A DNA Polymorphism Discovery Resource for Research on Human Genetic Variation

Francis S. Collins,¹ Lisa D. Brooks,^{1,3} and Aravinda Chakravarti²

¹National Human Genome Research Institute, National Institutes of Health (NIH), Bethesda, Maryland 20892 USA;

²Department of Genetics and Center for Human Genetics, Case Western Reserve University and University Hospitals of Cleveland, Cleveland, Ohio 44106 USA

Identifying the genes conferring susceptibility or resistance to common human diseases should become increasingly feasible with improved methods for finding DNA sequence variants on a genome-wide scale (Collins et al. 1997; Landegren et al. 1998; Wang et al. 1998). To facilitate the discovery of DNA sequence variants, the National Human Genome Research Institute (NHGRI) of NIH, working with the Centers for Disease Control and Prevention, the National Institute of Environmental Health Sciences, and several individual investigators, has assembled a DNA Polymorphism Discovery Resource of samples from 450 U.S. residents with ancestry from all the major regions of the world. This DNA Polymorphism Discovery Resource will be immensely valuable for the discovery of human genetic variation, which other follow-up studies can relate to health and disease.

Most successes so far in finding genes that contribute to disease risk have been for highly penetrant diseases caused by single genes, such as cystic fibrosis (Kerem et al. 1989; Rommens et al. 1989). To locate genes affecting these rare disorders, researchers perform linkage analysis on families, which requires 300–500 highly informative genetic markers spanning the entire human genome. However, it has been considerably harder to locate the genes contributing to the risk of common diseases such as diabetes, heart disease, cancers, and psychiatric disorders, because these phenotypes are affected by multiple genes, each with small effect; environmental contributions are also important. Instead of linkage analysis on families it may be much more efficient to

perform association analysis on many affected and unaffected individuals, which would require hundreds of thousands of variants spread over the entire genome (Risch and Merikangas 1996). Such a large number of variants is currently not available. The DNA Polymorphism Discovery Resource is designed to promote their discovery.

About 90% of sequence variants in humans are differences in single bases of DNA, called single nucleotide polymorphisms (SNPs). SNPs in the coding regions of genes (cSNPs) or in regulatory regions are more likely to cause functional differences than SNPs elsewhere. Although most SNPs do not affect gene function, a large number of mapped SNPs will be valuable as markers throughout the genome for finding SNPs that do affect gene function, as linkage disequilibrium over tens to hundreds of kilobases is expected to be found in many regions of the human genome. Both SNPs and cSNPs can be identified by using the DNA Polymorphism Discovery Resource.

When two random chromosomes are compared, they differ at $\sim 1/1000$ nucleotides (Kwok et al. 1996). When all chromosomes from 40 individuals are screened, about 17 million SNPs are expected to be found, out of the 3 billion bases in human DNA. Only a small proportion of these SNPs are expected to be in coding regions, as coding regions are $\sim 5\%$ of the genome and are less likely to have SNPs (Nickerson et al. 1998). Thus the number of cSNPs is estimated to be $\sim 500,000$, an average of about 6 per gene.

There is thus widespread interest in finding SNPs. They are also more numerous, more stable, and potentially easier to score than the microsatellite repeat variants currently used for mapping genes. Given the large potential role of

SNPs in human disease it is important to have these data in the public domain (Heller and Eisenberg 1998). Consequently NIH recently began an initiative for large-scale discovery of SNPs and for improving the technology to detect them. For this initiative, as well as others that are just starting, a common, geographically diverse DNA resource for SNP discovery is crucial, so that researchers can benefit from the cumulative power gained by sharing a common resource, analogous to the demonstrated benefits of the common CEPH panel for genetic mapping and the RH panels for physical mapping. Accumulating information on the same samples will allow validation, quality control, and comparisons of different methods of detecting SNPs.

The DNA Polymorphism Discovery Resource has been assembled to serve this function. It includes cell lines and DNA from 450 anonymous, unrelated individuals, with equal numbers of females and males. No medical, phenotypic, or ethnicity information is included. There are predefined subsets with 8, 24, 44, and 90 samples as well as the complete set, with each subset containing the smaller subsets. The subsets have the same range of diversity as the complete set. This span of sample sizes will allow researchers to use common sets of samples that are of the appropriate size to address various questions. Fewer samples will be needed when researchers are developing new technologies or looking for common variants; however, a more extensive set of samples will be needed when researchers are scaling up technologies or looking for rarer variants.

The sampling strategy for the DNA Polymorphism Discovery Resource facilitates finding genetic variants in the entire human population (Table 1). Any

³Corresponding author.

E-MAIL brooks@exchange.nih.gov; FAX (301) 480-2770.

Table 1. Composition of the DNA Polymorphism Discovery Resource

Population group	Propor. admix.	No. of indiv.	No. of genomes by continent			
			Europe	Africa	America	Asia
European–American	0.01	120	119	1	0	0
African–American	0.17	120	20	100	0	0
Mexican–American	0.39	60	36	5	19	0
Native American	0.05	30	2	0	28	0
Asian–American	0.10	120	12	0	0	108
Total no. of individuals		450				
Total no. of genomes			189	106	47	108

population contains ~85% of the world-wide genetic variation, but none contains all of it (Barbujani et al. 1997). Because a random sample of U.S. residents would include genomes of mostly European origin, the DNA Polymorphism Discovery Resource includes individuals with non-European ancestry at more than their frequency in the U.S. population, although no attempt was made to be exhaustive or precisely balanced. The individuals sampled are U.S. residents who have ancestors from the major geographic regions of the world—Europe, Africa, the Americas, and Asia (Weiss 1998). Many U.S. residents have ancestors from more than one region, and such individuals are included in the DNA Polymorphism Discovery Resource. The European–American group includes non-Hispanic whites; the African–American group includes non-Hispanic blacks; the Americas group includes Mexican–Americans and Native Americans; and the Asian–American group includes individuals whose ancestors came from several countries in East and South Asia.

Table 1 shows the number of individuals sampled from each population group and the expected number of genomes corresponding to the proportion of their ancestry from each geographic region. The second column shows current estimates of the average amounts of admixture for the groups sampled: African admixture for the European–Americans, Native American and African admixture for the Mexican–Americans, and European admixture for the other groups (Hanis et al. 1991; Parra et al. 1998).

All samples came from individuals who gave informed consent explicitly to be part of this DNA Polymorphism Discovery Resource. The consent forms ex-

plain that the purpose of the DNA Polymorphism Discovery Resource is to discover genetic variation. All collection of consents and samples received Institutional Review Board (IRB) approval. For the Native American samples, consent was obtained first from the tribe and then from individuals; in addition, community issues were discussed with other Native Americans and representatives of the Indian Health Service.

To ensure a diverse collection, information on geographic origin and gender was collected for each individual sampled, but once the DNA Polymorphism Discovery Resource was assembled, all identifying and demographic information was removed from the individual samples. Because 52% more individuals gave consent than were included in the DNA Polymorphism Discovery Resource, no one, not even those sampled, knows which individuals are actually included. A summary of the number of individuals sampled from each group is available for the complete collection and the predefined subsets, but no identifiers are associated with individual samples.

The DNA Polymorphism Discovery Resource was designed to be used to discover variants in human DNA, not to assess the frequency of variants in particular groups. Thus, the DNA Polymorphism Discovery Resource is not useful for population-specific medical or anthropological studies, such as the Human Genome Diversity Project (Committee on Human Genome Diversity 1997). The lack of information on geographic origin and phenotype may be seen by some as a lost opportunity for research. However, many ethical issues are raised by including such information, and addressing these issues will take time. The Ethical, Legal, and Social

Implications research program of NHGRI has made these issues a high priority for consideration; they include avoidance of stigmatization, population definition, community consultation, and education about the meaning of genetic variation. These issues must be addressed so that any potential harmful effects of research on human genetic variation are minimized while the benefits are made widely available. Delay in the development of the DNA Polymorphism Discovery Resource while these issues were being addressed would have resulted in lost research opportunities, so the admittedly limited approach described here was adopted as an initial step in this area.

A concern has been raised that researchers might try to identify the ethnicity of the samples (Foster and Freeman 1998). This probably cannot be done precisely, as most variants occur in most populations, and some individuals have ancestry from multiple regions. Nonetheless, the Native Americans agreed to participate only on the condition that such identification would not be attempted. Consequently, attempting to define the population affiliation of the samples in the DNA Polymorphism Discovery Resource is a violation of the consent form and thus a violation of regulation 45 CFR 46 for the protection of human subjects. Users will be required to agree not to attempt to identify ethnicity when they obtain samples and when they access the data derived from the DNA Polymorphism Discovery Resource in the NIH SNP database (see below).

The samples are available from the Coriell Institute for Medical Research as part of the National Institute of General Medical Sciences Human Genetic Mutant Cell Repository (<http://umdnj.edu/locus/nigms/>). The NHGRI, in consultation with the Office for Protection from Research Risks, considers the material in the DNA Polymorphism Discovery Resource to be in the category of human subjects, for which exemption 4, use of anonymous samples, should apply. All use of material in the DNA Polymorphism Discovery Resource must be reviewed by an IRB and approved or designated as exempt. The Coriell Institute requires that researchers submit their proposed research plans so it can check that the plans are in accordance with the consent forms signed by the indi-

viduals who agreed to participate in the DNA Polymorphism Discovery Resource.

The NIH National Center for Biotechnology Information has created a database to collect information on all SNPs found for each sample in the DNA Polymorphism Discovery Resource, as part of their SNP database, dbSNP (<http://www.ncbi.nlm.nih.gov/SNP/>). SNP discoverers are encouraged to submit their data to dbSNP because a central database will give researchers ready access to data on the variants found using the DNA Polymorphism Discovery Resource as well as the ability to verify the SNP data and to find associations among SNPs.

Finding genetic variants on a large scale is a natural extension of the Human Genome Project and has become one of its new goals (Collins et al. 1998). At least 100,000 SNPs are expected to be discovered in the next 3 years and placed in the public domain. These variants will allow researchers to identify the genetic basis for common diseases and to improve the efficacy of drugs and other therapies.

ACKNOWLEDGMENTS

We particularly thank the individuals who agreed to participate in the DNA Polymorphism Discovery Resource and the research groups who provided the samples. We thank the participants in the DNA Polymorphism Discovery Resource planning meeting, held at the NIH on December 8–9, 1997, which laid out the blueprint for the plan described here: Kenneth Buetow, Linda Burhansstipanov, Aravinda Chakravarti, Georgia Dunston, Jonathan Friedlaender, Bronya Keats, Charles Langley, Andrew Merriwether, John Moore, Robert Nussbaum, Madison Powers, Nancy Press, Edward Sondik, Karen Steinberg, Diane Wagener, LeRoy Walters, Bruce Weir, and Kenneth Weiss. We also thank Jeanne Beck, Christine Beiswanger, Jean Findlay, William Freeman, Bettie Graham, Judith Greenberg, Mark Guyer, Clifford Johnson, Robert Johnson, Elke Jordan, Cay Loria, Jennifer Madans, Geraldine McQuillan, Glenn Pinder, Edward Sondik, Elizabeth Thomson, and Lorraine Toji for assistance with the project. We thank the National Institute of General Medical Sciences for supporting this project.

REFERENCES

Barbujani, G., A. Magagni, E. Minch, and L.L. Cavalli-Sforza. 1997. *Proc. Natl. Acad. Sci.* **94**: 4516–4519.

Collins, F.S., M.S. Guyer, and A. Chakravarti. 1997. *Science* **278**: 1580–1581.

Collins, F.S., A. Patrinos, E. Jordan, A. Chakravarti, R. Gesteland, L. Walters. 1998. *Science* **282**: 682–689.

Committee on Human Genome Diversity, National Research Council. 1997. *Evaluating human genetic diversity*. National Academy of Sciences, Washington, D.C.

Foster, M.W. and W.L. Freeman. 1998. *Genome Res.* **8**: 755–757.

Hanis, C.L., D. Hewett-Emmett, T.K. Bertin, and W.J. Schull. 1991. *Diabetes Care* (Suppl. 3) **14**: 618–627.

Heller, M.A. and R.S. Eisenberg. 1998. *Science* **280**: 698–701.

Kerem, B.-S., J.M. Rommens, J.A. Buchanan, D. Markiewicz, T.K. Cox, A. Chakravarti, M. Buchwald, and L.-C. Tsui. 1989. *Science* **245**: 1073–1080.

Kwok, P.-Y., Q. Deng, H. Zakeri, S.L. Taylor, and D.A. Nickerson. 1996. *Genomics* **31**: 123–126.

Landegren, U., M. Nilsson, and P.-Y. Kwok. 1998. *Genome Res.* **8**: 769–776.

Nickerson, D.A., S.L. Taylor, K.M. Weiss, A.G. Clark, R.G. Hutchinson, J. Stengård, V. Salomaa, E. Vartiainen, E. Boerwinkle, and C.F. Sing. 1998. *Nat. Genet.* **19**: 233–240.

Parra, E.J., A. Marcini, J. Akey, J. Martinson, M.A. Batzer, R. Cooper, T. Forrester, D.B. Allison, R. Deka, R.E. Ferrell, and M.D. Shriver. 1998. *Am. J. Hum. Genet.* **63**: 1839–1851.

Risch, N. and K. Merikangas. 1996. *Science* **273**: 1516–1517.

Rommens, J.M., M.C. Iannuzzi, B.-S. Kerem, M.L. Drumm, G. Melmer, M. Dean, R. Rozmahel, J.L. Cole, D. Kennedy, N. Hidaka et al. 1989. *Science* **245**: 1059–1065.

Wang, D.G., J.-B. Fan, C.-J. Siao, A. Berno, P. Young, R. Sapolsky, G. Ghandour, N. Perkins, E. Winchester, J. Spencer et al. 1998. *Science* **280**: 1077–1082.

Weiss, K.M. 1998. *Genome Res.* **8**: 691–697.

Genome Research 8: 1229–1231

A DNA Polymorphism Discovery Resource for Research on Human Genetic Variation

Francis S. Collins, Lisa D. Brooks, and Aravinda Chakravarti

The URL for the Coriell Institute of Medical Research, which was provided in this article, should be <http://locus.umdj.edu/nigms>.

Genome Research 8 (1998)

Author Index

Because of an error in printing, the first page of the Author Index was unalphabetized. The entire Author Index for 1998 appears on the following pages.

Author Index, Volume 8, 1998

- Åslund, L., 809
 Abajian, C., 195
 Acharya, C., 1022
 Adamson, A.A., 791
 Agarwala, R., 211
 Ajioka, J.W., 18
 Aksentijevich, I., 1172
 Alland, D., 435
 Altenhofen, J.L., 404
 Alward, W.L.M., 377
 Ambros, P.F., 929
 Andersson, B., 809
 Andersson, L., 399, 826
 Angrist, M., 683
 Ankener, M., 1022
 Ansari-Lari, M.A., 29
 Apoltolou, S., 1172
 Aravind, L., 1038
 Arbieva, Z.H., 404
 Arbour, N.C., 377
 Assadnia, S., 711
 Auburger, G., 1216
 Audic, S., 524
 Avner, P., 608
 Bagherzadeh, A., 135
 Bailey, E., 569
 Bailey, L.C., Jr., 234, 362
 Bairoch, A., 348
 Baldock, R.A., 859
 Bankier, A.T., 599
 Baptista, P.R., 385
 Barbon, A., 817
 Bard, J.B.L., 859
 Barrett, J.C., 666
 Baskin, D., 1022, 1131
 Beaudet, A.L., 146
 Beck, S., 493
 Beier, D.R., 9
 Belmont, J.W., 29
 Belosludtsev, Y., 741
 Berkes, C., 354
 Bernaola-Galván, P., 916
 Berno, A., 435
 Bhatt, N.K., 146
 Biesecker, L.G., 211
 Bird, A.P., 621
 Blackman, C., 354
 Blake, T., 1172
 Boeke, J.D., 464
 Boguski, M.S., 168
 Boitard, C., 608
 Bono, H., 203
 Boothroyd, J.C., 18
 Boright, A., 1060
 Borodovsky, M., 1154
 Bortoluzzi, S., 817
 Bouck, J., 1074
 Bourgade, F., 531
 Brázma, A., 1202
 Breen, M., 951
 Brignac, S., 741
 Brown, S.D.M., 531
 Brunialti, A.L.B., 531
 Brunk, B.P., 18
 Bucan, M., 698
 Bumgarner, R.E., 1131
 Burke, J., 276
 Burmeister, M., 737
 Burmeister, R., 741
 Byrne, M., 83
 Cabin, D.E., 940
 Callen, D.F., 1172
 Cannata, N., 817
 Carlstén, J., 951
 Carrasquillo, M.M., 111
 Centola, M., 1172
 Cercek, A., 1172
 Chakravarti, A., 111
 Chan, H.M., 135
 Chee, M.S., 1142
 Chen, E.Y., 557
 Chen, L., 1022
 Chen, S.-M., 557
 Chen, X., 549
 Chen, X., 1172
 Chen, X., 1172
 Chevillard, C., 673
 Chinault, A.C., 29, 146
 Choo, K.H.A., 81
 Chowdhary, B.P., 577
 Christensen, B.M., 41
 Christian, S.L., 146
 Cicila, G.T., 711
 Ciufo, S.A., 1131
 Claverie, J.-M., 524
 Clifton, S.W., 331
 Collins, F.S., 1172
 Constancia, M., 881
 Cook, M.W., 543
 Cooper, C., 1022
 Cooper, P.R., 48, 57
 Cowell, L.G., 124
 Crabtree, J., 234
 Crane, C.F., 479
 Cribiu, E.P., 901
 Czihal, R., 842
 d'Alessi, F., 817
 Danieli, G.A., 817
 DasSarma, S., 1131
 Davidson, D.R., 859
 Davies, A.F., 631
 Davies, C., 57
 Davis, E., 509
 Davis, R.W., 848
 Davison, D.B., 276
 Davoine, C.-S., 1216
 Day, C.D., 57
 de Jong, P.J., 57
 Dear, P.H., 599
 Dear, S., 161, 260, 975
 Dearlove, A., 531
 Dedhia, N.N., 313
 Deming, M.S., 599
 Demorest, D.M., 69
 Dene, H., 711
 Deng, A.Y., 711
 Deng, Z., 1172
 Desmond, E., 435
 Dogget, N.A., 1172
 Drenkow, J., 435
 Drobniowski, F., 435
 Drouot, N., 1216
 Dürr, A., 1216
 Durbin, R., 161, 260
 Duret, L., 348
 Dyer, K.D., 599
 Easton, J., 929
 Edfors-Lilja, I., 826
 Efcavitch, J.W., 69
 Eichler, E.E., 758, 791
 Eisen, J.A., 163
 Ellegren, H., 951
 Evans, A., 531
 Evans, G.A., 57, 741
 Ewing, B., 175, 186
 Faraco, J., 427
 Faust, J., 1131
 Ferdig, M.T., 41
 Fernando, S., 531
 Fingert, J.H., 377
 Fischel-Ghodsian, N., 1172
 Fischer, S., 234
 Fizames, C., 1216
 Florea, L., 967
 Foley, R., 339
 Fontaine, B., 1216
 Foster, M.W., 755
 Francomano, C.A., 211
 Freeman, W.L., 755
 Friedman, J.M., 985
 Fröncke, L., 577
 Funa, K., 826
 Gabriel, A., 464
 Galperin, M.Y., 779
 Ganai, M.W., 842
 Garey, J.R., 590
 Garner, H.R., 741
 Garrett, M.R., 711
 Gautheret, D., 524
 Gerhard, D.S., 48
 Ghandour, G., 435
 Gibbs, R.A., 29, 1074
 Gibson, K., 531
 Gibson, M., 234
 Giddings, M.C., 644
 Gilbert, D.A., 69
 Gingeras, T.R., 435
 Giraud-Delville, C., 901
 Glass, J.I., 557
 Glöckner, G., 1060
 Goodman, L., 997
 Goodman, N., 509
 Gordon, D., 195
 Gordon, L.A., 791
 Gorrell, J.H., 29, 1074
 Goto, S., 203
 Grant, O., 741
 Green, P., 175, 186, 195, 414
 Grenet, J., 929
 Greystrom, J., 531
 Groet, J., 385
 Gruber, I., 929
 Gu, Z., 748
 Guénet, J.-L., 531

AUTHOR INDEX

- Guex, N., 348
 Gumucio, D., 1172
 Gunderson, K.L., 1142
 Gururajan, R., 929
 Guyer, M., 413
 Gyapay, G., 1216
 Hall, B., 1131
 Halleck, M.S., 354
 Hamon, M., 1172
 Hannappel, U., 842
 Hanson, R.E., 479
 Hartzell, G., 967
 Hayes, W.S., 1154
 Haynes, A., 531
 Hazan, J., 1216
 Hehl, A., 18
 Heiner, C.R., 557
 Hejtmancik, F., 57
 Hellsten, E., 724
 Helt, G.A., 291
 Herberg, J.A., 631
 Herring, C.D., 673
 Hide, W., 276
 Higgins, M.J., 57
 Hillier, L., 18, 175, 260, 748, 975
 Hodgson, D., 975
 Hoffman, R., 404
 Hoffman, S.M., 791
 Hoheisel, J.D., 809
 Holodniy, M., 435
 Hood, L., 1131
 Hood, L.E., 1022
 Hopkins, K.A., 211
 Horelli-Kuitunen, N., 724
 Horrigan, S.K., 404
 Huang, B., 146
 Huang, X.C., 1142
 Hudson, T.J., 509
 Humphray, S.J., 631
 Hunicke-Smith, S.P., 848
 Hunkapiller, K.L., 557
 Huo, Y.K., 940
 Ivens, A.C., 135
 Ives, J.H., 385
 Jacob, H.J., 268
 Jalanko, A., 724
 Janitz, M., 124
 Jeon, J.-T., 399
 Jiang, J., 268
 Johnston, S.L., 673
 Joly, F., 608
 Jonassen, I., 1202
 Jones, T.A., 385
 Kadotani, H., 427
 Kahan, T., 1172
 Kanehisa, M., 203, 1048
 Karlsson, M., 1085
 Kashuk, C., 111
 Kastner, D.L., 1172
 Kawaguchi, T., 509
 Kawamoto, K., 666
 Kelley, M., 531
 Kelsey, G., 881
 Kenmochi, N., 509
 Kepler, T.B., 124
 Kidd, V.J., 929
 Kijas, J., 826
 Kim, J.M., 464
 Kim, S.Y., 404
 King, M.-C., 306
 Kloos, D.-U., 842
 Koi, M., 666
 Koonin, E.V., 779, 1038
 Korenberg, J.R., 940
 Kouprina, N., 666
 Krizman, D., 1172
 Kubota, T., 146
 Kwok, P.-Y., 549, 748, 769
 Lacey, T., 531
 Lahti, J.M., 929
 Lamerdin, J.E., 791
 Landegren, U., 769
 Lanfranchi, G., 817
 Lange, D., 826
 Lange, K., 222
 Larionov, V., 666
 Lathrop, M., 608
 Lauster, R., 124
 Lavedan, C., 871
 Ledbetter, D.H., 146
 Lee, I.Y., 1022
 Lee, M.K., 306
 Lehrach, H., 385, 493
 Leonard, C.J., 1038
 Lewis, S., 291
 Lewis, S.M., 135
 Li, Q., 748
 Li, W., 916
 Linblad, K., 1085
 Lindgren, G., 951
 Ling, H.-Q., 842
 Lipshutz, R.J., 11142
 Liu, J., 1172
 Liu, L.X., 590
 Liu, P.P., 1172
 Livak, K.J., 549
 Lockhart, D.J., 1142
 Lopez, F., 524
 Loraine, A.E., 291
 Loretz, C., 1131
 Lu, J., 29
 Lyall, A., 493
 Lynch, E.D., 306
 Mahtani, M.M., 100
 Manger, I.D., 18
 Mansfield, E., 1172
 Mardis, E.R., 543
 Marklund, L., 399
 Marklund, S., 826, 951
 Marquardt, A., 48
 Marquette, C., 1216
 Marra, M., 18
 Marth, G., 260
 Martin, J., 590
 Martin, S.A., 146
 Mason, R., 631
 Matesic, L.E., 940
 Mavel, D., 1216
 Mazzarella, R., 1007
 McCombie, W.R., 306
 McCready, P., 791
 McGrane, R.M., 543
 McKee-Johnson, J.W., 940
 McKie, J.M., 834
 McMurray, A.A., 562
 McQueen, H.A., 621
 Melanitou, E., 608
 Menchen, S., 69
 Micheltmore, R.W., 1113
 Mignot, E., 427
 Miller, C.L., 737
 Miller, W., 29, 967, 1074
 Mitchison, N.A., 124
 Mjaatvedt, A.E., 940
 Mohrenweiser, H.W., 791
 Moller, M., 826
 Montagutelli, X., 531
 Morris, M.S., 1142
 Mott, R., 260
 Moyzis, R.K., 1172
 Mundy, C., 531
 Muselet, D., 1216
 Mushegian, A.R., 590
 Mutirangura, A., 146
 Muzny, D., 1074
 Muzny, D.M., 29
 Myers, B.C., 1113
 Newell, W., 493
 Ng, W.V., 1131
 Ni, L., 57
 Nierras, C.R., 419
 Nilsson, M., 769
 Nižetić, D., 385
 Nizetic, D., 631
 Nowak, N.J., 48, 57
 Nystuen, A.M., 377
 Oaks, F., 69
 O'Brien, K., 741
 Oefner, P.J., 848
 Oeltjen, J.C., 29
 Ogata, H., 203
 Oliver, J.L., 916
 Olson, M., 414
 Orias, E., 91
 Oustry, A., 901
 Overton, G.C., 18, 234, 362
 Page, D.C., 509
 Pallavicini, A., 817
 Panussis, D.A., 543
 Paternotte, C., 1216
 Paterson, A.H., 479
 Peitsch, M.C., 348
 Peltonen, L., 724
 Persson, H., 951
 Pettersson, U., 809
 Pickard, B., 881
 Pilgrim, D., 1192
 Piper, M.B., 599
 Poirier, C., 531
 Poirot, O., 524
 Polley, A., 842
 Potier, M.-C., 385
 Pradhan, D., 354
 Price, H.J., 479
 Pruitt, K.D., 4, 86, 170, 334, 422, 572, 686, 763, 864, 1000, 1109
 Prusiner, S.B., 1022
 Puffenberger, E.G., 111
 Quail, M.A., 562
 Ragoussis, J., 631
 Rampoldi, L., 817
 Rapp, J.P., 711
 Raudsepp, T., 577
 Rayner, S., 741
 Reeves, R.H., 940
 Reik, W., 881
 Rhodes, M., 531

- Riblet, R., 673
 Richards, N., 1172
 Richards, R.I., 1172
 Richterich, P., 251
 Ricke, D.O., 1172
 Rifkin, L.L., 543
 Rivera, A., 48
 Rönnstrand, L., 826
 Robertson, H.M., 449
 Robertson, J.M., 69
 Rodriguez-Martinez, H., 826
 Roe, B., 331
 Roos, D.S., 18
 Rosenberg, H.F., 599
 Rosenblum, B.B., 69
 Rosenthal, A., 1060
 Rozen, S., 509
 Rubin, G.M., 291, 967
 Rudnicki, D., 1216
 Rue, E.E., 940
 Salonen, T., 724
 Samson, D., 1216
 Sandberg, K., 951
 Sandgren, B., 951
 Sandmeyer, S., 416
 Scambler, P.J., 834
 Schadt, E.E., 222
 Schaffer, A.A., 211
 Schalling, M., 1085
 Schattevoy, R., 1060
 Scheibler, D., 69
 Scherer, S., 1060
 Scherthan, H., 577
 Schibler, L., 901
 Schimenti, J., 698
 Schlegel, R.A., 354
 Schlessinger, D., 1007
 Schug, J., 234
 Schwartz, S., 29
 Searle, J.B., 1
 Searls, D.B., 362
 Senger, G., 631
 Seto, J., 1022, 1131
 Settles, A.M., 83
 Severin, J., 644
 Severson, D.W., 41
 Shafran, N., 1172
 Shaw, S.H., 111
 Sheffield, V.C., 377
 Shows, T.B., 48, 57
 Si, Y., 479
 Sibley, L.D., 18
 Simionati, B., 817
 Simon, D., 531
 Sinsheimer, J.S., 222
 Siriaco, G., 621
 Sjöberg, K., 1085
 Slagel, J., 1131
 Small, P.M., 435
 Smilinich, N.J., 57
 Smit, A.F.A., 1022
 Smith, D.F., 135
 Smith, L.M., 644
 Smith, R.J.H., 57
 Smith, T.M., 1131
 Snider, J.E., 543
 Sood, R., 1172
 South, A.P., 385
 Stelly, D.M., 479
 Stöhr, H., 48
 Stolovitzky, G., 916
 Stone, E.M., 377
 Straw, R., 531
 Strong, J.T., 543
 Sulston, J.E., 562
 Sutcliffe, J.S., 146
 Sutherland, H.F., 834
 Swiderski, R.E., 377
 Taft, A.S., 41
 Taillon-Miller, P., 748
 Tammi, M., 809
 Tanaka, T., 509
 Taylor, C.L., 834
 Taylor, D., 531
 The Sanger Centre, 1097
 The Washington University Genome Sequencing Center, 1097
 Thelaus, J., 1085
 Thierry-Mieg, J., 260
 Thompson, R.C., 737
 Thorstenson, Y.R., 848
 Tiso, N., 817
 Tomii, K., 1048
 Toppo, S., 817
 Tran, A.-N., 809
 Tripodis, N., 631
 Trowsdale, J., 631
 Tsui, L.-C., 1060
 Ukkonen, E., 1202
 Vaiman, D., 901
 Valle, G., 817
 Van Broeckhoven, C., 385
 Vanguri, S., 464
 Vedula, A., 1172
 Vega-Czarny, N., 1216
 Vilo, J., 1202
 Voit, T., 1216
 Voytas, D.F., 464
 Wadey, R.B., 834
 Walder, R., 711
 Walker, D.R., 779
 Walker, J., 531
 Wan, K.-L., 18
 Wang, E., 435
 Wang, H., 276
 Wang, K., 1022
 Ward, T., 741
 Warner, J.R., 419
 Waterston, R., 18
 Watson, P., 531
 Weber, B.H.F., 48
 Weber, J., 1060
 Weiss, K.M., 691
 Weissenbach, J., 1216
 Wendel, J.F., 479
 Wendl, M.C., 175, 975
 Wenz, H.-M., 69
 Westaway, D., 1022
 Westbrook, C.A., 404
 Weston, P., 531
 Westphall, M., 644
 Wettstein, P.J., 673
 Wheelan, S.J., 168
 Wike, C., 69
 Willard, H.F., 100
 Williamson, P., 354
 Wilson, R., 543
 Wiltshire, T., 940
 Winick, J.D., 985
 Womack, J.E., 731
 Wood, G., 1172
 Wu, J., 644
 Yang, Y.-P., 731
 Yao, H., 1022
 Yaspo, M.-L., 385
 Ying, L., 377
 Zaks, N., 1172
 Zander, C., 1085
 Zhang, L., 135
 Zhang, M.Q., 319
 Zhang, Q.-Y., 711
 Zhang, Z., 29, 967
 Zhao, X.-p., 479
 Zimbello, R., 817

A DNA Polymorphism Discovery Resource for Research on Human Genetic Variation

Francis S. Collins, Lisa D. Brooks and Aravinda Chakravarti

Genome Res. 1998 8: 1229-1231

Access the most recent version at doi:[10.1101/gr.8.12.1229](https://doi.org/10.1101/gr.8.12.1229)

Related Content **Errata for vol. 8, p. 1229**
[Genome Res. February , 1999 9: 210](#)

References This article cites 14 articles, 11 of which can be accessed free at:
<http://genome.cshlp.org/content/8/12/1229.full.html#ref-list-1>

Articles cited in:
<http://genome.cshlp.org/content/8/12/1229.full.html#related-urls>

License

Email Alerting Service Receive free email alerts when new articles cite this article - sign up in the box at the top right corner of the article or [click here](#).

Affordable, Accurate
Sequencing.

To subscribe to *Genome Research* go to:
<https://genome.cshlp.org/subscriptions>