Supplementary

Table 8: Algorithm parameters and descriptions.

ID	Year	Algorithm	Parameter	Description
1	2023	$MCOR$	No parameters required	The method simultaneously considers functional annotation information and network topology to construct a weighted network and comprehensively mines protein complexes based on both density and modularity
2	2022	$LCDA-GO$	$HL=4$	A community detection algorithm based on Gene Ontology (GO) functional annotation
3	2021	$TADW-SC$	$\nu=0.1, \mu=0.5$	A spectral clustering method based on text-associated DeepWalk, matrices, and cosine similarity
4	2021	GE	No parameters required	A graph clustering algorithm based on entropy and GO functional annotation
5	2021	$PC2P$	No parameters required	A protein complex prediction algorithm based on biclique spanned subgraphs and a greedy approximation algorithm
6	2018	PMD_{pc}	$c_1=0.25\times\sqrt{n}, c_2=0.25\times\sqrt{p}$	A protein complex identification algorithm based on penalized matrix decomposition and normalization
7	2017	$SEGC$	$(\beta_1,\beta_2,k,\varepsilon,r,\theta)=(0.6,0,3,0.4,0.3,2)$	A graph clustering algorithm for protein complex formation based on extending from seed nodes selected through roulette wheel selection
8	2017	$NABCAM$	$T_s=0.3, T_p=0.3, T_n=0$	A Core-Attachment method for mining protein complexes from PPI networks based on neighbor affinity

Table 9: 24 protein complexes identified by MCOR.

ID	Recognised Complexes
1	**CBX7, PCGF1, PHC2, CBX8, CBX4, CBX2, PCGF3, RNF2, PCGF6, SAMD13, RING1, BMI1, PHC3,** BCAS4
2	**BLOC1S6, HPS5, HPS3, HPS6, BLOC1S4, HPS1, DTNBP1, BCAS4, SNAPIN, BLOC1S2, BLOC1S5, HPS4**
3	**ACTL6B, SMARCC1, SMARCD3, SMARCB1, SMARCA2, SMARCC2, ARID1A, SMARCE1, SS18L1, ARID1B, DPF1,** PCGF2
4	**SESN2, TELO2, MAPKAP1, RICTOR, MTOR, TTI1, PRR5L, PRR5**
5	**ACTL6B, ACTR6, HMGXB4, CSNK2A1, CHRAC1, INO80B, ACTR5, SMARCC1, BRD8, SMARCD3, YY1, CHD5, SRCAP, SMARCB1, SMARCA2, SMARCC2, RB1, MTA2, SMARCA5, NCR1, EN1, EN2, ZNHIT1, BPTF, RSF1, ATAD5, GLTSCR1L, SUZ12, RUVBL1, ARID1A, ING3, SMARCE1, SS18L1, MTA1, ACTR8, KAT5, CECR2, PHF10, ARID1B, DPF1, CHD4, MCRS1, VCP, TRRAP, BAZ1A, GATAD2A, INO80, UCHL5, GATAD2B, SMARCA1, DMAP1, RBBP4, HDAC1, POLE3, RBBP7, CHD3, RFC1, EP400, TFPT, RFC4, PBRM1, SMARCD1, GLTSCR1, MTA3, INO80C, SMARCD2, SMARCA4, ACTL6A, MBD3, SS18, MYSM1,** MLST8
6	**MYO15A, MYH9, MYL12A, MYL7, MYH1, MYL2, MYH2, MYH4, CCDC102A, MYO1G, MYO5C, MYH7B, MYO3A, CGN, MYH15, MYL9, CGNL1, MYO5B, MYO1E, MYL1, MYO1D, MYLPF, MYO18B, MYO1F, BMF, MYL4, MYH7, MYO9A, MYO1C, MYH10, MYO6, MYO1B, MYL3, MYH11, MYO5A, MYL5, MYH8, MYH6, MYO3B, MYO7A, MYO1A, MYO16, MYH13,** DPF3
7	**KIF22, KIF17, KLC4, KIF13A, KIF23, KIF11, KIF18A, KIF1B, YWHAE, KIF3C, CENPE, KIF2B, KIF6, KIF27, KIFC2, KIF5B, KIF1C, KIF15, KIF9, NDEL1, KIFAP3, KIF21A, DISC1, KIF14, KIF20B, KIF2C, KIF12, KIF4A, KIF3B, KIF24, KIFC3, KIF19, KLC3,** DYNLL2, MYO9B

Table 9: 24 protein complexes identified by MCOR (Continued).

ID	Recognised Complexes
8	**NDUFA7, NDUFS4, NDUFA12, NDUFA10, NDUFB9, NDUFS8, NDUFB11, NDUFB7, NDUFB8, NDUFS6, NDUFC2, NDUFB10, NDUFAF1, NDUFS7, NDUFB5, NDUFB3, NDUFV1, WDR93, NDUFB4, FOXRED1, NDUFA2, NDUFS3, NDUFV2, NDUFA9,** INO80E, HDAC2
9	**YER022W, YBR253W, YGL151W, YHR058C, YBR193C, YDL005C, YNR010W, YGR104C, YBL093C, YKL161C, YCR081W, YCR033W, YGL127C, YOL051W, YMR112C, YHR041C, YNL025C, YNL236W, YDR308C, YDR443C, YLR071C, YBR193C,** YLR026C
10	**YAL014C, YAL030W, YBL050W, YDR468C, YDR498C, YGL095C, YGL098W, YGL212W, YGR009C, YHL031C, YIL004C, YKL006C-A, YKL196C, YLR026C, YLR078C, YLR093C, YLR268W, YMR017W, YMR183C, YMR197C, YNR049C,** YHR071W
11	**YDR392W, YCL010C, YBR111W-A, YDR145W, YGR252W, YER164W, YBR081C, YGL112C, YDR448W, YMR223W, YDR176W, YLR055C, YGL066W, YBR198C, YDR167W, YHR099W**
12	**YDL008W, YGL116W, YHR166C, YDR260C, YBL084C, YIR025W, YKL022C, YGL003C, YLR102C, YFR036W, YGR225W, YGL240W, YDR118W**
13	**YAL009W, YAL016W, YBL046W, YBR045C, YBR050C, YDL047W, YDL134C, YDR028C, YDR075W, YDR130C, YER054C, YER133W, YFR003C, YGL190C, YHR004C, YIL153W, YKL190W, YKL193C, YKR075C, YLR273C,** YGL215W, YGL048C
14	**YBL063W, YBR156C, YDR106W, YDR424C, YDR488C, YEL061C, YGL216W, YGR200C, YHR129C, YHR199C-A, YJR089W, YKL079W, YKR054C, YLL049W, YMR198W, YMR294W,** YOR362C
15	**YAL026C, YCR094W, YDR244W, YDR265W, YDR424C, YEL020W-A, YER145C, YER166W, YGL153W, YGR077C, YGR181W, YHR005C-A, YJL210W, YJR040W,** YFR004W
16	**YAL033W, YAR008W, YBL018C, YBR098W, YBR167C, YBR257W, YDR386W, YDR478W, YGR030C, YHR062C, YIR015W, YLR105C, YML091C,** YLR423C

Table 9: 24 protein complexes identified by MCOR (Continued).

ID	Recognised Complexes
17	**YBR135W, YBR160W, YDL108W, YDL127W, YDL179W, YDR079C-A, YDR311W, YDR422C, YDR460W, YDR477W, YER027C, YER059W, YER171W, YGL115W, YGL134W, YGL180W, YGL208W, YGL215W, YGR108W, YHR071W, YIL050W, YIL143C, YJL006C, YKL139W, YLR005W, YLR226W, YLR423C, YML112W, YNL025C, YNL289W,** YBR198C, YDR260C, YGL190C
18	**YDR427W, YGL011C, YIL075C, YDL097C, YDR394W, YJL001W, YFR004W, YKL145W, YDL007W, YER012W, YDR363W-A, YOL038W, YER094C, YGR253C, YBL041W, YML092C, YMR314W, YFR050C, YFR052W, YGR135W, YDL147W, YGL048C, YHR027C, YLR421C, YFL007W**
19	**YAR003W, YBR057C, YBR175W, YBR258C, YDL201W, YDR140W, YDR165W, YDR469W, YGL130W, YGL192W, YHR119W, YJL125C, YKL018W, YLR015W, YMR180C, YNL062C, YNL196C**
20	**YDR280W, YGR158C, YNL232W, YGR195W, YCR035C, YDR293C, YHR069C, YMR287C, YGR095C, YDL111C, YHR081W**
21	**Gnai3, Gna12, Gnat1, Gna13, Gng4, Gnb3, Gnal, Gnaq, Gna14, Gnat3, Gnb1, Gng11, Gngt1, Gnb2, Gnaz, Gng10, Gna11, Gngt2, Gna15, Gnat2, Gnai2, Gnai1, Gnb5, Gng8, Gnas, Gng5,** Nfkb1, Cdkn2a, Tgfb1, Fasn, Hbegf, Mef2c
22	**Cdh1, Cdh4, Jup, Ctnnb1, Cdh2, Cdh9, Smad7, Cdh17, Cdh5, Cdh15, Cdh6, Cdh10, Cdh26, Ctnna1, Cdh20, Ctnnd1, Cdh24,** Srebf1, Ppp3ca, Dnase2b, Dusp1
23	**Gje1, Gjd4, Gjb6, Gjb5, Gjb3, Gja8, Gjb2, Gjd3, Gja3, Gja10, Gja4, Gjb1, Gja1, Gja6, Gjc3, Gjd2, Gja5, Gjb4**
24	**Lamb1, Lama5, Lamb3, Pmp22, Ntn4, Lamc1, Lamc2, Lama1, Lamb2**

The first column is the ID of the protein complex identified by MCOR, and the second column is the composition of the protein complex, where proteins that match functional annotation terms are highlighted in bold.

Table 10: Functions and associated diseases of 8 biologically significant protein complexes identified by MCOR.

Term	Complex Function
GO:0035102	Polycomb Repressive Complexes (PRCs) are a group of protein complexes that play a crucial role in many biological processes, especially in the repression of gene transcription. PRC1 is one of the primary complexes, and it represses gene transcription by altering chromatin structure. Abnormalities in the PRC1 complex can lead to the development of tumors, developmental disorders, and neurodegenerative diseases.
GO:0031082	The BLOC (Biogenesis of Lysosome-related Organelles Complex) is a set of protein complexes associated with vesicle transport within the endoplasmic reticulum-to-lysosome pathway. It plays essential roles in vesicle trafficking, especially between the endoplasmic reticulum and lysosomes, as well as in the formation and sorting of vesicles within the cell. Dysfunctions in the BLOC complexes are linked to genetic diseases, notably Hermansky-Pudlak syndrome (HPS), characterized by pigment deficiencies in the skin, eyes, and hair, increased risk of bleeding and bruising, and lung diseases in some patients.
GO:0071565	The nBAF complex is a subtype of the SWI/SNF chromatin-remodeling complexes, vital for regulating gene expression by modifying chromatin structures. By facilitating access to DNA, nBAF aids in various cellular processes, including neuronal development and differentiation. Dysfunctions or mutations in components of the nBAF complex have been linked to several neurodevelopmental disorders and syndromic intellectual disabilities, highlighting its crucial role in brain development and function.
GO:0031932	The TORC2 complex, part of the Target of Rapamycin (TOR) signaling pathways, plays a crucial role in regulating cell growth and survival, actin cytoskeleton reorganization, and lipid metabolism. By sensing and responding to various environmental cues, TORC2 ensures cellular homeostasis and adaptation. Dysregulation or abnormalities in TORC2 signaling can lead to a variety of disorders, including metabolic diseases, age-related conditions, and certain types of cancers, underscoring its significance in maintaining cellular and organismal health.
GO:1904949	The ATPase complex is a central enzyme responsible for hydrolyzing adenosine triphosphate (ATP) into adenosine diphosphate (ADP) and inorganic phosphate, a process that releases energy essential for numerous cellular functions, including muscle contraction, ion transport, and synthesis of macromolecules. Dysfunction or mutations in the ATPase complex can lead to a variety of disorders, such as certain neurodegenerative diseases, muscular dystrophies, and imbalances in ion homeostasis, emphasizing its pivotal role in cellular energetics and physiological processes.
GO:0016459	The myosin complex, primarily known for its motor protein components, plays a fundamental role in muscle contraction, intracellular transport, and cell motility by converting chemical energy from ATP into mechanical work. Abnormalities or mutations in myosin proteins can result in various disorders, including myopathies, cardiomyopathies, and hearing impairments, highlighting its indispensable role in both muscle function and various cellular processes.
GO:0005871	The kinesin complex is a motor protein family critical for intracellular transport, moving cellular cargoes along microtubules primarily toward their positive ends. By powering vesicle and organelle trafficking, kinesins ensure proper cell division, signaling, and structure. Dysfunctions or mutations in kinesin proteins can lead to a range of disorders, including neurodegenerative diseases, developmental abnormalities, and certain forms of cancer, underscoring the significance of kinesin-mediated transport in cellular health and functionality.
GO:0005747	Mitochondrial respiratory chain complex I, also known as NADH:ubiquinone oxidoreductase, is the first and largest enzyme of the mitochondrial electron transport chain. It plays a pivotal role in cellular respiration, facilitating the transfer of electrons from NADH to ubiquinone, and coupling this to proton translocation across the inner mitochondrial membrane. Dysfunction or mutations in complex I can lead to various disorders, including mitochondrial encephalomyopathies, Leigh syndrome, and Parkinson's disease, emphasizing its critical role in energy production and cellular health.