

SUPPLEMENTAL TABLES

Details of modularized genes from *Shewanella* data

Module	Gene#	Name	TIGR annotation	Linked genes	Assigned color
Module 1	1	so1538	isocitrate dehydrogenase, NAD-dependent	2 3	Red
	2	so1789	conserved hypothetical protein	1 4	Gray10
	3	gla	citrate synthase	6 1	Red
	4	so2391	conserved hypothetical protein	2 5	Gray10
	5	astb	succinylarginine dihydrolase	4	Red
	6	lpda	pyruvate dehydrogenase complex, E3 component, lipoamide dehydrogenase	3	Red
Module 2	7	mmsa	methylmalonate-semialdehyde dehydrogenase	8 10	Red
	8	pccb-1	3-methylcrotonyl CoA carboxylase, beta subunit	7 9	Red
	9	ivd	isovaleryl-CoA dehydrogenase	8	Red
	10	so2339	alpha keto acid dehydrogenase complex, E1 component, alpha subunit	7	Red
Module 3	11	succ	succinyl-CoA synthase, beta subunit	14	Lavender
	12	cora	magnesium and cobalt transport protein CorA	13 14	Red
	13	so3099	long-chain fatty acid transport protein, putative	12	Red
	14	atpa	ATP synthase F1, alpha subunit	11 12	Lavender
Module 4	15	so2291	hypothetical protein	18	Gray10
	16	cvsp	sulfate ABC transporter, periplasmic sulfate-binding protein	22	Red
	17	so3705	5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase, putative	18 23	Red
	18	so3725	hypothetical protein	15 17 20 22	Gray10
	19	cysn	sulfate adenylyltransferase, subunit 1	20 22 24	Red
	20	cysd	sulfate adenylyltransferase, subunit 2	18 19 21 22	Red
	21	coba	uroporphyrin-III C-methyltransferase	20 22 23	Lavender
	22	cysj	sulfite reductase (NADPH) flavoprotein alpha-component	16 18 19 20 21	Red
	23	so4150	transporter, putative	17 21	Gray10
	24	leud	3-isopropylmalate dehydratase, small subunit	19	Lavender
	Module 5	25	so1165	rare lipoprotein A	90 106 124 128 129 149 154 167 168 236 258 305 332 341
26		so1166	membrane-bound lytic transglycosylase, putative	244 305	Gray10
27		roda	rod shape-determining protein RodA	398 405 99 111 116 150 236	Black
28		so1169	conserved hypothetical protein TIGR00246	394 30 36 59 72 73 76 147 277 349	Gray10
29		so1179	conserved hypothetical protein TIGR00043	328	Gray10
30		so1180	PhoH family protein	380 278 327 328 394 398 415 416 417 28 35 40 52 59 60 72 73 74 76 84 88 89 94 107 131 147 153 164 172 187 188 230 237 239 247 265 271 289 320 321 343 349 354	Gray10
31		so1189	conserved hypothetical protein	32	Gray10
32		so1190	conserved hypothetical protein	31 98	Gray10
33		so0112	conserved hypothetical protein	186	Gray10
34		rrmj	ribosomal RNA large subunit methyltransferase J	425 269 288	Purple
35		ftsh	cell division protein FtsH	30 60 106 240 257 258 269 288 289	Black
36		tpia	triosephosphate isomerase	155 28 59 72 73 94 107 222 237 286 302	Red
37		nusa	N utilization substance protein A	315	Red
38		infb	translation initiation factor IF-2	107 194 280 302	Purple
39		rbfa	ribosome-binding factor A	394 417 40 88 196 276 369	Purple
40		rpso	ribosomal protein S15	155 394 417 30 39 59 74 84 88 89 114 147 193 222 237 294 302 349 369	Purple
41		deoa	thymidine phosphorylase	156 158 248 42 176 281 319	Red
42		deob	phosphopentomutase	158 41 43 60 74 319	Red
43		deod-2	purine nucleoside phosphorylase	413 42 60 247 281 331	Red
44		so1242	hypothetical protein	423 227 317	Gray10
45		so1264	conserved hypothetical protein	46 178 318 396 57 70 100 131 138 154 182 184 191 200 246 249 282 315 332 359 370	Gray10
46		so0119	conserved hypothetical protein	396 45 272 282 315 336 359 360	Gray10
47		so1340	hypothetical protein	72 73 94 122	Gray10
48		so0126	conserved hypothetical protein	100 131 164 172 282 332 343	Gray10
49		lepb	signal peptidase I	85 147 150 237 265 296	Black
50		era	GTP-binding protein Era	155 94 107 222 286 302 319	Red
51		so1364	iron-sulfur cluster-binding protein	392 160 324	Red
52	so1376	conserved hypothetical protein	389 398 30 57 59 72 73 91 114 138 147 154 172 200 237 247 258 264 271 304 332	Gray10	
53	so1391	conserved hypothetical protein	61	Gray10	
54	so1410	hypothetical protein	327 389 59 72 84 185 277	Gray10	
55	so0136	hypothetical protein	318 396 57 108 182 233 280 282 283 359	Gray10	
56	so1459	hypothetical protein	390 393 424 161 221 222 237 270 271 286 304 365	Gray10	
57	acea	isocitrate lyase	55 318 45 52 73 84 91 114 131 154 185 198 200 271 275 332	Red	
58	so0141	sensory box protein	330 351	Gray10	

	59	adhb	alcohol dehydrogenase II	380 155 327 389 391 394 398 416 417 28 30 36 40 52 54 60 72 73 74 76 84 88 89 94 107 114 122 147 172 230 234 237 247 271 277 286 291 294 321 349 354 369	Red
	60	grpe	heat shock protein GrpE	380 328 398 415 417 30 35 42 43 59 63 74 106 147 150 172 188 222 237 239 240 247 258 265 269 271 288 289 321 343 348 349 354	Yellow
	61	thii	thiamine biosynthesis protein ThiI	422 53 78 92 119 166 169 170 171 173 210 211 212 215 216 217 220 227 306 342 367 375	Red
	62	so151	conserved hypothetical protein	119 342	Gray10
	63	so1646	GGDEF family protein	398 419 424 60 129 172 237 247 258 271 289 296 304 343	Gray10
	64	so160	transporter, putative	106 258 271 286	Gray10
	65	so1690	ABC transporter, ATP-binding protein	418 152 66 300 366	Red
	66	so1743	hydrolase, alpha/beta hydrolase fold family	65	Gray10
	67	gspg	general secretion pathway protein G	242 296 331	Black
	68	so1757	conserved hypothetical protein	398 200 305	Gray10
	69	so1769	glutamate decarboxylase, putative	383 300	Red
	70	mitrb	outer membrane protein precursor MtrB	45 181 182 184 359	Red
	71	mitra	decaheme cytochrome c MtrA	163 339	Red
	72	omcb	decaheme cytochrome c	155 327 389 394 398 416 417 28 30 36 47 52 54 59 73 84 88 89 94 122 147 186 234 271 277 291 294 349 354	Red
	73	omca	decaheme cytochrome c	155 327 368 389 394 398 416 417 28 30 36 47 52 57 59 72 76 84 88 94 107 114 122 147 186 230 234 237 247 271 277 286 294 349	Red
	74	lon	ATP-dependent protease La	380 390 391 394 400 416 417 30 40 42 59 60 88 89 222 256 289 321 326 348 349 354 374	Yellow
	75	so1815	histone deacetylase/AcuC/AphA family protein	82 313 332 376	Gray10
	76	so1818	conserved hypothetical protein	28 30 59 73 131 147 349	Gray10
	77	ding	ATP-dependent helicase DinG	78 113 173 192 211 212 220 250 261 266 306 307 308	Black
	78	polb	DNA polymerase II	422 61 77 92 119 171 173 210 211 212 213 214 216 217 220 227 229 261 306 342	Black
	79	so1851	conserved hypothetical protein	107 193 230 237 293 302	Gray10
	80	so1868	conserved hypothetical protein	381	Gray10
	81	sucd	succinyl-CoA synthase, alpha subunit	143	Red
	82	phoq	sensor protein PhoQ	385 403 75 94 100 103 109 118 138 147 153 172 199 206 230 237 247 249 281 296 315 331 356 376	Black
	83	so1966	conserved hypothetical protein TIGR00266	194 195	Gray10
	84	so1986	RNA polymerase sigma-70 factor, ECF subfamily	327 389 394 398 417 30 40 54 57 59 72 73 88 91 114 147 200 271 294 349 369	Black
	85	so2006	NifR3/SmmI family protein	290 393 398 417 49 88 94 104 120 130 140 147 150 179 197 221 222 226 228 237 286 364	Gray10
	86	so2011	conserved hypothetical protein	399 157 160 162	Gray10
	87	so194	acyltransferase family protein	360	Gray10
	88	htpg	heat shock protein HtpG	380 409 155 327 390 391 393 394 398 400 416 417 30 39 40 59 72 73 74 84 85 89 114 147 193 196 197 222 234 237 266 271 291 294 321 338 349 354 364 369 374	Yellow
	89	so2017	conserved hypothetical protein	380 159 390 391 394 416 417 30 40 59 72 74 88 294 321 349 354 374	Gray10
	90	so2039	conserved domain protein	152 383 25 101 104 106 112 128 149 258 287 323 366	Gray10
	91	so2042	conserved hypothetical protein	389 398 52 57 84 129 147 154 172 200 236 247 258 271 304 305 332 370	Gray10
	92	so2064	conserved domain protein	61 78 119 214 215 216 342	Gray10
	93	phes	phenylalanyl-tRNA synthetase, alpha subunit	244	Purple
	94	so2088	lipid A biosynthesis acyltransferase, putative	155 158 398 30 36 47 50 59 72 73 82 85 122 138 140 147 165 172 230 237 286	Red
	95	hydc	quinone-reactive Ni/Fe hydrogenase, cytochrome b subunit	163 339	Red
	96	so2111	hypothetical protein	209 242	Gray10

	97	so2175	conserved hypothetical protein	178 131 147 164 370	Gray10
	98	subh	extragenic suppressor protein SuhB	146 406 32 99	Gray10
	99	so2261	RNA methyltransferase, TrmH family, group 1	27 98	Gray10
	100	infc	translation initiation factor IF-3	48 358 45 82 109 138 142 153 168 172 199 206 245 246 282 284 310 313 332	Purple
	101	so2329	conserved hypothetical protein	90 104 128 149 168 260 287 366	Gray10
	102	rpob	DNA-directed RNA polymerase, beta subunit	304	Black
	103	gapa-2	glyceraldehyde 3-phosphate dehydrogenase	82 109 117 138 153 296	Red
	104	so2354	conserved hypothetical protein	152 383 85 90 101 106 124 150 237 287 300 366 377	Gray10
	105	trme	tRNA modification GTPase TrmE	409	Purple
	106	so2375	membrane protein, putative	414 64 144 146 383 398 25 35 60 90 104 111 150 236 247 258 269 271 288 289 300 304 305 377	Gray10
	107	so2380	RecQ domain protein	155 30 36 38 50 59 73 79 114 123 188 193 194 222 230 237 247 275 280 286 293 302 319 346 349 376	Gray10
	108	dacb	penicillin-binding protein 4	55 359	Gray10
	109	so2399	conserved hypothetical protein	156 178 82 100 103 138 153 168 172 247 296 315 319 356	Gray10
	110	cmk	cytidylate kinase	237 271	Red
	111	ansa	L-asparaginase I	144 398 27 106 116 150 258	Red
	112	so2426	DNA-binding response regulator	90	Gray10
	113	so2439	srpA-related protein	393 77 173 197 220 221 222 223 226 228 250 266 307	Gray10
	114	so2451	conserved hypothetical protein	398 40 52 57 59 73 84 88 107 131 147 172 193 198 200 237 271 273 275 286 293 361 369	Gray10
	115	rplb	ribosomal protein L2	237 271 304	Purple
	116	so2474	carbonic anhydrase family protein	414 398 417 27 111 133 244 291	Gray10
	117	pyka	pyruvate kinase II	103 142 206	Red
	118	so2500	conserved hypothetical protein	403 82 224 372	Gray10
	119	exsb	exsB protein	62 422 61 78 92 169 171 173 211 215 216 306 342	Gray10
	120	so2540	response regulator	85 237	Gray10
	121	dnaq-2	DNA polymerase III, epsilon subunit	306 307	Purple
	122	rnha	ribonuclease HI	47 59 72 73 94	Black
	123	so2563	metallo-beta-lactamase family protein	107 193 194 302	Gray10
	124	so2564	transglycosylase, Slt family	25 104 341	Gray10
	125	asma	asmA protein	126	Gray10
	126	so2570	lipoprotein, putative	125 251	Gray10
	127	rnd	ribonuclease D	414 381 304 369	Black
	128	so2589	oxidoreductase, iron/ascorbate family	25 90 101 129 236 258 304 305	Red
	129	so2590	GTP-binding protein	424 25 63 91 128 147 154 236 237 247 258 271 296 304 305 332 370 377	Red
	130	so2610	hydrolase, TatD family	85 165	Black
	131	holb	DNA polymerase III, delta prime subunit	48 174 178 385 396 30 45 57 76 97 114 147 154 164 172 198 200 247 249 262 264 271 282 293 310 332 343 344 349 370 371 376	Black
	132	secy	preprotein translocase, SecY subunit	174	Purple
	133	so2647	cytosolic long-chain acyl-CoA thioester hydrolase family protein	116	Red
	134	so2648	DNA-binding response regulator, LuxR family	199	Gray10
	135	so2652	prophage MuSo2, transcriptional regulator, Cro/CI family	207	Gray10
	136	so2710	conserved hypothetical protein	280 283	Gray10
	137	so2724	protease, putative	188 221 222 226 237 239 250	Yellow
	138	so2725	transcriptional regulator, LuxR family	156 174 178 385 392 396 403 45 52 82 94 100 103 109 147 153 164 172 199 206 247 249 282 310 315 332 336 356 376	Gray10
	139	so2727	cytochrome c3	276 369	Red
	140	htpx	peptidase HtpX	85 94 179	Yellow
	141	biod	dethiobiotin synthase	404 142 311	Red
	142	bioc	biotin synthesis protein BioC	404 358 100 117 141 143 206 311	Red
	143	biof	8-amino-7-oxononanoate synthase	81 142	Red
	144	ccme	cytochrome c biogenesis protein CcmE	414 398 106 111 150 244 258 271 300 340	Red
	145	upp	uracil phosphoribosyltransferase	394 276 279	Red
	146	ccmc	heme exporter protein CcmC	148 152 330 383 98 106 165 255 287 300 335 340	Red
	147	fabf-1	3-oxoacyl-(acyl-carrier-protein) synthase II	178 397 398 417 28 30 40 49 52 59 60 72 73 76 82 84 85 88 91 94 97 114 129 131 138 150 153 154 164 172 198 200 230 236 237 247 249 258 265 271 286 289 296 304 332 349 354 370 376	Red
	148	ccmb	heme exporter protein CcmB	146 152	Red
	149	fabd	malonyl CoA-acyl carrier protein transacylase	425 25 90 101 150	Red

				240 258 269 288 341 363	
150	fabh-1	3-oxoacyl-(acyl-carrier-protein) synthase III		144 383 398 27 49 60 85 104 106 111 147 149 237 258 271 289 296 304 321 354 377	Red
151	plsx	fatty acid/phospholipid synthesis protein PlsX		258	Red
152	cema	heme exporter protein CcmA		146 148 383 386 65 90 104 255 287 300 366	Red
153	cdd	cytidine deaminase		398 30 82 100 103 109 138 147 167 172 247 296 310	Red
154	lpxk	tetraacyldisaccharide 4'-kinase		178 389 398 25 45 52 57 91 129 131 147 172 200 236 237 243 246 247 258 271 304 305 332 370	Red
155	so0265	conserved hypothetical protein		394 417 36 40 50 59 72 73 88 94 107 222 237 271 286 319	Gray10
156	ccmf-1	cytochrome c-type biogenesis protein CcmF		248 399 41 109 138 165 258 335	Red
157	nrdd	anaerobic ribonucleoside-triphosphate reductase		86 160 162 208	Red
158	dsbe	thiol:disulfide interchange protein DsbE		248 41 42 94 247 319	Red
159	ccmh	cytochrome c-type biogenesis protein CcmH		416 89	Red
160	nhab	Na ⁺ /H ⁺ antiporter		399 51 86 157 162 285	Red
161	zipa	cell division protein ZipA		424 56 221 226 377	Black
162	so2911	formate transporter, putative		399 86 157 160 285	Red
163	pfib	formate acetyltransferase		71 95 200	Red
164	glts	sodium/glutamate symporter		48 174 178 396 30 97 131 138 147 172 247 249 262 282 293 315 343 344 349 376	Red
165	so2929	hypothetical protein		146 156 395 94 130 296 334	Gray10
166	so2988	conserved hypothetical protein		61	Gray10
167	so2991	conserved hypothetical protein		419 25 153 168 258 296	Gray10
168	so2992	hypothetical protein		25 100 101 109 167 258	Gray10
169	so2997	hypothetical protein		61 119	Gray10
170	so2998	hypothetical protein		61 171	Gray10
171	so3000	conserved hypothetical protein		422 61 78 119 170 211 215 216 217 220 367	Gray10
172	so3013	site-specific recombinase, phage integrase family		48 174 178 368 398 403 30 52 59 60 63 82 91 94 100 109 114 131 138 147 153 154 164 199 237 247 249 258 271 296 304 315 331 332 343 349 356 376	Black
173	so3015	conserved hypothetical protein		422 61 77 78 113 119 211 212 217 219 220 229 261 306 307 342	Gray10
174	arob	3-dehydroquinate synthase		132 178 396 131 138 164 172 283 293 309 315 376	Red
175	so3047	conserved hypothetical protein		255	Gray10
176	so3052	methyl-accepting chemotaxis protein		248 41	Tan
177	so3065	colicin V production protein		197	Red
178	dam	DNA adenine methylase		174 45 97 109 131 138 147 154 164 172 247 376	Black
179	so3078	major facilitator family protein, putative		85 140 314	Gray10
180	so3089	fatty oxidation complex, beta subunit		282	Red
181	so3090	MoxR domain protein		70 182 184 359	Gray10
182	so3091	conserved hypothetical protein		55 45 70 181 184 200 246 253 359	Gray10
183	so3092	hypothetical protein		200	Gray10
184	so3093	von Willebrand factor type A domain protein		45 70 181 182 359	Gray10
185	so3094	TPR domain protein		54 57 200	Gray10
186	so3101	conserved hypothetical protein		33 416 72 73 268	Gray10
187	sec-2	protein-export membrane protein SecD		30 188 349	Black
188	yajc	preprotein translocase, YajC subunit		380 328 415 30 60 107 137 187 222 237 239 247 265 288 289 320 321 343 349 354	Black
189	tgt	queuine tRNA-ribosyltransferase		239 240	Purple
190	so3119	hypothetical protein		395 242	Gray10
191	so3121	conserved hypothetical protein		45 200 332 359	Gray10
192	so3128	ABC transporter, ATP-binding/permease protein, putative		77 211 261 308	Red
193	dctp	C4-dicarboxylate-binding periplasmic protein		40 79 88 107 114 123 197 222 230 237 265 266 286 302 349	Gray10
194	etfa	electron transfer flavoprotein, alpha subunit		38 83 107 123 195 302 361	Red
195	etfb	electron transfer flavoprotein, beta subunit		83 194	Red
196	so3157	lipoprotein, putative		417 39 88 197 364	Gray10
197	so3159	conserved hypothetical protein		391 393 417 85 88 113 177 193 196 221 222 223 226 228 231 237 266 364 373	Gray10
198	rfbc	dTDP-4-dehydrohamose 3,5-epimerase		385 57 114 131 147 200 247 249 264 315 376	Red
199	so3164	conserved hypothetical protein		396 82 100 134 138 172 206 246 272 282 284 315 336 356	Gray10
200	so3168	DnaJ domain protein		318 45 52 57 68 84 91 114 131 147 154 163 182 183 185 191 198 246 249 271 305 332 359 370	Yellow
201	asnb-2	asparagine synthetase, glutamine-hydrolyzing		203	Red

	202	so3176	glycosyl transferase, group 1 family protein	203	Red
	203	so3177	formyl transferase domain protein	201 202 205	Red
	204	so3179	lipopolysaccharide biosynthesis polymerase, putative	205 206	Red
	205	so3183	perosamine synthetase-related protein	203 204	Red
	206	rfba	glucose-1-phosphate-thymidyltransferase	358 82 100 117 138 142 199 204 207 356	Red
	207	so3191	chain length determinant protein	135 206	Gray10
	208	so3194	transcriptional activator rfaH, putative	157 246	Gray10
	209	chey-3	chemotaxis protein CheY	96 242	Tan
	210	flhf	flagellar biosynthetic protein FlhF	61 78 211 212 217 220 261	Tan
	211	flha	flagellar biosynthesis protein FlhA	422 61 77 78 119 171 173 192 210 212 216 217 220 227 228 261 306 367	Tan
	212	so3214	hypothetical protein	61 77 78 173 210 211 217 220 227 229 261 266	Gray10
	213	flir	flagellar biosynthetic protein FlhR	391 78 221 227 228 229	Tan
	214	flfo	flagellar protein FlhO	78 92 342	Tan
	215	flim	flagellar motor switch protein FlhM	61 92 119 171 216 342	Tan
	216	flil	flagellar protein FlhL	61 78 92 119 171 211 215 217 306 367	Tan
	217	flik	flagellar hook-length control protein FlhK	61 78 171 173 210 211 212 216 220 227 229 261	Tan
	218	flii	flagellum-specific ATP synthase FlhI	307	Tan
	219	flig	flagellar motor switch protein FlhG	263 173 342	Tan
	220	flif	flagellar M-ring protein FlhF	61 77 78 113 171 173 210 211 212 217 221 222 223 228 229 235 261 266 306 307	Tan
	221	flie	flagellar hook-basal body complex protein FlhE	390 391 393 417 420 56 85 113 137 161 197 213 220 222 223 226 228 237 266 373	Tan
	222	flrc	flagellar regulatory protein C	155 390 391 393 400 417 420 36 40 50 56 60 74 85 88 107 113 137 188 193 197 220 221 223 226 228 230 237 250 266 271 286 302 373	Tan
	223	flrb	flagellar regulatory protein B	393 113 197 220 221 222 226 228 235 266 373	Tan
	224	flid	flagellar hook-associated protein FlhD	118 225	Tan
	225	flag	flagellin FlaG	224	Tan
	226	flgj	flagellar protein FlgJ	393 420 85 113 137 161 197 221 222 223 228 237	Tan
	227	flgi	flagellar P-ring protein FlgI	44 61 78 211 212 213 217 261	Tan
	228	flgh	flagellar L-ring protein FlgH	390 391 393 420 85 113 197 211 213 220 221 222 223 226 266	Tan
	229	flgg	flagellar basal-body rod protein FlgG	78 173 212 213 217 220 261 266	Tan
	230	flgf	flagellar basal-body rod protein FlgF	368 30 59 73 79 82 94 107 147 193 222 237 247 265 296 349	Tan
	231	flgd	basal-body rod modification protein FlgD	393 197 364	Tan
	232	so3257	conserved hypothetical protein	315	Gray10
	233	so3277	transcriptional regulator, TetR family	55 318	Gray10
	234	cyda	cytochrome d ubiquinol oxidase, subunit I	327 394 398 417 59 72 73 88 294 352	Red
	235	so3288	transglycosylase, Slt family	220 223	Gray10
	236	so3298	conserved hypothetical protein	398 424 25 27 91 106 128 129 147 154 237 244 247 258 271 304 305 332 333 370 377	Gray10
	237	enga	GTP-binding protein EngA	115 155 368 393 398 417 420 424 30 36 40 49 52 56 59 60 63 73 79 82 85 88 94 104 107 110 114 120 129 137 147 150 154 172 188 193 197 221 222 226 230 236 247 254 265 271 286 289 296 304 321 331 349 354 365 369 377	Red
	238	so3335	conserved hypothetical protein	415 239 288 348	Gray10
	239	so3336	hypothetical protein	380 382 328 415 30 60 137 188 189 238 240 250 269 288 289 320 321 337 343 344 348 349 354	Gray10
	240	proc	pyrroline-5-carboxylate reductase	35 60 149 189 239 241 269 289 320 343	Red
	241	so3355	conserved hypothetical protein	240	Gray10
	242	so3357	conserved hypothetical protein	67 395 96 190 209 260 288	Gray10
	243	so3364	conserved hypothetical protein	154	Gray10
	244	glsa	glutaminase A	144 398 26 93 116 236 255 258 304 305	Red
	245	plrb	deoxyribodipyrimidine photolyase	100 246	Red
	246	so3386	conserved hypothetical protein	358 45 100 154 182 199 200 208 245 272 274 282 284 305 315 332 333 336 359	Gray10
	247	yfia-1	ribosomal subunit interface protein	158 178 328 385 398 403 30 43 52 59 60 63 73 82 91 106 107 109 129 131 138 147 153 154 164 172 188 198	Purple

				230 236 237 249 258 265 271 281 288 289 296 304 315 319 331 332 333 343 349 354 376	
	248	so0324	conserved hypothetical protein	156 158 41 176	Gray10
	249	pyrg	CTP synthase	403 45 82 131 138 147 164 172 198 200 247 282 315 332 343 376	Red
	250	recn	DNA repair protein RecN	77 113 137 222 239 266	Yellow
	251	thil	thiamin-monophosphate kinase	126 266	Red
	252	so0332	conserved hypothetical protein	308	Gray10
	253	lytb	penicillin tolerance protein LytB	182	Black
	254	so3542	conserved hypothetical protein	237	Gray10
	255	so3553	sulfate permease family protein	146 152 378 386 399 175 244 258	Red
	256	so3558	hypothetical protein	390 74	Gray10
	257	gsha	glutamate-cysteine ligase	35	Red
	258	clpb	clpB protein	64 144 156 398 419 424 25 35 52 60 63 90 91 106 111 128 129 147 149 150 151 154 167 168 172 236 244 247 255 269 271 288 289 296 304 305 331 332 333	Gray10
	259	putr	phosphoribosylglycinamide formyltransferase 2	278 389	Red
	260	so3616	hypothetical protein	401 101 242 331	Gray10
	261	ksga	dimethyladenosine transferase	77 78 173 192 210 211 212 217 220 227 229 308	Red
	262	apah	bis(5'-nucleosyl)-tetrakisphosphate (symmetrical)	131 164 343 376	Red
	263	so0342	conserved hypothetical protein	267 219	Gray10
	264	so3645	hypothetical protein	385 52 131 198	Gray10
	265	so3647	conserved hypothetical protein	328 30 49 60 147 188 193 230 237 247 296 349	Gray10
	266	so3649	GTP-binding protein, GTP1/Obg family	391 393 400 417 77 88 113 193 197 212 220 221 222 223 228 229 250 251	Red
	267	acna	aconitate hydratase I	263	Red
	268	rplu	ribosomal protein L21	186	Purple
	269	so3665	ABC transporter, ATP-binding/permease protein, putative	425 34 35 60 106 149 239 240 258 288 289 337 363	Red
	270	so3679	conserved hypothetical protein	56 271 331	Gray10
	271	so3681	universal stress protein family	64 115 144 155 389 397 398 417 424 30 52 56 57 59 60 63 72 73 84 88 91 106 110 114 129 131 147 150 154 172 200 222 236 237 247 258 270 273 275 286 289 296 304 305 331 332 333 343 345 349 365 369 370 377	Yellow
	272	so3683	coniferyl aldehyde dehydrogenase	46 199 246 282 315 336	Red
	273	so3684	transcriptional regulator, TetR family	114 271 365	Gray10
	274	so3690	ABC transporter, permease protein	246	Red
	275	so3709	ABC transporter, periplasmic substrate-binding protein, putative	57 107 114 271	Red
	276	so3715	oxygen-insensitive NAD(P)H nitroreductase	39 139 145	Red
	277	so3718	thiol:disulfide interchange protein, DsbA family	327 389 394 28 54 59 72 73	Red
	278	so0350	hypothetical protein	30 259 349	Gray10
	279	pnrb	NAD(P) transhydrogenase, beta subunit	145	Red
	280	so3747	sodium/hydrogen exchanger family/TrkA domain protein	55 329 38 107 136 283	Red
	281	so3762	hypothetical protein	41 43 82 247 315 319 331 356	Gray10
	282	so3764	conserved hypothetical protein	46 48 55 318 396 45 100 131 138 164 180 199 246 249 272 283 315 332 336 359 376	Gray10
	283	so3765	conserved hypothetical protein	55 174 318 396 136 280 282 316	Gray10
	284	so3766	hypothetical protein	100 199 246	Gray10
	285	cydc	ABC transporter, ATP-binding protein CydC	399 160 162 301	Red
	286	so3783	ATP-dependent RNA helicase, DEAD box family	64 155 36 50 56 59 73 85 94 107 114 147 193 222 237 271 365	Red
	287	so3797	peptidase, U32 family	146 152 383 90 101 104	Yellow
	288	so3801	ABC transporter, permease protein	380 328 425 34 35 60 106 149 188 238 239 242 247 258 269 289 337	Red
	289	so3802	ABC transporter, ATP-binding protein	380 382 328 398 415 30 35 60 63 74 106 147 150 188 237 239 240 247 258 269 271 288 296 320 321 349 354	Red
	290	spot	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	85	Red
	291	so3852	conserved hypothetical protein	327 398 417 59 72 88 116 294 369	Gray10
	292	sfca	malate oxidoreductase	411	Red
	293	so3861	iron-sulfur cluster-binding protein	174 396 79 107 114 131 164 343	Red
	294	moda	molybdenum ABC transporter, periplasmic molybdenum-binding protein	327 391 394 398 416 417 40 59 72 73 84 88 89 234 291 353 369	Red
	295	modb	molybdenum ABC transporter, permease protein	390	Red
	296	so3890	methyl-accepting chemotaxis protein	67 398 419 424 49 63	Tan

				82 103 109 129 147 150 153 165 167 172 230 237 247 258 265 271 289 304 331 334	
	297	so3892	hypothetical protein	361	Gray10
	298	so3896	outer membrane porin, putative	414 390 391 417	Gray10
	299	icc	lacZ expression regulator	378	Gray10
	300	so3915	conserved hypothetical protein	414 418 144 146 152 383 390 65 69 104 106 340	Gray10
	301	rpsf	ribosomal protein S6	285	Purple
	302	vacb	ribonuclease R	36 38 40 50 79 107 123 193 194 222	Black
	303	motx	sodium-type flagellar protein MotX	315	Tan
	304	pura	adenylosuccinate synthetase	102 115 379 381 398 424 52 56 63 91 106 127 128 129 147 150 154 172 236 237 244 247 258 271 296 305 331 332 333	Red
	305	so3942	serine protease, HtrA/DegQ/DegS family	389 398 25 26 68 91 106 128 129 154 200 236 244 246 258 271 304 332 333 370	Yellow
	306	so3984	magnesium transporter, putative	422 61 77 78 119 121 173 211 216 220 307 342	Red
	307	so3985	conserved hypothetical protein	77 113 121 173 218 220 306	Gray10
	308	so3990	dipeptidyl peptidase IV	252 77 192 261	Yellow
	309	so4006	hypothetical protein	174 329 376	Gray10
	310	so4011	conserved hypothetical protein	100 131 138 153	Gray10
	311	so4013	hypothetical protein	141 142	Gray10
	312	so4014	AcrB/AcrD/AcrF family protein	404	Gray10
	313	so4017	transglycosylase, Slt family	75 100	Gray10
	314	so4019	hypothetical protein	179	Gray10
	315	dead	ATP-dependent RNA helicase DeaD	46 174 329 385 392 396 403 37 45 82 109 138 164 172 198 199 232 246 247 249 272 281 282 303 325 332 336 356 357 376	Red
	316	so4035	hypothetical protein	283	Gray10
	317	so4068	hypothetical protein	393 44	Gray10
	318	so0388	site-specific recombinase, phage integrase family	55 45 57 200 233 282 283 359	Black
	319	udp	uridine phosphorylase	155 158 328 403 41 42 50 107 109 247 281	Red
	320	so4161	hypothetical protein	380 30 188 239 240 289 321 349 354	Gray10
	321	hslv	ATP-dependent protease HslV	380 382 390 391 398 405 415 416 417 30 59 60 74 88 89 150 188 237 239 289 320 348 349 354 374	Yellow
	322	so4164	conserved hypothetical protein	354	Gray10
	323	meng-2	S-adenosylmethionine:2-demethylmenaquinone methyltransferase	90	Red
	324	ubie	ubiquinone/menaquinone biosynthesis methyltransferase UbiE	51	Red
	325	so4210	hypothetical protein	315 356	Gray10
	326	so4263	conserved hypothetical protein	390 74	Gray10
	327	so0404	hypothetical protein	389 394 398 30 54 59 72 73 84 88 234 277 291 294 352	Gray10
	328	trxa	thioredoxin 1	380 29 30 60 188 239 247 265 288 289 319 349	Red
	329	gppa	guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	280 309 315 376	Red
	330	so4049	hypothetical protein	58 146 378 384 399	Gray10
	331	so4356	conserved domain protein	401 67 413 424 43 82 172 237 247 258 260 270 271 281 296 304 332 333	Gray10
	332	dmaa-2	anaerobic dimethyl sulfoxide reductase, A subunit	48 413 25 45 52 57 75 91 100 129 131 138 147 154 172 191 200 236 246 247 249 258 271 282 304 305 315 331 333 370 376	Red
	333	so4359	outer membrane protein, putative	236 246 247 258 271 304 305 331 332	Gray10
	334	so4418	trypanothione synthetase domain protein	165 296	Gray10
	335	moae	molybdenum cofactor biosynthesis protein E	146 156	Red
	336	so4468	transcriptional regulator, TetR family	46 138 199 246 272 282 315	Gray10
	337	so4492	conserved hypothetical protein	239 269 288	Gray10
	338	so4511	formate dehydrogenase, C subunit, putative	416 417 88	Red
	339	so4513	formate dehydrogenase, alpha subunit	71 95	Red
	340	so4515	formate dehydrogenase, C subunit, putative	144 146 300	Red
	341	so4556	transcriptional regulator, LysR family	25 124 149	Gray10
	342	so4565	transporter, putative	62 61 78 92 119 173 214 215 219 306	Gray10
	343	lexa	LexA repressor	48 396 30 60 63 131 164 172 188 239 240 247 249 262 271 293 344 349	Gray10
	344	so4604	conserved hypothetical protein	131 164 239 343 349	Gray10
	345	so4618	prolyl oligopeptidase family protein	271	Gray10
	346	so4680	conserved hypothetical protein	107	Gray10
	347	so4682	glycosyl transferase, group 1 family protein	396	Red
	348	so4686	NAD dependent epimerase/dehydratase family protein	416 60 74 238 239 321	Red
	349	prlc	oligopeptidase A	380 382 278 328 394 398 400 415 416 417 28 30 40 59 60 72 73 74 76 84 88 89 107 131 147 164 172 187	Yellow

				188 193 230 237 239 247 265 271 289 320 321 343 344 354	
	350	so4712	ABC transporter, ATP-binding protein, putative	406	Red
	351	so4713	menaquinone-specific isochorismate synthase, putative	58	Red
	352	so4719	conserved hypothetical protein	327 394 234	Gray10
	353	so4721	ABC transporter, ATP-binding protein	294 355	Red
	354	so4723	molybdopterin biosynthesis MoeA protein, putative	380 382 398 416 417 30 59 60 72 74 88 89 147 150 188 237 239 247 289 320 321 322 349	Red
	355	so4724	molybdenum cofactor biosynthesis protein A, putative	353	Red
	356	so4727	conserved hypothetical protein	82 109 138 172 199 206 281 315 325	Gray10
	357	so4728	conserved hypothetical protein	315	Gray10
	358	so4449	conserved hypothetical protein	100 142 206 246	Gray10
	359	soa0172		46 55 318 45 70 108 181 182 184 191 200 246 282	Black
	360	soa0165		46 87	Gray10
	361	soa0161		114 194 297 362	Red
	362	soa0160		361	Red
	363	soa0080		425 149 269	Gray10
	364	so3579		390 391 417 85 88 196 197 231	Purple
	365	soa0034		56 237 271 273 286	Gray10
	366	so1211		152 383 65 90 101 104	Yellow
	367	so2985		61 171 211 216	Gray10
	368	ubia	4-hydroxybenzoate polyprenyl transferase	73 172 230 237	Red
	369	so2784		394 398 417 39 40 59 84 88 114 127 139 237 271 291 294	Gray10
	370	so2783		397 45 91 97 129 131 147 154 200 236 271 305 332	Red
	371	so0590		131	Red
	372	so2754		118	Tan
	373	so3118		197 221 222 223	Purple
	374	so2277		380 391 416 417 74 88 89 321	Yellow
	375	so2154		61	Gray10
	376	so4328		174 178 329 385 396 75 82 107 131 138 147 164 172 198 247 249 262 282 309 315 332	Gray10
	377	soa0127		104 106 129 150 161 236 237 271	Gray10
	378	so0490	transcriptional regulator	330 384 389 398 399 255 299	Gray10
	379	so0549	chemotaxis protein CheY/response regulator receiver domain protein	304	Tan
	380	secb	protein-export protein SecB	382 328 390 398 415 416 417 30 59 60 74 88 89 188 239 288 289 320 321 349 354 374	Black
	381	smta	smtA protein	80 127 304	Gray10
	382	gpsa	glycerol-3-phosphate dehydrogenase (NAD(P)+)	380 398 239 289 321 349 354	Red
	383	bfd	bacterioferritin-associated ferredoxin	146 152 69 90 104 106 150 287 300 366	Red
	384	so0584	methyl-accepting chemotaxis protein	330 378 399 406	Tan
	385	so0591	conserved hypothetical protein TIGR00157	82 131 138 198 247 264 315 376	Gray10
	386	so0595	hypothetical protein	152 255	Gray10
	387	peta	ubiquinol-cytochrome c reductase, iron-sulfur subunit	406 407	Red
	388	petb	ubiquinol-cytochrome c reductase, cytochrome b	408	Red
	389	dsbd	thiol:disulfide interchange protein Dsbd	327 378 394 398 52 54 59 72 73 84 91 154 259 271 277 305	Red
	390	groes	chaperonin GroES	380 409 414 391 393 398 416 417 56 74 88 89 221 222 228 256 295 298 300 321 326 364	Yellow
	391	groel	chaperonin GroEL	409 390 393 394 416 417 59 74 88 89 197 213 221 222 228 266 294 298 321 364 374	Yellow
	392	so0740	melanin biosynthesis protein TyrA, putative	51 138 315	Red
	393	so0783	hypothetical protein	390 391 417 56 85 88 113 197 221 222 223 226 228 231 237 266 317	Gray10
	394	lldp	L-lactate permease	155 327 389 391 416 417 28 30 39 40 59 72 73 74 84 88 89 145 234 277 294 349 352 369	Red
	395	so0835	conserved hypothetical protein	165 190 242	Gray10
	396	dbpa	ATP-dependent RNA helicase Dbpa	46 55 174 45 131 138 164 199 282 283 293 315 343 347 376	Red
	397	srmB	ATP-dependent RNA helicase SrmB	147 271 370	Red
	398	so0970	fumarate reductase flavoprotein subunit precursor	380 382 414 144 327 378 389 390 402 405 416 417 419 424 27 30 52 59 60 63 68 72 73 84 85 88 91 94 106 111 114 116 147 150 153 154 172 234 236 237 244 247 258 271 289 291 294 296 304 305 321 349 354 369	Red
	399	so0975	hypothetical protein	156 330 378 384 86	Gray10

	400	so0987	methyl-accepting chemotaxis protein	160 162 255 285 416 417 74 88 222 266 349	Tan
	401	deod-1	purine nucleoside phosphorylase	260 331	Red
	402	so1007	conserved hypothetical protein	398	Gray10
	403	so1045	hypothetical protein	82 118 138 172 247 249 315 319	Gray10
	404	huth	histidine ammonia-lyase	141 142 312	Red
	405	so1074	tyrosine-specific transport protein, putative	398 27 321	Gray10
	406	nqra-2	NADH:ubiquinone oxidoreductase, Na translocating, alpha subunit	384 387 407 98 350	Red
	407	nqrb-2	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrB	387 406 408	Red
	408	nqrc-2	NADH:ubiquinone oxidoreductase, Na translocating, gamma subunit	388 407 411	Red
	409	fdhe	fdhE protein	105 421 423 390 391 417 88	Gray10
	410	nqrd-2	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrD	411 412	Red
	411	nqre-2	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrE	408 410 412 292	Red
	412	nqrf-2	NADH:ubiquinone oxidoreductase, Na translocating, beta subunit	410 411	Red
	413	bfr2	bacterioferritin subunit 2	43 331 332	Red
	414	sela	L-seryl-tRNA selenium transferase	418 144 390 398 417 106 116 127 298 300	Red
	415	so1125	integral membrane domain protein	380 30 60 188 238 239 289 321 349	Gray10
	416	dnak	chaperone protein DnaK	380 159 390 391 394 398 400 417 30 59 72 73 74 88 89 186 294 321 338 348 349 354 374	Yellow
	417	dnaj	chaperone protein DnaJ	380 409 414 155 390 391 393 394 398 400 416 30 39 40 59 60 72 73 74 84 85 88 89 116 147 196 197 221 222 234 237 266 271 291 294 298 321 338 349 354 364 369 374	Yellow
	418	selb	selenocysteine-specific translation elongation factor	414 65 300	Purple
	419	cara	carbamoyl-phosphate synthase, small subunit	398 424 63 167 258 296	Red
	420	carb	carbamoyl-phosphate synthase, large subunit	221 222 226 228 237	Red
	421	fdhd	formate dehydrogenase accessory protein FdhD	409 423	Red
	422	so1146	hypothetical protein	61 78 119 171 173 211 306	Gray10
	423	so0108	conserved hypothetical protein	409 421 44	Gray10
	424	so1158	Dps family protein	398 419 56 63 129 161 236 237 258 271 296 304 331	Gray10
	425	so1163	conserved hypothetical protein	34 149 269 288 363	Gray10
Module 6	426	so1520	conserved hypothetical protein	430 432	Gray10
	427	msra	peptide methionine sulfoxide reductase	430	Red
	428	so2860	thiol:disulfide interchange protein, DsbA family	429	Gray10
	429	so2861	conserved hypothetical protein	428 430	Gray10
	430	so2862	HDIG domain protein	426 427 429 433 434	Gray10
	431	so2865	L-lysine exporter, putative	434	Red
	432	so2869	conserved hypothetical protein	426	Gray10
	433	so3768	ion transporter	435 436 430 434	Red
	434	so4051	HlyD family secretion protein	430 431 433 437	Gray10
	435	pdhr	pyruvate dehydrogenase complex repressor	433	Red
	436	fkbp-1	peptidyl-prolyl cis-trans isomerase Fkbp	433	Black
	437	soa0013		434	Black
Module 7	438	cysw-1	sulfate ABC transporter, permease protein	439	Red
	439	cysa-1	sulfate ABC transporter, ATP-binding protein	438 441	Red
	440	so3696	hypothetical protein	441	Gray10
	441	cysi	sulfite reductase (NADPH) hemoprotein beta-component (cysI)	439 440	Red

References

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