

Table S1. Sequences for phylogenetic analysis.

Names	Accession	Description	Organisms	Length [aa]	Taxonomy
AF101058 - AAD1644 0.1	AAD16440.1	ethylene-forming enzyme	<i>Pseudomonas syringae</i> pv. <i>Phaseolicola</i>	350	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i>
MBW4490 662	MBW449066 2.1	MAG: hypothetical protein KME12_23050	<i>Trichocoleus desertorum</i> ATA4-8-CV12	339	Bacteria; Cyanobacteria; Synechococcales; Trichocoleusaceae; <i>Trichocoleus</i>
MBW4538 205	MBW453820 5.1	MAG: hypothetical protein KME43_03555	<i>Myxacorys chilensis</i> ATA2-1-KO14	352	Bacteria; Cyanobacteria; Pseudanabaenales; Leptolyngbyaceae; <i>Myxacorys</i> ; <i>Myxacorys chilensis</i>
RAM5295 8	RAM52958.1	MAG: MFS transporter	<i>Hapalosiphona ceae cyanobacteriu m</i> JJU2	360	Bacteria; Cyanobacteria; Nostocales; Hapalosiphonaceae
RCJ18531	RCJ18531.1	MFS transporter	Nostoc sp. ATCC 43529	361	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; <i>Nostoc</i>
RML4951 4	RML49514.1	2OG-Fe oxygenase	<i>Pseudomonas syringae</i> pv. <i>pisi</i>	344	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i> ; <i>Pseudomonas syringae</i>
TMH3290 0	TMH32900.1	MAG: isopenicillin N synthase family oxygenase	<i>Betaproteobact eria bacterium</i>	352	Bacteria; Proteobacteria; Betaproteobacteria
WP_01461 8742	WP_0146187 42.1	isopenicillin N synthase family oxygenase	<i>Ralstonia solanacearum</i>	347	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; <i>Ralstonia</i>
WP_01535 1455	WP_0153514 55.1	isopenicillin N synthase family oxygenase	<i>Myxococcus stipitatus</i>	360	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Myxococcus</i>
WP_01936 2686	WP_0193626 86.1	isopenicillin N synthase family oxygenase	<i>Pseudomonas fuscovaginae</i>	350	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i>
WP_05742 6137	WP_0574261 37.1	isopenicillin N synthase family oxygenase	<i>Pseudomonas syringae</i>	345	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i>
WP_06334 3083	WP_0633430 83.1	MULTISPECIES: isopenicillin N synthase family oxygenase	<i>Pseudomonas</i>	353	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae

WP_07178 0333	WP_0717803 33.1	isopenicillin N synthase family oxygenase	<i>Fischerella</i> sp. PCC 9431	385	Bacteria; Cyanobacteria; Nostocales; Hapalosiphonaceae; <i>Fischerella</i>
WP_07495 0276	WP_0749502 76.1	isopenicillin N synthase family oxygenase	<i>Myxococcus</i> <i>fulvus</i>	360	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Myxococcus</i>
WP_09656 2523	WP_0965625 23.1	isopenicillin N synthase family oxygenase	<i>Scytonema</i> sp. NIES-4073	359	Bacteria; Cyanobacteria; Nostocales; Scytonemataceae; <i>Scytonema</i> ; unclassified <i>Scytonema</i>
WP_11666 5714	WP_1166657 14.1	isopenicillin N synthase family oxygenase	<i>Pseudomonas</i> sp. GL93	346	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i>
WP_12349 6614	WP_1234966 14.1	isopenicillin N synthase family oxygenase	<i>Pseudomonas</i> <i>frederiksbergensis</i>	344	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i>
WP_13111 8892	WP_1311188 92.1	isopenicillin N synthase family oxygenase	<i>Mastigocladus</i> <i>laminosus</i>	360	Bacteria; Cyanobacteria; Nostocales; Hapalosiphonaceae; <i>Mastigocladus</i>
WP_14164 1058	WP_1416410 58.1	isopenicillin N synthase family oxygenase	<i>Myxococcus</i>	362	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Myxococcus</i>
WP_16386 1341	WP_1638613 41.1	isopenicillin N synthase family oxygenase	<i>Myxococcus</i> <i>eversor</i>	360	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Myxococcus</i>
WP_16398 9172	WP_1639891 72.1	isopenicillin N synthase family oxygenase	<i>Pyxidicoccus</i> <i>caerfyrddinensis</i>	358	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Pyxidicoccus</i>
WP_16934 3509	WP_1693435 09.1	isopenicillin N synthase family oxygenase	<i>Pyxidicoccus</i> <i>fallax</i>	356	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Pyxidicoccus</i>
WP_17447 5597	WP_1744755 97.1	isopenicillin N synthase family oxygenase	<i>Myxococcus</i> sp. CA033	360	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Myxococcus</i> ; unclassified <i>Myxococcus</i>
WP_17643 4236	WP_1764342 36.1	isopenicillin N synthase family oxygenase	<i>Myxococcus</i> sp. AM011	360	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Myxococcus</i> ; unclassified <i>Myxococcus</i>
WP_18108 0955	WP_1810809 55.1	isopenicillin N synthase family oxygenase	<i>Pseudomonas</i> <i>lurida</i>	351	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i>

WP_18128 6820	WP_1812868 20.1	isopenicillin N synthase family oxygenase	<i>Pseudomonas brassicacearum</i>	346	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i>
WP_19113 3867	WP_1911338 67.1	isopenicillin N synthase family oxygenase	<i>Phormidium tenue</i>	352	Bacteria; Cyanobacteria; Oscillatoriothyracaceae; Oscillatoriales; Oscillatoriaceae; <i>Phormidium</i>
WP_19387 4723	WP_1938747 23.1	isopenicillin N synthase family oxygenase	<i>Oculatella</i> sp. LEGE 06141	356	Bacteria; Cyanobacteria; Pseudanabaenales; Oculatellaceae; <i>Oculatella</i> ; unclassified <i>Oculatella</i>
WP_20671 5722	WP_2067157 22.1	isopenicillin N synthase family oxygenase	<i>Myxococcus</i> sp. SCHIC003	360	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Myxococcus</i> ; unclassified <i>Myxococcus</i>
WP_21667 0419	WP_2166704 19.1	hypothetical protein	<i>Microcoleus asticus</i>	369	Bacteria; Cyanobacteria; Oscillatoriothyracaceae; Oscillatoriales; Microcoleaceae; <i>Microcoleus</i>
WP_21785 5079	WP_2178550 79.1	MFS transporter	<i>Pseudomonas asgharzadehian a</i>	339	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i>
WP_22301 8911	WP_2230189 11.1	MFS transporter	<i>Pseudomonas</i> sp. P867	346	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i>
WP_22374 5345	WP_2237453 45.1	MFS transporter	<i>Myxococcus</i> sp. XM-1-1-1	360	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Myxococcus</i> ; unclassified <i>Myxococcus</i>
WP_22378 1934	WP_2237819 34.1	MFS transporter	<i>Myxococcus</i> sp. AS-1-15	352	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; <i>Myxococcus</i> ; unclassified <i>Myxococcus</i>
WP_22949 6330	WP_2294963 30.1	hypothetical protein	<i>Nostoc mirabile</i>	360	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; <i>Nostoc</i>

Table S2. Parameters of the five constructed models based on 6VP4.1.A.

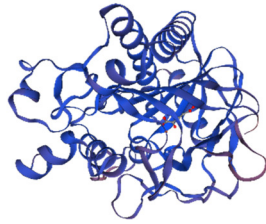
Proteins	Oligo-State	Seq Identity	GMQE	QMEANDisCo Global	Ligands
Efe_MS	Monomer	63.29%	0.87	0.86 ± 0.05	1xAKG, 1xFE
Efe_RS	Monomer	61.40%	0.87	0.84 ± 0.05	1xAKG, 1xFE
Efe_MA	Monomer	67.74%	0.85	0.87 ± 0.05	1xARG, 1xAKG, 1xFE
Efe_NS	Monomer	67.25%	0.87	0.87 ± 0.05	1xAKG, 1xFE
Efe_SS	Monomer	68.10%	0.88	0.87 ± 0.05	1xARG, 1xAKG, 1xFE

* 1 x AKG: α -ketoglutaric acid ligand binding sites; 1 x ARG: arginine ligand binding sites; 1 x FE: FE (III) ion ligand binding sites.

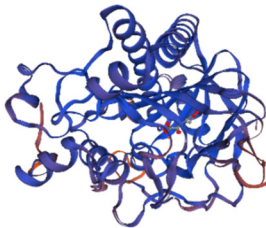
*GMQE (Global Model Quality Estimate) and QMEANDisCo global (QMEAN: Qualitative Model Energy Analysis) give an overall model quality measurement between 0 and 1, with higher numbers indicating higher expected quality. GMQE is coverage dependent, i.e., a model covering only half of the target sequence is unlikely to get a score above 0.5 QMEANDisCo on the other hand evaluates the model 'as is' without explicit coverage dependency.

(a)

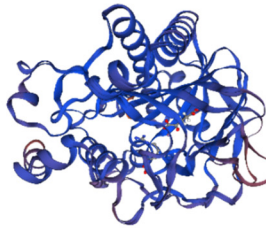
Efe_MS



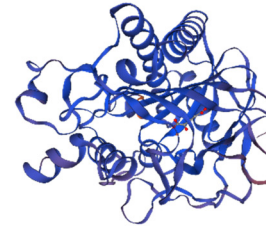
Efe_RS



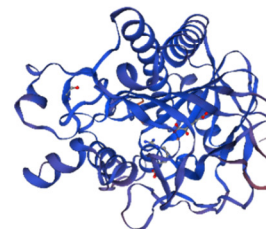
Efe_MA



Efe_NS

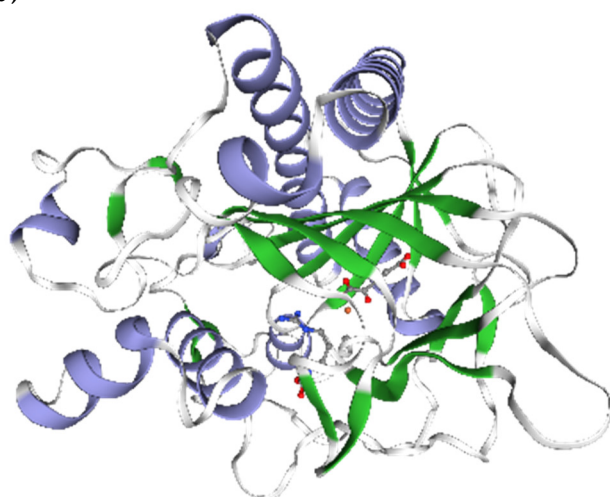


Efe_SS



```
Model_02 MTDLQDLPKPSITGQSDIDLAHQNIQAWRTDGIQVYMNIAQRTKTESAFES 55
6vp4.1.AMTNLQDLPTEVTGADISLGRALIQAWRTDGIQVYMNIAQRTKTESAFES 55
Model_02 RHFPRQSLERKARCVSDLTYSYVYASGEEDPAGSDISYEVETQCRWPLTDQV 110
6vp4.1.AKQFQSLERKARCVSDLTYSYVYASGEEDPAGSDISYEVETQCRWPLTDQV 110
Model_02 SKWPCDQGFNFDSMRQSQCAHASELGSYGERLLRLIALQGLDIDALITDTH 165
6vp4.1.AQWPCDQGFNFDSMRQSQCAHASELGSYGERLLRLIALQGLDIDALITDTH 165
Model_02 GRHHMRVLEDFALSKSTRGIGADTDYGLVIAAADDVGGLYRFPVEGEKRRN 220
6vp4.1.AGWHMRVLEDFALSKSTRGIGADTDYGLVIAAADDVGGLYRFPVEGEKRRN 220
Model_02 NLPHSSAGMYEHDEDFWVKEVFGVLTVPDQILQFDINGYLLSTHRYVLTN 275
6vp4.1.AWLPQESSAGMYEHDEDFWVKEVFGVLTVPDQILQFDINGYLLSTHRYVLTN 275
Model_02 RRFALAYTFEPNFCAQFLFAPSDEDEHYGTHFTNMFMRYYPDRVTTRRI 330
6vp4.1.ARRFALAYTFEPNFCAQFLFAPSDEDEHYGTHFTNMFMRYYPDRVTTRRI 330
Model_02 SKITLTLNLRQEAFLRTAFLEAVFLQRAAG 360
6vp4.1.AENRLAHLEDLKKYSDDR----- 360
Model_03 MGLTQDPLFERILHSEAHRLQGDQNVAAWRADGICFVYMNIAQRTKTESAFES 55
6vp4.1.AMTNLQDLPTEVTGADISLGRALIQAWRTDGIQVYMNIAQRTKTESAFES 55
Model_03 RHFPRQSLERKARCVSDLTYSYVYASGEEDPAGSDISYEVETQCRWPLTDQV 110
6vp4.1.AKQFQSLERKARCVSDLTYSYVYASGEEDPAGSDISYEVETQCRWPLTDQV 110
Model_03 SKWPCDQGFNFDSMRQSQCAHASELGSYGERLLRLIALQGLDIDALITDTH 165
6vp4.1.AQWPCDQGFNFDSMRQSQCAHASELGSYGERLLRLIALQGLDIDALITDTH 165
Model_03 GRHHMRVLEDFALSKSTRGIGADTDYGLVIAAADDVGGLYRFPVEGEKRRN 220
6vp4.1.AGWHMRVLEDFALSKSTRGIGADTDYGLVIAAADDVGGLYRFPVEGEKRRN 220
Model_03 NLPHSSAGMYEHDEDFWVKEVFGVLTVPDQILQFDINGYLLSTHRYVLTN 275
6vp4.1.AWLPQESSAGMYEHDEDFWVKEVFGVLTVPDQILQFDINGYLLSTHRYVLTN 275
Model_03 RRFALAYTFEPNFCAQFLFAPSDEDEHYGTHFTNMFMRYYPDRVTTRRI 330
6vp4.1.ARRFALAYTFEPNFCAQFLFAPSDEDEHYGTHFTNMFMRYYPDRVTTRRI 330
Model_03 SKITLTLNLRQEAFLRTAFLEAVFLQRAAG 360
6vp4.1.AENRLAHLEDLKKYSDDR----- 360
Model_02 MTDLQDLPKPSITGQSDIDLAHQNIQAWRTDGIQVYMNIAQRTKTESAFES 55
6vp4.1.AMTNLQDLPTEVTGADISLGRALIQAWRTDGIQVYMNIAQRTKTESAFES 55
Model_02 RHFPRQSLERKARCVSDLTYSYVYASGEEDPAGSDISYEVETQCRWPLTDQV 110
6vp4.1.AKQFQSLERKARCVSDLTYSYVYASGEEDPAGSDISYEVETQCRWPLTDQV 110
Model_02 SKWPCDQGFNFDSMRQSQCAHASELGSYGERLLRLIALQGLDIDALITDTH 165
6vp4.1.AQWPCDQGFNFDSMRQSQCAHASELGSYGERLLRLIALQGLDIDALITDTH 165
Model_02 GRHHMRVLEDFALSKSTRGIGADTDYGLVIAAADDVGGLYRFPVEGEKRRN 220
6vp4.1.AGWHMRVLEDFALSKSTRGIGADTDYGLVIAAADDVGGLYRFPVEGEKRRN 220
Model_02 NLPHSSAGMYEHDEDFWVKEVFGVLTVPDQILQFDINGYLLSTHRYVLTN 275
6vp4.1.AWLPQESSAGMYEHDEDFWVKEVFGVLTVPDQILQFDINGYLLSTHRYVLTN 275
Model_02 RRFALAYTFEPNFCAQFLFAPSDEDEHYGTHFTNMFMRYYPDRVTTRRI 330
6vp4.1.ARRFALAYTFEPNFCAQFLFAPSDEDEHYGTHFTNMFMRYYPDRVTTRRI 330
Model_02 SKITLTLNLRQEAFLRTAFLEAVFLQRAAG 360
6vp4.1.AENRLAHLEDLKKYSDDR----- 360
Model_02 MTDLQDLPKPSITGQSDIDLAHQNIQAWRTDGIQVYMNIAQRTKTESAFES 55
6vp4.1.AMTNLQDLPTEVTGADISLGRALIQAWRTDGIQVYMNIAQRTKTESAFES 55
Model_02 RHFPRQSLERKARCVSDLTYSYVYASGEEDPAGSDISYEVETQCRWPLTDQV 110
6vp4.1.AKQFQSLERKARCVSDLTYSYVYASGEEDPAGSDISYEVETQCRWPLTDQV 110
Model_02 SKWPCDQGFNFDSMRQSQCAHASELGSYGERLLRLIALQGLDIDALITDTH 165
6vp4.1.AQWPCDQGFNFDSMRQSQCAHASELGSYGERLLRLIALQGLDIDALITDTH 165
Model_02 GRHHMRVLEDFALSKSTRGIGADTDYGLVIAAADDVGGLYRFPVEGEKRRN 220
6vp4.1.AGWHMRVLEDFALSKSTRGIGADTDYGLVIAAADDVGGLYRFPVEGEKRRN 220
Model_02 NLPHSSAGMYEHDEDFWVKEVFGVLTVPDQILQFDINGYLLSTHRYVLTN 275
6vp4.1.AWLPQESSAGMYEHDEDFWVKEVFGVLTVPDQILQFDINGYLLSTHRYVLTN 275
Model_02 RRFALAYTFEPNFCAQFLFAPSDEDEHYGTHFTNMFMRYYPDRVTTRRI 330
6vp4.1.ARRFALAYTFEPNFCAQFLFAPSDEDEHYGTHFTNMFMRYYPDRVTTRRI 330
Model_02 SKITLTLNLRQEAFLRTAFLEAVFLQRAAG 360
6vp4.1.AENRLAHLEDLKKYSDDR----- 360
```

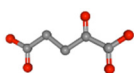
(b)



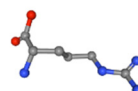
Efe_PS-AAD16440.1 (6vp4.1.A)



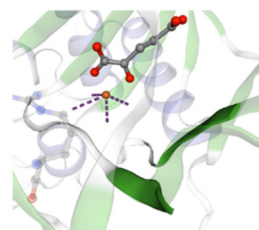
FE(III)ION



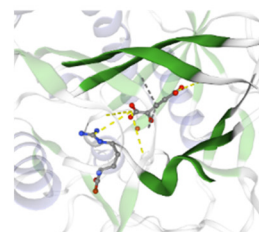
2-OXOGLUTARIC ACID



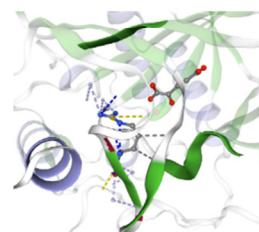
ARGININE



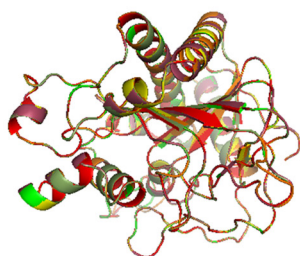
FE site



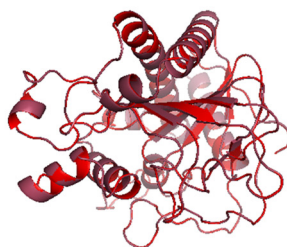
AKG site



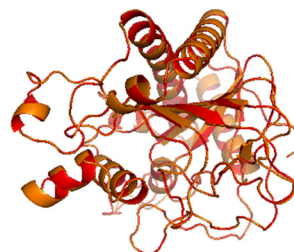
ARG site



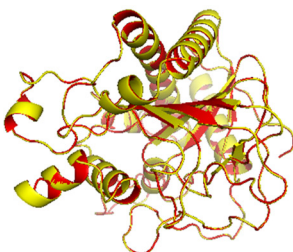
All the six



Efe_MS RMSD=0.057 (322 to 322 atoms)



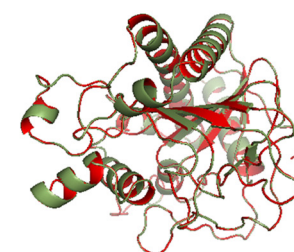
Efe_RS RMSD=0.056 (297 to 297 atoms)



Efe_MA RMSD=0.055 (312 to 312 atoms)



Efe_NS RMSD=0.054 (314 to 314 atoms)



Efe_SS RMSD=0.058 (318 to 318 atoms)

Figure S1. Model of Efes, 6VP4.1.A and its active sites. (a) Efe models constructed by SWISS MODEL and structure aligning to 6VP4.1.A. They are shown by confidence level: blue—red: high confidence—low confidence. α -helix: labeled with the arrow; β -helix: labeled with square. Little change shows in α -helix or β -helix and most sites are in high confidence. Changes are marked by red box. (b) Model of 6VP4.1.A and its active sites (α -helix: purple; β -helix: green; active sites are darker in the right figures). (c) Structure alignment by PyMOL between five Efes and 6vp4.1.A (in red). RMSD root-mean-square deviation, a parameter used to indicate differences in atomic positions between protein structures. RMSDs of these five aligning are all less than 0.1 (abnormal atoms were rejected during the cycle), which means these models have little difference in structures. There are slight fluctuations in atomic positions between protein structures, while the main frameworks remain the same.



Figure S2. Analysis of disulfide bond formation of cysteine residue in the original model 6VP4.1.A.

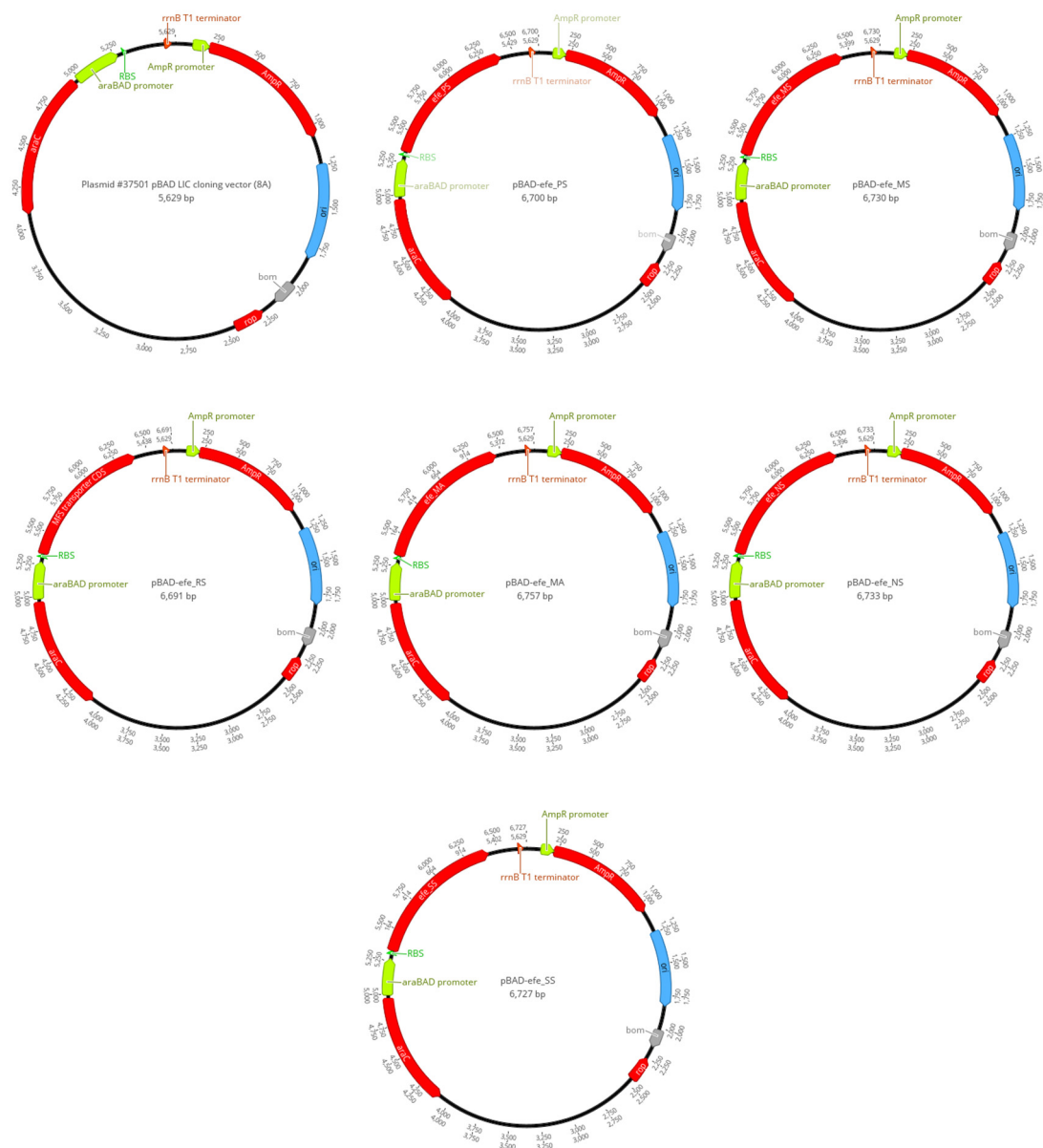


Figure S3. Plasmids profiles of pBAD_LIC_cloning vector and the six recombinant plasmids.

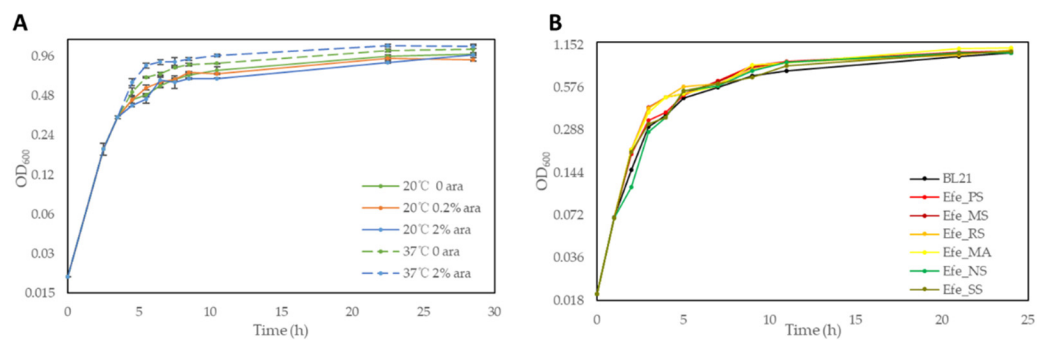


Figure S4. Growth curves of BL21_efe⁺ in LB medium with arabinose and antibiotic (ampicillin) in low temperature. **(A).** Growth in LB with arabinose concentration of 0 (green), 0.2% (orange) and 2% (blue) under 20 °C (full line) or 37 °C (dashed line); **(B).** Growth curve of the six engineering strains in LB with 2% arabinose and 50 µg/mL ampicillin: black: BL21_WT; red: Efe_PS; rose red: Efe_MS; orange: Efe_RS; yellow: Efe_MA; green: Efe_NS; brown: Efe_SS.

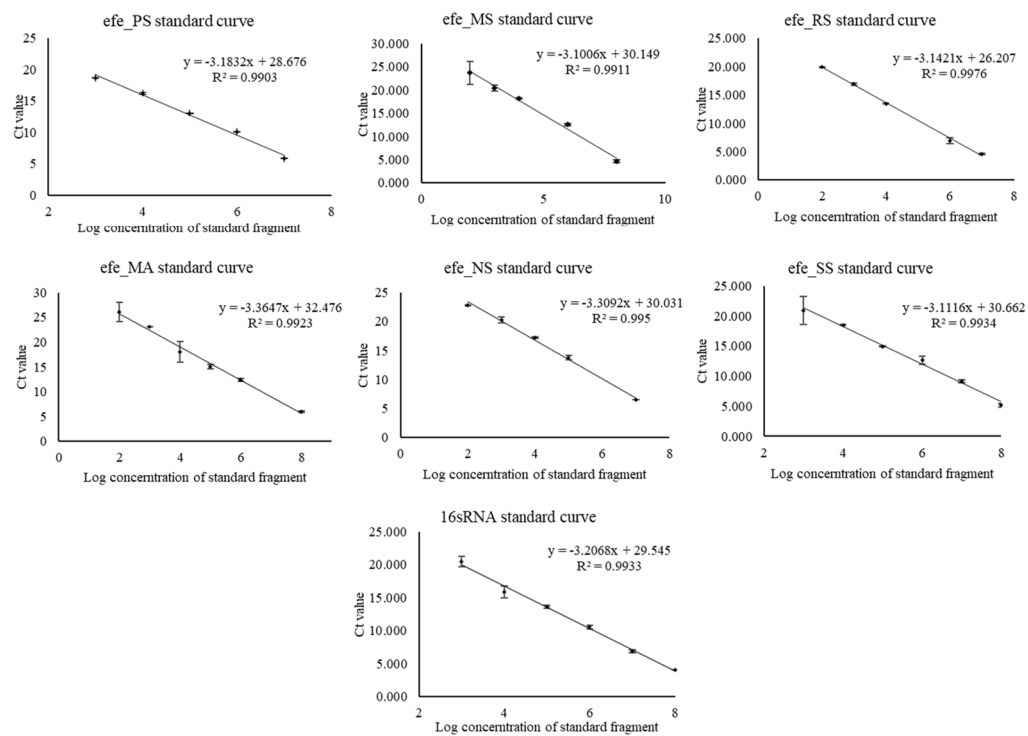


Figure S5. RT-qPCR standard curves of *efe* genes and 16sRNA gene.

Table S3. Protein MS (Q-E test) results of Efes.

Accession	Mass	Score	Matches ¹	Sequences ²	emPAI ³	Coverage
Efe_NS	39593	9040	268(233)	35(27)	49.86	71%
Efe_PS	39819	3179	160(113)	37(20)	12.90	70%
Efe_RS	41756	2542	89(70)	30(18)	12.35	68%
Efe_MS	40953	2060	129(74)	32(15)	8.50	58%
Efe_SS	39223	1406	70(33)	24(10)	1.44	47%
Efe_MA	42477	634	53(24)	21(10)	1.85	30%

¹Matches: the total number of peptide matches, in parentheses, is the number of matches above the significance threshold; ²Sequences: the total number of matched sequences is the number of sequences higher than the significance threshold in parentheses; ³emPAI: $10^{(\text{Nobserved}/\text{Nobservable})-1}$

<p>Efe_PS Score: 3179</p> <p>1 MTNLQTFELP TEVTGCAADI SLGRALIQAQ QKDGIPIKTI DSEQDRKTQE 51 AMAASKQFCK EPLTFKSSCV SDLTYSGYVA SGEEVTAGKP DFPEIFTVCK 101 DLSVGDRVK AGWPCGHPVP WPNNTYQKSM KTFMEELGLA GERLLKLTAL 151 GFELPINTFT DLTRDGWHHM RVLRFPPQTS TLSRGIGAHT DYGLLVIAAQ 201 DDVGGLYIRP PVEGEKRNRR WLPCESSAGM FEHDEPWTFF TPTPGWTVF 251 PGDILQFMIG QLLSTPHKV KLNTRERFAC AYFHEPNFEA SAYPLFEPSA 301 NERIHYGEHF TNMFMRCPYP RITTQRINKE NLAHLEDLK KYSDTRATGS 351 _</p>	<p>Efe_MS Score: 2060</p> <p>1 MIELETFLQP QSVSGREADI ALGLTMVRAW RRDGIQVVM SPAQAEKSQR 51 AFELSRHFFR QSLETKARCV SDLTYSGYIA SQQELTASEA DLSEVFTVCR 101 DVPLTDPRVQ SKWPCHGCPG WPDESWRQGM QAHAELGSV GERLLRLIAL 151 GLGLDIDALT TLTHDGWHHM RVLRFPPARP TTRTGIGAHT DYGLLVIAAQ 201 DDVGGLYIRP PVEGEKRNRR WLPHESSAGM YEHEDEPWTFF KPVPGVLTFF 251 PGDILQFLTR GYLLSTPHKV VLNTRERFAL AYFHEPQFEA CVRPLSAPTR 301 DEYIHYGTHF TNMFMRSYPD RVTTQRILDE SRLTTLSWLR QEAVLRTAPL 351 EAVPLQRAAG _</p>
<p>Efe_NS Score: 9040</p> <p>1 MTGLTTFHLP ERILHSEHR QLQDMVAAW RADGIFQIAL STPQQHTTDE 51 AFAQSRFFFE LDFETKRRHV SELTYSGYIA SREEITAGEA DYSEIFTICP 101 DIGMDDVRVR EGWPCGHPVP WPGTAYRDRM TDFTGMLGAF GERLLQLTAL 151 GLGLDDMETF TRLTRDGWHHM MRVLRFPVTP SSENARGIGA HTDYGLLVIAA 201 AQDDVGGLYV RPPIAGERRN RNWLPSESTA GMFEHDDGWT FIKPEPAVLT 251 VFPQDFLQFL TGGHLMSTPH KVLNTRERF AMAYFHEPNF DAWVEPLKAD 301 ADTDAPIHY GTHFTNFMFR CYPKRITTRR IEEQGLDLRL PALGEVA_ 351 _</p>	<p>Efe_MA Score: 634</p> <p>1 MTHKYQEKIE VSNLQIFHLP ESITGIQSDI DIARQMIQAW RRDGIHFHVA 51 NKIQERKSER TFAASRRFFG MPLESKSQFI SDLTYSGYIA SGEEVTAGES 101 DYSEIFTVCK DVPLNDRRVQ AQWPCGHPAP WPDEDYQSM KAYMDELGSI 151 GEKLLKLTAL GLELDDINAL TELTKDGWHH MRVLRFPALS QKSTRGIGAH 201 TDYGLLVIAA QDDVGGLYIR PPVEGEKRNRR NWLPTESMGG MYNEEPWIL 251 VKPVPSVLTV FPGDILQFLT NGYLLSTPHK VRLNTRERFA IAYFHEPNFE 301 ACVRPLFAPS SDEHIHYGSH FTNMFMRCPY DRITTRRIID ENRLSILGLV 351 KNEGLRRLTT AKKAIELQR</p>
<p>Efe_RS Score: 2542</p> <p>1 MTDLQTFDLP KSITGQSADI DLAHQMIQAW RTDGIFQVAT NAIQTRKTEN 51 AFEASRRFFR MPLDFKSQCI SNLTYSGYIA SGEEITAGES DYSEIFTICK 101 DVRLDDVRVQ AQWPCGHPVP WPDNNYHQN KAFMDLGLI GEKLLKLTAL 151 GLELDDINAL TKLTRDGWHH MRVLRFPALS EKSTRGIGAH TDYGLLVIAA 201 QDDVGGLYIR PPVEGEKRNRR NWLSDSSAG MYENDPWTFF VKPVPSVLTV 251 FPGDILQFMT HNYLLSTPHK VRLNTRERFA LAYFHEPNFD ACVRPLFDPS 301 NDDYIHYGTH FTNMFMRCPY YRITTRRIID EDRLSVLELL RNEALGMLR 351 PKYKTLVPSY L</p>	<p>Efe_SS Score: 1406</p> <p>1 MTDLQTFHLP KSITGQSADI DTAREIIQAW RTDGIFQVAT NTIQDRKTES 51 AFEASRRFFR MPKFKSQCI SDLNYYGYIA SGEEVTAGKS DYSEIYTICK 101 DIPLNDARVQ AQWPCGHPMP WPDQEHQSM KVFMDLGLI GEKLLKLTAL 151 GLGLDDINAL TKLTRDGWHH MRVLRFPPTS QKSARGIGAH TDYGLLVIAA 201 QDDVGGLYIR PPVEGEKRNRR NWLSTESMAG MYENDPWTFF VKPVPSVLTV 251 FPGDILQFLT NGYLLSTPHK VRLNTRERFA LAYFHEPNFD ACVRPLFDPS 301 SDEHIHYGTH FTNMFMRCPY DRITTRRIIN EDRLSILAR ENKTLGRLLT 351 MKNAYALQR</p>

Figure S6. Protein MS sequence alignment.