

RegPrecise

Collection of Manually Curated Inferences of Regulons in Prokaryotic Genomes

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Propagation of CodY regulon to *Staphylococcus aureus* subsp. aureus USA300_FPR3757

Reference regulon properties

Source regulon:	CodY - Staphylococcaceae
Regulator type:	Transcription factor
Regulator family:	CodY
Regulation mode:	repressor
Biological process:	Amino acid metabolism
Effector:	Branched-chain amino acids
Phylum:	Firmicutes
Propagated regulon:	
Target genome	Staphylococcus aureus subsp. aureus USA300_FPR3757
Orthologous TF(s)	SAUSA300_1148
Regulated genes	73



Predicted regulatory interactions in *Staphylococcus aureus* subsp. aureus USA300_FPR3757

Locus tag	Position	Score	Sequence
SAUSA300_0012	-314	4.6	AGTAATCAGAAAATT

Supported by regulated orthologs from reference regulons

Ortholog gene name: [metX](#)

Ortholog function: homoserine-o-acetyltransferase

Staphylococcus aureus subsp. aureus N315	SA0011	-293	4.6	AGTAATCAGAAAATT
Staphylococcus capitis SK14	STACA0001_1363	-236	4.6	ATTAATTAGAAAATT
		-227	4.6	AAAATTCAGACTATT
Staphylococcus epidermidis ATCC 12228	SE0011	-233	4.8	AATAATTAGAAAATT
		-224	4.5	AAAATTTAGACTATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0012	-230	4.8	AATAATTAGAAAATT
		-221	4	AAAATTATGATATTT

SAUSA300_0129	-102	4.7	AAATATCTGAATATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [butA](#)

Ortholog function: acetoin reductase

Staphylococcus aureus subsp. aureus N315	SA0122	-102	4.7	AAATATCTGAATATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0065	-68	4.6	ATTATTCAGAAAATA

SAUSA300_0135	-102	4.2	AAATTTTATATAATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [sodM](#)

Ortholog function: superoxide dismutase SodM

Staphylococcus aureus subsp. aureus N315	SA0128	-102	4.2	AAATTTTATATAATT
		-41	4	AATTATATAAAAGT

SAUSA300_0152	-205	4.1	ATTTTTTTAAATAAA
	-32	4.1	ATTTTAATGAAAATT

Supported by regulated orthologs from reference regulons

Ortholog gene name: [capA](#)

Ortholog function: capsular polysaccharide synthesis enzyme Cap5A

Staphylococcus aureus subsp. aureus N315	SA0144	-32	4.1	ATTTTAATGAAAATT
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SAUSA300_0160	3	4.2	AGAATTTTAAATATT
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	Locus tag	Position	Score	Sequence
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: capI				
Ortholog function: capsular polysaccharide synthesis enzyme Cap5I				
Staphylococcus aureus subsp. aureus N315	SA0152	-32	4.1	ATTTTAATGAAAATT
	SAUSA300_0173	-88	4.8	AATATTTAAAAAAAT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: SA0165				
Ortholog function: hypothetical protein				
Staphylococcus aureus subsp. aureus N315	SA0165	-97	4.2	TTTATCTAAATATT
		-88	4.8	AATATTTAAAAAAAT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0460	-99	4.8	ATTTATCAGAAAATT
	SAUSA300_0188	-117	5.2	AATTTTCAAAAAATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: brnQ1				
Ortholog function: branched-chain amino acid transport system				
Staphylococcus aureus subsp. aureus N315	SA0180	-117	5.2	AATTTTCAAAAAATT
Staphylococcus capitis SK14	STACA0001_0024	-81	4.7	TTTTTCTGAAAATT
Staphylococcus epidermidis ATCC 12228	SE0217	-173	4.4	AATATTAAAAATTTT
Staphylococcus haemolyticus JCSC1435	SH0145	-81	4.5	AATTTATTGAATATT
Micrococcus caseolyticus JCSC5402	MCCL_0050	-86	4.5	AATTTTTAATTAAT
		-77	4.8	ATTAATCAGAAAATT
	SAUSA300_0306	-85	4.5	ATTTTTCAGATTTT
		-76	4.5	ATTTTTTAAATTATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: brnQ2				
Ortholog function: branched-chain amino acid transport system				
Staphylococcus aureus subsp. aureus N315	SA0294	-55	4.5	ATTTTTCAGATTTT
		-46	4.5	ATTTTTTAAATTATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0418	-53	5	AATATTCAGAAATTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP2299	-112	4.3	AATACTTTAAATATT
		-103	4.1	AATATTATAAATTAT
		-94	4.5	AATTATCTGACATTT
	SAUSA300_0361	-167	5.1	ATTATTCAGAAAATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: SA0348				
Ortholog function: putative transcriptional regulator				
Staphylococcus aureus subsp. aureus N315	SA0348	-176	5.1	ATTATTCAGAAAATT
Staphylococcus capitis SK14	STACA0001_1417	-209	4.9	ACTTTTCTGAAAATT
		-75	4.8	AATTTTTAAAAATAAT
Staphylococcus epidermidis ATCC 12228	SE2378	-210	5.1	ATTTTCTGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0015	-192	5.1	AATTTTCAGAAATAAT
		-115	4.9	AATTTTTTGAATTTT
Staphylococcus haemolyticus JCSC1435	SH2634	-279	4.9	ACTTTTCTGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP2412	-127	4.6	ACTTATCTGAAAATT
	SAUSA300_0381	-121	4.5	AATATTTTAAAAAGT

Supported by regulated orthologs from reference regulons

	Locus tag	Position	Score	Sequence
Ortholog gene name: SA0367				
Ortholog function: putative NADPH-flavin oxidoreductase				
Staphylococcus aureus subsp. aureus N315	SA0367	-121	4.2	AATATTTTAAAAAGT
Staphylococcus capitis SK14	STACA0001_1449	-145	4.8	AAATATCTGAAAATT
Staphylococcus epidermidis ATCC 12228	SE2355	-114	5.1	AATTATCTGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0041	-140	4.3	AATATTTATATTATT
Staphylococcus haemolyticus JCSC1435	SH2590	-144	4.8	AAATATCTGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP2331	-193	4.3	AATAATTTAACTATT

	SAUSA300_0382	-29	4.4	TATATTCAAAAATTT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [tcyP](#)**Ortholog function:** L-cystine uptake protein tcyP

Staphylococcus aureus subsp. aureus N315	SA0368	-72	4.3	AATATTTTAAAAATTA
		-29	4.4	TATATTCAAAAATTT
Staphylococcus capitis SK14	STACA0001_1450	-133	5.1	ATTATTCAGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP2329	-138	4.6	AATTATCAGAAAATA

	SAUSA300_0444	-169	4.4	CTTTTTTAGAATATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [gltC](#)**Ortholog function:** transcription activator of glutamate synthase operon

Staphylococcus aureus subsp. aureus N315	SA0429	-169	4.4	CTTTTTTAGAATATT
		-160	4.3	AATATTCTGATATTA
Staphylococcus capitis SK14	STACA0001_1493	-179	5	AATTTTCTGACAATT
		-41	4.6	AAATTTTAGAATTTT
Staphylococcus epidermidis ATCC 12228	SE2313	-171	5	AATTTTCTGACAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0104	-113	4.7	AATTTTCAGATTTT
		-39	4.5	ATTATTCTAATTATT
Staphylococcus haemolyticus JCSC1435	SH2541	-138	5.4	AATTTTCAGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP2285	-118	5	AAAATTCTGAAAATT

	SAUSA300_0445	-26	4.4	AATATTCTAAAAAAG
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [gltB](#)**Ortholog function:** glutamate synthase large subunit

Staphylococcus aureus subsp. aureus N315	SA0430	-35	4.3	TAATATCAGAAATATT
		-26	4.4	AATATTCTAAAAAAG
Staphylococcus capitis SK14	STACA0001_1494	-174	4.6	AAAATTCTAAATTTT
		-36	5	AATTGTCAGAAAATT
Staphylococcus epidermidis ATCC 12228	SE2312	-35	5	AATTGTCAGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0105	-117	4.5	AATAATTAGAATAAT
		-43	4.7	AAAAATCTGAAAATT
Staphylococcus haemolyticus JCSC1435	SH2540	-34	5.4	AATTTTCTGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP2284	-34	5	AATTTTCTGAAAATT

	SAUSA300_0539	-92	5.2	AATTTTCTAGAAAATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [ilvE](#)**Ortholog function:** branched-chain amino acid aminotransferase

Staphylococcus aureus subsp. aureus N315	SA0512	-92	5.2	AATTTTCTAGAAAATT
Staphylococcus capitis SK14	STACA0001_0476	-101	4.4	TTTATTTTGAATATT
		-92	4.7	AATATTTAGAAAATT
Staphylococcus epidermidis ATCC 12228	SE0318	-99	4.1	TCTATTTTGAATATT
		-90	5.2	AATATTTAGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0215	-101	4.5	ATTTTCTTAAATTTT

	Locus tag	Position	Score	Sequence
Staphylococcus haemolyticus JCSC1435	SH2449	-92	4.8	AATTTTCTAAAAACT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP2163	-91	5.2	AATTTTGTAGAAAATT
Macroccoccus caseolyticus JCSC5402	MCCL_1855	-86	5.2	AATTTTGTGAAAATT
		-85	4.8	AATTTTCTAAAAACT

	SAUSA300_0632	-178	5	AAAATTCAGAATATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [SA0601](#)

Ortholog function: hypothetical protein

Staphylococcus aureus subsp. aureus N315	SA0601	-400	5	AAAATTCAGAATATT
		-391	4.1	AATATTTTAAATTAT
Staphylococcus capitis SK14	STACA0001_0382	-211	5	AAAATTCAGAATATT
Staphylococcus epidermidis ATCC 12228	SE0420	-206	5	AAAATTCAGAATATT
		-197	4.1	AATATTTAAATTTAT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0294	-120	4.8	AATTTTCAGAAATTAT
Staphylococcus haemolyticus JCSC1435	SH2248	-172	5	AAAATTCAGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP2074	-166	4.8	AAATTTTCAGAAATTTT

	SAUSA300_0657	-195	4.5	ATATTTTGTGAAAAAT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [SA0626](#)

Ortholog function: hypothetical protein

Staphylococcus aureus subsp. aureus N315	SA0626	-195	4.5	ATATTTTGTGAAAAAT
Staphylococcus capitis SK14	STACA0001_0358	-200	4.6	ATTAATTAGAAAATT
		-142	4.3	AATTTTAAGTAAATT
		-98	4.2	ATAATTTGTGAAAATA
Staphylococcus haemolyticus JCSC1435	SH2222	-200	4.1	TTTATTTAGAAATTTT
		-191	4.6	AATTTTCAGATAATA
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP2051	-190	5.1	AATTTTCAGAAAAT

	SAUSA300_0712	-112	4.6	AATATTCTCAATATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [tppB](#)

Ortholog function: di-tripeptide ABC transporter

Staphylococcus aureus subsp. aureus N315	SA0682	-112	4.6	AATATTCTCAATATT
		-103	4.1	AATATTTTATTTTT
Staphylococcus capitis SK14	STACA0001_0301	-124	4.3	AATTGACTGAATATT
		-115	4.5	AATATTCATATTATT
		-98	4.8	TATTTTGTGAAAATT
Staphylococcus epidermidis ATCC 12228	SE0509	-107	4	CTTTTTTAAATTTT
		-98	5.2	AATTTTGTGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0374	-114	5.3	AATATTCTGAAAATT
		-88	4.5	TATTTTAAGAAAATT
Staphylococcus haemolyticus JCSC1435	SH2166	-102	5	AAATTTCTAAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1991	-118	4.1	AAATAACAGAAATATT
		-109	4.6	AATATTCTCAATATT
Macroccoccus caseolyticus JCSC5402	MCCL_0478	-117	4.6	AACTTTTGTGAAAATT
		-36	5.3	AATTTTCAGAAATATT

	SAUSA300_0784	-41	4.6	TTTTTTCAGAAATATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [lysE](#)

Ortholog function: lysine exporter protein

Staphylococcus aureus subsp. aureus N315	SA0753	-41	4.6	TTTTTTCAGAAATATT
Staphylococcus capitis SK14	STACA0001_0229	-43	4.7	AATTATCAGAAATTTT
Staphylococcus haemolyticus JCSC1435	SH2058	-60	4.4	TATATTCTAAATTTT

	Locus tag	Position	Score	Sequence
		-51	4.3	AATTTTCAGATTTTA
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	SAUSA300_0864	-32	4.6	AATATTCAGATAACT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: argG				
Ortholog function: argininosuccinate synthase				
Staphylococcus aureus subsp. aureus N315	SA0822	-32	4.6	AATATTCAGATAACT
Staphylococcus capitis SK14	STACA0001_0165	-33	5	AAAATTCTGAAAATT
Staphylococcus epidermidis ATCC 12228	SE0657	-180	4.5	AATTTACAGAAATTT
		-171	4.3	AAATTTTAAAAATATA
Staphylococcus carnosus subsp. carnosus TM300	Sca_0569	-33	4.5	AAAATTCTAACTATT
Staphylococcus haemolyticus JCSC1435	SH1989	-31	5.1	AATTTTCAGAAAAAT
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	SAUSA300_0887	-66	4.7	AGATTTTCAGAAAATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: oppB				
Ortholog function: oligopeptide ABC transporter permease protein OppB				
Staphylococcus aureus subsp. aureus N315	SA0845	-66	4.7	AGATTTTCAGAAAATT
Staphylococcus capitis SK14	STACA0001_0146	-36	4.2	AATATACATAATATT
		-27	4.6	AATATTCTGAAAAAA
Staphylococcus epidermidis ATCC 12228	SE0680	-63	4.9	ATATTCTGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0588	-113	5.2	AATATTCTAAAAATT
		-65	4.2	AATATTAAAAATATT
		-56	4.9	ATATTCTGAAAATT
Staphylococcus haemolyticus JCSC1435	SH1970	-116	4.7	AATTTTGTGAAAATT
		-60	4.9	ATATTCTGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1794	-56	4.8	ATATTCTGAATATT
Macroccoccus caseolyticus JCSC5402	MCCL_0605	-186	4.8	AATTTTAAAAAAAT
		-132	4.8	AATCTTCTGAAAATT
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	SAUSA300_0892	-84	4.7	AATATTCTAAAAATA
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: appA				
Ortholog function: oligopeptide transport system oligopeptide-binding protein AppA				
Staphylococcus aureus subsp. aureus N315	SA0850	-93	4.1	AAATAACTGAATATT
		-84	4.7	AATATTCTAAAAATA
Staphylococcus carnosus subsp. carnosus TM300	Sca_0936	-65	4.6	AATAGTCAGACAATT
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	SAUSA300_0914	-78	5.1	AATATTCTGAAAAAT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: SA0871				
Ortholog function: sodium-alanine symporter homolog				
Staphylococcus aureus subsp. aureus N315	SA0871	-150	4.3	ATTTATAAGAATATT
		-141	5.1	AATATTCTGAAAAAT
Staphylococcus aureus subsp. aureus N315	SA0871	-150	4.3	ATTTATAAGAATATT
		-141	5.1	AATATTCTGAAAAAT
Macroccoccus caseolyticus JCSC5402	MCCL_0082	-101	4.7	AATATTCAGAAATTAT
Macroccoccus caseolyticus JCSC5402	MCCL_0082	-101	4.7	AATATTCAGAAATTAT
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	SAUSA300_0928	-186	4.9	AATATTCTGACTATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: comK				
Ortholog function: competence transcription factor				

	Locus tag	Position	Score	Sequence
Staphylococcus aureus subsp. aureus N315	SA0882	-147	4.9	AATATTCTGACTATT
Staphylococcus capitis SK14	STACA0001_0106	-151	4.7	AATATTCTGACATTT
Staphylococcus epidermidis ATCC 12228	SE0731	-147	4.7	AATATTCTGACATTT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0642	-145	4.6	AATATTCTGACTTTT
		-136	4.1	ACTTTTAAAAAATA
Staphylococcus haemolyticus JCSC1435	SH1926	-148	4.6	AATATTCTGACTTTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1755	-186	4.6	AATATTCAGACTTTT
		-92	4.5	AAATTTATAAAAATT
Macroccoccus caseolyticus JCSC5402	MCCL_1546	-195	4.8	ATAATTCTGAAAATT
		-186	4.4	AAAATTTAAATTATT
		-86	4.7	AAATTTCTTAAAATT

[SAUSA300_0929](#) -77 4.9 AATAGTCAGAATATT

Supported by regulated orthologs from reference regulons

Ortholog gene name: [SA0883](#)

Ortholog function: hypothetical protein

Staphylococcus aureus subsp. aureus N315	SA0883	-77	4.9	AATAGTCAGAATATT
Staphylococcus capitis SK14	STACA0001_0107	-83	4.7	AAATGTCAGAATATT
Staphylococcus epidermidis ATCC 12228	SE0729	-82	4.7	AAATGTCAGAATATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0643	-178	4.2	AATTATAAAAAAAT
		-91	4.1	TATTTTAAAAAAGT
		-82	4.6	AAAAGTCAGAATATT
Staphylococcus haemolyticus JCSC1435	SH1925	-80	4.6	AAAAGTCAGAATATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1756	-174	4.5	AATTTTATAAAATTT
		-80	4.6	AAAAGTCTGAATATT

[SAUSA300_0952](#) -50 4.2 TAATTTCTAAATTTT
-41 4.4 AATTTTGTAGACAATA
19 4.1 CTAATTTCTAAATATT

Supported by regulated orthologs from reference regulons

Ortholog gene name: [patA](#)

Ortholog function: putative aminotransferase A

Staphylococcus aureus subsp. aureus N315	SA0902	-50	4.2	TAATTTCTAAATTTT
		-41	4.4	AATTTTGTAGACAATA
Staphylococcus capitis SK14	STACA0001_2317	-58	4.1	ACTATTTTAACAATT
Staphylococcus epidermidis ATCC 12228	SE0747	-59	4.1	ACTATTTAAACAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0656	-108	4.2	TTTATTCTAAATTTT
Staphylococcus haemolyticus JCSC1435	SH1916	-65	4.9	ATTATTCTAAATTTT
Macroccoccus caseolyticus JCSC5402	MCCL_1585	-86	4.3	AATGTTCTAATAATT

[SAUSA300_1014](#) -109 4.4 TAAATTTTGAAAATT
-41 4.6 ATTAGTTAGAAAATT

Supported by regulated orthologs from reference regulons

Ortholog gene name: [pycA](#)

Ortholog function: pyruvate carboxylase

Staphylococcus aureus subsp. aureus N315	SA0963	-41	4.6	ATTAGTTAGAAAATT
Staphylococcus capitis SK14	STACA0001_2249	-42	4.6	ATTAGTTAGAAAATT
		-33	4.4	AAAATTCAAAAAATA
Staphylococcus epidermidis ATCC 12228	SE0813	-40	4.1	TATTATCTAATTATT
		-31	4.9	ATTATTAGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0740	-34	4.6	AAAATTCAAAATAATT
Staphylococcus haemolyticus JCSC1435	SH1838	-41	4.5	ATTAGTTAGAAATATT
		-32	4	AATATTCAAACTTTA
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1675	-38	4.7	ACTTTTGTAGAAAATT
		-29	4.1	AAAATTCAAAATTTA

[SAUSA300_1200](#) -187 4.4 ATTTATCAGATTATT
-178 4.2 ATTATTTTAAAAAT

	Locus tag	Position	Score	Sequence
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: glnR				
Ortholog function: HTH-type transcriptional regulator GlnR				
Staphylococcus aureus subsp. aureus N315	SA1149	-187	4.4	ATTTATCAGATTATT
		-178	4.2	ATTATTTTTAAAAAT
Staphylococcus capitis SK14	STACA0001_1553	-202	4.3	TTTTGTCAGAAAATT
		-191	4.1	AATTATAAAATTATT
		-150	4.2	ATTAATTAAAAATTT
Staphylococcus epidermidis ATCC 12228	SE0986	-194	4.8	AAATGTCTGAAAATT
		-185	4.7	AAAATTTTAAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0958	-157	4.8	AATTTACAGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1452	-179	4.2	ATTTTTTTGAATAAA
		-157	4.9	AATTTTCTAATAATT
		-56	4.4	ATTAATCTGATTATT
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	SAUSA300_1225	-87	4.6	AATATTCAAAATATA
		-35	4.7	AATTTTCTGATTTTT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: thrA				
Ortholog function: aspartokinase III				
Staphylococcus aureus subsp. aureus N315	SA1163	-87	4.6	AATATTCAAAATATA
		-35	4.7	AATTTTCTGATTTTT
Staphylococcus capitis SK14	STACA0001_1570	-33	4.7	AATTTTCTGATTTTT
Staphylococcus epidermidis ATCC 12228	SE1008	-33	4.7	AATTTTCTGATTTTT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0969	-97	4.4	AAAGTTCAAAAAATT
		-79	4.2	AATATGTTGAAATTT
Staphylococcus haemolyticus JCSC1435	SH1580	-35	4.7	AATTTTCTGATTTTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1439	-35	4.7	AATTTTCTGATTTTT
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	SAUSA300_1226	-170	4.7	AAAAATCAGAAAATT
		-118	4.6	TATATTTTGAATATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: hom				
Ortholog function: homoserine dehydrogenase				
Staphylococcus aureus subsp. aureus N315	SA1164	-170	4.7	AAAAATCAGAAAATT
		-118	4.6	TATATTTTGAATATT
Staphylococcus capitis SK14	STACA0001_1571	-170	4.7	AAAAATCAGAAAATT
		-91	4.3	AAAATTAAAGAATAAT
Staphylococcus epidermidis ATCC 12228	SE1009	-170	4.7	AAAAATCAGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0970	-127	4.2	AAATTTCAACATATT
		-109	4.4	AATTTTGTGAACTTT
Staphylococcus haemolyticus JCSC1435	SH1579	-178	4.7	AAAAATCAGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1438	-168	4.7	AAAAATCAGAAAATT
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	SAUSA300_1231	-110	4.7	AAAAATCAGAAAATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: rocC				
Ortholog function: amino acid permease				
Staphylococcus aureus subsp. aureus N315	SA1169	-110	4.7	AAAAATCAGAAAATT
		-101	4.1	AAAATTTTAATTTTT
Staphylococcus capitis SK14	STACA0001_1576	-112	5.1	AAATTTTCAGAAAATT
		-102	4.7	AAATTTTTAAATATT
Staphylococcus epidermidis ATCC 12228	SE1015	-112	4.6	AAATATCAGAAAAAT
		-103	4.1	AAAAATTTAACAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0975	-121	4.3	TTTTTTTCAGAAATTT
		-112	4.7	AATTTTTCAGAAATTT
Staphylococcus haemolyticus JCSC1435	SH1574	-114	5.1	AAATTTTCAGAAAATT

	Locus tag	Position	Score	Sequence
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305 Macrococcus caseolyticus JCSC5402	SSP1433 MCCL_0990	-105	4.4	AAAAATTTAAAAATTTT
		-111	4.4	AATATTTTAAACATTTT
		-56	4.4	AATTTTCTTAATTAT
	SAUSA300_1232	-117	4.1	AAAAATTAAAAATTTT
		-108	4.7	AATTTTCTGATTTT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: katA				
Ortholog function: catalase				
Staphylococcus aureus subsp. aureus N315	SA1170	-111	4.1	AAAAATTAAAAATTTT
		-102	4.7	AATTTTCTGATTTT
Staphylococcus capitis SK14	STACA0001_1577	-131	4.7	AATATTTTAAAAATTT
		-121	5.1	AATTTTCTGAAATTT
Staphylococcus epidermidis ATCC 12228	SE1016	-142	4.1	AATTGTTAAATTTT
		-133	4.6	ATTTTCTGATATTT
Staphylococcus carnosus subsp. carnosus TM300	Sca_2336	-28	4.1	ATTATTCTAAATAAG
Staphylococcus haemolyticus JCSC1435	SH1573	-123	4.4	AAAATTTTAAATTTT
		-114	5.1	AATTTTCTGAAATTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1432	-129	4.4	AAATGTTTAAATATT
	SAUSA300_1260	-34	5.1	ATTATTCTGAAAATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: tyrA				
Ortholog function: prephenate dehydrogenase				
Staphylococcus aureus subsp. aureus N315	SA1197	-34	5.1	ATTATTCTGAAAATT
Staphylococcus capitis SK14	STACA0001_1611	-35	4.8	ACTATTCTGAAAATT
Staphylococcus epidermidis ATCC 12228	SE1047	-251	4.4	AATTATCTGATTTT
		-242	4.6	ATTTTCTAATTATT
		-35	4.4	GTTATTCTGAAAATT
Staphylococcus haemolyticus JCSC1435	SH1544	-35	4.8	CATATTCTGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1387	-36	4.8	ACTATTCTGAAAATT
	SAUSA300_1262	-96	4.5	AATATTTCGAATATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: trpE				
Ortholog function: anthranilate synthase component I				
Staphylococcus aureus subsp. aureus N315	SA1199	-439	4.5	AATAATTAGAAATTTT
Staphylococcus capitis SK14	STACA0001_1613	-438	4.6	AATAATTAGAAAAAT
		-429	4.4	AAAAATCAGATAATT
Staphylococcus epidermidis ATCC 12228	SE1048	-431	4.6	AATAATTAGAAAAAT
		-422	4.4	AAAAATCAGATAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1012	-464	4.3	CATTATTAAAAAATT
Staphylococcus haemolyticus JCSC1435	SH1542	-453	4.3	AAATATCAAACAATT
	SAUSA300_1286	-342	4.4	AATTTTCAGGTTATT
		-324	4	AAAAATCTAAATTAT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: lysC				
Ortholog function: aspartokinase II				
Staphylococcus carnosus subsp. carnosus TM300	Sca_1037	-340	4.3	AAATTTCTAAAAATC
Staphylococcus haemolyticus JCSC1435	SH1518	-344	4.1	ATTTTTCAGTCTATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1357	-350	4.5	ATTTTTCAGTAAATT
		-341	4.3	TAAATTTAAAAAATT
	SAUSA300_1287	-45	5.2	AATATTCTAAAAATT

	Locus tag	Position	Score	Sequence
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: asd				
Ortholog function: aspartate semialdehyde dehydrogenase				
Staphylococcus aureus subsp. aureus N315	SA1226	-45	5.2	AATATTCTAAAAATT
Staphylococcus capitis SK14	STACA0001_1640	-44	5	AATTTTCTTAAAAATT
Staphylococcus epidermidis ATCC 12228	SE1074	-46	5.2	AATTTTCTAAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1038	-340	4.3	AAATTTCTAAAAATC
Staphylococcus haemolyticus JCSC1435	SH1517	-42	4.8	AATTTTTTTAAAAATT
		-33	4.3	AAAATTCAAACAAAT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1356	-350	4.5	ATTTTTCAGTAAATT
		-341	4.3	TAAATTTAAAAAATT
	SAUSA300_1330	-64	4.5	AATATTTTAAATATA
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: tcdB				
Ortholog function: threonine dehydratase				
Staphylococcus aureus subsp. aureus N315	SA1271	-64	4.5	AATATTTTAAATATA
	SAUSA300_1354	-101	4	AAAACTAGAAAAATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: SA1296				
Ortholog function: hypothetical protein				
Staphylococcus aureus subsp. aureus N315	SA1296	-150	4.6	AATATTAAGATAATT
		-141	4.2	ATAATTCTGACATTT
Staphylococcus epidermidis ATCC 12228	SE1152	-138	4	TCTTTTAAATATT
Staphylococcus haemolyticus JCSC1435	SH1449	-124	4.7	AATTATTAATATT
		-115	4.6	AATATTCTAATAAAT
	SAUSA300_1357	-150	4.6	AATATTAAGATAATT
		-141	4.2	ATAATTCTGACATTT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: aroC				
Ortholog function: chorismate synthase				
Staphylococcus aureus subsp. aureus N315	SA1299	-150	4.6	AATATTAAGATAATT
		-141	4.2	ATAATTCTGACATTT
Staphylococcus epidermidis ATCC 12228	SE1155	-138	4	TCTTTTAAATATT
Staphylococcus haemolyticus JCSC1435	SH1446	-124	4.7	AATTATTAATATT
		-115	4.6	AATATTCTAATAAAT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1278	-113	4.6	ATTTTATGAATATT
	SAUSA300_1494	-106	4.8	AATTATCAAAATATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: SA1363				
Ortholog function: Lipote-protein ligase A				
Staphylococcus aureus subsp. aureus N315	SA1363	-106	4.8	AATTATCAAAATATT
Staphylococcus capitis SK14	STACA0001_1770	-109	4.6	ATTTATCAAAATATT
Staphylococcus epidermidis ATCC 12228	SE1217	-108	4.6	ATTTATCAAAATATT
Staphylococcus haemolyticus JCSC1435	SH1383	-100	4.3	ATTTATCAAAATTTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1222	-121	4.6	ATTTATCAAAATATT
	SAUSA300_1495	-66	4.8	AATATTTTGATAATT

	Locus tag	Position	Score	Sequence
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: SA1364				
Ortholog function: putative sulfurtransferase				
Staphylococcus aureus subsp. aureus N315	SA1364	-66	4.8	AATATTTTGATAATT
Staphylococcus capitis SK14	STACA0001_1771	-66	4.6	AATATTTTGATAAAAT
Staphylococcus epidermidis ATCC 12228	SE1218	-66	4.6	AATATTTTGATAAAAT
Staphylococcus haemolyticus JCSC1435	SH1382	-66	4.3	AAAATTTTGATAAAAT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1221	-67	4.6	AATATTTTGATAAAAT
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	SAUSA300_1513	-140	4.1	AAATGTTTAATTATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: sodA				
Ortholog function: superoxide dismutase SodA				
Staphylococcus aureus subsp. aureus N315	SA1382	-140	4.1	AAATGTTTAATTATT
Staphylococcus capitis SK14	STACA0001_1791	-219	4.3	TATTTTCAAAAAACT
		-184	4.2	AATGGTCTGAAAAAT
Staphylococcus epidermidis ATCC 12228	SE1240	-101	4.4	AATAATTTAATAATT
Staphylococcus haemolyticus JCSC1435	SH1363	-248	4.3	AATTATTTAAAAATA
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1203	-182	4.2	AATTTTAAAAATTGT
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	SAUSA300_1669	-54	5.4	AATTTTCAGAAAATT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: SA1544				
Ortholog function: putative phosphoserine transaminase				
Staphylococcus aureus subsp. aureus N315	SA1544	-54	5.4	AATTTTCAGAAAATT
Staphylococcus capitis SK14	STACA0001_0615	-53	5.2	AATATTCAGAATATT
Staphylococcus epidermidis ATCC 12228	SE1400	-54	5	AATATTCAGAATTTT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1329	-55	4.9	TATTTTCAGAATATT
Staphylococcus haemolyticus JCSC1435	SH1201	-55	5	AATTATCAGAATATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1040	-55	4.9	TATTTTCTGAAAATT
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	SAUSA300_1679	-127	4.3	ATTATATAGAAAATT
		-78	4.6	AAAATTTTGAATAAT
		-69	4.1	AATAATTAGAAATGT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: acsA				
Ortholog function: acetyl-CoA synthetase				
Staphylococcus aureus subsp. aureus N315	SA1554	-78	4.6	AAAATTTTGAATAAT
		-69	4.1	AATAATTAGAAATGT
Staphylococcus capitis SK14	STACA0001_0626	-78	4.3	AGATTTTGTGAAAAAT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1338	-96	4.2	AAAAATCAGAATTAT
		-87	4.1	AATTATCATAATTAT
Staphylococcus haemolyticus JCSC1435	SH1189	-87	4.9	AATTATCTAAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1030	-75	4.9	ATTATTTTGTAAAAAT
Macroccoccus caseolyticus JCSC5402	MCCL_1409	-48	4.5	TATATTTTGTAAAAAT
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	SAUSA300_1680	-114	4.1	ACATTTCTAATTATT
		-105	4.6	ATTATTCAAAAATTTT
		-56	4.3	AATTTTCTATATAAT
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: acuA				
Ortholog function: hypothetical protein				
Staphylococcus aureus subsp. aureus N315	SA1555	-114	4.1	ACATTTCTAATTATT
		-105	4.6	ATTATTCAAAAATTTT

	Locus tag	Position	Score	Sequence
Staphylococcus capitis SK14	STACA0001_0627	-56	4.3	AATTTTCTATATAAT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1339	-110	4.3	ATTTTTCAAAAATCT
		-159	4.1	ATAATTATGATAATT
		-150	4.2	ATAATTCTGATTTTT
Staphylococcus haemolyticus JCSC1435	SH1188	-92	4.9	AATTTTCTAGATAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1029	-119	4.9	AATTTTCAAAAATAAT
Macroccoccus caseolyticus JCSC5402	MCCL_1410	-39	4.5	ATTTTTCAAAAATATA

	SAUSA300_1808	-35	4.3	ATAATTATGAATATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [artQ](#)

Ortholog function: Arginine ABC transport system ArtQ

Staphylococcus aureus subsp. aureus N315	SA1675	-167	4.3	ATAATTATGAATATT
Staphylococcus capitis SK14	STACA0001_0720	6	4.2	AAAATTATTAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1432	-83	5.1	AAATTTTCAGAAAATT
		-74	4	AAAATTTTAAAAATTA
Staphylococcus haemolyticus JCSC1435	SH1104	-72	4	CTTTTTTAAAAATTTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0937	-63	4.2	ATTATATTGAATATT
Macroccoccus caseolyticus JCSC5402	MCCL_1584	-87	4.3	AATTATTAGAACATT

	SAUSA300_1918	-318	4.4	AATTAAGTGAATATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [hly](#)

Ortholog function: truncated beta-hemolysin

Staphylococcus aureus subsp. aureus N315	SA1752	-315	4.4	AATTAAGTGAATATT
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	SAUSA300_1989	4	4.2	ATTATTTTGATAATA
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [agrB](#)

Ortholog function: accessory gene regulator B

Staphylococcus aureus subsp. aureus N315	SA1842	-261	4.6	AAAATTCTTAAAATT
Staphylococcus haemolyticus JCSC1435	SH0996	-124	4.1	ATATGTTAAAATATT

	SAUSA300_1996	-38	4.6	AATTGTCAGATTATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [nrgA](#)

Ortholog function: ammonium transporter

Staphylococcus aureus subsp. aureus N315	SA1848	-38	4.6	AATTGTCAGATTATT
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	SAUSA300_2006	-301	4.9	AATTTTCTAGACAATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [ilvD](#)

Ortholog function: dihydroxy-acid dehydratase

Staphylococcus aureus subsp. aureus N315	SA1858	-301	4.9	AATTTTCTAGACAATT
		-53	4.5	ATATTTTCAGAAATTTT
Staphylococcus capitis SK14	STACA0001_0526	-327	4.9	AATTGTTAGAAAATT
Staphylococcus epidermidis ATCC 12228	SE1654	-330	5.2	AATTTTCTAGAAAATT
		-321	4.1	AAAATCTTAAATTTA
Staphylococcus carnosus subsp. carnosus TM300	Sca_1559	-316	4.8	AATTTTAAAAAATTT
		-307	4.3	AAAATCTTAAATTTA
Staphylococcus haemolyticus JCSC1435	SH0980	-321	4.4	AGTTGTTAGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0825	-323	4.2	AATTGACAGAAAAT
		-266	4	ATTTATCAAATTTT

	Locus tag	Position	Score	Sequence
Macrococcus caseolyticus JCSC5402	MCCL_0860	-258	4.7	AATTTTGTAGATATTT
		-249	4.1	ATATTTCAAAACAAAT
		-266	5.2	AATTTTGTAGAAAATT
		-257	4.7	AAAATTTTAAATATT

SAUSA300_2087	-143	4.5	AGTTATTAGAAAATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [hmrA](#)

Ortholog function: N-acyl-L-amino acid amidohydrolase

Staphylococcus aureus subsp. aureus N315	SA1935	-143	4.5	AGTTATTAGAAAATT
Staphylococcus capitis SK14	STACA0001_0837	-235	4.6	AATTGTAAGAAAATT
Staphylococcus epidermidis ATCC 12228	SE1731	-113	4.6	AATTGTAAGAAAATT
		-102	4.2	AATTGTGTAAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1636	-176	4.1	AATTTATTAAATTTT
Staphylococcus haemolyticus JCSC1435	SH0902	-179	4.7	AATTTTCAAAATTAT
		-52	4.5	AATATCCAAAATATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0752	-190	4.1	TATTTTGTATAAATTT
		-181	4.6	AAATTTTCAGAAAATG

SAUSA300_2160	-220	5.2	AATTTTCAAAAAATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [SA2002](#)

Ortholog function: hypothetical regulator

Staphylococcus aureus subsp. aureus N315	SA2002	-220	5.1	AATTTTGTAAAAATT
Staphylococcus haemolyticus JCSC1435	SH0156	-76	4.8	AATTTTGTAAAAATT
		-51	4.2	AAATTTTGTAAATATT

SAUSA300_2265	-263	4.4	AATATTATTAAAAATT
	-183	4.7	ATTTTGTAGAAAAAT

Supported by regulated orthologs from reference regulons

Ortholog gene name: [SA2109](#)

Ortholog function: probable amino-acid or metabolite transporter

Staphylococcus aureus subsp. aureus N315	SA2109	-183	4.7	ATTTTGTAGAAAAAT
Staphylococcus capitis SK14	STACA0001_1171	-181	5.1	AATTTTTCAGAAAAAT
		-101	4.1	AATTGTAAAAATTTT
Staphylococcus epidermidis ATCC 12228	SE1892	-98	4.4	AATTGTAAAAATATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1812	-468	4.4	ATTATACTGAAAAAT
		-414	4.4	AATATTCAAATAATA
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0591	-88	4.4	AATTGTTTAAATTTT
		-79	4.4	AATTTTGTGAATTTA

SAUSA300_2268	-78	4.9	AATTTTTCAGAAAAGT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [yocS](#)

Ortholog function: Uncharacterized sodium-dependent transporter yocS

Staphylococcus aureus subsp. aureus N315	SA2112	-87	4.2	AATAATCTTAATTTT
		-78	4.9	AATTTTTCAGAAAAGT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0585	-90	4.5	AAAAATTAGAAATATT
		-81	5.2	AATATTGTAGAAAATT

SAUSA300_2383	-108	4.3	TATATTTAAAAAAAT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [aapA](#)

	Locus tag	Position	Score	Sequence
Ortholog function: D-serine/D-alanine/glycine transporter				
Staphylococcus aureus subsp. aureus N315	SA2226	-108	4.3	TATATTTAAAAAAAT
Staphylococcus aureus subsp. aureus N315	SA2227	-108	4.3	TATATTTAAAAAAAT
Staphylococcus capitis SK14	STACA0001_1050	-166	4.8	AATTTTTTGATTATT
		-157	4.7	ATTATTCTAAAAAAT
Staphylococcus epidermidis ATCC 12228	SE2004	-93	4.9	ATATTTCTGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1918	-126	4.6	AATTTTCTTATAATT
Staphylococcus haemolyticus JCSC1435	SH0623	-231	5.1	AATTTTCAGAAATTT

SAUSA300_2389	-85	4.7	AATTTTCTGCAAATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [SA2233](#)**Ortholog function:** integral membrane efflux protein

Staphylococcus aureus subsp. aureus N315	SA2233	-85	4.7	AATTTTCTGCAAATT
Staphylococcus capitis SK14	STACA0001_1042	-252	5.2	AATTTTCTAAAAATT
Staphylococcus epidermidis ATCC 12228	SE2010	-246	5.2	AATTTTCTAAAAATT

SAUSA300_2393	-82	4.1	ATTTGTTTAACAATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [opuCA](#)**Ortholog function:** glycine betaine/carnitine/choline ABC transporter opuCA

Staphylococcus aureus subsp. aureus N315	SA2237	-76	4.1	ATTTGTTTAACAATT
Staphylococcus epidermidis ATCC 12228	SE0222	-43	4	TATTTTTTAACAAT
Staphylococcus carnosus subsp. carnosus TM300	Sca_1934	-517	4.7	ATTTGTCTGAATATT

SAUSA300_2416	-271	4.9	AATTTTCAGAAAATA
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [SA2260](#)**Ortholog function:** putative short chain dehydrogenase

Staphylococcus aureus subsp. aureus N315	SA2260	-174	4.9	AATTTTCAGAAAATG
Staphylococcus capitis SK14	STACA0001_1022	-218	5.1	AATTTTCTGAAATTT
Staphylococcus epidermidis ATCC 12228	SE2032	-218	4.6	ATTTTCTGAAATAT
Staphylococcus haemolyticus JCSC1435	SH0590	-209	5.1	AATTTTCAGAAATTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0436	-165	4.9	AATATTCTGAAAATA

SAUSA300_2417	-75	4.9	TATTTTCTGAAAATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [SA2261](#)**Ortholog function:** putative p-aminobenzoyl-glutamate transporter

Staphylococcus aureus subsp. aureus N315	SA2261	-75	4.9	CATTTTCTGAAAATT
Staphylococcus capitis SK14	STACA0001_1021	-78	5.1	AAATTTTCAGAAAATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_2265	-83	4.8	AATTTTCAGAAATAT
Staphylococcus haemolyticus JCSC1435	SH0589	-75	5.1	AAATTTCTGAAAATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0435	-75	4.9	TATTTTTCAGAAATAT

SAUSA300_2497	-205	4.8	ATTAATCTGAAAATT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [mtnE](#)**Ortholog function:** transaminase MtnE involved in methionine biosynthesis via salvage pathway

Staphylococcus aureus subsp. aureus N315	SA2347	-205	4.8	ATTAATCTGAAAATT
Staphylococcus capitis SK14	STACA0001_0934	-212	4.2	AAATGTTTGAAAATA
		-93	4.6	ACTTATCTGAAAATT

	Locus tag	Position	Score	Sequence
Staphylococcus epidermidis ATCC 12228	SE2122	-61	4.4	TTATTTTCAGAAAATT
		-52	4.5	AAAATTCTAACTATT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0010	-257	4.4	AAATGTCAGAAATTTT
Staphylococcus haemolyticus JCSC1435	SH0492	-253	4.5	ATAAATCTGAAAATT
		-244	4.4	AAAATTATAAATATT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0294	-203	4.3	AATATTCTGATAAAA
Macroccoccus caseolyticus JCSC5402	MCCL_0180	-222	4.8	AATATTCTGAATACT

	SAUSA300_2538	-227	4.9	AATTGTTAGAAAATT
		-103	4.8	ATTTTTCAGAAATTTT

Supported by regulated orthologs from reference regulons

Ortholog gene name: [SA2396](#)

Ortholog function: putative amino acid transporter

Staphylococcus aureus subsp. aureus N315	SA2396	-226	4.9	AATTGTTAGAAAATT
		-103	4.8	ATTTTTCAGAAATTTT
		-94	4.2	AATTTTTCAGACAAAA
Staphylococcus capitis SK14	STACA0001_0893	-295	4.3	AATTTGTAAATATT
		-160	4.8	ATTTTTCAGAAATTTT
		-151	4.2	AATTTTTCAGACAAAA
Staphylococcus epidermidis ATCC 12228	SE2147	-165	4.8	ATTTTTCAGAAATTTT
		-156	4.2	AATTTTTCAGACAAAA
Staphylococcus haemolyticus JCSC1435	SH0460	-114	5.1	AATTTTCAGAAATTTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0274	-98	5.3	AATTTTCTGAATATT
		-89	4.3	AATATTAGATATAT

	SAUSA300_2539	-127	4.5	AATTATCAGAAATATA
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [gabT](#)

Ortholog function: 4-aminobutyrate aminotransferase

Staphylococcus aureus subsp. aureus N315	SA2397	-136	4	AAAATCTTAATTAT
		-127	4.5	AATTATCAGAAATATA
Staphylococcus capitis SK14	STACA0001_0892	-175	4.7	AATATTCTAATAATT
		-166	4.3	ATAATTCAGAAAATA
Staphylococcus epidermidis ATCC 12228	SE2148	-164	4.6	AATATTCTAATAATT
		-155	4.6	AATTATCAGAAAATA
Staphylococcus carnosus subsp. carnosus TM300	Sca_0283	-127	4.8	AAATATCTGAAAATT
Staphylococcus haemolyticus JCSC1435	SH0459	-145	4.6	ATTATTCAGAAAATA
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0353	-218	4.6	ATTTTTCAGAAATATA

	SAUSA300_2572	-199	4.3	AAATTTTAAATATA
		-175	4.7	AATTTTTCAGAAATTTT
		-68	4.6	ACTTTTCTGAAAAAT

Supported by regulated orthologs from reference regulons

Ortholog gene name: [aur](#)

Ortholog function: zinc metalloproteinase aureolysin

Staphylococcus aureus subsp. aureus N315	SA2430	-68	4.6	ACTTTTCTGAAAAAT
Staphylococcus capitis SK14	STACA0001_1850	-30	4.2	CTTTTTCAGAAATTTT
		7	4.4	ATTTTTCAGAAATATG
Staphylococcus epidermidis ATCC 12228	SE2219	-69	4.9	ACTTTTTCAGAAATTTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP1542	-104	4.3	ATAATTCAAAATAAT

	SAUSA300_2600	4	4.4	AATTTTTCAGAAATTTT
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Supported by regulated orthologs from reference regulons

Ortholog gene name: [icaA](#)

Ortholog function: intercellular adhesion protein A

Staphylococcus aureus subsp. aureus N315	SA2459	4	4.4	AATTTTTCAGAAATTTT
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	Locus tag	Position	Score	Sequence
Staphylococcus capitis SK14	STACA0001_0088	4	4.4	AATTTTTTAACTTTT
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	SAUSA300_2613	-142	4.6	AATTTTCTGAAAAAG
<hr/>				
<i>Supported by regulated orthologs from reference regulons</i>				
Ortholog gene name: hisZ				
Ortholog function: ATP phosphoribosyltransferase regulatory subunit				
Staphylococcus aureus subsp. aureus N315	SA2472	-142	4.6	AATTTTCTGAAAAAG
Staphylococcus epidermidis ATCC 12228	SE0270	-115	5.1	AATTTTCTGAAAAAT
Staphylococcus carnosus subsp. carnosus TM300	Sca_0637	-125	4.2	ATTTTATTAAATATT
		-116	5	AATATTCAGAAATTTT
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	SSP0431	-109	4.8	CATTTTCAGAAATATT