

### Proteins

- Most structurally & functionally diverse group of biomolecules
- Functions:
  - involved in almost everything
    - enzymes
    - structure (keratin, collagen)
    - carriers & transport (membrane channels)
    - receptors & binding (defense)
    - contraction (actin & myosin)
    - signaling (hormones)

### Proteins

- Structure:
  - monomer = amino acids
    - 20 different amino acids
  - polymer = polypeptide
    - protein can be 1 or more polypeptide chains folded & bonded together
    - large & complex molecules
    - complex 3-D shape

### Amino acids

- Structure:
  - central carbon
  - amino group
  - carboxyl group (acid)
  - R group (side chain)
    - variable group
    - confers unique chemical properties of the amino acid

### Nonpolar amino acids

- nonpolar & hydrophobic side chains

Glycine (Gly)	Alanine (Ala)	Valine (Val)	Leucine (Leu)	Isoleucine (Ile)
Methionine (Met)	Phenylalanine (Phe)	Tryptophan (Trp)	Proline (Pro)	

**Why are these considered nonpolar & hydrophobic?**

### Polar amino acids

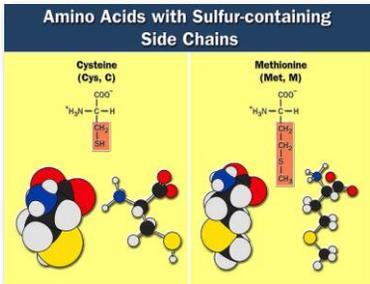
- polar or charged & hydrophilic side chains

Serine (Ser)	Threonine (Thr)	Cysteine (Cys)	Tyrosine (Tyr)	Asparagine (Asn)	Glutamine (Gln)
<b>Acidic</b>			<b>Basic</b>		
Aspartic acid (Asp)	Glutamic acid (Glu)	Lysine (Lys)	Arginine (Arg)	Histidine (His)	

**Why are these considered polar & hydrophilic?**

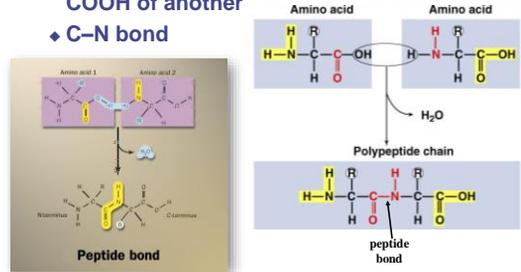
### Sulfur containing amino acids

- Disulfide bridges
  - cysteines form cross links



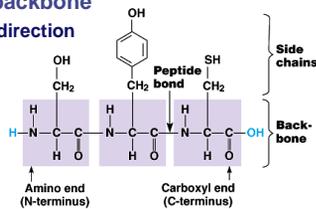
### Building proteins

- Peptide bonds: dehydration synthesis
  - linking NH<sub>2</sub> of 1 amino acid to COOH of another
  - C-N bond



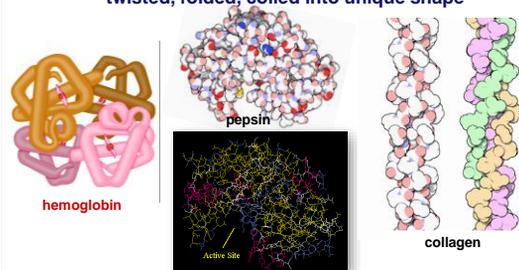
### Building proteins

- Polypeptide chains
  - N-terminal = NH<sub>2</sub> end (**BEGINNING**)
  - C-terminal = COOH end (**END**)
  - repeated sequence (N-C-C) is the polypeptide backbone
    - grow in one direction



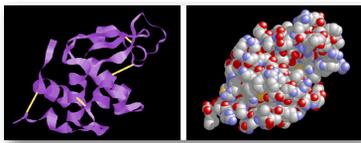
### Protein structure & function

- function depends on structure
  - 3-D structure
    - twisted, folded, coiled into unique shape

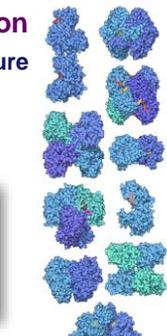


### Protein structure & function

- function depends on structure
  - all starts with the order of amino acids
    - what determines that order of amino acids?



lysozyme: enzyme in tears & mucus that kills bacteria



the 10 glycolytic enzymes used to breakdown glucose to make ATP

### Primary (1°) structure

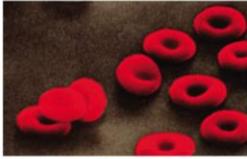
- Order of amino acids in chain
  - amino acid sequence determined by DNA
  - slight change in amino acid sequence can affect protein's structure & it's function
    - even just one amino acid change can make all the difference!

Tell 'em about the Colonie Youth in a lineup!



H<sub>2</sub>N - C<sub>1</sub> (Leu) - C<sub>2</sub> (Lys) - C<sub>3</sub> (Phe) - C<sub>4</sub> (Arg) - C<sub>5</sub> (Cys) - C<sub>6</sub> (Met) - C<sub>7</sub> (Ile) - C<sub>8</sub> (Val) - C<sub>9</sub> (Gly) - C<sub>10</sub> (Ala) - C<sub>11</sub> (Ser) - C<sub>12</sub> (Pro) - C<sub>13</sub> (Thr) - C<sub>14</sub> (Asp) - C<sub>15</sub> (Glu) - C<sub>16</sub> (Asn) - C<sub>17</sub> (Lys) - C<sub>18</sub> (Gln) - C<sub>19</sub> (Phe) - C<sub>20</sub> (Leu) - C<sub>21</sub> (Ile) - C<sub>22</sub> (Val) - C<sub>23</sub> (Met) - C<sub>24</sub> (Cys) - C<sub>25</sub> (Ser) - C<sub>26</sub> (Pro) - C<sub>27</sub> (Thr) - C<sub>28</sub> (Asp) - C<sub>29</sub> (Glu) - C<sub>30</sub> (Asn) - C<sub>31</sub> (Lys) - C<sub>32</sub> (Gln) - C<sub>33</sub> (Phe) - C<sub>34</sub> (Leu) - C<sub>35</sub> (Ile) - C<sub>36</sub> (Val) - C<sub>37</sub> (Met) - C<sub>38</sub> (Cys) - C<sub>39</sub> (Ser) - C<sub>40</sub> (Pro) - C<sub>41</sub> (Thr) - C<sub>42</sub> (Asp) - C<sub>43</sub> (Glu) - C<sub>44</sub> (Asn) - 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C<sub>132</sub> (Leu) - C<sub>133</sub> (Ile) - C<sub>134</sub> (Val) - C<sub>135</sub> (Met) - C<sub>136</sub> (Cys) - C<sub>137</sub> (Ser) - C<sub>138</sub> (Pro) - C<sub>139</sub> (Thr) - C<sub>140</sub> (Asp) - C<sub>141</sub> (Glu) - C<sub>142</sub> (Asn) - C<sub>143</sub> (Lys) - C<sub>144</sub> (Gln) - C<sub>145</sub> (Phe) - C<sub>146</sub> (Leu) - C<sub>147</sub> (Ile) - C<sub>148</sub> (Val) - C<sub>149</sub> (Met) - C<sub>150</sub> (Cys) - C<sub>151</sub> (Ser) - C<sub>152</sub> (Pro) - C<sub>153</sub> (Thr) - C<sub>154</sub> (Asp) - C<sub>155</sub> (Glu) - C<sub>156</sub> (Asn) - C<sub>157</sub> (Lys) - C<sub>158</sub> (Gln) - C<sub>159</sub> (Phe) - C<sub>160</sub> (Leu) - C<sub>161</sub> (Ile) - C<sub>162</sub> (Val) - C<sub>163</sub> (Met) - C<sub>164</sub> (Cys) - C<sub>165</sub> (Ser) - C<sub>166</sub> (Pro) - C<sub>167</sub> (Thr) - C<sub>168</sub> (Asp) - C<sub>169</sub> (Glu) - C<sub>170</sub> (Asn) - C<sub>171</sub> (Lys) - C<sub>172</sub> (Gln) - C<sub>173</sub> (Phe) - 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C<sub>468</sub> (Leu) - C<sub>469</sub> (Ile) - C<sub>470</sub> (Val) - C<sub>471</sub> (Met) - C<sub>472</sub> (Cys) - C<sub>473</sub> (Ser) - C<sub>474</sub> (Pro) - C<sub>475</sub> (Thr) - C<sub>476</sub> (Asp) - C<sub>477</sub> (Glu) - C<sub>478</sub> (Asn) - C<sub>479</sub> (Lys) - C<sub>480</sub> (Gln) - C<sub>481</sub> (Phe) - C<sub>482</sub> (Leu) - C<sub>483</sub> (Ile) - C<sub>484</sub> (Val) - C<sub>485</sub> (Met) - C<sub>486</sub> (Cys) - C<sub>487</sub> (Ser) - C<sub>488</sub> (Pro) - C<sub>489</sub> (Thr) - C<sub>490</sub> (Asp) - C<sub>491</sub> (Glu) - C<sub>492</sub> (Asn) - C<sub>493</sub> (Lys) - C<sub>494</sub> (Gln) - C<sub>495</sub> (Phe) - C<sub>496</sub> (Leu) - C<sub>497</sub> (Ile) - C<sub>498</sub> (Val) - C<sub>499</sub> (Met) - C<sub>500</sub> (Cys) - C<sub>501</sub> (Ser) - C<sub>502</sub> (Pro) - C<sub>503</sub> (Thr) - C<sub>504</sub> (Asp) - C<sub>505</sub> (Glu) - C<sub>506</sub> (Asn) - C<sub>507</sub> (Lys) - C<sub>508</sub> (Gln) - C<sub>509</sub> (Phe) - C<sub>510</sub> (Leu) - C<sub>511</sub> (Ile) - C<sub>512</sub> (Val) - C<sub>513</sub> (Met) - C<sub>514</sub> (Cys) - C<sub>515</sub> (Ser) - C<sub>516</sub> (Pro) - C<sub>517</sub> (Thr) - C<sub>518</sub> (Asp) - C<sub>519</sub> (Glu) - C<sub>520</sub> (Asn) - C<sub>521</sub> (Lys) - C<sub>522</sub> (Gln) - C<sub>523</sub> (Phe) - C<sub>524</sub> (Leu) - C<sub>525</sub> (Ile) - C<sub>526</sub> (Val) - C<sub>527</sub> (Met) - C<sub>528</sub> (Cys) - C<sub>529</sub> (Ser) - C<sub>530</sub> (Pro) - C<sub>531</sub> (Thr) - C<sub>532</sub> (Asp) - C<sub>533</sub> (Glu) - C<sub>534</sub> (Asn) - C<sub>535</sub> (Lys) - C<sub>536</sub> (Gln) - C<sub>537</sub> (Phe) - C<sub>538</sub> (Leu) - C<sub>539</sub> (Ile) - C<sub>540</sub> (Val) - C<sub>541</sub> (Met) - C<sub>542</sub> (Cys) - C<sub>543</sub> (Ser) - C<sub>544</sub> (Pro) - C<sub>545</sub> (Thr) - C<sub>546</sub> (Asp) - C<sub>547</sub> (Glu) - C<sub>548</sub> (Asn) - C<sub>549</sub> (Lys) - C<sub>550</sub> (Gln) - C<sub>551</sub> (Phe) - C<sub>552</sub> (Leu) - C<sub>553</sub> (Ile) - C<sub>554</sub> (Val) - C<sub>555</sub> (Met) - C<sub>556</sub> (Cys) - C<sub>557</sub> (Ser) - C<sub>558</sub> (Pro) - C<sub>559</sub> (Thr) - C<sub>560</sub> (Asp) - C<sub>561</sub> (Glu) - C<sub>562</sub> (Asn) - C<sub>563</sub> (Lys) - C<sub>564</sub> (Gln) - C<sub>565</sub> (Phe) - C<sub>566</sub> (Leu) - C<sub>567</sub> (Ile) - C<sub>568</sub> (Val) - C<sub>569</sub> (Met) - C<sub>570</sub> (Cys) - C<sub>571</sub> (Ser) - C<sub>572</sub> (Pro) - C<sub>573</sub> (Thr) - C<sub>574</sub> (Asp) - C<sub>575</sub> (Glu) - C<sub>576</sub> (Asn) - C<sub>577</sub> (Lys) - C<sub>578</sub> (Gln) - C<sub>579</sub> (Phe) - C<sub>580</sub> (Leu) - C<sub>581</sub> (Ile) - C<sub>582</sub> (Val) - C<sub>583</sub> (Met) - C<sub>584</sub> (Cys) - C<sub>585</sub> (Ser) - C<sub>586</sub> (Pro) - C<sub>587</sub> (Thr) - C<sub>588</sub> (Asp) - C<sub>589</sub> (Glu) - C<sub>590</sub> (Asn) - C<sub>591</sub> (Lys) - C<sub>592</sub> (Gln) - C<sub>593</sub> (Phe) - C<sub>594</sub> (Leu) - C<sub>595</sub> (Ile) - C<sub>596</sub> (Val) - C<sub>597</sub> (Met) - C<sub>598</sub> (Cys) - C<sub>599</sub> (Ser) - C<sub>600</sub> (Pro) - C<sub>601</sub> (Thr) - C<sub>602</sub> (Asp) - C<sub>603</sub> (Glu) - C<sub>604</sub> (Asn) - C<sub>605</sub> (Lys) - C<sub>606</sub> (Gln) - C<sub>607</sub> (Phe) - C<sub>608</sub> (Leu) - C<sub>609</sub> (Ile) - C<sub>610</sub> (Val) - C<sub>611</sub> (Met) - C<sub>612</sub> (Cys) - C<sub>613</sub> (Ser) - C<sub>614</sub> (Pro) - C<sub>615</sub> (Thr) - C<sub>616</sub> (Asp) - C<sub>617</sub> (Glu) - C<sub>618</sub> (Asn) - C<sub>619</sub> (Lys) - C<sub>620</sub> (Gln) - C<sub>621</sub> (Phe) - C<sub>622</sub> (Leu) - C<sub>623</sub> (Ile) - C<sub>624</sub> (Val) - C<sub>625</sub> (Met) - C<sub>626</sub> (Cys) - C<sub>627</sub> (Ser) - C<sub>628</sub> (Pro) - C<sub>629</sub> (Thr) - C<sub>630</sub> (Asp) - C<sub>631</sub> (Glu) - C<sub>632</sub> (Asn) - C<sub>633</sub> (Lys) - C<sub>634</sub> (Gln) - C<sub>635</sub> (Phe) - C<sub>636</sub> (Leu) - C<sub>637</sub> (Ile) - C<sub>638</sub> (Val) - C<sub>639</sub> (Met) - C<sub>640</sub> (Cys) - C<sub>641</sub> (Ser) - C<sub>642</sub> (Pro) - C<sub>643</sub> (Thr) - C<sub>644</sub> (Asp) - C<sub>645</sub> (Glu) - C<sub>646</sub> (Asn) - C<sub>647</sub> (Lys) - C<sub>648</sub> (Gln) - C<sub>649</sub> (Phe) - C<sub>650</sub> (Leu) - C<sub>651</sub> (Ile) - C<sub>652</sub> (Val) - C<sub>653</sub> (Met) - C<sub>654</sub> (Cys) - C<sub>655</sub> (Ser) - C<sub>656</sub> (Pro) - C<sub>657</sub> (Thr) - C<sub>658</sub> (Asp) - C<sub>659</sub> (Glu) - C<sub>660</sub> (Asn) - C<sub>661</sub> (Lys) - C<sub>662</sub> (Gln) - C<sub>663</sub> (Phe) - C<sub>664</sub> (Leu) - C<sub>665</sub> (Ile) - C<sub>666</sub> (Val) - C<sub>667</sub> (Met) - C<sub>668</sub> (Cys) - C<sub>669</sub> (Ser) - C<sub>670</sub> (Pro) - C<sub>671</sub> (Thr) - C<sub>672</sub> (Asp) - C<sub>673</sub> (Glu) - C<sub>674</sub> (Asn) - C<sub>675</sub> (Lys) - C<sub>676</sub> (Gln) - C<sub>677</sub> (Phe) - C<sub>678</sub> (Leu) - C<sub>679</sub> (Ile) - C<sub>680</sub> (Val) - C<sub>681</sub> (Met) - C<sub>682</sub> (Cys) - C<sub>683</sub> (Ser) - C<sub>684</sub> (Pro) - C<sub>685</sub> (Thr) - C<sub>686</sub> (Asp) - C<sub>687</sub> (Glu) - C<sub>688</sub> (Asn) - C<sub>689</sub> (Lys) - C<sub>690</sub> (Gln) - C<sub>691</sub> (Phe) - C<sub>692</sub> (Leu) - C<sub>693</sub> (Ile) - C<sub>694</sub> (Val) - C<sub>695</sub> (Met) - C<sub>696</sub> (Cys) - C<sub>697</sub> (Ser) - C<sub>698</sub> (Pro) - C<sub>699</sub> (Thr) - C<sub>700</sub> (Asp) - C<sub>701</sub> (Glu) - C<sub>702</sub> (Asn) - C<sub>703</sub> (Lys) - C<sub>704</sub> (Gln) - C<sub>705</sub> (Phe) - C<sub>706</sub> (Leu) - C<sub>707</sub> (Ile) - C<sub>708</sub> (Val) - C<sub>709</sub> (Met) - C<sub>710</sub> (Cys) - C<sub>711</sub> (Ser) - C<sub>712</sub> (Pro) - C<sub>713</sub> (Thr) - C<sub>714</sub> (Asp) - C<sub>715</sub> (Glu) - C<sub>716</sub> (Asn) - C<sub>717</sub> (Lys) - C<sub>718</sub> (Gln) - C<sub>719</sub> (Phe) - C<sub>720</sub> (Leu) - C<sub>7</sub>

### Primary (1°) structure: Sickle cell anemia



10 μm

Val | His | Leu | Thr | Pro | Glu | Glu | ...  
1 2 3 4 5 6 7

(a) Normal red blood cells and the primary structure of normal hemoglobin



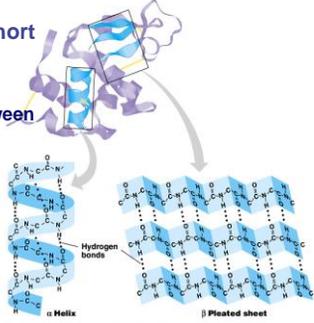
10 μm

Val | His | Leu | Thr | Pro | Val | Glu | ...  
1 2 3 4 5 6 7

(b) Sickled red blood cells and the primary structure of sickle-cell hemoglobin

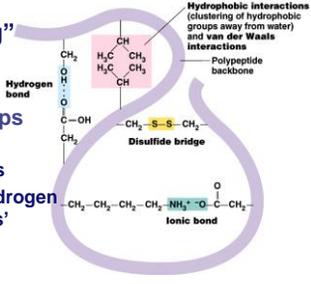
### Secondary (2°) structure

- “Local folding”
  - folding along short sections of polypeptide
    - interaction between adjacent amino acids
    - H bonds on backbone
    - α-helix
    - β-pleated sheet



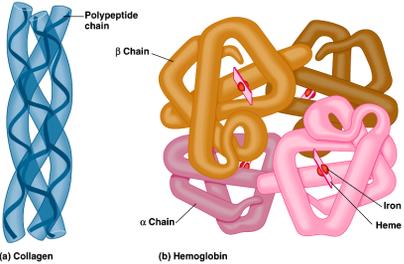
### Tertiary (3°) structure

- “Global (whole molecule) folding”
  - determined by interactions between R groups
    - anchored by disulfide bridges
    - stabilized by hydrogen and ionic ‘bonds’
    - hydrophobic interactions
      - effect of water in cell



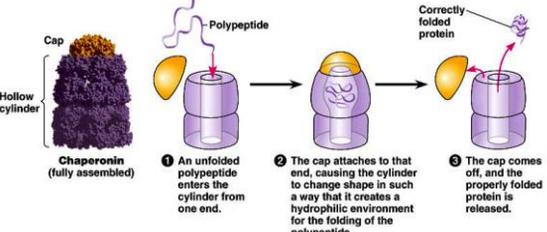
### Quaternary (4°) structure

- Joins together more than 1 polypeptide chain
  - only then is it a functional protein



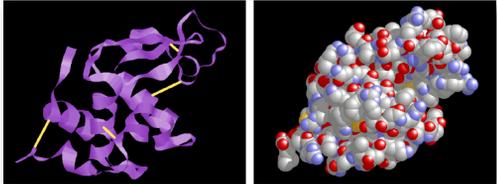
### Chaperonin proteins

- Guide protein folding
  - provide shelter for folding polypeptides
  - keep the new protein segregated from cytoplasmic influences



### Protein models

- Protein structure visualized by
  - X-ray crystallography
  - extrapolating from amino acid sequence
  - computer modelling



lysozyme

