

Usage of InChI in SPL Substance Indexing Files

Yulia Borodina

Office of Health Informatics

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Disclaimer

The views and opinions presented here represent those of the speaker and should not be considered to represent advice or guidance on behalf of the Food and Drug Administration.

SPL Substance Indexing Files

- Not to be confused with Drug Labels
- Link drug products to ingredient substances
- One Substance Indexing File describes one substance with UNII in *fully machine-readable format*

The screenshot shows the top navigation bar of the DailyMed website. It features the 'DAILYMED' logo on the left. Below the logo are three tabs: 'ALL DRUGS', 'HUMAN DRUGS', and 'ANIMAL DRUGS'. A search bar is positioned below these tabs, containing the placeholder text 'Enter drug, NDC code, drug class, or Set ID' and a magnifying glass icon. Below the search bar are three buttons: 'ADVANCED SEARCH', 'BROWSE DRUG CLASSES', and 'LABELING ARCHIVES'. At the bottom of the search bar area, there is a paragraph of text: 'The DailyMed database contains 137159 Labeling submitted to the Food and Drug Administration (FDA) by companies. DailyMed does not contain a complete listing of labeling for FDA-regulated products (e.g., labeling that is not submitted to the FDA). See ABOUT DAILYMED for more information.' To the right of this text is a 'SHARE' button with social media icons.

The screenshot shows the 'NEWS' section of the DailyMed website. It has a sub-header 'DailyMed Announcements' and a post date of 'August 17, 2020'. The main article is titled 'Pillbox Retiring' and discusses the retirement of the Pillbox in January 2021. A 'MORE INFO' link is provided. At the bottom, there is an RSS icon and a link to 'Get RSS News & Updates'.

The screenshot shows the 'FDA RESOURCES' section of the DailyMed website. It has a sub-header 'SPL, Other Prescription Drug Labeling Resources, and Guidances'. Below this are three links: 'FDA's Structured Product Labeling Resources', 'FDA's Prescription Drug Labeling Resources', and 'FDA's Drug Guidances'. The 'FDA's Structured Product Labeling Resources' link is highlighted with a red box and a red arrow. Below this is the 'NLM SPL RESOURCES' section, which states that the following Structured Product Labeling (SPL) resources have been created to assist industry professionals. Under the 'Download Data' sub-header, there are three links: 'All Drug Labels', 'All Indexing & REMS Files', and 'All Mapping Files'. The 'All Indexing & REMS Files' link is highlighted with a red box and a red arrow.

SPL XML schema and implementation guide are here

Substance Indexing Files are here

About role of InChI

One ring to rule them all, one ring to find them,

*One ring to bring them all, and in the ~~darkness~~ ^{data}
bind them.*

after J.R.R. Tolkien

Historic notes

2011 Task to develop structured *document* format for exchanging information on substances in medicinal products. Prerequisites:

- ISO IDMP 11238 standard for substances
- Data registered in FDA Substance Registration System (SRS, later **GSRS**)
- Syntactic platform used for Structured Product Labeling (SPL)

2012 **Decision to make InChI the “must be present” characteristic for the exchange format**

2014 Substance Indexing Initiative announced. First small molecules and mixtures in SPL format published on DailyMed

2017 First modified biologics published on DailyMed

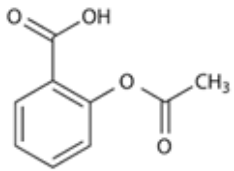
2021 First polymers published on DailyMed

About identification of medicinal substances

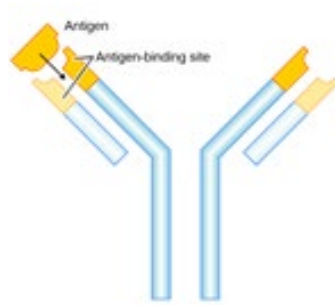
...it is easier for a camel to go through the eye of a needle...

Matthew

Chemical diversity of medicinal substances



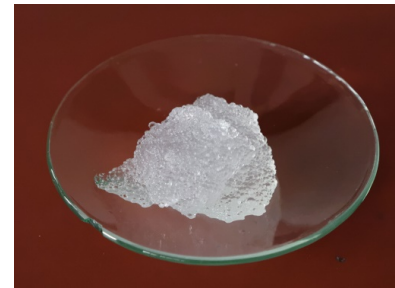
Small molecule



Antibody



DNA vector



Polymer



Botanical extract

Identification of complex (bio)chemical substance using InChI

Comprehensive approach	Complex (Bio)chemical Substance = Single InChI + other attributes
Modular approach	Complex (Bio)chemical Substance = Complex data model where InChI(s) is/are component(s)

Concerns about *comprehensive* approach

- When complexity of (bio)chemical substance increases it may become problematic to create a unique identifier by exploiting the algorithm designed for much simpler objects
- Implementation of such complex identifiers may influence the original algorithm and make backwards compatibility impossible

About modeling complex data

Everything should be made as simple as possible, but no simpler.

A. Einstein

Our data model uses *modular* approach

- **Concept of moiety:**

- Any part of a substance. Does not have to be a complete functional group. Does not have to be covalently connected to other moieties.

- **Two types of moieties:**

- Additive moiety

- contributes to a whole complex substance

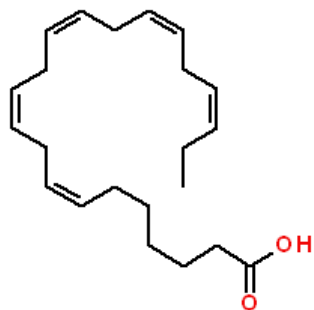
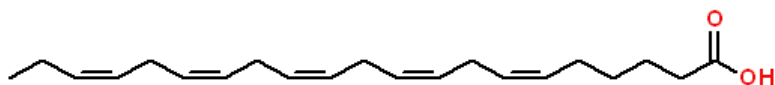
- Site of interest

- delineates features or sites of interests, such as amino acid connection points

Moiety “simple chemical”

- Is used to define a small molecule
- The structure of this moiety is represented by MOLFILE and/or SMILES
- **InChI is required for unique identification of the structure**
- Small proteins and nucleic acids (up to 999 atoms and 999 bonds) are also represented as simple chemicals

Moiety “mixture component”

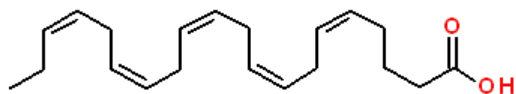


=

InChI=1S/C22H34O2/c1-2-3-4-5-6-7-8-9-10-11-12-13-14-15-16-17-18-19-20-21-22(23)24/h3-4,6-7,9-10,12-13,15-16H,2,5,8,11,14,17-21H2,1H3,(H,23,24)/b4-3-,7-6-,10-9-,13-12-,16-15-

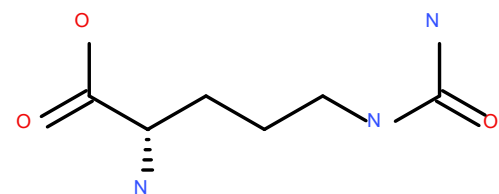
+

Amount expressed as mole fraction (f)



Molar mass of mixture: $M = \sum_{i=1}^{N \text{ of components}} (f_i M_i)$

Racemate is also a mixture

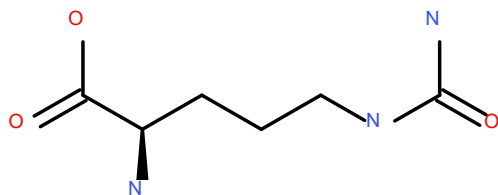


=

InChI=1S/C6H13N3O3/c7-4(5(10)11)2-1-3-9-6(8)12/h4H,1-3,7H2,(H,10,11)(H3,8,9,12)/t4-/m0/s1

+

1/2



=

InChI=1S/C6H13N3O3/c7-4(5(10)11)2-1-3-9-6(8)12/h4H,1-3,7H2,(H,10,11)(H3,8,9,12)/t4-/m1/s1

+

1/2

Molar mass calculation: $M = \frac{1}{2}M_1 + \frac{1}{2}M_2$

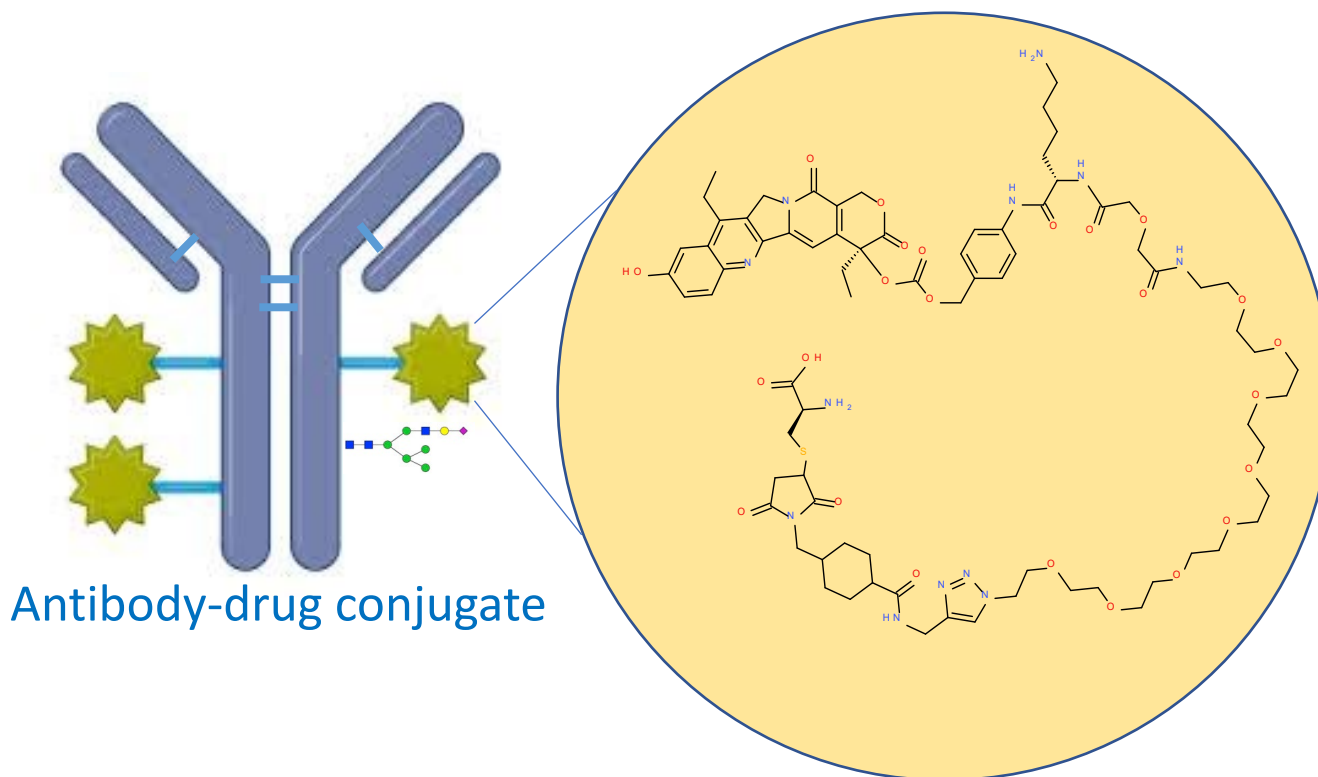
Moiety “protein subunit”

DIQMTQSPSSLSASVGDRVTITCRSSQSIVHSVGNTFLEWYQQKPG
KAPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCFQ
GSQFPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN
NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK
ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

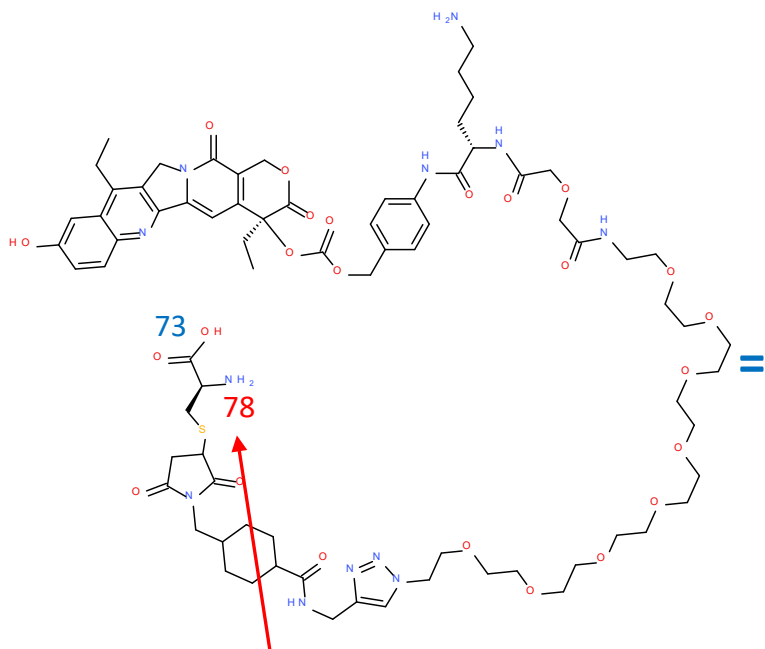
Moiety “polynucleotide”

CTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGGTCGCCCGGCCTCA
GTGAGCGAGCGAGCGCGCAGAGGAGCGCGCAGAGAGGGAGTGGCCAACCTCCATCACTAGGGGTTCTTGTAGTT
AATGATTAACCCGCCATGCTACTTATCTACGTAGCCATGCTCTAGGTACCATTGACGTCAATAATGACGTATGTTCCCAT
AGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACTTGGCAGTACATC
AAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACA
TGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTTCGAGGTGAGCCCCAC
GTTCTGCTTCACTCTCCCCATCTCCCCCCCCTCCCCACCCCAATTTTGTATTTATTTATTTTTAATTATTTTGTGCAGC
GATGGGGGGCGGGGGGGGGGGGGGGGGGGCGCGCGCCAGGCGGGGCGGGGCGGGGCGAGGGGCGGGGCGGGGC
GAGGCGGAGAGGTGCGGCGGCAGCCAATCAGAGCGGCGCGCTCCGAAAGTTTCCTTTTATGGCGAGGCGGCGGC
GGCGGCGGCCCTATAAAAAGCGAAGCGCGCGGCGGGGCGGGAGTCGCTGCGCGCTGCCTTCGCCCCGTGCCCCGC
TCCGCCGCCGCTCGCGCCGCCCGCCCCGGCTCTGACTGACCGCGTTACTCCCACAGGTGAGCGGGCGGGACGGC
CCTTCTCCTCCGGGCTGTAATTAGCGCTTGGTTTAAATGACGGCTTGTTTCTTTTCTGTGGCTGCGTGAAAGCCTTGAG
GGGCTCCGGGAGGGCCCTTTGTGCGGGGGGAGCGGCTCGGGGCTGTCCGCGGGGGGACGGCTGCCTTCGGGG
GGGACGGGGCAGGGCGGGGTTTCGGCTTCTGGCGTGTGACCGGCGGCTCTAGAGCCTCTGCTAACCATGTTTCATGC
CTTCTTCTTTTCTACAGCTCCTGGGCAACGTGCTGGTTATTGTGCTGTCTCATCATTTTGGCAAAGAATTGGATCCT
AGCTTGATATCGAATTCCTGCAGCCCCGGCGGCACCATGGCGGATACTCTCCCTTCGGAGTTTGATGTGATCGTAATAG
GGACGGGTTTGCCTGAATCCATCATTGCAGCTGCATGTTCAAGAAGTGGCCGGAGAGTTCTGCATGTTGATTCAAG
AAGCTACTATGGAGGAAACTGGGCCAGTTTTAGCTTTTTCAGGACTATTGTCTGGCTAAAGGAATACCAGGAAAAC
AGTGACATTGTAAGTGACAGTCCAGTGTGGCAAGACCAGATCCTTGAAAATGAAGAAGCCATTGCTCTTAGCAGGA
AGGACAAAACCTATTCAACATGTGGAAGTATTTTGTATGCCAGTCAGGATTTGCATGAAGATGTCGAAGAAGCTGGT
GCACTGCAGAAAAATCATGCTCTTGTGACATCTGCAAACCTCCACAGAAGCTGCAGATTCTGCCTTCTGCCTACGGA
GGATGAGTCATTAAGCACTATGAGCTGTGAAATGCTCACAGAACAACTCCAAGCAGCGATCCAGAGAATGCGCTA
GAAGTAAATGGTGTGAAGTGACAGGGGAAAAAGAAAACCATTGTGATGATAAACTTGTGTGCCATCAACTTCAG
CAGAAGACATGAGTGAAAATGTGCCTATAGCAGAAGATAACACAGAGCAACCAAAGAAAAACAGAATTACTTACTC¹⁶
ACAAATTATTAAAGAAGGCAGGAGATTTAATATTGATTTAGTATCAAAGCTGCTGTATTCTCGAGGATTACTAATTGAT

Moiety “structural modification” references a substituent defined in the same document



Definition of substituent relies on InChI *and* InChI canonical atom numbering



InChI=1S/C76H104N12O24S/c1-3-55-56-37-54(89)16-17-61(56)83-68-57(55)43-87-63(68)38-59-58(71(87)95)45-110-74(99)76(59,4-2)112-75(100)111-44-50-10-14-52(15-11-50)81-70(94)62(7-5-6-18-77)82-66(91)47-109-46-65(90)79-19-21-101-23-25-103-27-29-105-31-33-107-35-36-108-34-32-106-30-28-104-26-24-102-22-20-86-42-53(84-85-86)40-80-69(93)51-12-8-49(9-13-51)41-88-67(92)39-64(72(88)96)113-48-60(78)73(97)98/h10-11,14-17,37-38,42,49,51,60,62,64,89H,3-9,12-13,18-36,39-41,43-48,77-78H2,1-2H3,(H,79,90)(H,80,93)(H,81,94)(H,82,91)(H,97,98)/t49?,51?,60-,62-,64?,76-/m0/s1

+

InChI canonical atom numbers

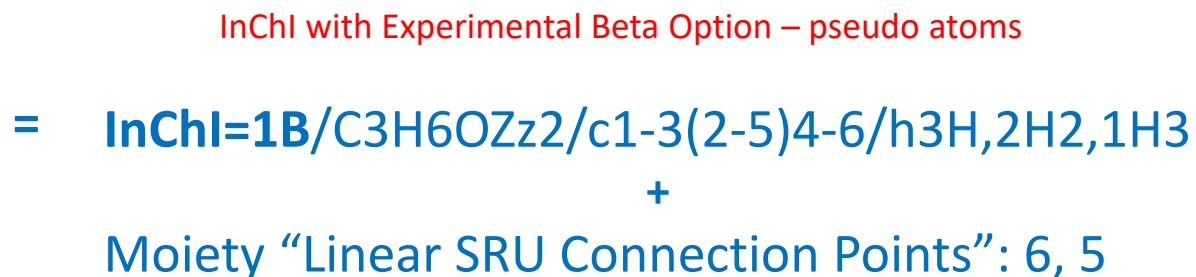
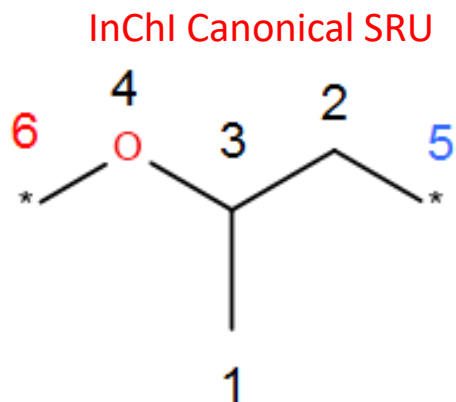


Moiety "Amino Acid Connection Points": 78, 73

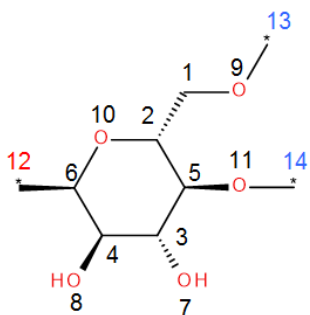
Moiety “polymer”

- Is used to define a stochastic (non-template driven) polymer
- Has one or more sub-moieties “**Structural Repeat Unit**” (SRU)
- Has amount associated with each SRU. Amount can be a range
- Does not include end groups
- End groups are moieties “structural modification”

Definition of SRU relies on InChI=1B/ (v. 1.06) and InChI canonical atom numbering



SRU can be non-linear

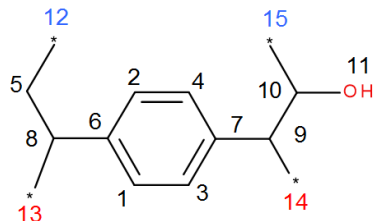


=

InChI=1B/C6H9O5Zz3/c7-3-4(8)6(12)10-2(1-9-13)5(3)11-14/h2-8H,1H2/t2-,3-,4-,5-/m1/s1

+

Moiety “Branched SRU Connection Points”: 12, 13, 14



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InChI=1B/C10H10OZz4/c11-10(15)9(14)7-3-1-6(2-4-7)8(13)5-12/h1-4,8-11H,5H2

+

Moiety “Cross-linked SRU Connection Points”: 13, 14, 12,15

Hash code

- Concatenation of InChIs and other characteristics of moieties sorted in lexicographical orders feeds into a hashing algorithm and a unique hash is computed
- MD5 hash code is currently used
- Hash is a 32 ASCII HEX character string (displayed as a GUID-like string)
- The hash code is added to each Substance Indexing File as follows

```
<code code="1bc32748-ed8-3a96-fd46-  
a5497a4683ad"codeSystem="2.16.840.1.113883.3.2705" />
```

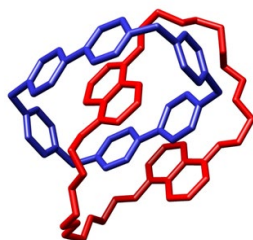
Summary

- SPL Substance Indexing File is a structured document that utilizes a modular approach in which InChI is ***not a single identifier*** of the substance but rather ***a contributor*** to a more complex data model
- All structural moieties represented by atoms and bonds are identified by their InChI
- Other structural moieties, such as protein subunits, are uniquely identified by the letter notation code
- Moieties of type “site of interest” use InChI canonical atom numbers
- All structural moieties and their modifications are uniquely identified within one document
- Linking between moieties is unambiguously defined, so that a complete molecular structure can be recreated
- Since all moieties are uniquely defined, it is possible to build independent canonical identifiers and hash codes including layered hash codes directly from the files

Improvements in InChI would be appreciated

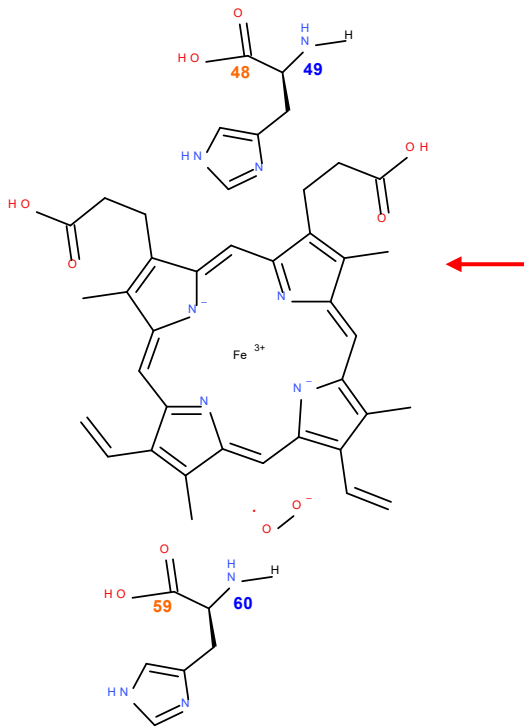
- E/Z stereochemistry of sulfoxides
- Tautomerism
- Organometallic and inorganic compounds
- Special stereo: hindered rotation, square planar, octahedral, etc.

- Topoisomerism ?



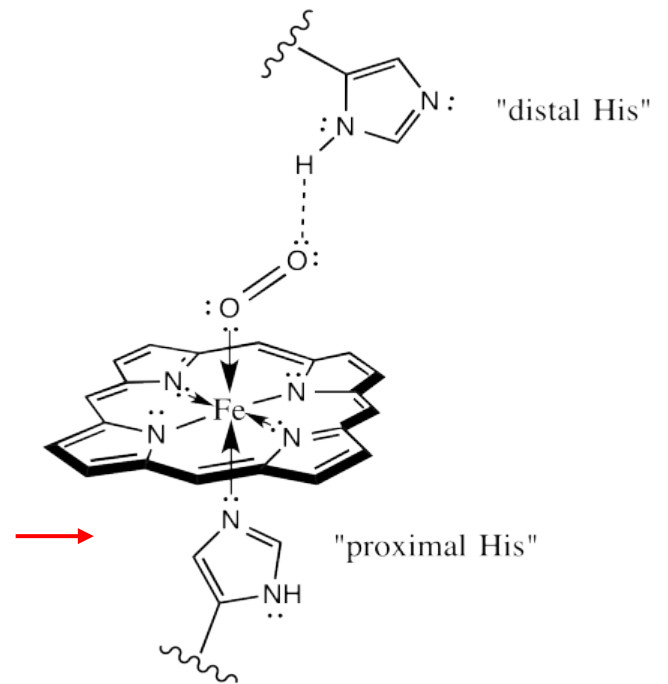
https://en.wikipedia.org/wiki/File:Catenane_Crystal_Structure_ChemComm_page634_1991_commons.png

Example organometallic compound: histidine-heme-histidine complex in Hemoglobin



Currently represented by disconnected fragments

Improvements could include coordination bond handling



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Devendra Dhaked
Laura Guasch
Wolf-Dietrich
Ihlenfeldt
Gregory Landrum
John W. Mayfield
Hitesh Patel
Igor Pletnev
Roger Sayle
Dmitrii Tchekhovskoi

InChI Working Groups

Organometallics

Colin Batchelor
Gerd Blanke
Evan Bolton
Ian Bruno
Andrei Erin
Jane Frommer
Jonathan
Goodman
Richard Hartshorn
Hinnerk Rey
Clare Tovee

Stereochemistry

Gerd Blanke
Andrey Erin
Jane Frommer
Burt Leland
Juergen Kammerer
Igor Pletnev
Clare Tovee

Questions?

Yulia.Borodina@fda.hhs.gov