

## Supporting information

### Supplementary figures and table legends

**Figure S1.** (A) The gel filtration curve for the purified recombinant PpgL in solution. The AUC results are presented as the ultraviolet absorption in 280 nm. The black solid curve refers to PpgL eluted from ENrich™ SEC 650 10×300 Column. (B) Then the eluted protein was analyzed by SDS-PAGE (purity >95%). The different mutant PA4204 proteins were purified using same method.

**Figure S2.** The major accessible pockets of different seven-bladed propeller lactone catalyzing enzymes (i-vii) and two conserved residues are shown.

**Figure S3.** The totally 21 sites for the diverse enzymatic activities are shown in ribbon diagram of PpgL viewed down the central axis. The 9 residues which are crucial to catalytic activity are indicated in red.

**Figure S4.** The growth curve of PA14- $\Delta ppgl$  and the PA14-WT grown in LB at 37°C. The OD600 of different groups were measured per hour. Each bar represents the mean of three independent measurements ( $\pm$ SEM).

**Figure S5.** Quantitative PCR and gene expression analysis of *ppgl*. Relative mRNA expression of *ppgl* from the WT, complementation plasmid pME6032-*ppgl* strain and different mutants. Each bar represents the mean of three independent measurements ( $\pm$ SEM).

**Table S1.** Statistics on the qualities of diffraction data and model

refinement.

**Table S2.** Primers used in the work.

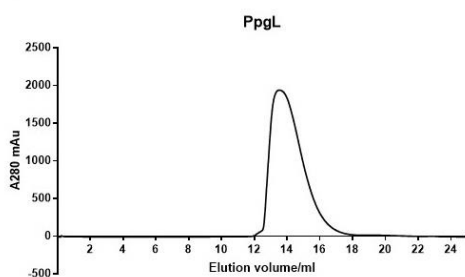
<b>Table S1   Data collection and refinement statistics.</b>		
<b>Space group</b>	<b>P 41 21 2</b>	
<b>Data collection</b>	<b>Cell dimension</b>	
	<i>a, b, c</i> (Å)	91.763, 91.763, 170.708
	$\alpha, \beta, \gamma$ (°)	90, 90, 90
	Wavelength	0.97853
	Resolution (Å)	39.9-1.651 (1.71-1.651) <sup>a</sup>
	I/ $\sigma$ I	15.90 (2.385)
	Completeness (%)	99.98 (99.99)
	Rmerge	0.174 (0.773)
	Redundancy	17.6 (12.2)
<b>Refinement</b>	Resolution (Å)	39.90-1.651 (1.71-1.651)
	No. of reflections	88036 (8682)
	Rwork/Rfree <sup>b</sup>	0.1972/0.2227
	<b>No. of atoms</b>	
	Protein	726
	Ligand/ion	18
	Water	305
	<b>B-factors(Å<sup>2</sup>)</b>	
	Protein	19.53
	Ligand/ion	27.01
	Water	27.57
	<b>R.m.s. deviations</b>	
	Bond lengths (Å)	0.018
	Bond angles (°)	1.73
	Ramachandran plot	97.65/2.35

<sup>a</sup>Numbers in parentheses are statistics of the outer shell. <sup>b</sup>5% of total reflections were set aside for the Rfree calculation.

<b>Table S2. Primers used in the work.</b>			
<b>Number</b>	<b>Primer name</b>	<b>Direction</b>	<b>Sequence</b>
1	ppgl-recombination	Forward	5'AAGAAGGAGATATACATATGGCCAGCCTCTACAACCTGCTG3'
2	ppgl-recombination	Reverse	5'TCCTCGCCCTTGCTCACCATCGGCACCGCCACGAAGCG3'
3	ppgl-pEX18	Forward	5'ACGACGGCCAGTGCCAAGCTTAGCCGCTGTCCGCGAGGAAC3'
4	ppgl-pEX18	Reverse	5'TTCGAGCTCGGTACCCGGGGATGTGGGATGAGGGGCTGACG3'
5	pEX18-Removal	Forward	5'CCTTGCCTCGGCCATCCGCCGATAC3'

	ppgl		
6	pEX18-Removal ppgl	Reverse	5'GGGCAACTCCTTGGCTCGCTATTG3'
7	ppgl-pME6032	Forward	5'GCTAGTCCGAGGCCTCGAGATCATGAGAAGACTGCCACCCCTC3'
8	ppgl-pME6032	Reverse	5'CACACAGGAAACAGAATTCGAGTCACGGCACCGCCACGAAG3'
9	ppgl/Tyr35Ala	Forward	5'GCGACCGAAGGCTCCAGCGAAG3'
10	ppgl/Tyr35Ala	Reverse	5'GGTCCCCACCAGCAGGTTGTAG3'
11	ppgl/Glu84Ala	Forward	5'GCGAACGGACGGGGCGCAAGG3'
12	ppgl/Glu84Ala	Reverse	5'GTTGACCACGAACAGAGTGCGTTG3'
13	ppgl/Tyr139Ala	Forward	5'GCGTCGGTACAGCCGGAAG3'
14	ppgl/ Tyr139Ala	Reverse	5'GTTGGCGACGAACAGGTAGC3'
15	ppgl/Arg175Ala	Forward	5'GCGCAGGTTCCGGTCATGTG3'
16	ppgl/Arg175Ala	Reverse	5'CGGATGCACCTTGTGGCTG3'
17	ppgl/His182Ala	Forward	5'GCGTCGGTGGTGTCTCGCCCGACGGCCAG3'
18	ppgl/His182Ala	Reverse	5'CACATGACCGGAAACCTGGCGCGGATGCAC3'
19	ppgl/Arg234Ala	Forward	5'GCGCATCTGATCTTCAGCGCCGACGGGCGT3'
20	ppgl/Arg234Ala	Reverse	5'CGGGCCGCTGCCGGGCGGGTTCGGGACG3'
21	ppgl/Glu250Ala	Forward	5'GCGCTGAGCGCCAGGTGATGGTGTTCT3'
22	ppgl/Glu250Ala	Reverse	5'CAGGGTCAGGTAGGCGAAACGCCCTC3'
23	ppgl/Arg302Ala	Forward	5'GCGGGCGACGACAACCAACTGGTGACC3'
24	ppgl/Arg302Ala	Reverse	5'ATTGAGCACGCCGAGGAAGCGGCCGTC3'
25	ppgl/Arg334Ala	Forward	5'GCGGAATTCGCTTTCTCG3'
26	ppgl/Arg334Ala	Reverse	5'CGGCTCGGTGCCTTCCAC3'
27	qPCR-ppgl	Forward	5'GAGAAGACTGCCACCCCTCT3'
28	qPCR-ppgl	Reverse	5'TCGGTATAGGTCCCCACCAG3'

**Fig.S1A**



**B**

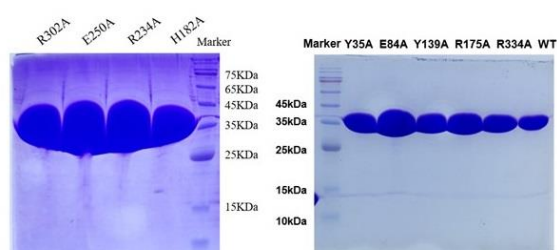


Fig.S2

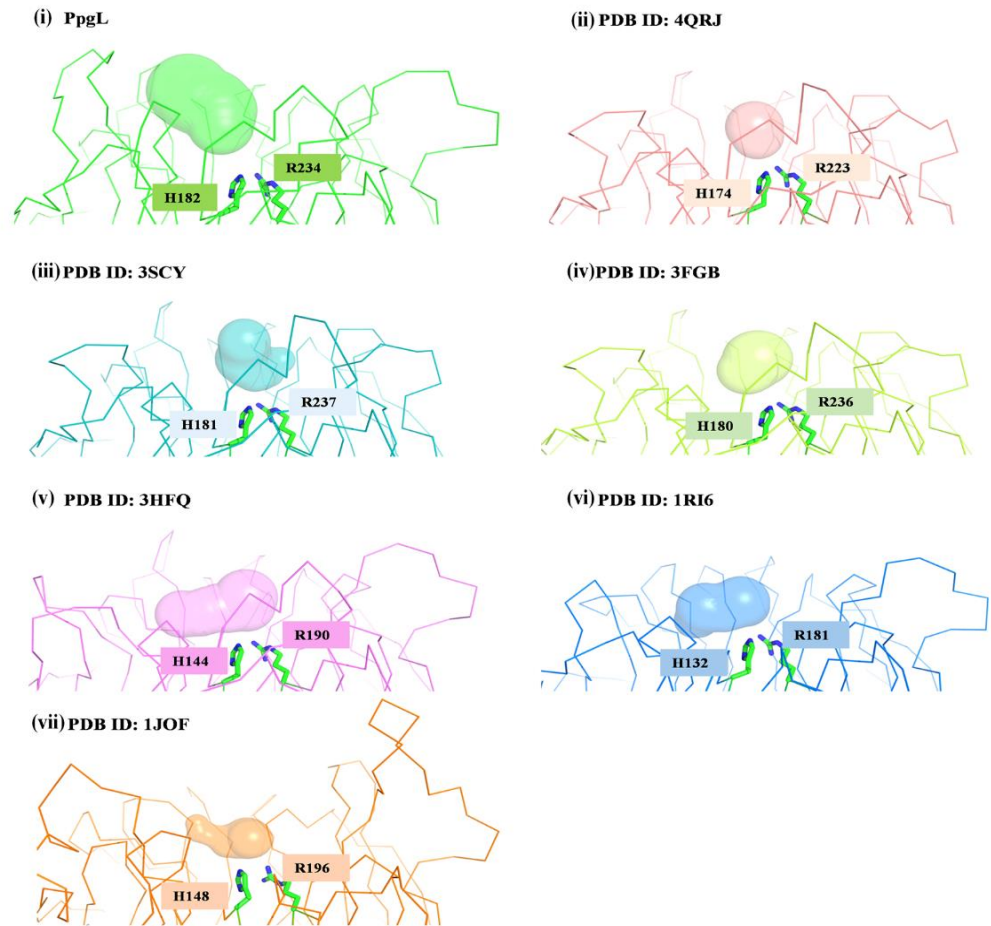


Fig.S3

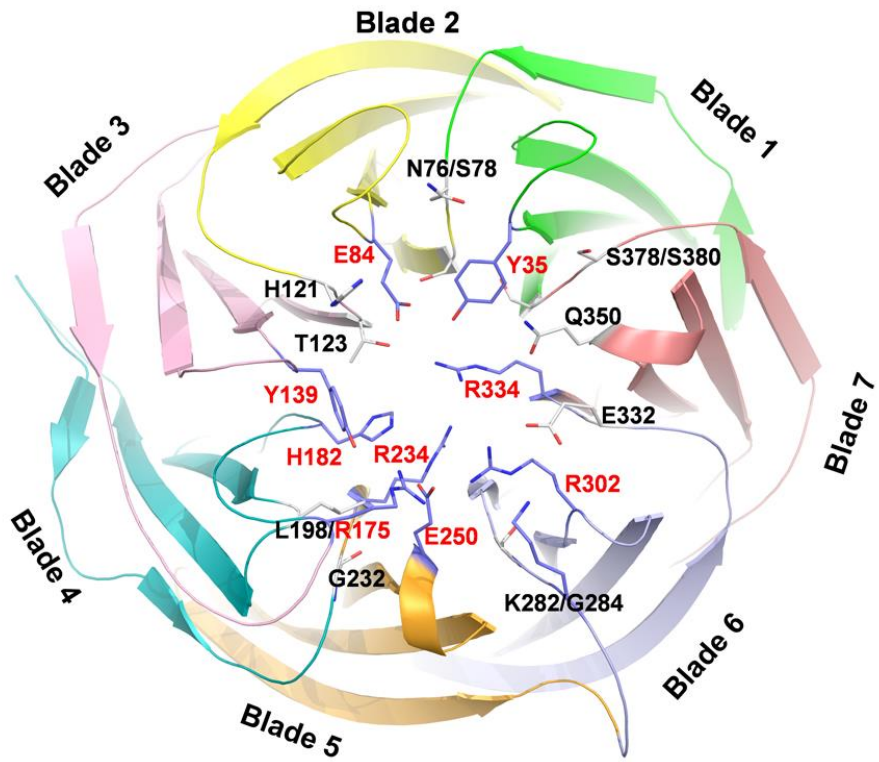


Fig.S4

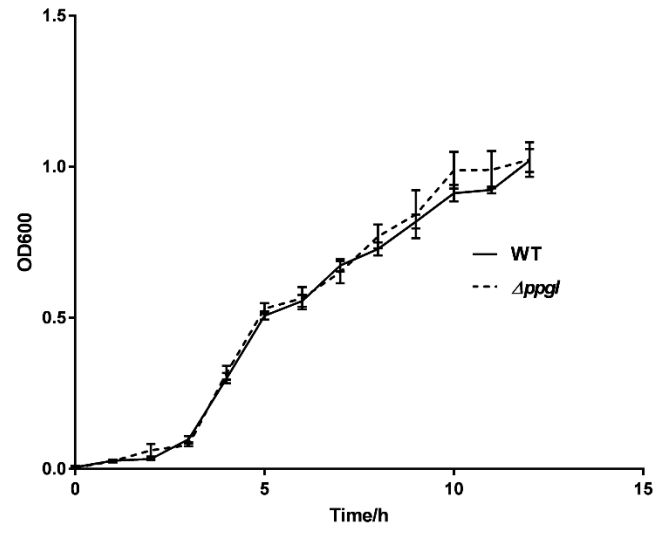


Fig.S5

