

Amino Acids

Session Slides with Notes

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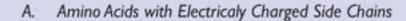


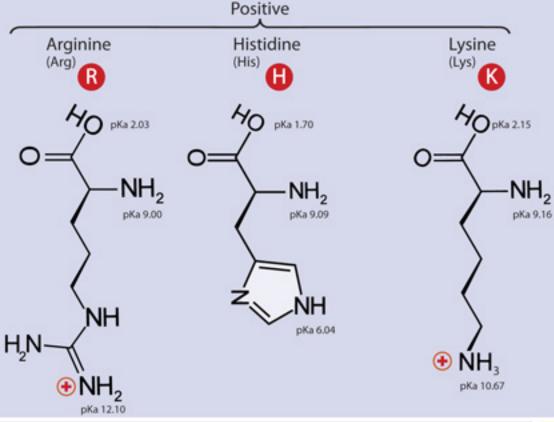
anino acids

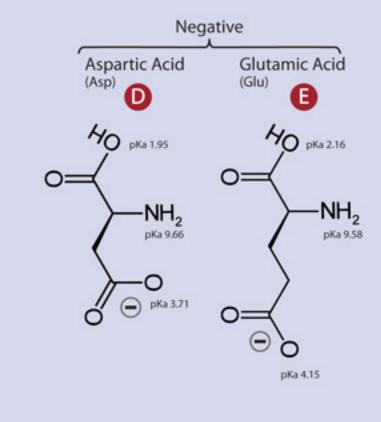
L amino acid

$$\rho H = \rho K_{a} + \log \left(\frac{[A]}{CHA} \right)$$

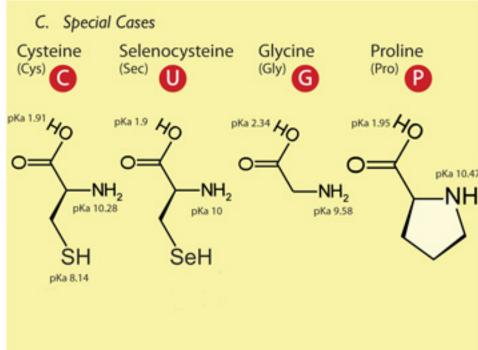
$$7 \qquad 2 + \log \left(\frac{100,000}{L} \right)$$







Amino Acids with Polar Uncharged Side Chains Serine Threonine Asparagine Glutamine (Thr) (Asn) S Q pKa 2.13 pKa 2.20 pKa 2.18 pKa 8.76 pKa 9.00 pKa 8.96 NH₂ NH₂ NH₂ NH₂ 0 OH 0: ŃH₂ NH₂



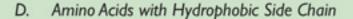
Valine

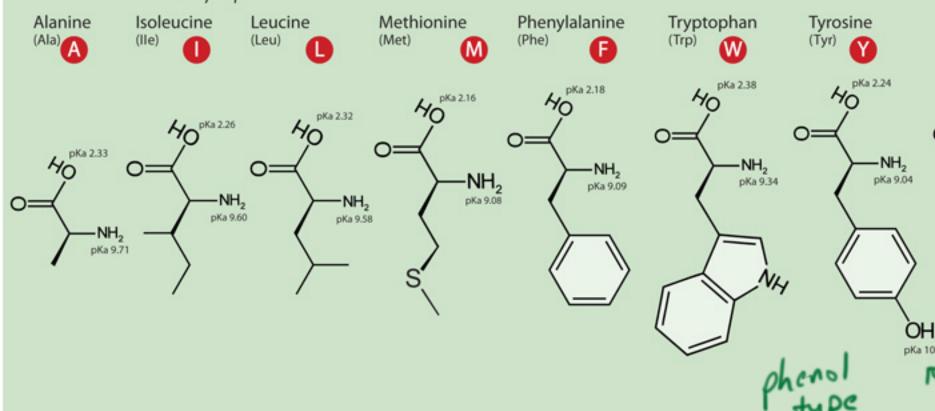
NH₂

pKa 9.52

(Val)

0:





$$H_3\overset{+}{\mathsf{N}}$$
 $CO_2\mathsf{H}$ $\xrightarrow{-\mathsf{H}^+}$ $H_3\overset{+}{\mathsf{N}}$ $CO_2^ \xrightarrow{-\mathsf{H}^+}$ $H_2\overset{-}{\mathsf{N}}$ $CO_2^ glycinium\ cation$ $glycine\ zwitterion$ $glycinate\ anion$

$$\begin{array}{c|c}
- & Gly \rightarrow & + \\
- & Gly \rightarrow & + \\
- & PH=9.5 & + \\
- & Gly & + \\
\end{array}$$

$$\frac{2.3 + 9.6}{2} = 6.2$$

Aspartate

$$COO^{-}$$
 pka 2.0

 COO^{-} pka 2.0

 COO^{-} pka 2.0

 COO^{-} pka 3.7

 COO^{-} pka 3.7

Amino Acid pKa

Asp (D) 3.9

Glu (E) 4.3

Arg (R) 12.0

Lys (K) 10.5

His (H) 6.08

Cys (C) 8.28 (-SH)

Tyr (Y) 10.1

$$H_{2}N$$
 $\alpha | A_{1}$
 $\alpha | A_{2}$
 $\alpha | A_{3}$
 $\alpha | A_{4}$
 $\alpha | A_{2}$
 $\alpha | A_{2}$
 $\alpha | A_{3}$
 $\alpha | A_{4}$
 $\alpha | A_{4}$
 $\alpha | A_{3}$
 $\alpha | A_{4}$
 $\alpha | A_{$

hydrophobic

(2)	, et al (3)	(1979)
(2)	(3)	***
	, · · ·	(4)
Cys	Gly,Leu,Ile	Cys
	Val,ala	Ile
Phe,Ile		Val
Val	Phe	Leu,Phe
Leu, Met, Trp	Cys	Met
70	Met	Ala,Gly,Trp
His	Thr,Ser	
Tyr	Trp,Tyr	His,Ser
Ala		Thr
Gly		Pro
Thr		Туг
		Asn
	Asp.Lvs.Gln	Asp
Ser		Gln,Glu
_		
any oppose		Arg
Lys	Arg	Lγs
	Val Leu, Met, Trp His Tyr Ala Gly Thr Ser Pro, Arg Asn Gln, Asp, Glu	Phe,lle Val Leu,Met,Trp Cys Met His Thr,Ser Trp,Tyr Ala Gly Thr Ser Pro,Arg Asn Gln,Asp,Glu Phe Cys Met Asp,Lys,Gln Glu,His Asp

hydnph.lk

- · like a missing book
 - · oxianion hole in serinc protease
 - · 30% of collagen
 -interior of triple
 - · backbone H bonding

- · achiral
- · important procusor
 such as with
 porphyrin
 organic
 component of
 component

- OOC - C - CH3

- OOC - C - CH3

- H alanne

- Hansoninase

- Hansoninase

- COO

- COO

- COOC - C - CH3

· prototype borned amino acid in protoms

. K293A

Lysino at 293 replaced

SCAAAAAAHHHHH

alanne spacers

for attenty reply chronehy richila

How alaine is

How alam is gluogenic · hydrophobic

$$^{+}H_{3}N - C - H$$
 ^{-}CH
 $^{-}CH_{3}C$

exaple monais.

· breaks down to successyl CoA

succesate

funarate

l
malate

oxaloacetate

It is glucogonic.

· breaks down to acetyl CoA ad acetoacetate

There's no path from actific CoA to glucose.

Leveine is ketogenic.

The level
$$COO^{-}$$
 $+H_3N-C-H$
 H_3C-C-H
 CH_2
 CH_3
 CH_3

$$^{+}H_{2}N \longrightarrow C \longrightarrow H$$
 $^{-}H_{2}C \longrightarrow CH_{2}$
 $^{-}CH_{2}$

- · Plays a big role in protein structure
- +H2N C H · locks \$ at 60° in polypephide - Todocis Configurated cutopy
 - . & helix disruptor and Bturns (cssontial poolnes bond of helix)

Hydroxyproline

- · hydroxyproline
- · profil hydroxylase requires ascorbate (vitamin c)

phosphorylation by leinase COO
(also threanine in throsms)

Kiness

H₃N — C — H

CH₂

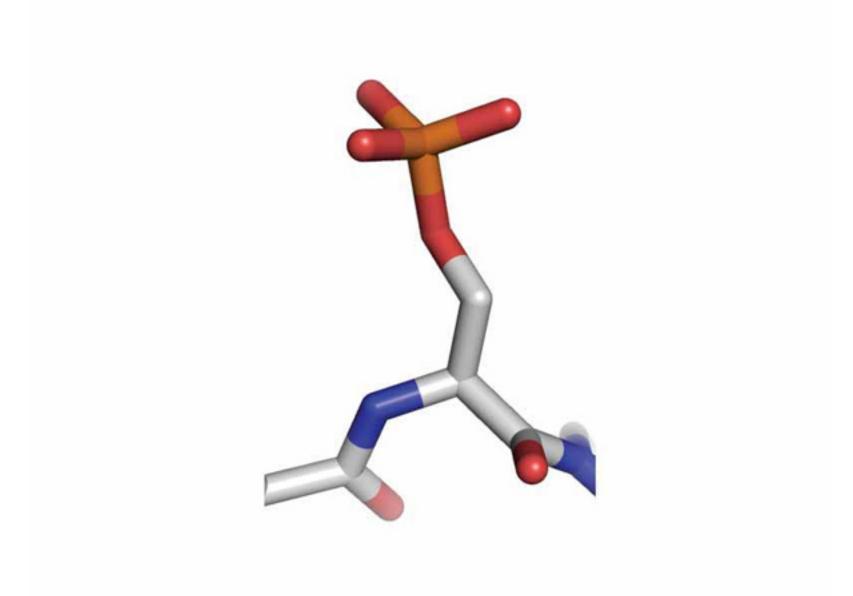
B: -0-19-0-19-A

OH

Ille SN2 across the phosphins

- · also tright of O-linked glynsylation
- phosphatidyl serine
- · Nucleophile in

Phosphorylated Scrine

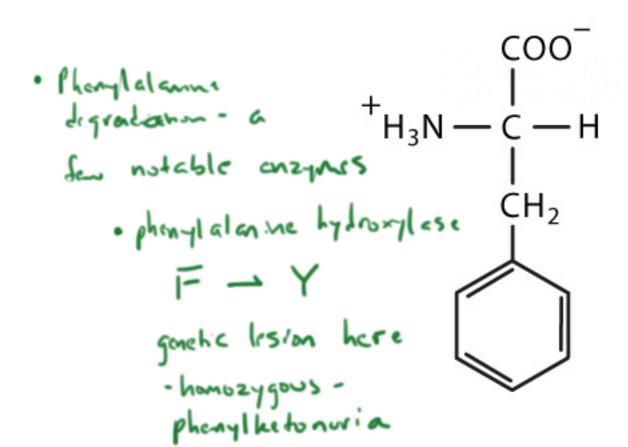


Serthe protecse such as chymotypism

RCX OHI gop

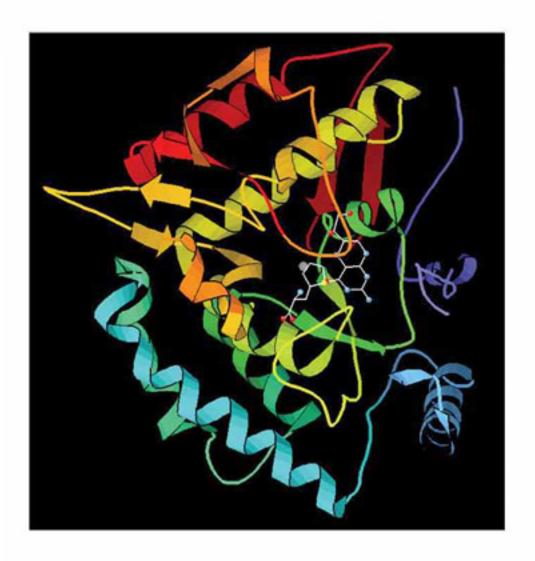
Muclesphlic Acyl Substitution

- · Target of kinase



- · Hydophobic
- · Monbrane

- · homogentisate oridose
 - lesion leads la alcaptonnia
 - Archibald Garrod one gene one orzyme



Phonylalane Hydronylase · Target of kinase

· Hrosina kinase

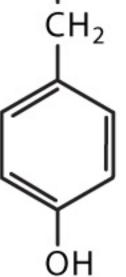
· catolyhe receptors

· growth factor receptors

- intrinsie receptor tyrosne lunese

· Cytokene recoplors

· nonvecaplor tyrosine Khase



· Hydrophobi c (a b'it of a dead occo)

· Precusor of catrcholamines chuchymu, muchquebhure dopamine

1) light booking likes to reciphor

transauto phosphary later

- Phosphorylated tyrosims some cs docking sites for signaling proteins acrivating than.

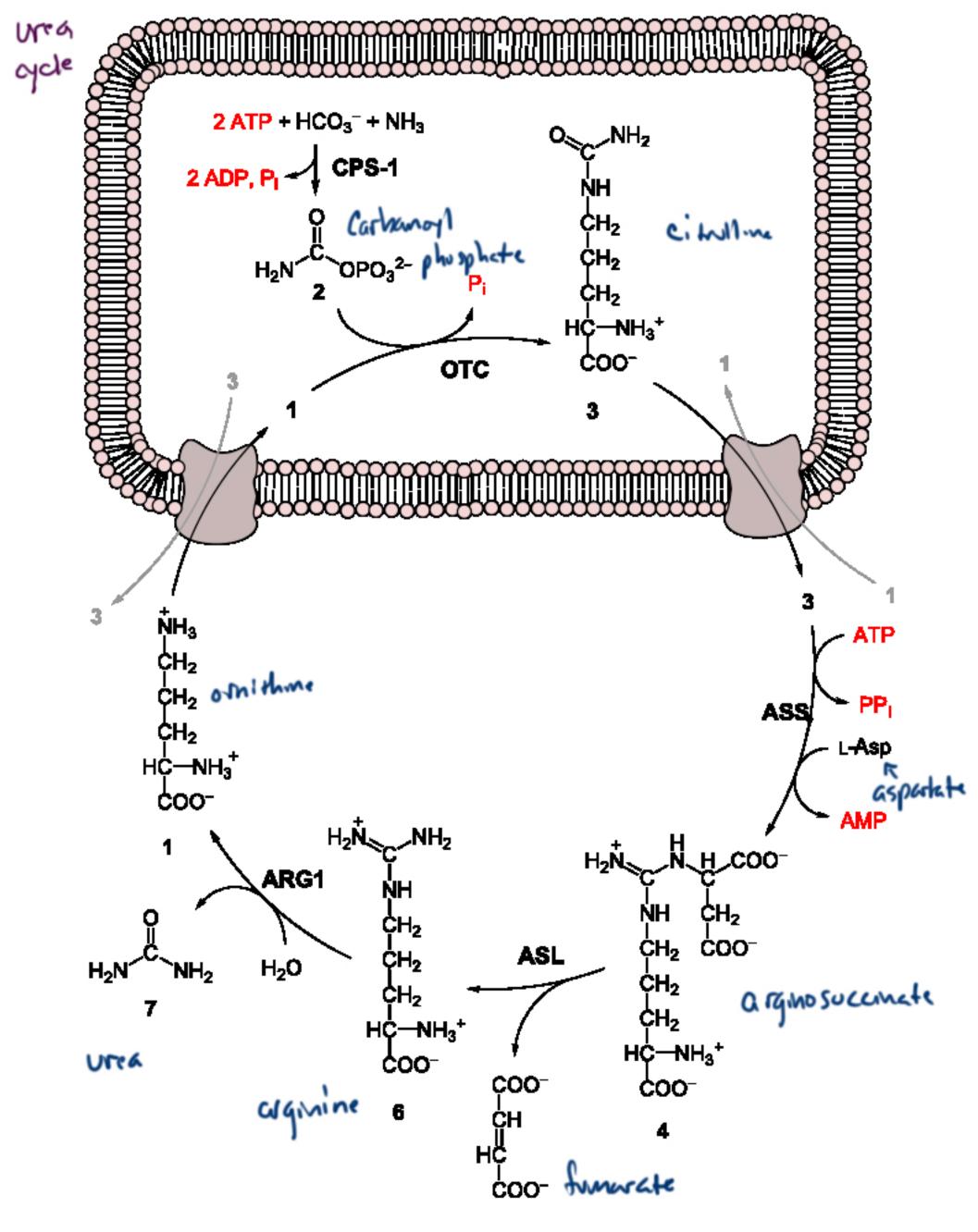
Imn. Funato · Reliable (CH_2 Ofthe Sin formers Schill bese with ÇH₂ anide linkages Imine N: Lonim (Schist base cation $\dot{N}H_3^+$ PA = pKa + log ([HA]) 10,5 + log (1000)

pyodoryl phosphate

" the amino acid chamshy

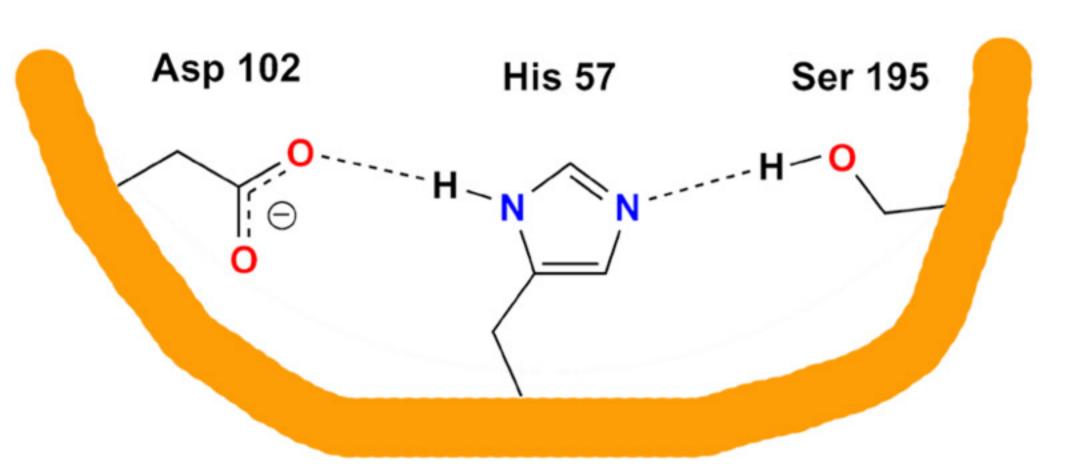
PLP-aniho acid Schia bese grandinium

H2N-C-NH2



Histdine





· Rliable 0

. and base cately st

· carbonglata nucleophile

. Just pudies

Glutamate

· rol'iable (

1 carboxyglutamate Cloths factor A COO - 1 - H3N - C - H glutanch requires vitanin K -ooc coo- 6 bidentate ligad

· H bonding - ofther

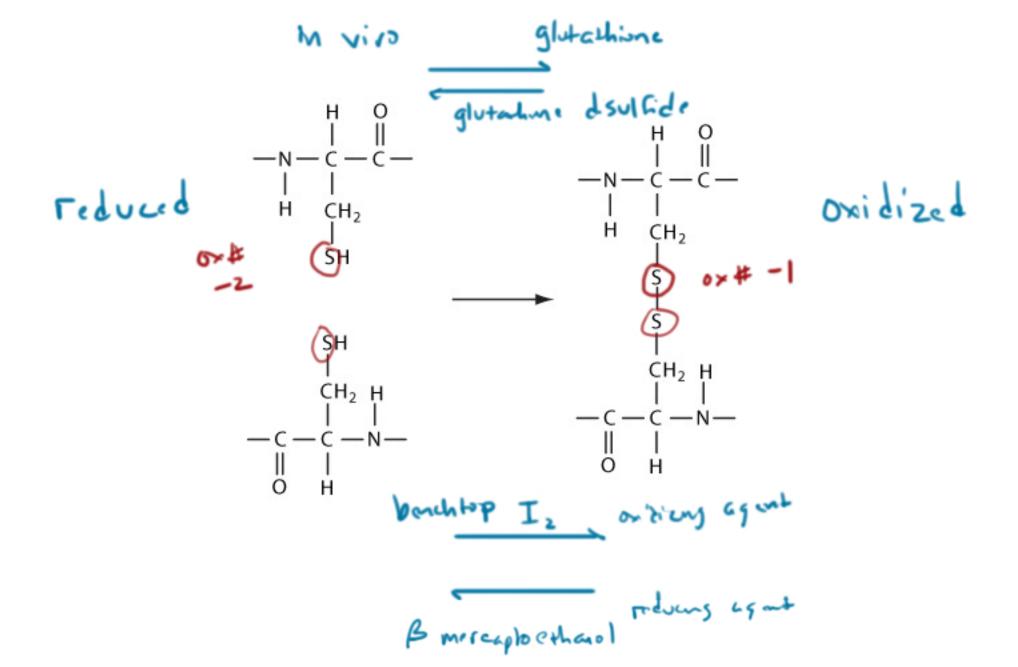
to be debone is

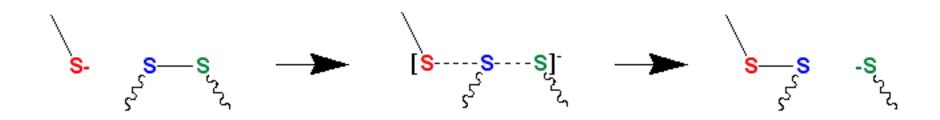
important for

poten smelve

Cysteine

- · Forms disultide bridges (covalunt)
- · Nucleophile
- · Ligad on coordnatures





Glutathione

(Riduced)

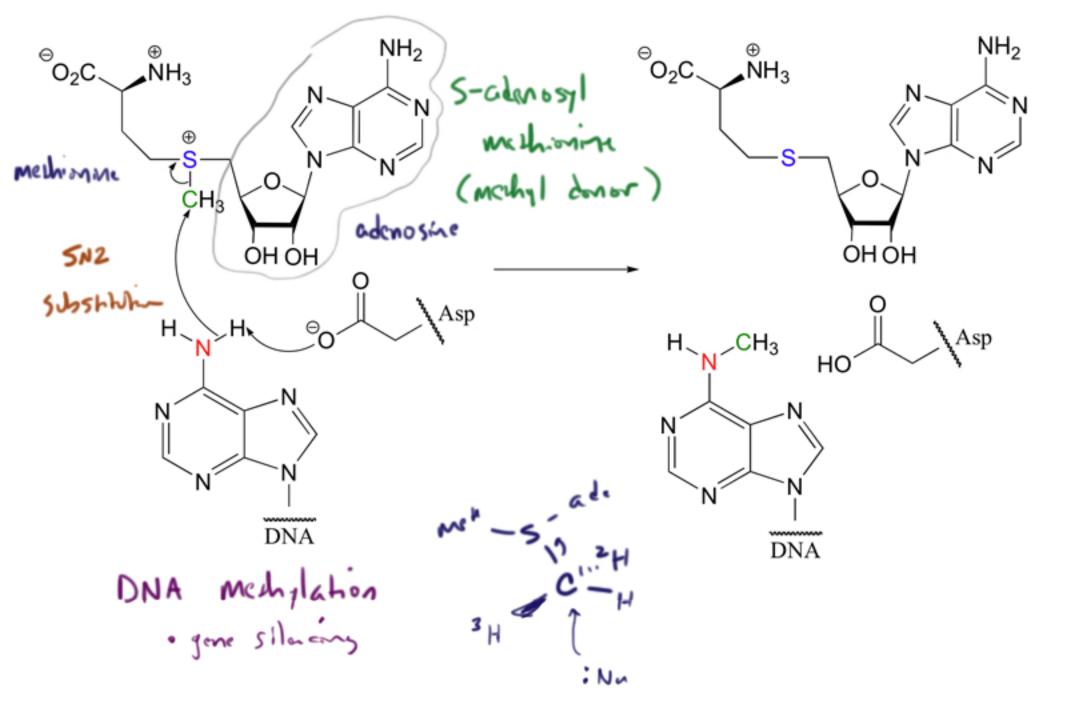
· the most important redox butter in the blood. Glutathone Disultido

(bridized)

reduced

· AUG ç00⁻ is le methionne codon ÇH₂ ĊH₂ | S | CH_3

* nonpolar · kydophobic



diethyl bromomalonate

$$K = \begin{pmatrix} A & A & A \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & \\ & & & \\$$

potassium phthalamide

$$C=0$$
 $C=0$
 $C=0$

of esta

Strecker Synthesis

$$COOH$$
 $R-C-H$
 $\frac{1.KCN, NH_4CI}{2.H^+, H_2O}$
 $\frac{1.KCN}{R}$
 $\frac{1.KCN}{R}$
 $\frac{1.KCN}{R}$
 $\frac{1.KCN}{R}$

$$= \begin{bmatrix} \overrightarrow{P} & \overrightarrow{Q} & \overrightarrow{P} & \overrightarrow{Q} & \overrightarrow{P} \\ \overrightarrow{P} & \overrightarrow{P} & \overrightarrow{P} & \overrightarrow{P} & \overrightarrow{P} \\ \overrightarrow{P} & \overrightarrow{P} & \overrightarrow{P} & \overrightarrow{P} & \overrightarrow{P} & \overrightarrow{P} & \overrightarrow{P} \\ \overrightarrow{P} & \overrightarrow{$$

$$= \begin{bmatrix} H & H & H & H \\ R - C - H & R - C - H \end{bmatrix}^{+}$$

$$= \begin{bmatrix} R & NH_{2} & R & NH_{2} \\ R - C - H & R - C - H \\ R - C - H & R - C - H \end{bmatrix}^{+}$$

$$= \begin{bmatrix} R & NH_{2} & R & NH_{2} \\ R - C - H & R - C - H \\ R - C - H & R - C - H \end{bmatrix}^{+}$$

$$= \begin{bmatrix} R & NH_{2} & R & NH_{2} \\ R - C - H & R - C - H \\ R - C - H & R - C - H \end{bmatrix}^{+}$$