Phyre2

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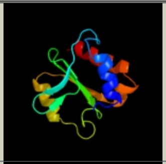
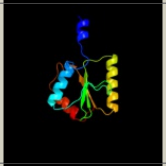
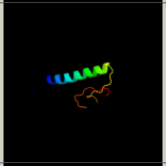
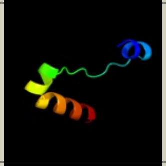
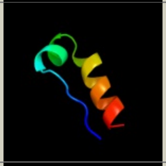
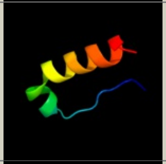
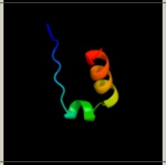
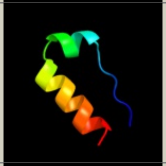
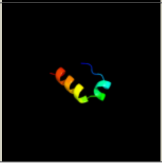
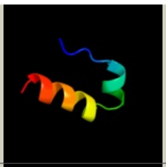
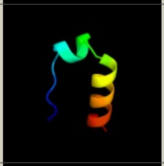
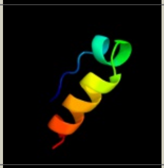
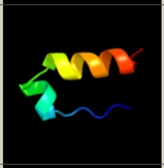
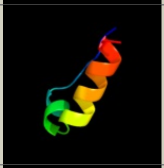
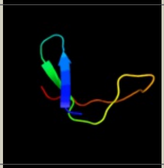
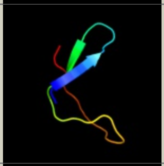
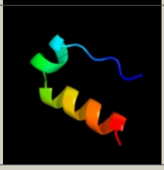
Description	P45736
Date	Thu Jan 5 12:03:28 GMT 2012
Unique Job ID	1fcf921c99401d5c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hrlA_	Alignment		100.0	49	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endonuclease-like protein; **PDBTitle:** crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
2	d1cw0a_	Alignment		99.9	25	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
3	d1vsra_	Alignment		99.7	25	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
4	d1m0da_	Alignment		87.7	22	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
5	c2fqzC_	Alignment		26.9	11	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**r.ecl18ki; **PDBTitle:** metal-depleted ecl18ki in complex with uncleaved dna
6	d1texa_	Alignment		25.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
7	c2ovfA_	Alignment		24.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stal; **PDBTitle:** crystal structure of stal-pap complex
8	c2kyrA_	Alignment		22.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
9	c3mg9A_	Alignment		20.0	14	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**teg12; **PDBTitle:** teg 12 binary structure complexed with the teicoplanin aglycone
10	c3mgbA_	Alignment		16.2	15	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**teg12; **PDBTitle:** teg 12 ternary structure complexed with pap and the teicoplanin2 aglycone
11	c3rnlA_	Alignment		15.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase; **PDBTitle:** crystal structure of sulfotransferase from alicyclobacillus2 acidocaldarius

12	d1xv1a_	Alignment		12.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
13	d1aqua_	Alignment		12.0	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
14	d1nsta_	Alignment		12.0	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
15	c1nstA_	Alignment		12.0	12	**PDB header:**sulfotransferase **Chain:** A: **PDB Molecule:**heparan sulfate n-deacetylase/n-sulfotransferase; **PDBTitle:** the sulfotransferase domain of human haparin sulfate n-2 deacetylase/n-sulfotransferase
16	c1zd1B_	Alignment		11.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfotransferase 4a1; **PDBTitle:** human sulfortransferase sult4a1
17	d3bfxa1	Alignment		11.2	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
18	c1xe1A_	Alignment		11.2	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf0907; **PDBTitle:** hypothetical protein from pyrococcus furiosus pfu-880080-001
19	d1xe1a_	Alignment		11.2	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
20	c2gwhA_	Alignment		10.1	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1c2; **PDBTitle:** human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol
21	d1j99a_	Alignment	not modelled	10.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
22	d1vkja_	Alignment	not modelled	9.7	4	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
23	c1vkjA_	Alignment	not modelled	9.7	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**heparan sulfate (glucosamine) 3-o- **PDBTitle:** crystal structure of heparan sulfate 3-o-sulfotransferase2 isoform 1 in the presence of pap
24	c2h8kA_	Alignment	not modelled	9.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sult1c3 splice variant d; **PDBTitle:** human sulfotranferase sult1c3 in complex with pap
25	c3fovA_	Alignment	not modelled	9.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0102 protein rpa0323; **PDBTitle:** crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris
26	c3u3oA_	Alignment	not modelled	9.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1a1; **PDBTitle:** crystal structure of human sult1a1 bound to pap and two 3-cyano-7-2 hydroxycoumarin
27	d1ls6a_	Alignment	not modelled	9.6	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
28	c3ap3A_	Alignment	not modelled	9.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-tyrosine sulfotransferase 2; **PDBTitle:** crystal structure of human tyrosylprotein sulfotransferase-2 complexed2 with pap
						Fold:P-loop containing nucleoside triphosphate hydrolases

29	d2a3ra1	Alignment	not modelled	9.4	20	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
30	d1g3ma_	Alignment	not modelled	9.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
31	d1fmja_	Alignment	not modelled	9.3	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
32	c2zvpX_	Alignment	not modelled	9.0	20	**PDB header:**transferase **Chain:** X: **PDB Molecule:**tyrosine-ester sulfotransferase; **PDBTitle:** crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol
33	d1jg5a_	Alignment	not modelled	8.7	36	**Fold:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Superfamily:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Family:**GTP cyclohydrolase I feedback regulatory protein, GFRP
34	c2zq5A_	Alignment	not modelled	7.9	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)
35	d1x9ga_	Alignment	not modelled	7.9	18	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
36	c2z6vA_	Alignment	not modelled	7.8	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of sulfotransferase stf9 from2 mycobacterium avium
37	c2vldA_	Alignment	not modelled	7.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
38	c3bm3A_	Alignment	not modelled	7.2	13	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**pspgi restriction endonuclease; **PDBTitle:** restriction endonuclease pspgi-substrate dna complex
39	d1q44a_	Alignment	not modelled	6.9	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
40	c2qjwA_	Alignment	not modelled	6.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein xcc1541; **PDBTitle:** crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
41	c1q1qA_	Alignment	not modelled	6.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase family, cytosolic, 2b, member 1 **PDBTitle:** crystal structure of human pregnenolone sulfotransferase2 (sult2b1a) in the presence of pap
42	c2i9iA_	Alignment	not modelled	6.2	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of helicobacter pylori protein hp0492
43	d2i9ia1	Alignment	not modelled	6.2	40	**Fold:**Anticodon-binding domain-like **Superfamily:**XCC0632-like **Family:**NLBH-like
44	d1t8ta_	Alignment	not modelled	6.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
45	d1q20a_	Alignment	not modelled	5.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
46	c3fcgB_	Alignment	not modelled	5.3	24	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** crystal structure analysis of the middle domain of the2 caf1a usher
47	c3bd9A_	Alignment	not modelled	5.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**heparan sulfate glucosamine 3-o-sulfotransferase **PDBTitle:** human 3-o-sulfotransferase isoform 5 with bound pap
48	c3gzbC_	Alignment	not modelled	5.1	32	**PDB header:**lyase **Chain:** C: **PDB Molecule:**putative snoal-like polyketide cyclase; **PDBTitle:** crystal structure of putative snoal-like polyketide cyclase2 (yp_001182657.1) from shewanella putrefaciens cn-32 at 1.44 a3 resolution
49	c1f3mB_	Alignment	not modelled	5.1	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** crystal structure of human serine/threonine kinase pak1
50	d1whza_	Alignment	not modelled	5.1	13	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like