

S3 Table. Pairwise comparison of protein sequence identities between all GntR/HutC transcription factors used in the multiple sequence alignment shown in S4 Fig. The sequence identities were calculated with CLUSTAL OMEGA [59].

Name	Protein sequence identity (%)																		
	DasR	PhnF	NagR	ScuR	PsuR	CguR	BbuR	EfuR	YurK	PhnF	SauR	EcuR	TreR	StuR	YydK	BauR	BcuR	TraR	
DasR	100																		
PhnF	39.6	100																	
NagR	38.8	31.1	100																
ScuR	34.6	24.4	34.6	100															
PsuR	30.5	21.7	27.7	26.6	100														
CguR	30.4	24.5	28.9	50.0	24.7	100													
BbuR	29.8	23.4	26.5	30.4	23.5	31.7	100												
EfuR	28.9	24.1	34.0	26.3	22.4	28.9	23.0	100											
YurK	26.4	20.5	26.1	24.7	23.5	27.2	24.3	29.4	100										
PhnF	25.3	25.4	20.3	27.9	19.1	27.9	23.0	23.3	23.3	100									
SauR	22.9	16.0	21.1	22.9	22.7	24.2	22.5	15.9	20.6	17.2	100								
EcuR	22.8	19.1	25.9	25.3	21.8	27.5	22.1	26.0	25.2	25.1	19.3	100							
TreR	21.8	21.1	24.5	21.8	17.2	19.3	18.8	25.3	19.9	20.0	14.5	21.5	100						
StuR	21.1	15.0	21.7	20.6	19.7	19.7	20.9	24.0	22.9	22.1	18.3	19.4	21.2	100					
YydK	20.4	16.6	26.6	23.0	16.2	18.8	19.6	25.3	21.6	23.0	15.7	22.6	25.3	39.9	100				
BauR	19.3	22.4	22.8	20.6	17.4	22.4	22.3	25.5	20.4	21.8	17.3	18.9	24.9	21.7	24.8	100			
BcuR	18.8	22.4	22.8	21.0	18.2	22.8	22.3	25.1	20.4	21.8	17.7	19.3	25.7	22.1	25.2	97.6	100		
TraR	16.6	20.5	21.3	21.4	20.2	19.7	19.5	21.5	18.2	18.4	20.9	17.8	15.9	16.7	16.2	19.1	18.7	100	