<table>
<thead>
<tr>
<th>Aligned proteins</th>
<th>Structures</th>
<th>In development and unpublished (available for user feedback)</th>
<th>Drugs + in-trial agents</th>
<th>Ligands</th>
<th>Structure constructs</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>28,014 (14,950)</td>
<td>464 (218)</td>
<td></td>
<td>2,223 (0)</td>
<td>198,577</td>
<td>464 (0)</td>
<td>10 (0)</td>
</tr>
<tr>
<td>Genetic variants</td>
<td>63,526 (0)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Structure models 939* (1,125)

Ligand interactions 23,346 (10,059)
Ligand site mutations 34,760 (30,328)

Deposited by the GPCR community

GPCRdb invites dissemination of published data here and in other sections (info is in the Join us section).

Drug statistics
Ligand statistics

Truncation & fusions sites

Stabilising mutation analyser

Ligand site mutation design tool

Construct design tool

Focused structure superposition (e.g. on ligand site residues) (inference)