Phyre^2

Email	l.a.kelley@imperial.ac.uk
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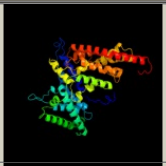
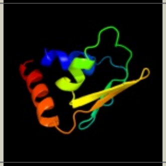
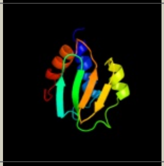
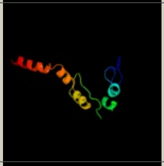
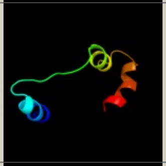
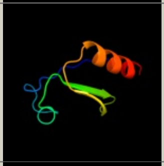
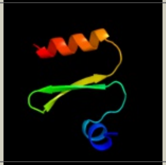
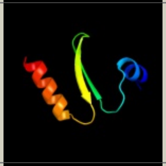
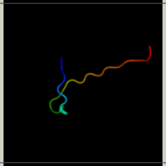
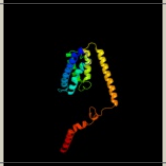
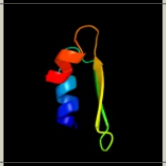
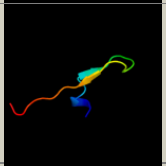
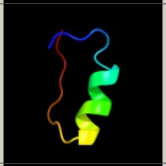
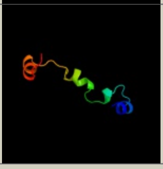
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	Alignment		100.0	16	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
2	d3bp8c1	Alignment		99.6	100	**Fold:**Homing endonuclease-like **Superfamily:**Glucose permease domain IIB **Family:**Glucose permease domain IIB
3	c1ibaA_	Alignment		99.5	99	**PDB header:**phoshphotransferase **Chain:** A: **PDB Molecule:**glucose permease; **PDBTitle:** glucose permease (domain iib), nmr, 11 structures
4	c3ipjB_	Alignment		99.4	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts system, iiabc component; **PDBTitle:** the crystal structure of one domain of the pts system, iiabc component2 from clostridium difficile
5	c3qm3C_	Alignment		59.0	19	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
6	c2dlaB_	Alignment		48.3	35	**PDB header:**replication **Chain:** B: **PDB Molecule:**397aa long hypothetical protein; **PDBTitle:** primase large subunit amino terminal domain from pyrococcus horikoshii
7	d2ifqa1	Alignment		40.3	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
8	c2diyA_	Alignment		38.6	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**thioredoxin-like protein 2; **PDBTitle:** the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2
9	d1gh2a_	Alignment		38.5	4	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
10	d1r26a_	Alignment		37.4	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
11	c2xbqB_	Alignment		34.2	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom

12	c2rddB_	Alignment		33.0	28	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
13	d1fzda_	Alignment		32.9	26	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
14	c3b9yA_	Alignment		32.8	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
15	d1cpza_	Alignment		32.0	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
16	c3gnjD_	Alignment		32.0	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**thioredoxin domain protein; **PDBTitle:** the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
17	c3zqsB_	Alignment		31.9	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase fancl; **PDBTitle:** human fancl central domain
18	d1osda_	Alignment		30.5	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
19	d1nh8a2	Alignment		30.5	16	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
20	d1l0wa3	Alignment		29.2	23	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
21	c1yjrA_	Alignment	not modelled	29.1	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
22	c2k5jB_	Alignment	not modelled	28.8	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
23	d2axtk1	Alignment	not modelled	28.6	37	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein K, PsbK **Family:**PsbK-like
24	c3d22A_	Alignment	not modelled	28.0	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
25	d1fida_	Alignment	not modelled	27.8	35	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
26	d1p6ta1	Alignment	not modelled	27.7	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
27	d1q8la_	Alignment	not modelled	27.4	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
28	c3mgjA_	Alignment	not modelled	27.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1480; **PDBTitle:** crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.

29	c2wz9A_	Alignment	not modelled	27.0	5	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
30	c2oarA_	Alignment	not modelled	26.9	4	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
31	d2v0fa1	Alignment	not modelled	26.8	17	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
32	d2cfua2	Alignment	not modelled	26.8	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
33	d1kvja_	Alignment	not modelled	26.7	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
34	c1jdpA_	Alignment	not modelled	26.5	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atrial natriuretic peptide clearance receptor; **PDBTitle:** crystal structure of hormone/receptor complex
35	d1jdpa_	Alignment	not modelled	26.5	21	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
36	c3a0bK_	Alignment	not modelled	26.1	33	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
37	c2ga7A_	Alignment	not modelled	26.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
38	c2l3mA_	Alignment	not modelled	25.4	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
39	c2oi2A_	Alignment	not modelled	25.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate
40	d1neea1	Alignment	not modelled	25.1	17	**Fold:**Ribosome binding domain-like **Superfamily:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain **Family:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain
41	c3a0hk_	Alignment	not modelled	25.0	33	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
42	c2ldiA_	Alignment	not modelled	24.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
43	c1p68A_	Alignment	not modelled	24.9	45	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein s-824; **PDBTitle:** solution structure of s-824, a de novo designed four helix2 bundle
44	d1a8ra_	Alignment	not modelled	24.3	27	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
45	c2cfuA_	Alignment	not modelled	24.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
46	d2oara1	Alignment	not modelled	23.9	14	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
47	d1wf3a2	Alignment	not modelled	23.7	21	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
48	d1afia_	Alignment	not modelled	23.5	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
49	d2qifa1	Alignment	not modelled	23.3	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
50	d1st6a5	Alignment	not modelled	22.1	35	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
51	d1lwub1	Alignment	not modelled	21.9	17	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
52	d2a9da1	Alignment	not modelled	21.8	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
53	c2e9hA_	Alignment	not modelled	21.7	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
54	d1lwuc1	Alignment	not modelled	21.6	32	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
						PDB header:electron transport

55	c3a0bk_	Alignment	not modelled	21.4	33	**Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
56	d1m1jc1	Alignment	not modelled	21.3	35	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
57	c2j61B_	Alignment	not modelled	20.6	30	**PDB header:**lectin **Chain:** B: **PDB Molecule:**ficolin-2; **PDBTitle:** l-ficolin complexed to n-acetylglucosamine (forme c)
58	d1l0wa2	Alignment	not modelled	20.6	19	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
59	d2axti1	Alignment	not modelled	20.5	17	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
60	d1h3da2	Alignment	not modelled	20.4	40	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
61	c2hpcF_	Alignment	not modelled	20.2	35	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
62	c3e6qL_	Alignment	not modelled	20.1	19	**PDB header:**isomerase **Chain:** L: **PDB Molecule:**putative 5-carboxymethyl-2-hydroxymuconate isomerase; **PDBTitle:** putative 5-carboxymethyl-2-hydroxymuconate isomerase from pseudomonas2 aeruginosa.
63	d1t4aa_	Alignment	not modelled	20.0	21	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
64	c3dxsX_	Alignment	not modelled	20.0	17	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
65	d1s6ua_	Alignment	not modelled	19.7	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
66	c2ofhX_	Alignment	not modelled	19.6	10	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
67	c3mp7A_	Alignment	not modelled	19.2	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
68	d2aw0a_	Alignment	not modelled	19.1	10	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
69	c1deqF_	Alignment	not modelled	19.0	29	**PDB header:** **PDB COMPND:**
70	c3bvhC_	Alignment	not modelled	18.7	38	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrinogen gamma chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
71	c3p2aA_	Alignment	not modelled	18.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
72	d1p6ta2	Alignment	not modelled	18.0	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
73	c1y3kA_	Alignment	not modelled	17.9	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
74	d1f9pa_	Alignment	not modelled	17.8	7	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
75	d1nkta3	Alignment	not modelled	17.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
76	d2bj7a1	Alignment	not modelled	17.7	16	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
77	c1d1rA_	Alignment	not modelled	17.6	32	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 11.4 kd protein ycih in pyrf-osmb **PDBTitle:** nmr solution structure of the product of the e. coli ycih2 gene.
78	d1d1ra_	Alignment	not modelled	17.6	32	**Fold:**eIF1-like **Superfamily:**eIF1-like **Family:**eIF1-like
79	c3p2aB_	Alignment	not modelled	17.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
80	c2hnhA_	Alignment	not modelled	16.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
81	c2fbiD	Alignment	not modelled	16.7	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**formylmethanofuran--tetrahydromethanopterin

81	[illegible]	Alignment	not modelled	16.7	22	**PDBTitle:** crystal structure of formylmethanofuran:2 tetrahydromethanopterin formyltransferase in complex with3 its coenzymes
82	d1xfla_	Alignment	not modelled	16.5	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
83	c2yx5A_	Alignment	not modelled	16.5	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
84	d1re3b1	Alignment	not modelled	16.4	26	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
85	d1r9ja3	Alignment	not modelled	16.2	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
86	d1h7sa2	Alignment	not modelled	16.0	26	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
87	c2ci2I_	Alignment	not modelled	15.9	19	**PDB header:**proteinase inhibitor (chymotrypsin) **Chain:** I: **PDB Molecule:**chymotrypsin inhibitor 2; **PDBTitle:** crystal and molecular structure of the serine proteinase2 inhibitor ci-2 from barley seeds
88	d2p02a3	Alignment	not modelled	15.9	31	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
89	c2vimA_	Alignment	not modelled	15.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
90	d1bkna2	Alignment	not modelled	15.4	26	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
91	d1syra_	Alignment	not modelled	15.4	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
92	c3dgpB_	Alignment	not modelled	15.3	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rna polymerase ii transcription factor b subunit 5; **PDBTitle:** crystal structure of the complex between tfb5 and the c-terminal2 domain of tfb2
93	d1otga_	Alignment	not modelled	15.1	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**5-carboxymethyl-2-hydroxymuconate isomerase (CHMI)
94	c2j5zA_	Alignment	not modelled	15.1	35	**PDB header:**lectin **Chain:** A: **PDB Molecule:**ficolin-3; **PDBTitle:** h-ficolin complexed to galactose
95	c2x7iA_	Alignment	not modelled	15.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252
96	d1wpla_	Alignment	not modelled	15.0	10	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
97	c2kncA_	Alignment	not modelled	15.0	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
98	d1tvxb_	Alignment	not modelled	14.9	7	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
99	c1is7F_	Alignment	not modelled	14.9	10	**PDB header:**hydrolase/protein binding **Chain:** F: **PDB Molecule:**gtp cyclohydrolase i; **PDBTitle:** crystal structure of rat gtpchi/gfrp stimulatory complex