



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:19 PM UTC

PDB ID : 7ARQ / pdb_00007arq
EMDB ID : EMD-11367
Title : Cryo EM of 3D DNA origami 16 helix bundle
Authors : Feigl, E.; Kube, M.; Kohler, F.
Deposited on : 2020-10-26
Resolution : 10.00 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:

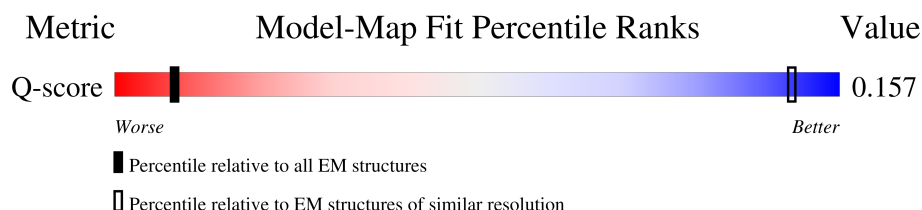
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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

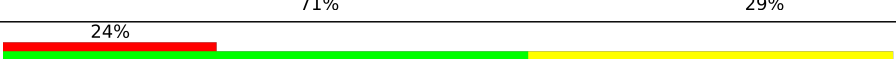
The reported resolution of this entry is 10.00 Å.

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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	147 (9.50 - 10.50)

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	AA	1317	 8% 73% 26% .
2	AB	49	 71% 29%
3	AC	42	 69% 31%
4	AD	33	 64% 33% .
5	AE	27	 70% 26% .
6	AF	35	 69% 31%
7	AG	49	 76% 24%
8	AH	34	 71% 29%
9	AI	34	 24% 59% 41%
10	AJ	30	 30% 80% 13% 7%

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Mol	Chain	Length	Quality of chain
11	AK	46	
12	AL	46	
13	AM	44	
14	AN	29	
15	AO	40	
16	AP	43	
17	AQ	40	
18	AR	30	
19	AS	34	
20	AT	40	
21	AU	42	
22	AV	37	
23	AW	41	
24	AX	33	
25	AY	35	
26	AZ	31	
27	Aa	49	
28	Ab	38	
29	Ac	48	
30	Ad	38	
31	Ae	27	
32	Af	36	
33	Ag	42	
34	Ah	35	
35	Ai	48	

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Mol	Chain	Length	Quality of chain
36	Aj	27	 78% 22%
37	Ak	40	 5% 68% 32%

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 54985 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 DNA chain called SCAFFOLD STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1317	Total	C	N	O	P	0	0
			26988	12825	4971	7876	1316		

- Molecule 2 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	49	Total	C	N	O	P	0	0
			1008	478	191	291	48		

- Molecule 3 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	42	Total	C	N	O	P	0	0
			863	412	152	258	41		

- Molecule 4 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	33	Total	C	N	O	P	0	0
			676	322	128	194	32		

- Molecule 5 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	27	Total	C	N	O	P	0	0
			546	262	95	163	26		

- Molecule 6 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	35	Total	C	N	O	P	0	0
			710	340	131	205	34		

- Molecule 7 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	49	Total	C	N	O	P	0	0
			1006	480	189	289	48		

- Molecule 8 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	34	Total	C	N	O	P	0	0
			698	334	125	206	33		

- Molecule 9 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	34	Total	C	N	O	P	0	0
			698	332	130	203	33		

- Molecule 10 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	30	Total	C	N	O	P	0	0
			611	292	110	180	29		

- Molecule 11 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	46	Total	C	N	O	P	0	0
			936	447	165	279	45		

- Molecule 12 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	46	Total	C	N	O	P	0	0
			940	451	167	277	45		

- Molecule 13 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	44	Total	C	N	O	P	0	0
			893	430	143	277	43		

- Molecule 14 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	29	Total	C	N	O	P	0	0
			584	282	96	178	28		

- Molecule 15 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	40	Total	C	N	O	P	0	0
			826	391	161	235	39		

- Molecule 16 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	43	Total	C	N	O	P	0	0
			877	417	156	262	42		

- Molecule 17 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	40	Total	C	N	O	P	0	0
			810	387	144	240	39		

- Molecule 18 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	30	Total	C	N	O	P	0	0
			610	294	108	179	29		

- Molecule 19 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	34	Total	C	N	O	P	0	0
			694	334	119	208	33		

- Molecule 20 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	40	Total	C	N	O	P	0	0
			831	396	150	246	39		

- Molecule 21 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	42	Total	C	N	O	P	0	0
			871	414	168	248	41		

- Molecule 22 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	37	Total	C	N	O	P	0	0
			749	360	129	224	36		

- Molecule 23 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	41	Total	C	N	O	P	0	0
			844	403	158	243	40		

- Molecule 24 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	33	Total	C	N	O	P	0	0
			668	321	114	201	32		

- Molecule 25 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	35	Total	C	N	O	P	0	0
			725	343	143	205	34		

- Molecule 26 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AZ	31	Total	C	N	O	P	0	0
			636	302	124	180	30		

- Molecule 27 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Aa	49	Total	C	N	O	P	0	0
			985	473	172	292	48		

- Molecule 28 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ab	38	Total	C	N	O	P	0	0
			776	373	131	235	37		

- Molecule 29 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ac	48	Total	C	N	O	P	0	0
			975	469	164	295	47		

- Molecule 30 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ad	38	Total	C	N	O	P	0	0
			774	370	140	227	37		

- Molecule 31 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ae	27	Total	C	N	O	P	0	0
			547	265	92	164	26		

- Molecule 32 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Af	36	Total	C	N	O	P	0	0
			727	348	132	212	35		

- Molecule 33 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ag	42	Total	C	N	O	P	0	0
			854	411	147	255	41		

- Molecule 34 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ah	35	Total	C	N	O	P	0	0
			713	340	134	205	34		

- Molecule 35 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ai	48	Total	C	N	O	P	0	0
			966	468	153	298	47		

- Molecule 36 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Aj	27	Total	C	N	O	P	0	0
			551	263	103	159	26		

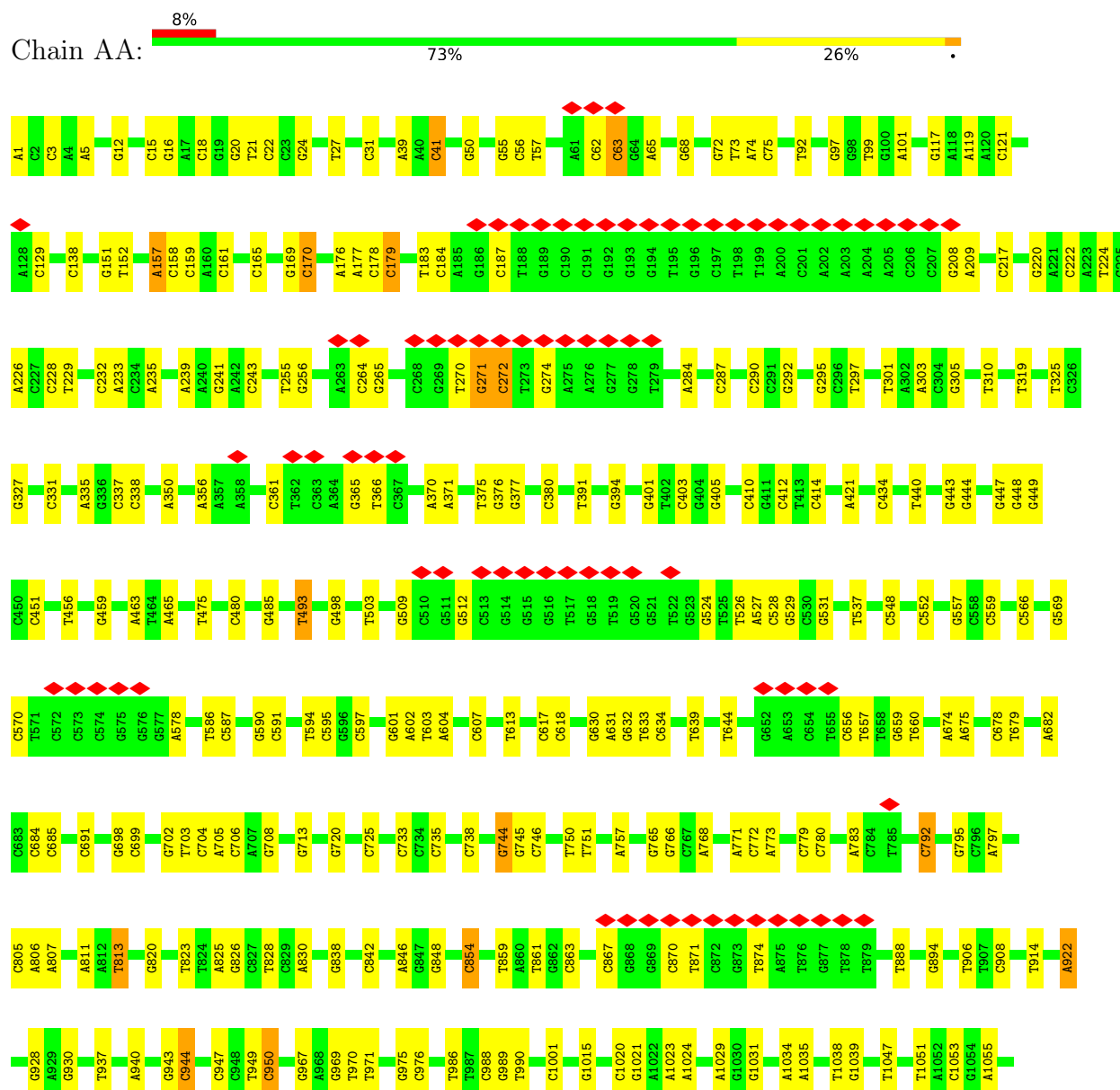
- Molecule 37 is a DNA chain called STAPLE STRAND.

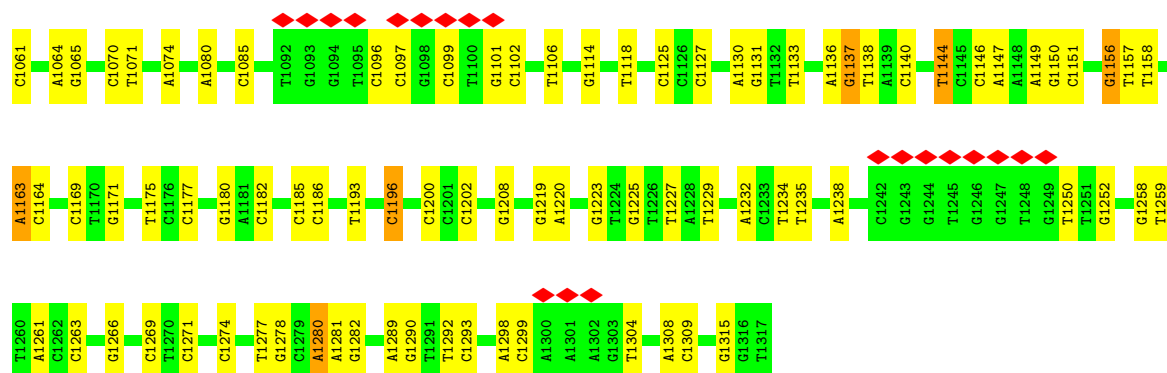
Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ak	40	Total	C	N	O	P	0	0
			819	386	163	231	39		

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: SCAFFOLD STRAND





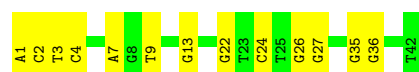
• Molecule 2: STAPLE STRAND

Chain AB: 71% 29%



• Molecule 3: STAPLE STRAND

Chain AC: 69% 31%



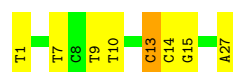
• Molecule 4: STAPLE STRAND

Chain AD: 64% 33%



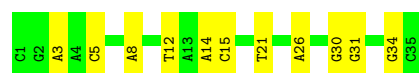
• Molecule 5: STAPLE STRAND

Chain AE: 70% 26%



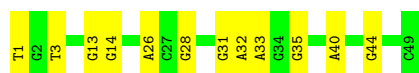
• Molecule 6: STAPLE STRAND

Chain AF: 69% 31%



• Molecule 7: STAPLE STRAND

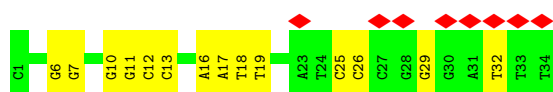
Chain AG: 76% 24%



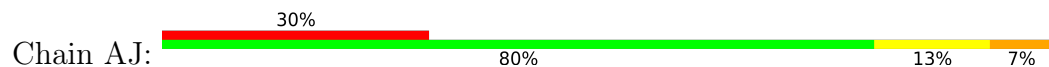
• Molecule 8: STAPLE STRAND



• Molecule 9: STAPLE STRAND



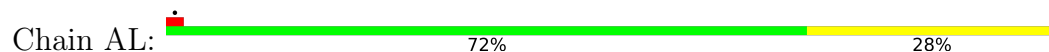
• Molecule 10: STAPLE STRAND



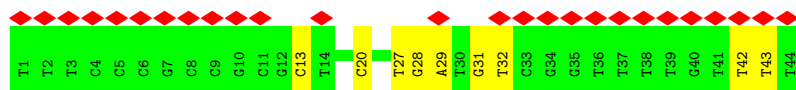
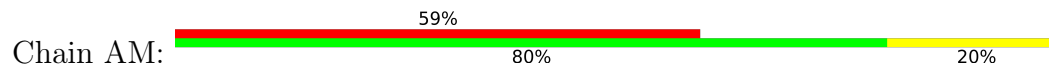
• Molecule 11: STAPLE STRAND



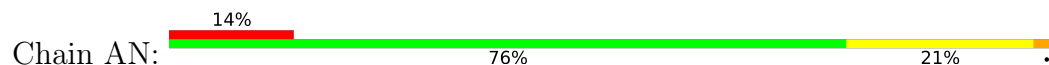
• Molecule 12: STAPLE STRAND



• Molecule 13: STAPLE STRAND



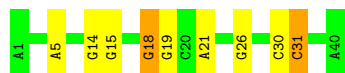
• Molecule 14: STAPLE STRAND





• Molecule 15: STAPLE STRAND

Chain AO: 78% 18% 5%



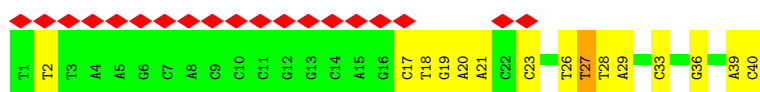
• Molecule 16: STAPLE STRAND

Chain AP: 58% 35% 7%



• Molecule 17: STAPLE STRAND

Chain AQ: 48% 62% 35% 0%



• Molecule 18: STAPLE STRAND

Chain AR: 27% 63% 30% 7%



• Molecule 19: STAPLE STRAND

Chain AS: 15% 65% 35% 0%



• Molecule 20: STAPLE STRAND

Chain AT: 70% 28% 0%



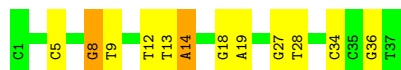
• Molecule 21: STAPLE STRAND

Chain AU: 81% 19% 0%



• Molecule 22: STAPLE STRAND

Chain AV: 68% 27% 5%



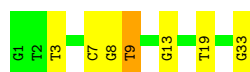
• Molecule 23: STAPLE STRAND

Chain AW: 66% 32% .



• Molecule 24: STAPLE STRAND

Chain AX: 79% 18% .



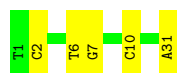
• Molecule 25: STAPLE STRAND

Chain AY: 77% 23%



• Molecule 26: STAPLE STRAND

Chain AZ: 84% 16%



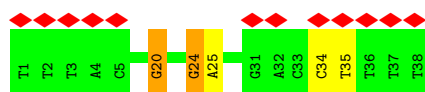
• Molecule 27: STAPLE STRAND

Chain Aa: 71% 27% .



• Molecule 28: STAPLE STRAND

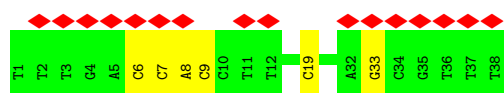
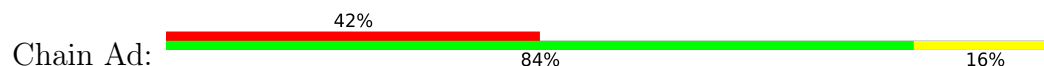
Chain Ab: 32% 87% 8% 5%



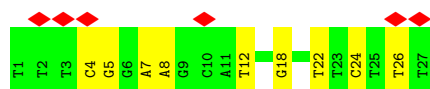
• Molecule 29: STAPLE STRAND



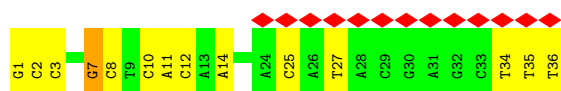
• Molecule 30: STAPLE STRAND



• Molecule 31: STAPLE STRAND



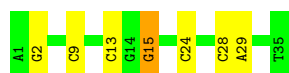
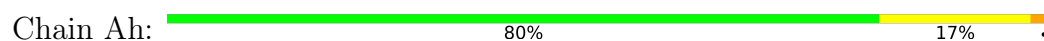
• Molecule 32: STAPLE STRAND



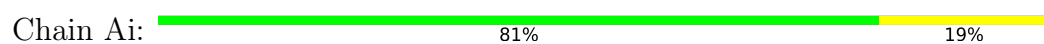
• Molecule 33: STAPLE STRAND



• Molecule 34: STAPLE STRAND

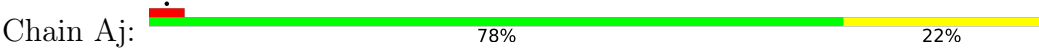


• Molecule 35: STAPLE STRAND

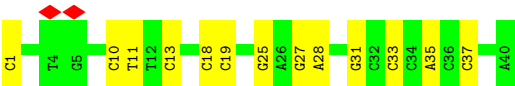




• Molecule 36: STAPLE STRAND



• Molecule 37: STAPLE STRAND



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44605	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.551	Depositor
Minimum map value	-0.116	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.17	Depositor
Map size (Å)	828.0, 828.0, 828.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.3, 2.3, 2.3	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	AA	0.72	0/30285	1.02	70/46736 (0.1%)
2	AB	0.75	0/1132	1.01	2/1747 (0.1%)
3	AC	0.76	0/966	1.05	2/1492 (0.1%)
4	AD	0.77	0/759	1.06	1/1170 (0.1%)
5	AE	0.74	0/610	1.08	1/939 (0.1%)
6	AF	0.71	0/796	1.02	0/1225
7	AG	0.72	0/1130	0.97	2/1743 (0.1%)
8	AH	0.75	0/782	1.08	2/1207 (0.2%)
9	AI	0.72	0/783	0.96	1/1208 (0.1%)
10	AJ	0.75	0/684	1.07	2/1054 (0.2%)
11	AK	0.74	0/1047	1.10	4/1614 (0.2%)
12	AL	0.75	0/1053	1.13	2/1624 (0.1%)
13	AM	0.70	0/995	0.99	0/1535
14	AN	0.71	0/651	1.06	1/1002 (0.1%)
15	AO	0.72	0/929	1.01	3/1434 (0.2%)
16	AP	0.75	0/981	1.09	4/1513 (0.3%)
17	AQ	0.74	0/906	1.06	3/1395 (0.2%)
18	AR	0.72	0/683	1.09	3/1052 (0.3%)
19	AS	0.72	0/776	0.99	0/1197
20	AT	0.76	0/932	1.07	2/1442 (0.1%)
21	AU	0.73	0/980	0.97	0/1514
22	AV	0.72	0/837	1.09	3/1289 (0.2%)
23	AW	0.72	0/948	1.11	5/1463 (0.3%)
24	AX	0.71	0/746	1.02	1/1149 (0.1%)
25	AY	0.75	0/816	1.02	1/1260 (0.1%)
26	AZ	0.74	0/715	0.99	0/1102
27	Aa	0.70	0/1101	1.11	1/1693 (0.1%)
28	Ab	0.71	0/867	1.09	2/1338 (0.1%)
29	Ac	0.71	0/1089	1.10	2/1679 (0.1%)
30	Ad	0.70	0/867	0.96	1/1336 (0.1%)
31	Ae	0.71	0/611	1.09	2/941 (0.2%)
32	Af	0.70	0/814	0.99	3/1252 (0.2%)
33	Ag	0.74	0/955	1.13	6/1472 (0.4%)
34	Ah	0.72	0/800	1.01	3/1232 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Ai	0.69	0/1076	1.04	0/1657
36	Aj	0.72	0/618	1.06	1/952 (0.1%)
37	Ak	0.74	0/921	1.01	3/1419 (0.2%)
All	All	0.73	0/61641	1.03	139/95077 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	3	313
2	AB	0	12
3	AC	0	11
4	AD	0	12
5	AE	0	8
6	AF	0	11
7	AG	0	10
8	AH	0	8
9	AI	0	13
10	AJ	0	6
11	AK	0	15
12	AL	0	11
13	AM	0	9
14	AN	0	7
15	AO	0	8
16	AP	0	17
17	AQ	0	13
18	AR	0	10
19	AS	0	12
20	AT	0	11
21	AU	0	8
22	AV	0	11
23	AW	0	10
24	AX	0	7
25	AY	0	7
26	AZ	0	5
27	Aa	0	14
28	Ab	1	5
29	Ac	0	14
30	Ad	0	5
31	Ae	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
32	Af	0	12
33	Ag	0	11
34	Ah	0	5
35	Ai	0	9
36	Aj	0	5
37	Ak	0	10
All	All	4	662

There are no bond length outliers.

The worst 5 of 139 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	Ab	20	DG	P-O3'-C3'	12.23	138.54	120.20
29	Ac	17	DG	P-O3'-C3'	11.38	137.26	120.20
27	Aa	41	DA	P-O3'-C3'	11.15	136.93	120.20
16	AP	16	DG	P-O3'-C3'	11.10	136.85	120.20
31	Ae	26	DT	P-O3'-C3'	11.09	136.83	120.20

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	272	DC	C3',C4'
1	AA	1272	DC	C3'
28	Ab	35	DT	C3'

5 of 662 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	DA	Sidechain
1	AA	12	DG	Sidechain
1	AA	15	DC	Sidechain
1	AA	3	DC	Sidechain
1	AA	5	DA	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	26988	0	14795	0	0
2	AB	1008	0	551	0	0
3	AC	863	0	478	0	0
4	AD	676	0	372	0	0
5	AE	546	0	307	0	0
6	AF	710	0	395	0	0
7	AG	1006	0	553	0	0
8	AH	698	0	387	0	0
9	AI	698	0	384	0	0
10	AJ	611	0	340	0	0
11	AK	936	0	519	0	0
12	AL	940	0	523	0	0
13	AM	893	0	505	0	0
14	AN	584	0	332	0	0
15	AO	826	0	449	0	0
16	AP	877	0	486	0	0
17	AQ	810	0	452	0	0
18	AR	610	0	342	0	0
19	AS	694	0	389	0	0
20	AT	831	0	456	0	0
21	AU	871	0	474	0	0
22	AV	749	0	421	0	0
23	AW	844	0	464	0	0
24	AX	668	0	376	0	0
25	AY	725	0	393	0	0
26	AZ	636	0	348	0	0
27	Aa	985	0	554	0	0
28	Ab	776	0	435	0	0
29	Ac	975	0	548	0	0
30	Ad	774	0	430	0	0
31	Ae	547	0	310	0	0
32	Af	727	0	406	0	0
33	Ag	854	0	479	0	0
34	Ah	713	0	394	0	0
35	Ai	966	0	551	0	0
36	Aj	551	0	305	0	0
37	Ak	819	0	445	0	0
All	All	54985	0	30348	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

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](#)

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.

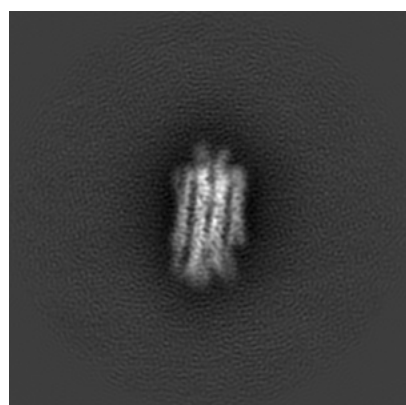
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11367. These allow visual inspection of the internal detail of the map and identification of artifacts.

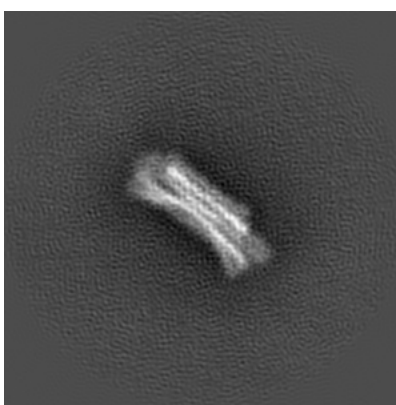
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

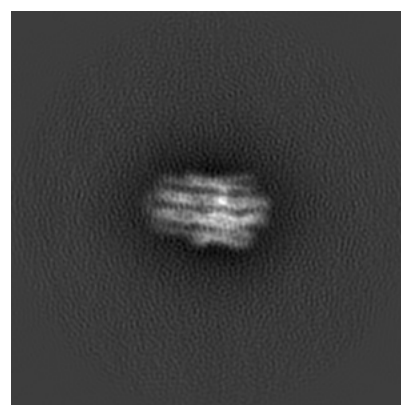
6.1.1 Primary map



X



Y

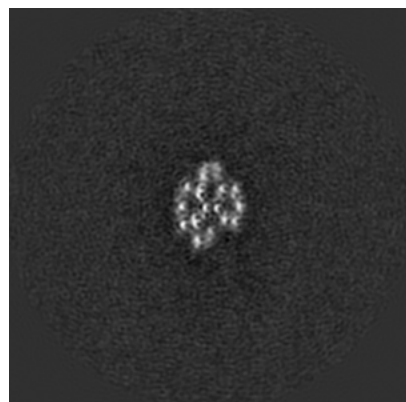


Z

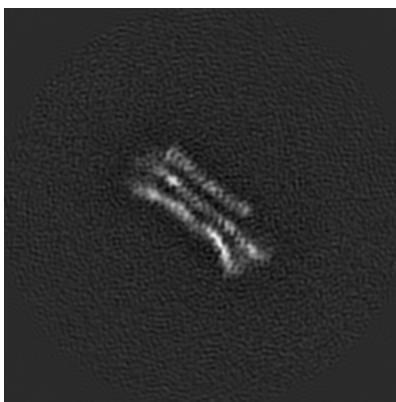
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

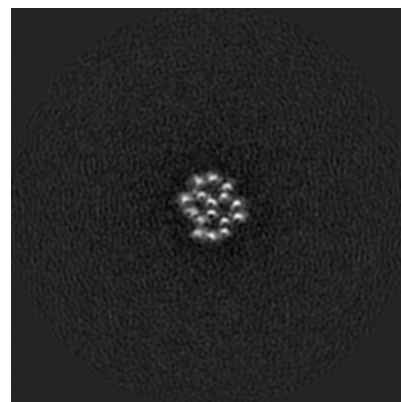
6.2.1 Primary map



X Index: 180



Y Index: 180

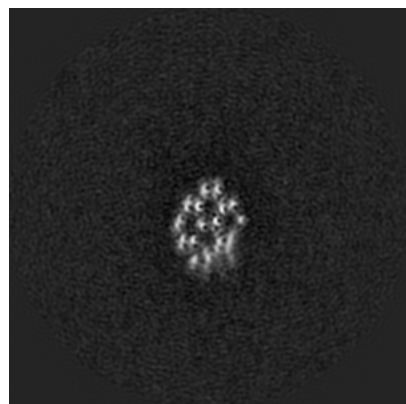


Z Index: 180

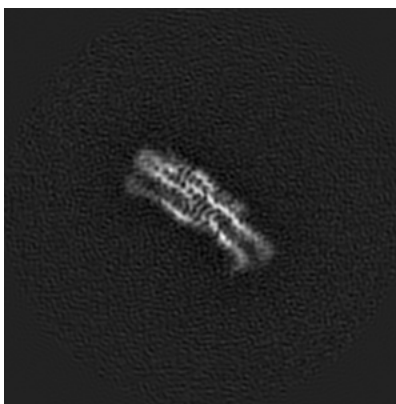
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

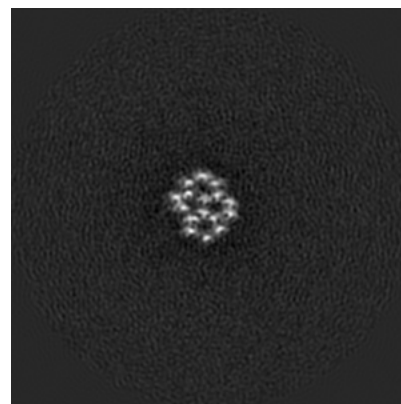
6.3.1 Primary map



X Index: 191



Y Index: 171

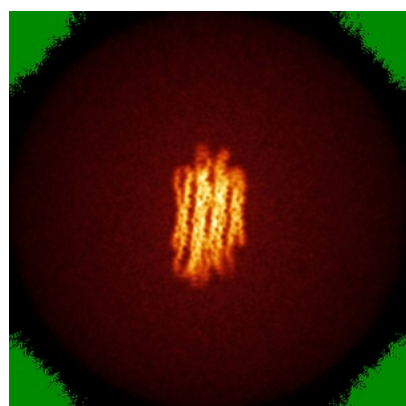


Z Index: 189

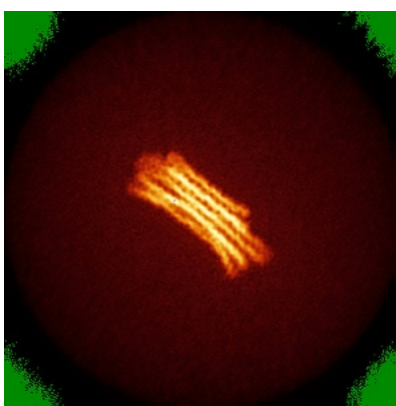
The images above show the largest variance slices of the map in three orthogonal directions.

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

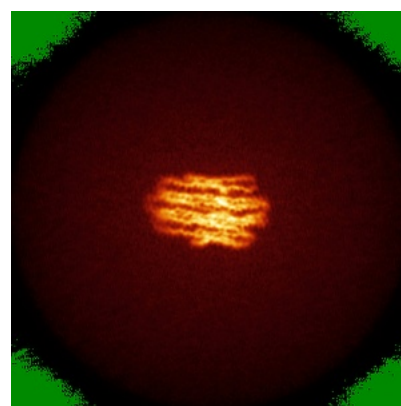
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views

This section was not generated.

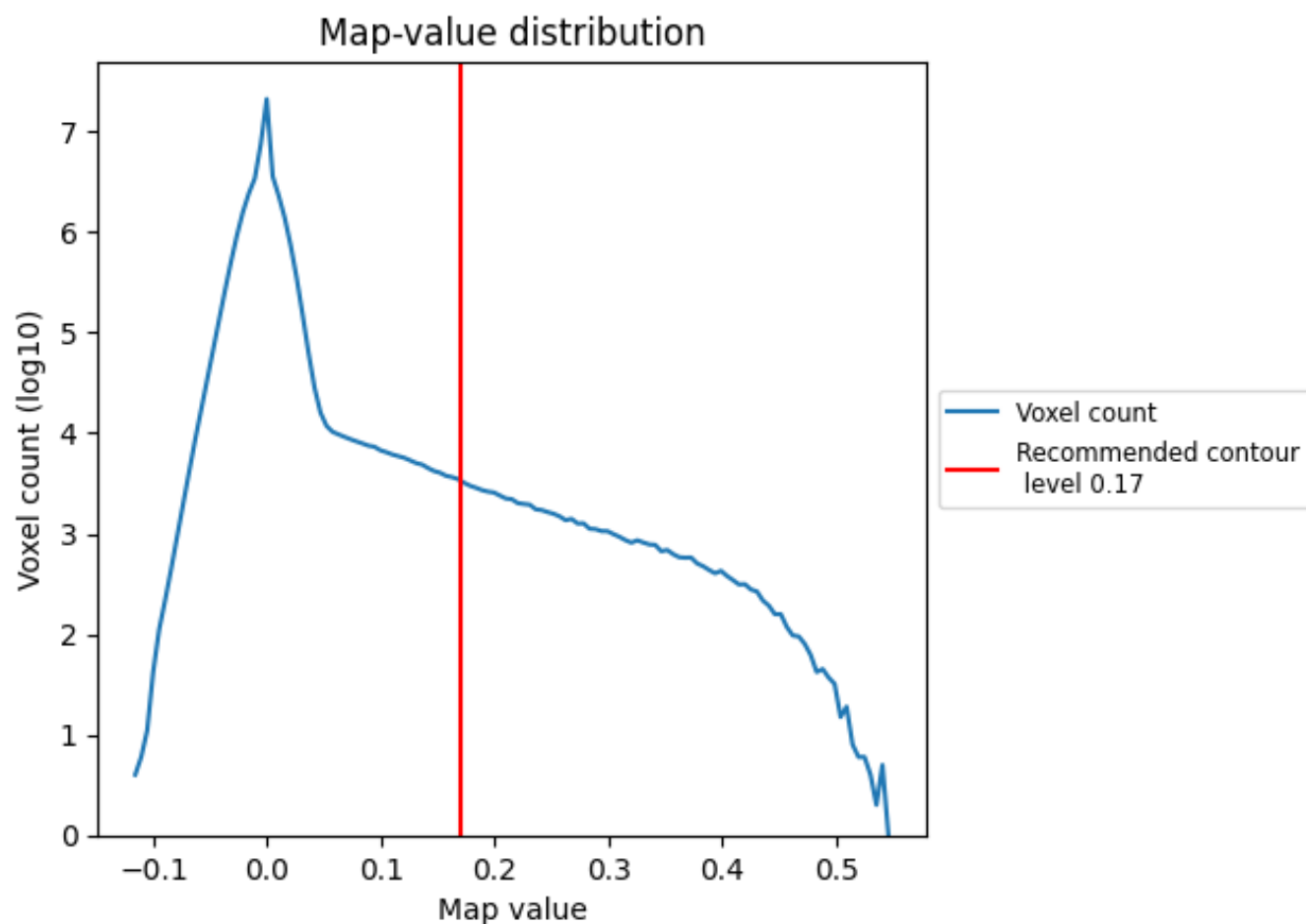
6.6 Mask visualisation

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

7 Map analysis [i](#)

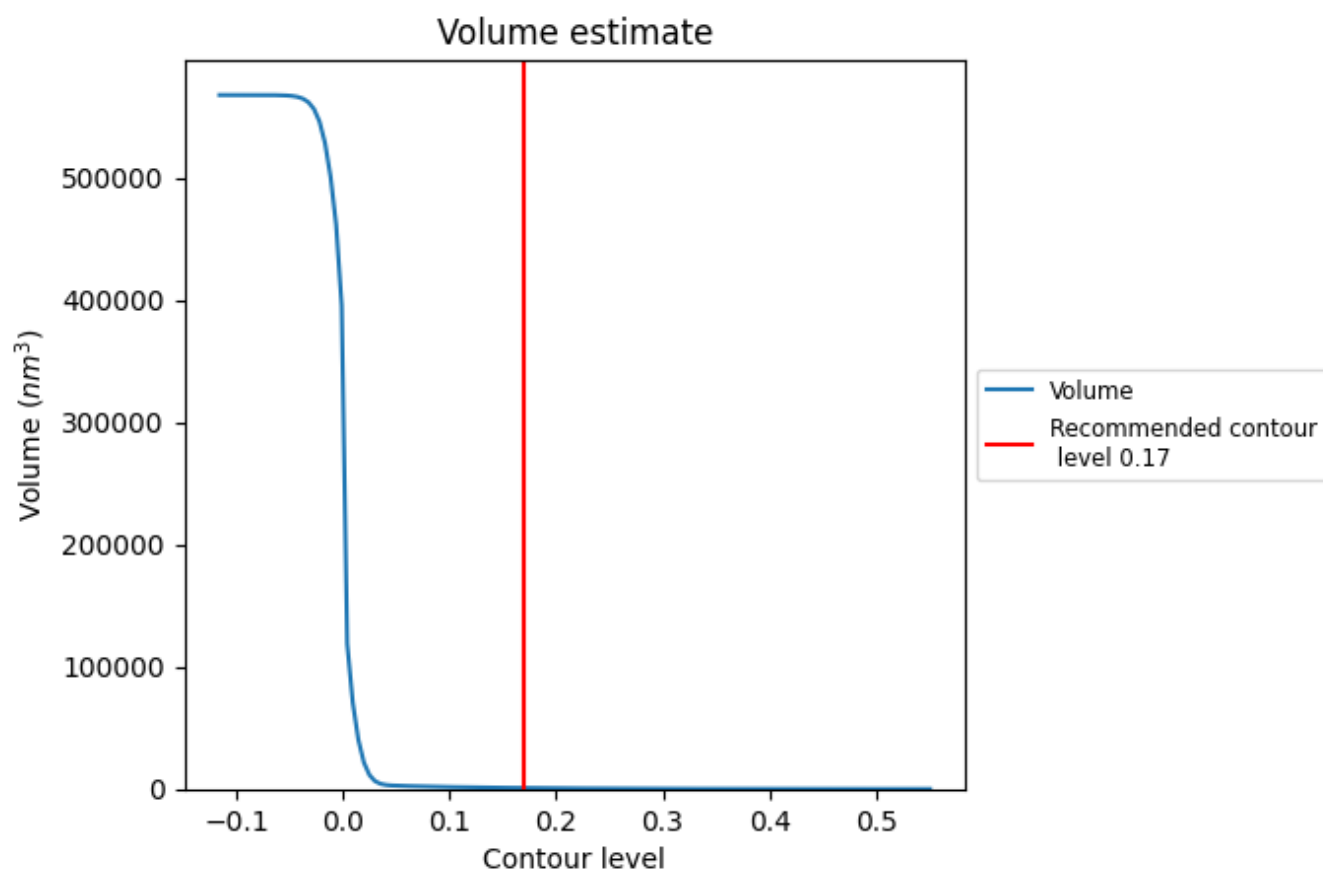
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

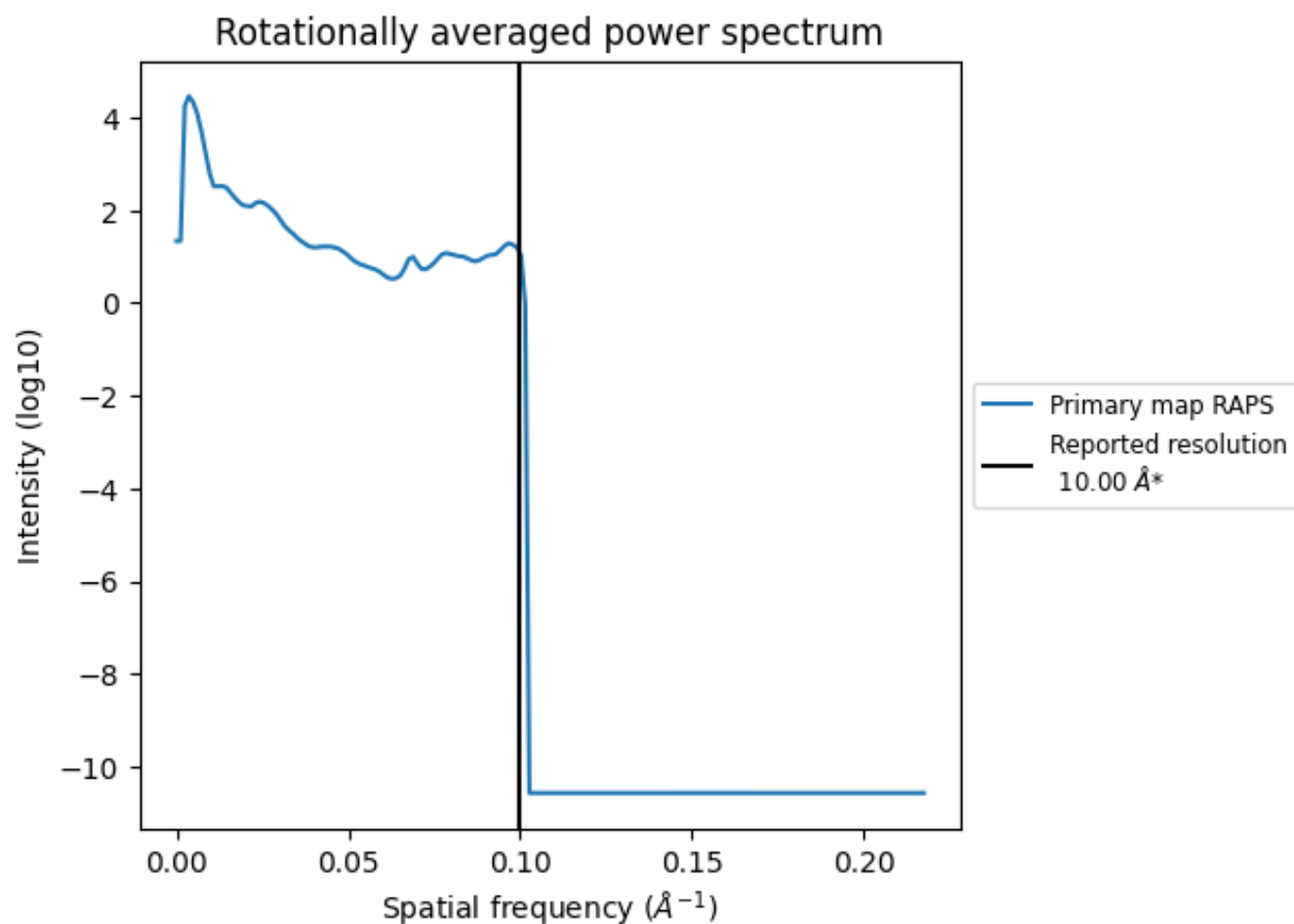
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 795 nm^3 ; this corresponds to an approximate mass of 719 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 ⓘ

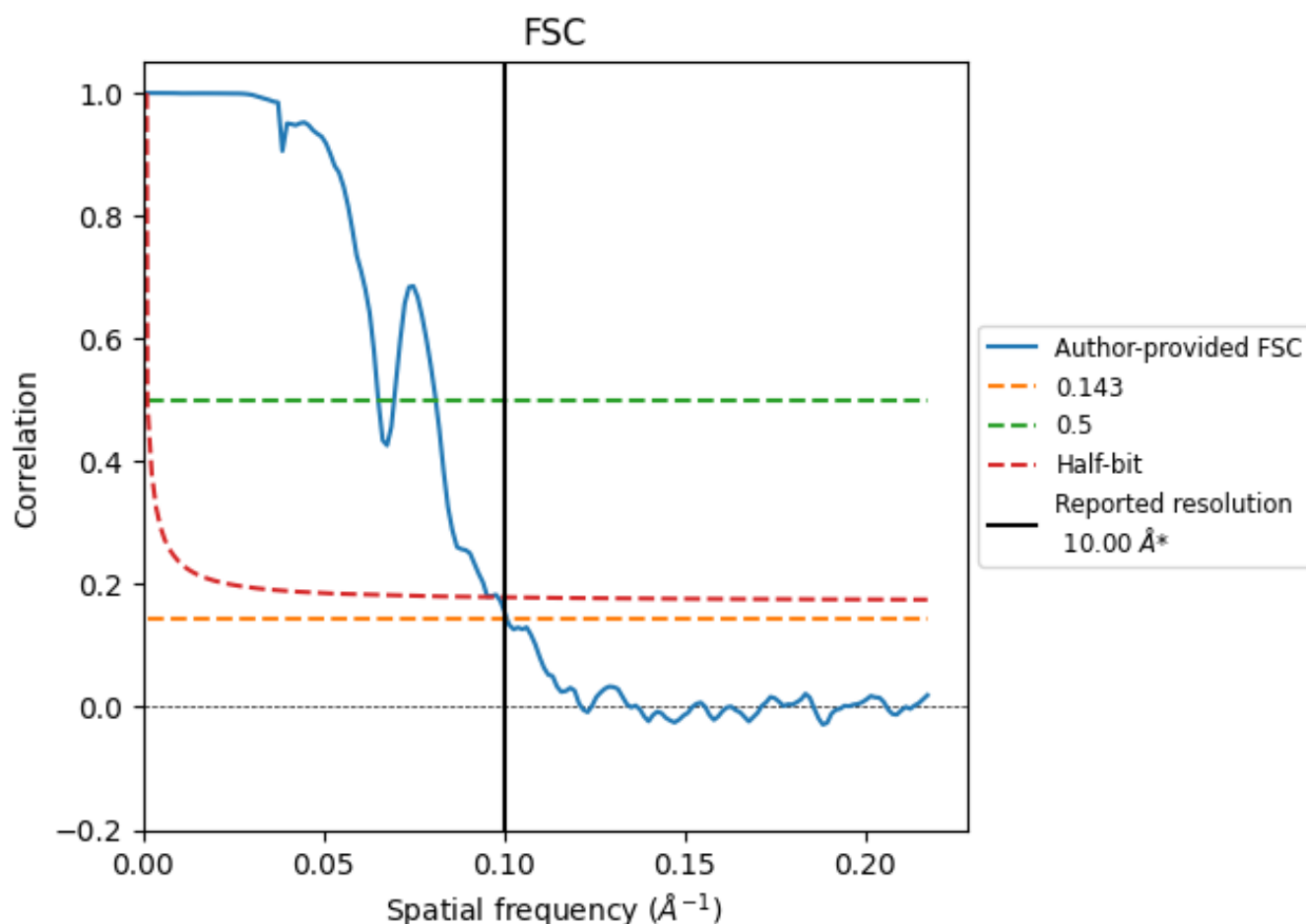


*Reported resolution corresponds to spatial frequency of 0.100 $\text{\AA}^{-1}$

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 0.100 Å⁻¹

8.2 Resolution estimates [i](#)

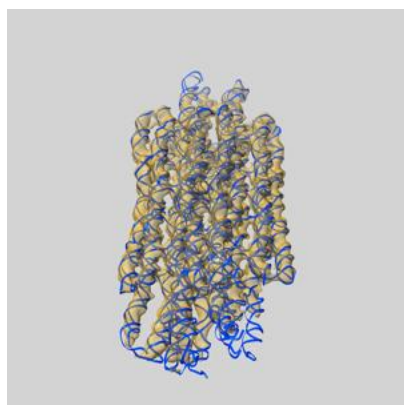
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	10.00	-	-
Author-provided FSC curve	9.91	15.34	10.17
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

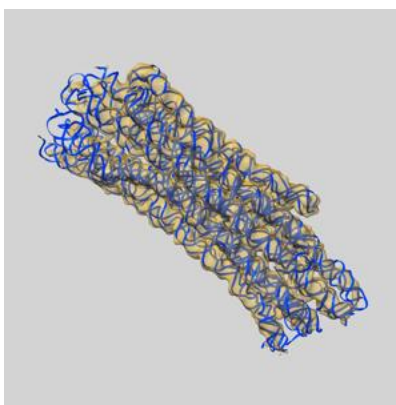
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11367 and PDB model 7ARQ. Per-residue inclusion information can be found in section [3](#) on page [11](#).

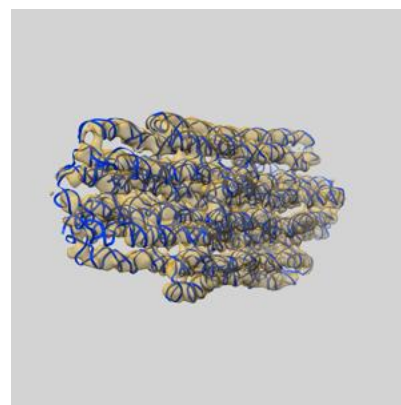
9.1 Map-model overlay [i](#)



X



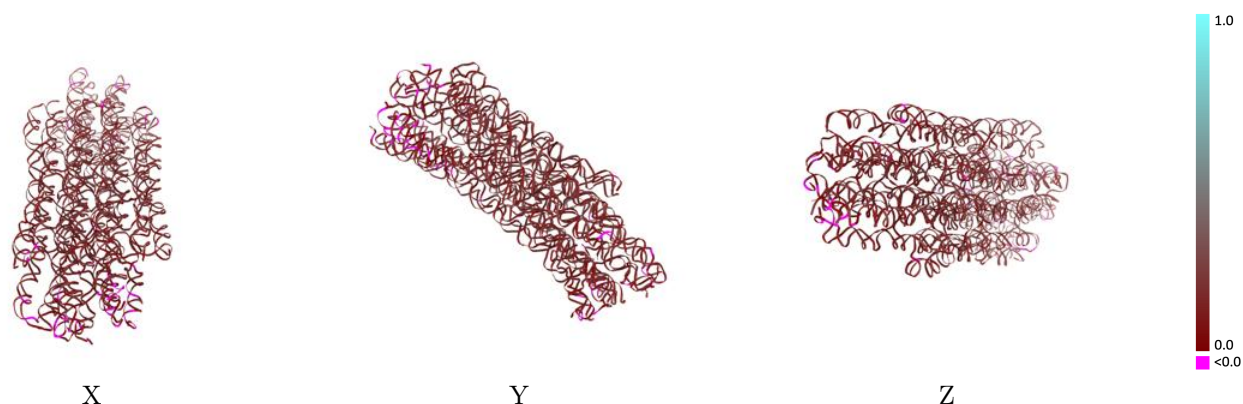
Y



Z

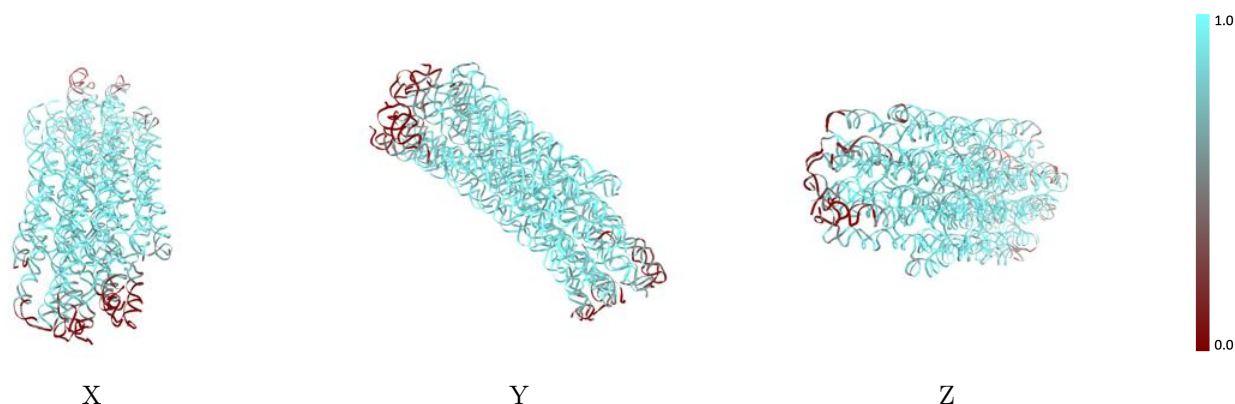
The images above show the 3D surface view of the map at the recommended contour level 0.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



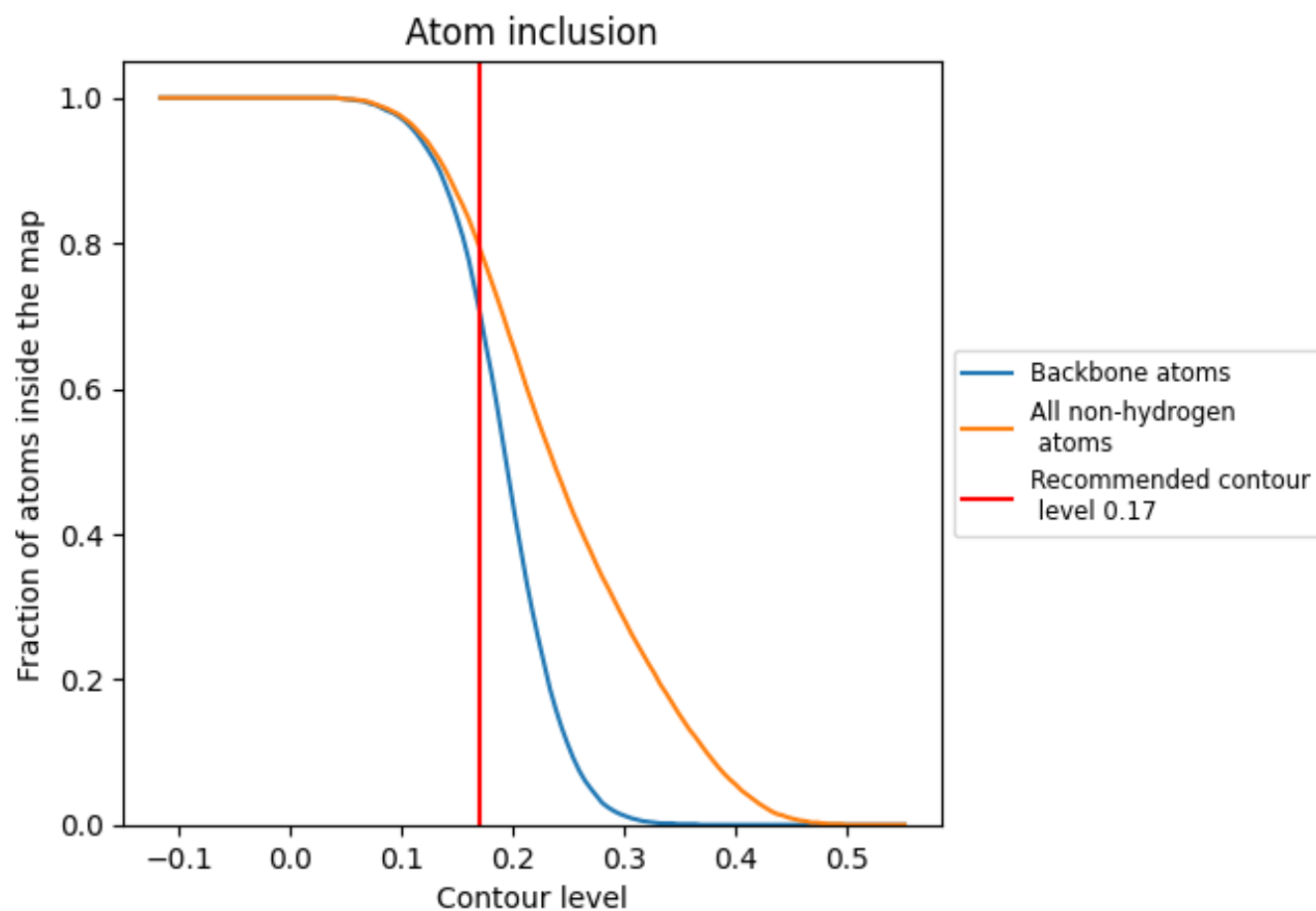
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.17).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 79% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7940	 0.1570
AA	 0.8090	 0.1630
AB	 0.8990	 0.1720
AC	 0.9250	 0.1730
AD	 0.7900	 0.1620
AE	 0.8970	 0.1670
AF	 0.9300	 0.1740
AG	 0.8820	 0.1670
AH	 0.9230	 0.1810
AI	 0.6660	 0.1290
AJ	 0.5940	 0.1150
AK	 0.7220	 0.1160
AL	 0.8800	 0.1570
AM	 0.3610	 0.0880
AN	 0.7190	 0.1390
AO	 0.8780	 0.1680
AP	 0.9010	 0.1620
AQ	 0.4100	 0.0700
AR	 0.6130	 0.1220
AS	 0.7420	 0.1510
AT	 0.8660	 0.1560
AU	 0.8540	 0.1610
AV	 0.8400	 0.1720
AW	 0.8350	 0.1480
AX	 0.8890	 0.1590
AY	 0.8990	 0.1670
AZ	 0.9210	 0.1850
Aa	 0.9090	 0.1730
Ab	 0.5360	 0.1160
Ac	 0.6890	 0.1530
Ad	 0.4680	 0.1320
Ae	 0.5700	 0.1220
Af	 0.5120	 0.1410
Ag	 0.9210	 0.1740
Ah	 0.9140	 0.1770



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Chain	Atom inclusion	Q-score
Ai	 0.8970	 0.1660
Aj	 0.8400	 0.1710
Ak	 0.8120	 0.1530