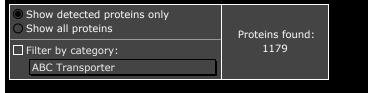
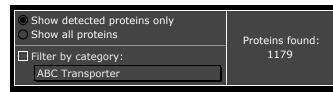
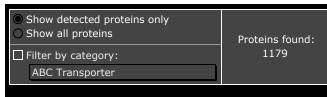
Cover	age							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 1
		Sg		SgFn	9	SgPg	Sg	<sub>I</sub> PgFn				Sg	SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0001	16 24	48.2% 57.3%	7 10	26.0% 34.2%	9	33.3% 32.9%	7	15.6% 26.4%	dnaA; chromosomal r	eplication initiator pr	otein DnaA				
SGO_0002	9	27.5% 30.7%	7	24.9% 27.8%	11 11	35.4% 33.3%	4	11.9% 11.9%	dnaN; DNA polymeras	se III, beta subunit					44
SGO_0004	15	62.2% 59.3%	11	51.7% 35.5%	11 12	52.3% 52.9%	8	43.6%	putative lipoprotein						
SGO_0005	8	10.9% 16.0%							hypothetical protein S	GGO_0005		01			
SGO_0006	17 20	41.5% 44.8%	17 15	44.8% 43.5%	21 18	52.2% 45.7%	10 9	26.7% 26.7%	ABC transporter, ATP-	-binding protein					
SGO_0007	8	34.7% 35.0%	7	28.8% 29.7%	9	34.4% 34.7%	7 5	28.2% 20.6%	trpS; tryptophanyl-tR	NA synthetase					••
SGO_0008	23 26	54.8% 58.2%	22 26	62.9% 64.5%	30 28	77.7% 70.4%	20 20	52.3% 57.0%	inosine-5'-monophosp	phate dehydrogenase	2				
SGO_0011	7	22.7% 27.2%	5	17.6%	3 4	11.3% 11.6%	8	25.1% 13.7%	proteinase, M16 famil	у		•		00	
SGO_0012	3	8.4%	3	13.7% 17.2%					mpp; peptidase, M16	family		04			
SGO_0013	4 5	18.1% 21.0%			4	18.1%			hypothetical protein S	GGO_0013		01		••	
SGO_0015	8	41.6% 42.3%	3	15.0%	5 6	24.8%	3	15.7%	ABC transporter (ATP	-binding protein)		01			••
SGO_0016	4	24.7% 17.9%			4	24.0% 16.8%			cbiO; ABC transporter	r, ATP-binding proteil	n	•		••	



Cover	rage							S	Streptococ	cus gora	lonii				Hac Labo	ratory UW
	5	Summai	гу Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgP	gFn vs SgPg	Coverage	Page 2
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	<b>_</b> SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Re	ep II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0017	4	12.5% 13.3%							ABC-type putative col	palt transport system	n, permease	•				
550, 0010									sdhA; L-serine dehydi	ratase. iron-sulfur-de	enendent.					
SGO_0019	6	24.1%							alpha subunit	acase, non sanar ac	spendency					
SGO_0020			3	26.9%					sdhB; L-serine dehydi	ratase, iron-sulfur-de	ependent,					
300_0020	3	19.7%	3	24.2%					beta subunit							
SGO_0022	6	20.4%	15	55.2%	8	28.4%	5	20.6%	trmU; tRNA (5-methy	laminomethyl-2-thio	uridylate)-					
330_332	8	29.5%	15	56.3%	11	31.1%	3	15.0%	methyltransferase					<b>J J</b>		
SGO_0025	10	23.8%	4	9.5%	11	23.9%	4	8.1%	gidA; glucose inhibite	d division protein A		4			44	
	10	22.8%	6	13.8%	10	22.1%	7	14.9%	g.a, g.acccc							
SGO_0026	20	32.3%			4	9.1%	4	6.8%	DHH subfamily 1 prot	ein						
	21	33.1%			5	7.3%			, '							
SGO_0027	7	54.7%	7	46.7%	8	63.3%	7	58.7%	rplI; ribosomal protei	n L9						
	11	72.0%	9	64.0%	8	55.3%	8	52.7%							-	3 3
SGO_0028	9	30.6%	4	11.8%	5	17.7%			dnaC; replicative DNA	helicase						
	13	41.9%	4	13.7%	7	27.5%	3	9.5%								
SGO_0030	12	47.3%	18	54.2%	15	57.7%	11	40.8%	aspB; aspartate trans	aminase						
	13	46.1%	19	59.7%	14	49.9%	11	42.8%							-	
SGO_0032	11	36.9%	7	30.0%	12	44.1%	5	18.0%	plsX; fatty acid/phosp	holipid synthesis pro	tein PlsX					
	16	42.6%	1	27.9%	11	39.3%	4	11.1%								
SGO_0033	6	41.8% 57.0%			3	40.5% 51.9%	3	40.5% 51.9%	acpP; acyl carrier pro	tein						
	O	31.0%		F F0'	4	31.9%	4	31.9%				_	_			
SGO_0035	3	3.6%	5	5.5% 6.4%	3	4.2%			phosphoribosylformyl	glycinamidine syntha	ise			00	00	
		0.070	J	0.770	1 3	7.2/0							_	_		



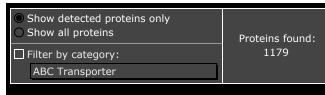
Cover	rage							S	Streptococ	cus gora	lonii				Hac Labor	kett atory UW
	5	Summar	у Та	ble S	SgFn '	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgP	gFn vs SgPg	Coverage	Page 3
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I R	ep II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0042	3 5	15.1% 26.5%	6 5	43.3% 35.3%	5 5	33.2% 29.8%	3	17.6%	transcription regulato	r, GntR family		•				
SGO_0044									PTS system, IIB comp	oonent						
SGO_0050	7	33.5% 40.4%							hypothetical protein S	GGO_0050						
SGO_0051	3	16.1% 28.6%							hypothetical protein S	GGO_0051		•				
SGO_0054	16 16	40.8% 38.5%	13 13	36.3% 37.7%	13 16	31.8% 38.9%	6 7	20.9%	dltA; D-alanine-activa	iting enzyme						••
SGO_0055	3	9.9%							dltB; integral membra	ane protein		•				
SGO_0056	3	39.2% 36.7%	3	31.6%					dltC; D-alanyl carrier	protein						
SGO_0057	20 26	58.3% 64.0%	14 9	48.8% 32.9%	13 12	43.8% 40.0%	7	25.4% 19.9%	dltD protein							••
SGO_0059	4	45.3% 45.3%	4	45.3% 45.3%	4 5	45.3% 45.3%	4 5	45.3% 45.3%	pXO1; hypothetical pr	rotein SGO_0059						
SGO_0060	36 45	45.3% 49.0%	3	5.0%					hypothetical protein S	GGO_0060				••		
SGO_0062	3	51.2%							hypothetical protein S	GGO_0062						
SGO_0063	14 17	32.1% 42.9%	7	10.8% 18.9%	7	22.3% 27.3%	5 7	14.4% 17.5%	hypothetical protein S	GGO_0063				••	••	••



Cover	rage							S	Streptococ	cus gora	lonii				Hac Labor	
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs S	gPg Cov	erage	Page 4
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg	SgFn	 n Sg	ıPg '	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Re	p II Rep I	Rep II	Rep I Rep II
SGO_0064	50 52	43.8% 42.8%	9	8.5% 11.8%	29 30	28.5% 30.6%	14 17	13.6% 16.4%	FtsK/SpoIIIE family p	rotein						00
SGO_0065	16 18	49.9% 50.4%	9	33.7% 38.1%	13 15	48.2% 56.2%	10 12	35.9% 37.0%	hypothetical protein S	GGO_0065						
SGO_0066			3	36.6%	4 5	36.6% 58.4%	3	36.6% 36.6%	D-3-phosphoglycerate	e dehydrogenase, pu	tative	0 (				
SGO_0067	8	25.7% 29.7%	4 5	14.6% 17.1%	13 14	37.3% 42.6%	8	28.1% 20.0%	protein with prophage	e function domain		•				99
SGO_0068	7	40.7% 40.7%	4	28.2%	7 6	40.7% 40.1%	3	24.3% 23.2%	lipoprotein, putative							••
SGO_0069	5 7	38.6% 45.7%			5 4	38.6% 31.0%	3	25.5% 31.0%	hypothetical protein S	GO_0069						
SGO_0070	4 5	33.6% 39.6%			4	34.3% 34.3%	4	38.8% 39.6%	merozoite surface pro	tein 1						
SGO_0075	4	23.6%							hypothetical protein S	GGO_0075						
SGO_0078	7	38.2% 38.6%	3	20.9%	5 4	25.0% 25.0%			hypothetical protein S	GO_0078						
SGO_0079	3	27.6%							hypothetical protein S	GGO_0079						
SGO_0080	17 22	38.7% 49.8%	9	20.8%	14 12	31.8% 29.7%	10 10	24.4% 23.3%	hypothetical protein S	GO_0080						••
SGO_0081	3	11.5% 11.5%	5 4	21.6% 13.3%	3 6	11.5% 29.8%			hypothetical protein S	GGO_0081		01				



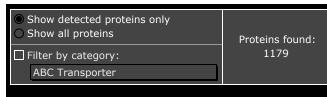
Cover	rage							S	Streptococ	ccus gora	lonii				Had Labo	ratory UW
	9	Summai	гу Та	ble S	SgFn	vs Sg	SgF	Pg vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPg	Fn vs SgPg	Coverage	Page 5
		Sg		SgFn	9	SgPg	Sg	<sub>I</sub> PgFn	_			Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0095			9	39.1% 47.3%	8 6	38.8% 34.4%			mccF; microcin immu	nity protein MccF, pu	ıtative					
SGO_0097	3	12.4%							hypothetical protein S	CO 0007						
545_557	5	22.5%							nypothetical protein s	SGO_0097						
SGO_0098	3	21.7%			3	21.7%			ribonucleotide reducta	aco-liko protoin						
565_555					3	21.7%			Tiboliucieotide Teducta	ase-like protein						
SGO_0099			4	11.3%	7	16.6%	3	5.6%	pulA-2; pullulanase, t	vne I						
			7	15.8%	6	16.6%			puiA 2, puilulaliase, e	урс 1						
SGO_0100	6	27.4%							maltose operon trans	crintion repressor		<b>4</b>				
	4	20.7%	4	21.6%	3	11.9%			matose operon trans-	сприон тергеззог						
SGO_0101	5	25.8%							malA; Maltodextrose	utilization protein ma	alΔ					
	10	37.5%							Than ty Transacki ose	atmzation protein me	-17 \					
SGO_0104	23	59.6%	19	56.8%	23	61.8%	20	57.7%	Maltose/maltodextrin-	-hindina protein prec	ursor					
	26	65.1%	18	56.8%	23	61.8%	17	50.1%								
SGO_0105	8	19.6%	8	24.6%	9	21.5%	4	9.1%	malQ; 4-alpha-glucan	otransferase		4			44	
	9	19.8%	8	22.3%	9	21.7%	3	6.6%	marę, raipila gracari							
SGO_0106	12	20.5%	27	49.1%	23	42.0%	17	31.9%	glgP-2; maltodextrin	phosphorylase		4				
	15	22.7%	24	47.5%	28	51.1%	15	29.3%	g.g,a.couoxe							
SGO_0107									LPXTG cell wall surface	e protein, collagen b	inding					
							4	5.6%	domain							
SGO_0108	8	30.7%	4	15.4%					ruvB; Holliday junctio	n DNA helicase RuvB	3					
	9	30.7%	3	13.9%												
SGO_0110					3	40.7%			phosphotyrosine prote	ein nhosphatase						
			4	46.4%					phosphocyrosine prote	ciii piiospiiatase						



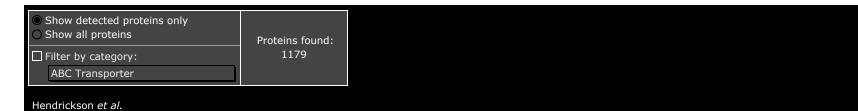
Cover	age							S	Streptococ	ccus gora	lonii					ratory UW
	5	Summar	гу Та	ble !	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs	SgPg	Coverage	Page 6
		Sg		SgFn		SgPg	Sg	<sub>I</sub> PgFn				Sg	Sgi	Fn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I	Rep II	Rep I Rep II	Rep I Rep II
SGO_0111	4 6	27.0% 36.5%							MORN motif family pr	rotein						
SGO_0112	10	22.0% 22.2%							putative acyltransfera	ise		96				
SGO_0113	53 57	63.8%	53 51	66.8%		60.5%	45 45	59.1% 60.2%	acdH; alcohol-acetald	ehyde dehydrogenas	e			•		
SGO_0128	5	60.7%							hypothetical protein S	GGO_0128						
SGO_0129	13 16	29.2% 31.6%			4	11.1% 8.8%			atpI; v-type sodium A	ATP synthase, chain I					00	
SGO_0131	6	34.7% 35.2%	3	27.6% 29.1%	_				v-type sodium ATP sy	nthase, chain E						
SGO_0132	3	13.1%			3 4	12.8% 15.4%			ATP synthase (C/AC3	9) subunit					00	
SGO_0134	6	27.3% 39.0%	4	17.7%	6 7	26.4% 35.1%			acetyltransferase, GN	AT family		•		•		
SGO_0135	22 24	49.0% 49.5%	16 10	34.9% 23.3%	_	28.4% 48.5%	8	16.1% 20.0%	v-type sodium ATP sy	nthase, subunit A				•		••
SGO_0136	22 22	54.7% 54.5%	16 14	48.9% 44.6%		43.5% 45.9%	10 10	36.2% 36.2%	v-type sodium ATP sy	nthase, chain B						
SGO_0137	3	16.4% 15.5%							V-type ATPase, D sub	ounit		01				
SGO_0138	4	17.7%	5	22.0%					LysM domain protein					•		



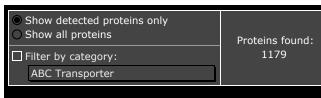
Cover	rage							5	Streptococ	ccus gora	lonii				Hac Labor	kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgP	gFn vs SgPg	Coverage	Page 7
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	<b>-</b> SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	ep II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0139	11	37.0%	14	44.9%	12	43.5%	10	30.0%	thrC; threonine synth	ase						
	12	38.3%	11	35.8%	13	42.9%	6	19.8%	,							
SGO_0142									hypothetical protein S	GGO 0142						
	3	15.5%							, p							
SGO_0144	14	15.6%	4	4.2%	3	1.9%			hypothetical protein S	GO 0144		4		44		
	18	18.1%	3	3.1%					, p							
SGO_0145	31	45.3%	25	41.1%	21	34.8%	11	19.9%	polI; DNA polymerase	ı T						
	25	37.6%	21	34.7%	22	38.1%	11	22.0%	poily brut polymerase							
SGO_0146	5	41.4%	7	58.6%	7	58.6%	5	41.4%	CoA-binding domain բ	orotein						
	6	46.2%	7	66.9%	5	46.2%	3	23.4%	cont smalling domain p							
SGO_0148	5	33.3%			3	21.1%			hypothetical protein S	GO 0148						
	7	38.2%							, p							
SGO_0150	3	10.0%							fucA1; alpha-L-fucosio	dase		4				
									, отрана = 1000							
SGO_0152	4	21.1%	6	31.3%	5	27.4%	3	17.9%	tgt; queuine tRNA-rib	osyltransferase						
	4	21.1%	4	17.4%	7	36.3%	4	19.7%	ege, queame aun m	osyntransierase						
SGO_0154	16	47.9%	32	71.3%	26	63.3%	18	53.9%	pgi; glucose-6-phospl	hate isomerase						
	21	48.6%	33	74.6%	23	61.0%	20	54.8%	pgi, gideose o pilospi	nate isomerase						
SGO_0155	15	52.6%			3	16.6%			hypothetical protein S	SGO 0155						
	15	57.0%			5	16.6%			nypotrictical protein s	.00_0133						
SGO_0156	9	41.0%			3	16.4%	3	16.4%	hypothetical protein S	GO 0156						
	11	42.5%			3	16.4%	3	17.2%	Trypodredical protein 3							
SGO_0157	4	16.8%							hypothetical protein S	SGO 0157						
330_3137	5	20.6%							Trypotrietical protein S	300_0137						



Cover	age							S	Streptococ	ccus gora	lonii				ratory UW
	5	Summar	y Tal	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	vs SgFn	SgPgFn vs SgPg	Coverage	Page 8
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0158	8	42.2% 42.2%	7	38.8%	7	41.4%	6 8	37.9% 45.3%	2,3,4,5-tetrahydropyr succinyltransferase, p		N-	01			
			3	10.6%	3	10.6%									
SGO_0159	5	19.9%				10.070			hippurate hydrolase						
SGO_0163	7	36.4%	11	48.3%	10	45.4%	6	29.1%	gallia LITD glugges 1	nhaanhata wideleltus	. n. a f a wa a a				
300_0103	8	40.1%	10	48.7%	9	41.7%	8	40.7%	galU; UTP-glucose-1-	рпоѕрпасе инфункта	insierase				
SGO_0164	12	55.9%	14	69.2%	11	56.2%	8	38.2%	Glycerol-3-phosphate (NAD(P)H-dependent						
330_01	13	61.5%	12	60.7%	11	58.6%	9	41.1%	dehydrogenase)	gryceror-5-priospriac	<b>E</b>				
SGO_0165	9	22.3%							ABC transporter, perr	nease/ATP-binding p	rotein	44			
	8	17.8%							SP2075						
SGO_0166	11	26.5%							ABC transporter, perr	nease/ATP-binding p	rotein	44			
	10	25.1%			3	3.7%			SP2073						
SGO_0167	5	27.1%							glutamine amidotrans	sferase					
	5	32.3%													
SGO_0168	4	30.2%							hydrolase, NUDIX fan	nily					
	5	39.6%	3	22.8%					, ,						
SGO_0169	5	41.5%	5	42.9%	4	42.9%	5	42.9%	dut; dUTP diphosphat	ase					
	5	52.4%	4	28.6%	4	44.2%	4	37.4%							
SGO_0171	7	21.7%	5	20.2%	9	31.8%	3	11.4%	radA; DNA repair prot	tein RadA					
	12	40.1%			10	35.0%									
SGO_0172	7	44.1%	3	25.4%	_				conserved hypothetic	al protein TIGR00266	5				
	7	44.5%													
SGO_0173	7	56.7%	3	34.1%	4	36.0%			Carbonic anhydrase						
	7	56.7%	5	50.0%	4	37.2%			,						



Cover	rage							S	Streptococ	cus gord	lonii				Had Labo	ratory UW
	9	Summai	гу Та	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgI	n vs SgPg	Coverage	Page 9
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	<b>-</b> SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	p II R	ep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0174	22	52.2%	19	45.4%	27	57.9%	17	44.9%	gltX; glutamyl-tRNA s	synthetase						
	22	53.2%	23	54.8%	23	56.9%	18	47.4%								
SGO_0179									Membrane protein ox	aA 1 precursor						
	3	7.0%														
SGO_0180	11	34.1%	7	30.9%	8	30.9%	3	10.3%	jag; hypothetical prot	ein SGO 0180						
	13	38.4%	4	19.7%	7	25.3%	8	28.1%	J. 37 / P P							
SGO_0181	12	40.4%							lipoprotein, putative							
	15	55.1%							iipoproteiii, putative							
SGO_0182			3	20.5%					canD, calcacia A avada	istian managan magu	latar					
300_0102	3	21.0%	4	32.4%					sapR; sakacin A produ	action response regu	iatoi					
SGO_0188	5	20.7%	6	35.9%					huduslass Tato fourill							
340_0188	6	27.0%	3	17.6%	3	14.5%			hydrolase, TatD famil	У						
CCO 0100																
SGO_0189	3	20.4%							primase-related prote	in			יוכ			
666 6466	9	34.2%			3	15.8%										
SGO_0190	16	51.8%			4	20.1%	3	15.5%	hypothetical protein S	GGO_0190						
666 6161	7	17.8%			4	14.9%										
SGO_0191	9	27.0%							hypothetical protein S	GGO_0191						
	3	14.1%	3	12.8%	7	32.8%										
SGO_0193	5	20.7%	4	17.9%	6	24.5%			ksgA; dimethyladenos	sine transferase		9		JJ		
			4	25.7%	3	20.2%			predicted ribosome sr	mall subunit-depends	ent GTPaco					
SGO_0197			6	39.7%	5	37.3%	3	17.8%	A	nan subumt-uepenue	ant GTF ase			JJ		
	8	51.1%	10	71.2%	10	65.3%	7	35.6%								
SGO_0198	7	37.9%	10	74.4%	9	58.9%	5	29.7%	rpe; ribulose-phospha	ate 3-epimerase						



Cover	age							S	Streptococ	cus gord	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 10
		Sg		SgFn		SgPg	Sg	PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	overage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0200	15 21	42.6% 51.9%	10	38.8%	12 11	45.0% 45.2%	5 7	20.3%	competence-induced	protein Ccs50					
SGO_0201	10	46.3%	12	48.2%	11	47.9%	6	26.2%	cmp-binding-factor 1						44
	12	51.1%	13	49.2%	13	52.1%	/	26.8%						-	
SGO_0202	3	20.3%	5	33.6%	5	25.5% 33.2%			pur operon repressor			01			
SGO_0203	4	27.9%							hypothetical protein S	GGO_0203		04		••	
SGO_0204	7	25.5% 25.5%	8	45.3% 43.8%	7	39.4% 39.4%	8	45.3% 45.3%	rpsL; ribosomal protei	in S12		•			
SGO_0205	12 14	67.3% 74.4%	11 13	62.8% 80.1%	11 10	59.6% 59.0%	9	60.3% 53.8%	rpsG; ribosomal prote	in S7					
SGO_0206	41 46	83.5% 86.0%	38 44	79.2% 97.4%	42 45	83.5% 83.8%	38 38	77.5% 79.8%	fusA; translation elon	gation factor G					
SGO_0207	14	47.9%	25	69.3%	19	62.2%	16	58.6%	gap; glyceraldehyde-3	3-phosphate dehydro	genase,				
	15	50.6%	27	91.1%	18	59.5%	18	58.9%	type I						-
SGO_0208	12 16	9.7%	13 12	11.3% 9.9%					LPXTG cell wall surfact	e protein, glycosyl h	ydrolase	44			
					07	04.50/	00	00.50/	,			) (			
SGO_0209	26 29	72.2% 72.9%	29 29	76.7% 87.2%	27 28	81.5% 82.5%	26 24	80.5% 72.2%	pgk; phosphoglycerat	e kinase					
SGO_0210	17	14.3%	20	21.1%	3	2.1%			sspA; streptococcal su	urface protein A			144	44	
	28	20.6%	15	18.4%	4	4.3%			osp, ocroptococcur st	and brocom n					
SGO_0211	20 18	13.4% 13.2%	5	3.0% 4.5%					sspB; streptococcal su	urface protein B		01			



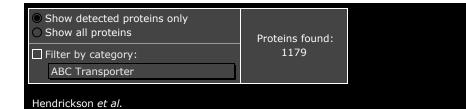
Cover	age							S	Streptococ	cus gord	lonii				ratory UW
	5	Summar	у Та	ble S	§gFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgP	g Coverage	Page 11
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep I	Rep I Rep II	Rep I Rep II
SGO_0214	4	30.6%							transcription regulato	r, MerR family					
SGO_0215	16	47.1%	17	48.7%	18	54.5%	15	49.6%		ahaaa baaa T					
300_0213	20	52.7%	19	56.3%	16	52.5%	12	34.4%	glnA; glutamine synth	letase, type I					
SGO_0219	17	44.3%	18	45.0%	20	51.3%	10	23.2%	metalle beta lastama	aa aynamfamily mustai	: 1				
300_0213	17	44.5%	15	38.8%	23	58.9%	11	27.0%	metallo-beta-lactama:	se superrannily protei	III I				
SGO_0220			3	53.9%	4	59.2%			Dustain of colons on the						
300_0220					5	68.4%			Protein of unknown fu	inction (DOF1447) Su	эрепаппіу				
SGO_0223	3	11.3%	3	11.6%					alveoprotoinase famili	, protoin					
330_0123	3	11.3%			3	12.2%			glycoproteinase family	y protein					
SGO_0230	4	25.6%	6	40.0%	6	37.8%	4	27.2%	Protoin of unknown fu	unction DUE536 fami	ilv				
330_0230	8	43.3%	5	31.1%	5	31.1%	7	44.4%	Protein of unknown fu	inction, Dorsso fami	iiy				
SGO_0231	4	11.1%							glycerophosphoryl die	ster phosphodiestera	ase family				
	6	17.1%							protein						
SGO_0232					3	26.9%	3	26.9%	conserved hypothetica	al protein TIGP00103	2				
	4	33.6%			3	26.9%	3	26.9%	conserved hypothetica	ar protein Trakooros	,				
SGO_0233	7	31.9%	3	26.7%					lipoprotein, putative						
555_555	10	48.9%	6	45.2%					iipoproteiii, patative						
SGO_0234	20	35.3%	18	35.6%	19	34.8%	13	23.7%	pepX; X-Pro dipeptidy	d-nentidase					
	21	36.2%	19	38.5%	18	30.8%	5	10.0%	pepx, x-rio dipeptidy	т-рершивзе					
SGO_0235	3	11.3%			4	21.9%			glycerol uptake facilita	ator protein-like prot	oin				
	4	14.1%			3	18.7%			gryceror uptake racilita	ator protein-like prot	Ciff				
SGO_0236	6	12.0%							hypothetical protein S						
-J05_0250	6	11.7%							nypothetical protein S	00_0230					

5	Dot P	Dot Plots
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Cover	rage							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 12
		Sg		SgFn		SgPg	Sg	<sub>1</sub> PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0237	3 8	18.0% 42.4%	6	26.1% 36.7%	7	38.0% 45.7%	3	17.1% 18.0%	ccpA; CcpA protein (p	proteinase)		01			••
SGO_0240	5	23.8%							mvaD; diphosphomev	valonate decarboxyla	se	44			
	4	21.3%													
SGO_0242	3	10.8%	3	14.7%					FMN-dependent dehy	AN-dependent dehydrogenase family protein  rdroxymethylglutaryl-CoA reductase, degradative					
SGO_0243			3	6.6% 9.4%	3	12.3% 15.8%	5	14.2%	hydroxymethylglutaryl-CoA reductase, degradative					00	
SGO_0244	3	8.7%	7	20.9%	8	31.6%	6	19.9%	FMN-dependent dehydrogenase family protein  hydroxymethylglutaryl-CoA reductase, degradative  hydroxymethylglutaryl-CoA synthase  pfl; formate acetyltransferase						40
	5	18.1%	7	28.3%	8	28.1%			hydroxymethylglutaryl-CoA reductase, degradative hydroxymethylglutaryl-CoA synthase						
SGO_0247	45	67.2%	43	66.4%	39	66.7%	33	51.1%	pfl; formate acetyltra	ydroxymethylglutaryl-CoA synthase					
	47	68.1%	43	69.3%	38	62.6%	30	51.9%	,						
SGO_0252	7	32.1% 26.9%	3	16.0% 14.6%	6	26.9% 14.6%	3	9.4%	possible TetR-type tra	anscriptional regulato	or	04			
	10	42.7%													
SGO_0253	12	36.9%							hypothetical protein S	GGO_0253					
SGO_0254	6	13.1%			6	12.1%			helicase, RecD/TraA f	amily					
555_555	11	21.3%			4	9.5%			Helicase, Reco, Han I	arriny					
SGO_0255	11	48.5%	7	46.5%	4	29.0%	5	19.0%	Signal peptidase I						
	13	48.5%	5	33.0%	6	39.5%	5	26.5%	c.gnar peptidase i						
SGO_0256	4	17.9%							rnhC; ribonuclease HI	III		44			
	6	22.3%	3	16.9%					.,						
SGO_0258	3	23.8%	3	56.4%			3	27.7%	hypothetical protein S	GGO_0258		04			



Cover	rage							S	Streptococ	cus gora	lonii					ackett oratory	UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	rs SgFn	SgPgFn	vs SgPg	Coverage	9	Page 13
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	_ SgPg	SgF	PgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep	I Rep II	Rep I Rep	II Rep I	Rep II
SGO_0260	16 23	29.7% 40.2%	8 11	17.5% 22.4%	13 15	24.3% 28.7%	6 7	8.4% 10.8%	DNA mismatch binding	g protein MutS2					04		
SGO_0261									CNI	AT Court							
300_0201	3	16.4%							acetyitransferase, Givi								
SGO_0262	11	34.1%	9	29.7%	12	32.8%	7	19.9%	dinentidase	000							
	9	30.5%	9	32.4%	12	30.3%	5	15.9%	агреричись								
SGO_0263	4	42.3%	4	42.3%	4	42.3%	4	42.3%	trx-1: thioredoxin	rx-1; thioredoxin					44		
	4	42.3%	6	67.3%	4	42.3%	3	41.3%									
SGO_0268	10	45.5%															
	8	38.7%			4	17.2%			mechanosensitive transport protein								
SGO_0269	3	22.5%							hypothetical protein S	GO_0269							
	4	31.9%															
SGO_0272	6	55.7%	7	54.9%	5	42.6%	4	39.3%	hypothetical protein S	GO_0272							
	5	48.4%	6	49.2%	5	42.6%	4	39.3%									
SGO_0276	19	44.9%	24	63.2%	23	59.2%	16	42.4%	gdhA; glutamate dehy	/drogenase (NADP)							
	24	48.2%	22	62.9%	25	65.4%	20	55.6%	, , ,								
SGO_0277	5	31.7%	4	28.8%	5	35.3%			pyrA; Dihydroorotate	dehydrogenase							
	5	31.7%	5	35.6%	4	27.9%											
SGO_0278			3	15.8%					msrA; Peptide methio msrA/msrB	nine sulfoxide reduct	tase						
	3	14.8%							IIISI AYIIISI B								
SGO_0279	6	29.4%							lipoprotein, putative								
	4	23.7%															
SGO_0280	6	20.4%	10	41.0%	7	20.9%			trzA; ethylammeline o	chlorohydrolase		4			44		
	7	23.4%	6	23.6%	6	20.6%				,							



Cover	age							S	Streptococ	ccus gord	'onii					ratory UW
	5	Summar	у Та	ble s	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPg	JFn vs SgPg	Coverage	Page 14
		Sg		SgFn	9	SgPg	Sg	PgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0282	9 11	27.1% 37.6%							cell wall polysaccharic	de biosynthesis prote	in					
SGO_0284	3	9.3%							transcriptional regulat	tor		•				
SGO_0286	7	16.0% 24.5%	3	7.7%			3	8.3%	DNA mismatch repair	DSL-like lipase/acylhydrolase					••	••
SGO_0288			3	21.6%	3	21.1% 30.9%			DNA mismatch repair protein MutS, putative  GDSL-like lipase/acylhydrolase  copper -translocating P-type ATPase					••	••	
SGO_0290	3	28.5% 28.5%			3	28.5% 28.5%	3	28.5%	copper -translocating	P-type ATPase						
SGO_0291	16 16	31.1% 33.5%	8	19.3% 13.4%	9	20.7%	7	16.6% 13.9%	copper-translocating I	P-type ATPase				90	••	••
SGO_0292	19 24	45.9% 51.1%	14 11	34.7% 35.4%	28 29	64.1% 64.1%	23 24	55.5% 60.2%	spxB; pyruvate oxida:	se						
SGO_0294	4 5	8.6% 10.1%							ABC transporter, puta	ative		0 (				
SGO_0297	4	11.5%	6 9	15.9% 27.6%					6-phospho-beta-glucc	osidase				••		
SGO_0299	3	11.0%							putative histidine kina	ase						
SGO_0301							3	14.2%	ABC transporter ATP-	binding protein-like p	rotein					••
SGO_0306	4	17.9% 21.9%							ABC transporter ATP-	binding protein-like p	rotein	•				

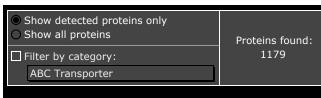
Cover	rage							S	Streptococ	ccus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 15
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0307	6	8.8% 12.5%							pabB; chorismate bin	ding enzyme		01			
SGO_0310	3	5.5% 4.9%	4 5	8.7% 8.3%	4	6.8%				OSPHOKETOIASE  OXTG cell wall surface protein, serine protease,			00	00	
SGO_0312	33	46.3% 48.5%	45 55	58.4% 71.2%	40 41	56.9% 57.2%	34 38	53.5% 55.5%	xfp; D-xylulose 5-pho phosphoketolase	fp; D-xylulose 5-phosphate/D-fructose 6-phosphate hosphoketolase  PXTG cell wall surface protein, serine protease,					
SGO_0317	43	46.8% 50.1%		71.270	71	37.270	3	2.6%	fp; D-xylulose 5-phosphate/D-fructose 6-phosphate					••	••
SGO_0321	8	57.8% 71.1%	8	61.3% 57.4%	7 8	51.5% 56.4%	5 6	42.2% 42.2%	PXTG cell wall surface protein, serine protease, ubtilase family						
SGO_0323	3	14.9%			3	18.6%			pseudouridine syntha	se rRNA-specific				••	
SGO_0324	10 10	22.6% 22.3%							hypothetical protein S	6GO_0324		•		••	
SGO_0325	7	25.4%							probable membrane p	protein, putative					
SGO_0326	19 23	38.9% 46.5%			3	8.5%			probable membrane p	protein, putative				00	
SGO_0327	5	17.2% 13.7%	4	12.4%	3	11.4%			Lipopolysaccharide N-	-acetylglucosaminyltr	ansferase			00	
SGO_0328	5 5	9.8% 9.8%							transmembrane prote	ein, putative		01		••	
SGO_0329	20 21	47.0% 49.4%			3	8.6%			hypothetical protein S	6GO_0329				••	



Cover	rage							S	Streptococ	cus gora	lonii					ckett cratory UW
	5	Summar	у Та	ble !	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn \	/s SgFn	SgPgFn	s SgPg	Coverage	Page 16
		Sg		SgFn		SgPg	Sg	<sub>1</sub> PgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep l	Rep II	Rep I Rep II	Rep I Rep II
SGO_0330	8	40.1% 38.5%							hypothetical protein S	GO_0330						
SGO_0331	4	19.7%							hathatian anatain C	vpothetical protein SGO_0331  vpothetical protein SGO_0332						
300_0331	6	23.3%							nypotnetical protein S	rpothetical protein SGO_0332						
SGO_0332	12	40.6%							hypothetical protein S							
	14	40.8%							, pour de de process de							
SGO_0333	8 11	34.8% 68.5%	9	68.5% 66.3%	_	68.5% 68.5%	10 10	38.2% 66.3%	rpsO; ribosomal prote	ein S15						
	11	00.5%	8	00.3%	_		10	00.3%								
SGO_0337	3	34.6%			3	33.7%			trx-2; thioredoxin							
			7	27.0%	3	11.8%										
SGO_0339	4	16.3%	7	31.9%					hypothetical protein S	GGO_0339						
SGO_0342	15	34.6%	19	44.5%	17	39.1%	12	26.9%	pepF-2; oligoendopep	tidasa						
333_33 12	15	33.4%	21	45.0%	18	43.0%	10	19.2%	pepi -z, oligoeridopep	liuase						
SGO_0344	27	48.1%	29	47.3%	28	48.4%	22	38.6%	pnpA; polyribonucleot	ide nucleotidyltransf	oraco					
	31	48.5%	27	44.1%	26	50.4%	16	26.0%	pripa, polyriboriacicoc	ide nacicottayittansi	crasc					
SGO_0345	3	16.1%							cysE; serine O-acetylt	ransferase		4				
	6	23.4%														
SGO_0348			5	48.0%	_	31.8%			reductase							
	4	36.4%			3	31.8%										
SGO_0349	11	32.2%	10	28.6%	_	36.5%	10	25.7%	cysS; cysteinyl-tRNA s	synthetase						
	11	31.8%	11	31.1%	_	32.7%	7	18.3%								
SGO_0352	14	42.3%	12	40.7%		48.4%	7	26.1%	ABC transporter, ATP-	-binding protein SP1	580					
	16	47.6%	12	37.8%	12	39.6%	6	21.5%	,	•						



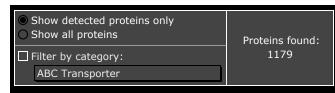
Cover	rage							S	Streptococ	ccus gora	lonii					lackett boratory	UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn	vs SgPg	Coverag	ge	Page 17
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	SgPg	Sgi	PgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep	I Rep II	Rep I Rep	II Rep I	Rep II
SGO_0353	3	6.0% 5.2%	3	7.6% 6.3%	5 3	7.8% 6.0%			transport protein			01		0	01		
SGO_0355	5	27.6%	4	20.6%	6	35.0%				- u.c. ii							
300_0333	7	28.0%	4	23.5%	5	30.9%			RNA metnyitransferas	NA methyltransferase, TrmH family, group 3  vpothetical protein SGO_0356  egV; DegV family fatty acid binding protein							
SGO_0356	3	16.4%							hypothetical protein S	pothetical protein SGO_0356							
SGO_0357	8	44.3% 47.4%	10	59.6% 39.0%	11 12	59.6% 63.8%	8	57.1% 47.7%	degV; DegV family fat	tty acid binding prote	ein						
SGO_0358	11	78.4%	10	73.0%	9	65.5%	8	70.3%	rplM; ribosomal prote	in I 13							
	11	79.1%	12	77.7%	11	79.1%	10	75.7%	Tpirity ribosomar proce								
SGO_0359	5	27.7%	6	28.5%	5	21.5%	5	21.5%	rpsI; ribosomal protei	in S9		4			44		
	6	28.5%	4	20.8%	5	21.5%	5	21.5%									
SGO_0361	5	33.1% 33.1%	5	35.5% 35.5%	5 3	40.7% 28.5%			immunity repressor p	rotein					0		
SGO_0368	3	9.8%	5	11.9%			3	9.4%	(TT)	1 1 - 1 - 1							
340_0308	4	10.9%	5	13.2%					merA; mercury(II) red	ductase							
SGO_0371									putative transcription	al regulator							
	4	39.7%															
SGO_0372	6	18.9%	12	25.7%	8	30.1%	7	25.1%	malate oxidoreductas	e							
	8	22.2%	10	24.0%	7	23.1%	6	17.4%									
SGO_0374	7 8	29.5% 34.4%	9	40.6%	8	40.6% 41.8%	5 4	23.4%	Response regulator of	f the LytR/AlgR famil	У						
					<u> </u>		4	24.3%									
SGO_0376	5	23.9%						,	ABC transporter ATP-	binding protein							



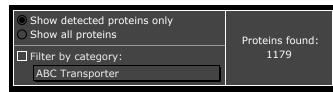
Cove	rage							S	Streptococ	cus gora	lonii					oratory UW
	5	Summar	у Та	ble s	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn	vs SgPg	Coverage	Page 18
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep	I Rep II	Rep I Rep I	I Rep I Rep II
SGO_0378			3	29.9%					hypothetical protein S	GGO_0378						
SGO_0379	6	31.6%							Protein of unknown fu	ınction (DUF421) fan	nily					
	7	34.9%														
SGO_0380	3	23.3%							hypothetical protein S	ypothetical protein SGO_0380  utative carboxylate-amine/thiol ligase						
	3	15.7%	4	23.1%	3	15.7%	4	25.3%								
SGO_0384	5	22.8%	6	29.2%	_	34.3%	5	29.2%	putative carboxylate-a	amine/thiol ligase		9				
SGO_0385	19	19.9%	21	21.7%					ava hata D frustacida	•••						
300_0303	24	27.5%	18	19.0%					exo-beta-D-fructosida	ise						
SGO_0387	4	22.1%							hypothetical protein S	SGO 0387						
	6	31.7%							nypothetical protein s	740_0307						
SGO_0388	19	25.3%	16	26.6%					LPXTG cell wall surfac	e protein, zinc carbo	xypeptidase					
	27	36.4%	13	18.7%					family							
SGO_0389			3	37.5%					possible phosphoserin	ne nhosnhatase						
	3	28.4%	3	45.5%					possible phosphoserm	те риозриченое						
SGO_0390	14	43.4%	19	51.2%	23	56.4%	11	34.4%	glycerol-3-phosphate	dehydrogenase (NAI	)(P)+)					
	18	50.3%	16	48.8%	18	49.7%	13	37.1%	gryceror 5 phosphate	denyarogenase (14/12	2(1)1)					
SGO_0392			7	36.4%	6	32.5%	3	14.5%	phosphoglycerate mu	tace						
303_0071	4	25.4%	5	28.9%	6	32.5%			phosphogrycerate mu	tase						
SGO_0393	8	53.7%	3	16.3%					D-alanyl-D-alanine ca	rhoxypentidase						
	10	63.8%							D didilyi D-didililie Ca	Doxypeptidase						
SGO_0396	3	25.2%							Transcriptional regula	tor, PadR family						



Cover	rage							S	Streptococ	cus gord	lonii				Hac Labo	ratory UW
	S	Summar	y Tal	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPg	Fn vs SgPg	Coverage	Page 19
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I Re	p II F	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0398	12 10	49.5% 35.1%	4 5	16.1% 20.7%	5 3	20.4%	4	17.5% 17.9%	ABC transporter ATP-I	binding protein				99	99	99
	4	12.8%	8	27.6%				111070						<del></del>		
SGO_0400	4	12.5%	4	16.6%					hrcA; heat-inducible t	ranscription represso	or HrcA	<b>U</b> (		JJ		
SGO_0401	8	41.8%	9	46.9%	7	33.9%	6	33.9%		pE; co-chaperone GrpE						
300_0401	10	53.7%	9	53.7%	8	41.8%	7	33.9%	grpE; co-chaperone G	E; co-chaperone GrpE  OK; DnaK chaperone protein						
SGO_0402	29	56.8%	40	71.3%	32	64.3%	29	61.6%	dnak: Dnak chanoron	o protoin						
330_0101	36	63.8%	42	74.6%	33	64.4%	33	64.6%	dilak, bilak cilaperon	е ргосент						
SGO_0404	15	42.0%	6	23.6%	8	28.9%	6	19.7%	dnaJ; DnaJ chaparone	e protein						
	21	50.1%	9	26.2%	13	35.7%	8	27.8%	,							
SGO_0407			3	17.3%	3	19.7%			truA; tRNA pseudourio	dine synthase A						
	3	16.9%	3	17.3%												
SGO_0408	65	42.9%						0.00/	zmpB; zinc metallopro	oteinase B						
	68	42.0%					4	3.6%								
SGO_0409	3	17.0%	14	67.2%	3	28.5%			pyridoxine kinase							
			13	70.8%	4	26.9%	•	40.00/					_			
SGO_0411			12	80.7% 84.5%	3	12.8% 12.8%	3	12.8%	conserved hypothetica	al protein TIGR01440	)				00	
	20	72 00/	33		32	81.0%	07	72 10/					-			
SGO_0412	28 35	73.8% 85.9%	30	83.8%	32	81.0%	27 27	73.1% 73.1%	tig; trigger factor							
	5	45.1%	6	46.2%	5	33.3%	4	32.3%						•		
SGO_0413	3	22.6%	7	35.9%	5	33.3%	5	33.3%	DNA-directed RNA pol	lymerase delta chain				JJ		
	41	59.2%	34	53.6%	39	59.8%	29	46.2%								
SGO_0415	45	61.2%	30	50.6%	34	54.9%	33	55.5%	secA; preprotein trans	slocase, SecA subuni	t			JJ		



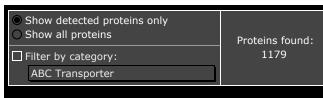
Cover	rage							S	Streptococ	cus gora	lonii				Hac Labo	ratory UW
	5	Summar	y Tal	ble S	igFn '	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPg	gFn vs SgPg	Coverage	Page 20
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	⊒ SgPg	SgPgFn
Protein	n (	Coverage	n C	Coverage	n C	Coverage				Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0416	12 14	44.9% 53.6%	15 14	51.0% 50.7%	15 12	59.5% 46.4%	11 6	42.3% 27.4%	phospho-2-dehydro-3	-deoxyheptonate ald	lolase					
SGO_0418			7	26.4% 22.8%	4	18.5% 12.5%			alr; alanine racemase					••	••	
SGO_0425	3	16.9%	4	22.5%	3	16.9%			ansB; asparaginase			•		••	••	
SGO_0426	10 13	24.6% 31.3%	6 11	16.6% 32.2%	7	14.9% 13.2%	5	14.3%	Cof family protein					••	00	••
SGO_0427	5 7	38.7% 44.7%	8	62.7% 76.7%	6	57.3% 57.3%	4	30.7% 51.3%	universal stress protei	in family						
SGO_0429	18 18	56.7% 59.2%	18 17	57.2% 56.7%	20 19	61.6% 59.9%	15 16	51.7% 51.5%	aspartate transaminas	se						
SGO_0430	29 38	48.6% 57.1%	17 14	29.0% 25.3%					LPXTG cell wall surfac	e protein						
SGO_0431	8	32.1% 23.7%	4	16.4%	6 5	28.6%			GTP-sensing transcrip	tional pleiotropic rep	ressor codY					
SGO_0432	4 5	36.2% 40.0%	4	36.2%	3	29.2% 29.2%	3	29.2% 29.2%	entB; isochorismatase	e family protein						
SGO_0434	19 22	47.6% 49.7%	12 17	33.2% 42.0%	14 13	40.1% 36.3%	11	26.6% 22.5%	aspS-2; aspartyl-tRNA	A synthetase						••
SGO_0435	5 5	59.0% 51.0%	5 5	80.0% 89.0%	5 5	79.0% 78.0%	4	41.0% 49.0%	gatC; glutamyl-tRNA( subunit	Gln) amidotransferas	se, C					
SGO_0436	22 25	55.9% 54.9%	16 18	42.2% 43.9%	21 19	52.7% 50.6%	16 19	43.6% 52.7%	gatA; glutamyl-tRNA( subunit	Gln) amidotransferas	se, A					



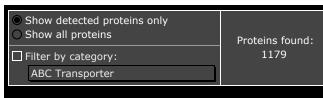
Cover	rage							S	Streptococ	ccus gora	lonii					ckett cratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn	vs SgPg	Coverage	Page 21
		Sg		SgFn		SgPg	Sg	<sub>I</sub> PgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep	I Rep II	Rep I Rep II	Rep I Rep II
SGO_0437	20 21	47.0% 48.8%	19 19	55.6% 52.0%	22 21	57.2% 56.6%	17 13	43.8% 30.2%	gatB; glutamyl-tRNA( subunit	(Gln) amidotransferas	se, B					
SGO_0440	4	21.6%	11	49.7%	7	37.1%	4	29.0%	L-iditol 2-dehydrogen	ase BH3949						
	5	26.1%	13	62.4%	4	25.3%			HAD superfamily (subfamily IIIA) phosphatase,							
SGO_0444	3	19.5%							HAD superfamily (sub TIGR01668	GR01668						
	11	42.1%	12	42.9%	14	54.6%	6	22.0%							0 0	0 0
SGO_0445	13	48.1%	10	38.6%	14	45.9%	6	21.2%	HAD superfamily (subfamily IIIA) phosphatase, TIGR01668  GTP-binding protein						99	
SGO_0446	3	53.4%							GTP-binding protein  conserved hypothetical protein TIGR00253							
			_	10.00/		00.40/										
SGO_0447	4	34.3% 24.8%	5	43.8% 48.6%	3	38.1%			nadD; nicotinate (nico adenylyltransferase	otinamide) nucleotide	2					
	5	32.7%	9	50.8%	5	35.2%	3	22.1%							0 0	0 0
SGO_0448	4	28.1%	6	40.7%	7	49.2%	3	22.170	conserved hypothetic	al protein TIGR00488	3					90
SGO_0449																
300_0449	3	18.6%							isochorismatase famil	ly protein						
SGO_0450			3	24.0%	4	32.2%			iojap-related protein							
	4	38.0%	4	30.6%	3	32.2%			lojap-related protein							
SGO_0451					4	20.9%			methyltransferase						44	
					4	20.9%			mediyid ansierase							
SGO_0453	18	56.2%							lipoprotein, putative							
	26	64.5%							iipoproteiii, patative							
SGO_0454	6	31.9%	4	25.6%	6	32.8%	3	20.2%	conserved hypothetic	al protein TIGR01033	3					44
	8	40.3%	4	25.6%	4	26.9%	3	20.2%	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,							



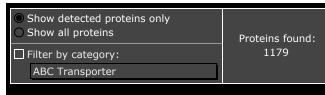
Cover	rage							S	Streptococ	ccus gora	lonii				ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgP	Coverage	Page 22
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep I	Rep I Rep II	Rep I Rep II
SGO_0455	21 21	61.0% 59.9%	3	8.7%	10 9	40.9% 35.5%	6 7	24.4%	lipoprotein, putative						
	4	13.8%	5	26.8%		00.070	,	27.070							
SGO_0456	5	17.0%	9	42.2%					ILL5; amino acid amii		91				
SCO 0457	17	48.8%	6	27.7%	11	36.8%	9	33.0%							
SGO_0457	23	57.5%	7	34.0%	12	40.0%	6	20.4%	ABC transporter, substrate-binding protein SP0148  hlpA; lipoprotein  succinyl-diaminopimelate desuccinylase						
SGO_0458	24	71.4%	17	67.9%	17	61.3%	15	59.2%	Idea Processor						
300_0438	27	70.7%	11	55.1%	16	61.0%	16	60.6%	hlpA; lipoprotein						
SGO_0459	8	30.9%	6	21.2%	8	24.7%			augainul diaminanima	lata daguasinulasa					
340_0433	10	35.2%	7	25.2%	4	14.2%			Succinyi-diaminopime	late desuccifylase					
SGO_0460	12	34.2%	5	13.8%	10	31.4%	6	14.7%	ABC transporter, ATP	-hinding protoin SD01	151				
330_0100	12	33.6%	6	17.8%	8	23.7%	6	18.1%	Abc transporter, ATP	-binding protein 370.	131				
SGO_0463	3	6.5%							cydD; putative ABC tr	ransporter (ATP-hindi	ing protein)				
	5	10.9%							cydb, patative Abe ti	ansporter (ATT binds	ing protein)				
SGO_0468	7	26.3%	7	26.3%	7	29.2%	6	28.5%	hypothetical protein S	SGO 0468					
	8	31.0%	7	26.3%	11	42.3%	5	24.9%	mypothetical protein s						
SGO_0469	3	10.2%							integral membrane pr	rotein					
	3	10.2%													
SGO_0476	7	31.7%			12	46.6%	9	38.1%	rhodanese family prot	tein		44			
	6	25.0%	3	15.5%	11	48.2%	7	30.5%	, , , , , , , , , , , , , , , , , , , ,						
SGO_0480			8	62.8%	3	30.7%			hypothetical protein S	SGO 0480					
	3	32.8%	6	58.4%	3	30.7%	3	30.7%	,,						
SGO_0483	11	45.7%	7	37.1%	7	33.1%	5	26.2%	hypothetical protein S	GO 0483					
	10	40.1%	5	33.8%	12	55.3%	7	32.1%	, potrictical protein c	200_0 100					



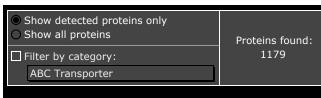
Cover	rage							S	Streptococ	cus gora	lonii					ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	Pg vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs	s SgPg	Coverage	Page 23
		Sg		SgFn		SgPg	Sg	gPgFn				Sg	S	gFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n	Coverage		Description		Rep I Rep	II Rep I	Rep II	Rep I Rep II	Rep I Rep II
SGO_0484	5 6	18.0% 18.5%	4	12.9%					sensor histidine kinas	e		0				
SGO_0488	19	39.8%	4	10.9%	8	21.9%			ABC transporter, ATP-	-binding protein SP04	183			4	44	
	18	35.7%	7	21.9%	6	19.1%										
SGO_0491			5	31.6% 22.4%	4	21.1%			gidB; methyltransfera	se GidB					99	
		0= =0/														
SGO_0494	5 8	27.5% 50.8%	15 11	72.0% 68.3%	8 9	51.3% 53.4%			lemA; LemA-like prot	ein						
SGO_0495	4	21.2%	4	23.2%	3	19.2%			htpx; heat shock prot	oin						
	6	28.6%	5	32.3%					перх, пеас зноек ргос	CIII						
SGO_0497			44	38.3%			3	2.5%	gtfG; glucosyltransfer	ase G						
			45	39.5%												
SGO_0500	3	12.1%							rggD; putative transc	riptional regulator Rg	jgD	0				
200 0704	7	43.2%			8	43.2%	6	34.1%								
SGO_0501	8	50.0%	3	22.7%	7	43.2%	6	34.1%	Uncharacterized ACR,	COG1399						
SGO_0502	29	58.4%	20	47.5%	25	56.2%	22	51.1%	floL; flotillin-like prote	ein						
	34	61.9%	15	37.1%	27	57.6%	21	51.9%	not, notimir like prote	2111						
SGO_0503	23	62.2%	33	77.6%	28	74.3%	25	69.2%	gnd; 6-phosphogluco	nate dehydrogenase,						
	27	65.2%	32	81.9%	31	78.7%	27	66.9%	decarboxylating							
SGO_0505	21	35.2%	16	34.2%	16	31.0%	10	21.6%	PTS system, IIBC con	nonent						
	22	37.5%	14	31.8%	20	36.2%	11	23.6%	1.5 System, Tibe con	iponent						
SGO_0506	3	15.5%			3	14.8%			rgfB; RgfB						•	



Cover	rage							S	Streptococ	ccus gora	lonii					ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn \	/s SgFn	SgPgFn v	s SgPg	Coverage	Page 24
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg	S	gFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I	Rep II	Rep I Rep II	Rep I Rep II
SGO_0508	3	19.7% 19.7%	4	22.3%	3	19.7% 19.7%	3	19.7% 22.3%	nrdR; transcriptional	regulator, NrdR famil	у	0			99	
SGO_0509	5	16.9%							Replication initiation a protein (DnaB) superf		nment	44			<b>64</b>	
	10	23.7%			4	11.5%			protein (Dhab) superi							
SGO_0510	7	30.1%	8	31.1%	13	60.2%	8	34.4%	dnaI; primosomal pro	otein DnaI		4				
	7	26.1%	7	34.4%	10	37.8%	6	15.1%	, ,							
SGO_0511	3	16.4%	6	38.2%	5	29.4%	3	17.2%	NADPH-flavin oxidore	ductase -like protein						
	8	36.6%	7	42.9%	7	34.9%	3	17.2%								
SGO_0512	13	35.1%	11	31.0%	11	34.2%	10	33.5%	GTP-binding protein e	enaA						
	17	42.0%	8	27.8%	11	36.9%	10	32.8%	, , , , , , , , , , , , , , , , , , ,							
SGO_0513			6	10.2%					Snf2 family protein							
	4	5.3%	3	4.6%												
SGO_0514					4	14.4%			hypothetical protein S	SGO 0514					44	
					4	24.6%			, potarotada protein c							
SGO_0515	12	35.4%	16	47.4%	15	50.3%	8	26.0%	murC; UDP-N-acetyln	nuramatealanine lic	iase					
	14	41.5%	15	51.5%	15	50.3%	9	31.8%	mare, obt it deceyin		,430					
SGO_0518	21	48.4%	9	21.0%	15	42.7%	10	26.3%	aminodeoxychorismat	te Ivase-like protein						
	26	51.4%	8	23.2%	17	45.9%	9	26.9%								
SGO_0519	8	51.3%	6	61.9%	10	71.3%	5	51.3%	greA; transcription el	ongation factor greA						
	10	58.1%	4	39.4%	9	58.8%	6	53.1%	3. 2, a. a							
SGO_0521	5	18.7%	3	8.4%	3	8.4%			Membrane protein ox	aA 2 precursor						
	7	22.6%			3	11.0%				a E precarsor						
SGO_0523			7	52.4%	6	34.6%			spoU rRNA Methylase	family protein						
	6	33.7%	9	59.3%	4	26.4%			Spoot intra methylase	ranning protein						



Cover	age							S	Streptococ	cus gord	lonii					kett ratory UW
	5	Summar	ry Tal	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPg	gFn vs SgPg	Coverage	Page 25
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0526	11 13	29.4% 29.6%	6 9	14.2% 19.4%	12 13	31.5% 28.9%	3	5.4% 9.6%	ilvB; acetolactate syn biosynthetic type	thase, large subunit,				44		44
							7	9.070				)	<u> </u>	-	0 0	0 0
SGO_0527	5	25.3% 32.3%	3	25.9% 12.7%	3	19.0%	3	20.9%	ilvN; acetolactate syn	thase, small subunit				90	99	
	12	40.9%	14	42.9%	16	50.6%	10	38.5%								
SGO_0528	13	43.2%	14	42.4%	17	50.9%	10	33.2%	ilvC; ketol-acid reduct	toisomerase				JJ		
SCO 0530	3	11.5%	5	16.8%	6	28.1%										
SGO_0529	7	19.2%	7	26.9%	7	27.6%	3	12.5%	ilvA; threonine dehyd	ratase						
SGO_0530	6	33.3%	5	29.6%	4	27.8%			Cof family protein							
	7	37.8%	7	40.0%	6	33.3%			corramny protein							
SGO_0533	3	18.8%	3	21.3%					conserved hypothetica	al protein TIGR00150	)	4		40		
					3	18.8%										
SGO_0535	10	33.3%	4	16.4%	4	16.9%	3	12.4%	putative transcription	al regulator LytR					44	
	13	40.2%			5	18.9%										
SGO_0536	6	60.0%			7	73.0%	7	79.0%	hypothetical protein S	GO_0536						
	6	60.0%		20.00/	6	60.0%	4	57.0%					-	0 0		
SGO_0537	6	38.7% 43.4%	3	32.9% 50.9%	4	38.7%	5	42.8% 44.5%	HIT family protein							
	8	39.9%	6	28.0%	4	20.2%		1 1.0 70						<u> </u>		
SGO_0538	7	39.9%	8	31.7%	4	22.2%			ABC transporter, ATP-	-binding protein SP05	522			JJ	77	
SCO 0530	6	13.1%														
SGO_0539	7	16.5%							ABC transporter, pern	nease protein		U				
SGO_0540	11	55.7%	12	58.0%	14	73.5%	10	47.3%	hypothetical protein S	SGO 0540						
<del>530_051</del> 0	11	53.0%	13	59.1%	12	59.5%	10	46.2%	nypothetical protein S	000_0340						



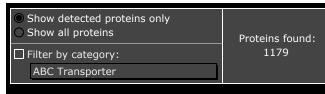
Cover	rage							S	Streptococ	ccus gora	lonii				Hac Labo	ratory UW
	5	Summai	гу Та	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPg	Fn vs SgPg	Coverage	Page 26
		Sg		SgFn	9	SgPg	Sg	ıPgFn	_			Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	p II R	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0541	6 9	36.3% 49.5%	5 5	32.1% 39.2%	7	20.3% 49.1%			methyltransferase, pu	utative						
SGO_0542	3	14.2%			4	24.7%			hypothetical protein S	5GO_0542						
SGO_0543	17 18	40.0% 41.9%	9	26.9% 25.4%	15 16	37.0% 44.1%	10 11	27.6% 30.5%	nusA; transcription te	ermination factor Nus	A					
SGO_0544	3	24.5%							Protein of unknown fu	unction (DUF448) sup	perfamily					
SGO_0545	3	39.4%							ribosomal protein L7A	A family						
SGO_0546	25 32	33.4% 39.0%	22 21	29.9% 35.0%	26 27	31.5% 32.8%	15 15	22.1% 19.7%	infB; Translation initia	ation factor IF-2						••
SGO_0547					3	36.5%			rbfA; ribosome-bindin	ng factor A						
SGO_0548	12 14	27.4% 26.3%	3	9.2%	7 6	14.7% 14.5%	4	9.0%	Na/Pi-cotransporter fa	amily protein				••		••
SGO_0549	3	9.1%	3	14.4%	3	11.0%			nagA; N-acetylglucosa	amine-6-phosphate c	deacetylase	0 (		<b>V</b> •	00	
SGO_0552	4	20.6%	15 14	67.3% 60.1%	10	53.0% 42.3%	6	33.8% 37.4%	oxidoreductase, aldo/	keto reductase famil	у	•			00	
SGO_0554	19 24	26.5% 32.5%	10 13	15.4% 20.9%	8	12.2% 21.0%	4	5.8%	hsdR; type I site-spec	cific deoxyribonucleas	se			99	00	••
SGO_0556	6 5	7.0% 8.5%							DNA helicase-like pro	tein, putative		0 (				

<ul><li>Show detected proteins only</li><li>Show all proteins</li></ul>	Proteins found:
☐ Filter by category:	1179
ABC Transporter	

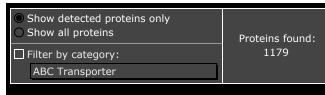
Cover	age							S	Streptococ	ccus gord	lonii				ratory UW
	5	Summar	гу Та	ble !	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	vs SgFn	SgPgFn vs SgPg	Coverage	Page 27
		Sg		SgFn		SgPg	Sg	gPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0557	4	13.9%							HsdS specificity prote modification system	ein of type I restriction	n-	• 4			
SGO_0558	5	32.7%	3	20.5%	3	26.0% 20.9%	3	18.5%	hypothetical protein S	GGO_0558					
SGO_0560	6 7	20.7% 18.1%	3	12.1%	5 4	18.1% 15.7%	5 4	17.8% 15.3%	hsdM; type I restriction	on-modification syste	m, M	01		90	99
SGO_0565	14	70.0% 74.7%	19	73.2% 72.6%	14	60.3%	11	46.8%	adhA; alcohol dehydr	ogenase					
SGO_0566	34 43	28.4% 32.7%	23 23	21.9% 23.1%					sgc; serine protease o	challisin		01		••	
SGO_0568	9	41.6% 36.1%	6 5	25.6% 19.0%	-	42.3% 51.1%	7	28.9% 35.1%	glyQ; glycyl-tRNA syn	nthetase, alpha subur	nit				
SGO_0569	21 23	35.3% 35.9%	19 16	34.8% 30.0%		49.5% 47.4%	19 22	33.3% 40.8%	glyS; glycyl-tRNA syn	nthetase, beta subuni	t				
SGO_0570	4	37.6%			3	29.4% 29.4%			hypothetical protein S	GGO_0570					
SGO_0571	3	7.8%							hypothetical protein S	6GO_0571		04			
SGO_0573	7	36.4% 50.6%	5 5	23.7% 28.5%	6	32.3% 33.5%	3 4	18.4% 19.0%	mraW; S-adenosyl-m	ethyltransferase Mra	W				••
SGO_0575	25 23	47.8% 46.7%			3	5.6% 6.5%			pbp2X; penicillin-bind	ling protein 2X				00	
SGO_0576	3	11.0%							mraY; phospho-N-ace transferase	etylmuramoyl-pentap	eptide-	04			



Cover	age							S	Streptococ	cus gora	lonii				ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 28
	·	Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0577	14 17	42.1% 45.2%	12 10	35.6% 27.5%	16 17	46.3% 52.3%	8	26.8%	ATP-dependent RNA h	nelicase					99
SCO 0579	5	24.5%	10	21.070	<u>''</u>	02.070		21.070							
SGO_0578	6	29.7%							amino acid ABC trans	porter permease pro	tein				
SGO_0579	8	54.3%	3	24.7%	9	51.8%			amino acid ABC trans	norter ATP hinding n	rotein				
	12	63.2%	3	21.9%	4	28.7%			animo acia Abe trans	porter ATT billding pi	roteiri				
SGO_0581	7	25.7%	5	24.3%	6	29.9%	6	25.0%	trxB; thioredoxin-disu	ılfide reductase					
	8	29.9%	5	17.8%	9	38.5%	4	16.1%	·						
SGO_0582	14	28.2%	22	48.8%	17	45.9%	8	23.5%	nicotinate phosphorib	osyltransferase, puta	ntive				
	16	35.2%	18	39.9%	19	47.3%	12	34.4%							
SGO_0583	6 5	29.9%	7	29.6% 32.1%	9	42.3% 29.2%	5	19.3% 25.5%	nadE; NAD+ syntheta	ise					
	-		22												
SGO_0585	13	21.2% 30.2%	16	53.2%	11	37.6% 39.6%	6 5	21.8%	pepC; aminopeptidase	e C		94			99
	26	50.0%	13	20.8%	19	41.6%	9	21.8%							
SGO_0586	26	48.5%	12	23.3%	17	35.0%	12	25.7%	pbp1a; penicillin-bind	ing protein 1A					77
SGO_0589	6	61.2%	4	52.6%	6	61.2%	5	61.2%							
300_0389	6	61.2%	4	45.7%	6	61.2%	6	61.2%	methylase						
SGO_0590	7	23.2%	9	22.9%	7	18.8%	4	12.6%	Methyltransferase						
	10	25.0%	10	26.0%	7	20.9%			ricuryiu arisiei ase						
SGO_0591	24	60.3%	11	39.7%	14	40.8%	7	23.7%	hypothetical protein S	GGO 0591					
	26	60.7%	9	26.9%	15	44.7%	8	19.9%	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,						
SGO_0592	5	30.6%	3	18.1%	7	56.9%	5	33.8%	luxS; autoinducer-2 p	roduction protein Lu	xS				
	4	25.6%	4	34.4%	7	55.6%			,	,					



Cover	age							S	Streptococ	cus gora	lonii					ratory UW
	S	Summar	ry Tal	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgF	Fn vs SgPg	Coverage	Page 29
		Sg		SgFn		SgPg		ıPgFn		Description		Sg		SgFn	SgPg	SgPgFn
Protein	n C	overage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	p II R	lep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0593	25 30	45.2% 47.3%	8 10	21.3%	21 20	43.9% 39.3%	11	27.5% 16.3%	HD/KH domain protei	n						
SGO_0594	8	40.4%	8	48.1%	8	48.6%	5	20.2%		(CMD Linear)						
340_0394	8	40.4%	7	41.3%	8	55.8%	5	30.3%	gmk; Guanylate kinas	se (GMP kinase)						
SGO_0595	5	43.7%	4	43.7%	6	59.2%	6	58.3%	DNA-directed RNA pol	lvmerase, omega sub	ounit					
	6	59.2%	4	43.7%	7	59.2%	6	59.2%	, , , , , , , , , , , , , , , , , , , ,	, ,			ין			
SGO_0596	5	8.8%	6	14.0%					priA; primosomal prot	tein N''		4				
			5	8.7%												
SGO_0597	6	32.5%	10	37.6%	11	46.9%	3	14.8%	fmt; methionyl-tRNA	formyltransferase						44
	6	27.7%	9	39.9%	8	39.5%	3	16.7%								
SGO_0598	7	20.4%		00.40/	10	30.2%			sun; sun protein						44	
	6	17.8%	6	20.4%	6	17.4%										
SGO_0599	11	48.0%	15	64.6%	9	39.8%	5	20.3%	phosphoprotein phosp	ohatase						
	11	43.9%	13	52.4%	7	35.4%	6	30.9%								
SGO_0600	22 24	48.8% 52.5%	9	19.8%	12 12	28.5% 32.4%	5	13.6%	serine/threonine prote	ein kinase			DI		44	
			1	10.9%	12	32.4%										
SGO_0602	7	24.0%							histidine kinase							
	4	21.5%	7	35.0%	5	25.7%								<u> </u>	4 4	
SGO_0603	5	25.7%	6	30.8%	4	20.1%			response regulator			9		JJ	99	
550 0504	14	46.9%	20	62.1%	18	59.3%	8	19.3%	hydrolase, haloacid de	ehalogenase family/r	entidyl-					
SGO_0604	18	54.8%	21	69.0%	20	63.6%	12	35.8%	prolyl cis-trans isome							
SGO_0606	17	70.2%	14	77.7%	15	75.1%	16	82.5%	cysK; cysteine syntha	.c. Λ						
	15	69.6%	13	76.7%	16	81.2%	15	81.9%	cysk, cystellie sylltiid	SC A						



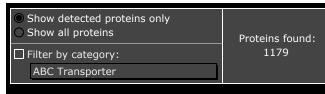
Cover	age							S	Streptococ	cus gora	lonii					ackett oratory	
	5	Summar	у Та	ble s	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs	SgPg	Coverag	е	Page 30
		Sg		SgFn		SgPg	Sg	gPgFn				Sg	Sg	Fn	SgPg	Sg	ıPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I	Rep II	Rep I Rep	II Rep	I Rep II
SGO_0608	4	13.4% 14.1%							comFA; competence (	ComFA-like protein		0					
SGO_0610	8	48.9%	11	55.6%	9	52.8%	8	51.7%	ribosomal subunit inte	orface protein							
555_55	9	53.9%	9	54.4%	9	52.8%	6	37.8%	Tibosomai subunit inte	errace protein							
SGO_0626	7	42.2%	3	13.6%	4	18.6%	3	15.5%	recX; Regulatory prot	ein recX					44		
	4	23.6%			5	22.9%			room, regulator, proc								
SGO_0628	3	21.1%							ymdC; 3"-aminoglyco protein (kanamycin ki		rase-like						
SGO_0629	4	15.9%			3	10.6%			rumA-1; 23S rRNA (u	racil-5-)-methyltrans	sferase						
	6	23.1%							RumA								
SGO_0631	4	10.0%	4	9.4%	18	36.2%	6	14.6%	alpha-glycerophospha	te oxidase							
					17	36.7%	5	10.0%	a.pa g., ee. epeepa								
SGO_0632					6	17.9%	5	19.9%	glpK; glycerol kinase						44		
					6	18.9%	4	13.9%									
SGO_0635									hypothetical protein S	GO 0635							
	5	21.4%	4	17.4%					Trypodrieded protein s								
SGO_0636	3	41.4%							hypothetical protein S	GO 0636							
	3	39.1%							7,1								
SGO_0639	23	35.6%	16	27.8%	-	46.0%	19	31.3%	valS; valyl-tRNA syntl	netase							
	23	38.5%	19	37.8%	29	44.4%	17	28.9%	, , , , , , , , , , , , , , , , , , ,								
SGO_0640	4	17.7%			4	12.6%			modification methylas	e							
	4	16.2%			3	13.4%	4	14.3%	meanication methylas								
SGO_0641	17	30.0%	17	34.6%	_	40.1%	9	16.9%	ATPase, histidine kina	se-, DNA gyrase B-,	and HSP90-						
	15	27.8%	13	24.5%	18	37.7%	6	11.0%	like domain protein pr	otein							



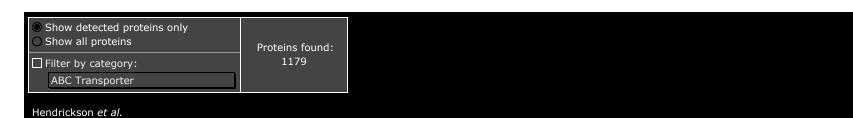
Cover	rage							S	Streptococ	cus gord	lonii					ackett ooratory	UW
	5	Summai	y Tal	ble S	SgFn '	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPg	gFn vs SgPg	Coverag	е	Page 31
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	 SgPg	Sgi	PgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I Re	ep II	Rep I Rep II	Rep I Rep	II Rep I	Rep II
SGO_0642	15 19	35.5% 37.2%	5	14.7% 11.8%	10 10	23.4%	7 6	21.2% 15.9%	hypothetical protein S	GO_0642				00	01		
SGO_0643	8	24.6%	3	12.1%	5	15.0%	3	8.9%	cytosine-specific meth	nyltransferase				44	44		
	7	24.6%	3	9.9%	7	25.9%											
SGO_0644	9	28.1%	7	20.5%	16	42.5%	9	30.6%	hypothetical protein S	GO 0644				44			
	11	34.3%	8	23.7%	14	39.1%	11	34.0%	, p			j					
SGO_0649	3	19.1%							hypothetical protein S	GGO_0649					0		
SCO 06F3	16	39.5%	3	11.8%	7	21.6%	4	13.8%						4			
SGO_0652	19	48.7%	4	14.7%	4	15.3%	4	11.0%	hypothetical protein S	GO_0652							
SGO_0653					4	24.2%			conserved hypothetica	al protein of unknowi	n function						
300_0033	5	28.1%			3	19.1%			(DUF1027)								
SGO_0654	13	48.1%	4	17.7%	10	35.4%	6	21.3%	radical SAM enzyme,	Cfr family							
300_0034	20	53.9%			10	35.4%	5	18.2%	radical SAM elizyille,	Cir iaililiy							
SGO_0656	7	23.9%	8	29.0%	5	20.4%	5	18.6%	trnP 21 truntanhan su	enthaca hata cubunit							
300_0030	8	28.8%	10	30.5%	6	22.4%	4	17.6%	trpB-2; tryptophan sy	minase, beta subunit	•						
SGO_0657									trpE; anthranilate syn	thase component I							
565_5657	4	10.0%							tipe, antinamate syn	itilase component i							
SGO_0662			5	19.9%					trnR_1: truntanhan av	enthaco hota cubusit							
300_0002	3	9.8%	3	10.3%					trpB-1; tryptophan sy	mulase, peta subunit							
SGO_0663									trnA 21 truntonban av	enthace alpha cultura	i+						
	3	13.1%							trpA-2; tryptophan sy	minase, aipna subun	IL						
SGO_0665	9	71.3%	8	66.7%	8	66.7%	6	53.8%	non-homo iron contai	ning forritin							
200_0005	8	66.7%	10	74.3%	8	64.3%	6	53.8%	non-heme iron-contai	ining remuit							

O Show all proteins	Proteins found:
☐ Filter by category:	1179
ABC Transporter	

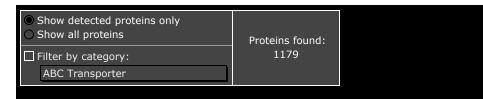
Cover	rage							S	Streptococ	ccus gora	lonii				ratory UW
	9	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn \	/s SgFn	SgPgFn vs SgP	g Coverage	Page 32
	·	Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg	SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep I	Rep I Rep II	Rep I Rep II
SGO_0667	4 5	38.3% 39.1%			3	38.3% 29.7%			rhodanese family prot	tein					
SGO_0669	15	33.3%	12	27.6%	18	35.1%	14	30.1%	typA; GTP-binding pro	otein TypA					
	16	35.8%	17	38.2%	16	34.8%	12	26.7%							
SGO_0671	11	31.6%	19	58.4%	18	54.0%	3	13.6%	murD; UDP-N-acetyln	nuramoylalanineD-	glutamate				
	15	39.1%	14	46.7%	17	51.3%	5	17.3%	ligase						
SGO_0672	18 16	61.5% 54.2%	10	32.6% 37.6%	7 10	28.4% 39.3%	3	9.6%	murG; undecaprenyl- UDPGlcNAc GlcNAc tra		otide-				
							_	40.40/							
SGO_0673	12 18	29.2% 32.2%	5	17.4% 16.4%	4	15.1%	3	10.1%	DivIB; cell division pro	otein DivIB					
550 0574	19	52.4%	19	53.0%	18	54.3%	15	47.9%							
SGO_0674	23	59.2%	17	52.1%	19	55.4%	15	46.6%	ftsA; cell division prot	ein FtsA					
SGO_0675	17	49.2%	20	52.3%	17	48.9%	15	43.9%	ftsZ; cell division prot	ein Fts7					
	19	49.4%	18	50.6%	17	50.8%	15	46.1%	1.62, 66 arrision pro-						
SGO_0676	5	32.7%	5	27.4%	4	24.7%	4	31.4%	conserved hypothetica	al nrotein TIGR00044	1				
	7	39.0%	5	32.3%	6	38.1%	3	17.9%	conserved hypothetic	ar protein Traktoo					
SGO_0677	8	50.3%	7	55.6%	4	37.0%	3	31.7%	ylmF protein						
	9	63.5%	6	53.4%	7	56.6%	3	31.7%	yiiii proceiii						
SGO 0680	13	57.3%	12	56.5%	15	57.3%	13	52.4%	cell division protein D	ivIVA					
	13	57.3%	9	43.9%	15	57.3%	12	54.5%	cell division protein b						
SGO_0681	23	32.5%	22	33.9%	30	40.6%	21	33.2%	ileS; isoleucyl-tRNA s	vnthetase					
	28	36.1%	21	39.6%	29	41.0%	19	30.8%	iles, isoleucyi-titiva s	ynthictase					
SGO 0684	4	41.4%	5	41.4%	5	41.4%	4	41.4%	hypothetical protein S	SGO 0684					
J36_0001	5	42.4%	6	42.4%	4	41.4%	4	41.4%	nypotrietical protein S	JGO_0004					



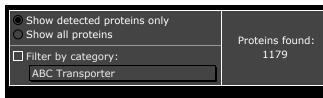
Cover		Streptococcus gordonii											Hackett Laboratory			
	9	Summai	mary Table   SgFn vs Sg				SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	vs SgFn	SgPgFn vs	SgPg	Coverage	Page 3
		Sg SgFn SgPg n Coverage n Coverage n Coverage		SgFn		SgPg		<sub>I</sub> PgFn				Sg	Sg	gFn	SgPg	SgPgFn
Protein	n (			Coverage	n C	Coverage	e Description Rep I Rep				II Rep I	Rep II	Rep I Rep II	Rep I Rep I		
SGO_0685	3	32.7%	3	34.0%					MutT/nudix family pro							
SGO_0688	27	48.1%	15	24.7%	24	41.7%	14	27.6%	ATP dependent Clp pr	otease, ATP-binding	subunit,					
340_000	35	50.2%	16	31.6%	26	48.2%	13	23.4%	CIPE							
SGO_0689	4	31.6%							hypothetical protein SGO_0689							
	3	17.3%	3	17.3%												
SGO_0690	4	20.8%	5	25.0%		17.3%			foID; methenyltetrahydrofolate cyclohydrolase							
	12	33.6%	8	24.7%	3	10.8%										
SGO_0693	14	33.2%	15	39.2%	3	10.8%	3	8.5%	xseA; exodeoxyribonu	uclease VII, large sub	ounit					
					3	45.7%										
SGO_0694	3	61.4%							xseB; exodeoxyribonuclease VII, small subunit							
SGO_0695			3	9.6%					goranyltranstransfora	foraço						
300_0033					3	16.5%			geranyltranstransfera	se						
SGO_0696	3	10.3%							hemolysin-like proteir							
	4	18.1%							Tiernorysin-like protein							
SGO_0697	3	34.3%			3	32.9%			transcription regulato							
	4	34.3%							transcription regulator							
SGO_0698	8	24.6%	10	27.0%		17.8%			recN: DNA repair prot	cein RecN		4				
	14	38.2%	7	18.3%	12	33.3%										
SGO_0699	3	26.4%	5	41.7%		31.4%			Serine/threonine prot	ein phosphatase						
	3	25.2%	6	35.1%	4	35.1%			, , , , , , , , , , , , , , , , , , , ,							
SGO_0700	7	39.4%	6	31.4%		42.2%	3	11.6%	DegV family protein	Serine/threonine protein phosphatase						
	7	33.6%	4	16.2%	9	45.1%	4	18.1%								



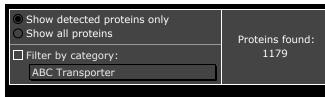
Coverage			Streptococcus gordonii										Hackett Laboratory		
	9	Summar	mary Table   SgFn vs Sg				SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 34
		Sg SgFn		SgFn		SgPg	Sg	ıPgFn			Sg	SgFn	SgPg	SgPgFn	
Protein	n (	n Coverage n Coverage			e n (	Coverage	n C	Coverage	Description			Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0701	7 10	59.3% 73.6%	8	73.6% 70.3%	6 7	49.5% 62.6%	7	62.6% 64.8%	hup; DNA-binding his	tone-like protein HU		00			
SGO_0704	15	70.9%	17	79.1%	21	80.4%	18	81.3%		gpmA; 2,3-bisphosphoglycerate-dependent					
	20	72.6%	18	83.9%	22	82.6%	18	77.4%	phosphoglycerate mutase						
SGO_0705	3	45.5%							Protein of unknown fu	Protein of unknown function (DUF1250) superfamily					
	3	12.0%	11	47.3%	7	32.8%									
SGO_0706	6	24.7%	10	42.8%	7	32.8%	5	17.8%	phoH-like protein						
SGO_0707	36	28.7%	32	25.8%	10	11.6%	6	4.9%	LPXTG cell wall surface protein						44
	46	33.0%	30	25.5%	4	3.2%	3	2.3%							
SGO_0708	18	65.1%	23	92.7%	19	77.6%	16	71.9%	ald; alanine dehydrog	enase					
-500 <u>-</u> 0700	20	76.8%	28	98.4%	22	88.6%	17	68.9%	all, delinic deli, diogenale						
SGO_0711	3	12.7%	4	20.6%					conserved hypothetica	conserved hypothetical protein TIGR00043		0			
	14	51.8%	15	61.9%	14	54.8%	7	29.1%					4		
SGO_0713	10	41.5%	16	59.5%	12	45.5%	9	36.8%	sgg; GTP-binding prot	tein Era					
SGO_0715															
300_0/13	3	18.2%			3	19.0%			mutM; formamidopyri	ımıdine-DNA giycosyi	ase				
SGO_0719	14	22.9%	6	11.3%	4	8.6%			rnri ribonucloaco D						
	15	25.3%	6	11.4%	5	10.9%			Till, Tiboliuciease R	rnr; ribonuclease R					
SGO_0721	7	13.7%	4	8.0%	4	7.5%	6	11.1%	abpB-like dipeptidase	lipoprotein					44
	10	19.8%	4	6.6%	3	6.3%	3	5.4%	abpb like dipeptidase	проргоссии					
SGO_0722	4	19.2%	5	22.0%	5	19.6%			tehB; tellurite resistar	nce protein TehB				44	
	9	37.1%	5	22.0%	5	19.9%									



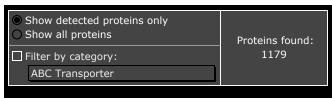
Cover		Streptococcus gordonii										Hackett Laboratory UW			
	5	Summar	mary Table SgFn vs Sg					g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	vs SgFn	SgPgFn vs SgPg	Coverage	Page 35
		Sg	Sg SgFn SgPg			SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage n Coverage n Coverage			n C	Coverage		Rep I Rep II	Rep I Rep II						
SGO_0724	12 14	32.5% 36.0%	6 5	20.5% 14.4%	5 6	16.1% 18.1%			dipeptidase					••	
SGO_0728	4	27.0%							ABC transporter, ATP-binding protein SP1653						
SGO_0729	7	5.2% 9.7%							ABC transporter perm						
SGO_0731	4	41.6% 41.6%							RRF2 family protein						
SGO_0736	9	43.1% 37.9%	10	46.3% 42.8%	5 5	22.8% 21.5%	3	11.9%	hprK; HPr(Ser) kinase/phosphatase					••	••
SGO_0737	3	14.5% 14.5%							lgt; prolipoprotein dia	04					
SGO_0738	5 5	57.5% 57.5%			3	51.2% 28.3%			Bacterial protein of ur family	Bacterial protein of unknown function (DUF948) family					
SGO_0739	7	43.5% 46.9%	4	28.6%	8	63.9% 63.9%	4	43.5% 55.8%	hypothetical protein S	GGO_0739					
SGO_0742	4	17.2% 20.7%	7	29.8% 29.4%	4 5	18.8% 25.9%	4	16.8%	peptidase, U32 family	,		04		••	••
SGO_0743	13	38.1% 48.8%	9	27.3% 17.8%	10	30.1%	7	21.5%	peptidase, U32 family	peptidase, U32 family					••
SGO_0745	3	44.3% 44.3%	3	38.6%	4	44.3% 44.3%	4	44.3% 44.3%	hypothetical protein S	GGO_0745		01			
SGO_0749	5	19.2% 29.0%	12 12	48.6% 45.4%	11	45.9% 38.8%	7	20.3%	glutathione reductase			01			••



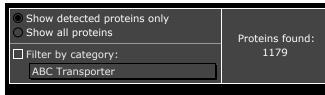
Coverage								S	Streptococ	cus gora	lonii			Hackett Laboratory						
	9	Summar	mary Table SgFn vs Sg				SgF	g vs S	SgPgFn vs Sg SgPg vs SgFn SgPgFn vs			s SgFn	SgPgFn vs SgPg	Coverage	Page 36					
		Sg SgFn		SgPg		Sg	ıPgFn			Sg	SgFn	 SgPg	SgPgFn							
Protein	n (	n Coverage n Coverage		ige n Coverage		n Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II							
SGO_0750	21 20	64.0% 61.9%	5 4	16.8% 18.8%	16 18	53.8% 60.9%	12 12	49.0% 41.4%	efflux transporter, RN	D family, MFP subun	it subfamily									
SGO_0751	9	45.0%	3	20.8%	13	74.5%	7	44.6%	ABC transporter, ATP-binding protein SP0786		144									
330_0/31	11	56.3%	5	34.2%	11	68.4%	7	40.3%												
SGO_0752	10	28.5%			5	17.5%			ABC transporter, ATP-											
	14	36.6%			6	16.7%	5	13.0%												
SGO_0753	22	45.8%	20	38.1%	24	48.0%	16	32.5%	lysS; lysyl-tRNA synth	sS; lysyl-tRNA synthetase										
	26	45.4%	19	40.3%	22	45.8%	16	33.3%												
SGO_0754			4	42.3%	3	27.7%			phosphoglycerate mu	tase family protein										
SGO_0755	6	57.0%	1	39.2%	4	43.7%														
	6	55.1%	5	44.9%	6	55.1%	4	41.8%	regulatory protein											
666 6757	10	49.2%																		
SGO_0757	9	52.4%							peptidase, U32 family											
SGO_0760	37	44.2%	34	42.7%	40	50.7%	18	24.1%	nna, nhaanhaanalniin											
300_0700	41	44.4%	29	40.4%	38	45.9%	18	23.8%	ppc; phosphoenolpyruvate carboxylase											
SGO_0761	31	78.1%	42	82.2%	37	79.9%	36	79.4%	tuf: translation along	ation factor Tu										
555_5751	32	78.1%	52	98.0%	36	79.9%	36	81.2%	tuf; translation elongation factor Tu											
SGO_0762	12	54.0%	13	55.2%	14	55.2%	12	54.0%	tpiA; triosephosphate isomerase											
	12	54.0%	13	54.0%	13	55.2%	12	54.0%	tpin, triosephosphate	13011161 036										
SGO_0763	19	59.9%	11	41.1%	14	45.5%	9	26.3%	murA-1; UDP-N-acety											
	17	58.2%	12	40.4%	15	54.2%	8	24.4%	carboxyvinyltransfera	se										
SGO_0765	4	21.9%							endA; DNA-entry nucl	lease										
	8	49.1%							Silarly Divit Chary Hack											



Cover	rage							S	Streptococ	ccus gora	lonii				ratory UW
	5	Summar	у Та	ble s	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 37
		Sg		SgFn		SgPg	Sg	<sub>I</sub> PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	10 46.4% 6 33.2% 8 42.2						n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0767			5%         11         50.5%         6         33.2%         4%         6         33.2%         8         42.2%         42.2%         44         6         42.2%         44						transport protein			01			
SGO_0771	12	45.0%     16     64.7%     12     58.9%     12     4       52.8%     14     60.3%     15     65.3%     10     4       82.3%     14     65.3%     18     74.6%     13     6						48.1%	pepq; proline dipeptid	lase					
	13 52.8% 14 60.3% 15 65.3% 10 41.4% per 25 82.3% 14 65.3% 18 74.6% 13 60.5%					41.4%	, .					-			
SGO_0773	26 82.6% 14 65.3%				_				ccpA; catabolite contr	rol protein A					
	26	82.6%	14	65.3%	17	74.3%	12	61.7%	, , , ,						
SGO_0774	12 17	38.0% 47.0%	5 6	15.9% 20.9%	5 7	20.6% 31.5%	4	17.1%	glycosyl transferase,	group 1 family protei	n	01		99	
SGO_0775	13	32.3%	11	30.9%	9	23.8%	4	12.4%	glycosyl transferase,	aroun 1					
	12	29.3%	10	30.2%	8	23.6%	7	19.7%	grycosyr trunsieruse, y	group i					
SGO_0778	23	46.7%	24	56.0%	25	53.8%	18	33.2%	thrS; threonyl-tRNA s	synthetase					
	25	43.7%	21	50.4%	28	56.1%	19	39.7%	tino, tinconyi titivi s	ynthetase					
SGO_0779	7	45.5% 54.1%	16 15	70.0% 65.2%	13 13	65.2% 61.4%	5	30.0% 14.2%	response regulator						
			7		_		3	14.2 /0				•		0 0	
SGO_0780	14	37.7% 36.9%	1	19.4% 14.8%	3	5.3% 13.2%			histidine kinase					00	
	11	43.8%	-	14.070	1 7	13.2 /0									0 0
SGO_0781	13	51.3%	3	23.2%					vicX; Zn-dependent h superfamily)	ıydrolase (beta-lactaı	mase				
	3	16.9%		20.270											
SGO_0782	3	16.9%							Protein of unknown fu	unction (DUF454) fan	nily	91			
CCC 4504	53	48.3%	18	21.9%	24	24.9%	9	10.0%							
SGO_0784	57	50.8%	18	21.6%	27	30.6%	8	10.0%	smc; chromosome se	gregation protein SM	С				
6CO 079E	4	20.4%	3	15.8%	3	20.0%			0.66 11 11						
SGO_0785	6	33.6%							Cof family protein						



Cover	rage							S	Streptococ	ccus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 38
	n Coverage n Coverage n Cove		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn			
Protein	86 6 39.4% 6					Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0786	6 5	39.4% 33.8%	9.4%     6     39.4%       8.8%     4     25.7%     7     46.1%       7.1%     14     38.9%     12     31.4%				5 5	33.8%	Cof family protein						
SGO_0787	20	47.1%     14     38.9%     12     31.4%       54.6%     9     23.8%     14     33.5%       18.5%     19     47.5%     15     40.7%					6	15.3% 17.4%	ftsY; cell division prot	ein FtsY					44
SGO_0788	7		54.6%     9     23.8%     14     33.5%     7     17       18.5%     19     47.5%     15     40.7%     7     19       30.5%     18     47.5%     13     38.5%     9     20       34.6%     7     13.5%     21     35.4%     11     18				7	19.8%	zwf; glucose-6-phosp	hate 1-dehydrogenas	se				••
SGO_0792	21	34.6% 34.9%	7				11	18.5% 18.0%	hypothetical protein S	6GO_0792		04		00	••
SGO_0794	16 19	38.9% 41.6%	19 15	43.4% 39.2%	20 19	35.6% 39.4%	9	20.4% 25.9%	metallo-beta-lactama:	se family protein					••
SGO_0795	4 5	24.0% 31.2%	6 9	31.2% 44.9%	5 6	32.3% 41.8%	4	26.6% 21.7%	tributyrin esterase						••
SGO_0797	6	12.8%	4	12.3%					RocB protein, putative	e					
SGO_0798	11	64.8% 55.1%	8	49.0% 48.2%	11 11	63.2% 60.3%	5 6	29.6% 35.2%	ABC transporter, ATP-	-binding protein SP13	381				
SGO_0800	11	48.2% 48.2%	4	23.0% 16.3%	6 5	29.7% 23.3%	3	15.7%	polysaccharide deacet	tylase family protein					••
SGO_0801	15 16	48.4% 53.5%	16 17	54.9% 55.4%	18 17	60.0% 54.2%	16 12	50.5% 42.5%	hom; homoserine deh	nydrogenase					
SGO_0802	10 12	54.9% 60.1%	8	43.1% 63.5%	10 10	55.6% 60.1%	5 8	28.1% 41.0%	thrB; homoserine kina	ase					
SGO_0803	7 8	20.8%			7 8	21.8% 23.8%	3	15.3% 15.3%	hypothetical protein S	GGO_0803		•		••	••



Cover	rage							S	Streptococ	cus gord	lonii				Hac Labo	ratory UW
	5	Summar	y Tal	ble S	SgFn '	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgP	gFn vs SgPg	Coverage	Page 39
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I Re	ep II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0804	5	17.2%	4	20.5%	4	11.9%			murB; UDP-N-acetyle reductase	nolpyruvoylglucosam	ine			44	44	
	6	25.2%	4		4	22.2%										
SGO_0805	12	30.9%	4 21.0% 3 13.8% 4 21.8% 5 11.7%						potA; spermidine/puti binding subunit	rescine ABC transpor	ter, ATP-					
	12	28.1%	4	21.8%	5	11.7%			- Sinding Subunit							
SGO_0806	4	15.7%							potB; spermidine/puti permease protein	rescine ABC transpor	ter,					
	4	15.7%							permease protein							
SGO_0808	13	57.0%	3	12.4%					potD; spermidine/put	rescine ABC transpor	ter					
	16	57.3%			6	29.2%										
SGO_0812	7	35.6%	5	31.5%	5	25.6%			hypothetical protein S	GO 0812						
	8	39.6%	7	38.9%	5	30.0%										
SGO_0813			3	3.8%					fructose-bisphosphata	ase				44		
	3	4.4%	3	7.7%												
SGO_0814							3	7.4%	aminotransferase, cla	ss-V						
	5	27.4%			3	13.9%			a							
SGO_0815	15	51.2%	8	31.4%	14	47.3%	6	22.0%	thiI; thiamine biosynt	hesis protein Thil						
	18	59.2%	9	33.4%	13	41.6%	7	26.5%	till, tillallille blosyfic	nesis protein mii						
SGO_0817	5	22.3%							hypothetical protein S	GO 0817						
	3	18.8%							nypothetical protein a	740_0017						
SGO_0818	3	49.0%	3	49.0%	4	57.7%	3	49.0%	rolli, ribocomal arota	in I 21						
	4	54.8%			3	49.0%	3	49.0%	rpIU; ribosomal protei							
SGO_0820	3	37.1%			5	49.5%	3	37.1%	rnmAı ribacamal azət	oin 1 27						
500_0020	3	37.1%	3	37.1%	5	49.5%	3	37.1%	rpmA; ribosomal prot	eiii LZ/						
SGO_0822	3	30.3%							linoprotoin sytatics							
-5GO_0622	5	36.0%							lipoprotein, putative							

○ Show all proteins	Proteins found:
☐ Filter by category:	1179
ABC Transporter	

Cover	rage							S	Streptococ	cus gora	lonii					ckett ratory UW
	9	Summar	у Та	ble s	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn \	/s SgFn	SgPgF	n vs SgPg	Coverage	Page 40
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	verage n Coverage n Coverage n 4 21.5%					Coverage		Description		Rep I Rep	p II Re	ep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0823	4	23.7%	4     21.5%       %     3       13.7%     4       25.9%       %     10       26.5%     15       38.9%     11       29						Cof family protein							
SGO_0824	11	31.3%	10	10     26.5%     15     38.9%     11     29.8%       13     32.1%     12     34.3%     10     27.8%					Local CTD bindings							
3GO_0824	19	46.5%	13	32.1%	12	34.3%	10	27.8%	lepA; GTP-binding pro	otein LepA						
SGO_0825	9	54.0%	3	20.4%	4	27.5%			linearetein nutative							
300_0023	7	35.1%			3	20.4%			iipoproteiii, putative							
SGO_0830	3	7.0%			3	8.5%			uvrC: ovcinucloaco AF	0.0						
333_333	3	7.4%	3	10.8%					uvrC; excinuclease ABC, C subunit							
SGO_0832	7	73.7%	3	43.0%	3	39.5%			hypothetical protein S	SGO 0832						
	8	78.9%			3	47.4%	3	40.4%	nypotnetical protein s	,GO_0032						
SGO_0833			7	40.2%	3	19.2%			phosphoesterase-rela	ted gene					44	
			7	31.3%	5	28.1%			phosphosoccius rela							
SGO_0834	4	8.1%							hypothetical protein S	GO 0834		4				
	5	9.2%	3	7.4%					,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,							
SGO_0835	8	39.8%	12	62.7%	12	58.7%	10	57.2%	nitroreductase							
	11	63.7%	11	62.7%	11	58.7%	10	61.2%							33	3 3
SGO_0836	17	52.2%	21	60.0%	21	65.5%	15	54.4%	pepV; dipeptidase Pep	οV						
	16	46.5%	22	69.2%	22	66.0%	13	48.4%								
SGO_0841			14	51.8%					oxidoreductase							
	4	13.9%	15	56.1%												
SGO_0842	4	51.0%	8	62.2%	3	40.8%	3	34.7%	rhodanese family prot	cein						
	4	51.0%	5	58.2%	5	58.2%	3	34.7%	, '							
SGO_0848	3	59.6%	5	60.6%	5	60.6%	5	60.6%	rpmE; ribosomal proto	ein L31						
	3	59.6%	3	59.6%	6	61.7%	4	60.6%	, , , , , , , , , , , , , , , , , , , ,							



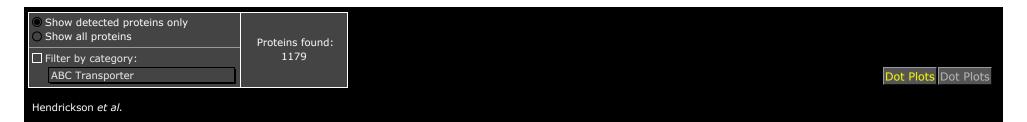
Cover	age							S	Streptococ	ccus gora	lonii					oratory UM
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn \	/s SgFn	SgPgFn	vs SgPg	Coverage	Page 4
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	overage         n Coverage         n Coverage         n Coverage         n           31.2%         10         41.1%         10         43.3%           43.0%         7         32.5%         8         34.7%						Coverage		Description		Rep I Rep	II Rep	I Rep II	Rep I Rep	II Rep I Rep II
SGO_0849	9 12		31.2%     10     41.1%     10       43.0%     7     32.5%     8       51.7%     5     55.8%     4       38.1%     4     51.7%     4						DHH subfamily 1 prot	ein					04	
SGO_0850	4	51.7%	5		4	51.7%	4	51.7%	flavodoxin						44	
	3 38.1% 4 51.7% 4					51.7%	4	51.7%								
SGO_0851	_	18.8%     3     15.5%     3     15.2%       11.1%     3     15.7%       29.9%     4     15.8%     4     14.8%							putative permease			44			44	
SGO_0852	8 7	29.9%	5	15.8% 17.8%	3	14.8% 12.3%			TPR domain protein					00		
SGO_0853	6	37.2%	3	21.8%	3	19.7%			budA; alpha-acetolact	tato docarbovylaco						
330_333	4	25.1%	4	24.7%	3	22.2%			buuA, aipila-acetolact	tate decarboxylase						
SGO_0854	65	33.6%	23	18.9%	7	5.9%	4	3.1%	cshA; surface-associa	ted protein CshA					44	
	71	35.1%	18	15.7%	10	9.1%	4	2.6%	,	·						
SGO_0855	10 12	24.2%	6	14.0%	9	24.5% 18.4%			fbpA; fibronectin-bind	ling protein A		4			44	
		28.9%						0= 00/								
SGO_0856	14	68.3%	6	32.3%	12	60.8%	6	27.8%	ABC transporter, subs	strate binding protein	1					
	19	73.1%	5	24.6%	12	56.3%	6	27.2%								
SGO_0858	4	16.7%			_				ABC transporter, ATP-	-binding protein						
	7	33.7%					_									
SGO_0859	13	44.4% 42.1%	10	34.7%	11	39.0% 39.3%	6 9	20.6% 31.2%	pheS; phenylalanyl-tF	RNA synthetase, alph	a subunit				01	
	25	42.9%	15	29.0%	26	50.2%	16	30.3%								3 3
SGO_0861	27	40.2%	15	33.6%	26	44.9%	16	29.8%	pheT; phenylalanyl-tR	RNA synthetase, beta	subunit					
	3	14.3%														
SGO_0862	4	24.5%							hypothetical protein S	GGO_0862						



Streptococcus gordonii							kett ratory UW								
	9	Summa	гу Та	ble s	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 42
		Sg	overage n Coverage n Cov				Sg	<sub>1</sub> PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	nC	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0868	3	59.7%							hypothetical protein S	GO_0868					
SGO_0877	3	13.9%		39.1% 4 24.9% 3 17.6%					permease domain pro	tein					
SGO_0885	7	44.4%	14.4%     6     40.6%     4     24.9%     3     20.3       17.9%     6     39.1%     4     24.9%     3     17.6				3	20.3%	cohumic poid cumthoco						
300_0003	8	47.9%	6	39.1%	4	24.9%	3	17.6%	cobyric acid synthase						
SGO_0886	4	13.4% 21.5%	6 5	18.1% 13.6%	4 5	12.8% 17.7%			Mur ligase family prot	ein		9		99	
	7	24.6%		10.070		17.770									
SGO_0887	10	28.5%							conserved hypothetica	al protein TIGR00159	)	9			
	6	41.5%			3	25.8%									
SGO_0888	8	48.0%			3	25.8%	3	25.8%	hypothetical protein S	GGO_0888					
666 6666	14	42.0%	6	19.3%	14	40.9%	9	24.2%							
SGO_0889	15	49.1%	9	28.9%	14	47.1%	4	12.9%	glmM; phosphoglucos	amine mutase					70
SGO_0890	7	11.0%	9	17.3%					LPXTG cell wall surfac	e protein, collagen b	inding				
300_0890	9	12.5%	8	15.7%					domain	. , ,	J				
SGO_0893	16	53.2%	15	56.7%	15	54.4%	10	39.0%	GTP-binding protein						
566_6655	18	56.9%	14	53.9%	18	58.3%	11	42.0%	GTP-billding protein						
SGO_0899	4	15.0%							putative hydrolase or	acyltransferase					
	7	24.6%							putative flyurolase of	acylci alisiei ase					
SGO_0901	10	28.1%	10	29.9%	10	26.8%	3	10.3%	DNA-directed DNA pol	lymerase III					
	8	21.0%	8	23.4%	11	32.9%	6	18.3%	Divit directed Divit poi	rymerase III					
SGO_0904	3	10.5%							purR; galactose opero	on repressor GalR		•			



Cover	Streptococcus gordonii					lonii			Hac Labor	_					
	9	Summai	гу Та	ble s	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 43
				SgFn		SgPg		<sub>1</sub> PgFn		Danasialian		Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II	
SGO_0905				1 Coverage n Coverage					lipoprotein, putative						
SGO_0906	9	25.7%	5.9%   5.7%   15   33.39 5.1%   15   35.19 6.6%			36.0%	10	29.3%	l. A 2 l						
300_0900	9	24.1%	24.1% 15 35.1° 1.6%			35.1%	13	38.1%	ieuA; 2-isopropyimaia	ite syntnase					
SGO_0907	3	11.6%		15     35.1%     14     35.1%       3     11.6%					lau.D. 2 iaaanaan laaala						
300_0907	3	12.8%			3	11.6%	13 38.1% leuB: 3-isopropylmalate dehydrogenase								
SGO_0909			4	18.7%					laC. 2 :	to deliciduates a lava					
300_0909			3	16.1%	4	10.4%			ieuC; 3-isopropyimaia	ite denydratase, iarg	e subunit				
SGO_0911	6	36.3%	leuB; 3-isopropylmalate dehydrogenase  4 18.7%  leuC; 3-isopropylmalate dehydratase,					200 0011							
300_0311	12	57.9%	11	58.7%	10	57.1%	9	48.3%	nypotnetical protein S	GO_0911					
SGO_0915	6	43.4%			3	21.9%			pro//. ABC type prolin	o/alveino hotaino tra	ncportor				
300_0313	8	47.5%			3	25.2%			proV; ABC-type prolin	e/grycine betaine tra	insporter				
SGO_0916	12	32.4%							proWX; ABC transport	ter membrane-spann	ning				
565_6515	13	36.4%							permease						
SGO_0932	6	15.3%							galK; galactokinase						
	5	17.1%							gaik, galactokillase						
SGO_0934			3	15.9%					galE-2; UDP-glucose 4	1-enimerase					
	5	22.2%	3	15.9%					gail 2, obi giacosc -	т срипстазс					
SGO_0936	4	6.4%							phosphoenolpyruvate	synthase nutative					
	3	4.9%					3	5.5%	phosphoenolpyravate	synthase, putative					
SGO_0938							3	15.2%	Phosphatidylserine de	carboxylase proenzy	me 2				
									, ,	, , , ,					
SGO_0940	8	16.1%					3	7.6%	ppsA; phosphoenolpyi	ruvate synthase		4			
	5	8.6%							, p , p	, , , , , , , , , , , , , , , , , , , ,					



Cover	Streptococcus gordonii								Hackett boratory	_							
	9	Summa	гу Та	ble s	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	's SgFn	SgF	gFn vs SgPg	Covera	ge Page 4	14
		Sg	g SgFn SgPg Sg. verage n Coverage n Coverage n C		ıPgFn				Sg		SgFn	SgPg	SgPgFn				
Protein	n (	Coverage	age n Coverage n Coverag					Coverage		Description		Rep I Re	ep II	Rep I Rep II	Rep I Re	o II Rep I Rep I	I
SGO_0941	4	18.2%	n Coverage n Coverage n (						hypothetical protein S	GO_0941							)
SGO_0942	17	8.7%							zmnC: zinc motallonro	otoinaso C							
340_0342	17	10.7%	7% 4%						zmpC; zinc metallopro	otemase C							,
SGO_0944	3	20.4%		7 05 00/ 7 04 00/ 4 45 40					ADC transporter ATD	binding pustoin							$\Box$
300_0344	4	27.4%							ABC transporter, ATP-	-binding protein							<b>,</b>
SGO_0946	6	21.2%	7	25.8%	7	24.6%	4	15.4%	Deble dring aminopont	bi daga							$\Box$
340_0340	7	26.1%	8	32.5%	4	15.1%	5	18.3%	Deblocking aminopept	lidase						,	
SGO_0948	9	28.0%	7	16.1%					pgdA; peptidoglycan N	N-acetylglucosamine	deacetylase						
340_0340	8	20.6%	10	29.2%					Α								,
SGO_0949	8	27.0%	5	24.0%	5	17.0%	3	10.0%	deaD; DEAD RNA helio	caso							
340_0343	8	24.0%	4	15.9%	5	18.6%			dead, DEAD RIVA Helio	case							,
SGO_0950			7	31.9%	3	16.9%	3	22.4%	oxidoreductase								
365_0350	6	28.8%	5	23.3%	3	16.9%			oxidoreductase			j					,
SGO_0951	7	43.8%	6	44.8%	7	44.3%	4	27.6%	udk; uridine kinase								
363_0351	8	48.1%	6	44.8%	7	54.8%	3	22.9%	uuk, ullulle killase								,
SGO_0953					3	42.1%			endoribonuclease L-PS	SP putativo							
363_0355					3	42.1%			endoribonaciease E-F3	or, putative							,
SGO_0954	8	32.1%	7	26.0%	6	28.7%	3	11.8%	ATP-binding protein								
555_551	7	30.4%	6	26.4%	9	37.5%	4	18.6%	ATP-billuling protein								,
SGO_0955	5	22.8%	5	21.3%					transporter								
	6	26.5%	4	17.3%	6	27.2%			transporter								,
SGO_0957	6	46.6%							hypothotical protein C	CO 0057							
200_0337	6	46.6%	3	24.5%					hypothetical protein S	00_0937							,

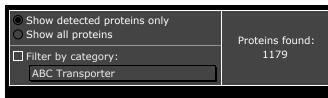


Cover	rage							S	treptococ	cus gora	lonii					ratory UW
	5	Summar	у Та	ble S	gFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPg	JFn vs SgPg	Coverage	Page 45
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_0959	5	36.2% 24.8%	% 6 45.7% 5 36.2% % 6 37.6% 5 36.2% %						copper homeostasis p	rotein CutC						
			0									)	_			
SGO_0961	5 7	15.4%	7.6%						ABC transporter, pern	nease/ATP-binding p	rotein					
SGO_0962	3	7.6%	9% 6% 3% STATE OF THE TRANSPORT OF THE T						ADC transporter norm	oogga/ATD binding n	watain					
300_0302	3	8.3%							ABC transporter, pern	nease/ATP-binding p	rotein					
SGO_0966	9	5.6%		4.2%					hsa; streptococcal her	magalutinin				44		
	10	6.3%	5	3.8%					, , , , , , , , , , , , , , , , , , , ,							
SGO_0969	4	17.1%	3	13.8%					nss; nucleotide sugar	synthetase-like prot	ein					
	3	17.1%		5 3.8%												
SGO_0971	4	9.1%							asp1; accessory secre	etory protein		4				
	-	3.370											_			
SGO_0972	5	12.0%							asp2; accessory sescr	etory protein						
	6	16.6%														
SGO_0975	4	10.3%							gtaA; glycosyl transfe	rase, group 1 SP175	8					
CCO 0070	4	15.7%														
SGO_0979	4	16.7%							degV family protein							
SGO_0980	3	18.0%							transcriptional regulat	or TetR family dom:	ain protein					
										or, reactaining dollar	uni protein					
SGO_0981	6	40.6%			4	31.6%			comE operon protein	2 family						
	5	41.9%	3	20.6%						,						
SGO_0982	19	68.0%	4	25.4%	11	47.9%	4		amino acid ABC trans	porter, amino acid-bi	inding			44		44
	23	70.8%	3	17.6%	10	49.6%	4	25.4%	protein							

lots Dot Plots

Cover	rage							S	Streptococ	ccus gora	lonii					Hack abora	
	5	Summa	гу Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgP	gFn vs SgP	Covera	age	Page 46
		Sg		SgFn	9	SgPg	Sg	<sub>I</sub> PgFn				Sg		SgFn	 SgPg	,_ 7	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Re	ep II	Rep I Rep II	Rep I Re	ep II	Rep I Rep II
SGO_0983	5 5	36.9% 36.9%	rage n Coverage n Coverage n Soverage n Coverage n Cove						amino acid ABC trans SP0709	porter, ATP-binding រុ	orotein						
			16 38.4% 16 40.4% 11 35.99										_			_	
SGO_0986	5 5	26.5% 26.5%		38.4% 16 40.4% 11 35.9%					hypothetical protein S	GO_0986							
			40	20.40/	40	40.40/	44	25.00/				)	_	0 0		_	
SGO_0987	12	30.6%					_		metK; S-adenosylmet	etK; S-adenosylmethionine synthetase							
			14	39.4%	10	30.3%	10	20.0%			)	_			_		
SGO_0991	3	53.6%			3	53.6%			hypothetical protein S								
550,0003			3	8.5%			4	12.9%									
SGO_0993			4	10.2%	5	13.8%			GTP-binding protein H	lfIX							
SGO_0994	3	21.7%			3	24.6%			la contration of a state of	200 0004							
300_0994	5	39.1%			3	24.6%			hypothetical protein S	GGO_0994							
SGO_0995	7	23.0%	4	22.7%	13	56.0%	4	20.4%	motalla hata lastama	aa ay namfamily muata	·						
340_0333	7	31.4%	6	28.5%	6	27.5%			metallo-beta-lactama	se superrannily protei	III						
SGO_0996	5	25.5%							oxidoreductase, short	-chain dehydrogenas	se/reductase						
546_6556	6	38.6%							family								
SGO_0997	7	34.6%	3	17.5%	4	23.1%			hypothetical protein S	SCO 0007							
566_6557	7	34.6%	3	17.5%	3	17.5%			nypothetical protein s	340_0997							
SGO_1000	4	8.1%	9	19.2%	9	17.9%			recJ; single-stranded-	-DNA-specific exerus	lesse Pecl						
555_1555			11	22.9%	7	14.1%			recs, single-stranded-	-DNA-specific exolluc	ilease Recj						
SGO_1001	11	67.1%	9	67.6%	11	78.2%	12	72.9%	apt; adenine phospho	rihosyltransferase							
	11	77.6%	8	68.8%	13	82.9%	10	75.9%	ape, ademine phospho	in bosyntransicrase							
SGO_1002									metA; homoserine O-	succinyltransferase							
	4	15.3%							,	,							

Cover	age							S	Streptococ	cus gord	lonii				kett atory UW
	5	Summar	у Та	ble s	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 47
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1003	7 5	38.5% 29.6%	3	16.4% 23.9%	5	29.6% 32.3%			DNA replication protei	in DnaD		04			
SGO_1004	3	14.1%	3 5	14.1% 25.2%	4 3	17.2% 13.4%			glutathione S-transfer	rase family protein		04		••	
SGO_1005	3 5	21.0% 30.1%	5 5	34.5% 27.1%	5	27.1% 39.3%	4	27.5% 23.1%	Bcl-2 family protein						••
SGO_1006	3	14.3%	3	15.8%	3	22.6% 15.8%			conserved hypothetica	al protein TIGR00486	5			••	
SGO_1007					3	11.5% 11.5%			oxidoreductase, DadA	family protein SP16	08			••	
SGO_1009	13 16	63.3% 65.4%	23 21	87.9% 92.0%	17 19	77.2% 85.1%	15 15	77.5% 70.6%	rfbA-1; glucose-1-pho	osphate thymidylyltra	nsferase				
SGO_1010	7	42.6% 47.2%	8 7	47.2% 48.2%	7	42.6% 42.6%	7 6	42.6% 38.1%	rmIC; dTDP-4-keto-6-	-deoxyglucose-3,5-ep	oimerase				
SGO_1011	10 16	38.2% 53.2%	20 17	64.4% 57.5%	16 17	51.7% 51.7%	14 13	47.7% 49.1%	rfbB-1; dTDP-glucose	4,6-dehydratase					
SGO_1012	14 12	50.1% 48.1%	17 18	56.9% 62.8%	14 14	47.5% 57.8%	11 14	43.4% 55.8%	galE-1; UDP-glucose 4	4-epimerase		01			
SGO_1013	6 7	37.3% 41.5%	3	16.9%	3	23.7%	3	17.8%	Glycosyltransferase in	nvolved in cell wall bio	ogenesis				
SGO_1016	8	41.5% 46.9%	3	12.3%	5	26.9% 27.3%	3	15.8%	putative glycosyltrans	sferase		01			
SGO_1018	4	9.1% 8.1%							hypothetical protein S	GGO_1018		04			



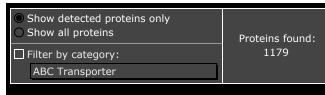
Cover	rage							S	Streptococ	cus gora	lonii					oracor y	N
	9	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn	/s SgFn	SgPgFn	vs SgPg	Coverage	Page	48
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	SgPg	SgPgFn	
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	o II Rep	Rep II	Rep I Rep I	I Rep I Rep	II
SGO_1019	7 8	29.2% 29.2%	4	24.0%	4	19.2% 19.5%	3	13.6%	glycosyl transferase			94			94		
	13	55.1%	15	62.5%	12	57.2%	8	32.9%									
SGO_1020	14	60.1%	15	67.8%	15	67.1%	7	29.0%	rfbD; dTDP-4-dehydro	orhamnose reductase	2						
SGO_1021	9	38.2%							rgpA; rhamnosyltrans	ferase nutative							
	14	47.6%							Typit, mammosylerans	reruse, patative							•
SGO_1022	8 7	35.8% 31.3%							rhamnosyltransferase								
	15	37.8%	4	15.5%	9	26.5%											
SGO_1024	17	40.3%	5	17.4%	7	17.7%			putative polysacchario	de ABC transporter					7		
SGO_1025	12	39.6%	8	30.7%	9	28.1%	9	24.7%	rgp; glycosyltransfera	ise						44	
	15	45.4%	5	22.7%	10	31.6%	6	19.8%	3,7,3,444,444								
SGO_1026	22 29	34.7% 40.4%	9 10	16.0% 17.7%	8 12	19.2% 26.5%	3	5.8% 5.8%	rhamnosyltransferase						44	04	
			10	17.770	12	20.5%	3	5.0%									$\dot{-}$
SGO_1027	11	20.2%							hypothetical protein S	GGO_1027		0					
	3	28.4%															$\overline{}$
SGO_1028	4	28.4%							hypothetical protein S	GO_1028							
SGO_1030									hunothatical protein C	200 1020							
300_1030	3	28.9%							hypothetical protein S	0GU_1030							
SGO_1031	6	39.1%	6	43.1%	7	48.0%	3	23.1%	cmk; cytidylate kinase	e							
	7	45.3%	5	34.2%	7	51.1%	3	23.6%									
SGO_1032	4	29.0%			4	30.7%	4	24.4%	infC; translation initia	tion factor IF-3						144	
	4	29.0%			4	30.7%	3	20.5%									_



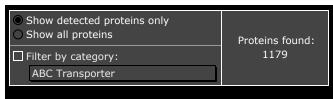
Cover	rage							S	Streptococ	cus gora	lonii				ratory UW
	5	Summar	у Та	ble s	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 49
		Sg		SgFn	9	SgPg	Sg	<sub>1</sub> PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1033	3 5	18.2% 30.3%	5	33.3% 18.2%			3 4	18.2% 18.2%	rpmI; ribosomal prote	ein L35		04			
SGO_1034	7	52.1% 52.1%	6	54.6% 73.9%	7	52.1% 52.1%	5 5	47.1% 51.3%	rplT; ribosomal protei	n L20					
SGO_1035	4	34.1% 34.1%	5	36.5% 38.1%	3	28.6%	3	28.6%	gloA; lactoylglutathio	ne Iyase					
SGO_1036	10	54.9% 52.0%	13 6	69.1% 35.8%	7 10	45.5% 64.6%	3	17.5% 20.3%	amino acid ABC trans SP1242	porter, ATP-binding p	orotein				••
SGO_1037	9	26.6% 37.1%	3	8.0% 14.2%	5 8	9.5% 21.6%			glutamine ABC transp binding protein	orter permease and	substrate			00	
SGO_1038	6	10.6% 15.6%	9	19.2% 19.9%	7 8	14.8% 16.0%	6 7	10.1% 13.1%	uvrB; excinuclease AE	3C, B subunit				••	••
SGO_1039	3	18.2% 10.5%							hypothetical protein S	GGO_1039					
SGO_1041	3	24.3%	3	32.0%	3 4	27.1% 40.3%			hypothetical protein S	GGO_1041					
SGO_1044	3	22.6%	3	23.9%	3	26.5% 32.9%			MutT/nudix family pro	otein		04		90	
SGO_1047	10 14	29.2% 35.4%	3	9.7%	8 9	22.2% 27.1%	5 3	14.6% 9.4%	hypothetical protein S	GGO_1047				99	••
SGO_1049	3	18.8% 29.8%			4	21.6% 22.6%	3	20.5%	tRNA pseudouridine s	ynthase B				99	••
SGO_1050	3	9.8%	3	10.5%	4	15.4% 12.1%	4	16.4%	ribF; riboflavin biosyn	thesis protein RibF		01		00	••



Cover	rage							S	Streptococ	ccus gora	lonii					lackett boratory	
	9	Summar	у Та	ble !	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn	vs SgPg	Coverag	je	Page 50
		Sg		SgFn	9	SgPg	Sg	<sub>1</sub> PgFn				Sg		SgFn	SgPg	S	gPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	nC	Coverage		Description		Rep I Rep	II Rep	I Rep II	Rep I Rep	II Rep	I Rep II
SGO_1051					5	43.6%	3	21.8%	negative regulator of	proteolysis							
SGO_1054	4	13.8%			3	14.5%			NOL1/NOP2/sun famil	ly protoin							
330_2331	5	18.2%							NOLI/NOFZ/Sull famili	ry protein							
SGO_1055	12	67.2%			4	21.2%			phosphate ABC transp	porter, phosphate-bir	nding						
330_1055	13	71.3%			5	25.9%			protein								
SGO_1057	4	10.2%							pstA; phosphate ABC PstA	transporter, permea	se protein	•					
CCO 1050	12	40.8%			5	17.6%	4	13.1%	pstB; Phosphate impo								
SGO_1058	14	46.1%			4	15.4%			(Phosphate-transporti transporter 2)	ing ATPase 2) (ABC p	phosphate						
SGO_1059	9	46.4%	3	17.9%	7	48.4%	7	44.8%	pstB; Phosphate impo								
300_1039	9	46.4%	3	17.9%	8	48.8%	6	38.5%	(Phosphate-transporti transporter 1)	ing AlPase 1) (ABC p	onospnate						
SGO_1060	11	55.8%	7	39.2%	9	54.4%	6	37.8%		sustana va sulatanu nu	atain						
300_1000	11	55.8%	7	41.0%	12	57.6%	6	37.8%	phosphate transport s	system regulatory pri	otein						
SGO_1065	8	41.7%	7	42.8%	4	32.1%	4	32.1%	hypothetical protein S	SCO 1065							
330_1003	8	43.3%	4	32.1%	4	32.1%	3	27.8%	nypothetical protein s	3GO_1003							
SGO_1066	12	37.3%	8	23.9%	5	12.0%			hypothetical protein S								
	14	37.0%	10	25.0%	4	11.1%			nypotnetical protein s	340_1000							
SGO_1067			3	64.3%					hypothetical protein S	SGO 1067							
	3	57.1%							nypotnetical protein s	330_1007							
SGO_1069	32	45.6%	27	44.3%	36	53.5%	21	37.5%	membrane alanyl ami	inonentidase							
	27	40.0%	35	54.9%	31	51.0%	20	35.1%	membrane alanyi ami	порершазе							
SGO_1072			5	31.3%	4	21.4%			ciaD: Transcriptional	regulatory protoin Ci	a D						
	3	14.7%	7	34.4%					ciaR; Transcriptional i	regulatory protein Cl	aix						



Cover	age							S	Streptococ	ccus gora	lonii				kett ratory UW
	5	Summar	у Та	ble :	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 51
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1073	6	17.6% 17.6%	5	15.2%	4	9.9%			Sensor protein CiaH					00	
SGO_1075	4	12.2%	7	22.8% 15.3%	_	11.2%			alpha-amylase precur	rsor				00	
SGO_1077	5	19.6% 25.2%	3	13.7% 18.6%	4	14.4%			coaA; pantothenate k	inase		01		00	
SGO_1078			3	35.0% 42.6%	_	35.0% 35.0%			methyltransferase do	main protein		0 (			
SGO_1079	10	31.3% 28.9%	9	29.2% 36.5%		39.8% 35.5%	5 7	20.0% 25.6%	pdp; pyrimidine-nucle	eoside phosphorylase					••
SGO_1080	11 12	68.6% 70.9%	12 10	70.9% 61.4%		70.9% 72.3%	13 12	72.3% 70.9%	deoC; deoxyribose-ph	nosphate aldolase					
SGO_1081	3 5	38.8% 55.0%			3	58.1% 44.2%	3	44.2%	cdd; cytidine deamina	ase					
SGO_1082	22 31	66.5% 75.0%	22 20	65.9% 62.2%	_	65.9% 63.4%	20 18	65.9% 63.4%	lipoprotein						
SGO_1083			19 20	53.8% 49.1%	-	61.1% 58.1%	19 18	43.4% 47.6%	sugar ABC transporte	r, ATP-binding protei	n SP0846				
SGO_1088	3	17.9% 24.8%			7	28.5%	3	23.2%	transcription regulato	r, LysR family		04			
SGO_1090	7	31.1% 33.1%	4	20.9%	9	33.1% 33.4%			pseudouridine syntha	se, RluA family					
SGO_1091	3	20.5%							hypothetical protein S	6GO_1091		01		••	



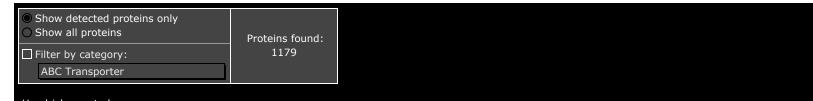
Cover	rage							S	Streptococ	ccus gora	lonii				Hac Labo	ratory UW
	5	Summai	y Tal	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgI	Fn vs SgPg	Coverage	Page 52
		Sg		SgFn	9	SgPg	Sg	<sub>I</sub> PgFn				Sg		SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	p II R	ep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1096	10	53.1%	15	64.6%	12	61.4%	12	61.4%	butA; acetoin dehydro	ogenase						
	10	58.3%	20	82.7%	12	61.4%	11	61.4%								-
SGO_1097			3	9.8%					proB; glutamate 5-kir	nase						
	3	8.7%														
SGO_1098			8	31.4%	6	22.9%	3	13.8%	proA; gamma-glutam	vl nhosnhate reducta	ise					
	4	11.9%	6	21.4%	7	26.4%	3	14.3%	proviy gariina gratain	yr priospriate reducte	.50					
SGO_1099			4	18.7%					proCi pyrrolino E carl	hovulato roductaco						
340_1033	3	19.0%	5	23.9%					proC; pyrroline-5-carl	boxylate reductase						
SGO_1100									phnA; alkylphosphona	ate utilization operon	protein					
300_1100	4	34.8%							PhnA	·	•					
660 1103	3	13.4%														
SGO_1103	3	14.8%							carA; carbamoyl-phos	sphate synthase, sma	all subunit		יוכ			
666 4464	14	20.8%					4	4.2%								4
SGO_1104	9	11.2%	4	5.9%					carB; carbamoyl-phos	sphate synthase, larg	je subunit		יוכ			
	7	49.1%														
SGO_1107	7	49.1%	3	28.3%	4	33.5%	3	26.6%	PyrR bifunctional prot	ein						
	14	50.3%	9	38.6%	14	48.0%	10	45.1%								
SGO_1109	15	52.9%	10	38.9%	16	57.8%	8	37.3%	pyrB; aspartate carba	imoyltransferase				JJ		
	15	26.4%														
SGO_1110	21	35.4%	4	7.9%					surface antigen SCP-I	ike domain						
	13	59.1%	4	21.5%	7	40.1%	4	21.9%								
SGO_1111	14	60.3%	3	18.2%	4	22.7%			fruR; phosphotransfer	rase system represso	or			JJ		
	11	51.8%	5	32.7%	8	37.3%										
SGO_1112	14	60.4%	4	22.4%	11	59.4%	3	14.9%	fruB; 1-phosphofructo	okinase				JJ		

<ul><li>Show detected proteins only</li><li>Show all proteins</li></ul>	Proteins found:
☐ Filter by category:	1179
ABC Transporter	

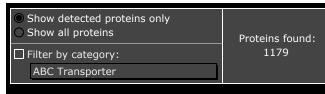
Cover	rage							S	Streptococ	ccus gora	lonii					ackett oratory	UW
	5	Summar	y Tal	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgF	Fn vs SgPg	Coverag	е	Page 53
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	SgPg	Sg	PgFn
Protein	n (	Coverage	n C	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	p II R	ep I Rep II	Rep I Rep	II Rep I	I Rep II
SGO_1113	21 26	34.8% 41.3%	9 5	16.8%	13 14	27.6% 27.4%	8 11	18.7% 24.2%	fruA; PTS system, fru	ctose specific IIABC	components			90	01		
SGO_1114	7	42.7% 36.3%	5	42.7% 29.8%	7 5	51.6% 31.5%	4	31.5% 25.0%	Protein of unknown fu	unction (DUF1149) su	uperfamily				04		
SGO_1115	0	30.3%	3	29.070	3	13.4%	3	25.0%	DegV family protein								
	3	12.0%	3	13.4%	3	12.0%			zegr ranni, protein								
SGO_1116	6	43.1% 43.5%	7	39.6% 37.6%	7	43.5% 43.5%	6	43.1% 43.1%	dapB; dihydrodipicolir	nate reductase							
SGO_1117			7	30.8% 17.3%	4	9.8% 15.8%			pcnA; polynucleotide	adenylyltransferase		0 (			01		
SGO_1118			5	12.4%	4	8.9%			ABC transporter, ATP-	-binding protein SP15	553						
	6	12.7%	8	14.8%	5	9.7%											
SGO_1119	3	9.4% 5.8%							Abi-alpha protein, put	tative							
CCO 1120	21	50.4%	20	49.0%	21	54.4%	15	46.3%									
SGO_1120	25	57.3%	25	64.3%	24	54.1%	17	45.8%	guaA; GMP synthase				יוע				
SGO_1121		40.00/				00.40/			transcription regulato	r, GntR family					04		
	5	16.8%			3	22.4%										4	
SGO_1123	11	28.4% 38.7%	16 14	47.1% 43.3%	20 21	54.4% 54.4%	13 14	41.2% 44.7%	ffh; signal recognition	n particle protein							
SGO_1124	3	18.0%							cell surface hydrolase			4					
	4	22.5%															
SGO_1128	6	10.3%							bacteriocin-associated subfamily	d integral membrane	protein						



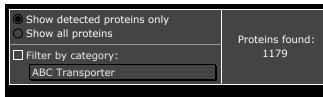
Cover	age							S	Streptococ	cus gora	lonii				H Lal	ackett poratory	
	5	Summar	y Tal	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPg	Fn vs SgPg	Coverag	e	Page 54
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	_ SgPg	Sg	<sub>I</sub> PgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Re	p II F	Rep I Rep II	Rep I Rep	II Rep	I Rep II
SGO_1129	9	33.1% 35.6%	6 4	14.9% 14.9%	8	35.3% 33.7%	7	26.4% 26.4%	lpIA; lipoate protein li	gase A					04		
SGO_1130	21	39.7% 42.0%	4 5	8.1% 14.8%	14 17	28.6% 35.4%	13 11	30.0% 24.2%	dihydrolipoamide deh	ydrogenase				44	41		
													_				
SGO_1131	10	34.9% 40.3%	4	18.4%	8	32.3% 35.4%	5	19.3% 23.9%	sucB; dihydrolipoamic	de S-acetyltransferas	е						
	16				9												
SGO_1132	5 7	22.4% 28.5%			5	26.1% 26.1%	3	17.6%	acetoin dehydrogenas	se					94		
SGO_1133	7	30.1%			6	26.7%	6	29.2%	acoA; acetoin dehydro	ngonaco							
330_1133	8	33.2%	5	15.8%	7	30.7%	4	20.5%	acoA, acetoin denyuro	ogenase							
SGO_1134	6	16.5%	7	20.9%	4	14.4%			hypothetical protein S	SCO 1134							
330_1151	6	22.9%	12	37.6%			4	12.4%	nypothetical protein 3	300_1134							
SGO_1139	9	58.9%	10	55.8%	13	73.1%	7	49.2%	GTP-binding protein								
	12	64.5%	8	49.7%	14	78.7%	8	43.7%				-					
SGO_1140	15	43.8%	15	46.9%	20	67.5%	12	35.9%	clpX; ATP-dependent subunit ClpX	Clp protease, ATP-bi	nding						
	20	49.1%	16	46.0%	20	67.2%	14	45.7%	Suburiit Cipx								
SGO_1141	5	40.6%	4	36.5%	4	36.5%	3	23.5%	folA; dihydrofolate red	ductase							
	4	25.9%	7	53.5%	4	36.5%											
SGO_1143	3	16.5%	3	17.2%	4	21.1%	3	16.5%	thyA; thymidylate syr	nthase					44		
	4	21.1%	4	23.7%	4	19.7%											
SGO_1144	14	45.5%	19	79.6%	19	72.1%	13	58.6%	glcK; glucokinase								
	19	63.9%	19	77.1%	18	69.0%	13	64.3%									
SGO_1145	4	21.7% 17.8%							cell surface hydrolase								
	4	11.070															



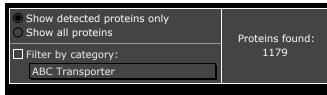
Cover	age							S	Streptococ	cus gord	lonii					ckett cratory UW
	S	Summar	y Tal	ole S	SgFn '	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPg	gFn vs SgPg	Coverage	Page 55
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	<b>_</b> SgPg	SgPgFn
Protein	n C	Coverage	n C	Coverage	e n C	Coverage	n C	Coverage		Description		Rep I Re	ep II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1148	46 48	28.8% 29.5%	11 11	9.0%					cshB; surface-associa	ted protein CshB				00		
	5	36.0%		0.070												
SGO_1149	6	42.0%							Pneumococcal vaccine	e antigen A-like prote	ein					
	-	12.070	8	32.1%	8	37.0%										
SGO_1150	9	37.3%	5	22.8%	9	38.0%	3	12.7%	hypothetical protein S	GGO_1150				JJ	JJ	
	15	45.0%	25	68.6%	19	55.0%	16	49.8%						<b>A A</b>		
SGO_1151	16	46.0%	22	67.4%	22	58.3%	14	44.0%	glyA; serine hydroxyn	nethyltransferase						
	10	36.2%	10	46.2%	11	37.6%	11	38.2%								
SGO_1154	12	44.3%	8	33.1%	13	46.5%	10	38.4%	prfA; peptide chain re	lease factor 1				JJ		
200 4455	7	41.9%	4	29.8%	5	24.1%										
SGO_1155	8	46.1%	4	28.8%	5	26.2%	4	16.2%	tdk; thymidine kinase					JJ		
CCO 1150			3	12.2%	4	21.1%										
SGO_1159	3	18.3%	3	12.2%	5	30.9%			guaC; guanosine mon	ophosphate reductas	se			UU		
SGO_1163							3	7.8%	Ivon normana ETD1 6	in mails a						
300_1103									Iron permease FTR1 f	amiiy						
SGO_1166	3	9.1%							voltage-gated chloride	channel family prot	ein					
330_1100	3	9.9%							voitage-gated chloride	e channel family proc	em.					
SGO_1167	13	31.7%	8	27.9%	17	48.9%	15	42.4%	nox; NADH oxidase							
	18	39.7%	7	21.6%	16	43.2%	14	39.7%	nox, NADIT Oxidase							
SGO_1169	12	53.7%	4	29.9%	12	53.2%	6	35.3%	NADPH-dependent FM	IN reductase						
	11	48.8%	4	29.9%	11	46.8%	7	40.8%	TWO IT dependent IP	iiv i caactase						
SGO_1170	13	42.8%	6	21.5%	15	45.4%	8	30.4%	NADPH-dependent FM	IN reductase						
	15	43.5%	8	31.4%	13	42.8%	10	35.5%	NADETI-dependent III	iiv reductase						



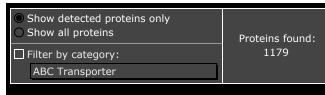
Cover	rage							S	Streptococ	cus gord	lonii				Hac Labor	kett atory UW
	5	Summai	ry Tal	ble S	SgFn '	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgP	gFn vs SgPg	Coverage	Page 56
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	<b>-</b> SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1171	12	76.9%	4	36.3%	5	46.3%			thioredoxin family pro	otein						
	14	76.9%	4	39.4%	4	35.0%										
SGO_1174	3	7.1%							histidine kinase			4				
	6	12.0%														
SGO_1176	3	11.0%							peptide methionine su	ulfoxide reductase-lik	e protein					
	3	8.9%											_			0 0
SGO_1182	3	0.9%							LPXTG cell wall surface	e protein		0				
SGO_1184	4	23.2%							GdmH			4				
	4	19.4%														
SGO_1185	4	21.7%	3	26.1%	5	27.7%	3	15.8%	acetyltransferase, GN	ΔT family						
	4	21.7%			4	21.7%	3	16.3%	acceyterationerase, or	, tr raininy						
SGO_1186	12	30.5%							ABC transporter, pern	nease/ATP-hinding n	rotein					
	14	34.6%							7.50 dianoporton, pon							
SGO_1187	13	27.2%							ABC transporter, pern	nease/ATP-hinding n	rotein					
	16	34.4%							ABC transporter, peri	neusc/7111 binding pi	TOTCH!					
SGO_1189	8	45.8%	6	50.3%	4	28.8%	3	22.2%	lipoprotein, putative							44
	12	60.8%	3	20.3%	5	30.1%	3	22.2%	iipoproteiii, putative							
SGO_1191	12	93.4%	13	82.8%	15	89.3%	13	86.9%	rplL; ribosomal protei	n I 7/I 12						
	11	82.8%	10	82.8%	13	89.3%	12	82.8%	TPIL, TIDOSOTTAL PROCE							
SGO_1192	9	53.6%	5	47.0%	12	75.9%	10	68.7%	BL5; 50S ribosomal p	rotein I 10						
	11	64.5%	8	60.8%	13	72.9%	10	63.3%	525, 303 прозопагр	TOTOM LIO						
SGO_1193	9	31.1%	12	51.4%	12	48.2%	4	16.9%	gid; Glucose inhibited	division protein A						
	10	38.1%	14	62.4%	14	62.2%	4	15.8%	gia, Giacose illilibitea	division protein A						



Cover	rage							S	Streptococ	cus gora	lonii					Hacke aborat	ory U	JW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn v	/s SgPg	Covera	ige	Pag	je 57
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	 SgPg		SgPgF	n
Protein	n (	n Coverage n Coverage n Covera						Coverage		Description		Rep I Rep	II Rep I	Rep II	Rep I Re	p II F	Rep I Re	ep II
SGO_1196	3						3	17.2%	satD; SatD-like protei	in								
SGO_1197	197			14	30.0%	10	21.1%	tonA. DNA tonoisomo	wasa I									
300_1137	33 52.2% 9 23.4%			23.4%	18	35.7%	10	19.5%	topA; DNA topoisome	rase I								
SGO 1198	O_1198 14 50.4%				13	51.8%	12	46.1%	DNA processing 5mf r	aratain								
300_1130	0_1198     14     50.4%       16     57.5%				10	44.3%	10	45.7%	DNA processing Smf p	protein								
SGO_1199	3	26.0%			3	26.0%			acetyltransferace Cyc	SE/LacA/LavA/NodLif	amily							
560_1155	3 26.0% 3 26.0% 5 34.4%						acetyltransferase, Cys	SE/Laca/Lpxa/NouL I	allilly									
SGO_1202	6	26.9%	7	33.9%	8	37.1%			GTP-binding protein									
555_1151	9	34.6%	5	19.8%	10	44.5%			GTF-billding protein									
SGO_1203	4	36.6%	7	77.7%	6	63.4%	4	51.8%	anaerobic ribonucleoti	ide reductace								
555_335	6	67.0%	9	79.5%	8	78.6%	4	51.8%	anderobic ribonacieoti	ide reductase								
SGO_1205	4	17.0%	7	24.4%	6	24.8%	4	15.8%	dapA; dihydrodipicolir	nate synthase							<b>A</b>	
	5	20.3%	3	13.8%	6	26.7%	4	19.6%	dapa, diriyardalpicolii	late synthase								
SGO_1206	9	41.3%	9	36.6%	11	48.6%	8	36.9%	asd; aspartate-semial	dehyde dehydrogens	200							
	12	49.4%	10	46.4%	10	41.3%	7	29.3%	asa, aspartate sermai	denyae denyarogene	130							
SGO_1208	3	25.8%							Hypothetical FAD-dep	endent ovidoreducta	se nutative							
	5	36.8%							Trypothetical TAD dep	chache oxidoredaeta	sc, putative							
SGO_1210	6	13.3%	11	25.7%	6	13.3%	3	9.2%	fhs-1; formatetetral	nydrofolate ligase								
	6	14.4%	9	25.4%	4	8.8%			ms 1, formate tetral	Tydrorolate figase								
SGO_1213						37.7%			coaC; phosphopantotl	henovicysteine decar	hoxylase							
	GO_1213			25.7%					code, phosphopantoti	inchioyicystellie decal	DOXYIGSE							
SGO_1215	9 62.8% 3				31	78.0%	26	69.8%	manR: phocphomann	omutaco								
500_1215	32	75.0%	32	78.3%	35	79.5%	26	66.1%	manB; phosphomanno	omutase								



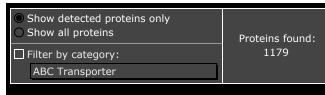
Cover	rage							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble s	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn S	gPgFn vs SgPg	Coverage	Page 58
	Sg SgFn Sg.						Sg	<sub>I</sub> PgFn				Sg	SgFn	 SgPg	SgPgFn
Protein	n Coverage n Coverage n Cov					Coverage	n C	Coverage		Description		Rep I Rep I	I Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1216	6 5	5 53.0% 5 53.0%			7 8	60.9% 78.3%	7	68.7% 60.9%	bta; Possible bacterio	cin transport accesso	ory protein				
SGO_1219	-				10	45.5%	8	33.8%	pta; phosphate acety	transferase		01			
	11 45.8% 11 50.8% 12 57.3% 3 14.6%			11	52.9%	/	30.8%								
SGO_1221	17 70.4% 9 42.3% 4 21.3%							ppnK; Probable inorga kinase	anic polyphosphate/A	TP-NAD					
SGO_1222	17 70.4% 9 42.3% 4 21.3% 6 33.5% 3 18.6% 4 26.2%					GTP pyrophosphokina	se-like protein		• •						
SGO_1224	17 17	58.4% 59.6%	13 10	51.6% 41.3%	16 14	54.0% 52.2%	11 14	39.8% 51.6%	Ribose-phosphate pyr	ophosphokinase 2		00			
SGO_1225	6	24.3%	6	27.2% 21.1%	7 8	34.1% 36.8%	4	20.0%	pyridoxal-phosphate (	dependent aminotran	isferase	44			40
SGO_1226	6	50.4% 45.2%	5	45.2% 40.9%	5	45.2% 45.2%	4	45.2% 40.9%	hypothetical protein S	GGO_1226		01			
SGO_1228	6	34.4% 36.3%	5	21.4%	6	27.9% 35.3%			DNA-binding protein I	3H0551				90	
SGO_1230	9	46.6% 34.7%			4	23.9%			srtA; sortase A			04		••	
SGO_1231	28	40.0% 44.3%	20	37.0% 19.6%	17	26.9% 34.0%	11 10	14.0% 14.9%	gyrA; DNA gyrase, A	subunit		01			••
SGO_1232	12 12	51.5% 49.7%	18 15	59.8% 51.5%	20 18	58.5% 57.6%	14 15	55.2% 55.2%	L-lactate dehydrogena	ase					
SGO_1234	23 28	56.6% 57.9%	31 24	69.3% 60.3%	28 26	67.3% 58.1%	26 27	63.6% 62.6%	rpsA; 30S ribosomal į	orotein S1					



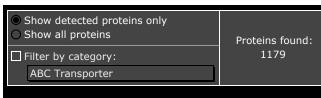
Cover	rage							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 59
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n Coverage n Coverage n Coverage n Co						n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1237	5 6	6 82.9% 6 82.9				82.9% 82.9%	4 5	44.7% 82.9%	hypothetical protein S	GO_1237		00			
SGO_1238	7	30.3%	11	47.4%	9	37.6%	7	30.0%							
SGO_1236	8 35.3% 10 40.9% 18 26.6% 3 6.4%			40.9%	11	47.1%	8	32.9%	ilvE; branched-chain a	amino acid aminotrar	nsferase				
SGO 1239	0_1239			6.4%	11	19.7%	3	4.5%	narCı DNA tanaisama	raco IV A cubunit					
560_1255	O_1239				9	14.3%	3	5.6%	parC; DNA topoisome	rase IV, A subunit					
SGO_1241	19 29.4% 7 12.7% 9 14.3% 3 5.6 4 18.4% 3 15.9%					aminoglycoside adeny	rlyltransferase		9						
	6	42.2%					3	36.2%							
SGO_1242	8	49.1%			3	36.2%			lipoprotein, putative						
SGO_1244	9	22.3%			5	18.9%			by mathatical protein C	CO 1244					
300_12++	5	15.5%			5	17.0%			hypothetical protein S	GO_1244					
SGO_1245	12	22.7%			6	12.3%			parE; DNA topoisome	race IV B subunit					
	12	23.1%			6	12.8%			pare, but topolsome	ruse IV, B subume					
SGO_1246	3	13.6%							hypothetical protein S	GO 1246					
	3	13.6%							Trypochecieal process of						
SGO_1247	36	55.2%	25	40.7%					5'-nucleotidase family	protein		44			
	41	61.8%	21	49.6%						p					
SGO_1248	5	13.5%	9	32.2%	7	16.6%	4	12.6%	pyrC; dihydroorotase			44			
	7	18.0%	8	24.6%	7	18.2%	4	13.7%	,, ,, , ,, ,, ,, ,, ,, ,, ,, ,, ,, ,, ,						
SGO_1250	GO_1250			21.7%					ung; uracil-DNA glyco	sylase					
	5 35.9% 4			33.2%					3,	•					
SGO_1251	GO_1251 3 16.4%								hypothetical protein S	GO 1251		44			
	3	16.4%							,						



Cover	age							S	Streptococ	ccus gord	lonii					ckett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	vs SgFn	SgPgFn v	s SgPg	Coverage	Page 60
		Sg		SgFn		SgPg	Sg	gPgFn				Sg	5	SgFn	SgPg	SgPgFn
Protein	n Coverage n Covera				e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I	Rep II	Rep I Rep II	Rep I Rep II
SGO_1252	3	5 42.1% 8 55.0%						integral membrane pr	rotein, putative		01					
SGO_1253	5	42.1%	8	55.0%	9	72.2%	4	38.8%								
300_1233	7	43.5%	5	43.5%	7	62.2%	4	37.8%	pyrE; orotate phospho	oribosyitransferase						
SGO 1254	6	42.2%							nurEi orotidino El nho	ocabata dacarbayylac	•					
300_1254	7 49.1%				4	33.9%			pyrF; orotidine 5'-pho	ospriace decarboxylas	е					
SGO_1255	4	31.1%							pyrd; dihydroorotate	dehydrogenase B						
330_1233	4					pyra, amyaroorotate	denydrogenase b									
SGO_1257	4	15.2%	8	31.1%	6	27.8%			probable transcriptior	nal regulator (LysR fa	mily)	4				
	7	22.5%	6	28.8%	8	30.1%			probable transcription	iai regulator (Lysix ra	,					
SGO_1258	3	16.5%	4	22.2%					NAD-dependent deace	etylase (Regulatory p	rotein					
	5	25.5%	4	27.2%					SIR2-like protein)							
SGO_1260	10	53.2%	8	52.3%	10	61.6%	7	40.1%	deoD; purine nucleos	ide phosphorvlase						
	10	51.9%	9	58.2%	9	57.8%	7	40.1%							-	
SGO_1261									glutamine amidotrans	sferase, class I						
	5	27.5%							<b>.</b>							
SGO_1263	9	45.7%	6	40.1%	6	40.5%	7	43.5%	purine nucleoside pho	sphorylase I, inosine	and					
	7	43.5%	8	49.8%	6	40.5%	10	48.7%	guanosine-specific							
SGO_1264	22	65.0%	22	64.5%	23	66.7%	21	65.0%	deoB; phosphopentor	nutase						
	22	65.3%	18	66.7%	23	66.7%	22	66.5%	, , , , ,							-
SGO_1265	9	59.1%	6	30.2%	6	41.8%	5	28.0%	rpiA; ribose 5-phosph	ate isomerase						
	9	59.1%	4	23.6%	9	59.1%	5	28.0%								
SGO_1266	12	33.0%	9	31.9%	8	19.7%	6	12.0%	trmE; tRNA modificati	ion GTPase TrmE		4			44	
	10	26.7%	9	23.6%	11	27.1%	6	10.3%								



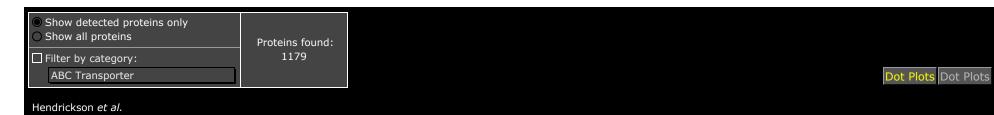
Cover	rage							S	Streptococ	cus gora	lonii					ckett oratory UW
	9	Summai	гу Та	ble S	SgFn	vs Sg	SgF	Pg vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn v	s SgPg	Coverage	Page 61
		Sg		SgFn	9	SgPg	Sg	gPgFn				Sg	S	gFn	SgPg	SgPgFn
Protein	n Coverage n Coverage n C					Coverage	n C	Coverage		Description		Rep I Rep	II Rep I	Rep II	Rep I Rep I	Rep I Rep II
SGO_1267	6 7				3	28.1%			thioredoxin family pro	otein						
	15		13	47.6%	17	56.8%	17	56.5%								
SGO_1273	15	51.9%	8	34.9%	17	57.6%	13	49.2%	rpoD; RNA polymeras	e sigma factor						
SGO_1274	4 86%			5	12.6%			dnaG; DNA primase								
330_1274	0_1274				7	17.2%			unad, DNA primase							
SGO_1276	7     12.6%     7     17.2%       4     36.2%     3     34.5%     5     36.2%     4				4	36.2%	rpsU; ribosomal prote	sin S21								
	5	37.9%	4	37.9%	5	37.9%	4	36.2%	Tp30, Tib030mar prote	321						
SGO_1280	4	20.4%							putative membrane-a	ssociated Zn-depend	lent	4				
	4	17.9%							protease							
SGO_1281	4	44.8%			5	59.2%			penicillinase repressor	r, putative						
	4	44.8%	3	36.8%	5	59.2%	3									
SGO_1283	13	45.2%	8	27.4%	18	59.6%	11	39.5%	oxidoreductase							
	14	44.1%	8	32.2%	16	52.1%	10	35.8%								
SGO_1284	7	33.2%	6	33.9%	9	45.0%	4	17.4%	thioredoxin-disulfide r	reductase						
	9	45.3%	10	43.5%	7	34.8%	6	28.9%								
SGO_1290	6	17.1%							ABC transporter, pern	nease/ATP-binding p	rotein					
	7	21.6%														
SGO_1291	6	13.8%							ABC transporter, pern SP1358	nease/ATP-binding p	rotein	44				
	3	5.0%							3, 1330							
SGO_1293	GO_1293		30.3%	16	37.8%	8	20.4%	asnS; asparaginyl-tRN	NA synthetase							
	15 38.1% 13			36.1%	14	34.4%	9	25.6%								
SGO_1297	9	28.8%	10	42.3%	9	44.6%	8	30.9%	aspC; aspartate amin	otransferase						
	8	27.0%	10	42.3%	10	42.1%	8	30.4%								



Cover	rage							S	Streptococ	cus gora	lonii				ratory UW
	5	Summar	у Та	ble	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn \	/s SgFn	SgPgFn vs SgPg	Coverage	Page 62
		Sg		SgFn		SgPg	Sg	<sub>1</sub> PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n Coverage n Coverage n Co						n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1298	5 4	28.4% 25.9%							hypothetical protein S	GGO_1298					
SGO_1305	15	42.7%			12	38.2%	6	22.7%	substants hinding aus	tain Mam E					
300_1303	18 45.2% 6 19.1% 14 49				12	35.0%	4	14.5%	substrate-binding pro	tem MSME					
SGO 1312	10_1312			49.5%	17	60.5%	13	46.6%	pepT; peptidase T						
	10_1312			56.6%	16	56.6%	12	40.4%	pepi, pepudase i						
SGO_1314	5	21.9%							metal binding lipoprot	ein					
SGO_1315	4	21.9%       5       26.7%       4       23.5%		trmD; tRNA (guanine-	-N1)-methyltransfera	ise			99						
SGO_1316	6	37.2%	3	26.2%	5	34.9%			16S rRNA processing	nrotain DimM					
566_1516	6	38.4%	3	18.6%	4	33.1%			105 TRIVA processing	protein Killin					
SGO_1323	3	43.3%	4	50.0%		43.3%	3	43.3%	rpsP; ribosomal prote	in S16					
	3	43.3%	3	43.3%	3	43.3%	3	43.3%							
SGO_1324	5	30.6%							hypothetical protein S	GGO_1324					
	6	30.6%													
SGO_1327	7	35.5%	6	24.2%	8	38.7%	3	15.6%	HAD-superfamily subf	family IIA hydrolase,	TIGR01457				
	10	43.4%	4	18.0%	8	38.7%	5	21.1%							
SGO_1328	3 11.8%							hypothetical protein S	GGO_1328						
SGO 1330	GO_1330 3 9.1%								transportor						
500_1550	7	16.5%							transporter						
SGO_1331	5	13.1%						_	HlyB/MsbA family ABO	C transporter					



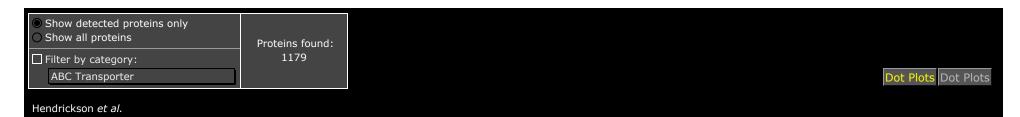
Cover	rage							S	Streptococo	cus gord	onii			Hac Labor	
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	rs SgFn S	gPgFn vs SgPg	Coverage	Page 63
		Sg SgFn SgPg					Sg	PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	n Coverage n Coverage n Coverage 1				n C	overage	De	escription		Rep I Rep I	I Rep I Rep II	Rep I Rep II	Rep I Rep II	
SGO_1336	12 15			5 6	7.1% 9.7%	pcrA; ATP-dependent D	NA helicase PcrA		••			••			
SGO_1337	3	9.1%							cation efflux family prot	tein		• 4			
SGO_1338	8	42.2% 60.5%	4	30.8%	3	15.7%			Signal peptidase I					••	
SGO_1339	25 32	56.1% 69.5%	35 36	79.2% 81.0%	29 34	72.5% 78.6%	27 28	69.1% 74.7%	pyk; pyruvate kinase						
SGO_1340	14 20	43.8% 60.4%	20 19	52.7% 50.3%	20 20	61.3% 60.1%	15 15	42.9% 42.9%	Phosphofructokinase						
SGO_1341	10	14.4% 12.2%	7	5.8% 10.0%	4	5.7%			dnaE; DNA-directed DN	IA polymerase III a	lpha chain	••	00	00	
SGO_1342	18 18	68.4% 68.4%	18 19	67.5% 74.8%	18 17	65.4% 65.4%	16 16	65.0% 65.0%	ABC transporter, ATP-bi	inding protein SP17	'15				
SGO_1343	5 5	15.4% 15.4%			3	10.5%			ABC transporter, ATP-bi	inding protein SP17	'15	94		••	
SGO_1347	10 13	37.4% 45.6%	3	13.5%					membrane associated li	ipoprotein					
SGO_1355	4	27.9% 22.1%	3	16.2%					lipoprotein, putative			94			
SGO_1360	3	9.0% 14.6%							ABC transporter domain	n protein		00			
SGO_1361	3	21.1%	3	23.2%					ADP-ribosylhydrolase			04			



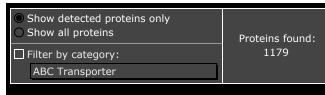
Cover	rage							S	Streptococ	ccus gora	lonii				ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	Sgl	Pg vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 64
		Sg		SgFn		SgPg	Sg	gPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n coverage in covera					Coverage	n (	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1364	17 44.5% 7 27 14 40.2% 5 13			16.4% 27.0%	13 13	42.1% 43.6%	4	12.3%	rumA-2; 23S rRNA (u RumA	ıracil-5-)-methyltrans	sferase	01			
SGO_1365		40.2%	5	13.8%	5	19.4%			transcription regulato	r vrfE				44	
	18 45.6% 6 14			14.0%	3	8.4%	3	13.5%		. ,					
SGO_1366	4 21.5%				pheA; prephenate del	hydratase									
	_	40.00/	^	20.40/										0 0	0 0
SGO_1367	5     42.2%     6     39.1%     3     21.1%       6     40.4%     6     42.2%     3     18.0%				aroK; shikimate kinas	se				99					
SGO_1368	3	8.7%	8	30.9%	5	20.4%			aroA; 3-phosphoshiki	mate 1-carboxyvinyli	transferase	44		44	
	6	20.4%	8	32.1%	5	24.1%									
SGO_1369	6 8	28.3% 32.2%	9	40.8%	5 6	25.3% 35.9%	3	15.5%	L-2-hydroxyisocaproa	ite dehydrogenase		44			
			_					22.22							
SGO_1370	6	73.2% 73.2%	5	73.2% 56.3%	6 4	73.2% 51.8%	4	33.9% 51.8%	Protein of unknown fu	unction (DUF964) sup	perfamily				
	3	10.1%			6	30.4%						<b>A A</b>			
SGO_1372	8	33.8%	3	15.2%	11	41.8%	3	12.6%	aroC; chorismate syn	thase					
SGO_1373	3	15.8%			5	26.8%	3	17.2%	araBu 2 dahydra awina	ata synthasa					
300_1373	6	25.9%	3	16.9%	5	26.8%			aroB; 3-dehydroquina	ate synthase					
SGO_1374	3	13.0%			6	28.4%			aroEi chikimato 5-dok	hydrogonaco					
360_13/-1	D_1374								aroE; shikimate 5-deh	nyui ogenase					
SGO_1375	7 41.3%			26.2%	6	37.8%	4	23.1%	aroD; 3-dehydroquina	ate dehydratase tyng					
	8 50.7%		3	17.8%	6	38.2%			arob, 5 deriyaroquina	are deligaratase, type					
SGO_1376	8 50. 5 17.								Methyltransferase			44			
	5	18.3%													



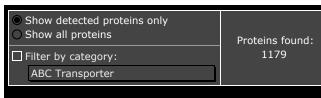
Cover	rage							S	Streptococ	cus gora	lonii				ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 65
						SgPg	Sg	<sub>I</sub> PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n Coverage n Coverage n Co				Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II	
SGO_1377	22 27	7 49.0% 14 31.8% 13 26			23.6% 26.2%	4	6.7% 8.8%	sulfatase						00	
SGO_1381	18	20.0%	12	13.9%	9	11.6%	3	3.1%	csn1; CRISPR-associa	ited protein, Csn1 far	nily	44	144	44	44
	28 27.6% 13 13.4%			12	14.8%	4	4.4%								
SGO_1383	0_1383			47.0%	6	46.1%	6	40.0%	rplS; ribosomal protei	in L19					
	10	60.9%	10	57.4%	6	40.0%	9	53.0%	. ,						
SGO_1386	3	30.7%	7	72.7% 68.2%	5 3	62.5% 48.9%			chorismate mutase						
SGO_1388	9	16.9%	3	6.4%					pulA-1; pullulanase, t	ype I		44			
	14	27.1%	6	13.1%											
SGO_1389	6	21.4%	3	11.9%					conserved hypothetica	al protein TIGR00147	7				
SGO_1390	13	26.8%	8	16.0%	7	15.5%	6	12.7%	liga. DNA ligage NAD	danandant					
300_1330	13	29.9%	10	23.6%	7	15.3%	6	12.7%	ligA; DNA ligase, NAD	-dependent					
SGO_1394			6	46.8%	3	14.5%			hypothetical protein S	GGO 1394					
					3	16.2%			, p						
SGO_1397	8	42.8%	9	41.8%	8	45.6%	6	30.2%	map; methionine ami	nonentidase tyne I					
	9	48.1%	8	39.6%	8	44.2%	5	26.3%							
SGO_1398	15	47.8%	3	8.9%	5	14.1%			hypothetical protein S	GO_1398					
	14	38.4%	3	8.5%	4	10.8%									
SGO_1400	GO_1400			20.7%	9	29.0%	6	22.6%	murA-2; UDP-N-acety						
	11	37.6%	6	24.8%	7	23.8%	3	14.8%	carboxyvinyltransfera	se					
SGO_1405					3	13.8%			hisA; phosphoribosylficarboxamide ribotide		idazole			00	



Cover	rage							S	Streptococ	cus gord	lonii					Had Labo	kett ratory	JW
	5	Summai	ry Tal	ble S	SgFn '	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	rs SgFn	SgF	gFn vs Sgl	Pg	Coverage	Pa	age 66
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn		SgPg	SgPg	Fn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I R	ep II	Rep I Rep	II R	ep I Rep II	Rep I R	Rep II
SGO_1413	8	8.7%	6	7.4%	8	8.6%			first chain of major ex	conuclease RexA		4		44				
	16	18.0%	12	15.9%	7	7.7%												
SGO_1414	8	11.5%	6	8.3%	4	5.6%	3	4.8%	rexB; putative exonuc	clease RexB								
	10	14.7%	8	12.2%	6	9.0%	4	5.9%							4			
SGO_1415	4	5.7%								PXTG cell wall surface protein, X-prolyl peptidylaminopeptidase, putative								
	5	6.3%							dipeptidylaminopeptid	lase, putative					4			
SGO_1416	5	14.8%							putative histidine kina	utative histidine kinase								
SGO_1417									response regulator pr	otoin								
330_1117					4	27.1%			response regulator pro	otem					4			
SGO_1422	9	28.9%	10	39.0%	9	34.2%	6	20.8%	h and halfred a state of	200 1422								
300_1422	10	29.8%	10	31.3%	8	25.9%	6	20.8%	hypothetical protein S	GGO_1422					4			
SGO_1426	31	75.1%	32	77.9%	32	77.2%	27	75.1%										
3GO_1420	31	77.0%	33	85.7%	30	77.2%	31	77.2%	eno; enolase									
CCO 1421	31	53.5%	21	43.6%	25	47.7%	18	39.0%										
SGO_1431	28	50.3%	20	41.3%	27	49.0%	20	40.1%	EzrA; Septation ring f	ormation regulator e	zrA					JJ		
666 4433	18	33.4%	12	26.5%	16	33.3%	6	10.9%										
SGO_1432	20	38.7%	14	34.1%	19	37.9%	6	9.4%	gyrB; DNA gyrase, B	subunit						JJ		
			4	29.1%	4	40.1%	3	22.0%	thiJ; 4-methyl-5(beta	-hvdrovvethyl)-thiaz	nle							
SGO_1434	4	32.4%	3	28.0%	3	25.8%			monophosphate synth							JJ		
	6 92%							DnaQ family exonucle	ase/DinG family heli	rase								
SGO_1437	7	11.0%							putative	ase, bills faililly field	cusc,							
550 1439	8	23.4%	5	19.5%	5	17.5%	3	17.2%		V. call division makein Flow								
SGO_1439	10	25.6%	5	21.4%	4	17.2%	3	17.2%	ftsX; cell division prot	ein FtsX						JU		



Cover	rage							S	Streptococ	cus gora	lonii				kett ratory UW
	9	Summar	гу Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 67
	·	Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg	SgFn	 SgPg	SgPgFn
Protein	n (	n Coverage n Coverage						Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1440	14 18	74.3% 13 67.4% 10 55.2			59.1% 55.2%	7 6	43.5% 45.7%	cell-division ATP-bindi	ing protein FtsE						
SGO_1441	8	29.9% 22.8%	22.8% 7 27.5% 11 35.2%			5 3	20.3% 11.8%	prfB; peptide chain re	elease factor 2		94			••	
SGO_1446	12     36.0%     9     27.6%     12     37.3%     4       14     39.7%     8     25.2%     12     34.2%     3			4	11.2% 11.4%	murF; UDP-N-acetylm alanine ligase	nuramoyl-tripeptide	-D-alanyl-D-	01			00			
SGO_1447	14     39.7%     8     25.2%     12     34.2%     3     11.4       13     45.1%     8     32.2%     14     52.0%     6     26.       15     53.2%     8     28.7%     14     50.6%     5     23.				26.1% 23.3%	ddlA; D-Ala-D-Ala liga	ase					••			
SGO_1449	24 26	47.7% 50.6%			9	21.9% 26.3%			pbp2b; penicillin-bind	ing protein 2B				••	
SGO_1450	6 7	27.1% 30.6%	4 5	19.0% 23.6%	6 5	28.2% 22.2%	3 6	14.8% 28.2%	hypothetical protein S	GGO_1450					••
SGO_1451	6 7	43.8% 44.3%	4	33.5% 33.5%	6 7	42.7% 43.8%	6 6	40.0% 39.5%	frr; ribosome recyclin	g factor		01			
SGO_1452	10 9	46.9% 45.2%	6	38.6% 27.4%	7 7	45.6% 45.6%	9	54.4% 34.0%	pyrH; uridylate kinase	2		01			
SGO_1453			3	8.7%	4	11.7%	3	6.4% 8.3%	glycosyl transferase, i	family 8 SP1766				••	00
SGO_1454	3	6.6% 6.6%							amino acid permease	family protein		01			
SGO_1455	8 39.3% 10 59.4% 9			45.0% 49.3%	9	49.3% 45.0%	rpIA; ribosomal protei	in L1							
SGO_1456	4 5	30.5% 37.6%	4 5	35.5% 51.8%	4	30.5% 30.5%	6	44.7% 42.6%	rplK; ribosomal protei	in L11		01			



Cover	age							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 68
		Sg	SgFn		SgPg	Sg	<sub>1</sub> PgFn				Sg	SgFn	SgPg	SgPgFn	
Protein	n (	n Coverage n Coverage n Cove					n C	Coverage		Description		Rep I Rep	I Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1458	19 21	21 38.2% 8 15.1% 4 9			8.2% 9.0%	4	7.7%	aha1; cation-transpor	ting ATPase yfgQ				00		
SGO_1459			6 5	67.2% 65.6%	3	35.2%			glyoxylase family prot	tein					
SGO_1460	17 32.5% 4 8.7% 11 23.0% 4 6. 19 34.3% 4 8.5% 7 12.3% 14 61.4% 5 27.0% 11 52.1% 5 27.				6.4%	DNA translocase ftsK				00	••	00			
SGO_1463	14 15	61.4% 61.4%	5 4	27.0% 17.6%	11 7	52.1% 40.1%	5 6	27.0% 28.5%	peptidyl-prolyl cis-tra	ns isomerase					
SGO_1464	10 11	94.9% 100.0%			8 7	85.9% 85.9%	5 4	84.6% 50.0%	uncharacterized proba	able metal-binding pr	rotein				
SGO_1465	17 20	43.9% 50.5%	8	25.5% 19.1%	13 10	34.3% 31.4%	8	26.7% 21.4%	ABC transporter, ATP-	-binding protein SP07	770				••
SGO_1466	7	40.0% 19.6%	6	33.0% 27.0%	7 6	42.2% 37.0%			MTA/SAH nucleosidas	e					
SGO_1468	3	20.2%							MutT/nudix family pro	otein		7			
SGO_1469	12 13	35.9% 43.1%	10 7	31.2% 23.7%	13 14	48.4% 45.8%	13 13	44.0% 38.6%	glmU; UDP-N-acetylg	lucosamine pyrophos	phorylase				
SGO_1472	13     43.1%     7     23.7%     14     45.8%       5     24.7%     5     32.0%       3     20.6%     3     15.0%     5     30.4%				3	24.7%	acetyltransferase, GN	AT family		04					
SGO_1475	7 22 1%							lipoprotein, putative			01				
SGO_1483	4	9.8%							ABC transporter, pern	nease protein, proba	ble SP0913	00			



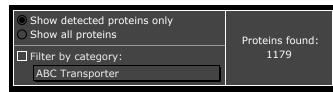
Coverage			Streptococcus gordonii												Hackett Laboratory		
	9	Summai	mary Table SgFn vs Sg				SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn v	s SgPg	Coverage	Page 69	
		Sg		SgFn		SgPg	SgPgFn			D		Sg		igFn	SgPg	SgPgFn	
Protein	n (	Coverage	n (	Coverage	e n (		n C	Coverage	Description			Rep I Rep	o II Rep I	Rep II	Rep I Rep II	Rep I Rep II	
SGO_1484					3	20.8%			ABC transporter, ATP-binding protein								
SGO_1486			8	5.9%			4	3.2%	beta-galactosidase								
555_1 155	5	3.1%					5	3.9%	oca galactosidase								
SGO_1487	12	9.4%	11	10.5%					LPXTG cell wall surface	e protein, Cna protei	in B-type						
555_1 157	18	12.8%	7	5.0%	4	4.0%			domain								
SGO_1493	10	25.3%	4	12.7%					hypothetical protein C	CO 1402							
566_1455	14	38.9%	6	19.9%	4	16.1%			hypothetical protein S								
SGO_1495	3	34.6%							putative transcriptiona								
555_1155	6	53.4%							putative transcriptions								
SGO_1498	3	5.7%							ABC transporter, permease protein, probable SP0913			•					
	3	13.8%															
SGO_1504	5	20.9%							histidine kinase		9						
	7	23.6%								nypothetical protein SGO_1507							
SGO_1507	11	30.5%							hypothetical protein S								
660 1513	3	9.2%	4	18.2%	5	13.7%									4		
SGO_1512			5	18.4%					lacG; 6-phospho-beta	-galactosidase							
CCO 1513																	
SGO_1513	3	5.5%							lacE; PTS system, lact	cose-specific IIBC co	mponent						
SGO 1516	8	37.1%			9	44.2%	4	22.4%	1	distribution of the state of th							
SGO_1516	9	31.3%			13	53.4%	6	31.3%	IacD-2; tagatose 1,6-0	-diphosphate aldolase							
SGO 1519	4	28.1%			6	46.2%			lacB-2; galactose-6-pl	hosphate isomerase.	LacB						
SGO_1518	6	33.9%			6	46.2%			subunit								



Cover		Streptococcus gordonii													Hackett Laboratory		
	5	Summar	nary Table SgFn vs Sg				SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgl	Fn vs SgPg	Coverage	Page 70	
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg		SgFn	SgPg	SgPgFn	
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage	Description			Rep I Rep	o II R	ep I Rep II	Rep I Rep II	Rep I Rep II	
SGO_1520	4	10.4%							PTS system, IIC comp		•						
SGO_1521	4	47.5%							PTS system IIB component (galactitol/fructose specific)								
SGO_1523									lacD-1; tagatose 1,6-diphosphate aldolase								
SGO_1527	3	17.9%							Lactose phosphotransferase system repressor								
SGO_1529	6 10	32.3% 46.7%	6	27.4% 34.7%	5 3	27.7% 18.2%			hypothetical protein SGO_1529					99			
SGO_1530	23 27	46.4% 53.5%	22 16	47.0% 33.3%	26 24	52.9% 50.2%	17 15	36.6% 35.0%	methionine-tRNA ligase								
SGO_1531	11 11	54.9% 59.6%	6 5	29.1% 26.5%	10 8	60.0% 49.5%	6 5	34.9% 33.1%	xth; exodeoxyribonuc	lease III							
SGO_1534	5 6	35.9% 49.6%	4 5	46.2% 57.3%	8 6	68.4% 62.4%	4	34.2%	ArsC family								
SGO_1536	10 11	40.5% 45.8%	5	19.4% 26.1%	9	43.0% 42.3%	4	17.3% 18.7%	conserved hypothetica	al protein TIGR00096	5						
SGO_1538	4	20.4%							DNA-directed DNA po	lymerase III, delta'' (	chain	•					
SGO_1539	7	42.0% 41.5%	7	36.3% 29.7%	8	48.1% 48.6%	4	22.2% 42.0%	tmk; thymidylate kina	ase						40	
SGO_1540	3	12.2% 19.2%	3	23.1 /0	4	23.0%		72.0 /0	YitT family protein								

	ot Plots Dot Plo
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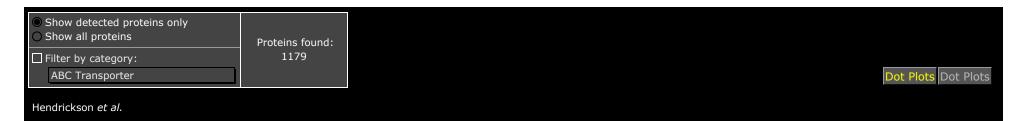
Cover		Streptococcus gordonii													ratory UW	
	S	Summai	mmary Table   SgFn vs Sg				SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPg	JFn vs SgPg	Coverage	Page 71
		Sg		SgFn		SgPg		PgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n C	Coverage	n (	Coverage	n (	Coverage	n C	overage	Description			Rep I Rep	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1541	4 5	33.3%	8	40.6% 31.2%	5 4	32.6% 32.6%	3 6	27.5% 39.9%	atpC; ATP synthase F1	, epsilon subunit						
SCO 1542	25	73.3%	30	75.9%	24	64.1%	19	58.5%								
SGO_1542	30	75.4%	29	72.6%	22	62.2%	20	58.8%	atpD; ATP synthase F1	., beta subunit		<b>)</b>				
SGO_1543	15	55.6%	12	55.6%	10	36.9%	4	21.2%	atnG: ATP synthase F1	atpG; ATP synthase F1, gamma subunit						
	16	50.2%	10	44.4%	11	47.1%	4	19.8%	aspo, o, include 12, gaining subunit							
SGO_1544	17	41.9%	15	43.7%	17	45.1%	9	26.1%	atpA; ATP synthase F1							
	16	41.9%	17	48.3%	17	45.1%	9	22.8%								
SGO_1545	5	42.1%	6	39.9%	4	28.7%	4	33.7%	atpH; ATP synthase F1	, delta subunit						
	6	46.6%	8	58.4%	4	33.7%	4	33.7%		,						
SGO_1546	14	56.1%	15	61.6%	10	49.4%	10	47.0%	atpF; ATP synthase F0,	, B subunit						
	15	61.6%	8	39.0%	11	49.4%	9	48.8%								
SGO_1550	22	38.1%	19	30.2%	25	45.0%	13	22.4%	glgP-1; glycogen phosp	phorylase						
	27	44.4%	26	42.7%	27	44.2%	20	32.7%								
SGO_1551	5	17.4%	14	38.0%	9	25.0%	3	9.0%	glgA; Glycogen syntha	ase						
	14	36.8%	15	42.6%	6	16.8%	5	14.7%								
SGO_1552	8	28.6%	13	47.7%	12	41.7%	8	26.6%	glgD; glucose-1-phosp	hate adenylyltransfe	erase, GlgD					
	9	26.9%	11	42.0%	12	43.7%	8	33.4%	subunit							
SGO_1553	7	23.9%	14	46.1%	14	45.5%	7	27.6%	glgC; glucose-1-phospl	hate adenvivitransfe	erase	4				
	10	33.9%	18	53.4%	15	50.5%	7	27.1%	5 5 - 7 5 E E E E E E E E							
SGO_1554	13	30.8%	24	47.4%	16	33.6%	12	28.9%	glgB; 1,4-alpha-glucan	branching enzyme						
	15	34.6%	22	48.0%	20	38.5%	8	21.5%	, , , , , , , , , , , , , , , , , , ,							
SGO_1555	25	62.2%	28	68.3%	28	66.6%	24	55.3%	ptsI; phosphoenolpyru	vate-protein						
	31	69.8%	31	74.5%	26	65.3%	21	54.4%	phosphotransferase							



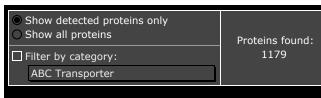
Coverage					Hackett Laboratory										
	5	Summar	mary Table SgFn vs Sg				SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 72
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n C	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1556	3 5	39.1% 41.4%	5	41.4% 39.1%	3	39.1% 39.1%	3	39.1% 39.1%	phosphocarrier protei	01					
SCO 1557	3	68.1%													
SGO_1557	3	68.1%							NrdH-redoxin						
SGO_1558	27	48.0%	31	53.8%	25	47.3%	19	38.8%	nrdE; ribonucleoside-o	diphosphate reductase large					
300_1330	32	49.4%	23	40.3%	30	52.0%	16	30.7%	chain						
SGO_1559	12	40.4%	11	46.4%	13	46.4%	9	33.9%	rihonucleoside-dinhos	nhate reductase, het					
	13	41.1%	10	38.9%	13	46.4%	9	28.2%	ribonucleoside-diphosphate reductase, beta subunit						
SGO_1561	3	13.6%							putative zinc metallop	eptidase		44			
	3	13.6%													
SGO_1562	4	10.6%							hypothetical protein S	GO_1562		44			
	3	10.6%													
SGO_1564	3	53.7%			3	53.7%			transcription regulator	r, probable -related բ	orotein				
	3	53.7%			3	53.7%								-	
SGO_1570	33	43.5%	29	42.4%	37	47.0%	23	35.4%	alaS: alanvl-tRNA svn	nthetase					
	41	50.2%	24	38.6%	34	42.4%	29	37.4%							
SGO_1571	6	43.5%							Protein of unknown fu	nction (DUF567) sup	erfamily				
	7	44.7%		00.007											
SGO_1572	26 26	69.3% 70.9%	8 5	32.0%			4	17.8%	proteinase maturation	protein, putative					
	20	10.970	-		2	20.40/	4	17.0%							
SGO_1573	4	17.5%	3	23.2%	5	29.4% 39.5%			O-methyltransferase f	family protein					
	17	35.5%	22	44.2%	21	49.8%	15	29.8%							
SGO_1574	18	37.0%	21	44.7%	24	52.7%	15	30.8%	pepF-1; oligoendopep	otidase F					



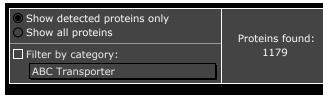
Cover	rage							S	Streptococ	cus gora	lonii					ckett cratory UW
	5	Summar	ry Ta	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgP	gFn vs SgPg	Coverage	Page 73
		Sg		SgFn		SgPg		<sub>1</sub> PgFn		D		Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1576	3	8.9% 8.2%							ptcC; PTS system, IIC	component		•				
SGO_1580			3	45.2%	4	49.0%	4	49.0%	DTC avetom Lastace/	D. aubumit						
300_1380			3	49.0%	4	49.0%	3	49.0%	P15 system, Lactose/	B SUDUNIT						
SGO_1585	14	40.4%			3	13.3%			D Alexad D Alexandra							
300_1383	13	37.8%			5	19.6%	3	6.7%	D-Alanyi-D-Alanine ca							
SGO_1587	5	26.9%	4	23.4%	4	24.3%	4	24.3%	ptcC; PTS system, IIC component  PTS system, Lactose/Cellobiose specific IIB subur  D-Alanyl-D-Alanine carboxypeptidase  queA; S-adenosylmethionine:tRNA ribosyltransfer							
300_1367	9	42.1%	8	33.0%	4	24.3%	3	19.0%	isomerase							
SGO_1588	4	48.1%							and and and an analysis							
300_1300	5	48.1%							arck; arginine repress							
SGO_1589	5	13.5%	11	29.3%					arcTi nutativo trancar							
500_1505	7	19.8%	10	30.0%					arci, putative transar	mnase/peptidase						
SGO_1590	5	9.9%	4	9.1%					arcD; arginine-ornithi	no antinortor						
555_1556	6	11.7%	3	9.1%					arcb, argilline-ornicin	ne antiportei						
SGO_1591	10	43.5%	17	70.8%	9	39.0%	5	27.6%	arcC; carbamate kinas	50						
550_1551	13	54.3%	17	65.4%	7	27.6%	6	32.4%	arcc, carbaniate kinas	se .						
SGO_1592	15	53.8%	25	64.8%	12	49.4%	10	42.3%	arcB; ornithine carbar	movitransferace						
	15	52.7%	26	73.1%	12	46.7%	11	45.3%	arcb, ornicilile carbar	noyiciansierase						
SGO_1593	28	72.6%	42	88.3%	20	62.3%	18	60.4%	arcA; arginine deimina	250						
	30	76.5%	38	84.8%	24	66.7%	17	53.3%	arch, argilline delilline	130						
SGO_1594	5	22.8%							Crp/Fnr family protein							
	6	26.3%							Cip/iiii lailiiiy proteiii							
SGO_1598	3	11.8%							hypothetical protein S	GO 1598						
	5	17.4%							nypotnetical protein 3	00_1390						



Cover	rage							S	Streptococ	ccus gora	lonii				ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 74
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg	SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage	<u> </u>	Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1599	10 9	56.2% 52.2%	15 13	57.2% 57.2%	10 10	52.2% 52.2%	10 11	56.2% 56.2%	sodA; manganese-dep	pendent superoxide (	dismutase				
SGO_1600	6	25.8%							DNA polymerase III, o	delta chain		44			
	7	27.8%													
SGO_1601	3	4.0% 5.6%							celB; DNA internalizat celB	tion-related compete	nce protein	01			
	12	48.3%	6	30.5%	6	28.4%								4	
SGO_1604	15	55.9%	5	32.6%	5	23.7%	3	18.6%	acyltransferase family	/ protein				99	
SGO_1605	16	29.3%	3	6.5%	5	11.0%									
300_1005	20	31.3%	3	8.0%	5	11.9%	3	6.1%	P-type ATPase, metai	cation transport					
SGO_1606	4	25.0%			4	25.0%			acyltransferase family protein P-type ATPase, metal cation transport						
300_1000	4	25.0%			3	19.2%			DNA methyltransferas	se signature protein					
SGO_1609	18	45.9%	7	17.2%	14	38.4%	12	35.2%	ATP-dependent RNA h	policaco DEAD/DEAH	l hav family				
330_233	22	51.2%	6	17.0%	15	42.8%	13	35.0%	ATF-dependent KNAT	ielicase, DLAD/DLAII	I DOX TAITING				
SGO_1614	9	32.5%							magnosium and sobal	It transporter CorA fa	mily				
330_1014	8	25.2%							magnesium and cobal	it transporter CorA ra	illily				
SGO_1617	12	37.0%	8	20.6%	10	23.9%	9	24.1%	prfC; peptide chain re	Nonco factor 3					
560_1017	19	48.2%	10	20.4%	16	38.1%	9	25.9%	pric, peptide chain re	elease factor 3					
SGO_1619	26	34.0%	10	17.4%	21	32.7%	12	19.7%	cation-transporting A	TPace F1-F2 family					
	26	34.0%	15	26.8%	20	35.2%	11	18.3%	cadon-d anspording A	Trase, LI-EZ Idililly					
SGO_1621	8	25.2%	6	21.7%	5	16.9%	3	10.4%	HD domain protein						
J00_1021	9	26.3%	9	31.2%	7	25.2%			TID domain protein						
SGO_1622	9	40.5%	6	30.5%	6	29.0%	6	29.0%	Cof family protoin						
000_1022	10	43.1%	4	21.2%	6	29.7%	4	20.1%	Cof family protein						



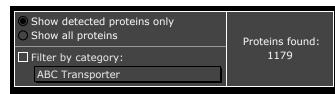
Cover	age							S	Streptococ	cus gora	lonii				kett ratory UW
	S	Summai	ry Tal	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 75
		Sg		SgFn		SgPg		PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1623	10 15	31.5% 48.7%	8	23.2%	11 11	37.2% 39.1%	5	20.5%	murM; MurM						
	8	25.1%	7	17.8%	5	15.6%						•		0 0	
SGO_1624	10	25.1%	7	24.1%	5	13.1%	5	14.8%	murN; MurN protein					99	
SCO 163E	15	77.1%	11	61.9%	13	64.2%	9	57.8%							
SGO_1625	16	77.5%	10	55.5%	12	59.6%	6	39.4%	acetoin utilization put	ative/CBS domain pr	otein				
SGO_1626	9	50.8%			8	45.3%	4	23.7%	branched-chain amino	o acid ABC transporte	er, ATP-				
3GO_1020	9	46.6%	5	32.2%	8	42.8%	6	35.2%	binding protein	·	,				
SGO_1627	7	41.7%			6	37.0%	5	33.1%	branched-chain amino	acid ABC transporte	er, ATP-				
	10	46.9%			5	27.6%	5	33.1%	binding protein						
SGO_1630	25	62.9%	15	50.0%	20	61.1%	17	52.3%	branched-chain amino	acid ABC transporte	er, amino				
	30	70.4%	14	45.6%	20	59.3%	16	47.9%	acid-binding protein					33	
SGO_1631	3	28.1%							hypothetical protein S	GO_1631					
	3	29.2%							,, ,						
SGO_1632	4	15.8%	5	39.8%	5	37.8%	6	36.7%	clpP; ATP-dependent	Clp protease, proteol	ytic subunit				
	5	21.4%	5	39.8%	5	37.8%	4	15.8%	ClpP						
SGO_1633	9	58.9%	14	67.5%	14	67.5%	12	66.5%	upp; uracil phosphoril	bosyltransferase					
	12	59.8%	14	72.2%	13	67.5%	10	54.1%							
SGO_1634	34	42.7% 44.0%	5	9.5%	8	13.9% 8.7%			magnesium-transloca	ting P-type ATPase					
	35		-		6										
SGO_1638	6	15.4% 15.6%	10	22.2%	8	25.6% 16.8%			murE; UDP-N-acetylm -2,6-diaminopimelate		itamate-	96			
	-	43.4%		59.5%		58.8%	10	12 10/							
SGO_1648	10	46.6%	12	59.5%	12 12	58.8%	8	43.1%	ppx1; inorganic pyrop dependent	hosphatase, mangar	nese-				
	14	<del>+</del> 0.0 /0	11	JJ. <del>4</del> /0	12	JU.U /0	U	JU.U /0				)			



Cover	rage							S	Streptococ	ccus gora	lonii				Hac Labor	kett ratory UW
	5	Summar	y Tal	ble S	SgFn '	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgP	gFn vs SgPg	Coverage	Page 76
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1649	9	45.7% 58.0%	6 10	33.1% 48.0%	3 5	14.1% 23.4%	3	14.1%	act; pyruvate formate	e-lyase-activating en	zyme				44	40
			10	40.0 /0	3	23.4 /0						)	_	-		
SGO_1650	14	22.5% 24.8%							LPXTG cell wall surfact domain	ce protein, collagen b	inding	0				
560 1651	28	45.6%	20	32.7%					LPXTG cell wall surfac	ce protein, nuclease/r	ohosphatase					
SGO_1651	31	46.6%	18	34.1%					domain	,, ,,	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,					
560 1653	13	31.2%	5	13.9%	12	31.1%	7	18.3%								
SGO_1652	12	28.7%	4	10.9%	10	29.4%	7	19.2%	intracellular glycosyl i	PXTG cell wall surface protein, nuclease/phospha				UU		99
SGO_1653	20	32.4%	9	18.5%	12	25.9%	5	10.9%	trehalose PTS enzyme	- II				44		
	25	35.0%	5	9.6%	12	24.5%	7	14.1%								
SGO_1655	10	27.1%	5	16.1%	4	12.1%			CBS domain protein/p	oossible hemolysin				44	44	
	15	33.0%	6	20.2%	4	13.0%				,						
SGO_1657	4	5.3%							membrane protein			4				
	6	8.0%														
SGO_1661	3	11.2%							radical SAM protein, T	ΓIGR01212 family						
	6	31.7%	6	26.9%												
SGO_1665		05.70/							rRNA methylase							
	4	35.7%														
SGO_1666	16	39.5%	14	34.8%	13	35.8%	6	19.6%	trkA; potassium uptak	ke protein, Trk family	/					
	20	47.0%	14	38.3%	13	36.9%	4	14.3%								
SGO_1669	12	45.0%	11	55.8%	11	40.5%	10	47.1%	ribosomal large subur	nit pseudouridine syn	thase B					
	17	57.4%	8	36.4%	13	45.9%	8	33.9%								
SGO_1670	4	30.9%							scpB; segregation and	d condensation prote	in B					

<ul><li>Show detected proteins only</li><li>Show all proteins</li></ul>	Proteins found:
☐ Filter by category:	1179
ABC Transporter	

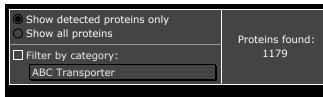
Cover	rage							S	Streptococ	ccus gora	lonii				kett atory UW
	5	Summar	у Та	ble !	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 77
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1674	5 5	32.4% 32.4%	5	29.5% 37.0%	-	27.7% 22.5%			phosphodiesterase, M	J0936 family					
SCO 167E	7	26.2%	6	20.9%	9	40.3%	3	12.6%							
SGO_1675	11	37.5%	8	31.7%	7	35.4%	4	16.9%	HAM1 protein-like protein  murI; glutamate racemase  lysA; diaminopimelate decarboxylase						
SGO_1676	4	22.3%	4	23.5%	9	45.5%	4	23.1%	murI; glutamate racemase						
300_1070	4	25.4%	4	21.6%	11	59.8%	6	29.9%	murI; glutamate racemase						
SGO_1678	4	13.9%	6	24.0%	6	23.8%	3	13.0%	murI; glutamate racemase						
	5	19.2%	6	22.4%	3	13.0%			murI; glutamate racemase  lysA; diaminopimelate decarboxylase						
SGO_1679	19	60.8%	15	64.7%	-	60.8%	16	61.4%							
	23	68.1%	19	68.4%	16	59.9%	15	59.6%				33	-		
SGO_1680	4	18.7%			4	18.7%	4	18.7%	phosphotransferase s	ystem enzyme II		44			
	4	18.7%			4	18.7%									
SGO_1681	13	44.2%	10	41.9%	-	41.9%	9	38.6%	PTS system, mannose component	e/fructose/sorbose fa	mily, IID				
	15	44.2%	7	35.6%	_	41.9%	9	38.6%	Component						
SGO_1683	19	55.1%	17	60.2%	-	61.9%	11	40.0%	serS; seryl-tRNA synt	hetase					
	19	56.5%	13	50.6%	_	63.3%	13	43.5%						-	
SGO_1684	7	26.3%			12	46.6%	7	28.0%	acyl-CoA dehydrogena	ase family					
	6	24.3%	_	0.4.404	12	43.8%	9	36.7%							
SGO_1685	4	33.0% 26.9%	5	34.1% 33.0%	-	37.4% 37.4%	3	26.4% 25.3%	putative peroxidase /	antioxidase					
			4		_		7							0 0	
SGO_1687	10	48.0% 36.3%	11	48.4% 35.2%	_	48.0% 44.5%	9	35.9% 39.1%	accA; acetyl-CoA carb alpha subunit	ooxylase, carboxyl tra	ansferase,				
	7	25.4%	8	36.2%	10	43.6%	5	22.3%				•		4	
SGO_1688	13	41.1%	9	35.2%	_	45.3%	4	17.1%	accD; acetyl-CoA cart beta subunit	ooxylase, carboxyl tra	ansferase,				



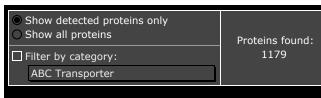
Cover	age							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	§gFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 78
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1689	14 14	48.1% 45.8%	13 14	48.4% 52.3%	13 15	44.9% 51.0%	9	29.0% 32.2%	accC; acetyl-CoA carb	oxylase, biotin carbo	oxylase				
SGO_1690			3 5	27.1% 40.7%	6 7	40.0% 46.4%	4	34.3%	fabZ; beta-hydroxyac dehydratase FabZ	yl-(acyl-carrier-prote	ein)				
SGO_1691	4 5	25.3% 28.4%	8	42.0% 47.5%	7	39.5% 46.3%	6	27.8% 39.5%	accB; acetyl-CoA carb protein	oxylase, biotin carbo	oxyl carrier				
SGO_1692	15 17	65.4% 62.0%	25 27	74.1% 77.3%	22 21	78.8% 71.2%	17 16	63.7% 61.2%	3-oxoacyl-[acyl-carrie	r-protein] synthase					
SGO_1693	7	39.3% 47.5%	11 12	55.7% 59.4%	15 13	73.0% 63.5%	9	50.0% 20.9%	fabG; 3-oxoacyl-(acyl	-carrier-protein) red	uctase				••
SGO_1694	10 13	45.4% 55.9%	9	43.5% 42.2%	11 13	58.5% 60.8%	10	43.8% 38.2%	fabD; malonyl CoA-ac	ccB; acetyl-CoA carboxylase, biotin carboxyl carrrotein  -oxoacyl-[acyl-carrier-protein] synthase  abG; 3-oxoacyl-(acyl-carrier-protein) reductase  abD; malonyl CoA-acyl carrier protein transacylase					
SGO_1695	12 13	52.2% 52.8%	15 12	57.1% 52.2%	17 13	60.8% 50.0%	13 10	54.9% 45.4%	enoyl-acyl carrier prot	tein(ACP) reductase					
SGO_1698	4 7	22.8% 32.1%			6	27.2% 22.5%			3-oxoacyl-[acyl-carrie	r-protein] synthase	III	•			
SGO_1699	4 5	48.3% 48.3%	3	40.8% 50.8%	4	47.5% 48.3%	3	40.8%	transcriptional regulat	or, MarR family					
SGO_1700	7	33.8% 25.5%	9	45.6% 47.9%	7	30.4% 30.4%	4	18.6%	enoyl-CoA hydratase/	isomerase family pro	otein				••
SGO_1701	11 14	28.7% 37.3%	12 16	40.8% 45.6%	17 19	52.4% 55.9%	11 10	31.6% 27.4%	aspartate kinase						
SGO_1708	16 20	62.9% 74.6%	11 10	42.7% 51.1%	14 13	65.5% 65.1%	9	43.6% 49.5%	amiF; Oligopeptide tra amiF	ansport ATP-binding	protein				



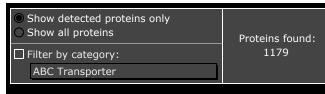
Cover	rage							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn \	/s SgFn	SgPgFn vs SgPg	Coverage	Page 79
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg	SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1709	16 17	49.6% 51.8%	9 10	34.1% 33.2%	11 11	40.0% 40.0%	12 12	42.5% 44.5%	amiE; Oligopeptide tra	ansport ATP-binding	protein				
SGO_1710	6	16.2%			5	15.6%	4	13.0%		ansport system perm	nease	44		44	44
	9	24.7%			4	15.3%	4	17.9%	procent						
SGO_1711	19	31.1%	7	14.9%	11	23.1%	10	20.1%	hppB; Oligopeptide transport system permease hppB; Oligopeptide transport system permease hppA; oligopeptide-binding lipoprotein						44
	22	38.0%	7	15.1%	14	30.1%	12	25.5%	hppB; Oligopeptide transport system permease						
SGO_1712	36 42	53.2% 57.0%	27	45.9% 45.6%	31 31	51.3% 50.1%	31 27	53.5% 49.2%	hppB; Oligopeptide transport system permease hppA; oligopeptide-binding lipoprotein						
	35	57.1%	29	54.2%	33	58.0%	28	54.4%	hppB; Oligopeptide transport system permease  hppA; oligopeptide-binding lipoprotein						
SGO_1713	38	58.5%	22	47.6%	30	52.6%	20	43.6%							
CCO 1715	32	61.7%	23	49.5%	31	62.4%	21	42.9%							
SGO_1715	35	64.1%	23	48.5%	29	57.5%	23	47.9%	hppH; oligopeptide-bi	nding lipoprotein					
SGO_1716	40	68.0%	24	47.2%	26	50.7%	21	46.1%	oligopeptide binding p	protein					
	38	66.9%	18	38.6%	29	58.3%	17	37.8%	ongopeptide binding p	or occini					
SGO_1717	16	58.5%	4	16.3%	4	13.3%			pbp3; penicillin-bindir	na protein 3		4			
	16	59.5%	4	13.6%					рърз, решенит виш	ig procein 5					
SGO_1718	16	36.4%	10	30.2%	16	51.5%	9	23.6%	sufB-1; FeS assembly	nrotein SufB		44			
	20	50.9%	14	36.8%	13	39.1%	11	26.4%	Suib 17 res assembly	protein Suib					
SGO_1719	4	33.8%							SUF system FeS asser	mbly protein. Nift! fa	milv				
	3	33.8%							22. 2,333 23 43361	, p. 555,	1				
SGO_1720	4	15.1%			8	34.4%	4	19.3%	aminotransferase, cla	ss-V					44
	9	38.5%			6	25.6%	3	16.1%	and and crace, cla						
SGO_1721	9	28.8%	8	28.6%	10	31.2%	10	31.2%	sufD; FeS assembly p	rotein SufD					
_	8	26.0%	8	28.6%	11	34.3%	6	23.3%	ca.z, res assertibly p						



Cover	age							S	Streptococ	cus gora	'onii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 80
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1722	9	34.8% 39.1%	11 5	50.0% 25.4%	14 10	56.3% 48.4%	7 5	25.8% 19.5%	sufC; FeS assembly A	TPase SufC					••
SGO_1724	3	13.6%							mecA: Adapter protei	n mec					
	6	32.6%	3	23.6%	4	24.8%			mech, Adapter protein	ii iiicc					
SGO_1725	3	12.4%							bacA; bacitracin resist	acA; bacitracin resistance protein					
	3	12.4%							mecA; Adapter protein mec bacA; bacitracin resistance protein hypothetical protein SGO_1726						
SGO_1726	10	16.7% 18.3%							hypothetical protein S	GGO_1726		01			
SGO_1727	16	44.3%	7	24.8%	8	28.4%	4	16.9%	pacA; bacitracin resistance protein						
300_1727	16	43.6%	7	23.8%	10	33.2%	4	16.7%	nypothetical protein SGO_1726 amino acid ABC transporter, amino acid-						
SGO_1728	8	44.7%	6	45.1%	7	44.3%	7	33.3%	glnQ; glutamine ABC	transporter ATD bind	ing protoin				
330_1/13	9	47.6%	6	40.7%	6	40.7%	6	38.6%	giriQ, giutarrille ABC	transporter ATF-billu	ing protein				
SGO_1729			5	68.1%	4	61.1%	3	50.0%	hypothetical protein S	SGO 1729					
			4	61.1%	4	61.1%	4	61.1%	nypotnetical protein s						
SGO_1730	26	75.6%	25	71.5%	19	61.7%	13	51.9%	SPFH domain/Band 7	family					
	32	78.3%	25	70.5%	21	63.4%	19	54.9%	or reading and rea	,					
SGO_1731	3	23.6%	4	22.1%	6	38.2%	4	26.1%	DNA-binding response	e regulator		44			
	3	18.6%	3	24.1%	8	49.7%	6	37.2%	3 3 3						
SGO_1732	6	19.1%							histidine kinase			44			
	7	23.0%			3	9.6%									
SGO_1735	22	61.0%	21	58.5%	21	56.0%	18	50.7%	hypothetical protein S	GGO_1735					
	23	64.6%	25	60.6%	21	56.0%	16	47.3%					7 - 3	-	
SGO_1736	4	33.1%	4	33.1%	4	33.1%	3	28.9%	alkaline shock protein						
	4	33.1%	4	33.1%	4	33.1%									



Cover	rage							S	Streptococ	cus gord	lonii					ratory UW
	5	Summa	ry Ta	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFr	n vs SgPg	Coverage	Page 81
		Sg		SgFn	9	SgPg	Sg	<sub>I</sub> PgFn				Sg		SgFn		SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	p II Re	p I Rep II	Rep I Rep II	Rep I Rep II
SGO_1737	3	38.7% 40.3%					4	40.3%	rpmB; ribosomal prot	ein L28						
	4	21.2%					7	40.070						-		0 0
SGO_1738	4	21.2%	3	14.0%					ytTr DNA-binding domain family			9				
SGO_1739	6	36.5%	3	27.7%					LytTr DNA-binding do	ytTr DNA-binding domain family						
	7	36.5%														
SGO_1744	9	34.8%	7	25.8%					LytTr DNA-binding domain family ABC transporter, ATP-binding protein SP0636							
SGO_1745	15	51.9%	18	54.9%	14	51.2%	16	54.9%	LytTr DNA-binding domain family ABC transporter, ATP-binding protein SP0636							
	17	56.7%	22	63.8%	15	51.2%	16	54.9%	LytTr DNA-binding domain family  ABC transporter, ATP-binding protein SP0636  fba; fructose-1,6-bisphosphate aldolase, class II							
SGO_1747					3	25.0%	3	27.2%	hypothetical protein S	SGO 1747						
			3	27.2%	3	33.1%			Trypochecical protein a	700_17 17						
SGO_1748	9	25.0%		44.40/	7	23.8%	6	21.0%	pyrG; CTP synthase			44			44	44
	11	24.2%	3		12	36.5%	6	17.9%								
SGO_1749	7	36.6%	6	28.0%	8	43.6%	3	11.5%	manA; mannose-6-ph	nosphate isomerase,	class I					
	9	42.7%	10	47.1%	7	36.6%	6	28.0%								
SGO_1750	11	21.4%							ABC-type multidrug/p ATPase component	rotein/lipid transport	system,					
	13	25.1%				0.40/										
SGO_1751	13	27.0%			6	6.1%			ABC-type multidrug/p ATPase component	rotein/lipid transport	system,				00	
	3	22.8%			"	11.4/0										
SGO_1753		22.070							hypothetical protein S	GGO_1753		9				
SGO 1755	8	47.2%	6	39.5%	11	67.6%	11	67.6%	and K. C. alalian							
SGO_1755	8	43.5%	7	47.2%	12	67.6%	9	57.5%	scrK; fructokinase							



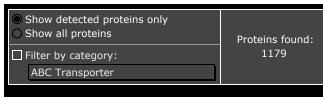
Cover	rage							S	Streptococ	cus gord	lonii					oratory UW
	5	Summai	ry Ta	ble s	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPg	gFn vs SgPg	Coverag	Page 82
		Sg		SgFn		SgPg		ıPgFn_		Dagariakian		Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverag	e n (	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep	II Rep I Rep II
SGO_1756	6	49.4%							hypothetical protein S	GO_1756						
SGO_1757	19	44.4%	13	34.3%	24	54.6%	14	39.3%	glmS; glucosaminefi	ructose-6-phosphate						
300_1/3/	24	48.4%	12	35.0%	25	61.0%	17	47.6%	aminotransferase	minotransferase  NA-binding response regulator						
SGO_1760			3	9.6%	4	14.3%			DNA-binding response	NA-binding response regulator				••	04	
	6	13.8%														
SGO_1761	10	18.9%							histidine kinase	9	<b>y</b>					
	18	48.4%	17	46.1%	17	54.5%	15	53.9%	DNA-binding response regulator					<b>A A</b>	<b>A A</b>	
SGO_1763	20	56.6%	11	39.3%		56.4%	12	40.7%	ABC transporter, subs	n SP0092			JJ			
	6	13.8%	12	23.7%	3	7.9%										
SGO_1768	5	10.5%	13	26.6%	8	15.5%			glycosyl hydrolase, fai	mily 38				JJ		
666 4772																
SGO_1772	3	11.8%							integral membrane pr	otein						
SGO_1774	5	27.5%	8	36.5%	6	30.4%	4	21.2%	alaskal dakada asasas							
300_1774	8	40.6%	8	39.4%	6	29.0%	4	23.8%	alcohol dehydrogenas	e, zinc-containing						
SGO_1780									hypothetical protein C	CO 1780						
300_1700	3	16.7%	3	14.3%					hypothetical protein S	GO_1780						
SGO_1784	14	20.6%	20	28.6%	16	25.1%	12	20.9%	lous, lough tRNA sus	thotaco						
500_1704	18	25.1%	12	21.4%	16	26.9%	16	27.7%	leuS; leucyl-tRNA syn	inetase						
SGO_1792			3	12.8%					transcription regulator	- <u> </u>						
500 <u>-</u> 1752	3	13.7%							u anscription regulator							
SGO_1799	19	42.5%	32	72.1%	26	63.3%	23	59.8%	endopeptidase O							
300_1/33	25	51.6%	27	65.1%	28	64.3%	16	41.7%	епиорерииаѕе О							



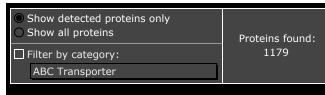
Cover	rage							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn S	gPgFn vs SgPg	Coverage	Page 83
		Sg		SgFn		SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep I	I Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1800	18 19	76.2% 75.7%			10 10	56.1% 53.1%	6	34.3% 30.1%	troB; manganese ABC protein SP1648	C transporter, ATP-bii	nding	00			
SGO_1802	26	75.2%	7	38.4%	21	70.6%	16	71.6%	Metal ABC transporte	r substrate-binding li	poprotein				
300_1002	32	85.8%	4	27.4%	18	66.8%	16	72.6%							
SGO_1803	4	37.4%	5	51.5%	5	51.5%	4	29.4%	tpx; thioredoxin peroxidase						
300_1003	5	38.0%	5	51.5%	7	52.1%	3	28.8%	tpx; thioredoxin peroxidase  hutI; imidazolonepropionase						
SGO_1804			6	23.0%	10	40.1%									
566_1664	4	18.1%	4	17.8%	10	37.1%			hutI; imidazolonepropionase						
SGO_1805	3	7.0%	3	7.1%	16	29.4%	8	16.3%							
					20	39.1%	3	5.6%	nutI; imidazolonepropionase						
SGO_1806					9	38.5%	5	20.7%	ftcD; glutamate formi	minotransferase					
					9	29.4%	4	16.4%	resp, gracamate rorm	Timioti diisierase					
SGO_1807					3	23.6%			serine cycle enzyme,	nutative				44	
					3	23.6%				patati v o					
SGO_1808					6	18.7%	3	7.9%	fhs-2; formatetetral	nvdrofolate ligase					
			4	9.5%	6	18.3%	5	13.5%							
SGO_1811	4	12.3%			5	15.4%			hutH; histidine ammo	nia-lyase					
	5	15.4%	3	10.7%	7	22.2%	4	12.3%	,	,					
SGO_1813			3	12.8%					hutG; formimidoylglu	tamase					
	3	11.6%							, , , , , ,						
SGO_1814	6	7.9%	6	7.7%					putative regulatory pr	otein		44			
	5	6.5%	5	8.8%											
SGO_1816	3	15.8%	6	33.0%					scaR; ScaR Manganes	se-dependent regulat	or of				
	4	23.7%	5	24.7%	5	27.9%			scaCBA						



Cover	rage							S	Streptococ	cus gora	lonii				ckett cratory UW
	9	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs Sg	Pg Coverage	Page 84
	·	Sg		SgFn		SgPg	Sg	<sub>I</sub> PgFn				Sg	SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep	II Rep I Rep II	Rep I Rep II
SGO_1822	22 25	33.7% 39.8%	9	15.3% 15.6%	10 5	19.5% 11.0%	4	7.0%	relA; GTP diphosphok	inase					
SGO_1823					4	28.3% 19.0%			conserved hypothetica	al protein TIGR00046	5				
SGO_1824	6 8	34.6% 40.6%	4 5	25.5% 27.7%	4	25.5% 36.2%	5 5	30.8% 29.6%	prmA; ribosomal prot						
SGO_1827	5 4	35.3% 27.6%	3	27.6%	3	27.6% 27.6%			hypothetical protein S	06					
SGO_1828	6	19.7% 12.8%	5 3	15.4% 10.4%	3 4	12.6% 15.6%	3	11.4%	hypothetical protein SGO_1827  ATPase, AAA family			•			
SGO_1834	5 5	27.6% 28.1%	11 11	69.9% 73.5%	6 7	43.4% 52.6%	8	54.1% 55.6%	hypothetical protein S	GGO_1834					
SGO_1835	3	29.9%	3	29.9%	3	29.9% 29.9%	3	47.8%	hypothetical protein S	GGO_1835					
SGO_1843	11	33.4% 40.0%	14 11	49.4% 43.8%	13 13	38.0% 38.0%	10 10	31.2% 29.5%	pepS; aminopeptidase	e PepS					
SGO_1844	5 12	7.9% 20.0%	6 9	10.5% 16.1%	10 12	18.9% 18.6%	3 5	6.5% 10.0%	cbxX/cfqX family prot	ein		06			00
SGO_1847	13 15	12.5% 14.6%	10 11	8.7% 12.0%	10 14	9.4% 13.9%	6	4.8%	polC; DNA polymerase positive type	e III, alpha subunit,	Gram-	06			
SGO_1848	9	47.8% 48.3%			4	23.9% 23.9%	5 4	22.2% 17.8%	lipoprotein, putative						••
SGO_1849	8	68.4% 63.2%							hypothetical protein S	GGO_1849					



Cover	rage							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	rs SgFn	SgPgFn vs SgPg	Coverage	Page 85
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1851	25 28	54.5% 55.8%	21	45.9% 53.7%	25 28	54.7% 60.2%	19 20	37.2% 45.0%	proS; prolyl-tRNA syn	thetase					
SGO_1852	9	27.6%			5	17.7%	4	16.8%	mombrano-accociatos	d zinc motallanrotaas	o putativo				
330_1032	10	29.7%			5	18.5%			membrane-associated	mbrane-associated zinc metalloprotease, putative					
SGO_1854	12	57.0%	6	34.5%	6	32.1%	6	32.1%	unnS: undecanrenyl d	ppS; undecaprenyl diphosphate synthase					
	12	50.6%	6	32.1%	7	39.4%	6	28.5%	upps, undecapteriyi c	iipiiospiiate syntiiase					
SGO_1855	4	47.3%			3	47.3%			preprotein translocase	e. YaiC subunit					
	4	47.3%			3	47.3%			p. sp. stem t. a.i.s. state	.,					
SGO_1856	17	35.8%	37	69.2%	12	22.9%	8	18.2%	ATP-dependent protei	nase ATP-binding ch	ain				
	19	34.7%	26	54.8%	12	26.7%	4	9.8%							
SGO_1857	4	11.3%			3	8.5%			PTS system, IIABC co	mponents		44			
	7	15.3%													
SGO_1858			4	17.8%	5	17.6%			beta-fructofuranosida	se/sucrose 6 phosha	te hydrolase				
	3	9.3%	5	16.7%	5	19.6%									
SGO_1860	10	47.4%	17	61.8%	11	48.1%	7	41.4%	5'-nucleotidase, lipopi	rotein e(P4) family					
	14	55.8%	13	55.8%	9	47.0%	5	29.5%							
SGO_1861	3	23.4%			4	40.1%			nusB; transcription ar	ntitermination factor	NusB				
					4	40.1%	3	23.4%							
SGO_1862	3	40.3%	4	46.5%	3	38.8%	3	40.3%	alkaline shock protein						
	3	40.3%	5	63.6%	3	38.8%	4	47.3%							
SGO_1863	8	58.1%	7	61.3%	7	50.5%	6	41.4%	efp; Elongation factor	P (EF-P)					
	8	58.1%	5	46.2%	8	66.1%	6	41.4%							
SGO_1864	10	46.2%	13	58.4%	10	43.1%	6	25.2%	X-Pro aminopeptidase	2					
	13	51.6%	13	63.7%	10	52.7%	6	25.2%							



Cover	rage							S	Streptococ	cus gord	lonii				Had Labo	ratory UW
	5	Summar	y Tal	ble S	SgFn '	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgP	gFn vs SgPg	Coverage	Page 86
		Sg		SgFn	9	SgPg	Sg	ıPgFn				Sg		SgFn	 SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n (	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1865	26 30	35.1% 43.4%	15 14	28.7%	17 20	29.2% 35.9%	8	16.5% 16.3%	uvrA; excinuclease AB	3C, A subunit						44
	30	43.4 /0	14	20.2 /0								)	_		0 0	
SGO_1866					3	11.1%	3	8.3%	corA; magnesium and cobalt transporter hypothetical protein SGO_1867							
SGO_1867	5	23.2%	3	15.6%	4	22.8%	3	20.1%						44		
300_1007	5	23.2%	4	22.8%	4	22.8%	4	22.8%	nypotnetical protein S							
SGO_1869	9	29.8%							hypothetical protein S							
300_1003	13	46.3%							nypothetical protein 3							
SGO_1870	14	28.8%			4	8.9%			hypothetical protein S	GO 1870						
	16	34.4%			3	6.3%			Trypochecieur procein s							
SGO_1871	11	34.0%							lipoprotein, putative							
	11	34.3%														
SGO_1872	6	25.1%			5	21.0%			hypothetical protein S	GO_1872						
	11	40.2%							,, ,	_						
SGO_1878	3	20.6%							transcriptional regulat	or, TetR family doma	ain protein	4				
	3	17.2%	4	29.9%					. ,	, , , , , , , , , , , , , , , , , , ,						
SGO_1879	7	44.3%	4	43.0%	5	41.8%	3	31.6%	rpsR; ribosomal prote	in S18						
	7	44.3%	7	59.5%	6	41.8%	5	44.3%								
SGO_1880	8	79.8%	7	69.3%	8	79.8%	8	79.8%	ssb-1; single-strand b	inding protein						
	8	79.8%	6	57.1%	8	79.8%	7	73.0%								
SGO_1881	7	74.0%	8	76.0%	8	74.0%	8	78.1%	rpsF; ribosomal protei	in S6						
	8	82.3%	9	78.1%	7	72.9%	8	74.0%								
SGO_1882	3	19.8%	4	20.3%	4	20.3%	3	19.8%	folE; GTP cyclohydrola	ase I						
	5	46.0%	5	40.1%	4	20.3%	4	25.1%								

<ul><li>Show detected proteins only</li><li>Show all proteins</li></ul>	Proteins found:
☐ Filter by category:	1179
ABC Transporter	

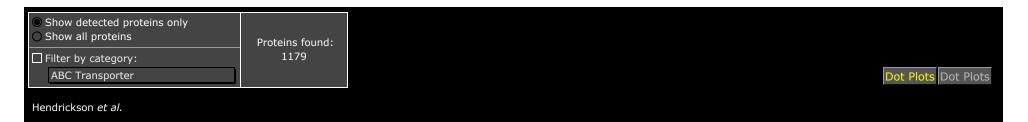
Cover	age							S	Streptococ	cus gord	lonii					ckett cratory UW
	9	Summai	гу Та	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPg	Fn vs SgPg	Coverage	Page 87
		Sg		SgFn		SgPg		<sub>1</sub> PgFn		Decemention		Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I Re	p II F	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1884	8	30.6% 43.3%							hypothetical protein S	GO_1884						
SGO_1885	30	60.7%	40	73.5%	29	63.5%	25	56.7%		. , =,						
3GO_1883	36	65.2%	35	75.4%	34	70.6%	24	61.1%	groL; 60 kDa chapero	nin/groEL protein						
SGO 1996	O_1886 4 54.8% 4 5		54.8%	4	54.8%	3	41.9%		) I D							
3GU_1880	4 54.8% 4 5			51.6%	3	41.9%	3	41.9%	groes; chaperonin, 10	) кра				J		
SGO_1887	3	13.9%							roES; chaperonin, 10 kDa  BC transporter, ATP-binding protein							
	7	29.6%														
SGO_1888	5	11.6%							ABC transporter, perm	nease protein						
	7	12.8%							, p							
SGO_1890	3	11.2%							PTS system, fructose(	mannose)-specific II	:D	4				
	3	11.2%														
SGO_1891	3	13.8%							PTS system, IIC comp	onent						
	4	24.7%	_	-0.404	_	-0.40/	_	-0.40/								
SGO_1892	5	52.4%		56.1%	5	52.4%	5	52.4%	PTS system, fructose(	mannose)-specific II	В					
	6	56.1%	6	59.8%	5	52.4%	4	42.7%							-	
SGO_1894	7	12.4%							sugar-binding cell env	elope protein						
		27.4%											_			
SGO_1895	3	15.0% 14.5%							response regulator							
															0 0	
SGO_1897	- 3 - 6	12.9% 22.7%							rbsB; ribose ABC transcomponent) CAC1453		ng					
			45	74.001	46	00.467	47	40.007	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,							
SGO_1898	10	40.6%	15 17	71.3% 70.1%	13 13	63.4% 63.4%	11	49.9% 40.6%	glutamyl aminopeptida	ase						
	10	49.5%	17	10.1%	13	03.4%	9	40.0%								



Cover	rage							S	Streptococ	cus gord	lonii					kett ratory UW
	9	Summai	ry Ta	ble s	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgP	gFn vs SgPg	Coverage	Page 88
		Sg		SgFn		SgPg		<sub>1</sub> PgFn		Dagawiakian		Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1899	3	30.5%							hypothetical protein S	GO_1899						
SGO_1900	4	48.6%			3	36.2% 43.8%			thioredoxin family pro	tein						
500 1001	6	36.1%	4	22.6%	7	44.7%	5	31.7%								
SGO_1901	5	31.7%	5	26.4%	7	36.1%	5	30.3%	tRNA binding domain							
SGO_1902	5	57.3%			6	59.5%	6	59.5%	sch: single-stranded F	NA binding domain b; single-stranded DNA-binding protein						
	6	64.1%			6	59.5%	6	59.5%	33b, Single Stranded E	on a binding protein						
SGO_1903	17	39.1%	25	50.0%	20	46.4%	15	44.2%	ATP-dependent Zn pro	otease						
	19	39.3%	20	49.0%	23	52.8%	13	39.5%						J		
SGO_1907									sensor protein							
	3	15.7%														
SGO_1912	4	20.4%	4	25.6%	5 3	29.3%			Bifunctional folate syn	thesis protein					99	
	4	21.4/0	4	15.0%	3	14.6%							_	-	0 0	0 0
SGO_1914	4	15.6%	5	21.2%	4	18.1%	3	11.8%	folP; dihydropteroate	synthase			9	99	99	
	19	61.4%	13	41.4%	19	61.4%	14	48.0%								
SGO_1916	19	60.6%	13	47.7%	21	68.7%	12	46.7%	ackA; acetate kinase					JJ		
	3	17.7%	3	18.6%	6	37.5%	5	29.3%								
SGO_1917	4	20.5%	6	34.4%	6	37.5%	3	18.9%	hypothetical protein S	GO_1917						
SGO_1923	5	17.2%							com/D. compater	a wata in						
3d0_1923									comYB; competence p	protein						
SGO_1924	17	54.9%			11	41.1%	7	23.5%	comYA; competence p	protein comVA						
300_1721	16	54.9%			9	34.5%	5	15.4%	contra, competence p	orotein contra						



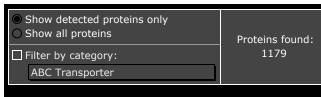
Cover	rage							S	Streptococ	cus gora	lonii					kett ratory UW
	5	Summa	ry Ta	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPg	gFn vs SgPg	Coverage	Page 89
		Sg		SgFn		SgPg		<sub>1</sub> PgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n C	Coverage	n C	Coverage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1926	55 69	49.6% 57.0%	51 56	52.1% 57.9%	69 73	57.5% 62.6%	55 55	48.3% 50.3%	rpoC; DNA-directed R	NA polymerase, beta	chain					
SGO_1927	50	53.6%	44	55.0%	61	63.4%	44	52.1%		NA l l . l .	. 19					
300_1327	53	54.5%	37	49.8%	57	63.7%	43	51.9%	poB; DNA-directed RNA polymerase, beta subunit				J			
SGO_1928	27	36.4%			9	17.0%	5	10.4%	photh, popicillin hind	bp1b; penicillin-binding protein 1B						
300_1320	30	42.4%			12	24.0%			popio; penicilin-bina	pp1b; penicillin-binding protein 1B						
SGO_1929	11	37.6%	17	56.2%	19	56.0%	13	41.6%	turs: turocul tBNA cur	bp1b; penicillin-binding protein 1B  vrS; tyrosyl-tRNA synthetase						
300_1717	16	40.2%	16	57.4%	21	60.3%	13	46.7%	tyro, tyrosyr-triva syr	op1b; penicillin-binding protein 1B vrS; tyrosyl-tRNA synthetase						
SGO_1930	4	15.2%			3	12.1%			rrmA; Ribosomal RNA	large subunit methy	/ltransferase					
	6	24.5%			3	12.1%			Α							
SGO_1931					3	30.9%			lipoprotein, putative							
									iipoproteiii, patative							
SGO_1934	11	26.9%							copper-translocating F	P-tyne ATPase						
	14	32.5%					3	5.4%	copper transfocuting r	type /// use						
SGO_1935	5	49.0%							negative transcription	al regulator ConY						
	3	27.3%							negative transcription							
SGO_1936	25	58.2%	8	24.2%	18	50.8%	5	16.2%	adcA; metal-binding (	Mn) permease precu	ırsor,			44		
	35	65.6%	8	24.8%	15	41.2%	6	18.2%	lipoprotein							
SGO_1938	6	43.2%			3	22.9%			adcC; ATP-binding pro	otein. Mn					44	
	8	48.3%			3	22.9%			adde, / billallig pro							
SGO_1939									adcR; repressor prote	in adcR						
					4	30.6%										
SGO_1957	8	30.8%	4	12.0%					hypothetical protein S	GO 1957						
	12	41.3%	6	19.5%	3	13.4%			ny potrictical protein 3	.00_1737						



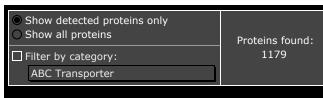
Cover	rage							S	Streptococ	cus gora	lonii					ratory UW
	9	Summar	ry Tal	ble S	SgFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgP	gFn vs SgPg	Coverage	Page 90
		Sg		SgFn		SgPg	Sg	PgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	overage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1958	5 7	47.7% 54.7%	5 5	47.7% 51.6%	6	48.4% 48.4%	6 5	54.7% 47.7%	rplQ; ribosomal protei	in L17						
SGO_1959	17	50.3%	20	59.0%	20	68.3%	15	54.8%	rpoA; DNA-directed R	NA polymoraco, alph	a cubunit					
330_1333	19 55.8% 15 56.7% 19 3 22.8% 4 33.9% 5				62.2%	18	63.5%	TPOA, DIVA-directed K	NA polymerase, alpm	ia Subuilit						
SGO_1960	3 22.8% 4 33.9% 5					50.4%	4	33.9%	rnck, ribocomal proto	in C11						
300_1300	3     22.8%     4     33.9%     5       4     33.1%     5     47.2%     4					33.9%	3	22.8%	rpsK; ribosomal prote	III 511						
SGO_1961	16	69.4%	11	62.8%	17	69.4%	13	59.5%	rncMi ribocomal proto	in C12n/C19a						
300_1301	16	69.4%	8	47.9%	14	69.4%	14	69.4%	rpsM; ribosomal prote	:iii 513p/518e						
SGO_1962					3	60.5%	3	60.5%	rpmJ; ribosomal prote	ain 136						
					3	60.5%			Tpms, moosomar proce	SIII ESO						
SGO_1964	10	64.6%	13	62.7%	13	68.9%	12	67.9%	adk; Adenylate kinase	A (ΔTP-ΔMP transpho	enhonylase)					
	11	64.6%	11	62.3%	14	79.2%	9	58.0%	duk, Adenyidte kiildse	2 (7117 71111 Cranspile	эрпогушэсу					
SGO_1965	8	20.2%			6	15.4%	3	8.5%	Preprotein translocase	secY subunit		4				
	9	20.6%			5	13.8%	3	8.5%	Treprotein translocase	2 See 1 Suburne						
SGO_1966	6	49.3%	7	50.7%	7	50.7%	12	56.2%	rplO; ribosomal protei	in I 15						
	5	28.8%	5	47.3%	8	50.7%	9	50.7%	Tpio, fibosomai protei							
SGO_1967	4	54.1%	3	54.1%	4	54.1%	5	54.1%	50S ribosomal protein	. I 30 -related protein	n					
	4	54.1%	3	35.1%	4	54.1%	4	54.1%	303 Hb030Hdi protein	reso related protein	'					
SGO_1968	11	65.9%	8	60.4%	10	71.3%	12	72.0%	rpsE; ribosomal prote	in S5						
	12	67.1%	9	76.2%	11	71.3%	11	72.0%	rpsz/ ribosomai prote							
SGO_1969	4	39.8%	4	39.8%	4	39.8%	5	47.5%	rpIR; ribosomal protei	n I 18						
	5	50.0%	4	39.8%	4	39.8%	4	39.8%	TPIRT, TIDOSOMAI PROCEI							
SGO_1970	9	59.6%	12	71.9%	9	59.6%	9	59.6%	BL10; 50S ribosomal	protein I 6						
	10	65.7%	6	49.4%	11	66.3%	8	59.6%	DETU, 303 HD050Hd1	protein Lo						



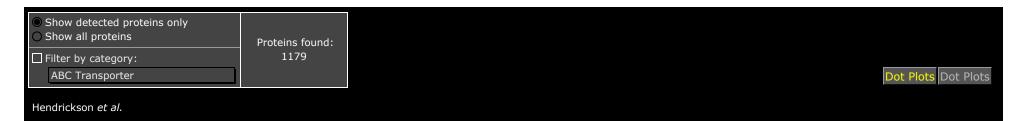
Cover	age							S	Streptococ	cus gora	lonii				Hac Labor	kett ratory UW
	S	Summar	у Та	ble S	gFn	vs Sg	SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgP	gFn vs SgPg	Coverage	Page 91
		Sg		SgFn		SgPg	Sg	PgFn				Sg		SgFn	SgPg	SgPgFn
Protein	n C	Coverage	n (	Coverage	n (	Coverage	n C	overage		Description		Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1971	12 12	59.8% 59.8%	13 10	59.8% 50.0%	12 13	58.3% 59.8%	12 11	58.3% 58.3%	rpsH; ribosomal prote	ein S8						
200 4070																
SGO_1972	3 49.2% 18 83.9% 15 70.6% 16 80.6% 14								rpsN; ribosomal prote	ein S14p/S29e						
SGO_1973	18 83 9% 15 70 6% 16 80 6%						14	77.2%	BL6; 50S ribosomal p	rotein I 5						
330_1375	18 83.9% 15 70.6% 16 80.6%						15	75.0%	beo, 303 fibosoffiai p	rotein E3						
SGO_1974	17 81.7% 15 88.3% 17 78.3% 15 8 47.5% 9 63.4% 9 52.5% 8						8	47.5%	rpIX; ribosomal protei	in 1.24						
	9	63.4%	6	54.5%	9	52.5%	8	47.5%	TPIX, TIBOSOMAI Protei	III LZŦ						
SGO_1975	4	27.0%	4	22.1%	5	34.4%	5	32.0%	rplN; ribosomal protei	in I 14				44		
	6	36.1%	4	22.1%	4	27.0%	5	32.0%	Tpirty Tibosomai proces	22 1						
SGO_1976	4	25.6%	3	25.6%	5	38.4%	5	38.4%	BS16; 30S ribosomal	protein						
	4	25.6%	6	53.5%	6	58.1%	5	38.4%	2010, 000 1120011141	p. 0 co						
SGO_1977	4	42.6%	4	50.0%	5	45.6%	4	57.4%	rpmC; ribosomal prote	ein L29						
	8	73.5%			5	58.8%	3	50.0%	, ., , p							
SGO_1978	4	33.6%	6	42.3%	6	44.5%	4	33.6%	rpIP; ribosomal protei	n L16						
	8	52.6%	4	40.1%	6	44.5%	4	37.2%	. ,							
SGO_1979	12	55.8%	14	58.1%	11	53.9%	10	49.8%	rpsC; ribosomal prote	in S3						
	14	59.4%	13	69.6%	10	53.5%	9	53.9%					_		-	
SGO_1980	8	58.8%	6	50.9%	7	57.0%	6	54.4%	rplV; ribosomal protei	in L22						
	9	69.3%	5	49.1%	8	61.4%	7	60.5%							-	-
SGO_1981	8	57.0%	8	48.4%	8	57.0%	6	55.9%	rpsS; ribosomal prote	in S19						
	9	58.1%	10	64.5%	9	57.0%	8	57.0%							-	33
SGO_1982	10	47.3%	10	52.0%	11	56.0%	10	50.2%	rplB; ribosomal protei	in L2						
	12	52.7%	11	54.2%	11	45.5%	12	56.0%	•							



Cover	rage							S	Streptococ	cus gora	lonii				ratory UW
	5	Summai	y Tal	ble S	SgFn	vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPgFn vs SgPg	Coverage	Page 92
		Sg		SgFn		SgPg	Sg	<sub>I</sub> PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_1983	7	69.4% 84.7%	6	59.2% 68.4%	8 7	69.4% 69.4%	7 8	69.4% 76.5%	rplW; ribosomal prote	ein L23					
SGO_1984	7	8     41.5%     9     49.8%     8     51.7%       8     45.2%     11     63.9%     9     53.8%				51.7%	7	51.7% 51.7%	rplD; ribosomal prote	in L4/L1 family					
SGO_1985	8 41.5% 9 49.8% 8 51.7% 8 45.2% 11 63.9% 9 53.8% 10 48.1% 10 64.9% 10 56.7% 5 38.2% 5 38.2% 5 38.2%				10	59.6% 59.6%	rpIC; ribosomal protei	in L3		01					
SGO_1986	5		45.2%     11     63.9%     9     53.8%     10     59.1       48.1%     10     64.9%     10     56.7%     10     59.1       38.2%     5     38.2%     5     38.2%     6     45.1       38.2%     5     45.1%     5     38.2%     6     45.1				6	45.1% 45.1%	rpsJ; ribosomal protei	in S10		01			00
SGO_1988	6	26.6% 25.7%	5	20.6%					hydrolase, haloacid de	ehalogenase-like fam	nily	•4			
SGO_1989	25 26	67.0% 67.2%	24 25	61.9% 63.3%	31 29	69.5% 65.8%	26 26	67.0% 66.7%	purA; adenylosuccina	te synthetase					
SGO_1990	7	6.4% 10.9%	10 12	23.7% 26.4%	7 8	15.3% 19.8%	4	8.7%	glutamatecysteine li ligase, putative	igase, putative/amino	o acid	04		00	•
SGO_1991	3 8	12.8% 32.4%	6 5	23.1% 19.7%	3	16.2% 19.7%			hsIO; 33 kDa chapero protein	nin /Heat shock prot	ein 33-like			••	
SGO_1993	10 14	49.8% 70.3%	6	35.6% 45.1%	9	49.8% 49.8%	3 5	22.4% 29.7%	possible transcription	al regulator					••
SGO_1994	3	25.9%							lipoprotein, putative			•			
SGO_1995	4	16.0% 16.0%	3	11.8% 22.1%			3	13.4%	MutT/nudix family pro	otein		01	00		••
SGO_1998	19 24	30.2% 32.6%	13 15	20.6% 24.2%	21 23	32.3% 34.7%	10 8	17.2% 13.6%	clpB; ATP-dependent chain	Clp proteinase, ATP-	binding				••



Cover	rage							S	Streptococ	cus gora	lonii				kett ratory UW
	5	Summar	у Та	ble S	SgFn	vs Sg	SgF	g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	gPgFn vs SgPg	Coverage	Page 93
		Sg		SgFn		SgPg	Sg	PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage		Description		Rep I Rep I	I Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_2000	16 16	67.4% 67.4%	17 19	68.6% 78.4%	20 18	79.8% 78.1%	16 15	66.9%	tsf; translation elonga	ation factor Ts					
SGO_2001	17	63.8%	23	69.2%	19	65.8%	19	66.9%	rpsB; ribosomal prote	in S2					
	19	68.5%	23	80.8%	18	63.1%	20	69.2%							
SGO_2004	20 25	41.9% 41.3%	5	13.1%					LPXTG cell wall surface protein			01			
	46	19.3%		11.070	5	1.8%	9	3.6%				0 0	0 0	0 0	0 0
SGO_2005	54	21.0%	4	1.9%	5	2.3%	5	1.9%	LPXTG cell wall surfac	e protein	94		00	00	
SGO_2006	3	27.3%							thioredoxin signature	protein					
	3	28.9%								F					
SGO_2007	7	47.8%	8	56.7%	6	43.3%	5	36.5%	nusG; transcription te	ermination/antitermir	nation factor				
	8	53.4%	7	48.9%	7	55.6%	7	47.8%	NusG						
SGO_2008	3	31.0% 31.0%							preprotein translocase protein	e secE component -re	elated				
	17	33.1%	6	17.3%											
SGO_2010	17	33.2%	4	8.4%					pbp2a; penicillin-bind	ing protein 2A					
	35	48.2%	5	6.0%											
SGO_2013	40	53.4%	5	6.6%					putative N-acetylmura	amidase/lysin					
SGO_2015									nossible nelvensebasis	do transport protein					
300_2015	3	6.4%							possible polysaccharic	de transport protein					
SGO_2016	4	10.50/							nucleotide sugar dehy	dratase, putative		04			
	4	10.5%												-	
SGO_2017	5	41.3%			3	29.6%			nucleotidyl transferas	e, putative					



Cover	rage							S	Streptococ	cus gord	lonii			Hac Labor	_
	5	Summar	у Та	ble S	§gFn	vs Sg	SgF	Pg vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 94
		Sg		SgFn	9	SgPg	Sg	gPgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Coverage	n C	Coverage	n C	Coverage		Description		Rep I Rep	II Rep I Rep II	Rep I Rep II	Rep I Rep II
SGO_2019	9	34.7% 38.2%			6 4	22.6% 18.8%			licD; licD3 protein					••	
SGO_2020	4	16.0%							glycosyltransferase						
SGO_2021	7	34.9% 45.5%							Extracellular polysacci	haride glycosyltransf	erase				
SGO_2022	4	17.7%							UDP-glucose 4-epimer	lycosyltransferase xtracellular polysaccharide glycosyltrans DP-glucose 4-epimerase BH3715					
SGO_2023	7	33.3% 33.3%							galactosyltransferase						
SGO_2024	19 24	32.3% 38.8%			10 8	18.9% 14.9%	3 4	6.5% 10.0%	Extracellular polysacci	haride biosynthesis				••	00
SGO_2025	13 12	60.2% 54.5%			10 9	43.7% 44.2%	3 5	16.9% 28.6%	wze; putative autopho kinase	osphorylating protein	tyrosine				••
SGO_2026	5	31.6% 31.6%			6 5	37.7% 31.6%			wzd; polysaccharide e	export protein, MPA1	family				
SGO_2027	5	12.3%							wzh; wzh/Putative pho phosphatase	osphotyrosine-protei	n				
SGO_2028	12 13	29.8% 31.5%			3	8.6%			wzg; transcriptional re	egulator				••	
SGO_2033	22 31	40.2% 48.2%	23 16	39.0% 30.4%	14 14	33.4% 31.9%	7 9	17.7% 21.1%	nrdD; ribonucleoside-	triphosphate reducta	se				••
SGO_2034	8	14.0% 19.3%	3	7.1%	4	7.6%			hypothetical protein S	GO_2034		0 (		••	



Cover	rage		Streptococcus gordonii													Hackett Laboratory		
	9	Summai	ry Table SgFn vs Sg			vs Sg	SgPg vs Sg		SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgF	n vs SgPg	Coverage	Page 95		
		Sg		SgFn		SgPg	Sg	PgFn			Sg		SgFn	SgPg	SgPgFn			
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n Coverage		Description			Rep I Rep	p II Re	p I Rep II	Rep I Rep II	I Rep I Rep II		
SGO_2037	9	21.0%	5 6	11.4% 14.0%					cardiolipin synthase			•						
SGO_2039	5	16.7%																
3d0_2039	6	18.7%			3	8.7%			dinydrofolate synthase	dihydrofolate synthase								
SGO_2041	4	33.8%			6	43.9%	3	23.0%	concerned by motheries	al amatain TICD003E0								
300_2041	5	38.1%			4	33.8%			conserved hypothetica	)								
SGO_2042	5	67.0%	5	68.2%	3	53.4%	4	63.6%	Bacterial protein of un	nknown function (DU	F965)							
340_2042	4	63.6%	4	63.6%	3	53.4%	4	63.6%	superfamily									
SGO_2043	8	58.9%							lipoprotein, putative									
000_=010	7	44.7%			3	21.6%			iipoproteiii, patative									
SGO_2045	18	52.2%	16	49.3%	18	53.3%	17	51.4%	recA; recA protein									
	22	54.8%	13	41.0%	19	55.6%	17	54.3%	reck, reck protein									
SGO_2046	7	19.9%	5	14.4%	4	10.0%	4	8.6%	cinA; competence indu	iced protein								
	5	12.2%	5	10.0%	4	9.6%	4	9.8%	cint, competence mat	acea protein								
SGO_2049									tagI; DNA-3-methylac	denine alvcosvlase I								
	3	29.3%							tagi, bin s memilia	zemie grycosynase i								
SGO_2050	5	37.2%			3	25.5%			ruvA; Holliday junction	n DNA helicase RuvA								
	3	17.3%	3	23.5%	4	26.0%												
SGO_2052									hypothetical protein S	GO 2052								
	4	25.4%							, pounduous processi o									
SGO_2053	9	20.2%	9	23.5%	5	13.8%	5	13.3%	- DNA mismatch repair p	protein hexB								
	12	28.4%	6	14.4%	10	27.5%	7	17.3%										
SGO_2056	15	20.2%	13	21.3%	11	21.4%	5	8.0%	mutS: DNA mismatch	ch repair protein MutS					44			
200_2050	17	28.1%	18	31.5%	14	28.6%	10	22.6%	dcg/ Drive information									



Cover	rage		Streptococcus gordonii												Hackett Laboratory		
	5	Summai	гу Та	ble s	ble SgFn vs Sg			g vs Sg	SgPgFn vs Sg	SgPg vs SgFn	SgPgFn vs SgFn		SgPgFn vs SgPg		Coverage	Page 96	
		Sg		SgFn		SgPg	Sg	PgFn	_			Sg		SgFn	SgPg	SgPgFn	
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	overage		Description			p II	Rep I Rep II	Rep I Rep II	Rep I Rep II	
SGO_2057	7 6	59.3% 49.0%							argR; arginine repressor								
SGO_2058	31	59.8%	39	69.4%	37	66.2%	25	56.6%	a Carata Libbia								
3GO_2038	37	65.7%	36	70.5%	36	64.1%	24	52.0%	argS; arginyl-tRNA sy	ntnetase							
SGO_2059	5	19.0%							hypothetical protein SGO_2059								
500 2060	15	31.5%	12	28.1%	21	43.0%	8	16.6%									
SGO_2060	22	42.0%	15	37.0%	19	39.4%	8	19.7%	aspS-1; aspartyl-tRNA	A synthetase					99		
SGO_2062	16	45.8%	19	63.1%	21	66.0%	14	37.1%	higC, highidal tDNA av	nthatasa							
300_2002	17	48.6%	18	55.2%	20	62.4%	14	40.4%	hisS; histidyl-tRNA sy	ntnetase							
SGO_2064	16	40.0%	19	48.8%	22	54.0%	15	41.9%	ilyDr dibydrowy acid d	obydrataco							
555_2551	18	40.3%	18	47.7%	24	60.4%	14	40.3%	ilvD; dihydroxy-acid d	icia acriyaratase							
SGO_2065									rpmF; ribosomal prote	ein L32							
SGO_2066	3	34.7%	5	65.3%	4	44.9%	3	34.7%									
300_2000	4	53.1%			3	34.7%	4	44.9%	rpmG; ribosomal prote	ein L33							
SGO_2070	7	31.4%	7	37.1%	9	48.8%	7	34.8%	hypothetical protein S	GO 2070							
555_2075	9	40.1%	3	15.7%	8	42.8%	3	12.4%	nypothetical protein 3	GO_2070							
SGO_2073							3	13.0%	FtsK/SpoIIIE family su	uhfamily nutative							
									Tony opoint family st	abraininy, putative							
SGO_2080	7	29.7%			4	20.6%			transcription activator	nlcR							
	6	29.7%			5	22.9%			and a priori delivator	picit							
SGO_2081	10	47.4%							lipoprotein, putative								
	15	60.9%			3	24.3%											



Cover	rage		Streptococcus gordonii												Hackett Laboratory		
	9	Summai	ry Tal	ble s	SgFn	vs Sg	SgPg vs Sg		SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgPg	Fn vs SgPg	Coverage	Page 97	
		Sg		SgFn		SgPg	Sg	<sub>1</sub> PgFn				Sg		SgFn	SgPg	SgPgFn	
Protein	n (	Coverage	n (	Coverage	e n (	Coverage	n C	Coverage	Description			Rep I Re	p II F	Rep I Rep II	Rep I Rep II	Rep I Rep II	
SGO_2082	9 12	43.0% 50.6%	3	17.7%					lipoprotein, putative								
SGO_2084	4	27.7%	3	13.3%					NAD (D) 1 1 1								
3GU_2084	5	27.7%	4	25.5%	5	42.0%			NAD(P)H dehydrogena	ase, quinone ramily							
SGO_2085	21	58.7%	12	37.4%	16	50.6%	13	46.4%	D. adam.daainat	ha l							
300_2083	23	56.8%	13	43.6%	17	53.4%	9	32.7%	purB; adenylosuccinate lyase								
SGO_2086	6	15.6%							hypothetical protein S	CO 2086							
566_2666	8	18.9%							nypothetical protein 5	3GO_2086							
SGO_2094	8	26.0%							general stress protein	GSP-781							
	11	37.7%							general stress protein	701							
SGO_2096	16	51.8%							comB; transport prote	ein ComB							
	21	60.6%							comb, transport prote	, statispart protein comb							
SGO_2097	30	47.3%			10	16.0%	3	2.9%	comA: ATP-hinding Tr	ransport protein ComA							
	32	49.7%			8	17.6%											
SGO_2098	17	65.0%	16	69.0%	20	61.6%	21	75.4%	rpsD; ribosomal prote	in S4							
	21	65.5%	16	58.6%	21	66.5%	22	76.4%	- Tpob/ Hooseman proce	AII ST							
SGO_2099									ABC transporter ATP-l	hindina protein							
					4	22.9%											
SGO_2100	14	45.8%	7	27.1%	25	60.5%	18	49.7%	ABC transporter subst	trate-binding protein							
	12	42.5%	5	22.3%	22	59.3%	18	54.2%									
SGO_2102					5	60.4%			hypothetical protein S	GGO 2102							
					5	60.4%	3	45.8%	, ,	.00_210Z							
SGO_2103			3	21.5%					hydrolase, haloacid de	ehalogenase-like fam	nilv						
	4	21.0%							n, a olase, haloacia ac	enalogenase-like faililly							



Cover	age		Streptococcus gordonii													Hackett Laboratory UW		
	S	Summar	mary Table SgFn vs Sg			SgF	g vs Sg	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	/s SgFn	SgP	gFn vs SgPg	Coverage	Page 98			
		Sg		SgFn		SgPg		PgFn		Danasialian		Sg		SgFn	SgPg	SgPgFn		
Protein	n C	Coverage	n (	Coverage	n C	Coverage	n C	overage	Description			Rep I Re	p II	Rep I Rep II	Rep I Rep II	Rep I Rep II		
SGO_2104	15 18	48.4% 57.9%	13 13	53.7% 51.9%	13 13	54.4% 57.2%	9	34.7% 35.4%	srtB; sortase B									
SGO_2105	9	55.9%	11	55.9%	5	39.0%	6	48.2%	abpA; amylase-bindin	a protein AhnA								
	12	69.7%	12	69.7%	7	48.2%	6	44.6%	abpri, amylase bilang procent rispri									
SGO_2106	13	44.2%	14	40.8%	14	43.0%	14	45.5%	ribose-phosphate diph	nosphokinase								
	16	48.0%	15	44.9%	14	40.8%	10	34.3%										
SGO_2107	4	22.7%							general stress protein	GSP-781		4						
	4	23.5%																
SGO_2108	10	55.1%			5	32.4%			mreC; cell shape-determining protein MreC		<b>C</b>							
	11	57.8%			3	20.6%						_						
SGO_2133	32 40	50.5% 57.6%	33 26	53.6% 47.3%	25 22	47.4% 40.9%	19 18	37.6% 37.9%	Cell division protein ft	tsH-like protein								
													_					
SGO_2134	6 7	26.7% 33.3%	12 12	52.8% 52.8%	11	46.7% 46.7%	8	38.3%	hpt; hypoxanthine ph	osphoribosyltransfera	ase							
SGO_2138	5	42.6%							Septum formation init	iator family								
SGO_2139	3	43.2%							SA DNA binding doma	in protoin								
									S4 RNA-binding doma	iii proteiri								
SGO_2140	6	6.6%							transcription-repair co	ounling factor								
	8	9.5%							transcription repair co	Japining ractor								
SGO_2141									pth; peptidyl-tRNA hy	drolase								
	3	18.5%							, , , popular,									
SGO_2142	15	56.9%	14	53.4%	16	61.2%	13	44.7%	GTP-binding protein									
	17	62.0%	16	58.5%	18	61.2%	15	56.9%	5.									



Cover					kett atory UW										
	9	Summa	nmary Table SgFn vs Sg			vs Sg	SgF	g vs S	g SgPgFn vs Sg	SgPg vs SgFn	SgPgFn v	s SgFn	SgPgFn vs SgPg	Coverage	Page 99
		Sg	SgFn SgPg				Sg	PgFn				Sg	SgFn	SgPg	SgPgFn
Protein	n (	Coverage	n (	Covera	ge n	Coverage	n C	overage		Description Rep I Rep II Rep I Rep					Rep I Rep II
SGO_2145	17	56.5%			15	56.1%	15	56.9%	comE; competence re	cnonco rogulator Co	mE				
555_11.5	20	61.6%			17	56.1%	16	56.9%	come, competence re	sponse regulator Col	IIIL				
SGO 2146	11	29.4%			7	23.2%			aanaDa histidina musta	in Linna Camp					
340_2140	11	32.0%			6	19.9%	3	6.0%	comb; histidine prote	ein kinase ComD				99	
SGO 2150	11	44.8%	9	34.5%	6 8	39.3%	7	34.8%							
300_2130	14	52.1%	9	32.7%	6 9	39.5%	5	24.4%	degP; serine protease						

