



Protein Crystallization: Simply *grab* the needle from the haystack

Burg Warberg, September 29th 2016

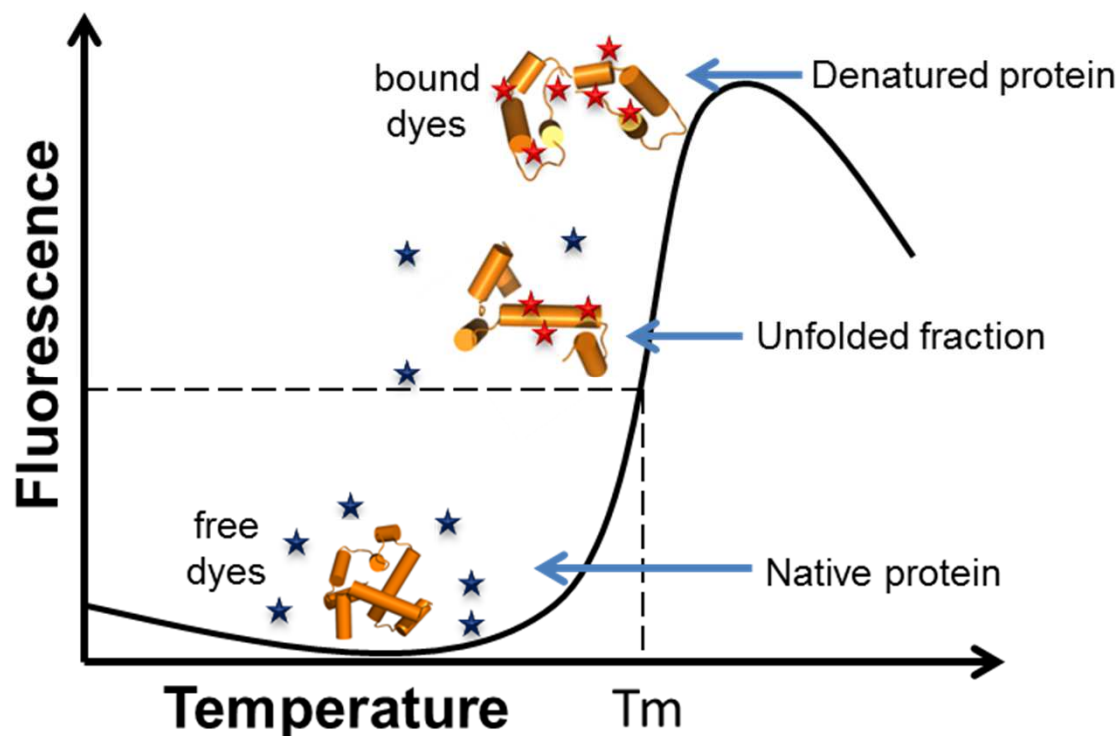
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Agenda

1. **JBScreen Thermofluor**
2. **Membrane Proteins: JBScreen LCP & LCP Lipids**
3. **Frag Xtal Screen**

Crystallizability depends on a protein's thermostability^(1,2)



JBScreen Thermofluor determines thermostability
as a protein's melting temperature (T_m)

(1) Ericsson *et al.* (2006) Thermofluor-based high-throughput stability optimization of proteins for structural studies. *Anal. Biochem.* 357(2):289.

(2) Dupeux *et al.* (2011) A thermal stability assay can help to estimate the crystallization likelihood of biological samples. *Acta Cryst. D* 67:915.

A protein's thermostability is affected by **FUNDAMENTAL** and **SPECIFIC** buffer components

FUNDAMENTAL FACTORS
affect
the whole protein molecule

- Proton concentration (i.e. pH):
Determines protein net charge
- Ionic strength:
Influences size of hydration shells

SPECIFIC FACTORS
affect
**energetically important hot spots
on the protein surface**

- Salt:
Ions with valency-specific effects on distinct sites
- Additives:
Cofactors/Ligands that interact with active site

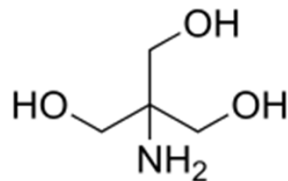
How to screen for thermostability systematically ...?

**Conventional buffers do not allow an independent pH-screen...
...since pH, ionic strength and additives are interdependent variables**

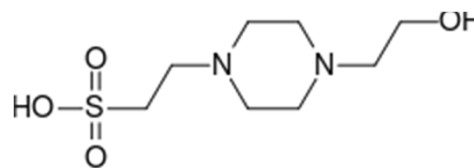
Buffer Solution = Multi-Parameter System of

- pH
- Ionic Strength
- Chemistry (specific ions & additives)

Same
pH...



50 mM TRIS/HCl pH 8.0

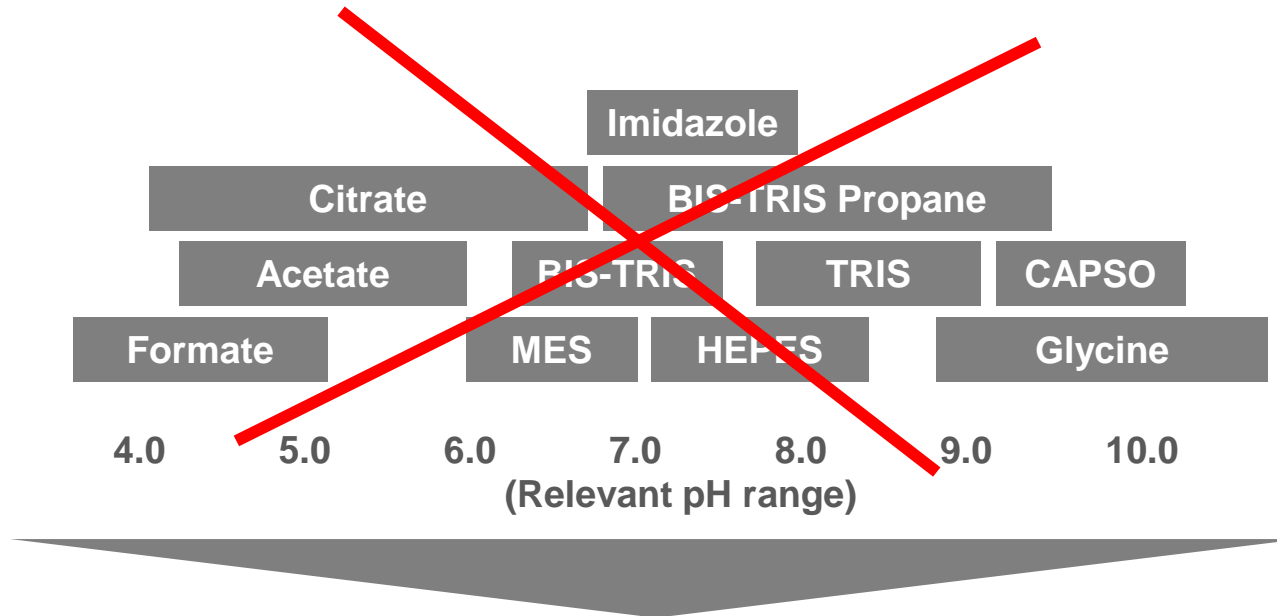


50 mM HEPES/NaOH pH 8.0

...but different
chemistry

Conventional Screening inevitably changes multiple parameters simultaneously

Solution: JBScreen Thermofluor is based on “Super Buffers”⁽¹⁾

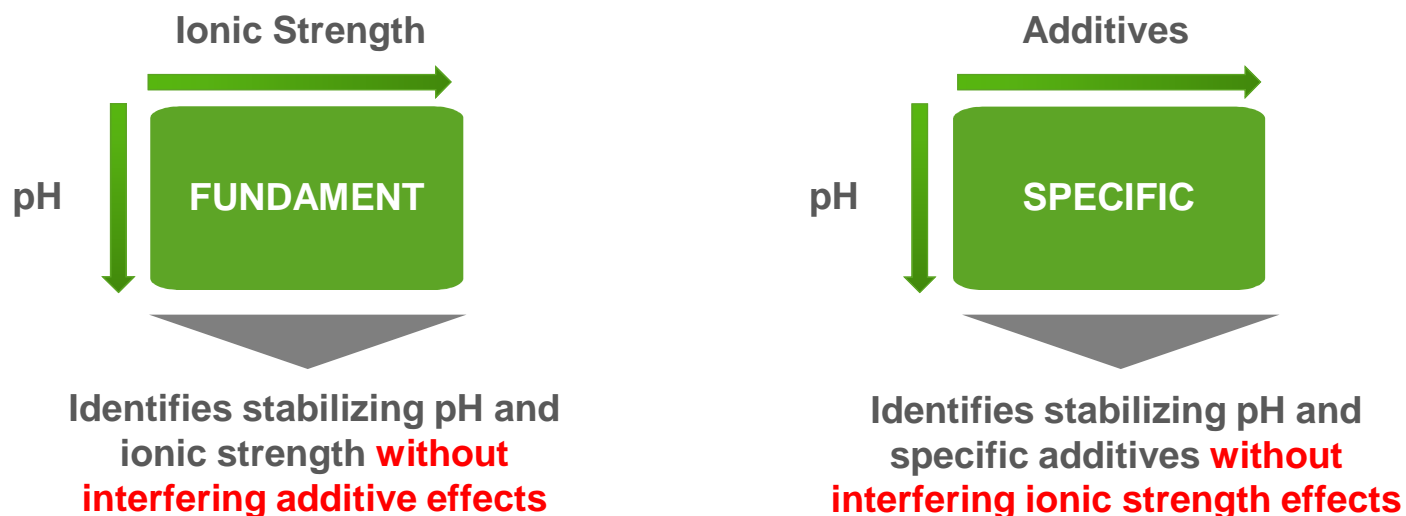


Super Buffer

- Composed of a mixture of three individual buffers with distinct pK_a values
- Specific ratio of individual buffers
- Cover the entire pH range from 4.0 – 10.0
- Maintain a constant chemical environment for screening

(1) Newman (2004) Novel buffer systems for macromolecular crystallization. *Acta Cryst. D* 60:610.

With Super-Buffer based JBScreen Thermofluor FUNDAMENT and SPECIFIC simply grab for the needle in the haystack



Optimization / Refinement

- Different Buffers @ optimum pH (JBScreen Buffers & Buffers Xtreme)
- Concentration of specific ion(s)

Small money and time with JBScreen Thermofluor may save big money and time during crystallization!

Screen	Cat.No.
JBScreen Thermofluor FUNDAMENT → pure pH effect at various ionic strengths	CS-332
JBScreen Thermofluor SPECIFIC → additive effects using high-scoring mono, di- and trivalent ions ⁽¹⁾	CS-333
JBScreen Buffers → common buffers @ neutral pH	CS-214
JBScreen Buffers Xtreme → common buffers @ extreme pH	CS-215

JBScreen Thermofluor is the first commercially available **systematic** protein stability screen

(1) <http://www.rcsb.org/pdb/home/home.do>

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JBScreen LCP is combined from the latest successful conditions



192 integral membrane proteins⁽¹⁾ were analyzed from the pdb⁽²⁾, evaluated and arranged to the novel JBScreen LCP:

- 96 conditions
- Structured by main precipitant
- Elimination of cacodylate and other highly toxic chemicals
- Elimination of metastable conditions

Product	Cat.No.
JBScreen LCP 4 x 24 solutions (10 ml each)	CS-340
JBScreen LCP HTS 96 solutions (1,7 ml each)	CS-213L

(1) Caffrey (2015) A comprehensive review of the lipid cubic phase or *in meso* method for crystallizing membrane and soluble proteins and complexes. *Acta Cryst F* 71:3

(2) <http://www.rcsb.org/pdb/home/home.do>

LCP Lipids: There is more than Monoolein^(1,2)

Cat. No.	Common Name	Abbreviation	Lipid#	C–C double bond
X-LCP-101	Monoolein	9.9 MAG	C18:1	9 cis
X-LCP-102	Monopalmitolein	9.7 MAG	C16:1	9 cis
X-LCP-103	Monovaccenin	11.7 MAG	C18:1	11 cis
X-LCP-104	Monoeicosenin	11.9 MAG	C20:1	11 cis

Change LCP parameters

- Bilayer thickness
- Bending elasticity
- Packaging
- Polarity

Crystallization in LCP: Screen for the optimum condition **and** the optimum LCP Lipid

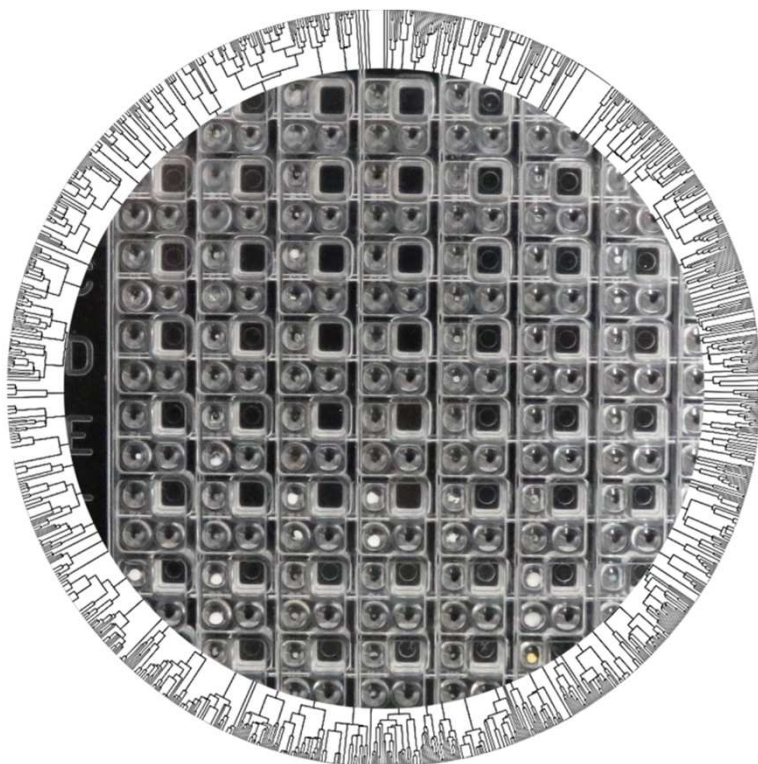
(1) Caffrey (2015) A comprehensive review of the lipid cubic phase or *in meso* method for crystallizing membrane and soluble proteins and complexes. *Acta Cryst F* 71:3

(2) Caffrey and Cherezov (2009) Crystallizing Membrane Proteins Using Lipidic Mesophases. *Nat Protoc.* 4(5):706.

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3. Frag Xtal Screen

Frag Xtal Screen is coming soon



- 96 solid fragments
- Provided in 3 well crystallization plate
- Designed for crystal soaking
- Direct and easy crystallographic analysis of fragment binding⁽¹⁻³⁾

(1) Huschmann *et al.* (2016) Structures of endothiapepsin-fragment complexes from crystallographic fragment screening using a novel, diverse and affordable 96-compound fragment library. *Acta Cryst F* 72:346.

(2) Schiebel *et al.* (2016) Six Biophysical Screening Methods Miss a Large Proportion of Crystallographic Discovered Fragment Hits: A Case Study. *ACS Chem. Biol.* 11:1693.

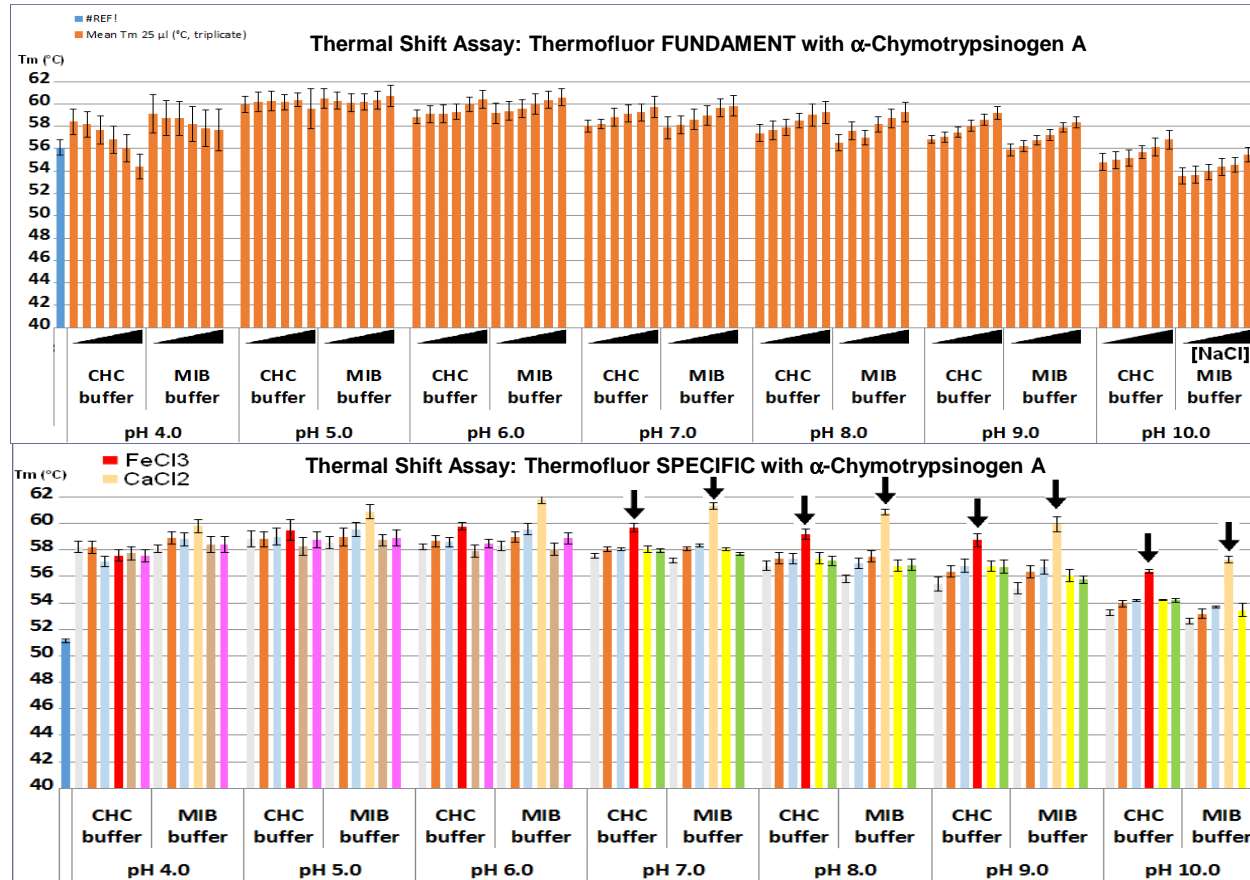
(3) Schiebel *et al.* (2015) One Question, Multiple Answers: Biochemical and Biophysical Screening Methods Retrieve Deviating Fragment Hit Lists. *ChemMedChem* 10:1511.

Our Xtal group is very pleased to answer your inquiries!
xtals@jenabioscience.com



Backups

Stabilizing effects on α -Chymotrypsinogen are directly correlated with crystallizability



FUNDAMENT:
stable from pH 5-8; stability dependent on ionic strength at pH>6

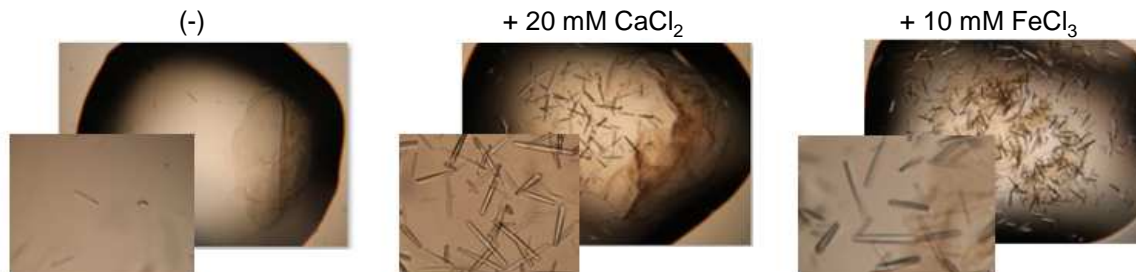
SPECIFIC:
stabilization is induced by either FeCl₃ or CaCl₂ (iron-binding properties are not described so far)

Buffer for crystallization

20 mg/ml α -Chymotrypsinogen in 20 mM HEPES (pH 7.0), 500 mM NaCl

Droplets with CaCl₂ and FeCl₃

Crystallization: 100 mM Phosphate (pH 7.5), 20% PEG 3350, 25% PEG 400



Crystal growth is promoted by CaCl₂ and FeCl₃

Apply JBScreen Thermofluor for hydrophobic targets

**Hydrophobic
protein target**

- Apply the intrinsic red shift of tryptophan residues (e.g. in the Prometheus machine from NanoTemper)
- Apply the new thiol-specific dye (JBS, in development)

Little protein

- Apply 5 μ l total assay volume instead of 25 μ l and save 80% of protein

Promising approach for membrane proteins, ligands, ...

JBScreen Thermofluor FUNDAMENT covers pH 4-10 and ionic strength 0...1,000 mM

	1	2	3	4	5	6	7	8	9	10	11	12
A	CP + Dye CB-1	CP + Dye CB-1	CP + Dye CB-1	CP + Dye CB-2	CP + Dye CB-2	CP + Dye CB-2	CP + Dye CB-3	CP + Dye CB-3	CP + Dye CB-3	TP + Dye Original Buffer	TP + Dye Original Buffer	TP + Dye Original Buffer
B	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0
C	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0
D	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0
E	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0
F	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0
G	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0
H	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0
	100 mM Super Buffer 1						100 mM Super Buffer 2					
	Ionic Strength						Ionic Strength					

Super Buffer 1: composed of Citric acid, HEPES and CHES buffers

Super Buffer 2: composed of Malonic acid, Imidazole and Boric acid buffers

JBScreen Thermofluor SPECIFIC screens for high-scoring⁽¹⁾ mono-, di- and trivalent cations

	1	2	3	4	5	6	7	8	9	10	11	12
	CP + Dye	CP + Dye	CP + Dye	CP + Dye	CP + Dye	CP + Dye	CP + Dye	CP + Dye	CP + Dye	TP + Dye	TP + Dye	TP + Dye
	CB-1	CB-1	CB-1	CB-2	CB-2	CB-2	CB-3	CB-3	CB-3	Original Buffer	Original Buffer	Original Buffer
A	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0
B			20 mM MgSO ₄	10 mM FeCl ₃	10 mM ZnCl ₂	10 mM MnCl ₂			20 mM MgSO ₄	20 mM CaCl ₂	10 mM ZnCl ₂	10 mM MnCl ₂
C	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0
D			20 mM MgSO ₄	10 mM FeCl ₃	10 mM ZnCl ₂	10 mM MnCl ₂			20 mM MgSO ₄	20 mM CaCl ₂	10 mM ZnCl ₂	10 mM MnCl ₂
E	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0
F			20 mM MgSO ₄	10 mM FeCl ₃	20 mM LiCl	20 mM KCl			20 mM MgSO ₄	20 mM CaCl ₂	20 mM LiCl	20 mM KCl
G	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0
H			20 mM MgSO ₄	10 mM FeCl ₃	20 mM LiCl	20 mM KCl			20 mM MgSO ₄	20 mM CaCl ₂	20 mM LiCl	20 mM KCl
	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0
			20 mM MgSO ₄	10 mM FeCl ₃	20 mM LiCl	20 mM KCl			20 mM MgSO ₄	20 mM CaCl ₂	20 mM LiCl	20 mM KCl
	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0
			20 mM MgSO ₄	10 mM FeCl ₃	20 mM LiCl	20 mM KCl			20 mM MgSO ₄	20 mM CaCl ₂	20 mM LiCl	20 mM KCl
	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0
			20 mM MgSO ₄	10 mM FeCl ₃	20 mM LiCl	20 mM KCl			20 mM MgSO ₄	20 mM CaCl ₂	20 mM LiCl	20 mM KCl

100 mM Super Buffer 1
100 mM Super Buffer 2

150 mM NaCl
150 mM NaCl

Super Buffer 1: composed of Citric acid, HEPES and CHES buffers

Super Buffer 2: composed of Malonic acid, Imidazole and Boric acid buffers

(1) Mostly occurring cations that appear as ligands in protein structures on the PDB (Protein Data Bank)