S2 Table. Structurally characterized members of the GntR/HutC transcription factor family. The listed regulators were identified by a protein structure database search (Dali Lite v.3, [60]) *via* the Dali server using the crystal structure of full-length DasR (PDB-ID 4ZS8) as a search model. From the resulting structures only those containing a GntR-family-specific wHTH domain as well as a HutC-subfamily-specific UTRA domain (as described in the respective entry in the UniProt database [19]) were used for a subsequent multiple sequence alignment *via* CLUSTAL OMEGA [59] that is shown in S4 Fig. For a better discrimination, regulators without an individual gene or protein name and mostly of unknown function were given unambiguous acronyms, e.g. ScuR for <u>S</u>. <u>coelicolor</u> <u>u</u>nnamed <u>R</u>egulator. The panel "Match of characteristic residues" describes residues that are explicitly involved in DNA binding of NagR [11] and in effector binding of DasR and/or NagR (Fig 9), and their equivalents from other GntR/HutC family members inferred by structural comparison with DasR and NagR. Residues marked in red were only inferred by sequence due to the lack of structural information.

Name	Organism	Gene	Uniprot ID PDB-ID	Function	Residues in structure (total)	Sequence identity to DasR (%)	Match of characteristic residues		Additional information
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DasR	*Streptomyces coelicolor*	*dasR*	Q9K492 4ZS8	global regulator; part of nutrient sensing system	22-251 (254)	100	R48 R58 G79	R142 R144 E154 Y177 R221 Y238	
PhnF	*Mycobacterium smegmatis*	*phnF*	A0QQ72 3F8M	transcr. regulator of unknown function	2-244 (244)	39.6	R36 R46 G66	R129 L131 E141 Y164 R207 Y224	S84 & R89 for phosphate moiety interaction [18]
NagR	*Bacillus subtilis*	*yvoA*	O34817 4U0V	local regulator; part of nutrient sensing system	1-243 (243)	38.8	R38 R48 G69	R133 R135 E145 Y167 R211 Y228	
ScuR	*Streptomyces coelicolor*	*SCO6256*	Q9RKT6 2RA5	transcr. regulator of unknown function	1-245 (245)	34.6	I42 R52 G73	R136 R138 L148 Y170 R213 Y230	S,R meso-tartaric acid in binding pocket
PsuR	*Pseudomonas syringae*	*hutC*	Q87UX0 2PKH	repressor of histidine utilization	105-249 (249)	30.5	S48 R58 G79	I143 H145 E155 Y178 R220 H236	R156 for phosphate moiety interaction?

CguR	*Corynebacterium glutamicum*	*cg0196*	Q8NTZ4 2P19	transcr. regulator of unknown function	105-253 (253)	30.4	I51 R61 G82	R145 R147 L157 Y177 R222 Y239	
BbuR	*Bacillus bronchiseptica*	*BB3683*	Q7WD95 3CNV	transcr. regulator of unknown function	98-259 (259)	29.8	I54 Q64 G85	R149 L151 D161 Y186 R230 Y247	R99 & R243 for phosphate moiety interaction? Citrate anion in binding pocket
EfuR	*Enterococcus faecalis*	*EF1328*	Q835P8 3DDV	transcr. regulator of unknown function	91-235 (235)	28.9	R34 R44 G65	R128 R130 E141 F163 Q207 L224	
YurK	*Bacillus subtilis*	*yurK*	O32152 2IKK	transcr. regulator of unknown function	94-242 (242)	26.4	N37 R47 G68	R132 L134 E144 H167 K211 M228	Sulphate anion in binding pocket
PhnF	*Escherichia coli*	*phnF*	K16684 2FA1	transcr. regulator of unknown function	85-241 (241)	25.3	Q39 R49 G70	T134 R136 I146 H168 R212 T230	R133 for phosphate moiety interaction?
SauR	*Streptomyces avermitilis*	*SAV3189*	Q82IF8 3EET	transcr. regulator of unknown function	1-250 (250)	22.9	A35 D45 G66	Y137 F139 S149 V177 R220 V236	R36 for DNA interaction? R86 & R95 for phosphate moiety interaction?
EcuR	*Escherichia coli*	*c4276*	Q8FCM7 3HFI	transcr. regulator of unknown function	82-251 (251)	22.8	Y42 R52 G73	R138 R140 I150 F173 Q217 L234	No dimerization of EBD
TreR	*Bacillus subtilis*	*treR*	P39796 2OGG	repressor of trehalose operon	90-238 (238)	21.8	H32 R42 G63	R128 R130 D140 Y162 N206 H223	Sulphate anion in binding pocket
StuR	*Staphylococcus aureus*	*SA0254*	Q7A7U1 2OOI	transcr. regulator of unknown function	73-234 (234)	21.1	T30 K40 G61	R126 R128 E138 F160 Q204 F221	Two ethylene glycol molecules in area of binding pocket
YydK	*Bacillus subtilis*	*yydK*	Q45591 3BWG	transcr. regulator of unknown function	1-236 (236)	20.4	E30 K40 G61	R125 R127 E137 F159 S203 Y220	
BauR	*Bacillus anthracis*	*BA3458*	Q81MW2 3LHE	transcr. regulator of unknown function	93-232 (245)	19.3	P36 V46 G67	R131 R133 E143 Y165 Q209 H226	High identity (>97%) to BcuR (*B. cereus*) No dimerization of EBD
BcuR	*Bacillus cereus*	*BC3424*	Q735I1 3L5Z	transcr. regulator of unknown function	92-245 (245)	18.8	P36 V46 G67	R131 R133 E143 Y165 Q209 H226	High identity (>97%) to BauR (*B. anthracis*)
TraR	*Streptomyces phaeochromogenes*	*traR*	Q54677 1V4R	transcr. regulator of unknown function	7-99 (245)	16.6	T36 A46 A66	R133 R136 G145 Y174 T218 Y235	NMR structure