



wwPDB EM Validation Summary Report i

Feb 24, 2022 – 12:59 am GMT

PDB ID : 7YXX
EMDB ID : EMD-14368
Title : Cryo-EM structure of USP9X
Authors : Deme, J.C.; Halabelian, L.; Arrowsmith, C.H.; Lea, S.M.; Structural Genomics Consortium (SGC)
Deposited on : 2022-02-16
Resolution : 3.30 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 following versions of software and data (see [references](#) ①) were used in the production of this report:

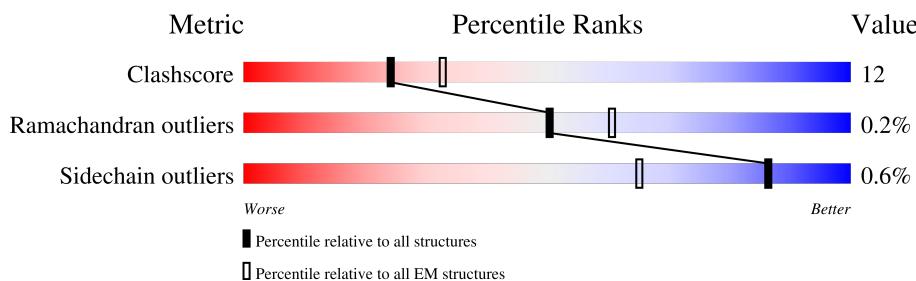
EMDB validation analysis : 0.0.0.dev97
MolProbitiy : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.26

1 Overall quality at a glance

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

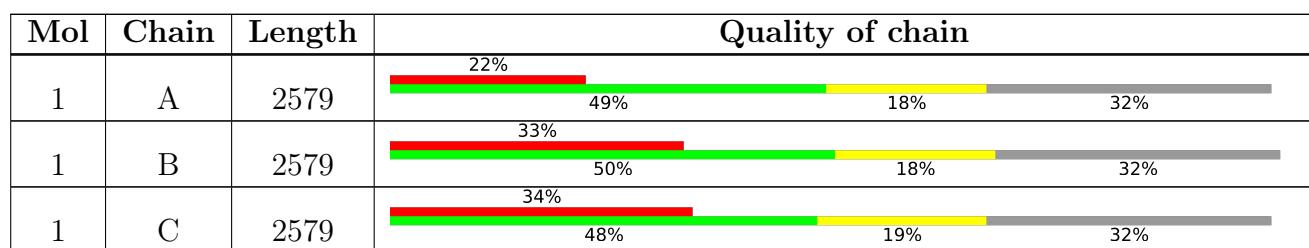
The reported resolution of this entry is 3.30 Å.

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.



2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 42357 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 Probable ubiquitin carboxyl-terminal hydrolase FAF-X.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1754	Total	C	N	O	S		
			14155	9062	2426	2571	96	1	0
1	B	1754	Total	C	N	O	S		
			14155	9062	2426	2571	96	1	0
1	C	1741	Total	C	N	O	S		
			14047	8997	2407	2547	96	1	0

There are 75 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	initiating methionine	UNP Q93008
A	-16	HIS	-	expression tag	UNP Q93008
A	-15	HIS	-	expression tag	UNP Q93008
A	-14	HIS	-	expression tag	UNP Q93008
A	-13	HIS	-	expression tag	UNP Q93008
A	-12	HIS	-	expression tag	UNP Q93008
A	-11	HIS	-	expression tag	UNP Q93008
A	-10	SER	-	expression tag	UNP Q93008
A	-9	SER	-	expression tag	UNP Q93008
A	-8	GLY	-	expression tag	UNP Q93008
A	-7	ARG	-	expression tag	UNP Q93008
A	-6	GLU	-	expression tag	UNP Q93008
A	-5	ASN	-	expression tag	UNP Q93008
A	-4	LEU	-	expression tag	UNP Q93008
A	-3	TYR	-	expression tag	UNP Q93008
A	-2	PHE	-	expression tag	UNP Q93008
A	-1	GLN	-	expression tag	UNP Q93008
A	0	GLY	-	expression tag	UNP Q93008
A	2555	ASP	-	expression tag	UNP Q93008
A	2556	TYR	-	expression tag	UNP Q93008
A	2557	LYS	-	expression tag	UNP Q93008
A	2558	ASP	-	expression tag	UNP Q93008
A	2559	ASP	-	expression tag	UNP Q93008
A	2560	ASP	-	expression tag	UNP Q93008

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2561	LYS	-	expression tag	UNP Q93008
B	-17	MET	-	initiating methionine	UNP Q93008
B	-16	HIS	-	expression tag	UNP Q93008
B	-15	HIS	-	expression tag	UNP Q93008
B	-14	HIS	-	expression tag	UNP Q93008
B	-13	HIS	-	expression tag	UNP Q93008
B	-12	HIS	-	expression tag	UNP Q93008
B	-11	HIS	-	expression tag	UNP Q93008
B	-10	SER	-	expression tag	UNP Q93008
B	-9	SER	-	expression tag	UNP Q93008
B	-8	GLY	-	expression tag	UNP Q93008
B	-7	ARG	-	expression tag	UNP Q93008
B	-6	GLU	-	expression tag	UNP Q93008
B	-5	ASN	-	expression tag	UNP Q93008
B	-4	LEU	-	expression tag	UNP Q93008
B	-3	TYR	-	expression tag	UNP Q93008
B	-2	PHE	-	expression tag	UNP Q93008
B	-1	GLN	-	expression tag	UNP Q93008
B	0	GLY	-	expression tag	UNP Q93008
B	2555	ASP	-	expression tag	UNP Q93008
B	2556	TYR	-	expression tag	UNP Q93008
B	2557	LYS	-	expression tag	UNP Q93008
B	2558	ASP	-	expression tag	UNP Q93008
B	2559	ASP	-	expression tag	UNP Q93008
B	2560	ASP	-	expression tag	UNP Q93008
B	2561	LYS	-	expression tag	UNP Q93008
C	-17	MET	-	initiating methionine	UNP Q93008
C	-16	HIS	-	expression tag	UNP Q93008
C	-15	HIS	-	expression tag	UNP Q93008
C	-14	HIS	-	expression tag	UNP Q93008
C	-13	HIS	-	expression tag	UNP Q93008
C	-12	HIS	-	expression tag	UNP Q93008
C	-11	HIS	-	expression tag	UNP Q93008
C	-10	SER	-	expression tag	UNP Q93008
C	-9	SER	-	expression tag	UNP Q93008
C	-8	GLY	-	expression tag	UNP Q93008
C	-7	ARG	-	expression tag	UNP Q93008
C	-6	GLU	-	expression tag	UNP Q93008
C	-5	ASN	-	expression tag	UNP Q93008
C	-4	LEU	-	expression tag	UNP Q93008
C	-3	TYR	-	expression tag	UNP Q93008
C	-2	PHE	-	expression tag	UNP Q93008

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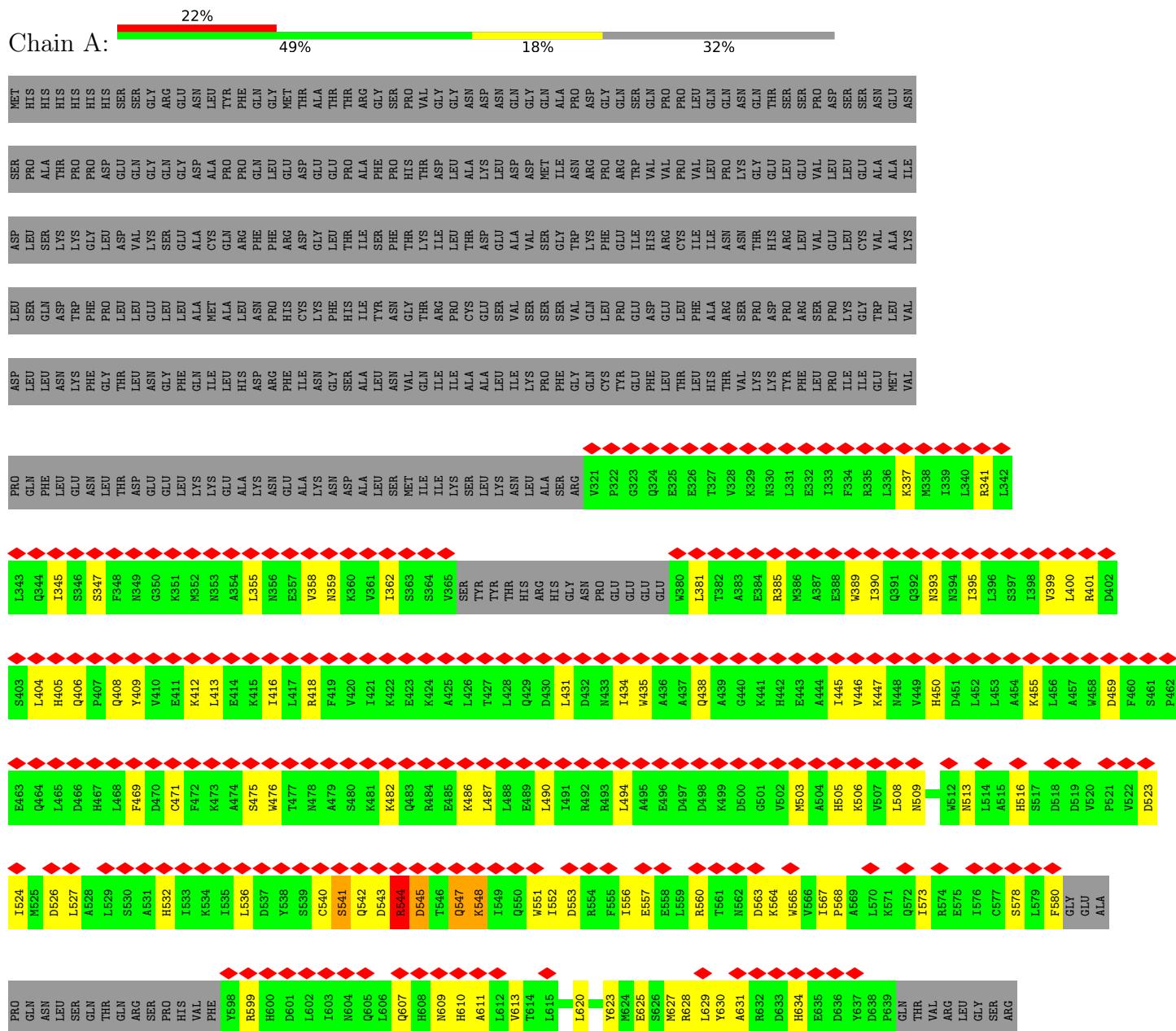
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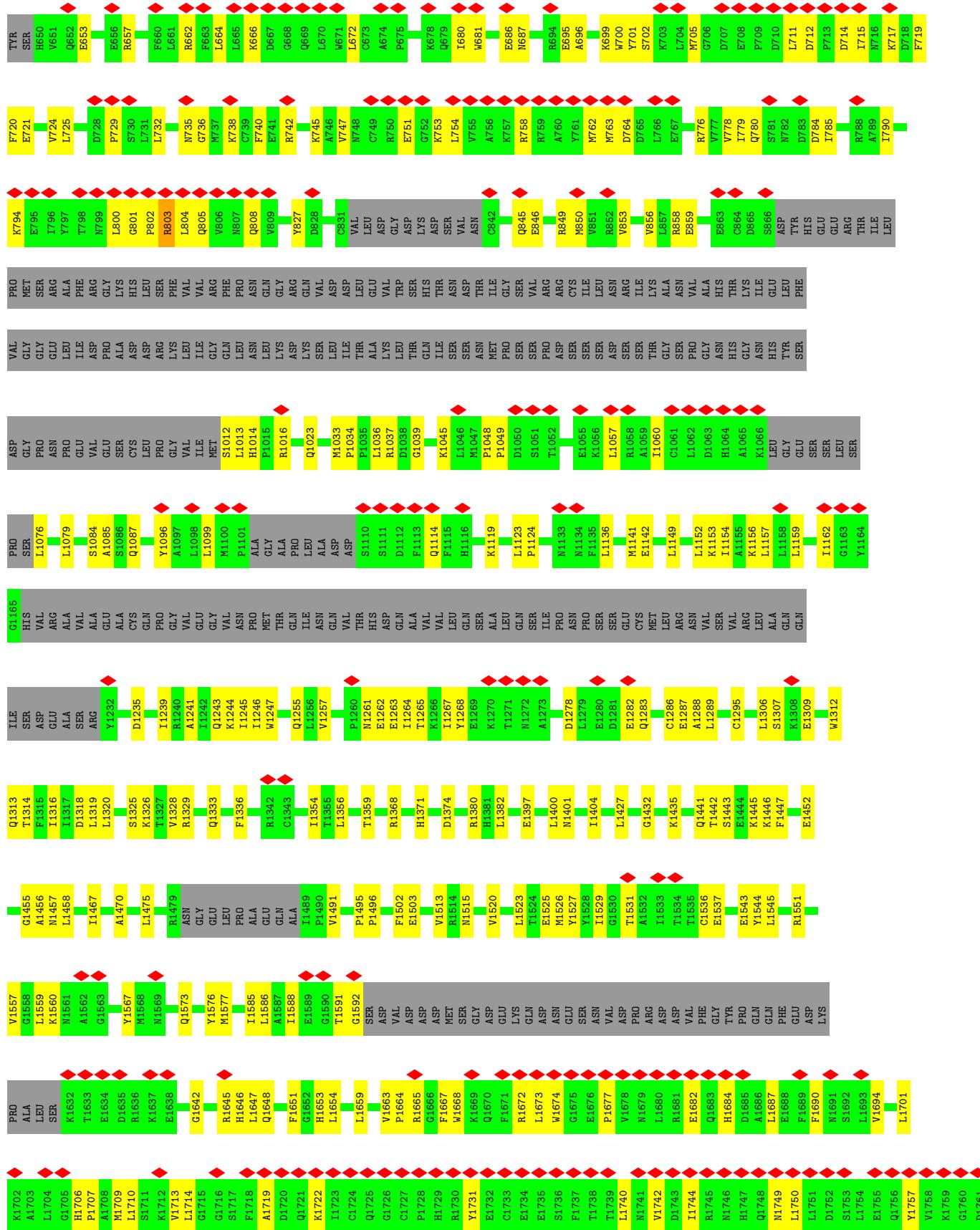
Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLN	-	expression tag	UNP Q93008
C	0	GLY	-	expression tag	UNP Q93008
C	2555	ASP	-	expression tag	UNP Q93008
C	2556	TYR	-	expression tag	UNP Q93008
C	2557	LYS	-	expression tag	UNP Q93008
C	2558	ASP	-	expression tag	UNP Q93008
C	2559	ASP	-	expression tag	UNP Q93008
C	2560	ASP	-	expression tag	UNP Q93008
C	2561	LYS	-	expression tag	UNP Q93008

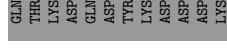
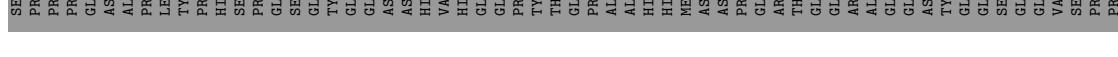
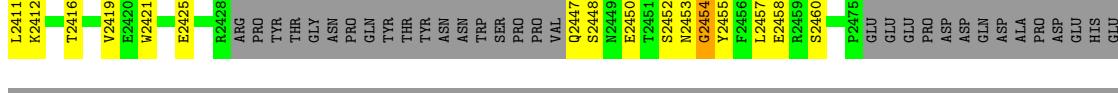
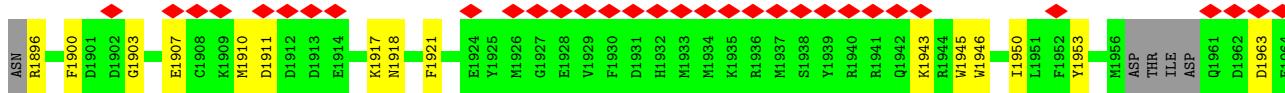
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Probable ubiquitin carboxyl-terminal hydrolase FAF-X



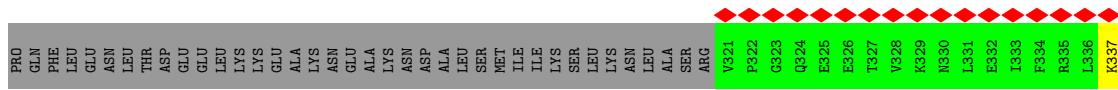
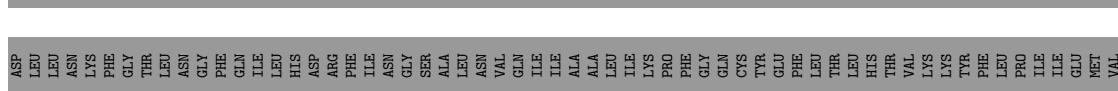
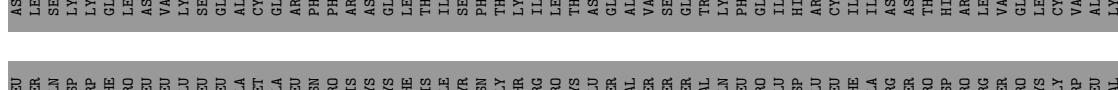
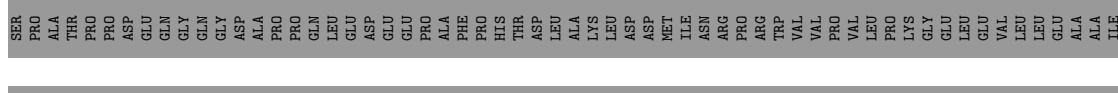




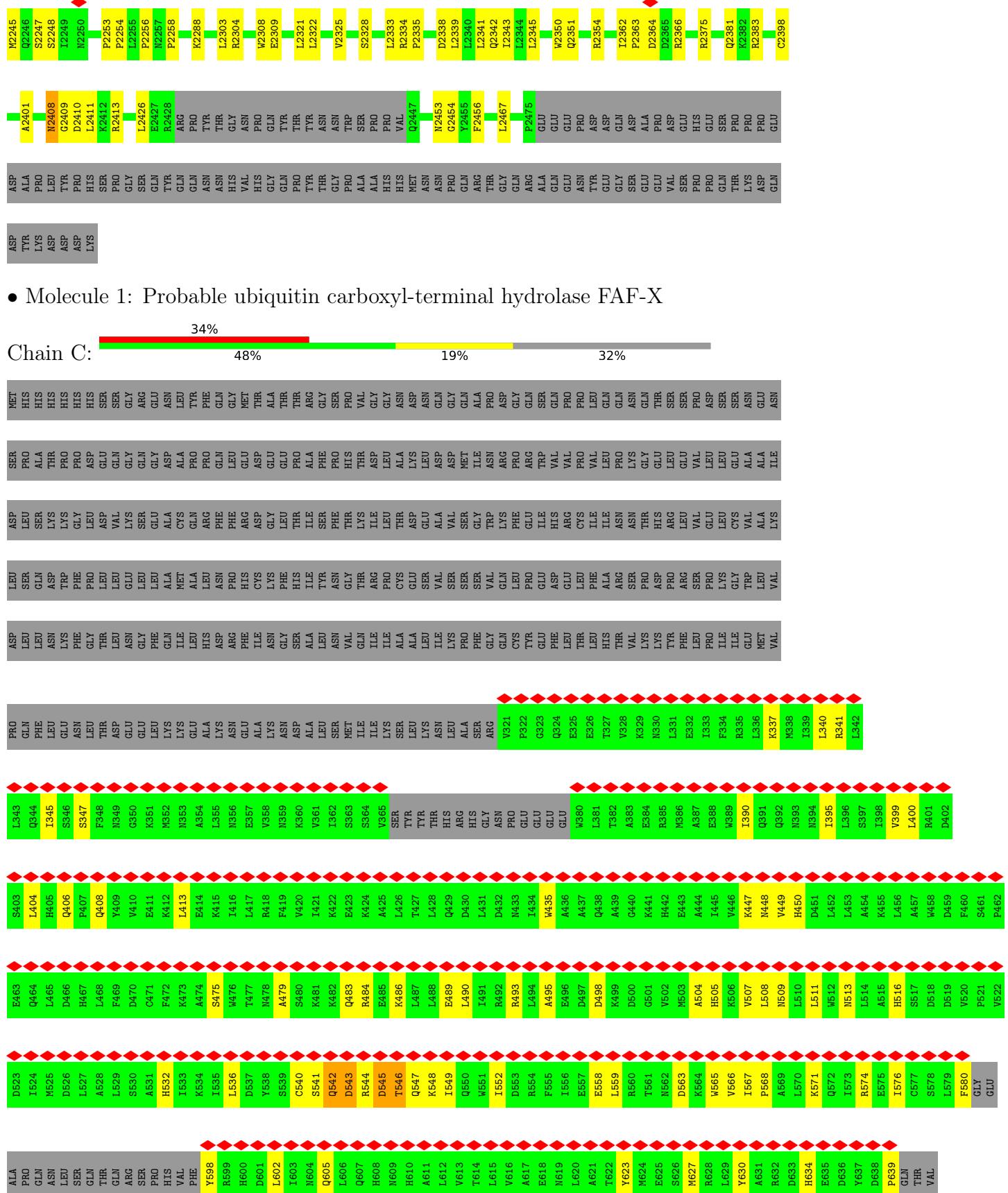
- Molecule 1: Probable ubiquitin carboxyl-terminal hydrolase FAF-X

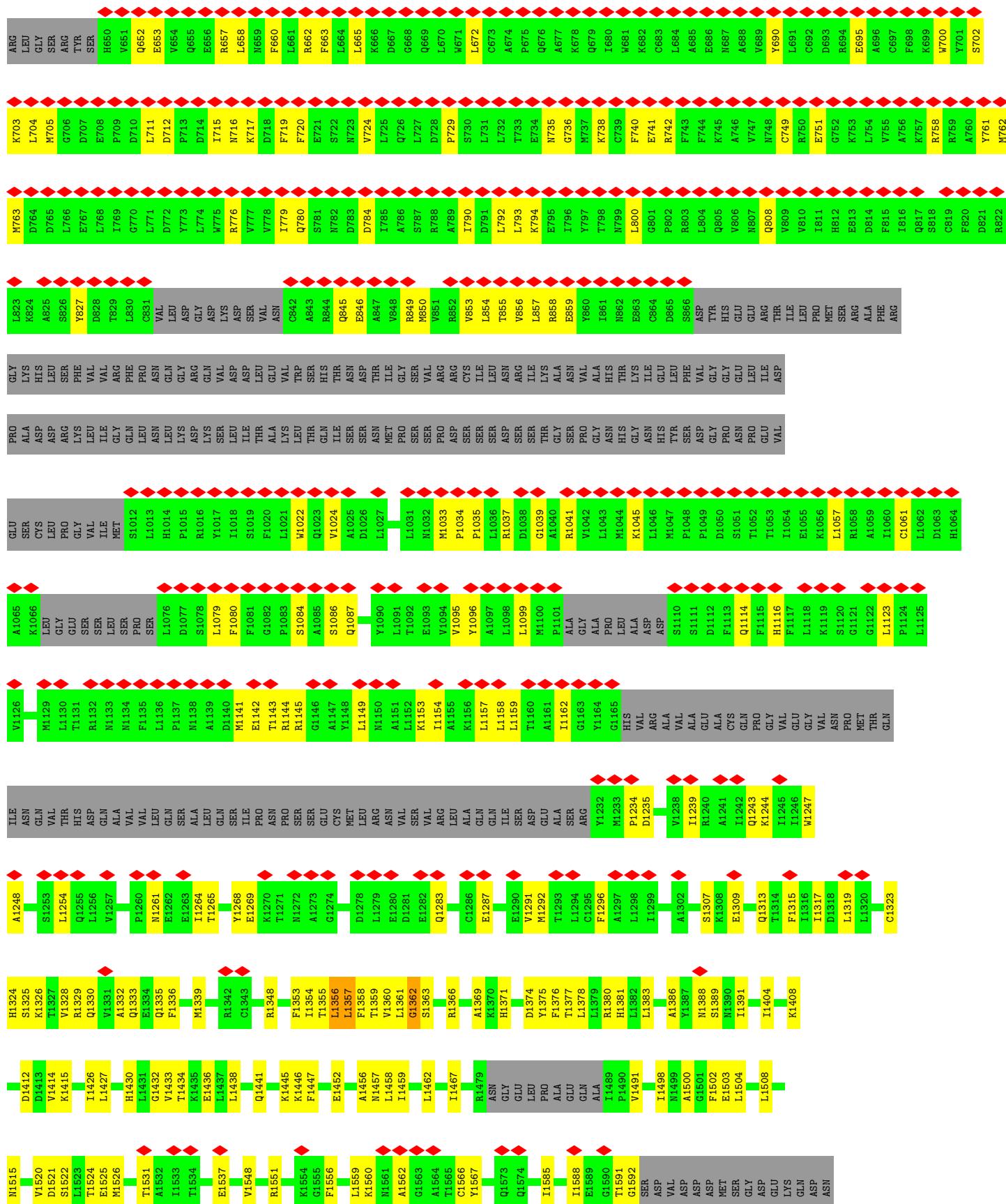


Chain B:



S1128	H1064	L823	W763	K703	E463	S403	L343
M1129	A1065	C7VS	ASP	LEU	LEU	LEU	Q344
L1130	K1066	LEU	ASP	GLN	GLN	GLN	I345
T1131	R1132	GLY	ASP	ASP	GLY	GLY	S346
N1133	N1133	VAL	VAL	TYR	TYR	TYR	S347
SER	SER	ILE	ILE	SER	SER	SER	Y407
N1134	SER	GLY	ARG	GLN	GLN	GLN	Q408
F1135	LEU	PHE	GLN	PHE	PHE	PHE	F348
L1136	SER	LEU	LEU	ASP	ASP	ASP	N349
P1137	PRO	ASP	ASN	GLN	GLN	GLN	G350
N1138	SER	GLY	GLY	ASP	ASP	ASP	K351
A1139	L1076	P1015	LYS	VAL	VAL	VAL	M352
D1077	R1016	P1015	LYS	VAL	VAL	VAL	N353
F1140	Y1017	Y1017	SER	VAL	VAL	VAL	A354
M1141	F1080	I1018	I1018	ASP	LYS	LYS	L355
E1142	F1081	S1019	S1019	ASP	ASP	ASP	K416
T1143	G1082	F1020	F1020	THR	LEU	LEU	I411
R1144	P1083	L1021	L1021	ALA	GLU	GLN	C471
R1145	W1022	W1022	W1022	LYS	VAL	VAL	H472
G1146	Q1023	V1024	V1024	TRP	TRP	TRP	K473
A1147	Q1087	V1088	V1088	SER	VAL	VAL	E474
Y1148	E1093	E1093	E1093	THR	VAL	VAL	E475
L1149	L1089	L1090	L1090	ASP	ASP	ASP	K476
N1150	Y1090	I1091	I1091	ASP	ASP	ASP	R477
L1151	T1092	I1092	I1092	ASP	ASP	ASP	A478
K1153	E1093	A1025	A1025	PRO	PRO	PRO	A479
T1154	A1094	D1026	D1026	SER	VAL	VAL	V479
A1155	W1095	L1090	L1090	SER	VAL	VAL	C480
K1156	Y1096	M033	M033	ASP	ASP	ASP	A481
L1157	A1097	P1034	P1034	SER	VAL	VAL	A482
L1158	L1098	S1035	S1035	ASP	ASP	ASP	A483
K1159	L1099	L1036	L1036	SER	VAL	VAL	A484
T1160	A1100	L1031	L1031	SER	VAL	VAL	A485
A1161	M1032	A1037	A1037	ASP	ASP	ASP	V486
K1162	A1162	ALA	ALA	ASP	ASP	ASP	C487
G1163	GLY	G1039	G1039	SER	VAL	VAL	A488
T1164	ALA	A1040	A1040	ASP	ASP	ASP	A489
G1165	ALA	R1041	R1041	GLY	GLY	GLY	A490
LEU	LEU	V1042	V1042	ALA	ALA	ALA	A491
A1166	K1166	M1047	M1047	SER	VAL	VAL	A492
H1167	L1167	L1043	L1043	THR	GLY	GLY	A493
V1168	V1043	M044	M044	ASP	ASP	ASP	A494
P1169	ALA	K045	K045	ASP	ASP	ASP	A495
S1170	ALA	L1046	L1046	VAL	VAL	VAL	W495
A1171	VAL	Q1046	Q1046	TYR	TYR	TYR	I496
F1172	ALA	E1047	E1047	SER	VAL	VAL	A497
I1173	I1173	T1052	T1052	ASP	ASP	ASP	A498
M1174	ALA	P1048	P1048	GLY	GLY	GLY	A499
G1175	ALA	P1049	P1049	PRO	PRO	PRO	A500
C1176	CYS	K1054	K1054	ASN	ASN	ASN	A501
Q1177	GLN	D1050	D1050	TYR	TYR	TYR	W502
P1178	PRO	F1115	F1115	ILE	ILE	ILE	H503
H1179	GLY	S1061	S1061	SER	VAL	VAL	M503
T1180	VAL	T1062	T1062	ASP	ASP	ASP	E443
A1181	GLU	L1047	L1047	GLY	GLY	GLY	A444
I1182	VAL	M1048	M1048	ASP	ASP	ASP	A445
F1183	ALA	D1049	D1049	PRO	PRO	PRO	A446
M1184	ALA	K1055	K1055	ASP	ASP	ASP	A505
V1185	VAL	E1055	E1055	ASP	ASP	ASP	A506
A1186	VAL	E1055	E1055	VAL	VAL	VAL	A507
E1187	ALA	E1056	E1056	ASP	ASP	ASP	A508
K1188	ALA	E1056	E1056	VAL	VAL	VAL	A509
T1189	ALA	T1053	T1053	ASP	ASP	ASP	A510
R1190	GLY	K1119	K1119	VAL	VAL	VAL	A511
S1190	VAL	S1120	S1120	ASP	ASP	ASP	A512
L1191	ALA	L1127	L1127	ASP	ASP	ASP	A513
A1192	ALA	C1061	C1061	THR	THR	THR	A514
R1193	VAL	L1062	L1062	THR	THR	THR	A515
R1194	ALA	D1063	D1063	THR	THR	THR	A516
A1195	ALA	A1126	A1126	ASP	ASP	ASP	A517
D1196	GLN	D1126	D1126	ASP	ASP	ASP	A518
F1197	GLN	E1126	E1126	ASP	ASP	ASP	A519
M1198	VAL	D1126	D1126	ASP	ASP	ASP	A520
P1199	ALA	A1126	A1126	ASP	ASP	ASP	A521
C1200	ALA	F1126	F1126	ASP	ASP	ASP	A522
K1201	VAL	S1127	S1127	ASP	ASP	ASP	A523
A1202	VAL	S1127	S1127	ASP	ASP	ASP	A524
R1203	ALA	S1127	S1127	ASP	ASP	ASP	A525
M1204	ALA	S1127	S1127	ASP	ASP	ASP	A526





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	330000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.7	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.330	Depositor
Minimum map value	-0.608	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.221	Depositor
Map size (Å)	372.73602, 372.73602, 372.73602	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8320001, 0.8320001, 0.8320001	Depositor

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.26	0/14461	0.47	0/19559
1	B	0.26	0/14461	0.47	0/19559
1	C	0.26	0/14351	0.47	0/19411
All	All	0.26	0/43273	0.47	0/58529

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts i

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	14155	0	14051	332	0
1	B	14155	0	14051	327	0
1	C	14047	0	13957	348	0
All	All	42357	0	42059	1000	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 12.

The worst 5 of 1000 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2413:ARG:O	1:C:2416:THR:HG22	1.31	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1521:ASP:O	1:C:1524:THR:HG22	1.38	1.20
1:B:540:CYS:HB2	1:B:544:ARG:HA	1.29	1.07
1:C:1789:LEU:HB3	1:C:1863:TYR:OH	1.58	1.02
1:A:1265:THR:HA	1:A:1268:TYR:CD2	2.02	0.95

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	1721/2579 (67%)	1631 (95%)	86 (5%)	4 (0%)	47 77
1	B	1721/2579 (67%)	1631 (95%)	90 (5%)	0	100 100
1	C	1708/2579 (66%)	1614 (94%)	88 (5%)	6 (0%)	34 66
All	All	5150/7737 (67%)	4876 (95%)	264 (5%)	10 (0%)	50 77

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	544	ARG
1	A	2454	GLY
1	C	2365	ASP
1	C	546	THR
1	C	1348	ARG

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	1544/2286 (68%)	1532 (99%)	12 (1%)	81 89
1	B	1544/2286 (68%)	1536 (100%)	8 (0%)	88 93
1	C	1532/2286 (67%)	1522 (99%)	10 (1%)	84 90
All	All	4620/6858 (67%)	4590 (99%)	30 (1%)	86 91

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	544	ARG
1	C	1357	LEU
1	B	794	LYS
1	C	2050	ARG
1	C	545	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1813	ASN
1	C	1653	HIS
1	B	1947	ASN
1	C	2221	GLN
1	C	406	GLN

5.3.3 RNA [\(i\)](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [\(i\)](#)

There are no ligands in this entry.

5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

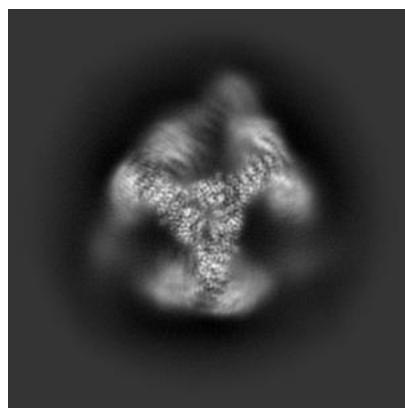
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-14368. These allow visual inspection of the internal detail of the map and identification of artifacts.

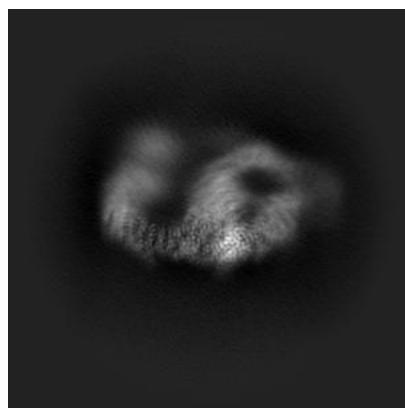
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

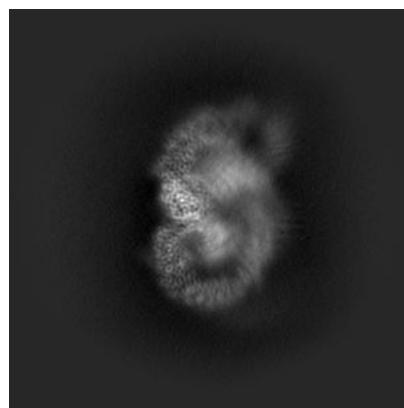
6.1.1 Primary map



X

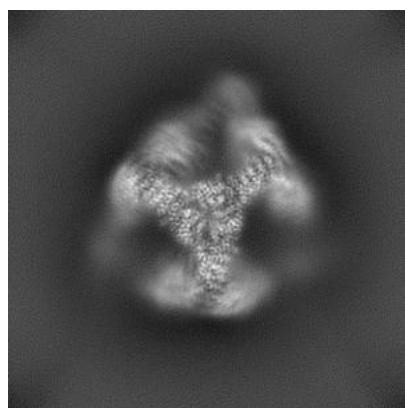


Y

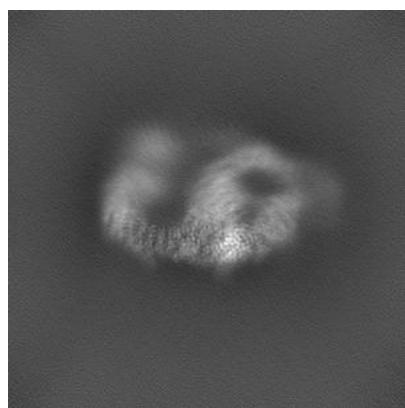


Z

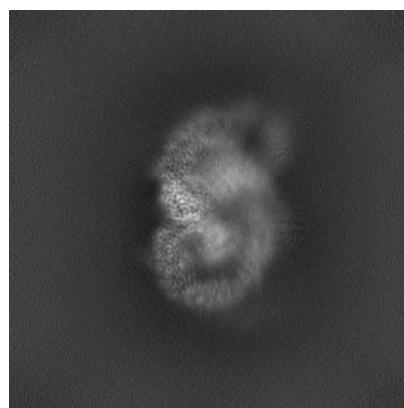
6.1.2 Raw map



X



Y

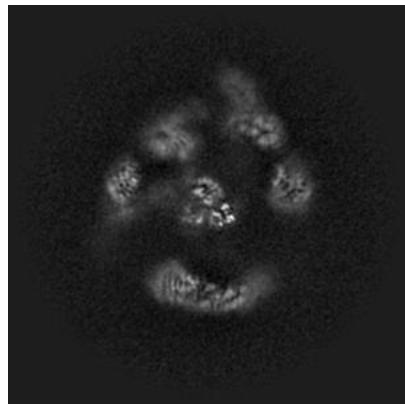


Z

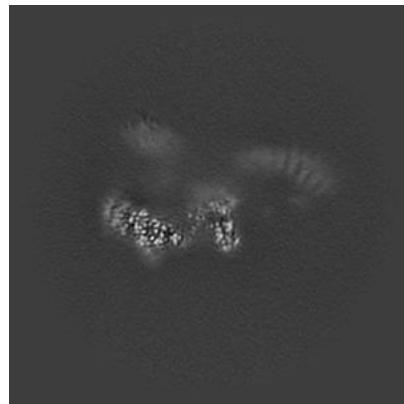
The images above show the map projected in three orthogonal directions.

6.2 Central slices [\(i\)](#)

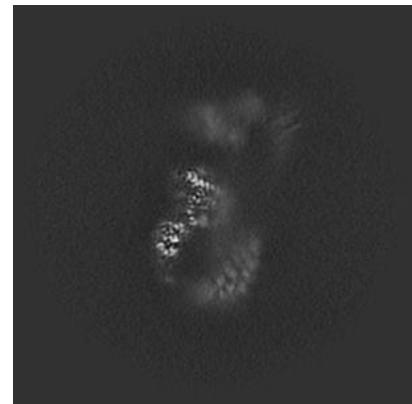
6.2.1 Primary map



X Index: 224

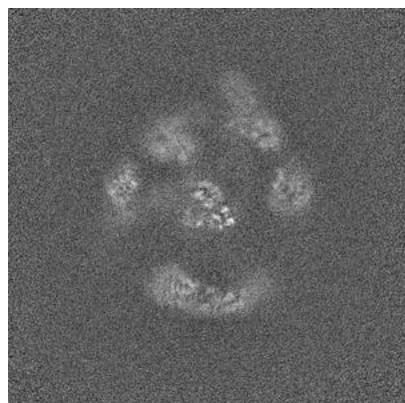


Y Index: 224



Z Index: 224

6.2.2 Raw map



X Index: 224



Y Index: 224

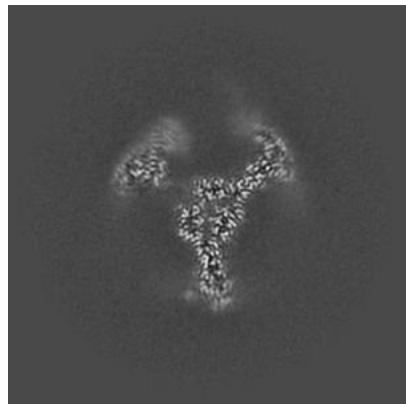


Z Index: 224

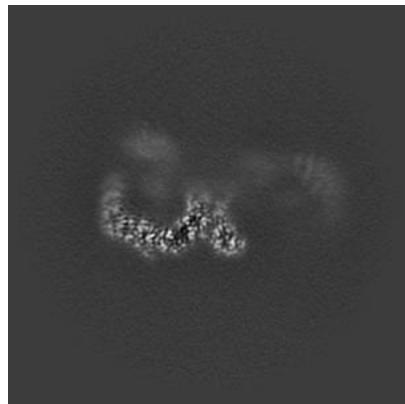
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

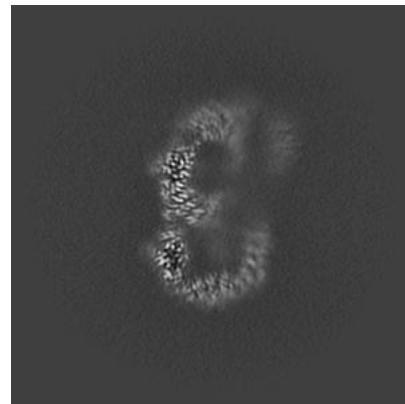
6.3.1 Primary map



X Index: 196

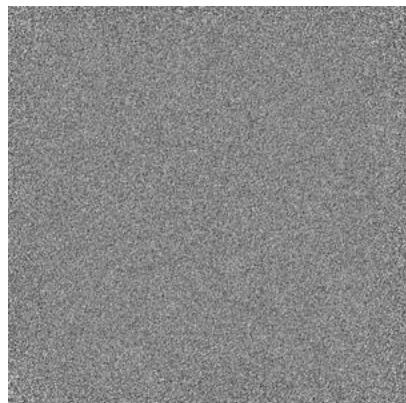


Y Index: 237

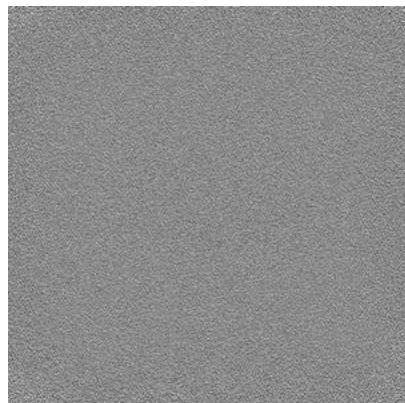


Z Index: 248

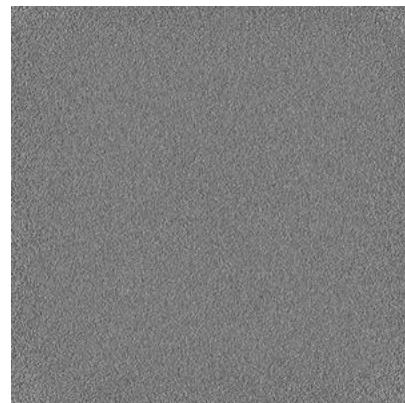
6.3.2 Raw map



X Index: 0



Y Index: 0



Z Index: 0

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

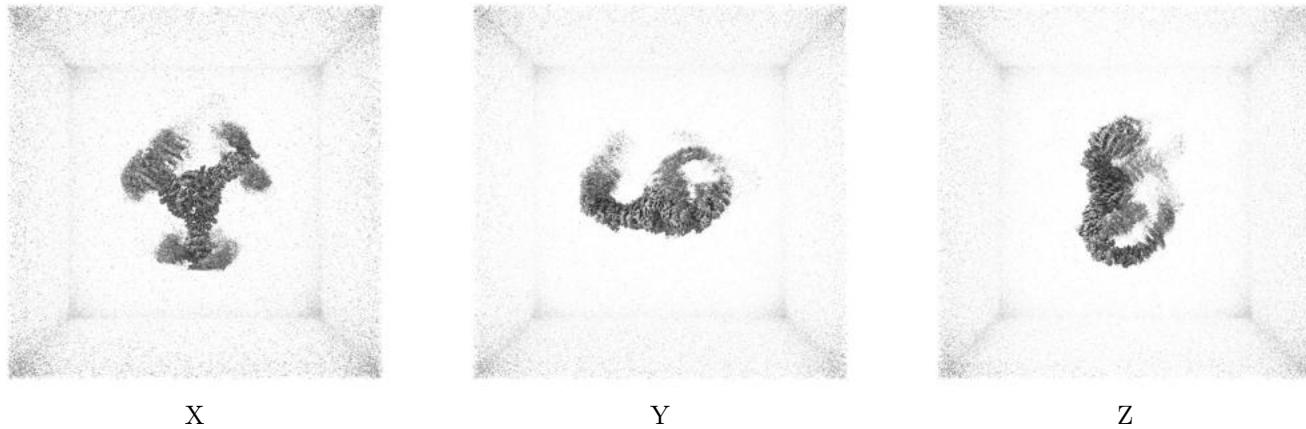
6.4 Orthogonal surface views [\(i\)](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.221. 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



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.

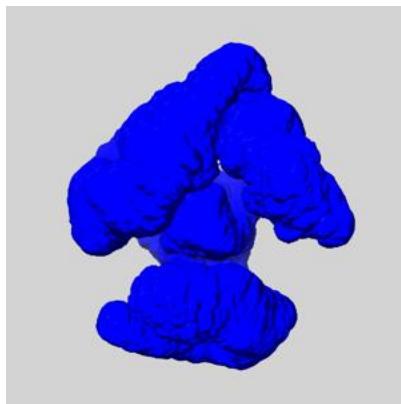
6.5 Mask visualisation [\(i\)](#)

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

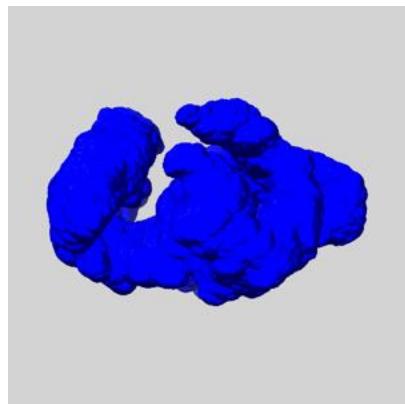
A mask typically either:

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

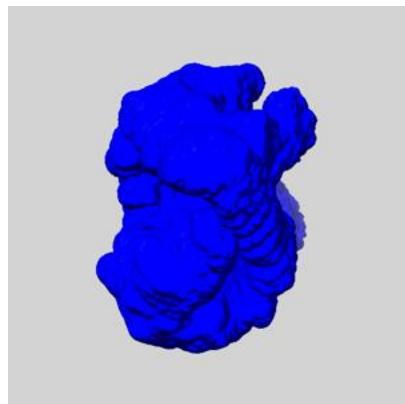
6.5.1 emd_14368_msk_1.map [\(i\)](#)



X



Y

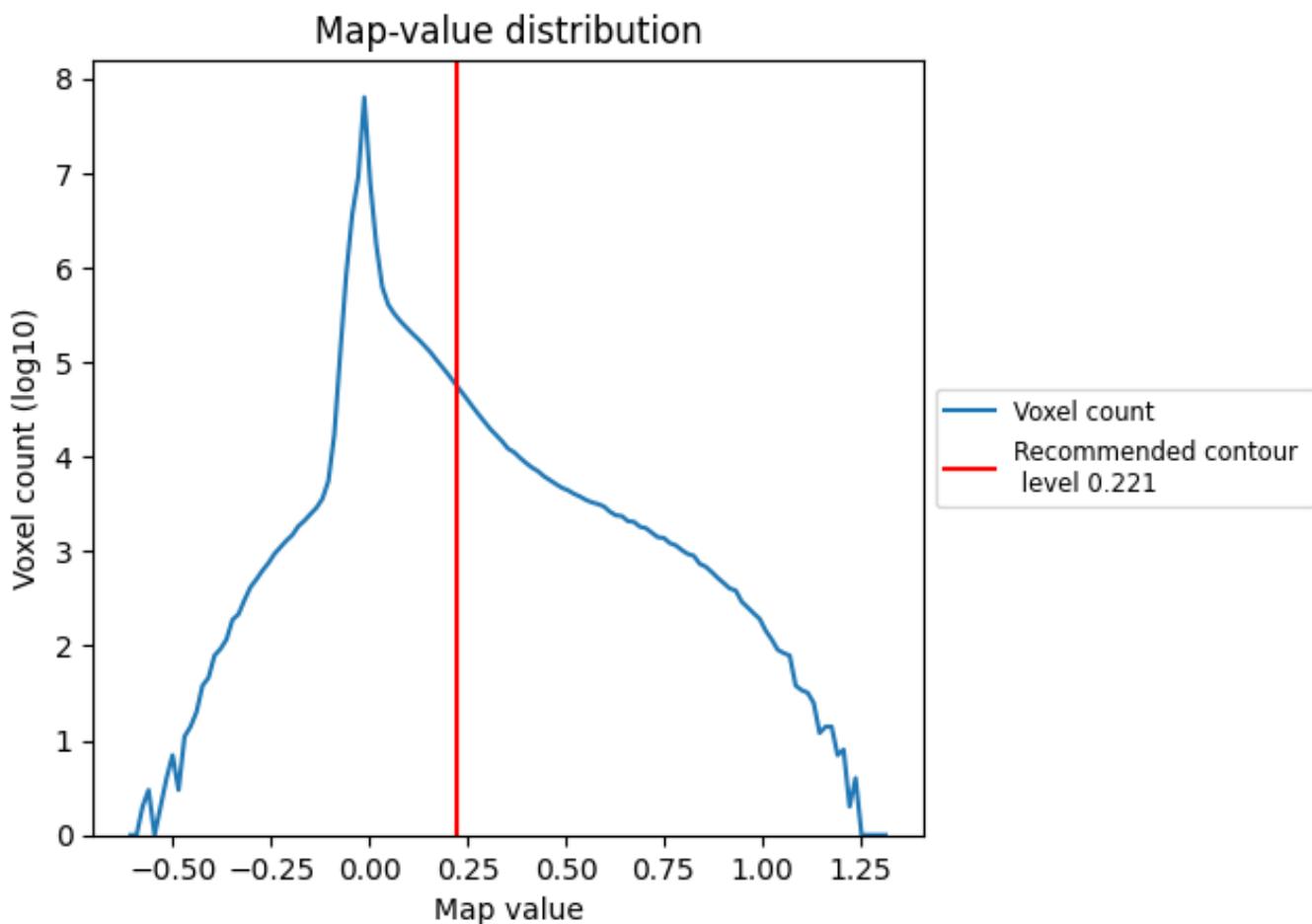


Z

7 Map analysis (i)

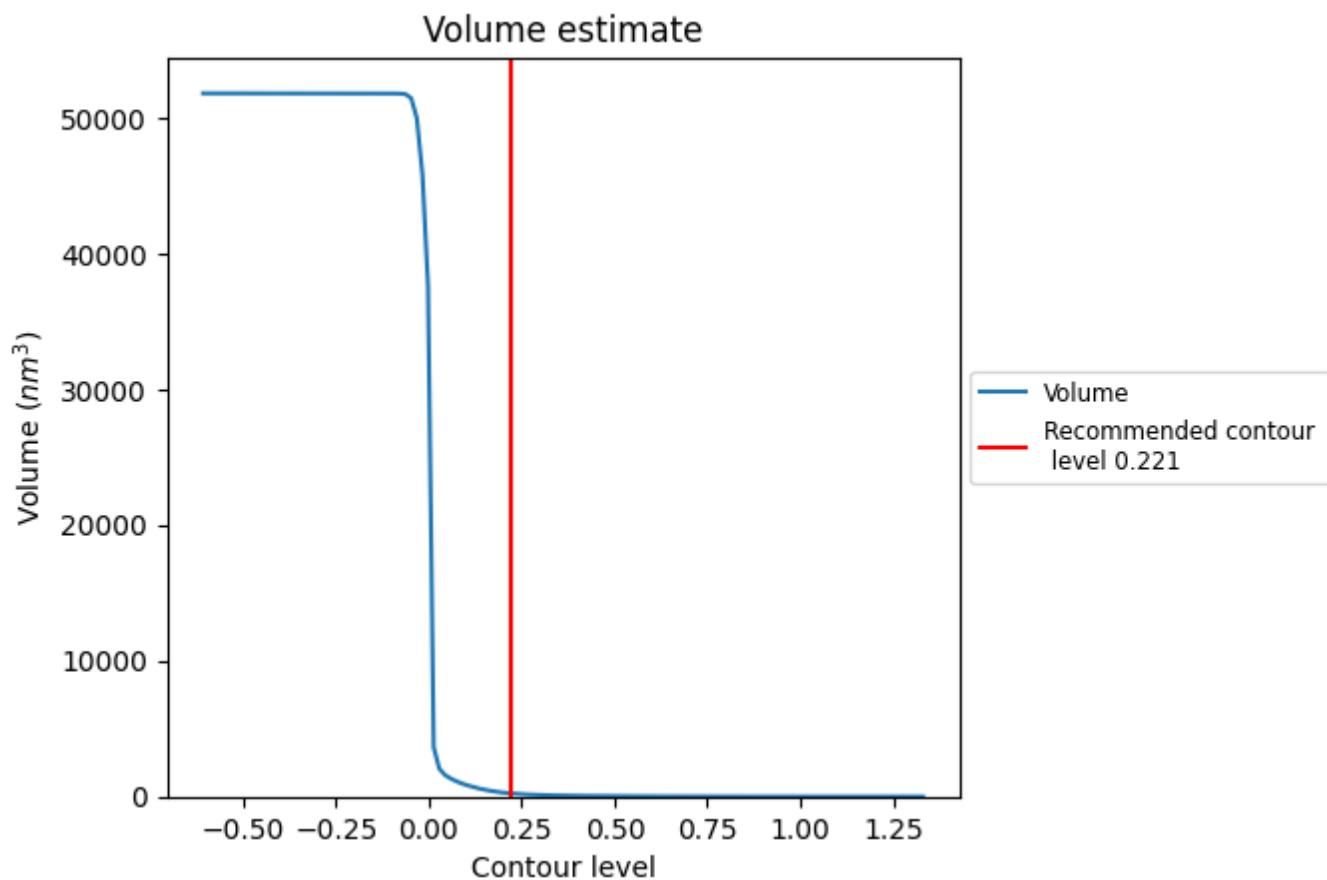
This section contains the results of statistical analysis of the map.

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.

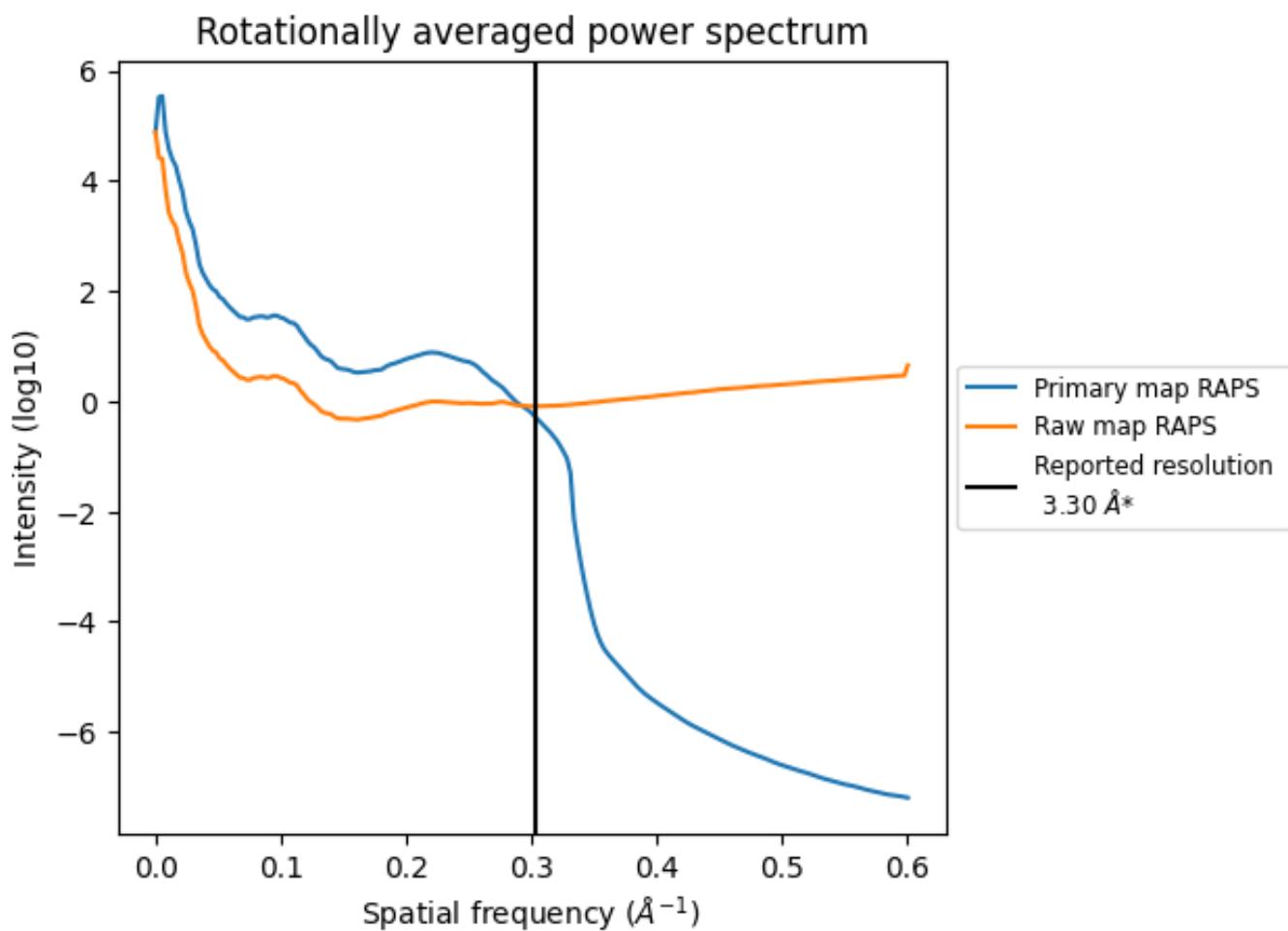
7.2 Volume estimate (i)



The volume at the recommended contour level is 235 nm^3 ; this corresponds to an approximate mass of 212 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 [\(i\)](#)

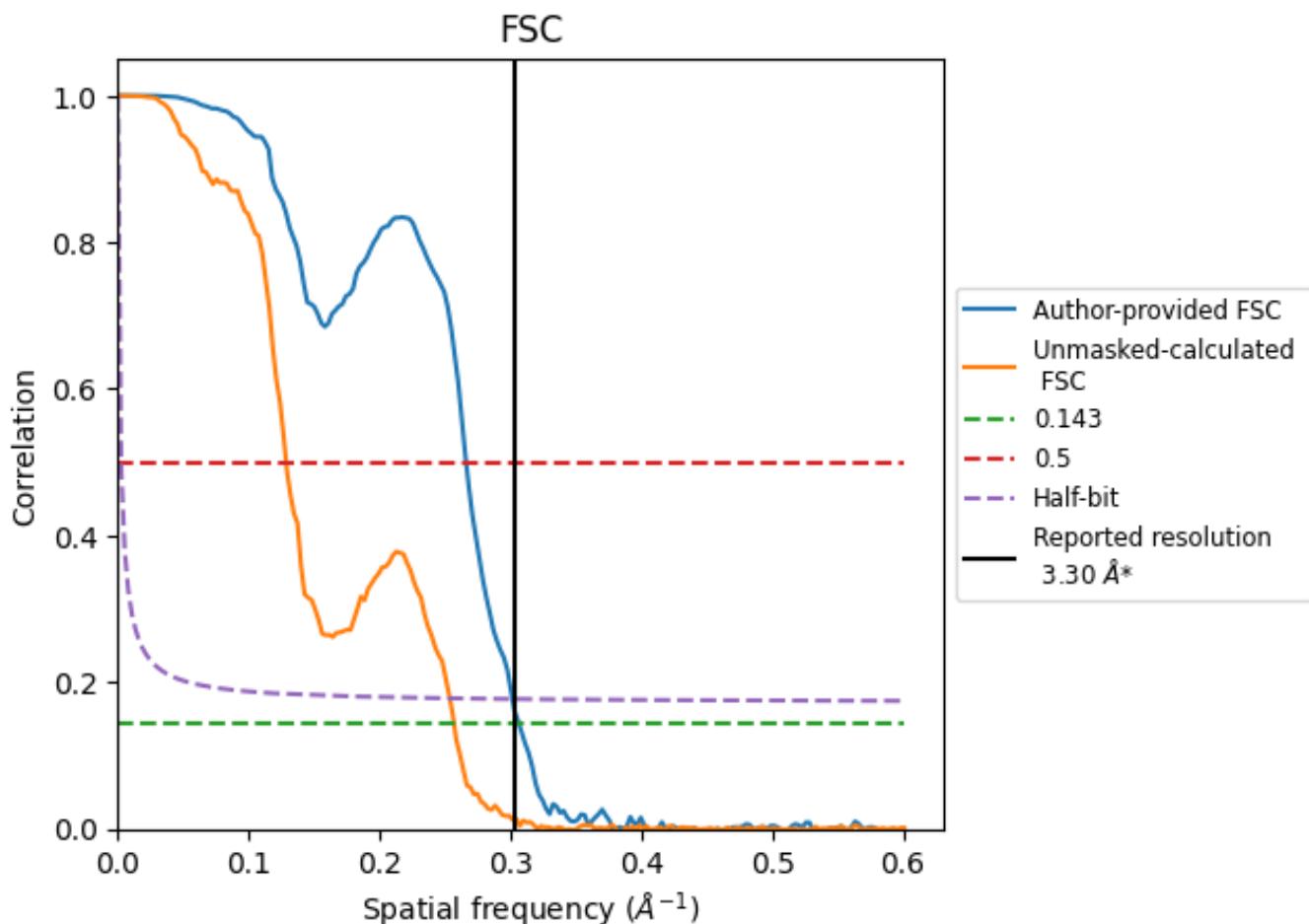


*Reported resolution corresponds to spatial frequency of 0.303 \AA^{-1}

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 0.303\AA^{-1}

8.2 Resolution estimates [\(i\)](#)

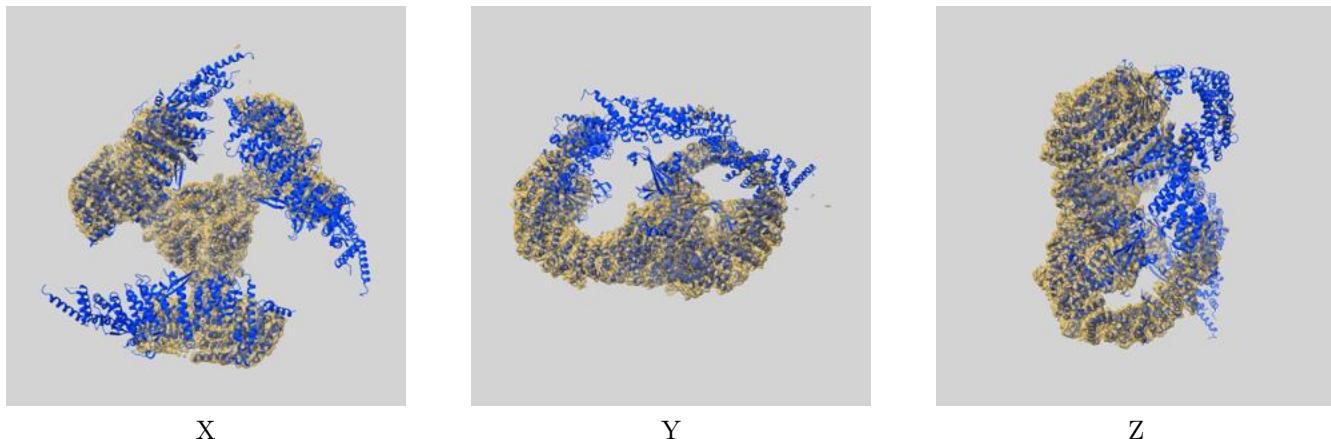
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.26	3.76	3.32
Unmasked-calculated*	3.89	7.77	3.94

*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 3.89 differs from the reported value 3.3 by more than 10 %

9 Map-model fit (i)

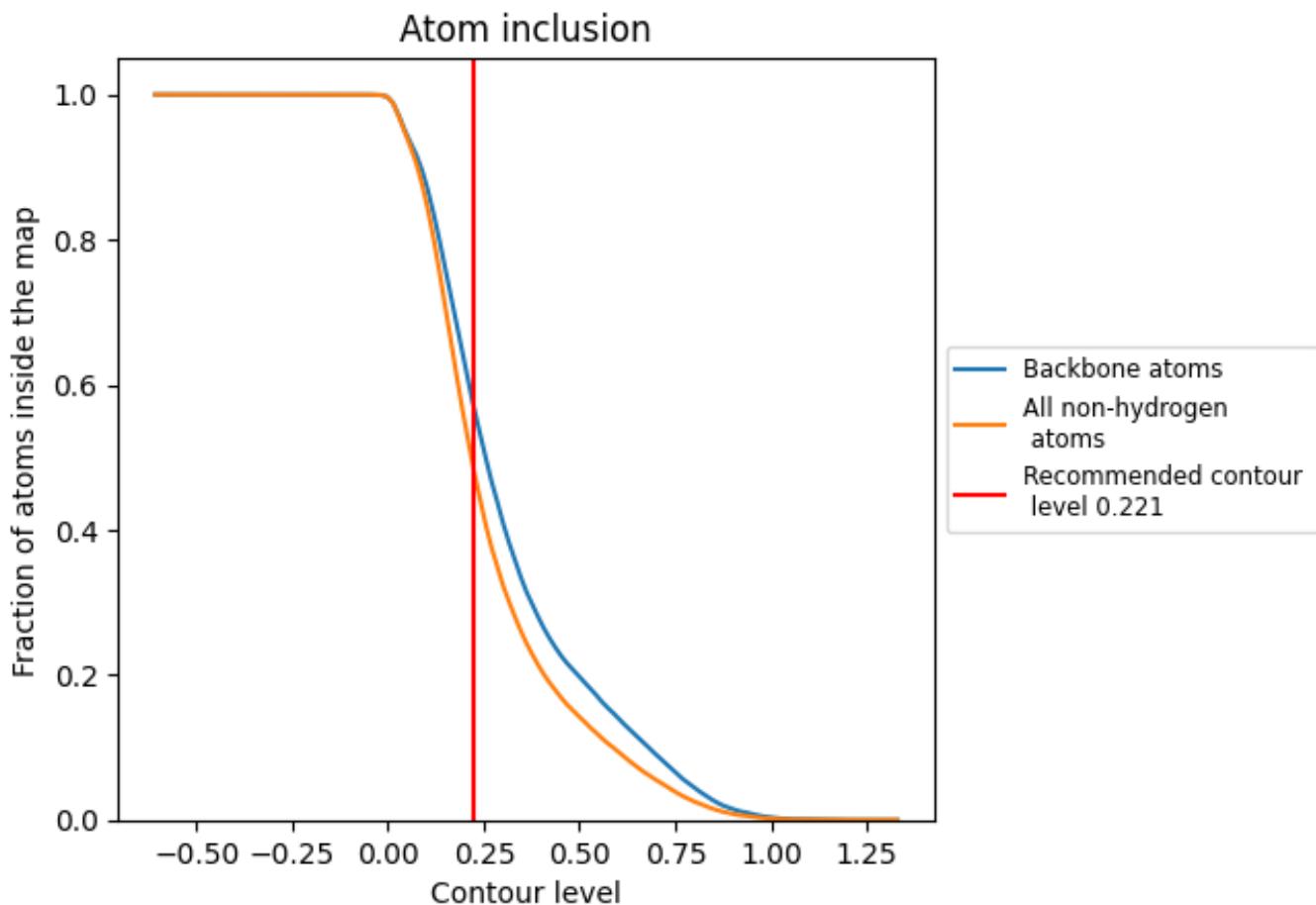
This section contains information regarding the fit between EMDB map EMD-14368 and PDB model 7YXX. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.221 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 Atom inclusion [\(i\)](#)



At the recommended contour level, 58% of all backbone atoms, 49% of all non-hydrogen atoms, are inside the map.