

Post Match Reporting

2018/2019 Match Cohort Data

Specialty: Radiation Oncology
N= 3 (1.0% match cohort)

Item	N	% of specialty cohort	Mean	Standard Deviation
Graduation year				
2016	1	33.3%		
2018	1	33.3%		
2019	1	33.3%		
Three digit Step 1 score			247.7	15.6
MSPE Adjective:				
Outstanding	1	33.3%		
Superior	1	33.3%		
Excellent	1	33.3%		
Very Good	0	0.0%		
Good	0	0.0%		
AOA elected	0	0.0 %		
Applied to preliminary or transitional programs:	2	66.7%		
Other specialties applied to:				
Internal Medicine				
Number of categorical programs applied to			2.5	2.1
Honors Received:				
Anesthesia	1	33.3%		
FCM	0	0.0%		
Internal Medicine	1	33.3%		
Neurology	2	66.7%		
Obstetrics/Gynecology	1	33.3%		
Pediatrics	0	0.0%		
Psychiatry	2	66.7%		
Surgery	2	66.7%		

Post Match Reporting

2018/2019 Survey Respondent Cohort Data

Specialty: Radiation Oncology
N= 2 (0.9% survey respondents)

Item	N	% of specialty cohort	Mean	Standard Deviation	Min	Max
How many programs invited you to interview?			12.0	5.7	8	16
How many interviews did you accept?			7.5	3.5	5	10
Did you review your application with a career advisor before applying?	0	0.0%				
Before ranking programs, did you review your rank list with a career advisor?	0	0.0%				
Total Spent on Interviews						
\$0-\$500	0	0.0%				
\$501-\$1000	1	50.0%				
\$1001-\$2000	0	0.0%				
\$2001-\$3000	1	50.0%				
\$3001-\$4000	0	0.0%				
>\$4000	0	0.0%				
Did you complete a Pathway project?	1	50.0%				
Did you complete a research project in the field you matched?	2	100.0%				
Did you have a publication during medical school?	2	100.0%				

The field project was in:

Cancer Genomics
Brain cancer radiation

Describe any publications:

1. Liu SJ, Lim DA. Modulating the expression of long non-coding RNAs for functional studies. *EMBO Reports*. 2018;e46955; doi 10.15252/embr.201846955
2. Kline CN*, Liu SJ*, Duriseti S, Banerjee A, Nicolaides T, Raber S, Gupta N, Haas-Kogan D, Braunstein S, Mueller S. Reirradiation and PD-1 inhibition with nivolumab for the treatment of recurrent diffuse intrinsic pontine glioma: a single-institution experience. *J Neuro-Oncol*. 2018;86:1064-10 *Equal Contribution
3. Cho SW, Xu J, Sun R, Mumbach MR, Carter AC, Chen YG, Yost KE, Kim J, He J, Nevins SA, Chin SF, Caldas C, Liu SJ, Horlbeck MA, Lim DA, Weissman JS, Curtis C, Chang HY. Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. *Cell*. 2018; doi.org/10.1016/j.cell.2018.03.068
4. Maller S, Cho A, Liu SJ, Lim DA, Diaz A. CONICS integrates scRNA-seq with DNA sequencing to map gene expression to tumor sub-clones. *Bioinformatics*. 2018; bty316
5. Nowakowski TJ, Bhaduri A, Pollen AA, Alvarado B, Mostajo-Radji MA, Di Lullo E, Haeussler M, Sandoval-Espinosa C, Liu SJ, Velmeshev S, Ounadjela JR, Shuga J, Wang X, Lim DA, West JA, Leyrat AA, Kent WJ, Kriegstein AR. Spatiotemporal gene expression trajectories reveal developmental hierarchies of the human cortex. *Science*. 2017;358:1318-1323
6. Maller S, Kohanbash G, Liu SJ, Alvarado B, Carrera D, Bhaduri A, Watchmaker PB, Yagnik G, Di Lullo E, Malatesta M, Amankulor NM, Kriegstein AR, Lim DA, Aghi M, Okada H, Diaz A. Single-cell profiling of human gliomas reveals macrophage ontogeny as a basis for regional differences in macrophage activation in the tumor microenvironment. *Genome Biology* 2017;18:234
7. Liu SJ*, Horlbeck MA*, Cho SW, Birk HS, Malatesta M, He D, Attenello FJ, Villalta JE, Cho MY, Chen Y, Mandegar MA, Olvera MP, Gilbert LA, Conklin BR, Chang HY, Weissman JS, Lim DA. CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. *Science*. 2017;355 aah7111 *Equal Contribution
8. Maller S*, Liu SJ*, Di Lullo E, Malatesta M, Pollen AA, Nowakowski TJ, Kohanbash G, Aghi M, Kriegstein AR, Lim DA, Diaz A. Single-cell sequencing maps gene expression to mutational phylogenies in PDGF- and EGF-driven gliomas. *Mol Syst Biol*. 2016;12(11) PMID 27888226 *Equal Contribution
9. Liu SJ, Nowakowski TJ, Pollen AA, Lui JH, Horlbeck MA, Attenello FJ, He D, Weissman JS, Kriegstein AR, Diaz AA, Lim DA. Single-cell analysis of long non-coding RNAs in the developing human neocortex. *Genome Biol*. 2016;17:67 PMID 27081004
10. Diaz AA, Liu SJ, Sandoval C, Pollen AA, Nowakowski TJ, Lim DA, Kriegstein AR. SCell: integrated analysis of single-cell RNA-seq data *Bioinformatics*. 2016; doi:10.1093/bioinformatics/btw201
11. Pollen AA, Nowakowski TJ, Chen J, Retallack H, Sandoval-Espinosa C, Nicholas CR, Shuga J, Liu SJ, Oldham MC, Diaz A, Lim DA, Leyrat AA, West JA, Kriegstein AR. Molecular identity of human outer radial glia during cortical development. *Cell*. 2015;163(1):55-67. PMID 26406371
12. Ramos AD, Andersen RE, Liu SJ, Nowakowski TJ, Hong SJ, Gertz CC, Salinas RD, Zarabi H, Kriegstein AR, Lim DA. The long noncoding RNA Pnky regulates neuronal differentiation of embryonic and postnatal neural stem cells. *Cell Stem Cell*. 2015;16(4):439-47. PMID 25800779
13. Park DH, Hong SJ, Salinas RD, Liu SJ, Sun SW, Sgualdino J, Testa G, Matzuk MM, Iwamori N, Lim DA. Activation of neuronal gene expression by the JMJD3 demethylase is required for postnatal and adult brain neurogenesis. *Cell Rep*. 2014;8(5):1290-9. PMID 25176653

One preclinical paper / One clinical paper

**Who was your most effective career advisor in field matched?
(number of multiple mentions)**

Steve Braunstein (2)

What were your most useful career resources?

Faculty in the department I was applying into

SDN section on RadOnc (avoid the annoying posts by hyper-competitive weirdos and focus on details regarding interview dates and such)

If you had to do anything differently in the residency matching process, what would it be?

Overall satisfied with application process

I wouldn't have applied to programs that, realistically, I would have never actually gone to.

Is there any other information helpful to UCSF students who will apply to your specialty choice in the future?

When applying to very small fields it is imperative to discuss with attendings in that department to assess the strategy for the interview process.

Don't skimp on prelim applications!