



# wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 11:48 AM UTC

PDB ID : 8CH6 / pdb\_00008ch6  
EMDB ID : EMD-16658  
Title : Structure of a late-stage activated spliceosome (BAqr) arrested with a dominant-negative Aquarius mutant (state B complex).  
Authors : Cretu, C.; Schmitzova, J.; Pena, V.  
Deposited on : 2023-02-07  
Resolution : 5.90 Å (reported)  
Based on initial models : 5Z57, 6FF7, 6FF4

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

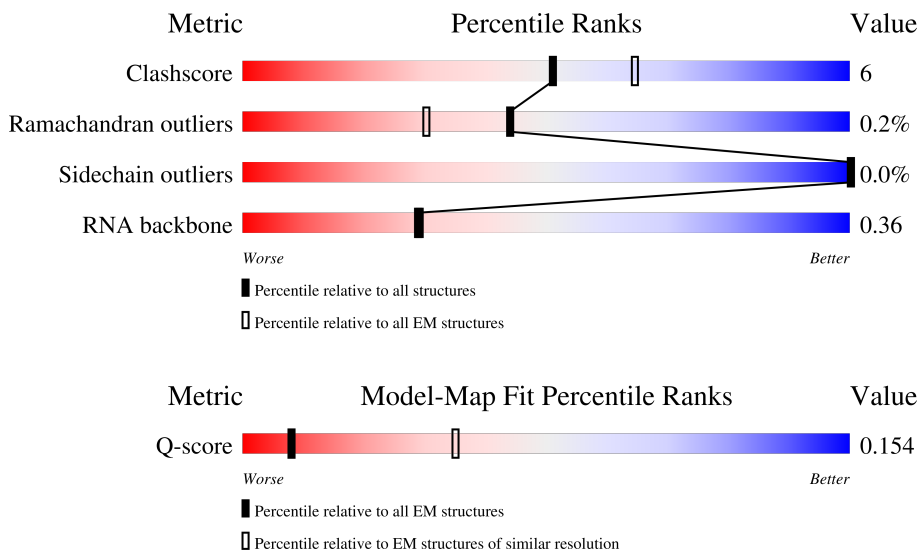
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 5.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





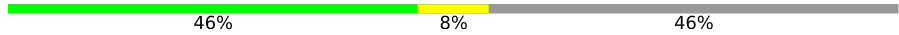






















Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	501 ( 5.40 - 6.40 )

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  $\geq 3$ , 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	92	85% (green), 14% (grey), 1% (yellow), 1% (orange), 1% (red)
1	i	92	72% (green), 24% (grey), 2% (yellow), 2% (orange), 2% (red)
2	2	86	76% (green), 10% (yellow), 14% (grey)

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Mol	Chain	Length	Quality of chain
2	h	86	
3	3	126	
3	j	126	
4	4	118	
4	l	118	
5	5	119	
5	k	119	
6	8	240	
6	n	240	
7	9	76	
7	m	76	
8	A	1217	
9	B	86	
10	C	1304	
11	D	110	
12	E	895	
13	F	424	
14	G	476	
15	H	793	
16	I	464	
17	J	501	
18	K	504	
18	M	504	
18	R	504	
18	v	504	







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Mol	Chain	Length	Quality of chain
19	L	619	5% 95%
20	N	1041	61% 15% 24%
21	O	514	48% 14% 38%
22	P	802	11% 35% 6% 59%
23	Q	229	33% 10% 56%
24	S	225	36% 60% 11% 29%
25	T	144	81% 18% .
26	U	420	55% 15% 30%
27	V	492	51% 6% 42%
28	W	908	47% . 49%
29	X	848	27% . 72%
30	Y	536	49% 7% 43%
31	Z	343	26% . 72%
32	a	2335	78% 15% 7%
33	b	972	74% 18% 8%
34	c	2136	7% 80% . 19%
35	d	106	42% 41% 6% 12%
36	e	117	45% 34% . 16%
37	f	188	50% 19% . 27%
38	g	319	11% 10% . 76%
39	o	357	64% 20% 16%
40	p	166	89% 7% .
41	q	2752	. 97%
42	r	255	. 64% 36%
43	s	225	6% 72% . 27%

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Mol	Chain	Length	Quality of chain
44	t	285	 14% 83%
45	u	520	 63% 7% 29%
46	w	301	 69% 5% 26%
47	x	579	 61% 37%
48	y	1485	 13% 77% 13% 11%
49	z	855	 19% 76% 19%

## 2 Entry composition [i](#)

There are 53 unique types of molecules in this entry. The entry contains 119058 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 Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	1	79	391	233	79	79	0	0
1	i	70	346	206	70	70	0	0

- Molecule 2 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	2	74	361	213	74	74	0	0
2	h	66	322	190	66	66	0	0

- Molecule 3 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	3	76	373	221	76	76	0	0
3	j	68	335	199	68	68	0	0

- Molecule 4 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	4	85	422	252	85	85	0	0
4	l	68	337	201	68	68	0	0

- Molecule 5 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	5	82	Total	C	N	O	0	0
			406	242	82	82		
5	k	78	Total	C	N	O	0	0
			388	232	78	78		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	8	86	Total	C	N	O	0	0
			422	250	86	86		
6	n	64	Total	C	N	O	0	0
			315	187	64	64		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	9	68	Total	C	N	O	0	0
			334	198	68	68		
7	m	63	Total	C	N	O	0	0
			309	183	63	63		

- Molecule 8 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	A	1158	Total	C	N	O	0	0
			5714	3398	1158	1158		

- Molecule 9 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	B	70	Total	C	N	O	0	0
			350	210	70	70		

- Molecule 10 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	815	Total	C	N	O	S	0	0
			5115	3242	928	930	15		

- Molecule 11 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	D	89	649	399	117	120	13	0	0

- Molecule 12 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	E	198	1350	855	249	241	5	0	0

- Molecule 13 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	F	78	383	227	78	78	0	0

- Molecule 14 is a protein called G-patch domain and KOW motifs-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	G	67	364	228	68	68	0	0

- Molecule 15 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	H	106	530	318	106	106	0	0

- Molecule 16 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	I	185	1034	620	215	197	2	0	0

- Molecule 17 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	J	410	2187	1326	431	426	4	0	0

- Molecule 18 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	118	Total	C	N	O	S	0	0
			938	586	167	181	4		
18	M	125	Total	C	N	O	S	0	0
			988	618	176	190	4		
18	R	118	Total	C	N	O	S	0	0
			938	586	167	181	4		
18	v	125	Total	C	N	O	S	0	0
			988	618	176	190	4		

- Molecule 19 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	28	Total	C	N	O	S	0	0
			177	111	32	32	2		

- Molecule 20 is a protein called Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	791	Total	C	N	O	S	0	0
			6147	3893	1089	1137	28		

- Molecule 21 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	320	Total	C	N	O	S	0	0
			2517	1592	457	460	8		

- Molecule 22 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	330	Total	C	N	O	S	0	0
			2432	1522	446	454	10		

- Molecule 23 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	100	Total	C	N	O	S	0	0
			823	509	161	151	2		

- Molecule 24 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	S	159	1323	820	246	248	9	0	0

- Molecule 25 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	T	142	1176	741	216	208	11	0	0

- Molecule 26 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	U	295	2080	1290	380	392	18	0	0

- Molecule 27 is a protein called Peptidyl-prolyl cis-trans isomerase-like 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	V	285	1996	1252	338	396	10	0	0

- Molecule 28 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	W	459	2921	1817	533	559	12	0	0

- Molecule 29 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	X	241	1587	1017	298	270	2	0	0

- Molecule 30 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Y	306	2250	1412	411	417	10	0	0

- Molecule 31 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	95	Total	C	N	O	S	0	0
			607	378	109	117	3		

- Molecule 32 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	2183	Total	C	N	O	S	0	0
			16415	10472	2956	2922	65		

- Molecule 33 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	898	Total	C	N	O	S	0	0
			7046	4513	1172	1327	34		

- Molecule 34 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	1722	Total	C	N	O		0	0
			8530	5086	1722	1722			

- Molecule 35 is a RNA chain called RNU6-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	93	Total	C	N	O	P	0	0
			1989	889	364	643	93		

- Molecule 36 is a RNA chain called RNU5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	98	Total	C	N	O	P	0	0
			2070	926	347	699	98		

- Molecule 37 is a RNA chain called RNU2-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	137	Total	C	N	O	P	0	0
			2906	1298	501	970	137		

- Molecule 38 is a RNA chain called MINX-M3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
38	g	76	1559	697	250	536	76	0	0

- Molecule 39 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	o	299	2338	1470	410	445	13	0	0

- Molecule 40 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	p	159	776	457	159	160	0	0

- Molecule 41 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	q	74	461	285	89	85	2	0	0

- Molecule 42 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	N			O
42	r	162	804	480	162	162	0	0

- Molecule 43 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	N			O
43	s	165	813	483	165	165	0	0

- Molecule 44 is a protein called Pre-mRNA-splicing factor ISY1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	t	48	407	261	64	81	1	0	0

- Molecule 45 is a protein called RING-type E3 ubiquitin-protein ligase PPIL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	u	367	1963	1181	382	399	1	0	0

- Molecule 46 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	w	224	1093	645	224	224	0	0

- Molecule 47 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	x	362	1787	1063	362	362	0	0

- Molecule 48 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	y	1327	10878	6988	1871	1965	54	0	0

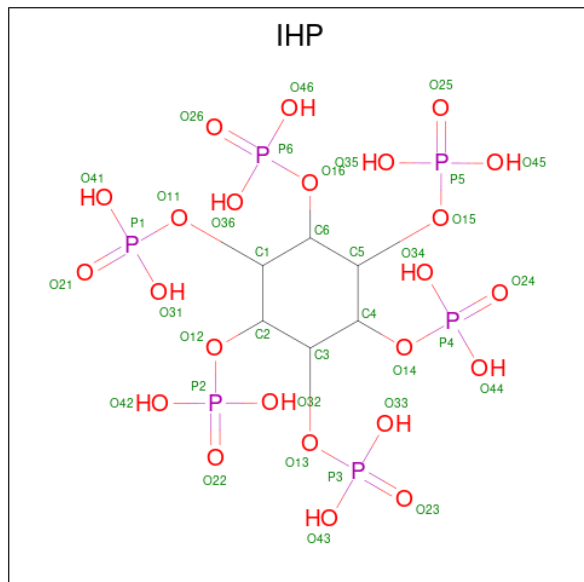
- Molecule 49 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	z	692	4511	2853	837	807	14	0	0

- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn).

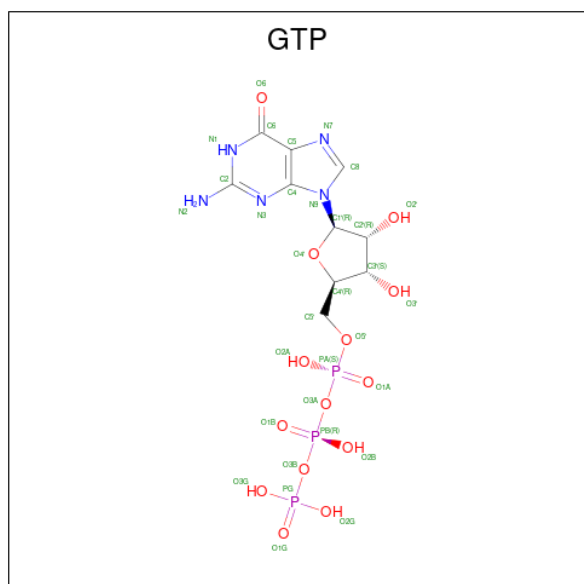
Mol	Chain	Residues	Atoms		AltConf
50	D	3	Total	Zn	0
			3	3	
50	I	1	Total	Zn	0
			1	1	
50	J	1	Total	Zn	0
			1	1	
50	T	3	Total	Zn	0
			3	3	
50	U	3	Total	Zn	0
			3	3	
50	Z	1	Total	Zn	0
			1	1	

- Molecule 51 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula:  $C_6H_{18}O_{24}P_6$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
51	a	1	36	6	24	6	0

- Molecule 52 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	b	1	32	10	5	14	3	0

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	b	1	Total 1	Mg 1	0
53	d	6	Total 6	Mg 6	0















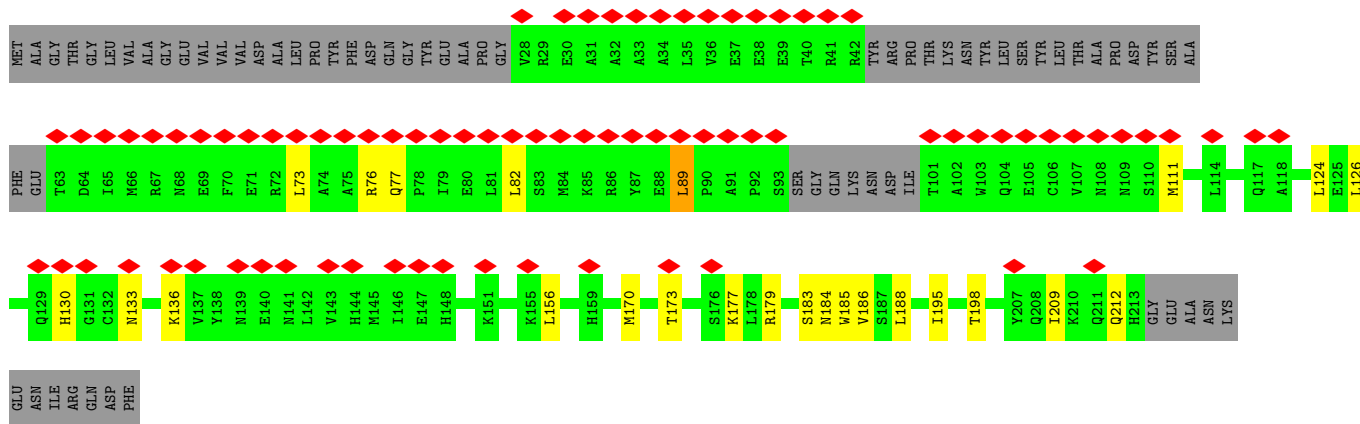




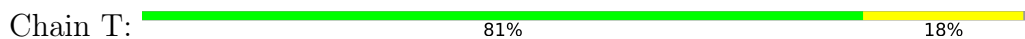




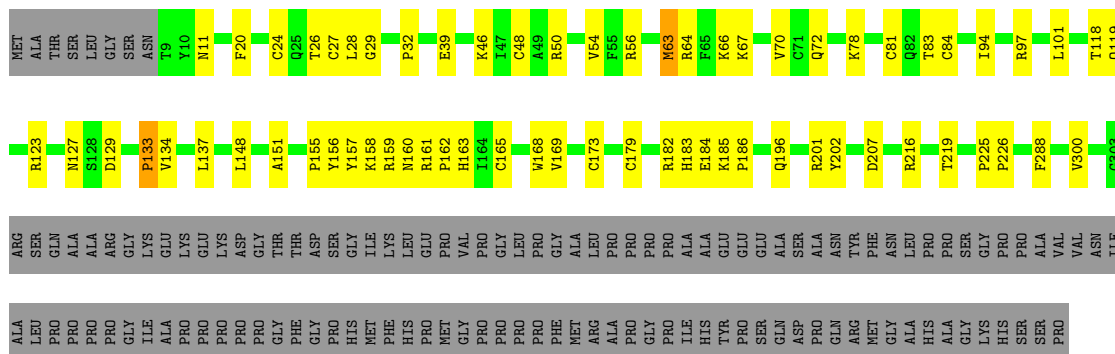




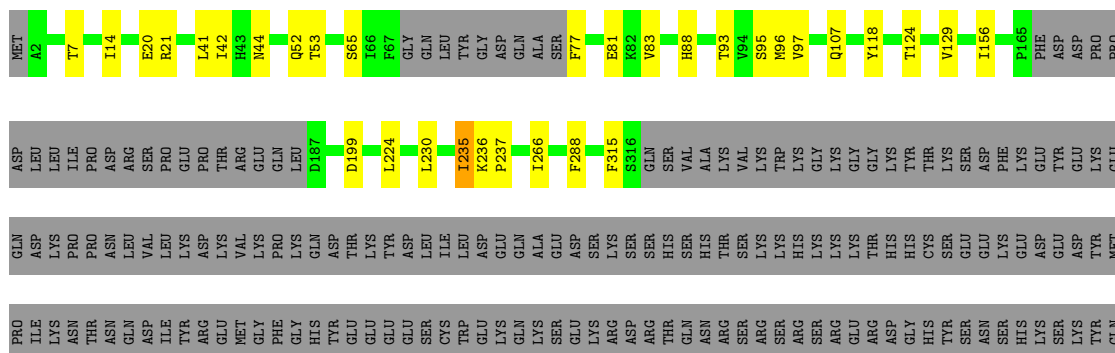
• Molecule 25: Protein BUD31 homolog



• Molecule 26: Pre-mRNA-splicing factor RBM22



• Molecule 27: Peptidyl-prolyl cis-trans isomerase-like 4

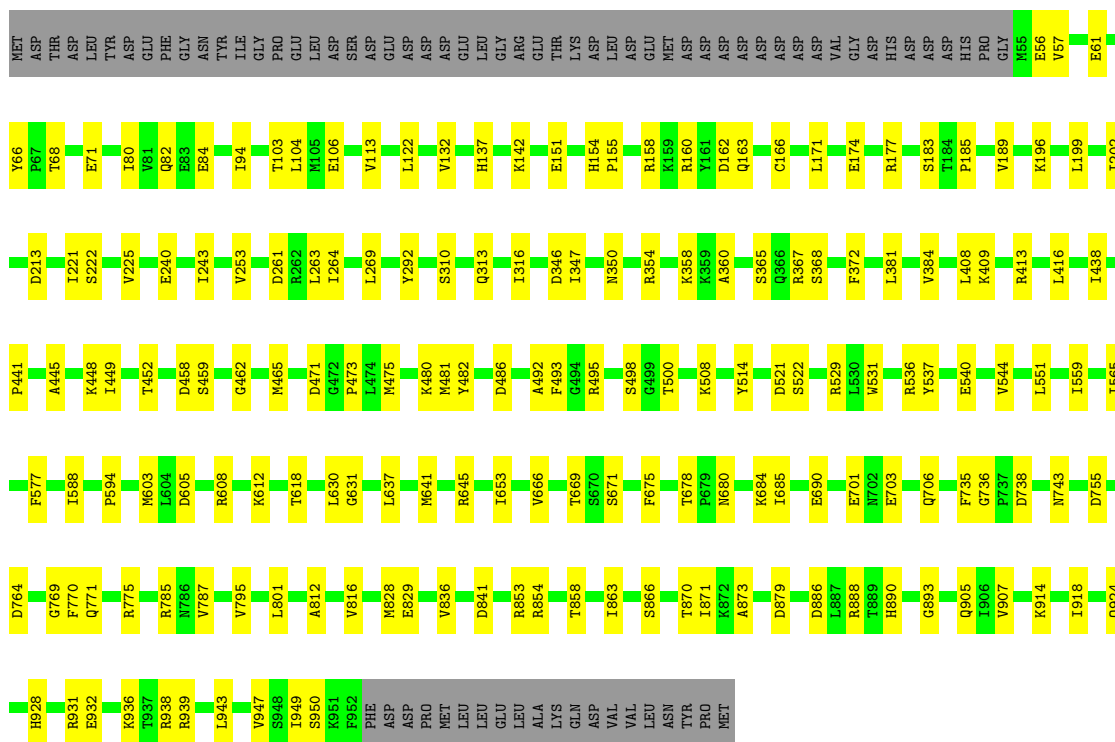






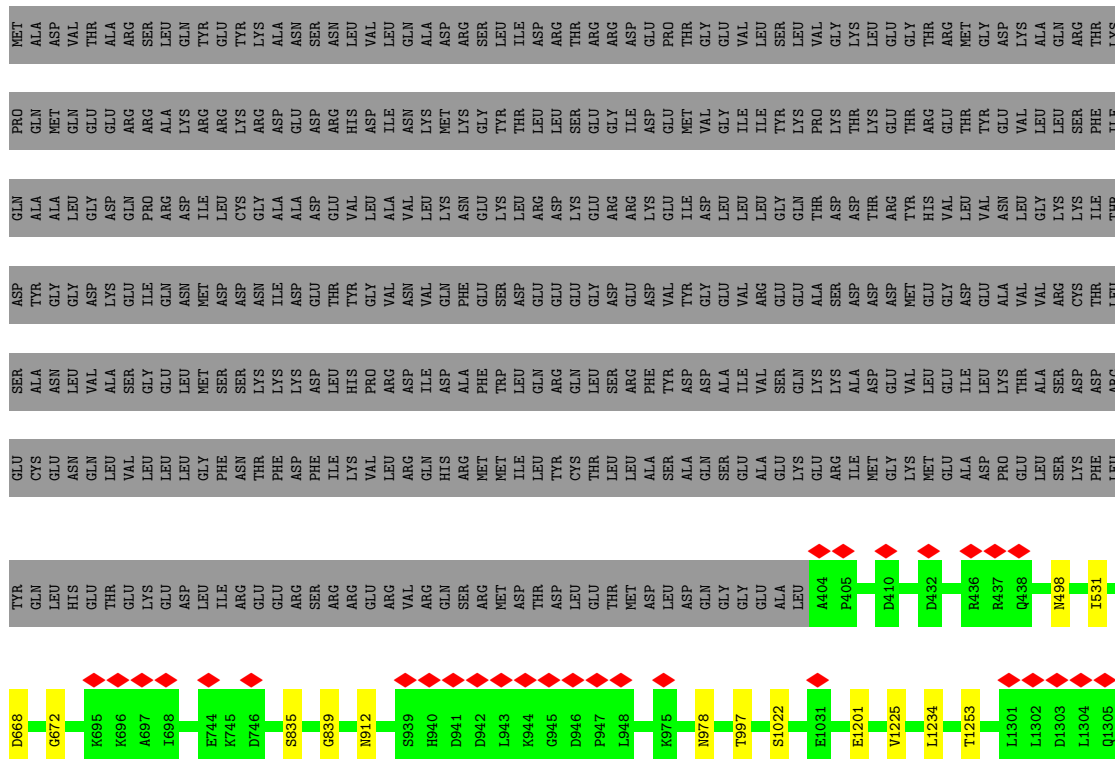


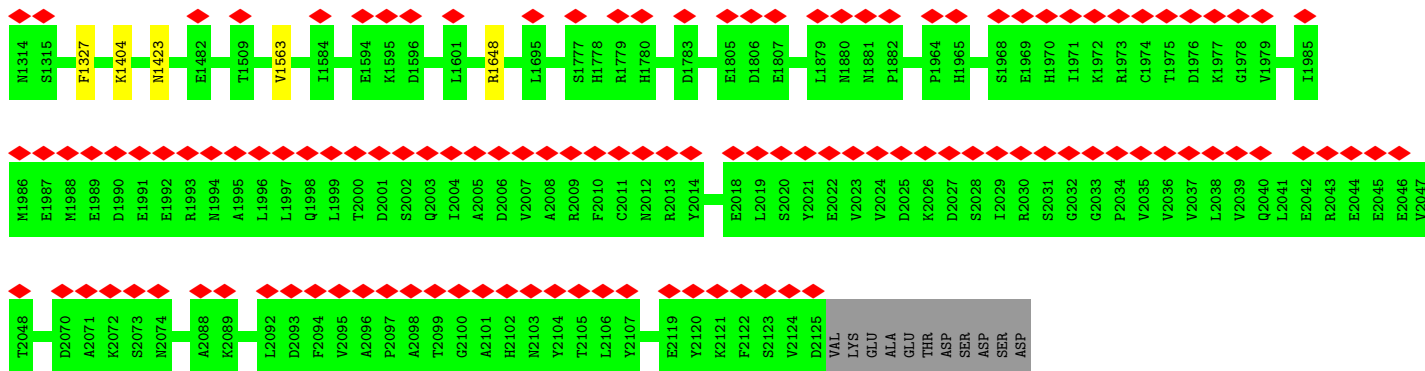
Chain b: 74% 18% 8%



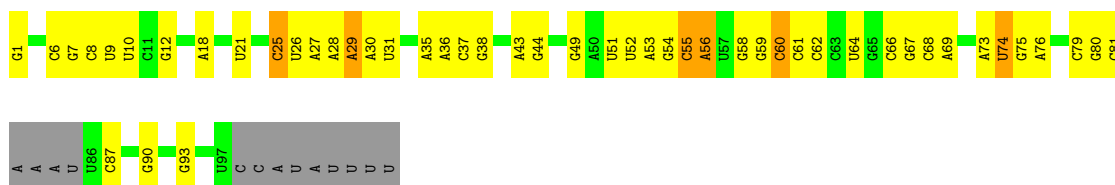
• Molecule 34: U5 small nuclear ribonucleoprotein 200 kDa helicase

Chain c: 7% 80% 19%

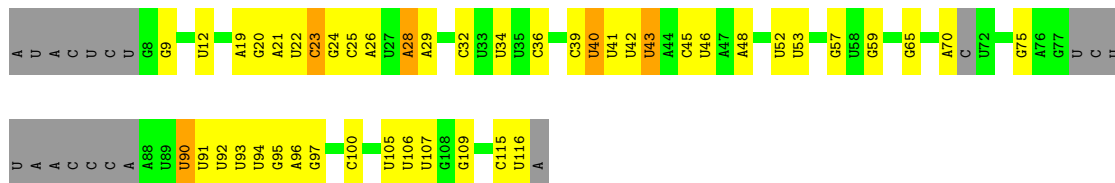




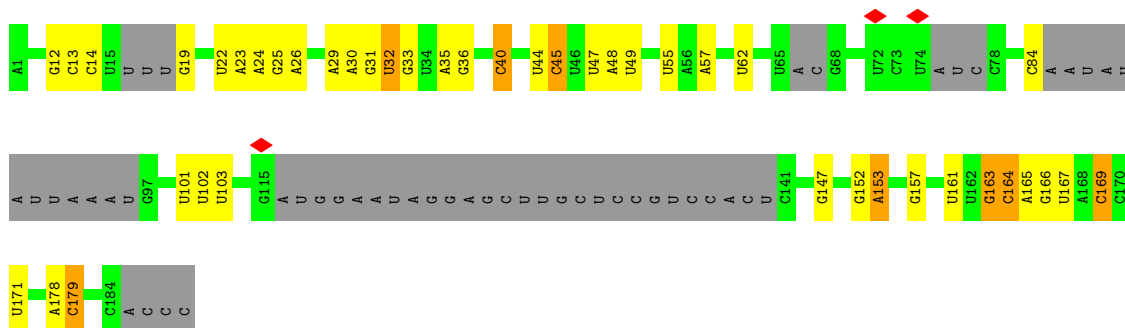
• Molecule 35: RNU6-1



• Molecule 36: RNU5A-1

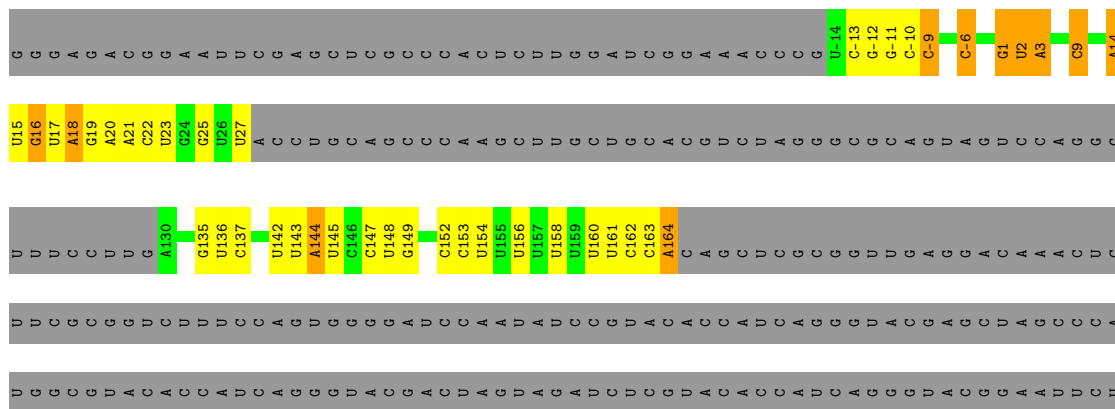


• Molecule 37: RNU2-1

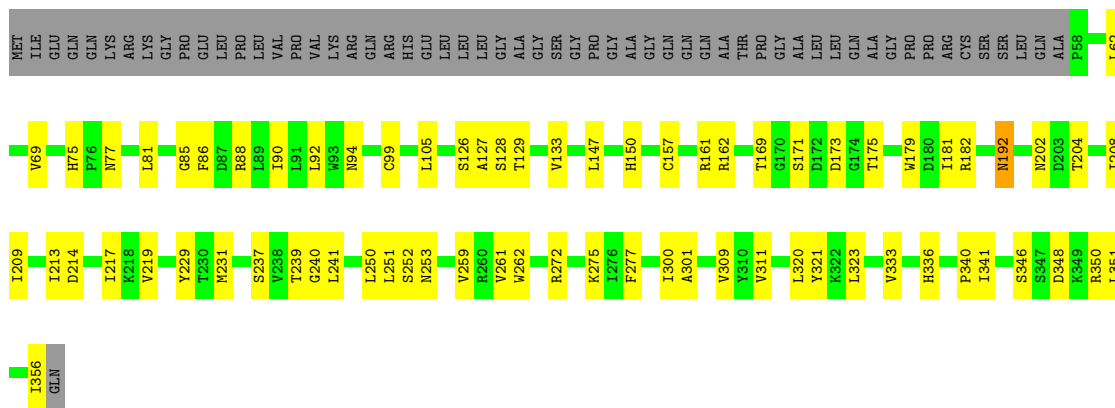


• Molecule 38: MINX-M3

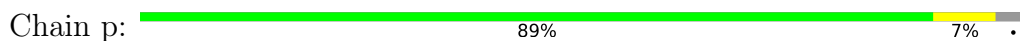




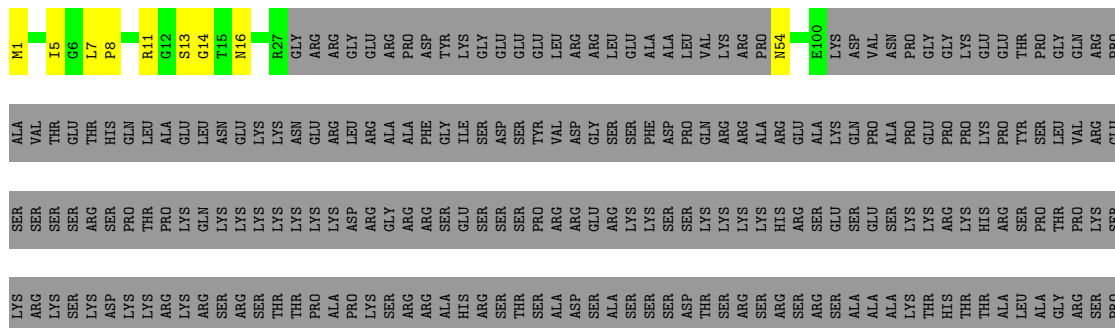
• Molecule 39: U5 small nuclear ribonucleoprotein 40 kDa protein



• Molecule 40: Peptidyl-prolyl cis-trans isomerase-like 1



• Molecule 41: Serine/arginine repetitive matrix protein 2

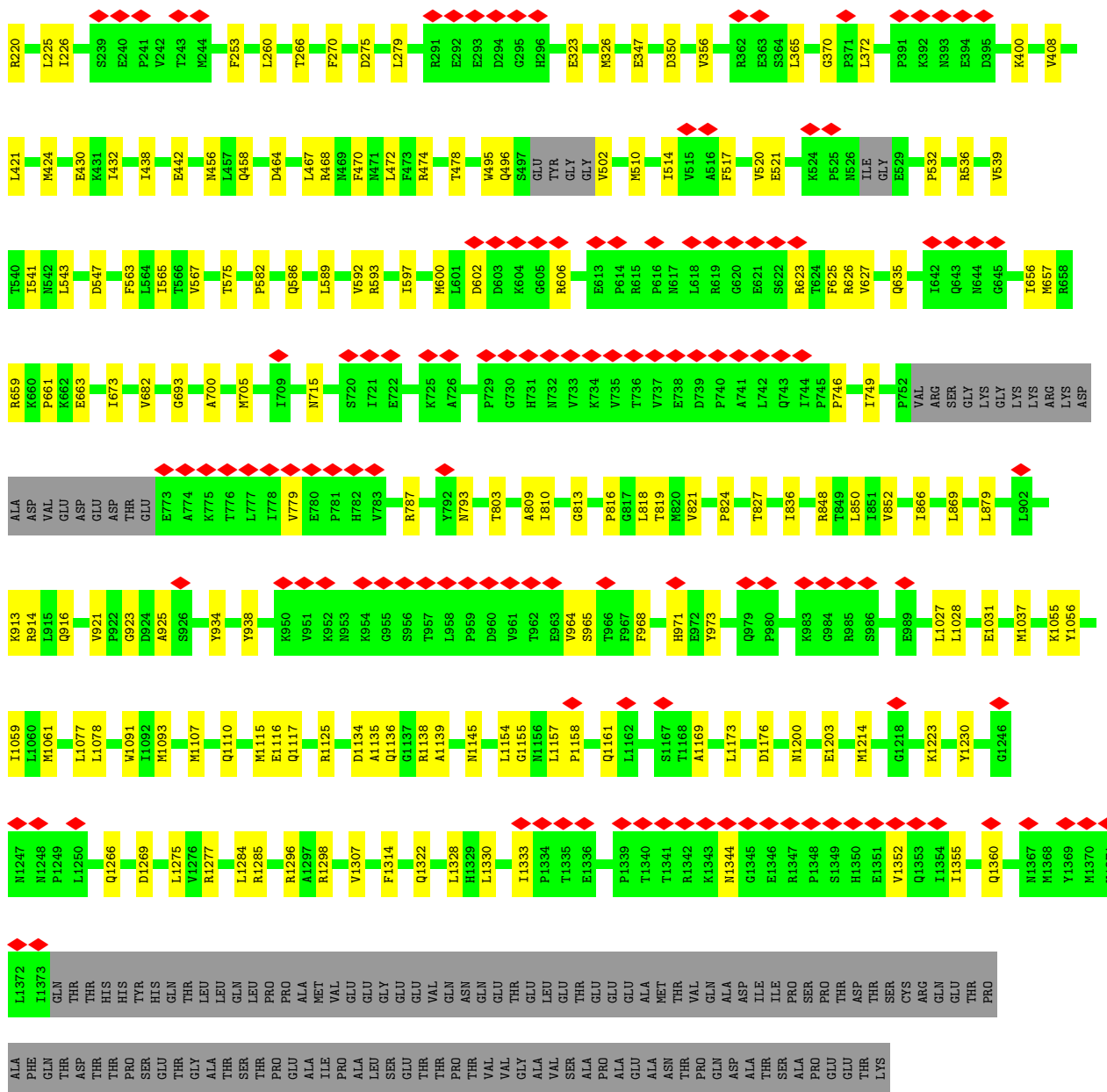




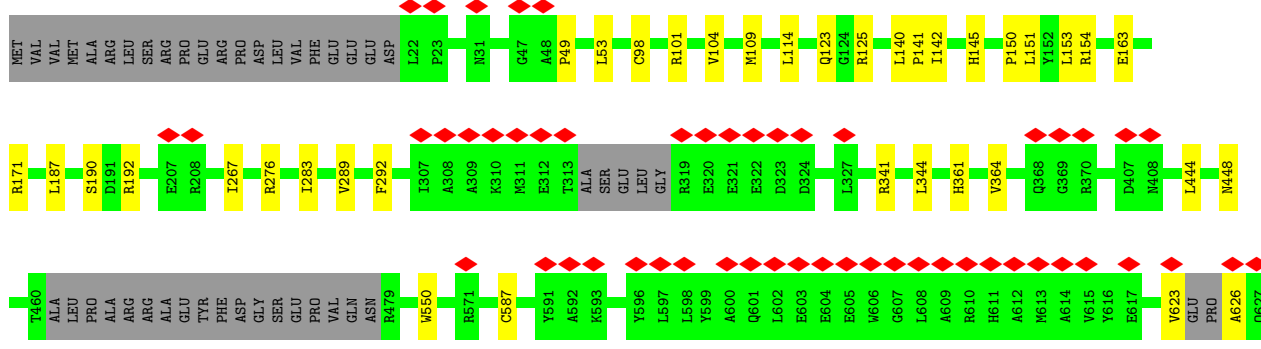
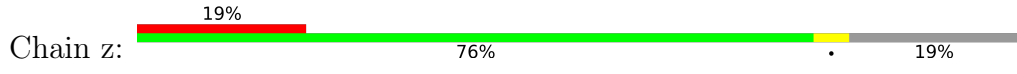








● Molecule 49: Pre-mRNA-splicing factor SYF1



Q628 Y629 Y630 D630 M631 F632 M633 I634 Y635 I636 K637 R638 A639 A640 E641 I642 Y643 G644 V645 T646 H647 T648 R649 G650 I651 Y652 Q653 K654 A655 I656 E657 V658 L659 S660 D661 E662 H663 A664 R665 E666 M667 C668 L669 R670 F671 A672 D673 M674 E675 C676 K677 L678 G679 E680 I681 D682 R683 A684 R685 A686 I687

Y688 S689 F690 C691 S692 Q693 I694 C695 D696 P697 R698 T699 T700 G701 A702 F703 W704 Q705 T706 W707 K708 D709 F710 E711 V712 R713 H714 G715 N716 E717 D718 T719 I720 K721 E722 M723 L724 R725 I726 R727 R728 S729 V730 Q731 A732 T733 Y734 N735 T736 V738 ASN PHE MET ALA SER GLN MET LEU LYS

VAL SER GLY SER ALA THR GLY THR VAL SER ASP LEU ALA PRO GLY GLN SER MET ASP ASP MET LYS LEU LEU LEU GLN PRO ASN ARG GLU ALA VAL GLN LEU LEU ALA GLN SER VAL ARG ASP ALA VAL PHE LEU ARG VAL SER ASP ALA SER ILE LEU PHE VAL ARG SER ASP ALA SER ARG LEU LEU ASP

ALA LEU ALA GLN GLN VAL ASN GLU ILE LEU LEU GLY GLN ASP ASP MET ASP LEU GLN ASN ARG VAL ARG LEU GLN SER VAL PHE LEU SER LEU LYS GLU ASP

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	12395	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 ( $e^-/\text{\AA}^2$ )	45.47	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.059	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	546.0, 546.0, 546.0	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GTP, IHP, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	1	0.17	0/390	0.48	0/542
1	i	0.16	0/344	0.46	0/476
2	2	0.15	0/360	0.41	0/497
2	h	0.14	0/320	0.42	0/440
3	3	0.13	0/372	0.47	0/515
3	j	0.18	0/334	0.50	0/463
4	4	0.17	0/420	0.45	0/583
4	l	0.16	0/335	0.44	0/464
5	5	0.24	0/405	0.42	0/563
5	k	0.15	0/387	0.42	0/537
6	8	0.16	0/421	0.45	0/583
6	n	0.15	0/313	0.40	0/432
7	9	0.14	0/332	0.39	0/458
7	m	0.16	0/306	0.46	0/420
8	A	0.15	0/5706	0.41	0/7930
9	B	0.12	0/351	0.39	0/489
10	C	0.24	1/5209 (0.0%)	0.55	0/7211
11	D	0.20	0/660	0.68	2/893 (0.2%)
12	E	0.18	0/1383	0.49	0/1887
13	F	0.14	0/382	0.46	0/529
14	G	0.25	0/370	0.62	0/513
15	H	0.11	0/524	0.44	0/724
16	I	0.19	0/1037	0.47	0/1420
17	J	0.15	0/2195	0.48	0/3036
18	K	0.22	0/953	0.53	0/1295
18	M	0.23	0/1004	0.60	2/1365 (0.1%)
18	R	0.19	0/953	0.49	0/1295
18	v	0.21	0/1004	0.52	0/1365
19	L	0.22	0/178	0.57	0/240
20	N	0.25	0/6267	0.62	0/8491
21	O	0.22	0/2586	0.55	0/3527
22	P	0.19	0/2463	0.53	0/3317

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
23	Q	0.23	0/836	0.62	0/1117
24	S	0.22	0/1342	0.69	1/1804 (0.1%)
25	T	0.23	0/1202	0.61	0/1611
26	U	0.24	0/2118	0.61	3/2881 (0.1%)
27	V	0.19	0/2026	0.53	0/2760
28	W	0.19	0/2954	0.50	0/4033
29	X	0.18	0/1623	0.48	0/2240
30	Y	0.19	0/2290	0.54	0/3103
31	Z	0.16	0/618	0.54	0/845
32	a	0.20	0/16807	0.53	5/22895 (0.0%)
33	b	0.22	0/7206	0.56	2/9800 (0.0%)
34	c	0.15	0/8529	0.41	0/11891
35	d	0.17	0/2225	0.34	0/3464
36	e	0.18	0/2307	0.36	0/3584
37	f	0.14	0/3239	0.26	0/5031
38	g	0.17	0/1734	0.37	0/2691
39	o	0.21	0/2392	0.54	0/3242
40	p	0.14	0/775	0.39	0/1070
41	q	0.22	0/466	0.58	0/639
42	r	0.18	0/803	0.51	0/1119
43	s	0.14	0/810	0.43	0/1122
44	t	0.25	0/414	0.58	0/555
45	u	0.18	0/1969	0.51	2/2722 (0.1%)
46	w	0.15	0/1087	0.41	0/1497
47	x	0.16	0/1785	0.47	0/2482
48	y	0.20	0/11144	0.48	2/15101 (0.0%)
49	z	0.24	1/4593 (0.0%)	0.60	2/6317 (0.0%)
All	All	0.20	2/121558 (0.0%)	0.50	21/168116 (0.0%)

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
11	D	0	1
20	N	0	1
24	S	0	2
39	o	0	1
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	C	729	LYS	C-N	5.80	1.39	1.33
49	z	341	ARG	C-N	5.06	1.40	1.34

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	M	70	SER	CA-C-N	7.03	124.67	120.24
18	M	70	SER	C-N-CA	7.03	124.67	120.24
32	a	519	ASP	CA-C-N	6.25	133.48	121.54
32	a	519	ASP	C-N-CA	6.25	133.48	121.54
32	a	192	GLN	N-CA-C	5.74	117.62	110.91

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	D	45	ILE	Peptide
20	N	504	GLU	Peptide
24	S	77	GLN	Peptide
24	S	89	LEU	Peptide
39	o	192	ASN	Peptide

## 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	1	391	0	163	1	0
1	i	346	0	144	3	0
2	2	361	0	158	5	0
2	h	322	0	138	10	0
3	3	373	0	163	0	0
3	j	335	0	148	6	0
4	4	422	0	175	3	0
4	l	337	0	139	6	0
5	5	406	0	170	3	0
5	k	388	0	164	2	0
6	8	422	0	177	1	0
6	n	315	0	134	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	9	334	0	143	3	0
7	m	309	0	135	3	0
8	A	5714	0	2549	42	0
9	B	350	0	167	0	0
10	C	5115	0	4128	46	0
11	D	649	0	597	17	0
12	E	1350	0	1111	21	0
13	F	383	0	173	4	0
14	G	364	0	226	2	0
15	H	530	0	218	1	0
16	I	1034	0	621	7	0
17	J	2187	0	1161	10	0
18	K	938	0	938	8	0
18	M	988	0	994	13	0
18	R	938	0	938	10	0
18	v	988	0	994	8	0
19	L	177	0	140	0	0
20	N	6147	0	5981	103	0
21	O	2517	0	2466	52	0
22	P	2432	0	2205	38	0
23	Q	823	0	779	22	0
24	S	1323	0	1311	16	0
25	T	1176	0	1178	19	0
26	U	2080	0	1803	47	0
27	V	1996	0	1727	22	0
28	W	2921	0	2168	14	0
29	X	1587	0	1176	14	0
30	Y	2250	0	2095	34	0
31	Z	607	0	402	6	0
32	a	16415	0	14878	232	0
33	b	7046	0	7030	111	0
34	c	8530	0	3747	10	0
35	d	1989	0	1006	23	0
36	e	2070	0	1046	19	0
37	f	2906	0	1473	13	0
38	g	1559	0	794	22	0
39	o	2338	0	2275	43	0
40	p	776	0	358	8	0
41	q	461	0	354	6	0
42	r	804	0	350	0	0
43	s	813	0	366	2	0
44	t	407	0	393	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	u	1963	0	1065	22	0
46	w	1093	0	497	8	0
47	x	1787	0	780	3	0
48	y	10878	0	10826	108	0
49	z	4511	0	3545	22	0
50	D	3	0	0	0	0
50	I	1	0	0	0	0
50	J	1	0	0	0	0
50	T	3	0	0	0	0
50	U	3	0	0	0	0
50	Z	1	0	0	0	0
51	a	36	0	6	2	0
52	b	32	0	12	0	0
53	b	1	0	0	0	0
53	d	6	0	0	0	0
All	All	119058	0	91198	1113	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 6.

The worst 5 of 1113 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)
25:T:139:CYS:SG	25:T:142:CYS:HB3	1.98	1.02
26:U:24:CYS:SG	26:U:81:CYS:HB2	2.12	0.90
32:a:972:GLU:HA	32:a:1101:PHE:O	1.72	0.90
36:e:90:U:HO2'	7:m:4:ALA:N	1.75	0.84
39:o:217:ILE:O	39:o:231:MET:HB3	1.79	0.82

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	77/92 (84%)	77 (100%)	0	0	100	100
1	i	66/92 (72%)	64 (97%)	2 (3%)	0	100	100
2	2	72/86 (84%)	72 (100%)	0	0	100	100
2	h	62/86 (72%)	58 (94%)	4 (6%)	0	100	100
3	3	74/126 (59%)	72 (97%)	2 (3%)	0	100	100
3	j	66/126 (52%)	63 (96%)	3 (4%)	0	100	100
4	4	81/118 (69%)	79 (98%)	2 (2%)	0	100	100
4	l	64/118 (54%)	61 (95%)	3 (5%)	0	100	100
5	5	80/119 (67%)	78 (98%)	2 (2%)	0	100	100
5	k	74/119 (62%)	68 (92%)	6 (8%)	0	100	100
6	8	84/240 (35%)	81 (96%)	3 (4%)	0	100	100
6	n	60/240 (25%)	60 (100%)	0	0	100	100
7	9	64/76 (84%)	64 (100%)	0	0	100	100
7	m	57/76 (75%)	55 (96%)	2 (4%)	0	100	100
8	A	1142/1217 (94%)	1069 (94%)	73 (6%)	0	100	100
9	B	68/86 (79%)	65 (96%)	2 (3%)	1 (2%)	8	39
10	C	813/1304 (62%)	779 (96%)	34 (4%)	0	100	100
11	D	87/110 (79%)	75 (86%)	11 (13%)	1 (1%)	11	46
12	E	190/895 (21%)	177 (93%)	13 (7%)	0	100	100
13	F	76/424 (18%)	68 (90%)	8 (10%)	0	100	100
14	G	63/476 (13%)	60 (95%)	3 (5%)	0	100	100
15	H	94/793 (12%)	94 (100%)	0	0	100	100
16	I	173/464 (37%)	161 (93%)	10 (6%)	2 (1%)	10	43
17	J	394/501 (79%)	369 (94%)	25 (6%)	0	100	100
18	K	114/504 (23%)	113 (99%)	1 (1%)	0	100	100
18	M	121/504 (24%)	120 (99%)	1 (1%)	0	100	100
18	R	114/504 (23%)	111 (97%)	3 (3%)	0	100	100
18	v	121/504 (24%)	121 (100%)	0	0	100	100
19	L	26/619 (4%)	24 (92%)	2 (8%)	0	100	100
20	N	779/1041 (75%)	723 (93%)	53 (7%)	3 (0%)	30	67
21	O	318/514 (62%)	304 (96%)	14 (4%)	0	100	100
22	P	316/802 (39%)	308 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	Q	96/229 (42%)	89 (93%)	7 (7%)	0	100	100
24	S	153/225 (68%)	142 (93%)	11 (7%)	0	100	100
25	T	140/144 (97%)	130 (93%)	10 (7%)	0	100	100
26	U	293/420 (70%)	270 (92%)	20 (7%)	3 (1%)	12	48
27	V	279/492 (57%)	257 (92%)	21 (8%)	1 (0%)	30	67
28	W	455/908 (50%)	439 (96%)	16 (4%)	0	100	100
29	X	237/848 (28%)	232 (98%)	5 (2%)	0	100	100
30	Y	294/536 (55%)	270 (92%)	22 (8%)	2 (1%)	18	56
31	Z	91/343 (26%)	83 (91%)	7 (8%)	1 (1%)	11	46
32	a	2171/2335 (93%)	2070 (95%)	95 (4%)	6 (0%)	36	72
33	b	896/972 (92%)	849 (95%)	42 (5%)	5 (1%)	21	59
34	c	1720/2136 (80%)	1668 (97%)	51 (3%)	1 (0%)	48	83
39	o	297/357 (83%)	278 (94%)	19 (6%)	0	100	100
40	p	157/166 (95%)	145 (92%)	12 (8%)	0	100	100
41	q	70/2752 (2%)	65 (93%)	5 (7%)	0	100	100
42	r	160/255 (63%)	154 (96%)	6 (4%)	0	100	100
43	s	159/225 (71%)	153 (96%)	6 (4%)	0	100	100
44	t	46/285 (16%)	45 (98%)	1 (2%)	0	100	100
45	u	359/520 (69%)	339 (94%)	19 (5%)	1 (0%)	36	72
46	w	213/301 (71%)	207 (97%)	6 (3%)	0	100	100
47	x	358/579 (62%)	332 (93%)	23 (6%)	3 (1%)	16	54
48	y	1319/1485 (89%)	1272 (96%)	47 (4%)	0	100	100
49	z	684/855 (80%)	636 (93%)	44 (6%)	4 (1%)	21	59
All	All	16637/30344 (55%)	15818 (95%)	785 (5%)	34 (0%)	44	77

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	I	139	PRO
16	I	218	PRO
26	U	225	PRO
26	U	226	PRO
33	b	57	VAL

### 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	
5	k	1/101 (1%)	1 (100%)	0	100	100
9	B	2/77 (3%)	2 (100%)	0	100	100
10	C	342/1104 (31%)	342 (100%)	0	100	100
11	D	69/95 (73%)	69 (100%)	0	100	100
12	E	102/776 (13%)	102 (100%)	0	100	100
14	G	10/397 (2%)	10 (100%)	0	100	100
16	I	33/382 (9%)	33 (100%)	0	100	100
17	J	42/446 (9%)	42 (100%)	0	100	100
18	K	106/435 (24%)	106 (100%)	0	100	100
18	M	111/435 (26%)	111 (100%)	0	100	100
18	R	106/435 (24%)	106 (100%)	0	100	100
18	v	111/435 (26%)	111 (100%)	0	100	100
19	L	11/545 (2%)	11 (100%)	0	100	100
20	N	624/897 (70%)	624 (100%)	0	100	100
21	O	274/441 (62%)	274 (100%)	0	100	100
22	P	208/709 (29%)	208 (100%)	0	100	100
23	Q	83/203 (41%)	83 (100%)	0	100	100
24	S	144/196 (74%)	144 (100%)	0	100	100
25	T	129/130 (99%)	129 (100%)	0	100	100
26	U	181/361 (50%)	181 (100%)	0	100	100
27	V	180/451 (40%)	180 (100%)	0	100	100
28	W	180/838 (22%)	177 (98%)	3 (2%)	53	68
29	X	85/751 (11%)	85 (100%)	0	100	100
30	Y	209/459 (46%)	209 (100%)	0	100	100
31	Z	35/294 (12%)	35 (100%)	0	100	100
32	a	1496/2108 (71%)	1496 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	b	784/866 (90%)	784 (100%)	0	100	100
39	o	256/300 (85%)	256 (100%)	0	100	100
41	q	30/2432 (1%)	30 (100%)	0	100	100
44	t	41/240 (17%)	41 (100%)	0	100	100
45	u	45/456 (10%)	45 (100%)	0	100	100
48	y	1200/1336 (90%)	1200 (100%)	0	100	100
49	z	290/749 (39%)	290 (100%)	0	100	100
All	All	7520/19880 (38%)	7517 (100%)	3 (0%)	100	100

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

Mol	Chain	Res	Type
28	W	458	THR
28	W	557	THR
28	W	575	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
33	b	575	GLN
48	y	330	HIS
33	b	856	HIS
39	o	257	ASN
48	y	586	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	d	91/106 (85%)	34 (37%)	0
36	e	95/117 (81%)	31 (32%)	0
37	f	131/188 (69%)	32 (24%)	0
38	g	74/319 (23%)	35 (47%)	0
All	All	391/730 (53%)	132 (33%)	0

5 of 132 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	d	6	C
35	d	7	G
35	d	8	C
35	d	9	U
35	d	10	U

There are no RNA pucker outliers to report.

## 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](#)

Of 21 ligands modelled in this entry, 19 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
52	GTP	b	1500	53	33,34,34	0.90	1 (3%)	50,54,54	1.57	8 (16%)
51	IHP	a	3001	-	36,36,36	1.59	6 (16%)	60,60,60	1.36	6 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
52	GTP	b	1500	53	-	5/22/38/38	0/3/3/3
51	IHP	a	3001	-	-	4/30/54/54	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	a	3001	IHP	P3-O13	3.82	1.66	1.59
51	a	3001	IHP	P4-O14	3.70	1.66	1.59
51	a	3001	IHP	P2-O12	3.25	1.65	1.59
51	a	3001	IHP	P6-O16	3.19	1.65	1.59
51	a	3001	IHP	P5-O15	3.15	1.65	1.59

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	b	1500	GTP	C5-C4-N3	-4.57	121.12	128.39
52	b	1500	GTP	C2-N3-C4	4.49	120.04	112.30
51	a	3001	IHP	C6-C5-C4	3.85	118.86	110.43
51	a	3001	IHP	O13-C3-C2	3.76	116.77	108.76
51	a	3001	IHP	C5-C6-C1	3.75	118.66	110.43

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
51	a	3001	IHP	C2-C3-O13-P3
51	a	3001	IHP	C5-C4-O14-P4
52	b	1500	GTP	C5'-O5'-PA-O3A
51	a	3001	IHP	C1-O11-P1-O21
52	b	1500	GTP	C5'-O5'-PA-O1A

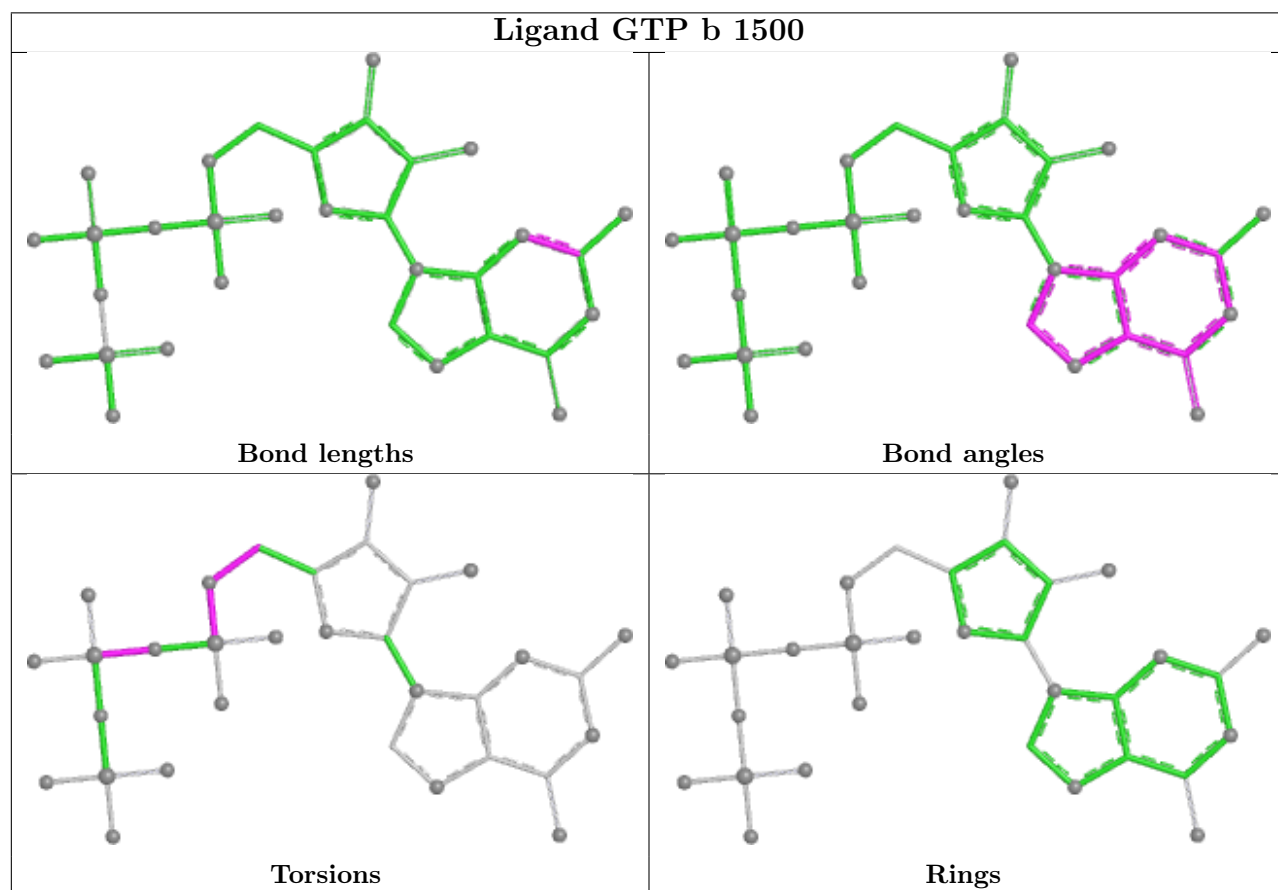
There are no ring outliers.

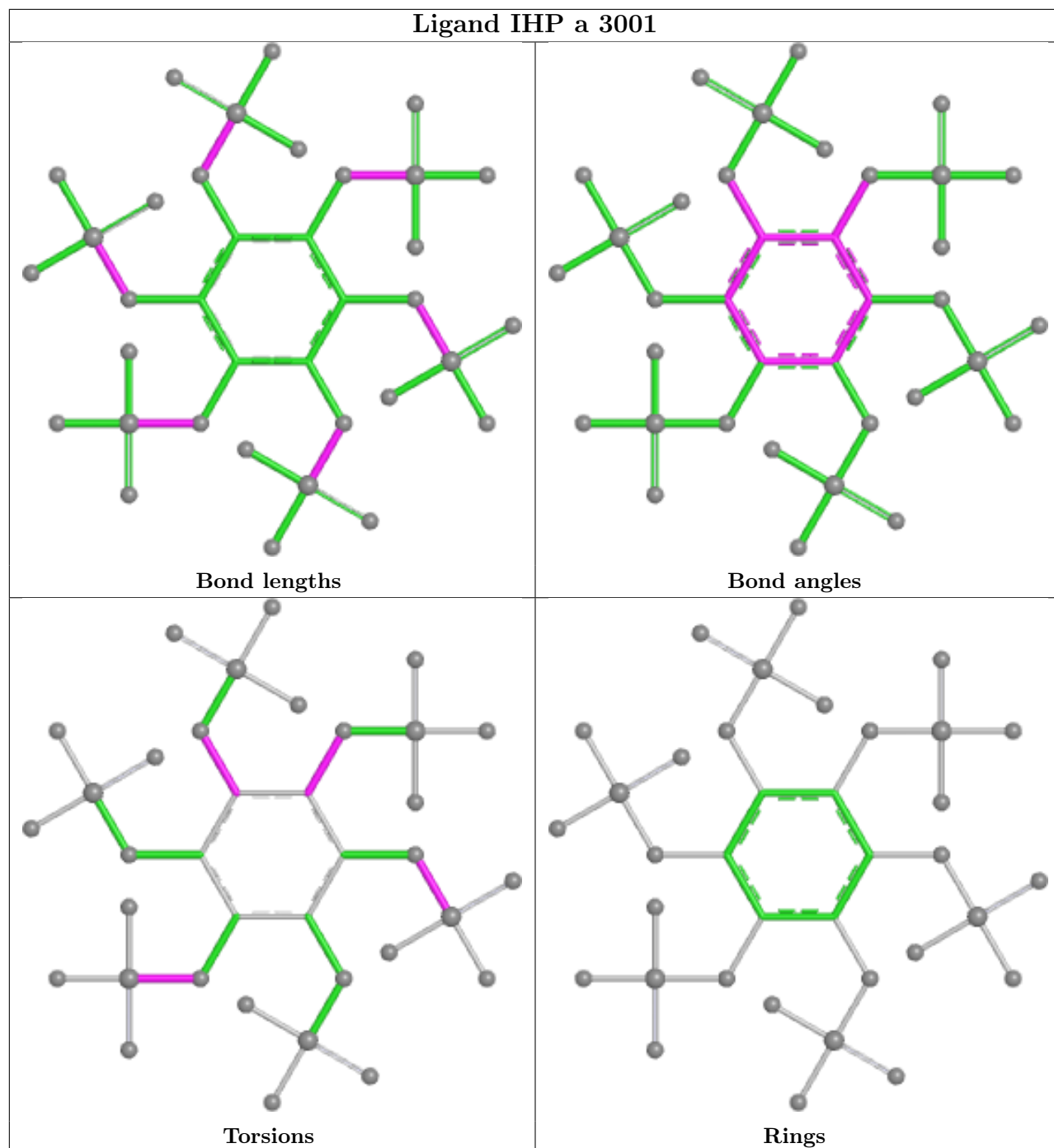
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
51	a	3001	IHP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

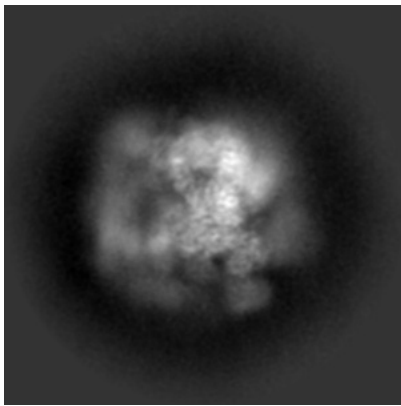
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16658. These allow visual inspection of the internal detail of the map and identification of artifacts.

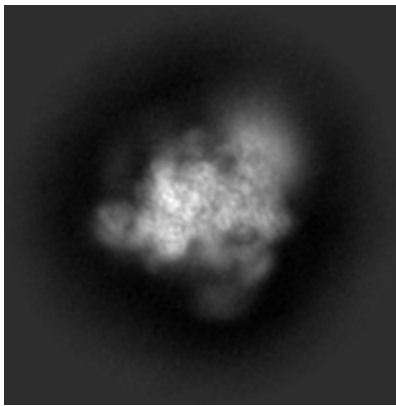
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

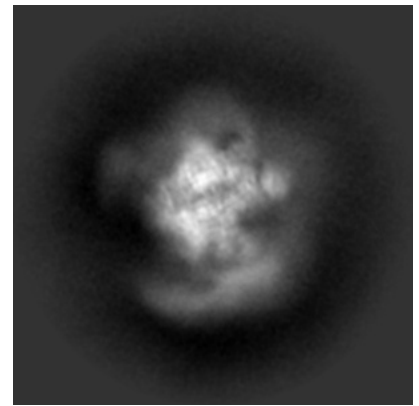
#### 6.1.1 Primary map



X

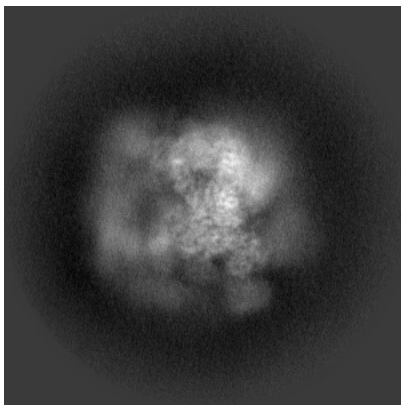


Y

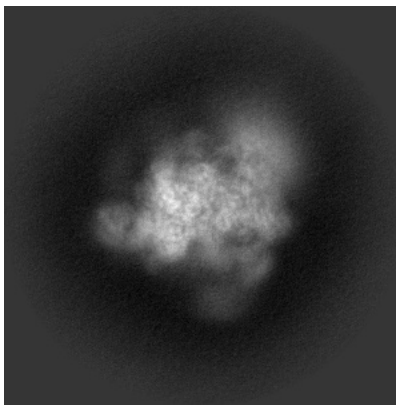


Z

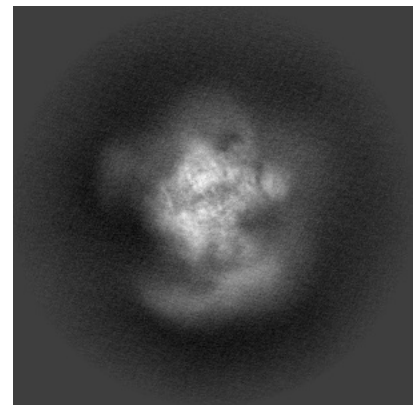
#### 6.1.2 Raw map



X



Y

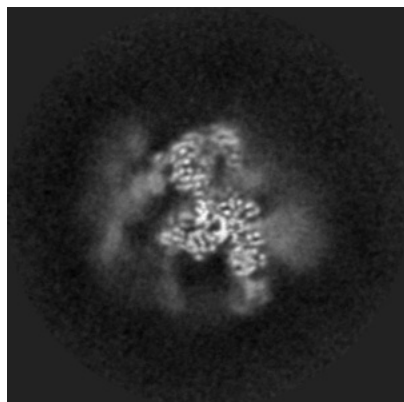


Z

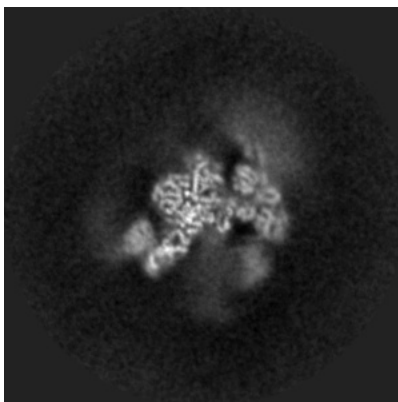
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

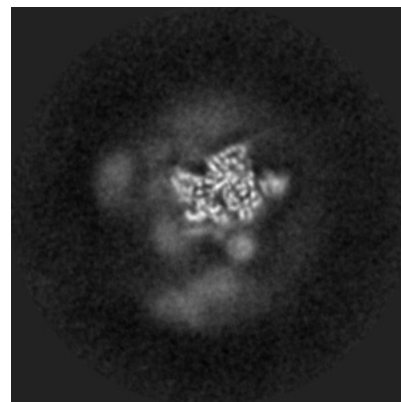
### 6.2.1 Primary map



X Index: 260

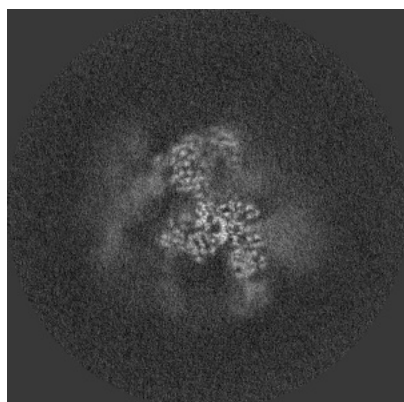


Y Index: 260

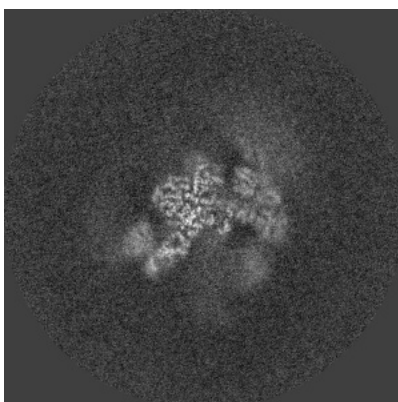


Z Index: 260

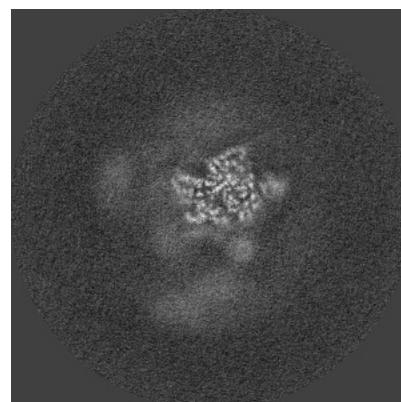
### 6.2.2 Raw map



X Index: 260



Y Index: 260

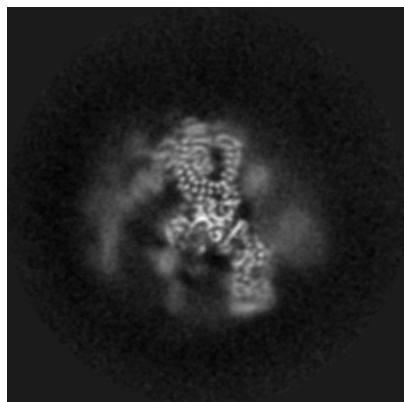


Z Index: 260

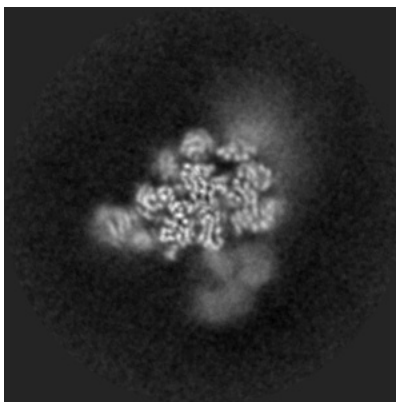
The images above show central slices of the map in three orthogonal directions.

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

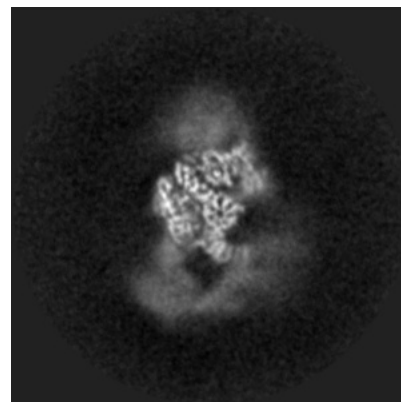
### 6.3.1 Primary map



X Index: 248

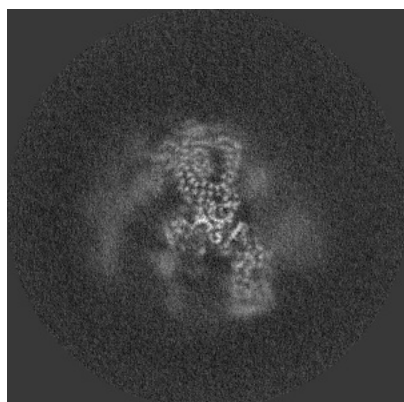


Y Index: 295

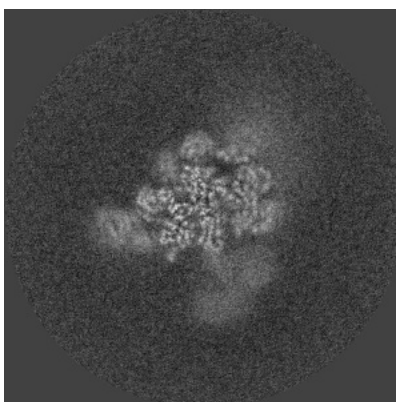


Z Index: 216

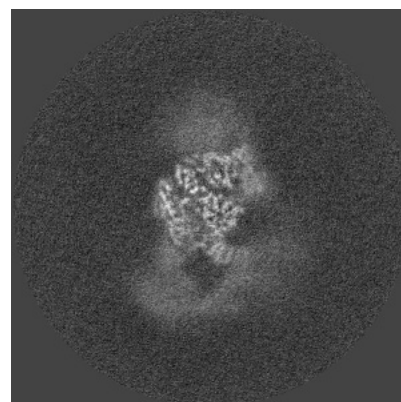
### 6.3.2 Raw map



X Index: 248



Y Index: 295

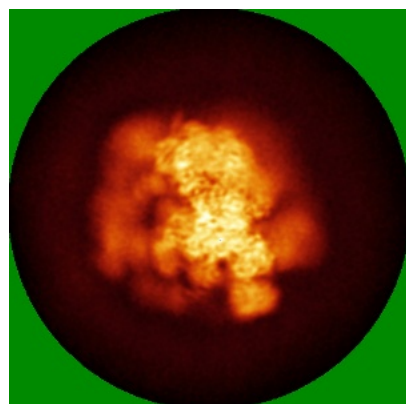


Z Index: 215

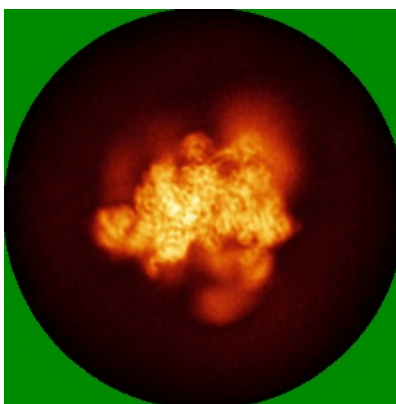
The images above show the largest variance slices of the map in three orthogonal directions.

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

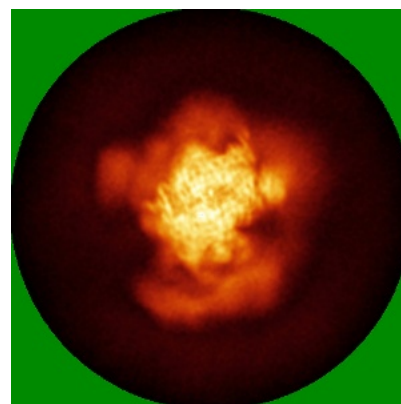
### 6.4.1 Primary map



X

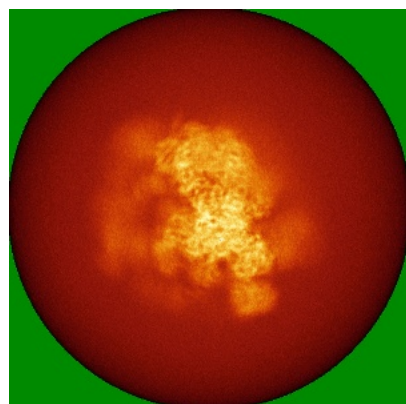


Y

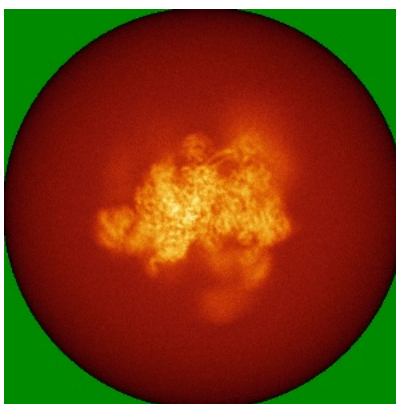


Z

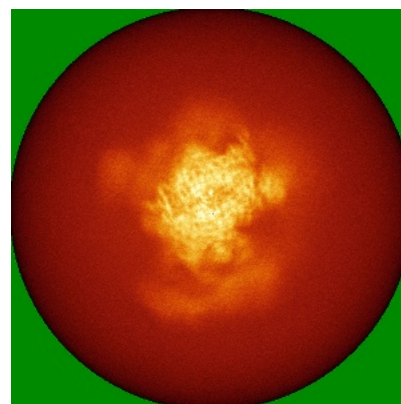
### 6.4.2 Raw map



X



Y

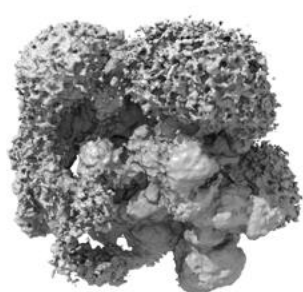


Z

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](#)

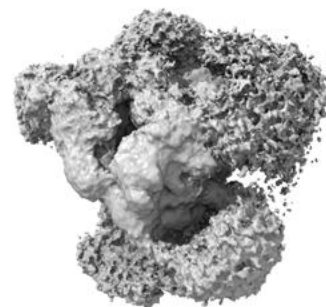
### 6.5.1 Primary map



X



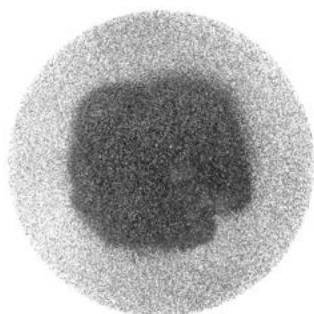
Y



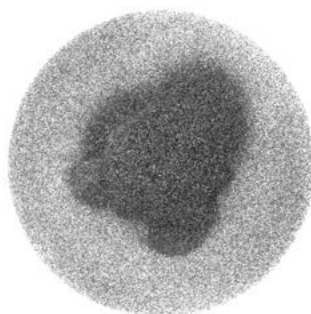
Z

The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

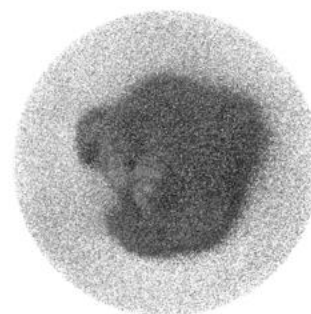
### 6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

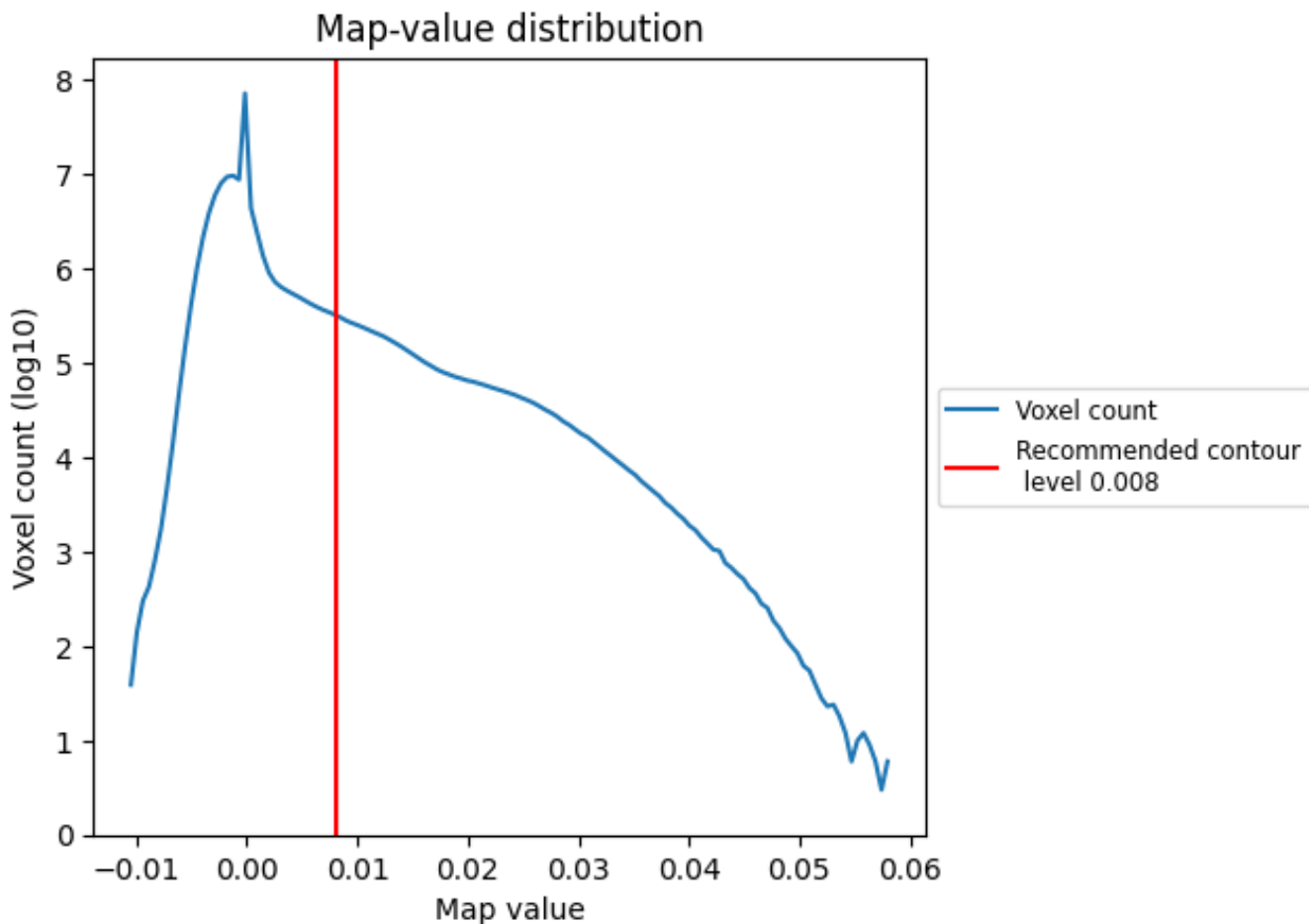
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

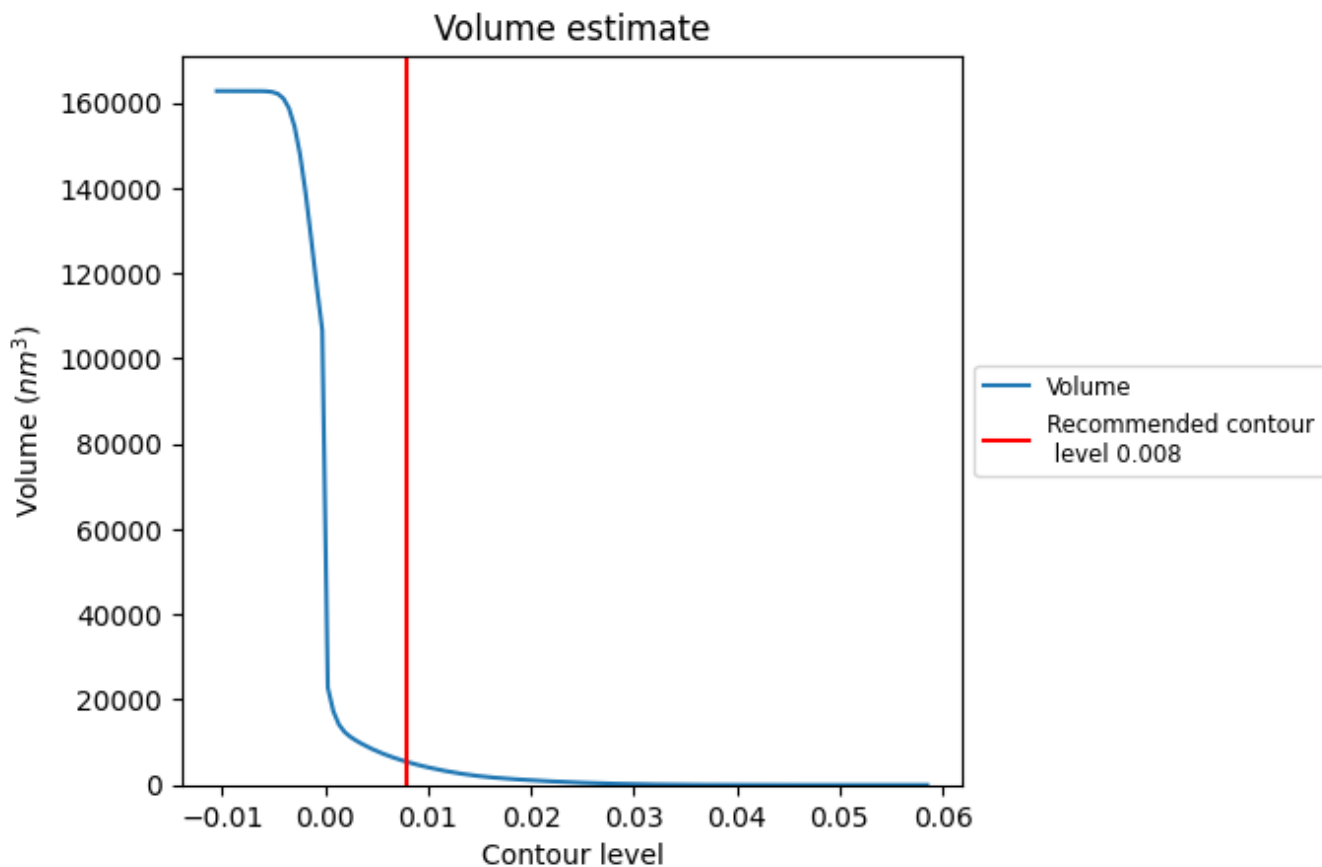
This section contains the results of statistical analysis of the map.

### 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.

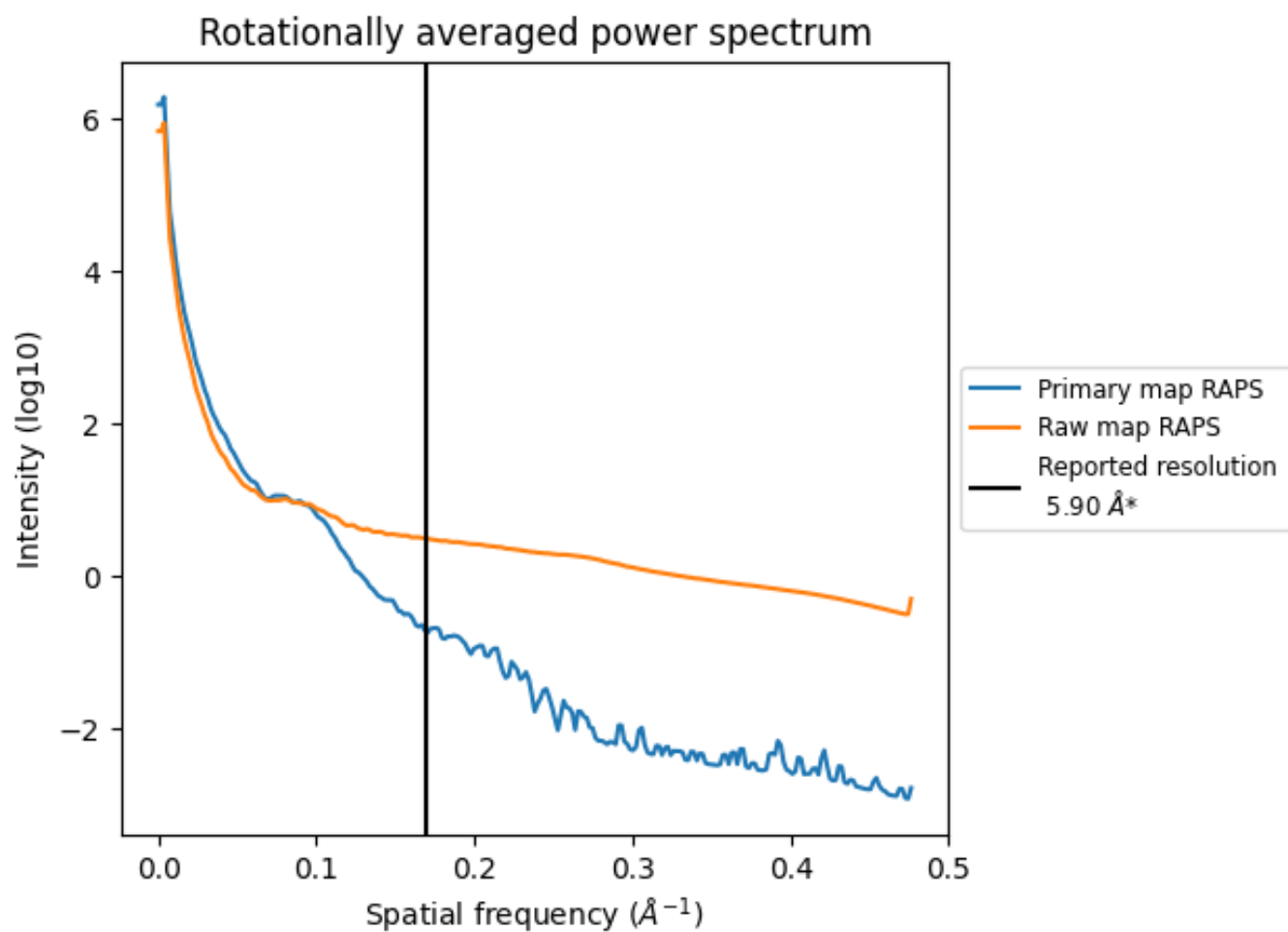
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 5401 nm<sup>3</sup>; this corresponds to an approximate mass of 4879 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

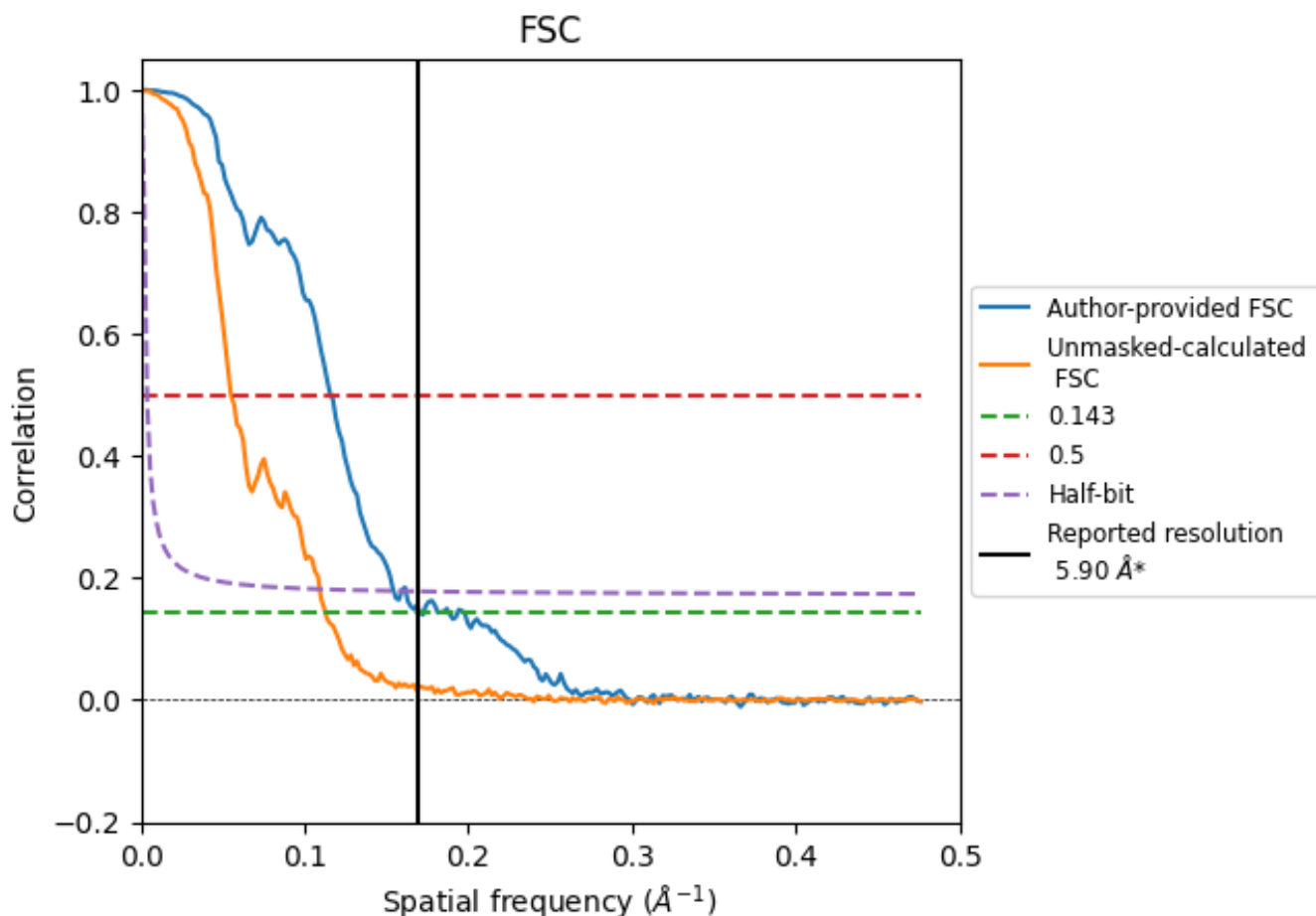


\*Reported resolution corresponds to spatial frequency of  $0.169 \text{ \AA}^{-1}$

## 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 0.169 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

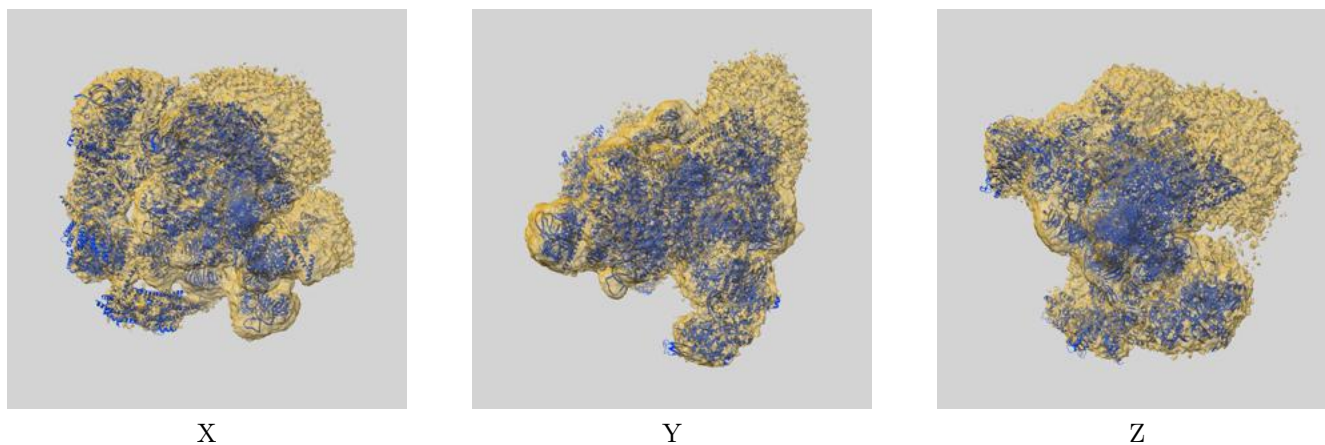
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.90	-	-
Author-provided FSC curve	5.85	8.63	6.48
Unmasked-calculated*	8.88	18.21	9.17

\*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 8.88 differs from the reported value 5.9 by more than 10 %

## 9 Map-model fit [i](#)

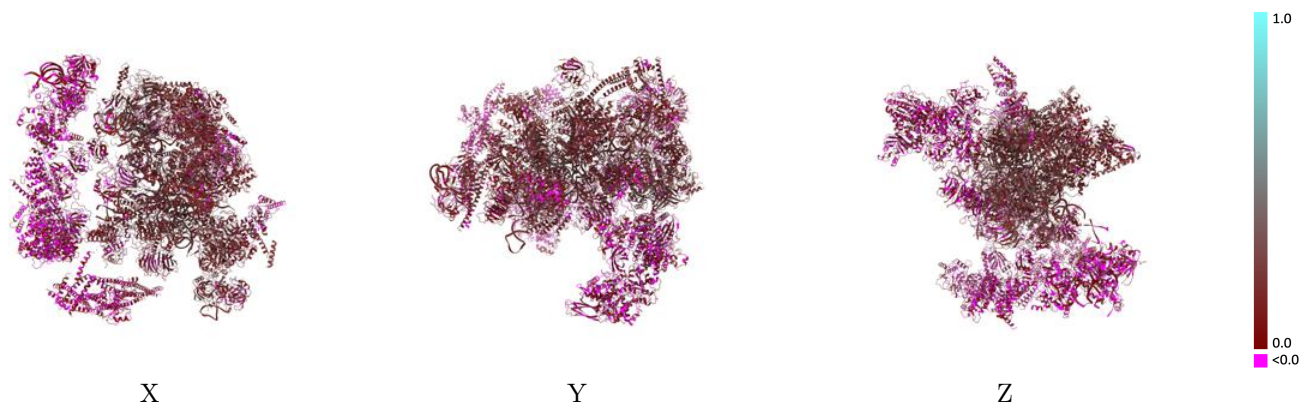
This section contains information regarding the fit between EMDB map EMD-16658 and PDB model 8CH6. Per-residue inclusion information can be found in section 3 on page 16.

### 9.1 Map-model overlay [i](#)



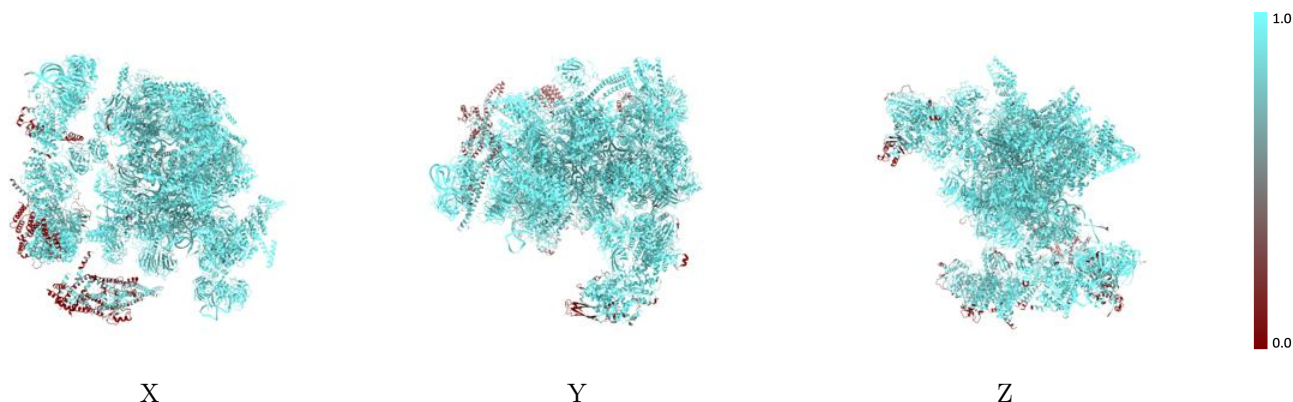
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



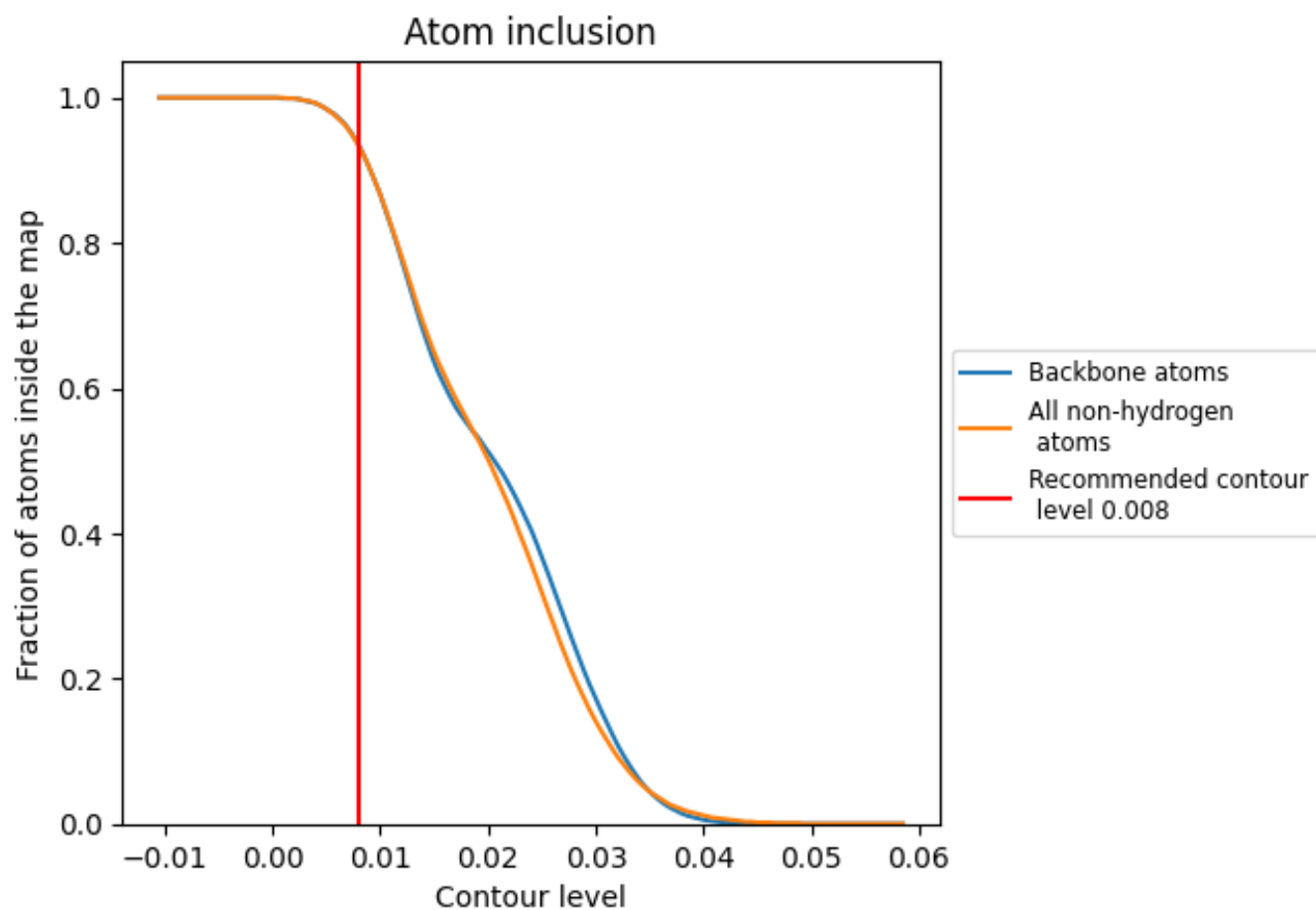
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9340	 0.1540
1	 1.0000	 0.0660
2	 0.9970	 0.0750
3	 1.0000	 0.0880
4	 0.9760	 0.0500
5	 1.0000	 0.0540
8	 1.0000	 0.0560
9	 1.0000	 0.1280
A	 1.0000	 0.2080
B	 1.0000	 0.2630
C	 1.0000	 0.2250
D	 1.0000	 0.1730
E	 1.0000	 0.2060
F	 0.9240	 0.1030
G	 1.0000	 0.2420
H	 0.9060	 0.0660
I	 0.9500	 0.1610
J	 0.7820	 0.0980
K	 0.4960	 0.0470
L	 1.0000	 0.2100
M	 0.5760	 0.0740
N	 1.0000	 0.1800
O	 1.0000	 0.2300
P	 0.7290	 0.1480
Q	 1.0000	 0.2160
R	 0.4040	 0.0800
S	 0.4540	 0.0980
T	 1.0000	 0.1910
U	 1.0000	 0.1740
V	 1.0000	 0.1690
W	 1.0000	 0.1580
X	 1.0000	 0.2050
Y	 1.0000	 0.2280
Z	 0.9970	 0.1790
a	 1.0000	 0.2030



*Continued on next page...*

Continued from previous page...

Chain	Atom inclusion	Q-score
b	 1.0000	 0.2060
c	 0.9060	 0.0830
d	 1.0000	 0.2540
e	 1.0000	 0.2500
f	 0.9650	 0.1380
g	 1.0000	 0.2490
h	 1.0000	 0.2580
i	 1.0000	 0.1840
j	 1.0000	 0.1550
k	 1.0000	 0.2230
l	 1.0000	 0.2280
m	 1.0000	 0.1410
n	 1.0000	 0.1570
o	 0.9970	 0.1020
p	 1.0000	 0.1470
q	 1.0000	 0.2510
r	 0.9690	 0.0720
s	 0.9130	 0.0600
t	 0.7880	 0.0750
u	 0.9840	 0.1530
v	 0.3870	 0.0640
w	 0.9930	 0.0850
x	 0.9730	 0.0850
y	 0.8370	 0.0520
z	 0.8100	 0.0550