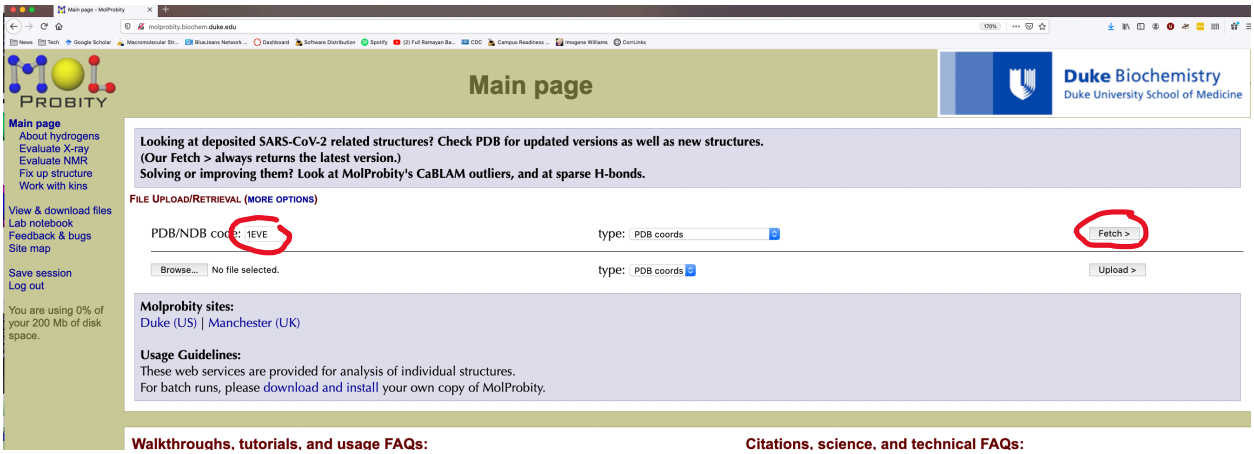
Main page
PROBITY
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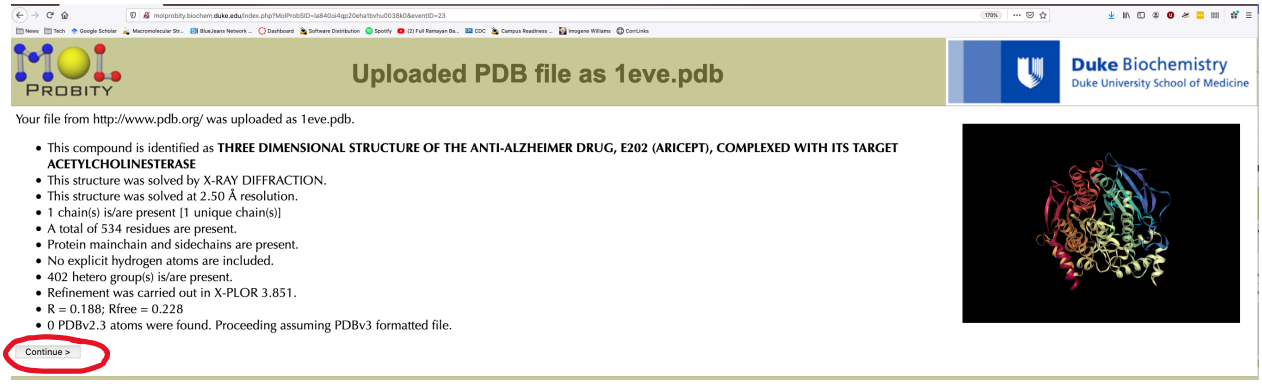
Log out
You are using 0% of your 200 Mb of disk space.
Looking at deposited SARS-CoV-2 related structures? Check PDB for updated versions as well as new structures.
(Our Fetch > always returns the latest version.)
Solving or improving them? Look at MolProbity's CaBLAM outliers, and at sparse H-bonds.
FILE UPLOAD/RETRIEVAL (MORE OPTIONS)
PDB/NDB code: 1EVE
type: PDB coords
Fetch >
Browse... No file selected.
type: PDB coords
Upload >
Molprobity sites:
Duke (US) | Manchester (UK)
Usage Guidelines:
These web services are provided for analysis of individual structures.
For batch runs, please download and install your own copy of MolProbity.
Walkthroughs, tutorials, and usage FAQs:
Citations, science, and technical FAQs:


Uploaded PDB file as 1eve.pdb
PROBITY
Duke Biochemistry
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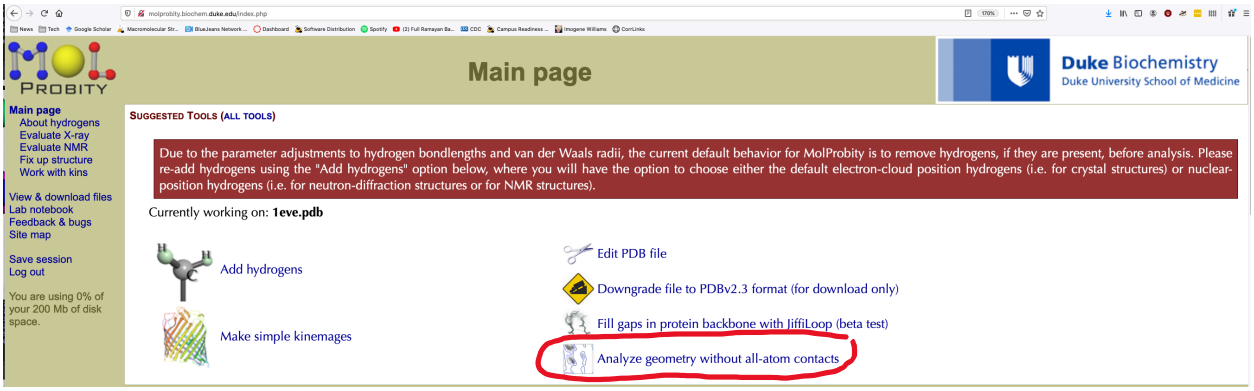
Your file from http://www.pdb.org/ was uploaded as 1eve.pdb.
This compound is identified as THREE DIMENSIONAL STRUCTURE OF THE ANTI-ALZHEIMER DRUG, E202 (ARICEPT), COMPLEXED WITH ITS TARGET ACETYLCHOLINESTERASE
This structure was solved by X-RAY DIFFRACTION.
This structure was solved at 2.50 Å resolution.
1 chain(s) is/are present [1 unique chain(s)]
A total of 534 residues are present.
Protein mainchain and sidechains are present.
No explicit hydrogen atoms are included.
402 hetero group(s) is/are present.
Refinement was carried out in X-PLOR 3.851.
R = 0.188; Rfree = 0.228
0 PDBv2.3 atoms were found. Proceeding assuming PDBv3 formatted file.
Continue >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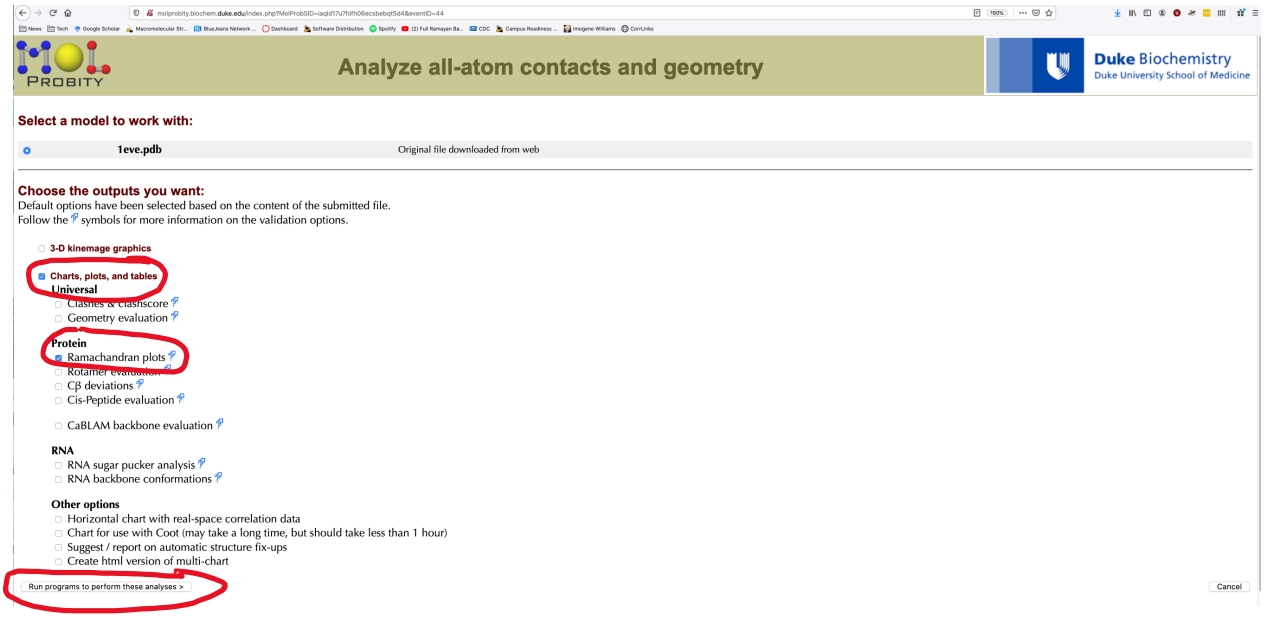
You are using 0% of your 200 Mb of disk space.
SUGGESTED TOOLS (ALL TOOLS)
Due to the parameter adjustments to hydrogen bondlengths and van der Waals radii, the current default behavior for MolProbity is to remove hydrogens, if they are present, before analysis. Please re-add hydrogens using the "Add hydrogens" option below, where you will have the option to choose either the default electron-cloud position hydrogens (i.e. for crystal structures) or nuclear-position hydrogens (i.e. for neutron-diffraction structures or for NMR structures).
Currently working on: 1eve.pdb
Add hydrogens
Make simple kinemages
Edit PDB file
Downgrade file to PDBv2.3 format (for download only)
Fill gaps in protein backbone with JiffiLoop (beta test)
Analyze geometry without all-atom contacts


MolProbity
Analyze all-atom contacts and geometry
Duke Biochemistry
Duke University School of Medicine
Select a model to work with:
1eve.pdb
Original file downloaded from web
Choose the outputs you want:
Default options have been selected based on the content of the submitted file.
Follow the symbols for more information on the validation options.
3-D kinemage graphics
Universal
Clashes
Hydrogen bonds
van der Waals contacts
Geometry evaluation
Protein
Ramachandran plots
Rotamer evaluation
Cβ deviations
Cis-Peptide evaluation
CaBLAM backbone markup
RNA
RNA sugar pucker analysis
RNA backbone conformations
Other options
Make views of trouble spots even if it takes longer
Alternate conformations
Model colored by B-factors
Model colored by occupancy
Ribbons
Charts, plots, and tables
Clashes & clashscore
Geometry evaluation
Protein
Ramachandran plots
Cβ deviations
Cis-Peptide evaluation
Show cis-nonPro and twisted peptide statistics even if the model has none
CaBLAM backbone evaluation
RNA


MolProbity
Analyze all-atom contacts and geometry
Duke Biochemistry
Duke University School of Medicine
Select a model to work with:
1eve.pdb
Original file downloaded from web
Choose the outputs you want:
Default options have been selected based on the content of the submitted file.
Follow the symbols for more information on the validation options.
3-D kinemage graphics
Charts, plots, and tables
Universal
Clashes & clashscore
Geometry evaluation
Protein
Ramachandran plots
Rotamer evaluation
Cβ deviations
Cis-Peptide evaluation
CaBLAM backbone evaluation
RNA
RNA sugar pucker analysis
RNA backbone conformations
Other options
Horizontal chart with real-space correlation data
Chart for use with Coot (may take a long time, but should take less than 1 hour)
Suggest / report on automatic structure fix-ups
Create html version of multi-chart
Run programs to perform these analyses >
Cancel

Analysis output: geometry for 1eve.pdb

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Summary statistics

Protein Geometry	Ramachandran outliers	0	0.00%	Goal: <0.05%
	Ramachandran favored	501	94.17%	Goal: >98%
	Rama distribution Z-score	-2.20 ± 0.31		Goal: abs(Z score) < 2

In the two column results, the left column gives the raw count, right column gives the percentage.
Key to table colors and cutoffs here:

Multi-criterion visualizations

View (966 bytes)

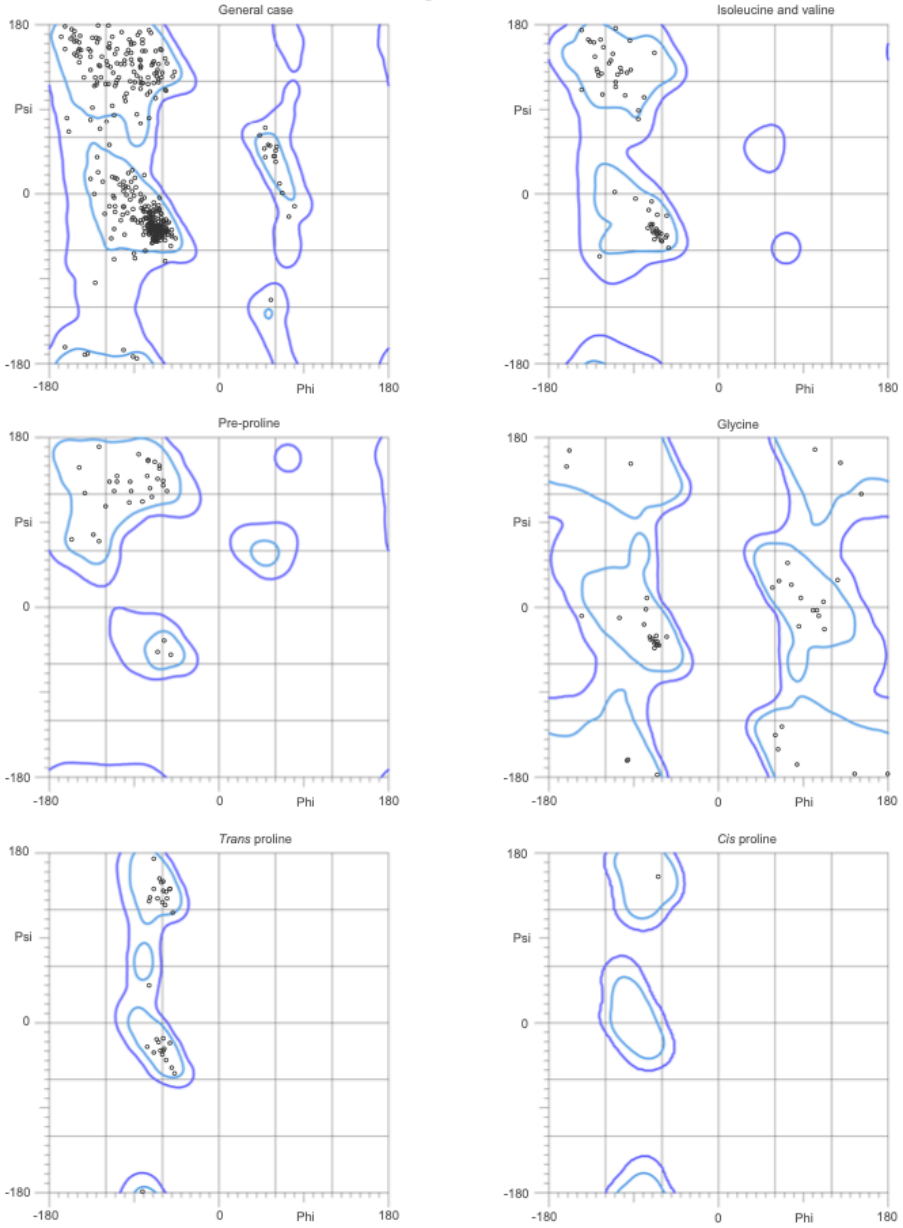
Single-criterion visualizations

- **Ramachandran plot** (435 Kb): View in KiNG | View in NGL | Download
- **Ramachandran plot PDF** (1.7 Mb): View
- **Ramachandran distribution Z-score analysis** (26 Kb): View

Continue >

MolProbity Ramachandran analysis

1eve.pdb, model 1



94.2% (501/532) of all residues were in favored (98%) regions.
100.0% (532/532) of all residues were in allowed (>99.8%) regions.

There were no outliers.