

**Supplementary Table 4**

**Time-course prediction sub-challenge (SC2) results, metadata, and inclusion of teams in Consortium.**

**Column heading color:**

	metadata
	metric for SC2A (experimental data task)
	metric for SC2B ( <i>in silico</i> data task)
	Consortium

**Explanations for metrics can be found in Online Methods. For convenience, a few definitions are provided below:**

SC2A mean rank: Teams were ranked within each (*cell line, phosphoprotein*) pair based on RMSE, resulting in a set of ranks.

SC2B mean rank: Teams were ranked within each (*test inhibitor, predicted node*) pair based on RMSE, resulting in a set of ranks.

SC2A/B combined score: Average of SC2A final rank and SC2B final rank.

**Top-performing teams are indicated by a \* in the final rank columns for SC2A, SC2B and SC2A/B combined. Note that "Mean RMSE" CAUTIONARY NOTE: SC2A and SC2B final rank is based on "mean rank" and not "mean RMSE". Mean I**  
**Team names are anonymized. Team's with an "X" in their anonymized name did not provide any details of their approach.**

Synapse project IDs link to individual team Synapse project pages, where team submission files and code can be found.  
 Further metrics can be found on the final challenge leaderboards on Synapse ([https://www.synapse.org/HPN\\_DREAM](https://www.synapse.org/HPN_DREAM)).

		Final t		
Anonymized Name	Summary of approach	SC2A mean RMSE (see cautionary note above)	SC2A mean rank	SC2A final rank (based on mean rank)
Team42	For the experimental data challenge, protein expression data for a given cell line, stimulus and time point are averaged across inhibitors. For the <i>in silico</i> data challenge, correlation was used to find a sparse causality network and fit a "pseudo-linear" system identified by minimizing mean squared error.	0.500	3.94	2*
Team10	Predicts the projection of phosphorylation levels under unseen inhibitors using truncated singular value decomposition based on Markov and stationarity assumption	0.467	3.97	3*
Team43	Partial least squares and a prior knowledge network are used to predict time-courses.	0.523	4.48	4
Team8	Gradient tree boosting is used to predict forward steps in time series data, represented as successive points under a Markov assumption.	0.529	5.83	6
Team28	The mean value of the inhibitor-free training perturbations was used to predict the time-course of phosphorylation kinetics for all test inhibitors.	0.517	6.68	7
Team34	Time series data prediction was carried out using consensus networks and generalized linear models.	0.861	7.76	9
Team3	We used COPASI to model reactions using mass-action kinetics with phosphorylated species as essential modifiers for subsequent reactions.	1.344	8.80	10
Team6	Predictions on real data are based on the network models learned in the network inference sub-challenge, using Ordinary Differential Equations (ODE) models and least squares method for parameter identification.	8.068	13.54	14

Team44	For a given protein, cell line, stimulus and time point, training data were averaged across inhibitors. This simple approach outperformed more complex Bayesian network approaches.	0.500	3.80	1
Team20		0.489	5.37	5
Team4		0.694	9.52	11
TeamX84		0.591	6.84	8
TeamX85		1.956	11.24	12
TeamX86		4.879	13.22	13
Team33				

anks for each team. These were averaged to produce a mean rank score for each team.  
of ranks for each team. These were averaged to produce a mean rank score for each team.

: two teams (ranked 2nd and 3rd) were named as top-performers for SC2A - see Notes column.  
RMSE is not a good indicator of performance due to scaling issues (see Supplementary Note 9).  
oach and are therefore not members of the HPN-DREAM Consortium (see Supplementary Note 7).

id. Links to all team pages can also be found under the "HPN-DREAM Community Resource" section of the  
M\_Network\_Challenge).

eam rankings and associated metrics					Statistical significance		Synapse project ID
SC2B mean RMSE (see cautionary note above)	SC2B mean rank	SC2B final rank (based on mean rank)	SC1A/B combined score	SC1A/B combined final rank (based on SC1A/B combined score)	SC2A statistical significance of mean rank (FDR)	SC2B statistical significance of mean rank (FDR)	
0.331	7.27	9	5.5	5	3.23E-27	1.00	<a href="#">syn2341971</a>
0.251	4.72	3	3.0	1*	6.47E-27	1.82E-10	<a href="#">syn2341963</a>
0.312	6.71	8	6.0	6	3.73E-20	1.00	<a href="#">syn2331401</a>
0.252	4.60	2	4.0	2	3.49E-07	4.46E-12	<a href="#">syn2337247</a>
0.341	7.37	10	8.5	8	0.01	1.00	n/a
0.241	4.15	1*	5.0	4	1.00	7.31E-20	<a href="#">syn2343054</a>
0.281	5.15	5	7.5	7	1.00	2.19E-05	<a href="#">syn2356612</a>
0.322	6.02	6	10.0	9	1.00	0.91	<a href="#">syn2343026</a>

					5.74E-29		<a href="#">syn2344994</a>
0.257	5.13	4	4.5	3	9.33E-11	1.46E-05	
0.440	8.84	11	11.0	10	1.00	1.00	
					0.04		
					1.00		
					1.00		
0.310	6.04	7				9.09E-01	

e challenge webpage at [https://www.synapse.org/HPN\\_DREAM\\_Network\\_Challenge](https://www.synapse.org/HPN_DREAM_Network_Challenge).

See Supplementary Note 7	
Member of HPN-DREAM Consortium?	Notes
Yes	SC2A top-performer (joint with Team10; Team42 was not robustly ranked above Team10)
Yes	SC2A top-performer (joint with Team42; Team42 was not robustly ranked above Team10) and most consistent performer across SC2A & SC2B.
Yes	
Yes	
Yes	
Yes	SC2B top-performer.
Yes	
Yes	

[illegible]