

SAOUIHSC_01606	peptidase T					0.777	0.470	8.9E-01	0.163	0.062	5.6E-01	1.315	0.039	8.2E-02	0.814	0.139	3.5E-01	0.973	0.028	2.5E-01
SAOUIHSC_01658	endonuclease IV					1.124	1.298	3.6E-01	0.152	0.078	1.0E-01	0.767	0.356	2.9E-02	1.044	0.090	4.2E-02	1.087	0.288	9.6E-02
SAOUIHSC_02358	HenK family modification methylase					0.425	0.187	7.7E-01	0.104	0.044	5.1E-01	1.208	0.099	6.8E-02	0.711	0.237	6.4E-01	0.350	0.225	6.4E-01
SAOUIHSC_01248	tRNA pseudouridine synthase B					0.132	0.086	4.2E-01	0.265	0.112	7.9E-01	1.452	0.049	2.2E-02	0.885	0.075	1.6E-01	1.279	0.065	3.0E-02
SAOUIHSC_01328	SOS ribosomal protein L33					0.152	0.019	6.0E-02	0.387	0.121	6.1E-01	0.739	0.707	1.5E-01	0.568	0.308	1.5E-01	1.950	0.066	2.3E-01
SAOUIHSC_01469	endonuclease III					0.063	0.015	2.3E-01	0.614	0.478	7.3E-01	1.602	0.216	4.2E-01	1.070	0.026	7.7E-01	1.516	0.115	4.5E-01
SAOUIHSC_01587	ribosomal large subunit pseudouridine synthase B					0.142	0.026	5.9E-01	0.400	0.314	8.5E-01	1.308	0.197	3.5E-04	1.098	0.104	5.5E-04	1.271	0.076	5.8E-04
SAOUIHSC_01759	rod shape-determining protein MrcC					0.046	0.010	7.0E-02	0.371	0.340	2.5E-01	1.412	0.064	1.0E-01	0.652	0.247	2.0E-02	1.170	0.208	4.9E-02
SAOUIHSC_01942	serine protease SpaIA					0.176	0.025	5.5E-02	0.533	0.237	1.5E-01	0.526	0.163	1.0E-02	0.505	0.163	8.7E-03	0.420	0.143	4.5E-03
SAOUIHSC_02299	serine-protein kinase RsbW					0.153	0.034	6.1E-01	1.803	1.639	1.0E-01	0.547	0.043	6.8E-04	0.916	0.062	2.6E-01	1.509	0.092	4.8E-11
SAOUIHSC_02423	UDP-N-acetylglucosamine pyrophosphorylase					0.144	0.022	2.9E-01	0.353	0.077	7.3E-01	1.370	0.178	1.6E-01	0.910	0.012	7.3E-01	1.188	0.043	3.1E-01
SAOUIHSC_02441	alkaline shock protein Z3					0.131	0.101	5.5E-02	0.317	0.018	8.0E-02	1.165	0.189	8.0E-02	1.178	0.052	5.8E-02	1.068	0.018	2.8E-02
SAOUIHSC_01695	hypothetical protein					0.188	0.052	6.3E-02	0.227	0.262	9.0E-02	2.331	0.741	1.5E-01	1.123	0.955	3.6E-02	1.27	0.034	4.2E-02
SAOUIHSC_01673	hypothetical protein					0.071	0.025	2.9E-01	0.275	0.050	7.0E-01	1.386	0.132	1.0E-01	0.775	0.150	5.2E-01	1.049	0.035	2.6E-01
SAOUIHSC_02013	hypothetical protein					0.213	0.031	3.3E-02	0.772	3.782	8.3E-01	2.216	0.351	2.3E-01	1.307	0.441	7.0E-02	1.129	0.140	1.6E-02
SAOUIHSC_01165	uracil permease					0.020	0.013	3.4E-02	0.001	0.001	5.6E-02	1.824	0.286	7.6E-03	1.970	0.029	5.2E-02	3.22	0.372	6.4E-01
SAOUIHSC_01967	ABC transporter ATP-binding protein					0.003	0.004	7.2E-02	0.022	0.021	7.7E-02	0.841	0.031	1.0E-02	1.359	0.141	6.2E-02	1.176	0.333	3.4E-02
SAOUIHSC_02152	ABC transporter ATP-binding protein					0.036	0.015	8.7E-02	0.134	0.006	1.3E-01	1.202	0.125	1.7E-01	0.522	0.141	2.2E-02	0.401	0.071	1.4E-02
SAOUIHSC_02481	cobalt transport protein					0.018	0.020	2.5E-02	0.002	0.002	3.0E-02	1.224	0.094	1.5E-03	0.846	0.050	6.4E-05	0.900	0.099	3.9E-05
SAOUIHSC_02482	cobalt transporter ATP-binding subunit					0.010	0.009	1.5E-01	0.028	0.006	1.9E-01	0.898	0.063	3.6E-01	0.882	0.102	4.2E-01	1.159	0.284	6.5E-01
SAOUIHSC_02483	cobalt transporter ATP-binding subunit					0.059	0.003	2.7E-02	0.003	0.003	4.8E-02	0.781	0.088	1.6E-03	0.824	0.099	1.6E-03	0.355	0.069	7.5E-04
SAOUIHSC_01966	hypothetical protein					0.119	0.095	4.3E-03	0.059	0.035	8.6E-03	0.970	0.430	7.5E-07	1.581	0.493	2.5E-05	1.629	0.199	6.6E-07
SAOUIHSC_01029	phosphoenolpyruvate-protein phosphotransferase					0.135	0.030	5.3E-01	0.125	0.016	6.7E-01	0.519	0.053	6.0E-01	1.402	0.044	5.9E-04	0.409	0.078	9.3E-01
SAOUIHSC_01354	sodium-alanine symporter family protein					0.183	0.050	2.3E-01	0.120	0.097	3.6E-01	0.781	0.041	1.2E-16	0.819	0.700	1.5E-22	0.630	0.026	9.4E-11
SAOUIHSC_01656	hypothetical protein					0.141	0.079	1.8E-01	0.174	0.076	3.2E-01	1.076	0.224	5.9E-01	1.102	0.254	8.3E-01	1.113	0.147	8.2E-01
SAOUIHSC_00670	hypothetical protein					0.093	0.018	1.6E-01	0.125	0.014	2.6E-01	1.868	0.044	3.2E-01	1.773	0.153	3.8E-01	0.274	0.171	3.5E-01
SAOUIHSC_01992	phosphotransferase system EIC domain-containing protein					0.099	0.025	7.6E-01	0.254	0.063	5.3E-01	1.021	0.049	6.8E-05	0.851	0.086	1.5E-05	2.021	0.077	1.0E-04
SAOUIHSC_00652	iron compound ABC transporter ATP-binding protein					0.088	0.026	1.1E-01	0.242	0.134	2.0E-01	1.189	0.327	1.1E-01	0.904	0.076	3.1E-01	1.068	0.018	9.6E-02
SAOUIHSC_01046	ABC transporter					0.690	0.365	9.3E-01	0.157	0.056	7.4E-01	0.700	0.384	5.9E-03	1.348	0.055	8.2E-04	1.120	0.169	8.8E-02
SAOUIHSC_02389	cation efflux family protein					0.844	0.559	7.2E-01	0.221	0.003	7.8E-01	0.851	0.214	3.5E-01	1.031	0.081	8.5E-02	1.200	0.071	4.8E-02
SAOUIHSC_02699	hypothetical protein					0.694	0.545	9.9E-01	0.200	0.024	7.0E-01	0.722	0.066	3.1E-01	0.589	0.048	5.9E-01	0.688	0.117	5.8E-01
SAOUIHSC_01047	spermidine/putrescine ABC transporter permease					0.185	0.043	3.2E-01	0.407	0.098	7.5E-01	0.916	0.097	8.4E-01	0.842	0.043	8.6E-01	0.673	0.030	7.0E-01
SAOUIHSC_01378	peptide ABC transporter ATP-binding protein					0.205	0.050	6.0E-01	0.520	0.367	7.8E-01	0.795	0.067	2.8E-01	0.589	0.106	6.4E-01	0.650	0.220	4.5E-01
SAOUIHSC_01657	ABC transporter					0.066	0.016	8.3E-01	0.271	0.205	5.1E-01	1.505	0.191	1.2E-02	0.940	0.022	5.5E-06	0.788	0.019	2.3E-04
SAOUIHSC_02763	peptide ABC transporter ATP-binding protein					0.207	0.014	9.2E-01	0.368	0.055	7.2E-01	0.777	0.021	1.5E-02	0.979	0.023	9.0E-04	0.926	0.101	3.5E-03
SAOUIHSC_02765	nickel ABC transporter permease					0.134	0.095	4.0E-01	0.314	0.029	8.3E-01	0.812	0.033	1.6E-01	1.118	0.057	3.8E-02	1.093	0.064	1.1E-01
SAOUIHSC_02767	nickel ABC transporter peptide-binding protein					0.062	0.020	2.3E-01	0.046	0.036	2.6E-01	0.742	0.067	7.0E-02	0.847	0.028	2.8E-02	0.928	0.067	9.2E-01
SAOUIHSC_02873	cation transporter E1-E2 family ATPase					0.209	0.016	2.6E-01	0.405	0.149	6.2E-01	0.947	0.124	7.5E-01	1.012	0.208	7.0E-01	1.139	0.070	6.5E-01
SAOUIHSC_00647	hypothetical protein					0.196	0.050	3.4E-01	0.783	0.688	5.0E-01	0.689	0.122	1.3E-03	0.712	0.258	6.5E-01	1.310	0.275	1.7E-02
SAOUIHSC_00084	hypothetical protein					0.126	0.124	1.4E-02	0.145	0.015	9.0E-03	0.709	0.022	1.0E-03	1.621	0.226	8.1E-03	0.831	0.111	3.5E-04
SAOUIHSC_00551	hypothetical protein					0.093	0.105	2.1E-01	0.069	0.012	2.4E-01	0.674	0.168	5.3E-01	1.480	0.542	9.3E-01	1.009	0.160	6.9E-01
SAOUIHSC_00678	hypothetical protein					0.009	0.004	8.2E-03	0.155	0.054	2.7E-03	2.308	0.753	4.8E-03	0.552	0.144	2.6E-06	1.353	0.350	5.5E-06
SAOUIHSC_00694	hypothetical protein					0.015	0.015	9.3E-02	0.020	0.023	1.1E-01	0.754	0.077	1.2E-01	1.888	0.286	5.9E-01	1.099	0.030	1.9E-01
SAOUIHSC_00941	hypothetical protein					0.014	0.016	3.8E-02	0.000	0.000	3.9E-02	0.367	0.089	9.6E-03	0.385	0.275	5.9E-03	0.175	0.265	7.1E-03
SAOUIHSC_00880	hypothetical protein					0.016	0.016	2.7E-05	0.010	0.011	3.5E-02	0.261	0.361	1.4E-05	0.716	0.061	6.1E-07	0.170	0.363	8.3E-06
SAOUIHSC_01256	hypothetical protein					0.058	0.028	6.9E-01	0.030	0.011	6.2E-02	2.007	0.132	1.2E-06	0.186	0.107	6.0E-08	1.037	0.076	2.4E-05
SAOUIHSC_01271	hypothetical protein					0.017	0.017	2.0E-01	0.003	0.001	2.5E-01	1.955	0.185	5.6E-01	1.506	0.481	6.0E-01	0.922	0.218	6.2E-01
SAOUIHSC_01353	hypothetical protein					0.062	0.007	6.0E-02	0.107	0.044	1.8E-02	0.802	0.034	7.7E-41	0.927	0.026	7.0E-54	0.679	0.137	3.4E-28
SAOUIHSC_01391	hypothetical protein					0.138	0.044	5.9E-02	0.125	0.080	8.8E-02	2.380	0.145	7.3E-01	1.453	0.458	1.3E-01	1.418	0.072	9.9E-02
SAOUIHSC_01419	hypothetical protein					0.001	0.001	4.9E-02	0.020	0.023	4.4E-02	0.778	0.055	8.5E-05	0.379	0.142	2.2E-04	1.138	0.059	3.8E-04
SAOUIHSC_01422	hypothetical protein					0.000	0.000	1.1E-01	0.106	0.122	1.2E-01	2.268	0.519	7.3E-01	0.706	0.051	7.3E-02	1.767	0.070	2.8E-01
SAOUIHSC_02775	hypothetical protein					0.183	0.078	6.5E-04	0.000	0.000	6.2E-04	0.688	0.219	1.1E-04	0.021	0.136	5.1E-05	3.727	0.177	1.9E-02
SAOUIHSC_02660	hypothetical protein					0.115	0.072	7.7E-02	0.105	0.017	1.4E-01	1.174	0.092	1.3E-01	1.183	0.070	1.1E-01	1.242	0.089	1.8E-01
SAOUIHSC_02853	hypothetical protein					0.066	0.071	3.9E-01	0.089	0.036	5.9E-01	1.172	0.440	7.4E-01	1.216	0.262	6.5E-01	1.048	0.425	9.4E-01
SAOUIHSC_00380	hypothetical protein					0.000	0.000	1.1E-04	0.214	0.248	1.1E-05	0.519	0.026	2.2E-07	0.379	0.227	3.5E-07	1.039	0.059	3.2E-07
SAOUIHSC_01264	hypothetical protein					0.000	0.000	2.4E-02	0.150	0.149	2.6E-02	2.054	2.372	1.3E-01	3.486	1.077	2.3E-01	0.516	0.069	3.3E-03
SAOUIHSC_01568	hypothetical protein					0.035	0.042	3.9E-02	0.178	0.187	3.7E-02	0.599	0.542	1.5E-02	1.113	0.393	3.9E-02	0.918	0.236	1.2E-02
SAOUIHSC_00369	hypothetical protein					0.128	0.110	2.7E-01	0.175	0.104	4.6E-01	1.050	0.110	4.0E-01	0.747	0.124	8.7E-01	0.890	0.256	8.1E-01
SAOUIHSC_01436	hypothetical protein					0.240	0.261	7.8E-02	0.100	0.054	6.5E-02	0.839	0.440	4.1E-02	0.317	0.236	1.8E-02	0.811	0.610	2.3E-02
SAOUIHSC_01860	hypothetical protein					0.179	0.103	6.3E-01	0.008	0.002	5.3E-0									

SAOUHSC_00798	phosphoglyceromutase					1.202	0.411	1.2E-01	5.140	0.100	9.8E-01	3.133	0.703	1.9E-01	4.266	0.175	6.2E-01	4.159	0.119	5.8E-01
SAOUHSC_01065	heme A synthase					0.048	0.056	4.2E-06	4.253	0.622	4.7E-04	21.504	4.628	1.9E-02	8.469	2.472	4.6E-05	12.856	2.249	6.5E-04
SAOUHSC_01037	hypothetical protein					0.000	0.000	1.4E-05	1.315	1.545	3.9E-06	18.817	18.551	3.8E-02	9.619	1.524	7.1E-03	5.124	1.181	2.0E-04
SAOUHSC_01068	hypothetical protein					4.312	2.115	2.6E-02	18.114	12.387	3.0E-01	5.055	2.114	1.6E-03	6.638	3.775	8.4E-03	6.431	1.806	4.1E-03
SAOUHSC_01659	hypothetical protein					0.014	0.016	5.3E-04	0.007	0.008	3.0E-04	9.019	0.574	7.0E-03	6.412	1.607	1.6E-05	4.416	3.452	1.1E-05
SAOUHSC_00650	hypothetical protein					8.519	10.926	5.5E-04	21.610	27.716	1.9E-03	32.886	34.971	1.9E-02	22.524	16.678	1.5E-03	42.003	40.313	2.0E-02
SAOUHSC_02838	hypothetical protein					72.967	78.737	4.6E-01	4.477	5.042	1.4E-03	5.761	6.237	3.0E-03	14.175	7.151	1.0E-02	3.811	1.026	2.6E-05
SAOUHSC_00372	xanthine phosphoribosyltransferase					3.965	1.143	1.4E-01	1.852	0.238	1.5E-02	4.798	1.305	7.6E-02	5.238	0.309	9.1E-02	3.713	0.735	1.9E-02
SAOUHSC_00373	xanthine permease					2.050	0.999	7.8E-02	1.993	0.419	1.1E-01	4.392	0.279	2.3E-01	4.496	0.195	1.2E-01	3.140	0.448	1.9E-02
SAOUHSC_00881	hypothetical protein					6.235	5.965	1.1E-01	1.782	0.086	5.2E-03	7.190	3.380	1.2E-01	5.157	2.261	3.7E-02	3.564	1.038	7.8E-03
SAOUHSC_01986	hypothetical protein					0.967	1.156	8.7E-04	3.680	3.406	7.3E-02	5.118	4.804	1.1E-02	6.969	3.567	1.5E-02	1.040	0.981	9.4E-06
SAOUHSC_01423	hypothetical protein					8.864	8.163	9.0E-02	1.475	0.725	5.4E-04	9.379	4.267	3.0E-02	3.965	1.182	2.5E-04	5.628	0.553	1.8E-03
SAOUHSC_00807	hypothetical protein					0.000	0.000	1.5E-02	0.080	0.048	9.1E-03	1.631	1.830	8.2E-02	5.933	0.736	4.4E-01	5.956	5.316	3.8E-01
SAOUHSC_02202	hypothetical protein					0.708	0.827	1.6E-02	2.498	1.210	2.0E-01	1.225	0.789	1.2E-03	5.959	0.766	9.6E-02	4.913	2.972	5.4E-02
SAOUHSC_00034	hypothetical protein					37.980	15.019	1.5E-02	55.220	36.607	1.1E-01	3.666	4.173	8.3E-07	19.552	12.720	6.9E-06	18.270	12.542	3.0E-09
SAOUHSC_01067	hypothetical protein					0.000	0.000	2.1E-03	2.604	0.721	4.2E-04	8.910	3.760	6.8E-04	15.609	15.644	1.8E-02	13.767	5.739	9.7E-04
SAOUHSC_00998	fnt protein					7.015	1.867	9.9E-02	13.141	0.888	7.0E-02	0.697	0.056	8.4E-07	0.386	0.088	9.7E-03	0.956	0.030	2.9E-12
SAOUHSC_00620	accessory regulator A					2.734	0.909	5.3E-01	26.350	12.802	4.7E-01	1.490	0.389	1.3E-01	2.718	0.371	4.5E-01	1.321	0.504	7.7E-02
SAOUHSC_00536	branched-chain amino acid aminotransferase					4.607	2.590	9.4E-01	24.750	23.487	7.6E-01	2.175	0.068	8.8E-02	1.244	0.037	8.0E-04	1.198	0.236	5.9E-04
SAOUHSC_00667	ABC transporter ATP-binding protein					8.864	1.644	2.1E-01	13.898	6.288	1.4E-01	0.506	0.089	6.2E-01	0.583	0.024	1.8E-01	0.642	0.193	3.8E-01
SAOUHSC_00668	ABC transporter permease					9.602	1.574	1.3E-01	13.209	0.509	7.2E-02	0.629	0.001	5.8E-06	0.723	0.019	1.8E-07	0.833	0.007	8.7E-08
SAOUHSC_02834	sortase					2.000	0.306	2.3E-01	8.289	4.192	7.7E-01	1.317	0.468	5.8E-03	1.602	0.321	9.6E-03	1.917	0.132	1.4E-02
SAOUHSC_00665	hypothetical protein					9.219	1.444	1.9E-01	19.663	5.741	1.4E-01	0.662	0.112	1.4E-01	0.852	0.054	3.6E-02	0.891	0.149	5.0E-02
SAOUHSC_00666	hypothetical protein					7.282	1.799	2.5E-01	14.630	5.385	2.0E-01	0.653	0.038	4.4E-01	0.852	0.034	2.0E-01	0.803	0.080	3.0E-01
SAOUHSC_02664	transcriptional regulator					3.737	0.071	4.5E-01	5.648	1.286	2.5E-01	0.566	0.021	3.6E-01	1.620	0.097	1.5E-01	0.934	0.057	8.3E-01
SAOUHSC_01025	hypothetical protein					4.980	0.305	5.3E-01	7.785	2.595	3.4E-01	0.746	0.115	3.3E-02	0.637	0.066	2.1E-02	0.887	0.029	5.6E-02
SAOUHSC_01821	hypothetical protein					5.560	0.346	3.4E-01	4.968	1.571	2.5E-01	1.518	0.270	5.8E-01	1.350	0.353	3.2E-01	1.337	0.500	5.7E-01
SAOUHSC_02961	hypothetical protein					6.183	5.663	3.9E-01	5.512	0.561	5.0E-01	1.422	0.237	2.4E-03	1.916	1.214	9.3E-03	1.164	0.363	2.9E-04
SAOUHSC_00664	hypothetical protein					2.737	1.179	4.7E-01	8.500	2.319	2.2E-01	1.006	0.130	7.6E-01	3.391	0.081	2.7E-01	1.302	0.224	4.7E-01
SAOUHSC_02936	hypothetical protein					1.144	0.344	3.1E-01	5.133	0.634	4.2E-01	0.916	0.293	8.0E-02	1.053	0.208	5.7E-02	1.057	0.056	1.1E-01
SAOUHSC_00751	hypothetical protein					33.371	31.877	6.7E-01	0.677	0.582	5.0E-01	2.274	0.644	9.1E-01	1.569	0.763	7.2E-01	1.682	0.728	7.0E-01
SAOUHSC_02190	hypothetical protein					6.443	0.401	2.1E-01	0.274	0.090	7.3E-01	1.243	0.225	4.5E-01	1.124	0.487	3.6E-01	0.776	0.074	6.2E-01
SAOUHSC_02059	phi PVL orf 52-like protein					0.275	0.318	1.0E-05	0.520	0.235	1.2E-04	4.211	1.968	1.1E-04	1.180	1.073	1.7E-08	0.529	0.466	4.1E-08
SAOUHSC_02366	fructose-bisphosphate aldolase					1.769	2.269	4.5E-06	0.959	1.229	5.8E-08	32.856	18.336	4.8E-03	11.362	8.580	2.9E-05	14.745	9.319	7.5E-05
SAOUHSC_02333	sceD protein					1.700	1.763	5.3E-03	1.824	1.378	2.6E-02	4.229	0.323	2.6E-02	1.543	0.713	4.9E-04	2.576	0.724	5.6E-05
SAOUHSC_01077	hypothetical protein					0.000	0.000	1.6E-02	0.032	0.017	6.6E-03	6.643	0.687	3.1E-01	2.294	0.336	1.2E-02	1.917	1.063	1.8E-03
SAOUHSC_01526	hypothetical protein					1.333	1.420	1.0E-01	0.125	0.144	6.5E-03	6.538	3.169	9.3E-01	3.088	1.044	8.1E-02	1.163	0.229	3.3E-03
SAOUHSC_01500	hypothetical protein					0.817	0.943	1.7E-03	2.092	0.901	9.3E-04	5.446	5.235	9.7E-03	2.539	0.829	4.6E-05	0.761	0.701	3.2E-07
SAOUHSC_01181	hypothetical protein					2.390	1.787	6.8E-02	1.208	0.580	1.6E-03	4.839	0.342	5.6E-03	3.387	0.146	0.6E-04	3.691	1.825	1.2E-02
SAOUHSC_01874	hypothetical protein					5.042	5.124	2.0E-01	0.143	0.057	3.8E-03	4.295	0.918	6.4E-02	3.689	1.961	4.1E-02	2.400	0.370	4.2E-03
SAOUHSC_00718	hypothetical protein					0.000	0.000	2.8E-05	0.040	0.010	3.1E-07	4.242	1.217	1.4E-07	1.540	0.283	1.2E-13	2.241	0.329	1.1E-10
SAOUHSC_02083	bacteriophage L54a, Cro-like protein					0.000	0.000	5.9E-06	0.000	0.000	1.7E-06	13.359	5.816	4.8E-03	2.363	1.130	6.4E-09	3.912	3.883	3.4E-05
SAOUHSC_02041	phi Mu50B-like protein					0.599	0.420	3.6E-02	0.169	0.099	7.0E-02	5.138	0.293	3.7E-01	0.683	0.013	1.6E-03	2.892	0.683	1.1E-01
SAOUHSC_00573	putative heme peroxidase					4.974	3.732	1.5E-02	2.414	1.454	8.3E-04	1.708	1.147	7.2E-07	6.521	0.570	1.3E-03	1.779	0.881	5.4E-09
SAOUHSC_01504	ferredoxin					0.668	0.000	2.8E-03	0.000	0.000	7.2E-04	2.819	2.215	4.0E-02	4.410	3.710	1.9E-01	2.537	0.290	3.4E-03
SAOUHSC_01421	hypothetical protein					0.668	0.337	2.1E-03	1.058	0.154	1.7E-03	3.409	3.564	1.9E-04	4.059	1.444	4.3E-04	2.299	0.591	1.4E-04
SAOUHSC_02170	peptidoglycan hydrolase					1.219	0.470	1.2E-01	1.647	1.213	2.2E-01	3.504	0.845	3.5E-01	2.424	0.409	1.3E-01	6.098	3.495	6.5E-01
SAOUHSC_01135	hypothetical protein					12.194	13.579	4.7E-02	11.915	1.824	5.5E-02	3.308	0.310	6.0E-02	13.373	6.289	4.6E-03	63.279	72.373	8.6E-02
SAOUHSC_02391	hypothetical protein					1.402	1.399	2.9E-07	87.663	97.773	1.9E-01	1.825	2.107	1.2E-08	6.981	8.061	9.4E-08	38.703	43.993	4.4E-02
SAOUHSC_01325	hypothetical protein					0.921	1.068	4.0E-03	1.027	0.259	5.1E-04	0.211	0.245	4.7E-06	0.851	0.678	2.2E-06	4.523	5.248	6.2E-03
SAOUHSC_01783	hypothetical protein					0.266	0.307	2.9E-07	0.230	0.265	5.1E-06	2.383	2.752	8.7E-10	0.914	0.775	2.5E-10	7.124	7.666	5.9E-10
SAOUHSC_02378	hypothetical protein					8.100	7.732	8.9E-02	1.840	2.163	4.2E-04	1.444	0.326	1.9E-05	1.659	0.313	8.6E-07	4.594	2.366	1.3E-05

Curated as under-represented in condition (Blue box) or over-represented in condition; 'Supergrowers' (Green box)
 *Abs, abscess; BI, blood; VH, vitreous fluid; AH, aqueous fluid.