

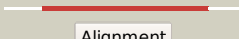

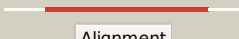




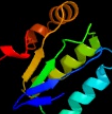











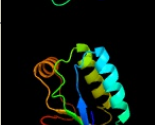

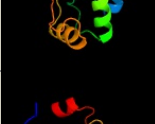






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1904 (- )_2150961_2151392
Date	Fri Aug 2 13:30:52 BST 2019
Unique Job ID	78d820eaa30595f6

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3t6oA_</a>	 Alignment		99.9	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate transporter/antisigma-factor antagonist stas; <b>PDBTitle:</b> the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
2	<a href="#">c4hylB_</a>	 Alignment		99.9	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> stage ii sporulation protein; <b>PDBTitle:</b> the crystal structure of an anti-sigma-factor antagonist from2 haliangium ochraceum dsm 14365
3	<a href="#">d1th8b_</a>	 Alignment		99.9	22	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Anti-sigma factor antagonist Spollaa
4	<a href="#">d1lauza_</a>	 Alignment		99.9	21	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Anti-sigma factor antagonist Spollaa
5	<a href="#">c3f43A_</a>	 Alignment		99.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative anti-sigma factor antagonist tm1081; <b>PDBTitle:</b> crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
6	<a href="#">d1vc1a_</a>	 Alignment		99.9	21	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Anti-sigma factor antagonist Spollaa
7	<a href="#">c4xs5D_</a>	 Alignment		99.9	8	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> sulfate transporter/antisigma-factor antagonist stas; <b>PDBTitle:</b> crystal structure of sulfate transporter/antisigma-factor antagonist2 stas from dyadobacter fermentans dsm 18053
8	<a href="#">c2vy9A_</a>	 Alignment		99.8	21	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> anti-sigma-factor antagonist; <b>PDBTitle:</b> molecular architecture of the stressosome, a signal2 integration and transduction hub
9	<a href="#">d1h4xa_</a>	 Alignment		99.8	18	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Anti-sigma factor antagonist Spollaa
10	<a href="#">c2klnA_</a>	 Alignment		99.8	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable sulphate-transport transmembrane protein, cog0659; <b>PDBTitle:</b> solution structure of stas domain of rv1739c from m. tuberculosis
11	<a href="#">c3mg1A_</a>	 Alignment		99.8	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate permease family protein; <b>PDBTitle:</b> crystal structure of permease family protein from vibrio cholerae

12	<a href="#">c3oirA_</a>	Alignment		99.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate transporter sulfate transporter family protein; <b>PDBTitle:</b> crystal structure of sulfate transporter family protein from wolinnella2 succinogenes
13	<a href="#">c5ezbB_</a>	Alignment		99.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chicken prestin stas domain,chicken prestin stas domain; <b>PDBTitle:</b> chicken prestin stas domain
14	<a href="#">c3ny7A_</a>	Alignment		99.8	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate transporter; <b>PDBTitle:</b> stas domain of ychm bound to acp
15	<a href="#">c3lloA_</a>	Alignment		99.8	15	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> prestine; <b>PDBTitle:</b> crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
16	<a href="#">c6rtfA_</a>	Alignment		99.7	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 26 member 9,solute carrier family 26 <b>PDBTitle:</b> structure of murine solute carrier 26 family member a9 (slc26a9) anion2 transporter in an intermediate state
17	<a href="#">c6ic4K_</a>	Alignment		99.6	21	<b>PDB header:</b> protein transport <b>Chain:</b> K: <b>PDB Molecule:</b> ttg2e; <b>PDBTitle:</b> cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
18	<a href="#">c3lkiB_</a>	Alignment		99.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> antisigma-factor antagonist stas; <b>PDBTitle:</b> crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
19	<a href="#">c5da0A_</a>	Alignment		99.2	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulphate transporter; <b>PDBTitle:</b> structure of the the slc26 transporter slc26dg in complex with a2 nanobody
20	<a href="#">d2q3la.1</a>	Alignment		95.6	11	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Sfri0576-like
21	<a href="#">c3ih9A_</a>	Alignment	not modelled	94.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> salt-tolerant glutaminase; <b>PDBTitle:</b> crystal structure analysis of mglu in its tris form
22	<a href="#">c3bl4B_</a>	Alignment	not modelled	91.1	12	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
23	<a href="#">c3bezC_</a>	Alignment	not modelled	78.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease 4; <b>PDBTitle:</b> crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
24	<a href="#">c2pr7A_</a>	Alignment	not modelled	72.7	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase/epoxide hydrolase family; <b>PDBTitle:</b> crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
25	<a href="#">c3ghfA_</a>	Alignment	not modelled	70.3	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> septum site-determining protein minc; <b>PDBTitle:</b> crystal structure of the septum site-determining protein minc from2 salmonella typhimurium
26	<a href="#">c2mwgB_</a>	Alignment	not modelled	65.8	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> blue-light photoreceptor; <b>PDBTitle:</b> full-length solution structure of ytvA, a lov-photoreceptor protein2 and regulator of bacterial stress response
27	<a href="#">d2ooka.1</a>	Alignment	not modelled	64.1	10	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Sfri0576-like
28	<a href="#">c3kc2A_</a>	Alignment	not modelled	48.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ykr070w; <b>PDBTitle:</b> crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae

29	<a href="#">c4eogA</a>	Alignment	not modelled	48.1	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of csx1 of pyrococcus furiosus
30	<a href="#">d1t3va</a>	Alignment	not modelled	44.6	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
31	<a href="#">c2deoA</a>	Alignment	not modelled	44.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 441aa long hypothetical nfd protein; <b>PDBTitle:</b> 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
32	<a href="#">d1o13a</a>	Alignment	not modelled	41.7	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
33	<a href="#">d2csua3</a>	Alignment	not modelled	37.7	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
34	<a href="#">c3rstH</a>	Alignment	not modelled	36.7	8	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> signal peptide peptidase sppa; <b>PDBTitle:</b> crystal structure of bacillus subtilis signal peptide peptidase a
35	<a href="#">c4vajA</a>	Alignment	not modelled	31.5	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
36	<a href="#">c3re1B</a>	Alignment	not modelled	29.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen-iii synthetase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
37	<a href="#">c2yx6C</a>	Alignment	not modelled	28.8	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein ph0822; <b>PDBTitle:</b> crystal structure of ph0822
38	<a href="#">c4es6A</a>	Alignment	not modelled	26.2	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen-iii synthase; <b>PDBTitle:</b> crystal structure of hemd (pa5259) from pseudomonas aeruginosa (pao1)2 at 2.22 a resolution
39	<a href="#">d1eol1a</a>	Alignment	not modelled	24.2	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
40	<a href="#">d1rdua</a>	Alignment	not modelled	23.1	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
41	<a href="#">c2csuB</a>	Alignment	not modelled	22.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> 457aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of ph0766 from pyrococcus horikoshii ot3
42	<a href="#">d1jr2a</a>	Alignment	not modelled	19.2	14	<b>Fold:</b> HemD-like <b>Superfamily:</b> HemD-like <b>Family:</b> HemD-like
43	<a href="#">c1jr2A</a>	Alignment	not modelled	19.2	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen-iii synthase; <b>PDBTitle:</b> structure of uroporphyrinogen iii synthase
44	<a href="#">c4hgnB</a>	Alignment	not modelled	17.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
45	<a href="#">c3mw8A</a>	Alignment	not modelled	14.7	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen-iii synthase; <b>PDBTitle:</b> crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
46	<a href="#">d1ccwa</a>	Alignment	not modelled	13.9	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
47	<a href="#">d1wd7a</a>	Alignment	not modelled	13.5	9	<b>Fold:</b> HemD-like <b>Superfamily:</b> HemD-like <b>Family:</b> HemD-like
48	<a href="#">d1ptma</a>	Alignment	not modelled	13.2	13	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> PdxA-like
49	<a href="#">c2wfbA</a>	Alignment	not modelled	12.1	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein orp; <b>PDBTitle:</b> high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
50	<a href="#">c2hroA</a>	Alignment	not modelled	11.3	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
51	<a href="#">d2g0ta1</a>	Alignment	not modelled	11.3	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
52	<a href="#">c1tg6G</a>	Alignment	not modelled	11.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> putative atp-dependent clp protease proteolytic subunit; <b>PDBTitle:</b> crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
53	<a href="#">c4rl6A</a>	Alignment	not modelled	10.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> crystal structure of the q04I03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
						<b>PDB header:</b> unknown function

54	<a href="#">c2obnA</a>	Alignment	not modelled	10.9	33	<b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
55	<a href="#">c2qtdA</a>	Alignment	not modelled	10.3	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0327; <b>PDBTitle:</b> crystal structure of a putative dinitrogenase (mj0327) from2 methanocaldococcus jannaschii dsm at 1.70 a resolution
56	<a href="#">c2dfwA</a>	Alignment	not modelled	10.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> salt-tolerant glutaminase; <b>PDBTitle:</b> crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
57	<a href="#">c2dgdD</a>	Alignment	not modelled	9.5	10	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 223aa long hypothetical arylmalonate decarboxylase; <b>PDBTitle:</b> crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
58	<a href="#">d2ap9a1</a>	Alignment	not modelled	9.5	10	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> N-acetyl-l-glutamate kinase
59	<a href="#">d1qvia</a>	Alignment	not modelled	9.5	8	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Hypothetical protein MW1667 (SA1546)
60	<a href="#">d1ro5a</a>	Alignment	not modelled	9.3	8	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> Autoinducer synthetase
61	<a href="#">d1owxa</a>	Alignment	not modelled	9.3	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
62	<a href="#">d1yg6a1</a>	Alignment	not modelled	9.1	5	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
63	<a href="#">d7reqa2</a>	Alignment	not modelled	8.7	3	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
64	<a href="#">d3c9ua2</a>	Alignment	not modelled	8.5	17	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
65	<a href="#">c3bdkB</a>	Alignment	not modelled	8.2	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mannonate dehydratase; <b>PDBTitle:</b> crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
66	<a href="#">d1n1ea2</a>	Alignment	not modelled	8.2	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
67	<a href="#">c4k05B</a>	Alignment	not modelled	8.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical exported protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0371) from2 bacteroides fragilis nctc 9343 at 1.65 a resolution
68	<a href="#">c3kthD</a>	Alignment	not modelled	7.9	8	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit; <b>PDBTitle:</b> structure of clpp from bacillus subtilis in orthorhombic crystal form
69	<a href="#">d1tg6a1</a>	Alignment	not modelled	7.8	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
70	<a href="#">c4jjaA</a>	Alignment	not modelled	7.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0379) from2 bacteroides fragilis nctc 9343 at 1.30 a resolution
71	<a href="#">c4zdiE</a>	Alignment	not modelled	7.7	10	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
72	<a href="#">c3dcmX</a>	Alignment	not modelled	7.5	15	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> uncharacterized protein tm_1570; <b>PDBTitle:</b> crystal structure of the thermotoga maritima spout family rna-2 methyltransferase protein tm1570 in complex with s-adenosyl-l-3 methionine
73	<a href="#">c2hwgA</a>	Alignment	not modelled	7.4	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
74	<a href="#">c2g0bG</a>	Alignment	not modelled	7.0	10	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> feem; <b>PDBTitle:</b> the structure of feem, an n-acyl amino acid synthase from uncultured2 soil microbes
75	<a href="#">d1kjna</a>	Alignment	not modelled	6.9	9	<b>Fold:</b> Hypothetical protein MTH777 (MT0777) <b>Superfamily:</b> Hypothetical protein MTH777 (MT0777) <b>Family:</b> Hypothetical protein MTH777 (MT0777)
76	<a href="#">c5u03C</a>	Alignment	not modelled	6.9	12	<b>PDB header:</b> ligase, protein fibril <b>Chain:</b> C: <b>PDB Molecule:</b> ctp synthase 1; <b>PDBTitle:</b> cryo-em structure of the human ctp synthase filament
77	<a href="#">c3nvaB</a>	Alignment	not modelled	6.9	12	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> dimeric form of ctp synthase from sulfolobus solfataricus
78	<a href="#">c4e1rA</a>	Alignment	not modelled	6.7	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
79	<a href="#">c4e1pA</a>	Alignment	not modelled	6.7	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group

80	<a href="#">c3c00B_</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> escu; <b>PDBTitle:</b> crystal structural of the mutated g247t escu/spas c-terminal domain
81	<a href="#">c6emsA_</a>	Alignment	not modelled	6.6	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(9)-/adenine(9)-n1)-methyltransferase; <b>PDBTitle:</b> crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis.
82	<a href="#">d1ydfa1</a>	Alignment	not modelled	6.1	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
83	<a href="#">d1ezra_</a>	Alignment	not modelled	6.0	12	<b>Fold:</b> Nucleoside hydrolase <b>Superfamily:</b> Nucleoside hydrolase <b>Family:</b> Nucleoside hydrolase
84	<a href="#">c6k4fU_</a>	Alignment	not modelled	5.9	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> U: <b>PDB Molecule:</b> duf1987 domain-containing protein; <b>PDBTitle:</b> siac of pseudomonas aeruginosa
85	<a href="#">c3uosH_</a>	Alignment	not modelled	5.8	25	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 50s ribosomal protein l10; <b>PDBTitle:</b> crystal structure of release factor rf3 trapped in the gtp state on a2 rotated conformation of the ribosome (without viomycin)
86	<a href="#">c1vcnA_</a>	Alignment	not modelled	5.8	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp synthetase; <b>PDBTitle:</b> crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
87	<a href="#">c4ix1B_</a>	Alignment	not modelled	5.8	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
88	<a href="#">c3t7yB_</a>	Alignment	not modelled	5.7	18	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> yop proteins translocation protein u; <b>PDBTitle:</b> structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
89	<a href="#">c2hx1D_</a>	Alignment	not modelled	5.7	8	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> predicted sugar phosphatases of the had superfamily; <b>PDBTitle:</b> crystal structure of possible sugar phosphatase, had superfamily2 (zp_00311070.1) from cytophaga hutchinsonii atcc 33406 at 2.10 a3 resolution
90	<a href="#">d1wzca1</a>	Alignment	not modelled	5.7	5	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
91	<a href="#">d2ef1a1</a>	Alignment	not modelled	5.5	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N-(deoxy)ribosyltransferase-like <b>Family:</b> ADP ribosyl cyclase-like
92	<a href="#">c6hxiB_</a>	Alignment	not modelled	5.5	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-citrate lyase alpha-subunit; <b>PDBTitle:</b> structure of atp citrate lyase from chlorobium limicola in complex2 with citrate and coenzyme a.
93	<a href="#">d1un8a4</a>	Alignment	not modelled	5.5	16	<b>Fold:</b> DAK1/DegV-like <b>Superfamily:</b> DAK1/DegV-like <b>Family:</b> DAK1
94	<a href="#">c3c01H_</a>	Alignment	not modelled	5.5	16	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> H: <b>PDB Molecule:</b> surface presentation of antigens protein spas; <b>PDBTitle:</b> crystal structural of native spas c-terminal domain
95	<a href="#">c1pggA_</a>	Alignment	not modelled	5.4	7	<b>PDB header:</b> oxidoreductase (choh(d)-nadp+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
96	<a href="#">c2re2A_</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ta1041; <b>PDBTitle:</b> crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
97	<a href="#">c3et4A_</a>	Alignment	not modelled	5.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein p4, nadp phosphatase; <b>PDBTitle:</b> structure of recombinant haemophilus influenzae e(p4) acid phosphatase
98	<a href="#">d2bufa1</a>	Alignment	not modelled	5.3	12	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> N-acetyl-l-glutamate kinase
99	<a href="#">c3b0zB_</a>	Alignment	not modelled	5.2	30	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar biosynthetic protein flhb; <b>PDBTitle:</b> crystal structure of cytoplasmic domain of flhb from salmonella2 typhimurium