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| Table of crystallographic statistics |  |  |
| Protein, PDB code | *Se*Tsr LBD (pH 7.5-9.7)PDB: 8FYV | *Se*Tsr LBD (pH 7-7.5)PDB: 8VL8 |
| Space Group | C 1 2 1 | C 1 2 1 |
| Cell dimensions and angle (a, b, c, beta) (Å, º) | 125.8, 75.2, 129.6, 116.5 | 126.0, 74.8, 128.9, 116.1 |
| Resolution (Å) a | 58.0-2.2 (2.26-2.20) | 62.4-2.12 (2.18-2.12) b |
| Completeness (%) a | 100.0 (100.0) | 98.3 (88.5) |
| Total reflections | 1,039,561 | 367,890 |
| Unique reflections  | 55,162 | 60,193 |
| Average *I/σ* a | 7.7 (3.6) | 5.4 (2.0) |
| CC1/2 a | 0.994 (0.838) | 0.977 (0.568) |
| Rwork (%) | 24.1 | 22.7 b |
| Rfree (%) | 25.8 | 27.4 b |
| Ramachandran favored, allowed, outliers (%) | 99.1, 0.9, 0.0 | 99.6, 0.4, 0.0 |
| Protein non-hydrogen atoms | 5604 | 5617 |
| Solvent atoms | 283 | 224 |
| Protein chains, residues | 5, 705 | 5, 705 |
| Average B-factor of protein atoms (Å2) | 49 | 35 |
| Average B-factor  of solvent atoms (Å2) | 43 | 37 |
| rms bond lengths (Å) | 0.002 | 0.013 |
| rms bond angles (°) | 0.42 | 1.22 |
| a Values in parentheses indicate statistics for the highest resolution shell.b Refinement was restricted to 2.5 Ǻ resolution. |  |  |
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