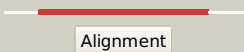
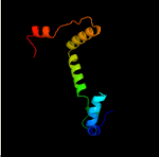
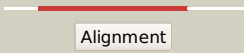



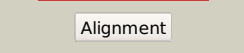
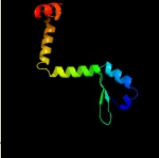


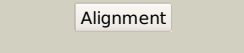

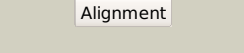


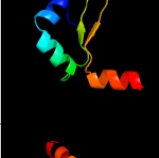
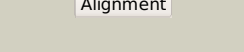

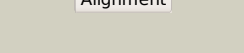

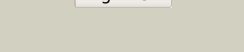
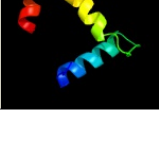
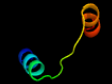

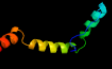
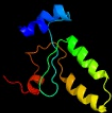




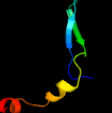


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3357 (-)_3770944_3771219
Date	Fri Aug 9 18:20:01 BST 2019
Unique Job ID	008bb43b60e07789

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3oeiB_	 Alignment		100.0	100	PDB header: toxin, protein binding Chain: B: PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
2	c3d55A_	 Alignment		99.9	100	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
3	d2a6qa1	 Alignment		99.9	44	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
4	c3g5oA_	 Alignment		99.9	28	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
5	d2a6qb1	 Alignment		99.7	46	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
6	c3hs2H_	 Alignment		99.5	29	PDB header: antitoxin Chain: H: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
7	c3hryA_	 Alignment		99.3	30	PDB header: antitoxin Chain: A: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd in a trigonal space group and partially2 disordered
8	c2odkD_	 Alignment		99.0	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
9	d2odka1	 Alignment		98.9	17	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
10	c3k6qB_	 Alignment		95.4	19	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
11	c5ytpA_	 Alignment		53.0	22	PDB header: dna binding protein Chain: A: PDB Molecule: ttha0139; PDBTitle: crystal structure of ttha0139 l34a from thermus thermophilus hb8

12	c4q2uM_	Alignment		39.7	20	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
13	d1n0ea_	Alignment		34.5	14	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ
14	c3ia7A_	Alignment		34.3	16	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
15	c1n0fF_	Alignment		33.4	14	PDB header: biosynthetic protein Chain: F: PDB Molecule: protein mraz; PDBTitle: crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
16	c4q8jE_	Alignment		33.2	11	PDB header: hydrolase Chain: E: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan3; PDBTitle: structure of the saccharomyces cerevisiae pan2-pan3 core complex
17	c4cyiH_	Alignment		31.7	9	PDB header: transferase Chain: H: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan3- PDBTitle: chaetomium thermophilum pan3
18	c6r5kO_	Alignment		30.8	11	PDB header: rna binding protein Chain: O: PDB Molecule: pan2-pan3 deadenylation complex subunit pan3; PDBTitle: cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
19	d1qrja1	Alignment		28.1	25	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
20	c6nklD_	Alignment		25.2	13	PDB header: antitoxin Chain: D: PDB Molecule: antitoxin vapb1; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
21	c1nexC_	Alignment	not modelled	25.0	14	PDB header: ligase, cell cycle Chain: C: PDB Molecule: centromere dna-binding protein complex cbf3 PDBTitle: crystal structure of scsckp1-sccdc4-cpd peptide complex
22	c2iyfA_	Alignment	not modelled	24.7	25	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
23	c4bwpA_	Alignment	not modelled	23.6	10	PDB header: gene regulation Chain: A: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan-3; PDBTitle: structure of drosophila melanogaster pan3 pseudokinase
24	d2ovra1	Alignment	not modelled	22.2	15	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
25	c2ovqA_	Alignment	not modelled	21.7	14	PDB header: transcription/cell cycle Chain: A: PDB Molecule: s-phase kinase-associated protein 1a; PDBTitle: structure of the skp1-fbw7-cyclinedegc complex
26	d1nexa1	Alignment	not modelled	21.3	15	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
27	c4xsuB_	Alignment	not modelled	21.2	6	PDB header: transferase Chain: B: PDB Molecule: alr3699 protein; PDBTitle: crystal structure of anaerobaculum alr3699/hepe in complex with udp and2 glucose
28	d1y0ua_	Alignment	not modelled	20.1	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
						PDB header: ligase

29	c4ebrB	Alignment	not modelled	19.1	21	Chain: B: PDB Molecule: ubiquitin-like-conjugating enzyme atg10; PDBTitle: crystal structure of autophagic e2, atg10
30	d1fs2b1	Alignment	not modelled	18.2	15	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
31	c4d0kC	Alignment	not modelled	17.5	9	PDB header: gene regulation Chain: C: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit PDBTitle: complex of chaetomium thermophilum pan2 (wd40-cs1) with pan3 (c-term)
32	c5l6mA	Alignment	not modelled	17.3	5	PDB header: hydrolase Chain: A: PDB Molecule: vapb family protein; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
33	c2jimH	Alignment	not modelled	16.6	16	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
34	c2qzsA	Alignment	not modelled	16.1	8	PDB header: transferase Chain: A: PDB Molecule: glycogen synthase; PDBTitle: crystal structure of wild-type e.coli gs in complex with adp and2 glucose(wtgsb)
35	d1rzua	Alignment	not modelled	15.4	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
36	c3zvK	Alignment	not modelled	14.6	12	PDB header: antitoxin/toxin/dna Chain: G: PDB Molecule: antitoxin of toxin-antitoxin system vapb; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
37	c2p1nD	Alignment	not modelled	14.6	14	PDB header: signaling protein Chain: D: PDB Molecule: skp1-like protein 1a; PDBTitle: mechanism of auxin perception by the tir1 ubiquitin ligase
38	c6ct6B	Alignment	not modelled	14.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from eimeria maxima with2 nadh and oxamate
39	c3iaaB	Alignment	not modelled	13.9	13	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
40	d1ghca	Alignment	not modelled	13.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
41	c3fiwB	Alignment	not modelled	13.5	13	PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor
42	c4bwxB	Alignment	not modelled	13.4	10	PDB header: gene regulation Chain: B: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan-3; PDBTitle: structure of neurospora crassa pan3 pseudokinase mutant
43	c5d00A	Alignment	not modelled	13.4	14	PDB header: transferase Chain: A: PDB Molecule: n-acetyl-alpha-d-glucosaminyl l-malate synthase; PDBTitle: crystal structure of bsha from b. subtilis complexed with n-2 acetylglucosaminyl-malate and ump
44	c2fy2A	Alignment	not modelled	13.0	18	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: structures of ligand bound human choline acetyltransferase provide2 insight into regulation of acetylcholine synthesis
45	c2p6pB	Alignment	not modelled	12.5	16	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
46	c5zmyF	Alignment	not modelled	12.3	14	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
47	c2m4hA	Alignment	not modelled	12.2	42	PDB header: viral protein Chain: A: PDB Molecule: feline calicivirus vpg protein; PDBTitle: solution structure of the core domain (10-76) of the feline2 calicivirus vpg protein
48	c6d9tA	Alignment	not modelled	12.0	14	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
49	d1ez4a2	Alignment	not modelled	11.9	9	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
50	c3ctoE	Alignment	not modelled	11.8	100	PDB header: toxin inhibitor Chain: E: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
51	c3okaA	Alignment	not modelled	11.7	14	PDB header: transferase Chain: A: PDB Molecule: gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol PDBTitle: crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
52	c3himA	Alignment	not modelled	11.4	14	PDB header: transcription regulator Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of a bacterial regulatory protein in the tetr2 family from rhodococcus rha1 to 2.2a
53	d1ui5a1	Alignment	not modelled	11.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain

54	c1grjA_	Alignment	not modelled	11.0	24	PDB header: transcription regulation Chain: A: PDB Molecule: grea protein; PDBTitle: grea transcript cleavage factor from escherichia coli
55	c2dg7A_	Alignment	not modelled	11.0	25	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
56	c3tndF_	Alignment	not modelled	10.6	15	PDB header: translation, toxin Chain: F: PDB Molecule: antitoxin vapb; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
57	c5du2B_	Alignment	not modelled	10.1	14	PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
58	d2id3a1	Alignment	not modelled	10.1	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
59	c2ktiA_	Alignment	not modelled	10.0	14	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of c-terminal domain from mttyrss of a. nidulans
60	c4qxzA_	Alignment	not modelled	9.9	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from staphylococcus aureus
61	c2hxoB_	Alignment	not modelled	9.8	15	PDB header: transcription regulator; Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structure of the transcriptional regulator sco7222, a tetr from2 streptomyces coelicolor
62	d2i10a1	Alignment	not modelled	9.7	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
63	c5d5nA_	Alignment	not modelled	9.5	13	PDB header: viral protein Chain: A: PDB Molecule: virion egress protein ul34 homolog; PDBTitle: crystal structure of the human cytomegalovirus pul50-pul53 complex
64	d2fq4a1	Alignment	not modelled	8.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
65	c3msqC_	Alignment	not modelled	8.7	33	PDB header: biosynthetic protein Chain: C: PDB Molecule: putative ubiquinone biosynthesis protein; PDBTitle: crystal structure of a putative ubiquinone biosynthesis protein2 (npun02000094) from nostoc punctiforme pcc 73102 at 2.85 a resolution
66	c2p4vA_	Alignment	not modelled	8.5	18	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
67	c2iyaB_	Alignment	not modelled	8.0	19	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
68	c5xvmB_	Alignment	not modelled	8.0	5	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
69	c3s29C_	Alignment	not modelled	7.7	14	PDB header: transferase Chain: C: PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
70	d1lvaa3	Alignment	not modelled	7.7	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
71	c3beoA_	Alignment	not modelled	7.7	16	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcnaC 2-epimerases
72	c3wadA_	Alignment	not modelled	7.4	17	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicienistatin
73	c5hjzA_	Alignment	not modelled	7.3	31	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
74	c2mxdA_	Alignment	not modelled	7.2	35	PDB header: viral protein Chain: A: PDB Molecule: viral protein genome-linked; PDBTitle: solution structure of vpg of porcine sapovirus
75	d1f6da_	Alignment	not modelled	7.1	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
76	c4leiB_	Alignment	not modelled	7.1	16	PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminyltransferase spnp
77	d1o6ca_	Alignment	not modelled	7.0	23	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
78	c3no5C_	Alignment	not modelled	6.9	15	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
79	c6expD_	Alignment	not modelled	6.9	11	PDB header: viral protein Chain: D: PDB Molecule: sirv3 acrid1 (gp02) anti-crispr protein; PDBTitle: crystal structure of the sirv3 acrid1 (gp02) anti-crispr protein

80	c5ngwA	Alignment	not modelled	6.9	6	PDB header: hydrolase Chain: A: PDB Molecule: opgh99a; PDBTitle: glycoside hydrolase-like protein
81	d1rp3a1	Alignment	not modelled	6.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
82	c5d17L	Alignment	not modelled	6.7	21	PDB header: dna binding protein Chain: L: PDB Molecule: transposon tn7 transposition protein tnse; PDBTitle: structure of the c-terminal domain of tnse at 2.85 resolution
83	c5yhha	Alignment	not modelled	6.7	25	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized conserved protein yiiim; PDBTitle: crystal structure of yiiim from geobacillus stearothermophilus
84	d1nm8a1	Alignment	not modelled	6.3	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
85	c3ot5D	Alignment	not modelled	6.2	21	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
86	d1g8ma1	Alignment	not modelled	6.2	11	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
87	c4e1pA	Alignment	not modelled	6.2	27	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
88	c4e1rA	Alignment	not modelled	6.2	27	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
89	c6ejjA	Alignment	not modelled	6.0	14	PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
90	c3iuvA	Alignment	not modelled	6.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized tetr family protein; PDBTitle: the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3
91	c6fqbe	Alignment	not modelled	6.0	19	PDB header: ligase Chain: E: PDB Molecule: coobyric acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
92	c2qkoA	Alignment	not modelled	5.9	21	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, tetr family protein; PDBTitle: crystal structure of transcriptional regulator rha06399 from2 rhodococcus sp. rha1
93	c5gl5B	Alignment	not modelled	5.9	5	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c): udpg complex
94	d1m1fa	Alignment	not modelled	5.8	0	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
95	c3kb4D	Alignment	not modelled	5.7	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr8543 protein; PDBTitle: crystal structure of the alr8543 protein in complex with2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
96	c3co5B	Alignment	not modelled	5.5	32	PDB header: transcription regulator Chain: B: PDB Molecule: putative two-component system transcriptional response PDBTitle: crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
97	d1j2ga2	Alignment	not modelled	5.4	25	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
98	d1vi0a1	Alignment	not modelled	5.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
99	d2csua2	Alignment	not modelled	5.1	11	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains