

SUPPLEMENTAL MATERIAL:

The structure of *Clostridioides difficile* SecA2 ATPase exposes regions responsible for differential target recognition of the SecA1 and SecA2-dependent systems

Nataša Lindič¹, Jure Loboda¹, Aleksandra Usenik^{1,2}, Robert Vidmar¹ and Dušan Turk^{1,2*}

¹ Department of Biochemistry, Molecular and Structural Biology, Jozef Stefan Institute, Jamova cesta 39, 1000 Ljubljana, Slovenia

² Centre of Excellence for Integrated Approaches in Chemistry and Biology of Proteins (CIPKeBiP), Jamova cesta 39, 1000 Ljubljana, Slovenia

* Correspondence: dusan.turk@ijs.si; Tel.: +386 1 477 3857

SUPPLEMENTAL FIGURES:

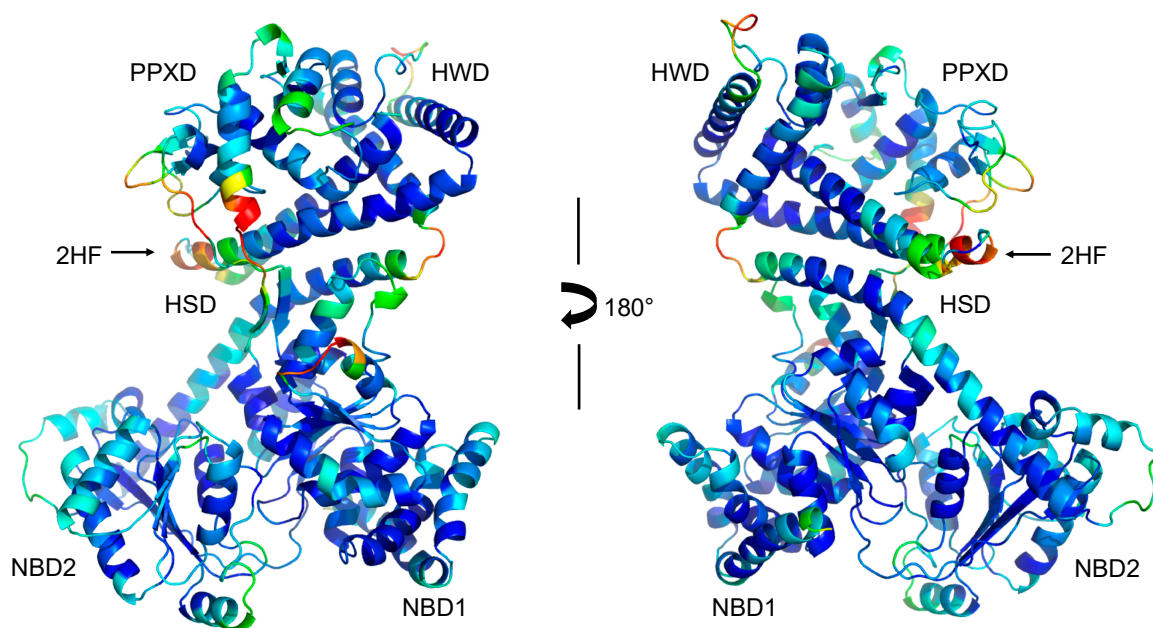


Figure S1, related to Figure 1: B-factor representation of the CDSecA2 crystal structure. All the objects are coloured according to the B-factor values (blue, low B-factors; red, high B-factors), and domains are depicted. 2HF with its loop is pointed out with an arrow. The molecule is shown in two different orientations. The figure was made with PyMOL [1].

Conservation:					5	5	6	7	5	5											
SECA1_GEO_thermodenitrifi	1	-----	MLGV	-LKKV	----	FDPNKRQLARLEKIADQVDALGP	EMARLSDEQLRQKTEEFKARY	----	QQGES	-----	57										
SECA1_GEO_kaustophilus	1	-----	MLGV	-LKKV	----	FDPNKRQLARLEKIADQVDALGP	EMARLSDEQLRQKTEEFKARY	----	QQGES	-----	57										
SECA1_LAC_johnsonii	1	-----	MANI	-LKKI	----	YDNRRLRELLKFEKLATKVESLG	DEYEKLSDBEQLQAKTPEFRKRL	----	KNGET	-----	57										
SECA1_STR_parasanguinis	1	-----	MANL	-LKTI	----	IENDRGEIKRLEKMADKVFVS	YEDQMAALTDDLELAKTVEFKORY	----	QDGES	-----	57										
SECA1_STR_gordonii	1	-----	MANI	-LRTI	----	IENDKGELRKLEKMANKVIAYS	DQMAALSDEBLKACTDEFKORY	----	QNSES	-----	57										
SECA1_STR_pneumoniae	1	-----	MANI	-LKTI	----	IENDKGIEIRLEKMADKVFV	KYEDQMAALTDDQLKAKTVEFKERY	----	QNSES	-----	57										
SECA1_STR_agalactiae	1	-----	MANI	-LRTV	----	IENDKGELKKLDKIAKKVDS	YADHMAALSDBALQAKTPEFKERY	----	QNGET	-----	57										
SECA1_LIS_monocytogenes	1	-----	MAGL	-LKKI	----	FESGKKDVKYLERKADEIIA	LADETAALSDDLAKTVEFKERV	----	QKGET	-----	57										
SECA1_LIS_innocua	1	-----	MAGL	-LKKI	----	FESGKKDVKYLERKADEIIA	LADETAALSDEALREKTVEFKERV	----	QKGET	-----	57										
SECA1_LIS_welshimeri	1	-----	MAGL	-LKKI	----	FESGKKDVKYLERKADEIIA	LADETAALSDDLAKTVEFKERV	----	QKGET	-----	57										
SECA_BAC_subtilis	1	-----	MLGI	-LNKM	----	FDPTKRTLNRYEKIANDIDA	IRGDYENLSDALKHKHTIEFKERL	----	EKGAT	-----	57										
SECA1_BAC_anthraxis	1	-----	MIGI	-LKKV	----	FDVNQRQIKRMQKTVEQIDALE	SSIKPLTDBQLKGKTLFVKERL	----	TKGET	-----	57										
SECA1_BAC_thuringiensis	1	-----	MIGI	-LKKV	----	FDVNQRQIKRMQKTVEQIDALE	SSIKPLTDBQLKGKTLFVKERL	----	TKGET	-----	57										
SECA1_BAC_cereus	1	-----	MIGI	-LKKV	----	FDVNQRQIKRMQKTVEQIDALE	SSIKPLTDBQLKGKTLFVKERL	----	TKGET	-----	57										
SECA1_STA_epidermidis	1	-----	MGF	-LSKI	----	VDGNKKEIKRLGKLADKVLAE	EDTAILTDEEIREKTSKFQKELAEIEDVKKQNDY	----		-----	63										
SECA1_STA_haemolyticus	1	-----	MGF	-LSKI	----	VDGNKKETKRLSKIADEVLS	LEEDMAILTDEEIKNKTKQFQQEQVEIEDVKKQNDY	----		-----	63										
SECA1_STA_aureus	1	-----	MGF	-LSKI	----	LDGNNKEIKGLGLADKVIAL	EKEKTAILTDEEIRNKTKQFOTELADIDNVKKQNDY	----		-----	63										
SECA1_ALK_metalliredigens	1	-----	MKRL	-FEKV	----	FGSSEEREIKKIDKLADRVEA	LDEEYKSLSDQALQSCTAELKGRIL	----	SQGEA	-----	58										
SECA1_PBP_difficile	1	-----	MSF	-MDNL	----	FNMAKKELKKPKNTVDIIDS	LEPFKFSMADSLENMTNIIFKERL	----	ANGES	-----	57										
SECA2_PBP_difficile	1	-----	MSV	-IDSI	----	LDKADEQEIKLNLNVI	VDKIDALEDSDKMNLSEBELKDMTAIFKNRL	----	KKGET	-----	57										
SECA2_model_opened_conf	1	-----			----	BQEIKKLNVI	VDKIDALEDSDKMNLSEBELKDMTAIFKNRL	----	KKGET	-----	45										
SECA_E_coli	1	-----	MLIKL	-LTKV	----	FGSRNDRTLRRMRKVNNI	INAMEPEMEKLSDEELKGGTAEPFARL	----	EKGEV	-----	59										
SECA1_MYC_vanbaalenii	1	-----	M	-LSKL	----	LRLGEGRMVKRLKGVADYVNT	LSDDIEKLSDAELRGKTDFPRARL	----	AGKE	-----	57										
SECA1_MYC_ulcerans	1	-----	M	-LSKL	----	LRVGEGRMVKRLKKVADYVES	LSGDEVELTDLAELRAKTDEFKKRH	----	AEGES	-----	55										
SECA1_MYC_paratuberculosis	1	-----	M	-LSKL	----	LRLGEGRMVKRLKKVADYVNT	LSDEVELTDLAELRAKTDEFKKRH	----	ADGES	-----	55										
SECA1_MYC_tuberculosis	1	-----	M	-LSKL	----	LRLGEGRMVKRLKKVADYVGT	LSDDVEKLTDAELRAKTDEFKRRILA	----	DQKNPET	-----	58										
SECA1_MYC_bovis	1	-----	M	-LSKL	----	LRLGEGRMVKRLKKVADYVGT	LSDDVEKLTDAELRAKTDEFKRRILA	----	DQKNPET	-----	58										
SECA1_MYC_leprae	1	-----	M	-LSKL	----	LRLGEGRIVKRLKRVAEYVNT	LSDNVEKLTDLVELAKTDEFKORLA	----	DEKNPES	-----	58										
SECA1_MYC_smegmatis	1	-----	M	-LSKL	----	LRLGEGRMVKRLKRVADYNAL	SDDVEKLSDAELRAKTEEFKKRV	----	ADGED	-----	55										
SECA1_COR_diphtheriae	1	-----			----	LRVGEGRAVKRLKKIADDVIA	LEADYTDLTDEELKAKTHEFQERI	----	AQGGS	-----	57										
SECA1_COR_efficiens	1	-----			----	LRVGEGRAVKRLKKIADQVIA	LEDQYANLTDEELKAKTEEFKORI	----	AQGET	-----	57										
SECA1_COR_glutamicum	1	-----			----	LRVGEGRAVKRLKHIAHQVIA	LEDKFAANLTDEELKAKTAEFKERI	----	AGGEG	-----	57										
SECA1_COR_jeikeium	1	-----			----	LRMGEGRAVKRLAKIADQVMD	LDEEYTKLTDEELQAKTDELKKRV	----	QEDGES	-----	58										
SECA1_THE_fusca	1	-----	MPGILD	RDV	----	LRIGEKGILRLKLNKLKDQINS	IEDDFVDSLDAELRALTDEYKORL	----	KDGE	-----	58										
SECA2_MYC_vanbaalenii	1	-----	M	-LADV	----	LRLGEARTVKQLSAIAHDHVS	LARGVENLTDAELSSRTDVFRRRV	----	ADGDV	-----	55										
SECA2_THE_maritima	1	-----			----	LPDKNKRILKKYAKMVSKINQ	IESDLRSKNSELIRLSMVLKEKV	----	NSPED	-----	52										
SECA2_GEO_kaustophilus	1	-----	MFAK	-VKQL	----	FDESAREVQRLAKLAAQIN	EWEPITSSLSDBQLRQKTUVFKERL	----	ERGET	-----	57										
SECA2_GEO_thermodenitrifi	1	-----	MLSL	-LKRA	----	IGYTNERQLKKYMRVVEQIN	RMEPQMEKLTDAELRRKTDEFKEQL	----	ASGKS	-----	58										
SECA2_BAC_anthraxis	1	-----	MLNS	-VKKL	----	LGDSQKRKLKKYEQLVQEI	NNLEEKLSDLSEBELRHKHTITFKDML	----	RDGKT	-----	58										
SECA2_BAC_thuringiensis	1	-----	MLNS	-VKKL	----	LGDSQKRKLKKYEQLVQEI	NNLEEKLSDLSEBELRHKHTITFKDML	----	RDGKT	-----	58										
SECA2_BAC_cereus	1	-----	MLNS	-VKKL	----	LGDSQKRKLKKYEQLVQEI	NNLEEKLSDLSEBELRHKHTITFKDML	----	RDGKT	-----	58										
SECA2_LIS_welshimeri	1	-----	MKQN	----	----	FDDRKIVKQYREIARQIVK	KEGLYKNMDQELREQTNFYREKF	----	KTKEM	-----	52										
SECA2_LIS_monocytogenes	1	-----	MRQN	----	----	YDDRKIVKQYREIARQIVK	KEGLYKNMQEALCEQTNFYREKF	----	KTKPM	-----	52										
SECA2_LIS_innocua	1	-----	MRQN	----	----	YDDRKIVKQYREIARQIVR	KEGLYKNMDQELREQTNFYREKF	----	KTKPM	-----	52										
SECA2_ALK_metalliredigens	1	-----	MLKN	----	----	ISSVSKRFENFKNEVYDIEL	YKKTVEEINNTNRYKNASDTFELREISENLKNKV	----	KEGIP	-----	62										
SECA2_LAC_johnsonii	1	-----			----	MLTDRLRLKKARKLLNKIN	KLGPQMAMSDEKLQQTAFKKQL	----	KEGKS	-----	49										
SECA2_STA_haemolyticus	1	-----	M	-ANQV	----	SNVINSMLRLKRLQKQLVA	VNRLSDQMRNCSDEALQAKTADFQRL	----	EKRET	-----	55										
SECA2_STA_aureus	1	-----	M	-KHL	----	DVTINELRLKSIRKIVKRIN	TSWDEVKSYSDDALQKQTEFKERL	----	ASGVD	-----	55										
SECA2_STA_epidermidis	1	-----	M	-AKGV	----	NQIINNIRLRLKRLKILNQ	INALSEEFNFSDEALQAKTEFKVYL	----	NDNKA	-----	55										
SECA2_STR_Agal	1	-----	MTA	-FNSL	----	FSLDKKRLKKLQRTLNTIN	SLKDQMATLSNEELQAKTTEFRKRL	----	VNGET	-----	56										
SECA2_STR_Gordon	1	-----	M	-VKNP	----	PHIIRLKKILAKIKSFEKE	MSSSLSDLDLQKKTDEFKKRL	----	ADGEN	-----	49										
SECA2_STR_Pneum	1	-----	MFRL	LGQD	----	FQLRKVKKILKQINALKG	KMSSSLSDQLVAKTVEFQRL	----	SEGES	-----	52										
SECA2_STR_Sanguin	1	-----	M	-IKNH	----	FQIQLRKLKILAKVKSFE	SESMAGLTDAELRKKTOEFKERL	----	AAGET	-----	49										
SECA2_COR_efficiens	1	-----	MAGFD	FWKA	----	LGKGQGRNQKRSLAIVDQA	EAHTRDLEALDDLAHLARA	----	RTLTV	-----	55										
SECA2_MYC_ulcerans	1	--MR	SCTAAPGVSRNTNTHARR	GLGVAYRWAVSKTT	RAQSGRLSSRFWRL	----	LGATTEKNQNRSLAQVTA	SAEFDKEAADLNDEKLRKAA	----	GLLN	----	LEDLA	94								
SECA2_MYC_paratuberculosis	1	----			----	MPKTNRAQPGRLSSRFWRL	----	LGASTEKNRSRSLTLVTD	SSEYDDEAAGLTDEQLRKA	----	GLLN	----	LEDLA	96							
SECA2_MYC_tuberculosis	1	MNVH	GCPRIAACRCTDTHPRGR	PAFAYRWFPKTT	RAQPGRLSSRFWRL	----	LGASTEKNRSRLADVTASA	EYDKEAADLSDDEBLRKA	----	GLLN	----	LDDLA	96								
SECA2_MYC_bovis	1	MNVH	GCPRIAACRCTDTHPRGR	PAFAYRWFPKTT	RAQPGRLSSRFWRL	----	LGASTEKNRSRSLADVTASA	EYDKEAADLSDDEBLRKA	----	GLLN	----	LDDLA	96								
SECA2_MYC_leprae	1	----			----	MSKTPRTQPGLSSRFWRL	----	LGASTDKNLNYSAEVTA	AAAAHYHKEAADLGDEQLRKAC	----	GLLN	----	LNDLA	96							
SECA2_MYC_smegmatis	1	----			----	MPKTSAAKPGRLSSKFWL	----	LGASTERNQARSLSEVK	GAADEFKKAADLDDBQLTKAA	----	KLLK	----	LEDLA	66							
SECA2_THE_fusca	1	----			----	MAEG	----	VRRL	----	----	----	----	TELG	----	NAELP	55					
SECA2_COR_diphtheriae	1	----			----	MAGFRWFWD	----	----	----	----	----	----	HECA	----	QHS	55					
SECA2_COR_glutamicum	1	----			----	MAGFDWFWKA	----	----	----	----	----	----	KDLA	----	SGG	55					
SECA2_COR_jeikeium	1	----			----	MAFDW	----	FWKA	----	----	----	----	MGSSPKKNQKKSRAVVA	QAD	----	SSRYSGLSDAELRDA	----	SDVV	----	TEQSTSEDGHHFG	62
Consensus_aa:						h.ph		p..p	pph.phhpp1..hp.ph..	hoD.pLp..o..F+p.h		psbs									
Consensus_ss:						h	hhhh		hhhhhhhhhhhhhhhhhhhh	hhhhhhhhhhhhhhhh		h									

		Walker A																						
Conservation:		5585	6765	9	565	55	89	7	6	8	6	89	99999999	6	55	66	9	565568	9	996	78	6	5	685
SECA1_GEO_thermodenitrifi	58	-LDDLLVEAFVAVREGAKRVLGLYPYKQVIMGGVVLHGGDIAE	MKTG	BGGKTL	TATMPVYLNAL	TGRGVHVVTVN	VEYLASRD	AKEMQGLYEF	LGLTVGLNLSGM															159
SECA1_GEO_kaustophilus	58	-LDDLLVEAFVAVREGAKRVLGLYPYKQVIMGGVVLHGGDIAE	MKTG	BGGKTL	TATMPVYLNAL	TGRGVHVVTVN	VEYLATRD	ATEMGKLYEFL	GMTVGLNLSGM															159
SECA1_LAC_johnsonii	58	-LDDILPEAFATAREGAKRVLGLYPFRVQIIGGIALHYGNIAE	MMTG	BGGKTL	TATLPVYLNAL	TGKGVHVVTVN	EYLSRR	DESEMGLYKWL	GLSVGLNLSNM															159
SECA1_STR_parasanguinis	58	-LDDLLVEAFVAVREGAKRVLGLFPYKQVIMGGVVLHGGDVE	MRTG	BGGKTL	TATMPVYLNAL	SGKGVHVVTVN	EYLTERT	DATEMBGLYSWL	GLSVGINLAAK															159
SECA1_STR_gordonii	58	-LDDLLVEAFVAVREGAKRVLGLYPYKQVIMGGVVLHGGDVE	MRTG	BGGKTL	TATMPVYLNAL	AGEGVHVVTVN	EYLTERT	DATEMBGLYSWL	GLSVGINLAAK															159
SECA1_STR_pneumoniae	58	-LDSLLVEAFVAVREGAKRVLGLFPYKQVIMGGVVLHGGDVE	MRTG	BGGKTL	TATMPVYLNAL	SGKGVHVVTVN	EYLSER	DATAMEGLYSWL	GLSVGINLATK															159
SECA1_STR_agalactiae	58	-LDQLLPEAFVAVREASRVLGLYPYHVGIMGGVVLHGGDIE	PMRT	BGGKTL	TATMPVYLNAL	ISGLGVHVVTVN	EYLSER	DATAMEGVVYSWL	GLSVGINLAAK															159
SECA1_LIS_monocytogenes	58	-LDDLLVEAFVAVREGAKRALGLYPFKVQMLGGIVLHEGNIAE	MKTG	BGGKTL	TATLPVYLNAL	SGEGVHVVTVN	EYLAHRD	AEEMGVLYN	FLGLSVGLNLSAL															159
SECA1_LIS_innocua	58	-LDDLLVEAFVAVREGAKRALGLYPFKVQMLGGIVLHEGNIAE	MKTG	BGGKTL	TATLPVYLNAL	SGEGVHVVTVN	EYLAHRD	AEEMGVLYN	FLGLSVGLNLSAL															159
SECA1_LIS_welshimeri	58	-LDDLLVEAFVAVREGAKRALGLYPFKVQMLGGIVLHEGNIAE	MKTG	BGGKTL	TATLPVYLNAL	SGEGVHVVTVN	EYLAHRD	AEEMGVLYN	FLGLSVGLNLSAL															159
SECA_BAC_subtilis	58	-TDDLLVEAFVAVREASRRVTGMFPFKVQMLGGIVLHGGDIAE	MKTG	BGGKTL	TSLPVYLNAL	TGKGVHVVTVN	EYLSARD	AEQMGKLYEFL	GLTVGLNLSNM															159
SECA1_BAC_anthraxis	58	-VDDLLPEAFVAVREAAATRVLMGRPYPGVQMLGGIALHEGNI	SE	MKTG	BGGKTL	TSLPVYLNAL	TGKGVHVVTVN	EYLAQRD	ANEMQLHEFL	GLTVGINLSNM														159
SECA1_BAC_thuringiensis	58	-VDDLLPEAFVAVREAAATRVLMGRPYPGVQMLGGIALHEGNI	SE	MKTG	BGGKTL	TSLPVYLNAL	TGKGVHVVTVN	EYLAQRD	ANEMQLHEFL	GLTVGINLSNM														159
SECA1_BAC_cereus	58	-VDDLLPEAFVAVREAAATRVLMGRPYPGVQMLGGIALHEGNI	SE	MKTG	BGGKTL	TSLPVYLNAL	TGKGVHVVTVN	EYLAQRD	ANEMQLHEFL	GLTVGINLSNM														159
SECA1_STA_epidermidis	64	-LDKILPEAYALVREGSKRVFNMPYKQVIMGGIAIHKGDI	AE	MRTG	BGGKTL	TATMPYLYNAL	LAGRGVHVITV	NLEYLSS	QSEEMAE	LYNGLTVGLNLSNK														165
SECA1_STA_haemolyticus	64	-LDKILPQAYALVREGAKRVFNMTYKQVIMGGIAIHKGDI	AE	MRTG	BGGKTL	TATMPYLYNAL	LAGRGVHVITV	NLEYLSS	QSEEMAE	LYNGLTVGLNLSNK														165
SECA1_STA_aureus	64	-LDKILPEAYALVREGSKRVFNMTYKQVIMGGIAIHKGDI	AE	MRTG	BGGKTL	TATMPYLYNAL	LAGRGVHVITV	NLEYLSS	QSEEMAE	LYNGLTVGLNLSNK														165
SECA1_ALK_metalliredigens	59	-LDDILPEAFATMREAAWRVLGMKHYRVQIYGAIIHKGRI	SE	MKTG	BGGKTL	MTATLPVYLNAL	AGKGVHVVTVN	DYLAQRD	CEWMGKLYEFL	GLSVGVIVHGI														160
SECA1_PBP_difficile	58	-TDDILPEAFVAVREVSRRVLGLRHYRVQMTIGGIVIHQKRI	AE	MKTG	BGGKTL	VEATAPVYLNAL	TGKGVHVVTVN	DYLAQRD	KDQMAKLYEFL	GLSMGVGVI	IHQ													159
SECA2_PBP_difficile	58	-LDDILPEAFVAVREVSRRKRLGMRQYRVQMTIGGIVIHQKRI	AE	MKTG	BGGKTL																			

Conservation:		75	9	7768	5	5	8997957575	6	6666996996	7769595697	6676	5											
SECA1_GEO_thermodenitrifi	160	----	SREEKQ	AAYNAD	ITYGT	NNEFG	FDYLR	DNMVL	YKEHI	VQRPL	FAV	DEVD	SILIDEART	PLII	ISGT	-AQKST	KLYVQ	ANAFV	RTL	245			
SECA1_GEO_kaustophilus	160	----	SREEKQ	AAYNAD	ITYGT	NNEFG	FDYLR	DNMVL	YKEHI	VQRPL	YAI	IDEVD	SILIDEART	PLII	ISGT	-AQKST	KLYVQ	ANAFV	RTL	245			
SECA1_LAC_johnsonii	160	----	SADEKR	DAYNCD	VTYST	NSELG	FDYLR	DNMVL	YKQDM	VQRPL	N	YAI	IDEVD	SILIDEART	PLII	ISGQ	-AEQAN	SEYIR	ADR	FVKTL	245		
SECA1_STR_parasanguinis	160	----	SPA EKKEA	YALCD	ITYST	NSEIG	FDYLR	DNMVL	YRAEN	MVQRPL	N	YAL	IDEVD	SILIDEART	PLII	IVSG	QGTAS	DTSLQ	LYHMAD	YVKTLL	246		
SECA1_STR_gordonii	160	----	SPA EKREAY	ACD	ITYST	NSEIG	FDYLR	DNMVL	YRAEN	MVQRPL	N	YAL	IDEVD	SILIDEART	PLII	IVSG	GPVSE	TNQLY	HMAAD	YVKS LN	246		
SECA1_STR_pneumoniae	160	----	SPMEKKEA	YEC	ITYST	NSEIG	FDYLR	DNMVL	YRAEN	MVQRPL	N	YAL	IDEVD	SILIDEART	PLII	IVSG	CANAV	ETSQ	LYHMAD	HYVKS LN	246		
SECA1_STR_agalactiae	160	----	SPFEKREAY	NC	ITYST	NAE	VGF	FDYLR	DNMVL	YQED	MVQRPL	N	YAL	IDEVD	SILIDEART	PLII	IVSG	GPVSE	MMQLY	TRADM	FVKTLN	246	
SECA1_LIS_monocytogenes	160	----	SSTEKREAY	ACD	ITYST	NNELG	FDYLR	DNMVL	YKEEM	VQRPL	A	FAV	IDEVD	SILVDEART	PLII	ISGE	-AEKST	ILYVR	ANT	FVRTLT	245		
SECA1_LIS_innocua	160	----	SSTEKREAY	ACD	ITYST	NNELG	FDYLR	DNMVL	YKEEM	VQRPL	A	FAV	IDEVD	SILVDEART	PLII	ISGE	-AEKST	ILYVR	ANT	FVRTLT	245		
SECA1_LIS_welshimeri	160	----	SSTEKREAY	ACD	ITYST	NNELG	FDYLR	DNMVL	YKEEM	VQRPL	S	FAV	IDEVD	SILVDEART	PLII	ISGE	-AEKST	ILYVR	ANT	FVRTLT	245		
SECA_BAC_subtilis	160	----	SKDEKREAY	ACD	ITYST	NNELG	FDYLR	DNMVL	YKEQ	MVQRPL	H	FAV	IDEVD	SILIDEART	PLII	ISGQ	-AAKST	KLYVQ	ANAFV	RTL	245		
SECA1_BAC_anthraxis	160	----	SREEKQ	EAYAAD	ITYST	NNELG	FDYLR	DNMVL	YKEQ	CVQRPL	H	FAI	IDEVD	SILVDEART	PLII	ISGQ	-AQKST	ELYMF	ANAFV	RTL	245		
SECA1_BAC_thuringiensis	160	----	SREEKQ	EAYAAD	ITYST	NNELG	FDYLR	DNMVL	YKEQ	CVQRPL	H	FAI	IDEVD	SILVDEART	PLII	ISGQ	-AQKST	ELYMF	ANAFV	RTL	245		
SECA1_BAC_cereus	160	----	SREEKQ	EAYAAD	ITYST	NNELG	FDYLR	DNMVL	YKEQ	CVQRPL	H	FAI	IDEVD	SILVDEART	PLII	ISGQ	-AQKST	ELYMF	ANAFV	RTL	245		
SECA1_STA_epidermidis	166	----	STEEKREAY	AQD	ITYST	NNELG	FDYLR	DNMVL	YAEER	VMRPL	H	FAI	IDEVD	SILIDEART	PLII	ISGE	-AEKST	SLY	TQANV	FAKMLK	251		
SECA1_STA_haemolyticus	166	----	STNEKREAY	AQD	ITYST	NNELG	FDYLR	DNMVL	YAEER	VMRPL	H	FAI	IDEVD	SILIDEART	PLII	ISGE	-AEKST	SLY	TQANV	FAKMLK	251		
SECA1_STA_aureus	166	----	TTEEKREAY	AQD	ITYST	NNELG	FDYLR	DNMVL	YNSED	RVMRPL	H	FAI	IDEVD	SILIDEART	PLII	ISGE	-AEKST	SLY	TQANV	FAKMLK	251		
SECA1_ALK_metalloedigens	161	----	TIEQRR	AAYNAD	VTYGT	NNEFG	FDYLR	DNMVL	YQKDM	VQREON	Y	AI	IDEVD	SILIDEART	PLII	ISGQ	-GEKST	KLYHI	VDQ	FVKTLK	246		
SECA1_PBP_difficile	160	----	NPKVRKEQ	YDCD	ITYGT	NNEYG	FDYLR	DNMVL	YHKE	QRVQ	GLN	Y	AI	IDEVD	SILIDEART	PLII	ISGP	-GDKST	HLYS	DANT	FVLTLL	245	
SECA2_PBP_difficile	160	----	DPNIRK	QYQKCD	ITYGT	NSEFG	FDYLR	DNMVL	YDL	SHKVQ	RELN	Y	AI	IDEVD	SILIDEART	PLII	ISGP	-GDEDL	KLYEL	ANS	FVKTVK	245	
SECA2_model_opened_conf	148	----	DPNIRK	QYQKCD	ITYGT	NSEFG	FDYLR	DNMVL	YDL	SHKVQ	RELN	Y	AI	IDEVD	SILIDEART	PLII	ISGP	-GDEDL	KLYEL	ANS	FVKTVK	245	
SECA_E_coli	162	----	PAPAKREAY	AAD	ITYGT	NNEYG	FDYLR	DNMVL	YSP	ERVQ	RKL	Y	AI	IDEVD	SILIDEART	PLII	ISGP	-AEDSS	SNMY	KRVNK	I	PHLI	247
SECA1_MYC_vanbaalenii	159	----	TPDQRR	AAYNAD	ITYGT	NNELG	FDYLR	DNMVL	Y														

[illegible]

Conservation: 9889 5 5 6568 8555 57 6998887 77 9 5 8 7766 9 9 8 67 8 5 6 569 9657 6 77 6 8 6

SECA1_GEO_thermodenitrifi 338 EAKEGLEIQNESMTLATITPQNYFRMYEKLAMGTGTAKEEEEFNRNIYNMRVVVITPNRPVIREDRPDLIYRTMEGKFRAVVEDIAQRHAKGQPVLVGTVAIETSELLSEMLKKRGIPHN 457

SECA1_GEO_kaustophilus 338 EAKEGLEIQNESMTLATITPQNYFRMYEKLAMGTGTAKEEEEFNRNIYNMRVVVITPNRPVIREDRPDLIYRTMEGKFRAVVEDIAARHAKGQPVLVGTVAIETSEMLSEMLKKRGIPHN 457

SECA1_LAC_johnsonii 350 EAKEGVKIQEESKTQATITTYQNFRMYKLAGMTGTAKEEEEFREIYNMEVITITPNRPIARKDLPLDIYPTLDSKFQAVVKEIKERHAKGQPVLVGTVAIETSESSRLSQMLNQAGIPHA 469

SECA1_STR_parasanguinis 339 EAKEGVPVQDEETKTASITYQNLFMRMYKLSGMTGTGTAKEEEEFREIYNIRVPIPTNRPVQIRIDHEDLLYPSLESKFKAUVEDVKERHLKGQPVLVGTVAIVETSDYLSKKLVAAGIPHE 458

SECA1_STR_gordonii 339 EAKEGVPVQDEETKTASITYQNLFMRMYKLSGMTGTGTAKEEEEFREIYNIRVPIPTNRPVQIRIDHEDLLYPSLESKFKAUVEDVKERHLKGQPVLVGTVAIVETSDYLSKKLVAAGIPHE 458

SECA1_STR_pneumoniae 339 EAKEGVPIQDEETKTASITYQNLFMRMYKLSGMTGTGTAKEEEEFREIYNIRVPIPTNRPVQIRIDHEDLLYPSLESKFKAUVEDVKERHLKGQPVLVGTVAIVETSDYLSKKLVAAGVPHE 458

SECA1_STR_agalactiae 339 EAKESVPIQEESKTASITYQNLFMRMYKLAGMTGTGTAKEEEEFREIYNMRVIEIPTNKVIRIDRDPDLIYTTIEAKFNAVVEDIAERHAKGQPVLVGTVAIETSELISSKLKRKGIKHD 457

SECA1_LIS_monocytogenes 338 EAKEGVTIQNESKTMATITPQNYFRMYKLAGMTGTAKEEEEFNRNIYNMRVIEIPTNKVIRIDRDPDLIYTTIEAKFNAVVEDIAERHAKGQPVLVGTVAIETSELISSKLKRKGIKHD 457

SECA1_LIS_innocua 338 EAKEGVTIQNESKTMATITPQNYFRMYKLAGMTGTAKEEEEFNRNIYNMRVIEIPTNKVIRIDRDPDLIYTTIEAKFNAVVEDIAERHAKGQPVLVGTVAIETSELISSKLKRKGIKHD 457

SECA1_LIS_welshimeri 338 EAKEGVTIQNESKTMATITPQNYFRMYKLAGMTGTAKEEEEFNRNIYNMRVIEIPTNKVIRIDRDPDLIYTTIEAKFNAVVEDIAERHAKGQPVLVGTVAIETSELISSKLKRKGIKHD 457

SECA_BAC_subtilis 338 EAKEGLEIQNESMTLATITPQNYFRMYEKLAMGTGTAKEEEEFNRNIYNMQVVTIPTNRPVVRDRPDLIYRTMEGKFKAUAEDVAQRVMTGQPVLVGTVAIVETSELISKLLKNKGIPHQ 457

SECA1_BAC_anthraxis 338 EAKEGVEIQNESMTLATITPQNYFRMYEKLAMGTGTAKEEEEFNRNIYNMNVIPTNKP1IRDDRADLIYFKSMKGKFAVVEDIYNRHKQGPVLVGTVAIETSELISKMLTRKGVVRHN 457

SECA1_BAC_thuringiensis 338 EAKEGVEIQNESMTLATITPQNYFRMYEKLAMGTGTAKEEEEFNRNIYNMNVIPTNKP1IRDDRADLIYFKSMKGKFAVVEDIYNRHKQGPVLVGTVAIETSELISKMLTRKGVVRHN 457

SECA1_BAC_cereus 338 EAKEGVEIQNESMTLATITPQNYFRMYEKLAMGTGTAKEEEEFNRNIYNMNVIPTNKP1IRDDRADLIYFKSMKGKFAVVEDIYNRHKQGPVLVGTVAIETSELISKMLTRKGVVRHN 457

SECA1_STA_epidermidis 344 EAKEGVAIQNESKTASITPQNYFRMYKLAGMTGTAKEEEEFNRNIYNMTVQIPTNKPVRQKDSLDLIYISQKGKFAVVEDVVEKHKQGPVLLGTVAIVETSEYISNLLKKRGVRHD 463

SECA1_STA_haemolyticus 344 EAKEGVKIQNESKTASITPQNYFRMYKLAGMTGTAKEEEEFNRNIYNMTVQIPTNKPVRQKDSLDLIYISQKGKFAVVEDVVEKHKQGPVLLGTVAIVETSEYISNLLKKRGVRHD 463

SECA1_STA_aureus 344 EAKEGVQIQNESKTASITPQNYFRMYKLAGMTGTAKEEEEFNRNIYNMTVQIPTNKPVRQKDSLDLIYISQKGKFAVVEDVVEKHKQGPVLLGTVAIVETSEYISNLLKKRGVRHD 463

SECA1_ALK_metalloedigens 339 EAKEGLQIQRESKTALATITPQNYFRMYKLAGMTGTAKEEEEFNRNIYNMDVIEIPTNRPVIRDDQDLYYKGEQKGFALAKDIEGRYKQGPVLVGTISIEKSEELATLLKRGKIPCE 458

SECA1_PEP_difficile 337 EAKEGLKIQRESKTALATITPQNYFRMYKLAGMTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 456

SECA2_PEP_difficile 337 EAKEGVEIKNESKTMAITVTVQNFRRLYEKLAMGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 456

SECA2_model_opened_conf 325 EAKEGVEIKNESKTMAITVTVQNFRRLYEKLAMGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 444

SECA_E_coli 358 EAKEGVQIQNESKTALATITPQNYFRMYKLAGMTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 477

SECA1_MYC_vanbaalenii 337 EAKEHVEIKAESNTVAQVTLQNYFRMYEKLAMGTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 456

SECA1_MYC_ulcerans 336 EAKEHVEIKAESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 455

SECA1_MYC_paratuberculosis 336 EAKEHVEIKAESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 455

SECA1_MYC_tuberculosis 339 EAKEHVEIKAESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 458

SECA1_MYC_bovis 339 EAKEHVEIKAESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 458

SECA1_MYC_leprae 339 EAKEHVEIKAESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 458

SECA1_MYC_smegmatis 336 EAKERVEIKAESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 455

SECA1_COR_diphtheriae 338 EAKENVEIKNESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 457

SECA1_COR_efficiens 338 EAKERVEIKNESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 457

SECA1_COR_glutamicum 338 EAKERVEIKNESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 457

SECA1_COR_jeikeium 339 EAKEHVEIKNESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 458

SECA1_THE_fusca 339 EAKEHVEIKNESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 458

SECA2_MYC_vanbaalenii 337 EAKEGVEIKNESNTLATITLQNYFRMYKLAGMTGTAETEAALHEIYKLGVPVPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 456

SECA_THE_maritima 383 EAKEGVPIKEESNTIYATITPQNYFRMYEKLAMGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 502

SECA2_GEO_kaustophilus 338 EAKEGVEITEENDIYATITPQNYFRMYEKLAMGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 457

SECA2_GEO_thermodenitrifi 339 EAKEGLEITEENTYASITITQNYFRMYPLSGMTGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 458

SECA2_BAC_anthraxis 339 EAKEGLEITEENTYASITITQNYFRMYPLSGMTGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 458

SECA2_BAC_thuringiensis 339 EAKEGLEITEENTYASITITQNYFRMYPLSGMTGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 458

SECA2_BAC_cereus 339 EAKEGLEITEENTYASITITQNYFRMYPLSGMTGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 458

SECA2_LIS_welshimeri 332 EAKEEVEVKEESRTLATITITQNYFRMYKISGMTGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 451

SECA2_LIS_monocytogenes 332 EAKEEVEVKEESRTLATITITQNYFRMYKISGMTGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 451

SECA2_LIS_innocua 332 EAKEEVEVKEESRTLATITITQNYFRMYKISGMTGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 451

SECA2_ALK_metalloedigens 343 EAKEGLVSETKGRIMGSIALQYFLKLYPKLAGMTGTAISVMNDELDRMYQLKVLIPTNKP1IRKDDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 462

SECA2_LAC_johnsonii 337 EAKEKVELTKIQKTAASITPPALFALFNKVSMSGTAKVNEEEFLQTYNLKVVTIPTNRPVVRQDQSDLIYKTEEAQYIAVDDVAERYEKGQPVVIGTTSVERSEFLSRQFEKRRIPHN 456

SECA2_STA_haemolyticus 342 EAKEGVELSQDLVSMATITPQNLFLKLFNGFSGMTGTGKLGKEEFFDLYSKLVVEIPTNHP1IRKDDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 461

SECA2_STA_aureus 342 EAKEGMEVSTDKSVMATITPQNLFLKLFNGFSGMTGTGKLGKEEFFDLYSKLVVEIPTNHP1IRKDDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 461

SECA2_STA_epidermidis 342 EALENVEIQSDMSVSMATITPQNLFLKLFNGFSGMTGTGKLGKEEFFDLYSKLVVEIPTNHP1IRKDDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 461

SECA2_STR_Agal 342 EQKEHLNVTPESRAMASITYQNLFMRMYKLAGMTGTGTAKEEEEFNRNIYNMDVQVPTNKLMIREDPDCVYKSEIKGFNAVQEIIRHKNVQPIVLVGTISIEKSELLSQLLKKKGIPHE 461

SECA2_STR_Gordon 339 EAKEHVKLTQETRAMASITYQNLFMRMYKLAGMTGTGKLVVEEFFDLYSKLVVEIPTNHP1IRKDDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 458

SECA2_STR_Pneum 338 EAKEHVKLTQETRAMASITYQNLFMRMYKLAGMTGTGKLVVEEFFDLYSKLVVEIPTNHP1IRKDDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 457

SECA2_STR_Sanguin 339 EAKEHVKLTQETRAMASITYQNLFMRMYKLAGMTGTGKLVVEEFFDLYSKLVVEIPTNHP1IRKDDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 458

SECA2_COR_efficiens 336 EAKEGLAVTEGGRIIDLITLQALINRYATVCGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 455

SECA2_MYC_ulcerans 379 EAKEGIETTETGEVLDTITVQALINRYATVCGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 498

SECA2_MYC_paratuberculosis 347 EAKEGIETTETGEVLDTITVQALINRYATVCGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 466

SECA2_MYC_tuberculosis 381 EAKEGIETTETGEVLDTITVQALINRYATVCGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 500

SECA2_MYC_bovis 381 EAKEGIETTETGEVLDTITVQALINRYATVCGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 500

SECA2_MYC_leprae 347 EAKEGIETTETGEVLDTITVQALINRYATVCGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 466

SECA2_MYC_smegmatis 347 EAKEGIETTETGEVLDTITVQALINRYATVCGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 466

SECA2_THE_fusca 336 EAKEHVTPESTGEVLDSITVQSLIVRGVPIRCGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 455

SECA2_COR_diphtheriae 336 EAKEGLVVTBEGGRIDLTLQSLMGRYPIVCGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 455

SECA2_COR_glutamicum 336 EAKEGLAVSEGGKILDTITLQALIGRYPMACGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 455

SECA2_COR_jeikeium 342 EAKEGLDVTDGGRIDLDTITLQALIGRYPMACGMTGTALAAEQQLRQFYKLGVSPIPPNKPNIREDPDLIYFTCKEIKKTLILEIKNINATGQPIVLIGTSSVEESERIATTLNTEGICKN 461

Consensus_aa: EAKE.1p1pppsphhhtoIThQshhpb.p1tGMTGTtbb..pEh.phYph.Vh.IPNpP..R.D..D.l@o..K..Allccl.p.@.pGpPILlSt.sl.pSEb1tp.L.p.sl.hp

Consensus_ss: hhhh eeee hhhhhhhhhhhh hhhhhhhhhh eeee eeeee eeeee hhhhhhhhhhhhhhhh eeee hhhhhhhhhhhh ee

Conservation:	69895	99	75	79	5	67679	89999898	97		7	999	768	575	5		
SECA1_GEO_thermodenitrifi	458	VLNAKNHAKAEI	IAAQAGQKGAVT	IATNMAGRGT	DI	KLGE	-----	GVKELGGLAVIGTERHESR	516							
SECA1_GEO_kaustophilus	458	VLNAKNHAKAEI	IAAQAGQKGAVT	IATNMAGRGT	DI	KLGE	-----	GVKELGGLAVIGTERHESR	516							
SECA1_LAC_johnsonii	470	VLNAKNHAKAEI	IMNAGQRGAVT	IATNMAGRGT	DI	KLGP	-----	GVKELGGLAVIGTERHESR	528							
SECA1_STR_parasanguinis	459	VLNAKNHYKEAQI	IMNAGQRGAVT	IATNMAGRGT	DI	KLGE	-----	GVRELGGLCVIGTERHESR	517							
SECA1_STR_gordonii	459	VLNAKNHYREAQI	IMNAGQRGAVT	IATNMAGRGT	DI	KLGE	-----	GVRELGGLCVIGTERHESR	517							
SECA1_STR_pneumoniae	459	VLNAKNHYREAQI	IMNAGQRGAVT	IATNMAGRGT	DI	KLGE	-----	GVRELGGLCVIGTERHESR	517							
SECA1_STR_agallactiae	459	VLNAKNHFKEAQI	IMNAGQRGAVT	IATNMAGRGT	DI	KLGE	-----	GVRELGGLCVIGTERHESR	517							
SECA1_LIS_monocytogenes	458	VLNAKQHEREADI	IKHAGERGAVT	IATNMAGRGT	DI	KLGE	-----	GTIEAGGLAVIGTERHESR	516							
SECA1_LIS_innocua	458	VLNAKQHEREADI	IKNAGERGAVT	IATNMAGRGT	DI	KLGE	-----	GTIDAGGLAVIGTERHESR	516							
SECA1_LIS_welshimeri	458	VLNAKQHEREADI	IKHAGERGAVT	IATNMAGRGT	DI	KLGE	-----	GTIEAGGLAVIGTERHESR	516							
SECA_BAC_subtilis	458	VLNAKNHEREAQI	IEEAGQKGAVT	IATNMAGRGT	DI	KLGE	-----	GVKELGGLAVVGTGRHESR	516							
SECA1_BAC_anthraxis	458	ILNAKNHAREADI	IAEAGMKGAVT	IATNMAGRGT	DI	KLGD	-----	DIKNI-GLAVIGTERHESR	515							
SECA1_BAC_thuringiensis	458	ILNAKNHAREADI	IAEAGMKGAVT	IATNMAGRGT	DI	KLGD	-----	DIKNI-GLAVIGTERHESR	515							
SECA1_BAC_cereus	458	ILNAKNHAREADI	IAEAGMKGAVT	IATNMAGRGT	DI	KLGD	-----	DIKNI-GLAVIGTERHESR	515							
SECA1_STA_epidermidis	464	VLNAKNHEREAEI	VSNAQQKGAVT	IATNMAGRGT	DI	KLGD	-----	GVEELGGLAVIGTERHESR	522							
SECA1_STA_haemolyticus	464	VLNAKNHEREAEI	IVANAGQKGAVT	IATNMAGRGT	DI	KLGE	-----	GVEEIGGLAVIGTERHESR	522							
SECA1_STA_aureus	464	VLNAKNHEREAEI	IVAGAGQKGAVT	IATNMAGRGT	DI	KLGE	-----	GVEELGGLAVIGTERHESR	522							
SECA1_ALK_metalliredigens	459	VLNAKHHEREAEI	VAQAGRKGI	IT	IATNMAGRGT	DI	ILGGN- - -	PEFLAKREMKKRGYADELIANATSHHETDDEELQAARKVYNDLLEKFKKETEQEHKDVIEAGGLHI	IGTERHESR	574						
SECA1_PEP_difficile	457	VLNAKHQDKEAEI	IAQAGRLGAVT	IATNMAGRGT	DI	VLGGNPD	LT	TREMRNRNGFKEEIVNRVDTPIEGIPVKGNEILFEAREEYKELFEKFKQQTQEEQKQVVAAGGLAI	IGTERHESR	576						
SECA2_PEP_difficile	457	VLNAKHQDKEAEI	ISKAGKLD	AIT	IATNMAGRGT	DI	SLGA	-GDKEEEQ	-	EVKDLGGLYVIGTERHESR	522					
SECA2_model_opened_conf	445	VLNAKHQDKEAEI	ISKAGKLD	AIT	IATNMAGRGT	DI	SLGA	-GDKEEEQ	-	EVKDLGGLYVIGTERHESR	510					
SECA_E_coli	478	VLNAKPHANEAAI	IVAQAGYPAAVT	IATNMAGRGT	DI	VLGG	-----	SWQAEVAALENP	TAEQIEKI	KADWQVRHDA	-----	VLEAGGLHI	IGTERHESR	565		
SECA1_MYC_vanbaalenii	457	VLNAKYHEQEAQI	IVAEAGRLG	AIT	VATNMAGRGT	DI	VLGG	-----	NVDVLLDRRLR	QGLDPIET	PEEYEQGWHEELPHIKA	EA	VAAEAKDVI	AAGGLVVLGTERHESR	559	
SECA1_MYC_ulcerans	456	VLNAKYHEQEAQI	IAEAGRRG	AIT	VATNMAGRGT	DI	VLGG	-----	NVDFLT	DKRLR	NDGLDPVET	PDEYEQA	WHQELPKVKEE	AGDEATEVI	KAGGLVVLGTERHESR	558
SECA1_MYC_paratuberculosis	456	VLNAKYHEQEAQI	IVAGRRGGVT	VATNMAGRGT	DI	VLGG	-----	NVDFLT	DQRLR	ERGLDPVET	PDEYEAAWHEELPKVKA	AAAAEAK	EVIEAGGLVVLGTERHESR	558		
SECA1_MYC_tuberculosis	459	VLNAKYHEQEAQI	IVAGRRGGVT	VATNMAGRGT	DI	VLGG	-----	NVDFLT	DQRLR	ERGLDPVET	PEEYEA	AHWSELPIVKEE	ASKEAKEVI	EAGGLVVLGTERHESR	561	
SECA1_MYC_bovis	459	VLNAKYHEQEAQI	IVAGRRGGVT	VATNMAGRGT	DI	VLGG	-----	NVDFLT	DQRLR	ERGLDPVET	PEEYEA	AHWSELPIVKEE	ASKEAKEVI	EAGGLVVLGTERHESR	561	
SECA1_MYC_leprae	459	VLNAKYHEQEAQI	IVAGRRGGVT	VATNMAGRGT	DI	VLGG	-----	NVDFLT	DQRLR	RRRGLDPVET	PDEYEQA	WHSELPKVKEE	AGQEA	AAEVI	EAGGLVVLGTERHESR	561
SECA1_MYC_smegmatis	456	VLNAKYHEQEAQI	IVAEAGRRG	AVT	VATNMAGRGT	DI	VLGG	-----	NVDFLAD	KLRLR	ERGLDPVET	PEEYEA	AAWHEVL	LPQVKA	ECAKEAQVIEAGGLVVLGTERHESR	558
SECA1_COR_diphtheriae	458	VLNAKFHBEQEAQI	IAKAGLPGAVT	VATNMAGRGT	DI	VLGG	-----	NPDIIAD	INL	RERGLN	DPVET	PEEYEA	AWDAELARVKEKGAELAEK	AKVREAGGLVVLGTERHESR	560	
SECA1_COR_efficiens	458	VLNAKHHEQEAQI	IVAQAGLPGAVT	VATNMAGRGT	DI	VLGG	-----	NPDILL	DI	KL	RERGLDPF	FEDEEAYQV	AWHEELPKMKQRC	EERAEK	VREAGGLVVLGTERHESR	560
SECA1_COR_glutamicum	458	VLNAKHHEQEAQI	IVAQAGLPGAVT	VATNMAGRGT	DI	VLGG	-----	NPEILL	DI	KL	RERGLDPF	FEDEESYQ	EAWDDEL	PAMKQRC	EEGRDKVREAGGLVVL	

Conservation: 958 9869978989959 7 85585 955 5 5 8 8 7 5 98 5 9 56

SECA1_GEO_thermodenitrifi 517 RIDNQLRGRSGRQGDGPGVSQFYLSLEDELMRRFGSESLMAMMDRLGM-----DDSQPIQSKMVTRAVESAQKRVEGNFDFARKQLLYQDDVLRQREVIYRQRFVEVLADN--LRGIIIEK 629

SECA1_GEO_kaustophilus 517 RIDNQLRGRSGRQGDGPGVSQFYLSLEDELMRRFGSESLMAMMDRLGM-----DDSQPIQSKMVTRAVESAQKRVEGNFDFARKQLLYQDDVLRQREVIYRQRFVEVLADN--LRGIIIEK 629

SECA1_LAC_johnsonii 529 RIDNQLRGRSGRQGDGPGVTRFYLSLEDDLMLKRFGGDRVKFLDRLISDN---DDDKVIESRMIKQVESAQKRVEGNNDTRKQTLQYDDVMTRQREIYICERMQVISEDK-SLKPVLM 643

SECA1_STR_parasanguinis 518 RIDNQLRGRSGRQGDGPGVSQFYLSLEDELMRRFGSERIKAVLDRFLKLS---EEBSVIRSMFTTRQVEAQKRVEGNNDTRKQVLYQDDVMRQREIYIAERYDVITANR-DLAPETHA 632

SECA1_STR_gordonii 518 RIDNQLRGRSGRQGDGPGVSQFYLSLEDELMRRFGSERIKAVLDRFLKLS---EEBSVIRSMFTTRQVEAQKRVEGNNDTRKQVLYQDDVMRQREIYIAERYDVITANR-DLAPETHA 632

SECA1_STR_pneumoniae 518 RIDNQLRGRSGRQGDGPGVSQFYLSLEDDLMLKRFGGSERLKGIFERLMS----EEATIESRMLTRQVEAQKRVEGNNDTRKQVLYQDDVMRQREIYIAERYDVITADR-DLAPETHA 630

SECA1_STR_agalactiae 518 RIDNQLRGRSGRQGDGPGVSQFYLSLEDDLMLKRFGGTDRIKVLERLMLA---EDDVTIKSMLTRQVEAQKRVEGNNDTRKQVLYQDDVMRQREIYIANRREVITAEER-DLGPBELLK 632

SECA1_LIS_monocytogenes 517 RIDNQLRGRSGRQGDGPGVTQFYLSMEDELMRRFGSDNMKSMERFGM-----AED-AIQSKMVSRAVESAQKRVEGNNDSRKQVLYQDDVLRQREVIYKQRYEVINAEN-SLREIIEQ 629

SECA1_LIS_innocua 517 RIDNQLRGRSGRQGDGPGVTQFYLSMEDELMRRFGSDNMKSMERFGM-----AED-AIQSKMVSRAVESAQKRVEGNNDSRKQVLYQDDVLRQREVIYKQRYEVINAEN-SLREIIEQ 629

SECA1_LIS_welshimeri 517 RIDNQLRGRSGRQGDGPGVTQFYLSMEDELMRRFGSDNMKSMERFGM-----AED-AIQSKMVSRAVESAQKRVEGNNDSRKQVLYQDDVLRQREVIYKQRYEVINAEN-SLREIIEQ 629

SECA_BAC_subtilis 517 RIDNQLRGRSGRQGDGPGITQFYLSMEDELMRRFGAERTMAMLDRLGM-----DDSTPIESKMVSRAVESAQKRVEGNNDSRKQVLYQDDVLRQREVIYKQRYEVIDSEN-LREIVEN 629

SECA1_BAC_anthraxis 516 RIDNQLRGRAGRQGDGPGVTQFYLSMEDELMRRFGSDNMKAMMDRLGM-----DDSQPIESKMVSRAVESAQKRVEGNNDARKQLLYQDDVLRQREVIYKQRYEVMESSEN-LRGIIIEG 628

SECA1_BAC_thuringiensis 516 RIDNQLRGRAGRQGDGPGVTQFYLSMEDELMRRFGSDNMKAMMDRLGM-----DDSQPIESKMVSRAVESAQKRVEGNNDARKQLLYQDDVLRQREVIYKQRYEVMESSEN-LRGIIIEG 628

SECA1_BAC_cereus 516 RIDNQLRGRAGRQGDGPGVTQFYLSMEDELMRRFGSDNMKAMMDRLGM-----DDSQPIESKMVSRAVESAQKRVEGNNDARKQLLYQDDVLRQREVIYKQRYEVMESSEN-LRGIIIEG 628

SECA1_STA_epidermidis 523 RIDNQLRGRSGRQGDGRDSRFYLSLQDELMLVRFGSERLQKMMNRLGM-----DDSTPIESKMVSRAVESAQKRVEGNNDARKRILEYDEVLRKQREIYINERNEIIDSEE--SSQVVNA 635

SECA1_STA_haemolyticus 523 RIDNQLRGRSGRQGDGRDSRFYLSLQDELMLVRFGSERLQKMMNRLGM-----DDSTPIESKMVSRAVESAQKRVEGNNDARKRILEYDEVLRKQREIYINERNEIIDSEE--SSQVVNA 635

SECA1_STA_aureus 523 RIDNQLRGRSGRQGDGRDSRFYLSLQDELMLVRFGSERLQKMMNRLGL-----DDSTPIESKMVSRAVESAQKRVEGNNDARKRILEYDEVLRKQREIYINERNEIIDSEE--SSQVVNA 635

SECA1_ALK_metalliregignis 575 RIDNQLRGRAGRQGDGPGSSKFYISLEDDLMLRFGGDKMLSIKVMGL-----EDDEAIEHGLMSRSIENAKKQVEGNFIRKHVLYQDDVMNKQREVIYGERKKVLGAGES--LKDHLVN 687

SECA1_PEP_difficile 577 RIDNQLRGRSGRQGDGPGSSRFYISLEDDLMLRFGGDRISGIVDKILG-----EEDMPIEHLISKSIEGAKQKVEGNFIRKHVLYQDDVMNKQREIYIAERYKRVLEGED-LQEQIQS 689

SECA2_PEP_difficile 523 RIDNQLRGRSGRQGDGPTSRFFVSLDEDDVIKLYGGKTIKLMKRTSS-----NENTAIESKALTRAIERAQKQVEGNFIRKHVLYQDDTINEQRKVIYINERKNVLNDEE-IQEDIQK 635

SECA2_model_opened_conf 511 RIDNQLRGRSGRQGDGPTSRFFVSLDEDDVIKLYGGKTIKLMKRTSS-----NENTAIESKALTRAIERAQKQVEGNFIRKHVLYQDDTINEQRKVIYINERKNVLNDEE-IQEDIQK 623

SECA_E_coli 566 RIDNQLRGRSGRQGDGAGSRFYLSMEDALMRIFASDRVSGMMRLKLM-----KPEGAIEHPWVTAKIANAQKQVEGNFIRKHVLYQDDVDMNQRAIYQRENEILLVSD-VSETINS 678

SECA1_MYC_vanbaalenii 566 RIDNQLRGRSGRQGDGPGESRFYLSLQDELMLRRFGATLETLTLRLNL-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_MYC_ulcerans 559 RIDNQLRGRSGRQGDGPGESRFYLSLQDELMLRRFGAALLESLLTLRLNL-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_MYC_paratuberculosis 559 RIDNQLRGRSGRQGDGPGESRFYLSLQDELMLRRFGAALLESLLTLRLNL-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_MYC_tuberculosis 562 RIDNQLRGRSGRQGDGPGESRFYLSLQDELMLRRFGAALLESLLTLRLNL-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_MYC_bovis 562 RIDNQLRGRSGRQGDGPGESRFYLSLQDELMLRRFGAALLESLLTLRLNL-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_MYC_leprae 562 RIDNQLRGRSGRQGDGPGESRFYLSLQDELMLRRFGAALLESLLTLRLNL-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_MYC_smegmatis 559 RIDNQLRGRSGRQGDGPGESRFYLSLQDELMLRRFGAALLESLLTLRLNL-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_COR_diphtheriae 561 RIDNQLRGRAGRQGDGPGTRFYLSMRDDLMLVRFVGTMTENMMNRLNV-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_COR_efficiens 561 RIDNQLRGRAGRQGDGPGTRFYLSMRDDLMLVRFVGTMTENMMNRLNV-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_COR_glutamicum 561 RIDNQLRGRAGRQGDGPGTRFYLSMRDDLMLVRFVGTMTENMMNRLNV-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_COR_jeikeium 562 RIDNQLRGRAGRQGDGPGTRFYLSMRDDLMLVRFVGTMTENMMNRLNI-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA1_THE_fusca 562 RIDNQLRGRAGRQGDGPGSRFYLSLQDELMLRRFGAALLESLLTLRLNL-----PDDVPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA2_MYC_vanbaalenii 560 RIDNQLRGRSGRQGDGPGTRFYLSLQDELMLRRSATAFLEKMLSRKLM-----PEREPIEAKMVSRAIKSAQTQVEQNFIEVRKNVLYKDEVMNQQRKVIYAEERRRILEGEN-LQOQVND 671

SECA2_THE_maritima 562 RIDNQLRGRAGRQGDGPGSIFFLSLEDDLMLRFGGSEIKGVMNLIK-----EBEQPIQHPLMSKLIENIQKQVEGNFIRKHVLYQDDVDMNQRAIYQRENEILLVSD-VSETINS 678

SECA2_GEO_kaustophilus 517 RIDNQLRGRAGRQGDGPGSSQFIISLDDDLFLRYDDELKWKKSQVET-----DETGRIVSPDPIKFQVQVQTTIENAHYSARLHLLKLDITVDAQKVIYHMRDRVLAHQAEVLSSELLR 631

SECA2_GEO_thermodenitrifi 518 RIDNQLRGRAGRQGDGPGSSQFIISLDDDLMLRFRFAAETELKAKLTK-----DETGLILNDIHEFDVFNRTQLICEGSHFSMREYNKLDDVINDQRNVIYKLRNLLCEDT-NMIEIIP 631

SECA2_BAC_anthraxis 518 RIDNQLRGRAGRQGDGPGSSQFIISLDDDLMLRFRFAAETELKAKLTK-----DETGLILNDIHEFDVFNRTQLICEGSHFSMREYNKLDDVINDQRNVIYKLRNLLCEDT-NMIEIIP 631

SECA2_BAC_thuringiensis 518 RIDNQLRGRAGRQGDGPGSSQFIISLDDDLMLRFRFAAETELKAKLTK-----DETGLILNDIHEFDVFNRTQLICEGSHFSMREYNKLDDVINDQRNVIYKLRNLLCEDT-NMIEIIP 631

SECA2_BAC_cereus 518 RIDNQLRGRAGRQGDGPGSSQFIISLDDDLMLRFRFAAETELKAKLTK-----DETGLILNDIHEFDVFNRTQLICEGSHFSMREYNKLDDVINDQRNVIYKLRNLLCEDT-NMIEIIP 631

SECA2_LIS_welshimeri 511 RIDLQLMGRSGRRGDPGSGKPMISLEDDLLEQFESKWEKLSVLKLRK--APRDGKPVNSKRIHVSIVDAQKRLEGANDIRKDLLSYDEVIDLQRMVYKERDOLLERNK-LGVSEK 626

SECA2_LIS_monocytogenes 511 RIDLQLMGRSGRRGDPGSGKPMISLEDDLLEQFESKWEKLSVLKLRK--APRDGKPVNSKRIHVSIVDAQKRLEGANDIRKDLLSYDEVIDLQRMVYKERDOLLERNK-LGVSEK 626

SECA2_LIS_innocua 511 RIDLQLMGRSGRRGDPGSGKPMISLEDDLLEQFESKWEKLSVLKLRK--APRDGKPVNSKRIHVSIVDAQKRLEGANDIRKDLLSYDEVIDLQRMVYKERDOLLERNK-LGVSEK 626

SECA2_ALK_metalliregignis 529 RIDNQLRGRAGRQGDGPGSKFIFISLEDDLKYYEIKPMIYQY-YTQ-----KQESLDNTMINKINSQRIYEGVNSIDIRKQVLEYSVIDEQRRIHQKHREILVIRE-PLSLLSN 630

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SECA1_GEO_thermodenitrifi	630	MIRSVIERVVNTYTPKEDLP	EEWNKLG-VVDYLNAYLL	PEGDVT-EGDLR-----	GKEPEEMIELI	WAKVKARYDEKETQI	----	PPEQMREFERVV	VLRAVDMKMMNHID	AMEQLR	735																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_GEO_kaustophilus	630	MIHSVIERVNAHTPK	EEVNKLG-LVEYLN	NAHLLPEGDVT-EADLR-----	GKEPEEMIELI	WAKVKARYDEKEAQI	----	PPEQMREFERVV	VLRAVDMKMMNHID	AMEQLR	735																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_LAC_johnsonii	644	MIKRTIDHQIDMYTQ	GDKG--KDWNRDQ-IR	DFISSAITDEETTK-KLNMK-----	HLSAEELKKRLY	QIAEDNYAEKEKQI	----	ADPEQMLEFEK	QVILRVVDERWTD	HDIDAMDQLR	748																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_STR_parasanguinis	633	MIKRTIKRIVEGASH	SSK--EERVEA-ILN	FAKYNLVPEDTIS-ESDIE-----	GKSDKEVIDYLYA	RAEEIYASQVAKI	----	RDEESVQEFQK	VLILRVVDSKWT	DDHIDALDQLR	736																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_STR_gordonii	633	MIKRTIDRFVDGMS	RAPQ---BEKLDS-ILY	FAKYNLVPESIS-LSDLQ-----	GLSDEEIKANLY	ERALEVYNSQIAKI	----	RDEEAVREFQK	VLILRVVDNKWT	DDHIDALDQLR	736																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_STR_pneumoniae	631	MIKRTIERVVDGHAR	AKQ---DEKLEA-ILN	FAKYNLLPEDSIT-MEDLS-----	GLSDKAIKEELF	QSRSLKVYDSQVSKI	----	RDEEAVKEFQK	VLILRVVDNKWT	DDHIDALDQLR	734																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_STR_agalactiae	633	MIKRTIKRAVDASH	RSBK---NTAAEA-IVN	FARSALLDEEAIT-VSELR-----	GLKEAEIKELLY	ERALEVYEQQIAKI	----	KDPEAIEFQK	VLILMVVDNQWTE	HDIDALDQLR	736																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_LIS_monocytogenes	630	MIQRTVNFIVSSN	ASHEPEEAWNLOG-I	IDYVDANLLPEGTIT-LEDLQ-----	NRTSEDIQNL	ILDKIKAAAYDEKETLL	----	PPEEFNEFEK	QVLLRVVDTKW	VDHIDAMDHLR	735																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_LIS_innocua	630	MIQRTVNFIVSSN	ASHEPEEAWNLOG-I	IDYVDANLLPEGTIT-LEDLQ-----	NRTSEDIQNL	ILDKIKAAAYDEKETLL	----	PPEEFNEFEK	QVLLRVVDTKW	VDHIDAMDHLR	735																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_LIS_welshimeri	630	MIQRTVNFIVSSN	ASHEPEEAWNLOG-I	IDYVDANLLPEGTIT-LEDIQ-----	NRSSEDIQNL	ILDKIKVAYDEKETLL	----	PPEEFNEFEK	QVLLRVVDTKW	VDHIDAMDHLR	735																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA_BAC_subtilis	630	MIKSSLERAIAAYT	PREELPEEWKLDG-L	VDLINTTYLDEGALE-KSDIF-----	GKEPDEMELIMDRI	ITKYNEKEEQI	----	GKEQMREFEK	QVILRAVDSKWM	DHIDAMDQLR	735																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_BAC_anthraxis	629	MMKSTVERAVALHT	-QEEIEEDWNIG-L	VDYLNNTLLQEGDVK-EELR-----	RLAPEEMSEPI	IAKLIERYNDKEKLM	----	PEEQMREFEK	QVVFVRVVDTKW	TEHIDAMDHLR	733																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_BAC_thuringiensis	629	MMKSTVERAVALHT	-QEEIEEDWNIG-L	VDYLNNTLLQEGDVK-EELR-----	RLAPEEMSEPI	IAKLIERYNDKEKLM	----	PEEQMREFEK	QVVFVRVVDTKW	TEHIDAMDHLR	733																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_BAC_cereus	629	MMKSTVERAVALHT	-QEEIEEDWNIG-L	VDYLNNTLLQEGDVK-EELR-----	RLAPEEMSEPI	IAKLIERYNDKEKLM	----	PEEQMREFEK	QVVFVRVVDTKW	TEHIDAMDHLR	733																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_STA_epidermidis	636	MLRSTLQRAINHF	INEED--DNDPYTP-F	INYVNDVFLQEGDLQ-DTEIK-----	GKDSEDI	FEIVWSKIEKAYAQOQETI	----	GDQMSFEFER	MILLRSIDTHWTD	HIDTMDQLR	738																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_STA_haemolyticus	636	MLRSTLQRGVTYH	ISEED--DNDPYTP-F	INYVNDVFLQEGDLK-EEBIN-----	GKDSEDI	FEIVWSKIEKAYAQOQETI	----	GDQMAEFER	MILLRSIDTHWTD	HIDTMDQLR	738																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_STA_aureus	636	MLRSTLQRSINYY	INTAD--DEPEYQP-F	IDYINDIFLQEGDIT-EDDIK-----	GKDAEDI	FEVWAKIEAAYQSQKDIL	----	EEQMEFER	MILLRSIDSHWTD	HIDTMDQLR	738																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_ALK_metalliredigens	688	MARNIINEAVAIYT	ADAKYPEEWDLVG-L	GEYLAGIYMQRATLS-FDNIE-----	ELTVETLQEQI	YETSEKLYEAKKEEI	----	EAERMRELER	IIVLQVIDTKW	MDHIDAMDQLR	793																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_PEP_difficile	690	MTHSIEEAVTLTQ	TDKG---DDEEG-F	KHEMYNLFPGKSIE-IPEIE-----	KLNPNVEIT	TKVYEIAMKIYTSKEEQV	----	GYERMREVER	VILLQAVDNHWH	IDHIDAMDQLR	791																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_PEP_difficile	636	MVKDIIQEA	GETYLIGRK---RDY	YG-YFKHLYSTFMPADTLL-IPGVD-----	KKSQVEI	IDSTYEISKRVDLKKMML	----	GIDKVAELEK	TVLLKVVDQYV	IDHIDAMEQLR	737																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_model_opened_conf	624	MVKDIIQEA	GETYLIGRK---RDY	YG-YFKHLYSTFMPADTLL-IPGVD-----	KKSQVEI	IDSTYEISKRVDLKKMML	----	GIDKVAELEK	TVLLKVVDQYV	IDHIDAMEQLR	725																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA_E_coli	679	IREDVFKATIDAY	IPQSLEEMWDIPG-L	QERLKNDFDLDLPIAEWLDEP-----	ELHEETLRER	ILAQSIIEVYQRKEEVV	----	GAEMMRHFE	KGVMLQTLDSL	DKWHEHLAMDYL	786																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_MYC_vanbaalenii	673	ILVDVITAYVDGAT	ABEG-YSEDWDLK-L	WEGRLQYLPVGDHHL-DLDS	DAVGEFGELTREEL	QALLADAERAYAAEAIEE	IAEGEGAMRQ	LERNVLLNVLD	RKWRHLYEMDYL	R	788																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_MYC_ulcerans	672	MLTDVITAYVDGAT	VEG-YAEDWDLA-L	WTALKTLYPVGIKTD-TLMRR	QDSDRDDLTRDEL	QALLQDADQAYAAEAIEE	IAEGEGAMRQ	LERNVLLNVLD	RKWRHLYEMDYL	R	787																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_MYC_paratuberculosis	672	MVRDVITAYVNGAT	ABEG-YAEDWDLA-L	WTALKTLYPVGIDYA-TLTRR	DADGGFDDLTRDEL	LEALLKDAERAYATREAEIEE	IAEGEGAMRQ	LERNVLLNVLD	RKWRHLYEMDYL	R	787																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_MYC_tuberculosis	675	MVRDVITAYVDGAT	GEG-YAEDWDLA-L	WTALKTLYPVGITAD-SLTRK	DHEFERDDLTRDEL	LEALLKDAERAYAAEAIEE	IAEGEGAMRQ	LERNVLLNVLD	RKWRHLYEMDYL	R	790																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_MYC_bovis	675	MVRDVITAYVDGAT	GEG-YAEDWDLA-L	WTALKTLYPVGITAD-SLTRK	DHEFERDDLTRDEL	LEALLKDAERAYAAEAIEE	IAEGEGAMRQ	LERNVLLNVLD	RKWRHLYEMDYL	R	790																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_MYC_leprae	675	MVRDVITAYIDGAT	TPDS-YVEDWDLA-L	WNALEALYLPVGIKHE-SLTRH	ADESDCEDDLTRDEL	LEALLDAHAYAAEAIEE	IAELAGEGAMRQ	LERNVLLNVLD	RKWRHLYEMDYL	R	790																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_MYC_smegmatis	672	MLVDVITAYVDGAT	ABEG-YAEDWDLT-L	WTALKTLYPVGDHHR-DLDS	DAVGEFGELTREEL	DALIKDAERAYAEERQIEA	IAEGEGAMRQ	LERNVLLNVLD	RKWRHLYEMDYL	R	787																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_COR_diphtheriae	674	MIDDTIGAYVDAAT	ATG-YVEDWDLT-L	WNALESYLGPSFSAQ-ELIDG	DSYGESGELSASDL	RKAVLEDAHKQYAELEENV	TAIGGEAQM	RNIERMVILP	IDTKWRHLYEMDYL	R	789																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_COR_efficiens	674	MVDETISAYVAAAT	TANG-YVEDWDLK-L	WNALEALYGPFTTWQ-SLVDG	SEYGAPELSAEDL	RALTALDAHAYAKLEAAV	TALGGEAQM	RNIERMVILP	IDTKWRHLYEMDYL	R	789																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_COR_glutamicum	674	MIETVSAYVDGAT	ANG-YVEDWDLK-L	WNALEALYDPSINWT-DLVEG	SEYGPGLSABDL	RALTALVNDAAHAYAKLEAAV	SAIGGEAQ	RNIERMVILP	IDTKWRHLYEMDYL	R	789																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_COR_jeikeium	675	MLKDTIEAYVDGAT	ABEG-YVEDWDLT-L	WNALEALYGPFTTTE-ELVEG	DEYGRPGELSSQL	DALLEDANREYDELEEKV	SEVAGEEQ	MRGMERAA	LNVVDQKWRHLYEMDYL	R	790																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA1_THE_fusca	675	MIDDVLSYVRSAT	ABEG-DEPDWDLB-L	WTFQSQIFPVSFTAD-QLIE	BEGG-DISVLT	PTDISQVRDEDAHEVYDRREABE	----	GEETMREVER	QVILQVMDRKWRHLYEMDYL	R	785																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_MYC_vanbaalenii	673	MIGDVVITAYVNE	CTAGR-RTADWDLT-L	RAALSTLYPV-----VWQ	PDRPHMRGLTRSV	LREHVIADARRALVRKKAIEARS	GLRVMLRELER	ALLDCLDS	KWRHLYEMDYLA	R	782																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA_THE_maritima	675	IFEDVVSTRVEEFC	---SGKNWDIES-L	KNSLSFFPAGLFDL-----DEKQ	-----FSSSEEL	HDYLFNRLWEEYQRRKQEI	----	GEDYRKVIR	FLMLRIIDDDH	WRRYLEVEHVK	773																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_GEO_kaustophilus	632	HIHRHITQIDRYC	PNVPFEEWNIG-L	HNELRRAFPFPAYP-IDDLR	-----HKQKEI	AQLVWEYKSLAALADLP	----	CDEQTMRL	KHLMVETIDA	HWIRHLNQMLLK	736																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_GEO_thermodenitrifi	631	MIRSACDRIVDAY	ALSEQIPEEWDVRR-M	TEELNRI-VYRTP	I-TFDQP-----	PADLEDV	KRVKVAEAVES	VALLEKKK	----	AHTQLQTL	LKSVMLTVIDDY	WMRHL																																																																																																																																																																																																																																																																																																																																																																																																																															
SECA2_BAC_anthraxis	632	MIDHAVEAISKQYL	VEGMLPEEWFAS-L	TASLNEILSVENMPS-LSANN-----	VHSPEDLQSVL	KETLSLYKERVNELD	----	SNTDLQQS	RLRYVALHFLDQ	NNVNHLDAMTHLK	737																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_BAC_thuringiensis	632	MIDHAVEAISKQYL	VEGMLPEEWFAS-L	TASLNEILSVENMPS-LSANN-----	VHSPEDLQSVL	KETLSLYKERVNELD	----	SHTDLQQS	RLRYVALHFLDQ	NNVNHLDAMTHLK	737																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_BAC_cereus	632	MIDHAVEAISKQYL	VEGMLPEEWFAS-L	TASLNEILSVENMPS-LSANN-----	VHSPEDLQSVL	KETLSLYKERVNELD	----	SNTDLQQS	RLRYVALHFLDQ	NNVNHLDAMTHLK	737																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_LIS_welshimeri	627	ILREVAEYAFIHPV	---DIQEKLK-YYAR	QKELLGGTKFPV-SFDEVS-----	LMSPAEEVBEKI	---VTWHKKERDKF	----	PIETITAI	BEKVEYVLLNMDQ	MVWHLDMVQLR	725																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_LIS_monocytogenes	627	ILREVAEYSFTHPS	---DIPEELEI-YYSR	QKELLGGTKFPV-SFDQVT-----	LMSPREVVBEI	---VSWHKKERNKF	----	PAETITAI	BEREYVLLNMDQ	MVWHLDMVQLR	725																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_LIS_innocua	627	ILREVAEYSFHPL	---ELEEELEK-YYSR	QKELLGGTKFPV-SFDQVT-----	LMSPREVVBEI	---VAWHKKERNKF	----	PVETITAI	EKEVYVLLNMDQ	MVWHLDMVQLR	725																																																																																																																																																																																																																																																																																																																																																																																																																																
SECA2_ALK_metalliredigens	641	KCPVLYDRYLDLVG	-----	-----	-----	-----	-----	-----	KDVL	YKVEKITLPH	INKKVAEYLYEVS	YIR																																																																																																																																																																																																																																																																																																																																																																																																																															
SECA2_LAC_johnsonii	633	IIDNALNLYLEKQD	---LSNKS	DLKY-FINQ	HVTYQQVNV	PDN-----	LKTKKAI	KDFL	KELAYKILDEK	KHVI-----	INKKQAND	FQQQVI	ISSMDGN	IVDQ	VRI	EKIK	730																																																																																																																																																																																																																																																																																																																																																																																																																										
SECA2_STA_haemolyticus	638	SLARDVFYDLRTKH	---IHNKD	DIINYI	EQLSFS	FKDDA-----	ISQO-----	IQTREQ	ITVFL	VQQFN	KQLNK	MMKIA-----	NDNY	FKLRF	FQKAIL	KAID	VEWINQ	VDQLQ	LK	738																																																																																																																																																																																																																																																																																																																																																																																																																							
SECA2_STA_aureus	638	ALAKDVPEMFVNEEK	---VLTKSR	VEYIYQ	NLSFN	KNDV-----	ACVN-----	FKDKQ	AVTV	FLLE	QFQK	ALN	RKNM-----	QSAYY	INI	FQVK	FLKAID	SCLE	QVQD	LQ	LK	738																																																																																																																																																																																																																																																																																																																																																																																																																					
SECA2_STA_epidermidis	638	QLARDVFTKDVKNLD	---LSSER	ALVNIY	ENLSF	VFDEDV-----	SNIN-----	QMND	EEI	IQFLI	QQFT	QQFN	NLEVA-----	ADSYL	KLRF	QTS	ILKAID	SEWIE	QVDN	LQ	LK	738																																																																																																																																																																																																																																																																																																																																																																																																																					
SECA2_STR_Agal	638	IIDTVISSFIAYLGE	-VEKELEF-ENRF	IFDN	MSY	NLQ-----	GISK-----	EMSLEE	KNL	FKIAE	ILREK	HNLI-----	GDS	FGDF	QERT	AALKAID	EAVE	EDV	YLQ	LK	737																																																																																																																																																																																																																																																																																																																																																																																																																						
SECA2_STR_Gordon	636	VEIYVIKQVAYEQS	-FENRAD	FYR-FIL	HHFS	NRAERIP-----	QEPD-----	HTSPEK	VSHY	LQAI	ABQELL	KASKYL-----	KSDPK	LYSQ	FOR	LAI	KAID	NNWE	QVDY	LQ	LK	735																																																																																																																																																																																																																																																																																																																																																																																																																					
SECA2_STR_Pneum	634	IIERVTEEVAADH	---YASRE	LLFH-FI	TNIS	SFH	KEVP-----	DYID-----	VTDKT	AVRS	FMQ	QV	DKEL	SEK	ELL-----	NQHD	LYEQ	FLRL	SL	LKAID	NNWE	QVDY	LQ	LK	732																																																																																																																																																																																																																																																																																																																																																																																																																		
SECA2_STR_Sanguin	636	ILVSQVIHQAAEQS	---YETR	ADLYR-FIL	DHFS	YHAERIP-----	YDFD-----	IYSPEK	IAELL	QDIA	EQEL	QAKKAYI-----	KSDKL	FTFH	FOR	VSL	KAID	NNWE	QVDY	LQ	LK	735																																																																																																																																																																																																																																																																																																																																																																																																																					
SECA2_COR_efficiens	631	RAQDRAAAGLEG-V	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	

		2H loop															
		5	5	6	6	5	7	5									
Conservation:																	
SECA1_GEO_thermodenitrifi	736	QGIHLRAYGQVDP	LR	REYQ	MEGY	AMFEN	MIAAIEE	EEVATY	IMKAEI	H-----	HNLERQEVAK -GEA-	794					
SECA1_GEO_kaustophilus	736	QGIHLRAYGQVDP	LR	REYQ	MEGY	AMFEN	MIAAIEE	EEVATY	IMKAEI	H-----	HNLERQEVAK -GEA-	794					
SECA1_LAC_johnsonii	749	QSISLRGYQQLNPL	VEYQ	ESG	YRMFE	EMISN	IEFDAT	RLFMKAQ	IR-----	QNISR		799					
SECA1_STR_parasanguinis	737	NAVGLRGYAQNPNP	VEYQ	SES	FRMFND	MIGSIE	FDVTRL	MMKAQI	H-----	EQERPRT	TEH--SI-	793					
SECA1_STR_gordonii	737	NAVGLRGYAQNPNP	VEYQ	SES	FRMFND	MIGSIE	FDVTRL	MMKAQI	H-----	EQERPRT	TEH--NI-	793					
SECA1_STR_pneumoniae	735	NAVGLRGYAQNPNP	VEYQ	AEGR	FRMFND	MIGSIE	FDVTRL	MMKAQI	H-----	EQERPQ	AE--HI-	791					
SECA1_STR_agalactiae	737	NSVGLRGYAQNPNP	VEYQ	SES	FRMFND	MIGSIE	FDVTRL	MMKAQI	H-----	EQERERAS	Q--HA-	793					
SECA1_LIS_monocytogenes	736	DGIHLRAYGQIDP	LR	REYQ	SEG	FEMFAM	VSSIDED	VARYIMKAE	IR-----	QNLEREQ	VAK-GEA-	794					
SECA1_LIS_innocua	736	DGIHLRAYGQIDP	LR	REYQ	SEG	FEMFAM	VSSIDED	VARYIMKAE	IR-----	QNLEREQ	VAK-GEA-	794					
SECA1_LIS_welshimeri	736	DGIHLRAYGQIDP	LR	REYQ	SEG	FEMFAM	VSSIDED	VARYIMKAE	IR-----	QNLEREQ	VAK-GEA-	794					
SECA_BAC_subtilis	736	QGIHLRAYAQTNPL	LR	REYQ	MEGFAM	FHEM	IESIDE	VAKFVMKAE	IE-----	NNLEREE	VVQ-GOTTA-	796					
SECA1_BAC_anthraxis	734	EGIHRLRAYGQIDP	LR	REYQ	MEGFAM	FESMIASIEE	EISRYIMKAE	IE-----	QNLEREQ	VVQ-GEA-		792					
SECA1_BAC_thuringiensis	734	EGIHRLRAYGQIDP	LR	REYQ	MEGFAM	FESMIASIEE	EISRYIMKAE	IE-----	QNLEREQ	VVQ-GEA-		792					
SECA1_BAC_cereus	734	EGIHRLRAYGQIDP	LR	REYQ	MEGFAM	FESMIASIEE	EISRYIMKAE	IE-----	QNLEREQ	VVQ-GEA-		792					
SECA1_STA_epidermidis	739	QGIHLRSYAQQNPL	LR	DYQNE	GHELFD	IMMONE	EEDTCK	YILKSVVQ	F-----	EDDVERE	KSKS-FGEAKH-	802					
SECA1_STA_haemolyticus	739	QGIHLRSYAQQNPL	LR	DYQNE	GHELFD	IMMONE	EEDTCK	YILKSVVQ	F-----	DENIERE	KTTD-FGTAQH-	802					
SECA1_STA_aureus	739	QGIHLRSYAQQNPL	LR	DYQNE	GHELFD	IMMONE	EEDTCK	YILKSVVQ	F-----	EDNIERE	KTTE-FGEAKH-	802					
SECA1_ALK_metalliredigens	794	QGIHLRAIGQIDP	VR	AYQVE	GDFM	FNAMINSI	QEDTVK	YLFNV	EPQ-----	AKVERK	QVAK--P-	850					
SECA1_PBP_difficile	792	QGIHLRAVGQDDP	VR	AYKME	GDFM	FDMNKH	IKEDTV	RYLFN	ITIE-----	TPVERK	AVVD--VEN-	850					
SECA2_PBP_difficile	738	QYIGLKSAYAQKDDP	VR	EYALE	GDFM	FEALNKN	IREATV	QYLYKF	N-----			781					
SECA2_model_opened_conf	726	QYIGLKSAYAQKDDP	VR	EYALE	GDFM	FEALNKN	IREATV	QYLYKF	N-----			769					
SECA_E_coli	787	QGIHLRGYAQKDDP	VR	EYKRE	SFMA	AMLES	LKYEVIST	LSKVQVR	MP-----	EEVEELE	QQRMEALQ--MQQ-	856					
SECA1_MYC_vanbaalenii	789	EGIGLRGLAQRRPE	VR	EYARE	GDFM	FIAMLDG	MKEESV	GLFNVQ	VE-----	RAPSA	PTVAA-QAAPAGLA	FAFAAAAAEQAAQTGGVATKERPA-	876				
SECA1_MYC_ulcerans	788	EGIGLRAMAQRDPL	VR	EYQRE	GDFM	FAMMLD	GVKESV	GLFNV	SVE-----	AVPA-PQVE	AVPAEPDLAE	FATAAAAAAQEGGAGRKNAAREE-	877				
SECA1_MYC_paratuberculosis	788	EGIGLRAMAQRDPL	VR	EYQRE	GDFM	FAMMLD	GVKESV	GLFNV	TVE-----	AVPA-PQVAP	-VQTPEGLAEL	GAPABGGGTATAARDEAPT-	871				
SECA1_MYC_tuberculosis	791	EGIGLRAMAQRDPL	VR	EYQRE	GDFM	FAMMLD	GVKESV	GLFNV	TVE-----	AVPA-PPVAP	-AAEPAELAE	FAAAAAAAQQRSAVDGGARERA-	877				
SECA1_MYC_bovis	791	EGIGLRAMAQRDPL	VR	EYQRE	GDFM	FAMMLD	GVKESV	GLFNV	TVE-----	AVPA-PPVAP	-AAEPAELAE	FAAAAAAAQQRSAVDGGARERA-	877				
SECA1_MYC_leprae	791	EGIGLRAMAQRDPL	VR	EYQRE	GDFM	FAMMLD	GVKESV	GLFNV	LAVE-----	AVPA-SHVAP	-VEIPEGFTGL	VAADVVAIRPREEASSAL-	872				
SECA1_MYC_smegmatis	788	EGIGLRAMAQRDPL	VR	EYQRE	GDFM	FVGMLE	ALKEESV	GLFNVQ	VE-----	AAQPQ	PQVAP-QAPPPTL	SEFAAAAAKASDSAAPDSGGSVATKERA-	879				
SECA1_COR_diphtheriae	790	EGIGLRAMAQRDPL	VR	EYQRE	GEGDM	FNAMKDAV	KEETVR	QLFL	LLRKQ-----	FAVAN-	EQPAETE	EEGTVEA-	853				
SECA1_COR_efficiens	790	EGIGLRAMAQRDPL	VR	EYQRE	GEGDM	FNAMKEA	KEETVR	QLFL	MLRKQ-----	FVKQD-	EEANA-		845				
SECA1_COR_glutamicum	790	EGIGLRAMAQRDPL	VR	EYQRE	GEGDM	FNGMKDA	KEETVR	QLFL	LLRKQ-----	FVKQD-	EEANA-		845				
SECA1_COR_jeikeium	791	EGIGLRAMAQRDPL	VR	EYQRE	GEGDM	FNRMKD	GKEETVR	QLFL	VRNQ-----	LKQA-GQVHV-	EDPAAGN	EGVAVDR-	859				
SECA1_THE_fusca	786	EGIGLRAMAQRNPL	VR	EYQRE	GDFM	QEMLEG	IKESIR	FLN	VEVR-----	VNQ	PQESQIT	TAASAATASAIPLVAPEAK	TEDKAEDAQEAEBESAASAEAAESAKDTAQDKDAE	895			
SECA2_MYC_vanbaalenii	783	AGIGMRALAGADNP	VR	EYHRE	GHRM	FVRML	EAUVKE	QSIR	SLFDATTR-----	MLAP	IMP	SA--ARSPGT	PDPRWPF-	850			
SECA2_THE_maritima	774	EAVQLRSYGQKDDP	VR	EYKRE	TYMF	DEMRR	INDT	IANY	VLRRVKV-----	SEKDE	KEAKE--ELGKIRL	VLHVEE	FLNVRAMRR--	850			
SECA2_GEO_kaustophilus	737	EGIHRLRSYGQDDP	VR	EYQRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	QFVID	DEAAAA--AANKP-			797			
SECA2_GEO_thermodenitrifi	735	EGIHRLRHYQQDDP	VR	EYQRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	LEQE	EEGQS--			788			
SECA2_BAC_anthraxis	738	EGIGLRQYQQDDP	VR	EYQRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	PENVQ				788			
SECA2_BAC_thuringiensis	738	EGIGLRQYQQDDP	VR	EYQRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	PENVQ				788			
SECA2_BAC_cereus	738	EGIGLRQYQQDDP	VR	EYQRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	PENVQ				788			
SECA2_LIS_welshimeri	726	EGIHRLRAYGQDDP	VR	EYQRE	GEGA	QLFEK	QADYH	FFA	HALLELDPD-----	GLVQ				776			
SECA2_LIS_monocytogenes	726	EGIHRLRAYGQDDP	VR	EYQRE	GEGA	QLFEK	QADYH	FFA	HALLELDPD-----	GLIQ				776			
SECA2_LIS_innocua	726	EGIHRLRAYGQDDP	VR	EYQRE	GEGA	QLFEK	QADYH	FFA	HALLELDPD-----	GLIQ				776			
SECA2_ALK_metalliredigens	686	EGIHVLVVGKNDPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	KDGD	IEKEK--LKGPS	STWTY	LISDSPNQFSRLP-	764			
SECA2_LAC_johnsonii	731	INAQQWGRSGRPOD	LR	REYQ	MEGY	AMFEN	MIAAIEE	EEVATY	IMKAEI	H-----	TNEK	QQLVVV--FN-		788			
SECA2_STA_haemolyticus	739	ASVNNRQNGQRNAL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	FDKQ	QDLVVH--FP-			796			
SECA2_STA_aureus	739	ASVNNRQNGQRNAL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	FDKE	GMPVIH--FP-			796			
SECA2_STA_epidermidis	739	ASVNNRQNGQRNVL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	FDK	QDMVIH--FP-			796			
SECA2_STR_Agal	738	TVATARQTAQRNPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	FNENG	DLQIY--FI-			795			
SECA2_STR_Gordon	736	SALSGFHTSNKKPI	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	LNP	KEVIMY--FP-			793			
SECA2_STR_Pneum	733	MAIGQSASQKNPI	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	VTP	KEIVTH--FP-			790			
SECA2_STR_Sanguin	736	TALSQGHFSMKNPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	LNP	KEVIMY--FP-			793			
SECA2_COR_efficiens	675	ESIHRLRATARETPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	DRGA	HL	EDAG--LAR	PSATWTY	MVSD-	744		
SECA2_MYC_ulcerans	719	ESIHRLRALGRQNPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	EDE	PGL	DL	SK--LAR	PTSTWTY	MVND-	788	
SECA2_MYC_paratuberculosis	690	ESIHRLRALGRQNPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	EDE	PGL	DL	SK--LAR	PTSTWTY	MVND-	759	
SECA2_MYC_tuberculosis	721	ESIHRLRALGRQNPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	DHE	PGL	DL	SK--LAR	PTSTWTY	MVND-	790	
SECA2_MYC_bovis	721	ESIHRLRALGRQNPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	DHE	PGL	DL	SK--LAR	PTSTWTY	MVND-	790	
SECA2_MYC_leprae	691	ESIHRLRALGRQSP	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	DGA	PGL	DL	SK--LAR	PTSTWTY	MVND-	760	
SECA2_MYC_smegmatis	697	ESIHRLRALGRQNPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	ADE	P	VD	SK--LAR	PTSTWTY	MVND-	766	
SECA2_THE_fusca	676	EGIHRLRFLGRDPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	DGR	L	D	VAAG--VKR	PTSTWTY	MVND-	745	
SECA2_COR_diphtheriae	676	ESIHRLRTIARETPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	QDGA	HL	ADAG--L	TR	PSATWTY	MVSD-	745	
SECA2_COR_glutamicum	675	ESIHRLRATARETPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	HEGA	HL	DD	EG--LAR	PSATWTY	MVSD-	744	
SECA2_COR_jeikeium	683	ESIHRLRATARETPL	VR	EYHRE	GFEM	FKA	MYE	IEKEIS	VHTARLLQS-----	SDGA	Q	L	G	GMG--LHK	PSATWTY	MVND-	752
Consensus aa: pt1.hR.httpsP1.b@ppbt.hP..h.php..hhp.h																	
Consensus ss: hhhhhhhhhhh hhhhhhhhhhhhhhhhhhhhhhhhhhhhh hhh h																	

Conservation:				
SECA1_GEO_thermodenitrifi	795	-----VHPKE--DGEEPPKKKPIR----	KAVRVGRNDPCPCGS-----GKKYKHCCGRAV-----	837
SECA1_GEO_kaustophilus	795	-----VHPKE--DGEEPPKKRPVR----	KAVRVGRNDPCPCGS-----GKKYKHCCGRTV-----	837
SECA1_LAC_johnsonii				
SECA1_STR_parasanguinis	794	-----TTTAT--RNIAAQQQDIPA-DIDL	SQVKRNDLCPCGS-----GKKFKNCHGRKF-----	839
SECA1_STR_gordonii	794	-----VTTAT--RNISAQESDLPA-DVDL	AKVGRNELCPCGS-----GKKFKNCHGRR-----	838
SECA1_STR_pneumoniae	792	-----TTTAT--RNIAAHQASMPE-DL	LSQIGRNELCPCGS-----GKKFKNCHGKRQ-----	837
SECA1_STR_agalactiae	794	-----TTTAE--QNISAQHVPMNNESPEYQGI	KRNDKPCGS-----GKKFKNCHGLR-CLQ-----	842
SECA1_LIS_monocytogenes	795	-----INPAE--GKPEAKRPPIR----	KDQHIGRNDPCPCGS-----GKKYKNCHGKEA-----	837
SECA1_LIS_innocua	795	-----INPAE--GKPEAKRPVR----	KDQHIGRNDPCPCGS-----GKKYKNCHGKEA-----	837
SECA1_LIS_welshimeri	795	-----INPAE--GKPEAKRPVR----	KDQHIGRNDPCPCGS-----GKKYKNCHGKEA-----	837
SECA_BAC_subtilis	797	-----HQPQEGDDNKKAKKAPVR----	KVVDIGRNAPCHCGS-----GKKYKNCCGRTE-----	841
SECA1_BAC_anthraxis	793	-----VHPSS--DGEEAKKKPVV----	KGDQVGRNDLCCKGS-----GKKYKNCCGIGK-----	835
SECA1_BAC_thuringiensis	793	-----VHPSS--DGEEAKKKPVV----	KGDQVGRNDLCCKGS-----GKKYKNCCGIGK-----	835
SECA1_BAC_cereus	793	-----VHPSS--DGEEAKKKPVV----	KGDQVGRNDLCCKGS-----GKKYKNCCGIGK-----	835
SECA1_STA_epidermidis	803	-----VTAED--GKEAKKPPIV----	KGDQVGRNDPCPCGS-----GKKYKNCHGKA-----	844
SECA1_STA_haemolyticus	803	-----VSAED--GKEAKKPPIV----	KGDQVGRNDPCPCGS-----GKKYKNCHGKEE-----	845
SECA1_STA_aureus	803	-----VSAED--GKEKVKPKPIV----	KGDQVGRNDPCPCGS-----GKKYKNCHGKEE-----	843
SECA1_ALK_metalliredigens	851	-----IEASH--GDGNRKAPVV----	KEKEAGRNDPCPCGS-----GKKYKCCGE-----	891
SECA1_PEP_difficile	851	-----LSSPS--DGTLPSTKTVK----	KDEKVGRNDLCPCGS-----GKKYKNCCGR-----	891
SECA2_PEP_difficile				
SECA2_model_opened_conf				
SECA_E_coli	857	-----LSHQD--DDSAAAAALAAQ----	TGERKVGRNDPCPCGS-----GKKYKQCHGRLO-----	901
SECA1_MYC_vanbaalenii	877	-----VGGLRAKGIDDKAQPLTYTGPSE--	DGG-----VEVKRSGGGTPTST-----	938
SECA1_MYC_ulcerans	878	-----APSRLRAKGIEDESPALTYSGPSE--	DGS-----AQVQRNGGGAAKTPAG----	950
SECA1_MYC_paratuberculosis	872	-----QLRAKGIDNEAPAMTYSGPSE--	DGS-----AQVQRNGGDAKTPAG----	940
SECA1_MYC_tuberculosis	878	-----PSALRAKGVASESPALTYSGPAE--	DGS-----AQVQRNGGGAHKTAPAG----	949
SECA1_MYC_bovis	878	-----PSALRAKGVASESPALTYSGPAE--	DGS-----AQVQRNGGGAHKTAPAG----	949
SECA1_MYC_leprae	873	-----RTKDIDNESTGLTYSGPSE--	DGS-----TQVQLNSGGGQKTPAG----	940
SECA1_MYC_smegmatis	880	-----EAERPAPALRAKGIDNEAPPLTYTGPSE--	DGT-----AQVQRSGNGGRHAA-----	953
SECA1_COR_diphtheriae				
SECA1_COR_efficiens				
SECA1_COR_glutamicum				
SECA1_COR_jeikeium	860	-----ATQTT--MGG-----		867
SECA1_THE_fusca	896	SVAKKAQAVVPALGKEEKQPEKLQYSGPSE--	GGG-----VEKRTEDTGPDIYANTPRNAPCPCSG	968
SECA2_MYC_vanbaalenii				
SECA_THE_maritima	851	-----ATEKKKKKDGLHS-----	FGRIRVKR-----	871
SECA2_GEO_kaustophilus				
SECA2_GEO_thermodenitrifi				
SECA2_BAC_anthraxis				
SECA2_BAC_thuringiensis				
SECA2_BAC_cereus				
SECA2_LIS_welshimeri				
SECA2_LIS_monocytogenes				
SECA2_LIS_innocua				
SECA2_ALK_metalliredigens	765	-----FIVKGVLFSLRSISN-----	GIVRKVQETINVVIQK-----	795
SECA2_LAC_johnsonii				
SECA2_STA_haemolyticus				
SECA2_STA_aureus				
SECA2_STA_epidermidis				
SECA2_STR_Agal				
SECA2_STR_Gordon				
SECA2_STR_Pneum				
SECA2_STR_Sanguin				
SECA2_COR_efficiens	745	-----NPLSGS-----	GNS-VISGI--GNIFR--	763
SECA2_MYC_ulcerans	789	-----NPLSDD-----	TLS-TLSLP---GVFR--	806
SECA2_MYC_paratuberculosis	760	-----NPLSDD-----	TLS-TLSLP---GVFR--	777
SECA2_MYC_tuberculosis	791	-----NPLSDD-----	TLS-ALSLP---GVFR--	808
SECA2_MYC_bovis	791	-----NPLSDD-----	TLS-ALSLP---GVFR--	808
SECA2_MYC_leprae	761	-----APLSDD-----	TLS-PLSLP---GVFR--	778
SECA2_MYC_smegmatis	767	-----NPLADD-----	TMS-ALSLP---GVFR--	784
SECA2_THE_fusca	746	-----QPFSTD-----	LEN-IVGRV---KNLMGRD	766
SECA2_COR_diphtheriae	746	-----NPLSNN-----	NRS-VINGI--GSIFR--	764
SECA2_COR_glutamicum	745	-----NPLSGS-----	GNS-VISGI--GNIFR--	763
SECA2_COR_jeikeium	753	-----NPLSSS-----	GGG-VMGSI--VQMFR--	771
Consensus_aa:				
Consensus_ss:				

Figure S2, related to Figures 1, 2, 3 and 5: Structure-restrained sequence alignment of SecA1 and SecA2 sequences from 30 SecA2-encoding organisms. PROMALS3D alignment [2] of the 30 sequences encoding SecA1 (30 seq) and SecA2 (30 seq) was performed using default parameters, the coordinate file for CDSecA2 and the structure-based constraints from therein. So far, most of the SecA-protein interaction studies were based on the *T. maritima*, *E. coli* and *B. subtilis* SecAs. Thus, their sequences are added for orientation, but were not included in the Consurf analyses presented in main text (Figure 5). The highly conserved ATP binding site within Walker motifs is highlighted in red, the PPDX loop in cyan (coloured cyan in Figure 3A), the 2HF loop in yellow, and HWD domain in purple. The signal and nascent peptide binding sites (see Figures 3A, 3C and 5) involve residues present at the surface of the SecA molecule that make up or surround the groove. The ones that have been previously implicated in interaction with the signal peptide are highlighted in blue [3–7], and the ones implicated in the nascent protein binding in yellow [8–10]. The red frames represent the differences we observed when structurally aligning the CDSecA2 with *T. maritima* SecA, and refer to Figure 3B. The grey colouring represents the residues predicted to interact with the SecY channel [11–13]. The first line of each block shows conservation indices for positions with a conservation index above 4. Consensus predicted secondary structures (ss) are presented as symbols h for α -helix and b for β -strand. Conserved amino acids are shown in bold uppercase letters, aliphatic as *l*, aromatic as *@*, hydrophobic as *h*, alcohol as *o*, polar as *p*, tiny as *t*, small as *s*, bulky as *b*, positively charged as *+*, negatively charged as *-*, charged as *c*.

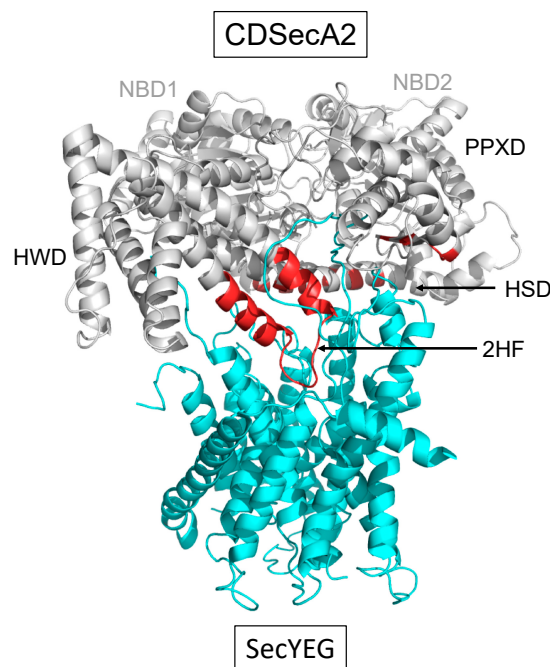


Figure S3, related to Figure 3, 4 and 5. Interface residues (red) of CDSecA2 (grey) that would contact the SecYEG (cyan), based on superposition with *T. maritima* SecA (PDB ID 3DIN; [11]).

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