

**Table 1– Statistics of constructed networks**

Networks	Number of nodes	Number of edges	Average degree	Clustering coefficient	Connected components
Co-Neighbor	2696	13728	10.184	0.645	25
Co-Domain	2448	18123	14.806	0.743	471
Co-Complex	1595	10886	13.650	0.798	279
PN	3082	57256	37.155	0.673	185

**Table 2- Comparison of the original network and the constructed network**

Networks	Number of nodes	Number of edges	Characteristic path length	Clustering coefficient
BioGRID	4113	26105	3.461	0.309
PN	3082	57256	3.710	0.673

**Table 3 - Basic information of prediction by various algorithms**

Methods	MP	PMP	MMP	ZP
NPF	1503	891	1213	885
NC	1945	1428	771	100
Zhang	727	421	1989	432
DCS	1269	743	1447	742
DSCP	1358	810	1358	799
PON	536	229	2180	277
<i>GrAPFI</i>	774	384	1942	432

**Table 4 – Basic information of selected target proteins**

Proteins	Degree	Number of domains	Number of complexes
YNL262W	13	2	1
YBR278W	9	0	1
YPR175W	9	1	1

**Table 5 - Description of selected GO Terms**

GO Term	Description
GO:0006272	<u>Leading strand elongation</u> , which is continuous as it proceeds in the same direction as the replication fork.
GO:0006273	<u>Lagging strand elongation</u> proceeds by discontinuous synthesis of short stretches of DNA, known as Okazaki fragments, from RNA primers; these fragments are then joined by DNA ligase.
GO:0006289	<u>Nucleotide excision</u> repair recognizes a wide range of substrates, including damage caused by UV irradiation and chemicals.
GO:0006298	The <u>mismatch repair system</u> promotes genomic fidelity by repairing base-base mismatches, insertion-deletion loops and heterologies generated during DNA replication and recombination.
GO:0006303	The <u>repair of a double-strand break</u> in DNA in which the two broken ends are re-joined with little or no sequence complementarity.
GO:0006348	<u>Chromatin silencing at telomere</u> means the repression of transcription of telomere DNA by altering the structure of chromatin.
GO:0007064	<u>Mitotic sister chromatid cohesion</u> . The cell cycle process in which the sister chromatids of a replicated chromosome are joined along the entire length of the chromosome.

**Table 6 – The prediction results using ten-fold validation**

Methods	Precision		Recall		F-measure	
	mean value	standard deviations	mean value	standard deviations	mean value	standard deviations
NPF	0.424	0.025	0.429	0.022	0.426	0.022
NC	0.176	0.014	0.610	0.023	0.273	0.018
Zhang	0.198	0.019	0.196	0.019	0.197	0.019
DCS	0.352	0.025	0.354	0.027	0.353	0.025
DSCP	0.378	0.027	0.382	0.028	0.380	0.027
PON	0.139	0.017	0.129	0.016	0.134	0.016
<i>GrAPFI</i>	0.219	0.018	0.209	0.018	0.214	0.018