



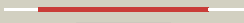


























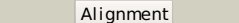
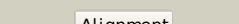

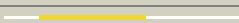

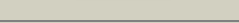
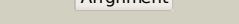





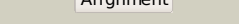

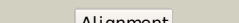

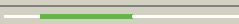

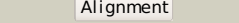


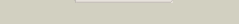
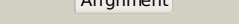
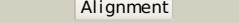
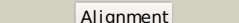



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ne7a_	 Alignment		100.0	25	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: NagB-like
2	c3hn6D_	 Alignment		100.0	23	PDB header: isomerase Chain: D: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
3	d1fsfa_	 Alignment		100.0	25	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: NagB-like
4	c3e15D_	 Alignment		100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: 6-phosphogluconolactonase from plasmodium vivax
5	c3icoA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from mycobacterium tuberculosis
6	c3oc6A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
7	c1y89B_	 Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: devb protein; PDBTitle: crystal structure of devb protein
8	c2j0eA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
9	c1pbtA_	 Alignment		100.0	21	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
10	d1vl1a_	 Alignment		100.0	21	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: NagB-like
11	c3cssA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis

12	c3lwdA	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
13	c3nwpA	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
14	c3lhiA	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative 6-phosphogluconolactonase; PDBTitle: crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
15	c2bkxB	Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
16	c2ri0B	Alignment		100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
17	d2gnpa1	Alignment		99.8	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
18	c2w48D	Alignment		99.7	13	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
19	d3efba1	Alignment		99.7	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
20	c3nzeB	Alignment		99.6	15	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator, sugar-binding family; PDBTitle: the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
21	d2o0ma1	Alignment	not modelled	99.6	11	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
22	c2o0mA	Alignment	not modelled	99.6	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, sorc family; PDBTitle: the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
23	d2okga1	Alignment	not modelled	99.2	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
24	c3kv1A	Alignment	not modelled	98.5	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional repressor; PDBTitle: crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
25	d2r5fa1	Alignment	not modelled	98.4	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
26	d1xnga1	Alignment	not modelled	89.7	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
27	d1zuna1	Alignment	not modelled	87.6	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
28	c2e21A	Alignment	not modelled	87.0	7	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysidine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
29	c3a2kB	Alignment	not modelled	85.7	9	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysidine synthase; PDBTitle: crystal structure of tils complexed with trna

30	c1zunA	 Alignment	not modelled	85.6	10	PDB header: transferase Chain: A: PDB Molecule: sulfate adenyllyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
31	c1ni5A	 Alignment	not modelled	79.1	10	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
32	c3dpiA	 Alignment	not modelled	77.2	12	PDB header: ligase Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
33	d1ni5a1	 Alignment	not modelled	74.3	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
34	d1wxia1	 Alignment	not modelled	71.7	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
35	c1gpmD	 Alignment	not modelled	69.5	14	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
36	c3uowB	 Alignment	not modelled	67.8	9	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
37	c2gaaA	 Alignment	not modelled	66.4	13	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 39.9 kda protein; PDBTitle: crystal structure of yfh7 from saccharomyces cerevisiae: a2 putative p-loop containing kinase with a circular3 permutation.
38	c3i3wB	 Alignment	not modelled	65.0	10	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis
39	c3p52B	 Alignment	not modelled	62.7	8	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
40	c3u7jA	 Alignment	not modelled	61.3	21	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
41	c3tqiB	 Alignment	not modelled	58.1	16	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
42	d1kqpa	 Alignment	not modelled	55.9	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
43	c3hheA	 Alignment	not modelled	54.3	17	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
44	d1ydha	 Alignment	not modelled	50.9	16	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
45	c2q4dB	 Alignment	not modelled	48.3	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lysine decarboxylase-like protein at5g11950; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
46	c3l7oB	 Alignment	not modelled	44.9	13	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
47	c1k5C	 Alignment	not modelled	43.1	28	PDB header: isomerase Chain: C: PDB Molecule: d-ribose-5-phosphate isomerase; PDBTitle: structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
48	c2vxoB	 Alignment	not modelled	42.8	13	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
49	d1gpm1	 Alignment	not modelled	38.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
50	c3ewbX	 Alignment	not modelled	38.5	10	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
51	d1pjq3	 Alignment	not modelled	37.6	13	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
52	c2hnkC	 Alignment	not modelled	36.6	13	PDB header: transferase Chain: C: PDB Molecule: sam-dependent o-methyltransferase; PDBTitle: crystal structure of sam-dependent o-methyltransferase from2 pathogenic bacterium leptospira interrogans
53	c3pdkB	 Alignment	not modelled	36.3	16	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis
54	c3fiuD	 Alignment	not modelled	35.9	14	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
55	c1uj6A	 Alignment	not modelled	35.5	18	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate

56	c3q4gA	Alignment	not modelled	34.8	13	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
57	c2f7lA	Alignment	not modelled	33.5	10	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfobolus tokodaii2 phosphomannomutase/phosphoglucosomutase
58	d1iv0a	Alignment	not modelled	33.4	23	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
59	c3kwmC	Alignment	not modelled	32.5	23	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
60	c2pjmA	Alignment	not modelled	31.3	23	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
61	c3tr6A	Alignment	not modelled	30.5	18	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: structure of a o-methyltransferase from coxiella burnetii
62	c2dplA	Alignment	not modelled	29.5	16	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
63	d1t35a	Alignment	not modelled	28.3	17	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
64	d1uj4a1	Alignment	not modelled	28.3	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
65	c3r3hA	Alignment	not modelled	28.1	16	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase, sam-dependent; PDBTitle: crystal structure of o-methyltransferase from legionella pneumophila
66	c2x9qA	Alignment	not modelled	27.1	17	PDB header: ligase Chain: A: PDB Molecule: cyclodipeptide synthetase; PDBTitle: structure of the mycobacterium tuberculosis protein, rv2275.2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.
67	d1wy5a1	Alignment	not modelled	27.0	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
68	d1wd5a	Alignment	not modelled	26.5	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
69	c1xtzA	Alignment	not modelled	25.8	11	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
70	c2e18B	Alignment	not modelled	25.1	13	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of project ph0182 from pyrococcus horikoshii ot3
71	c3oqhB	Alignment	not modelled	23.8	4	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein yvmc; PDBTitle: crystal structure of b. licheniformis cdps yvmc-blic
72	c2oq2B	Alignment	not modelled	22.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
73	c3d3uA	Alignment	not modelled	21.3	20	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
74	d1nvma2	Alignment	not modelled	20.6	6	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
75	c1m0sA	Alignment	not modelled	19.6	13	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: northeast structural genomics consortium (nesg id ir21)
76	c3c04A	Alignment	not modelled	19.5	11	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucosomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
77	c3dqqB	Alignment	not modelled	18.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative trna synthase; PDBTitle: the crystal structure of the putative trna synthase from salmonella2 typhimurium lt2
78	d2fvta1	Alignment	not modelled	17.1	12	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
79	c1ydnA	Alignment	not modelled	17.1	15	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
80	d1p5dx1	Alignment	not modelled	16.6	12	Fold: Phosphoglucosomutase, first 3 domains Superfamily: Phosphoglucosomutase, first 3 domains Family: Phosphoglucosomutase, first 3 domains

81	d2q4oa1	Alignment	not modelled	15.6	16	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
82	c2q4oA	Alignment	not modelled	15.6	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at2g37210/t2n18.3; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
83	c3g8rA	Alignment	not modelled	15.4	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
84	c2f8mB	Alignment	not modelled	15.3	15	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum
85	c2ywcC	Alignment	not modelled	15.2	15	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
86	dlyza1	Alignment	not modelled	15.1	13	Fold: YgbK-like Superfamily: YgbK-like Family: YgbK-like
87	c1lkzB	Alignment	not modelled	15.0	17	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA)2 from escherichia coli.
88	c3dr5A	Alignment	not modelled	14.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative o-methyltransferase; PDBTitle: crystal structure of the q8nrd3_corgl protein from2 corynebacterium glutamicum. northeast structural genomics3 consortium target cgr117.
89	d1m0sa1	Alignment	not modelled	13.8	16	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
90	clydoC	Alignment	not modelled	13.4	15	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
91	d1w77a1	Alignment	not modelled	13.3	39	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
92	d1sura	Alignment	not modelled	13.1	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
93	c2infB	Alignment	not modelled	12.7	12	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
94	c3sftA	Alignment	not modelled	12.4	13	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
95	c1rcuB	Alignment	not modelled	12.4	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein vt76; PDBTitle: x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
96	d1rcua	Alignment	not modelled	12.4	10	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
97	d1vl2a1	Alignment	not modelled	12.4	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
98	d1vhxa	Alignment	not modelled	12.0	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
99	d1vbka1	Alignment	not modelled	12.0	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like