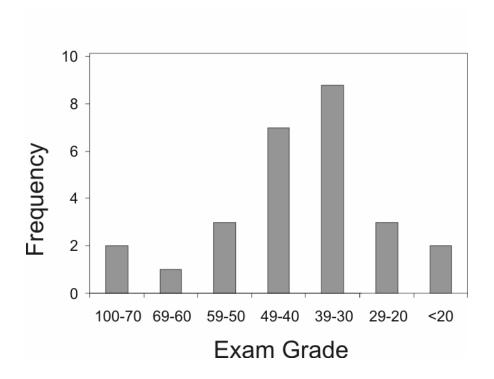
Midterm Exam 3 Answer Key

Exam 3 Mean: 41 Exam 3 Median: 39 Exam 3 St. Dev.: 16



EXAM 3 SOLUTIONS

1. a) THE PARENT MOLECULE, 1 HAS MASS MON DISOTOPIC MASS 288 (FOR C12H7[35CR]3 02).

M/2 = 218 CORRESPONDS TO LOSS OF 70.

THERE ISN'T ANY EASY WAY TO LOSE 70 AMU
WITH CARBONS, OXYGENS & HYDROGENS, BUT
IT WOULD BE # EASY TO LOSE 2 (CL.) = 70.

SO,

m/2=218: [C12 H7 CL O2]+

m/z= 146 CORRESPONDS TO LOSS OF 142.

STRUCTURALLY CLEAVAGE HAPPENS

WITH H. MOVING SOMEHOW FROM RIGHT TO

LEFT TO CIVE (ce) (m/2 = 146), so,

3 POINTS FOR EACH FORMULA. GIVING STRUCTURE

'INSTEAD OF FORMULA IS FINE, AND STRUCTURE INSEED

ONLY CORRESPOND TO CORRECT FORMULA FOR FULL CREDIT.

DON'T NEED POSITIVE CHARGE.

b) FOR BOTH FORMULAE (M+2) AND (M+4)

INTENSITIES ARE DETERMINED BY FREQUENCY

OF 37CL, (M+1) IS DETERMINED BY [37CL '3C]

AND (M+3) IS DETERMINED BY [37CL '3C]

TOGETHER. CONTRIBUTIONS OF 2H, 170 & 180

ARE NEGLICIBLE (<1%) BY COMPARISON.

$$m/2 = 218$$
: $(M+1) = 12 \times (1.1\%)^{13} = 13.2\%$
 $(M+2) = 1 \times (32\%)^{37} = 32\%$
 $(M+3) = 32\% \times 13.2\% = 4.2\%$
probability of probability of

(M+4) = 0%. THERE IS ONLY ONE CHLORINE IN THE MOLECULE.

$$m/z = 146$$
: $(M+1) = 6 \times (1.170^{-13}C) = 6.670$
 $(M+2) = 2 \times (3270^{-37}Ce) = 6470$
 $(M+3) = 6470 \times 6.670 = 4.270$
 $(M+4) = 3270 \times 3270 = 1070$

IN BOTH CASES, THE M+2 & M+4 INTENSITIES

ARE CONSISTENT WITH DOUG'S SPECTRUM, BUT

M+1 & M+3 INTENSITIES ARE TOO HIGH. DON'T

KNOW WHY.

POINT FOR EACH MENTER PERCENT (TO WITHIN 5%); ;

POINT FOR EITHER "YES" OR "NO" IN CONSISTENCY (

(NO GOOD ANSWER HERE)

C) PARENT MASS IN EI-MS OF 2 IS m/z = 252.

ISOTOPE RATIOS ARE CONSISTENT W/ 2 CHLORINES
SO ONE CHLORINE IS CONE FROM 1. ACTUALLY,

LOSS OF HCR FROM MASS 288 EXPLAINS m/z = 252 PARENT. SO WHERE DOES HCR COME

FROM IN 1?

NMR SHOWS THAT PRODUCT 2 IS MUCH LESS

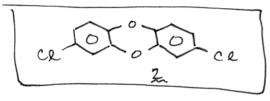
COMPLEX THAN PRODUCT 1 (THOUGH IT APPEARS AS

THOUGH LOW DU/J IS CAUSING SOME COMPLEXITY

IN SPLITTING. PRODUCT MOLECULE MIGHT BE

SYMMETRIC. ONE WAY OF CETTING THERE WOULD

BE



, HCL HAS BEEN LOST.

TRANSITIONS IN ARYL RINGS.

IN THIS MOLECULE, CONJUGATION IS NOT CONTINUOUS BECAUSE STERICALLY, TWO ARYL RINGS CAN'T LIE IN THE SAME PLANE:

steric repulsion twists rings out of planarity

SO, IN 1, CONJUGATION IS NOT MAXIMIZED.

IN 2, HOWEVER, MOLECULE IS COMPLETELY
PLANAR & CONJUGATED:

THIS SHIFTS UV-VIS

CR ABSORPTION TO LONGER

WAVELENGTH.

PLANARITY! NO NEED TO EXPLAIN IT > IT + TRANSITION. I

POINTS FOR ANY INCREASE IN CONSULATION ARGUMENT.

OPOINTS ALSO AVAILABLE FOR FUNCTIONAL CROSP
RELATED ARGUMENTS, BUT ONLY IF CONSISTENT N/

YOUR STRUCTURE IN PART (C) AND IF THEY ARE

TRUE (BACKED BY CHARTS). THIS IS RESTRICTIVE.

e) MOST IMPORTANT QUESTION HERE: HOW OO WE
DISTINGUISH ENDOGENOUS TRICLOSAN FROM
OUR TRICLOSAN? IN CLASS, WE TALKED ABOUT
RUNNING PARALLEL EXPERIMENTS W/ BACTERIA
IN WHICH ONE SAMPLE WAS ISOTOPICALLY
MODIFIED; HERE, SIMILAR STRATEGY WOULD BE
EFFECTIVE, USING ISOTOPICALLY LABELED
TRICLOSAN AS OUR TRICLOSAN:

PRODUCTS AS NORMAL TRICLOSAN, ONLY 6 MASS UNITS HIGHER.

- SO EXPERIMENT GOES SOMETHING LIKE
- ADD TRICLOSAN-d6 UPSTREAM ON A SUNNY DAY;
- COLLECT WATER DOWNSTREAM;
- INJECT THIS INTO GC-MS, MAYBE AFTER EXTRACTING WI CHLOROFORM;
- LOOK AT REI-MS OF PEAKS FROM TOTAL

 10N CHROMATOGRAM FOR SAME COMPOUNDS IN

 8 2, ONLY 6 MASS UNITS HEAVIER.

FROM ENDOGENOUS TRICADSAN.

- FULL CREDIT FOR ANY ISOTOPIC SUBSTITUTION THAT

 MAKES PARENT MORE THAN 4 MASS UNITS HEAVIER.

 IF NOT, (M+4) PEAK INTERFERES
 - 3 POINTS FOR ANY OTHER ISOTOPE SUBSTITUTION

 (ALL 37CE; 180; MONOCEUTERATED)
- 2 POINTS FOR OTHER CHEMICAL VARIANT OF TRICLOSAND e.g.

 (DICHLORINATED STARTING MATERIAL) CHEMISTRY

 WON'T BE THE SAME, BUT WILL GIVE INFO.
- 5 POINTS FOR ANY DESCRIPTION OF MASS SPEC

 EXPERIMENT. COULD BE ANYTHING GC-MS,

 ESI-MS, JUST ABOUT ANYTHING MUST BE

 REASONABLE.

2 a) THE CHART ON PAGE IN LISTS MASSES FOR EACH AMINO ACID FRAGMENT

HOWEVER, THE PEPTIDE WIN FULL LOOKS

$$\begin{array}{c|c} & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\$$

SO THE MASS OF THE PERTIDE WILL BE THE SUM OF THE FRAGMENT MASSES, PLUS I amu FOR THE C-TERMINAL-H, PLUS IT AMU FOR THE C-TERMINAL-OH, IN ADDITION, THE MASSES OBJECTED ARE FOR [M+H] IN MALDI-MS. IN ACID MATRIX, SO, ANOTHER I AMU IS ADDED.

m 2 (NON-PHOSPHORYLATED PEPTIDE) =

$$Y + F + R + P + S + G + F + Y* + D$$

 $+ 17 + 1 + 1 = \boxed{1196.5}$
IF ONE -OH IS CONVERTED TO $-0-\ddot{p}-OH$
 OH ,

m/2 (PHOSPHORYLATED) = m/2 (NON-PHOSPHORYLATED)

OKAY, SO THE PROBLEM PROBABLY WOULDN'T EXIST

IF THE PEPTIDE WEREN'T PHOSPHORYLATED, SO

THE APPEARANCE OF m/z = 1276.4 IN SPECTRUM

(i) IS NO SURPRISE. BUT IMPORTANTLY,

m/z = 1178.4 IS NOT NON-PHOSPHORYLATED PEPTIDE
IT MUST BE A FRAGMENT.

12 POINTS FOR EACH MASS.

b) FOLLOWING THE SHOKAT PROTOCOL RESULTED IN NEW CHEMICAL SPECIES - WHICH SUCCESTS

THAT IT IS SERINE THAT IS PHOSPHORYLATED.

(BELAUSE THAT IS WHAT THE METHOD IS DESIGNED TO DETECT.) SO, THE PHOSPHORYLATED PEPTIDE

MUST BE

m/z = 1276.4: [YFRP(pS)GF(Y*)D +H], or

(PS) RESIDUE INTO K*:

PROTEASE THEN CLEAVES THIS TO THE RIGHT OF K*:

m/z= 728.3.

THAT'S 3 OUT OF 4. THE LAST m/z: 1178.4,

IS ALREADY PRESENT FROM THE PURE

PHOSPHORYLATED PEPTIDE. IT IS ALSO AN

INTERMEDIATE GENERATED BY THE KOH.

H-1 YFRP-H GF (Y*) D 1 OH

or YFRP(dhA) GF(Y*) D; m/z= 1178.4.

WARREN SEL

IN SUM, m/z = 1276.4 YFRP(pS) $GF(Y^*)D$ 1255.4 YFRP(K*) $GF(Y^*)D$ 1178.4 YFRP(dhA) $GF(Y^*)D$ 728.3 YFRP(K*)

POINTS EACH BOX, THOUGH THE QUESTION MAKS SOME STORMAT IS RECOMMENDATIONS ON FORMAT, ANY FORMAT IS

C) THREE EXPLANATIONS:

#1: KOH-MEDIATED ELIMINATION (SEE ABOVE),
HAPPENS DURING SHOKAT METHOD (SAMPLE PREP),

#2: MATRIX-MEDIATED ELIMINATION, SAME
MECHANISM AS ABOVE, BUT HAPPENS DURING
IRRADIATION/VAPORIZATION.

#3: UNIMOLECULAR FRACMENTATION, HAPPENS
DURING VAPORIZATION.

d) ONLY ONE FUNCTIONAL GROUP IN PEPTIDE ABSORBS

>300 nm: NITRO, GROUP IN Y*

OH.

4 POINTS FOR ANY OF THESE ANSWERS

e) ALL OF THE OBSERVED PEAKS CORRESPOND TO LOSSES OF 16 AND 32 FROM PEAKS IN (ii).
IRRADIATED GROUP IS -NO2, SO MY BET IS THAT OXYGEN ATOMS COME OFF (VIA MULTISTEP PROCESS) FROM THIS.

POINTS EACH STRUCTURE.

TOTOM MUST BE CORRECT.

CAN BE ANYTHING THAT HAS LOST MASS 32.

(EACH)

2 POINTS FOR "16" AND "32".