

Redox State-Dependent Structural Changes in [NiFeSe] Hydrogenase from *Desulfovibrio vulgaris* Hildenborough

www.itqb.unl.pt



INSTITUTO
DE TECNOLOGIA
QUÍMICA E BIOLÓGICA
/UNL

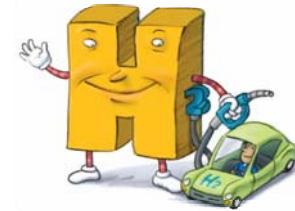
Knowledge Creation

Pedro M. Matias
Industry and Medicine Applied Crystallography

10th International Hydrogenase Conference
Szeged, Hungary – July 9, 2013

[NiFeSe] Hases

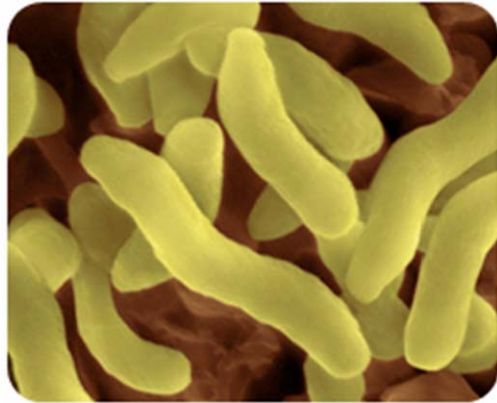
- ✓ Included in the [NiFe] group
- ✓ Higher activities for H₂ production
- ✓ Less H₂ inhibition
- ✓ Fast reactivation at a low redox potential
- ✓ Display some level of protection to O₂ exposure



Attractive candidates for:

- Biological H₂ production from renewable sources
- Use in bioelectrical devices

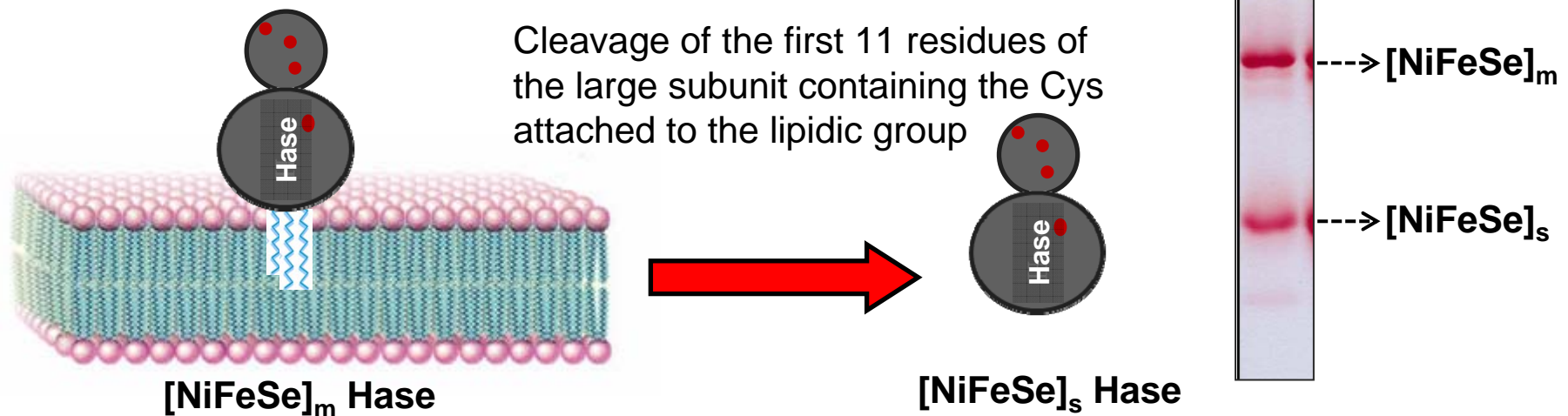
Desulfovibrio vulgaris Hildenborough



- ✓ 7 Hases in genome, 4 are periplasmic
- ✓ [NiFeSe] Hase uses Type I cytochrome c_3 as electron acceptor
- ✓ Expression levels of different Hases depend on metal availability and H_2 concentration
- ✓ [NiFeSe] Hase is preferentially expressed in the presence of Se

D. vulgaris Hildenborough [NiFeSe] Hase

- Periplasmic bacterial lipoprotein (lipobox)
- Two subunits
- Three [4Fe-4S] clusters
- The large subunit binds the NiFe active site
- One of the terminal Ni-bound Cys is a SeCys
- During purification a soluble protein is also obtained



D. vulgaris Hildenborough [NiFeSe] Hase

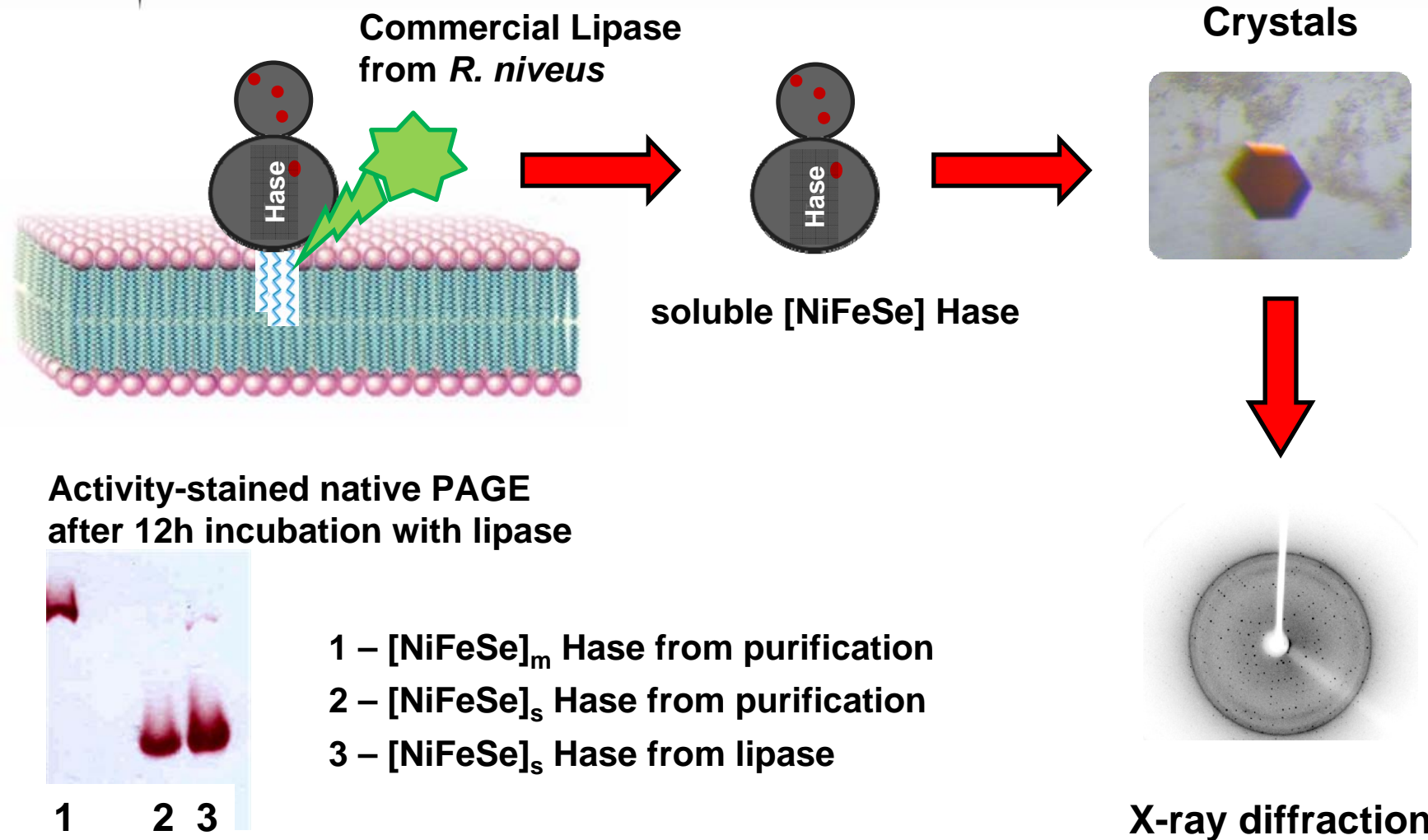


Specific activity (U mg⁻¹)

Hase	Phospholipids	Tris-HCl buffer
[NiFeSe] _m	6908	2755
[NiFeSe] _s	-	460
[NiFe] ₁	495	366

Valente, FMA et al., 2005, J. Biol. Inorg. Chem, 10:667-682.

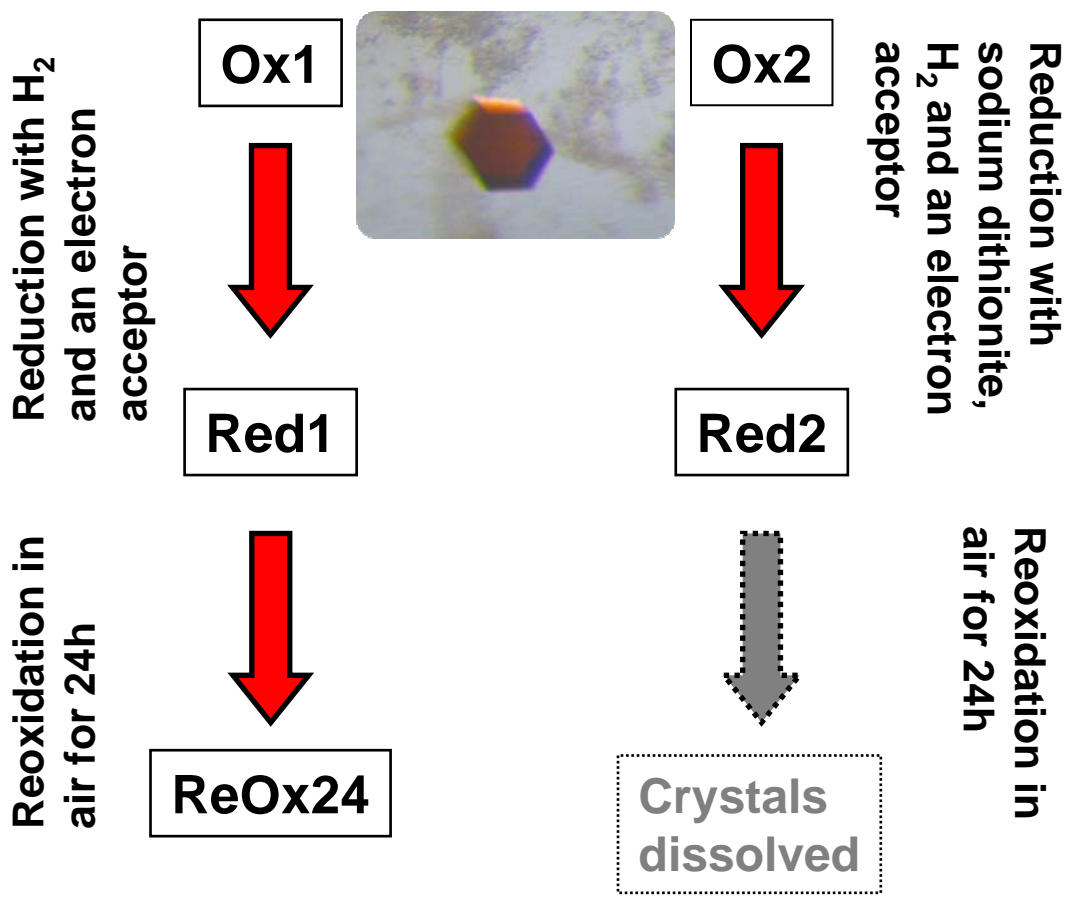
Production of $[\text{NiFeSe}]_s$ Hase from $[\text{NiFeSe}]_m$



Crystals of $[\text{NiFeSe}]_s$ in different redox forms

Aerobic crystallization

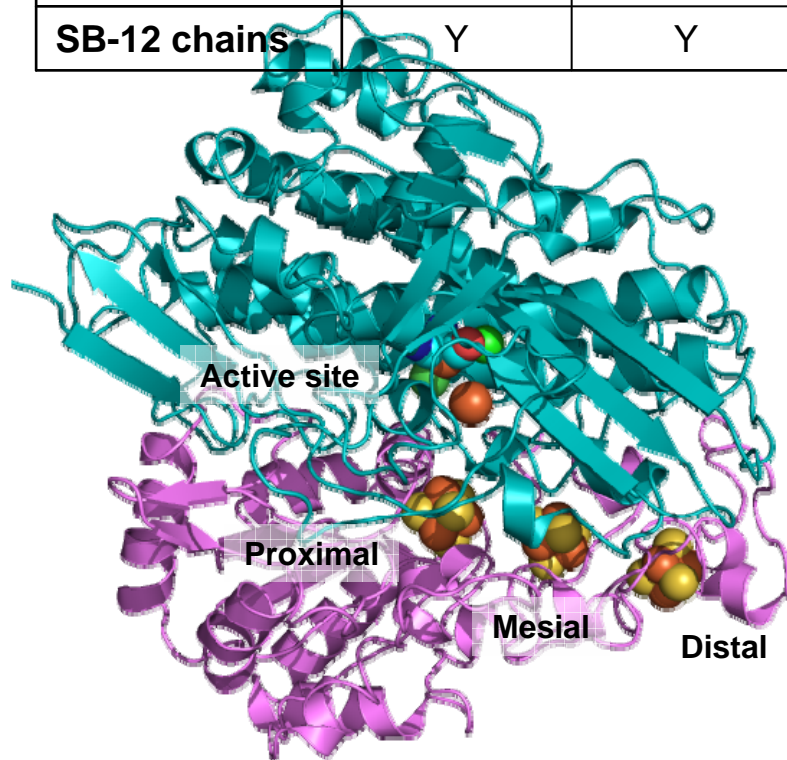
Purified $[\text{NiFeSe}]_s$ Hase, “native”



$[\text{NiFeSe}]_s$ Hase from $[\text{NiFeSe}]_m$

X-ray data collection & 3D structure

Dataset	Ox	Ox1	Ox2	Red1	Red2	ReOx24
Beamline	DLS I04	SLS PXIII	ESRF ID29	SLS PXIII	ESRF ID29	SLS PXIII
Resolution (Å)	2.05	1.50	1.33	1.95	1.82	1.80
R / R _{free} (%)	14.4 / 20.1	13.5 / 15.4	13.1 / 14.8	15.3 / 19.0	12.4 / 14.7	13.5 / 16.6
Space Group	$P 2_1$	$P 2_1 2_1 2_1$	$C 2$	$P 2_1 2_1 2_1$	$P 3_1 21$	$P 2_1 2_1 2_1$
SB-12 chains	Y	Y	N	N	N	Y



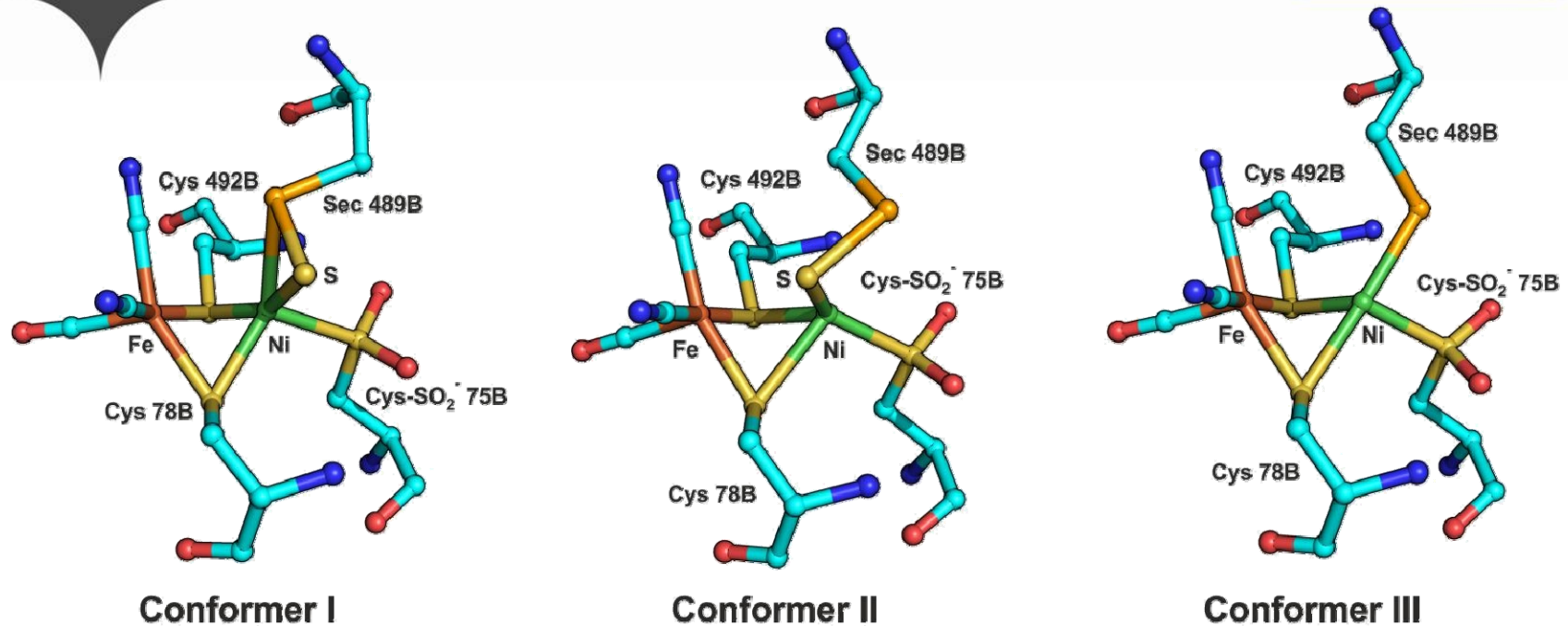
Large subunit (B)

Typical fold of a [NiFe] Hase

Small subunit (A)

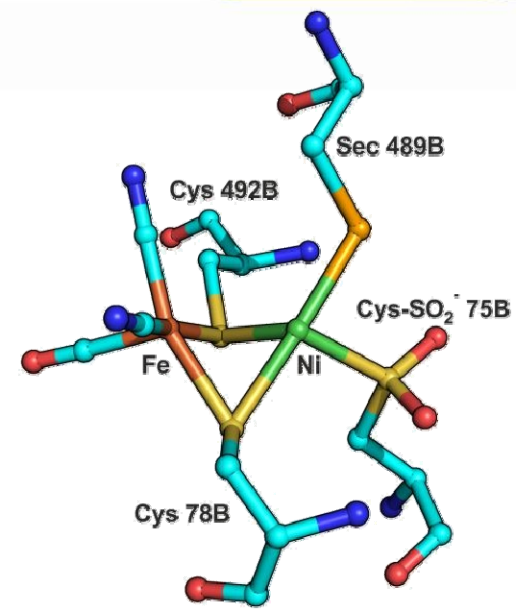
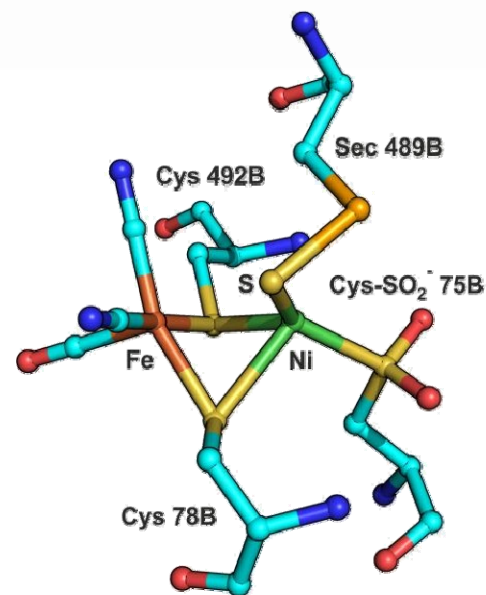
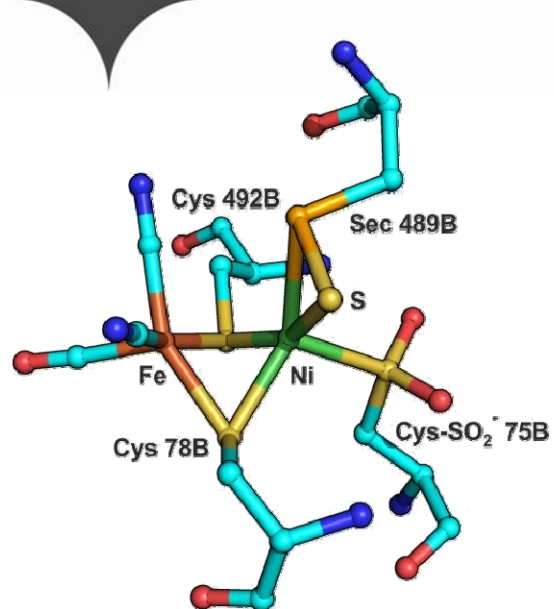
Marques *et al.* 2010, *J Mol Biol*, 396:893-907
 Marques *et al.* 2013, *Int J Hydrogen Energy*, 38:8664-8682

The active site



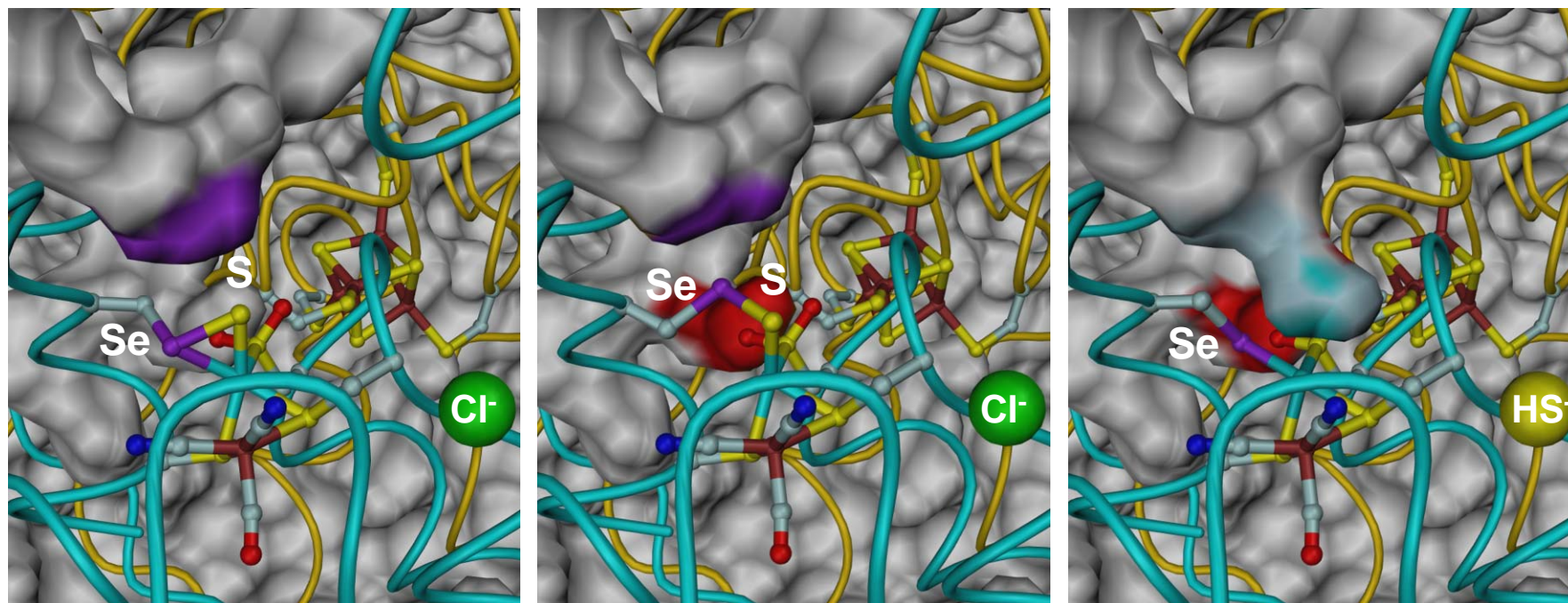
- ❖ Side chain of SeCys 489B in **three different conformers**
- ❖ Terminal Cys 75B **irreversibly** oxidized to **sulfinate**

The active site



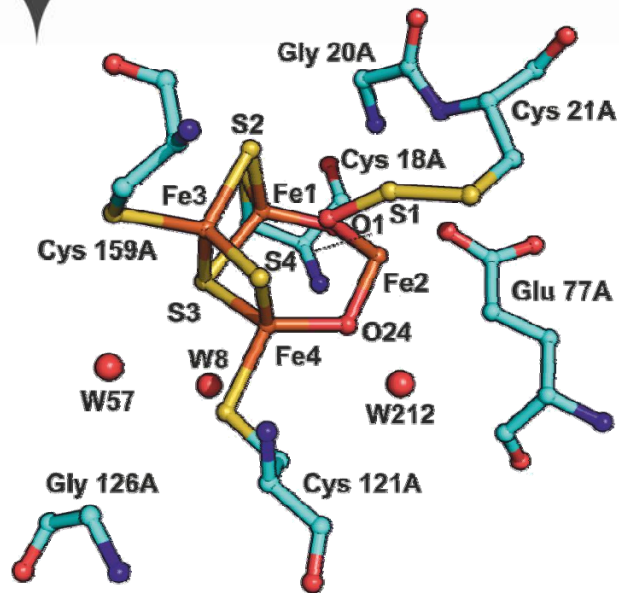
Ox	70 %	15 %	15 %
Ox1	74 %	16 %	10 %
Ox2	73 %	13 %	14 %
Red1	-	-	100 %
Red2	-	12 %	88 %
ReOx24	-	38 %	62 %

The active site

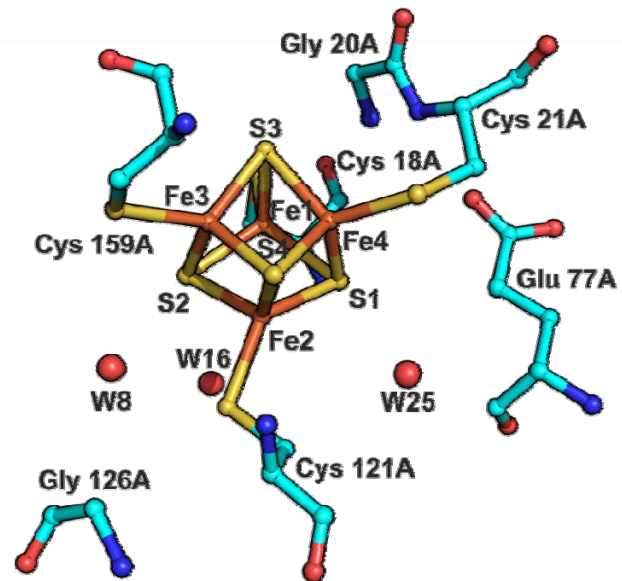


- ❖ Se atom in conformers I and II **blocks access to bridging position**
- ❖ No oxy/hydroxy bridging species
- ❖ **No Ni-A/Ni-B EPR signal**

The proximal [4Fe-4S] cluster



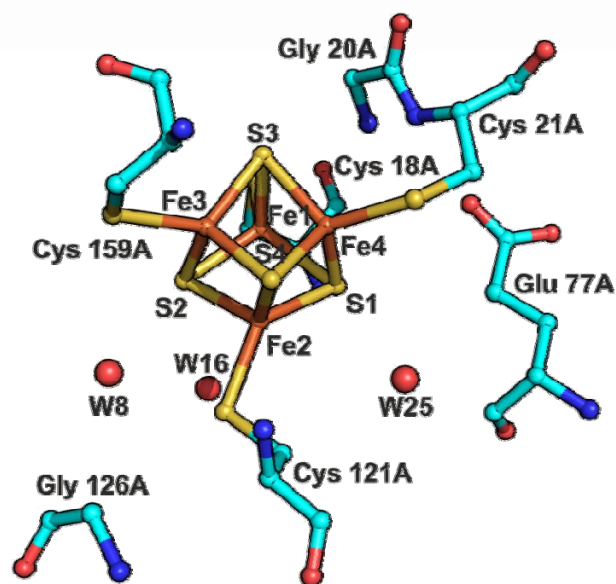
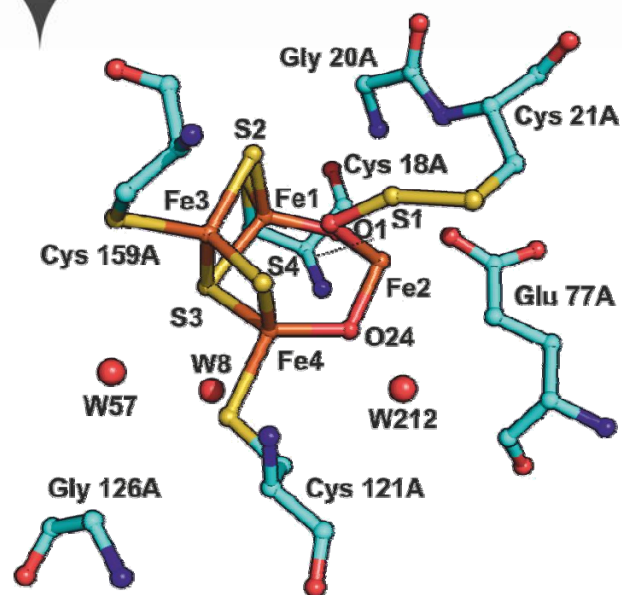
Ox, Ox1, Ox2



Red1, Red2, ReOx24

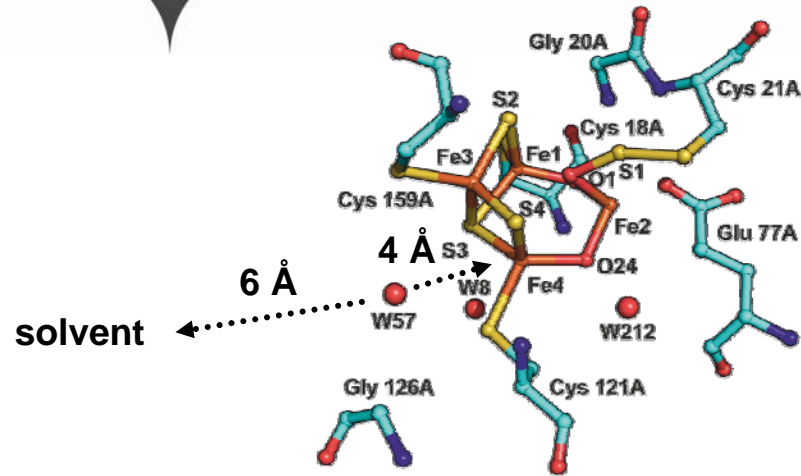
- ❖ [4Fe-4S] **reversibly** oxidized to [4Fe-4S-O3]
- ❖ oxidation occurs during aerobic purification and crystallization

The proximal [4Fe-4S] cluster

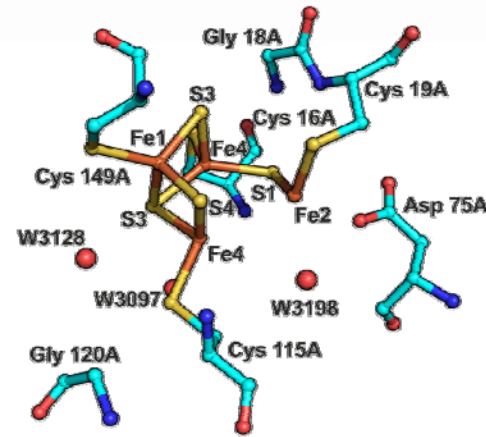


	[Fe ₄ S ₄ O ₃]	[Fe ₄ S ₄]
Ox	40 %	60 %
Ox1	80 %	20 %
Ox2	~100 %	-
Red1	-	100 %
Red2	-	100 %
ReOx24	-	100 %

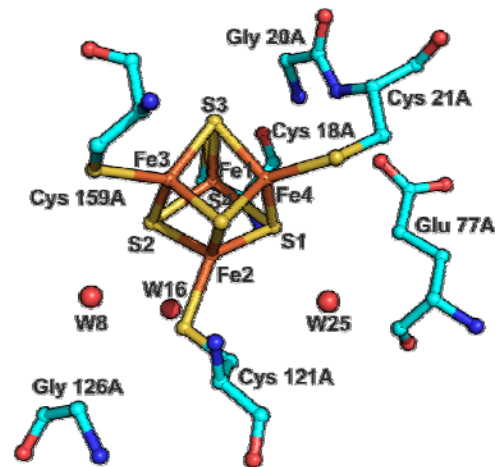
The proximal [4Fe-4S] cluster



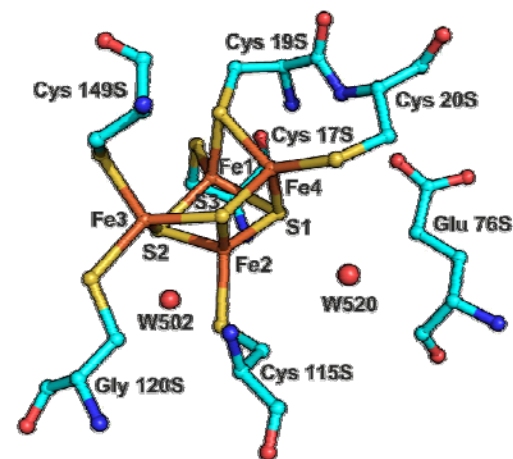
D. Vulgaris Hildenborough Ox



A. vinosum [NiFe] Ni-A – 3myr
(Ogata et al, 2010)



D. Vulgaris Hildenborough Red



E. coli Red – 3uqy
(Volbeda et al., (2012)

The inactivation of [NiFeSe] Hase from *DvH*

Inactive states of [NiFeSe] Hases different from [NiFe] Hases?

In *D. vulgaris* Hildenborough:

- ❖ **No access** to bridging site by oxy/hydroxy bridging species
- ❖ Proximal [4Fe-4S] cluster **reversibly** oxidized to [4Fe-4S-3O]
- ❖ Terminal Cys 75B **irreversibly** oxidized to sulfinate
 - ❖ Does this modification completely inactivate the enzyme ?

New activity measurements of [NiFeSe]_s Hase :

5707 U mg⁻¹ after purification

782 U mg⁻¹ after 16 days (from redissolved crystals with ~100% sulfinate)



INSTITUTO
DE TECNOLOGIA
QUÍMICA E BIOLÓGICA
/UNL

INDUSTRY AND MEDICINE APPLIED CRYSTALLOGRAPHY LAB (ITQB)

Pedro Matias

Ricardo Coelho
Marta Marques

PROTEIN MODELLING LAB (ITQB)

Cláudio Soares

Carla Baltazar

DATA COLLECTIONS

Diamond Light Source (Didcot, UK)
Swiss Light Source (Villigen, CH)
European Synchrotron Radiation Facility (Grenoble, FR)



FCT grants SFRH/BD/60879/2009, PTDC/BIA-PRO/70429/2006 and PTDC/BBB-BEP/0934/2012

BACTERIAL ENERGY METABOLISM LAB (ITQB)

Inês Pereira

Isabel Pacheco
Marta Marques
Mónica Neves
Raquel Ramos
Sofia Venceslau
André Santos
Fabian Grein



Instituto de Catalisis y Petroleoquimica (Madrid)

Departamento de Biocatálisis

Antonio De Lacey

Marisela Velez
Cristina Gutiérrez-Sanchez
David Olea
Oscar Gutiérrez



PROJECT COFUNDED BY
THE EUROPEAN UNION