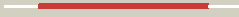





















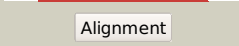







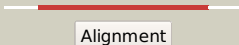

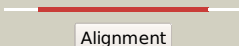

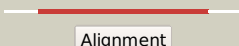





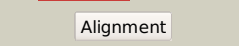

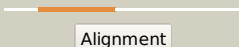
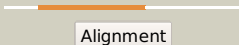
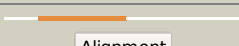





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2465c_(-)_2767681_2768169
Date	Wed Aug 7 12:50:09 BST 2019
Unique Job ID	25b748f5b977d184

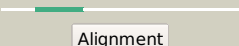
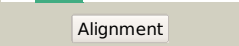
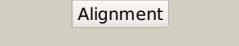
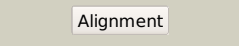
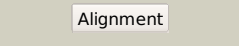

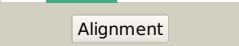
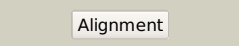
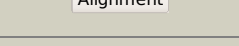
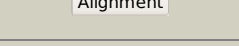
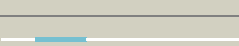



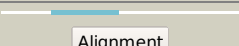



Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2vvpA1	 Alignment		100.0	100	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
2	c4lfnD	 Alignment		100.0	29	PDB header: isomerase Chain: D: PDB Molecule: galactose-6-phosphate isomerase subunit b; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-ribose
3	c6mu0A	 Alignment		100.0	39	PDB header: isomerase Chain: A: PDB Molecule: probable ribose-5-phosphate isomerase b; PDBTitle: crystal structure of ribose-5-phosphate isomerase b from mycoplasma2 genitalium with bound ribulose-5-phosphate
4	c3he8A	 Alignment		100.0	37	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
5	c3qd5B	 Alignment		100.0	24	PDB header: isomerase Chain: B: PDB Molecule: putative ribose-5-phosphate isomerase; PDBTitle: crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
6	d1nn4a	 Alignment		100.0	32	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
7	c6fxwA	 Alignment		100.0	33	PDB header: isomerase Chain: A: PDB Molecule: putative ribose 5-phosphate isomerase; PDBTitle: structure of leishmania infantum type b ribose 5-phosphate isomerase
8	c3m1pA	 Alignment		100.0	36	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
9	c3k7pA	 Alignment		100.0	36	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
10	d1o1xa	 Alignment		100.0	36	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
11	c4lfmA	 Alignment		100.0	28	PDB header: isomerase Chain: A: PDB Molecule: galactose-6-phosphate isomerase subunit a; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-psicose

12	c4em8A_	 Alignment		100.0	35	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
13	c6fxsA_	 Alignment		100.0	36	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase, putative; PDBTitle: structure of trypanosoma brucei type b ribose 5-phosphate isomerase
14	c3s5pA_	 Alignment		100.0	33	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
15	c5ifzA_	 Alignment		100.0	34	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase from brucella2 melitensis 16m
16	c3onoA_	 Alignment		100.0	17	PDB header: isomerase Chain: A: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase lacab_rpb from2 vibrio parahaemolyticus
17	c2ppwA_	 Alignment		100.0	17	PDB header: isomerase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
18	c3c5yD_	 Alignment		100.0	19	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
19	c2pjka_	 Alignment		94.6	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
20	d1y5ea1	 Alignment		93.2	22	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
21	d1mkza_	 Alignment	not modelled	93.1	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
22	c2xecD_	 Alignment	not modelled	91.1	19	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
23	c2is8A_	 Alignment	not modelled	89.4	20	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
24	d1v7ra_	 Alignment	not modelled	88.1	11	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
25	c4fq5B_	 Alignment	not modelled	87.0	18	PDB header: isomerase Chain: B: PDB Molecule: maleate cis-trans isomerase; PDBTitle: crystal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate
26	c4xcwF_	 Alignment	not modelled	87.0	18	PDB header: transferase Chain: F: PDB Molecule: molybdopterin adenyltransferase; PDBTitle: crystal structure of molybdenum cofactor biosynthesis protein moga2 from helicobacter pylori str. j99
27	c3rfqC_	 Alignment	not modelled	84.6	22	PDB header: biosynthetic protein Chain: C: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase moab2; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
28	c6gyzB_	 Alignment	not modelled	84.5	28	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus

29	d1p5dx1	Alignment	not modelled	83.5	33	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
30	d1jja_	Alignment	not modelled	83.2	12	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
31	d1uuya_	Alignment	not modelled	82.4	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
32	c3pdkB_	Alignment	not modelled	81.7	26	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis
33	c1tvmA_	Alignment	not modelled	80.2	20	PDB header: transferase Chain: A: PDB Molecule: pts system, galactitol-specific iib component; PDBTitle: nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
34	c2rirA_	Alignment	not modelled	79.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
35	c2f7IA_	Alignment	not modelled	79.4	23	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
36	d2f7wa1	Alignment	not modelled	78.7	15	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
37	d2g2ca1	Alignment	not modelled	78.6	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
38	c3uw2A_	Alignment	not modelled	78.4	16	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase/phosphomannomutase family protein; PDBTitle: x-ray crystal structure of phosphoglucomutase/phosphomannomutase2 family protein (bth_11489)from burkholderia thailandensis
39	c2qq1A_	Alignment	not modelled	78.4	21	PDB header: structural protein Chain: A: PDB Molecule: molybdenum cofactor biosynthesis mog; PDBTitle: crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vF5
40	c3kbqA_	Alignment	not modelled	78.2	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ta0487; PDBTitle: the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
41	c4ix1B_	Alignment	not modelled	76.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
42	d1di6a_	Alignment	not modelled	76.6	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
43	d2ftsa3	Alignment	not modelled	76.3	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
44	c1wqaB_	Alignment	not modelled	75.6	33	PDB header: isomerase Chain: B: PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
45	c5zi9B_	Alignment	not modelled	74.4	24	PDB header: hydrolase Chain: B: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal structure of type-ii log from streptomyces coelicolor a3
46	c2yxbA_	Alignment	not modelled	74.3	22	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
47	c1vkrA_	Alignment	not modelled	73.4	29	PDB header: transferase Chain: A: PDB Molecule: mannitol-specific pts system enzyme iibc components; PDBTitle: structure of iib domain of the mannitol-specific permease enzyme ii
48	d1vkra_	Alignment	not modelled	73.4	29	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
49	c1tuoA_	Alignment	not modelled	73.0	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative phosphomannomutase; PDBTitle: crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
50	d1uz5a3	Alignment	not modelled	71.5	15	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
51	c1kgsA_	Alignment	not modelled	70.6	24	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
52	c3czcA_	Alignment	not modelled	70.6	19	PDB header: transferase Chain: A: PDB Molecule: rmpb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from streptococcus2 mutans
53	d3bula2	Alignment	not modelled	68.7	22	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain

				Family:Cobalamin (vitamin B12)-binding domain		
54	c2hunB	Alignment	not modelled	68.6	17	PDB header: lyase Chain: B: PDB Molecule: 336aa long hypothetical dtdp-glucose 4,6-dehydratase; PDBTitle: crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
55	c3i3wB	Alignment	not modelled	67.5	28	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis
56	c3vpbC	Alignment	not modelled	66.2	19	PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
57	d1p5dx2	Alignment	not modelled	65.5	18	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
58	c3c04A	Alignment	not modelled	64.1	30	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
59	d2nqra3	Alignment	not modelled	62.1	31	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
60	c1k98A	Alignment	not modelled	61.1	22	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
61	c4leiB	Alignment	not modelled	60.7	28	PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminyltransferase spnp
62	c3ezxA	Alignment	not modelled	59.8	14	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
63	c3ptjA	Alignment	not modelled	58.0	11	PDB header: hydrolase Chain: A: PDB Molecule: upf0603 protein at1g54780, chloroplastic; PDBTitle: structural and functional analysis of arabidopsis thaliana thylakoid2 lumen protein attp18.3
64	c2nqgA	Alignment	not modelled	58.0	31	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
65	c3tquD	Alignment	not modelled	56.3	18	PDB header: hydrolase Chain: D: PDB Molecule: non-canonical purine ntp pyrophosphatase; PDBTitle: structure of a ham1 protein from coxiella burnetii
66	c5bmpA	Alignment	not modelled	55.7	13	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
67	c2g4rB	Alignment	not modelled	55.3	22	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
68	c2fuvB	Alignment	not modelled	54.7	28	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucomutase; PDBTitle: phosphoglucomutase from salmonella typhimurium.
69	c1yr3A	Alignment	not modelled	52.9	32	PDB header: transferase Chain: A: PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the product of2 the xapa gene
70	c3bq9A	Alignment	not modelled	51.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted rossmann fold nucleotide-binding domain- PDBTitle: crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
71	c3d4oA	Alignment	not modelled	51.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
72	c5g2rA	Alignment	not modelled	50.9	18	PDB header: transferase Chain: A: PDB Molecule: molybdopterin biosynthesis protein cnx1; PDBTitle: crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
73	c3dz1A	Alignment	not modelled	50.7	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
74	c4r3uD	Alignment	not modelled	50.2	27	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
75	c4zrmB	Alignment	not modelled	49.7	26	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase (tm0509) from2 hyperthermophilic eubacterium thermotoga maritima
76	c4mgeB	Alignment	not modelled	48.7	13	PDB header: transferase Chain: B: PDB Molecule: pts system, cellobiose-specific iib component; PDBTitle: 1.85 angstrom resolution crystal structure of pts system cellobiose-2 specific transporter subunit iib from bacillus anthracis.
77	c5yvmA	Alignment	not modelled	48.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
78	c1bmtB	Alignment	not modelled	48.5	22	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase

79	c6oecD	 Alignment	not modelled	48.4	11	PDB header: structural protein Chain: D: PDB Molecule: response regulator/sensory box protein/ggdef domain PDBTitle: yeast spc42 trimeric coiled-coil amino acids 181-211 fused to pdb:2 3h5i
80	c2x4gA	 Alignment	not modelled	48.4	7	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa
81	d1dbwa	 Alignment	not modelled	48.3	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
82	d2gaxa1	 Alignment	not modelled	46.3	11	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
83	d1ka9h	 Alignment	not modelled	46.1	25	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
84	c5gqsA	 Alignment	not modelled	45.0	19	PDB header: transport protein Chain: A: PDB Molecule: pts galactitol transporter subunit iib; PDBTitle: nmr based solution structure of pts system, galactitol-specific iib2 component from methicillin resistant staphylococcus aureus
85	c2dgdD	 Alignment	not modelled	43.5	9	PDB header: lyase Chain: D: PDB Molecule: 223aa long hypothetical arylmalonate decarboxylase; PDBTitle: crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
86	d1weha	 Alignment	not modelled	42.9	13	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
87	c4hjhA	 Alignment	not modelled	42.4	19	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase; PDBTitle: iodide sad phased crystal structure of a phosphoglucomutase from2 brucella melitensis complexed with glucose-6-phosphate
88	c2fu3A	 Alignment	not modelled	41.7	18	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
89	d1fmfa	 Alignment	not modelled	41.5	24	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
90	c5iejA	 Alignment	not modelled	41.5	15	PDB header: protein Chain: A: PDB Molecule: sdrq; PDBTitle: solution structure of the bef3-activated conformation of sdrq from2 pseudomonas melonis fr1
91	c5wq3A	 Alignment	not modelled	40.8	25	PDB header: hydrolase Chain: A: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal structure of type-ii log from corynebacterium glutamicum
92	c5f64C	 Alignment	not modelled	40.1	17	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
93	d1gy8a	 Alignment	not modelled	39.8	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
94	c3h5dD	 Alignment	not modelled	39.7	15	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
95	c2jimH	 Alignment	not modelled	39.7	13	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
96	c2iyaB	 Alignment	not modelled	39.6	12	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
97	d1ws6a1	 Alignment	not modelled	37.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
98	c1rcuB	 Alignment	not modelled	36.4	11	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
99	d1rcua	 Alignment	not modelled	36.4	11	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
100	c1y80A	 Alignment	not modelled	35.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
101	c2i2xD	 Alignment	not modelled	35.8	22	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
102	c2q1wC	 Alignment	not modelled	35.7	26	PDB header: sugar binding protein Chain: C: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
103	c4v8A	 Alignment	not modelled	35.4	15	PDB header: dna binding protein Chain: A: PDB Molecule: response regulator chra;

103	c4ynbA	Alignment	not modelled	33.4	13	PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system PDB header: lyase
104	c3qayC	Alignment	not modelled	35.1	17	Chain: C; PDB Molecule: endolysin; PDBTitle: catalytic domain of cd27l endolysin targeting clostridia difficile
105	d3pma1	Alignment	not modelled	35.0	20	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
106	c6d9tA	Alignment	not modelled	34.7	15	PDB header: transferase Chain: A; PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
107	d1iiba	Alignment	not modelled	34.1	13	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
108	c5t3uA	Alignment	not modelled	32.9	6	PDB header: transport protein Chain: A; PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the pts iia protein associated with the fucose2 utilization operon from streptococcus pneumoniae
109	c4m6iA	Alignment	not modelled	32.6	27	PDB header: hydrolase Chain: A; PDB Molecule: peptidoglycan amidase rv3717; PDBTitle: structure of the reduced, zn-bound form of mycobacterium tuberculosis2 peptidoglycan amidase rv3717
110	c3c4vB	Alignment	not modelled	31.9	18	PDB header: transferase Chain: B; PDB Molecule: predicted glycosyltransferases; PDBTitle: structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
111	c4lhbC	Alignment	not modelled	31.4	24	PDB header: transferase Chain: C; PDB Molecule: molybdopterin adenylyltransferase; PDBTitle: crystal structure of tungsten cofactor synthesizing protein moab from2 pyrococcus furiosus
112	d1qe5a	Alignment	not modelled	31.1	26	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
113	d1fp1d2	Alignment	not modelled	30.7	23	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
114	c4s05B	Alignment	not modelled	30.6	25	PDB header: transcription/dna Chain: B; PDB Molecule: dna-binding transcriptional regulator basr; PDBTitle: crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
115	c4qs9A	Alignment	not modelled	30.1	18	PDB header: transferase Chain: A; PDB Molecule: hexokinase-1; PDBTitle: arabidopsis hexokinase 1 (athxk1) mutant s177a structure in glucose-2 bound form
116	c3whpA	Alignment	not modelled	30.1	13	PDB header: gene regulation Chain: A; PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
117	c4o6mA	Alignment	not modelled	30.1	28	PDB header: transferase Chain: A; PDB Molecule: af2299, a cdp-alcohol phosphotransferase; PDBTitle: structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
118	c2esrB	Alignment	not modelled	30.0	14	PDB header: transferase Chain: B; PDB Molecule: methyltransferase; PDBTitle: conserved hypothetical protein- streptococcus pyogenes
119	c1kfiA	Alignment	not modelled	29.3	17	PDB header: isomerase Chain: A; PDB Molecule: phosphoglucomutase 1; PDBTitle: crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
120	c2pzb	Alignment	not modelled	29.2	43	PDB header: sugar binding protein Chain: B; PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmj in2 complex with nad and udp