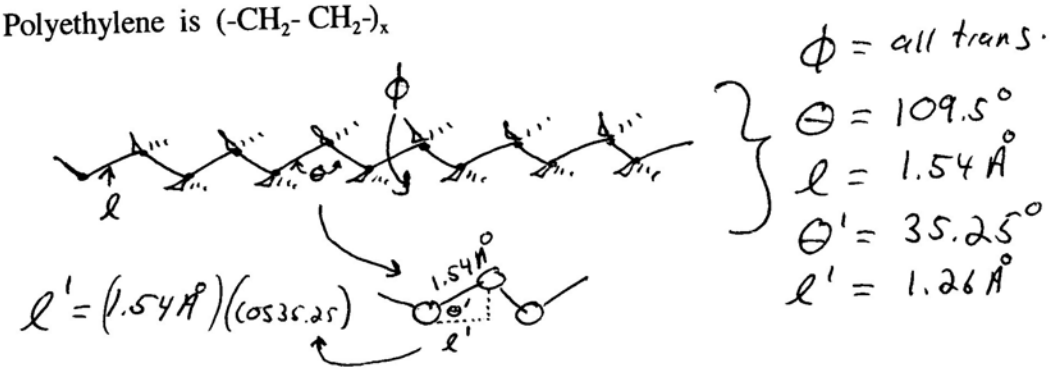
In the fully extended zig-zag chain, all carbon-carbon bonds are arranged in the trans conformation as shown below (hydrogen atoms not shown). For sp^3 hybridized carbon atoms, the bond angles are 109.5° and the length of each carbon-carbon single bond is 1.54 Å. Thus, geometry shows that each bond contributes about 1.26Å to the length of the chain.

Polyethylene is $(-CH_2- CH_2-)_x$



To calculate the length of this fully extended chain, we need to determine the number of bonds in the polymer chain.

Recall that $\overline{M}_n = \overline{Dp}_n(\overline{M}_o)$ In this case $\overline{M}_o = 28$ g/mole (structural unit molecular weight). Hence, for a $\overline{M}_n$ of 80, 000 g/mole, the degree of polymerization $(\overline{Dp}_n) = 2857$.

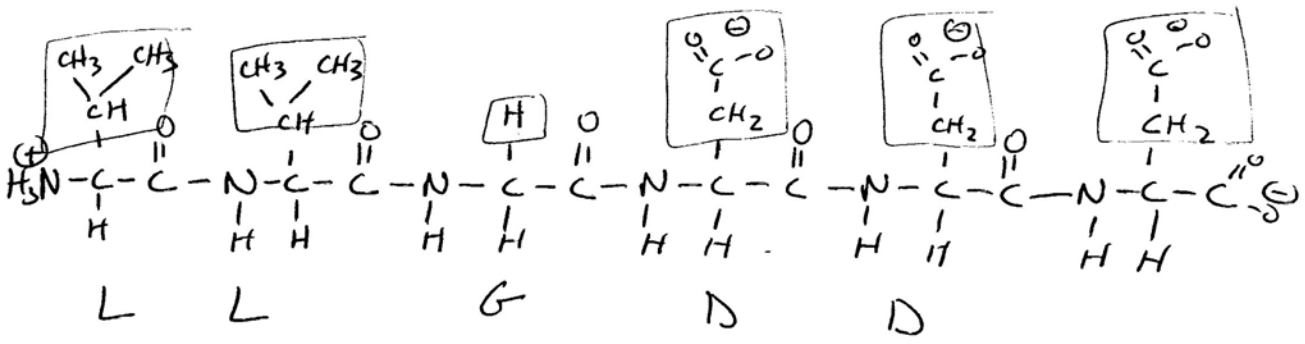
Since we have 2 bonds per structural unit (also a repeat unit in this case), the length of the fully extended chain is $= 2x\ 2857x(1.26Å) = 7199$ Å or 719.9 nm.

2) many different hexapeptide sequences will work. I would draw a peptide that is half hydrophobic, half polar charged. Acidic amino acids are very good at binding Ca^{+2} out of solution

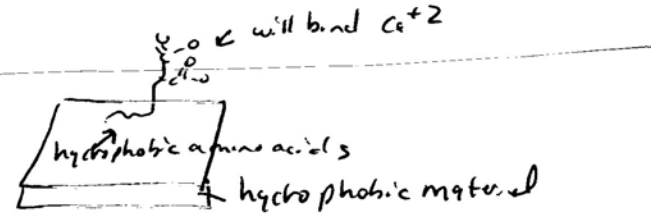
hydrophobic could be G, A, V, L, I, M, P (I probably would not use proline), F, W also ok

Charged: could be D or E; postive charge might work also to bind PO_4^{-3}. positive charge would be better. Un Natural or modified amino acids O-phosphoserine or γ carboxyglutamate would also be interesting.

I would use 3 hydrophobic with glycine at position #3 to give flexible transition between hydrophobic and charged. I would use 3 asparatic acid groups. Not sure if 1 or 3 is best. I would start with 3, see how it works, then maybe try 2

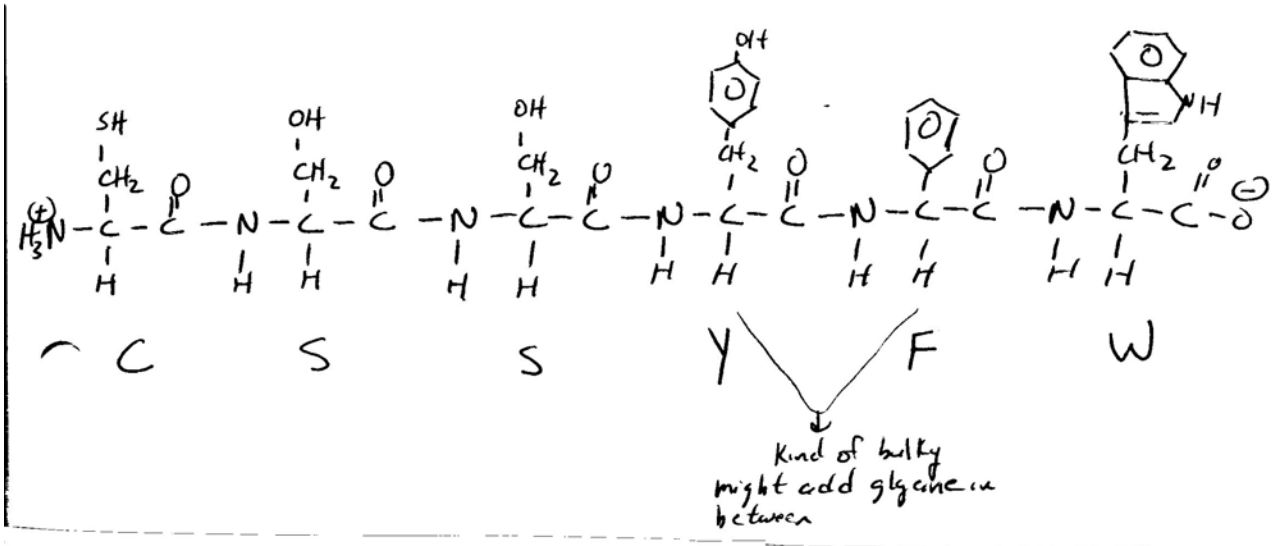


here is an example,



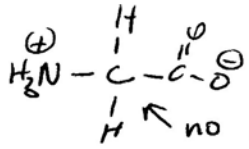
3) If I was going to do this for real I would use directed peptide evolution. But for this homework I would use a hydrophobic ring amino acid with a Cysteine on one end. The built in way I was thinking about would be following the UV absorbance spectra of the aromatic side chains of (T, W or F), between 100-400nm. There could be other ways as well.

Because I know the drug is a small organic ring, I am going to have my peptide with both F and W, not sure which would be best, so try both. I will also add tyrosine because it is also a ring but has OH group which might increase solubility of my peptide in water. I am going to use water as my solvent so I am going to add some polar hydrogen bonders to increase solubility. I am also going to use only 1 cysteine, so 2 cysteines don't bind together (SH) to form a disulfide bond.

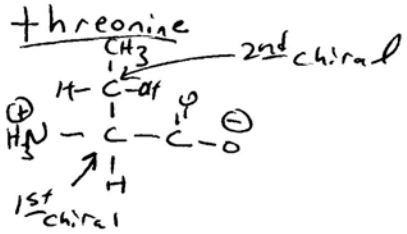


4) I would use pH as my environmental control. Aspartic acid, glutamic acid, Histidine & cysteine are all good metal binders. All have pKR that can be titrated. I would use cysteine & histidine, but you could use any. Aspartic acid & glutamic acid would be reversible at low pH.

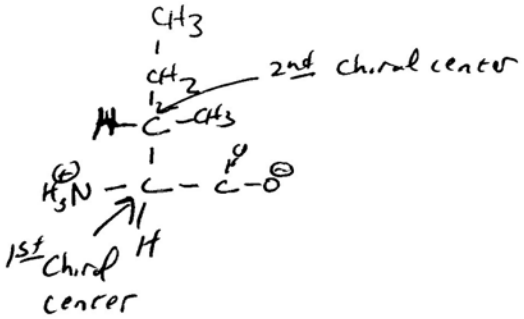
5) glycine



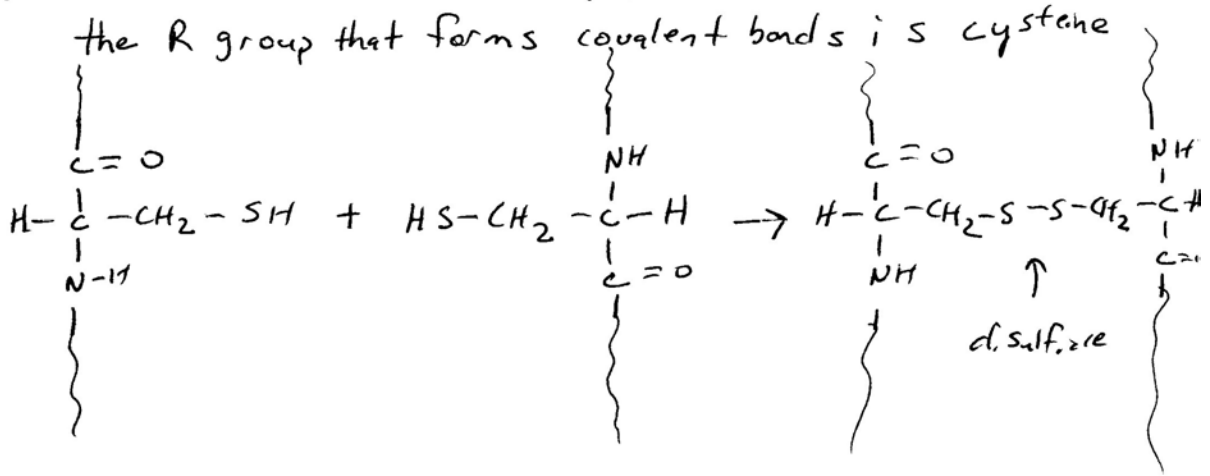
threonine



Isoleucine



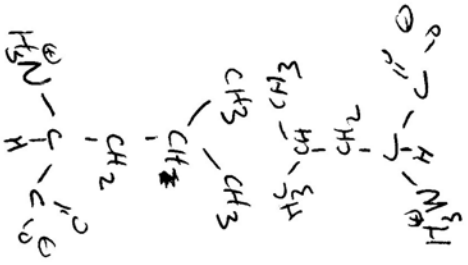
6) the back bone is covalent, peptide bond (amide)
the R group that forms covalent bonds is cysteine



6) cont.

hydrophobic, pick two hydrophobic amino acids, or two of the same hydrophobic amino acids

2 Leucines, nonpolar side chains

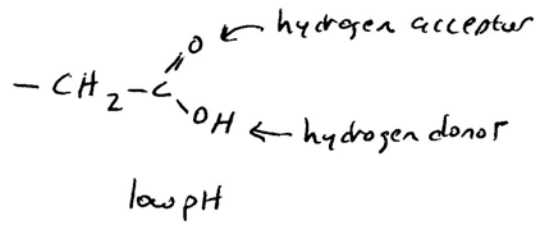


2 amino acids that could hydrogen bond:

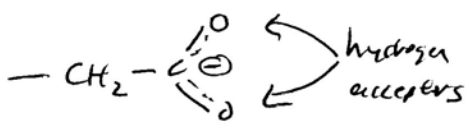
looking for amino acids that could act as hydrogen donors or hydrogen acceptors

- The side chains of tryptophan & arginine can serve as hydrogen bonds donors only
- The side chains of asparagine, glutamine, serine and threonine can serve as hydrogen bonders and acceptors
- The ability of lysine, aspartic acid, glutamic acid, tyrosine and histidine side groups to hydrogen bond, depends on pH. These side groups can serve as ~~both~~ donors or acceptors at certain pH value or donor and acceptors at other pH values.

Example:

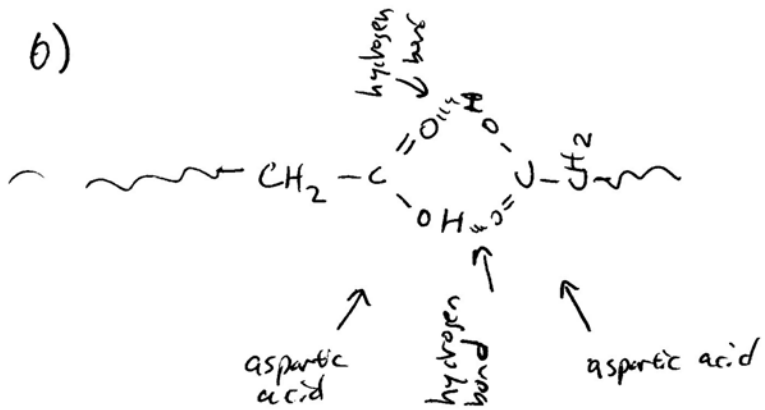


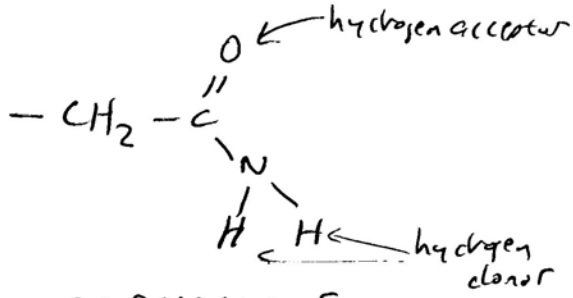
low pH



higher pH

6)





asparagine or glutamine

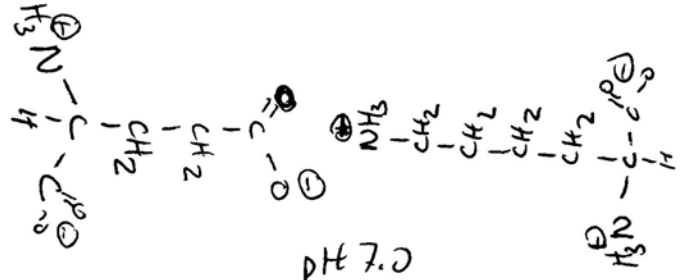
Ionic interactions:

full postive + full negative charged side groups

examples: Aspartic acid/ glutamic acid with Lysine, Arginine, or histidine

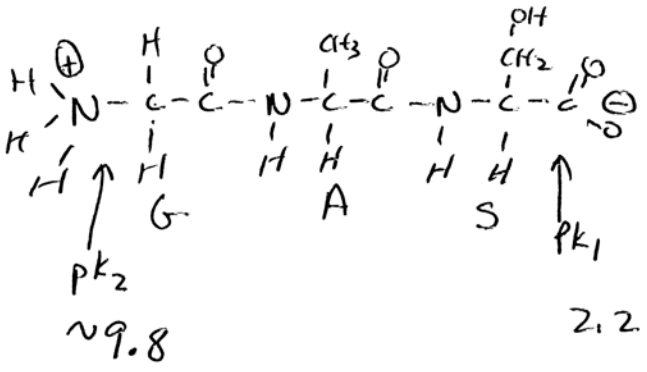
histidine will be 50% postive charged around pH 6.0

aspartic/glutamic acid are negatively charged above pH 3



pH 7.0

7) a) I would do this the easy way which is to use amino acids with no ionizable side groups



$$pI = \frac{1}{2}(pk_1 + pk_2)$$
$$= \frac{1}{2}(9.8 + 2.2)$$
$$pI = 6$$

This is the pH where the peptide has no net charge & will have no net movement in electric field

b) remember that it is better to measure the iso electric point for large proteins & peptides These proteins & peptide will take on a structure that changes the environment of the amino acid side groups, this enviro local environment will/or could change the pK_R of the individual amino acids, hard to predict from individual pK_R values.

c) Yes, remember that the environment such as solvent, temperature, salt concentration will effect hydrogen bonding & electrostatic interactions.