

Biological information about PhaP protein
PhaP蛋白功能结构的生物信息学收集

By Group 07th,

赵亮, 赵丹, 甘婷婷, 何艳云

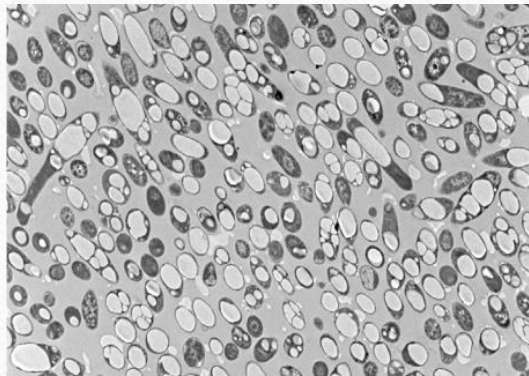
2017.01.07

Breif introduction——PHA

PHA, **p**oly**h**ydroxy**a**lkanooates, 聚羟基脂肪酸酯;

微生物的储能性物质;

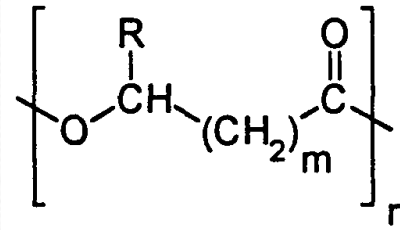
特点: 可生物降解, 绿色环保材料, 医学植入材料、药物缓释剂;



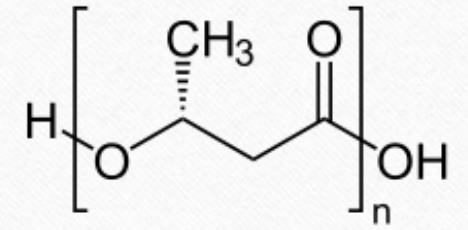
CRISPRi engineering *E. coli* for morphology diversification

Dina Elhadi^{a,1}, Li Lv^{a,1}, Xiao-Ran Jiang^a, Hong Wu^a, Guo-Qiang Chen^{a,b,c,*}

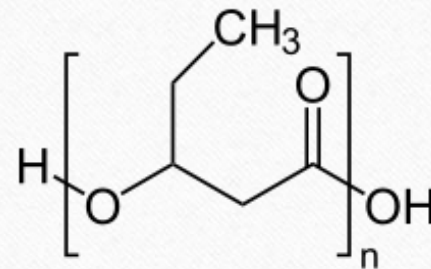
Metabolic Engineering



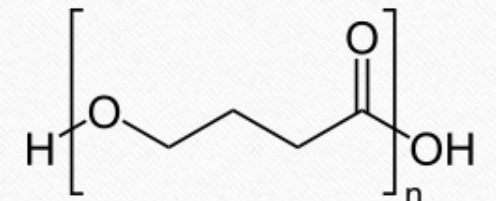
PHA 通式



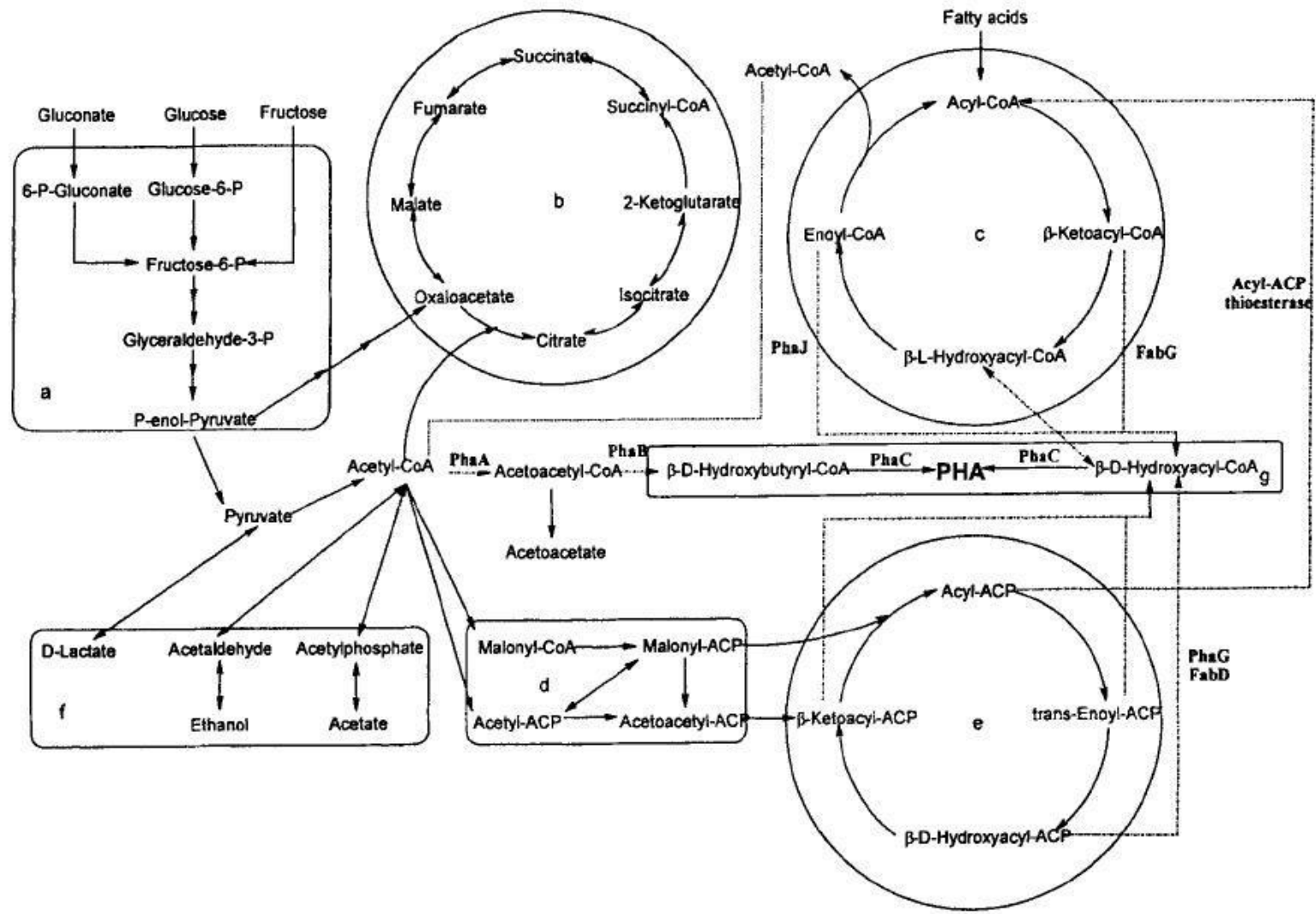
P3HB (聚3-羟基丁酸)



P3HV (聚3-羟基戊酸)



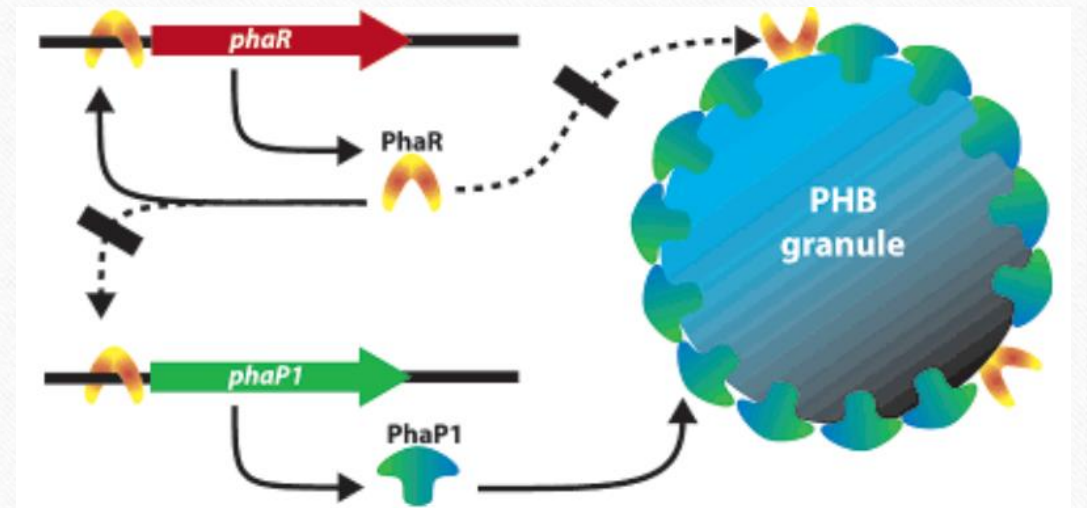
P4HB (聚4-羟基丁酸)



a: 糖酵解途径; b: TCA 循环; c: 脂肪酸 β -氧化途径; d: 脂肪酸生物合成起始途径; e: 脂肪酸生物合成延长途径; f: 其它相关途径; g: PHA 生物合成途径

Brief introduction——PhaP

- PhaP, **Halo**ferax mediterranei;
- Phap, PHA granule-associated proteins, 也称Phasins;
- 结合在PHA表面, 用于PHA的稳定;
- 具有类似功能的蛋白 PhaR, PhaF等;



Biomacromolecules 2005, 6, 552–560

Poly(3-hydroxybutyrate) Granule-Associated Proteins: Impacts on Poly(3-hydroxybutyrate) Synthesis and Degradation[†]


Markus Pötter and Alexander Steinbüchel*

GO information

Term Ancestry

Term info

Settings

 **GO:0070088** PHA granule

An inclusion body located in the cytoplasm that consists of polyhydroxyalkanoate (PHA) molecules and associated proteins, surrounded by a phospholipid monolayer; the proteins include PHA synthase, PHA depolymerase and 3HB-oligomer hydroxylase, phasins (PhaPs), which are thought to be the major structural proteins of the membrane surrounding the inclusion, and the regulator of phasin expression PhaR.

Child Terms

Term Information


Ancestor Chart

Child Terms

Protein Annotation

Co-occurring Terms

Change Log

ID	 GO:0042619
Name	poly-hydroxybutyrate biosynthetic process
Ontology	Biological Process
Definition	The chemical reactions and pathways resulting in the formation of poly-hydroxybutyrate (PHB), a polymer of beta-hydroxybutyrate and a common storage material of prokaryotic cells.
GONUTS	GO:0042619 Wiki Page

Synonyms

Cross-Ontology Relations

Cross-references

Uniprot information

Functionⁱ

Polyhydroxyalkanoate (PHA) granule structural protein. Important for PHA granule formation and separation, and for cell growth. [1 Publication](#) ▼

Names & Taxonomyⁱ

Protein names ⁱ	<i>Recommended name:</i> PHA granule-associated protein PhaP <i>Alternative name(s):</i> <ul style="list-style-type: none">Major haloarchaeal phasin
Gene names ⁱ	<i>Name:</i> phaP Ordered Locus Names: HFX_5219 ORF Names: BM92_17940, C439_00150
Encoded on ⁱ	Plasmid HMPLAS2 1 Publication ▼ Plasmid pHM300 1 Publication ▼
Organism ⁱ	<i>Haloferax mediterranei</i> (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) (<i>Halobacterium mediterranei</i>)
Taxonomic identifier ⁱ	523841 [NCBI]
Taxonomic lineage ⁱ	Archaea > Euryarchaeota > Halobacteria > Haloferacales > Haloferacaceae > Haloferax > ▶▶
Proteomes ⁱ	UP000011603 Component ⁱ : Unassembled WGS sequence UP000006469 Component ⁱ : Plasmid pHM300 UP000027075 Component ⁱ : Plasmid HMPLAS2

Subcellular locationⁱ

Graphical	SL-0281 Cytoplasmic granule
Definition	Protein found in or associated with cytoplasmic granules.
Category	> Cellular component

Uniprot information

Pathology & Biotechⁱ

Disruption phenotypeⁱ

Deletion mutant is defective in both PHA biosynthesis and cell growth. The number of PHA granules is significantly lower. 1 Publication

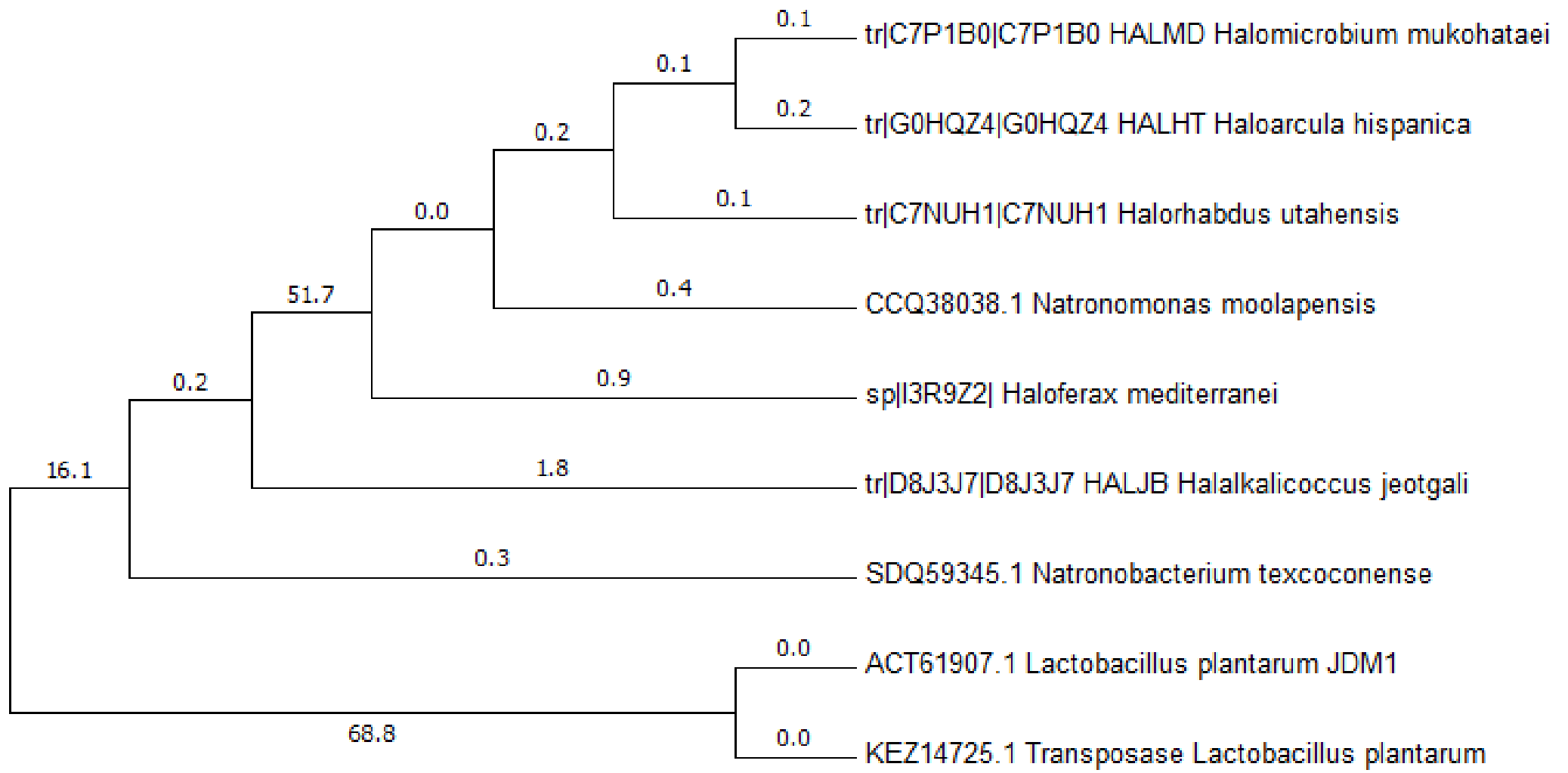
Family & Domainsⁱ

Phylogenomic databases

OMAⁱ IEQSQA.

Taxon	Protein ID	Cross reference	Function annotation
A <i>Halalkalicoccus jeotgali</i> (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	HALJB01911	★ D8J3J7@	Putative uncharacterized protein
A <i>Haloarcula hispanica</i> (strain ATCC 33960 / DSM 4426 / JCM 8911 / NBRC 102182 / NCIMB 2187 / VKM B-1755)	HALHT00148	★ G0HQZ4@	conserved hypothetical protein
A <i>Haloarcula marismortui</i> (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809)	HALMA02541	★ Q5UYM2@	unknown
A <i>Halomicrobium mukohataei</i> (strain ATCC 700874 / DSM 12286 / JCM 9738 / NCIMB 13541)	HALMD00964	★ C7P1B0@	Putative uncharacterized protein
A <i>Halorhabdus utahensis</i> (strain DSM 12940 / JCM 11049 / AX-2)	HALUD02138	★ C7NUH1@	Putative uncharacterized protein
A <i>Natronomonas moolapensis</i> (strain DSM 18674 / JCM 14361 / 8.8.11)	NATM802831	★ M1XU04@	arCOG06342 family protein
A <i>Haloferax mediterranei</i> (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4)	HALMT03644	★ PHAP_HALMT@	PHA granule-associated protein/haloarchaeal phasin (PhaP)
A <i>Halogeometricum borinquense</i> (strain ATCC 700274 / DSM 11551 / JCM 10706 / PR3)	HALBP02916	★ E4NU11@	hypothetical protein
A <i>Haloquadratum walsbyi</i> (strain DSM 16790 / HBSQ001)	HALWD01376	★ Q18HU7@	conserved hypothetical protein
A <i>Haloquadratum walsbyi</i> (strain DSM 16854 / JCM 12705 / C23)	HALWC01408	★ G0LKV8@	conserved hypothetical protein
A <i>Halopiger xanaduensis</i> (strain DSM 18323 / JCM 14033 / SH-6)	HALXS02055	★ F8D3L4@	hypothetical protein KEGG: htu:Htur_2457 hypothetical protein
A <i>Natrinema pellirubrum</i> (strain DSM 15624 / JCM 10476 / NCIMB 786)	NATP101149	★ L0JL80@	hypothetical protein
A <i>Natronobacterium gregoryi</i> (strain ATCC 43098 / CCM 3738 / NCIMB 2189 / SP2)	NATGS00349	★ L0AF11@	hypothetical protein

Alignments						
Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> hypothetical protein [Haloferax mediterranei]	312	312	100%	5e-108	100%	WP_004056140.1
<input type="checkbox"/> hypothetical protein [Haloferax mucosum]	262	262	100%	4e-88	82%	WP_008320239.1
<input type="checkbox"/> hypothetical protein [Haloferax larsenii]	255	255	100%	4e-85	79%	WP_007542256.1
<input type="checkbox"/> hypothetical protein [Haloferax larsenii]	252	252	100%	4e-84	78%	WP_074796501.1
<input type="checkbox"/> hypothetical protein [Haloferax elongans]	252	252	100%	6e-84	78%	WP_008321926.1
<input type="checkbox"/> hypothetical protein HSB1_32060 [Haloqranum salarium B-1]	149	149	100%	2e-43	43%	EJN58728.1
<input type="checkbox"/> hypothetical protein SAMN04487948_101244 [Haloqranum amylolyticum]	147	147	100%	1e-42	42%	SEO23408.1
<input type="checkbox"/> hypothetical protein [Haloqranum salarium]	135	135	92%	6e-38	41%	WP_049894087.1
<input type="checkbox"/> hypothetical protein SAMN04487949_2305 [Haloqranum gelatinilyticum]	128	128	96%	4e-35	39%	SDM62520.1
<input type="checkbox"/> hypothetical protein [Natronomonas pharaonis]	102	102	95%	3e-24	31%	WP_011322310.1
<input type="checkbox"/> MULTISPECIES: hypothetical protein [Haloarcula]	97.4	97.4	95%	1e-22	33%	WP_050037369.1
<input type="checkbox"/> hypothetical protein SAMN05444271_11431 [Halo]hastata [litchfieldiae]	97.8	97.8	89%	1e-22	31%	SEI97161.1
<input type="checkbox"/> hypothetical protein SAMN05216218_105135 [Halo]orientalis [regularis]	97.1	97.1	92%	1e-22	35%	SDF30947.1
<input type="checkbox"/> hypothetical protein SAMN05216559_0241 [Halo]microbium [zhouii]	97.1	97.1	95%	2e-22	35%	SFR86604.1
<input type="checkbox"/> hypothetical protein [Halorhabdus utahensis]	96.3	96.3	95%	3e-22	31%	WP_015789899.1
<input type="checkbox"/> hypothetical protein [Haloarcula hispanica]	95.9	95.9	95%	4e-22	33%	WP_014039169.1
<input type="checkbox"/> MULTISPECIES: hypothetical protein [Haloarcula]	95.9	95.9	95%	5e-22	33%	WP_050007574.1
<input type="checkbox"/> hypothetical protein [Haloarcula amylolytica]	95.5	95.5	95%	7e-22	33%	WP_008306975.1
<input type="checkbox"/> hypothetical protein [Halalkalicoccus paucihalophilus]	97.8	97.8	98%	7e-22	32%	WP_066380719.1
<input type="checkbox"/> hypothetical protein [Halo]microbium [katesii]	94.7	94.7	95%	1e-21	32%	WP_018256939.1
<input type="checkbox"/> hypothetical protein [Halo]microbium [mukohataei]	94.4	94.4	95%	2e-21	32%	WP_015761964.1
<input type="checkbox"/> MULTISPECIES: hypothetical protein [Natrialbaeae]	74.7	74.7	96%	5e-14	26%	WP_007261347.1
<input type="checkbox"/> hypothetical protein [Natronorubrum tibetense]	74.7	74.7	88%	5e-14	29%	WP_006090695.1
<input type="checkbox"/> hypothetical protein SAMN04515672_1017 [Natronorubrum texcoconense]	73.9	73.9	96%	9e-14	28%	SDJ56867.1
<input type="checkbox"/> hypothetical protein SAMN04489841_0303 [Natri]nema [salaciae]	73.6	73.6	96%	1e-13	27%	SEP69641.1
<input type="checkbox"/> transducer protein [Natronomonas pharaonis]	74.7	74.7	82%	1e-13	30%	WP_011322084.1
<input type="checkbox"/> hypothetical protein [Halo]quadratum [walsbyi]	73.2	73.2	96%	1e-13	27%	WP_014556028.1
<input type="checkbox"/> hypothetical protein SAMN04488065_0739 [Halo]planus [vescus]	72.8	72.8	79%	2e-13	31%	SDZ84598.1
<input type="checkbox"/> hypothetical protein [Halo]quadratum [walsbyi]	72.8	72.8	94%	2e-13	27%	WP_011571564.1
<input type="checkbox"/> hypothetical protein [Natri]nema [altunense]	72.4	72.4	96%	3e-13	27%	WP_007109153.1
<input type="checkbox"/> transducer protein [Natronomonas pharaonis]	73.9	73.9	88%	3e-13	24%	WP_011323082.1
<input type="checkbox"/> hypothetical protein SAMN05192554_103166 [Halo]archaeobius [iranensis]	72.0	72.0	85%	4e-13	30%	SDM51877.1
<input type="checkbox"/> hypothetical protein [Natri]nema [pallidum]	71.2	71.2	96%	9e-13	26%	WP_006184360.1
<input type="checkbox"/> hypothetical protein [Natronorubrum sulfidifaciens]	71.2	71.2	96%	9e-13	31%	WP_008159630.1
<input type="checkbox"/> hypothetical protein [Halalkalicoccus paucihalophilus]	70.5	70.5	87%	2e-12	33%	WP_066382199.1
<input type="checkbox"/> MULTISPECIES: hypothetical protein [Natri]nema	70.5	70.5	96%	2e-12	26%	WP_014863684.1
<input type="checkbox"/> Helix-hairpin-helix domain-containing protein [Natronorubrum texcoconense]	73.2	73.2	88%	2e-12	36%	SDK24433.1
<input type="checkbox"/> hypothetical protein C486_09200 [Natri]nema [qari JCM 14663]	71.6	71.6	92%	5e-12	29%	ELY80172.1
<input type="checkbox"/> hypothetical protein [Natri]nema [qari]	69.3	69.3	96%	6e-12	26%	WP_008453421.1
<input type="checkbox"/> hypothetical protein NJ7G_2660 [Natri]nema [sp. J7-2]	70.9	70.9	92%	8e-12	29%	AFO57889.1
<input type="checkbox"/> hypothetical protein J07HQW2_00898 [Halo]quadratum [walsbyi J07HQW2]	68.6	68.6	94%	8e-12	26%	ERG94464.1
<input type="checkbox"/> hypothetical protein [Halo]piquer [salifodinae]	70.5	70.5	88%	1e-11	34%	WP_049992299.1
<input type="checkbox"/> hypothetical protein [Natronorubrum tibetense]	70.1	70.1	84%	2e-11	31%	WP_006091742.1
<input type="checkbox"/> hypothetical protein [Halo]terri[gena] [salina]	68.9	68.9	83%	6e-11	34%	WP_008896838.1
<input type="checkbox"/> Helix-hairpin-helix domain-containing protein [Natri]nema [salaciae]	67.8	67.8	88%	2e-10	34%	SEQ39161.1
<input type="checkbox"/> hypothetical protein [Natri]nema [qari]	66.6	66.6	86%	2e-10	30%	WP_049910322.1
<input type="checkbox"/> MULTISPECIES: hypothetical protein [Natri]nema	66.2	66.2	86%	4e-10	30%	WP_049888537.1
<input type="checkbox"/> Mobile element protein [Lactobacillus plantarum]	37.0	37.0	46%	2.1	32%	KZU13890.1
<input type="checkbox"/> Transposase [Lactobacillus plantarum]	38.1	38.1	46%	2.1	32%	KEZ14725.1
<input type="checkbox"/> transposase [Lactobacillus plantarum JDM1]	38.1	38.1	46%	2.3	32%	ACT61907.1
<input type="checkbox"/> transposase [Lactobacillus selanorensis]	38.5	38.5	38%	2.4	37%	WP_057771279.1
<input type="checkbox"/> hypothetical protein [Nocardia sp. BMG111209]	36.6	36.6	41%	2.4	34%	WP_019930111.1



KEGG motif

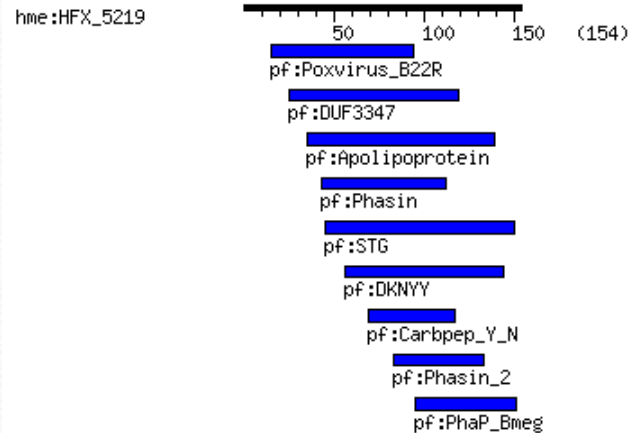
Organism : *Haloferax mediterranei*

Gene : [HFX_5219](#)

Definition : no KO assigned | (GenBank) phaP; poly(3-hydroxyalkanoate) granule-associated protein(phasin)

Motif id	From	To	Definition	E value	Score
pf:Poxvirus_B22R	15	94	Poxvirus B22R protein	0.0064	-
pf:DUF3347	25	119	Protein of unknown function (DUF3347)	0.019	-
pf:Apolipoprotein	35	139	Apolipoprotein A1/A4/E domain	0.062	-
pf:Phasin	43	112	Poly(hydroxyalkanoate) granule associated protein (phasin)	0.015	-
pf:STG	45	150	Simian taste bud-specific gene product family	0.035	-
pf:DKNYY	56	144	DKNYY family	0.095	-
pf:Carbpep_Y_N	69	117	Carboxypeptidase Y pro-peptide	0.19	-
pf:Phasin_2	83	133	Phasin protein	0.0033	-
pf:PhaP_Bmeg	95	151	Polyhydroxyalkanoic acid inclusion protein (PhaP_Bmeg)	0.037	-

[Search GENES with the same motifs](#)



The structure of PhaP

- PhaP, from *Aeromonas hydrophila*; Uniprot-KB O32470.
- PDB no. 5IP0

Unreleased Structure ID	Title / Authors / Dates	Status	Sequence Available?
5IP0	PHA Binding Protein PhaP (Phasin) Chen, G.Q., Wang, X.Q., Zhao, H.Y.	HPUB	--

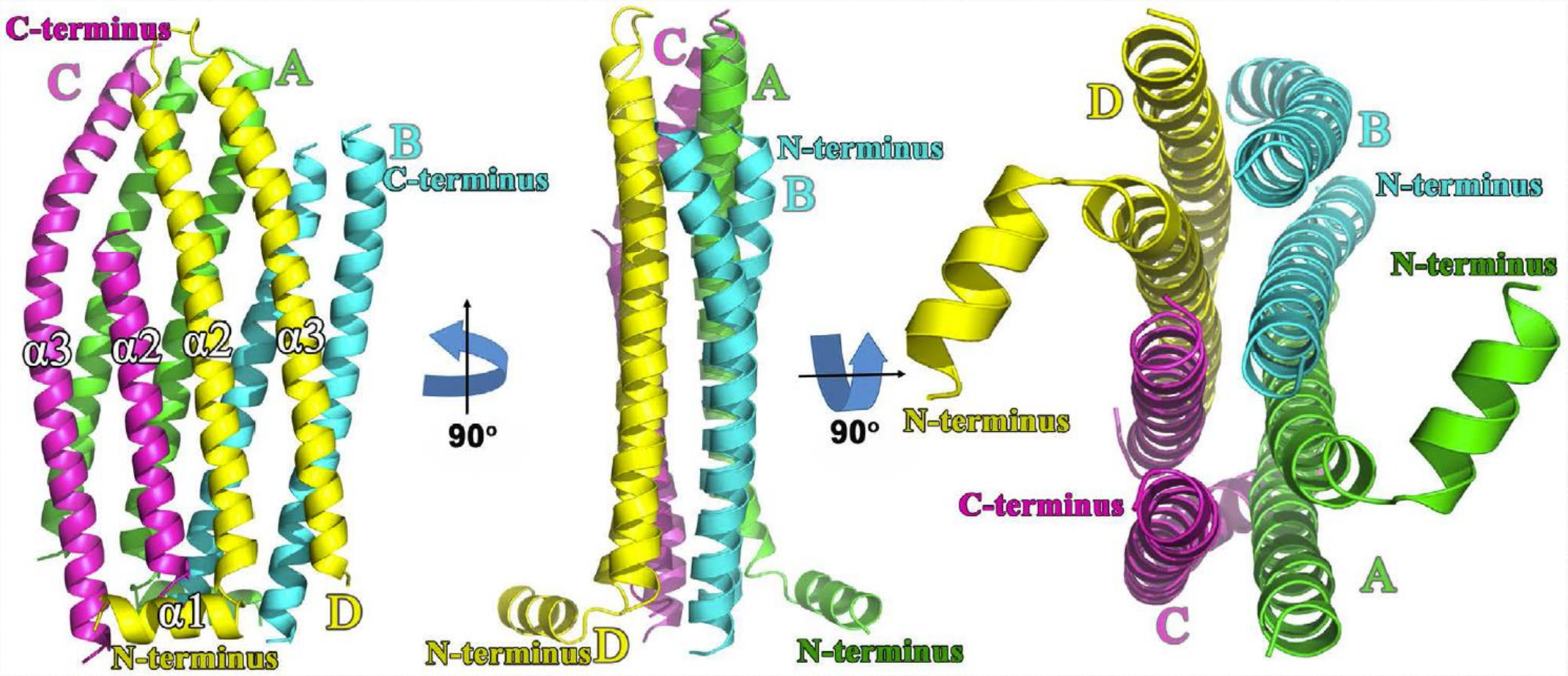
SCIENTIFIC REPORTS

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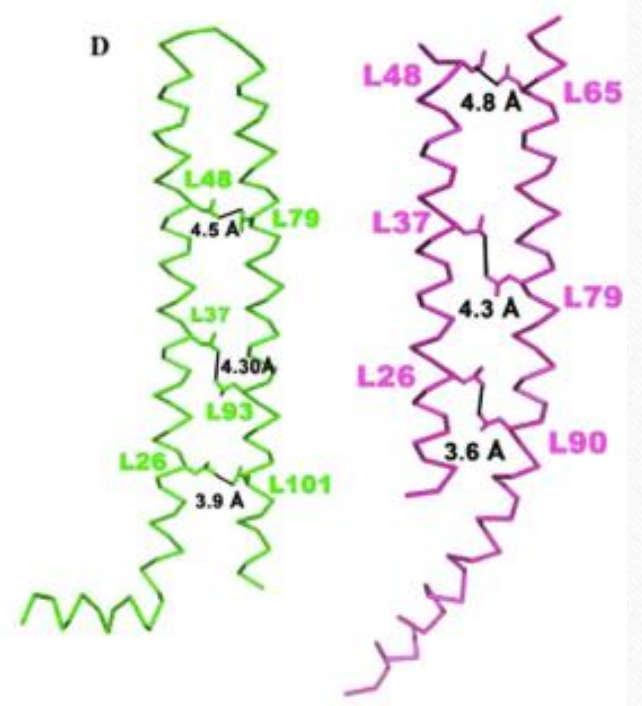
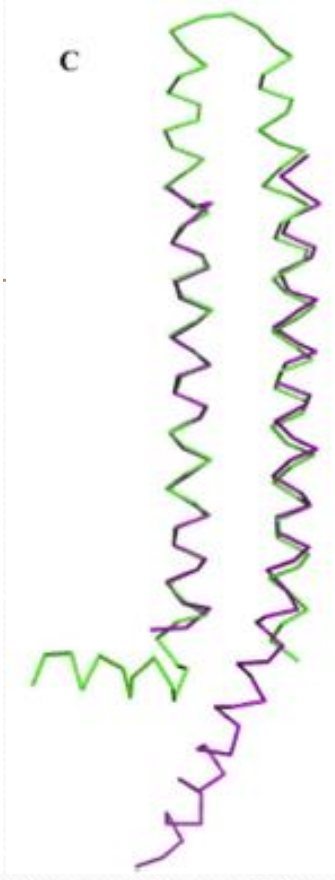
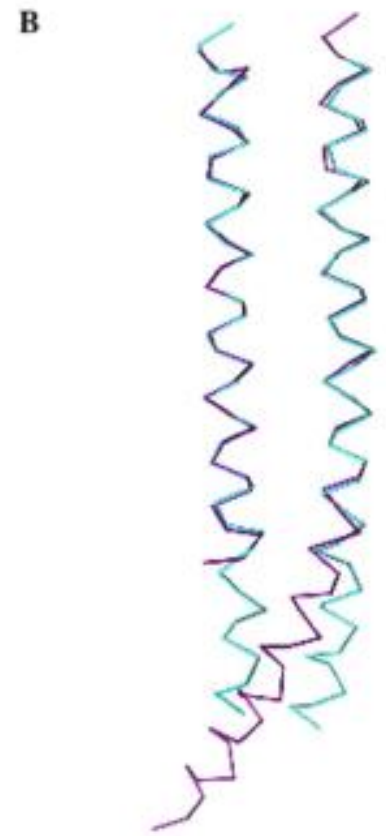
Structural Insights on PHA Binding Protein PhaP from *Aeromonas hydrophila*

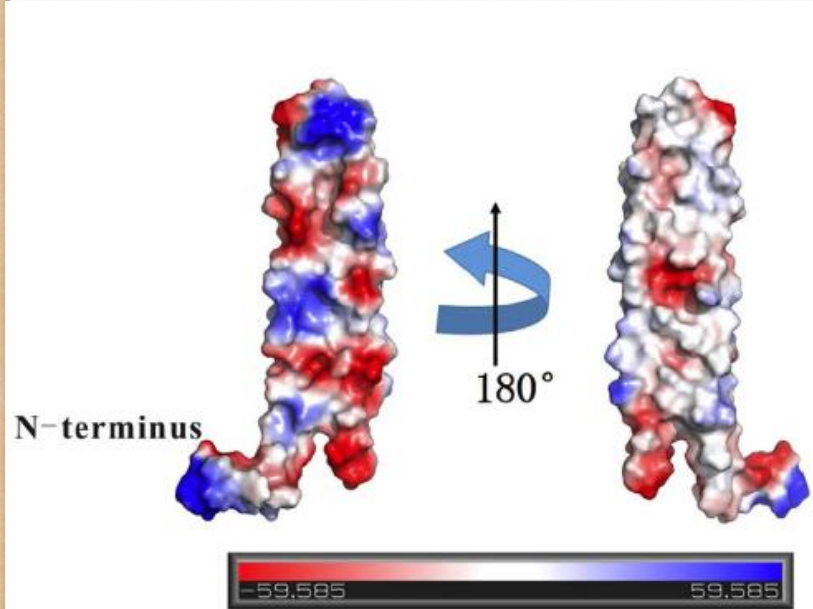
Received: 08 April 2016
Accepted: 22 November 2016
Published: 23 December 2016

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Xinquan Wang^{3,4} & Guo-Qiang Chen^{1,5,6}



The structure of PhaP(Ah) tetramer, consisting of the A(green), B(cyan), C(purple), D(yellow) four chains. The N-terminus and the C-terminus are indicated.



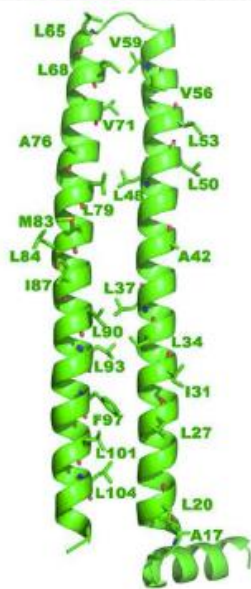


N-terminus

180°

Type I hydrophilic surface

Type I hydrophobic surface

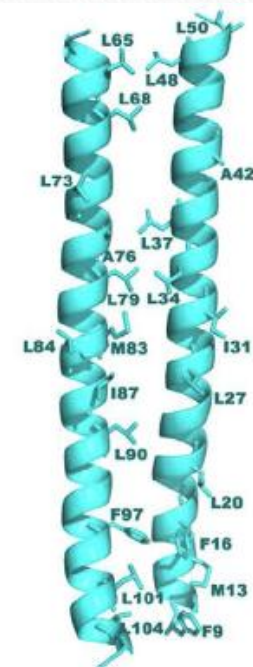
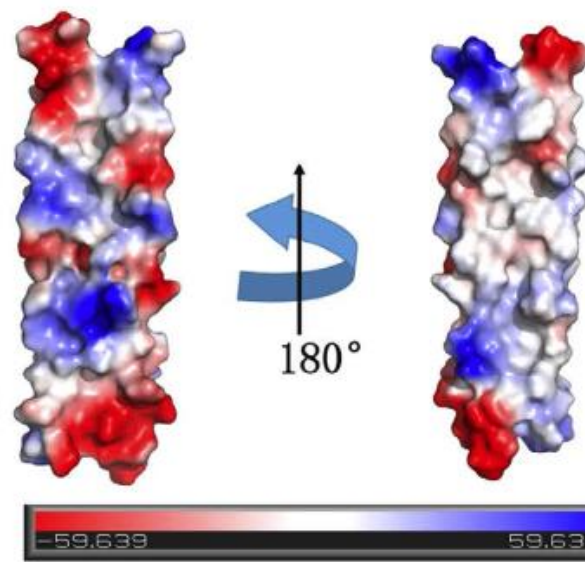


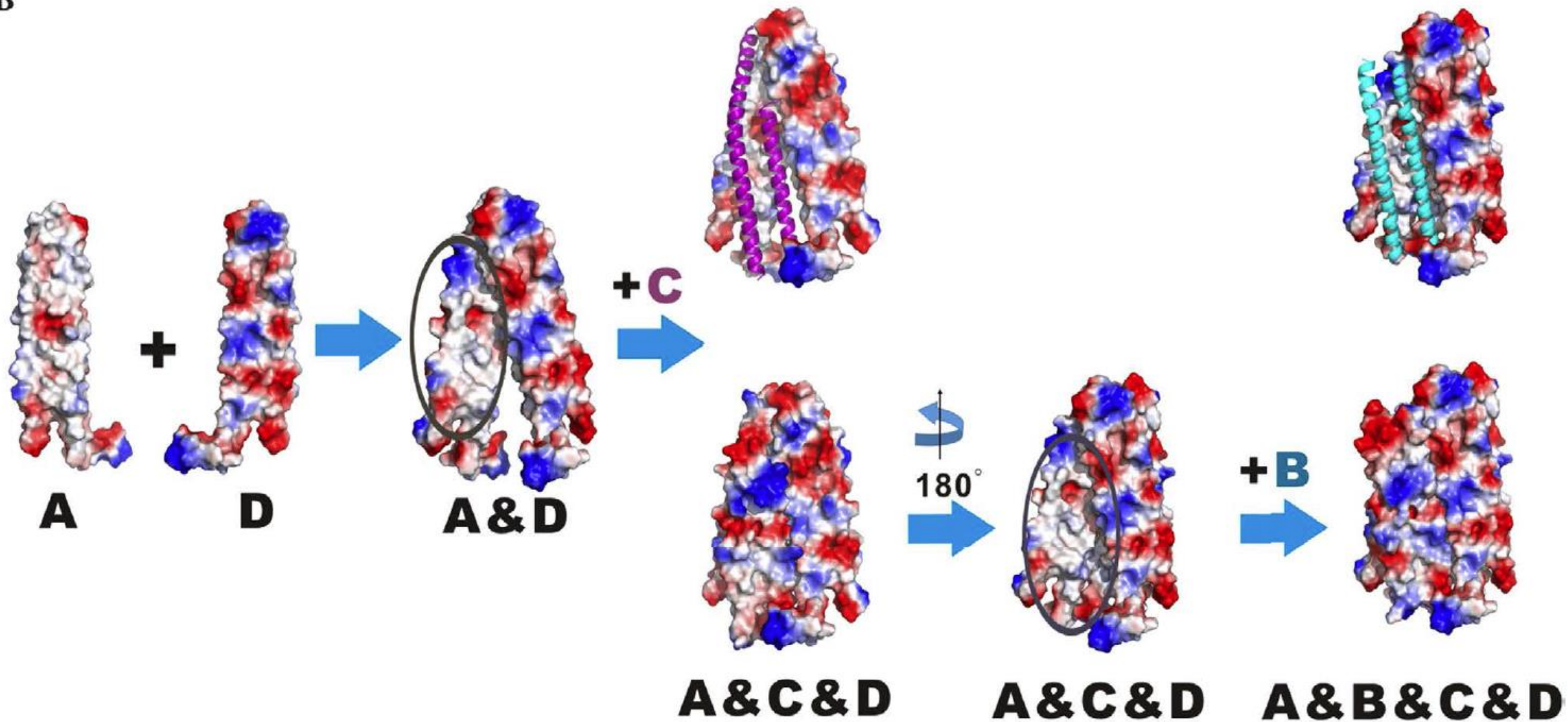
N-terminus

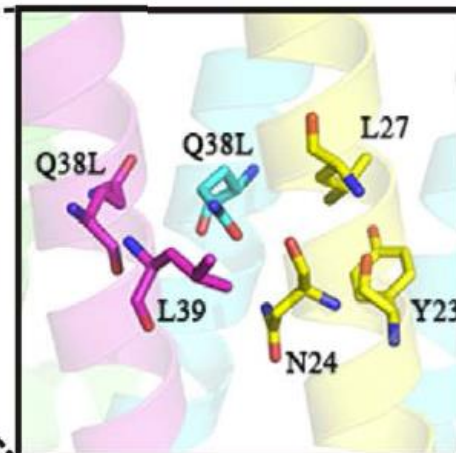
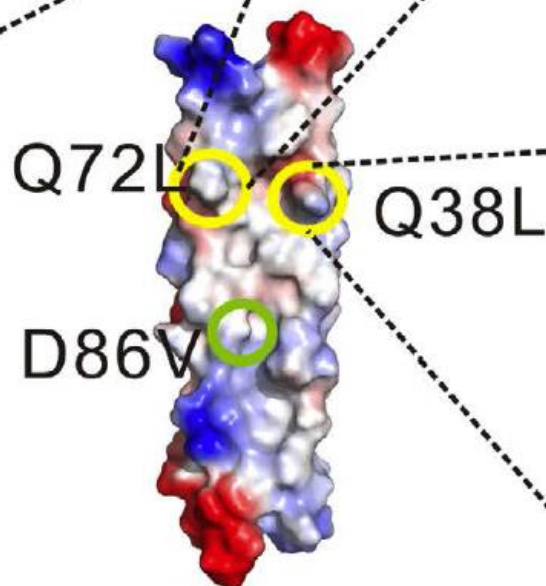
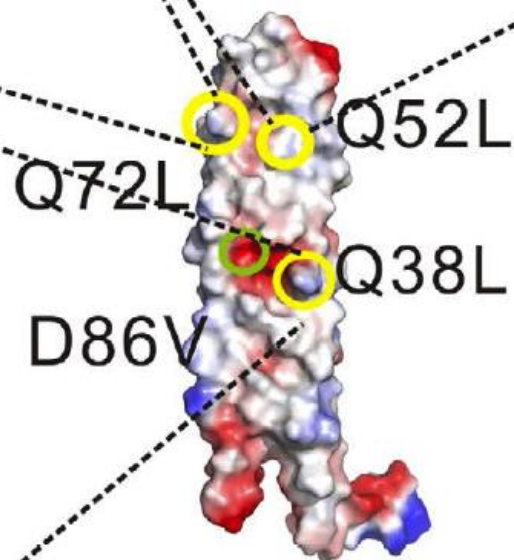
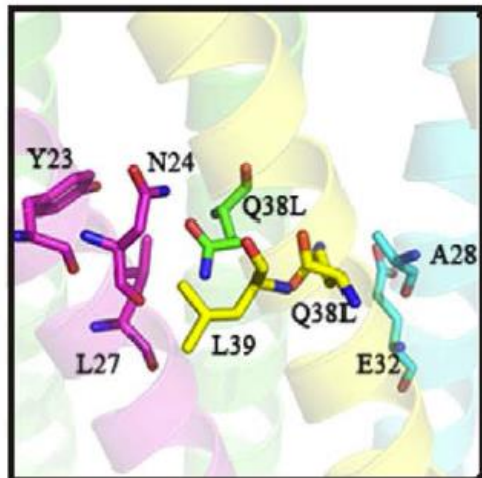
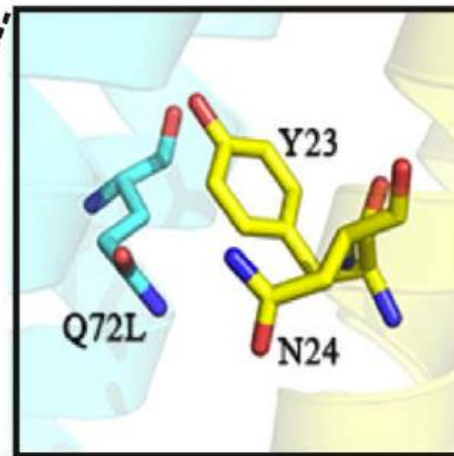
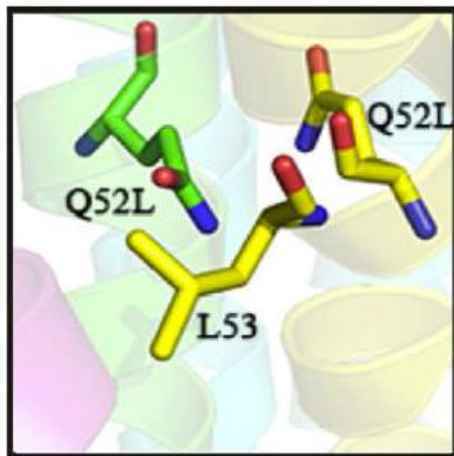
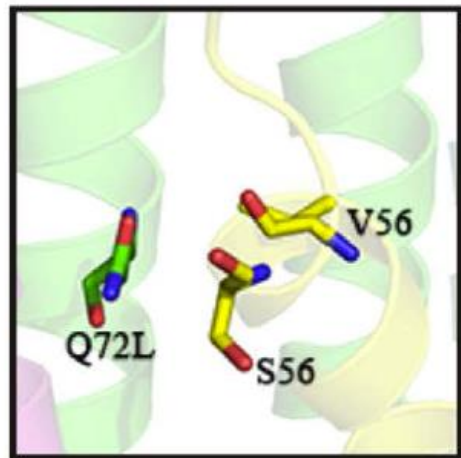
180°

Type II hydrophilic surface

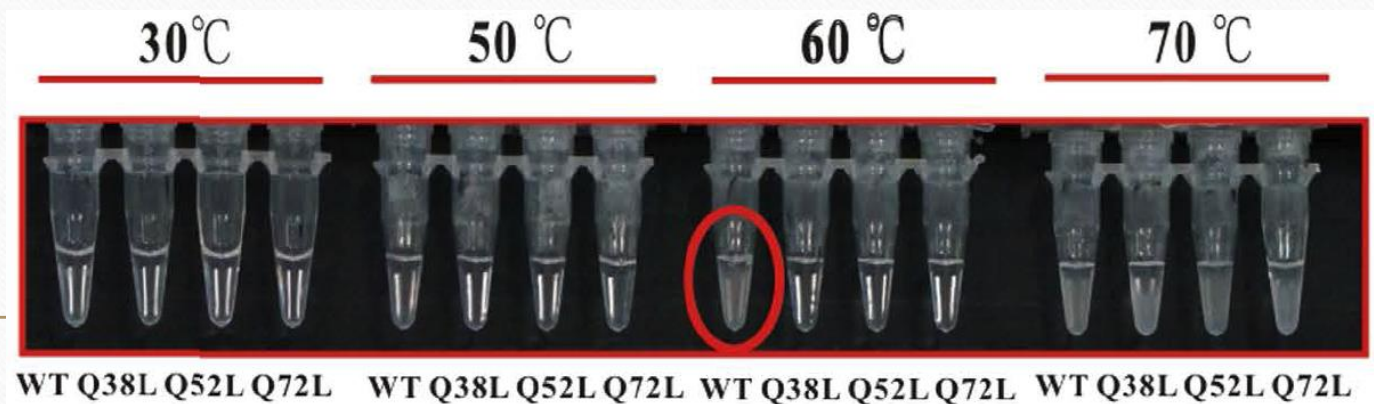
Type II hydrophobic surface



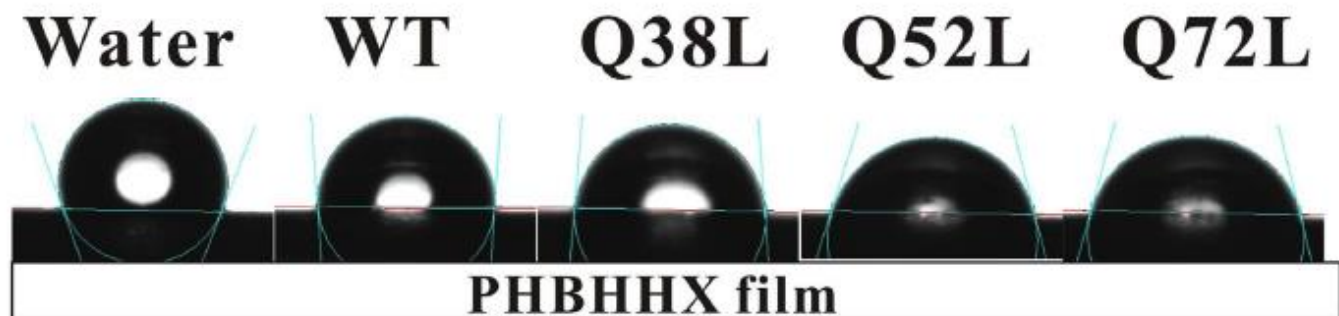
B



Type I hydrophobic surface Type II hydrophobic surface



c

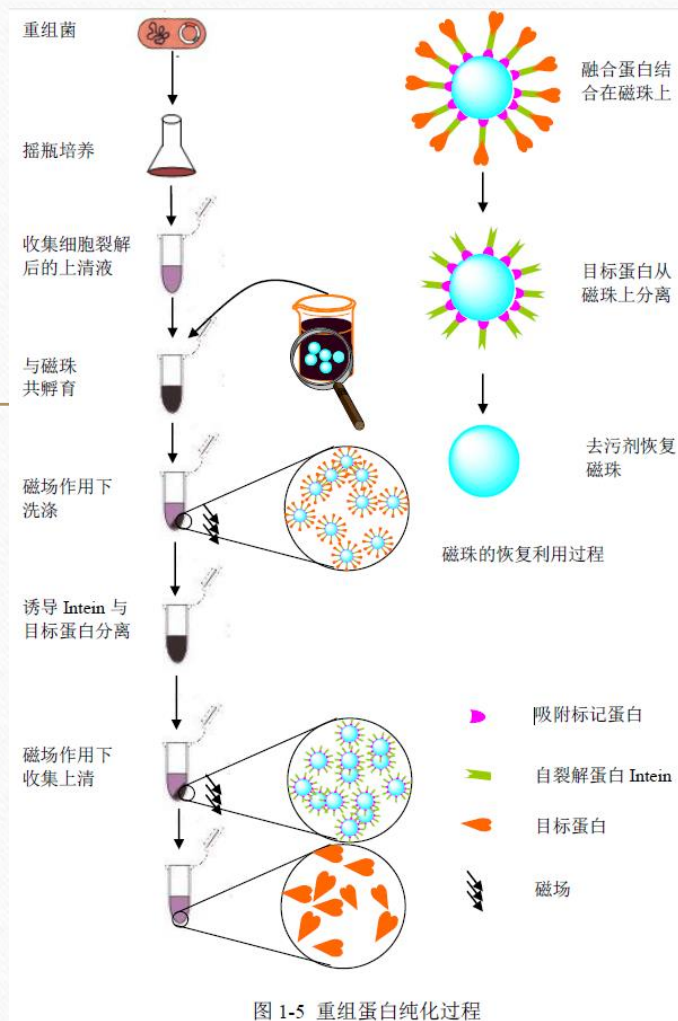


Left: 110.6 Left: 94.3 Left: 86.0 Left: 73.4 Left: 75.9
Right: 110.2 Right: 93.5 Right: 85.1 Right: 74.8 Right: 75.0

功能和应用



(一) 化工洗涤剂的优良替代品



(二) 创新型的蛋白分离纯化技术

Acknowledge

- Prof. Luo;
- TA Ke Lan;
- The author, Zhao Hongyu;
- Memnners of Group 07;
- All classmates in ABC;
- Prof. Chen



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生命学院生物新馆103

Thank you !

Group 07th

2017.01.07