

# ***XBio, Focus on Protein***

清泓生物技术(上海)有限公司  
www.xbioservice.com

# Platform for active protein production

- **Mammalian expression for correct protein phosphorylation and modification**
- **Optimized procedure for protein expression in insect cells from Bacmid to Virus**
- **Soluble protein expression in *E.Coli***
- **Delicate process for protein purification**
- **Unique experience for assay development based on protein activity, protein and protein interaction**

# Capacity

- **Mammalian cells: Pilot study of 50 constructs in parallel, 5-25 mg per batch**
- **Insect cells: Pilot study of 50 constructs in parallel, 10-50 mg per batch**
- ***E.Coli*: Pilot study of 50 constructs in parallel, 10-100 mg per batch**
- **The capacity could be expanded upon request**

**Case study:**  
**Gene to Structure of Kinase S**

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# Expression of recombinant Protein S

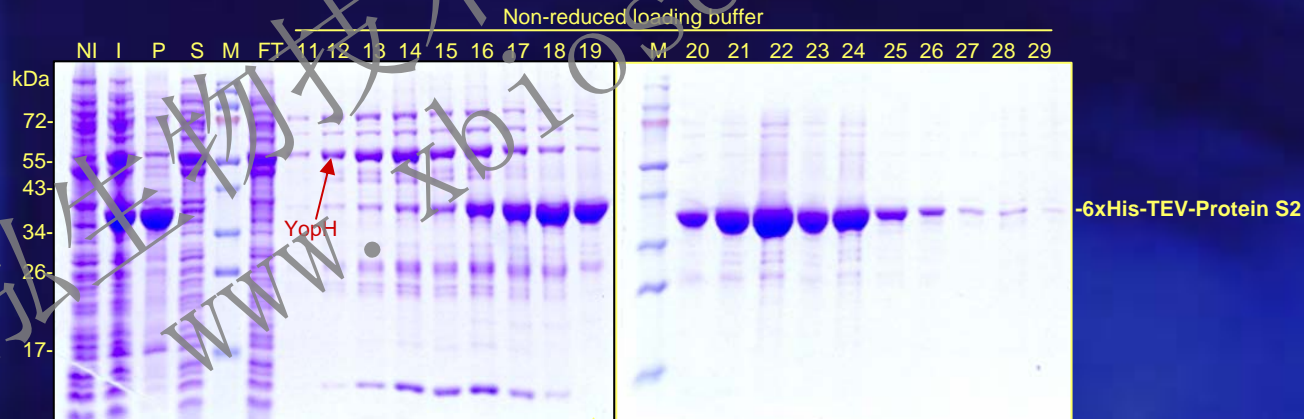
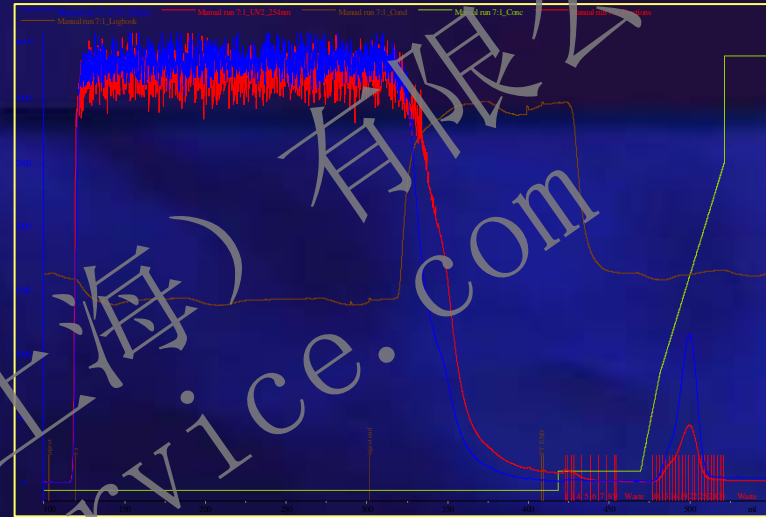
Recombinant plasmids	Expressed protein	Co-transformed plasmid	E.Coli Strain	Medium	Induced Conditions
pET28B-TEV-Protein S2	His tag-thrombin-TEV-Protein S2	pCDFDuet1-YopH	BL21 (DE3)	TB	18 °C, 14hrs, 0.2mM IPTG

Protein	MW (Da)	Theoretical PI	Amino acids
His tag-thrombin-TEV-Protein S2	35495.856	6.075	311
Protein S2	32349.409	5.315	283

Plasmids	OD600
	pET28b-TEV-Protein S2 pCDFDuet1-YopH
Seed-13:10	2.0211
Theoretical-13:10	0.0396
14:10	0.2060
14:41	0.4208
15:11	0.8290 Lower the temperature to 18°C
16:10	1.5227 Add IPTG
2nd day, 8:10	16.4340 Collect the culture.

# Purification step one: Ni-Column

Sample	1.5L cell lysate supernatant
Column	HisTrap HP 5mL
Lysis buffer	50mM Tris, 500mM NaCl, 25mM Imidazole, 20mM $\beta$ -mercaptoethanol, 0.2mM PMSF, pH8.0
Ni Buffer	A: 50mM Tris, 500mM NaCl, 25mM Imidazole, 20mM $\beta$ -mercaptoethanol, pH8.0 B: 50mM Tris, 1M NaCl, 25mM Imidazole, 20mM $\beta$ -mercaptoethanol, pH8.0 C: 50mM Tris, 500mM NaCl, 25mM Imidazole, 20mM $\beta$ -mercaptoethanol, pH8.0
Elution	Target proteins were eluted with a line gradient of 4.5-75% buffer C in 10CV.



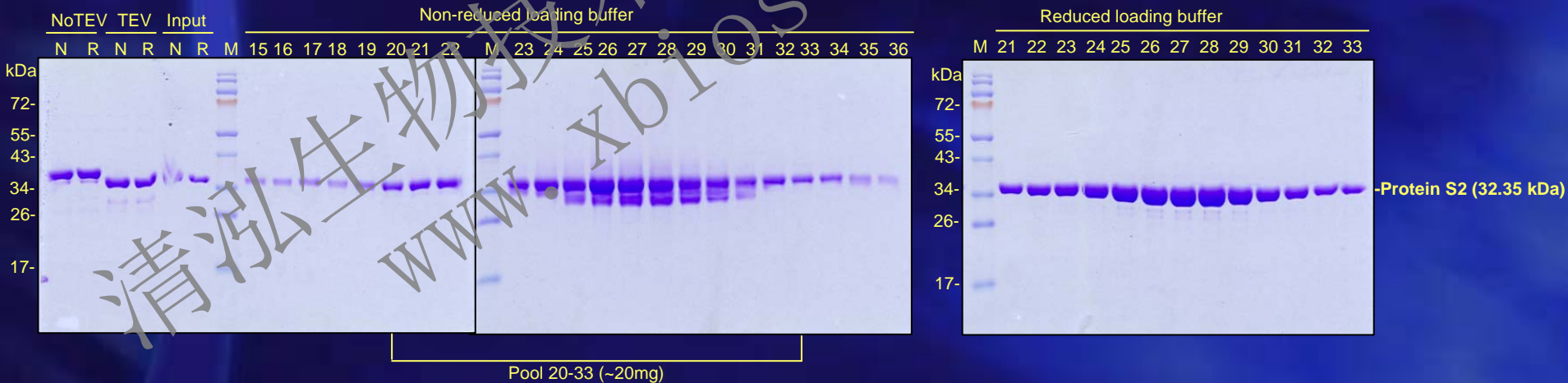
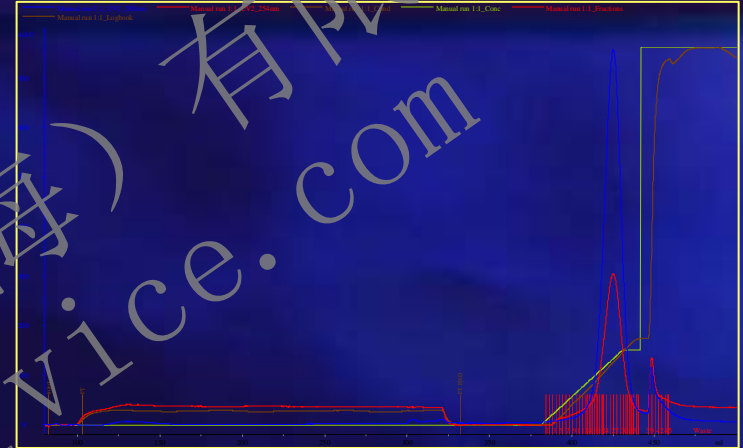
NI: non-induced  
I: induced  
P: cell pellets  
S: cell supernatant

Pool 19-25 (~40mg)

TEV cleavage  
50ug/mg protein  
Overnight at 4°C

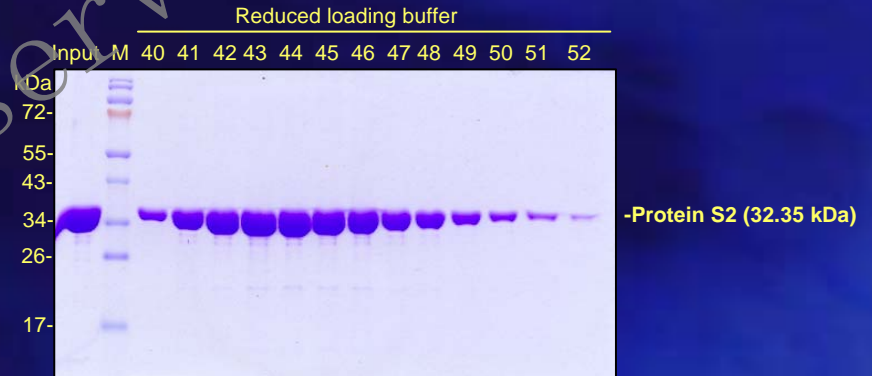
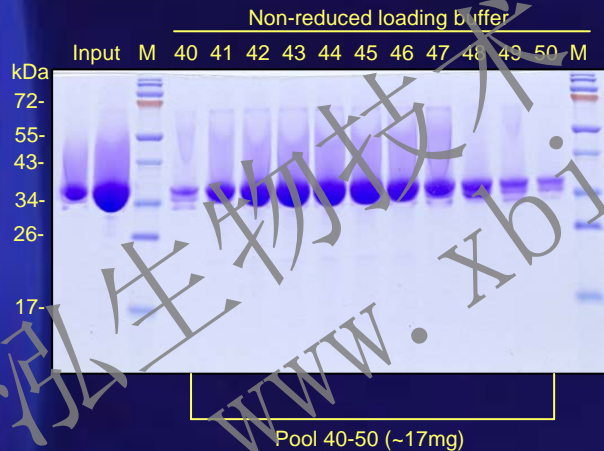
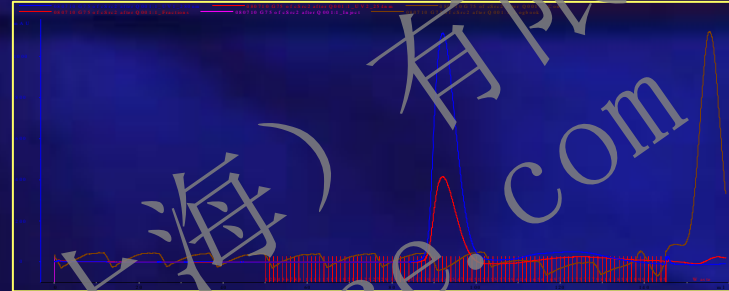
# Purification step two: TEV&Q-Column

Sample	Protein S2 after TEV cleavage
Column	HiTrap Q FF 5mL
Q Buffer	A: 50mM Tris, 20mM NaCl ,5mM DTT , pH8.0 B: 50mM Tris, 1M NaCl , 5mM DTT , pH8.0
Elution	Target proteins were eluted with a line gradient of 0-20% buffer C in 10CV.



# Purification step three: Sizing Column

Sample	Protein S2 Q-Column pool 20-33
Column	Superdex 75
Buffer	50mM Tris, 100mM NaCl, 5mM DTT, pH8.0





# Purification step four: Concentration

	Concentration (mg/ml)	Volume (ml)	Total (mg)	method
Protein S2	9	0.6	5.40	Bradford*
Buffer	50mM Tris, 100mM NaCl, 5mM DTT, pH8.0			

Note, BSA is always used as the reference protein in Bradford method to measure the protein concentration at SG.



# Better crystals of native Protein S grew in the 2<sup>nd</sup> round of screening

Crystals of native Protein S2, 60x



Native Protein S2

Temperature: 18°C

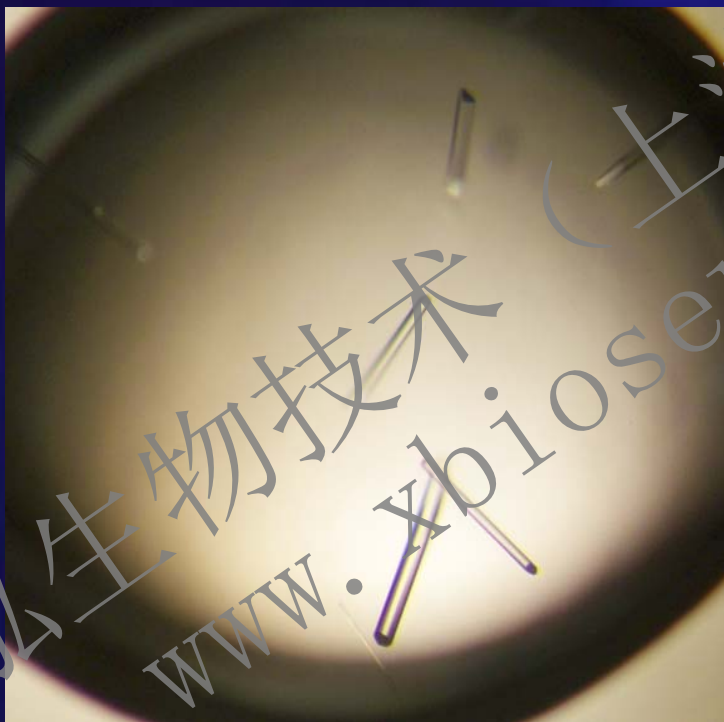
Protein concentration: 3.7 mg/ml

Reservoir solution: IHT G11,  
0.2 M Magnesium Chloride hexahydrate  
0.1 M Bis-Tris pH 6.5  
25% w/v PEG 3350

Diffraction data was collected with resolution at 2.63 Å.

# Better crystals of Protein S co-crystallized with compound 43 was obtained when using additive to optimize the crystallization

Crystals of Protein S2 & 43, 60x



**Protein S2 & 43**

**Temperature: 18°C**

**Reservoir solution:** IHT G11,  
0.2 M Magnesium Chloride hexahydrate  
0.1 M Bis-Tris pH 6.5  
25% w/v PEG 3350

**Additive: C6**  
30% w/v 6-Aminohexanoic acid  
From Additive Screen™ kit  
(Hampton Research Corp, HR2-428)

Mixture: 1  $\mu$ l of protein, 0.8  $\mu$ l of reservoir  
solution and 0.2  $\mu$ l of additive were used.

**Diffraction data was collected with resolution at 1.8 Å.**

# Strong and clear electric density map may be found around the compound binding area

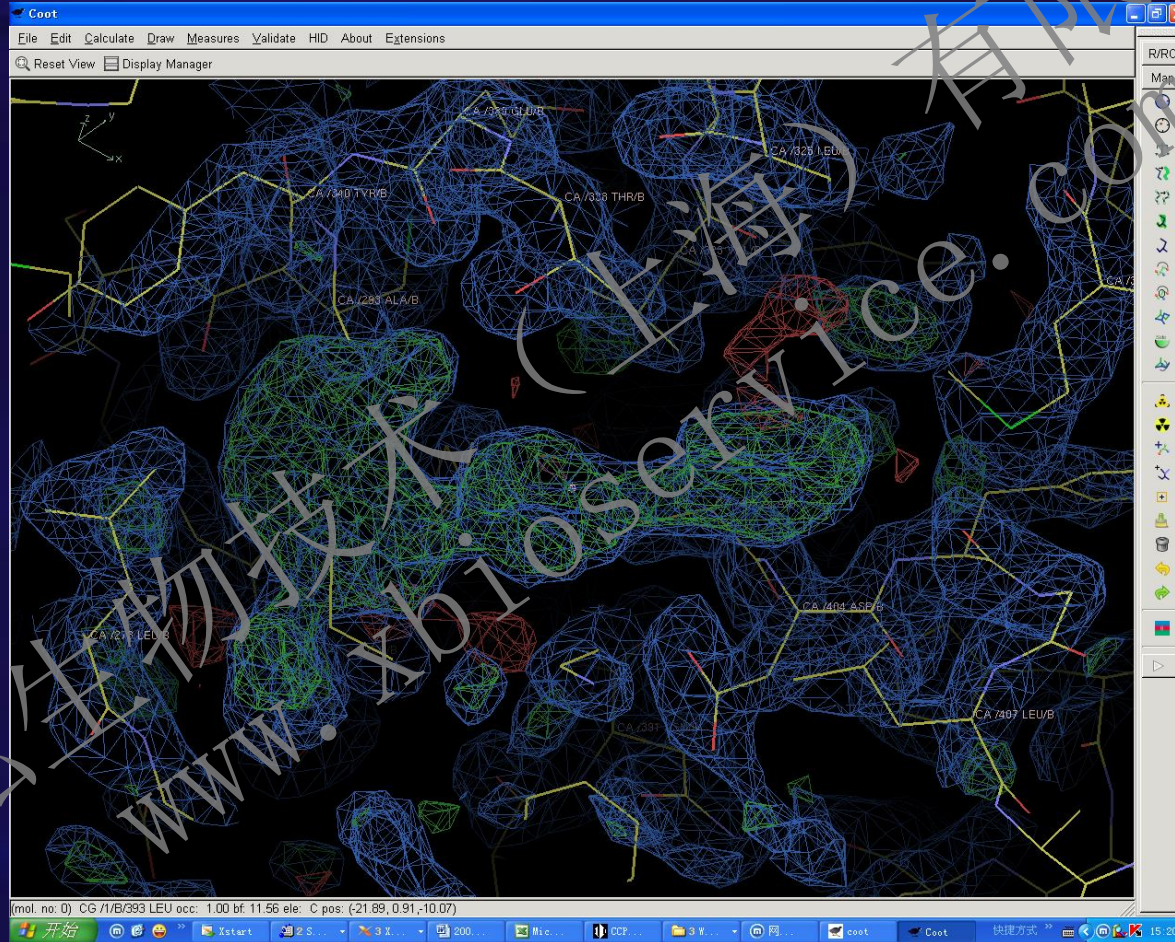


Fig 1: Strong and clear electric density map around the compound binding area (1.00 sigma 2Fo-Fc map in blue and 3.00 sigma Fo-Fc map in green)

# Summary for case study

- **Protein S protein was purified with good purity and yield.**
- **Succeed in crystallization of native Protein S kinase, high quality diffraction data was collected.**
- **Succeed in crystallization of Protein S kinase complexed with compound 43, excellent quality diffraction data was collected.**