wwPDB EM Validation Summary Report (i)

Dec 18, 2022 – 07:53 pm GMT

PDB ID	:	7AY1
EMDB ID	:	EMD-11934
Title	:	Cryo-EM structure of USP1-UAF1 bound to mono-ubiquitinated FANCD2, and FANCI
Authors	:	Rennie, M.L.; Arkinson, C.; Walden, H.
Deposited on	:	2020-11-10
Resolution	:	3.70 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 (i) 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 (i)) were used in the production of this report:

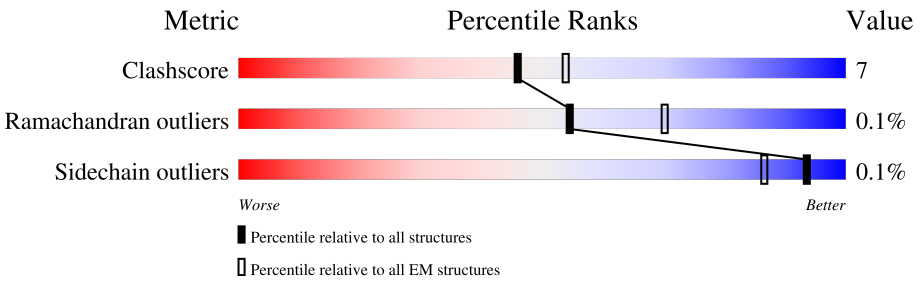
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 3.70 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)
Clashscore	158937	4297
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	1335	6% 65% 12% 23%
2	B	1455	9% 59% 12% 29%
3	C	80	86% 10% •
4	D	786	• 34% 9% 57%
5	E	694	5% 71% 14% 14%
6	S	29	100% 90% 10%
6	T	29	100% 90% 10%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 25186 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 Fanconi anemia group I protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1033	8215	5273	1371	1522	49	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP Q9NVI1
A	-5	HIS	-	expression tag	UNP Q9NVI1
A	-4	HIS	-	expression tag	UNP Q9NVI1
A	-3	HIS	-	expression tag	UNP Q9NVI1
A	-2	HIS	-	expression tag	UNP Q9NVI1
A	-1	HIS	-	expression tag	UNP Q9NVI1
A	0	HIS	-	expression tag	UNP Q9NVI1

- Molecule 2 is a protein called Fanconi anemia group D2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1033	8263	5316	1373	1523	51	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP Q9BXW9
B	-2	PRO	-	expression tag	UNP Q9BXW9
B	-1	GLY	-	expression tag	UNP Q9BXW9
B	0	SER	-	expression tag	UNP Q9BXW9

- Molecule 3 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	77	607	381	106	119	1	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP P62987
C	-2	PRO	-	expression tag	UNP P62987
C	-1	GLY	-	expression tag	UNP P62987
C	0	SER	-	expression tag	UNP P62987

- Molecule 4 is a protein called Ubiquitin carboxyl-terminal hydrolase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	341	2742	1757	445	527	13	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	GLY	-	expression tag	UNP O94782
D	90	SER	CYS	engineered mutation	UNP O94782
D	670	ALA	GLY	engineered mutation	UNP O94782
D	671	ALA	GLY	engineered mutation	UNP O94782

- Molecule 5 is a protein called WD repeat-containing protein 48.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	596	4720	2986	829	879	26	0	0

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-16	MET	-	initiating methionine	UNP Q8TAF3
E	-15	HIS	-	expression tag	UNP Q8TAF3
E	-14	HIS	-	expression tag	UNP Q8TAF3
E	-13	HIS	-	expression tag	UNP Q8TAF3
E	-12	HIS	-	expression tag	UNP Q8TAF3
E	-11	HIS	-	expression tag	UNP Q8TAF3
E	-10	HIS	-	expression tag	UNP Q8TAF3
E	-9	LEU	-	expression tag	UNP Q8TAF3
E	-8	GLU	-	expression tag	UNP Q8TAF3
E	-7	VAL	-	expression tag	UNP Q8TAF3
E	-6	LEU	-	expression tag	UNP Q8TAF3
E	-5	PHE	-	expression tag	UNP Q8TAF3
E	-4	GLN	-	expression tag	UNP Q8TAF3

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-3	GLY	-	expression tag	UNP Q8TAF3
E	-2	PRO	-	expression tag	UNP Q8TAF3
E	-1	GLY	-	expression tag	UNP Q8TAF3
E	0	SER	-	expression tag	UNP Q8TAF3

- Molecule 6 is a DNA chain called DNA (61-MER).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	O	P		
6	S	29	319	145	145	29	0	0
			Total	C	O	P		
6	T	29	319	145	145	29	0	0

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

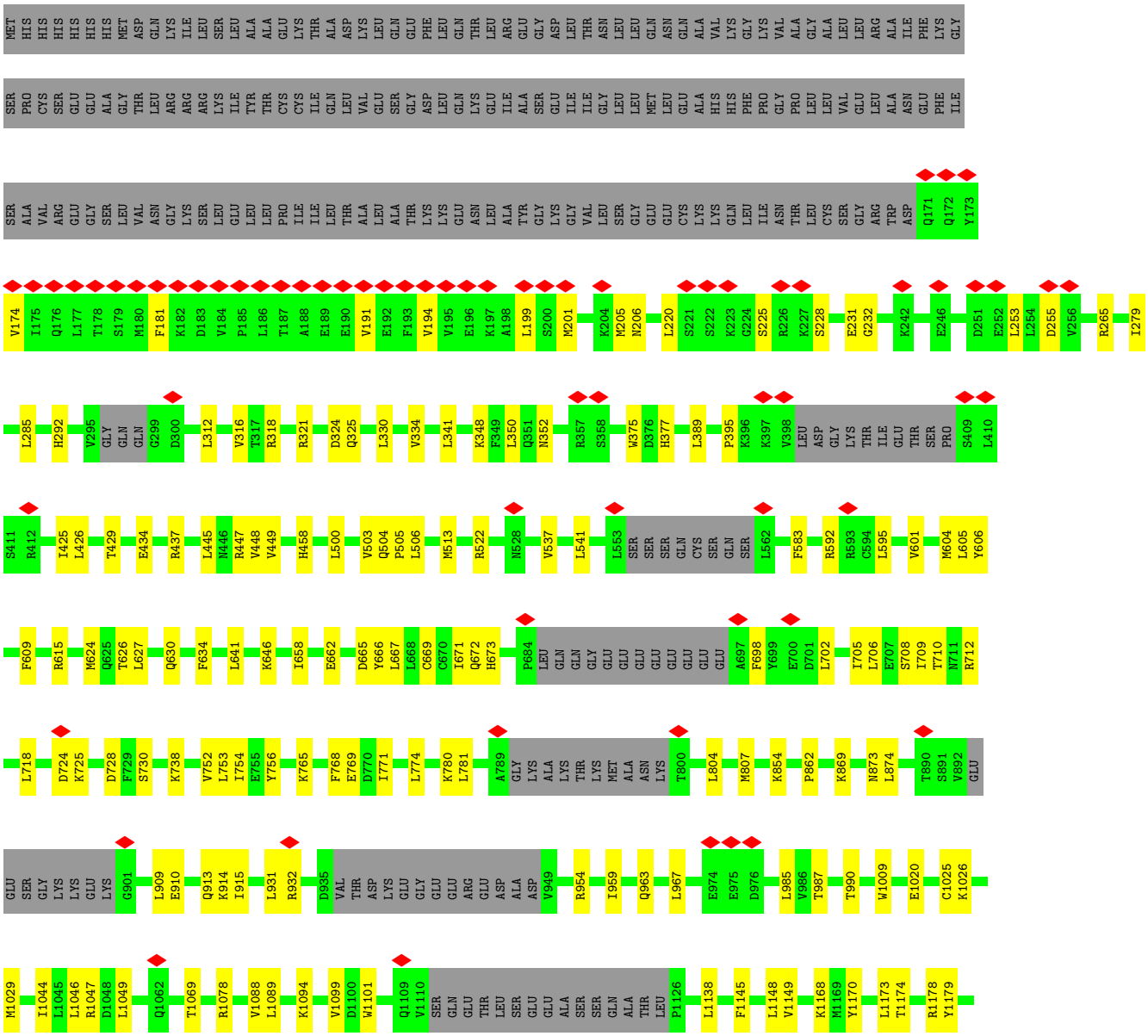
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
7	D	1	1	1	0

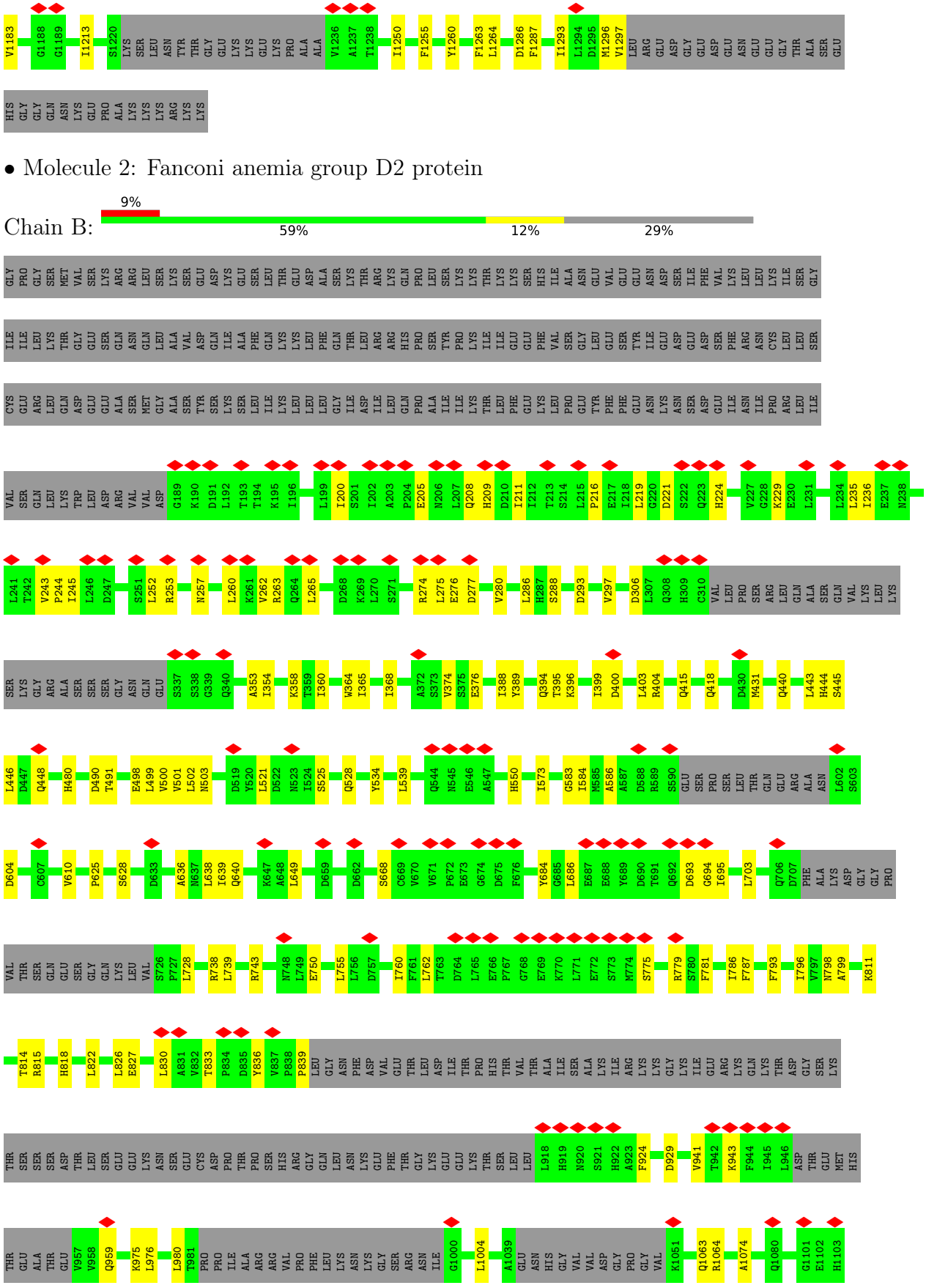
3 Residue-property plots (i)

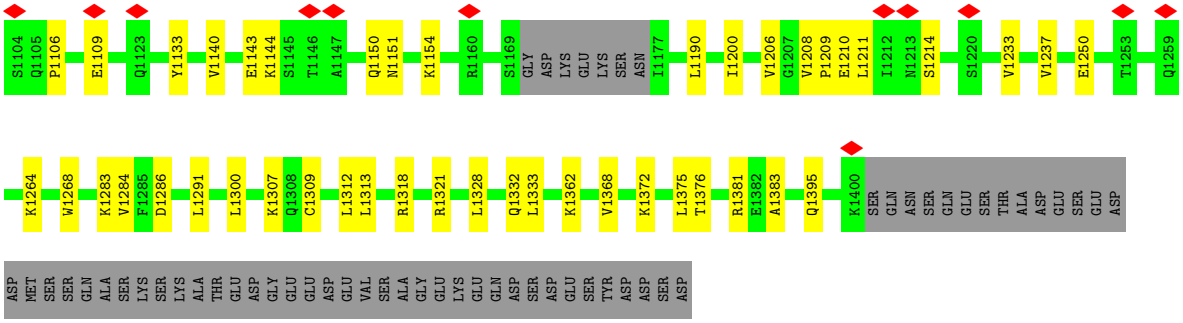
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

Chain A:

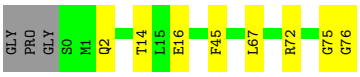



V1183 G1188 G1189 I1213 S1220 LYS SER LEU ASN TYR THR GLY GLU LYS LYS GLU LYS PRO ALA ALA V1236 A1237 T1238 I1250 F1255 Y1260 F1263 L1264 D1286 F1287 I1293 L1294 D1295 M1296 V1297 LEU ARG GLU ASP GLY GLU ASP GLU ASN GLU GLU GLY THR ALA SER GLU
HIS GLY GLY GLN ASN LYS GLU PRO ALA LYS LYS LYS ARG LYS LYS
• Molecule 2: Fanconi anemia group D2 protein
Chain B:
9%
59%
12%
29%
GLY PRO GLY SER MET VAL SER LYS ARG ARG LEU SER LYS SER GLU ASP LYS GLU SER LEU THR GLU ASP ALA SER LYS THR ARG LYS GLN PRO LEU SER LYS LYS THR LYS LYS SER HIS ILE ALA ASN GLU VAL GLU GLU ASN ASP SER ILE PHE VAL LYS LEU LEU LYS ILE SER GLY
ILE ILE LEU LYS THR GLY GLU SER GLN ASN GLN LEU ALA VAL ASP GLN ILE ALA PHE GLN LYS LYS LEU PHE GLN THR LEU ARG ARG HIS PRO SER TYR PRO LYS LYS ILE ILE GLU GLU PHE VAL SER GLY LEU GLU SER TYR ILE GLU ASP SER PHE ARG ASN CYS LEU LEU SER
CYS GLU ARG LEU GLN ASP GLU GLU ALA SER MET GLY ALA SER TYR SER LYS SER LEU ILE LYS LEU LEU LEU GLY ILE ASP ILE LEU GLN PRO ALA ILE ILE LYS THR LEU PHE GLU LYS LEU PRO GLU TYR PHE PHE GLU ASN LYS ASN SER ASP GLU ILE ASN ILE PRO ARG LEU LEU ILE
VAL SER GLN LEU LYS TRP LEU ASP ARG VAL VAL ASP G139 K190 D191 L192 T193 T194 K195 I196 L199 I200 S201 I202 A203 P204 E205 N206 L207 Q208 H209 D210 I211 I212 T213 S214 L215 P216 E217 I218 L219 G220 D221 S222 Q223 H224 V227 G228 K229 E230 L231 L234 L235 I236 E237 N238
L241 T242 V243 P244 I245 L246 D247 S251 L252 R253 N257 L260 K261 V262 R263 Q264 L265 D268 K269 L270 S271 R274 L275 E276 D277 V280 L286 H287 S288 D293 V297 D306 L307 Q308 H309 C310 VAL LEU PRO SER ARG LEU GLN ALA SER GLN VAL LYS LEU LYS
SER LYS GLY ARG ALA SER SER GLY ASN GLN GLU S337 S338 G339 Q340 A353 I354 K358 T359 I360 W364 I365 I368 A372 S373 V374 S375 E376 I388 Y389 Q394 T395 K396 I399 D400 L403 R404 Q415 Q418 D430 M431 Q440 L443 H444 S445
L446 D447 Q448 H480 D490 T491 E498 L499 V500 V501 L502 N503 D519 Y520 L521 D522 N523 I524 S525 Q528 Y534 L539 Q544 N545 E546 A547 H550 I573 G583 I584 M585 A586 A587 D588 R589 S590 GLU SER PRO SER LEU THR GLN GLU ARG ALA ASN L602 S603
D604 C607 V610 P625 S628 D633 A636 N637 L638 I639 Q640 K647 A648 L649 D659 D662 S668 C669 V670 V671 P672 E673 G674 D675 F676 Y684 G685 L686 E687 E688 Y689 D690 T691 Q692 D693 G694 I695 L703 Q706 D707 PHE ALA LYS ASP GLY GLY PRO
VAL THR SER GLN GLU SER GLY GLN LYS LEU VAL S726 P727 L728 R738 L739 R743 N748 L749 E750 L755 L756 D757 I760 F761 L762 T763 D764 L765 E766 P767 G768 E769 K770 L771 E772 S773 M774 S775 R779 S780 F781 I786 F787 F793 I796 V797 N798 A799 K811
T814 R815 H818 L822 L826 E827 L830 A831 V832 T833 P834 D835 Y836 V837 P838 P839 LEU GLY ASN PHE ASP VAL GLU THR LEU ASP ILE THR PRO HIS THR VAL THR ALA ILE SER ALA LYS ILE ARG LYS LYS GLY LYS ILE GLU ARG LYS GLN LYS THR ASP GLY SER LYS
THR SER SER SER ASP THR LEU SER GLU GLU LYS ASN SER GLU CYS ASP PRO THR PRO SER HIS ARG GLY GLN LEU ASN LYS GLU PHE THR GLY LYS GLU GLU LYS THR HIS SER LEU LEU L918 H919 N920 S921 H922 A923 F924 D929 V941 T942 K943 F944 I945 L946 ASP THR GLU MET HIS
THR GLU ALA THR GLU V957 V958 Q959 K975 L976 L980 T981 PRO PRO ILE ALA ARG ARG VAL PRO PHE LEU LYS ASN LYS GLY SER ARG ASN ILE G1000 L1004 A1039 GLU ASN HIS GLY VAL VAL ASP GLY PRO GLY VAL K1051 Q1063 R1064 A1074 Q1080 G1101 E1102 H1103



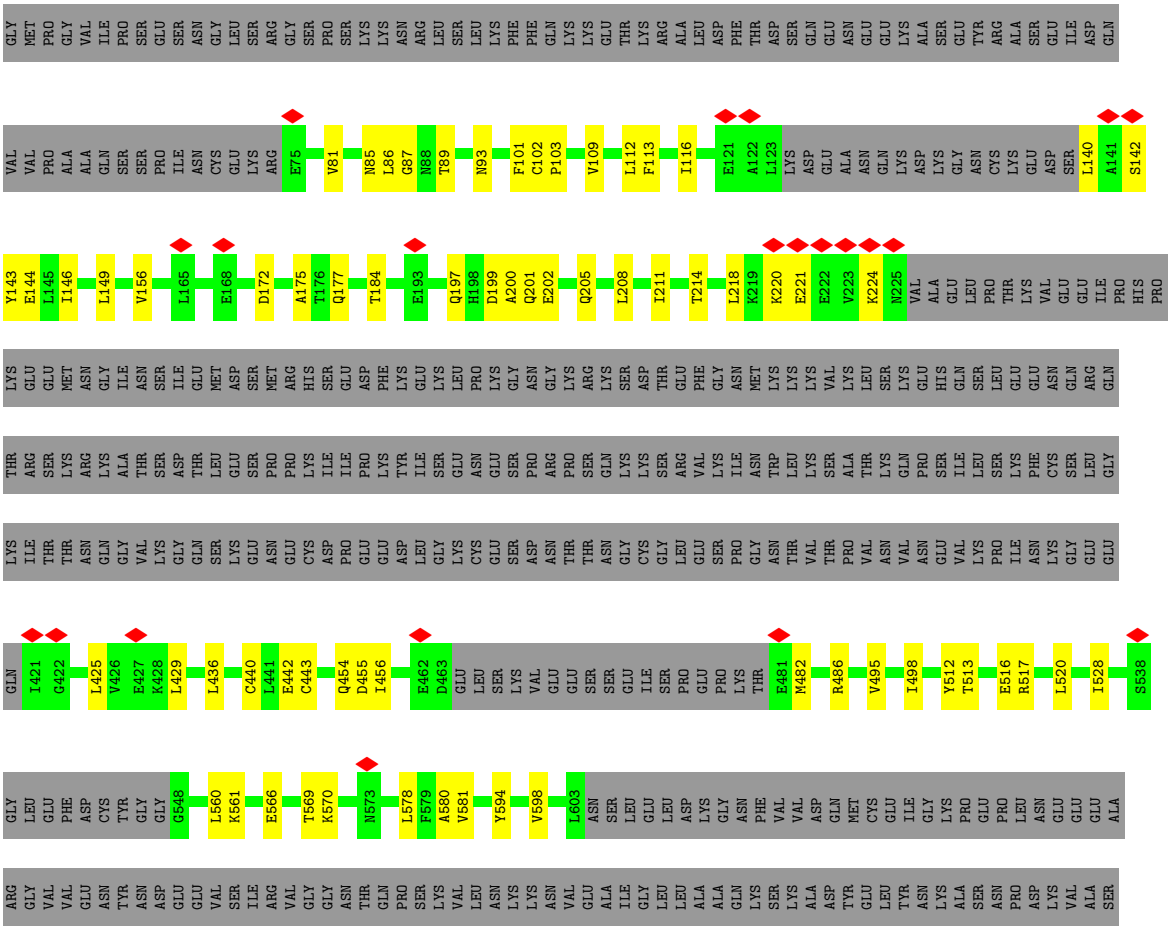
- Molecule 3: Ubiquitin-60S ribosomal protein L40

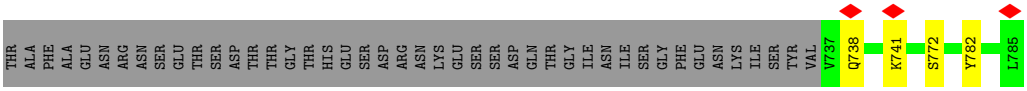
Chain C:



- Molecule 4: Ubiquitin carboxyl-terminal hydrolase 1

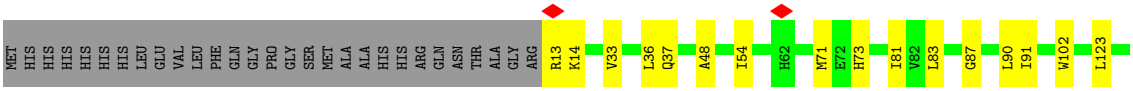
Chain D:

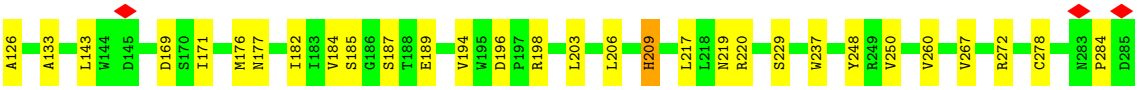


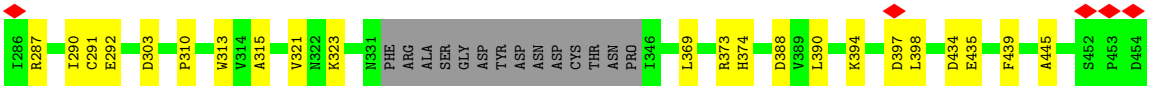


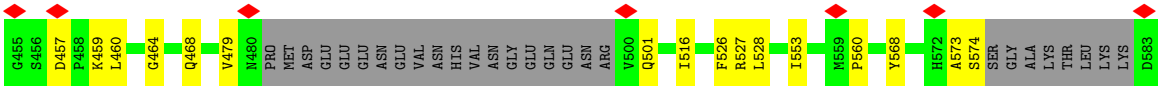
• Molecule 5: WD repeat-containing protein 48

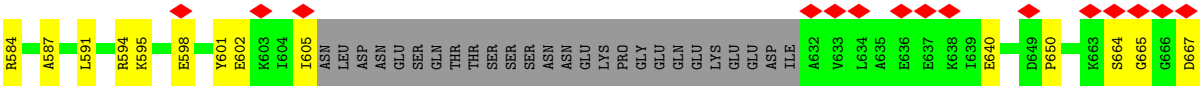
Chain E:

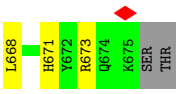






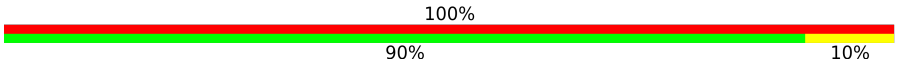


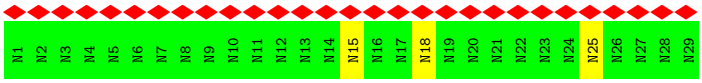




• Molecule 6: DNA (61-MER)

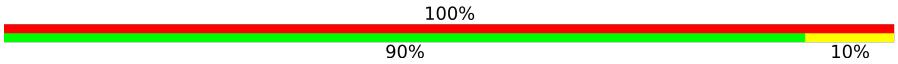
Chain S:

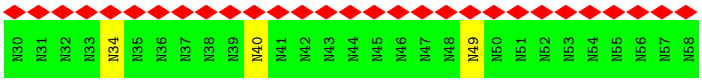




• Molecule 6: DNA (61-MER)

Chain T:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	391552	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	65	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-64 (8k x 8k)	Depositor
Maximum map value	1.765	Depositor
Minimum map value	-0.829	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	324.8, 324.8, 324.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.015, 1.015, 1.015	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: DN, ZN

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	0.29	0/8347	0.52	0/11270
2	B	0.28	0/8421	0.51	0/11396
3	C	0.26	0/613	0.52	0/824
4	D	0.30	0/2791	0.51	0/3769
5	E	0.30	0/4815	0.63	1/6528 (0.0%)
All	All	0.29	0/24987	0.54	1/33787 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	E	398	LEU	CA-CB-CG	6.60	130.47	115.30

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	8215	0	8482	106	0
2	B	8263	0	8385	119	0
3	C	607	0	634	8	0
4	D	2742	0	2746	50	0
5	E	4720	0	4735	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	S	319	0	233	0	0
6	T	319	0	233	0	0
7	D	1	0	0	0	0
All	All	25186	0	25448	335	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 7.

The worst 5 of 335 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:B:1268:TRP:HE1	2:B:1309:CYS:HG	1.20	0.90
2:B:1313:LEU:HD21	2:B:1328:LEU:HD21	1.63	0.79
2:B:1268:TRP:NE1	2:B:1309:CYS:SG	2.58	0.77
5:E:587:ALA:HB1	5:E:591:LEU:HD12	1.66	0.76
4:D:85:ASN:ND2	4:D:87:GLY:O	2.24	0.71

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	1013/1335 (76%)	954 (94%)	58 (6%)	1 (0%)	51 83
2	B	1015/1455 (70%)	963 (95%)	52 (5%)	0	100 100
3	C	75/80 (94%)	70 (93%)	5 (7%)	0	100 100
4	D	329/786 (42%)	314 (95%)	15 (5%)	0	100 100
5	E	586/694 (84%)	560 (96%)	25 (4%)	1 (0%)	47 78
All	All	3018/4350 (69%)	2861 (95%)	155 (5%)	2 (0%)	54 83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	73	HIS
1	A	1069	THR

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	956/1209 (79%)	954 (100%)	2 (0%)	93 97
2	B	947/1326 (71%)	947 (100%)	0	100 100
3	C	69/70 (99%)	69 (100%)	0	100 100
4	D	315/713 (44%)	315 (100%)	0	100 100
5	E	526/612 (86%)	525 (100%)	1 (0%)	93 97
All	All	2813/3930 (72%)	2810 (100%)	3 (0%)	93 98

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	615	ARG
1	A	725	LYS
5	E	209	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	93	ASN
5	E	167	ASN
5	E	177	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)

58 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
6	DN	T	43	6	8,11,12	0.55	0	9,14,17	0.92	0
6	DN	T	36	6	8,11,12	0.58	0	9,14,17	0.89	0
6	DN	T	45	6	8,11,12	0.58	0	9,14,17	0.85	0
6	DN	T	58	6	8,11,12	0.52	0	9,14,17	0.82	0
6	DN	S	1	6	8,11,12	0.52	0	9,14,17	0.82	0
6	DN	S	9	6	8,11,12	0.58	0	9,14,17	0.35	0
6	DN	T	55	6	8,11,12	0.51	0	9,14,17	0.82	0
6	DN	S	28	6	8,11,12	0.51	0	9,14,17	0.82	0
6	DN	T	35	6	8,11,12	0.52	0	9,14,17	0.90	0
6	DN	S	12	6	8,11,12	0.53	0	9,14,17	0.78	0
6	DN	T	33	6	8,11,12	0.49	0	9,14,17	0.86	0
6	DN	S	18	6	8,11,12	0.55	0	9,14,17	1.07	1 (11%)
6	DN	S	27	6	8,11,12	0.52	0	9,14,17	0.81	0
6	DN	T	52	6	8,11,12	0.55	0	9,14,17	0.84	0
6	DN	T	30	6	8,11,12	0.52	0	9,14,17	0.81	0
6	DN	S	16	6	8,11,12	0.59	0	9,14,17	0.88	0
6	DN	T	39	6	8,11,12	0.52	0	9,14,17	0.80	0
6	DN	S	19	6	8,11,12	0.44	0	9,14,17	0.77	0
6	DN	S	23	6	8,11,12	0.56	0	9,14,17	0.91	0
6	DN	T	41	6	8,11,12	0.56	0	9,14,17	0.78	0
6	DN	T	49	6	8,11,12	0.57	0	9,14,17	0.92	1 (11%)
6	DN	T	40	6	8,11,12	0.57	0	9,14,17	0.93	1 (11%)
6	DN	T	44	6	8,11,12	0.68	0	9,14,17	0.60	0
6	DN	T	50	6	8,11,12	0.58	0	9,14,17	0.71	0
6	DN	S	10	6	8,11,12	0.55	0	9,14,17	0.80	0
6	DN	T	48	6	8,11,12	0.70	0	9,14,17	0.52	0
6	DN	S	21	6	8,11,12	0.48	0	9,14,17	0.87	0
6	DN	S	8	6	8,11,12	0.56	0	9,14,17	0.82	0
6	DN	S	2	6	8,11,12	0.50	0	9,14,17	0.90	0
6	DN	T	32	6	8,11,12	0.61	0	9,14,17	0.32	0
6	DN	T	38	6	8,11,12	0.55	0	9,14,17	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	DN	T	51	6	8,11,12	0.52	0	9,14,17	0.81	0
6	DN	S	4	6	8,11,12	0.51	0	9,14,17	0.80	0
6	DN	S	25	6	8,11,12	0.56	0	9,14,17	0.98	1 (11%)
6	DN	S	13	6	8,11,12	0.62	0	9,14,17	0.33	0
6	DN	S	7	6	8,11,12	0.59	0	9,14,17	0.73	0
6	DN	T	34	6	8,11,12	0.48	0	9,14,17	0.95	1 (11%)
6	DN	S	20	6	8,11,12	0.48	0	9,14,17	0.84	0
6	DN	S	24	6	8,11,12	0.54	0	9,14,17	0.80	0
6	DN	T	31	6	8,11,12	0.54	0	9,14,17	0.80	0
6	DN	S	3	6	8,11,12	0.51	0	9,14,17	0.84	0
6	DN	T	46	6	8,11,12	0.62	0	9,14,17	0.31	0
6	DN	S	6	6	8,11,12	0.53	0	9,14,17	0.89	0
6	DN	T	42	6	8,11,12	0.52	0	9,14,17	0.81	0
6	DN	T	54	6	8,11,12	0.64	0	9,14,17	0.54	0
6	DN	S	11	6	8,11,12	0.53	0	9,14,17	0.88	0
6	DN	S	29	6	8,11,12	0.54	0	9,14,17	0.45	0
6	DN	S	15	6	8,11,12	0.55	0	9,14,17	0.92	1 (11%)
6	DN	T	47	6	8,11,12	0.55	0	9,14,17	0.78	0
6	DN	S	14	6	8,11,12	0.49	0	9,14,17	0.79	0
6	DN	T	57	6	8,11,12	0.54	0	9,14,17	0.81	0
6	DN	T	37	6	8,11,12	0.54	0	9,14,17	0.86	0
6	DN	S	26	6	8,11,12	0.45	0	9,14,17	0.79	0
6	DN	T	56	6	8,11,12	0.52	0	9,14,17	0.89	0
6	DN	S	22	6	8,11,12	0.56	0	9,14,17	0.77	0
6	DN	T	53	6	8,11,12	0.51	0	9,14,17	0.81	0
6	DN	S	5	6	8,11,12	0.65	0	9,14,17	0.61	0
6	DN	S	17	6	8,11,12	0.53	0	9,14,17	0.83	0

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
6	DN	T	43	6	-	0/3/15/16	0/1/1/1
6	DN	T	36	6	-	0/3/15/16	0/1/1/1
6	DN	T	45	6	-	0/3/15/16	0/1/1/1
6	DN	T	58	6	-	0/3/15/16	0/1/1/1
6	DN	S	1	6	-	1/3/15/16	0/1/1/1
6	DN	S	9	6	-	2/3/15/16	0/1/1/1
6	DN	T	55	6	-	0/3/15/16	0/1/1/1
6	DN	S	28	6	-	0/3/15/16	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	DN	T	35	6	-	0/3/15/16	0/1/1/1
6	DN	S	12	6	-	3/3/15/16	0/1/1/1
6	DN	T	33	6	-	0/3/15/16	0/1/1/1
6	DN	S	18	6	-	0/3/15/16	0/1/1/1
6	DN	S	27	6	-	0/3/15/16	0/1/1/1
6	DN	T	52	6	-	2/3/15/16	0/1/1/1
6	DN	T	30	6	-	0/3/15/16	0/1/1/1
6	DN	S	16	6	-	3/3/15/16	0/1/1/1
6	DN	T	39	6	-	0/3/15/16	0/1/1/1
6	DN	S	19	6	-	0/3/15/16	0/1/1/1
6	DN	S	23	6	-	0/3/15/16	0/1/1/1
6	DN	T	41	6	-	1/3/15/16	0/1/1/1
6	DN	T	49	6	-	0/3/15/16	0/1/1/1
6	DN	T	40	6	-	0/3/15/16	0/1/1/1
6	DN	T	44	6	-	1/3/15/16	0/1/1/1
6	DN	T	50	6	-	0/3/15/16	0/1/1/1
6	DN	S	10	6	-	0/3/15/16	0/1/1/1
6	DN	T	48	6	-	0/3/15/16	0/1/1/1
6	DN	S	21	6	-	0/3/15/16	0/1/1/1
6	DN	S	8	6	-	0/3/15/16	0/1/1/1
6	DN	S	2	6	-	0/3/15/16	0/1/1/1
6	DN	T	32	6	-	0/3/15/16	0/1/1/1
6	DN	T	38	6	-	0/3/15/16	0/1/1/1
6	DN	T	51	6	-	0/3/15/16	0/1/1/1
6	DN	S	4	6	-	0/3/15/16	0/1/1/1
6	DN	S	25	6	-	0/3/15/16	0/1/1/1
6	DN	S	13	6	-	0/3/15/16	0/1/1/1
6	DN	S	7	6	-	1/3/15/16	0/1/1/1
6	DN	T	34	6	-	2/3/15/16	0/1/1/1
6	DN	S	20	6	-	0/3/15/16	0/1/1/1
6	DN	S	24	6	-	0/3/15/16	0/1/1/1
6	DN	T	31	6	-	0/3/15/16	0/1/1/1
6	DN	S	3	6	-	0/3/15/16	0/1/1/1
6	DN	T	46	6	-	3/3/15/16	0/1/1/1
6	DN	S	6	6	-	0/3/15/16	0/1/1/1
6	DN	T	42	6	-	0/3/15/16	0/1/1/1
6	DN	T	54	6	-	0/3/15/16	0/1/1/1
6	DN	S	11	6	-	0/3/15/16	0/1/1/1
6	DN	S	29	6	-	0/3/15/16	0/1/1/1
6	DN	S	15	6	-	0/3/15/16	0/1/1/1
6	DN	T	47	6	-	0/3/15/16	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	DN	S	14	6	-	0/3/15/16	0/1/1/1
6	DN	T	57	6	-	1/3/15/16	0/1/1/1
6	DN	T	37	6	-	0/3/15/16	0/1/1/1
6	DN	S	26	6	-	0/3/15/16	0/1/1/1
6	DN	T	56	6	-	0/3/15/16	0/1/1/1
6	DN	S	22	6	-	0/3/15/16	0/1/1/1
6	DN	T	53	6	-	0/3/15/16	0/1/1/1
6	DN	S	5	6	-	0/3/15/16	0/1/1/1
6	DN	S	17	6	-	2/3/15/16	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	S	18	DN	C1'-C2'-C3'	-2.66	100.21	103.20
6	S	25	DN	C1'-C2'-C3'	-2.30	100.61	103.20
6	T	34	DN	C1'-C2'-C3'	-2.24	100.68	103.20
6	T	49	DN	C1'-C2'-C3'	-2.01	100.94	103.20
6	T	40	DN	C1'-C2'-C3'	-2.01	100.94	103.20

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	S	12	DN	O4'-C4'-C5'-O5'
6	S	12	DN	C3'-C4'-C5'-O5'
6	T	46	DN	C3'-C4'-C5'-O5'
6	T	46	DN	O4'-C4'-C5'-O5'
6	T	34	DN	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

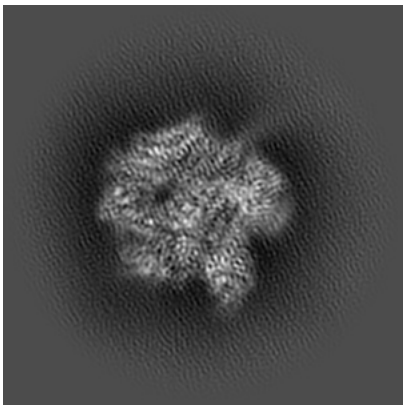
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-11934. These allow visual inspection of the internal detail of the map and identification of artifacts.

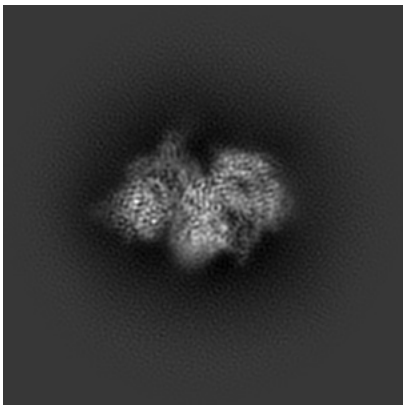
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

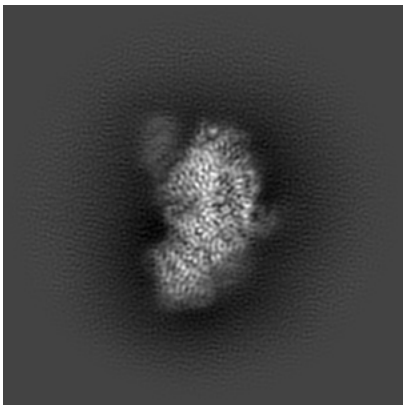
6.1.1 Primary map



X

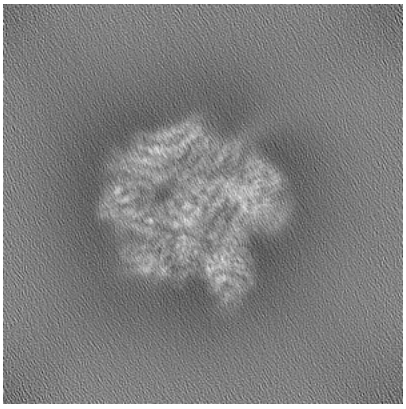


Y

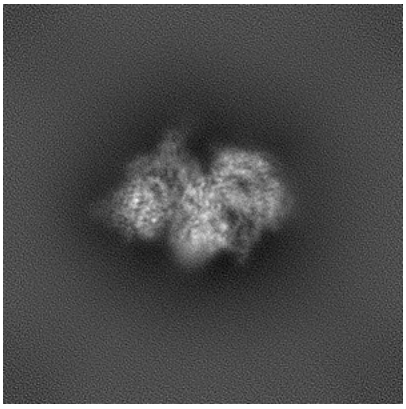


Z

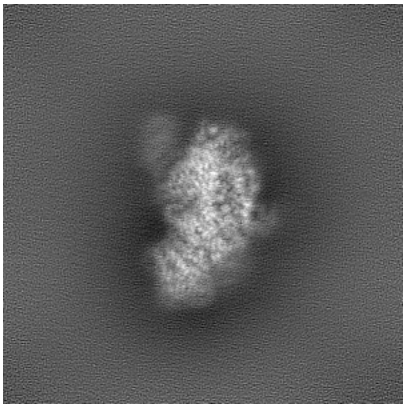
6.1.2 Raw map



X



Y

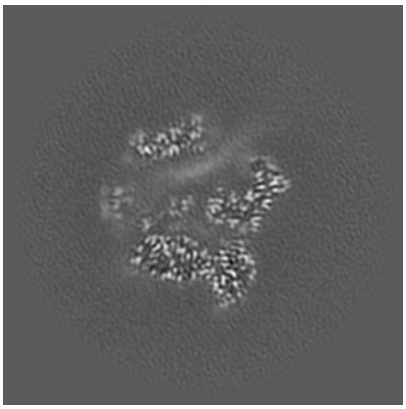


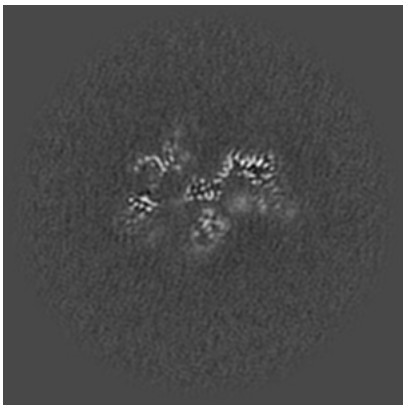
Z

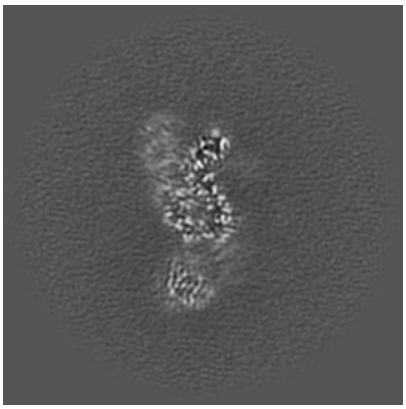
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

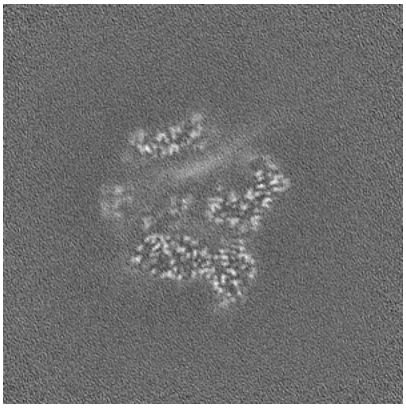
6.2.1 Primary map


X Index: 160

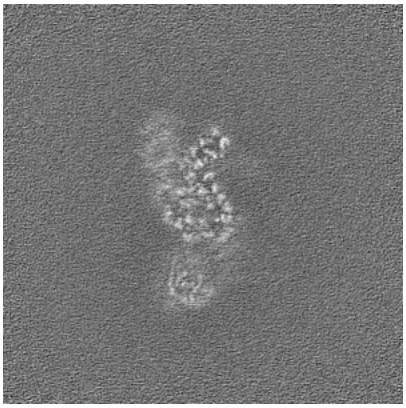

Y Index: 160


Z Index: 160

6.2.2 Raw map


X Index: 160

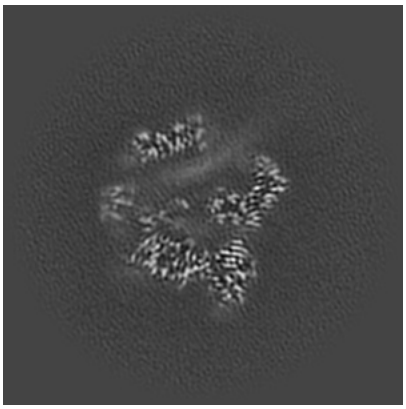
Y Index: 160


Z Index: 160

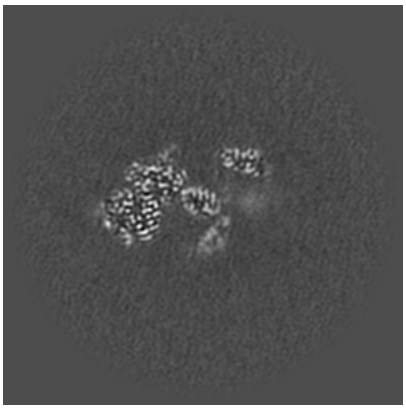
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

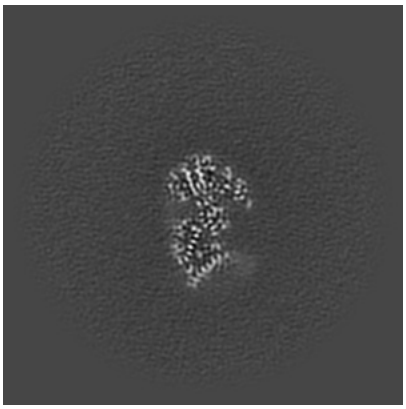
6.3.1 Primary map



X Index: 158

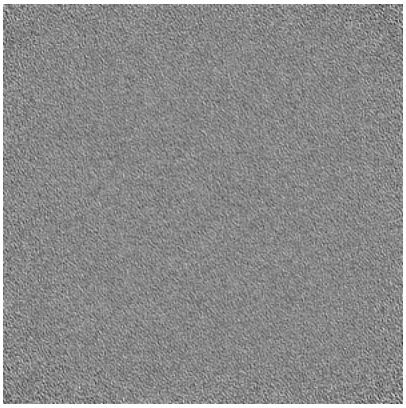


Y Index: 175

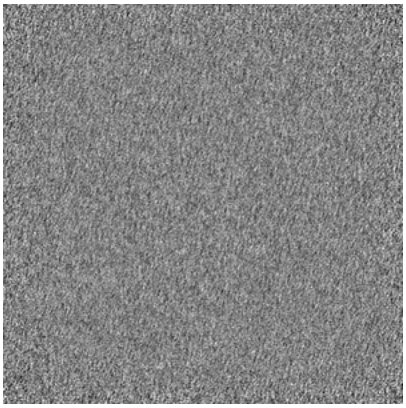


Z Index: 116

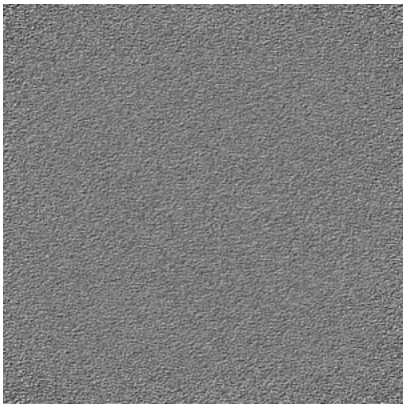
6.3.2 Raw map



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 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 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

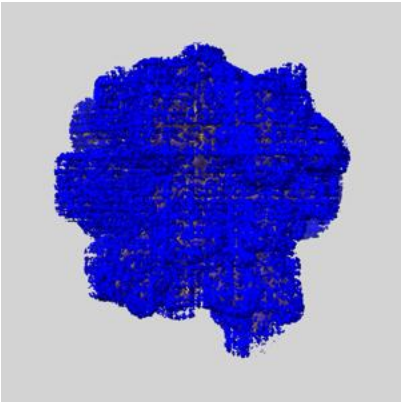
6.5 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

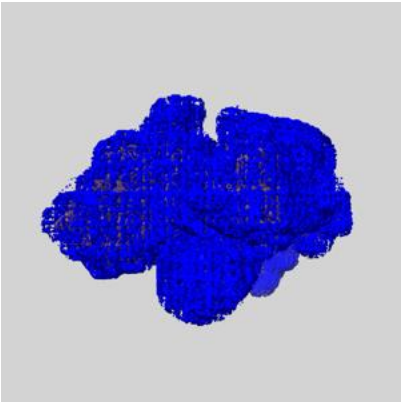
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

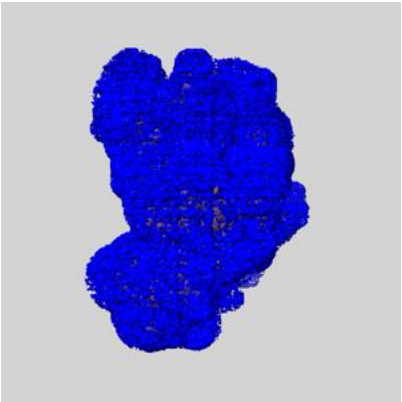
6.5.1 emd_11934_msk_1.map (i)



X



Y

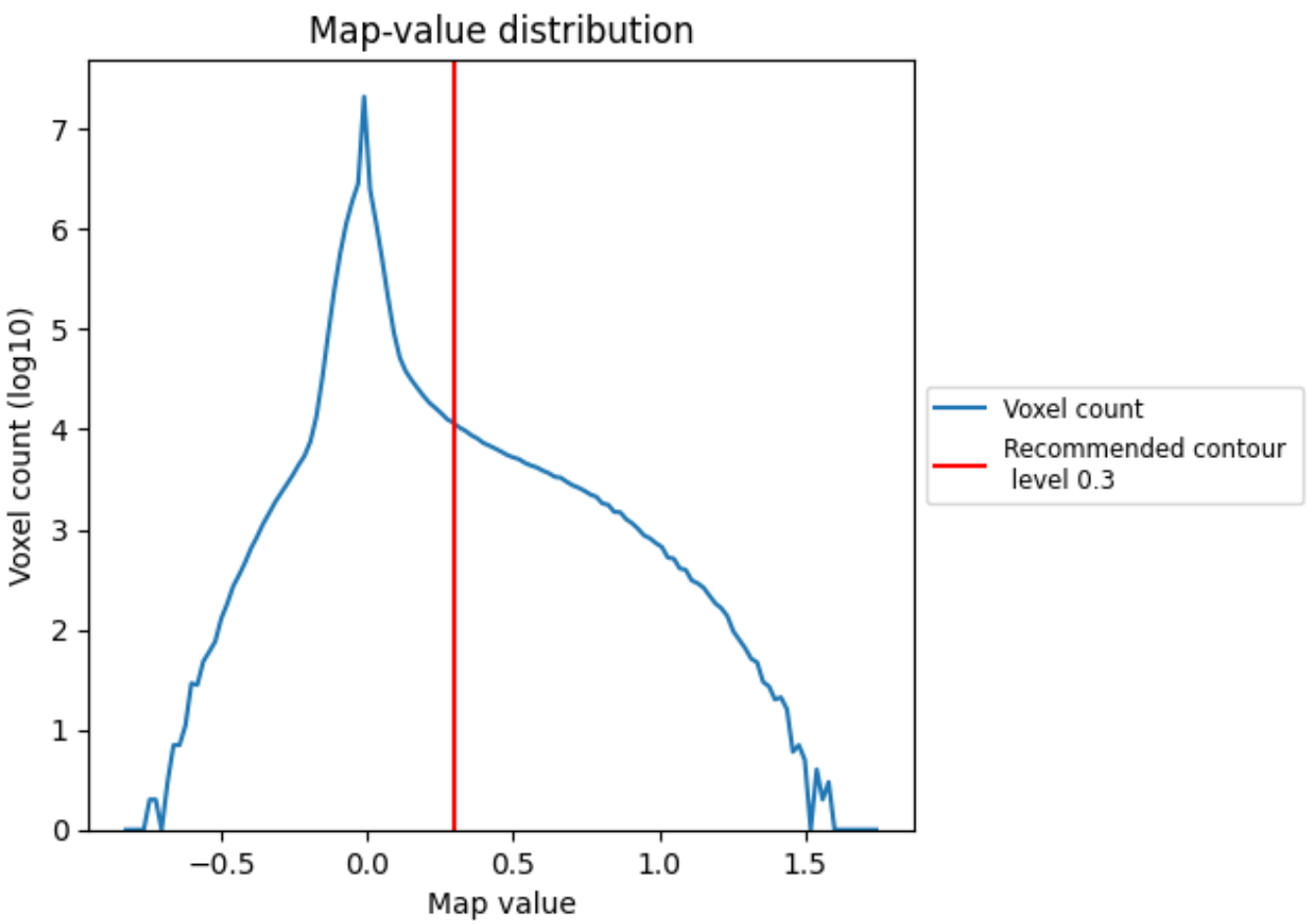


Z

7 Map analysis (i)

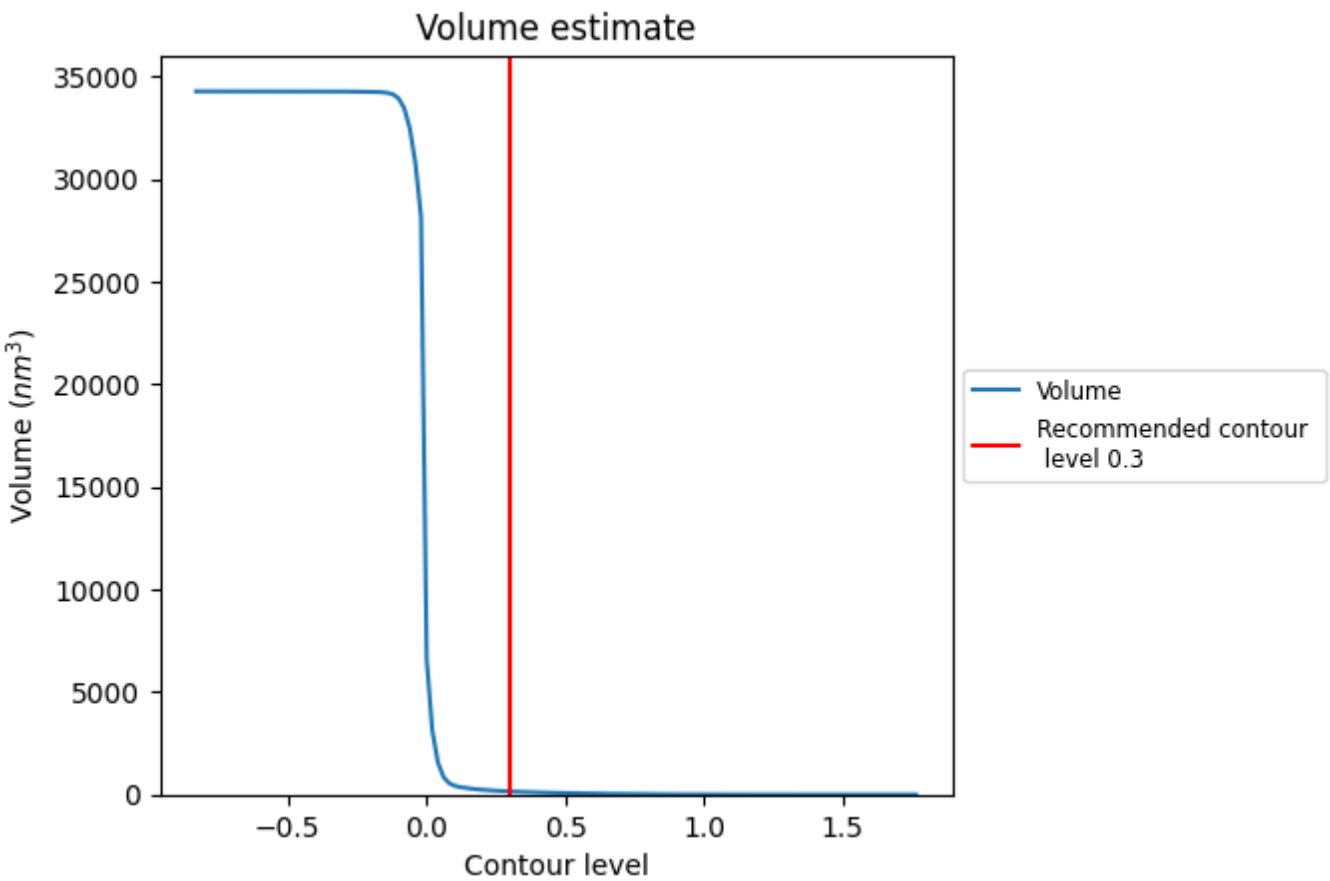
This section contains the results of statistical analysis of the map.

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.

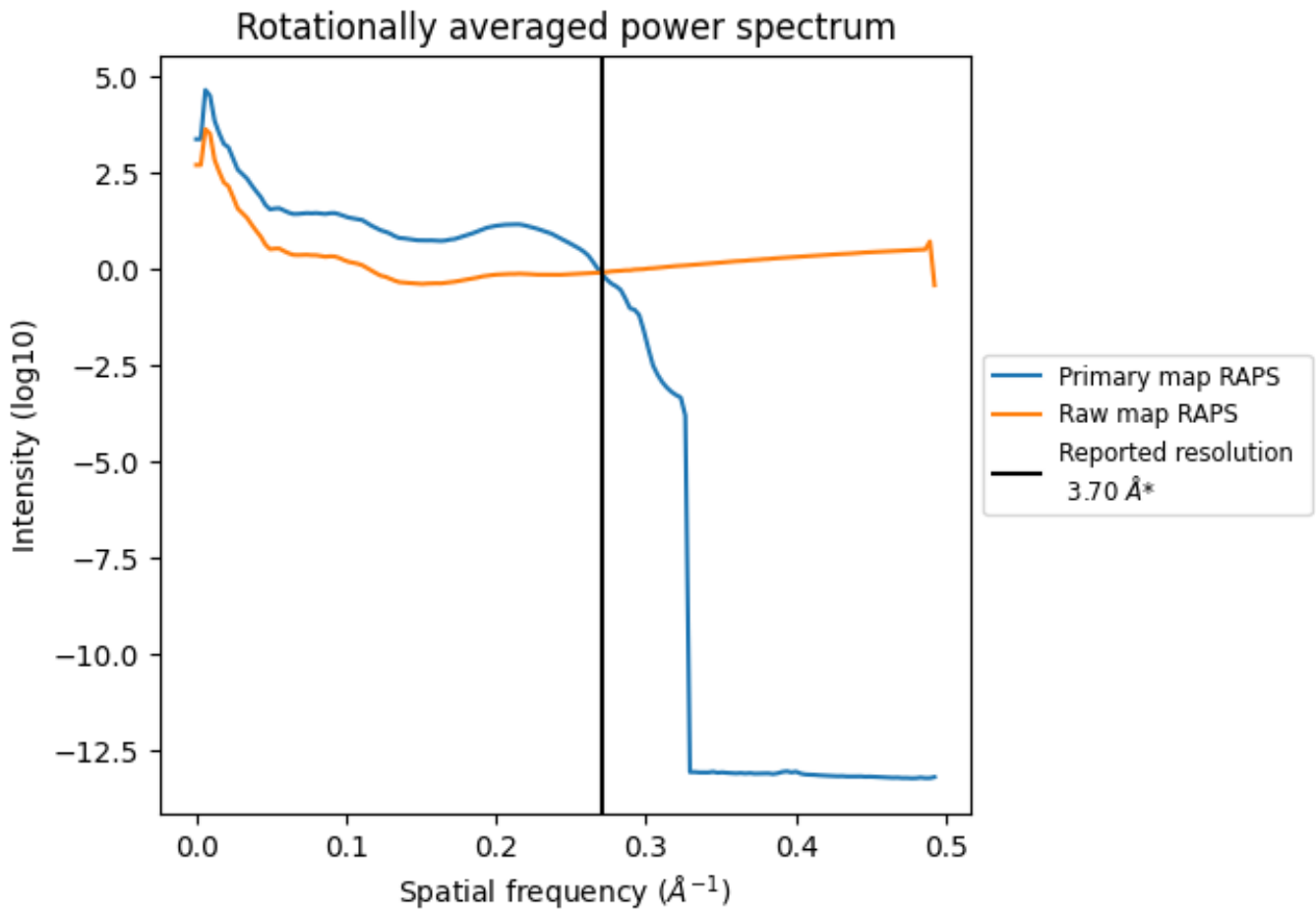
7.2 Volume estimate (i)



The volume at the recommended contour level is 154 nm^3; this corresponds to an approximate mass of 139 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)

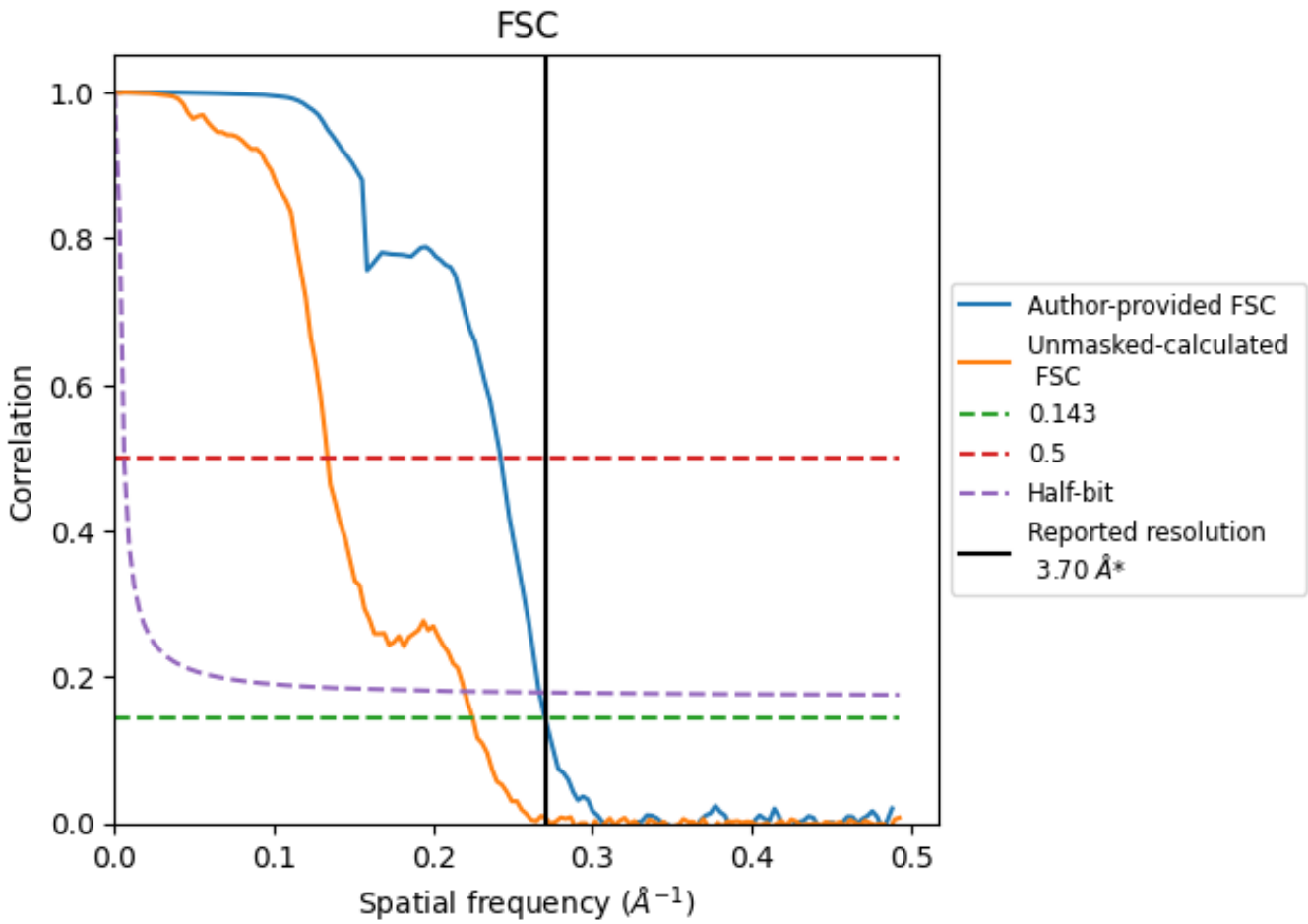


*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

8.2 Resolution estimates (i)

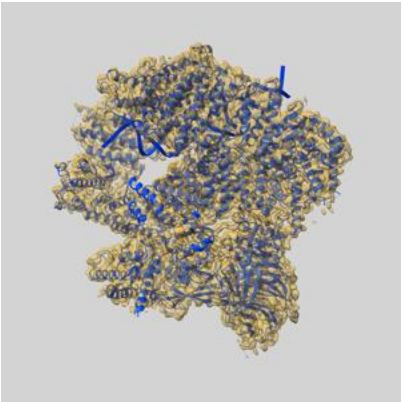
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.70	4.13	3.75
Unmasked-calculated*	4.45	7.48	4.55

*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 4.45 differs from the reported value 3.7 by more than 10 %

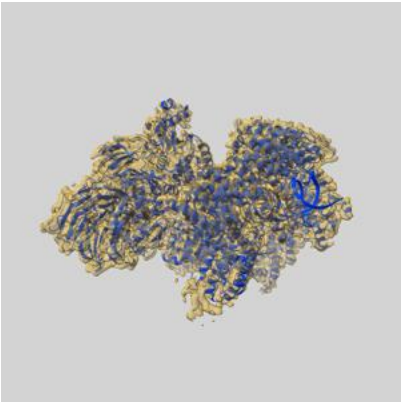
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-11934 and PDB model 7AY1. Per-residue inclusion information can be found in section 3 on page 6.

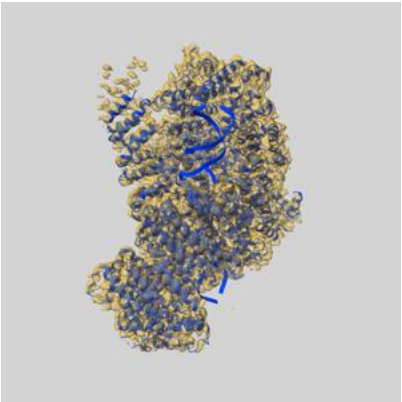
9.1 Map-model overlay (i)



X



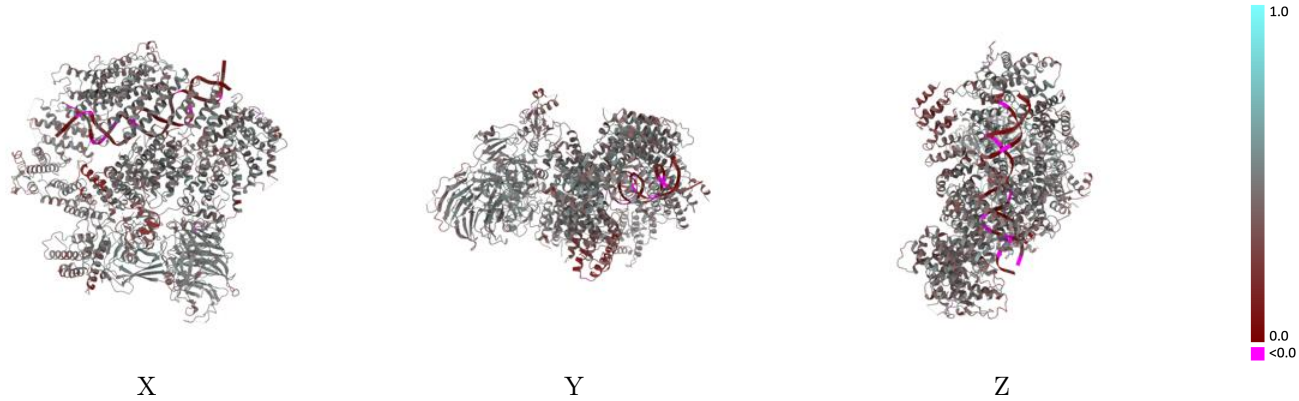
Y



Z

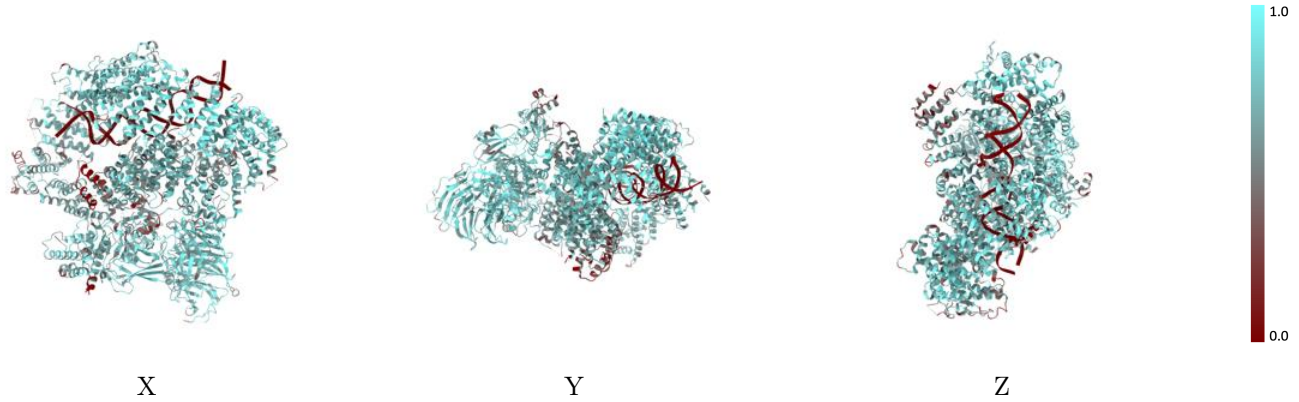
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



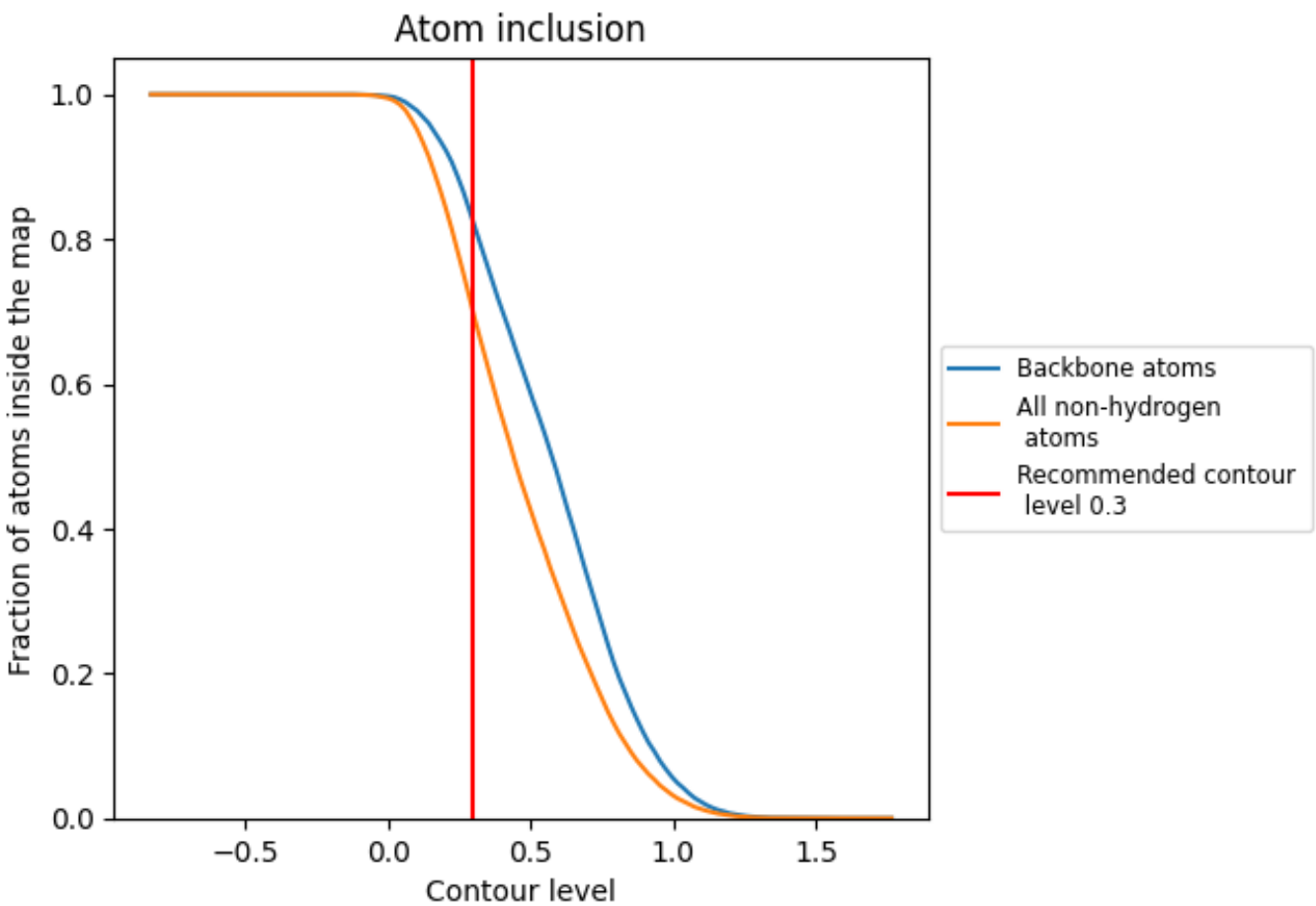
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6982	0.4320
A	0.7350	0.4480
B	0.6743	0.4170
C	0.7525	0.4960
D	0.7386	0.4620
E	0.7396	0.4490
S	0.0157	0.1100
T	0.0094	0.0950