With the complete human genomic sequence being unraveled, the focus will shift to gene identification and to the functional analysis of gene products. The generation of a set of cDNAs, both sequences and physical clones, which contains the complete and noninterrupted protein coding regions of all human genes will provide the indispensable tools for the systematic and comprehensive analysis of protein function to eventually understand the molecular basis of man. Here we report the sequencing and analysis of 500 novel human cDNAs containing the complete protein coding frame. Assignment to functional categories was possible for 52% (259) of the encoded proteins, the remaining fraction having no similarities with known proteins. By aligning the cDNA sequences with the sequences of the finished chromosomes 21 and 22 we identified a number of genes that either had been completely missed in the analysis of the genomic sequences or had been wrongly predicted. Three of these genes appear to be present in several copies. We conclude that full-length cDNA sequencing continues to be crucial also for the accurate identification of genes. The set of 500 novel cDNAs, and another 1000 full-coding cDNAs of known transcripts we have identified, adds up to cDNA representations covering 2%–5% of all human genes. We thus substantially contribute to the generation of a gene catalog, consisting of both full-coding cDNA sequences and clones, which should be made freely available and will become an invaluable tool for detailed functional studies.

[The sequence data described in this paper have been submitted to the EMBL database under the accession nos. given in Table 2.]
protein coding open reading frame (ORF). The majority of the respective cDNA clones are most likely not accessible. The generation of a physical clone set representing all human genes that should be made freely accessible is consequently regarded to have an extremely high impact (Schuler 1997; Pruitt et al. 2000). This would permit the establishment of a catalog of clones to provide the resources needed in the proteomics era where the functions of proteins, their action in pathways, and the possible disease relation are deciphered.

Until recently, the long-cDNA sequencing project carried out at the Kazusa Institute (Nomura et al. 1994; Nagase et al. 2000) Consortium had been the only systematic full-length cDNA sequencing project with a significant output of novel sequence information. The initiation of a new large-scale cDNA sequencing project has been announced lately that is coordinated by the National Institute of Health (Strausberg et al. 1999). We founded a cDNA Consortium in 1997 as part of the German Genome Project and aim at the characterization of the complete sequences of novel human transcripts at the cDNA level.

Here, we report the sequences and analysis of 500 novel human cDNAs that all contain the complete protein coding region. These cDNAs constitute the most valuable essence of 30,000 clones that have been EST sequenced and 3630 fully sequenced cDNAs. Over 1000 cDNAs that cover the complete coding sequence of already known transcripts have been identified in the EST-sequenced clone set. All clones are made available through the Resource Center of the German Genome Project (RZPD).

RESULTS

Libraries and Clones

To identify and sequence novel human cDNAs we have 5‘-EST sequenced >30,000 independent cDNA clones. Bioinformatic evaluation of these sequences (Fig. 1) led to the identification of full-coding clones of already known proteins (>1000), and to cDNA clones lacking database hits, which are potential targets for full-length sequencing. Presumably novel cDNAs were 3‘-EST sequenced and again analyzed for novelty. Out of the initial clones, 3630 cDNAs have been fully sequenced thus far, totaling 8.8 Mb. The sequence subset described here comprises 500 novel human cDNAs that are representations of the complete protein coding part of the original transcripts. Also the other fully sequenced cDNAs represent mostly genes that have not been fully sequenced elsewhere; however, the clones are not likely to contain the complete protein coding region of the respective transcripts, or they contain frame-shift mutations that have probably been introduced during reverse transcription in the cloning process. Therefore, these clones are only of reduced value for functional analysis. The number of bases reported for the 500 full-coding cDNAs is 1,264,620 bp; the average insert size of the clones is 2529 bp. The clones originate from five different cDNA libraries that have been sampled in varying numbers of clones (Table 1) to maximize the likelihood of identifying novel cDNAs.

The calculated average size of the encoded proteins was 470 amino acid residues, which equals the number that has been reported previously for some 1200 genes (Malakowski and Boguski 1998). There was, however, a wide variation between 66 and 1805 residues. The cDNA identifiers, the respective sequence ac-
As with the 5'-UTRs compared with that observed in the previous studies. This discrepancy probably derives from the different average size of the cDNAs described here, as reported by Maka et al. (1998) and Pesole et al. (1996), respectively. This discrepancy probably derives from the different average size of the cDNAs described here, as reported by Maka et al. (1998) and Pesole et al. (1996), respectively.

Features of 5'- and 3'-Untranslated Regions
The 5'-untranslated regions (UTRs) averaged 148 nt, which is the same range as that reported previously (Pesole et al. 1996) but considerably shorter than the number (215 nt) calculated in the UTRdb (Pesole et al. 2000). There was a wide variation in size ranging up to >800 nt (e.g., DKFZp761F182). Even this long 5'-UTR was consistent with the scanning model for translational initiation (Kozak 1999) as there was no AUG codon in this stretch of sequence. In-frame stop codons upstream from the initiator AUG were present in 56.4% (282) of the cDNAs. This number is consistent with that observed with cDNAs isolated from oligo-nucleotide cap ligation libraries (Suzuki et al. 2000), where the cDNAs have been selected to contain the extreme 5' ends of the respective transcripts. The overall GC content in the 5'-UTRs (56.3%) was considerably higher than that in the coding regions (52.6%) and the 3'-UTRs (45.7%). This is consistent with the finding that CpG islands frequently extend into the transcribed sequence (Cross and Bird 1995) whereas elements present in the 3'-UTR are often AU rich (Xu et al. 1997).

The average size of the 3'-UTRs was 926 nt [not including the poly(A) tail], which is considerably larger than the 388 nt and 820 nt reported by Makalowski and Boguski (1998) and Pesole et al. (1996), respectively. This discrepancy probably derives from the longer average size of the cDNAs described here, as compared with that observed in the previous studies. As with the 5'-UTR there was great variability with the size of the 3'-UTR. The translation terminator codon TAA could be part of the polyadenylation signal (e.g., in clone DKFZp564F1272) whereas in other cDNAs the 3'-UTR was found to be >4000 nucleotides (e.g., DKFZp486C1218).

We screened for the presence of repeat structures across the cDNA sequences. The Alu repeat family was most frequently contained in the cDNAs; 7.6% (38) of the cDNA inserts carried this type of repeat. L1 repeats were present in two cDNAs; one cDNA contained both LTR2 and Alu repeats (DKFZp761G18121). The repeat structures were, without exception, located in the 3'-UTR of the respective cDNAs. However, in a number of other cDNAs we found repeats also in the presumed 5'-UTRs. All of these clones turned out to be not completely spliced and/or partial upon further analysis, and having intronic sequence at the 5' ends. We therefore reason that the presence of repeat structures in 5'-UTRs of transcripts is rather rare. The lack of repeat structures in 5' EST sequences has since been implemented as criterion in the selection process of cDNA clones that are targeted to full-insert sequencing to further increase the impact of the project.

Functional Classification
We grouped the cDNAs into functional classes according to homologies of their encoded proteins with already known proteins (Table 2 and Fig. 2): cell cycle, differentiation and development, membrane protein, metabolism, nucleic acid management, protein management, signaling and communication, structure and motility, transport and traffic, and unknown. Sequence annotations in databases sometimes were misleading, and the putative function of a protein could not be simply deduced by regarding the hit with the highest similarity as being the most significant. The integration of results from several search algorithms was necessary to draw relevant conclusions. For example, the deduced protein sequences were evaluated for the presence of specific (protein) sequence patterns necessary for the function/activity of a particular protein [e.g., the DFG/DWG and aPE motifs had to be present in a protein kinase, as reported by Hanks et al. (1988)]. The results of this functional classification are given in Table 2. The largest class constitutes proteins of unknown function (202 cDNAs, 41%). Considering that for another 39 cDNAs (8%) the only prediction that had been possible was that the deduced proteins would contain a putative transmembrane domain, no function could be inferred to a total of 241 cDNAs (48%) of the predicted proteins. But even if functional

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**Table 1. Library Distribution of cDNA Clones Analyzed**

<table>
<thead>
<tr>
<th>RZPD library identifier</th>
<th>Tissue</th>
<th>No. of clones</th>
<th>% of the clones reported</th>
<th>Average insert size (bp)</th>
<th>Average ORF size (aa)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DKFZp434</td>
<td>Testis</td>
<td>204</td>
<td>40.8</td>
<td>2766</td>
<td>562</td>
</tr>
<tr>
<td>DKFZp564</td>
<td>Fetal brain</td>
<td>142</td>
<td>28.4</td>
<td>2049</td>
<td>354</td>
</tr>
<tr>
<td>DKFZp566</td>
<td>Fetal kidney</td>
<td>43</td>
<td>8.6</td>
<td>2210</td>
<td>328</td>
</tr>
<tr>
<td>DKFZp586</td>
<td>Uterus</td>
<td>50</td>
<td>10.0</td>
<td>2506</td>
<td>492</td>
</tr>
<tr>
<td>DKFZp761</td>
<td>Amygdala (brain)</td>
<td>61</td>
<td>12.2</td>
<td>3055</td>
<td>506</td>
</tr>
</tbody>
</table>

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cession numbers (EMBL/GenBank/DDBJ), cDNA sizes, the length of ORFs, the chromosomal location, and functional details for the individual cDNAs are broken down in Table 2. This table is available in its entirety at http://www.dkfz-heidelberg.de/abt0840/GCC.
<table>
<thead>
<tr>
<th>Clone ID</th>
<th>Accession no.</th>
<th>Contig size (bp)</th>
<th>ORF size (aa)</th>
<th>Chromosomal location</th>
<th>Description of best hit</th>
<th>Database accession no.</th>
<th>P-value</th>
<th>Gene family</th>
<th>Tissue</th>
<th>Score</th>
<th># ESTs</th>
</tr>
</thead>
<tbody>
<tr>
<td>DKFZp434A0530</td>
<td>AL136842</td>
<td>2768</td>
<td>254</td>
<td>2p22.1</td>
<td>gene: Borg2; product: “CRIB-containing BORG2 protein”; Homo sapiens CRIB-containing BORG2 protein (BORG2) mRNA, complete cds.</td>
<td>EMBL AF164118</td>
<td>2.1e-99</td>
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<td></td>
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<td></td>
</tr>
<tr>
<td>DKFZp434A1135</td>
<td>AL122068</td>
<td>3010</td>
<td>670</td>
<td>5q13</td>
<td>Homo sapiens Rad 17-like protein (RAD17) mRNA, complete cds. product: “F1N21.3”; The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence.</td>
<td>EMBL AF076838</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>DKFZp434A1315</td>
<td>AL136755</td>
<td>1848</td>
<td>387</td>
<td>1q21.2</td>
<td>Homo sapiens mRNA for cyclin B2, complete cds. cell growth regulating nucleolar protein LYAR—mouse gene: cd23; “SPBC1347.10”; product: “cell division cycle protein 23”; S. pombe chromosome II cosmid c1347.</td>
<td>EMBL AL035548</td>
<td>7e-21</td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>DKFZp434B174</td>
<td>AL80146</td>
<td>1546</td>
<td>398</td>
<td>1p21.3</td>
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<td>4619</td>
<td>855</td>
<td>1q13</td>
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<td>EMBL AL035548</td>
<td>7e-21</td>
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<tr>
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<td>AL136891</td>
<td>3443</td>
<td>628</td>
<td>1q32.1</td>
<td>Homo sapiens mRNA for cyclin B2, complete cds. cell growth regulating nucleolar protein LYAR—mouse gene: cd23; “SPBC1347.10”; product: “cell division cycle protein 23”; S. pombe chromosome II cosmid c1347.</td>
<td>EMBL AB011109</td>
<td>2.6e-148</td>
<td>protein kinase</td>
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<td></td>
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</tr>
<tr>
<td>DKFZp434N0250</td>
<td>AL117525</td>
<td>1584</td>
<td>462</td>
<td>1p43-q44</td>
<td>Homo sapiens AKT3 protein kinase mRNA, complete cds. product: “AKT3 protein kinase”; Homo sapiens AKT3 protein kinase mRNA, complete cds.</td>
<td>EMBL AF135794</td>
<td>2.1e-249</td>
<td>protein kinase</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>DKFZp434P107</td>
<td>AL136894</td>
<td>2380</td>
<td>422</td>
<td>9q34</td>
<td>Homo sapiens AKT3 protein kinase mRNA, complete cds. product: “AKT3 protein kinase”; Homo sapiens AKT3 protein kinase mRNA, complete cds.</td>
<td>PIR S53818</td>
<td>5.9e-10</td>
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Table 2. (Continued)

<table>
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<th>cDNA data</th>
<th>Cell cycle</th>
</tr>
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<tbody>
<tr>
<td>Clone ID</td>
<td>Accession no.</td>
</tr>
<tr>
<td>-----------</td>
<td>---------------</td>
</tr>
<tr>
<td>DKFZp434P2235 AL136860</td>
<td>2027</td>
</tr>
<tr>
<td>DKFZp64A0723 AL80116</td>
<td>2524</td>
</tr>
<tr>
<td>DKFZp64E2182 AL50261</td>
<td>2367</td>
</tr>
<tr>
<td>DKFZp64G1816 AL136599</td>
<td>4775</td>
</tr>
<tr>
<td>DKFZp64K142 AL136636</td>
<td>2241</td>
</tr>
<tr>
<td>DKFZp64L0562 AL80090</td>
<td>941</td>
</tr>
<tr>
<td>DKFZp64N0582 AL50264</td>
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<td>1646</td>
</tr>
<tr>
<td>DKFZp566G0346 AL136719</td>
<td>4503</td>
</tr>
</tbody>
</table>

The cDNAs have been grouped into ten functional categories (see Statistics—Classification) based on sequence similarity data and have been grouped accordingly. The cDNA clones are available from the Resource Center of the German Genome project using the clone ID shown in the first column. The respective sequences are available at the EMBL/GenBank/DDJ databases under the accession numbers shown in the second column. The third column provides the size of the individual cDNA inserts, and the fourth column shows the size of the encoded/predicted proteins. The chromosomal location of the respective genes is shown in the fifth column. Columns 6–8 describe database hits with the highest similarity: The accession number of the best hit (and the database where this hit was found), the description of the best hit, and the p-value of this hit is provided in these three columns, respectively. Similarities were predicted based on BLASTX and BLASTN analyses. Selection of the “representative = best” hit was done using the following criteria: (1) A BLASTX hit was judged better than a BLASTN hit. (2) In cases where the best BLASTX (only with TREMBL database) hit had been calculated from the same nucleotide sequence entry that was the best hit in the BLASTN analysis, the BLASTN hit is given, and (3) Only when no other hits were available, genomic sequence entries are given. If classification of a protein to a major gene family was possible (based on similarity information), the respective family is shown in column 9. Based on the availability of EST information, tissue-specific expression of transcripts has been depicted in columns 10–13, showing the tissue, an arbitrary score (see WWW2001) and the absolute number of ESTs sequenced from that particular tissue (at the time of analysis), respectively.

*This section is excerpted from the full table, available on-line at http://www.dkfz-heidelberg.de/abt0840/GCC.
predictions were possible, the identification, for example, of a protein kinase, neither provides information on its substrates nor on the pathway(s) in which it is involved. Comprehensive functional analyses should be specifically indicated for a set of cDNAs encoding candidates for genes related to disease, such as putative GTP binding proteins, ion channels, and a cDNA encoding a protein that is highly similar to an oncogene.

We further analyzed the cDNAs for the presence of function-related sequence motifs to also identify novel members of gene families. We identified 41 potential leucine zipper proteins (Struhl 1989), 11 proteins with WD-domains (Neer et al. 1994), 11 proteins with predicted zinc finger domains (Parraga et al. 1988), 7 potential protein kinases, and 5 RNA helicases. The respective clones are indicated in Table 2 (column 9). Two cDNAs (DKFZpS66l021 and DKFZp434O1826) contain both a WD-domain and a leucine zipper. A zinc-finger domain is predicted additionally for the deduced protein of the former cDNA.

**Alternative Splicing**

We found 39 (7.8%) cDNAs to represent putative splice variants of already known transcripts. This number is likely to represent the lower end of the fraction of transcripts that are alternatively spliced in vivo as any cDNAs representing already fully-known transcripts were excluded from further sequencing and alternative splice forms should therefore be under-represented in our set. We found ORFs with additional exons (e.g., DKFZp761B192), skipped exons (e.g., DKFZpS64A032), and alternative exons including one containing the translational start codon and resulting in a different N terminus of the deduced peptide (e.g., DKFZp434J154).

The percentage of alternatively spliced cDNAs appeared to be slightly higher in fetal brain, 40% of the alternatively spliced cDNAs originate from fetal brain whereas only 28% of all cDNAs analyzed originate from this tissue. This finding is consistent with reports by Sutcliffe and Milner (1988) and Hanke et al. (1999). The presence of intron sequences reminiscent in many cDNA sequences available in public databases, however, might lead to an overestimation of the extent of alternative splicing that is taking place in vivo. Experimental evidence will therefore be needed to confirm presumed alternative splice forms.

**Representation of cDNAs in the UniGene Data Set**

Depending on the true number of human genes, about 60%–90% have already been identified by partial sequencing of >2,000,000 cDNAs (EST sequencing). Overlapping EST sequences have been clustered to break down this large number of ESTs to comprehensive collections that should consist of nonredundant data sets having one representation (cluster) for every gene. The most widely accepted clustering data set is the UniGene (Schuler et al. 1996) resource at the NCBI (http://www.ncbi.nlm.nih.gov/UniGene/). This dataset currently consists of >90,000 clusters of mostly partial sequences. Consensus sequences of these clusters are available from http://www.rzpd.de. To investigate the representation of the novel cDNAs reported here in the UniGene data set and to evaluate the maximum number of genes that could be represented there, we aligned the full-length sequences with the UniGene database. The version of UniGene (Build 105) that was used in the analysis consisted of 92,931 clusters with 10,501 clusters containing known genes.

In total, 626 UniGene clusters matched with 472 out of the 500 full-coding cDNA sequences. The majority of cDNAs (342, 68%) was represented by one UniGene cluster. An additional 130 (26%) cDNAs were represented by 284 separate UniGene clusters (Fig. 3). Thus, a number of UniGene clusters could be linked by the full-length cDNA sequences. An example of three UniGene clusters that were joined with one cDNA is given in Figure 4. We analyzed the ESTs and clusters that were placed internal to the cDNAs reported here and found that most of the EST clones making up these clusters had originated from internal priming events (mostly in reminiscent intron sequences) and not from alternative polyadenylation. The number of 640 clusters that was hit with 472 cDNA sequences implies that there is ~35% redundancy in UniGene. As the average size of the human transcripts in general has been estimated to be in the same range as the average size of the cDNAs reported here (by quantification of Northern blots that had been hybridized with a labeled oligonucleotide dT probe; N. Nomura, pers. comm.), our finding should be representative. However, the true
number of genes represented in UniGene will further condense as a considerable fraction of the UniGene clusters are singletons (~39%), which are clusters made up by only one cDNA, and several of these will eventually turn out to be artifacts. Consequently, we estimate the number of independent genes that are represented in UniGene to be 50,000 at most.

A fraction of 6% (28 cDNAs) did not have hits in the UniGene database (cutoff, sequence identity >95% in 50 bp). The low number of the novel cDNAs without UniGene matches might in turn imply that >90% of all human genes were already represented in this database. However, we would rather assume that an unknown number of genes has escaped cloning and/or identification so far as the respective transcripts might be expressed only at extremely low levels or in very specialized cell types or differentiation stages. A proper selection of tissues or even single cell types for cDNA library production will be a critical issue for the detection and cloning also of these rarely expressed transcripts. For example, fetal brain, although very complex in expression, has been so deeply sampled in EST projects especially the IMAGE 1NIB library (Soares et al. 1994) but also in full-length cDNA sequencing (Nagase et al. 2000) that the novelty rate (3 of 142 cDNAs, 2%) is rather low in this tissue. In contrast, testis currently appears to have a higher potential for identifying transcripts not yet covered by ESTs (19 of 204 cDNAs, 9%).

Tissue Specificity of Expression
To analyze for a possible tissue specificity of expression we aligned the cDNA sequences with the EST database dbEST. ESTs originating from pooled tissues and tissues with unclear origin were excluded. Each cDNA received a score indicating the degree of tissue specificity. The higher this score, the higher the likelihood that expression of the particular transcript should be restricted to that tissue. A ubiquitously expressed transcript would have had a score of one. Only cDNAs with scores of five or higher are indicated in Table 2 (columns 10–12). In total, the expression of 22 transcripts appeared to be restricted to only one tissue with matching tissues of our cDNA and the ESTs (Table 2). Six brain-derived cDNAs only matched ESTs that had derived from brain tissues. Most of the cDNAs encode proteins that are either involved in the cell cycle or signaling pathways, for example, a stathmin-like protein and a protein similar to a calmodulin-binding protein. Only one of the six cDNAs encodes a protein of unknown function. Another 15 testis cDNAs had hits only with ESTs from testis/male genital tract. Although predictions could be made for three of the encoded proteins (a predicted sperm flagellar protein, a putative neurotransmitter transporter, and a possible nuclear pore protein), the other 12 cDNAs encode proteins of unknown function. The only uterus cDNA predicted to be specifically expressed in uterus/ovary encodes a putative chaperone-associated protease, which could indicate that this protein might be involved in the differentiation of the egg or embryo. The expression of several testis-derived transcripts appeared to be very selective as the scores calculated for these cDNAs were rather high, compared with scores obtained with other cDNAs and tissues (Table 2). This also matches the observation that the novelty rate, counting cDNAs without EST hits, was highest in the testis library (see above).

cDNAs Mapping to Human Chromosomes 21 and 22
To demonstrate the power of mapping genes by aligning cDNA with genomic sequences we downloaded the sequences of the first two completely sequenced human chromosomes 21 (Hattori et al. 2000) and 22...
respective cDNAs are given in columns 6 and 7. The number of amino acid residues is given first, followed by the number of the residues deduced from the cDNA sequence. A dash (-) is inserted for proteins that were not predicted. The predicted localization as based on mainly STS data is given in the fourth column, followed by the exact localization of the genes (gene locus in bp as defined in the published sequences of chromosome 21, http://hgp.gsc.riken.go.jp, and chromosome 22, http://www.sanger.ac.uk/cgi-bin/cwa/22cwa.pl). The accession numbers of the genomic clone(s) covering the genes, identifiers of predicted transcripts (if available; dashes indicate nonpredicted genes), the number of predicted exons out of the number of identified exons (based on cDNA sequence), and the number of UniGene clusters that were hit with the respective cDNAs are given in columns 6–9.

Whereas 13 of the novel cDNAs map to chromosome 22, only two cDNAs map to chromosome 21. This could either be a reflection of the generally higher gene content of chromosome 22 (554 compared with the 225 predicted genes on chromosome 21) or be a result of the fact that the percentage of genes that had been known previously is higher for chromosome 21 (this chromosome had long been carefully investigated because of its clinical implications, e.g., in Down syndrome). A third explanation could be a correlation between chromosomal location and global expression levels of the individual genes, as has been proposed by Ewing and Green (2000), with genes mapping to chromosome 21 in general possibly being expressed at lower levels compared with genes located on chromosome 22.

By combining the genomic and cDNA data, the exact gene structures of all 15 cDNAs could be determined. Although all cDNAs were covered by UniGene clusters, only 8 of the 15 genes had been predicted from the genomic sequence. Most of these gene predictions were precise, identifying the majority or all exons. The number of amino acid residues varied in most cases only marginally from the number deduced from the cDNA sequence. However, one cDNA (DKFZp564B212) merged three predicted transcripts to only one gene and overlapped another gene (bK445C9.C22.3) predicted on the opposite strand. In total, seven genes had completely failed to be predicted, some of which encode rather large ORFs and consist of several exons.

The mapping information that is based on genomic sequence not only gives the exact localization of individual genes but also provides information on the context of these genes in view of neighboring genes (e.g., DKFZp434B194 and DKFZp564B212 are only 13 kb apart) and the presence of probable additional gene copies. For example, the genes of cDNAs DKFZp434N035 and DKFZp434P211 appear to be present on chromosome 22 in 2 and 9 highly similar copies (>85% sequence identity on nucleotide level), respectively. DKFZp434P211 could indicate a cluster of highly similar POM121 related genes (Fig. 5), the first of which was described by Kawasaki et al. (1997). Two copies (2850458 and 2871777) seem to be ancient and inactive as they are incomplete, contain several frame shifts, and share only 89% and 87% sequence identity with the cDNA sequence in exon 1, respectively. The other copies are highly similar (>95% identity on nucleotide level). Further experiments will be necessary to investigate how many of the gene copies are expressed and to explain the presence of the stop codon at position 429 in three of the gene copies (and in the cDNA) but a sense codon in this position in four other gene copies, possibly leading to an extended protein product. EST evidence is available for transcripts of both types of genes (e.g., for copies 5055694 and 8220566).

**DISCUSSION**

The considerable fraction of genes that were not predicted in the analysis of the chromosome 21 and 22 sequences was somewhat surprising, as EST data and UniGene clusters (Table 3) were available for these genes. Three of the genes that were not predicted even appear to be present in more than one copy on the same chromosome, namely, within 6 Mb on chromosome 22. But even if all genes could be identified via bioinformatic procedures, the alternative use of exons and promoters (alternative splicing) constitutes a problem that cannot currently be solved with knowledge of the genomic sequence alone. Consequently, only the availability of cDNA sequences enables us to define the precise protein coding parts of the genome and, in conjunction with the genomic counterpart, to also define the composition of exons in alternatively spliced transcripts of the same gene. Both the sequence and the chromosomal location of genes are important pieces of information supportive also in the process of defining and analyzing candidate disease genes.

Most of the genome has been unraveled as draft sequence, where sequence submissions of individual genomic clones are released in several contigs of varying length. These contigs are usually not ordered relative to one another. However, automated assembly and annotation tools like GoldenPath (http://genome.ucsc.edu/goldenPath/hgTracks.html) try to overcome this problem and prove to be extremely helpful for the mapping of cDNAs. The availability of cDNA sequences in turn immediately helps to identify the genes that are located on the respective chromosomes 21, http://hgp.gsc.riken.go.jp, and chromosomal 22, http://www.sanger.ac.uk/cgi-bin/cwa/22cwa.pl). The accession numbers of the genomic clone(s) covering the genes, identifiers of predicted transcripts (if available; dashes indicate nonpredicted genes), the number of predicted exons out of the number of identified exons (based on cDNA sequence), and the number of UniGene clusters that were hit with the respective cDNAs are given in columns 6–9.

Whereas 13 of the novel cDNAs map to chromosome 22, only two cDNAs map to chromosome 21. This could either be a reflection of the generally higher gene content of chromosome 22 (554 compared with the 225 predicted genes on chromosome 21) or be a result of the fact that the percentage of genes that had been known previously is higher for chromosome 21 (this chromosome had long been carefully investigated because of its clinical implications, e.g., in Down syndrome). A third explanation could be a correlation between chromosomal location and global expression levels of the individual genes, as has been proposed by Ewing and Green (2000), with genes mapping to chromosome 21 in general possibly being expressed at lower levels compared with genes located on chromosome 22.

By combining the genomic and cDNA data, the exact gene structures of all 15 cDNAs could be determined. Although all cDNAs were covered by UniGene clusters, only 8 of the 15 genes had been predicted from the genomic sequence. Most of these gene predictions were precise, identifying the majority or all exons. The number of amino acid residues varied in most cases only marginally from the number deduced from the cDNA sequence. However, one cDNA (DKFZp564B212) merged three predicted transcripts to only one gene and overlapped another gene (bK445C9.C22.3) predicted on the opposite strand. In total, seven genes had completely failed to be predicted, some of which encode rather large ORFs and consist of several exons.

The mapping information that is based on genomic sequence not only gives the exact localization of individual genes but also provides information on the context of these genes in view of neighboring genes (e.g., DKFZp434B194 and DKFZp564B212 are only 13 kb apart) and the presence of probable additional gene copies. For example, the genes of cDNAs DKFZp434N035 and DKFZp434P211 appear to be present on chromosome 22 in 2 and 9 highly similar copies (>85% sequence identity on nucleotide level), respectively. DKFZp434P211 could indicate a cluster of highly similar POM121 related genes (Fig. 5), the first of which was described by Kawasaki et al. (1997). Two copies (2850458 and 2871777) seem to be ancient and inactive as they are incomplete, contain several frame shifts, and share only 89% and 87% sequence identity with the cDNA sequence in exon 1, respectively. The other copies are highly similar (>95% identity on nucleotide level). Further experiments will be necessary to investigate how many of the gene copies are expressed and to explain the presence of the stop codon at position 429 in three of the gene copies (and in the cDNA) but a sense codon in this position in four other gene copies, possibly leading to an extended protein product. EST evidence is available for transcripts of both types of genes (e.g., for copies 5055694 and 8220566).

**DISCUSSION**

The considerable fraction of genes that were not predicted in the analysis of the chromosome 21 and 22 sequences was somewhat surprising, as EST data and UniGene clusters (Table 3) were available for these genes. Three of the genes that were not predicted even appear to be present in more than one copy on the same chromosome, namely, within 6 Mb on chromosome 22. But even if all genes could be identified via bioinformatic procedures, the alternative use of exons and promoters (alternative splicing) constitutes a problem that cannot currently be solved with knowledge of the genomic sequence alone. Consequently, only the availability of cDNA sequences enables us to define the precise protein coding parts of the genome and, in conjunction with the genomic counterpart, to also define the composition of exons in alternatively spliced transcripts of the same gene. Both the sequence and the chromosomal location of genes are important pieces of information supportive also in the process of defining and analyzing candidate disease genes.

Most of the genome has been unraveled as draft sequence, where sequence submissions of individual genomic clones are released in several contigs of varying length. These contigs are usually not ordered relative to one another. However, automated assembly and annotation tools like GoldenPath (http://genome.ucsc.edu/goldenPath/hgTracks.html) try to overcome this problem and prove to be extremely helpful for the mapping of cDNAs. The availability of cDNA sequences in turn immediately helps to identify the genes that are located on the respective chromosomes.
### Table 3. Analysis of Gene Structures of cDNAs Mapping to Human Chromosomes 21 and 22

<table>
<thead>
<tr>
<th>Clone D</th>
<th>Contig size (bp)</th>
<th>ORF size (aa)</th>
<th>Predicted chromosomal location</th>
<th>Chromosomal location relative to the published genomic sequences</th>
<th>Accession no. of genomic sequence entry</th>
<th>Annotation of predicted transcript</th>
<th>No. predicted/No. true exons</th>
<th>No. of UniGene clusters</th>
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<tr>
<td><strong>CHROMOSOME 21</strong></td>
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<td>21q</td>
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<td>45/45</td>
<td>22q13.2-q13.33</td>
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<td>AL035658</td>
<td>dJ756G23.3</td>
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<td>0/2</td>
<td>1</td>
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</table>
genomic clones, to support the ordering of the draft sequence contigs, and to narrow down the regions where putative regulatory elements should reside. Thus, cDNA and genomic sequences are complementary and synergistically add information. The BLAST analysis of cDNAs and matching genomic sequences showed that only 32 cDNAs did not have corresponding genomic matches (not covered, NC in Table 2, column 5), which is the number expected because >91% of the genomic sequence are reported to be unraveled. The chromosomal localization could be approximated for 449 cDNAs using the GoldenPath web browser; 21 BACs had not been mapped (NM). The accession numbers of these BACs are provided in column 5 of Table 2. The combination of genomic and cDNA sequence provides the gene structures with precise exon–intron boundaries and defined intron sequences. Furthermore, it will become increasingly important to not only have the human genes identified but rather to characterize the precise functions of the en-

Figure 5 Multiple sequence alignment of cDNA DKFZp434P211 with POM121-related 1 (accession no. D87002) and sequences from chromosome 22 demonstrate the presence of a cluster of POM121-related genes. The individual genomic sequences were named after the start of the first exon relative to the cDNA: The open reading frame (ORF) was defined according to the predicted protein of the cDNA and of POM121-related 1. Genes located on the plus and minus strands of chromosome 22 are indicated with + and −, respectively. The cDNA sequence of DKFZp434P211 was taken as reference; identical residues in other sequences are indicated with a dot, residues deviating from the consensus are printed. Asterisks (*) indicate stop codons. The genomic sequences 2850458 and 2871777 are in italics because these copies deviate from the other copies by a premature stop or frame shifts and a large insertion, respectively, and are probably not expressed. In these two gene copies the initiator ATG is mutated. Dashes (-) were inserted by the software (CLUSTAL) to optimize the alignment.
coded proteins and also the functions of those transcripts that are not translated. To this end, full-coding cDNA representations are indispensable tools, for example, for the subcloning of exactly defined ORFs into expression vectors. However, currently only -11,000 nonredundant cDNA sequences have been deposited in public databases which are supposed to contain the complete protein coding ORF. An even lower number of these full-coding ORFs can be obtained as cDNA clones through commercial or noncommercial providers (e.g., ATCC, Genome Systems, Research Genetics, HGMP, Resource Center of the German Genome Project) and would thus be available for functional research.

Recently, the range of estimates given for the number of human genes has evolved to the lower end, because in two calculations only -35,000 human genes have been predicted (Ewing and Green 2000; Roest Crollius et al. 2000). Our data would also hint at a lower than previously expected number, as we would estimate the number of genes currently represented in UniGene to be 50,000 at most. Still, the real number of human genes needs to be established by further cDNA and also by comparative genomic sequencing (e.g., of the mouse). If it should hold true, however, that the number of genes in human was indeed only about two-fold higher than the -18,000 genes that have been predicted for Caenorhabditis elegans by The C. elegans Sequencing Consortium (1998) the question would arise as to where the difference in complexity between these two life forms originated. Because the sheer doubling of gene number would not be likely to account for all differences, the comprehensive analysis of gene and protein function(s) would become an even greater problem. This is because one solution to this apparent paradox could be the acquisition of multiple functions by many of the proteins expressed in human. This would add another order of complexity to the line starting with the genome and continuing through the transcriptome with alternative splicing, the proteome with post-translational modifications, and finally (?) to a ‘functome,’ which would cover the acquisition of diverse functions by the same protein depending on its cellular and subcellular environment. Several examples of such multiple usages of proteins have already been described (Jeffery 1999).

In the set of 500 novel cDNAs described here, only about half of the deduced proteins could be functionally classified, while identification, for example, of a protein kinase does not provide information on substrates or pathways in which this protein is involved. Additionally, half of the predicted proteins remain without any hint as to their possible function. With this in mind, the establishment of a gene catalog which will eventually contain a nonredundant set of full-coding cDNA sequences and clones covering every human gene, is prerequisite to carry out the experiments needed to precisely identify the protein function(s). This catalog should be the result of a global enterprise integrating the data and clones from as many projects and researchers as possible and could be an extension of already existing databases such as GeneCards (Rebhan et al. 1998) and RefSeq (Pruitt et al. 2000) with, for example, links to the clone providers mentioned above. In addition to the novel full-coding cDNA sequences and clones described here, we have identified over 1000 cDNAs which comprise full-coding representations of previously known genes. In combination, these cDNAs represent 2%–5% of all human genes and will thus be a substantial part of the catalog and be ideal tools to carry out functional analyses. Although the 500 novel cDNAs have been fully sequenced and can be directly used in functional analysis, the cDNAs representing known genes need further characterization because these are not fully sequenced. To this end, we amplify the ORFs from these cDNAs and verify the predicted size. These ORFs are then cloned into a bacterial expression vector which contains a N-terminal fusion with the GFP. As the Gateway system (Life Technologies) is employed in the cloning process, ORFs can be shuttled into any expression vector (Simpson et al. 2000). Only intact reading frames (no PCR frame shifts, no introns, no frame shifts in the clone) lead to fluorescent colonies as the ORF extends uninterrupted into the GFP. The Gateway entry clones of the verified genes are also made available through the Resource Center.

To address the systematic functional analysis of the novel proteins, a large-scale project dealing with the subcellular localization and functional analysis of the proteins encoded by newly identified cDNAs reported here is underway (Simpson et al. 2000). Thus, the gene catalog in upcoming years will form the basis for the large-scale and comprehensive functional analysis of human genes and proteins, which is crucial to understand the basis of human life, disease, and death.

METHODS

Library Construction

SMART Libraries
The DKFZpS64 (human fetal brain) and DKFZpS66 (human fetal kidney) libraries were generated using the SMART kit (Clontech). PCR amplification of the cDNA was necessary to obtain enough cDNA for cloning. The first-strand primer did contain the KS sequence of the pBluescript vector (Stratagene) and any base but T (IUB code = V) in the 3’-terminal position of the primer [TCGAGTCGACGGTATCGATAAG(T)_{19}]_{11032}. Amplification of the primary cDNA with AmpliTaq (Perkin Elmer) and Pfu (Stratagene) DNA polymerases in a ratio of 19/1 (vol/vol) was carried out with primers that contained...
uracil residues (3’ primer: CAUCAUCAUCAUGAGGTCGAC
GGTATCGTAAAG; 5’ primer: CAUCAUCAUCAUTACGCT
GGAGAGAGACGAGACAA) and that were compatible with
the pAMP1 (Life Technologies) cloning sites for directional
cloning. Prior to cloning, the cDNA was size fractionated on
an agarose gel. Fragments >2 kb were excised and extracted
from the gel using GE LAse (Epicent er). Cloning was done us-
ing uracil deglycosilase (UDG, LifeTechnologies) and chemi-
cally competent bacterial cells (XL-2 Blue, Stratagen e).

Conventional Libraries
The DKFZp434 (human adult testis), DKFZp86 (human adult
uterus), and DKFZp761 (human adult amygdala) libraries were
generated using conventional approaches (Gubler and Hof-
man 1983), employing a NotI-dT V primer for first-strand
synthesis [GAGGGAGGGC(T)3]5V]. After second-strand syn-
thesis, SauI adapters were ligated to the blunted cDNA. Then
the cDNA was cut with NotI to generate SauI–NotI-compatible
ends at the 5’ and 3’ ends of the cDNA, respectively, to
allow directional cloning. The cDNAs were then size-selected
on agarose gels in two dimensions and cloned into pSPORT1 pre-
cut with SauI and NotI (Life Technologies).

Availability of cDNA Libraries and Clones
All libraries have been arrayed into 384-well microtiter plates
and spotted on high-density nylon membranes. Each library
consists of 27,000 clones or multiples thereof. High-density
clone filters and individual clones are available through the
Resource Center of the German Genome Project (http://
www2.mips.biochem.mpg.de; clone@pzd.de).

Selection of Clones for Sequencing
First, 5’ ESTs were systematically generated from all clones of
384-well microtiter plates. The sequences were analyzed with
BLASTN (Altschul et al. 1990) and BLASTX (Gish and States
1993) against EMBL, PIR, SWISSPROT, and TREMBL databases
for the lack of identical (>95% identity over 50 bp) matches
with known cDNAs, and for the presence of ORFs.

Clones with novel sequences were 3’ end sequenced. These 3’
ESTs were checked for the lack of matches with known genes in public databases, for repeat structures, and for the
presence of polyadenylation signals. Clones matching the
selection criteria were subjected to full-length sequencing.

Sequencing Methodology and Strategy
Sequencing was done preferentially using dye terminator
chemistry (Applied Biosystems or Amersham) on ABI 377 au-
tomated DNA sequencers; one partner used EMBL prototype
instruments (Wiemann et al. 1995) mainly with dye primer
chemistry. Primer walking (Straus et al. 1986) was the pre-
ferr ed sequencing strategy for the full-length sequencing of
cDNAs. Design of walking primers was done preferentially
using software (e.g., Schwager et al. 1995; Haas et al. 1998)
that permitted the complete automation of this usually-time-
consuming process and thus helped in the parallel processing
of large numbers of clones.

Bioinformatic Analysis
Every complete cDNA sequence was compared with the se-
quences in EMBL, EMBL-EST, EMBL-STS using BLASTN
(Altschul et al. 1990). Searches against EMBL were done to
determine whether the cDNAs were already known and to
identify any genomic sequence information available that
would cover the respective genes. Searches against EMBL-EST
were performed to analyze for the abundance of transcripts,
to obtain information on a possible tissue specificity of ex-
pression, and to identify putative alternative splice forms or
alternative use of polyadenylation signals. The annotations
on the source tissue of the respective EST clones were parsed
from the database entries to calculate the real ratio versus the
expected ratio of expression according to the equation: (# hits
tissue/total # hits)/(# ESTs tissue/total # ESTs). A gene that was
transcribed at a constant level in many tissues would have a
ratio of one. Significant higher or lower ratios would indicate
increased or decreased levels of transcription in the tissue,
respectively. To identify tissue-specific expression, the para-
eters were set to >4 ESTs matching the respective cDNA that
needed to have been sequenced from a given tissue, and the
cutoff for the ratio of overexpression was set to five. ESTs
originating from pooled tissues or that were of unspecified
origin were disregarded in this analysis. To obtain chromo-
osomal mapping information, the sequences were aligned with
the EMBL-STS database.

The potential protein-sequences were identified by a
search for the longest ORF in each of the three forward frames
with a minimum length of 90 codons. The deduced protein
sequences were searched against the nonredundant protein
data set of PIR, SWISSPROT, and TREMBL (BLASTP, using
the SEG-filter by Wootton (1994)). Any cDNAs without ORF >50
codons were analyzed with BLASTN against TREMBL to iden-
tify even shorter ORFs present.

BLASTX searches were performed against a nonredund-
ant protein database comprising PIR, SWISSPROT, and
TREMBL. The SEG-filter was used to screen for potential frame
shifts in the coding sequences of the cDNAs and to identify
cDNAs that were not fully spliced or were alternatively
spliced. The protein sequence was then transferred to PEDANT
(Frishman and Mewes 1997). PEDANT performed automated
database searches: psiBLAST (Altschul et al. 1997), an iterated
profile search procedure; HHMER (Sonnhammer et al. 1997), a
Hidden Model vector software which uses statistical descrip-
tions of a sequence family’s consensus; and BLIMPS (Wallace
and Henikoff 1992) for similarity searches against the
BLOCKS (Henikoff et al. 2000) database. PROSITE protein
sequence patterns were identified by ProSearch (Kolakovski
et al. 1992), CLUSTAL-W (Thompson et al. 1994) was used for
multiple sequence alignments of DNA and proteins. Trans-
membrane regions were identified by ALOM2 (Klein et al.
1984), and signal peptides in secreted proteins by SIGNALP
(Nielsen et al. 1997). SEO (Wootton and Federhen 1993) has
been employed to detect low-complexity regions in protein
sequences and COILS (Lupas et al. 1991) for the detection of
coiled coils. For the functional classification of the cDNAs
sequence, identities with E-values <10E–30 (BLASTN) and
<10E–10 (BLASTX) were accepted to be significant. The com-
prehensive bioinformatic data on all cDNAs analyzed by the
Consortium are accessible at http://www2.mips.biochem.
mpg.de/proj/cDNA/index.html. Mapping of the cDNAs to
chromosomes was done first by BLAST analysis of the cDNA
sequences against the human genomic sequence (NCBI–htgs
database), followed by identifying the mapping position with
help of the GoldenPath (Jim Kent, UCSC) browser (http://
genome.ucsc.edu/goldenPath/hgTracks.html).

Availability of Clones and Further Information
All clones described here, and the other clones analyzed by
the German cDNA Consortium, are available from the Re-
source Center of the German Genome Project (http://
genome.org)
www.rzpd.de; clone@rzpd.de). The comprehensive bioinformatic data on all cDNAs analyzed by the Consortium are accessible at http://www2.mips.biochem.mpg.de/proj/cDNA/index.html. Additional information about the analysis of the described set of cDNAs is available at http://www.dkfz-heidelberg.de/abt0840/GCC. The full version of Table 2 can be obtained at this location in Excel, tab-delineated text, and pdf formats.

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