

A**CC0374** : a putative DsbA homolog**CC0375** : a putative DsbA homolog**CC1879** : CcScsC**CC0220** : CcPrxL**CC2210** : thiol:disulfide interchange protein **TipA**

MNEVQSGQNGEEAKKRNP**MALAGVILLGVA**AVLYVIASAS**FKPSG**PADL**TEFK**
 KGAF**EKL**DVPATPRP**APTTVFTSMDGKPTTLAD**FKGRVV**VMNLWATW**CA**PC**KAE
 MPTLAKLQAA**YATQP**VT**VLPI**SVD**RSDLN**LVREEMAAN**PPLVTY**RDP**SYKLS**FDL
 QPRAQGYPTT**IIYDR**QGRERARLAGPADWSA**PEVRGIVEK**L**LAEK**

CC3666 : hypothetical protein

MRS**MRKAALS**LFSLVLS**GVVATLSWGGV**AWAQPPVV**VELFTAQGCSS**CGKAN
 QVAADLAKQDGVLALTYAVDYWDYLGW**KDTFAK**PVFAERQRAYAK**KFALRD**VPTP
 QMVVAGRVQASG**TKAE**AVEDLVKTAARAR**LNP**DMQFIGAARVAVGSG**PAPRGG**
 GEVWLVRYPREQDIAIKRGDNKGQTLVHRNVREL**VRLGPWAGKPKLYR**LPAAN
 DADLVTVVLVQGA**KGRILGVL**QSAGEAKR

CC3674 : thiol:disulfide interchange protein CycY (**CcmG** homolog)

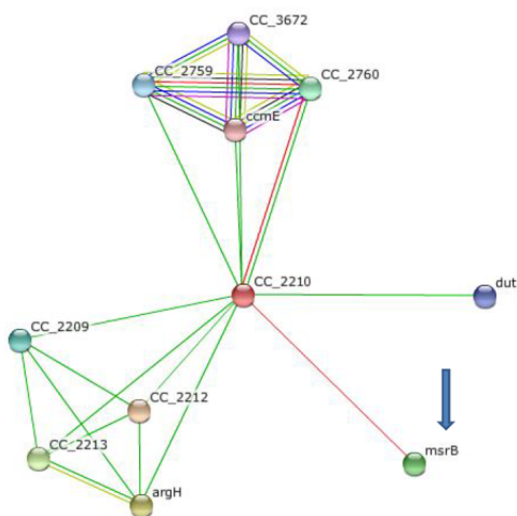
MKR**WLA**FSPL**IVLVALAVL**FAGYALQRDPRVQ**PQALV**GK**PMPALMLP**DLDTGRPA
 PLRQ**TGEG**PILV**NFFASW**CA**PC**EV**EH**PQLM**ALKAQ**GV**TVVGI**AYKDAPANTQA**FLT**
 RLGDPFAAKR**VDRDGR**AGLEFGVTGVPETYLVGSDGV**IIAKHTG**PLTPDAAEDLLK
 QAK

CC0249 : SCO1/2 family protein

MPRHRL**VLILACV**GLAVAVGLAW**NVGV**FRSEPA**VTVGGPF**ELVDQNGAPTSEKA
 LKGKWSAVFFGFTY**CPDVC**PGTLQGLAAATDQLGPKAKDFQIVFISIDPARDTV**KQ**
 MKAYLSAPYVPKATIGLTGTQAQV**DAAKAYRVYHAKV**GDGVDYTM**DHSTAI**YLMD
 PKGRFKTVIPY**NLPPDEI**ARRIKDAVREG

CC3503 : SCO1/2 family protein

MRAIALTLALLAAT**PLAGC**GEKAAQDAAGAVIKGGPFQ**L**TDMNGK**PVTEK**SLLGK
 PTAVFFGFTY**CPEV**CP**PTTL**EMTAWL**KALGK**DADK**LN**VV**LITV**DPERDTPAQL**KEYL**
 SNFD**PRIQ**GFTGTPDAIAKTARAYRVY**YQKV**PLDGGGYTIDHSSAIY**L**FD**AKGR**FVS
 PIAYQAPQDRALGQLRDLLK

B**C**

Score = 99.8 bits (247), Expect = 8e-27, Method: Compositional matrix adjust
 Identities = 65/204 (32%), Positives = 100/204 (49%), Gaps = 12/204 (6%)

Query	7	SATRRIP	LV	IATVAVG	LAGFAALYGL	LSRAP	TGDPACRAAVATAQKI	APLAHGEVAAL	66
		A +R	P+	+A	V L A LY + +	PA	+ G L		
Sbjct	12	EAKKRNP	M	RMALAGV	ILLGVA	AVLYVIASAS	FKPSGPA-----	DLTEFKKGA	FEKL 62
Query	67	TMASAP	LKLPDLAFEDADGKPKKLSDFR	GKTL	LVNLWATWCVPCR	KEMPALDE	LOGKLSG	126	
		+ + P	P F DGKP	L+DF+G+	+++NLWATWC	PC+ EMP	L +LQ +		
Sbjct	63	DVPATPR	PAPTTVFTSMDGKPTTLAD	FKGRVV	VMNLWATWCA	PCKAEMPTLAKL	QAA	YAT 122	
Query	127	PNFEVVA	INIDTRDPEKPKTFLKEANL	TRLGYFNDQKAKVFQDL	KAIGRALGMPT	SVLVD	186		
		V+ I++D	RD + + A	L + D	K+ DL+ RA	G PT+++	D		
Sbjct	123	QPVT	VLPI	SVDRSDLN	LVREEMAANP	PLVTYRDP	SYKLSFDLQP--	RAQGYPTTIIYD 179	
Query	187	POGCE	IATIAGPAEWASE	DALKLI	210				
		QG E A	+AGPA+W++	+ +					
Sbjct	180	ROGRERAR	LAGPADWSA	PEVRGIV	203				

← **BrTipA**← **CcTipA**