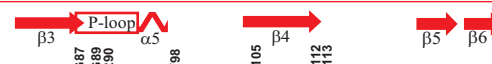


NAD⁺/NADH binding domain



Secondary structure and residues numbers corresponds to the *Thermus aquaticus* Rex protein (PDB: 3IKT)

Phylum	Accession	Protein Name	Residues
Deinococcus/Thermus	3IKT	Taq 4998	NRKGLGICVGRIGLSALADYVPGF-GESE- FELR GFVDPDE- KVGR PVR-GGVIEHVD- LLP QRVPRGR- I
	2DT5	TTIC1293	NRKGLGICVGRIGLSALADYVPGF-GESE- FELR GFVDPDE- KVGR PVR-GGVIEHVD- LLP QRVPRGR- I
		Dgeo 0630	NQTNNVVIVGMRIGLQALANYPGA-SDYQFQVGLFDVNEA-LIGTVQR-GLTVRHDV- ELRAF QVTR- I
		Deide 14030	NQTNNVVIVGMRIGLQALANYPGA-SDYQFQVGLFDVNEA-LIGTVQR-GLTVRHDV- ELRAF QVTR- I
		DR0939	DQTNNVVIVGMRIGLQALANYPGA-SDYQFQVGLFDVNEA-LIGTVQR-GLTVRHDV- ELRAF QVTR- I
		CTC02428	TKEVRCIIILGGNIGQALANYNPK-EKLGFLRLAIFDINPK-LVGLKTR-DIEIKRID- TLED YLKRN- V
		CKL 0453	TKVVRVILIGAGNIGQALANYNPK-EKLGFLRLAIFDINPK-LVGLKTR-DIEIKRID- TLED YLKRN- V
		CB03306	NNEPNTIILIGAGNIGQALANYNPK-EKLGFLRLAIFDINPK-LVGLKTR-DIEIKRID- TLED YLKRN- V
		GAZ2713	TKMNTIILIGAGNIGQALANYNPK-EKLGFLRLAIFDINPK-LVGLKTR-DIEIKRID- TLED YLKRN- V
		NT01CX 0475	DENNNTIILIGAGNIGQALANYNPK-EKLGFLRLAIFDINPK-LVGLKTR-DIEIKRID- TLED YLKRN- V
Clostridiaceae		Cbei 0320	DRGEAALVAGNIGQAVSYRSE-ENLEFKITAFIDANPK-LIGMKTR-DVEIMDD- EMES VLSEHK- I
		CBY 3040	DRGKAALVAGNIGQAVSYRSE-ENLEFKITAFIDANPK-LIGMKTR-DVEIMDD- EMK ILENEK- I
		CPF 2586	TRDYNVILIGAGNIGQALANYNPK-NRLEFKLIGLFDANPK-MFGIKTR-DVEIQDVE- KLKD FKVKNY- I
		Clos 2464	DKTVKLILIGAGNIGQALANYNPK-ERSGFELIALFDINPK-LGLKTR-DIEFRDID- ELRQ FINENY- I
		CD0171	DRPNVAVLIGAGNIGQALANYNPK-RKAGFELKALFDANPK-MIGLKTR-EFEVLDS- TLED FKNNK- I
		CLOHR 00042	DRPNVAVLIGAGNIGQALANYNPK-RKAGFELKALFDANPK-MIGLKTR-EFEVLDS- TLED FKNNK- I
		CLOBAR 00711	DRPNVAVLIGAGNIGQALANYNPK-RKAGFELKALFDANPK-MIGLKTR-EFEVLDS- TLED FKNNK- I
		CLOEX 01590	DVNHMIIILIGAGNIGQALANYNPK-ERSGFVLRKIGFDVNR-LEGVTR- GIE TRMD- ELSD FKNNK- I
		CLOSC 00613	EEDHNTIILIGAGNIGQALANYNPK-EKRGFLKIGFDVNR-LEGVTR- GIE TRMD- GLKT FKNNK- V
		Cphy 0901	DKKNNVILIGAGNIGQALANYNPK-ERSGFVLRKIGFDVNR-LEGVTR- GIE TRMD- ELRQ FINENY- I
Thermoanaerobacterales		CLOBL 04148	DRQENVTIILIGAGNIGQALANYNPK-ERSGFVLRKIGFDVNR-LGLVTR- GIE TRMD- ELRQ FINENY- I
		CLOS21 01144	DKRNDMIIIGAGNIGQALANYNPK-ERSGFVLRKIGFDVNR-LGLVTR- GIE TRMD- ELRQ FINENY- I
		Cce1 2882	NKTFYCIILIGAGNIGQALANYNPK-IRKGFVLRKIGFDVNR-VVGGKIK-NLEVMD- SLEP FLNHR- V
		CLOLEP 02947	SNRFNAILIGAGNIGQALANYNPK-ERSGFVLRKIGFDVNR-LGLVTR- GIE TRMD- ELRQ FINENY- I
		TTE0543	DKTNNVILIGAGNIGQALANYNPK-EKSGFNLKIGFDINPK-LFGLKTR-DVEIMDD- KVEE FINHR- I
		Teth514 0496	DKTNNVILIGAGNIGQALANYNPK-EKSGFNLKIGFDINPK-LFGLKTR-DVEIMDD- KVEE FINHR- I
		Csac 1220	DKNFKMLIIGAGNIGQALANYNPK-YKGFVLRVGLFDVDEQ-KVGRKTR-NVKIQHD- ELDK FKNNK- I
		Arth 3297	TRDKVAVLIGAGNIGQALANYNPK-ERSGFVLRVGLFDVDEQ-KVGRKTR-NVKIQHD- ELDK FKNNK- I
		AAur 3294	THDKVAVLIGAGNIGQALANYNPK-ERSGFVLRVGLFDVDEQ-KVGRKTR-NVKIQHD- ELDK FKNNK- I
		Amir 6731	TRKHSVAVVIGLGHGALANYNPK-ERSGFVLRVGLFDVDEQ-KVGRKTR-NVKIQHD- ELDK FKNNK- I
Actinobacteria		SACE 6947	TRKHSVAVVIGLGHGALANYNPK-ERSGFVLRVGLFDVDEQ-KVGRKTR-NVKIQHD- ELDK FKNNK- I
		Svi 02840	TRKHSVAVVIGLGHGALANYNPK-ERSGFVLRVGLFDVDEQ-KVGRKTR-NVKIQHD- ELDK FKNNK- I
		Franceal 612	TRKHSVAVVIGLGHGALANYNPK-ERSGFVLRVGLFDVDEQ-KVGRKTR-NVKIQHD- ELDK FKNNK- I
		Francecl3 0484	TRKHSVAVVIGLGHGALANYNPK-ERSGFVLRVGLFDVDEQ-KVGRKTR-NVKIQHD- ELDK FKNNK- I
		SCO3320	TQDPVVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		SAV 4738	TQDPVVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		SGR 4154	TQDPVVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		Noca 0493	TQDPVVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		Acel 0239	TQDPVVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		JNB 09294	TQDPVVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
Desulfobrivionales		Namu 0919	HRHRVALVGLGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		RHA1 z02054	DRGHKVVVIGVGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		ROP 17260	DRGHKVVVIGVGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		REK 16400	DRGHKVVVIGVGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		nfa 710	SDGRGFTVIGVGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		DWPF 1390	NRENRVIVGIGLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		DVU0916	NRENRVIVGIGLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		Dde 2702	DREKNTVILIGAGNIGQALANYNPK-ERSGFVLRKIGFDVNR-LGLVTR- GIE TRMD- ELRQ FINENY- I
		Ddes 2257	DREKNTVILIGAGNIGQALANYNPK-ERSGFVLRKIGFDVNR-LGLVTR- GIE TRMD- ELRQ FINENY- I
		DESPIG 02066	DREKNTVILIGAGNIGQALANYNPK-ERSGFVLRKIGFDVNR-LGLVTR- GIE TRMD- ELRQ FINENY- I
Rex Thermotogales		L11059	NREKVALVGLGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		Dret 2085	DRTNNVALVGLGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		Dbac 2793	DRTNNVALVGLGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		DMR 42180	DRVVKCALVGLGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		Desal 3723	DRVVKCALVGLGNLQALGAGYSGF-AGRFVLSALFDVDEQ-RVGRV- GRV TRHD- SAG CVRA- R
		THA 1697	NKYNNVIVGAGNIGSALADYVPGF-GESE- FELR GFVDPDE- KVGR PVR-GGVIEHVD- LLP QRVPRGR- I
		Tmal 1209	TQDPVVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		Fnod 0423	NKEMNVVIGAGNIGSALADYVPGF-GESE- FELR GFVDPDE- KVGR PVR-GGVIEHVD- LLP QRVPRGR- I
		Tlet 0332	HRRNNVIVGAGNIGSALADYVPGF-GESE- FELR GFVDPDE- KVGR PVR-GGVIEHVD- LLP QRVPRGR- I
		Tpet 0756	KKEKLVVAGNIGRAVSYRSE-ENLEFKITAFIDANPK-LIGMKTR-DVEIMDD- EMES VLSEHK- I
Chloroflexi		Tnap 0799	KKEKLVVAGNIGRAVSYRSE-ENLEFKITAFIDANPK-LIGMKTR-DVEIMDD- EMES VLSEHK- I
		TRO2 0779	KKEKLVVAGNIGRAVSYRSE-ENLEFKITAFIDANPK-LIGMKTR-DVEIMDD- EMES VLSEHK- I
		TM0169	KKEKLVVAGNIGRAVSYRSE-ENLEFKITAFIDANPK-LIGMKTR-DVEIMDD- EMES VLSEHK- I
		CTN 0518	KKEKLVVAGNIGRAVSYRSE-ENLEFKITAFIDANPK-LIGMKTR-DVEIMDD- EMES VLSEHK- I
		Kole 1558	KKEKLVVAGNIGRAVSYRSE-ENLEFKITAFIDANPK-LIGMKTR-DVEIMDD- EMES VLSEHK- I
		Emob 0343	ERVNVVAVLIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		Cagg 0157	NQHVPVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		Chy400 3940	HHHPVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		TQDPVVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V	
		RoseRS 4103	TREPVAVVIGLGHGALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
Streptococcaceae		Haur 4427	HEVNVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		LACR 1156	DOEHIALIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		L71932	DOEHIALIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		SP 1090	NSINVMVIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		smi 1188	NSINVMVIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		SGO 1228	NSINVMVIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		SSA 1216	NAINVMVIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		SMU 1053	TSTNNVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		SSU05 1069	TSINVMVIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		st1463	NATKVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
Lactobacillales		SP1120	HSTNVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		SDEG 0880	HSTNVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		Sub 1050	HSTNVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		SUB0845	HSTNVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		GALL0 1010	HSTNVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		SAG1100	HSTNVVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		LGG 01260	HSEQMLVIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		LAF 0324	DKLSVALVGVGLSALLNPK-FHQSTNLRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		LAR 0341	DSLVSVALVGVGLSALLNPK-FHQSTNLRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		LVI5 0616	DRLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
Staphylococcaceae		lp 0725	DTLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		LSL 1214	DTLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		LQ455	DTLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		LBUL 1498	DTLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		LB0398	DTLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		lhv 0416	DTLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		LSEI 2245	DRLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		LS0356	DRLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		LEUM 1774	DSLINVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		OEOE 1398	DKLNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
Bacillales		PEPE 1470	DTANVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		SE1647	SDQIKIIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		STACA0001 0533	SDEIKIIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		SA1851	SDQIKIIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		SA0933	SDQIKIIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		SH0886	SDQIKIIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		Sca 1553	SDQIKIIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		MCCL 1721	DMIKVAVLIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		RBAM 06420	DETNVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		B5U05970	DETNVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
Rex1 Thermotogales		BLi00618	DETNVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		BPUM 0528	DETNVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		GK0242	DEVVALVGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		Aflv 0208	DETVALVGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		BC0291	DDIIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		CB0652	HEIIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		AB0487	DERNVIVGIGLGAALANYNPK-ASRGRFVAALIDADPA-MAGKPA- GIV QHD- ELKI IQD- V
		BH0551	DELKVMVIGVGNLGRALLNPK-ELRQFINENY- ELDK FKNNK- I
		Pjdr2 2450	DQRNVALVGVGNLGRALLNPK-FHQSNVIRISAADFVDEQ-LANTVKSQVIVYVSE- DMKQ LKQ- Q
		Tpet 1366	NNTNMIIVGANDLARALLSLD- ESKAG - VKV VAVFDEKE- NVGK FTG-EFAVRELD- VLER VRFRD- A
	Tnap 1384	NNTNMIIVGANDLARALLSLD- ESKAG - VKV VAVFDEKE- NVGK FTG-EFAVRELD- VLER VRFRD- A	
	TRO2 1320	NNTNMIIVGANDLARALLSLD- ESKAG - VKV VAVFDEKE- NVGK FTG-EFAVRELD- VLER VRFRD- A	
	TM1427	NNTNMIIVGANDLARALLSLD- ESKAG - VKV VAVFDEKE- NVGK FTG-EFAVRELD- VLER VRFRD- A	
	CTN 1066	NSTNMIIVGANDLARALLSLD- ESKAG - VKV VAVFDEKE- NVGK FTG-EFAVRELD- VLER VRFRD- A	
	THA 788	GVMNIIIVGAGNIGSALADYVPGF-GESE- FELR GFVDPDE- KVGR PVR-GGVIEHVD- LLP QRVPRGR- I	
	Tml 0489	GVMNIIIVGAGNIGSALADYVPGF-GESE- FELR GFVDPDE- KVGR PVR-GGVIEHVD- LLP QRVPRGR- I	
	Fnod 0224	KDRDSIIIVGAGNIGSALADYVPGF-GESE- FELR GFVDPDE- KVGR PVR-GGVIEHVD- LLP QRVPRGR- I	
	Tlet 0951	RKTQVILVIGAGNIGSALADYVPGF-GESE- FELR GFVDPDE- KVGR PVR-GGVIEHVD- LLP QRVPRGR- I	
	ruler	140.....150.....160.....170.....180.....190.....200.....210.....	

Secondary structure and residues numbers corresponds to the *Thermus aquaticus* Rex protein (PDB: 3IKT)

Residues that are essential for NADH-binding and dimer formation are shown by red and gray asterisks, respectively.

NAD⁺/NADH binding domain



Secondary structure and residues numbers corresponds to the *Thermus aquaticus* Rex protein (PDB: 3IKT)

Phylum	Accession	Protein Name	Sequence	Residue
Deinococcus/Thermus	3IKT	Taq 4998	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	1143
	2DT5	TTG1293	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	1148
	Dgeo	0630	DMGLAV [*] PREAQA [*] AAQALADAGV [*] RGILNFAPV [*] IQPS	
	Deide	14030	DMGLAV [*] PREAQA [*] AAQALADAGV [*] RGILNFAPV [*] IQPS	
Clostridiaceae	DRO939	DMGLLV [*] PAEHAQA [*] AAQALV [*] AAVGGILNFAPV [*] LVLE [*] V		
	CTC02428	DVGLI [*] CVPS [*] SAQK [*] VC [*] ILIR [*] NNV [*] KGIW [*] NFAPV [*] DLK [*] VE		
	CKL	0453	DIGIIC [*] VPSS [*] NNGK [*] VC [*] INIL [*] VKNV [*] KGIW [*] NFAPV [*] DLV [*] PE	
	CB03306	DIGIIC [*] VPSS [*] NNGK [*] VC [*] INIL [*] VKNV [*] KGIW [*] NFAPV [*] DLV [*] PE		
	CAC2713	DIGIIC [*] VPSS [*] NNGK [*] VC [*] INIL [*] VKNV [*] KGIW [*] NFAPV [*] DLV [*] PE		
	NT01CX	0475	HGVIC [*] VPSS [*] NNGK [*] VC [*] INIL [*] VKNV [*] KGIW [*] NFAPV [*] DLV [*] PE	
	CGIC	0320	CGICLV [*] CPKKA [*] NA [*] YV [*] ADRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
	CBY	3040	CGICLV [*] CPKKA [*] NA [*] YV [*] ADRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
	CPF	2586	HGVIC [*] VPSS [*] NNGK [*] VC [*] INIL [*] VKNV [*] KGIW [*] NFAPV [*] DLV [*] PE	
	Clos	2464	DIVVLS [*] PEKVA [*] SVV [*] IK [*] LNK [*] IN [*] VGGI [*] WNFAPV [*] DLK [*] VSD	
	CD0171	DIAVLC [*] IPKNGA [*] QELN [*] RVKAG [*] IGVW [*] NFAPV [*] DLV [*] PE		
	CLOHIR	00042	DIAVLC [*] IPKNGA [*] QELN [*] RVKAG [*] IGVW [*] NFAPV [*] DLV [*] PE	
	CLOBAR	00711	DIGIIC [*] VPSS [*] NNGK [*] VC [*] INIL [*] VKNV [*] KGIW [*] NFAPV [*] DLV [*] PE	
	CLONEX	01590	E [*] IAVL [*] ITPK [*] KA [*] TE [*] VADML [*] VESG [*] IKAI [*] WNFAPV [*] DLV [*] PE	
	CLOSCI	00613	E [*] IAVL [*] ITPK [*] KA [*] TE [*] VADML [*] VESG [*] IKAI [*] WNFAPV [*] DLV [*] PE	
Thermoanaerobacterales	Cphy	0901	N [*] AAAL [*] ITPK [*] KA [*] TE [*] VADML [*] VESG [*] IKAI [*] WNFAPV [*] DLV [*] PE	
	CLOBOL	01448	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	CLOSS21	01144	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Cosl	2132	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	CLOLEI	02947	D [*] MAIL [*] CPK [*] NDNA [*] YV [*] ADRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
	TT0543	D [*] MAIL [*] CPK [*] NDNA [*] YV [*] ADRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V		
	Teth514	0496	DIGIIC [*] VPSS [*] NNGK [*] VC [*] INIL [*] VKNV [*] KGIW [*] NFAPV [*] DLV [*] PE	
	Csac	1220	DIGIIC [*] VPSS [*] NNGK [*] VC [*] INIL [*] VKNV [*] KGIW [*] NFAPV [*] DLV [*] PE	
	Arth	3297	NMVVIAL [*] PAVA [*] AAQV [*] CV [*] DRV [*] LAAG [*] RSIL [*] SFAPV [*] LVLE [*] V	
	AAur	3294	NMVVIAL [*] PAVA [*] AAQV [*] CV [*] DRV [*] LAAG [*] RSIL [*] SFAPV [*] LVLE [*] V	
	Amir	6731	SIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
	SACE	6947	TIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
	Svir	02840	SIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
	FraneanI	6132	TIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
	Actinobacteria	Franc31	0484	TIGMICH [*] PA [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V
SC0332		SIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V		
SAV		4738	SIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
SGR		4154	SIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
Noca		0493	AIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
Acel		0239	AIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
JNB		09294	AIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
Namu		0919	SIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
RHAL		ro02054	TIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
ROP		17260	TIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
RER		16400	TIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V	
nfa51710		TIGVIA [*] PP [*] AAQA [*] QV [*] CDRL [*] VAGC [*] IGLNFAPV [*] LVLE [*] V		
DvMF		1390	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
DV0916		E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
Dde		2702	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
Desulfovibrionales	Ddes	2257	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	DESPIG	02066	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	L11059	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	Dret	2085	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Dbac	2793	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	DMR	42180	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Desal	3723	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	THA	1697	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Tme1	1209	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Fnod	0423	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Tlet	0332	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Tpe	0756	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Tnap	0799	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	TRQ2	0779	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	TM0169	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
CTN	0518	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
Chloroflexi	Kole	1558	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Fmob	0343	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Cagg	0157	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Chy400	3940	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Rcas	1392	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	RoseRS	4103	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Hau	4427	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	LACK	1156	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	L71932	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	SP	1090	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	smi	1188	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	SGO	1228	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	SSA	1216	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	SMU	1053	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	SSU05	1069	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
Streptococcaceae	str1463	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	Spy1120	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	SDBG	0880	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Seq	1050	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	SUB0845	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	GALLO	1010	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	SAG1100	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	LGG	01260	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	LAF	0324	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	LAR	0341	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	LVIS	0616	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	lp	0725	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	LSL	1214	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	LJ0455	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	LBUL	1498	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
Lactobacillales	LB0398	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	lhv	0416	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	LSEI	2245	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	LSA0356	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	LEUM	1774	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	OEOE	1398	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	PEPE	1470	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	SE1647	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	STACA0001	0533	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	SA1851	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	SSP0833	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	SH0986	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	SCIL	553	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	MCC1	1721	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	RBAM	06420	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
Staphylococcaceae	BSU05970	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	Bli00618	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	BPUM	0528	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	GR0242	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	Aflv	0208	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	BC0291	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	OB0652	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	ABC0873	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	BH0551	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	Pjdd2	2450	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Tpet	1366	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Tnap	1384	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	TRQ2	1320	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	TM1427	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
	CTN	1066	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
THA	788	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V		
Bacillales	Tme1	0489	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Fnod	0224	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	Tlet	0951	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
	zuler	220	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
		230	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
		240	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
		250	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
		260	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	
		270	E [*] IALLV [*] PREAAK [*] AADLLV [*] AAIGIK [*] GLNFAPV [*] LVLE [*] V	

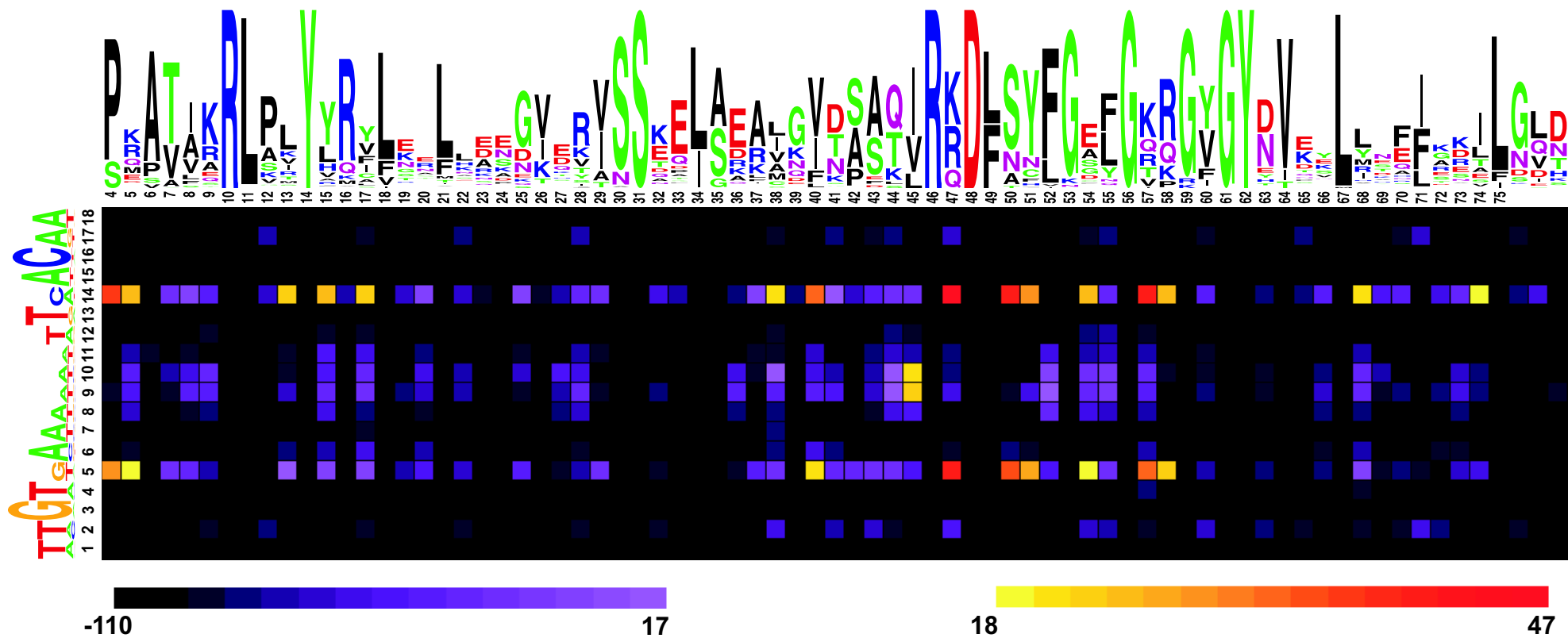


Figure S3. Heatmap of correlations between amino acid and nucleotide pairs for Rex proteins and their operator sites.

Sequence logos of Rex DNA-binding domains and operator DNAs are displayed above and to the left of the heatmap, respectively. The total height of the symbols in each position equals the positional information content, whereas the height of individual symbols is proportional to the positional amino acid/nucleotide frequency. The correlation scores are color ramped from yellow to red for amino acid nucleotide pairs with statistical significance greater than automatically defined threshold. 26 significantly correlated pairs of residues/nucleotides correspond to 16 amino acid positions in Rex proteins and 4 nucleotide positions in DNA operators.

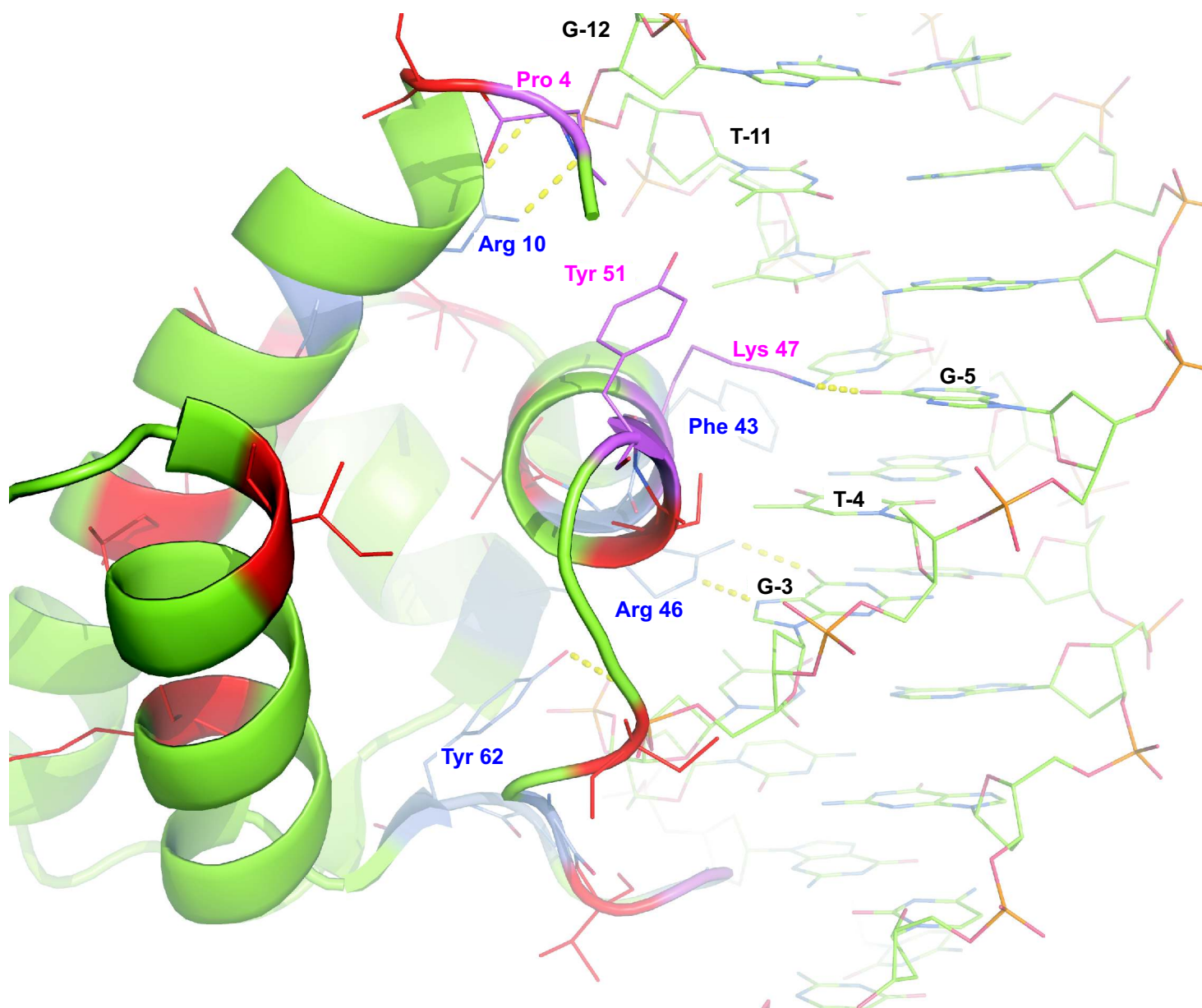


Figure S4. Correlated residues on the structure of Rex regulator from *Thermus aquaticus* (3IKT). Correlated residues are shown in red; residues contacting with DNA are in blue; correlated residues that are in contact with DNA are in magenta. Some hydrogen bonds are shown by yellow dashes.

Figure S5. Multiple alignments of upstream regions of Rex regulated genes in *Thermotoga* spp.

Candidate Rex-binding sites are highlighted in yellow. Candidate promoter elements (-35 and -10 boxes) are underlined. Transcription start sites and translation initiation codons are in red. Genome abbreviations are *Thermotoga maritima* MSB8 (TM), *Thermotoga neapolitana* DSM 4359 (CTN), *Thermotoga petrophila* RKU-1 (Tpet), *Thermotoga naphthophila* RKU-10 (Tnap), *Thermotoga* sp. RQ2 (TRQ2).

sat (TM1400) upstream region

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-35          -10          TSS
TM1400      TGTTTACACCATCAATGGTCGTTGTATAATATTCCAACACCTCTCAAGATTATAGCAAACAGA-TTTTTGCTTTCTCGTTC-----CTTTTGATAAAATATGCTTCATCCG
CTN_1191    TGTTTACCTCCCTGTGGATCGTTGTATAATATTCCAACATCTTCCAAAATTATAGCAA-----TTCGGAACACACCTTCGGGAGCTTTTGATAAAATATGCTTCACTGA
Tpet_1383   TGTTTACACTGTTCGATGGCCATTGTATAATATTCCAACACCTCTCAAGATTATAGCAAACAGATTTTTTGGTTTCTCGTCT-----CTTTTGATAAAATATGCTTCATCCG
TRQ2_1429   TGTTTACACCATCAATGGTCGTTGTATAATATTCCAACACCTCTCAAGATTATAGCAAACAGA-TTTTTGCTTTCTCGTTC-----CTTTTGATAAAATATGCTTCATCCG
Tnap_1403   TGTTTACACCATCGATGGCCATTGTATAATATTCCAACACCTCTCAAGATTATAGCAAACAGATTTTTTGGTTTCTCGTTC-----CTTTTGATAAAATATGCTTCATCCG
*****          * * ***** ** *** ***** ** * * *****

                Rex-site                                start
TM1400      TCTGTAAAAATTCTGGTAGTATAATTAGTTAAAAAATAACAAGCACCACCATCCTGGAAAGGGGGAGTTCCATG
CTN_1191    TTTGTAAAAATACCGTGGTATAATTAGTTAAAAAATAACAAGCACCACCATCCTGGAAAGGGGGAGTTCCATG
Tpet_1383   TCTGTAAAAATTCTGGTAGTATAATTAGTTAAAAAATAACAAGCACCACCATCCTGGAAAGGGGGAGTTCCATG
TRQ2_1429   TCTGTAAAAATTCTGGTAGTATAATTAGTTAAAAAATAACAAGCACCACCATCCTGGAAAGGGGGAGTTCCATG
Tnap_1403   TCTGTAAAAATTCTGGTAGTATAATTAGTTAAAAAATAACAAGCACCATCATCCTGGAAAGGGGGAGTTCCATG
* ***** * *** ***** *****

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TM1586 upstream region

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                Rex-site
-35          -10          TSS
TM1586      TTTTGGAAATTCGTCTTCGAAAAGAGTAAAATATTTCACAAGGAACGACCTGGTTCCCGTGCTCTCGTAGAGTTCCTCGGGAAAATCCACCGAGAGCGGCACAAGATACAGGAAA
Tnap_1222   TTTTGGAAATTCGTCTTCGAAAAGAGTAAAATATTTCACAAGGAACGACCTGGTTCCCGTGCTCTCGTAGAGTTCCTCGGGAAAATCCACCGAGAGCGGCACAAGATACAGGAAA
Tpet_1206   TTTTGGAAATTCGTCTTCGAAAAGAGTAAAATATTTCACAAGGAACGACCTGGTTCCCGTGCTCTCGTAGAGTTCCTCGGGAAAATCCACCGAGAGCGGCACAAGATACAGGAAA
TRQ2_1249   TTTTGGAAATTCGTCTTCGAAAAGAGTAAAATATTTCACAAGGAACGACCTGGTTCCCGTGCTCTCGTAGAGTTCCTCGGGAAAATCCACCGAGAGCGGCACAAGATACAGGAAA
*****

                start
TM1586      TCCCCAAAAGAAATTGAAAGCAGAACAGAAACAATCAAAAAGCCAGTGATTTTCTCACGTCGCTCACCCCGGAGGTGGTAGAGGTG
Tnap_1222   GATCCAAAAGAAATTGAAAGCAGAACAGAAACAATCAAAAAGCCAGTGATTTTCTCACGTCGCTCACCCCGGAGGTGGTAGAGGTG
Tpet_1206   GATCCAAAAGAAATTGAAAGCAGAACAGAAACAATCAAAAAGCCAGTGATTTTCTCACGTCGCTCACCCCGGAGGTGGTAGAGGTG
TRQ2_1249   TCCCCAAAAGAAATTGAAAGCAGAACAGAAACAATCAAAAAGCCAGTGATTTTCTCACGTCGCTCACCCCGGAGGTGGTAGAGGTG
*****

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gldA (TM0423) upstream region

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-35 Rex-site -10 TSS start
TM0423      CTTCGTGAAAAATTTAACAAATTAAGGTTGATAATAATGGTAGGGAGGTGATAATCATG
CTN_0247    CATTGTGAAATACGTAACATGTAGGTTTAAAATGGAACCGGGAGGTGAT-GTGATG
Tpet_0498   CTTCGTGAAAAATTTAACAAATTAAGGTTGATAATAATGGTAGGAGGTGATAATCATG
TRQ2_0522   CTTCGTGAAAAATTTAACAAATTAAGGTTGATAATAATGGTAGGAGGTGATAATCATG
* * ***** * ***** ** ***** * *** ***** * ***

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TM1420 upstream region

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-35          Rex1-site      -10          TSS          Rex-site          start
TM1420      TTTACAAAACTTGTGAAGTAGGTAACAACATAGAGCATTCCTTGACTTCTCCTGAAAATAGTGAAAAATATAACGTGAAAAGGTTACGATTTGAAAGGAACGATGGACATG
Tpet_1372   TTTACAAAACTTGTGAAGTAGGTAACAACATATATCACTCCCTTGACTTCTCCTGAAAATAGTGAAAAATATAACGTGAAAAGGTTACGATTTGAAAGGAACGATGGACATG
Tnap_1390   TTTACAAAACTTGTGAAGTAGGTAACAACATATATCACTCCCTTGACTTCTCCTGAAAATAGTGAAAAATATAACGTGAAAAGGTTACGATTTGAAAGGAACGATGGACATG
TRQ2_1314   TTTACAAAACTTGTGAAGTAGGTAACAACATATATCACTCCCTTGACTTCTCCTGAAAATAGTGAAAAATATAACGTGAAAAGGTTACGATTTGAAAGGAACGATGGACATG
CTN_1072    TTTACTTTTCTTTGTGAATACAGTAACAACATGGTGTACTCCCTTGACTTTTGTCGAAAAATAGTGAAAAATATAACGTGAAAAGGTTACGATTTGAGGAAAACCACCGATG
          *****          *****          * *****          *****          *          *****          ***

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TM1814 upstream region

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-35          -10          TSS          Rex-site          start
TM1814      AAAAAAAGGATAG-----TATGCAA-----AGAAAATTTTAATGATAAAATTATCACAAAGACATCCAAGGGGGAAACAGTATG
Tpet_1099   AAAAAAAGGATAG-----TATGCAA-----AGAAAATTTTAATGATAAAATTATCACAAAGACATCCAAGGGGGAAACAGTATG
Tnap_1013   AAAAAAAGGATAG-----TATGCAA-----AGAAAATTTTAATGATAAAATTATCACAAAGACATCCAAGGGGGAAACAGTATG
TRQ2_1007   AAAAAAAGGATAG-----TATGCAA-----AGAAAATTTTAATGATAAAATTATCACAAAGACATCCAAGGGGGAAACAGTATG
CTN_0700    AAAGTACGGAGGGAGGGCCTTCCCTTCTTACGTGCAACTTATTACCGTTTCTTGGTGGACAAAATGATAAAATTATCACAA-----AAAGGGGGTGTGGTATG
          *** * *** *          *****          * *          *****          ** ****          *****

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TM0179 upstream region

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-35          Rex-site      -10          TSS          start
TM0179      TTTTTTATAGATCACCTTTTGTTATAATAGTAACAAGGGGGTGATCTCGTG
CTN_0508    TCTTTCAGAGCCCTTTTGTTATAATGATATCAAGGGGGTGATCCAGTG
Tnap_0810   TTTTTTATAGATCACA-TTTTGTTATAATAGTAACAAGGGGGTGATCTCATG
Tpet_0745   TTTTTTATAGATCACCTTTTGTTATAATAGTAACAAGGGGGTGATATCGTG
TRQ2_0769   TTTTTTATAGATCACCTTTTGTTATAATAGTAACAAGGGGGTGATCTCGTG
          * *** *          * *          *****          ** *****          **

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TM0983 upstream region

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-35          Rex-site      -10          TSS          Rex-site          start
TM0983      ATATCGTAATATTATTCAACGTCTATGTAACATTAGAATATTATTTTCACGAGGATTGAGA-TTTTTTTCACAAAAACTCAAGGGGAGGTGTGCAGTATG
Tpet_1758   ATATCGTAACATTATTCAACGTCTATGTAACATTAGAATATTATTTTCACGAGGATTGAGA-TTTTTTTCACAAAAACTCAAGGGGAGGTGTGCGGTATG
TRQ2_1812   ATATCGTAACATTATTCAACGTCTATGTAACATTAGAATATTATTTTCACGAGGATTGAGA-TTTTTTTCACAAAAACTCAAGGGGAGGTGTGCGGTATG
Tnap_1770   ATATCGTAACATTATTCAACGTCTATGTAACATTAGAATATTATTTTCACGAGGATTGAGA-TTTTTTTCACAAAAACTCAAGGGGAGGTGTGCGGTATG
CTN_1595    ATATCGTAATATTATTCAACGTCTATGTAACATTAGAATATTATTTTCACGAGGATTGAGA-TTTTTTTCACAAAAACTCAAGGGGAGGTGTGCAGTATG
          *****          *****          *****          *****          *****          *****

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TM1427(Rex1)	-	-	-	+	+
TM0169 (Rex)	-	+	+	-	-
DNA	+	+	+	+	+
T, °C	37	60	37	60	37

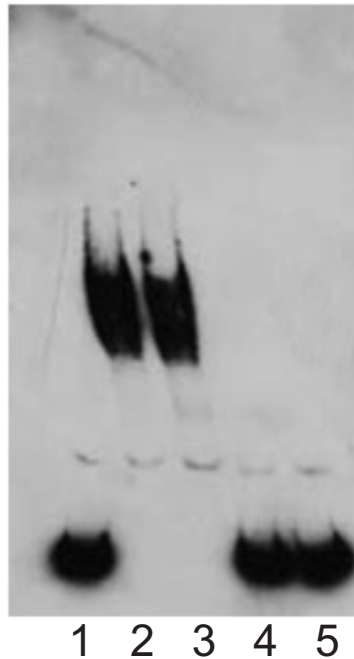


Figure S6. Assessment of interaction between the *T. maritima* Rex (TM0169) and Rex1 (TM1427) proteins with 200-bp DNA fragment containing the promoter region of *TM1420* gene using EMSA.. Concentrations of Rex and Rex1 proteins are 100nM and 1μM, respectively. Concentration of DNA fragment is 0.03nM.

Table S1. Synthetic oligonucleotides containing the *Thermotoga* Rex binding regions used in the binding assays.

Target gene	Fragment used for EMSA or FPA ¹⁾
TM0012 (<i>hycA</i>)	gggggATGTGAAAAAATATCAGgggg t
TM0179	gggggTTGTTATAATAGTAACAAGgggg t
TM0201 (<i>hycD</i>) ²⁾	gggggTTGAGAAATTTATCACAAgggg t
TM0227 (<i>hycE</i>)	gggggTTGTGAAATTTTGGACGAGgggg t
TM0379 (<i>noxE</i>)	gggggTCGTGAAAAATTTCTCTTgggg t
TM0423 (<i>gldA</i>)	gggggTCGTGAAAAATTTAACAAGgggg t
TM0686 (<i>dnaX</i>)	gggggTAGTTATTTTTTTCACGAGgggg t
TM0983	gggggTTGAGATTTTTTTCACAAGgggg t
TM1400 (<i>sat</i>)	gggggTAGTTAAAAAATAACAAGgggg t
TM1420	gggggTAGTGAAAAATATAACGTgggg t
TM1586	gggggGAGTAAAATATTTCACAAgggg t
TM1814	gggggATGATAAAATTATCACAAgggg t
TRQ2_0578-1 (<i>adhE</i>)	gggggGTGAGAAATTTTCACAAGgggg t
TRQ2_0578-2 (<i>adhE</i>)	gggggTTGTTATGAAATTCACAAGgggg t
TM0808 (<i>chiR</i>) ³⁾	gggggAAGTTGTTTGCGGCATGCAACTAgggg t

¹⁾ Rex-binding sites are capitalized. For each DNA fragment, two complimentary single-stranded oligonucleotides have been synthesized by IDT, at that one of these fragments (5'-3' shown here) was labeled by either biotin or 6-carboxyfluorescein at 3' end (marked by blue and red, respectively). All analyzed Rex-binding sites are from *Thermotoga maritima* MSB8, except two sites marked TRQ2_0578 that are from *Thermotoga* sp. RQ2.

²⁾ Fragment was used for both EMSA and FPA, all other fragments were used only for FPA.

³⁾ Negative control DNA fragment, contains a binding site of the chitobiose responsive regulator ChiR (TM0808).

Table S2. Distribution of Rex orthologs in Bacteria

#	Phylum	Class	Order	Family	Organism name	rex gene locus_tag	Reconstructed regulog in RegPrecise
1	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Solibacter usitatus Ellin6076	Acid_6962	-
2	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Janibacter sp. HTCC2649	JNB_09294	Rex - Actinomycetales
	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Nakamurella multipartita DSM 44233	Namu_0919	Rex - Actinomycetales
	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus erythropolis PR4	RER_16400	Rex - Actinomycetales
	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus opacus B4	ROP_17260	Rex - Actinomycetales
	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Saccharomonospora viridis DSM 43017	Svir_02840	Rex - Actinomycetales
	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Saccharopolyspora erythraea NRRL 2338	SACE_6947	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Acidothermaceae	Acidothermus cellulolyticus 11B	Acel_0239	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Actinosynnemataceae	Actinosynnema mirum DSM 43827	Amir_6731	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Brevibacteriaceae	Brevibacterium linens BL2	BlinB01001404	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Catenulisporineae	Catenulispora acidiphila DSM 44928	Caci_8327	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Cellulomonadaceae	Cellulomonas flavigena DSM 20109	Cfla_2738	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Dermacoccaceae	Dermacoccus sp. Ellin185	HMPREF0321_2048	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Frankiaceae	Frankia sp. Ccl3	Francci3_0484	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Frankiaceae	Frankia sp. EAN1pec	Franean1_6132	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Geodermatophilaceae	Geodermatophilus obscurus DSM 43160	Gobs_4581	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Glycomycetaceae	Stackebrandtia nassauensis DSM 44728	Snas_5695	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Gordoniaceae	Gordonia bronchialis DSM 43247	Gbro_1012	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Kineosporiaceae	Kineococcus radiotolerans SRS30216	Krad_0616	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcaceae	Arthrobacter aurescens TC1	AAur_3294	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcaceae	Arthrobacter sp. FB24	Arth_3297	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Micromonosporaceae	Micromonospora aurantiaca ATCC 27029	Micau_5643	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Nocardiaceae	Nocardia farcinica IFM 10152	nfa51710	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Nocardiaceae	Nocardioides sp. JS614	Noca_0493	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Nocardiaceae	Rhodococcus sp. RHA1	RHA1_ro02054	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Nocardioidaceae	Nocardioides sp. JS614	Noca_0493	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Nocardiopsaceae	Thermobifida fusca YX	Tfu_2734	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Promicromonosporaceae	Xylanimonas cellulositytica DSM 15894	Xcel_0440	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Sanguibacteraceae	Sanguibacter keddieii DSM 10542	Sked_07160	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Streptomycetaceae	Streptomyces avermitilis MA-4680	SAV_4738	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Streptomycetaceae	Streptomyces coelicolor A3(2)	SCO3320	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Streptomycetaceae	Streptomyces griseus NBRC 13350	SGR_4154	Rex - Actinomycetales
	Actinobacteria	Actinobacteridae	Actinomycetales	Streptosporangiaceae	Streptosporangium roseum DSM 43021	Sros_0547	-
	Actinobacteria	Actinobacteridae	Actinomycetales	Thermomonosporaceae	Thermomonospora curvata DSM 43183	Tcur_4441	-
3	Bacteroidetes	Bacteroidetes	Bacteroidales	Bacteroidaceae	Bacteroides fragilis NCTC 9343	BF3782	-
	Bacteroidetes	Bacteroidetes	Bacteroidales	Bacteroidaceae	Bacteroides thetaiotaomicron VPI-5482	BT3882	-
	Bacteroidetes	Bacteroidetes	Bacteroidales	Bacteroidaceae	Bacteroides vulgatus ATCC 8482	BVU_1637	-
	Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	Parabacteroides distasonis ATCC 8503	BDI_2578	-
	Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	Porphyromonas gingivalis W83	PG0024	-

4	Chloroflexi	Chloroflexi	Chloroflexales	Chloroflexaceae	Chloroflexus aggregans DSM 9485	Cagg_0157	Rex - Chloroflexi
	Chloroflexi	Chloroflexi	Chloroflexales	Chloroflexaceae	Chloroflexus sp. Y-400-fl	Chy400_3940	Rex - Chloroflexi
	Chloroflexi	Chloroflexi	Chloroflexales	Chloroflexaceae	Herpetosiphon aurantiacus ATCC 23779	Haur_4427	Rex - Chloroflexi
	Chloroflexi	Chloroflexi	Chloroflexales	Chloroflexaceae	Roseiflexus castenholzii DSM 13941	Rcas_1392	Rex - Chloroflexi
	Chloroflexi	Chloroflexi	Chloroflexales	Chloroflexaceae	Roseiflexus sp. RS-1	RoseRS_4103	Rex - Chloroflexi
5	Deinococcus-Ther	Deinococci	Deinococcales	Deinococcaceae	Deinococcus deserti VCD115	Deide_14030	Rex - Deinococcus-Thermus
	Deinococcus-Ther	Deinococci	Deinococcales	Deinococcaceae	Deinococcus geothermalis DSM 11300	Dgeo_0630	Rex - Deinococcus-Thermus
	Deinococcus-Ther	Deinococci	Deinococcales	Deinococcaceae	Deinococcus radiodurans R1	DR0939	Rex - Deinococcus-Thermus
	Deinococcus-Ther	Deinococci	Thermales	Thermaceae	Thermus aquaticus Y51MC23	Taq_4998	Rex - Deinococcus-Thermus
	Deinococcus-Ther	Deinococci	Thermales	Thermaceae	Thermus thermophilus HB27	TTC1293	Rex - Deinococcus-Thermus
6	Dictyoglomi	Dictyoglomia	Dictyoglomales	Dictyoglomaceae	Dictyoglomus thermophilum H-6-12	DICTH_0414	-
7	Elusimicrobia	Elusimicrobia	Elusimicrobiales	Elusimicrobiaceae	Elusimicrobium minutum Pei191	Emin_0756	-
8	Firmicutes	Bacilli	Bacillales	Bacillaceae	Anoxybacillus flavithermus WK1	Aflv_0208	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus amyloliquefaciens FZB42	RBAM_006420	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus cereus ATCC 14579	BC0291	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus clausii KSM-K16	ABC0873	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus halodurans C-125	BH0551	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus licheniformis ATCC 14580	BLI00618	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus pumilus SAFR-032	BPUM_0528	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus subtilis 168	BSU05970	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Geobacillus kaustophilus HTA426	GK0242	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Oceanobacillus iheyensis HTE831	OB0652	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus sp. JDR-2	Pjdr2_2450	Rex - Bacillales
	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Macrocococcus caseolyticus JCSC5402	MCCL_1721	Rex - Staphylococcus
	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus aureus N315	SA1851	Rex - Staphylococcus
	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus capitis SK14	STACA0001_0533	Rex - Staphylococcus
	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus carnosus TM300	Sca_1553	Rex - Staphylococcus
	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus epidermidis ATCC 12228	SEI1647	Rex - Staphylococcus
	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus haemolyticus JCSC1435	SH0986	Rex - Staphylococcus
	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus saprophyticus ATCC 15305	SSP0833	Rex - Staphylococcus
	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus faecalis V583	EF2638, EF2933	-
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus acidophilus NCFM	LBA0398	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus brevis ATCC 367	LVIS_0616	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus casei ATCC 334	LSEI_2245, LSEI_1250	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus delbrueckii subsp. bulgaricus	LBUL_1498	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus fermentum IFO 3956	LAF_0324	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus helveticus DPC 4571	lhv_0416	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus johnsonii NCC 533	LJ0455	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus plantarum WCFS1	lp_0725	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus reuteri JCM 1112	LAR_0341	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus rhamnosus GG	LGG_01260, LGG_02247	Rex - Lactobacillaceae
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus sakei 23K	LSA0356, LSA0848	Rex - Lactobacillaceae

Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus salivarius UCC118	LSL_1214	Rex - Lactobacillaceae	
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Pediococcus pentosaceus ATCC 25745	PEPE_1470	Rex - Lactobacillaceae	
Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Leuconostoc mesenteroides ATCC 8293	LEUM_1774	Rex - Lactobacillaceae	
Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Oenococcus oeni PSU-1	OEOE_1398	Rex - Lactobacillaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus lactis SK11	LACR_1156	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus lactis subsp. lactis II1403	L71932	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus agalactiae 2603V/R	SAG1100	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus dysgalactiae subsp. equisiri	SDEG_0880	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus equi MGCS10565	Sez_1050	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus gallolyticus UCN34	GALLO_1010	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus gordonii CH1	SGO_1228	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus mitis B6	smi_1188	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus mutans UA159	SMU.1053	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus pneumoniae TIGR4	SP_1090	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus pyogenes M1 GAS	SPY1120	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus sanguinis SK36	SSA_1216	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus suis 05ZYH33	SSU05_1069	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus thermophilus CNRZ1066	str1463	Rex - Streptococcaceae	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus uberis 0140J	SUB0845	Rex - Streptococcaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Alkaliphilus oremlandii OHILAs	Clos_2464	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium acetobutylicum ATCC 824	CAC2713	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium bartlettii DSM 16795	CLOBAR_00711, CLOBAR_01830	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium beijerinckii NCIMB 8052	Cbei_0320	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium boltea ATCC BAA-613	CLOBOL_04148	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium botulinum A str. ATCC 3502	CBO3306	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium butyricum 5521	CBY_3040	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium cellulolyticum H10	Ccel_2882	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium difficile 630	CD0171	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium hiranonis DSM 13275	CLOHIR_00042	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium kluyveri DSM 555	CKL_0453	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium leptum DSM 753	CLOLEP_02947	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium nexile DSM 1787	CLONEX_01590	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium novyi NT	NT01CX_0475	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium perfringens ATCC 13124	CPF_2586	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium phytofermentans ISDg	Cphy_0901	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium scindens ATCC 35704	CLOSCI_00613	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium sp. SS2/1	CLOSS21_01144	Rex - Clostridiaceae	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium tetani E88	CTC02428	Rex - Clostridiaceae	
Firmicutes	Clostridia	Thermoanaerobactera	Thermoanaerobacterales	F Caldicellulosiruptor saccharolyticus DSM 1220	CSac_1220	Rex - Thermoanaerobacterales	
Firmicutes	Clostridia	Thermoanaerobactera	Thermoanaerobacteraceae	Thermoanaerobacter ethanolicus CCSD1	TeCCSD1DRAFT_0298	Rex - Thermoanaerobacterales	
Firmicutes	Clostridia	Thermoanaerobactera	Thermoanaerobacteraceae	Thermoanaerobacter tengcongensis MB4	TTE0543	Rex - Thermoanaerobacterales	
9	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Leptotrichia buccalis DSM 1135	Lebu_0168	-

	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Sebaldella termitidis ATCC 33386	Sterm_1177	-
	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Streptobacillus moniliformis DSM 12112	Smon_0374	-
10	Gemmatimonadet	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas aurantiaca T-27	GAU_1881	-
11	Lentisphaerae	Lentisphaerae	Lentisphaerales	Lentisphaeraceae	Lentisphaera araneosa HTCC2155	LNTAR_20783	-
	Lentisphaerae	Lentisphaerae	Victivallales	Victivallaceae	Victivallis vadensis ATCC BAA-548	Vvad_PD0169	-
	Lentisphaerae	Lentisphaerae	Victivallales	Victivallaceae	Victivallis vadensis ATCC BAA-548	Vvad_PD0204	-
12	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfatibacillum alkenivorans AK-01	Dalk_2860	-
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfohalobiaceae	Desulfohalobium retbaense DSM 5692	Dret_2085	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfomicrobiaceae	Desulfomicrobium baculatum DSM 4028	Dbac_2793	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio desulfuricans G20	Dde_2702	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio desulfuricans subsp. desulfu	Ddes_2257	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio magneticus RS-1	DMR_42180	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio piger ATCC 29098	DESPIG_02066	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio salexigens DSM 2638	Desa_3723	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio vulgaris Hildenborough	DVU0916	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio vulgaris Miyazaki F	DvMF_1390	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Lawsonia intracellularis PHE/MN1-00	LI1059	Rex - Desulfovibrionales
	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae	Pelobacter carbinolicus DSM 2380	Pcar_1593	-
	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Syntrophobacteraceae	Syntrophobacter fumaroxidans MPOB	Sfum_1603	-
13	Spirochaetes	Spirochaetes	Spirochaetales	Brachyspiraceae	Brachyspira murdochii DSM 12563	Bmur_1396	-
	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaeaceae	Treponema denticola ATCC 35405	TDE1912	-
14	Synergistetes	Synergistia	Synergistales	Synergistaceae	Aminobacterium colombiense DSM 12261	HMPREF1705_01340	-
	Synergistetes	Synergistia	Synergistales	Synergistaceae	Dethiosulfovibrio peptidovorans DSM 110C	Dpep_1901	-
	Synergistetes	Synergistia	Synergistales	Synergistaceae	Jonquetella anthropi E3_33 E1	GCWU000246_01870	-
	Synergistetes	Synergistia	Synergistales	Synergistaceae	Pyramidobacter piscolens W5455	HMPREF7215_0958	-
	Synergistetes	Synergistia	Synergistales	Synergistaceae	Thermanaerovibrio acidaminovorans DSM	Taci_1219	-
15	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Fervidobacterium nodosum Rt17-B1	Fnod_0423, Fnod_0224	Rex - Thermotogales, Rex1 - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Kosmotoga olearia TBF 19.5.1	Kole_1558	Rex - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Petrotoga mobilis SJ95	Pmob_0343	Rex - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermosipho africanus TCF52B	THA_1697, THA_788	Rex - Thermotogales, Rex1 - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermosipho melanesiensis BI429	Tmel_1209, Tmel_0489	Rex - Thermotogales, Rex1 - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermotoga lettingae TMO	Tlet_0332, Tlet_0951	Rex - Thermotogales, Rex1 - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermotoga maritima MSB8	TM0169, TM1427	Rex - Thermotogales, Rex1 - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermotoga naphthophila RKU-10	Tnap_0799, Tnap_1384	Rex - Thermotogales, Rex1 - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermotoga neapolitana DSM 4359	CTN_0518, CTN_1066	Rex - Thermotogales, Rex1 - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermotoga petrophila RKU-1	Tpet_0756, Tpet_1366	Rex - Thermotogales, Rex1 - Thermotogales
	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermotoga sp. RQ2	TRQ2_0779, TRQ2_1320	Rex - Thermotogales, Rex1 - Thermotogales
16	Verrucomicrobia	Spartobacteria	-	-	Chthoniobacter flavus Ellin428	CfE428DRAFT_5455	-

Organisms with reconstructed Rex regulons (available for view in RegPrecise database) are in bold

Experimentally studies Rex regulators are in red

Rex duplicates are in purple

