

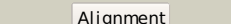
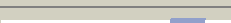
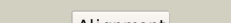
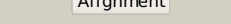
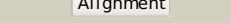
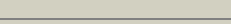
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pg3a1	 Alignment		100.0	82	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
2	c3bl5E_	 Alignment		100.0	57	PDB header: hydrolase Chain: E: PDB Molecule: queuosine biosynthesis protein quec; PDBTitle: crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
3	c2c5sA_	 Alignment		99.9	21	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
4	d2c5sa1	 Alignment		99.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
5	c2hmaA_	 Alignment		99.8	21	PDB header: transferase Chain: A: PDB Molecule: probable trna (5-methylaminomethyl-2-thiouridylate)- PDBTitle: the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
6	c2derA_	 Alignment		99.8	21	PDB header: transferase/rna Chain: A: PDB Molecule: trna-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
7	d1gpma1	 Alignment		99.8	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
8	c2vxob_	 Alignment		99.8	20	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
9	d1k92a1	 Alignment		99.8	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
10	c2dplA_	 Alignment		99.8	26	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
11	d1j20a1	 Alignment		99.8	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases

12	c2ywcC_	Alignment		99.8	17	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
13	d1vl2a1	Alignment		99.7	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
14	c2nz2A_	Alignment		99.7	16	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
15	c3tqiB_	Alignment		99.7	21	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
16	c3k32D_	Alignment		99.7	21	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein mj0690; PDBTitle: the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
17	c1vl2C_	Alignment		99.7	11	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
18	c1gpmD_	Alignment		99.7	14	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
19	c1k97A_	Alignment		99.7	17	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
20	c1kh2D_	Alignment		99.7	25	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
21	c3p52B_	Alignment	not modelled	99.7	16	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
22	d1vbka1	Alignment	not modelled	99.7	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
23	c2e21A_	Alignment	not modelled	99.7	17	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysidine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
24	c3fiuD_	Alignment	not modelled	99.7	16	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
25	d1ni5a1	Alignment	not modelled	99.7	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
26	c3a2kB_	Alignment	not modelled	99.7	16	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysidine synthase; PDBTitle: crystal structure of tils complexed with trna
27	d1wy5a1	Alignment	not modelled	99.7	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
28	c1ni5A_	Alignment	not modelled	99.6	22	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
29	c3uowB_	Alignment	not modelled	99.6	14	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase;

29	c3u0wB	Alignment	not modelled	99.0	14	PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
30	c1vbkA	Alignment	not modelled	99.6	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
31	d1xnga1	Alignment	not modelled	99.6	16	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of project ph0182 from pyrococcus horikoshii ot3
32	c2e18B	Alignment	not modelled	99.5	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
33	d1sura	Alignment	not modelled	99.5	13	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
34	c3q4gA	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: paps reductase in a covalent complex with thioredoxin c35a
35	c2o8vA	Alignment	not modelled	99.4	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
36	d1ru8a	Alignment	not modelled	99.4	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
37	d1kqpa	Alignment	not modelled	99.4	15	PDB header: ligase Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
38	c3dpiA	Alignment	not modelled	99.3	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
39	d1wxia1	Alignment	not modelled	99.2	13	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
40	c3n05B	Alignment	not modelled	99.1	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
41	d2d13a1	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: adenosine phosphosulfate reductase; PDBTitle: crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
42	c2goyC	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
43	c2oq2B	Alignment	not modelled	99.0	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
44	d1zuna1	Alignment	not modelled	98.9	11	PDB header: transferase Chain: A: PDB Molecule: sulfate adenyllyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
45	c1zunA	Alignment	not modelled	98.8	11	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli
46	c1ct9D	Alignment	not modelled	98.6	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
47	d1jgtal	Alignment	not modelled	98.5	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
48	d1q15a1	Alignment	not modelled	98.5	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
49	d1ct9a1	Alignment	not modelled	98.5	18	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
50	c3ilvA	Alignment	not modelled	98.2	18	PDB header: ligase Chain: D: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
51	c3dlaD	Alignment	not modelled	98.2	17	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
52	c1m1zB	Alignment	not modelled	98.1	26	PDB header: biosynthetic protein Chain: A: PDB Molecule: cara; PDBTitle: carbapenam synthetase
53	c1q15A	Alignment	not modelled	98.1	16	PDB header: transferase Chain: A: PDB Molecule: fmn adenyllyltransferase; PDBTitle: crystal structure of candida glabrata fmn2 adenyllyltransferase in complex with atp
54	c3g59A	Alignment	not modelled	98.1	16	PDB header: transferase Chain: A: PDB Molecule: fad synthetase;
55	c2wsiA	Alignment	not modelled	97.7	17	

55	c2wslA	Alignment	not modelled	97.7	17	PDBTitle: crystal structure of yeast fad synthetase (fad1) in complex2 with fad PDB header: lyase
56	c2ejbA	Alignment	not modelled	79.4	13	Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
57	c2c40B	Alignment	not modelled	79.4	21	PDB header: hydrolase Chain: B: PDB Molecule: inosine-uridine preferring nucleoside hydrolase family PDBTitle: crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
58	c3fojA	Alignment	not modelled	72.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
59	c3louB	Alignment	not modelled	69.6	11	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
60	c3p9xB	Alignment	not modelled	68.6	17	PDB header: transferase Chain: B: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
61	d2fug11	Alignment	not modelled	68.5	44	Fold: Bromodomain-like Superfamily: Nqo1C-terminal domain-like Family: Nqo1C-terminal domain-like
62	c3fz0C	Alignment	not modelled	66.7	17	PDB header: hydrolase Chain: C: PDB Molecule: nucleoside hydrolase, putative; PDBTitle: inosine-guanosine nucleoside hydrolase (ig-nh)
63	c1wv9B	Alignment	not modelled	65.0	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
64	c3o1lB	Alignment	not modelled	61.7	18	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
65	c3n0vD	Alignment	not modelled	59.4	14	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
66	d1vhqa	Alignment	not modelled	53.7	27	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
67	d2j13a1	Alignment	not modelled	48.7	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
68	c3nbmA	Alignment	not modelled	47.1	16	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
69	d1yt8a4	Alignment	not modelled	43.6	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
70	c2fugA	Alignment	not modelled	43.2	40	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-quinone oxidoreductase chain 1; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
71	d2hy5b1	Alignment	not modelled	40.5	19	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
72	c3etjB	Alignment	not modelled	38.0	23	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
73	c1zxxA	Alignment	not modelled	36.8	32	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
74	d1iiba	Alignment	not modelled	36.7	14	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellbiose specific IIB subunit
75	c3nrBD	Alignment	not modelled	36.2	15	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
76	d1ffva1	Alignment	not modelled	35.5	26	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
77	c2l2qA	Alignment	not modelled	35.2	8	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
78	c2jtaA	Alignment	not modelled	34.2	10	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli

79	d1t3qa1	Alignment	not modelled	34.0	22	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
80	d1tq8a_	Alignment	not modelled	33.7	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
81	c2k0zA_	Alignment	not modelled	33.4	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein hp1203; PDBTitle: solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
82	d4pfka_	Alignment	not modelled	33.4	45	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
83	c2iy3A_	Alignment	not modelled	33.2	19	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein ffh; PDBTitle: structure of the e. coli signal recognition particle2 bound to a translating ribosome
84	c3g5jA_	Alignment	not modelled	33.1	14	PDB header: nucleotide binding protein Chain: A: PDB Molecule: putative atp/gtp binding protein; PDBTitle: crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
85	c2jyiA_	Alignment	not modelled	32.8	33	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein hrx; PDBTitle: solution structure of mll cxxc domain
86	c1jr3E_	Alignment	not modelled	32.1	33	PDB header: transferase Chain: E: PDB Molecule: dna polymerase iii, delta' subunit; PDBTitle: crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii
87	c2dzdB_	Alignment	not modelled	31.7	10	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
88	c3noyA_	Alignment	not modelled	31.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
89	c2x7vA_	Alignment	not modelled	31.6	11	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
90	c1gqqa_	Alignment	not modelled	31.5	10	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
91	d2d1pb1	Alignment	not modelled	31.4	28	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
92	c3c1oA_	Alignment	not modelled	31.3	9	PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol synthase; PDBTitle: the multiple phenylpropane synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
93	c3dhnA_	Alignment	not modelled	29.6	29	PDB header: isomerase, lyase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
94	c2ehdB_	Alignment	not modelled	29.2	24	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family; PDBTitle: crystal structure analysis of oxidoreductase
95	c3qmhA_	Alignment	not modelled	28.5	45	PDB header: dna binding protein/dna Chain: A: PDB Molecule: cpg-binding protein; PDBTitle: structural basis of selective binding of non-methylated cpg islands2 (dna-tcga) by the cxxc domain of cfp1
96	c3mcfF_	Alignment	not modelled	27.8	27	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
97	c3qjgD_	Alignment	not modelled	27.7	17	PDB header: oxidoreductase Chain: D: PDB Molecule: epidermin biosynthesis protein epid; PDBTitle: epidermin biosynthesis protein epid from staphylococcus aureus
98	c2q1wC_	Alignment	not modelled	27.3	22	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+
99	c3p19A_	Alignment	not modelled	27.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative blue fluorescent protein; PDBTitle: improved nadph-dependent blue fluorescent protein
100	c3gpiA_	Alignment	not modelled	27.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
101	d1jroa1	Alignment	not modelled	26.7	44	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
102	c3emeA_	Alignment	not modelled	26.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: rhodanese-like domain protein; PDBTitle: crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
103	c2kakA_	Alignment	not modelled	26.5	54	PDB header: metal binding protein Chain: A: PDB Molecule: rec protein i/ii; PDBTitle: solution structure of the beta-e-domain of wheat ec-12 metallothionein

104	c3ilmD_	 Alignment	not modelled	26.2	10	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr3790 protein; PDBTitle: crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
105	c3k2qA_	 Alignment	not modelled	26.1	45	PDB header: transferase Chain: A: PDB Molecule: pyrophosphate-dependent phosphofructokinase; PDBTitle: crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
106	c2dcqA_	 Alignment	not modelled	26.1	6	PDB header: unknown function Chain: A: PDB Molecule: putative protein at4g01050; PDBTitle: fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
107	c3mt0A_	 Alignment	not modelled	25.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1789; PDBTitle: the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
108	d1v97a1	 Alignment	not modelled	25.8	22	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
109	c1xxhB_	 Alignment	not modelled	24.7	26	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
110	c1j8yF_	 Alignment	not modelled	24.2	14	PDB header: signaling protein Chain: F: PDB Molecule: signal recognition 54 kda protein; PDBTitle: signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
111	c3swrA_	 Alignment	not modelled	24.1	46	PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 1; PDBTitle: structure of human dnmt1 (601-1600) in complex with sinefungin
112	d1rm6c1	 Alignment	not modelled	23.9	19	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
113	d1n62a1	 Alignment	not modelled	23.8	19	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
114	c2fsxA_	 Alignment	not modelled	23.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
115	c1t3qD_	 Alignment	not modelled	23.3	22	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
116	d1dgja1	 Alignment	not modelled	23.1	33	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
117	d1ezra_	 Alignment	not modelled	22.9	19	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
118	d1yt8a1	 Alignment	not modelled	22.9	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
119	c3lqkA_	 Alignment	not modelled	22.8	10	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
120	d1pfka_	 Alignment	not modelled	22.4	39	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase