```
In [1]: from genefab import get_datasets, GLDS
```

Dataset search:

```
In [2]:
       datasets = get datasets(
           ptype="flight", organism="mus", factor="radiation", assay="transcript",
        )
In [3]: datasets
Out[3]: [GLDS-87 (number of assays: 1; factors: Spaceflight, Absorbed Radiati
       on Dose),
        GLDS-173 (number of assays: 1; factors: Space Flight, Absorbed Radia
        tion Dose),
        GLDS-25 (number of assays: 1; factors: Space Flight, Absorbed Radiat
        ion Dose).
        GLDS-116 (number of assays: 2; factors: Microgravity, Absorbed Radia
        tion Dose),
        GLDS-21 (number of assays: 1; factors: Gravitation, Absorbed Radiati
        on Dose),
        GLDS-50 (number of assays: 1; factors: Space Flight, Absorbed Radiat
        ion Dose),
        GLDS-135 (number of assays: 1; factors: Microgravity, Absorbed Radia
        tion Dose).
        GLDS-4 (number of assays: 1; factors: MESH:Gravitation, absorbed rad
        iation dose).
        GLDS-111 (number of assays: 1; factors: Microgravity, Absorbed Radia
        tion Dose)]
```

Filtering search results for assays with derived array data:

Requesting a dataset directly:

```
In [5]: glds = GLDS("GLDS-42")
    assay = glds.assays[0]
    assay.name
Out[5]: 'a E-GEOD-32949 GeneChip assay-txt'
```

```
In [6]: | assay.fields
Out[6]: {'Sample Name': {'a100000samplename'},
         'Extract Name': {'a100001extractname'},
         'Material Type': {'a100002materialtype'},
         'Protocol REF': {'a100005protocolref',
          'a100010protocolref',
          'a100013protocolref',
          'a100014protocolref',
          'a100017protocolref'},
         'Labeled Extract Name': {'a100006labeledextractname'},
         'Label': {'a100007label'},
         'Hybridization Assay Name': {'a100011hybridizationassayname'},
         'Array Design REF': {'a100012arraydesignref'},
         'Array Data File': {'a100015arraydatafile'},
         'Comment: ArrayExpress FTP file': {'a100016commentarrayexpressftpfi
       le'},
         'Normalization Name': {'a100018normalizationname'},
         'Derived Array Data File': {'a100019derivedarraydatafile'},
         'Comment: Derived ArrayExpress FTP file': {'a100020commentderivedar
        rayexpressftpfile'}}
```

Getting the combined matrix for the assay:

In [7]: matrix = assay.get_combined_matrix()
matrix[::5000]

Out[7]:

	ID_REF	VALUE	ABS_CALL	DETECTION P-VALUE	Sample Name
0	AFFX-BioB-5_at	385.51300	Р	0.001593	GSM815905 extract 1
5000	189216_at	40.07840	Α	0.366211	GSM815905 extract 1
10000	184223_at	132.49500	Α	0.219482	GSM815905 extract 1
15000	179220_s_at	49.42860	Α	0.129639	GSM815905 extract 1
20000	174219_at	241.49500	Р	0.030273	GSM815905 extract 1
25000	191859_at	210.43100	Р	0.023926	GSM815904 extract 1
30000	186831_s_at	270.50400	Р	0.000244	GSM815904 extract 1
35000	181862_at	5.77048	Α	0.696289	GSM815904 extract 1
40000	176828_s_at	532.64200	Р	0.000732	GSM815904 extract 1
45000	171858_x_at	214.57800	Р	0.046143	GSM815904 extract 1
50000	189471_at	539.19400	Р	0.008057	GSM815903 extract 1
55000	184478_at	61.41010	Α	0.246094	GSM815903 extract 1
60000	179443_s_at	10.22280	Α	0.753906	GSM815903 extract 1
65000	174474_at	1332.14000	Р	0.000244	GSM815903 extract 1
70000	192114_s_at	3855.12000	Р	0.000244	GSM815902 extract 1
75000	187086_at	186.97700	Р	0.037598	GSM815902 extract 1
80000	182118_s_at	103.42500	Α	0.334473	GSM815902 extract 1
85000	177083_at	3.22085	Α	0.985840	GSM815902 extract 1
90000	172073_x_at	9.60776	Α	0.888428	GSM815902 extract 1
95000	189694_at	153.34100	Р	0.000732	GSM815901 extract 1
100000	184732_at	31.38190	Α	0.274170	GSM815901 extract 1
105000	179697_at	56.63130	Α	0.334473	GSM815901 extract 1
110000	174730_at	1877.49000	Р	0.000244	GSM815901 extract 1
115000	192341_s_at	599.46700	Р	0.000244	GSM815900 extract 1
120000	187341_s_at	994.73900	Р	0.000244	GSM815900 extract 1
125000	182337_at	26.31630	Α	0.500000	GSM815900 extract 1
130000	177344_at	158.76100	Р	0.010742	GSM815900 extract 1
				0.943848	GSM815900 extract 1