

Table S8. CETHREADER threading alignment results for the 905 query-template pairs using native contact maps or contact maps predicted using 18 different contact predictors [1-16]. Different contact predictors are sorted in descending order of contact accuracy, *CMOacc*. ‘cm’ and ‘dp’ correspond to alignments generated using the contact map score from Eq. (6) and the dot-product score from Eq. (S9) as proposed by Di Lena et al. [17], respectively.

Methods	CMOacc	TM-score		CMOq	
		cm	dp	cm	dp
native	1	0.6492	0.5975	0.5814	0.5021
ResPRE	0.8462	0.6334	0.5853	0.4802	0.4165
DeepContact	0.7634	0.6114	0.5724	0.4269	0.3775
DeepCov	0.6561	0.5830	0.5473	0.3726	0.3349
NeBcon	0.6244	0.5738	0.5412	0.3489	0.3140
PconsC2	0.5796	0.5632	0.5287	0.3276	0.2908
MetaPSICOV	0.5731	0.5700	0.5406	0.3350	0.3011
GREMLIN	0.3586	0.4931	0.4714	0.1956	0.1767
CCMpred	0.3579	0.4910	0.4676	0.1940	0.1752
SVMcon	0.3573	0.4684	0.4713	0.2242	0.2127
BETAcon	0.3319	0.4658	0.4712	0.2173	0.2074
SVMSEQ	0.3316	0.4606	0.4664	0.2234	0.2122
plmDCA	0.3160	0.4699	0.4567	0.1691	0.1550
PSICOV	0.3033	0.4750	0.4615	0.1738	0.1598
NNcon	0.2897	0.4342	0.4435	0.2002	0.1889
PSpro.beta	0.2633	0.4215	0.4374	0.1847	0.1754
DNcon	0.1986	0.4590	0.4599	0.2134	0.1987
FreeContact	0.1497	0.3127	0.3053	0.1287	0.1208
PSpro	0.1314	0.4277	0.4317	0.3266	0.3053

References

1. Li Y, Hu J, Zhang C, Yu D, Zhang Y (2019) ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. *Bioinformatics*.
2. Liu Y, Palmedo P, Ye Q, Berger B, Peng J (2018) Enhancing Evolutionary Couplings with Deep Convolutional Neural Networks. *Cell Systems* 6: 65-74.e63.
3. Jones DT, Kandathil SM (2018) High precision in protein contact prediction using fully convolutional neural networks and minimal sequence features. *Bioinformatics* 34: 3308-3315.
4. Skwark MJ, Raimondi D, Michel M, Elofsson A (2014) Improved Contact Predictions Using the Recognition of Protein Like Contact Patterns. *PLoS Comput Biol* 10: e1003889.
5. Jones DT, Singh T, Kosciółek T, Tetchner S (2015) MetaPSICOV: Combining coevolution methods for accurate prediction of contacts and long range hydrogen bonding in proteins. *Bioinformatics* 31 (7): 999-1006.
6. Kamisetty H, Ovchinnikov S, Baker D (2013) Assessing the utility of coevolution-based residue-residue contact predictions in a sequence- and structure-rich era. *Proc Natl Acad Sci U S A* 110: 15674-15679.
7. Seemayer S, Gruber M, Söding J (2014) CCMpred—fast and precise prediction of protein residue–residue contacts from correlated mutations. *Bioinformatics*.
8. Cheng J, Baldi P (2007) Improved residue contact prediction using support vector machines and a large feature set. *BMC Bioinformatics* 8: 1-9.

9. Cheng J, Baldi P (2005) Three-stage prediction of protein β -sheets by neural networks, alignments and graph algorithms. *Bioinformatics* 21: i75-i84.
10. Wu S, Zhang Y (2008) A comprehensive assessment of sequence-based and template-based methods for protein contact prediction. *Bioinformatics* 24: 924-931.
11. Magnus E, Cecilia L, Yueheng L, Martin W, Erik A (2013) Improved contact prediction in proteins: using pseudolikelihoods to infer Potts models. *Phys Rev E Stat Nonlin Soft Matter Phys* 87.
12. Jones DT, Buchan DWA, Cozzetto D, Pontil M (2012) PSICOV: Precise structural contact prediction using sparse inverse covariance estimation on large multiple sequence alignments. *Bioinformatics* 28 (2): 184-190.
13. Tegge AN, Wang Z, Eickholt J, Cheng J (2009) NNcon: improved protein contact map prediction using 2D-recursive neural networks. *Nucleic Acids Research* 37: W515-W518.
14. Eickholt J, Cheng J (2013) A study and benchmark of DNcon: a method for protein residue-residue contact prediction using deep networks. *BMC Bioinformatics* 14: S12.
15. Kaján L, Hopf TA, Kalaš M, Marks DS, Rost B (2014) FreeContact: fast and free software for protein contact prediction from residue co-evolution. *BMC Bioinformatics* 15: 1-6.
16. He B, Mortuza SM, Wang Y, Shen HB, Zhang Y (2017) NeBcon: protein contact map prediction using neural network training coupled with naive Bayes classifiers. *Bioinformatics* 33: 2296-2306.
17. Di Lena P, Fariselli P, Margara L, Vassura M, Casadio R (2010) Fast overlapping of protein contact maps by alignment of eigenvectors. *Bioinformatics* 26: 2250-2258.