



wwPDB EM Validation Summary Report ⓘ

Aug 18, 2026 – 04:26 PM EDT

PDB ID : 9NQL / pdb_00009nql
EMDB ID : EMD-49668
Title : Cryo electron microscopic analysis of the adduct of syringolin analog with the Mtb 20S proteasome
Authors : Gu, X.; Yu, Z.
Deposited on : 2025-03-12
Resolution : 2.16 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

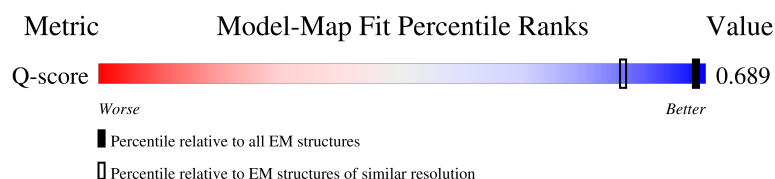
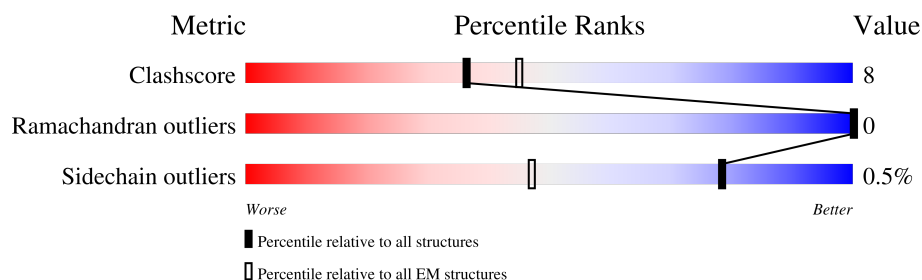
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.16 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



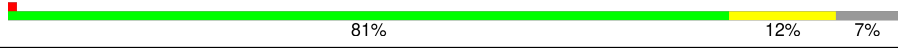
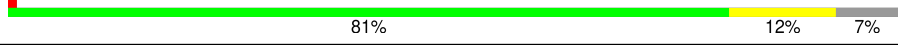
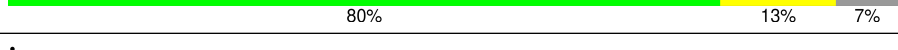
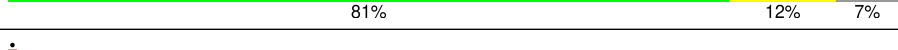
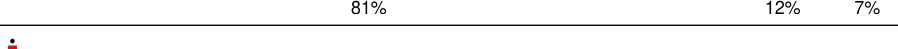
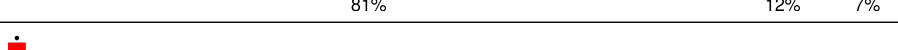
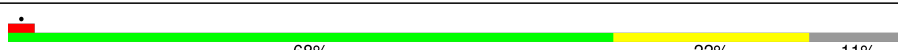
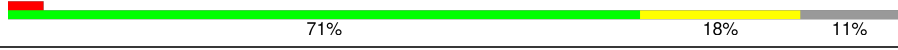
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2609 (1.67 - 2.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	240	
1	2	240	
1	O	240	
1	P	240	

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Mol	Chain	Length	Quality of chain
1	Q	240	
1	R	240	
1	S	240	
1	T	240	
1	U	240	
1	V	240	
1	W	240	
1	X	240	
1	Y	240	
1	Z	240	
2	A	240	
2	B	240	
2	C	240	
2	D	240	
2	E	240	
2	F	240	
2	G	240	
2	H	240	
2	I	240	
2	J	240	
2	K	240	
2	L	240	
2	M	240	
2	N	240	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 93515 atoms, of which 46763 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	2	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	O	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	P	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	Q	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	R	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	S	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	T	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	U	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	V	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	W	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	X	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	Y	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		
1	Z	224	Total	C	H	N	O	S	0	0
			3286	1032	1639	284	326	5		

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	535	HIS	-	expression tag	UNP A5U4D6
1	536	HIS	-	expression tag	UNP A5U4D6

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Chain	Residue	Modelled	Actual	Comment	Reference
1	537	HIS	-	expression tag	UNP A5U4D6
1	538	HIS	-	expression tag	UNP A5U4D6
1	539	HIS	-	expression tag	UNP A5U4D6
1	540	HIS	-	expression tag	UNP A5U4D6
2	535	HIS	-	expression tag	UNP A5U4D6
2	536	HIS	-	expression tag	UNP A5U4D6
2	537	HIS	-	expression tag	UNP A5U4D6
2	538	HIS	-	expression tag	UNP A5U4D6
2	539	HIS	-	expression tag	UNP A5U4D6
2	540	HIS	-	expression tag	UNP A5U4D6
O	535	HIS	-	expression tag	UNP A5U4D6
O	536	HIS	-	expression tag	UNP A5U4D6
O	537	HIS	-	expression tag	UNP A5U4D6
O	538	HIS	-	expression tag	UNP A5U4D6
O	539	HIS	-	expression tag	UNP A5U4D6
O	540	HIS	-	expression tag	UNP A5U4D6
P	535	HIS	-	expression tag	UNP A5U4D6
P	536	HIS	-	expression tag	UNP A5U4D6
P	537	HIS	-	expression tag	UNP A5U4D6
P	538	HIS	-	expression tag	UNP A5U4D6
P	539	HIS	-	expression tag	UNP A5U4D6
P	540	HIS	-	expression tag	UNP A5U4D6
Q	535	HIS	-	expression tag	UNP A5U4D6
Q	536	HIS	-	expression tag	UNP A5U4D6
Q	537	HIS	-	expression tag	UNP A5U4D6
Q	538	HIS	-	expression tag	UNP A5U4D6
Q	539	HIS	-	expression tag	UNP A5U4D6
Q	540	HIS	-	expression tag	UNP A5U4D6
R	535	HIS	-	expression tag	UNP A5U4D6
R	536	HIS	-	expression tag	UNP A5U4D6
R	537	HIS	-	expression tag	UNP A5U4D6
R	538	HIS	-	expression tag	UNP A5U4D6
R	539	HIS	-	expression tag	UNP A5U4D6
R	540	HIS	-	expression tag	UNP A5U4D6
S	535	HIS	-	expression tag	UNP A5U4D6
S	536	HIS	-	expression tag	UNP A5U4D6
S	537	HIS	-	expression tag	UNP A5U4D6
S	538	HIS	-	expression tag	UNP A5U4D6
S	539	HIS	-	expression tag	UNP A5U4D6
S	540	HIS	-	expression tag	UNP A5U4D6
T	535	HIS	-	expression tag	UNP A5U4D6
T	536	HIS	-	expression tag	UNP A5U4D6

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Chain	Residue	Modelled	Actual	Comment	Reference
T	537	HIS	-	expression tag	UNP A5U4D6
T	538	HIS	-	expression tag	UNP A5U4D6
T	539	HIS	-	expression tag	UNP A5U4D6
T	540	HIS	-	expression tag	UNP A5U4D6
U	535	HIS	-	expression tag	UNP A5U4D6
U	536	HIS	-	expression tag	UNP A5U4D6
U	537	HIS	-	expression tag	UNP A5U4D6
U	538	HIS	-	expression tag	UNP A5U4D6
U	539	HIS	-	expression tag	UNP A5U4D6
U	540	HIS	-	expression tag	UNP A5U4D6
V	535	HIS	-	expression tag	UNP A5U4D6
V	536	HIS	-	expression tag	UNP A5U4D6
V	537	HIS	-	expression tag	UNP A5U4D6
V	538	HIS	-	expression tag	UNP A5U4D6
V	539	HIS	-	expression tag	UNP A5U4D6
V	540	HIS	-	expression tag	UNP A5U4D6
W	535	HIS	-	expression tag	UNP A5U4D6
W	536	HIS	-	expression tag	UNP A5U4D6
W	537	HIS	-	expression tag	UNP A5U4D6
W	538	HIS	-	expression tag	UNP A5U4D6
W	539	HIS	-	expression tag	UNP A5U4D6
W	540	HIS	-	expression tag	UNP A5U4D6
X	535	HIS	-	expression tag	UNP A5U4D6
X	536	HIS	-	expression tag	UNP A5U4D6
X	537	HIS	-	expression tag	UNP A5U4D6
X	538	HIS	-	expression tag	UNP A5U4D6
X	539	HIS	-	expression tag	UNP A5U4D6
X	540	HIS	-	expression tag	UNP A5U4D6
Y	535	HIS	-	expression tag	UNP A5U4D6
Y	536	HIS	-	expression tag	UNP A5U4D6
Y	537	HIS	-	expression tag	UNP A5U4D6
Y	538	HIS	-	expression tag	UNP A5U4D6
Y	539	HIS	-	expression tag	UNP A5U4D6
Y	540	HIS	-	expression tag	UNP A5U4D6
Z	535	HIS	-	expression tag	UNP A5U4D6
Z	536	HIS	-	expression tag	UNP A5U4D6
Z	537	HIS	-	expression tag	UNP A5U4D6
Z	538	HIS	-	expression tag	UNP A5U4D6
Z	539	HIS	-	expression tag	UNP A5U4D6
Z	540	HIS	-	expression tag	UNP A5U4D6

- Molecule 2 is a protein called Proteasome subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	A	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	B	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	C	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	D	213	Total	C	H	N	O	S	0	0
			3297	1030	1652	301	310	4		
2	E	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	F	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	G	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	H	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	I	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	J	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	K	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	L	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	M	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		
2	N	214	Total	C	H	N	O	S	0	0
			3316	1036	1663	302	311	4		

There are 14 discrepancies between the modelled and reference sequences:

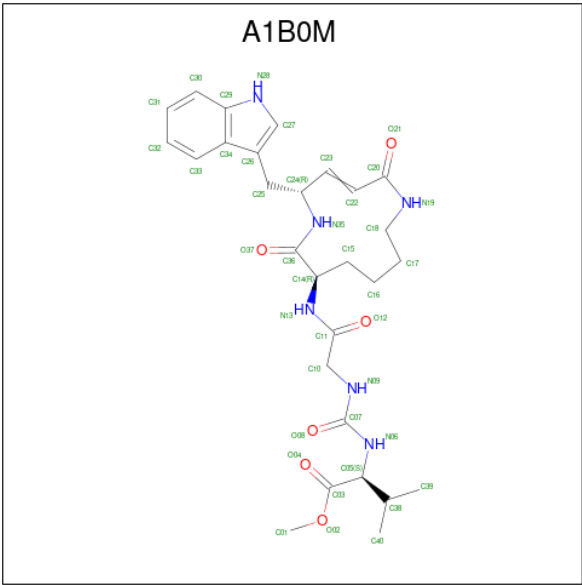
Chain	Residue	Modelled	Actual	Comment	Reference
A	9	MET	-	initiating methionine	UNP A5U4D5
B	9	MET	-	initiating methionine	UNP A5U4D5
C	9	MET	-	initiating methionine	UNP A5U4D5
D	9	MET	-	initiating methionine	UNP A5U4D5
E	9	MET	-	initiating methionine	UNP A5U4D5
F	9	MET	-	initiating methionine	UNP A5U4D5
G	9	MET	-	initiating methionine	UNP A5U4D5
H	9	MET	-	initiating methionine	UNP A5U4D5
I	9	MET	-	initiating methionine	UNP A5U4D5
J	9	MET	-	initiating methionine	UNP A5U4D5
K	9	MET	-	initiating methionine	UNP A5U4D5
L	9	MET	-	initiating methionine	UNP A5U4D5

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Chain	Residue	Modelled	Actual	Comment	Reference
M	9	MET	-	initiating methionine	UNP A5U4D5
N	9	MET	-	initiating methionine	UNP A5U4D5

- Molecule 3 is methyl N-{[2-((3Z,5R,8R)-5-[(1H-indol-3-yl)methyl]-2,7-dioxo-1,6-diazacyc lododec-3-en-8-yl)amino]-2-oxoethyl}carbamoyl}-L-valinate (CCD ID: A1B0M) (formula: C₂₈H₃₈N₆O₆).



Mol	Chain	Residues	Atoms					AltConf
3	1	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	2	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	O	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	P	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	Q	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	R	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	S	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	T	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	U	1	Total	C	H	N	O	0
			79	28	39	6	6	

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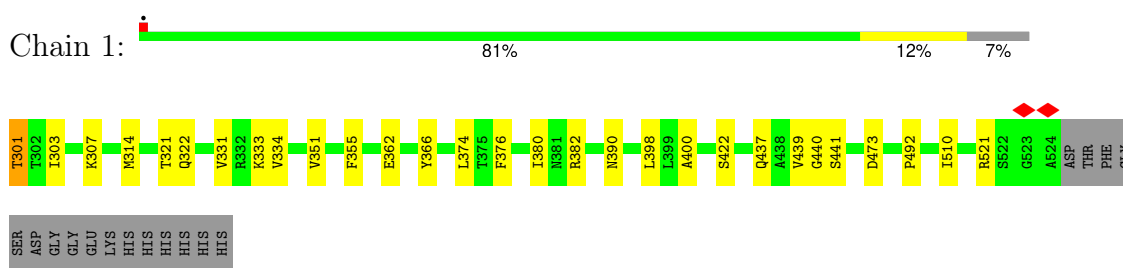
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Mol	Chain	Residues	Atoms					AltConf
3	V	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	W	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	X	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	Y	1	Total	C	H	N	O	0
			79	28	39	6	6	
3	Z	1	Total	C	H	N	O	0
			79	28	39	6	6	

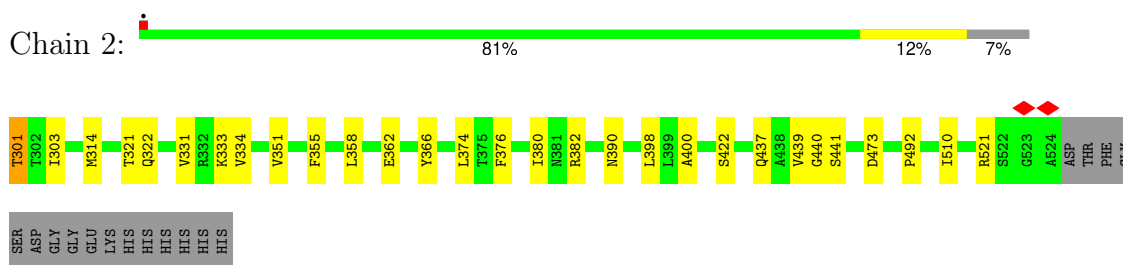
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

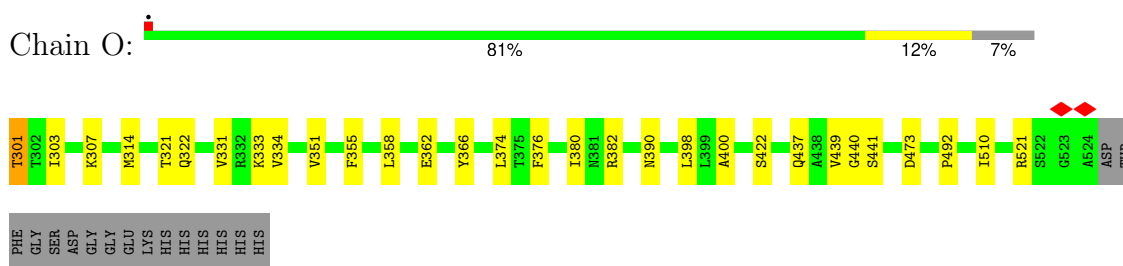
- Molecule 1: Proteasome subunit beta



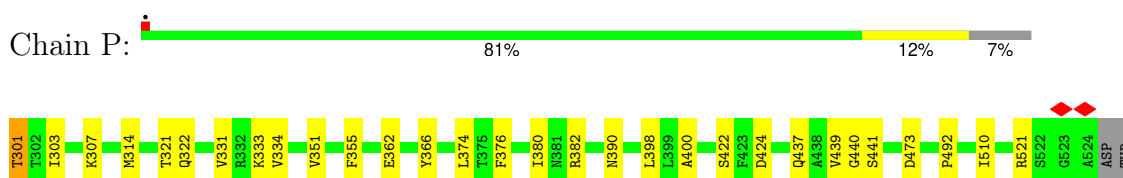
- Molecule 1: Proteasome subunit beta



- Molecule 1: Proteasome subunit beta



- Molecule 1: Proteasome subunit beta



PHE
GLY
SER
ASP
GLY
GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome subunit beta

Chain Q:  81% 12% 7%

T301 T302 T303 K307 K314 T321 Q322 V331 R332 K333 V334 V351 F355 E362 Y366 L374 T375 F376 N380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR PHE GLY

SER
ASP
GLY
GLY
LYS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome subunit beta

Chain R:  81% 12% 7%

T301 T302 T303 K314 T321 Q322 V331 R332 K333 V334 V351 F355 L358 E362 Y366 L374 T375 F376 N380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR PHE GLY

SER
ASP
GLY
GLY
LYS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome subunit beta

Chain S:  81% 12% 7%

T301 T302 T303 K307 K314 T321 Q322 V331 R332 K333 V334 V351 F355 E362 Y366 L374 T375 F376 A377 G378 K379 N380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR

PHE
GLY
SER
ASP
GLY
GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome subunit beta

Chain T:  81% 12% 7%

T301 T302 T303 K307 K314 T321 Q322 V331 R332 K333 V334 V351 F355 E362 Y366 L374 T375 F376 A377 G378 K379 N380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR

PHE
GLY
SER
ASP
GLY
GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome subunit beta

Chain U:  81% 12% 7%

T301 T302 T303 K307 K314 T321 Q322 V331 R332 K333 V334 V351 F355 E362 Y366 L374 T375 F376 A377 G378 K379 N380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR

PHE
GLY
SER
ASP
GLY
GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome subunit beta

Chain V:  81% 12% 7%

T301 T302 T303 K307 M314 T321 Q322 V331 F332 K333 V334 V351 F355 E362 Y366 L374 T375 F376 I380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR PHE GLY

SER
ASP
GLY
GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome subunit beta

Chain W:  80% 13% 7%

T301 T302 T303 K307 M314 T321 Q322 S327 V331 R332 K333 V334 V351 F355 F358 E362 Y366 L374 T375 F376 I380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR PHE GLY

G523 A524 ASP THR PHE GLY SER ASP GLY GLU LYS HIS HIS K333 V334 V351 F355 F358 E362 Y366 L374 T375 F376 I380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR PHE GLY

• Molecule 1: Proteasome subunit beta

Chain X:  81% 12% 7%

T301 T302 T303 M314 T321 Q322 V331 R332 K333 V334 V351 F355 F358 E362 Y366 L374 T375 F376 I380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR PHE GLY

SER
ASP
GLY
GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome subunit beta

Chain Y:  81% 12% 7%

T301 T302 T303 K307 M314 T321 Q322 V331 R332 K333 V334 V351 F355 E362 Y366 E370 L374 T375 F376 I380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR PHE GLY

PHE
GLY
SER
ASP
GLY
GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome subunit beta

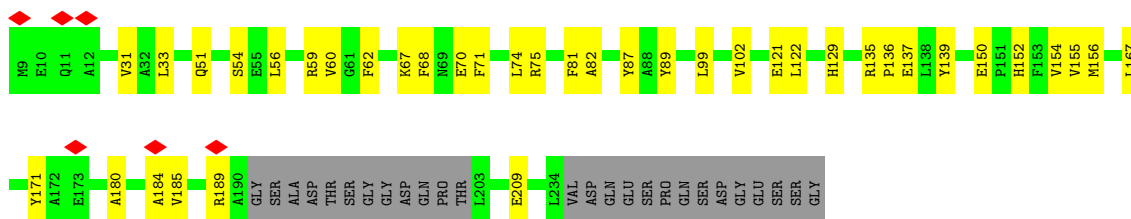
Chain Z:  81% 12% 7%

T301 T302 T303 K307 M314 T321 Q322 V331 R332 K333 V334 V351 F355 E362 Y366 L374 T375 F376 I380 N381 R382 N390 L398 L399 A400 S422 Q437 A438 V439 G440 S441 D473 P492 I510 R521 S522 G523 A524 ASP THR PHE GLY

SER
ASP
GLY
GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS
HIS

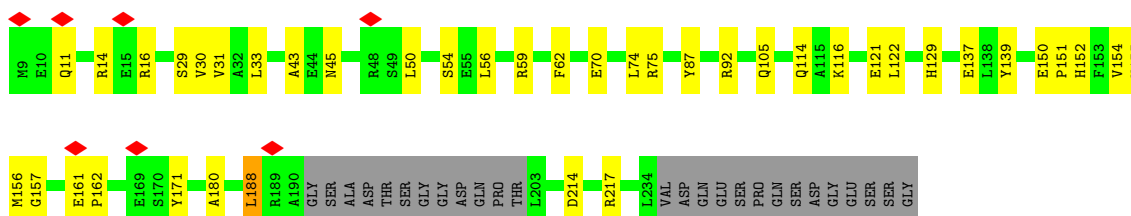
• Molecule 2: Proteasome subunit alpha

Chain A: 



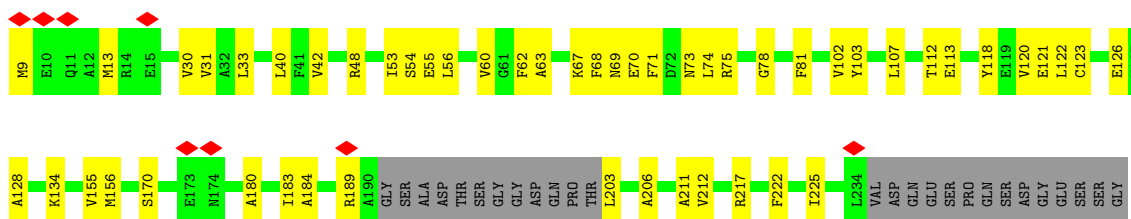
• Molecule 2: Proteasome subunit alpha

Chain B: 



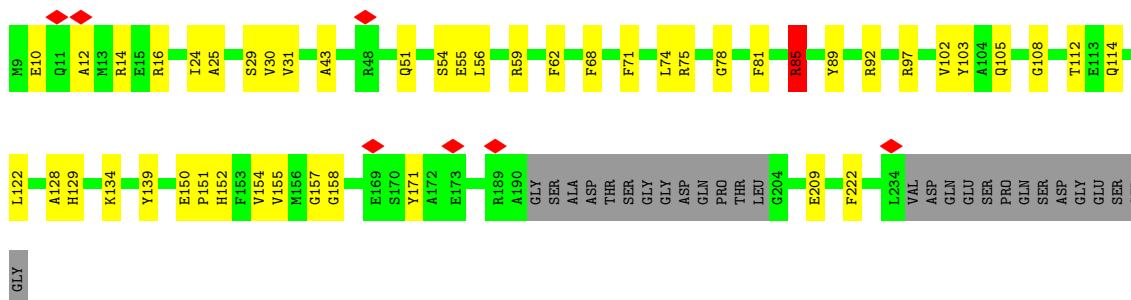
• Molecule 2: Proteasome subunit alpha

Chain C: 

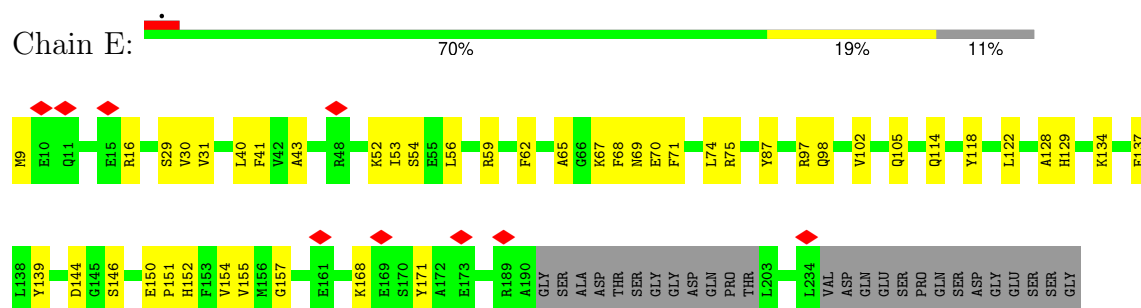


• Molecule 2: Proteasome subunit alpha

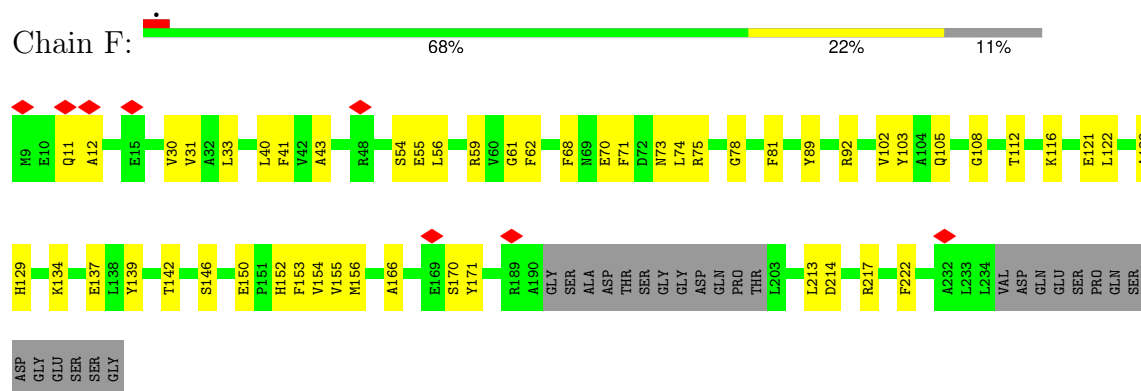
Chain D: 



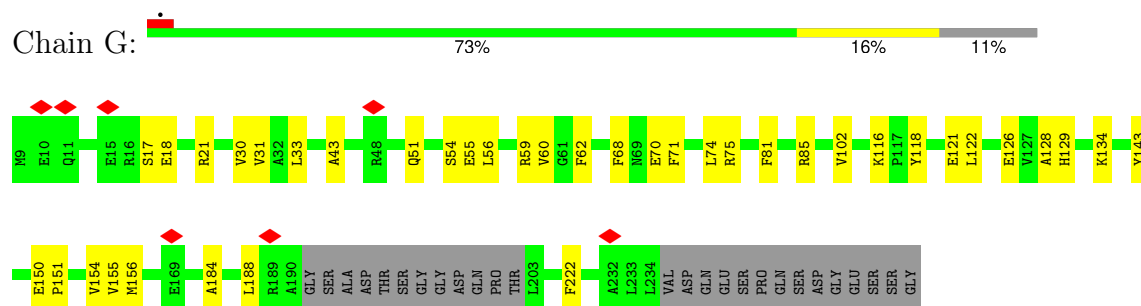
- Molecule 2: Proteasome subunit alpha



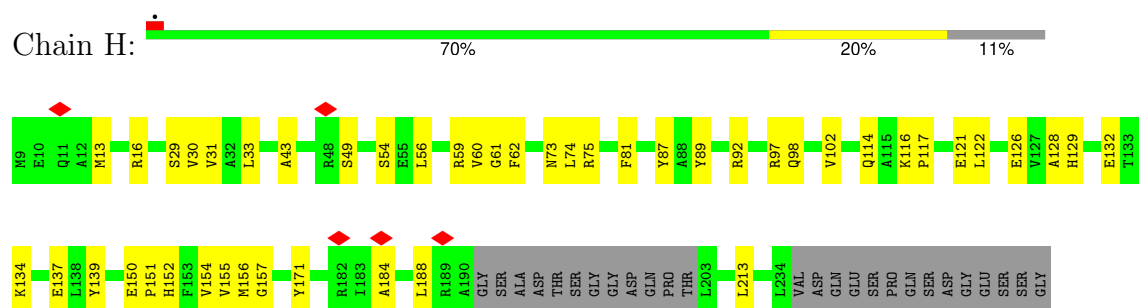
- Molecule 2: Proteasome subunit alpha



- Molecule 2: Proteasome subunit alpha

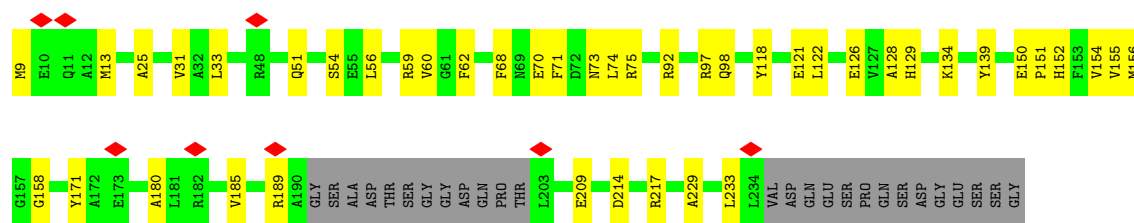


- Molecule 2: Proteasome subunit alpha

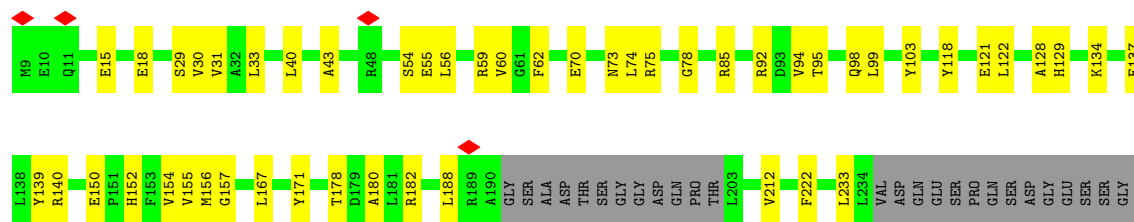


- Molecule 2: Proteasome subunit alpha

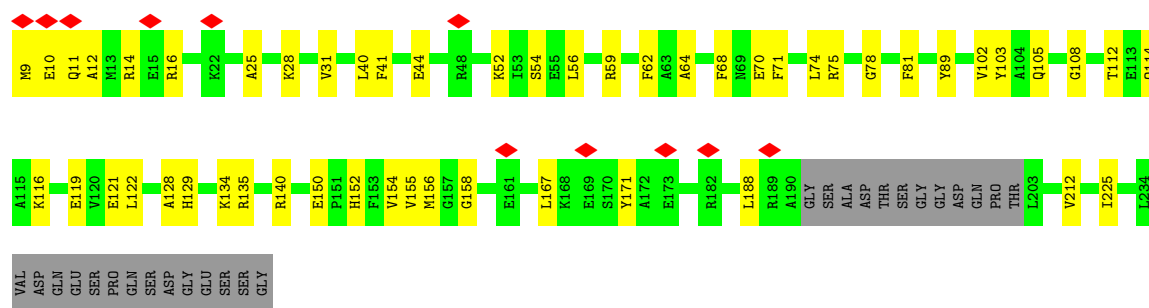




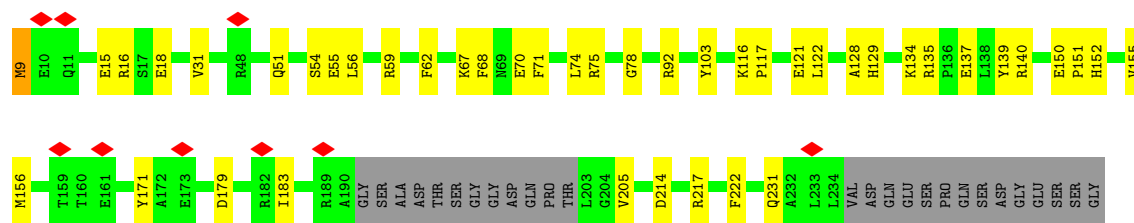
• Molecule 2: Proteasome subunit alpha



• Molecule 2: Proteasome subunit alpha

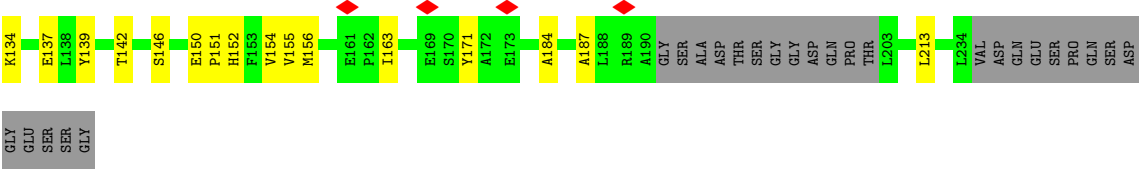


• Molecule 2: Proteasome subunit alpha

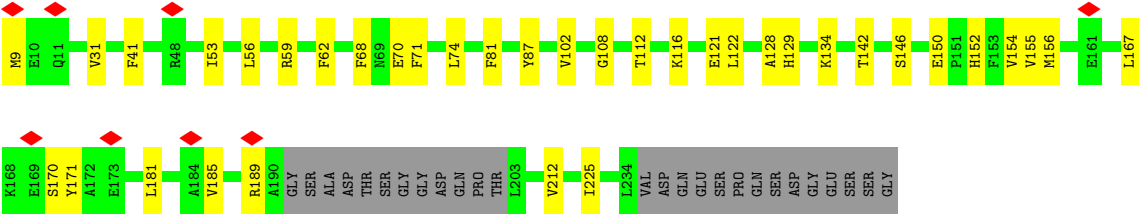


• Molecule 2: Proteasome subunit alpha





● Molecule 2: Proteasome subunit alpha



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	375837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	103.592	Depositor
Minimum map value	-59.854	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	3.416	Depositor
Recommended contour level	8	Depositor
Map size ($\text{\AA}$)	353.28, 353.28, 353.28	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.92, 0.92, 0.92	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: A1B0M

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.35	0/1671	0.49	0/2266
1	2	0.35	0/1671	0.49	0/2266
1	O	0.35	0/1671	0.49	0/2266
1	P	0.35	0/1671	0.49	0/2266
1	Q	0.35	0/1671	0.49	0/2266
1	R	0.35	0/1671	0.49	0/2266
1	S	0.35	0/1671	0.49	0/2266
1	T	0.35	0/1671	0.49	0/2266
1	U	0.35	0/1671	0.49	0/2266
1	V	0.35	0/1671	0.49	0/2266
1	W	0.35	0/1671	0.49	0/2266
1	X	0.35	0/1671	0.49	0/2266
1	Y	0.35	0/1671	0.49	0/2266
1	Z	0.35	0/1671	0.49	0/2266
2	A	0.26	0/1677	0.42	0/2264
2	B	0.29	0/1677	0.43	0/2264
2	C	0.28	0/1677	0.49	0/2264
2	D	0.31	0/1669	0.45	1/2253 (0.0%)
2	E	0.32	0/1677	0.49	0/2264
2	F	0.27	0/1677	0.46	0/2264
2	G	0.28	0/1677	0.45	0/2264
2	H	0.27	0/1677	0.44	0/2264
2	I	0.27	0/1677	0.45	0/2264
2	J	0.27	0/1677	0.46	0/2264
2	K	0.30	0/1677	0.51	0/2264
2	L	0.29	0/1677	0.45	0/2264
2	M	0.27	0/1677	0.45	0/2264
2	N	0.27	0/1677	0.46	0/2264
All	All	0.32	0/46864	0.47	1/63409 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	85	ARG	CB-CG-CD	-5.04	99.71	111.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	85	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1647	1639	1637	25	0
1	2	1647	1639	1637	24	0
1	O	1647	1639	1637	25	0
1	P	1647	1639	1637	25	0
1	Q	1647	1639	1637	24	0
1	R	1647	1639	1637	24	0
1	S	1647	1639	1637	25	0
1	T	1647	1639	1637	25	0
1	U	1647	1639	1637	26	0
1	V	1647	1639	1637	24	0
1	W	1647	1639	1637	27	0
1	X	1647	1639	1637	24	0
1	Y	1647	1639	1637	27	0
1	Z	1647	1639	1637	24	0
2	A	1653	1663	1656	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1653	1663	1656	28	0
2	C	1653	1663	1656	34	0
2	D	1645	1652	1645	28	0
2	E	1653	1663	1656	29	0
2	F	1653	1663	1656	32	0
2	G	1653	1663	1656	23	0
2	H	1653	1663	1656	32	0
2	I	1653	1663	1656	26	0
2	J	1653	1663	1656	29	0
2	K	1653	1663	1656	35	0
2	L	1653	1663	1656	28	0
2	M	1653	1663	1656	29	0
2	N	1653	1663	1656	22	0
3	1	40	39	0	4	0
3	2	40	39	0	4	0
3	O	40	39	0	4	0
3	P	40	39	0	4	0
3	Q	40	39	0	4	0
3	R	40	39	0	5	0
3	S	40	39	0	4	0
3	T	40	39	0	4	0
3	U	40	39	0	4	0
3	V	40	39	0	4	0
3	W	40	39	0	4	0
3	X	40	39	0	4	0
3	Y	40	39	0	4	0
3	Z	40	39	0	4	0
All	All	46752	46763	46091	717	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 717 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:301:THR:HG22	1:U:441:SER:H	1.32	0.93
1:Y:301:THR:HG22	1:Y:441:SER:H	1.32	0.93
1:O:301:THR:HG22	1:O:441:SER:H	1.32	0.92
1:2:301:THR:HG22	1:2:441:SER:H	1.32	0.92
1:1:301:THR:HG22	1:1:441:SER:H	1.32	0.92

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	2	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	O	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	P	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	Q	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	R	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	S	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	T	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	U	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	V	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	W	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	X	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	Y	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	Z	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
2	A	210/240 (88%)	205 (98%)	5 (2%)	0	100	100
2	B	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	C	210/240 (88%)	207 (99%)	3 (1%)	0	100	100
2	D	209/240 (87%)	206 (99%)	3 (1%)	0	100	100
2	E	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	F	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	G	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	H	210/240 (88%)	205 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	I	210/240 (88%)	207 (99%)	3 (1%)	0	100	100
2	J	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	K	210/240 (88%)	207 (99%)	3 (1%)	0	100	100
2	L	210/240 (88%)	207 (99%)	3 (1%)	0	100	100
2	M	210/240 (88%)	207 (99%)	3 (1%)	0	100	100
2	N	210/240 (88%)	205 (98%)	5 (2%)	0	100	100
All	All	6047/6720 (90%)	5966 (99%)	81 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	2	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	O	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	P	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	Q	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	R	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	S	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	T	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	U	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	V	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	W	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	X	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	Y	165/178 (93%)	164 (99%)	1 (1%)	78	84
1	Z	165/178 (93%)	164 (99%)	1 (1%)	78	84
2	A	164/184 (89%)	164 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	164/184 (89%)	163 (99%)	1 (1%)	78	84
2	C	164/184 (89%)	164 (100%)	0	100	100
2	D	163/184 (89%)	162 (99%)	1 (1%)	78	84
2	E	164/184 (89%)	164 (100%)	0	100	100
2	F	164/184 (89%)	164 (100%)	0	100	100
2	G	164/184 (89%)	163 (99%)	1 (1%)	78	84
2	H	164/184 (89%)	164 (100%)	0	100	100
2	I	164/184 (89%)	163 (99%)	1 (1%)	78	84
2	J	164/184 (89%)	163 (99%)	1 (1%)	78	84
2	K	164/184 (89%)	163 (99%)	1 (1%)	78	84
2	L	164/184 (89%)	162 (99%)	2 (1%)	63	70
2	M	164/184 (89%)	164 (100%)	0	100	100
2	N	164/184 (89%)	164 (100%)	0	100	100
All	All	4605/5068 (91%)	4583 (100%)	22 (0%)	78	87

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	301	THR
1	V	301	THR
1	U	301	THR
1	W	301	THR
2	J	233	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
2	M	152	HIS
1	T	396	GLN
2	N	98	GLN
1	Q	396	GLN
1	V	396	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	A1B0M	W	601	1	42,42,42	3.09	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	T	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	S	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	X	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	P	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	2	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	Q	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	R	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	U	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	V	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	Y	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	Z	601	1	42,42,42	3.09	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	O	601	1	42,42,42	3.08	14 (33%)	54,56,56	2.93	17 (31%)
3	A1B0M	1	601	1	42,42,42	3.09	14 (33%)	54,56,56	2.93	17 (31%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	A1B0M	W	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	T	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	S	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	X	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	P	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	2	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	Q	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	R	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	U	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	V	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	Y	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	Z	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	O	601	1	-	10/48/48/48	0/2/3/3
3	A1B0M	1	601	1	-	10/48/48/48	0/2/3/3

The worst 5 of 196 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	V	601	A1B0M	C22-C23	14.46	1.64	1.32
3	W	601	A1B0M	C22-C23	14.45	1.64	1.32
3	Z	601	A1B0M	C22-C23	14.44	1.64	1.32
3	P	601	A1B0M	C22-C23	14.43	1.64	1.32
3	1	601	A1B0M	C22-C23	14.43	1.64	1.32

The worst 5 of 238 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Y	601	A1B0M	C25-C24-N35	11.86	128.66	110.53
3	P	601	A1B0M	C25-C24-N35	11.86	128.66	110.53
3	W	601	A1B0M	C25-C24-N35	11.86	128.66	110.53
3	1	601	A1B0M	C25-C24-N35	11.85	128.65	110.53
3	U	601	A1B0M	C25-C24-N35	11.85	128.64	110.53

There are no chirality outliers.

5 of 140 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	1	601	A1B0M	C20-C22-C23-C24
3	1	601	A1B0M	C23-C24-C25-C26

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	1	601	A1B0M	N35-C24-C25-C26
3	1	601	A1B0M	C23-C24-N35-C36
3	1	601	A1B0M	C25-C24-N35-C36

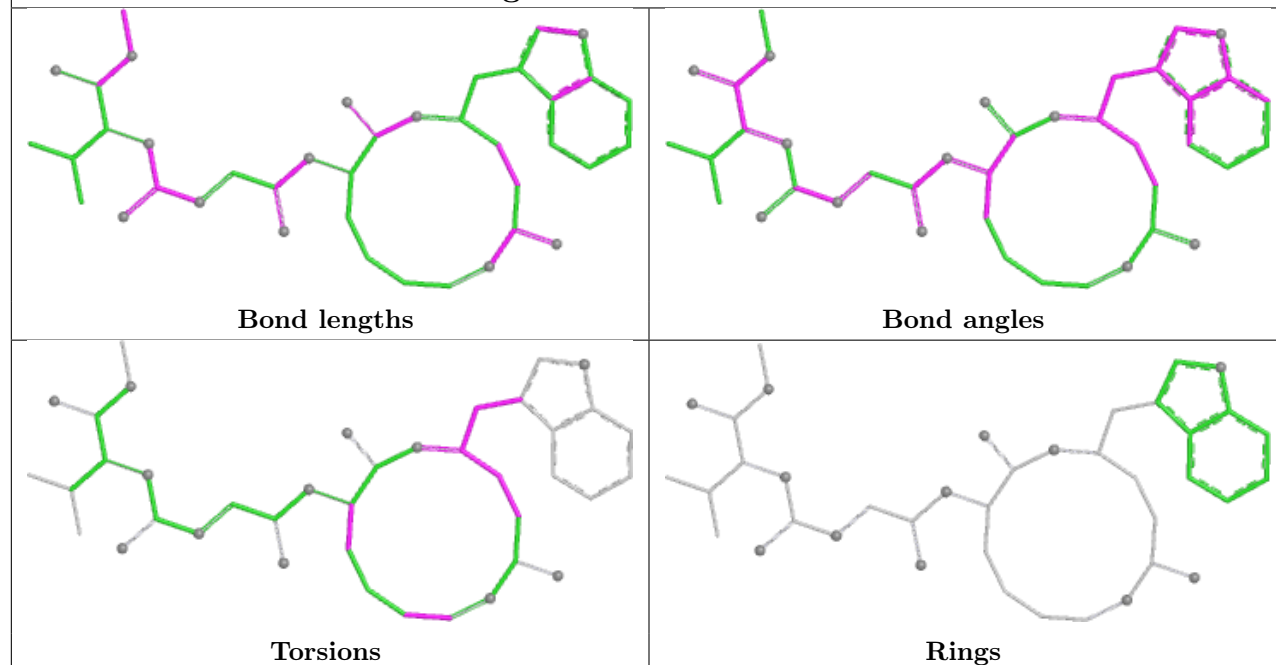
There are no ring outliers.

14 monomers are involved in 57 short contacts:

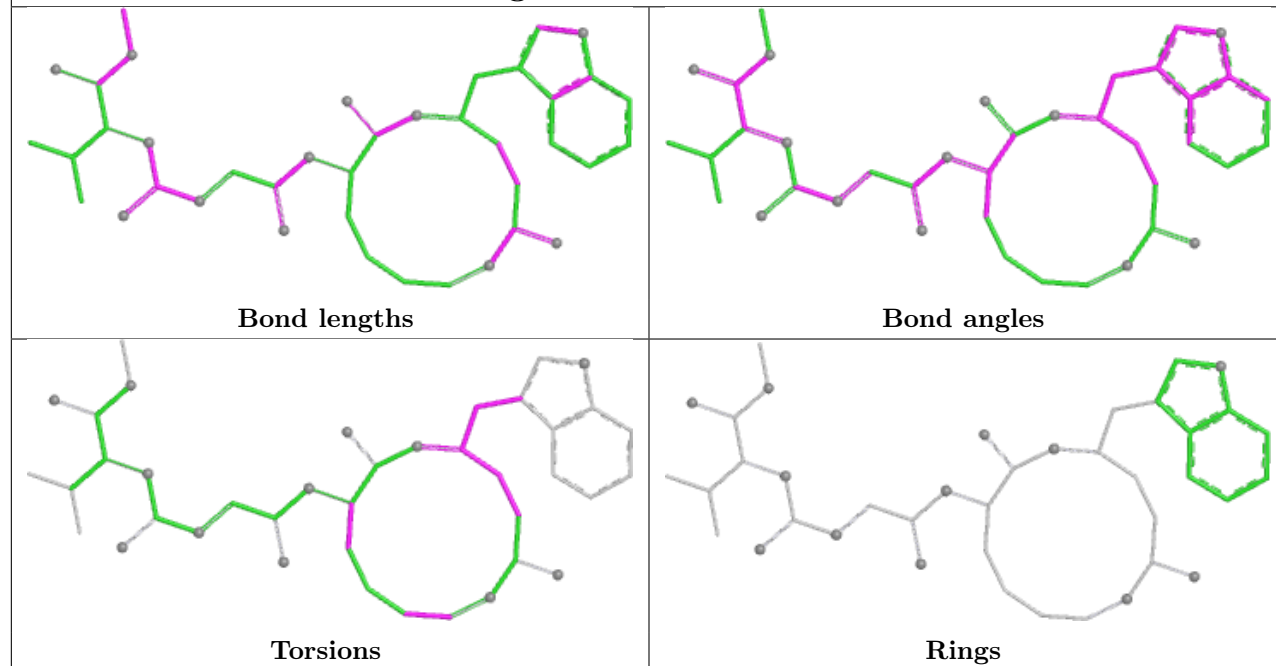
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	W	601	A1B0M	4	0
3	T	601	A1B0M	4	0
3	S	601	A1B0M	4	0
3	X	601	A1B0M	4	0
3	P	601	A1B0M	4	0
3	2	601	A1B0M	4	0
3	Q	601	A1B0M	4	0
3	R	601	A1B0M	5	0
3	U	601	A1B0M	4	0
3	V	601	A1B0M	4	0
3	Y	601	A1B0M	4	0
3	Z	601	A1B0M	4	0
3	O	601	A1B0M	4	0
3	1	601	A1B0M	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

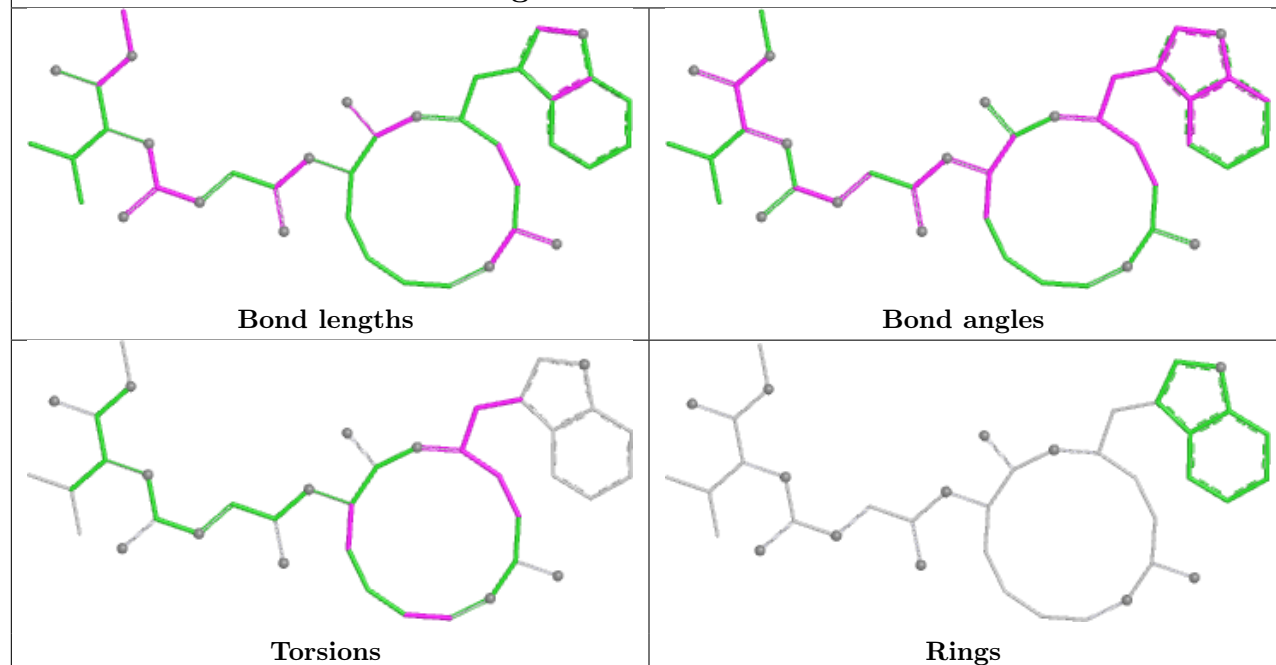
Ligand A1B0M W 601



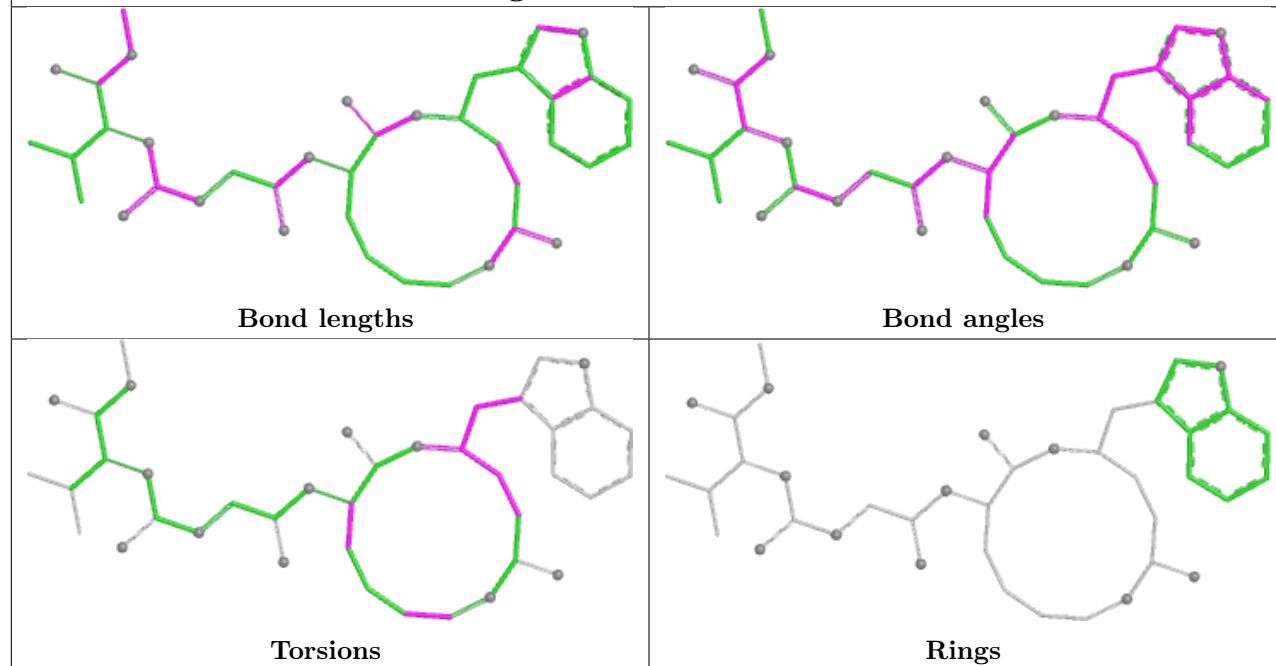
Ligand A1B0M T 601



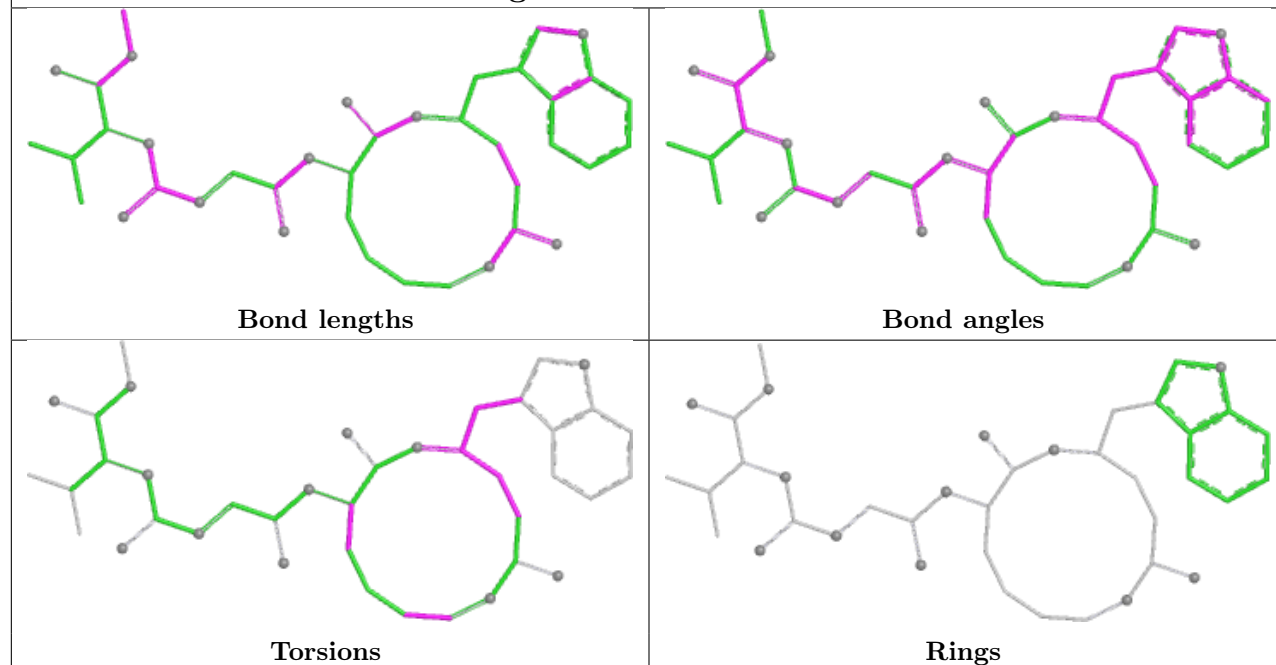
Ligand A1B0M S 601



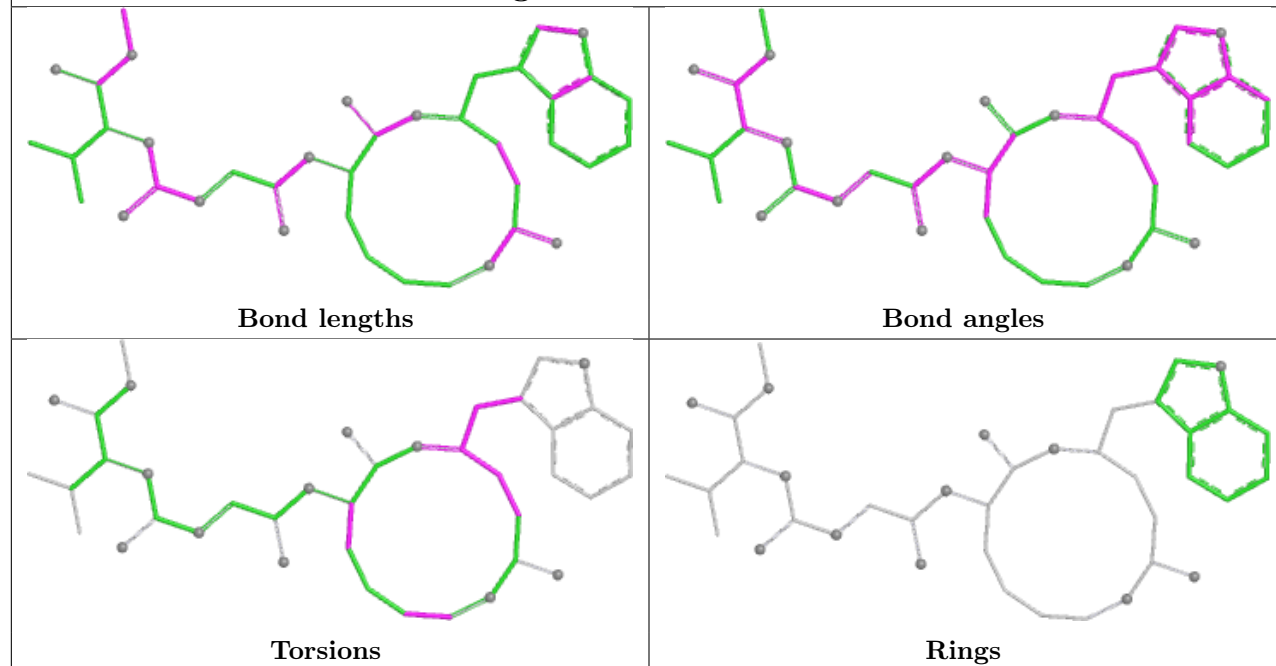
Ligand A1B0M X 601

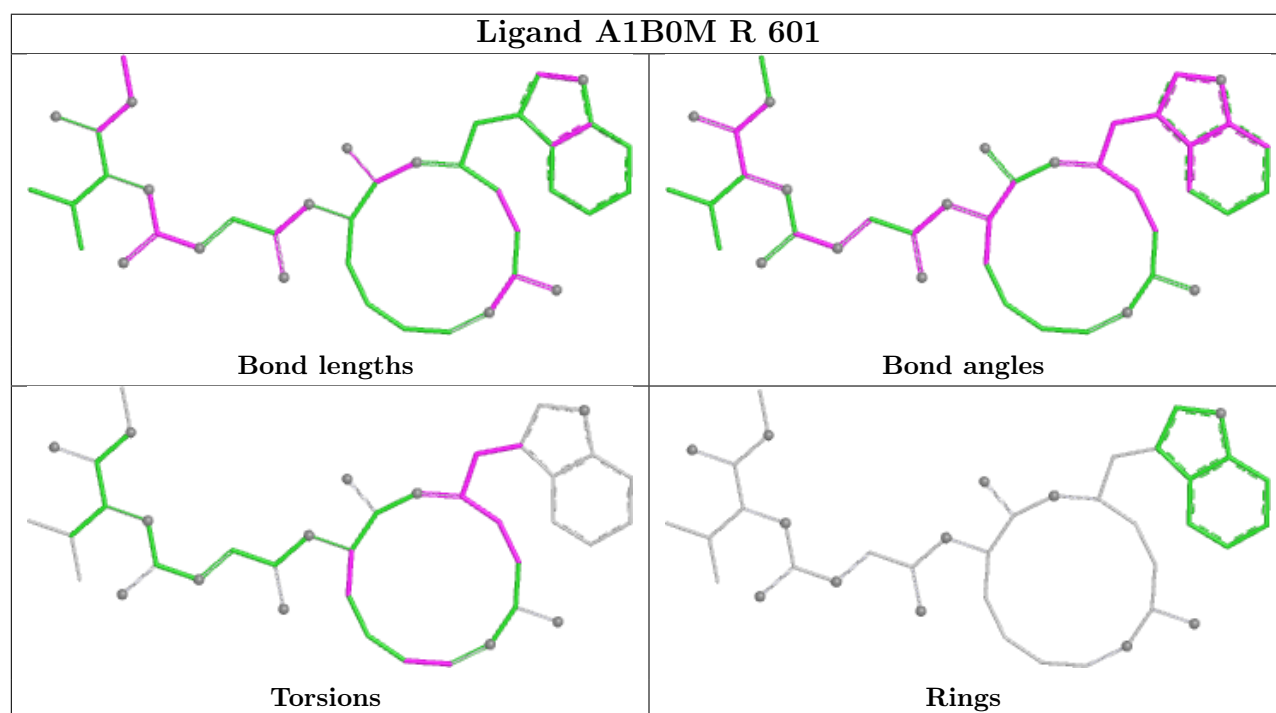
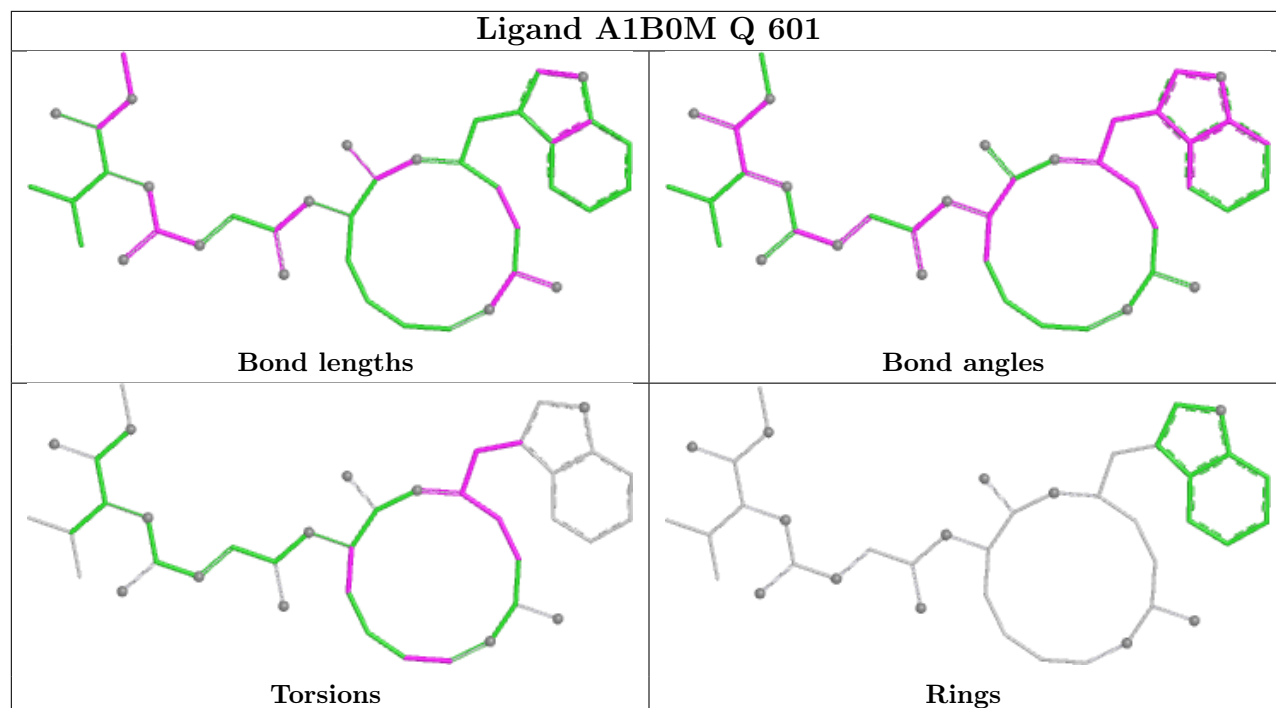


Ligand A1B0M P 601

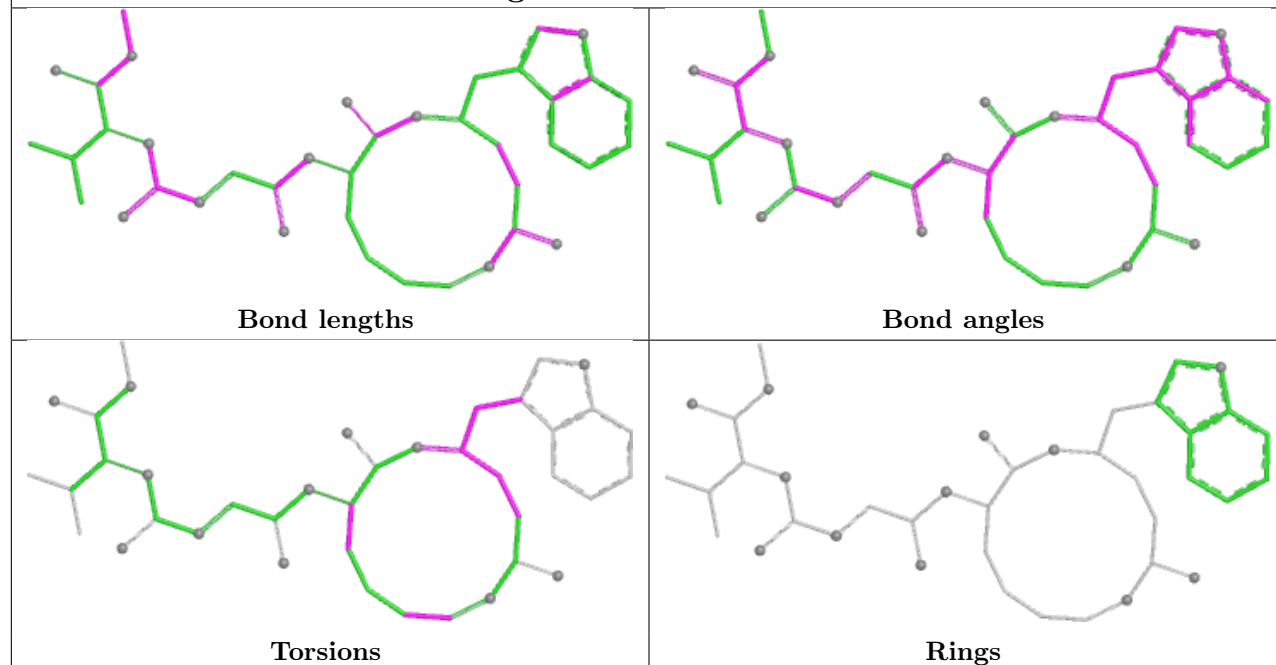


Ligand A1B0M 2 601

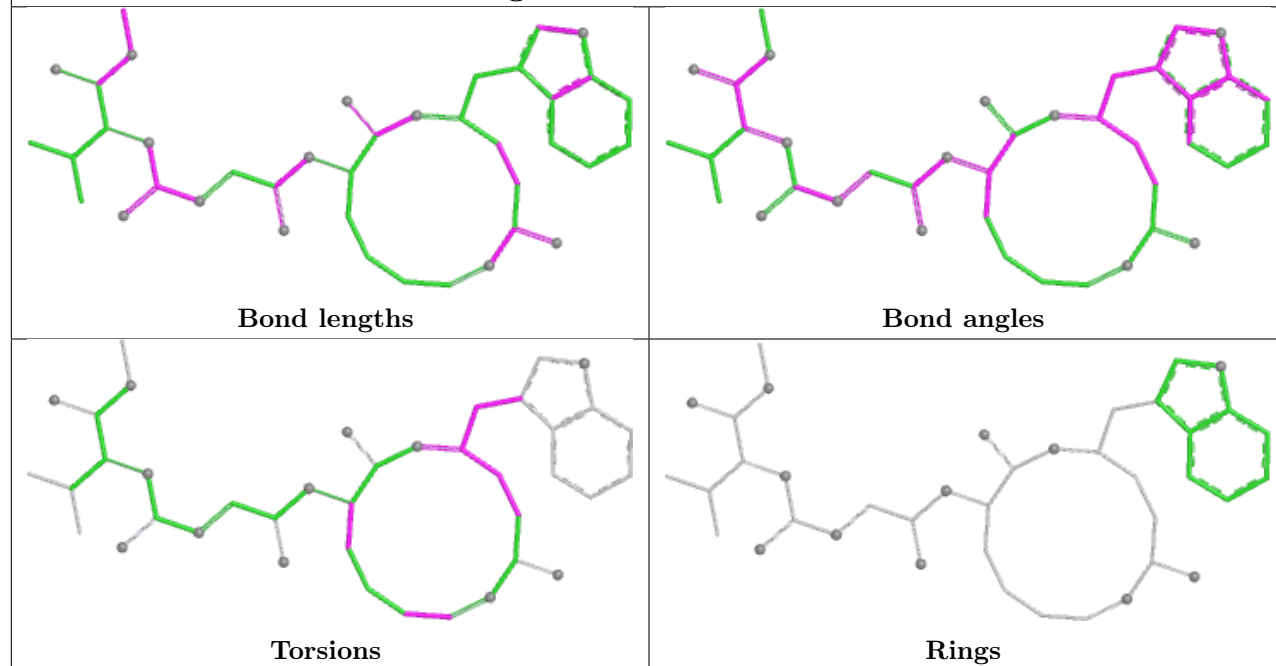




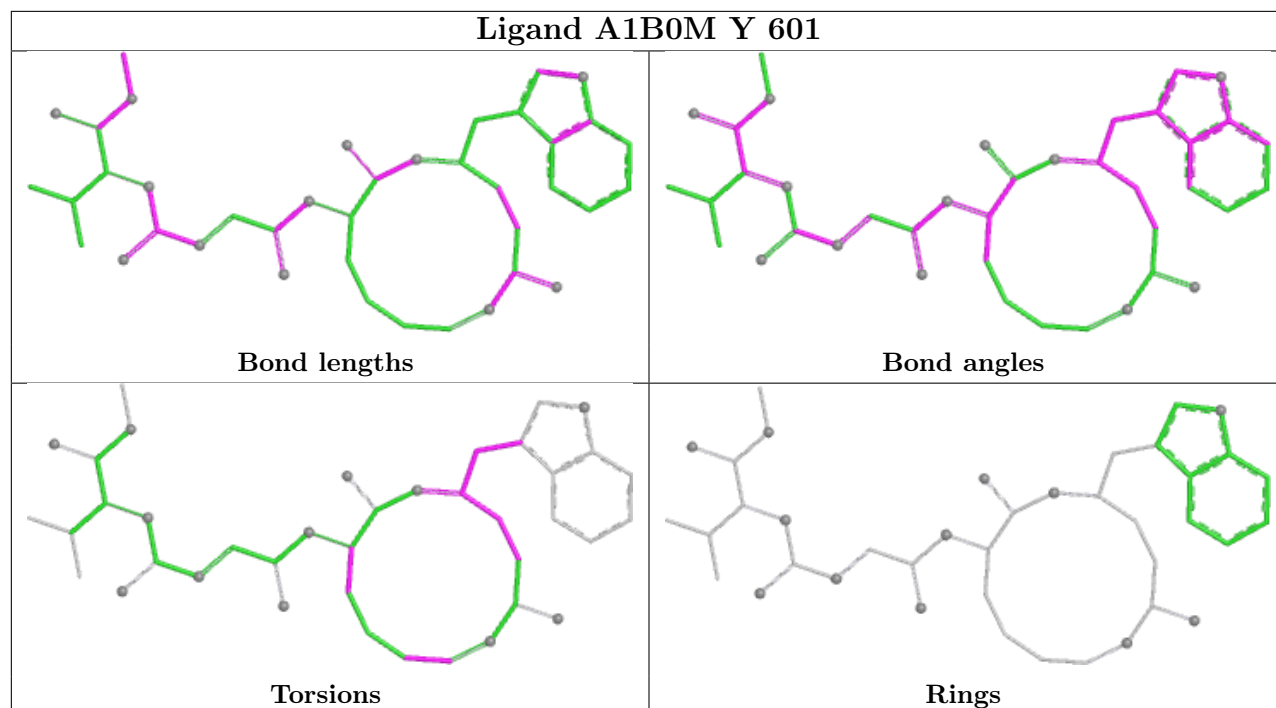
Ligand A1B0M U 601



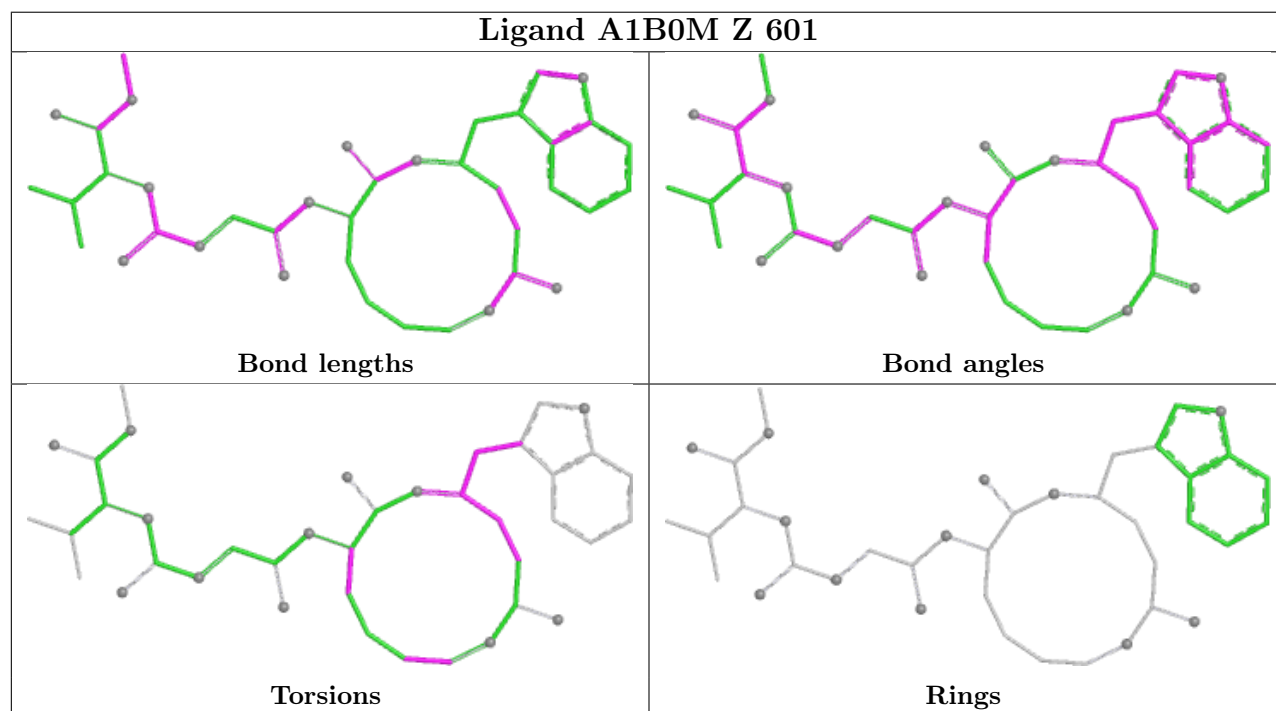
Ligand A1B0M V 601

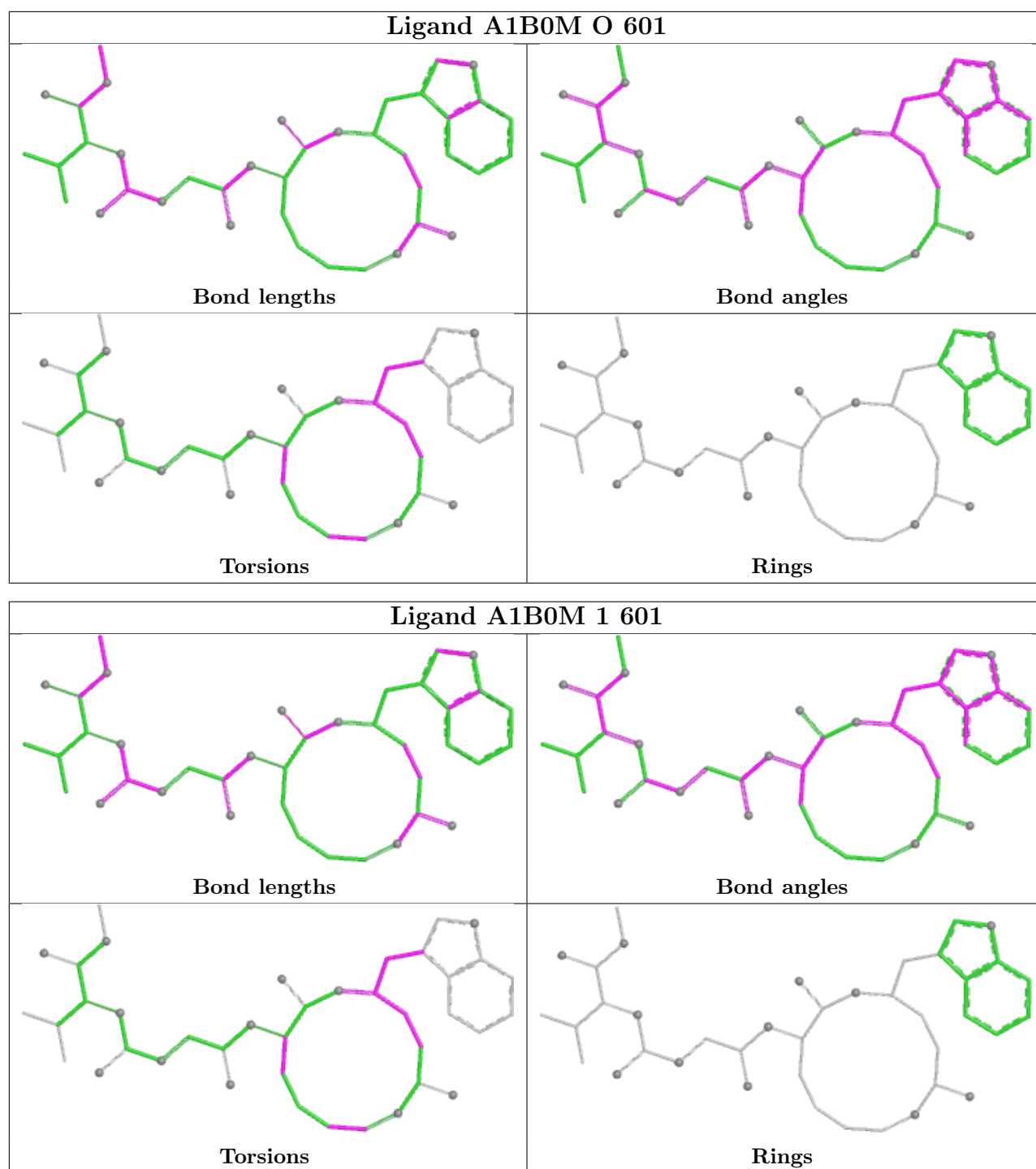


Ligand A1B0M Y 601



Ligand A1B0M Z 601





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

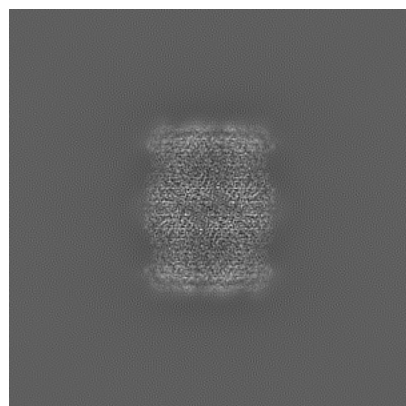
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49668. These allow visual inspection of the internal detail of the map and identification of artifacts.

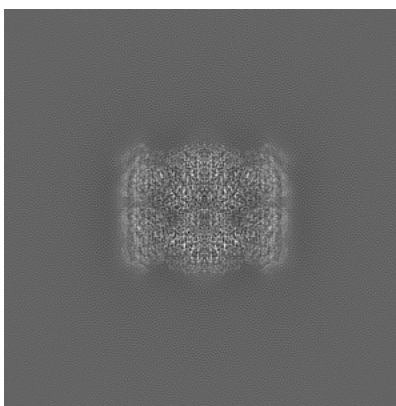
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

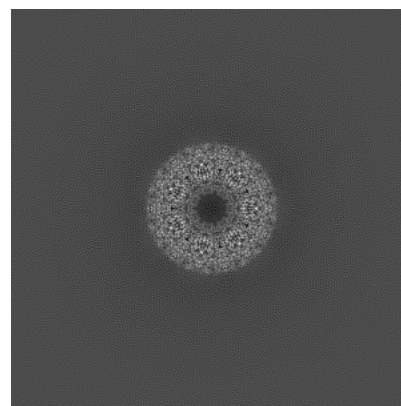
6.1.1 Primary map



X

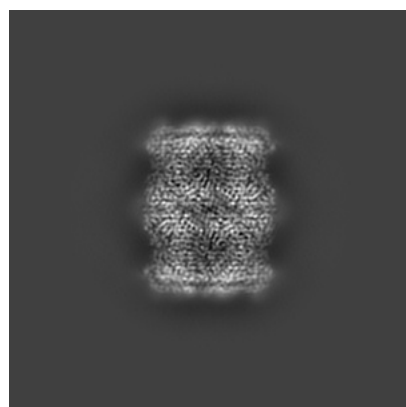


Y

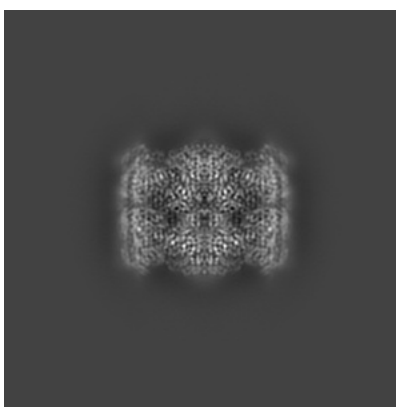


Z

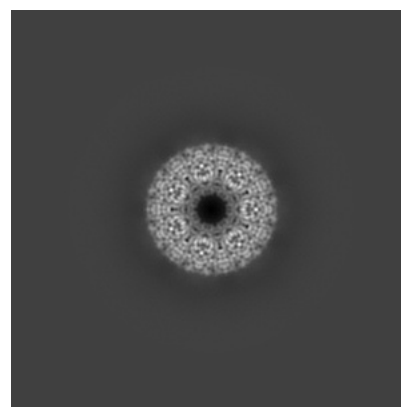
6.1.2 Raw map



X



Y

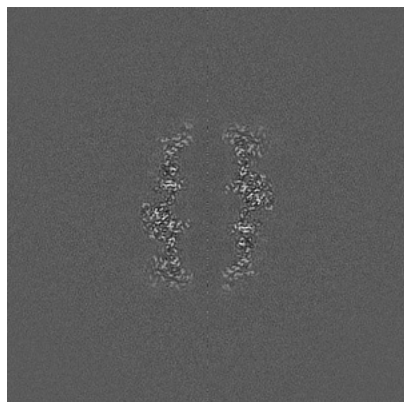


Z

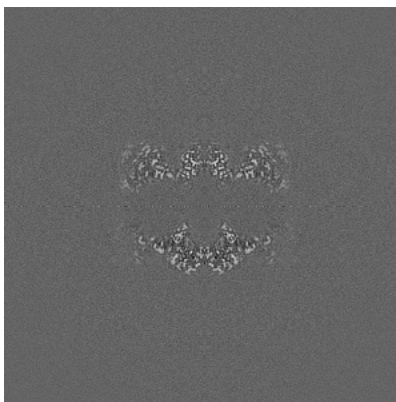
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

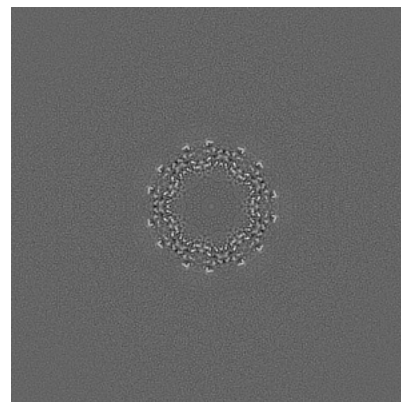
6.2.1 Primary map



X Index: 192

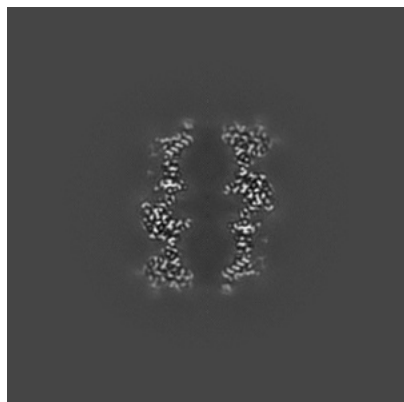


Y Index: 192

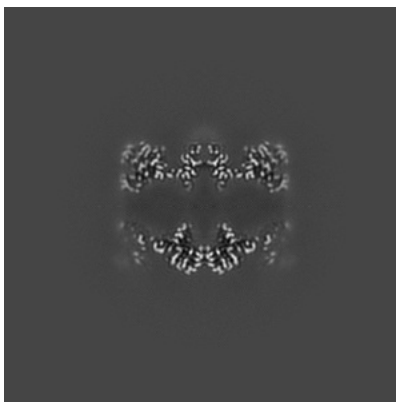


Z Index: 192

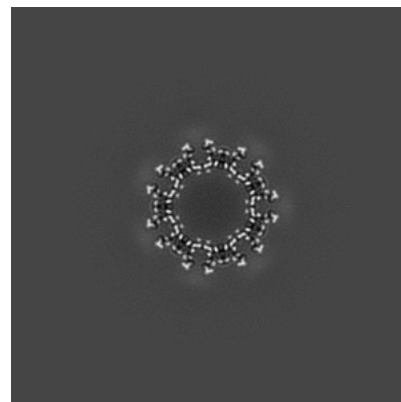
6.2.2 Raw map



X Index: 192



Y Index: 192

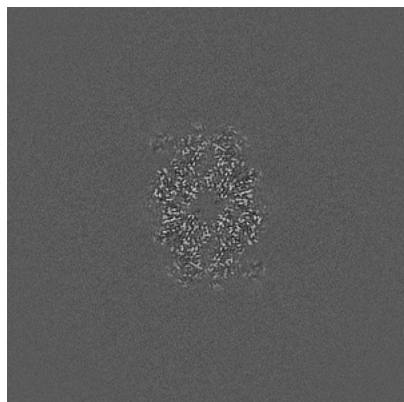


Z Index: 192

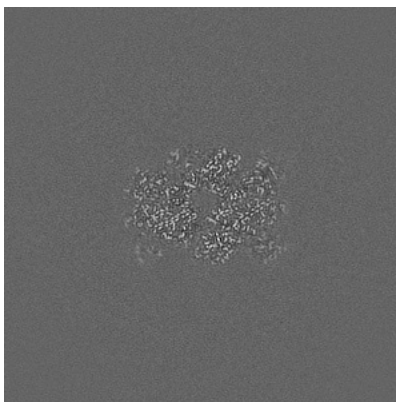
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

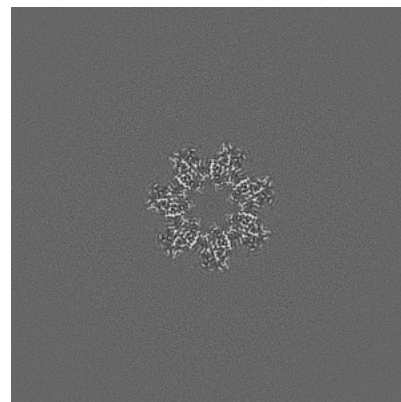
6.3.1 Primary map



X Index: 164

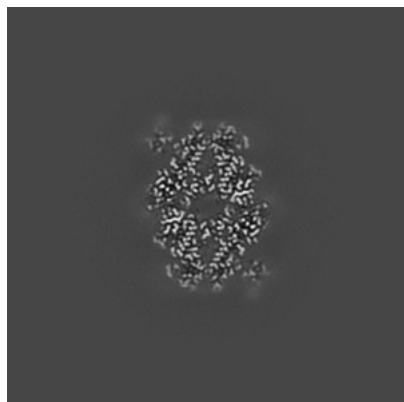


Y Index: 222

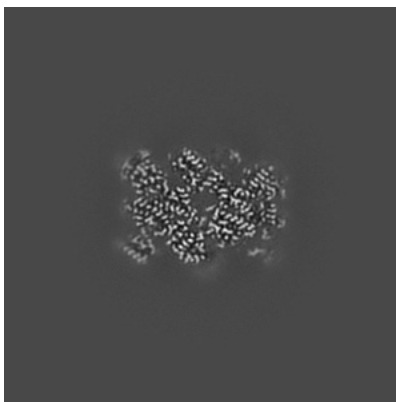


Z Index: 172

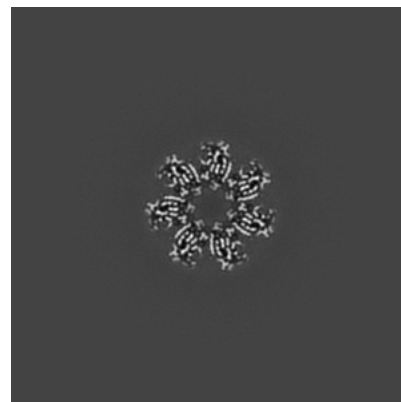
6.3.2 Raw map



X Index: 165



Y Index: 160

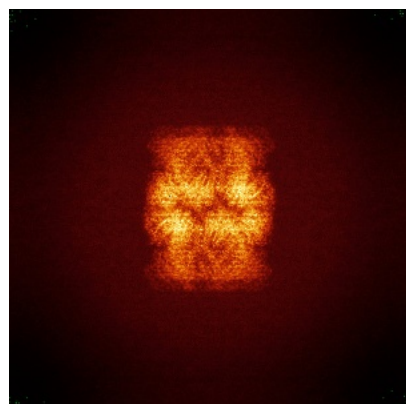


Z Index: 212

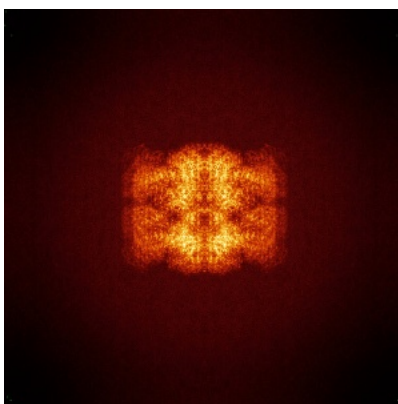
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

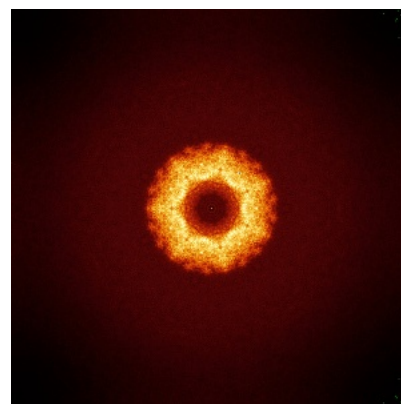
6.4.1 Primary map



X

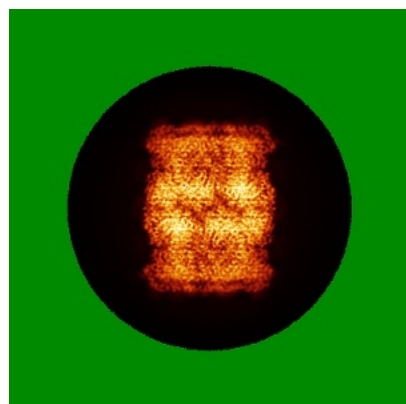


Y

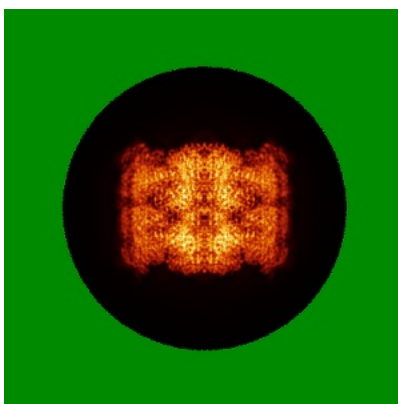


Z

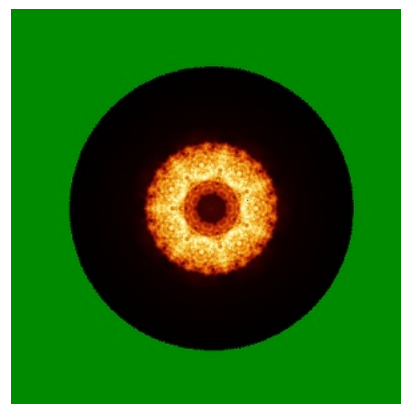
6.4.2 Raw map



X



Y

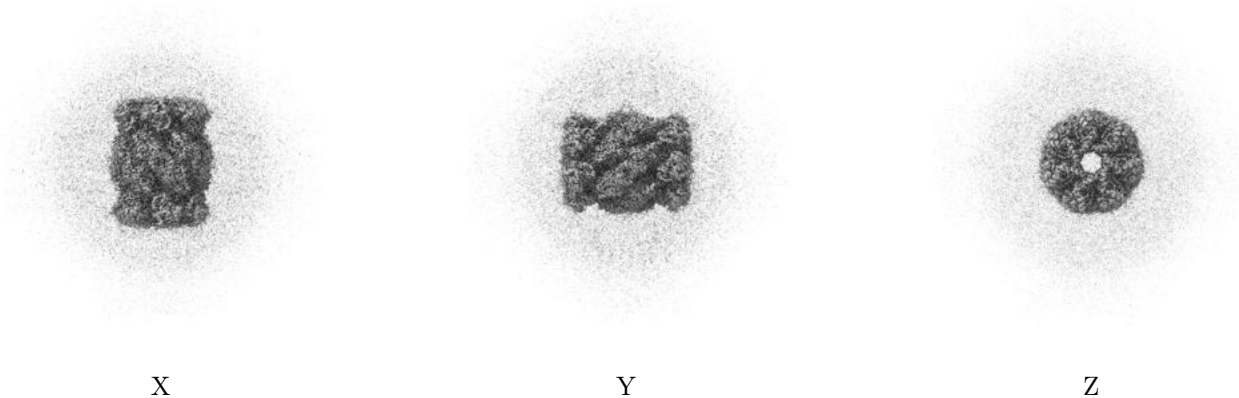


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

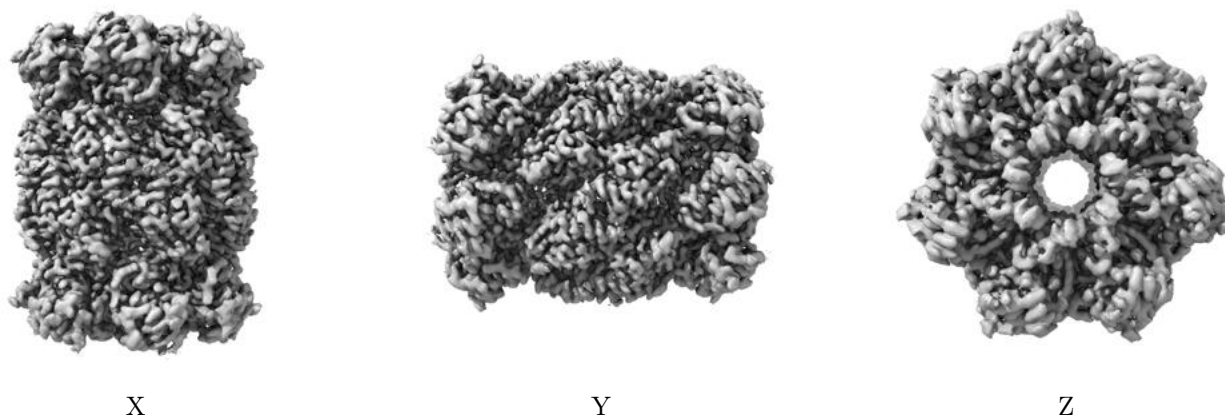
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 8.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

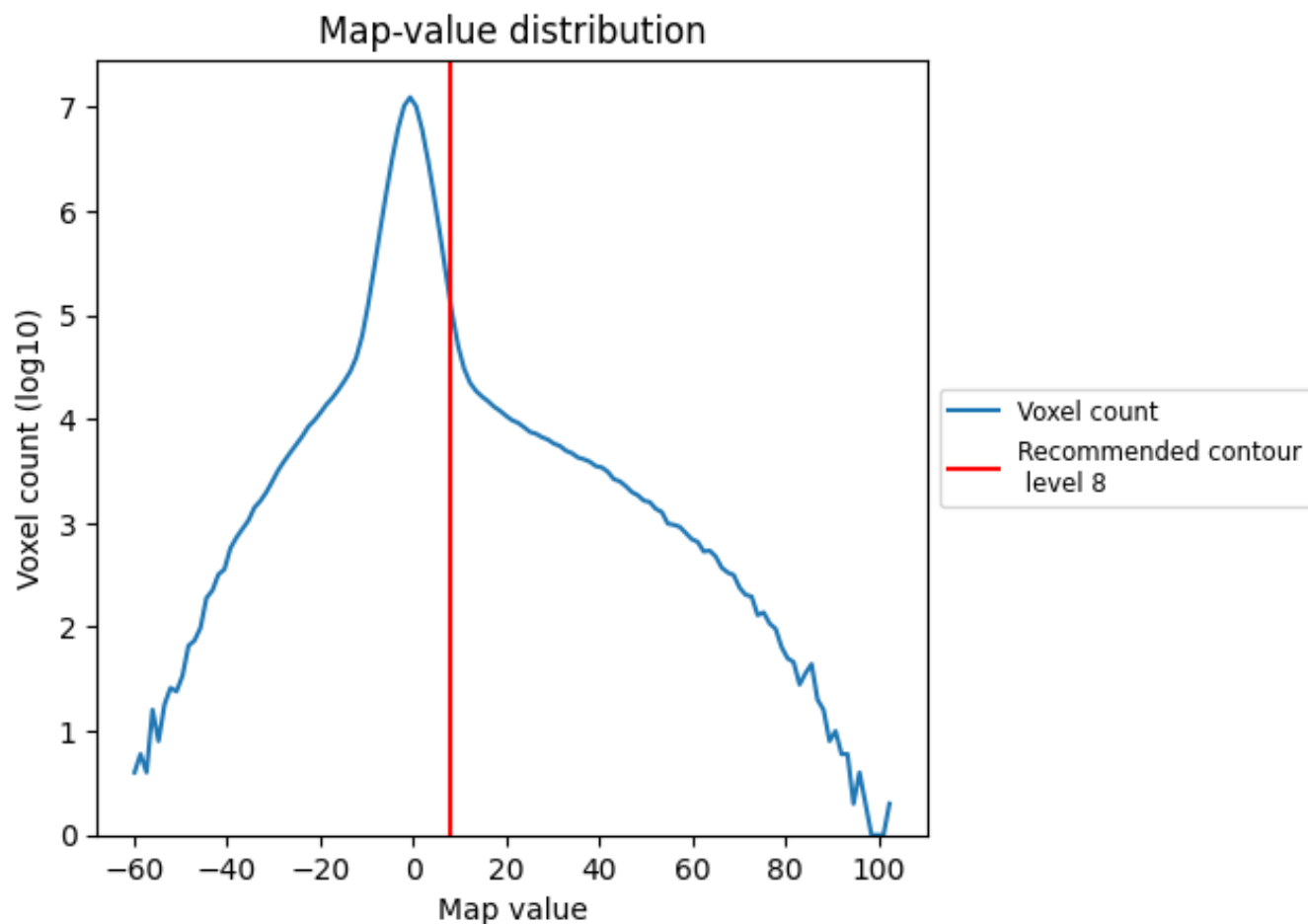
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

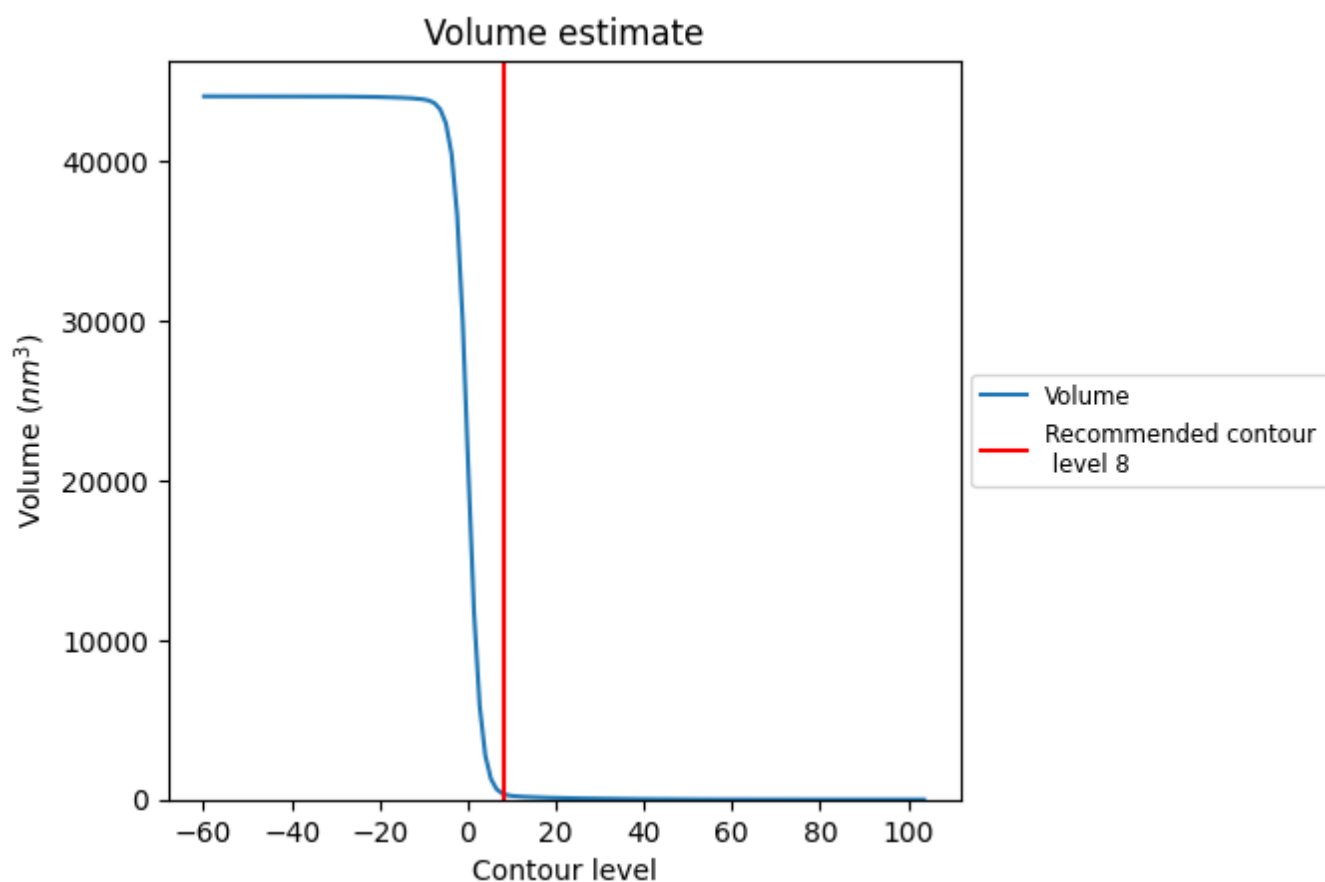
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

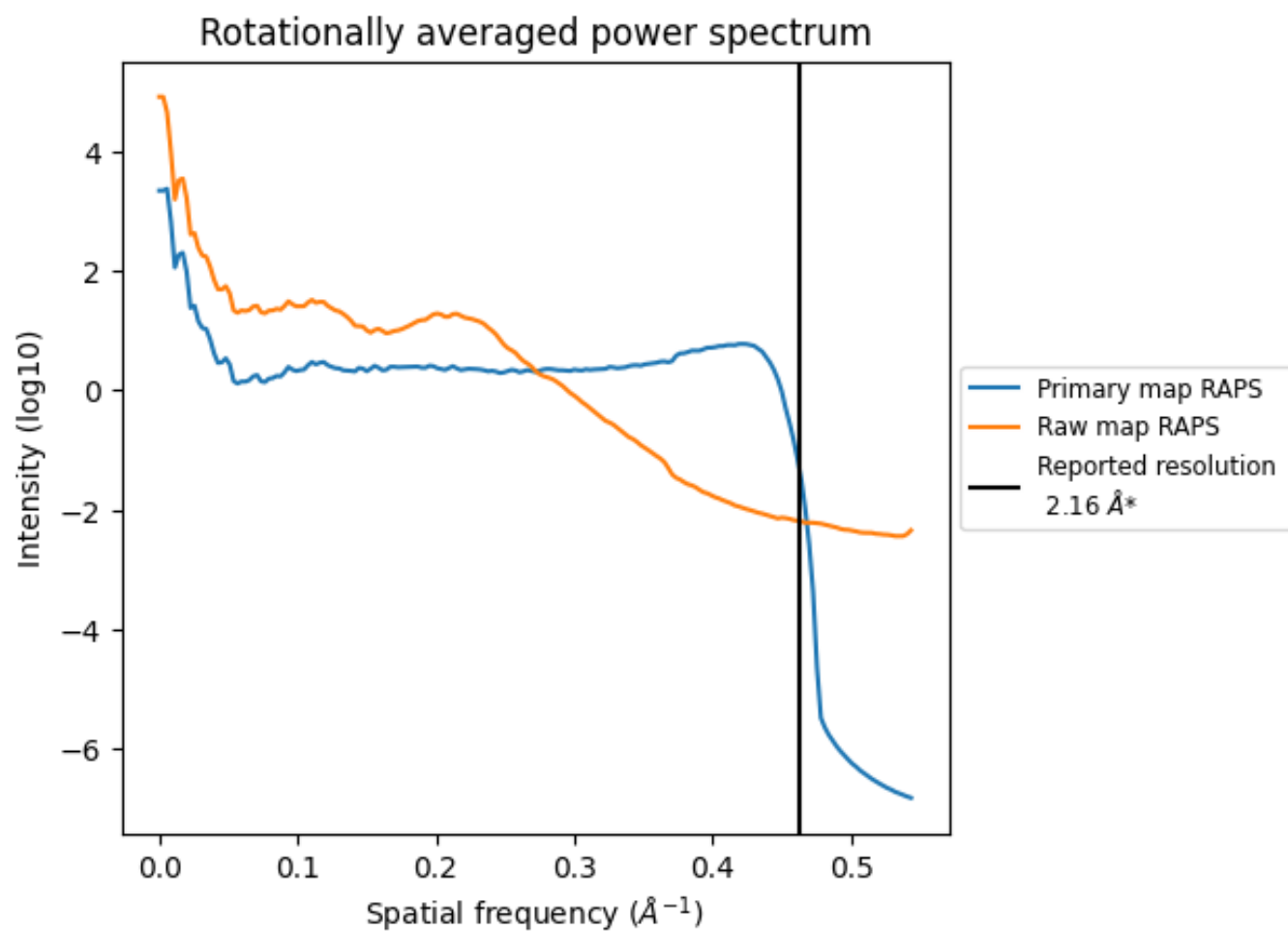
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 368 nm³; this corresponds to an approximate mass of 333 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

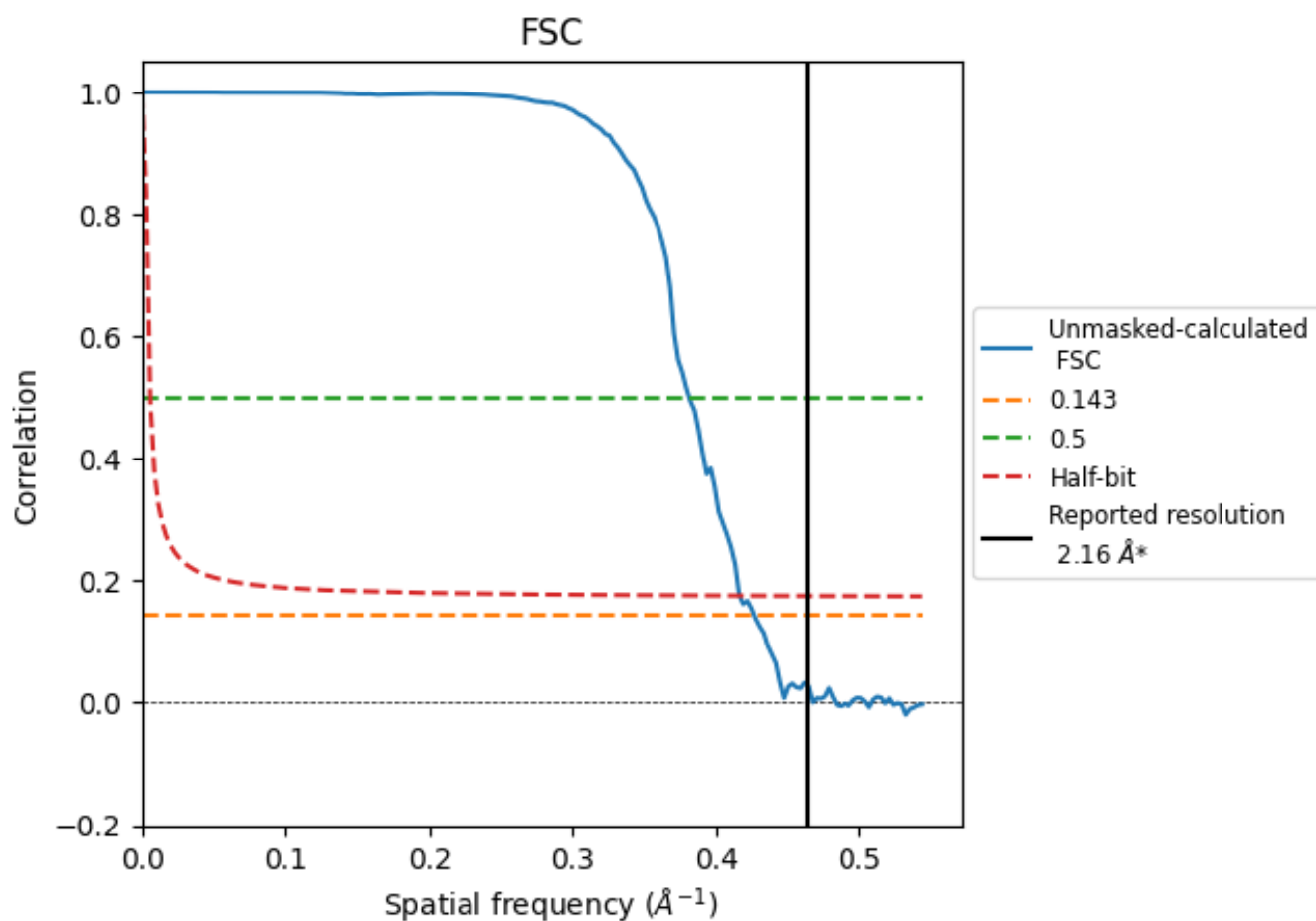


*Reported resolution corresponds to spatial frequency of 0.463 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.463 Å⁻¹

8.2 Resolution estimates [i](#)

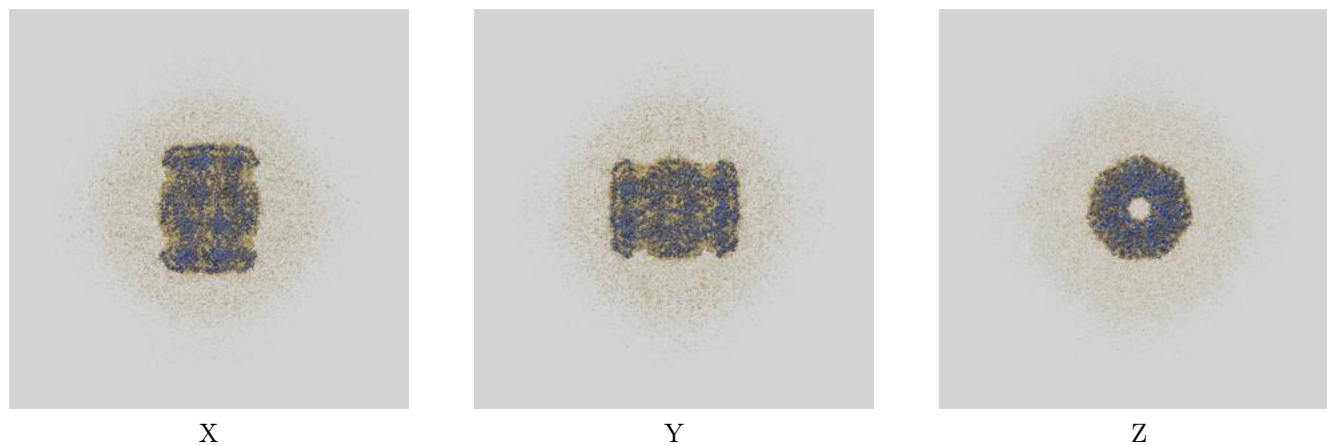
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.16	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.34	2.62	2.40

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

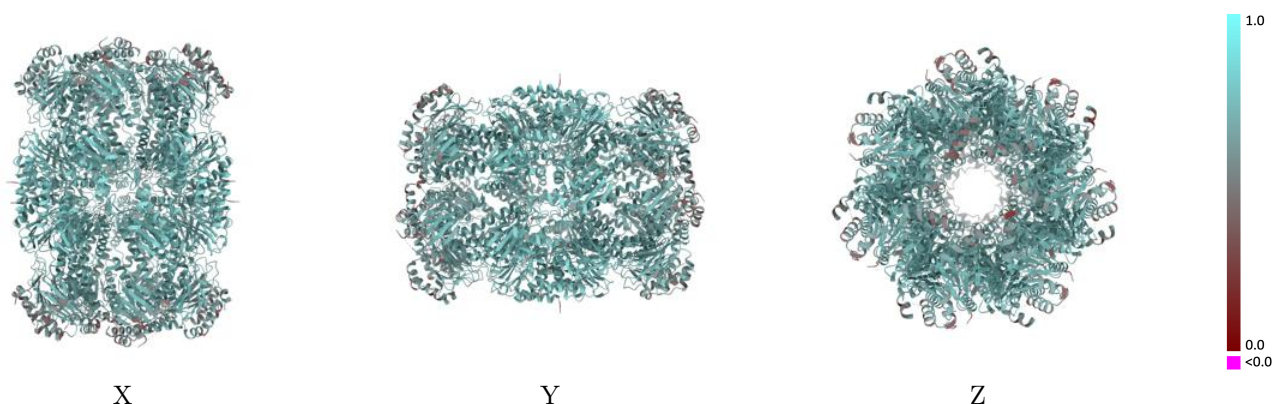
This section contains information regarding the fit between EMDB map EMD-49668 and PDB model 9NQL. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



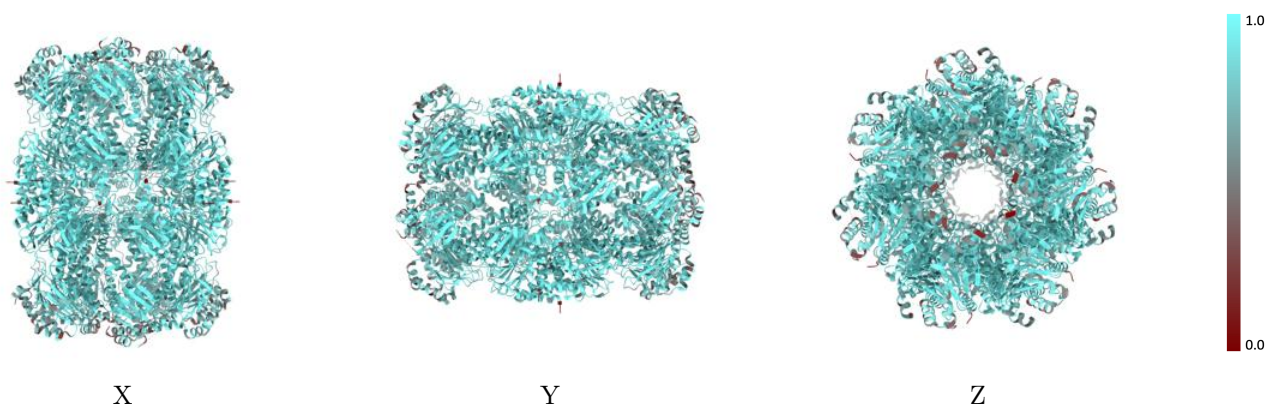
The images above show the 3D surface view of the map at the recommended contour level 8.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



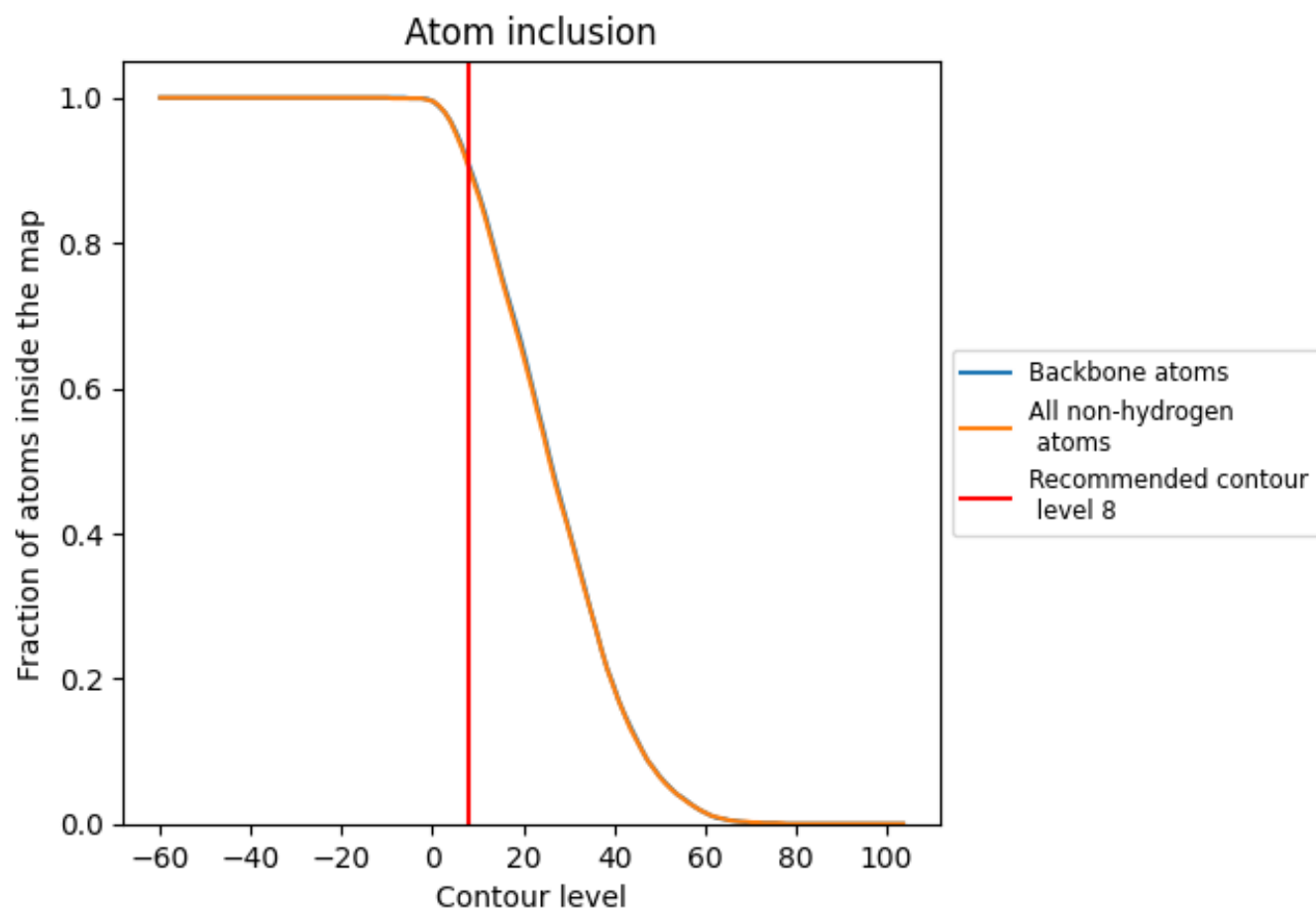
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9040	 0.6890
1	 0.9590	 0.7310
2	 0.9610	 0.7330
A	 0.8780	 0.6670
B	 0.8600	 0.6440
C	 0.8480	 0.6390
D	 0.8700	 0.6600
E	 0.8430	 0.6250
F	 0.8510	 0.6360
G	 0.8610	 0.6490
H	 0.8780	 0.6770
I	 0.8680	 0.6560
J	 0.8640	 0.6540
K	 0.8410	 0.6300
L	 0.8520	 0.6420
M	 0.8530	 0.6440
N	 0.8620	 0.6540
O	 0.9590	 0.7300
P	 0.9550	 0.7220
Q	 0.9570	 0.7290
R	 0.9590	 0.7300
S	 0.9590	 0.7290
T	 0.9580	 0.7290
U	 0.9600	 0.7300
V	 0.9580	 0.7290
W	 0.9560	 0.7270
X	 0.9580	 0.7280
Y	 0.9580	 0.7300
Z	 0.9540	 0.7270

