

**Supplementary material S1. Proteins identified in the IB-AuNPs of *S. pneumoniae* TIGR4 strain**

Cellular location	Row	Scores	MW [kDa]	Peptides	Accession number	Protein name	Molecular function	Chemical nature
	1	656.4	86.8	14	PEPX_STRP2	Xaa-Pro dipeptidyl-peptidase	Aminopeptidase, Hydrolase, Protease, Serine protease	
	2	2837.5	76.8	45	EFG_STRPN	Elongation factor G	Elongation factor	
	3	124.8	57.1	3	CH60_STRP2	60 kDa chaperonin	Chaperone	
	4	118.2	57.0	2	CH60_STRPI	60 kDa chaperonin	Chaperone	
	5	387.0	49.8	7	G6PI_STRPS	Glucose-6-phosphate isomerase	Isomerase	
	6	292.2	48.4	6	MURD_STRPS	UDP-N-acetylmuramoylalanine--D-glutamate ligase	Ligase	
	7	95.5	45.8	2	MURA1_STRPN	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	Cell cycle, Cell division, Cell shape, Cell wall biogenesis/degradation, Peptidoglycan synthesis	
	8	111.1	44.7	2	RECA_STRPS	Protein RecA	DNA damage, DNA recombination, DNA	

						repair, SOS response	
9	111.1	44.7	2	PEPT_STRPS	Peptidase T	Aminopeptidase, Hydrolase, Metalloprotease, Protease	
10	1744.3	43.9	28	EFTU_STRPI	Elongation factor Tu	Elongation factor	
11	1230.4	43.9	18	RS1_STRR6	30S Ribosomal protein S1	Ribonucleoprotein, Ribosomal protein, RNA-binding	Phosphoprotein
12	200.9	42.0	4	DPO3B_STRR6	DNA polymerase III subunit beta	DNA-directed DNA polymerase, Nucleotidyltrans ferase, Transferase	
13	557.5	41.9	11	RECA_STRPI	Protein RecA	DNA damage, DNA recombination, DNA repair, SOS response	
14	989.4	41.9	6	PGK_STRPN	Phosphoglycerate kinase	Kinase, Transferase	
15	877.4	37.6	16	ASNA_STRPI	Aspartate--ammonia ligase	Ligase	
16	794.6	35.2	14	PFKA_STRPJ	ATP-dependent 6- phosphofructokinase	Kinase, Transferase	

	17	718.7	35.2	13	PFKA_STRP2	ATP-dependent 6-phosphofructokinase	Kinase, Transferase	
	18	155.0	34.9	3	PLSX_STRZP	Phosphate acyltransferase	Transferase	
	19	103.5	33.5	3	PPAC_STRPI	Probable manganese-dependent inorganic pyrophosphatase	Hydrolase	
<b>Membrane</b>	20	955.1	72.2	10	STKP_STRPN	Serine/threonine-protein kinase StkP	Kinase, Serine/threonine-protein kinase, Transferase	Phosphoprotein
	21	333.7	50.9	5	ATPB_STRP4	ATP synthase subunit beta	ATP synthesis, Hydrogen ion transport, Ion transport, Transport	
	22	207.6	34.6	4	MTSA_STRPN	Manganese ABC transporter substrate-binding lipoprotein	Transport	Lipoprotein
	23	115.0	34.4	3	PRSA_STRPN	Foldase protein PrsA	Isomerase, Rotamase	Lipoprotein
	24	537.4	34.4	10	PRSA_STRPI	Foldase protein PrsA	Isomerase, Rotamase	Lipoprotein
<b>Cell surface, secreted and cytoplasm</b>	25	1581.2	47.1	23	ENO_STRPI	Enolase	Lyase	

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<b>No data</b>	26	157.4	64.8	3	DNAK_STRP4	Chaperone protein DnaK	Chaperone Phosphoprotein
	27	874.7	49.1	17	DER_STRPI	GTPase Der	Ribosome biogenesis
	28	236.0	36.3	6	LACD_STRPN	Tagatose 1,6-diphosphate aldolase	Lyase
	29	233.3	35.9	5	GUAC_STRP4	GMP reductase	Oxidoreductase

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**Supplementary material S1. Proteins identified in the IB-AuNPs of *S. pneumoniae* R6 strain**

Cellular location	Row	Scores	MW [kDa]	#Peptides	Accession	Protein name	Molecular function	Chemical nature
	1	372.1	100.8	11	SYV_STRR6	Valine--tRNA ligase	Aminoacyl-tRNA synthetase, Ligase	
	2	537.6	96.4	12	SYA_STRPI	Alanine--tRNA ligase	Aminoacyl-tRNA synthetase, Ligase, RNA-binding, tRNA-binding	
	3	2798.4	76.8	47	EFG_STRPN	Elongation factor G	Elongation factor	
	4	1313.1	63.4	25	SYR_STRZP	Arginine--tRNA ligase	Aminoacyl-tRNA synthetase, Ligase	
	5	559.6	62.0	12	DEXB_STRPN	Glucan 1,6-alpha-glucosidase	Glycosidase, Hydrolase	
	6	132.9	59.2	3	PYRG_STRR6	CTP synthase	Ligase	
	7	821.9	58.0	17	MALQ_STRPN	4-alpha-glucanotransferase	Glycosyltransferase, Transferase	
	8	944.5	57.1	16	CH60_STRZP	60 kDa chaperonin	Chaperone	
	9	526.7	51.7	12	DNAA_STRZP	Chromosomal replication initiator protein DnaA	DNA replication	

10	196.2	49.3	3	GLMU_STRP4	Bifunctional protein GImU	Acyltransferase, Nucleotidyltransferase, Transferase	
11	959.6	48.4	18	OBG_STRP2	GTPase Obg OS	Hydrolase	
12	909.8	47.5	16	SYU_STRPJ	Tyrosine--tRNA ligase	Aminoacyl-tRNA synthetase, Ligase, RNA-binding	
13	319.3	45.8	7	MURA1_STRPN	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	Cell cycle, Cell division, Cell shape, Cell wall biogenesis/degradation, Peptidoglycan synthesis	
14	1902.1	43.9	30	EFTU_STRPI	Elongation factor Tu	Elongation factor	
15	1297.6	43.9	25	RS1_STRR6	30S Ribosomal protein S1	Ribonucleoprotein, Ribosomal protein, RNA-binding	Phosphoprotein
16	142.4	42.0	3	DPO3B_STRR6	DNA polymerase III subunit beta	DNA-directed DNA polymerase, Nucleotidyltransferase, Transferase	
17	460.1	41.9	9	RECA_STRPI	Protein RecA	DNA-binding	
18	678.8	41.9	9	RECA_STRPS	Protein RecA	DNA damage, DNA recombination, DNA repair, SOS response	

	19	117.4	39.8	2	PROB_STRPI	Glutamate 5-kinase	Kinase, Transferase	
	20	1166.7	37.6	18	ASNA_STRP2	Aspartate--ammonia ligase	Ligase	
	21	354.6	35.4	7	KPRS1_STRPN	Ribose-phosphate pyrophosphokinase 1	Kinase, Transferase	
	22	566.1	35.3	8	KPRS2_STRPN	L-lactate dehydrogenase	Oxidoreductase	
	23	614.7	30.2	12	DIV4A_STRR6	Cell division protein DivIVA	Cell cycle, Cell division, Cell shape, Septation	Phosphoprotein
<b>Membrane</b>	24	1055.6	72.2	19	STKP_STRPN	Serine/threonine-protein kinase StkP	Kinase, Serine/threonine- protein kinase, Transferase	Lipoprotein
	25	184.1	60.8	3	MLTG_STRP2	Endolytic murein transglycosylase	Lyase	
	26	684.0	59.8	12	RNY_STRPN	Ribonuclease Y	Endonuclease, Hydrolase, N uclease, RNA-binding	
	27	525.8	50.9	11	ATPB_STRP4	ATP synthase subunit beta	ATP synthesis, Hydrogen ion transport, Ion transport, Transport	



	28	920.0	45.3	17	MALX_STRR6	Maltose/maltodextrin-binding protein	Sugar transport, Transport	
	29	159.1	34.6	4	MTSA_STRPN	Manganese ABC transporter substrate-binding lipoprotein	Transport	Lipoprotein
	30	374.4	34.4	6	PRSA_STRPN	Foldase protein PrsA	Isomerase, Rotamase	Lipoprotein
	31	452.4	30.4	11	PRSA_STRPI	Foldase protein PrsA	Isomerase, Rotamase	Lipoprotein
<b>Cell surface, secreted and cytoplasm</b>	32	1581.2	47.1	23	ENO_STRPI	Enolase	Lyase	
	33	1868.2	65.2	24	POXB_STRPN	Pyruvate oxidase	Oxidoreductase	
	34	227.0	59.8	5	ILVD_STRPI	Dihydroxy-acid dehydratase	Lyase	
<b>No data</b>	35	320.5	49.1	6	DER_STRPI	GTPase Der	Ribosome biogénesis	
	36	628.4	45.8	12	CLPX_STRPN	ATP-dependent Clp protease ATP-binding subunit ClpX	Chaperone	
	37	411.3	45.0	7	CINA_STRR6	Putative competence-damage inducible protein	No data	

