wwPDB EM Validation Summary Report

Oct 31, 2022 – 04:35 PM EDT

PDB ID	:	8D6X
EMDB ID	:	EMD-27225
Title	:	Structure of the Mycobacterium tuberculosis 20S proteasome bound to the ATP-bound Mpa ATPase
Authors	:	Xiao, X.; Li, H.
Deposited on	:	2022-06-06
Resolution	:	3.20 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:

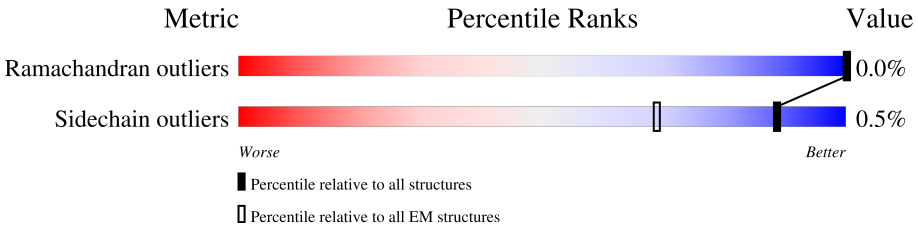
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.20 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	A	609	76% 23%
1	B	609	5% 78% 22%
1	C	609	7% 76% 24%
1	D	609	6% 73% 26%
1	E	609	6% 78% 22%
1	F	609	8% 78% 22%
2	G	248	86% 13%
2	H	248	85% 13%
2	I	248	87% 13%

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Mol	Chain	Length	Quality of chain
2	J	248	86% 13%
2	K	248	86% 13%
2	L	248	86% 13%
2	M	248	85% 13%
2	N	248	86% 13%
2	O	248	86% 13%
2	k	248	86% 13%
2	l	248	87% 13%
2	m	248	85% 13%
2	n	248	87% 13%
2	o	248	86% 13%
3	P	291	76% 24%
3	Q	291	76% 24%
3	R	291	76% 24%
3	S	291	76% 24%
3	T	291	76% 24%
3	U	291	76% 24%
3	V	291	76% 24%
3	W	291	76% 24%
3	X	291	76% 24%
3	Y	291	76% 24%
3	Z	291	76% 24%
3	a	291	76% 24%
3	b	291	76% 24%
3	c	291	76% 24%

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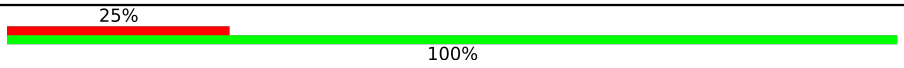
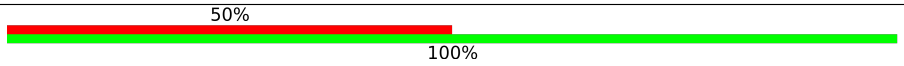
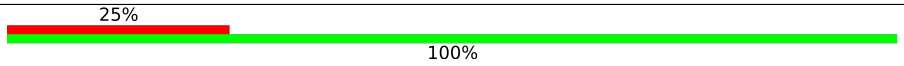
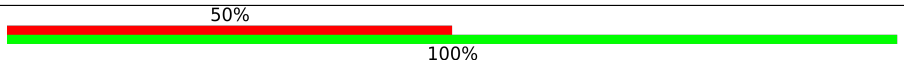
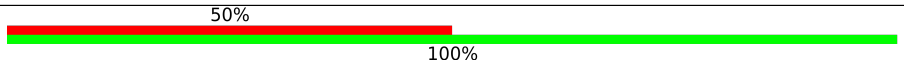
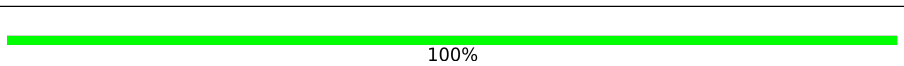
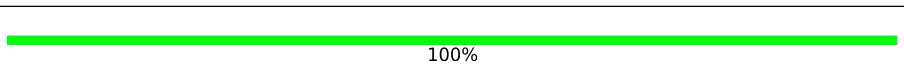
Mol	Chain	Length	Quality of chain
4	d	4	
4	e	4	
4	f	4	
4	g	4	
4	h	4	
4	i	4	
4	j	4	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 68362 atoms, of which 0 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 AAA ATPase forming ring-shaped complexes.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	466	Total	C	N	O	S	0	0
			3650	2306	630	703	11		
1	B	476	Total	C	N	O	S	0	0
			3719	2343	642	723	11		
1	C	464	Total	C	N	O	S	0	0
			3629	2291	625	702	11		
1	D	452	Total	C	N	O	S	0	0
			3542	2242	607	682	11		
1	E	476	Total	C	N	O	S	0	0
			3719	2343	642	723	11		
1	F	477	Total	C	N	O	S	0	0
			3723	2345	643	724	11		

- Molecule 2 is a protein called Proteasome subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	k	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	l	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	m	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	n	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	o	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	G	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	H	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	I	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	J	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	L	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	M	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	N	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
2	O	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		

- Molecule 3 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	Q	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	R	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	S	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	T	222	Total	C	N	O	S	0	0
			1636	1026	282	323	5		
3	U	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	V	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	W	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	X	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	Y	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	Z	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	a	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	b	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		
3	c	222	Total	C	N	O	S	0	0
			1638	1027	282	324	5		

- Molecule 4 is a protein called Proteasome-associated ATPase.

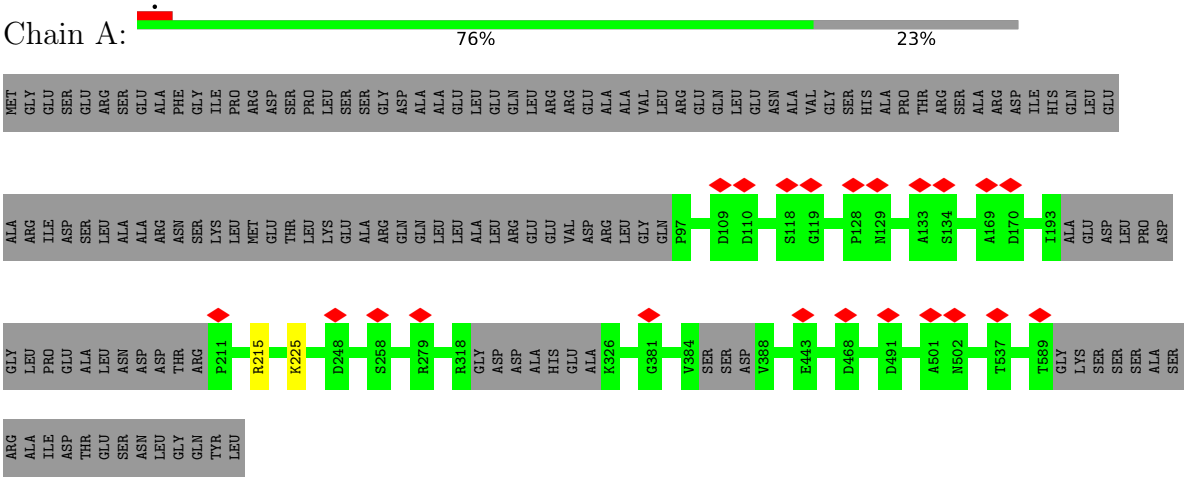
Mol	Chain	Residues	Atoms				AltConf	Trace
4	d	4	Total	C	N	O	0	0
			34	22	5	7		
4	e	4	Total	C	N	O	0	0
			34	22	5	7		
4	f	4	Total	C	N	O	0	0
			34	22	5	7		
4	g	4	Total	C	N	O	0	0
			34	22	5	7		
4	h	4	Total	C	N	O	0	0
			34	22	5	7		
4	i	4	Total	C	N	O	0	0
			34	22	5	7		
4	j	4	Total	C	N	O	0	0
			34	22	5	7		

3 Residue-property plots (i)

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.

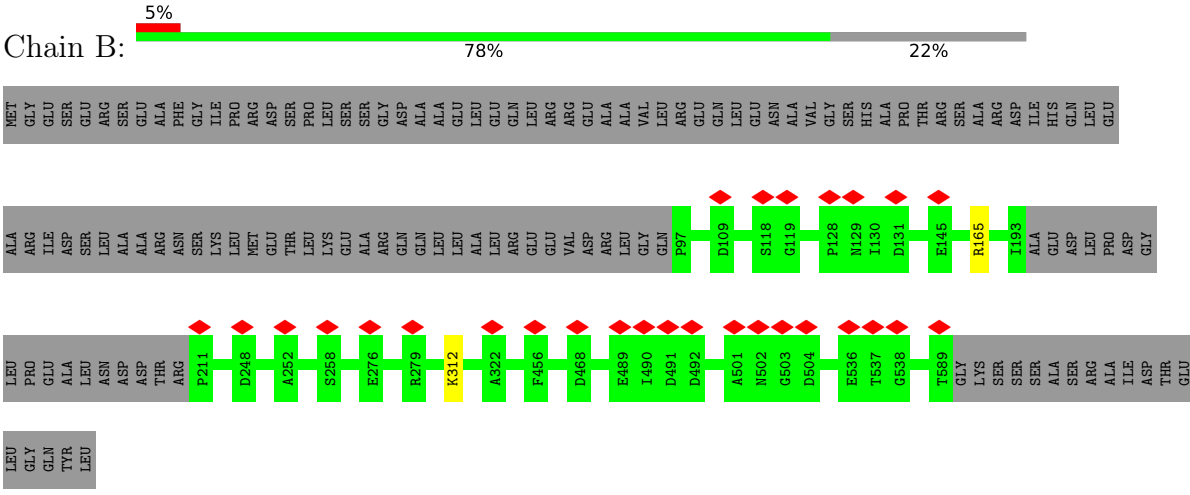
• Molecule 1: AAA ATPase forming ring-shaped complexes

Chain A:



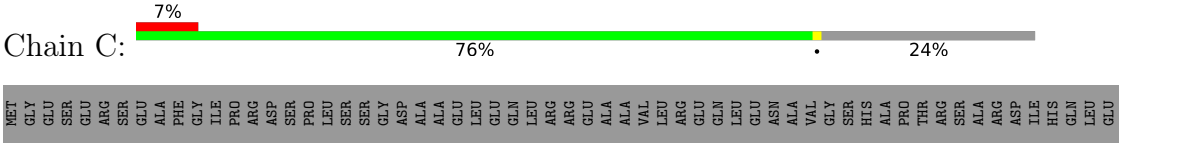
• Molecule 1: AAA ATPase forming ring-shaped complexes

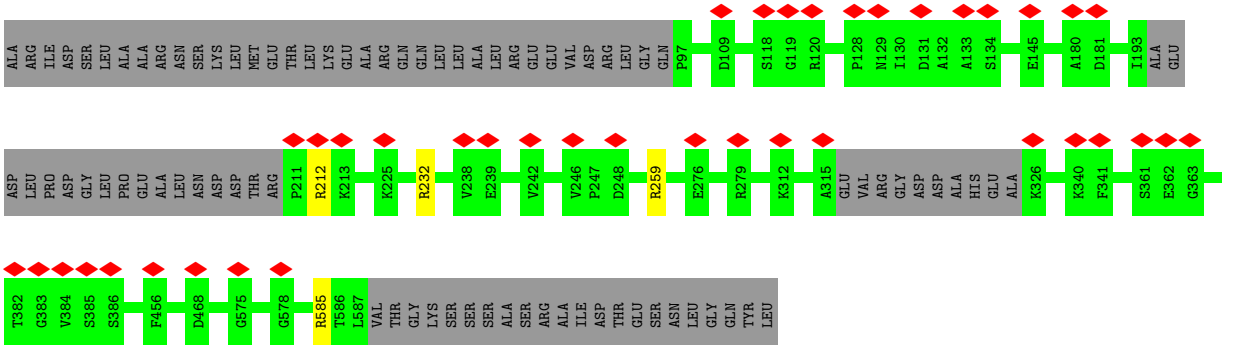
Chain B:



• Molecule 1: AAA ATPase forming ring-shaped complexes

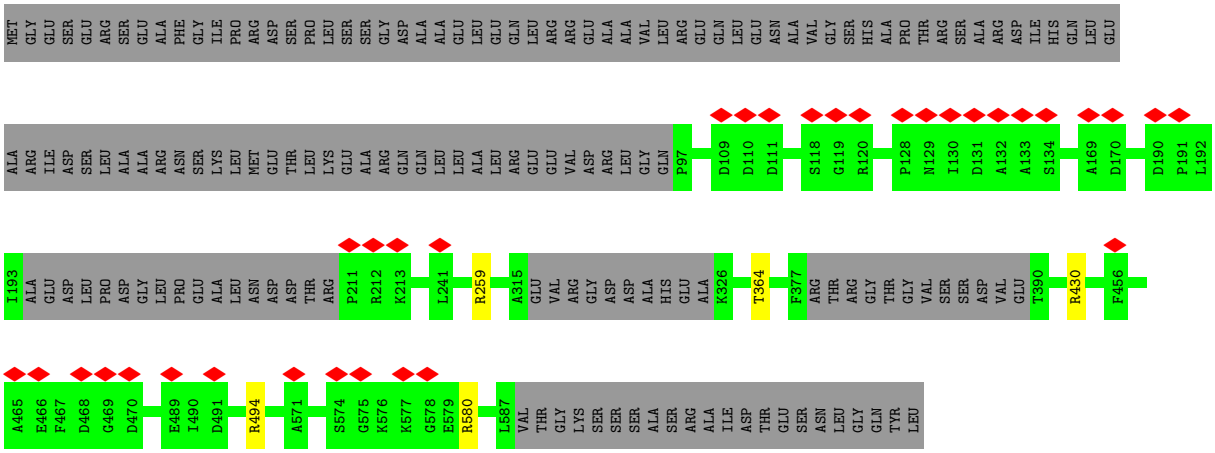
Chain C:





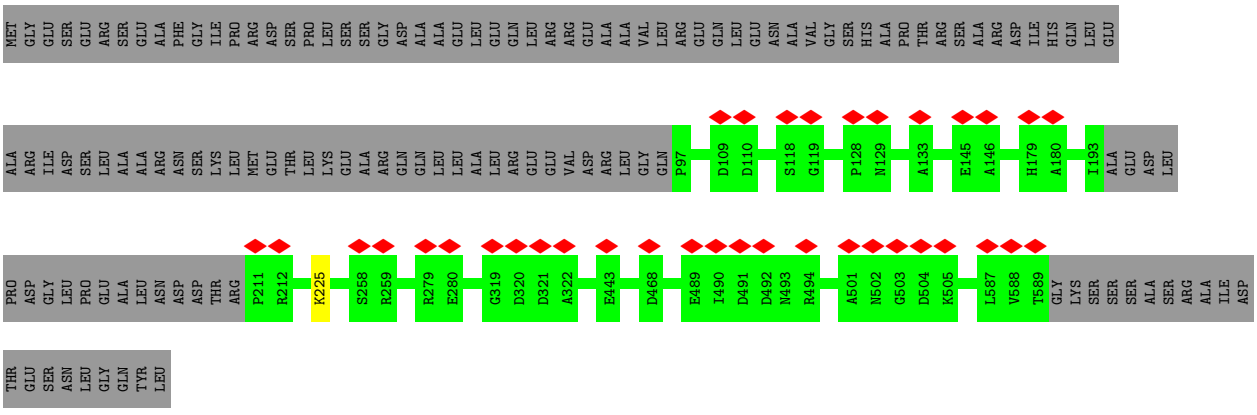
• Molecule 1: AAA ATPase forming ring-shaped complexes

Chain D:



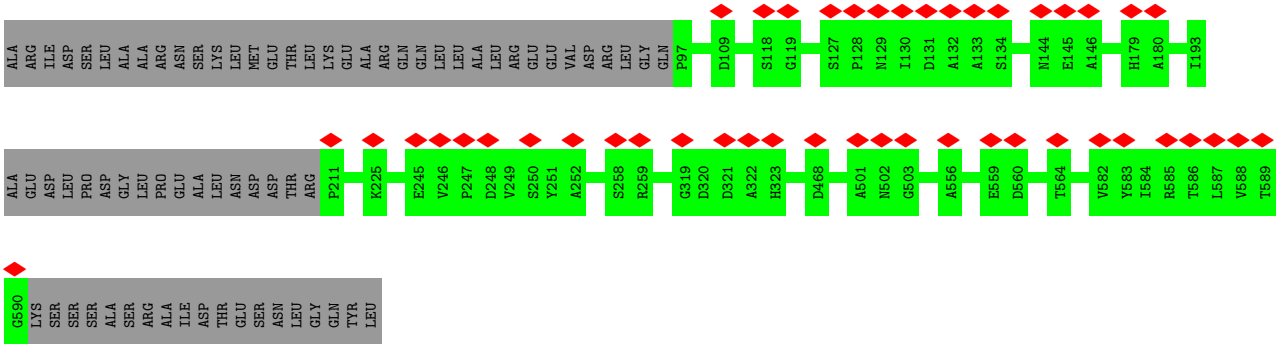
• Molecule 1: AAA ATPase forming ring-shaped complexes

Chain E:



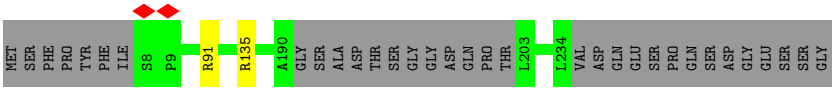
• Molecule 1: AAA ATPase forming ring-shaped complexes

Chain F:



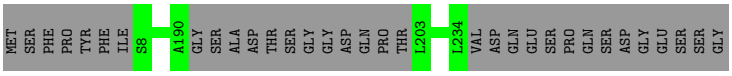
• Molecule 2: Proteasome subunit alpha

Chain k:



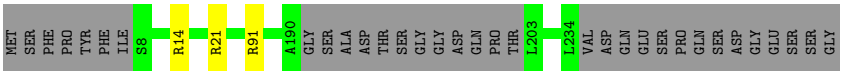
• Molecule 2: Proteasome subunit alpha

Chain l:



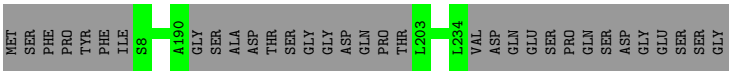
• Molecule 2: Proteasome subunit alpha

Chain m:



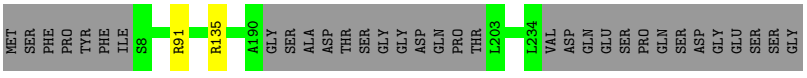
• Molecule 2: Proteasome subunit alpha

Chain n:



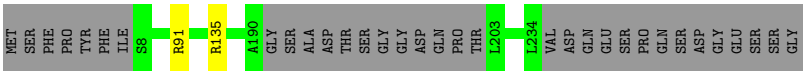
• Molecule 2: Proteasome subunit alpha

Chain o:



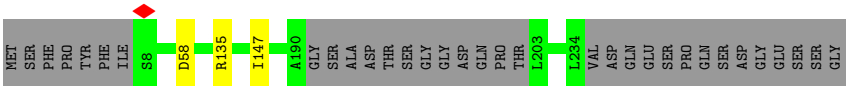
• Molecule 2: Proteasome subunit alpha

Chain G:



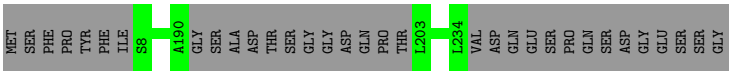
• Molecule 2: Proteasome subunit alpha

Chain H:



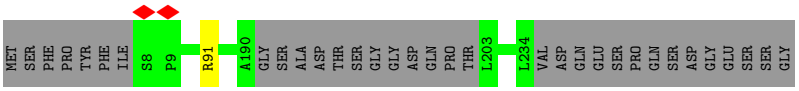
• Molecule 2: Proteasome subunit alpha

Chain I:



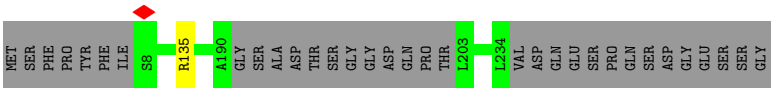
• Molecule 2: Proteasome subunit alpha

Chain J:



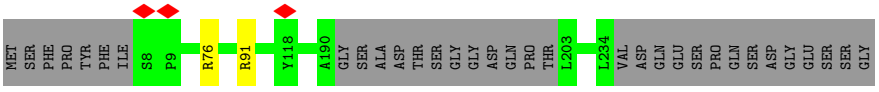
• Molecule 2: Proteasome subunit alpha

Chain K:



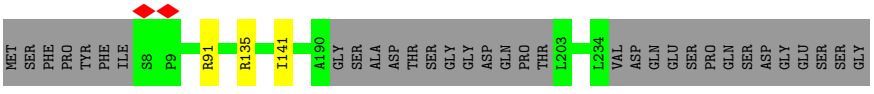
• Molecule 2: Proteasome subunit alpha

Chain L:



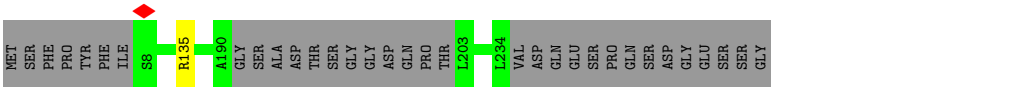
• Molecule 2: Proteasome subunit alpha

Chain M:



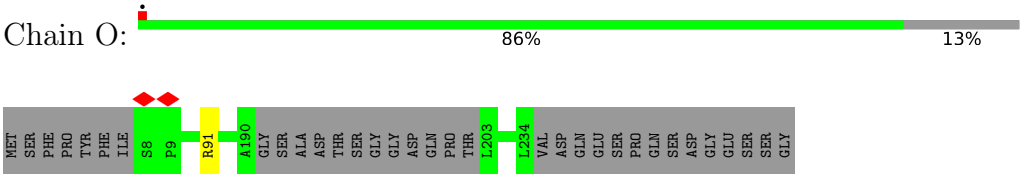
• Molecule 2: Proteasome subunit alpha

Chain N:



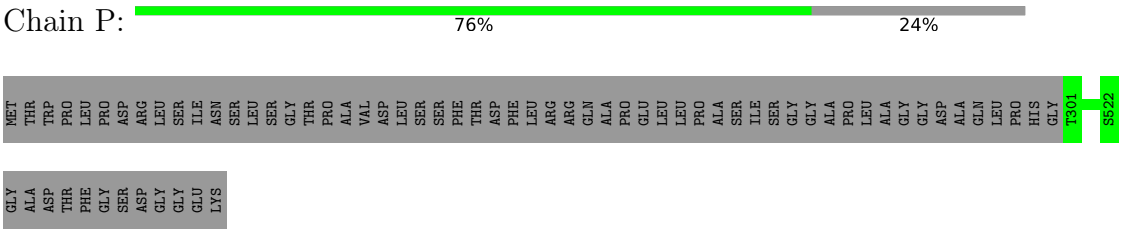
• Molecule 2: Proteasome subunit alpha

Chain O:



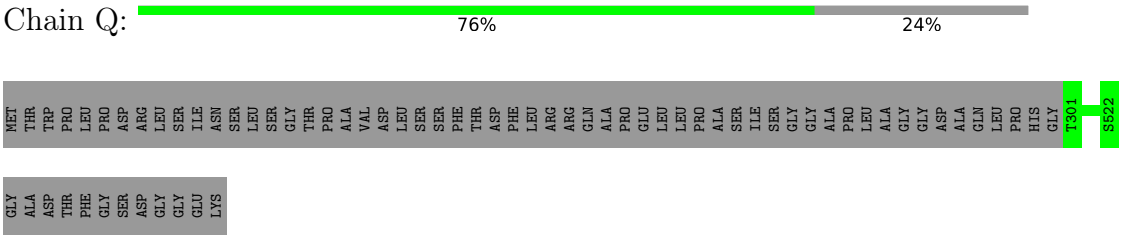
• Molecule 3: Proteasome subunit beta

Chain P:



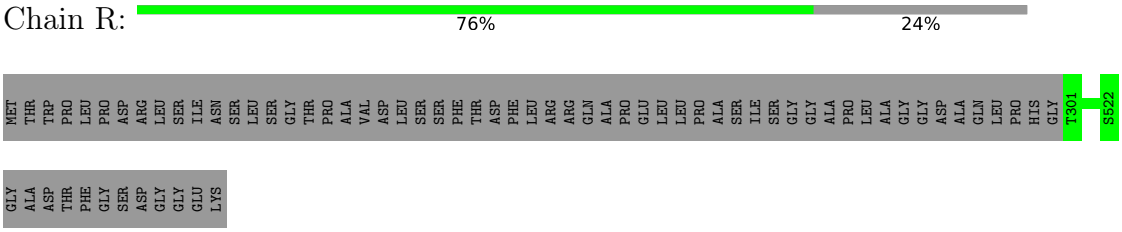
• Molecule 3: Proteasome subunit beta

Chain Q:



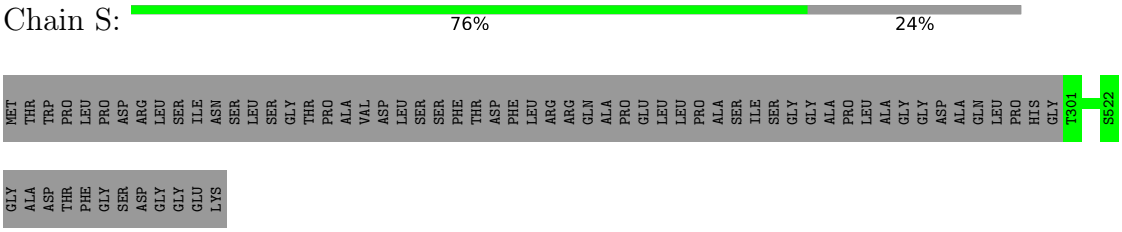
• Molecule 3: Proteasome subunit beta

Chain R:



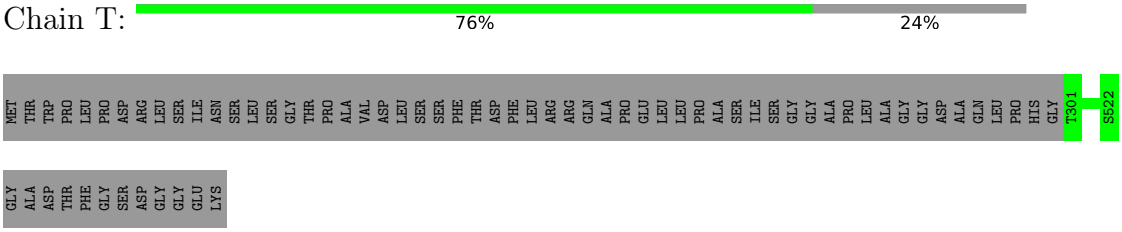
• Molecule 3: Proteasome subunit beta

Chain S:



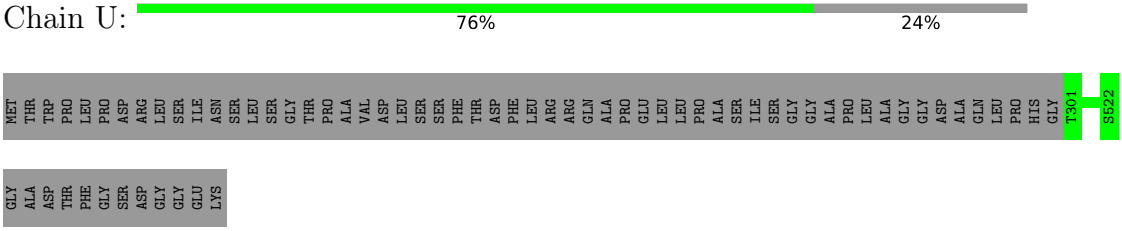
• Molecule 3: Proteasome subunit beta

Chain T:



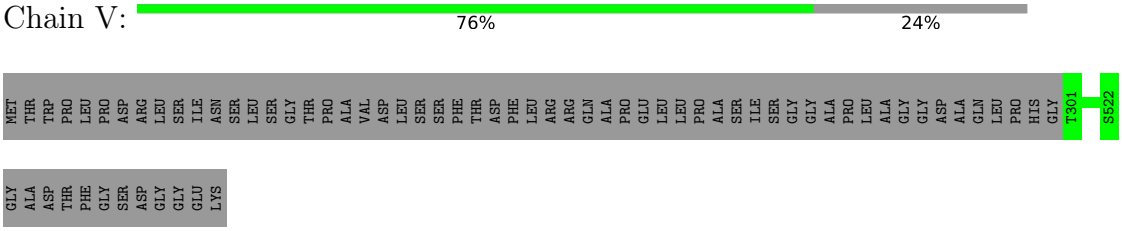
• Molecule 3: Proteasome subunit beta

Chain U:



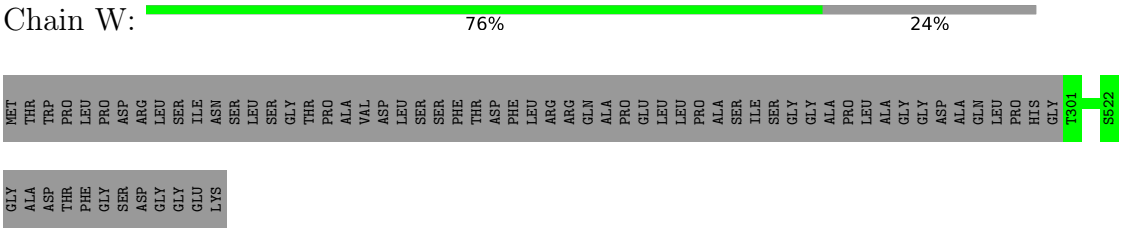
• Molecule 3: Proteasome subunit beta

Chain V:



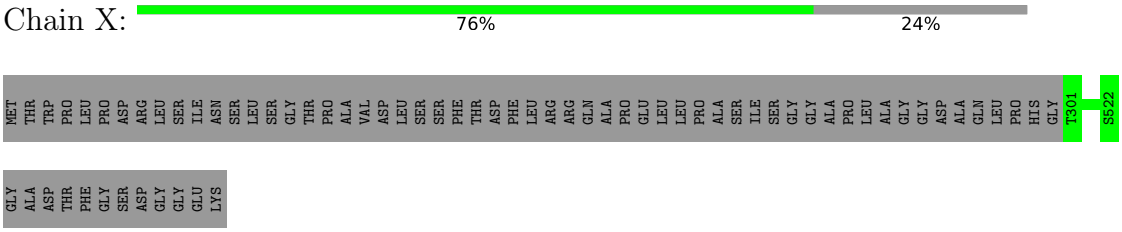
• Molecule 3: Proteasome subunit beta

Chain W:



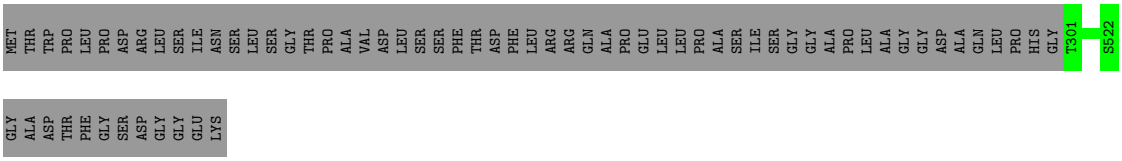
• Molecule 3: Proteasome subunit beta

Chain X:



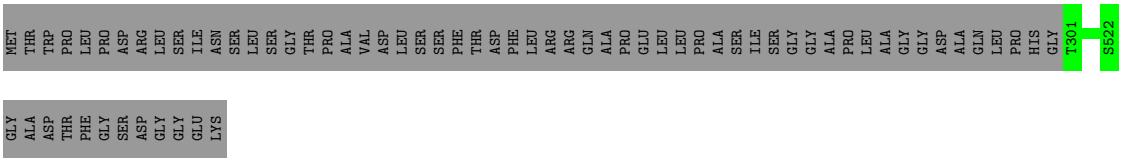
• Molecule 3: Proteasome subunit beta

Chain Y:



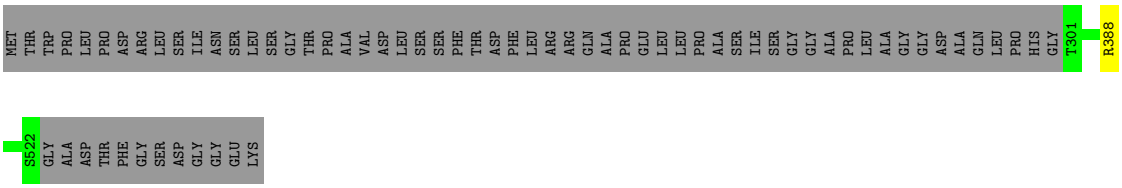
• Molecule 3: Proteasome subunit beta

Chain Z:



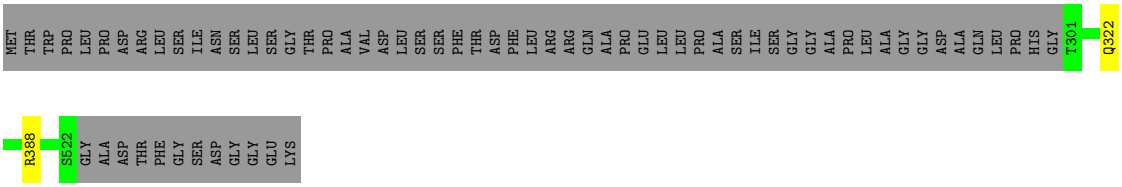
• Molecule 3: Proteasome subunit beta

Chain a:



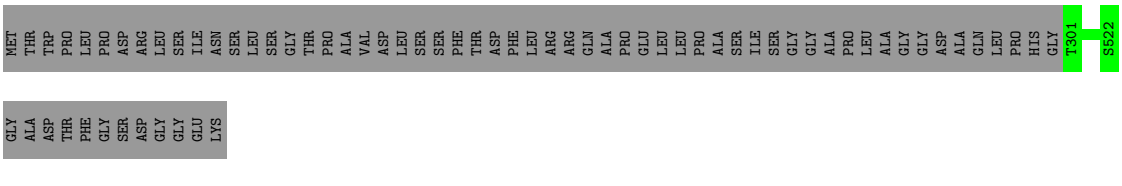
• Molecule 3: Proteasome subunit beta

Chain b:



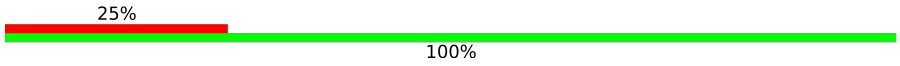
• Molecule 3: Proteasome subunit beta

Chain c:



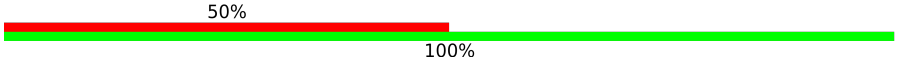
• Molecule 4: Proteasome-associated ATPase

Chain d:



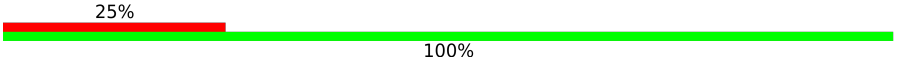
• Molecule 4: Proteasome-associated ATPase

Chain e:



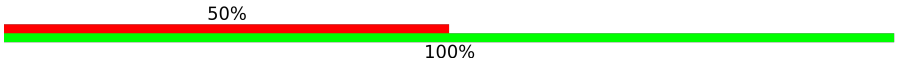
• Molecule 4: Proteasome-associated ATPase

Chain f:



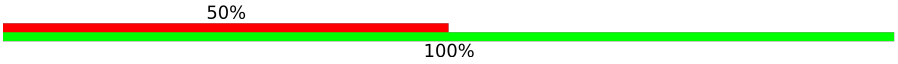
• Molecule 4: Proteasome-associated ATPase

Chain g:



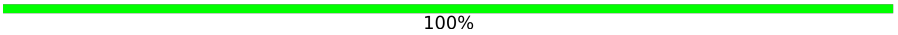
• Molecule 4: Proteasome-associated ATPase

Chain h:



• Molecule 4: Proteasome-associated ATPase

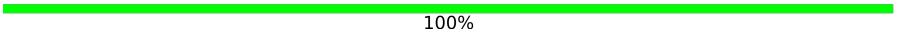
Chain i:



There are no outlier residues recorded for this chain.

• Molecule 4: Proteasome-associated ATPase

Chain j:



There are no outlier residues recorded for this chain.

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	213000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	1.2	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	25.608	Depositor
Minimum map value	-13.771	Depositor
Average map value	-0.122	Depositor
Map value standard deviation	1.501	Depositor
Recommended contour level	3.2	Depositor
Map size (Å)	440.832, 440.832, 440.832	wwPDB
Map dimensions	96, 96, 96	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	4.592, 4.592, 4.592	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	A	0.25	0/3709	0.49	0/5015
1	B	0.24	0/3781	0.50	0/5116
1	C	0.25	0/3689	0.50	0/4989
1	D	0.26	0/3601	0.50	0/4869
1	E	0.24	0/3781	0.50	0/5116
1	F	0.24	0/3785	0.49	0/5121
2	G	0.28	0/1683	0.54	0/2274
2	H	0.31	0/1683	0.54	0/2274
2	I	0.28	0/1683	0.55	0/2274
2	J	0.25	0/1683	0.54	0/2274
2	K	0.30	0/1683	0.54	0/2274
2	L	0.26	0/1683	0.55	0/2274
2	M	0.27	0/1683	0.53	0/2274
2	N	0.29	0/1683	0.54	0/2274
2	O	0.26	0/1683	0.55	0/2274
2	k	0.25	0/1683	0.53	0/2274
2	l	0.29	0/1683	0.54	0/2274
2	m	0.28	0/1683	0.55	0/2274
2	n	0.28	0/1683	0.55	0/2274
2	o	0.29	0/1683	0.54	0/2274
3	P	0.26	0/1662	0.53	0/2254
3	Q	0.26	0/1662	0.53	0/2254
3	R	0.26	0/1662	0.52	0/2254
3	S	0.26	0/1662	0.51	0/2254
3	T	0.26	0/1660	0.53	0/2251
3	U	0.27	0/1662	0.52	0/2254
3	V	0.30	0/1662	0.53	0/2254
3	W	0.28	0/1662	0.54	0/2254
3	X	0.28	0/1662	0.56	0/2254
3	Y	0.27	0/1662	0.53	0/2254
3	Z	0.32	0/1662	0.54	0/2254
3	a	0.27	0/1662	0.51	0/2254
3	b	0.27	0/1662	0.54	0/2254
3	c	0.26	0/1662	0.52	0/2254

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
4	d	0.22	0/34	0.51	0/43
4	e	0.22	0/34	0.31	0/43
4	f	0.25	0/34	0.55	0/43
4	g	0.21	0/34	0.41	0/43
4	h	0.22	0/34	0.43	0/43
4	i	0.23	0/34	0.52	0/43
4	j	0.28	0/34	0.67	0/43
All	All	0.27	0/69412	0.52	0/93916

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	A	458/609 (75%)	446 (97%)	12 (3%)	0	100	100
1	B	472/609 (78%)	459 (97%)	13 (3%)	0	100	100
1	C	458/609 (75%)	444 (97%)	14 (3%)	0	100	100
1	D	444/609 (73%)	427 (96%)	17 (4%)	0	100	100
1	E	472/609 (78%)	453 (96%)	19 (4%)	0	100	100
1	F	473/609 (78%)	463 (98%)	10 (2%)	0	100	100
2	G	211/248 (85%)	206 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	211/248 (85%)	204 (97%)	6 (3%)	1 (0%)	29	67
2	I	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
2	J	211/248 (85%)	202 (96%)	9 (4%)	0	100	100
2	K	211/248 (85%)	203 (96%)	8 (4%)	0	100	100
2	L	211/248 (85%)	206 (98%)	5 (2%)	0	100	100
2	M	211/248 (85%)	206 (98%)	5 (2%)	0	100	100
2	N	211/248 (85%)	208 (99%)	3 (1%)	0	100	100
2	O	211/248 (85%)	207 (98%)	4 (2%)	0	100	100
2	k	211/248 (85%)	207 (98%)	4 (2%)	0	100	100
2	l	211/248 (85%)	204 (97%)	7 (3%)	0	100	100
2	m	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
2	n	211/248 (85%)	200 (95%)	11 (5%)	0	100	100
2	o	211/248 (85%)	206 (98%)	5 (2%)	0	100	100
3	P	220/291 (76%)	215 (98%)	5 (2%)	0	100	100
3	Q	220/291 (76%)	214 (97%)	6 (3%)	0	100	100
3	R	220/291 (76%)	216 (98%)	4 (2%)	0	100	100
3	S	220/291 (76%)	215 (98%)	5 (2%)	0	100	100
3	T	220/291 (76%)	217 (99%)	3 (1%)	0	100	100
3	U	220/291 (76%)	216 (98%)	4 (2%)	0	100	100
3	V	220/291 (76%)	216 (98%)	4 (2%)	0	100	100
3	W	220/291 (76%)	213 (97%)	7 (3%)	0	100	100
3	X	220/291 (76%)	218 (99%)	2 (1%)	0	100	100
3	Y	220/291 (76%)	217 (99%)	3 (1%)	0	100	100
3	Z	220/291 (76%)	216 (98%)	4 (2%)	0	100	100
3	a	220/291 (76%)	216 (98%)	4 (2%)	0	100	100
3	b	220/291 (76%)	215 (98%)	5 (2%)	0	100	100
3	c	220/291 (76%)	217 (99%)	3 (1%)	0	100	100
4	d	2/4 (50%)	2 (100%)	0	0	100	100
4	e	2/4 (50%)	2 (100%)	0	0	100	100
4	f	2/4 (50%)	1 (50%)	1 (50%)	0	100	100
4	g	2/4 (50%)	2 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	h	2/4 (50%)	1 (50%)	1 (50%)	0	100	100
4	i	2/4 (50%)	2 (100%)	0	0	100	100
4	j	2/4 (50%)	2 (100%)	0	0	100	100
All	All	8825/11228 (79%)	8594 (97%)	230 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	58	ASP

5.3.2 Protein sidechains (i)

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	A	396/511 (78%)	394 (100%)	2 (0%)	88	95
1	B	403/511 (79%)	401 (100%)	2 (0%)	88	95
1	C	394/511 (77%)	390 (99%)	4 (1%)	76	90
1	D	384/511 (75%)	379 (99%)	5 (1%)	69	87
1	E	403/511 (79%)	402 (100%)	1 (0%)	93	98
1	F	403/511 (79%)	403 (100%)	0	100	100
2	G	165/192 (86%)	163 (99%)	2 (1%)	71	88
2	H	165/192 (86%)	163 (99%)	2 (1%)	71	88
2	I	165/192 (86%)	165 (100%)	0	100	100
2	J	165/192 (86%)	164 (99%)	1 (1%)	86	94
2	K	165/192 (86%)	164 (99%)	1 (1%)	86	94
2	L	165/192 (86%)	163 (99%)	2 (1%)	71	88
2	M	165/192 (86%)	162 (98%)	3 (2%)	59	82
2	N	165/192 (86%)	164 (99%)	1 (1%)	86	94
2	O	165/192 (86%)	164 (99%)	1 (1%)	86	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	k	165/192 (86%)	163 (99%)	2 (1%)	71 88
2	l	165/192 (86%)	165 (100%)	0	100 100
2	m	165/192 (86%)	162 (98%)	3 (2%)	59 82
2	n	165/192 (86%)	165 (100%)	0	100 100
2	o	165/192 (86%)	163 (99%)	2 (1%)	71 88
3	P	165/217 (76%)	165 (100%)	0	100 100
3	Q	165/217 (76%)	165 (100%)	0	100 100
3	R	165/217 (76%)	165 (100%)	0	100 100
3	S	165/217 (76%)	165 (100%)	0	100 100
3	T	164/217 (76%)	164 (100%)	0	100 100
3	U	165/217 (76%)	165 (100%)	0	100 100
3	V	165/217 (76%)	165 (100%)	0	100 100
3	W	165/217 (76%)	165 (100%)	0	100 100
3	X	165/217 (76%)	165 (100%)	0	100 100
3	Y	165/217 (76%)	165 (100%)	0	100 100
3	Z	165/217 (76%)	165 (100%)	0	100 100
3	a	165/217 (76%)	164 (99%)	1 (1%)	86 94
3	b	165/217 (76%)	163 (99%)	2 (1%)	71 88
3	c	165/217 (76%)	165 (100%)	0	100 100
4	d	3/3 (100%)	3 (100%)	0	100 100
4	e	3/3 (100%)	3 (100%)	0	100 100
4	f	3/3 (100%)	3 (100%)	0	100 100
4	g	3/3 (100%)	3 (100%)	0	100 100
4	h	3/3 (100%)	3 (100%)	0	100 100
4	i	3/3 (100%)	3 (100%)	0	100 100
4	j	3/3 (100%)	3 (100%)	0	100 100
All	All	7023/8813 (80%)	6986 (100%)	37 (0%)	89 95

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	91	ARG
3	b	388	ARG

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Mol	Chain	Res	Type
2	M	91	ARG
2	N	135	ARG
1	D	580	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
3	Y	390	ASN
3	b	322	GLN
4	h	172	GLN
3	c	381	ASN
3	a	396	GLN

5.3.3 RNA (i)

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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

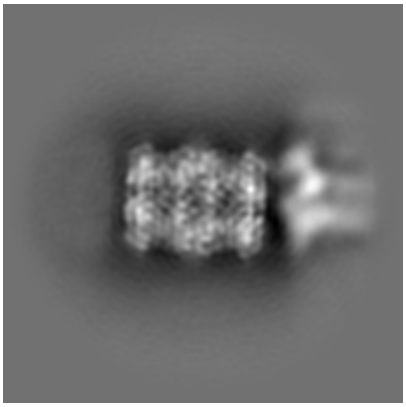
This section contains visualisations of the EMDB entry EMD-27225. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

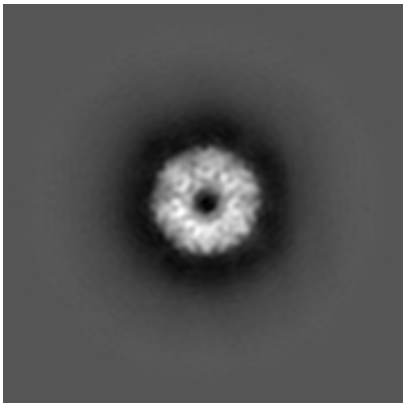
6.1 Orthogonal projections

6.1.1 Primary map

X



Y

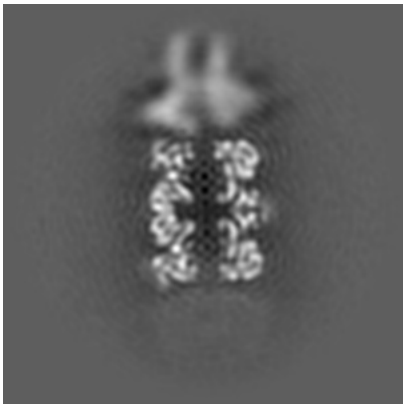


Z

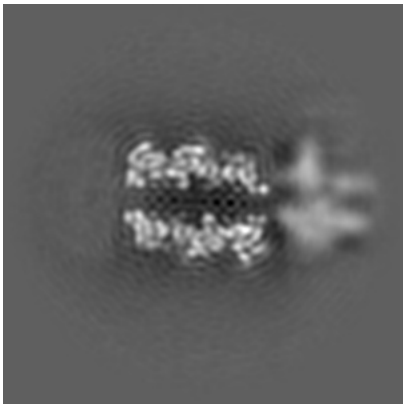
The images above show the map projected in three orthogonal directions.

6.2 Central slices

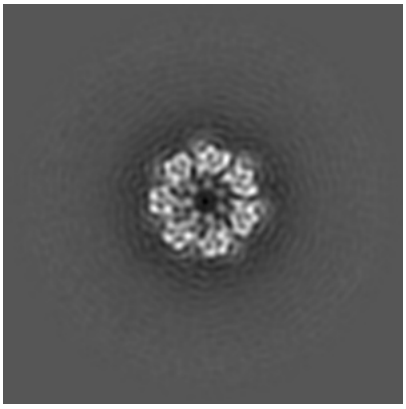
6.2.1 Primary map



X Index: 48



Y Index: 48

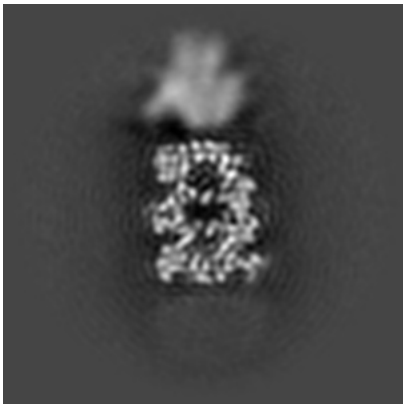


Z Index: 48

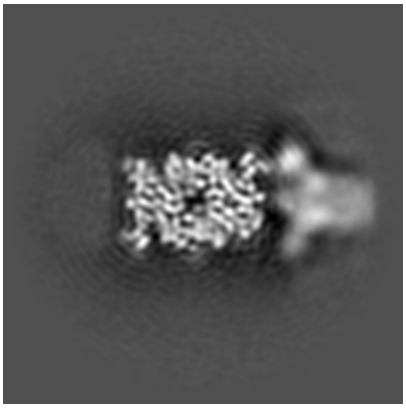
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

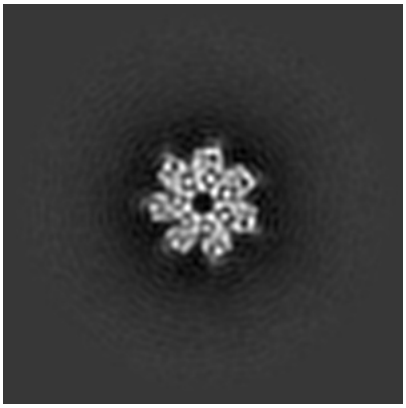
6.3.1 Primary map



X Index: 44



Y Index: 42



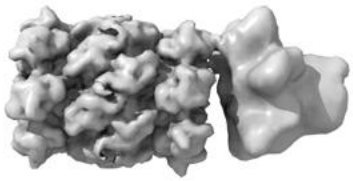
Z Index: 59

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X



Y

Z

The images above show the 3D surface view of the map at the recommended contour level 3.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

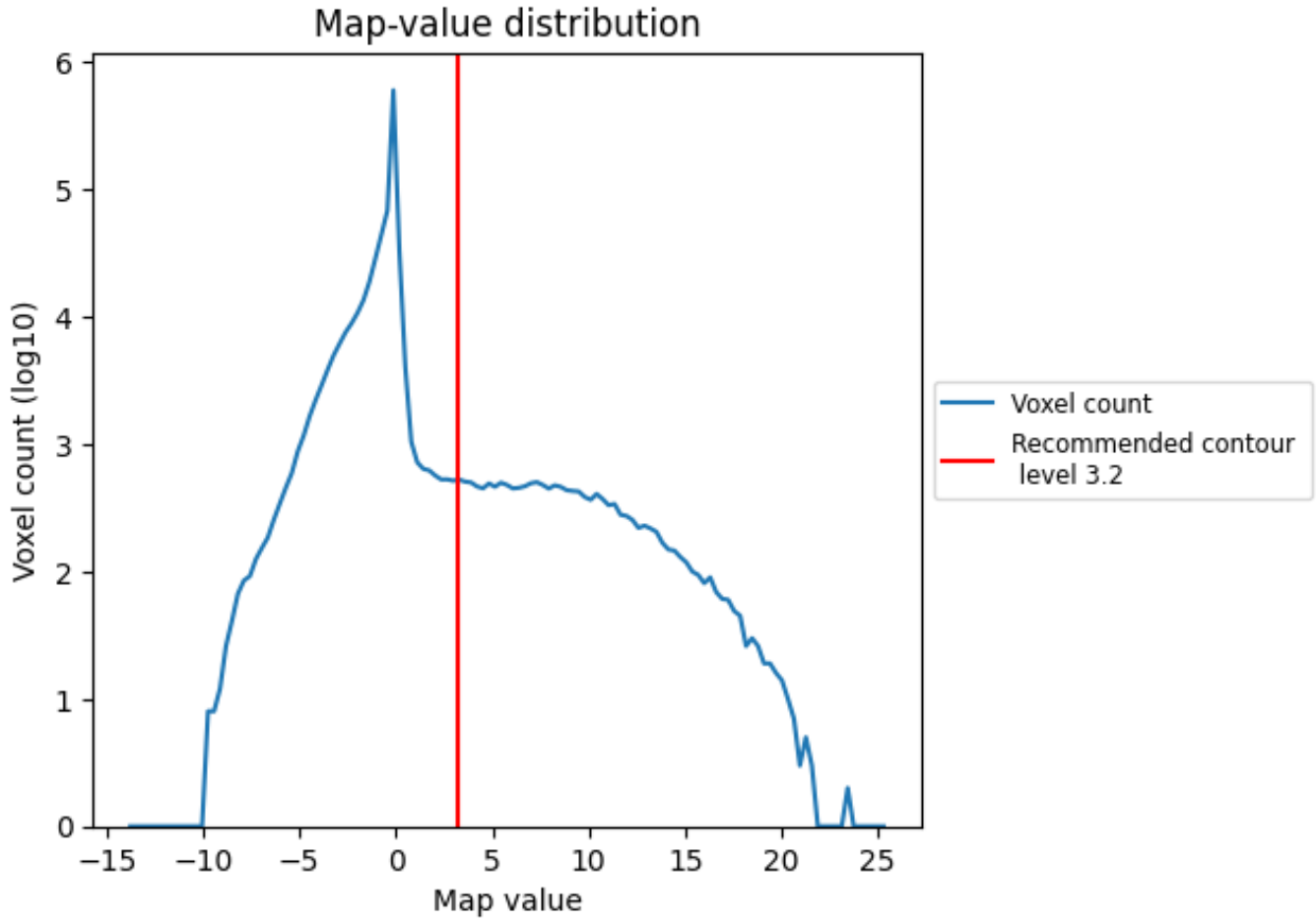
6.5 Mask visualisation (i)

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

7 Map analysis

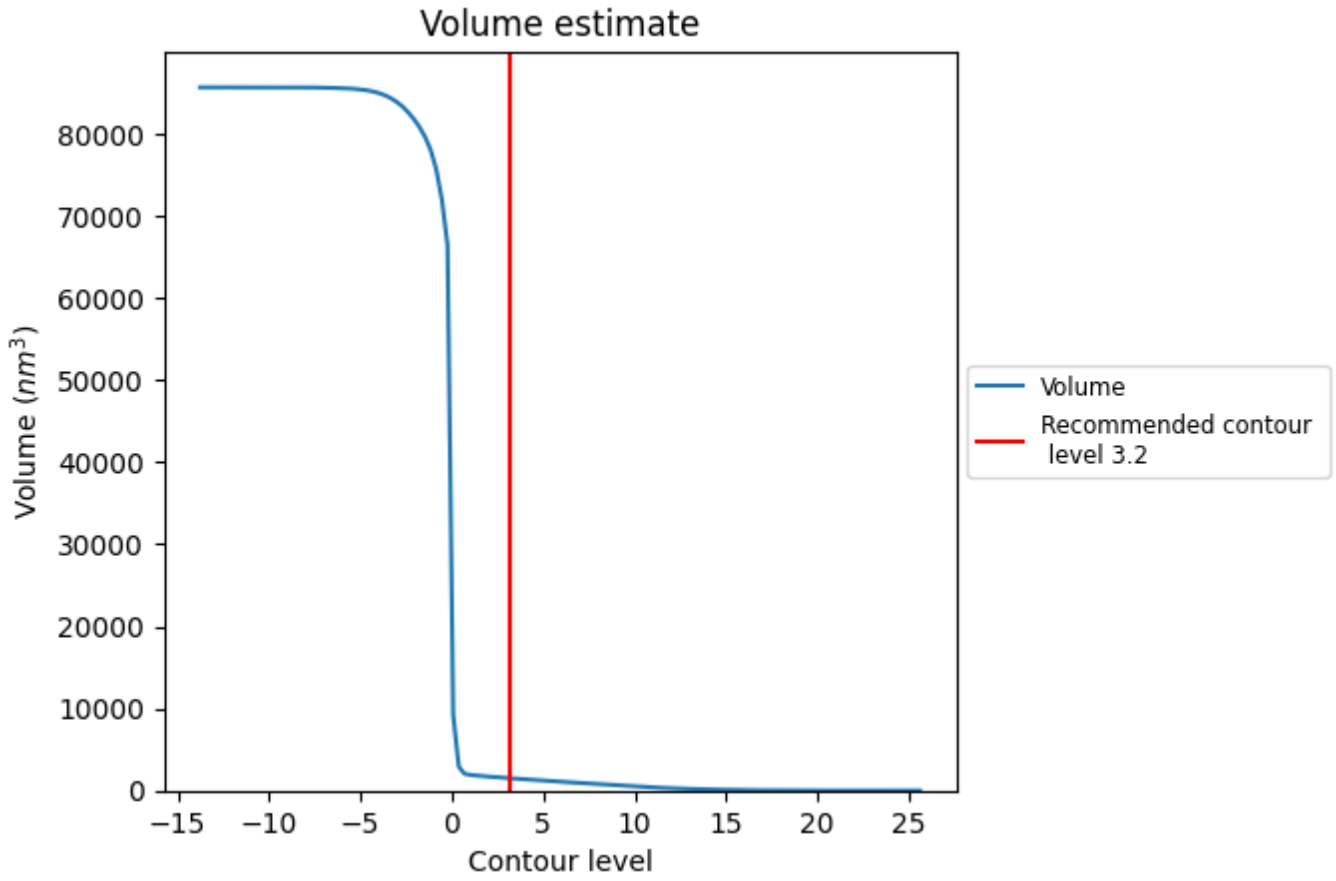
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

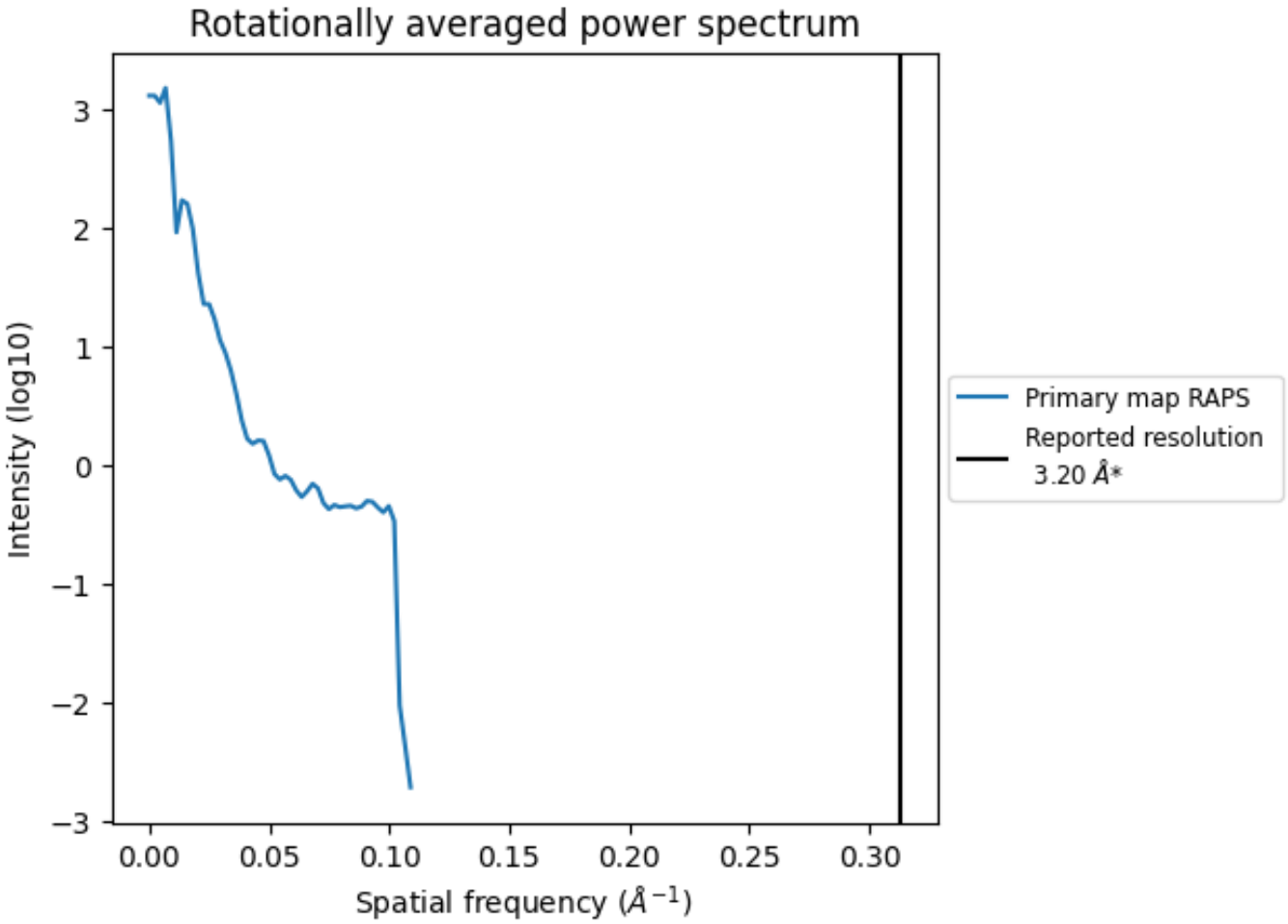
7.2 Volume estimate (i)



The volume at the recommended contour level is 1496 nm^3; this corresponds to an approximate mass of 1352 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 (i)



*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

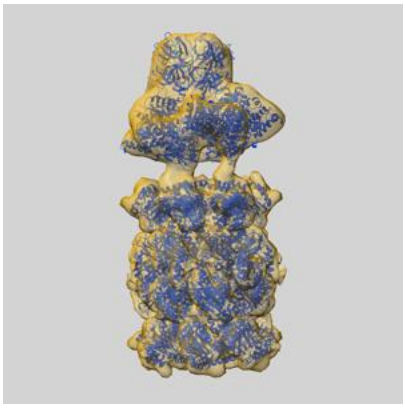
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

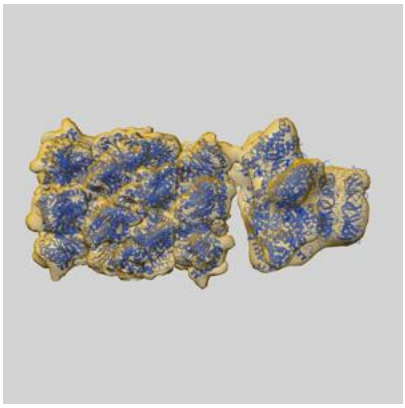
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-27225 and PDB model 8D6X. Per-residue inclusion information can be found in section 3 on page 8.

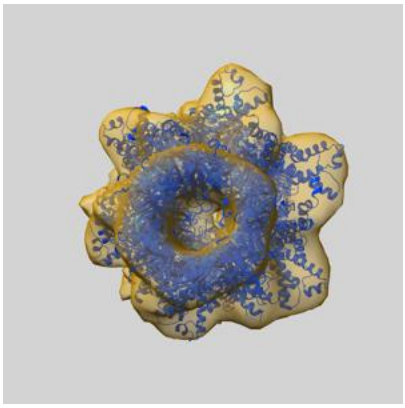
9.1 Map-model overlay



X



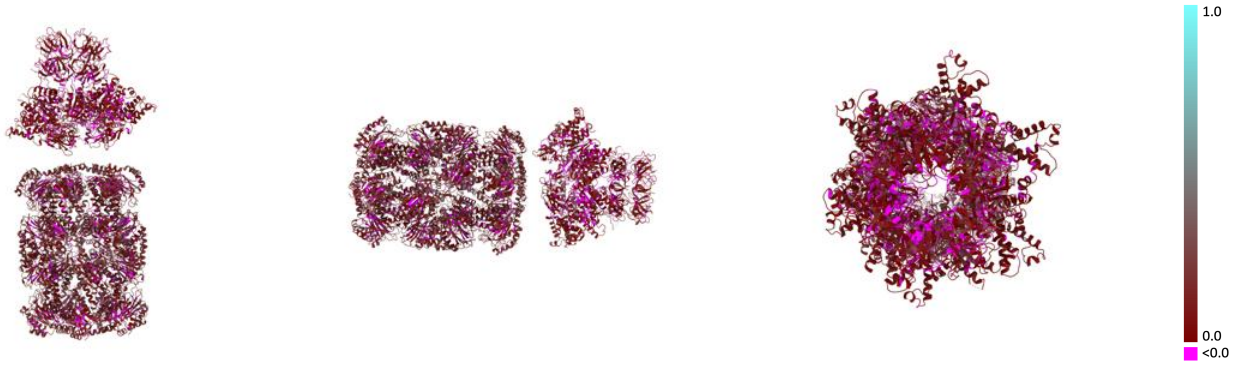
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.2 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.

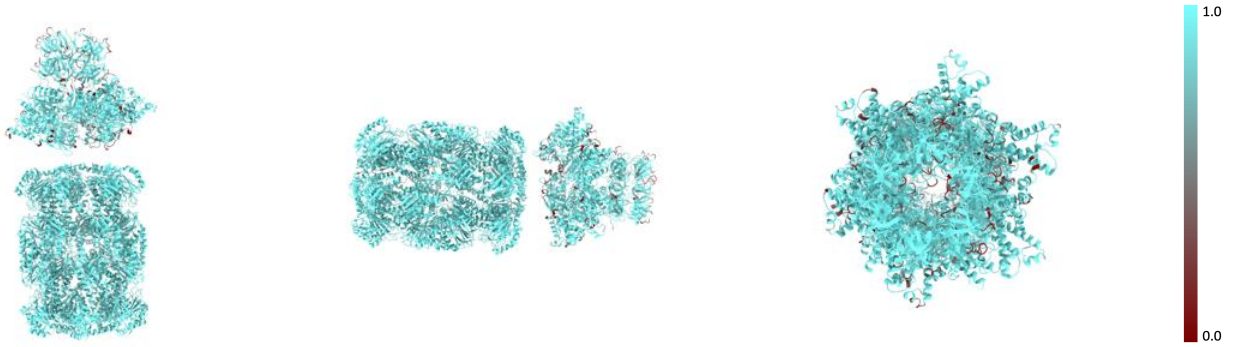
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

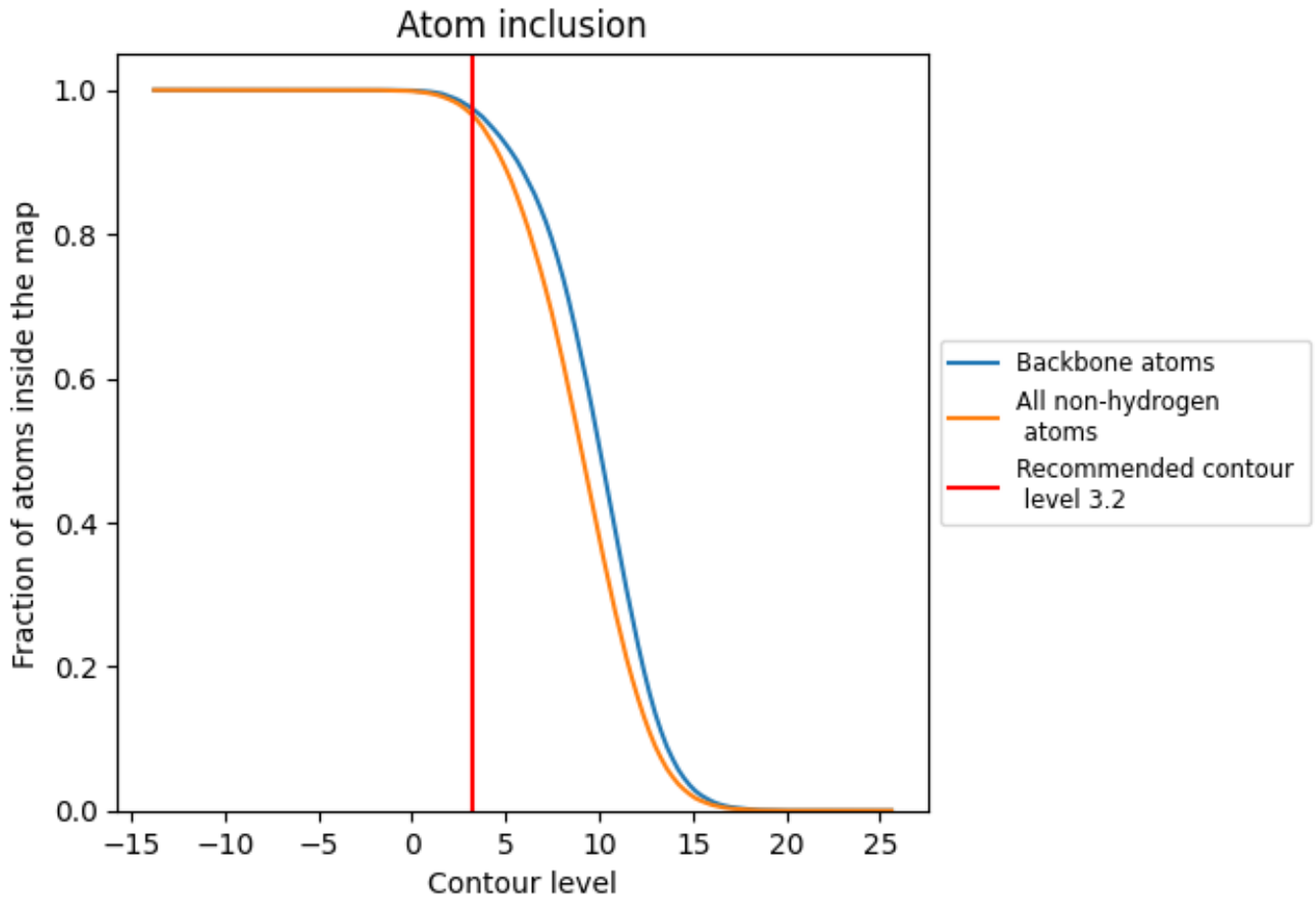
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (3.2).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (3.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9657	0.1130
A	0.9471	0.0640
B	0.9415	0.0520
C	0.9054	0.0630
D	0.9210	0.0650
E	0.9170	0.0510
F	0.8949	0.0490
G	0.9863	0.1440
H	0.9851	0.1450
I	0.9913	0.1470
J	0.9851	0.1430
K	0.9875	0.1370
L	0.9807	0.1380
M	0.9801	0.1450
N	0.9832	0.1440
O	0.9807	0.1390
P	0.9925	0.1410
Q	0.9913	0.1340
R	0.9931	0.1350
S	0.9913	0.1350
T	0.9925	0.1350
U	0.9913	0.1340
V	0.9906	0.1380
W	0.9888	0.1390
X	0.9888	0.1430
Y	0.9888	0.1450
Z	0.9894	0.1380
a	0.9925	0.1440
b	0.9888	0.1430
c	0.9956	0.1390
d	0.6970	-0.1050
e	0.3939	-0.0410
f	0.6061	-0.0890
g	0.5152	-0.0890
h	0.5152	-0.0930

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Chain	Atom inclusion	Q-score
i	0.9091	-0.0120
j	0.8788	-0.0480
k	0.9795	0.1430
l	0.9950	0.1420
m	0.9925	0.1440
n	0.9950	0.1460
o	0.9869	0.1410