

# Browse demo

⌵ Sort by pLDDT

⌵ Sort by name

🔄 Refresh

Name	Structure	pLDDT	MSA	Annotation
CP00000106	<div>PDBCIF</div>	98.23	A3M	Thioredoxin
CP00004462	<div>PDBCIF</div>	98.10	A3M	retinal dehydrogenase 2-like isoform X1
CP00001235	<div>PDBCIF</div>	98.04	A3M	Glutathione transferase
CP00000602	<div>PDBCIF</div>	97.99	A3M	Peptidyl-prolyl cis-trans isomerase
CP00004464	<div>PDBCIF</div>	97.99	A3M	aldehyde dehydrogenase X, mitochondrial
CP00002762	<div>PDBCIF</div>	97.98	A3M	Glyceraldehyde-3-phosphate dehydrogenase
CP00000604	<div>PDBCIF</div>	97.96	A3M	Peptidyl-prolyl cis-trans isomerase
CP00001477	<div>PDBCIF</div>	97.94	A3M	Type 1 glutamine amidotransferase domain-containing protein
CP00001394	<div>PDBCIF</div>	97.93	A3M	Type 1 glutamine amidotransferase domain-containing protein
CP00001479	<div>PDBCIF</div>	97.92	A3M	Type 1 glutamine amidotransferase domain-containing protein
CP00000098	<div>PDBCIF</div>	97.90	A3M	Uncharacterized protein
CP00002573	<div>PDBCIF</div>	97.89	A3M	Transaldolase
CP00000606	<div>PDBCIF</div>	97.87	A3M	Peptidyl-prolyl cis-trans isomerase
CP00000596	<div>PDBCIF</div>	97.87	A3M	Peptidyl-prolyl cis-trans isomerase
CP00000366	<div>PDBCIF</div>	97.86	A3M	Profilin
CP00000510	<div>PDBCIF</div>	97.84	A3M	Superoxide dismutase [Cu-Zn]

## Generate command for importing

System

ColabFold

Repository

demo

Naming mode

0: Use prefix

Path to data

/tmp/data

Path to python3

/usr/bin/python3

Path to MineProt scripts

/toolkit/scripts

Parameters

☒ --zip

☒ --amber

Generate

```
cd ./toolkit/scripts

# If your data are raw outputs from colabfold, run:

colabfold/import.sh /tmp/data --repo demo \
--name-mode 0 \
--zip \
--relax \
--python /usr/bin/python3 \
--url http://223.3.59.192

# If your data have been preprocessed by colabfold/transform.py, run:

/usr/bin/python3 import2es.py -n demo -i /tmp/data -a --url http://223.3.59.192/api/es
/usr/bin/python3 import2repo.py -n demo -i /tmp/data --url http://223.3.59.192/api/import2repo/
```