

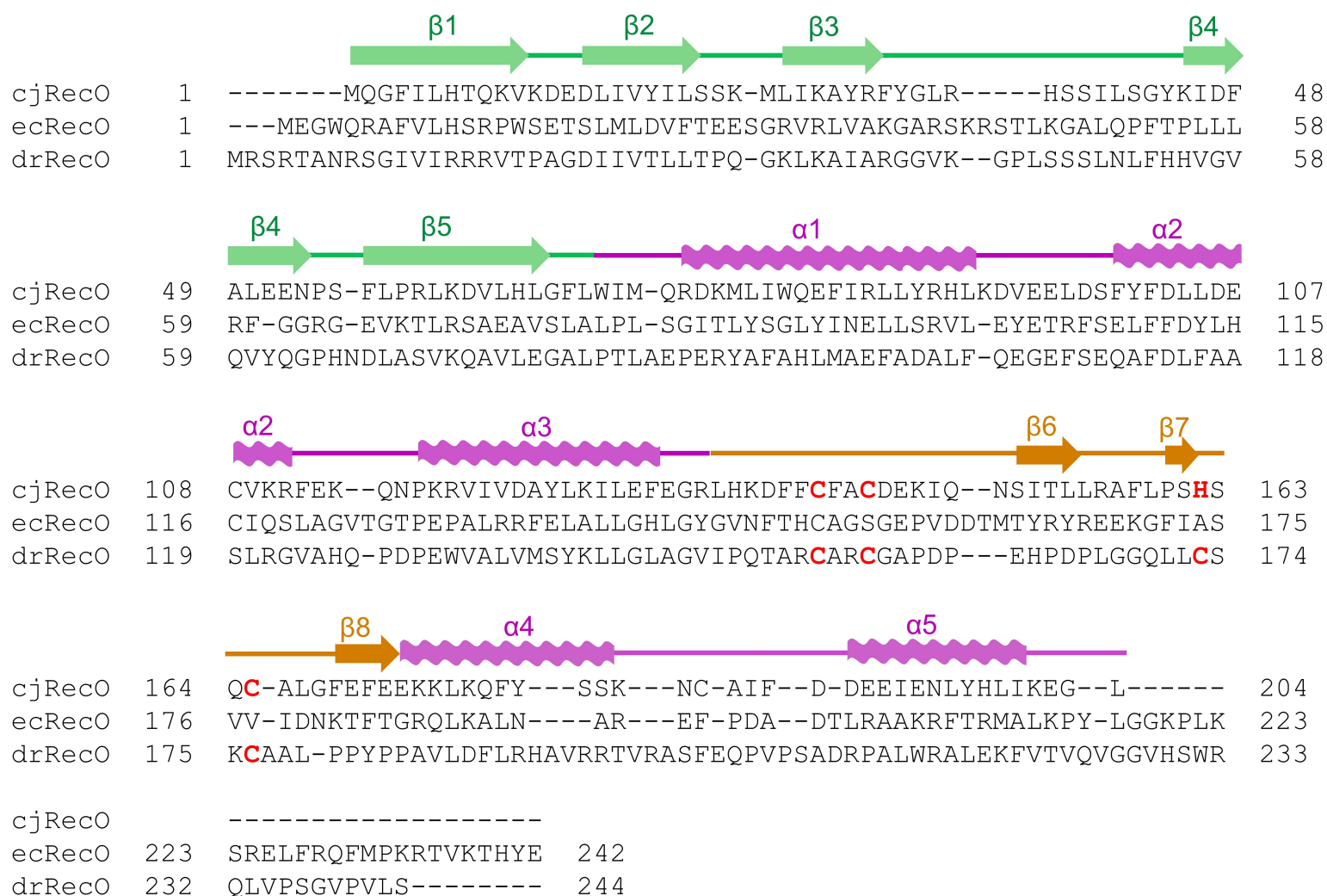
Figure S1

Figure S1. Structure-based sequence alignment of cjRecO, ecRecO, and drRecO. The Zn²⁺-coordinating residues of cjRecO and drRecO are colored red. The secondary structures of cjRecO (α -helices, waves; β -strands, arrows) are shown above the cjRecO sequence in domain-specific colors (NTD, green; CTD, magenta; ZnD, orange). Structure-based sequence alignment was performed using the PROMALS3D program [33].

Figure S2

cjRecO	-----MQGFILHTQKVKDEDLIVYILSSKMLIKAYRFYGLRHSSILSGYKIDFALE	51
hpRecO	-----MQGFLLQTQSIRDEDLIVHILTKNQ LKTL YRFYGRHSVVLNVGRKIDFEE	51
rlRecO	-----MQWQDHAI ILGVKRHGETSV LAEVMTRDRGRHLGLVRSGR SR-----	42
bsRecO	-----MLTKCEGIVLRTNDYGETNKLIVTLL TREHGKIGVMARGAK-KP-----	42
bpRecO	-----MLHSYPYRETS LVIDVL TRDHGRIALVAKGAK-RP-----	34
ecRecO	-----MEGWQRAFVLH SRPWSETS LMLDVFTESGRVRLVAKGAR-SK-----	42
vpRecO	MSNL SAEGFQRCFV LHRRPYSESSLILDVFS EYGRLTLMAGAR-SK-----	47
drRecO	-MRSRTANRSG-IVIRRRVTPAGDIIVTLLTPQ GK-LKAIARGGVKG P-----	45
bbRecO	----MTQGKDRFI ILKKIKYAEADLI IHGLSPRGEKLA FFIARGALKSK-----	44
cjRecO	ENPSFLPRLKDVHLGLFWIMQRDKM--L-----IW	80
hpRecO	NDDKFLPKLRNILLHGYIWEREMERL--F-----FW	80
rlRecO	---AMQFVLQAGNAVEVIWRARLD-EHLGEFRVEPVT LRAARLMETA-----TAVYG	90
bsRecO	-NSRLSAVSQPF LYGSFLMQKTSG---LG-----TLQQGEMILSMRGIREDLFLTAYA	91
bpRecO	-HSALRGVLQTFQPLSLSWSGKSE---LR-----TLTGAEWVGGMLPLAGDALL--CG	81
ecRecO	-RSTLKGALQPFTPLLLRFGGRGE---VK-----TLRSAEAVSLALPLSGITLY--SG	89
vpRecO	-RSNLKGALQPFTPLLLKWSGKGS---MK-----TLRQAEPISLGLPLFGINLY--SA	94
drRecO	-LSSSLNL---FHHVGVQVY-QGPHNDLA-----SVKQAVLEGALPTLAEP-ERYAFA	92
bbRecO	-KRFGGGVLEP THFVTFTYKQANEHGQLN-----VLQEATIVNDFPGLRTDYDRLETA	96
cjRecO	QEFIRLLYRHLKDVEELDSFYFDLLDECVKRFEK--QNPKRVIVDAYLKILEFEGRLHKD	138
hpRecO	QRFCALLFRHLEGVHSLDSIYFDTLDDGASKLSK--QHPLRVVLEMYATLLNFEGRLQSY	138
rlRecO	VQAMGALLRLLPERDPH-PHLFDALEVILDHLHN-PADAGELFVRFELAVLNDLGFGLDL	148
bsRecO	AYVAELVDRGT EKKPN-PYLF EFIEESLKQLNE-GTDPDVITFIVQMKMLGVMGLYPEL	149
bpRecO	FYANELLVKFCAREDPH-PPLFQH YLVTLTRLAH-GEPPVQVLR SFERVLRETGYAMTL	139
ecRecO	LYINELL SRVLEYETRF-SE LFFDYLHC IQSLAGVTGTPEPALRRFELALLGHLGYGVNF	148
vpRecO	MYVNELVGRV LMAEVPM-PALFHDYLHALTELAQ-CENPEPALRRFELALLSSMGYGVDF	152
drRecO	HLMAEFADALFQEGE-FSEQAFDLFAASLRGVAH-QPDPEWVALVMSYKLLGLAGVIPQT	150
bbRecO	LHILECVSKVSQEGDRDSEFLFNLLGNTLKVLES-TPDILVLKMHFY LKFL LQQGVVNAE	155
cjRecO	FFCFACDEKIQNSIT----LLRAFLPSHS-----QCALGF EFEEKKLKQFYS--SK	183
hpRecO	HSCFLCDKKLENSVT----LAQGFIL AHP-----SCLKTKSLDLEKIQAFFR--TQ	183
rlRecO	AECAATGTRSD--LV--YVSPKSGRAVSRAA-GAPWADKMLLLPPFLS-----IE	193
bsRecO	NHCVHC KSQ---DGT FHFVSVRDNGFICHRCFEKDPYRIP- IKPQTARLLRLFY YFDLSRL	205
bpRecO	KRTVA--RRAVEPDKLYVFD-PQHGV RDAGGDA--PSHWPVIAQTLLDMEEDDY-----	189
ecRecO	THCAGSGEPVDDTMTYR YR-EEKGF IASVV-----IDNKTF TGRQLKALNAREF-----	196
vpRecO	LHCAGTGE PVAPEMTYR YR-EQKGF IASVR-----RDNLTF LGNELIAISERRF-----	200
drRecO	ARCARC GAPDPEH----PDPLGGQL LSKCAALPPYP PAVLD-----FLRHAVRRT	197
bbRecO	PWMA PF-----LKTNL-AD SANLISYRQTVDD-----EMYN-VEQM	189
cjRecO	NCAIFDDEEIEN----LYHLIKEGL-----	204
hpRecO	STIDLETEEVEE----LWRTLNLGF-----	204
rlRecO	GNHAADFDLSLAAFRLTGF FLHRHVYEP-----RGIESVAARDGFVQAALKALN	242
bsRecO	GNVSLKEETKAELKQVIDLYEEY-----SGLYLKSKRFLDQME-----	244
bpRecO	----HRAQTVAQSKTLMRFL LNTYL-----GGTPLATRQILIDLQ-----	225
ecRecO	----PDADTLRAAKRFTRMAL KPYL-----GGKPLKSRELFRQFM-----	232
vpRecO	----VTKEQLKA AKRFTRIAL KPYL-----GGKPLKSRELFIQTP-----	236
drRecO	VRASF EQPVPSADRPALWRALEKFVTVQVG VHSWRQLVPSGVPVLS-----	244
bbRecO	VKHYLAN----A---TL-----	199
cjRecO	-----	204
hpRecO	-----	204
rlRecO	PTPRTLSPNGVSA	256
bsRecO	-SMKHLMGENKS--	255
bpRecO	-NL-----	227
ecRecO	-PKRTVKTHYE---	242
vpRecO	-RARSNGK-----	243
drRecO	-----	244
bbRecO	-----	199

Figure S2. Residue type-based sequence alignment of cjRecO, *H. pylori* RecO (hpRecO), *Rhizobium leguminosarum* RecO (rlRecO), *Bacillus subtilis* RecO (bsRecO), *Burkholderia pseudomallei* RecO (bpRecO), ecRecO, *Vibrio parahaemolyticus* RecO (vpRecO), drRecO, and *Bdellovibrio bacteriovorus* RecO (bbRecO). The Zn²⁺-coordinating residues of cjRecO and drRecO are colored red. The residues of RecO orthologs that are identical to those of cjRecO are highlighted by a cyan background. Residue type-based sequence alignment was performed using the Clustal Omega program [34].

Figure S3

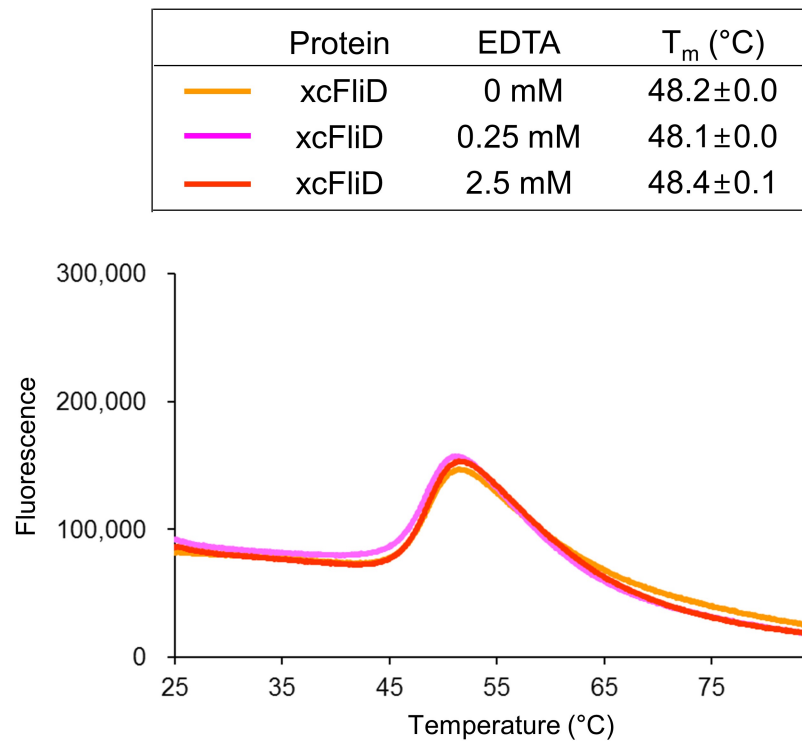


Figure S3. Thermal shift assay of the control protein xcFliD in the absence and presence of EDTA. EDTA did not change the protein stability of xcFliD, which does not have a metal-binding capacity. The data in the figure are representative of three independent experiments that yielded similar results. T_m values are shown as means \pm S.D. from the three independent experiments.

Figure S4

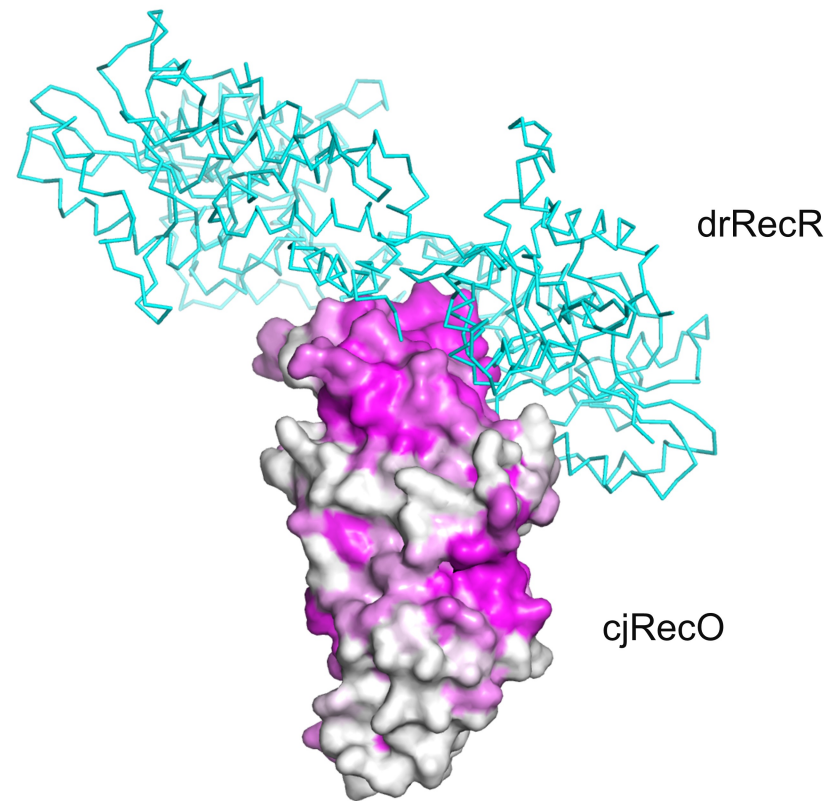


Figure S4. Sequence conservation of RecO proteins on the cjRecO structure in the backside view of Figure 5B. The cjRecO structure is shown as surfaces that represent the sequence conservation of cjRecO orthologs (high sequence conservation, magenta; low sequence conservation, white). The drRecR structure from the drRecO-drRecR complex (PDB ID 4JCV) is depicted as cyan α traces with the cjRecO structure. The RecR-binding region of RecO exhibits high sequence conservation.