Table 2. Annotated list of RNA database files

NDB ID	PDB ID	Resol.	No.res.	Name
ar0001	402D	2.30	16	8-mer duplex
ar0002	405D	2.50	32	16-mer duplex
ar0004	409D	2.50	16	8-mer duplex
ar0005	413D	1.80	13	13-mer (one strand)
ar0006	420D	1.90	32	16-mer duplex
ar0007	422D	2.60	24	12-mer duplex
ar0008	433D	2.10	28	14-mer duplex
ar0009	434D	1.16	14	7-bp ala-tRNA acceptor stem*
ar0011	438D	2.50	18	8-mer duplex*
ar0012	439D	1.6	16	8-mer duplex (with "wobble-like" G.C.)
ar0013	466D	1.16	14	7-mer duplex from ala-tRNA of *Escherichia coli*
ar0020	1QCU	1.20	22	Plasmid copy control*
ar0021	1QCO	1.55	57	Plasmid copy control
ar0022	472D	1.90	16	8-mer duplex (with GG/UU)
ar0023	1CSL	1.6	28	RRE high-affinity site
ar0024	1D4R	2.00	58	Fragment of human SRP RNA helix 6
ar0027	1DQH	1.70	19	Helix II of *Xenopus laevis* somatic 5S RNA*
ar0028	1DUQ	2.10	22	Rev. binding element of HIV-1
ar0030	1G2J	1.97	8	8-mer with phenyl ribonucleotide*
ar0032	1I9X	2.18	26	BPS-U2 snRNA duplex
ar0036	1KD3	1.80	22	11-mer duplex, thallium
ar0038	1KD5	1.58	22	11-mer duplex, metal-free*
ar0040	1L3Z	2.01	14	7-mer duplex*
ar0044	1NLC	1.85	46	HIV-1 DIS(MAL) genomic RNA
arb002		0.8	4	AU duplex*
arb003		1.1	4	GC duplex–calcium*
arb004		0.89	4	GC duplex-sodium*
arb005		0.85	4	GC duplex-ammonium octahydrate*
arf0108	377D	1.76	12	6-mer duplex
arh064	1RXB	1.80	16	8-mer duplex*
arh074	259D	1.46	16	8-mer duplex, hydration study*
arl037	255D	2.00	12	One strand of duplex*
arl048	157D	1.80	24	12-mer duplex
arl062	1SDR	2.60	24	*E. coli* Shine--Dalgarno seq*
arn035	1RNA	2.25	28	14-mer [U(U-A)6A]2
dr0005	1F27	1.30	30	Biotin-binding RNA pseudoknot
dr0008	1MWL	2.40	43	Eubacterial 16S rRNA A site
dr0010	1NTB	2.90	40	Streptomycin RNA-aptamer complex
drb002		0.90	2	AA + proflavine*
drb003		1.00	2	AU + 9-aminoacridine*
drb005		0.8	2	CA + proline*
drb007		1.34	4	CG duplex + ethidium*
drb008		0.85	2	CG + proflavin*
drb018		1.1	4	UA duplex + ethidium
drd004		1.00	4	CA/UG duplex + proflavine*
pd0345	1MSW	2.10	10	RNA message, phage T7 RNA
pr0005	1DRZ	2.30	72	Hepatitis delta virus genomic ribozyme
pr0006	1QF6	2.90	76	Threonine tRNA from *E. coli*
pr0007	1CVJ	2.60	9	Polyadenylate 9-mer [with poly(A)-bdg protein]
pr0008	2A8V	2.40	9	RNA/rho transcription termination F
pr0009	1C9S	1.90	5	GAGAU-repeats/TRP RNA-bdg attenuation protein
pr0010	1CX0	2.30	72	Hepatitis delta virus nested double pseudoknot
pr0011	1B7F	2.60	12	TRA pre-mRNA
pr0015	1QA6	2.80	58	1051-1108 from *E. coli* 23S rRNA
pr0017	1DDL	2.7	9	RNA from desmodium yellow mottle tymovirus
pr0018	1DFU	1.80	38	Loop E-helix IV fragments from 5S rRNA *E. coli*
pr0019	1C0A	2.40	76	Asp-tRNA
pr0020	1DI2	1.90	20	10-mer (with dsRNA-binding domain)
pr0021	1DUL	1.80	48	4.5S RNA domain IV
pr0022	1EC6	2.40	20	20-mer RNA hairpin

pr0026	1EUY	2.60	75	Gln-tRNA
pr0030	1F7U	2.2	76	Arg-tRNA
pr0032	1FFY	2.2	74	Ile-tRNA
pr0033	1FXL	1.80	7	Fragment of C-FOS AU-rich element
pr0034	1G2E	2.30	10	Fragment of AU-rich element of TNF alpha RNA
pr0036	1F8V	3.00	25	RNA from pariacoto virus
pr0037	1HQ1	1.52	48	4.5S RNA domain 4 (res 32-74)
pr0040	1E7X	2.38	16	RNA hairpin (with coat protein) from phage MS2
pr0046	1I5L	2.75	3	UUU with snRNP SM-like protein AF-SM1
pr0047	1I6U	2.60	37	16S rRNA fragment from *Methanococus jannaschii*, with S8P
pr0051	1JBR	2.15	62	Ribotoxin and 31-mer SRD RNA inhibitor
pr0053	1JBT	2.7	29	Sarcin/ricin domain RNA analog
pr0055	1E7K	2.90	22	U4 snRNA
pr0057	1H4S	2.85	66	Pro-tRNA + tRNApro(CGG) from *T. thermophilus*
pr0060	1K8W	1.85	22	T stem-loop RNA
pr0062	1GKW	2.56	26	MS2 RNA hairpin
pr0063	1KNZ	2.45	5	Rotavirus mRNA 3' consensus
pr0065	1KQ2	2.71	7	RNA with host factor for Q beta
pr0067	1L9A	2.90	137	Signal recognition particle RNA S domain
pr0069	1IVS	2.90	75	Val-tRNA
pr0071	1GTF	1.75	4	GAGUU repeat RNA with TRP-protein
pr0073	1LNG	2.30	97	7S.S SRP RNA
pr0075	1M50	2.20	21	RNA hairpin ribozyme with U1A, STR virus
pr0078	1M8V	2.60	41	Uridine heptamer (with snRNP sm-like protein)
pr0079	1M8W	2.20	30	NRE1-19 RNA
pr0080	1M8X	2.20	15	NRE1-14 RNA
pr0081	1M8Y	2.60	10	NRE2-10 RNA
pr0083	1MJI	2.50	34	5S rRNA fragment
pr0085	1MZP	2.65	55	23S rRNA fragment (L1 protuberance)
pr0090	1N78	2.10	76	Glu-tRNA
pr0091	1NB7	2.90	4	U-template for HC-JR RNA polymerase
prv001	1BMV	3.00	11	RNA in icosahedral virus (bountiful bean)
prv004	2BBV	2.80	10	RNA in black beetle virus
prv010	6MSF	2.80	24	RNA in MS2
prv020	1A34	1.81	21	RNA in satellite tobacco mosaic virus
prv021	1ZDJ	2.90	16	8-NT MS2 variant RNA fragment
pte003	1QTQ	2.25	76	Gln-tRNA
ptr004	1SER	2.90	66	Ser-tRNA
ptr016	1A9N	2.38	24	U2 snRNA hairpin IV
rr0005	1DK1	2.80	52	rRNA fragment with S15 (30S)
rr0010	1F7Y	2.80	52	16S rRNA fragment (w/ UUCG tetraloops)
rr0016	1FJG	3.00	1513	30S ribosomal subunit
rr0019	1G1X	2.60	84	16S rRNA fragments
rr0033	1JJ2	2.40	2876	*Haloarcula marismortui* large ribosomal subunit
tr0001	1EHZ	1.93	76	Phe-tRNA
trna12	1YFG	3.00	76	Yeast initiator tRNA
uh0001	1BR3	3.00	13	RNA complex with 10-23 DNA enzyme
uhx026	1HMH	2.60	34	Hammerhead ribozyme (RNA-DNA) RNA strand
ur0001	429D	2.7	24	Lead-dependent ribozyme
ur0004	437D	1.6	28	RNA pseudoknot from beet western yellow virus
ur0005	462D	2.30	46	HIV-1 genomic RNA dimerization initiation site
ur0007	483D	1.11	27	Sarcin/ricin rRNA domain from *E. coli*
ur0009	1DUH	2.7	45	Conserved domain IV of *E. coli* 4.5S RNA
ur0012	1HR2	2.25	157	PR-P6 DELC209 mut, tetrahymena group I intron
ur0014	1J8G	0.61	24	RNA tetraplex
ur0015	1JJM	2.60	46	HIV-1(LAI) genomic RNA 265-287
ur0019	1KXK	3.00	70	Domains 5,6 of AI5G group II self-splicing intron
ur0020	1L2X	1.25	28	RNA pseudoknot, beet western yellow virus
ur0022	1L8V	2.80	157	P4-P6 RNA ribozyme domain group I intron
ur0026	1MSY	1.41	27	GUAA tetraloop mutant, sarcin/ricin from 23S*
urb003		1.00	2	AA*
urb008		1.00	2	UA*

urb016		0.86	4	UA/UA*
urc002		0.95	3	AAA*
urf042	1OSU	1.40	6	Half of double helix, with UU overhang*
url029	205D	2.64	24	Double helix with UU-pair in internal loop
url050	280D	2.40	24	RNA dodecamer with internal loop
urt068	361D	3.00	20	Domain E of *Thermus flavus* 5S rRNA, with tetraloop
urx053	1GID	2.50	158	P4-P6 ribozyme domain
urx059	301D	3.00	41	RNA hammerhead ribozyme
urx063	353D	2.40	24	Domain A of *T. flavus* 5S rRNA*
urx075	397D	1.30	27	HIV-1 transactivation response region

NDB, Nucleic Acid Database; PDB, Protein Data Bank; ID, identification; Resol., resolution.

*No backbone clashes.