



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:49 AM UTC

PDB ID : 7YPH / pdb_00007yph
EMDB ID : EMD-34000
Title : Open-spiral pentamer of the substrate-free Lon protease with a Y224S mutation
Authors : Li, S.; Hsieh, K.Y.; Kuo, C.I.; Lee, S.H.; Ho, M.R.; Wang, C.H.; Zhang, K.; Chang, C.I.
Deposited on : 2022-08-03
Resolution : 3.68 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:

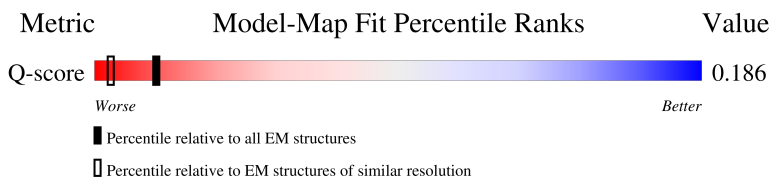
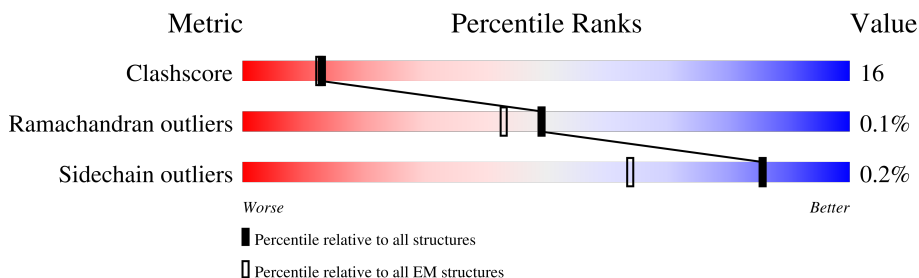
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

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 3.68 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	11376 (3.18 - 4.18)

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	A	793	30% 66% 32% .
1	B	793	28% 60% 37% ..
1	C	793	26% 64% 34% .
1	D	793	28% 61% 37% .

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Mol	Chain	Length	Quality of chain
1	E	793	37% 66% 31%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 30407 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.

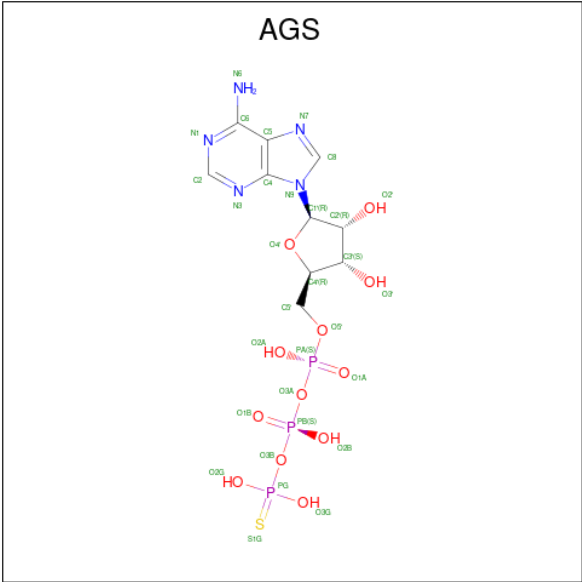
- Molecule 1 is a protein called Lon protease.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	773	Total	C	N	O	S	0	0
			6069	3832	1067	1149	21		
1	B	773	Total	C	N	O	S	0	0
			6069	3832	1067	1149	21		
1	C	773	Total	C	N	O	S	0	0
			6069	3832	1067	1149	21		
1	D	773	Total	C	N	O	S	0	0
			6069	3832	1067	1149	21		
1	E	773	Total	C	N	O	S	0	0
			6069	3832	1067	1149	21		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	224	SER	TYR	engineered mutation	UNP A0A059VAZ3
B	224	SER	TYR	engineered mutation	UNP A0A059VAZ3
C	224	SER	TYR	engineered mutation	UNP A0A059VAZ3
D	224	SER	TYR	engineered mutation	UNP A0A059VAZ3
E	224	SER	TYR	engineered mutation	UNP A0A059VAZ3

- Molecule 2 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S) (labeled as "Ligand of Interest" by depositor).

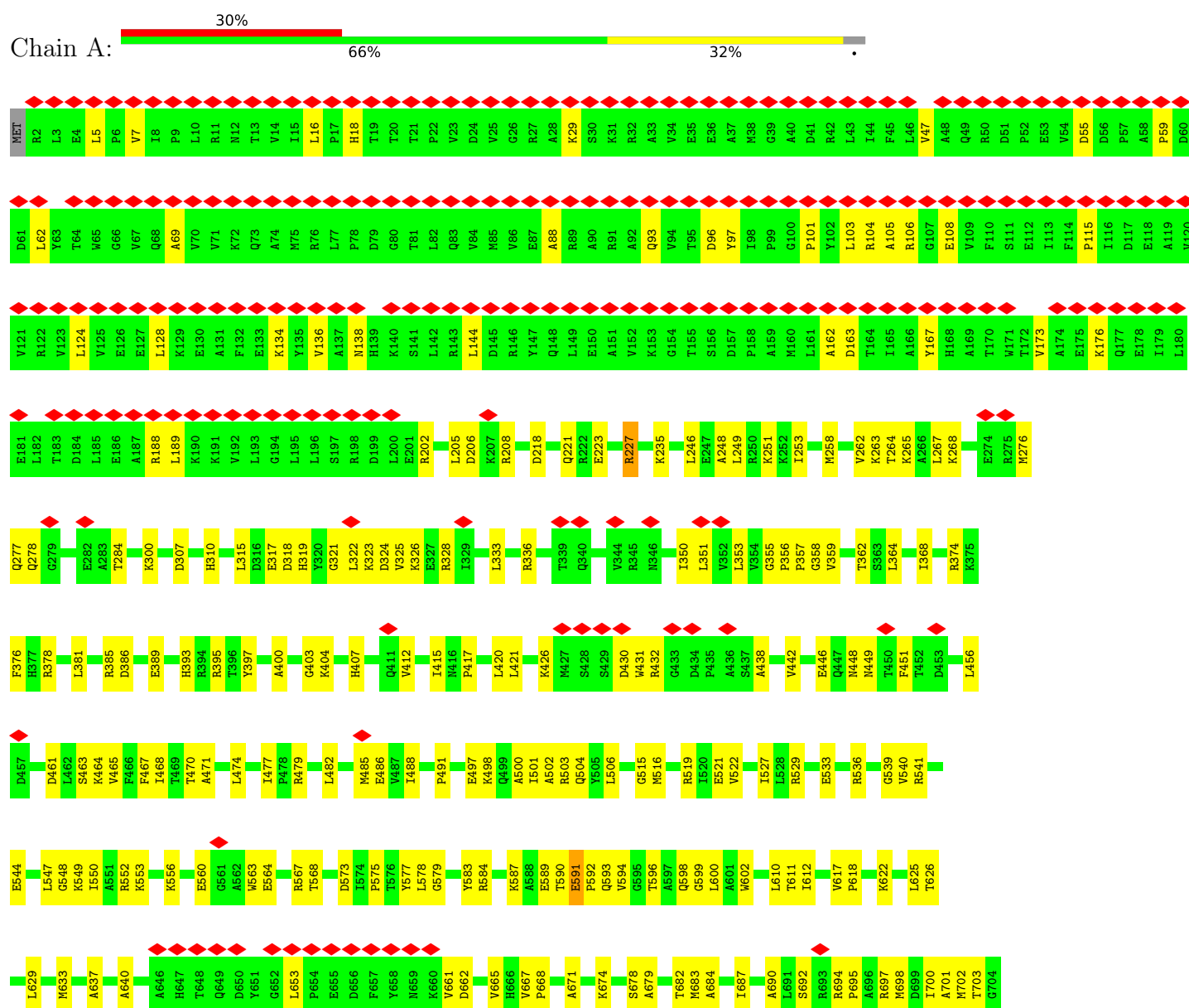


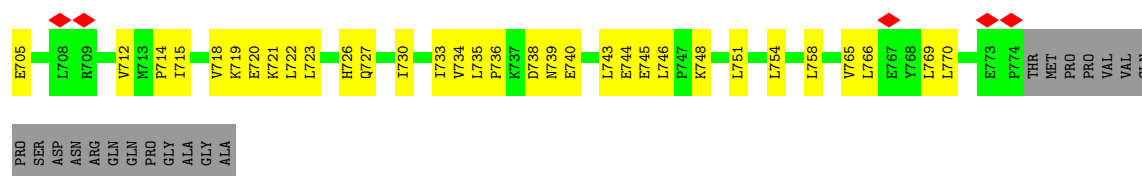
Mol	Chain	Residues	Atoms						AltConf
2	B	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	D	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

3 Residue-property plots

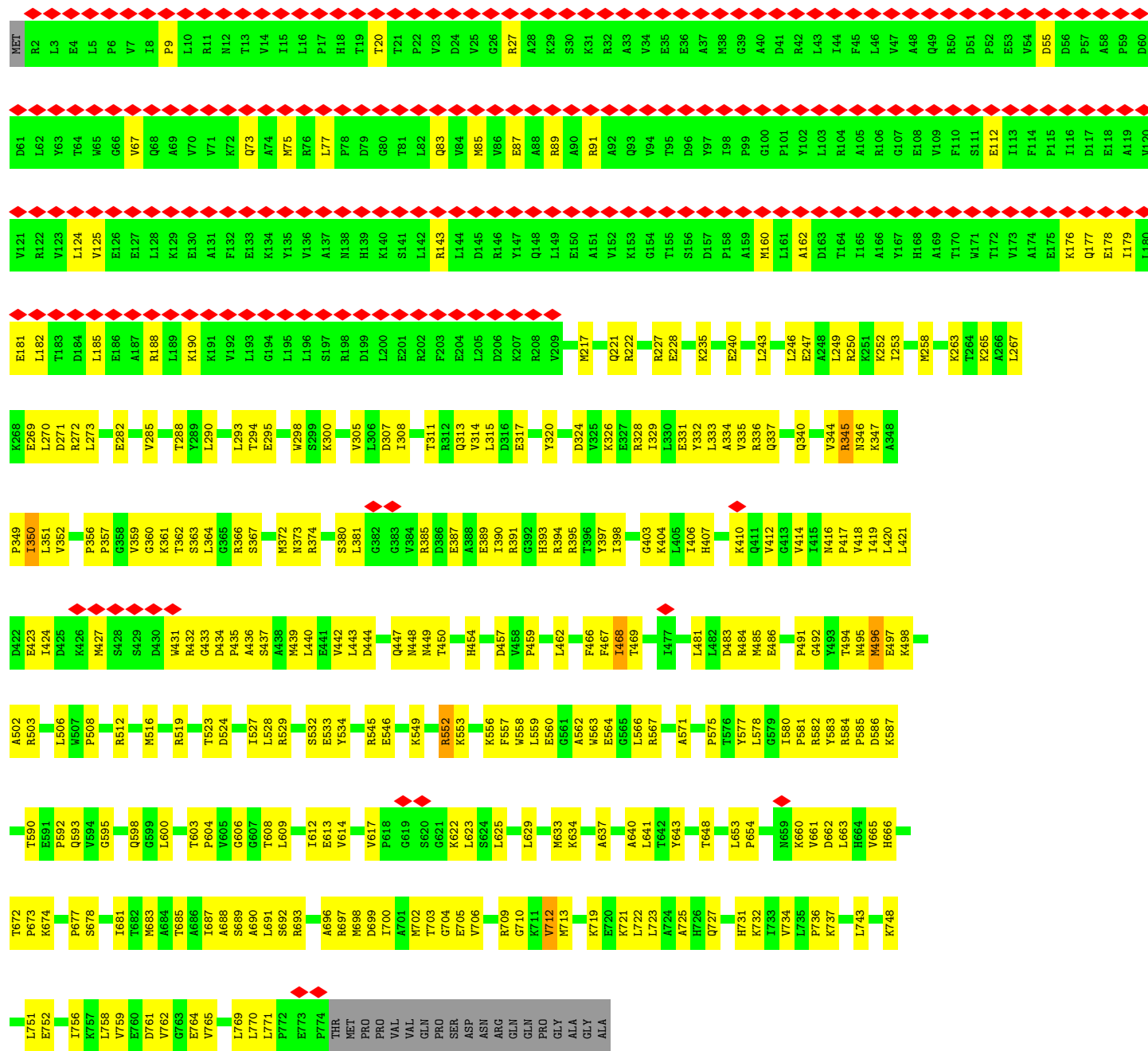
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Lon protease

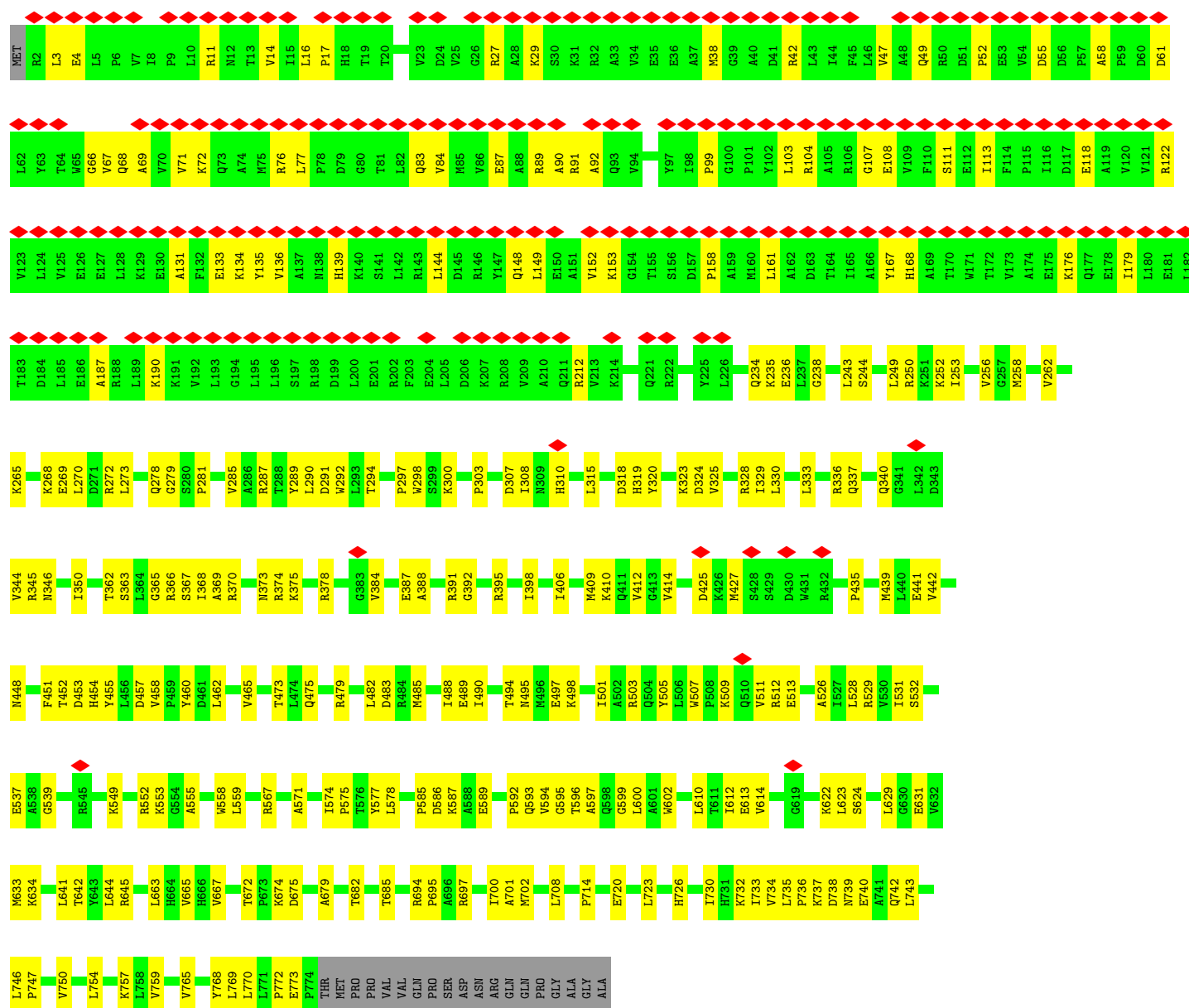




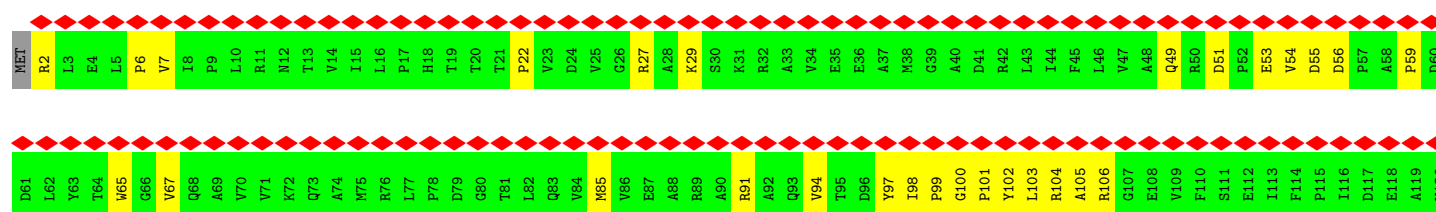
• Molecule 1: Lon protease

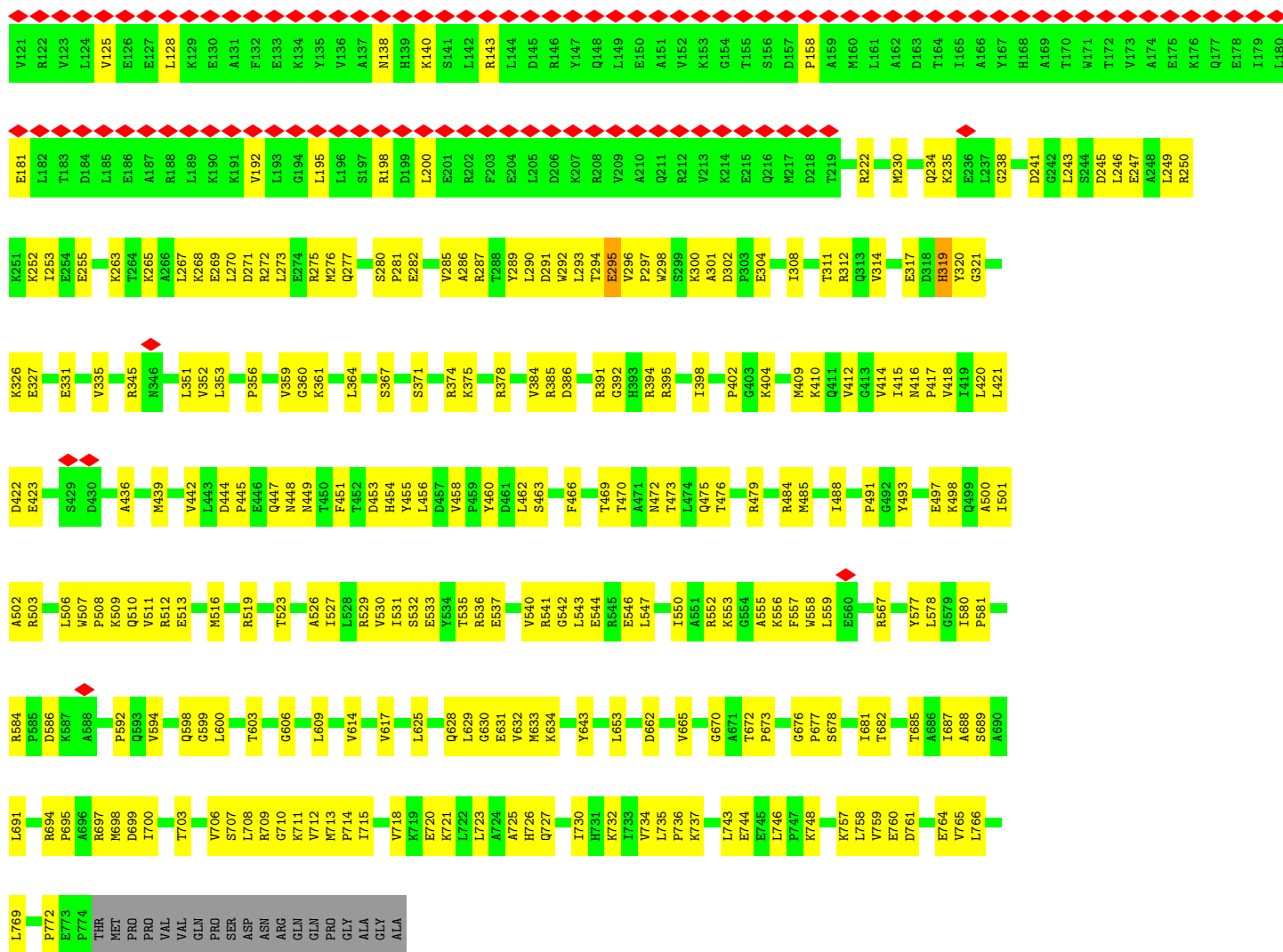


• Molecule 1: Lon protease

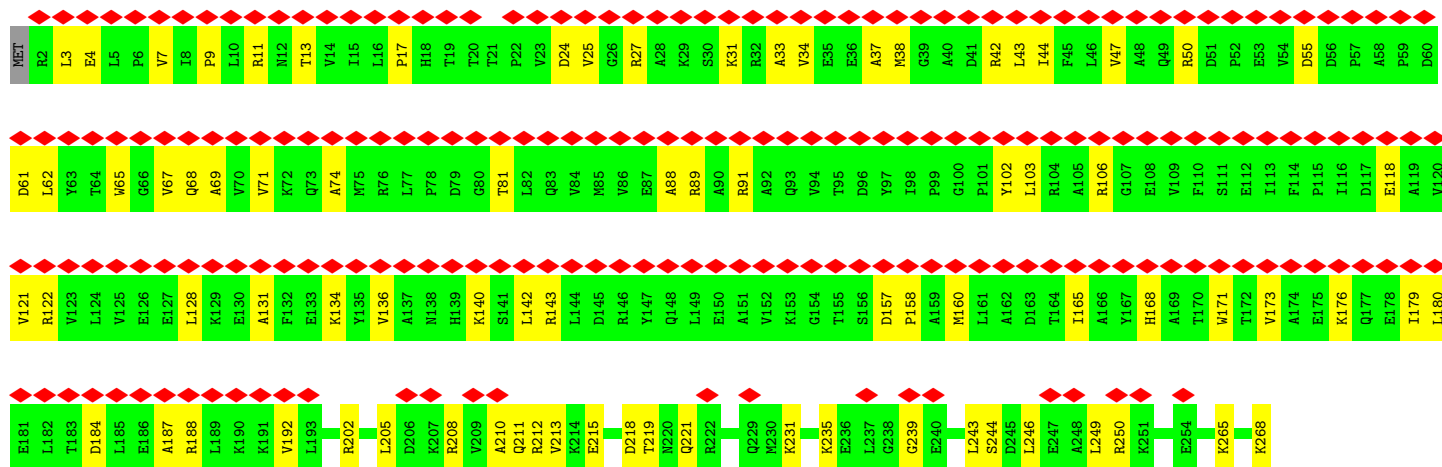


• Molecule 1: Lon protease





• Molecule 1: Lon protease



GLN	K711	L623	R529	P417	L342	E269
PRO	V712	T626	V530	V418	D343	L270
SER	W713		I531	I419	V344	D271
ASP		G630		L420	R345	R272
ASN	P714		Y534	L421	N346	L273
ARG	I715	K634	G542	D422	K347	E274
GLN	G716		L543	E423	V352	R275
GLN	G717	L641	E544	I424	L353	M276
PRO	V718		R545	D425	V354	Q277
GLY	K719	R645	E546	S428	G355	Q278
ALA	A725	A646	L547	D434	P356	G279
GLY		H647	G548	P435		S280
ALA	G729	T648	K549	A436	K361	
	K732	Q649	I550	L443	T362	A283
	I733	D650	K553	D444	S363	T284
		Y651	W558	Q447	G365	V285
	K737	G652	N563	D453	S367	A286
	D738	L653	E564	H454	I368	R287
	W739	P654	G565	Y455	I369	
	E740	D656	L566	K464	A369	L290
		F657	R567	V465	R370	D291
	L743	Y658	T568	T469	F376	W292
	E744	K660	A571	T470	H377	L293
	E745	L663	S572	A471	I378	T294
	E746	H664	D573	N472	I379	E295
	L746	V665	I574	T473	S380	V296
	P747	G670		L474	L381	P297
	K748	G676	I580	P478		W298
	E749		P581	R479	K300	S299
	V750		R582	P480		
	L751	I681	K587	L481	I308	I308
	E752	T682	A588	L482	N309	H310
	G753	M683	E589	D483	T311	R312
	E755	A684	T590	R484	Q813	Q813
	L756	T685	E591		V814	V814
	W757	A690	P592	I488	L315	L315
	K757	L691	Q593	E489	D316	D316
	L758	S692	V594	I490	E317	E317
	W759	R693	G595	Q499	D318	
	E760		T596	I501	L322	L322
	D761	A696	L600	Y505	K323	K323
	V762	R697	A601		D324	D324
	G763	M698	W602	G518	V325	V325
	E764	G699	T603	R519	K326	K326
	V765	D699	P604	I520	E327	E327
	L766	I700	E613	E521	R328	R328
	E767	A701	V614	V522	I329	I329
	W768	M702	A615	T523	L330	L330
	L769	T703	A616	D524	E331	E331
	L770	G704	V617		A334	A334
	L771	E705			L338	L338
	P772	L708			T339	T339
	E773	R709			Q340	Q340
	P774	G710			G341	G341
	THR					
	MET					
	PRO					
	PRO					
	VAL					
	VAL					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	777117	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	73.8	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.276	Depositor
Minimum map value	-0.130	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.035	Depositor
Map size ($\text{\AA}$)	318.72, 318.72, 318.72	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	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: AGS

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	0.34	0/6177	0.72	1/8370 (0.0%)
1	B	0.42	0/6177	0.77	6/8370 (0.1%)
1	C	0.40	0/6177	0.80	0/8370
1	D	0.43	0/6177	0.79	2/8370 (0.0%)
1	E	0.28	0/6177	0.67	2/8370 (0.0%)
All	All	0.38	0/30885	0.75	11/41850 (0.0%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	E	324	ASP	CA-C-N	5.96	132.69	121.97
1	E	324	ASP	C-N-CA	5.96	132.69	121.97
1	B	345	ARG	CA-C-N	-5.88	114.48	121.90
1	B	345	ARG	C-N-CA	-5.88	114.48	121.90
1	B	228	GLU	N-CA-CB	5.81	120.04	110.39

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	A	6069	0	6184	187	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	6069	0	6184	227	0
1	C	6069	0	6184	199	0
1	D	6069	0	6184	251	0
1	E	6069	0	6184	179	0
2	B	31	0	12	5	0
2	D	31	0	12	3	0
All	All	30407	0	30944	1004	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 16.

The worst 5 of 1004 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:C:685:THR:HG21	1:C:702:MET:HE1	1.40	1.04
1:B:564:GLU:HB2	1:B:567:ARG:HG2	1.41	1.00
1:B:712:VAL:HB	1:B:736:PRO:HG3	1.48	0.91
1:D:711:LYS:HA	1:D:761:ASP:HA	1.57	0.86
1:B:418:VAL:HG13	1:B:466:PHE:HB3	1.59	0.83

There are no symmetry-related clashes.

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	771/793 (97%)	707 (92%)	63 (8%)	1 (0%)	48	78
1	B	771/793 (97%)	700 (91%)	71 (9%)	0	100	100
1	C	771/793 (97%)	707 (92%)	64 (8%)	0	100	100
1	D	771/793 (97%)	710 (92%)	61 (8%)	0	100	100
1	E	771/793 (97%)	703 (91%)	67 (9%)	1 (0%)	48	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	3855/3965 (97%)	3527 (92%)	326 (8%)	2 (0%)	49 78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	325	VAL
1	A	591	GLU

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	A	649/665 (98%)	648 (100%)	1 (0%)	87 86
1	B	649/665 (98%)	646 (100%)	3 (0%)	81 80
1	C	649/665 (98%)	649 (100%)	0	100 100
1	D	649/665 (98%)	648 (100%)	1 (0%)	87 86
1	E	649/665 (98%)	649 (100%)	0	100 100
All	All	3245/3325 (98%)	3240 (100%)	5 (0%)	85 86

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	317	GLU
1	B	350	ILE
1	B	468	ILE
1	B	712	VAL
1	D	295	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	49	GLN
1	C	472	ASN

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Mol	Chain	Res	Type
1	E	277	GLN
1	C	234	GLN
1	C	593	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	$\# Z > 2$
2	AGS	B	801	-	32,33,33	0.56	0	45,52,52	0.67	2 (4%)
2	AGS	D	801	-	32,33,33	0.97	3 (9%)	45,52,52	1.08	1 (2%)

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
2	AGS	B	801	-	-	7/21/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AGS	D	801	-	-	9/21/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	801	AGS	PB-O3B	-3.28	1.56	1.59
2	D	801	AGS	PA-O3A	-2.72	1.56	1.59
2	D	801	AGS	PB-O3A	-2.16	1.57	1.59

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	AGS	PB-O3B-PG	-6.66	108.79	133.17
2	B	801	AGS	O2G-PG-O3B	2.74	113.78	104.64
2	B	801	AGS	PB-O3B-PG	-2.17	125.22	133.17

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	801	AGS	PB-O3B-PG-O2G
2	B	801	AGS	PB-O3B-PG-O3G
2	B	801	AGS	C5'-O5'-PA-O1A
2	B	801	AGS	C5'-O5'-PA-O2A
2	B	801	AGS	C5'-O5'-PA-O3A

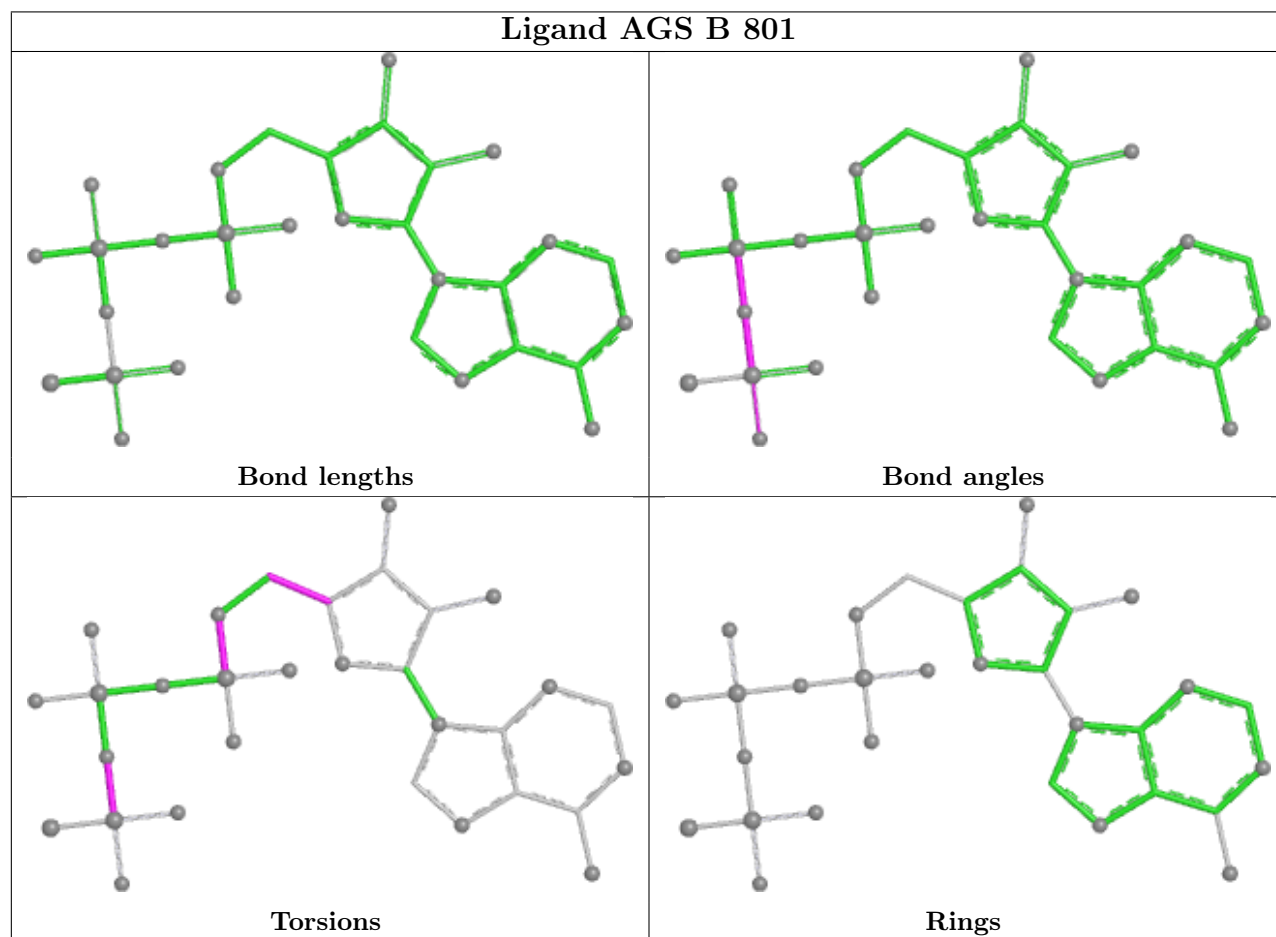
There are no ring outliers.

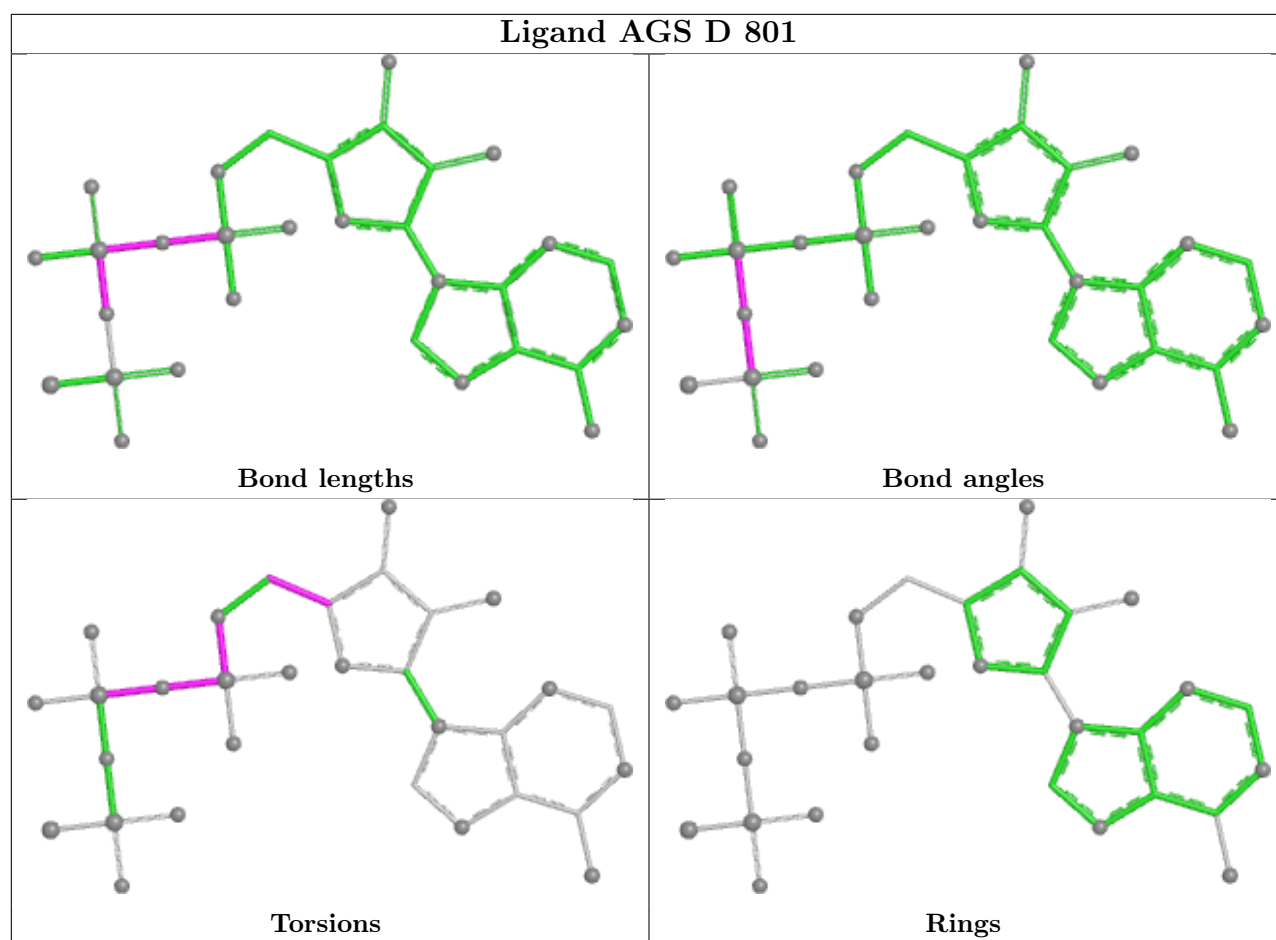
2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	AGS	5	0
2	D	801	AGS	3	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.





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.

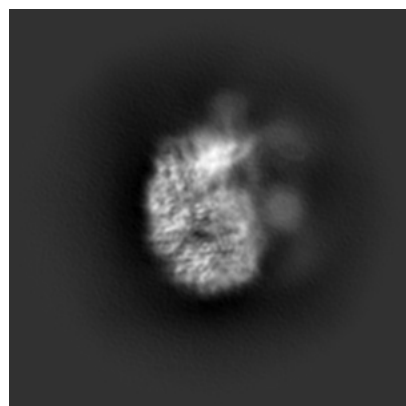
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34000. These allow visual inspection of the internal detail of the map and identification of artifacts.

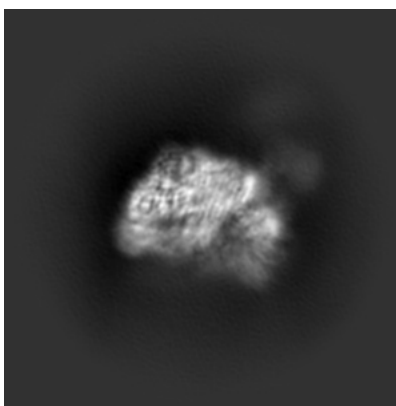
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

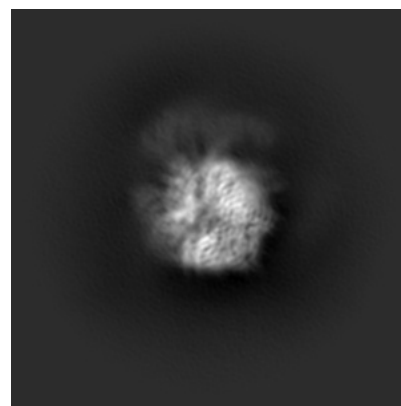
6.1.1 Primary map



X

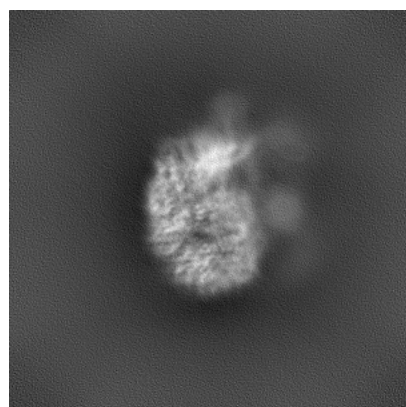


Y

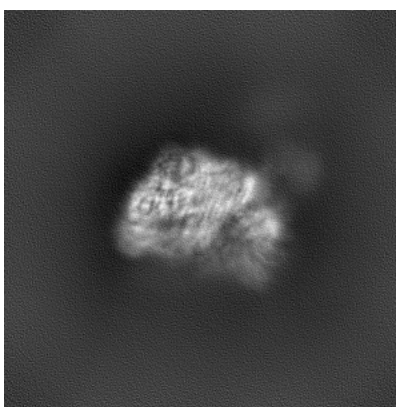


Z

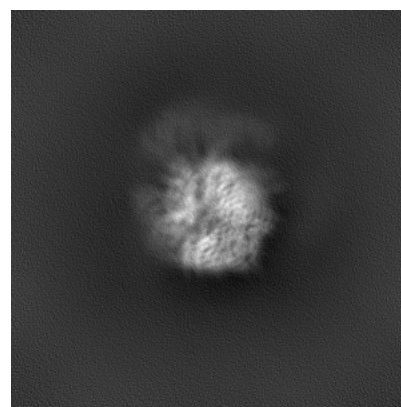
6.1.2 Raw map



X



Y

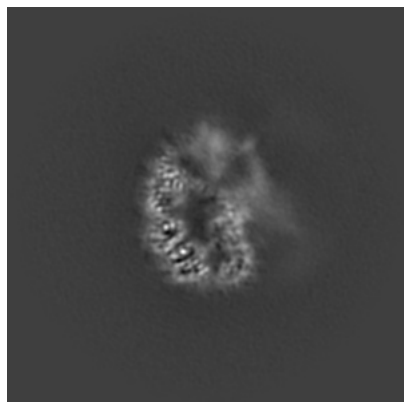


Z

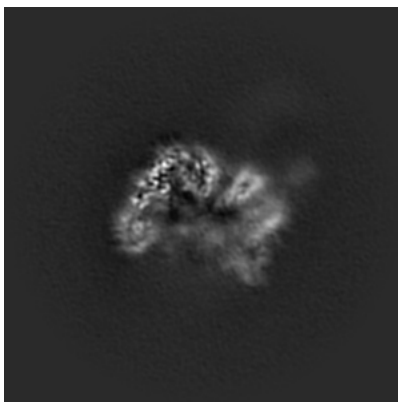
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

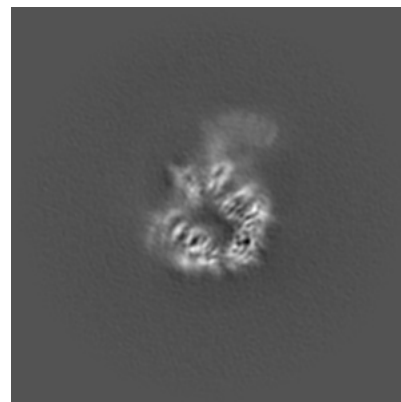
6.2.1 Primary map



X Index: 192

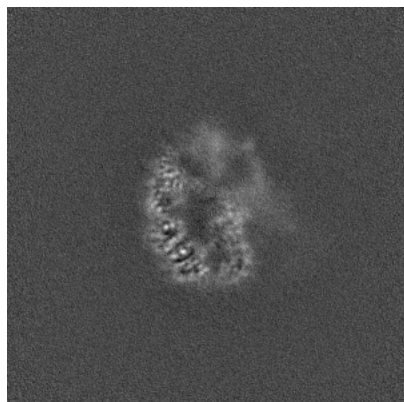


Y Index: 192

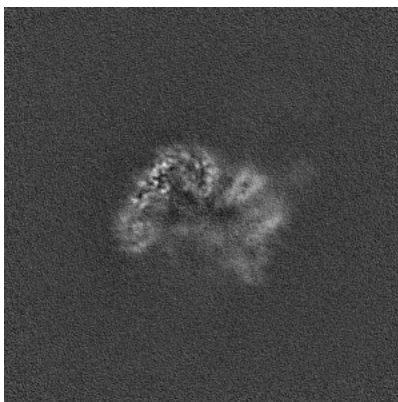


Z Index: 192

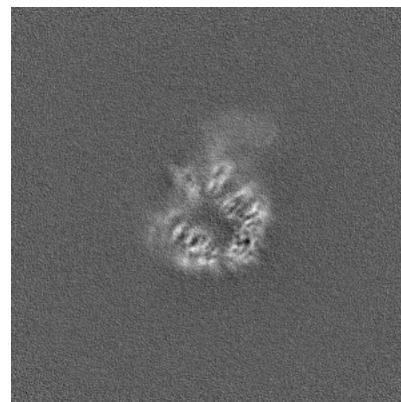
6.2.2 Raw map



X Index: 192



Y Index: 192

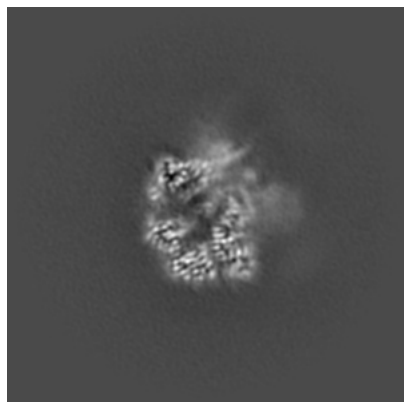


Z Index: 192

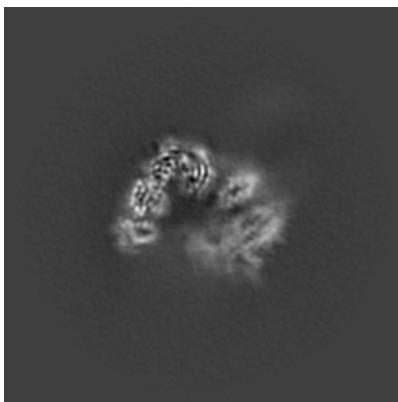
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

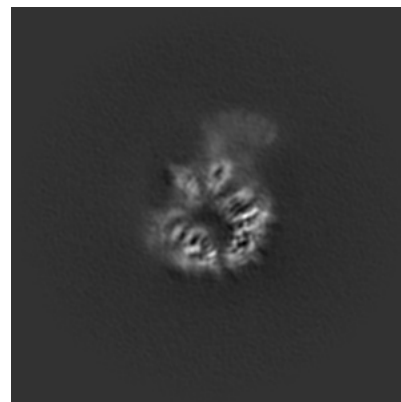
6.3.1 Primary map



X Index: 203

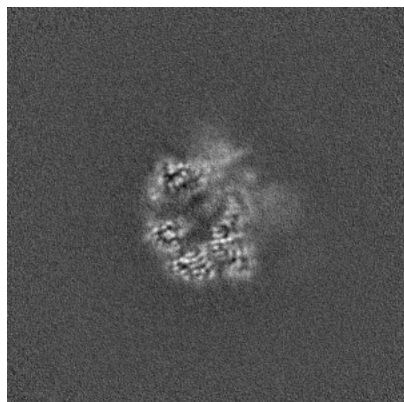


Y Index: 184

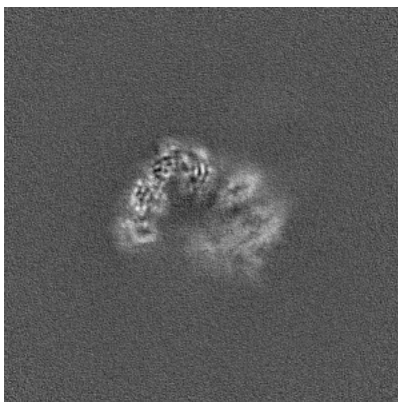


Z Index: 190

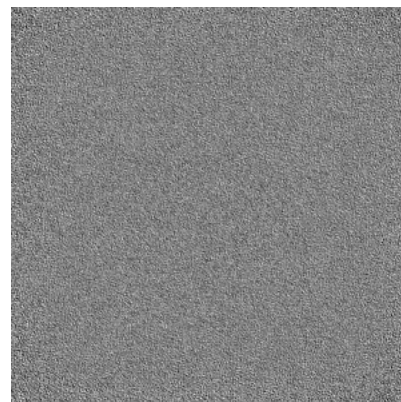
6.3.2 Raw map



X Index: 202



Y Index: 185



Z Index: 0

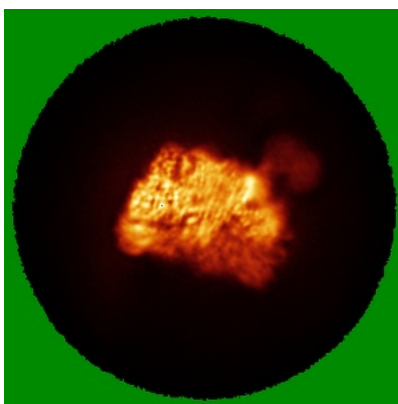
The images above show the largest variance slices of the map in three orthogonal directions.

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

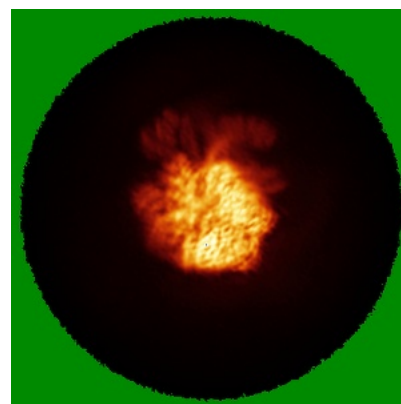
6.4.1 Primary map



X

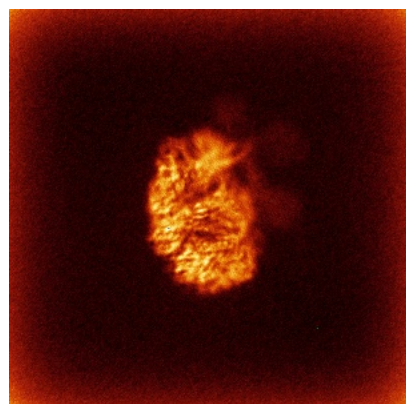


Y

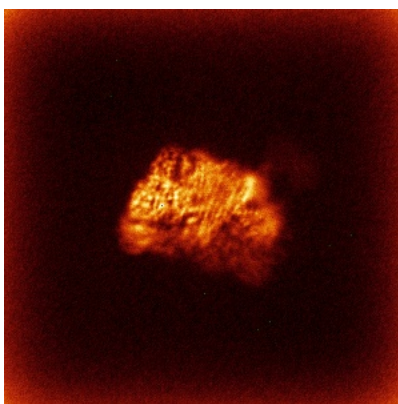


Z

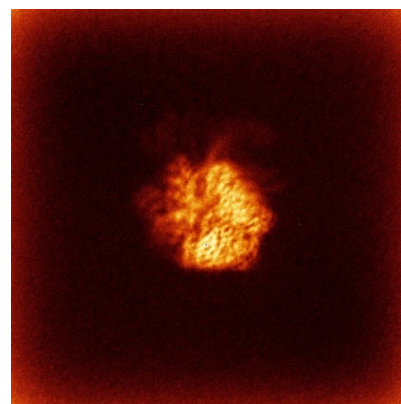
6.4.2 Raw map



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



X



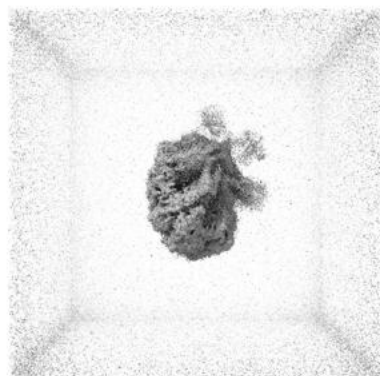
Y



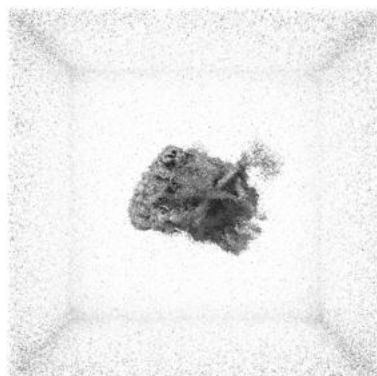
Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

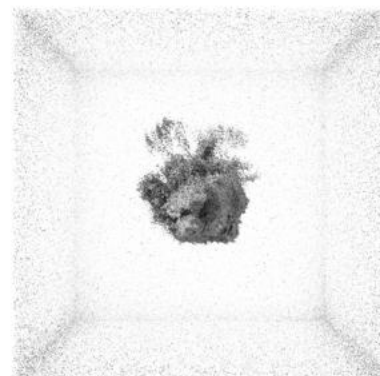
6.5.2 Raw map



X



Y



Z

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.

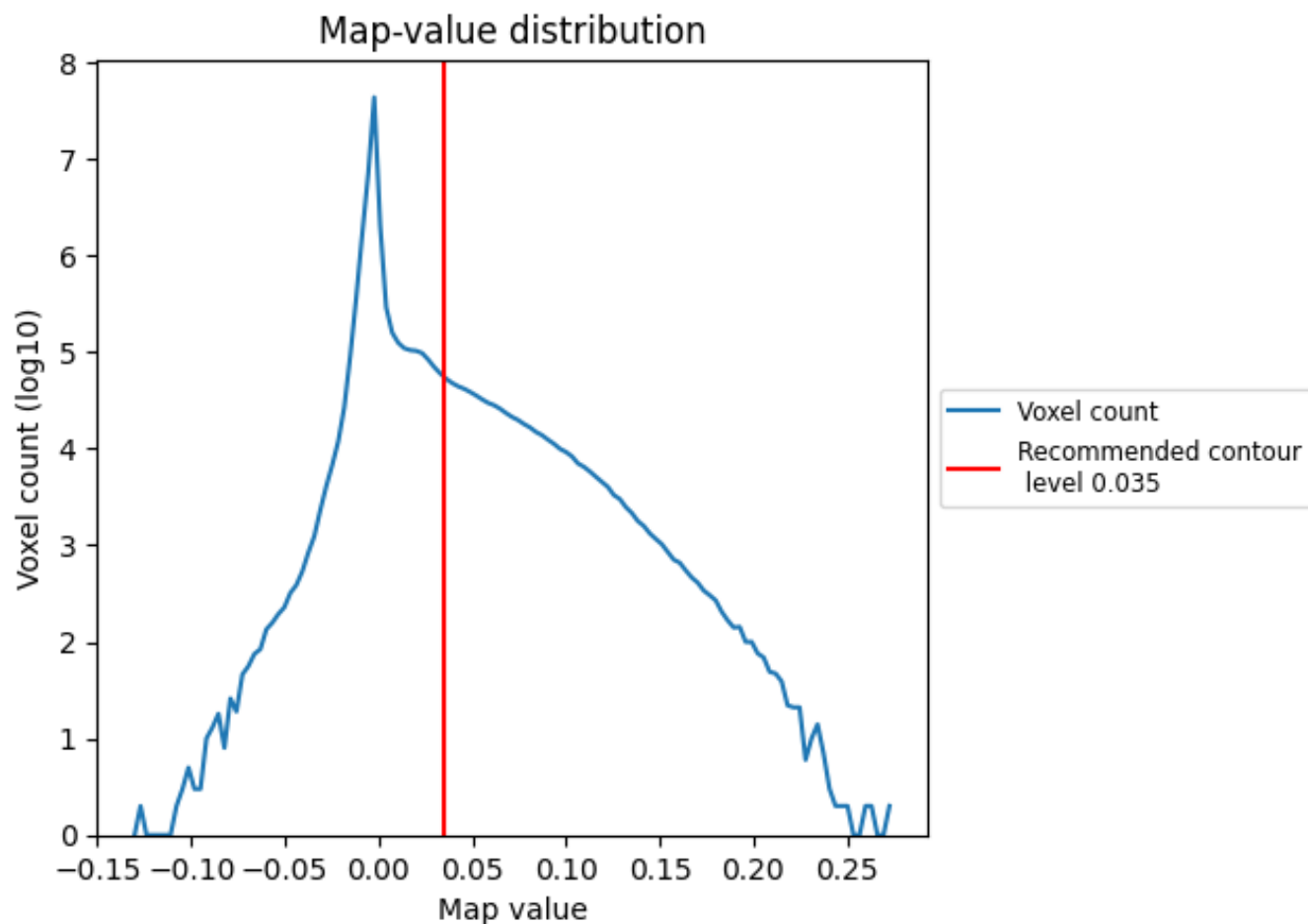
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

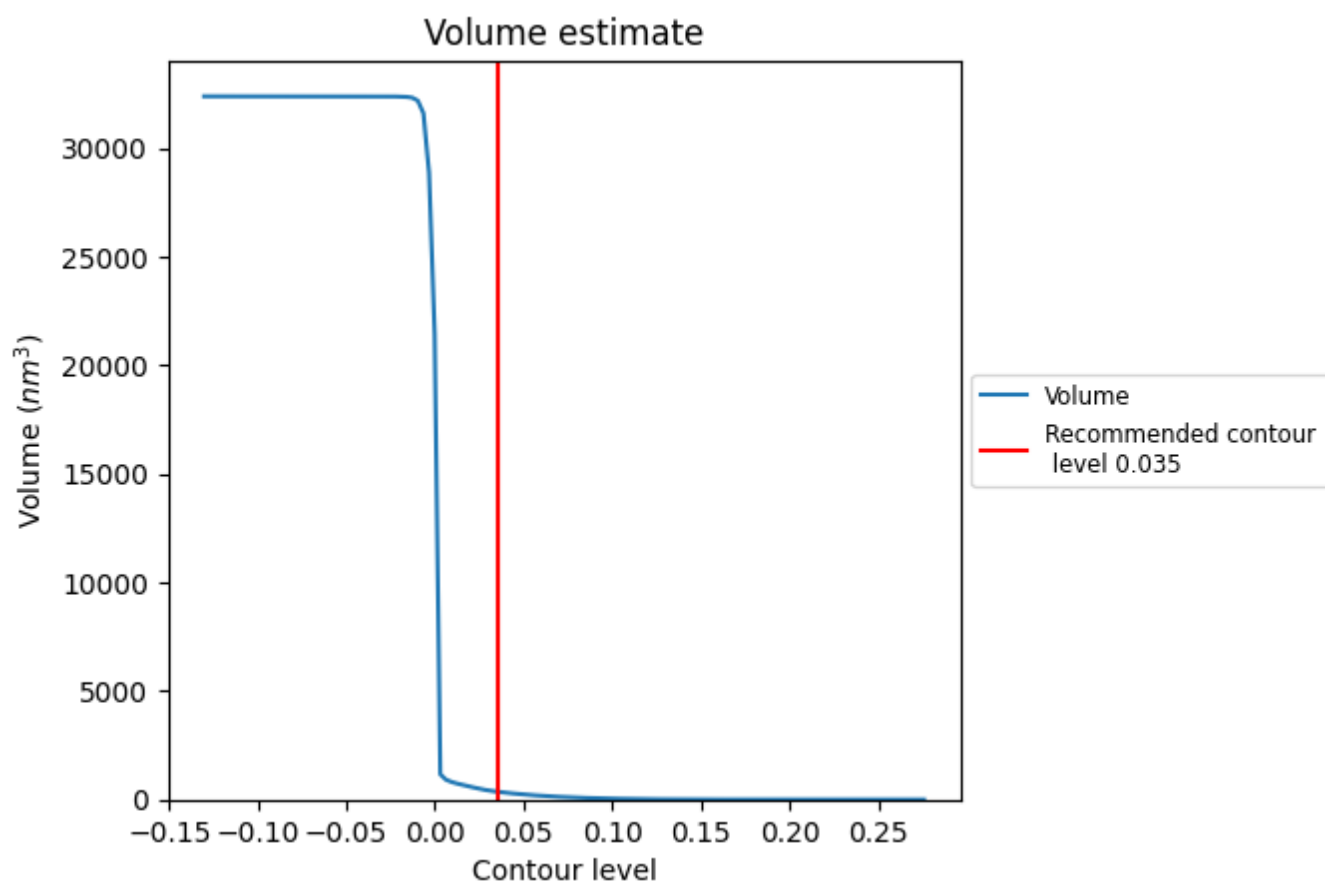
This section contains the results of statistical analysis of the map.

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.

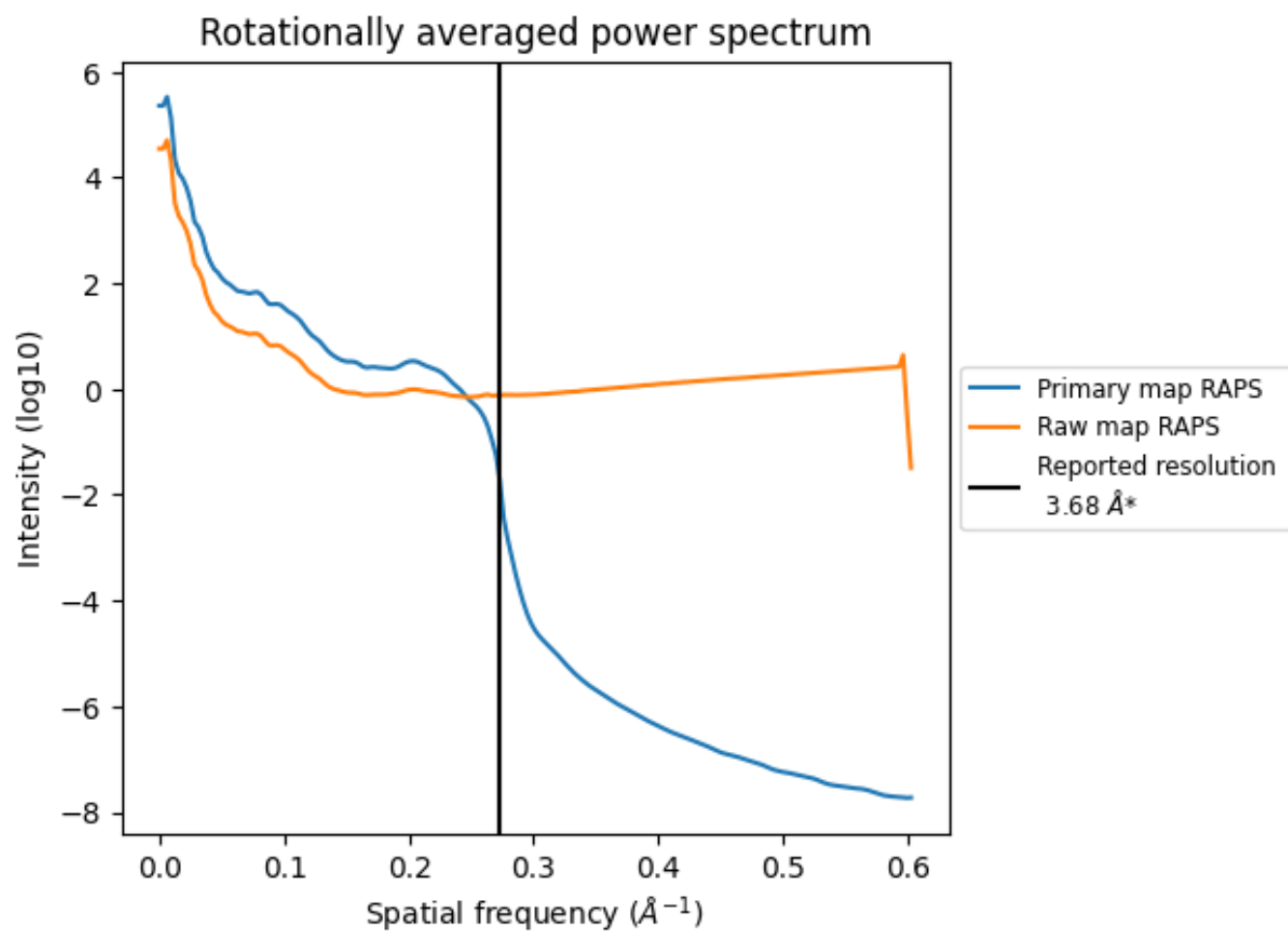
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 362 nm^3 ; this corresponds to an approximate mass of 327 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 ⓘ

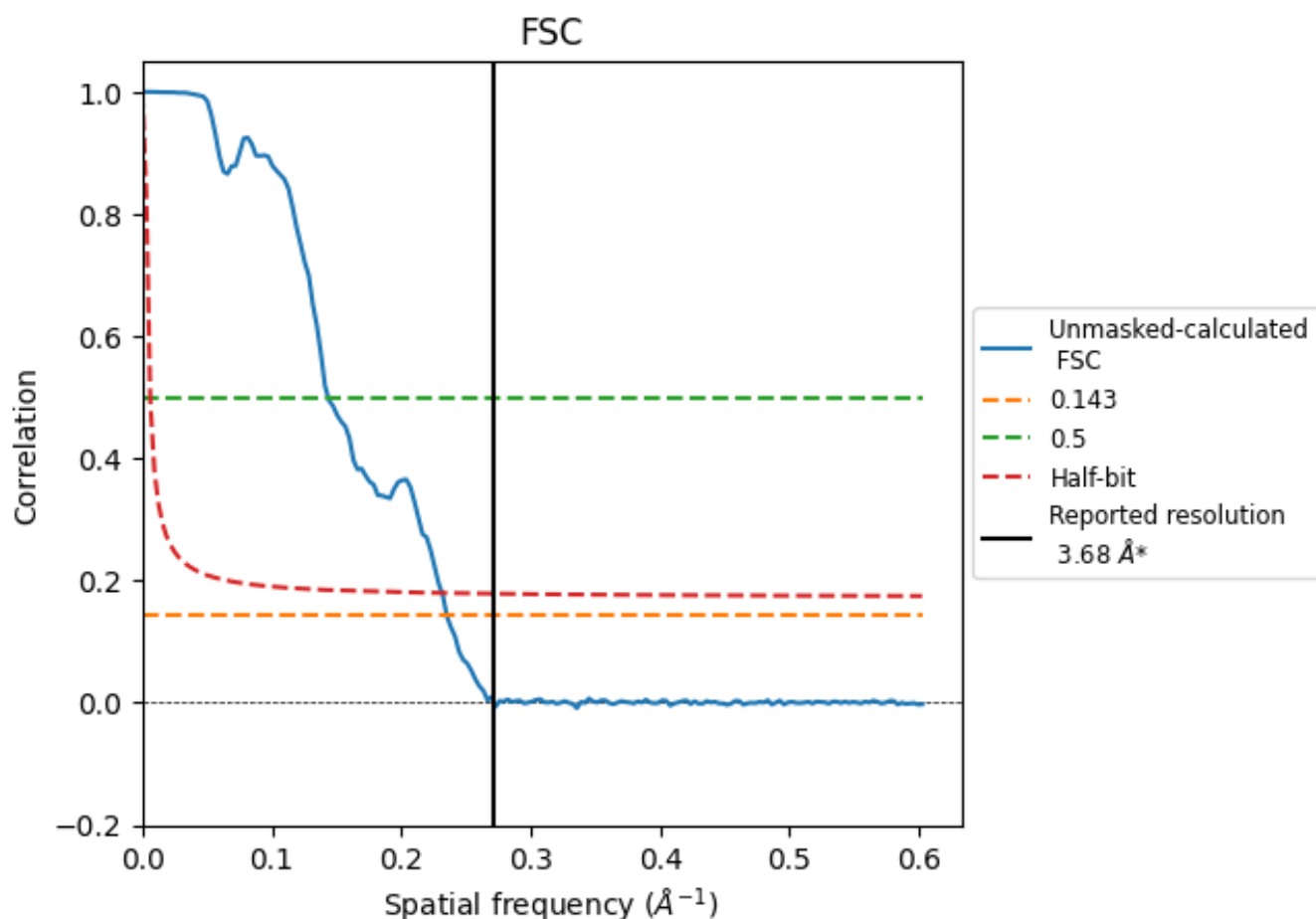


*Reported resolution corresponds to spatial frequency of 0.272 $\text{\AA}^{-1}$

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 0.272 Å⁻¹

8.2 Resolution estimates [i](#)

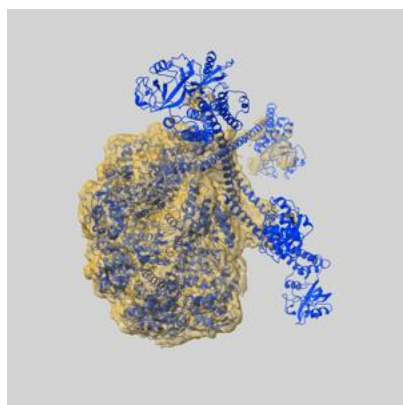
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.68	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.25	6.96	4.32

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.25 differs from the reported value 3.68 by more than 10 %

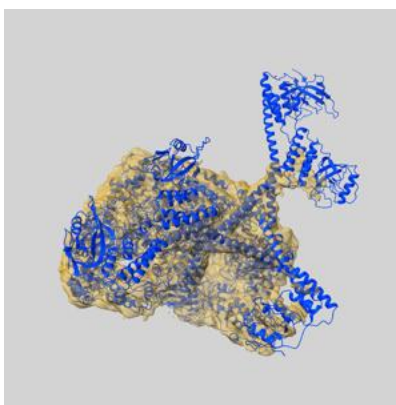
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34000 and PDB model 7YPH. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

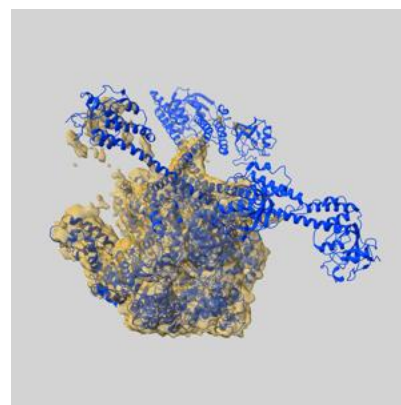
9.1 Map-model overlay [i](#)



X



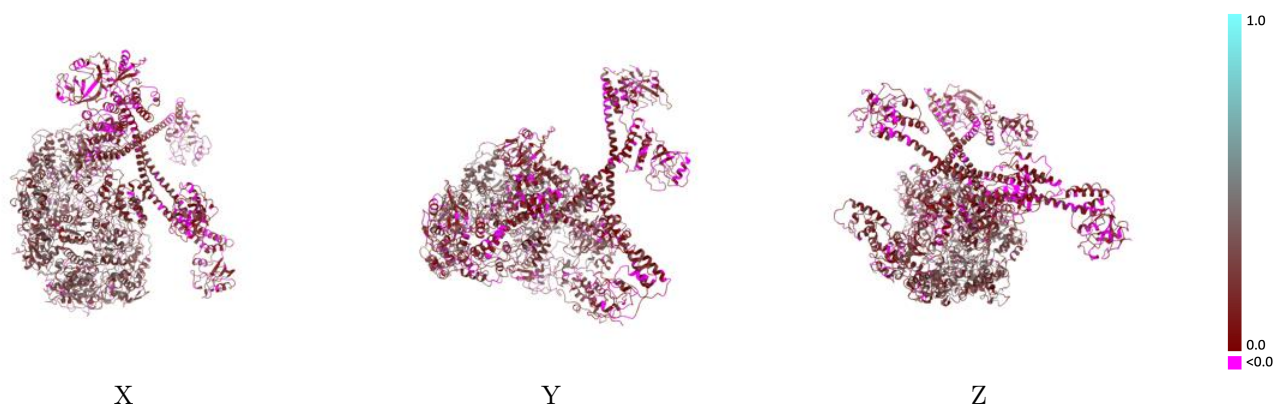
Y



Z

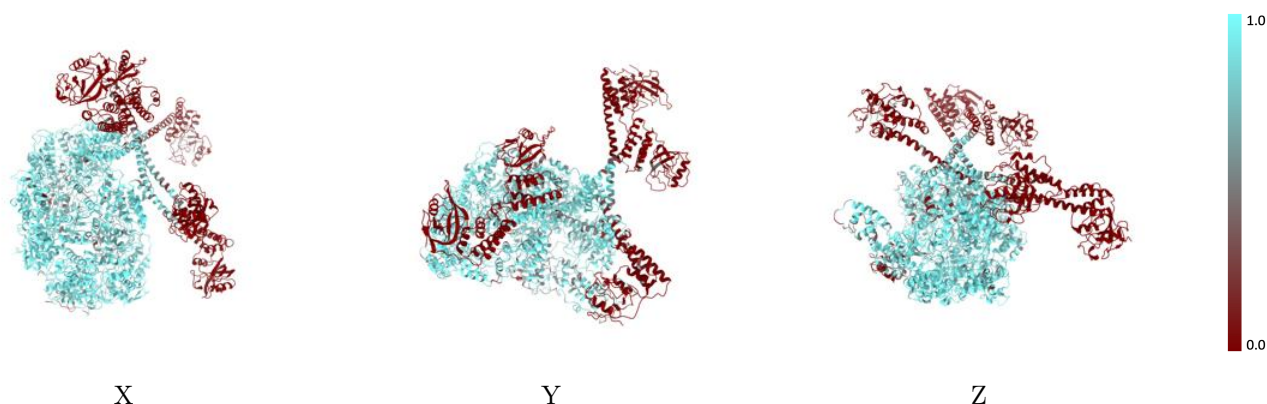
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



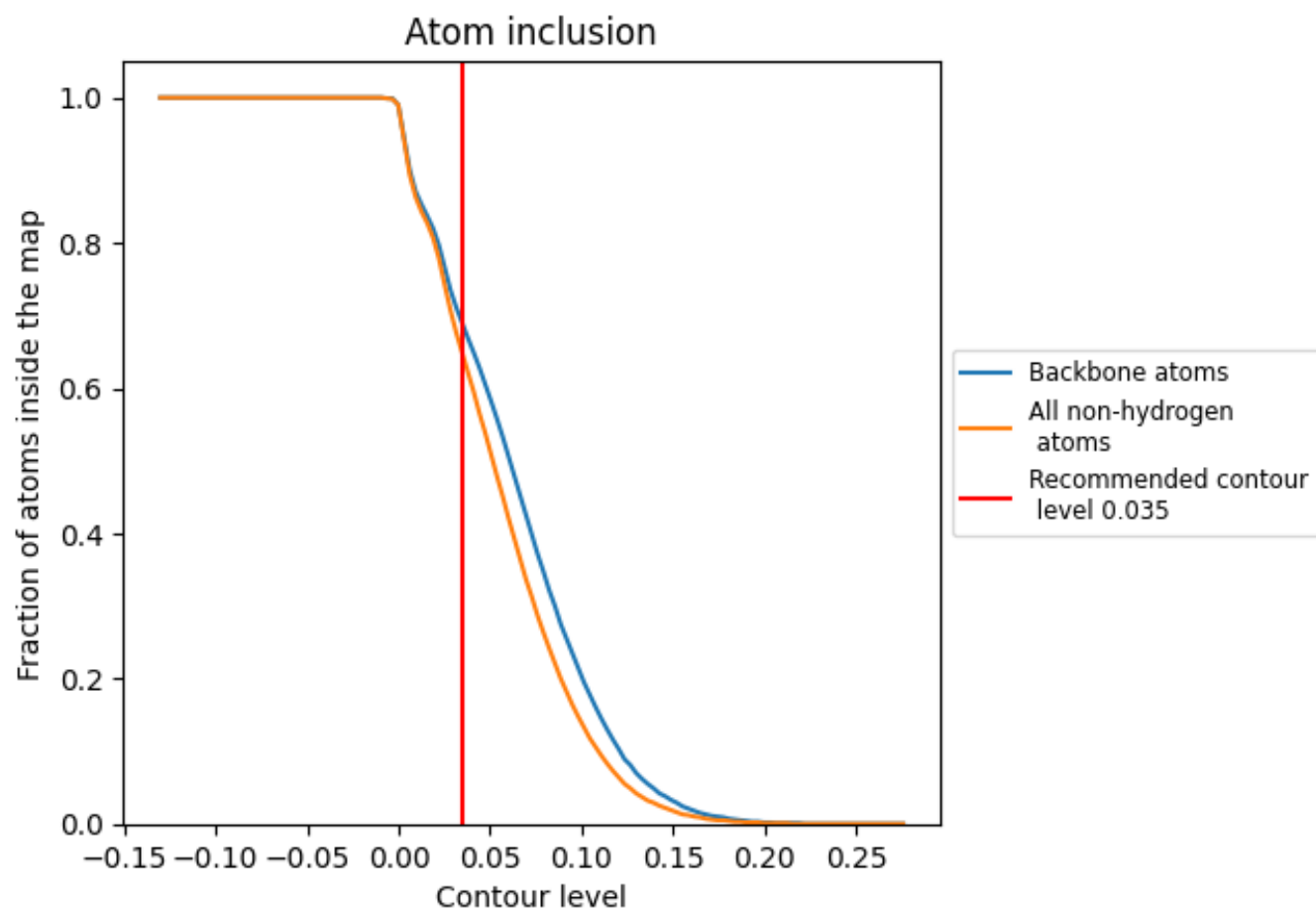
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 65% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6470	0.1860
A	0.6420	0.1630
B	0.6670	0.2210
C	0.6830	0.2110
D	0.6750	0.1950
E	0.5700	0.1390

