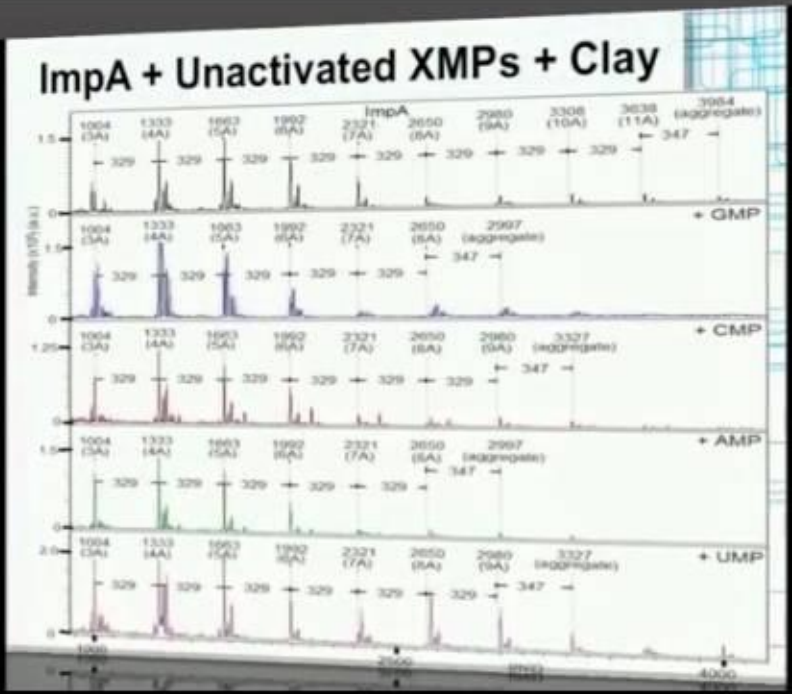
ImpA + Unactivated XMPs + Clay
ImpA
+ GMP
+ CMP
+ AMP
+ UMP
Intensity (x10^5 a.u.)
1004 (3A)
1333 (4A)
1663 (5A)
1992 (6A)
2321 (7A)
2650 (8A)
2980 (9A)
3306 (10A)
3638 (11A)
3964 (aggregate)
2997 (aggregate)
3327 (aggregate)
329
347
1500
2500
3500
4000

1
00:00:09,670 --> 00:00:08,320
so as you might have noticed I've

2
00:00:12,220 --> 00:00:09,680
changed the title of my talk just a

3
00:00:13,570 --> 00:00:12,230
little bit from what my abstract is in

4
00:00:15,370 --> 00:00:13,580
part because I think this will be more

5
00:00:16,330 --> 00:00:15,380
interesting but if you really want to

6
00:00:18,070 --> 00:00:16,340
talk to me about the trials and

7
00:00:19,900 --> 00:00:18,080
tribulations of using maldi-tof mass

8
00:00:23,800 --> 00:00:19,910
spec later I'd be happy to take this

9
00:00:26,830 --> 00:00:23,810
offline so as we went over this morning

10
00:00:28,569 --> 00:00:26,840
in our morning talk I think we're all

11
00:00:31,409 --> 00:00:28,579
acquainted now with the structure of RNA

12
00:00:35,110 --> 00:00:31,419
so again we have those ribose sugars

13
00:00:36,940 --> 00:00:35,120

phosphates and nucleobases and all these

14
00:00:41,319 --> 00:00:36,950
are connected via phosphodiester

15
00:00:44,380 --> 00:00:41,329
backbone a backbone sorry what I'm most

16
00:00:45,759 --> 00:00:44,390
interested in are these nucleobases so

17
00:00:48,610 --> 00:00:45,769
we know that we have four that are

18
00:00:50,380 --> 00:00:48,620
included in modern RNA and that includes

19
00:00:52,509 --> 00:00:50,390
two purines which are adenine and

20
00:00:55,779 --> 00:00:52,519
guanine and two parameters which are

21
00:00:59,139 --> 00:00:55,789
uracil and cytosine and we also know

22
00:01:01,569 --> 00:00:59,149
that the purines will base pair via

23
00:01:06,310 --> 00:01:01,579
hydrogen bonds to the respective periods

24
00:01:08,140 --> 00:01:06,320
so again a tu gu ji tusi what's most

25
00:01:09,010 --> 00:01:08,150
interesting about these nucleobases is

26
00:01:11,679 --> 00:01:09,020
that there could have been a whole

27
00:01:15,039 --> 00:01:11,689
library of possibilities to be included

28
00:01:18,399 --> 00:01:15,049
in our genomic DNA and RNA yet we only

29
00:01:19,960 --> 00:01:18,409
see four included in modern RNA so what

30
00:01:21,370 --> 00:01:19,970
I'm most interested in is trying to

31
00:01:23,910 --> 00:01:21,380
determine how we ended up with just

32
00:01:28,270 --> 00:01:23,920
these four and most specifically I'm

33
00:01:30,249 --> 00:01:28,280
interested in guanine so guanine is

34
00:01:33,100 --> 00:01:30,259
relatively unique compared to the other

35
00:01:36,459 --> 00:01:33,110
modern nucleobases and this is because

36
00:01:38,560 --> 00:01:36,469
guanine can actually base sort of base

37
00:01:42,160 --> 00:01:38,570
pair of with itself via hydrogen bonds

38
00:01:43,749 --> 00:01:42,170

in the very concentrated solutions so if

39
00:01:47,350 --> 00:01:43,759
we have a concentrated solution of

40
00:01:49,209 --> 00:01:47,360
guanine or guanosine monomers we can get

41
00:01:51,099 --> 00:01:49,219
these structures of jeet at RADS that

42
00:01:53,380 --> 00:01:51,109
are again hydrogen bonding to each other

43
00:01:55,899 --> 00:01:53,390
very much like we see in base pairs if

44
00:01:58,690 --> 00:01:55,909
we increase the concentration of guanine

45
00:02:02,200 --> 00:01:58,700
even further we can get even larger

46
00:02:04,630 --> 00:02:02,210
aggregate structures of these g tetrads

47
00:02:08,760 --> 00:02:04,640
so these gchat treads are just planar a

48
00:02:11,880 --> 00:02:08,770
certain range minus the guanine on these

49
00:02:14,190 --> 00:02:11,890
g-quadruplexes are just a G tetrad

50
00:02:16,440 --> 00:02:14,200
stabilized by

51
00:02:19,170 --> 00:02:16,450
cation typically potassium sodium and

52
00:02:22,890 --> 00:02:19,180
then another layer of duty at red Melky

53
00:02:25,500 --> 00:02:22,900
on duty at red etc etc and as far as we

54
00:02:27,150 --> 00:02:25,510
can tell dhwani is the only one of is

55
00:02:30,150 --> 00:02:27,160
really the only nucleobase that we see a

56
00:02:33,360 --> 00:02:30,160
modern IRNA that really does this or at

57
00:02:39,300 --> 00:02:33,370
least to any extreme extent so this

58
00:02:41,699 --> 00:02:39,310
brings us to yg so if G can form these

59
00:02:43,949 --> 00:02:41,709
large aggregate systems that are much

60
00:02:47,699 --> 00:02:43,959
easier to assemble then having it go

61
00:02:51,570 --> 00:02:47,709
into RNA then why is it included in RNA

62
00:02:53,370 --> 00:02:51,580
when it can do this so it could be in

63
00:02:55,410 --> 00:02:53,380

spite of this ability to form these

64
00:02:56,819 --> 00:02:55,420
aggregate structures but we like to

65
00:02:59,370 --> 00:02:56,829
think in our group that's because of

66
00:03:02,160 --> 00:02:59,380
this so this leads to what my work is

67
00:03:04,680 --> 00:03:02,170
which is looking at the effect of GMP or

68
00:03:08,729 --> 00:03:04,690
guanosine monophosphate on a biotic

69
00:03:10,229 --> 00:03:08,739
polymerization so this means i'm looking

70
00:03:13,530 --> 00:03:10,239
at the inclusion of other nucleotides

71
00:03:15,449 --> 00:03:13,540
based on the presence of GMP or sequence

72
00:03:17,460 --> 00:03:15,459
effects that are caused by constraints

73
00:03:20,190 --> 00:03:17,470
by the caused by these g aggregate

74
00:03:22,170 --> 00:03:20,200
structures what the focus of my talk

75
00:03:24,479 --> 00:03:22,180
today is though is just looking at the

76
00:03:27,599 --> 00:03:24,489
inclusion of these other nucleotides in

77
00:03:32,849 --> 00:03:27,609
our synthesis reaction so to make

78
00:03:36,030 --> 00:03:32,859
polymers from a various unactivated

79
00:03:38,879 --> 00:03:36,040
species it's impossible so we need some

80
00:03:41,160 --> 00:03:38,889
sort of catalytic reaction to happen and

81
00:03:44,430 --> 00:03:41,170
so we use a catalytic montmorillonite

82
00:03:46,650 --> 00:03:44,440
clay so this is clay that you've already

83
00:03:49,170 --> 00:03:46,660
heard about several times now that are

84
00:03:51,180 --> 00:03:49,180
just layers of tetrahedral and

85
00:03:52,920 --> 00:03:51,190
octahedral arrangements of atoms with

86
00:03:56,550 --> 00:03:52,930
the space in between that can hold

87
00:03:58,199 --> 00:03:56,560
cations and we've seen there has been

88
00:04:00,569 --> 00:03:58,209

some previous work especially done by

89
00:04:03,930 --> 00:04:00,579
the ferris group at rpi that shows that

90
00:04:06,509 --> 00:04:03,940
you can get RNA molecules both inside

91
00:04:08,509 --> 00:04:06,519
and around the edges of the clay and

92
00:04:13,319 --> 00:04:08,519
that this will lead to polymerization of

93
00:04:18,089 --> 00:04:13,329
activated nucleotides too as long as 50

94
00:04:20,759 --> 00:04:18,099
bases long but again this clay is not

95
00:04:22,529 --> 00:04:20,769
enough for our reaction to happen so we

96
00:04:25,740 --> 00:04:22,539
also have to have an activated species

97
00:04:27,690 --> 00:04:25,750
so if we think of some nucleoside

98
00:04:32,550 --> 00:04:27,700
monophosphate like GMP

99
00:04:34,590 --> 00:04:32,560
cmp a.m. PU NP this hydroxyl group is

100
00:04:36,390 --> 00:04:34,600
not a strong enough leaving group to

101
00:04:40,050 --> 00:04:36,400
allow it to polymerize into long strands

102
00:04:41,880 --> 00:04:40,060
of RNA so what we do is we exchange out

103
00:04:44,190 --> 00:04:41,890
the one of these hydroxyl groups for

104
00:04:45,900 --> 00:04:44,200
Anna middle right here and this makes

105
00:04:48,180 --> 00:04:45,910
for a very good leaving group and water

106
00:04:50,940 --> 00:04:48,190
systems which makes it significantly

107
00:04:56,100 --> 00:04:50,950
easier to create these long strands of

108
00:04:57,900 --> 00:04:56,110
polymers to analyze my polymers I use

109
00:05:00,180 --> 00:04:57,910
something called matrix assisted laser

110
00:05:04,820 --> 00:05:00,190
desorption ionization or maldi

111
00:05:08,130 --> 00:05:04,830
time-of-flight Tov mass spectrometry ms

112
00:05:10,350 --> 00:05:08,140
and in short all I'm really doing is

113
00:05:13,530 --> 00:05:10,360

hitting my sample with a laser causing

114
00:05:16,320 --> 00:05:13,540
it to ionize and then I have it it flies

115
00:05:19,830 --> 00:05:16,330
through a long tube it separates base

116
00:05:22,080 --> 00:05:19,840
fonts mass mass to charge ratio which

117
00:05:23,970 --> 00:05:22,090
you can see a determined via kinetics

118
00:05:26,130 --> 00:05:23,980
equations and look at how long it takes

119
00:05:28,260 --> 00:05:26,140
the supply through the tube so in short

120
00:05:30,030 --> 00:05:28,270
what I get our spectra that look like

121
00:05:32,490 --> 00:05:30,040
just separation of peaks and I'm

122
00:05:37,710 --> 00:05:32,500
identifying my polymers based upon the

123
00:05:42,150 --> 00:05:37,720
separations between those Peaks so again

124
00:05:44,430 --> 00:05:42,160
I need to put my put my activated

125
00:05:47,580 --> 00:05:44,440
species in clay and I can get a

126
00:05:49,950 --> 00:05:47,590
polymerization in the case of em peso

127
00:05:51,720 --> 00:05:49,960
activated adenosine monophosphate to

128
00:05:55,710 --> 00:05:51,730
about somewhere between eight to twelve

129
00:05:58,620 --> 00:05:55,720
verse which means eight to twelve units

130
00:06:00,600 --> 00:05:58,630
of a so this one appeared shows an

131
00:06:04,830 --> 00:06:00,610
eleven mer up to 11 mar which is pretty

132
00:06:08,160 --> 00:06:04,840
cool and if we add in any unactivated

133
00:06:10,140 --> 00:06:08,170
species we can see that we get still a

134
00:06:12,540 --> 00:06:10,150
similar mad polymerization a little bit

135
00:06:14,220 --> 00:06:12,550
less but it still kind of works we're

136
00:06:16,980 --> 00:06:14,230
still getting a decent amount of polymer

137
00:06:18,270 --> 00:06:16,990
formation but if you were listening to

138
00:06:20,250 --> 00:06:18,280

what i was talking about earlier you

139
00:06:23,280 --> 00:06:20,260
might expect that we'd only get one peak

140
00:06:24,960 --> 00:06:23,290
but if you look even closely even closer

141
00:06:28,230 --> 00:06:24,970
you'll see that we get multiple peaks

142
00:06:31,890 --> 00:06:28,240
for one species so if we zoom in on just

143
00:06:33,930 --> 00:06:31,900
one side peak so i'll zoom in on a 5a we

144
00:06:37,500 --> 00:06:33,940
can see that we we do get several peaks

145
00:06:41,100 --> 00:06:37,510
so our base peak is the 1663 in the case

146
00:06:43,170 --> 00:06:41,110
of 5a so again this corresponds to a

147
00:06:45,660 --> 00:06:43,180
polymer of a that has five adenosine

148
00:06:47,550 --> 00:06:45,670
monophosphate units in it we can see

149
00:06:50,310 --> 00:06:47,560
that we get some peak separation that's

150
00:06:53,760 --> 00:06:50,320
like plus 22 for a sodium RNA aggregate

151
00:06:56,310 --> 00:06:53,770
plus 3338 for a potassium RNA aggregate

152
00:06:58,380 --> 00:06:56,320
and a few other species as well but

153
00:07:01,800 --> 00:06:58,390
what's most interesting is not these

154
00:07:03,300 --> 00:07:01,810
aggregates with salts to us but if you

155
00:07:07,050 --> 00:07:03,310
look at the UH the addition of

156
00:07:09,330 --> 00:07:07,060
unactivated species cmp A&P UMP they

157
00:07:12,630 --> 00:07:09,340
look fairly similar to just implode in

158
00:07:15,750 --> 00:07:12,640
clay but GMP pops up with this other

159
00:07:19,800 --> 00:07:15,760
random peak at plus 6 that is plus 16

160
00:07:22,620 --> 00:07:19,810
difference from the 1663 peak that plus

161
00:07:25,770 --> 00:07:22,630
16 corresponds to the addition of a G

162
00:07:30,470 --> 00:07:25,780
instead of an a so what that means this

163
00:07:33,720 --> 00:07:30,480

is that this peak here is for a and 1 G

164
00:07:37,080 --> 00:07:33,730
so again a polymer of RNA for a base

165
00:07:39,360 --> 00:07:37,090
pair of base units and 1 G so this is

166
00:07:41,490 --> 00:07:39,370
really cool we see that G&P seems to

167
00:07:44,340 --> 00:07:41,500
force itself into Palmer inclusion

168
00:07:45,600 --> 00:07:44,350
whereas the rest of these don't so of

169
00:07:47,160 --> 00:07:45,610
course when the next things we want to

170
00:07:49,320 --> 00:07:47,170
do is look at entirely different system

171
00:07:52,920 --> 00:07:49,330
well not entirely but fairly similar

172
00:07:55,620 --> 00:07:52,930
system so of course we look at G so this

173
00:07:58,710 --> 00:07:55,630
here is a this here at the top is our mg

174
00:08:00,270 --> 00:07:58,720
polymerization and clay so again you can

175
00:08:03,780 --> 00:08:00,280
see that we get a little bit less

176
00:08:07,650 --> 00:08:03,790
polymerization than we do for a but we

177
00:08:09,870 --> 00:08:07,660
still get up to 7 which isn't bad if we

178
00:08:12,930 --> 00:08:09,880
add in the unactivated species we get

179
00:08:14,730 --> 00:08:12,940
fairly similar extensive reaction but

180
00:08:17,120 --> 00:08:14,740
again we are getting multiple peaks

181
00:08:19,680 --> 00:08:17,130
where we might only expect to find one

182
00:08:21,840 --> 00:08:19,690
so if we look again much more closely

183
00:08:24,840 --> 00:08:21,850
we'll see the sodium pig we'll see

184
00:08:26,820 --> 00:08:24,850
potassium and stuff if we look at the mg

185
00:08:29,790 --> 00:08:26,830
polymerization we see that we have a 3g

186
00:08:31,230 --> 00:08:29,800
here at 1052 and if we look at the one

187
00:08:33,000 --> 00:08:31,240
that includes GMP it looks fairly

188
00:08:34,920 --> 00:08:33,010

similar a little bit of extra base line

189
00:08:37,710 --> 00:08:34,930
noise but essentially the same as our

190
00:08:39,450 --> 00:08:37,720
empty reaction up top but the minute we

191
00:08:42,450 --> 00:08:39,460
look at the cmp we know it's an entirely

192
00:08:47,010 --> 00:08:42,460
different Peaks that's minus 40 mass

193
00:08:49,110 --> 00:08:47,020
units from our base peak of 1052 and if

194
00:08:52,200 --> 00:08:49,120
you want to map it out you'll notice

195
00:08:54,840 --> 00:08:52,210
that C is different in mass from g x

196
00:08:57,660 --> 00:08:54,850
minus 40 so this

197
00:09:02,040 --> 00:08:57,670
that we are getting a different type of

198
00:09:04,019 --> 00:09:02,050
polymer here that is 2g and 1c and if we

199
00:09:06,120 --> 00:09:04,029
look again at a we're getting a similar

200
00:09:09,389 --> 00:09:06,130
thing where we're getting minus 16 for

201
00:09:11,579 --> 00:09:09,399
2g and 1a and we can even make an

202
00:09:13,889 --> 00:09:11,589
argument down here for the you where

203
00:09:17,749 --> 00:09:13,899
we're gaining again minus 40 because you

204
00:09:21,540 --> 00:09:17,759
and c are approximately the same mass

205
00:09:23,370 --> 00:09:21,550
for 2g and one you so this is really

206
00:09:25,710 --> 00:09:23,380
cool that we're getting in our abiotic

207
00:09:27,360 --> 00:09:25,720
polymerization that's using act and

208
00:09:29,220 --> 00:09:27,370
activated nucleotide and unactivated

209
00:09:32,400 --> 00:09:29,230
species we're gaining inclusion of these

210
00:09:35,040 --> 00:09:32,410
unactivated species in our polymers but

211
00:09:37,379 --> 00:09:35,050
this still isn't enough so we've

212
00:09:40,730 --> 00:09:37,389
recently tried to get some preliminary

213
00:09:43,139 --> 00:09:40,740

data on the polymerization of c and

214
00:09:45,210 --> 00:09:43,149
unfortunately this is only a first run

215
00:09:47,550 --> 00:09:45,220
so our seed to not polymerize quite to

216
00:09:50,189 --> 00:09:47,560
the extent that we had hoped for but

217
00:09:53,069 --> 00:09:50,199
what's most important is that if we look

218
00:09:54,900 --> 00:09:53,079
at the inclusion of low concentrations

219
00:09:56,790 --> 00:09:54,910
and high concentrations of GMP into

220
00:09:59,819 --> 00:09:56,800
these reactions we can see that we are

221
00:10:03,179 --> 00:09:59,829
getting Peaks that correspond to again

222
00:10:05,790 --> 00:10:03,189
the addition of a G in place of a see in

223
00:10:07,829 --> 00:10:05,800
our polymerization reactions so it does

224
00:10:11,550 --> 00:10:07,839
appear that g likes the force itself

225
00:10:15,179 --> 00:10:11,560
into our other polymerizations so some

226
00:10:16,829 --> 00:10:15,189
quick conclusions hey whatever we make

227
00:10:19,800 --> 00:10:16,839
our poly a from our info and clay

228
00:10:21,509 --> 00:10:19,810
reactions we get a G incorporated and

229
00:10:23,309 --> 00:10:21,519
while no other nucleotide likes to

230
00:10:26,400 --> 00:10:23,319
incorporate itself into its power

231
00:10:29,759 --> 00:10:26,410
polymers if we look at our poly g

232
00:10:31,740 --> 00:10:29,769
reaction we will see the incorporation

233
00:10:33,960 --> 00:10:31,750
of all the unactivated species of

234
00:10:36,210 --> 00:10:33,970
nucleotides and we even have some

235
00:10:37,559 --> 00:10:36,220
evidence that suggests that g will

236
00:10:41,340 --> 00:10:37,569
incorporate itself into the sea

237
00:10:43,439 --> 00:10:41,350
polymerization so this all is stated

238
00:10:46,679 --> 00:10:43,449

together is starting to suggest us that

239
00:10:48,929 --> 00:10:46,689
maybe g is including itself because of

240
00:10:51,540 --> 00:10:48,939
its a weird properties its unique

241
00:10:53,670 --> 00:10:51,550
property properties and helping to bring

242
00:10:56,819 --> 00:10:53,680
others in in addition to these because

243
00:10:58,290 --> 00:10:56,829
of these unique properties so obviously

244
00:11:00,960 --> 00:10:58,300
some future worked we want to make our

245
00:11:03,900 --> 00:11:00,970
MC reaction look better and additionally

246
00:11:07,259 --> 00:11:03,910
we want to get imputed polymer a gift

247
00:11:08,470 --> 00:11:07,269
polymers of using our mpu reaction and

248
00:11:13,079 --> 00:11:08,480
also look at using

249
00:11:17,350 --> 00:11:13,089
unactivated species as well um excuse me

250
00:11:19,180 --> 00:11:17,360
and eventually we do want to get to

251
00:11:21,040 --> 00:11:19,190
quantitation and sequencing of the

252
00:11:25,629 --> 00:11:21,050
species that we're making because

253
00:11:27,610 --> 00:11:25,639
maldita can't quantify or sequence our

254
00:11:30,850 --> 00:11:27,620
species we can only determine the

255
00:11:31,930 --> 00:11:30,860
general contents of what we have so I'd

256
00:11:33,790 --> 00:11:31,940
like to finish up with some quick

257
00:11:36,430 --> 00:11:33,800
acknowledgments so thanks to my advisor

258
00:11:37,870 --> 00:11:36,440
dr. Linda McGowan of course thanks to my

259
00:11:40,740 --> 00:11:37,880
group especially Bradley Burke our who

260
00:11:43,030 --> 00:11:40,750
gave a talk yesterday and Lauren Cassidy

261
00:11:46,120 --> 00:11:43,040
thanks to the ferris group downstairs

262
00:11:48,519 --> 00:11:46,130
from us at rpi especially dr. Prakash G

263
00:11:51,009 --> 00:11:48,529

of XI my committee members and of course

264
00:11:53,199 --> 00:11:51,019
I do all my work at rpi which is one of

265
00:12:01,110 --> 00:11:53,209
the NASA centers for astrobiology and

266
00:12:08,410 --> 00:12:04,800
thanks for not make me go to UM

267
00:12:09,460 --> 00:12:08,420
interesting is there what is the sort of

268
00:12:10,389 --> 00:12:09,470
the mechanism that you're seeing because

269
00:12:12,250 --> 00:12:10,399
it seems like there could be two

270
00:12:13,930 --> 00:12:12,260
competing processes one is going into

271
00:12:15,490 --> 00:12:13,940
the tetrad formation and then the other

272
00:12:17,230 --> 00:12:15,500
is actually being absorbed to the

273
00:12:21,939 --> 00:12:17,240
mountain Morla night and that seems like

274
00:12:26,470 --> 00:12:21,949
they might be mutually exclusive do you

275
00:12:29,170 --> 00:12:26,480
have the idea um I'm not exactly certain

276
00:12:31,689 --> 00:12:29,180
what what things are going into the clay

277
00:12:33,879 --> 00:12:31,699
and what are not some data that I

278
00:12:36,100 --> 00:12:33,889
haven't showed suggests that all of our

279
00:12:38,530 --> 00:12:36,110
unactivated species do get absorbed into

280
00:12:42,129 --> 00:12:38,540
the clay at some point or at least in

281
00:12:44,110 --> 00:12:42,139
varying concentrations and so I would

282
00:12:45,189 --> 00:12:44,120
guess that a decent amount is going into

283
00:12:51,910 --> 00:12:45,199
the clay allowing us to do our

284
00:12:53,889 --> 00:12:51,920
polymerization that make sense at most

285
00:12:56,710 --> 00:12:53,899
these concentrations if we do get some

286
00:12:59,410 --> 00:12:56,720
tetrad formation it's very low so it's

287
00:13:03,490 --> 00:12:59,420
possible but it shouldn't be having as

288
00:13:06,069 --> 00:13:03,500

much of an effect in fact the MC if I

289
00:13:08,860 --> 00:13:06,079
can go back so I was trying to get

290
00:13:12,670 --> 00:13:08,870
higher concentrations of GMP 24 set of

291
00:13:14,199 --> 00:13:12,680
quadruplex and tetrad formation but we

292
00:13:15,579 --> 00:13:14,209
can look at it and doesn't look like it

293
00:13:18,280 --> 00:13:15,589
had too much of a difference in effect

294
00:13:21,120 --> 00:13:18,290
may be slightly lower polymerization and

295
00:13:33,720 --> 00:13:21,130
more aggregation instead

296
00:13:35,490 --> 00:13:33,730
any other questions for Kristen so um

297
00:13:37,800 --> 00:13:35,500
because we both do this i have a very

298
00:13:39,810 --> 00:13:37,810
specific question for you so I'm can you

299
00:13:42,510 --> 00:13:39,820
actually go back one more slide so you

300
00:13:46,260 --> 00:13:42,520
you use your empty and you in corp and

301
00:13:48,690 --> 00:13:46,270
you used the fork anukul nucleobases as

302
00:13:51,720 --> 00:13:48,700
inactivated species and because you're

303
00:13:53,310 --> 00:13:51,730
trying to figure out why we use those

304
00:13:55,500 --> 00:13:53,320
for and other nucleobases have you

305
00:13:57,810 --> 00:13:55,510
considered using the non-canonical

306
00:14:00,140 --> 00:13:57,820
nucleobases as the inactive species I

307
00:14:02,760 --> 00:14:00,150
know they're expensive but have you

308
00:14:06,080 --> 00:14:02,770
that's a beautiful question and actually

309
00:14:09,300 --> 00:14:06,090
that's a long term project okay so in

310
00:14:11,310 --> 00:14:09,310
the work that I'm doing hopefully by

311
00:14:12,780 --> 00:14:11,320
next year I'll start this it's starting

312
00:14:14,670 --> 00:14:12,790
to include some of the other purines

313
00:14:17,490 --> 00:14:14,680

that we find especially meteorite so

314
00:14:19,770 --> 00:14:17,500
like a santhan hypo xanthine purine and

315
00:14:21,390 --> 00:14:19,780
some of the diamine appearance I have

316
00:14:23,790 --> 00:14:21,400
not yet done it but I'm really excited

317
00:14:25,020 --> 00:14:23,800
to do it okay because we can go halfsies

318
00:14:30,540 --> 00:14:25,030
on some of the expensive ones if you