

Supplemental File 1:

Deep Learning for RNA Secondary Structure Determination: Gauging Generalizability and Broadening the Scope of Traditional Methods

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1 Aptamers

1.1 Theophylline aptamer

1.1.1 8d28_A

Crystal structure of theophylline aptamer in complex with theophylline

Release date: 2022-11-30

Method: x-ray diffraction

Resolution: 1.42 Å

Chain length: 33

Extracted length: 33

Total clashes: 4

Clashes per residue: 0.121

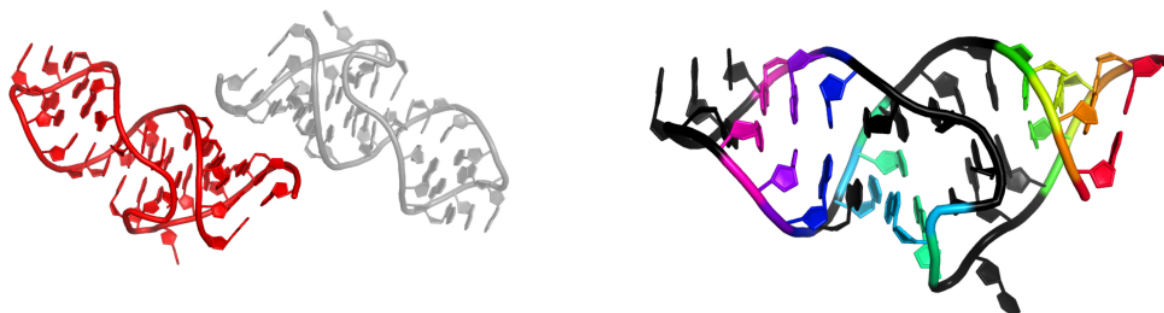
Clashscore: 1.840

Description: RNA (33-MER)

Organism: synthetic construct

Menichelli, E., Lam, B.J., Wang, Y., Wang, V.S., Shaffer, J., Tjhung, K.F., Bursulaya, B., Nguyen, T.N., Vo, T., Alper, P.B., McAllister, C.S., Jones, D.H., Spraggon, G., Michellys, P.Y., Joslin, J., Joyce, G.F., Rogers, J. (2022) Discovery of small molecules that target a tertiary-structured RNA. *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.2213117119](https://doi.org/10.1073/pnas.2213117119)



GGCGAUACCAGCCGAAAGGCCCUUGGCAGCGCC
(((...((.((((...)))...))...)))

1.1.2 8d29_C

Crystal structure of theophylline aptamer - apo form

Release date: 2022-11-30

Method: x-ray diffraction

Resolution: 1.81 Å

Chain length: 34

Extracted length: 34

Total clashes: 4

Clashes per residue: 0.118

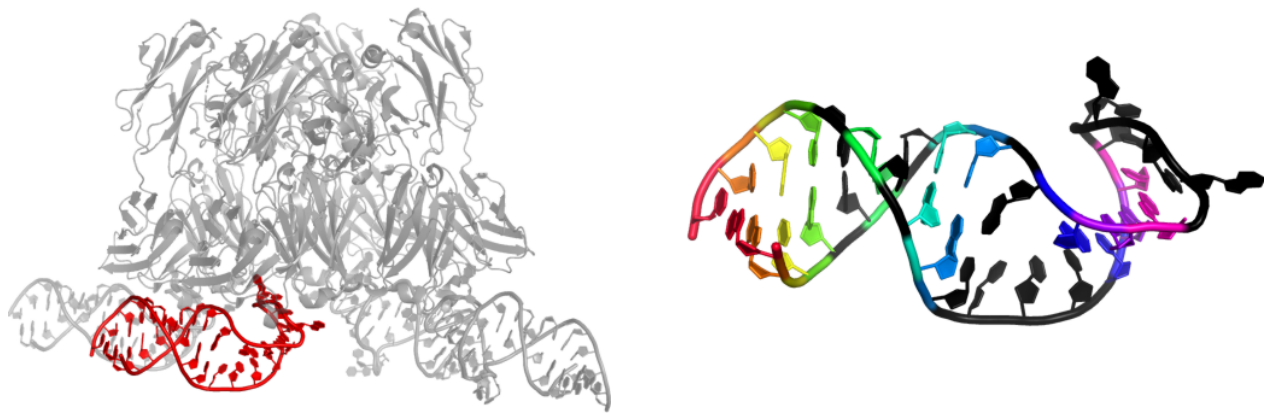
Clashscore: 4.310

Description: RNA (34-MER)

Organism: synthetic construct

Menichelli, E., Lam, B.J., Wang, Y., Wang, V.S., Shaffer, J., Tjhung, K.F., Bursulaya, B., Nguyen, T.N., Vo, T., Alper, P.B., McAllister, C.S., Jones, D.H., Spraggon, G., Michellys, P.Y., Joslin, J., Joyce, G.F., Rogers, J. (2022) Discovery of small molecules that target a tertiary-structured RNA. *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.2213117119](https://doi.org/10.1073/pnas.2213117119)



GGCGAUACCAGCGAAACACGCCCUUGGCAGCGUC

(((((.(.(.(((.....))).....)).)).)))

1.1.3 8dk7_C

Crystal structure of theophylline aptamer soaked with TAL2

Release date: 2022-11-30

Method: x-ray diffraction

Resolution: 2.46 Å

Chain length: 34

Extracted length: 34

Total clashes: 4

Clashes per residue: 0.118

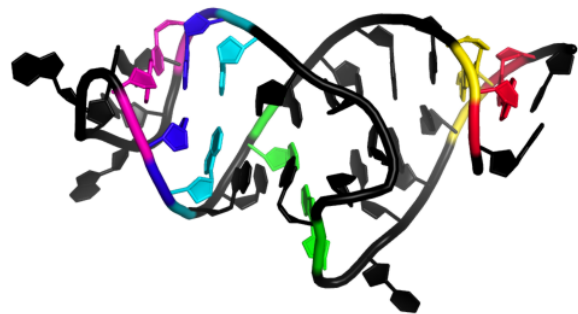
Clashscore: 24.590

Description: RNA (34-MER)

Organism: synthetic construct

Menichelli, E., Lam, B.J., Wang, Y., Wang, V.S., Shaffer, J., Tjhung, K.F., Bursulaya, B., Nguyen, T.N., Vo, T., Alper, P.B., McAllister, C.S., Jones, D.H., Spraggon, G., Michellys, P.Y., Joslin, J., Joyce, G.F., Rogers, J. (2022) Discovery of small molecules that target a tertiary-structured RNA. *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.2213117119](https://doi.org/10.1073/pnas.2213117119)



GGCGAUACCAGCGAAACACGCCCUUGGCAGCGUC

.((.....(.....(((.....))).....).....))..

1.2.1 4m4o_B

Release date: 2013-12-18

Method: x-ray diffraction

Resolution: 2.00 Å

Chain length: 59

Extracted length: 59

Total clashes: 14

Clashes per residue: 0.237

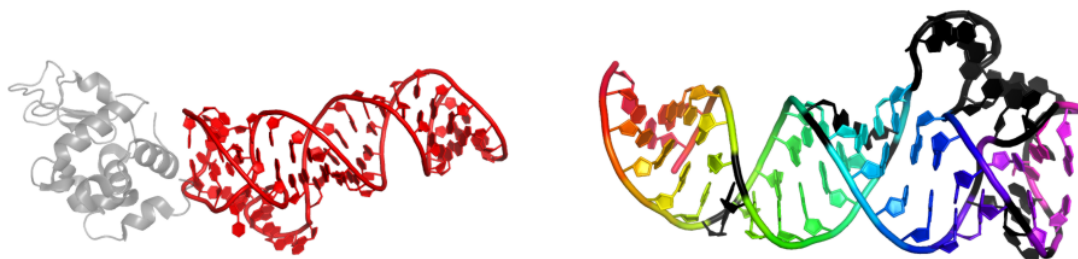
Clashscore: 2.830

Description: RNA (59-MER)

Organism: nan

Malashkevich, V.N., Padlan, F.C., Toro, R., Girvin, M., Almo, S.C. (N/A) Crystal structure of the aptamer minE-lysozyme complex. to be published.

DOI: nan



GGGUUCAUCAGGGCUAAAGAGUGCAGAGUUACUAGUUCACUGCAGACUUGACGAACCC
(((.(((.(.(.....(((.(.(.<.>..)).)))..)))).)))))

1.2.2 4m6d_L

Crystal structure of the aptamer minF-lysozyme complex.

Release date: 2013-12-11

Method: x-ray diffraction

Resolution: 2.68 Å

Chain length: 45

Extracted length: 43

Total clashes: 62

Clashes per residue: 1.378

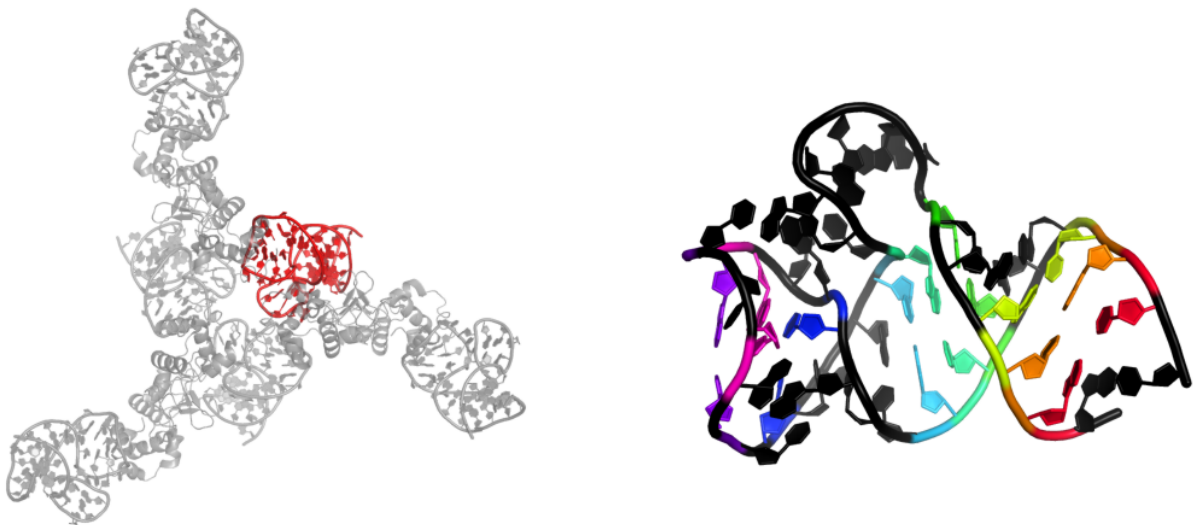
Clashscore: 18.470

Description: aptamer

Organism: nan

Malashkevich, V.N., Padlan, F.C., Toro, R., Girvin, M., Almo, S.C. (N/A) Crystal structure of the aptamer minF-lysozyme complex. To be Published.

DOI: [nan](#)



GGGCGGCUAAAGAGUGCAGAGUUACUUAGUUCACUGCAGACGCCC
..(((..(.....((...(.(<...>...))...))...))..

1.3 RhoBAST aptamer

1.3.1 9bun_A

RhoBAST aptamer RNA in complex with 5(6)-carboxytetramethylrhodamine

Release date: 2024-06-05

Method: x-ray diffraction

Resolution: 2.10 Å

Chain length: 48

Extracted length: 48

Total clashes: 9

Clashes per residue: 0.188

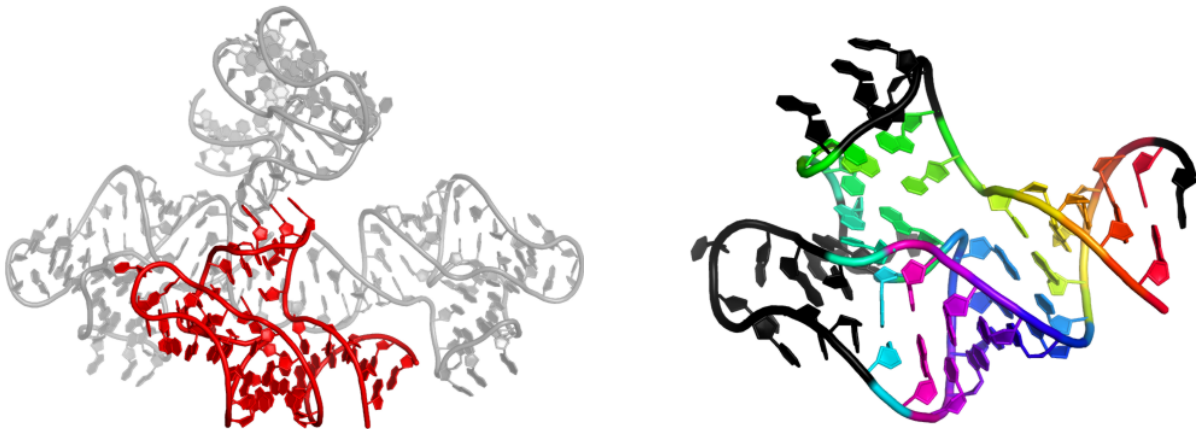
Clashscore: 11.130

Description: RNA (48-MER)

Organism: synthetic construct

Batey, R.T., Siwik, S.H. (N/A) Structure of RhoBAST RNA aptamer in complex with 5(6)-carboxytetramethylrhodamine (TAMRA). To Be Published.

DOI: [nan](#)



GGACUCGGAAACGUGAAGGAGAGGCGCAAGGUUAACGCCUCAGUCCA
(((((((.....))(<...<(((((>.....>)))))))))..

1.3.2 8jy0_D

Crystal structure of RhoBAST complexed with TMR-DN

Release date: 2024-05-29

Method: x-ray diffraction

Resolution: 2.75 Å

Chain length: 64

Extracted length: 64

Total clashes: 41

Clashes per residue: 0.641

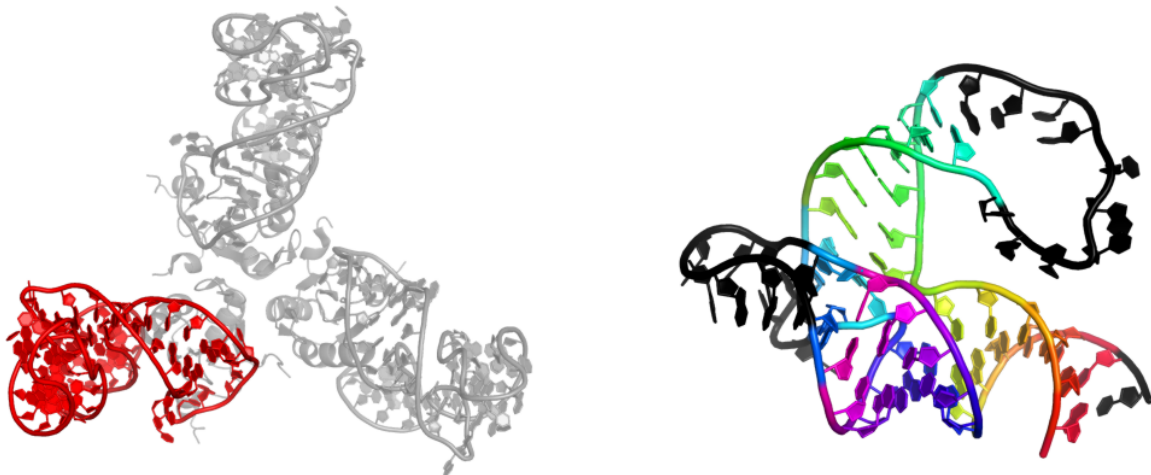
Clashscore: 5.150

Description: RhoBAST

Organism: artificial sequences

Zhang, Y., Xu, Z., Xiao, Y., Jiang, H., Zuo, X., Li, X., Fang, X. (2024) Structural mechanisms for binding and activation of a contact-quenched fluorophore by RhoBAST. Nat Commun.

DOI: [10.1038/s41467-024-48478-9](https://doi.org/10.1038/s41467-024-48478-9)



GAACCUCGCCCCAUUGCACUCCGGGCGGUGAAGGAGAGGCGCAAGGUUAACCGCCUCAGGUUCC
(((((((.....))))))(<...<((((>.....>))))))..

1.4.1 6b14_R

Release date: 2017-12-27

Resolution: 1.64 Å

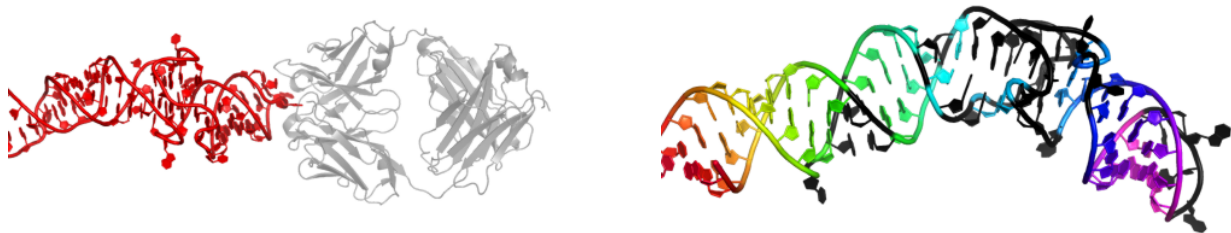
Extracted length: 83

Clashes per residue: 0.000

Description: RNA (86-MER)

Organism: synthetic construct

DOI: [10.1093/nar/gkx1292](https://doi.org/10.1093/nar/gkx1292)



GACGCGACCGAAAUGGUGAAGGACGGGUCCAGUGCGAAACACGCACUGUUGAGUAGAGUGUGAGCUCGCCUAACUGGUCGCGUC
((((((((((. (. (. (. (.)

1.4.2 6b3k_R

Crystal structure of mutant Spinach RNA aptamer in complex with Fab BL3-6

Release date: 2017-12-27

Method: x-ray diffraction

Resolution: 2.09 Å

Chain length: 83

Extracted length: 83

Total clashes: 0

Clashes per residue: 0.000

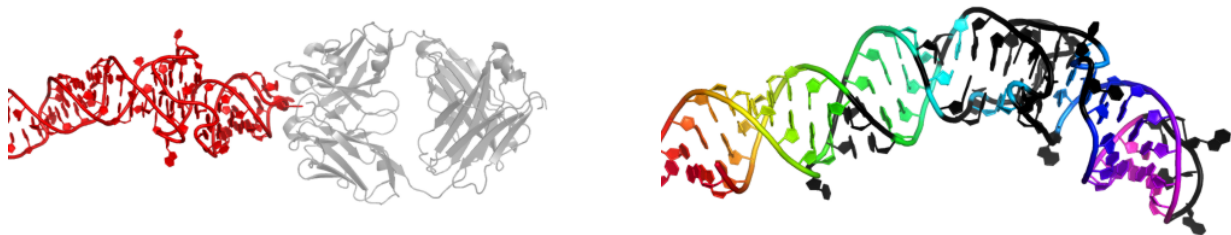
Clashscore: 4.330

Description: RNA (83-MER),RNA (83-MER)

Organism: synthetic construct

Koirala, D., Shelke, S.A., Dupont, M., Ruiz, S., DasGupta, S., Bailey, L.J., Benner, S.A., Piccirilli, J.A. (2018) Affinity maturation of a portable Fab-RNA module for chaperone-assisted RNA crystallography. *Nucleic Acids Res.*

DOI: [10.1093/nar/gkx1292](https://doi.org/10.1093/nar/gkx1292)



GACGCGACCGAAAUGGUGAAGGACGGGUCCAGUGCGAGACCCGCACUGUUGAGUAGAGUGAGCUCGGUAACUGGUCGCGUC
(((((((((.....(((((((.....)))))).....)))))).....)))))).....)))))).....)))))).....))))))

1.5 Mango aptamer

1.5.1 8u5t_A

Structure of Mango II variant aptamer bound to T01-6A-B

Release date: 2024-03-27

Method: x-ray diffraction

Resolution: 2.20 Å

Chain length: 36

Extracted length: 36

Total clashes: 0

Clashes per residue: 0.000

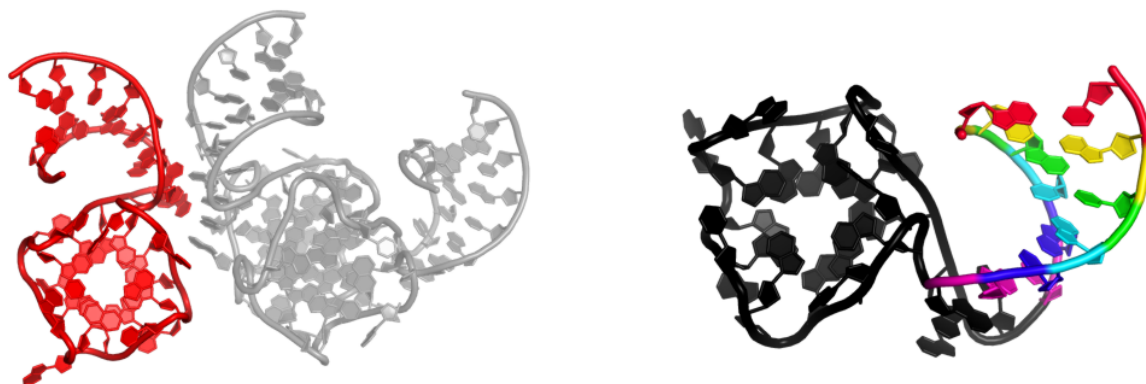
Clashscore: 2.450

Description: Mango II variant

Organism: synthetic construct

Passalacqua, L.F.M., Ferre-D'Amare, A.R. (N/A) Structure of Mango II variant aptamer bound to T01-6A-B. To Be Published.

DOI: [nan](#)



GCGUACGAAGGUGAGGAGAGGCGAGGAAGAGUACGC
((((((.....))))))

1.5.2 6e8u_B

Structure of the Mango-III (A10U) aptamer bound to TO1-Biotin

Release date: 2019-04-17

Method: x-ray diffraction

Resolution: 1.55 Å

Chain length: 37

Extracted length: 37

Total clashes: 0

Clashes per residue: 0.000

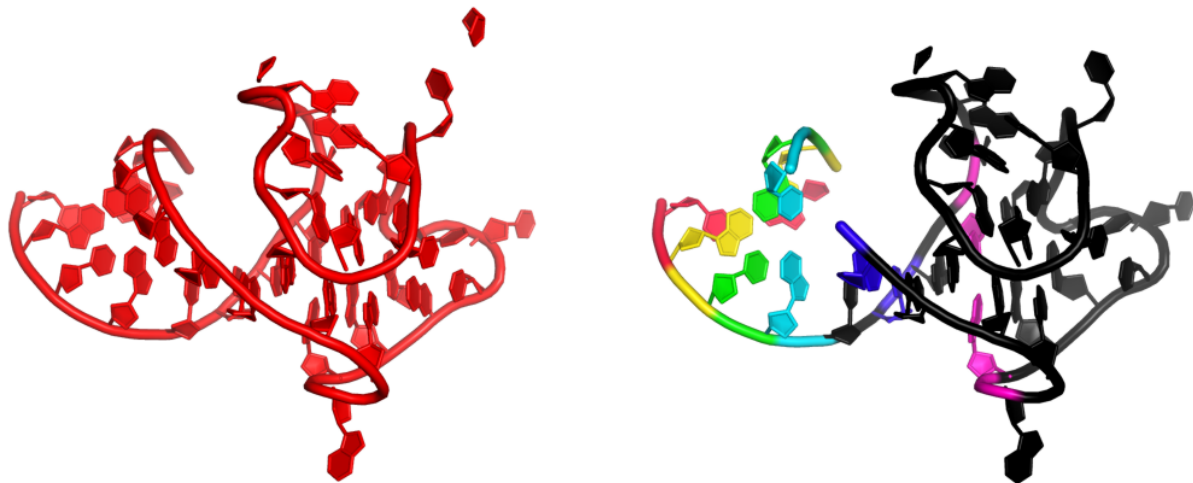
Clashscore: 4.540

Description: RNA (37-MER)

Organism: synthetic construct

Trachman 3rd., R.J., Autour, A., Jeng, S.C.Y., Abdolazadeh, A., Andreoni, A., Cojocaru, R., Garipov, R., Dolgosheina, E.V., Knutson, J.R., Ryckelynck, M., Unrau, P.J., Ferre-D'Amare, A.R. (2019) Structure and functional reselection of the Mango-III fluorogenic RNA aptamer. Nat. Chem. Biol.

DOI: [10.1038/s41589-019-0267-9](https://doi.org/10.1038/s41589-019-0267-9)



GUACGAAGGAAGGUUGGUAUGGGGUAGUUGUCGUAC

(((((.(.....(.).).)))

1.5.3 6e8t_D

Structure of the Mango-III (A10U) aptamer bound to TO1-Biotin

Release date: 2019-04-17

Method: x-ray diffraction

Resolution: 2.90 Å

Chain length: 36

Extracted length: 36

Total clashes: 31

Clashes per residue: 0.861

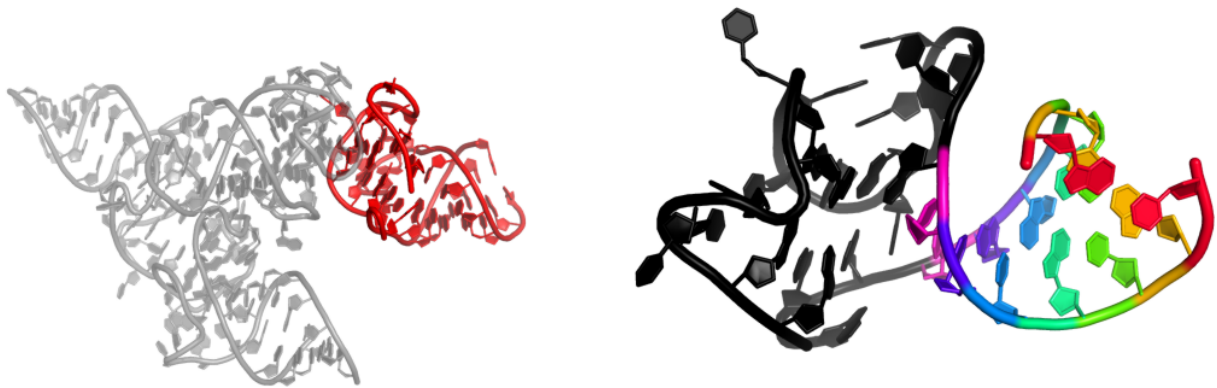
Clashscore: 12.160

Description: RNA (35-MER)

Organism: synthetic construct

Trachman 3rd., R.J., Autour, A., Jeng, S.C.Y., Abdolazadeh, A., Andreoni, A., Cojocaru, R., Garipov, R., Dolgosheina, E.V., Knutson, J.R., Ryckelynck, M., Unrau, P.J., Ferre-D'Amare, A.R. (2019) Structure and functional reselection of the Mango-III fluorogenic RNA aptamer. Nat. Chem. Biol.

DOI: [10.1038/s41589-019-0267-9](https://doi.org/10.1038/s41589-019-0267-9)



GUACGAAGGAAGGUUGGUAUGUGGUAUAUUCGUAC
((((((.....))))))

1.5.4 8u5j_A

Structure of Mango III variant aptamer bound to T01-07M-B

Release date: 2024-03-27

Method: x-ray diffraction

Resolution: 1.70 Å

Chain length: 36

Extracted length: 36

Total clashes: 20

Clashes per residue: 0.556

Clashscore: 7.820

Description: Mango III variant

Organism: synthetic construct

Passalacqua, L.F.M., Ferre-D'Amare, A.R. (N/A) Structure of Mango III variant aptamer bound to T01-07M-B. To Be Published.

DOI: [nan](#)



GUACGAAGGAAGGUUGGUAUGUGGUAGAUUCGUAC
(((((((.....))))))

1.5.5 6c65_B

Crystal Structure of the Mango-II-A22U Fluorescent Aptamer Bound to TO1-Biotin

Release date: 2018-08-08

Method: x-ray diffraction

Resolution: 2.80 Å

Chain length: 36

Extracted length: 36

Total clashes: 41

Clashes per residue: 1.139

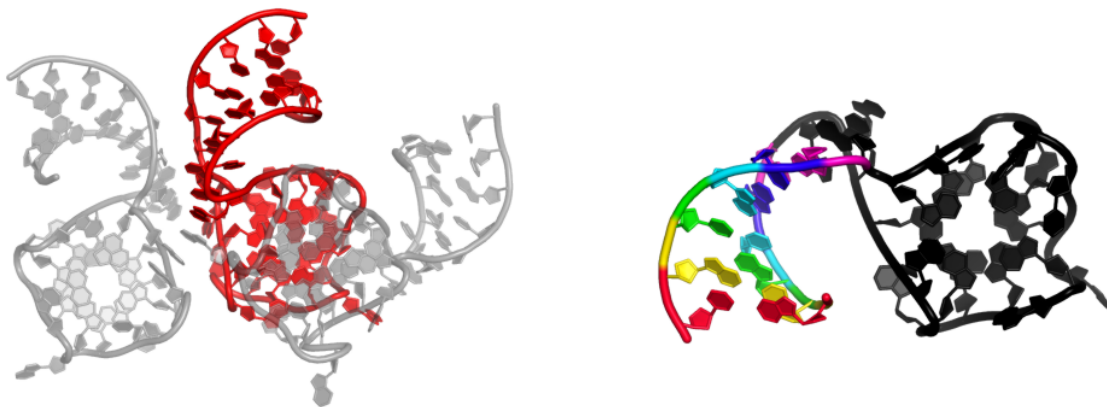
Clashscore: 23.160

Description: RNA (36-MER)

Organism: synthetic construct

Trachman 3rd., R.J., Abdolazadeh, A., Andreoni, A., Cojocaru, R., Knutson, J.R., Ryckelynck, M., Unrau, P.J., Ferre-D'Amare, A.R. (2018) Crystal Structures of the Mango-II RNA Aptamer Reveal Heterogeneous Fluorophore Binding and Guide Engineering of Variants with Improved Selectivity and Brightness. *Biochemistry*.

DOI: [10.1021/acs.biochem.8b00399](https://doi.org/10.1021/acs.biochem.8b00399)



GCGUACGAAGGAGAGGAGAGGUAGAGGAGAGUACGC
((((((.....))))))

1.5.6 6e8s_B

Structure of the iMango-III aptamer bound to TO1-Biotin

Release date: 2019-04-17

Method: x-ray diffraction

Resolution: 2.35 Å

Chain length: 38

Extracted length: 38

Total clashes: 34

Clashes per residue: 0.895

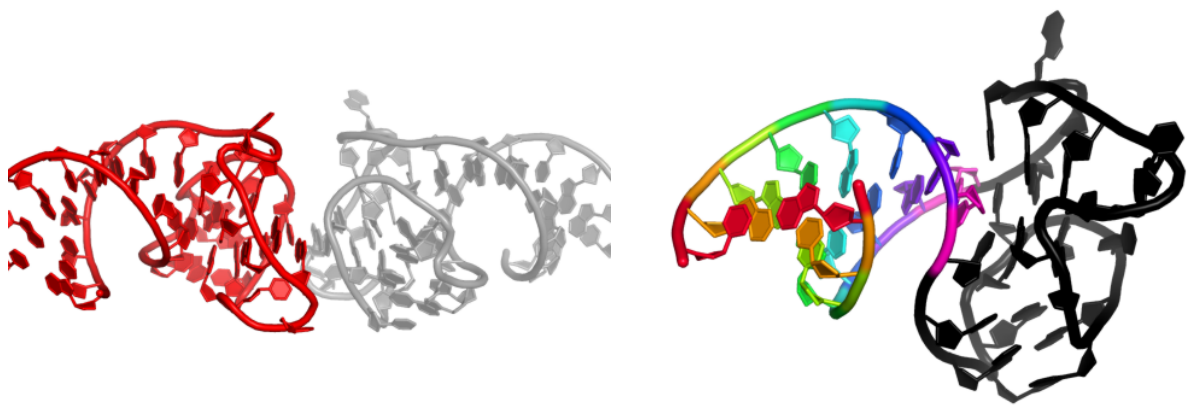
Clashscore: 12.660

Description: iMango-III aptamer

Organism: synthetic construct

Trachman 3rd., R.J., Autour, A., Jeng, S.C.Y., Abdolazadeh, A., Andreoni, A., Cojocaru, R., Garipov, R., Dolgosheina, E.V., Knutson, J.R., Ryckelynck, M., Unrau, P.J., Ferre-D'Amare, A.R. (2019) Structure and functional reselection of the Mango-III fluorogenic RNA aptamer. Nat. Chem. Biol.

DOI: [10.1038/s41589-019-0267-9](https://doi.org/10.1038/s41589-019-0267-9)



GCUACGAAGGAAGGAUUGGUAUGUGGUAUAUUCGUAGC
(((((((.)))))))

1.6 Vitamin B12 aptamer

1.6.1 1et4_E

CRYSTAL STRUCTURE OF A VITAMIN B12 BINDING RNA APTAMER WITH LIGAND AT 2.3 Å

Release date: 2000-11-13

Method: x-ray diffraction

Resolution: 2.30 Å

Chain length: 35

Extracted length: 35

Total clashes: 24

Clashes per residue: 0.686

Clashscore: 10.070

Description: RNA APTAMER, 35-MER

Organism: nan

Sussman, D., Wilson, C. (2000) A water channel in the core of the vitamin B(12) RNA aptamer. Structure Fold.Des.

DOI: [10.1016/S0969-2126\(00\)00159-3](https://doi.org/10.1016/S0969-2126(00)00159-3)



GGAACCGGUGCGCAUAACCACCUCAGUGCGAGCAA

.....<<<.(.(...((>>>...).).).)..

1.7 Squash aptamer

1.7.1 7kvu_G

Crystal structure of Squash RNA aptamer in complex with DFHBI-1T

Release date: 2022-01-19

Method: x-ray diffraction

Resolution: 2.68 Å

Chain length: 83

Extracted length: 83

Total clashes: 0

Clashes per residue: 0.000

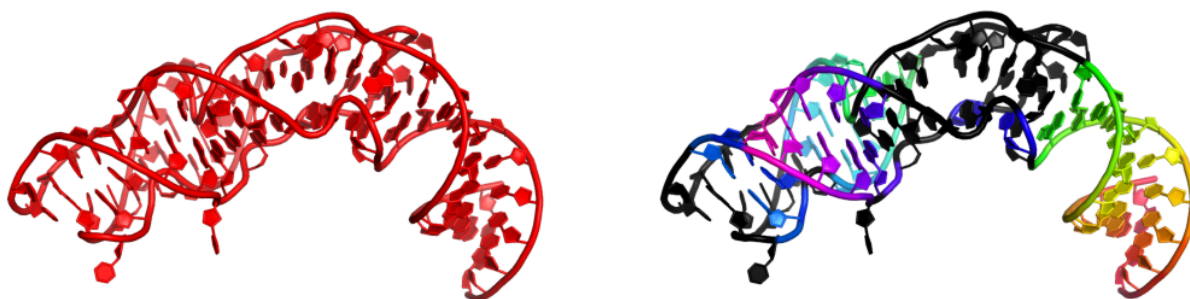
Clashscore: 3.680

Description: Squash RNA aptamer

Organism: synthetic construct

Truong, L., Kooshapur, H., Dey, S.K., Li, X., Tjandra, N., Jaffrey, S.R., Ferre-D'Amare, A.R. (2022) The fluorescent aptamer Squash extensively repurposes the adenine riboswitch fold. Nat.Chem.Biol.

DOI: [10.1038/s41589-021-00931-2](https://doi.org/10.1038/s41589-021-00931-2)



GGGAAGAUACAAGGUGAGCCCAUAAUAUGGUUUGGGUUAGGAUAGGAAGUAGAGCCUUAACUCUCUAAGCGGUAUCUUC
((((((.....(((.....<.>))).....(.(((>.....)))).....).))))))

1.8 Pepper aptamer

1.8.1 7eoh_A

Crystal structure of the Pepper aptamer in complex with HBC

Release date: 2021-11-24

Method: x-ray diffraction

Resolution: 1.64 Å

Chain length: 49

Extracted length: 49

Total clashes: 0

Clashes per residue: 0.000

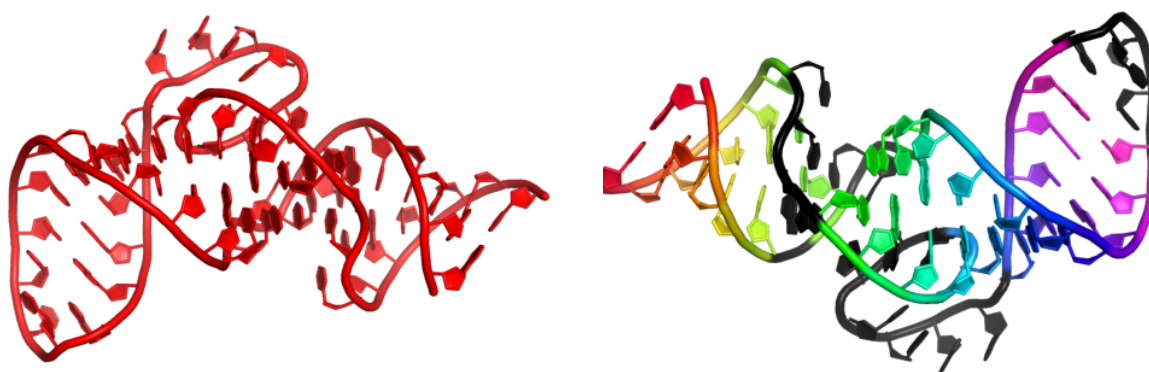
Clashscore: 0.620

Description: Pepper (49-MER)

Organism: synthetic construct

Huang, K., Chen, X., Li, C., Song, Q., Li, H., Zhu, L., Yang, Y., Ren, A. (2021) Structure-based investigation of fluorogenic Pepper aptamer. Nat.Chem.Biol.

DOI: [10.1038/s41589-021-00884-6](https://doi.org/10.1038/s41589-021-00884-6)



GGCGCACUGGCGCUGCGCCUUCGGGCGCCAAUCGUAGCGUGUCGGCGCC
(((. . . ((((((((((. . .)))) . . .)))) . . .))))

1.10 Corn aptamer

1.10.1 5bjo_Y

Crystal structure of the Corn RNA aptamer in complex with DFHO, site-specific 5-iodo-U

Release date: 2017-09-27

Method: x-ray diffraction

Resolution: 2.35 Å

Chain length: 36

Extracted length: 36

Total clashes: 0

Clashes per residue: 0.000

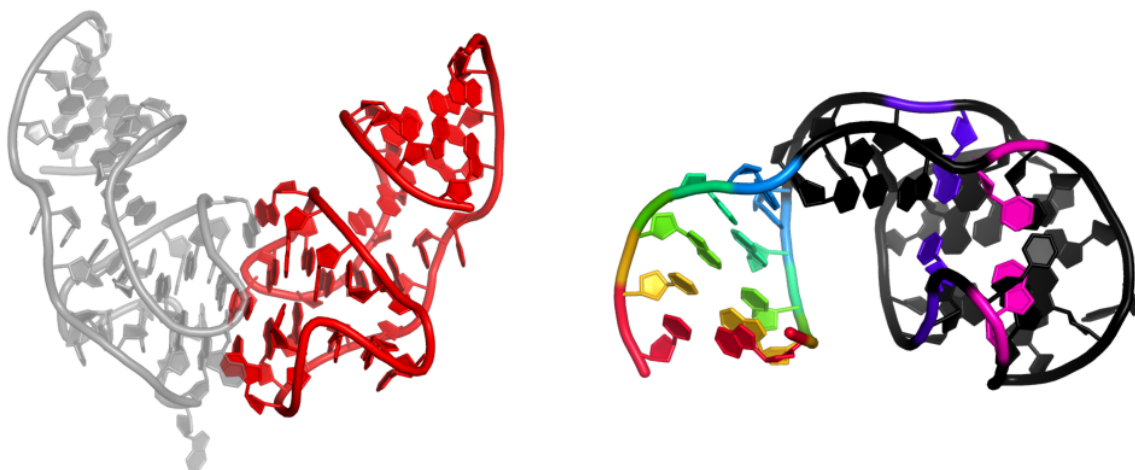
Clashscore: 4.190

Description: RNA (36-MER)

Organism: synthetic construct

Warner, K.D., Sjekloca, L., Song, W., Filonov, G.S., Jaffrey, S.R., Ferre-D'Amare, A.R. (2017)
A homodimer interface without base pairs in an RNA mimic of red fluorescent protein. Nat.
Chem. Biol.

DOI: [10.1038/nchembio.2475](https://doi.org/10.1038/nchembio.2475)



GGCGCGAGGAAGGAGGUCUGAGGAGGUCACUGCGCC
((((...((.....).(.....).....))))

1.11 DIR2s aptamer

1.11.1 6db8_R

Structural basis for promiscuous binding and activation of fluorogenic dyes by DIR2s RNA aptamer

Release date: 2018-11-14

Method: x-ray diffraction

Resolution: 1.87 Å

Chain length: 60

Extracted length: 60

Total clashes: 0

Clashes per residue: 0.000

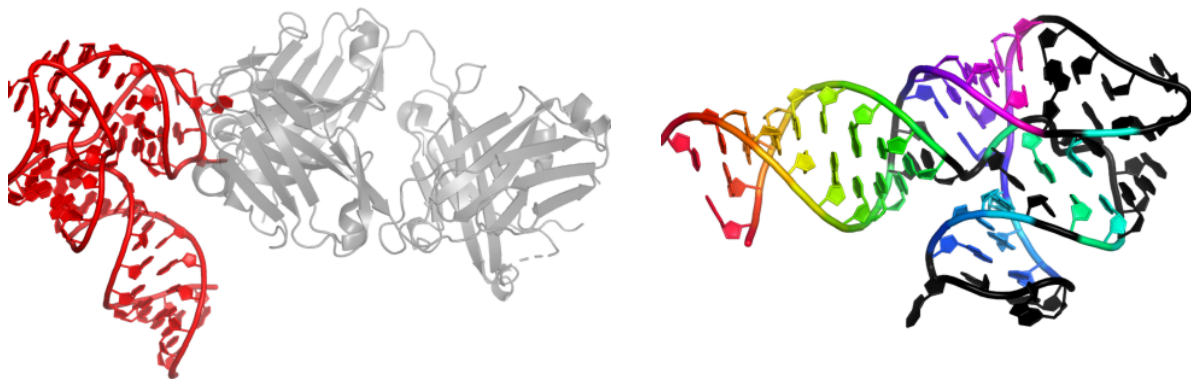
Clashscore: 4.480

Description: RNA (60-MER)

Organism: synthetic construct

Shelke, S.A., Shao, Y., Laski, A., Koirala, D., Weissman, B.P., Fuller, J.R., Tan, X., Constantin, T.P., Waggoner, A.S., Bruchez, M.P., Armitage, B.A., Piccirilli, J.A. (2018) Structural basis for activation of fluorogenic dyes by an RNA aptamer lacking a G-quadruplex motif. Nat Commun.

DOI: [10.1038/s41467-018-06942-3](https://doi.org/10.1038/s41467-018-06942-3)



GGAUGCGCCUUGAAAAGCCUGCGAAACACGCAGCUGGUGAAUGACAGCUAUGGCGCAUCC
((((((.....<)).((((.....)))((((.....>..))))..)))..)))

1.12 Clivia aptamer

1.12.1 8hze_B

A new fluorescent RNA aptamer bound with N

Release date: 2024-06-19

Method: x-ray diffraction

Resolution: 1.59 Å

Chain length: 35

Extracted length: 35

Total clashes: 0

Clashes per residue: 0.000

Clashscore: 2.480

Description: RNA (36-MER)

Organism: synthetic construct

Huang, K., Song, Q., Fang, M., Yao, D., Shen, X., Xu, X., Chen, X., Zhu, L., Yang, Y., Ren, A. (2024) Structural basis of a small monomeric Clivia fluorogenic RNA with a large Stokes shift. *Nat.Chem.Biol.*

DOI: [10.1038/s41589-024-01633-1](https://doi.org/10.1038/s41589-024-01633-1)



GAAGAUUGUAAACAUGCCGAAAGGCAGACACUUCC
(((.....(((.....))).....)))..

1.12.2 8hzj_A

A new fluorescent RNA aptamer bound with N571

Release date: 2024-06-19

Method: x-ray diffraction

Resolution: 2.60 Å

Chain length: 35

Extracted length: 35

Total clashes: 2

Clashes per residue: 0.057

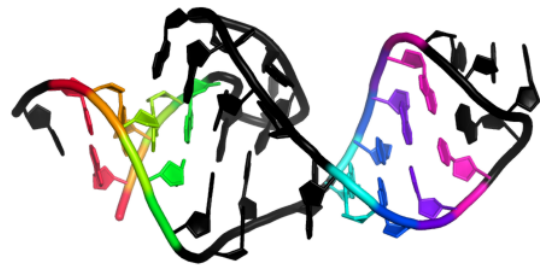
Clashscore: 2.500

Description: RNA (36-MER)

Organism: synthetic construct

Huang, K., Song, Q., Fang, M., Yao, D., Shen, X., Xu, X., Chen, X., Zhu, L., Yang, Y., Ren, A. (2024) Structural basis of a small monomeric Clivia fluorogenic RNA with a large Stokes shift. *Nat.Chem.Biol.*

DOI: [10.1038/s41589-024-01633-1](https://doi.org/10.1038/s41589-024-01633-1)



GAAGAUUGUAAACAUGCCGAAAGGCAGACACUCC
(((.....((((.....))).....)))..

1.12.3 8hzl_B

A new fluorescent RNA aptamer_III bound with N

Release date: 2024-06-19

Method: x-ray diffraction

Resolution: 2.60 Å

Chain length: 84

Extracted length: 84

Total clashes: 26

Clashes per residue: 0.310

Clashscore: 5.170

Description: RNA (84-MER)

Organism: synthetic construct

Huang, K., Song, Q., Fang, M., Yao, D., Shen, X., Xu, X., Chen, X., Zhu, L., Yang, Y., Ren, A. (2024) Structural basis of a small monomeric Clivia fluorogenic RNA with a large Stokes shift. Nat.Chem.Biol.

DOI: [10.1038/s41589-024-01633-1](https://doi.org/10.1038/s41589-024-01633-1)



GGAAGAUUGUAAACAGCGAGAUUGUAAACAGCGAGAUUGUAAACAUGCCGAAAGGCAGACACUCGCGACACUCGCGACACUUUC
((((.....(((.....((((.....(((.....)))).....)))).....))))

1.13 A9g aptamer

1.13.1 6rti_X

X-ray structure of human glutamate carboxypeptidase II (GCPII) in complex with aptamer A9g

Release date: 2020-06-10

Method: x-ray diffraction

Resolution: 2.20 Å

Chain length: 43

Extracted length: 43

Total clashes: 0

Clashes per residue: 0.000

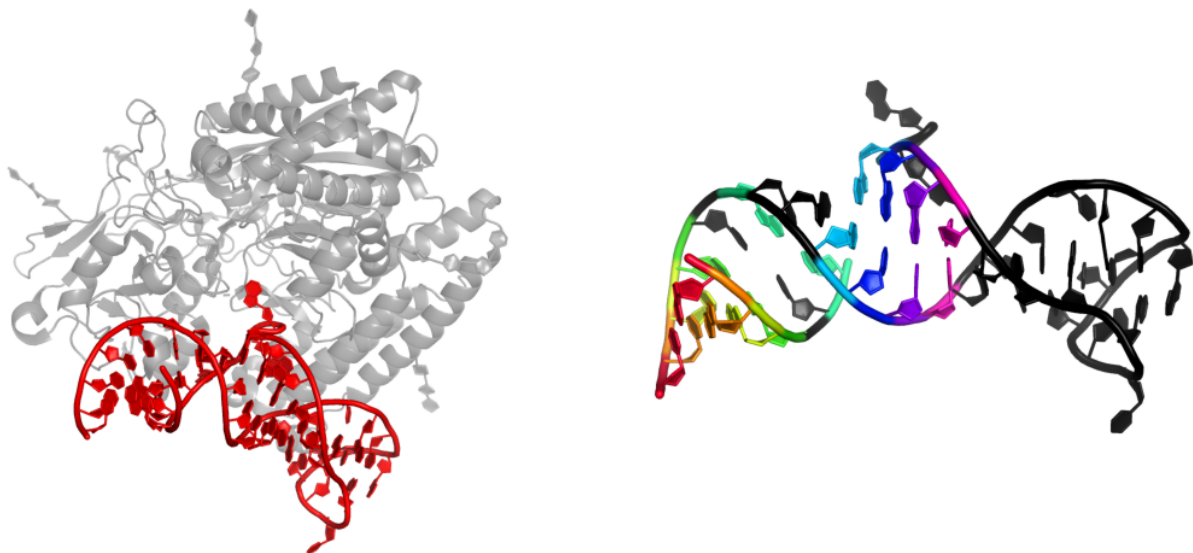
Clashscore: 3.130

Description: Aptamer A9g, RNA (43-MER)

Organism: synthetic construct

Ptacek, J., Zhang, D., Qiu, L., Kruspe, S., Motlova, L., Kolenko, P., Novakova, Z., Shubham, S., Havlinova, B., Baranova, P., Chen, S.J., Zou, X., Giangrande, P., Barinka, C. (2020) Structural basis of prostate-specific membrane antigen recognition by the A9g RNA aptamer. Nucleic Acids Res.

DOI: [10.1093/nar/gkaa494](https://doi.org/10.1093/nar/gkaa494)



GGGACCGAAAAAGACCUGACUUCUAUACUAAGUCUACGUUCCC
(((.(.....(((.....)))...)))

1.14 Beetroot aptamer

1.14.1 8eyu_B

Structure of Beetroot dimer bound to DFAME

Release date: 2023-05-31

Method: x-ray diffraction

Resolution: 1.95 Å

Chain length: 49

Extracted length: 49

Total clashes: 5

Clashes per residue: 0.102

Clashscore: 3.240

Description: RNA (49-MER)

Organism: synthetic construct

Passalacqua, L.F.M., Starich, M.R., Link, K.A., Wu, J., Knutson, J.R., Tjandra, N., Jaffrey, S.R., Ferre-D'Amare, A.R. (2023) Co-crystal structures of the fluorogenic aptamer Beetroot show that close homology may not predict similar RNA architecture. Nat Commun.

DOI: [10.1038/s41467-023-38683-3](https://doi.org/10.1038/s41467-023-38683-3)



GCGCCGGUUAGGCAGAGGUGGGUGGUGGAGGAGUAUCUGUCCGGCGC
((((((.....(((((((.....(.....)))))))))

1.14.2 8f0n_B

Wobble Beetroot (A16U-U38G) dimer bound to DFHO

Release date: 2023-05-31

Method: x-ray diffraction

Resolution: 2.85 Å

Chain length: 49

Extracted length: 49

Total clashes: 26

Clashes per residue: 0.531

Clashscore: 10.100

Description: RNA (49-MER)

Organism: synthetic construct

Passalacqua, L.F.M., Starich, M.R., Link, K.A., Wu, J., Knutson, J.R., Tjandra, N., Jaffrey, S.R., Ferre-D'Amare, A.R. (2023) Co-crystal structures of the fluorogenic aptamer Beetroot show that close homology may not predict similar RNA architecture. Nat Commun.

DOI: [10.1038/s41467-023-38683-3](https://doi.org/10.1038/s41467-023-38683-3)



GCGCCGGUUAGGCAGUGGUGGGUGGUGGAGGAGUAGCUGUCCGGCGC
(((((((.....(((((((.....(.)))))))))

1.15 Malachite green aptamer

1.15.1 1flt_A

CRYSTAL STRUCTURE OF THE MALACHITE GREEN APTAMER COMPLEXED WITH TETRAMETHYL-ROSAMINE

Release date: 2000-09-04

Method: x-ray diffraction

Resolution: 2.80 Å

Chain length: 38

Extracted length: 38

Total clashes: 92

Clashes per residue: 2.421

Clashscore: 35.830

Description: MALACHITE GREEN APTAMER RNA

Organism: nan

Baugh, C., Grate, D., Wilson, C. (2000) 2.8 Å crystal structure of the malachite green aptamer. J.Mol.Biol.

DOI: [10.1006/jmbi.2000.3951](https://doi.org/10.1006/jmbi.2000.3951)



GGAUCCCGACUGGCGAGAGCCAGGUAACGAAUGGAUCC
(((((((((.....)))))).....))))))

1.16 11F7t aptamer

1.16.1 5voe_A

DesGla-XaS195A Bound to Aptamer 11F7t

Release date: 2018-06-20

Method: x-ray diffraction

Resolution: 2.00 Å

Chain length: 36

Extracted length: 36

Total clashes: 0

Clashes per residue: 0.000

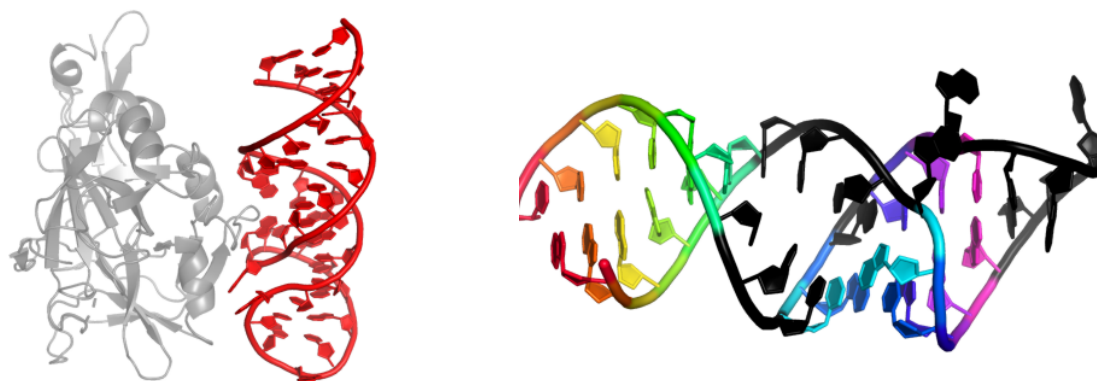
Clashscore: 12.260

Description: Aptamer 11F7t (36-MER)

Organism: synthetic construct

Gunaratne, R., Kumar, S., Frederiksen, J.W., Stayrook, S., Lohrmann, J.L., Perry, K., Bompiani, K.M., Chabata, C.V., Thalji, N.K., Ho, M.D., Arepally, G., Camire, R.M., Krishnaswamy, S., Sullenger, B.A. (2018) Combination of aptamer and drug for reversible anticoagulation in cardiopulmonary bypass. Nat. Biotechnol.

DOI: [10.1038/nbt.4153](https://doi.org/10.1038/nbt.4153)



GAGAGCCCCAGCGAGAUAAUACUUGGCCCCGCUCUU
(((((((.....((((((.....)))))).....))))))

1.17 K1 aptamer

1.17.1 6sy4_C

TetR in complex with the TetR-binding RNA-aptamer K1

Release date: 2020-02-05

Method: x-ray diffraction

Resolution: 2.69 Å

Chain length: 43

Extracted length: 38

Total clashes: 4

Clashes per residue: 0.093

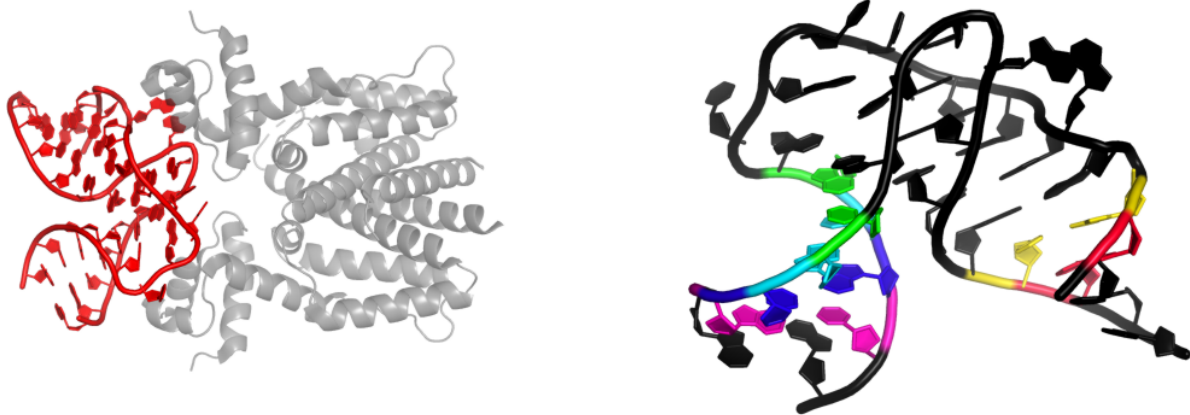
Clashscore: 3.720

Description: TetR-binding aptamer K1 (43-MER)

Organism: *Escherichia coli*

Grau, F.C., Jaeger, J., Groher, F., Suess, B., Muller, Y.A. (2020) The complex formed between a synthetic RNA aptamer and the transcription repressor TetR is a structural and functional twin of the operator DNA-TetR regulator complex. *Nucleic Acids Res.*

DOI: [10.1093/nar/gkaa083](https://doi.org/10.1093/nar/gkaa083)



GGCCGGAGAAUGUUAUGGCGCGAAAGCGCAGAGAAAACCGGUC
.....((.....(((.....))).....)).....

1.18 Tetracycline aptamer

1.18.1 3egz_B

Crystal structure of an in vitro evolved tetracycline aptamer and artificial riboswitch

Release date: 2008-10-28

Method: x-ray diffraction

Resolution: 2.20 Å

Chain length: 65

Extracted length: 65

Total clashes: 136

Clashes per residue: 2.092

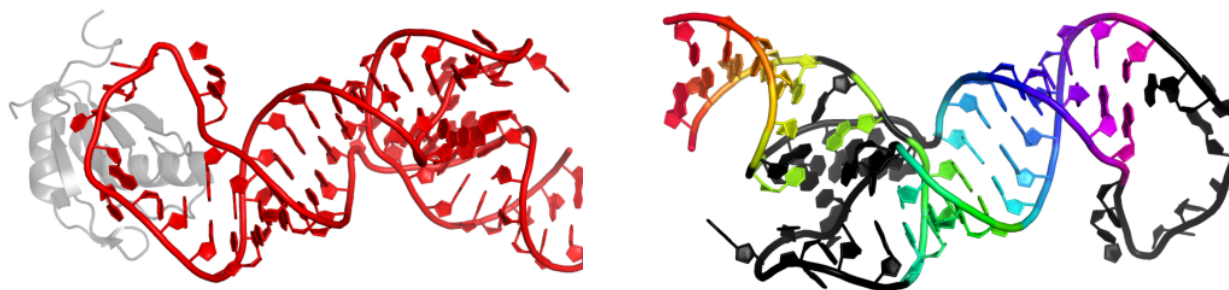
Clashscore: 24.650

Description: Tetracycline aptamer and artificial riboswitch

Organism: nan

Xiao, H., Edwards, T.E., Ferre-D'Amare, A.R. (2008) Structural basis for specific, high-affinity tetracycline binding by an in vitro evolved aptamer and artificial riboswitch. Chem.Biol.

DOI: [10.1016/j.chembiol.2008.09.004](https://doi.org/10.1016/j.chembiol.2008.09.004)



GAGGGAGAGGUGAAGAAUACGACCACCUAGGUACCAUUGCACUCCGGUACCUGAAAACAUACCCUC
((((((.....))))))((((((.....)))))).....)))))

2 CRISPR guides

2.1 Cas9 guide

2.1.1 7el1_B

Structure of a protein from bacteria

Release date: 2021-07-28

Method: x-ray diffraction

Resolution: 2.22 Å

Chain length: 73

Extracted length: 53

Total clashes: 9

Clashes per residue: 0.123

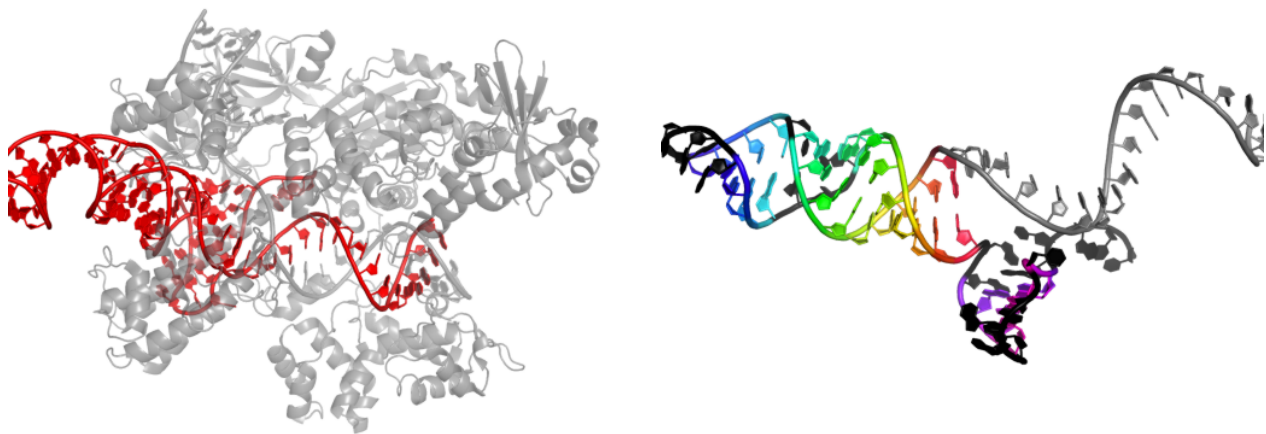
Clashscore: 6.160

Description: RNA (73-MER)

Organism: *Staphylococcus aureus*

Liu, H., Zhu, Y., Lu, Z., Huang, Z. (2021) Structural basis of *Staphylococcus aureus* Cas9 inhibition by AcrIIA14. *Nucleic Acids Res.*

DOI: [10.1093/nar/gkab487](https://doi.org/10.1093/nar/gkab487)



GGAAAUUAGGUGCGCUUGGCGUUUUAGUACUCUGGAAACAGAAUCUACUAAAACAAGGCAAAAUGCCGUGUUU
.....((((((.....))).....))).....(((.....))).....

2.1.2 6wbr_B

Crystal structure of AceCas9 bound with guide RNA and DNA with 5'-NNNCC-3' PAM

Release date: 2020-11-18

Method: x-ray diffraction

Resolution: 2.91 Å

Chain length: 94

Extracted length: 74

Total clashes: 73

Clashes per residue: 0.777

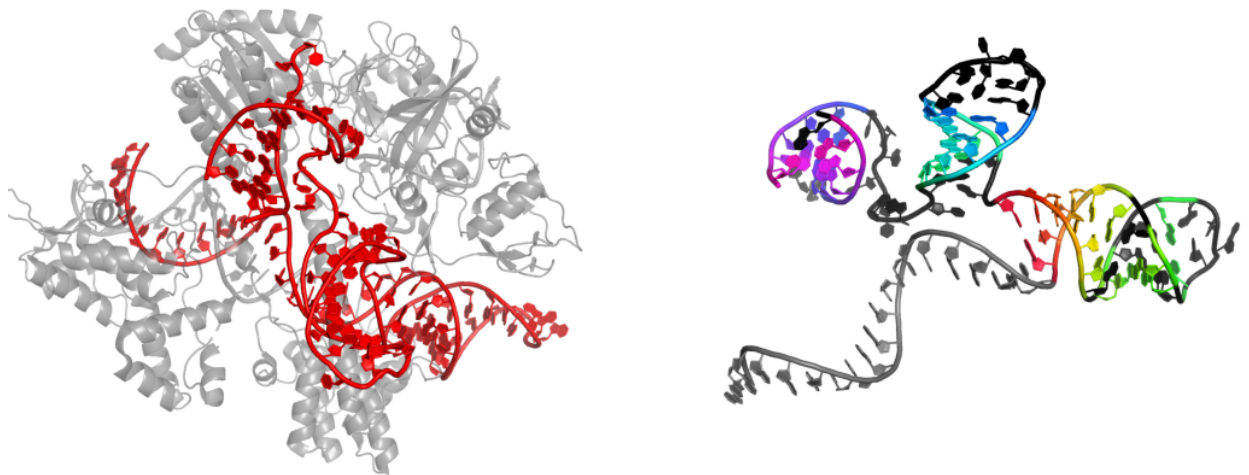
Clashscore: 11.650

Description: RNA (94-MER)

Organism: *Acidothermus cellulolyticus* 11B

Das, A., Hand, T.H., Smith, C.L., Wickline, E., Zawrotny, M., Li, H. (2020) The molecular basis for recognition of 5'-NNNCC-3' PAM and its methylation state by *Acidothermus cellulolyticus* Cas9. *Nat Commun.*

DOI: [10.1038/s41467-020-20204-1](https://doi.org/10.1038/s41467-020-20204-1)



GGAUGGCAAGAUCUGGUAUGCUGGGGAGCCUGAAAAGGCUACCUAGCAAGACCCCUUCGUGGGGUCGCAUUCUUCACCCCCAGCAGGGGGUUC
.....(((((.(.(.)))))..(((.....))).....((((.....))))..

2.1.3 8umf_B

Structure of PsCas9 in complex with gRNA and DNA in product state

Release date: 2024-10-02

Method: electron microscopy

Resolution: 2.90 Å

Chain length: 131

Extracted length: 101

Total clashes: 50

Clashes per residue: 0.382

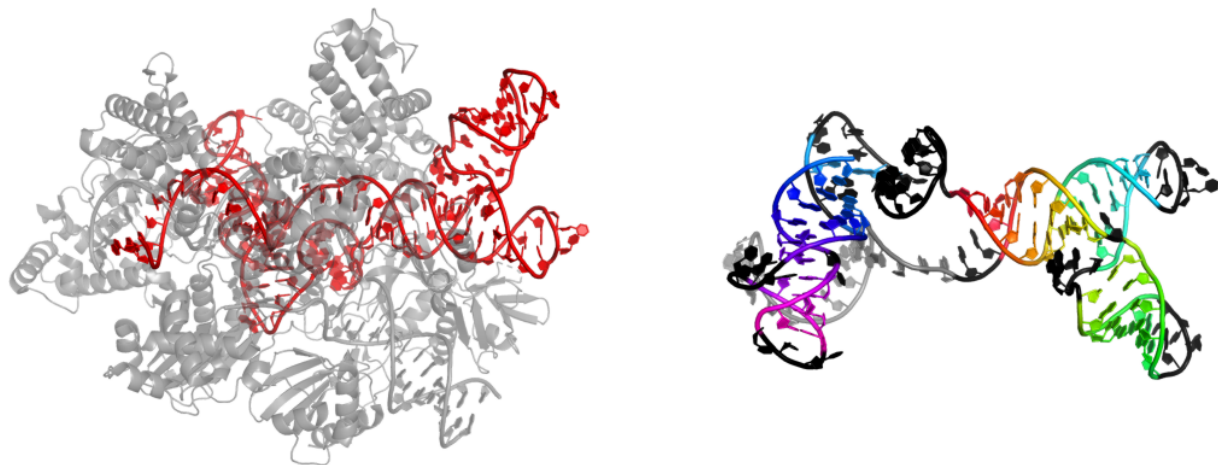
Clashscore: 4.930

Description: RNA (121-MER)

Organism: synthetic construct

Bravo, J.P.K., Taylor, D.W. (N/A) Structure-guided engineering of PsCas9 yields a high fidelity and activity enzyme for in vivo gene editing. To Be Published.

DOI: [nan](#)



AUGUCACCUCCAAUGACUAGGGGUUUCAGUUAUUCGUGAAAACGAAUGAAGUCACUCUAAAAGUGAGCUGAAAUCACUAAAAUUAAAGAUUGAACCCGGCUACUGACUCUGUCAUCCGGGUUUACUUAUUU
.....(((((((.....)))))).....((((.....)))))).....((((.....)))))).....((((.....)))))).....((((.....)))))).....((((.....)))))).....

2.1.4 8hud_B

Cryo-EM structure of the EvCas9-sgRNA-target DNA ternary complex

Release date: 2023-12-27

Method: electron microscopy

Resolution: 3.43 Å

Chain length: 75

Extracted length: 52

Total clashes: 19

Clashes per residue: 0.253

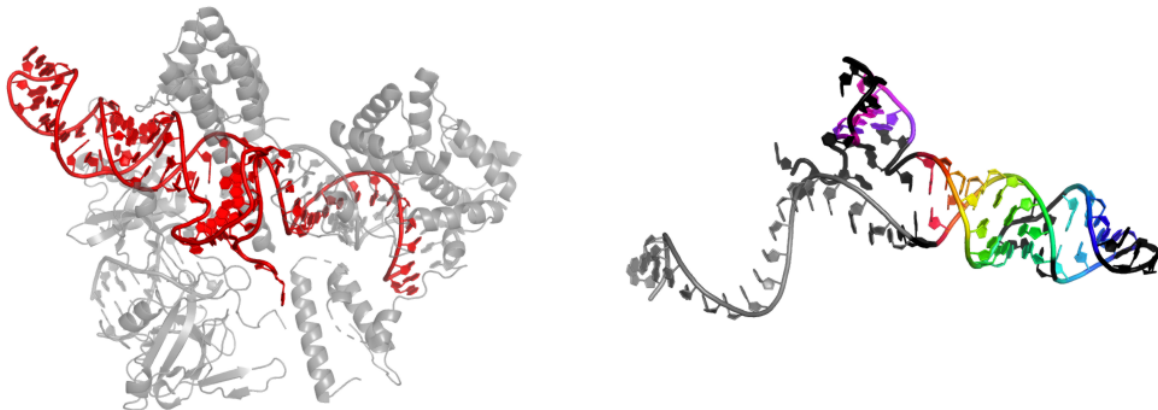
Clashscore: 10.270

Description: sgRNA

Organism: synthetic construct

Tang, N., Wu, Z., Gao, Y., Chen, W., Wang, Z., Su, M., Ji, W., Ji, Q. (2024) Molecular Basis and Genome Editing Applications of a Compact *Eubacterium ventriosum* CRISPR-Cas9 System. *Acs Synth Biol.*

DOI: [10.1021/acssynbio.3c00501](https://doi.org/10.1021/acssynbio.3c00501)



GGUAAUCGCUCUCCUCCGGCGAUUUUAGUACCUGAGAAAUCAGAUCUACUAAAACAAGGCUUUAUGCCGAAAUCA
.....((((((.((((.....))).....)))))).....(((.....))).....

2.2 sgRNA guide

2.2.1 8rdu_1

Conformational Landscape of the Type V-K CRISPR-associated Transposon Integration Assembly CAST
V-K composite map

Release date: 2024-06-19

Method: electron microscopy

Resolution: 2.30 Å

Chain length: 261

Extracted length: 227

Total clashes: 16

Clashes per residue: 0.061

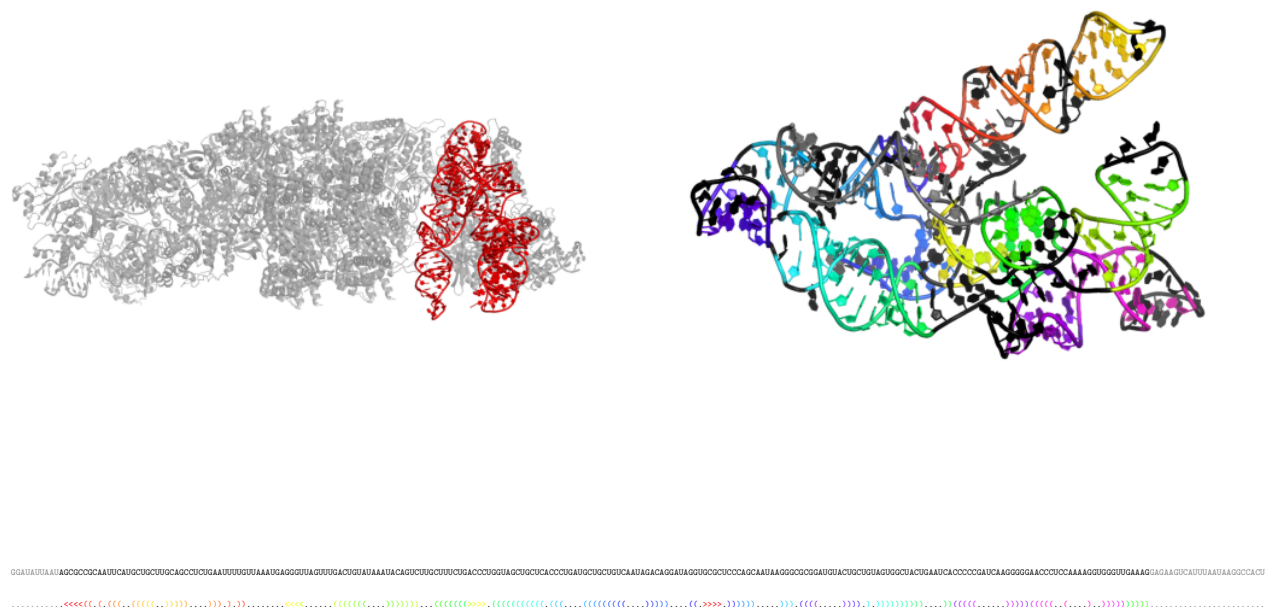
Clashscore: 3.440

Description: sgRNA

Organism: *Scytonema hofmannii*

Tenjo-Castano, F., Sofos, N., Stutzke, L.S., Temperini, P., Fuglsang, A., Pape, T., Mesa, P., Montoya, G. (2024) Conformational landscape of the type V-K CRISPR-associated transposon integration assembly. *Mol.Cell.*

DOI: 10.1016/j.molcel.2024.05.005



2.2.2 8x5v_B

BlCas9-sgRNA-target DNA complex

Release date: 2024-07-10

Method: x-ray diffraction

Resolution: 2.00 Å

Chain length: 110

Extracted length: 91

Total clashes: 2

Clashes per residue: 0.018

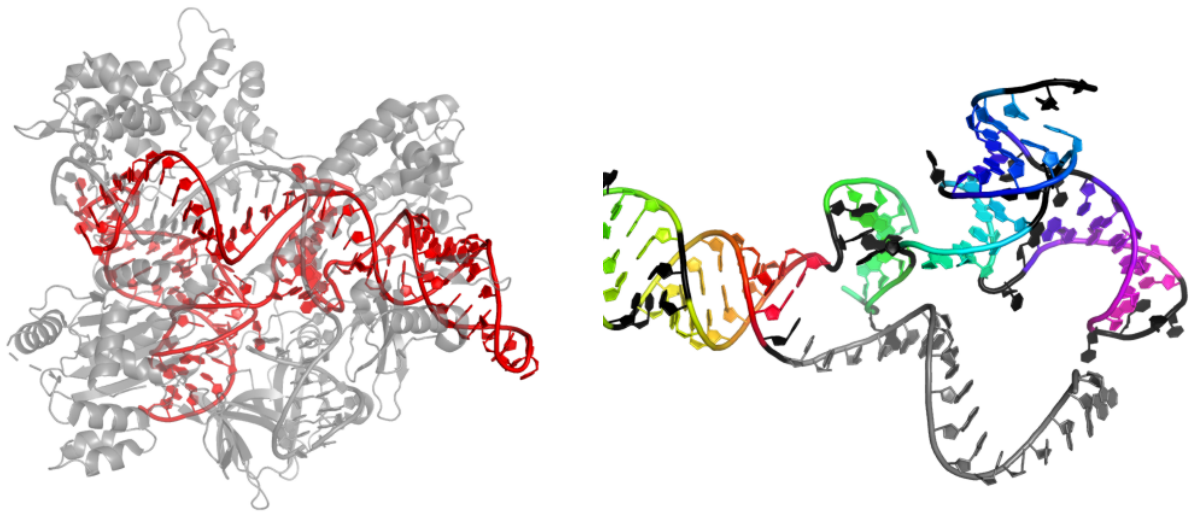
Clashscore: 0.940

Description: RNA (110-mer)

Organism: *Brevibacillus laterosporus*

Nakane, T., Nakagawa, R., Ishiguro, S., Okazaki, S., Mori, H., Shuto, Y., Yamashita, K., Yachie, N., Nishimasu, H., Nureki, O. (2024) Structure and engineering of *Brevibacillus laterosporus* Cas9. *Commun Biol.*

DOI: [10.1038/s42003-024-06422-z](https://doi.org/10.1038/s42003-024-06422-z)



GGAAAUAGGUGCGCUUGCGCUAUAGUCCUUGAAAAAGUUGCUAUAGUAAGGGCAACAGACCCGAGGCGUUGGGGAUCGCCUAGCCCGUUUUUACGGGCUCUCCCCAU
.....(((((((.....))).....))).....((((.....))).....<<<.....(((.....))).....((((.....))).....

2.2.3 7c7l_C

Cryo-EM structure of the Cas12f1-sgRNA-target DNA complex

Release date: 2020-12-23

Method: electron microscopy

Resolution: 3.30 Å

Chain length: 180

Extracted length: 110

Total clashes: 29

Clashes per residue: 0.161

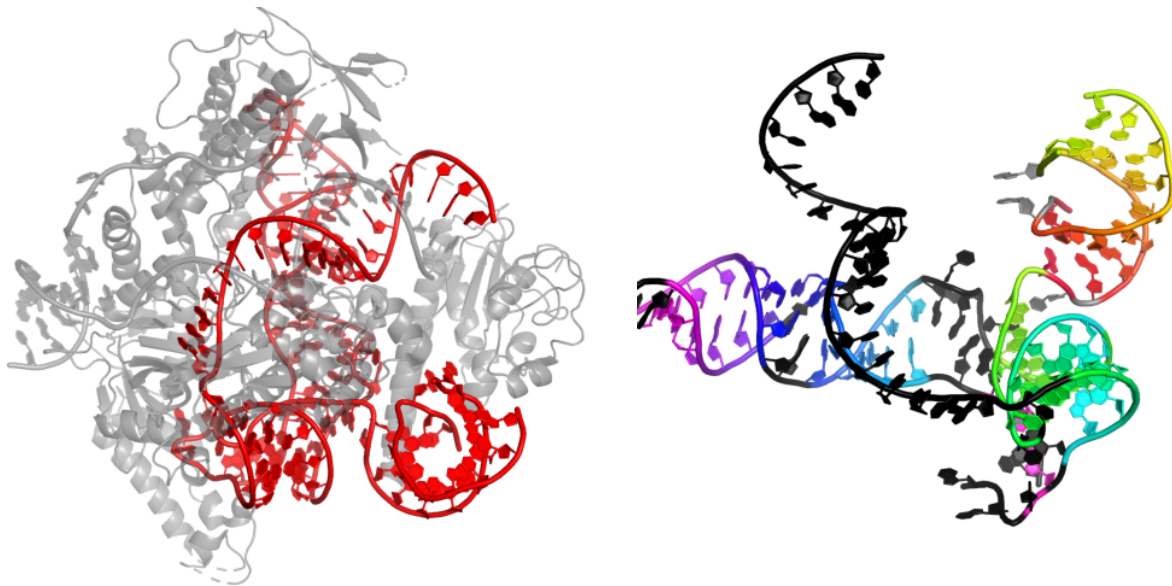
Clashscore: 4.790

Description: sgRNA

Organism: uncultured archaeon

Takeda, S.N., Nakagawa, R., Okazaki, S., Hirano, H., Kobayashi, K., Kusakizako, T., Nishizawa, T., Yamashita, K., Nishimasu, H., Nureki, O. (2021) Structure of the miniature type V-F CRISPR-Cas effector enzyme. *Mol.Cell.*

DOI: [10.1016/j.molcel.2020.11.035](https://doi.org/10.1016/j.molcel.2020.11.035)



UUCACUGAUAAAGUGGAGAACOGCUUACAACAAAGCUGUCCCUUAGGGGAUUGAGAACUUGAGUGAAGGUGGGCUGCUUGCAUCAGCCUAAUGUCGAGAAAGUGCUUUCUUCGGAAGUAAACCCUCGAAACAAAUUCAUUUGAAAGAAUGAAGGAATUGCAACGGAAAUUAGGUGGCUUGGC
.....((((((((.....))))))>><<<((((>>>.....(((((((.....))))))>>..((.....))>>>.....

2.2.4 5wti_B

Crystal structure of the CRISPR-associated protein in complex with crRNA and DNA

Release date: 2017-11-01

Method: x-ray diffraction

Resolution: 2.68 Å

Chain length: 123

Extracted length: 104

Total clashes: 0

Clashes per residue: 0.000

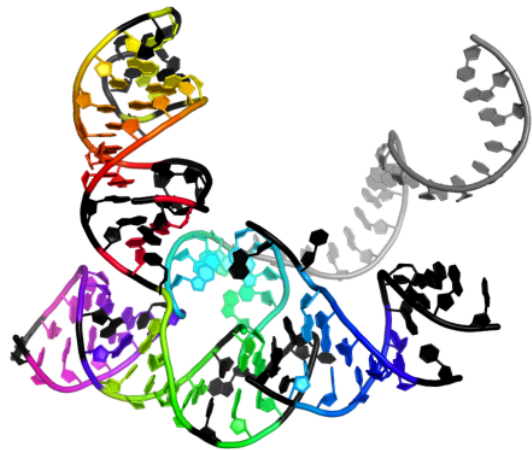
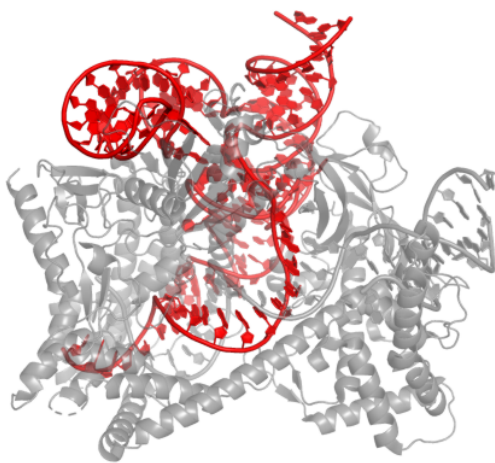
Clashscore: 7.540

Description: RNA (123-MER)

Organism: RNA transcription vector pBRDI1

Wu, D., Guan, X., Zhu, Y., Ren, K., Huang, Z. (2017) Structural basis of stringent PAM recognition by CRISPR-C2c1 in complex with sgRNA. Cell Res.

DOI: [10.1038/cr.2017.46](https://doi.org/10.1038/cr.2017.46)



GGCGAGGUUCUGUCUUUUGGUCAGGACAACCGUCUAGCUAUAAGUGCUGCAGGGGUGUGAGAAACUCCUAUUGCUGGACGAUGUCUCUUUCGAGGCAUAGCACCGGGGAGAAGUCAUUUAAU
.(.....(((((((.....)))))).....)(((((.....<<<<.....((((.....)))).....))))(((((.....)))).....>>>>.....

2.3 Cas12 guide

2.3.1 8bf8_B

ISDra2 TnpB in complex with reRNA

Release date: 2023-04-12

Method: electron microscopy

Resolution: 2.80 Å

Chain length: 150

Extracted length: 123

Total clashes: 49

Clashes per residue: 0.327

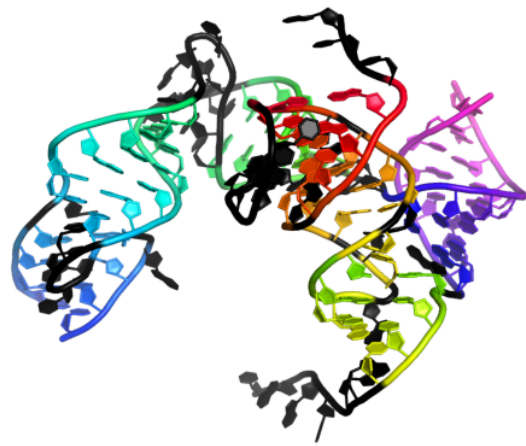
Clashscore: 8.730

Description: Deinococcus radiodurans R1 chromosome 1

Organism: Deinococcus radiodurans R1 = ATCC 13939 = DSM 20539

Sasnauskas, G., Tamulaitiene, G., Druteika, G., Carabias, A., Silanskas, A., Kazlauskas, D., Venclovas, C., Montoya, G., Karvelis, T., Siksnys, V. (2023) TnpB structure reveals minimal functional core of Cas12 nuclease family. *Nature*.

DOI: [10.1038/s41586-023-05826-x](https://doi.org/10.1038/s41586-023-05826-x)



CAUUCGGCGUGAAGCGUUGUGGGUCUGCGGAAUCUCAGACACCUUAAACGCUCAUGGAGGCUAUGUCAGACCUUCUUCGGCGGGCAUUGGUCUGCGAAGUGAGAAUACACGCGACUUUAGUCGUGUGAGGUUCAAGAGUCCCUUGGGGCCC
.....(((((((.<<<<)).))).....(((((((.....(((.....)))).....)))).....(((((((.....)))).....)))).....>>>>.....

2.3.2 8j3r_C

Cryo-EM structure of the AsCas12f-HKRA-sgRNA3-5v7-target DNA

Release date: 2023-09-27

Method: electron microscopy

Resolution: 2.95 Å

Chain length: 118

Extracted length: 109

Total clashes: 18

Clashes per residue: 0.153

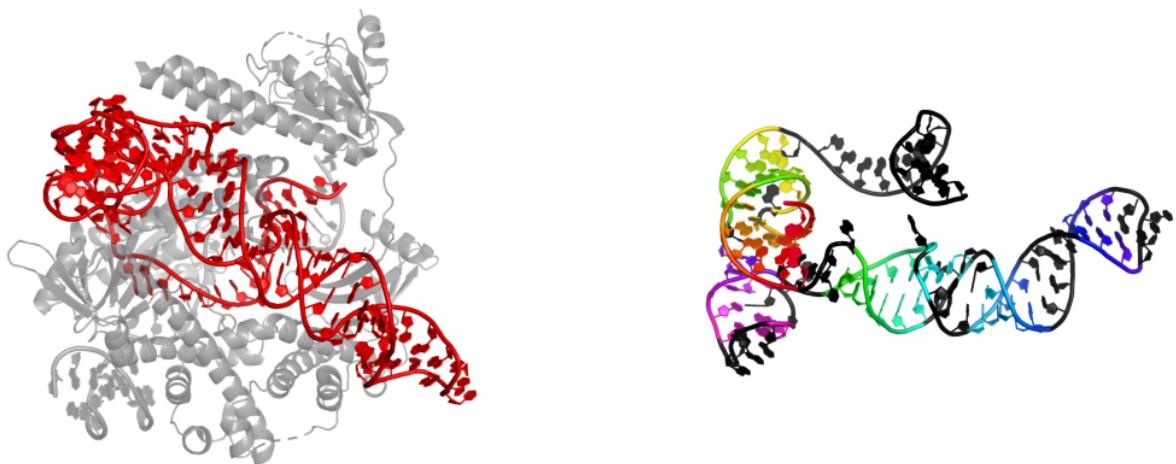
Clashscore: 5.620

Description: RNA (118-MER)

Organism: *Sulfoacidibacillus thermotolerans*

Hino, T., Omura, S.N., Nakagawa, R., Togashi, T., Takeda, S.N., Hiramoto, T., Tasaka, S., Hirano, H., Tokuyama, T., Uosaki, H., Ishiguro, S., Kagieva, M., Yamano, H., Ozaki, Y., Motooka, D., Mori, H., Kirita, Y., Kise, Y., Itoh, Y., Matoba, S., Aburatani, H., Yachie, N., Karvelis, T., Siksnys, V., Ohmori, T., Hoshino, A., Nureki, O. (2023) An AsCas12f-based compact genome-editing tool derived by deep mutational scanning and structural analysis. *Cell*.

DOI: [10.1016/j.cell.2023.08.031](https://doi.org/10.1016/j.cell.2023.08.031)



GGAUUCGUCGGUUCAGCGACGAUAAGCCGAGAAGUGCCAAUAAAACUGUUAAGUGGUUUGGUAAACGCUCGGUAAAGGUCCGAAAGGAGAACACUGAACGGAAAAUAGGCGCGCUUGGC
.....(((((((.<=<=<=<=<))))))....(((((((.....((((.....))))))....))))))....((((.....))))>>>>>>.....

2.3.3 6xmf_C

Cryo-EM structure of Cas12g binary complex

Release date: 2021-01-13

Method: electron microscopy

Resolution: 3.10 Å

Chain length: 122

Extracted length: 119

Total clashes: 0

Clashes per residue: 0.000

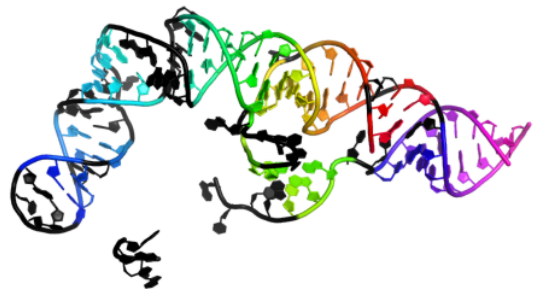
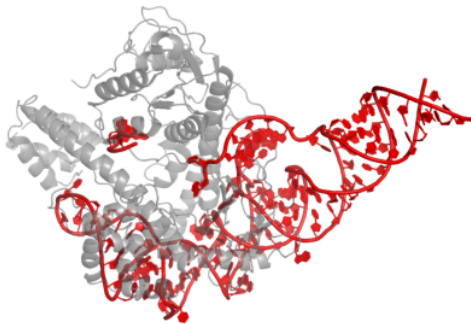
Clashscore: 8.600

Description: RNA (116-MER)

Organism: metagenome

Li, Z., Zhang, H., Xiao, R., Han, R., Chang, L. (2021) Cryo-EM structure of the RNA-guided ribonuclease Cas12g. *Nat.Chem.Biol.*

DOI: [10.1038/s41589-020-00721-2](https://doi.org/10.1038/s41589-020-00721-2)



GGGAUGCUUACUUAGUCAUCUGGUUGGCAAACCUCGCGGACCUUCGGGACCA AUGGAGAGGAACCCAGCCGAGAAGCAUCGAGCCGGUAAAUGUUUACCGGCUCUGACACCAACUGGUGAA
..((.(((.(.(<<.....((((.....(((.....((.....)).....)).....)).....)).....)).....)).....)).....)).....)).....>>.....

2.4 Cas13 guide

2.4.1 6dtd_C

High-resolution crystal structure of Cas13b from *Prevotella buccae*

Release date: 2019-02-20

Method: x-ray diffraction

Resolution: 1.65 Å

Chain length: 37

Extracted length: 37

Total clashes: 0

Clashes per residue: 0.000

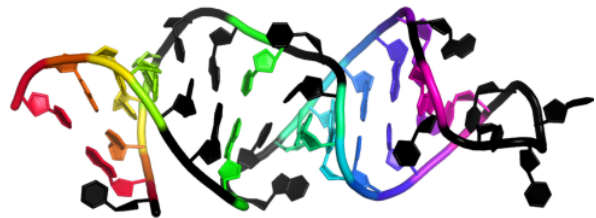
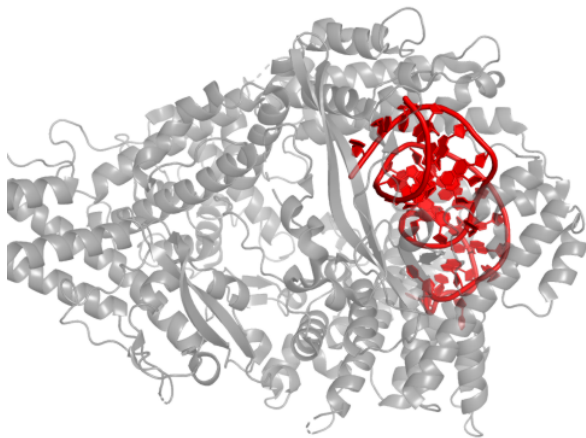
Clashscore: 4.840

Description: RNA (37-MER)

Organism: *Segatella buccae*

Slaymaker, I.M., Mesa, P., Kellner, M.J., Kannan, S., Brignole, E., Koob, J., Feliciano, P.R., Stella, S., Abudayyeh, O.O., Gootenberg, J.S., Strecker, J., Montoya, G., Zhang, F. (2019) High-Resolution Structure of Cas13b and Biochemical Characterization of RNA Targeting and Cleavage. *Cell Rep.*

DOI: [10.1016/j.celrep.2019.02.094](https://doi.org/10.1016/j.celrep.2019.02.094)



UGUUGCAUCUGCCUUCUUUUUGAAAGGUAAAAACAAC
.(.(((.(((((.)))..)))..)))..))

2.4.2 8wcs_G

Cryo-EM structure of Cas13h1-crRNA binary complex

Release date: 2024-05-22

Method: electron microscopy

Resolution: 3.10 Å

Chain length: 66

Extracted length: 66

Total clashes: 0

Clashes per residue: 0.000

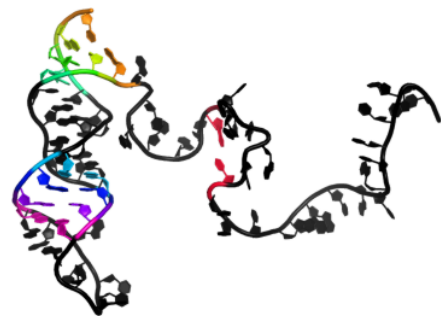
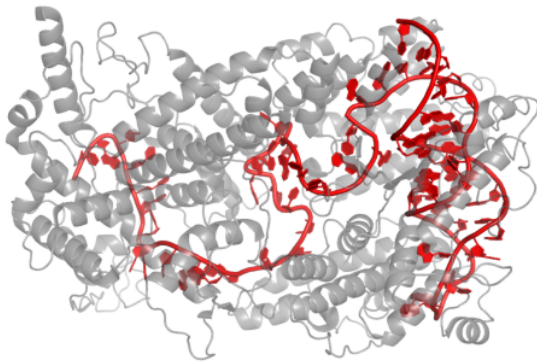
Clashscore: 4.750

Description: 66-nt crRNA

Organism: synthetic construct

Chen, F., Zhang, C., Xue, J., Wang, F., Li, Z. (2024) Molecular mechanism for target RNA recognition and cleavage of Cas13h. *Nucleic Acids Res.*

DOI: [10.1093/nar/gkae324](https://doi.org/10.1093/nar/gkae324)



UGC UUCACGUAGGCCUUGGAGCCGUACAUGGUUGUAACAAGCCUAAGUUUGAAAGGUAAAAACAAC
..... (.....) (((..... (((..... (((.....))))))

2.4.3 6aay_B

the Cas13b binary complex

Release date: 2019-03-13

Method: x-ray diffraction

Resolution: 2.79 Å

Chain length: 59

Extracted length: 59

Total clashes: 49

Clashes per residue: 0.831

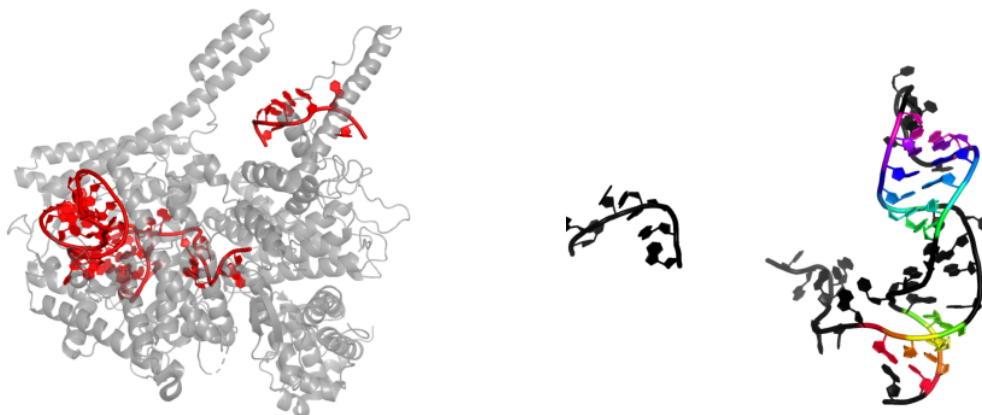
Clashscore: 26.170

Description: RNA (52-MER)

Organism: *Bergeyella zoohelcum*

Zhang, B., Ye, W.W., Ye, Y.M., Zhou, H., Saeed, A.F.U.H., Chen, J., Lin, J.Y., Perculija, V., Chen, Q., Chen, C.J., Chang, M.X., Choudhary, M.I., Ouyang, S.Y. (2018) Structural insights into Cas13b-guided CRISPR RNA maturation and recognition. *Cell Res.*

DOI: [10.1038/s41422-018-0109-4](https://doi.org/10.1038/s41422-018-0109-4)



AAAAAGGGUUUAAAAAUGAAAGUUGGAACUGCUCUCAUUUUGGAGGGUAAUCACAACA
.....(((.....((((.....)))).....)))..

2.4.4 8ewg_B

Cryo-EM structure of a ribonuclease

Release date: 2023-08-30

Method: electron microscopy

Resolution: 2.90 Å

Chain length: 60

Extracted length: 57

Total clashes: 27

Clashes per residue: 0.450

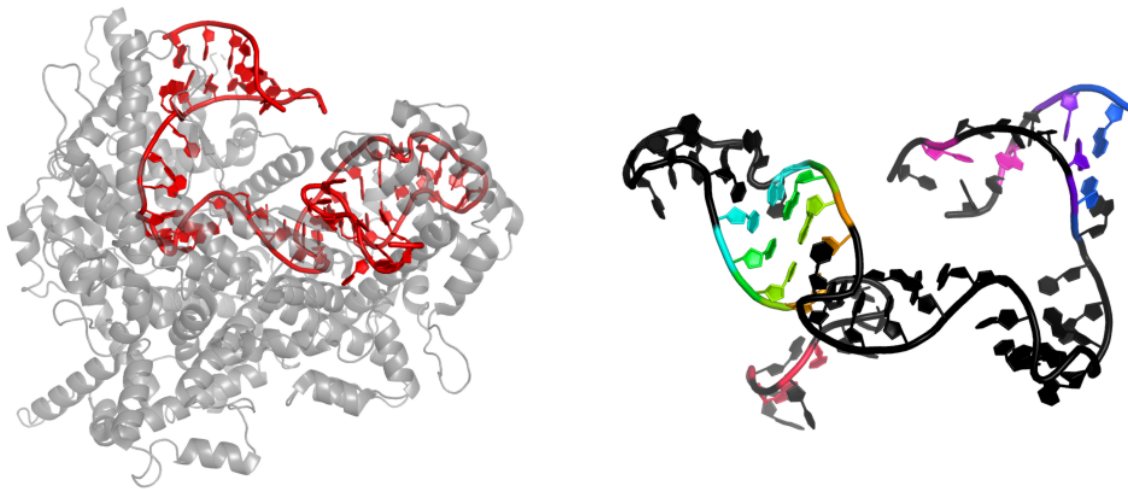
Clashscore: 5.360

Description: RNA (56-MER)

Organism: *Thermoclostridium caenicola*

Wang, F., Zhang, C., Xu, H., Zeng, W., Ma, L., Li, Z. (2023) Structural Basis for the Ribonuclease Activity of a Thermostable CRISPR-Cas13a from *Thermoclostridium caenicola*. *J.Mol.Biol.*

DOI: [10.1016/j.jmb.2023.168197](https://doi.org/10.1016/j.jmb.2023.168197)



UAGGGUCACAACUCCCAUGUAGGCGGAGACUGCAACCCGAAGGUGUGACUCCAUGCCAA
.....(.).....(((.....))).....((.....))..

2.5.1 8gkh_W

Release date: 2023-07-05

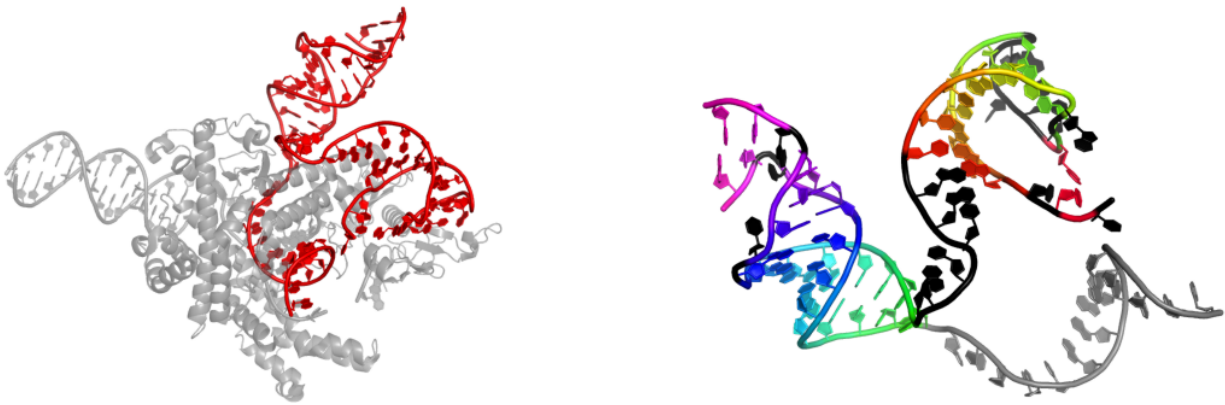
Resolution: 2.70 Å

Extracted length: 63

Clashscore: 5.490

Organism: *Spizellomyces punctatus*

DOI: [10.1038/s41586-023-06356-2](https://doi.org/10.1038/s41586-023-06356-2)



UCCGAGCCGGUAGUCGCGGGUUAUCCUUGGUGCGGGUGCUAGUGCACCGGCUCCGCACUAUCUAUAGGUUAUGAA
 .<(((((((.....>).))))).....(((((((.(.((.(.)))))())))).....

2.6 Fanzor guide

2.6.1 9cf2_W

Parasitella parasitica Fanzor (PpFz) State 3

Release date: 2024-09-11

Method: electron microscopy

Resolution: 3.15 Å

Chain length: 61

Extracted length: 42

Total clashes: 0

Clashes per residue: 0.000

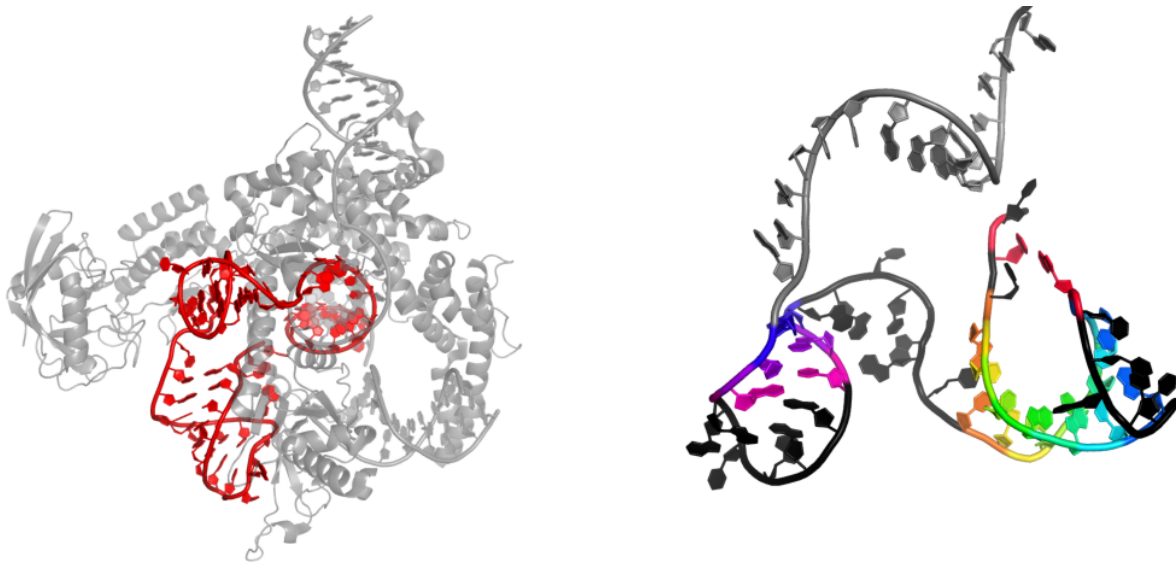
Clashscore: 3.490

Description: *Parasitella parasitica* Fanzor 1 omegaRNA

Organism: *Parasitella parasitica*

Xu, P., Saito, M., Faure, G., Maguire, S., Chau-Duy-Tam Vo, S., Wilkinson, M.E., Kuang, H., Wang, B., Rice, W.J., Macrae, R.K., Zhang, F. (2024) Structural insights into the diversity and DNA cleavage mechanism of Fanzor. *Cell*.

DOI: [10.1016/j.cell.2024.07.050](https://doi.org/10.1016/j.cell.2024.07.050)



UUAUCCACCAAAGUUAUCGCUUUGGUCAAUUAUAGCAGGUAAAGCAACAUCAGCAAAACAGA
.....<((((((.....>)))))).....(((.....))).....

3.1.2 6p5n_1

Structure of a mammalian 80S ribosome in complex with a single translocated Israeli Acute Paralysis Virus IRES and eRF1

Release date: 2019-09-25

Method: electron microscopy

Resolution: 3.20 Å

Chain length: 251

Extracted length: 207

Total clashes: 0

Clashes per residue: 0.000

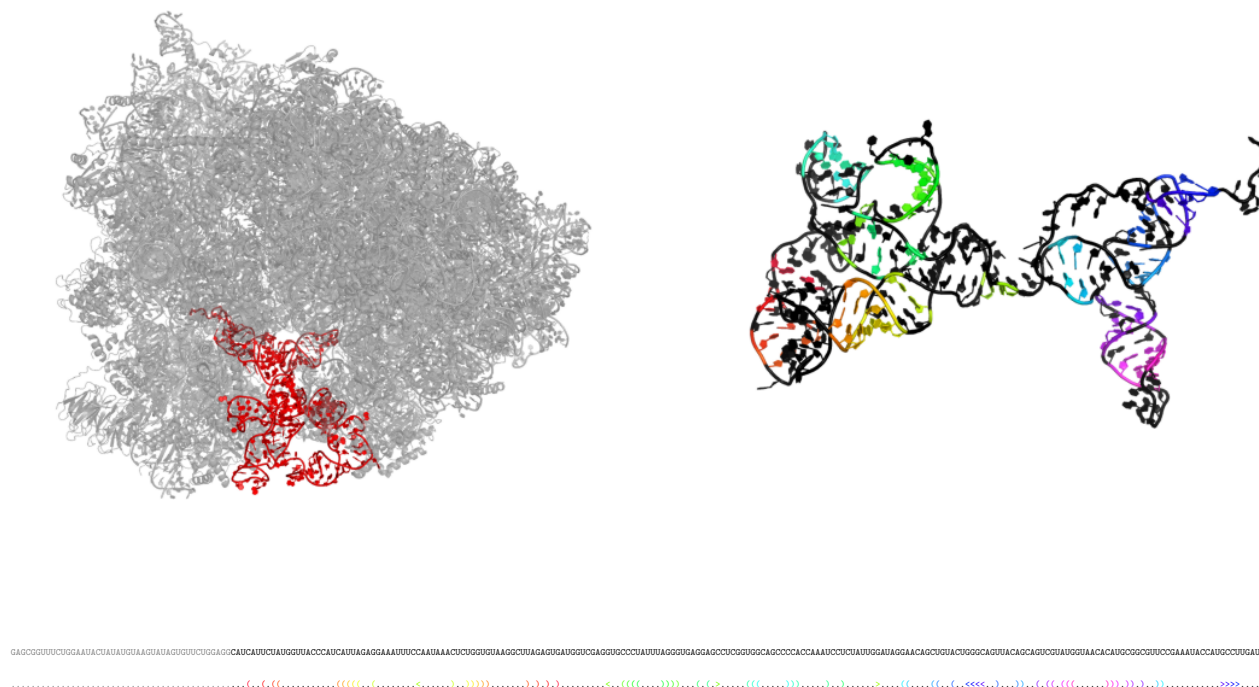
Clashscore: 2.150

Description: IAPV-IRES

Organism: Israeli acute paralysis virus

Acosta-Reyes, F., Neupane, R., Frank, J., Fernandez, I.S. (2019) The Israeli acute paralysis virus IRES captures host ribosomes by mimicking a ribosomal state with hybrid tRNAs. *Embo J.*

DOI: [10.15252/emboj.2019102226](https://doi.org/10.15252/emboj.2019102226)



3.3 TSV IRES

3.3.1 8evp_EC

Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), Structure I

Release date: 2023-09-06

Method: electron microscopy

Resolution: 2.38 Å

Chain length: 202

Extracted length: 196

Total clashes: 0

Clashes per residue: 0.000

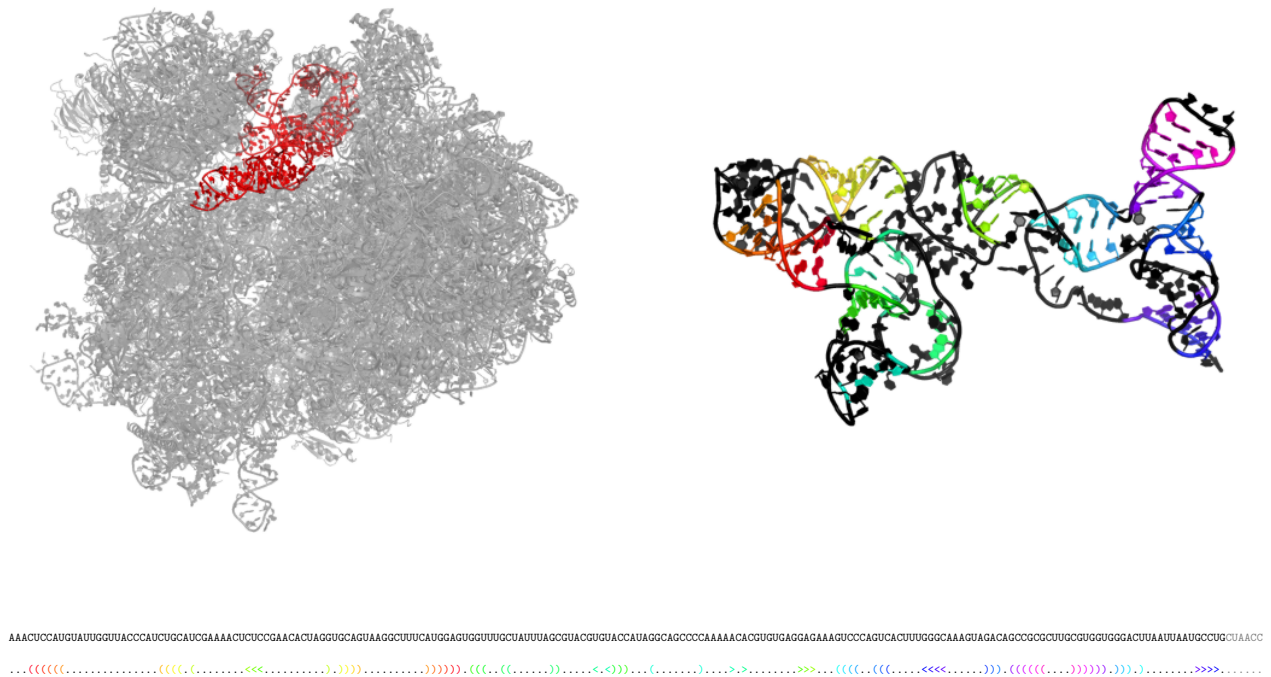
Clashscore: 5.910

Description: Internal ribosome entry site

Organism: Taura syndrome virus

Zhao, Y., Rai, J., Li, H. (2023) Regulation of translation by ribosomal RNA pseudouridylation.
Sci Adv.

DOI: [10.1126/sciadv.adg8190](https://doi.org/10.1126/sciadv.adg8190)



3.4 PSIV IGR IRES

3.4.1 4v83_CV

Crystal structure of a complex containing domain 3 from the PSIV IGR IRES RNA bound to the 70S ribosome.

Release date: 2014-07-09

Method: x-ray diffraction

Resolution: 3.50 Å

Chain length: 35

Extracted length: 35

Total clashes: 0

Clashes per residue: 0.000

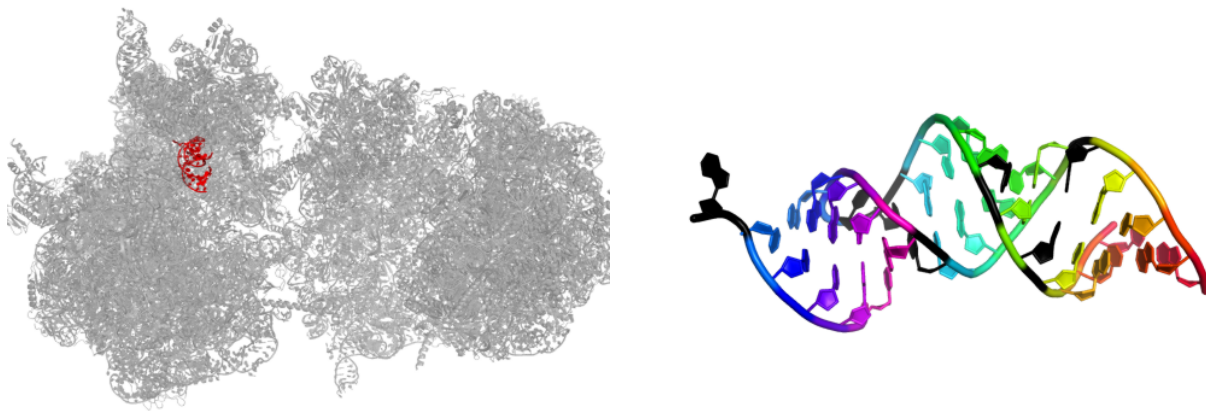
Clashscore: 20.140

Description: domain 3 of PSIC IGR IRES RNA

Organism: *Thermus thermophilus* HB27

Zhu, J., Korostelev, A., Costantino, D.A., Donohue, J.P., Noller, H.F., Kieft, J.S. (2011) Crystal structures of complexes containing domains from two viral internal ribosome entry site (IRES) RNAs bound to the 70S ribosome. *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.1018582108](https://doi.org/10.1073/pnas.1018582108)



UCGCUCAAACAUUAAGUGGUGUUGUGCGACACUUA
(((. (. ((((. <<<<(.))))(.))))>>>>.

4.1.2 3ivk_C

Crystal Structure of the Catalytic Core of an RNA Polymerase Ribozyme Complexed with an Antigen Binding Antibody Fragment

Release date: 2010-03-02

Method: x-ray diffraction

Resolution: 3.10 Å

Chain length: 128

Extracted length: 128

Total clashes: 0

Clashes per residue: 0.000

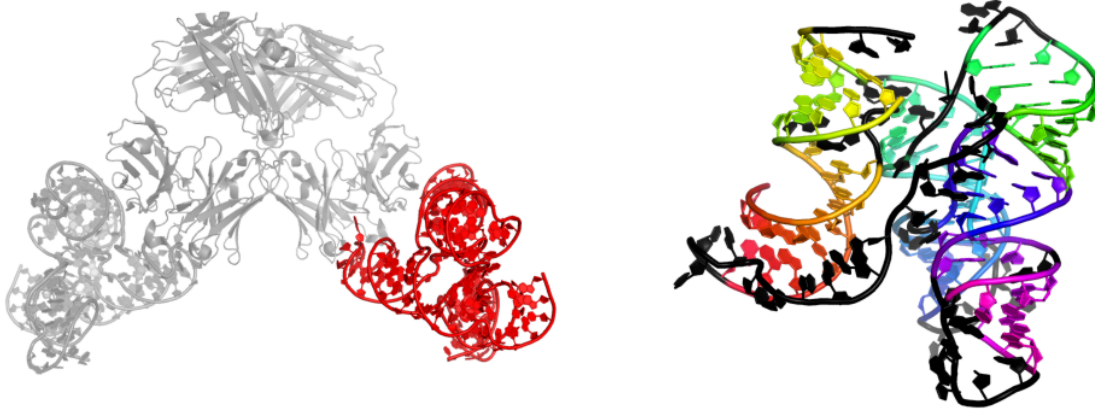
Clashscore: 31.380

Description: class I ligase product

Organism: nan

Shechner, D.M., Grant, R.A., Bagby, S.C., Koldobskaya, Y., Piccirilli, J.A., Bartel, D.P. (2009)
Crystal structure of the catalytic core of an RNA-polymerase ribozyme. *Science*.

DOI: [10.1126/science.1174676](https://doi.org/10.1126/science.1174676)



UCCAGUAGGAACACUAUACUACUGGAUAAUCAAAAGACAAAUUCGCCGAAGGGCUUGAGAACAUCGAAACACGAUGCAGAGGUGGCAGCCUCCGGUGGGUUAAAACCCCAACGUUCUCAAACAAUAGUGA
(((((((.....<<<<.>>>>)))))).....<<<<(..).....((((((((((((.....)))))).....((((>>>>))))((.((((.....))))..)))))).....>>>>..

4.1.3 8t2p_B

5TU-t1 - heterodimeric triplet polymerase ribozyme

Release date: 2024-01-24

Method: electron microscopy

Resolution: 5.00 Å

Chain length: 152

Extracted length: 152

Total clashes: 0

Clashes per residue: 0.000

Clashscore: 0.000

Description: RNA (152-MER)

Organism: synthetic construct

McRae, E.K.S., Wan, C.J.K., Kristoffersen, E.L., Hansen, K., Gianni, E., Gallego, I., Curran, J.F., Attwater, J., Holliger, P., Andersen, E.S. (2024) Cryo-EM structure and functional landscape of an RNA polymerase ribozyme. *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.2313332121](https://doi.org/10.1073/pnas.2313332121)



GGAUUCUUCGUAUCUAAACAAAAAGACAAUUGCCACAAAGCUUGAGAGCAUCUUCGGAUGCAGAGGCGGCAGCCUUCGGUGGCGCGAUAGCGCCAACGUUCUCAAACUAUGACACGCAAAACGCGUGCUCGUGAAUGGAGUUUAUCAUG
..(((.....))).....<<<<.....(((((.....))))).(((.....>>>>)))(((((.....))))).(((.....))).....(((.....))).....(((.....))).....(((.....))).....(((.....))).....

4.2.1 4r4v_A

Release date: 2015-09-30

Resolution: 3.07 Å

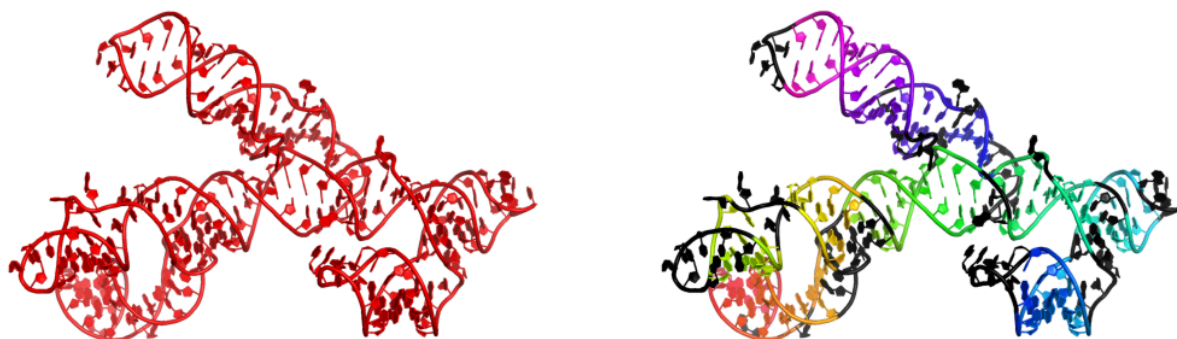
Extracted length: 186

Clashes per residue: 0.204

Clashscore: 3.260

Organism: Neurospora

DOI: 10.1038/nchembio.1929



.(((((((.....(((((.....))))))..)))....))))).(((((((.....(((((.....))))))..)))....))))).(((((((.....(((((.....))))))..)))....))))).

4.4 Diels-Alder ribozyme

4.4.1 1ykv_D

Crystal structure of the Diels-Alder ribozyme complexed with the product of the reaction between N-pentylmaleimide and covalently attached 9-hydroxymethylantracene

Release date: 2005-02-22

Method: x-ray diffraction

Resolution: 3.30 Å

Chain length: 38

Extracted length: 31

Total clashes: 26

Clashes per residue: 0.684

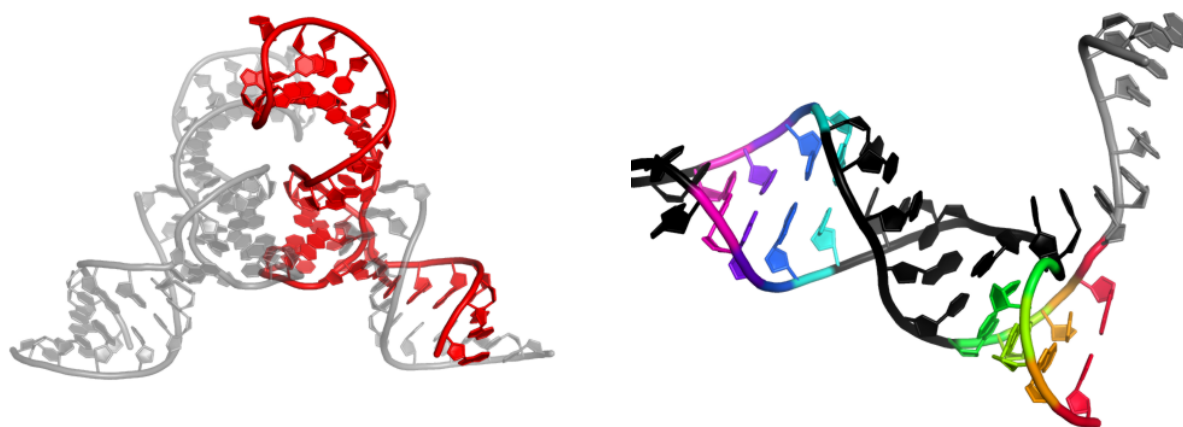
Clashscore: 12.520

Description: Diels-Alder ribozyme

Organism: nan

Serganov, A., Keiper, S., Malinina, L., Tereshko, V., Skripkin, E., Hobartner, C., Polonskaia, A., Phan, A.T., Wombacher, R., Micura, R., Dauter, Z., Jaschke, A., Patel, D.J. (2005) Structural basis for Diels-Alder ribozyme-catalyzed carbon-carbon bond formation. *Nat.Struct.Mol.Biol.*

DOI: [10.1038/nsm906](https://doi.org/10.1038/nsm906)



GGGCGAGGCCGUGCCAGCUCUUCGGAGCAAUACUCGGC
.....(((.....(((.....)))).....))

4.4.2 1yls_D

Crystal structure of selenium-modified Diels-Alder ribozyme complexed with the product of the reaction between N-pentylmaleimide and covalently attached 9-hydroxymethylantracene

Release date: 2005-02-22

Method: x-ray diffraction

Resolution: 3.00 Å

Chain length: 38

Extracted length: 31

Total clashes: 43

Clashes per residue: 1.132

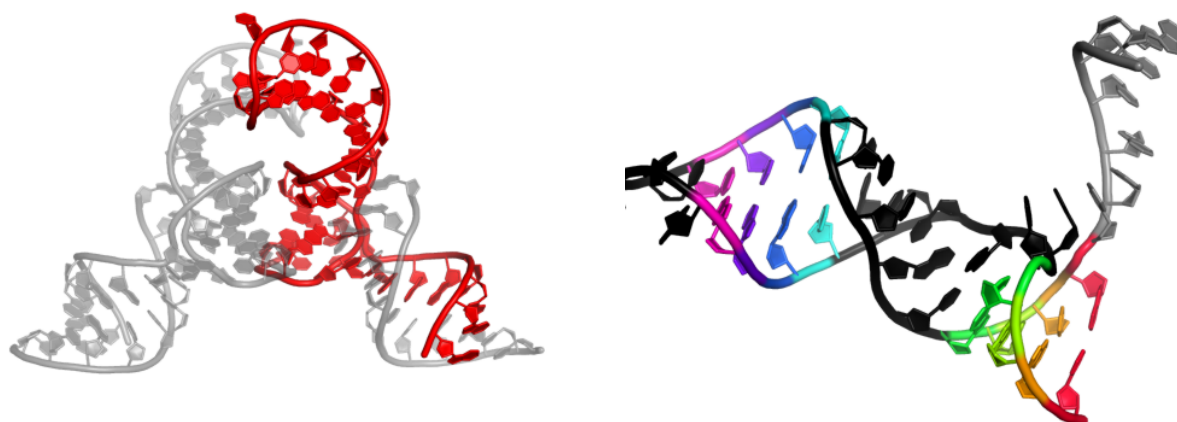
Clashscore: 14.760

Description: RNA Diels-Alder ribozyme

Organism: nan

Serganov, A., Keiper, S., Malinina, L., Tereshko, V., Skripkin, E., Hobartner, C., Polonskaia, A., Phan, A.T., Wombacher, R., Micura, R., Dauter, Z., Jaschke, A., Patel, D.J. (2005) Structural basis for Diels-Alder ribozyme-catalyzed carbon-carbon bond formation. *Nat.Struct.Mol.Biol.*

DOI: [10.1038/nsmb906](https://doi.org/10.1038/nsmb906)



GGGCGAGGCCGUGCCGGCUCUUCGGAGCAAUACUCGGC
.....(((.....(((.....)))).....)))

4.5 Methyltransferase ribozyme

4.5.1 7dlz_Y

Crystal Structure of Methyltransferase Ribozyme

Release date: 2021-10-27

Method: x-ray diffraction

Resolution: 3.00 Å

Chain length: 45

Extracted length: 45

Total clashes: 0

Clashes per residue: 0.000

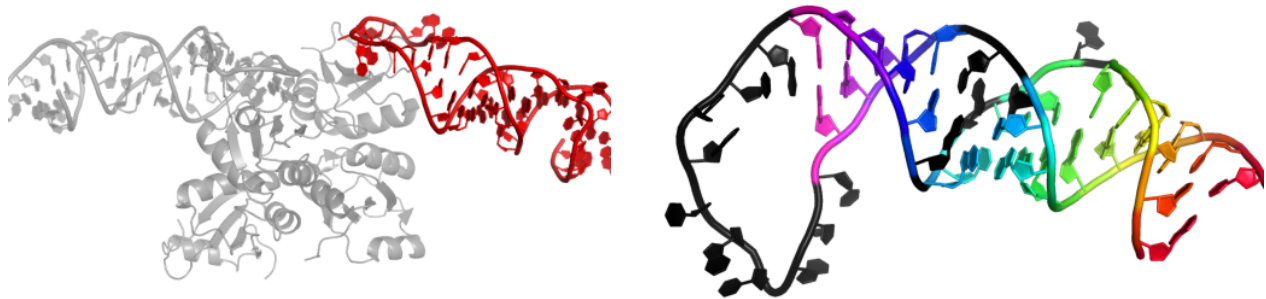
Clashscore: 8.240

Description: RNA (45-MER)

Organism: synthetic construct

Jiang, H.Y., Gao, Y.Q., Zhang, L., Chen, D.R., Gan, J.H., Murchie, A.I.H. (2021) The identification and characterization of a selected SAM-dependent methyltransferase ribozyme that is present in natural sequences. Nat Catal.

DOI: [10.1038/s41929-021-00685-z](https://doi.org/10.1038/s41929-021-00685-z)



GGACCUACUACGAGCGCCAUUGCACUCCGGCGCCACGGGGGUCC
((((((.(.((.(.(((.(.....))))).)))))))))

4.5.2 7v9e_A

Crystal structure of a methyl transferase ribozyme

Release date: 2022-03-23

Method: x-ray diffraction

Resolution: 2.30 Å

Chain length: 68

Extracted length: 68

Total clashes: 4

Clashes per residue: 0.059

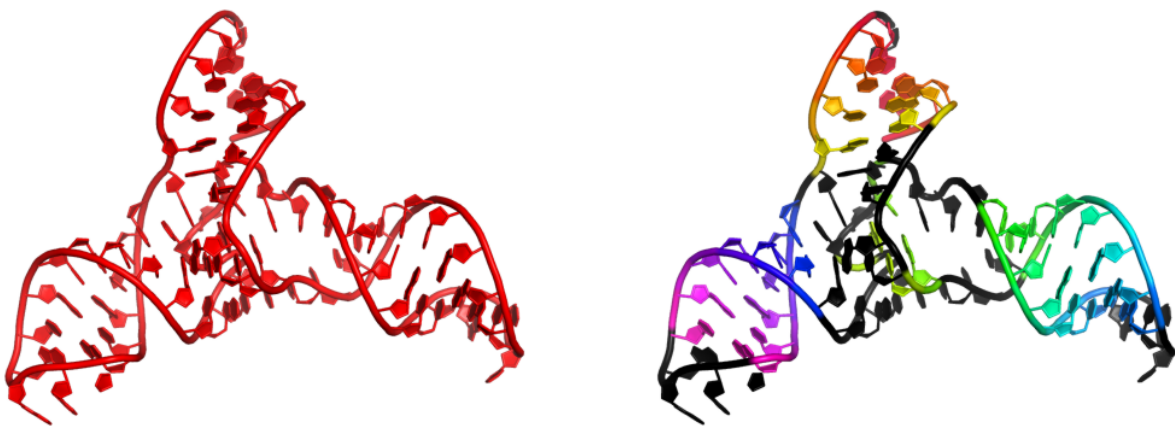
Clashscore: 1.360

Description: RNA (68-MER)

Organism: Homo sapiens

Deng, J., Wilson, T.J., Wang, J., Peng, X., Li, M., Lin, X., Liao, W., Lilley, D.M.J., Huang, L. (2022) Structure and mechanism of a methyltransferase ribozyme. Nat.Chem.Biol.

DOI: [10.1038/s41589-022-00982-z](https://doi.org/10.1038/s41589-022-00982-z)



CGGGCUGACCGACCCCCGAGUUCGCUCGGGGACAACUAGACAUACAGUAUGAAAAUACUGAGCCCGC
((((.....((((((.....)))))).....)).....((((.....)))))).

5.2 r(CCUG)

5.2.1 4k27_U

Myotonic Dystrophy Type 2 RNA: Structural Studies and Designed Small Molecules that Modulate RNA Function

Release date: 2013-11-27

Method: x-ray diffraction

Resolution: 2.35 Å

Chain length: 55

Extracted length: 55

Total clashes: 0

Clashes per residue: 0.000

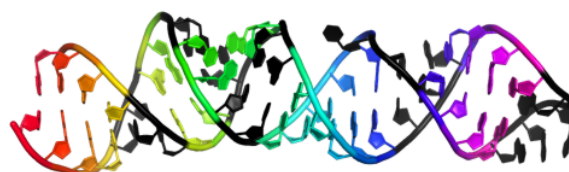
Clashscore: 1.170

Description: Myotonic Dystrophy Type 2 RNA

Organism: nan

Childs-Disney, J., Yildirim, I., Park, H., Lohman, J., Guan, L., Tran, T., Sarkar, P., Schatz, G.C., Disney, M.D. (2013) Myotonic Dystrophy Type 2 RNA: Structural Studies and Designed Small Molecules that Modulate RNA Function. ACS CHEM.BIOL.

DOI: [nan](#)



GCCCCUGCCUGCCUGCAGCUAAGGAUGAAAGUCUAUGCUGCCUGCCUGCCUGGGC
((((...((...(((...(((...(((...)))...)))...)))...)))

5.3 r(AUUCU)

5.3.1 5btm_A

Crystal structure of AUUCU repeating RNA that causes spinocerebellar ataxia type 10 (SCA10)

Release date: 2015-07-15

Method: x-ray diffraction

Resolution: 2.78 Å

Chain length: 55

Extracted length: 43

Total clashes: 6

Clashes per residue: 0.109

Clashscore: 2.200

Description: RNA (55-mer)

Organism: Homo sapiens

Park, H., Gonzalez, A.L., Yildirim, I., Tran, T., Lohman, J.R., Fang, P., Guo, M., Disney, M.D. (2015) Crystallographic and Computational Analyses of AUUCU Repeating RNA That Causes Spinocerebellar Ataxia Type 10 (SCA10). *Biochemistry*.

DOI: [10.1021/acs.biochem.5b00551](https://doi.org/10.1021/acs.biochem.5b00551)



GUCAUUCUAUUCUAUCGGCUAAGGAUGAAAGUCUAUGCCGAUUCUAUUCUAUGGC
.....(((.....((((.....(((.....)))).....)))).)).....

6 Miscellaneous (synthetic)

6.1 Nanoarchitecture 1

6.1.1 7jrr_A

Crystal structures of artificially designed homomeric RNA nanoarchitectures

Release date: 2021-09-08

Method: x-ray diffraction

Resolution: 2.16 Å

Chain length: 51

Extracted length: 51

Total clashes: 14

Clashes per residue: 0.275

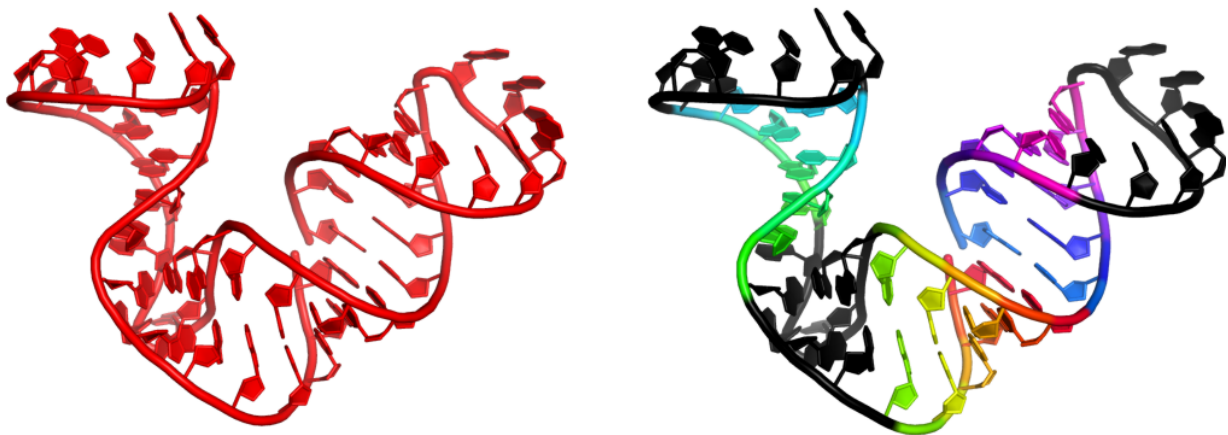
Clashscore: 4.790

Description: RNA (50-MER)

Organism: synthetic construct

Liu, D., Shao, Y., Piccirilli, J.A., Weizmann, Y. (2021) Structures of artificially designed discrete RNA nanoarchitectures at near-atomic resolution. Sci Adv.

DOI: [10.1126/sciadv.abf4459](https://doi.org/10.1126/sciadv.abf4459)



GGACGGGAGCUGAACCAUCCAGCGAAGAACGUCCCGACGGAUGGUUCGUCG
(((((((.....(((((((.....)))))).....))))))(((((((.....))))))

6.2.1 7jrs_A

Release date: 2021-09-08

Method: x-ray diffraction

Resolution: 3.21 Å

Chain length: 129

Extracted length: 129

Total clashes: 19

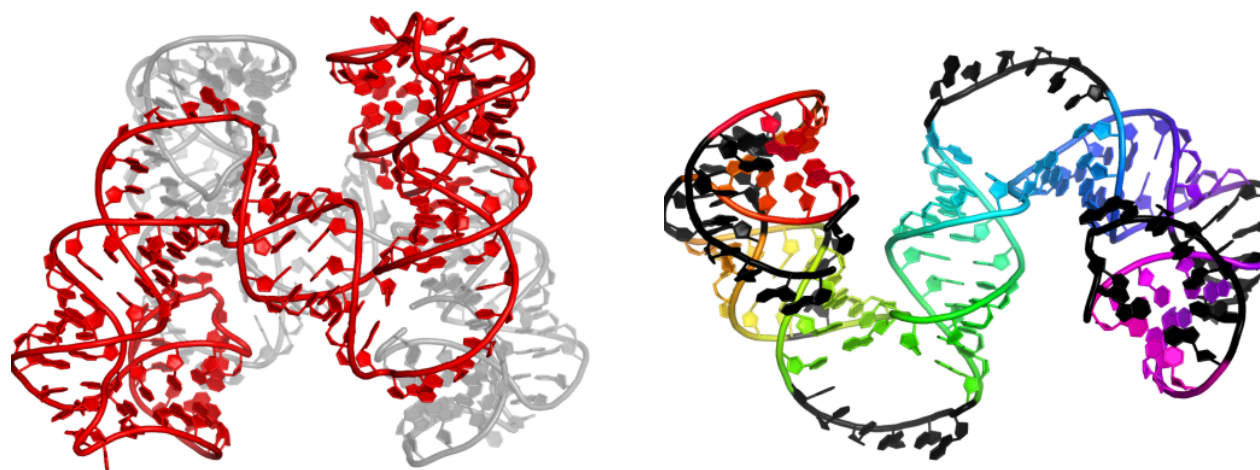
Clashes per residue: 0.147

Clashscore: 3.950

Description: RNA 3D nanocage

Organism: synthetic construct

Liu, D., Shao, Y., Piccirilli, J.A., Weizmann, Y. (2021) Structures of artificially designed discrete RNA nanoarchitectures at near-atomic resolution. *Sci Adv.*

DOI: [10.1126/sciadv.abf4459](https://doi.org/10.1126/sciadv.abf4459)

GGACGCGGUAGCGAAGAACCaucGCAUGCGCAUAGCGGAGCCUGCCUGGCAUGGGAGCCUGAAGCAGGCACGGGCGAAGAACAUCUGCAGGUGCUGAGUCGCGGUCUCCAGUUAUGGGGAGCUACC

6.3 Synthetic hairpin

6.3.1 6az4_A

RNA hairpin complex with guanosine dinucleotide ligand G(5')ppp(5')G

Release date: 2018-02-21

Method: x-ray diffraction

Resolution: 2.98 Å

Chain length: 32

Extracted length: 21

Total clashes: 0

Clashes per residue: 0.000

Clashscore: 0.720

Description: RNA (32-MER)

Organism: synthetic construct

Zhang, W., Tam, C.P., Zhou, L., Oh, S.S., Wang, J., Szostak, J.W. (2018) Structural Rationale for the Enhanced Catalysis of Nonenzymatic RNA Primer Extension by a Downstream Oligonucleotide. *J. Am. Chem. Soc.*

DOI: [10.1021/jacs.7b11750](https://doi.org/10.1021/jacs.7b11750)



CUGCUGCUGCCGCUAAGGAUGAAAGUCUAUGC
.....((. . .(((. . .))) . . .))

6.5 Synthetic G-quadruplex

6.5.1 5dea_C

Crystal structure of the complex between human FMRP RGG motif and G-quadruplex RNA, cesium bound form.

Release date: 2015-09-23

Method: x-ray diffraction

Resolution: 2.80 Å

Chain length: 35

Extracted length: 35

Total clashes: 4

Clashes per residue: 0.114

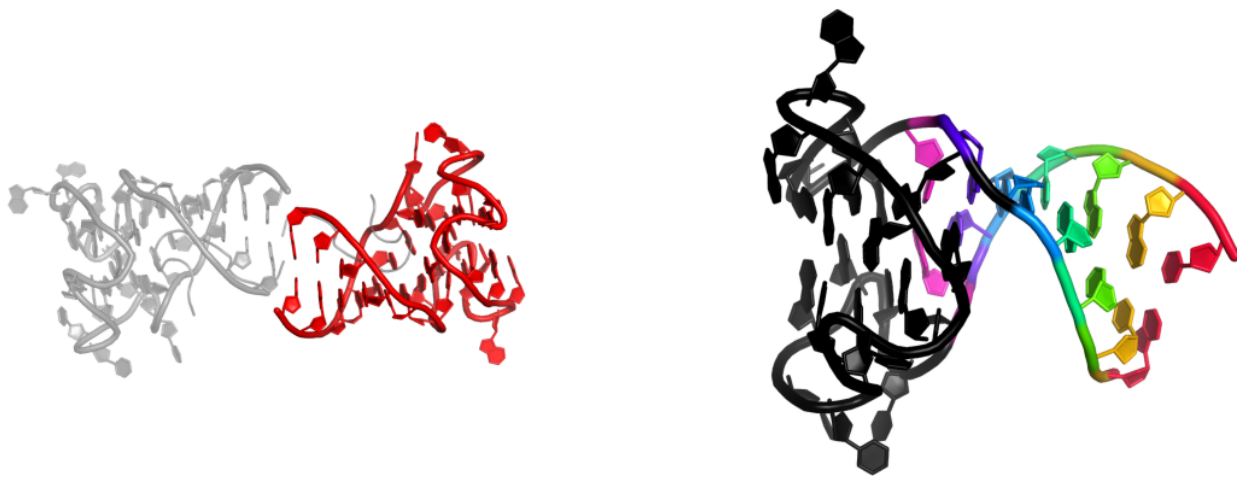
Clashscore: 3.840

Description: sc1

Organism: synthetic construct

Vasilyev, N., Polonskaia, A., Darnell, J.C., Darnell, R.B., Patel, D.J., Serganov, A. (2015) Crystal structure reveals specific recognition of a G-quadruplex RNA by a beta-turn in the RGG motif of FMRP. *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.1515737112](https://doi.org/10.1073/pnas.1515737112)



GCUGCGGUGUGGAAGGAGUGGCUGGGUUGCGCAGC
((((((.....))))))

7 Miscellaneous

7.1 ToXI

7.1.1 7d8o_L

Crystal structure of E. coli ToxIN type III toxin-antitoxin complex

Release date: 2022-01-05

Method: x-ray diffraction

Resolution: 2.10 Å

Chain length: 37

Extracted length: 37

Total clashes: 4

Clashes per residue: 0.108

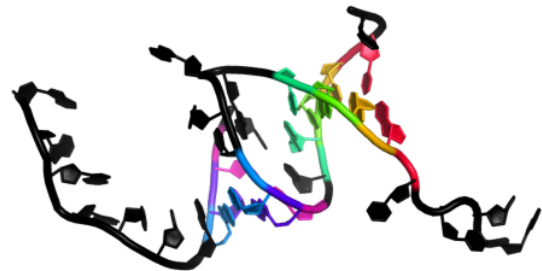
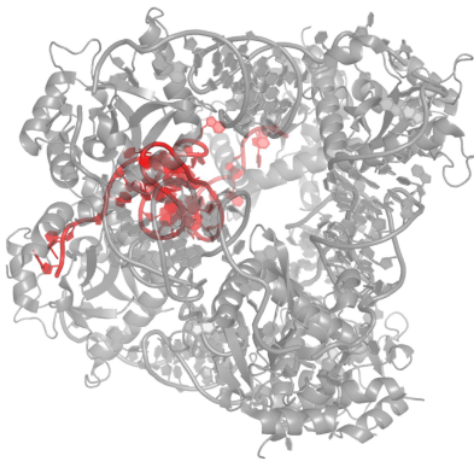
Clashscore: 2.640

Description: Antitoxin RNA

Organism: Escherichia coli

Manikandan, P., Sandhya, S., Nadig, K., Paul, S., Srinivasan, N., Rothweiler, U., Singh, M. (2022) Identification, functional characterization, assembly and structure of ToxIN type III toxin-antitoxin complex from E. coli. Nucleic Acids Res.

DOI: [10.1093/nar/gkab1264](https://doi.org/10.1093/nar/gkab1264)



AUUUAGGUGAUUUGCUACCUUUUAGUGCAGCUAGAAA

.....(((.....<<.....)).....>>.....

7.1.2 2xdb_G

A processed non-coding RNA regulates a bacterial antiviral system

Release date: 2011-01-12

Method: x-ray diffraction

Resolution: 2.55 Å

Chain length: 40

Extracted length: 36

Total clashes: 0

Clashes per residue: 0.000

Clashscore: 12.800

Description: TOXI

Organism: *Pectobacterium atrosepticum*

Blower, T.R., Pei, X.Y., Short, F.L., Fineran, P.C., Humphreys, D.P., Luisi, B.F., Salmond, G.P.C. (2011) A Processed Noncoding RNA Regulates an Altruistic Bacterial Antiviral System. Nat.Struct.Mol.Biol.

DOI: [10.1038/NSMB.1981](https://doi.org/10.1038/NSMB.1981)



AUUCAGGUGAUUUGCUACCUUUAAGUGCAGCUAGAAUUC
.....(((.(...<<.)...))>>.....>>>.....

7.1.3 4rmo_H

Crystal Structure of the CptIN Type III Toxin-Antitoxin System from *Eubacterium rectale*

Release date: 2015-09-30

Method: x-ray diffraction

Resolution: 2.20 Å

Chain length: 45

Extracted length: 45

Total clashes: 19

Clashes per residue: 0.422

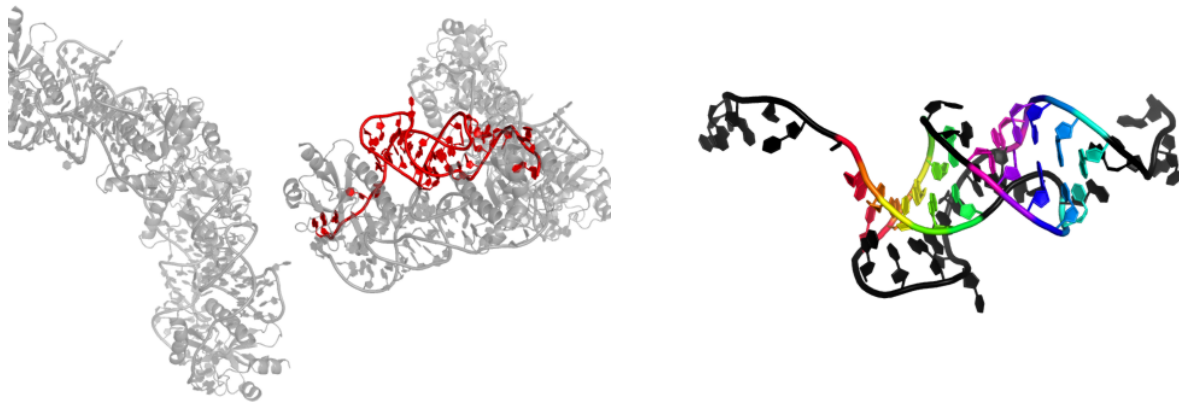
Clashscore: 6.710

Description: RNA (45-MER)

Organism: synthetic construct

Rao, F., Short, F.L., Voss, J.E., Blower, T.R., Orme, A.L., Whittaker, T.E., Luisi, B.F., Salmond, G.P. (2015) Co-evolution of quaternary organization and novel RNA tertiary interactions revealed in the crystal structure of a bacterial protein-RNA toxin-antitoxin system. *Nucleic Acids Res.*

DOI: [10.1093/nar/gkv868](https://doi.org/10.1093/nar/gkv868)



AAGUUUACCACUGACCGAU AUGUGGUAUAUAAAUGGUCGGGUUGA
.....((((((...<<<<...)))...>>>>.....

7.2 Structured part of acrIF8-aca2 5' UTR

7.2.1 8w35_C

Aca2 from Pectobacterium phage ZF40 bound to RNA

Release date: 2024-07-24

Method: electron microscopy

Resolution: 2.61 Å

Chain length: 42

Extracted length: 37

Total clashes: 0

Clashes per residue: 0.000

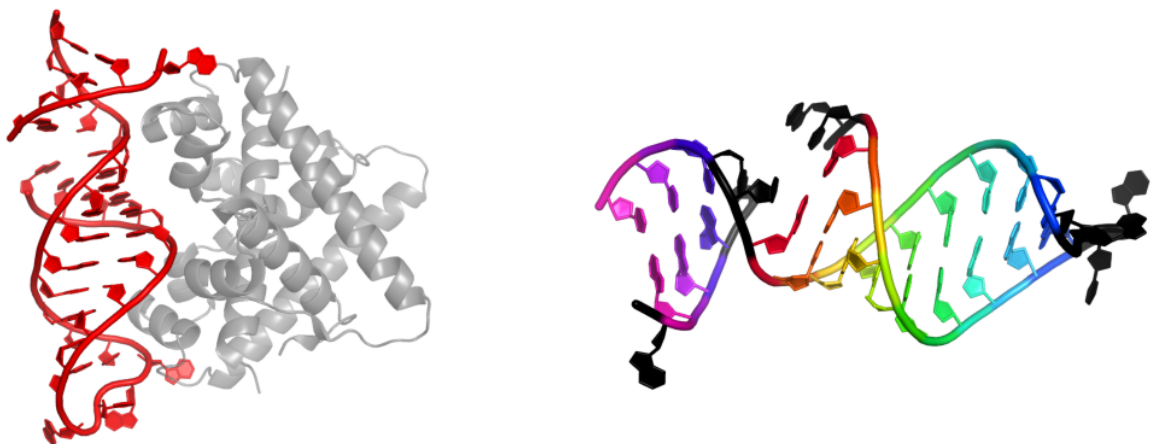
Clashscore: 0.620

Description: IR2 and IR-RBS RNA

Organism: Pectobacterium phage ZF40

Birkholz, N., Kamata, K., Feussner, M., Wilkinson, M.E., Cuba Samaniego, C., Migur, A., Kimanius, D., Ceelen, M., Went, S.C., Usher, B., Blower, T.R., Brown, C.M., Beisel, C.L., Weinberg, Z., Fagerlund, R.D., Jackson, S.A., Fineran, P.C. (2024) Phage anti-CRISPR control by an RNA- and DNA-binding helix-turn-helix protein. *Nature*.

DOI: [10.1038/s41586-024-07644-1](https://doi.org/10.1038/s41586-024-07644-1)



AUCGGUUCGAGAUGGCUCGAAUCGCUCCUAACGAGGAUCCA
..((((((.....))))))..(((.....))).....

7.3 Saguaro cactus viral mRNA structure

7.3.1 8t2a_R

Crystal structure of SCV PTE G18A mutant RNA in complex with Fab BL3-6

Release date: 2024-01-10

Method: x-ray diffraction

Resolution: 3.17 Å

Chain length: 90

Extracted length: 90

Total clashes: 55

Clashes per residue: 0.611

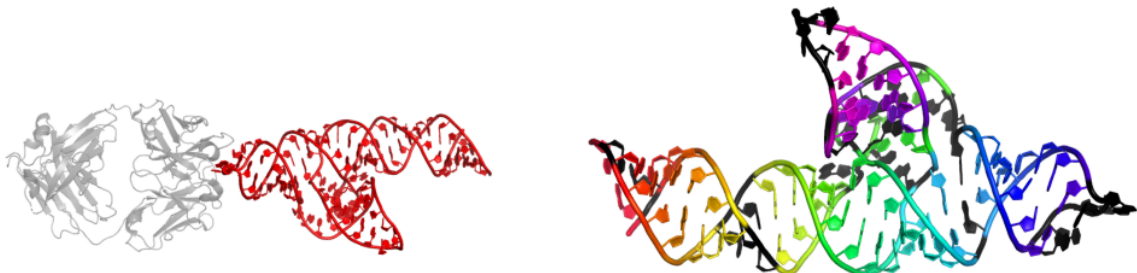
Clashscore: 9.760

Description: RNA (90-MER)

Organism: Saguaro cactus virus

Ojha, M., Vogt, J., Das, N.K., Redmond, E., Singh, K., Banna, H.A., Sadat, T., Koirala, D. (2024) Structure of saguaro cactus virus 3' translational enhancer mimics 5' cap for eIF4E binding. *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.2313677121](https://doi.org/10.1073/pnas.2313677121)



GGUUGCUCGACUGUGAGAGGACCUACCCACUGUGGAAACACCACAGGAACUCCAACCUUCGGGUGGCGAGGUAGGGCAGAAGAGUGACC
(.((((((...(((...<...((((((...((((((...)))...>...(((((...)))...)))))...)))...)))...))

7.3.2 8t29_R

Crystal structure of SCV PTE RNA in complex with Fab BL3-6

Release date: 2024-01-10

Method: x-ray diffraction

Resolution: 3.13 Å

Chain length: 90

Extracted length: 90

Total clashes: 61

Clashes per residue: 0.678

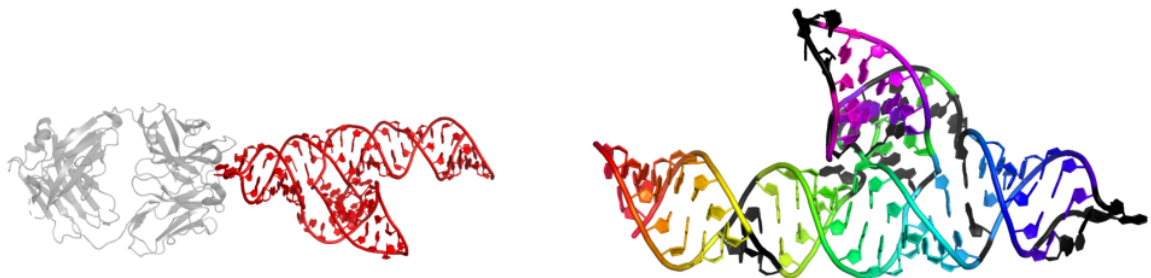
Clashscore: 10.320

Description: RNA (90-MER)

Organism: Saguaro cactus virus

Ojha, M., Vogt, J., Das, N.K., Redmond, E., Singh, K., Banna, H.A., Sadat, T., Koirala, D. (2024) Structure of saguaro cactus virus 3' translational enhancer mimics 5' cap for eIF4E binding. *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.2313677121](https://doi.org/10.1073/pnas.2313677121)



GGUUGCUCGACUGUGAGGGGACCUACCCACUGUGGAAACACCACAGGAACUCCAACCUUCGGGUGGCGAGGUAGGGCAGAAGAGUGACC
(((((((...(((...<...((((((((((((((...)))))...>...(((...)))))...)))))...)))))

7.3.3 8t2b_R

Crystal structure of SCV PTE G18C mutant RNA in complex with Fab BL3-6

Release date: 2024-01-10

Method: x-ray diffraction

Resolution: 3.18 Å

Chain length: 90

Extracted length: 90

Total clashes: 49

Clashes per residue: 0.544

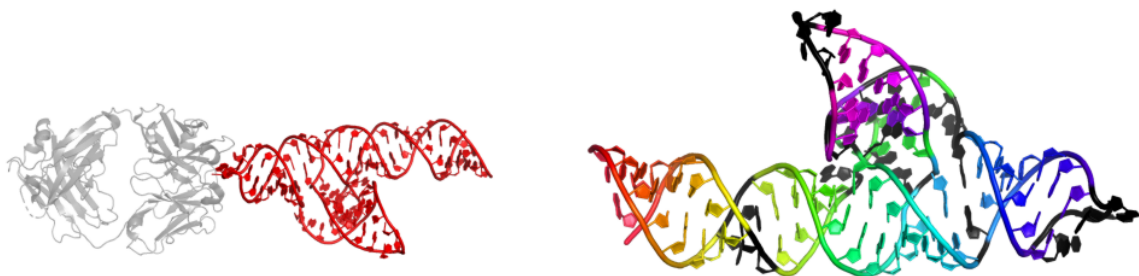
Clashscore: 9.440

Description: RNA (90-MER)

Organism: Saguaro cactus virus

Ojha, M., Vogt, J., Das, N.K., Redmond, E., Singh, K., Banna, H.A., Sadat, T., Koirala, D. (2024) Structure of saguaro cactus virus 3' translational enhancer mimics 5' cap for eIF4E binding. *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.2313677121](https://doi.org/10.1073/pnas.2313677121)



GGUUGCUCGACUGUGAGCGGACCUACCCACUGUGGAAACACCACAGGAACUCCAACCUUCGGGUGGCGAGGUAGGGCAGAAGAGUGACC
(((((((((...(((...<...(((((((...(((...))))))...>...(((...))))...))))))...))))))

7.4 ITS-2

7.4.1 7r6q_6

State E2 nucleolar 60S ribosome biogenesis intermediate - Foot region model

Release date: 2022-11-09

Method: electron microscopy

Resolution: 2.98 Å

Chain length: 87

Extracted length: 87

Total clashes: 0

Clashes per residue: 0.000

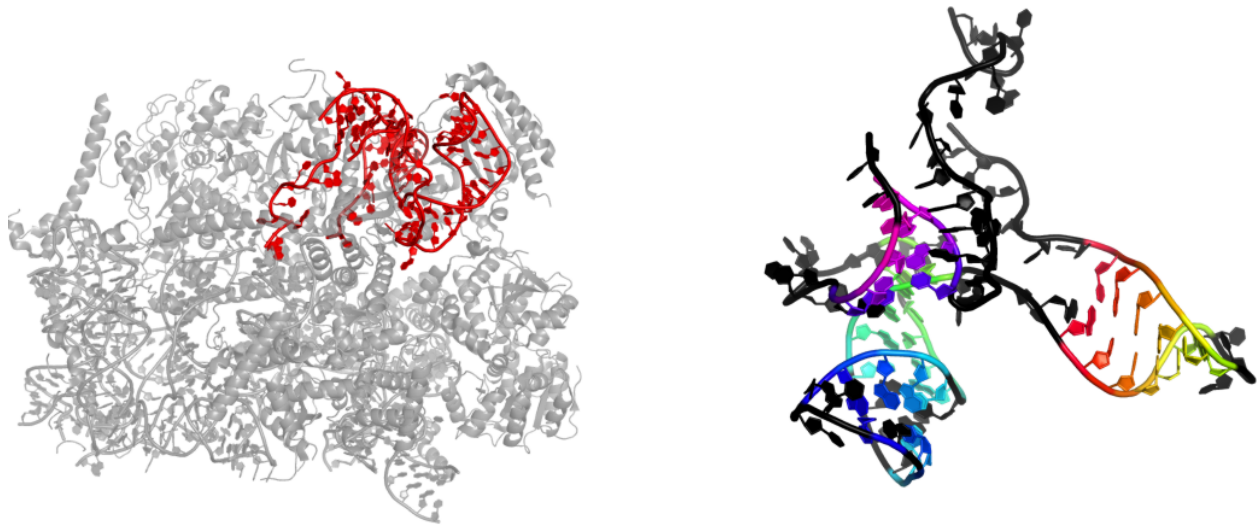
Clashscore: 6.420

Description: ITS-2

Organism: *Saccharomyces cerevisiae* BY4741

Cruz, V.E., Sekulski, K., Peddada, N., Sailer, C., Balasubramanian, S., Weirich, C.S., Stengel, F., Erzberger, J.P. (2022) Sequence-specific remodeling of a topologically complex RNP substrate by Spb4. *Nat.Struct.Mol.Biol.*

DOI: [10.1038/s41594-022-00874-9](https://doi.org/10.1038/s41594-022-00874-9)



CCUUCUCAACAUAUCUGUUUGGUAGUGAGUGAUACUCUUUGGAGUUAACUUGAAAUUGCUGGCCUUUAGGCGAACAAUGUUCUAAA
.....((((((.....))))).(((.....(((.....))))).)).....((((.....)))).....

7.4.2 7u0h_6

State NE1 nucleolar 60S ribosome biogenesis intermediate - Overall model

Release date: 2022-12-14

Method: electron microscopy

Resolution: 2.76 Å

Chain length: 87

Extracted length: 87

Total clashes: 60

Clashes per residue: 0.690

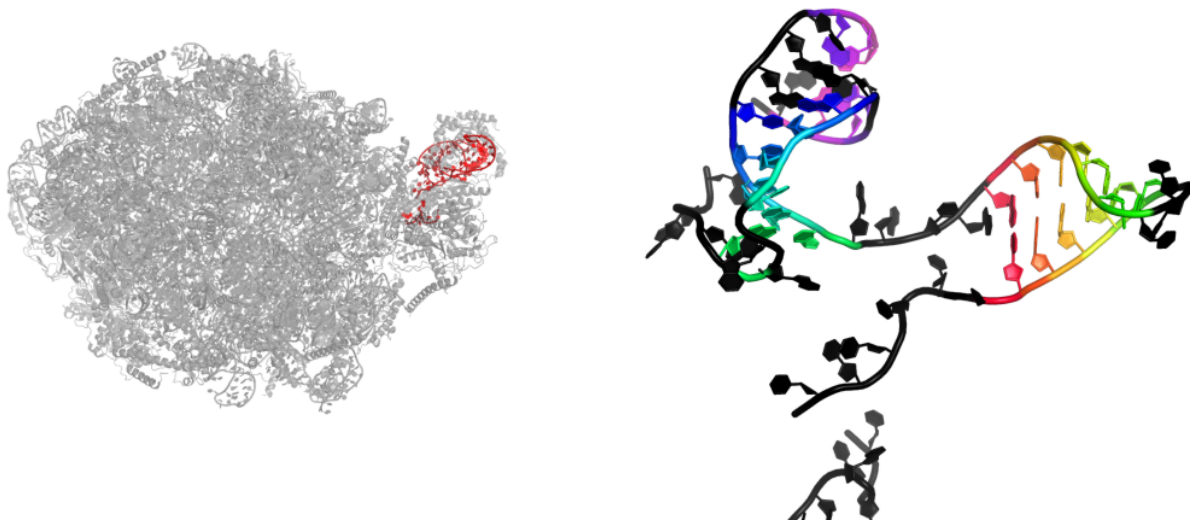
Clashscore: 7.920

Description: ITS2 rRNA

Organism: *Saccharomyces cerevisiae* BY4741

Cruz, V.E., Sekulski, K., Peddada, N., Sailer, C., Balasubramanian, S., Weirich, C.S., Stengel, F., Erzberger, J.P. (2022) Sequence-specific remodeling of a topologically complex RNP substrate by Spb4. *Nat.Struct.Mol.Biol.*

DOI: [10.1038/s41594-022-00874-9](https://doi.org/10.1038/s41594-022-00874-9)



CCUUCUCAAACAUCUGUUUGGUAGUGAGUGAUACUCUUUGGAGUUAACUUGAAAUUGCUGGCCUUUAGGCGAACAAUGUUCUAAA
.....((((((.....))))).(((.....(((.....))))).)).....

7.5 ENE

7.5.1 7ljy_B

Cryo-EM structure of the B dENE construct complexed with a 28-mer poly(A)

Release date: 2021-04-14

Method: electron microscopy

Resolution: 5.60 Å

Chain length: 76

Extracted length: 76

Total clashes: 5

Clashes per residue: 0.066

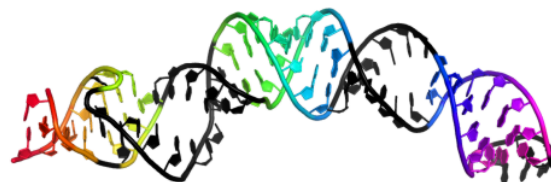
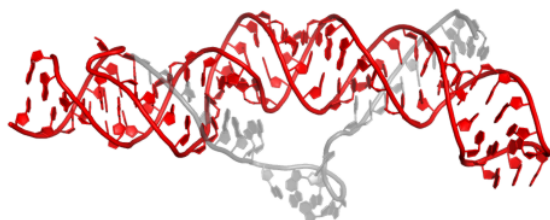
Clashscore: 1.860

Description: B dENE construct

Organism: *Oryza sativa*

Torabi, S.F., Chen, Y.L., Zhang, K., Wang, J., DeGregorio, S.J., Vaidya, A.T., Su, Z., Pabit, S.A., Chiu, W., Pollack, L., Steitz, J.A. (2021) Structural analyses of an RNA stability element interacting with poly(A). *Proc.Natl.Acad.Sci.USA*.

DOI: [10.1073/pnas.2026656118](https://doi.org/10.1073/pnas.2026656118)



GGGUACUCUUUUCUUUGUCAUGGUUUUCUCAGGCGAAAGUCUGAGUUUUUACAUGACAAAGUUUUUAACGAGGCC
(((.(.(((.....((((((.....(((((((.....)))))).....)))))).....))))))

7.5.2 3p22_A

Crystal structure of the ENE, a viral RNA stability element, in complex with A9 RNA

Release date: 2010-12-08

Method: x-ray diffraction

Resolution: 2.50 Å

Chain length: 40

Extracted length: 40

Total clashes: 3

Clashes per residue: 0.075

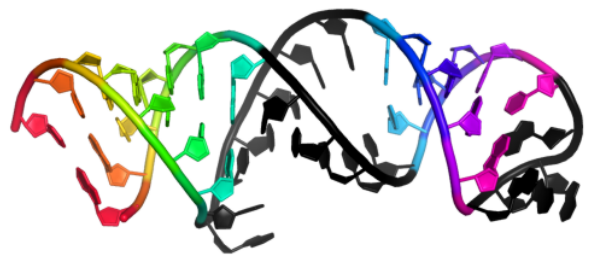
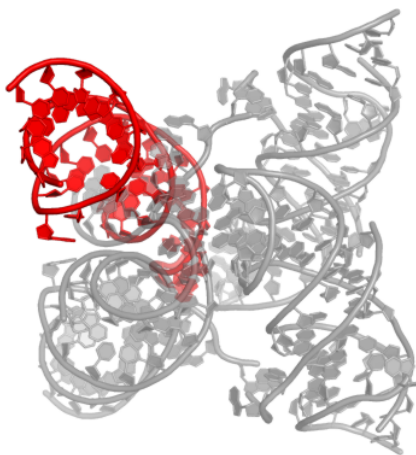
Clashscore: 3.530

Description: Core ENE hairpin from KSHV PAN RNA

Organism: nan

Mitton-Fry, R.M., DeGregorio, S.J., Wang, J., Steitz, T.A., Steitz, J.A. (2010) Poly(A) tail recognition by a viral RNA element through assembly of a triple helix. *Science*.

DOI: [10.1126/science.1195858](https://doi.org/10.1126/science.1195858)



GGCUGGGUUUUUCCUUCGAAAGAAGGUUUUUAUCCAGUC
((((((.....((((.....)))))).....))))))

7.5.3 7jnh_B

Crystal structure of a double-ENE RNA stability element in complex with a 28-mer poly(A) RNA

Release date: 2021-01-20

Method: x-ray diffraction

Resolution: 2.89 Å

Chain length: 86

Extracted length: 86

Total clashes: 62

Clashes per residue: 0.721

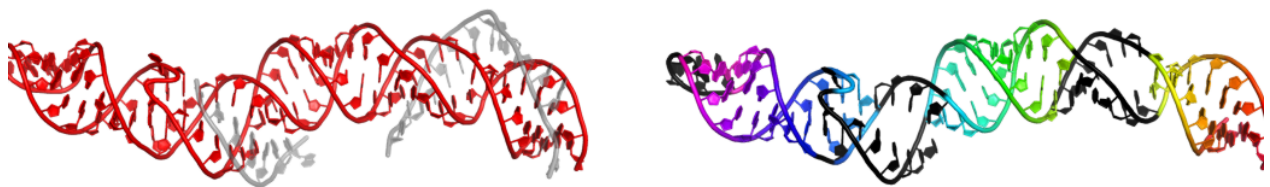
Clashscore: 13.540

Description: Core double ENE RNA (Xtal construct) from Oryza sativa transposon,Core double ENE RNA (Xtal construct) from Oryza sativa transposon

Organism: Oryza sativa

Torabi, S.F., Vaidya, A.T., Tycowski, K.T., DeGregorio, S.J., Wang, J., Shu, M.D., Steitz, T.A., Steitz, J.A. (2021) RNA stabilization by a poly(A) tail 3'-end binding pocket and other modes of poly(A)-RNA interaction. Science.

DOI: [10.1126/science.abe6523](https://doi.org/10.1126/science.abe6523)



GGGCUGAGUUUUACAUGACAAAGUUUUUAAACGAGGCAGCGGCGAAAGUCGCUGUACUCUUUUCUUUGUCAUGGUUUUCUCAGCCC
(((((((.....(((((((.....(((((((((((.....)))))))).))).....))))))))).....)))))))))

7.5.4 3p22_E

Crystal structure of the ENE, a viral RNA stability element, in complex with A9 RNA

Release date: 2010-12-08

Method: x-ray diffraction

Resolution: 2.50 Å

Chain length: 40

Extracted length: 40

Total clashes: 8

Clashes per residue: 0.200

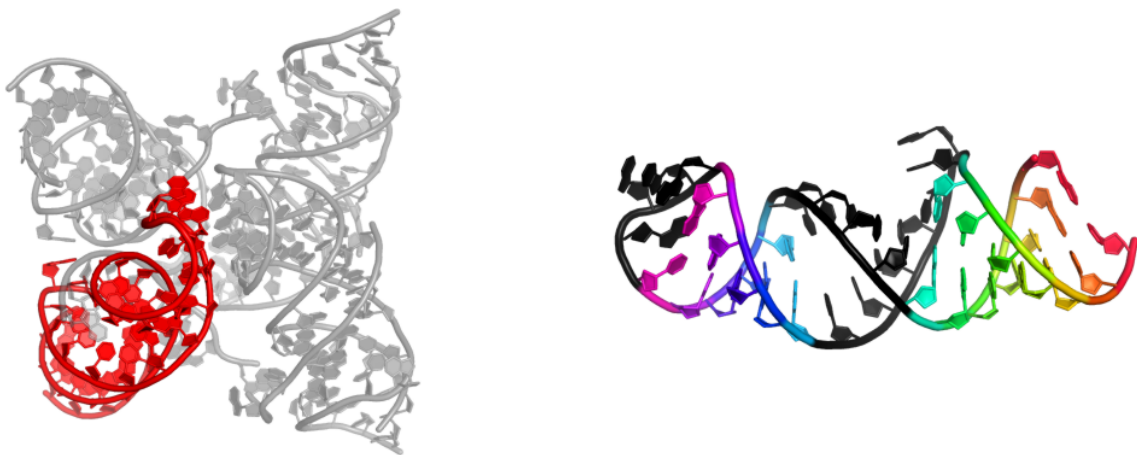
Clashscore: 3.530

Description: Core ENE hairpin from KSHV PAN RNA

Organism: nan

Mitton-Fry, R.M., DeGregorio, S.J., Wang, J., Steitz, T.A., Steitz, J.A. (2010) Poly(A) tail recognition by a viral RNA element through assembly of a triple helix. *Science*.

DOI: [10.1126/science.1195858](https://doi.org/10.1126/science.1195858)



GGCUGGGUUUUUCCUUCGAAAGAAGGUUUUUAUCCAGUC
((((((.....((((.....)))))).....))))))

7.7 SCNMV xrRNA

7.7.1 6d3p_A

Crystal structure of an exoribonuclease-resistant RNA from Sweet clover necrotic mosaic virus (SCNMV)

Release date: 2018-06-20

Method: x-ray diffraction

Resolution: 2.90 Å

Chain length: 45

Extracted length: 45

Total clashes: 18

Clashes per residue: 0.400

Clashscore: 6.560

Description: RNA (45-MER)

Organism: Sweet clover necrotic mosaic virus

Steckelberg, A.L., Akiyama, B.M., Costantino, D.A., Sit, T.L., Nix, J.C., Kieft, J.S. (2018)
A folded viral noncoding RNA blocks host cell exoribonucleases through a conformationally
dynamic RNA structure. *Proc. Natl. Acad. Sci. U.S.A.*

DOI: [10.1073/pnas.1802429115](https://doi.org/10.1073/pnas.1802429115)



GGGCGUAACCUCCAUCCGAGUUGCAAGAGAGGGAAACGCAGUCUC
..(((..(((.....))..)).....

7.9 NAD-II riboswitch

7.9.1 8hb8_A

Crystal structure of NAD-II riboswitch (single strand) with NMN

Release date: 2023-03-22

Method: x-ray diffraction

Resolution: 2.30 Å

Chain length: 55

Extracted length: 55

Total clashes: 8

Clashes per residue: 0.145

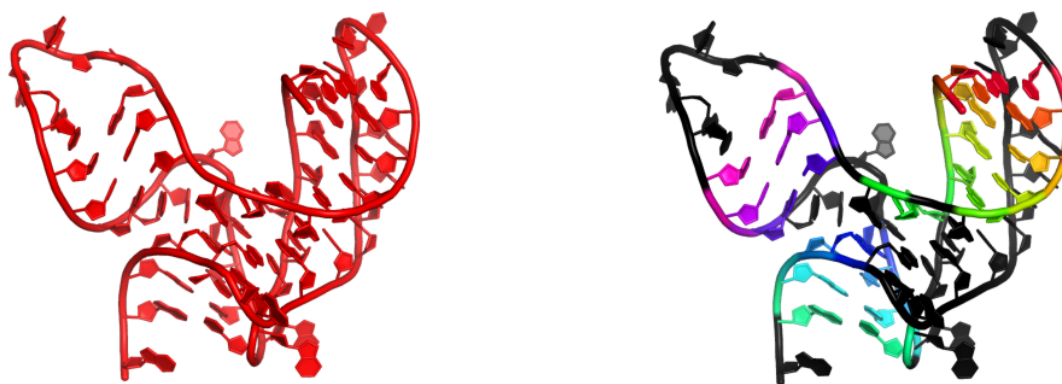
Clashscore: 2.180

Description: RNA (55-MER)

Organism: *Streptococcus parasanguinis*

Peng, X., Liao, W., Lin, X., Lilley, D.M.J., Huang, L. (2023) Crystal structures of the NAD⁺-II riboswitch reveal two distinct ligand-binding pockets. *Nucleic Acids Res.*

DOI: [10.1093/nar/gkad102](https://doi.org/10.1093/nar/gkad102)



GCGGCGUUGCGUCCGAAAGUCUAAACAGACACGGCCGCUAAAAACAAAAGGAGA
((((((...<.<<<...(((.....)))..)))...>>>..

7.9.2 8hba_A

Crystal structure of NAD-II riboswitch (single strand) with NAD

Release date: 2023-03-22

Method: x-ray diffraction

Resolution: 2.64 Å

Chain length: 56

Extracted length: 56

Total clashes: 53

Clashes per residue: 0.946

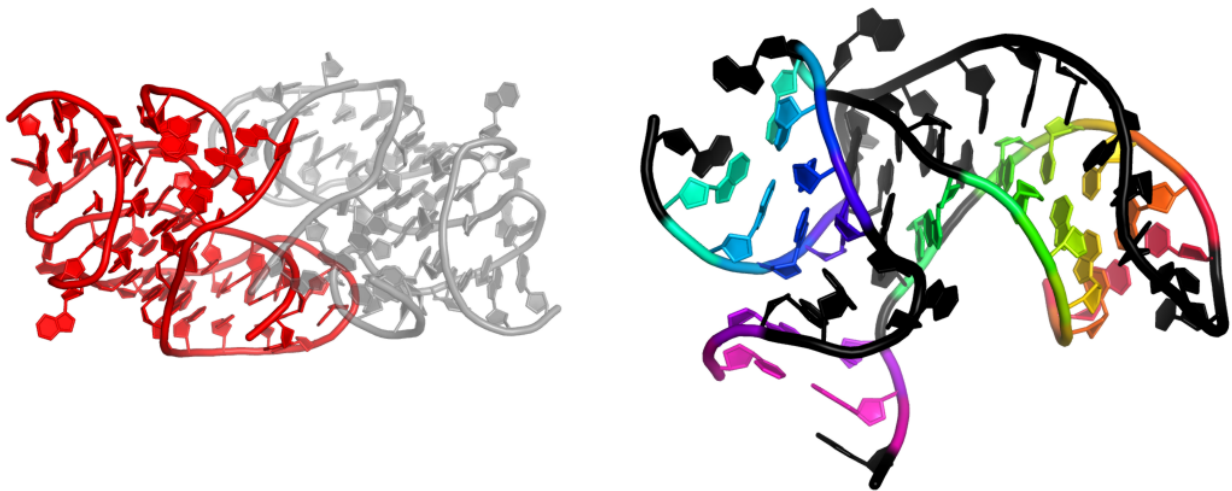
Clashscore: 15.750

Description: RNA (55-MER)

Organism: *Streptococcus parasanguinis*

Peng, X., Liao, W., Lin, X., Lilley, D.M.J., Huang, L. (2023) Crystal structures of the NAD⁺-II riboswitch reveal two distinct ligand-binding pockets. *Nucleic Acids Res.*

DOI: [10.1093/nar/gkad102](https://doi.org/10.1093/nar/gkad102)



CGCGGCGUUGCGUCCGAAAGUCUAAACAGACACGGCCGCUAAAAACAAAAGGAGA
.(.(((.((...<.<<...((.....))..))...>>>..