Phyre^2

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Description	Q9H305
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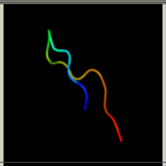
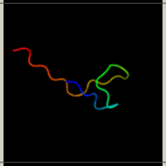
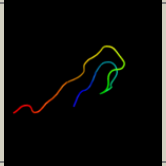
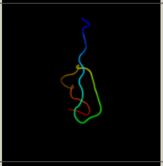
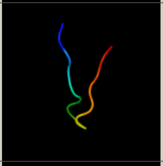
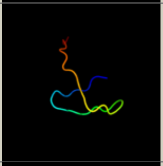
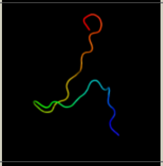
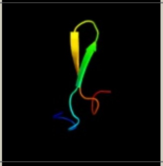
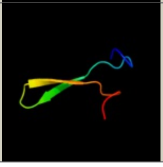
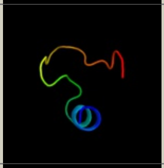
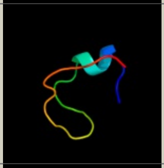
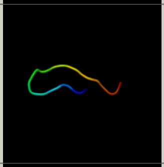
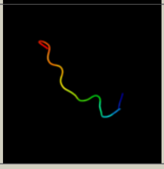
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2joxA_	Alignment		62.6	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**churchill protein; **PDBTitle:** embryonic neural inducing factor churchill is not a dna-2 binding zinc finger protein: solution structure reveals a3 solvent-exposed beta-sheet and zinc binuclear cluster
2	d1hk8a_	Alignment		55.7	32	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
3	c1hk8A_	Alignment		55.7	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
4	c2kdxA_	Alignment		50.4	29	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
5	d2ct1a1	Alignment		39.8	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
6	c3na7A_	Alignment		39.0	33	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
7	c3eb6A_	Alignment		38.0	23	**PDB header:**apoptosis, ligase **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 3; **PDBTitle:** structure of the ciap2 ring domain bound to ubch5b
8	d2cona1	Alignment		35.8	22	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
9	d1wiia_	Alignment		35.6	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
10	c2opfA_	Alignment		35.4	23	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
11	c1k82D_	Alignment		34.5	23	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna

12	d1v87a_	Alignment		34.4	38	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
13	d1vdda_	Alignment		34.0	35	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
14	c1vddC_	Alignment		32.3	35	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
15	d1x6ma_	Alignment		30.7	33	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
16	c2eclA_	Alignment		29.5	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring-box protein 2; **PDBTitle:** solution structure of the ring domain of the human ring-box2 protein 2
17	c2yhoE_	Alignment		29.3	12	**PDB header:**ligase **Chain:** E: **PDB Molecule:**e3 ubiquitin-protein ligase mylip; **PDBTitle:** the idol-ube2d complex mediates sterol-dependent degradation of the2 ldl receptor
18	c1zzaA_	Alignment		28.6	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**stannin; **PDBTitle:** solution nmr structure of the membrane protein stannin
19	c3facE_	Alignment		28.6	25	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rhodobacter sphaeroides protein2 rsp_2168. northeast structural genomics target rhr83.
20	d1qf8a_	Alignment		28.3	35	**Fold:**Rubredoxin-like **Superfamily:**Casein kinase II beta subunit **Family:**Casein kinase II beta subunit
21	c2d8tA_	Alignment	not modelled	28.3	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 146; **PDBTitle:** solution structure of the ring domain of the human ring2 finger protein 146
22	c3cc4Z_	Alignment	not modelled	28.3	26	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
23	d1iyma_	Alignment	not modelled	28.2	21	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
24	c2djbA_	Alignment	not modelled	27.7	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 6; **PDBTitle:** solution structure of the ring domain of the human polycomb2 group ring finger protein 6
25	d1x63a2	Alignment	not modelled	27.2	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
26	d1lv3a_	Alignment	not modelled	26.9	19	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Hypothetical zinc finger protein YacG
27	c2lo2A_	Alignment	not modelled	25.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** solution structure of sgf11(63-99) zinc finger domain
28	c2ea5A_	Alignment	not modelled	25.4	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell growth regulator with ring finger domain **PDBTitle:** solution structure of the ring domain of the human cell2 growth regulator with ring finger domain 1 protein

29	c2qa4Z_	Alignment	not modelled	25.3	26	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
30	c2kluA_	Alignment	not modelled	24.7	13	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
31	d1jwhc_	Alignment	not modelled	24.5	35	**Fold:**Rubredoxin-like **Superfamily:**Casein kinase II beta subunit **Family:**Casein kinase II beta subunit
32	c2jvyA_	Alignment	not modelled	24.4	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** solution structure of the eda-id-related c417f mutant of2 human nemo zinc finger
33	d1ffkw_	Alignment	not modelled	24.1	22	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
34	d1rb9a_	Alignment	not modelled	21.8	38	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
35	c2jmdA_	Alignment	not modelled	21.8	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of human traf6
36	d2dsxa1	Alignment	not modelled	21.3	33	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
37	c2ecmA_	Alignment	not modelled	21.1	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain- **PDBTitle:** solution structure of the ring domain of the ring finger2 and chy zinc finger domain-containing protein 1 from mus3 musculus
38	d2fu5a1	Alignment	not modelled	20.4	11	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
39	c1bi6H_	Alignment	not modelled	20.3	27	**PDB header:**cysteine protease inhibitor **Chain:** H: **PDB Molecule:**bromelain inhibitor vi; **PDBTitle:** nmr structure of bromelain inhibitor vi from pineapple stem
40	c2kn9A_	Alignment	not modelled	20.1	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin; **PDBTitle:** solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
41	c2l0bA_	Alignment	not modelled	20.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase praja-1; **PDBTitle:** solution nmr structure of zinc finger domain of e3 ubiquitin-protein2 ligase praja-1 from homo sapiens, northeast structural genomics3 consortium (nesg) target hr4710b
42	c1s24A_	Alignment	not modelled	20.0	33	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
43	d1s24a_	Alignment	not modelled	20.0	33	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
44	c2ep4A_	Alignment	not modelled	19.9	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ring finger protein 24; **PDBTitle:** solution structure of ring finger from human ring finger2 protein 24
45	c3fl2A_	Alignment	not modelled	19.8	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the ring domain of the e3 ubiquitin-2 protein ligase uhrf1
46	c4a17Y_	Alignment	not modelled	19.6	18	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rpl37a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
47	d1wgma_	Alignment	not modelled	19.5	10	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
48	d2rdva_	Alignment	not modelled	19.4	43	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
49	c1z6uA_	Alignment	not modelled	19.1	35	**PDB header:**ligase **Chain:** A: **PDB Molecule:**np95-like ring finger protein isoform b; **PDBTitle:** np95-like ring finger protein isoform b [homo sapiens]
50	d1fbva4	Alignment	not modelled	19.0	23	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
51	d1dx8a_	Alignment	not modelled	18.8	24	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
52	d1h7va_	Alignment	not modelled	18.7	24	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
53	c2v3bB_	Alignment	not modelled	18.7	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
54	d4rxna_	Alignment	not modelled	18.6	38	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin

55	d1hxra_	Alignment	not modelled	18.4	11	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
56	d1qcva_	Alignment	not modelled	18.2	29	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
57	c2zkrz_	Alignment	not modelled	18.0	25	**PDB header:**ribosomal protein/rna **Chain:** Z: **PDB Molecule:**e site t-rna; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
58	c1yshD_	Alignment	not modelled	18.0	13	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
59	d1jj2y_	Alignment	not modelled	18.0	25	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
60	d1iu5a_	Alignment	not modelled	17.8	43	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
61	c2ecgA_	Alignment	not modelled	17.7	15	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** solution structure of the ring domain of the baculoviral2 iap repeat-containing protein 4 from homo sapiens
62	d1iroa_	Alignment	not modelled	17.7	38	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
63	d1vqoz1	Alignment	not modelled	17.6	31	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
64	c3jyw9_	Alignment	not modelled	17.4	13	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
65	d6rxna_	Alignment	not modelled	17.3	28	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
66	c3l11A_	Alignment	not modelled	17.2	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rnf168; **PDBTitle:** crystal structure of the ring domain of rnf168
67	c2ecyA_	Alignment	not modelled	17.2	20	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 3; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger)" domain of tnf receptor-associated factor 3
68	d1brfa_	Alignment	not modelled	17.1	38	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
69	c1x4jA_	Alignment	not modelled	17.0	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ring finger protein 38; **PDBTitle:** solution structure of ring finger in ring finger protein 38
70	c2vjfB_	Alignment	not modelled	16.9	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**mdm4 protein; **PDBTitle:** crystal structure of the mdm2-mdmx ring domain heterodimer
71	c2zxeG_	Alignment	not modelled	16.8	13	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
72	c1s1i9_	Alignment	not modelled	16.5	13	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
73	c3vk6A_	Alignment	not modelled	16.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hakai; **PDBTitle:** crystal structure of a phosphotyrosine binding domain
74	c2h0dB_	Alignment	not modelled	15.9	21	**PDB header:**metal binding protein/ligase **Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2; **PDBTitle:** structure of a bmi-1-ring1b polycomb group ubiquitin ligase complex
75	c3s8pA_	Alignment	not modelled	15.8	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv420h1; **PDBTitle:** crystal structure of the set domain of human histone-lysine n-2 methyltransferase suv420h1 in complex with s-adenosyl-l-methionine
76	c2ysoA_	Alignment	not modelled	15.4	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 95 homolog; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 656-2 688) of human zinc finger protein 95 homolog
77	c2xeuA_	Alignment	not modelled	15.1	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein 4; **PDBTitle:** ring domain
78	d1g25a_	Alignment	not modelled	14.6	25	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
79	c2hdpB_	Alignment	not modelled	14.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ubiquitin-protein ligase e3 mdm2; **PDBTitle:** solution structure of hdm2 ring finger domain

80	d1vzya2	Alignment	not modelled	14.4	27	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
81	c2kizA_	Alignment	not modelled	14.3	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase arkadia; **PDBTitle:** solution structure of arkadia ring-h2 finger domain
82	c2ectA_	Alignment	not modelled	14.3	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 126; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger) domain of ring finger protein 126
83	c2jo1A_	Alignment	not modelled	14.3	13	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
84	d2k4xa1	Alignment	not modelled	14.1	30	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
85	c1x31D_	Alignment	not modelled	13.8	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**sarcosine oxidase delta subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
86	c2zkr4_	Alignment	not modelled	13.4	24	**PDB header:**ribosomal protein/rna **Chain:** 4: **PDB Molecule:**60s ribosomal protein l44e; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
87	c2lcqA_	Alignment	not modelled	13.3	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
88	d1xjha_	Alignment	not modelled	13.1	14	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
89	c2jp3A_	Alignment	not modelled	12.9	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
90	d1vq0a2	Alignment	not modelled	12.9	19	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
91	d2qam01	Alignment	not modelled	12.8	6	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
92	d1vqo31	Alignment	not modelled	12.7	29	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L44e
93	d2j0151	Alignment	not modelled	12.2	29	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
94	d2cu8a1	Alignment	not modelled	12.1	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
95	c2cklA_	Alignment	not modelled	12.1	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 4; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
96	d2dloa1	Alignment	not modelled	12.1	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
97	d1e4ua_	Alignment	not modelled	12.1	25	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
98	d1ee8a3	Alignment	not modelled	11.9	56	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
99	c3d5d6_	Alignment	not modelled	11.8	27	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**50s ribosomal protein l33; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of the second 70s ribosome. the entire3 crystal structure contains two 70s ribosomes as described in remark4 400.