

Fundamentals of Protein Structure

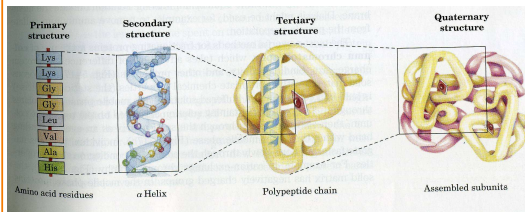
Thomas Funkhouser
Princeton University
CS597A, Fall 2007

Outline

Protein structure

- Primary
- Secondary
- Tertiary
- Quaternary

Levels of Protein Structure



Lehninger Principles of Biochemistry (3rd edition)
David L. Nelson, Michael M. Cox

Outline

Protein structure

- Primary
- Secondary
- Tertiary
- Quaternary

Primary Structure

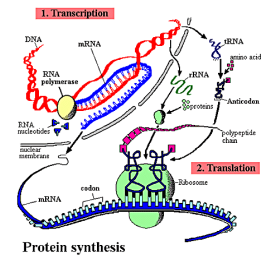
DNA

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GCAGCCCTGCTGCTTGGCCCGCTCGCTCCCGCATGGCTCCAGGAGTCTTCTGGTGGAGCACTGGAGATGAAAG  
GGAGCAGAGAGCTTGGCCAGCTGCTCCAGACCTGATGGCCCGAGCTTCTGGCCAGCAGCGAGGCTTGGGGAG  
CCCTTCAATCTACCTGATTTGGCCCGAGAGCTGATGCAAGATTTGAGCTTGCAGCAGCAAACTGTTGAAAGCTAC  
CGAAGGTCCTTACAGGAGAGATCAGCCAGCAATGATCAAAAGATTTGAGCTGCAATGGGATCTGGCCACTCAG  
AGCGAGGATTTTTGGAGATCTGATGATTTGATTTGGCAGAAAGTGGCTCATGCTCTGCTGAAGGC . [Strauss5]
```

Sequence of Nucleic Acids

Primary Structure

Transcription and translation (DNA→Protein)



<http://www.accessexcellence.org>

Primary Structure



Transcription and translation (DNA→Protein)

First Position	Second Position				Third Position
	U(T)	C	A	G	
U(T)	Phe	Ser	Tyr	Cys	U(T)
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	STOP	STOP	A
C	Leu	Pro	His	Arg	U(T)
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U(T)
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U(T)
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

Primary Structure



Transcription and translation (DNA→Protein)

Alanine	Ala	A
Cysteine	Cys	C
Aspartic Acid	Asp	D
Glutamic Acid	Glu	E
Phenylalanine	Phe	F
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Lysine	Lys	K
Leucine	Leu	L
Methionine	Met	M
Asparagine	Asn	N
Proline	Pro	P
Glutamine	Gln	Q
Arginine	Arg	R
Serine	Ser	S
Threonine	Thr	T
Valine	Val	V
Tryptophan	Trp	W
Tyrosine	Tyr	Y

Short-hand Names for Amino Acids

Primary Structure



Transcription and translation (DNA→Protein)

```
GGGGCTAAGGGGGTGGGGCTTCGCGCCGCCGCGGCTAAGAGCGCGCGCGCGCTCCGCTGCGCTTCGCGACCTTGGCTG
GGCGCCCTGCTGCTTGGCGCCCTCCGCTCCGCGAGGCTTCCTGCGGGCGCACTGGAGAGTGAACG
CGCGCAGAGAGACTTGGCGAGCTTCGCGACGCTGATGGCGCGAGCTCCGCGCAGCAGCGAGTGGTTGGCGAG
CCCTTCAATCTACCTTGATTTGGCGCGAGGCTTATGCGAAGATTTGAGGTTGCGAGCAGCAAACTGTTACAAAGTAC
CGAAGGGTCTTACAGAGAGATCAGCCGACGATGATCAAAAGATATGAGGTCGATGGTATGATCTGGCGCCACTGAG
AGCGGAGCATGTTTTGGGAGGCTGATGAGTTGATTTGGCGAAGGTTGCTCATGCTCTGCTGAGGCG...
```

Sequence of Nucleic Acids



```
APRKFYVGGNWKMGDKKSLGELIHTLNGAKLSADTEVCGAPSIYLDFA
RQKLDKIGVAAQNCYKVPKGAFTGEISPAKIDGAAWVILGHSERRHVFGE
SDELIGQKVAHALAEGLVIAICIGEKLDEREAGITEKVVFEQTKAIADNVKDW
SKVVLAYEPVVAIGTGKTATPQQAQEVHEKLRGLKSHVSDAVAQSTRI
IYGGSVTGGNCKELASQHDVDFLVGGASLKEPFDIINAKH
```

Sequence of Amino Acids

[Straus85]

Primary Structure



Transcription and translation (DNA→Protein)

```
GGGGCTAAGGGGGTGGGGCTTCGCGCCGCCGCGGCTAAGAGCGCGCGCGCGCTCCGCTGCGCTTCGCGACCTTGGCTG
GGCGCCCTGCTGCTTGGCGCCCTCCGCTCCGCGAGGCTTCCTGCGGGCGCACTGGAGAGTGAACG
CGCGCAGAGAGACTTGGCGAGCTTCGCGACGCTGATGGCGCGAGCTCCGCGCAGCAGCGAGTGGTTGGCGAG
CCCTTCAATCTACCTTGATTTGGCGCGAGGCTTATGCGAAGATTTGAGGTTGCGAGCAGCAAACTGTTACAAAGTAC
CGAAGGGTCTTACAGAGAGATCAGCCGACGATGATCAAAAGATATGAGGTCGATGGTATGATCTGGCGCCACTGAG
AGCGGAGCATGTTTTGGGAGGCTGATGAGTTGATTTGGCGAAGGTTGCTCATGCTCTGCTGAGGCG...
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Sequence of Nucleotides



```
APRKFYVGGNWKMGDKKSLGELIHTLNGAKLSADTEVCGAPSIYLDFA
RQKLDKIGVAAQNCYKVPKGAFTGEISPAKIDGAAWVILGHSERRHVFGE
SDELIGQKVAHALAEGLVIAICIGEKLDEREAGITEKVVFEQTKAIADNVKDW
SKVVLAYEPVVAIGTGKTATPQQAQEVHEKLRGLKSHVSDAVAQSTRI
IYGGSVTGGNCKELASQHDVDFLVGGASLKEPFDIINAKH
```

Sequence of Amino Acids

[Straus85]

Primary Structure



Transcription and translation (DNA→Protein)

```
GGGGCTAAGGGGGTGGGGCTTCGCGCCGCCGCGGCTAAGAGCGCGCGCGCGCTCCGCTGCGCTTCGCGACCTTGGCTG
GGCGCCCTGCTGCTTGGCGCCCTCCGCTCCGCGAGGCTTCCTGCGGGCGCACTGGAGAGTGAACG
CGCGCAGAGAGACTTGGCGAGCTTCGCGACGCTGATGGCGCGAGCTCCGCGCAGCAGCGAGTGGTTGGCGAG
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CGAAGGGTCTTACAGAGAGATCAGCCGACGATGATCAAAAGATATGAGGTCGATGGTATGATCTGGCGCCACTGAG
AGCGGAGCATGTTTTGGGAGGCTGATGAGTTGATTTGGCGAAGGTTGCTCATGCTCTGCTGAGGCG...
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Sequence of Nucleotides



```
APRKFYVGGNWKMGDKKSLGELIHTLNGAKLSADTEVCGAPSIYLDFA
RQKLDKIGVAAQNCYKVPKGAFTGEISPAKIDGAAWVILGHSERRHVFGE
SDELIGQKVAHALAEGLVIAICIGEKLDEREAGITEKVVFEQTKAIADNVKDW
SKVVLAYEPVVAIGTGKTATPQQAQEVHEKLRGLKSHVSDAVAQSTRI
IYGGSVTGGNCKELASQHDVDFLVGGASLKEPFDIINAKH
```

Sequence of Amino Acids

[Straus85]

Primary Structure



Transcription and translation (DNA→Protein)

```
GGGGCTAAGGGGGTGGGGCTTCGCGCCGCCGCGGCTAAGAGCGCGCGCGCGCTCCGCTGCGCTTCGCGACCTTGGCTG
GGCGCCCTGCTGCTTGGCGCCCTCCGCTCCGCGAGGCTTCCTGCGGGCGCACTGGAGAGTGAACG
CGCGCAGAGAGACTTGGCGAGCTTCGCGACGCTGATGGCGCGAGCTCCGCGCAGCAGCGAGTGGTTGGCGAG
CCCTTCAATCTACCTTGATTTGGCGCGAGGCTTATGCGAAGATTTGAGGTTGCGAGCAGCAAACTGTTACAAAGTAC
CGAAGGGTCTTACAGAGAGATCAGCCGACGATGATCAAAAGATATGAGGTCGATGGTATGATCTGGCGCCACTGAG
AGCGGAGCATGTTTTGGGAGGCTGATGAGTTGATTTGGCGAAGGTTGCTCATGCTCTGCTGAGGCG...
```

Sequence of Nucleotides



```
APRKFYVGGNWKMGDKKSLGELIHTLNGAKLSADTEVCGAPSIYLDFA
RQKLDKIGVAAQNCYKVPKGAFTGEISPAKIDGAAWVILGHSERRHVFGE
SDELIGQKVAHALAEGLVIAICIGEKLDEREAGITEKVVFEQTKAIADNVKDW
SKVVLAYEPVVAIGTGKTATPQQAQEVHEKLRGLKSHVSDAVAQSTRI
IYGGSVTGGNCKELASQHDVDFLVGGASLKEPFDIINAKH
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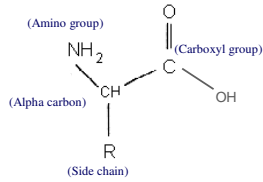
Sequence of Amino Acids

[Straus85]

Primary Structure



Amino acid:

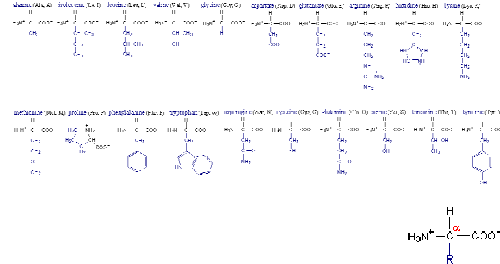


[<http://www.cryst.bbk.ac.uk>]

Primary Structure



Twenty amino acids:

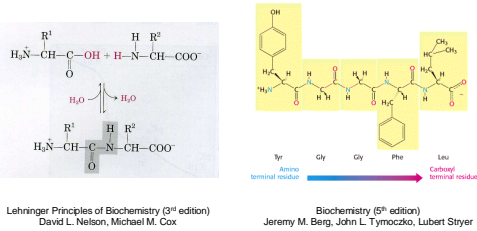


[<http://www.cryst.bbk.ac.uk>]

Primary Structure



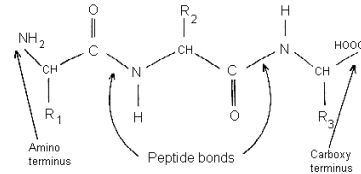
Amino acids are linked by peptide bonds



Primary Structure



Polypeptide chain:



APRKFYVGGNWKMGDKKSLGELIHLTLNGAKLSADTEVVCGAPSIYLDFA
RQKLDKIGVAAQNCYKVPKGAFTGEISPAIKDIGAAWVILGHSERRHVFGE
DELIGQKVAHALAEGLVIAICIGEKLDEREAGITEKVVFEQTKAIADNVKDW
SKVVLAYEPVVAIGTGKTATPQQAQEVHEKLRGLWLSHVSDAVAQSTRI
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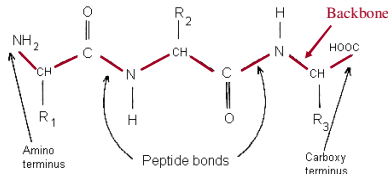
Sequence of Amino Acids

[<http://www.cryst.bbk.ac.uk>]

Primary Structure



Polypeptide chain:



APRKFYVGGNWKMGDKKSLGELIHLTLNGAKLSADTEVVCGAPSIYLDFA
RQKLDKIGVAAQNCYKVPKGAFTGEISPAIKDIGAAWVILGHSERRHVFGE
DELIGQKVAHALAEGLVIAICIGEKLDEREAGITEKVVFEQTKAIADNVKDW
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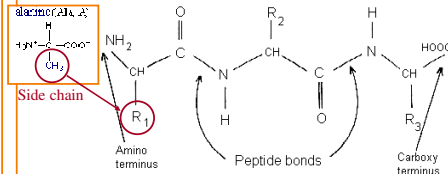
Sequence of Amino Acids

[<http://www.cryst.bbk.ac.uk>]

Primary Structure



Polypeptide chain:



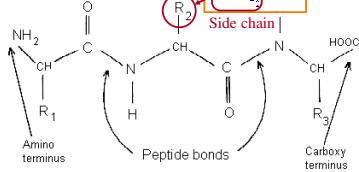
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SKVVLAYEPVVAIGTGKTATPQQAQEVHEKLRGLWLSHVSDAVAQSTRI
IYGGSVTGGNCKELASQHDVDFLGGASLKPFEVDIINAKH

Sequence of Amino Acids

[<http://www.cryst.bbk.ac.uk>]

Primary Structure

Polypeptide chain:



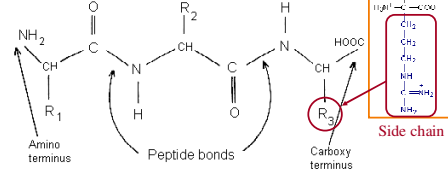
APRKFYVGGNWKMGDKKSLGELIHLNGLAKLSADTEVCGAPSIYLDFA
 SKLDAKIGVAAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGE
 DELIGQKVAHALAEGLGVIACIGEKLDEREAGITEKVVEFQTKAIADNVKDW
 SKVVLAYEPVVAIGTGKTATPQQAQEVHEKLRGWLKSHVSDAVAQSTRI
 IYGGSVTGGNCKELASQHDVDFLGGASLKPFPVDIINAKH

Sequence of Amino Acids

[\[http://www.cryst.bbk.ac.uk\]](http://www.cryst.bbk.ac.uk)

Primary Structure

Polypeptide chain:



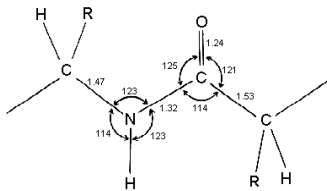
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 SKLDAKIGVAAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGE
 DELIGQKVAHALAEGLGVIACIGEKLDEREAGITEKVVEFQTKAIADNVKDW
 SKVVLAYEPVVAIGTGKTATPQQAQEVHEKLRGWLKSHVSDAVAQSTRI
 IYGGSVTGGNCKELASQHDVDFLGGASLKPFPVDIINAKH

Sequence of Amino Acids

[\[http://www.cryst.bbk.ac.uk\]](http://www.cryst.bbk.ac.uk)

Primary Structure

Peptide bond:

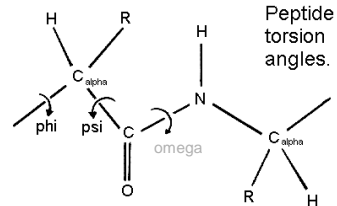


Most bond angles are constrained

[\[http://www.cryst.bbk.ac.uk\]](http://www.cryst.bbk.ac.uk)

Primary Structure

Peptide bond:

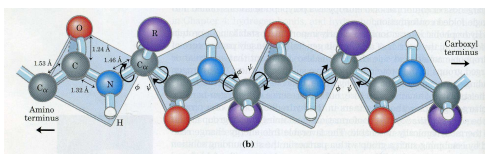


Peptides have at most two free torsion angles
 (omega is 180° (trans) or 0° (cis))

[\[http://www.cryst.bbk.ac.uk\]](http://www.cryst.bbk.ac.uk)

Primary Structure

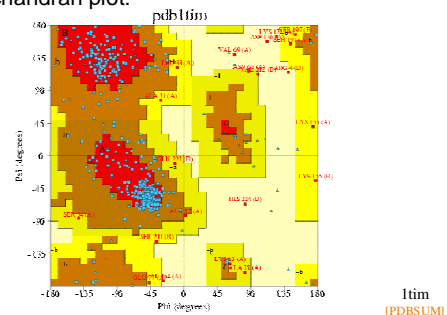
N-Cα and Cα-C bonds can rotate



Lehninger Principles of Biochemistry (3rd edition)
 David L. Nelson, Michael M. Cox

Primary Structure

Ramachandran plot:



Primary Structure



Important properties of amino acids:

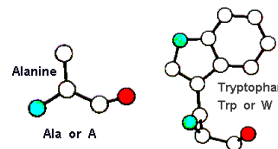
- Size
- Charge
- Polarity
- Aromaticity
- Hydrophobicity
- Conformational constraints

Primary Structure



Important properties of amino acids:

- ~~Size~~
- Charge
- Polarity
- Aromaticity
- Hydrophobicity
- Conformational constraints



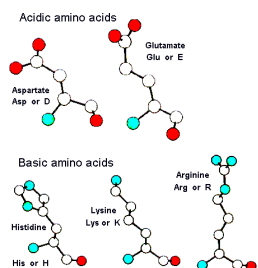
[<http://www.cryst.bbk.ac.uk>]

Primary Structure



Important properties of amino acids:

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- ~~Charge~~
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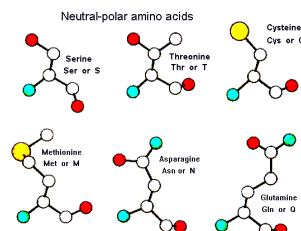
[<http://www.cryst.bbk.ac.uk>]

Primary Structure



Important properties of amino acids:

- Size
- Charge
- ~~Polarity~~
- Aromaticity
- Hydrophobicity
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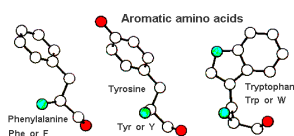
[<http://www.cryst.bbk.ac.uk>]

Primary Structure



Important properties of amino acids:

- Size
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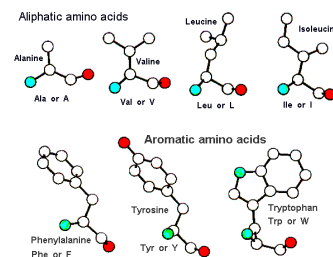
[<http://www.cryst.bbk.ac.uk>]

Primary Structure



Important properties of amino acids:

- Size
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- Polarity
- Aromaticity
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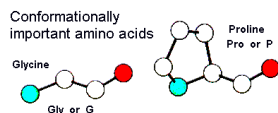
[<http://www.cryst.bbk.ac.uk>]

Primary Structure



Important properties of amino acids:

- Size
- Charge
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- Aromaticity
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- Ø Conformational constraints



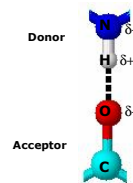
[<http://www.cryst.bbk.ac.uk>]

Structure



Forces affecting structure:

- Ø H-bonding
- Van der Waals
- Electrostatics
- Hydrophobicity
- Disulfide Bridges



H-bonds form when a hydrogen is shared by two partially negatively charged atoms

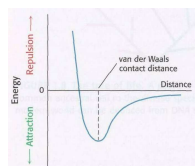
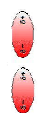
- In proteins, the participating atoms are always N/N, O/O, or N/O, usually in polar residues or backbone

Structure



Forces affecting structure:

- H-bonding
- Ø Van der Waals
- Electrostatics
- Hydrophobicity
- Disulfide Bridges



Van de Waals forces are caused by fluctuation in the positions of electrons on uncharged atoms

They are repulsive or attractive, depending on the proximity of interacting atoms

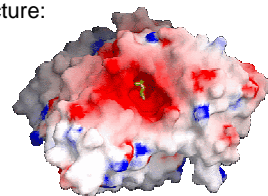
*Biochemistry, 5th Edition
Berg, Tymoczko, and Stryer*

Structure



Forces affecting structure:

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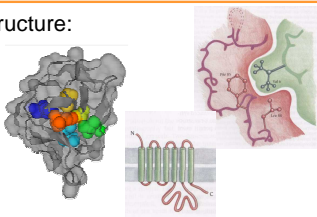
<http://honiglab.cpmc.columbia.edu/grasp/pictures.html>

Structure



Forces affecting structure:

- H-bonding
- Van der Waals
- Electrostatics
- Ø Hydrophobicity
- Disulfide Bridges



Hydrophobic (nonpolar) residues generally pack together away from polar solutions (water) ...

- e.g., in core of proteins in water, in binding sites, on the surface of proteins in membranes, etc.

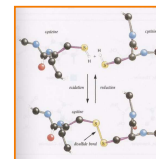
Branden and Tooze, Introduction to Protein Structure, 2nd Edition

Structure

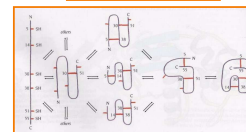


Forces affecting structure:

- H-bonding
- Van der Waals
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Cysteines can be oxidized to form covalent S-S bonds between amino acids distant in primary sequence



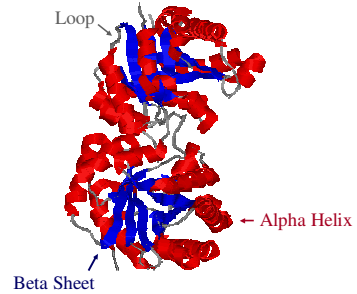
Introduction to Protein Structure, 2nd Edition, Branden and Tooze

Outline

Protein structure

- Primary
- ∅ Secondary
- Tertiary
- Quaternary

Secondary Structure

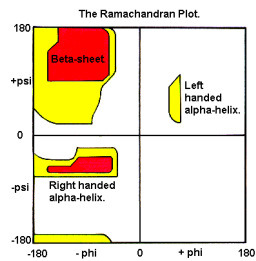


Itim
[Jena]

Secondary Structure

Some repeating sequences of torsion angles are very stable

- Alpha helix
- Beta sheet

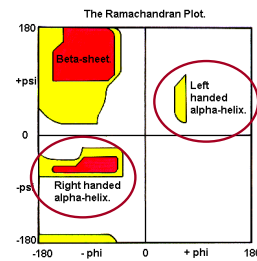


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Secondary Structure

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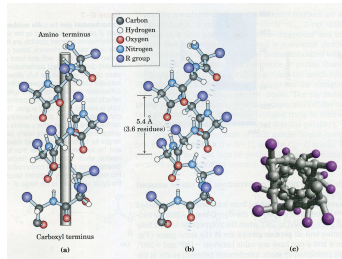


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Secondary Structure

Some repeating sequences of torsion angles are very stable

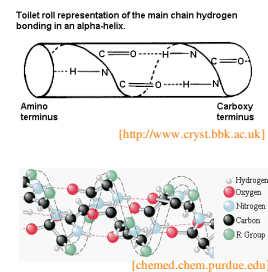
- ∅ Alpha helix
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Secondary Structure

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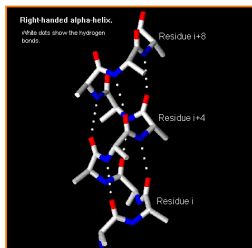


Secondary Structure



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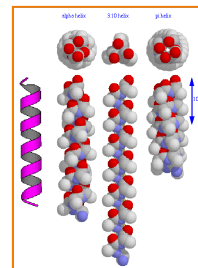
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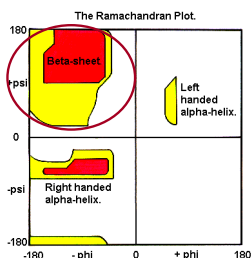
[<http://www.cryst.bbk.ac.uk>]

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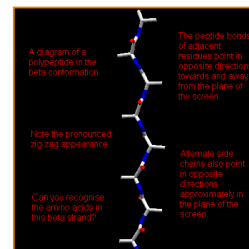
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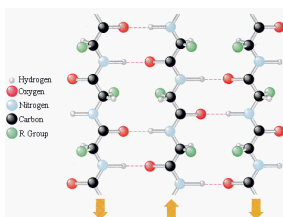
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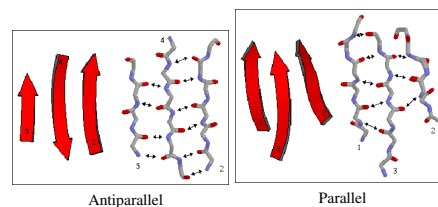
[chemed.chem.purdue.edu]

Secondary Structure



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- Alpha helix
- Beta sheet



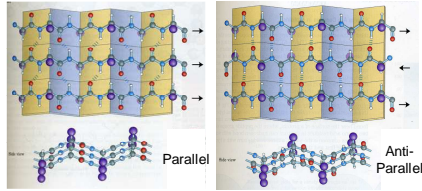
[<http://www.cryst.bbk.ac.uk>]

Secondary Structure



Some repeating sequences of torsion angles are very stable

- Alpha helix
- Beta sheet



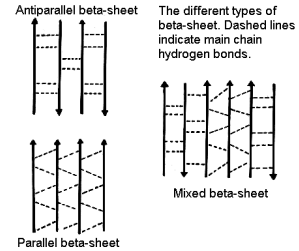
Lehninger Principles of Biochemistry (3rd edition)
David L. Nelson, Michael M. Cox

Secondary Structure



Some repeating sequences of torsion angles are very stable

- Alpha helix
- Beta sheet

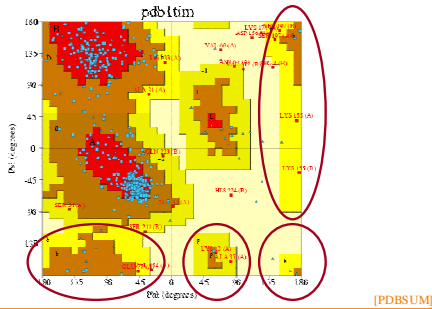


[<http://www.cryst.bbk.ac.uk>]

Secondary Structure



Others form loops, turns etc.

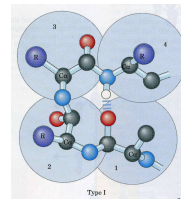


[PDBSUM]

Secondary Structure



Others form loops, turns etc.

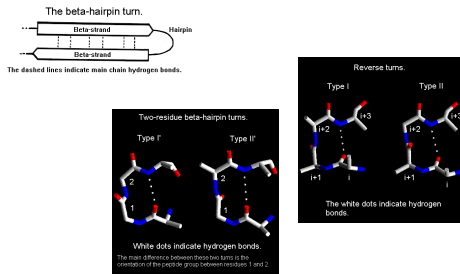


Lehninger Principles of Biochemistry (3rd edition)
David L. Nelson, Michael M. Cox

Secondary Structure

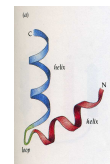


Others form loops, turns etc.

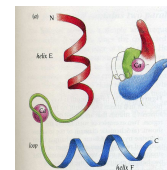


[<http://www.cryst.bbk.ac.uk>]

Supersecondary structure / motifs



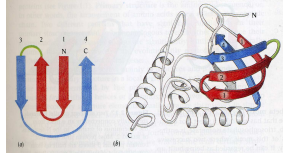
Helix – loop – helix



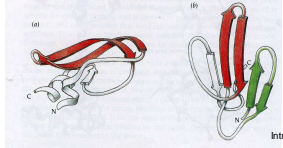
Helix – loop – helix
Calcium-binding motif

Introduction to protein structure (2nd edition)
Carl Branden, John Tooze

Supersecondary structure / motifs



Geek Key motif



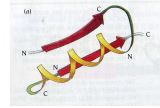
Hairpin motif

Introduction to protein structure (2nd edition)
Carl Branden, John Tooze

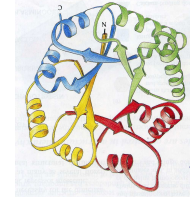
Supersecondary structure / motifs

Four classes:

- All α
- All β
- α/β
- $\alpha+\beta$



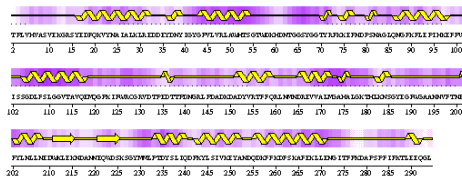
β - α - β motif



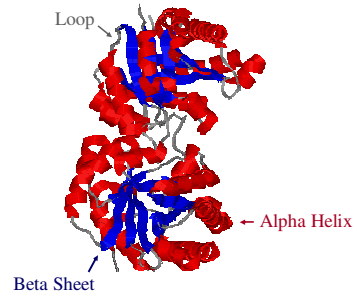
Introduction to protein structure (2nd edition)
Carl Branden, John Tooze

Secondary Structure Visualization

Secondary structure pdb2cyp



Secondary Structure Visualization



Itim
[Jena]

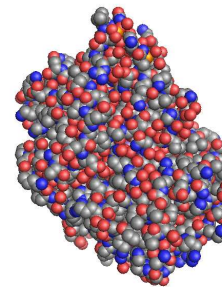
Outline

Protein structure

- Primary
- Secondary
- ◊ Tertiary
- Quaternary

Tertiary Structure

Arrangement of atoms:

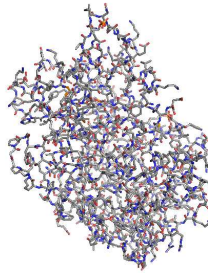


Iatp
[pymol]

Tertiary Structure



How protein folds:

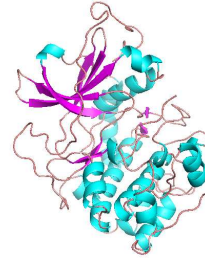


1atp
[pymol]

Tertiary Structure



How protein folds:

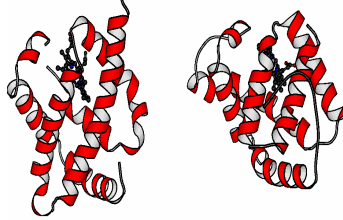


1atp
[pymol]

Tertiary Structure



Sequence → Structure → Function



The globin fold is resilient to amino acid changes. *V. stercoraria* (bacterial) hemoglobin (left) and *P. marinus* (eukaryotic) hemoglobin (right) share just 8% sequence identity, but their overall fold and function is identical.

Slide courtesy of Philip Bourne

Tertiary Structure

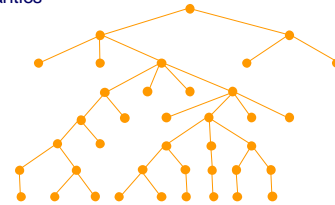


Structural classifications

- Fold similarities
- Evolutionary relationships
- Sequence similarities

Examples:

- CATH
- SCOP



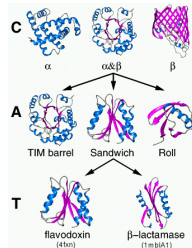
Tertiary Structure



CATH hierarchy:

- Class
- Architecture
- Topology
- Homology
- S35 (Family)
- S95
- S100

Structural Layout



<http://cathwww.biochem.ucl.ac.uk/> [Orengo97]



Tertiary Structure



SCOP hierarchy:

- Class
- Fold
- Superfamily
- Family
- Protein Domain
- Species
- PDB

SCOP: 1gsa

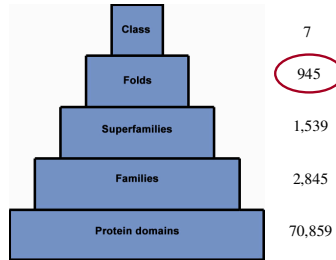
1. Root: [scop](#)
2. Class: [Alpha and beta proteins \(a/b\)](#) [51349]
3. Fold: [PreATP-grasp domain](#) [52439]
4. Superfamily: [PreATP-grasp domain](#) [52440]
5. Family: [Prokaryotic glutathione synthetase, N-terminal domain](#) [52457]
6. Protein: [Prokaryotic glutathione synthetase, N-terminal domain](#) [52458]
7. Species: [Escherichia coli](#) [52459]

<http://scop.mrc-lmb.cam.ac.uk/scop/> [Murzin95]

Tertiary Structure



SCOP hierarchy:



SCOP: Structural Classification of Proteins (1.69 release)

Outline



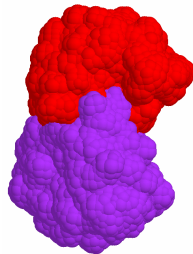
Protein structure

- Primary
- Secondary
- Tertiary
- Quaternary

Quaternary Structure



How multiple chains/proteins form a complex:

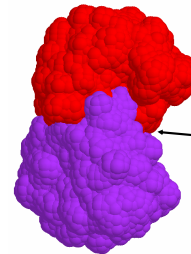


1tim
[Rasurf]

Quaternary Structure



How multiple chains/proteins form a complex:



Active binding site
may be at interface
between two chains

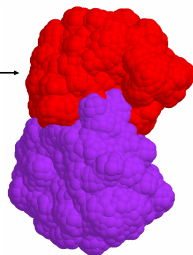
1tim
[Rasurf]

Quaternary Structure



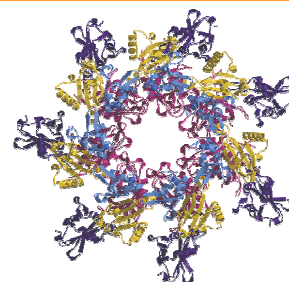
How multiple chains/proteins form a complex:

Chain may take
a new (active)
conformation
when bound
to another



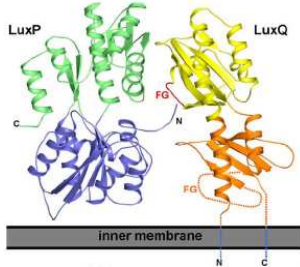
1tim
[Rasurf]

Quaternary structure



Ribbon diagram of a heptameric, 63 kDa cleavage fragment (PA63) of the protective antigen (PA) protein, produced by *Bacillus anthracis* as part of the anthrax toxin. The quaternary structure is that of a pre-pore, which later forms a channel that allows other toxins into the cytosol of the target cell, so the pathogen can cause damage to the host. [<http://www3.niaid.nih.gov/>]

Quaternary structure



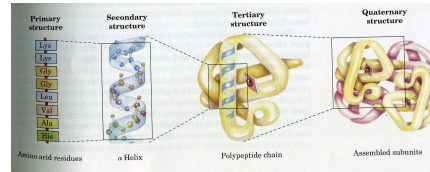
Quorum Sensing Activity in *Vibrio harveyi*
[Megan Pomianek, Chemistry, Princeton University]

Protein Structure Level Summary



Protein structure description

- Primary ← amino acid sequence
- Secondary ← local fold pattern of small subsequence
- Tertiary ← fold of entire protein chain
- Quaternary ← complex of multiple chains



Lehninger Principles of Biochemistry (3rd edition)
David L. Nelson, Michael M. Cox

Protein Structure Databases



Repositories:

- Primary ← UniProt
- Secondary ← DSSP
- Tertiary ← PDB
- Quaternary ← PQS

Chain 1 GSA:_
Compound Glutathione Synthetase
Type Protein
Molecular Weight 35547
Number of Residues 316

```

1 MKELGTWDP IANINIKEDS SPANLEAQR ROVELTYNEM GELYLINDRA
51 RAHTSTLANK QNYERFSPY GRQLGLADL DVILMRSKQD FOTEFIVATY
101 ILSEAREKOT LVNNDQSLR DNEKLEPTAM FEGLTFTSLV TNSAQLAF
151 WEKNSDILK PLDONGASL FRWKEKDPNL OVIARTLTER QTRYCNAGRY
201 LPARDGKER YLVVDGKFPV YCLARIPQDG EYHNKLAAGD RGEWPLRES
251 DMKIASQIDP TLKEREGLFV GLDNIIDRLT EINVTSPTCI REIASFPVS
301 ITDGMGAIE ARLQQQ
    
```

<http://www.uniprot.org/> [Apweiler04]

Protein Structure Databases



Repositories:

- Primary ← UniProt
- Secondary ← DSSP
- Tertiary ← PDB
- Quaternary ← PQS

Chain 1 GSA:_
Compound Glutathione Synthetase
Type Protein
Molecular Weight 35547
Number of Residues 316
Number of Alpha 9 Content of Alpha 27.22
Number of Beta 19 Content of Beta 28.16

```

1 MKELGTWDP IANINIKEDS SPANLEAQR ROVELTYNEM GELYLINDRA
   EEEE S QNITTTTH HRRHRRHH HT EEEE Q QDEKETTVE
51 RAHTSTLANK QNYERFSPY GRQLGLADL DVILMRSKQD FOTEFIVATY
   EEEEEEEE S SS EEE EEEKGGGGS EEEEE HRRHRRHH
   HRRHRRHTT EEE HRRHH HTTYGGGGG GTTTS EEE ES HRRHRRH
101 ILSEAREKOT LVNNDQSLR DNEKLEPTAM FEGLTFTSLV TNSAQLAF
   HRRHRRHTT EEE HRRHH HTTYGGGGG GTTTS EEE ES HRRHRRH
151 WEKNSDILK PLDONGASL FRWKEKDPNL OVIARTLTER QTRYCNAGRY
   HRRHSEEE SS TTT EEE TTTTH HRRHRRHTT TTS EEEEE
201 LPARDGKER YLVVDGKFPV YCLARIPQDG EYHNKLAAGD RGEWPLRES
   GGGG EEE EEEETEE S EEEEE SS S GQDT EEEEE HH
251 DMKIASQIDP TLKEREGLFV GLDNIIDRLT EINVTSPTCI REIASFPVS
   HRRHRRHT HRRHTT DE EEEETTEE EEE SS H HRRHRRHS
301 ITDGMGAIE ARLQQQ
   HRRHRRHH HRT
    
```

H = helix
E = residue in isolated beta bridge
E = extended beta strand
G = 310 helix
T = hydrogen bonded turn
S = bend

[Kabsch83]

Protein Structure Databases



Repositories:

- Primary ← UniProt
- Secondary ← DSSP
- Tertiary ← PDB
- Quaternary ← PQS



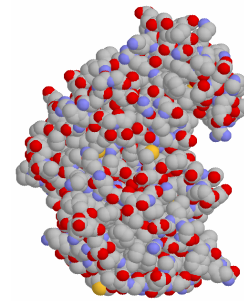
[Kabsch83]

Protein Structure Databases



Repositories:

- Primary ← UniProt
- Secondary ← DSSP
- Tertiary ← PDB
- Quaternary ← PQS



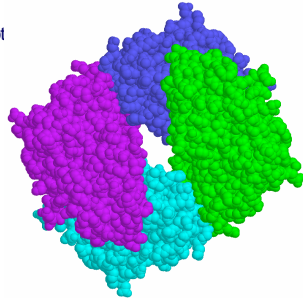
<http://www.rcsb.org/pdb/> [Berman00]

Protein Structure Databases



Repositories:

- Primary ← UniProt
- Secondary ← DSSP
- Tertiary ← PDB
- Quaternary ← PQS



<http://pqs.ebi.ac.uk/> [Hendrick98]

Summary

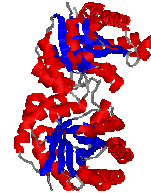


Protein structure description

- Primary ← amino acid sequence
- Secondary ← local fold pattern of small subsequence
- Tertiary ← fold of entire protein chain
- Quaternary ← complex of multiple chains

Protein folding/binding

- Disulfide linkages
- Hydrogen bonding
- Electrostatic interactions
- Hydrophobic interactions
- Van der Waals forces



Itim
[Lena]

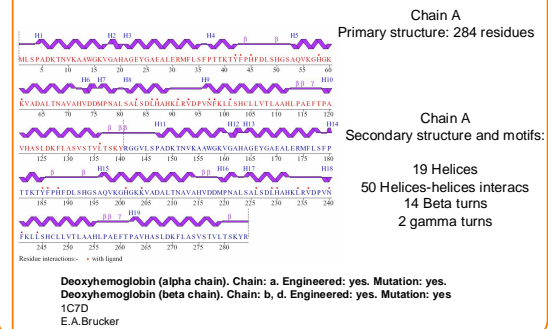
References



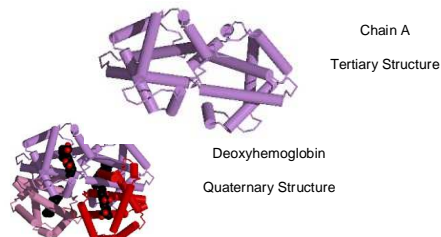
Information and figures were taken from:

- *Introduction to protein structure* (2nd edition)
Carl Branden, John Tooze
- *Lehninger Principles of Biochemistry* (3rd edition)
David L. Nelson, Michael M. Cox
- *Biochemistry* (5th edition)
Jeremy M. Berg, John L. Tymoczko, Lubert Stryer
- <http://www.cs.cryst.bbk.ac.uk>
- <http://www.access Excellence.org>
- <http://chemmed.chem.purdue.edu>

Example: Hemoglobin



Example: Hemoglobin



Deoxyhemoglobin (alpha chain). Chain: a. Engineered: yes. Mutation: yes.
Deoxyhemoglobin (beta chain). Chain: b, d. Engineered: yes. Mutation: yes
1C7D
E.A.Brucker

Example: Hemoglobin



Deoxyhemoglobin (alpha chain). Chain: a. Engineered: yes. Mutation: yes.
Deoxyhemoglobin (beta chain). Chain: b, d. Engineered: yes. Mutation: yes
1C7D
E.A.Brucker