| Domain superfamily | LBD type             | Domain model | No. of LBDs | % of each domain model |
|--------------------|----------------------|--------------|-------------|------------------------|
| 4HB_MCP            | Single 4HB           | 4HB_MCP_1    | 12754       | 17.597                 |
|                    | TarH                 |              | 2840        | 3.918                  |
|                    | CHASE3               |              | 1133        | 1.563                  |
|                    | HBM                  |              | 906         | 1.250                  |
|                    | **Subtotal:**        |              | **17633**   | **24.328**             |
|                    | Double 4HB           |              | 12754       | 17.597                 |
|                    | TarH                 |              | 2840        | 3.918                  |
|                    | CHASE3               |              | 1133        | 1.563                  |
|                    | HBM                  |              | 906         | 1.250                  |
|                    | **Subtotal:**        |              | **17633**   | **24.328**             |
| Cache-like         | Double Cache         | dCache_1     | 11216       | 15.475                 |
|                    |                      | Cache_1-Cache_2 | 1381     | 1.905                  |
|                    |                      | dCache_3     | 598         | 0.825                  |
|                    |                      | dCache_2     | 560         | 0.773                  |
|                    |                      | Yku1_C       | 5           | 0.007                  |
|                    | **Subtotal:**        |              | **12754**   | **17.597**             |
|                    | Single Cache         | scache_2     | 4049        | 5.586                  |
|                    |                      | scache_3_3   | 779         | 1.075                  |
|                    |                      | scache_3_2   | 179         | 0.247                  |
|                    |                      | Dcisf_rec    | 90          | 0.124                  |
|                    |                      | CHASE4       | 35          | 0.048                  |
|                    |                      | CHASE8       | 23          | 0.032                  |
|                    | **Subtotal:**        |              | **18915**   | **26.097**             |
| Unknown            | Unknown              | UNKNOWN      | 15776       | 21.766                 |
| PAS                | PAS                  | PAS_3        | 6704        | 9.249                  |
|                    |                      | PAS_4        | 1459        | 2.013                  |
|                    |                      | PAS_8        | 430         | 0.593                  |
|                    |                      | PAS_7        | 316         | 0.436                  |
|                    |                      | PAS_10       | 3           | 0.004                  |
|                    |                      | PAS_6        | 1           | 0.001                  |
|                    | **Subtotal:**        |              | **11028**   | **15.215**             |
| GAF                | GAF                  | GAF          | 786         | 1.084                  |
|                    |                      | GAF_3        | 232         | 0.320                  |
|                    |                      | GAF_1        | 1           | 0.001                  |
|                    | **Subtotal:**        |              | **1019**    | **1.406**              |
| Protoglobin        | Protoglobin          | Protoglobin  | 1682        | 2.321                  |
|                    |                      | Globin       | 20          | 0.028                  |
|                    |                      | Bac_globe    | 6           | 0.008                  |
|                    | **Subtotal:**        |              | **1708**    | **2.357**              |
| PBP                | Periplasmic Binding Proteins | Phosphonate-bd | 74         | 0.102                  |
|                    |                      | SBP_bac_5    | 64          | 0.088                  |
|                    |                      | SBP_bac_3    | 60          | 0.083                  |
|                    |                      | Peripla_BP_4 | 50          | 0.069                  |
|                    |                      | SBP_bac_6    | 36          | 0.050                  |
|                    |                      | OpuAC        | 13          | 0.018                  |
|                    |                      | Peripla_BP_5 | 9           | 0.012                  |
|                    |                      | DctP         | 8           | 0.011                  |
|                    |                      | SBP_bac_1    | 5           | 0.007                  |
|                    |                      | Peripla_BP_3 | 4           | 0.006                  |
|                    |                      | NMT1_2       | 4           | 0.006                  |
|                    |                      | Peripla_BP_6 | 3           | 0.004                  |
|                    |                      | NMT1         | 2           | 0.003                  |
|                    | **Subtotal:**        |              | **332**     | **0.458**              |
| HNOX-like          | Heme and NO binding  | HNOB         | 235         | 0.324                  |
| 4Fe-4S             | Iron-sulfur cluster binding | FeS         | 78         | 0.108                  |
|                    |                      | Fe4_10       | 54         | 0.075                  |
|                    |                      | Fe4^-        | 46         | 0.063                  |
|                    |                      | Fe4_7        | 14         | 0.019                  |
|                    |                      | Fe4_9        | 11         | 0.015                  |
|                    |                      | Fe4_6        | 3          | 0.004                  |
|                    |                      | Fe4_20       | 3          | 0.004                  |
|                    | **Subtotal:**        |              | **209**     | **0.288**              |
| GPCR-A             | GPCR-like            | 7TMR-DISM_7TM | 43         | 0.059                  |
| NADP-Rossman       | NAD binding          | GFO_IDH_MocA | 15         | 0.021                  |
|                    |                      | Semialdehyde_dh | 4        | 0.006                  |
|                    | **Subtotal:**        |              | **19**      | **0.026**              |
| Gx-transp          | Transporter          | 5TM-5MR_LYT  | 26         | 0.036                  |
| Beta-propeller     | Extracellular binding | Reg_prop   | 38         | 0.052                  |
| GBD                | Galactose binding    | 7TMR-DISMED2 | 10         | 0.014                  |
|                    |                      | CBM_4_9      | 2           | 0.003                  |
|                    | **Subtotal:**        |              | **12**      | **0.017**              |
| TPR                | Protein-Protein interactions | TPR_19     | 6           | 0.008                  |
| Superfamily | Annotation | Clan | Score |
|-------------|------------|------|-------|
| ANAPC3      |            |      | 1     |
| ANAPC3      |            |      | 1     |
| Cupin       | Nucleotide binding | cNMP_binding | 1 | 0.010 |
| HHH         | Helix-turn-Helix | HHH_5 | 2 | 0.003 |
| E-set       | Sugar binding | Y_Y_Y | 10 | 0.014 |
| Phosphatase  | Cyanide binding | Rhodanese | 10 | 0.014 |
| P-loop-NTPase | Nucleotide binding | ABC_tran | 1 | 0.001 |
| P-loop-NTPase | Nucleotide binding | ABC_sub_bind | 1 | 0.001 |
| No assigned superfamily | Zinc binding | CZB | 1629 | 2.248 |
| No assigned superfamily | PIU | PIU | 1095 | 1.511 |
| No assigned superfamily | Nitrate and nitrite binding | NT | 923 | 1.273 |
| No assigned superfamily | Oxygen binding | Hemerythrin | 276 | 0.381 |
| No assigned superfamily | PocR | PocR | 166 | 0.229 |
| No assigned superfamily | c-di-GMPbinding | Piz | 270 | 0.373 |
| No assigned superfamily | Ammonium transporter | Ammonium_transp | 64 | 0.088 |
| No assigned superfamily | Integral membrane sensor | MHTY | 36 | 0.050 |
| No assigned superfamily | Ligand binding | PrnP_N | 18 | 0.025 |
| No assigned superfamily | Putative LBD | He_PiG | 8 | 0.011 |
| No assigned superfamily | Putative LBD | Response_reg | 7 | 0.010 |
| No assigned superfamily | Putative LBD | Hr2 | 7 | 0.010 |
| No assigned superfamily | Domain of unknown function | DUF3365 | 213 | 0.294 |
| No assigned superfamily | Hydrogen binding | Fe_hyd_lg_C | 124 | 0.171 |
| No assigned superfamily | Adenosyl group binding | CBS | 65 | 0.090 |
| No assigned superfamily | Ammonium transporter | Ammonium_transp | 64 | 0.088 |
| No assigned superfamily | Integral membrane sensor | MHTY | 36 | 0.050 |
| No assigned superfamily | Ligand binding | PrnP_N | 18 | 0.025 |
| No assigned superfamily | Putative LBD | He_PiG | 8 | 0.011 |
| No assigned superfamily | Putative LBD | Response_reg | 7 | 0.010 |
| No assigned superfamily | Putative LBD | Hr2 | 7 | 0.010 |
| No assigned superfamily | Domain of unknown function | DUF4077 | 5 | 0.007 |
| No assigned superfamily | Putative LBD | AhpC-TSA | 5 | 0.007 |
| No assigned superfamily | Putative LBD | Pro_CA | 4 | 0.006 |
| No assigned superfamily | Integral membrane domain | MASE3 | 4 | 0.006 |
| No assigned superfamily | Putative LBD | DapB_N | 4 | 0.006 |
| No assigned superfamily | Putative LBD | Pyr_redx_2 | 3 | 0.004 |
| No assigned superfamily | Putative LBD | NAHD_4Fe-4S | 3 | 0.004 |
| No assigned superfamily | Putative LBD | H kinase_N | 3 | 0.004 |
| No assigned superfamily | Domain of unknown function | DUF2222 | 3 | 0.004 |
| No assigned superfamily | Putative LBD | TPR_16 | 2 | 0.003 |
| No assigned superfamily | Putative LBD | TSS_ESX_EspC | 2 | 0.003 |
| No assigned superfamily | Phosphatase/sugar binding | PTS_EllC | 2 | 0.003 |
| No assigned superfamily | Putative LBD | MASE4 | 2 | 0.003 |
| No assigned superfamily | Putative LBD | GGDEF | 2 | 0.003 |
| No assigned superfamily | Domain of unknown function | DUF948 | 2 | 0.003 |
| No assigned superfamily | Putative LBD | B12-binding | 2 | 0.003 |
| No assigned superfamily | Putative LBD | Alp3 | 2 | 0.003 |
| No assigned superfamily | Putative LBD | YykA | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Vps53_N | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Vps28 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Usher | 1 | 0.001 |
| No assigned superfamily | Putative LBD | UPF0184 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Ufd2P_core | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Tranegly | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Tox_URII | 1 | 0.001 |
| No assigned superfamily | Putative LBD | TnpV | 1 | 0.001 |
| No assigned superfamily | Putative LBD | THF_DHM_CYH_C | 1 | 0.001 |
| No assigned superfamily | Putative LBD | THF_DHM_CYH | 1 | 0.001 |
| No assigned superfamily | Putative LBD | SURF1 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | SpoIIAA-like | 1 | 0.001 |
| No assigned superfamily | Putative LBD | SOR_SNZ | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Sensor_TM1 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | SDH_alpha | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Porin_4 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | PhoU | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Pentapeptide_4 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Pentapeptide | 1 | 0.001 |
| No assigned superfamily | Putative LBD | PapC_N | 1 | 0.001 |
| No assigned superfamily | Putative LBD | OMS26_protin | 1 | 0.001 |
| No assigned superfamily | Putative LBD | NAAD_1 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Mul7-C | 1 | 0.001 |
| No assigned superfamily | Putative LBD | MerR_1 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | LxG | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Lipoprotein_7 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | ion_trans_2 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | ING | 1 | 0.001 |
| No assigned superfamily | Putative LBD | IGPD | 1 | 0.001 |
| No assigned superfamily | Putative LBD | lcIR | 1 | 0.001 |
| No assigned superfamily | Putative LBD | HTH_ParB | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Glyco_hydro_2_N | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Glyco_hydro_106 | 1 | 0.001 |
| No assigned superfamily | Putative LBD | FRB_dom | 1 | 0.001 |
| No assigned superfamily | Putative LBD | FhiPPE | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Fe-ADH | 1 | 0.001 |
| No assigned superfamily | Putative LBD | F420_oxidored | 1 | 0.001 |
| No assigned superfamily | Putative LBD | Exonuc_VII_L | 1 | 0.001 |
| Domain Type                | Domain Name       | Count | p-value |
|---------------------------|-------------------|-------|---------|
| Putative LBD              | EMC3_TMCO1        | 1     | 0.001   |
| Putative LBD              | EF-hand_11        | 1     | 0.001   |
| Putative LBD              | EAL               | 1     | 0.001   |
| Domain of unknown function| DUF442            | 1     | 0.001   |
| Domain of unknown function| DUF411B           | 1     | 0.001   |
| Domain of unknown function| DUF3235           | 1     | 0.001   |
| Domain of unknown function| DUF1640           | 1     | 0.001   |
| Putative LBD              | DNA_pol_A_exo1    | 1     | 0.001   |
| Putative LBD              | CHASE             | 1     | 0.001   |
| Putative LBD              | Cas_DxTHG         | 1     | 0.001   |
| Putative LBD              | bZIP_2            | 1     | 0.001   |
| Putative LBD              | BLUF              | 1     | 0.001   |
| Putative LBD              | Band_7            | 1     | 0.001   |
| Putative LBD              | Bac_rhodopsin     | 1     | 0.001   |
| Putative LBD              | Asparaginase      | 1     | 0.001   |
| Quorum sensing            | AI-2E_transport   | 1     | 0.001   |
| Putative LBD              | 5_3_exonuc_N      | 1     | 0.001   |
| Putative LBD              | 5_3_exonuc       | 1     | 0.001   |
| Putative LBD              | 2CSK_N            | 1     | 0.001   |

Subtotal: 5449 7.52

TOTAL: 72460 100