

# La TEI dans ...

A decorative graphic consisting of a blue line with circular markers and several location pin icons, overlaid on a background of green and yellow wavy shapes, spans the width of the slide above the "ISTEX" text.

# ISTEX

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## TEI-ISTEX : Ce que nous allons aborder

- ❑ Présentation d'**ISTEX**
- ❑ Schéma **ODD-ISTEX**
- ❑ **Transformations** en TEI
- ❑ **Annotations** en TEI

*Construire le socle de la bibliothèque scientifique numérique nationale.*

## ISTEX ...

Initiative d'excellence en Information Scientifique et Technique

- ❑ **Accès en ligne aux collections rétrospectives** de la littérature scientifique dans toutes les disciplines
- ❑ Pour les abonnés de la communauté de l'**enseignement supérieur et de la recherche**

<https://www.istex.fr/>



ISTEX aujourd'hui, c'est :



**23 027 718**  
documents

**26**

corpus éditeurs

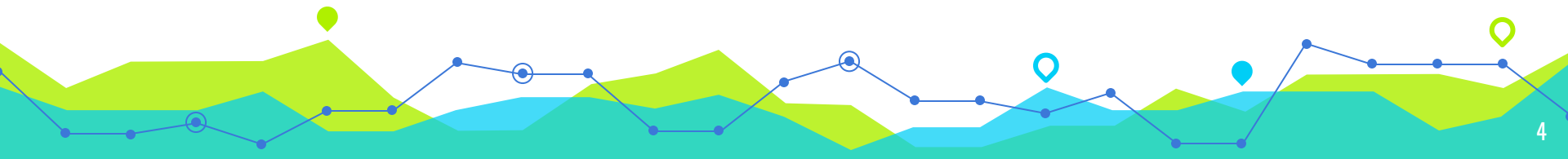
**9 279**

revues

*De 1473 à  
2016*

**345 369**

monographies



## ISTEX : quels services ?

The screenshot shows the ISTEX website interface. At the top left is a hamburger menu icon. At the top right are icons for a heart, a notification bell, and a grid. Below the navigation is a large green button containing the URL <https://www.istex.fr>. To the right of the button, the word "ISTEX" is displayed in large, bold, blue and green letters. Below the logo, a text block states: "23 millions de documents provenant de 26 corpus de littérature scientifique dans toutes les disciplines, soit plus de 9 279 revues et 345 369 ebooks entre 1473 et 2016 pour l'ESR". At the bottom, there is a search bar with the placeholder text "Testez ISTEX : indiquez un titre, des mots-clés ou un DOI" and a magnifying glass search icon on the right.

## ISTEX : quels services ?

The screenshot shows the ISTEX website interface. At the top left is a hamburger menu icon. At the top right are icons for a heart, a notification bell, and a grid. Below the menu is a green rounded rectangle containing the URL <https://www.istex.fr>. The main heading is 'ISTEX' in large blue and green letters. Below it, the text reads: '23 millions de documents provenant de 26 corpus de littérature scientifique dans toutes les disciplines, soit plus de 9 279 revues et 345 369 ebooks entre 1473 et 2016 pour l'ESR'. At the bottom, there is a search bar with the placeholder text 'Testez ISTEX : indiquez un titre, des mots-clés ou un DOI' and a magnifying glass icon. A large green arrow on the right side of the screenshot points from the top right towards the search bar.

## ISTEX : quels services ?

The screenshot shows the ISTEX website interface. At the top left, there is a hamburger menu icon. Below it, a green button contains the URL <https://www.istex.fr>. The main header area features the text "23 millions de documents de littérature scientifique dans toutes les disciplines", "9 279 revues et 345 369 ebooks", and a search bar with the placeholder text "Testez ISTEX : indiquez un titre, des mots-clés ou un DOI". A central menu overlay is displayed, listing various services: Bouton (puzzle icon), Scholar (graduation cap icon), Zotero (bookmarks icon), Télécharger (download icon), API (cloud with arrows icon), Harvester (terminal icon), SPARQL (network icon), data.istex.fr (book icon), and Rechercher (search icon). A green arrow points from the Harvester icon to the search bar on the right side of the interface.

## ISTEX : quels services ?

The screenshot shows the ISTEX website interface. A green box highlights the URL <https://www.istex.fr>. The main text reads: "23 millions de documents pour la littérature scientifique dans toutes les disciplines, 9 279 revues et 345 369 ebooks". Below this, a search bar contains the text "Testez ISTEX : indiquez un titre, des mots-clés ou un auteur". A dark overlay menu is positioned on the right, listing various services with icons: Bouton (puzzle piece), Scholar (graduation cap), Zotero (bookmarks), Télécharger (download arrow) - highlighted with a green border, API (cloud with arrows), Harvester (terminal), SPARQL (network graph), data.istex.fr (book icon), and Rechercher (magnifying glass). A green arrow points from the Harvester icon to the search bar. A TEI logo (Text Encoding Initiative) is also visible in the bottom center of the overlay area.



Le démonstrateur est une interface à **vocation pédagogique** branchée sur l'API ISTEEX qui permet de :

- Construire sa requête (en mode simple ou en mode avancé)
- Visualiser et filtrer les résultats

<https://demo.istex.fr>

**ISTEEX**

Bienvenue sur le **démonstrateur ISTEEX**

[En savoir plus](#)

Titre ou mot clef

Requête `https://api.istex.fr/document?q=*%&facet=corpusName[*]&size=10&rankBy=qualityOverRelevance&output=*%&stats`

**Astuce**

Vous pouvez sélectionner une facette en cliquant sur Corpus ci-dessous.

**Corpus**  26

- elsevier 6015990
- wiley 5345607
- springer-journals 3905350
- oup 1450708
- springer-ebooks 930986
- cambridge 836349
- acs 816147

Résultats : 23027718 (528 ms)   1/ 2302772 Tri par : Aucun

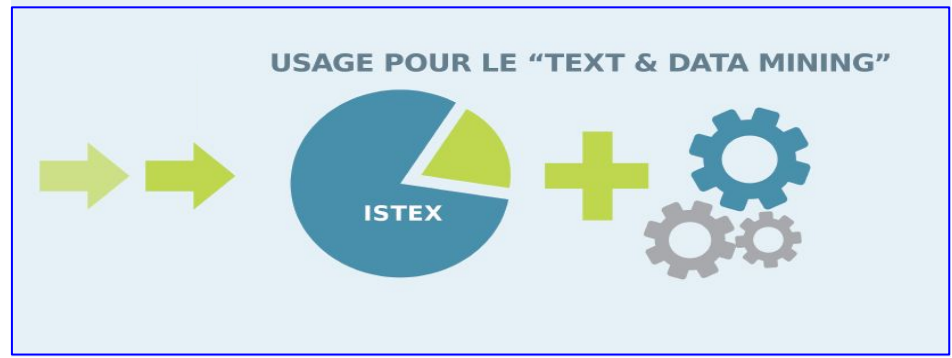
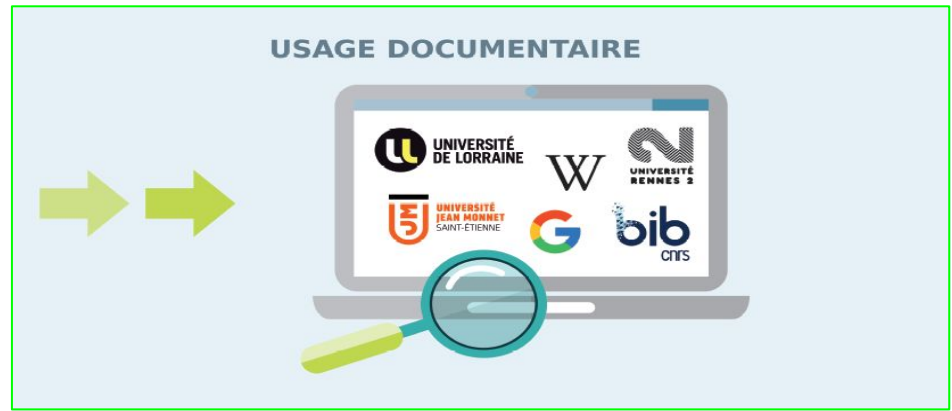
**5'-(2-Phosphoryl-1,4-dioxobutane) as a Product of 5'-Oxidation of Deoxyribose in DNA: Elimina...**

Oxidation of deoxyribose in DNA leads to the formation of a spectrum of electrophilic products unique to each position in the sugar. For example, chemical reactions following abstraction of the C5'-hydrogen atom partition to form either a nucleoside 5'-aldehyde residue attached to the 5'-end of the DNA strand or a 5'-formyl phosphate...

Fulltext     Annexes   Enrichments

# ISTEX : quels usages ?

L'un classique,



... l'autre plus avancé !



# La TEI dans ISTEX





# Schéma TEI - ISTEEX

<https://tei-istex.fr>

1


# Schéma TEI-ISTEX = ODD-ISTEX

## > modélisation des données

- ODD (**O**ne **D**ocument **D**oes it all) → pour personnaliser la TEI
- Implémentations techniques du modèle
  - De façon générale: correspondre aux Guidelines TEI
  - De façon particulière: répondre à des besoins spécifiques
- Adapter les modules de la TEI en fonction des cas rencontrés

Pour en savoir plus sur ce qu'est un ODD → [https://halshs.archives-ouvertes.fr/cel-01706530/file/06\\_TEI\\_ODD\\_Camps\\_20170202.pdf](https://halshs.archives-ouvertes.fr/cel-01706530/file/06_TEI_ODD_Camps_20170202.pdf)

- Génération grâce à l'outil [ROMA](#)
  - Création d'un schéma TEI **adapté**
  - Prise en charge de la **structuration** de  
abstracts
  - **Exports** de schémas XSD, relaxNG



## Roma: generating customizations for the TEI

A new version of Roma is available! It is currently in beta, [try it at romabeta.tei-c.org](http://try.it.at.romabeta.tei-c.org)

TEI Roma is a tool for working with TEI customizations. A TEI customization is a document from which you can generate a schema documentation of it. The schema generated can be expressed in any of DTD, RELAXNG W3C Schema or Schematron language.

You can make or modify your TEI customization in several different ways:

- Build up: create a new customization by adding elements and modules to the smallest recommended schema
- Reduce: create a new customization by removing elements and modules from the largest possible schema
- Create a new customization starting from a template
- Use or modify an existing TEI-defined customization
- Upload a customization

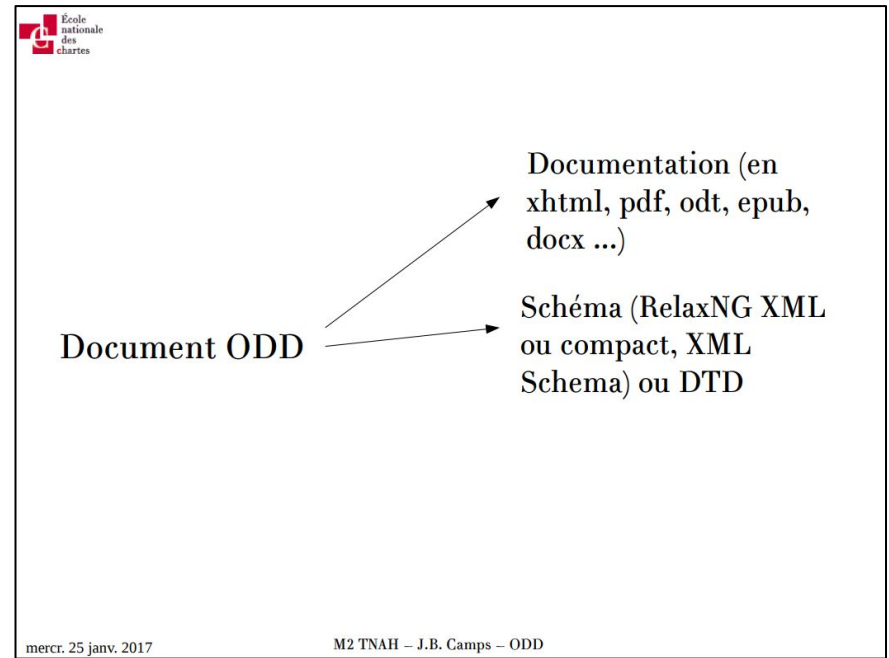
Community-maintained customizations can be downloaded from [the TEI website](#)

Start

A TEI customization is informally referred to as an ODD (for "One Document Does it all")

<https://roma2.tei-c.org/>

- Génération grâce à l'outil [ROMA](#)
  - Export de la **documentation**



Source: [https://halshs.archives-ouvertes.fr/cel-01706530/file/06\\_TEI\\_ODD\\_Camps\\_20170202.pdf](https://halshs.archives-ouvertes.fr/cel-01706530/file/06_TEI_ODD_Camps_20170202.pdf)



Mise à disposition

Schéma TEI pour le projet ISTEX

Schéma ODD-ISTEX -  
 Disponible sur GitHub -  
 Autres formats disponibles à télécharger -

Schéma ODD-ISTEX  
 Codes  
 Schéma XSD ...

## Table of contents



- 1. Elements
  - 1.1. <TEI>
  - 1.2. <ab>
  - 1.3. <abbr>
  - 1.4. <abstract>
  - 1.5. <accMat>
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  - 1.31. <bibFull>
  - 1.32. <bibScope>

- ◉ Guidelines personnalisés (version Bêta) pour le format TEI-ISTEX  
 extrait de l'outil [ROMA](https://roma.istex.fr)

<https://tei.istex.fr>





# pub2TEI-ISTEX

<https://github.com/istex/Pub2TEI>

# 2

- Développé au départ dans le cadre du projet européen [PEER](#) par L. Romary et P. Lopez
- Propose un **ensemble de feuilles de style** → conversion documents XML en **format TEI**
- Déploiement et adaptation pour **ISTEX** (*en cours*)
  - Entraînements, développements

<https://github.com/istex/pub2te>

istex / Pub2TEI  
forked from kermitt2/Pub2TEI

Join GitHub today  
GitHub is home to over 40 million developers working together to host and review code, manage projects, and build software together.  
[Sign up](#)

Set of XSL stylesheets for converting heterogeneous publisher XML formats into TEI

321 commits 2 branches 0 packages 2 releases 5 contributors BSD-2-Clause

Branch: master Pull request Find file Clone or download

This branch is 55 commits ahead, 18 commits behind kermitt2:master.

File	Description	Commit Date
Schemas	First commit	4 years ago
Stylesheets	Add OpenEdition editor	2 days ago
.gitignore	add a 'true' version number, which will be increased (and not fixed t...	3 months ago
LICENSE	First commit	4 years ago
Pub2TEI.xpr	reprise revisionDesc	4 months ago
README.md	It's better with the good email	3 years ago
get-version.js	add package.json and postversion script to update version number in P...	3 months ago
package.json	1.0.4	22 days ago
update-version.sh	update format for version date	2 months ago

istex / Pub2TEI  
forked from kermitt2/Pub2TEI

Code Pull requests Projects Security Insights

Branch: master Pub2TEI / Stylesheets / Create new file Find file History

This branch is 55 commits ahead, 18 commits behind kermitt2:master.

File	Description	Commit Date
ArticleSetNLMV2.0.xsl	reprise tableau + email	last month
BMJ.xsl	reprise tableau + email	last month
Bibliography.xsl	Nature - reprise auteurs rebib: ajout persName - reprise affiliation...	22 days ago
BookChapter.xsl	reprise tableau + email	last month
BookComponents.xsl	Elsevier suite travaux monogr	2 years ago
CountryCodes.xml	RSL structuration + coup pays des affiliations non structurées	2 years ago
Default.xsl	ajout de note, reprise affiliation	2 years ago
Duke.xsl	reprise tableau + email	last month
EDPSArticle.xsl	reprise tableau + email	last month
EDPSedp-article.xsl	reprise tableau + email	last month
Elsevier.xsl	reprise tableau + email	last month
ElsevierFormula.xsl	Elsevier suite travaux monogr	2 years ago
Figures.xsl	ACS - ajout des tableaux en format oasis	last year
FullTextTags.xsl	reprise tableau + email	last month
IOP.xsl	reprise tableau + email	last month
IOPPatch.xsl	Simplification de la sortie et petite mise à jour TEI	5 years ago
ISOifiers.xsl	reprise volume et numero erronés	11 months ago
Imports.xsl	Add NPG coverage (header, full text and biblio), as provided to ISTEX	4 years ago
JournalComponents.xsl	NML- reprise author group	14 days ago
JournalList.xml	Premiers exemples opérationnels	5 years ago
KeywordsAbstract.xsl	rebase - all namespace make big errors in process	last year
NLM2TEI-article.xsl	Nature - découpage fin des affiliations	10 days ago
NameComponents.xsl	reprise informations book-reviews	last month
NamesDatesPlaces.xsl	Add OpenEdition editor	2 days ago



nature publishing group

PDF

# pub2TEI-ISTEX < modélisation >

## articles

### A novel protein–mineral interface

Dmitriy Alexeev<sup>1</sup>, Haizhong Zhu<sup>2</sup>, Maolin Guo<sup>2,3</sup>, Weiqing Zhong<sup>2,4</sup>, Dominic J.B. Hunter<sup>2</sup>, Weiping Yang<sup>2,4</sup>, Dominic J. Campopiano<sup>2</sup> and Peter J. Sadler<sup>2</sup>

Published online 24 February 2003; corrected 10 March 2003 (details online); doi:10.1038/nsb903

**Transferrins transport Fe<sup>3+</sup> and other metal ions in mononuclear-binding sites. We present the first evidence that a member of the transferrin superfamily is able to recognize multi-nuclear oxo-metal clusters, small mineral fragments that are the most abundant forms of many metals in the environment. We show that the ferric iron-binding protein from *Neisseria gonorrhoeae* (nFBp) readily binds clusters of Fe<sup>3+</sup>, Ti<sup>3+</sup>, Zr<sup>4+</sup> or Hf<sup>4+</sup> in solution. The 1.7 Å resolution crystal structure of Hf-nFBp reveals three distinct types of clusters in an open, positively charged cleft between two hinged protein domains. A di-tyrosyl cluster nucleation motif (Tyr195–Tyr196) is situated at the bottom of this cleft and binds either a trinuclear oxo-Hf cluster, which is capped by phosphate, or a pentanuclear cluster, which in turn can be capped with phosphate. This first high-resolution structure of a protein–mineral interface suggests a novel metal-uptake mechanism and provides a model for protein-mediated mineralization/dissimilation, which plays a critical role in geochemical processes.**

Organisms have developed sophisticated mechanisms for the uptake of Fe<sup>3+</sup> and other metal ions from the environment. Metals in mineral form are used as sources of energy by geobacteria<sup>1</sup>, which are critical in the control of mineral growth and phase transformations. The recognition of minerals by microbial proteins is of current interest because microbes can affect the chemistry and distribution of nearly all elements in the periodic table<sup>2,3</sup>. Little structural information is currently available about the interactions between proteins and metal clusters during the initial stages of protein-mediated mineralization and mineral acquisition by bacteria. Here we report the surprising discovery that an iron-binding protein in the transferrin superfamily can recognize a variety of metal clusters in its iron-binding cleft, a finding that has potential implications for our understanding of metal uptake mechanisms. Many pathogenic microorganisms require iron for virulence<sup>4</sup>. However, iron acquisition is a major problem for them in aerobic environments because aquated Fe<sup>3+</sup> ions are highly acidic and readily form hydroxide- and oxo-bridged polymers and insoluble Fe(OH)<sub>3</sub> (rust) at neutral or alkaline pH. Therefore, pathogenic Gram-negative bacteria, such as *Neisseria gonorrhoeae*, *Neisseria meningitidis* and *Haemophilus influenzae*, synthesize the iron-binding protein fbp to capture iron presented at the outer membrane and transport it across the periplasm. Fbp, a single polypeptide chain of 309 amino acids, shows the same polypeptide topology as the two lobes of serum transferrin and lactoferrin despite a lack of significant sequence similarity<sup>5,6</sup>. The Fe<sup>3+</sup>-binding site is in an interdomain cleft — a 'Venus fly-trap' — that is open in the apo protein and closed when Fe<sup>3+</sup> is bound. Fbp has been reported to bind one Fe<sup>3+</sup> strongly but reversibly<sup>7</sup>, as does each lobe of transferrin<sup>8</sup>. We sought to determine whether other metals bind strongly to fbp from *N. gonorrhoeae* (nFBp) as a possible basis for the design of novel metalantibiotics.

transferrin<sup>9</sup>. They have a high affinity for oxygen ligands — for example, hydroxide, oxide, phosphate and phenolate — and can be found along with Fe<sup>3+</sup> in the same geological minerals<sup>10</sup>. Ti<sup>3+</sup> has antibacterial properties<sup>11</sup> and binds strongly to human transferrin<sup>12</sup>. There is interest in the binding of Hf<sup>4+</sup> to transferrin because of its chemical similarity to Pu<sup>4+</sup>: injected Hf<sup>4+</sup> is almost totally bound to transferrin in animal serum<sup>13</sup>.

The molar ratio of protein:ferric phosphate (P) in isolated recombinant holo-nFBp overexpressed in the *Escherichia coli* periplasm is 1:1:1 (Table 1). Addition of an equimolar amount of Hf<sup>4+</sup> (as the mononuclear complex [Hf(NTA)<sub>3</sub>]<sup>2-</sup>) to holo-nFBp led to displacement of 47% of the bound Fe (monitored by the intensity decrease of the tyrosinate-to-Fe<sup>3+</sup> charge-transfer band at 493 nm in 100 mM NaCl, 4 mM phosphate and 25 mM NaHCO<sub>3</sub>, pH 7.4, at 310 K). To fully load nFBp with Hf, apo-nFBp was reacted with a 50-fold molar excess of the mononuclear chelated Hf<sup>4+</sup> complex. Unexpectedly, the Hf-nFBp product contained 4.0 Hf and 1.4 P per mol protein (Table 1). The presence of bound phosphate was confirmed by <sup>31</sup>P-NMR spectroscopy (new peaks shifted downfield from free phosphate by 2–3 p.p.m.; data not shown). Other metal ions, including Fe<sup>3+</sup> itself, yielded similar binding patterns. Treatment of apo-nFBp with excess chelated Fe<sup>3+</sup> in the presence of phosphate gave rise to 2–3 mol Fe per mol protein (Table 1). Attempts to remove the excess bound Fe<sup>3+</sup> by treatment with phosphate (FePO<sub>4</sub> is insoluble) did not restore the 1:1 Fe:P ratio (Table 1). Treatment of native mono-ferric holo-nFBp with a large excess of chelated Fe<sup>3+</sup> did not lead to additional binding of Fe, although the bound phosphate was readily removed. The pathway for multinuclear loading, therefore, does not seem to involve the mononuclear form of the protein, which is isolated from bacteria.

**Conformational heterogeneity in crystals**  
We crystallized and solved the three-dimensional structure of Hf-nFBp, containing 4.8 Hf<sup>4+</sup> per mol protein, at 1.7 Å resolution by molecular replacement (Table 2). Hemidradal twinning

**Multinuclear metal binding**  
The group four metal ions Ti<sup>3+</sup>, Zr<sup>4+</sup> and Hf<sup>4+</sup>, similar to Fe<sup>3+</sup>, are highly acidic and, therefore, expected to bind strongly to

<sup>1</sup>Institute of Cell and Molecular Biology, Michael Swann Building, University of Edinburgh, Mayfield Road, Edinburgh EH9 3JR, U.K. <sup>2</sup>School of Chemistry, University of Edinburgh, West Mains Road, Edinburgh EH9 3JJ, U.K. <sup>3</sup>Current address: Department of Molecular Biology and Biochemistry, University of California, Irvine, California 92697, USA. <sup>4</sup>Current address: School of Pharmacy, Second Military Medical University, Shanghai 200433, China.

Correspondence should be addressed to P.J.S. e-mail: P.J.Sadler@ed.ac.uk

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Format XML éditeur

# < modélisation des affiliations semi-structurées >



Article Journal Nature  
<https://api.istex.fr/ark:/67375/GT4-LHM354SF-Z/fulltext.pdf?sid=istex-api-demo>

## Format XML éditeur

## Reformatage en TEI

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Découpage de façon automatique des organismes afin de les baliser

ISO 3166-1 alpha-2 + verbalisation



### Format XML éditeur

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  <title type="short">Electron transfer to minerals</title>
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<p>Many pathogenic microorganisms require iron for virulence<ref type="bibr" rId="b5"/>. However, iron acquisition is a major problem for them in aerobic environments because aquated Fe<sup>3+</sup> ions are highly acidic and readily form hydroxide- and oxide-bridged polymers and insoluble FeO(OH) (rust) at neutral or alkaline pH<ref type="bibr" rId="b6"/>. Therefore, pathogenic Gram-negative bacteria, such as <i>Neisseria gonorrhoeae</i>, <i>Neisseria meningitidis</i> and <i>Haemophilus influenzae</i>, synthesize the iron-binding protein Fbp to capture iron presented at the outer membrane and transport it across the periplasm. Fbp, a single polypeptide chain of 309 amino acids, shows the same polypeptide topology as the two lobes of serum transferrin and lactoferrin despite a lack of significant sequence similarity<ref type="bibr" rId="b7 b8"/>. The Fe<sup>3+</sup>-binding site is in an interdomain cleft mdash; a 'Venus fly-trap' mdash; that is open in the apo protein and closed when Fe<sup>3+</sup> is bound. Fbp has been reported to bind one Fe<sup>3+</sup> strongly but reversibly<ref type="bibr" rId="b9"/>, as does each lobe of transferrin<ref type="bibr" rId="b10"/>. We sought to determine whether other metals bind strongly to Fbp from <i>N. gonorrhoeae</i> (nFbp) as a possible basis for the design of novel metalloantibiotics.</p>  
<crossid>Multinuclear metal binding</crossid>  
<p>The group four metal ions Ti<sup>4+</sup>, Zr<sup>4+</sup> and Hf<sup>4+</sup>, similar to Fe<sup>3+</sup>, are highly acidic and, therefore, expected to bind strongly to transferrin<ref type="bibr" rId="b11"/>. They have a high affinity for oxygen ligands mdash; for example, hydroxide, oxide, phosphate and phenolate mdash; and can be found along with Fe<sup>3+</sup> in the same geological minerals<ref type="bibr" rId="b12"/>. Ti<sup>4+</sup> has antibacterial properties<ref type="bibr" rId="b13"/> and binds strongly to human transferrin<ref type="bibr" rId="b14"/>. There is interest in the binding of Hf<sup>4+</sup> to transferrin because of its chemical similarity to Pu<sup>4+</sup>; injected Hf<sup>4+</sup> is almost totally bound to transferrin in animal serum<ref type="bibr" rId="b15"/>.</p>  
<p>The molar ratio of protein:Fe:phosphate (P) in isolated recombinant holo-nFbp overexpressed in the <i>Escherichia coli</i> periplasm is 1:1:1 (<table border="1"><tr><td>1</td></tr></table>). Addition of an equimolar amount of HF<sup>4+</sup> to holo-nFbp led to displacement of 47% of the bound Fe (monitored by the intensity decrease of the tyrosinate-to-Fe<sup>3+</sup> charge-transfer band at 481 nm in 100 mM NaCl, 4 mM phosphate and 25 mM NaHCO<sub>3</sub>, pH 7.4, at 310 K). To fully load nFbp with Hf, apo nFbp was reacted with a 50-fold molar excess of the mononuclear chelated HF<sup>4+</sup> complex. Unexpectedly, the Hfndash;nFbp product contained 4.0 Hf and 1.4 P per mol protein (<table border="1"><tr><td>4</td><td>1.4</td></tr></table>). The presence of bound phosphate was confirmed by <sup>31</sup>P-NMR spectroscopy (new peaks shifted downfield from free phosphate by 2ndash;3 p.p.m.; data not shown). Other metal ions, including Fe<sup>3+</sup> itself, yielded similar binding patterns. Treatment of apo nFbp with excess chelated Fe<sup>3+</sup> in the presence of phosphate gave rise to 2ndash;3 mol Fe per mol protein (<table border="1"><tr><td>2</td><td>3</td></tr></table>). Attempts to remove the excess bound Fe<sup>3+</sup> by treatment with phosphate (FePO<sub>4</sub> is insoluble) did not restore the 1:1 Fe:P ratio (<table border="1"><tr><td>1</td><td>1</td></tr></table>). Treatment of native mono-ferric holo-nFbp with a large excess of chelated Fe<sup>3+</sup> did not lead to additional binding of Fe, although the bound phosphate was readily removed. The pathway for multinuclear loading, therefore, does not

<body>  
<p>Organisms have developed sophisticated mechanisms for the uptake of Fe<sup>3+</sup> and other metal ions from the environment. Metals in mineral form are used as source of energy by geobacteria<ref type="bibr" target="#1"/>, which are critical in the control of mineral growth and phase transformations<ref type="bibr" target="#2"/>. The recognition of minerals by microbial proteins is of current interest because microbes can affect the chemistry and distribution of nearly all elements in the periodic table<ref type="bibr" target="#3 b4"/>. Little structural information is currently available about the interactions between proteins and metal clusters during the initial stages of protein-mediated mineralization and mineral acquisition by bacteria. Here we report the surprising discovery that an iron-binding protein in the transferrin superfamily can recognize a variety of metal clusters in its iron-binding cleft, a finding that has potential implications for our understanding of metal uptake mechanisms.</p>  
<p>Many pathogenic microorganisms require iron for virulence<ref type="bibr" target="#5"/>. However, iron acquisition is a major problem for them in aerobic environments because aquated Fe<sup>3+</sup> ions are highly acidic and readily form hydroxide- and oxide-bridged polymers and insoluble FeO(OH) (rust) at neutral or alkaline pH<ref type="bibr" target="#6"/>. Therefore, pathogenic Gram-negative bacteria, such as <i>Neisseria gonorrhoeae</i>, <i>Neisseria meningitidis</i> and <i>Haemophilus influenzae</i>, synthesize the iron-binding protein Fbp to capture iron presented at the outer membrane and transport it across the periplasm. Fbp, a single polypeptide chain of 309 amino acids, shows the same polypeptide topology as the two lobes of serum transferrin and lactoferrin despite a lack of significant sequence similarity<ref type="bibr" target="#7 b8"/>. The Fe<sup>3+</sup>-binding site is in an interdomain cleft mdash; a 'Venus fly-trap' mdash; that is open in the apo protein and closed when Fe<sup>3+</sup> is bound. Fbp has been reported to bind one Fe<sup>3+</sup> strongly but reversibly<ref type="bibr" target="#9"/>, as does each lobe of transferrin<ref type="bibr" target="#10"/>. We sought to determine whether other metals bind strongly to Fbp from (nFbp) as a possible basis for the design of novel metalloantibiotics.</p>  
<hi>Multinuclear metal binding</hi>  
<p>The group four metal ions Ti<sup>4+</sup>, Zr<sup>4+</sup> and Hf<sup>4+</sup>, similar to Fe<sup>3+</sup>, are highly acidic and, therefore, expected to bind strongly to transferrin<ref type="bibr" target="#11"/>. They have a high affinity for oxygen ligands mdash; for example, hydroxide, oxide, phosphate and phenolate mdash; and can be found along with Fe<sup>3+</sup> in the same geological minerals<ref type="bibr" target="#12"/>. Ti<sup>4+</sup> has antibacterial properties<ref type="bibr" target="#13"/> and binds strongly to human transferrin because of its chemical similarity to Pu<sup>4+</sup>; injected Hf<sup>4+</sup> is almost totally bound to transferrin in animal serum<ref type="bibr" target="#15"/>.</p>  
<p>The molar ratio of protein:Fe:phosphate (P) in isolated recombinant holo-nFbp overexpressed in the periplasm is 1:1:1 (<ref type="table" target="#1">Table 1</ref>). Addition of an equimolar amount of Hf<sup>4+</sup> to holo-nFbp led to displacement of 47% of the bound Fe (monitored by the intensity decrease of the tyrosinate-to-Fe<sup>3+</sup> charge-transfer band at 481 nm in 100 mM NaCl, 4 mM phosphate and 25 mM NaHCO<sub>3</sub>, pH 7.4, at 310 K). To fully load nFbp with Hf, apo nFbp was reacted with a 50-fold molar excess of the mononuclear chelated HF<sup>4+</sup> complex. Unexpectedly, the Hfndash;nFbp product contained 4.0 Hf and 1.4 P per mol protein (<ref type="table" target="#1">Table 1</ref>). The presence of bound phosphate was confirmed by <sup>31</sup>P-NMR spectroscopy (new peaks shifted downfield from free phosphate by 2ndash;3 p.p.m.; data not shown). Other metal ions, including Fe<sup>3+</sup> itself, yielded similar binding patterns. Treatment of apo nFbp with excess chelated Fe<sup>3+</sup> in the presence of phosphate gave rise to 2ndash;3 mol Fe per mol protein (<ref type="table" target="#1">Table 1</ref>). Attempts to remove the excess bound Fe<sup>3+</sup> by treatment with phosphate (FePO<sub>4</sub> is insoluble) did not restore the 1:1 Fe:P ratio (<ref type="table" target="#1">Table 1</ref>). Treatment of native mono-ferric holo-nFbp with a large excess of chelated Fe<sup>3+</sup> did not lead to additional binding of Fe, although the bound phosphate was readily removed. The pathway for multinuclear loading, therefore, does not seem to involve the mononuclear form of the protein<ref type="bibr" target="#7"/> which is isolated

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Appel Ref Tableau

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Style



# Enrichissements ISTE ou “annotations”

3





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Détection de 9 types d'entités nommées (lieux géographiques, organismes financeurs, etc.)

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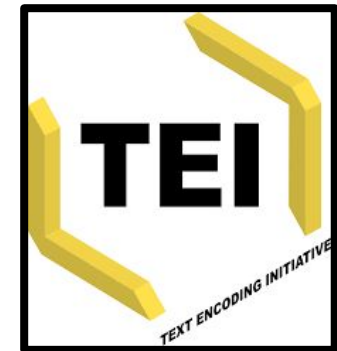


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Article Journal *Nature*

<https://api.istex.fr/ark:/67375/GT4-LHM354SF-Z/fulltext.pdf?sid=istex-api-demo>

## A novel protein–mineral interface

Transferrins transport Fe<sup>3+</sup> and other metal ions in mononuclear-binding sites. We present the first evidence that a member of the transferrin superfamily is able to recognize multi-nuclear oxo-metal clusters, small mineral fragments that are the most abundant forms of many metals in the environment. We show that the ferric...

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ark:/67375/GT4-LHM354SF-Z

Score : 9.88

Mots : 4880

Publication : 2003

Fulltext



Metadata



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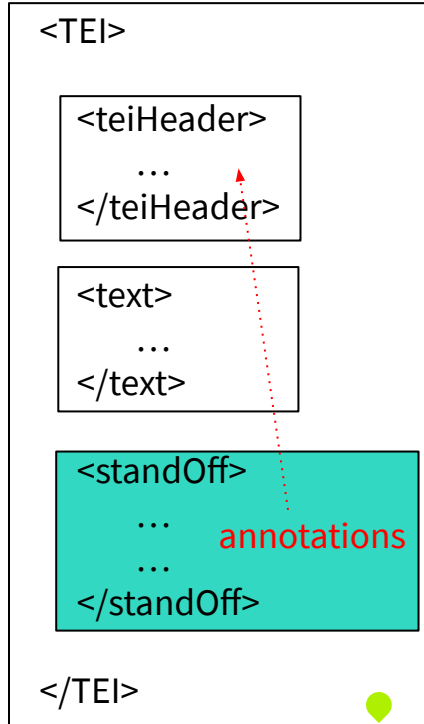
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*Revue internationale de sémiotique juridique* Vol.VI no.18 [1993]

## TROIS FIGURES D'INTERACTI

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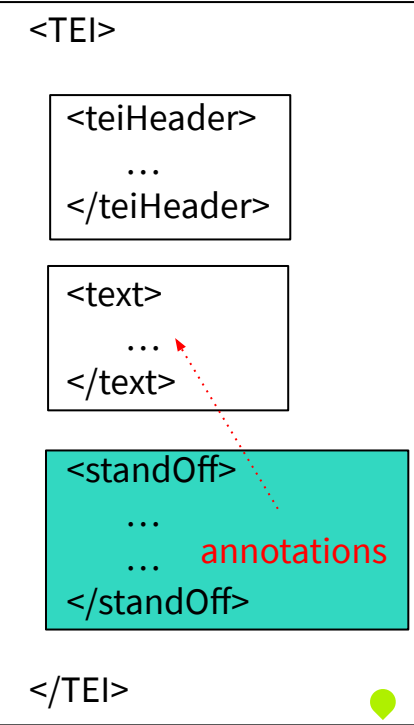
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Danièle Bourcier qui rappelle, dans sa présentation, c  
tives sont définies "comme l'étude interdisciplinaire  
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Fréquence d'apparition  
dans le texte



# Conclusion

Article Journal *Nature*

<https://api.istex.fr/ark:/67375/GT4-LHM354SF-Z/fulltext.pdf?sid=istex-api-demo>

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nature research-article

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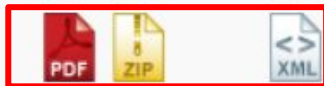
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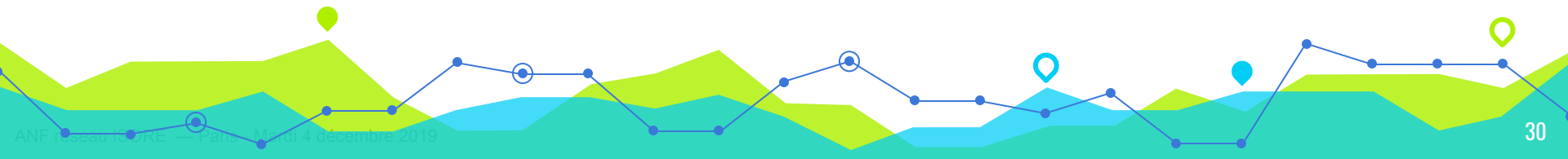
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Annexes

Enrichments



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## A novel protein–mineral interface

Transferrins transport Fe<sup>3+</sup> and other metal ions in mononuclear-binding sites. We present the first evidence that a member of the transferrin superfamily is able to recognize multi-nuclear oxo-metal clusters, small mineral fragments that are the most abundant forms of many metals in the environment. We show that the ferric...

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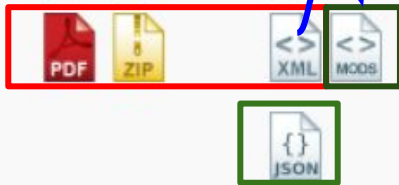
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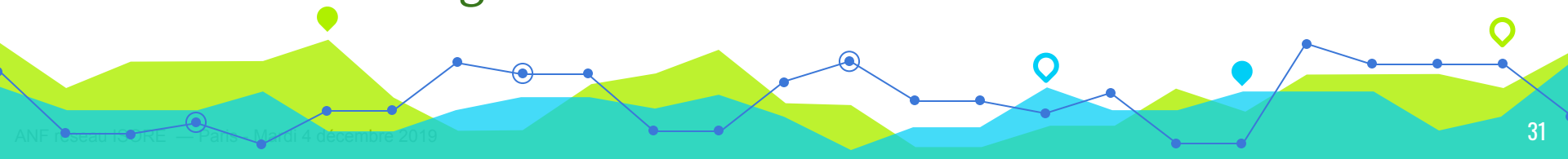
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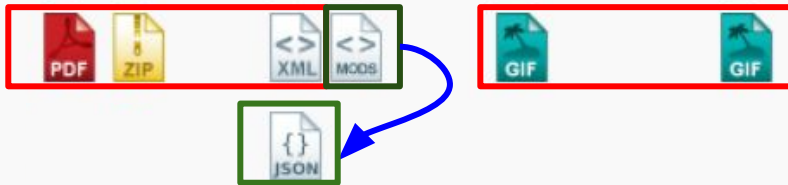
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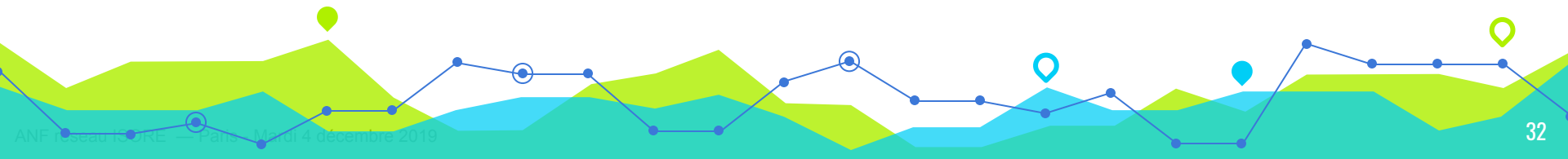
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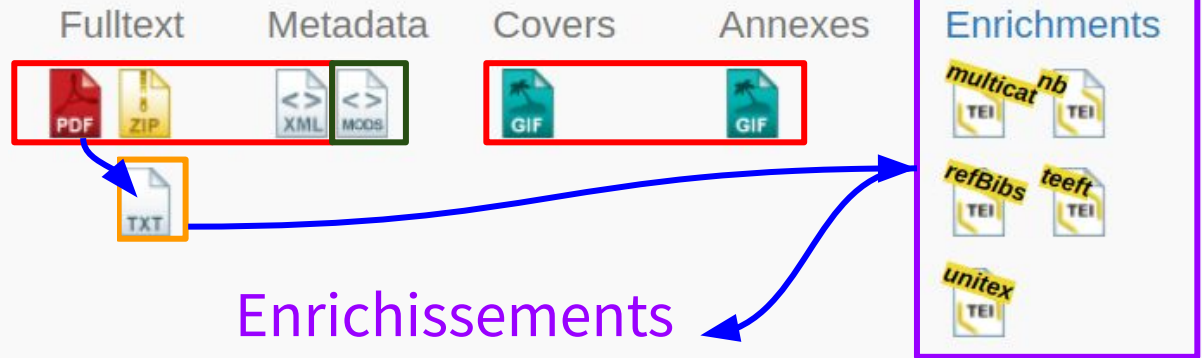
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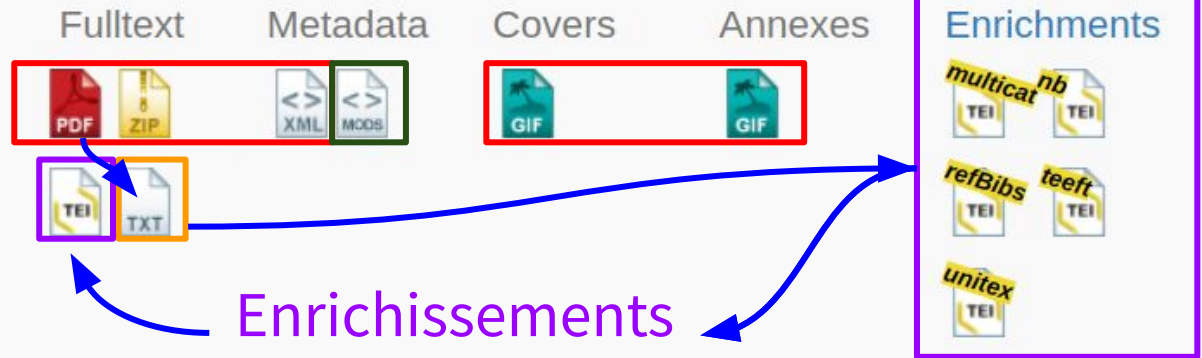
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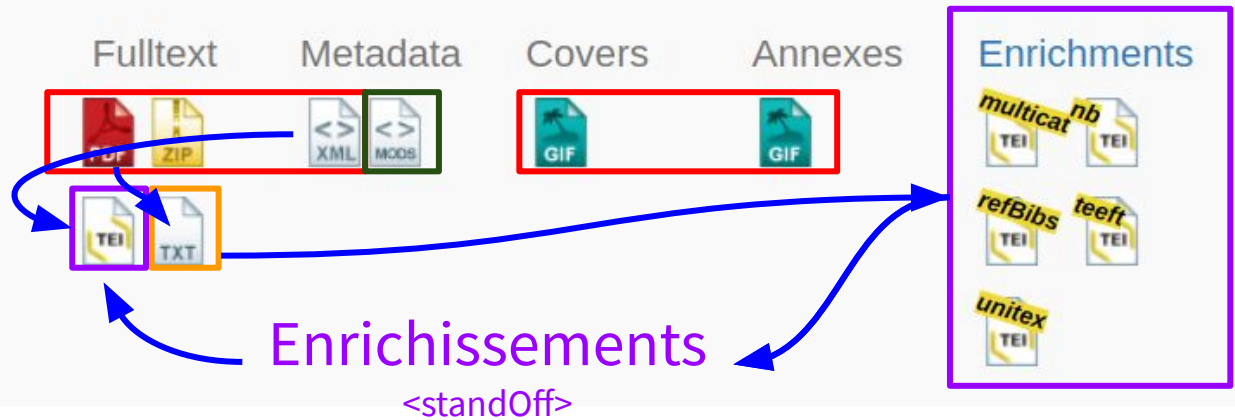
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