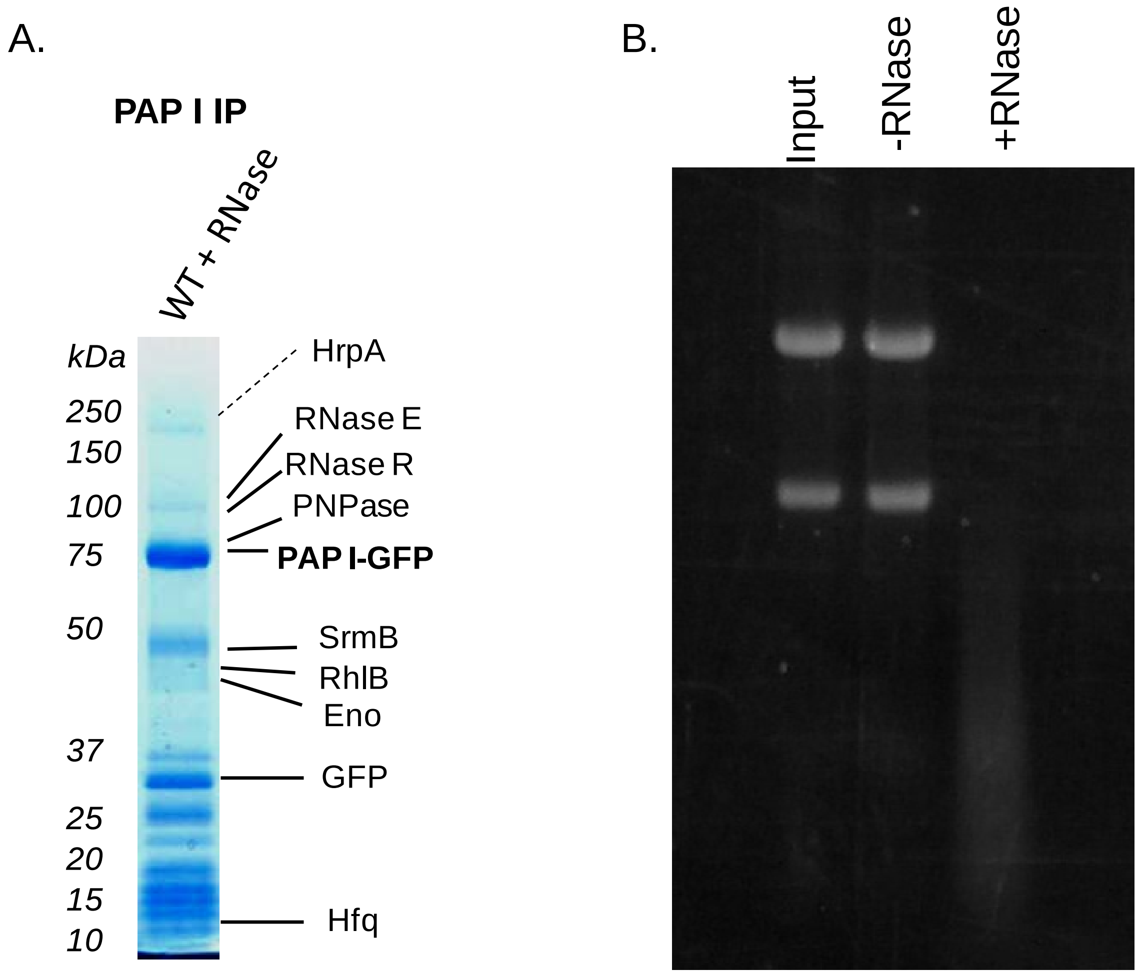
Appendix

Supplementary Figures

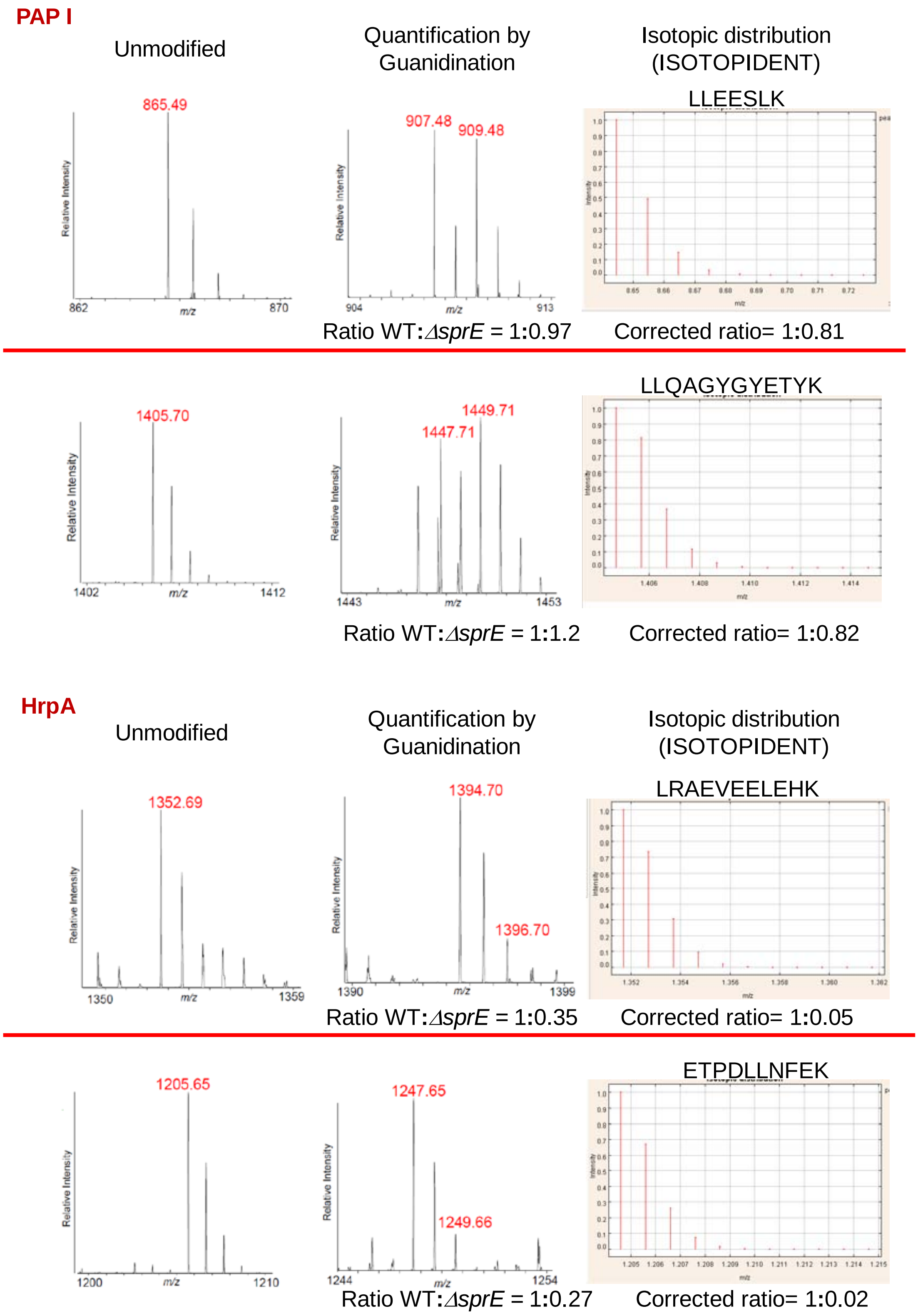
Supplementary Tables

Supplementary figure S1: *A GFP control immunopurification reveals non-specific interactions*

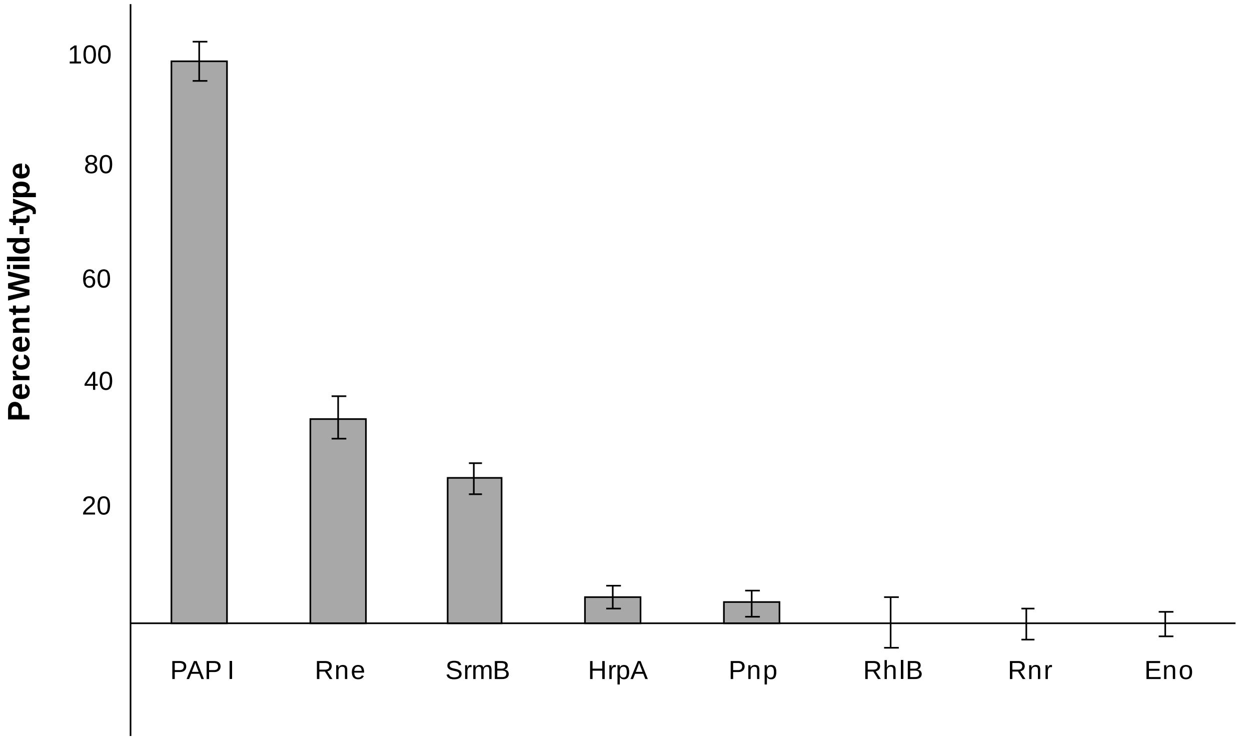
Supplementary figure S2: *PAP I-GFP immunopurification from wild-type cells in the presence of RNase A, during stationary phase*



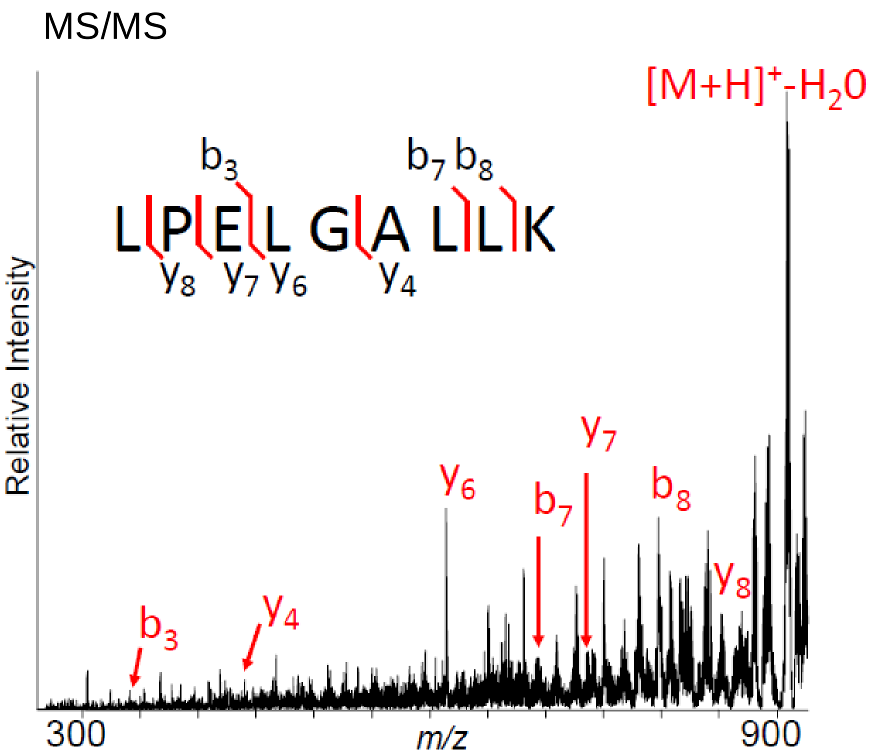
Supplementary figure S3: *Examples of the correction for the heavy labeled ΔsprE peptides*



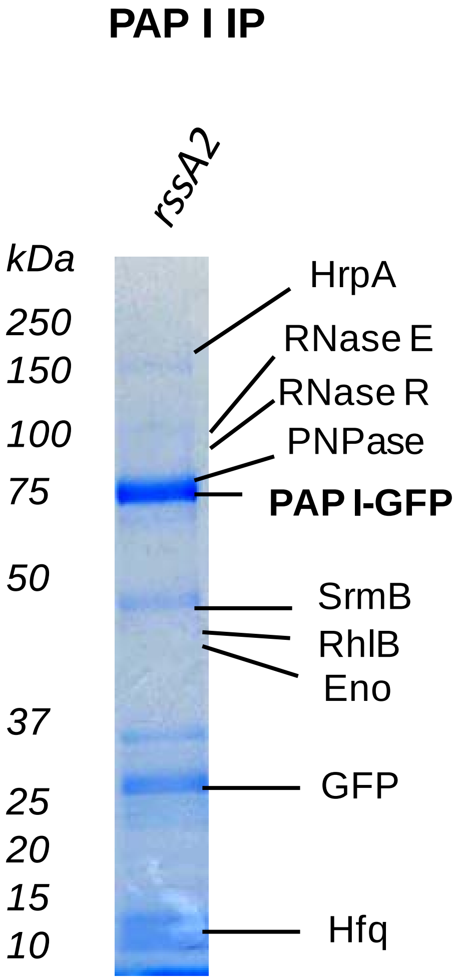
Supplementary figure S4: *Relative quantification of PAP I interacting partners using Lys-N digestion and switched isotopic labeling (ΔsprE peptides derivatized with [N^{14}]- and the wild-type peptides with [N^{15}]-O-methylisourea).*



Supplementary figure S5: *Single confirmed SprE peptide during stationary phase*



Supplementary figure S6: *PAP I-GFP immunopurification from cells overproducing SprE (rssA2)*



Supplementary Table S1: PAP I-GFP isolation from wild type cells

Protein Information		**Summary**		**Exponential Phase**				**Stationary Phase**			
Name	gi #	Exponential	Stationary	# peptides from MS	% sequence coverage	XProteo Score [d’]	Peptides confirmed by MS/MS	# peptides from MS	% sequence coverage	XProteo Score [d’]	Peptides confirmed by MS/MS
GFP-tag	93278674	+	+	11	43.1%	7.5	AEVKFEGDTLVNR SAMPEGYVQER GIDFKEDGNILGHK	10	32.5%	9.6	FEGDTLVNR TIFFKDDGNYK
PAP I	89107024	+	+	21	48.4%	30.6	AGYAEWLVGGGVR DIWQLQLR ISPETAEPIPR	22	45.7%	24.1	LATLLNDIAPPAR DNIFGSIEEDAQR
Rne	26247224	+	+	29	37.7%	22.5	IEPSLEAAFVDYGAER ALFSGGEETKPTEQPAPK	29	46.5%	22.7	GMLNELDEEPSPR ISPETAEPIPR DFDVTTNATPEQVR
Pnp	110643405	+	+	15	19.0%	11.2	GDISEFAPR IEEITAEIEVGR	22	45.7%	24.1	GDISEFAPR EGRPSEGETLIAR IEEITAEIEVGR
Eno	15803300	+	+	10	38.1%	3.5	IQLVGDDLFVTNTK FNQIGSLTETLAAIK	14	40.0%	3.8	IQLVGDDLFVTNTK AFTEEFTHFLEELTK
RhlB	148184	+	+	10	21.1%	4.9	VLESGVDILIGTTR LLQTLIEEEWPDR	13	31.3%	10.8	LLQTLIEEEWPDR YNPDALMTDLPKPLR
Hfq	15804761	+	+	3	15.5%	2.7	GQSLQDPFLNALR LQGQIESFDQFVILLK	3	15.5%	6.7	GQSLQDPFLANALRR GQSLQDPFLANALR AKGQSLQDPFLANALR
HrpA	75239959	+	+	20	12.5%	N/O	ERGSLQDLK YVIDPGTAR SLNIDFLLGYLK	43	24.7%	24.3	YVIDPGTAR YRPIVEEADDTER
Rnr	83585083	+	+	10	5.5%	N/O	EFILEHLTK DLPVTIDGEDAR EFILEHLTKR	26	36.7%	23.9	EFILEHLTK VNFEPDSAFR DLPLVTIDGEDAR
SmrB	75234075	+	+	16	36.9%	11.7	VHELANWLR LLEDPVEVSANPSTR	23	50.3%	18	GIDIPDVSHVFNFDMPR AVETLILDEADR LLEDPVEVSANPSTR
CsdA*	75176236	-	+	-	-	-	-	33	55.2%	37.2	FLEAEDFDAAIIFVR VQQQLESSDLDQYR ALLFVENR
SprE	26247564	-	?	-	-	-	-	3	5.00%	N/O	LPELAGLLK
RpoC	223476	+	+	29	21.2%	15.4	* See GFP control pullout	36	21.5%	17.7	*See GFP control pullout

RpoB	15804577	+	+	30	23.3%	13.4		32	18.5%	13.4	
AceE	434010	-	+	-	-	-		26	31.1%	23.6	
AdhE	15801467	-	+	-	-	-		21	28.8%	14.7	
PflB	15800764	-	+	-	-	-		25	26.1%	9.8	
DnaK	75235743	+	+	17	31.3%	2.5		20	29.3%	6.1	
RpsA	223404	+	+	29	50.0%	38.1		22	46.2%	19	
OppA	147014	-	+	-	-	-		20	42.6%	13.4	
EF-Tu	26249935	+	+	20	69.0%	19.4		22	58.3%	17.3	
GatZ	75196143	-	+	-	-	-		12	31.6%	2.2	
Pgk	1942721	-	+	-	-	-		18	52.8%	7.4	
SucC	115512045	-	+	-	-	-		14	38.0%	2.8	
Mdh	91074230	-	+	-	-	-		12	41.2%	N/O	
EF-G	33357902	+	+	15	55.8%	10.4		20	67.6%	5.2	
RbsB	3318870	-	+	-	-	-		14	59.2%	6.8	
GatY	7436618	-	+	-	-	-		12	59.2%	4.1	
RplL	223571	+	+	22	67.0%	23.3		14	52.7%	2.2	
RpsC	15803841	+	+	10	38.9%	1.9		16	51.3%	8.5	
RplA	81247737	+	+	15	71.1%	15.2		10	49.8%	3.0	
RplD	115514721	-	+	-	-	-		8	42.6%	2.5	
Dps	91071421	-	+	-	-	-		16	74.9%	12.1	
RplI	110346152			11	70.7%	6.2		16	70.0%	16.8	
RplQ	15803821	-	+	-	-	-		7	43.8%	2.7	
RpsI	223001	-	+	-	-	-		8	48.8%	2.3	
RplO	606235	-	+	-	-	-		7	44.1%	N/O	
RplS	15803128	-	+	-	-	-		11	69.0%	2.7	
RplY	12516517	+	-	11	75.8%	N/O		9	55.8%	N/O	
AtpB	112791342	+	-	12	35.3%	3.7		-	-	-	
Rho	15833970	+	-	15	39.8%	6.2		-	-	-	
PrsA	75228259	+	-	13	45.9%	7.6		-	-	-	
RplB	15803844	+	-	18	47.8%	10.4		-	-	-	
RpsB	26246115	+	-	14	56.2%	11.6		-	-	-	
RplM	15803765	+	-	15	79.7%	16.2		-	-	-	
RpsJ	15803848	+	-	10	57.7%	N/O		-	-	-	

Supplementary Table S2: Control GFP isolations

Name	gi #	# of peptides from MS	% sequence coverage	XProteo Score [d']	Peptides confirmed by MS/MS
GFP	1277124	12	48.10%	5.8	AEVKFEGDTLVNR FSVSGEGEGDATYGK
AdhE	15801467	24	34.30%	14.8	IAELAGFSVPENTK AVTNVAELNALVER
RpoB	110345914	43	35.90%	25.4	FIEQDPEGQYGLEAAFR STGSYSLVTQQPLGGK LIEVPVEYIAGK
RpoC	85676082	46	37.10%	35.1	VIDIWAAANDR VTAEDVLKPGTADILVPR LGIQAFEPVLIEGK
PheT	73855444	15	22.70%	N/O	IGFVGVVHPELER IEGGIVVR LDDNTIEISVTPNR
EF-G	223649	37	71.70%	24.5	GGVIPGEYIPAVDK IATDPFVGNLTFFR
TnaA	91074807	23	53.20%	26.6	AVEIGSFLLGR GNFDLEGLER
AceE	99032369	19	44.70%	17.7	FNIDADKVNPR AQYLIDQLLAEAR
PflB	6730181	13	53.70%	22.9	TSTFLDVYIER SGVLTGLPDAYGR
GroEL	61679908	-	-	-	AAVEEGVVAGGGVALIR DTTTIIDGVGEEAAIQGR
PtsA	110344192	23	39.20%	4.8	ALLLKEDEIVIDR EENPFLGWR
AtpA	148137	19	47.10%	8.0	EAFPGDVFYLHSR DRGEDALIIYDDLSK
AtpB	75197628	18	50.80%	10.3	DVLLFVDNIYR QLDPLVVGQEHYDTAR
ThrS	75195791	19	26.10%	9.4	TLTQEDVEALEKR
Pck	1943496	17	44.00%	4.1	VIFLTADAFGVLPPVSR EAEPEIYAAIRR
TreC	12519243	24	39.10%	10.2	DGEPETPPNNWR, NDGRDADELLAILASK
GadB	81245467	16	31.90%	6.2	YWDVELR LKDGEDPGYTLYDLSER
PykF	110641972	18	48.60%	4.3	TAALIGVDYLAVSFPR TAAILLDTKGPEIR
LysU	9954999	31	54.90%	20.5	GANEAIDFNDELR WDLGDIIGAR
DnaK	75194239	23	40.30%	17.6	SLGQFNLDGINPAPR VAEFFGKEPR
RpsA	110614467	25	64.00%	23.6	GATVELADGVEGYLR AFLPGSLVDVRPVR
OppA	147014	19	37.30%	2.0	TFLDTR VTDEAHGTALYTKAEQQLDK
Oma87	75226693	20	29.30%	11.4	DIHFEGLQR GLEDFYYSVGK
PutA	115512334	30	21.30%	N/O	ATRDALIR VMEELYPR AQMDGLEGYPVYTR
Pgk	26249339	16	61.10%	12.9	DYLDGDVAEGELVVLENVR SLYEADLVDEAKR
OmpF	6729727	10	53.40%	10.7	NSNFFGLVDGLNFAVQYLGK YADVGSFDYGR
GapA	146099	11	44.10%	13.9	AGIALNDNFVK VPTPNVSVVDLTVR
FbaA	12517457	10	40.40%	6.3	ANEAYLQGQLGNPK LLPWIDGLLDAGEK
Rho	25299646	20	45.90%	14.8	VNEVNFDKPENAR VLTGGVDANALHRPK
SucC	110342528	15	37.30%	14.2	GLTDAAQQVVAAVEGK LGADGNALFR
Gnd	146940	15	30.50%	5.7	AGAGTDAAIDSLKPYLDK DYFGAHTYKR EFVESLETPRR
EF-Tu	110345172	37	61.00%	24.5	GITINTSHVEYDTPTR VGEEVEIVGIKETQK
GatZ	91211381	13	41.60%	7.8	EAIFALAQIEQELIAPENR TGFNDSLLDIR
rpsC	12517946	11	52.60%	N/O	VVADIAGVPAQINIAEVR KVVADIAGVPAQINIAEVR
OmpA	51235578	12	51.90%	16.2	LGYPITDDLDIYTR SDVLFNFNK

GatY	89108914	11	59.60%	4.7	SVMIDASHLPFAQNISR VKEVVDFCHR
Mdh	1455852	16	61.70%	1.7	LFGVTTLDIIR SDLFNVAGIVK
Prs	75255057	-	-	-	VVADFLSSVGVDR LFAGNATPELAQR
RplF	110616701	-	-	-	GADKQVIGQVAADLR HADNTLTFGPR
GpmM	75189769	10	41.00%	N/O	VIPYWNETILPR FTGWYDVDLSEK
Icd	33383669	14	42.90%	6.7	DVIADAFLQQILLR TVTYDFER
DapD	26246112	13	49.50%	9.5	EAVNQVIALLDSGALR FADYDEAR
RplA	110617382	9	47.60%	N/O	FVESVDVAVNLGIDAR SDQNRGATVLPHGTGR
RbsB	576079	11	53.30%	5	FNVLASQPADFDR ILLINPTDSDAVGNAVK
RpsB	110341980	9	51.90%	N/O	MATVSMRDMLK TVPMFNEALAELNK
Dps	85376196	14	78.40%	4.8	DLDKFLWFIESNIE GANFIAVHEMLDGFR AVQLGGVALGTTQVINSK
RplJ	110345912	-	-	-	AAAFEGELIPASQIDR LATLPTYEEAIAR
RplE	110345139	-	-	-	LLDNAAADLAAISGQKPLITK ALLAAFDFPFRK
RplM	91212650	11	66.40%	N/O	VYAGNEHNHAAQQPQVLDI DWYVVDATGK
OmpX	81244671	10	73.30%	N/O	INDWASIYGVVGVGYGK SVDVGTWIAGVGYR
RplP	83584670	-	-	-	VLYEMDGVPEELAR GLAQGTDVSFGSFGLK
DeoD	110346413	12	56.30%	3.1	FKDHDFAAIADFDMVR YIAETFLEDAR
OmpC	9714150	16	65.40%	9.2	YVDVGATYYFNK FQDVGSFDYGR
OmpW	88192838	8	53.50%	N/O	DSWGAAGQVGVDYLINR HEAGEFFMR
NarG	75235264	17	15.50%	12.1	AYTPAWAEQITGVSR EFHLDNPSQYFTDYVR DFGESLLVYRPPIDTR
GyrA	290547	24	36.50%	11.6	GLLEEDAFIER DGKEDHFHYEGGIK
TktA	115514288	17	31.60%	8.8	AYPQEAAEFTR TEEQLANIAR
GlmS	290577	25	45.20%	9.3	DVAEILLEGLR FIFLEEGDIAEITR
ProRS	227122	21	40.00%	4.7	TGDIVEYLVK TIAELVEQFNLPIEK
BtuB	145440	20	50.10%	2.4	YDKDYSSYPYQTVK SKQWEGAFEGLTAGVNWR
GlpK	1134966	16	35.30%	6.1	MLEVLDIPR VKWILDHVEGSR
AspC	1127182	8	17.60%	1.9	LREEFGVYAVASGR GLEEDAEGLR
ManX	15802230	17	54.60%	1.7	IIVVSDEVAADTVR DDDPSFDELVALAVETGR
AccA	26246132	14	41.20%	N/O	LAFDEFDELAGDR LIDSIIPEPLGGAHR
Tsx	26246416	11	44.10%	1.9	NDTYLEYEAFAK FSIDKLTNTDLSFGPFK LTNTDLSFGPFK
RplC	15803847	11	58.60%	2.6	DYLANDGYR VTKPEAGHFAK
AhpC	15800320	13	60.10%	1.7	YAMIGDPTGALTR LGVDVYAVSTDTHFTHK
RplI	15804792|	9	52.70%	N/O	NIEFFEAR AGDEGKLFGSIGTR

Supplementary Table S3: *PAP I-GFP isolation from wild type cells in the presence of RNase*

	gi number	**# of peptides from MS**	**% Sequence Coverage**	**XProteo score [d']**	**Peptides confirmed by MS/MS**
PAP I	89107024	24	42.9%	36.1	LATLLNDIAPPAR DNIFGSIEEDAQR
RNase E	26247224	30	43.4%	33.3	ISPETAEPIPR DFDVTTNATPEQVR
RNase R	83585083	31	34.3%	34.2	GDISEFAPR IEEITAEIEVGR
PNPase	110643405	14	20.0%	13.2	EFILEHLTK DLPLVTIDGEDAR
HrpA	75239959	10	6.5%	N/O	YVIDPGTAR ERGSLQDLK
SrmB	75234075	12	25.0%	10.2	AVETLILDEADR LLEDPVEVSANPSTR
Eno	15803300	6	14.0%	3.6	IQLVGDDLFVTNTK AFTEEFTHFLEELTK
RhlB	148184	10	20.5%	8.5	LLQTLIEEEWPDR VLESGVDILIGTTR
Hfq	15804761	4	20.0%	3.7	GQSLQDPFLANALRR GQSLQDPFLANALR AKGQSLQDPFLANALR

Supplementary Table S4: PAP I-GFP isolation in *ΔsprE* cells

Protein Information		**Summary**		**Exponential Phase**				**Stationary Phase**			
Name	gi #	Exponential	Stationary	# peptides from MS	% sequence coverage	XProteo Score [d’]	Peptides confirmed by MS/MS	# peptides from MS	% sequence coverage	XProteo Score [d’]	Peptides confirmed by MS/MS
GFP-tag	26892271	+	+	10	40.6%	7.5	AEVKFEGDTLVNR TIFFKDDGNYK GIDFKEDGNILGHK	10	45.6%	2.9	TIFFKDDGNYK AEVKFEGDTLVNR
PAP I	89107024	+	+	26	54.1%	30.2	AGYAEWLVGGGVR DIWQLQLR AAYDLLALR	30	55.8%	35.8	DNIFGSIEEDAQR AAYDLLALR
Rne	16129047	+	+	35	41.4%	22.8	IEPSLEAAFVDYGAER SAEALQWDLSFR	17	17.0%	N/O	DNESLSLSILR SAEALQWDLSFR
Pnp	110643405	+	-	15	23.0%	9.1	GDISEFAPR IEEITAEIEVGR EGRPSEGETLIAR	-	-	-	-
Eno	563868	+	-	12	33.1%	N/O	IQLVGDDLFVTNTK FNQIGSLTETLAAIK	-	-	-	-
RhlB	148184	+	-	14	39.8%	5.1	DIRWLFR MYDLGFIKDIR IKEELFYPSNEEK	-	-	-	-
Hfq	15804761	+	+	3	30.1%	2.8	GQSLQDPFLNALR LQGQIESFDQFVILLK AKGQSLQDPFLNALR	2	14.6%	1.8	AKGQSLQDPFLNALR GQSLQDPFLNALR
HrpA	49176106	+	+	19	12.7%	N/O	ERGSLQDLK HALVEGDWQTR EVWMIEELR	19	9.7%	N/O	ESDLLAFVNLWNYLGEQQK YVIDPGTAR
Rnr	91214001	+	-	10	5.5%	N/O	EKVVLDDDVFK	-	-	-	-
RpoC	409789	+	+	34	23.6%	19.6	* See GFP control isolation	48	30.1%	35.2	*See GFP control isolation
RpoB	15804577	+	+	37	26.7%	18.6		46	31.4%	32.8	
AceE	434010	+	+	25	24.9%	17		31	35.4%	25.3	
AdhE	15801467	-	+	-	-	-		32	38.6%	30.2	
PflB	15800764	+	+	13	13.3%	N/O		36	45.8%	29.3	
TnaA	41936	-	+	-	-	-		19	37.9%	14.4	
RpsA	223404	+	+	25	43.4%	22.2		24	50.9%	21.6	
EF-Tu	26249935	+	+	20	58.0%	16		25	47.8%	19.3	

RpoA	42812	+	-	11	42.7%	10.1		-	-	-	
Pgk	1942721	-	+	-	-	-		17	64.5%	2.5	
OmpF	26246956	-	+	-	-	-		14	54.5%	11	
OmpC	16130152	+	+	10	42.7%	4.9		15	56.0%	12.5	
EF-G	33357902	+	+	22	67.4%	25.6		12	42.7%	9.2	
RpsD	15803823	+	-	10	37.2%	2.3		-	-	-	
RplL	223571	+	+	14	37.7%	2.3		15	50.2%	2.1	
RpsC	15803841	+	+	6	28.6%	N/O		9	41.5%	2.5	
RplA	15804574	+	+	8	35.7%	N/O		9	43.0%	N/O	
RplD	15803846	+	-	10	51.0%	2.1		-	-	-	
Dps	91071421	-	+	-	-	-		10	50.3%	2.9	
RplI	15804792	+	+	12	74.7%	13.4		10	55.3%	6.8	
RplQ	16131180	+	+	12	69.7%	9.4		7	39.1%	N/O	
RpsK	15803824	+	-	9	66.2%	6.8		-	-	-	
RpsJ	15803848	+	+	10	60.6%	6.3		10	72.1%	2.8	
RplY	15802741	+	+	11	87.4%	12.6		8	55.8%	N/O	
OmpX	30749947	+	+	8	58.4%	3.8		8	62.8%	4.5	
Rho	15833970	+	-	16	25.7%	6.6		-	-	-	
PrsA	75228259	+	+	15	45.4%	11.2		13	37.0%	3.1	
RplB	15803844	+	-	8	27.7%	N/O		-	-	-	
RpsB	26246115	+	-	6	32.5%	N/O		-	-	-	
RplM	15803765	+	+	16	72.7%	21.6		10	61.5%	8.0	
RplJ	15804575	+	+	6	44.0%	N/O		9	57.2%	2.4	
RplC	15803847	+	-	17	66.7%	10.3		-	-	-	
DnaK	75235743	-	+	-	-	-		12	22.8%	2.5	
AtpA	15804334	-	+	-	-	-		15	39.3%	7.5	
AtpB	15804332	-	+	-	-	-		17	38.6%	8.7	
LysU	7523127	-	+	-	-	-		21	32.2%	11.3	
PykF	1310978	-	+	-	-	-		17	47.8%	12.5	
PckA	1942693	-	+	-	-	-		14	31.4%	3.6	
TreC	16132061	-	+	-	-	-		12	23.7%	2.8	
GapA	1421424	-	+	-	-	-		17	57.1%	11.6	
RplE	15803835	-	+	-	-	-		10	56.7%	5.1	

Supplementary Table S5: Detection of Interacting partners in Flow Through

		Wild-type			**Peptides confirmed by MS/MS[a]**	***ΔsprE***		
Name	**gi #**	**# peptides from MS**	**% sequence coverage**	**XProteo Score [d’]**		**# peptides from MS**	**% sequence coverage**	**XProteo Score [d’]**
Rne	26247224	39	42.2%	8.7	GMLNELDEEPSPR ISPETAEPIPR DFDVTTNATPEQVR	25	29.9%	12.1
Pnp	110643405	27	43.7%	12.3	GDISEFAPR EGRPSEGETLIAR IEEITAEIEVGR	20	33.0%	7.0
Eno	15803300	13	35.1%	N/O	IQLVGDDLFVTNTK FNQIGSLTETLAAIK	11	29.4%	N/O
RhlB	148184	8	14.0%	N/O	LLQTLIEEEWPDR YNPDALMTDLPKPLR	5	10.3%	N/O
HrpA	75239959	50	26.5%	7.7	ERGSLQDLK YVIDPGTAR	35	24.1%	N/O
Rnr	83585083	35	23.7%	4.2	EFILEHLTK VNFEPDSAFR DLPLVTIDGEDAR	29	22.0%	7.3
SmrB	75234075	8	15.5%	N/O	VHELANWLR LLEDPVEVSANPSTR	5	13.3%	N/O

[a] The same peptides were confirmed for both strains.

Supplementary Table S6: *PAP I-GFP isolation from rssA2 cells*

	gi number	**# of peptides from MS**	**% Sequence Coverage**	**XProteo score [d']**	**Peptides confirmed by MS/MS**
PAPI	89107024	29	50.0%	25.9	AAYDLLALR GMLNELDEESPR
RNase E	16129047	7	10.2%	3.3	APAPEYVPEAPR SAEALQWDLSFR IEPSLEAAFVDYGAER
RNase R	83585083	22	25.2%	9.3	FDQVGQR AKEPALFR DLPLVTIDGEDAR
PNPase	75187972	13	14.9%	5.5	GDISEFAPR IEEITAEIEVGR
HrpA	75190465	16	17.2%	10.2	EGRSLQDLK ESDFLAFVNLWNYLGEQQK
SmrB	15832696	21	52.8%	20.9	GGVDVLVATPGR AVAEQGYR
Eno	15803300	10	35.0%	4.6	IQLVGDDLFVTNTK AFTEEFTHFLEELTK
RhlB	148184	7	12.3%	0.8	VLESGVDILIGTTGR EELFYPSNEEKMR
Hfq	15804761	2	15.0%	1.2	GQSLQDPFLANALR AKGQSLQDPFLANALR
SprE	26247564	-	-	-	LPELAGLLK

Supplementary Table S7: *PAP I-GFP isolation from ΔrpoS cells*

	gi number	**# of peptides from MS**	**% Sequence Coverage**	**XProteo score [d']**	**Peptides confirmed by MS/MS**
PAP I	89107024	29	48.5%	42.8	LATLLNDIAPPAR DNIFGSIEEDAQR
RNase E	26247224	11	13.3%	9.9	ISPETAEPIPR DFDVTTNATPEQVR
RNase R	83585083	21	20.4%	27.3	EFILEHLTK DLPLVTIDGEDAR
PNPase	110643405	15	26.8%	18	GDISEFAPR EGRPSEGETLIAR
HrpA	75239959	25	27.6%	15.5	YVIDPGTAR YRPIVEEADDTER
SrmB	75234075	15	30.0%	14.3	AVETLILDEADR LLEDPVEVSANPSTR
Eno	15803300	7	15.9%	4.6	IQLVGDDLFVTNTK AFTEEFTHFLEELTK
RhlB	148184	12	25.0%	4	LLQTLIEEEWPDR YNPDALMTDLPKPLR
Hfq	15804761	3	18.0%	3.2	GQSLQDPFLANALRR GQSLQDPFLANALR AKGQSLQDPFLANALR