



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:47 PM UTC

PDB ID : 7Y4W / pdb_00007y4w
EMDB ID : EMD-33608
Title : The cryo-EM structure of human ERAD retro-translocation complex
Authors : Cao, Y.; Rao, B.; Wang, Q.; Yao, D.; Xia, Y.; Li, W.; Li, S.; Shen, Y.
Deposited on : 2022-06-16
Resolution : 3.67 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

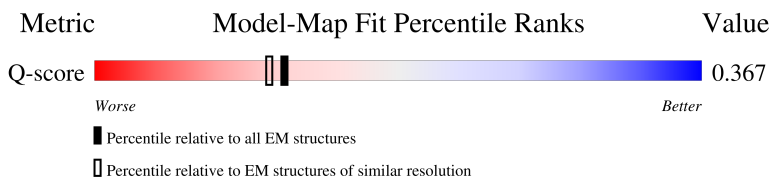
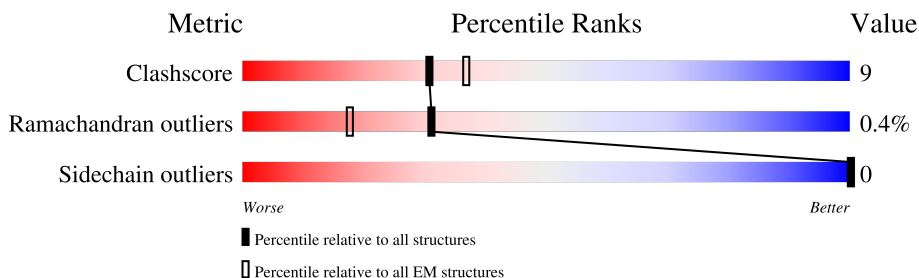
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.67 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.



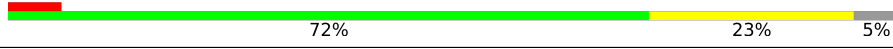
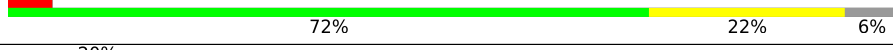
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11424 (3.17 - 4.17)

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	W	226	
1	X	226	
1	Y	226	
1	Z	226	

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Mol	Chain	Length	Quality of chain
2	A	787	
2	B	787	
2	C	787	
2	D	787	
2	E	787	
2	F	787	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 42776 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 Derlin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	W	225	Total	C	N	O	S	0	0
			1870	1267	297	295	11		
1	X	225	Total	C	N	O	S	0	0
			1870	1267	297	295	11		
1	Y	225	Total	C	N	O	S	0	0
			1870	1267	297	295	11		
1	Z	225	Total	C	N	O	S	0	0
			1870	1267	297	295	11		

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	?	-	ARG	deletion	UNP Q9BUN8
W	?	-	GLY	deletion	UNP Q9BUN8
W	?	-	GLY	deletion	UNP Q9BUN8
W	?	-	VAL	deletion	UNP Q9BUN8
W	?	-	SER	deletion	UNP Q9BUN8
W	?	-	GLY	deletion	UNP Q9BUN8
W	?	-	PHE	deletion	UNP Q9BUN8
W	?	-	GLY	deletion	UNP Q9BUN8
W	?	-	VAL	deletion	UNP Q9BUN8
W	?	-	PRO	deletion	UNP Q9BUN8
W	?	-	PRO	deletion	UNP Q9BUN8
W	?	-	ALA	deletion	UNP Q9BUN8
W	?	-	SER	deletion	UNP Q9BUN8
W	?	-	MET	deletion	UNP Q9BUN8
W	?	-	ARG	deletion	UNP Q9BUN8
W	?	-	ARG	deletion	UNP Q9BUN8
W	?	-	ALA	deletion	UNP Q9BUN8
W	?	-	ALA	deletion	UNP Q9BUN8
W	?	-	ASP	deletion	UNP Q9BUN8
W	?	-	GLN	deletion	UNP Q9BUN8
W	?	-	ASN	deletion	UNP Q9BUN8
W	?	-	GLY	deletion	UNP Q9BUN8

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Chain	Residue	Modelled	Actual	Comment	Reference
W	?	-	GLY	deletion	UNP Q9BUN8
W	?	-	GLY	deletion	UNP Q9BUN8
W	?	-	GLY	deletion	UNP Q9BUN8
X	?	-	ARG	deletion	UNP Q9BUN8
X	?	-	GLY	deletion	UNP Q9BUN8
X	?	-	GLY	deletion	UNP Q9BUN8
X	?	-	VAL	deletion	UNP Q9BUN8
X	?	-	SER	deletion	UNP Q9BUN8
X	?	-	GLY	deletion	UNP Q9BUN8
X	?	-	PHE	deletion	UNP Q9BUN8
X	?	-	GLY	deletion	UNP Q9BUN8
X	?	-	VAL	deletion	UNP Q9BUN8
X	?	-	PRO	deletion	UNP Q9BUN8
X	?	-	PRO	deletion	UNP Q9BUN8
X	?	-	ALA	deletion	UNP Q9BUN8
X	?	-	SER	deletion	UNP Q9BUN8
X	?	-	MET	deletion	UNP Q9BUN8
X	?	-	ARG	deletion	UNP Q9BUN8
X	?	-	ARG	deletion	UNP Q9BUN8
X	?	-	ALA	deletion	UNP Q9BUN8
X	?	-	ALA	deletion	UNP Q9BUN8
X	?	-	ASP	deletion	UNP Q9BUN8
X	?	-	GLN	deletion	UNP Q9BUN8
X	?	-	ASN	deletion	UNP Q9BUN8
X	?	-	GLY	deletion	UNP Q9BUN8
X	?	-	GLY	deletion	UNP Q9BUN8
X	?	-	GLY	deletion	UNP Q9BUN8
X	?	-	GLY	deletion	UNP Q9BUN8
Y	?	-	ARG	deletion	UNP Q9BUN8
Y	?	-	GLY	deletion	UNP Q9BUN8
Y	?	-	GLY	deletion	UNP Q9BUN8
Y	?	-	VAL	deletion	UNP Q9BUN8
Y	?	-	SER	deletion	UNP Q9BUN8
Y	?	-	GLY	deletion	UNP Q9BUN8
Y	?	-	PHE	deletion	UNP Q9BUN8
Y	?	-	GLY	deletion	UNP Q9BUN8
Y	?	-	VAL	deletion	UNP Q9BUN8
Y	?	-	PRO	deletion	UNP Q9BUN8
Y	?	-	PRO	deletion	UNP Q9BUN8
Y	?	-	ALA	deletion	UNP Q9BUN8
Y	?	-	SER	deletion	UNP Q9BUN8
Y	?	-	MET	deletion	UNP Q9BUN8

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	?	-	ARG	deletion	UNP Q9BUN8
Y	?	-	ARG	deletion	UNP Q9BUN8
Y	?	-	ALA	deletion	UNP Q9BUN8
Y	?	-	ALA	deletion	UNP Q9BUN8
Y	?	-	ASP	deletion	UNP Q9BUN8
Y	?	-	GLN	deletion	UNP Q9BUN8
Y	?	-	ASN	deletion	UNP Q9BUN8
Y	?	-	GLY	deletion	UNP Q9BUN8
Y	?	-	GLY	deletion	UNP Q9BUN8
Y	?	-	GLY	deletion	UNP Q9BUN8
Y	?	-	GLY	deletion	UNP Q9BUN8
Z	?	-	ARG	deletion	UNP Q9BUN8
Z	?	-	GLY	deletion	UNP Q9BUN8
Z	?	-	GLY	deletion	UNP Q9BUN8
Z	?	-	VAL	deletion	UNP Q9BUN8
Z	?	-	SER	deletion	UNP Q9BUN8
Z	?	-	GLY	deletion	UNP Q9BUN8
Z	?	-	PHE	deletion	UNP Q9BUN8
Z	?	-	GLY	deletion	UNP Q9BUN8
Z	?	-	VAL	deletion	UNP Q9BUN8
Z	?	-	PRO	deletion	UNP Q9BUN8
Z	?	-	PRO	deletion	UNP Q9BUN8
Z	?	-	ALA	deletion	UNP Q9BUN8
Z	?	-	SER	deletion	UNP Q9BUN8
Z	?	-	MET	deletion	UNP Q9BUN8
Z	?	-	ARG	deletion	UNP Q9BUN8
Z	?	-	ARG	deletion	UNP Q9BUN8
Z	?	-	ALA	deletion	UNP Q9BUN8
Z	?	-	ALA	deletion	UNP Q9BUN8
Z	?	-	ASP	deletion	UNP Q9BUN8
Z	?	-	GLN	deletion	UNP Q9BUN8
Z	?	-	ASN	deletion	UNP Q9BUN8
Z	?	-	GLY	deletion	UNP Q9BUN8
Z	?	-	GLY	deletion	UNP Q9BUN8
Z	?	-	GLY	deletion	UNP Q9BUN8
Z	?	-	GLY	deletion	UNP Q9BUN8

- Molecule 2 is a protein called Transitional endoplasmic reticulum ATPase.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	745	Total	C	N	O	S	0	0
			5846	3667	1035	1113	31		

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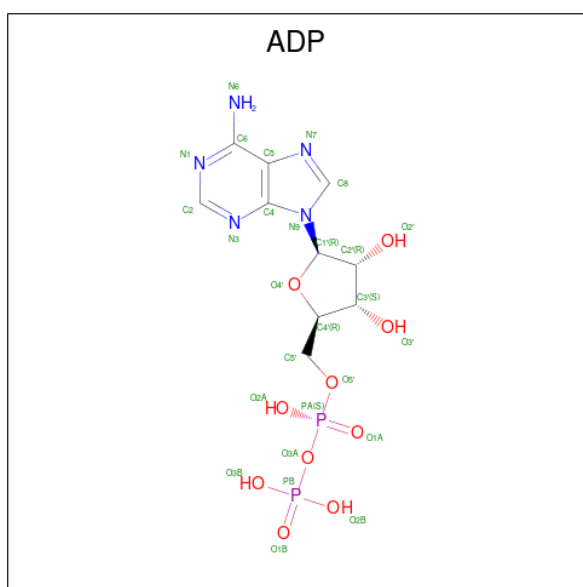
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	745	Total	C	N	O	S	0	0
			5846	3667	1035	1113	31		
2	C	744	Total	C	N	O	S	0	0
			5835	3661	1031	1112	31		
2	D	743	Total	C	N	O	S	0	0
			5829	3658	1030	1110	31		
2	E	753	Total	C	N	O	S	0	0
			5911	3712	1046	1122	31		
2	F	755	Total	C	N	O	S	0	0
			5921	3717	1048	1125	31		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	initiating methionine	UNP P55072
B	20	MET	-	initiating methionine	UNP P55072
C	20	MET	-	initiating methionine	UNP P55072
D	20	MET	-	initiating methionine	UNP P55072
E	20	MET	-	initiating methionine	UNP P55072
F	20	MET	-	initiating methionine	UNP P55072

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			27	10	5	10	2	

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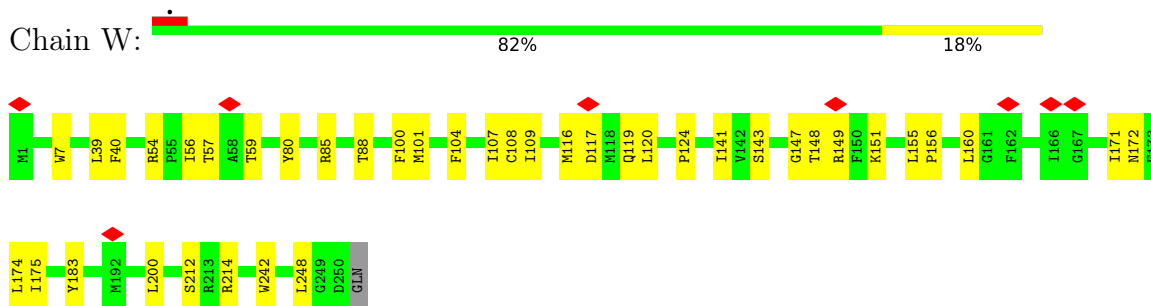
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Mol	Chain	Residues	Atoms					AltConf
3	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	F	1	Total	C	N	O	P	0
			27	10	5	10	2	

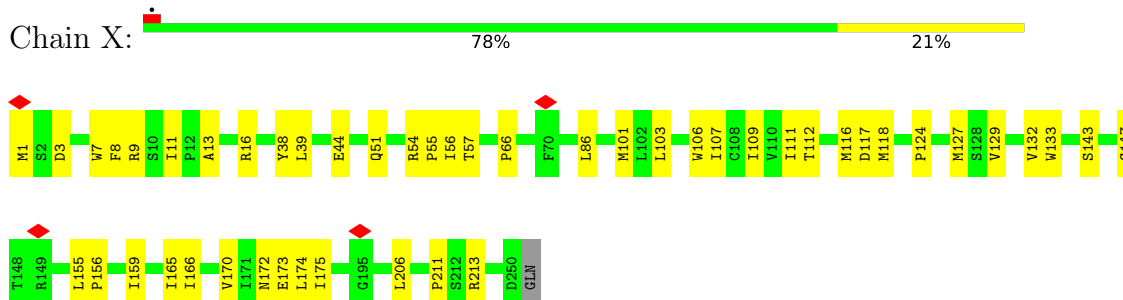
3 Residue-property plots [i](#)

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.

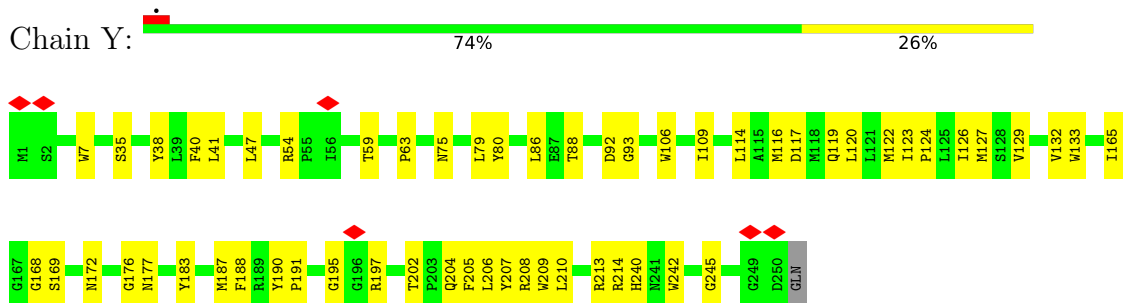
• Molecule 1: Derlin-1



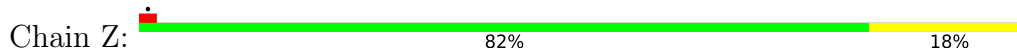
• Molecule 1: Derlin-1

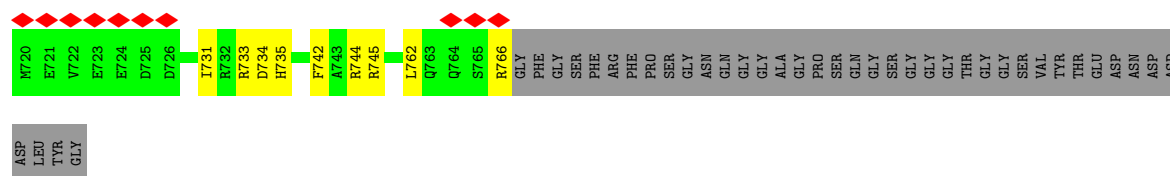


• Molecule 1: Derlin-1

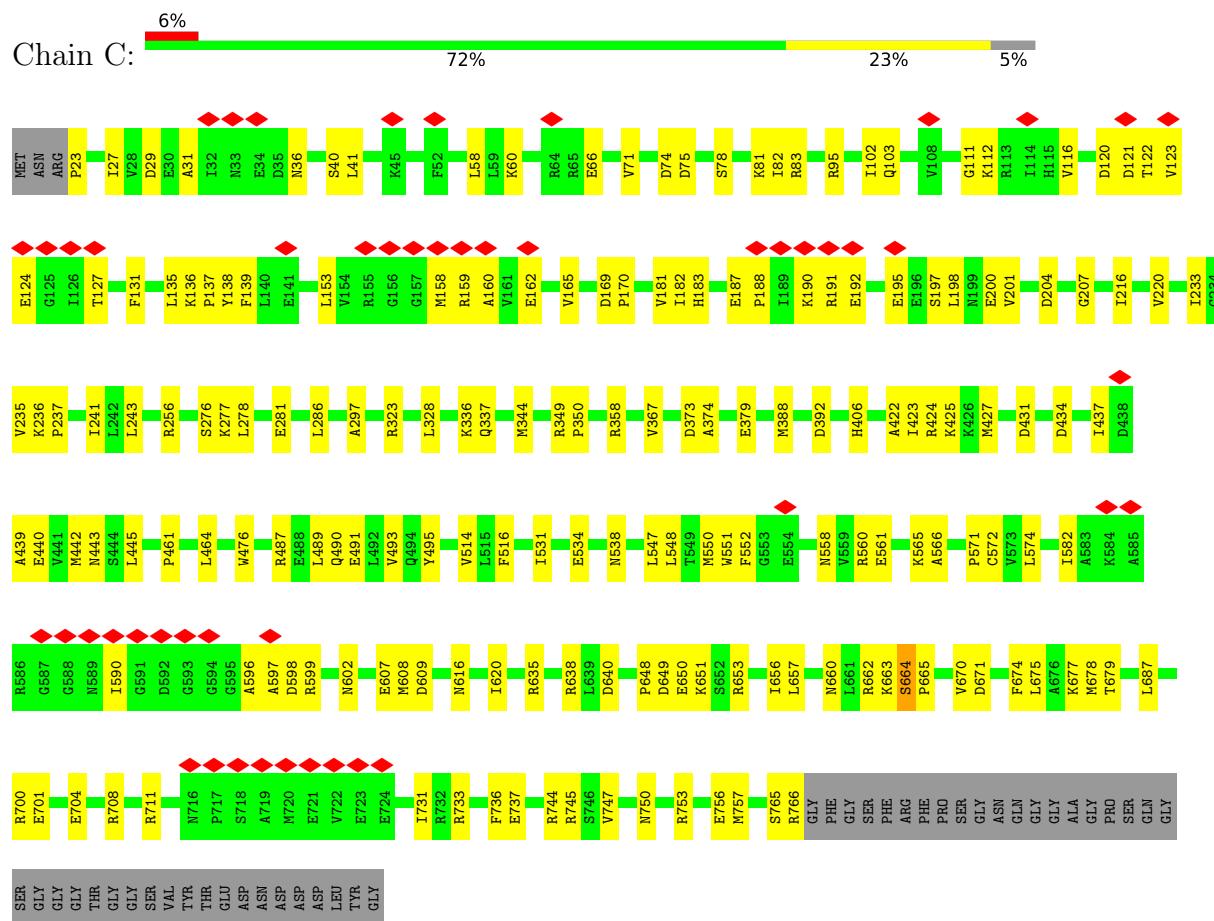


• Molecule 1: Derlin-1

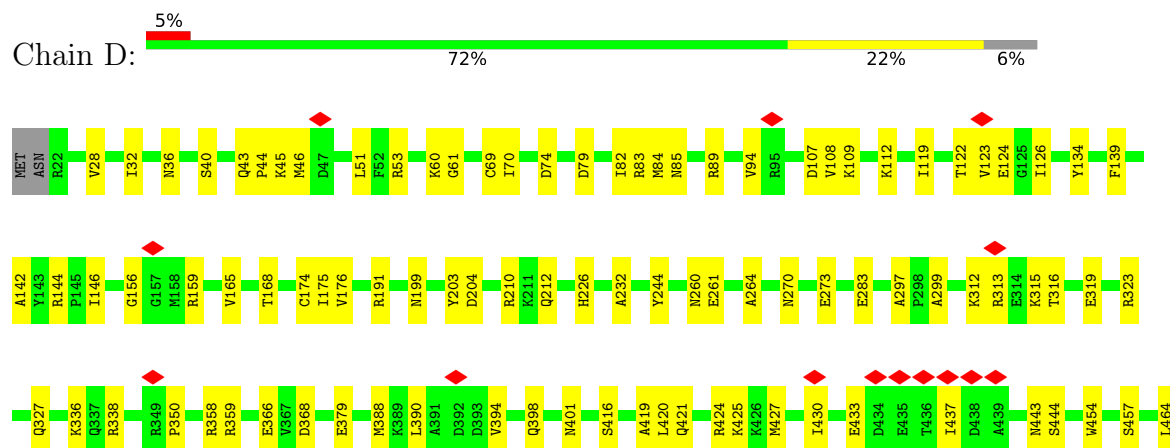


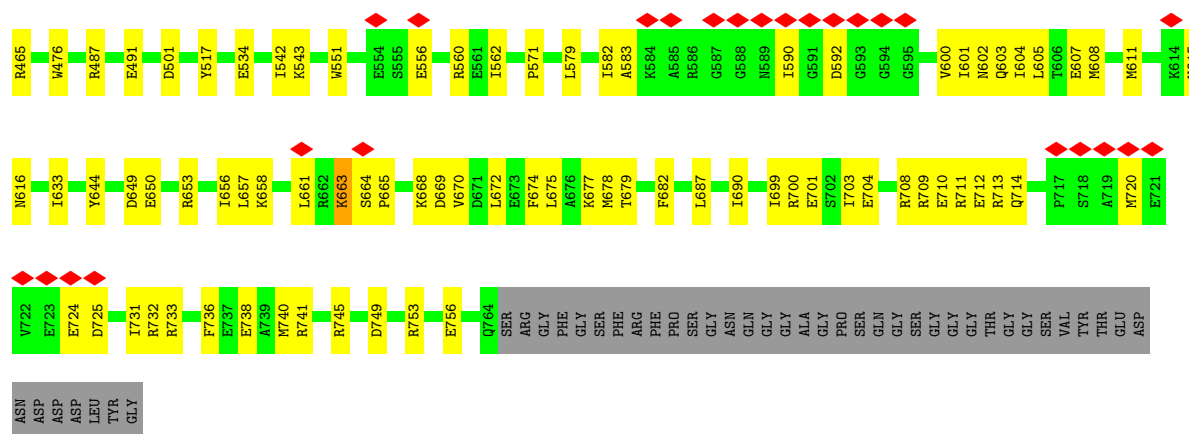


• Molecule 2: Transitional endoplasmic reticulum ATPase

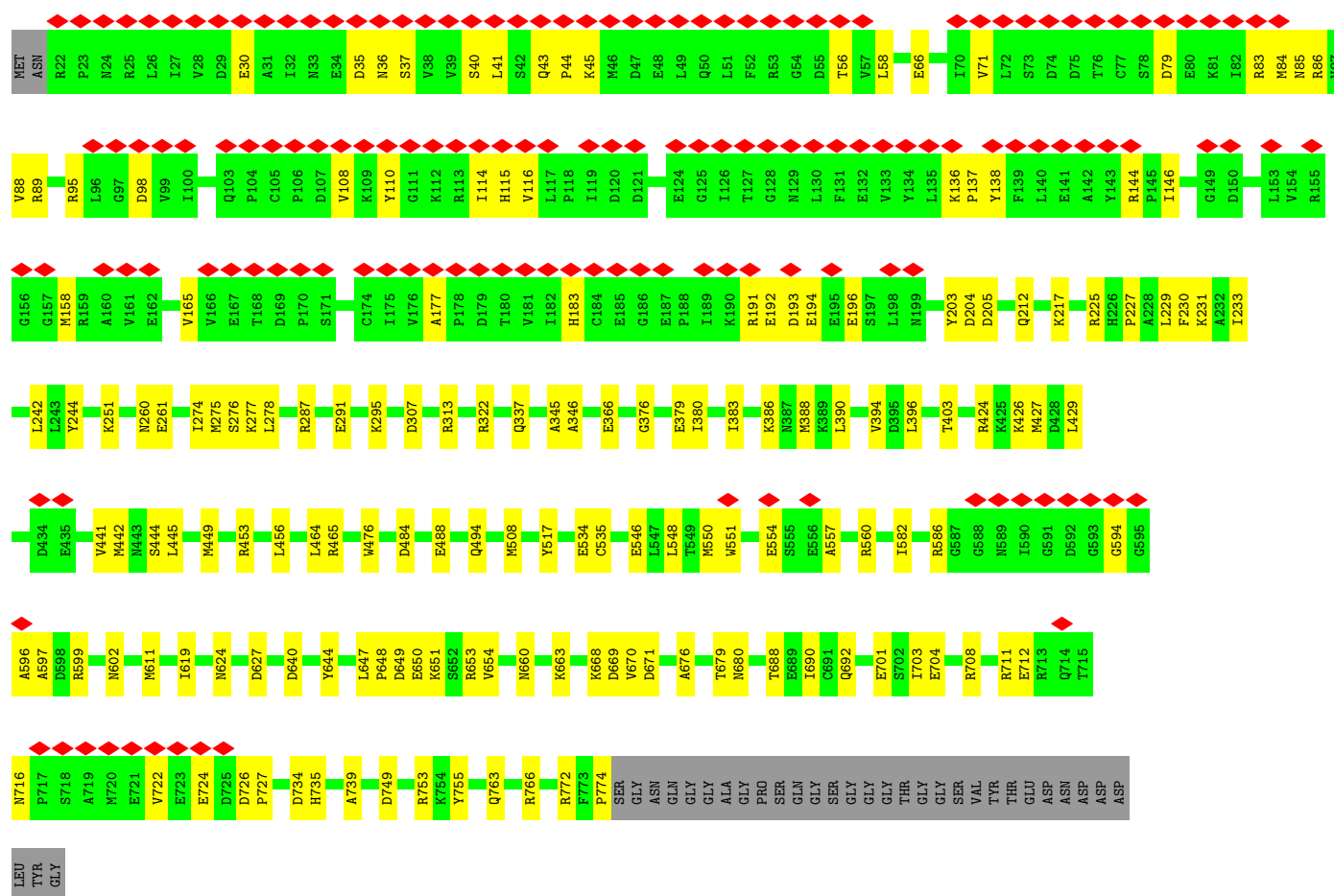
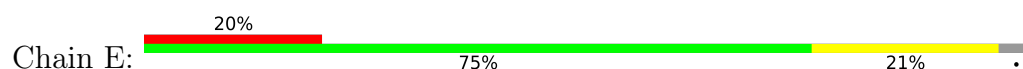


• Molecule 2: Transitional endoplasmic reticulum ATPase





• Molecule 2: Transitional endoplasmic reticulum ATPase



• Molecule 2: Transitional endoplasmic reticulum ATPase



GLN	E701	W551	T347	G202	E141	K81	MET
GLY	S702	F552	N348	Y203	A142	I82	ASN
SER	I703	E556	D364	D204	Y143	R83	R22
GLY	E704	A557	R365	I206	R144	M84	P23
GLY	I707	R560	E366	G207	P145	N85	N24
THR	R708	R567	A374	R210	I146	R86	R25
GLY	R709	R578	R377	K211	K147	V87	L26
GLY	R713	E578	I380	L212	K148	V88	I27
SER	T715	S581	L420	L213	G149	R89	V28
VAL	R716	G587	E435	L224	D150	N90	D29
THR	P717	G588	T436	L229	I151	N91	E30
GLU	S718	N589	D434	I269	F152	L92	A31
ASN	A719	I590	E436	K288	L153	R93	I32
ASP	W720	I591	T436	A289	V154	V94	I32
ASP	W721	D592	L445	E291	R155	R95	N33
ASP	W722	G593	W454	E294	G156	L96	E34
LEU	T723	G594	Q458	E297	G157	G97	D35
TYR	E724	A596	D484	P298	M158	D98	N36
GLY	D725	A597	E484	I303	R159	V99	S37
	D726	L605	L492	D304	A160	V38	V38
	R733	E606	Q494	E305	V161	I100	V39
	D734	E607	Y495	R313	E162	S101	S40
	H735	M608	D501	E314	F163	I102	L41
	F736	G611	E502	E315	K164	Q103	S42
	F737	I619	F503	E316	V165	P104	S43
	E738	G627	F506	E317	V166	C105	P44
	R741	I633	G507	E318	E167	P106	K45
	F742	Y644	G514	E319	T168	D107	M46
	A743	Y644	D506	E320	D169	V108	D47
	R744	N660	V514	E321	P170	K109	E48
	R745	K663	Y517	E322	P172	Y110	L49
	S748	S664	Y517	E323	C174	G111	Q50
	D749	F674	C535	E324	I175	K112	L51
	N750	M678	L547	E325	I176	R113	F52
	D751	N680	L548	E326	V177	H115	R83
	I752	L687	M550	E327	A177	V116	G54
	R753			E328	P178	L117	D55
	K754			E329	D179	P118	T56
	L762			E330	T180	I119	V57
	S770			E331	V181	D120	L58
	F771			E332	I182	D121	L59
	R772			E333	H183	T122	K60
	G776			E334	C184	V123	G61
ASN				E335	E185	E124	K62
GLN				E336	E186	G125	K63
GLY				E337	E187	I126	R64
GLY				E338	P188	T127	R65
ALA				E339	I189	G128	E66
PRO				E340	K190	N129	C69
SER				E341	R191	L130	I70
				E342	E192	F131	V71
				E343	D193	E132	L72
				E344	E194	V133	S73
				E345	E195	Y134	D74
				E346	E196	L135	D75
				E347	S197	K136	T76
				E348	L198	P137	C77
				E349	V201	Y139	S78
				E350		F139	D79
				E351		L140	E80

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	183316	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.567	Depositor
Minimum map value	-0.666	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.057	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	352.0, 352.0, 352.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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: ADP

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	W	0.12	0/1941	0.35	0/2647
1	X	0.12	0/1941	0.34	0/2647
1	Y	0.12	0/1941	0.33	0/2647
1	Z	0.11	0/1941	0.32	0/2647
2	A	0.11	0/5941	0.31	1/8023 (0.0%)
2	B	0.10	0/5941	0.31	0/8023
2	C	0.11	0/5930	0.34	0/8008
2	D	0.12	0/5924	0.33	0/8001
2	E	0.12	0/6010	0.34	0/8115
2	F	0.13	0/6020	0.35	0/8128
All	All	0.12	0/43530	0.33	1/58886 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	337	GLN	CB-CA-C	-5.04	110.38	117.23

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	W	1870	0	1856	28	0
1	X	1870	0	1856	35	0
1	Y	1870	0	1856	46	0
1	Z	1870	0	1856	26	0
2	A	5846	0	5905	100	0
2	B	5846	0	5905	92	0
2	C	5835	0	5893	125	0
2	D	5829	0	5887	134	0
2	E	5911	0	5963	111	0
2	F	5921	0	5971	125	0
3	A	27	0	12	2	0
3	B	27	0	12	2	0
3	E	27	0	12	1	0
3	F	27	0	12	2	0
All	All	42776	0	42996	763	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 9.

The worst 5 of 763 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)
2:D:604:ILE:HG22	2:D:608:MET:HE2	1.56	0.86
2:A:395:ASP:H	2:A:449:MET:HE2	1.41	0.86
1:Y:127:MET:HE1	1:Y:177:ASN:HB2	1.63	0.81
2:F:43:GLN:HG2	2:F:44:PRO:HD3	1.61	0.81
1:X:101:MET:HE1	1:X:132:VAL:HG11	1.63	0.80

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	W	223/226 (99%)	205 (92%)	18 (8%)	0	100	100
1	X	223/226 (99%)	203 (91%)	20 (9%)	0	100	100
1	Y	223/226 (99%)	202 (91%)	21 (9%)	0	100	100
1	Z	223/226 (99%)	202 (91%)	20 (9%)	1 (0%)	30	60
2	A	743/787 (94%)	678 (91%)	62 (8%)	3 (0%)	30	60
2	B	743/787 (94%)	685 (92%)	53 (7%)	5 (1%)	18	50
2	C	742/787 (94%)	679 (92%)	59 (8%)	4 (0%)	24	56
2	D	741/787 (94%)	678 (92%)	59 (8%)	4 (0%)	24	56
2	E	751/787 (95%)	683 (91%)	66 (9%)	2 (0%)	36	65
2	F	753/787 (96%)	691 (92%)	57 (8%)	5 (1%)	18	50
All	All	5365/5626 (95%)	4906 (91%)	435 (8%)	24 (0%)	31	60

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	663	LYS
2	E	337	GLN
2	F	298	PRO
2	F	434	ASP
2	F	770	SER

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	W	193/194 (100%)	193 (100%)	0	100	100
1	X	193/194 (100%)	193 (100%)	0	100	100
1	Y	193/194 (100%)	193 (100%)	0	100	100
1	Z	193/194 (100%)	193 (100%)	0	100	100
2	A	636/664 (96%)	636 (100%)	0	100	100
2	B	636/664 (96%)	636 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	635/664 (96%)	635 (100%)	0	100	100
2	D	634/664 (96%)	634 (100%)	0	100	100
2	E	642/664 (97%)	642 (100%)	0	100	100
2	F	643/664 (97%)	643 (100%)	0	100	100
All	All	4598/4760 (97%)	4598 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	85	ASN
2	F	443	ASN
2	E	337	GLN
2	F	285	ASN
2	F	602	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](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	ADP	A	901	-	28,29,29	1.39	4 (14%)	43,45,45	1.84	9 (20%)
3	ADP	F	901	-	28,29,29	1.40	4 (14%)	43,45,45	1.84	9 (20%)
3	ADP	B	901	-	28,29,29	1.39	4 (14%)	43,45,45	1.80	9 (20%)
3	ADP	E	901	-	28,29,29	1.40	4 (14%)	43,45,45	1.82	10 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	A	901	-	-	9/16/32/32	0/3/3/3
3	ADP	F	901	-	-	4/16/32/32	0/3/3/3
3	ADP	B	901	-	-	4/16/32/32	0/3/3/3
3	ADP	E	901	-	-	7/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	901	ADP	C5-C4	4.65	1.47	1.39
3	E	901	ADP	C5-C4	4.64	1.47	1.39
3	B	901	ADP	C5-C4	4.62	1.47	1.39
3	A	901	ADP	C5-C4	4.62	1.47	1.39
3	F	901	ADP	C5-C6	2.68	1.48	1.41

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	901	ADP	C5-C4-N3	-5.84	118.68	126.72
3	A	901	ADP	C5-C4-N3	-5.81	118.72	126.72
3	B	901	ADP	C5-C4-N3	-5.78	118.76	126.72
3	E	901	ADP	C5-C4-N3	-5.74	118.82	126.72
3	F	901	ADP	N3-C4-N9	4.71	135.17	127.17

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

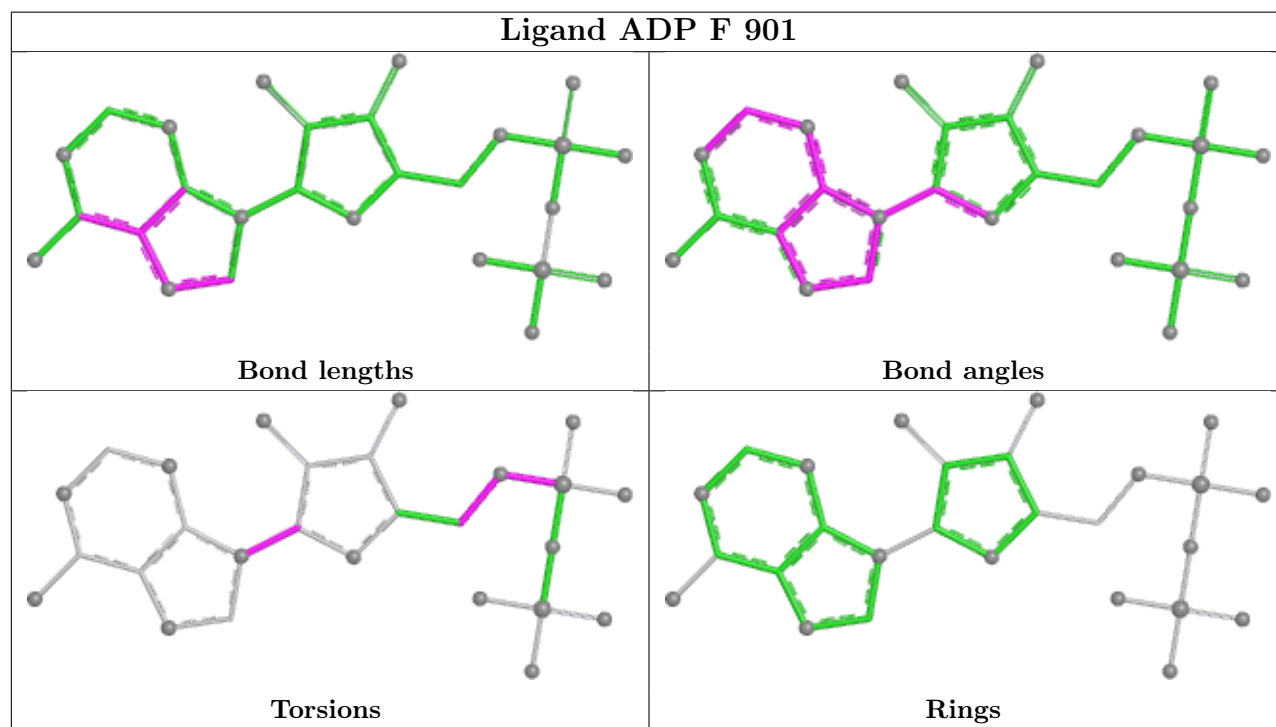
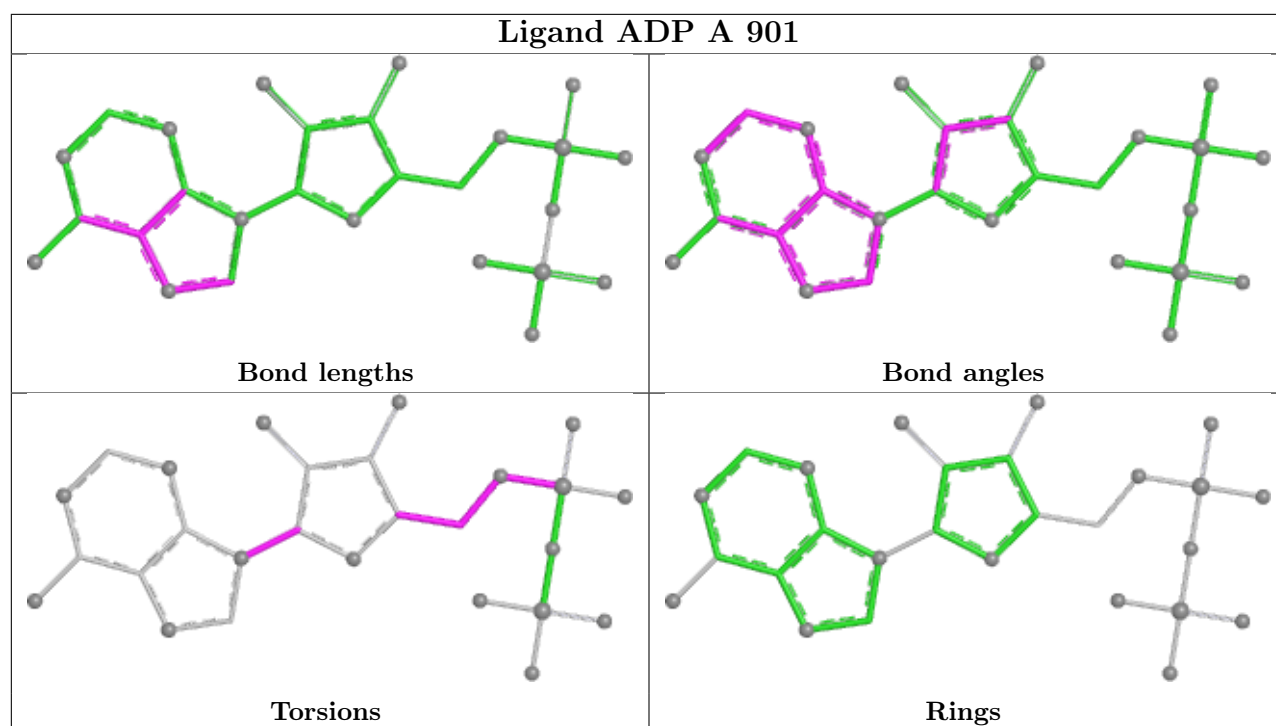
Mol	Chain	Res	Type	Atoms
3	A	901	ADP	C5'-O5'-PA-O1A
3	A	901	ADP	C5'-O5'-PA-O2A
3	A	901	ADP	C5'-O5'-PA-O3A
3	E	901	ADP	C5'-O5'-PA-O3A
3	A	901	ADP	O4'-C4'-C5'-O5'

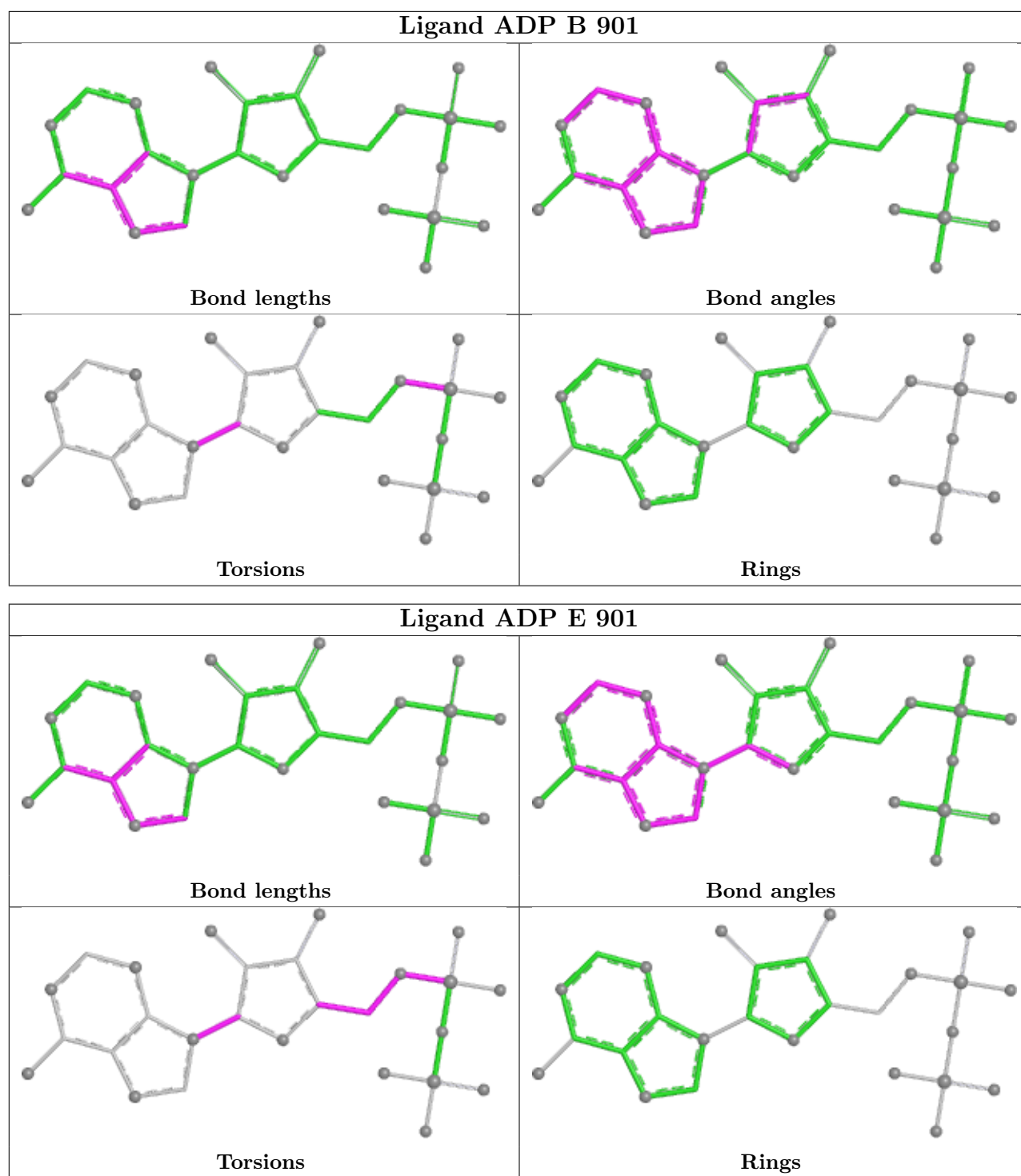
There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	901	ADP	2	0
3	F	901	ADP	2	0
3	B	901	ADP	2	0
3	E	901	ADP	1	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

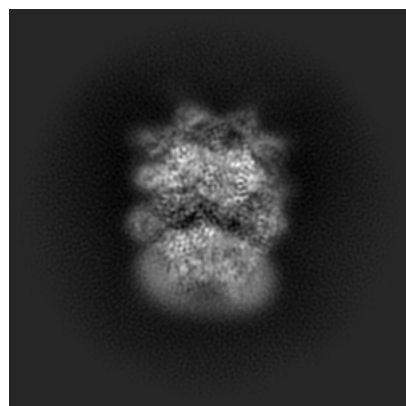
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33608. These allow visual inspection of the internal detail of the map and identification of artifacts.

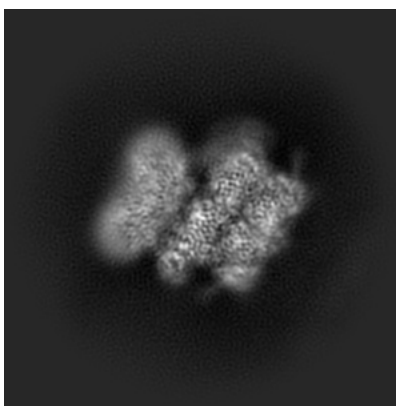
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

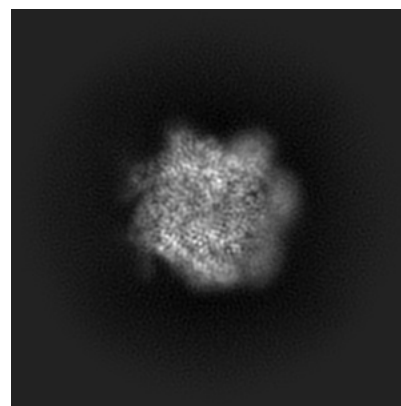
6.1.1 Primary map



X

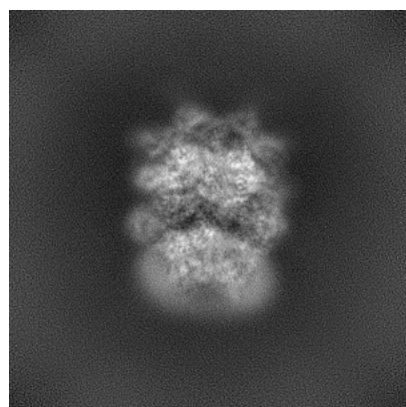


Y

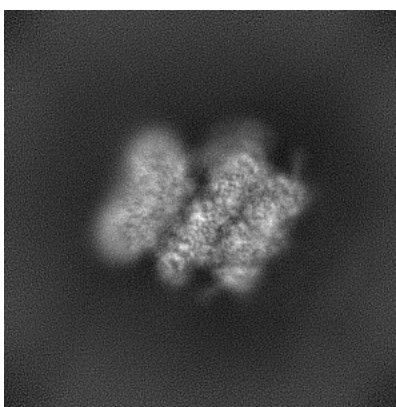


Z

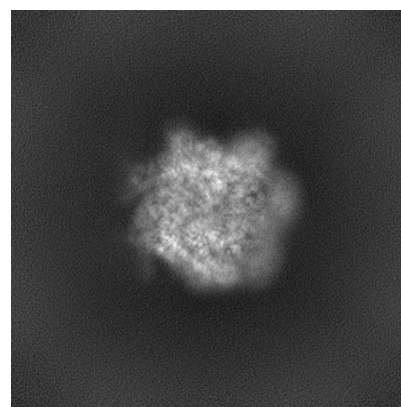
6.1.2 Raw map



X



Y

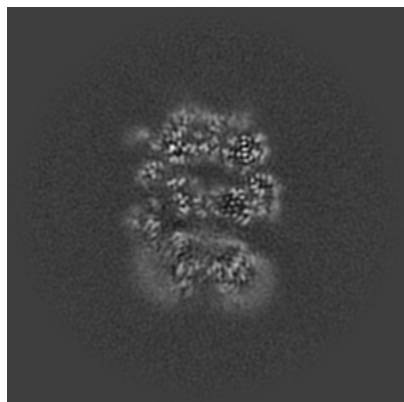


Z

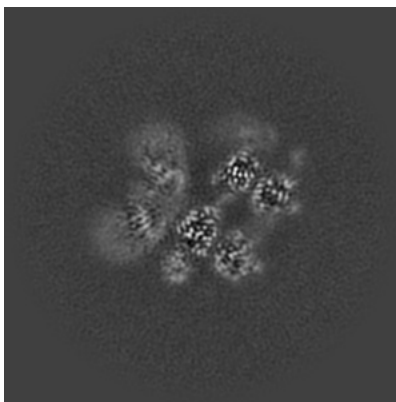
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

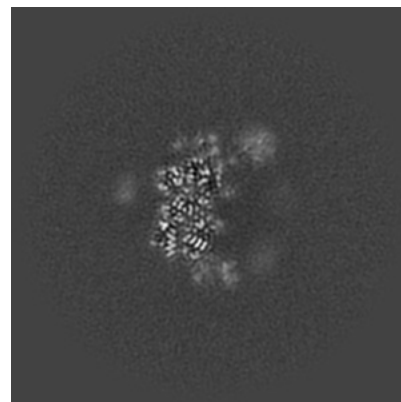
6.2.1 Primary map



X Index: 160

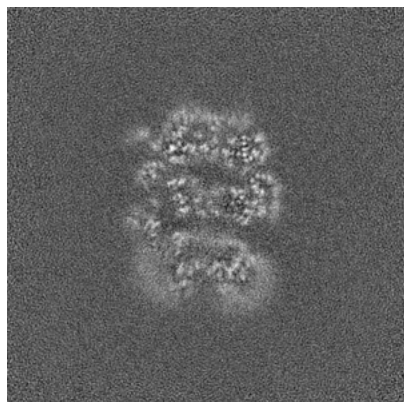


Y Index: 160

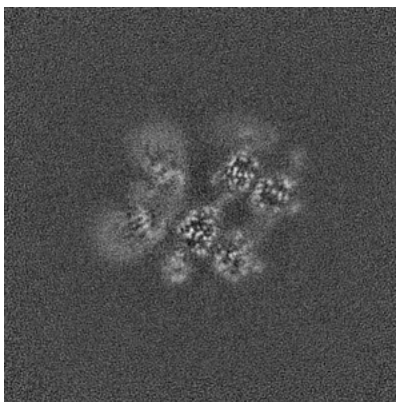


Z Index: 160

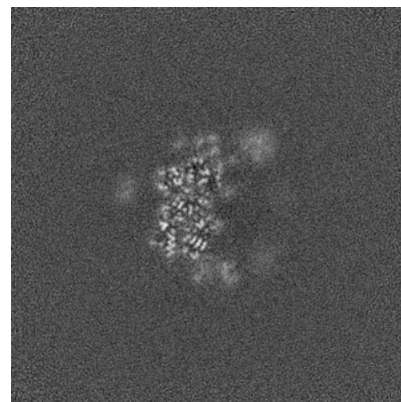
6.2.2 Raw map



X Index: 160



Y Index: 160

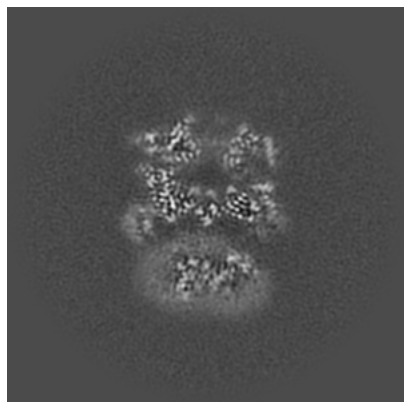


Z Index: 160

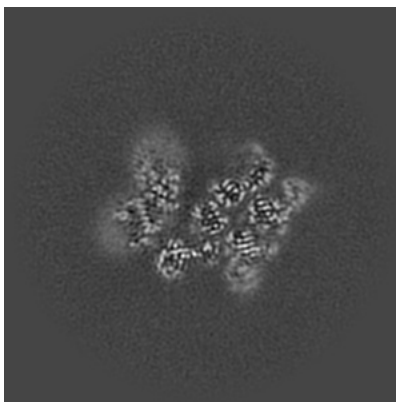
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

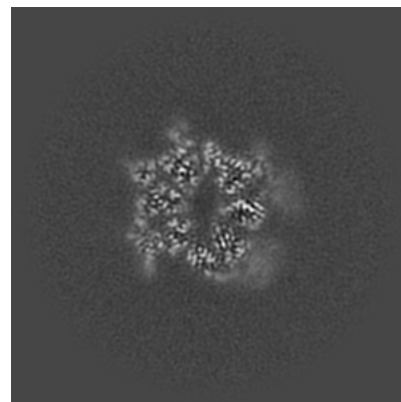
6.3.1 Primary map



X Index: 151

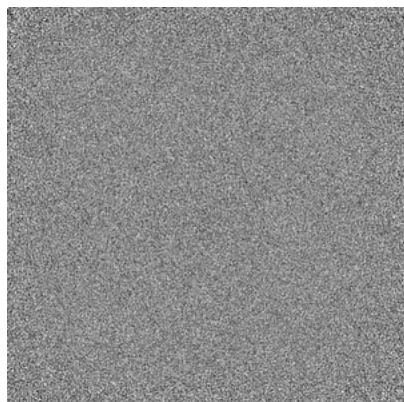


Y Index: 137

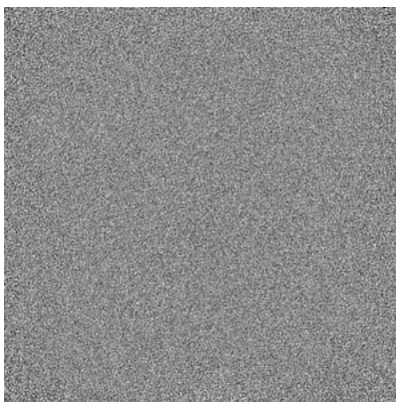


Z Index: 184

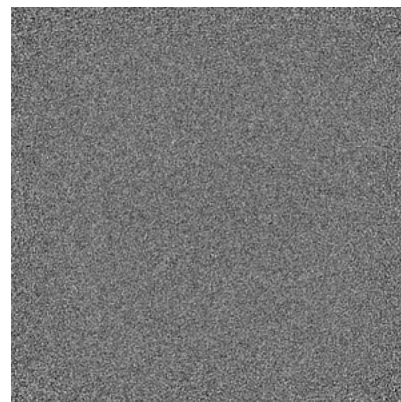
6.3.2 Raw map



X Index: 0



Y Index: 0

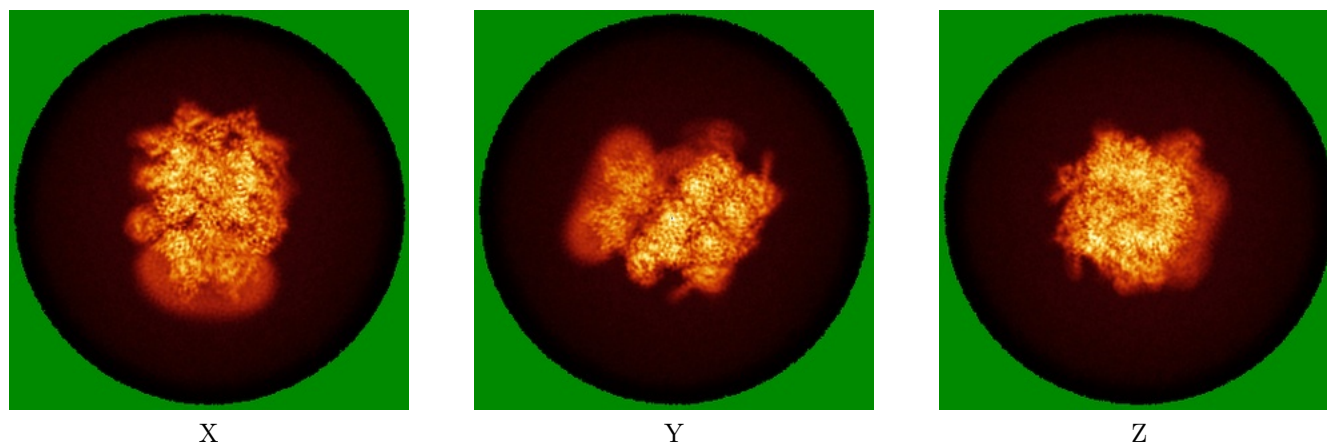


Z Index: 0

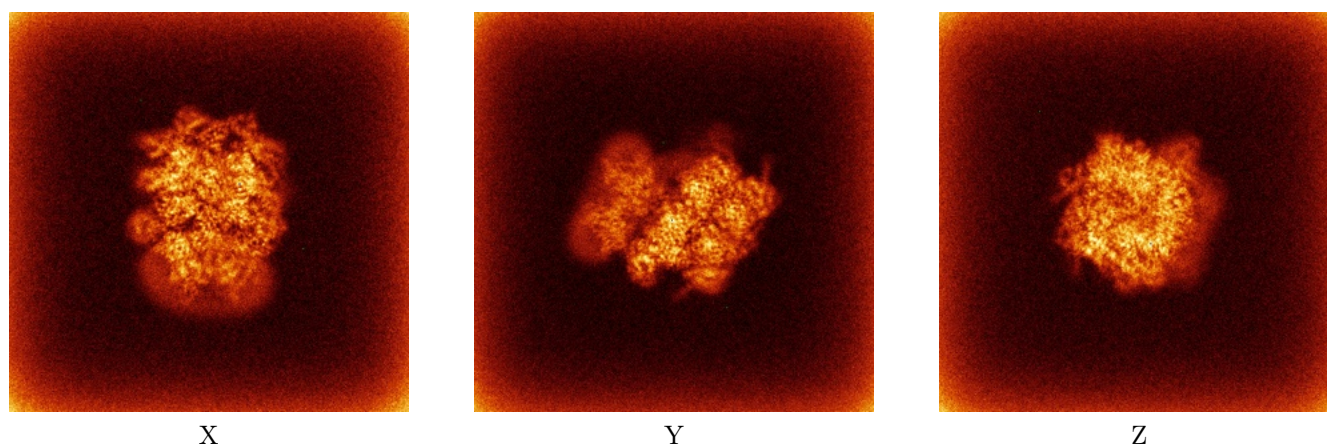
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

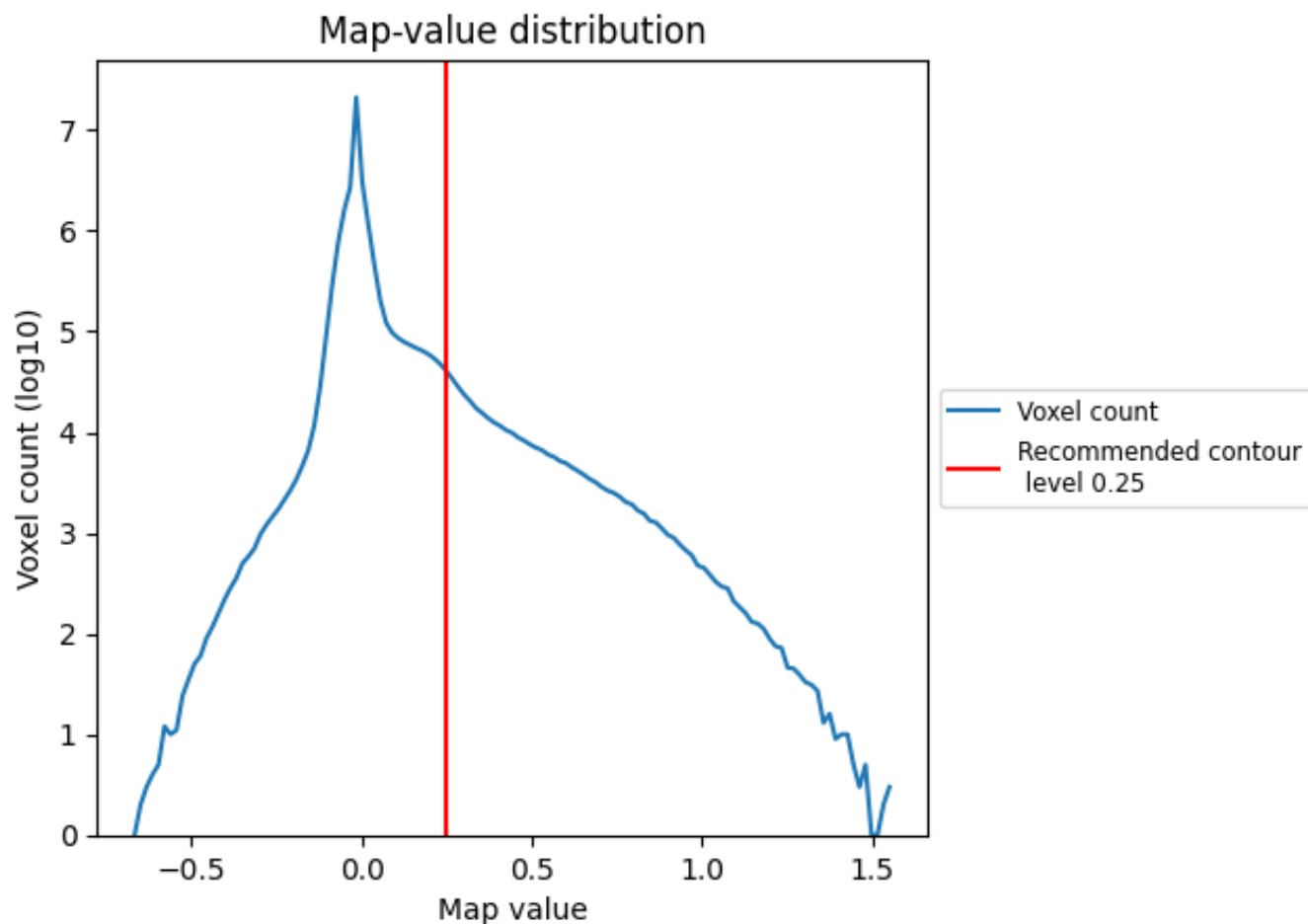
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

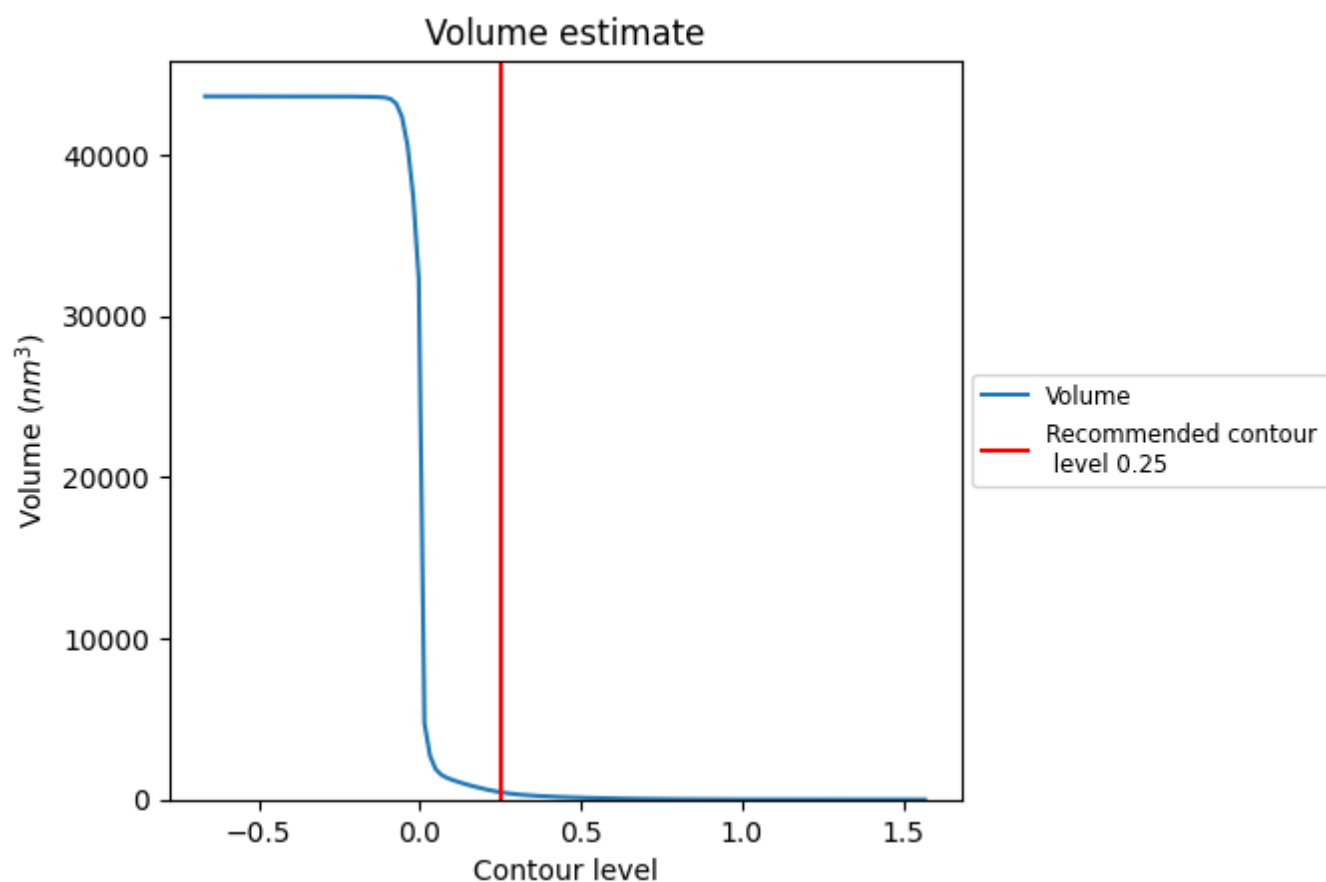
This section contains the results of statistical analysis of the map.

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.

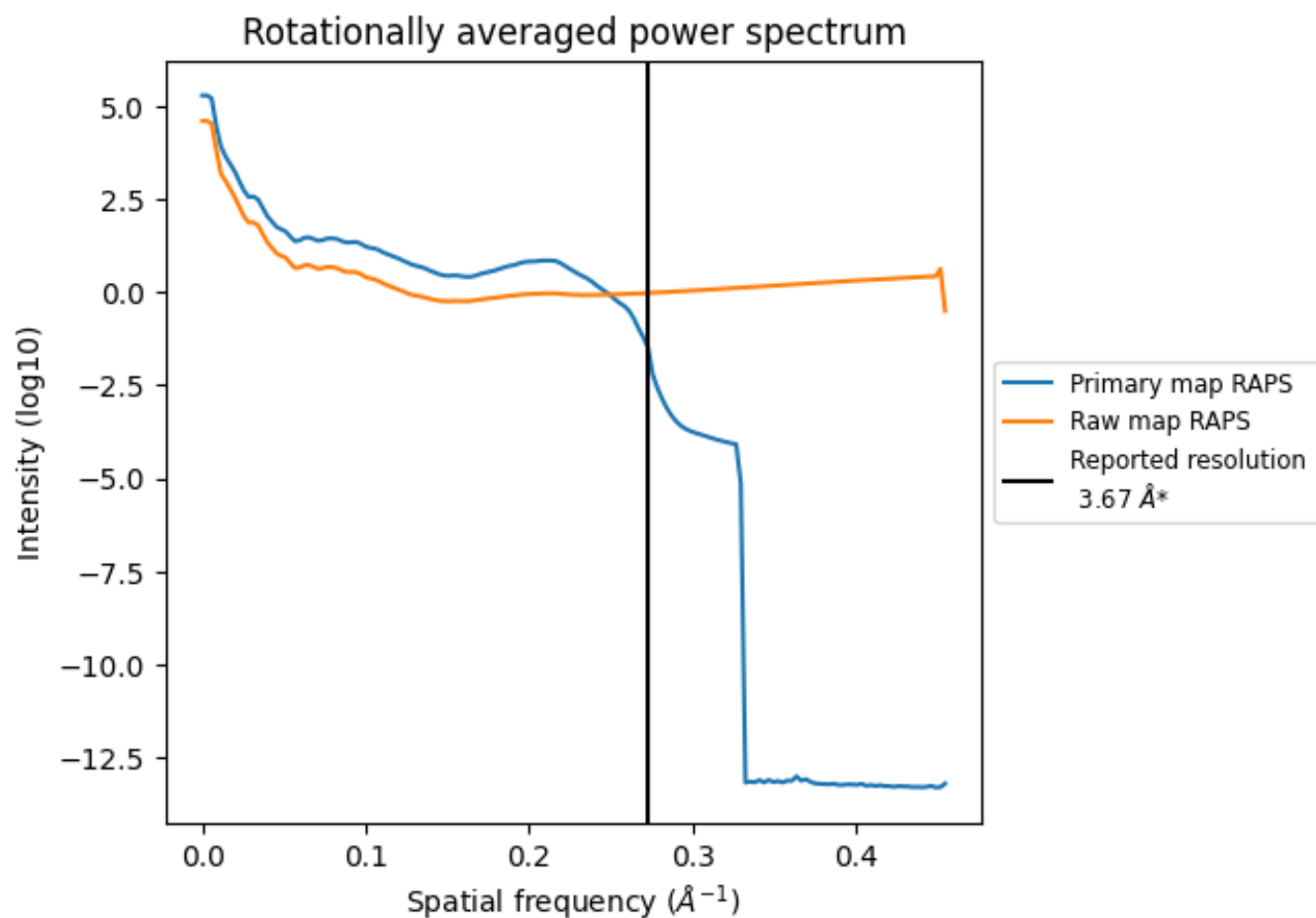
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 456 nm³; this corresponds to an approximate mass of 412 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 ⓘ

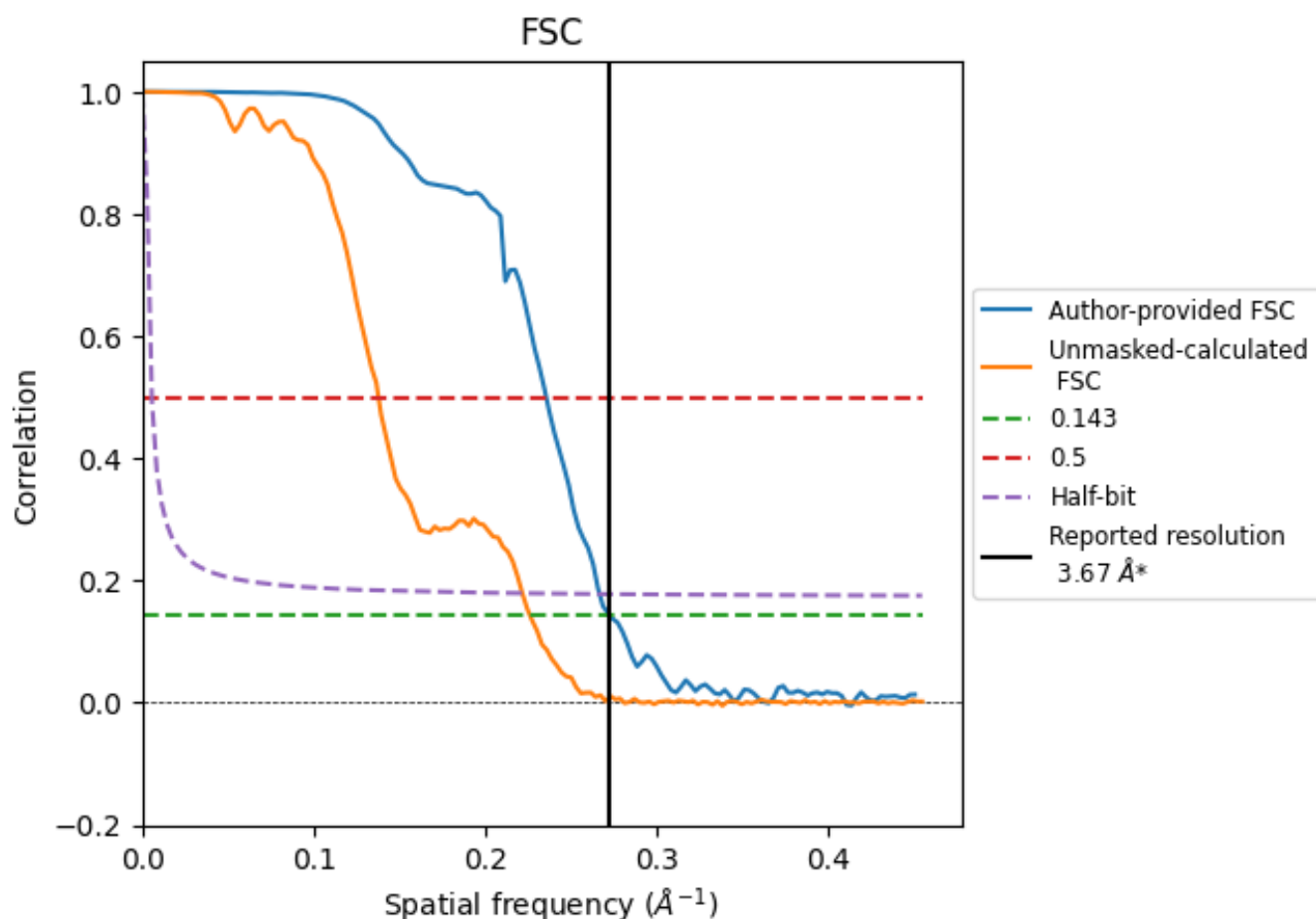


*Reported resolution corresponds to spatial frequency of 0.272 $\text{\AA}^{-1}$

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 $0.272 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.67	-	-
Author-provided FSC curve	3.67	4.25	3.75
Unmasked-calculated*	4.42	7.26	4.51

*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 4.42 differs from the reported value 3.67 by more than 10 %

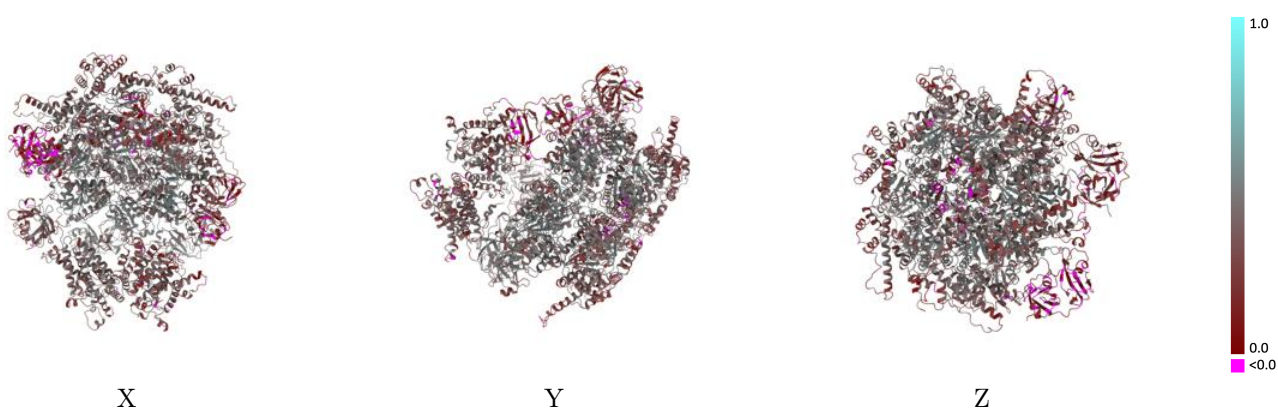
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33608 and PDB model 7Y4W. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)

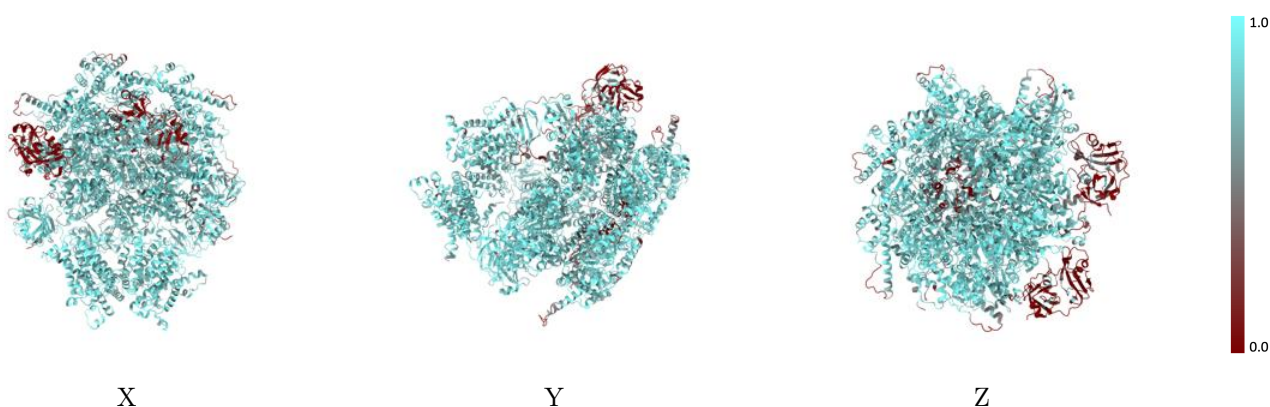
This section was not generated.

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



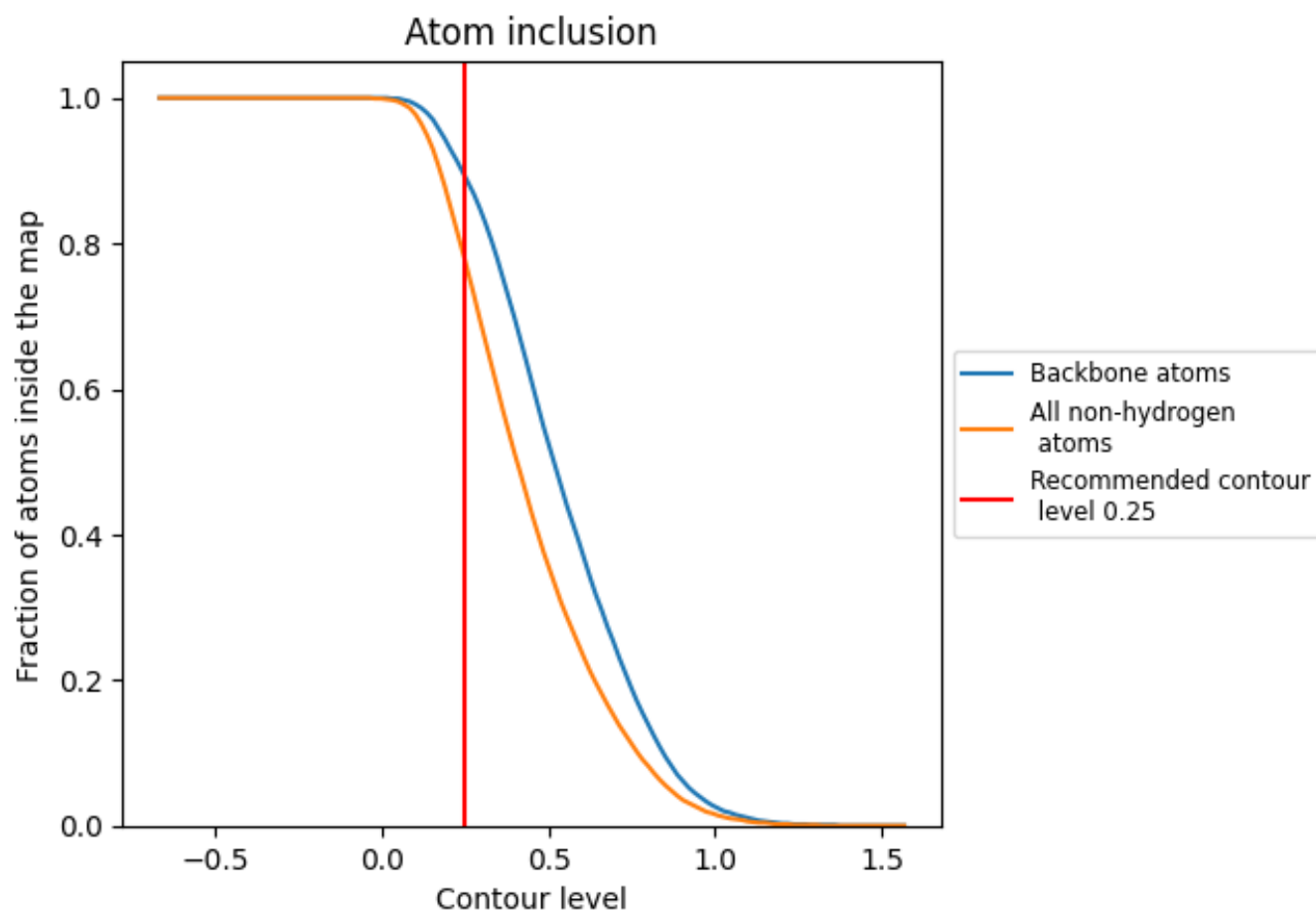
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 78% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7760	0.3670
A	0.8320	0.4100
B	0.8220	0.4050
C	0.7860	0.3540
D	0.8100	0.3780
E	0.6770	0.3580
F	0.6430	0.3200
W	0.8320	0.3290
X	0.8580	0.3650
Y	0.8310	0.3280
Z	0.8600	0.3800

1.0

0.0

<0.0