Supplementary materials

to **"What bacteria want"** by Michael Y. Galperin**,** published in *Environmental Microbiology,*

https://onlinelibrary.wiley.com/doi/abs/10.1111/1462-2920.14398

Table 1. Distribution of environmental sensors in selected bacteria (updated, with hyperlinks)

Organism, strain name	**Genome size, kb**	**HK**	**MCP**	**PTS EIIC**	**cAMP**		**c-di-GMP signaling**				**c-di-AMP signaling**			**ECF sigma**	**Ser/Thr/Tyr~P**	
					ACI, ACIII	**CPD**	**GGDEF**	**GGDEF +EAL**	**EAL**	**HD-GYP**	**DisA _N**	**GbpP**	**PgpH**		**STYK**	**PP2C**
Escherichia coli K-12	4,639	30	5	23	1	1	12	7	10	–	–	–	–	2	5	3
Bacillus subtilis 168	4,216	36	10	16	–	–	3	1	2	–	3	1	1	7	10	7
Mycobacterium tuberculosis H37Rv	4,412	14	–	–	16	1	–	1	1	–	1	1	–	10	13	2
Porphyromonas gingivalis W83	2,343	6	–	–	–	–	–	–	–	–	1	1	1	6	1	1
Neisseria gonorrhoeae FA 1090	2,154	4	–	–	–	–	–	–	–	–	–	–	–	1	1	–
Streptococcus pyogenes M1 GAS	1,852	12	–	14	–	–	–	–	–	–	1	2	–	2	1	1
Haemophilus influenzae Rd KW20	1,830	4	–	1	1	1	–	–	–	–	–	–	–	2	1	–
Helicobacter pylori 26695	1,668	4	4	–	–	–	–	–	–	–	–	–	–	–	1	1
Treponema pallidum str. Nichols	1,138	1	4	–	1	–	1	–	–	3	1	1	1	1	1	3
Rickettsia typhi str. Wilmington	1,111	4	–	–	–	–	1	–	1	–	–	–	–	–	1	–
Chlamydia trachomatis D/UW-3/Cx	1,043	1	–	–	–	1	–	–	–	–	1	–	–	–	3	3
Mycoplasma pneumoniae M129	816	–	–	4	–	–	–	–	–	–	1	2	–	1	1	1

Please address corrections and comments to galperin@ncbi.nlm.nih.gov

Table S1. Sensor proteins of *Escherichia coli* K-12

No.	Gene	UniProt entry		Sensed ligand, parameter, or the sensor domain	Regulated genes, processes	PubMed reference[a]
Histidine kinases						
1	*arcB*	P0AEC3	ARCB_ECOLI	Redox status of the respiratory chain	Anerobic respiration	27656164 29945971
2	*atoS*	Q06067	ATOS_ECOLI	Acetoacetate, spermidine	*atoDAEB*, fatty acid degradation, polyhydroxy-butyrate biosynthesis	19198978 22083893
3	*baeS*	P30847	BAES_ECOLI	Envelope stress, iron, tungstate	*spy, mdtABCD; acrD*	21515766
4	*barA*	P0AEC5	BARA_ECOLI	Redox stress, O_2, H_2O_2	*csrA*/*csrB*; carbon storage, metabolism	14619967
5	*basS*	P30844	BASS_ECOLI	Fe, Zn	*csgD, elbA, csrB*, *inaA*; LPS, membrane tranporters	22442305
6	*btsS (yehU)*	P0AD14	BTSS_ECOLI	Pyruvate, serine	*yjiY*; nutrient assimilation	28469239
7	*cheA*	P07363	CHEA_ECOLI	Activated MCPs	Chemotaxis	22494339 24163342
8	*cpxA*	P0AE82	CPXA_ECOLI	Envelope stress	*cpxP*, *degP*, *dsbA*, *ppiA*, adhesion to surfaces	12670966 23335416
9	*creC (phoM)*	P08401	CREC_ECOLI	Phosphate (and Ca^{2+}, Mg^{2+})	*ackA, pta, malE, talA;* carbon metabolism	11350954 26497466
10	*cusS*	P77485	CUSS_ECOLI	High levels of Cu^+, Ag^+	Export of Cu^+, Ag^+	27583660
11	*dcuS*	P0AEC8	DCUS_ECOLI	Fumarate, other C4-dicarboxylates	*frdABCD*; *nuoAN*; *dcuBC*; *sdhCDAB*	25135747 29203472
12	*dpiB (citA)*	P77510	DPIB_ECOLI	Citrate	Citrate, SOS response	11889485
13	*envZ*	P0AEJ4	ENVZ_ECOLI	Osmotic shock	*ompF*, *ompC*; osmoregulation	22543870 24681325
14	*evgS*	P30855	EVGS_ECOLI	Acid pH, Na^+, K^+	Acid resistance, multidrug efflux pumps	24957621 28674068
15	*glnL* (*ntrB*)	P0AFB5	NTRB_ECOLI	Nitrogen limitation	*glnA, glnB*	7961767
16	*glrK (yfhK)*	P52101	GLRK_ECOLI	Epinephrine, sulfate?	*glmY* sRNA	19843219
17	*hprS* (*yedV*)	P76339	HPRS_ECOLI	H_2O_2, DNA damage	*cyoA, hiuH, cusC*	25568260 27983483
18	*kdpD*	P21865	KDPD_ECOLI	K^+ gradient	*kdpABC;* K^+ uptake	23651428 26350129
19	*narQ*	P27896	NARQ_ECOLI	Nitrate, nitrite	*narDHIJ*; *fdnGHI*; *frdABCD*; nitrate, formate, fumarate reductases	18375557 19968795
20	*narX*	P0AFA2	NARX_ECOLI	Nitrite, nitrate		
21	*phoQ*	P23837	PHOQ_ECOLI	Low Mg^{2+} levels	*hemL*, *mgrB*, *mgtA*, *nagA*, *rstAB*, *slyB*, *vboR*; Mg^{2+} uptake	12218035 19889087 29183977
22	*phoR*	P08400	PHOR_ECOLI	Phosphate limitation (and/or Ca^{2+}, Mg^{2+})	Phosphate regulon	12533489 24563032

[a] – Here and below, the references are not exhaustive and are provided only as pointers to the functions of the respective proteins. Many additional references can be found on the UniProt web site

23	*qseC*	P40719	QSEC_ECOLI	Quorum sensing	*flhDC*; flagella	16803956 21542868
24 25	*rcsC*, *rcsD*	P0DMC5 P39838	RCSC_ECOLI RCSD_ECOLI	Envelope stress (via RcsF)	Capsule biosynthesis, biofilm formation, cell division	13129944 14651646 28691662
26	*rstB*	P18392	RSTB_ECOLI	General stress?	No data	25461694 30011323
27	*torS*	P39453	TORS_ECOLI	Trimethylamine oxide	Anaerobic respiration	25825431
28	*uhpB*	P09835	UHPB_ECOLI	Glucose-6-phosphate bound to UhpC	Hexose phosphate transport	8349544 12107138
29	*ypdA*	P0AA93	YPDA_ECOLI	Pyruvate	*yhjX*	23222720 29038258
30	*zraS*	P14377	ZRAS_ECOLI	High Zn^{2+}, Pb^{2+}	Export of Zn^{2+}, Pb^{2+}	26438879
Chemotaxis sensors (MCPs)						
1	*aer*	P50466	AER_ECOLI	Redox state of respiratory chain	Aerotaxis	17824925 27803157
2	*tsr*	P02942	MCP1_ECOLI	Serine	Chemotaxis	24205875
3	*tar*	P07017	MCP2_ECOLI	Asp, maltose	Chemotaxis	27292793
4	*trg*	P05704	MCP3_ECOLI	Ribose, galactose	Chemotaxis	11133962
5	*tap*	P07018	MCP4_ECOLI	Dipeptides, pyrimidine	Chemotaxis	18065551
Sugar PTS membrane components EIIC						
1	*ascF*	P24241	PTIBC_ECOLI	Arbutin, cellobiose	Sugar uptake, chemotaxis	1630307
2,3	*agaC*, *agaW*	P42910, P42905	PTPC1_ECOLI, PTPC2_ECOLI	N-acetyl-galactosamine	Sugar uptake, chemotaxis	10931310
4	*bglF*	P08722	PTV3B_ECOLI	β-Glucosides	Sugar uptake, chemotaxis	12923168
5	*chbC*	P17334	PTQC_ECOLI	Diacetylchitobiose	Sugar uptake, chemotaxis	24593230
6	*cmtA*	P69826	PTMCB_ECOLI	Mannitol	Sugar uptake, chemotaxis	8353127
7	*fruA*	P20966	PTFBC_ECOLI	Fructose	Sugar uptake, chemotaxis	11361065
8	*frvB*	P32154	PTFLB_ECOLI	Fructose	Sugar uptake, chemotaxis	11361065
9	*frwC*	P32672	PTFC2_ECOLI	Fructose	Sugar uptake, chemotaxis	11361065
10	*fryG*	P77579	PTFC1_ECOLI	Fructose?	Sugar uptake, chemotaxis	
11	*gatC*	P69831	PTKC_ECOLI	Galactitol	Sugar uptake, chemotaxis	8955298
12	*glvC*	P31452	PTXC_ECOLI	α-Glucosides?	Sugar uptake, chemotaxis	
13	*malX*	P19642	PTOCB_ECOLI	Maltose	Sugar uptake, chemotaxis	1856179
14	*manY*	P69801	PTNC_ECOLI	Mannose	Sugar uptake, chemotaxis	2951378
15	*mngA*	P54745	MNGA_ECOLI	Mannosylglycerate	Sugar uptake, chemotaxis	14645248
16	*mtlA*	P00550	PTM3C_ECOLI	Mannitol	Sugar uptake, chemotaxis	2407724
17	*murP (yfeV)*	P77272	PTYBC_ECOLI	N-acetylmuramic acid	Sugar uptake, chemotaxis	15060041
18	*nagE*	P09323	PTW3C_ECOLI	N-acetylglucosamine	Sugar uptake, chemotaxis	19617367
19	*ptsG*	P69786	PTGCB_ECOLI	Glucose	Sugar uptake, chemotaxis	21996078
20	*sgcC*	P39365	SGCC_ECOLI	Galactitol?	Sugar uptake, chemotaxis	
21	*srlA*	P56579	PTHC_ECOLI	Sorbitol, glucitol	Sugar uptake, chemotaxis	1100608
22	*treB*	P36672	PTTBC_ECOLI	Trehalose	Sugar uptake, chemotaxis	24586369
23	*ulaA*	P39301	ULAA_ECOLI	Ascorbate	Sugar uptake, chemotaxis	12644495
Adenylate cyclase						
1	*cyaA*	P00936	CYAA_ECOLI	PTS $EIIA^{Glc}$	Transcription of cAMP-CRP-dependent operons	11988530

cAMP phosphodiesterase						
1	*cpdA*	P0AEW4	CPDA_ECOLI	Uncharacterized C-terminal domain	cAMP levels	8810311
Diguanylate cyclases (GGDEF domains)						
1	*dgcC* (*adrA*)	P0AAP1	DGCC_ECOLI	Unknown, MASE2 sensor domain	Cellulose biosynthesis	11260463
2	*dgcE* (*yegE*)	P38097	DGCE_ECOLI	Aspartate? MASE1 sensor domain	Curli fimbriae	19332833 23740576
3	*dgcF* (*yneF*)	P76147	DGCF_ECOLI	Aspartate? MASE1 sensor domain	Motility, biofilm formation	21181144 23740576
4	*dgcI* (*yliF*)	P75801	DGCI_ECOLI	Unknown, GAPES2 sensor domain	No data, low expression	19332833 26148715
5	*dgcJ* (*yeaJ*)	P76237	DGCJ_ECOLI	Unknown, GAPES1 sensor domain	Motility	18765794 26148715
6	*dgcM* (*ydaM*)	P77302	DGCM_ECOLI	Unknown, two PAS sensor domains	Curli fimbriae, biofilm formation	17010156 19332833
7	*dgcN* (*yfiN*)	P46139	DGCN_ECOLI	Unknown, CHASE8 sensor domain	Motility, biofilm formation	21181144 26148715
8	*dgcO* (*yddV*)	P0AA89	DOSC_ECOLI	Oxygen, CO, NO	Exopolysaccharide, biofilm	20576684
9	*dgcP* (*yeaP*)	P76245	DGCP_ECOLI	cAMP? GAF sensor domain	Curli finbiae	19332833
10	*dgcQ* (*yedQ*)	P76330	DGCQ_ECOLI	Unknown, CHASE7 sensor domain	Motility, biofilm formation	21181144 26148715
11	*dgcT* (*ycdT*)	P75908	DGCT_ECOLI	Unknown, MASE4 sensor domain	Motility	18713317 26148715
12	*dgcZ* (*ydeH*)	P31129	DGCZ_ECOLI	Zn^{2+}, surface sensing	Motility, surface adhesion, biofilm formation	23769666 27402625
c-di-GMP phosphodiesterases (EAL domains)						
1	*pdeA* (*yfeA*)	P23842	PDEA_ECOLI	Aspartate? MASE1 sensor domain	Biofilm formation	23047748 23740576
2	*pdeB* (*ylaB*)	P77473	PDEB_ECOLI	Redox status in the periplasm, CSS domain	Poly-GlcNAc production	26553851 29018125 29514851
3	*pdeC* (*yjcC*)	P32701	PDEC_ECOLI	Redox status in the periplasm, CSS domain	Poly-GlcNAc production	26553851 29514851
4	*pdeD* (*yoaD*)	P76261	PDED_ECOLI	Redox status in the periplasm, CSS domain	Biofilm formation	23047748 29514851
5	*pdeF* (*yfgF*)	P77172	PDEF_ECOLI	Aspartate? MASE1 sensor domain	Biofilm formation (low-level expression)	23047748 23740576
6	*pdeG* (*ycgG*)	P75995	PDEG_ECOLI	Redox status in the periplasm, CSS domain	Biofilm formation (low-level expression)	20385176 29514851
7	*pdeH* (*yhjH*)	P37646	PDEH_ECOLI	No sensor domain	Flagellar motility, curli (major c-di-GMP hydrolase)	19332833
8	*pdeI* (*yliE*)	P75800	PDEI_ECOLI	t°; CHASE9 sensor domain	Biofilm formation	26148715 26553851

9	*pdeK* (*yhjK*)	P37649	PDEK_ECOLI	Unknown, GAPES3 sensor domain	Cellulose biosynthesis, biofilm formation	23047748 26148715
10	*pdeL* (*yahA*)	P21514	PDEL_ECOLI	DNA? Contains DNA-binding LuxR HTH domain	Transcriptional regulator, biofilm formation	17827157 24451384 26553851
11	*pdeN* (*rtn*)	P76446	PDEN_ECOLI	Redox status in the periplasm, CSS domain	Biofilm formation	23047748 26553851 29514851
12	*pdeO* (*dosP*)	P76129	DOSP_ECOLI	Oxygen, CO, NO	RNA turnover	21320509 25586128
13	*pdeR* (*yciR*)	P77334	PDER_ECOLI	Unknown, PAS sensor domain	CsgD, MlrA; Curli fimbriae, biofilm formation	19332833 23708798
Enzymatically inactive GGDEF and EAL domains						
1	*bluF* (*ycgF*)	P75990	BLUF_ECOLI	Blue light, BLUF sensor domain	*rcs* genes; no phosphodiesterase activity	16107542 22783906
2	*cdgI* (*yeaI*)	P76236	CDGI_ECOLI	Unknown, MASE4 sensor domain	Motility, biofilm formation (low expression)	21181144 26148715
3	*csrD* (*yhdA*)	P13518	CSRD_ECOLI	Unknown, GAPES4 sensor domain	Carbon storage and metabolism	16980588 27235416
4	*rflP* (*ydiV*)	P76204	YDIV_ECOLI	No sensor domain	Flagellar biosynthesis, P fimbriae	23002140 28652301
Extracytoplasmic function (ECF) sigma factors						
1	*rpoE*	P0AGB6	RPOE_ECOLI	Heat shock, envelope stress	*dsbC*, *fkpA*, *skp*, surA *htrA*, *cutC*, *nlpB*, *purA*, *mdoG*, *mdoH*, *yggN*, *ytfJ*	18983936 28924029 29941590
2	*fecI*	P23484	FECI_ECOLI	Ferric citrate via FecA, FecR	*fecABCDE*	12618442 12732308
Ser/Thr/Tyr protein kinases						
1	*ubiB*	P0A6A0	UBIB_ECOLI	No sensor domain	Ubiquinone biosynthesis enzymes UbiG, UbiE	10960098 25498144
2	*hipA*	P23874	HIPA_ECOLI	PF13657 domain (uncharacterized)	GltX; amino acid starvation, stringent response	17041039 25848049
3	*rdoA (yihE)*	P0C0K3	SRKA_ECOLI	ROS, no sensor domain	Programmed cell death	17302814 23416055
4	*yeaG*	P0ACY3	YEAG_ECOLI	N-terminal AAA domain; nitrogen starvation	Methionine biosynthesis	29957170 26621053
5	*yegI*	P76393	YEGI_ECOLI	Unknown, contains DNA-binding HTH domain	Persistence?	25911659 29967116
Ser/Thr/Tyr protein phosphatases						
1	*prpA*	P55798	PRP1_ECOLI	Misfolded proteins	*htrA*; heat shock response	9130712
2	*prpB*	P55799	PRP2_ECOLI	Misfolded proteins	*htrA*; heat shock response	9130712
3	*yegK*	P76395	YEGK_ECOLI	Unknown short C-terminal domain	No data	29967116

Table S2. Sensor proteins of *Bacillus subtilis* strain 168[a]

No.	Gene	UniProt entry		Sensed signal and/or the sensor domain	Regulated genes, processes	PubMed reference[b]
Histidine kinases						
1	*bceS*	O35044	BCES_BACSU	Bacitracin, nisin	Bacitracin resistance	25118291 27997719
2	*cheA*	P29072	CHEA_BACSU	Activated MCPs	Chemotaxis	21515776
3	*citS*	O34427	CITS_BACSU	Citrate	*citM*; citrate utilization	10972810
4	*comP*	Q99027	COMP_BACSU	Quorum sensing	Competence	16091051
5	*cssS*	O32193	CSSS_BACSU	Misfolded proteins	*htrA, htrB*; protein secretion	22307758
6	*dctS*	P96601	DCTS_BACSU	C4-dicarboxylates	*dctA*, *dctB*; transport of dicarboxylic acids	24375102
7	*degS*	P13799	DEGS_BACSU	Mechanosensing through flagellar rotation	Competence, flagella formation; proteases	23888912 24317403
8	*desK*	O34757	DESK_BACSU	t^{o}, membrane fluidity	Δ5 acyl-lipid desaturase	27528507
9	*glnK*	P40758	GLNK_BACSU	Glutamine	*glsA-glnT* operon, nitrogen metabolism	17001076 25691471
10	*kinA*	P16497	KINA_BACSU	Starvation? 3 N-terminal PAS sensor domains	*spo0A*, *spo0F*; sporulation	19561131 23504013
11	*kinB*	Q08430	KINB_BACSU	Starvation? ATP, GTP levels	*spo0A*, *spo0F*; sporulation	29314743
12	*kinC*	P39764	KINC_BACSU	Membrane potential, flotilin; PAS sensor domain	*spo0A*; sporulation, biofilm formation	20971918 26297017
13	*kinD*	O31671	KIND_BACSU	Glycerol, Mg^{2+}; dCache_1 sensor domain	*spo0F*, *spo0A*; sporulation, biofilm formation	23436677 23564171
14	*kinE*	O31661	KINE_BACSU	Unknown; 4 PAS sensor domains	*spo0A*, *spo0F*; sporulation, biofilm formation	11069677
15	*liaS*	O32198	LIAS_BACSU	Cell wall stress, bacitracin	*lialH* operon	24666271
16	*lytS*	P94513	LYTS_BACSU	Pyruvate? 5TM-5TMR_LYT and GAF sensor domains	*ysbA*; cell wall metabolism, pyruvate consumption	27422364
17	*malK*	O05250	MALK_BACSU	Malate; sCache sensor domain	*maeA*, *maeN*, *yflS*	12949160
18	*natK*	P70954	NATK_BACSU	Unknown	*natAB*; sodium export	17322186
19	*phoR*	P23545	PHOR_BACSU	Phosphate limitation; sCache sensor domain	Switch from cell wall teichoic acid to teichuronic acid	25315493 29644746
20	*resE*	P35164	RESE_BACSU	Anaerobiosis? PAS sensor domain	Aerobic and anaerobic respiration	17189364 22287527
21	*walK*	Q45614	WALK_BACSU	Unknown; dCache_3 sensor domain	*ftsAZ*, *yocH*, *ykvT*, *cwlO*, *lytE*, *ydjM*, *yjeA*, *tagAB*, *tagDEF*	19019149 29465029
22	*ybdK*	O31433	YBDK_BACSU	Unknown, 2TM domain	No data	20035725
23	*ycbM*	P42245	YCBM_BACSU	Unknown	No data	
24	*yclK*	P94414	YCLK_BACSU	Unknown	*yclIH, yfjR, ykcBC, yngABC, yycA*	20512483
25	*ydfH*	P96685	YDFH_BACSU	Unknown; 6TM domain	*ydfJ*	15941986

[a] – For more details and additional proteins, please see SubtiWiki, http://www.subtiwiki.uni-goettingen.de/.

[b] – Here and below, the references are not exhaustive and are provided only as pointers to the functions of the respective proteins. Additional references can be found at the UniProt and SubtiWiki web sites

26	*yesM*	O31516	YESM_BACSU	Unknown, dCache_1 domain	No data	
27	*lnrJ* (*yfiJ*)	P94438	LNRJ_BACSU	Linearmycin?	*lnrLMN*; Biofilm morphology	28461449
28	*yhcY*	O07527	YHCY_BACSU	Unknown, GAF domain	No data	29785949
29	*ykoH*	O34638	YKOH_BACSU	Unknown	No data	
30	*yrkQ*	P54444	YRKQ_BACSU	Unknown	*ykcBC, yrkON*, *yrkPQR*	18175906
31	*psdS* (*yvcQ*)	O06979	YVCQ_BACSU	Nisin, gallidermin, 2TM domain	*psdAB*	21078927 27997719
32	*yvfT*	Q795K2	YVFT_BACSU	Unknown, 5TM domain	No data	
33	*yvrG*	O34989	YVRG_BACSU	Unknown	*dltABCDE, lytABC, sigO-rsoA, sigX-rsiX, wprA, wapAI, sunAT-bdbA-yolJ-bdbB,* and others	16306698
34	*ywpD*	P94586	YWPD_BACSU	Unknown, truncated?	No data	
35	*yxdK*	P42422	YXDK_BACSU	Cationic antimicrobial peptide LL-37, 2TM domain	*yxdLM-yxeA*; ABC-type transporter	15289557 15870467
36	*yxjM*	P55183	YXJM_BACSU	Unknown, 6TM domain	No data	
Chemotaxis sensors (MCPs)						
1	*hemAT*	O07621	HEMAT_BACSU	Oxygen	Aerotaxis	12962628
2	*mcpA*	P39214	MCPA_BACSU	Glucose, αMeGlc; dCache_1 sensor domain	Chemotaxis	8188684
3	*mcpB*	P39215	MCPB_BACSU	Asp/Asn, Glu, His; dCache_1 sensor domain	Chemotaxis	19864420
4	*mcpC*	P54576	MCPC_BACSU	PTS sugars, amino acids, dCache_1 sensor domain	Chemotaxis	23038252
5	*tlpA*	P39216	TLPA_BACSU	Unknown; dCache_1 sensor domain	Chemotaxis?	
6	*tlpB*	P39217	TLPB_BACSU	Unknown; dCache_1 sensor domain	Chemotaxis?	
7	*tlpC*	P39209	TLPC_BACSU	*Arabidopsis* root exudates, sCache_3 sensor domain	Chemotaxis	27899502
8	*yfmS*	O06477	YFMS_BACSU	Unknown, CHASE3 sensor domain	Chemotaxis?	
9	*yoaH*	O34576	YOAH_BACSU	Unknown, CHASE3 sensor domain	Chemotaxis?	
10	*yvaQ*	O32239	YVAQ_BACSU	Unknown, 4HB_MCP_1 sensor domain	Chemotaxis?	
Sugar PTS membrane component EIIC						30038046
1	*bglP*	P40739	PTV3B_BACSU	β-Glucosides	LicT; β-glucoside metabolism	12169607 23475962
2	*fruA*	P71012	PTF3A_BACSU	Fructose	Chemotaxis, sugar utilization	20487301
3	*gamP*	P39816	PTW3C_BACSU	Glucosamine	Chemotaxis, sugar utilization	23667565
4	*gmuC*	O05507	PTEC_BACSU	Cellobiose, mannobiose	Chemotaxis, sugar utilization	18177310
5	*levF*	P26381	PTFC_BACSU	Fructose	Chemotaxis, sugar utilization	9033408
6	*licC* (*celB*)	P46317	PTJC_BACSU	Cellobiose , lichenan	LicR; metabolism of oligo-β-glucosides	8990303 10438772
7	*malP*	P54715	PTOCB_BACSU	Maltose	Chemotaxis, sugar utilization	16707683
8	*manP*	O31645	PTN3B_BACSU	Mannose	ManR, mannose utilization	23551403
9	*mtlA*	P42956	PTMCB_BACSU	Mannitol	MtlR; mannitol utilization	23279188
10	*murP* (*ybbF*)	Q797S1	PTXBC_BACSU	*N*-acetylmuramic acid	Chemotaxis, sugar utilization	20400549 23504016

11	*nagP*	O34521	PTWCB_BACSU	N-acetylglucosamine	Chemotaxis, sugar utilization	23667565
12	*ptsG*	P20166	PTG3C_BACSU	Glucose	GlcT; sugar utilization	11902727 22722928
13	*sacP*	P05306	PTSBC_BACSU	Sucrose	SacT; sugar utilization	1577686 21278164
14	*sacX*	P15400	SACX_BACSU	Sucrose	SacY; sugar utilization	9202047
15	*treP*	P39794	PTTBC_BACSU	Trehalose	Chemotaxis, sugar utilization	18977770
16	*ywbA*	P39584	YWBA_BACSU	Unknown	No data	
c-di-GMP synthases (GGDEF domains)						
1	*dgcK* (*yhcK*)	P54595	YHCK_BACSU	Unknown, 5TM-5TMR_LYT sensor domain	Swarming motility	23893111 27897378 28536559
2	*dgcP* (*ytrP*)	O34325	YTRP_BACSU	Unknown, two GAF domains	Swarming motility	23893111 27897378 28536559
3	*ydaK*	P96585	YDAK_BACSU	Binds c-di-GMP but does not synthesize it	*ydaKLMN;* extracellular matrix	27897378 28536559
c-di-GMP related enzymes (both GGDEF and EAL domains)						
1	*dgcW* (*ykoW*)	O34311	YKOW_BACSU	Nitric oxide? Contains MHYT sensor domain	Biofilm formation, dispersal	11728710 23893111
c-di-GMP phosphodiesterase (EAL domain)						
1	*ykuI*	O35014	YKUI_BACSU	Binds c-di-GMP but does not hydrolyze it	No data	19244251
2	*pdeH* (*yuxH*)	P14203	YUXH_BACSU	Contains C-terminal HDOD domain (uncharacterized)	Swarming motility, biofilm formation	23893111 22821967
c-di-AMP synthases						
1	*disA*	P37573	DISA_BACSU	DNA damage	Sporulation, DNA repair	18439896 21566650
2	*cdaA* (*ybbP*)	Q45589	CDAA_BACSU	Regulated by CdaR (YbbR), contains N-terminal 3TM domain	Potassium homeostasis	23192352 26240071 28420751
3	*cdaS* (*yojjJ*)	O31854	CDAS_BACSU	Unknown; contains autoin-hibitory N-terminal domain	Germination	24939848
c-di-AMP phosphodiesterases						
1	*gdpP*	P37484	GDPP_BACSU	Oxygen, CO, NO; PAS-like domain	Potassium homeostasis, cell growth	26240071
2	*pgpH*	P46344	PGPH_BACSU	Unknown; contains 7TM-HDED extracellular sensor domain and 7TM-7TMR_HD integral membrane domain	Potassium homeostasis, cell growth	26240071
Ser/Thr/Tyr protein kinases						
1	*prkA*	P39134	PRKA_BACSU	Unknown	Control of SigK, sporulation	25983726
2	*prkC* (*yloP*)	O34507	PRKC_BACSU	Muropeptides; contains 3 PASTA sensor domains	AbrB, CpgA, EF-Tu, GlmR, GngF (YvcK), GpsB, YezB, PtkA, WalR, SpoIIAB; sporulation, biofilm formation	12399479 19246764 25278935 25012659
3	*prkD* (*ybdM*)	O31435	YBDM_BACSU	Unknown, no sensor domain	AbrB, DegS, HprK, RsbT, RsbW, SpoIIAB	21304896 25278935

4	*yabT*	P37562	PKN1_BACSU	DNA; forespore-specific	AbrB, YabA, DegS, SpoIIAB, EF-Tu; sporulation	23634894 25278935 29619013
5	*hprK*	O34483	HPRK_BACSU	Unknown; combines kinase and phosphorylase domain	Hpr, Crh, PrkD; carbohydrate metabolism	12359880 12779331 22001508
6	*ptkA* (*ywqD*)	P96716	YWQD_BACSU	Interaction with EpsA, TkmA (YwqC), SalA	Ugd/YwqF, DnaK, TuaD, SsbA, SsbB, Eno, Ldh, InfA, OppA, YabT	12970183 20497499 27725816
7	*epsB* (*ptkB*)	P71051	YVEL_BACSU	Interaction with TkmA (YwqC), TkmB	Exopolysaccharide production	24493247 25085422 25667587
8	*rsbT*	P42411	RSBT_BACSU	Environmental stress	RsbR, RsbRB, RsbRC, RsbRD, RsbS; control of SigB	9786195 21362065
9	*rsbW*	P17904	RSBU_BACSU	Energy stress, ATP/ADP ratio?	RsbV; control of SigB	8144446 12270815
10	*spoIIAB*	P10728	SP2AB_BACSU	ATP/ADP ratio?	SpoIIAA; control of SigF	8358793
11	*yrzF*	O32057	YRZF_BACSU	Unknown	No data	
–	*mcsB*	P37570	MCSB_BACSU	Arg kinase, no Ser/Thr/Tyr kinase activity	Stress response	27749819 25610436
Ser/Thr/Tyr protein phosphatases						
1	*prpC*	O34779	PRPC_BACSU	No sensor domain	PrkC, CpgA, EF-Tu, YezB; sporulation, biofilm formation	12399479 19246764
2	*ptpZ* (*ywqE*)	P96717	YWQE_BACSU	Unknown	PtkA, Ugd/YwqF, SsbA, SsbB	15866923 16549871
3	*rsbP*	O07014	RSBP_BACSU	Energy stress, red light; PAS sensor domain	RsbV, SigB	10632888 19948797
4	*rsbU*	P40399	RSBU_BACSU	Environmental stress; KaiA/RsbU (PF08673) domain	RsbV, SigB	10632888 17303566
5	*rsbX*	P17906	RSBX_BACSU	Environmental stress	RsbR, RsbS	15466036
6	*spoIIE*	P37475	SP2E_BACSU	10-TM N-terminal domain	SpoIIAA; sporulation	8830262 22115775
7	*yfkJ*	O35016	YFKJ_BACSU	Unknown	Stress response?	15995210
–	*ywlE*	P39155	PAP_BACSU	pArg phosphatase, no pTyr phosphatase activity	–	15995210 23770242
–	*prpE* (*yjbP*)	O31614	PRPE_BACSU	Ap4A hydrolase, can dephosphorylate pTyr	Spore germination?	12059787 23824080
Extracytoplasmic function (ECF) sigma factors						
1	*sigM*	O07582	SIGM_BACSU	Cell wall-targeting antibiotics, ethanol, heat and acid stress, superoxide	*bcrC, yacK, ydaH, yfnI, yjbD, ypbG, ypuA, yraA, ysxA*; integrity of the membrane and cell wall	17675383 22211522
2	*sigV*	O05404	SIGV_BACSU	Envelope stress, no sensor domain	*asnB, bcrC, divIC, dltA, pbpX, ycgQ, ydjF, ypuA, ywaC*, lysozyme resistance	21926231 23687273
3	*sigW*	Q45585	SIGW_BACSU	Envelope and membrane stress, no sensor domain	*rsiW, spo0M, yeaA, ysdB, yjoB, ydjP*, etc; bacteriocin production	16899079 23155385
4	*sigX*	P35165	SIGX_BACSU	Heat shock, cationic antimicrobial peptides	Abh; septum and wall synthesis; biofilm formation	17675383
5	*sigY*	P94370	SIGY_BACSU	Nitrogen starvation	*ybgB, yxlCDEFG*; maintenance of the Spβ prophage	12897008 22400495
6	*sigZ*	O05409	SIGZ_BACSU	Unknown	No data	
7	*ylaC*	O07627	YLAC_BACSU	Redox changes, Mn^{2+} levels	*clpP, sigH*; oxidative stress	29760236

Table S3. Environmental sensor proteins of some common bacterial pathogens

No	Locus tag (gene)	UniProt entry	Sensor type	Sensed ligand, sensor domain	Regulated genes, processes	PubMed reference
***Chlamydia trachomatis* D/UW-3/Cx**						
1	CT_467 (*ctcB*)	O84473	HK	Unknown, PAS sensor domain	Cell development	12600998
1	CT_754 (*cpdA*)	O84759	CPD	Metallophophoesterase, no sensor domain	No data	3023286
1	CT_145 (*pkn1*)	O84147	STYK	Unknown, C-type lectin (FGE-sulfatase) sensor domain	Phosphorylates inclusion membrane protein IncG	14500499
2	CT_301 (*pknD*)	O84303	STYK	Unknown, contains a TPR-like helical domain	Phosphorylates the FHA domain in the T3SS protein CdsD (CT_664)	14500499 17766419
3	CT_673 (*pkn5*)	O84680	STYK	Unknown, may be inactive	No data	
1	CT_259 (*cppA*)	O84592	PP2C	No sensor domain	Unknown, protein phosphatase activity shown *in vitro* and *in vivo*	27114464 30038048
2	CT_588 (*rsbU*)	O84592	PPM	Unknown, uncharacterized Chlamydia-specific domain	Regulation of sigma subunit	16390455 26313645
3	CT_589	O84593	PPM	Unknown, uncharacterized Chlamydia-specific domain	Competence, synthesis of proteases, flagella	
***Haemophilus influenzae* Rd KW20**						
1	HI0220 (*arcB)*	Q9L746	HK	Redox status of the respiratory chain	Anerobic respiration	11717280
2	HI0267 (*narQ)*	P44604	HK	Nitrate/nitrite	*narDHIJ*; *fdnGHI*; *frdABCD*; nitrate, formate, fumarate reductases	16199562
3	HI1378 (*phoR)*	P71380	HK	Phosphate limitation (and/or Ca^{2+}, Mg^{2+})	Phosphate regulon	8892843
4	HI1707 (*basS)*	P45336	HK	Quorum sensing	*flhDC*; flagella	8892843
1	HI0446 (*fruA*)	P44714	EIIC	Fructose	Competence, fermentation of ribose and galactose	8885265 8763608 12949188
1	HI0604 (*cyaA)*	P40134	ACI	PTS component EIIA^{Glc}	Various cAMP-CRP-dependent operons	8226661; 8892843
1	HI0399 (*cpdA*)	P44685	CPD	Uncharacterized C-terminal domain	cAMP levels, competence	9721275
1	HI0628 (*rpoE)*	P44790	ECF	Heat shock, envelope stress	No data	11796603
2	HI1459	P45215	ECF	No sensor domain	Virulence, host survival	12473436
1	HI1326	P44162	STYK	Unknown	No data	

No	Locus tag (gene)	UniProt entry	Sensor type	Sensed ligand, sensor domain	Regulated genes, processes	PubMed reference
***Helicobacter pylori* 26695**						
1	HP_0164 (*arsS*)	O24971	HK	pH? No sensor domain	Acid resistance	17609149 22865848
2	HP_0244 (*flgS*)	O25026	HK	Unknown sensor domain	Flagellar motility	25802298
3	HP_0392 (*cheA*)	O25153	HK	CheA, interacts with MCPs	Chemotaxis	10722597 15664919 28242706
4	HP_1364 (*crdS*)	O25917	HK	Unknown sensor domain	Cu^{2+} resistance	15968080
1	HP_0082 (*tlpC*)	O24911	MCP	Lactate, other acids	Chemotaxis	12228322 29075010
2	HP_0099 (*tlpA*)	O24925	MCP	Arginine, bicarbonate	Chemotaxis, virulence	12892880 12228322
3	HP_0103 (*tlpB*)	O24929	MCP	Urea, acidic pH, quorum-sensing autoinducer-2; sCache_2 sensor domain	pH taxis, colonization	16547053 22705207 21602215 26269952
4	HP_0599 (*tlpD*)	O25321	MCP	Zn^{2+}, acid, reactive oxygen species; SZB sensor domain	Chemotaxis, stomach infection	22802346 23139399 18245281 27002127
1	HP_0432	O25182	STYK	No sensor domain	No data	10427715 21360674
1	HP_0431	O25181	PP2C	No sensor domain	No data	
***Mycobacterium tuberculosis* H37Rv**						
1	Rv0490 (*senX3*)	P9WGK5	HK	Low phosphate; unknown sensor domain	Virulence	25344463
2	Rv0601c+ Rv0600c	O07777 O07778	HK	Unknown sensor domain	No data	17434492
3	Rv0758 (*phoR*)	P71815	HK	Unknown sensor domain	Virulence?	28782049 18757548
4	Rv0845 (*narS*)	O53857	HK	Nitrite? Unknown sensor domain	Nitrate metabolism	12595424 25659431
5	Rv0902c (*prrB*)	P9WGK7	HK	Unknown sensor domain	Early intracellular multiplication	11953357
6	Rv0982 (*mprB*)	P9WGL1	HK	Unknown sensor domain, possible autoinhibition	Persistent infection	11675502 17379732 24187094
7	Rv1028c (*kdpD*)	P9WGL3	HK	Turgor? Unknown sensor domain	Potassium transport	12595424 12581360 24667597
8	Rv1032c (*trcS*)	P96368	HK	Unknown sensor domain	Multiple genes	12595424 12499293
9	Rv2027c (*dosT*)	P9WGK1	HK	O_2, CO; two heme-binding GAF sensor domains	Persistence, latency	28977726 15033981 19276084 18980385

10	Rv3132c (*devS, dosS*)	P9WGK3	HK	O_2, CO; two heme-binding GAF sensor domains	Latency, nitrate metabolism	15033981 25659431 28977726
11	Rv3220c (*pdtaS*)	P9WGL5	HK	H-kinase_N and PAS sensor domains	Respiration?	12595424 16026786 22115998
12	Rv3245c (*mtrB*)	P9WGK9	HK	Unknown sensor domain	Cell division	22610443
13	Rv3365c	Q93IG6	HK	No phosphorylatable His; unknown sensor domain	Inhibition of macrophage apoptosis	22275911
14	Rv3764c (*tcrY*)	O69729	HK	Iron limitation? Unknown sensor domain	No data	12595424 22001925
1	Rv0386	O53720	ACIII	Contains ATPase, TPR and a DNA-binding domain	Virulence	15955067 19516256
2	Rv0891c	P9WMV1	ACIII	No sensor domain	Expressed in hypoxia	26025969
3	Rv1120c	O06572	ACIII	Pseudogene? No sensor domain	No data	15908099
4	Rv1264	P9WMU9	ACIII	pH, contains N-terminal PF16701 regulatory domain	May be active in early phago-somes, regulates slow growth via small RNA MTS0997	11839758 15890882 17005450 26573524
5	Rv1318c	P9WQ33	ACIII	Unknown integral membrane sensor domain	No data	15182360
6	Rv1319c	P9WQ31	ACIII	Unknown integral membrane sensor domain	No data	15182360
7	Rv1320c	P9WQ29	ACIII	Unknown integral membrane sensor domain	No data	15182360
8	Rv1358	Q11028	ACIII	Contains ATPase, TPR and a DNA-binding domain	No clear data	28650996 22307756
9	Rv1359	P9WM05	ACIII	No sensor domain	No data	
10	Rv1625c	P9WQ35	ACIII	Unknown integral membrane sensor domain	Appears to be the most active of *Mtub* adenylate cyclases	11447108 15500449
11	Rv1647	P94982	ACIII	Unknown sensor domain	Works during log phase	15500449
12	Rv1900c	O07732	ACIII	Contains an N-terminal α/β hydrolase domain	No data	15678099
13	Rv2212	P9WMU7	ACIII	Unknown, contains PF16701 regulatory domain	Intracellular survival, virulence, recovery from dormancy	27481930 28861399
14	Rv2435c	P71914	ACIII	dCache sensor domain	No data	27049771
15	Rv2488c	O53213	ACIII	Contains ATPase, TPR and a DNA-binding domain	Transcriptional regulator, control of DNA damage?	26270051
16	Rv3645	I6X7Z3	ACIII	Unknown integral membrane sensor domain	No data	15182360 22094466
1	Rv0805 (*cpdA*)	P9WP65	CPD	No sensor domain	Virulence?	16313172 17059828
1	Rv1354c	P9WM13	DGC	GAF sensor domain; also contains EAL domain	Cell length, colony morphology, long-term survival	21151497 22343354 25037163
1	Rv1357c	P9WM07	PDE	No sensor domain		
1	Rv3586	P9WNW5	DAC	No sensor domain	Virulence, expression of CRISPR-Cas	22529992 24806618 26668313 29378893
1	Rv2837c	P71615	CDA	No sensor domain		
1	Rv2069 (*sigC*)	P9WGH1	ECF	No sensor domain	*hspX, mtrA, senX*; important for pathogenicity	15049808

2	Rv3414c (*sigD*)	P9WGG9	ECF	No sensor domain	*rpfC*, *recR*, *pks10*; stationary phase genes; essential for virulence	15659067 15375142
3	Rv1221 (*sigE*)	P9WGG7	ECF	Unknown sensor domain	*clgR, aceA, gltA, fadB, fadE, pspA*; heat shock, detergent, oxidative stress	11489128 18657035
4	Rv0182c (*sigG*)	P9WGG5	ECF	Contains C-terminal SnoaL_2 domain	*aceA*, *clpB*, *dnaK*, *fadE*, *lexA*; survival in macrophages	21169493 28934483
5	Rv3223c (*sigH*)	P9WGH9	ECF	No sensor domain	Heat shock, detergent, oxidative stress	11567012 12123450
6	Rv1189 (*sigI*)	P9WGH3	ECF	Contains C-terminal SnoaL_2 domain	No data	18248429 28934483
7	Rv3328c (*sigJ*)	L0TCG5	ECF	Contains C-terminal SnoaL_2 domain	Oxidative stress?	28934483
8	Rv0445c (*sigK*)	P9WGH7	ECF	No sensor domain	*dipZ*, *mpt70*, *mpt83*, *rskA*	15882422
9	Rv0735 (*sigL*)	P9WGH5	ECF	No sensor domain	*mpt53*, *pks7*, *pks10*; secreted proteins, polyketide synthase	16199577 16552079
10	Rv3911 (*sigM*)	O53590	ECF	No sensor domain	*esxT, esxU, esxE, esxF;* surface proteins, lipids, mycolic acids	17028284
1	Rv0014c (*pknB*)	P9WI81	STYK	Contains 4 C-terminal PASTA domains	Cell division, survival in the host	16980473 24706757
2	Rv0015c (*pknA*)	P9WI83	STYK	Unknown sensor domain	Cell division, survival in the host	15985609 25713147
3	Rv0410c (*pknG*)	P9WI73	STYK	Contains rubredoxin and TPR-like domains	Growth in the host, Glu/Gln levels	15186418 19638631
4	Rv0647c (*ubiB*)	P9WQI1	STYK	Unknown sensor domain	Ubiquinone biosynthesis	
5	Rv0931c (*pknD*)	P9WI79	STYK	Contains C-terminal β-propeller domain (6xNHL)	Invasion of host brain endothelia	17411339 22243650
6	Rv1266c (*pknH*)	P9WI71	STYK	Contains C-terminal PF14032 domain	Transcriptional regulator EmbR, HK DevR	17286964 16585755
7	Rv1743 (*pknE*)	P9WI77	STYK	Contains thioredoxin-like PF13462 domain	NO stress, macrophage apoptosis	17892498
8	Rv1746 (*pknF*)	P9WI75	STYK	Unknown sensor domain	GroEL; glucose transport, cell division	15135525 15866927 19201798
9	Rv2088 (*pknJ*)	P9WI67	STYK	Contains C-terminal PF14032 domain	EmbR, PykA, Mdh; mycolic acid biosynthesis	20185505 20520732
10	Rv2176 (*pknL*)	P9WI63	STYK	Unknown sensor domain	DNA-binding protein Rv2175c	19457863
11	Rv2232 (*ptkA*)	P9WPI9	STYK	Tyr-specific, disordered N-terminal domain	Virulence?	19366344 29884774
12	Rv2914c (*pknI*)	P9WI69	STYK	Unknown sensor domain	Oxidative stress?	27818650
13	Rv3080c (*pknK*)	P9WI65	STYK	Contains ATPase and TPR-like domains	VirS; persistent infection	19251699 20522497
14	Rv3197 (*abc1*)	O53343	STYK	Belongs to the ABC1 family	Assists in host survival	20394526
1	Rv0018c (*pstP*)	P9WHW5	PP2C	Unknown sensor domain	Dephosphorylation of mycobacterial STY kinases	14575702 27758870
2	Rv1364c	P9WLZ7	PP2C	PAS, HSP90 ATPase, and STAS anti-sigma domain		19700407 20541534
3	Rv0153c (*ptpB*)	I6WXK4	LMWP	pTyr-specific, no sensor domain	Virulence, survival in the host	10986245 14617138 29888212
4	Rv2234 (*ptpA*)	P9WIA1	LMWP	pTyr-specific, no sensor domain	Virulence, survival in the host	10986245 18474358 25743628

No	Locus tag (gene)	UniProt entry	Sensor type	Sensed ligand, sensor domain	Regulated genes, processes	PubMed reference
***Mycoplasma pneumoniae* M129**						
1	MPN_078 (*fruA*)	P75039	EIIC	Fructose	Sugar utilization	15547265
2	MPN_207 (*ptsG*)	P75569	EIIC	Glucose	Sugar utilization	15547265
3	MPN_496 (*ulaA*)	P75291	EIIC	Ascorbate?	Sugar utilization	
4	MPN_651 (*mtlA*)	P75146	EIIC	Mannitol	Sugar utilization	15547265
1	MPN_244 *(cdaM)*	P75528	DAC	No sensor domain	Potassium homeostasis	28751888
1	MPN_140 *(nrnA)*	P75144	CDA	No sensor domain	Not active against c-di-AMP	28751888
2	MPN_549 (*pdeM*)	P75229	CDA	No sensor domain	Potassium homeostasis	28751888
1	MPN_626 (*sigD*)	P75169	ECF	No sensor domain	No data	25925568
1	MPN_248 (*prkC*)	P75524	STYK	No sensor domain	Gliding motility	19858294 23396910
1	MPN_247 (*prpC*)	P75525	PP2C	No sensor domain	Gliding motility	16857667 23396910
***Neisseria gonorrhoeae* FA 1090**						
1	NGO_0112	Q5FAB5	HK	Unknown sensor domain	No data	
2	NGO_0176 (*misS*)	Q5FA56	HK	Unknown sensor domain	Virulence, resistance to aminoglycosides and antimicrobial peptides	27216061 27353397 28652307
3	NGO_0753 (*narQ/narX*)	Q5F8L9	HK	PilJ-type sensor domain, nitrite is not a signal	Oxygen-limited growth	10972806 16954205
4	NGO_1867 (hydH)	Q5F5Q0	HK	Unknown sensor domain	No data	16194237
1	NGO_1944 (*rpoE*)	Q5F5I1	ECF	No sensor domain	Methionine sulfoxide reductase	16672599
1	NGO_1424 (*ubiB*)	Q5F6W9	STYK	No sensor domain	Ubiquinone biosynthesis	
1	NGO_0541	Q5F962	LMWP	No sensor domain	No data	

No	Locus tag (gene)	UniProt entry	Sensor type	Sensed ligand, sensor domain	Regulated genes, processes	PubMed reference
***Porphyromonas gingivalis* W83**						
1	PG_0017	Q7MXX9	HK	Unknown, PAS-like sensor domain	No data	
2	PG_0052 (*porY*)	Q7MXV5	HK	Unknown sensor domain	Type IX secretion system	27630829 29209465
3	PG_0719 (*haeS*)	Q7MWB2	HK	Unknown sensor domain	Hemin transport	24039921
4	PG_0746	Q7MW90	HK	Unknown, PAS sensor domain	No data	
5	PG_1432 (*fimS*)	Q7MUR1	HK	Unknown, 4 TPR repeats in the sensor domain	Production of fimbriae	10832973 20061484 20118268
6	PG_1797 (*gppX*)	Q7MTY1	HK	Unknown, contains TPR-like sensor domain and C-terminal REC and DNA-binding domains	Gingipain secretion, pigmentation, biofilm formation	14638996 23194602
1	PG_1588	Q7MUE0	DAC	No sensor domain	No data	
1	PG_1091	Q7MVH2	CDA	No sensor domain	No data	
2	PG_1592	Q7MUD7	CDA	Unknown; contains 7TM-HDED extracellular sensor domain and 7TM-7TMR_HD integral membrane domain	No data	
1	PG_0162	Q7MXL2	ECF	No sensor domain	Gingipain, virulence, biofilm formation	20807237 26216199 25596817
2	PG_0214	Q7MXH4	ECF	No sensor domain	No data	20807237
3	PG_0985	Q7MVR1	ECF	No sensor domain	H_2O_2 sensitivity	20807237
4	PG_1318	Q7MV00	ECF	No sensor domain	Proteinase secretion, pigmentation	19702950
5	PG_1660	Q7MU87	ECF	No sensor domain	Gingipain, H_2O_2 sensitivity	20807237
6	PG_1827 (*sigH*)	Q7MTV5	ECF	No sensor domain	*sod, trx, tpx, ftn, feoB2 hmu*; oxidative stress, biofilm formation	20807237 22520389 25596817
1	PG_0436	Q7MWZ2	STYK	Unknown	No data	
1	PG_0435	Q7MWZ3	PP2C	Unknown	No data	
2	PG_1641	Q7MU97	LMWP	No sensor domain	No data	
***Rickettsia typhi* str. Wilmington**						
1	RT0221	Q68XD9	HK	Unknown sensor domain	No data	
2	RT0412	Q68WV3	HK	Unknown sensor domain	No data	
3	RT0452	Q68WR4	HK	SSS family sensor domain, may be sensing Pro and/or Na^+ gradient	No data	
4	RT0603	Q68WC5	HK	Unknown sensor domain	No data	
1	RT0229	Q68XD2	DGC	PleD-type response regulator, two REC domains	No data	
1	RT0238	Q68XC3	PDE	Unknown sensor domain	No data	
1	RT0674 (*ubiB*)	Q68W58	STYK	UbiB domain	Ubiquinone biosynthesis	

No	Locus tag (gene)	UniProt entry	Sensor type	Sensed ligand, sensor domain	Regulated genes, processes	PubMed reference
***Streptococcus pyogenes* M1 GAS**						
1	SPy_0242	Q9A1J7	HK	Integral membrane sensor domain	No data	
2	SPy_0244	Q9A1J6	HK	Integral membrane sensor domain	No data	
3	SPy_0337 (*covS*, *csrS*)	O87528	HK	Mg^{2+}? Unknown sensor domain	Synthesis of hyaluronic acid capsule, streptokinase, streptolysin S	15175307 12646707
4	SPy_0529	Q9A107	HK	PAS sensor domain	No data	
5	SPy_0875	Q9A099	HK	Unknown sensor domain	No data	
6	SPy_1061	Q99ZV0	HK	Unknown sensor domain	No data	
7	SPy_1082	Q99ZT6	HK	Unknown sensor domain	No data	
8	SPy_1236	Q99ZG9	HK	Unknown sensor domain	No data	
9	SPy_1588	Q99YQ6	HK	Unknown sensor domain	No data	
10	SPy_1605	Q99YP4	HK	Integral membrane sensor domain	No data	
11	SPy_1622 (*liaS*)	Q99YN2	HK	Integral membrane sensor domain	No data	19118347 23704792
12	SPy_2026	Q99XU6	HK	Unknown sensor domain	No data	
1	SPy_0146 (*frwC*)	Q9A1Q9	EIIC	Fructose?	No data	27862457
2	SPy_0174 (*ulaA*)	Q9A1N9	EIIC	3-keto-L-gulonate, ascorbate	No data	27862457
3	SPy_0572	Q9A0X4	EIIC	β-Glucosides	No data	27862457
4	SPy_0630 (*agaW*)	Q9A0T5	EIIC	N-acetylgalactosamine?	No data	26787724
5	SPy_0855 (*fruA*)	Q9A0B0	EIIC	Fructose	*fruRBA*; carbohydrate utilization	26787724
6	SPy_1059	Q99ZV2	EIIC	Mannose? Sorbose?	No data	27862457
7	SPy_1709	Q99YH0	EIIC	Galactose?	No data	26787724
8	SPy_1739 (*manM*)	Q99YE5	EIIC	Mannose	No data	27862457
9	SPy_1815 (*scrA*)	Q99Y91	EIIC	Sucrose?	No data	27862457
10	SPy_1917 (*lacE*)	Q99Y17	EIIC	Lactose?	No data	27862457
11	SPy_1949	Q99XZ3	EIIC	Ascorbate?	No data	27862457
12	SPy_1986	Q99XX0	EIIC	N-acetylglucosamine?	No data	27862457
13	SPy_2050	Q99XT2	EIIC	Cellobiose?	No data	27862457
14	SPy_2097	Q99XQ4	EIIC	Trehalose?	No data	27862457
1	SPy_1036	Q99ZX0	DAC	No sensor domain	No data	21614937
1	SPy_0720	Q9A0L5	CDA	No sensor domain	No data	
2	SPy_2184 (*gdpP*)	Q99XI9	CDA	No sensor domain	Secreted protease SpeB	23869242
1	SPy_1902	Q99Q57	ECF?	No sensor domain	No data	
2	SPy_2144	Q99XM1	ECF?	No sensor domain	No data	
1	Spy_1625 (*stk*)	Q99YN0	STYK	3 PASTA domains, senses envelope stress	Stress response, virulence, penicillin tolerance	21788381
1	SPy_1626	Q99YM9	PP2C	No sensor domain	No data	28127804
2	SPy_0039	Q9A1Y0	LMWP	No sensor domain	Virulence	25939957

No	Locus tag (gene)	UniProt entry	Sensor type	Sensed ligand, sensor domain	Regulated genes, processes	PubMed reference
Treponema pallidum **subsp.** ***pallidum*** **str. Nichols**						
1	TP_0363	P96123	HK	CheA, interacts with MCPs	Chemotaxis	
1	TP_0040	Q56344	MCP	Unknown sensor domain	No data	
2	TP_0488	O83501	MCP	Unknown, dCache_1 sensor domain	No data	
3	TP_0639	O83646	MCP	Unknown integral membrane sensor domain	No data	
4	TP_0640	O52778	MCP	Unknown integral membrane sensor domain	No data	
1	TP0485	O83498	ACIII	Unknown sensor domain	No data	
1	TP_0981	O83946	DGC	Unknown, GAF sensor domain	No data	
2	*TP_0172	O83202	*DGC	Unknown sensor domain, truncated GGDEF domain	No data	
1	TP_0764	O83745	PDE	Unknown sensor domain	No data	
2	TP_0877	O83847	PDE	Unknown sensor domain	No data	
3	TP_0912	O83882	PDE	DUF3391 sensor domain (uncharacterized)	No data	
1	TP_0826	O83798	DAC	No sensor domain	No data	
1	TP_0436	O83450	CDA	No sensor domain	No data	
2	TP_0803	O83781	CDA	No sensor domain	No data	
3	TP_0651	O83657	CDA	Unknown; contains 7TM-HDED extracellular sensor domain and 7TM-7TMR_HD integral membrane domain	No data	
1	TP_0092 *(rpoE)*	O83130	ECF	No sensor domain	No data	
1	TP_0591 (*hprK*)	O83600	STYK	No sensor domain	Phosphorylates Hpr protein	9570401
1	TP_0218	O83247	PP2C	Unknown sensor	No data	
2	TP_0219	O83248	PP2C	Integral membrane sensor domain	No data	
3	TP_0854	O83826	PP2C	Unknown sensor domain, contains a sialidase-like fragment	No data	