

Supporting Information

Application of a Cytochrome P450 Enzyme eluted from Encapsulated Biomaterials to the Catalysis of Enantioselective Oxidation

*Hiroyuki Nagaoka**

Sanyo Shokuhin Co., Ltd. R & D, 555-4 Asakura, Maebashi, Gunma 371-0811, Japan

E-mail: hnagaoka@sanyofoods.co.jp, Tel: +81-27-220-3471, Fax: +81-27-220-3477

Abbreviations: ME: membrane-bound enzyme, GA: glutaraldehyde, FD: freeze-dried, Has: heme acquisition system, NAD(P): nicotinamide adenine dinucleotide, FAD: flavin adenine dinucleotide, PP-gel: calcium-alginate-gel-containing PP, CLME: cross-linked ME, CMME: a compound-modified ME, AGME: PEG (MW: 1000/4000 = 2/1)-aggregated ME, *S-1*: *S*-(+)-1-(6-methoxynaphthalen-2-yl)ethanol, *S-2*: *S*-(+)-1-(2-naphthyl) ethanol, HBP: heme-binding protein. PQQ-ADH: pyrroloquinoline quinone alcohol dehydrogenase, Cyt c O: cytochrome *c* oxidase, Cyt-P450: oxygen-driven cytochrome P450 enzyme, P450: cytochrome P450 enzyme.

Table of Contents

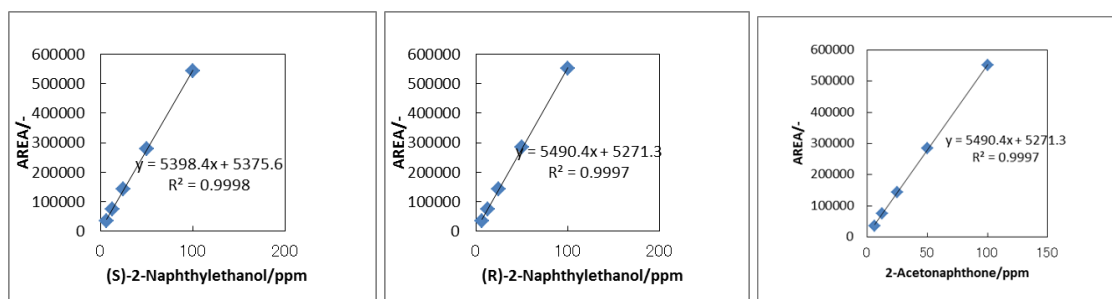
1. General procedure for reactions using CMMEs and AGME.....	S2
2. Data of FTIR/ICP-AES/IC analysis for the no necessity of (NH ₄) ₂ SO ₄ process.....	S5
3. Optimum scale of compound modification for asymmetric redox activity of the ME.....	S10
4. Data for the specific activity (unit/(mg·min)) of CMME and AGME.....	S13
5. Gel filtration for given a single band-F from many band-A in SDS-PAGE.....	S14
6. Physicochemical analysis for the detection of PP-HBP.	S16
7. Chromatograms of the N-terminal amino-acid sequence of band-F.....	S18
8. References attached by PDF.....	S18

1. General procedure for reactions using CMME and AGME

A calibration curve configured, the chromatograms of the *rac*-1 biotransformation with ME derivatives were shown. Enantiomeric excess (ee) values, chemical yield ratio (% yield)/conversion ratio of all compounds were obtained from chiral HPLC analysis.¹

1-1. Calibration curve configured using HPLC.

The ee was calculated for either *rac*-1 (0.8 mM or 1.2 mM) or *rac*-2 (0.8 mM or 1.2 mM), which were separated with either a Daicel Chiralcel OB-H column ((S)-isomer/(R)-isomer/product ketone = 7.8/8.8/11.6 min) or a Daicel Chiralpak AS-H column ((S)-isomer/(R)-isomer/product ketone = 7.5/8.25/9.5 min) connected to an HPLC LC-10A system (Shimadzu). Analytical conditions were as follows: mobile phase, n-hexane/IPA: 9/1, flow rate: 1.0 mL/min, temperature: 30 °C, wavelength: UV 254 nm. The stereochemistry of the isolated optically active alcohol was identified by comparing the values (+ or –) for the specific rotation detected using a polarimeter, as done previously.¹

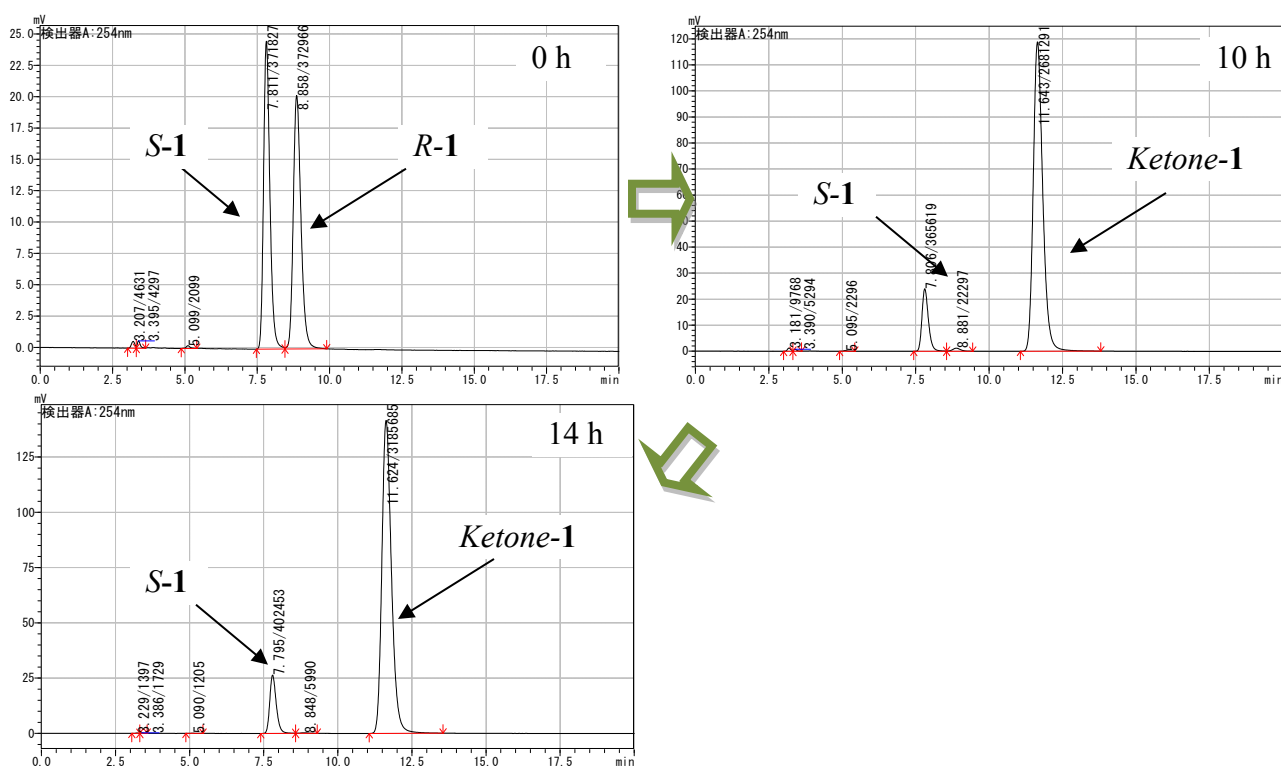


Conc./ppm	(R)-2/abs [‡]	(S)-2/abs [‡]	ketone/abs [†]
3.125	18408	18403	-
6.25	34455	34671	64884
12.5	69207	69837	129479
25	133042	134274	256966
50	263249	267577	509690
100	515506	524152	983200

[‡]Absorbance of HPLC analysis, [†]Average

1-2. Data of chromatograms

The time course/chromatograms of the asymmetric oxidation of *rac*-**1** (1.2 mM) using a CLME_a (20 mg) was monitored and quantitatively analyzed under the suggested conditions.¹



Time/h	S-1/Abs [‡]	R-1/abs [‡]	Ketone/Abs [‡]	%ee	Avg [†] (%ee)
0	384592	386537	-	0.252	0.20
	371827	372966	-	0.152	
10	341321	27703	2437138	84.985	86.74
	365619	22297	2681291	88.50	
14	421760	2286	3429781	98.92	99.17
	402453	1190	3185685	99.41	

[‡]Absorbance of HPLC analysis, [†]Average

Differences in the activity between ME-fractions separated by centrifugation and the ME-derivatives.

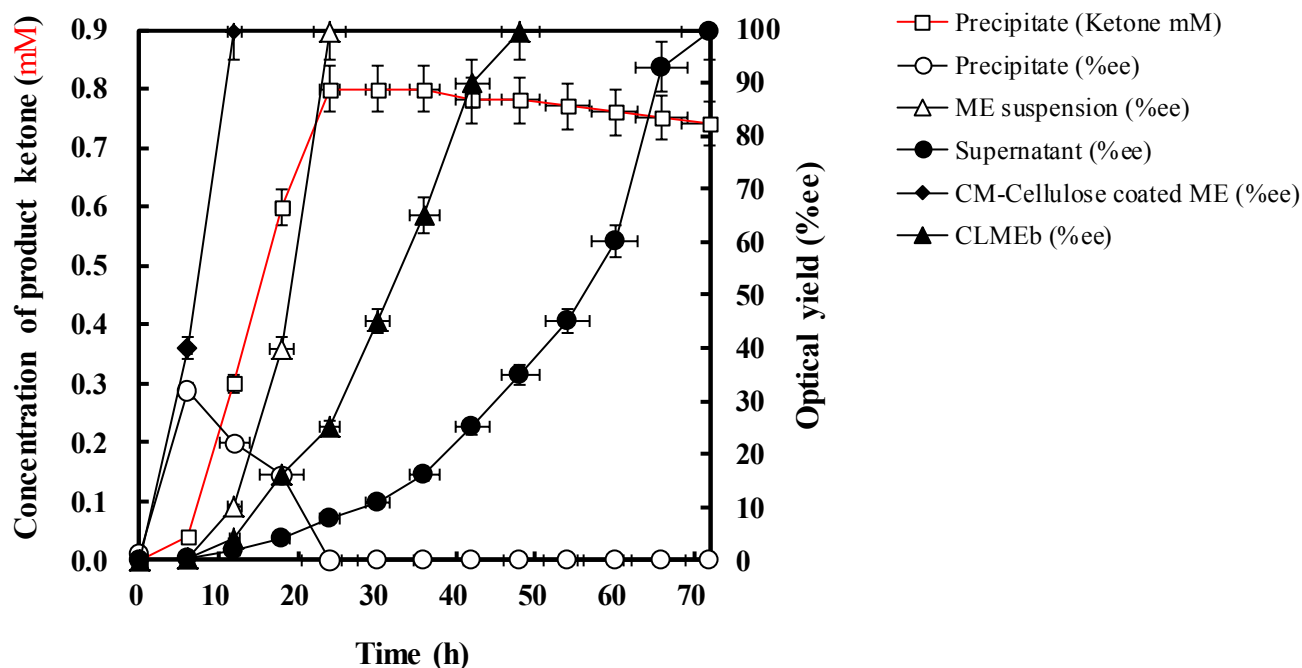


Figure S1. Time course of the asymmetric oxidation activity: (-Δ-) eluent from the ME-suspension of the PP-gel (5.0 mL), (-●-) supernatant of the ME-suspension acquired via centrifugation (5.0 mL), (-□-: mM, -○-: %ee) aqueous suspension of the sample 1 precipitate acquired via centrifugation (100 mg/5.0 mL D.W.), (-◆-) CM-cellulose-coated ME (20 mg/5.0 mL D.W.), and (-▲-) cross-linked ME_b (CLME_b) treated with 30% (w/v) aqueous (NH₄)₂SO₄ (20 mg/5.0 mL 50 mM glycine-NaOH (pH 9.0)). A substrate solution (*rac*-1: 20 μL, 20,000 ppm) was then poured into a test tube (18 mm × 15 mL) containing each of the samples prepared above.

As shown in Figure 1, while the activity of the ME suspension shows a 24 h biotransformation time, the highest asymmetric oxidation activity was observed in the CMC-ME reaction (13 h), and the lowest activities were observed for the CLME_b reaction (48 h) and ME supernatant reaction (72 h). The ME-suspension, supernatant, precipitate, and CMC-ME may function in the presence of O₂ via a reactive oxygen species ($\text{Fe}^{2+} + \text{O}_2 \rightarrow \text{Fe}^{3+}\text{-O-O}^- \rightarrow \text{Fe}^{4+}=\text{O} (+ \text{rac-1}) \rightarrow \text{Fe}^{2+} + \text{H}_2\text{O}$).^{3c} This suggests that the iron electron-transfer system may lie in the hydrogen peroxide-driven P450_{BSB}—an HBP that depends on oxygen instead of a redox cofactor (e.g., NAD(P)H).³

2. Data of FTIR/ICP-ACS/IC analysis for the no necessity of $(\text{NH}_4)_2\text{SO}_4$ process.

To investigate the reason relevant for the poor activity of CLME_b , the residue content (%) of raw materials (i.e., $(\text{NH}_4)_2\text{SO}_4$ and sodium alginate) per CMME was examined. To investigate functional group of 1) PP, 2) sodium alginate, 3) PEG (4000), 4) SC1 (PEG (4000)-ME (1) not treated with $(\text{NH}_4)_2\text{SO}_4$), 5) SC2 (PEG (4000)-ME (2) treated by the precipitation process using 30% (w/v) aqueous $(\text{NH}_4)_2\text{SO}_4$), and 6) SC3 (CLME_b treated by $(\text{NH}_4)_2\text{SO}_4$), these samples were analyzed using a portable ATR instrument (A2 Technologies; ML version).

2-1. ML FTIR instrument analysis

A single bounce internal reflection method using a diamond crystal was applied to acquire spectra of the PP, PEG (4000)-MEs (SC1 and SC2), CLME_b , and sodium alginate. The samples were placed on the diamond crystal to acquire their spectra.

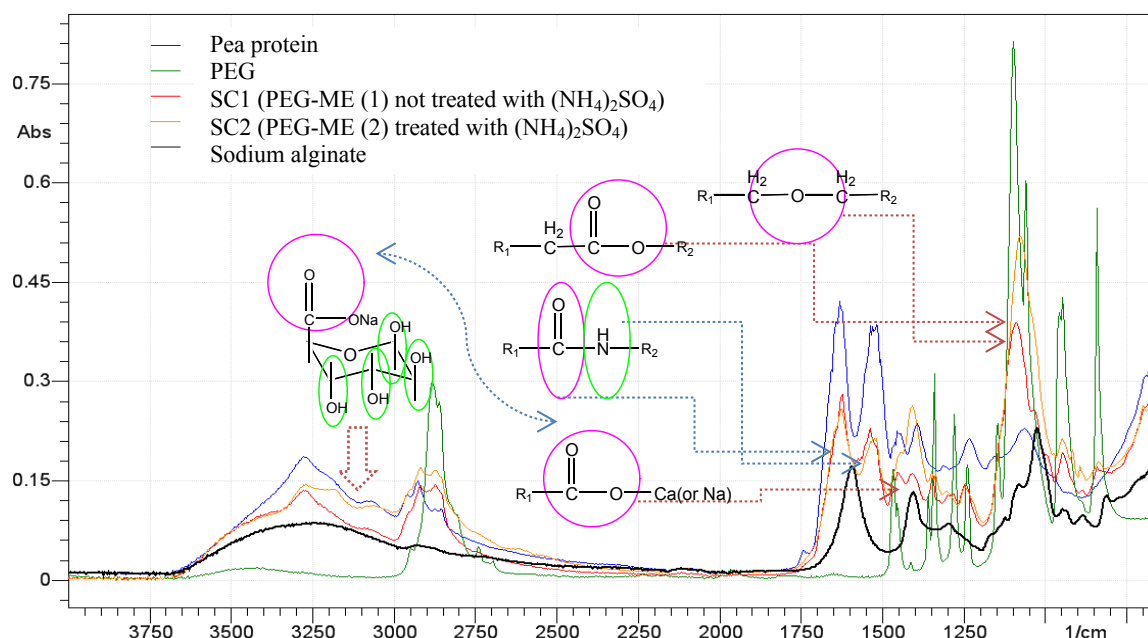


Figure S2. Differences in the content of functional groups among four samples: (1) SC1 (PEG (4000)-ME (1) not treated with $(\text{NH}_4)_2\text{SO}_4$), (2) SC2 (PEG (4000)-ME (2) treated with 30% (w/v) aqueous $(\text{NH}_4)_2\text{SO}_4$), (3) pea protein (PP), and (4) sodium alginate.

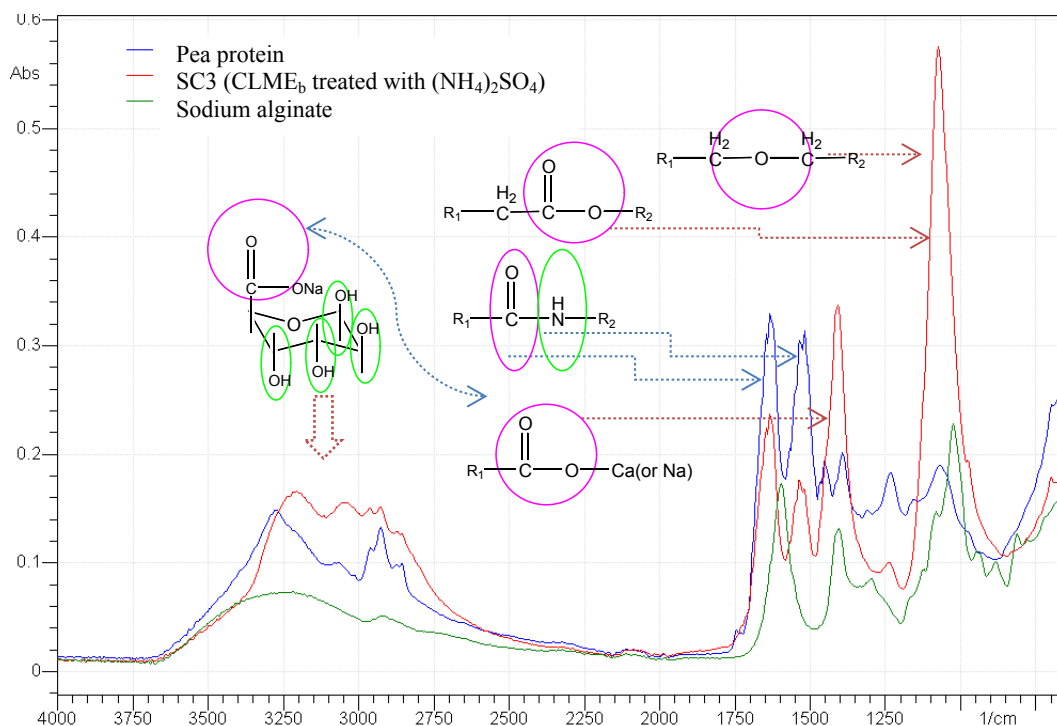


Figure S3. Difference in the content of functional groups among three samples: (1) CLME_b (SC3: cross-linked ME treated with 30% (w/v) aqueous (NH₄)₂SO₄), (2) pea protein (PP), and (3) sodium alginate. *To ensure uniform contact, each sample was pressed to a crystal by a pressure device that was attached to the ML FTIR instrument. SC1 shows the PEG (4000)-MEs (1) treated without the saturated (NH₄)₂SO₄; whereas SC2 and SC3 show the PEG-MEs (2) and cross-linked MEs, respectively, treated with the 30 (v/v%) saturated (NH₄)₂SO₄ process.

Table S1. Content of elements: improvement of the purification processes of raw materials residue content for MEs treated or not treated with (NH₄)₂SO₄ from elements identified in **Figures S1 and S2**.

Sample	FTIR analysis			
	950–1250 cm ⁻¹ i.e., sulfate	1250–1500 cm ⁻¹ i.e., calcium alginate	1500–1750 cm ⁻¹ i.e., Pea Protein	Residues
PP	0.19 abs	0.24 abs	0.4 abs	—
SC3: CLME _b ^a	0.58 abs	0.32 abs	0.24 abs	(NH ₄) ₂ SO ₄ Calcium-Alginate
SC1: PEG (4000)-ME ^b	0.42 abs	0.17 abs	0.3 abs	—
SC2: PEG (4000)-ME ^c	0.58 abs	0.28 abs	0.3 abs	(NH ₄) ₂ SO ₄ Calcium-Alginate

^aCLME_b includes the process of “(NH₄)₂SO₄” precipitation.

^bPEG (4000)-ME (SC1) does not include the process of “(NH₄)₂SO₄” precipitation but centrifugation.

^cPEG (4000)-ME (SC2) includes the process of “(NH₄)₂SO₄” for precipitation.

^dhighest wt% (red) shows the remainder of “(NH₄)₂SO₄” in the precipitation process.

^elowest wt% (blue) shows no remainder but a higher oxygen (O₂) is detected to PP.

2-2. Result of the section 2-1

The FTIR spectra showed a significant difference between the ME not treated with (NH₄)₂SO₄ (i.e., SC1) and ME treated with (NH₄)₂SO₄ (i.e., SC2 and SC3). As shown in **Figures S2 and S3**, when SC1 is compared with SC2 and SC3 (CLME_b), it can be seen that both sodium alginate (range, 1250–1500 cm⁻¹) and (NH₄)₂SO₄ (range, 950–1250 cm⁻¹) were dramatically reduced in the untreated catalyst. This result indicated that when preparing SC1, not treated with (NH₄)₂SO₄, the raw materials (i.e., sodium alginate and (NH₄)₂SO₄) can be removed successfully. This means the ME-redox protein incorporating an iron electron-transfer system may be effectively concentrated, reducing the activity of CLME_b (i.e., direct evidence) (see **Table S1**). Furthermore, to explain why SC1 has a spectrum apparently showing a sulfate (SO)₃^c it was speculated that oxygen absorption in the PP gel is processed under aeration, and then an oxygen-driven cytochrome P450 enzyme (Cyt-P450, a HBP) is formed/eluted, which leads to the formation of a reactive oxygen species via an iron electron-transfer system (Cyt-P450^{3a-3c}: cysteine–Fe²⁺ + O₂ → Fe³⁺–O–O⁻ → Fe⁴⁺=O (oxidizing *rac-1*) → Fe²⁺ + H₂O), resulting in water solubility (PP → ME), leading to the appearance of sulfate (SO: a superoxoiron–cysteinate) in the range 950–1250 cm⁻¹.³

2-3. ICP-AES analysis and IC analysis in between PP and ME derivatives

In the measurements of metal contents of between PP, CLME_b (before FD and after FD), and PEG(4000)-ME (1: without (NH₄)₂SO₄ process and 2: with (NH₄)₂SO₄ process), the each samples (0.5 g) was added to a 100 mL beaker with purified water (50 mL) and 60%-HNO₃ (Kokusan, 10 mL), and then digested by heating on a hotplate about 1 h: the ICP-AES analysis was done.

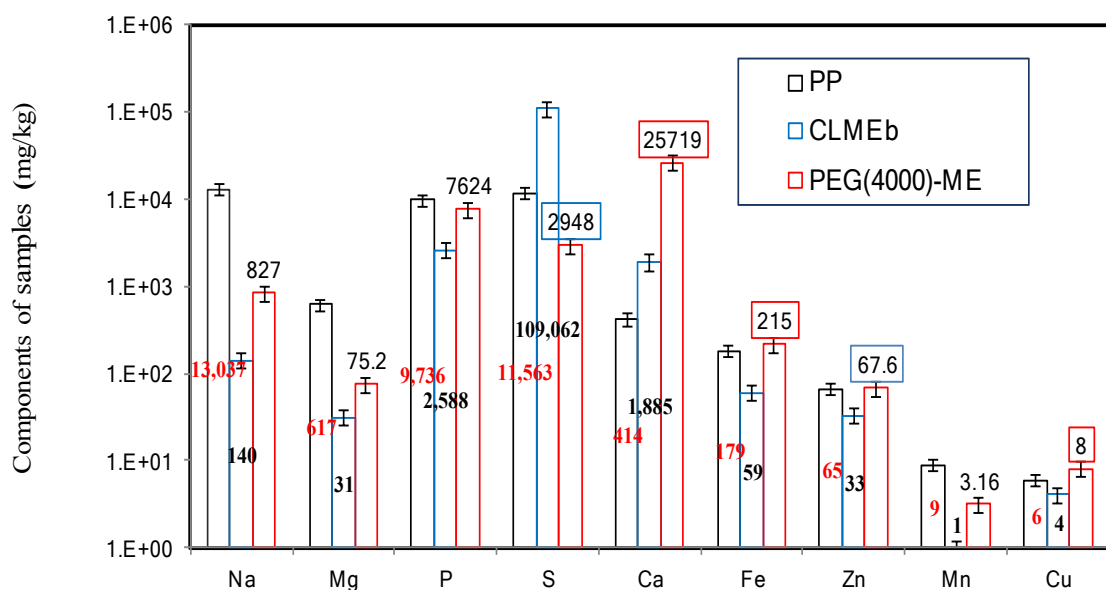


Figure S4. ICP-AES (metal) analysis results: (-□-) pea protein (PP), (-□-) CLME_b (cross-linked ME treated with 30% (w/v) aqueous (NH₄)₂SO₄), and (-□-) PEG (4000)-ME (not treated with (NH₄)₂SO₄).

Table S2. ICP-AES analysis (n=1: PP, and CLME_b (before FD and after FD))

	Sample	g	mL	Status	ICP								
					Na	Mg	Si	P	S	Ca	Fe	Zn	Mn
	Blank	—	—		0.15	0.00	0.17	0.00	0.03	0.00	0.00	0.00	0.01
N=1	PP	0.5012	100	Raw data (ppm)	65.49	3.09	0.58	48.80	57.99	2.48	0.90	0.33	0.05
				Actual (mg/kg)	13037	617	81.2	9736	11563	495	179	65.4	8.91
	CLMEb before FD	1.0033	100	Raw data (ppm)	0.85	0.24	0.31	17.48	374.99	117.63	0.35	0.11	0.04
				Actual (mg/kg)	69.4	24.2	13.5	1742	37372	11725	34.9	11.3	3.08
	CLMEb after FD	0.5010	100	Raw data (ppm)	0.85	0.16	0.47	12.97	95.47	9.45	0.30	0.16	0.01
				Actual (mg/kg)	140	31.3	58.9	2588	98890	1885	59.4	32.8	1.00

Table S3. ICP-AES analysis (n=2: PP, and CLME_b (before FD-drying and after FD-drying))

	Sample	g	mL	Status	ICP								
					Na	Mg	Si	P	S	Ca	Fe	Zn	Mn
	Blank	—	—		0.15	0.00	0.32	0.00	0.15	0.00	0.01	0.00	0.00
N=2	PP	0.4999	100	Raw data (ppm)	67.98	2.87	0.95	53.58	30.12	2.50	0.89	0.34	0.03
				Actual (mg/kg)	13568	573	125.2	10718	5995	500	176	68.2	6.39
	CLMEb ^a before FD	1.0027	100	Raw data (ppm)	0.86	0.24	0.61	19.38	389.76	117.83	0.39	0.13	0.02
				Actual (mg/kg)	70.9	23.9	28.7	1932	38856	11751	38.2	13.3	2.27
	CLMEb ^a	0.5005	100	Raw data (ppm)	0.80	0.14	0.75	13.11	392.09	9.43	0.30	0.18	0.00
				Actual (mg/kg)									

	after FD			Actual (mg/kg)	129	28.6	85.8	2619	78310	1885	58.5	36.8	0.00
--	----------	--	--	-------------------	-----	------	------	------	-------	------	------	------	------

^aCLME_b includes the process of “(NH₄)₂SO₄” precipitation.

Table S4. ICP-AES analysis (n=3: PEG (4000)-MEs and CLME_b)

	Sample	g	mL	Status	ICP								
					Na	Mg	Si	P	S	Ca	Fe	Zn	Mn
	Blank	—	—		0.00000	0.00000	0.18382	0.00241	0.12336	0.00000	0.00000	0.000	0.000
N=3	PEG (4000)-ME (1) ^a	0.4994	100	Raw data (ppm)	4.1305	0.37584	0.78668	38.0755	14.7225	128.443	1.0747	0.337	0.015
				Actual (mg/kg)	827	75.3	158	7624	2948	25719	215	67.6	3.16
	PEG (4000)-ME (2) ^b	0.0399	25	Raw data (ppm)	0.9753	0.43717	0.46021	6.2873	22.0515	1.5947	0.2682	0.138	0.009
				Actual (mg/kg)	611	274	288	3939	13817	999	168	86.8	5.62
	CLME _b ^c	0.4986	100	Raw data (ppm)	0.8374	0.22764	0.46703	23.4985	549.375	22.5460	0.2937	0.042	0.027
				Actual (mg/kg)	168	45.7	56.8	4712	110159	4515	58.8	8.40	5.36

^aPEG (4000)-ME (1) does not includes the process of “(NH₄)₂SO₄” precipitation but centrifugation.

^bPEG (4000)-ME (2) includes the process of “(NH₄)₂SO₄” for precipitation.

^cCLPX_b includes the process of “(NH₄)₂SO₄” precipitation.

Table S5. ICP-AES analysis of the Cu contents of PP and CLME_b.

Sample		n	g	mL	Status	Cu	
						ppm	average
Blank			—	—		0.00128	—
N=1	PP	1	0.5000	100	Raw data (ppm)	0.03112	5.83
					Actual (mg/kg)	5.97	
		2	0.5018	100	Raw data (ppm)	0.02981	
					Actual (mg/kg)	5.69	
	CLME _b	1	0.5005	100	Raw data (ppm)	0.02114	4.07
					Actual (mg/kg)	3.96	
		2	0.5016	100	Raw data (ppm)	0.02220	
					Actual (mg/kg)	4.17	

2-3-5. IC analysis

Further, the IC analysis was done by the measurements of anions of between PP, CLME_b, and PEG (4000)-ME. The each sample (0.5 g) was stirred in purified water (10 mL) at room temperature for overnight. This mixture was centrifuged at 15,000 rpm for 15min. The resulting supernatant (0.1 mL) was diluted to 10 ml with purified water, and measured anions by an ion chromatography (DIONEX, ICS-90).

Table S6. IC analysis for the anions/element detections

Sample	N =	IC analysis
--------	-----	-------------

		C	H	N	S
PEG (4000)-ME (1) ^a	1	45.99	8.19	6.91	1.54
	2	46.08	8.48	6.93	1.63
	average	46.04	8.34	6.92	1.59
PEG (4000)-ME (2) ^b	1	43.56	8.81	9.63	4.61
	2	43.13	8.97	9.71	4.81
	average	43.35	8.89	9.67	4.71
CLME _b ^c	1	26.56	7.42	16.22	11.74
	2	26.05	7.30	16.36	12.38
	average	26.31	7.36	16.29	12.06

^aPEG (4000)-ME (1) does not include the process of “(NH₄)₂SO₄” precipitation but centrifugation.

^bPEG (4000)-ME (2) includes the process of “(NH₄)₂SO₄” for precipitation.

^cCLME_b includes the process of “(NH₄)₂SO₄” precipitation.

2-4. Result of the section 2-3.

The raw material of (NH₄)₂SO₄ was retained in CLME_b. In addition, a comparison of the PEG (4000)-ME (not treated with (NH₄)₂SO₄) with CLME_b shows that the former contains four times the level of iron (215 mg/kg, PEG (4000)-MEs vs 59 mg/kg, CLME_b) suggesting that the activity of PEG (4000)-ME could be approximately four times greater than that of CLME_b, if an iron electron-transfer system is incorporated. These results indicate that the initial ME-redox oxidant may be more active owing to the existence of a greater proportion of incorporated Fe.

3. Optimum scale of compound modification for asymmetric redox activity of the ME.

Using CMME (20 mg) and *rac*-**1** (1.2 mM), the activity of PEG-ME (MW: 4000) was compared for different concentrations of coating to determine the optimum concentration of PEG (4000), as shown in **Figure S5**.

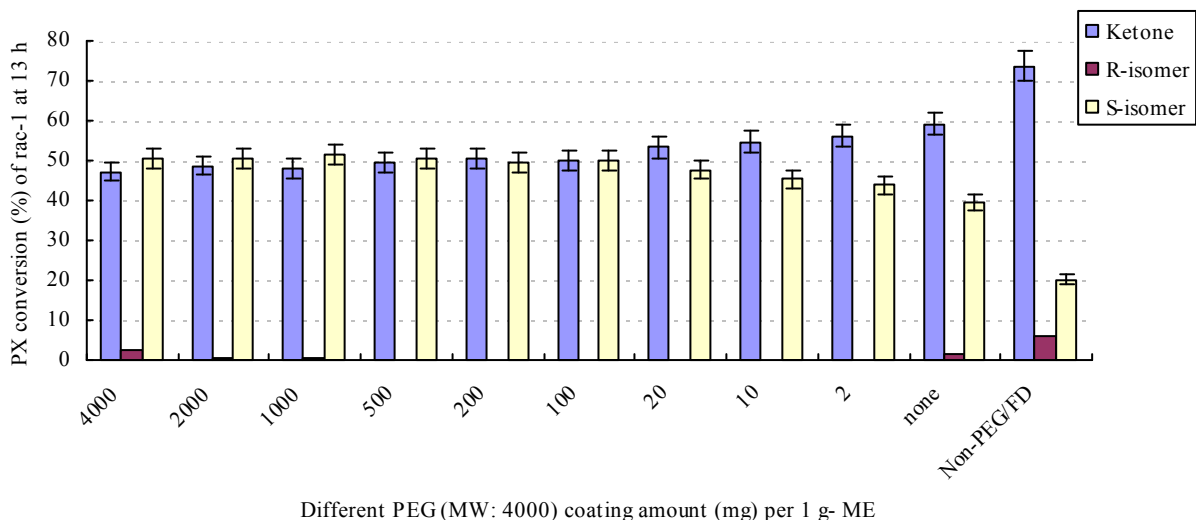


Figure S5. Conversion ratio (%) for the reaction of CMME (20 mg) with *rac*-1 (1.2 mM) in distilled water (4.0 mL) and DMSO (0.6% (v/v)) at 40 °C with magnetic stirring at 700 rpm for 13 h: Differences in the amount of PEG (4000) coating (0–4000 mg) on the ME (1 g).

The reaction was further examined to determine whether the substrate solution (30 μ L, 20,000 ppm) can be added in three portions (0 h, 8 h, and 12 h) to the CMME (20 mg) in 4.0 mL deionized water (D.W.) without any loss of optical purity or chemical yield, as shown in **Figure S6**.

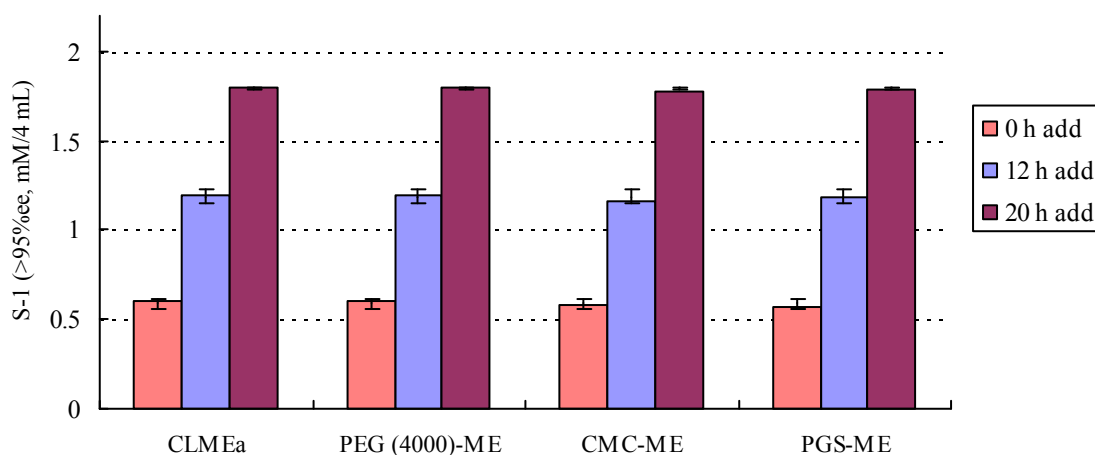
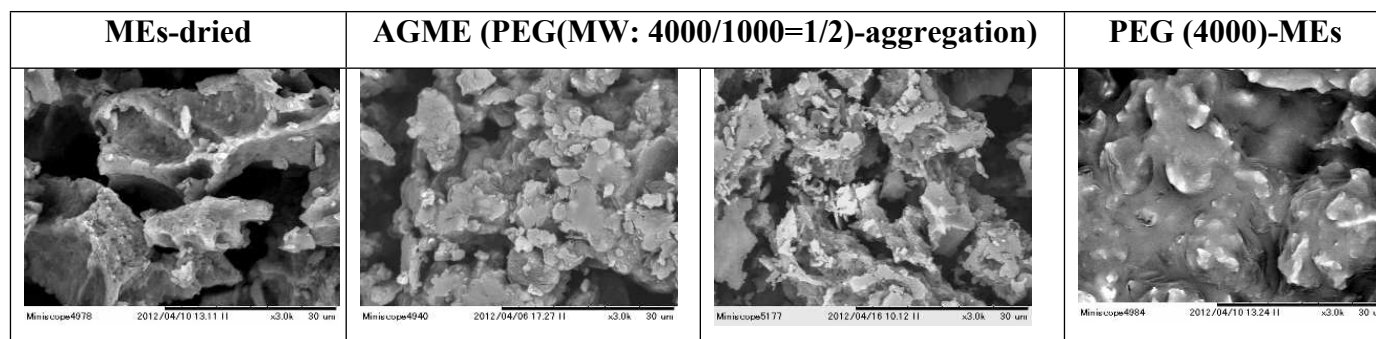


Figure S6. Conversion ratio (%) for the reaction of CMME (20 mg) with *rac*-**1** (1.2 mM) in distilled water (4.0 mL) and DMSO (0.6% (v/v)) at 40 °C with magnetic stirring at 700 rpm for 13 h: 30 h reaction of *rac*-**1** added in three portions at reaction times of 0, 12, and 20 h (1.2 mM \times 3).

Scheme 1S. Microscope photographs of the ME-surfaces that are surrounded by 2.6%-Ca²⁺ or Ca²⁺-compound



3-2. Result of the section 3-1

When an equimolecular amount of the highly polymerized compound compared to ME is used, the PEG (4000)-ME, CMC-ME, and PGS-ME (20 mg) systems only oxidize the (*R*)-isomer with high enantioselectivity at 13 h; thus, greater than 99% ee of the (*S*)-isomer was obtained from *rac*-**1**. In addition, the increase in both the product ketone and unreacted (*S*)-isomer in the aqueous medium was not lost until after three additions (30 h reaction), and the substrate could be added in three portions at 0 h, 8 h and 12 h without any decrease in optical purity or yield. Thus, using CMME (20 mg in 4.0 mL D.W.), (*S*)-**1** (approximately 1.0 mg, 99% ee) was generated from *rac*-**1** (3.6 mM) in 30 h, as shown in **Figure S6**. Furthermore, if no compound modification was applied, no stereoselectivity was observed in the reaction (i.e., non-PEG/freeze-dried (FD): no PEG (4000) and no freeze-drying) with *rac*-**1**, and both isomers were oxidized to the corresponding ketone. These results thus indicated that ME-compound modification improves the intensity and/or stereoselectivity of asymmetric oxidation in aqueous media, as shown in **Figures S5 and S6**, and implies that a ME-active site surrounded by 2.6% Ca²⁺ or Ca²⁺-compounds may affect the ability of the reactant to enter beyond the metallic surface after GA-/highly polymerized compound treatment.

4. Data for the specific activity (unit/(mg·min)) of CMME and AGME.

This section examines the asymmetric oxidation activity of CLME_a and the oxidation activity of AGME (5, 10, 15, and 20 mg) with *rac*-1 (1.2 mM) at 40 °C under magnetic stirring at 700 rpm for 34-h bioconversions in aqueous media (4.0 mL D.W.) with water miscible DMSO (<1.0%) to determine the unit of activity.

4-1. Specific activity (unit/(mg·min))

During the 34-h incubation at 40 °C, the substrate solution (30 µL, 20,000 ppm) was added in three portions at 0, 12, and 20 h. Table 3-1 show the dependence of the specific activity (unit/(mg·min)) on the quantity of CLME_a and AGME (mg), respectively. The unit indicates that the enzyme amount is capable of oxidizing *rac*-1 (1 µmol) per minute. The unit indicates that the enzyme amount (mg) is capable of oxidizing *rac*-1 (1 µmol) per minute.

Table S7. Differences in the specific activity (unit/(mg·min)) of CLME_a and AGME. Details of the calculation formulas and results are noted below the table.

CLME _a (mg)	Instant velocity (IV) (mM/h)	Activity (AC) (unit/(4 mL·min))	Specific activity (SA) (unit/(mg·min))
5	0.045 ^a	0.003 ^a	0.0006^a
10	0.0675 ^a 0.085 ^b	0.0045 ^a 0.00567 ^b	0.00045 ^a 0.000567 ^b
15	0.068333333 ^a 0.125 ^b	0.004555556 ^a 0.008333333 ^b	0.000303704 ^a 0.000555556 ^b
20	0.075 ^a 0.15 ^b	0.005 ^a 0.01 ^b	0.00025 ^a 0.0005 ^b
AGME (mg)	Instant velocity (IV) (mM/h)	Activity (AC) (unit/(4 mL·min))	Specific activity (SA) (unit/(mg·min))
5	0.06 ^c	0.004 ^c	0.0008^c
10	0.098 ^c 0.13 ^d	0.006533 ^c 0.0867 ^d	0.000653 ^c 0.000867 ^d
15	0.12 ^c 0.20 ^d	0.008 ^c 0.01333333 ^d	0.000533 ^c 0.00088 ^d
20	0.15 ^c 0.25 ^d	0.01 ^c 0.016667 ^d	0.0005 ^c 0.0008 ^d

Calculation formula and data in CLME and AGME

IV (see Figure 5a) = Δ ketone (mM) ÷ Time (h)

AC = IV (mM/h) × 0.004 (4 mL/L) × 1000 (M/mM) ÷ 60 (min/h), SA = AC (unit/4 mL per min) ÷ CLPC_a (mg)

^aUpper shows the data of “Max IV in the 1st stage (0.6 mM: 8–12 h)”

^bUnder shows the data of “Max IV in the 2nd stage (0.6 mM– 1.2 mM: 16–18 h)”

^cUpper shows the data of “Max IV in the 1st stage (1.2 mM: 8– 12 h)”

^dUnder shows the data of “Max IV in the 2nd stage (1.2 mM– 2.4 mM: 1– 18 h)”

4-2. Results of section 4-1.

The results indicate that the activity of CLME_a/AGME is approximately 0.6 mU/0.8 mU. Overall, in comparison to AGME, the unit of CLME_a appears to be lower because of the particle sizes of PEG (1000 or 4000) being utilized. The solubility of *rac*-1 (1.2 mM) is difference with PEG (MW: 4000/1000 = 1/2 or MW: 4000) in water (4 mL) containing 0.6% (v/v) DMSO: In the solubility, PEG (MW: 4000/1000 = 1/2) may be higher than PEG (4000). Thus, the ME-dried (20 h) working with a pure dehydrogenase activity for biotransformation may be surmountable in the presence of added PEG (MW: 1000/4000 = 2/1 or MW: 4000).

5. Gel-filtration for given a single band in F from many band in A (see SDS-PAGE)

The ME-suspension (10 mL) eluted from the PP-gel, which was incubated for 48 h, was first separated using a gel-filtration system. These were determined using a ÄKTA explorer 10S system. Sample (10 mL or 2 mL) was injected onto a HiLoad16/60 Superdex 200 pg column at 4 °C. Conductivity-**brown**, 280 nm-**blue**, 254 nm-**pink**, and 340 nm-**red**.

Figure S7. Gel-filtration chromatograms:

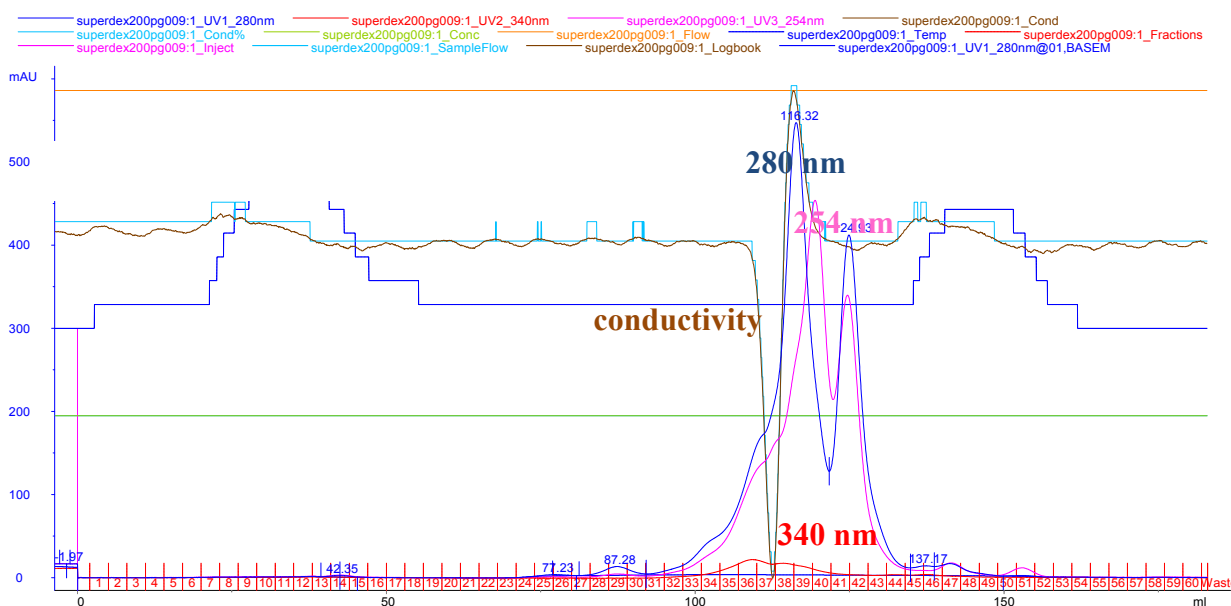


Figure S8. The supernatant of the 5% PP aqueous suspension acquired by centrifugation (2 mL).

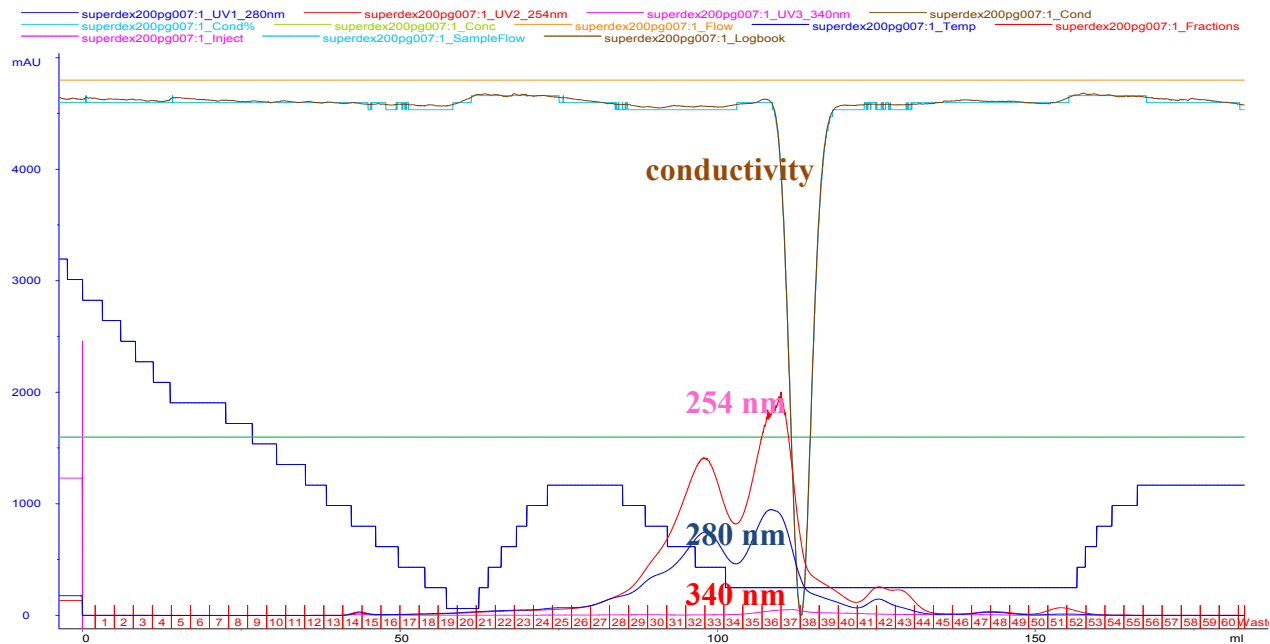
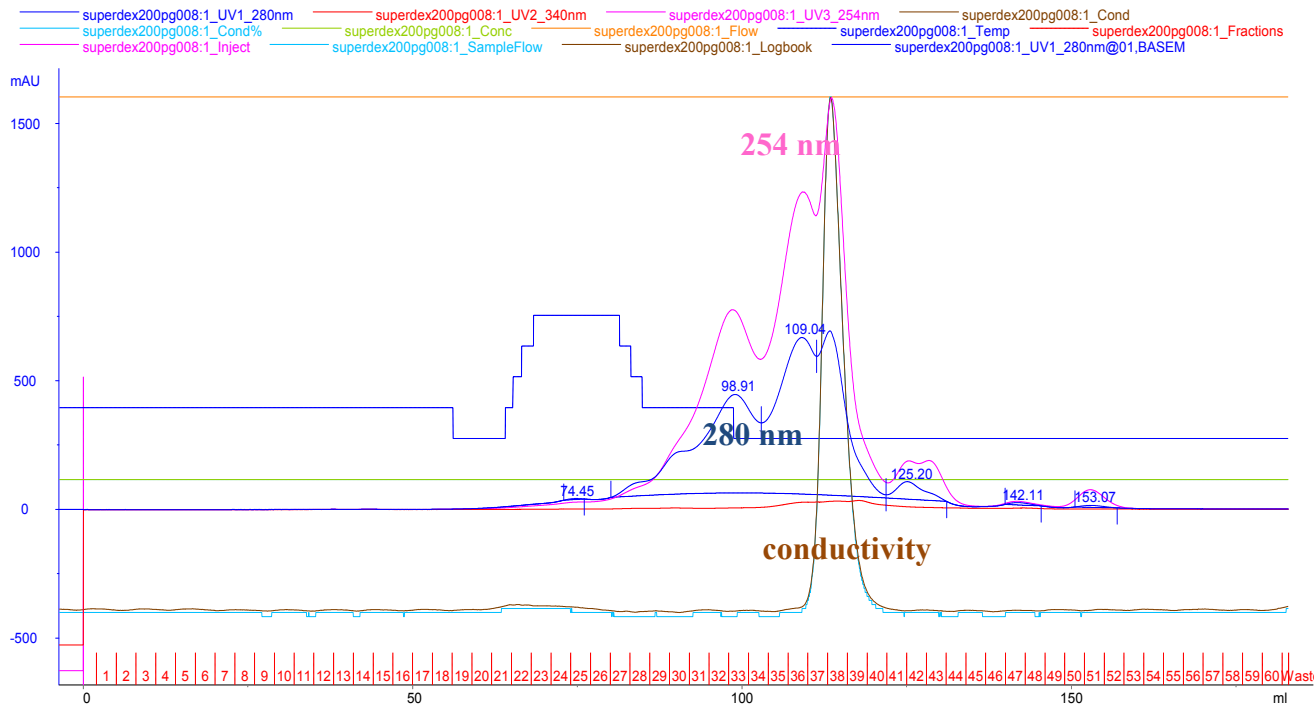


Figure S9. Data of the supernatant (2 mL) of the molecular standard: a, ferritin (440 kDa); b, aldolase (158 kDa); c, conalbumin (75 kDa); d, ovalbumin (44 kDa); e, carbonic anhydrase (29 kDa); f, ribonuclease A (13.7 kDa); g, aprotinin (6.5 kDa).



5-2. Results of the section 5-1.

As shown in **Figures S7-S9**, there are significant differences in the absorbance chromatograms of conductivity (**brown**). This is caused by the deferent conductivity between Tris-HCl (50 mM) NaCl (150 mM, pH8.0) and ME-suspension (10 mM, water). Interestingly, the suspension-injected (10 mL) can be successfully purified with sample **A** in SDS-PAGE to give a single band in **F**: the molecular mass of fraction 36 is not detected by 20 kDa but by 6.5 kDa. This means that the purpose of the gel-filtration chromatograms could be in the purification of sample **A** to sample **F**.

6. Physicochemical analysis for the detection of ME-HBP

6-1. Bradford method for the sample of SDS-PAGE

In SDS-PAGE result, the different concentrations of sample **F** (ME-redox protein), sample **A**, and sample **B** (i.e., **A** and **B** are the suspensions for producing CLME_a) was evaluated for the ME-redox protein concentration, and therefore, their concentrations were examined using the Bradford method

Table S8. Bradford method for the sample **F**, and the **F**s in sample **A** and **B**.

Samples		Bradford method for protein conc. analysis			
		whole conc.(X)	F conc.(Y)	X/Y	Y/X% (v/v)
A	MEs suspension eluted from PP-gel	270 µg/mL	14.9 µg/mL	18.1	5.5%
B	Aqueous suspension of A precipitate by centrifugation	298 µg/mL	20.5 µg/mL	14.5	6.9%
F	Fraction 36 gel-filtrated from sample A	49 µg/mL	—	—	—

*In the SDS-PAGE result, **Red** is precipitate, **Green** is supernatant, **DE** are treated with (NH₄)₂SO₄).

6-1-2. PMF /LCMS-IT-TOF analyses and MASCOT analyses for six bands

Further, In-gel digestion of the other six obtained bands (single bands 1–6 monitored by SDS-Page) was optionally performed by PMF. Also, the data obtained by MASCOT analyses are shown below.

Table S9. MASCOT analysis of the band 1-6 in SDS-PAGE

Band	Score	MASCOT hit
------	-------	------------

1	77	Na ⁺ -type flagellar protein MotY precursor
2	79	unnamed protein product [Clostridium ljungdahlii DSM 13528]
3	79	GTP diphosphokinase [Phascolarctobacterium succinatutens YIT 12067]
4	80	extracellular ligand-binding receptor [Desulfovibrio africanus str. Walvis Bay]
5	> 46	oligopeptide ABC transporter substrate-binding protein [Brevibacillus brevis NBRC 100599]
6	72	conserved hypothetical protein [Wolbachia endosymbiont of Drosophila ananassae]

6-2. Result of the section 6-1.

These result also indicated that the ratio of the ME-redox protein per MEs is approximately 1/15– 1/20 (~5%– 7%) (see **Table S8**), and the others (>90%) of MEs mainly contain PP's wreck from the cell membrane or cell wall, such as an extracellular ligand-binding receptor (band 4) or oligopeptide ABC transporter substrate-binding protein (band 5) (see **Table S9**).

6-3. N-terminal amino acid sequence and BLAST analysis of fraction 36 (band 7 in SDS-PAGE).

N-terminal amino acid sequence (protein sequencing) was accomplished using the protein sequencer PPSQ-21A (Shimadzu) with single band 7 of the ME-redox protein in sample F monitored by SDS-Page.

Table S10. BLAST query sequence analysis with N-terminal sequence (33 residues) identified.

Accession	Region	MW	Length	Query coverage	E value
YP 262445.1^a	HasAp	20853	205	93%	2e-11
3ELL A	HasAp	NA ^b	185	93%	4e-8
YP 001347105.1	HasAp	20717	205	93%	5e-8
ZP 01366858.1	HasAp	20786	205	93%	5e-8
NP 252097.1	HasAp	20772	205	93%	5e-8
AAT49927.1	HasAp	NA ^b	206	93%	5e-8
GAA21312.1	HasAp	NA ^b	219	93%	5e-8

3MOL A	HasAp	NA ^b	184	93%	7e-6
--------	-------	-----------------	-----	-----	------

^aYP 262445.1: The accession hit on the query sequence was limited between the query coverage (>93%) and E value (2e-11), a 20.853 kDa HasAp gene product [*Pseudomonas fluorescens Pf-5*] from plant commensal bacteria, that can inhibit the rhizosphere and produce secondary metabolites that suppress soilborne plant pathogens.⁹

^bNA = no BLAST correlation.

6-4. Result of the section 6-3.

Although no BLAST-hit data exemplifying an HasAp gene was detected from the plant (**Table S10**), for the connection between HBP [*Pseudomonas fluorescens Pf-5*]² and PP, it is thought that the existence of the PP-HasAp gene (hemophore)⁵ may be due to broad acquisition by the plant rather than by bacterial contamination (e.g., PP). This is indicated by the consistency of both the location of pea utilized (i.e., PP-origin: not rhizosphere but bean therein²) and the germfree process of MEs-purification. In addition, as direct evidence of PP-heme, it has been reported that the plant-HBP^{3a} and bacterial-HBP^{3b} produce secondary metabolites.³ Thus, the PP-HBP, incorporating iron electron-transfer system in the presence of oxygen ($\text{Fe}^{2+} \rightleftharpoons \text{Fe}^{3+}$ with O_2), being seen when O_2 is varied, as occurs for P450 and/or CytC_o,^{4a-4c} may be enabled.⁴⁻⁵ In addition, the MEs-activity is competitively inhibited by the addition of a chelating agent such as 1.0 mM EDTA.¹

7. Chromatograms of the N-terminal amino-acid sequence of band-F

Another PDF file “Protein sequence chromatogram” shows the raw data of 33 amino-acid sequence (see Table 4) detected by PPSS-21A protein sequencer (Shimazu).

8. References attached by PDF

- (1) H. Nagaoka, K. Udagawa, K. Kirimura, *Biotechnol. Prog.* **2012**, 28, 953–961.
- (2) I. T. Paulsen, C. M. Press, J. Ravel, D. Y. Kobayashi, G. S. Myers, D. V. Mavrodi, R. T. DeBoy, R. Seshadri, Q. Ren, R. Madupu, R. J. Dodson, A. S.

Durkin, L. M. Brinkac, S. C. Daugherty, S. A. Sullivan, M. J. Rosovitz, M. L. Gwinn, L. Zhou, D. J. Schneider, S. W. Cartinhour, W. C. Nelson, J. Weidman, K. Watkins, K. Tran, H. Khouri, E. A. Pierson, L. S Pierson 3rd, L. S. Thomashow, J. E. Loper, *Nat. Biotechnol.* 2005, **23**(7), 873.

- (3) (a) W. Adam, W. Boland, J. Hartmann-Schreier, H-U. Hump, M. Lazarus, A. Saffert, C. R. Saha-Moller, P. Schreier, *J. Am. Chem. Soc.* 1998, **120**, 11044. (b) M. Landwehr, L. Hochrein, R. C. Otey, A. Kasrayan, E. J. Bäckvall, H. F. Arnold, *J. Am. Chem. Soc.* 2006, **128**, 6058. (c) A. R. McDonald, M. R. Bukowski, E. R. Farquhar, T. A. Jackson, K. D. Koehntop, Mi Sook Seo, R. F. De Hont, A. Stubna, J. A. Halfen, E. Muonck, W. Nam, L. Que Jr. *J. Am. Chem. Soc.* 2010, **132**, 17118.
- (4) (a) D. S. Lee, H. Yamada, H. Sugimoto, I. Matsunaga, H. Ogura, K. Ichihara, S. Adachi, S. Y. Park, Y. Shiro, *J. Biol. Chem.* 2003, **278**, 9761. (b) O. Shoji, T. Fujishiro, H. Nakajima, M. Kim, S. Nagano, Y. Shiro, Y. Watanabe, *Angew. Chem. Int. Ed.* 2007, **46**, 3656. (c) T. H. Yosca, J. Rittle, C. M. Krest, E. L. Onderko, A.-R. K. Beham, M. T. Green, *Science* 2013, **342**, 825. (d) P. R. Ortiz de Montellano, *Cytochrome P450: Structure, Mechanism, and Biochemistry*, 3rd ed.; Kluwer Academic/Plenum: New York, Boston, Dorcrecht, London, Mosow, 2004.
- (5) (a) M. L. Oldham, D. Khare, F. A. Quioco, A. L. Davidson, J. Chen, *Nature* 2007, **450**, 515. (b) S. Krieg, F. Huché, K. Diederichs, N. Izadi-Pruneyre, A. Lecroisey, C. Wandersman, P. Delepelaire, W. Welte, *PNAS* 2009, **106**(4), 1045. (c) N. Izadi-Pruneyre, N. Wolff, V. Redeker, C. Wandersman, M. Delepierre, A. Lecroisey, *J. Bacteriol.* 1999, **261**, 562. (d) S. Létoffé, K. Omori, C. Wandersman, *J. Bacteriol.* 2000, **182** (16), 4401.