



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 03:31 AM UTC

PDB ID : 7WI4 / pdb_00007wi4
EMDB ID : EMD-32521
Title : Cryo-EM structure of E.Coli FtsH protease cytosolic domains
Authors : Qiao, Z.; Gao, Y.G.
Deposited on : 2022-01-02
Resolution : 3.40 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

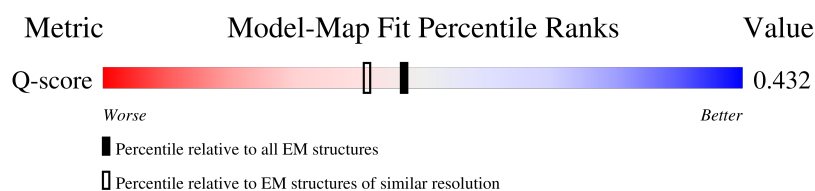
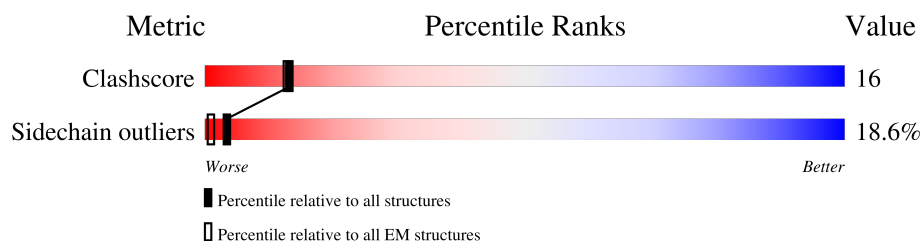
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

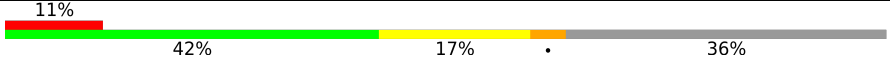
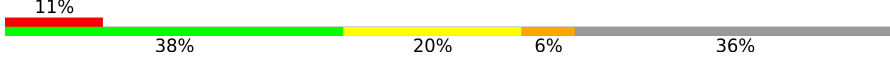
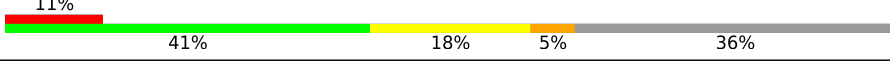
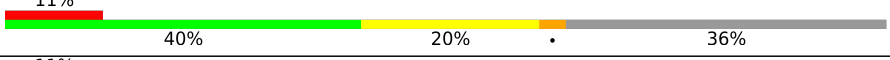
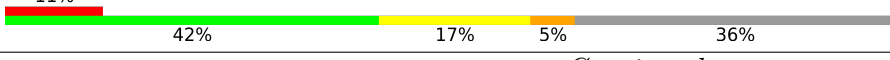
The reported resolution of this entry is 3.40 Å.

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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	644	
1	B	644	
1	C	644	
1	D	644	
1	E	644	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	644	10% 42% 18% • 36%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19284 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.

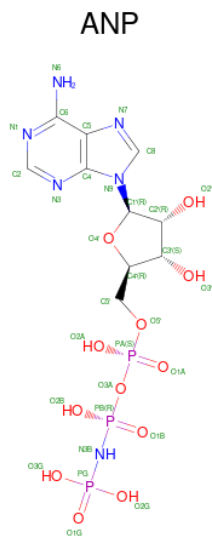
- Molecule 1 is a protein called ATP-dependent zinc metalloprotease FtsH.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	410	Total	C	N	O	S	5	0
			3181	1996	571	594	20		
1	D	410	Total	C	N	O	S	5	0
			3181	1996	571	594	20		
1	E	410	Total	C	N	O	S	5	0
			3181	1996	571	594	20		
1	F	410	Total	C	N	O	S	5	0
			3181	1996	571	594	20		
1	B	410	Total	C	N	O	S	5	0
			3181	1996	571	594	20		
1	C	410	Total	C	N	O	S	5	0
			3181	1996	571	594	20		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	252	GLN	GLU	engineered mutation	UNP P0AAI3
A	415	GLN	GLU	engineered mutation	UNP P0AAI3
D	252	GLN	GLU	engineered mutation	UNP P0AAI3
D	415	GLN	GLU	engineered mutation	UNP P0AAI3
E	252	GLN	GLU	engineered mutation	UNP P0AAI3
E	415	GLN	GLU	engineered mutation	UNP P0AAI3
F	252	GLN	GLU	engineered mutation	UNP P0AAI3
F	415	GLN	GLU	engineered mutation	UNP P0AAI3
B	252	GLN	GLU	engineered mutation	UNP P0AAI3
B	415	GLN	GLU	engineered mutation	UNP P0AAI3
C	252	GLN	GLU	engineered mutation	UNP P0AAI3
C	415	GLN	GLU	engineered mutation	UNP P0AAI3

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



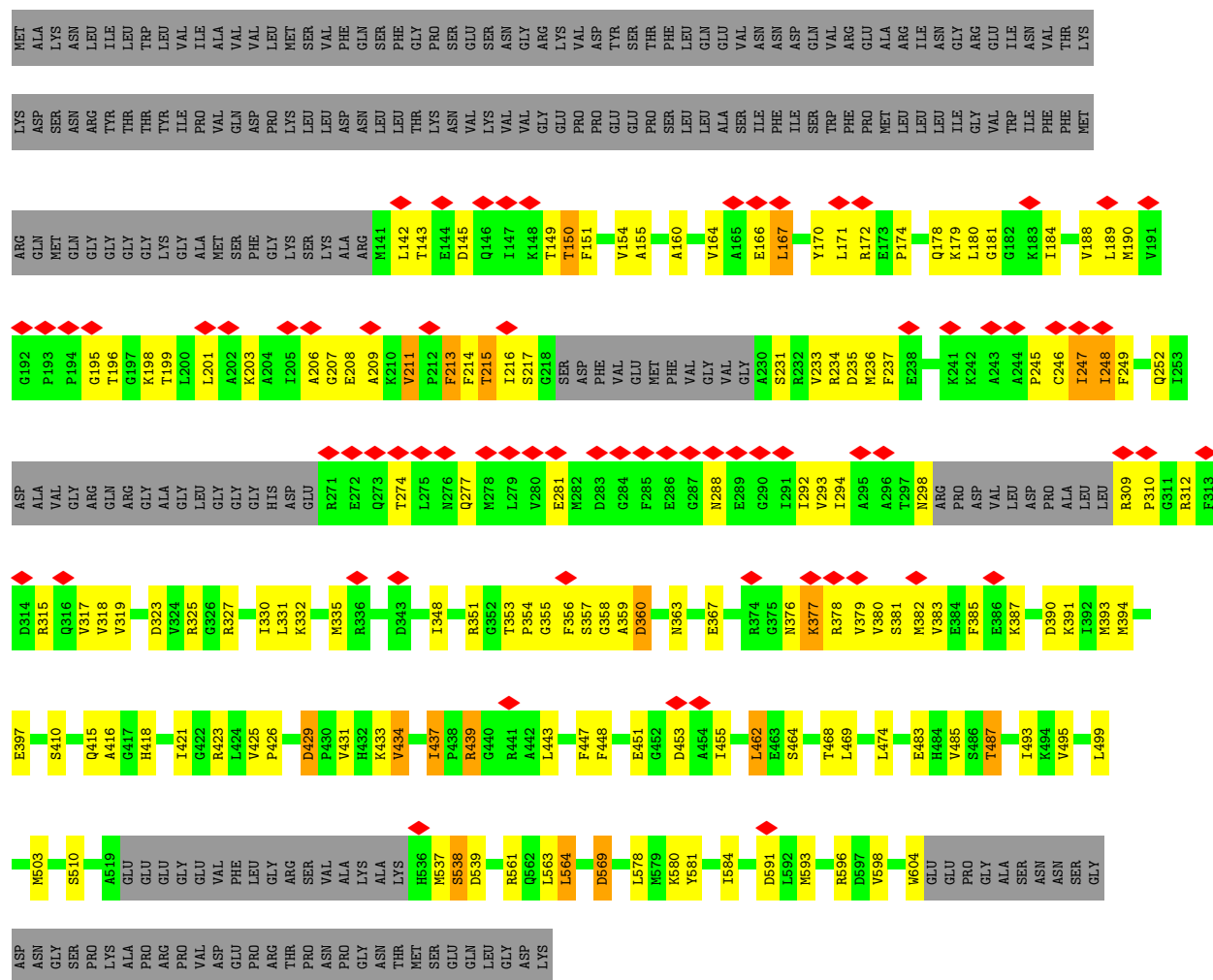
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total 31	C 10	N 6	O 12	P 3	0
2	D	1	Total 31	C 10	N 6	O 12	P 3	0
2	E	1	Total 31	C 10	N 6	O 12	P 3	0
2	F	1	Total 31	C 10	N 6	O 12	P 3	0
2	B	1	Total 31	C 10	N 6	O 12	P 3	0
2	C	1	Total 31	C 10	N 6	O 12	P 3	0

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

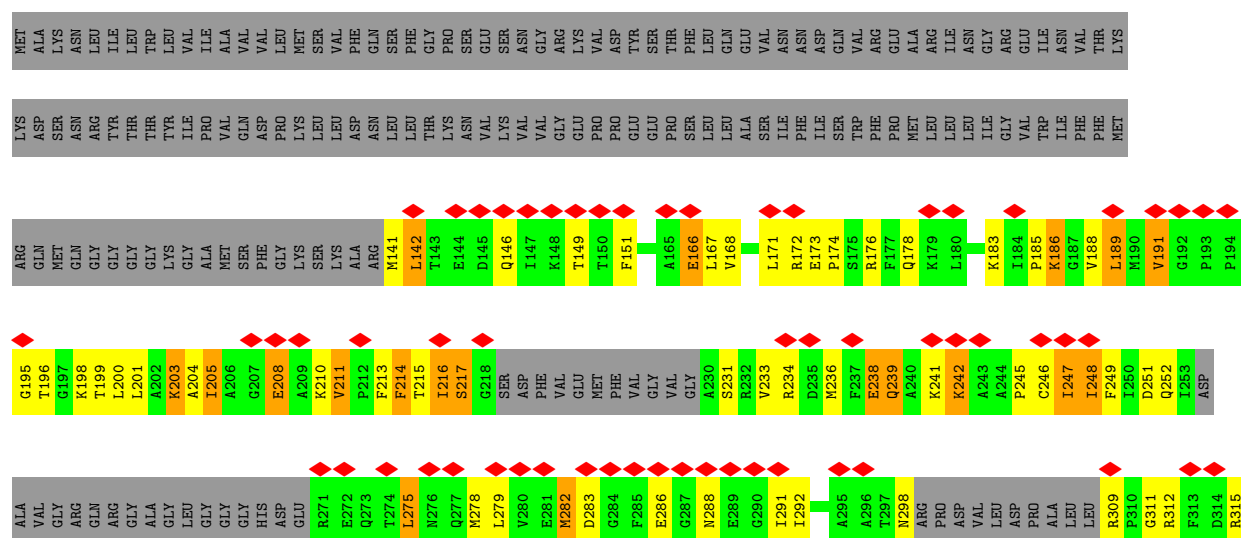
Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total Zn 1 1	0
3	D	1	Total Zn 1 1	0
3	E	1	Total Zn 1 1	0
3	F	1	Total Zn 1 1	0
3	B	1	Total Zn 1 1	0
3	C	1	Total Zn 1 1	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

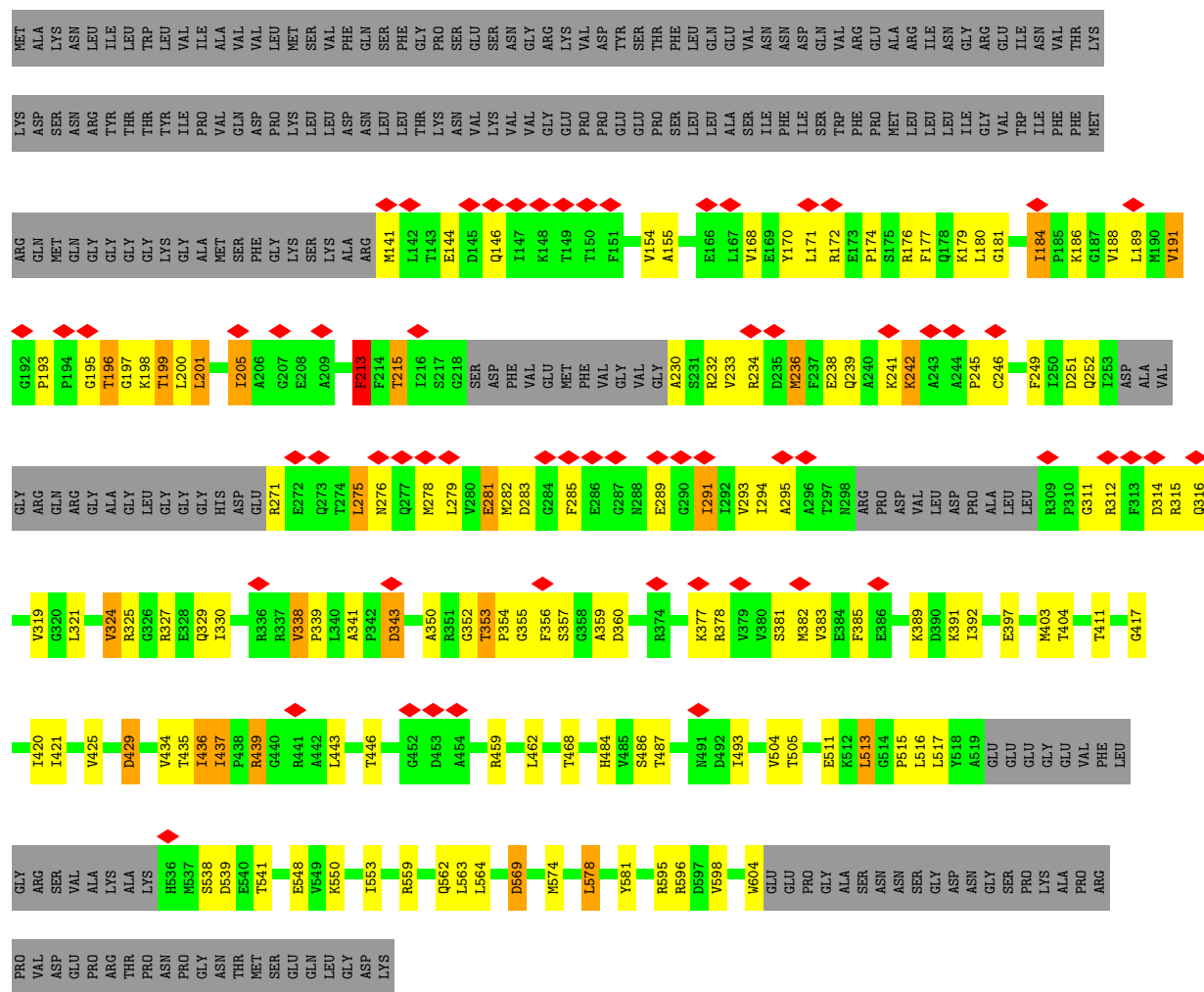
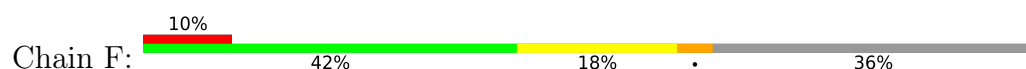
Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total 1	Mg 1	0
4	D	1	Total 1	Mg 1	0
4	E	1	Total 1	Mg 1	0
4	F	1	Total 1	Mg 1	0
4	B	1	Total 1	Mg 1	0
4	C	1	Total 1	Mg 1	0



● Molecule 1: ATP-dependent zinc metalloprotease FtsH

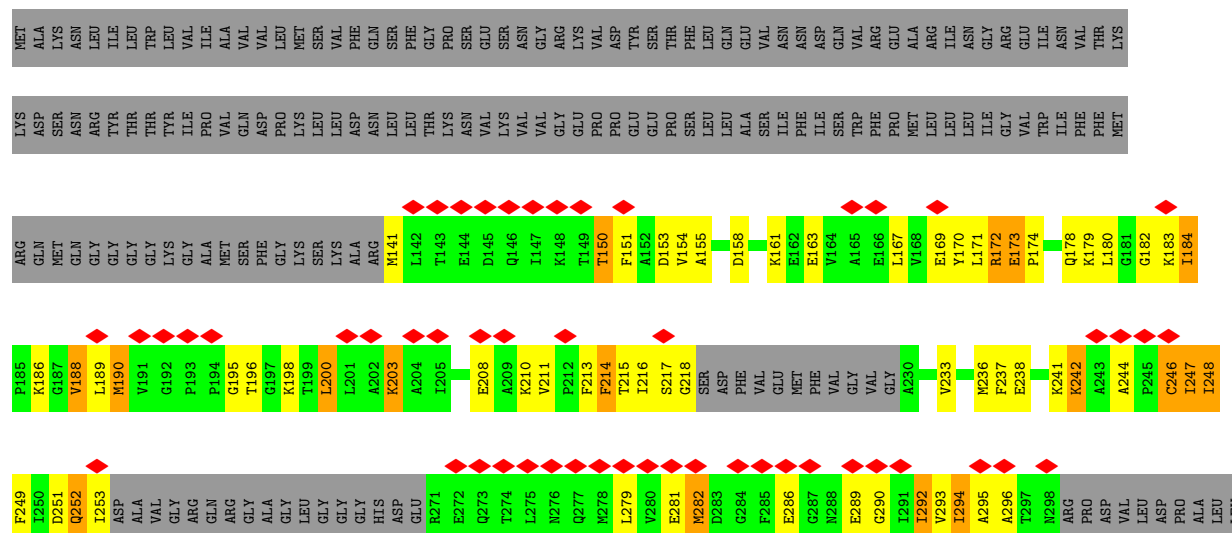


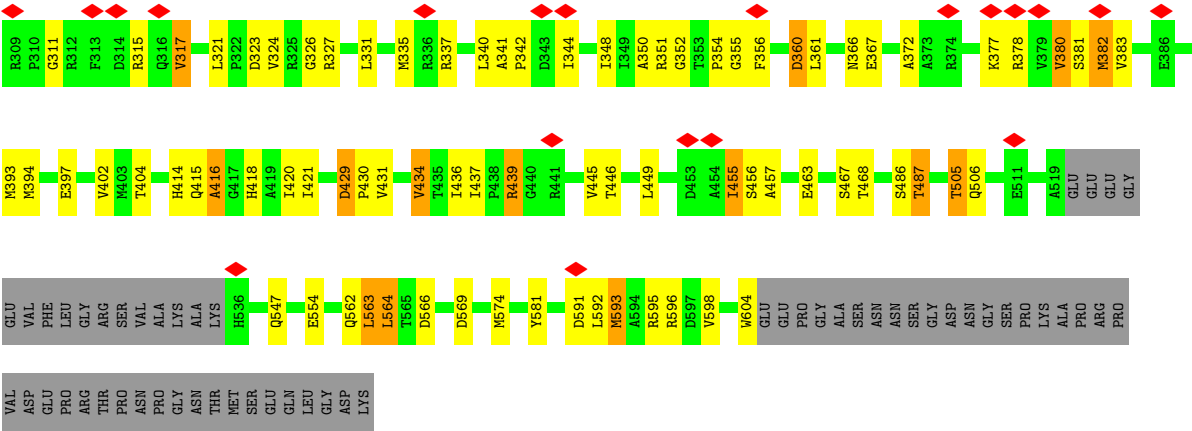
- Molecule 1: ATP-dependent zinc metalloprotease FtsH



- Molecule 1: ATP-dependent zinc metalloprotease FtsH







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32359	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.617	Depositor
Minimum map value	-0.003	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.172	Depositor
Map size ($\text{\AA}$)	219.648, 219.648, 219.648	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3728, 1.3728, 1.3728	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, ANP, MG

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	0.53	0/3254	0.57	0/4383
1	B	0.54	0/3254	0.57	0/4383
1	C	0.55	0/3254	0.60	2/4383 (0.0%)
1	D	0.54	0/3254	0.56	0/4383
1	E	0.56	0/3254	0.59	0/4383
1	F	0.55	0/3254	0.61	0/4383
All	All	0.55	0/19524	0.58	2/26298 (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
1	A	0	2
1	B	0	1
1	D	0	2
1	F	0	5
All	All	0	10

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	416	ALA	CA-C-N	-5.38	110.87	121.41
1	C	416	ALA	C-N-CA	-5.38	110.87	121.41

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	417	GLY	Peptide
1	A	455	ILE	Peptide
1	D	181	GLY	Peptide
1	D	415	GLN	Peptide
1	F	213	PHE	Peptide

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	A	3181	0	3231	107	0
1	B	3181	0	3231	123	0
1	C	3181	0	3230	98	0
1	D	3181	0	3231	98	0
1	E	3181	0	3231	103	0
1	F	3181	0	3231	98	0
2	A	31	0	13	8	0
2	B	31	0	13	3	0
2	C	31	0	12	5	0
2	D	31	0	13	7	0
2	E	31	0	13	5	0
2	F	31	0	13	6	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
All	All	19284	0	19462	625	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 625 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:A:184:ILE:HD11	1:A:292:ILE:HG22	1.53	0.90
1:B:215:THR:HB	1:B:249:PHE:HB3	1.55	0.88
1:E:327:ARG:NH1	1:E:353:THR:O	2.07	0.87
1:C:141:MET:N	1:C:218:GLY:O	2.10	0.83
1:B:238:GLU:O	1:B:241:LYS:NZ	2.10	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	337/527 (64%)	279 (83%)	58 (17%)	2	8
1	B	337/527 (64%)	267 (79%)	70 (21%)	1	4
1	C	337/527 (64%)	280 (83%)	57 (17%)	2	9
1	D	337/527 (64%)	275 (82%)	62 (18%)	1	7
1	E	337/527 (64%)	271 (80%)	66 (20%)	1	5
1	F	337/527 (64%)	278 (82%)	59 (18%)	2	8
All	All	2022/3162 (64%)	1650 (82%)	372 (18%)	3	7

5 of 372 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	541	THR
1	B	411	THR

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Mol	Chain	Res	Type
1	F	564	LEU
1	B	216	ILE
1	B	487	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	178	GLN
1	C	418	HIS
1	C	498	ASN
1	C	465	GLN
1	E	276	ASN

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](#)

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 for Mogul analysis.

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	ANP	B	701	-	33,33,33	1.28	4 (12%)	45,52,52	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ANP	E	701	4	33,33,33	1.28	3 (9%)	45,52,52	0.77	2 (4%)
2	ANP	C	701	4	33,33,33	1.26	3 (9%)	45,52,52	0.91	3 (6%)
2	ANP	A	701	4	33,33,33	1.55	3 (9%)	45,52,52	0.90	4 (8%)
2	ANP	D	701	4	33,33,33	1.31	3 (9%)	45,52,52	0.92	4 (8%)
2	ANP	F	701	4	33,33,33	1.49	3 (9%)	45,52,52	0.72	3 (6%)

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	ANP	B	701	-	-	4/18/38/38	0/3/3/3
2	ANP	E	701	4	-	4/18/38/38	0/3/3/3
2	ANP	C	701	4	-	5/18/38/38	0/3/3/3
2	ANP	A	701	4	-	4/18/38/38	0/3/3/3
2	ANP	D	701	4	-	9/18/38/38	0/3/3/3
2	ANP	F	701	4	-	10/18/38/38	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	ANP	PA-O3A	-6.42	1.52	1.59
2	F	701	ANP	PA-O3A	-5.98	1.53	1.59
2	D	701	ANP	PA-O3A	-4.91	1.54	1.59
2	F	701	ANP	PB-O3A	-4.81	1.53	1.59
2	C	701	ANP	PA-O3A	-4.77	1.54	1.59

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	701	ANP	O3G-PG-O1G	-3.43	104.85	113.45
2	A	701	ANP	O3G-PG-O1G	-3.23	105.34	113.45
2	C	701	ANP	O2B-PB-O3A	2.95	114.49	104.64
2	A	701	ANP	O1G-PG-N3B	-2.75	107.72	111.77
2	C	701	ANP	O1B-PB-N3B	-2.54	108.02	111.77

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

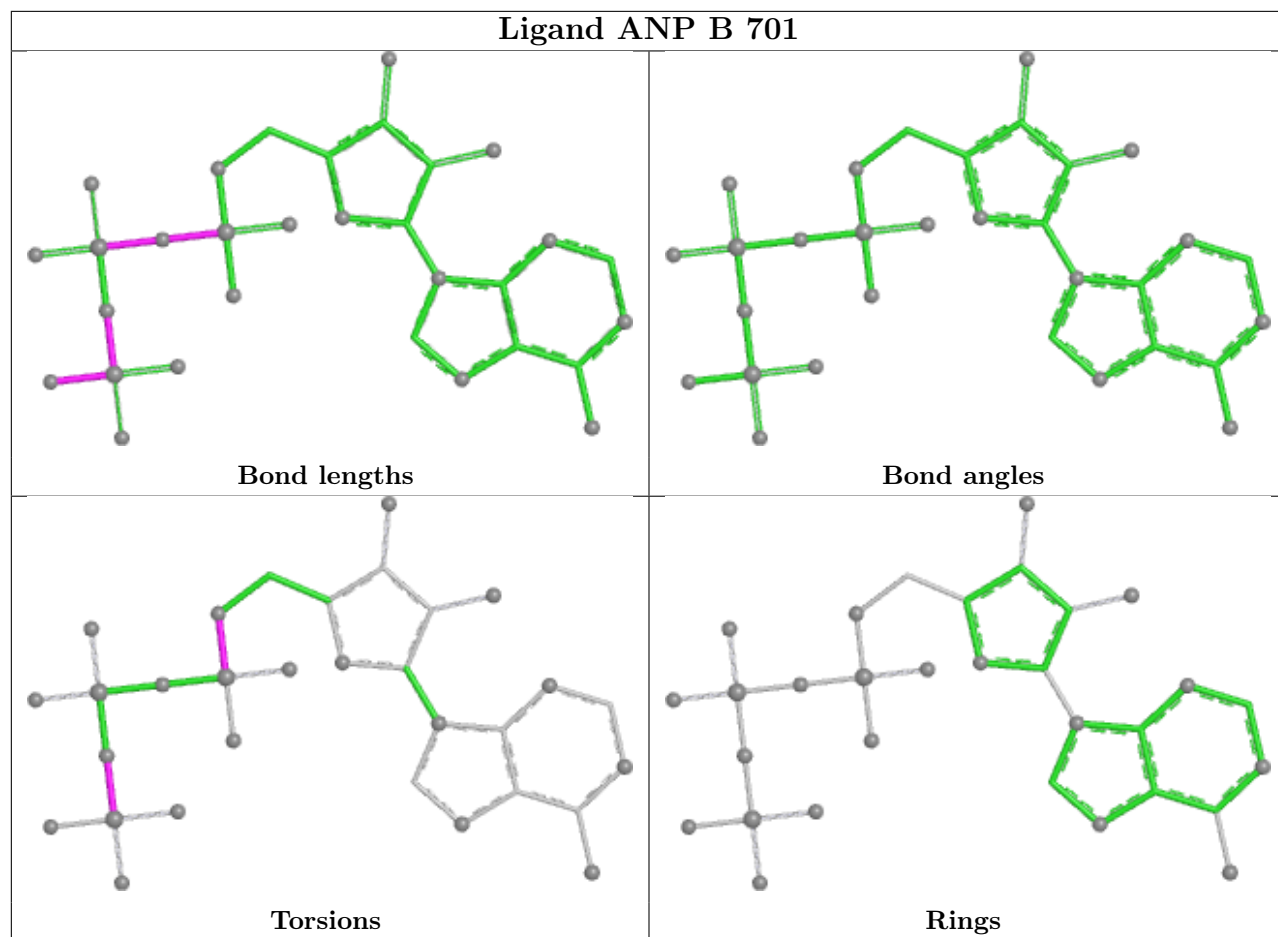
Mol	Chain	Res	Type	Atoms
2	A	701	ANP	PG-N3B-PB-O1B
2	D	701	ANP	PG-N3B-PB-O1B
2	D	701	ANP	O4'-C4'-C5'-O5'
2	D	701	ANP	C3'-C4'-C5'-O5'
2	E	701	ANP	PB-N3B-PG-O1G

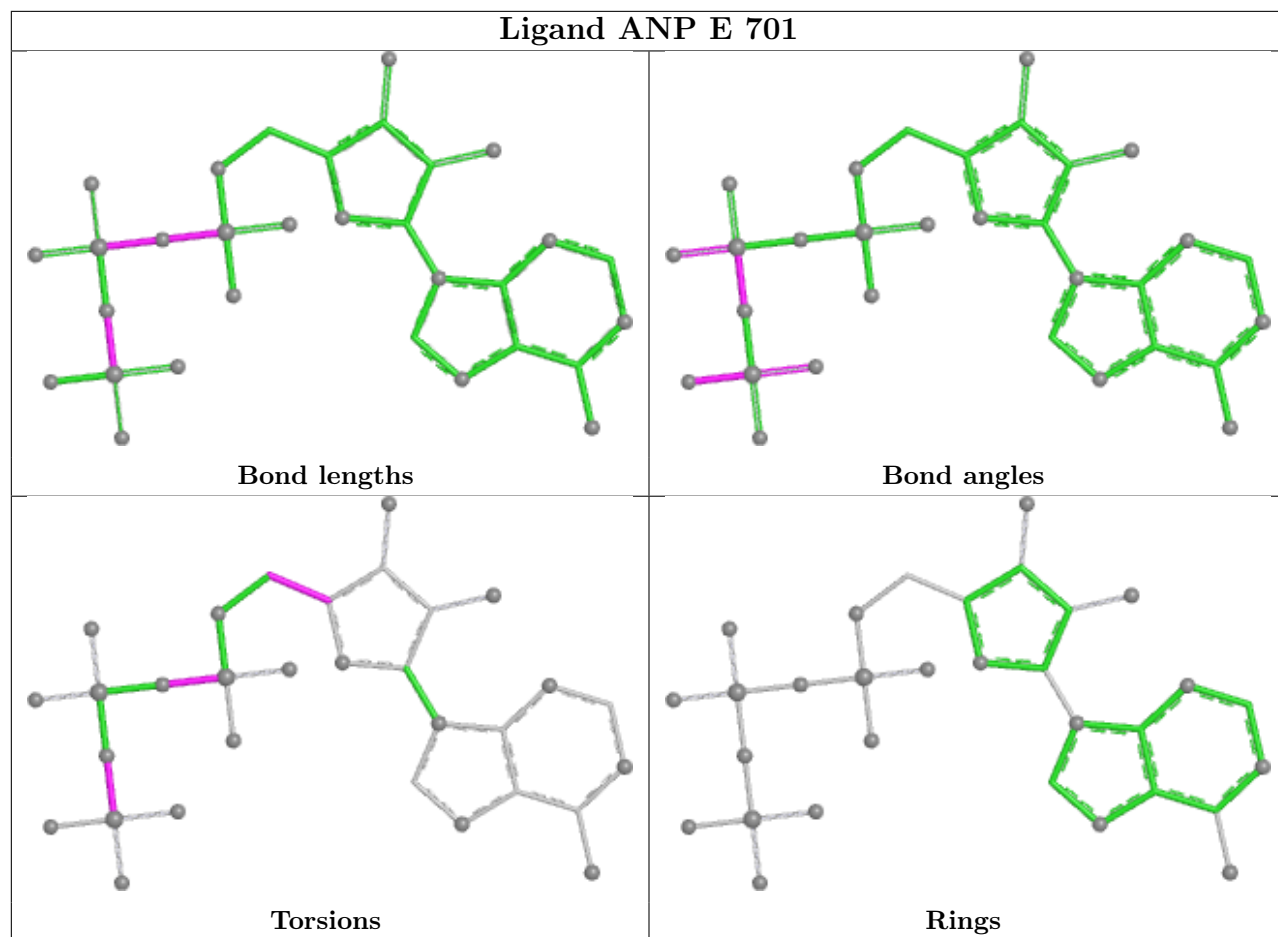
There are no ring outliers.

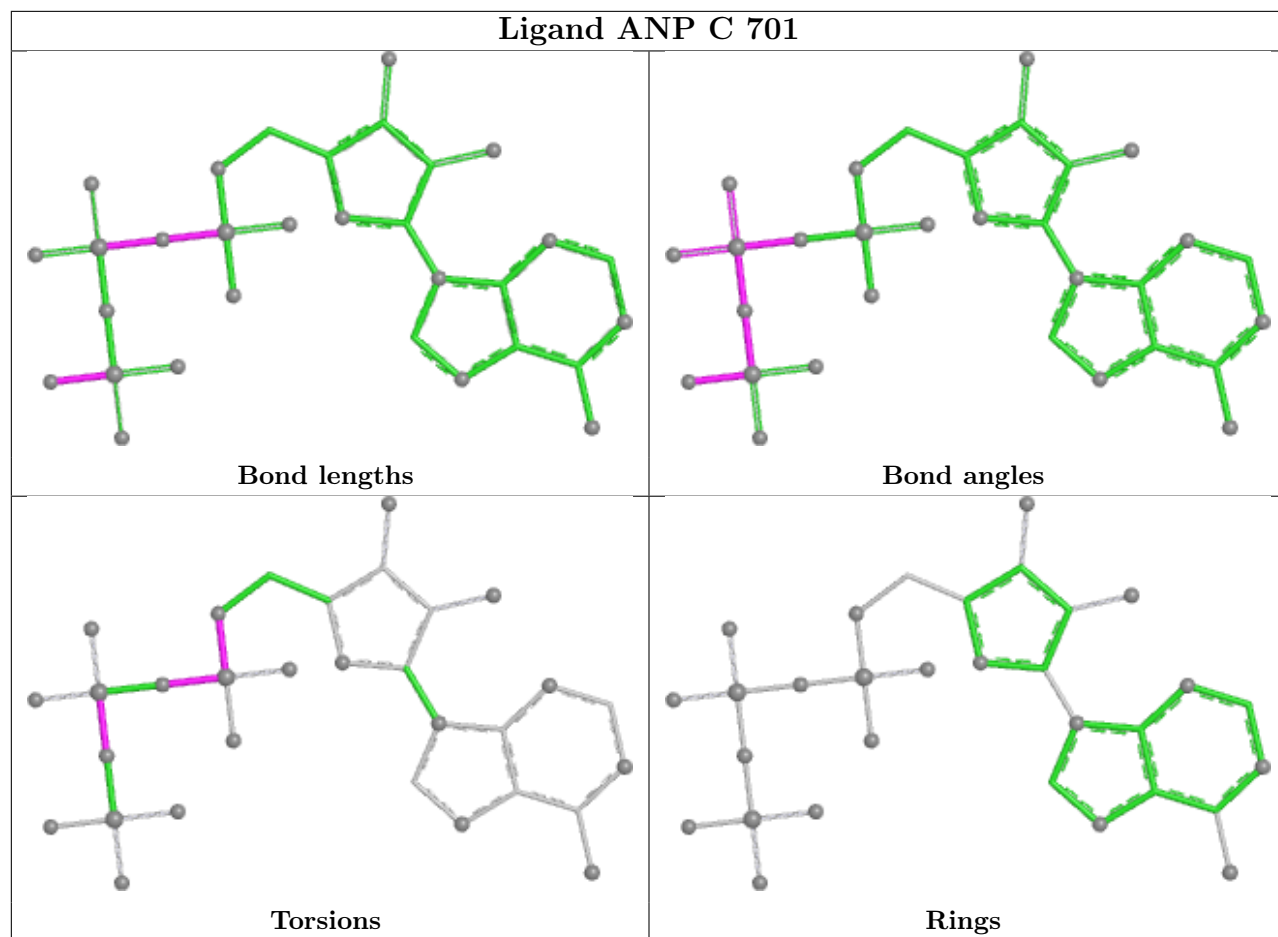
6 monomers are involved in 34 short contacts:

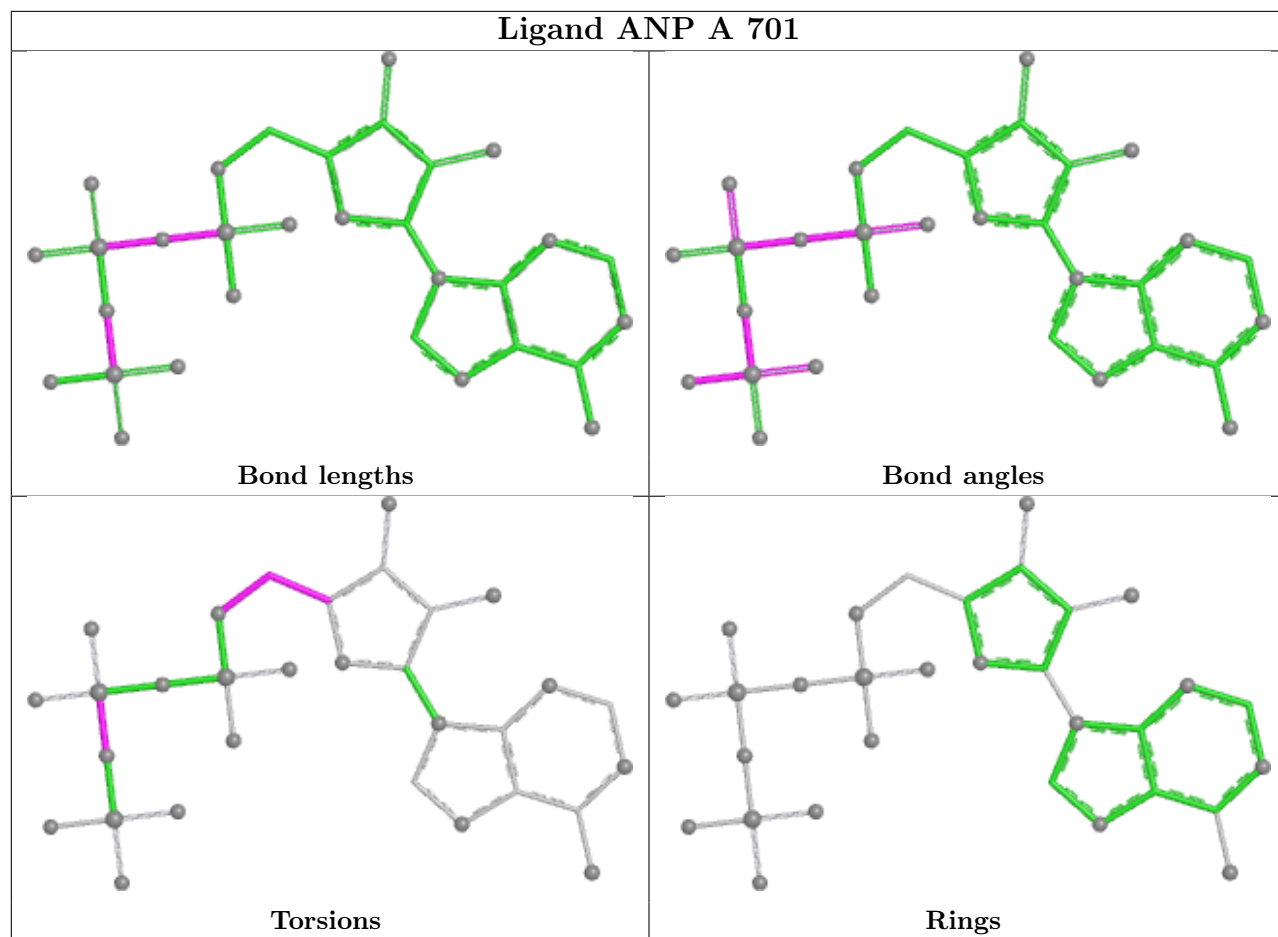
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	ANP	3	0
2	E	701	ANP	5	0
2	C	701	ANP	5	0
2	A	701	ANP	8	0
2	D	701	ANP	7	0
2	F	701	ANP	6	0

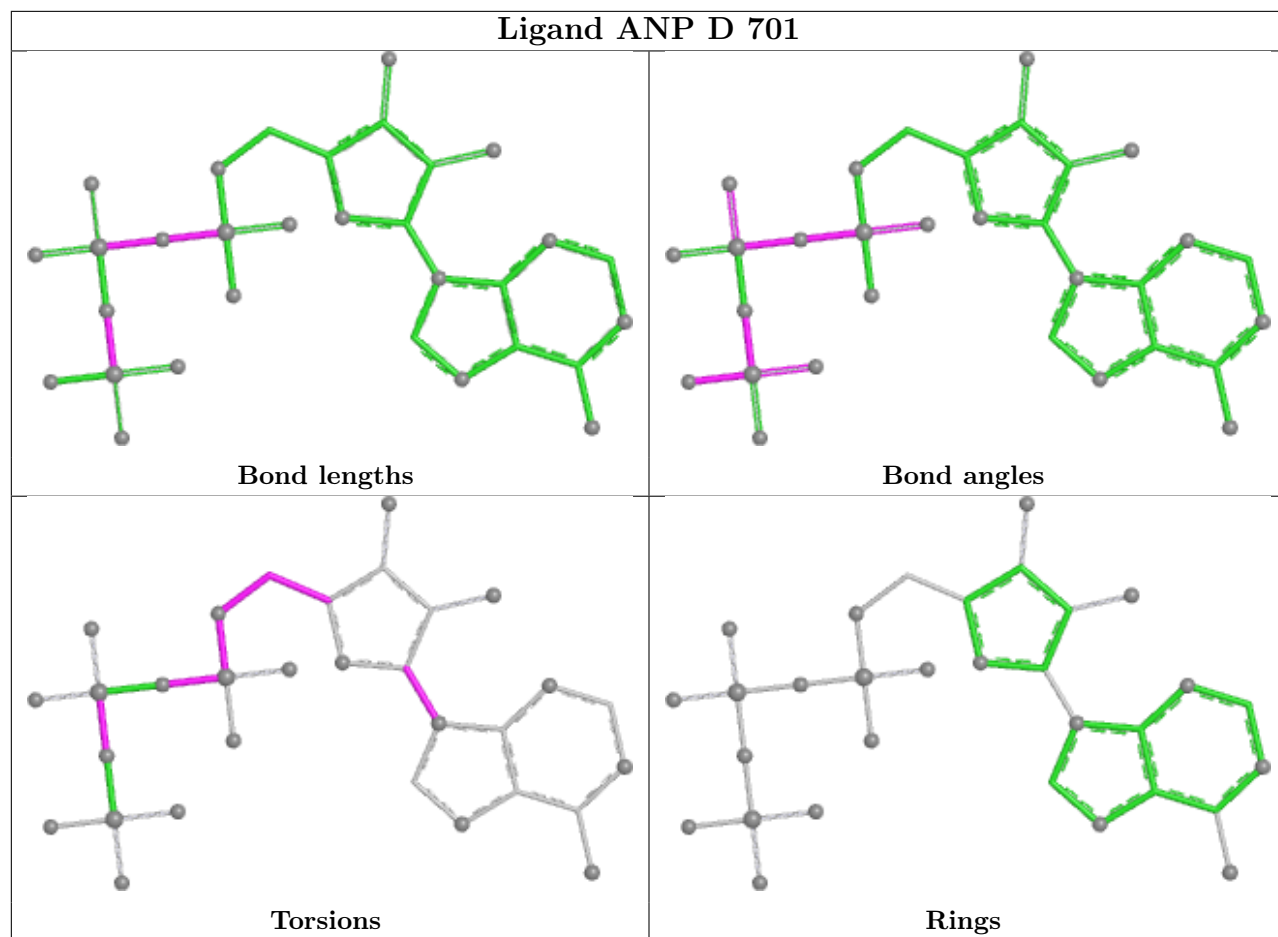
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

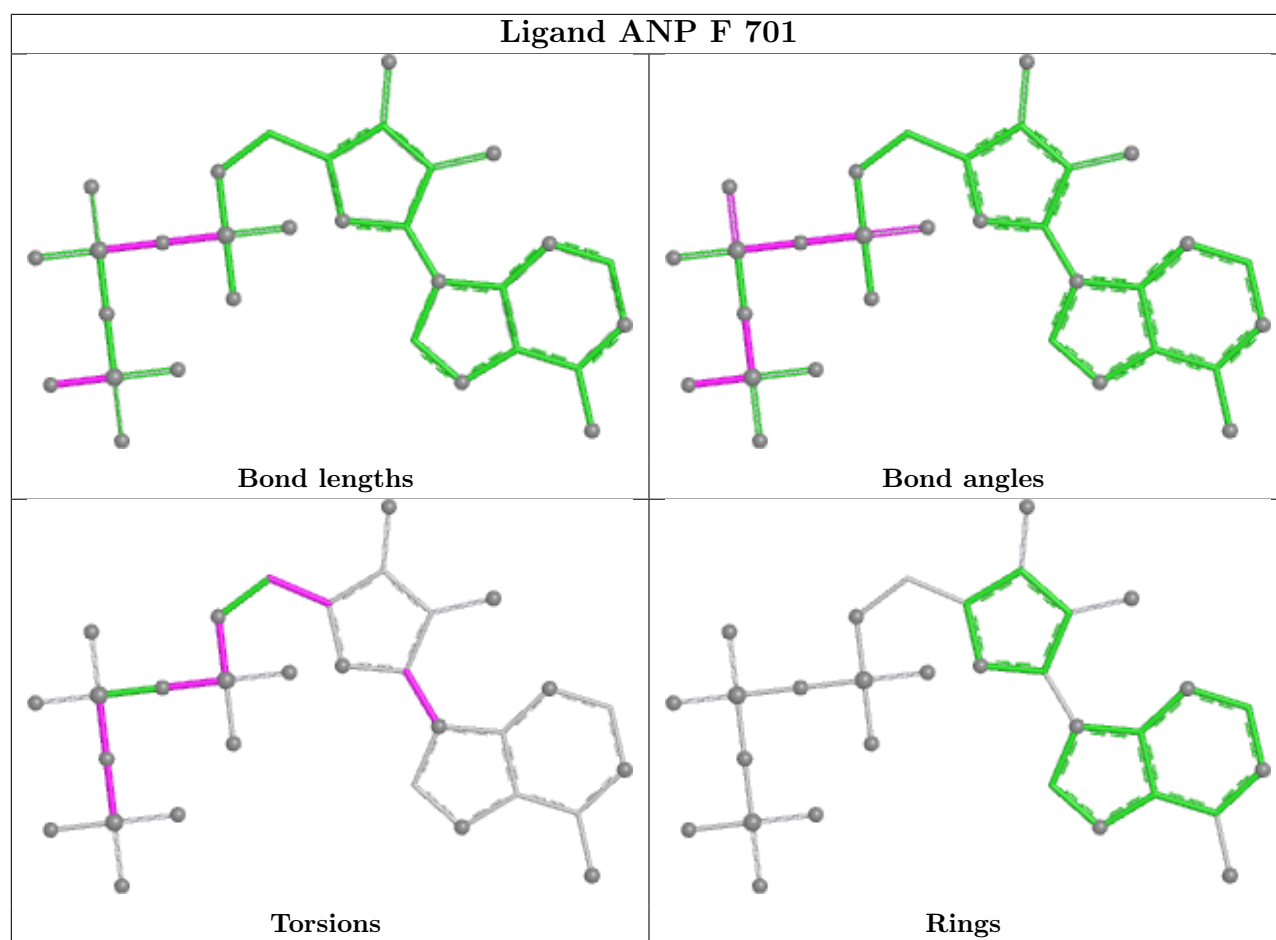












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

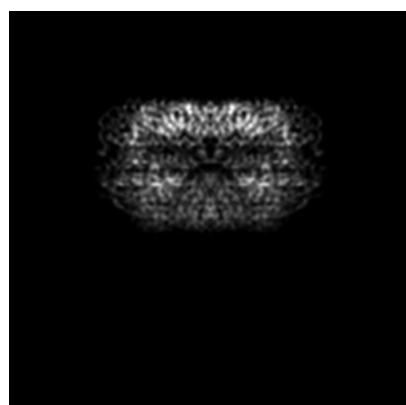
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32521. These allow visual inspection of the internal detail of the map and identification of artifacts.

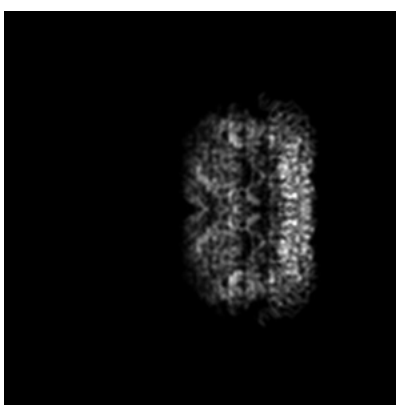
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

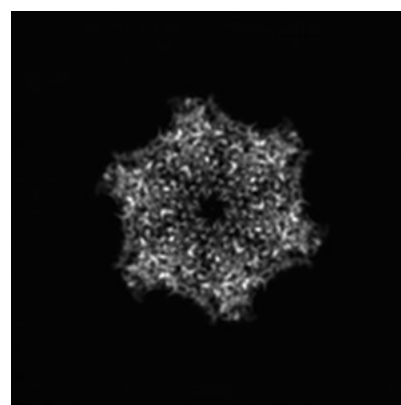
6.1.1 Primary map



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: 80



Y Index: 80



Z Index: 80

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: 64



Y Index: 72



Z Index: 113

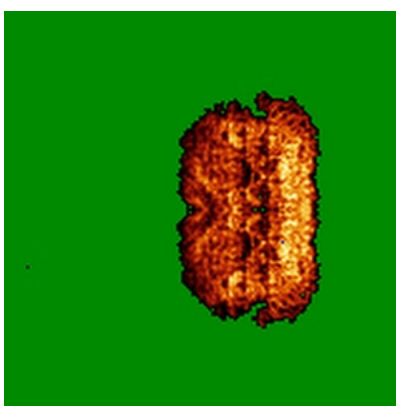
The images above show the largest variance slices of the map in three orthogonal directions.

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

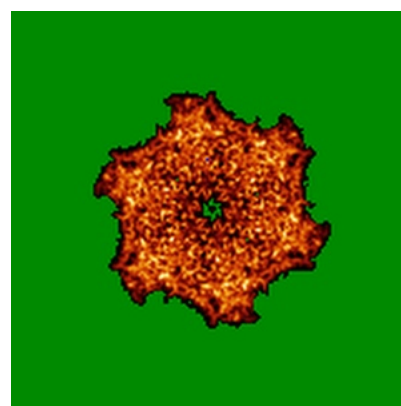
6.4.1 Primary map



X



Y



Z

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

This section was not generated.

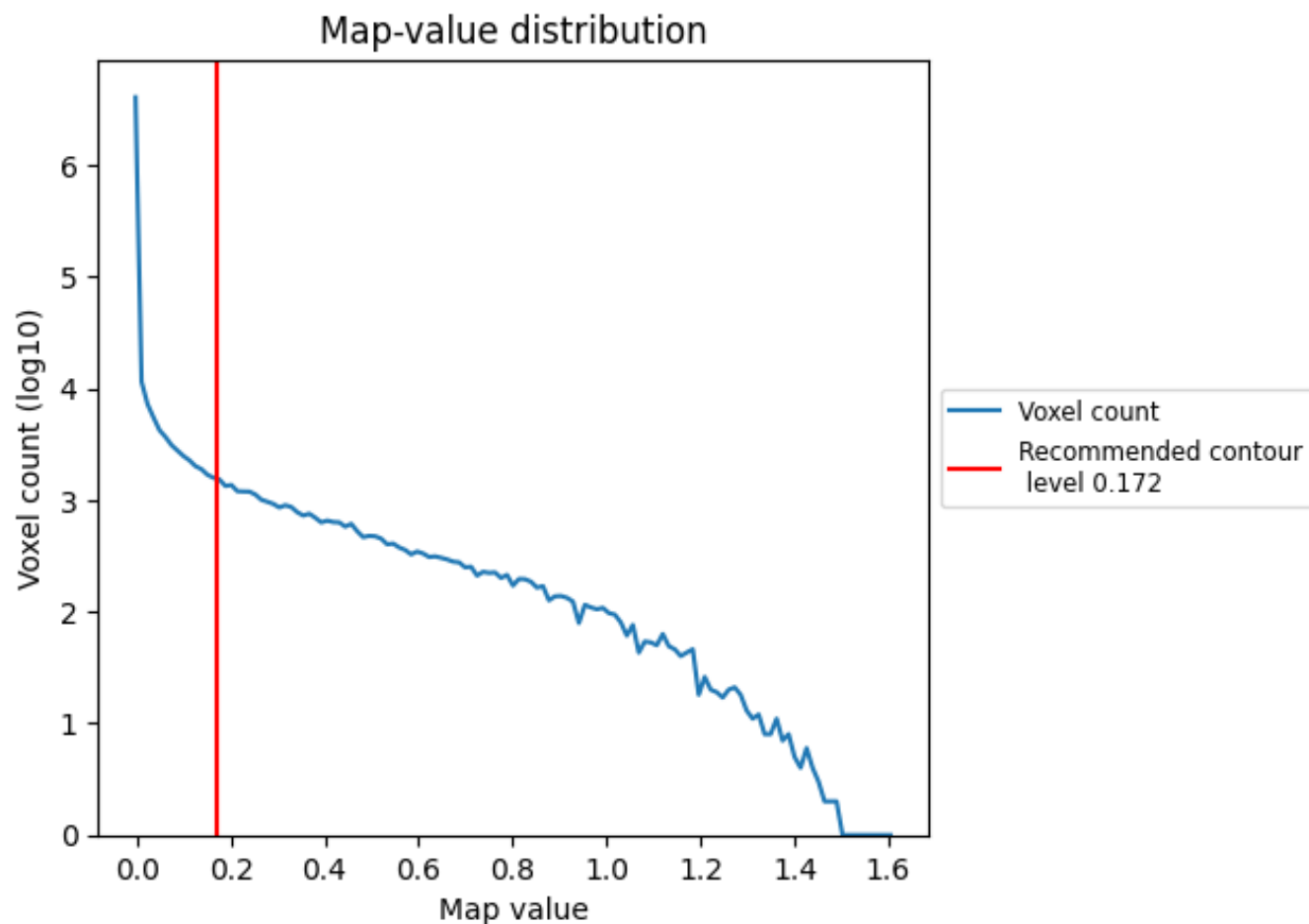
6.6 Mask visualisation

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

7 Map analysis [i](#)

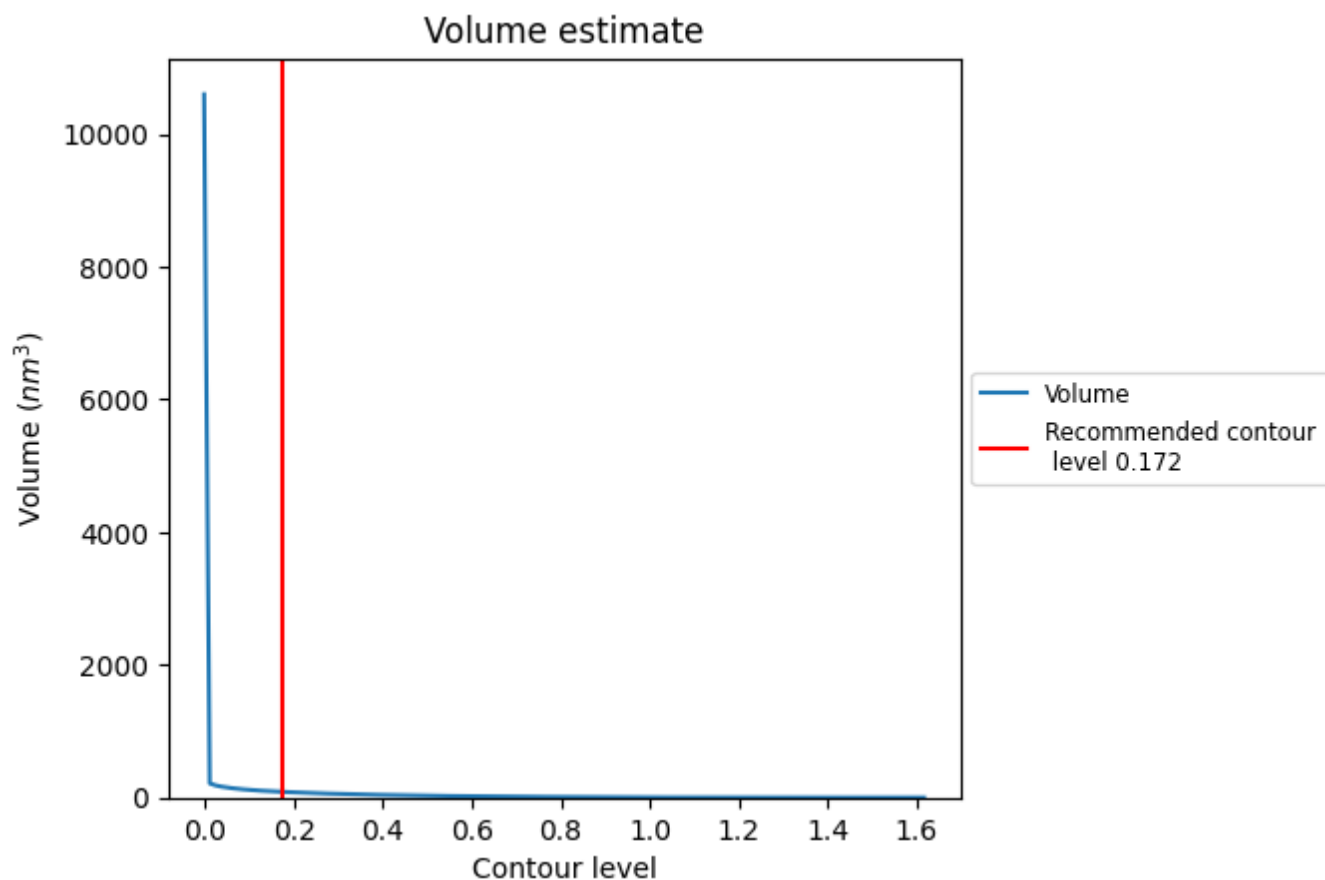
This section contains the results of statistical analysis of the map.

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.

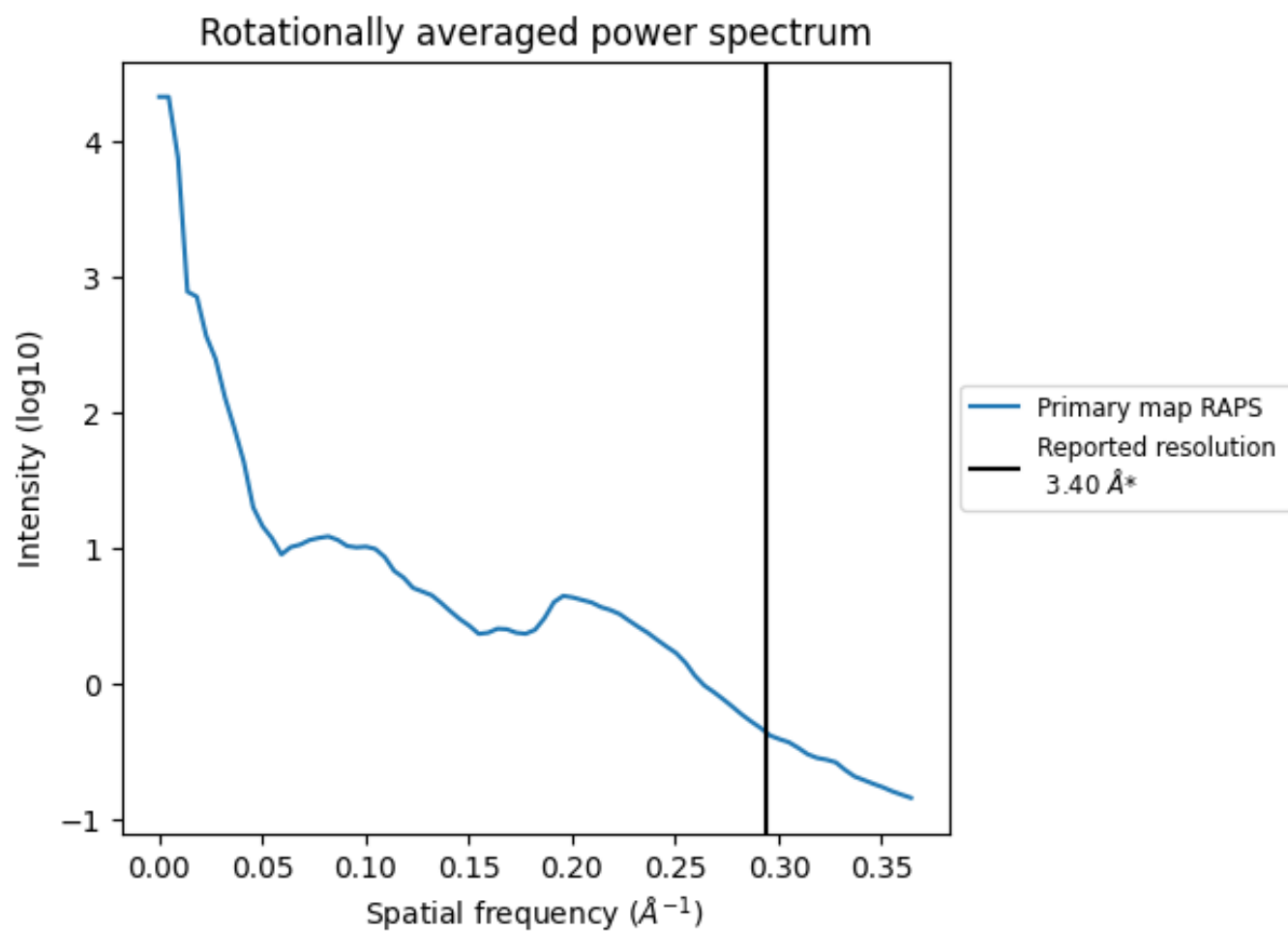
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 87 nm³; this corresponds to an approximate mass of 78 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 0.294 Å⁻¹

8 Fourier-Shell correlation

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

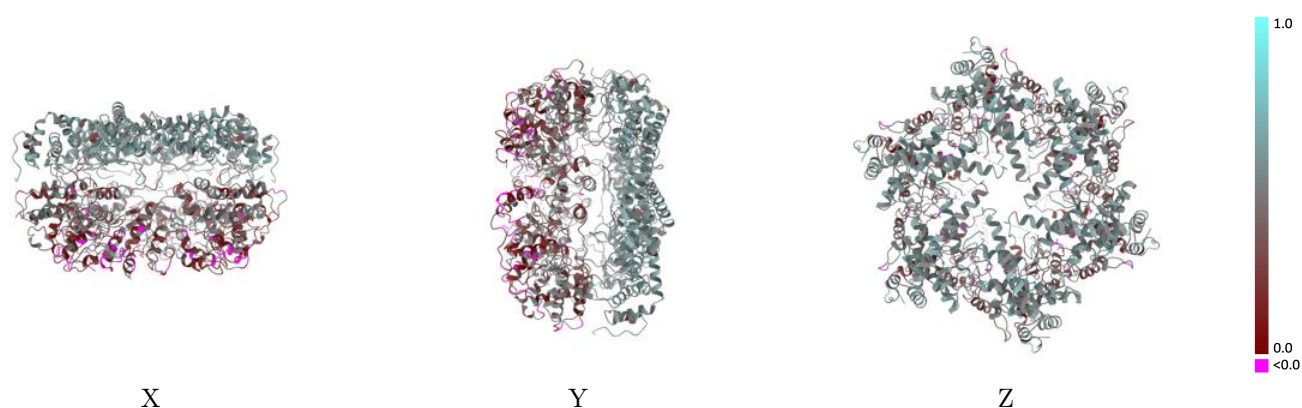
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-32521 and PDB model 7WI4. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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



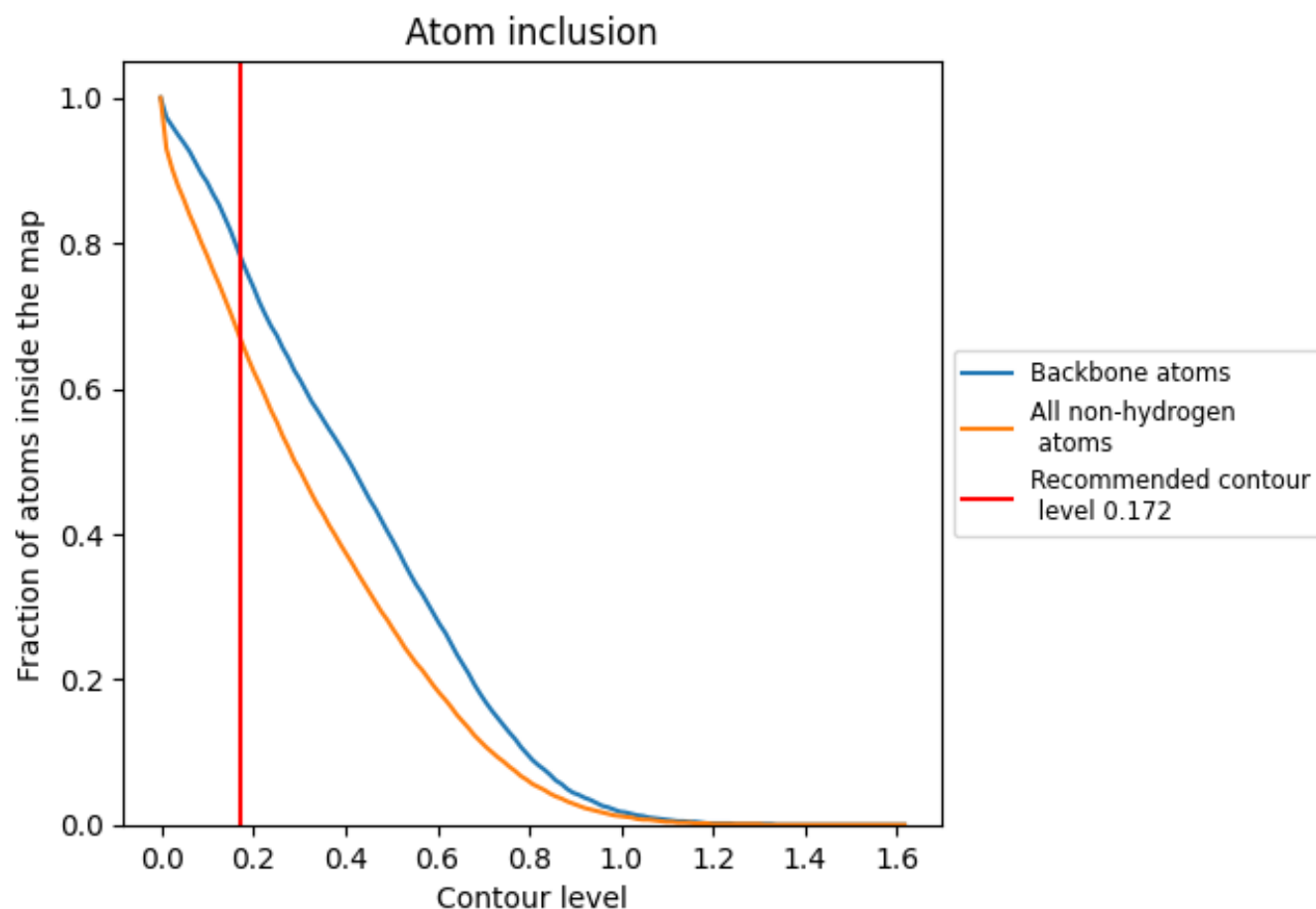
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.172).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 67% 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 (0.172) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6670	0.4320
A	0.6650	0.4350
B	0.6630	0.4270
C	0.6640	0.4340
D	0.6620	0.4290
E	0.6730	0.4340
F	0.6760	0.4360

