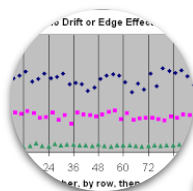


CACHE#3 Compounds Advancing to
Round #2 (hit expansion)

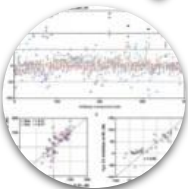
HTS flowchart

Final hit rate: 1.6%

1.



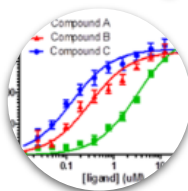
2.



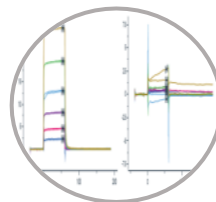
3.

Cmpd 1 @ 50	No protein	No protein
Cmpd 5 @ 100	No protein	Cmpd 6 @ 50
No protein	No protein	No protein
Cmpd 9 @ 100	Cmpd 9 @ 50	Cmpd 9 @ 25
No protein	No protein	No protein
Cmpd 13 @ 100	Cmpd 13 @ 50	Cmpd 13 @ 25
No protein	No protein	No protein
Cmpd 17 @ 100	Cmpd 17 @ 50	Cmpd 17 @ 25
No protein	No protein	No protein
Cmpd 21 @ 100	Cmpd 21 @ 50	Cmpd 21 @ 25
No protein	No protein	No protein

4.



5.



SPR Counter screening: 18 confirmed hits were tested by SPR against NSP3_SARS2 and PARP14 proteins with a 6-points concentration range starting from 100/50/30 μM in duplicates. Another 18 HTRF hits that misbehaved with 2% DMSO in the SPR buffer were re-tested with 4% DMSO.

28 final hits confirmed to bind NSP3 by HTRF and SPR are advancing to Round #2, regardless of their PARP14 binding status

SPR Dose response: 166 compounds selected from the HTRF hit confirmation step were tested by SPR against NSP3_SARS2 protein with a 6-points concentration range (top concentration selected according to DLS aggregation/solubility data at 100 and 50 μM) in duplicate.

Hit criteria: ($K_D < 100 \mu\text{M}$, % of binding > 30 , $\chi^2 < 10\%$ Rmax) – 16 hits and 2 possible hits ($K_D < 100 \mu\text{M}$, % of binding > 15)

HTRF Hit confirmation for 302 compounds selected from primary screen: 3 concentration points 100, 50 and 25 μM were tested by HTRF for each compound in duplicate. In parallel compound-only controls (without protein) were tested at the same concentrations in duplicate.

Confirmed hit criteria: dose dependency trend with $> 30\%$ inhibition @100 μM and no fluorescence interference by control – 150 compounds with dose-dependency and 16 additional could be hits

HTRF Primary HTS: 1738 compounds were tested in duplicates as 2 independent runs @100 μM by HTRF.

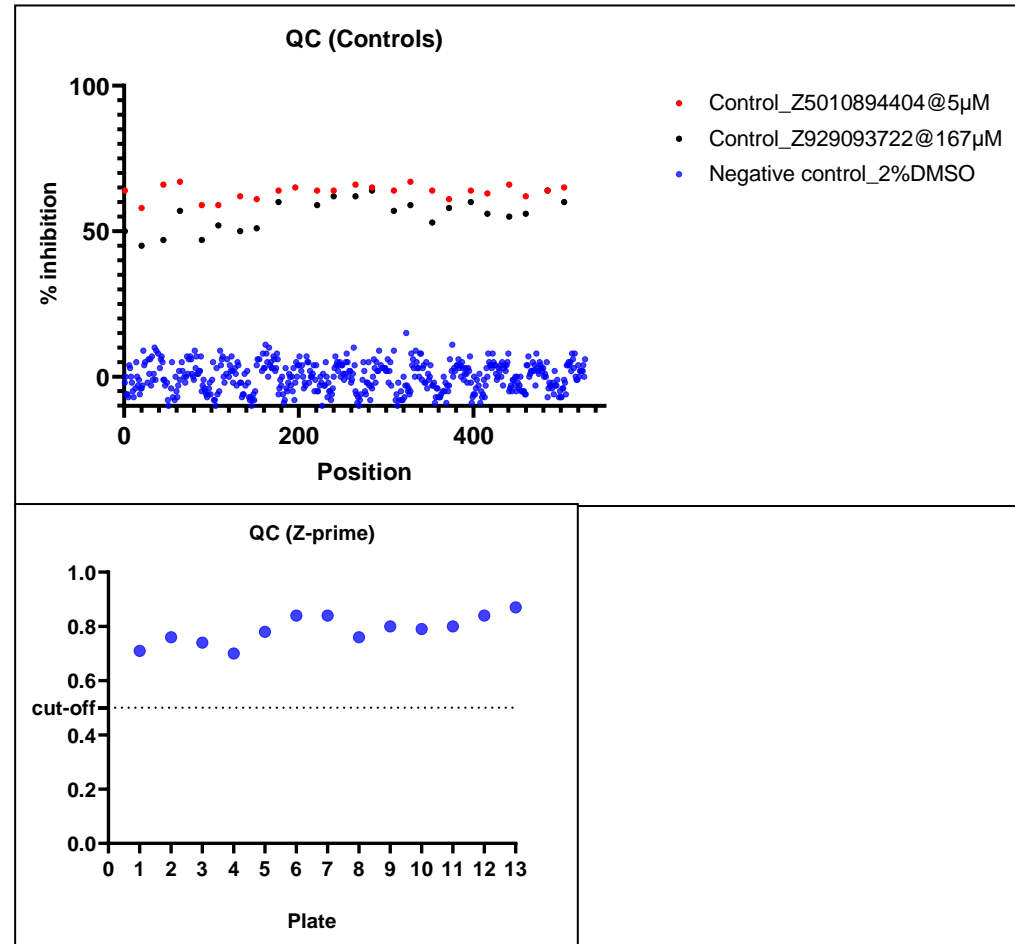
Initial hit criteria: $> 30\%$ inhibition in a single run - 281 compounds selected

Criteria#2: compounds demonstrating “overflow” signal in 2 runs – 21 compounds selected

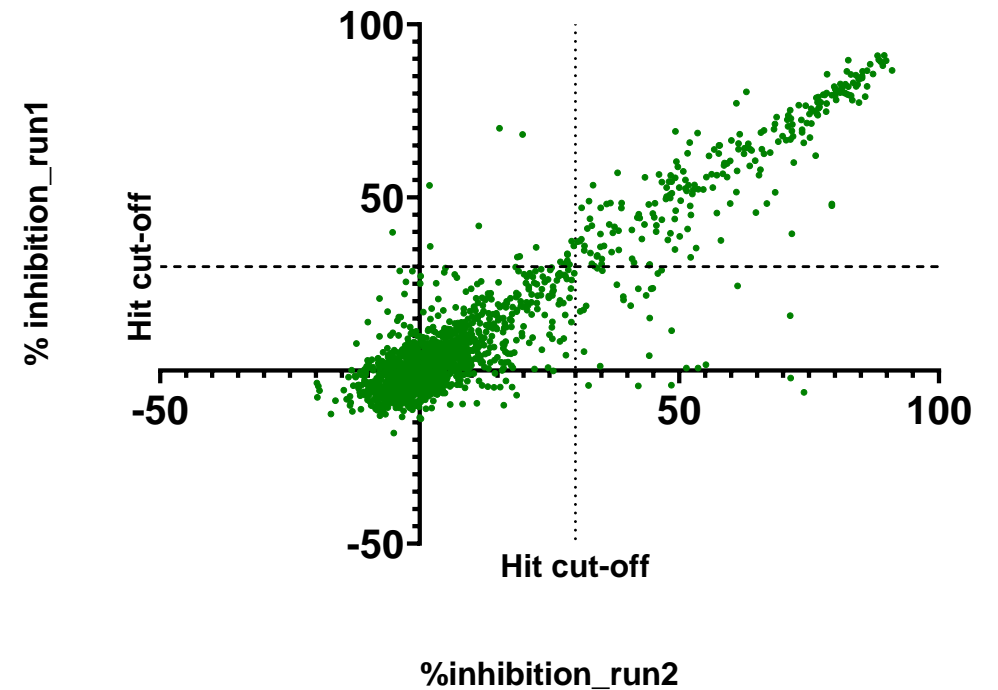
Assay setup and validation: 8 previously published reference compounds (doi.org/10.1073/pnas.2212931120) were used for HTRF and SPR assays optimization and for Uniformity test (<http://www.ncbi.nlm.nih.gov/books/NBK83783/>)

Primary screen (HTRF)

QC plots

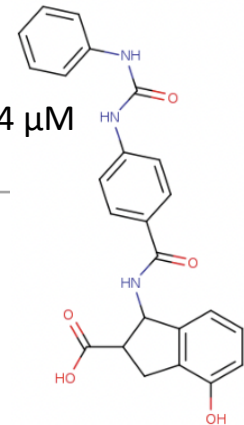


Single point (100 uM compound concentration) in duplicate; correlation between runs



SPR QC data

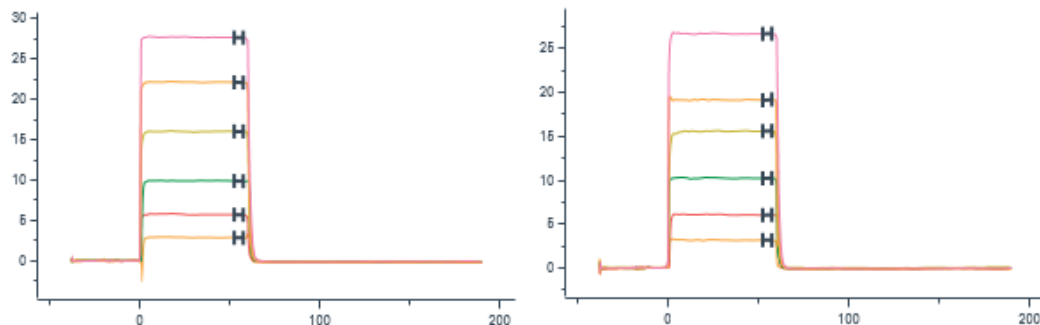
published K_i : 0.4 μM



QC data (Positive Controls)

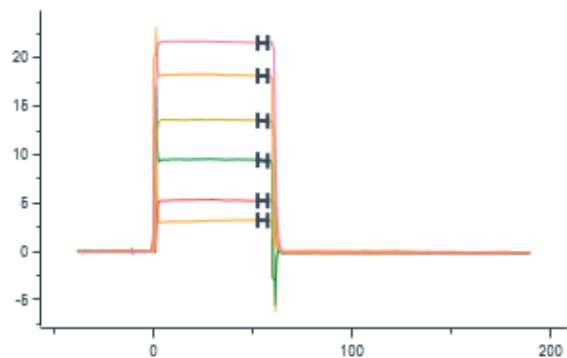
NSP3_SARS2

ADP-ribose



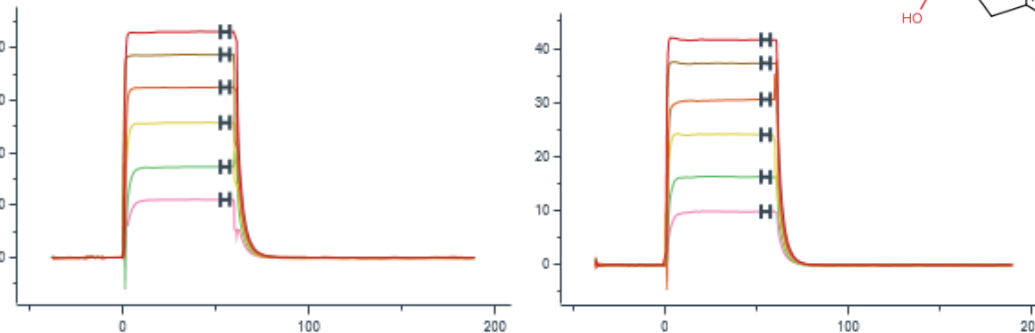
Run first: $K_D = 9.5 \mu\text{M}$, 100% binding
Run last: $K_D = 10 \mu\text{M}$, 92% binding
 $K_{\text{disp}}/\text{IC}_{50}$ (HTRF) = 12 μM

PARP14a

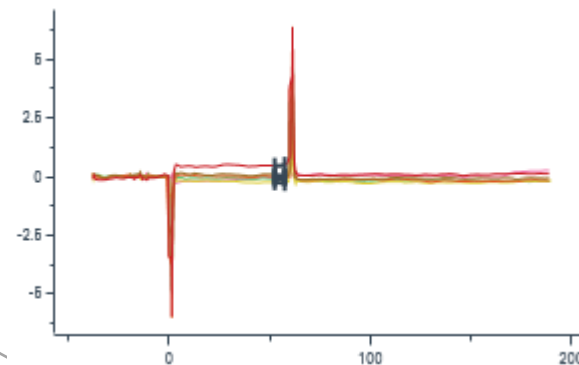


$K_D = 7.2 \mu\text{M}$
Binding = 88%

Z5010894404

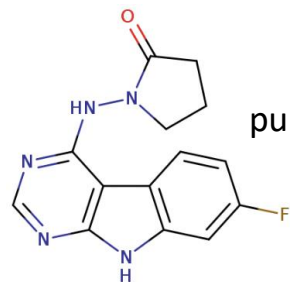


Run first: $K_D = 1.2 \mu\text{M}$, 124% binding
Run last: $K_D = 1.3 \mu\text{M}$, 121% binding
 $K_{\text{disp}}/\text{IC}_{50}$ (HTRF) = 2.5-5 μM



$K_D = \text{NA}$
No binding

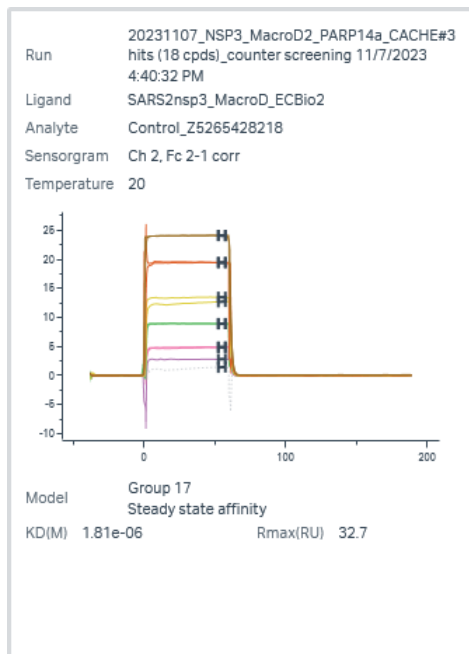
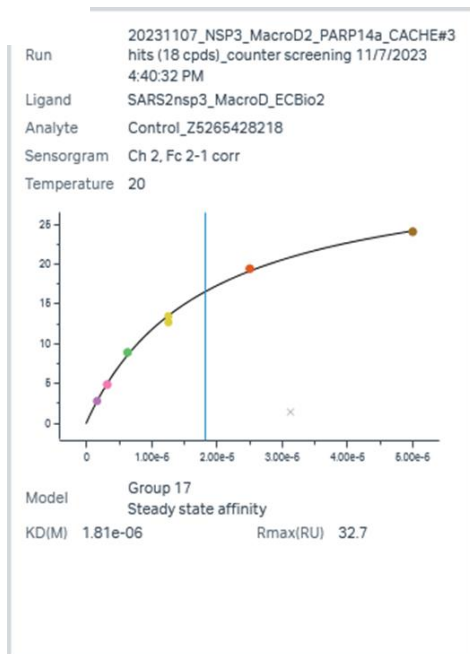
SPR QC data



published Ki: 1.5 μ M

NSP3_SARS2

Z5265428218



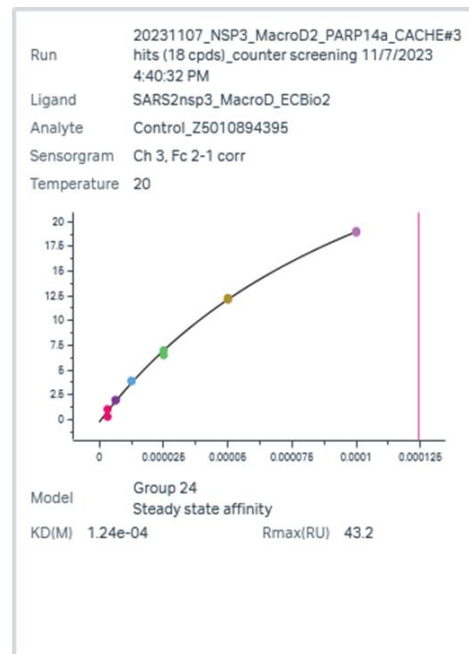
Binding = 125%

$K_D = 1.8 \mu$ M

K_{disp}/IC_{50} (HTRF) = 5.7 μ M

QC data (Additional Positive Controls)

Z5010894395

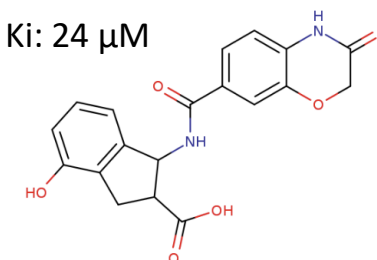


Binding = 130%

$K_D = 124 \mu$ M

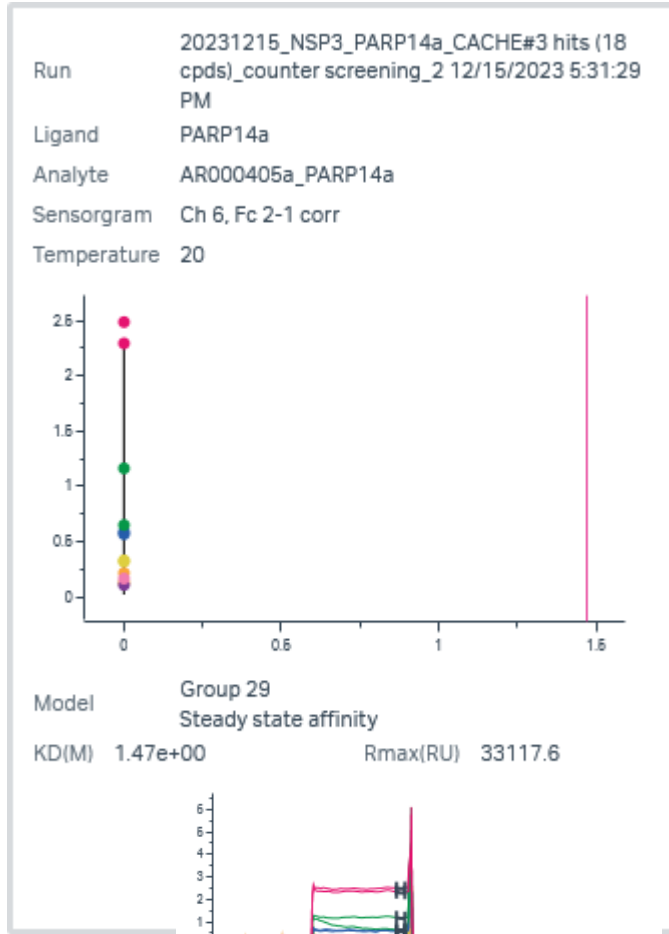
K_{disp}/IC_{50} (HTRF) = 240 μ M

published Ki: 24 μ M

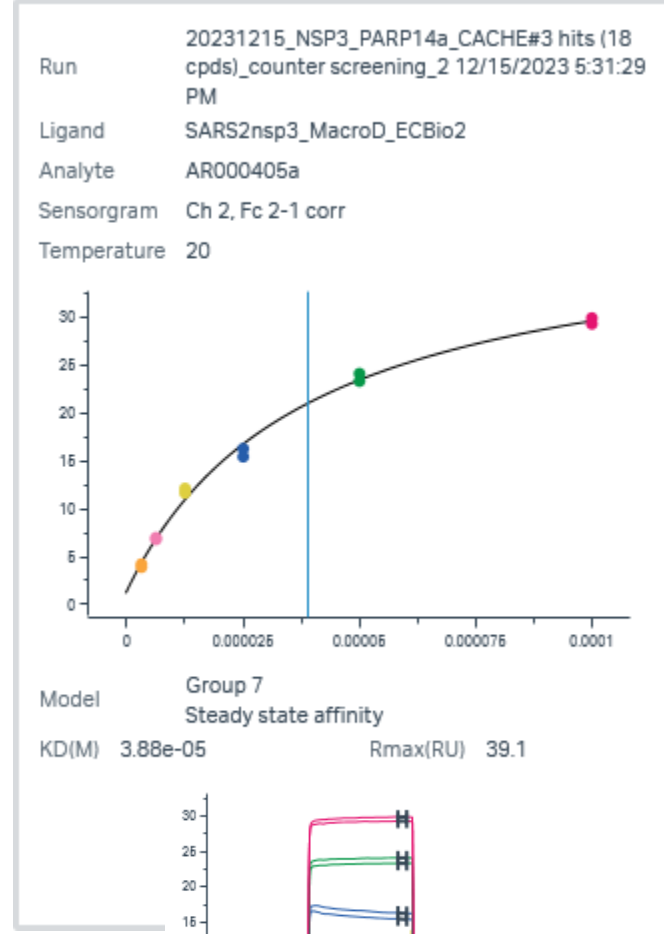


CACHE3HI_1690_45

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement results

confirmation:

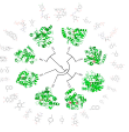
%inh@100 μ M = 60.1

%inh@50 μ M = 39.6

%inh@25 μ M = 27.6

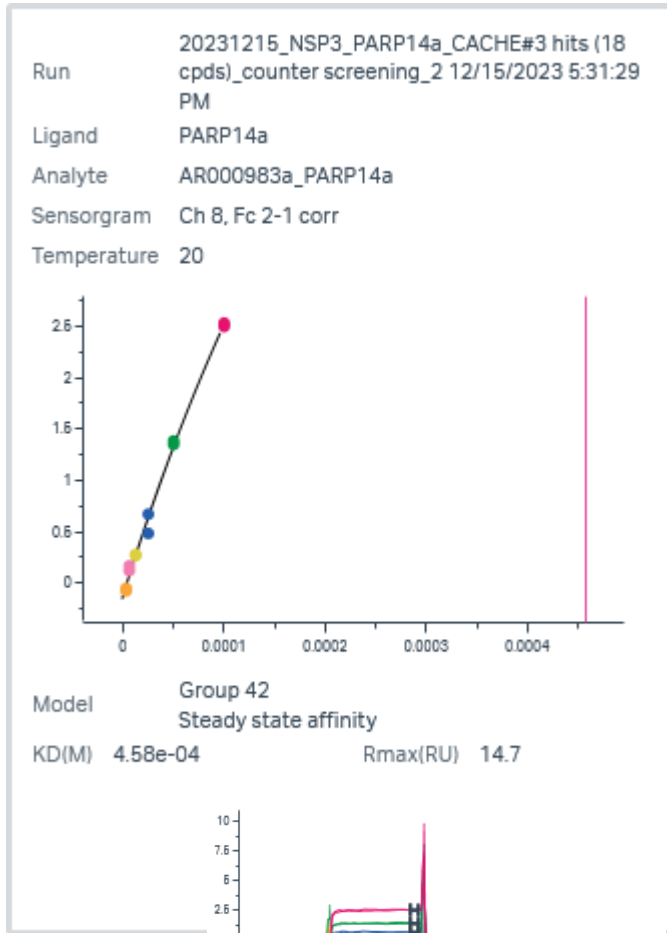
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μ M, n=2
NSP3_SARS2	39	35	111	38.8
PARP14a	1470774.4	29	NA	no binding

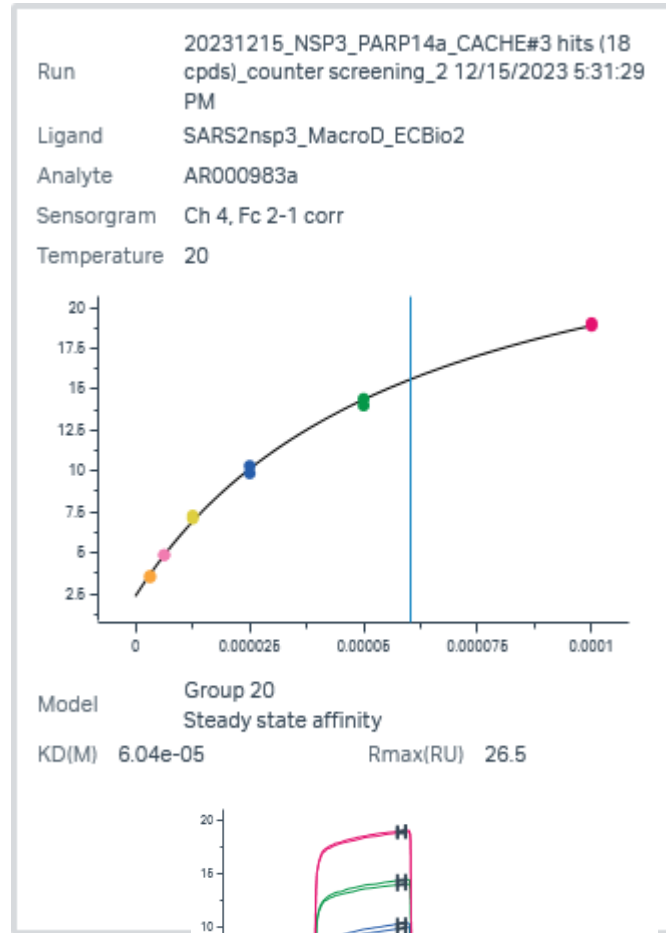


CACHE3HI_1690_48

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement results

confirmation:

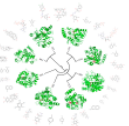
%inh@100 μ M = 46.5

%inh@50 μ M = 34.0

%inh@25 μ M = 18.4

SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μ M, n=2
NSP3_SARS2	27	30	87	60.4
PARP14a	14.7	28	53	no binding



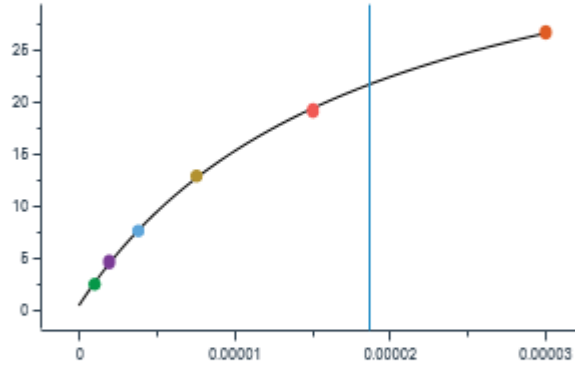
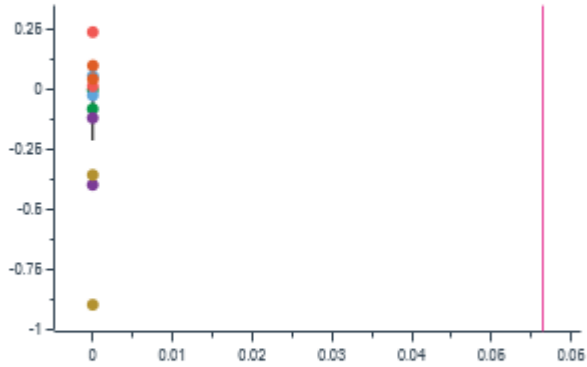
CACHE3HI_1690_63

PARP14a

NSP3_SARS2

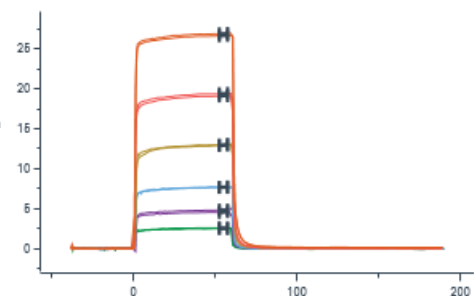
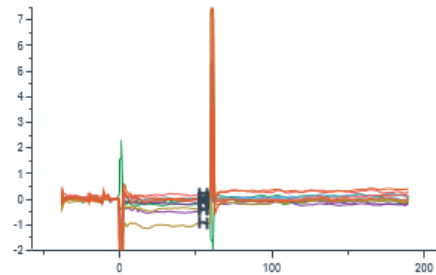
Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand PARP14a
 Analyte AR000761a_PARP14a
 Sensorgram Ch 7, Fc 2-1 corr
 Temperature 20

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand SARS2nsp3_MacroD_ECBio2
 Analyte AR000761a
 Sensorgram Ch 3, Fc 2-1 corr
 Temperature 20



Model Group 36
 Steady state affinity
 KD(M) 5.66e-02 Rmax(RU) 534.2

Model Group 14
 Steady state affinity
 KD(M) 1.87e-05 Rmax(RU) 42.2



Previous data:

HTRF displacement results

confirmation:

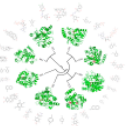
%inh@100 μM = 86.9

%inh@50 μM = 42.5

%inh@25 μM = 20.2

SPR confirmation/selectivity test

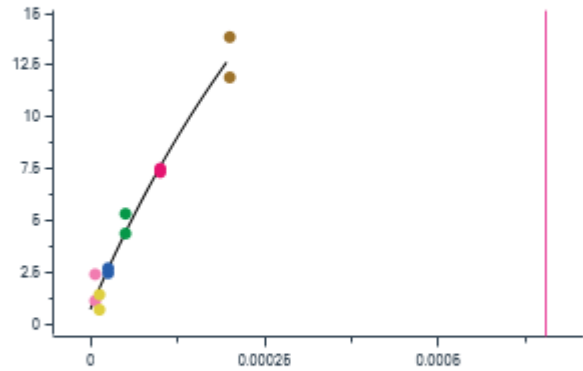
Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	42	43	98	18.7
PARP14a	534.2	37	NA	no binding



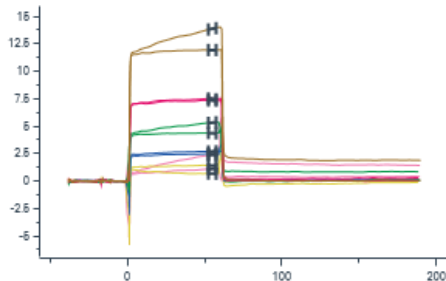
CACHE3HI_1690_87

PARP14a

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand PARP14a
 Analyte AR001560a_PARP14a
 Sensorgram Ch 8, Fc 2-1 corr
 Temperature 20

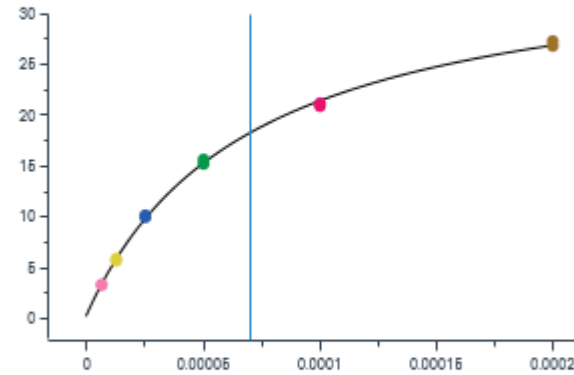


Model Group 44
 Steady state affinity
 KD(M) 6.56e-04 Rmax(RU) 51.8

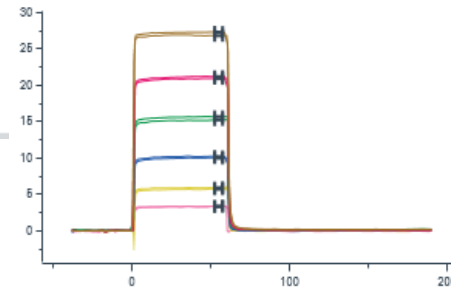


NSP3_SARS2

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand SARS2nsp3_MacroD_ECBio2
 Analyte AR001560a
 Sensorgram Ch 4, Fc 2-1 corr
 Temperature 20



Model Group 22
 Steady state affinity
 KD(M) 7.03e-05 Rmax(RU) 35.7



Previous data:

HTRF displacement results

confirmation:

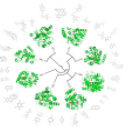
%inh@100 μM = 47.6

%inh@50 μM = 35.6

%inh@25 μM = 20.4

SPR confirmation/selectivity test

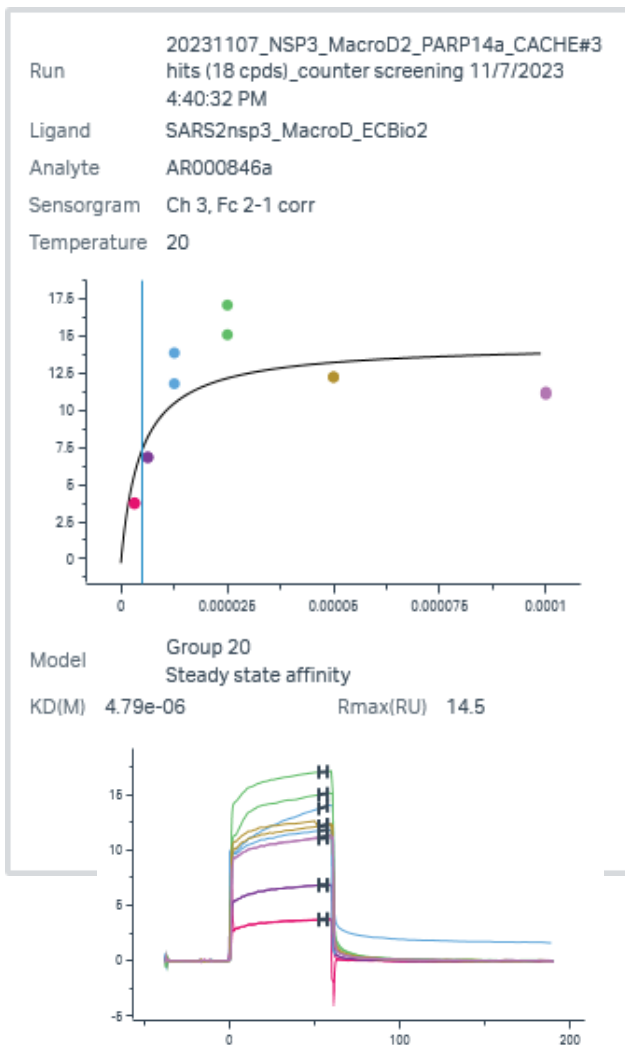
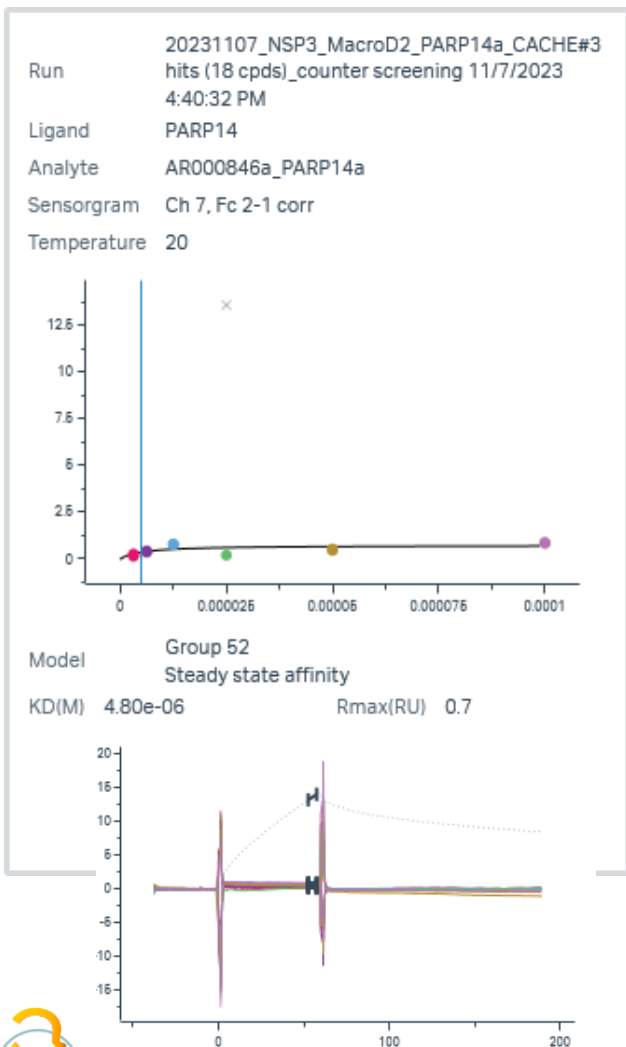
Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μM, n=2
NSP3_SARS2	36	34	105	70
PARP14a	52	31	167	Linear



CACHE3HI_1690_36

PARP14a

NSP3_SARS2



Previous data:

HTRF displacement hit

confirmation:

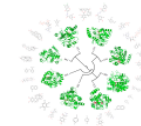
%inh@100 uM = 83

%inh@50 uM = 78

%inh@25 uM = 67

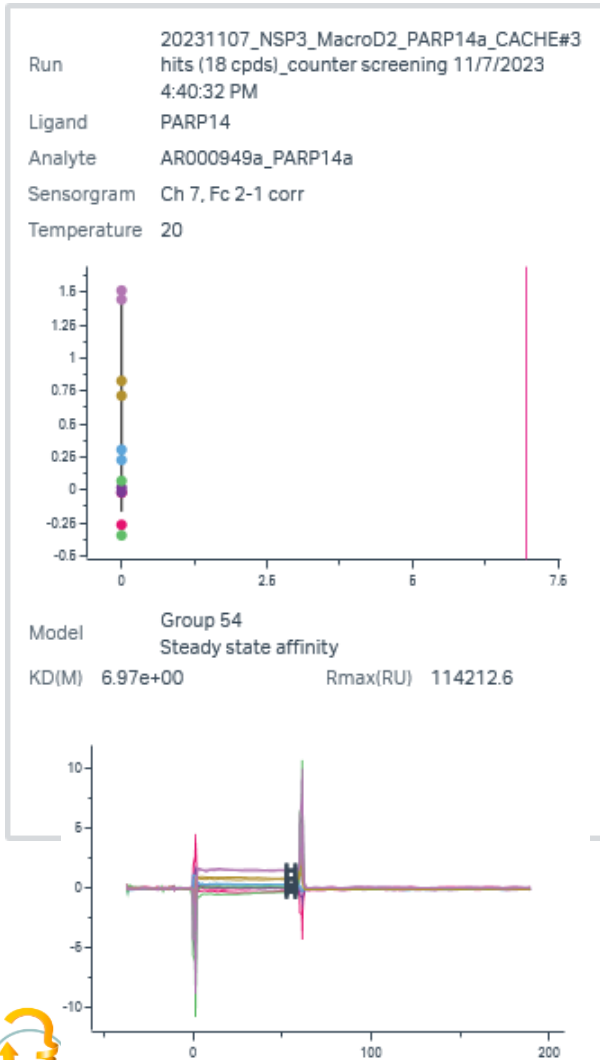
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	14.5	31.0	47	48
PARP14a	0.7	24.5	3.0	NB

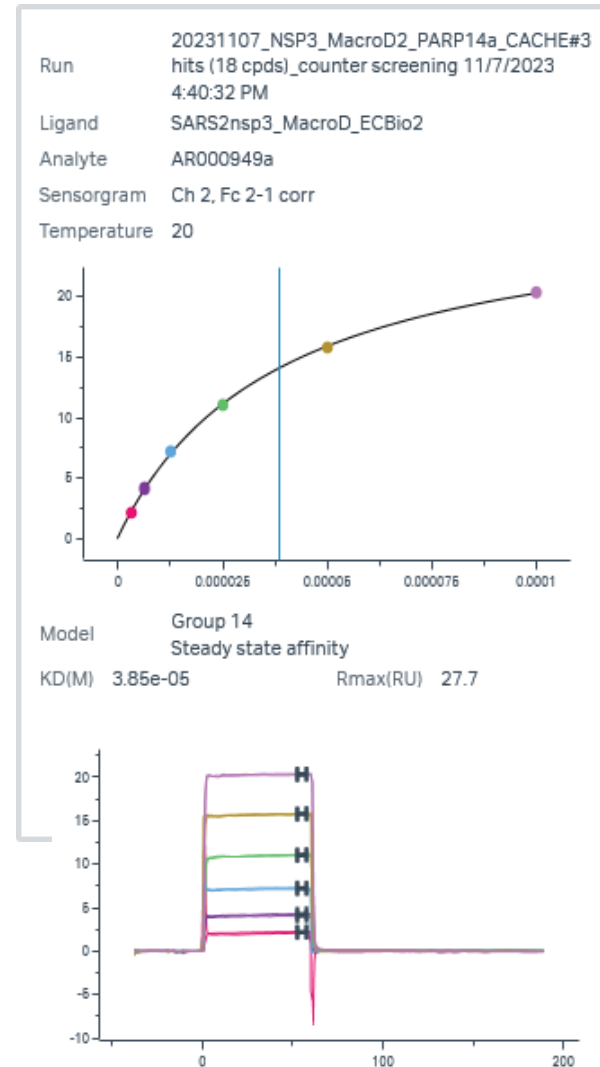


CACHE3HI_1690_92

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement hit
confirmation:

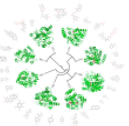
%inh@100 uM = 67

%inh@50 uM = 50

%inh@25 uM = 29

SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	27.7	23.9	116	38.5
PARP14a	114212.6	18.5	NA	NB

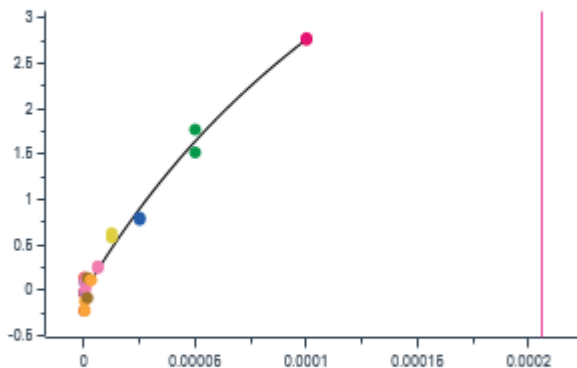


CACHE3HI_1696_50

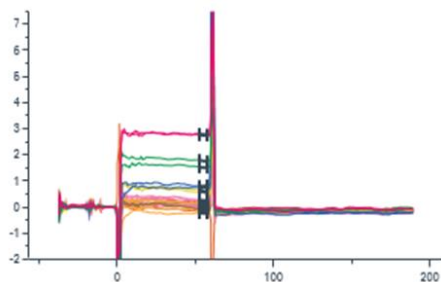
PARP14a

NSP3_SARS2

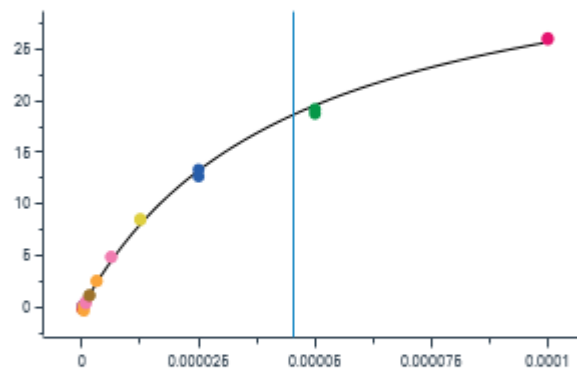
Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand PARP14a
 Analyte AR000657a_PARP14a
 Sensorgram Ch 8, Fc 2-1 corr
 Temperature 20



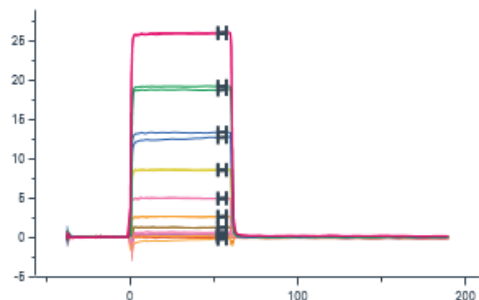
Model Group 40
 Steady state affinity
 KD(M) 2.06e-04 Rmax(RU) 8.5



Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand SARS2nsp3_MacroD_ECBio2
 Analyte AR000657a
 Sensorgram Ch 4, Fc 2-1 corr
 Temperature 20



Model Group 18
 Steady state affinity
 KD(M) 4.53e-05 Rmax(RU) 37.2



Previous data:

HTRF displacement results

confirmation:

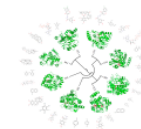
%inh@100 μM = 56.5

%inh@50 μM = 40.0

%inh@25 μM = 25.7

SPR confirmation/selectivity test

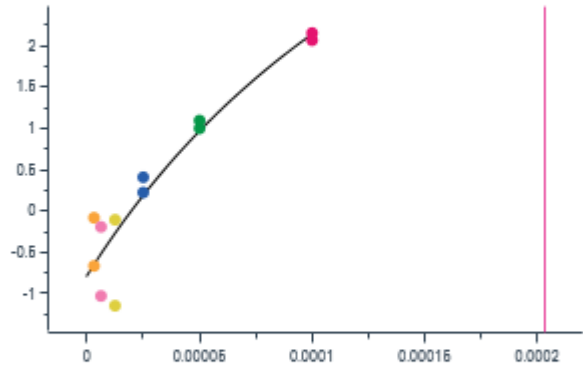
Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	37	36	104	45
PARP14a	8.5	33	26	no binding



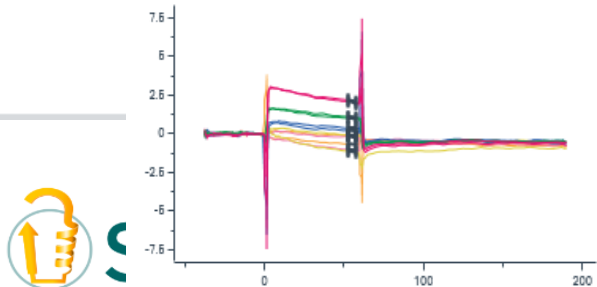
CACHE3HI_1696_6

PARP14a

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand PARP14a
 Analyte AR000475a_PARP14a
 Sensorgram Ch 7, Fc 2-1 corr
 Temperature 20

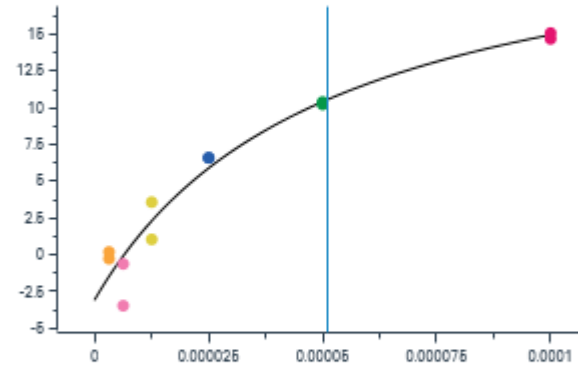


Model Group 35
 Steady state affinity
 KD(M) 2.04e-04 Rmax(RU) 8.9

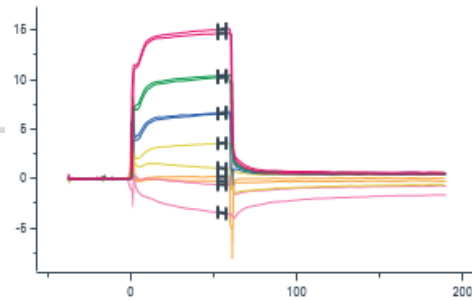


NSP3_SARS2

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand SARS2nsp3_MacroD_ECBio2
 Analyte AR000475a
 Sensorgram Ch 3, Fc 2-1 corr
 Temperature 20



Model Group 13
 Steady state affinity
 KD(M) 5.10e-05 Rmax(RU) 27.2



Previous data:

HTRF displacement results

confirmation:

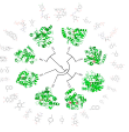
%inh@100 μM = 44.6

%inh@50 μM = 25.0

%inh@25 μM = 10.3

SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μM, n=2
NSP3_SARS2	27	37	73	51
PARP14a	9	32	28	no binding

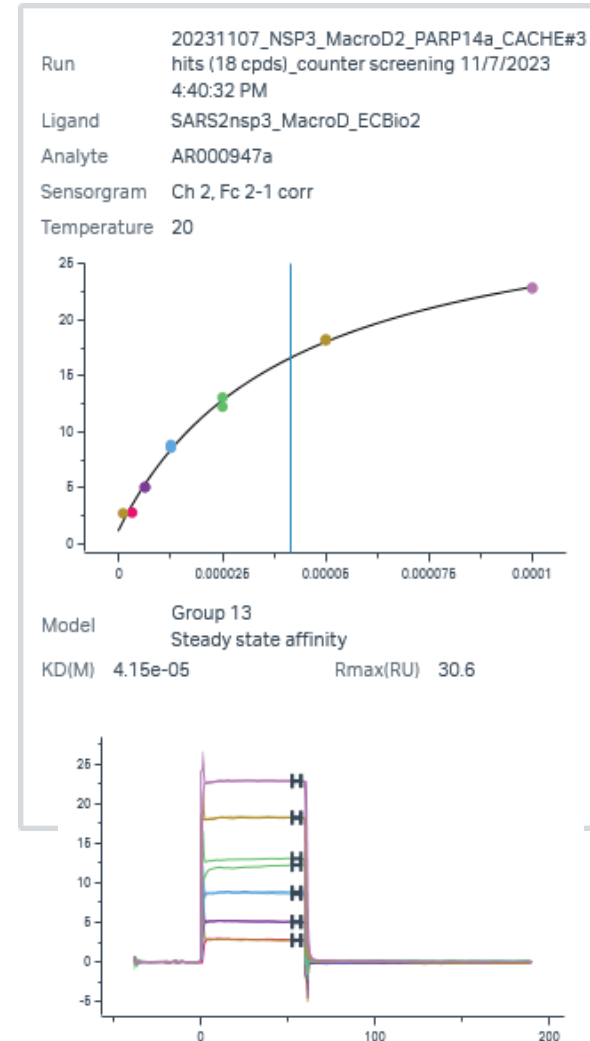
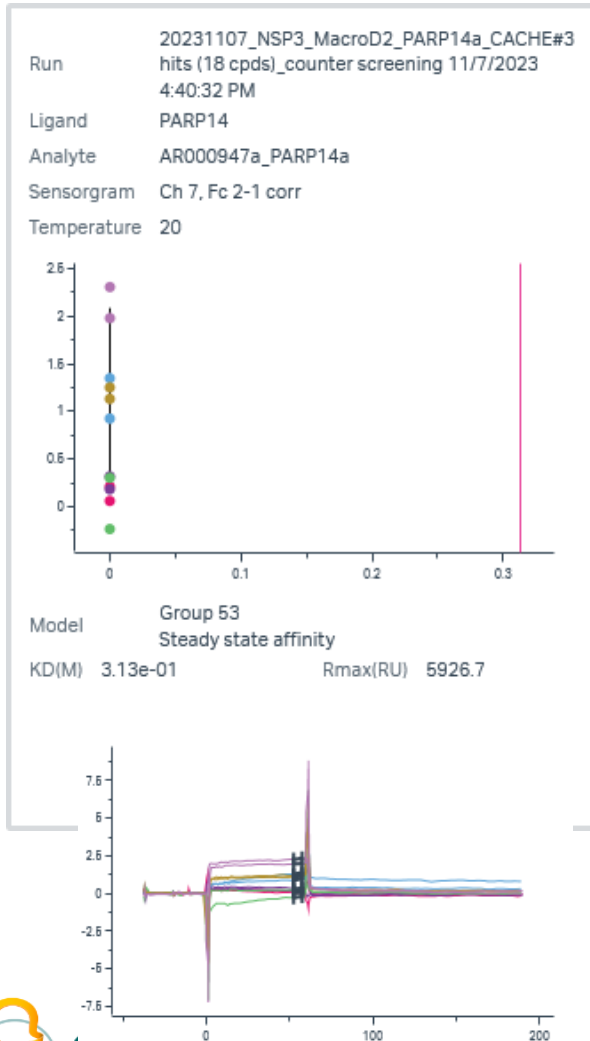


CACHE3HI_1696_67

PARP14a

4% DMSO

NSP3_SARS2



Previous data:

HTRF displacement hit
confirmation:

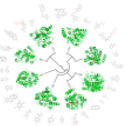
%inh@100 uM = 56

%inh@50 uM = 40

%inh@25 uM = 26

SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	30.6	29.7	103	41.5
PARP14a	5926.7	23	NA	NB

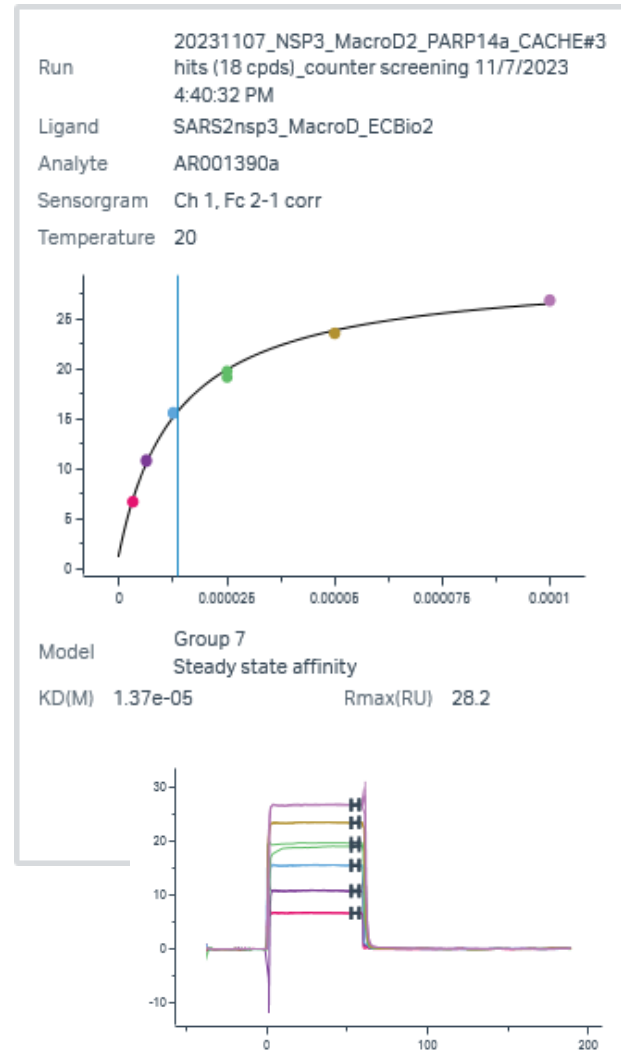
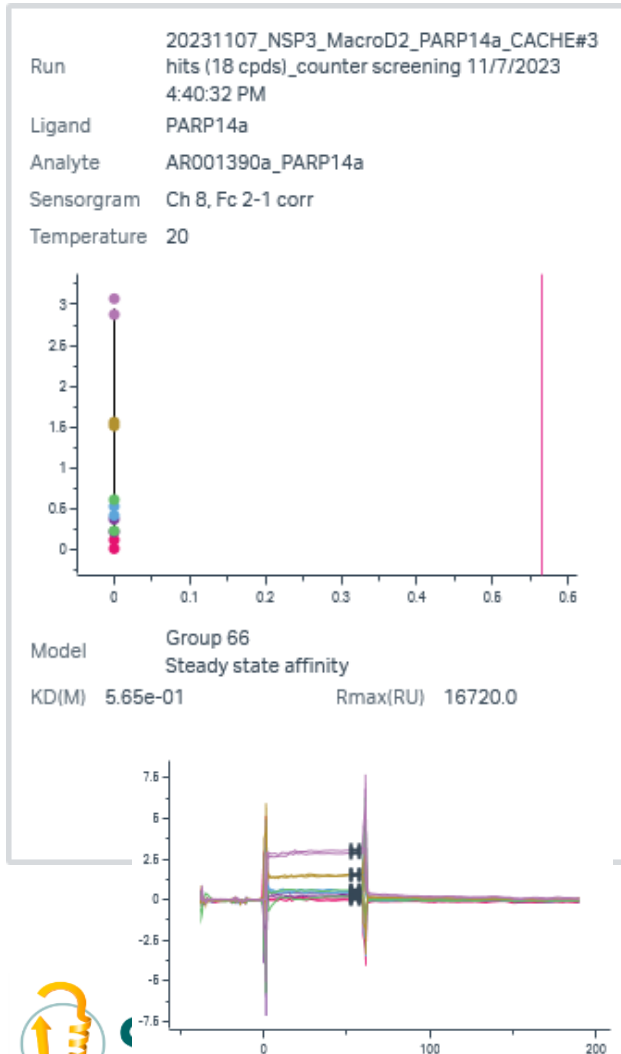


CACHE3HI_1696_78

PARP14a

4% DMSO

NSP3_SARS2



Previous data:

HTRF displacement hit
confirmation:

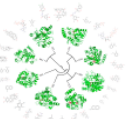
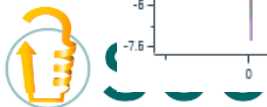
%inh@100 uM = 78

%inh@50 uM = 66

%inh@25 uM = 48

SPR confirmation/selectivity test

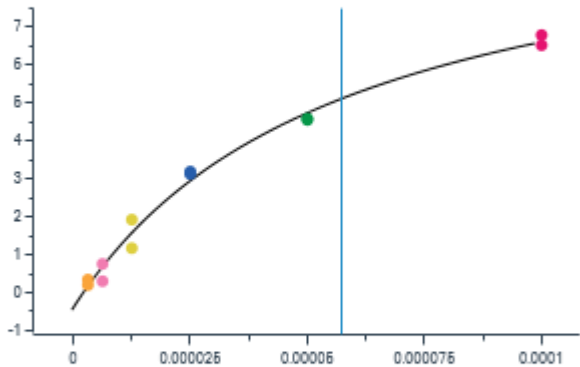
Protein	RUmax_ experime nt	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	28.2	34	83	13.7
PARP14a	16720.0	25.6	NA	NB



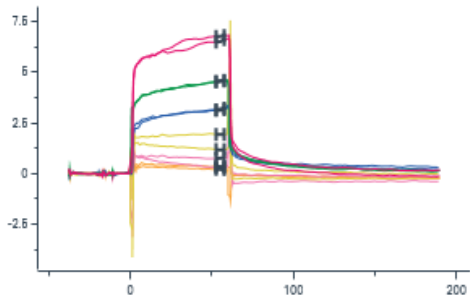
CACHE3HI_1700_52

PARP14a

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand PARP14a
 Analyte AR000861a_PARP14a
 Sensorgram Ch 6, Fc 2-1 corr
 Temperature 20

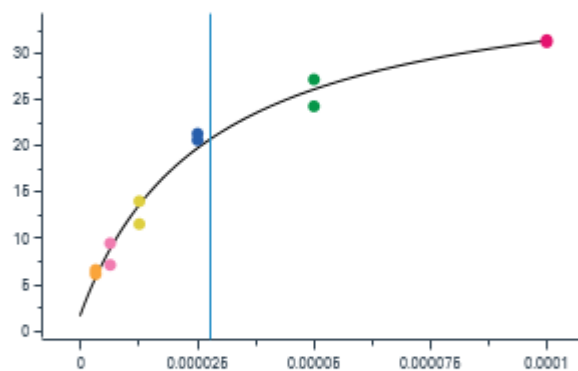


Model Group 30
 Steady state affinity
 KD(M) 5.73e-05 Rmax(RU) 11.0

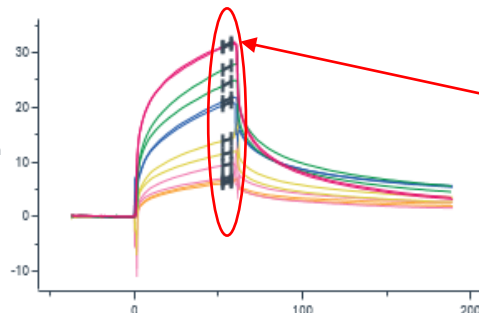


NSP3_SARS2

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand SARS2nsp3_MacroD_ECBio2
 Analyte AR000861a
 Sensorgram Ch 2, Fc 2-1 corr
 Temperature 20



Model Group 8
 Steady state affinity
 KD(M) 2.78e-05 Rmax(RU) 37.6



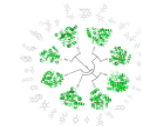
Previous data:

HTRF displacement
results confirmation:
%inh@100 μM = 81.1
%inh@50 μM = 69.0
%inh@25 μM = 31.7

SPR confirmation/selectivity test

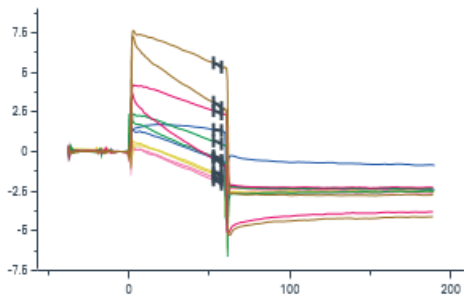
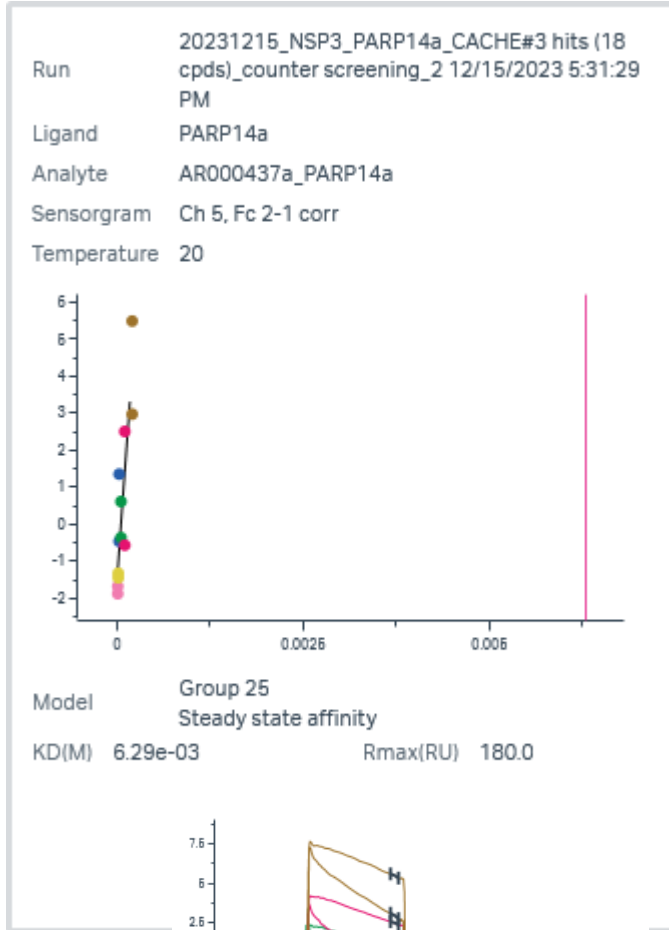
Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μM, n=2
NSP3_SARS2	38	40	94	28
PARP14a	11	32	34	57

Estimated K_D is not reliable, binding profile does not show steady state

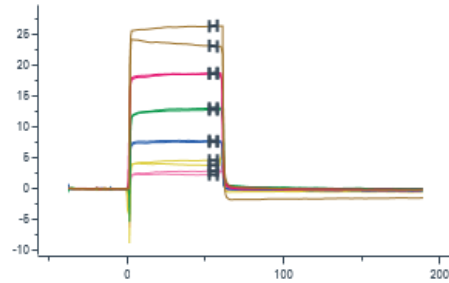
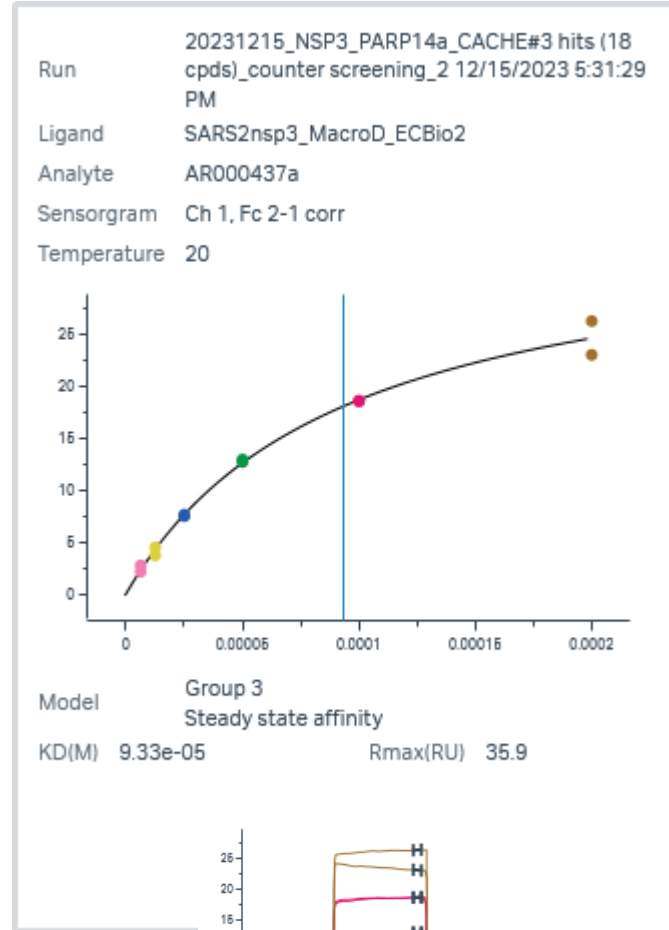


CACHE3HI_1705_4

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement results

confirmation:

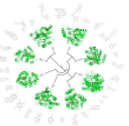
%inh@100 μ M = 37.5

%inh@50 μ M = 20.3

%inh@25 μ M = 9.9

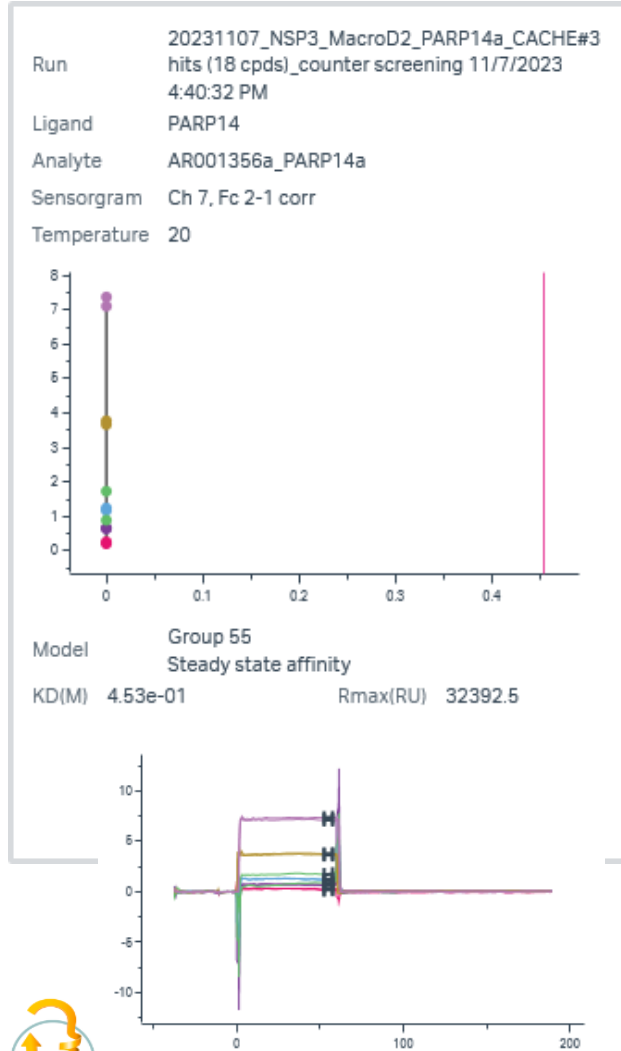
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μ M, n=2
NSP3_SARS2	36	33	109	93
PARP14a	180	29	NA	weak binding

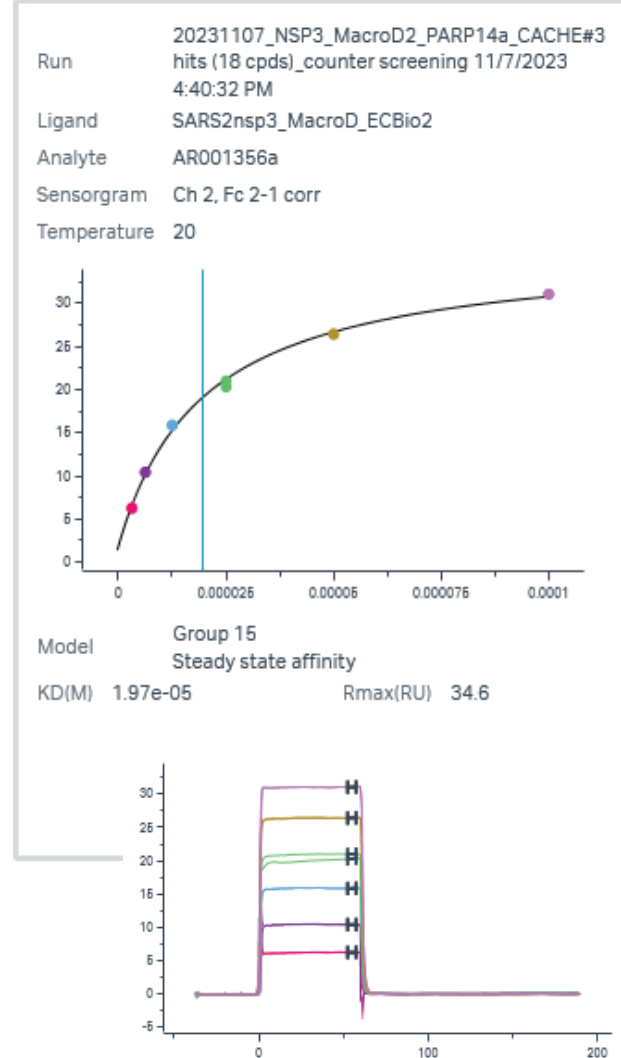


CACHE3HI_1706_56

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement hit confirmation:

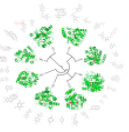
%inh@100 uM = 84

%inh@50 uM = 72

%inh@25 uM = 54

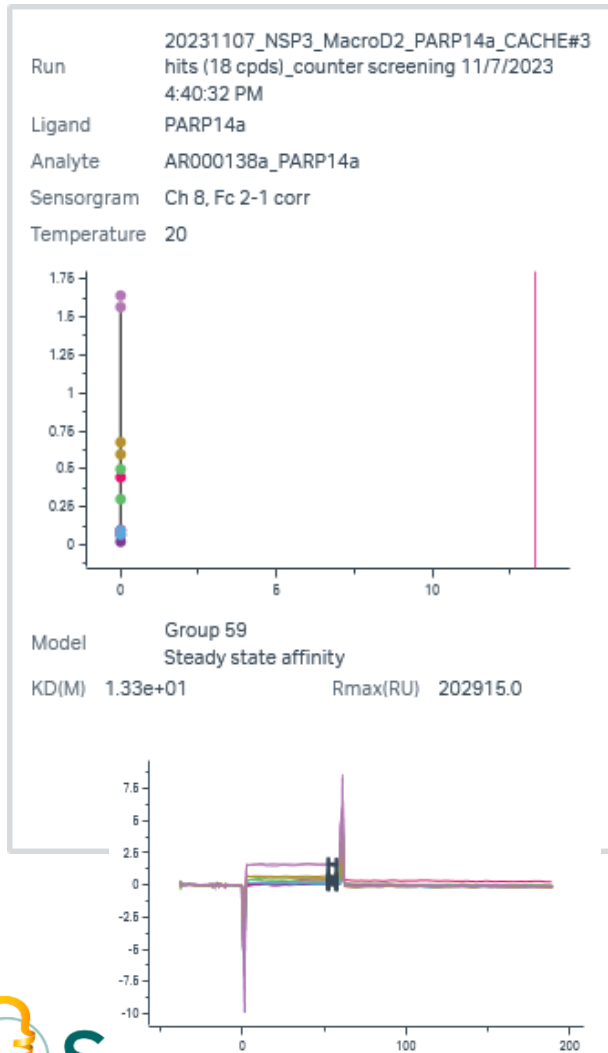
SPR confirmation/selectivity test

Protein	RUmax_experimnt	RUmax_expected	% binding	K _D _μM, n=2
NSP3_SARS2	34.6	39.1	89	19.7
PARP14a	32392.5	23.9	NA	Weak

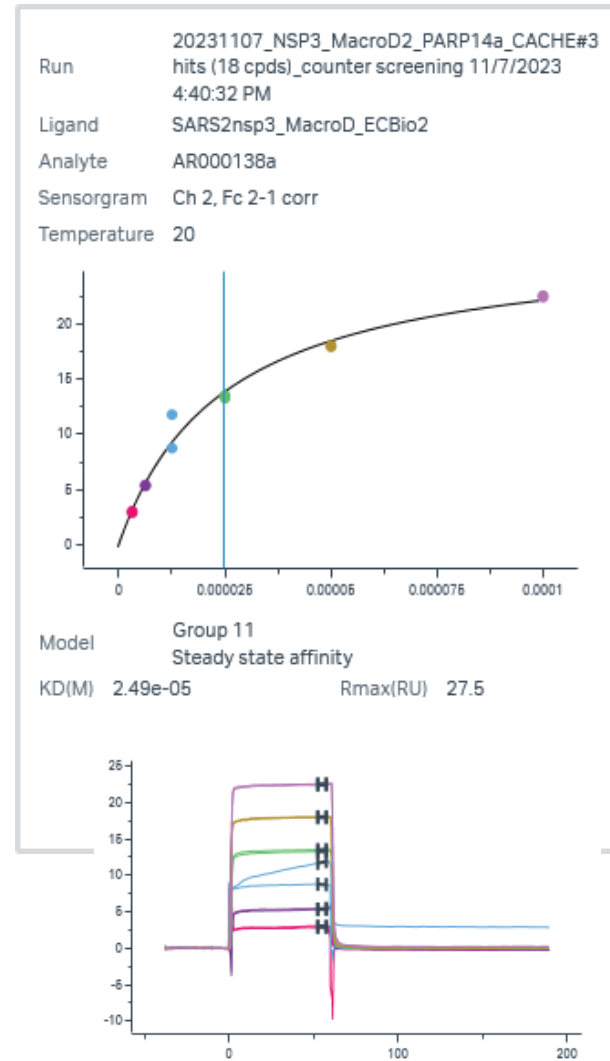


CACHE3HI_1708_42

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement hit
confirmation:

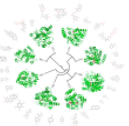
%inh@100 uM = 66

%inh@50 uM = 46

%inh@25 uM = 34

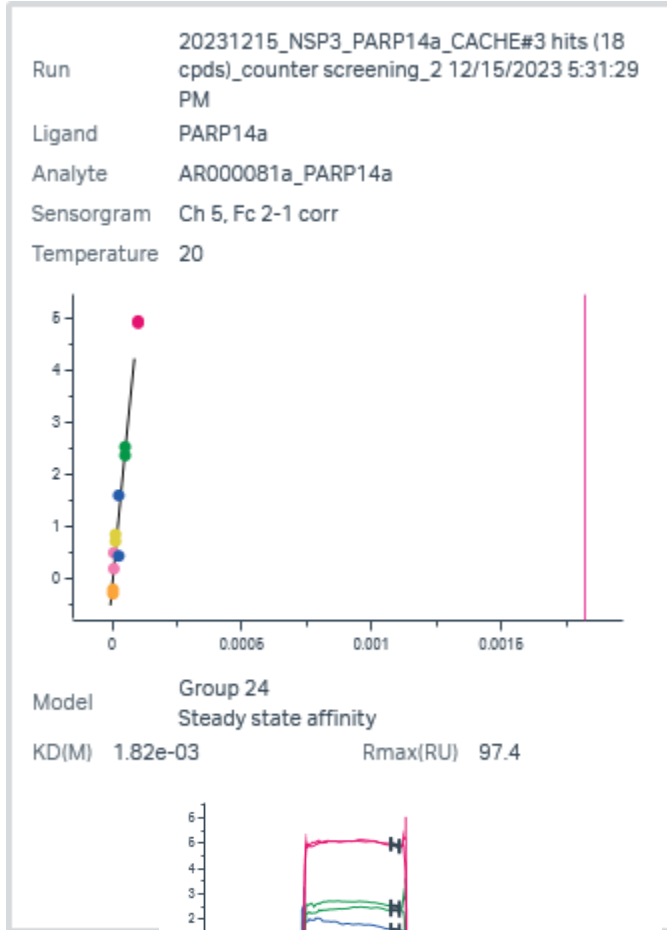
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	27.5	24.1	114	25
PARP14a	202915.0	19	NA	NB

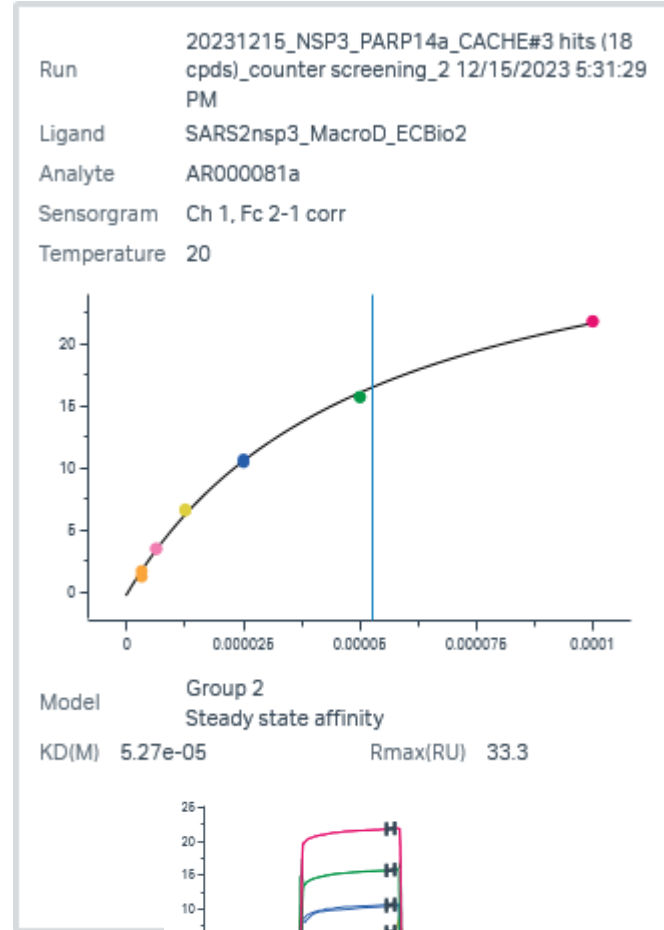


CACHE3HI_1708_87

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement results

confirmation:

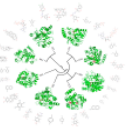
%inh@100 μ M = 51.6

%inh@50 μ M = 38.2

%inh@25 μ M = 20.3

SPR confirmation/selectivity test

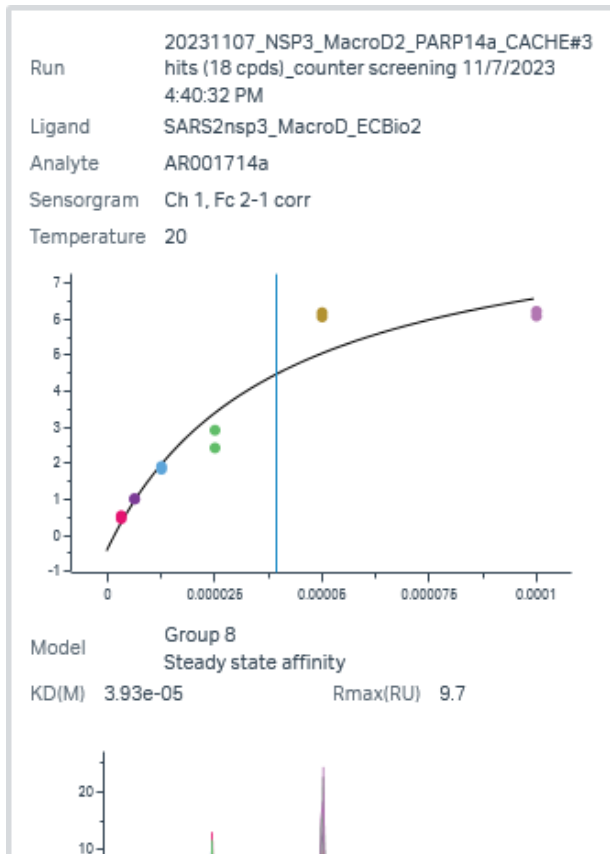
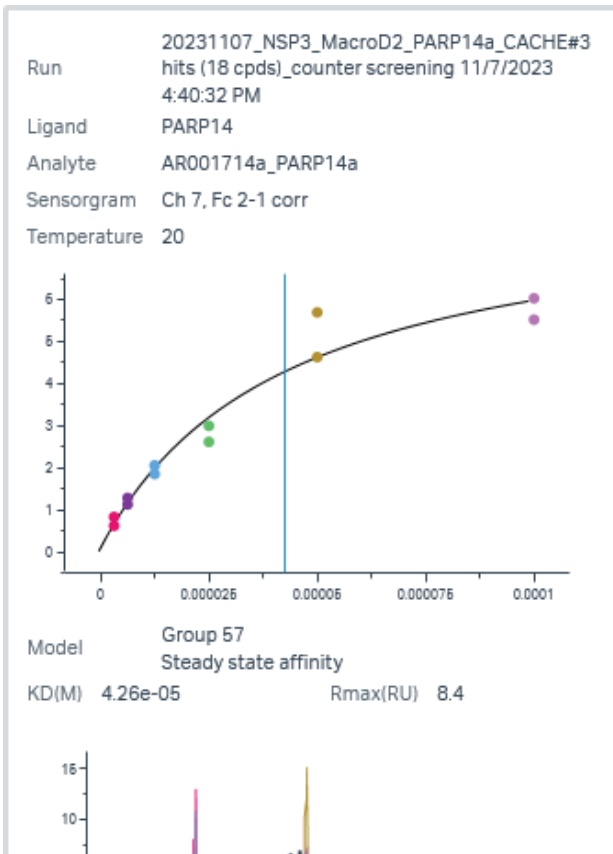
Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μ M, n=2
NSP3_SARS2	33	32	106	53
PARP14a	1819.9	28	NA	weak binding



CACHE3HI_1714_34

PARP14a

NSP3_SARS2



Previous data:

HTRF displacement hit
confirmation:

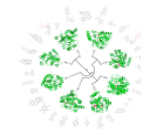
%inh@100 uM = 40

%inh@50 uM = 15

%inh@25 uM = 1

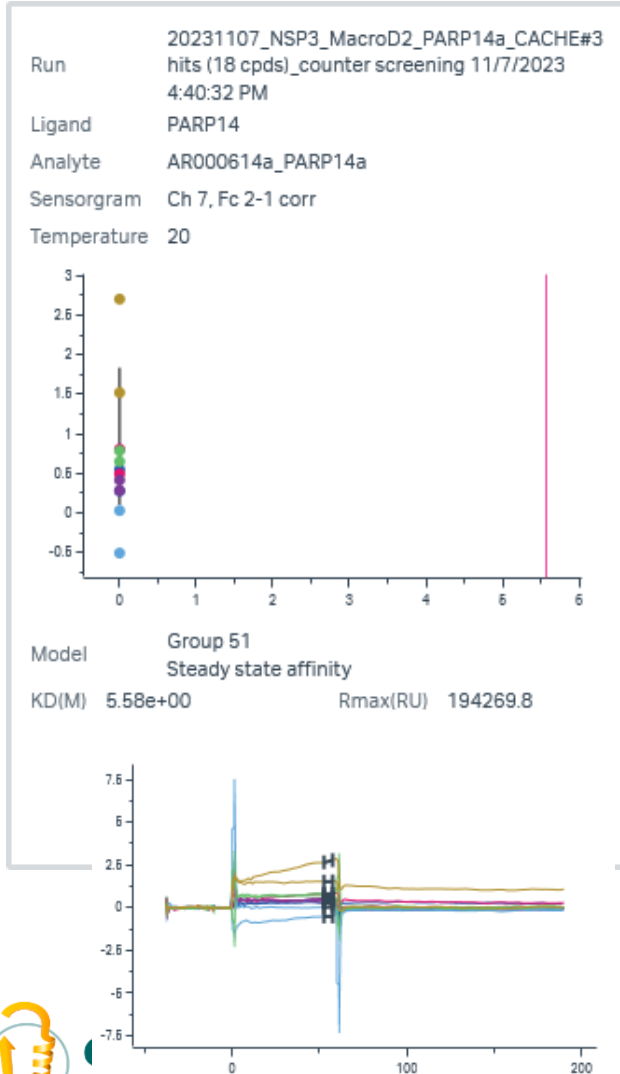
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	9.7	37.7	25.6	39.3
PARP14a	8.4	30.8	27.2	43

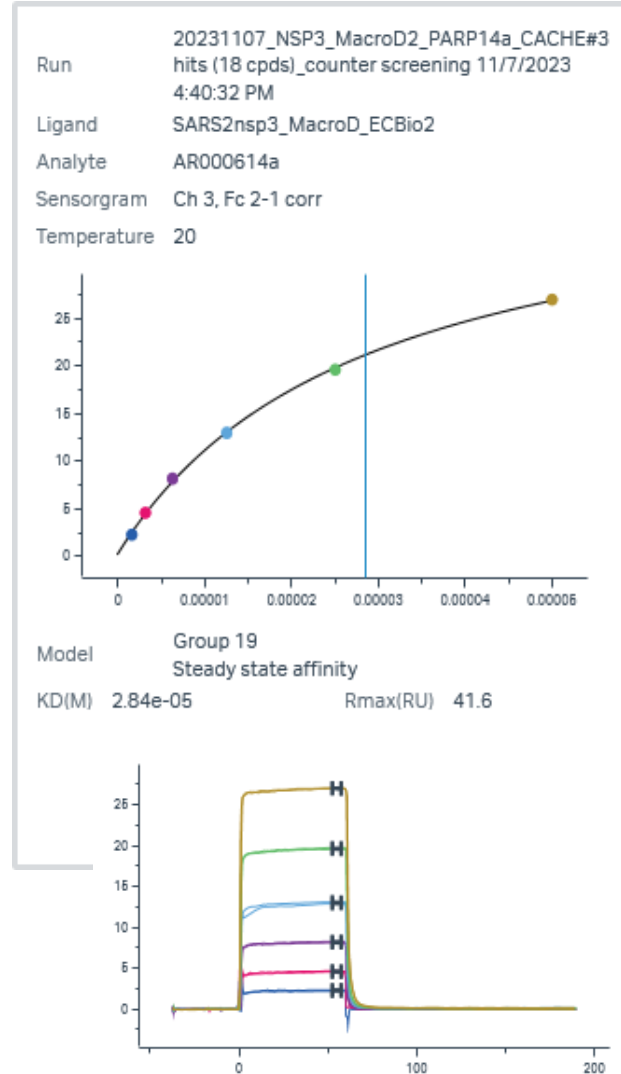


CACHE3HI_1715_71

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement hit

confirmation:

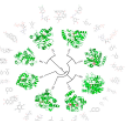
%inh@100 uM = 66

%inh@50 uM = 93

%inh@25 uM = 23

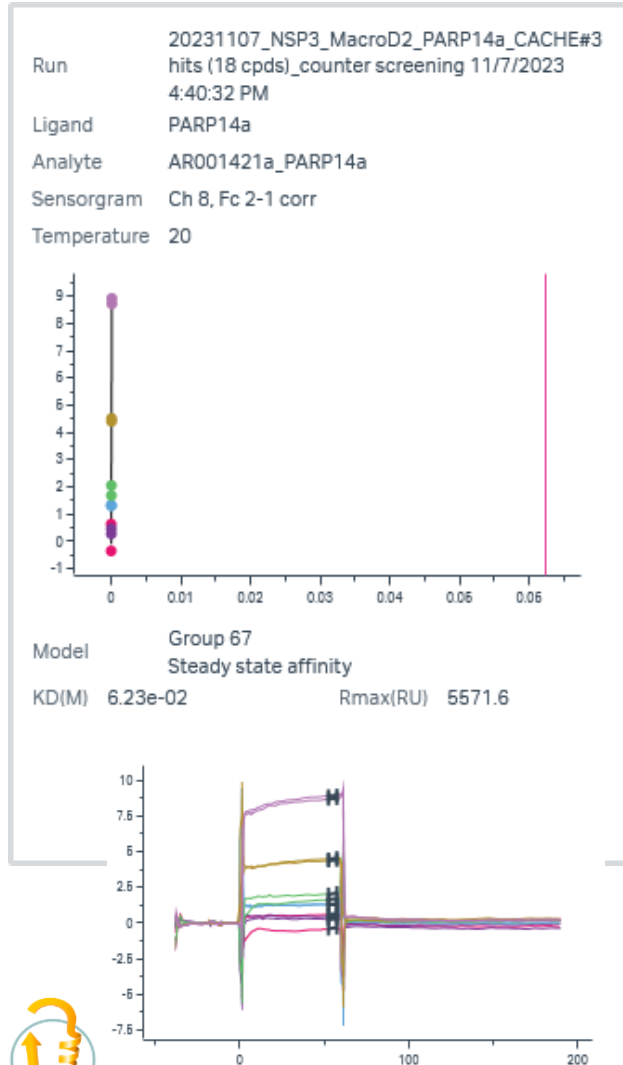
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	41.6	32.6	127.5	28.4
PARP14a	194269.8	25.8	NA	NB

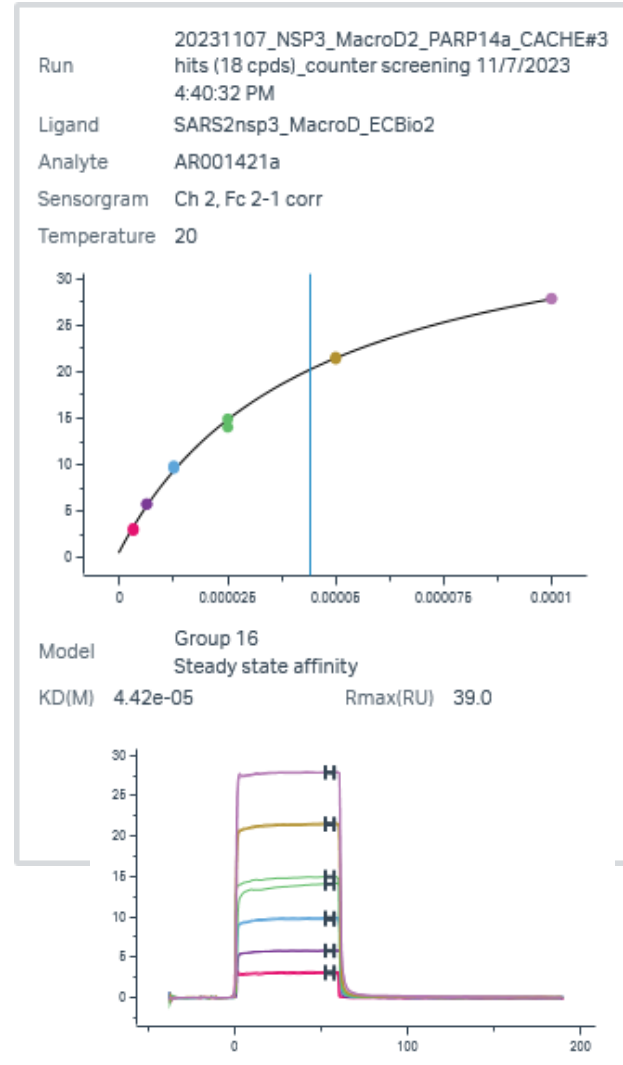


CACHE3HI_1715_85

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement hit

confirmation:

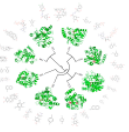
%inh@100 uM = 67

%inh@50 uM = 47

%inh@25 uM = 32

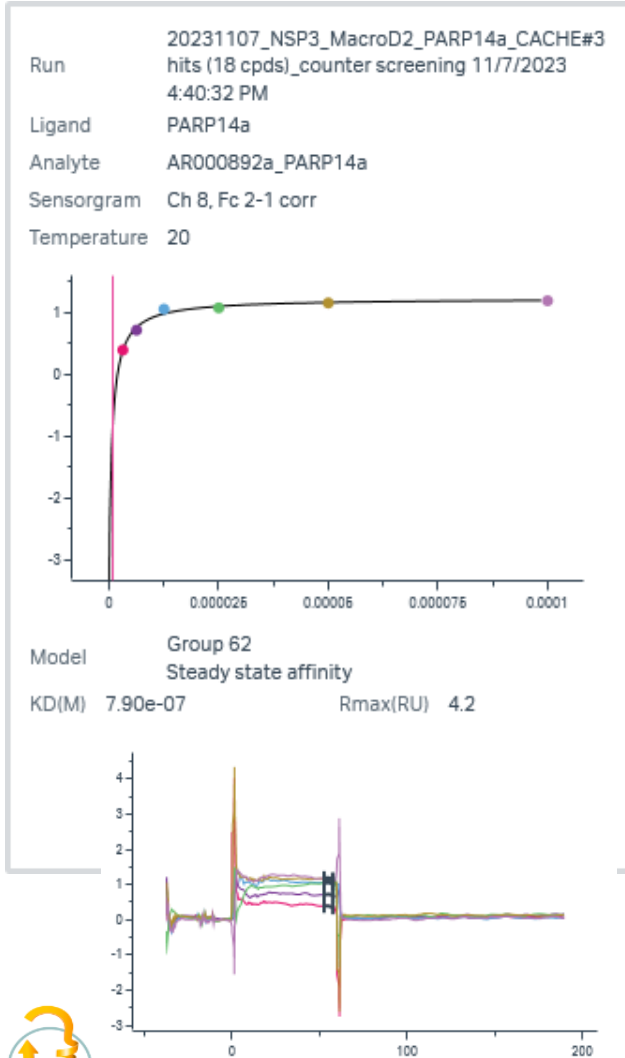
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	39.0	31.3	124.4	44
PARP14a	5571.6	24.7	NA	weak

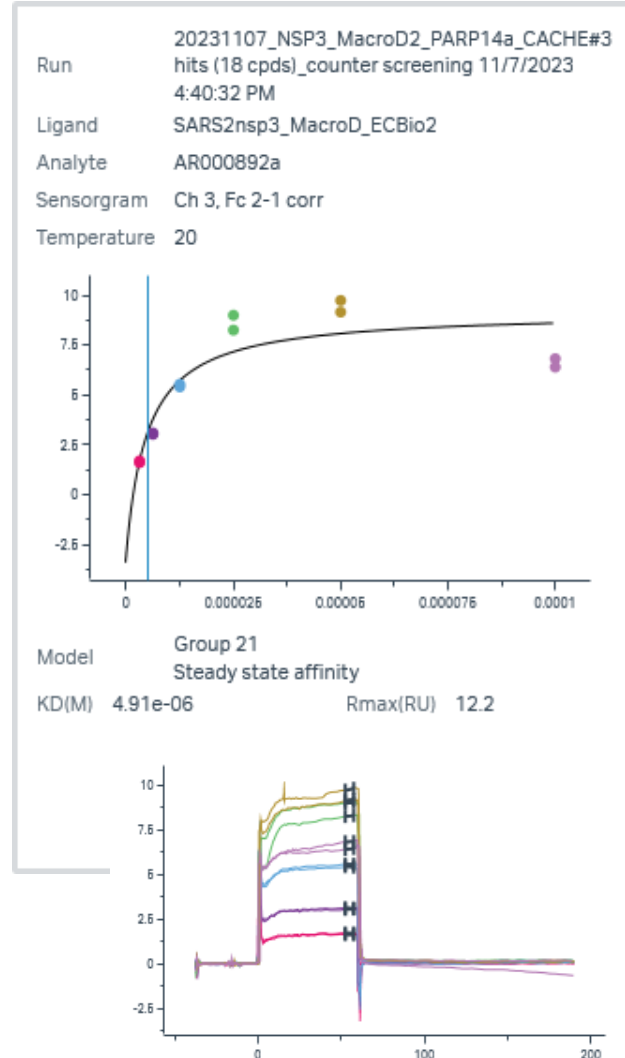


CACHE3HI_1715_88

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement hit
confirmation:

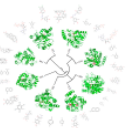
%inh@100 uM = 80

%inh@50 uM = 65

%inh@25 uM = 22

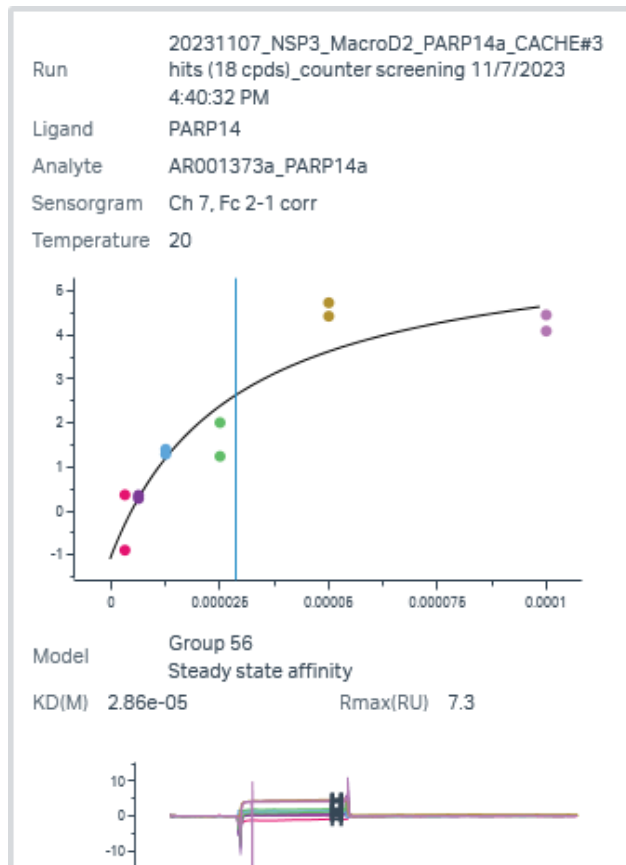
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	12.2	35.3	34.6	49
PARP14a	1.3	22.7	5.7	NB

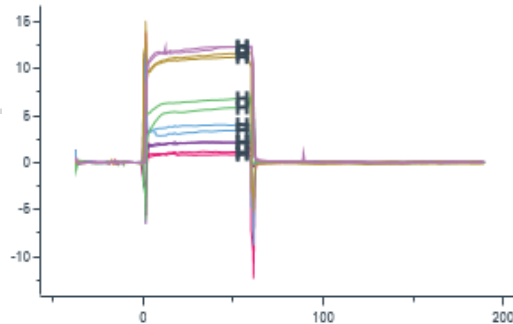
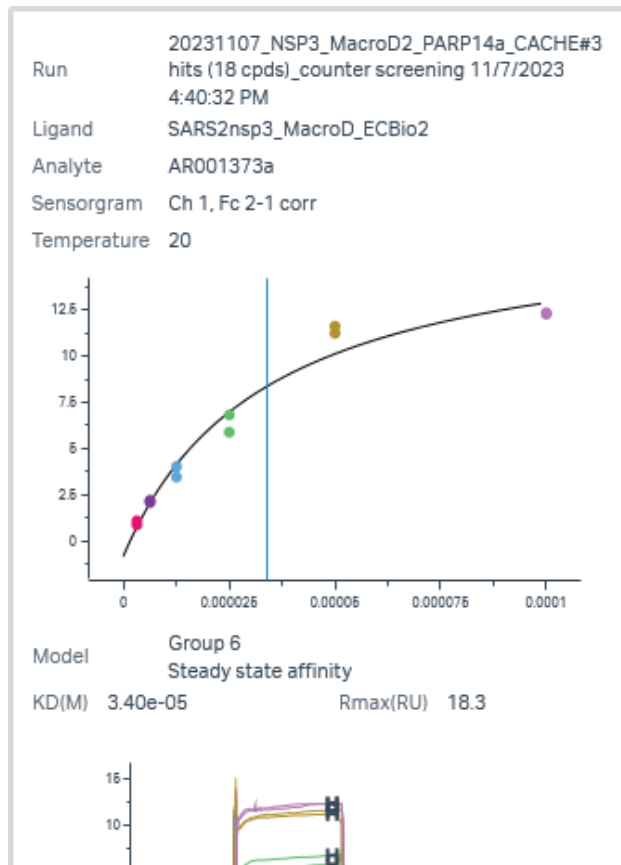


CACHE3HI_1715_92

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement hit confirmation:

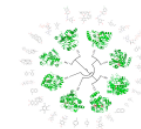
%inh@100 uM = 47

%inh@50 uM = 27

%inh@25 uM = 16

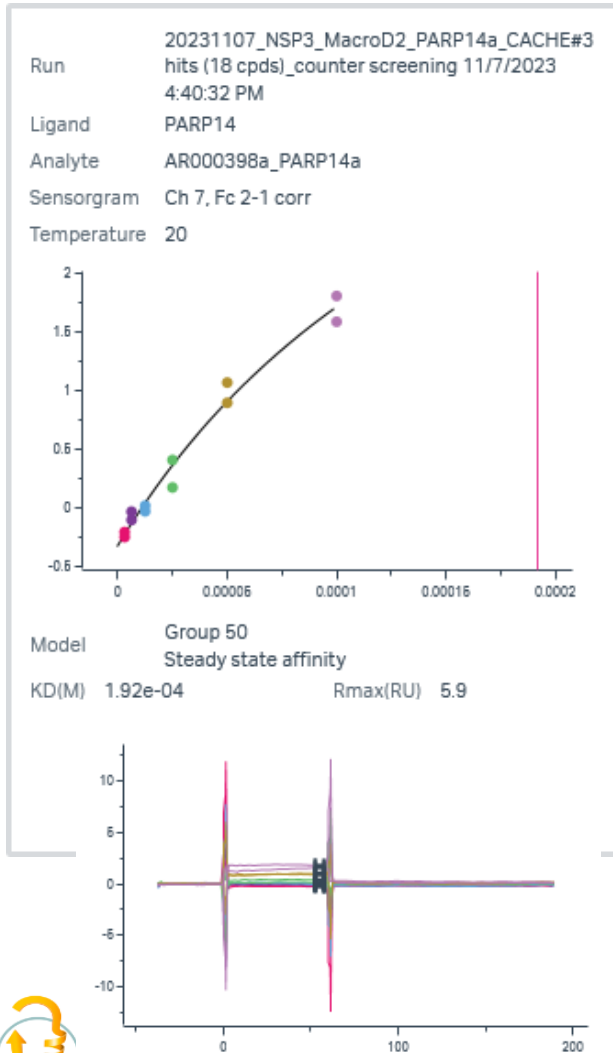
SPR confirmation/selectivity test

Protein	RUmax_experimnt	RUmax_expected	% binding	K _D _μM, n=2
NSP3_SARS2	28.5	18.3	64	34
PARP14a	7.3	23	31	29

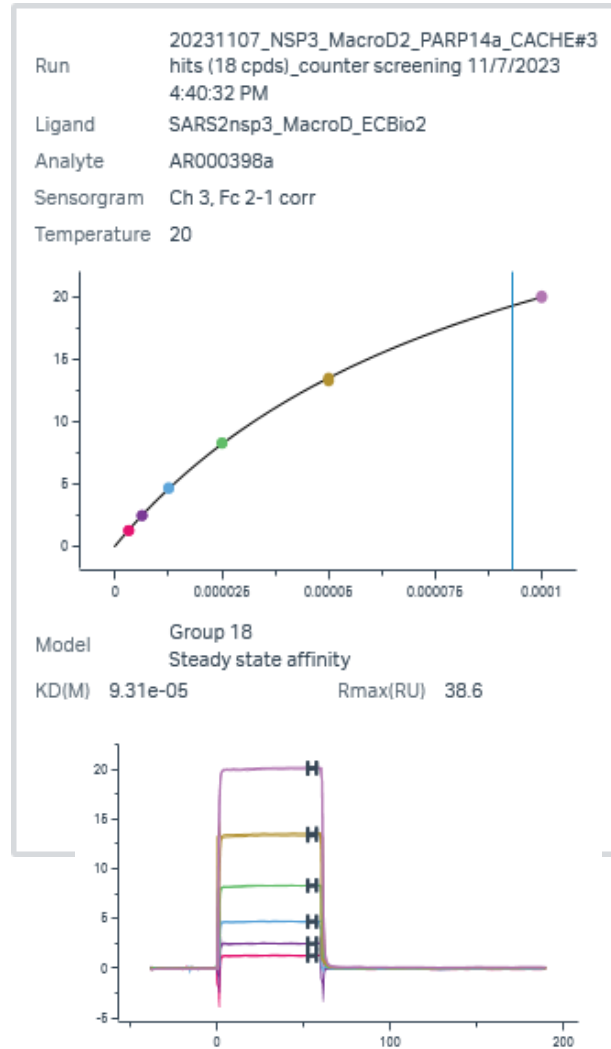


CACHE3HI_1715_95

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement hit
confirmation:

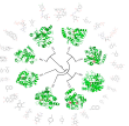
%inh@100 uM = 35

%inh@50 uM = 21

%inh@25 uM = 11

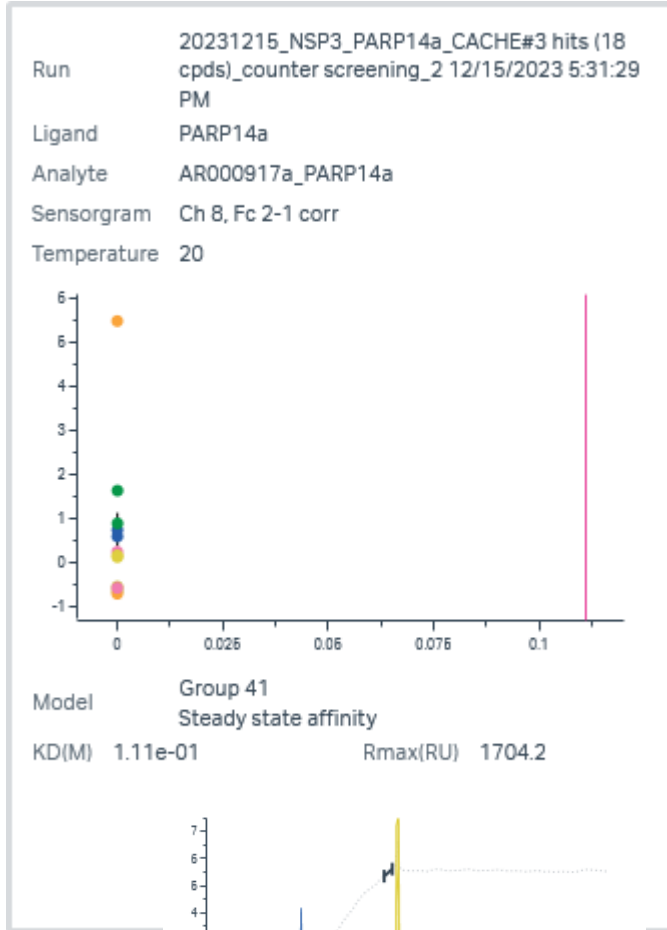
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	38.6	29.8	129.4	93
PARP14a	5.9	23.6	25.2	NB

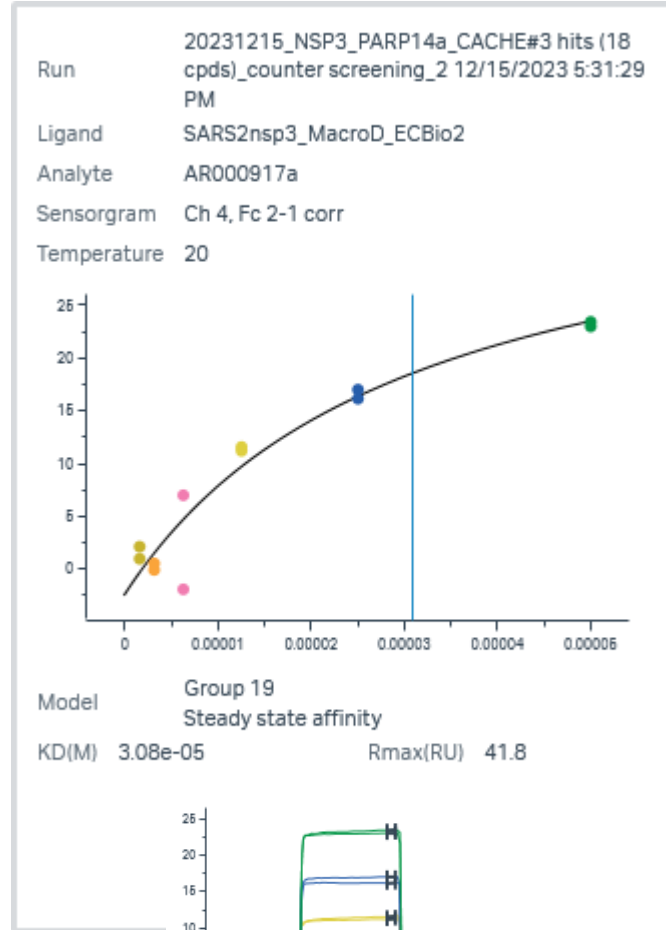


CACHE3HI_1715_91

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement results

confirmation:

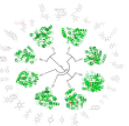
%inh@100 μM = 56.8

%inh@50 μM = 40.2

%inh@25 μM = 23.2

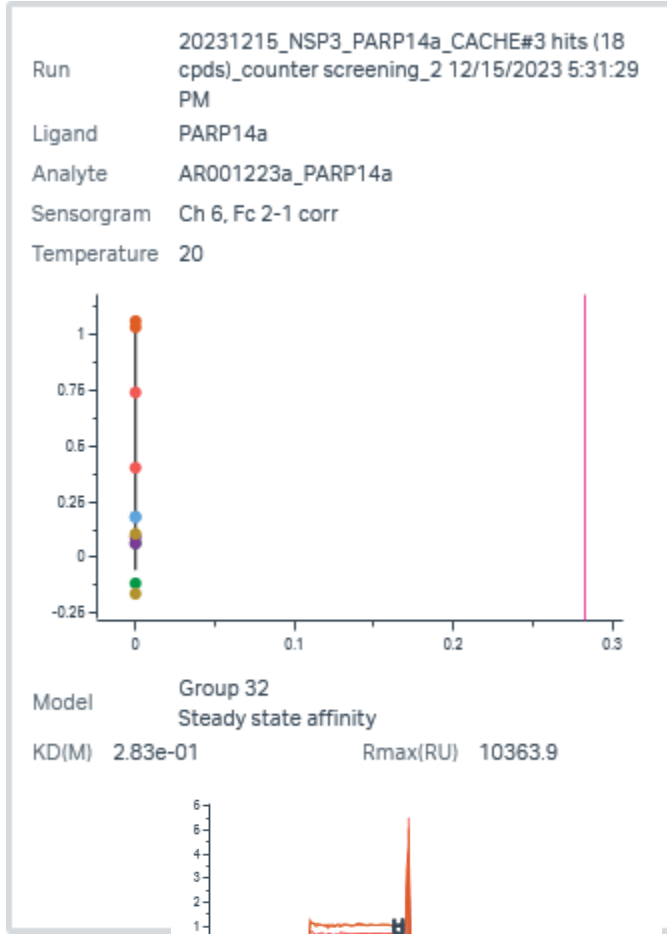
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	31	34	124	31
PARP14a	111033.2	31	NA	no binding

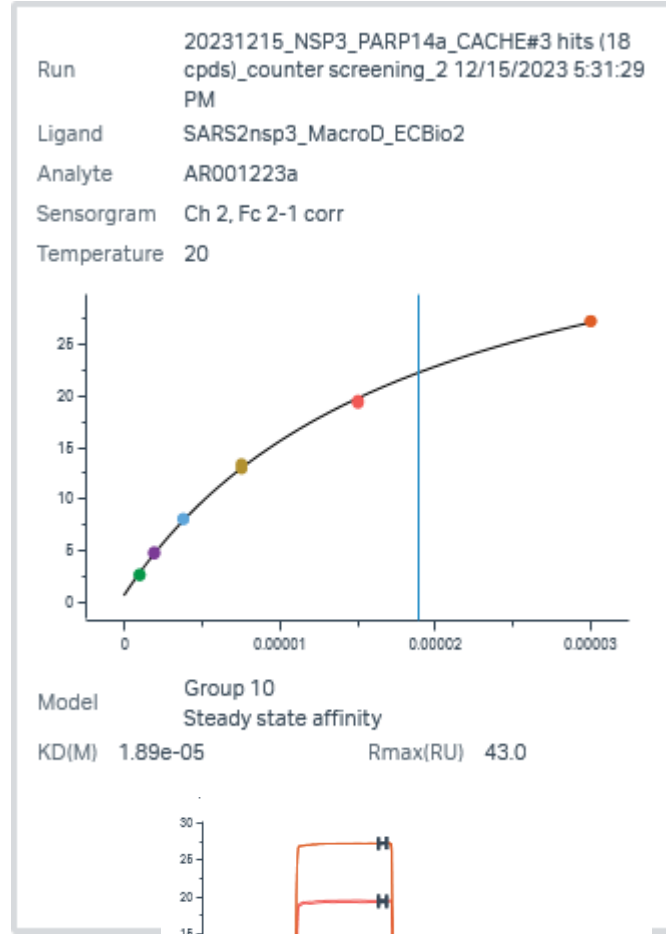


CACHE3HI_1715_76

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement results

confirmation:

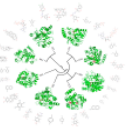
%inh@100 μM = 48.0

%inh@50 μM = 36.5

%inh@25 μM = 23.5

SPR confirmation/selectivity test

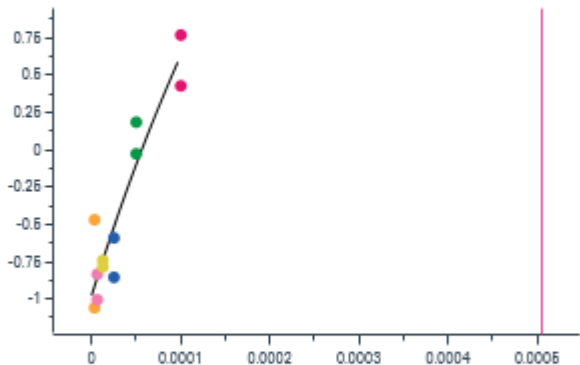
Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	43	42	103	19
PARP14a	283427.3	34	NA	no binding



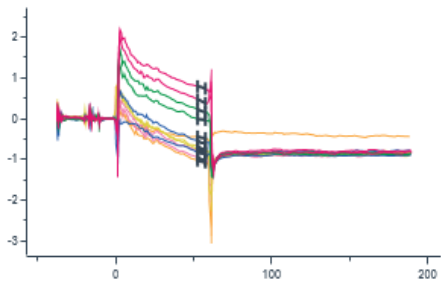
CACHE3HI_1715_89

PARP14a

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand PARP14a
 Analyte AR001694a_PARP14a
 Sensorgram Ch 6, Fc 2-1 corr
 Temperature 20

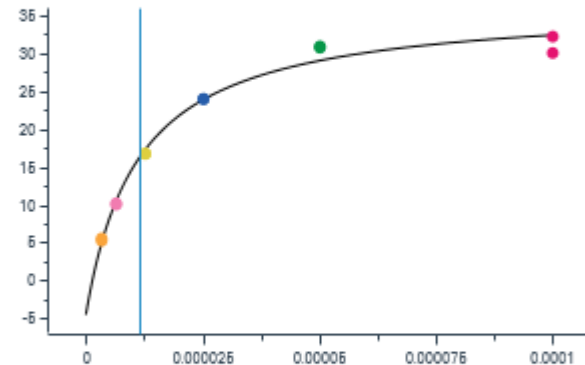


Model Group 33
 Steady state affinity
 KD(M) 5.06e-04 Rmax(RU) 9.8

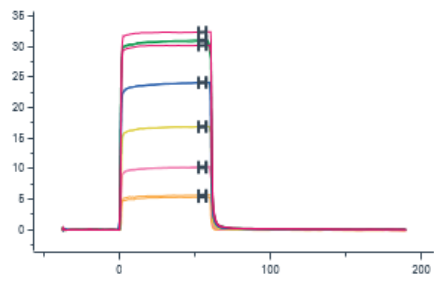


NSP3_SARS2

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand SARS2nsp3_MacroD_ECBio2
 Analyte AR001694a
 Sensorgram Ch 2, Fc 2-1 corr
 Temperature 20



Model Group 11
 Steady state affinity
 KD(M) 1.15e-05 Rmax(RU) 40.2



Previous data:

HTRF displacement results

confirmation:

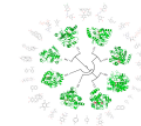
%inh@100 μM = 81.9

%inh@50 μM = 48.4

%inh@25 μM = 30.5

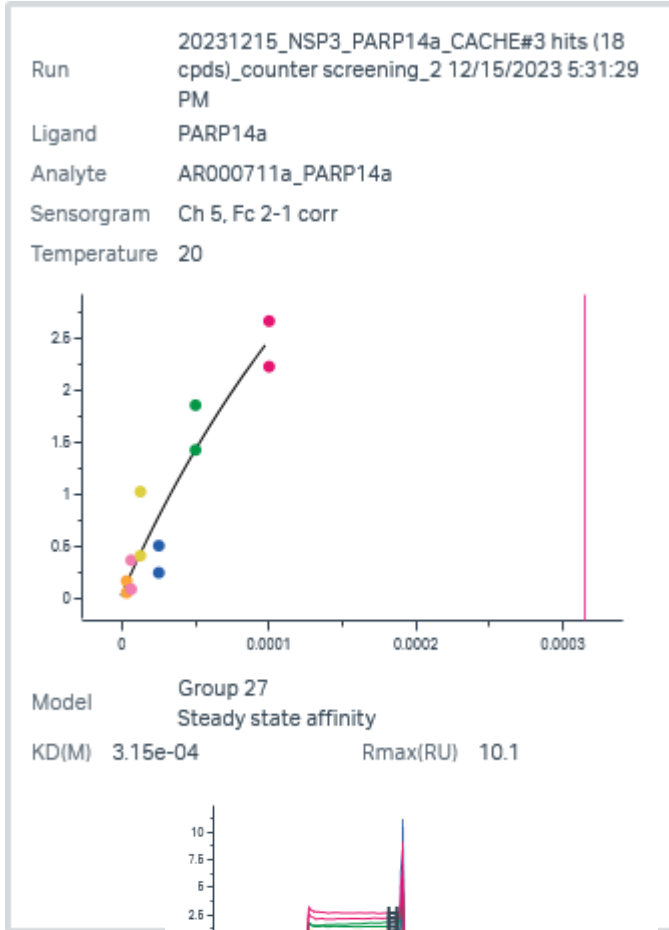
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D _μM, n=2
NSP3_SARS2	40	46	87	11.5
PARP14a	9.8	38	26	no binding

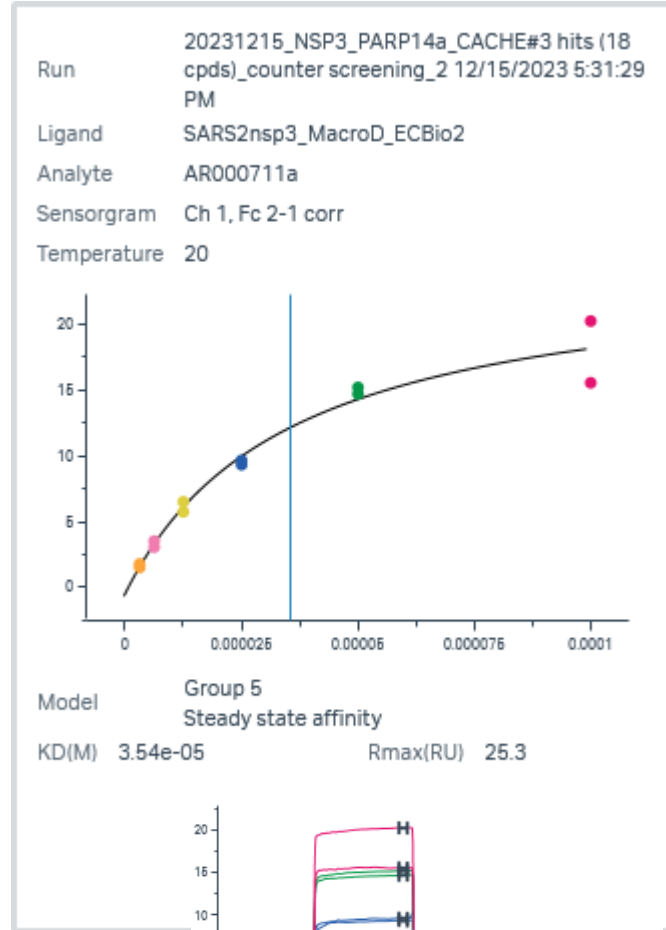


CACHE3HI_1715_83

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement results

confirmation:

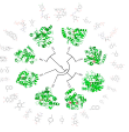
%inh@100 μ M = 81.6

%inh@50 μ M = 37.4

%inh@25 μ M = 14.8

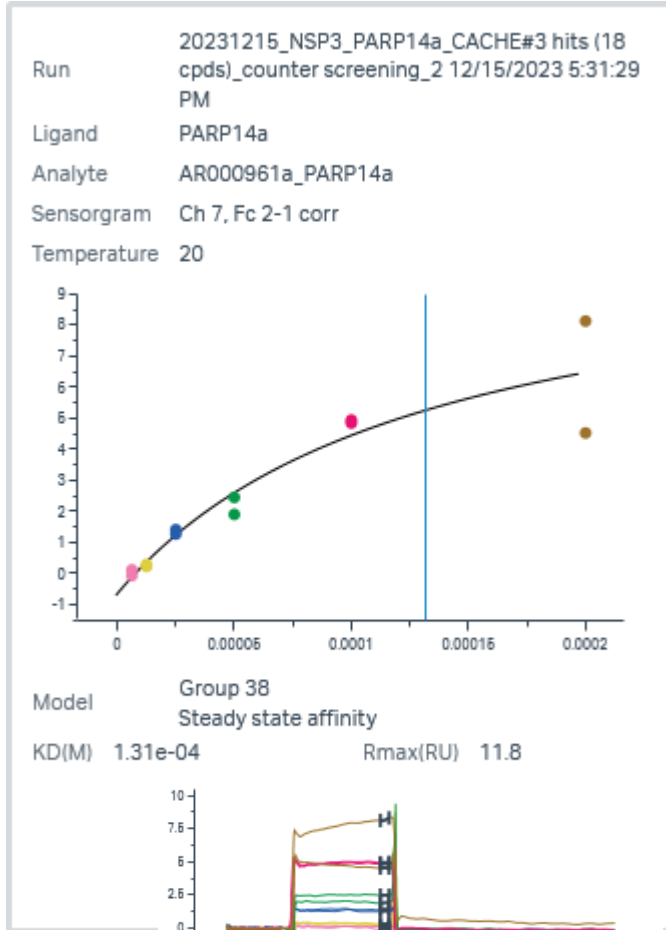
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μ M, n=2
NSP3_SARS2	25	41	61	35.4
PARP14a	10	36	28	no binding

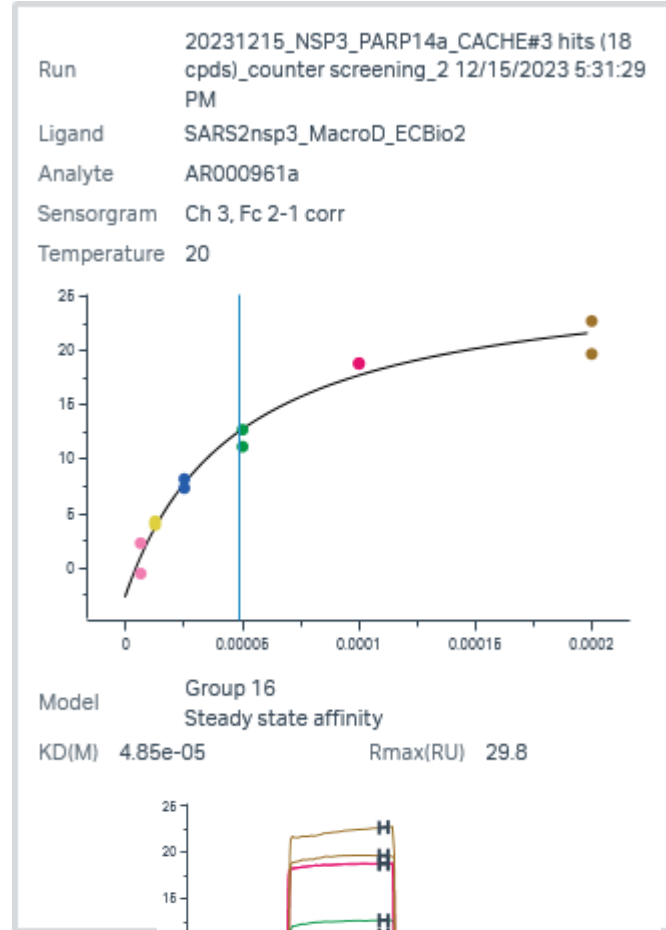


CACHE3HI_1715_82

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement

results confirmation:

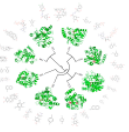
%inh@100 μM = 68.2

%inh@50 μM = 24.8

%inh@25 μM = 8.6

SPR confirmation/selectivity test

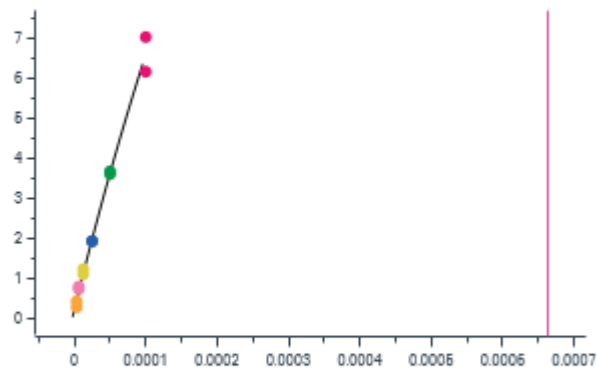
Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μM, n=2
NSP3_SARS2	30	46	64	49
PARP14a	12	40	30	131



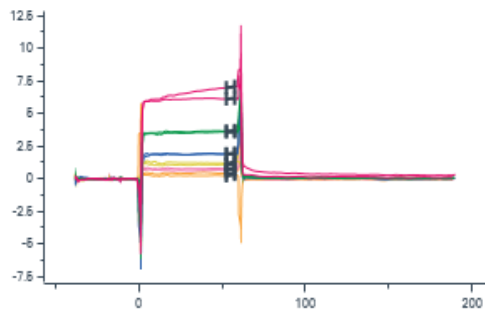
CACHE3HI_1718_58

PARP14a

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand PARP14a
 Analyte AR001533a_PARP14a
 Sensorgram Ch 8, Fc 2-1 corr
 Temperature 20

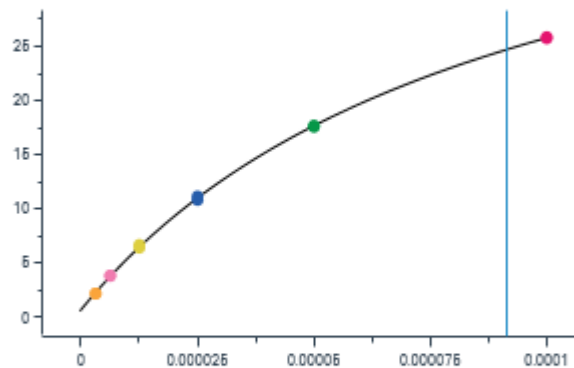


Model Group 43
 Steady state affinity
 KD(M) 6.62e-04 Rmax(RU) 48.6

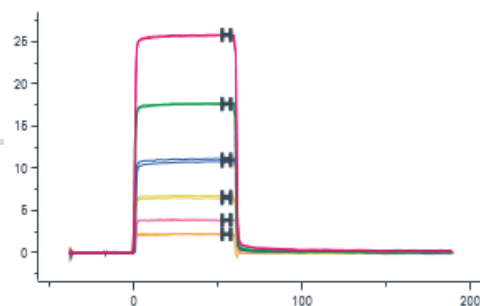


NSP3_SARS2

Run 20231215_NSP3_PARP14a_CACHE#3 hits (18 cpds)_counter screening_2 12/15/2023 5:31:29 PM
 Ligand SARS2nsp3_MacroD_ECBio2
 Analyte AR001533a
 Sensorgram Ch 4, Fc 2-1 corr
 Temperature 20



Model Group 21
 Steady state affinity
 KD(M) 9.15e-05 Rmax(RU) 48.0



Previous data:

HTRF displacement results

confirmation:

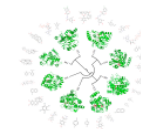
%inh@100 μ M = 35.8

%inh@50 μ M = 17.1

%inh@25 μ M = 9.7

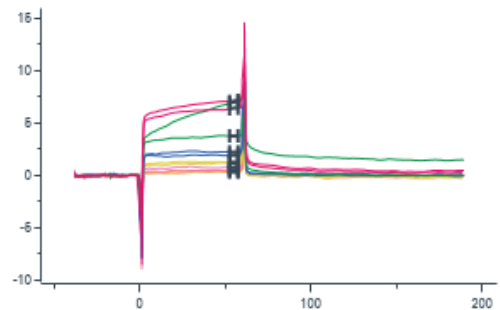
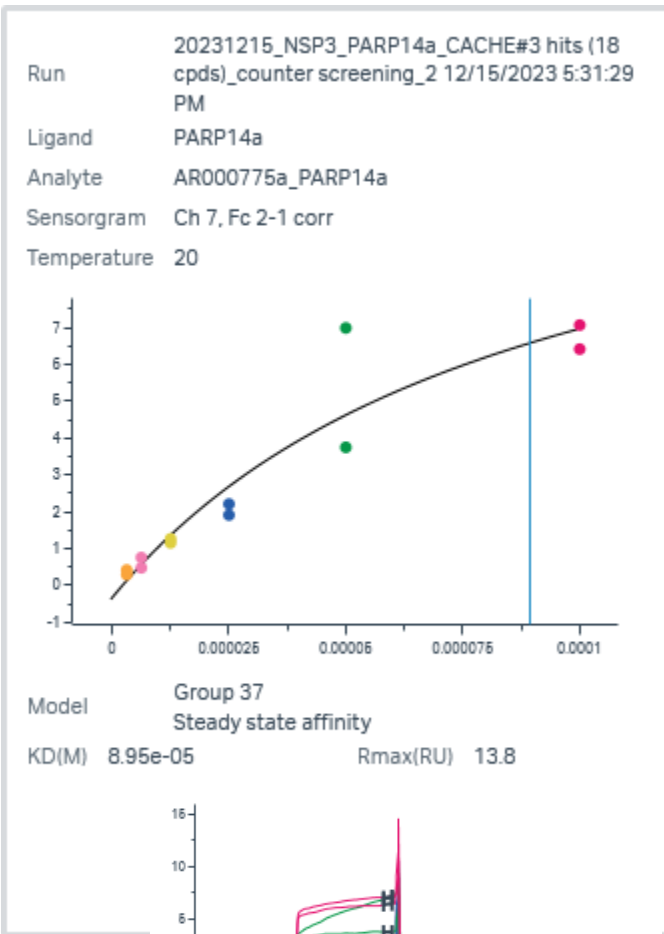
SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μ M, n=2
NSP3_SARS2	48	35	139	91.5
PARP14a	49	32	153	weak binding

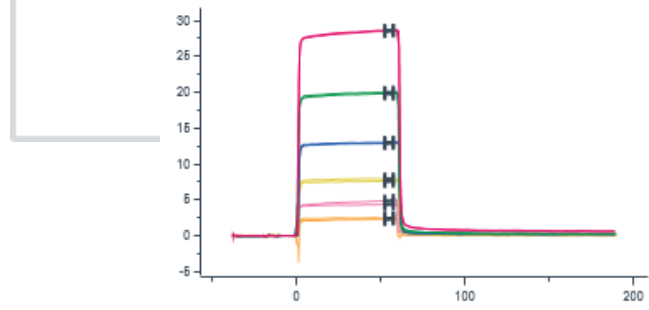
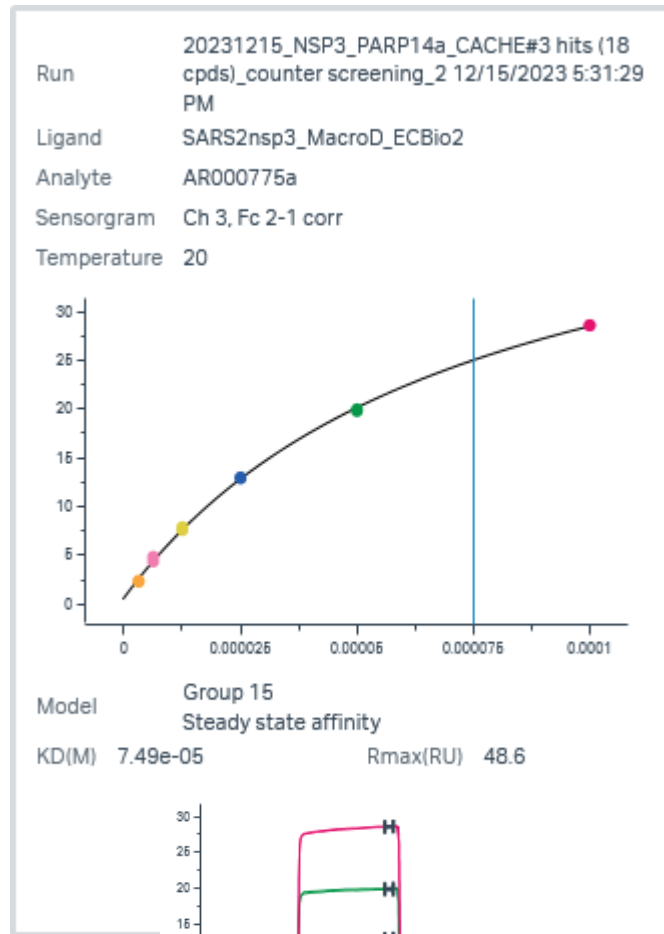


CACHE3HI_1718_59

PARP14a



NSP3_SARS2



Previous data:

HTRF displacement

results confirmation:

%inh@100 μ M = 43.5

%inh@50 μ M = 18.7

%inh@25 μ M = 9.1

SPR confirmation/selectivity test

Protein	RUmax_ experiment	RUmax_ expected	% binding	K _D μ M, n=2
NSP3_SARS2	49	39	125	75
PARP14a	14	34	41	90

