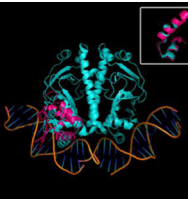
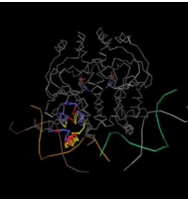
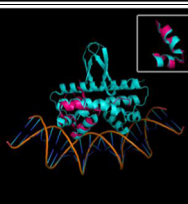
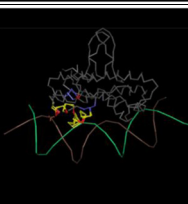
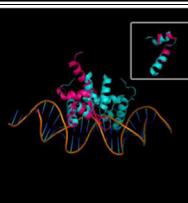
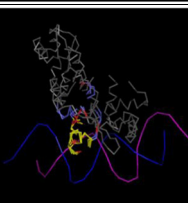
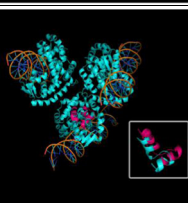
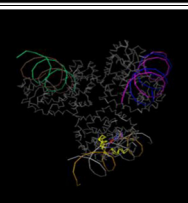
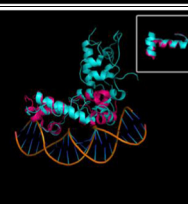
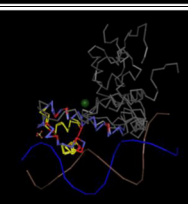


PDB # - Function	RMSD - % Identity	Images from PyMOL and Cn3D		References
<p>Example 1</p> <ul style="list-style-type: none"> - 1Q1H_Chain A: The alpha subunit of transcription factor TFIIE homolog from archae <i>Sulfolobus solfataricus</i>. - 1RUN_Chain A: DNA binding domain of <i>Escherichia coli</i> regulatory proteins which belongs to catabolite activator protein family. 	<p>RMSD: 1.0 Identity: 22.7%</p>			<p>47, 48</p>
<p>Example 2</p> <ul style="list-style-type: none"> - 1D1L_Chain A: Cro repressor of <i>Enterobacteria phage lambda</i>. - 3JRH_Chain B: <i>Escherichia coli</i> protein from Fis family which binds to unspecific DNA. 	<p>RMSD: 2.0 Identity: 21.4%</p>			<p>50, 49</p>
<p>Example 3</p> <ul style="list-style-type: none"> - 1R1T_Chain A: Negatively allogeostic regulated DNA binding of SmtB protein in presence of metals. <i>Synechococcus elongatus</i>. - 1ZLK_Chain A: Hypoxia – induced DosR protein. <i>Mycobacterium tuberculosis</i>. 	<p>RMSD: 1.5 Identity: 20.5%</p>			<p>51, 52</p>
<p>Example 4</p> <ul style="list-style-type: none"> - 1RES_Chain A: DNA-binding domains of <i>Escherichia coli</i> $\gamma\delta$ resolvase. - 1Z9C_Chain F: Chimeric winged helix-turn-helix (wHTH) DNA-binding domain of OhrR-ohrA complex. <i>Bacillus subtilis</i>. 	<p>RMSD: 1.4 Identity: 10.7%</p>			<p>53, 54</p>
<p>Example 5</p> <ul style="list-style-type: none"> - 3OIO_Chain A: Bacterial regulatory helix-turn-helix proteins of AraC family from <i>Chromobacterium violaceum</i>. - 1XS9_Chain A: MarA <i>Escherichia coli</i> regulatory helix-turn-helix protein that binds DNA as a monomer. 	<p>RMSD: 2.2 Identity: 20.7%</p>			<p>⁵⁵ Chang et al., deposited in PDB, not published</p>