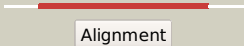

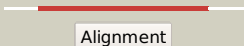
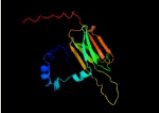
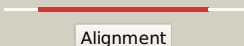


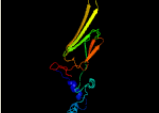

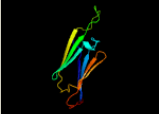

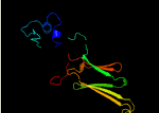
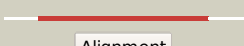


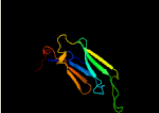



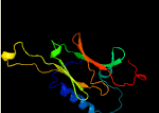


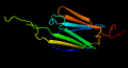

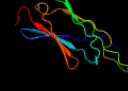
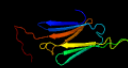
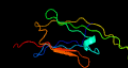
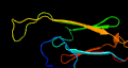
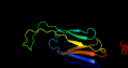




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2031c_(hspX)_2278506_2278940
Date	Mon Aug 5 13:25:14 BST 2019
Unique Job ID	d8bfd95f635e7bcb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5mb8J_</a>	 Alignment		100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> J: <b>PDB Molecule:</b> 25.3 kda heat shock protein, chloroplastic; <b>PDBTitle:</b> hsp21 dodecamer, structural model based on cryo-em and homology2 modelling
2	<a href="#">d1gmea_</a>	 Alignment		100.0	30	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
3	<a href="#">c3w1zA_</a>	 Alignment		99.9	33	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 16; <b>PDBTitle:</b> heat shock protein 16.0 from schizosaccharomyces pombe
4	<a href="#">c2ygdV_</a>	 Alignment		99.9	23	<b>PDB header:</b> chaperone <b>Chain:</b> V: <b>PDB Molecule:</b> <b>PDBTitle:</b> molecular architectures of the 24meric eye lens chaperone alphab-2 crystallin elucidated by a triple hybrid approach
5	<a href="#">c3w1zD_</a>	 Alignment		99.9	33	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> heat shock protein 16; <b>PDBTitle:</b> heat shock protein 16.0 from schizosaccharomyces pombe
6	<a href="#">c6dv5T_</a>	 Alignment		99.9	21	<b>PDB header:</b> chaperone <b>Chain:</b> T: <b>PDB Molecule:</b> heat shock protein beta-1; <b>PDBTitle:</b> oligomeric complex of a hsp27 24-mer at 3.6 a resolution
7	<a href="#">c4ydzA_</a>	 Alignment		99.9	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> stress-induced protein 1; <b>PDBTitle:</b> stress-induced protein 1 from caenorhabditis elegans
8	<a href="#">c5mb8L_</a>	 Alignment		99.9	26	<b>PDB header:</b> chaperone <b>Chain:</b> L: <b>PDB Molecule:</b> 25.3 kda heat shock protein, chloroplastic; <b>PDBTitle:</b> hsp21 dodecamer, structural model based on cryo-em and homology2 modelling
9	<a href="#">d1gmeb_</a>	 Alignment		99.9	36	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
10	<a href="#">c2bolA_</a>	 Alignment		99.9	16	<b>PDB header:</b> heat shock protein <b>Chain:</b> A: <b>PDB Molecule:</b> small heat shock protein; <b>PDBTitle:</b> crystal structure and assembly of tsp36, a metazoan small heat shock2 protein
11	<a href="#">c1shsD_</a>	 Alignment		99.9	23	<b>PDB header:</b> heat shock protein <b>Chain:</b> D: <b>PDB Molecule:</b> small heat shock protein; <b>PDBTitle:</b> small heat shock protein from methanococcus jannaschii

12	<a href="#">d1shsa_</a>	Alignment		99.9	23	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
13	<a href="#">c3glaA_</a>	Alignment		99.9	31	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight heat shock protein; <b>PDBTitle:</b> crystal structure of the hspa from xanthomonas axonopodis
14	<a href="#">c4feiA_</a>	Alignment		99.9	22	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein-related protein; <b>PDBTitle:</b> hsp17.7 from deinococcus radiodurans
15	<a href="#">c3l1eA_</a>	Alignment		99.9	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-crystallin a chain; <b>PDBTitle:</b> bovine alphas crystallin zinc bound
16	<a href="#">c6ewnA_</a>	Alignment		99.8	34	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hspa; <b>PDBTitle:</b> hspa from thermosynechococcus vulcanus in the presence of 2m urea with2 initial stages of denaturation
17	<a href="#">c5ltwK_</a>	Alignment		99.8	20	<b>PDB header:</b> protein binding <b>Chain:</b> K: <b>PDB Molecule:</b> heat shock protein beta-6; <b>PDBTitle:</b> complex of human 14-3-3 sigma clu1 mutant with phosphorylated heat2 shock protein b6
18	<a href="#">c6f2rK_</a>	Alignment		99.8	20	<b>PDB header:</b> chaperone <b>Chain:</b> K: <b>PDB Molecule:</b> hspb2,heat shock protein beta-2,heat shock protein beta-2, <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3
19	<a href="#">c4ylcF_</a>	Alignment		99.8	18	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> heat shock protein hsp20; <b>PDBTitle:</b> crystal structure of del-c4 mutant of hsp14.1 from sulfolobus2 solfatataricus p2
20	<a href="#">c3aabA_</a>	Alignment		99.8	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein st1653; <b>PDBTitle:</b> small heat shock protein hsp14.0 with the mutations of i120f and i122f2 in the form i crystal
21	<a href="#">c6f2rE_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> hspb2,heat shock protein beta-2,heat shock protein beta-2, <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3
22	<a href="#">c6f2rI_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> chaperone <b>Chain:</b> I: <b>PDB Molecule:</b> hspb2,heat shock protein beta-2,heat shock protein beta-2, <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3
23	<a href="#">c2wj5A_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein beta-6; <b>PDBTitle:</b> rat alpha crystallin domain
24	<a href="#">d2h50a1</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
25	<a href="#">c2n3jA_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein beta-1; <b>PDBTitle:</b> solution structure of the alpha-crystallin domain from the redox-2 sensitive chaperone, hspb1
26	<a href="#">c4zjdF_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> aggregation suppressing protein; <b>PDBTitle:</b> small heat shock protein agsa from salmonella typhimurium: truncations2 at n- and c- termini
27	<a href="#">c4rzka_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> small heat shock protein hsp20 family; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus hsp20.1 acid
28	<a href="#">c5ds1B_</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> 17.1 kda class ii heat shock protein; <b>PDBTitle:</b> core domain of the class ii small heat-shock protein hsp 17.7 from2 pisum sativum
						<b>PDB header:</b> chaperone

29	<a href="#">c6f2rA_</a>	Alignment	not modelled	99.8	21	<b>Chain:</b> A: <b>PDB Molecule:</b> hspb2,heat shock protein beta-2,heat shock protein beta-2, <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3
30	<a href="#">c2klrA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-crystallin b chain; <b>PDBTitle:</b> solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
31	<a href="#">c5zulB_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> small heat shock protein; <b>PDBTitle:</b> small heat shock protein from mycobacterium marinum m : form-3
32	<a href="#">c3q9qB_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock protein beta-1; <b>PDBTitle:</b> hspb1 fragment second crystal form
33	<a href="#">c6f2rT_</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> chaperone <b>Chain:</b> T: <b>PDB Molecule:</b> heat shock protein beta-3,heat shock protein beta-3,heat <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3
34	<a href="#">c2wj7D_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-crystallin b chain; <b>PDBTitle:</b> human alphab crystallin
35	<a href="#">c4pbdA_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein shq1 homolog; <b>PDBTitle:</b> crystal structure of the n-terminal cs domain of human shq1
36	<a href="#">c6gxzD_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> pih1 domain-containing protein 1; <b>PDBTitle:</b> crystal structure of the human rpap3(tp2)-pih1d1(cs) complex
37	<a href="#">d1rl1a_</a>	Alignment	not modelled	98.4	11	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> GS domain
38	<a href="#">c2jkiS_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> chaperone <b>Chain:</b> S: <b>PDB Molecule:</b> sgt1-like protein; <b>PDBTitle:</b> complex of hsp90 n-terminal and sgt1 cs domain
39	<a href="#">c3iqfB_</a>	Alignment	not modelled	97.8	29	<b>PDB header:</b> atp binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> all4481 protein; <b>PDBTitle:</b> crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
40	<a href="#">c1x5mA_</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> apoptosis, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcyclin-binding protein; <b>PDBTitle:</b> solution structure of the core domain of calcyclin binding2 protein; siah-interacting protein (sip)
41	<a href="#">d1ejfa_</a>	Alignment	not modelled	97.5	12	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> Co-chaperone p23-like
42	<a href="#">c3eudE_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> nuclear protein <b>Chain:</b> E: <b>PDB Molecule:</b> protein shq1; <b>PDBTitle:</b> structure of the cs domain of the essential h/aca rnp assembly protein2 shq1p
43	<a href="#">c2o30A_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear movement protein; <b>PDBTitle:</b> nuclear movement protein from e. cuculi gb-m1
44	<a href="#">d1wgva_</a>	Alignment	not modelled	97.3	14	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> Nuclear movement domain
45	<a href="#">d1wfia_</a>	Alignment	not modelled	97.3	11	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> Nuclear movement domain
46	<a href="#">c6mv2A_</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b5 reductase 4; <b>PDBTitle:</b> 2.05a resolution structure of the cs-b5r domains of human ncb5or2 (nadp+ form)
47	<a href="#">d1wh0a_</a>	Alignment	not modelled	96.8	8	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> GS domain
48	<a href="#">d1xo9a_</a>	Alignment	not modelled	96.6	16	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> Co-chaperone p23-like
49	<a href="#">c2k8qA_</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein shq1; <b>PDBTitle:</b> nmr structure of shq1p n-terminal domain
50	<a href="#">c2rh0B_</a>	Alignment	not modelled	95.5	8	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucd domain-containing protein 2; <b>PDBTitle:</b> crystal structure of nucd domain-containing protein 2 (13542905) from2 mus musculus at 1.95 a resolution
51	<a href="#">c2cg9Y_</a>	Alignment	not modelled	90.5	7	<b>PDB header:</b> chaperone <b>Chain:</b> Y: <b>PDB Molecule:</b> co-chaperone protein sba1; <b>PDBTitle:</b> crystal structure of an hsp90-sba1 closed chaperone complex
52	<a href="#">d2fq1a1</a>	Alignment	not modelled	38.3	13	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> Frataxin/Nqo15-like <b>Family:</b> Frataxin-like
53	<a href="#">c3em0A_</a>	Alignment	not modelled	35.8	14	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ileal bile acid-binding protein; <b>PDBTitle:</b> crystal structure of zebrafish ileal bile acid-bindin protein2 complexed with cholic acid (crystal form b).
54	<a href="#">d1rl6a1</a>	Alignment	not modelled	30.0	31	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
55	<a href="#">c6c1zA_</a>	Alignment	not modelled	26.5	11	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid binding protein; <b>PDBTitle:</b> crystal structure of apo caenorhabditis elegans lipid binding protein2 8 (lbp-8)

56	<a href="#">d2ga5a1</a>	Alignment	not modelled	25.1	13	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> Frataxin/Nqo15-like <b>Family:</b> Frataxin-like
57	<a href="#">d1vqoe1</a>	Alignment	not modelled	23.0	33	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
58	<a href="#">d1eala</a>	Alignment	not modelled	21.8	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
59	<a href="#">d1yiva1</a>	Alignment	not modelled	21.7	14	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
60	<a href="#">d1ekga</a>	Alignment	not modelled	21.2	27	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> Frataxin/Nqo15-like <b>Family:</b> Frataxin-like
61	<a href="#">d2ftba1</a>	Alignment	not modelled	21.2	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
62	<a href="#">c2lbaA</a>	Alignment	not modelled	20.7	9	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> babp protein; <b>PDBTitle:</b> solution structure of chicken ileal babp in complex with2 glycochenodeoxycholic acid
63	<a href="#">d1p6pa</a>	Alignment	not modelled	20.2	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
64	<a href="#">c4jpdA</a>	Alignment	not modelled	20.1	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein cyay; <b>PDBTitle:</b> the structure of cyay from burkholderia cenocepacia
65	<a href="#">d2j01h1</a>	Alignment	not modelled	19.8	11	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
66	<a href="#">c4hs5B</a>	Alignment	not modelled	19.5	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein cyay; <b>PDBTitle:</b> frataxin from psychromonas ingrahamii as a model to study stability2 modulation within cyay protein family
67	<a href="#">c2q9sA</a>	Alignment	not modelled	18.3	10	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid-binding protein; <b>PDBTitle:</b> linoleic acid bound to fatty acid binding protein 4
68	<a href="#">d1pmpa</a>	Alignment	not modelled	17.5	21	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
69	<a href="#">d1tw4a</a>	Alignment	not modelled	17.5	17	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
70	<a href="#">d2cqla1</a>	Alignment	not modelled	17.1	11	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
71	<a href="#">c1nvpC</a>	Alignment	not modelled	17.0	27	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> transcription initiation factor iia beta chain; <b>PDBTitle:</b> human tfiia/tbp/dna complex
72	<a href="#">d1nvpC</a>	Alignment	not modelled	17.0	27	<b>Fold:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Family:</b> Transcription factor IIA (TFIIA), beta-barrel domain
73	<a href="#">c1nh2C</a>	Alignment	not modelled	16.9	27	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> transcription initiation factor iia large chain; <b>PDBTitle:</b> crystal structure of a yeast tfiia/tbp/dna complex
74	<a href="#">d1nh2c</a>	Alignment	not modelled	16.9	27	<b>Fold:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Family:</b> Transcription factor IIA (TFIIA), beta-barrel domain
75	<a href="#">c5ggeA</a>	Alignment	not modelled	16.5	12	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid bindin protein, isoform b; <b>PDBTitle:</b> fatty acid-binding protein in brain tissue of drosophila melanogaster
76	<a href="#">d1ggla</a>	Alignment	not modelled	16.4	14	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
77	<a href="#">d1yafc</a>	Alignment	not modelled	16.2	27	<b>Fold:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Family:</b> Transcription factor IIA (TFIIA), beta-barrel domain
78	<a href="#">c3jx8B</a>	Alignment	not modelled	16.1	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> crystal structure of putative lipid binding protein (yp_001304415.1)2 from parabacteroides distasonis atcc 8503 at 2.16 a resolution
79	<a href="#">c5xnaB</a>	Alignment	not modelled	15.9	13	<b>PDB header:</b> lipid transport <b>Chain:</b> B: <b>PDB Molecule:</b> sahs1; <b>PDBTitle:</b> crystal structure of a secretory abundant heat soluble (sahs) protein2 from ramazzottius varieornatus (from dimer sample)
80	<a href="#">d1crba</a>	Alignment	not modelled	15.8	17	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
81	<a href="#">d1lfoa</a>	Alignment	not modelled	15.5	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
82	<a href="#">d2f73a1</a>	Alignment	not modelled	15.5	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like

83	<a href="#">d2hnxa1</a>	Alignment	not modelled	14.9	7	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
84	<a href="#">d1o1va_</a>	Alignment	not modelled	14.8	7	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
85	<a href="#">d1g7na_</a>	Alignment	not modelled	14.8	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
86	<a href="#">d1b56a_</a>	Alignment	not modelled	14.7	12	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
87	<a href="#">d1kqwa_</a>	Alignment	not modelled	14.5	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
88	<a href="#">d2nwtal</a>	Alignment	not modelled	14.2	23	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AF2212/PG0164-like <b>Family:</b> AF2212-like
89	<a href="#">d1qw9a1</a>	Alignment	not modelled	13.8	7	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
90	<a href="#">d1mdca_</a>	Alignment	not modelled	13.7	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
91	<a href="#">c5iydN_</a>	Alignment	not modelled	13.2	27	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> N: <b>PDB Molecule:</b> transcription initiation factor iia subunit 1; <b>PDBTitle:</b> human core-pic in the initial transcribing state (no iis)
92	<a href="#">d1lpja_</a>	Alignment	not modelled	13.1	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
93	<a href="#">c2n93A</a>	Alignment	not modelled	12.2	21	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid-binding protein; <b>PDBTitle:</b> solution structure of lcfabp
94	<a href="#">d1hmsa_</a>	Alignment	not modelled	12.2	7	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
95	<a href="#">d1opaa_</a>	Alignment	not modelled	12.0	9	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
96	<a href="#">d1ew4a_</a>	Alignment	not modelled	11.4	21	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> Frataxin/Nqo15-like <b>Family:</b> Frataxin-like
97	<a href="#">d1a5fh2</a>	Alignment	not modelled	11.1	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
98	<a href="#">d1u8ib2</a>	Alignment	not modelled	11.0	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
99	<a href="#">c3rswA</a>	Alignment	not modelled	10.2	7	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid-binding protein, heart; <b>PDBTitle:</b> crystal structure of heart fatty acid binding protein (fabp3)