## Dali server: conservation mapping in 3D

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**Citation Report** 

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456 457 458 459 460	DNA Recognition of 5-Carboxylcytosine by a Zfp57 Mutant at an Atomic Resolution of 0.97 Å         Biochemistry, 2013, 52, 9310-9317.         Crystal Structure and Computational Characterization of the Lytic Polysaccharide Monooxygenase         GH61D from the Basidiomycota Fungus Phanerochaete chrysosporium. Journal of Biological         Chemistry, 2013, 288, 12828-12839.         Biochemical and Structural Studies of Conserved Maf Proteins Revealed Nucleotide Pyrophosphatases         with a Preference for Modified Nucleotides. Chemistry and Biology, 2013, 20, 1386-1398.         Neuroglobins, Pivotal Proteins Associated with Emerging Neural Systems and Precursors of Metazoan         Globin Diversity. Journal of Biological Chemistry, 2013, 288, 6957-6967.         Rubella virus capsid protein structure and its role in virus assembly and infection. Proceedings of the         National Academy of Sciences of the United States of America, 2013, 110, 20105-20110.         A PilT N-terminus domain protein SSO1118 from hyperthemophilic archaeon Sulfolobus solfataricus	<ol> <li>2.5</li> <li>3.4</li> <li>6.0</li> <li>3.4</li> <li>7.1</li> </ol>	19 158 15 31 34

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1338       (Cispp Rk/scp) polycep Nk/scp) 345holdenzyme and the type III secretion export apparatus in cirb Chlamydla       7.6         1349       Structure alignment of membrane proteins: Accuracy of available tools and a consensus strategy.       2.6         1349       Structure, Function and Bioinformatics, 2015, 83, 1720-1732.       2.6         1349       Crystal structure, Function and Bioinformatics, 2015, 83, 1720-1732.       4.7         1340       A Novel Peptide Binding Motifs Inference Approach to Understand Deoxynivalenol Molecular Toxicity.       3.4         1341       Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between       3.3         1343       Sequence and Structure Analysis of Distantly-Related Viruses, 2015, 7, 6424-640.       3.3         1349       Structure of the Receptor Binding Carboxy-Terminal Domain of the Bacteriophage T5 L-Shaped Tail       3.3         1340       Structure of the Acceptor Binding Carboxy-Terminal Domain of the Bacteriophage T5 L-Shaped Tail       3.3         1341       Domain organization of DNase from Thinalkallubito sp. provides insights into retention of activity in       3.6         1342       betructure di sovery of symergistic inhibitors against E. coll and S. enterica seroural Typhilmurium       3.5         1344       basis of death domain signaling in the p75 neurotrophin receptor. Elife, 2015, 6, 958.       3.5         1344       betructure di a Novel T	1132		7.6	4
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1133       journal, 2015, 282, 3126-3135.       4.7         1134       A Novel Peptide-Binding Motifs Inference Approach to Understand Deoxynivalenol Molecular Toxicity.       3.4         1137       Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between       3.3         1137       Sequence and Structure Analysis of Distantly-Related Viruses, Reveals Extensive Gene Transfer between       3.3         1138       Structure of the Receptor-Binding Carboxy-Terminal Domain of the Bacteriophage 15 L-Shaped Tall       5.3         1139       Structural basis of death domain signaling in the p75 neurotrophin receptor. ELife, 2015, 4, e11692.       6.0         1140       Domain organization of DNase from Thioalkallybrio sp. provides insights into retention of activity in       3.5         1141       Model-driven discovery of synergistic inhibitors against E. coli and S. enterica serovar Typhimurium       3.5         1142       The Structure of a Novel Thermophilic Esterase from the Planctomycetes Species, Thermoguita terrifortis Reveals an Open Active Site Due to a Minimal & Cap#E <sup>IM</sup> Domain. Frontiers in Microbiology, 2015, 6, 51.       3.5         1143       Positively-Charged Semi-Tunnel Is a Structural and Surface Characteristic of Polyphosphate-Binding Proteins: An In-Silico Study. PLoS ONE, 2015, 10, e0123713.       2.5         1144       Structure and Assembly of Group B Streptococcus Pilus 2b Backbone Protein. PLoS ONE, 2015, 10, e0125875.       2.5         1145 </td <td>1134</td> <td>Structure alignment of membrane proteins: Accuracy of available tools and a consensus strategy. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1720-1732.</td> <td>2.6</td> <td>12</td>	1134	Structure alignment of membrane proteins: Accuracy of available tools and a consensus strategy. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1720-1732.	2.6	12
1136       Toxins, 2015, 7, 1989-2005.       3.4         1137       Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between       3.3         1138       Structure of the Receptor-Binding Carboxy-Terminal Domain of the Bacteriophage 15 LShaped Tail       3.3         1138       Structure of the Receptor-Binding Carboxy-Terminal Domain of the Bacteriophage 15 LShaped Tail       3.3         1139       Structural basis of death domain signaling in the p75 neurotrophin receptor. ELife, 2015, 4, e11692.       6.0         1140       Domain organization of DNase from Thioalkalivibrio sp. provides insights into retention of activity in       3.5         1141       targeting a novel synthetic lethal pair, aldA and pr0. Frontiers in Microbiology, 2015, 6, 661.       3.5         1141       targeting a novel synthetic lethal pair, aldA and pr0. Frontiers in Microbiology, 2015, 6, 958.       3.5         1142       terrifontis Reveals an Open Active Site Due to a Minimal & Cap& Monain. Frontiers in Microbiology, 2015, 6, 12.       3.5         1143       Positively-Charged Semi-Tunnel Is a Structural and Surface Characteristic of Polyphosphate-Binding       2.5         1144       Structure and Assembly of Group B Streptococcus Pilus 2b Backbone Protein. PLoS ONE, 2015, 10, e012575.       2.5         1145       Optimization of Translation Profiles Enhances Protein Expression and Solubility. PLoS ONE, 2015, 10, e012503.       2.5 <td< td=""><td>1135</td><td></td><td>4.7</td><td>32</td></td<>	1135		4.7	32
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1140high salt environments. Frontiers in Microbiology, 2015, 6, 661.3.51141Model-driven discovery of synergistic inhibitors against E. coli and S. enterica serovar Typhimurium targeting a novel synthetic lethal pair, aldA and prpC. Frontiers in Microbiology, 2015, 6, 958.3.51141The Structure of a Novel Thermophilic Esterase from the Planctomycetes Species, Thermogutta terrifontis Reveals an Open Active Site Due to a Minimal †Capâ€ <sup>TM</sup> Domain. Frontiers in Microbiology, 2015, 6, 1294.3.51142Positively-Charged Semi-Tunnel Is a Structural and Surface Characteristic of Polyphosphate-Binding Proteins: An In-Silico Study. PLoS ONE, 2015, 10, e0123713.2.51143Structure and Assembly of Group B Streptococcus Pilus 2b Backbone Protein. PLoS ONE, 2015, 10, e0125875.2.51144Optimization of Translation Profiles Enhances Protein Expression and Solubility. PLoS ONE, 2015, 10, e0127039.2.51145Structure Analysis Uncovers a Highly Diverse but Structurally Conserved Effector Family in Phytopathogenic Fungi. PLoS Pathogens, 2015, 11, e1005228.4.71147Structural and Biochemical Characterization of the Francisella tularensis Pathogenicity Regulator, Macrophage Locus Protein A (MgIA). PLoS ONE, 2015, 10, e0128225.2.5	1139	Structural basis of death domain signaling in the p75 neurotrophin receptor. ELife, 2015, 4, e11692.	6.0	69
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