Additional File

MEGADOCK-Web: an integrated database of highthroughput structure-based protein-protein interaction predictions

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Supporting Figures

Figure S1: Precision and recall at each threshold value with complete cross-docking on protein-protein docking benchmark version 4.0*



*Hwang H, Vreven T, Janin J, Weng Z. Protein-protein docking benchmark version 4.0. Proteins 2010;78:3111-4.

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TOP ABOUT US	AGE STATISTICS CONTACT LOGIN	
	Free Word •	Search
	MEGADOCK-Web	
	Search Single Protein	
Free Word	e.g.1A4I	٩
	Search Pair Proteins	
Free Word	e.g.1A4I	

MEGADOCK-Web is a database of protein-protein interactions (PPIs) predicted by an FFT-grid-based protein-protein docking software, MEGADOCK.

Q

e.g.1A4I

v

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In the top page, there are two functions, i.e., "Search Single Protein" and "Search Pair Proteins".

Figure S2: MEGADOCK-Web top page

Free Word

Figure S3: Protein selection page

UniProt AC	Organism	Protein Names	Gene Names	PDB ID	Chain	
P18754	Homo sapiens	Regulator of chromosome condensation	RCC1 CHC1	1A12	А	View
P18754	Homo sapiens	Regulator of chromosome condensation	RCC1 CHC1	1A12	в	View
P18754	Homo sapiens	Regulator of chromosome condensation	RCC1 CHC1	1A12	С	View

There are 3 matches for the query "1a12". Please click "View" to go to your protein page.



This page shows candidate protein structure hits after making a query. The table contains basic information on proteins, including PDB ID, chain, UniProt AC, gene name, and protein name for each protein.

Figure S4: *PPIScore* list page

Protein Information				
Your Query: 1oa8				
Protein Names Ataxin-1				
ATXN1 ATX1 SCA1				
10A8 (Chain A)				
UniProt AC P54253				

Predicted PPI Information Show KEGG pathways in candidates PPIScore > & Show Pathway

UniProt AC	Organism	Protein Names	Gene Names	PDB ID	PPI Score	View	Databases
P54253	Homo sapiens	Ataxin-1	ATXN1 ATX1 SCA1	1OA8 (Chain B)	20.3817	View	3M
P54253	Homo sapiens	Ataxin-1	ATXN1 ATX1 SCA1	1OA8 (Chain D)	18.2159	View	9M
P21583	Homo sapiens	Kit ligand [Cleaved into: Soluble KIT ligand]	KITLG MGF SCF	1EXZ (Chain C)	10.8461	View	
P01130	Homo sapiens	Low-density lipoprotein receptor	LDLR	1IJQ (Chain B)	10.5583	View	
Q15797	Homo sapiens	Mothers against decapentaplegic homolog 1	SMAD1 BSP1 MADH1 MADR1	1KHU (Chain A)	10.4384	View	
O14936	Homo sapiens	Peripheral plasma membrane protein CASK	CASK LIN2	1KWA (Chain B)	10.3444	View	
P23381	Homo sapiens	TryptophantRNA ligsse; cytoplasmic [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS IFI53 WRS	1ULH (Chain A)	9.9297	View	
P04234	Homo sapiens	T-cell surface glycoprotein CD3 delts chain	CD3D T3D	1XIW (Chain B)	9.9288	View	
Q9HAN9	Homo sapiens	Nicotinsmide/nicotinic scid mononucleotide adenylyltransferase 1	NMNAT1 NMNAT	1KQN (Chain B)	9.9102	View	
Q9UKK6	Homo sapiens	NTF2-related export protein 1	NXT1	1JKG (Chain A)	9.9045	View	
		« <mark>1</mark> 2 3	×.				

This page shows candidate proteins interacting with the query protein on the basis of *PPIScore*. Specifying the threshold of *PPIScore* and pressing the "Show Pathway" button at the top of the page results in transition to the pathway selection page, whereas clicking the "View" link in the table takes the viewer to the predicted complex page.

Figure S5: Predicted complex page

Docking Information

PPIScore: 11.1101 Show KEGG Pathway

	Protein Names	Gene Names	PDB ID
Protein 1	N–L-asparaginase [Cleaved into: Glycosylasparaginase alpha chain; Glycosylasparaginase beta chain]	AGA.	1APY (Chain A)
Protein2	Regulator of chromosome condensation	RCC1 CHC1	1A12 (Chain A)

Docking results from rank 1 to 10 Download complex in this page



In this page, complex structures predicted by MEGADOCK for the two proteins are displayed with the 3D molecular viewer, Molmil. A PDB-format file can be downloaded for each predicted complex, and 10 PDB files can be compressed into zip format from the "Download complexes in this page" link at the top of the page.

Figure S6: Pathway selection page

	Pathway Filtering	
e.g.c	ancer	filter
hsa01100 Metabolic pa	athways - Homo sapiens (human) (19)	
hsa05200 Pathways in	cancer - Homo sapiens (human) (12)	
hsa04060 Cytokine-cyt	tokine receptor interaction - Homo sapiens (human) (9)	
hsa05166 HTLV-I infec	ction - Homo sapiens (human) (9)	
hsa05203 Viral carcino	genesis - Homo sapiens (human) (8)	
hsa04657 IL-17 signali	ing pathway - Homo sapiens (human) (6)	
hsa04062 Chemokine	signaling pathway - Homo sapiens (human) (6)	
hsa04668 TNF signalin	ng pathway - Homo sapiens (human) (6)	
hsa01200 Carbon met	abolism - Homo sapiens (human) (6)	
hsa05205 Proteoglyca	ns in cancer - Homo sapiens (human) (6)	
hsa01522 Endocrine re	esistance - Homo sapiens (human) (δ)	
hsa04151 PI3K-Akt sig	naling pathway - Homo sapiens (human) (6)	
hsa04630 Jak-STAT si	gnaling pathway - Homo sapiens (human) (6)	
hsa05152 Tuberculosis	s - Homo sapiens (human) (6)	
hsa05224 Breast cano	er - Homo sapiens (human) (6)	
hsa03040 Spliceosome	e - Homo sapiens (human) (5)	
hsa05202 Transcriptior	nal misregulation in cancer - Homo sapiens (human) (5)	
hsa04010 MAPK signa	aling pathway - Homo sapiens (human) (5)	
hsa05160 Hepatitis C -	- Homo sapiens (human) (5)	
hsa05168 Herpes simp	olex infection - Homo sapiens (human) (5)	
hsa05169 Epstein-Barr	r virus infection - Homo sapiens (human) (5)	
hsa04144 Endocytosis	s - Homo sapiens (human) (5)	
hsa04390 Hippo signal	ling pathway - Homo sapiens (human) (5)	
hsa04722 Neurotrophi	n signaling pathway - Homo sapiens (human) (5)	
hsa04611 Platelet activ	vation - Homo sapiens (human) (5)	
hsa05418 Fluid shears	stress and atherosclerosis - Homo sapiens (human) (5)	
hsa04068 FoxO signal	ling pathway - Homo sapiens (human) (5)	
hsa04550 Signaling pa	athways regulating pluripotency of stem cells - Homo sapiens (human) (5)
hsa05161 Hepatitis B -	- Homo sapiens (human) (5)	

hsa05164 Influenza A - Homo sapiens (human) (5)

In this page, the pathways to which the predicted binders belong are shown as a list. The pathways can be filtered according to a word or phrase typed in the "Pathway Filtering" box at the top of the page. The number in parentheses next to the pathway name indicates the number of predicted binders included in the pathway.

Figure S7: Protein pair selection page

Your Query 1:axin

	UniProt AC	Organism	Protein Names	Gene Names	PDB ID	Chain
0	O15169	Homo sapiens	Axin-1	AXIN1 AXIN	1DK8	Α
0	O15169	Homo sapiens	Axin-1	AXIN1 AXIN	1EMU	A
0	P54253	Homo sapiens	Ataxin-1	ATXN1 ATX1 SCA1	10A8	A
0	P54253	Homo sapiens	Ataxin-1	ATXN1 ATX1 SCA1	10A8	в
0	P54253	Homo sapiens	Ataxin-1	ATXN1 ATX1 SCA1	10A8	с
0	P54253	Homo sapiens	Ataxin-1	ATXN1 ATX1 SCA1	10A8	D

Your Query 2:apc

	UniProt AC	Organism	Protein Names	Gene Names	PDB ID	Chain
0	P25054	Homo sapiens	Adenomatous polyposis coli protein	APC DP2.5	1DEB	A
0	P25054	Homo sapiens	Adenomatous polyposis coli protein	APC DP2.5	1DEB	в
0	P25054	Homo sapiens	Adenomatous polyposis coli protein	APC DP2.5	1M5I	A

Submit

PPI Score Information

Protein1 (PDBID_Chain)	Protein2 (PDBID_Chain)	PPI Score	
1DEB_B	10A8_D	8.1506	View
1DK8_A	1DEB_A	8.13	View
1DEB_B	10A8_C	7.8709	View
10A8_D	1DEB_A	7.6317	View
10A8_A	1DEB_B	7.1811	View
10A8_A	1DEB_A	7.0214	View
1EMU_A	1M5I_A	6.9516	View
1M5I_A	10A8_D	6.8361	View
1EMU_A	1DEB_A	6.836	View
1M5I_A	10A8_C	6.7529	View
1DK8_A	1M5I_A	6.7018	View
1DEB_B	1DK8_A	6.5972	View
1DEB B	1048 B	6 55	View

In this page, a list of candidate hits for the two queries is displayed. In addition, at the bottom of the page, a table showing the all-to-all *PPIScore* of the protein hit by query 1 and the protein hit by query 2 is displayed.