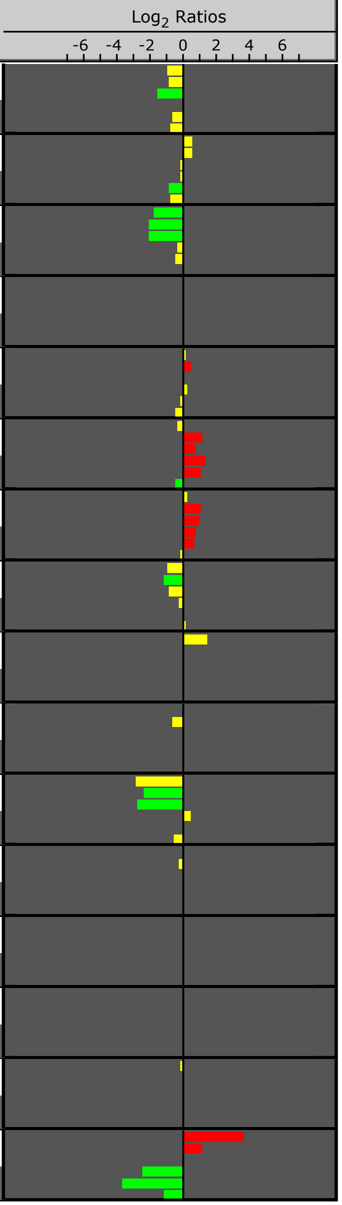
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory **UW**

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0001 dnaA; chromosomal replication initiator protein DnaA	-0.902	7.046	0.0101	0.0398	-0.754	7.101	0.0159	0.0586	-1.455	6.882	0.0038	0.0189	0.148	6.069	0.0468	0.3152	-0.553	5.134	0.0078	0.0292	-0.702	5.838	0.0183	0.0240
SGO_0002 dnaN; DNA polymerase III, beta subunit	0.640	7.258	0.0146	0.0633	0.550	7.204	0.0242	0.0969	-0.140	6.846	0.0591	0.5301	-0.090	6.961	0.0299	0.1843	-0.780	6.060	0.0016	0.0035	-0.691	6.614	0.0067	0.0043
SGO_0004 putative lipoprotein	-1.661	8.780	0.0020	0.0050	-1.979	8.713	0.0019	0.0040	-2.017	8.695	0.0009	0.0028	-0.318	7.080	0.0514	0.3501	-0.356	6.431	0.0274	0.1457	-0.038	6.879	0.2009	0.7232
SGO_0005 hypothetical protein SGO_0005		4.640				4.640				4.640														
SGO_0006 ABC transporter, ATP-binding protein	0.158	7.655	0.0485	0.2750	0.462	7.817	0.0017	0.0033	0.100	7.626	0.0516	0.4541	0.304	7.378	0.0161	0.0882	-0.058	6.587	0.1084	0.7696	-0.362	7.354	0.0348	0.0653
SGO_0007 trpS; tryptophanyl-tRNA synthetase	-0.294	6.164	0.0417	0.2311	1.153	6.977	0.0003	0.0002	0.785	6.734	0.0005	0.0012	1.447	6.385	0.0006	0.0008	1.079	5.516	0.0015	0.0031	-0.368	6.754	0.0012	0.0001
SGO_0008 inosine-5'-monophosphate dehydrogenase	0.310	9.371	0.0149	0.0651	1.064	9.833	0.0005	0.0007	0.961	9.763	0.0004	0.0008	0.755	9.426	0.0009	0.0014	0.651	8.752	0.0013	0.0020	-0.103	9.703	0.0397	0.0811
SGO_0011 proteinase, M16 family	-0.863	5.257	0.0270	0.1369	-1.064	5.482	0.0036	0.0090	-0.825	5.581	0.0082	0.0486	-0.201	4.002	0.0922	0.6812	0.038	3.580	0.1191	0.8484	0.238	4.509	0.1464	0.4687
SGO_0012 mpp; peptidase, M16 family	1.455	4.510	0.0205	0.0948		1.807				1.807				3.756				3.145						
SGO_0013 hypothetical protein SGO_0013		4.813			-0.643	5.212	0.0434	0.1881		4.813				2.648								2.648		
SGO_0015 ABC transporter (ATP-binding protein)	-2.771	6.426	0.0058	0.0196	-2.256	6.598	0.0001	0.0000	-2.738	6.428	0.0039	0.0197	0.514	3.987	0.0097	0.0458	0.033	2.445			-0.482	3.996	0.0283	0.0484
SGO_0016 cbiO; ABC transporter, ATP-binding protein		3.787			-0.241	4.669	0.0423	0.1825		3.787				3.028								3.028		
SGO_0017 ABC-type putative cobalt transport system, permease		2.351				2.351				2.351														
SGO_0019 sdhA; L-serine dehydratase, iron-sulfur-dependent, alpha subunit		2.807				2.807				2.807														
SGO_0020 sdhB; L-serine dehydratase, iron-sulfur-dependent, beta subunit	-0.115	4.222	0.1386	0.9320		2.585				2.585				3.149				2.538						
SGO_0022 trmU; tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	3.662	7.860	0.0001	0.0000	1.241	5.854	0.0025	0.0057	0.104	5.176	0.0906	0.8591	-2.421	7.479	0.0000	0.0000	-3.558	6.740	0.0001	0.0000	-1.137	5.357	0.0037	0.0010



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1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

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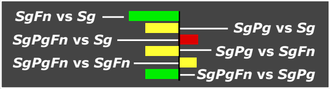

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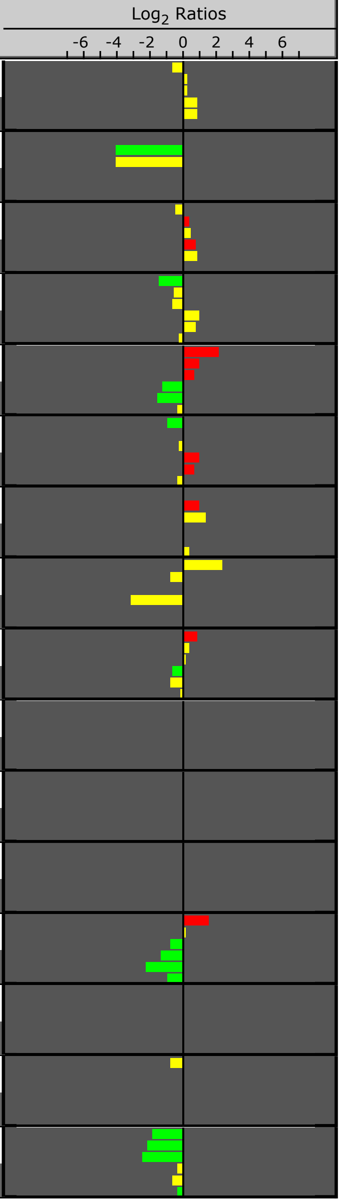
Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0025 gidA; glucose inhibited division protein A	-0.570	5.781	0.0268	0.1355	0.338	6.207	0.0477	0.2100	0.343	6.230	0.0332	0.2749	0.908	5.502	0.0157	0.0846	0.913	4.918	0.0230	0.1173	0.005	5.892	0.2382	0.9134
SGO_0026 DHH subfamily 1 protein		7.420			-3.976	7.514	0.0005	0.0007	-4.015	7.463	0.0109	0.0718		3.020				1.272			-0.039	3.561	0.2247	0.8413
SGO_0027 rplI; ribosomal protein L9	-0.380	6.937	0.0100	0.0393	0.376	7.312	0.0046	0.0126	0.520	7.410	0.0109	0.0722	0.756	6.646	0.0011	0.0021	0.900	6.144	0.0071	0.0259	0.144	7.060	0.1271	0.3931
SGO_0028 dnaC; replicative DNA helicase	-1.442	5.255	0.0034	0.0101	-0.451	5.614	0.0507	0.2268	-0.610	5.208	0.0357	0.2993	0.991	4.452	0.0119	0.0590	0.832	3.141	0.0235	0.1219	-0.159	4.394	0.1982	0.7084
SGO_0030 aspB; aspartate transaminase	2.151	7.906	0.0001	0.0000	0.967	7.027	0.0008	0.0011	0.689	6.851	0.0018	0.0069	-1.184	7.625	0.0001	0.0000	-1.462	6.935	0.0001	0.0000	-0.278	6.784	0.0184	0.0244
SGO_0032 plsX; fatty acid/phospholipid synthesis protein PlsX	-0.944	7.088	0.0028	0.0077	0.024	7.492	0.1697	0.8926	-0.245	7.365	0.0180	0.1364	0.968	6.584	0.0006	0.0007	0.699	5.805	0.0031	0.0086	-0.269	6.860	0.0188	0.0254
SGO_0033 acpP; acyl carrier protein		3.725			0.994	5.306	0.0039	0.0102	1.403	5.651	0.0085	0.0517		4.205				4.086			0.409	5.472	0.0935	0.2631
SGO_0035 phosphoribosylformylglycinamidine synthase	2.367	5.314	0.0174	0.0779	-0.709	2.496				1.807			-3.076	4.751	0.0137	0.0713		4.058				0.585		
SGO_0042 transcription regulator, GntR family	0.918	6.144	0.0003	0.0002	0.355	5.804	0.0083	0.0260	0.243	5.283	0.0113	0.0752	-0.563	5.766	0.0019	0.0045	-0.675	4.801	0.0136	0.0616	-0.112	5.007	0.1627	0.5485
SGO_0044 PTS system, IIB component																								
SGO_0050 hypothetical protein SGO_0050		4.640				4.640				4.640														
SGO_0051 hypothetical protein SGO_0051		3.351				3.351				3.351														
SGO_0054 dltA; D-alanine-activating enzyme	1.565	8.469	0.0001	0.0001	0.238	7.609	0.0136	0.0480	-0.677	7.186	0.0010	0.0031	-1.327	8.019	0.0002	0.0001	-2.242	7.201	0.0001	0.0000	-0.915	6.823	0.0031	0.0007
SGO_0055 dltB; integral membrane protein		2.058				2.058				2.058														
SGO_0056 dltC; D-alanyl carrier protein	-0.711	3.805	0.0112	0.0452		3.420				3.420				1.196				0.585						
SGO_0057 dltD protein	-1.818	8.223	0.0010	0.0018	-2.098	8.163	0.0008	0.0012	-2.415	8.108	0.0005	0.0010	-0.280	6.397	0.0215	0.1239	-0.596	5.653	0.0078	0.0291	-0.316	6.092	0.0050	0.0020



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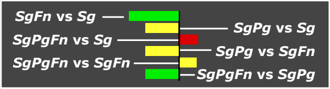

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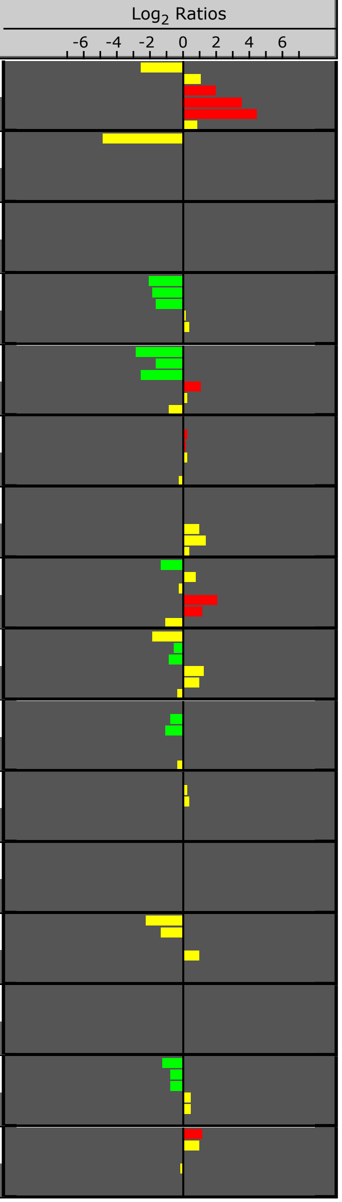
	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0059	-2.492	11.167	0.0067	0.0235	1.097	12.538	0.0073	0.0222	1.992	13.189	0.0006	0.0015	3.589	11.564	0.0007	0.0009	4.484	11.789	0.0004	0.0002	0.895	12.958	0.0058	0.0034
	pXO1; hypothetical protein SGO_0059																							
SGO_0060	-4.809	8.069	0.0112	0.0455		8.043				8.043				1.717				1.107						
	hypothetical protein SGO_0060																							
SGO_0062		1.379				1.380				1.380														
	hypothetical protein SGO_0062																							
SGO_0063	-1.969	7.830	0.0001	0.0000	-1.765	7.875	0.0002	0.0001	-1.618	7.907	0.0000	0.0000	0.204	6.135	0.0400	0.2615	0.350	5.597	0.0071	0.0258	0.146	6.304	0.1104	0.3266
	hypothetical protein SGO_0063																							
SGO_0064	-2.780	8.948	0.0001	0.0000	-1.647	9.154	0.0003	0.0002	-2.484	8.988	0.0001	0.0000	1.133	7.144	0.0027	0.0079	0.296	6.006	0.0101	0.0407	-0.837	7.241	0.0120	0.0121
	FtsK/SpoIIIE family protein																							
SGO_0065	0.041	7.328	0.0927	0.5936	0.339	7.484	0.0009	0.0013	0.159	7.386	0.0007	0.0020	0.298	6.991	0.0071	0.0294	0.118	6.285	0.0397	0.2305	-0.179	7.043	0.0094	0.0077
	hypothetical protein SGO_0065																							
SGO_0066		2.446				4.494				4.900			1.034	4.293	0.0278	0.1684	1.422	4.018	0.0352	0.2001	0.388	5.198	0.0661	0.1647
	D-3-phosphoglycerate dehydrogenase, putative																							
SGO_0067	-1.326	6.056	0.0003	0.0004	0.784	7.024	0.0059	0.0173	-0.170	6.487	0.0082	0.0489	2.110	6.156	0.0015	0.0035	1.156	4.815	0.0012	0.0019	-0.954	6.452	0.0122	0.0126
	protein with prophage function domain																							
SGO_0068	-1.848	6.075	0.0116	0.0478	-0.510	6.655	0.0016	0.0031	-0.815	6.537	0.0004	0.0009	1.338	5.123	0.0075	0.0324	1.033	4.262	0.0063	0.0223	-0.305	5.719	0.0051	0.0023
	lipoprotein, putative																							
SGO_0069		5.402			-0.728	6.084	0.0007	0.0009	-1.033	5.980	0.0006	0.0015		4.162				3.258			-0.305	5.023	0.0396	0.0796
	hypothetical protein SGO_0069																							
SGO_0070		5.452			0.264	6.588	0.0177	0.0667	0.351	6.637	0.0080	0.0470		5.199				4.678			0.087	6.244	0.1261	0.3884
	merozoite surface protein 1																							
SGO_0075		1.379				1.380				1.380														
	hypothetical protein SGO_0075																							
SGO_0078	-2.233	5.972	0.0356	0.1899	-1.267	6.328	0.0090	0.0292		5.830			0.966	4.360	0.0387	0.2518		1.429				4.038		
	hypothetical protein SGO_0078																							
SGO_0079		1.379				1.380				1.380														
	hypothetical protein SGO_0079																							
SGO_0080	-1.239	7.315	0.0013	0.0026	-0.712	7.484	0.0011	0.0018	-0.691	7.490	0.0004	0.0007	0.527	6.346	0.0125	0.0629	0.548	5.745	0.0105	0.0445	0.021	6.581	0.2181	0.8060
	hypothetical protein SGO_0080																							
SGO_0081	1.176	4.906	0.0041	0.0126	1.034	4.842	0.0181	0.0685		3.266			-0.142	4.788	0.0913	0.6734		3.224				3.740		
	hypothetical protein SGO_0081																							



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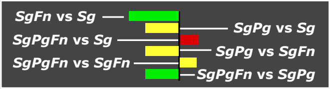

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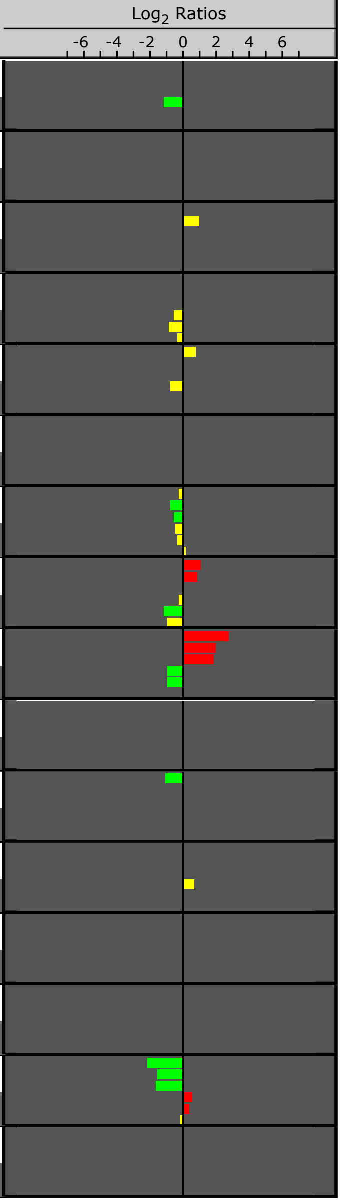
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0095 mccF; microcin immunity protein MccF, putative		6.401				5.271							-1.125	6.431	0.0009	0.0016		5.277				4.758		
SGO_0097 hypothetical protein SGO_0097		6.097				6.097				6.097														
SGO_0098 ribonucleotide reductase-like protein		4.012			0.979	6.324	0.0344	0.1448		4.012				5.487								5.487		
SGO_0099 pulA-2; pullulanase, type I		4.372				3.712				2.396			-0.483	4.566	0.0416	0.2746	-0.792	3.575	0.0732	0.4882	-0.310	3.686	0.0956	0.2721
SGO_0100 maltose operon transcription repressor	0.845	4.371	0.0570	0.3329	0.127	4.089	0.1827	0.9834		3.499			-0.717	3.403				2.107				2.000		
SGO_0101 malA; Maltodextrose utilization protein malA		4.874				4.874				4.874														
SGO_0104 Maltose/maltodextrin-binding protein precursor	-0.242	9.829	0.0207	0.0962	-0.689	9.636	0.0001	0.0000	-0.524	9.703	0.0008	0.0024	-0.447	8.985	0.0077	0.0334	-0.282	8.448	0.0219	0.1109	0.165	8.825	0.0450	0.0968
SGO_0105 malQ; 4-alpha-glucanotransferase	1.097	6.362	0.0042	0.0127	0.873	6.200	0.0011	0.0019	-0.043	5.689	0.0920	0.8746	-0.225	6.182	0.0330	0.2061	-1.140	5.228	0.0045	0.0140	-0.915	5.676	0.0067	0.0043
SGO_0106 glgP-2; maltodextrin phosphorylase	2.848	8.574	0.0005	0.0007	1.969	7.831	0.0002	0.0001	1.923	7.794	0.0001	0.0001	-0.879	8.496	0.0019	0.0044	-0.925	7.869	0.0018	0.0039	-0.046	7.963	0.0238	0.0370
SGO_0107 LPXTG cell wall surface protein, collagen binding domain										2.907								1.783				2.394		
SGO_0108 ruvB; Holliday junction DNA helicase RuvB	-1.035	6.092	0.0022	0.0058		5.505				5.505				3.998				3.387						
SGO_0110 phosphotyrosine protein phosphatase		2.231				2.898							0.668	3.090				1.107				2.385		
SGO_0111 MORN motif family protein		4.115				4.115				4.115														
SGO_0112 putative acyltransferase		5.366				5.366				5.366														
SGO_0113 acdH; alcohol-acetaldehyde dehydrogenase	-2.089	13.012	0.0001	0.0000	-1.505	13.143	0.0002	0.0001	-1.648	13.107	0.0001	0.0001	0.584	11.427	0.0014	0.0031	0.441	10.731	0.0011	0.0015	-0.143	11.620	0.0405	0.0836
SGO_0128 hypothetical protein SGO_0128		3.170				3.170				3.170														



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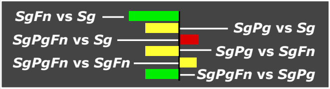

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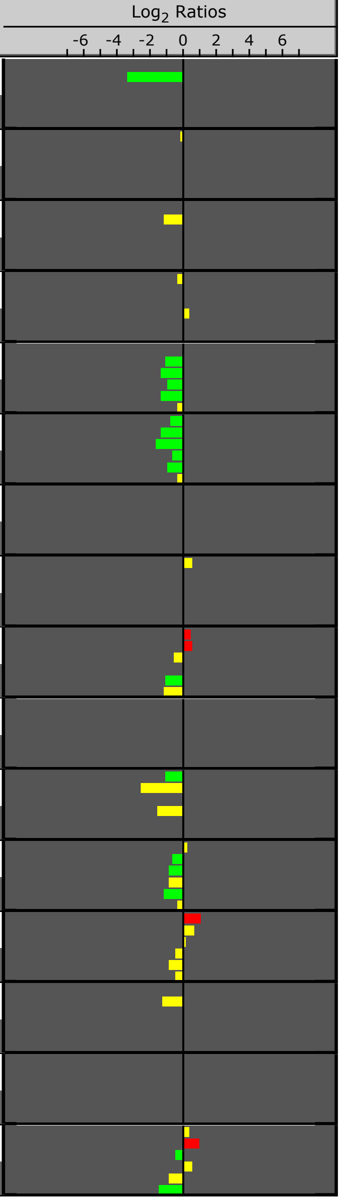
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0129 atpI; v-type sodium ATP synthase, chain I		6.741			-3.290	6.881	0.0002	0.0001		6.741				2.937								2.937		
SGO_0131 v-type sodium ATP synthase, chain E	-0.135	6.282	0.0858	0.5442		5.425				5.425				4.611				4.000						
SGO_0132 ATP synthase (C/AC39) subunit		3.524			-1.088	4.528	0.0494	0.2205		3.524				3.020								3.020		
SGO_0134 acetyltransferase, GNAT family	-0.328	4.635	0.0580	0.3390	0.106	5.225	0.1182	0.5924		4.154			0.434	4.222	0.0641	0.4482		1.692				3.779		
SGO_0135 v-type sodium ATP synthase, subunit A	-0.017	8.321	0.1433	0.9713	-0.954	7.926	0.0003	0.0003	-1.286	7.825	0.0004	0.0008	-0.937	7.410	0.0031	0.0095	-1.269	6.698	0.0026	0.0068	-0.332	6.712	0.0532	0.1238
SGO_0136 v-type sodium ATP synthase, chain B	-0.696	8.587	0.0016	0.0037	-1.309	8.383	0.0007	0.0010	-1.600	8.309	0.0005	0.0011	-0.613	7.410	0.0019	0.0047	-0.904	6.696	0.0022	0.0052	-0.291	6.942	0.0664	0.1660
SGO_0137 V-type ATPase, D subunit		3.653				3.653				3.653														
SGO_0138 LysM domain protein	0.579	3.778				2.459				2.459				2.525				1.914						
SGO_0139 thrC; threonine synthase	0.506	7.391	0.0013	0.0027	0.581	7.434	0.0007	0.0010	-0.511	6.896	0.0090	0.0555	0.074	7.146	0.0368	0.2375	-1.017	6.088	0.0023	0.0056	-1.092	6.748	0.0063	0.0038
SGO_0142 hypothetical protein SGO_0142		1.585				1.585				1.585														
SGO_0144 hypothetical protein SGO_0144	-1.032	5.671	0.0020	0.0050	-2.511	5.213	0.0174	0.0651		5.092			-1.478	3.796	0.0265	0.1585		2.951				1.063		
SGO_0145 polI; DNA polymerase I	0.275	8.112	0.0341	0.1807	-0.566	7.699	0.0007	0.0009	-0.848	7.593	0.0004	0.0009	-0.841	7.372	0.0061	0.0248	-1.124	6.669	0.0048	0.0153	-0.282	6.743	0.0224	0.0329
SGO_0146 CoA-binding domain protein	1.056	6.377	0.0048	0.0152	0.659	6.116	0.0087	0.0278	0.244	5.991	0.0505	0.4436	-0.397	6.110	0.0195	0.1112	-0.812	5.412	0.0355	0.2024	-0.416	5.791	0.1828	0.6415
SGO_0148 hypothetical protein SGO_0148		4.387			-1.225	4.667	0.0139	0.0492		4.387				1.648								1.648		
SGO_0150 fucA1; alpha-L-fucosidase		1.379				1.380				1.380														
SGO_0152 tgt; queuine tRNA-ribosyltransferase	0.387	5.773	0.0519	0.2961	1.009	6.079	0.0003	0.0003	-0.431	5.291	0.0027	0.0119	0.622	5.762	0.0322	0.1998	-0.818	4.490	0.0268	0.1420	-1.441	5.438	0.0019	0.0003



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ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

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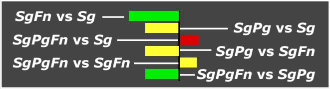

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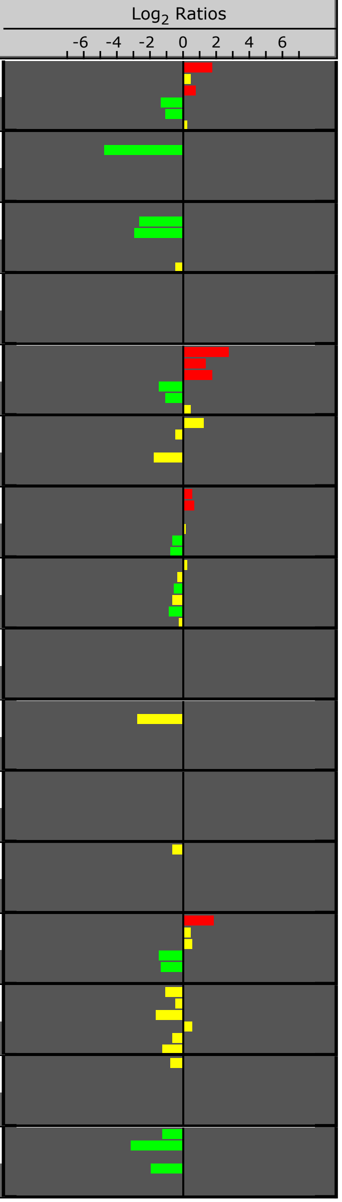
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory **UW**

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0154	1.787	11.314	0.0007	0.0010	0.517	10.445	0.0109	0.0367	0.826	10.628	0.0007	0.0018	-1.270	10.934	0.0011	0.0022	-0.961	10.418	0.0014	0.0025	0.309	10.324	0.0256	0.0417
	pgi; glucose-6-phosphate isomerase																							
SGO_0155		8.348			-4.703	8.402	0.0009	0.0014		8.348				3.118								3.118		
	hypothetical protein SGO_0155																							
SGO_0156		7.444			-2.580	7.668	0.0004	0.0004	-2.949	7.620	0.0003	0.0003		4.357				3.370			-0.369	5.181	0.0319	0.0567
	hypothetical protein SGO_0156																							
SGO_0157		3.357				3.357				3.357														
	hypothetical protein SGO_0157																							
SGO_0158	2.802	8.548	0.0003	0.0002	1.379	7.403	0.0009	0.0014	1.833	7.756	0.0014	0.0050	-1.423	8.300	0.0006	0.0007	-0.969	7.832	0.0020	0.0047	0.454	7.674	0.0376	0.0735
	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase, putative																							
SGO_0159	1.294	3.787			-0.424	2.804				2.000			-1.718	3.164				2.170				1.063		
	hippurate hydrolase																							
SGO_0163	0.563	7.521	0.0030	0.0085	0.746	7.631	0.0010	0.0016	0.009	7.216	0.1026	0.9909	0.182	7.353	0.0069	0.0286	-0.555	6.398	0.0013	0.0022	-0.737	7.118	0.0007	0.0000
	galU; UTP-glucose-1-phosphate uridylyltransferase																							
SGO_0164	0.296	7.639	0.0213	0.0992	-0.280	7.349	0.0252	0.1009	-0.524	7.239	0.0018	0.0071	-0.577	7.010	0.0080	0.0354	-0.821	6.303	0.0038	0.0111	-0.244	6.572	0.0594	0.1433
	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)																							
SGO_0165		4.275				4.275				4.275														
	ABC transporter, permease/ATP-binding protein SP2075																							
SGO_0166		6.237			-2.723	6.342	0.0082	0.0256		6.237				2.000								2.000		
	ABC transporter, permease/ATP-binding protein SP2073																							
SGO_0167		4.020				4.020				4.020														
	glutamine amidotransferase																							
SGO_0168	-0.600	4.566	0.0250	0.1212		4.156				4.156				2.039				1.429						
	hydrolase, NUDIX family																							
SGO_0169	1.929	6.595	0.0023	0.0059	0.502	5.611	0.0352	0.1490	0.646	5.680	0.0064	0.0364	-1.427	6.200	0.0032	0.0101	-1.283	5.622	0.0033	0.0094	0.144	5.383	0.1609	0.5407
	dut; dUTP diphosphatase																							
SGO_0171	-0.989	5.628	0.0409	0.2246	-0.402	6.118	0.0338	0.1424	-1.565	5.530	0.0219	0.1728	0.587	4.795	0.0400	0.2623	-0.576	2.911			-1.163	4.672	0.0664	0.1664
	radA; DNA repair protein RadA																							
SGO_0172	-0.682	6.005	0.0089	0.0337		5.614				5.614				3.418				2.807						
	conserved hypothetical protein TIGR00266																							
SGO_0173	-1.237	7.924	0.0003	0.0002	-3.121	7.570	0.0001	0.0000		7.412			-1.884	6.016	0.0008	0.0013		5.058				3.790		
	Carbonic anhydrase																							



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ABC Transporter

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1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

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🟩	yes	–	ratios, bars
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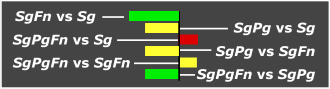
▨	yes	–	



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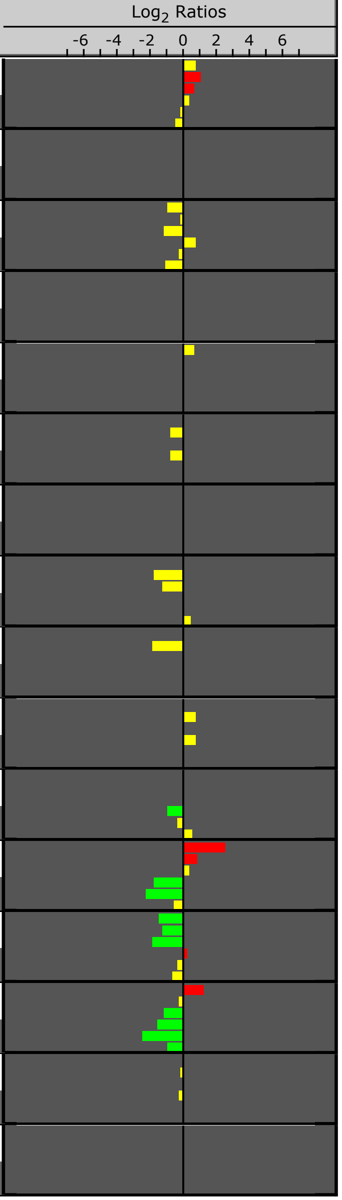
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0174 gltX; glutamyl-tRNA synthetase	0.758	8.458	0.0073	0.0266	1.114	8.678	0.0001	0.0000	0.684	8.400	0.0008	0.0023	0.356	8.459	0.0157	0.0841	-0.073	7.627	0.0875	0.6035	-0.429	8.419	0.0055	0.0029
SGO_0179 Membrane protein oxaA 1 precursor		2.585				2.585				2.585														
SGO_0180 jag; hypothetical protein SGO_0180	-0.946	6.660	0.0122	0.0506	-0.132	7.007	0.1414	0.7291	-1.123	6.647	0.0120	0.0809	0.815	6.068	0.0151	0.0803	-0.177	4.949	0.1287	0.9284	-0.991	6.054	0.0521	0.1201
SGO_0181 lipoprotein, putative		5.217				5.217				5.217														
SGO_0182 sapR; sakacin A production response regulator	0.723	4.937	0.0798	0.4978		2.700				2.700				4.080				3.469						
SGO_0188 hydrolase, TatD family	-0.017	5.264	0.1383	0.9279	-0.745	4.646	0.0473	0.2076		4.272			-0.729	4.120	0.0340	0.2137		3.132				2.000		
SGO_0189 primase-related protein		1.585				1.585				1.585														
SGO_0190 hypothetical protein SGO_0190		5.130			-1.685	5.563	0.0110	0.0370	-1.173	5.410	0.0326	0.2689		3.103				1.783			0.512	3.791	0.2040	0.7382
SGO_0191 hypothetical protein SGO_0191		4.351			-1.774	4.548	0.0060	0.0179		4.351				1.063								1.063		
SGO_0193 ksgA; dimethyladenosine transferase	0.004	4.805	0.1428	0.9653	0.844	5.139	0.0514	0.2304		3.820			0.840	4.614	0.0309	0.1910		2.666				3.887		
SGO_0197 predicted ribosome small subunit-dependent GTPase A		4.429				3.541				3.170			-0.890	4.539	0.0020	0.0048	-0.253	3.809	0.0515	0.3175	0.637	3.854	0.0520	0.1190
SGO_0198 rpe; ribulose-phosphate 3-epimerase	2.600	8.472	0.0001	0.0001	0.896	7.170	0.0011	0.0017	0.364	6.853	0.0122	0.0827	-1.704	8.123	0.0002	0.0001	-2.236	7.405	0.0002	0.0001	-0.532	6.794	0.0089	0.0068
SGO_0200 competence-induced protein Ccs50	-1.421	7.784	0.0001	0.0001	-1.166	7.858	0.0002	0.0001	-1.758	7.706	0.0003	0.0003	0.255	6.525	0.0010	0.0018	-0.337	5.633	0.0212	0.1059	-0.591	6.391	0.0165	0.0202
SGO_0201 cmp-binding-factor 1	1.296	8.289	0.0028	0.0079	-0.173	7.404	0.0277	0.1122	-1.090	7.048	0.0011	0.0034	-1.470	7.726	0.0022	0.0060	-2.387	6.927	0.0016	0.0032	-0.917	6.416	0.0048	0.0017
SGO_0202 pur operon repressor	0.149	5.698	0.0870	0.5536	-0.101	5.559	0.1063	0.5282		4.619			-0.250	5.128	0.0384	0.2496		3.648				3.983		
SGO_0203 hypothetical protein SGO_0203		2.700				2.700				2.700														



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1179

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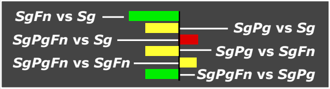

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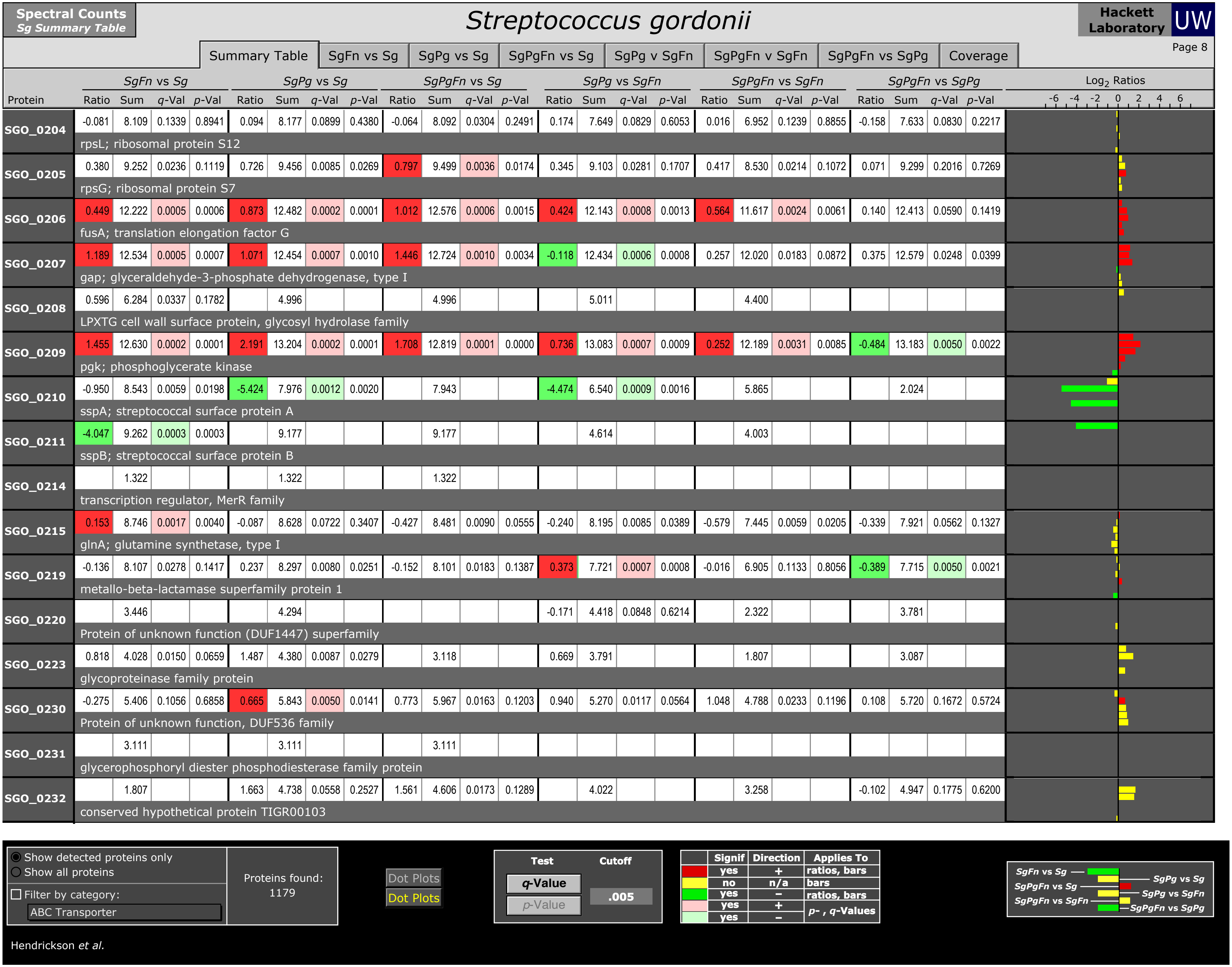

Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0204	-0.081	8.109	0.1339	0.8941	0.094	8.177	0.0899	0.4380	-0.064	8.092	0.0304	0.2491	0.174	7.649	0.0829	0.6053	0.016	6.952	0.1239	0.8855	-0.158	7.633	0.0830	0.2217
	rpsL; ribosomal protein S12																							
SGO_0205	0.380	9.252	0.0236	0.1119	0.726	9.456	0.0085	0.0269	0.797	9.499	0.0036	0.0174	0.345	9.103	0.0281	0.1707	0.417	8.530	0.0214	0.1072	0.071	9.299	0.2016	0.7269
	rpsG; ribosomal protein S7																							
SGO_0206	0.449	12.222	0.0005	0.0006	0.873	12.482	0.0002	0.0001	1.012	12.576	0.0006	0.0015	0.424	12.143	0.0008	0.0013	0.564	11.617	0.0024	0.0061	0.140	12.413	0.0590	0.1419
	fusA; translation elongation factor G																							
SGO_0207	1.189	12.534	0.0005	0.0007	1.071	12.454	0.0007	0.0010	1.446	12.724	0.0010	0.0034	-0.118	12.434	0.0006	0.0008	0.257	12.020	0.0183	0.0872	0.375	12.579	0.0248	0.0399
	gap; glyceraldehyde-3-phosphate dehydrogenase, type I																							
SGO_0208	0.596	6.284	0.0337	0.1782		4.996				4.996				5.011				4.400						
	LPXTG cell wall surface protein, glycosyl hydrolase family																							
SGO_0209	1.455	12.630	0.0002	0.0001	2.191	13.204	0.0002	0.0001	1.708	12.819	0.0001	0.0000	0.736	13.083	0.0007	0.0009	0.252	12.189	0.0031	0.0085	-0.484	13.183	0.0050	0.0022
	pgk; phosphoglycerate kinase																							
SGO_0210	-0.950	8.543	0.0059	0.0198	-5.424	7.976	0.0012	0.0020		7.943			-4.474	6.540	0.0009	0.0016		5.865				2.024		
	sspA; streptococcal surface protein A																							
SGO_0211	-4.047	9.262	0.0003	0.0003		9.177				9.177				4.614				4.003						
	sspB; streptococcal surface protein B																							
SGO_0214		1.322				1.322				1.322														
	transcription regulator, MerR family																							
SGO_0215	0.153	8.746	0.0017	0.0040	-0.087	8.628	0.0722	0.3407	-0.427	8.481	0.0090	0.0555	-0.240	8.195	0.0085	0.0389	-0.579	7.445	0.0059	0.0205	-0.339	7.921	0.0562	0.1327
	glnA; glutamine synthetase, type I																							
SGO_0219	-0.136	8.107	0.0278	0.1417	0.237	8.297	0.0080	0.0251	-0.152	8.101	0.0183	0.1387	0.373	7.721	0.0007	0.0008	-0.016	6.905	0.1133	0.8056	-0.389	7.715	0.0050	0.0021
	metallo-beta-lactamase superfamily protein 1																							
SGO_0220		3.446				4.294							-0.171	4.418	0.0848	0.6214		2.322				3.781		
	Protein of unknown function (DUF1447) superfamily																							
SGO_0223	0.818	4.028	0.0150	0.0659	1.487	4.380	0.0087	0.0279		3.118			0.669	3.791				1.807				3.087		
	glycoproteinase family protein																							
SGO_0230	-0.275	5.406	0.1056	0.6858	0.665	5.843	0.0050	0.0141	0.773	5.967	0.0163	0.1203	0.940	5.270	0.0117	0.0564	1.048	4.788	0.0233	0.1196	0.108	5.720	0.1672	0.5724
	Protein of unknown function, DUF536 family																							
SGO_0231		3.111				3.111				3.111														
	glycerophosphoryl diester phosphodiesterase family protein																							
SGO_0232		1.807			1.663	4.738	0.0558	0.2527	1.561	4.606	0.0173	0.1289		4.022				3.258			-0.102	4.947	0.1775	0.6200
	conserved hypothetical protein TIGR00103																							

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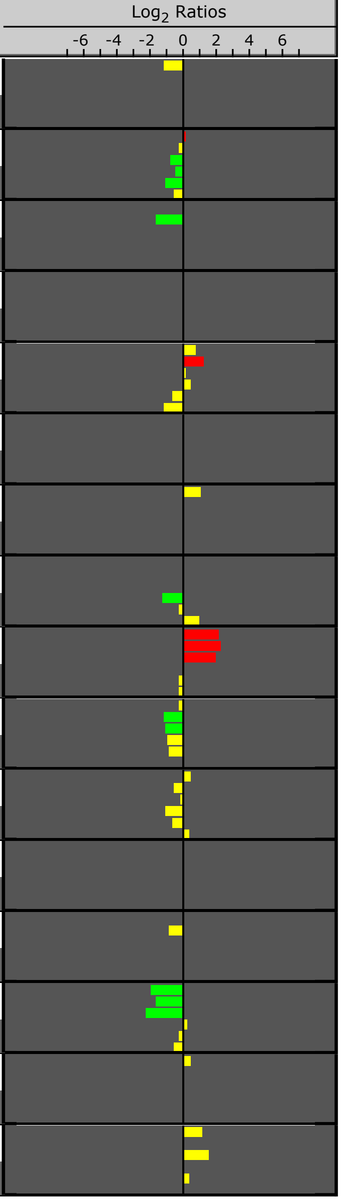
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

		SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0233	lipoprotein, putative	-1.071	6.570	0.0111	0.0442		5.976				5.976				4.491				3.881						
SGO_0234	pepX; X-Pro dipeptidyl-peptidase	0.223	7.887	0.0036	0.0108	-0.219	7.669	0.0216	0.0849	-0.741	7.449	0.0004	0.0009	-0.442	7.280	0.0043	0.0153	-0.964	6.469	0.0008	0.0008	-0.522	6.807	0.0178	0.0227
SGO_0235	glycerol uptake facilitator protein-like protein		6.742			-1.563	7.157	0.0048	0.0133		6.742				4.642								4.642		
SGO_0236	hypothetical protein SGO_0236		4.509				4.509				4.509														
SGO_0237	ccpA; CcpA protein (proteinase)	0.811	5.501	0.0302	0.1571	1.319	5.790	0.0038	0.0097	0.200	5.141	0.0774	0.7214	0.508	5.557	0.0255	0.1510	-0.611	4.436	0.0348	0.1970	-1.119	5.325	0.0099	0.0084
SGO_0240	mvaD; diphosphomevalonate decarboxylase		2.836				2.836				2.836														
SGO_0242	FMN-dependent dehydrogenase family protein	1.066	2.687				1.058				1.058				1.611				1.000						
SGO_0243	hydroxymethylglutaryl-CoA reductase, degradative		4.989				3.791				3.755			-1.190	4.998	0.0013	0.0029	-0.226	4.377	0.0612	0.3979	0.965	4.260	0.0166	0.0206
SGO_0244	hydroxymethylglutaryl-CoA synthase	2.219	5.446	0.0014	0.0029	2.252	5.461	0.0003	0.0002	2.049	4.551	0.0023	0.0095	0.032	5.664	0.1189	0.9011	-0.170	4.570	0.0834	0.5695	-0.203	5.193	0.0935	0.2633
SGO_0247	pfl; formate acetyltransferase	-0.232	11.349	0.0506	0.2878	-1.086	11.004	0.0005	0.0006	-0.986	11.037	0.0004	0.0007	-0.854	10.354	0.0067	0.0274	-0.755	9.779	0.0088	0.0343	0.100	9.898	0.0316	0.0559
SGO_0252	possible TetR-type transcriptional regulator	0.478	5.107	0.0169	0.0754	-0.542	4.617	0.0297	0.1218	-0.114	4.382	0.0432	0.3739	-1.020	4.417	0.0086	0.0395	-0.593	3.619	0.0510	0.3132	0.427	3.562	0.1586	0.5274
SGO_0253	hypothetical protein SGO_0253		5.655				5.655				5.655														
SGO_0254	helicase, RecD/TraA family		4.018			-0.810	4.643	0.0299	0.1228		4.018				2.622								2.622		
SGO_0255	Signal peptidase I	-1.915	7.565	0.0021	0.0053	-1.618	7.630	0.0027	0.0065	-2.151	7.519	0.0013	0.0045	0.297	5.938	0.0082	0.0371	-0.236	5.062	0.0282	0.1521	-0.533	5.836	0.0073	0.0051
SGO_0256	rnhC; ribonuclease HIII	0.549	4.962	0.0603	0.3566		4.191				4.191				3.177				2.566						
SGO_0258	hypothetical protein SGO_0258	1.231	3.328				1.585			1.585	3.585				2.302			0.355	2.880				2.657		



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Test	Cutoff
q-Value	.005
p-Value	

	Signif	Direction	Applies To
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🟨	no	n/a	bars
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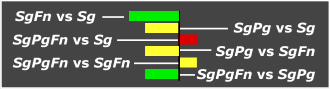

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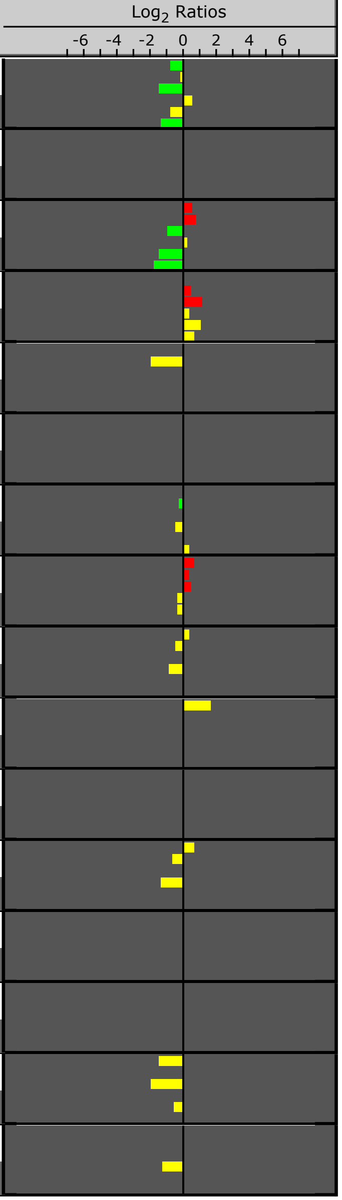
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0260 DNA mismatch binding protein MutS2	-0.703	6.887	0.0044	0.0135	-0.106	7.135	0.0376	0.1609	-1.380	6.661	0.0004	0.0008	0.597	6.310	0.0062	0.0249	-0.677	5.083	0.0123	0.0543	-1.274	6.073	0.0045	0.0014
SGO_0261 acetyltransferase, GNAT family		1.585				1.585				1.585														
SGO_0262 dipeptidase	0.568	6.914	0.0032	0.0094	0.829	7.073	0.0008	0.0012	-0.877	6.228	0.0006	0.0017	0.261	6.793	0.0115	0.0553	-1.445	5.499	0.0010	0.0014	-1.706	6.302	0.0019	0.0003
SGO_0263 trx-1; thioredoxin	0.095	7.290	0.0900	0.5751	0.527	7.504	0.0012	0.0020	1.216	7.973	0.0040	0.0199	0.431	7.051	0.0237	0.1383	1.121	6.893	0.0087	0.0340	0.690	7.637	0.0306	0.0536
SGO_0268 mechanosensitive transport protein		5.055			-1.945	5.229	0.0268	0.1082		5.055				1.585								1.585		
SGO_0269 hypothetical protein SGO_0269		4.194				4.194				4.194														
SGO_0272 hypothetical protein SGO_0272	0.119	6.592	0.0674	0.4081	-0.248	6.402	0.0007	0.0009	0.120	6.586	0.0310	0.2548	-0.367	5.966	0.0163	0.0892	0.001	5.530	0.1304	0.9477	0.368	5.959	0.0212	0.0303
SGO_0276 gdhA; glutamate dehydrogenase (NADP)	0.718	9.428	0.0029	0.0083	0.383	9.225	0.0017	0.0034	0.460	9.271	0.0031	0.0143	-0.334	9.070	0.0083	0.0379	-0.258	8.496	0.0206	0.1025	0.077	8.931	0.1104	0.3263
SGO_0277 pyrA; Dihydroorotate dehydrogenase	0.354	6.057	0.0447	0.2509	-0.412	5.671	0.0422	0.1820		4.856			-0.766	5.384	0.0153	0.0815		4.110				3.945		
SGO_0278 msrA; Peptide methionine sulfoxide reductase msrA/msrB	1.709	3.094				1.000				1.000				2.196				1.585						
SGO_0279 lipoprotein, putative		3.902				3.902				3.902														
SGO_0280 trzA; ethylammeline chlorohydrolase	0.678	7.016	0.0256	0.1260	-0.591	6.340	0.0170	0.0629		5.584			-1.269	6.326	0.0124	0.0620		5.224				4.531		
SGO_0282 cell wall polysaccharide biosynthesis protein		5.347				5.347				5.347														
SGO_0284 transcriptional regulator		1.058				1.058				1.058														
SGO_0286 DNA mismatch repair protein MutS, putative	-1.447	5.729	0.0117	0.0484		5.487			-1.900	5.668	0.0073	0.0419		2.525			-0.453	2.705				2.072		
SGO_0288 GDSL-like lipase/acylhydrolase		3.231				3.007							-1.232	3.610	0.0111	0.0536		2.107				2.494		



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p-Value	

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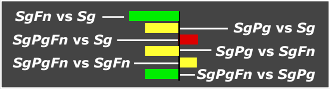

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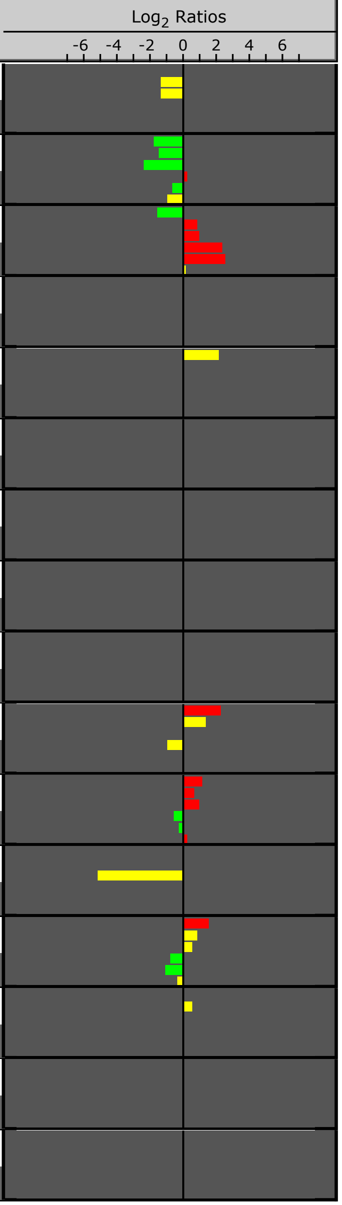
Streptococcus gordonii

Protein	Description	*SgFn vs Sg* Ratio	Sum	*q*-Val	*p*-Val	*SgPg vs Sg* Ratio	Sum	*q*-Val	*p*-Val	*SgPgFn vs Sg* Ratio	Sum	*q*-Val	*p*-Val	*SgPg vs SgFn* Ratio	Sum	*q*-Val	*p*-Val	*SgPgFn vs SgFn* Ratio	Sum	*q*-Val	*p*-Val	*SgPgFn vs SgPg* Ratio	Sum	*q*-Val	*p*-Val
SGO_0290	copper -translocating P-type ATPase		5.411			-1.343	5.871	0.0144	0.0519	-1.342	5.657	0.0373	0.3152		3.486				1.857			0.001	4.065	0.2458	0.9518
SGO_0291	copper-translocating P-type ATPase	-1.699	7.622	0.0005	0.0008	-1.402	7.697	0.0008	0.0011	-2.286	7.507	0.0004	0.0006	0.297	6.175	0.0019	0.0045	-0.587	5.151	0.0046	0.0146	-0.884	5.946	0.0057	0.0032
SGO_0292	spxB; pyruvate oxidase	-1.515	8.103	0.0001	0.0000	0.881	9.177	0.0004	0.0005	1.040	9.282	0.0003	0.0005	2.395	8.289	0.0002	0.0001	2.555	7.814	0.0003	0.0001	0.159	9.120	0.0391	0.0774
SGO_0294	ABC transporter, putative		4.271				4.271				4.271														
SGO_0297	6-phospho-beta-glucosidase	2.180	5.828	0.0348	0.1852		2.459				2.459				5.168				4.557						
SGO_0299	putative histidine kinase		0.585				0.585				0.585														
SGO_0301	ABC transporter ATP-binding protein-like protein										1.981								0.857				1.468		
SGO_0306	ABC transporter ATP-binding protein-like protein		3.886				3.886				3.886														
SGO_0307	pabB; chorismate binding enzyme		2.718				2.718				2.718														
SGO_0310	metE; 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	2.302	4.772	0.0011	0.0022	1.387	3.401	0.0144	0.0522		2.202			-0.916	4.329	0.0290	0.1782		3.382				2.063		
SGO_0312	xfp; D-xylulose 5-phosphate/D-fructose 6-phosphate phosphoketolase	1.214	11.377	0.0002	0.0002	0.735	11.059	0.0001	0.0000	0.992	11.225	0.0001	0.0000	-0.479	11.127	0.0008	0.0013	-0.222	10.630	0.0039	0.0115	0.258	11.002	0.0042	0.0012
SGO_0317	LPXTG cell wall surface protein, serine protease, subtilase family		8.639				8.639			-5.050	8.661	0.0082	0.0481						1.461				2.072		
SGO_0321	polypeptide deformylase	1.577	7.033	0.0012	0.0024	0.887	6.560	0.0098	0.0322	0.594	6.384	0.0162	0.1194	-0.690	6.785	0.0021	0.0052	-0.983	6.071	0.0015	0.0030	-0.292	6.267	0.0650	0.1584
SGO_0323	pseudouridine synthase rRNA-specific		1.000			0.576	2.317				1.000				1.063								1.063		
SGO_0324	hypothetical protein SGO_0324		5.618				5.618				5.618														
SGO_0325	probable membrane protein, putative		3.058				3.058				3.058														



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***q*-Value**	**.005**
p-Value	

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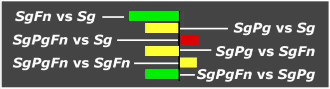

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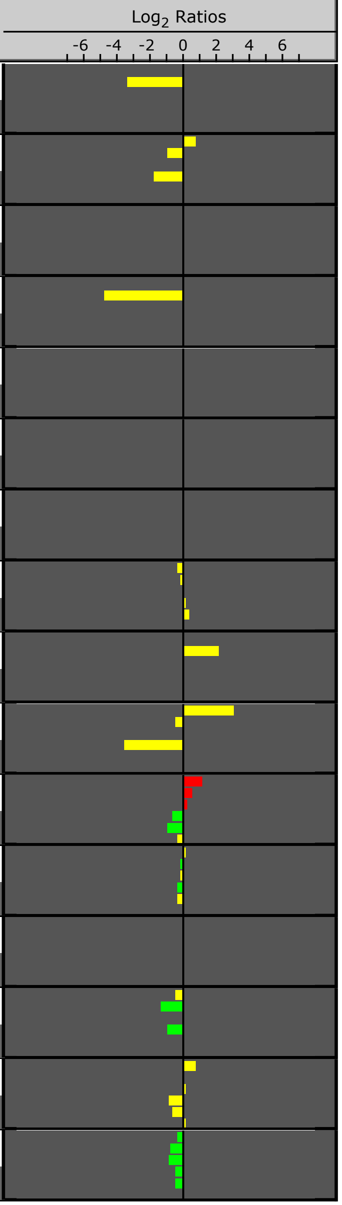
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0326 probable membrane protein, putative		6.681			-3.296	6.752	0.0097	0.0317		6.681				1.871								1.871		
SGO_0327 Lipopolysaccharide N-acetylglucosaminyltransferase	0.798	3.924	0.0200	0.0913	-0.856	3.376	0.0346	0.1462		3.025			-1.654	2.700				1.692				0.648		
SGO_0328 transmembrane protein, putative		4.383				4.383				4.383														
SGO_0329 hypothetical protein SGO_0329		6.839			-4.732	6.866	0.0187	0.0718		6.839				0.585								0.585		
SGO_0330 hypothetical protein SGO_0330		5.031				5.031				5.031														
SGO_0331 hypothetical protein SGO_0331		5.455				5.455				5.455														
SGO_0332 hypothetical protein SGO_0332		5.722				5.722				5.722														
SGO_0333 rpsO; ribosomal protein S15	-0.323	8.323	0.0334	0.1757	-0.089	8.419	0.0644	0.2989	0.039	8.488	0.0801	0.7503	0.234	7.759	0.0419	0.2768	0.362	7.225	0.0310	0.1718	0.128	7.930	0.1089	0.3178
SGO_0337 trx-2; thioredoxin		1.000			2.161	3.452				1.000				2.648								2.648		
SGO_0339 hypothetical protein SGO_0339	3.050	5.724	0.0138	0.0594	-0.424	2.389				1.585			-3.474	5.190	0.0118	0.0574		4.516				0.648		
SGO_0342 pepF-2; oligoendopeptidase	1.201	8.387	0.0004	0.0004	0.572	7.982	0.0036	0.0093	0.291	7.819	0.0031	0.0143	-0.629	8.075	0.0021	0.0050	-0.909	7.359	0.0009	0.0010	-0.280	7.594	0.0330	0.0606
SGO_0344 pnpA; polyribonucleotide nucleotidyltransferase	0.219	9.215	0.0124	0.0516	-0.124	9.039	0.0049	0.0139	-0.094	9.053	0.0059	0.0326	-0.343	8.646	0.0046	0.0170	-0.313	8.048	0.0061	0.0214	0.030	8.477	0.0735	0.1898
SGO_0345 cysE; serine O-acetyltransferase		3.663				3.663				3.663														
SGO_0348 reductase	-0.407	4.511			-1.348	4.537	0.0036	0.0090		3.700			-0.942	3.810	0.0043	0.0151		2.170				2.839		
SGO_0349 cysS; cysteinyl-tRNA synthetase	0.798	7.081	0.0084	0.0315	0.002	6.611	0.1832	0.9875	0.188	6.710	0.0171	0.1270	-0.796	6.568	0.0072	0.0301	-0.611	6.029	0.0125	0.0552	0.186	6.196	0.0419	0.0871
SGO_0352 ABC transporter, ATP-binding protein SP1580	-0.349	7.992	0.0015	0.0032	-0.745	7.834	0.0012	0.0022	-0.788	7.816	0.0003	0.0003	-0.396	7.112	0.0042	0.0144	-0.438	6.480	0.0007	0.0007	-0.043	6.880	0.1733	0.6020



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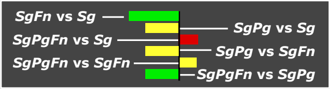

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Spectral Counts
Sg Summary Table

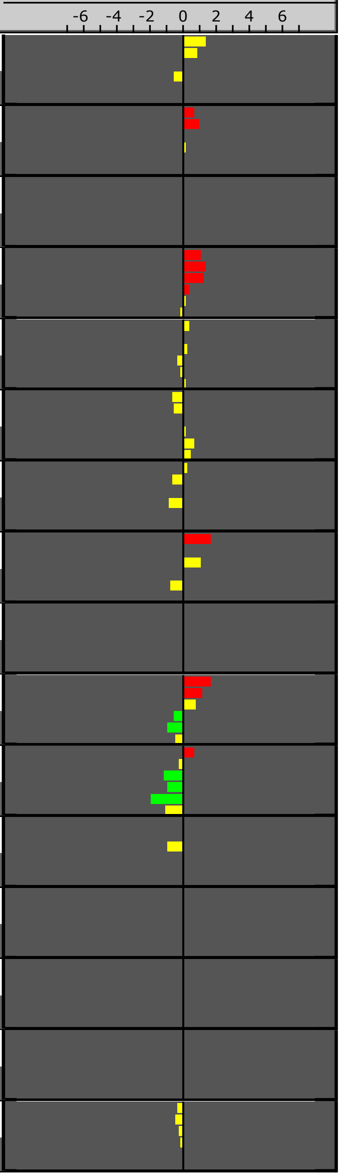
Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0353	1.406	4.544	0.0136	0.0580	0.905	4.160	0.0171	0.0639		2.619			-0.501	4.341	0.0414	0.2728		2.979				3.040		
	transport protein																							
SGO_0355	0.730	5.564	0.0047	0.0149	0.966	5.720	0.0046	0.0127		4.154			0.236	5.496	0.0349	0.2222		3.759				4.612		
	RNA methyltransferase, TrmH family, group 3																							
SGO_0356		1.379				1.380				1.380														
	hypothetical protein SGO_0356																							
SGO_0357	1.098	7.238	0.0022	0.0058	1.449	7.485	0.0013	0.0025	1.313	7.388	0.0012	0.0041	0.351	7.343	0.0025	0.0070	0.214	6.658	0.0091	0.0360	-0.137	7.442	0.0627	0.1523
	degV; DegV family fatty acid binding protein																							
SGO_0358	0.443	9.550	0.0112	0.0451	0.122	9.371	0.0784	0.3765	0.343	9.490	0.0083	0.0498	-0.321	9.085	0.0082	0.0369	-0.100	8.576	0.0520	0.3226	0.221	9.027	0.0116	0.0115
	rplM; ribosomal protein L13																							
SGO_0359	-0.649	8.262	0.0156	0.0689	-0.466	8.319	0.0137	0.0485	0.022	8.546	0.0981	0.9422	0.184	7.477	0.0730	0.5246	0.671	7.145	0.0101	0.0418	0.488	7.813	0.0120	0.0122
	rpsI; ribosomal protein S9																							
SGO_0361	0.296	4.951	0.0570	0.3323	-0.553	4.546	0.0329	0.1384		3.789			-0.849	4.222	0.0132	0.0679		2.972				2.740		
	immunity repressor protein																							
SGO_0368	1.733	4.471	0.0048	0.0150		2.345			1.075	3.371	0.0148	0.1064		3.583			-0.659	3.359	0.0554	0.3497		1.883		
	merA; mercury(II) reductase																							
SGO_0371		2.000				2.000				2.000														
	putative transcriptional regulator																							
SGO_0372	1.711	6.450	0.0017	0.0040	1.166	6.049	0.0026	0.0062	0.792	5.806	0.0059	0.0319	-0.545	6.289	0.0048	0.0177	-0.919	5.539	0.0025	0.0064	-0.374	5.811	0.0055	0.0029
	malate oxidoreductase																							
SGO_0374	0.739	6.858	0.0028	0.0079	-0.169	6.358	0.0363	0.1547	-1.123	6.002	0.0022	0.0094	-0.908	6.283	0.0019	0.0047	-1.862	5.419	0.0013	0.0022	-0.954	5.376	0.0145	0.0161
	Response regulator of the LytR/AlgR family																							
SGO_0376		3.322				3.322			-0.926	3.932								1.272				1.883		
	ABC transporter ATP-binding protein																							
SGO_0378		4.294												3.781				3.170						
	hypothetical protein SGO_0378																							
SGO_0379		4.594				4.594				4.594														
	Protein of unknown function (DUF421) family																							
SGO_0380		3.459				3.459				3.459														
	hypothetical protein SGO_0380																							
SGO_0384	-0.291	5.820	0.0649	0.3905	-0.385	5.773	0.0578	0.2637	-0.243	5.827	0.0418	0.3577	-0.094	5.081	0.0912	0.6706	0.048	4.532	0.1293	0.9361	0.142	5.090	0.1416	0.4514
	putative carboxylate-amine/thiol ligase																							

Log$_2$ Ratios



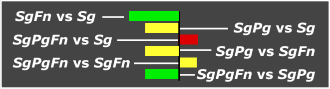
● Show detected proteins only
○ Show all proteins
☐ Filter by category:
ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
🟨	no	n/a	bars
🟩	yes	–	ratios, bars
▨	yes	+	*p*- , *q*-Values
▨	yes	–	



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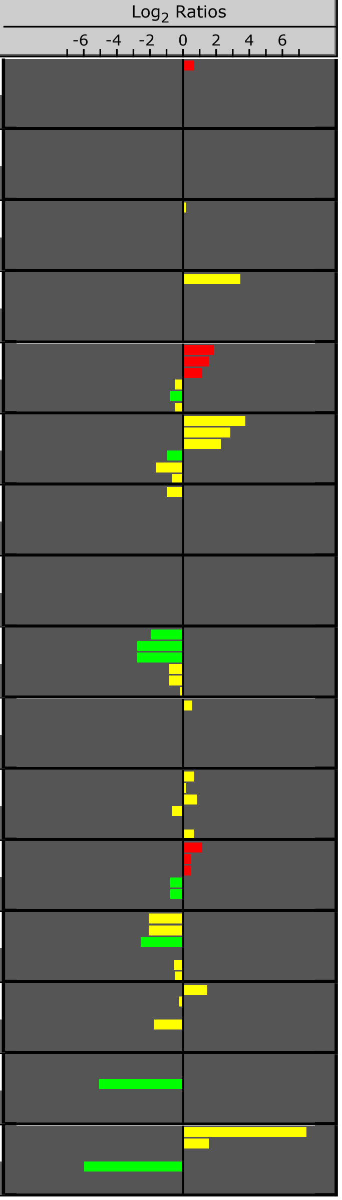
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory **UW**

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

		SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0385	exo-beta-D-fructosidase	0.670	7.728	0.0026	0.0070		6.351				6.351				6.514				5.903						
SGO_0387	hypothetical protein SGO_0387		4.194				4.194				4.194														
SGO_0388	LPXTG cell wall surface protein, zinc carboxypeptidase family	0.224	7.351	0.0555	0.3217		6.251				6.251				5.931				5.320						
SGO_0389	possible phosphoserine phosphatase	3.458	5.613	0.0418	0.2326		1.000				1.000				5.039				4.429						
SGO_0390	glycerol-3-phosphate dehydrogenase (NAD(P)+)	1.938	8.321	0.0014	0.0028	1.564	8.027	0.0010	0.0015	1.196	7.757	0.0003	0.0005	-0.374	8.298	0.0161	0.0876	-0.742	7.537	0.0050	0.0165	-0.369	7.920	0.0236	0.0363
SGO_0392	phosphoglycerate mutase	3.821	6.458	0.0090	0.0344	2.875	5.566	0.0232	0.0922	2.271	4.127			-0.946	6.501	0.0011	0.0021	-1.550	5.511	0.0113	0.0485	-0.604	5.365	0.0830	0.2216
SGO_0393	D-alanyl-D-alanine carboxypeptidase	-0.858	5.430	0.0702	0.4299		5.105				5.105				2.611				2.000						
SGO_0396	Transcriptional regulator, PadR family		2.322				2.322				2.322														
SGO_0398	ABC transporter ATP-binding protein	-1.902	7.059	0.0021	0.0053	-2.695	6.928	0.0017	0.0033	-2.749	6.912	0.0009	0.0028	-0.794	4.991	0.0183	0.1028	-0.848	4.338	0.0119	0.0517	-0.054	4.508	0.2021	0.7300
SGO_0400	hrcA; heat-inducible transcription repressor HrcA	0.608	4.887	0.0421	0.2346		3.423				3.423				3.724				3.113						
SGO_0401	grpE; co-chaperone GrpE	0.727	7.007	0.0294	0.1511	0.166	6.709	0.1742	0.9248	0.875	7.096	0.0122	0.0835	-0.561	6.510	0.0076	0.0327	0.148	6.218	0.0233	0.1210	0.708	6.598	0.0127	0.0135
SGO_0402	dnaK; DnaK chaperone protein	1.202	11.615	0.0001	0.0001	0.461	11.142	0.0013	0.0022	0.487	11.157	0.0007	0.0019	-0.741	11.257	0.0002	0.0001	-0.715	10.656	0.0003	0.0001	0.026	10.853	0.1603	0.5363
SGO_0404	dnaJ; DnaJ chaparone protein	-2.009	7.978	0.0052	0.0171	-2.045	7.970	0.0057	0.0167	-2.460	7.910	0.0032	0.0147	-0.036	6.073	0.0706	0.5026	-0.451	5.300	0.0313	0.1735	-0.415	5.889	0.0769	0.2007
SGO_0407	truA; tRNA pseudouridine synthase A	1.455	4.510	0.0205	0.0948	-0.231	2.696				1.807			-1.686	3.963	0.0161	0.0876		3.145				1.063		
SGO_0408	zmpB; zinc metalloproteinase B		8.890				8.890			-4.983	8.913	0.0027	0.0117						1.783				2.394		
SGO_0409	pyridoxine kinase	7.517	9.176	0.0184	0.0834	1.598	3.467	0.0233	0.0929		0.643			-5.919	8.682	0.0007	0.0010		8.048				2.735		



● Show detected proteins only
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☐ Filter by category:
ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
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🟨	no	n/a	bars
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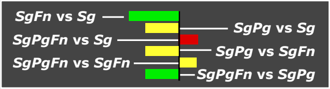
▨	yes	+	*p*- , *q*-Values
▨	yes	−	



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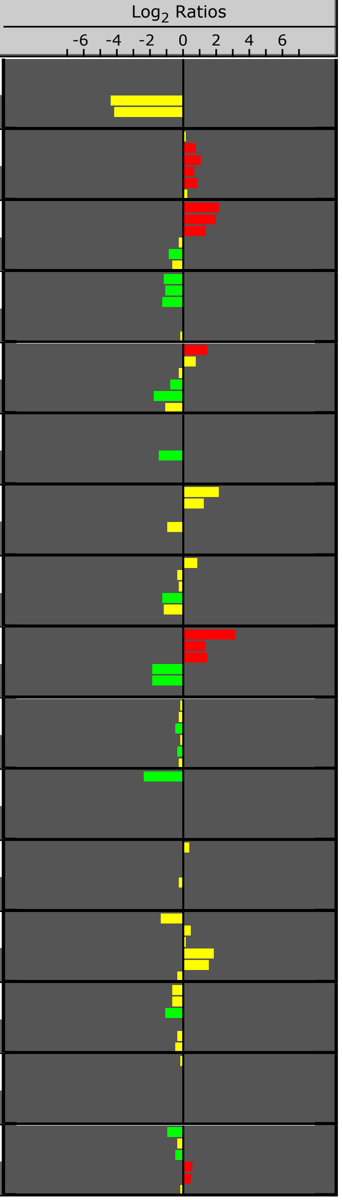
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0411 conserved hypothetical protein TIGR01440		8.854				4.454				3.566			-4.261	8.407	0.0072	0.0303	-4.144	7.766	0.0451	0.2683	0.118	4.564	0.1587	0.5290
SGO_0412 tig; trigger factor	0.157	10.717	0.0298	0.1538	0.831	11.109	0.0005	0.0006	1.089	11.280	0.0002	0.0002	0.673	10.654	0.0006	0.0008	0.932	10.208	0.0004	0.0003	0.259	11.086	0.0051	0.0025
SGO_0413 DNA-directed RNA polymerase delta chain	2.206	7.129	0.0003	0.0004	2.022	7.008	0.0040	0.0107	1.445	6.540	0.0007	0.0018	-0.184	7.251	0.0657	0.4612	-0.761	6.382	0.0007	0.0007	-0.577	6.900	0.0368	0.0718
SGO_0415 secA; preprotein translocase, SecA subunit	-1.134	10.674	0.0005	0.0007	-1.044	10.702	0.0005	0.0006	-1.184	10.658	0.0003	0.0005	0.090	9.530	0.0349	0.2222	-0.050	8.850	0.0760	0.5089	-0.140	9.505	0.0226	0.0337
SGO_0416 phospho-2-dehydro-3-deoxyheptonate aldolase	1.455	7.692	0.0001	0.0001	0.754	7.228	0.0087	0.0280	-0.211	6.715	0.0597	0.5367	-0.702	7.428	0.0028	0.0085	-1.666	6.527	0.0009	0.0010	-0.964	6.657	0.0227	0.0340
SGO_0418 alr; alanine racemase		5.266				3.870							-1.405	5.217	0.0004	0.0004		4.142				3.357		
SGO_0425 ansB; asparaginase	2.236	3.572			1.326	2.868				1.058			-0.910	3.396				2.170				1.871		
SGO_0426 Cof family protein	0.886	6.136	0.0062	0.0214	-0.316	5.480	0.0492	0.2190	-0.210	5.146	0.0650	0.5907	-1.201	5.513	0.0025	0.0071	-1.096	4.682	0.0291	0.1586	0.105	4.407	0.1979	0.7048
SGO_0427 universal stress protein family	3.220	7.650	0.0005	0.0006	1.411	6.151	0.0006	0.0008	1.454	6.180	0.0001	0.0001	-1.809	7.352	0.0008	0.0012	-1.766	6.750	0.0009	0.0012	0.043	6.199	0.1767	0.6150
SGO_0429 aspartate transaminase	-0.087	9.283	0.0341	0.1809	-0.208	9.238	0.0673	0.3144	-0.434	9.126	0.0012	0.0042	-0.121	8.678	0.0795	0.5757	-0.347	7.952	0.0016	0.0034	-0.226	8.510	0.0878	0.2406
SGO_0430 LPXTG cell wall surface protein	-2.297	9.650	0.0001	0.0000		9.382				9.382				6.577				5.967						
SGO_0431 GTP-sensing transcriptional pleiotropic repressor codY	0.352	4.954	0.0932	0.5974	0.147	5.310	0.1464	0.7587		4.268			-0.204	4.493	0.0326	0.2026		2.429				3.837		
SGO_0432 entB; isochorismatase family protein	-1.338	6.161	0.0267	0.1349	0.535	7.190	0.0066	0.0198	0.234	7.019	0.0184	0.1401	1.873	6.100	0.0126	0.0633	1.572	5.226	0.0121	0.0526	-0.301	6.773	0.0214	0.0309
SGO_0434 aspS-2; aspartyl-tRNA synthetase	-0.624	7.577	0.0152	0.0669	-0.559	7.587	0.0084	0.0265	-0.962	7.443	0.0026	0.0113	0.066	6.756	0.1206	0.9195	-0.338	5.963	0.0483	0.2909	-0.404	6.589	0.0524	0.1213
SGO_0435 gatC; glutamyl-tRNA(Gln) amidotransferase, C subunit	-0.058	6.298	0.0814	0.5104	-0.003	6.327	0.1779	0.9549	0.062	6.359	0.0647	0.5867	0.055	5.782	0.0639	0.4458	0.120	5.204	0.0298	0.1626	0.065	5.843	0.1504	0.4844
SGO_0436 gatA; glutamyl-tRNA(Gln) amidotransferase, A subunit	-0.868	9.074	0.0011	0.0021	-0.300	9.301	0.0091	0.0294	-0.390	9.261	0.0025	0.0108	0.568	8.373	0.0013	0.0027	0.478	7.708	0.0009	0.0010	-0.090	8.584	0.0541	0.1266



● Show detected proteins only
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☐ Filter by category:
ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	.005
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
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🟩	yes	−	ratios, bars
▨	yes	+	*p-* , *q*-Values
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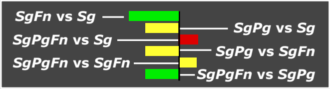

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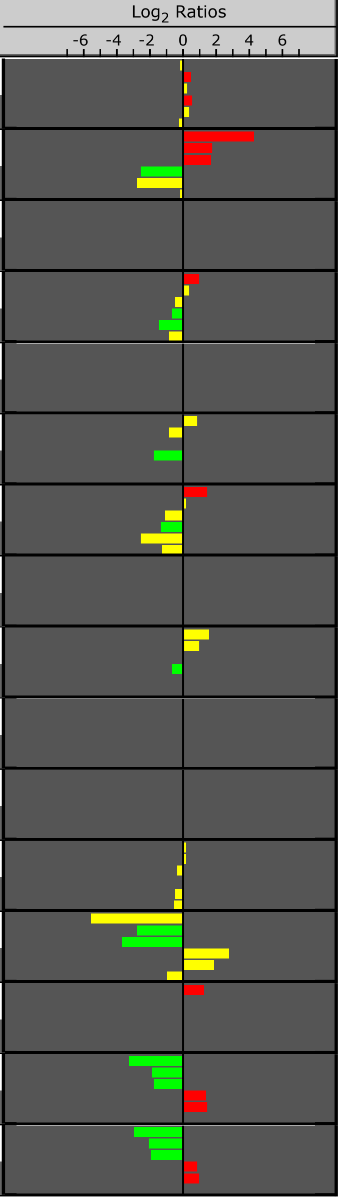
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0437 gatB; glutamyl-tRNA(Gln) amidotransferase, B subunit	-0.052	8.674	0.1104	0.7212	0.549	8.996	0.0018	0.0038	0.341	8.903	0.0263	0.2113	0.601	8.467	0.0037	0.0121	0.393	7.762	0.0355	0.2029	-0.208	8.655	0.1558	0.5048
SGO_0440 L-iditol 2-dehydrogenase BH3949	4.334	7.132	0.0002	0.0002	1.808	4.908	0.0017	0.0035	1.671	4.100	0.0035	0.0167	-2.526	6.782	0.0004	0.0003	-2.663	6.048	0.0122	0.0534	-0.137	4.572	0.1770	0.6170
SGO_0444 HAD superfamily (subfamily IIIA) phosphatase, TIGR01668		3.087				3.087				3.087														
SGO_0445 GTP-binding protein	0.991	7.156	0.0005	0.0006	0.374	6.781	0.0137	0.0486	-0.388	6.403	0.0100	0.0638	-0.617	6.781	0.0019	0.0044	-1.379	5.916	0.0006	0.0005	-0.762	6.115	0.0125	0.0132
SGO_0446 conserved hypothetical protein TIGR00253		3.585				3.585				3.585														
SGO_0447 nadD; nicotinate (nicotinamide) nucleotide adenylyltransferase	0.891	5.986	0.0080	0.0300	-0.822	5.135	0.0144	0.0518		4.453			-1.713	5.261	0.0044	0.0155		4.251				3.212		
SGO_0448 conserved hypothetical protein TIGR00488	1.496	5.978	0.0028	0.0078	0.170	5.137	0.1330	0.6801	-1.036	4.384	0.0375	0.3180	-1.326	5.495	0.0019	0.0046	-2.532	4.521	0.0206	0.1025	-1.206	3.960	0.0358	0.0691
SGO_0449 isochorismatase family protein		1.585				1.585				1.585														
SGO_0450 iojap-related protein	1.587	4.981	0.0111	0.0443	1.018	4.508	0.0199	0.0773		2.170			-0.570	4.989	0.0013	0.0029		3.635				3.677		
SGO_0451 methyltransferase						3.791								3.278								3.278		
SGO_0453 lipoprotein, putative		7.985				7.985				7.985														
SGO_0454 conserved hypothetical protein TIGR01033	0.166	7.715	0.0699	0.4277	0.236	7.740	0.0327	0.1365	-0.263	7.542	0.0681	0.6242	0.070	7.311	0.1040	0.7740	-0.429	6.514	0.0563	0.3573	-0.499	7.151	0.0878	0.2397
SGO_0455 lipoprotein, putative	-5.504	8.234	0.0133	0.0563	-2.675	8.428	0.0004	0.0005	-3.589	8.338	0.0003	0.0004	2.829	5.127	0.0111	0.0532	1.915	3.733	0.0398	0.2313	-0.914	5.663	0.0166	0.0204
SGO_0456 ILL5; amino acid aminohydrolase	1.256	5.488	0.0003	0.0003		3.732				3.732				4.469				3.858						
SGO_0457 ABC transporter, substrate-binding protein SP0148	-3.171	9.200	0.0001	0.0000	-1.812	9.410	0.0002	0.0001	-1.713	9.432	0.0001	0.0001	1.359	7.198	0.0002	0.0001	1.458	6.659	0.0001	0.0000	0.099	7.774	0.0397	0.0810
SGO_0458 hlpA; lipoprotein	-2.885	10.776	0.0004	0.0004	-1.995	10.913	0.0005	0.0005	-1.927	10.927	0.0003	0.0006	0.889	8.708	0.0015	0.0034	0.958	8.142	0.0015	0.0029	0.069	9.113	0.0419	0.0868



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Dot Plots

Test	Cutoff
***q*-Value**	**.005**
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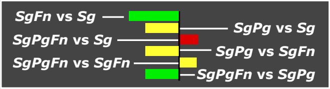

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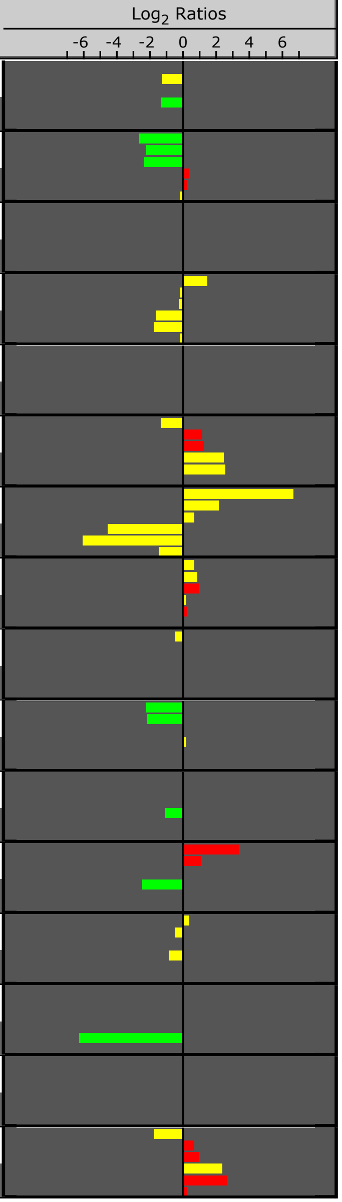
Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0459	0.112	5.970	0.1341	0.8978	-1.190	5.463	0.0169	0.0627		4.950			-1.303	4.977	0.0023	0.0064		3.866				3.209		
	succinyl-diaminopimelate desuccinylase																							
SGO_0460	-2.640	7.625	0.0007	0.0010	-2.214	7.691	0.0008	0.0013	-2.331	7.671	0.0005	0.0012	0.425	5.479	0.0025	0.0072	0.308	4.801	0.0014	0.0024	-0.117	5.619	0.0524	0.1210
	ABC transporter, ATP-binding protein SP0151																							
SGO_0463		2.723				2.723				2.723														
	cydD; putative ABC transporter (ATP-binding protein)																							
SGO_0468	1.460	7.214	0.0095	0.0367	-0.141	6.233	0.1049	0.5199	-0.209	6.214	0.0553	0.4919	-1.602	6.634	0.0051	0.0196	-1.669	6.013	0.0058	0.0201	-0.067	5.563	0.2181	0.8046
	hypothetical protein SGO_0468																							
SGO_0469		4.352				4.352				4.352														
	integral membrane protein																							
SGO_0476	-1.320	4.817	0.0152	0.0670	1.201	6.277	0.0008	0.0012	1.297	6.342	0.0002	0.0002	2.521	5.363	0.0119	0.0583	2.617	4.838	0.0082	0.0313	0.096	6.290	0.0979	0.2804
	rhodanese family protein																							
SGO_0480	6.692	9.969	0.0405	0.2217	2.150	5.482	0.0231	0.0917	0.737	3.585			-4.542	9.506	0.0050	0.0191	-5.955	8.849	0.0388	0.2230	-1.413	5.063	0.0499	0.1131
	hypothetical protein SGO_0480																							
SGO_0483	0.666	6.247	0.0052	0.0168	0.911	6.419	0.0108	0.0362	0.979	6.445	0.0011	0.0035	0.245	6.162	0.0367	0.2361	0.313	5.573	0.0011	0.0015	0.069	6.312	0.2214	0.8252
	hypothetical protein SGO_0483																							
SGO_0484	-0.367	4.981	0.0680	0.4142		4.515				4.515				2.611				2.000						
	sensor histidine kinase																							
SGO_0488	-2.214	6.635	0.0018	0.0041	-2.054	6.608	0.0002	0.0001		6.297			0.160	4.799	0.1077	0.8086		3.254				3.730		
	ABC transporter, ATP-binding protein SP0483																							
SGO_0491		4.342				3.343							-1.048	4.414	0.0033	0.0108		3.218				2.830		
	gidB; methyltransferase GidB																							
SGO_0494	3.418	8.065	0.0010	0.0018	1.064	6.136	0.0009	0.0013		4.516			-2.354	7.679	0.0013	0.0025		6.813				5.055		
	lemA; LemA-like protein																							
SGO_0495	0.441	5.691	0.0257	0.1271	-0.397	4.932	0.0987	0.4863		4.481			-0.838	4.717	0.0118	0.0577		3.751				2.523		
	htpx; heat shock protein																							
SGO_0497		9.226								1.981				8.713			-6.245	8.111	0.0022	0.0054		1.468		
	gtfG; glucosyltransferase G																							
SGO_0500		2.058				2.058				2.058														
	rggD; putative transcriptional regulator RggD																							
SGO_0501	-1.705	5.727	0.0055	0.0183	0.653	6.885	0.0004	0.0004	0.967	7.084	0.0000	0.0000	2.358	5.796	0.0062	0.0253	2.672	5.473	0.0013	0.0023	0.314	6.827	0.0037	0.0010
	Uncharacterized ACR, COG1399																							



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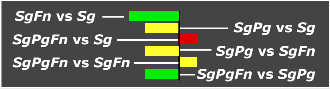
☐ Filter by category:
ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
🟨	no	n/a	bars
🟩	yes	–	ratios, bars
▨	yes	+	*p-* , *q*-Values
▧	yes	–	



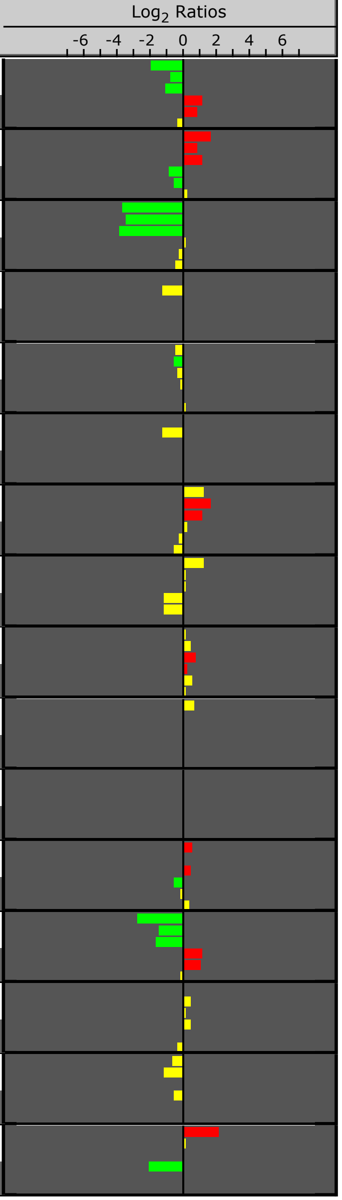
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0502 floL; flotillin-like protein	-1.901	9.535	0.0003	0.0003	-0.710	9.878	0.0016	0.0032	-1.046	9.757	0.0002	0.0002	1.192	8.502	0.0023	0.0064	0.856	7.662	0.0028	0.0076	-0.336	8.810	0.0263	0.0431
SGO_0503 gnd; 6-phosphogluconate dehydrogenase, decarboxylating	1.705	11.551	0.0001	0.0001	0.873	10.962	0.0003	0.0002	1.201	11.183	0.0002	0.0003	-0.832	11.295	0.0004	0.0003	-0.504	10.811	0.0012	0.0018	0.328	10.994	0.0086	0.0064
SGO_0505 PTS system, IIBC component	-3.594	10.971	0.0001	0.0000	-3.384	10.986	0.0001	0.0000	-3.763	10.957	0.0001	0.0000	0.210	7.872	0.0512	0.3479	-0.169	7.069	0.0565	0.3604	-0.379	7.786	0.0264	0.0435
SGO_0506 rgfB; RgfB		3.000			-1.165	3.532				3.000				1.322								1.322		
SGO_0508 nrdR; transcriptional regulator, NrdR family	-0.432	6.099	0.0118	0.0489	-0.519	6.409	0.0010	0.0016	-0.317	6.498	0.0061	0.0338	-0.087	5.228	0.0712	0.5085	0.116	4.756	0.0856	0.5856	0.202	5.722	0.0616	0.1493
SGO_0509 Replication initiation and membrane attachment protein (DnaB) superfamily		4.188			-1.245	4.446	0.0735	0.3492		4.188				1.322								1.322		
SGO_0510 dnaI; primosomal protein DnaI	1.340	5.852	0.0052	0.0170	1.688	6.091	0.0010	0.0015	1.171	5.714	0.0011	0.0038	0.348	6.032	0.0275	0.1659	-0.169	5.157	0.0612	0.3971	-0.517	5.948	0.0158	0.0183
SGO_0511 NADPH-flavin oxidoreductase -like protein	1.306	5.805	0.0113	0.0460	0.194	5.117	0.1773	0.9470	0.216	5.138	0.0919	0.8722	-1.112	5.300	0.0054	0.0209	-1.090	4.703	0.0072	0.0263	0.022	4.638	0.2139	0.7868
SGO_0512 GTP-binding protein engA	0.201	7.827	0.0613	0.3659	0.530	8.008	0.0100	0.0333	0.771	8.160	0.0043	0.0222	0.329	7.571	0.0043	0.0149	0.571	7.105	0.0060	0.0210	0.241	7.855	0.0443	0.0950
SGO_0513 Snf2 family protein	0.668	4.254	0.0524	0.3005		2.170				2.170				3.353				2.742						
SGO_0514 hypothetical protein SGO_0514						3.791								3.278								3.278		
SGO_0515 murC; UDP-N-acetylmuramate--alanine ligase	0.612	8.759	0.0031	0.0092	0.105	8.471	0.0142	0.0507	0.490	8.689	0.0047	0.0250	-0.507	8.288	0.0038	0.0126	-0.122	7.853	0.0635	0.4155	0.385	8.219	0.0246	0.0388
SGO_0518 aminodeoxychorismate lyase-like protein	-2.664	8.637	0.0001	0.0000	-1.438	8.879	0.0001	0.0001	-1.560	8.849	0.0002	0.0001	1.227	6.988	0.0002	0.0001	1.104	6.297	0.0015	0.0027	-0.123	7.418	0.0956	0.2702
SGO_0519 greA; transcription elongation factor greA	0.050	7.158	0.1070	0.6966	0.526	7.415	0.0087	0.0280	0.177	7.214	0.0112	0.0744	0.476	6.929	0.0132	0.0679	0.127	6.121	0.0722	0.4804	-0.349	6.975	0.0315	0.0556
SGO_0521 Membrane protein oxaA 2 precursor	-0.573	5.942	0.0557	0.3239	-1.082	6.092	0.0080	0.0248		5.531			-0.509	4.706	0.0488	0.3295		2.807				3.945		
SGO_0523 spoU rRNA Methylase family protein	2.159	6.704	0.0005	0.0007	0.164	5.107	0.1254	0.6344		3.392			-1.995	6.366	0.0002	0.0001		5.427				4.070		



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p-Value	

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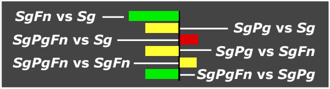

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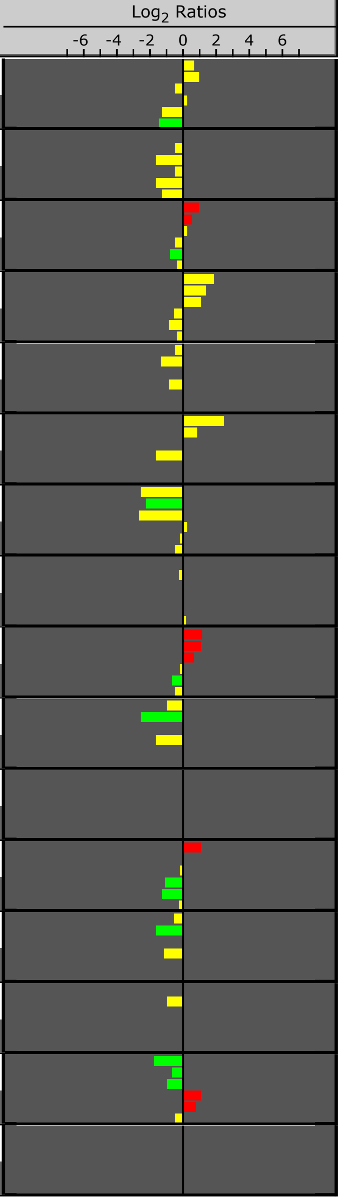
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein		*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0526	ilvB; acetolactate synthase, large subunit, biosynthetic type	0.727	6.089	0.0277	0.1410	0.991	6.225	0.0078	0.0239	-0.429	5.467	0.0284	0.2290	0.264	5.998	0.0611	0.4254	-1.156	4.798	0.0101	0.0413	-1.420	5.561	0.0050	0.0022
SGO_0527	ilvN; acetolactate synthase, small subunit	0.008	5.759	0.1306	0.8672	-0.395	5.587	0.0288	0.1179	-1.584	4.978	0.0063	0.0350	-0.403	5.078	0.0196	0.1122	-1.592	3.861	0.0089	0.0352	-1.189	4.162	0.0867	0.2343
SGO_0528	ilvC; ketol-acid reductoisomerase	1.026	8.815	0.0020	0.0049	0.581	8.528	0.0018	0.0039	0.292	8.366	0.0128	0.0887	-0.445	8.520	0.0078	0.0339	-0.734	7.797	0.0048	0.0157	-0.289	8.143	0.0423	0.0885
SGO_0529	ilvA; threonine dehydratase	1.907	5.080	0.0065	0.0226	1.401	4.686	0.0093	0.0302	1.149	3.915	0.0332	0.2748	-0.507	4.959	0.0259	0.1541	-0.759	3.952	0.0542	0.3391	-0.252	4.168	0.1566	0.5093
SGO_0530	Cof family protein	-0.427	5.304	0.0251	0.1236	-1.277	5.023	0.0059	0.0174		4.486			-0.849	4.253	0.0220	0.1276		2.972				2.826		
SGO_0533	conserved hypothetical protein TIGR00150	2.481	3.362			0.871	2.143				0.643			-1.611	3.019				2.000				1.000		
SGO_0535	putative transcriptional regulator LytR	-2.494	6.747	0.0178	0.0800	-2.237	6.905	0.0008	0.0011	-2.636	6.736	0.0117	0.0784	0.257	4.384	0.0652	0.4574	-0.143	2.930			-0.400	4.343	0.1153	0.3452
SGO_0536	hypothetical protein SGO_0536		6.082			-0.177	6.995	0.0193	0.0745	0.019	7.090	0.0847	0.7979		5.390				4.975			0.196	6.491	0.0198	0.0277
SGO_0537	HIT family protein	1.242	6.570	0.0008	0.0013	1.124	6.487	0.0008	0.0011	0.678	6.200	0.0029	0.0130	-0.118	6.485	0.0126	0.0637	-0.564	5.678	0.0016	0.0033	-0.446	6.219	0.0051	0.0025
SGO_0538	ABC transporter, ATP-binding protein SP0522	-0.908	6.861	0.0075	0.0275	-2.541	6.463	0.0012	0.0020		6.232			-1.633	5.245	0.0054	0.0210		4.236				3.195		
SGO_0539	ABC transporter, permease protein		4.667				4.667				4.667														
SGO_0540	hypothetical protein SGO_0540	1.134	7.814	0.0003	0.0003	0.148	7.214	0.0131	0.0456	-0.100	7.089	0.0204	0.1589	-0.986	7.348	0.0004	0.0003	-1.234	6.659	0.0004	0.0002	-0.248	6.654	0.0094	0.0078
SGO_0541	methyltransferase, putative	-0.545	5.797	0.0064	0.0223	-1.602	5.480	0.0030	0.0073		5.047			-1.057	4.580	0.0057	0.0224		3.371				3.020		
SGO_0542	hypothetical protein SGO_0542		2.700			-0.865	3.332				2.700				1.322								1.322		
SGO_0543	nusA; transcription termination factor NusA	-1.692	7.929	0.0001	0.0000	-0.585	8.276	0.0002	0.0001	-0.940	8.146	0.0003	0.0004	1.107	6.991	0.0000	0.0000	0.752	6.151	0.0016	0.0032	-0.355	7.276	0.0105	0.0098
SGO_0544	Protein of unknown function (DUF448) superfamily		2.000				2.000				2.000														



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p-Value	

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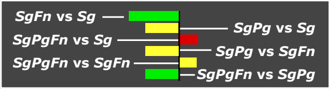

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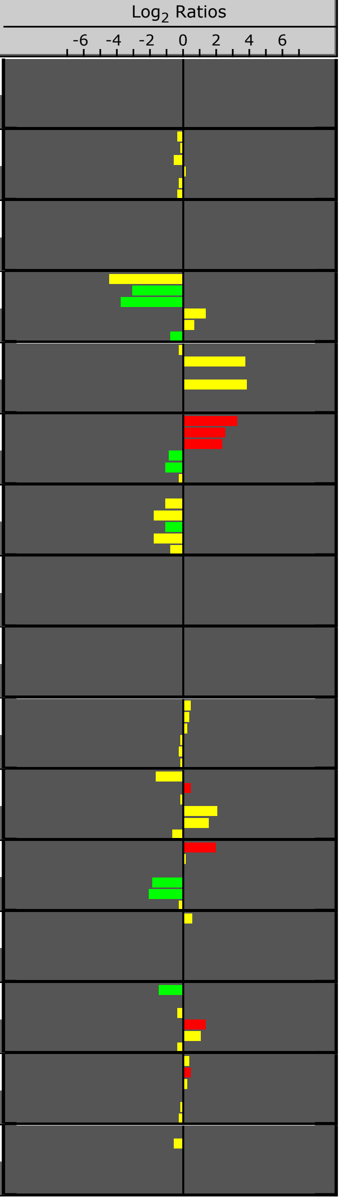
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0545		1.807				1.807				1.807														
	ribosomal protein L7A family																							
SGO_0546	-0.307	8.766	0.0250	0.1222	-0.138	8.842	0.0729	0.3461	-0.475	8.700	0.0122	0.0836	0.170	8.171	0.0265	0.1583	-0.168	7.401	0.0612	0.3987	-0.338	8.102	0.0476	0.1054
	infB; Translation initiation factor IF-2																							
SGO_0547						1.098								0.585								0.585		
	rbfA; ribosome-binding factor A																							
SGO_0548	-4.413	7.683	0.0137	0.0590	-2.975	7.822	0.0004	0.0004	-3.700	7.756	0.0003	0.0004	1.438	4.402	0.0127	0.0642	0.714	3.205	0.0101	0.0417	-0.725	4.840	0.0050	0.0019
	Na/Pi-cotransporter family protein																							
SGO_0549	-0.156	2.789			3.756	5.724				1.865			3.912	5.200				0.585				5.108		
	nagA; N-acetylglucosamine-6-phosphate deacetylase																							
SGO_0552	3.347	7.019	0.0005	0.0007	2.595	6.355	0.0004	0.0004	2.390	6.185	0.0004	0.0009	-0.752	7.028	0.0022	0.0058	-0.957	6.345	0.0017	0.0037	-0.205	6.502	0.0184	0.0242
	oxidoreductase, aldo/keto reductase family																							
SGO_0554	0.061	6.972	0.1305	0.8645	-0.957	6.566	0.0297	0.1216	-1.664	6.199	0.0395	0.3367	-1.018	6.007	0.0028	0.0083	-1.725	5.015	0.0204	0.1000	-0.707	4.799	0.0921	0.2571
	hsdR; type I site-specific deoxyribonuclease																							
SGO_0556		3.279				3.279				3.279														
	DNA helicase-like protein, putative																							
SGO_0557		1.807				1.807				1.807														
	HsdS specificity protein of type I restriction-modification system																							
SGO_0558	0.494	3.590			0.356	4.186	0.1015	0.5010	0.263	3.460			-0.137	3.826	0.1100	0.8286	-0.230	2.581			-0.093	3.750	0.2118	0.7732
	hypothetical protein SGO_0558																							
SGO_0560	-1.604	4.640	0.0073	0.0263	0.516	5.703	0.0024	0.0054	-0.051	5.401	0.0810	0.7600	2.120	4.582	0.0118	0.0572	1.553	3.483	0.0247	0.1292	-0.567	5.174	0.0151	0.0173
	hsdM; type I restriction-modification system, M subunit																							
SGO_0565	2.010	9.293	0.0008	0.0013	0.214	8.069	0.0140	0.0500	0.010	7.962	0.0921	0.8777	-1.797	8.825	0.0009	0.0015	-2.000	8.171	0.0010	0.0013	-0.204	7.560	0.0246	0.0387
	adhA; alcohol dehydrogenase																							
SGO_0566	0.575	8.380	0.0109	0.0434		7.073				7.073				7.120				6.510						
	sgc; serine protease challisin																							
SGO_0568	-1.401	6.686	0.0013	0.0025	0.047	7.232	0.0949	0.4663	-0.300	7.076	0.0184	0.1403	1.448	6.209	0.0014	0.0031	1.101	5.369	0.0073	0.0268	-0.346	6.590	0.0499	0.1129
	glyQ; glycyl-tRNA synthetase, alpha subunit																							
SGO_0569	0.390	8.405	0.0137	0.0586	0.474	8.445	0.0001	0.0001	0.301	8.362	0.0214	0.1686	0.084	8.115	0.0814	0.5918	-0.089	7.432	0.1037	0.7297	-0.173	8.079	0.1338	0.4182
	glyS; glycyl-tRNA synthetase, beta subunit																							
SGO_0570		3.170			-0.455	4.468	0.0111	0.0375		3.170				3.202								3.202		
	hypothetical protein SGO_0570																							



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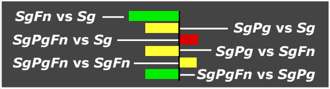

Streptococcus gordonii

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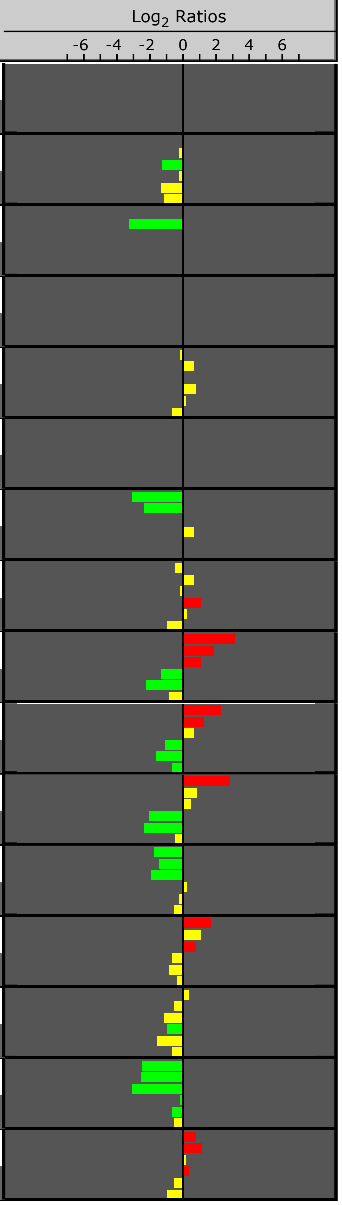
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0571		1.322				1.322				1.322														
	hypothetical protein SGO_0571																							
SGO_0573	0.013	6.729	0.1339	0.8953	-0.163	6.619	0.0727	0.3439	-1.240	6.233	0.0046	0.0239	-0.176	6.126	0.0588	0.4067	-1.254	5.136	0.0101	0.0414	-1.078	5.593	0.0120	0.0121
	mraW; S-adenosyl-methyltransferase MraW																							
SGO_0575		6.904			-3.188	7.054	0.0001	0.0001		6.904				3.202								3.202		
	pbp2X; penicillin-binding protein 2X																							
SGO_0576		3.087				3.087				3.087														
	mraY; phospho-N-acetylmuramoyl-pentapeptide-transferase																							
SGO_0577	-0.084	6.915	0.1306	0.8687	0.720	7.329	0.0064	0.0189	0.118	7.003	0.0712	0.6568	0.804	6.796	0.0075	0.0319	0.202	5.854	0.0868	0.5957	-0.602	6.863	0.0238	0.0368
	ATP-dependent RNA helicase																							
SGO_0578		6.489				6.489				6.489														
	amino acid ABC transporter permease protein																							
SGO_0579	-3.048	6.975	0.0001	0.0000	-2.330	7.076	0.0002	0.0001		6.811			0.718	4.668	0.0075	0.0323		2.639				3.991		
	amino acid ABC transporter ATP binding protein																							
SGO_0581	-0.401	5.554	0.0381	0.2059	0.719	6.131	0.0084	0.0264	-0.136	5.652	0.0353	0.2946	1.121	5.490	0.0046	0.0168	0.265	4.348	0.0563	0.3569	-0.856	5.563	0.0121	0.0124
	trxB; thioredoxin-disulfide reductase																							
SGO_0582	3.236	8.876	0.0000	0.0000	1.890	7.748	0.0025	0.0058	1.063	7.143	0.0042	0.0212	-1.346	8.699	0.0006	0.0007	-2.174	7.897	0.0002	0.0001	-0.827	7.536	0.0224	0.0331
	nicotinate phosphoribosyltransferase, putative																							
SGO_0583	2.312	6.694	0.0022	0.0058	1.345	5.936	0.0033	0.0083	0.732	5.536	0.0130	0.0915	-0.967	6.490	0.0045	0.0163	-1.580	5.703	0.0027	0.0071	-0.613	5.640	0.0045	0.0014
	nadE; NAD+ synthetase																							
SGO_0585	2.877	8.679	0.0002	0.0002	0.921	7.164	0.0065	0.0193	0.528	6.916	0.0092	0.0570	-1.956	8.313	0.0004	0.0004	-2.349	7.628	0.0004	0.0002	-0.393	6.850	0.0426	0.0898
	pepC; aminopeptidase C																							
SGO_0586	-1.742	8.755	0.0002	0.0001	-1.402	8.842	0.0003	0.0003	-1.931	8.713	0.0001	0.0001	0.341	7.309	0.0144	0.0754	-0.188	6.424	0.0303	0.1667	-0.529	7.227	0.0163	0.0197
	pbp1a; penicillin-binding protein 1A																							
SGO_0589	1.676	7.845	0.0038	0.0113	1.105	7.429	0.0068	0.0204	0.840	7.241	0.0028	0.0124	-0.571	7.688	0.0196	0.1119	-0.835	6.970	0.0101	0.0417	-0.265	7.239	0.0979	0.2806
	methylase																							
SGO_0590	0.366	6.294	0.0250	0.1225	-0.529	5.876	0.0308	0.1271	-1.104	5.408	0.0263	0.2109	-0.895	5.577	0.0044	0.0159	-1.470	4.571	0.0188	0.0905	-0.575	4.491	0.1229	0.3763
	Methyltransferase																							
SGO_0591	-2.414	8.988	0.0000	0.0000	-2.495	8.975	0.0000	0.0000	-3.040	8.906	0.0000	0.0000	-0.081	6.773	0.0005	0.0005	-0.626	5.925	0.0013	0.0021	-0.545	6.487	0.0058	0.0034
	hypothetical protein SGO_0591																							
SGO_0592	0.770	5.593	0.0015	0.0034	1.171	5.856	0.0003	0.0002	0.243	4.825	0.0276	0.2220	0.401	5.626	0.0027	0.0078	-0.527	4.232	0.0281	0.1510	-0.928	5.148	0.0264	0.0438
	luxS; autoinducer-2 production protein LuxS																							



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1179

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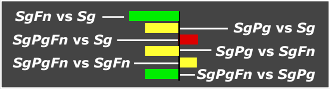
Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
🟨	no	n/a	bars
🟩	yes	−	ratios, bars
🟥	yes	+	*p*- , *q*-Values
🟩	yes	−	



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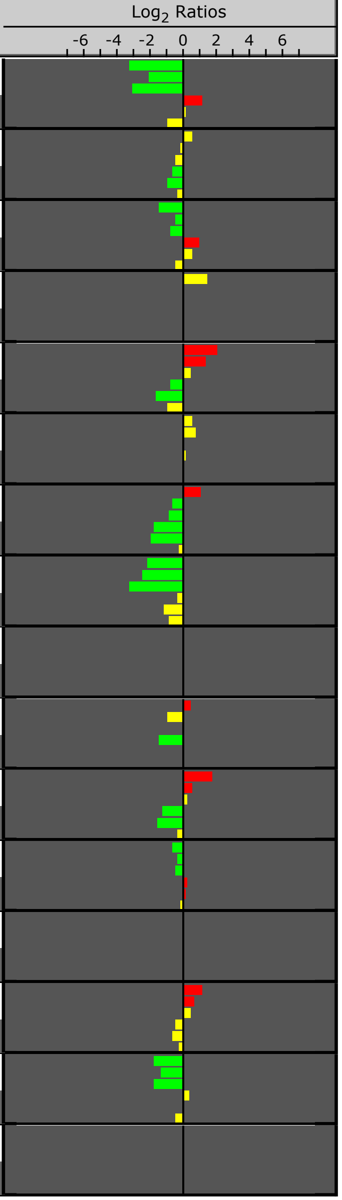
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0593 HD/KH domain protein	-3.236	8.876	0.0001	0.0000	-2.047	9.043	0.0002	0.0001	-2.992	8.903	0.0001	0.0001	1.189	6.701	0.0013	0.0027	0.245	5.513	0.0449	0.2657	-0.945	6.782	0.0089	0.0068
SGO_0594 gmk; Guanylate kinase (GMP kinase)	0.562	6.622	0.0052	0.0169	-0.071	6.280	0.1194	0.6001	-0.356	6.147	0.0097	0.0616	-0.633	6.078	0.0028	0.0086	-0.918	5.361	0.0014	0.0025	-0.285	5.592	0.0336	0.0621
SGO_0595 DNA-directed RNA polymerase, omega subunit	-1.365	6.899	0.0004	0.0006	-0.368	7.248	0.0003	0.0002	-0.733	7.101	0.0004	0.0006	0.997	6.131	0.0011	0.0021	0.632	5.291	0.0054	0.0183	-0.365	6.369	0.0086	0.0063
SGO_0596 priA; primosomal protein N''	1.535	4.408	0.0093	0.0359		1.643				1.643				3.665				3.054						
SGO_0597 fmt; methionyl-tRNA formyltransferase	2.095	6.308	0.0012	0.0024	1.413	5.785	0.0025	0.0057	0.482	5.192	0.0290	0.2349	-0.682	6.173	0.0032	0.0104	-1.613	5.275	0.0013	0.0022	-0.930	5.400	0.0057	0.0031
SGO_0598 sun; sun protein	0.617	4.435	0.0067	0.0238	0.767	5.065	0.0098	0.0324		3.614			0.150	4.423	0.0894	0.6563		2.107				3.895		
SGO_0599 phosphoprotein phosphatase	1.085	7.939	0.0005	0.0006	-0.624	7.019	0.0012	0.0022	-0.816	6.954	0.0019	0.0077	-1.709	7.255	0.0004	0.0003	-1.901	6.606	0.0006	0.0005	-0.192	6.080	0.1225	0.3743
SGO_0600 serine/threonine protein kinase	-2.104	8.114	0.0001	0.0001	-2.409	8.059	0.0001	0.0000	-3.243	7.883	0.0037	0.0182	-0.306	6.059	0.0240	0.1406	-1.139	4.891	0.0315	0.1751	-0.833	5.248	0.0549	0.1291
SGO_0602 histidine kinase		4.115				4.115				4.115														
SGO_0603 response regulator	0.459	5.665	0.0023	0.0062	-0.916	5.074	0.0148	0.0537		4.419			-1.375	4.866	0.0031	0.0096		3.751				3.106		
SGO_0604 hydrolase, haloacid dehalogenase family/peptidyl-prolyl cis-trans isomerase, cyclophilin type	1.785	8.952	0.0001	0.0001	0.579	8.119	0.0028	0.0068	0.298	7.959	0.0102	0.0659	-1.206	8.588	0.0001	0.0000	-1.487	7.899	0.0001	0.0000	-0.281	7.730	0.0121	0.0124
SGO_0606 cysK; cysteine synthase A	-0.606	9.178	0.0004	0.0005	-0.319	9.299	0.0034	0.0086	-0.436	9.248	0.0006	0.0014	0.287	8.481	0.0032	0.0103	0.171	7.806	0.0019	0.0043	-0.116	8.560	0.0452	0.0978
SGO_0608 comFA; competence ComFA-like protein		4.069				4.069				4.069														
SGO_0610 ribosomal subunit interface protein	1.162	8.870	0.0022	0.0058	0.727	8.578	0.0016	0.0031	0.525	8.478	0.0148	0.1065	-0.434	8.621	0.0095	0.0444	-0.637	7.943	0.0136	0.0613	-0.202	8.303	0.1450	0.4632
SGO_0626 recX; Regulatory protein recX	-1.694	5.610	0.0047	0.0149	-1.293	5.901	0.0004	0.0005	-1.685	5.612	0.0032	0.0150	0.400	4.071	0.0495	0.3347	0.009	2.590			-0.391	4.073	0.1141	0.3401
SGO_0628 ymdC; 3''-aminoglycoside phosphotransferase-like protein (kanamycin kinase)		1.322				1.322				1.322														



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1179

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Test	Cutoff
***q*-Value**	**.005**
p-Value	

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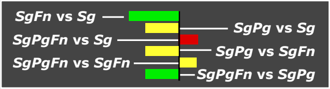
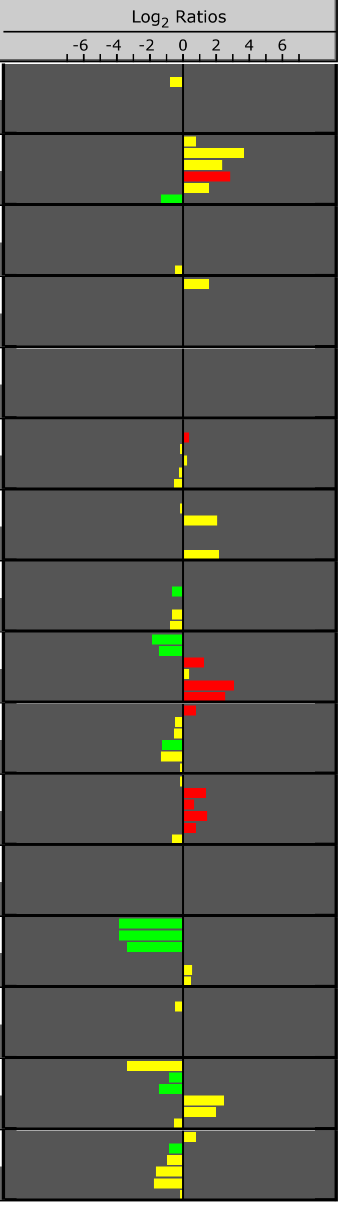
🟨	no	n/a	bars
🟩	yes	–	ratios, bars
▨	yes	+	*p*- , *q*-Values
▨	yes	–	



Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0629		3.342			-0.706	3.714	0.0791	0.3819		3.342				1.063								1.063		
	rumA-1; 23S rRNA (uracil-5-)-methyltransferase RumA																							
SGO_0631	0.803	3.099			3.710	6.407	0.0052	0.0151	2.433	5.206	0.0084	0.0510	2.906	5.932	0.0044	0.0161	1.630	4.171	0.0136	0.0613	-1.276	6.339	0.0012	0.0001
	alpha-glycerophosphate oxidase																							
SGO_0632						5.243				4.816				4.730				3.692			-0.428	5.532	0.0101	0.0091
	glpK; glycerol kinase																							
SGO_0635	1.553	3.976				2.000				2.000				3.039				2.429						
	hypothetical protein SGO_0635																							
SGO_0636		2.930				2.930				2.930														
	hypothetical protein SGO_0636																							
SGO_0639	0.072	8.074	0.0676	0.4110	0.402	8.251	0.0020	0.0044	-0.081	8.001	0.0655	0.5956	0.330	7.771	0.0060	0.0237	-0.153	6.917	0.0555	0.3511	-0.483	7.708	0.0168	0.0211
	valS; valyl-tRNA synthetase																							
SGO_0640		3.285			-0.116	4.207	0.1194	0.5995	2.061	4.870	0.0095	0.0595		2.612				3.162			2.176	4.306	0.0195	0.0266
	modification methylase																							
SGO_0641	0.022	6.939	0.1313	0.8744	0.103	6.975	0.0807	0.3916	-0.590	6.661	0.0043	0.0221	0.081	6.473	0.0774	0.5594	-0.612	5.552	0.0071	0.0258	-0.693	6.206	0.0057	0.0032
	ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein protein																							
SGO_0642	-1.789	6.945	0.0020	0.0050	-1.357	7.044	0.0027	0.0063	1.284	8.338	0.0006	0.0014	0.432	5.530	0.0425	0.2821	3.073	6.884	0.0005	0.0003	2.641	7.544	0.0019	0.0003
	hypothetical protein SGO_0642																							
SGO_0643	0.835	5.351	0.0028	0.0078	-0.367	4.720	0.0490	0.2176	-0.469	4.323	0.0371	0.3127	-1.201	4.722	0.0021	0.0051	-1.303	3.846	0.0181	0.0853	-0.102	3.563	0.2074	0.7545
	cytosine-specific methyltransferase																							
SGO_0644	-0.099	5.966	0.0866	0.5505	1.368	6.862	0.0033	0.0081	0.731	6.424	0.0024	0.0102	1.467	6.326	0.0028	0.0083	0.830	5.269	0.0045	0.0138	-0.638	6.594	0.0262	0.0428
	hypothetical protein SGO_0644																							
SGO_0649		2.322				2.322				2.322														
	hypothetical protein SGO_0649																							
SGO_0652	-3.825	7.262	0.0001	0.0000	-3.768	7.285	0.0002	0.0001	-3.269	7.309	0.0001	0.0000	0.057	3.991	0.0810	0.5877	0.556	3.540	0.0164	0.0761	0.499	4.282	0.1697	0.5840
	hypothetical protein SGO_0652																							
SGO_0653		3.322			-0.400	4.660	0.0528	0.2379		3.322				3.420								3.420		
	conserved hypothetical protein of unknown function (DUF1027)																							
SGO_0654	-3.313	7.518	0.0183	0.0826	-0.815	8.095	0.0039	0.0102	-1.356	7.923	0.0011	0.0036	2.498	6.237	0.0141	0.0739	1.957	5.141	0.0205	0.1015	-0.541	6.872	0.0183	0.0237
	radical SAM enzyme, Cfr family																							
SGO_0656	0.786	6.720	0.0347	0.1846	-0.846	5.780	0.0012	0.0020	-0.917	5.799	0.0092	0.0574	-1.633	5.978	0.0164	0.0904	-1.703	5.379	0.0202	0.0985	-0.070	4.817	0.2354	0.8955
	trpB-2; tryptophan synthase, beta subunit																							



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1179

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Test	Cutoff
q-Value	.005
p-Value	

	Signif	Direction	Applies To
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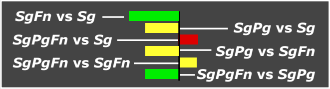

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Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

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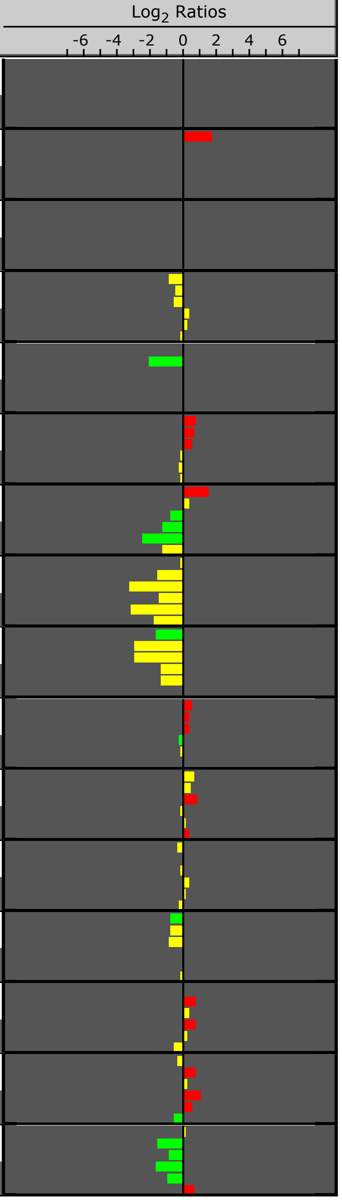
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0657 trpE; anthranilate synthase component I		1.322				1.322				1.322														
SGO_0662 trpB-1; tryptophan synthase, beta subunit	1.838	4.612	0.0045	0.0139		1.585				1.585				3.910				3.299						
SGO_0663 trpA-2; tryptophan synthase, alpha subunit		1.000				1.000				1.000														
SGO_0665 non-heme iron-containing ferritin	-0.806	10.143	0.0079	0.0292	-0.422	10.290	0.0218	0.0858	-0.506	10.265	0.0144	0.1037	0.384	9.366	0.0119	0.0585	0.300	8.721	0.0397	0.2299	-0.084	9.511	0.2049	0.7441
SGO_0667 rhodanese family protein		4.807			-1.961	5.142	0.0011	0.0019		4.807				2.360								2.360		
SGO_0669 typA; GTP-binding protein TypA	0.790	8.186	0.0019	0.0045	0.694	8.122	0.0002	0.0001	0.640	8.090	0.0006	0.0015	-0.097	7.966	0.0429	0.2855	-0.151	7.331	0.0325	0.1814	-0.054	7.888	0.0984	0.2826
SGO_0671 murD; UDP-N-acetylmuramoylalanine--D-glutamate ligase	1.635	7.976	0.0003	0.0004	0.437	7.176	0.0084	0.0267	-0.744	6.613	0.0005	0.0010	-1.199	7.584	0.0008	0.0012	-2.380	6.703	0.0004	0.0002	-1.181	6.393	0.0058	0.0033
SGO_0672 murG; undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase	-0.119	7.180	0.0814	0.5114	-1.494	6.719	0.0073	0.0224	-3.241	6.316	0.0161	0.1181	-1.375	6.114	0.0055	0.0216	-3.122	5.069	0.0180	0.0847	-1.747	4.555	0.1156	0.3479
SGO_0673 DivIB; cell division protein DivIB	-1.650	6.736	0.0020	0.0049	-2.932	6.419	0.0241	0.0961	-2.920	6.420	0.0136	0.0962	-1.282	4.462	0.0387	0.2526	-1.270	3.853	0.0431	0.2539	0.012	2.877		
SGO_0674 ftsA; cell division protein FtsA	0.569	9.226	0.0003	0.0004	0.359	9.105	0.0012	0.0021	0.429	9.145	0.0011	0.0037	-0.210	8.869	0.0037	0.0120	-0.140	8.291	0.0145	0.0659	0.070	8.796	0.0972	0.2773
SGO_0675 ftsZ; cell division protein FtsZ	0.657	9.878	0.0130	0.0548	0.507	9.775	0.0084	0.0266	0.860	9.992	0.0013	0.0044	-0.149	9.573	0.0515	0.3515	0.204	9.139	0.0478	0.2859	0.353	9.672	0.0028	0.0006
SGO_0676 conserved hypothetical protein TIGR00044	-0.268	5.946	0.0808	0.5048	0.129	6.116	0.1080	0.5380	-0.086	5.997	0.0553	0.4930	0.397	5.507	0.0465	0.3128	0.182	4.768	0.0997	0.6987	-0.215	5.555	0.0878	0.2400
SGO_0677 ylmF protein	-0.741	8.345	0.0045	0.0138	-0.679	8.372	0.0077	0.0236	-0.787	8.346	0.0071	0.0406	0.062	7.443	0.0778	0.5626	-0.046	6.798	0.1359	0.9911	-0.108	7.445	0.2139	0.7877
SGO_0680 cell division protein DivIVA	0.018	8.598	0.1210	0.7945	0.819	9.042	0.0017	0.0035	0.360	8.769	0.0084	0.0506	0.801	8.548	0.0049	0.0186	0.341	7.668	0.0356	0.2039	-0.460	8.674	0.0226	0.0338
SGO_0681 ileS; isoleucyl-tRNA synthetase	-0.268	8.346	0.0217	0.1021	0.809	8.932	0.0014	0.0026	0.282	8.622	0.0122	0.0830	1.077	8.323	0.0001	0.0000	0.551	7.377	0.0007	0.0008	-0.526	8.524	0.0026	0.0005
SGO_0684 hypothetical protein SGO_0684	0.170	8.754	0.0141	0.0608	-1.462	8.112	0.0000	0.0000	-0.754	8.337	0.0001	0.0000	-1.632	7.728	0.0004	0.0004	-0.924	7.324	0.0010	0.0012	0.708	7.087	0.0016	0.0002



● Show detected proteins only
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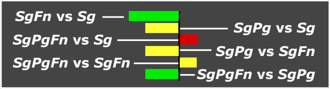
ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
🟨	no	n/a	bars
🟩	yes	–	ratios, bars
▨	yes	+	*p*- , *q*-Values
▨	yes	–	



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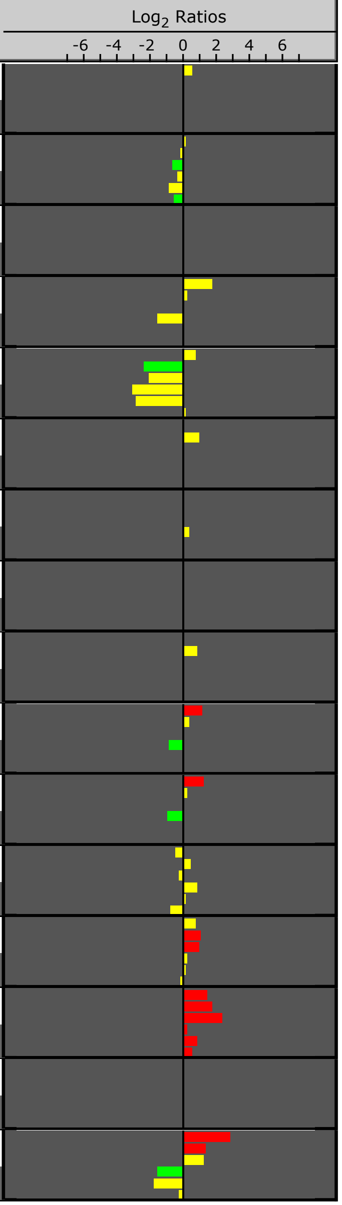
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0685 MutT/nudix family protein	0.646	3.529				2.170				2.170				2.302				1.692						
SGO_0688 ATP dependent Clp protease, ATP-binding subunit, ClpE	0.228	8.363	0.0550	0.3181	-0.104	8.168	0.0159	0.0586	-0.604	7.948	0.0002	0.0003	-0.332	7.804	0.0336	0.2103	-0.832	6.996	0.0118	0.0511	-0.500	7.374	0.0031	0.0007
SGO_0689 hypothetical protein SGO_0689		3.170				3.170				3.170														
SGO_0690 folD; methenyltetrahydrofolate cyclohydrolase	1.809	5.251	0.0084	0.0320	0.338	3.866	0.1779	0.9520		3.260			-1.471	4.553	0.0349	0.2212		3.709				1.807		
SGO_0693 xseA; exodeoxyribonuclease VII, large subunit	0.753	6.673	0.0237	0.1130	-2.268	5.513	0.0024	0.0053	-2.019	5.369	0.0151	0.1091	-3.021	5.697	0.0055	0.0215	-2.773	4.999	0.0401	0.2338	0.248	3.226	0.2508	0.9789
SGO_0694 xseB; exodeoxyribonuclease VII, small subunit		3.248			0.972	4.814				3.248				3.707								3.707		
SGO_0695 geranyltranstransferase		2.931				3.321							0.389	3.626				1.807				2.807		
SGO_0696 hemolysin-like protein		3.029				3.029				3.029														
SGO_0697 transcription regulator		2.339			0.936	3.253	0.0636	0.2947		2.339				1.648								1.648		
SGO_0698 recN; DNA repair protein RecN	1.171	6.257	0.0039	0.0118	0.402	5.779	0.0587	0.2686		4.604			-0.769	5.857	0.0019	0.0043		4.580				4.421		
SGO_0699 Serine/threonine protein phosphatase	1.280	5.382	0.0018	0.0043	0.342	4.783	0.0207	0.0805		3.609			-0.938	4.974	0.0023	0.0060		3.759				3.426		
SGO_0700 DegV family protein	-0.380	5.870	0.0479	0.2708	0.522	6.310	0.0140	0.0498	-0.170	5.972	0.0741	0.6885	0.903	5.663	0.0060	0.0237	0.210	4.677	0.0820	0.5588	-0.692	5.746	0.0354	0.0673
SGO_0701 hup; DNA-binding histone-like protein HU	0.805	12.498	0.0064	0.0221	1.056	12.649	0.0002	0.0001	0.991	12.614	0.0019	0.0078	0.251	12.458	0.0282	0.1725	0.186	11.819	0.0600	0.3839	-0.065	12.543	0.1866	0.6611
SGO_0704 gpmA; 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	1.491	10.896	0.0009	0.0016	1.791	11.120	0.0004	0.0004	2.431	11.636	0.0001	0.0001	0.300	11.092	0.0038	0.0127	0.940	10.868	0.0004	0.0002	0.640	11.588	0.0012	0.0001
SGO_0705 Protein of unknown function (DUF1250) superfamily		1.807				1.807				1.807														
SGO_0706 phoH-like protein	2.946	6.245	0.0001	0.0001	1.431	5.021	0.0017	0.0035	1.279	4.295	0.0196	0.1513	-1.515	5.980	0.0001	0.0000	-1.667	5.147	0.0054	0.0186	-0.152	4.568	0.0575	0.1368



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ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

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🟥	yes	+	*p*- , *q*-Values
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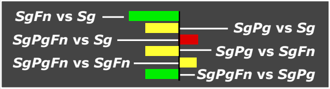

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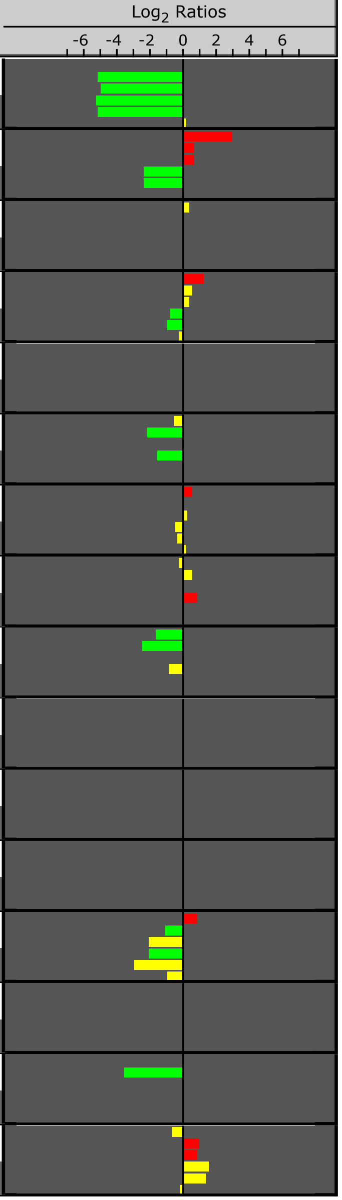
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0707 LPXTG cell wall surface protein	0.131	9.804	0.0405	0.2218	-5.103	8.777	0.0000	0.0000	-4.949	8.783	0.0000	0.0000	-5.234	8.398	0.0005	0.0005	-5.080	7.793	0.0006	0.0005	0.154	4.307	0.1982	0.7097
SGO_0708 ald; alanine dehydrogenase	3.041	11.420	0.0000	0.0000	0.702	9.607	0.0002	0.0001	0.711	9.617	0.0018	0.0071	-2.339	11.001	0.0000	0.0000	-2.330	10.393	0.0001	0.0000	0.009	9.410	0.2272	0.8553
SGO_0711 conserved hypothetical protein TIGR00043	0.408	4.363				3.145				3.145				3.039				2.429						
SGO_0713 sgg; GTP-binding protein Era	1.330	7.661	0.0001	0.0001	0.586	7.177	0.0059	0.0173	0.405	7.070	0.0056	0.0304	-0.744	7.343	0.0012	0.0024	-0.925	6.666	0.0007	0.0007	-0.181	6.841	0.0893	0.2463
SGO_0715 mutM; formamidopyrimidine-DNA glycosylase		2.322			-0.001	3.321				2.322				1.807								1.807		
SGO_0719 rnr; ribonuclease R	-0.545	6.065	0.0077	0.0282	-2.061	5.620	0.0009	0.0013		5.311			-1.516	4.686	0.0013	0.0029		3.644				2.735		
SGO_0721 abpB-like dipeptidase lipoprotein	0.551	5.573	0.0013	0.0026	0.112	5.337	0.0947	0.4647	0.287	5.501	0.0435	0.3781	-0.439	5.111	0.0072	0.0300	-0.265	4.636	0.1044	0.7373	0.174	5.042	0.1577	0.5139
SGO_0722 tehB; tellurite resistance protein TehB	-0.229	5.726	0.0706	0.4330	0.624	6.153	0.0651	0.3027		4.921			0.853	5.475	0.0002	0.0001		3.376				4.839		
SGO_0724 dipeptidase	-1.628	6.596	0.0007	0.0011	-2.408	6.437	0.0004	0.0003		6.186			-0.780	4.723	0.0077	0.0334		3.454				3.275		
SGO_0728 ABC transporter, ATP-binding protein SP1653		2.000				2.000				2.000														
SGO_0729 ABC transporter permease protein		3.022				3.022				3.022														
SGO_0731 RRF2 family protein		4.120				4.120				4.120														
SGO_0736 hprK; HPr(Ser) kinase/phosphatase	0.917	6.466	0.0009	0.0015	-1.037	5.520	0.0033	0.0081	-1.951	5.113	0.0111	0.0738	-1.954	5.676	0.0005	0.0005	-2.868	4.823	0.0101	0.0416	-0.914	3.749	0.0956	0.2697
SGO_0737 lgt; prolipoprotein diacylglyceryl transferase		4.348				4.348				4.348														
SGO_0738 Bacterial protein of unknown function (DUF948) family		6.938			-3.482	7.062	0.0005	0.0006		6.938				2.941								2.941		
SGO_0739 hypothetical protein SGO_0739	-0.567	4.807	0.0334	0.1759	0.984	5.964	0.0021	0.0046	0.854	5.875	0.0006	0.0015	1.551	5.087	0.0174	0.0968	1.421	4.361	0.0109	0.0466	-0.130	5.795	0.0902	0.2502



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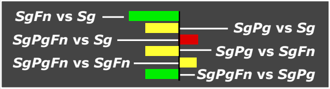
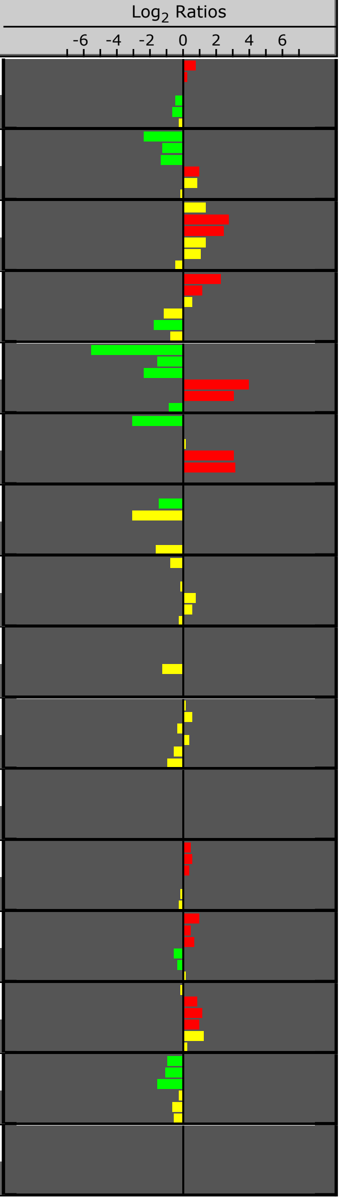


Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0742 peptidase, U32 family	0.753	6.494	0.0004	0.0005	0.310	6.232	0.0039	0.0104	0.136	5.701	0.0463	0.4048	-0.443	6.102	0.0000	0.0000	-0.616	5.103	0.0023	0.0056	-0.174	5.394	0.0184	0.0243
SGO_0743 peptidase, U32 family	-2.254	7.696	0.0001	0.0000	-1.241	7.933	0.0005	0.0007	-1.304	7.921	0.0007	0.0019	1.012	6.258	0.0031	0.0096	0.950	5.620	0.0085	0.0330	-0.062	6.660	0.2296	0.8666
SGO_0745 hypothetical protein SGO_0745	1.409	5.643	0.0205	0.0948	2.842	7.443	0.0002	0.0001	2.462	7.139	0.0015	0.0057	1.433	6.982	0.0106	0.0504	1.053	6.078	0.0389	0.2241	-0.380	7.571	0.0455	0.0988
SGO_0749 glutathione reductase	2.313	7.691	0.0032	0.0094	1.249	6.844	0.0018	0.0038	0.577	6.407	0.0069	0.0395	-1.065	7.467	0.0068	0.0278	-1.737	6.673	0.0041	0.0126	-0.672	6.517	0.0067	0.0042
SGO_0750 efflux transporter, RND family, MFP subunit subfamily	-5.485	10.400	0.0005	0.0007	-1.521	10.797	0.0013	0.0023	-2.349	10.625	0.0005	0.0012	3.963	8.415	0.0001	0.0000	3.135	7.045	0.0004	0.0002	-0.828	8.970	0.0037	0.0010
SGO_0751 ABC transporter, ATP-binding protein SP0786	-3.035	7.519	0.0002	0.0002	0.115	8.412	0.0791	0.3822	0.176	8.439	0.0142	0.1021	3.150	7.118	0.0009	0.0015	3.211	6.554	0.0004	0.0003	0.061	7.986	0.1979	0.7045
SGO_0752 ABC transporter, ATP-binding protein		7.159			-1.394	7.621	0.0017	0.0034	-2.977	7.247	0.0130	0.0914		5.241				2.046			-1.583	5.463	0.0073	0.0049
SGO_0753 lysS; lysyl-tRNA synthetase	-0.738	8.826	0.0084	0.0316	0.038	9.150	0.1267	0.6427	-0.113	9.075	0.0303	0.2481	0.776	8.336	0.0061	0.0244	0.624	7.633	0.0121	0.0526	-0.152	8.582	0.0514	0.1174
SGO_0754 phosphoglycerate mutase family protein		3.038				1.835							-1.203	3.045				1.914				1.322		
SGO_0755 regulatory protein	0.217	5.320	0.0517	0.2947	0.647	5.566	0.0123	0.0424	-0.282	4.691	0.0355	0.2972	0.430	5.150	0.0253	0.1495	-0.500	3.740	0.0565	0.3592	-0.930	4.679	0.0843	0.2256
SGO_0757 peptidase, U32 family		6.945				6.945				6.945														
SGO_0760 ppc; phosphoenolpyruvate carboxylase	0.523	9.217	0.0019	0.0046	0.615	9.269	0.0000	0.0000	0.431	9.163	0.0019	0.0079	0.092	8.988	0.0338	0.2120	-0.093	8.287	0.0546	0.3434	-0.184	8.944	0.0275	0.0469
SGO_0761 tuf; translation elongation factor Tu	0.986	13.763	0.0007	0.0011	0.462	13.435	0.0010	0.0017	0.656	13.549	0.0001	0.0000	-0.524	13.422	0.0022	0.0058	-0.330	12.893	0.0045	0.0138	0.194	13.234	0.0122	0.0126
SGO_0762 tpiA; triosephosphate isomerase	-0.128	10.618	0.0596	0.3510	0.868	11.183	0.0047	0.0131	1.175	11.402	0.0039	0.0197	0.996	10.630	0.0038	0.0129	1.303	10.244	0.0054	0.0182	0.307	11.217	0.0902	0.2505
SGO_0763 murA-1; UDP-N-acetylglucosamine 1-carboxyvinyltransferase	-0.883	8.224	0.0007	0.0010	-1.037	8.173	0.0008	0.0011	-1.499	8.053	0.0010	0.0030	-0.153	7.128	0.0151	0.0803	-0.615	6.340	0.0148	0.0673	-0.462	6.864	0.0656	0.1614
SGO_0765 endA; DNA-entry nuclease		4.959				4.959				4.959														



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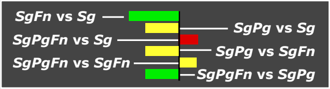

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Streptococcus gordonii

Hackett Laboratory UW

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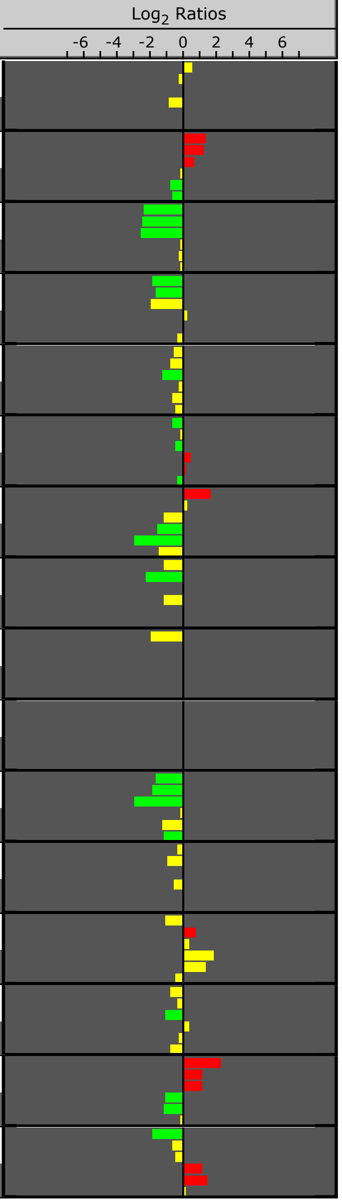
	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0767	0.649	5.851	0.0207	0.0965	-0.180	5.377	0.0674	0.3152		4.456			-0.829	5.279	0.0144	0.0755		4.038				3.781		
	transport protein																							
SGO_0771	1.357	8.365	0.0016	0.0037	1.279	8.306	0.0013	0.0023	0.699	7.925	0.0046	0.0243	-0.078	8.325	0.0501	0.3396	-0.658	7.462	0.0020	0.0046	-0.580	8.022	0.0012	0.0001
	pepq; proline dipeptidase																							
SGO_0773	-2.320	10.237	0.0002	0.0001	-2.406	10.223	0.0002	0.0001	-2.492	10.209	0.0001	0.0001	-0.087	8.100	0.0601	0.4177	-0.172	7.448	0.0253	0.1330	-0.086	8.013	0.1168	0.3541
	ccpA; catabolite control protein A																							
SGO_0774	-1.831	7.074	0.0009	0.0018	-1.574	7.142	0.0017	0.0036	-1.853	6.904	0.0142	0.1017	0.257	5.516	0.0357	0.2284	-0.022	4.332	0.1048	0.7413	-0.279	5.141	0.1579	0.5182
	glycosyl transferase, group 1 family protein																							
SGO_0775	-0.533	6.511	0.0127	0.0537	-0.719	6.433	0.0052	0.0149	-1.162	6.276	0.0009	0.0028	-0.186	5.622	0.0562	0.3873	-0.629	4.816	0.0103	0.0434	-0.443	5.309	0.0248	0.0395
	glycosyl transferase, group 1																							
SGO_0778	-0.632	9.020	0.0003	0.0002	-0.132	9.237	0.0068	0.0204	-0.413	9.110	0.0003	0.0004	0.500	8.428	0.0005	0.0005	0.220	7.659	0.0011	0.0016	-0.280	8.523	0.0045	0.0014
	thrS; threonyl-tRNA synthetase																							
SGO_0779	1.732	7.769	0.0006	0.0008	0.258	6.808	0.0709	0.3336	-1.147	6.246	0.0082	0.0488	-1.473	7.317	0.0007	0.0008	-2.878	6.457	0.0005	0.0004	-1.405	5.902	0.0158	0.0186
	response regulator																							
SGO_0780	-1.119	5.893	0.0058	0.0196	-2.189	5.620	0.0017	0.0034		5.337			-1.070	4.283	0.0082	0.0369		3.126				2.617		
	histidine kinase																							
SGO_0781	-1.851	5.277	0.0213	0.0999		5.091				5.091				1.717				1.107						
	vicX; Zn-dependent hydrolase (beta-lactamase superfamily)																							
SGO_0782		3.665				3.665				3.665														
	Protein of unknown function (DUF454) family																							
SGO_0784	-1.644	8.363	0.0015	0.0033	-1.759	8.327	0.0011	0.0018	-2.876	8.139	0.0005	0.0010	-0.115	6.752	0.0695	0.4919	-1.232	5.715	0.0055	0.0190	-1.117	6.222	0.0007	0.0000
	smc; chromosome segregation protein SMC																							
SGO_0785	-0.328	4.940	0.0462	0.2608	-0.875	4.804	0.0299	0.1232		4.457			-0.548	3.363				2.000				2.063		
	Cof family protein																							
SGO_0786	-1.050	4.921	0.0257	0.1273	0.800	6.061	0.0010	0.0015	0.377	5.816	0.0142	0.1012	1.850	5.077	0.0050	0.0193	1.427	4.116	0.0282	0.1522	-0.423	5.701	0.0238	0.0369
	Cof family protein																							
SGO_0787	-0.721	7.421	0.0055	0.0182	-0.273	7.598	0.0142	0.0509	-0.953	7.335	0.0016	0.0064	0.448	6.741	0.0087	0.0402	-0.232	5.787	0.0490	0.2959	-0.680	6.644	0.0078	0.0056
	ftsY; cell division protein FtsY																							
SGO_0788	2.261	8.231	0.0012	0.0024	1.244	7.437	0.0003	0.0002	1.161	7.380	0.0002	0.0002	-1.017	8.020	0.0028	0.0083	-1.100	7.383	0.0027	0.0071	-0.083	7.373	0.0165	0.0200
	zwf; glucose-6-phosphate 1-dehydrogenase																							
SGO_0792	-1.830	6.869	0.0014	0.0031	-0.585	7.246	0.0105	0.0350	-0.372	7.330	0.0097	0.0613	1.245	5.922	0.0025	0.0071	1.458	5.456	0.0009	0.0011	0.213	6.515	0.0667	0.1684
	hypothetical protein SGO_0792																							



● Show detected proteins only
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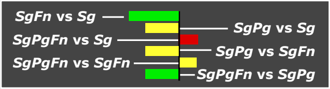
ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
🟨	no	n/a	bars
🟩	yes	–	ratios, bars
🟥	yes	+	*p*- , *q*-Values
🟩	yes	–	

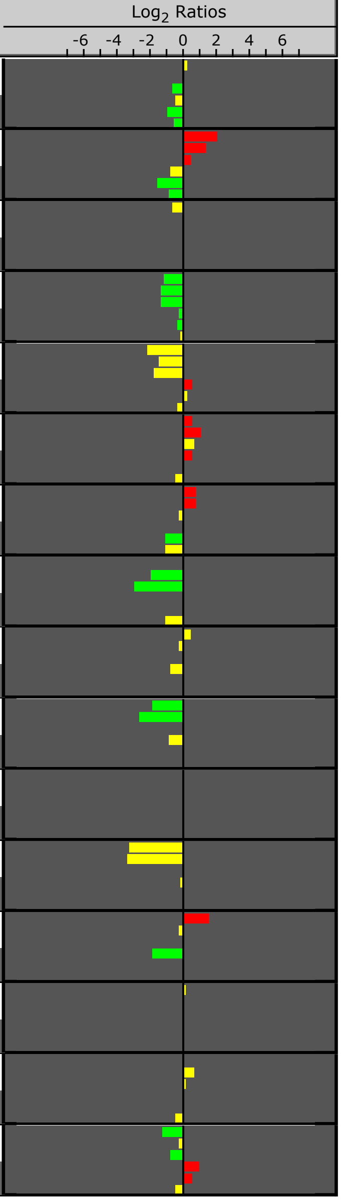


Hendrickson *et al.*

Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

		SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0794	metallo-beta-lactamase family protein	0.304	7.978	0.0206	0.0955	-0.049	7.789	0.1049	0.5188	-0.592	7.547	0.0015	0.0055	-0.353	7.442	0.0119	0.0588	-0.896	6.619	0.0029	0.0081	-0.543	7.003	0.0048	0.0017
SGO_0795	tributyrin esterase	2.063	5.813	0.0022	0.0058	1.371	5.264	0.0002	0.0001	0.525	4.707	0.0008	0.0022	-0.692	5.681	0.0081	0.0360	-1.539	4.805	0.0031	0.0086	-0.846	4.916	0.0016	0.0002
SGO_0797	RocB protein, putative	-0.613	4.048				3.322				3.322				2.196				1.585						
SGO_0798	ABC transporter, ATP-binding protein SP1381	-1.060	7.828	0.0009	0.0017	-1.256	7.768	0.0009	0.0013	-1.346	7.742	0.0005	0.0011	-0.196	6.593	0.0045	0.0162	-0.286	5.940	0.0007	0.0007	-0.090	6.447	0.0451	0.0973
SGO_0800	polysaccharide deacetylase family protein	-2.065	6.313	0.0072	0.0261	-1.446	6.450	0.0120	0.0409	-1.735	6.211	0.0329	0.2721	0.619	4.705	0.0019	0.0047	0.330	3.454	0.0202	0.0988	-0.289	4.477	0.0893	0.2470
SGO_0801	hom; homoserine dehydrogenase	0.572	8.591	0.0014	0.0028	1.139	8.955	0.0003	0.0002	0.695	8.684	0.0080	0.0468	0.567	8.645	0.0005	0.0004	0.123	7.802	0.0693	0.4577	-0.444	8.709	0.0357	0.0679
SGO_0802	thrB; homoserine kinase	0.760	6.777	0.0003	0.0003	0.767	6.782	0.0003	0.0002	-0.222	6.252	0.0335	0.2779	0.008	6.597	0.0826	0.6016	-0.982	5.582	0.0015	0.0031	-0.990	6.198	0.0056	0.0030
SGO_0803	hypothetical protein SGO_0803		7.539			-1.866	7.889	0.0002	0.0001	-2.851	7.738	0.0002	0.0002		5.159				3.654			-0.985	5.780	0.0183	0.0238
SGO_0804	murB; UDP-N-acetylenolpyruvoylglucosamine reductase	0.475	5.314	0.0954	0.6141	-0.227	4.969	0.0921	0.4499		4.183			-0.701	4.607	0.0102	0.0483		3.311				3.205		
SGO_0805	potA; spermidine/putrescine ABC transporter, ATP-binding subunit	-1.847	6.699	0.0005	0.0007	-2.598	6.570	0.0004	0.0005		6.344			-0.751	4.677	0.0092	0.0427		3.382				3.272		
SGO_0806	potB; spermidine/putrescine ABC transporter, permease protein		4.271				4.271				4.271														
SGO_0808	potD; spermidine/putrescine ABC transporter	-3.175	6.779	0.0410	0.2259	-3.301	6.773	0.0501	0.2239		6.705			-0.125	2.871				1.322				1.807		
SGO_0812	hypothetical protein SGO_0812	1.605	6.051	0.0014	0.0029	-0.235	4.916	0.0150	0.0547		4.031			-1.840	5.482	0.0012	0.0023		4.519				3.278		
SGO_0813	fructose-bisphosphatase	0.162	3.519	0.0963	0.6216		1.807				1.807				2.480				1.869						
SGO_0814	aminotransferase, class-V		2.170			0.665	3.541			0.226	3.287				2.322				1.272			-0.439	3.119		
SGO_0815	thiI; thiamine biosynthesis protein ThiI	-1.223	7.201	0.0008	0.0014	-0.231	7.574	0.0182	0.0693	-0.667	7.389	0.0012	0.0041	0.991	6.530	0.0013	0.0026	0.556	5.645	0.0041	0.0124	-0.436	6.739	0.0128	0.0137



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ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
q-Value	.005
p-Value	

	Signif	Direction	Applies To
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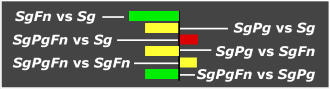
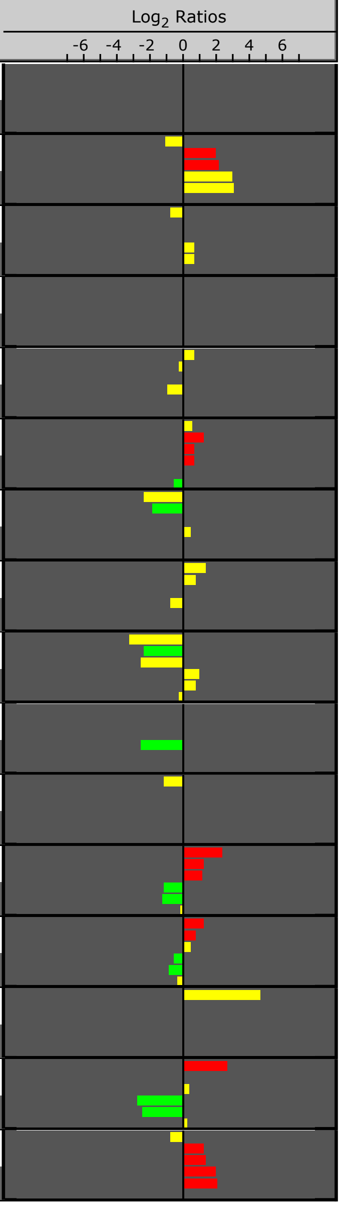
🟨	no	n/a	bars
🟩	yes	−	ratios, bars
	yes	+	*p*- , *q*-Values
	yes	−	



Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0817 hypothetical protein SGO_0817		3.556				3.556				3.556														
SGO_0818 rplU; ribosomal protein L21	-0.991	7.586	0.0392	0.2131	2.010	9.582	0.0005	0.0006	2.156	9.701	0.0004	0.0007	3.001	8.832	0.0110	0.0524	3.147	8.361	0.0134	0.0601	0.146	9.821	0.0805	0.2119
SGO_0820 rpmA; ribosomal protein L27	-0.660	7.245	0.0675	0.4089	0.025	7.846	0.1704	0.8971	0.074	7.887	0.0933	0.8915	0.685	6.704	0.0229	0.1335	0.734	6.156	0.0515	0.3181	0.049	7.356	0.1989	0.7149
SGO_0822 lipoprotein, putative		3.621				3.621				3.621														
SGO_0823 Cof family protein	0.742	4.129	0.0368	0.1974	-0.165	2.920				2.000			-0.907	3.580	0.0282	0.1720		2.630				1.322		
SGO_0824 lepA; GTP-binding protein LepA	0.590	7.350	0.0082	0.0310	1.254	7.781	0.0010	0.0017	0.727	7.433	0.0035	0.0168	0.663	7.458	0.0000	0.0000	0.136	6.548	0.0078	0.0297	-0.527	7.513	0.0019	0.0003
SGO_0825 lipoprotein, putative	-2.331	6.193	0.0250	0.1222	-1.794	6.419	0.0019	0.0042		6.057			0.536	4.160	0.0096	0.0448		1.585				3.732		
SGO_0830 uvrC; excinuclease ABC, C subunit	1.409	3.045	0.0116	0.0479	0.755	2.710	0.0282	0.1150		1.832			-0.654	2.427				1.107				1.063		
SGO_0832 hypothetical protein SGO_0832	-3.238	6.446	0.0184	0.0838	-2.252	6.649	0.0010	0.0016	-2.454	6.497	0.0130	0.0915	0.985	3.942	0.0356	0.2272	0.783	2.444			-0.202	4.135	0.1685	0.5790
SGO_0833 phosphoesterase-related gene		5.529				3.120							-2.479	5.265	0.0007	0.0009		4.405				2.606		
SGO_0834 hypothetical protein SGO_0834	-1.079	4.671	0.0550	0.3178		4.377				4.377				1.717				1.107						
SGO_0835 nitroreductase	2.378	8.920	0.0001	0.0000	1.275	8.064	0.0004	0.0004	1.176	8.008	0.0025	0.0110	-1.103	8.702	0.0000	0.0000	-1.203	8.066	0.0008	0.0008	-0.100	8.008	0.1676	0.5747
SGO_0836 pepV; dipeptidase PepV	1.291	9.572	0.0004	0.0004	0.793	9.237	0.0004	0.0004	0.471	9.046	0.0053	0.0283	-0.497	9.336	0.0013	0.0026	-0.820	8.604	0.0015	0.0029	-0.322	8.917	0.0227	0.0344
SGO_0841 oxidoreductase	4.736	7.573	0.0111	0.0444		1.807				1.807				7.033				6.422						
SGO_0842 rhodanese family protein	2.744	6.552	0.0028	0.0078	0.073	4.710	0.1825	0.9811	0.388	4.835	0.0615	0.5534	-2.671	6.038	0.0025	0.0072	-2.356	5.463	0.0027	0.0073	0.314	4.316	0.1271	0.3929
SGO_0848 rpmE; ribosomal protein L31	-0.727	7.350	0.0071	0.0254	1.269	8.420	0.0000	0.0000	1.395	8.511	0.0001	0.0001	1.996	7.739	0.0004	0.0003	2.122	7.230	0.0005	0.0003	0.126	8.471	0.0199	0.0280



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ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

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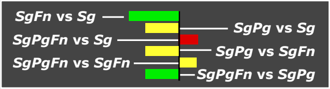

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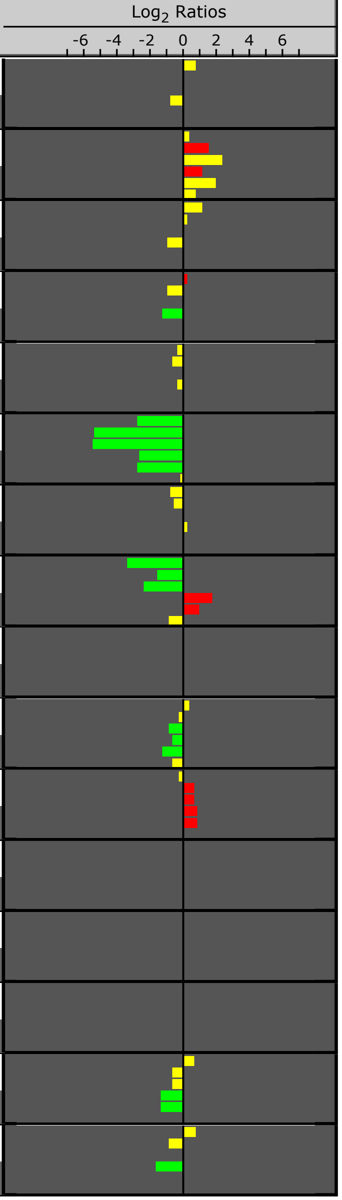
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory **UW**

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	Description	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0849	DHH subfamily 1 protein	0.752	6.415	0.0126	0.0528	0.055	6.011	0.1464	0.7609		4.979			-0.697	5.926	0.0132	0.0684		4.626				4.529		
SGO_0850	flavodoxin	0.386	6.736	0.0152	0.0673	1.562	7.506	0.0004	0.0004	2.383	8.256	0.0063	0.0348	1.176	7.105	0.0011	0.0020	1.997	7.200	0.0101	0.0422	0.821	8.115	0.0532	0.1238
SGO_0851	putative permease	1.157	4.915	0.0416	0.2304	0.281	4.984	0.1267	0.6444		3.898			-0.875	4.486	0.0156	0.0837		2.807				3.551		
SGO_0852	TPR domain protein	0.346	5.338	0.0035	0.0103	-0.862	4.813	0.0092	0.0300		4.156			-1.209	4.527	0.0025	0.0071		3.376				2.848		
SGO_0853	budA; alpha-acetolactate decarboxylase	-0.298	5.096	0.0590	0.3462	-0.638	4.965	0.0412	0.1775		4.288			-0.340	4.208	0.0129	0.0661		2.751				3.036		
SGO_0854	cshA; surface-associated protein CshA	-2.737	9.701	0.0002	0.0001	-5.332	9.527	0.0001	0.0000	-5.415	9.525	0.0001	0.0000	-2.595	6.521	0.0044	0.0160	-2.678	5.896	0.0048	0.0152	-0.083	4.618	0.1668	0.5698
SGO_0855	fbpA; fibronectin-binding protein A	-0.735	5.591	0.0050	0.0161	-0.453	5.699	0.0089	0.0287		4.908			0.282	4.813	0.0271	0.1633		3.061				3.941		
SGO_0856	ABC transporter, substrate binding protein	-3.308	8.206	0.0001	0.0000	-1.459	8.517	0.0003	0.0003	-2.301	8.333	0.0001	0.0000	1.850	6.458	0.0011	0.0021	1.007	5.228	0.0013	0.0022	-0.843	6.741	0.0099	0.0084
SGO_0858	ABC transporter, ATP-binding protein		3.727				3.727				3.727														
SGO_0859	pheS; phenylalanyl-tRNA synthetase, alpha subunit	0.405	7.841	0.0093	0.0357	-0.216	7.523	0.0440	0.1920	-0.807	7.283	0.0037	0.0179	-0.621	7.234	0.0007	0.0010	-1.212	6.420	0.0006	0.0004	-0.591	6.628	0.0101	0.0091
SGO_0861	pheT; phenylalanyl-tRNA synthetase, beta subunit	-0.152	8.497	0.0448	0.2521	0.743	8.986	0.0008	0.0012	0.727	8.977	0.0010	0.0033	0.895	8.418	0.0007	0.0009	0.878	7.798	0.0013	0.0023	-0.016	8.788	0.2193	0.8146
SGO_0862	hypothetical protein SGO_0862		3.475				3.475				3.475														
SGO_0868	hypothetical protein SGO_0868		1.058				1.058				1.058														
SGO_0877	permease domain protein		1.585				1.585				1.585														
SGO_0885	cobyric acid synthase	0.700	6.064	0.0149	0.0652	-0.639	5.374	0.0115	0.0390	-0.567	5.403	0.0086	0.0525	-1.339	5.333	0.0042	0.0146	-1.267	4.744	0.0049	0.0163	0.072	4.529	0.1023	0.2951
SGO_0886	Mur ligase family protein	0.806	5.586	0.0240	0.1154	-0.777	4.851	0.0434	0.1880		4.225			-1.583	4.790	0.0009	0.0015		3.751				2.830		



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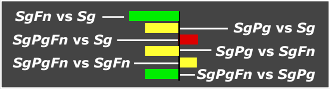


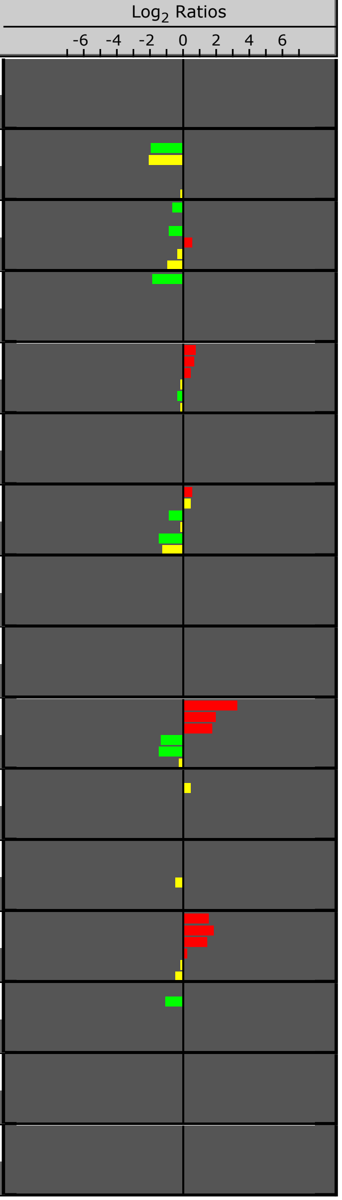
Hendrickson *et al.*

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0887 conserved hypothetical protein TIGR00159		7.303				7.303				7.303														
SGO_0888 hypothetical protein SGO_0888		5.203			-1.894	5.554	0.0025	0.0055	-2.014	5.369	0.0175	0.1316		2.830				1.046			-0.120	3.360	0.2049	0.7437
SGO_0889 glmM; phosphoglucosamine mutase	-0.553	6.939	0.0003	0.0003	0.013	7.195	0.1403	0.7211	-0.844	6.839	0.0020	0.0083	0.566	6.433	0.0003	0.0003	-0.291	5.387	0.0344	0.1939	-0.857	6.334	0.0094	0.0079
SGO_0890 LPXTG cell wall surface protein, collagen binding domain	-1.796	8.439	0.0006	0.0010		8.059				8.059				5.817				5.206						
SGO_0893 GTP-binding protein	0.773	7.832	0.0005	0.0008	0.666	7.769	0.0040	0.0106	0.522	7.678	0.0010	0.0033	-0.107	7.603	0.0440	0.2940	-0.251	6.921	0.0001	0.0000	-0.144	7.478	0.0694	0.1766
SGO_0899 putative hydrolase or acyltransferase		3.334				3.334				3.334														
SGO_0901 DNA-directed DNA polymerase III	0.594	6.466	0.0011	0.0021	0.470	6.395	0.0052	0.0150	-0.769	5.823	0.0046	0.0238	-0.125	6.162	0.0425	0.2819	-1.363	5.098	0.0016	0.0033	-1.239	5.624	0.0092	0.0073
SGO_0904 purR; galactose operon repressor GalR		1.058				1.058				1.058														
SGO_0905 lipoprotein, putative		4.857				4.857				4.857														
SGO_0906 leuA; 2-isopropylmalate synthase	3.270	8.067	0.0000	0.0000	1.999	6.978	0.0001	0.0000	1.830	6.859	0.0013	0.0047	-1.270	7.911	0.0000	0.0000	-1.439	7.258	0.0005	0.0004	-0.169	7.067	0.1085	0.3157
SGO_0907 leuB; 3-isopropylmalate dehydrogenase		2.828			0.546	3.597	0.0772	0.3701		2.828				1.807								1.807		
SGO_0909 leuC; 3-isopropylmalate dehydratase, large subunit		4.074				2.683							-0.372	4.027	0.0561	0.3851		2.951				2.170		
SGO_0911 hypothetical protein SGO_0911	1.606	7.986	0.0001	0.0000	1.860	8.180	0.0001	0.0000	1.485	7.903	0.0009	0.0027	0.254	8.195	0.0012	0.0024	-0.121	7.397	0.0554	0.3488	-0.375	8.145	0.0196	0.0271
SGO_0915 proV; ABC-type proline/glycine betaine transporter		4.909			-1.047	5.481	0.0012	0.0021		4.909				3.357								3.357		
SGO_0916 proWX; ABC transporter membrane-spanning permease		5.255				5.255				5.255														
SGO_0932 galK; galactokinase		2.845				2.845				2.845														



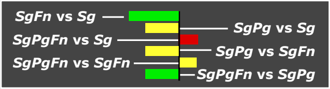
● Show detected proteins only
○ Show all proteins
☐ Filter by category:
ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

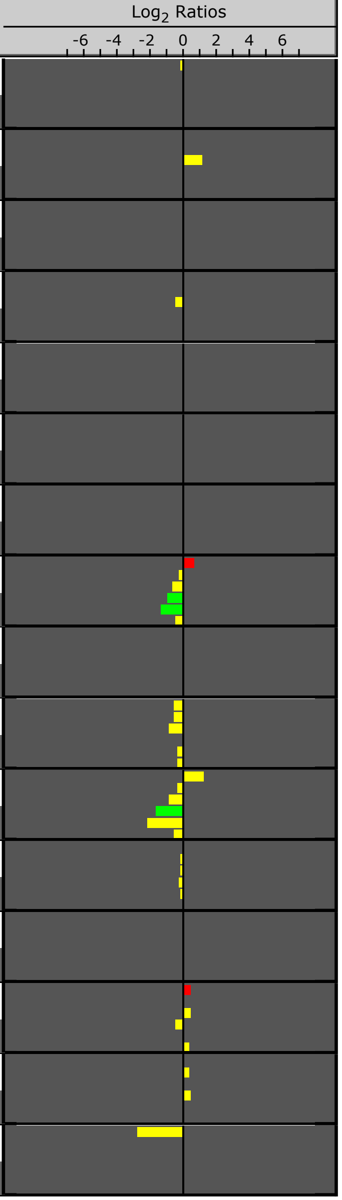
	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
🟨	no	n/a	bars
🟩	yes	−	ratios, bars
▨	yes	+	*p*- , *q*-Values
▨	yes	−	



Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0934 galE-2; UDP-glucose 4-epimerase	-0.121	3.967	0.0745	0.4594		2.459				2.459				2.829				2.218						
SGO_0936 phosphoenolpyruvate synthase, putative		2.036				2.036			1.188	3.105	0.0184	0.1408						1.046				1.657		
SGO_0938 Phosphatidylserine decarboxylase proenzyme 2										2.718								1.594				2.205		
SGO_0940 ppsA; phosphoenolpyruvate synthase		3.894				3.894			-0.447	4.331	0.0526	0.4634						1.272				1.883		
SGO_0941 hypothetical protein SGO_0941		1.322				1.322				1.322														
SGO_0942 zmpC; zinc metalloproteinase C		5.201				5.201				5.201														
SGO_0944 ABC transporter, ATP-binding protein		5.012				5.012				5.012														
SGO_0946 Deblocking aminopeptidase	0.714	7.288	0.0005	0.0007	-0.217	6.786	0.0285	0.1162	-0.622	6.632	0.0098	0.0625	-0.931	6.698	0.0008	0.0011	-1.336	5.975	0.0016	0.0033	-0.405	5.997	0.0811	0.2141
SGO_0948 pgdA; peptidoglycan N-acetylglucosamine deacetylase A	0.086	6.180	0.0837	0.5279		5.141				5.141				4.705				4.094						
SGO_0949 deaD; DEAD RNA helicase	-0.475	5.295	0.0377	0.2032	-0.476	5.268	0.0151	0.0552	-0.757	4.862	0.0284	0.2286	-0.001	4.522	0.1088	0.8182	-0.281	3.421	0.0875	0.6042	-0.280	3.985	0.0869	0.2354
SGO_0950 oxidoreductase	1.300	5.753	0.0324	0.1703	-0.275	4.609	0.1251	0.6319	-0.774	3.834			-1.575	5.402	0.0029	0.0089	-2.074	4.525	0.0255	0.1345	-0.499	3.856	0.1382	0.4363
SGO_0951 udk; uridine kinase	0.064	6.011	0.1114	0.7288	-0.138	5.905	0.0714	0.3362	-0.083	5.935	0.0662	0.6035	-0.202	5.426	0.0329	0.2049	-0.146	4.844	0.0608	0.3924	0.056	5.347	0.1726	0.5963
SGO_0953 endoribonuclease L-PSP, putative						5.155								4.642								4.642		
SGO_0954 ATP-binding protein	0.510	6.460	0.0041	0.0126	0.095	6.263	0.1169	0.5847	0.496	6.475	0.0164	0.1211	-0.415	6.016	0.0367	0.2361	-0.015	5.584	0.1274	0.9148	0.400	6.031	0.1104	0.3269
SGO_0955 transporter	-0.040	4.797	0.1102	0.7184	0.411	4.555	0.0759	0.3630		3.830			0.451	4.001	0.0127	0.0640		2.639				2.700		
SGO_0957 hypothetical protein SGO_0957	-2.699	5.625	0.0124	0.0518		5.518				5.518				1.302				0.692						



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ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
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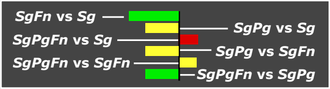

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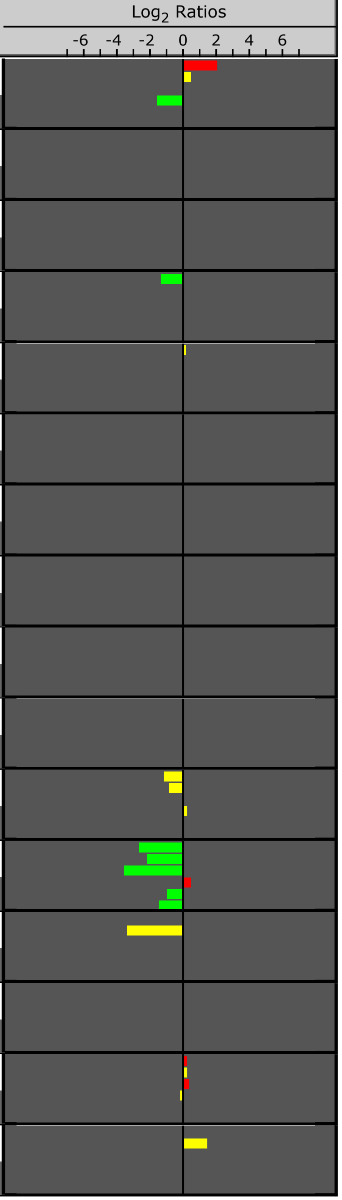
	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0959 copper homeostasis protein CutC	2.052	5.945	0.0046	0.0144	0.527	4.866	0.0492	0.2185		3.624			-1.525	5.534	0.0049	0.0184		4.499				3.560		
SGO_0961 ABC transporter, permease/ATP-binding protein		3.776				3.776				3.776														
SGO_0962 ABC transporter, permease/ATP-binding protein		1.841				1.841				1.841														
SGO_0966 hsa; streptococcal hemagglutinin	-1.271	6.593	0.0003	0.0003		6.093				6.093				4.307				3.696						
SGO_0969 nss; nucleotide sugar synthetase-like protein	0.191	3.585	0.0379	0.2044		2.934				2.934				1.611				1.000						
SGO_0971 asp1; accessory secretory protein		2.609				2.609				2.609														
SGO_0972 asp2; accessory sescretory protein		1.585				1.585				1.585														
SGO_0975 gtaA; glycosyl transferase, group 1 SP1758		3.272				3.272				3.272														
SGO_0979 degV family protein		3.279				3.279				3.279														
SGO_0980 transcriptional regulator, TetR family domain protein		0.643				0.643				0.643														
SGO_0981 comE operon protein 2 family	-1.139	4.303	0.0531	0.3053	-0.793	4.371	0.0772	0.3697		4.020			0.346	2.486				0.692				1.648		
SGO_0982 amino acid ABC transporter, amino acid-binding protein	-2.577	8.302	0.0002	0.0002	-2.052	8.392	0.0004	0.0003	-3.500	8.201	0.0002	0.0002	0.524	6.278	0.0049	0.0186	-0.924	4.987	0.0004	0.0002	-1.448	5.968	0.0050	0.0022
SGO_0983 amino acid ABC transporter, ATP-binding protein SP0709		5.795			-3.281	5.868	0.0096	0.0314		5.795				1.000								1.000		
SGO_0986 hypothetical protein SGO_0986		3.992				3.992				3.992														
SGO_0987 metK; S-adenosylmethionine synthetase	0.344	7.742	0.0021	0.0052	0.274	7.714	0.0366	0.1563	0.420	7.786	0.0008	0.0021	-0.070	7.365	0.0982	0.7269	0.076	6.818	0.0052	0.0176	0.146	7.404	0.1271	0.3950
SGO_0991 hypothetical protein SGO_0991		6.865			1.525	8.820				6.865				7.877								7.877		



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ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	.005
p-Value	

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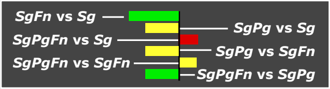


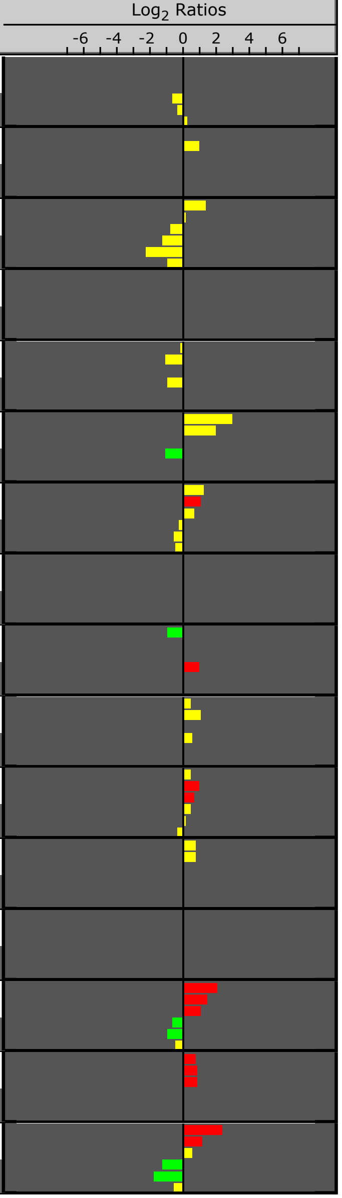
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory **UW**

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_0993 GTP-binding protein HflX		3.772				2.098				2.396			-0.644	3.652	0.0469	0.3163	-0.346	3.118	0.0694	0.4602	0.298	2.742		
SGO_0994 hypothetical protein SGO_0994		2.718			0.996	4.243	0.0136	0.0479		2.718				3.114								3.114		
SGO_0995 metallo-beta-lactamase superfamily protein	1.419	6.066	0.0067	0.0234	0.171	5.395	0.1330	0.6801	-0.740	4.614	0.0526	0.4645	-1.248	5.629	0.0117	0.0566	-2.159	4.605	0.0271	0.1436	-0.910	4.300	0.1485	0.4762
SGO_0996 oxidoreductase, short-chain dehydrogenase/reductase family		3.351				3.351				3.351														
SGO_0997 hypothetical protein SGO_0997	-0.144	5.713	0.0609	0.3621	-1.025	5.451	0.0317	0.1312		4.781			-0.881	4.852	0.0342	0.2148		3.519				3.508		
SGO_1000 recJ; single-stranded-DNA-specific exonuclease RecJ	2.968	5.438	0.0074	0.0270	1.958	4.529	0.0329	0.1379		1.380			-1.010	5.423	0.0013	0.0025		4.224				3.844		
SGO_1001 apt; adenine phosphoribosyltransferase	1.289	8.028	0.0064	0.0223	1.111	7.883	0.0025	0.0058	0.748	7.654	0.0066	0.0376	-0.178	7.924	0.0588	0.4071	-0.540	7.161	0.0225	0.1147	-0.363	7.652	0.0482	0.1077
SGO_1002 metA; homoserine O-succinyltransferase		1.000				1.000				1.000														
SGO_1003 DNA replication protein DnaD	-0.915	5.035	0.0023	0.0059	0.078	5.464	0.1208	0.6096		4.424			0.993	4.573	0.0021	0.0054		2.376				3.989		
SGO_1004 glutathione S-transferase family protein	0.470	3.945	0.0697	0.4252	1.083	4.433	0.0635	0.2929		2.000			0.613	4.345	0.0244	0.1438		2.387				3.625		
SGO_1005 Bcl-2 family protein	0.530	5.015	0.0122	0.0505	0.994	5.306	0.0039	0.0102	0.682	5.098	0.0013	0.0047	0.464	4.993	0.0129	0.0658	0.152	4.203	0.0501	0.3034	-0.311	5.052	0.0394	0.0786
SGO_1006 conserved hypothetical protein TIGR00486	0.802	2.778			0.787	3.497	0.0576	0.2617		1.322			-0.015	3.203	0.1268	0.9734		1.000				2.622		
SGO_1007 oxidoreductase, DadA family protein SP1608						2.854								2.341								2.341		
SGO_1009 rfbA-1; glucose-1-phosphate thymidylyltransferase	2.074	9.379	0.0003	0.0003	1.501	8.934	0.0003	0.0002	1.149	8.693	0.0021	0.0088	-0.573	9.300	0.0019	0.0047	-0.925	8.563	0.0020	0.0047	-0.352	8.825	0.0358	0.0687
SGO_1010 rmlC; dTDP-4-keto-6-deoxyglucose-3,5-epimerase	0.815	7.342	0.0017	0.0041	0.919	7.414	0.0033	0.0084	0.915	7.403	0.0001	0.0001	0.105	7.238	0.0678	0.4775	0.100	6.619	0.0511	0.3146	-0.004	7.284	0.2348	0.8913
SGO_1011 rfbB-1; dTDP-glucose 4,6-dehydratase	2.376	9.181	0.0022	0.0055	1.150	8.223	0.0022	0.0049	0.641	7.895	0.0064	0.0362	-1.226	8.918	0.0039	0.0133	-1.735	8.174	0.0028	0.0076	-0.510	7.930	0.0092	0.0074



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ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
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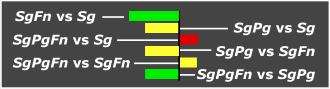

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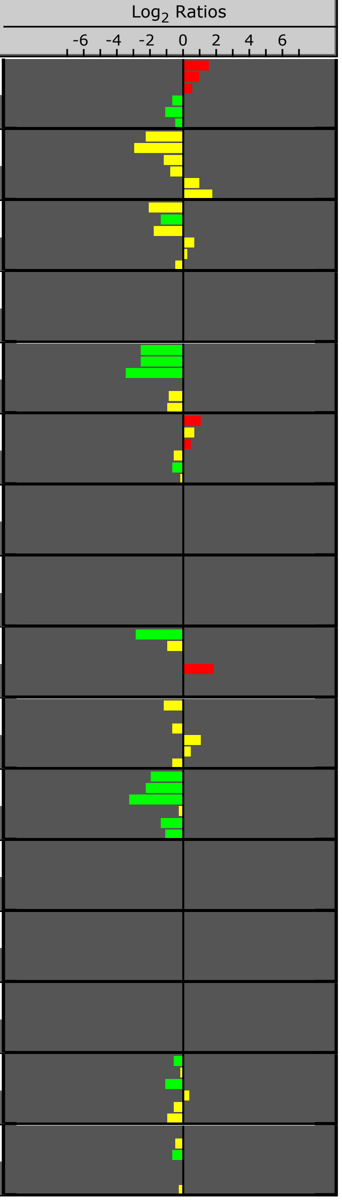
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	Description	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1012	galE-1; UDP-glucose 4-epimerase	1.633	9.235	0.0001	0.0000	0.993	8.779	0.0001	0.0000	0.585	8.521	0.0002	0.0002	-0.640	9.034	0.0002	0.0001	-1.048	8.277	0.0001	0.0000	-0.408	8.489	0.0012	0.0001
SGO_1013	Glycosyltransferase involved in cell wall biogenesis	-2.184	6.159	0.0202	0.0930	-2.901	6.102	0.0214	0.0839	-1.144	6.302	0.0175	0.1311	-0.717	2.988			1.040	3.303			1.757	3.716		
SGO_1016	putative glycosyltransferase	-1.977	5.619	0.0303	0.1580	-1.298	5.936	0.0047	0.0130	-1.705	5.652	0.0215	0.1691	0.679	4.010	0.0282	0.1722	0.272	2.464			-0.407	4.079	0.0910	0.2534
SGO_1018	hypothetical protein SGO_1018		3.669				3.669				3.669														
SGO_1019	glycosyl transferase	-2.526	6.462	0.0035	0.0105	-2.504	6.579	0.0001	0.0000	-3.361	6.410	0.0023	0.0096	0.022	3.918	0.1180	0.8916	-0.835	2.334			-0.856	3.694	0.0874	0.2378
SGO_1020	rfbD; dTDP-4-dehydrorhamnose reductase	1.139	7.938	0.0003	0.0002	0.660	7.639	0.0101	0.0334	0.517	7.544	0.0030	0.0137	-0.479	7.674	0.0085	0.0391	-0.622	6.999	0.0020	0.0046	-0.143	7.350	0.1361	0.4272
SGO_1021	rgpA; rhamnosyltransferase, putative		5.625				5.625				5.625														
SGO_1022	rhamnosyltransferase		5.593				5.593				5.593														
SGO_1024	putative polysaccharide ABC transporter	-2.758	6.575	0.0023	0.0063	-0.897	6.994	0.0133	0.0467		6.371			1.861	5.327	0.0044	0.0154		2.528				4.969		
SGO_1025	rgp; glycosyltransferase	-1.071	6.306	0.0103	0.0406	-0.018	6.700	0.1714	0.9072	-0.576	6.464	0.0131	0.0922	1.052	5.779	0.0087	0.0402	0.495	4.844	0.0527	0.3287	-0.558	5.938	0.0438	0.0934
SGO_1026	rhamnosyltransferase	-1.947	8.073	0.0048	0.0151	-2.178	8.025	0.0046	0.0126	-3.207	7.890	0.0021	0.0088	-0.231	6.138	0.0308	0.1900	-1.260	5.145	0.0030	0.0084	-1.030	5.584	0.0017	0.0002
SGO_1027	hypothetical protein SGO_1027		5.739				5.739				5.739														
SGO_1028	hypothetical protein SGO_1028		4.110				4.110				4.110														
SGO_1030	hypothetical protein SGO_1030		4.129				4.129				4.129														
SGO_1031	cmk; cytidylate kinase	-0.494	5.534	0.0028	0.0079	-0.051	5.735	0.1206	0.6069	-0.973	5.369	0.0025	0.0107	0.443	4.994	0.0067	0.0276	-0.479	3.944	0.0246	0.1287	-0.922	4.825	0.0158	0.0184
SGO_1032	infC; translation initiation factor IF-3		4.700			-0.408	5.564	0.0853	0.4151	-0.623	5.422	0.0007	0.0018		3.902				2.955			-0.215	4.744	0.1382	0.4357



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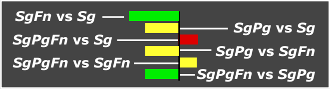

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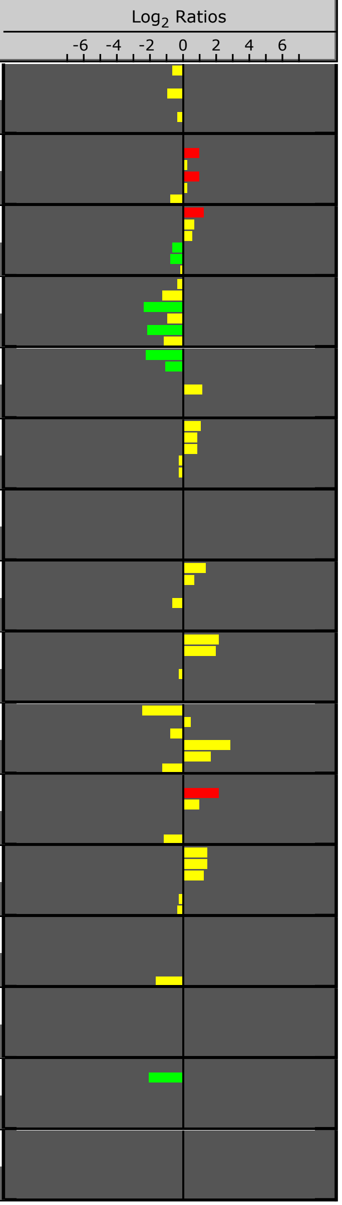
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1033	-0.590	7.556	0.0312	0.1631		6.858			-0.863	7.498	0.0208	0.1629		5.660			-0.273	5.973	0.0937	0.6504		5.504		
	rpmI; ribosomal protein L35																							
SGO_1034	0.007	9.370	0.1242	0.8190	1.019	9.964	0.0000	0.0000	0.317	9.575	0.0337	0.2807	1.012	9.453	0.0001	0.0000	0.310	8.455	0.0481	0.2893	-0.702	9.592	0.0321	0.0574
	rplT; ribosomal protein L20																							
SGO_1035	1.252	6.060	0.0022	0.0058	0.688	5.690	0.0127	0.0439	0.599	5.642	0.0130	0.0914	-0.564	5.768	0.0013	0.0027	-0.653	5.126	0.0027	0.0070	-0.089	5.418	0.1403	0.4457
	gloA; lactoylglutathione lyase																							
SGO_1036	-0.270	7.310	0.0668	0.4036	-1.212	6.966	0.0083	0.0259	-2.329	6.684	0.0011	0.0035	-0.942	6.292	0.0161	0.0871	-2.060	5.362	0.0045	0.0142	-1.118	5.294	0.0358	0.0685
	amino acid ABC transporter, ATP-binding protein SP1242																							
SGO_1037	-2.158	5.957	0.0010	0.0019	-0.955	6.229	0.0002	0.0001		5.628			1.204	4.743	0.0083	0.0375		2.538				4.162		
	glutamine ABC transporter permease and substrate binding protein																							
SGO_1038	1.093	5.266	0.0097	0.0377	0.889	5.145	0.0229	0.0908	0.907	5.145	0.0101	0.0649	-0.205	5.088	0.0722	0.5173	-0.187	4.477	0.0694	0.4605	0.018	4.993	0.2552	0.9977
	uvrB; excinuclease ABC, B subunit																							
SGO_1039		3.272				3.272				3.272														
	hypothetical protein SGO_1039																							
SGO_1041	1.365	4.298			0.719	4.572	0.0490	0.2172		2.459			-0.646	4.507	0.0268	0.1605		2.700				3.680		
	hypothetical protein SGO_1041																							
SGO_1044	2.231	3.094			2.045	3.796	0.0095	0.0310		0.585			-0.186	3.767	0.0278	0.1681		1.692				3.118		
	MutT/nudix family protein																							
SGO_1047	-2.388	5.361	0.0294	0.1515	0.514	6.503	0.0197	0.0765	-0.691	5.932	0.0115	0.0768	2.902	5.310	0.0170	0.0942	1.697	3.631	0.0356	0.2046	-1.205	5.745	0.0107	0.0100
	hypothetical protein SGO_1047																							
SGO_1049		3.011			2.154	5.188	0.0027	0.0065	1.047	3.872	0.0552	0.4899		4.315				1.594			-1.108	4.615	0.0348	0.0652
	tRNA pseudouridine synthase B																							
SGO_1050	1.494	3.254			1.530	4.146	0.0605	0.2783	1.263	3.088			0.036	3.963	0.1129	0.8522	-0.230	2.581			-0.267	3.894	0.1782	0.6234
	ribF; riboflavin biosynthesis protein RibF																							
SGO_1051						3.576				1.981				3.063				0.857			-1.595	3.476		
	negative regulator of proteolysis																							
SGO_1054		3.033			0.144	3.662	0.1254	0.6353		3.033				1.648								1.648		
	NOL1/NOP2/sun family protein																							
SGO_1055		6.557			-1.995	6.887	0.0009	0.0014		6.557				4.083								4.083		
	phosphate ABC transporter, phosphate-binding protein																							
SGO_1057		2.585				2.585				2.585														
	pstA; phosphate ABC transporter, permease protein PstA																							



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ABC Transporter

Proteins found:
1179

Dot Plots
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Test	Cutoff
***q*-Value**	**.005**
p-Value	

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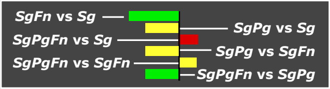

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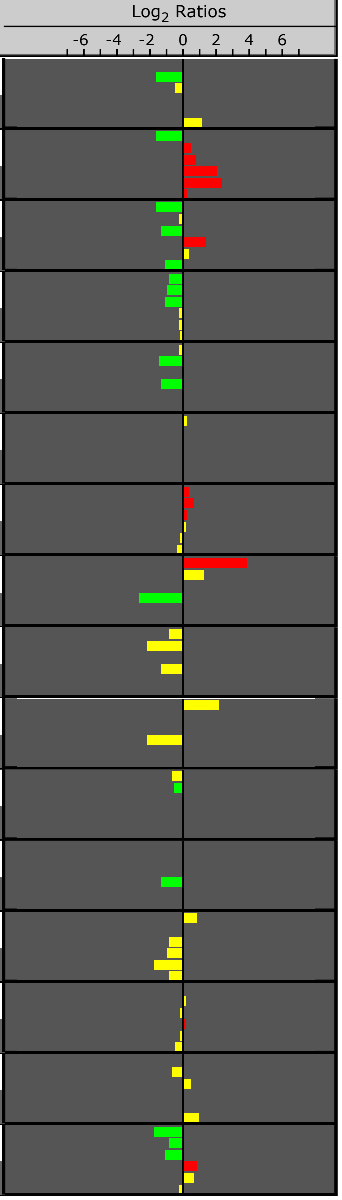
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1058		6.104			-1.604	6.514	0.0002	0.0001	-0.384	6.571	0.0169	0.1253		3.985				3.594			1.220	5.099	0.0073	0.0050
	pstB; Phosphate import ATP-binding protein pstB 2 (Phosphate-transporting ATPase 2) (ABC phosphate transporter 2)																							
SGO_1059	-1.598	5.982	0.0001	0.0001	0.545	6.866	0.0004	0.0004	0.849	7.054	0.0001	0.0000	2.143	5.896	0.0001	0.0001	2.447	5.537	0.0001	0.0000	0.304	6.760	0.0048	0.0016
	pstB; Phosphate import ATP-binding protein pstB 1 (Phosphate-transporting ATPase 1) (ABC phosphate transporter 1)																							
SGO_1060	-1.641	7.306	0.0009	0.0016	-0.234	7.789	0.0257	0.1035	-1.276	7.399	0.0007	0.0018	1.407	6.618	0.0009	0.0014	0.365	5.333	0.0135	0.0606	-1.042	6.723	0.0043	0.0012
	phosphate transport system regulatory protein																							
SGO_1065	-0.762	6.548	0.0014	0.0031	-0.937	6.481	0.0002	0.0001	-0.993	6.465	0.0004	0.0009	-0.175	5.520	0.0316	0.1956	-0.231	4.888	0.0351	0.1995	-0.056	5.401	0.1849	0.6538
	hypothetical protein SGO_1065																							
SGO_1066	-0.160	6.695	0.0523	0.2992	-1.426	6.237	0.0027	0.0065		5.779			-1.266	5.599	0.0009	0.0016		4.482				3.844		
	hypothetical protein SGO_1066																							
SGO_1067	0.317	2.974				1.807				1.807				1.611				1.000						
	hypothetical protein SGO_1067																							
SGO_1069	0.425	8.560	0.0023	0.0062	0.674	8.712	0.0038	0.0100	0.331	8.508	0.0047	0.0248	0.250	8.375	0.0127	0.0644	-0.094	7.585	0.0233	0.1204	-0.344	8.334	0.0248	0.0395
	membrane alanyl aminopeptidase																							
SGO_1072	3.899	6.269	0.0019	0.0046	1.254	3.081				1.322			-2.645	5.819	0.0021	0.0051		5.097				2.063		
	ciaR; Transcriptional regulatory protein CiaR																							
SGO_1073	-0.816	5.409	0.0184	0.0834	-2.149	5.203	0.0133	0.0468		5.049			-1.332	3.200				2.107				1.385		
	Sensor protein CiaH																							
SGO_1075	2.151	5.320	0.0250	0.1226	0.098	3.050				2.000			-2.053	4.817	0.0216	0.1250		4.044				1.585		
	alpha-amylase precursor																							
SGO_1077	-0.574	5.673	0.1462	0.9937	-0.543	5.427	0.0040	0.0106		4.671			0.031	4.917	0.0724	0.5199		3.552				3.620		
	coaA; pantothenate kinase																							
SGO_1078		5.392				4.180							-1.252	5.397	0.0030	0.0090		4.268				3.667		
	methyltransferase domain protein																							
SGO_1079	0.866	7.696	0.0238	0.1139	-0.010	7.139	0.1705	0.8989	-0.826	6.789	0.0056	0.0302	-0.876	7.174	0.0185	0.1042	-1.692	6.333	0.0101	0.0421	-0.816	6.258	0.0107	0.0101
	pdp; pyrimidine-nucleoside phosphorylase																							
SGO_1080	-0.018	8.282	0.1194	0.7822	0.227	8.409	0.0119	0.0406	-0.127	8.229	0.0176	0.1329	0.245	7.887	0.0045	0.0165	-0.109	7.094	0.0180	0.0847	-0.354	7.838	0.0064	0.0039
	deoC; deoxyribose-phosphate aldolase																							
SGO_1081		3.660			-0.569	4.373	0.0588	0.2694	0.464	4.360	0.0716	0.6617		2.500				1.857			1.033	3.484	0.0735	0.1892
	cdd; cytidine deaminase																							
SGO_1082	-1.703	12.818	0.0002	0.0001	-0.805	13.082	0.0002	0.0001	-1.016	13.028	0.0024	0.0103	0.898	11.735	0.0011	0.0019	0.686	11.027	0.0202	0.0984	-0.212	12.037	0.1609	0.5401
	lipoprotein																							



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ABC Transporter

Proteins found:
1179

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Test	Cutoff
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p-Value	

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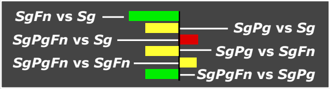

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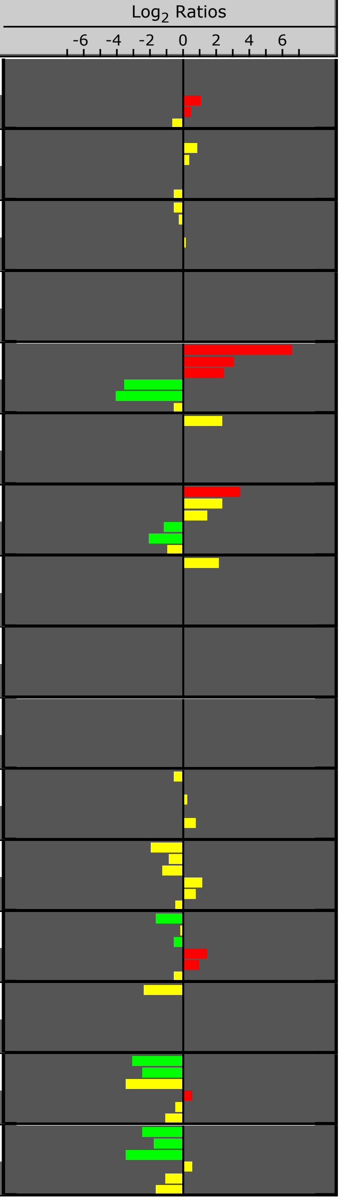
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1083 sugar ABC transporter, ATP-binding protein SP0846		7.517				8.625				7.979			1.096	8.662	0.0021	0.0055	0.463	7.643	0.0001	0.0000	-0.634	8.825	0.0148	0.0168
SGO_1088 transcription regulator, LysR family		2.718			0.884	4.195	0.0275	0.1112	0.367	3.396	0.0737	0.6830		3.040				0.857			-0.517	3.458	0.1390	0.4396
SGO_1090 pseudouridine synthase, RluA family	-0.494	5.182	0.0601	0.3543	-0.245	5.633	0.0727	0.3447		4.751			0.249	4.491	0.0722	0.5174		2.107				3.991		
SGO_1091 hypothetical protein SGO_1091		2.022				2.022				2.022														
SGO_1096 butA; acetoin dehydrogenase	6.559	13.354	0.0001	0.0000	3.057	10.001	0.0001	0.0000	2.511	9.539	0.0010	0.0031	-3.502	12.948	0.0001	0.0001	-4.048	12.301	0.0002	0.0001	-0.546	10.083	0.0167	0.0208
SGO_1097 proB; glutamate 5-kinase	2.446	3.689				1.000				1.000				2.933				2.322						
SGO_1098 proA; gamma-glutamyl phosphate reductase	3.518	6.387	0.0016	0.0037	2.384	5.365	0.0434	0.1888	1.476	4.525	0.0115	0.0771	-1.135	6.369	0.0019	0.0043	-2.043	5.516	0.0001	0.0000	-0.908	5.326	0.0271	0.0453
SGO_1099 proC; pyrroline-5-carboxylate reductase	2.177	5.178	0.0740	0.4560		1.322				1.322				4.561				3.950						
SGO_1100 phnA; alkylphosphonate utilization operon protein PhnA		3.807				3.807				3.807														
SGO_1103 carA; carbamoyl-phosphate synthase, small subunit		3.944				3.944				3.944														
SGO_1104 carB; carbamoyl-phosphate synthase, large subunit	-0.461	4.724	0.0114	0.0463		4.277			0.289	4.965	0.0092	0.0571		2.302			0.750	3.115				3.053		
SGO_1107 PyrR bifunctional protein	-1.932	4.963	0.0370	0.1991	-0.775	5.151	0.0690	0.3237	-1.162	5.074	0.0311	0.2563	1.157	2.994			0.770	2.127			-0.387	3.279		
SGO_1109 pyrB; aspartate carbamoyltransferase	-1.562	7.655	0.0005	0.0008	-0.059	8.205	0.0928	0.4547	-0.527	7.996	0.0029	0.0129	1.503	7.095	0.0001	0.0000	1.035	6.157	0.0011	0.0017	-0.468	7.446	0.0077	0.0055
SGO_1110 surface antigen SCP-like domain	-2.330	6.283	0.0068	0.0242		6.147				6.147				2.302				1.692						
SGO_1111 fruR; phosphotransferase system repressor	-2.986	6.930	0.0008	0.0012	-2.353	7.016	0.0010	0.0016	-3.352	6.828	0.0127	0.0882	0.633	4.603	0.0021	0.0054	-0.366	3.112	0.0209	0.1038	-0.999	4.208	0.0466	0.1029
SGO_1112 fruB; 1-phosphofructokinase	-2.373	7.196	0.0001	0.0000	-1.735	7.327	0.0004	0.0004	-3.355	7.010	0.0028	0.0123	0.638	5.431	0.0121	0.0598	-0.983	3.774	0.0214	0.1074	-1.620	4.938	0.0735	0.1901



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1179

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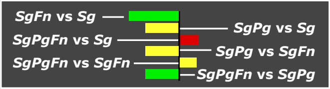

Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory **UW**

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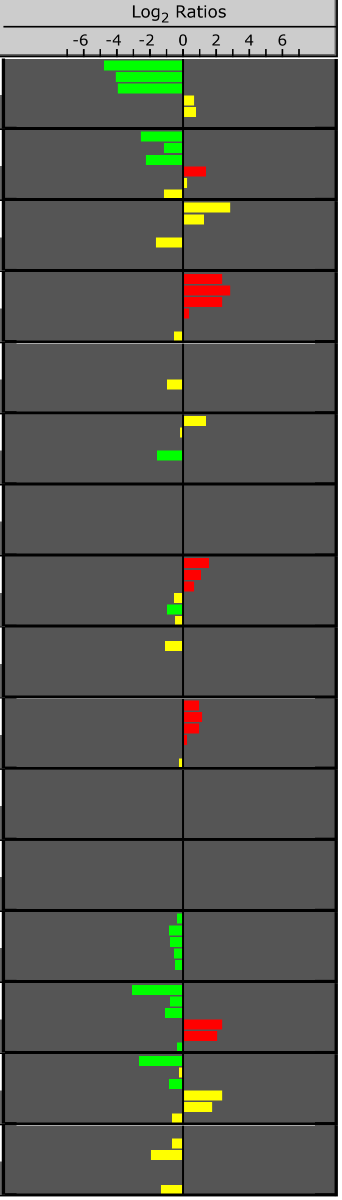
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1113 fruA; PTS system, fructose specific IIABC components	-4.663	11.177	0.0000	0.0000	-3.955	11.208	0.0000	0.0000	-3.884	11.211	0.0000	0.0000	0.709	7.396	0.0246	0.1456	0.779	6.817	0.0182	0.0864	0.070	7.700	0.2139	0.7865
SGO_1114 Protein of unknown function (DUF1149) superfamily	-2.537	6.777	0.0003	0.0002	-1.137	7.080	0.0005	0.0005	-2.238	6.815	0.0001	0.0001	1.400	5.373	0.0022	0.0060	0.299	4.065	0.0612	0.3976	-1.101	5.443	0.0051	0.0023
SGO_1115 DegV family protein	2.947	4.930			1.302	4.389	0.0357	0.1516		1.807			-1.645	4.960	0.0095	0.0441		3.630				3.612		
SGO_1116 dapB; dihydrodipicolinate reductase	2.419	6.592	0.0002	0.0001	2.860	6.972	0.0002	0.0001	2.399	6.582	0.0006	0.0013	0.440	7.068	0.0022	0.0059	-0.021	6.214	0.1274	0.9159	-0.461	7.063	0.0163	0.0196
SGO_1117 pcnA; polynucleotide adenylyltransferase		4.237				3.130							-0.898	4.274	0.0269	0.1619		3.113				2.617		
SGO_1118 ABC transporter, ATP-binding protein SP1553	1.378	4.957	0.0183	0.0825	-0.081	3.858	0.1344	0.6881		2.322			-1.459	4.639	0.0008	0.0011		3.580				2.735		
SGO_1119 Abi-alpha protein, putative		2.036				2.036				2.036														
SGO_1120 guaA; GMP synthase	1.559	8.789	0.0013	0.0025	1.050	8.420	0.0004	0.0005	0.698	8.203	0.0049	0.0263	-0.509	8.618	0.0052	0.0203	-0.861	7.879	0.0041	0.0122	-0.352	8.177	0.0319	0.0570
SGO_1121 transcription regulator, GntR family		2.807			-0.972	3.402				2.807				1.322								1.322		
SGO_1123 ffh; signal recognition particle protein	0.954	7.773	0.0005	0.0007	1.244	7.970	0.0002	0.0001	1.001	7.805	0.0004	0.0010	0.290	7.812	0.0038	0.0129	0.048	7.074	0.0814	0.5514	-0.243	7.834	0.0198	0.0276
SGO_1124 cell surface hydrolase		3.025				3.025				3.025														
SGO_1128 bacteriocin-associated integral membrane protein subfamily		2.000				2.000				2.000														
SGO_1129 lplA; lipoate protein ligase A	-0.262	6.672	0.0032	0.0095	-0.806	6.457	0.0025	0.0058	-0.672	6.501	0.0006	0.0016	-0.544	5.782	0.0047	0.0173	-0.410	5.221	0.0013	0.0022	0.133	5.556	0.1407	0.4477
SGO_1130 dihydrolipoamide dehydrogenase	-3.046	7.970	0.0000	0.0000	-0.666	8.509	0.0002	0.0001	-0.959	8.402	0.0001	0.0000	2.380	6.880	0.0001	0.0000	2.087	6.027	0.0001	0.0000	-0.293	7.485	0.0045	0.0014
SGO_1131 sucB; dihydrolipoamide S-acetyltransferase	-2.627	6.185	0.0028	0.0079	-0.208	6.974	0.0108	0.0364	-0.836	6.722	0.0014	0.0050	2.419	5.484	0.0116	0.0560	1.791	4.327	0.0283	0.1530	-0.628	6.083	0.0172	0.0217
SGO_1132 acetoin dehydrogenase		5.344			-0.631	6.047	0.0181	0.0688	-1.908	5.520	0.0242	0.1926		4.160				1.272			-1.277	4.431	0.0092	0.0072



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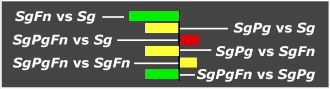
🟩	yes	−	



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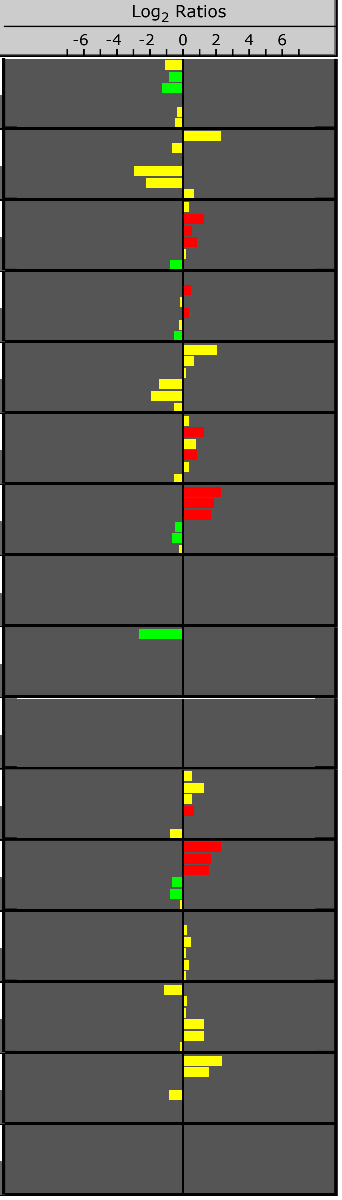
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1133	-0.959	6.337	0.0317	0.1660	-0.813	6.658	0.0048	0.0135	-1.214	6.539	0.0027	0.0117	0.146	5.214	0.0706	0.5025	-0.255	4.367	0.0958	0.6663	-0.401	5.511	0.0753	0.1952
	acoA; acetoin dehydrogenase																							
SGO_1134	2.321	6.119	0.0067	0.0238	-0.566	3.898	0.0626	0.2887	0.121	4.103	0.0782	0.7301	-2.886	5.443	0.0357	0.2287	-2.199	4.884	0.0423	0.2490	0.687	2.769		
	hypothetical protein SGO_1134																							
SGO_1139	0.405	6.420	0.0116	0.0478	1.267	6.969	0.0006	0.0007	0.580	6.523	0.0034	0.0164	0.862	6.582	0.0002	0.0001	0.176	5.568	0.0074	0.0275	-0.687	6.647	0.0017	0.0002
	GTP-binding protein																							
SGO_1140	0.128	8.431	0.0388	0.2102	0.482	8.625	0.0017	0.0033	-0.066	8.332	0.0435	0.3780	0.354	8.166	0.0015	0.0034	-0.194	7.274	0.0080	0.0304	-0.548	8.083	0.0007	0.0000
	clpX; ATP-dependent Clp protease, ATP-binding subunit ClpX																							
SGO_1141	2.133	6.005	0.0060	0.0203	0.710	4.941	0.0144	0.0518	0.201	4.191	0.0695	0.6387	-1.422	5.648	0.0080	0.0352	-1.932	4.762	0.0407	0.2387	-0.510	4.166	0.1108	0.3287
	folA; dihydrofolate reductase																							
SGO_1143	0.391	5.180	0.0534	0.3075	1.268	5.705	0.0018	0.0037	0.799	4.852	0.0299	0.2442	0.877	5.319	0.0041	0.0140	0.407	3.951	0.0709	0.4709	-0.469	5.119	0.0256	0.0415
	thyA; thymidylate synthase																							
SGO_1144	2.268	9.727	0.0002	0.0001	1.912	9.437	0.0000	0.0000	1.707	9.282	0.0004	0.0009	-0.356	9.774	0.0022	0.0056	-0.562	9.079	0.0024	0.0060	-0.205	9.487	0.0330	0.0604
	glcK; glucokinase																							
SGO_1145		3.781				3.781				3.781														
	cell surface hydrolase																							
SGO_1148	-2.650	8.527	0.0003	0.0003		8.314				8.314				5.151				4.540						
	cshB; surface-associated protein CshB																							
SGO_1149		3.830				3.830				3.830														
	Pneumococcal vaccine antigen A-like protein																							
SGO_1150	0.600	4.826	0.0397	0.2158	1.321	5.394	0.0177	0.0671	0.585	4.130			0.721	5.305	0.0023	0.0062	-0.014	3.870	0.1271	0.9104	-0.736	4.996	0.0458	0.1000
	hypothetical protein SGO_1150																							
SGO_1151	2.287	9.772	0.0000	0.0000	1.725	9.323	0.0000	0.0000	1.614	9.238	0.0001	0.0000	-0.562	9.736	0.0001	0.0000	-0.674	9.082	0.0002	0.0001	-0.112	9.374	0.0151	0.0172
	glyA; serine hydroxymethyltransferase																							
SGO_1154	0.128	7.465	0.0957	0.6170	0.348	7.523	0.0322	0.1340	0.523	7.625	0.0085	0.0520	0.220	7.107	0.1010	0.7485	0.396	6.592	0.0614	0.4010	0.176	7.252	0.0328	0.0595
	prfA; peptide chain release factor 1																							
SGO_1155	-1.087	5.504	0.0219	0.1031	0.258	6.054	0.1207	0.6079	0.196	5.567	0.0922	0.8799	1.345	5.132	0.0082	0.0365	1.283	3.830	0.0310	0.1716	-0.062	5.189	0.2203	0.8197
	tdk; thymidine kinase																							
SGO_1159	2.423	4.557	0.0157	0.0696	1.630	3.910	0.0590	0.2706		1.000			-0.794	4.599	0.0100	0.0472		3.305				3.191		
	guaC; guanosine monophosphate reductase																							
SGO_1163										1.981								0.857				1.468		
	Iron permease FTR1 family																							



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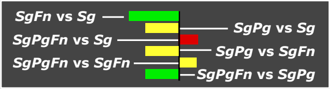
Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
q-Value	.005
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
🟨	no	n/a	bars
🟩	yes	–	ratios, bars
▨	yes	+	*p*- , *q*-Values
▨	yes	–	



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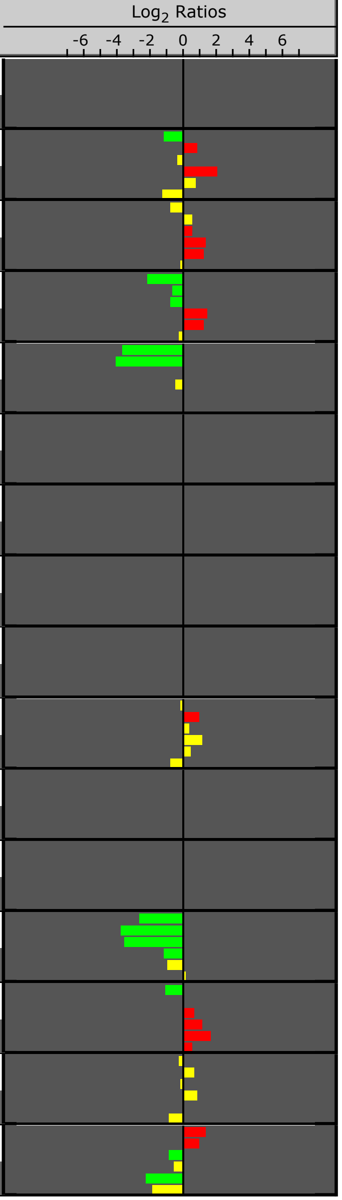
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1166		3.272				3.272				3.272														
	voltage-gated chloride channel family protein																							
SGO_1167	-1.132	7.433	0.0004	0.0005	0.927	8.426	0.0002	0.0001	-0.299	7.772	0.0371	0.3123	2.059	7.614	0.0000	0.0000	0.833	6.143	0.0129	0.0571	-1.225	7.832	0.0061	0.0037
	nox; NADH oxidase																							
SGO_1169	-0.745	6.887	0.0056	0.0186	0.631	7.557	0.0079	0.0244	0.557	7.504	0.0004	0.0009	1.376	6.806	0.0027	0.0078	1.302	6.132	0.0011	0.0015	-0.074	7.287	0.1579	0.5196
	NADPH-dependent FMN reductase																							
SGO_1170	-2.073	8.329	0.0001	0.0000	-0.581	8.759	0.0002	0.0001	-0.745	8.696	0.0002	0.0002	1.493	7.367	0.0002	0.0001	1.328	6.638	0.0006	0.0005	-0.164	7.848	0.0268	0.0445
	NADPH-dependent FMN reductase																							
SGO_1171	-3.650	7.609	0.0001	0.0001	-4.040	7.574	0.0001	0.0000		7.489			-0.390	4.216	0.0429	0.2851		2.839				2.937		
	thioredoxin family protein																							
SGO_1174		3.417				3.417				3.417														
	histidine kinase																							
SGO_1176		0.585				0.585				0.585														
	peptide methionine sulfoxide reductase-like protein																							
SGO_1182		1.058				1.058				1.058														
	LPXTG cell wall surface protein																							
SGO_1184		3.412				3.412				3.412														
	GdmH																							
SGO_1185	-0.148	4.148	0.1009	0.6525	1.029	5.215	0.0048	0.0134	0.351	4.801	0.0232	0.1848	1.176	4.409	0.0260	0.1546	0.498	3.270	0.0501	0.3038	-0.678	4.825	0.0219	0.0318
	acetyltransferase, GNAT family																							
SGO_1186		5.718				5.718				5.718														
	ABC transporter, permease/ATP-binding protein																							
SGO_1187		6.301				6.301				6.301														
	ABC transporter, permease/ATP-binding protein																							
SGO_1189	-2.586	9.364	0.0003	0.0004	-3.706	9.249	0.0003	0.0003	-3.464	9.278	0.0003	0.0004	-1.120	6.592	0.0013	0.0026	-0.877	6.105	0.0154	0.0708	0.243	6.125	0.1382	0.4349
	lipoprotein, putative																							
SGO_1191	-1.030	11.163	0.0007	0.0010	0.125	11.651	0.0327	0.1371	0.717	11.990	0.0008	0.0022	1.155	10.733	0.0002	0.0001	1.746	10.556	0.0004	0.0002	0.592	11.525	0.0050	0.0022
	rplL; ribosomal protein L7/L12																							
SGO_1192	-0.243	9.189	0.0417	0.2316	0.701	9.702	0.0111	0.0375	-0.130	9.230	0.0106	0.0690	0.944	9.110	0.0071	0.0297	0.112	7.996	0.0872	0.5997	-0.831	9.141	0.0196	0.0270
	BL5; 50S ribosomal protein L10																							
SGO_1193	1.446	6.759	0.0004	0.0005	0.996	6.452	0.0037	0.0096	-0.784	5.522	0.0004	0.0007	-0.451	6.593	0.0082	0.0371	-2.230	5.464	0.0004	0.0003	-1.780	5.724	0.0061	0.0036
	gid; Glucose inhibited division protein A																							



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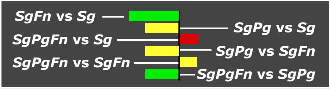

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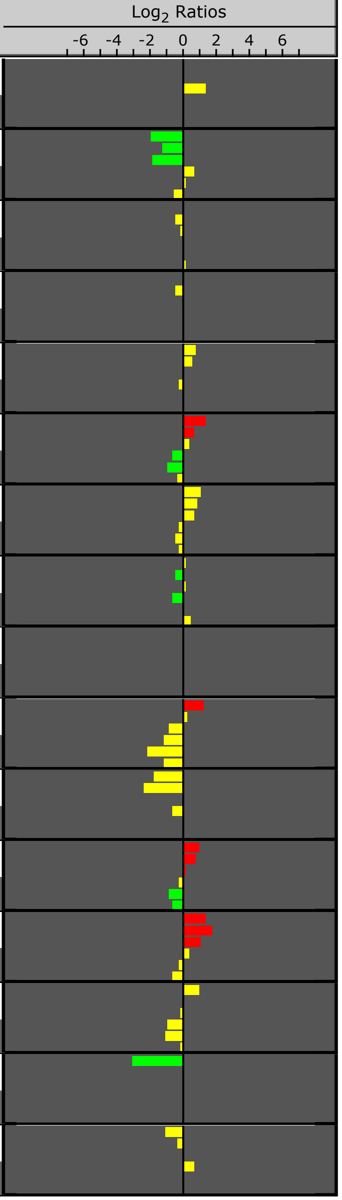
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1196		2.227				2.227			1.358	4.061								2.461				3.072		
	satD; SatD-like protein																							
SGO_1197	-1.919	7.885	0.0011	0.0021	-1.218	8.057	0.0018	0.0038	-1.756	7.913	0.0006	0.0017	0.702	6.511	0.0076	0.0330	0.163	5.590	0.0770	0.5164	-0.539	6.562	0.0140	0.0154
	topA; DNA topoisomerase I																							
SGO_1198		8.008			-0.387	8.825	0.0055	0.0161	-0.145	8.938	0.0296	0.2408		7.103				6.739			0.242	8.232	0.0289	0.0498
	DNA processing Smf protein																							
SGO_1199		2.934			-0.356	3.409	0.0322	0.1336		2.934				1.063								1.063		
	acetyltransferase, CysE/LacA/LpxA/NodL family																							
SGO_1202	0.838	5.772	0.0078	0.0290	0.592	5.619	0.0154	0.0563		4.275			-0.246	5.510	0.0543	0.3719		4.017				4.383		
	GTP-binding protein																							
SGO_1203	1.365	7.031	0.0011	0.0022	0.746	6.612	0.0027	0.0066	0.435	6.426	0.0071	0.0404	-0.619	6.766	0.0034	0.0112	-0.930	6.041	0.0020	0.0048	-0.311	6.275	0.0295	0.0509
	anaerobic ribonucleotide reductase																							
SGO_1205	1.087	5.095	0.0245	0.1182	0.892	4.892	0.0147	0.0533	0.719	4.781	0.0129	0.0899	-0.195	4.889	0.0680	0.4795	-0.368	4.202	0.0507	0.3092	-0.173	4.641	0.1033	0.2994
	dapA; dihydrodipicolinate synthase																							
SGO_1206	0.207	7.665	0.0140	0.0604	-0.353	7.392	0.0040	0.0107	0.164	7.642	0.0130	0.0915	-0.559	6.998	0.0013	0.0029	-0.043	6.619	0.0817	0.5556	0.517	6.972	0.0053	0.0027
	asd; aspartate-semialdehyde dehydrogenase																							
SGO_1208		3.604				3.604				3.604														
	Hypothetical FAD-dependent oxidoreductase, putative																							
SGO_1210	1.322	6.338	0.0019	0.0045	0.250	5.689	0.0723	0.3419	-0.802	4.885	0.0098	0.0626	-1.072	5.922	0.0057	0.0223	-2.125	4.887	0.0218	0.1097	-1.052	4.625	0.1103	0.3245
	fhs-1; formate--tetrahydrofolate ligase																							
SGO_1213	-1.696	5.911	0.0075	0.0273	-2.296	5.647	0.0472	0.2066		5.513			-0.601	3.733	0.0674	0.4737		2.734				1.648		
	coaC; phosphopantothenoylcysteine decarboxylase																							
SGO_1215	0.991	10.269	0.0005	0.0007	0.815	10.153	0.0002	0.0001	0.239	9.813	0.0014	0.0051	-0.176	10.082	0.0080	0.0351	-0.753	9.229	0.0009	0.0010	-0.577	9.730	0.0000	0.0000
	manB; phosphomannomutase																							
SGO_1216	1.372	6.913	0.0009	0.0017	1.790	7.228	0.0010	0.0016	1.150	6.754	0.0004	0.0009	0.419	7.152	0.0080	0.0349	-0.222	6.206	0.0131	0.0582	-0.641	7.060	0.0103	0.0094
	bta; Possible bacteriocin transport accessory protein																							
SGO_1219	0.989	8.278	0.0179	0.0802	0.089	7.683	0.0652	0.3035	-0.058	7.613	0.0681	0.6240	-0.901	7.792	0.0163	0.0896	-1.048	7.136	0.0161	0.0745	-0.147	7.143	0.0656	0.1621
	pta; phosphate acetyltransferase																							
SGO_1221	-2.962	7.363	0.0009	0.0017		7.145				7.145				4.019				3.408						
	ppnK; Probable inorganic polyphosphate/ATP-NAD kinase																							
SGO_1222	-1.021	4.154	0.0070	0.0250	-0.323	4.321	0.0170	0.0631		3.836			0.698	2.693				0.692				2.000		
	GTP pyrophosphokinase-like protein																							



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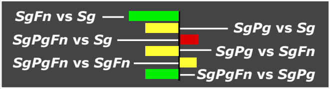

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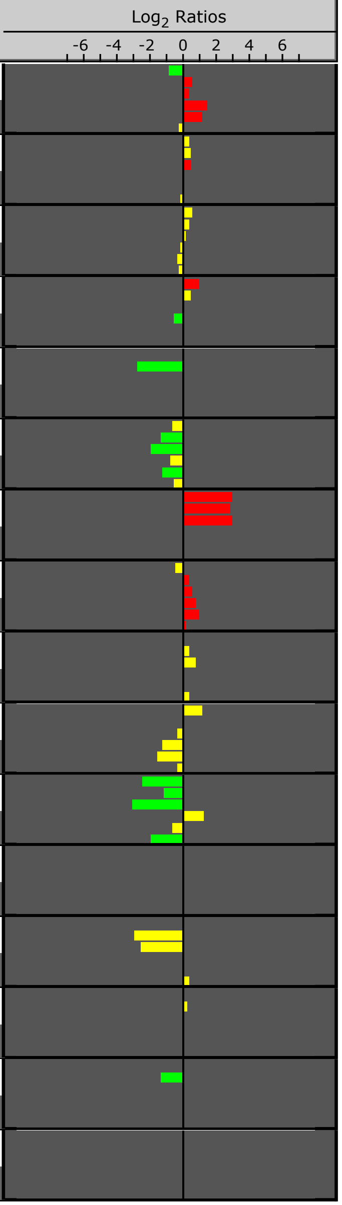
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory **UW**

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1224	-0.808	8.161	0.0001	0.0001	0.647	8.869	0.0008	0.0012	0.425	8.740	0.0033	0.0157	1.455	8.092	0.0003	0.0002	1.233	7.325	0.0011	0.0015	-0.222	8.539	0.0384	0.0755
	Ribose-phosphate pyrophosphokinase 2																							
SGO_1225	0.444	5.289	0.0259	0.1290	0.546	5.333	0.0081	0.0252	0.465	5.279	0.0018	0.0070	0.103	5.035	0.1024	0.7602	0.021	4.378	0.1295	0.9390	-0.082	5.027	0.1579	0.5157
	pyridoxal-phosphate dependent aminotransferase																							
SGO_1226	0.554	6.560	0.0306	0.1599	0.436	6.473	0.0366	0.1558	0.231	6.360	0.0532	0.4709	-0.118	6.216	0.0701	0.4969	-0.323	5.511	0.0327	0.1832	-0.205	6.039	0.0203	0.0288
	hypothetical protein SGO_1226																							
SGO_1228	1.028	5.079	0.0021	0.0053	0.534	4.773	0.0171	0.0636		3.494			-0.494	4.758	0.0045	0.0167		3.371				3.494		
	DNA-binding protein BH0551																							
SGO_1230		6.030			-2.690	6.240	0.0003	0.0003		6.030				2.844								2.844		
	srtA; sortase A																							
SGO_1231	-0.634	8.407	0.0061	0.0209	-1.323	8.182	0.0024	0.0054	-1.868	8.032	0.0004	0.0008	-0.689	7.258	0.0135	0.0698	-1.234	6.445	0.0028	0.0078	-0.544	6.626	0.0495	0.1114
	gyrA; DNA gyrase, A subunit																							
SGO_1232	2.961	10.386	0.0001	0.0000	2.941	10.367	0.0001	0.0000	3.026	10.443	0.0000	0.0000	-0.020	10.687	0.0601	0.4179	0.065	10.119	0.0078	0.0295	0.085	10.720	0.0113	0.0108
	L-lactate dehydrogenase																							
SGO_1234	-0.416	10.488	0.0136	0.0581	0.414	10.895	0.0030	0.0073	0.581	10.993	0.0008	0.0023	0.829	10.222	0.0014	0.0032	0.997	9.720	0.0011	0.0016	0.167	10.658	0.0048	0.0016
	rpsA; 30S ribosomal protein S1																							
SGO_1237		5.031			0.373	6.228	0.0055	0.0159	0.822	6.561	0.0153	0.1106		4.888				4.824			0.449	6.187	0.0848	0.2281
	hypothetical protein SGO_1237																							
SGO_1238	1.196	7.844	0.0074	0.0267	0.021	7.106	0.1464	0.7601	-0.322	6.950	0.0122	0.0839	-1.175	7.336	0.0066	0.0269	-1.517	6.634	0.0056	0.0194	-0.343	6.447	0.0305	0.0530
	ilvE; branched-chain amino acid aminotransferase																							
SGO_1239	-2.435	6.547	0.0006	0.0010	-1.117	6.822	0.0003	0.0003	-2.990	6.446	0.0001	0.0001	1.318	5.182	0.0052	0.0202	-0.555	3.569	0.0403	0.2359	-1.874	4.994	0.0012	0.0001
	parC; DNA topoisomerase IV, A subunit																							
SGO_1241		2.946				2.946				2.946														
	aminoglycoside adenylyltransferase																							
SGO_1242		7.113			-2.894	7.207	0.0175	0.0659	-2.541	7.232	0.0106	0.0688		2.700				2.442			0.352	3.887		
	lipoprotein, putative																							
SGO_1244		4.043			0.288	5.085	0.1646	0.8635		4.043				3.612								3.612		
	hypothetical protein SGO_1244																							
SGO_1245		5.347			-1.278	5.846	0.0026	0.0059		5.347				3.560								3.560		
	parE; DNA topoisomerase IV, B subunit																							
SGO_1246		3.940				3.940				3.940														
	hypothetical protein SGO_1246																							



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Proteins found:
1179

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Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
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🟨	no	n/a	bars
🟩	yes	−	ratios, bars
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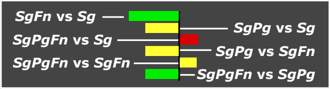
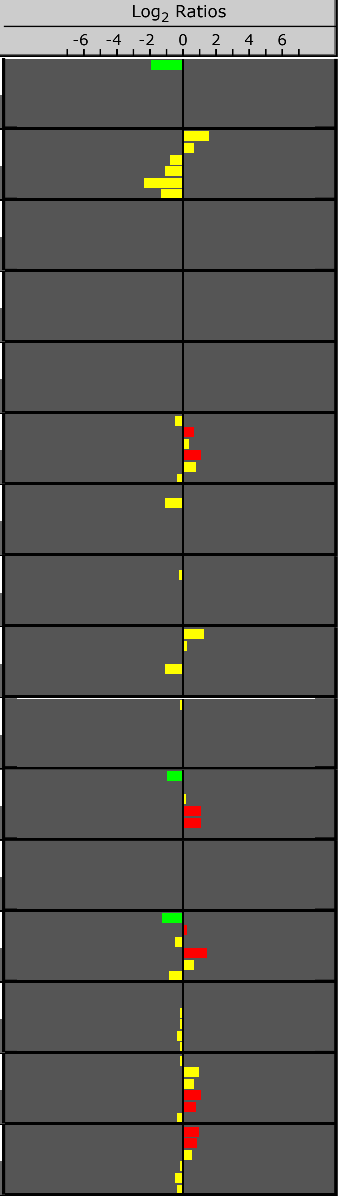


Hendrickson *et al.*

Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1247 5'-nucleotidase family protein	-1.887	9.490	0.0001	0.0000		9.144				9.144				6.747				6.136						
SGO_1248 pyrC; dihydroorotase	1.629	6.962	0.0102	0.0400	0.664	6.259	0.0221	0.0871	-0.668	5.583	0.0094	0.0593	-0.965	6.635	0.0161	0.0872	-2.297	5.699	0.0069	0.0249	-1.332	5.511	0.0136	0.0148
SGO_1250 ung; uracil-DNA glycosylase	0.002	5.377	0.1241	0.8174		4.412				4.412				3.829				3.218						
SGO_1251 hypothetical protein SGO_1251		1.841				1.841				1.841														
SGO_1252 integral membrane protein, putative		1.322				1.322				1.322														
SGO_1253 pyrE; orotate phosphoribosyltransferase	-0.416	6.262	0.0462	0.2609	0.695	6.813	0.0038	0.0099	0.357	6.621	0.0183	0.1387	1.111	6.169	0.0032	0.0103	0.773	5.347	0.0134	0.0603	-0.339	6.446	0.0353	0.0668
SGO_1254 pyrF; orotidine 5'-phosphate decarboxylase		4.699			-1.011	5.018	0.0244	0.0978		4.699				2.170								2.170		
SGO_1255 pyrd; dihydroorotate dehydrogenase B		2.824			-0.177	3.313	0.1403	0.7201		2.824				1.000								1.000		
SGO_1257 probable transcriptional regulator (LysR family)	1.286	5.778	0.0098	0.0384	0.296	5.116	0.0467	0.2042		3.977			-0.991	5.347	0.0106	0.0504		4.167				3.730		
SGO_1258 NAD-dependent deacetylase (Regulatory protein SIR2-like protein)	-0.144	4.608	0.0885	0.5643		3.718				3.718				2.976				2.366						
SGO_1260 deoD; purine nucleoside phosphorylase	-0.908	7.764	0.0001	0.0001	0.150	8.225	0.0058	0.0171	0.150	8.227	0.0123	0.0845	1.058	7.351	0.0002	0.0002	1.059	6.742	0.0009	0.0010	0.001	7.787	0.2478	0.9628
SGO_1261 glutamine amidotransferase, class I		1.807				1.807				1.807														
SGO_1263 purine nucleoside phosphorylase I, inosine and guanosine-specific	-1.173	8.218	0.0007	0.0011	0.330	8.861	0.0049	0.0137	-0.436	8.496	0.0106	0.0693	1.503	7.938	0.0002	0.0001	0.737	6.819	0.0083	0.0316	-0.766	8.178	0.0100	0.0088
SGO_1264 deoB; phosphopentomutase	0.143	10.075	0.0658	0.3970	0.019	10.003	0.1710	0.9034	-0.125	9.941	0.0572	0.5115	-0.124	9.567	0.0535	0.3653	-0.269	8.897	0.0403	0.2361	-0.144	9.434	0.1271	0.3944
SGO_1265 rpiA; ribose 5-phosphate isomerase	-0.125	7.240	0.0847	0.5356	0.958	7.844	0.0077	0.0238	0.677	7.670	0.0125	0.0861	1.083	7.260	0.0003	0.0002	0.802	6.467	0.0014	0.0026	-0.281	7.570	0.0190	0.0257
SGO_1266 trmE; tRNA modification GTPase TrmE	0.968	6.266	0.0005	0.0007	0.882	6.214	0.0025	0.0058	0.563	6.020	0.0059	0.0320	-0.086	6.119	0.0707	0.5041	-0.405	5.365	0.0117	0.0504	-0.319	5.932	0.0570	0.1353



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p-Value	

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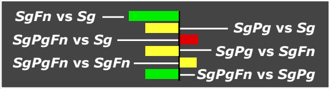


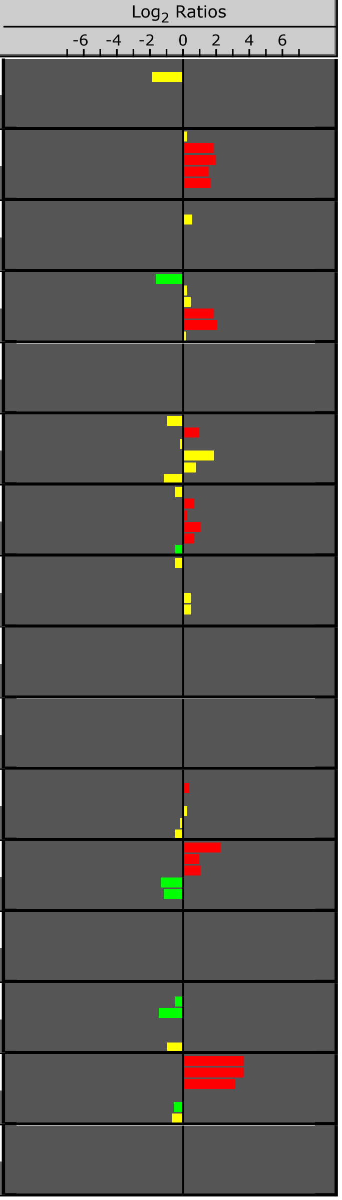
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory **UW**

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1267 thioredoxin family protein		5.406			-1.825	5.596	0.0185	0.0707		5.406				2.063								2.063		
SGO_1273 rpoD; RNA polymerase sigma factor	0.309	7.412	0.0431	0.2413	1.903	8.469	0.0001	0.0000	1.987	8.558	0.0018	0.0070	1.594	8.036	0.0006	0.0008	1.678	7.509	0.0037	0.0108	0.084	8.669	0.1635	0.5535
SGO_1274 dnaG; DNA primase		3.105			0.563	4.342	0.0490	0.2164		3.105				3.032								3.032		
SGO_1276 rpsU; ribosomal protein S21	-1.596	7.134	0.0001	0.0000	0.281	7.872	0.0142	0.0507	0.481	7.989	0.0059	0.0324	1.877	6.842	0.0007	0.0010	2.077	6.395	0.0013	0.0021	0.200	7.602	0.0874	0.2374
SGO_1280 putative membrane-associated Zn-dependent protease		3.549				3.549				3.549														
SGO_1281 penicillinase repressor, putative	-0.896	4.066	0.0337	0.1781	0.982	5.300	0.0047	0.0128	-0.127	4.265	0.0675	0.6167	1.879	4.379	0.0216	0.1249	0.770	2.127			-1.109	4.494	0.0665	0.1670
SGO_1283 oxidoreductase	-0.373	7.916	0.0112	0.0452	0.742	8.503	0.0003	0.0003	0.335	8.261	0.0009	0.0029	1.115	7.864	0.0006	0.0008	0.708	6.989	0.0018	0.0041	-0.407	8.123	0.0016	0.0002
SGO_1284 thioredoxin-disulfide reductase	-0.375	5.791	0.0754	0.4661	0.132	6.048	0.1080	0.5381	0.103	5.968	0.0455	0.3963	0.508	5.424	0.0537	0.3677	0.479	4.727	0.0518	0.3205	-0.029	5.586	0.1982	0.7089
SGO_1290 ABC transporter, permease/ATP-binding protein		4.483				4.483				4.483														
SGO_1291 ABC transporter, permease/ATP-binding protein SP1358		3.115				3.115				3.115														
SGO_1293 asnS; asparaginyl-tRNA synthetase	0.127	7.656	0.0294	0.1508	0.430	7.822	0.0034	0.0085	0.069	7.646	0.0692	0.6353	0.303	7.365	0.0076	0.0328	-0.058	6.586	0.1292	0.9336	-0.362	7.357	0.0731	0.1879
SGO_1297 aspC; aspartate aminotransferase	2.252	7.245	0.0019	0.0046	0.992	6.280	0.0004	0.0005	1.112	6.360	0.0001	0.0000	-1.260	6.958	0.0033	0.0109	-1.140	6.383	0.0042	0.0127	0.120	6.240	0.0340	0.0635
SGO_1298 hypothetical protein SGO_1298		3.425				3.425				3.425														
SGO_1305 substrate-binding protein MsmE		5.520			-0.420	6.325	0.0004	0.0004	-1.367	5.998	0.0004	0.0007		4.586				3.048			-0.947	5.196	0.0053	0.0026
SGO_1312 pepT; peptidase T	3.698	7.531	0.0000	0.0000	3.727	7.558	0.0001	0.0000	3.152	7.040	0.0004	0.0009	0.028	7.925	0.0440	0.2936	-0.546	7.056	0.0025	0.0065	-0.574	7.684	0.0079	0.0057
SGO_1314 metal binding lipoprotein		1.807				1.807				1.807														



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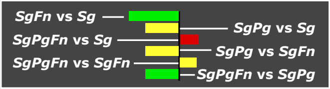

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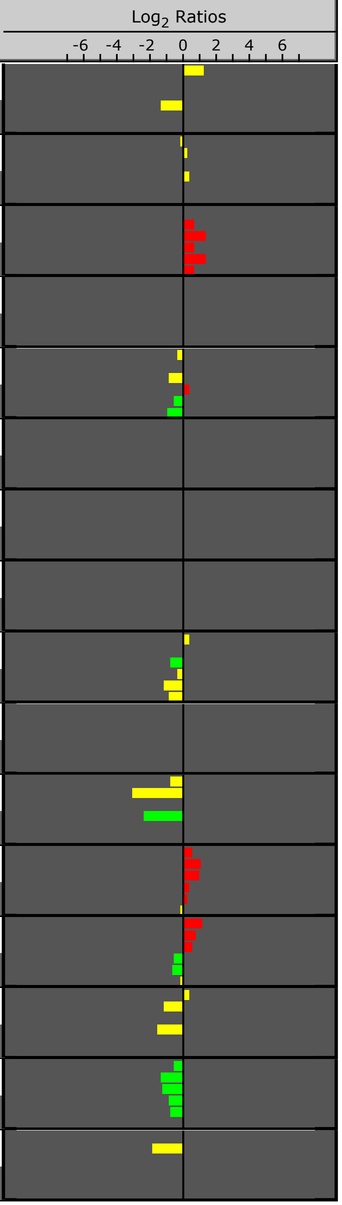
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein		*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1315	trmD; tRNA (guanine-N1)-methyltransferase	1.317	3.611			0.030	3.428	0.1661	0.8725		1.807			-1.287	3.485	0.0152	0.0809		2.000				2.348		
SGO_1316	16S rRNA processing protein RimM	-0.094	4.561	0.0829	0.5220	0.266	4.747	0.0494	0.2206		3.619			0.360	4.180	0.0050	0.0190		2.376				3.351		
SGO_1323	rpsP; ribosomal protein S16	-0.001	7.305	0.1420	0.9590	0.691	7.691	0.0033	0.0082	1.424	8.182	0.0002	0.0003	0.692	7.175	0.0021	0.0051	1.425	7.057	0.0003	0.0002	0.733	7.891	0.0043	0.0012
SGO_1324	hypothetical protein SGO_1324		5.595				5.595				5.595														
SGO_1327	HAD-superfamily subfamily IIA hydrolase, TIGR01457	-0.272	5.984	0.0425	0.2370	0.123	6.174	0.1330	0.6792	-0.794	5.775	0.0079	0.0463	0.395	5.518	0.0009	0.0015	-0.522	4.460	0.0011	0.0014	-0.917	5.317	0.0026	0.0005
SGO_1328	hypothetical protein SGO_1328		1.585				1.585				1.585														
SGO_1330	transporter		3.772				3.772				3.772														
SGO_1331	HlyB/MsbA family ABC transporter		1.807				1.807				1.807														
SGO_1336	pcrA; ATP-dependent DNA helicase PcrA	0.376	6.355	0.0261	0.1308	0.050	6.164	0.0802	0.3879	-0.743	5.818	0.0010	0.0032	-0.326	5.865	0.0282	0.1730	-1.119	4.961	0.0062	0.0218	-0.793	5.338	0.0073	0.0051
SGO_1337	cation efflux family protein		1.585				1.585				1.585														
SGO_1338	Signal peptidase I	-0.729	6.239	0.0050	0.0161	-3.036	5.648	0.0253	0.1018		5.564			-2.307	4.446	0.0012	0.0024		3.696				1.000		
SGO_1339	pyk; pyruvate kinase	0.635	11.550	0.0014	0.0030	1.066	11.826	0.0001	0.0001	0.963	11.757	0.0003	0.0003	0.431	11.551	0.0019	0.0043	0.328	10.883	0.0048	0.0154	-0.104	11.699	0.0426	0.0899
SGO_1340	Phosphofructokinase	1.240	10.517	0.0002	0.0001	0.758	10.195	0.0001	0.0000	0.630	10.116	0.0002	0.0003	-0.483	10.273	0.0008	0.0011	-0.610	9.611	0.0008	0.0008	-0.128	9.949	0.0114	0.0111
SGO_1341	dnaE; DNA-directed DNA polymerase III alpha chain	0.393	5.498	0.0437	0.2450	-1.076	4.546	0.0154	0.0566		4.239			-1.469	4.431	0.0448	0.3009		3.594				1.648		
SGO_1342	ABC transporter, ATP-binding protein SP1715	-0.526	10.529	0.0026	0.0071	-1.281	10.262	0.0001	0.0001	-1.216	10.281	0.0001	0.0000	-0.755	9.403	0.0030	0.0092	-0.690	8.816	0.0033	0.0095	0.066	9.004	0.1095	0.3209
SGO_1343	ABC transporter, ATP-binding protein SP1715		5.350			-1.773	5.547	0.0085	0.0271		5.350				2.063								2.063		



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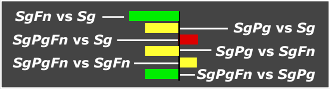
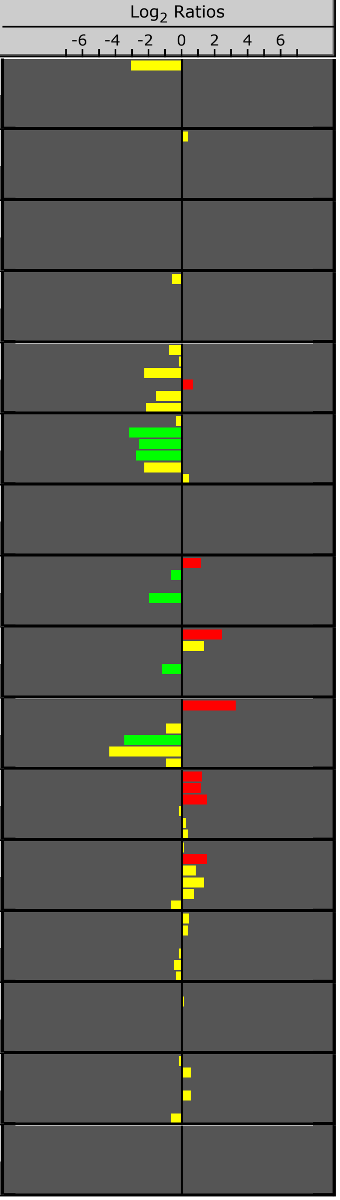


Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	Description	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1347	membrane associated lipoprotein	-3.010	6.238	0.0236	0.1122		6.152				6.152				1.611				1.000						
SGO_1355	lipoprotein, putative	0.352	4.188	0.0603	0.3566		3.483				3.483				2.302				1.692						
SGO_1360	ABC transporter domain protein		2.832				2.832				2.832														
SGO_1361	ADP-ribosylhydrolase	-0.470	3.485				2.700				2.700				1.717				1.107						
SGO_1364	rumA-2; 23S rRNA (uracil-5-)-methyltransferase RumA	-0.705	6.491	0.0080	0.0301	-0.053	6.770	0.1267	0.6436	-2.201	5.952	0.0174	0.1299	0.652	5.934	0.0013	0.0028	-1.496	4.199	0.0205	0.1008	-2.148	5.375	0.0143	0.0158
SGO_1365	transcription regulator yrfE	-0.327	6.965	0.0064	0.0221	-3.071	6.289	0.0001	0.0001	-2.531	6.236	0.0012	0.0040	-2.745	5.496	0.0007	0.0010	-2.204	4.820	0.0169	0.0791	0.541	3.376	0.1526	0.4924
SGO_1366	pheA; prephenate dehydratase						3.719								3.205								3.205		
SGO_1367	aroK; shikimate kinase	1.206	5.508	0.0015	0.0034	-0.645	4.492	0.0027	0.0065		3.781			-1.851	4.827	0.0009	0.0014		3.866				2.617		
SGO_1368	aroA; 3-phosphoshikimate 1-carboxyvinyltransferase	2.491	5.517	0.0015	0.0034	1.405	4.704	0.0175	0.0655		3.098			-1.086	5.261	0.0005	0.0005		4.094				3.617		
SGO_1369	L-2-hydroxyisocaproate dehydrogenase	3.346	8.392	0.0001	0.0000	-0.018	5.905	0.1710	0.9038	-0.928	5.247	0.0072	0.0414	-3.364	7.878	0.0001	0.0000	-4.275	7.170	0.0063	0.0223	-0.910	4.724	0.0565	0.1337
SGO_1370	Protein of unknown function (DUF964) superfamily	1.319	6.800	0.0022	0.0058	1.245	6.740	0.0010	0.0015	1.637	7.025	0.0003	0.0004	-0.075	6.763	0.0826	0.6023	0.318	6.355	0.0193	0.0935	0.392	6.928	0.0178	0.0228
SGO_1372	aroC; chorismate synthase	0.153	4.305	0.0774	0.4805	1.553	5.640	0.0003	0.0002	0.923	4.628	0.0109	0.0717	1.399	4.953	0.0083	0.0379	0.770	3.127			-0.629	5.106	0.0352	0.0663
SGO_1373	aroB; 3-dehydroquinate synthase	0.481	4.716	0.0699	0.4266	0.379	5.146	0.0473	0.2080	0.062	4.562	0.1026	0.9899	-0.102	4.405	0.0224	0.1302	-0.419	3.082			-0.318	4.272	0.0284	0.0487
SGO_1374	aroE; shikimate 5-dehydrogenase		3.196			0.232	4.333	0.0655	0.3054		3.196				2.945								2.945		
SGO_1375	aroD; 3-dehydroquinate dehydratase, type I	-0.075	5.682	0.0821	0.5164	0.563	6.044	0.0214	0.0838	0.006	5.308	0.1015	0.9771	0.638	5.497	0.0111	0.0536	0.081	4.126	0.0571	0.3649	-0.556	5.207	0.1164	0.3516
SGO_1376	Methyltransferase		3.982				3.982				3.982														



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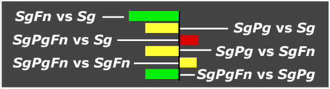
☐ Filter by category:
ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
🟨	no	n/a	bars
🟩	yes	−	ratios, bars
▨	yes	+	*p*- , *q*-Values
▨	yes	−	



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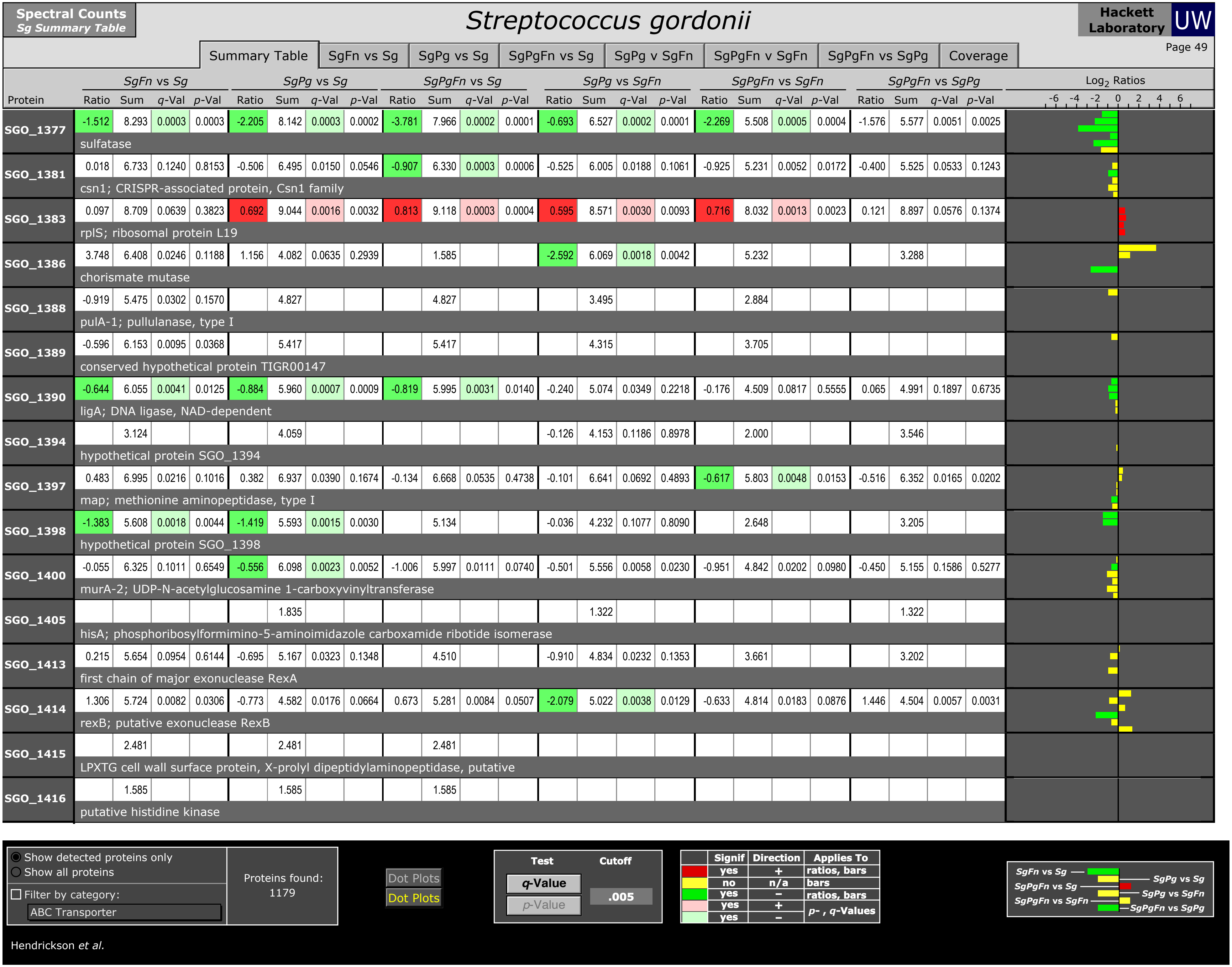

Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*				Log_2 Ratios
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	-6 -4 -2 0 2 4 6
SGO_1377	-1.512	8.293	0.0003	0.0003	-2.205	8.142	0.0003	0.0002	-3.781	7.966	0.0002	0.0001	-0.693	6.527	0.0002	0.0001	-2.269	5.508	0.0005	0.0004	-1.576	5.577	0.0051	0.0025	
	sulfatase																								
SGO_1381	0.018	6.733	0.1240	0.8153	-0.506	6.495	0.0150	0.0546	-0.907	6.330	0.0003	0.0006	-0.525	6.005	0.0188	0.1061	-0.925	5.231	0.0052	0.0172	-0.400	5.525	0.0533	0.1243	
	csn1; CRISPR-associated protein, Csn1 family																								
SGO_1383	0.097	8.709	0.0639	0.3823	0.692	9.044	0.0016	0.0032	0.813	9.118	0.0003	0.0004	0.595	8.571	0.0030	0.0093	0.716	8.032	0.0013	0.0023	0.121	8.897	0.0576	0.1374	
	rplS; ribosomal protein L19																								
SGO_1386	3.748	6.408	0.0246	0.1188	1.156	4.082	0.0635	0.2939		1.585			-2.592	6.069	0.0018	0.0042		5.232				3.288			
	chorismate mutase																								
SGO_1388	-0.919	5.475	0.0302	0.1570		4.827				4.827				3.495				2.884							
	pulA-1; pullulanase, type I																								
SGO_1389	-0.596	6.153	0.0095	0.0368		5.417				5.417				4.315				3.705							
	conserved hypothetical protein TIGR00147																								
SGO_1390	-0.644	6.055	0.0041	0.0125	-0.884	5.960	0.0007	0.0009	-0.819	5.995	0.0031	0.0140	-0.240	5.074	0.0349	0.2218	-0.176	4.509	0.0817	0.5555	0.065	4.991	0.1897	0.6735	
	ligA; DNA ligase, NAD-dependent																								
SGO_1394		3.124				4.059							-0.126	4.153	0.1186	0.8978		2.000				3.546			
	hypothetical protein SGO_1394																								
SGO_1397	0.483	6.995	0.0216	0.1016	0.382	6.937	0.0390	0.1674	-0.134	6.668	0.0535	0.4738	-0.101	6.641	0.0692	0.4893	-0.617	5.803	0.0048	0.0153	-0.516	6.352	0.0165	0.0202	
	map; methionine aminopeptidase, type I																								
SGO_1398	-1.383	5.608	0.0018	0.0044	-1.419	5.593	0.0015	0.0030		5.134			-0.036	4.232	0.1077	0.8090		2.648				3.205			
	hypothetical protein SGO_1398																								
SGO_1400	-0.055	6.325	0.1011	0.6549	-0.556	6.098	0.0023	0.0052	-1.006	5.997	0.0111	0.0740	-0.501	5.556	0.0058	0.0230	-0.951	4.842	0.0202	0.0980	-0.450	5.155	0.1586	0.5277	
	murA-2; UDP-N-acetylglucosamine 1-carboxyvinyltransferase																								
SGO_1405						1.835								1.322								1.322			
	hisA; phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase																								
SGO_1413	0.215	5.654	0.0954	0.6144	-0.695	5.167	0.0323	0.1348		4.510			-0.910	4.834	0.0232	0.1353		3.661				3.202			
	first chain of major exonuclease RexA																								
SGO_1414	1.306	5.724	0.0082	0.0306	-0.773	4.582	0.0176	0.0664	0.673	5.281	0.0084	0.0507	-2.079	5.022	0.0038	0.0129	-0.633	4.814	0.0183	0.0876	1.446	4.504	0.0057	0.0031	
	rexB; putative exonuclease RexB																								
SGO_1415		2.481				2.481				2.481															
	LPXTG cell wall surface protein, X-prolyl dipeptidylaminopeptidase, putative																								
SGO_1416		1.585				1.585				1.585															
	putative histidine kinase																								

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ABC Transporter

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1179

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Dot Plots

Test	Cutoff
q-Value	.005
p-Value	

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🟨	no	n/a	bars
🟩	yes	–	ratios, bars
▨	yes	+	*p*- , *q*-Values
▨	yes	–	

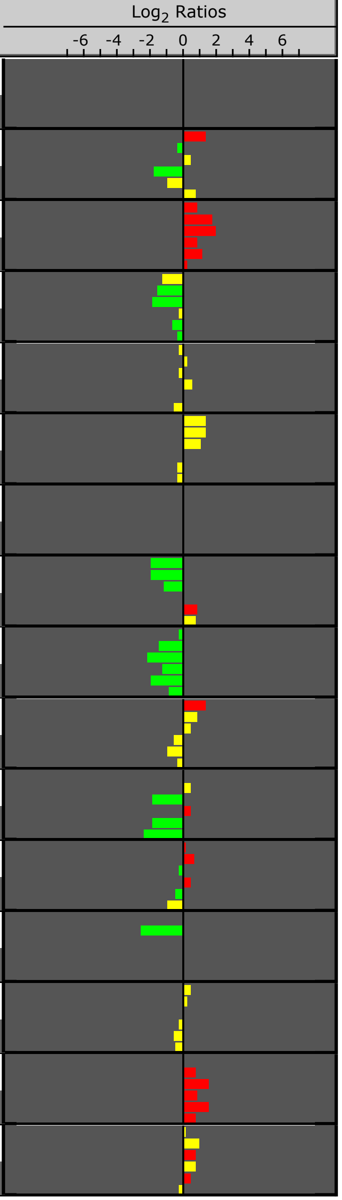
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1417						2.973								2.459								2.459		
	response regulator protein																							
SGO_1422	1.421	7.816	0.0049	0.0157	-0.278	6.778	0.0007	0.0009	0.474	7.184	0.0121	0.0817	-1.700	7.234	0.0037	0.0120	-0.947	6.844	0.0101	0.0413	0.752	6.562	0.0229	0.0351
	hypothetical protein SGO_1422																							
SGO_1426	0.877	13.890	0.0009	0.0017	1.751	14.510	0.0001	0.0000	2.044	14.741	0.0001	0.0000	0.874	14.250	0.0003	0.0003	1.167	13.835	0.0002	0.0001	0.293	14.775	0.0037	0.0009
	eno; enolase																							
SGO_1431	-1.232	10.435	0.0057	0.0190	-1.476	10.366	0.0048	0.0136	-1.818	10.285	0.0024	0.0100	-0.244	9.039	0.0119	0.0586	-0.585	8.282	0.0028	0.0076	-0.341	8.748	0.0026	0.0005
	EzrA; Septation ring formation regulator ezrA																							
SGO_1432	-0.233	7.339	0.0479	0.2714	0.327	7.630	0.0534	0.2414	-0.175	7.394	0.0706	0.6504	0.560	7.005	0.0084	0.0385	0.058	6.137	0.0965	0.6723	-0.502	7.053	0.0667	0.1681
	gyrB; DNA gyrase, B subunit																							
SGO_1434	1.420	4.000	0.0260	0.1301	1.419	4.025	0.0515	0.2317	1.074	2.957			-0.001	4.256	0.1190	0.9037	-0.346	3.106	0.0544	0.3410	-0.345	3.738	0.1566	0.5087
	thiJ; 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis protein																							
SGO_1437		3.669				3.669				3.669														
	DnaQ family exonuclease/DinG family helicase, putative																							
SGO_1439	-1.950	7.156	0.0001	0.0000	-1.888	7.169	0.0001	0.0000	-1.087	7.383	0.0003	0.0006	0.062	5.394	0.0593	0.4113	0.863	5.252	0.0027	0.0072	0.801	5.885	0.0103	0.0094
	ftsX; cell division protein FtsX																							
SGO_1440	-0.192	8.633	0.0018	0.0041	-1.350	8.204	0.0001	0.0000	-2.111	8.027	0.0001	0.0000	-1.158	7.555	0.0000	0.0000	-1.919	6.748	0.0000	0.0000	-0.761	6.532	0.0017	0.0002
	cell-division ATP-binding protein FtsE																							
SGO_1441	1.397	6.689	0.0036	0.0106	0.860	6.328	0.0120	0.0413	0.530	6.167	0.0258	0.2063	-0.537	6.479	0.0212	0.1216	-0.867	5.769	0.0186	0.0894	-0.331	6.072	0.1586	0.5279
	prfB; peptide chain release factor 2																							
SGO_1446	0.050	6.385	0.1420	0.9578	0.547	6.652	0.0188	0.0726	-1.757	5.755	0.0038	0.0190	0.497	6.145	0.0048	0.0181	-1.806	4.641	0.0016	0.0034	-2.303	5.644	0.0026	0.0006
	murF; UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase																							
SGO_1447	0.192	6.727	0.0003	0.0002	0.694	7.021	0.0026	0.0059	-0.234	6.516	0.0002	0.0002	0.502	6.584	0.0037	0.0122	-0.426	5.499	0.0000	0.0000	-0.928	6.423	0.0057	0.0032
	ddlA; D-Ala-D-Ala ligase																							
SGO_1449		7.043			-2.494	7.277	0.0006	0.0007		7.043				4.030								4.030		
	pbp2b; penicillin-binding protein 2B																							
SGO_1450	0.488	5.729	0.1066	0.6933	0.312	5.654	0.1740	0.9221	-0.049	5.584	0.0945	0.9050	-0.175	5.241	0.0703	0.4995	-0.537	4.565	0.0809	0.5462	-0.361	5.099	0.2139	0.7870
	hypothetical protein SGO_1450																							
SGO_1451	-0.022	6.949	0.1451	0.9850	0.844	7.426	0.0011	0.0018	1.596	7.952	0.0003	0.0004	0.866	6.911	0.0024	0.0066	1.618	6.827	0.0008	0.0008	0.752	7.695	0.0032	0.0008
	frr; ribosome recycling factor																							
SGO_1452	0.222	6.908	0.0294	0.1514	1.012	7.403	0.0077	0.0237	0.769	7.227	0.0011	0.0036	0.790	6.962	0.0074	0.0313	0.547	6.184	0.0004	0.0002	-0.243	7.184	0.0848	0.2275
	pyrH; uridylate kinase																							



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Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	.005
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
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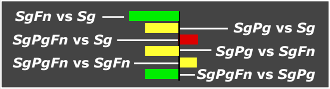

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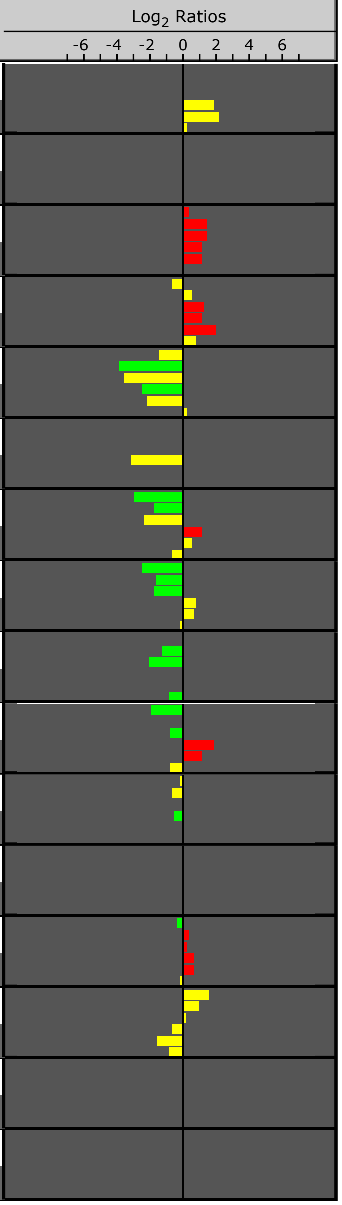
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory **UW**

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1453 glycosyl transferase, family 8 SP1766		2.231				4.100				5.420			1.869	3.936			2.151	4.446	0.0325	0.1818	0.282	5.393	0.1618	0.5445
SGO_1454 amino acid permease family protein		4.989				4.989				4.989														
SGO_1455 rplA; ribosomal protein L1	0.360	9.165	0.0027	0.0075	1.547	9.960	0.0027	0.0064	1.539	9.954	0.0016	0.0063	1.187	9.545	0.0031	0.0097	1.180	8.929	0.0033	0.0095	-0.007	10.022	0.2492	0.9697
SGO_1456 rplK; ribosomal protein L11	-0.623	7.371	0.0080	0.0297	0.563	7.956	0.0124	0.0428	1.340	8.456	0.0002	0.0002	1.186	7.235	0.0044	0.0159	1.963	7.189	0.0006	0.0004	0.777	8.133	0.0094	0.0079
SGO_1458 aha1; cation-transporting ATPase yfgQ	-1.358	7.397	0.0062	0.0213	-3.777	7.025	0.0025	0.0057	-3.490	6.985	0.0199	0.1543	-2.418	5.291	0.0023	0.0064	-2.131	4.587	0.0298	0.1627	0.287	3.299	0.1503	0.4830
SGO_1459 glyoxylase family protein		5.269				1.161							-3.101	4.837	0.0133	0.0686		4.145				0.648		
SGO_1460 DNA translocase ftsK	-2.935	6.888	0.0009	0.0018	-1.693	7.097	0.0017	0.0034	-2.301	6.850	0.0154	0.1116	1.242	5.000	0.0001	0.0000	0.634	3.467	0.0102	0.0427	-0.608	4.901	0.0251	0.0404
SGO_1463 peptidyl-prolyl cis-trans isomerase	-2.423	7.258	0.0002	0.0002	-1.582	7.422	0.0003	0.0002	-1.721	7.388	0.0001	0.0001	0.841	5.569	0.0059	0.0232	0.702	4.869	0.0085	0.0325	-0.139	5.848	0.1013	0.2915
SGO_1464 uncharacterized probable metal-binding protein		7.031			-1.171	7.558	0.0021	0.0045	-1.964	7.359	0.0007	0.0020		5.336				3.939			-0.793	5.996	0.0050	0.0018
SGO_1465 ABC transporter, ATP-binding protein SP0770	-1.851	6.642	0.0016	0.0037	0.016	7.297	0.1771	0.9448	-0.670	6.990	0.0048	0.0254	1.867	6.138	0.0013	0.0026	1.182	5.013	0.0011	0.0016	-0.686	6.485	0.0158	0.0184
SGO_1466 MTA/SAH nucleosidase	-0.133	5.958	0.0658	0.3968	-0.616	5.754	0.0142	0.0510		5.034			-0.483	5.149	0.0044	0.0157		3.755				3.893		
SGO_1468 MutT/nudix family protein		1.585				1.585				1.585														
SGO_1469 glmU; UDP-N-acetylglucosamine pyrophosphorylase	-0.341	7.526	0.0005	0.0007	0.365	7.880	0.0011	0.0018	0.313	7.853	0.0043	0.0221	0.705	7.228	0.0004	0.0003	0.653	6.587	0.0017	0.0038	-0.052	7.514	0.1588	0.5306
SGO_1472 acetyltransferase, GNAT family	1.625	4.942	0.0553	0.3203	0.998	4.385	0.0738	0.3513	0.170	3.088			-0.627	4.934	0.0371	0.2402	-1.454	3.841	0.0537	0.3353	-0.828	3.906	0.1256	0.3862
SGO_1475 lipoprotein, putative		4.513				4.513				4.513														
SGO_1483 ABC transporter, permease protein, probable SP0913		1.643				1.643				1.643														



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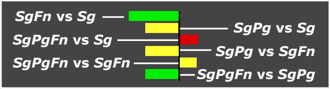

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Spectral Counts
Sg Summary Table

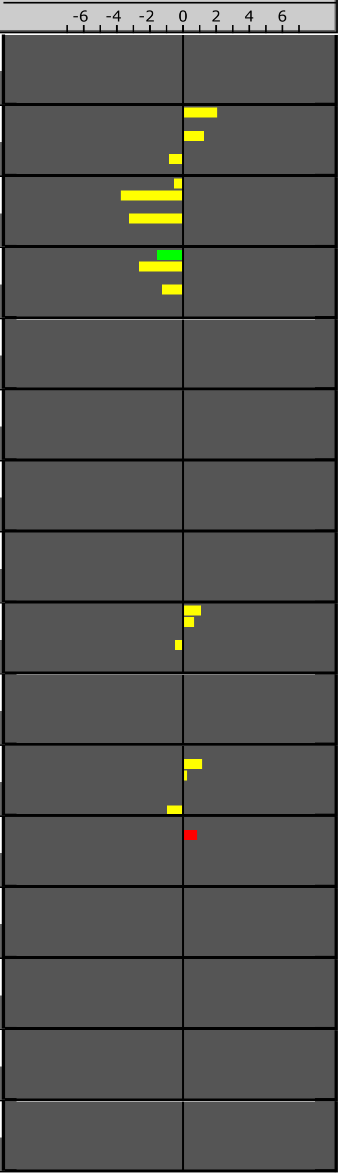
Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein		*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1484	ABC transporter, ATP-binding protein						3.135								2.622								2.622		
SGO_1486	beta-galactosidase	2.124	3.744				1.322			1.330	3.932	0.0225	0.1786		2.933			-0.794	3.441	0.0286	0.1547		3.161		
SGO_1487	LPXTG cell wall surface protein, Cna protein B-type domain	-0.501	7.346	0.0093	0.0359	-3.730	6.626	0.0185	0.0708		6.572			-3.229	5.637	0.0167	0.0923		4.952				1.322		
SGO_1493	hypothetical protein SGO_1493	-1.485	7.194	0.0009	0.0015	-2.649	6.864	0.0185	0.0704		6.754			-1.164	5.045	0.0191	0.1084		4.145				2.585		
SGO_1495	putative transcriptional regulator		4.523				4.523				4.523														
SGO_1498	ABC transporter, permease protein, probable SP0913		1.643				1.643				1.643														
SGO_1504	histidine kinase		3.785				3.785				3.785														
SGO_1507	hypothetical protein SGO_1507		5.334				5.334				5.334														
SGO_1512	lacG; 6-phospho-beta-galactosidase	1.099	4.069	0.0412	0.2271	0.741	3.060				1.643			-0.358	3.726	0.0645	0.4512		2.648				1.871		
SGO_1513	lacE; PTS system, lactose-specific IIBC component		1.807				1.807				1.807														
SGO_1516	lacD-2; tagatose 1,6-diphosphate aldolase		4.452			1.216	6.199	0.0050	0.0144	0.291	5.601	0.0057	0.0306		5.175				3.613			-0.925	5.776	0.0172	0.0219
SGO_1518	lacB-2; galactose-6-phosphate isomerase, LacB subunit		3.417			0.892	4.926	0.0015	0.0030		3.417				3.788								3.788		
SGO_1520	PTS system, IIC component		3.058				3.058				3.058														
SGO_1521	PTS system IIB component (galactitol/fructose specific)		2.170				2.170				2.170														
SGO_1523	lacD-1; tagatose 1,6-diphosphate aldolase																								
SGO_1527	Lactose phosphotransferase system repressor		1.865				1.865				1.865														

Log$_2$ Ratios



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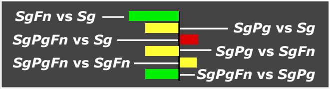
Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
🟥	yes	+	ratios, bars
🟨	no	n/a	bars
🟩	yes	–	ratios, bars
	yes	+	*p*- , *q*-Values
	yes	–	



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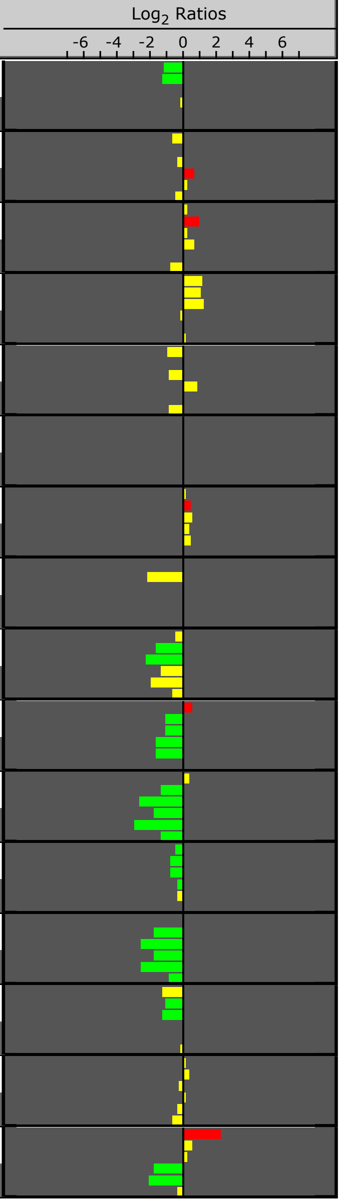
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1529	-1.110	6.071	0.0007	0.0011	-1.199	6.053	0.0017	0.0037		5.519			-0.089	4.876	0.1076	0.8056		3.294				3.846		
	hypothetical protein SGO_1529																							
SGO_1530	-0.620	8.210	0.0111	0.0443	0.080	8.516	0.1062	0.5268	-0.321	8.323	0.0092	0.0575	0.700	7.741	0.0048	0.0180	0.299	6.897	0.0330	0.1849	-0.402	7.851	0.0073	0.0049
	methionine-tRNA ligase																							
SGO_1531	0.311	5.961	0.0299	0.1548	0.988	6.363	0.0013	0.0023	0.273	5.947	0.0295	0.2398	0.677	5.972	0.0060	0.0243	-0.038	4.984	0.1282	0.9234	-0.715	5.962	0.0212	0.0304
	xth; exodeoxyribonuclease III																							
SGO_1534	1.195	5.714	0.0220	0.1038	1.089	5.713	0.0490	0.2161	1.284	5.196	0.0428	0.3687	-0.106	5.567	0.1294	0.9952	0.089	4.573	0.0468	0.2795	0.195	5.182	0.2345	0.8886
	ArsC family																							
SGO_1536	-0.922	6.083	0.0065	0.0228	-0.019	6.475	0.1779	0.9526	-0.798	6.124	0.0053	0.0282	0.903	5.581	0.0127	0.0647	0.124	4.493	0.0921	0.6369	-0.779	5.622	0.0396	0.0794
	conserved hypothetical protein TIGR00096																							
SGO_1538		3.266				3.266				3.266														
	DNA-directed DNA polymerase III, delta'' chain																							
SGO_1539	0.151	6.166	0.0639	0.3839	0.530	6.365	0.0031	0.0075	0.614	6.430	0.0085	0.0520	0.379	5.928	0.0213	0.1226	0.463	5.379	0.0278	0.1490	0.084	6.150	0.1727	0.5986
	tmk; thymidylate kinase																							
SGO_1540		4.984			-2.147	5.138	0.0124	0.0428		4.984				1.322								1.322		
	YitT family protein																							
SGO_1541	-0.363	8.032	0.0624	0.3731	-1.636	7.569	0.0014	0.0025	-2.232	7.454	0.0008	0.0022	-1.273	6.843	0.0107	0.0508	-1.869	6.097	0.0086	0.0335	-0.596	5.759	0.0271	0.0458
	atpC; ATP synthase F1, epsilon subunit																							
SGO_1542	0.619	11.040	0.0001	0.0001	-1.008	10.281	0.0002	0.0001	-1.022	10.277	0.0002	0.0002	-1.626	10.208	0.0000	0.0000	-1.641	9.594	0.0001	0.0000	-0.014	9.171	0.2260	0.8480
	atpD; ATP synthase F1, beta subunit																							
SGO_1543	0.383	8.135	0.0131	0.0553	-1.291	7.418	0.0002	0.0001	-2.555	7.153	0.0001	0.0001	-1.674	7.196	0.0013	0.0029	-2.938	6.372	0.0011	0.0015	-1.264	5.625	0.0026	0.0005
	atpG; ATP synthase F1, gamma subunit																							
SGO_1544	-0.415	10.250	0.0008	0.0014	-0.726	10.124	0.0001	0.0001	-0.675	10.144	0.0002	0.0003	-0.311	9.368	0.0025	0.0072	-0.260	8.780	0.0054	0.0184	0.051	9.229	0.1101	0.3231
	atpA; ATP synthase F1, alpha subunit																							
SGO_1545	0.015	8.292	0.1306	0.8681	-1.669	7.677	0.0004	0.0004	-2.474	7.521	0.0002	0.0003	-1.684	7.176	0.0007	0.0008	-2.489	6.412	0.0006	0.0005	-0.805	5.751	0.0010	0.0001
	atpH; ATP synthase F1, delta subunit																							
SGO_1546	-1.156	8.155	0.0064	0.0223	-1.026	8.163	0.0016	0.0031	-1.162	8.114	0.0003	0.0005	0.130	7.047	0.1240	0.9498	-0.007	6.360	0.1038	0.7314	-0.137	6.983	0.1164	0.3521
	atpF; ATP synthase F0, B subunit																							
SGO_1550	0.171	7.857	0.0596	0.3503	0.394	7.975	0.0120	0.0408	-0.160	7.692	0.0416	0.3558	0.224	7.536	0.0179	0.1003	-0.330	6.657	0.0181	0.0857	-0.554	7.392	0.0092	0.0072
	glgP-1; glycogen phosphorylase																							
SGO_1551	2.324	7.034	0.0017	0.0041	0.606	5.888	0.1122	0.5606	0.335	5.734	0.0978	0.9376	-1.718	6.594	0.0009	0.0014	-1.989	5.919	0.0006	0.0006	-0.272	5.395	0.1285	0.4007
	glgA; Glycogen synthase																							



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Test	Cutoff
***q*-Value**	**.005**
p-Value	

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▨	yes	+	*p*- , *q*-Values
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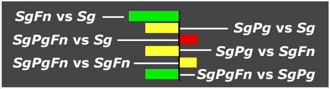

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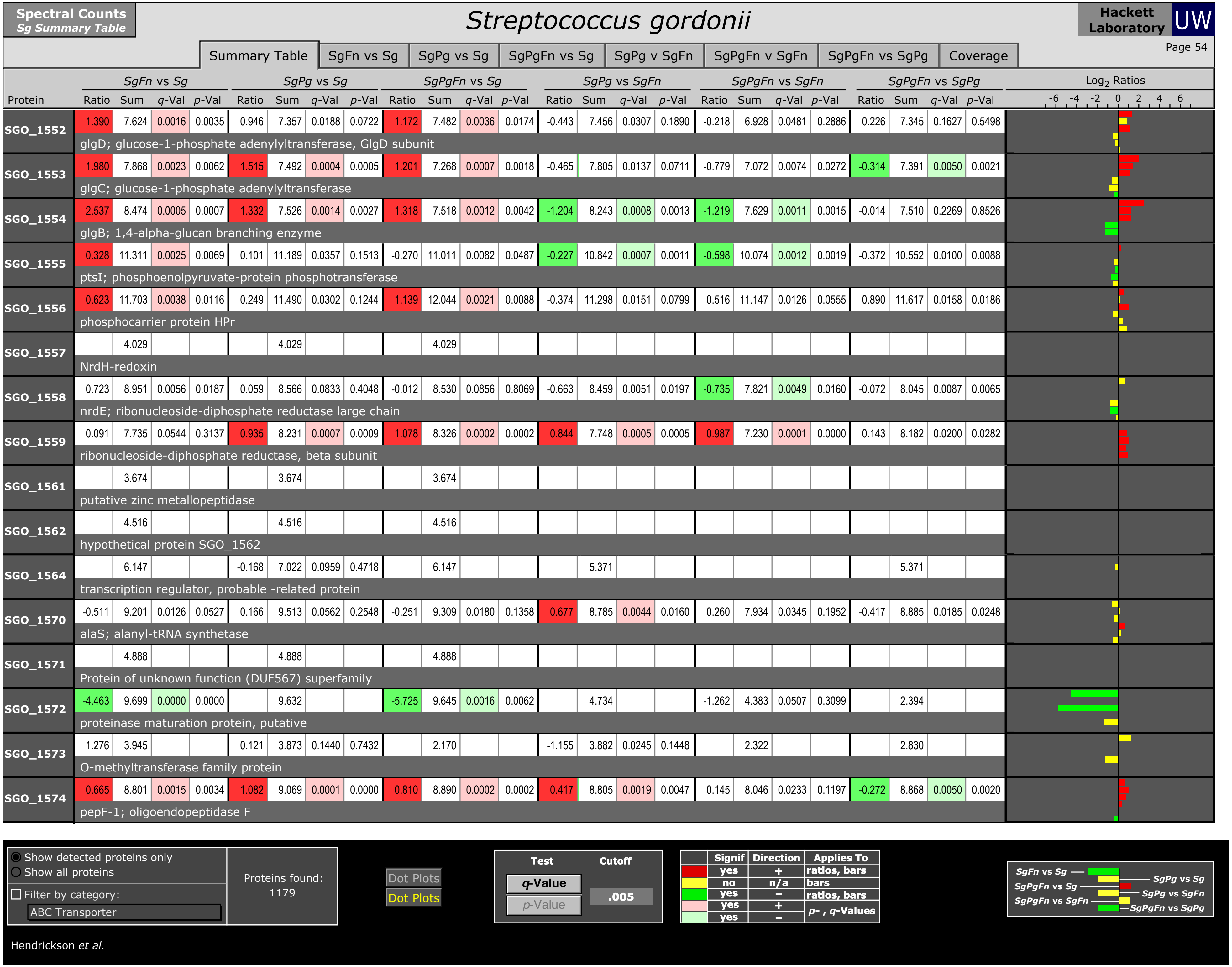

Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1552	1.390	7.624	0.0016	0.0035	0.946	7.357	0.0188	0.0722	1.172	7.482	0.0036	0.0174	-0.443	7.456	0.0307	0.1890	-0.218	6.928	0.0481	0.2886	0.226	7.345	0.1627	0.5498
	glgD; glucose-1-phosphate adenylyltransferase, GlgD subunit																							
SGO_1553	1.980	7.868	0.0023	0.0062	1.515	7.492	0.0004	0.0005	1.201	7.268	0.0007	0.0018	-0.465	7.805	0.0137	0.0711	-0.779	7.072	0.0074	0.0272	-0.314	7.391	0.0050	0.0021
	glgC; glucose-1-phosphate adenylyltransferase																							
SGO_1554	2.537	8.474	0.0005	0.0007	1.332	7.526	0.0014	0.0027	1.318	7.518	0.0012	0.0042	-1.204	8.243	0.0008	0.0013	-1.219	7.629	0.0011	0.0015	-0.014	7.510	0.2269	0.8526
	glgB; 1,4-alpha-glucan branching enzyme																							
SGO_1555	0.328	11.311	0.0025	0.0069	0.101	11.189	0.0357	0.1513	-0.270	11.011	0.0082	0.0487	-0.227	10.842	0.0007	0.0011	-0.598	10.074	0.0012	0.0019	-0.372	10.552	0.0100	0.0088
	ptsI; phosphoenolpyruvate-protein phosphotransferase																							
SGO_1556	0.623	11.703	0.0038	0.0116	0.249	11.490	0.0302	0.1244	1.139	12.044	0.0021	0.0088	-0.374	11.298	0.0151	0.0799	0.516	11.147	0.0126	0.0555	0.890	11.617	0.0158	0.0186
	phosphocarrier protein HPr																							
SGO_1557		4.029				4.029				4.029														
	NrdH-redoxin																							
SGO_1558	0.723	8.951	0.0056	0.0187	0.059	8.566	0.0833	0.4048	-0.012	8.530	0.0856	0.8069	-0.663	8.459	0.0051	0.0197	-0.735	7.821	0.0049	0.0160	-0.072	8.045	0.0087	0.0065
	nrdE; ribonucleoside-diphosphate reductase large chain																							
SGO_1559	0.091	7.735	0.0544	0.3137	0.935	8.231	0.0007	0.0009	1.078	8.326	0.0002	0.0002	0.844	7.748	0.0005	0.0005	0.987	7.230	0.0001	0.0000	0.143	8.182	0.0200	0.0282
	ribonucleoside-diphosphate reductase, beta subunit																							
SGO_1561		3.674				3.674				3.674														
	putative zinc metallopeptidase																							
SGO_1562		4.516				4.516				4.516														
	hypothetical protein SGO_1562																							
SGO_1564		6.147			-0.168	7.022	0.0959	0.4718		6.147				5.371								5.371		
	transcription regulator, probable -related protein																							
SGO_1570	-0.511	9.201	0.0126	0.0527	0.166	9.513	0.0562	0.2548	-0.251	9.309	0.0180	0.1358	0.677	8.785	0.0044	0.0160	0.260	7.934	0.0345	0.1952	-0.417	8.885	0.0185	0.0248
	alaS; alanyl-tRNA synthetase																							
SGO_1571		4.888				4.888				4.888														
	Protein of unknown function (DUF567) superfamily																							
SGO_1572	-4.463	9.699	0.0000	0.0000		9.632			-5.725	9.645	0.0016	0.0062		4.734			-1.262	4.383	0.0507	0.3099		2.394		
	proteinase maturation protein, putative																							
SGO_1573	1.276	3.945			0.121	3.873	0.1440	0.7432		2.170			-1.155	3.882	0.0245	0.1448		2.322				2.830		
	O-methyltransferase family protein																							
SGO_1574	0.665	8.801	0.0015	0.0034	1.082	9.069	0.0001	0.0000	0.810	8.890	0.0002	0.0002	0.417	8.805	0.0019	0.0047	0.145	8.046	0.0233	0.1197	-0.272	8.868	0.0050	0.0020
	pepF-1; oligoendopeptidase F																							

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Proteins found:
1179

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Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
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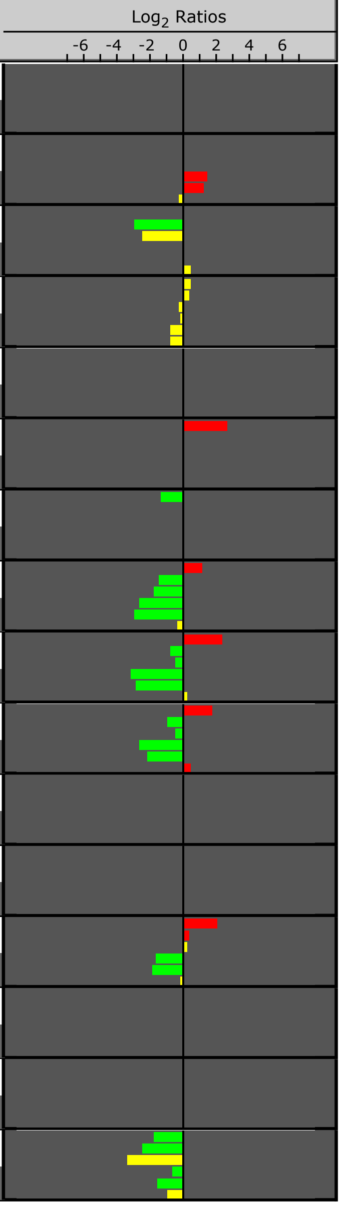
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1576 ptcC; PTS system, IIC component		2.832				2.832				2.832														
SGO_1580 PTS system, Lactose/Cellobiose specific IIB subunit		3.178				4.634				4.506			1.452	4.570	0.0007	0.0009	1.302	3.866	0.0039	0.0118	-0.150	5.058	0.1529	0.4943
SGO_1585 D-Alanyl-D-Alanine carboxypeptidase		6.024			-2.854	6.245	0.0039	0.0104	-2.399	6.151	0.0222	0.1761		2.920				1.461			0.456	3.557	0.2327	0.8803
SGO_1587 queA; S-adenosylmethionine:tRNA ribosyltransferase-isomerase	0.505	6.189	0.0397	0.2167	0.437	6.170	0.0692	0.3251	-0.217	5.809	0.0458	0.3997	-0.068	5.865	0.1190	0.9045	-0.722	4.947	0.0075	0.0278	-0.654	5.537	0.0426	0.0902
SGO_1588 arcR; arginine repressor		3.890				3.890				3.890														
SGO_1589 arcT; putative transaminase/peptidase	2.726	6.450	0.0001	0.0000		3.546				3.546				5.730				5.120						
SGO_1590 arcD; arginine-ornithine antiporter	-1.292	7.433	0.0008	0.0014		6.934				6.934				5.146				4.535						
SGO_1591 arcC; carbamate kinase	1.169	8.010	0.0009	0.0015	-1.436	6.786	0.0047	0.0131	-1.727	6.702	0.0018	0.0070	-2.605	7.184	0.0002	0.0001	-2.896	6.530	0.0001	0.0000	-0.291	5.239	0.0865	0.2333
SGO_1592 arcB; ornithine carbamoyltransferase	2.366	11.142	0.0009	0.0016	-0.713	9.197	0.0000	0.0000	-0.397	9.329	0.0032	0.0149	-3.079	10.535	0.0008	0.0012	-2.763	9.962	0.0010	0.0014	0.316	8.455	0.0271	0.0457
SGO_1593 arcA; arginine deiminase	1.771	10.509	0.0002	0.0001	-0.870	8.998	0.0009	0.0015	-0.377	9.191	0.0021	0.0090	-2.641	9.840	0.0002	0.0001	-2.148	9.308	0.0002	0.0001	0.493	8.251	0.0030	0.0007
SGO_1594 Crp/Fnr family protein		3.486				3.486				3.486														
SGO_1598 hypothetical protein SGO_1598		2.836				2.836				2.836														
SGO_1599 sodA; manganese-dependent superoxide dismutase	2.054	10.580	0.0002	0.0002	0.417	9.437	0.0020	0.0044	0.277	9.360	0.0057	0.0308	-1.637	10.158	0.0003	0.0002	-1.777	9.514	0.0004	0.0002	-0.140	9.050	0.0520	0.1195
SGO_1600 DNA polymerase III, delta chain		3.975				3.975				3.975														
SGO_1601 celB; DNA internalization-related competence protein celB		2.604				2.604				2.604														
SGO_1604 acyltransferase family protein	-1.738	6.821	0.0006	0.0009	-2.382	6.699	0.0006	0.0007	-3.267	6.516	0.0101	0.0647	-0.644	4.907	0.0028	0.0085	-1.529	3.806	0.0025	0.0063	-0.886	3.902	0.0769	0.2010



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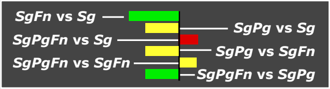

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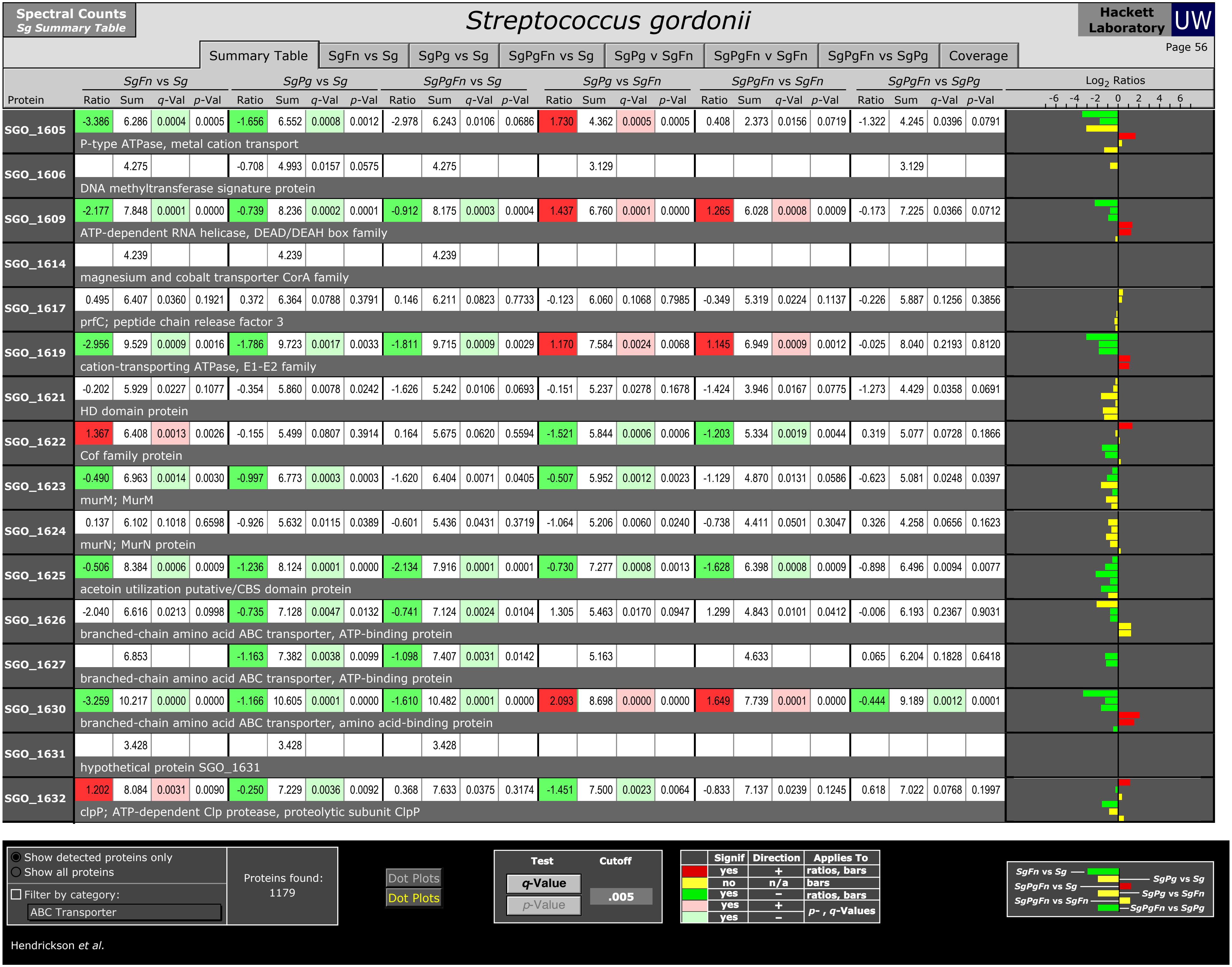

Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1605 P-type ATPase, metal cation transport	-3.386	6.286	0.0004	0.0005	-1.656	6.552	0.0008	0.0012	-2.978	6.243	0.0106	0.0686	1.730	4.362	0.0005	0.0005	0.408	2.373	0.0156	0.0719	-1.322	4.245	0.0396	0.0791
SGO_1606 DNA methyltransferase signature protein		4.275			-0.708	4.993	0.0157	0.0575		4.275				3.129								3.129		
SGO_1609 ATP-dependent RNA helicase, DEAD/DEAH box family	-2.177	7.848	0.0001	0.0000	-0.739	8.236	0.0002	0.0001	-0.912	8.175	0.0003	0.0004	1.437	6.760	0.0001	0.0000	1.265	6.028	0.0008	0.0009	-0.173	7.225	0.0366	0.0712
SGO_1614 magnesium and cobalt transporter CorA family		4.239				4.239				4.239														
SGO_1617 prfC; peptide chain release factor 3	0.495	6.407	0.0360	0.1921	0.372	6.364	0.0788	0.3791	0.146	6.211	0.0823	0.7733	-0.123	6.060	0.1068	0.7985	-0.349	5.319	0.0224	0.1137	-0.226	5.887	0.1256	0.3856
SGO_1619 cation-transporting ATPase, E1-E2 family	-2.956	9.529	0.0009	0.0016	-1.786	9.723	0.0017	0.0033	-1.811	9.715	0.0009	0.0029	1.170	7.584	0.0024	0.0068	1.145	6.949	0.0009	0.0012	-0.025	8.040	0.2193	0.8120
SGO_1621 HD domain protein	-0.202	5.929	0.0227	0.1077	-0.354	5.860	0.0078	0.0242	-1.626	5.242	0.0106	0.0693	-0.151	5.237	0.0278	0.1678	-1.424	3.946	0.0167	0.0775	-1.273	4.429	0.0358	0.0691
SGO_1622 Cof family protein	1.367	6.408	0.0013	0.0026	-0.155	5.499	0.0807	0.3914	0.164	5.675	0.0620	0.5594	-1.521	5.844	0.0006	0.0006	-1.203	5.334	0.0019	0.0044	0.319	5.077	0.0728	0.1866
SGO_1623 murM; MurM	-0.490	6.963	0.0014	0.0030	-0.997	6.773	0.0003	0.0003	-1.620	6.404	0.0071	0.0405	-0.507	5.952	0.0012	0.0023	-1.129	4.870	0.0131	0.0586	-0.623	5.081	0.0248	0.0397
SGO_1624 murN; MurN protein	0.137	6.102	0.1018	0.6598	-0.926	5.632	0.0115	0.0389	-0.601	5.436	0.0431	0.3719	-1.064	5.206	0.0060	0.0240	-0.738	4.411	0.0501	0.3047	0.326	4.258	0.0656	0.1623
SGO_1625 acetoin utilization putative/CBS domain protein	-0.506	8.384	0.0006	0.0009	-1.236	8.124	0.0001	0.0000	-2.134	7.916	0.0001	0.0001	-0.730	7.277	0.0008	0.0013	-1.628	6.398	0.0008	0.0009	-0.898	6.496	0.0094	0.0077
SGO_1626 branched-chain amino acid ABC transporter, ATP-binding protein	-2.040	6.616	0.0213	0.0998	-0.735	7.128	0.0047	0.0132	-0.741	7.124	0.0024	0.0104	1.305	5.463	0.0170	0.0947	1.299	4.843	0.0101	0.0412	-0.006	6.193	0.2367	0.9031
SGO_1627 branched-chain amino acid ABC transporter, ATP-binding protein		6.853			-1.163	7.382	0.0038	0.0099	-1.098	7.407	0.0031	0.0142		5.163				4.633			0.065	6.204	0.1828	0.6418
SGO_1630 branched-chain amino acid ABC transporter, amino acid-binding protein	-3.259	10.217	0.0000	0.0000	-1.166	10.605	0.0001	0.0000	-1.610	10.482	0.0001	0.0000	2.093	8.698	0.0000	0.0000	1.649	7.739	0.0001	0.0000	-0.444	9.189	0.0012	0.0001
SGO_1631 hypothetical protein SGO_1631		3.428				3.428				3.428														
SGO_1632 clpP; ATP-dependent Clp protease, proteolytic subunit ClpP	1.202	8.084	0.0031	0.0090	-0.250	7.229	0.0036	0.0092	0.368	7.633	0.0375	0.3174	-1.451	7.500	0.0023	0.0064	-0.833	7.137	0.0239	0.1245	0.618	7.022	0.0768	0.1997

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	Signif	Direction	Applies To
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▨	yes	+	*p*- , *q*-Values
▨	yes	−	

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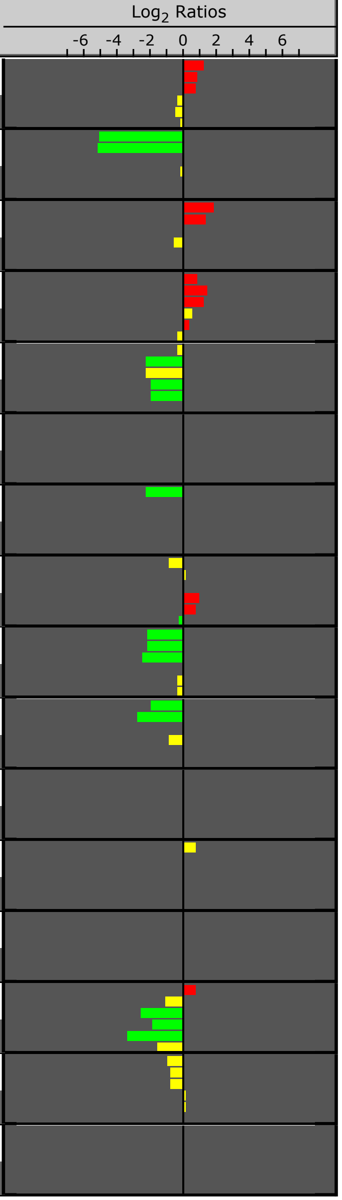
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1633 upp; uracil phosphoribosyltransferase	1.254	8.358	0.0018	0.0044	0.909	8.114	0.0001	0.0000	0.812	8.067	0.0046	0.0242	-0.346	8.175	0.0121	0.0602	-0.442	7.533	0.0195	0.0946	-0.097	7.949	0.1841	0.6500
SGO_1634 magnesium-translocating P-type ATPase	-4.978	9.104	0.0000	0.0000	-5.111	9.102	0.0000	0.0000		9.059			-0.133	4.535	0.1063	0.7935		2.958				3.500		
SGO_1638 murE; UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	1.909	5.438	0.0023	0.0061	1.421	5.055	0.0014	0.0027		3.205			-0.488	5.348	0.0125	0.0623		3.968				4.073		
SGO_1648 ppx1; inorganic pyrophosphatase, manganese-dependent	0.910	8.722	0.0009	0.0016	1.546	9.176	0.0020	0.0044	1.285	8.978	0.0004	0.0007	0.636	8.950	0.0052	0.0203	0.375	8.178	0.0014	0.0026	-0.261	9.108	0.0541	0.1270
SGO_1649 act; pyruvate formate-lyase-activating enzyme	-0.303	6.470	0.0116	0.0477	-2.242	5.905	0.0010	0.0017	-2.213	5.763	0.0122	0.0831	-1.939	5.143	0.0006	0.0007	-1.910	4.362	0.0027	0.0073	0.029	3.498	0.2429	0.9375
SGO_1650 LPXTG cell wall surface protein, collagen binding domain		7.977				7.977				7.977														
SGO_1651 LPXTG cell wall surface protein, nuclease/phosphatase domain	-2.162	9.827	0.0000	0.0000		9.536				9.536				6.862				6.251						
SGO_1652 intracellular glycosyl hydrolase	-0.823	6.776	0.0058	0.0195	0.184	7.218	0.0578	0.2631	-0.012	7.118	0.0881	0.8335	1.008	6.371	0.0005	0.0005	0.811	5.633	0.0010	0.0012	-0.197	6.691	0.0007	0.0000
SGO_1653 trehalose PTS enzyme II	-2.067	8.997	0.0002	0.0002	-2.054	8.998	0.0002	0.0001	-2.355	8.961	0.0004	0.0007	0.013	7.115	0.1226	0.9373	-0.288	6.406	0.0813	0.5500	-0.301	7.020	0.1579	0.5204
SGO_1655 CBS domain protein/possible hemolysin	-1.918	7.001	0.0023	0.0060	-2.739	6.857	0.0016	0.0030		6.653			-0.821	4.901	0.0162	0.0886		3.653				3.417		
SGO_1657 membrane protein		4.486				4.486				4.486														
SGO_1661 radical SAM protein, TIGR01212 family	0.772	4.627	0.0794	0.4944		3.822				3.822				2.887				2.277						
SGO_1665 rRNA methylase		2.585				2.585				2.585														
SGO_1666 trkA; potassium uptake protein, Trk family	0.784	7.821	0.0022	0.0057	-0.970	6.980	0.0056	0.0162	-2.475	6.630	0.0011	0.0038	-1.754	7.016	0.0001	0.0000	-3.259	6.176	0.0001	0.0000	-1.505	5.335	0.0052	0.0026
SGO_1669 ribosomal large subunit pseudouridine synthase B	-0.888	7.256	0.0099	0.0386	-0.728	7.307	0.0126	0.0436	-0.722	7.304	0.0063	0.0352	0.160	6.308	0.0762	0.5497	0.166	5.693	0.0746	0.4987	0.006	6.372	0.2463	0.9553
SGO_1670 scpB; segregation and condensation protein B		2.379				2.379				2.379														



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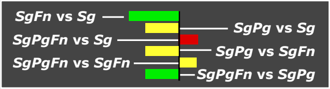

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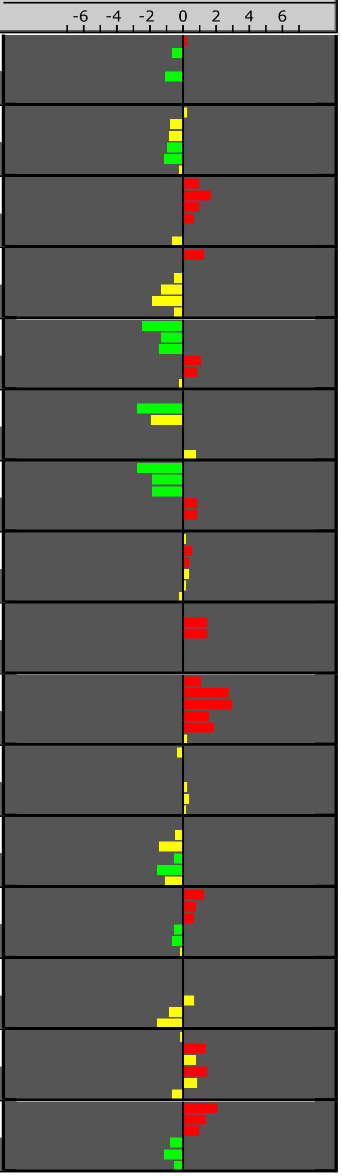
Streptococcus gordonii

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1674	0.340	5.823	0.0050	0.0159	-0.643	5.361	0.0040	0.0107		4.646			-0.983	5.062	0.0007	0.0010		3.858				3.494		
phosphodiesterase, MJ0936 family																								
SGO_1675	0.255	6.690	0.0603	0.3569	-0.654	6.276	0.0214	0.0834	-0.814	6.224	0.0104	0.0676	-0.908	5.903	0.0027	0.0079	-1.069	5.244	0.0031	0.0088	-0.161	5.315	0.1661	0.5658
HAM1 protein-like protein																								
SGO_1676	0.999	5.350	0.0014	0.0030	1.692	5.845	0.0003	0.0002	1.047	5.395	0.0034	0.0164	0.694	5.633	0.0003	0.0002	0.048	4.668	0.0972	0.6784	-0.645	5.659	0.0113	0.0108
murI; glutamate racemase																								
SGO_1678	1.280	6.005	0.0026	0.0070	0.029	5.328	0.1365	0.6999	-0.494	4.666	0.0386	0.3278	-1.251	5.548	0.0083	0.0379	-1.774	4.577	0.0233	0.1208	-0.523	4.291	0.1651	0.5609
lysA; diaminopimelate decarboxylase																								
SGO_1679	-2.373	10.552	0.0000	0.0000	-1.278	10.798	0.0004	0.0003	-1.444	10.749	0.0001	0.0000	1.095	9.069	0.0023	0.0062	0.929	8.341	0.0012	0.0019	-0.165	9.433	0.0933	0.2616
phosphotransferase system enzyme II																								
SGO_1680		7.797			-2.691	8.003	0.0007	0.0010	-1.867	7.981	0.0139	0.0989		4.584				3.796			0.823	5.498	0.0228	0.0348
phosphotransferase system enzyme II																								
SGO_1681	-2.678	10.136	0.0001	0.0000	-1.826	10.284	0.0000	0.0000	-1.822	10.287	0.0001	0.0001	0.852	8.227	0.0011	0.0020	0.855	7.626	0.0043	0.0131	0.003	8.594	0.2354	0.8967
PTS system, mannose/fructose/sorbose family, IID component																								
SGO_1683	0.183	8.135	0.0676	0.4105	0.563	8.319	0.0012	0.0021	0.372	8.211	0.0043	0.0219	0.380	7.907	0.0346	0.2185	0.189	7.196	0.0866	0.5936	-0.191	7.970	0.0457	0.0994
serS; seryl-tRNA synthetase																								
SGO_1684		4.578			1.477	6.486	0.0012	0.0020	1.486	6.497	0.0013	0.0044		5.526				4.931			0.009	6.534	0.2382	0.9134
acyl-CoA dehydrogenase family																								
SGO_1685	1.132	6.834	0.0008	0.0013	2.779	8.132	0.0001	0.0000	3.050	8.386	0.0008	0.0023	1.647	7.820	0.0001	0.0000	1.918	7.432	0.0017	0.0038	0.271	8.571	0.0582	0.1392
putative peroxidase / antioxidase																								
SGO_1687	-0.326	7.903	0.0149	0.0652	-0.031	8.036	0.1317	0.6708	0.122	8.112	0.0045	0.0231	0.295	7.374	0.0188	0.1060	0.448	6.848	0.0070	0.0253	0.153	7.586	0.0385	0.0760
accA; acetyl-CoA carboxylase, carboxyl transferase, alpha subunit																								
SGO_1688	0.081	6.923	0.1412	0.9507	-0.423	6.692	0.0434	0.1883	-1.406	6.366	0.0063	0.0357	-0.504	6.188	0.0000	0.0000	-1.487	5.254	0.0006	0.0005	-0.983	5.513	0.0057	0.0032
accD; acetyl-CoA carboxylase, carboxyl transferase, beta subunit																								
SGO_1689	1.308	7.985	0.0008	0.0013	0.770	7.623	0.0018	0.0039	0.660	7.554	0.0016	0.0063	-0.538	7.735	0.0021	0.0051	-0.648	7.080	0.0015	0.0031	-0.110	7.385	0.0381	0.0748
accC; acetyl-CoA carboxylase, biotin carboxylase																								
SGO_1690		5.237				5.878				3.396			0.686	6.080	0.0188	0.1070	-0.770	4.468	0.0601	0.3863	-1.456	5.603	0.0713	0.1821
fabZ; beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ																								
SGO_1691	-0.102	7.422	0.1200	0.7870	1.379	8.276	0.0017	0.0036	0.766	7.873	0.0089	0.0549	1.481	7.734	0.0013	0.0027	0.867	6.712	0.0097	0.0386	-0.614	8.006	0.0102	0.0092
accB; acetyl-CoA carboxylase, biotin carboxyl carrier protein																								
SGO_1692	2.086	10.166	0.0004	0.0004	1.429	9.656	0.0001	0.0000	0.957	9.329	0.0002	0.0002	-0.657	10.055	0.0015	0.0034	-1.129	9.280	0.0009	0.0011	-0.472	9.471	0.0019	0.0003
3-oxoacyl-[acyl-carrier-protein] synthase																								

Log$_2$ Ratios



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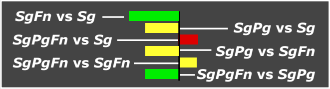

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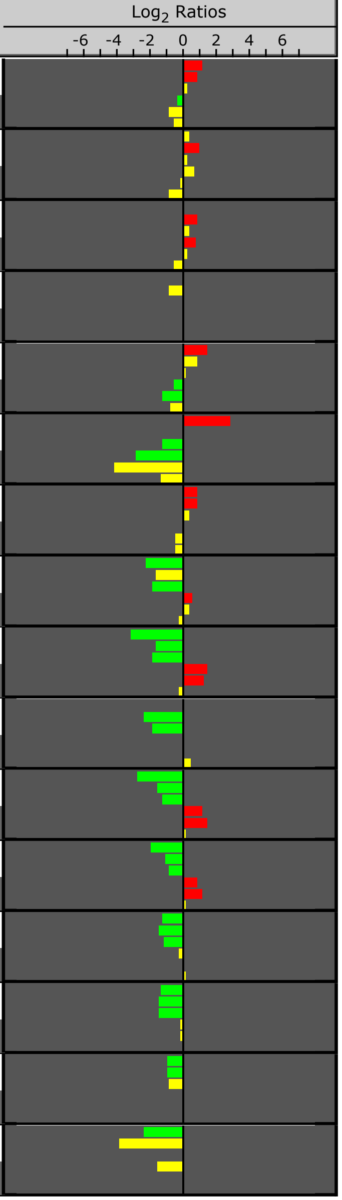
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1693 fabG; 3-oxoacyl-(acyl-carrier-protein) reductase	1.153	7.330	0.0003	0.0003	0.871	7.143	0.0014	0.0026	0.329	6.844	0.0297	0.2420	-0.282	7.146	0.0033	0.0107	-0.824	6.332	0.0053	0.0180	-0.542	6.773	0.0397	0.0812
SGO_1694 fabD; malonyl CoA-acyl carrier protein transacylase	0.376	6.814	0.0294	0.1515	1.047	7.221	0.0027	0.0064	0.254	6.757	0.0396	0.3378	0.671	6.845	0.0067	0.0276	-0.122	5.819	0.1009	0.7086	-0.793	6.806	0.0204	0.0291
SGO_1695 enoyl-acyl carrier protein(ACP) reductase	0.088	9.310	0.0294	0.1501	0.870	9.770	0.0028	0.0067	0.383	9.478	0.0104	0.0673	0.782	9.289	0.0030	0.0092	0.295	8.393	0.0233	0.1203	-0.487	9.411	0.0306	0.0534
SGO_1698 3-oxoacyl-[acyl-carrier-protein] synthase III		4.505			-0.756	5.106	0.0515	0.2316		4.505				3.040								3.040		
SGO_1699 transcriptional regulator, MarR family	1.460	6.054	0.0002	0.0002	0.913	5.685	0.0055	0.0160	0.250	4.823	0.0440	0.3827	-0.547	5.849	0.0043	0.0152	-1.210	4.762	0.0048	0.0154	-0.663	4.951	0.0888	0.2445
SGO_1700 enoyl-CoA hydratase/isomerase family protein	2.949	8.270	0.0006	0.0010	0.135	6.207	0.0097	0.0318	-1.156	5.429	0.0016	0.0063	-2.813	7.773	0.0007	0.0010	-4.105	7.012	0.0167	0.0776	-1.291	5.028	0.0264	0.0438
SGO_1701 aspartate kinase	0.868	7.787	0.0013	0.0027	0.897	7.802	0.0001	0.0000	0.450	7.536	0.0079	0.0461	0.028	7.657	0.1026	0.7627	-0.419	6.844	0.0121	0.0527	-0.447	7.468	0.0184	0.0246
SGO_1708 amiF; Oligopeptide transport ATP-binding protein amiF	-2.226	9.714	0.0047	0.0146	-1.595	9.842	0.0073	0.0220	-1.843	9.787	0.0037	0.0183	0.630	8.003	0.0022	0.0059	0.383	7.250	0.0103	0.0432	-0.248	8.165	0.0330	0.0603
SGO_1709 amiE; Oligopeptide transport ATP-binding protein	-3.054	9.803	0.0000	0.0000	-1.584	10.055	0.0001	0.0000	-1.751	10.017	0.0001	0.0001	1.471	7.990	0.0006	0.0007	1.303	7.267	0.0024	0.0059	-0.168	8.469	0.1043	0.3029
SGO_1710 amiD; Oligopeptide transport system permease protein		6.608			-2.268	6.883	0.0003	0.0002	-1.800	6.971	0.0002	0.0002		3.844				3.682			0.468	5.086	0.0227	0.0342
SGO_1711 hppB; Oligopeptide transport system permease	-2.691	8.366	0.0007	0.0012	-1.467	8.602	0.0014	0.0026	-1.236	8.671	0.0013	0.0049	1.224	6.684	0.0002	0.0001	1.455	6.248	0.0017	0.0038	0.231	7.297	0.0594	0.1436
SGO_1712 hppA; oligopeptide-binding lipoprotein	-1.923	10.854	0.0003	0.0003	-1.011	11.090	0.0001	0.0000	-0.769	11.175	0.0001	0.0001	0.912	9.612	0.0027	0.0079	1.154	9.163	0.0016	0.0033	0.242	10.111	0.0051	0.0024
SGO_1713 hppG; oligopeptide-binding lipoprotein	-1.214	10.762	0.0008	0.0013	-1.386	10.708	0.0004	0.0004	-1.142	10.780	0.0003	0.0005	-0.172	9.436	0.0368	0.2370	0.072	8.945	0.0937	0.6499	0.244	9.467	0.0073	0.0050
SGO_1715 hppH; oligopeptide-binding lipoprotein	-1.347	9.552	0.0001	0.0000	-1.406	9.535	0.0001	0.0000	-1.403	9.537	0.0001	0.0000	-0.060	8.185	0.0447	0.2998	-0.056	7.577	0.0676	0.4455	0.004	8.157	0.2404	0.9264
SGO_1716 oligopeptide binding protein	-0.893	9.573	0.0026	0.0072	-0.939	9.553	0.0017	0.0034	-0.817	9.616	0.0059	0.0323	-0.045	8.522	0.0912	0.6716	0.076	8.001	0.0978	0.6839	0.121	8.584	0.1586	0.5254
SGO_1717 pbp3; penicillin-binding protein 3	-2.333	6.693	0.0016	0.0037	-3.837	6.483	0.0278	0.1132		6.434			-1.505	3.809	0.0180	0.1005		2.965				1.063		



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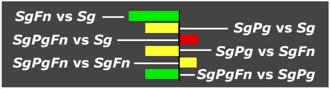
▨	yes	+	*p*- , *q*-Values
▨	yes	−	



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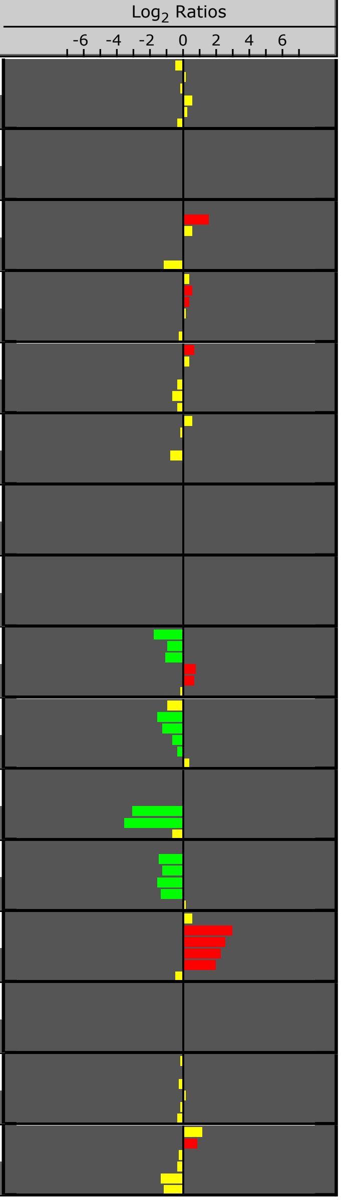
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	Description	*SgFn vs Sg* Ratio	Sum	*q*-Val	*p*-Val	*SgPg vs Sg* Ratio	Sum	*q*-Val	*p*-Val	*SgPgFn vs Sg* Ratio	Sum	*q*-Val	*p*-Val	*SgPg vs SgFn* Ratio	Sum	*q*-Val	*p*-Val	*SgPgFn vs SgFn* Ratio	Sum	*q*-Val	*p*-Val	*SgPgFn vs SgPg* Ratio	Sum	*q*-Val	*p*-Val
SGO_1718	sufB-1; FeS assembly protein SufB	-0.376	7.137	0.0406	0.2227	0.192	7.395	0.0742	0.3537	-0.096	7.275	0.0867	0.8195	0.568	6.721	0.0097	0.0454	0.280	5.976	0.0608	0.3913	-0.288	6.851	0.1156	0.3481
SGO_1719	SUF system FeS assembly protein, NifU family		2.946				2.946				2.946														
SGO_1720	aminotransferase, class-V		3.975			1.646	5.980	0.0008	0.0011	0.593	5.293	0.0194	0.1486		5.053				3.429			-1.053	5.634	0.0073	0.0051
SGO_1721	sufD; FeS assembly protein SufD	0.391	7.322	0.0192	0.0878	0.589	7.430	0.0033	0.0083	0.411	7.324	0.0029	0.0128	0.197	7.090	0.0384	0.2496	0.020	6.386	0.1345	0.9787	-0.178	7.092	0.0300	0.0521
SGO_1722	sufC; FeS assembly ATPase SufC	0.722	6.904	0.0017	0.0039	0.437	6.734	0.0079	0.0243	0.109	6.599	0.0647	0.5864	-0.285	6.570	0.0075	0.0318	-0.613	5.854	0.0224	0.1139	-0.328	6.304	0.1360	0.4258
SGO_1724	mecA; Adapter protein mec	0.591	4.101	0.0794	0.4935	-0.127	3.848	0.1462	0.7567		3.339			-0.717	2.988				1.692				1.585		
SGO_1725	bacA; bacitracin resistance protein		4.038				4.038				4.038														
SGO_1726	hypothetical protein SGO_1726		4.724				4.724				4.724														
SGO_1727	amino acid ABC transporter, amino acid-binding/permease protein	-1.722	7.502	0.0003	0.0003	-0.949	7.719	0.0005	0.0007	-1.039	7.688	0.0002	0.0003	0.773	6.329	0.0041	0.0141	0.683	5.661	0.0048	0.0156	-0.089	6.612	0.1273	0.3962
SGO_1728	glnQ; glutamine ABC transporter ATP-binding protein	-0.925	7.589	0.0068	0.0241	-1.549	7.411	0.0042	0.0114	-1.188	7.505	0.0032	0.0153	-0.625	6.253	0.0044	0.0160	-0.263	5.786	0.0020	0.0047	0.361	6.099	0.0393	0.0781
SGO_1729	hypothetical protein SGO_1729		9.102				6.111				5.593			-2.961	8.759	0.0025	0.0072	-3.517	8.099	0.0025	0.0064	-0.556	6.362	0.0426	0.0903
SGO_1730	SPFH domain/Band 7 family	0.138	10.208	0.0639	0.3830	-1.409	9.596	0.0011	0.0019	-1.177	9.659	0.0006	0.0016	-1.547	9.192	0.0021	0.0053	-1.314	8.639	0.0024	0.0058	0.232	8.334	0.0701	0.1788
SGO_1731	DNA-binding response regulator	0.649	4.113	0.0366	0.1959	2.963	5.857	0.0014	0.0026	2.608	5.540	0.0004	0.0007	2.314	5.420	0.0013	0.0029	1.960	4.510	0.0006	0.0004	-0.354	5.984	0.0428	0.0909
SGO_1732	histidine kinase		4.686			0.137	5.243	0.1748	0.9291		4.686				3.087								3.087		
SGO_1735	hypothetical protein SGO_1735	-0.145	9.384	0.0589	0.3452	0.067	9.482	0.0791	0.3811	-0.245	9.332	0.0086	0.0525	0.211	8.904	0.0244	0.1434	-0.100	8.136	0.0649	0.4266	-0.312	8.854	0.0071	0.0047
SGO_1736	alkaline shock protein	1.192	6.293	0.0068	0.0244	0.919	6.090	0.0042	0.0115	-0.151	5.089	0.0568	0.5072	-0.273	6.124	0.0440	0.2941	-1.343	4.908	0.0394	0.2279	-1.070	5.272	0.0656	0.1608



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ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

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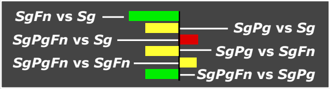

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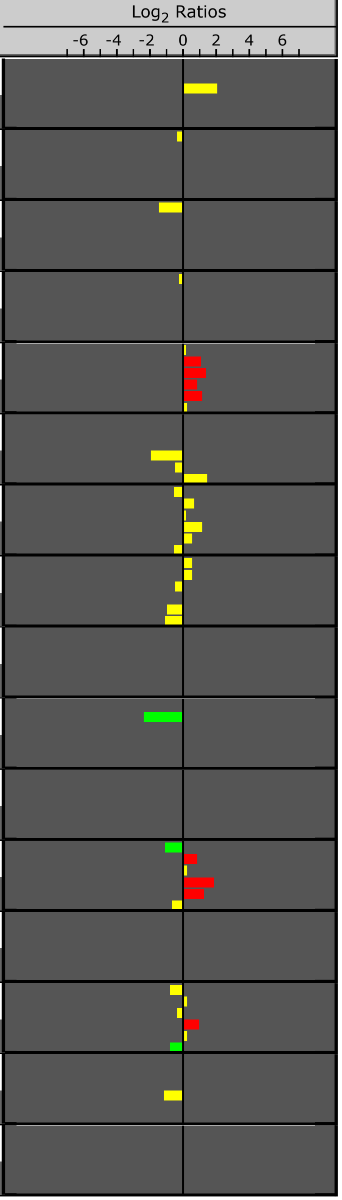
	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1737		5.867				5.867			2.134	7.515	0.0078	0.0454						5.836				6.447		
	rpmB; ribosomal protein L28																							
SGO_1738	-0.253	4.817	0.0847	0.5362		4.320				4.320				2.525				1.914						
	hypothetical protein SGO_1738																							
SGO_1739	-1.358	4.332	0.0238	0.1138		4.076				4.076				1.196				0.585						
	LytTr DNA-binding domain family																							
SGO_1744	-0.225	4.863	0.0260	0.1304		4.350				4.350				2.611				2.000						
	ABC transporter, ATP-binding protein SP0636																							
SGO_1745	0.223	11.665	0.0272	0.1384	1.138	12.225	0.0005	0.0006	1.424	12.436	0.0013	0.0044	0.915	11.782	0.0003	0.0002	1.201	11.373	0.0022	0.0053	0.286	12.325	0.0441	0.0943
	fba; fructose-1,6-bisphosphate aldolase, class II																							
SGO_1747		3.401				2.553				2.981			-1.902	3.525	0.0129	0.0660	-0.419	3.082			1.483	3.270	0.0461	0.1009
	hypothetical protein SGO_1747																							
SGO_1748	-0.482	4.963	0.0203	0.0936	0.671	5.923	0.0190	0.0733	0.167	5.622	0.0423	0.3624	1.153	5.008	0.0403	0.2643	0.649	3.985	0.0510	0.3132	-0.504	5.487	0.0660	0.1637
	pyrG; CTP synthase																							
SGO_1749	0.564	6.940	0.0184	0.0837	0.588	6.953	0.0186	0.0713	-0.386	6.448	0.0200	0.1552	0.024	6.688	0.1201	0.9143	-0.950	5.665	0.0052	0.0173	-0.974	6.290	0.0133	0.0144
	manA; mannose-6-phosphate isomerase, class I																							
SGO_1750		5.518				5.518				5.518														
	ABC-type multidrug/protein/lipid transport system, ATPase component																							
SGO_1751		5.926			-2.262	6.233	0.0014	0.0025		5.926				3.338								3.338		
	ABC-type multidrug/protein/lipid transport system, ATPase component																							
SGO_1753		2.643				2.643				2.643														
	hypothetical protein SGO_1753																							
SGO_1755	-0.956	6.493	0.0018	0.0044	0.917	7.427	0.0037	0.0097	0.304	7.053	0.0095	0.0602	1.873	6.648	0.0011	0.0021	1.260	5.573	0.0006	0.0006	-0.613	7.025	0.0163	0.0196
	scrK; fructokinase																							
SGO_1756		2.170				2.170				2.170														
	hypothetical protein SGO_1756																							
SGO_1757	-0.656	8.406	0.0149	0.0651	0.303	8.837	0.0214	0.0836	-0.347	8.518	0.0137	0.0974	0.959	8.074	0.0028	0.0085	0.309	7.076	0.0451	0.2675	-0.650	8.174	0.0050	0.0019
	glmS; glucosamine--fructose-6-phosphate aminotransferase																							
SGO_1760		3.231				2.098							-1.133	3.260				2.107				1.585		
	DNA-binding response regulator																							
SGO_1761		4.631				4.631				4.631														
	histidine kinase																							



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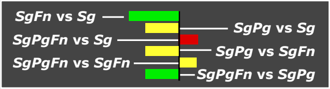


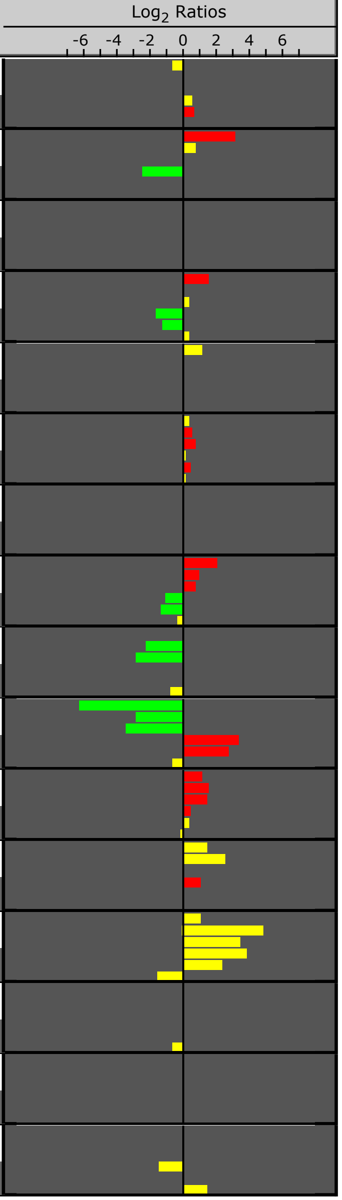
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1763 ABC transporter, substrate-binding protein SP0092	-0.583	7.656	0.0056	0.0188	0.005	7.920	0.1768	0.9410	0.099	7.963	0.0335	0.2787	0.588	7.148	0.0069	0.0284	0.682	6.589	0.0020	0.0048	0.094	7.454	0.1393	0.4415
SGO_1768 glycosyl hydrolase, family 38	3.248	6.256	0.0004	0.0004	0.808	4.468	0.0490	0.2172		2.946			-2.439	5.865	0.0010	0.0018		4.979				3.338		
SGO_1772 integral membrane protein		3.858				3.858				3.858														
SGO_1774 alcohol dehydrogenase, zinc-containing	1.620	6.691	0.0002	0.0002	0.032	5.695	0.1520	0.7951	0.393	5.898	0.0210	0.1646	-1.588	6.190	0.0005	0.0006	-1.227	5.684	0.0015	0.0028	0.361	5.406	0.0878	0.2411
SGO_1780 hypothetical protein SGO_1780	1.231	3.065				1.322				1.322				2.039				1.429						
SGO_1784 leuS; leucyl-tRNA synthetase	0.353	8.245	0.0126	0.0527	0.586	8.378	0.0027	0.0063	0.812	8.516	0.0005	0.0011	0.233	8.016	0.0129	0.0663	0.459	7.530	0.0023	0.0057	0.226	8.242	0.0100	0.0089
SGO_1792 transcription regulator	0.124	2.648				1.585				1.585				1.196				0.585						
SGO_1799 endopeptidase O	2.086	9.301	0.0001	0.0000	1.049	8.530	0.0008	0.0012	0.779	8.359	0.0031	0.0142	-1.037	9.053	0.0001	0.0000	-1.307	8.362	0.0004	0.0002	-0.270	8.319	0.0358	0.0694
SGO_1800 troB; manganese ABC transporter, ATP-binding protein SP1648		8.137			-2.160	8.427	0.0005	0.0007	-2.837	8.327	0.0003	0.0005		5.459				4.184			-0.676	6.165	0.0092	0.0071
SGO_1802 Metal ABC transporter substrate-binding lipoprotein precursor	-6.178	11.051	0.0003	0.0003	-2.784	11.227	0.0004	0.0004	-3.417	11.160	0.0003	0.0003	3.394	7.883	0.0013	0.0025	2.760	6.705	0.0014	0.0025	-0.634	8.464	0.0272	0.0462
SGO_1803 tpx; thioredoxin peroxidase	1.164	6.483	0.0010	0.0018	1.645	6.828	0.0001	0.0000	1.530	6.761	0.0021	0.0088	0.481	6.697	0.0022	0.0059	0.366	6.034	0.0255	0.1343	-0.115	6.871	0.1727	0.5975
SGO_1804 hutI; imidazolonepropionase	1.496	4.317	0.0079	0.0293	2.632	5.330	0.0096	0.0315		1.585			1.136	5.246	0.0003	0.0002		2.958				4.705		
SGO_1805 hutU; urocanate hydratase	1.066	2.272			4.930	6.617	0.0277	0.1125	3.472	5.269	0.0288	0.2332	3.863	6.129	0.0204	0.1167	2.406	4.208	0.0435	0.2567	-1.458	6.549	0.0146	0.0165
SGO_1806 ftcD; glutamate formiminotransferase						5.242				4.674				4.729				3.550			-0.584	5.473	0.0226	0.0335
SGO_1807 serine cycle enzyme, putative						4.350								3.837								3.837		
SGO_1808 fhs-2; formate--tetrahydrofolate ligase		3.816				3.454				4.970			-1.367	4.133	0.0081	0.0358	0.110	4.382	0.1057	0.7490	1.477	4.890	0.0163	0.0196



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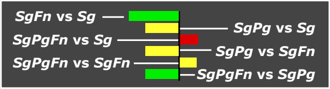

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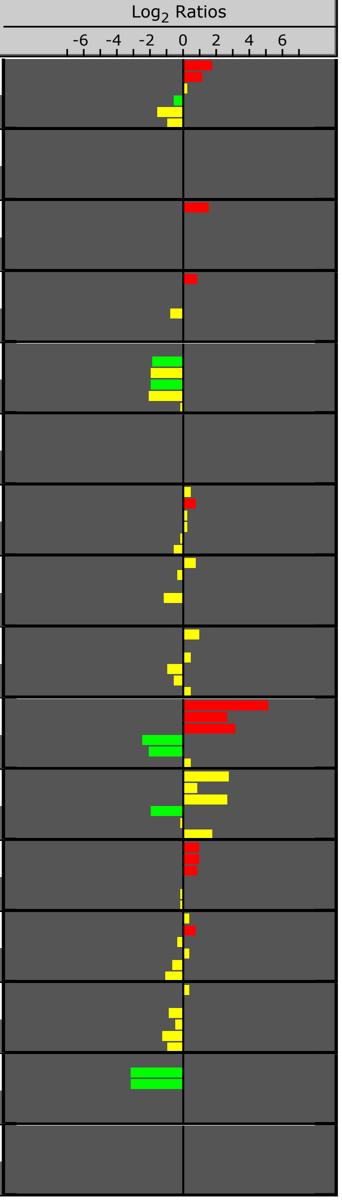
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1811 hutH; histidine ammonia-lyase	1.763	4.707	0.0030	0.0087	1.223	5.013	0.0001	0.0000	0.311	3.971	0.0125	0.0864	-0.540	4.773	0.0042	0.0146	-1.453	3.363			-0.913	4.325	0.0131	0.0141
SGO_1813 hutG; formimidoylglutamase	0.124	3.063				2.000				2.000				1.611				1.000						
SGO_1814 putative regulatory protein	1.632	5.980	0.0028	0.0079		3.940				3.940				5.065				4.454						
SGO_1816 scaR; ScaR Manganese-dependent regulator of scaCBA	0.877	5.790	0.0044	0.0135	0.145	4.910	0.0440	0.1916		4.275			-0.731	5.031	0.0357	0.2282		4.044				2.907		
SGO_1822 relA; GTP diphosphokinase	0.126	7.384	0.0609	0.3615	-1.768	6.687	0.0004	0.0004	-1.916	6.495	0.0097	0.0614	-1.893	6.278	0.0011	0.0022	-2.042	5.490	0.0212	0.1059	-0.149	4.569	0.0583	0.1398
SGO_1823 conserved hypothetical protein TIGR00046						3.722								3.209								3.209		
SGO_1824 prmA; ribosomal protein L11 methyltransferase	0.490	5.870	0.0226	0.1071	0.820	6.059	0.0028	0.0069	0.344	5.781	0.0208	0.1628	0.331	5.742	0.0167	0.0927	-0.145	4.892	0.0667	0.4389	-0.476	5.675	0.0116	0.0115
SGO_1827 hypothetical protein SGO_1827	0.838	5.024	0.0259	0.1289	-0.256	4.992	0.0635	0.2934		4.111			-1.094	4.383	0.0183	0.1026		2.807				3.348		
SGO_1828 ATPase, AAA family	0.994	5.002	0.0116	0.0472	0.056	4.482	0.1520	0.7952	0.528	4.191	0.0428	0.3679	-0.938	4.525	0.0147	0.0777	-0.466	3.724	0.0639	0.4192	0.472	3.741	0.1647	0.5585
SGO_1834 hypothetical protein SGO_1834	5.178	8.827	0.0008	0.0014	2.739	6.583	0.0043	0.0117	3.228	6.972	0.0001	0.0001	-2.439	8.524	0.0013	0.0027	-1.950	7.992	0.0015	0.0030	0.489	7.108	0.0493	0.1104
SGO_1835 hypothetical protein SGO_1835	2.787	4.567			0.863	3.800	0.0170	0.0631	2.701	4.492			-1.923	4.470	0.0032	0.0102	-0.086	4.206			1.837	4.414	0.0114	0.0111
SGO_1843 pepS; aminopeptidase PepS	0.982	8.061	0.0002	0.0001	0.981	8.067	0.0026	0.0060	0.922	8.025	0.0010	0.0032	-0.001	7.961	0.1224	0.9344	-0.060	7.319	0.0775	0.5213	-0.059	7.934	0.1835	0.6466
SGO_1844 cbxX/cfqX family protein	0.367	5.531	0.0241	0.1161	0.775	5.772	0.0050	0.0141	-0.266	5.225	0.0432	0.3728	0.408	5.399	0.0074	0.0314	-0.633	4.302	0.0107	0.0454	-1.041	5.171	0.0100	0.0089
SGO_1847 polC; DNA polymerase III, alpha subunit, Gram-positive type	0.427	6.251	0.0392	0.2126	0.057	6.008	0.1039	0.5132	-0.806	5.342	0.0155	0.1128	-0.370	5.761	0.0377	0.2442	-1.233	4.620	0.0507	0.3100	-0.863	4.872	0.0339	0.0631
SGO_1848 lipoprotein, putative		7.289			-3.095	7.448	0.0004	0.0005	-3.131	7.451	0.0003	0.0006		3.677				3.092			-0.036	4.690	0.2404	0.9247
SGO_1849 hypothetical protein SGO_1849		7.582				7.582				7.582														



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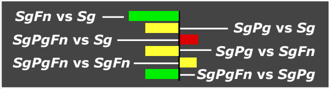
▨	yes	–	



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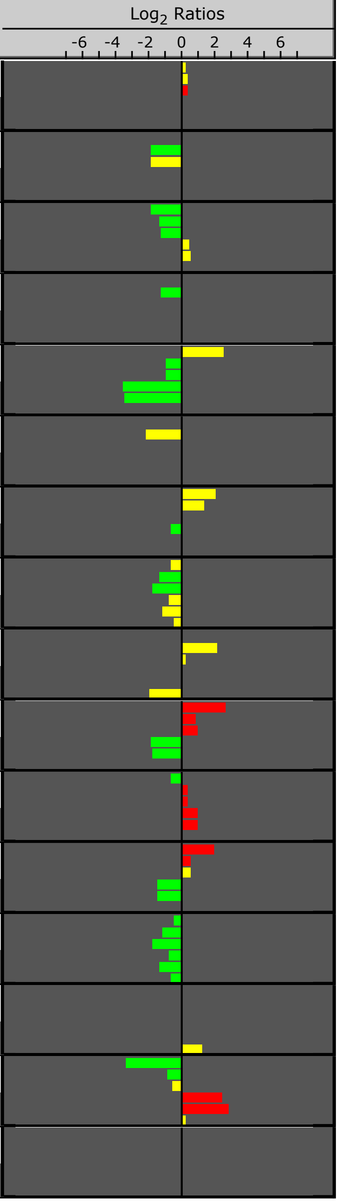
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1851 proS; prolyl-tRNA synthetase	0.331	8.944	0.0137	0.0588	0.365	8.961	0.0066	0.0196	0.354	8.954	0.0037	0.0181	0.035	8.603	0.1049	0.7821	0.024	7.987	0.1208	0.8624	-0.011	8.612	0.2296	0.8672
SGO_1852 membrane-associated zinc metalloprotease, putative		6.376			-1.841	6.734	0.0003	0.0003	-1.808	6.568	0.0073	0.0423		4.036				2.442			0.033	4.627	0.2454	0.9485
SGO_1854 uppS; undecaprenyl diphosphate synthase	-1.824	6.877	0.0003	0.0003	-1.307	7.017	0.0015	0.0028	-1.185	7.051	0.0011	0.0035	0.517	5.493	0.0244	0.1434	0.638	4.952	0.0188	0.0905	0.121	5.798	0.1989	0.7144
SGO_1855 preprotein translocase, YajC subunit		7.640			-1.217	8.163	0.0022	0.0049		7.640				5.932								5.932		
SGO_1856 ATP-dependent proteinase ATP-binding chain	2.577	8.999	0.0055	0.0181	-0.896	6.760	0.0005	0.0007	-0.872	6.771	0.0009	0.0027	-3.472	8.392	0.0042	0.0144	-3.449	7.784	0.0046	0.0145	0.023	5.751	0.2247	0.8416
SGO_1857 PTS system, IIABC components		4.723			-2.113	4.877	0.0396	0.1700		4.723				1.063								1.063		
SGO_1858 beta-fructofuranosidase/sucrose 6 phoshate hydrolase	2.081	4.249	0.0188	0.0855	1.448	3.696	0.0223	0.0881		1.000			-0.633	4.293	0.0040	0.0137		2.965				2.941		
SGO_1860 5'-nucleotidase, lipoprotein e(P4) family	-0.612	9.299	0.0202	0.0926	-1.332	9.034	0.0020	0.0044	-1.747	8.928	0.0009	0.0028	-0.721	8.138	0.0156	0.0833	-1.135	7.389	0.0101	0.0407	-0.414	7.507	0.0146	0.0165
SGO_1861 nusB; transcription antitermination factor NusB		1.865			2.171	5.189	0.0108	0.0360	0.305	3.026				4.524				1.046			-1.866	4.710	0.0246	0.0386
SGO_1862 alkaline shock protein	2.719	8.218	0.0003	0.0004	0.941	6.840	0.0011	0.0017	1.008	6.883	0.0004	0.0008	-1.778	7.869	0.0006	0.0006	-1.712	7.273	0.0007	0.0007	0.067	6.752	0.0956	0.2722
SGO_1863 efp; Elongation factor P (EF-P)	-0.622	8.044	0.0044	0.0134	0.394	8.526	0.0017	0.0034	0.360	8.507	0.0017	0.0065	1.017	7.780	0.0009	0.0014	0.982	7.147	0.0012	0.0019	-0.035	8.179	0.1094	0.3198
SGO_1864 X-Pro aminopeptidase	1.965	8.210	0.0001	0.0001	0.586	7.241	0.0040	0.0105	0.554	7.258	0.0189	0.1444	-1.379	7.834	0.0001	0.0000	-1.411	7.231	0.0014	0.0026	-0.032	7.000	0.2382	0.9116
SGO_1865 uvrA; excinuclease ABC, A subunit	-0.360	7.560	0.0050	0.0160	-1.073	7.288	0.0003	0.0003	-1.655	7.125	0.0002	0.0001	-0.713	6.543	0.0014	0.0032	-1.295	5.738	0.0008	0.0010	-0.582	5.878	0.0007	0.0000
SGO_1866 corA; magnesium and cobalt transporter						2.384				3.718				1.871				2.594			1.334	3.687		
SGO_1867 hypothetical protein SGO_1867	-3.307	7.508	0.0003	0.0003	-0.785	8.025	0.0012	0.0021	-0.450	8.165	0.0084	0.0500	2.522	6.302	0.0002	0.0001	2.857	5.997	0.0015	0.0030	0.335	7.252	0.0477	0.1060
SGO_1869 hypothetical protein SGO_1869		6.100				6.100				6.100														



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Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
p-Value	

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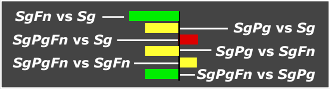

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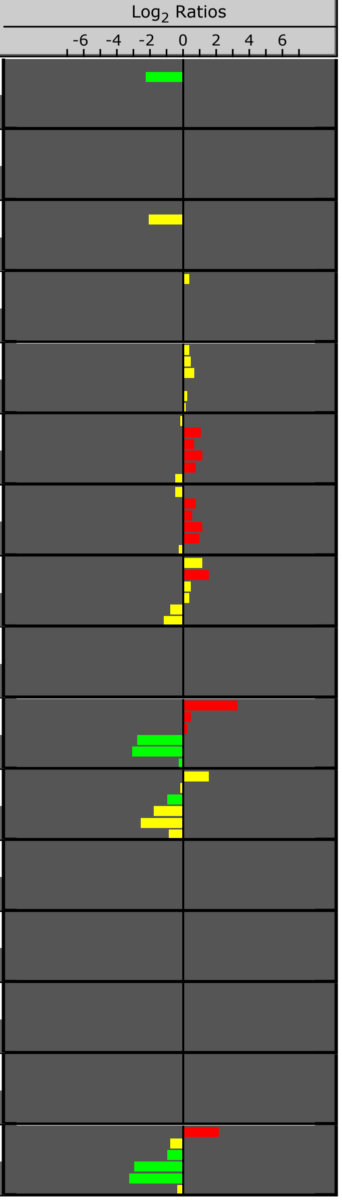
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1870 hypothetical protein SGO_1870		6.281			-2.154	6.573	0.0017	0.0036		6.281				3.612								3.612		
SGO_1871 lipoprotein, putative		5.486				5.486				5.486														
SGO_1872 hypothetical protein SGO_1872		5.232			-2.042	5.394	0.0376	0.1612		5.232				1.648								1.648		
SGO_1878 transcriptional regulator, TetR family domain protein	0.367	4.391	0.0261	0.1310		3.674				3.674				2.525				1.914						
SGO_1879 rpsR; ribosomal protein S18	0.354	7.776	0.0886	0.5656	0.485	7.843	0.0748	0.3573	0.700	7.966	0.0195	0.1505	0.132	7.433	0.0562	0.3870	0.347	6.937	0.0108	0.0460	0.215	7.603	0.0228	0.0348
SGO_1880 ssb-1; single-strand binding protein	-0.115	7.779	0.0501	0.2847	1.077	8.471	0.0008	0.0011	0.689	8.219	0.0009	0.0027	1.192	7.919	0.0004	0.0003	0.803	7.049	0.0001	0.0000	-0.388	8.214	0.0069	0.0045
SGO_1881 rpsF; ribosomal protein S6	-0.382	9.153	0.0271	0.1376	0.807	9.782	0.0045	0.0123	0.575	9.632	0.0010	0.0031	1.188	9.153	0.0034	0.0109	0.957	8.379	0.0031	0.0087	-0.231	9.505	0.0656	0.1618
SGO_1882 folE; GTP cyclohydrolase I	1.171	5.749	0.0060	0.0204	1.566	6.032	0.0038	0.0099	0.473	5.296	0.0155	0.1125	0.395	5.908	0.0260	0.1553	-0.698	4.773	0.0085	0.0331	-1.092	5.641	0.0125	0.0131
SGO_1884 hypothetical protein SGO_1884		4.239				4.239				4.239														
SGO_1885 groL; 60 kDa chaperonin/groEL protein	3.284	12.092	0.0000	0.0000	0.544	9.965	0.0001	0.0000	0.330	9.842	0.0005	0.0013	-2.739	11.639	0.0000	0.0000	-2.954	11.002	0.0000	0.0000	-0.214	9.596	0.0050	0.0022
SGO_1886 groES; chaperonin, 10 kDa	1.601	7.386	0.0137	0.0590	-0.062	6.280	0.1835	0.9903	-0.907	5.912	0.0036	0.0171	-1.663	6.874	0.0125	0.0626	-2.507	6.104	0.0097	0.0386	-0.844	5.401	0.0466	0.1028
SGO_1887 ABC transporter, ATP-binding protein		4.785				4.785				4.785														
SGO_1888 ABC transporter, permease protein		3.936				3.936				3.936														
SGO_1890 PTS system, fructose(mannose)-specific IID		4.754				4.754				4.754														
SGO_1891 PTS system, IIC component		5.077				5.077				5.077														
SGO_1892 PTS system, fructose(mannose)-specific IIB	2.240	8.409	0.0031	0.0089	-0.655	6.579	0.0076	0.0233	-0.914	6.496	0.0045	0.0231	-2.895	7.801	0.0024	0.0068	-3.155	7.166	0.0025	0.0065	-0.259	5.592	0.1219	0.3717



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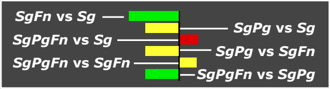

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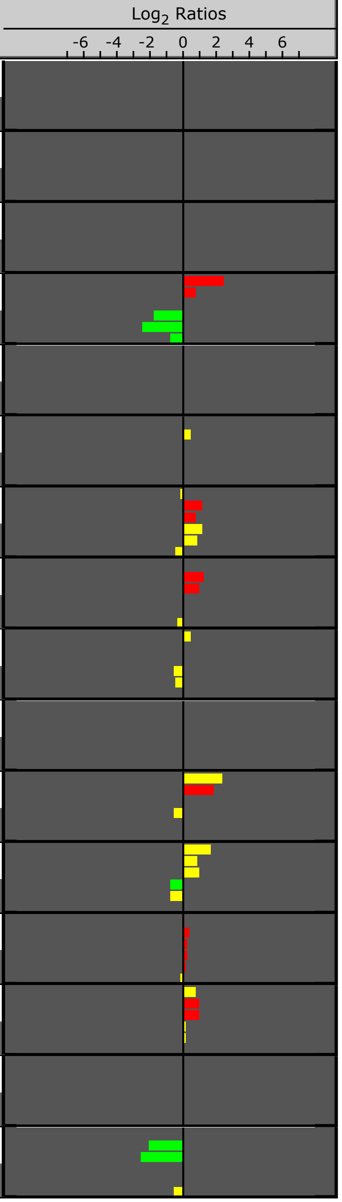
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1894 sugar-binding cell envelope protein		3.832				3.832				3.832														
SGO_1895 response regulator		2.202				2.202				2.202														
SGO_1897 rbsB; ribose ABC transporter (ribose-binding component) CAC1453		3.776				3.776				3.776														
SGO_1898 glutamyl aminopeptidase	2.530	9.291	0.0004	0.0005	0.820	7.993	0.0003	0.0002	0.145	7.601	0.0155	0.1136	-1.710	8.931	0.0007	0.0009	-2.385	8.189	0.0006	0.0006	-0.675	7.534	0.0026	0.0006
SGO_1899 hypothetical protein SGO_1899		2.700				2.700				2.700														
SGO_1900 thioredoxin family protein		1.322			0.545	3.292	0.0127	0.0442		1.322				2.354								2.354		
SGO_1901 tRNA binding domain	-0.053	6.001	0.1383	0.9288	1.151	6.682	0.0048	0.0136	0.799	6.435	0.0009	0.0026	1.204	6.178	0.0069	0.0283	0.852	5.322	0.0102	0.0424	-0.352	6.462	0.0503	0.1141
SGO_1902 ssb; single-stranded DNA-binding protein		8.290			1.319	10.098	0.0015	0.0028	0.981	9.865	0.0016	0.0059		9.099				8.151			-0.339	9.940	0.0402	0.0826
SGO_1903 ATP-dependent Zn protease	0.470	8.382	0.0109	0.0434	-0.014	8.113	0.1490	0.7754	0.042	8.146	0.0725	0.6714	-0.484	7.863	0.0087	0.0402	-0.428	7.280	0.0167	0.0781	0.056	7.626	0.1705	0.5878
SGO_1907 sensor protein		2.170				2.170				2.170														
SGO_1912 Bifunctional folate synthesis protein	2.439	4.026	0.0117	0.0484	1.890	4.365	0.0007	0.0009		2.189			-0.548	4.283	0.0072	0.0301		2.429				3.491		
SGO_1914 folP; dihydropteroate synthase	1.677	4.472	0.0060	0.0203	0.948	3.872	0.0322	0.1338	1.000	3.170			-0.729	4.433	0.0011	0.0020	-0.677	3.531	0.0094	0.0372	0.052	3.628	0.2193	0.8139
SGO_1916 ackA; acetate kinase	0.061	8.349	0.0764	0.4729	0.394	8.528	0.0030	0.0074	0.287	8.469	0.0046	0.0243	0.333	8.040	0.0002	0.0001	0.227	7.371	0.0018	0.0041	-0.106	8.144	0.0163	0.0194
SGO_1917 hypothetical protein SGO_1917	0.787	5.009	0.0052	0.0167	0.982	5.136	0.0039	0.0104	1.025	5.153	0.0001	0.0001	0.195	4.942	0.0506	0.3436	0.237	4.345	0.0275	0.1467	0.042	5.049	0.2247	0.8395
SGO_1923 comYB; competence protein		2.865				2.865				2.865														
SGO_1924 comYA; competence protein comYA		8.254			-2.018	8.576	0.0002	0.0001	-2.489	8.495	0.0001	0.0001		5.740				4.667			-0.471	6.528	0.0494	0.1109



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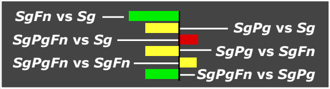

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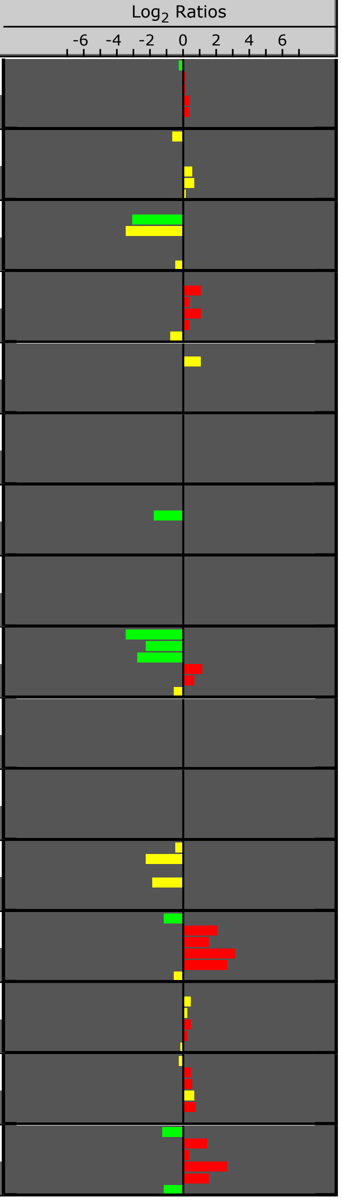
Streptococcus gordonii

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1926	-0.191	10.388	0.0027	0.0076	0.180	10.573	0.0033	0.0081	0.220	10.594	0.0018	0.0071	0.371	9.973	0.0006	0.0007	0.411	9.385	0.0008	0.0009	0.039	10.167	0.0956	0.2716
	rpoC; DNA-directed RNA polymerase, beta chain																							
SGO_1927	-0.581	10.200	0.0164	0.0731	-0.010	10.434	0.1496	0.7797	0.140	10.512	0.0173	0.1287	0.571	9.680	0.0141	0.0739	0.722	9.162	0.0101	0.0410	0.150	9.994	0.0423	0.0883
	rpoB; DNA-directed RNA polymerase, beta subunit																							
SGO_1928		7.371			-2.965	7.544	0.0003	0.0003	-3.385	7.438	0.0087	0.0531		3.889				1.857			-0.421	4.347	0.0219	0.0317
	pbp1b; penicillin-binding protein 1B																							
SGO_1929	-0.009	8.729	0.1251	0.8259	1.093	9.384	0.0010	0.0015	0.438	8.971	0.0031	0.0143	1.102	8.867	0.0008	0.0013	0.446	7.843	0.0035	0.0103	-0.655	9.026	0.0087	0.0065
	tyrS; tyrosyl-tRNA synthetase																							
SGO_1930		2.926			1.085	4.520	0.0051	0.0145		2.926				3.426								3.426		
	rrmA; Ribosomal RNA large subunit methyltransferase A																							
SGO_1931						1.161								0.648								0.648		
	lipoprotein, putative																							
SGO_1934		5.277				5.277			-1.691	5.485	0.0037	0.0184						1.461				2.072		
	copper-translocating P-type ATPase																							
SGO_1935		2.496				2.496				2.496														
	negative transcriptional regulator, CopY																							
SGO_1936	-3.425	8.816	0.0000	0.0000	-2.189	8.974	0.0001	0.0000	-2.739	8.890	0.0001	0.0000	1.236	6.497	0.0004	0.0004	0.686	5.528	0.0033	0.0095	-0.550	6.741	0.0107	0.0101
	adcA; metal-binding (Mn) permease precursor, lipoprotein																							
SGO_1938		5.090			0.029	6.096	0.1771	0.9448		5.090				4.589								4.589		
	adcC; ATP-binding protein, Mn																							
SGO_1939						2.321								1.807								1.807		
	adcR; repressor protein adcR																							
SGO_1957	-0.388	5.582	0.0561	0.3268	-2.186	4.917	0.0534	0.2415		4.774			-1.798	4.035	0.0345	0.2178		3.236				1.000		
	hypothetical protein SGO_1957																							
SGO_1958	-1.095	8.424	0.0024	0.0066	2.075	10.247	0.0004	0.0003	1.594	9.873	0.0005	0.0012	3.171	9.577	0.0002	0.0002	2.689	8.543	0.0006	0.0004	-0.481	10.205	0.0116	0.0114
	rplQ; ribosomal protein L17																							
SGO_1959	0.029	9.157	0.1289	0.8527	0.482	9.402	0.0056	0.0164	0.337	9.318	0.0063	0.0352	0.453	8.899	0.0029	0.0089	0.308	8.205	0.0048	0.0153	-0.145	9.035	0.0322	0.0578
	rpoA; DNA-directed RNA polymerase, alpha subunit																							
SGO_1960	-0.204	7.854	0.0710	0.4360	0.545	8.234	0.0033	0.0080	0.585	8.257	0.0012	0.0041	0.749	7.652	0.0050	0.0192	0.789	7.066	0.0045	0.0141	0.040	7.986	0.1586	0.5270
	rpsK; ribosomal protein S11																							
SGO_1961	-1.173	8.386	0.0006	0.0010	1.499	9.790	0.0003	0.0003	0.380	9.056	0.0015	0.0056	2.673	9.052	0.0002	0.0001	1.553	7.536	0.0006	0.0004	-1.119	9.386	0.0026	0.0006
	rpsM; ribosomal protein S13p/S18e																							



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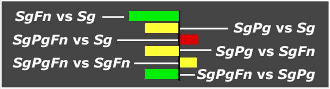
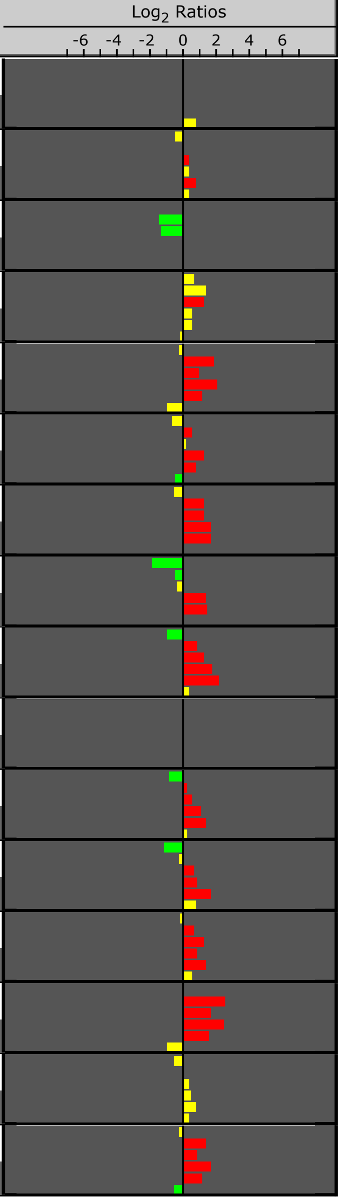


Hendrickson *et al.*

Streptococcus gordonii

Protein	*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1962 rpmJ; ribosomal protein L36						5.444				5.204				4.930				4.080			0.805	5.815	0.0818	0.2172
SGO_1964 adk; Adenylate kinase (ATP-AMP transphosphorylase)	-0.394	8.593	0.0246	0.1193	0.047	8.784	0.0231	0.0918	0.431	8.993	0.0013	0.0045	0.441	8.106	0.0161	0.0875	0.825	7.728	0.0045	0.0139	0.384	8.500	0.0076	0.0054
SGO_1965 Preprotein translocase secY subunit		6.268			-1.375	6.740	0.0004	0.0005	-1.253	6.773	0.0003	0.0003		4.386				3.889			0.121	5.444	0.0928	0.2595
SGO_1966 rplO; ribosomal protein L15	0.711	8.581	0.0250	0.1218	1.359	8.989	0.0068	0.0207	1.278	8.907	0.0009	0.0028	0.648	8.744	0.0282	0.1723	0.567	8.065	0.0299	0.1641	-0.081	8.956	0.1835	0.6466
SGO_1967 50S ribosomal protein L30 -related protein	-0.238	7.392	0.0767	0.4756	1.872	8.702	0.0003	0.0002	0.975	8.055	0.0016	0.0058	2.111	8.152	0.0006	0.0007	1.214	6.873	0.0039	0.0118	-0.897	8.463	0.0054	0.0028
SGO_1968 rpsE; ribosomal protein S5	-0.621	9.665	0.0078	0.0289	0.640	10.290	0.0024	0.0053	0.201	10.039	0.0195	0.1505	1.261	9.565	0.0006	0.0007	0.822	8.659	0.0017	0.0037	-0.439	9.855	0.0048	0.0017
SGO_1969 rplR; ribosomal protein L18	-0.461	9.203	0.0251	0.1230	1.259	10.158	0.0003	0.0003	1.285	10.176	0.0002	0.0003	1.721	9.530	0.0005	0.0005	1.746	8.939	0.0006	0.0005	0.025	10.151	0.0183	0.0240
SGO_1970 BL10; 50S ribosomal protein L6	-1.812	9.837	0.0001	0.0001	-0.442	10.269	0.0004	0.0004	-0.307	10.335	0.0120	0.0805	1.370	8.992	0.0003	0.0002	1.504	8.491	0.0022	0.0051	0.135	9.595	0.1111	0.3304
SGO_1971 rpsH; ribosomal protein S8	-0.883	9.958	0.0005	0.0007	0.875	10.836	0.0004	0.0005	1.268	11.111	0.0015	0.0056	1.758	10.068	0.0002	0.0001	2.151	9.780	0.0014	0.0024	0.393	10.912	0.0327	0.0590
SGO_1972 rpsN; ribosomal protein S14p/S29e		5.340				5.340				5.340														
SGO_1973 BL6; 50S ribosomal protein L5	-0.823	9.445	0.0007	0.0011	0.314	9.963	0.0026	0.0060	0.582	10.121	0.0019	0.0079	1.138	9.139	0.0002	0.0001	1.406	8.721	0.0009	0.0011	0.268	9.741	0.0248	0.0399
SGO_1974 rplX; ribosomal protein L24	-1.058	8.620	0.0046	0.0142	-0.172	8.962	0.0595	0.2735	0.659	9.413	0.0039	0.0194	0.886	7.983	0.0021	0.0053	1.717	7.964	0.0011	0.0016	0.831	8.830	0.0071	0.0046
SGO_1975 rplN; ribosomal protein L14	-0.135	8.279	0.0814	0.5114	0.740	8.750	0.0003	0.0003	1.293	9.123	0.0005	0.0012	0.875	8.196	0.0021	0.0051	1.428	7.967	0.0013	0.0021	0.553	8.865	0.0092	0.0073
SGO_1976 BS16; 30S ribosomal protein	0.116	7.182	0.1315	0.8772	2.575	8.892	0.0008	0.0012	1.712	8.214	0.0030	0.0137	2.459	8.387	0.0007	0.0009	1.596	7.102	0.0038	0.0111	-0.862	8.785	0.0140	0.0153
SGO_1977 rpmC; ribosomal protein L29	-0.463	5.951	0.0523	0.2993	0.014	6.513	0.1779	0.9553	0.375	6.717	0.0222	0.1763	0.476	5.445	0.0390	0.2551	0.837	5.125	0.0457	0.2725	0.361	6.208	0.0684	0.1734
SGO_1978 rplP; ribosomal protein L16	-0.239	7.841	0.0607	0.3602	1.442	8.829	0.0015	0.0028	0.912	8.468	0.0040	0.0201	1.680	8.238	0.0001	0.0000	1.151	7.242	0.0002	0.0001	-0.529	8.605	0.0007	0.0000



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Test	Cutoff
***q*-Value**	**.005**
p-Value	

	Signif	Direction	Applies To
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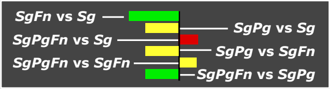

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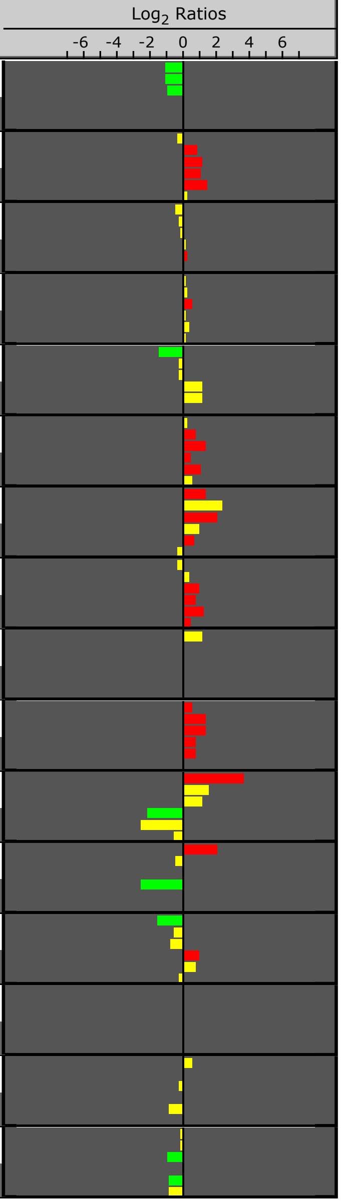
Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_1979	-1.001	10.336	0.0006	0.0010	-0.999	10.334	0.0003	0.0002	-0.865	10.382	0.0004	0.0010	0.002	9.240	0.1243	0.9528	0.136	8.699	0.0521	0.3237	0.134	9.307	0.0661	0.1645
	rpsC; ribosomal protein S3																							
SGO_1980	-0.272	8.907	0.0105	0.0417	0.869	9.533	0.0003	0.0003	1.192	9.751	0.0003	0.0005	1.141	8.930	0.0002	0.0002	1.464	8.550	0.0005	0.0003	0.323	9.561	0.0094	0.0076
	rplV; ribosomal protein L22																							
SGO_1981	-0.372	9.339	0.0070	0.0251	-0.198	9.418	0.0320	0.1328	-0.058	9.485	0.0642	0.5800	0.174	8.715	0.0107	0.0510	0.314	8.180	0.0049	0.0163	0.140	8.873	0.0680	0.1722
	rpsS; ribosomal protein S19																							
SGO_1982	0.174	9.007	0.0740	0.4556	0.327	9.069	0.0196	0.0760	0.562	9.205	0.0042	0.0214	0.153	8.650	0.0843	0.6166	0.388	8.167	0.0310	0.1712	0.235	8.829	0.0419	0.0871
	rplB; ribosomal protein L2																							
SGO_1983	-1.445	8.527	0.0028	0.0079	-0.214	8.948	0.0580	0.2650	-0.221	8.939	0.0161	0.1179	1.231	7.880	0.0079	0.0346	1.224	7.256	0.0069	0.0248	-0.007	8.326	0.2399	0.9214
	rplW; ribosomal protein L23																							
SGO_1984	0.348	9.327	0.0089	0.0341	0.821	9.611	0.0017	0.0035	1.443	10.038	0.0004	0.0009	0.473	9.229	0.0014	0.0030	1.096	9.013	0.0008	0.0008	0.622	9.793	0.0066	0.0041
	rplD; ribosomal protein L4/L1 family																							
SGO_1985	1.375	9.340	0.0021	0.0053	2.375	10.178	0.0072	0.0217	2.068	9.860	0.0001	0.0000	0.999	9.986	0.0136	0.0706	0.693	9.127	0.0024	0.0061	-0.307	10.243	0.1025	0.2963
	rplC; ribosomal protein L3																							
SGO_1986	-0.327	7.486	0.0238	0.1144	0.450	7.881	0.0131	0.0458	0.996	8.217	0.0008	0.0022	0.777	7.231	0.0011	0.0020	1.323	6.986	0.0002	0.0001	0.546	7.865	0.0050	0.0018
	rpsJ; ribosomal protein S10																							
SGO_1988	1.168	5.598	0.0404	0.2208		4.572				4.572				4.110				3.499						
	hydrolase, haloacid dehalogenase-like family																							
SGO_1989	0.601	9.267	0.0015	0.0034	1.403	9.800	0.0003	0.0002	1.422	9.815	0.0003	0.0004	0.802	9.478	0.0007	0.0008	0.821	8.880	0.0010	0.0013	0.019	9.834	0.2083	0.7590
	purA; adenylosuccinate synthetase																							
SGO_1990	3.661	6.835	0.0005	0.0008	1.608	5.146	0.0122	0.0419	1.153	4.157	0.0196	0.1515	-2.053	6.535	0.0013	0.0027	-2.509	5.718	0.0181	0.0858	-0.456	4.657	0.1579	0.5196
	glutamate--cysteine ligase, putative/amino acid ligase, putative																							
SGO_1991	2.067	6.131	0.0009	0.0016	-0.388	4.635	0.0674	0.3156		3.874			-2.454	5.522	0.0001	0.0000		4.668				2.835		
	hslO; 33 kDa chaperonin /Heat shock protein 33-like protein																							
SGO_1993	-1.499	6.875	0.0024	0.0063	-0.453	7.226	0.0175	0.0657	-0.658	7.153	0.0087	0.0534	1.046	6.030	0.0009	0.0014	0.841	5.299	0.0076	0.0285	-0.205	6.372	0.1151	0.3438
	possible transcriptional regulator																							
SGO_1994		1.379				1.380				1.380														
	lipoprotein, putative																							
SGO_1995	0.615	5.975	0.0425	0.2374		4.654			-0.155	5.158	0.0782	0.7315		4.724			-0.770	4.468	0.0601	0.3863		2.883		
	MutT/nudix family protein																							
SGO_1998	-0.114	7.258	0.0299	0.1545	-0.061	7.292	0.1442	0.7455	-0.905	6.939	0.0016	0.0059	0.053	6.720	0.0848	0.6222	-0.791	5.739	0.0021	0.0049	-0.844	6.394	0.0172	0.0218
	clpB; ATP-dependent Clp proteinase, ATP-binding chain																							



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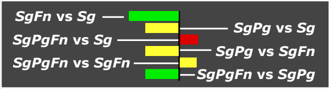

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Streptococcus gordonii

Hackett Laboratory UW

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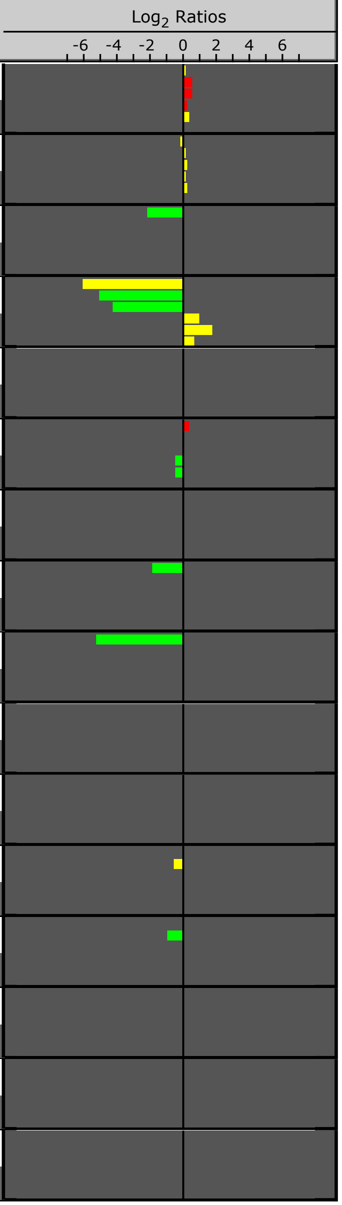
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_2000 tsf; translation elongation factor Ts	0.216	10.871	0.0174	0.0778	0.557	11.062	0.0011	0.0018	0.572	11.072	0.0014	0.0052	0.341	10.640	0.0032	0.0103	0.356	10.040	0.0060	0.0208	0.015	10.808	0.2122	0.7760
SGO_2001 rpsB; ribosomal protein S2	-0.063	10.783	0.0858	0.5436	0.163	10.895	0.0136	0.0480	0.252	10.944	0.0063	0.0353	0.226	10.354	0.0122	0.0605	0.316	9.794	0.0097	0.0386	0.089	10.507	0.0813	0.2151
SGO_2004 LPXTG cell wall surface protein	-2.079	7.088	0.0011	0.0023		6.780				6.780				4.196				3.585						
SGO_2005 LPXTG cell wall surface protein	-5.995	9.561	0.0089	0.0340	-4.964	9.595	0.0002	0.0001	-4.242	9.625	0.0001	0.0001	1.031	4.389	0.0158	0.0855	1.753	4.401	0.0290	0.1574	0.722	5.492	0.0219	0.0321
SGO_2006 thioredoxin signature protein		3.279				3.279				3.279														
SGO_2007 nusG; transcription termination/antitermination factor NusG	0.413	7.410	0.0001	0.0001	-0.015	7.182	0.1504	0.7846	0.048	7.214	0.0366	0.3079	-0.429	6.891	0.0009	0.0016	-0.365	6.308	0.0012	0.0019	0.063	6.694	0.1174	0.3566
SGO_2008 preprotein translocase secE component -related protein		5.872				5.872				5.872														
SGO_2010 pbp2a; penicillin-binding protein 2A	-1.834	6.616	0.0002	0.0002		6.259				6.259				3.916				3.305						
SGO_2013 putative N-acetylmuramidase/lysin	-5.238	9.019	0.0000	0.0000		8.980				8.980				3.259				2.648						
SGO_2015 possible polysaccharide transport protein		0.585				0.585				0.585														
SGO_2016 nucleotide sugar dehydratase, putative		2.170				2.170				2.170														
SGO_2017 nucleotidyl transferase, putative		2.700			-0.539	3.456				2.700				1.648								1.648		
SGO_2019 licD; licD3 protein		5.006			-0.881	5.633	0.0003	0.0002		5.006				3.614								3.614		
SGO_2020 glycosyltransferase		2.585				2.585				2.585														
SGO_2021 Extracellular polysaccharide glycosyltransferase		5.271				5.271				5.271														
SGO_2022 UDP-glucose 4-epimerase BH3715		2.000				2.000				2.000														



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p-Value	

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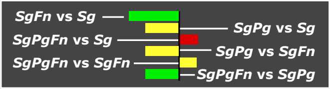

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Streptococcus gordonii

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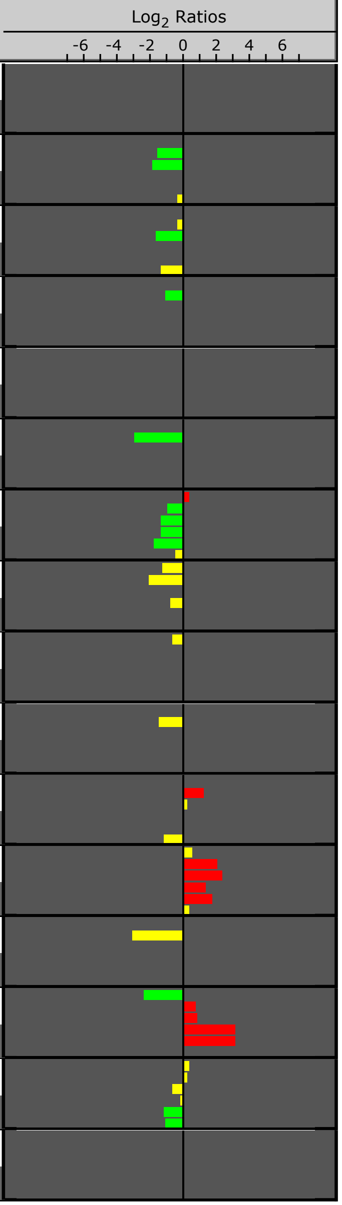
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_2023 galactosyltransferase		5.835				5.835				5.835														
SGO_2024 Extracellular polysaccharide biosynthesis		6.956			-1.523	7.385	0.0014	0.0026	-1.812	7.317	0.0008	0.0021		4.912				4.018			-0.289	5.777	0.0339	0.0630
SGO_2025 wze; putative autophosphorylating protein tyrosine kinase		6.005			-0.304	6.869	0.0257	0.1036	-1.636	6.420	0.0005	0.0011		5.206				3.296			-1.332	5.698	0.0123	0.0128
SGO_2026 wzd; polysaccharide export protein, MPA1 family		6.124			-0.991	6.710	0.0019	0.0042		6.124				4.614								4.614		
SGO_2027 wzh; wzh/Putative phosphotyrosine-protein phosphatase		2.170				2.170				2.170														
SGO_2028 wzg; transcriptional regulator		6.039			-2.941	6.130	0.0049	0.0138		6.039				1.585								1.585		
SGO_2033 nrdD; ribonucleoside-triphosphate reductase	0.426	8.356	0.0017	0.0041	-0.854	7.763	0.0003	0.0002	-1.279	7.627	0.0002	0.0003	-1.280	7.538	0.0003	0.0003	-1.704	6.817	0.0004	0.0002	-0.425	6.565	0.0099	0.0085
SGO_2034 hypothetical protein SGO_2034	-1.249	5.669	0.0365	0.1951	-1.989	5.567	0.0362	0.1540		5.398			-0.740	3.288				2.000				1.871		
SGO_2037 cardiolipin synthase	-0.611	6.209	0.0059	0.0199		5.472				5.472				4.374				3.763						
SGO_2039 dihydrofolate synthase		3.546			-1.419	3.789	0.0442	0.1931		3.546				0.585								0.585		
SGO_2041 conserved hypothetical protein TIGR00250		3.189			1.335	4.956	0.0032	0.0078	0.282	3.847	0.0764	0.7107		3.941				1.272			-1.052	4.251	0.0482	0.1073
SGO_2042 Bacterial protein of unknown function (DUF965) superfamily	0.631	7.574	0.0260	0.1299	2.054	8.549	0.0006	0.0008	2.436	8.867	0.0006	0.0013	1.423	8.197	0.0021	0.0052	1.805	7.874	0.0017	0.0037	0.382	8.928	0.0313	0.0550
SGO_2043 lipoprotein, putative		5.470			-2.954	5.560	0.0127	0.0442		5.470				1.000								1.000		
SGO_2045 recA; recA protein	-2.332	9.653	0.0005	0.0006	0.828	10.862	0.0006	0.0008	0.911	10.917	0.0007	0.0018	3.160	9.855	0.0000	0.0000	3.243	9.321	0.0003	0.0001	0.083	10.745	0.0818	0.2174
SGO_2046 cinA; competence induced protein	0.441	5.691	0.0257	0.1271	0.321	5.625	0.0568	0.2580	-0.649	5.179	0.0131	0.0925	-0.120	5.303	0.0188	0.1070	-1.090	4.310	0.0010	0.0012	-0.970	4.841	0.0050	0.0022
SGO_2049 tagI; DNA-3-methyladenine glycosylase I		1.000				1.000				1.000														



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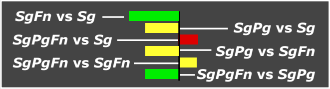

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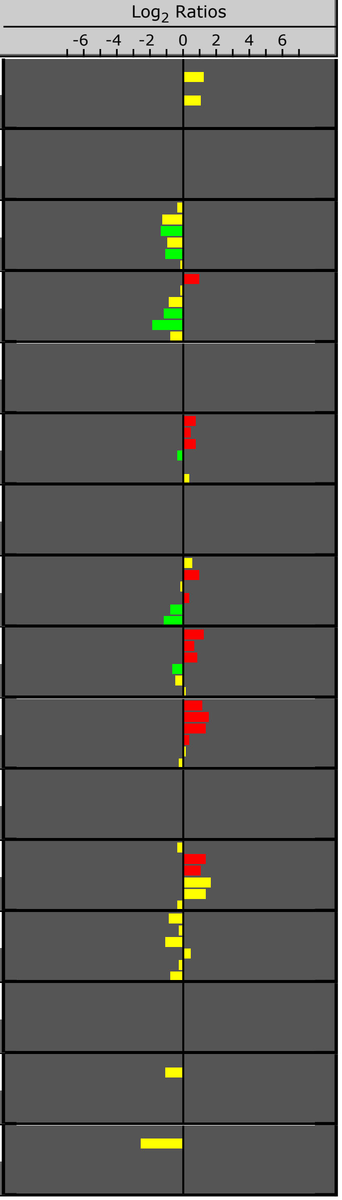
Streptococcus gordonii

Hackett Laboratory UW

Summary Table | SgFn vs Sg | SgPg vs Sg | SgPgFn vs Sg | SgPg v SgFn | SgPgFn v SgFn | SgPgFn vs SgPg | Coverage

	SgFn vs Sg				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
Protein	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_2050	0.126	3.423	0.1429	0.9676	1.259	4.533	0.0163	0.0602		2.849			1.133	3.770	0.0411	0.2701		0.692				3.483		
	ruvA; Holliday junction DNA helicase RuvA																							
SGO_2052		3.000				3.000				3.000														
	hypothetical protein SGO_2052																							
SGO_2053	-0.307	6.428	0.0257	0.1272	-1.164	6.120	0.0053	0.0152	-1.264	6.077	0.0018	0.0070	-0.856	5.395	0.0050	0.0190	-0.957	4.735	0.0014	0.0024	-0.100	4.861	0.1661	0.5663
	DNA mismatch repair protein hexB																							
SGO_2056	0.988	7.171	0.0049	0.0156	-0.084	6.562	0.1403	0.7223	-0.777	6.303	0.0176	0.1321	-1.072	6.628	0.0033	0.0109	-1.765	5.849	0.0027	0.0072	-0.693	5.734	0.0656	0.1610
	mutS; DNA mismatch repair protein MutS																							
SGO_2057		5.049				5.049				5.049														
	argR; arginine repressor																							
SGO_2058	0.776	10.075	0.0002	0.0001	0.451	9.878	0.0008	0.0011	0.830	10.111	0.0006	0.0014	-0.325	9.745	0.0011	0.0020	0.054	9.316	0.0612	0.3967	0.379	9.776	0.0103	0.0095
	argS; arginyl-tRNA synthetase																							
SGO_2059		2.058				2.058				2.058														
	hypothetical protein SGO_2059																							
SGO_2060	0.598	7.874	0.0093	0.0357	0.996	8.121	0.0014	0.0027	-0.098	7.496	0.0584	0.5233	0.399	7.832	0.0038	0.0130	-0.696	6.704	0.0031	0.0087	-1.094	7.569	0.0012	0.0001
	aspS-1; aspartyl-tRNA synthetase																							
SGO_2062	1.266	8.848	0.0012	0.0025	0.686	8.464	0.0046	0.0126	0.880	8.587	0.0018	0.0073	-0.579	8.567	0.0028	0.0084	-0.386	8.038	0.0077	0.0286	0.193	8.348	0.0506	0.1152
	hisS; histidyl-tRNA synthetase																							
SGO_2064	1.217	8.670	0.0002	0.0002	1.647	8.986	0.0005	0.0006	1.405	8.804	0.0002	0.0003	0.430	8.872	0.0029	0.0089	0.188	8.126	0.0073	0.0270	-0.242	8.955	0.0271	0.0454
	ilvD; dihydroxy-acid dehydratase																							
SGO_2065																								
	rpmF; ribosomal protein L32																							
SGO_2066	-0.335	6.614	0.0814	0.5094	1.393	7.977	0.0019	0.0041	1.056	7.749	0.0037	0.0182	1.727	7.190	0.0158	0.0853	1.390	6.300	0.0278	0.1487	-0.337	7.834	0.0466	0.1024
	rpmG; ribosomal protein L33																							
SGO_2070	-0.754	6.302	0.0416	0.2298	-0.247	6.477	0.0921	0.4498	-0.962	6.219	0.0204	0.1592	0.507	5.531	0.0345	0.2179	-0.208	4.559	0.0776	0.5231	-0.715	5.430	0.0332	0.0611
	hypothetical protein SGO_2070																							
SGO_2073										1.981								0.857				1.468		
	FtsK/SpoIIIE family subfamily, putative																							
SGO_2080		5.162			-0.970	5.772	0.0103	0.0343		5.162				3.723								3.723		
	transcription activator plcR																							
SGO_2081		6.027			-2.513	6.148	0.0099	0.0328		6.027				2.000								2.000		
	lipoprotein, putative																							



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ABC Transporter

Proteins found:
1179

Dot Plots
Dot Plots

Test	Cutoff
***q*-Value**	**.005**
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	Signif	Direction	Applies To
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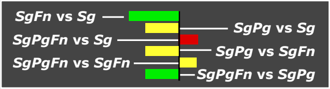

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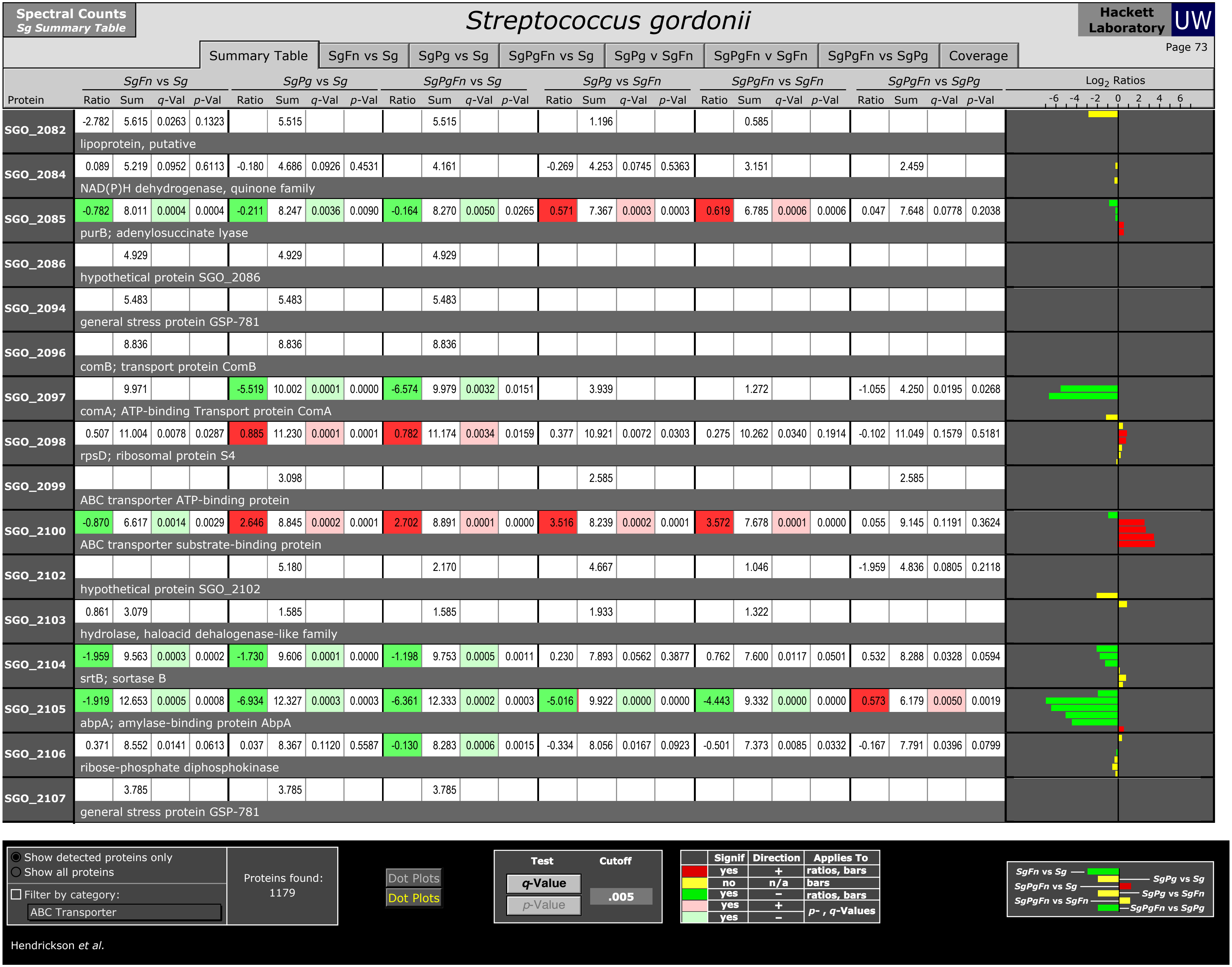

Spectral Counts
Sg Summary Table

Streptococcus gordonii

Hackett Laboratory UW

Protein		*SgFn vs Sg*				*SgPg vs Sg*				*SgPgFn vs Sg*				*SgPg vs SgFn*				*SgPgFn vs SgFn*				*SgPgFn vs SgPg*			
		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_2082	lipoprotein, putative	-2.782	5.615	0.0263	0.1323		5.515				5.515				1.196				0.585						
SGO_2084	NAD(P)H dehydrogenase, quinone family	0.089	5.219	0.0952	0.6113	-0.180	4.686	0.0926	0.4531		4.161			-0.269	4.253	0.0745	0.5363		3.151				2.459		
SGO_2085	purB; adenylosuccinate lyase	-0.782	8.011	0.0004	0.0004	-0.211	8.247	0.0036	0.0090	-0.164	8.270	0.0050	0.0265	0.571	7.367	0.0003	0.0003	0.619	6.785	0.0006	0.0006	0.047	7.648	0.0778	0.2038
SGO_2086	hypothetical protein SGO_2086		4.929				4.929				4.929														
SGO_2094	general stress protein GSP-781		5.483				5.483				5.483														
SGO_2096	comB; transport protein ComB		8.836				8.836				8.836														
SGO_2097	comA; ATP-binding Transport protein ComA		9.971			-5.519	10.002	0.0001	0.0000	-6.574	9.979	0.0032	0.0151		3.939				1.272			-1.055	4.250	0.0195	0.0268
SGO_2098	rpsD; ribosomal protein S4	0.507	11.004	0.0078	0.0287	0.885	11.230	0.0001	0.0001	0.782	11.174	0.0034	0.0159	0.377	10.921	0.0072	0.0303	0.275	10.262	0.0340	0.1914	-0.102	11.049	0.1579	0.5181
SGO_2099	ABC transporter ATP-binding protein						3.098								2.585								2.585		
SGO_2100	ABC transporter substrate-binding protein	-0.870	6.617	0.0014	0.0029	2.646	8.845	0.0002	0.0001	2.702	8.891	0.0001	0.0000	3.516	8.239	0.0002	0.0001	3.572	7.678	0.0001	0.0000	0.055	9.145	0.1191	0.3624
SGO_2102	hypothetical protein SGO_2102						5.180				2.170				4.667				1.046			-1.959	4.836	0.0805	0.2118
SGO_2103	hydrolase, haloacid dehalogenase-like family	0.861	3.079				1.585				1.585				1.933				1.322						
SGO_2104	srtB; sortase B	-1.959	9.563	0.0003	0.0002	-1.730	9.606	0.0001	0.0000	-1.198	9.753	0.0005	0.0011	0.230	7.893	0.0562	0.3877	0.762	7.600	0.0117	0.0501	0.532	8.288	0.0328	0.0594
SGO_2105	abpA; amylase-binding protein AbpA	-1.919	12.653	0.0005	0.0008	-6.934	12.327	0.0003	0.0003	-6.361	12.333	0.0002	0.0003	-5.016	9.922	0.0000	0.0000	-4.443	9.332	0.0000	0.0000	0.573	6.179	0.0050	0.0019
SGO_2106	ribose-phosphate diphosphokinase	0.371	8.552	0.0141	0.0613	0.037	8.367	0.1120	0.5587	-0.130	8.283	0.0006	0.0015	-0.334	8.056	0.0167	0.0923	-0.501	7.373	0.0085	0.0332	-0.167	7.791	0.0396	0.0799
SGO_2107	general stress protein GSP-781		3.785				3.785				3.785														

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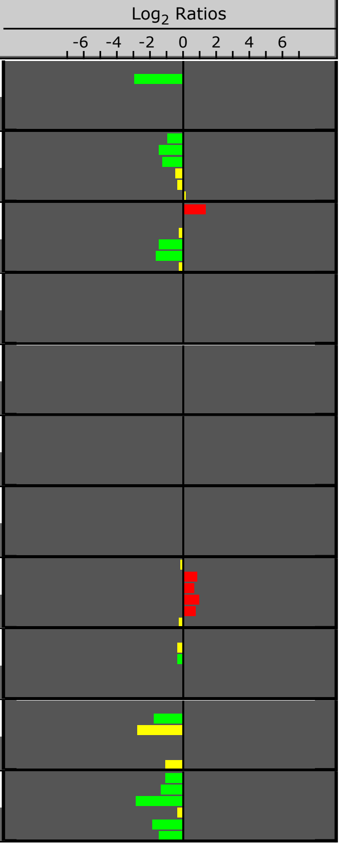
Protein		Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val	Ratio	Sum	*q*-Val	*p*-Val
SGO_2108	mreC; cell shape-determining protein MreC		6.472			-2.938	6.651	0.0001	0.0000		6.472				3.036								3.036		
SGO_2133	Cell division protein ftsH-like protein	-0.914	10.415	0.0008	0.0014	-1.361	10.272	0.0002	0.0001	-1.206	10.318	0.0002	0.0002	-0.447	9.169	0.0060	0.0240	-0.292	8.626	0.0149	0.0680	0.155	9.003	0.0195	0.0267
SGO_2134	hpt; hypoxanthine phosphoribosyltransferase	1.391	8.622	0.0005	0.0008	-0.013	7.764	0.1588	0.8316	-0.203	7.684	0.0476	0.4172	-1.405	8.099	0.0001	0.0000	-1.595	7.444	0.0006	0.0004	-0.190	7.151	0.1153	0.3458
SGO_2138	Septum formation initiator family		2.322				2.322				2.322														
SGO_2139	S4 RNA-binding domain protein		1.379				1.380				1.380														
SGO_2140	transcription-repair coupling factor		3.667				3.667				3.667														
SGO_2141	pth; peptidyl-tRNA hydrolase		1.000				1.000				1.000														
SGO_2142	GTP-binding protein	-0.098	7.739	0.0609	0.3630	0.906	8.309	0.0011	0.0018	0.662	8.157	0.0025	0.0106	1.004	7.762	0.0008	0.0011	0.760	6.995	0.0026	0.0067	-0.244	8.063	0.0397	0.0812
SGO_2145	comE; competence response regulator ComE		8.707			-0.255	9.587	0.0085	0.0270	-0.254	9.586	0.0013	0.0045		7.942				7.329			0.001	8.941	0.2492	0.9711
SGO_2146	comD; histidine protein kinase ComD		6.837			-1.707	7.223	0.0003	0.0003	-2.665	6.947	0.0073	0.0420		4.618				2.046			-0.958	4.948	0.0402	0.0827
SGO_2150	degP; serine protease	-0.999	8.352	0.0006	0.0008	-1.324	8.249	0.0002	0.0001	-2.772	7.969	0.0002	0.0001	-0.325	7.102	0.0081	0.0362	-1.773	6.029	0.0014	0.0025	-1.449	6.392	0.0050	0.0020



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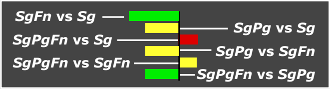

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