

Supplementary Material to the Article

A new thermophilic ene-reductase from the filamentous anoxygenic phototrophic bacterium *Chloroflexus aggregans*

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YqjM	-----MARKLFTPTITIKDMT	15
XenA	-----MSALFEPYTLKDV	14
RmER	-----MPHLFDYRIGNLE	14
DrER	-----MTVSSAAAPQSPAPALFTPLKLSLE	29
RhrER2718	-----VSVLFEPITLRGVT	14
OYERo2	-----MSVLFEPITFRGVT	14
Pfvc	-----MPALFRPLTLRSLE	14
CrOYE1	MGSATKASGSACHVPGAASTAFAQPVRKHQPMRQPLHAVGTPGPSGRPLLFEPTTLRQLT	60
AnabaenaER3	-----MDLFTPLIIRDIT	13
GloeoER	-----MHLFAPLTLRDIT	13
CaOYE	-----MQPHLFTPLTIGSVT	15
FOYE1	-----MSLLFSPYQLGSL	14
ChrOYE3	-----MLYTFVNFNRVE	12
GkOYE	-----MNTMLFSPYTIIRGLT	15
GeoER	-----METMLFSPYTIIRGVT	15
TsOYE	-----MALLFTPLLELGLR	14
TOYE	-----MSILHMLPKIKDIT	14
	*. * : :	
YqjM	LKNRIVMSFMCYSSHEKD---GKLTFFHMAHYISRAIGQVGLIIVEASAVNPQGRITDQ	72
XenA	LRNRRIAIPFMCYMA-ED---GLINDWHQVHYASMARGGAGLLVVEATAVAPEGRITPG	69
RmER	LANRIAIAIPFMCYSA-QE---GNATDWHMIHLGQMALSGAGLLIIEATAVSPEGRITPT	69
DrER	LPNRVVVSFMCYSA-TD---GVANEFHLVHLGQYALGGAGLILAEATAVSPEGRITPE	84
RhrER2718	IPNRVWMAFMCYSAADVIGDQVGVNPNEWHRTHLVSRAGGTGLILTEATAVSPEGRISAA	74
OYERo2	VPNRVWMAFMCYSAADVIGDQVGVNPNEWHRTHLVSRAGGTGLILTEATAVSPEGRISPA	74
Pfvc	LTHRGWVSFMCYSCGPDG---APGVPNWDHMLHLGSAAGGAALILTEAAAVNAAGRISPR	73
CrOYE1	IPNRVWMAFMCYSA-VD---GAPNTWHLVHLGARAAGCGGLVMTETACAVVPEGRISPS	115
AnabaenaER3	LPSRVAMSFMCYSA-EN---GFANDWHFVHLGSRVGGTGLIMVEATAVTPQGRITPG	68
GloeoER	LRNRVAVSFMCYSS-ID---GLANDWHFVHLGSRVGGAGLVIFEAAAVEARGRISPO	68
CaOYE	LRNRIGMSFMCYSA-VD---GFPTDWHMLHLGARAAGGVGLIILEATAVSPEGRISPF	70
FOYE1	LANRLVIAIPFMCYSA-VD---GIAQDWHMLHLGRLAISGAGLVIVEATGVNPEGRITPF	69
ChrOYE3	LKNRVVMSFMCYSS-ED---GLPNDHFHVFHYGSRAGGAGLLIVEATGVEPRGRITNH	67
GkOYE	LKNRIVMSFMCYSCDTKD---GAVRTWHKIHYPARAVGQVGLIIVEATGVTPQGRISER	72
GeoER	LKNRIVMSFMCYSCDTED---GKVRTWHKIHYPARAVGQVGLIIVEATAVTAQGRISAR	72
TsOYE	LKNRLAMSFMCYSATLE---GEVTDWHLLHYPTRALGGVGLIIVEATAVEPLGRISPY	70
TOYE	IKNRIMMSFMCYSASTD---GMPNDWHIVHYATRAIGGVGLIMQETAVESRGRITDH	70
	: * : *** * . * : * * . . : : ** * ***:	
YqjM	DLGIWSDEHIEGFAKLTQVKEQGS---KIGIQLAHAGRKAELE-----G---	114
XenA	CAGIWSDAHAQAFVPVQAIAKAGS---VPGIQIAHAGRKASANRPWE-GDDHIG-ADDA	124
RmER	DLGLYNDANEALGRVLGAVRNHSP--IAVTIQLAHAGRKASSEAPWD-GGGQIRPD-QP	125
DrER	DLGLWDDRIIVPLGHITDFVHQHGG---HIGVQLAHAGRKASTYAPWR-GKGAVPA--EL	138
RhrER2718	DLGIWNTQQAFAEINAQLEYFGA---VPGIQLAHAGRKASTQVPWR-GGKSLP-ADDR	129
OYERo2	DLGIWNTQTEFAEINAQLEYFGA---VPGIQLGHAGRKGSANHPWR-GGGSLD-GDDR	129
Pfvc	DAGLYNDEQAABAWQRITSFVHRHGAEEAKIGQLAHAGRKASTYWPFSGQRGSVPESD--	131
CrOYE1	DAGMNDNAQVFAWRPIADFIIRSHGA---VPSVQLAHAGRKASTFEPFVQGRPLYPGKDA	172
AnabaenaER3	DLGLWDDKQIEPLTRIVRFLRQGS---VTGIQLAHAGRKASCNVPWL-GGTPLTPEQ--	122
GloeoER	DLGLWDDKQIEPLTRINDFIHQES---VAGIQIAHAGRKASTARPE-GGGPLTEGE--	122
CaOYE	DLGIWSDDHIAALSRIVKLIESLGA---VAGIQLAHAGRKASVGRPWE-GGKPIAPAN--	124
FOYE1	CLGLYNDEQEAALGRIVAFAREFGQ--AKMATQLAHAGRKASTRRPWD-PGSPYSPE--E	124
ChrOYE3	CMGLYNDEQAQQLGRIVEFVHNSE--SKIGIQLSHSGRKGSTWNTK----QIS--VE	117
GkOYE	DLGIWSDDHIAGLRELVLVKEHGA---AIGIQLAHAGRKSQVP-----G---	114
GeoER	DLGIWSDEHVDGLRELVLVKEHGA---KIGIQLAHAGRKAEEVE-----G---	114
TsOYE	DLGIWSEDLPLKELARRIREAGA---VPGIQLAHAGRKAGTARPE-GGKPL-----	120
TOYE	DLGIWNEQVKELKKIVDICKANGA---VMGIQLAHAGRKCNIS-----	111
	*::: : : *:::***	
YqjM	----DIFAPSAIAFDEQSA-TPVEMSAEKVKETVQEFKQAAARAKEAGFDVIEIHAAGY	169
XenA	RGWE-TIAPSAIAFGAHLPNVPRAMTLDDIARVKQDFVDAARRARDAGFEWIELHFAHY	183
RmER	RGWQ-TFAPSAPVHAAGEV-PPAALDKAGMKKIRDDFVAAAKRAARLGIEGIEVHGAGY	183
DrER	GGWQ-VIGPDENSFHDLPF-TPAMMGADELGVVDASAAARRAQVAGFDAVEVHAAGY	196
RhrER2718	LSWQ-TVAPSAPVPG-HLA-DPVELTTEGIEKVVDFAAAATRALKAFFKVVEIHAAGY	186
OYERo2	LSWQ-TVAPSAGFG-DHT-PPAAATTADIRKVVADFAAAERASRAGFKVVEIHAAGY	186
Pfvc	GGWA-TVGPSAPFD-GYA-EPAAMTEEQIQGVISDFAAAAVRAVDAGFDTLELHGAHY	188
CrOYE1	AAWQ-VVAPSAPVFA-DFQ-TPREMTADIREVIDAFAAAAERSIKAGFQVVEIHAAGY	229
AnabaenaER3	GGWQ-PVAPSPIPQENAP-VPISLDERGIQETIFAFVAAQALQVGFQMIIEIHAAGY	180
GloeoER	GGWADSAPALPFDAGYP-VPEALDEAGIAATVQFAAAARRSLAAGFRVLEIHAAGY	181
CaOYE	GGWP-VVGPTAEPFAGYP-TPIPLDAAGIARVVDATATKRARAAGFRWIEIHAAGY	182
FOYE1	GGWQ-TWAPSAIKFYEESL-TPHPMSIEDLETVKQDFVNSAIRAERAGFKAIELHGAHY	182
ChrOYE3	EGWE-TIAPSPPIPYHPTER-IPHVLQEEIKEQVRNFREARRAVEAGFDVIEIHAAGY	175
GkOYE	----EIIAPSAPVDDSSP-TPKEMTKADIEETVQAFQNGARRAKEAGFDVIEIHAAGY	169
GeoER	----EIIAPSAPFNEKTR-TPKEMTKDIEETIQAFQNGARRAKEAGFDVIEIHAAGY	169
TsOYE	-GWR-VVGPSPIPFDEGYP-VPEPLDEAGMERILQAFVEGARRALRAGFQVIELHMAHY	177
TOYE	--YEDVVGSPSPKAGDRYK-LPRELSVEEIKSIVKAFGEAAKRALAGYDVVEIHAAGY	168
	. * * : * . : * : * * * *	

YqjM	LIHEFLSPLSNHRTDEYGGSPENRYRFLREI IDEV KQVWD--GPLFVRVSASDYTD----	223
XenA	LGQSFFSEHSNKRTDAYGGSFDNRSRFLLETAAVR EVWPENLPLTARFGVLEYDGR---	240
RmER	LLHQFLSPIANHRTDEYGGSLNRMRFPLEVFDVAREAFPAERPVMVRVSATDWVP----	239
DrER	LLHQFLSPLANTRTDDYGGSFENRTRLLEVVRAVR HVWPAHLPLFVRLSATDWAE----	252
RhrER2718	LLHQFLSPESNKRTDRYGGSFENRI RLLLEILTAVREVPAPLPLFVRVSATDWLTEERG	246
OYERo2	LLHQFLSPVSNHRTDEYGGSFAGRI RLLLEVVDAVRGVWPAELPVFVRVSATDWLSEEPG	246
PfvC	LLHQFQSPLTNTRTDSWGGNEAGNRMLLAVIDAVREVMPEMPLLLRISATDWAE----	244
CrOYE1	LLHQFLSPQANKRKDYGGSLANRMRLPLAVAEAVRAVIPPPLPLAVRISATDWAGP----	286
AnabaenaER3	LLHSFLSPLSNRRTDRYGGSLNRMRLLEVVRRVRDVLNMGMPFVRISATDWVE----	236
GloeoER	LLHSFLSPLSNRRTDRWGGLFENRI RLLLA VVEAVRGVWPERLPLFVRISATDWTE----	237
CaOYE	LLHNFLSPLGNDRNDEYGGDLRGVRLLSEVTAAVRAEWPSDPLAVRLSCSDWTP----	238
FOYE1	LIHQFLSPLSNQRODQYGGSLNRMRYPLEILSAVKHALSAEMVVMGRISAVDWAP----	238
ChrOYE3	LIHQFLSPLSNIRTDEYGGSFENRI RFLVEI DAVNQEELNDNVLFVRISGTEYAE----	231
GkOYE	LINEFLSPLSNRRODQYGGSPENRYRFLGEVIDAVREVD--GPLFVRISASDYHP----	223
GeoER	LINEFLSPLANKRODEYGGSENRYRFLGEVIDAVRQVWD--GPLFVRISASDYHP----	223
TsOYE	LLSSFLSPLSNQRTDAYGGSLENRMRFPLQVAQAVREVPRELPLFVRVSATDWGE----	233
TOYE	LIHEFLSPLSNKRKDEYGNSEIENRARFLIEVIDEVRKNWPKPIFVRVSADDDYME----	224
	* . * * * * : * . * * * : * . : :	
YqjM	---KGLDIADHIGFAKWKQGVLDIDCSSGALV-HADINVFPYQVQVFAEKIR-EQADM	278
XenA	---DEQTEESIELARRFKAGGLDLLSVSVGFTIPETNIPWGPAPMGPIAERVR-REAKL	296
RmER	---NGWDIEGTIALSHELKARGSAHVSTGGVSPQQAIGPGYQVPAQRVK-AEVGL	295
DrER	---GGWDLQEQVQLSKLLKYEGVDVLDISSGGLTAAQQIEVGPYQVFPAAVSAETEI	309
RhrER2718	LEVDSWTADQTVANILSDYGVLDVVDSTGGNSPAAQIPVEPGYQVFPFARRLQ-NESLL	305
OYERo2	LDADSWTPDQTVSVLQALADLGDVLDVSSGGVA-SARIPIGPGYQVFPFARRIQ-NEITV	304
PfvC	---GGIDIEASVRLAAQAHEHGVLDIDVSSGGVAHQIQPGPGYQVTFGARIR-RETRV	300
CrOYE1	LDGPAPWDVDQSVVLGALRDLGCDLIDVSSGGQLPRALIPVGPYQVFPFARRIR-REARV	345
AnabaenaER3	LDGWSWTPDQTVSVLQALADLGDVLDVSSGGVAHQIQPGPGYQVFPFARRIQ-NEITV	292
GloeoER	---GGWDLQEQVQLSKLLKYEGVDVLDISSGGLTAAQQIEVGPYQVFPFARRIR-REARV	293
CaOYE	---EGLTADITVEVARMLEQGVLDIDCSSGGIAPGITIPVGEYQVFPFAAQVR-REANI	294
FOYE1	---GGLTIEESITFSQCEKRGAGF IHVSTGGVLAHQIQIPVGPYQVVEHAQAIR-QNVNI	294
ChrOYE3	---NGWEITDSVELSKVLKNHSDVLDVSSGGNIHGKIPFDGYQVPLASQVR-NEADV	287
GkOYE	---DGLTAKDVVPYAKRMKEQGVLDVVDSSGAVV-PARMNVYPGYQVFPFAELIR-READI	278
GeoER	---EGLTAKDYIPYAKRMKEQGVLDIDVSSGAVV-PATINAYPGYQVFPFAELIR-REAEI	278
TsOYE	---GGWSLEDTLAFARRLKEVGVDLDCSSGGVLRVRIPLAPGFQVFPFADAVR-KRVGL	289
TOYE	---GGINIDMMVEYINMIKD-KVDLIDVSSGGLL-NVDINLYPGYQVQYAEITIK-KRCNI	278
	: : * * : . : : : . :	
YqjM	ATGAVGLMITDGSMAEELQNGRADLIFIGRELLRDPFFARTAAKQLNTEI--PAPVQYER	336
XenA	PVTSAWCFGTPQLAEALQANQLDLSVYGRAHLADPHWAYFAAKELGVEKA-SWTLPPAPY	355
RmER	PTMAVGLLITEAQAEI IANNEADI IS IARAMLIDPRWPWHAAKLGASV--NAPKQYWR	353
DrER	SVMVAVGLIETGAQAEAILQAGDADLIALGRPFLLRDPHWAQRAARELGLRPV-S-IDQYAR	367
RhrER2718	PAAAVGLLITEPEQAEKIVEDGSAAVAVLIGRELLRDPYWARRAARELNAEVGPHIPSQYAR	365
OYERo2	PAAAVGLLITEPEQAEKIVEDGSAAVAVLIGRELLRDPYWPRAALVLNAQVTPQIPAQYAR	364
PfvC	PTGTVGLLITSPGQAEHAVATGQADGVFIARAALRDPHWWLRAAFELGHDL--AWAPQYER	358
CrOYE1	ATGTVGLLITTKGQAEKILQEGKADVVLIGREMLRDPNWPLRAAAELGYEGA-RYPPQYER	404
AnabaenaER3	MTGAVGLLINEAEYADQIITRGADLVILIGRELLRNPYWSIYARCSLDEEP--NWPVPYGY	350
GloeoER	LFGAVGQITSAEQADHIVRTGQADLVILIGRQLLRDPYWLKAAVELRAPG--PWPEQYQY	351
CaOYE	ATAAVGLITRPEHADAIVRNGDADLVILIGRELLRDPHWPRAARALGHDL--APPPQYIL	352
FOYE1	PTMAVGLLITSAQAEITLKSEQADMIATARAALKNPWPWTAAELGDKP--FAPPQYQY	352
ChrOYE3	KTGAVGLLIKVSASHAEILEKGDADLIF IAREMLRNPYLAVQGSFEMNEEC--FFPHQYIL	345
GkOYE	PTGAVGLLITSGWQAEELQNGRADLVILIGRELLRNPYWPYAAARELGAKI--SAPVQYER	336
GeoER	ATGAVGLLITSGWQAEELRNGRADLVILARELLRNPYWPYAAARELGAKI--SAPVQYER	336
TsOYE	RTGAVGLLITTPQAEITLQAGSADLVILGRVLLRDPYFPLRAAKALGVAP--EVPPQYQY	347
TOYE	KTSVAVGLLITQELAEELSNERADLVILIGRELLRNPYWLHTYTS----KEDWPKQYER	333
	. . : * : : : : * * * *	
YqjM	GW-----	338
XenA	AHFLERYR-----	363
RmER	SQPRGLEKLFKDAHFGQR	371
DrER	AGW-----	370
RhrER2718	AF-----	367
OYERo2	AY-----	366
PfvC	AVPRHSF-----	365
CrOYE1	GKFPK-----	410
AnabaenaER3	AVKRQRR-----	357
GloeoER	AKP-----	354
CaOYE	AW-----	354
FOYE1	AR-----	354
ChrOYE3	AKISS-----	350
GkOYE	GWRF-----	340
GeoER	GWRF-----	340
TsOYE	GF-----	349
TOYE	AFKK-----	337

Figure S1. Sequence alignment of the putative ER from *Chloroflexus aggregans* performed by Clustal Omega. The catalytic residues are highlighted in pink and the finger print motifs of thermophilic-like OYEs reported by Oberdorfer et al. (2011) are highlighted in green and cyano. The residues shaded in grey are conserved among OYE family, and the one in bold indicate similar residues. Residues highlighted in yellow show the sequence conservation of FMN binding. Residues highlighted in petrol green are involved in dimer formation. The accession numbers are reported in Table S3.

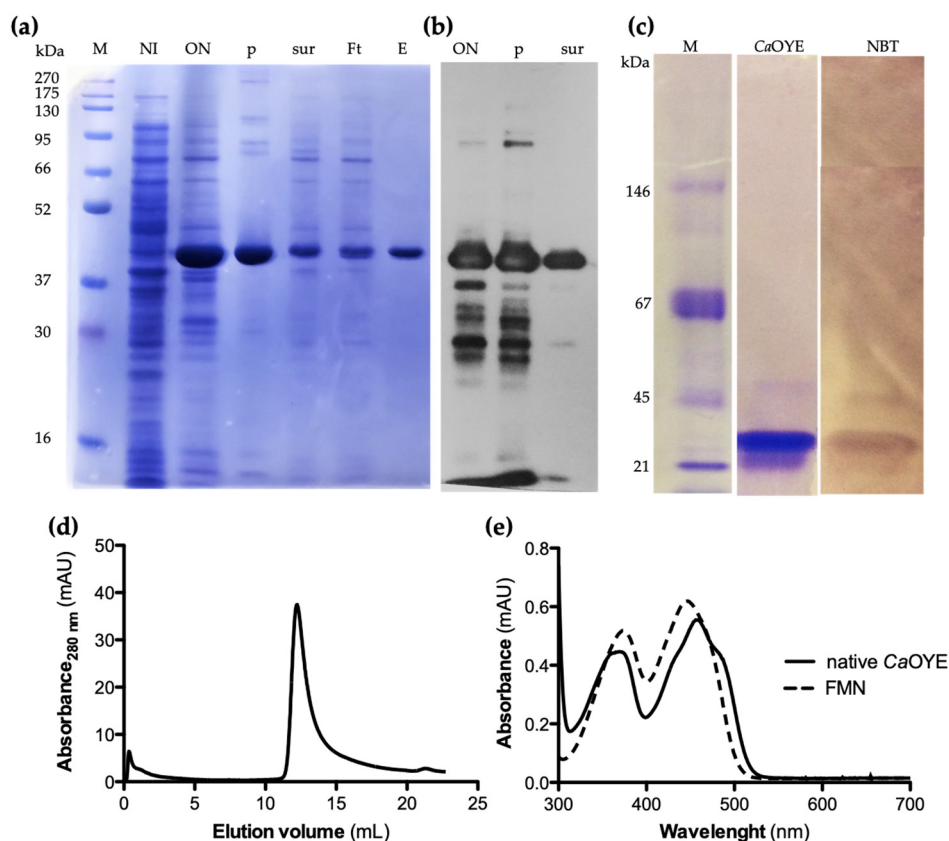


Figure S2. (a) SDS-PAGE 12% acrylamide: BL21(DE3) grown at 25 °C expressing *CaOYE*: Prestained SharpMass™ VII protein ladder (M), total cell extracts from not-induced cells (NI) and overnight induced cells with IPTG (ON), pellet fraction (p), soluble protein fraction (sur), flow-through (Ft) and pooled eluted fractions from IMAC (E); (b) Western blot assay with anti-His tag antibodies with samples of protein induced at 25 °C; (c) Native-PAGE using precast NuPAGE™ Tris-Acetate 3-8% gel from ThermoFisher: SERVA native marker (M), *CaOYE* samples stained by Coomassie brilliant blue and by NBT stain; (d) Analytical gel filtration of purified *CaOYE* sample eluted from a Superose 12 300/GL column.; (e) Determination of *CaOYE* concentration based on flavin absorption spectra of purified enzymes and released flavin after thermal denaturation (dotted line).

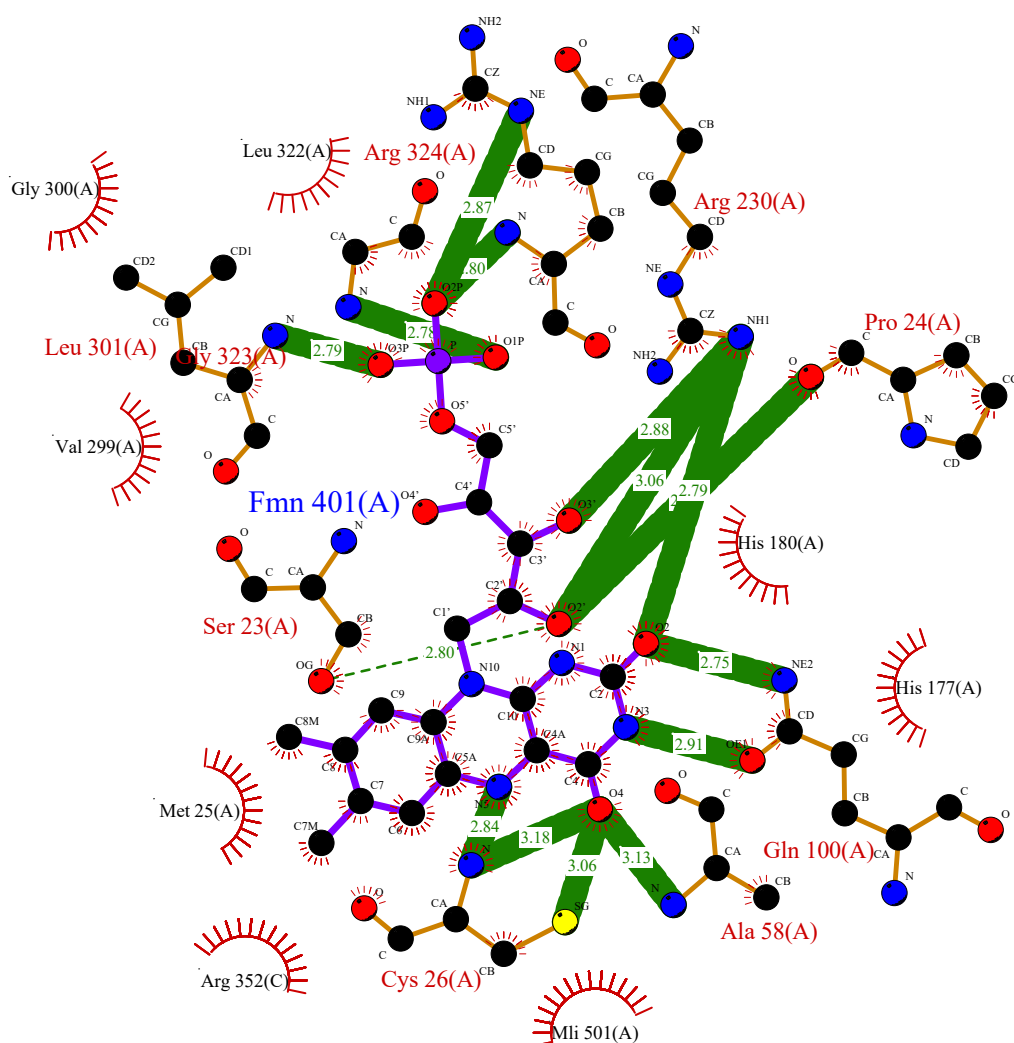


Figure S3. Schematic illustration of the interaction of FMN with active site residues of CaOYE. The thin green dotted lines illustrate hydrogen bonds.

Supplementary Tables

Table S1. Oligonucleotides used for PCR amplification of *CaOYE* sequence and cloning.

Primer	Sequence (5'→3') ¹
CaOYE 1_for	ATGATGCAATTAAGCAGCACGTCCG
CaOYE 2_rev	GCGCGCATGACGAATTTATCGTACC
CaOYE 3_for	TTCAACTACTGAGAGAGCC <u>ATATG</u> CAACCACATTTATTAC
CaOYE 4_rev	TATAG GATCCT CACCACGCCCGCAAATACTGC

¹ Restriction sites are shown in bold. Modifications introduced to mutate the original sequences are underlined.

Table S2. X-ray crystallographic data collection and refinement statistics of CaOYE (pdb 7O0T).

Data collection statistics	
Wavelength	0.97
Space group	C 2 2 21
Cell constants	
a, b, c (Å)	108.194 162.274 216.2
α, β, γ (°)	90 90 90
Resolution range for refinement (Å)	38.01 - 2.40 (2.641 - 2.40)
Total reflections	343346 (22759)
Number of Unique Reflections	73908 (4571)
R _{merge}	0.185 (0.522)
<I / sigma(I)>	4.9 (1.8)
Completeness (%)	99.3 (100.00)
Multiplicity	4.6 (5.0)
Refinement statistics	
R _{work} / R _{free}	0.22/0.26
RMSD bond lengths (Å)	0.0068
RMSD bond angles (°)	1.47
Average B factor	34.24
Main chain B factor	34.38
Ligands B factor	26.97
Water molecules B factor	29.45
No. of non-hydrogen atoms	
Number of protein atoms	10754
Number of ligands atoms	159
Number of water molecules atoms	188
Ramachandran plot (%)	
Most favoured	95.03
Generously allowed	4.54
Outliers	0.43

Table S3. List of OYE sequences used for the phylogenetic analysis, and their accession numbers from the National Center for Biotechnology Information (NCBI) or Phytosome (*).

Protein name	Organism	Accession number
AcaryoER1	<i>Acaryochloris marina</i> MBIC11017	ABW29811
AcaryoER3	<i>Acaryochloris marina</i> MBIC11017	ABW32756
AnabaenaER3	<i>Trichormus variabilis</i> ATCC 29413	ABA25236
AtOPR1	<i>Arabidopsis thaliana</i>	NP_177794
AtOPR3	<i>Arabidopsis thaliana</i>	NP_001077884
CaOYE	<i>Chloroflexus aggregans</i>	WP_015941499.1
Chr-OYE3	<i>Cryseobacterium</i> sp. CA49	AHV90721
CrOYE1	<i>Chlamydomonas reinhardtii</i>	Cre01.g050150*
CrOYE2	<i>Chlamydomonas reinhardtii</i>	Cre03.g210513*
CrOYE3	<i>Chlamydomonas reinhardtii</i>	Cre17.g727300*
CtOYE	<i>Chroococcidiopsis thermalis</i>	WP_015152687.1
CyanothER1	<i>Rippakea orientalis</i> PCC 8801	ACK64210
CyanothER2	<i>Rippakea orientalis</i> PCC 8801	ACK65723
DrER	<i>Deinococcus radiodurans</i> R1	AAF11740
FOYE-1	<i>Ferroplasma</i> sp. JA12	KRH78075
GeoER	<i>Geobacillus</i> sp. #30	BAO37313
GkOYE	<i>Geobacillus kaustophilus</i> HTA426	BAD76617
GloeoER	<i>Gloeobacter violaceus</i> PCC 7421	BAC91769
GsOYE	<i>Galdieria sulphuraria</i>	XP_005703492.1
LeOPR1	<i>Solanum lycopersicum</i>	NP_001234781
LeOPR2	<i>Solanum lycopersicum</i>	NP_001233868
LeOPR3	<i>Solanum lycopersicum</i>	NP_001233873
LyngbyaER1	<i>Lyngbya</i> sp. PCC 8106	EAW37813
NospuncER1	<i>Nostoc punctiforme</i> PCC 73102	ACC84535
NostocER1	<i>Nostoc</i> sp. PCC 7120	BAB73564
OYERo2	<i>Rhodococcus opacus</i> 1CP	ALL54975
Pfvc	<i>Arthrobacter</i> sp. JBH1	AFF18622
RhrER2718	<i>Rhodococcus rhodochrous</i> ATCC 17895	AMD82542
RmER	<i>Cupriavidus metallidurans</i> CH34	ABF11721
SynER	<i>Synechococcus elongatus</i> PCC 7942	ABB56505
TOYE	<i>Thermoanaerobacter pseudethanolicus</i> ATCC	ABY93685
TsOYE	<i>Thermus scotoductus</i> SA-01	CAP16804
XenA	<i>Pseudomonas putida</i>	AAF02538
YqjM	<i>Bacillus subtilis</i>	BAA12619

Table S4. Thermostability fingerprints. Parameters referring to primary sequence have been calculated with Protparam ExPASy; oligomerization states in solution have been obtained from literature data and derived from size exclusion, native gel or light scattering measurements; in crystal oligomerization data were deduced from crystallographic structures, as well as interface area and number of interactions (Hydrogen bonds, Hb, and Salt bridges, Sb) involving the dimerization surface, calculated by PISA software; T_{opt} corresponds to the optimal temperature for enzymatic activity and it has been deduced from literature data, while T_m corresponds to melting temperature of the corresponding recombinant enzymes, measured either by Fluorescence (ThermoFAD or ThermoFluor) or Circular dichroism.

Enzyme	Oligomerization								
	Sequence length (aa)	Arg/Lys ratio	Total proline content (%)	In solution	In crystal	T_{opt} (°C)	T_m (°C)	Interface (Å ² , %tot)	Interactions (Hb, Sb)
<i>CaOYE</i>	354	7.0	8.2	monomer	dimer	-	79	1451 (10.4%)	(16; 8)
<i>FOYE1</i>	354	1.6	6.2	-	-	50 ($t_{1/2}$ = 5h)	-	-	-
<i>GkOYE</i>	340	2.2	6.2	tetramer	dimer	70	76-82	1211 (8.9%)	(16; 0)
<i>GeoER</i>	340	1.7	5.0	trimer or tetramer	-	70	-	-	-
<i>TsOYE</i>	349	4.6	8.0	dimer	octamer of dimers	65	-	1273 (9.3%)	(16; 2)
<i>TOYE</i>	337	0.7	3.6	tetramer, octamer, dodecamer	dimer of dimers	-	> 70	1073 (8.0%)	(15; 0)
<i>YqjM</i>	338	0.9	3.8	tetramer	dimer of dimers	25-30 ($t_{1/2}$ = 9 days)	-	1152 (8.5%)	(13; 0)
<i>XenA</i>	363	2.9	6.1	dimer	dimer	-	50.4	1346 (9.7%)	(2; 2)
<i>RmER</i>	371	2.0	7.0	monomer	dimer	35	-	2132 (14%)	(28; 7)
<i>DrER</i>	370	4.4	6.2	dimer	-	30	-	-	-
<i>ChrOYE3</i>	350	1.3	4.0	dimers, tetramers	-	35 ($t_{1/2}$ = 233.5h)	-	-	-
<i>RhrER2718</i>	367	3.4	6.3	dimer	-	40	-	-	-
<i>OYERo2</i>	366	6.3	6.8	dimer/ tetramer conc. dependent	-	up to 20	-	-	-

PfvC	365	12.5	6.0	-	-	-	-	-	-
CrOYE1	410	2.5	9.0	-	-	40	-	-	-
						($t_{1/2}$ = 5.7 days)			
Anabaena ER3	357	4.8	7.0	-	-	-	-	-	-
GloeoER	354	10.7	6.2	-	-	-	-	-	-