

Euryarchaeota													
Archaeoglobi			15,162	38	42	32	5	1	0	0	0	0	4
Archaeoglobus fulgidus DSM 4304	AE000782	224325	2400	13	12	9	1	1	0	0	0	0	1
Archaeoglobus profundus DSM 5631	CP001857	572546	1818	3	7	4	1	0	0	0	0	0	2
Archaeoglobus sulfaticallidus PM70-1	CP005290	387631	2213	4	5	4	0	0	0	0	0	0	1
Archaeoglobus veneficus SNP6	CP002588	693661	2065	4	3	2	1	0	0	0	0	0	0
Ferroglobus placidus DSM 10642	CP001899	589924	2463	4	4	3	1	0	0	0	0	0	0
Geoglobus acetivorans SBH6	CP009552	565033	2,218	5	8	7	1	0	0	0	0	0	0
Geoglobus ahangari	CP011267	113653	1,985	4	3	3	0	0	0	0	0	0	0
Halobacteria			123,786	745	695	163	35	230	51	11	110	81	14
Halalkalicoccus jeotgali B3	CP002062	795797	3,873	6	14	4	0	2	2	1	2	3	0
Halanaeroarchaeum sulfurireducens HSR2	CP008874	1604004	2,228	27	8	1	1	3	1	0	2	0	0
Haloarcula hispanica ATCC 33960	CP002921	634497	3,865	26	36	3	1	18	6	0	6	2	0
Haloarcula marismortui ATCC 43049	AY596297	272569	4,240	37	45	7	1	21	7	1	6	2	0
Haloarcula sp. CBA1115	CP010529	1592728	3,916	26	36	3	1	19	5	0	6	2	0
Halobacterium hubeiense	LN831302	1407499	3,143	18	19	2	1	6	2	0	6	2	0
Halobacterium salinarum NRC-1	AE004437	64091	2,622	11	8	1	1	2	0	0	3	1	0
Halobacterium sp. DL1	CP007060	751944	3,280	18	17	5	1	4	1	0	4	1	1
Halobiforma lacisalsi AJ5	CP019285	358396	4,097	25	22	8	2	6	0	0	2	4	0
Halodesulfurarchaeum formicicum	CP016804	1873524	2079	15	6	1	1	2	0	0	1	1	0
Haloferax gibbonsii ATCC 33959	CP011947	1227459	3,744	27	24	3	1	10	3	0	2	4	1
Haloferax mediterranei ATCC 33500	CP001868	523841	3,752	22	17	3	1	4	3	0	1	4	1
Haloferax volcanii DS2	CP001956	309800	4,042	15	22	4	1	8	4	1	2	1	1
Halogeometricum borinquense DSM 11551	CP001690	469382	3,898	21	25	4	1	8	3	1	3	3	2
Halomicrobium mukohataei DSM 12286	CP001688	485914	3,349	21	25	3	1	8	1	0	9	1	2
Halopiger xanaduensis SH-6	CP002839	797210	4,221	26	18	10	2	2	0	0	2	2	0
Haloquadratum walsbyi DSM 16790	AM180088	768065	2,560	4	6	1	0	3	0	1	0	1	0
Halorhabdus tiamatea SARL4B	HF571520	1033806	3,023	18	17	4	1	7	0	0	4	1	0
Halorhabdus utahensis DSM 12940	CP001687	519442	2,998	31	29	4	1	11	4	0	7	2	0

Methanothermobacter marburgensis str. Marburg	CP001710	79929	1,757	11	11	1	0	5	1	0	0	0	4
Methanothermobacter sp. CaT2	AP011952	866790	1,725	12	10	1	0	4	0	0	0	0	5
Methanothermobacter thermautotrophicus str. Delta H	AE000666	187420	1,873	13	10	1	0	3	2	0	0	0	4
Methanothermobacter wolfeii	LT608329	145261	1,665	14	10	1	0	3	2	0	0	0	4
Methanothermus fervidus DSM 2088	CP002278	523846	1,285	0	0	0	0	0	0	0	0	0	0
Methanococci			19,966	19	23	15	8	0	0	0	0	0	0
Methanocaldococcus bathoardescens	CP009149	1301915	1,637	1	2	1	1	0	0	0	0	0	0
Methanocaldococcus fervens AG86	CP001696	573064	1,581	2	3	2	1	0	0	0	0	0	0
Methanocaldococcus infernus ME	CP002009	573063	1,442	1	2	1	1	0	0	0	0	0	0
Methanocaldococcus jannaschii DSM 2661	L77117	243232	1,786	0	0	0	0	0	0	0	0	0	0
Methanocaldococcus sp. FS406-22	CP001901	644281	1,816	1	1	1	0	0	0	0	0	0	0
Methanocaldococcus vulcanius M7	CP001787	579137	1,742	1	2	1	1	0	0	0	0	0	0
Methanococcus aeolicus Nankai-3	CP000743	419665	1,490	1	1	1	0	0	0	0	0	0	0
Methanococcus maripaludis S2	BX950229	402880	1,722	3	3	2	1	0	0	0	0	0	0
Methanococcus vannielii SB	CP000742	406327	1,678	5	3	2	1	0	0	0	0	0	0
Methanococcus voltae A3	CP002057	456320	1,717	2	3	2	1	0	0	0	0	0	0
Methanothermococcus okinawensis IH1	CP002792	647113	1,576	2	3	2	1	0	0	0	0	0	0
Methanotorris igneus Kol 5	CP002737	880724	1,779	0	0	0	0	0	0	0	0	0	0
Methanomicrobia			108,246	998	697	300	33	175	62	20	0	0	107
Methanocella arvoryzae MRE50	AM114193	351160	3,103	45	14	9	1	0	1	0	0	0	3
Methanocella conradii HZ254	CP003243	1041930	2,456	19	9	8	0	0	0	0	0	0	1
Methanocella paludicola SANAE	AP011532	304371	3,004	51	8	6	0	1	0	0	0	0	1
Methanococcoides burtonii DSM 6242	CP000300	259564	2406	26	18	8	1	4	2	1	0	0	2
Methanococcoides methylutens MM1	CP009518	1434104	2,203	27	14	7	0	4	1	1	0	0	1
Methanocorpusculum labreanum Z	CP000559	410358	1,739	1	1	0	0	0	0	0	0	0	1
Methanoculleus bourgensis MS2	HE964772	1201294	2,538	14	7	1	1	4	0	0	0	0	1

Methanoculleus marisnigri JR1	CP000562	368407	2,489	24	10	3	1	4	0	0	0	0	2
Methanoculleus sp. MAB1	LT158599	86622	3,450	15	5	1	1	1	1	0	0	0	1
Methanofollis liminatans DSM 4140	CM001555	28892	2,396	17	20	4	1	9	4	0	0	0	2
Methanohalobium evestigatum Z-7303	CP002069	644295	2,254	28	11	7	1	0	0	0	0	0	3
Methanohalophilus halophilus Z-7982	CP017921	2177	1,987	26	12	7	0	0	1	1	0	0	3
Methanohalophilus mahii DSM 5219	CP001994	547558	1,987	22	13	7	0	2	1	1	0	0	2
Methanolacinia petrolearia DSM 11571	CP002117	679926	2,785	32	30	7	1	10	6	0	0	0	6
Methanolobus psychrophilus R15	CP003083	1094980	2,841	36	20	8	1	5	2	1	0	0	3
Methanomethylovorans hollandica DSM 15978	CP003362	867904	2,525	11	9	4	1	2	1	1	0	0	0
Methanoplanus limicola DSM 2279	CM001436	937775	2,967	32	39	6	1	18	6	0	0	0	8
Methanoregula boonei 6A8	CP000780	456442	2,450	30	63	15	1	22	6	0	0	0	19
Methanoregula formicica SMSP	CP003167	593750	2,816	30	40	5	1	20	8	1	0	0	5
Methanosaeta concilii GP6	CP002565	990316	2,858	8	4	3	0	0	0	0	0	0	1
Methanosaeta harundinacea 6Ac	CP003117	1110509	2,399	2	6	2	0	1	1	1	0	0	1
Methanosaeta thermophila PT	CP000477	349307	1,696	7	4	3	0	0	0	0	0	0	1
Methanosalsum zhilinae DSM 4017	CP002101	679901	1,976	28	9	5	1	0	2	0	0	0	1
Methanosarcina acetivorans C2A	AE010299	188937	4,540	51	17	12	2	2	0	0	0	0	1
Methanosarcina barkeri str. Fusaro	CP000099	269797	3,625	25	12	8	1	1	0	1	0	0	1
Methanosarcina horonobensis HB-1 = JCM 15518	CP009516	1434110	4,095	67	23	17	1	3	0	1	0	0	1
Methanosarcina lacustris Z-7289	CP009515	1434111	3,264	18	10	7	1	0	0	1	0	0	1
Methanosarcina mazei Go1	AE008384	192952	3,371	33	15	10	2	1	0	1	0	0	1
Methanosarcina siciliae C2J	CP009508	1434118	4,401	43	17	11	2	2	0	1	0	0	1
Methanosarcina sp. 795	CP011449	1653396	2,416	15	14	10	1	0	0	1	0	0	2
Methanosarcina sp. Kolksee	CP009524	1434099	3,476	21	15	11	1	1	0	1	0	0	1
Methanosarcina sp. MTP4	CP009505	1434100	3,250	28	16	13	1	1	0	0	0	0	1
Methanosarcina sp. WH1	CP009504	1434102	3,198	22	15	11	1	1	0	1	0	0	1
Methanosarcina sp. WWM596	CP009503	1434103	3,408	22	16	11	1	1	0	1	0	0	2
Methanosarcina thermophila CHTI-55	CP009502	1434121	2,545	21	16	11	1	1	0	2	0	0	1

Thaumarchaeota			36,321	175	224	172	7	1	0	1	0	0	43
Candidatus Caldiarchaeum subterraneum	BA000048	311458	1,730	0	0	0	0	0	0	0	0	0	0
Candidatus Nitrocosmicus oleophilus	CP012850	1353260	3,725	22	24	16	0	0	0	0	0	0	8
Candidatus Nitrosoarchaeum limnia SFB1	CM001158	1007084	2,038	26	33	28	1	1	0	0	0	0	3
Candidatus Nitrosomarinus catalina	CP021324	1898749	1,677	0	1	0	0	0	0	0	0	0	1
Candidatus Nitrosopelagicus brevis	CP007026	1410606	1,445	0	0	0	0	0	0	0	0	0	0
Candidatus Nitrosopumilus adriaticus	CP011070	1580092	2,184	22	34	28	1	0	0	0	0	0	5
Candidatus Nitrosopumilus koreensis AR1	CP003842	1229908	1,890	12	15	12	0	0	0	0	0	0	3
Candidatus Nitrosopumilus piranensis	CP010868	1582439	2,161	2	3	1	0	0	0	0	0	0	2
Candidatus Nitrosopumilus sediminis	CP003843	1229909	1,974	6	9	5	0	0	0	0	0	0	4
Candidatus Nitrososphaera evergladensis SR1	CP007174	1459636	3,499	19	19	12	1	0	0	0	0	0	6
Candidatus Nitrososphaera gargensis Ga9.2	CP002408	1237085	3,565	19	31	25	1	0	0	0	0	0	5
Candidatus Nitrosotalea devanaterrea	LN890280	1078905	2103	19	19	16	1	0	0	0	0	0	2
Candidatus Nitrosotenuis cloacae	CP011097	1603555	1,717	6	15	12	1	0	0	0	0	0	2
Cenarchaeum symbiosum A	DP000238	414004	2,017	0	0	0	0	0	0	0	0	0	0
Nitrosopumilus maritimus SCM1	CP000866	436308	1,795	12	10	9	0	0	0	0	0	0	1
Nitrososphaera viennensis EN76	CP007536	926571	2801	10	11	8	1	0	0	1	0	0	1
unclassified Archaea			5,604	0	0	0	0	0	0	0	0	0	0
archaeon GW2011_AR10	CP010424	1579370	1,339	0	0	0	0	0	0	0	0	0	0
archaeon GW2011_AR15	CP010425	1579373	1,308	0	0	0	0	0	0	0	0	0	0
archaeon GW2011_AR20	CP010426	1579378	1,010	0	0	0	0	0	0	0	0	0	0
Uncultured archaeon clone ASS_A1	CP009479	115547	1,947	0	0	0	0	0	0	0	0	0	0
TOTAL	218		511,588	2,139	1,875	740	102	445	141	33	110	81	222

^a – Based in its 16S rRNA sequence, halophilic archaeon DL31 belongs to the family *Halorubraceae*, class *Halobacteria*.

Table S5. Details of the sequence analysis of the newly described archaeal domains

Domain name	Query ID (GenBank entry, aa boundaries)	Program used ^a	Hit ID and its annotation	HHpred probability (Pr) or PSI-BLAST E-value (E)	Comment
AcidOD1	MSA of four sequences related to ADD08891.1 (122-194 aa)	HHpred	PDB: 4UN1_A; Putative transcriptional regulator, AsnC family (126-165 aa)	Pr= 71.79	Partial overlap with the ligand binding domain of the Lrp/AsnC family regulators
HalOD2	ACV46423.1 (114-195 aa)	HHpred	PF08663.9, HalX domain	Pr=85.79	A HalX-related domain, followed by a Zn-finger
	ACV46423.1 (196-253 aa)	HHpred	PF13240.5, Zinc-ribbon domain	Pr=96.38	
MetOD1	AAM05831.1 (133-292 aa)	HHpred	PDB: 5FRW_A; Phenol-responsive sensory domain of PoxR. TIGR02019; BchJ; Bacteriochlorophyll 4-vinyl reductase	Pr=98.52	Related to the V4R (PF02830) hydrocarbon-binding domain
MetOD3	ABS55483.1 (20-200 aa)	TMHMM	Transmembrane helix, at positions 174..196		Membrane-anchored Ig-like domain, possibly involved in sugar binding (lectin-like). Ig-like domains are often seen in membrane- and S-layer-associated proteins
		HHpred	PF10648.8, Gmad2; Immunoglobulin-like domain of bacterial spore germination	Pr=53.38	
NitrOD1	AFS82515.1 (114-198 aa)	PSI-BLAST	KEQ56625.1, AsnC family transcriptional regulator protein	E=0.67	Related to the ligand binding domain of the Lrp/AsnC family regulators
NitrOD2	AIC16890.1 (1-100 aa)	PSI-BLAST, HHPred	AFU59294.1, hypothetical protein Ngar_c23690	E=0.023	Second iteration of the PSI-BLAST (with E=0.1 inclusion threshold) returns a hit to the Ngar_c23690 protein. When Ngar_c23690 is used as query for an HHpred search, it reveals similarity with the DUF3227 domain (Pr= 88.03%), which was recently shown to belong to the archaeal Death domain-like family (1)
NitrOD3	AIF83507.1 (1-142 aa)	HHpred	PDB: 3KYE_A; Roadblock/LC7 domain	Pr= 68.3	Related to the Roadblock/LC7 domain, expansion in Thaumarchaea
NitrOD4	AFS80878.1 (1-96 aa)	PSI-BLAST	AFU59889.1, hypothetical protein Ngar_c29710 (194-263 aa)	E=0.003	Second iteration of the PSI-BLAST returns a hit to the Ngar_c29710 protein. When used as query for HHpred, this protein reveals similarity with the DUF3227 family (Pr=97%), which was recently shown to belong to the archaeal Death domain-like family (1)

NitrOD5	ABX12603.1 (127-216 aa)	HHpred	PF11537.7; Protein of unknown function (DUF3227)	Pr=95.52	DUF3227 family was shown to belong to archaeal Death domain-like family (1)
TackOD1	AFS80801.1 (126-318 aa)	HHPred	PDB: 2JNE_A; <i>E. coli</i> Yfgj bound to two Zn ⁺² . PF12773; Double zinc ribbon domain	Pr=97.56	Similar to the Double zinc ribbon (PF12773) domain, in bacteria often fused to the GGDEF (diguanylate cyclase) domains

^a - PSI_BLAST searches were run against NCBI's non-redundant protein database with the following parameters: inclusion threshold E= 0.01; taxonomy restriction: "archaea" only; no low complexity filtering; composition based statistics: off, unless stated otherwise in comments. HHpred was run with default parameters with three HHblits iterations, against PDB, Pfam and CDD database. TMHMM 2.0 was run with default parameters.

Reference

1. **Makarova KS, Galperin MY, Koonin EV.** 2017. Proposed role for KaiC-like ATPases as major signal transduction hubs in Archaea. mBio01959-17, in press.

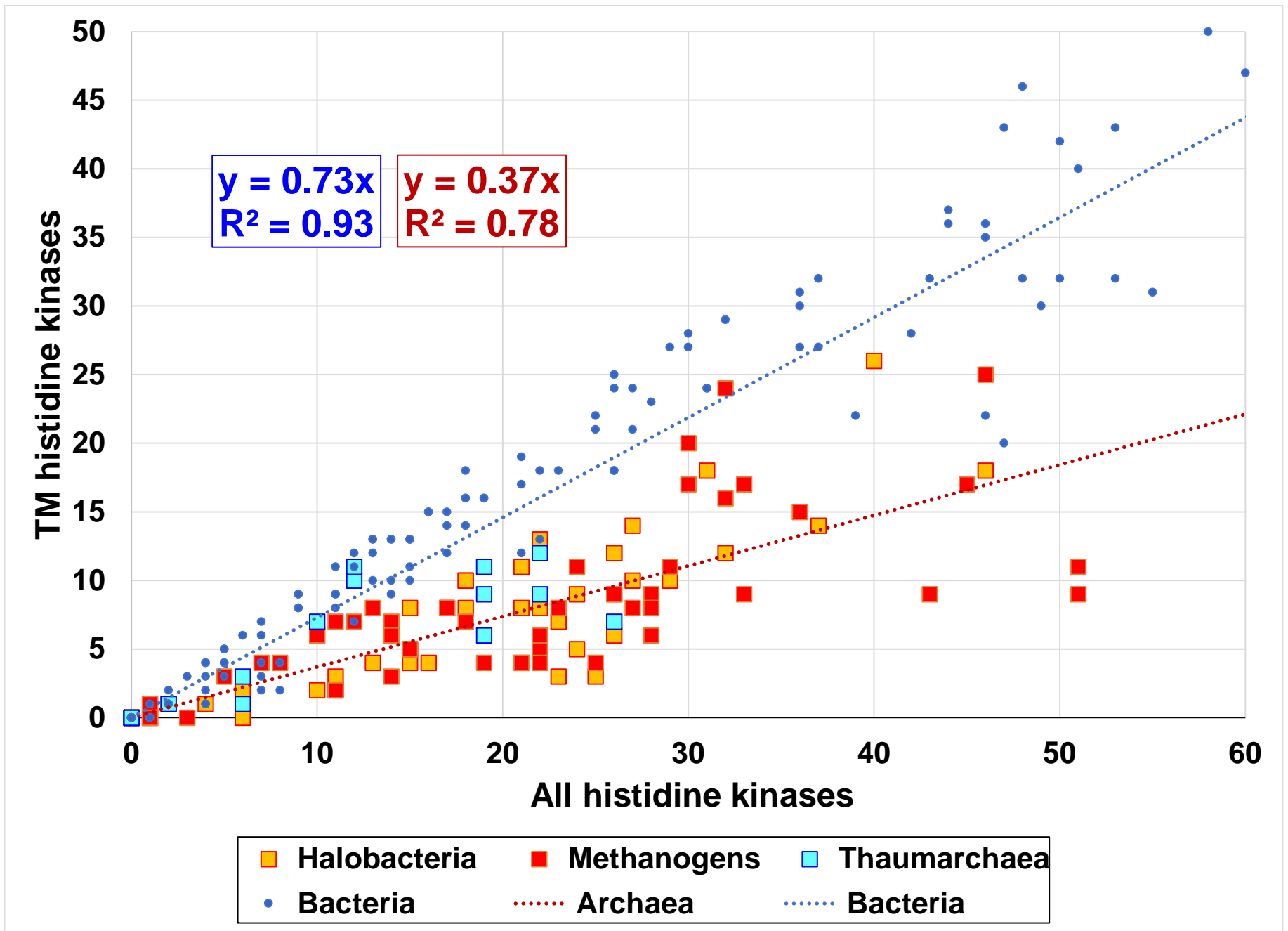


Figure S1. Transmembrane histidine kinase content in bacteria and archaea

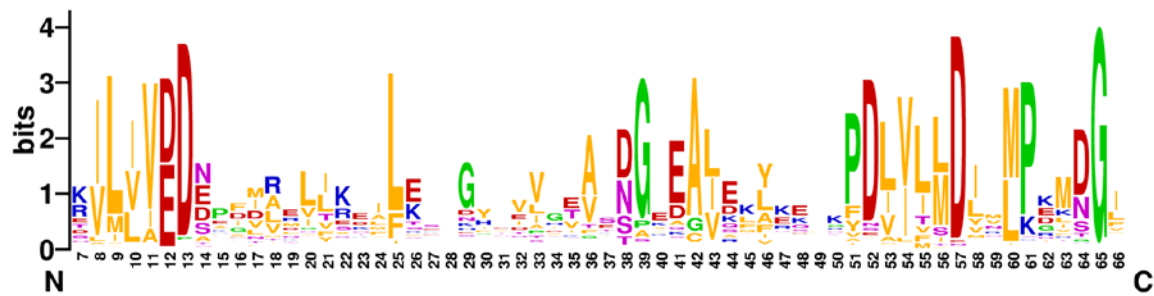
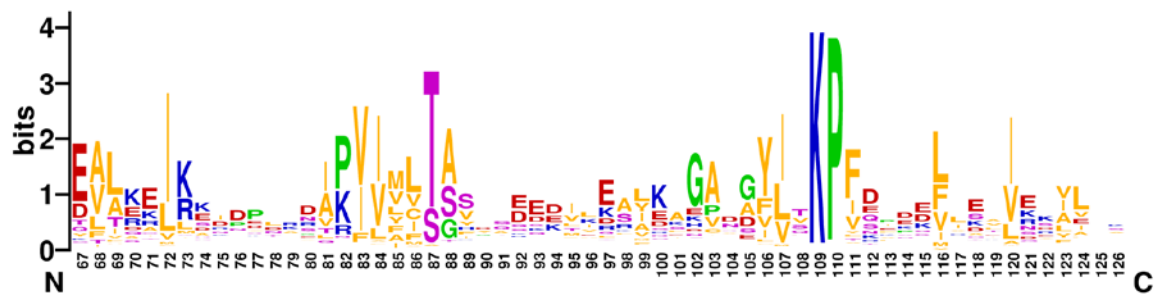
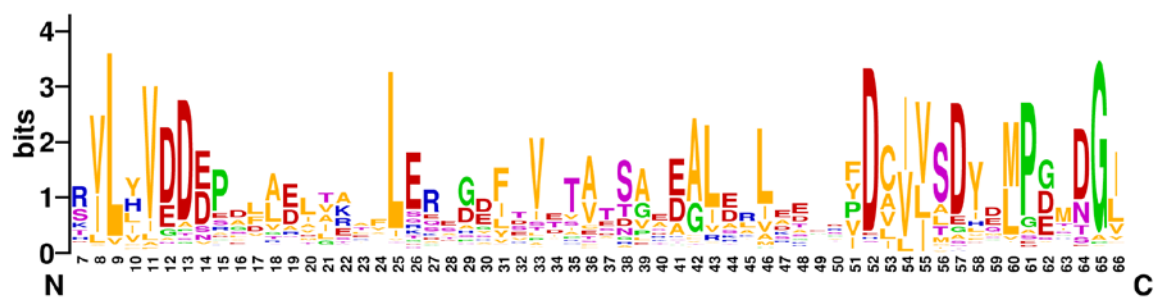
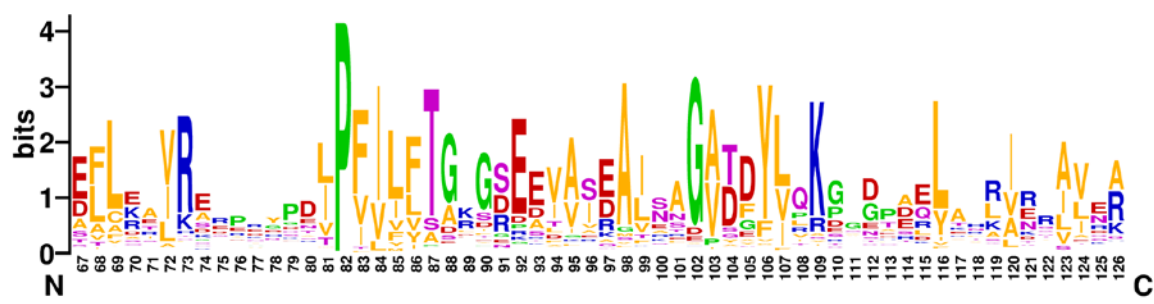
A**C****B****C****C****C**

Figure S2. Sequence conservation in archaeal receiver domains.

A, response regulators with stand-alone REC domains;
 B, REC domains of the response regulators with the REC-(PAS/GAF)_n-HisKA-HATPase domain architectures

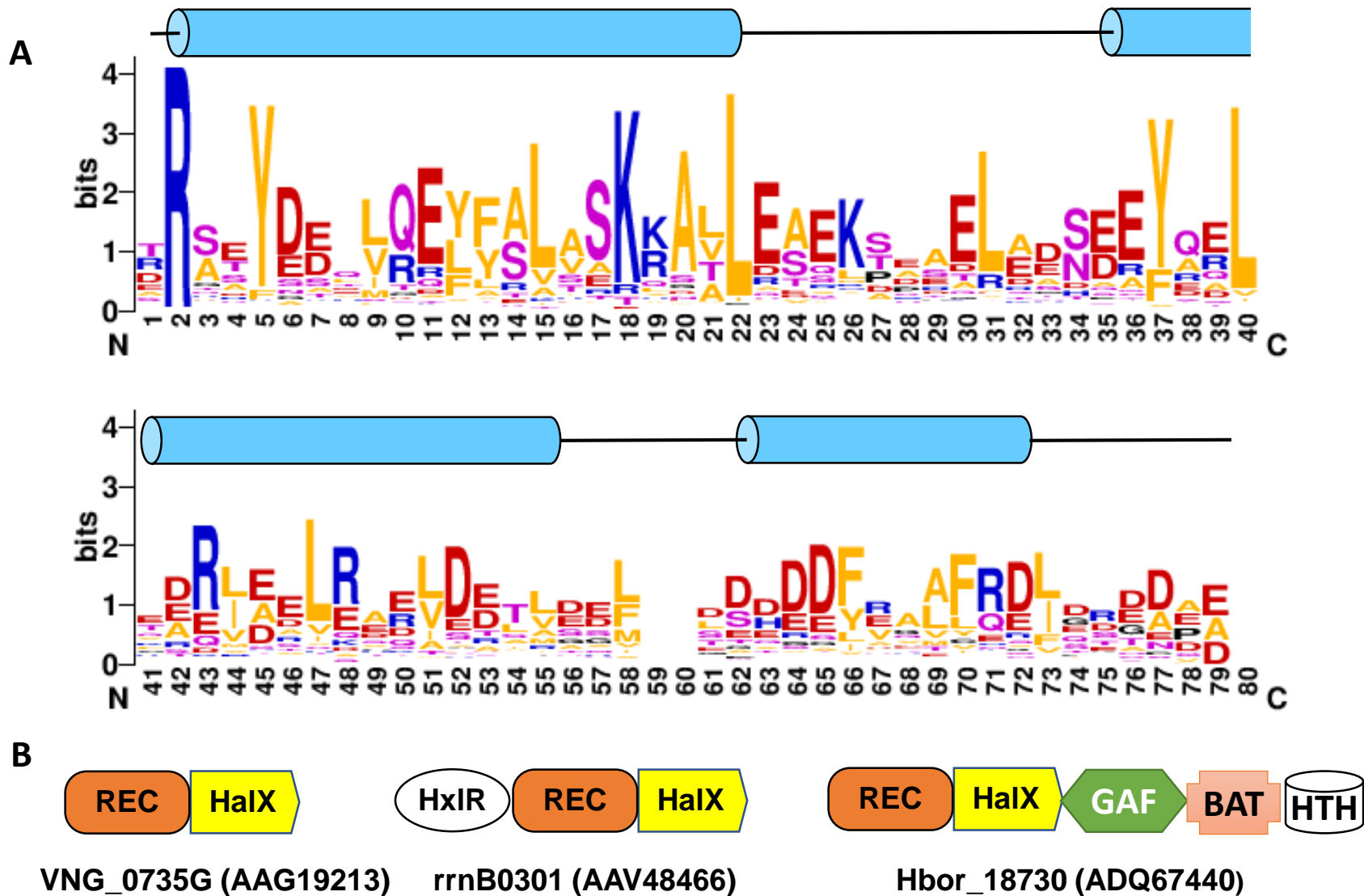


Figure S3. Sequence conservation and domain architectures of the HalX (PF08663) domain.
 A. Sequence logo of HalX, blue cylinders on top indicate α -helices predicted by the JPred program.
 B. Examples of HalX domain architectures

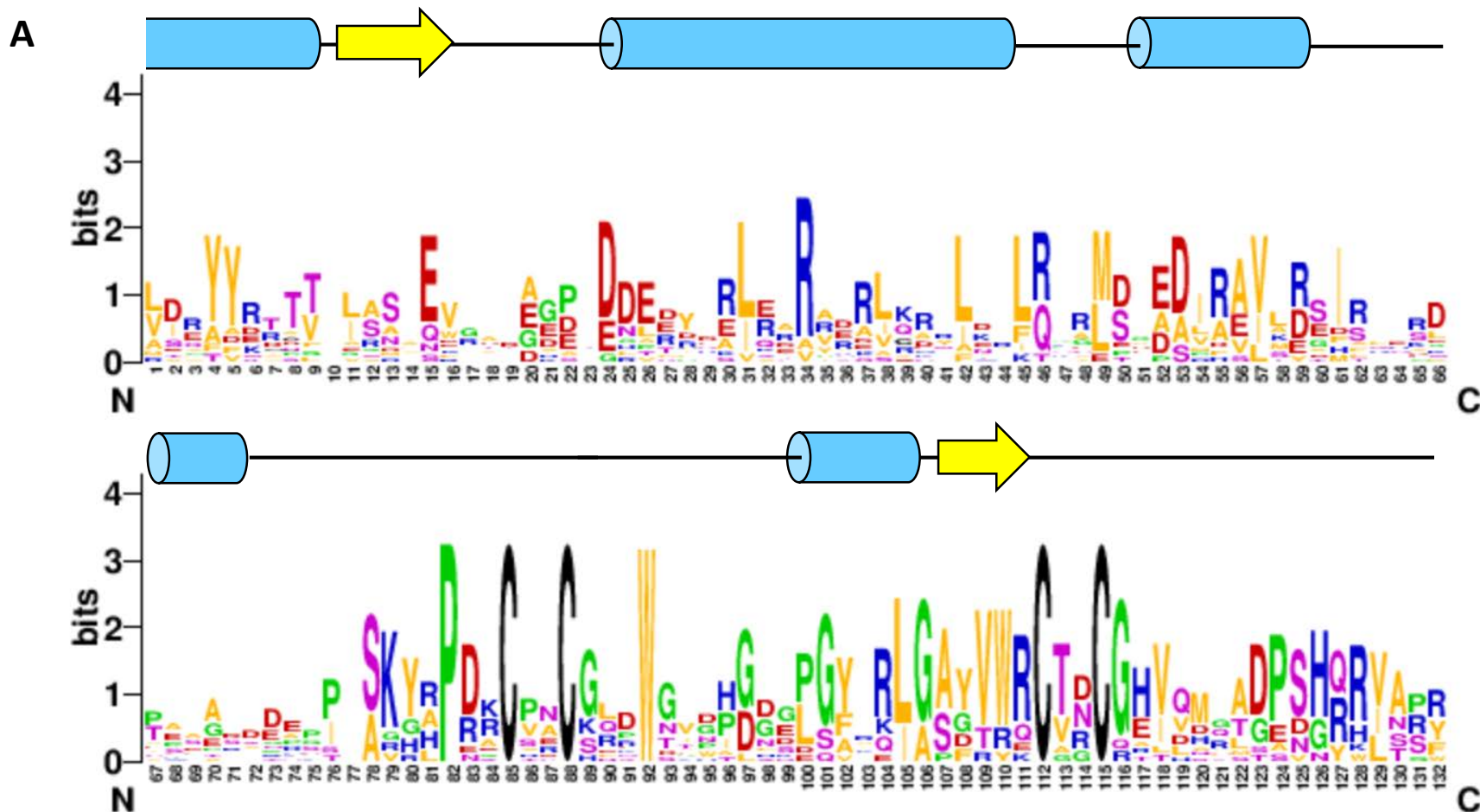


Figure S4. Sequence conservation in the HalOD2 domain. Residue numbering is based on the sequence of the response regulator Hmuk_0286 from *Halomicrobium mukohataei*. Logo position 1 corresponds to Leu122 of Hmuk_0286 (GenBank: ACV46423). Blue cylinders and yellow arrows indicate α -helices and β -strands, respectively, predicted by the JPred program.

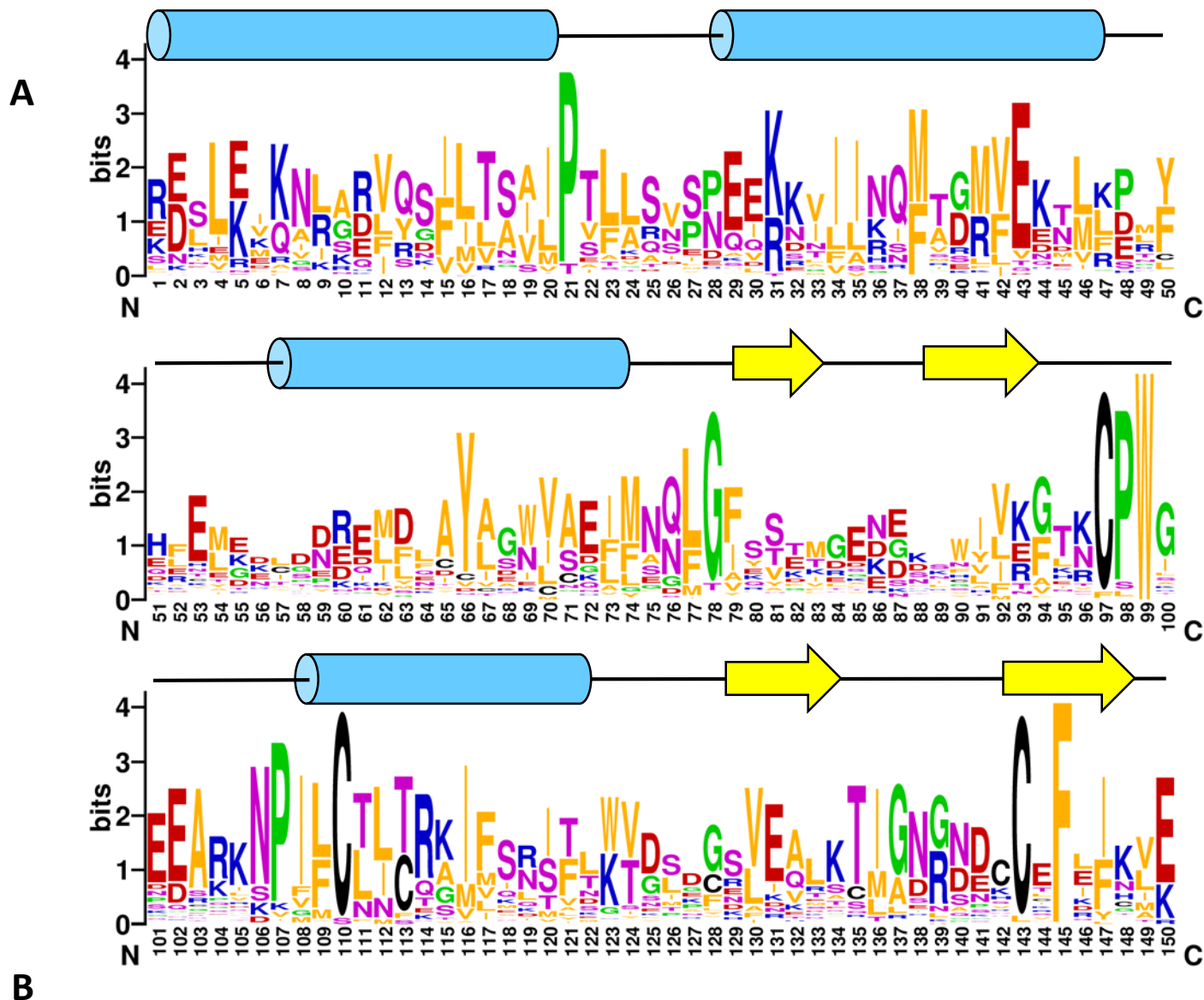


Figure S5. Sequence conservation of the MetOD1 domain and its domain combinations. The residue numbering is based on the sequence of MTH_447, the first position corresponds to the Lys128 of the GenBank entry AAB84953

MTH_447 (AAB84953)

MTH_440 (AAB84946)

Metev_2349(ADI75160)

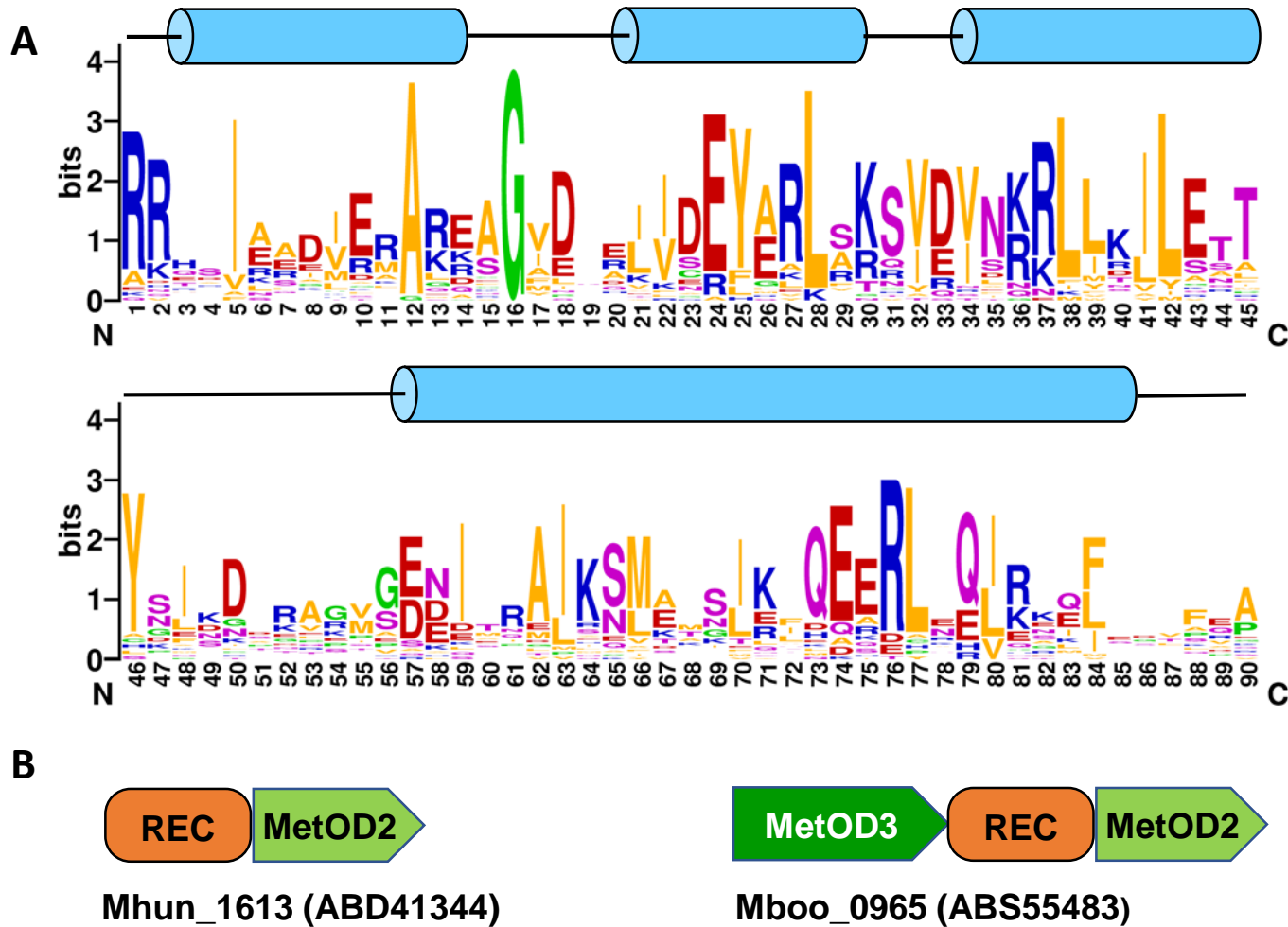


Figure S6. Sequence conservation of the MetOD2 domain and its domain combinations. The residue numbering is based on the sequence of Mhun_1613, the first position corresponds to Arg124 of the GenBank entry ABD41344. The cylinders on top indicate α -helices predicted by JPred.

A

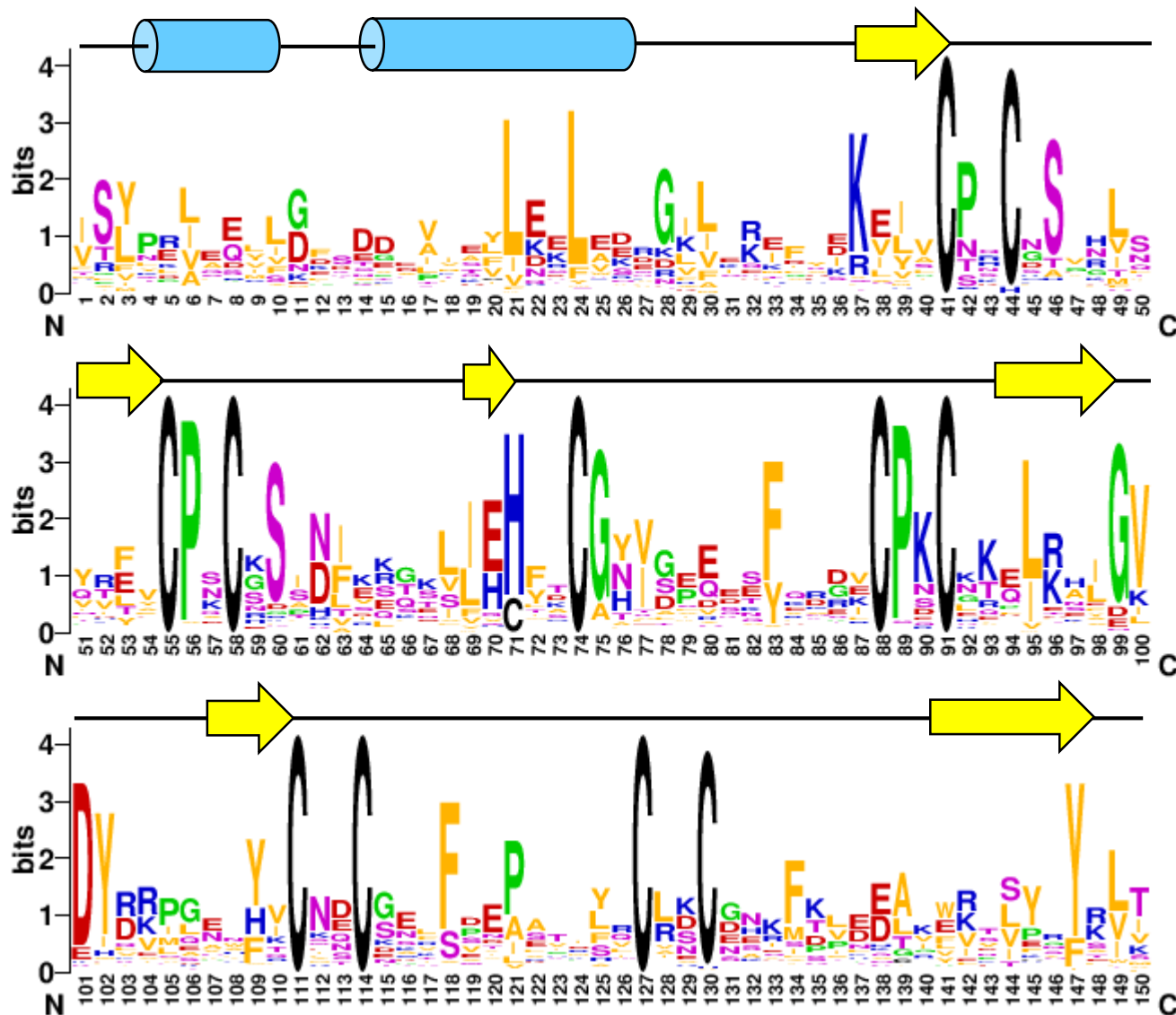


Figure S7. Sequence conservation of the TackOD1 domain. The residue numbering is based on the sequence of NKOR_04565 protein from *Candidatus Nitrosopumilus koreensis* AR1, the first position corresponds to Ile167 of the GenBank entry AFS80801