

A

Modeller Comparative
Sequence alignments

aligned_1.fasta

Target sequences

aligned_1.fasta HBA_HUMAN_P69905

Options

Basic Advanced

Make multichain model from multichain template ☐

Modeller license key

Number of models

Basic Advanced

Build models with hydrogens ☐

Include non-water HETATM residues from template ☒

Include water molecules from template ☐

Temporary folder location (optional)

Use fast/approximate mode (produces only one model) ☐

Publications using Modeller results should cite:
A. Sali and T.L. Blundell.
Comparative protein modelling by satisfaction of spatial restraints.
J. Mol. Biol. 234, 779-815, 1993.

Help Cancel OK

B

Modeller Results

	Model	GA341	zDOPE
1	#3.1	1	-1.19111
2	#3.2	1	-1.16015
3	#3.3	1	-1.19806
4	#3.4	1	-1.21929
5	#3.5	1	-1.166

C

Models

Name	ID		eye	green
axis_input.bild	1		<input checked="" type="checkbox"/>	<input type="checkbox"/>
1pbx.cif	2		<input checked="" type="checkbox"/>	<input type="checkbox"/>
HBA_HUMAN_P69905 ...	3		<input checked="" type="checkbox"/>	<input type="checkbox"/>
HBA_HUMAN_P69905	3.1		<input checked="" type="checkbox"/>	<input type="checkbox"/>
HBA_HUMAN_P69905	3.3		<input checked="" type="checkbox"/>	<input type="checkbox"/>
HBA_HUMAN_P69905	3.4		<input checked="" type="checkbox"/>	<input type="checkbox"/>
HBA_HUMAN_P69905	3.5		<input checked="" type="checkbox"/>	<input type="checkbox"/>
HBA_HUMAN_P69905	4		<input checked="" type="checkbox"/>	<input type="checkbox"/>

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