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	HMDB: a knowledgebase for the human metabolome	D.S.Wishart, C.Knox, A.C.Guo, R.Eisner, N.Young, B.Gautam, D.D.Hau, N.Psychogios, E.Dong, S.Bouatra, R.Mandal, I.Sinelnikov, J.Xia, L.Jia, J.A.Cruz, E.Lim, C.A.Sobsey, S.Shrivastava, P.Huang, P.Liu, L.Fang, J.Peng, R.Fradette, D.Cheng, D.Tzur, M.Clements, A.Lewis, A.D.Souza, A.Zuniga, M.Dawe, Y.Xiong, D.Clive, R.Greiner, A.Nazyrova, R.Shaykhutdinov, L.Li, H.J.Vogel and I.Forsythe	D603–D610
S	PMAP: databases for analyzing proteolytic events and pathways	Y.Igarashi, E.Heureux, K.S.Doctor, P.Talwar, S.Gramatikova, K.Gramatikoff, Y.Zhang, M.Blinov, S.S.Ibragimova, S.Boyd, B.Ratnikov, P.Cieplak, A.Godzik, J.W.Smith, A.L.Osterman and A.M.Eroshkin	D611–D618
	Reactome knowledgebase of human biological pathways and processes	L.Matthews, G.Gopinath, M.Gillespie, M.Caudy, D.Croft, B.de Bono, P.Garapati, J.Hemish, H.Hermjakob, B.Jassal, A.Kanapin, S.Lewis, S.Mahajan, B.May, E.Schmidt, I.Vastrik, G.Wu, E.Birney, L.Stein and P.D'Eustachio	D619–D622
S	ConsensusPathDB—a database for integrating human functional interaction networks	A.Kamburov, C.Wierling, H.Lehrach and R.Herwig	D623–D628
	EcID. A database for the inference of functional interactions in <i>E. coli</i>	E.Andres Leon, I.Ezkurdia, B.Garcia, A.Valencia and D.Juan	D629–D635
	Update of KDBI: Kinetic Data of Bio-molecular Interaction database	P.Kumar, B.C.Han, Z.Shi, J.Jia, Y.P.Wang, Y.T.Zhang, L.Liang, Q.F.Liu, Z.L.Ji and Y.Z.Chen	D636–D641
	Michigan molecular interactions r2: from interacting proteins to pathways	V.G.Tarcea, T.Weymouth, A.Ade, A.Bookvich, J.Gao, V.Mahavisno, Z.Wright, A.Chapman, M.Jayapandian, A.Özgür, Y.Tian, J.Cavalcoli, B.Mirel, J.Patel, D.Radev, B.Athey, D.States and H.V.Jagadish	D642–D646
	PIG—the pathogen interaction gateway	T.Driscoll, M.D.Dyer, T.M.Murali and B.W.Sobral	D647–D650
	PIPs: human protein–protein interaction prediction database	M.D.McDowall, M.S.Scott and G.J.Barton	D651–D656

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S	UniHI 4: new tools for query, analysis and visualization of the human protein–protein interactome	G.Chaurasia, S.Malhotra, J.Russ, S.Schnoegl, C.Hänig, E.E.Wanker and M.E.Futschik	D657–D660
S	VirHostNet: a knowledge base for the management and the analysis of proteome-wide virus–host interaction networks	V.Navratil, B.de Chasse, L.Meyniel, S.Delmotte, C.Gautier, P.André, V.Lotteau and C.Rabourdin-Combe	D661–D668
	VirusMINT: a viral protein interaction database	A.Chatr-aryamontri, A.Ceol, D.Peluso, A.Nardoza, S.Panni, F.Sacco, M.Tinti, A.Smolyar, L.Castagnoli, M.Vidal, M.E.Cusick and G.Cesareni	D669–D673
S	PID: the Pathway Interaction Database	C.F.Schaefer, K.Anthony, S.Krupa, J.Buchoff, M.Day, T.Hannay and K.H.Buetow	D674–D679
S	IUPHAR-DB: the IUPHAR database of G protein-coupled receptors and ion channels	A.J.Harmar, R.A.Hills, E.M.Rosser, M.Jones, O.P.Buneman, D.R.Dunbar, S.D.Greenhill, V.A.Hale, J.L.Sharman, T.I.Bonner, W.A.Catterall, A.P.Davenport, P.Delagrang, C.T.Dollery, S.M.Foord, G.A.Gutman, V.Laudet, R.R.Neubig, E.H.Ohlstein, R.W.Olsen, J.Peters, J.-P.Pin, R.R.Ruffolo, D.B.Searls, M.W.Wright and M.Spedding	D680–D685
	CleanEST: a database of cleansed EST libraries	B.Lee and G.Shin	D686–D689
	Ensembl 2009	T.J.P.Hubbard, B.L.Aken, S.Ayling, B.Ballester, K.Beal, E.Bragin, S.Brent, Y.Chen, P.Clapham, L.Clarke, G.Coates, S.Fairley, S.Fitzgerald, J.Fernandez-Banet, L.Gordon, S.Graf, S.Haider, M.Hammond, R.Holland, K.Howe, A.Jenkinson, N.Johnson, A.Kahari, D.Keefe, S.Keenan, R.Kinsella, F.Kokocinski, E.Kulesha, D.Lawson, I.Longden, K.Megy, P.Meidl, B.Overduin, A.Parker, B.Pritchard, D.Rios, M.Schuster, G.Slater, D.Smedley, W.Spooner, G.Spudich, S.Trevanion, A.Vilella, J.Vogel, S.White, S.Wilder, A.Zadissa, E.Birney, F.Cunningham, V.Curwen, R.Durbin, X.M.Fernandez-Suarez, J.Herrero, A.Kasprzyk, G.Proctor, J.Smith, S.Searle and P.Flicek	D690–D697
	EVOG: a database for evolutionary analysis of overlapping genes	D.-S.Kim, C.-Y.Cho, J.-W.Huh, H.-S.Kim and H.-G.Cho	D698–D702
S	ExDom: an integrated database for comparative analysis of the exon–intron structures of protein domains in eukaryotes	A.Bhasi, P.Philip, V.Manikandan and P.Senapathy	D703–D711
	The Mouse Genome Database genotypes::phenotypes	J.A.Blake, C.J.Bult, J.T.Eppig, J.A.Kadin and J.E.Richardson	D712–D719
	Mouse Phenome Database	S.C.Grubb, T.P.Maddatu, C.J.Bult and M.A.Bogue	D720–D730
	PhyloPat: an updated version of the phylogenetic pattern database contains gene neighborhood	T.Hulsen, P.M.A.Groenen, J.de Vlieg and W.Alkema	D731–D737
S	Pseudofam: the pseudogene families database	H.Y.K.Lam, E.Khurana, G.Fang, P.Cayting, N.Carriero, K.-H.Cheung and M.B.Gerstein	D738–D743
	The Rat Genome Database 2009: variation, ontologies and pathways	M.R.Dwinell, E.A.Worthey, M.Shimoyama, B.Bakir-Gungor, J.DePons, S.Laulederkind, T.Lowry, R.Nigram, V.Petri, J.Smith, A.Stoddard, S.N.Twigger, H.J.Jacob and the RGD Team	D744–D749

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	SpBase: the sea urchin genome database and web site	R.A.Cameron, M.Samanta, A.Yuan, D.He and E.Davidson	D750–D754
	The UCSC Genome Browser Database: update 2009	R.M.Kuhn, D.Karolchik, A.S.Zweig, T.Wang, K.E.Smith, K.R.Rosenbloom, B.Rhead, B.J.Raney, A.Pohl, M.Pheasant, L.Meyer, F.Hsu, A.S.Hinrichs, R.A.Harte, B.Giardine, P.Fujita, M.Diekhans, T.Dreszer, H.Clawson, G.P.Barber, D.Haussler and W.J.Kent	D755–D761
	Human Gene and Protein Database (HGPD): a novel database presenting a large quantity of experiment-based results in human proteomics	Y.Maruyama, A.Wakamatsu, Y.Kawamura, K.Kimura, J.-i.Yamamoto, T.Nishikawa, Y.Kisu, S.Sugano, N.Goshima, T.Isogai and N.Nomura	D762–D766
	Human Protein Reference Database—2009 update	T.S.Keshava Prasad, R.Goel, K.Kandasamy, S.Keerthikumar, S.Kumar, S.Mathivanan, D.Telikicherla, R.Raju, B.Shafreen, A.Venugopal, L.Balakrishnan, A.Marimuthu, S.Banerjee, D.S.Somanathan, A.Sebastian, S.Rani, S.Ray, C.J.Harrys Kishore, S.Kanth, M.Ahmed, M.K.Kashyap, R.Mohmood, Y.L.Ramachandra, V.Krishna, B.A.Rahiman, S.Mohan, P.Ranganathan, S.Ramabadrnan, R.Chaerkady and A.Pandey	D767–D772
S	Human Proteinpedia: a unified discovery resource for proteomics research	K.Kandasamy, S.Keerthikumar, R.Goel, S.Mathivanan, N.Patankar, B.Shafreen, S.Renuse, H.Pawar, Y.L.Ramachandra, P.K.Acharya, P.Ranganathan, R.Chaerkady, T.S.Keshava Prasad and A.Pandey	D773–D781
	BodyParts3D: 3D structure database for anatomical concepts	N.Mitsuhashi, K.Fujieda, T.Tamura, S.Kawamoto, T.Takagi and K.Okubo	D782–D785
	Comparative Toxicogenomics Database: a knowledgebase and discovery tool for chemical–gene–disease networks	A.P.Davis, C.G.Murphy, C.A.Saraceni-Richards, M.C.Rosenstein, T.C.Wiegers and C.J.Mattingly	D786–D792
	McKusick's Online Mendelian Inheritance in Man (OMIM®)	J.Amberger, C.A.Bocchini, A.F.Scott and A.Hamosh	D793–D796
	HGVbaseG2P: a central genetic association database	G.A.Thorisson, O.Lancaster, R.C.Free, R.K.Hastings, P.Sarmah, D.Dash, S.K.Brahmachari and A.J.Brookes	D797–D802
S	SNPLogic: an interactive single nucleotide polymorphism selection, annotation, and prioritization system	A.R.Pico, I.V.Smirnov, J.S.Chang, R.-F.Yeh, J.L.Wiemels, J.K.Wiencke, T.Tihan, B.R.Conklin and M.Wrens	D803–D809
	VarySysDB: a human genetic polymorphism database based on all H-InvDB transcripts	M.K.Shimada, R.Matsumoto, Y.Hayakawa, R.Sanbonmatsu, C.Gough, Y.Yamaguchi-Kabata, C.Yamasaki, T.Imanishi and T.Gojobori	D810–D815
	CTdatabase: a knowledge-base of high-throughput and curated data on cancer-testis antigens	L.G.Almeida, N.J.Sakabe, A.R.deOliveira, M.C.C.Silva, A.S.Mundstein, T.Cohen, Y.-T.Chen, R.Chua, S.Gurung, S.Gnjatic, A.A.Jungbluth, O.L.Caballero, A.Bairoch, E.Kiesler, S.L.White, A.J.G.Simpson, L.J.Old, A.A.Camargo and A.T.R.Vasconcelos	D816–D819
	Database for exploration of functional context of genes implicated in ovarian cancer	M.Kaur, A.Radovanovic, M.Essack, U.Schaefer, M.Maquungo, T.Kibler, S.Schmeier, A.Christoffels, K.Narasimhan, M.Choolani and V.B.Bajic	D820–D823
S	MoKCa database—mutations of kinases in cancer	C.J.Richardson, Q.Gao, C.Mitsopoulous, M.Zvelebil, L.H.Pearl and F.M.G.Pearl	D824–D831

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S	AutDB: a gene reference resource for autism research	S.N.Basu, R.Kollu and S.Banerjee-Basu	D832–D836
	DNAREplication: a database of information and resources for the eukaryotic DNA replication community	S.Cotterill and S.E.Kearsey	D837–D839
	ERGR: An ethanol-related gene resource	A.-Y.Guo, B.T.Webb, M.F.Miles, M.P.Zimmerman, K.S.Kendler and Z.Zhao	D840–D845
	G2Cdb: the Genes to Cognition database	M.D.R.Croning, M.C.Marshall, P.McLaren, J.D.Armstrong and S.G.N.Grant	D846–D851
S	INTERFEROME: the database of interferon regulated genes	S.A.Samarajiwa, S.Forster, K.Auchetl and P.J.Hertzog	D852–D857
	MDPD: an integrated genetic information resource for Parkinson's disease	S.Tang, Z.Zhang, G.Kavitha, E.-K.Tan and S.K.Ng	D858–D862
	RAPID: Resource of Asian Primary Immunodeficiency Diseases	S.Keerthikumar, R.Raju, K.Kandasamy, A.Hijikata, S.Ramabadran, L.Balakrishnan, M.Ahmed, S.Rani, L.D.N.Selvan, D.S.Somanathan, S.Ray, M.Bhattacharjee, S.Gollapudi, Y.L.Ramachandra, S.Bhadra, C.Bhattacharyya, K.Imai, S.Nonoyama, H.Kanegane, T.Miyawaki, A.Pandey, O.Ohara and S.Mohan	D863–D867
	ArrayExpress update—from an archive of functional genomics experiments to the atlas of gene expression	H.Parkinson, M.Kapushesky, N.Kolesnikov, G.Rustici, M.Shojatalab, N.Abeygunawardena, H.Berube, M.Dylag, I.Emam, A.Farne, E.Holloway, M.Lukk, J.Malone, R.Mani, E.Pilicheva, T.F.Rayner, F.Rezwan, A.Sharma, E.Williams, X.Z.Bradley, T.Adamusiak, M.Brandizi, T.Burdett, R.Coulson, M.Krestyaninova, P.Kurnosov, E.Maguire, S.G.Neogi, P.Rocca-Serra, S.-A.Sansone, N.Sklyar, M.Zhao, U.Sarkans and A.Brazma	D868–D872
S	BloodExpress: a database of gene expression in mouse haematopoiesis	D.Miranda-Saavedra, S.De, M.W.Trotter, S.A.Teichmann and B.Göttgens	D873–D879
	CleanEx: new data extraction and merging tools based on MeSH term annotation	V.Praz and P.Bucher	D880–D884
	NCBI GEO: archive for high-throughput functional genomic data	T.Barrett, D.B.Troup, S.E.Wilhite, P.Ledoux, D.Rudnev, C.Evangelista, I.F.Kim, A.Soboleva, M.Tomashevsky, K.A.Marshall, K.H.Phillippy, P.M.Sherman, R.N.Muertter and R.Edgar	D885–D890
	GermSAGE: a comprehensive SAGE database for transcript discovery on male germ cell development	T.-L.Lee, H.-H.Cheung, J.Claus, C.Sastry, S.Singh, L.Vu, O.Rennert and W.-Y.Chan	D891–D897
	Implementation of GenePattern within the Stanford Microarray Database	J.Hubble, J.Demeter, H.Jin, M.Mao, M.Nitzberg, T.B.K.Reddy, F.Wymore, Z.K.Zachariah, G.Sherlock and C.A.Ball	D898–D901
	MAPU 2.0: high-accuracy proteomes mapped to genomes	F.Gnad, M.Oroshi, E.Birney and M.Mann	D902–D906
	Sys-BodyFluid: a systematical database for human body fluid proteome research	S.-J.Li, M.Peng, H.Li, B.-S.Liu, C.Wang, J.-R.Wu, Y.-X.Li and R.Zeng	D907–D912
	SysPIMP: the web-based systematical platform for identifying human disease-related mutated sequences from mass spectrometry	H.Xi, J.Park, G.Ding, Y.-H.Lee and Y.Li	D913–D920

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	Cell Line Data Base: structure and recent improvements towards molecular authentication of human cell lines	P.Romano, A.Manniello, O.Aresu, M.Armento, M.Cesaro and B.Parodi	D925–D932
S	APD2: the updated antimicrobial peptide database and its application in peptide design	G.Wang, X.Li and Z.Wang	D933–D937
	OligoArrayDb: pangenomic oligonucleotide microarray probe sets database	J.-M.Rouillard and E.Gulari	D938–D941
	RTPrimerDB: the portal for real-time PCR primers and probes	S.Lefever, J.Vandesompele, F.Speleman and F.Pattyn	D942–D945
	GOBASE: an organelle genome database	E.A.O'Brien, Y.Zhang, E.Wang, V.Marie, W.Badejoko, B.F.Lang and G.Burger	D946–D950
	AutoSNPdb: an annotated single nucleotide polymorphism database for crop plants	C.Duran, N.Appleby, T.Clark, D.Wood, M.Imelfort, J.Batley and D.Edwards	D951–D953
	GabiPD: the GABI primary database—a plant integrative 'omics' database	D.M.Riaño-Pachón, A.Nagel, J.Neigenfind, R.Wagner, R.Basekow, E.Weber, B.Mueller-Roeber, S.Diehl and B.Kersten	D954–D959
	P³DB: a plant protein phosphorylation database	J.Gao, G.K.Agrawal, J.J.Thelen and D.Xu	D960–D962
	PhytAMP: a database dedicated to antimicrobial plant peptides	R.Hammami, J.B.Hamida, G.Vergoten and I.Fliss	D963–D968
S	PPDB, the Plant Proteomics Database at Cornell	Q.Sun, B.Zybailov, W.Majeran, G.Friso, P.D.B.Olinares and K.J.van Wijk	D969–D974
S	Arabidopsis Hormone Database: a comprehensive genetic and phenotypic information database for plant hormone research in Arabidopsis	Z.-y.Peng, X.Zhou, L.Li, X.Yu, H.Li, Z.Jiang, G.Cao, M.Bai, X.Wang, C.Jiang, H.Lu, X.Hou, L.Qu, Z.Wang, J.Zuo, X.Fu, Z.Su, S.Li and H.Guo	D975–D982
	AthaMap, integrating transcriptional and post-transcriptional data	L.Bülöw, S.Engelmann, M.Schindler and R.Hehl	D983–D986
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	OryGenesDB 2008 update: database interoperability for functional genomics of rice	G.Droc, C.Périn, S.Fromentin and P.Larmande	D992–D995
	RiceGeneThresher: a web-based application for mining genes underlying QTL in rice genome	S.Thongjuea, V.Ruanjaichon, R.Bruskiewich and A.Vanavichit	D996–D1000
	Update of the Diatom EST Database: a new tool for digital transcriptomics	U.Maheswari, T.Mock, E.V.Armbrust and C.Bowler	D1001–D1005
	IMGT[®], the international ImMunoGeneTics information system[®]	M.-P.Lefranc, V.Giudicelli, C.Ginestoux, J.Jabado-Michaloud, G.Folch, F.Bellahcene, Y.Wu, E.Gemrot, X.Brochet, J.Lane, L.Regnier, F.Ehrenmann, G.Lefranc and P.Duroux	D1006–D1012
	The IMGT/HLA database	J.Robinson, M.J.Waller, S.C.Fail, H.McWilliam, R.Lopez, P.Parham and S.G.E.Marsh	D1013–D1017
S	The HuRef Browser: a web resource for individual human genomics	N.Axelrod, Y.Lin, P.C.Ng, T.B.Stockwell, J.Crabtree, J.Huang, E.Kirkness, R.L.Strausberg, M.E.Frazier, J.C.Venter, S.Kravitz and S.Levy	D1018–D1024
	The YH database: the first Asian diploid genome database	G.Li, L.Ma, C.Song, Z.Yang, X.Wang, H.Huang, Y.Li, R.Li, X.Zhang, H.Yang, J.Wang and J.Wang	D1025–D1028