



Full wwPDB EM Validation Report ⓘ

Aug 11, 2026 – 04:52 pm BST

PDB ID : 30DR / pdb_000030dr
EMDB ID : EMD-57643
Title : Dynein-Dynactin-RAB11FIP3 complex - composite
Authors : d'Amico, E.A.; Carter, A.P.
Deposited on : 2026-04-21
Resolution : 10.00 Å(reported)
Based on initial model : .

This is a Full wwPDB EM Validation 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:

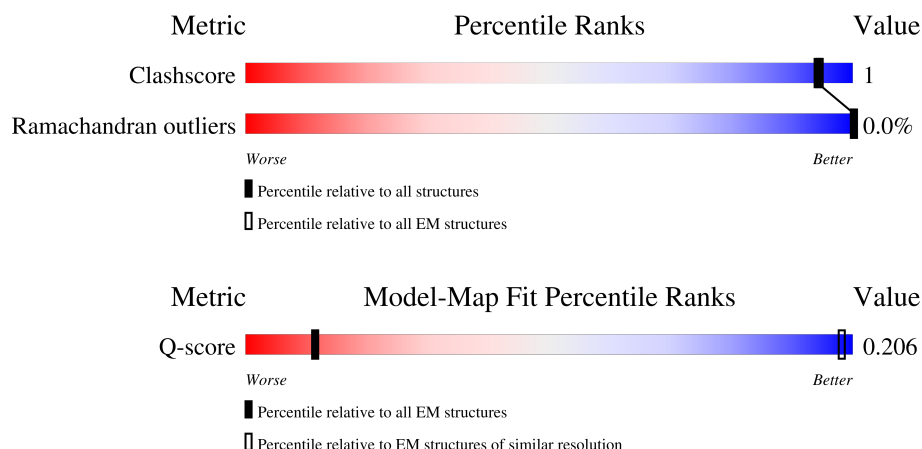
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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.



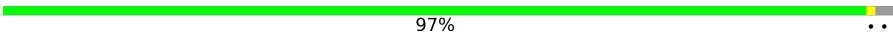
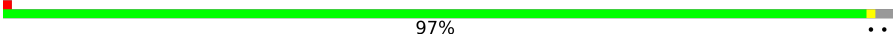
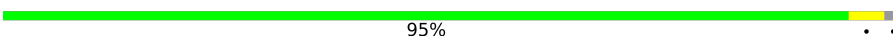
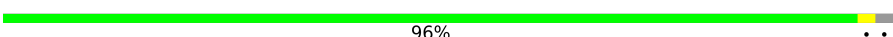
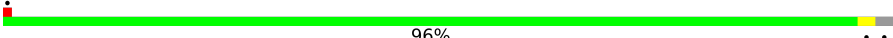
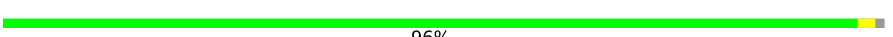
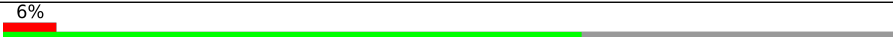
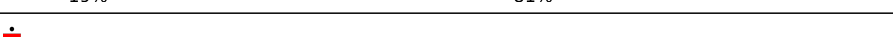
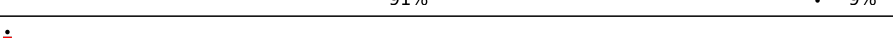
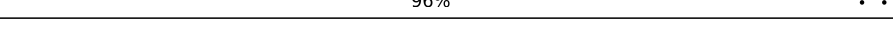
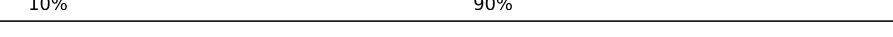
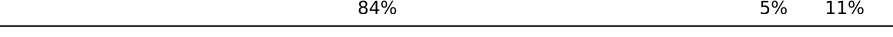
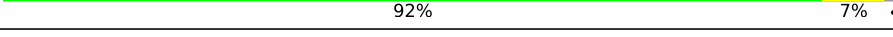
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	147 (9.50 - 10.50)

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	1	793	 30% 70%
1	2	793	 28% 72%
2	A	376	 98% ..
2	B	376	 97% ..
2	C	376	 98% .

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Mol	Chain	Length	Quality of chain
2	D	376	
2	E	376	
2	F	376	
2	G	376	
2	I	376	
3	H	375	
4	J	417	
5	K	286	
6	L	272	
7	M	405	
7	N	405	
7	P	405	
7	Q	405	
7	V	405	
8	O	186	
8	R	186	
9	S	1281	
9	T	1281	
10	U	190	
11	W	182	
12	Y	467	
13	e	4646	
13	f	4646	
13	m	4646	
13	n	4646	

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Mol	Chain	Length	Quality of chain
14	g	612	
14	h	612	
14	o	612	
14	p	612	
15	j	492	
15	q	492	
15	r	492	
16	s	96	
16	t	96	
16	w	96	
16	z	96	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 68795 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 Rab11 family-interacting protein 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	1	236	Total	C	N	O	0	0
			1176	704	236	236		
1	2	219	Total	C	N	O	0	0
			1091	653	219	219		

There are 74 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	-36	MET	-	initiating methionine	UNP O75154
1	-35	TRP	-	expression tag	UNP O75154
1	-34	SER	-	expression tag	UNP O75154
1	-33	HIS	-	expression tag	UNP O75154
1	-32	PRO	-	expression tag	UNP O75154
1	-31	GLN	-	expression tag	UNP O75154
1	-30	PHE	-	expression tag	UNP O75154
1	-29	GLU	-	expression tag	UNP O75154
1	-28	LYS	-	expression tag	UNP O75154
1	-27	GLY	-	expression tag	UNP O75154
1	-26	SER	-	expression tag	UNP O75154
1	-25	ALA	-	expression tag	UNP O75154
1	-24	GLY	-	expression tag	UNP O75154
1	-23	SER	-	expression tag	UNP O75154
1	-22	ALA	-	expression tag	UNP O75154
1	-21	ALA	-	expression tag	UNP O75154
1	-20	GLY	-	expression tag	UNP O75154
1	-19	SER	-	expression tag	UNP O75154
1	-18	GLY	-	expression tag	UNP O75154
1	-17	ALA	-	expression tag	UNP O75154
1	-16	GLY	-	expression tag	UNP O75154
1	-15	TRP	-	expression tag	UNP O75154
1	-14	SER	-	expression tag	UNP O75154
1	-13	HIS	-	expression tag	UNP O75154
1	-12	PRO	-	expression tag	UNP O75154
1	-11	GLN	-	expression tag	UNP O75154

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Chain	Residue	Modelled	Actual	Comment	Reference
1	-10	PHE	-	expression tag	UNP O75154
1	-9	GLU	-	expression tag	UNP O75154
1	-8	LYS	-	expression tag	UNP O75154
1	-7	LEU	-	expression tag	UNP O75154
1	-6	GLU	-	expression tag	UNP O75154
1	-5	VAL	-	expression tag	UNP O75154
1	-4	LEU	-	expression tag	UNP O75154
1	-3	PHE	-	expression tag	UNP O75154
1	-2	GLN	-	expression tag	UNP O75154
1	-1	GLY	-	expression tag	UNP O75154
1	0	PRO	-	expression tag	UNP O75154
2	-36	MET	-	initiating methionine	UNP O75154
2	-35	TRP	-	expression tag	UNP O75154
2	-34	SER	-	expression tag	UNP O75154
2	-33	HIS	-	expression tag	UNP O75154
2	-32	PRO	-	expression tag	UNP O75154
2	-31	GLN	-	expression tag	UNP O75154
2	-30	PHE	-	expression tag	UNP O75154
2	-29	GLU	-	expression tag	UNP O75154
2	-28	LYS	-	expression tag	UNP O75154
2	-27	GLY	-	expression tag	UNP O75154
2	-26	SER	-	expression tag	UNP O75154
2	-25	ALA	-	expression tag	UNP O75154
2	-24	GLY	-	expression tag	UNP O75154
2	-23	SER	-	expression tag	UNP O75154
2	-22	ALA	-	expression tag	UNP O75154
2	-21	ALA	-	expression tag	UNP O75154
2	-20	GLY	-	expression tag	UNP O75154
2	-19	SER	-	expression tag	UNP O75154
2	-18	GLY	-	expression tag	UNP O75154
2	-17	ALA	-	expression tag	UNP O75154
2	-16	GLY	-	expression tag	UNP O75154
2	-15	TRP	-	expression tag	UNP O75154
2	-14	SER	-	expression tag	UNP O75154
2	-13	HIS	-	expression tag	UNP O75154
2	-12	PRO	-	expression tag	UNP O75154
2	-11	GLN	-	expression tag	UNP O75154
2	-10	PHE	-	expression tag	UNP O75154
2	-9	GLU	-	expression tag	UNP O75154
2	-8	LYS	-	expression tag	UNP O75154
2	-7	LEU	-	expression tag	UNP O75154
2	-6	GLU	-	expression tag	UNP O75154

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Chain	Residue	Modelled	Actual	Comment	Reference
2	-5	VAL	-	expression tag	UNP O75154
2	-4	LEU	-	expression tag	UNP O75154
2	-3	PHE	-	expression tag	UNP O75154
2	-2	GLN	-	expression tag	UNP O75154
2	-1	GLY	-	expression tag	UNP O75154
2	0	PRO	-	expression tag	UNP O75154

- Molecule 2 is a protein called ARP1 actin related protein 1 homolog A.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	A	370	Total	C	N	O	0	0
			1822	1082	370	370		
2	B	370	Total	C	N	O	0	0
			1822	1082	370	370		
2	C	375	Total	C	N	O	0	0
			1847	1097	375	375		
2	D	370	Total	C	N	O	0	0
			1822	1082	370	370		
2	E	370	Total	C	N	O	0	0
			1822	1082	370	370		
2	F	370	Total	C	N	O	0	0
			1822	1082	370	370		
2	G	370	Total	C	N	O	0	0
			1822	1082	370	370		
2	I	370	Total	C	N	O	0	0
			1822	1082	370	370		

- Molecule 3 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	H	370	Total	C	N	O	0	0
			1822	1082	370	370		

- Molecule 4 is a protein called Arp11.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	J	379	Total	C	N	O	0	0
			1868	1110	379	379		

- Molecule 5 is a protein called Capping protein (Actin filament) muscle Z-line, alpha 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	K	278	Total	C	N	O	0	0
			1378	822	278	278		

- Molecule 6 is a protein called F-actin-capping protein subunit beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	L	269	Total	C	N	O	0	0
			1327	789	269	269		

- Molecule 7 is a protein called Dynactin subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	M	241	Total	C	N	O	0	0
			1201	719	241	241		
7	N	263	Total	C	N	O	0	0
			1310	784	263	263		
7	P	353	Total	C	N	O	0	0
			1757	1051	353	353		
7	Q	329	Total	C	N	O	0	0
			1632	974	329	329		
7	V	75	Total	C	N	O	0	0
			369	219	75	75		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	7	VAL	ALA	conflict	UNP A0A5G2QD80
N	7	VAL	ALA	conflict	UNP A0A5G2QD80
P	7	VAL	ALA	conflict	UNP A0A5G2QD80
Q	7	VAL	ALA	conflict	UNP A0A5G2QD80
V	7	VAL	ALA	conflict	UNP A0A5G2QD80

- Molecule 8 is a protein called Dynactin subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	O	170	Total	C	N	O	0	0
			844	504	170	170		
8	R	179	Total	C	N	O	0	0
			888	530	179	179		

- Molecule 9 is a protein called Dynactin subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	S	134	Total	C	N	O	0	0
			667	399	134	134		
9	T	192	Total	C	N	O	0	0
			952	568	192	192		

- Molecule 10 is a protein called Dynactin 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	U	169	Total	C	N	O	0	0
			832	494	169	169		

- Molecule 11 is a protein called Dynactin subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	W	179	Total	C	N	O	0	0
			881	523	179	179		

- Molecule 12 is a protein called Dynactin subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	Y	375	Total	C	N	O	0	0
			1863	1113	375	375		

- Molecule 13 is a protein called Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	e	884	Total	C	N	O	0	0
			4387	2619	884	884		
13	f	1097	Total	C	N	O	0	0
			5440	3246	1097	1097		
13	m	1075	Total	C	N	O	0	0
			5333	3183	1075	1075		
13	n	871	Total	C	N	O	0	0
			4324	2582	871	871		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	1567	GLU	ARG	engineered mutation	UNP Q14204
e	1610	GLU	LYS	engineered mutation	UNP Q14204
f	1567	GLU	ARG	engineered mutation	UNP Q14204
f	1610	GLU	LYS	engineered mutation	UNP Q14204

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Chain	Residue	Modelled	Actual	Comment	Reference
m	1567	GLU	ARG	engineered mutation	UNP Q14204
m	1610	GLU	LYS	engineered mutation	UNP Q14204
n	1567	GLU	ARG	engineered mutation	UNP Q14204
n	1610	GLU	LYS	engineered mutation	UNP Q14204

- Molecule 14 is a protein called Isoform 2C of Cytoplasmic dynein 1 intermediate chain 2.

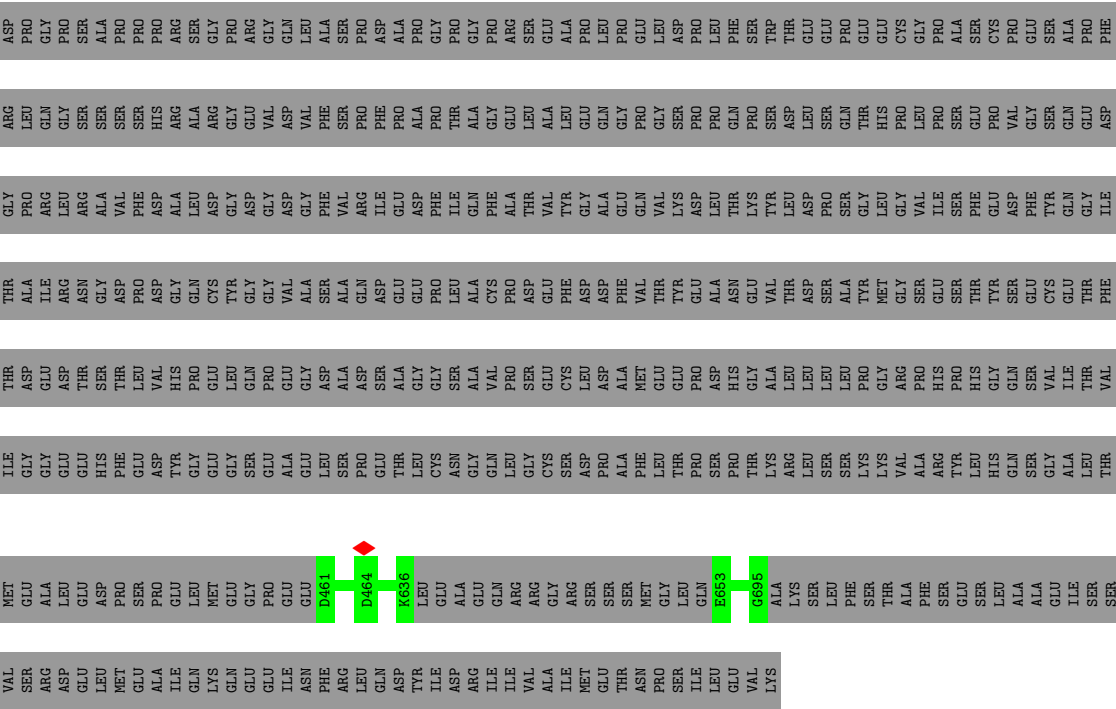
Mol	Chain	Residues	Atoms				AltConf	Trace
14	g	394	Total	C	N	O	0	0
			1947	1159	394	394		
14	h	396	Total	C	N	O	0	0
			1956	1164	396	396		
14	o	394	Total	C	N	O	0	0
			1946	1158	394	394		
14	p	401	Total	C	N	O	0	0
			1981	1179	401	401		

- Molecule 15 is a protein called Cytoplasmic dynein 1 light intermediate chain 2.

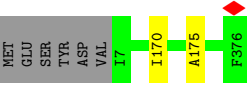
Mol	Chain	Residues	Atoms				AltConf	Trace
15	j	310	Total	C	N	O	0	0
			1535	915	310	310		
15	q	318	Total	C	N	O	0	0
			1574	938	318	318		
15	r	13	Total	C	N	O	0	0
			65	39	13	13		

- Molecule 16 is a protein called Dynein light chain roadblock-type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	s	93	Total	C	N	O	0	0
			462	276	93	93		
16	t	93	Total	C	N	O	0	0
			462	276	93	93		
16	w	93	Total	C	N	O	0	0
			462	276	93	93		
16	z	93	Total	C	N	O	0	0
			462	276	93	93		



• Molecule 2: ARP1 actin related protein 1 homolog A



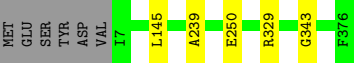
• Molecule 2: ARP1 actin related protein 1 homolog A



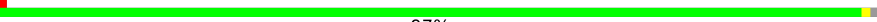
• Molecule 2: ARP1 actin related protein 1 homolog A



• Molecule 2: ARP1 actin related protein 1 homolog A

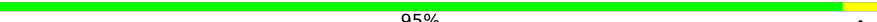


• Molecule 2: ARP1 actin related protein 1 homolog A

Chain E:  97%

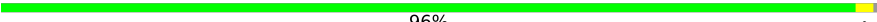


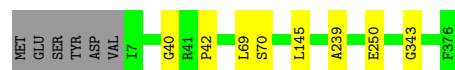
- Molecule 2: ARP1 actin related protein 1 homolog A

Chain F:  95%



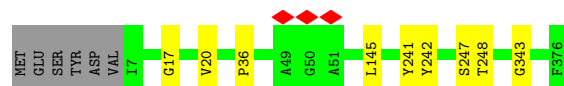
- Molecule 2: ARP1 actin related protein 1 homolog A

Chain G:  96%

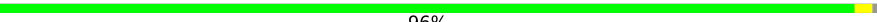


- Molecule 2: ARP1 actin related protein 1 homolog A

Chain I:  96%



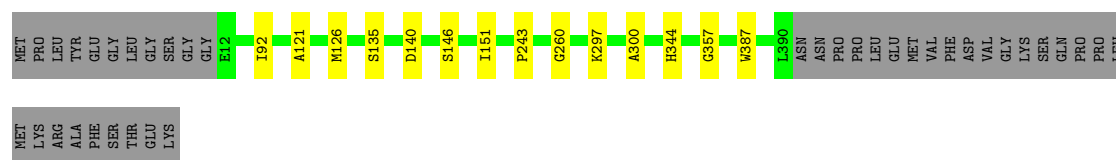
- Molecule 3: Actin, cytoplasmic 1

Chain H:  96%

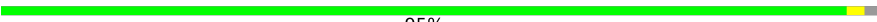


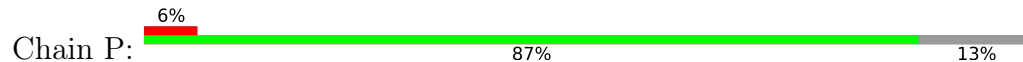
- Molecule 4: Arp11

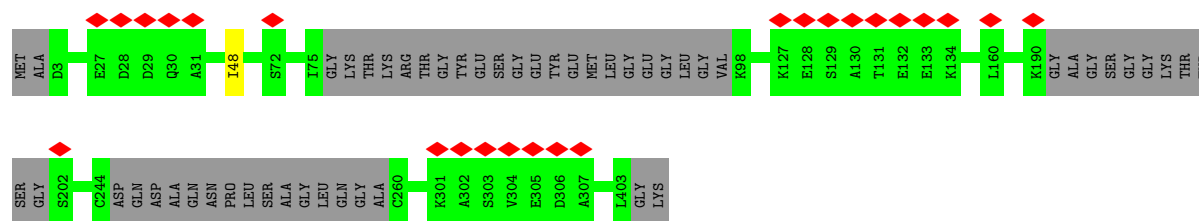
Chain J:  88%



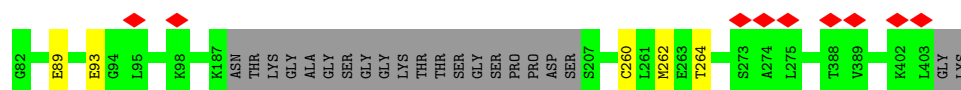
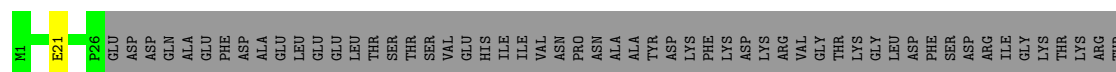
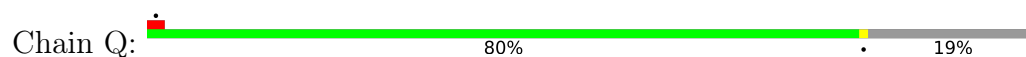
- Molecule 5: Capping protein (Actin filament) muscle Z-line, alpha 1

Chain K:  95%

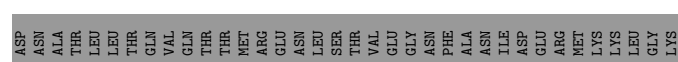
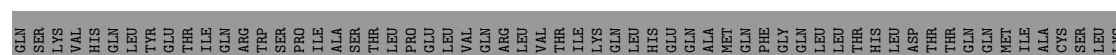
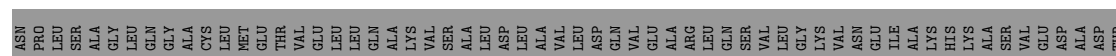
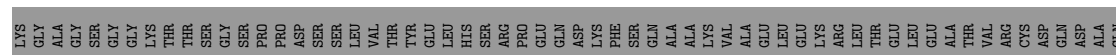
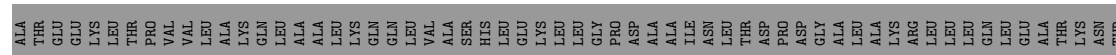
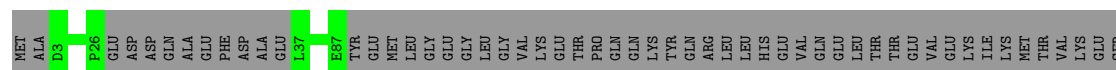




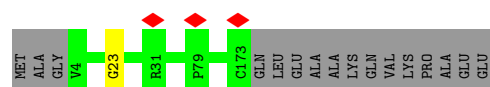
• Molecule 7: Dynactin subunit 2



• Molecule 7: Dynactin subunit 2



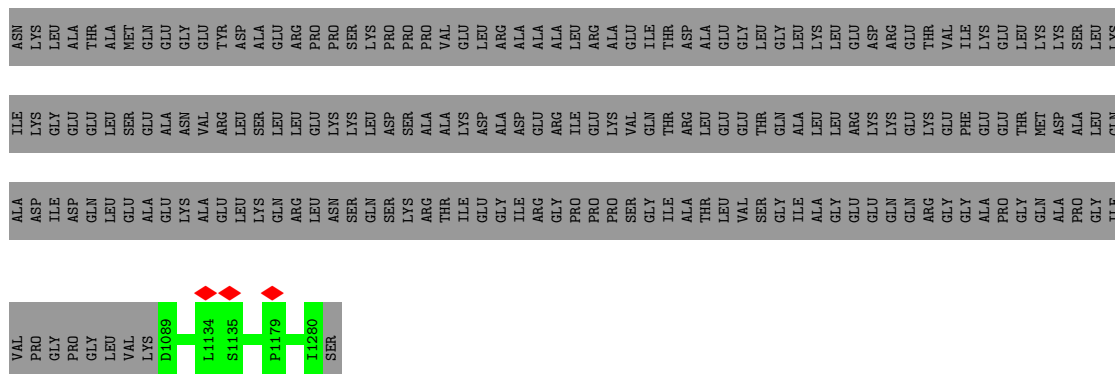
• Molecule 8: Dynactin subunit 3



• Molecule 8: Dynactin subunit 3

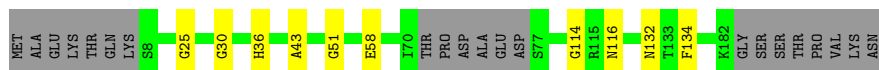


[illegible]



• Molecule 10: Dynactin 6

Chain U: 84% 5% 11%



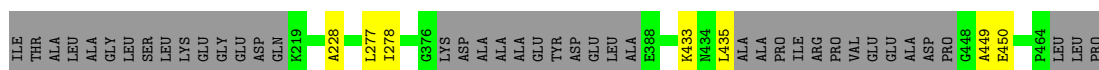
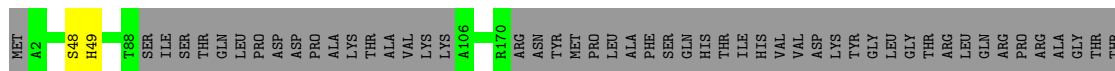
• Molecule 11: Dynactin subunit 5

Chain W: 92% 7% .



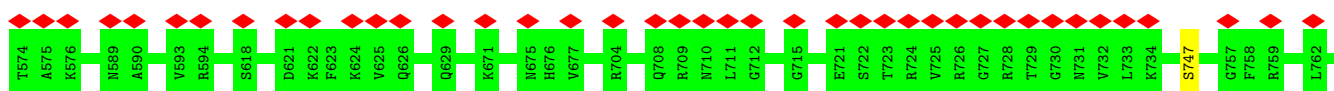
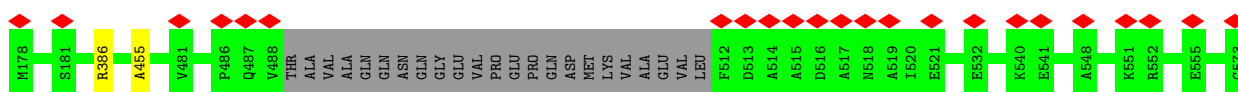
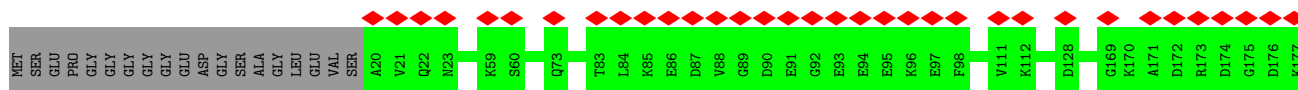
• Molecule 12: Dynactin subunit 4

Chain Y: 78% . 20%



• Molecule 13: Cytoplasmic dynein 1 heavy chain 1

Chain e: 19% 81%





















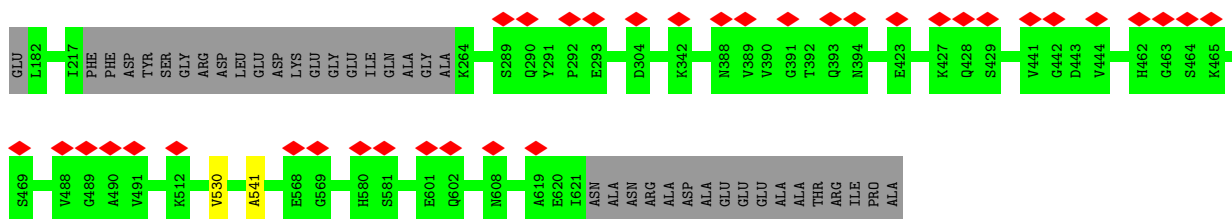






[illegible]

- Molecule 14: Isoform 2C of Cytoplasmic dynein 1 intermediate chain 2

[illegible]

- Molecule 14: Isoform 2C of Cytoplasmic dynein 1 intermediate chain 2



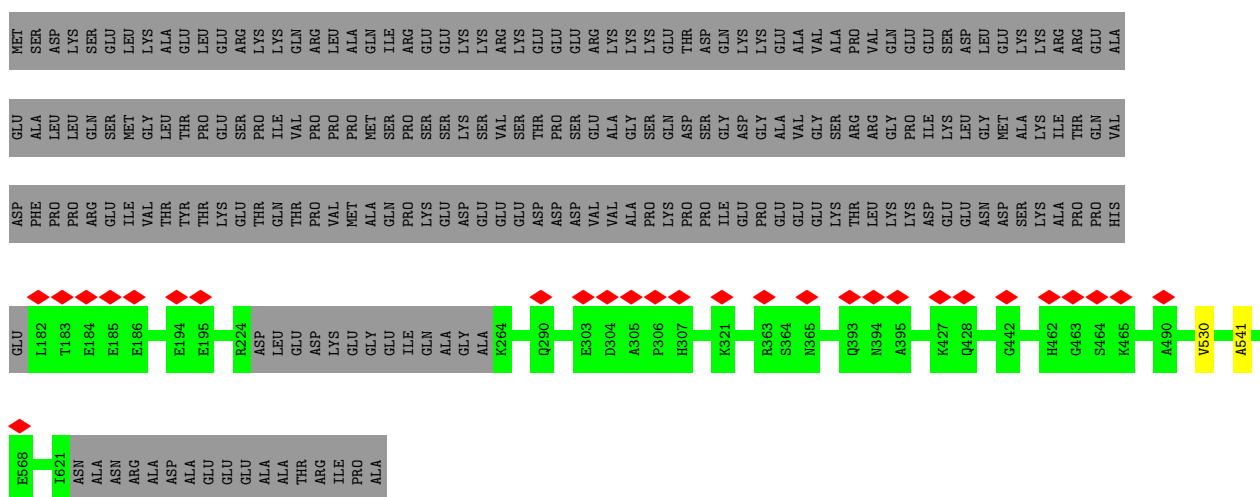
ALA	S409	GLU	ASP	GLU	ASP	GLU	MET
ALA	S421	LEU	PHE	LEU	PHE	ALA	SER
THR	S421	THR	PRO	THR	PRO	LEU	ASP
ARG	S452	GLU	ARG	GLU	ARG	LEU	SER
ILE	E452	GLU	ARG	GLU	GLN	GLN	SER
PRO	E453	GLU	ILE	GLU	GLU	MET	GLU
ALA	G454	K187	VAL	VAL	ILE	MET	LEU
	A459	Q188	THR	THR	THR	GLY	LYS
	A459	Q189	TYR	TYR	THR	LEU	ALA
	S469	I190	THR	THR	THR	GLU	GLU
	G477	S193	GLY	GLY	GLY	GLU	LEU
	A487	E194	THR	THR	THR	SER	ARG
	F502	E195	GLN	THR	GLN	PRO	LYS
	D503	G223	THR	PRO	VAL	VAL	GLN
	W504	R224	MET	VAL	MET	PRO	ALA
	T505	ASP	ALA	ALA	ALA	GLN	GLN
	V506	LEU	ILE	PRO	ILE	SER	ARG
	W509	GLU	LYS	LYS	GLU	GLU	GLU
	L517	GLY	GLY	GLY	SER	SER	GLU
	Y518	GLY	ASP	ASP	LYS	LYS	LYS
	SS19	GLU	GLU	GLU	GLN	VAL	ARG
	D529	ILE	GLU	GLU	GLU	SER	LYS
		GLN	ASP	THR	THR	GLU	GLU
	P537	ALA	ASP	ASP	PRO	GLU	GLU
	A538	GLY	ASP	ASP	GLU	SER	GLU
	L539	ALA	VAL	VAL	GLU	ARG	ARG
	C542	K264	VAL	VAL	ALA	LYS	LYS
	L549	N268	PRO	PRO	ALA	LYS	LYS
	D550	C284	LYS	LYS	GLN	SER	GLU
	W551	A297	PRO	PRO	ASP	THR	THR
	W552	L551	ILE	ILE	SER	ASP	ASP
	N555	W316	GLU	PRO	GLU	GLY	LYS
	P561	E326	GLU	GLU	GLU	ALA	GLU
	SS64	A341	LYS	GLU	VAL	VAL	VAL
	Y597	H344	THR	THR	SER	ALA	PRO
	G621	I357	LEU	LEU	ARG	VAL	VAL
	ASN	R372	LYS	LYS	GLY	GLN	GLN
	ALA	V384	ASP	ASP	ILE	GLU	GLU
	ASN	N388	GLU	ASN	LYS	LEU	SER
	ARG	L398	ASP	ASP	GLY	ASP	GLU
	ALA	S402	SER	SER	MET	LEU	LEU
	ASP		ALA	ALA	GLY	GLY	GLU
	ALA		LYS	LYS	ILE	ASP	GLU
	GLU		ALA	ILE	THR	THR	ARG
	GLU		PRO	THR	GLU	GLU	ALA
	GLU		PRO	THR	VAL	VAL	ALA

- Molecule 14: Isoform 2C of Cytoplasmic dynein 1 intermediate chain 2

36%

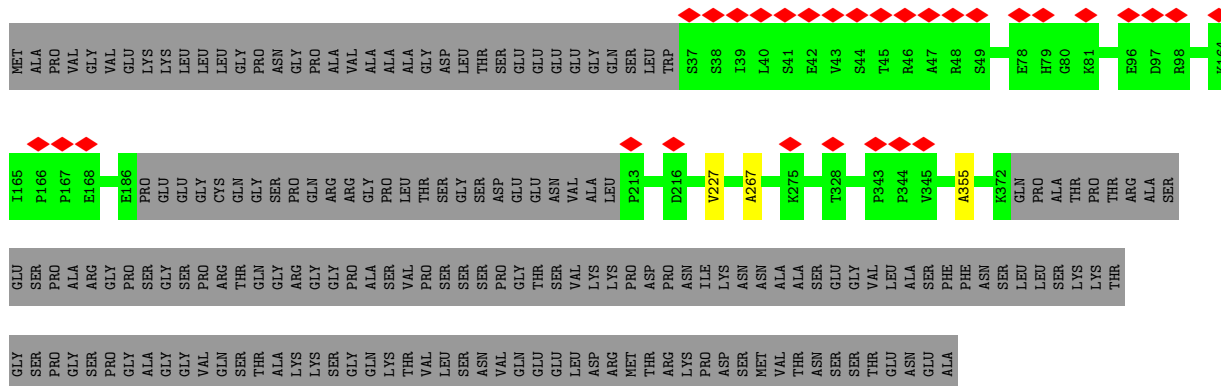
- Molecule 14: Isoform 2C of Cytoplasmic dynein 1 intermediate chain 2

34%

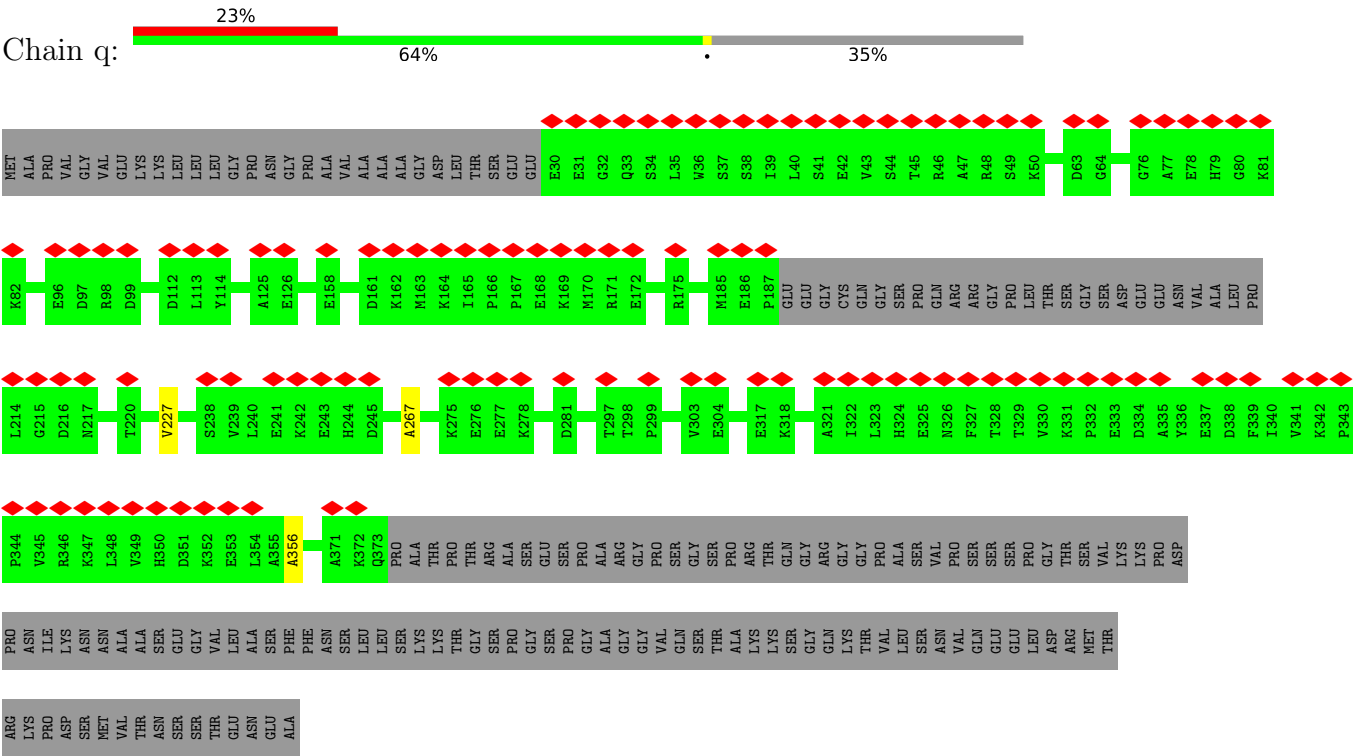


- Molecule 15: Cytoplasmic dynein 1 light intermediate chain 2

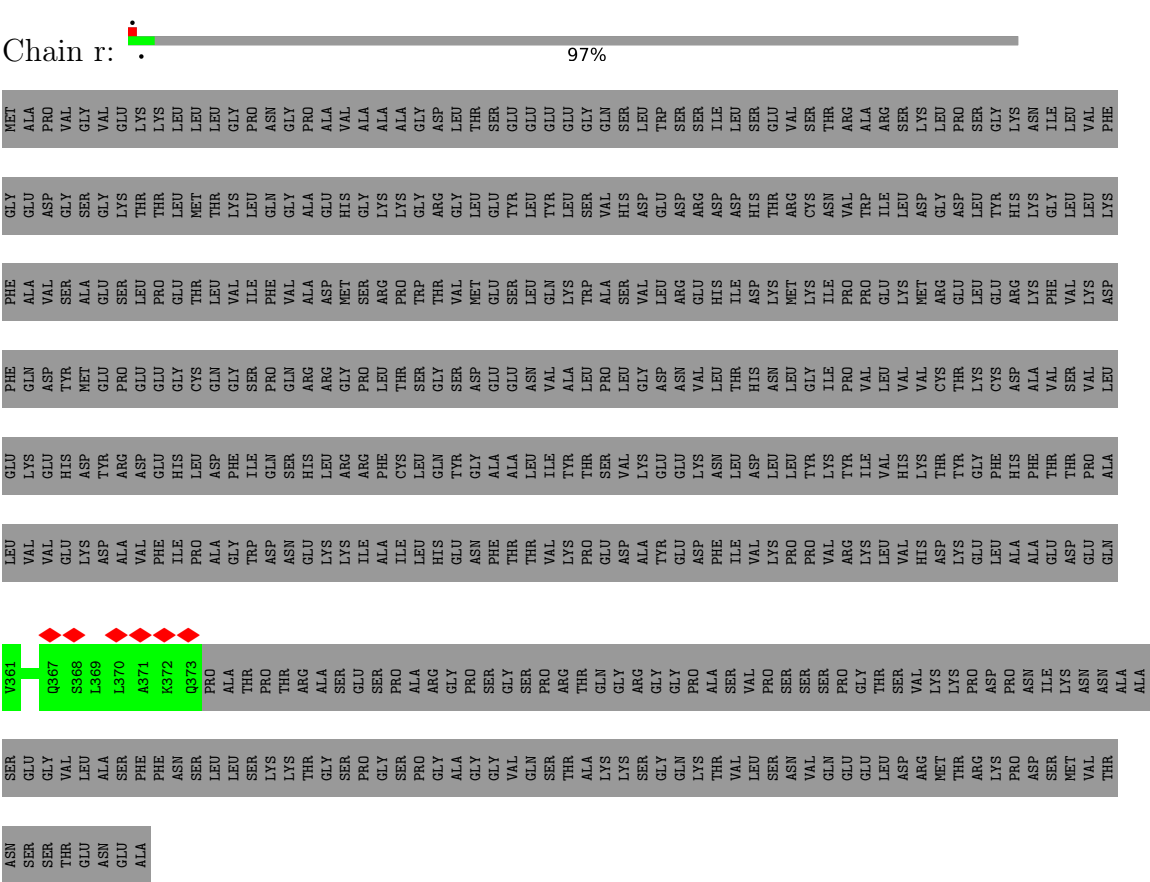
37%



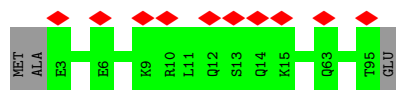
• Molecule 15: Cytoplasmic dynein 1 light intermediate chain 2



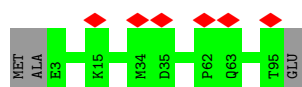
• Molecule 15: Cytoplasmic dynein 1 light intermediate chain 2



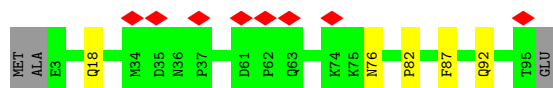
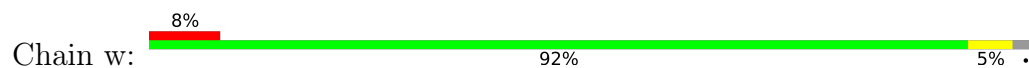
- Molecule 16: Dynein light chain roadblock-type 1



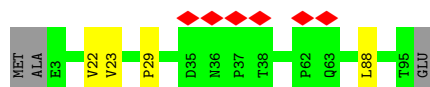
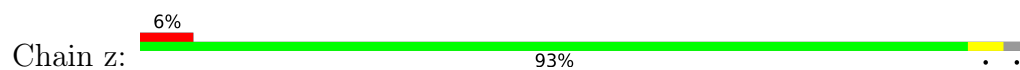
- Molecule 16: Dynein light chain roadblock-type 1



- Molecule 16: Dynein light chain roadblock-type 1



- Molecule 16: Dynein light chain roadblock-type 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	159084	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	881.39996, 881.39996, 881.39996	wwPDB
Map dimensions	678, 678, 678	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	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	1	0.29	0/1173	0.28	0/1635
1	2	0.29	0/1089	0.29	0/1519
2	A	0.23	0/1821	0.31	0/2531
2	B	0.27	0/1821	0.34	0/2531
2	C	0.27	0/1846	0.34	0/2566
2	D	0.27	0/1821	0.36	0/2531
2	E	0.28	0/1821	0.34	0/2531
2	F	0.31	0/1821	0.37	0/2531
2	G	0.26	0/1821	0.33	0/2531
2	I	0.30	0/1821	0.35	0/2531
3	H	0.32	0/1821	0.36	0/2531
4	J	0.33	0/1867	0.36	0/2596
5	K	0.23	0/1377	0.31	0/1919
6	L	0.25	0/1326	0.29	0/1844
7	M	0.17	0/1196	0.23	0/1664
7	N	0.17	0/1304	0.25	0/1813
7	P	0.20	0/1753	0.28	0/2443
7	Q	0.23	0/1629	0.32	0/2268
7	V	0.19	0/367	0.30	0/507
8	O	0.19	0/843	0.33	0/1175
8	R	0.20	0/887	0.32	0/1236
9	S	0.19	0/662	0.26	0/917
9	T	0.22	0/951	0.26	0/1325
10	U	0.24	0/830	0.31	0/1151
11	W	0.26	0/880	0.33	0/1222
12	Y	0.27	0/1858	0.36	0/2586
13	e	0.18	0/4385	0.28	0/6116
13	f	0.32	0/5438	0.32	0/7583
13	m	0.28	0/5330	0.31	0/7432
13	n	0.19	0/4321	0.28	0/6026
14	g	0.10	0/1945	0.26	0/2706
14	h	0.43	0/1954	0.44	0/2718
14	o	0.17	0/1944	0.31	0/2704
14	p	0.09	0/1979	0.26	0/2753

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	j	0.14	0/1533	0.23	0/2134
15	q	0.09	0/1572	0.25	0/2188
15	r	0.08	0/64	0.14	0/88
16	s	0.15	0/461	0.29	0/642
16	t	0.15	0/461	0.28	0/642
16	w	0.11	0/461	0.27	0/642
16	z	0.12	0/461	0.29	0/642
All	All	0.25	0/68715	0.31	0/95650

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 ⓘ

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	1	1176	0	508	0	0
1	2	1091	0	466	0	0
2	A	1822	0	820	1	0
2	B	1822	0	820	4	0
2	C	1847	0	830	3	0
2	D	1822	0	820	3	0
2	E	1822	0	820	3	0
2	F	1822	0	820	8	0
2	G	1822	0	820	4	0
2	I	1822	0	820	5	0
3	H	1822	0	835	5	0
4	J	1868	0	823	8	0
5	K	1378	0	611	3	0
6	L	1327	0	585	1	0
7	M	1201	0	545	1	0
7	N	1310	0	590	1	0
7	P	1757	0	789	1	0
7	Q	1632	0	752	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	V	369	0	158	0	0
8	O	844	0	385	1	0
8	R	888	0	413	1	0
9	S	667	0	285	0	0
9	T	952	0	434	0	0
10	U	832	0	371	5	0
11	W	881	0	379	6	0
12	Y	1863	0	794	5	0
13	e	4387	0	1950	3	0
13	f	5440	0	2412	5	0
13	m	5333	0	2365	7	0
13	n	4324	0	1921	3	0
14	g	1947	0	873	1	0
14	h	1956	0	878	23	0
14	o	1946	0	872	4	0
14	p	1981	0	888	1	0
15	j	1535	0	673	2	0
15	q	1574	0	689	2	0
15	r	65	0	28	0	0
16	s	462	0	192	0	0
16	t	462	0	192	0	0
16	w	462	0	192	3	0
16	z	462	0	192	2	0
All	All	68795	0	30610	116	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 1.

All (116) 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)
14:h:459:ALA:HA	14:h:469:SER:H	1.32	0.92
2:B:325:ASP:HA	7:Q:93:GLU:CB	2.05	0.87
13:f:806:ALA:HB1	15:j:355:ALA:HA	1.57	0.85
3:H:42:GLY:HA3	4:J:387:TRP:HA	1.67	0.75
4:J:344:HIS:HA	12:Y:228:ALA:HA	1.69	0.74
14:h:398:LEU:O	14:h:409:SER:HA	1.91	0.70
2:F:334:GLN:HA	7:N:13:ALA:HB3	1.75	0.68
2:B:329:ARG:CB	7:Q:89:GLU:HA	2.24	0.66
2:E:145:LEU:O	2:E:343:GLY:HA3	1.97	0.65
13:m:673:TRP:O	13:m:679:GLY:HA3	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:f:804:LEU:HA	13:f:894:SER:O	1.99	0.62
14:h:357:ILE:O	14:h:372:ARG:HA	1.99	0.62
3:H:140:LEU:O	3:H:342:GLY:HA3	2.00	0.61
2:I:145:LEU:O	2:I:343:GLY:HA3	2.01	0.60
4:J:92:ILE:HA	4:J:121:ALA:HB3	1.84	0.60
2:D:329:ARG:HA	7:Q:21:GLU:HA	1.82	0.59
12:Y:433:LYS:HA	12:Y:450:GLU:HA	1.84	0.59
14:h:487:ALA:HB3	14:h:537:PRO:HA	1.85	0.58
11:W:7:LEU:HA	11:W:177:LEU:O	2.04	0.58
16:z:22:VAL:HA	16:z:88:LEU:HA	1.87	0.57
2:A:170:ILE:HA	2:A:175:ALA:HA	1.87	0.57
4:J:126:MET:O	4:J:357:GLY:HA3	2.05	0.56
13:m:806:ALA:HA	15:q:356:ALA:HB2	1.88	0.55
2:B:145:LEU:O	2:B:343:GLY:HA3	2.06	0.54
2:G:145:LEU:O	2:G:343:GLY:HA3	2.08	0.54
10:U:114:GLY:HA3	10:U:132:ASN:HA	1.88	0.54
12:Y:435:LEU:H	12:Y:449:ALA:HB1	1.73	0.54
16:z:23:VAL:HA	16:z:29:PRO:HA	1.91	0.53
13:f:716:ARG:HA	13:f:823:VAL:HA	1.91	0.52
14:h:384:VAL:HA	14:h:402:SER:HA	1.92	0.52
11:W:53:ALA:HB1	11:W:84:PRO:HA	1.92	0.52
12:Y:48:SER:O	12:Y:278:ILE:HA	2.10	0.52
2:F:145:LEU:O	2:F:343:GLY:HA3	2.10	0.51
2:C:145:LEU:O	2:C:343:GLY:HA3	2.11	0.51
14:h:284:CYS:O	14:h:297:ALA:HA	2.10	0.51
2:E:200:LYS:O	2:F:117:PRO:HA	2.11	0.50
4:J:135:SER:HA	4:J:151:ILE:O	2.10	0.50
4:J:243:PRO:O	4:J:260:GLY:HA3	2.11	0.50
7:Q:262:MET:C	7:Q:264:THR:H	2.19	0.50
5:K:94:ILE:HA	5:K:110:PRO:HA	1.93	0.50
11:W:38:GLY:HA3	11:W:59:ARG:HA	1.92	0.50
15:j:227:VAL:O	15:j:267:ALA:HA	2.12	0.50
5:K:66:LYS:HA	5:K:73:GLN:HA	1.94	0.49
10:U:30:GLY:HA3	10:U:51:GLY:O	2.12	0.49
2:D:145:LEU:O	2:D:343:GLY:HA3	2.12	0.49
14:h:268:ASN:H	14:h:597:TYR:HA	1.76	0.49
14:h:509:TRP:HA	14:h:517:LEU:H	1.77	0.49
14:h:529:ASP:O	14:h:542:CYS:HA	2.13	0.49
14:o:284:CYS:O	14:o:297:ALA:HA	2.12	0.49
14:o:384:VAL:HA	14:o:402:SER:HA	1.94	0.49
11:W:58:GLY:HA3	11:W:89:ASP:HA	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:242:TYR:HA	2:F:247:SER:O	2.13	0.48
14:h:452:GLU:C	14:h:454:GLY:H	2.21	0.48
14:h:539:LEU:HA	14:h:552:TRP:O	2.14	0.47
14:h:506:VAL:O	14:h:519:SER:HA	2.15	0.47
3:H:237:GLU:HA	3:H:251:GLY:HA2	1.98	0.46
10:U:116:ASN:O	10:U:134:PHE:HA	2.14	0.46
13:m:40:LEU:HA	13:m:45:GLY:HA2	1.98	0.46
13:m:537:ASP:CB	13:m:542:GLY:HA3	2.45	0.46
13:n:673:TRP:O	13:n:679:GLY:HA3	2.16	0.46
5:K:141:CYS:HA	5:K:157:CYS:O	2.16	0.45
14:h:477:GLY:HA3	14:h:503:ASP:N	2.31	0.45
14:h:502:PHE:C	14:h:504:TRP:H	2.24	0.45
10:U:25:GLY:HA3	10:U:43:ALA:HB3	1.99	0.45
11:W:96:ASP:O	11:W:113:ASN:HA	2.17	0.45
2:I:242:TYR:HA	2:I:247:SER:O	2.17	0.45
6:L:166:HIS:HA	6:L:200:ASP:HA	1.99	0.45
14:h:549:LEU:O	14:h:564:SER:HA	2.16	0.45
2:G:40:GLY:HA2	2:G:70:SER:O	2.16	0.44
16:w:82:PRO:HA	16:w:87:PHE:HA	2.00	0.44
2:G:42:PRO:HA	2:G:69:LEU:HA	1.99	0.44
2:D:239:ALA:O	2:D:250:GLU:HA	2.17	0.44
2:F:108:VAL:O	2:F:137:LEU:HA	2.17	0.44
10:U:36:HIS:CB	10:U:58:GLU:H	2.30	0.44
14:o:341:ALA:HB3	14:o:344:HIS:O	2.17	0.44
13:f:537:ASP:CB	13:f:542:GLY:HA3	2.48	0.44
4:J:297:LYS:O	4:J:300:ALA:HB3	2.17	0.44
3:H:36:GLY:HA2	3:H:66:THR:O	2.18	0.43
11:W:60:HIS:O	11:W:90:HIS:HA	2.18	0.43
14:h:407:ILE:O	14:h:421:SER:HA	2.18	0.43
13:m:138:LEU:HA	13:n:137:VAL:O	2.18	0.43
15:q:227:VAL:O	15:q:267:ALA:HA	2.17	0.43
2:I:241:TYR:O	2:I:248:THR:HA	2.19	0.43
2:I:17:GLY:HA3	2:I:20:VAL:O	2.17	0.43
13:f:964:ILE:HA	13:f:968:VAL:O	2.19	0.43
13:e:386:ARG:HA	13:e:455:ALA:HB3	2.00	0.43
2:E:17:GLY:H	2:E:21:ILE:HA	1.83	0.42
3:H:150:GLY:HA2	3:H:293:LEU:HA	2.01	0.42
14:h:341:ALA:HB3	14:h:344:HIS:O	2.19	0.42
13:m:470:ARG:O	13:m:471:ARG:C	2.62	0.42
2:C:333:PRO:HA	7:P:48:ILE:O	2.20	0.42
14:p:530:VAL:HA	14:p:541:ALA:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:161:GLY:O	2:F:186:ALA:HB1	2.20	0.42
7:M:262:MET:H	8:R:21:VAL:HA	1.84	0.42
14:h:459:ALA:HA	14:h:469:SER:N	2.15	0.42
2:B:129:PHE:O	2:B:133:ASN:HA	2.19	0.42
16:w:76:ASN:HA	16:w:92:GLN:O	2.20	0.42
2:I:20:VAL:HA	2:I:36:PRO:HA	2.00	0.42
14:g:530:VAL:HA	14:g:541:ALA:O	2.18	0.42
14:h:388:ASN:O	14:h:398:LEU:HA	2.19	0.42
2:F:129:PHE:O	2:F:133:ASN:HA	2.20	0.42
14:o:357:ILE:O	14:o:372:ARG:HA	2.19	0.42
13:e:747:SER:HA	13:e:768:ALA:HB1	2.01	0.41
13:m:137:VAL:O	13:n:138:LEU:HA	2.19	0.41
2:C:239:ALA:O	2:C:250:GLU:HA	2.20	0.41
14:h:551:LEU:O	14:h:561:PRO:HA	2.20	0.41
12:Y:49:HIS:HA	12:Y:277:LEU:O	2.20	0.41
8:O:23:GLY:HA2	7:Q:260:CYS:O	2.21	0.41
16:w:18:GLN:H	16:w:92:GLN:HA	1.86	0.41
13:e:804:LEU:HA	13:e:893:TYR:HA	2.03	0.40
14:h:538:ALA:HB1	14:h:555:ASN:H	1.86	0.40
2:G:239:ALA:O	2:G:250:GLU:HA	2.21	0.40
14:h:452:GLU:C	14:h:454:GLY:N	2.79	0.40
4:J:140:ASP:O	4:J:146:SER:HA	2.21	0.40
2:F:241:TYR:O	2:F:248:THR:HA	2.21	0.40
14:h:316:TRP:HA	14:h:326:GLU:H	1.87	0.40

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	1	230/793 (29%)	230 (100%)	0	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	215/793 (27%)	215 (100%)	0	0	100	100
2	A	368/376 (98%)	356 (97%)	12 (3%)	0	100	100
2	B	368/376 (98%)	358 (97%)	10 (3%)	0	100	100
2	C	373/376 (99%)	358 (96%)	15 (4%)	0	100	100
2	D	368/376 (98%)	355 (96%)	13 (4%)	0	100	100
2	E	368/376 (98%)	354 (96%)	14 (4%)	0	100	100
2	F	368/376 (98%)	354 (96%)	14 (4%)	0	100	100
2	G	368/376 (98%)	355 (96%)	13 (4%)	0	100	100
2	I	368/376 (98%)	352 (96%)	16 (4%)	0	100	100
3	H	368/375 (98%)	355 (96%)	13 (4%)	0	100	100
4	J	377/417 (90%)	362 (96%)	15 (4%)	0	100	100
5	K	276/286 (96%)	266 (96%)	10 (4%)	0	100	100
6	L	267/272 (98%)	262 (98%)	5 (2%)	0	100	100
7	M	231/405 (57%)	229 (99%)	2 (1%)	0	100	100
7	N	251/405 (62%)	249 (99%)	2 (1%)	0	100	100
7	P	345/405 (85%)	334 (97%)	11 (3%)	0	100	100
7	Q	323/405 (80%)	316 (98%)	7 (2%)	0	100	100
7	V	71/405 (18%)	68 (96%)	3 (4%)	0	100	100
8	O	168/186 (90%)	158 (94%)	10 (6%)	0	100	100
8	R	177/186 (95%)	166 (94%)	11 (6%)	0	100	100
9	S	124/1281 (10%)	121 (98%)	2 (2%)	1 (1%)	16	54
9	T	190/1281 (15%)	186 (98%)	4 (2%)	0	100	100
10	U	165/190 (87%)	157 (95%)	8 (5%)	0	100	100
11	W	177/182 (97%)	170 (96%)	7 (4%)	0	100	100
12	Y	365/467 (78%)	342 (94%)	23 (6%)	0	100	100
13	e	880/4646 (19%)	860 (98%)	20 (2%)	0	100	100
13	f	1093/4646 (24%)	1071 (98%)	22 (2%)	0	100	100
13	m	1069/4646 (23%)	1059 (99%)	10 (1%)	0	100	100
13	n	865/4646 (19%)	854 (99%)	11 (1%)	0	100	100
14	g	390/612 (64%)	387 (99%)	3 (1%)	0	100	100
14	h	392/612 (64%)	378 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	o	390/612 (64%)	377 (97%)	13 (3%)	0	100	100
14	p	397/612 (65%)	392 (99%)	5 (1%)	0	100	100
15	j	306/492 (62%)	304 (99%)	2 (1%)	0	100	100
15	q	314/492 (64%)	310 (99%)	4 (1%)	0	100	100
15	r	11/492 (2%)	11 (100%)	0	0	100	100
16	s	91/96 (95%)	81 (89%)	10 (11%)	0	100	100
16	t	91/96 (95%)	87 (96%)	4 (4%)	0	100	100
16	w	91/96 (95%)	86 (94%)	5 (6%)	0	100	100
16	z	91/96 (95%)	76 (84%)	15 (16%)	0	100	100
All	All	13740/34634 (40%)	13361 (97%)	378 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	S	1137	PRO

5.3.2 Protein sidechains [i](#)

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

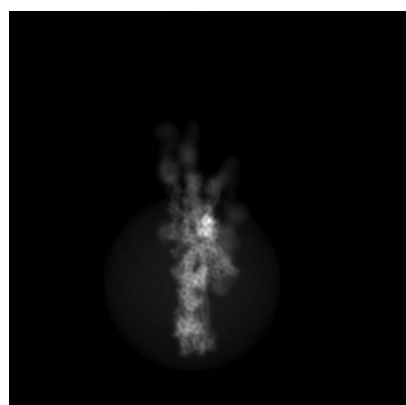
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-57643. These allow visual inspection of the internal detail of the map and identification of artifacts.

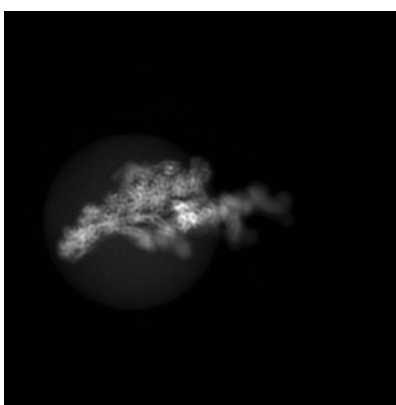
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

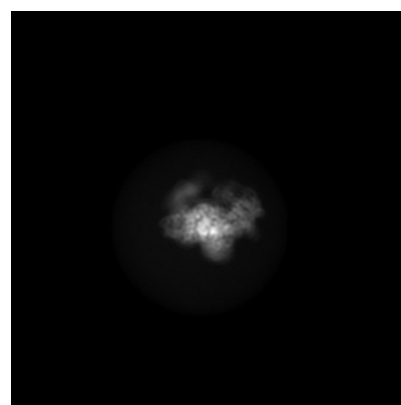
6.1.1 Primary map



X



Y

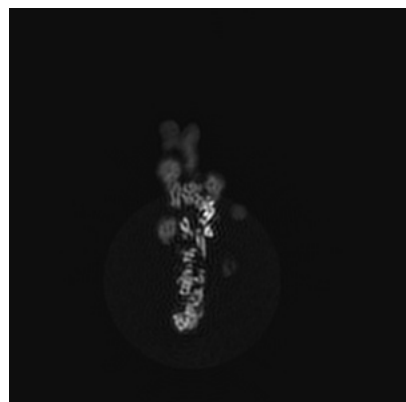


Z

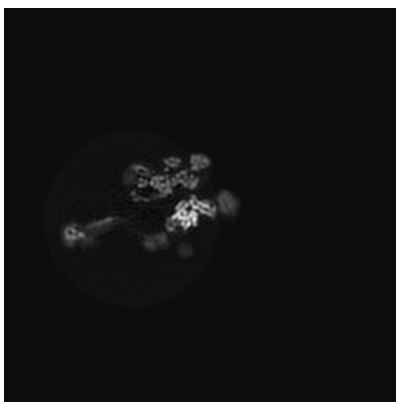
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

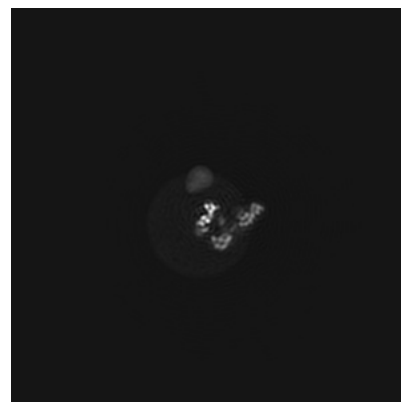
6.2.1 Primary map



X Index: 339



Y Index: 339

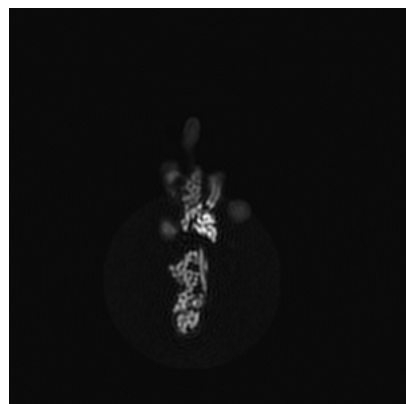


Z Index: 339

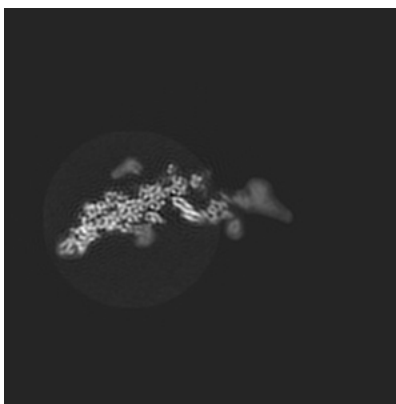
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

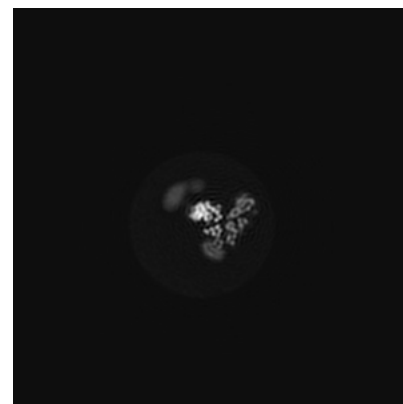
6.3.1 Primary map



X Index: 328



Y Index: 302

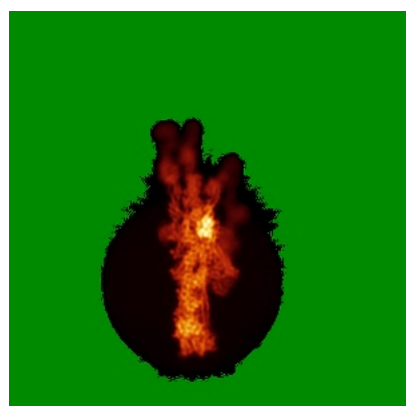


Z Index: 304

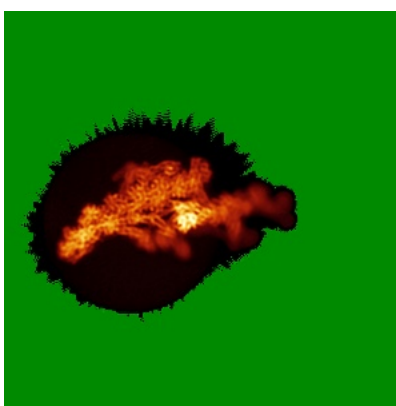
The images above show the largest variance slices of the map in three orthogonal directions.

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

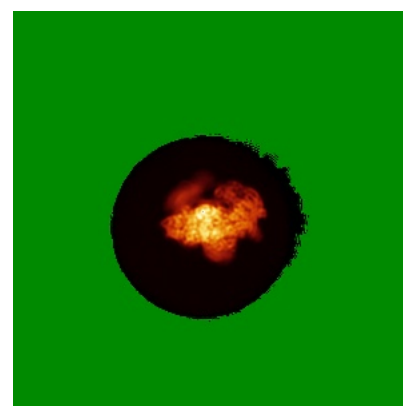
6.4.1 Primary map



X



Y



Z

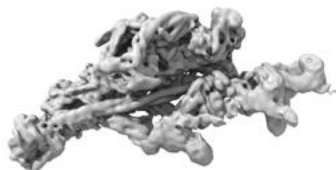
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

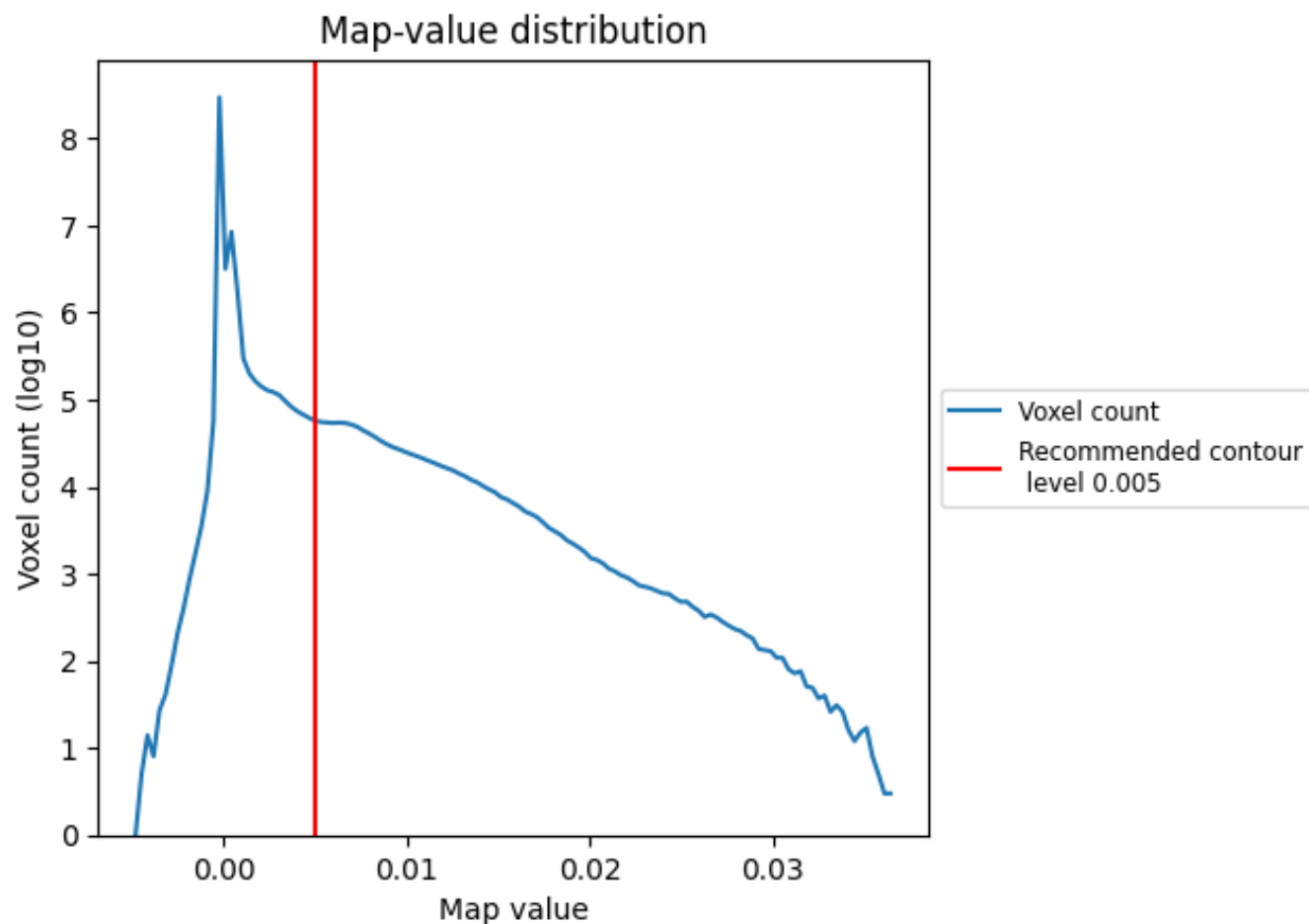
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

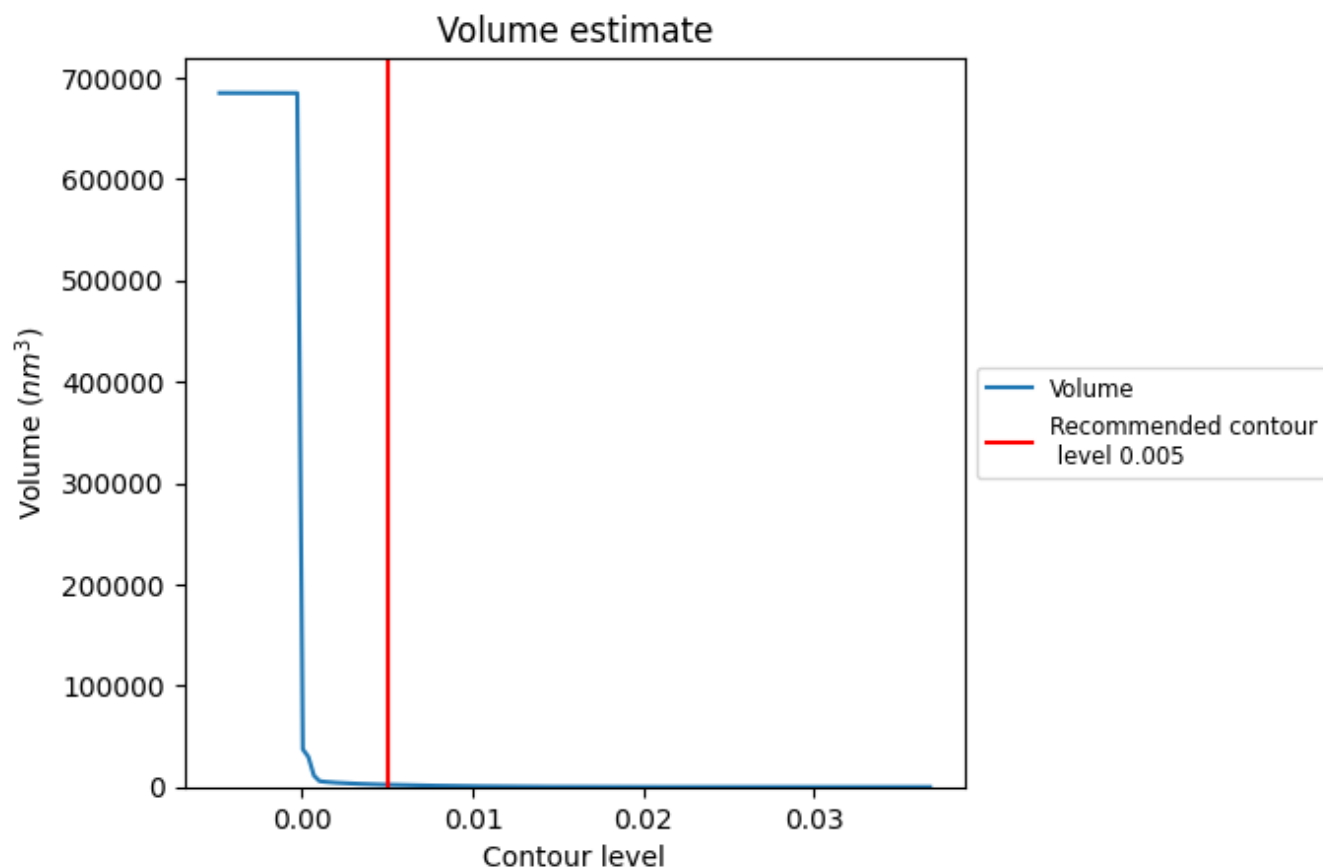
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

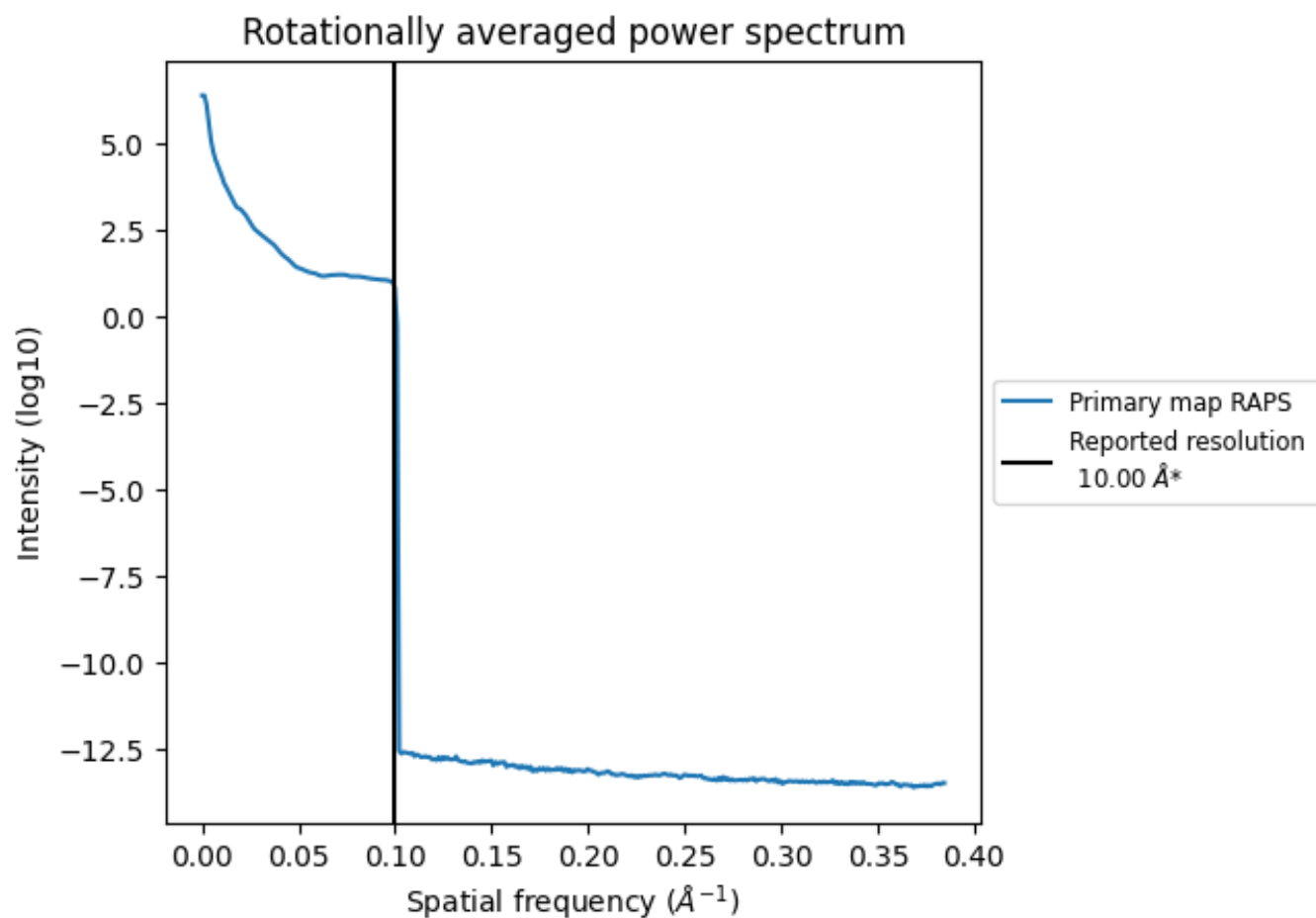
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2225 nm^3 ; this corresponds to an approximate mass of 2010 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 Å⁻¹

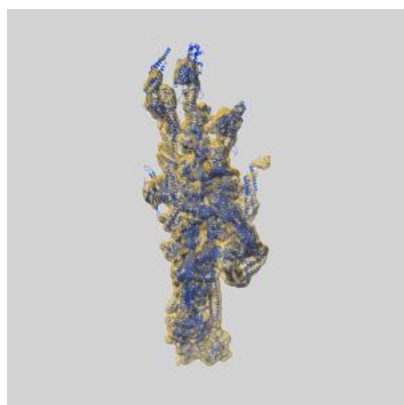
8 Fourier-Shell correlation

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

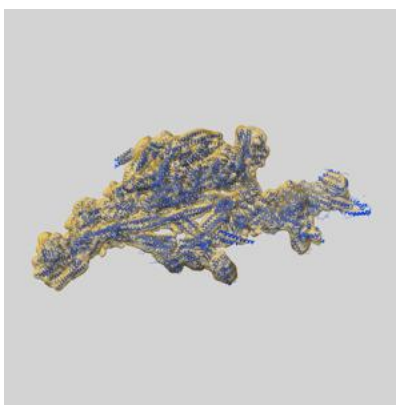
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-57643 and PDB model 30DR. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

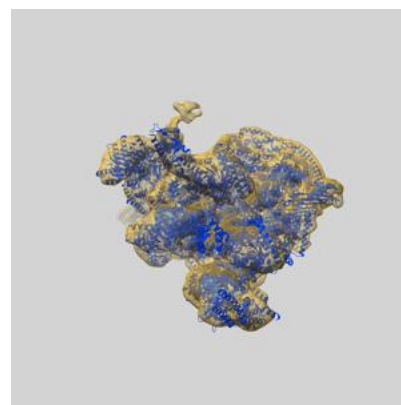
9.1 Map-model overlay [i](#)



X



Y



Z

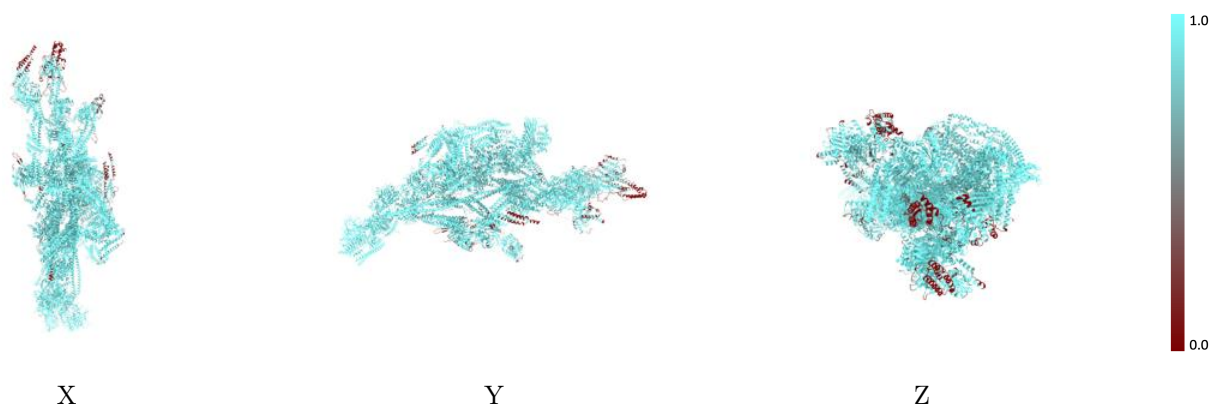
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



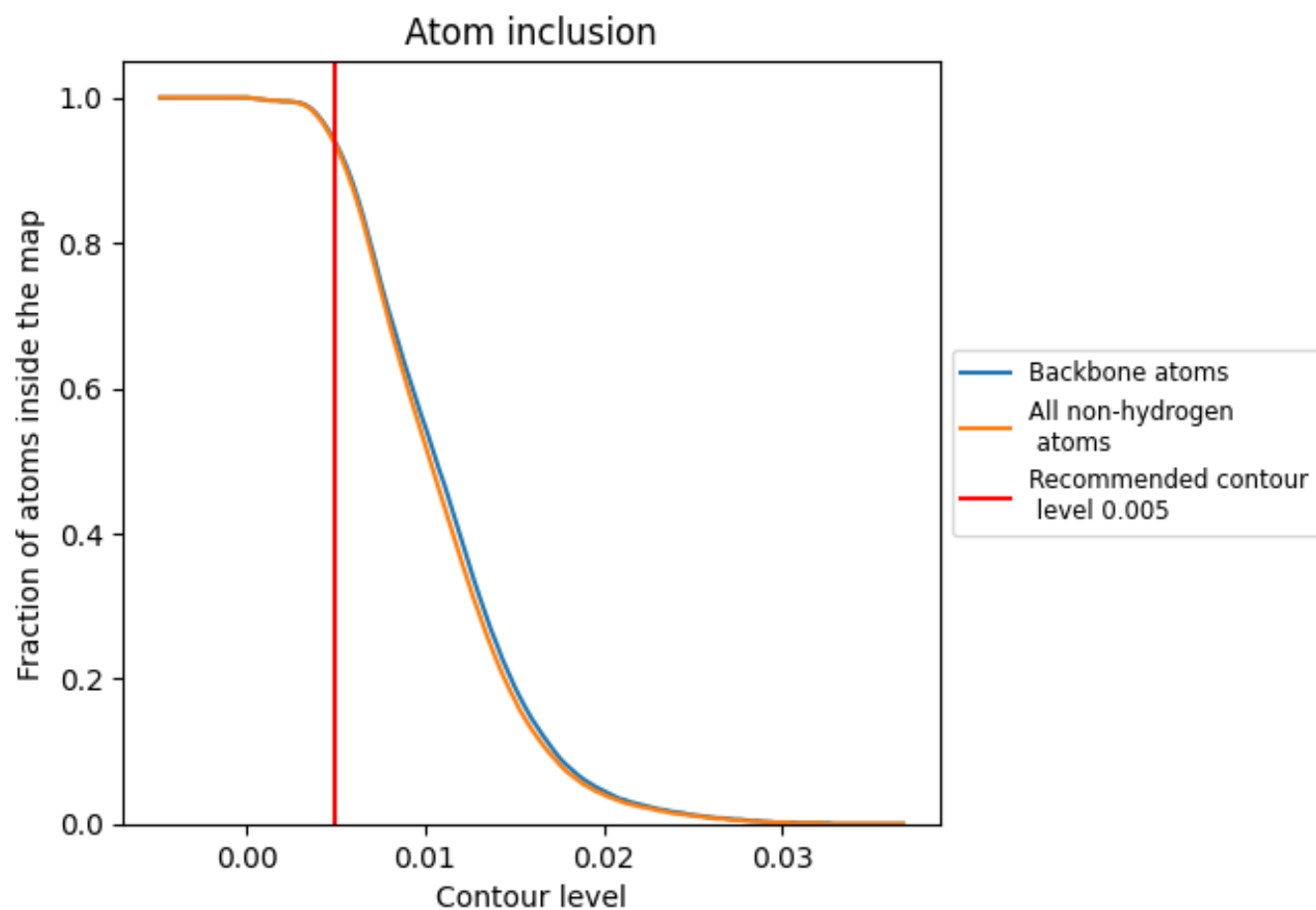
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9350	 0.2060
1	 0.9860	 0.2810
2	 0.9950	 0.2790
A	 0.9970	 0.2340
B	 0.9990	 0.2350
C	 0.9980	 0.2220
D	 0.9980	 0.2310
E	 0.9950	 0.2300
F	 0.9970	 0.2350
G	 0.9980	 0.2270
H	 1.0000	 0.2330
I	 0.9920	 0.2320
J	 1.0000	 0.2300
K	 0.9960	 0.2380
L	 0.9990	 0.2380
M	 0.9510	 0.2390
N	 0.9010	 0.2290
O	 0.9760	 0.2080
P	 0.9230	 0.2310
Q	 0.9610	 0.2350
R	 0.9760	 0.2340
S	 0.9810	 0.2100
T	 0.9780	 0.2250
U	 0.9990	 0.2180
V	 1.0000	 0.2320
W	 1.0000	 0.2200
Y	 1.0000	 0.2320
e	 0.7970	 0.1390
f	 0.9160	 0.2120
g	 0.9070	 0.0970
h	 0.9810	 0.1990
j	 0.8950	 0.1460
m	 0.8570	 0.2080
n	 0.8760	 0.2070
o	 0.9900	 0.1930



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Chain	Atom inclusion	Q-score
p	 0.9190	 0.1330
q	 0.6370	 0.0930
r	 0.5380	 0.1660
s	 0.8960	 0.1630
t	 0.9350	 0.1960
w	 0.8960	 0.1310
z	 0.9330	 0.1060