Phyre^2

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Description	RVBD0251c_(hsp)_302173_302652
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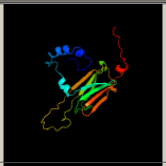
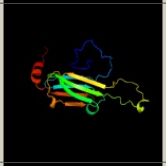
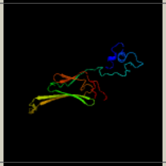
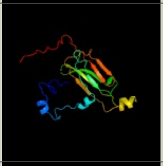
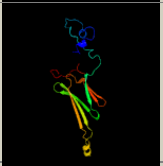
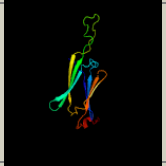
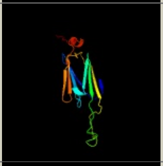
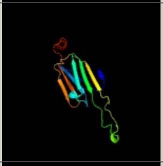
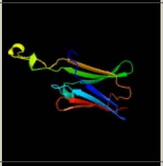
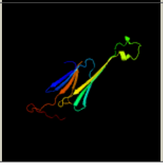
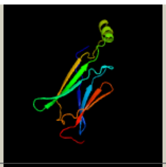
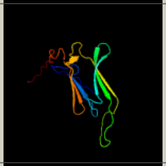
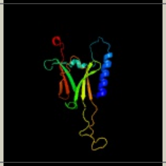
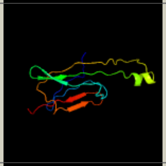
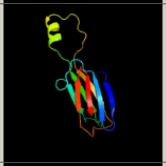
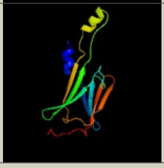
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gmea_	Alignment		99.9	23	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
2	c3w1zA_	Alignment		99.9	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 16; **PDBTitle:** heat shock protein 16.0 from schizosaccharomyces pombe
3	c2ygdV_	Alignment		99.9	26	**PDB header:**chaperone **Chain:** V: **PDB Molecule:** **PDBTitle:** molecular architectures of the 24meric eye lens chaperone alphab-2 crystallin elucidated by a triple hybrid approach
4	c5mb8J_	Alignment		99.9	19	**PDB header:**chaperone **Chain:** J: **PDB Molecule:**25.3 kda heat shock protein, chloroplastic; **PDBTitle:** hsp21 dodecamer, structural model based on cryo-em and homology2 modelling
5	c6dv5T_	Alignment		99.9	22	**PDB header:**chaperone **Chain:** T: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** oligomeric complex of a hsp27 24-mer at 3.6 a resolution
6	c3w1zD_	Alignment		99.9	31	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**heat shock protein 16; **PDBTitle:** heat shock protein 16.0 from schizosaccharomyces pombe
7	d1gmeb_	Alignment		99.9	30	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
8	d1shsa_	Alignment		99.9	23	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
9	c1shsD_	Alignment		99.9	23	**PDB header:**heat shock protein **Chain:** D: **PDB Molecule:**small heat shock protein; **PDBTitle:** small heat shock protein from methanococcus jannaschii
10	c3glaA_	Alignment		99.9	33	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**low molecular weight heat shock protein; **PDBTitle:** crystal structure of the hspa from xanthomonas axonopodis
11	c3l1eA_	Alignment		99.9	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**alpha-crystallin a chain; **PDBTitle:** bovine alphaa crystallin zinc bound

12	c4feiA_	Alignment		99.9	31	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein-related protein; **PDBTitle:** hsp17.7 from deinococcus radiodurans
13	c4ydzA_	Alignment		99.9	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stress-induced protein 1; **PDBTitle:** stress-induced protein 1 from caenorhabditis elegans
14	c5mb8L_	Alignment		99.8	25	**PDB header:**chaperone **Chain:** L: **PDB Molecule:**25.3 kda heat shock protein, chloroplastic; **PDBTitle:** hsp21 dodecamer, structural model based on cryo-em and homology2 modelling
15	c2bolA_	Alignment		99.8	17	**PDB header:**heat shock protein **Chain:** A: **PDB Molecule:**small heat shock protein; **PDBTitle:** crystal structure and assembly of tsp36, a metazoan small heat shock2 protein
16	c6ewnA_	Alignment		99.8	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hspa; **PDBTitle:** hspa from thermosynechococcus vulcanus in the presence of 2m urea with2 initial stages of denaturation
17	d2h50a1	Alignment		99.8	32	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
18	c5ds1B_	Alignment		99.8	30	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**17.1 kda class ii heat shock protein; **PDBTitle:** core domain of the class ii small heat-shock protein hsp 17.7 from2 pisum sativum
19	c4zjdF_	Alignment		99.8	31	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**aggregation suppressing protein; **PDBTitle:** small heat shock protein agsa from salmonella typhimurium: truncations2 at n- and c- termini
20	c3aabA_	Alignment		99.8	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**putative uncharacterized protein st1653; **PDBTitle:** small heat shock protein hsp14.0 with the mutations of i120f and i122f2 in the form i crystal
21	c5ltwK_	Alignment	not modelled	99.8	21	**PDB header:**protein binding **Chain:** K: **PDB Molecule:**heat shock protein beta-6; **PDBTitle:** complex of human 14-3-3 sigma clu1 mutant with phosphorylated heat2 shock protein b6
22	c4ylcF_	Alignment	not modelled	99.8	25	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock protein hsp20; **PDBTitle:** crystal structure of del-c4 mutant of hsp14.1 from sulfolobus2 solfatataricus p2
23	c6f2rK_	Alignment	not modelled	99.8	17	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**hspb2,heat shock protein beta-2,heat shock protein beta-2, **PDBTitle:** a hetrotetramer of human hspb2 and hspb3
24	c6f2rE_	Alignment	not modelled	99.8	19	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**hspb2,heat shock protein beta-2,heat shock protein beta-2, **PDBTitle:** a hetrotetramer of human hspb2 and hspb3
25	c2wj5A_	Alignment	not modelled	99.8	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein beta-6; **PDBTitle:** rat alpha crystallin domain
26	c6f2rI_	Alignment	not modelled	99.8	16	**PDB header:**chaperone **Chain:** I: **PDB Molecule:**hspb2,heat shock protein beta-2,heat shock protein beta-2, **PDBTitle:** a hetrotetramer of human hspb2 and hspb3
27	c4rzkA_	Alignment	not modelled	99.8	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**small heat shock protein hsp20 family; **PDBTitle:** crystal structure of sulfolobus solfataricus hsp20.1 acd
28	c2n3jA_	Alignment	not modelled	99.8	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** solution structure of the alpha-crystallin domain from the redox-2 sensitive chaperone, hspb1
						PDB header:chaperone

29	c5zulB_	Alignment	not modelled	99.8	26	**Chain:** B: **PDB Molecule:**small heat shock protein; **PDBTitle:** small heat shock protein from mycobacterium marinum m : form-3
30	c6f2rA_	Alignment	not modelled	99.7	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hspb2,heat shock protein beta-2,heat shock protein beta-2, **PDBTitle:** a hetrotetramer of human hspb2 and hspb3
31	c2klrA_	Alignment	not modelled	99.7	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
32	c3q9qB_	Alignment	not modelled	99.7	25	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** hspb1 fragment second crystal form
33	c6f2rT_	Alignment	not modelled	99.6	22	**PDB header:**chaperone **Chain:** T: **PDB Molecule:**heat shock protein beta-3,heat shock protein beta-3,heat **PDBTitle:** a hetrotetramer of human hspb2 and hspb3
34	c2wj7D_	Alignment	not modelled	99.5	30	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** human alphab crystallin
35	c4pbdA_	Alignment	not modelled	99.4	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein shq1 homolog; **PDBTitle:** crystal structure of the n-terminal cs domain of human shq1
36	c6gxzD_	Alignment	not modelled	99.1	22	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**pih1 domain-containing protein 1; **PDBTitle:** crystal structure of the human rpap3(tpr2)-pih1d1(cs) complex
37	d1rl1a_	Alignment	not modelled	98.0	16	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**GS domain
38	c2jkiS_	Alignment	not modelled	97.9	17	**PDB header:**chaperone **Chain:** S: **PDB Molecule:**sgt1-like protein; **PDBTitle:** complex of hsp90 n-terminal and sgt1 cs domain
39	c3eudE_	Alignment	not modelled	97.3	18	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**protein shq1; **PDBTitle:** structure of the cs domain of the essential h/aca rnp assembly protein2 shq1p
40	c3igfB_	Alignment	not modelled	97.2	31	**PDB header:**atp binding protein **Chain:** B: **PDB Molecule:**all4481 protein; **PDBTitle:** crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
41	d1ejfa_	Alignment	not modelled	96.6	12	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**Co-chaperone p23-like
42	c1x5mA_	Alignment	not modelled	96.5	8	**PDB header:**apoptosis, signaling protein **Chain:** A: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of the core domain of calcyclin binding2 protein; siah-interacting protein (sip)
43	c6mv2A_	Alignment	not modelled	96.2	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome b5 reductase 4; **PDBTitle:** 2.05a resolution structure of the cs-b5r domains of human ncb5or2 (nadp+ form)
44	c2k8qA_	Alignment	not modelled	96.2	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein shq1; **PDBTitle:** nmr structure of shq1p n-terminal domain
45	c2o30A_	Alignment	not modelled	96.2	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nuclear movement protein; **PDBTitle:** nuclear movement protein from e. cuniculi gb-m1
46	d1wgva_	Alignment	not modelled	96.1	17	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**Nuclear movement domain
47	d1wfia_	Alignment	not modelled	95.9	21	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**Nuclear movement domain
48	d1xo9a_	Alignment	not modelled	95.1	20	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**Co-chaperone p23-like
49	d1wh0a_	Alignment	not modelled	94.6	16	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**GS domain
50	c2rh0B_	Alignment	not modelled	82.6	13	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**nudc domain-containing protein 2; **PDBTitle:** crystal structure of nudc domain-containing protein 2 (13542905) from2 mus musculus at 1.95 a resolution
51	c2cg9Y_	Alignment	not modelled	62.4	10	**PDB header:**chaperone **Chain:** Y: **PDB Molecule:**co-chaperone protein sba1; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
52	d2fqla1	Alignment	not modelled	61.2	17	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
53	d1vyfa_	Alignment	not modelled	46.2	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
54	d2ga5a1	Alignment	not modelled	43.0	20	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
55	d1ekga_	Alignment	not modelled	41.9	41	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like

56	d1eala_	Alignment	not modelled	40.8	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
57	c4jpdA_	Alignment	not modelled	40.4	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein cyay; **PDBTitle:** the structure of cyay from burkholderia cenocepacia
58	c4i3dB_	Alignment	not modelled	40.0	14	**PDB header:**fluorescent protein **Chain:** B: **PDB Molecule:**bilirubin-inducible fluorescent protein unag; **PDBTitle:** crystal structure of fluorescent protein unag n57a mutant
59	c3em0A_	Alignment	not modelled	39.3	19	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**ileal bile acid-binding protein; **PDBTitle:** crystal structure of zebrafish ileal bile acid-bindin protein2 complexed with cholic acid (crystal form b).
60	d1o1va_	Alignment	not modelled	39.3	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
61	c4hs5B_	Alignment	not modelled	39.2	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**protein cyay; **PDBTitle:** frataxin from psychromonas ingrahamii as a model to study stability2 modulation within cyay protein family
62	c6fcoB_	Alignment	not modelled	36.0	28	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**mitochondrial frataxin-like protein; **PDBTitle:** structural and functional characterisation of frataxin (fxn) like2 protein from chaetomium thermophilum
63	d2a0aa1	Alignment	not modelled	35.2	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
64	c6c1zA_	Alignment	not modelled	34.4	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**lipid binding protein; **PDBTitle:** crystal structure of apo caenorhabditis elegans lipid binding protein2 8 (lbp-8)
65	d2j01h1	Alignment	not modelled	34.1	9	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
66	d2ftba1	Alignment	not modelled	33.8	29	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
67	c5bvtA_	Alignment	not modelled	33.4	15	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**epidermal fatty acid-binding protein; **PDBTitle:** palmitate-bound pfabp5
68	d1ggla_	Alignment	not modelled	32.0	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
69	c2lbaA_	Alignment	not modelled	31.7	14	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**babp protein; **PDBTitle:** solution structure of chicken ileal babp in complex with2 glycochenodeoxycholic acid
70	d1ew4a_	Alignment	not modelled	31.3	33	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
71	d1yiva1	Alignment	not modelled	29.2	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
72	d1tw4a_	Alignment	not modelled	29.1	31	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
73	d2cqla1	Alignment	not modelled	28.8	11	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
74	d1p6pa_	Alignment	not modelled	28.8	26	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
75	c5kz5H_	Alignment	not modelled	28.7	41	**PDB header:**transferase/oxidoreductase **Chain:** H: **PDB Molecule:**frataxin, mitochondrial; **PDBTitle:** architecture of the human mitochondrial iron-sulfur cluster assembly2 machinery: the complex formed by the iron donor, the sulfur donor,3 and the scaffold
76	d1crba_	Alignment	not modelled	28.4	24	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
77	d2f73a1	Alignment	not modelled	28.3	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
78	d1bwya_	Alignment	not modelled	27.9	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
79	c5xnaB_	Alignment	not modelled	26.7	11	**PDB header:**lipid transport **Chain:** B: **PDB Molecule:**sahs1; **PDBTitle:** crystal structure of a secretary abundant heat soluble (sahs) protein2 from ramazzottius varieornatus (from dimer sample)
80	c2q9sA_	Alignment	not modelled	26.5	26	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fatty acid-binding protein; **PDBTitle:** linoleic acid bound to fatty acid binding protein 4
81	d1pmpa_	Alignment	not modelled	26.0	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
82	d1mdca_	Alignment	not modelled	25.9	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like

83	d1rl6a1	Alignment	not modelled	25.9	9	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
84	d1lfoa_	Alignment	not modelled	24.8	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
85	c4nkbB_	Alignment	not modelled	24.3	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable serine/threonine-protein kinase zyg-1; **PDBTitle:** crystal structure of the cryptic polo box (cpb)of zyg-1
86	d2hnxa1	Alignment	not modelled	24.1	24	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
87	d1kqwa_	Alignment	not modelled	24.1	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
88	d1kzwa_	Alignment	not modelled	23.8	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
89	d1lpja_	Alignment	not modelled	23.6	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
90	d1fdqa_	Alignment	not modelled	23.5	19	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
91	d1b56a_	Alignment	not modelled	23.0	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
92	d1qw9a1	Alignment	not modelled	22.5	10	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
93	d1vqoe1	Alignment	not modelled	21.8	26	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
94	c5fu4B_	Alignment	not modelled	21.2	34	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**cbm74-rfgh5; **PDBTitle:** the complexity of the ruminococcus flavefaciens cellulosome reflects2 an expansion in glycan recognition
95	d1g7na_	Alignment	not modelled	19.5	26	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
96	d2zjre2	Alignment	not modelled	17.2	9	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
97	d1ifca_	Alignment	not modelled	15.4	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
98	c3pcsB_	Alignment	not modelled	15.2	15	**PDB header:**protein transport/transferase **Chain:** B: **PDB Molecule:**espg; **PDBTitle:** structure of espg-pak2 autoinhibitory ialpha3 helix complex
99	c2n93A_	Alignment	not modelled	14.9	11	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fatty acid-binding protein; **PDBTitle:** solution structure of lcfabp