSADSVEGGYGDFITANDKGEFEYPLNNRKIV HNQEIEVSSSSPDLGDDEEDEEVEESSTEKAGAEESTDAKATYTTPRYEKAYEIPKEQLKEKDG HHQVFIPIPEGSGIIKGHTSVKGKVALSINNKFINFEEERAKGGISKEDTKASSDGVWMPINEKGY FDFDFKKNPFDNLELKKNDEISLTFAPDDEDEALKSLIFKTKVTSLEDIDKAETKYDHTKVEKVK VLKDVKEDIHVDEIYGSLYHTEKGKGILDKQGTKEITGKTKFANAVVKVYSDLGDAQLFPDIQV DENGKFSFDAEKAGFRLQNGETLNFVVKPITGDLLHQGFVSKYIDVYESPEEKKEREFEEKLE NTPAYHKLHGDKIVGYDVQGNPSTWIFYPLGEKKVERTTPKLEK
21	A0A0H3JL12, SA0587 protein	12178	MKKLVPLLLALLLLVAACGTGGKQSSDKSNGKLVVTTNSILYDMAKNVGGDNVDIHSIVPVG QDPHEYEVPKPKDIKCLTDADVILYNGLNLETGNGWFEKALEQAGKSLKDKKVIASVDVKPIY LNGEENKDKQDPHAWLSLDNGIKYVKTIQQTIFDNDKKHKADYEKQGNKYIAQLEKLNND KDKFNDIPKEQRAMITSEGAFKYFSKQYGITPGYIWEINTEKQGTPEQMRQAIEFVKKHKLKHL VETSVDKKAMESLSEETKKDIFGEVYTD SIGKEG TKGDSYYKMMKSNIETVHGSMK
22		13018	MKKLVPLLLALLLLVAACGTGGKQSSDKSNGKLVVTTNSILYDMAKNVGGDNVDIHSIVPVG QDPHEYEVPKPKDIKCLTDADVILYNGLNLETGNGWFEKALEQAGKSLKDKKVIASVDVKPIY LNGEENKDKQDPHAWLSLDNGIKYVKTIQQTIFDNDKKHKADYEKQGNKYIAQLEKLNND KDKFNDIPKEQRAMITSEGAFKYFSKQYGITPGYIWEINTEKQGTPEQMRQAIEFVKKHKLKHL VETSVDKKAMESLSEETKKDIFGEVYTD SIGKEG TKGDSYYKMMKSNIETVHGSMK
23		12774	MKKLVPLLLALLLLVAACGTGGKQSSDKSNGKLVVTTNSILYDMAKNVGGDNVDIHSIVPVG QDPHEYEVPKPKDIKCLTDADVILYNGLNLETGNGWFEKALEQAGKSLKDKKVIASVDVKPIY LNGEENKDKQDPHAWLSLDNGIKYVKTIQQTIFDNDKKHKADYEKQGNKYIAQLEKLNND KDKFNDIPKEQRAMITSEGAFKYFSKQYGITPGYIWEINTEKQGTPEQMRQAIEFVKKHKLKHL VETSVDKKAMESLSEETKKDIFGEVYTD SIGKEG TKGDSYYKMMKSNIETVHGSMK
24	A0A0H3JT93, SA0620 protein	12178	MKKLAFAITATSGAAAF LTHHDAQASTQHTVQSGESLWSIAQKYNTSVESIKQNNQLDNNLVF PGQVISVGGSDAQNTSNTSPQAGSASSTVQAGESLNIIASRYGVSVDQLMAANNLRGYLIMP N QTLQIPNGSGGTTPTATTGSGNASSFNHQNLYTAGQCTWYVFDRAQAGSPISTYWSDAKY WAGNAANDGYQVNNTPSVGSIMQSTPGPYGHVAYVERVNGDGSILISEMNYTYGPYNMNYRT IPASEVSSYAFIH



			VVYNTAKSPVNVNQSYSIKSGTKLYTVPWGTSKQVAGSVSGSGNQTFKASKQQQIDKSIYLYG SVNGKSGWVSKAYLVDATAKPTPTPIPKPSTPTTNNKLTVSSLNGVAQINAKNNGLFTTVYDKTG KPTKEVQKTFAVTKEASLGGNKFYLVKDYNSTPLIGWVKQGDVIYNNAKSPVNMQTYTVKP GTKLYSVPWGTYKQEAGAVSGTGNQTFKATKQQQIDKSIYLFGTVNGKSGWVSKAYLAVPAA PKKAVAQPKTAVKAYTVTKPQTTQTVSKIAQVKPNNTGIRASVYEKTAKNGAKYADRTFYVT KERAHGNETYVLLNNTSHNIPLGWFNVKDLNVQNLGKEVKTTQKYTVNKSNNGLSMVPWGT KNQVILTGNNIAQGTFNATKQVSVGKDVYLYGTINNRTGWVNAKDLTAPTAVKPTTSAAKDY NYTYVIKNGNGYVTPNSDTAKYSLKAFNEQPFVAVKEQVINGQTWYYGKLSNGKLAWIKS TDLAKELIKYNQTMGTNLQVAQIQAGLQYKPQVQRPVKWTDANFNDVKHAMDTKRLAQDP ALKYQFLRLDQPQNISIDKINQFLKGKGVLENQGAAFNKAQMYGINEVYLISHALLETGNGTS QLAKGADVNNKVVNTSNTKYHNVFGIAAYDNDPLREGIKYAKQAGWDTVSKAIVGGAKFIG NSYVKAGQNTLYKMRWNPAPGTHQYATDVDWANINAKIIGYYDKIGEVGKYFDIPQYK
29		43355	MAKKFNYKLPSMVALTLVGSVTAHQVQAAETTQDQTTNKNVLDSNKKVATTEQAKAEVKN PTQNISGTQVYQDPAIVQPKTANNKTGNAQVSQKVDTAQVNGDTRANQSATTNNTQPAKSTS TTAPKTNTNVTNAGYSLVDEDDNSEHQINPELIKSAAKPAALETQYKAAAPKAKTEATPKVTT FSASAQPRVAATPKTSLPKYKPQVNSSINDYIRKNNLKAPKIEEDYTSYFPKYAYRNGVGRPEG IVVHDTANDRSTINGEISYMKNNYQNAFVHAFVDGDRIETAPTDYLSWGVGAVGNPRFINVEI VHTHDYASFARSMNNYADYAATQLQYYGLKPDSA EYDGNGTWVTHYAVSKYLGTDHADP HGYLRSHNYSYDQLYDLIN EKYLKMGKVAPWGTQFTTPTTPSKPTTPSKPSTGKLTVAANNG VAQIKPTNSGLYTTVYDKTGKATNEVQKTFVAVSKTATLGNQKFYLVQDYNNGKFGWVKEGD VVYNTAKSPVNVNQSYSIKSGTKLYTVPWGTSKQVAGSVSGSGNQTFKASKQQQIDKSIYLYG SVNGKSGWVSKAYLVDATAKPTPTPIPKPSTPTTNNKLTVSSLNGVAQINAKNNGLFTTVYDKTG KPTKEVQKTFAVTKEASLGGNKFYLVKDYNSTPLIGWVKQGDVIYNNAKSPVNMQTYTVKP GTKLYSVPWGTYKQEAGAVSGTGNQTFKATKQQQIDKSIYLFGTVNGKSGWVSKAYLAVPAA PKKAVAQPKTAVKAYTVTKPQTTQTVSKIAQVKPNNTGIRASVYEKTAKNGAKYADRTFYVT KERAHGNETYVLLNNTSHNIPLGWFNVKDLNVQNLGKEVKTTQKYTVNKSNNGLSMVPWGT KNQVILTGNNIAQGTFNATKQVSVGKDVYLYGTINNRTGWVNAKDLTAPTAVKPTTSAAKDY NYTYVIKNGNGYVTPNSDTAKYSLKAFNEQPFVAVKEQVINGQTWYYGKLSNGKLAWIKS TDLAKELIKYNQTMGTNLQVAQIQAGLQYKPQVQRPVKWTDANFNDVKHAMDTKRLAQDP ALKYQFLRLDQPQNISIDKINQFLKGKGVLENQGAAFNKAQMYGINEVYLISHALLETGNGTS QLAKGADVNNKVVNTSNTKYHNVFGIAAYDNDPLREGIKYAKQAGWDTVSKAIVGGAKFIG NSYVKAGQNTLYKMRWNPAPGTHQYATDVDWANINAKIIGYYDKIGEVGKYFDIPQYK
30		15146	MAKKFNYKLPSMVALTLVGSVTAHQVQAAETTQDQTTNKNVLDSNKKVATTEQAKAEVKN PTQNISGTQVYQDPAIVQPKTANNKTGNAQVSQKVDTAQVNGDTRANQSATTNNTQPAKSTS TTAPKTNTNVTNAGYSLVDEDDNSEHQINPELIKSAAKPAALETQYKAAAPKAKTEATPKVTT FSASAQPRVAATPKTSLPKYKPQVNSSINDYIRKNNLKAPKIEEDYTSYFPKYAYRNGVGRPEG IVVHDTANDRSTINGEISYMKNNYQNAFVHAFVDGDRIETAPTDYLSWGVGAVGNPRFINVEI VHTHDYASFARSMNNYADYAATQLQYYGLKPDSA EYDGNGTWVTHYAVSKYLGTDHADP HGYLRSHNYSYDQLYDLIN EKYLKMGKVAPWGTQFTTPTTPSKPTTPSKPSTGKLTVAANNG VAQIKPTNSGLYTTVYDKTGKATNEVQKTFVAVSKTATLGNQKFYLVQDYNNGKFGWVKEGD



			VVYNTAKSPVNVNQSYSIKSGTKLYTVPWGTSKQVAGSVSGSGNQTFKASKQQQIDKSIYLYG SVNGKSGWVSKAYLVDATAKPTPTPIPKPSTPTTNNKLTVSSLNGVAQINAKNNGLFTTVYDKTG KPTKEVQKTFAVTKEASLGGNKFYLVKDYNSTPLIGWVKQGDVIYNNAKSPVNVMQTYTVKP GTKLYSVPWGTYKQEAGAVSGTGNQTFKATKQQQIDKSIYLFGTVNGKSGWVSKAYLAVPAA PKKAVAQPKTAVKAYTVTKPQTTQTVSKIAQVKPNNTGIRASVYEKTAKNGAKYADRTFYVT KERAHGNETYVLLNNTSHNIPLGWFNVKDLNVQNLGKEVKTTQKYTVNKSNNGLSMVPWGT KNQVILTGNNIAQGTFNATKQVSVGKDVYLYGTINNRTGWVNAKDLTAPTAVKPTTSAAKDY NYTYVIKNGNGYVTPNSDTAKYSLKAFNEQPFVAVKEQVINGQTWYYGKLSNGKLAWIKS TDLAKELIKYNQTMGTNLNQAQIQAGLQYKPQVQRPVKWTDANFNDVKHAMDTKRLAQDP ALKYQFLRLDQPNISIDKINQFLKGKGVLENQGAAFNKAQMYGINEVYLISHALLETGNGTS QLAKGADVNNKVVVNTSNTKYHNVFGIAAYDNDPLREGIKYAKQAGWDTVSKAIVGGAKFIG NSYVKAGQNTLYKMRWNPAPGTHQYATDVDWANINAKIIGYYDKIGEVGKYFDIPQYK
31		10789	MAKKFNYKLPSMVALTLVGSVTAHQVQAAETTQDQTTNKNVLDNKNVKATTEQAKAEVKN PTQNISGTQVYQDPAIVQPKTANNKTGNAQVSQKVDTAQVNGDTRANQSATTNNTQPAKSTS TTAPKTNTNVTNAGYSLVDEDDNSEHQINPELIKSAAPAALETQYKAAAPKAKTEATPKVTT FSASAQPRVAATPKTSLPKYKQVNSSINDYIRKNNLKAPKIEEDYTSYFPKYAYRNGVGRPEG IVVHDTANDRSTINGEISYMKNNYQNAFVHAFVDGDRHETAPTDLVSWGVGAVGNPRFINVEI VHTHDYASFARSMNNYADYAATQLQYYGLKPDSAEYDNGTVWTHYAVSKYLGTDHADP HGYLRSHNYSYDQLYDLINKEYLIKMGKVAPWGTQFTTPTTPSKPTTPSKPSTGKLTVAANNG VAQIKPTNSGLYTTVYDKTGKATNEVQKTFVSKTATLGNQKFYLVQDYNNGKFGWVKEGD VVYNTAKSPVNVNQSYSIKSGTKLYTVPWGTSKQVAGSVSGSGNQTFKASKQQQIDKSIYLYG SVNGKSGWVSKAYLVDATAKPTPTPIPKPSTPTTNNKLTVSSLNGVAQINAKNNGLFTTVYDKTG KPTKEVQKTFAVTKEASLGGNKFYLVKDYNSTPLIGWVKQGDVIYNNAKSPVNVMQTYTVKP GTKLYSVPWGTYKQEAGAVSGTGNQTFKATKQQQIDKSIYLFGTVNGKSGWVSKAYLAVPAA PKKAVAQPKTAVKAYTVTKPQTTQTVSKIAQVKPNNTGIRASVYEKTAKNGAKYADRTFYVT KERAHGNETYVLLNNTSHNIPLGWFNVKDLNVQNLGKEVKTTQKYTVNKSNNGLSMVPWGT KNQVILTGNNIAQGTFNATKQVSVGKDVYLYGTINNRTGWVNAKDLTAPTAVKPTTSAAKDY NYTYVIKNGNGYVTPNSDTAKYSLKAFNEQPFVAVKEQVINGQTWYYGKLSNGKLAWIKS TDLAKELIKYNQTMGTNLNQAQIQAGLQYKPQVQRPVKWTDANFNDVKHAMDTKRLAQDP ALKYQFLRLDQPNISIDKINQFLKGKGVLENQGAAFNKAQMYGINEVYLISHALLETGNGTS QLAKGADVNNKVVVNTSNTKYHNVFGIAAYDNDPLREGIKYAKQAGWDTVSKAIVGGAKFIG NSYVKAGQNTLYKMRWNPAPGTHQYATDVDWANINAKIIGYYDKIGEVGKYFDIPQYK
32	A0A0H3JMD8, SA2094 protein	8962	MMKRKPTFLESISTMIVMVIVVVTGFFVDIPIQVLLIIASAYATWIAKRVLGTWQDLEKGIAERL NTAMPAILIILAVGIIVGSMFSGTVPALIYYGLDLLNPSYFLISAFFISAVTS VATGTAWGSASTAGIALISIGNQLGIPPGMAAGAIAGAVFGDKMSPLSDTTNLAALVTKVNIFK HIHSMWTTIPASIIIGLLVWFIAGFQFKGHSNDKQIQTLSELAQIYQINIWWV PLIVIIIVCLLFKMATVPAMVISSFSIIIVGTFNHFFKMTDGFKATFSGFNDSMIHQSHISSSVKSL EQGGMMSMTQILVTIFCGYAFAGIVEKAGCLEVLLTTISKGIHSGVSLICITV ICCIALVFAAGVASIIVMVGVLMDLFEKYQVSRVLSRTLEDSSTMVLPPLIPWGTSGIYYTNQL HVSVGEFFMWTPCYLCAIIIIYGFTGIGIKKSSNSRLT



33	P68800, Fibrinogen-binding protein	15790	MKNKLIAKSLLTIAAIGITTTTIASTADASEGYGPREKKPVSINHNIVEYNDGTFKYQSRPKFNST PKYIKFKHDYNILEFNDGTFEYGARPQFNKPAAKTDTATIKKEQKLIQAQNLVREFEKTHTVSAH RKAQKAVNLVSFEYKVKKMVLQERIDNVLKQGLVR
34		15790	MKNKLIAKSLLTIAAIGITTTTIASTADASEGYGPREKKPVSINHNIVEYNDGTFKYQSRPKFNST PKYIKFKHDYNILEFNDGTFEYGARPQFNKPAAKTDTATIKKEQKLIQAQNLVREFEKTHTVSAH RKAQKAVNLVSFEYKVKKMVLQERIDNVLKQGLVR
35		11106	MKNKLIAKSLLTIAAIGITTTTIASTADASEGYGPREKKPVSINHNIVEYNDGTFKYQSRPKFNST PKYIKFKHDYNILEFNDGTFEYGARPQFNKPAAKTDTATIKKEQKLIQAQNLVREFEKTHTVSAH RKAQKAVNLVSFEYKVKKMVLQERIDNVLKQGLVR
36	P60748, Foldase protein PrsA	14127	MKMINKLIVPVTASALLLGACGASATDSKENTLISSKAGDVTVADTMKKIGKDQIANASFTEML NKILADKYKNKVNDKKIDEQIEKMQKQYGGKDKFEKALQQQGLTADKYKENLRTAAYHKELL SDKIKISDSEIKEDSKKASHILIKVSKKSDKEGLDDKEAKQKAEEIQKEVSKDPSKFGEIAKKES MDTGSAKKDGELGYVLKGQTDKDFEKALFKLDGEVSEVVKSSFGYHIIKADKPTDFNSEKQS LKEKLVQKVQKNPKLLTDAYKDLLKEYDVDFKDRDIKSVVEDKILNPEKCLKQGGAQGGQSG MSQ
37		14901	MKMINKLIVPVTASALLLGACGASATDSKENTLISSKAGDVTVADTMKKIGKDQIANASFTEML NKILADKYKNKVNDKKIDEQIEKMQKQYGGKDKFEKALQQQGLTADKYKENLRTAAYHKELL SDKIKISDSEIKEDSKKASHILIKVSKKSDKEGLDDKEAKQKAEEIQKEVSKDPSKFGEIAKKES MDTGSAKKDGELGYVLKGQTDKDFEKALFKLDGEVSEVVKSSFGYHIIKADKPTDFNSEKQS LKEKLVQKVQKNPKLLTDAYKDLLKEYDVDFKDRDIKSVVEDKILNPEKCLKQGGAQGGQSG MSQ
38		14699	MKMINKLIVPVTASALLLGACGASATDSKENTLISSKAGDVTVADTMKKIGKDQIANASFTEML NKILADKYKNKVNDKKIDEQIEKMQKQYGGKDKFEKALQQQGLTADKYKENLRTAAYHKELL SDKIKISDSEIKEDSKKASHILIKVSKKSDKEGLDDKEAKQKAEEIQKEVSKDPSKFGEIAKKES MDTGSAKKDGELGYVLKGQTDKDFEKALFKLDGEVSEVVKSSFGYHIIKADKPTDFNSEKQS LKEKLVQKVQKNPKLLTDAYKDLLKEYDVDFKDRDIKSVVEDKILNPEKCLKQGGAQGGQSG MSQ
39		12878	MKMINKLIVPVTASALLLGACGASATDSKENTLISSKAGDVTVADTMKKIGKDQIANASFTEML NKILADKYKNKVNDKKIDEQIEKMQKQYGGKDKFEKALQQQGLTADKYKENLRTAAYHKELL SDKIKISDSEIKEDSKKASHILIKVSKKSDKEGLDDKEAKQKAEEIQKEVSKDPSKFGEIAKKES MDTGSAKKDGELGYVLKGQTDKDFEKALFKLDGEVSEVVKSSFGYHIIKADKPTDFNSEKQS LKEKLVQKVQKNPKLLTDAYKDLLKEYDVDFKDRDIKSVVEDKILNPEKCLKQGGAQGGQSG MSQ
40		23875	MKMINKLIVPVTASALLLGACGASATDSKENTLISSKAGDVTVADTMKKIGKDQIANASFTEML NKILADKYKNKVNDKKIDEQIEKMQKQYGGKDKFEKALQQQGLTADKYKENLRTAAYHKELL SDKIKISDSEIKEDSKKASHILIKVSKKSDKEGLDDKEAKQKAEEIQKEVSKDPSKFGEIAKKES MDTGSAKKDGELGYVLKGQTDKDFEKALFKLDGEVSEVVKSSFGYHIIKADKPTDFNSEKQS LKEKLVQKVQKNPKLLTDAYKDLLKEYDVDFKDRDIKSVVEDKILNPEKCLKQGGAQGGQSG MSQ

41		2083.2	MKMINKLIVPTASALLLGA CGASATDSKENTLISSKAGDVTVADTMKKIGKDQIANASFTEML NKILADKYKNKVNDKKIDEQIEKMQKQYGGKDKFEKALQQQGLTADKYKENLRTAAYHKELL SDKIKISDSEIKEDSKKASHILIKVSKKSDKEGLDDKEAKQKAEEIQKEVSKDPKSFGEIAKKES MDTGSAKKDGELGYVLKGQTDKDFEKALFKLDGEVSEVVKSSFGYHIIKADKPTDFNSEKQS LKEKLVQKVQKNPKLLTDAYKDLLKEYDVDFKDRDIKSVVEDKI LNPEKLKQGGAQGGQSGMSQ
41	A0A0H3JNJ9, Probable molybdate-binding protein	17366	MKMKRFIAIVMALFLVLGCSNSNDN NESKKDDADNGKKQEIQVAAAASLTDVTKKLASEFK KEHKNADIKFNYGGSGALRKQIESGAPVDVFMSANTKDVDALKDKNKAHDTYKYAKNSLVLI GDKDSNYTSVKDLKDNDKLALGEVKTVPAGKYAKQYLDNNNLFKEVESKIVYAKDVKQVLN YVEKGNAKQGFVYKTDLYKQNKKIDTVKVIKEVELKKPITYEAGATSDSKLAKEWMEFLKSD KAKEILKEYHFAA
43		19061	MKMKRFIAIVMALFLVLGCSNSNDN NESKKDDADNGKKQEIQVAAAASLTDVTKKLASEFK KEHKNADIKFNYGGSGALRKQIESGAPVDVFMSANTKDVDALKDKNKAHDTYKYAKNSLVLI GDKDSNYTSVKDLKDNDKLALGEVKTVPAGKYAKQYLDNNNLFKEVESKIVYAKDVKQVLN YVEKGNAKQGFVYKTDLYKQNKKIDTVKVIKEVELKKPITYEAGATSDSKLAKEWMEFLKSD KAKEILKEYHFAA
44		14127	MKMKRFIAIVMALFLVLGCSNSNDN NESKKDDADNGKKQEIQVAAAASLTDVTKKLASEFK KEHKNADIKFNYGGSGALRKQIESGAPVDVFMSANTKDVDALKDKNKAHDTYKYAKNSLVLI GDKDSNYTSVKDLKDNDKLALGEVKTVPAGKYAKQYLDNNNLFKEVESKIVYAKDVKQVLN YVEKGNAKQGFVYKTDLYKQNKKIDTVKVIKEVELKKPITYEAGATSDSKLAKEWMEFLKSD KAKEILKEYHFAA
45	Q7A423, Staphylococcal secretory antigen ssaA2	12164	MKKIATATIATAGFATIAIASGNQAHASEQDNYGYNPNDPTSYSYTYTIDAQGNHYHTWKGNW HPSQLNQDNGYYSYYYYNGYNNYNNYNNNGYSYNNYSRYNNYSNNNQSYNNYNNYSYNTNS YRTGGLGASYSTSSNNVQVTTTMAPSSNGRSISSGYTSGRNLYTSGQCTYYVFDRVGGKIGSTW GNASNWANAARAGYTVNNTPKAGAIMQTTQGAYGHVAYVESVNSNGSVRVSE MNYGYGPGVVTSTISASQAAGYNFIH
46		20300	MKKIATATIATAGFATIAIASGNQAHASEQDNYGYNPNDPTSYSYTYTIDAQGNHYHTWKGNW HPSQLNQDNGYYSYYYYNGYNNYNNYNNNGYSYNNYSRYNNYSNNNQSYNNYNNYSYNTNS YRTGGLGASYSTSSNNVQVTTTMAPSSNGRSISSGYTSGRNLYTSGQCTYYVFDRVGGKIGSTW GNASNWANAARAGYTVNNTPKAGAIMQTTQGAYGHVAYVESVNSNGSVRVSEMNYGYGP GVVTSTISASQAAGYNFIH
47	Q99RL2, Immunoglobulin-binding protein Sbi	11345	MKNKYISKLLVGAATITLATMISNGEAKASENTQQTSTKHQTTQNNYVTDQQKAFYQVLHLKG ITEEQRNQYIKTLREHPERAQEVFSESLKDSKNPDRRAQQNAFYNVLKNDNLTEQEKNNYIAQ IKENPDRSQQVWVESVQSSKAKERQNIENADKAIKDFQDNKAPHDKSAAYEANSKLPKDLRDK NNRFVEKVSIEKAIVRHDERVKSANDAIKSLNEKDSIENRRLAQREVNKAPMDVKEHLQKQLD ALVAQKDAEKKVAPKVEAPQIQSPQIEKPKAESPKVEVPQIQSPKVEVPQSKLLGYYQSLKDSF NYGYKYLTDYKSYKEKYDTAKYYYYNTYYKYKGAIQTVLTVLGSGSKSYIQPLKVDDKNGY LAKSYAQVRNYVTESINTGKVLTYFYQNPTLVKTAIKAQETASSIKNTLSNLLSFWK

48		16264	MKNKYISKLLVGAATITLATMISNGEAKASENTQQTSTKHQTTQNNYVTDQQKAFYQVLHLKG ITEEQRNQYIKTLREHPERAQEVFSESLKDSKNPDRRVAQQNAFYNVLKNDNLTEQEKNNYIAQ IKENPDRSQQVWVESVQSSKAKERQNIENADKAIKDFQDNKAPHDKSAAYEANSKLPKDLRDK NNRFVEKVSIEKAIVRHDERVKSANDAIKSLNEKDSIENRRLAQREVNKAPMDVKEHLQKQLD ALVAQKDAEKKVAPKVEAPQIQSPQIEKPKAESPKVEVPQIQSPKVEVPQSKLLGYYQSLKDSF NYGYKYLTDTYKSYKEKYDTAKYYYNTYYKYKGAIQTVLTVLGSGSKSYIQLKVDDKNGY LAKSYAQVRNYVTESINTGKVLTYTFYQNPTLVKTAIKAQETASSIKNTLSNLLSFWK
49		11668	MKNKYISKLLVGAATITLATMISNGEAKASENTQQTSTKHQTTQNNYVTDQQKAFYQVLHLKG ITEEQRNQYIKTLREHPERAQEVFSESLKDSKNPDRRVAQQNAFYNVLKNDNLTEQEKNNYIAQ IKENPDRSQQVWVESVQSSKAKERQNIENADKAIKDFQDNKAPHDKSAAYEANSKLPKDLRDK NNRFVEKVSIEKAIVRHDERVKSANDAIKSLNEKDSIENRRLAQREVNKAPMDVKEHLQKQLD ALVAQKDAEKKVAPKVEAPQIQSPQIEKPKAESPKVEVPQIQSPKVEVPQSKLLGYYQSLKDSF NYGYKYLTDTYKSYKEKYDTAKYYYNTYYKYKGAIQTVLTVLGSGSKSYIQLKVDDKNGY LAKSYAQVRNYVTESINTGKVLTYTFYQNPTLVKTAIKAQETASSIKNTLSNLLSFWK
50	P0A075, Gamma-hemolysin component B	10693	MKMNKLVKSSVATSMALLLSGTANAEGKITPVSVKKVDDKVTLYKTTATADSDKFKISQILTF NFIKDKSYDKDTLVLKATGNINSGFVKPNPNNDYDFSKLYWGAKYNVSISSQSNDVNVVDYAP KNQNEEFQVQNTLGYTFGGDISISNGLSGGLNGNTAFSETINYKQESYRTTLSRNTNYKNVGWG VEAHKIMNNGWGPYGRDSFHPTYGNELFLAGRQSSAYAGQNFIAQHQMPLLSRSNFNPEFLSV LSHRQDGAKKSKITVTYQREMDLYQIRWNGFYWAGANYKNFKTRTFKSTYEIDWENHKVKLL DTKETENNK
51		10300	MKMNKLVKSSVATSMALLLSGTANAEGKITPVSVKKVDDKVTLYKTTATADSDKFKISQILTF NFIKDKSYDKDTLVLKATGNINSGFVKPNPNNDYDFSKLYWGAKYNVSISSQSNDVNVVDYAP KNQNEEFQVQNTLGYTFGGDISISNGLSGGLNGNTAFSETINYKQESYRTTLSRNTNYKNVGWG VEAHKIMNNGWGPYGRDSFHPTYGNELFLAGRQSSAYAGQNFIAQHQMPLLSRSNFNPEFLSV LSHRQDGAKKSKITVTYQREMDLYQIRWNGFYWAGANYKNFKTRTFKSTYEIDWENHKVKLL DTKETENNK
52		22581	MKMNKLVKSSVATSMALLLSGTANAEGKITPVSVKKVDDKVTLYKTTATADSDKFKISQILTF NFIKDKSYDKDTLVLKATGNINSGFVKPNPNNDYDFSKLYWGAKYNVSISSQSNDVNVVDYAP KNQNEEFQVQNTLGYTFGGDISISNGLSGGLNGNTAFSETINYKQESYRTTLSRNTNYKNVGWG VEAHKIMNNGWGPYGRDSFHPTYGNELFLAGRQSSAYAGQNFIAQHQMPLLSRSNFNPEFLSV LSHRQDGAKKSKITVTYQREMDLYQIRWNGFYWAGANYKNFKTRTFKSTYEIDWENHKVKLL DTKETENNK
53	P65806, Peptidase T	4763	MKNQLIDRLTRYTTIDTQSDPKSTTTPSTEKQWDLHLLEKELQQLGLPTDLDENGYLFATLESN IDADVPTVGFLAHVDTSPDFNASNVPKQIHENYDGKPYKLGNTKRVLDPKVPPELNSLVGHTLM VTDGTSLLGADDKAGIVEIMEAICYLQEHPEIKHGTIRIGFTPDEEIGRPHKFDVDRFNADFAYT MDGSQYGELQYESFNAAEAVITCHGVNVHPGSAKNAMVNAILRGEQFDSLLPDSEVPERTEGY EGFYHLMNFEGTVEKATLQYIIRDHDKKQFELRKKRILEIRDDINAHFENYPVKVDISDQYFNM AEKILPLPHIIDIPKRVFAKLDIPANTEPIRGGTDGSQLSFMGLPTPNIFTGCGNFHGPYEYASIDV MEKAVQVVIIGIVEDIAENH

54	P66937, DNA gyrase subunit B (gyrB)	7348	MVTALSDVNNTDNYGAGQIQVLEGLEAVRKRPGMYIGSTSERGLHHLVWEIVDNSIDEALAGY ANKIEVVIEKDNWIKVTDNGRGIPVDIQEKMGRPAVEVILTVLHAGGKFGGGGYKVS <del>GGLHGV</del> <del>GSSVVNAL</del> SQDLEVYVHRNETIYHQAYKKGVPQFDLKEVGTTDKTGTVIRFKADGEIFTETTVY NYETLQQRIRELAFLNKGIQITLRDERDEENVREDSYHYEGGIKSVELLNENKEPIHDEPIYIHQ SKDDIEVEIAIQNSGYATNLLTYANNIHTYEGGTHEDGFKRALTRVLNSYGLSSKIMKEEKDR SGEDTREGMTAII <del>SIKHGDPQFEGQTKTKLGNSEVRQVVDKLFSEHFERFLYENPQVARTVVEK</del> GIMAAARVA <del>AAKAREVTRRKSALDVASLPGKLADCSSKSPEECEIFLVEGDSAGGSTKSGRDS</del> RTQAILPLRGKILNVEKARLDRILNNNEIRQMITAFGTGIGGDFDLAKARYHKIVIMTDADVDGA HIRTLLLTFYRFMRPLIEAGYVYIAQPPLYKLTQGKQKYVYNDRELDKLKSELNPTPKWSIAR YKGLGEMNADQLWETTMNPEHRALLQVKLEDAIEADQTFEMLMGDVVENRRQFIEDNAVYA NLDF
55	A0A0H3JL12, SA0587 protein	3635	MKKLVPLLLALLLLVAACGTGGKQSSDKSNGKLKVVTTNSILYDMAKNVGGDNVDIHSIVPVG QDPHEYE <del>VKPKDIK</del> LTADVILY <del>NGLNLETGNGWFEKALEQAGKSLKDKK</del> VIAVSKDVKPIY LNGEEGNKDKQDPHAWLSLDNGIKYVKTIQQT <del>FDNDKKHKADYEKQGNKYIAQLEKLN</del> NDS KDKFNDIPKEQRAMITSEGAFKYFSKQYGITPGYIWEINTEKQGTPEQMRQAIEFVKKHKLKHL VETSVDKKAMESLSEETKKDIFGEVYTD <del>SIGKEG</del> TKGDSYKMMKSNIETVHGSMK
56	A0A0H3JS82, Cassette chromosome recombinase B	3996	MQQLKTKRVGIYVRVSTEMQSTEGYSIDGQINQIKEYCDFHHFEVKDIYADRGISGKSMNRPEL QRILKDAKEGYIDCVMVYKTNRLARNTSDLLKIVEDLHKQNEFFSLSERMEVNTSSGKLMLQI LASFSEFERNNIVENVFMGQTRRAQEGYYQGNLPLGYDKIPNSKHELMINQHEANIVKYIFESY AKGHGYRKIANALNHKGYVTKKGKPFSSITYILANPFYIGKIQFAKYKDWSEKRRKGLNDKP VIAEGKHSPINQDLWDKVQMRKKQVSQKPQVHGKGTNLLTGIIHCPQCGAPMAASNTTNTLK DGTKKRIRYYSCSNFRNKGSKVCSANSVRADVIEDYVMKQILEIVKSDKVIQRVVTHVNQENQ VDGAALHH <del>DIAYKQQYDEVQIKLNN</del> LIKTIEDNPDLT <del>SVIRPSIQKYEKQLNDITNQINQLKNQ</del> QNE <del>DKPLF</del> DAKEISKLLQHIFHDIKHIEKSRLKALYLSVIDRIDIKKDG <del>NHKKQFYVTLKLNNEII</del> KQLFNNKQLDEVHLSTSSFLPQTLYLTI
57	A0A0H3JW57, SA2339 protein	11639	MAKFLYKMGTFIAKHKWSAVIAWIVIVAAILIPLATNAPKFDNDIKMTGLES <del>LDTNKKIEKHFN</del> QDSEKAQIRVVF <del>KTTKDDGIVQPNITEDIKKTLEDIKKDDKHIDKISDPYEN</del> KQISKDKTTAFADI TYDVSQTS <del>LKDGS</del> RDNVKSHLKDLRDNHNVQTELTGTGMTSTEVGGNSELVGIIVAFVLLITF GSVIAAGLPIISALIGLASGVGIISLLTYAFDIPNVTLTAVMIGLAVGIDYALFILFRYRQVMKTE TDYIKGIGLAIGTAGSAVVFAGVTVVIAVCGLSLVGIDFLAVMGFASAVISVIFAVFSALTLLPALIS IFHKRIKVNKLQSNFKKDIDTPWSKFITGNALAAVLLGLIILVAAAIPVSHMRLGIPDDGVKPADS TQKKAYDIISDKFGEGFNGQIPMLINVKDKKDDPQGLQQLQSVYKDIKDKKNVDIVTPPQMSK DNDYALMVVIPKQGPNAESTNDLVHDLRDYHKDAQDKYGFKTEISGQSVINIDMSKKLNEAIPL FATVIVVLAFFLLMIVFRSILIPLKAVLGFVLSMATLGFTTLMQDGMKGLFGIETTGPMLAFL PVITIGILFGLAMDYEVFLMSRIHEEYSKTGDNDYSIKVGLKESGPVIVAAALIMFSVFFAFVFQE DVMIKSMGMALAFGVLFDAFVVRMMLIPALTKLFGKGSWYLPAWLNRIIPRV <del>DIEGH</del> ALEKYK TVESQESEAKDSKETYDTTFKVYPQGATNVSKHQDVHGGQDDAHSIVLDDKT <del>MALYQEV</del> KQSS ASSLFLYDALIDYQNKHQLNSKQQVTNIEQLNKNIEKLNQLLEKNLRNKS

58	A0A0H3JNZ0, SA2437 protein	20300	MPKKNKILYLLSTTLVLPTLVSPAYADTPQKDTTAKTTSHDSKKSNDDETSKDTTSKDTDKAD NNNTSNQDNNDKKFKTIDDSTSDSNNIIDFIYKNLPQTNNQLLTKNKYDDNYSLTTLIQNLFNL NSDISDYEQPRNGEKSTNDSNKNSDNSIKNDTDTQSSKQDKADNQKAPKSNNTKPSTSNKQPNS PKPTQPNQSNSQPASDDKANQKSSSKDNQMSDSALDSILDQYSEDAKKTQKDYASQSKKDKN EKSNTKNPQLPTQDELKHKS KPAQSFNNDVNQKDTRATSLFETDPSISNNDDSGQFNVVDSKDT RQFVKSIAKDAHRIGQDNNDIYASVMIAQAILESDSGRSALAKSPNHNLFGIKGAFEGNSVPFNTL EADGNKLYSINAGFRKYPSTKESLKDYSDLIKNGIDGNRTIYKPTWKSEADSYKDATSHLSKTY ATDPNYAKKLNSIIKHYYLTQFDDERMPDLDKYERSIKDYDDSSDEFKPFREVSDSMYPYHGQC TWYVYNRMKQFGTSISGDLGDAHNWNNRAQYRDYQVSHTPKRHAAVVF EAGQFGADQHYG HVAFVEKVNSDGSIVISESNVKGLGIISHRTINAAAAEELSYITGK
59		14918	MPKKNKILYLLSTTLVLPTLVSPAYADTPQKDTTAKTTSHDSKKSNDDETSKDTTSKDTDKAD NNNTSNQDNNDKKFKTIDDSTSDSNNIIDFIYKNLPQTNNQLLTKNKYDDNYSLTTLIQNLFNL NSDISDYEQPRNGEKSTNDSNKNSDNSIKNDTDTQSSKQDKADNQKAPKSNNTKPSTSNKQPNS PKPTQPNQSNSQPASDDKANQKSSSKDNQMSDSALDSILDQYSEDAKKTQKDYASQSKKDKN EKSNTKNPQLPTQDELKHKS KPAQSFNNDVNQKDTRATSLFETDPSISNNDDSGQFNVVDSKDT RQFVKSIAKDAHRIGQDNNDIYASVMIAQAILESDSGRSALAKSPNHNLFGIKGAFEGNSVPFNTL EADGNKLYSINAGFRKYPSTKESLKDYSDLIKNGIDGNRTIYKPTWKSEADSYKDATSHLSKTY ATDPNYAKKLNSIIKHYYLTQFDDERMPDLDKYERSIKDYDDSSDEFKPFREVSDSMYPYHGQC TWYVYNRMKQFGTSISGDLGDAHNWNNRAQYRDYQVSHTPKRHAAVVF EAGQFGADQHYG HVAFVEKVNSDGSIVISESNVKGLGIISHRTINAAAAEELSYITGK
60		16019	MPKKNKILYLLSTTLVLPTLVSPAYADTPQKDTTAKTTSHDSKKSNDDETSKDTTSKDTDKAD NNNTSNQDNNDKKFKTIDDSTSDSNNIIDFIYKNLPQTNNQLLTKNKYDDNYSLTTLIQNLFNL NSDISDYEQPRNGEKSTNDSNKNSDNSIKNDTDTQSSKQDKADNQKAPKSNNTKPSTSNKQPNS PKPTQPNQSNSQPASDDKANQKSSSKDNQMSDSALDSILDQYSEDAKKTQKDYASQSKKDKN EKSNTKNPQLPTQDELKHKS KPAQSFNNDVNQKDTRATSLFETDPSISNNDDSGQFNVVDSKDT RQFVKSIAKDAHRIGQDNNDIYASVMIAQAILESDSGRSALAKSPNHNLFGIKGAFEGNSVPFNTL EADGNKLYSINAGFRKYPSTKESLKDYSDLIKNGIDGNRTIYKPTWKSEADSYKDATSHLSKTY ATDPNYAKKLNSIIKHYYLTQFDDERMPDLDKYERSIKDYDDSSDEFKPFREVSDSMYPYHGQC TWYVYNRMKQFGTSISGDLGDAHNWNNRAQYRDYQVSHTPKRHAAVVF EAGQFGADQHYG HVAFVEKVNSDGSIVISESNVKGLGIISHRTINAAAAEELSYITGK
61	P61598, Putative surface protein SA2285	43354	MRDKKGPVNKRVDFLSNKLNKYSIRKFTVGTASILIGSLMYLGTQQEAEAAENNIENPTTLKDN VQSKEVKIEEVTNKDTAPQGV EAKSEVTSNKDTIEHEASVKAEDISKKEDTPKEVANVAEVQPK SSVTHNAEAPKVRKARSVDEGSFDITRDSKNVVESTPITIQQKEHFEGYGSVDIQKNPTDLGVSE VTRFNVGNESNGLIGALQLKNKIDFSKDFNFKVRVANNHQSNTTGADGWGFLFSKGNAEEYLT NGGILGDKGLVNSGGFKIDTGYIYTSSMDKTEKQAGQGYRGYGAFVKNDSGNSQMVGENIDK SKTNFLNYADNSTNTSDGKFHGQRLNDVILTYVASTGKMRAEYAGKTWETSITDLGLSKNQAY NFLITSSQRWGLNQGINANGWMRTDLKGSEFTTPEAPKTITELEKKLKRHFHSRKNVNLIRI
62		23416	MRDKKGPVNKRVDFLSNKLNKYSIRKFTVGTASILIGSLMYLGTQQEAEAAENNIENPTTLKDN VQSKEVKIEEVTNKDTAPQGV EAKSEVTSNKDTIEHEASVKAEDISKKEDTPKEVANVAEVQPK SSVTHNAEAPKVRKARSVDEGSFDITRDSKNVVESTPITIQQKEHFEGYGSVDIQKNPTDLGVSE

			VTRFNVGNESNGLIGALQLKNKIDFSKDFNFKVRVANNHQSNTTGADGWGFLFSKGNAAEEYLT NGGILGDKGLVNSGGFKIDTGYIYTSSMDKTEKQAGQGYRGYGAFVKNDSSGNSQMVGENIDK SKTNFLNYADNSTNTSDGKFHQQRLNDVILTYVASTGKMRAEYAGKTWETSITDLGLSKNQAY NFLITSSQRWGLNQGINANGWMRTDLKGSEFTFTPEAPKTITELEKKLKRFRHSRKNVNLIRI
63		38919	MRDKKGPVNKRVDFLSNKLNKYSIRKFTVGTASILIGSLMYLGTQQEAEAAENNIENPTTLKDN VQSKEVKIEEVTNKDTAPQGVAKSEVTSNKDTIEHEASVKAEDISKKEDTPKEVANVAEVQPK SSVTHNAEAPKVRKARSVDEGSFDITRDSKNVVESTPITIQQKEHFEGYGSVDIQKNPTDLGVSE VTRFNVGNESNGLIGALQLKNKIDFSKDFNFKVRVANNHQSNTTGADGWGFLFSKGNAAEEYLT NGGILGDKGLVNSGGFKIDTGYIYTSSMDKTEKQAGQGYRGYGAFVKNDSSGNSQMVGENIDK SKTNFLNYADNSTNTSDGKFHQQRLNDVILTYVASTGKMRAEYAGKTWETSITDLGLSKNQAY NFLITSSQRWGLNQGINANGWMRTDLKGSEFTFTPEAPKTITELEKKLKRFRHSRKNVNLIRI
64		6642.1	MRDKKGPVNKRVDFLSNKLNKYSIRKFTVGTASILIGSLMYLGTQQEAEAAENNIENPTTLKDN VQSKEVKIEEVTNKDTAPQGVAKSEVTSNKDTIEHEASVKAEDISKKEDTPKEVA NVAEVQPKSSVTHNAEAPKVRKARSVDEGSFDITRDSKNVVESTPITIQQKEHFEGYGSVDIQKN PTDLGVSEVTRFNVGNESNGLIGALQLKNKIDFSKDFNFKVRVANNHQSNTTGADGWGFLFSK GNAAEEYLTNGGILGDKGLVNSGGFKIDTGYIYTSSMDKTEKQAGQGYRGYGAFVKNDSSGNSQ MVGENIDKSKTNFLNYADNSTNTSDGKFHQQRLNDVILTYVASTGKMRAEYAGKTWETSITDL GLSKNQAYNFLITSSQRWGLNQGINANGWMRTDLKGSEFTFTPEAPKTITELEKKLKRFRHSRKN VNLIRI
65		4484	MRDKKGPVNKRVDFLSNKLNKYSIRKFTVGTASILIGSLMYLGTQQEAEAAENNIENPTTLKDN VQSKEVKIEEVTNKDTAPQGVAKSEVTSNKDTIEHEASVKAEDISKKEDTPKEVANVAEVQPK SSVTHNAEAPKVRKARSVDEGSFDITRDSKNVVESTPITIQQKEHFEGYGSVDIQKNPTDLGVSE VTRFNVGNESNGLIGALQLKNKIDFSKDFNFKVRVANNHQSNTTGADGWGFLFSKGNAAEEYLT NGGILGDKGLVNSGGFKIDTGYIYTSSMDKTEKQAGQGYRGYGAFVKNDSSGNSQMVGENIDK SKTNFLNYADNSTNTSDGKFHQQRLNDVILTYVASTGKMRAEYAGKTWETSITDLGLSKNQAY NFLITSSQRWGLNQGINANGWMRTDLKGSEFTFTPEAPKTITELEKKLKRFRHSRKNVNLIRI
66		2278	MRDKKGPVNKRVDFLSNKLNKYSIRKFTVGTASILIGSLMYLGTQQEAEAAENNIENPTTLKDN VQSKEVKIEEVTNKDTAPQGVAKSEVTSNKDTIEHEASVKAEDISKKEDTPKEVANVAEVQPK SSVTHNAEAPKVRKARSVDEGSFDITRDSKNVVESTPITIQQKEHFEGYGSVDIQKNPTDLGVSE VTRFNVGNESNGLIGALQLKNKIDFSKDFNFKVRVANNHQSNTTGADGWGFLFSKGNAAEEYLT NGGILGDKGLVNSGGFKIDTGYIYTSSMDKTEKQAGQGYRGYGAFVKNDSSGNSQMVGENIDK SKTNFLNYADNSTNTSDGKFHQQRLNDVILTYVASTGKMRAEYAGKTWETSITDLGLSKNQAY NFLITSSQRWGLNQGINANGWMRTDLKGSEFTFTPEAPKTITELEKKLKRFRHSRKNVNLIRI
67	Q99SN7, Uncharacterized leukocidin-like protein 2	26908	MKNKKRVLIASSLSCAILLLSAATTQANSAHKDSQDQNKKEHVDKSQQKDKRNVNKNKDNST VPDDIGKNGKITRTETVYDEKTNILQNLQFDFIDDPYDKNVLLVKKQGSIHSLKFESHKEEK NSNWLKYPSEYHVDQVKRNRKTEILDQLPKNKISTAKVDSTFSYSSGGKFDSTKGIGRTSSNSY SKTISYNQQNYDTIASGKNNNWHVHWSVIANDLKYGGEVKNRNDELLFYRNTRIAATVENPELS FASKYRYPALVRSGFNPEFLTYLSNEKSNEKTQFEVYTRNQDILKNRPGIHYAPPILEKNKDGG RLIVTYEVDWKNKTVKVVDKYSDDNKPYPEG



68		12206	MKNKKRVLIASSLSCAILLLSAATTQANSAHKDSQDQNKKEHVVDKSQQKDKRNVTNKDKNST VPDDIGKNGKITKRTETVYDEKTNILQNLQFDFIDDPYDKNVLLVKKQGSIHNLKFESHKEEK NSNWLKYPSEYHVDVFQVKRNRKTEILDQLPKNKISTAKVDSTFSYSSGGKFDSTKGIGRTSSNSY SKTISYNQQNYDTIASGKNNNWHVHWSVIANDLKYGGEVKNRNDLLFYRNTRIATVENPELS FASKYRYPALVRSGFNPEFLTYSNEKSNEKTQFEVYTRNQDILKNRPGIHYAPPILEKNKDGO RLIVTYEVDWKNKTVKVVDKYSDDNKPYKEG
69	P0A072, Gamma- hemolysin component A	10287	MIKNKILTATLAVGLIAPLANPFIEISKAENKIEDIGQGAIEIKRTQDITSKRLAITQNIQFDFVKDK KYNKDALVVKMQGFISRTTYSCLKKYPYIKRMIWPFQYNISLKTKDSNVDLINYL PKNKIDSA DVSQKLGYNIGGNFQSAPSIGGSGSFNYSKTISYNQKNYVTEVESQNSKGKVGWKANSFVTPN GQVSAYDQYLFAQDPTGPAARDYFVPDNQLPPLIQSGFNPSFIT TLSHERGKGDKSEFEITYGRNMDATYAYVTRHRLAVDRKHDAFKNRNVTVKYEVNWKT THEVKIKSITPK
70		26908	MIKNKILTATLAVGLIAPLANPFIEISKAENKIEDIGQGAIEIKRTQDITSKRLAITQNIQFDFVKDK KYNKDALVVKMQGFISRTTYSCLKKYPYIKRMIWPFQYNISLKTKDSNVDLINYL PKNKIDSA DVSQKLGYNIGGNFQSAPSIGGSGSFNYSKTISYNQKNYVTEVESQNSKGKVGWKANSFVTPN GQVSAYDQYLFAQDPTGPAARDYFVPDNQLPPLIQSGFNPSFIT TLSHERGKGDKSEFEITYGRNMDATYAYVTRHRLAVDRKHDAFKNRNVTVKYEVNWKT THEVKIKSITPK
71	A0A0H3JLZ7, Probable L-asparaginase	12850	MKHLVVIHTGGTISMSQDQSNKVVNTNDINPISMHQDVINQYAQIDELNPFNVPSPHMTIQHVQK LKDIILEAVTNKYDGFVITHGTDTLEETAFLDLILGIEQPVVITGAMRSSNEIGSDGLYNYISAI RVASDEKARHKGVMMVFENDEIHTARNVTKTHTSNTNTFQSPNHGPLGVLT KD RVQFHHMPYR QQALENVNDKLVNPLVKAYMGMPGDIFSFYSREGIDGMVIEALGQGNIPPSALEGIQQLVSLNP IVLVSRSFNGIVSPTYAYDGGGYQLAQQGFIFSNNGSNGPKARLKLVALSNNLDKAEIKSYFEL
72	A0A0H3JJ69, YycI domain-containing protein	13616	MNWKLTKTLFIFVFILVNIVLSIYVNVKVNRSINEVESNNEVNFQQEEIKVPASILNKS VKGIKL EQITGRSKDFSSKAKGSDLTSSDGGKLLNANISQSVKVSNNLKDLDYVNRVFKGSEYQLS EINSGSVKYEQTYDNFPILNNSKAMLNFNIEDNKAASYKQSMDDIKPTDGADKKHQVIGVRK AIEALYYNRYLKKGDEVINARLGYYSVVNETNVQLLQPNWEIKVKHDGKDKTNTYYVEATNN NPKIINH
73	Q7A3E0, 4,4'- diaponeurosporenoate glycosyltransferase	10118	MKWLSRILTVIVTMSMACGALIFNRRHQLKTKTLNFNHKALTIIPARNEEKRIGHLLHSIIQQQV PVDVIVMNDGSTDETARVARSYGATVVDVDDTDGKWKYKSHACYQGVTHACTNRIAFVDA DVTFLRKDAVETLINQYQLQGEKGLLSVQPYHITKRFYEGFSAIFNLMTVVGMNVFSTLDDGRT NQHAFGPVTLTNKEDYYATGGHKSANRHHIEGFALGSAYTSQSLPVTVYEGFPFVAFRMYQEGF QSLQEGWTKHLSTGAGGTPKIMTAIVLWLFSGIASILGLCLSLKYRQMSVRKMVALYLSYTTQ FIYLHRRVGQFSNLLMVCHPLLFMFFTKIFIQSWKQTHRYGVVEWKGRQYSISKEQ
74	A0A0H3JVS7, SA2164 protein	14483	MNIFKNKLLWIPIATMILVIFSLAFYPAYNP KPKDLPIGILNEDKGTTIQDKNVNIGKKLEDKLL DSDSNKIKVWKVDSEKDL EKDLKDQKIFGVAIIDKDFSKDAMSKTQKVVMDSKKEEMQKQVA SGEIPPQVVQMKQKMGNQQVEVKQAKFKTIVSEGSSSQSIASAVLTGMGDNINAQITKQSL ETLTSQNVKVNAADINGLTNPVKVDNEKLNKVKDHQAGGNAPFLMFMPIWIGSIVTSILLFFAF RTSNNIVVQHRRIASIGQMIFAVVAFAAGSFVYIYFMQGVQGFDFDHPNRIAFVAFAILGFVGLIL

			GVMVWLGMKSVPIFFILMFFSMQLVTLPKQMLPESYQKYVVDWNPFTHYATSVRELLYLNHHI ELNSTMWMFIGFMIFGAVSSLVSAIVRKHSTKRTEVPS
75	Q7A6L9, UPF0337 protein SA0772	6886	MADESKFEQAKGNVKETVGNVTDNKNLENEGKEDKASGKAKEFVENAKEKATDFIDKVKG NKGE
76	Q7A5P3, Cold shock protein CspA	7320	MKQGTVKWFNAEKGFGFIEVEGENDVFVHFSAINQDGYKSLEEGQAVEFEVVEGDRGPQAA NVKL
77	P99154, 50S Ribosomal protein L7/L12	12578	MANHEQIIEAIKEMSVLELNDLVKAIEEEFGVTAAAPVAVAGAAGGADAAAETFDVELTSA GSSKIKVVKAVKEATGLGLKDAKELVDGAPKVIKEALPKEEAELKEQLEEVGATVELK
78	P99122, Thioredoxin	11305.8	MAIVKVTDAFDPSKVESGVQLVDFWATWCGPCKMIAPVLEELAADYEGKADILKLDVDEN PSTAAKYEVMSIPTLIVFKDQGPVDKVVGFQPKENLAEVLDKHL
79	Q7A5J1, DNA-binding protein HU	9626	MNKTDLINAVAEQADLTKEAGSAVDVAFESIQNSLAKGEKVQLIGFGNFEVRERAARKGRNP QTGKEIDIPASKVPAFKAGKALKDAVK
80	P0A0G0, 30S ribosomal protein L30	6420	MAKLQITLRSVIGRPETQRKTVEALGLKKTNSVVEDNPAIRGQINKVKHLVTVEEK
81	P66440, 30S ribosomal protein S16	10102	MAVKIRLTRLGSKRNPFYRIVVADARSPRDGRIIEQIGTYNPTSANAPEIKVDEALALKWLNDGA KPTDVTVHNILSKEGIMKKFDEQKKAK
82	Q7A5C0, 30S ribosomal protein S20	8888	MANIKSAIKRVKTTEKAEARNISQKSAMRTAVKNAKTAVSNNADRIKSQLMTANKADNKNEL VSLAVKLVDKAAQSNLIHSNK
83	P60735, 50S ribosomal protein L24	11533	MHIKKGDNVVKIAGKDKGKEGKVIATLPKKDRVVVEGVNIMKKHQKPTQLNPEGGILETEAAI HVSNNVQLLDPKTNEPTRVGYKFVDGKKVRIAKKSCEEIKSNN
84	P66494, 30S Ribosomal Protein S19	10525.3	MARSIKKGPFVDEHLMKKVEAQEGSEKKQVIKTWSRRSTIFPNFIGHTFAVDGRKHPVYVTE DMVGHLKGEFAPTRTFKGHVADDDKKTRR
85	P66299, 50S Ribosomal Protein L36	3693	MKVRPSVVKPICEKCKVIKRGKVMVICENPKHKQRQG
86	P66276, 30S Ribosomal Protein L35	5292	MPKMKTHRGAARKRVKRTASGQLKRSRAFTSHLFANKSTKQKRQLRKARLVSKSDMKRVKQL LAYKK
87	P66210, 30S Ribosomal Protein L32	6349	MAVPKRRTSKTRKNKRRTTHFKISVPGMTECPNCGEYKLSHRVCKNCGSYNGEEVAAK
88	P66521, 30S ribosomal protein S21	6840	MSKTVVRKNESLEDALRRFKRSVSKSGTIQEVKRREFYEKPSVKRKKKSEAARKRKFK
89	P99155, 50S ribosomal protein L10		MSAIIIEAKKQLVDEIAEVLNSVSTVIVDYRGLTVAEVTDLRSQLEAGVEYKVYKNTMVRRA AEKAGIEGLDEFLTGPATATSSEDA VAAAKVISGFAKDHEALEIKSGVMEGNVITAEVKTGVS LP SHDGLVSMLLSVLQAPVRNFAYAVKAIGEQQEENAE
90	P66108, 50S ribosomal protein L20		MPRVKG GTVTRARRKKTIKLAKGYFGSKHTLYKVAKQQVMKSGQYAFRDRRQRKRDRFKLW ITRINAAARQHEMSYSRLMNLKKGAGIDINRKMLSEIAISDEKAFQVLTKAKDALK
91	P66388, 30S ribosomal protein S13		MARIAGVDIPREKRVVISLTYIYGIGTSTAQKILEEANVSADTRVKDLTDELGRIREVVDGYKV EGDLRRETNLNIKRLMEISSYRGIRHRRGLPVRGQKTKNNARTRKGPVKTVANKKK



92	Q7A5X8, 30S ribosomal protein S15		MAISQERKNEIIEYRVHETDTGSPEVQIAVLTAEINAVNEHLRTHKKDHHSRRGLLKMGVRRRHLLNYLRSKDIQRYRELIKSLGIRR
93	Q7A593, UPF0337 protein SA1452	6551	MADESKFDQFKGNVKETVGNVTDNKELEKEGQQDKATGKAKEVVENAKNKITDAIDKLLK
94	P66173, 50S Ribosomal Protein L29	8090	MKAKEIRDLTTSIEIEEQIKSSKEELFNLRFLATGQLEETARIRTVRKTIARLKTVAREREIEQSKANQ
95	P66196, 50S Ribosomal Protein L31 Type B	9721	MKQGIHPEYHQVIFLDTTTFNFKFLSGSTKTSSEMMEWEDGKEYPVIRLDISSDSHPFYTGQRQKFAAADGRVERFNKKFGLKSNN
96	P66726, DNA-directed RNA polymerase subunit omega	8149	MLNPPLNQLTSQIKSKYLIATTAAKRAREIDEQPETELLSEYHSFKPVGRALEEIADGKIRPVISSDYGKE
97	P99132, Probable tautomerase SA1195.1	6611.5	MMPIVNVKLEGRSDEQLKNLVSEVTDAVEKTTGANRQAIHVVIEEMKPNHYGVAGVRKSDQ
98		6626(-14Da modification)	MPIVNVKLEGRSDEQLKNLVSEVTDAVEKTTGANRQAIHVVIEEMKPNHYGVAGVRKSDQ
99	A0A0H3JV47, Uncharacterized protein	8211	METKYELNNTKKVANAFGLNEADTNLLINAVDLDIKNNMQEISSELQQSEQSKQKQYGTTLQNLAKQNRIIK
100	Q7A473, 50S ribosomal protein L13	16332	MRQTFMANESNIERKWYVIDAEGQTLGRLSSEVASILRGKNKVITYTPHVDTG DYVIVINASKIEFTGNKETDKVYYRHSNHPGGIKSITAGELRRTNPERLIENSIKGMLPSTRLGEKQGKKLFFVYGGAEHPhAAQQPENYELRG
101	Q7A460, 50S ribosomal protein L22	12833	MEAKAVARTIRIAPRKVRLVLDLIRGKNAAEAIAILKLTNKASSPVIEKVLMSALANAEHNYDMNTDELVVKEAYANEGPTLKRFRPRAQGRASAINKRTSHITIVVSDGKEEAKA
102	P99142, 30S ribosomal protein S6	11594	MRTYEVMYIVRPNIEEDAKKALVERFNGILATEGAEVLEAKDWGKRRLAYEINDFKDGFYNIVRVKSDNNKATDEFQRLAKISDDIIRYMVIREDEDK
103	P66334, 30S ribosomal protein S10	11444	MAKQKIRIRLKAYDHRVIDQSAEKIVETAKRSGADVSGPIPLPTEKSVYTIIRAVHKYKDSREQFEQRTHKRLIDIVNPTPKTVDALMGLNLP SGVDIEIKL
104	P68800, Fibrinogen-binding protein (Efb)	11104	MKNKLIASLLTIAAIGITTTTIASTADASEGYGPREKKPVSINHNIVEYNDGTFKYQSRPKFNSTPKYIKFKHDYNILEFNDGTFEYGARPQFNKPAAKTDTATIKKEQKLIQAQNLVREFEKTHTVSAH RKAQKAVNLVSFEYKVKKMVLQERIDNVLKQGLVR
105	A0A0H3JPH2, Uncharacterized protein	3180	MKKKFVSSCIASITLFGTLLGVTYKAEAATVHVAGGVWSHGIGKHYVWSYYSHNKRNHGSTAVGKYSSFSGVARPGVQSKASAPKAWGGNKTFYSLH
106	Hypothetical protein	8620	MKKKFVSSCIASITLFGTLLGVTYKAEAATVHVAGGVWSHGIGKHYVWSYYSHNKRNHGSTAVGKYSSFSGVARPGVQSKASAPKAWGGNKTFYSLH
107	Hypothetical protein	8769	MKKKFVSSCIASITLFGTLLGVTYKAEAATVHVAGGVWSHGIGKHYVWSYYSHNKRNHGSTAVGKYSSFSGVARPGVQSKASAPKAWGGNKTFYSLH
108	Hypothetical protein	8239	MKKKFVSSCIASITLFGTLLGVTYKAEAATVHVAGGVWSHGIGKHYVWSYYSHNKRNHGSTAVGKYSSFSGVARPGVQSKASAPKAWGGNKTFYSLH
109		5457	MKKKFVSSCIASITLFGTLLGVTYKAEAATVHVAGGVWSHGIGKHYVWSYYSHNKRNHGSTAVGKYSSFSGVARPGVQSKASAPKAWGGNKTFYSLH

110	A0A0H3JLH5, Uncharacterized protein	7660	MKFKKVLVATAMVGVLATGVVGYGNQADAKVYSQNGLVLHDDANFLEHEL SYIDVLLDKNA DQATKDNLR SYFADKGLHSIKDIINKAKQDGF DVSKYEHVK
111	A0A0H3JVL1, SA2097 protein	15003	MKKLV TATTLTAGIGTALVGQAHHADA AENYTNYN NYNTTQT TTTTTTTTTTSSISHS GNL YTAGQCTWYVYDKVGGEIGSTWGNANNWAAAAQGAGFTVNHTPSKGAILQSSEGPFGHVAY VESVNSDGSVTISEMNYSGGPFSVSSRTISASEAGNYNYIHI
112	P65415, Putative 3- methyladenine DNA glycosylase	4208	MDFVNNDTRQIAKNLLGVKVIYQDTTQTYTGYIVETEAYLGLNDRAAHGYGGKITPKVTSLYK RGGTIYAHVMHTHLLINFVTKSEGIPEGVLIRAIEPEEGLSAMFRNRGKKGYEVTNGPGKWTKA FNIPRAIDGATLNDCLRSIDTKNRKYPKDIIASPRIGIPNKGDWTHKSLRYTVKGNPFVSRMRKSD CMFPEDTWK
113	Q99RL2, IgG-binding protein SBI	5285	MKNKYISKLLVGAA TITLATMISNGEAKASENTQQTSTKHQTTQNNYVTDQQKAFYQVHLKKG ITEEQRNQYIKTLREHPERAQEVFSESLKDSKNPDRRVAQQNAFY NVLKNDNLTEQEKNNYIAQ IKENPDRSQQVWVESVQSSKAKERQNIENADKA IKDFQDNKAPHDKSAAYEANSKLPKDLRDK NNRFVEKVSIEKAIVRHDERVKSANDAI SKLNEKDSIENRRLAQREVNKAPMDVKEHLQKQLD ALVAQKDAEKKVAPKVEAPQIQSPQIEKPKAESPKVEVPQIQSPKVEVPQSKLLGYYQSLKDSF NYGKYLTDTYKSYKEKYDTAKYYYNTYYKYKGAI DQTVLTVLGSGSKSYIQPLKVDDKNGY LAKSYAQVRNYVTESINTGKVLTYFYQNPTLVKTAIKAQETASSIKNTLSNLLSFWK
114		4007	MKNKYISKLLVGAA TITLATMISNGEAKASENTQQTSTKHQTTQNNYVTDQQKAFYQVHLKKG ITEEQRNQYIKTLREHPERAQEVFSESLKDSKNPDRRVAQQNAFY NVLKNDNLTEQEKNNYIAQ IKENPDRSQQVWVESVQSSKAKERQNIENADKA IKDFQDNKAPHDKSAAYEANSKLPKDLRDK NNRFVEKVSIEKAIVRHDERVKSANDAI SKLNEKDSIENRRLAQREVNKAPMDVKEHLQKQLD ALVAQKDAEKKVAPKVEAPQIQSPQIEKPKAESPKVEVPQIQSPKVEVPQSKLLGYYQSLKDSF NYGKYLTDTYKSYKEKYDTAKYYYNTYYKYKGAI DQTVLTVLGSGSKSYIQPLKVDDKNGY LAKSYAQVRNYVTESINTGKVL TYFYQNPTLVKTAIKAQETASSIKNTLSNLLSFWK
115	A0A0H3JLA2, Uncharacterized protein	10613	MKPYIQLVLFKQWLQYILLVTTIVIALVLIGIGYRVAHDNFKIPITIQDLDQTTASKSFVNKIKQSD YVTIKK VDEDESYIEDDVTKKEAILSMQIPKGF SQKLKENRLKETIQLYGRDDFIGGIAIEIVSSSL YEQQIPNIIYEHLEDMKQHQSIDAINKSYHKHTPESKIKFVSLTKQAQHSISISLIFAVILFVSAVQV VLHYRLNQQAALQRLSQYHLSRFKLYSTYVMTH TILLLLVLLAVSLYLSQPLSLIFYLKSLLLLILI YEIGIVFILFHIQTISHRLFM TFIYALAMGIVYLIIFM
116	Q99SU8, Chemotaxis inhibitory protein	14127	MKKKLATTVLALSFLTAGISTHHHSAKAFTFEPFPTNEEIESNKKMLEKEKAYKESFKNSGLPTT LGKLDERLRNYLEKGTKN TAQFEKMVILTENKGYTVYV LNTPLAEDRKNVELLGKMYKTYFF KKGESKSSYVINGPGKTNEYAY
117		10920	MKKKLATTVLALSFLTAGISTHHHSAKAFTFEPFPTNEEIESNKKMLEKEKAYKESFKNSGLPTT LGKLDERLRNYLEKGTKN TAQFEKMVILTENKGYTVYV LNTPLAEDRKNVELLGKMYKTYFF KKGESKSSYVINGPGKTNEYAY
118	A0A0H3JPQ1, SA1000 protein	10478	MKKNFIGKSILSIAAISLTVSTFAGESHAQTKNVEAAKKYDQYQTNFKKQVNKKV VDAQKAVN LFKRTRTVATHRKAQRAVNLIHFQHSYEKKKLQRQIDLVLKYNTLK
119	A0A0H3JVY4, Probable glycine betaine/ carnitine/	3995	MIEFLHEHGGQLMSKTLEHFYISIVALLLAIHVA VPIGILLSKTKRTANIVLTVAGVLQTIPTLAVL AIMIPFGVGKTPAIVALFIYVLLPILNNTVLGVQNIDSNIKEAGKSMGMTQFQLMKDVELPLALP

	choline ABC transporter opuCB		LIIGGIRLSSVYVISWATLASVVGAGGLGDFIFNGLNLYDPLMIVTATVLVTALALGVDALLALV EKWVVPKGLKVSG
120	0A0H3JMB8, Citrate synthase	12595	MAELQRGLEGVIAAETKISSIIESQLTYAGYDIDDLAENAQFEEVIFLLWNYRLPNEEELAHLKG KLNQYMTLNPVYTHFEEYVTDHVPMTALRTSLSYIAHFDPDAENESDENRYERAMRIQAKV ASLVTAFAFVRQDKEPLKPNPDLSYAAFLYMLRGELPTDIEVEAFNKALILHADHELNASFT ARCAVSSLSDMYSGIVAAGVSLKGPLHGGANEQVMTMLSEIGSIENVDAYLDEKFANKDKVM GFGHRVYKGDGPRAKYLREMSRQITKDAGREELFEMSVKMEKRMAEEKGLIPNVDFYSASVY HCMEIPHDLFPIFAVSRGAWIAHILEQYKDNRMRPRAKYIGETNRKYIPLEERK
121	A0A0H3JK15, Uncharacterized protein	17424	MKKLLTASIIACSVVMGVGLVNTSAEAASGNSIDTVKQLIKGDQSLNVKIGESIKDVLTKYKNP MYSYNEDGTEHYEFHTKKGMMLVTTDGKKNGKVTHISMMYNDANGPTYQAVKNYVGKA VTHTEYSKVAGNFGYIEKGKTTYQFASAPKDKNIKLYRIDLEK
122		17321	MKKLLTASIIACSVVMGVGLVNTSAEAASGNSIDTVKQLIKGDQSLNVKIGESIKDVLTKYKNP MYSYNEDGTEHYEFHTKKGMMLVTTDGKKNGKVTHISMMYNDANGPTYQAVKNYVGKA VTHTEYSKVAGNFGYIEKGKTTYQFASAPKDKNIKLYRIDLEK
123		16847	MKKLLTASIIACSVVMGVGLVNTSAEAASGNSIDTVKQLIKGDQSLNVKIGESIKDVLTKYKNP MYSYNEDGTEHYEFHTKKGMMLVTTDGKKNGKVTHISMMYNDANGPTYQAVKNYVGKA VTHTEYSKVAGNFGYIEKGKTTYQFASAPKDKNIKLYRIDLEK
124	A0A0H3JTC5, DM13 domain-containing protein	11668	MNTKYFLAVGAVASVLTGACGNSNSQDQGNKTEQKTKSEDSNVKTDKTKHLTGTFFSSKNGE TVEGKAEIKNGKLMMLTNYKSSKGPDLVYVLTKNNGDIKNGKEIAMVDYDKEKQTFDLKNVDLS KYDEVTIYCKKAHVIFGGAKLK
125		15146	MNTKYFLAVGAVASVLTGACGNSNSQDQGNKTEQKTKSEDSNVKTDKTKHLTGTFFSSKNGE TVEGKAEIKNGKLMMLTNYKSSKGPDLVYVLTKNNGDIKNGKEIAMVDYDKEKQTFDLKNVDLS KYDEVTIYCKKAHVIFGGAKLK
126		12894	MNTKYFLAVGAVASVLTGACGNSNSQDQGNKTEQKTKSEDSNVKTDKTKHLTGTFFSSKNGE TVEGKAEIKNGKLMMLTNYKSSKGPDLVYVLTKNNGDIKNGKEIAMVDYDKEKQTFDLKNVDLS KYDEVTIYCKKAHVIFGGAKLK
127	A0A0H3JMR5, Uncharacterized protein	10570	MALFLYKNLRRSFNMANEIIKKTERFILVQIDKEGTERVLYQDFVGSFTTSDSASYAQDFKSEEN AKKIAETLNLLYQLTGNQNGVKVVEKVVDRDLSSDKSVDSETM
128	Q7A377, Immunodominant staphylococcal antigen B	18565	MNKTSKVCVAATLALGTLIGVTVVENSAPTSKQAQAAITPYTYNGYIGNNANFILDKNFINAI KYDNVVFNGIKLAKTNTIKKVEKYDQTFKGVSAGNEASQLQFVVKNNISLKDIQKAYGKDLK KENGKTKEADSGIFYYQNAKKTGLIWFVVDHNRVVEVTVGHTPYKTSK
129		17837	MNKTSKVCVAATLALGTLIGVTVVENSAPTSKQAQAAITPYTYNGYIGNNANFILDKNFINAI KYDNVVFNGIKLAKTNTIKKVEKYDQTFKGVSAGNEASQLQFVVKNNISLKDIQKAYGKDLK KENGKTKEADSGIFYYQNAKKTGLIWFVVDHNRVVEVTVGHTPYKTSK
130		14699	MNKTSKVCVAATLALGTLIGVTVVENSAPTSKQAQAAITPYTYNGYIGNNANFILDKNFINAI KYDNVVFNGIKLAKTNTIKKVEKYDQTFKGVSAGNEASQLQFVVKNNISLKDIQKAYGKDLK KENGKTKEADSGIFYYQNAKKTGLIWFVVDHNRVVEVTVGHTPYKTSK
131		16575	MNKTSKVCVAATLALGTLIGVTVVENSAPTSKQAQAAITPYTYNGYIGNNANFILDKNFINAI KYDNVVFNGIKLAKTNTIKKVEKYDQTFKGVSAGNEASQLQFVVKNNISLKDIQKAYGKDLK KENGKTKEADSGIFYYQNAKKTGLIWFVVDHNRVVEVTVGHTPYKTSK

132	A0A0H3JMD3, Uncharacterized protein	3448(-14Da)	MDINVLATIFKFILFVVEIYYFGMIYFFTSWVPSIRETKVGYFLAKIYEPFLQPFRKVIPPIGIIDISS IAAIIVLVLFQKGLLQIFNWILIQLQ
133	Q99SU9, Staphylococcal complement inhibitor	9790	MKIRKSILAGTLAIVLASPLVTNLDKNEAQASTSLPTSNEYQNEKLANELKSLLDELNVNELATG SLNTYYKRTIKISGLKAMYALKSKDFKKMSEAKYQLQKIYNEIDEALKSKY
134		4133	MKIRKSILAGTLAIVLASPLVTNLDKNEAQASTSLPTSNEYQNEKLANELKSLLDELNVNELATG SLNTYYKRTIKISGLKAMYALKSKDFKKMSEAKYQLQKIYNEIDEALKSKY
135		9806	MKIRKSILAGTLAIVLASPLVTNLDKNEAQASTSLPTSNEYQNEKLANELKSLLDELNVNELATG SLNTYYKRTIKISGLKAMYALKSKDFKKMSEAKYQLQKIYNEIDEALKSKY
136		4133	MKIRKSILAGTLAIVLASPLVTNLDKNEAQASTSLPTSNEYQNEKLANELKSLLDELNVNELATG SLNTYYKRTIKISGLKAMYALKSKDFKKMSEAKYQLQKIYNEIDEALKSKY
137		9595.9	MKIRKSILAGTLAIVLASPLVTNLDKNEAQASTSLPTSNEYQNEKLANELKSLLDELNVNELATG SLNTYYKRTIKISGLKAMYALKSKDFKKMSEAKYQLQKIYNEIDEALKSKY