⌄ RFdiffusion

RFdiffusion is a method for structure generation, with or without conditional information (a motif, target etc). It can perform a whole range of protein design challenges as we have outlined in the RFdiffusion [manuscript](#).

NOTE: This notebook is in development, we are still working on adding all the options from the manuscript above.

For **instructions**, see end of Notebook.

See [diffusion_foldcond](#) for fold conditioning functionality.

See [original version](#) of this notebook (from 31Mar2023).

› setup **RFdiffusion** (~3min)

Show code

```
installing RFdiffusion...
installing ColabDesign...
downloading RFdiffusion params...
CPU times: user 5.93 s, sys: 946 ms, total: 6.87 s
Wall time: 2min 44s
```

› run **RFdiffusion** to generate a backbone

name: " try3 "

contigs: " 150 "

pdb: " LEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKT "

iterations: 50 ▼

hotspot: " Insert text here "

num_designs: 4 ▼

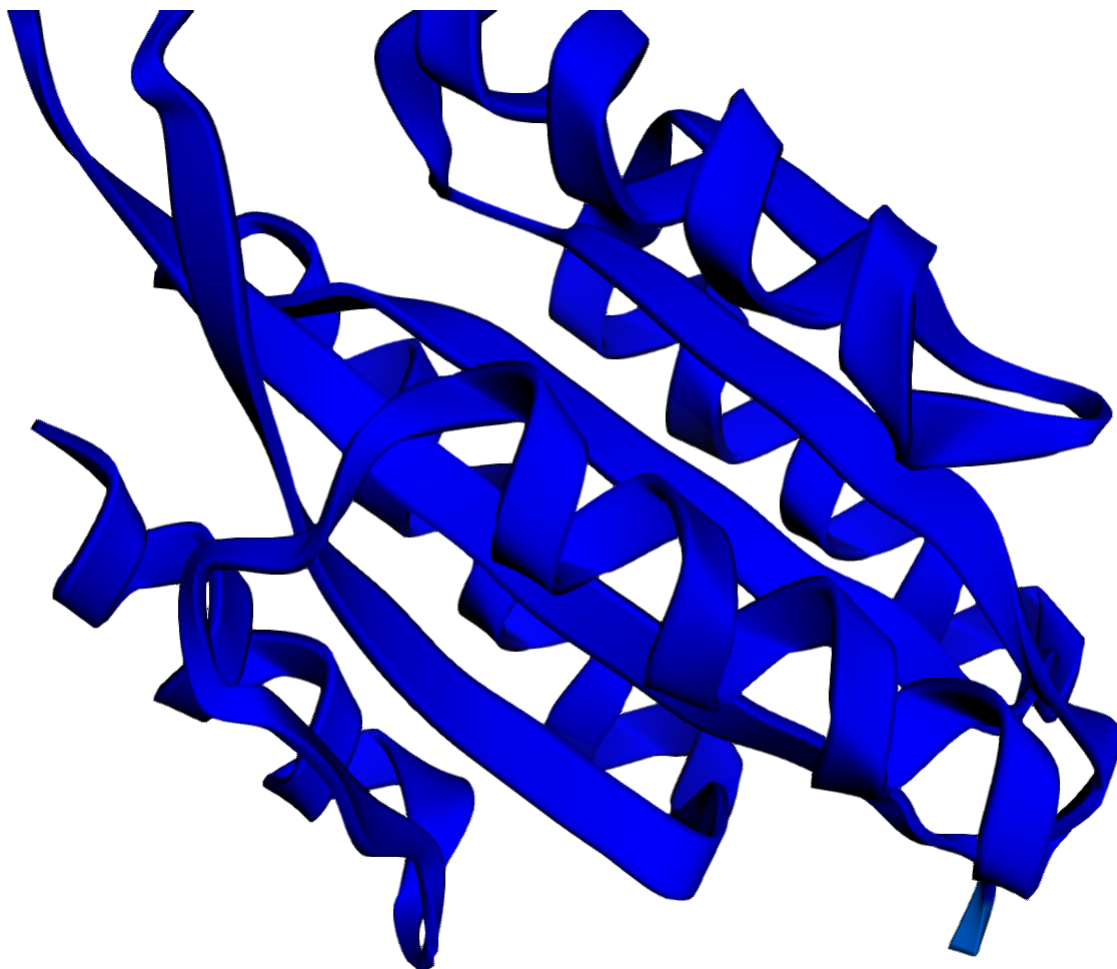**visual:** interactive ▼

symmetry settings

symmetry: none ▼

order: 1 ▼

chains: " Insert text here "

```
mode: free
output: outputs/try3
contigs: ['150-150']
./RFdiffusion/run_inference.py inference.output_prefix=outputs/try3 inference
```

running


```
CPU times: user 3.55 s, sys: 464 ms, total: 4.02 s
Wall time: 4min 27s
```

> Display 3D structure

animate: movie   ▼

color: chain   ▼

dpi: 100   ▼

Show code

design: 0

> run **ProteinMPNN** to generate a sequence and **AlphaFold** to validate

ProteinMPNN Settings

num_seqs: | 8 | ▼

mpnn_sampling_temp: | 0.1 | ▼

rm_aa: " | C | "

use_solubleMPNN: ☐

- `mpnn_sampling_temp` - control diversity of sampled sequences. (higher = more diverse).
- `rm_aa='C'` - do not use [C]ysteines.
- `use_solubleMPNN` - use weights trained only on soluble proteins. See [preprint](.).

AlphaFold Settings

initial_guess: ☑

- soft initialization with desired coordinates, see [paper](.).

num_recycles: 3   ▼

- for **binder** design, we recommend `initial_guess=True num_recycles=3`

use_multimer: ☐

- `use_multimer` - use AlphaFold Multimer v3 params for prediction.

Show code

⇥ `'num_seqs':8,'initial_guess':True,'use_multimer':False,'use_soluble':False,'nu`

```
GEVVGEKYLVRTVTLRFDDLAALAATIAEALAELADEKLSVLVIERRDGLLILRFYALNGSPEEITEQLTEIIIEAIE
EVVGERRLVERVTLAFDDREGLAAALAAALERLRDVRVSVVKFVLRDGRIEVTFYALEGDKEQIIEDLTELIIEAIE
GEILGEKELVKTLTFRRDDKEGLAKALKELIEEMKDEKLSVIVFELEDGLIIVRFYSLNGPKEEITKELTEIIIEAIK
GIVVGEKELVKIVTLDFNDKEEMKKTLKELLEELKDAKVSVIIFKLKDGKIIIEAYKLEGDEEQIVKDLTELIIKAIE
GEIVGEKYLYKIVKFSFDDLEGLKKEIEKELEKLKNEKVSVIIVEKKDGELILKFYVLNGDKEKIIEDLTEIIIEAIE
PEIKGEKELVKVLTFNFEDKEEIKKAIEELLKELEDARLSVLILEKKDGKIIVKFYRLNGDDEEIIEQLTEIIIEAIK
GTVKGEMYLVKIVTLSFDDLEGFKKTLEELLEELKDERLSVIEVIKEDGLLIIRFYALNGSPEQITKDLTKLIIRAI
GPVVLGERRLVRTVTLAWDDLEGLTAALRAALAEMADARVSVAELLREDGLLVLRFYELEGDPERITEELTELLVRAE
ASSSSGVTSLTLSTTISVKATDGTVVVTVTVTIDTATSDPAITVTLTASLSLATASAAATATISSSSGTATLVKTTTT
ISPNGVSSLTLSATITVAATAGTVTVTVTVTIQTSLSQGDVTVTVTLSLATPAAEAAVTATITSSDGTATLVSITTAP
TKTSATGVTSLTLNTTISVAATDGTIVVTATATIQTATSQPAVTVTLTVTLSTAAADAAVTATVTSSKGTATLTATTI
SSATGVTSLSLNETITVKATNGKVVLTATVTLTTAASQGATTVTLTLSFSTPTSESSVTATISSSSGTATLSSTTTTS
SSSSGVSSLSLTTTITVAATAGTVTVTVTVTISTASSDPTVTVTLTASLAVDAADAAVTATIASSDGTATLDAITITP
SSSSGVSSLTLNDTITVKATEGTVVVTVTVTLSTSSSQGPVTVTVTLSLSTAAASTDVTATVSSSSGTATLTSITKSP
SSSSGVTSLTLNTTITVKATEGTVVVTATVTITTSAAAGATTVTLTVSLKTDPAESDVTATVSDSAGTATLTSITKSP
SSSSGVSSLTLNTTITVQATAGTVVVTVTVTLQTSSSQGPVTVTVTLELSLPAAEAAATVTVSSSDGTATLTSLTITP
EEILKKLKEIGVPEEALEKAKEESKVEKLVDREETAARIRKLVEEGDVEGFAELVAESLERALIAYEVIKDTVPLDLA
IFKEVMEILKEMGVPEEALKKAEEEAEIKELYDREETKKKIRELAEKGDVEGLAELIAESLYRALIAYEVLKEEVPLE
AEILAILRRLGVPEEALALAEAEAAVRTLSDREETAARLRALVEAGDVEAAAALVAESLENALIFYEVARDTIPLELA
EEVLARLRALGVPEEALAAARAEAVVRELRDPAETAARLRALAEAGDVDGFAALVAESLENALIAYEVLRDTIPLDRA
TWERILELLREAGVPAEALARARAEAVVTELYDREAVAAKLRALVEAGDVAGAAALVAESLERALIAYEVLRDTAPLD
EEALEILKEVGVPEEALKLAREESEVRELVDRERAAAELRALAEAGDVDGLAALVAESLELAVIAYEVLRDTIPLDKA
TWAEILARLRALGVPAEALALAEAEAVVTELPDREAVAAQLRALAEAGDVDGAAALVAESLYRALVAYEVLVDTIPLD
EEIFEILREAGVPEEALELAREESKVTELPDREEVAARLRALYEAGDVEGAAELVAESLYNALIAYEVLRDTAPWELM
AGVEVLGETSFEEVAKRAAALARELGTRVHVFFSGVPEEVAEKMEAIARETFEDVTIHRGMTAEEVIAALTAIHEAGE
AGVEVLPETPIEEVVARAAALARELGTKVHVFLLGVPAAVAEEIEAIARATLEDVTIHRGMTAEEVIAALRALRDAGE
KGVEVLGKTSFEEVMKEAAEIAEKLGFDVHVFLSGVHPEVAERYEKIAKEILKNVTIHKGITAEEVIALLRALHEAGK
AGVEVLGETPIAEVLARAAALARELGTKVHVFLLSVPEEVADRYVALAEATLEDVTIHRGLTAEEVIALLRAIHEAGE
AGVEVLGETPVEEVFRRAAALARELGTRVHVFLLGVPEEVAEEYEAIARATFEDVTIRRGATAEEVIAALRALHEAGE
PGLEVLGETPIEEVFKRAAEIAKELGYKVYVFLSGVPEEVADEIIKIAKETFDDVNIFRGITSEEIIARLTALHDAGE
EGVEVLGETPAEAVFARAAAEAERLGTRVHVFLVGVPDEVADRMEAIARATFRDVTITRGATAEEVIARLRALHDAGE
EGVEVLGETSIEEVFERAAAEAERLGTKVHVFMLGVPEEAAERYERIARETFENVEIHRGITADEAIALLTKIHDAGE
```

> **Display best result**

Show code

design: | best |
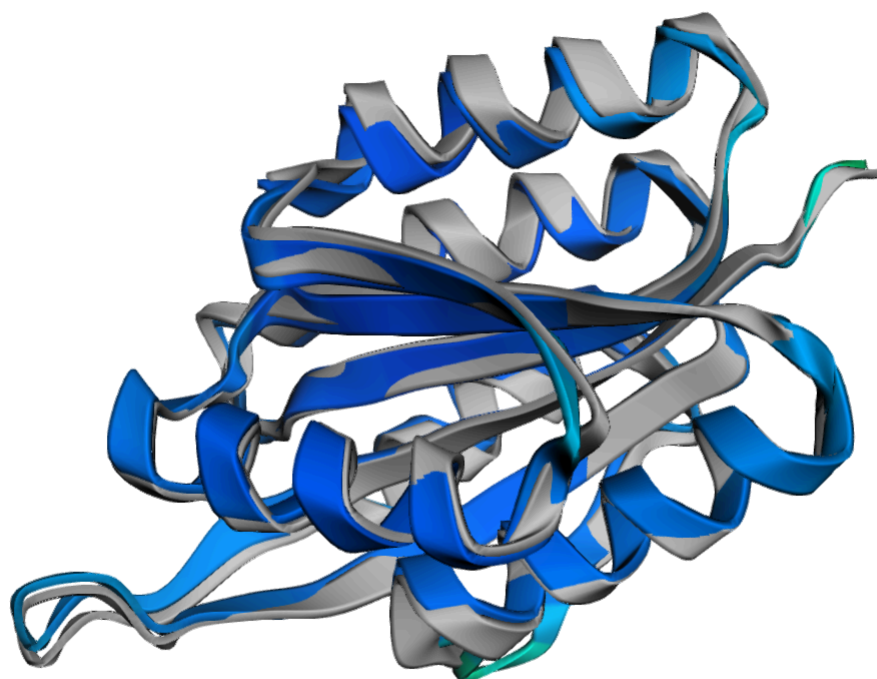
> ## Package and download results

If you are having issues downloading the result archive, try disabling your adblocker and run this cell again. If that fails click on the little folder icon to the left, navigate to file: `name.result.zip`, right-click and select "Download" (see [screenshot](#)).

Show code

```
adding: outputs/try3/ (stored 0%)
adding: outputs/try3/best.pdb (deflated 78%)
adding: outputs/try3/best_design0.pdb (deflated 78%)
adding: outputs/try3/best_design3.pdb (deflated 78%)
adding: outputs/try3/all_pdb/ (stored 0%)
adding: outputs/try3/all_pdb/design0_n1.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design2_n2.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design1_n7.pdb (deflated 77%)
adding: outputs/try3/all_pdb/design3_n2.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design1_n0.pdb (deflated 77%)
adding: outputs/try3/all_pdb/design3_n0.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design3_n6.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design1_n6.pdb (deflated 77%)
adding: outputs/try3/all_pdb/design1_n1.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design3_n3.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design0_n7.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design2_n4.pdb (deflated 77%)
adding: outputs/try3/all_pdb/design2_n7.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design1_n4.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design0_n0.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design3_n4.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design3_n7.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design1_n3.pdb (deflated 77%)
adding: outputs/try3/all_pdb/design2_n1.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design0_n4.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design0_n5.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design0_n2.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design2_n6.pdb (deflated 77%)
adding: outputs/try3/all_pdb/design2_n0.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design0_n6.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design0_n3.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design2_n3.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design3_n1.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design3_n5.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design1_n2.pdb (deflated 77%)
adding: outputs/try3/all_pdb/design2_n5.pdb (deflated 78%)
adding: outputs/try3/all_pdb/design1_n5.pdb (deflated 77%)
adding: outputs/try3/best_design2.pdb (deflated 78%)
adding: outputs/try3/best_design1.pdb (deflated 77%)
adding: outputs/try3/mpnn_results.csv (deflated 50%)
adding: outputs/try3/design.fasta (deflated 60%)
adding: outputs/try3_0.pdb (deflated 76%)
adding: outputs/try3_0.trb (deflated 15%)
adding: outputs/try3_1.pdb (deflated 76%)
adding: outputs/try3_1.trb (deflated 15%)
adding: outputs/try3_2.pdb (deflated 76%)
adding: outputs/try3_2.trb (deflated 15%)
adding: outputs/try3_3.pdb (deflated 76%)
adding: outputs/try3_3.trb (deflated 15%)
adding: outputs/traj/try3_0_pX0_traj.pdb (deflated 77%)
adding: outputs/traj/try3_0_Xt-1_traj.pdb (deflated 78%)
adding: outputs/traj/try3_1_pX0_traj.pdb (deflated 77%)
adding: outputs/traj/try3_1_Xt-1_traj.pdb (deflated 78%)
adding: outputs/traj/try3_2_pX0_traj.pdb (deflated 77%)
adding: outputs/traj/try3_2_Xt-1_traj.pdb (deflated 78%)
adding: outputs/traj/try3_3_pX0_traj.pdb (deflated 77%)
adding: outputs/traj/try3_3_Xt-1_traj.pdb (deflated 78%)
```

⌄ **Instructions**

Use `contigs` to define continious chains. Use a `:` to define multiple contigs and a `/` to define mutliple segments within a contig. For example:

Could not connect to the reCAPTCHA service. Please check your internet connection and reload to get a reCAPTCHA challenge.