
Nucleic Acids Research

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PROCOGNATE: a cognate ligand domain mapping for enzymes	M.Bashton, I.Nobeli and J.M.Thornton	D618–D622
s The MetaCyc Database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases	R.Caspi, H.Foerster, C.A.Fulcher, P.Kaipa, M.Krummenacker, M.Latendresse, S.Paley, S.Y.Rhee, A.G.Shearer, C.Tissier, T.C.Walk, P.Zhang and P.D.Karp	D623–D631
Bacteriome.org—an integrated protein interaction database for <i>E. coli</i>	C.Su, J.M.Peregrin-Alvarez, G.Butland, S.Phanse, V.Fong, A.Emili and J.Parkinson	D632–D636
The BioGRID Interaction Database: 2008 update	B.-J.Breitkreutz, C.Stark, T.Reguly, L.Boucher, A.Breitkreutz, M.Livstone, R.Oughtred, D.H.Lackner, J.Bähler, V.Wood, K.Dolinski and M.Tyers	D637–D640
The cell cycle DB: a systems biology approach to cell cycle analysis	R.Alfieri, I.Merelli, E.Mosca and L.Milanesi	D641–D645
CORUM: the comprehensive resource of mammalian protein complexes	A.Ruepp, B.Brauner, I.Dunger-Kaltenbach, G.Frishman, C.Montrone, M.Stransky, B.Waegele, T.Schmidt, O.N.Doudieu, V.Stümpflen and H.W.Mewes	D646–D650

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s	DOMINE: a database of protein domain interactions	B.Raghavachari, A.Tasneem, T.M.Przytycka and R.Jothi	D656–D661
	HotSprint: database of computational hot spots in protein interfaces	E.Guney, N.Tuncbag, O.Keskin and A.Gursoy	D662–D666
	LigASite—a database of biologically relevant binding sites in proteins with known <i>apo</i>-structures	B.H.Dessailly, M.F.Lensink, C.A.Orengo and S.J.Wodak	D667–D673
	Binding MOAD, a high-quality protein–ligand database	M.L.Benson, R.D.Smith, N.A.Khazanov, B.Dimcheff, J.Beaver, P.Dresslar, J.Nerothin and H.A.Carlson	D674–D678
	PepCyber:P~PEP: a database of human protein–protein interactions mediated by phosphoprotein-binding domains	W.Gong, D.Zhou, Y.Ren, Y.Wang, Z.Zuo, Y.Shen, F.Xiao, Q.Zhu, A.Hong, X.Zhou, X.Gao and T.Li	D679–D683
	STITCH: interaction networks of chemicals and proteins	M.Kuhn, C.von Mering, M.Campillos, L.J.Jensen and P.Bork	D684–D688
	EndoNet: an information resource about regulatory networks of cell-to-cell communication	J.Dönitz, B.Goemann, M.Lizé, H.Michael, N.Sasse, E.Wingender and A.P.Potapov	D689–D694
	NetworKIN: a resource for exploring cellular phosphorylation networks	R.Linding, L.Juhl Jensen, A.Pasulescu, M.Olhovsky, K.Colwill, P.Bork, M.B.Yaffe and T.Pawson	D695–D699
	The Molecule Pages database	B.Saunders, S.Lyon, M.Day, B.Riley, E.Chenette and S.Subramaniam	D700–D706
	Ensembl 2008	P.Flicek, B.L.Aken, K.Beal, B.Ballester, M.Caccamo, Y.Chen, L.Clarke, G.Coates, F.Cunningham, T.Cutts, T.Down, S.C.Dyer, T.Eyre, S.Fitzgerald, J.Fernandez-Banet, S.Gräf, S.Haider, M.Hammond, R.Holland, K.L.Howe, K.Howe, N.Johnson, A.Jenkinson, A.Kähäri, D.Keefe, F.Kokocinski, E.Kulesha, D.Lawson, I.Longden, K.Megy, P.Meidl, B.Overduin, A.Parker, B.Pritchard, A.Prlic, S.Rice, D.Rios, M.Schuster, I.Sealy, G.Slater, D.Smedley, G.Spudich, S.Trevanion, A.J.Vilella, J.Vogel, S.White, M.Wood, E.Birney, T.Cox, V.Curwen, R.Durbin, X.M.Fernandez-Suarez, J.Herrero, T.J.P.Hubbard, A.Kasprzyk, G.Proctor, J.Smith, A.Ureta-Vidal and S.Searle	D707–D714
	EuroPhenome and EMPReSS: online mouse phenotyping resource	A.-M.Mallon, A.Blake and J.M.Hancock	D715–D718
	Gallus GBrowse: a unified genomic database for the chicken	C.J.Schmidt, M.Romanov, O.Ryder, V.Magrini, M.Hickenbotham, J.Glasscock, S.McGrath, E.Mardis and L.D.Stein	D719–D723
	The Mouse Genome Database (MGD): mouse biology and model systems	C.J.Bult, J.T.Eppig, J.A.Kadin, J.E.Richardson, J.A.Blake and the Mouse Genome DatabaseGroup	D724–D728
	PBmice: an integrated database system of <i>piggyBac</i> (PB) insertional mutations and their characterizations in mice	L.V.Sun, K.Jin, Y.Liu, W.Yang, X.Xie, L.Ye, L.Wang, L.Zhu, S.Ding, Y.Su, J.Zhou, M.Han, Y.Zhuang, T.Xu, X.Wu, N.Gu and Y.Zhong	D729–D734

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TreeFam: 2008 Update	J.Ruan, H.Li, Z.Chen, A.Coghlan, L.J.M.Coin, Y.Guo, J.-K.Hériché, Y.Hu, K.Kristiansen, R.Li, T.Liu, A.Moses, J.Qin, S.Vang, A.J.Vilella, A.Ureta-Vidal, L.Bolund, J.Wang and R.Durbin	D735–D740
The UniTrap resource: tools for the biologist enabling optimized use of gene trap clones	G.Roma, M.Sardiello, G.Cobellis, P.Cruz, G.Lago, R.Sanges and E.Stupka	D741–D746
UTGB/medaka: genomic resource database for medaka biology	B.Ahsan, D.Kobayashi, T.Yamada, M.Kasahara, S.Sasaki, T.L.Saito, Y.Nagayasu, K.Doi, Y.Nakatani, W.Qu, T.Jindo, A.Shimada, K.Naruse, A.Toyoda, Y.Kuroki, A.Fujiyama, T.Sasaki, A.Shimizu, S.Asakawa, N.Shimizu, S.-i.Hashimoto, J.Yang, Y.Lee, K.Matsushima, S.Sugano, M.Sakaizumi, T.Narita, K.Ohishi, S.Haga, F.Ohta, H.Nomoto, K.Nogata, T.Morishita, T.Endo, T.Shin-I, H.Takeda, Y.Kohara and S.Morishita	D747–D752
The vertebrate genome annotation (Vega) database	L.G.Wilming, J.G.R.Gilbert, K.Howe, S.Trevanion, T.Hubbard and J.L.Harrow	D753–D760
Xenbase: a <i>Xenopus</i> biology and genomics resource	J.B.Bowes, K.A.Snyder, E.Segerdell, R.Gibb, C.Jarabek, E.Noumen, N.Pollet and P.D.Vize	D761–D767
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The UCSC Genome Browser Database: 2008 update	D.Karolchik, R.M.Kuhn, R.Baertsch, G.P.Barber, H.Clawson, M.Diekhans, B.Giardine, R.A.Harte, A.S.Hinrichs, F.Hsu, K.M.Kober, W.Miller, J.S.Pedersen, A.Pohl, B.J.Raney, B.Rhead, K.R.Rosenbloom, K.E.Smith, M.Stanke, A.Thakkapallayil, H.Trumbower, T.Wang, A.S.Zweig, D.Haussler and W.J.Kent	D773–D779
X:Map: annotation and visualization of genome structure for Affymetrix exon array analysis	T.Yates, M.J.Okoniewski and C.J.Miller	D780–D786
Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees	A.Matsuya, R.Sakate, Y.Kawahara, K.O.Koyanagi, Y.Sato, Y.Fujii, C.Yamasaki, T.Habara, H.Nakaoka, F.Todokoro, K.Yamaguchi, T.Endo, S.Oota, W.Makalowski, K.Ikeo, Y.Suzuki, K.Hanada, K.Hashimoto, M.Hirai, H.Iwama, N.Saitou, A.T.Hiraki, L.Jin, Y.Kaneko, M.Kanno, K.Murakami, A.O.Noda, N.Saichi, R.Sanbonmatsu, M.Suzuki, J.-i.Takeda, M.Tanaka, T.Gojobori, T.Imanishi and T.Itoh	D787–D792
The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts	C.Yamasaki, K.Murakami, Y.Fujii, Y.Sato, E.Harada, J.-i.Takeda, T.Taniya, R.Sakate, S.Kikugawa, M.Shimada, M.Tanino, K.O.Koyanagi, R.A.Barrero, C.Gough, H.-W.Chun, T.Habara, H.Hanaoka, Y.Hayakawa, P.B.Hilton, Y.Kaneko, M.Kanno, Y.Kawahara, T.Kawamura, A.Matsuya, N.Nagata, K.Nishikata, A.O.Noda, S.Nurimoto, N.Saichi, H.Sakai, R.Sanbonmatsu, R.Shiba, M.Suzuki, K.Takabayashi, A.Takahashi and T.Tamura	D793–D799

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EMAGE—Edinburgh Mouse Atlas of Gene Expression: 2008 update	S.Venkataraman, P.Stevenson, Y.Yang, L.Richardson, N.Burton, T.P.Perry, P.Smith, R.A.Baldock, D.R.Davidson and J.H.Christiansen	D860–D865
Many Microbe Microarrays Database: uniformly normalized Affymetrix compendia with structured experimental metadata	J.J.Faith, M.E.Driscoll, V.A.Fusaro, E.J.Cosgrove, B.Hayete, F.S.Juhn, S.J.Schneider and T.S.Gardner	D866–D870
The Stanford Tissue Microarray Database	R.J.Marinelli, K.Montgomery, C.L.Liu, N.H.Shah, W.Prapong, M.Nitzberg, Z.K.Zachariah, G.J.Sherlock, Y.Natkunam, R.B.West, M.van de Rijn, P.O.Brown and C.A.Ball	D871–D877
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An emerging cyberinfrastructure for biodefense pathogen and pathogen–host data	C.Zhang, O.Crasta, S.Cammer, R.Will, R.Kenyon, D.Sullivan, Q.Yu, W.Sun, R.Jha, D.Liu, T.Xue, Y.Zhang, M.Moore, P.McGarvey, H.Huang, Y.Chen, J.Zhang, R.Mazumder, C.Wu and B.Sobral	D884–D891
CEBS—Chemical Effects in Biological Systems: a public data repository integrating study design and toxicity data with microarray and proteomics data	M.Waters, S.Stasiewicz, B.Alex Merrick, K.Tomer, P.Bushel, R.Paules, N.Stegman, G.Nehls, K.J.Yost, C.H.Johnson, S.F.Gustafson, S.Xirasagar, N.Xiao, C.-C.Huang, P.Boyer, D.D.Chan, Q.Pan, H.Gong, J.Taylor, D.Choi, A.Rashid, A.Ahmed, R.Howle, J.Selkirk, R.Tennant and J.Fostel	D892–D900
DrugBank: a knowledgebase for drugs, drug actions and drug targets	D.S.Wishart, C.Knox, A.C.Guo, D.Cheng, S.Shrivastava, D.Tzur, B.Gautam and M.Hassanali	D901–D906
GLIDA: GPCR—ligand database for chemical genomics drug discovery—database and tools update	Y.Okuno, A.Tamon, H.Yabuuchi, S.Nijjima, Y.Minowa, K.Tonomura, R.Kunimoto and C.Feng	D907–D912
The pharmacogenetics and pharmacogenomics knowledge base: accentuating the knowledge	T.Hernandez-Boussard, M.Whirl-Carrillo, J.M.Hebert, L.Gong, R.Owen, M.Gong, W.Gor, F.Liu, C.Truong, R.Whaley, M.Woon, T.Zhou, R.B.Altman and T.E.Klein	D913–D918
SuperTarget and Matador: resources for exploring drug-target relationships	S.Günther, M.Kuhn, M.Dunkel, M.Campillos, C.Senger, E.Petsalaki, J.Ahmed, E.G.Urdiales, A.Gewiess, L.J.Jensen, R.Schneider, R.Skoblo, R.B.Russell, P.E.Bourne, P.Bork and R.Preissner	D919–D922
VIOLIN: vaccine investigation and online information network	Z.Xiang, T.Todd, K.P.Ku, B.L.Kovacic, C.B.Larson, F.Chen, A.P.Hodges, Y.Tian, E.A.Olenzek, B.Zhao, L.A.Colby, H.G.Rush, J.R.Gilsdorf, G.W.Jouradian and Y.He	D923–D928
The plant organelles database (PODB): a collection of visualized plant organelles and protocols for plant organelle research	S.Mano, T.Miwa, S.-i.Nishikawa, T.Mimura and M.Nishimura	D929–D937

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The Generation Challenge Programme comparative plant stress-responsive gene catalogue	S.Wanchana, S.Thongjuea, V.J.Ulat, M.Anacleto, R.Mauleon, M.Conte, M.Rouard, M.Ruiz, N.Krishnamurthy, K.Sjolander, T.van Hintum and R.M.Bruskiewich	D943–D946
Gramene: a growing plant comparative genomics resource	C.Liang, P.Jaiswal, C.Hebbard, S.Avraham, E.S.Buckler, T.Casstevens, B.Hurwitz, S.McCouch, J.Ni, A.Pujar, D.Ravenscroft, L.Ren, W.Spooner, I.Teclé, J.Thomason, C.-w.Tung, X.Wei, I.Yap, K.Youens-Clark, D.Ware and L.Stein	D947–D953
MetaCrop: a detailed database of crop plant metabolism	E.Grafahrend-Belau, S.Weise, D.Koschützki, U.Scholz, B.H.Junker and F.Schreiber	D954–D958
PlantGDB: a resource for comparative plant genomics	J.Duvick, A.Fu, U.Muppurala, M.Sabharwal, M.D.Wilkerson, C.J.Lawrence, C.Lushbough and V.Brendel	D959–D965
PlantTFDB: a comprehensive plant transcription factor database	A.-Y.Guo, X.Chen, G.Gao, H.Zhang, Q.-H.Zhu, X.-C.Liu, Y.-F.Zhong, X.Gu, K.He and J.Luo	D966–D969
PlantTribes: a gene and gene family resource for comparative genomics in plants	P.K.Wall, J.Leebens-Mack, K.F.Müller, D.Field, N.S.Altman and C.W.dePamphilis	D970–D976
ppdb: a plant promoter database	Y.Y.Yamamoto and J.Obokata	D977–D981
s Update of ASRP: the <i>Arabidopsis</i> Small RNA Project database	T.W.H.Backman, C.M.Sullivan, J.S.Cumbie, Z.A.Miller, E.J.Chapman, N.Fahlgren, S.A.Givan, J.C.Carrington and K.D.Kasschau	D982–D985
CATdb: a public access to <i>Arabidopsis</i> transcriptome data from the URGV-CATMA platform	S.Gagnot, J.-P.Tamby, M.-L.Martin-Magniette, F.Bitton, L.Taconnat, S.Balzergue, S.Aubourg, J.-P.Renou, A.Lecharny and V.Brunaud	D986–D990
GreenPhylDB: a database for plant comparative genomics	M.G.Conte, S.Gaillard, N.Lanau, M.Rouard and C.Périn	D991–D998
AtPID: <i>Arabidopsis thaliana</i> protein interactome database—an integrative platform for plant systems biology	J.Cui, P.Li, G.Li, F.Xu, C.Zhao, Y.Li, Z.Yang, G.Wang, Q.Yu, Y.Li and T.Shi	D999–D1008
The <i>Arabidopsis</i> Information Resource (TAIR): gene structure and function annotation	D.Swarbreck, C.Wilks, P.Lamesch, T.Z.Berardini, M.Garcia-Hernandez, H.Foerster, D.Li, T.Meyer, R.Muller, L.Ploetz, A.Radenbaugh, S.Singh, V.Swing, C.Tissier, P.Zhang and E.Huala	D1009–D1014
<i>PhosPhAt</i>: a database of phosphorylation sites in <i>Arabidopsis thaliana</i> and a plant-specific phosphorylation site predictor	J.L.Heazlewood, P.Durek, J.Hummel, J.Selbig, W.Weckwerth, D.Walther and W.X.Schulze	D1015–D1021
<i>Oryza Tag Line</i>, a phenotypic mutant database for the Génoplante rice insertion line library	P.Larmande, C.Gay, M.Lorieux, C.Périn, M.Bouniol, G.Droc, C.Sallaud, P.Perez, I.Barnola, C.Biderre-Petit, J.Martin, J.B.Morel, A.A.T.Johnson, F.Bourgis, A.Ghesquière, M.Ruiz, B.Courtois and E.Guiderdoni	D1022–D1027
The Rice Annotation Project Database (RAP-DB): 2008 update	T.Tanaka, B.A.Antonio, S.Kikuchi, T.Matsumoto, Y.Nagamura, H.Numata, H.Sakai, J.Wu, T.Itoh, T.Sasaki, R.Aono, Y.Fujii, T.Habara, E.Harada, M.Kanno, Y.Kawahara and H.Kawashima	D1028–D1033

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GDR (Genome Database for Rosaceae): integrated web-database for Rosaceae genomics and genetics data	S.Jung, M.Statton, T.Lee, A.Blenda, R.Svancara, A.Abbott and D.Main	D1034–D1040
Panzea: an update on new content and features	P.Canaran, E.S.Buckler, J.C.Glaubitx, L.Stein, Q.Sun, W.Zhao and D.Ware	D1041–D1043
Shanghai RAPESEED Database: a resource for functional genomics studies of seed development and fatty acid metabolism of <i>Brassica</i>	G.-Z.Wu, Q.-M.Shi, Y.Niu, M.-Q.Xing and H.-W.Xue	D1044–D1047
MUGEN mouse database; Animal models of human immunological diseases	V.Aidinis, C.Chandras, M.Manoloukos, A.Thanassopoulou, K.Kranidioti, M.Armaka, E.Douni, D.L.Kontoyiannis, M.Zouberakis, G.Kollias and the Mugen NoE consortium	D1048–D1054

S, Supplementary Material available at NAR Online