

## SI Legends

**Fig. S1.** A. Inactivation of wild-type OhrR (□), sc OhrR WT-WT (△), or WT-C15S scOhrR (×) in the presence of 0.5 mM Cys. As a control, the comparatively slow inactivation of OhrR in the absence of Cys is also shown (◊). B. Inactivation of OhrR (□), scOhrR WT-WT (△) or WT-C15S scOhrR (×) in the presence of 0.5 mM BSH.

**Fig. S2. S-bacillithiolated BrxB C54A does not transfer BSH to OhrR.** Immunoblot analysis usig anti-BSH antibodies to follow protein S-bacillithiolation. Purified OhrR-SSB (lane 1) and BrxB C54A-SSB (lane 2) are shown as controls. BSH does not de-bacillithiolate OhrR-SSB (lane 3), but incubation with BrxB C54A leads to de-bacillithiolation and transfer of the BSH moiety to BrxB (lane 4). The reverse reaction, transfer of BSH from BrxB C54A-SSB to OhrR is not observed (lane 5).

**Table S1: Detected MetE-SSB sites by Orbitrap LC-MS/MS analysis before and after reduction by BrxA and BrxB in an in vitro Brx-assay.** His-tagged MetE was expressed and purified from *E. coli* cells, in vitro bacillithiolated using BSSB and purified as described in the Methods section. MetE-SSB was reduced by purified BrxA and BrxB for 1 hour. The MetE-SSB control reaction and MetE-SSB that was treated with BrxA and BrxB were separated by SDS-PAGE. The MetE-SSB bands and the BrxA and BrxB bands were tryptically in gel-digested. The resulting MetE-SSB peptides were analyzed using LTQ Orbitrap Velos LC-MS/MS analysis as described in the Methods section (Chi et al., 2011). The Scaffold search results are shown and the Table includes the Xcorr, deltaCn scores,m/z of the precursor ions, neutral molecular masses of the peptides, peptide mass deviations (delta ppm) of all detected bacillithiolated peptides in MetE. The CID MS/MS spectrum of the modified Cys peptides are shown,with the b and y ion series labeled in red and blue, respectively. Two replicates each for the Brx assay using MetE-SSB were performed and the averages and SEM are shown for the bacillithiolated Cys peptides of MetE before and after Brx reduction in the Table below that is used for the Figure 5.

**Table S2: Detected BrxA-SSB sites by Orbitrap LC-MS/MS analysis before and after reduction of MetE-SSB by BrxA in the in vitro Brx-assay.** His-tagged MetE was expressed and purified from *E. coli* cells, in vitro bacillithiolated using BSSB and purified as described in the Methods section. MetE-SSB was reduced by purified BrxA for 1 hour. The MetE-SSB control reaction and MetE-SSB that was treated with BrxA and BrxB were separated by SDS-PAGE. The MetE-SSB bands and the BrxA and BrxB bands were tryptically in gel-digested. The resulting BrxA-SSB peptides were analyzed using LTQ Orbitrap Velos LC-MS/MS analysis as described in the Methods section (Chi et al., 2011). The Scaffold search results are shown and the Table includes the Xcorr, deltaCn scores,m/z of the precursor ions, neutral molecular masses of the peptides, peptide mass deviations (delta ppm) of all detected bacillithiolated peptides in BrxA. The CID MS/MS spectrum of the modified Cys peptides are shown,with the b and y ion series labeled in red and blue, respectively. Two replicates each for the Brx assay using MetE-SSB were performed and the averages and SEM are shown for the bacillithiolated Cys peptides of BrxA before and after Brx reduction of MetE-SSB in the Table below that is used for the Figure 5.

**Table S3: Detected BrxB-SSB sites by Orbitrap LC-MS/MS analysis before and after reduction of MetE-SSB by BrxB in the in vitro Brx-assay.** His-tagged MetE was expressed and purified from *E. coli* cells, in vitro bacillithiolated using BSSB and purified as described in the Methods section. MetE-SSB was reduced by purified BrxB for 1 hour. The MetE-SSB control reaction and MetE-SSB that was treated with BrxA and BrxB were separated by SDS-PAGE. The MetE-SSB bands and the BrxA and BrxB bands were tryptically in gel-digested. The resulting BrxB-SSB peptides were analyzed using LTQ Orbitrap Velos LC-MS/MS analysis as described in the Methods section (Chi et al., 2011). The Scaffold search results are shown and the Table includes the Xcorr, deltaCn scores,m/z of the precursor ions, neutral molecular masses of the peptides, peptide mass deviations (delta ppm) of all detected bacillithiolated peptides in BrxB. The CID MS/MS spectrum of the modified Cys peptides are shown,with the b

and y ion series labeled in red and blue, respectively. Two replicates each for the Brx assay using MetE-SSB were performed and the averages and SEM are shown for the bacillithiolated Cys peptides of BrxB before and after Brx reduction of MetE-SSB in the Table below that is used for the Figure 5.

**Table S4: BrxB C54A with the Cys52-SSB site (upper figure) and BrxA C55A with Cys53-SSB site (bottom figure) *in vivo*.** FLAG-tagged BrxB C54A and BrxA C55A proteins were purified from *B. subtilis* cells after NaOCl-stress, separated by SDS-PAGE and the Brx bands tryptically digested. The resulting peptides were analyzed using LTQ Orbitrap Velos LC-MS/MS analysis as described in the Methods section (Chi et al., 2011). The Scaffold search results are shown and the Table includes the Xcorr, deltaCn scores, m/z of the precursor ions, neutral molecular masses of the peptides, peptide mass deviations (delta ppm) of the S-bacillithiolated Cys52 peptide in BrxB C54A and Cys53 in BrxA C55A. The CID MS/MS spectra are shown with the b and y ion series labeled in red and blue, respectively.

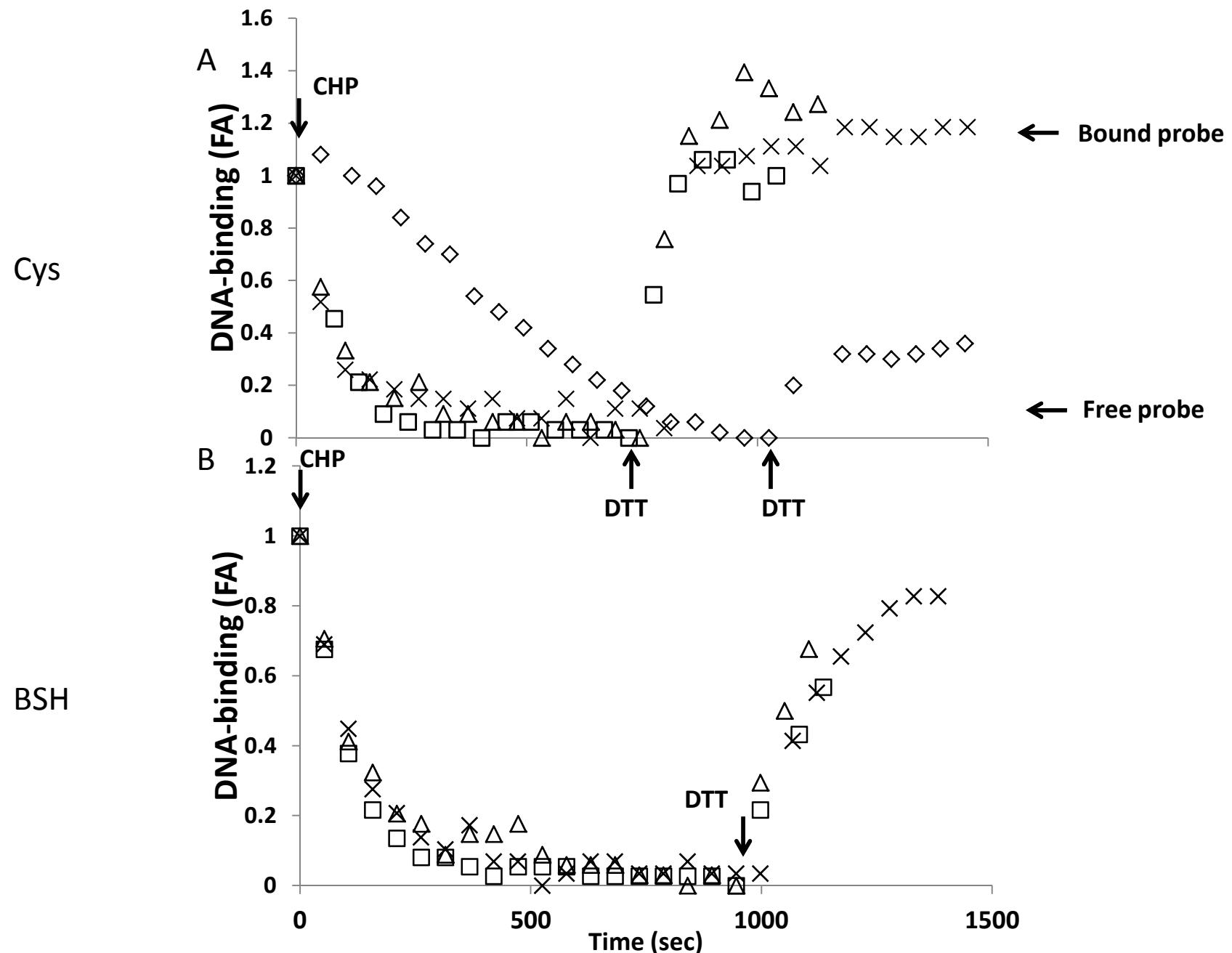
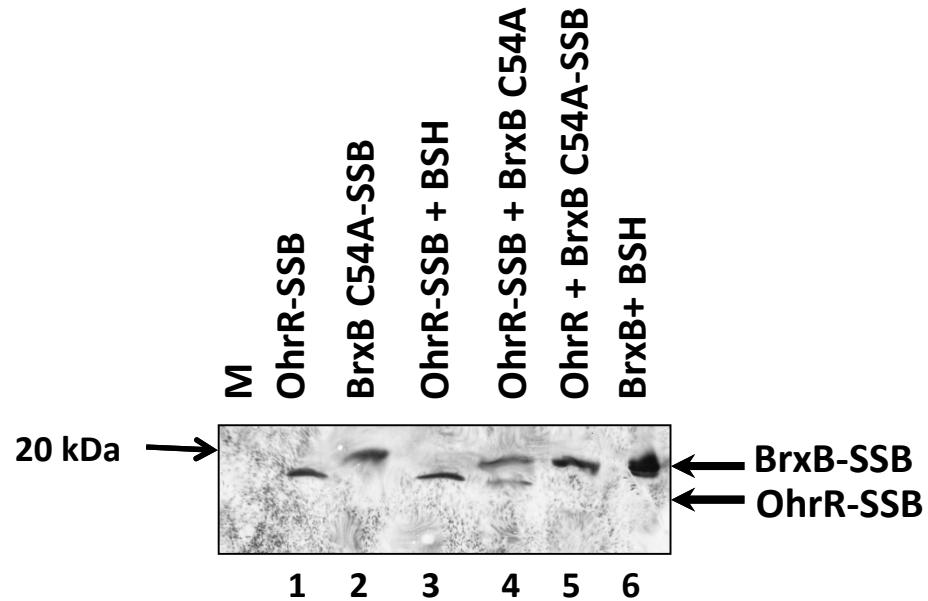


Fig. SI 1. . Inactivation of OhrR (□), scOhrR WT-WT (△) or WT-C15S scOhrR (×) in the presence of 0.5 mM L-Cys (A) or BSH (B). As a control, the comparatively slow inactivation of OhrR in the absence of thiols is also shown (◊).

**Fig. S2: S-bacillithiolated BrxB C54A does not transfer BSH to OhrR.**



**Table S1: MetE-SSB reduction by BrxA and BrxB in vitro (SI to MetE-SSB peptide informations to Fig. 5)**

Sequence	Prob	SEQUEST_Xcorr	SEQUEST_Acn	NTT	Modifications	Observed	Actual Mass	Charge	ΔAMU	ΔPPM	TIC	Start	Stop	Spectrum ID
<b>MetE-SSB control Replicate-1</b>														
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.1836	0.7028	2	~(+396)	944.7602	2831.2588	3	0.003419	1.207	14,591.20	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.12392.12392.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.0592	0.7896	2	~(+396)	944.7584	2831.2533	3	-0.002075	-0.7327	26,578.30	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.12343.1243.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.2177	0.6941	2	~(+396)	944.7583	2831.2531	3	-0.002258	-0.7974	27,220.40	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.12306.12306.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.9997	0.7969	2	~(+396)	944.7592	2831.2556	3	0.0003057	0.1079	13,520.70	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.12267.12267.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.0461	0.6715	2	~(+396)	944.7579	2831.2520	3	-0.003356	-1.185	6,669.91	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.11394.11394.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.5867	0.7053	2	~(+396)	944.7578	2831.2514	3	-0.003906	-1.379	7,123.97	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.11338.11338.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	3.5058	0.5981	2	~(+396)	944.7575	2831.2507	3	-0.004638	-1.638	8,693.21	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.11184.11184.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.3561	0.6894	2	~(+396)	944.7612	2831.2619	3	0.006531	2.306	11,118.70	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.11068.11068.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.5656	0.6957	2	~(+396)	944.7571	2831.2496	3	-0.005737	-2.026	8,588.09	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.11034.11034.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.0674	0.7613	2	~(+396)	944.7601	2831.2584	3	0.003052	0.1077	11,691.60	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10990.10990.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.5114	0.7231	2	~(+396)	944.7550	2831.2432	3	-0.01215	-4.288	12,948.00	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10884.10884.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.9779	0.6684	2	~(+396)	944.7634	2831.2685	3	0.01312	4.633	13,677.00	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10845.10845.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.8058	0.7143	2	~(+396)	944.7588	2831.2547	3	-0.006103	-0.2155	12,763.80	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10802.10802.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.0123	0.7767	2	~(+396)	944.7579	2831.2520	3	-0.003356	-1.185	12,107.90	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10742.10742.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.0021	0.7254	2	~(+396)	944.7594	2831.2564	3	0.001038	0.3664	17,197.70	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10660.10660.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.1924	0.6948	2	~(+396)	944.7564	2831.2474	3	-0.007934	-2.801	16,668.40	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10619.10619.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.1576	0.7643	2	~(+396)	944.7605	2831.2597	3	0.004334	1.53	17,913.90	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10576.10576.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.2905	0.7977	2	~(+396)	944.7609	2831.2608	3	0.005433	1.918	21,582.60	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10496.10496.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.7834	0.6853	2	~(+396)	944.7557	2831.2452	3	-0.01013	-3.577	19,462.80	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10456.10456.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.5139	0.6994	2	~(+396)	944.7586	2831.2540	3	-0.001342	-0.4739	16,986.40	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10384.10384.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.9454	0.7078	2	~(+396)	944.7587	2831.2544	3	-0.0009763	-0.3447	28,884.20	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10344.10344.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.9607	0.6636	2	~(+396)	944.7545	2831.2417	3	-0.01361	-4.805	27,961.80	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10242.10242.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.9153	0.7267	2	~(+396)	944.7619	2831.2369	3	0.008546	3.017	31,832.80	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10203.10203.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.3433	0.7273	2	~(+396)	944.7619	2831.2369	3	0.008546	3.017	33,131.10	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10163.10163.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.0397	0.6821	2	~(+396)	944.7561	2831.2465	3	-0.008849	-3.124	40,008.80	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10120.10120.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.1553	0.7324	2	~(+396)	944.7601	2831.2584	3	0.003052	1.077	39,504.60	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.10048.10048.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	4.9204	0.7729	2	~(+396)	944.7604	2831.2595	3	0.004151	1.466	50,752.70	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.09983.09983.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.2939	0.6514	2	~(+396)	944.7551	2831.2436	3	-0.01178	-4.159	55,685.70	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.09942.09942.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.2380	0.7827	2	~(+396)	944.7574	2831.2503	3	-0.005004	-1.767	77,989.70	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.08312.08312.3.dta
(R)VPSTEEMNYIIVDALAVcPTDR(F)	96%	5.0692	0.7421	2	~(+396)	944.7584	2831.2534	3	-0.001891	-0.6678	91,589.50	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.09826.09826.3.dta
(R)VPSTEEmNYIIVDALAVcPTDR(F)	100%	4.0605	0.7869	2	Ox(+16), ~(+396)	1424.6305	2847.2464	2	-0.003813	-1.339	14,667.10	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.08868.08868.2.dta
(R)VPSTEEmNYIIVDALAVcPTDR(F)	96%	5.3098	0.7701	2	Ox(+16), ~(+396)	950.0927	2847.2561	3	0.005879	2.064	1.12E+07	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.08854.08854.3.dta
(R)VPSTEEmNYIIVDALAVcPTDR(F)	96%	5.9281	0.7620	2	Ox(+16), ~(+396)	950.0905	2847.2497	3	-0.0005303	-0.1862	458115	702	723	130610_V3_P5_KB_MetE_SSB_co_2_2.08802.08802.3.dta
(R)cVRPPVIYGDVEFIEPMTVK(D)	96%	4.4106	0.6886	2	~(+396)	896.7585	2687.2538	3	0.0002747	0.1022	10,6475	520	539	130610_V3_P5_KB_MetE_SSB_co_2_2.08379.08379.3.dta
(R)cVRPPVIYGDVEFIEPMTVK(D)	96%	5.0547	0.6595	2	~(+396)	896.7588	2687.2547	3	0.00119	0.4426	382327	520	539	130610_V3_P5_KB_MetE_SSB_co_2_2.08312.08312.3.dta
(R)cVRPPVIYGDVEFIEPMTVK(D)	96%	3.8629	0.6606	2	(+396), Ox(+16)	902.0899	2703.2479	3	-0.0005613	-0.2076	366930	520	539	130610_V3_P5_KB_MetE_SSB_co_2_2.07605.07605.3.dta
(R)FWVNPNDcGLK(T)	98%													

**Table S2: BrxA-SSB peptides after *in vitro* MetE-SSB reduction by BrxA (SI to BrxA-SSB peptide informations to Fig. 5)**

Sequence	Prob	SEQUEST XCorr	SEQUEST ΔCn	NTT	Modifications	Observed	Actual Mass	Charge	ΔAMU	ΔPPM	TIC	Start	Stop	Spectrum ID
<b>BrxA Cys53-SSB peptide Replicate-1</b>														
(K)AEHTTLVVNSVCGAACGLAR(P)	99%	4.3439	0.6705	2	~(+396), IAM (+57)	1,222,5602	2,443,1058	2	0.002811	1.15	241284	41	61	130610_V3_P5_KB_BrxA_1_3.07377.07377.2.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	98%	4.0093	0.6601	2	~(+396), IAM (+57)	611,7833	2,443,1042	4	0.001199	0.4907	1368120	41	61	130610_V3_P5_KB_BrxA_1_3.07419.07419.4.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	99%	4.4746	0.6879	2	~(+396), IAM (+57)	1,222,5591	2,443,1036	2	0.0006144	0.2514	94,579,60	41	61	130610_V3_P5_KB_BrxA_1_3.07442.07442.2.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	99%	4.6582	0.6814	2	~(+396), IAM (+57)	1,222,5610	2,443,1075	2	0.00452	1.85	64,280,30	41	61	130610_V3_P5_KB_BrxA_1_3.07509.07509.2.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	99%	4.5244	0.6873	2	~(+396), IAM (+57)	1,222,5593	2,443,1041	2	0.001102	0.451	23,773,80	41	61	130610_V3_P5_KB_BrxA_1_3.07601.07601.2.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.6067	0.5882	2	~(+396), IAM (+57)	815,3757	2,443,1052	3	0.002188	0.8954	969805	41	61	130610_V3_P5_KB_BrxA_1_3.07670.07670.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.3809	0.5930	2	~(+396), IAM (+57)	815,3754	2,443,1043	3	0.001273	0.521	861204	41	61	130610_V3_P5_KB_BrxA_1_3.07733.07733.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.9883	0.6012	2	~(+396), IAM (+57)	815,3742	2,443,1008	3	-0.002206	-0.9024	881644	41	61	130610_V3_P5_KB_BrxA_1_3.07862.07862.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.9292	0.6176	2	~(+396), IAM (+57)	815,3759	2,443,1059	3	0.002921	1.195	393074	41	61	130610_V3_P5_KB_BrxA_1_3.08238.08238.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	5.1324	0.6490	2	~(+396), IAM (+57)	815,3751	2,443,1034	3	0.0003574	0.1462	325125	41	61	130610_V3_P5_KB_BrxA_1_3.08427.08427.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.6976	0.5816	2	~(+396), IAM (+57)	815,3749	2,443,1028	3	-0.0001916	-0.0784	276282	41	61	130610_V3_P5_KB_BrxA_1_3.08492.08492.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.1542	0.6129	2	~(+396), IAM (+57)	815,3755	2,443,1046	3	0.01639	0.6708	290393	41	61	130610_V3_P5_KB_BrxA_1_3.08959.08959.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.1945	0.6068	2	~(+396), IAM (+57)	815,3754	2,443,1043	3	0.001273	0.521	315465	41	61	130610_V3_P5_KB_BrxA_1_3.08659.08659.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.0174	0.5937	2	~(+396), IAM (+57)	815,3751	2,443,1034	3	0.0003574	0.1462	366688	41	61	130610_V3_P5_KB_BrxA_1_3.08721.08721.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.0835	0.5977	2	~(+396), IAM (+57)	815,3754	2,443,1045	3	0.001456	0.5959	495890	41	61	130610_V3_P5_KB_BrxA_1_3.08973.08973.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.7850	0.6616	2	~(+396), IAM (+57)	815,3751	2,443,1035	3	0.0005404	0.2211	502974	41	61	130610_V3_P5_KB_BrxA_1_3.09099.09099.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	95%	3.8743	0.4706	2	~(+396), IAM (+57)	815,3770	2,443,1090	3	0.006033	2.469	548015	41	61	130610_V3_P5_KB_BrxA_1_3.09162.09162.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.0708	0.6076	2	~(+396), IAM (+57)	815,3760	2,443,1063	3	0.003287	1.345	381624	41	61	130610_V3_P5_KB_BrxA_1_3.09607.09607.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.9460	0.6302	2	~(+396), IAM (+57)	815,3755	2,443,1048	3	0.001822	0.7456	361430	41	61	130610_V3_P5_KB_BrxA_1_3.09669.09669.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.3289	0.6000	2	~(+396), IAM (+57)	1,222,5563	2,443,1126	2	0.009647	3.947	11,465,60	41	61	130610_V3_P5_KB_BrxA_1_3.09716.09716.2.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.7169	0.6344	2	~(+396), IAM (+57)	815,3760	2,443,1061	3	0.003104	1.27	400496	41	61	130610_V3_P5_KB_BrxA_1_3.09733.09733.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.0753	0.6044	2	~(+396), IAM (+57)	815,3755	2,443,1059	3	0.002005	0.8205	387159	41	61	130610_V3_P5_KB_BrxA_1_3.09793.09793.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.0443	0.5498	2	~(+396), IAM (+57)	815,3752	2,443,1037	3	0.0007234	0.296	360887	41	61	130610_V3_P5_KB_BrxA_1_3.09856.09856.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	96%	3.9546	0.4937	2	~(+396), IAM (+57)	815,3755	2,443,1046	3	0.01639	0.6708	385756	41	61	130610_V3_P5_KB_BrxA_1_3.10024.10024.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.6452	0.6249	2	~(+396), IAM (+57)	815,3756	2,443,1050	3	0.002005	0.8205	362143	41	61	130610_V3_P5_KB_BrxA_1_3.10076.10076.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	95%	3.5188	0.4936	2	~(+396), IAM (+57)	815,3750	2,443,1032	3	0.0001744	0.7135	301162	41	61	130610_V3_P5_KB_BrxA_1_3.10294.10294.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	96%	3.5350	0.5500	2	~(+396), IAM (+57)	815,3753	2,443,1041	3	0.00109	0.4461	213113	41	61	130610_V3_P5_KB_BrxA_1_3.10419.10419.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	98%	3.5287	0.6572	2	~(+396), IAM (+57)	1,222,5542	2,443,0938	2	-0.009152	-3.744	6,865,67	41	61	130610_V3_P5_KB_BrxA_1_3.10546.10546.2.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.9731	0.5564	2	~(+396), IAM (+57)	815,3749	2,443,1030	3	-8.606E-06	-0.003521	157244	41	61	130610_V3_P5_KB_BrxA_1_3.10636.10636.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.6843	0.6101	2	~(+396), IAM (+57)	815,3755	2,443,1048	3	0.001822	0.7456	140262	41	61	130610_V3_P5_KB_BrxA_1_3.10720.10720.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	96%	3.8956	0.5092	2	~(+396), IAM (+57)	815,3748	2,443,1024	3	-0.0005576	-0.2281	107074	41	61	130610_V3_P5_KB_BrxA_1_3.10877.10877.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.5205	0.6364	2	~(+396), IAM (+57)	815,3748	2,443,1026	3	-0.0005576	-0.2281	84,877,60	41	61	130610_V3_P5_KB_BrxA_1_3.10993.10993.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.0513	0.6006	2	~(+396), IAM (+57)	815,3751	2,443,1034	3	0.0003574	0.1462	83,911,10	41	61	130610_V3_P5_KB_BrxA_1_3.11029.11029.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	4.0520	0.6034	2	~(+396), IAM (+57)	815,3749	2,443,1028	3	-0.0001916	-0.0784	67,207,40	41	61	130610_V3_P5_KB_BrxA_1_3.11148.11148.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.8423	0.5685	2	~(+396), IAM (+57)	815,3752	2,443,1039	3	0.0009064	0.3708	66,001,70	41	61	130610_V3_P5_KB_BrxA_1_3.11190.11190.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	96%	4.0039	0.5066	2	~(+396), IAM (+57)	815,3751	2,443,1034	3	0.0003574	0.1462	39,954,80	41	61	130610_V3_P5_KB_BrxA_1_3.11383.11383.3.dta
(K)AEHTTLVVNSVCGAACGLAR(P)	97%	3.8891	0.6026	2	~(+									

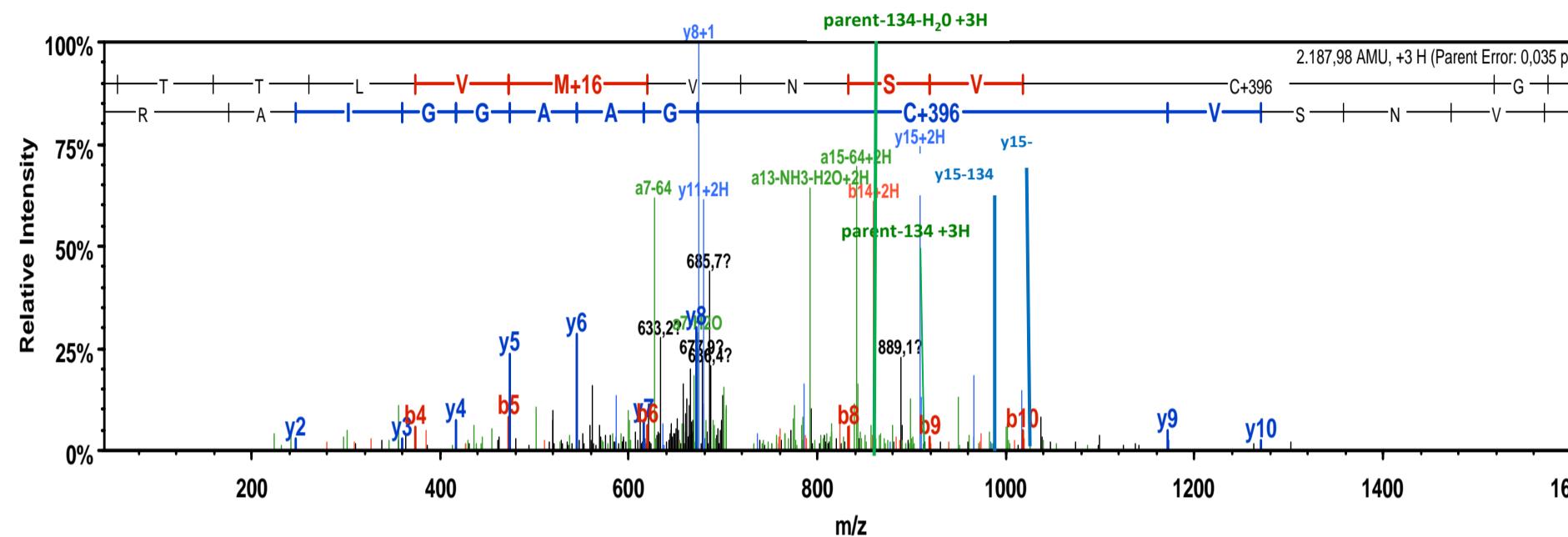
**Table S3: BrxB-SSB peptides after in vitro MetE-SSB reduction by BrxB (S1 to BrxB-SSB peptide informations to Fig. 5)**

Sequence	Prob	SEQUEST Xcorr	SEQUEST ACn	NTT	Modifications	Observed	Actual Mass	Charge	ΔAMU	ΔPPM	TIC	Start	Stop	Spectrum ID
<b>BrxB Cys52-SSB peptide 1</b>														
(K)IQEAEFEYCEEV(-)	99%	3.5339	0.9781	2	~(+396)	942.8559	1883.6972	2	0.0007077	0.3755	58,186.30	134	145	130610_V3_P5_KB_BrxB_1_5.06591.06591.2.dta
(K)IQEAEFEYCEEV(-)	99%	3.1124	0.9156	2	~(+396)	942.8558	1883.6971	2	0.0005857	0.3108	92,802.40	134	145	130610_V3_P5_KB_BrxB_1_5.06631.06631.2.dta
(K)IQEAEFEYCEEV(-)	99%	3.0009	0.8836	2	~(+396)	942.8558	1883.6970	2	0.0004637	0.246	45,494.70	134	145	130610_V3_P5_KB_BrxB_1_5.06677.06677.2.dta
(K)IQEAEFEYCEEV(-)	99%	2.4764	0.8904	2	~(+396)	942.8553	1883.6960	2	-0.0005133	-0.2724	21,657.90	134	145	130610_V3_P5_KB_BrxB_1_5.06856.06856.2.dta
(K)IQEAEFEYCEEV(-)	98%	2.5758	0.7802	2	~(+396)	942.8548	1883.6950	2	-0.001489	-0.7902	25,277.80	134	145	130610_V3_P5_KB_BrxB_1_5.06948.06948.2.dta
(K)IQEAEFEYCEEV(-)	99%	2.3117	0.891	2	~(+396)	942.8550	1883.6955	2	-0.001001	-0.5313	12,915.20	134	145	130610_V3_P5_KB_BrxB_1_5.07008.07008.2.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	99%	2.2767	0.9869	2	~(+396), IAM (+57)	942.8538	1883.6931	2	-0.003442	-1.826	11,019.00	134	145	130610_V3_P5_KB_BrxB_1_5.07095.07095.2.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	96%	3.6678	0.5241	2	~(+396), IAM (+57)	979.3649	2389.0728	3	-0.002022	-0.8458	119,590	41	60	130610_V3_P5_KB_BrxB_1_5.04815.04815.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	99%	4.5683	0.7697	2	~(+396), IAM (+57)	1195.5454	2389.0763	2	0.00147	0.6152	38,826.60	41	60	130610_V3_P5_KB_BrxB_1_5.04841.04841.2.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	96%	3.5027	0.5008	2	~(+396), IAM (+57)	797.3651	2389.0733	3	-0.001472	-0.6157	136079	41	60	130610_V3_P5_KB_BrxB_1_5.04901.04901.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.7127	0.6231	2	~(+396), IAM (+57)	797.3657	2389.0753	3	0.0005424	0.2269	61,904.50	41	60	130610_V3_P5_KB_BrxB_1_5.04943.04943.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	99%	4.3844	0.7465	2	~(+396), IAM (+57)	1131.4972	2260.9798	2	0.00003539	0.01565	102,764	42	60	130610_V3_P5_KB_BrxB_1_5.05626.05626.2.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	99%	4.2349	0.7763	2	~(+396), IAM (+57)	1131.4971	2260.9796	2	-0.0002086	-0.09222	78,814.20	42	60	130610_V3_P5_KB_BrxB_1_5.05668.05668.2.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.5031	0.6333	2	~(+396), IAM (+57)	754.6664	2260.9773	3	-0.00248	-1.096	395205	42	60	130610_V3_P5_KB_BrxB_1_5.05778.05778.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.791	0.7099	2	~(+396), IAM (+57)	754.6670	2260.9791	3	-0.0006486	-0.2867	239572	42	60	130610_V3_P5_KB_BrxB_1_5.05862.05862.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.5648	0.6629	2	~(+396), IAM (+57)	754.6666	2260.9780	3	-0.001748	-0.7726	16,0028	42	60	130610_V3_P5_KB_BrxB_1_5.05927.05927.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	4.0554	0.7564	2	~(+396), IAM (+57)	754.6671	2260.9793	3	-0.0004656	-0.2058	88,924.90	42	60	130610_V3_P5_KB_BrxB_1_5.06031.06031.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.689	0.7073	2	~(+396), IAM (+57)	754.6668	2260.9786	3	-0.001199	-0.5299	48,751.50	42	60	130610_V3_P5_KB_BrxB_1_5.06685.06685.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.6412	0.6866	2	~(+396), IAM (+57)	754.6669	2260.9788	3	-0.001016	-0.449	40,367.40	42	60	130610_V3_P5_KB_BrxB_1_5.06728.06728.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.3639	0.6342	2	~(+396), IAM (+57)	754.6679	2260.9819	3	0.002097	0.9272	41,799.80	42	60	130610_V3_P5_KB_BrxB_1_5.07075.07075.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.4168	0.7204	2	~(+396), IAM (+57)	754.6673	2260.9801	3	0.0002664	0.1178	32,758.50	42	60	130610_V3_P5_KB_BrxB_1_5.07369.07369.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.3314	0.6307	2	~(+396), IAM (+57)	754.6674	2260.9804	3	0.0006324	0.2796	43,543.50	42	60	130610_V3_P5_KB_BrxB_1_5.07833.07833.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.3249	0.7019	2	~(+396), IAM (+57)	754.6675	2260.9806	3	0.0008154	0.3605	65,119.20	42	60	130610_V3_P5_KB_BrxB_1_5.08162.08162.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.5985	0.7397	2	~(+396), IAM (+57)	754.6671	2260.9793	3	-0.0004656	-0.2058	65,215.30	42	60	130610_V3_P5_KB_BrxB_1_5.08346.08346.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.5049	0.6345	2	~(+396), IAM (+57)	754.6677	2260.9813	3	0.001548	0.6845	56,668.40	42	60	130610_V3_P5_KB_BrxB_1_5.08389.08389.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.4963	0.6768	2	~(+396), IAM (+57)	754.6671	2260.9795	3	-0.0002826	-0.1249	37,543.00	42	60	130610_V3_P5_KB_BrxB_1_5.08430.08430.3.dta
(K)KGTTLVMVNSVcGcAGGIAR(P)	97%	3.3583	0.6423	2	~(+396), IAM (+57)	754.6667	2260.9784	3	-0.001382	-0.6108	52,593.10	42	60	130610_V3_P5_KB_BrxB_1_5.08514.08514.3.dta
<b>BrxB Cys52-SSB peptide 2</b>														
(K)IQEAEFEYCEEV(-)	99%	3.4316	0.8598	2	~(+396)	942.8557	1883.6969	2	0.0003417	0.1813	51,842.80	134	145	130610_V3_P5_KB_BrxB_2_6.06715.06715.2.dta
(K)IQEAEFEYCEEV(-)	99%	3.0351	0.962	2	~(+396)	942.8558	1883.6971	2	0.0005857	0.3108	14,4311	134	145	130610_V3_P5_KB_BrxB_2_6.06752.06752.2.dta
(K)IQEAEFEYCEEV(-)	99%	3.2967	0.8768	2	~(+396)	942.8557	1883.6969	2	0.0003417	0.1813	63,913.80	134	145	130610_V3_P5_KB_BrxB_2_6.06794.06794.2.dta
(K)IQEAEFEYCEEV(-)	98%	2.2245	0.7763	2	~(+396)	942.8560	1883.6974	2	0.0008297	0.4402	12,0520	134	145	130610_V3_P5_KB_BrxB_2_6.06863.06863.2.dta
(K)IQEAEFEYCEEV(-)	99%	2.8494	0.9073	2	~(+396)	942.8559	1883.6972	2	0.0007077	0.3755	25,277.10	134	145	130610_V3_P5_KB_BrxB_2_6.06972.06972.2.dta
(K)IQEAEFEYCEEV(-)	99%	2.8524	0.9192	2	~(+396)	942.8552	1883.6959	2	-0.0006353	-0.3371	14,645.00	134	145	130610_V3_P5_KB_BrxB_2_6.07082.07082.2.dta
(K)IQEAEFEYCEEV(-)	99%	2.9067	0.8804	2	~(+396)	942.8560	1883.6975	2	0.0009517	0.505	12,190.50	134	145	130610_V3_P5_KB_BrxB_2_6.07141.07141.2.dta
(K)IQEAEFEYCEEV(-)	99%	2.8557	0.9298	2	~(+396)	942.8547	1883.6948	2	-0.001733	-0.9197	18,188.30	134	145	130610_V3_P5_KB_BrxB_2_6.07226.07226.2.dta
(K)IQEAEFEYCEEV(-)	99%	3.188	0.8686	2	~(+396)	942.8575	1883.7004	2	0.003882					

**Table S4: Identification of Cys52-SSB in BrxB C54A and Cys53-SSB in BrxA C55A in vivo after immunoprecipitation**

**BrxB-Cys52-SSB**

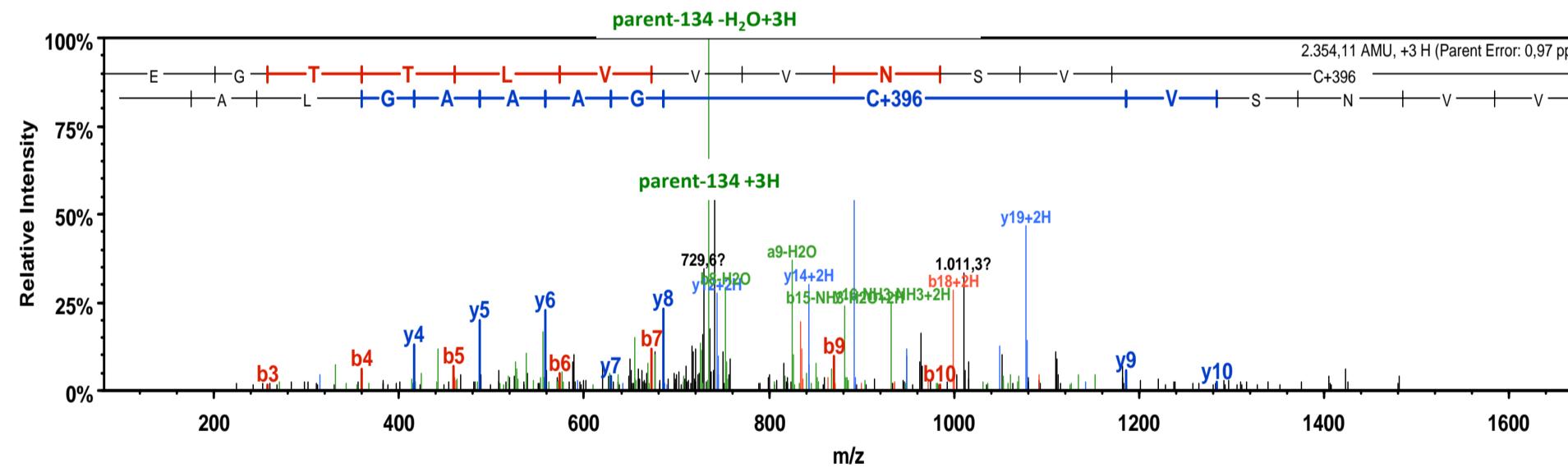
Sequence	Prob	SEQUEST XCorr	SEQUEST ΔCn	NTT	Modifications	Observed	Actual Mass	Charge	ΔAMU	ΔPPM	TIC	Start	Stop	Spectrum ID			
(K)GTTLVmVNSVcGAAGGIAR(P)	95%	3.0551	0.729	1	Ox (+16), ^ (+396)	730.3342	2187.9807	3	0.000076	0.03472	19,661.90	42	60	110328_OV3_P3_KG_HA_YqiWC54A_10.09955.09955.3.dta			



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	2,189.0	1,095.0	2,172.0	2,171.0	19
2	159.1			141.1	T	2,132.0	1,066.5	2,114.9	2,114.0	18
3	260.1		242.1	T	2,030.9	1,016.0	2,013.9	2,012.9	17	
4	373.2		355.2	L	1,929.9	965.4	1,912.8	1,911.9	16	
5	472.3		454.3	V	1,816.8	908.9	1,799.8	1,798.8	15	
6	619.3	310.2	601.3	M+16	1,717.7	859.4	1,700.7	1,699.7	14	
7	718.4	359.7	700.4	V	1,570.7	785.8	1,553.7	1,552.7	13	
8	832.4	416.7	815.4	N	1,471.6	736.3	1,454.6	1,453.6	12	
9	919.5	460.2	902.4	S	1,357.6	679.3	1,340.5	1,339.6	11	
10	1,018.5	509.8	1,001.5	1,000.5	V	1,270.5	635.8	1,253.5	10	
11	1,517.6	759.3	1,500.6	1,499.6	C+396	1,171.5	586.2	1,154.4	9	
12	1,574.6	787.8	1,557.6	1,556.6	G	672.4	336.7	655.4	8	
13	1,645.7	823.3	1,628.6	1,627.7	A	615.4	308.2	598.3	7	
14	1,716.7	858.9	1,699.7	1,698.7	A	544.3	272.7	527.3	6	
15	1,773.7	887.4	1,756.7	1,755.7	G	473.3		456.3	5	
16	1,830.8	915.9	1,813.7	1,812.7	G	416.3		399.2	4	
17	1,943.8	972.4	1,926.8	1,925.8	I	359.2		342.2	3	
18	2,014.9	1,007.9	1,997.8	1,996.9	A	246.2		229.1	2	
19	2,189.0	1,095.0	2,172.0	2,171.0	R	175.1		158.1	1	

**BrxA-Cys53-SSB**

Sequence	Prob	SEQUEST XCorr	SEQUEST ΔCn	NTT	Modifications	Observed	Actual Mass	Charge	ΔAMU	ΔPPM	TIC	Start	Stop	Spectrum ID			
(K)AEGTTLVVVNSVC <sub>53</sub> (+BSH)GAAAGLAR(P)	95%	2.4157	0.5477	1	^ (+396)	785.7110	2354.1112	3	0.002285	0.9702	7,578.04	41	61	110327_OV3_P3_KG_HA_YphPC55A_10.11736.11736.3.dta			



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	2,355.1	1,178.1	2,338.1	2,337.1	21
2	201.1			183.1	E	2,284.1	1,142.5	2,267.1	2,266.1	20
3	258.1			240.1	G	2,155.0	1,078.0	2,138.0	2,137.0	19
4	359.2			341.1	T	2,098.0	1,049.5	2,081.0	2,080.0	18
5	460.2			442.2	T	1,997.0	999.0	1,979.9	1,979.0	17
6	573.3	287.1		555.3	L	1,895.9	948.5	1,878.9	1,877.9	16
7	672.4	336.7		654.3	V	1,782.8	891.9	1,765.8	1,764.8	15
8	771.4	386.2		753.4	V	1,683.8	842.4	1,666.7	1,665.8	14
9	870.5	435.8		852.5	V	1,584.7	792.9	1,567.7	1,566.7	13
10	984.5	492.8		967.5	N	1,485.6	743.3	1,468.6	1,467.6	12
11	1,071.6	536.3	1,054.5	1,053.6	S	1,371.6	686.3	1,354.6	1,353.6	11
12	1,170.6	585.8	1,153.6	1,152.6	V	1,284.6	642.8	1,267.5		10
13	1,669.7	835.4	1,652.7	1,651.7	C+396	1,185.5	593.2	1,168.5		9
14	1,726.8	863.9	1,709.7	1,708.7	G	686.4	343.7	669.4		8
15	1,797.8	899.4	1,780.8	1,779.8	A	629.4	315.2	612.3		7
16	1,868.8	934.9	1,851.8	1,850.8	A	558.3	279.7	541.3		6
17	1,939.9	970.4	1,922.8	1,921.9	A	487.3		470.3		5
18	1,996.9	998.9	1,979.9	1,978.9	G	416.3		399.2		4
19	2,110.0	1,055.5	2,092.9	2,092.0	L	359.2		342.2		3
20	2,181.0	1,091.0	2,164.0	2,163.0	A	246.2		229.1		2
21	2,355.1	1,178.1	2,338.1	2,337.1	R	175.1		158.1		1

**Legend to Table S4:** BrxB C54A with the Cys52-SSB site (upper figure) and BrxA C55A with Cys53-SSB site (bottom figure) in vivo. FLAG-tagged BrxB C54A and BrxA C55A proteins were purified from *B. subtilis* cells after NaOCl-stress, separated by SDS-PAGE and the Brx bands tryptically digested. The resulting peptides were analyzed using LTQ Orbitrap Velos LC-MS/MS analysis as described in the Methods section (Chi et al., 2011). The Scaffold search results are shown and the Table includes the Xcorr, deltaCn scores, m/z of the precursor ions, neutral molecular masses of the peptides, peptide mass deviations (delta ppm) of the S-bacillithiolated Cys52 peptide in BrxB C54A and Cys53 in BrxA C55A. The CID MS/MS spectra are shown wth the b and y ion series labeled in red and blue, respectively.