



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 01:39 am GMT

PDB ID : 6G5I  
EMDB ID : EMD-4353  
Title : Cryo-EM structure of a late human pre-40S ribosomal subunit - State R  
Authors : Ameismeier, M.; Cheng, J.; Berninghausen, O.; Beckmann, R.  
Deposited on : 2018-03-29  
Resolution : 3.50 Å(reported)

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

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

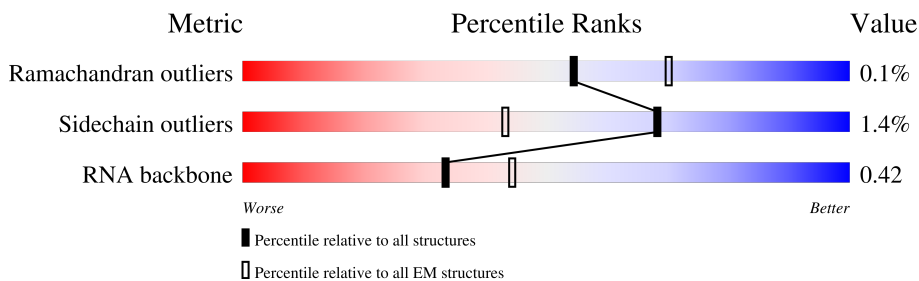
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 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.



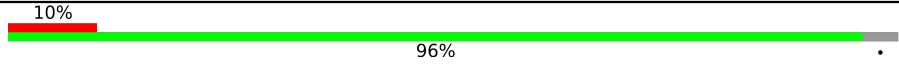
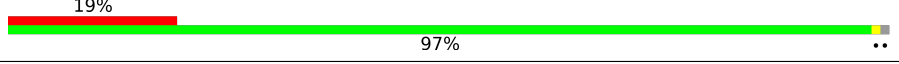
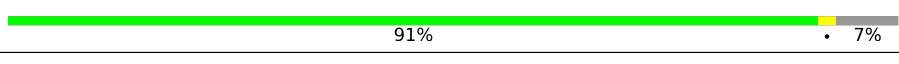


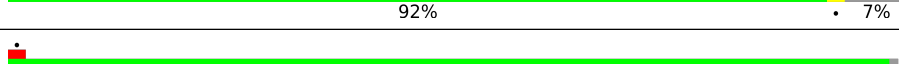
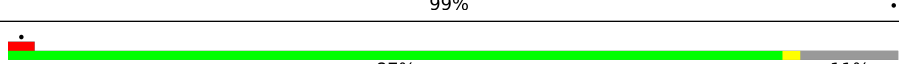
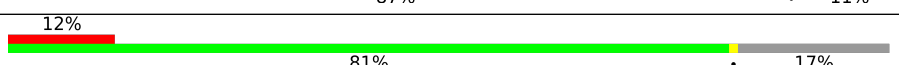
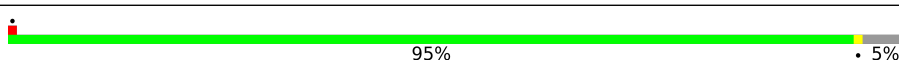

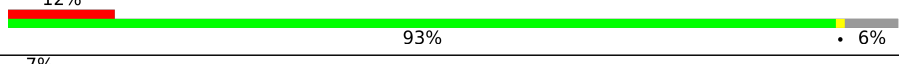
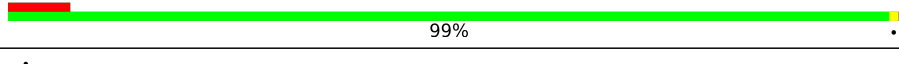
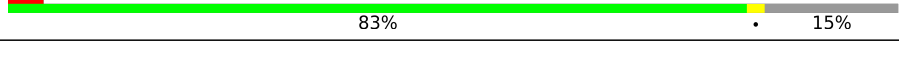
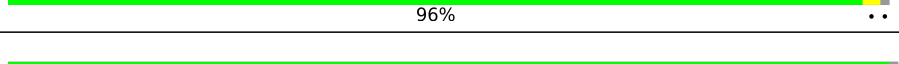
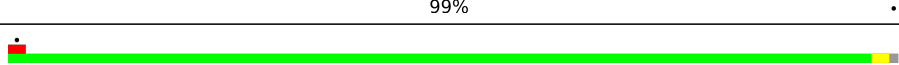
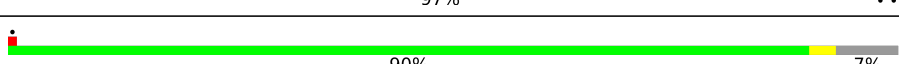

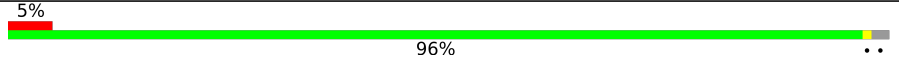

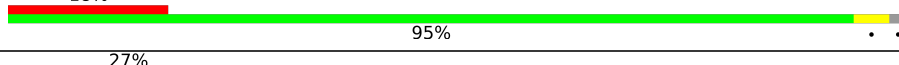
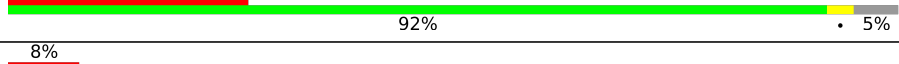

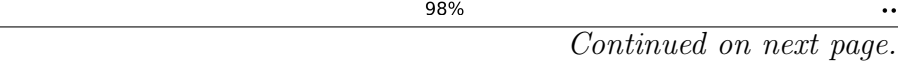


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	2	1882	
2	A	295	
3	B	264	
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	




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Mol	Chain	Length	Quality of chain
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	133	
27	Z	125	
28	b	84	
29	c	69	
30	d	56	
31	e	59	
32	f	156	
33	g	317	

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Mol	Chain	Length	Quality of chain
34	x	252	
35	y	412	
36	z	568	

## 2 Entry composition [i](#)

There are 37 unique types of molecules in this entry. The entry contains 77185 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 RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1657	35380	15792	6352	11579	1657	0	0

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	216	1705	1083	299	315	8	0	0

- Molecule 3 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	213	1729	1098	309	308	14	0	0

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	218	1690	1094	289	297	10	0	0

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	225	1752	1117	315	313	7	0	0

- Molecule 6 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	262	2076	1324	386	358	8	0	0

- Molecule 7 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	F	189	1495	934	284	270	7	0	0

- Molecule 8 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	230	1862	1164	371	320	7	0	0

- Molecule 9 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	186	1501	957	276	267	1	0	0

- Molecule 10 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	205	1682	1056	331	290	5	0	0

- Molecule 11 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	J	180	1499	955	300	242	2	0	0

- Molecule 12 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	95	800	522	142	131	5	0	0

- Molecule 13 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	151	1229	782	230	211	6	0	0

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	123	Total	C	N	O	S	0	0
			953	598	169	177	9		

- Molecule 15 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 16 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1009	618	198	187	6		

- Molecule 17 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	120	Total	C	N	O	S	0	0
			984	625	184	168	7		

- Molecule 18 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 19 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	122	Total	C	N	O	S	0	0
			990	621	184	182	3		

- Molecule 20 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 21 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	T	144	1122	703	217	199	3	0	0

- Molecule 22 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	U	101	803	504	153	142	4	0	0

- Molecule 23 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	V	82	625	384	116	120	5	0	0

- Molecule 24 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	W	129	1034	659	193	176	6	0	0

- Molecule 25 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	X	141	1098	693	219	183	3	0	0

- Molecule 26 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Y	124	1014	641	198	170	5	0	0

- Molecule 27 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Z	72	574	368	104	101	1	0	0

- Molecule 28 is a protein called 40S ribosomal protein S27.



Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 29 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 30 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	55	Total	C	N	O	S	0	0
			458	286	94	73	5		

- Molecule 31 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	56	Total	C	N	O	S	0	0
			442	273	96	72	1		

- Molecule 32 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	63	Total	C	N	O	S	0	0
			510	320	97	86	7		

- Molecule 33 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 34 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	x	175	Total	C	N	O	S	0	0
			1365	878	249	234	4		

- Molecule 35 is a protein called RNA-binding protein NOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	y	317	2490	1576	456	448	10	0	0

- Molecule 36 is a protein called Serine/threonine-protein kinase RIO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	z	29	257	160	57	39	1	0	0

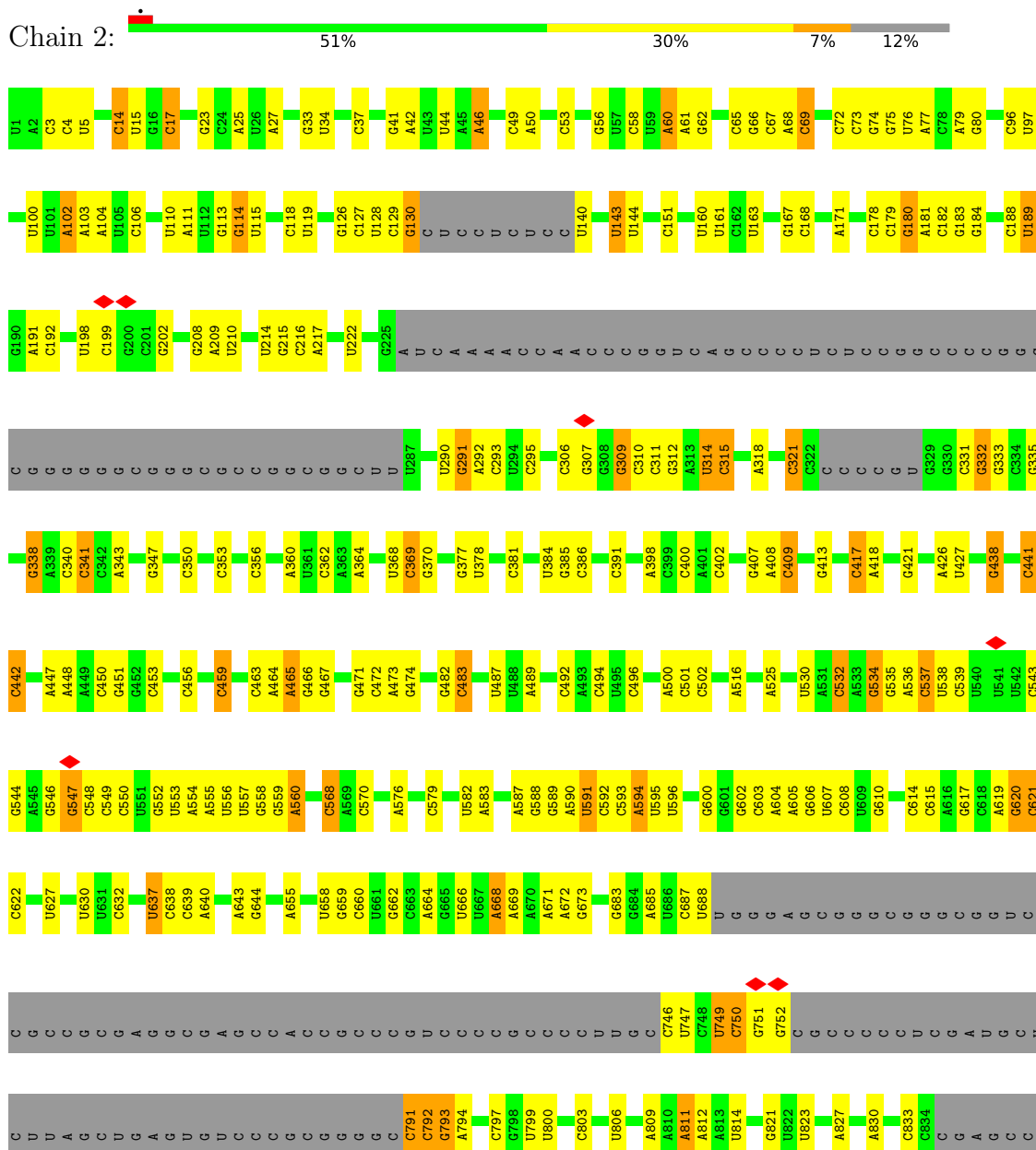
- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

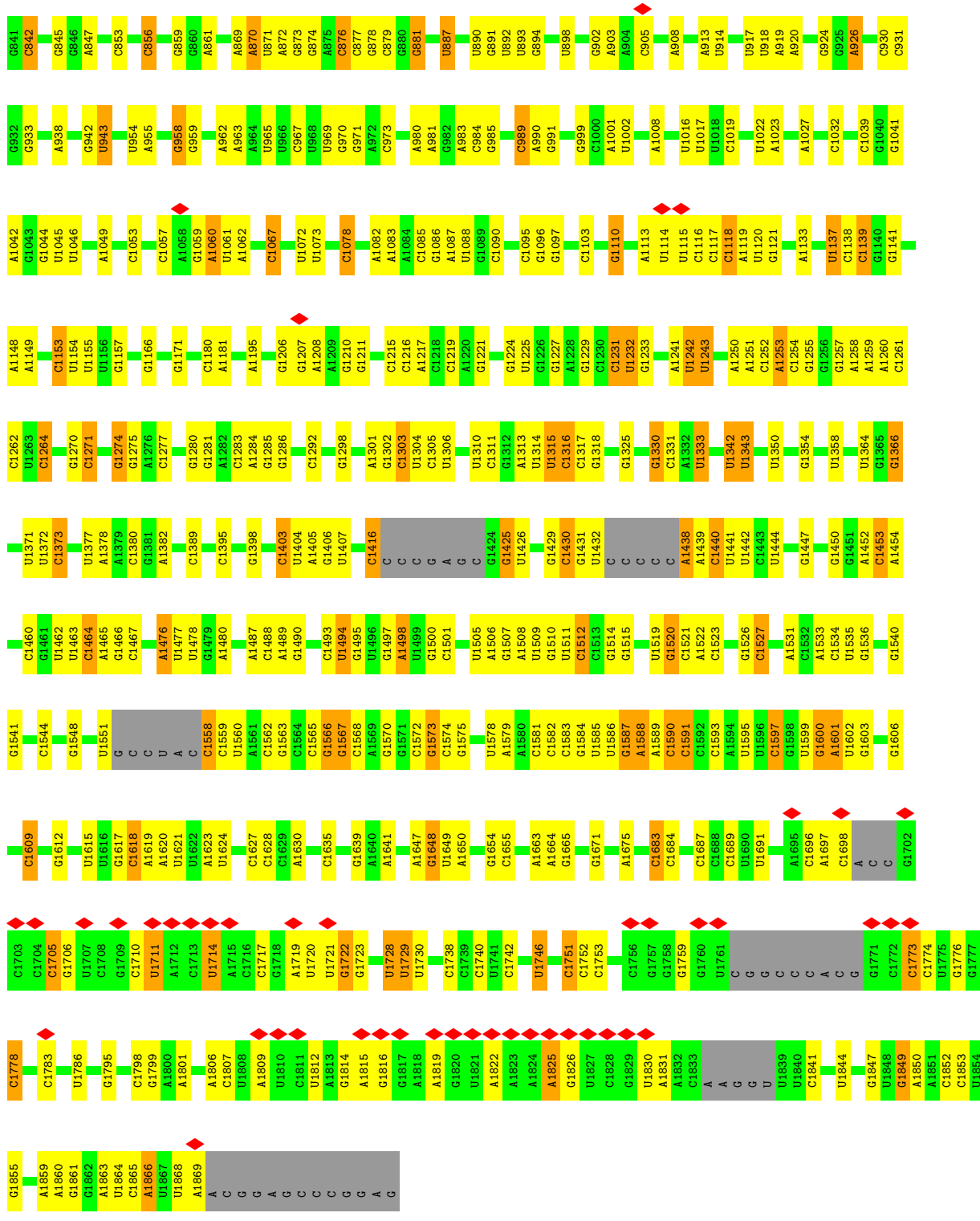
Mol	Chain	Residues	Atoms		AltConf
37	d	1	Total	Zn	0
			1	1	
37	f	1	Total	Zn	0
			1	1	
37	y	1	Total	Zn	0
			1	1	

### 3 Residue-property plots [i](#)

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

- Molecule 1: 18S ribosomal RNA



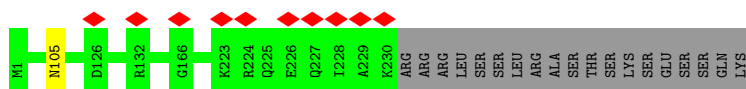


• Molecule 2: 40S ribosomal protein SA



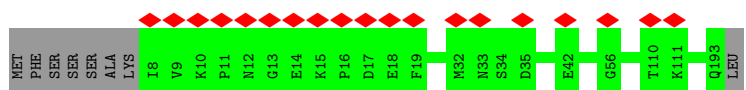


Chain G:  92% 8%



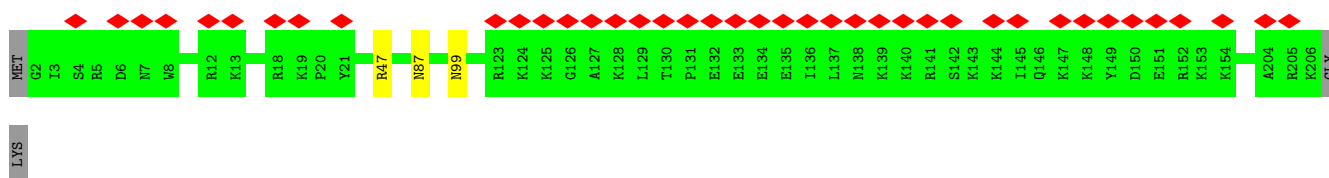
- Molecule 9: 40S ribosomal protein S7

Chain H:  10% 96%




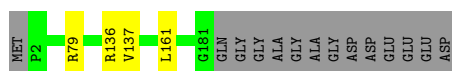
- Molecule 10: 40S ribosomal protein S8

Chain I:  19% 97%



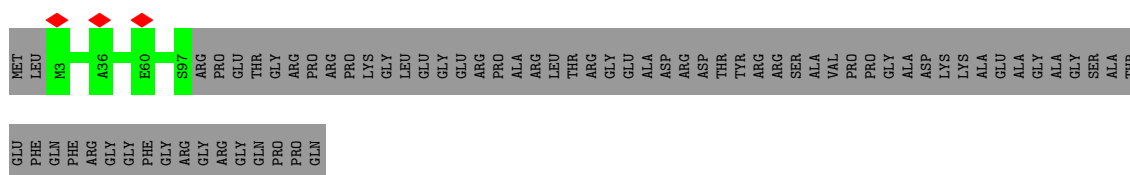
- Molecule 11: 40S ribosomal protein S9

Chain J:  91% 7%




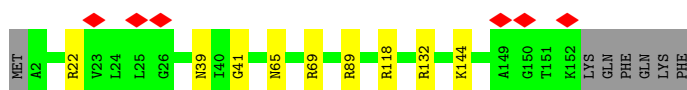
- Molecule 12: 40S ribosomal protein S10

Chain K:  58% 42%

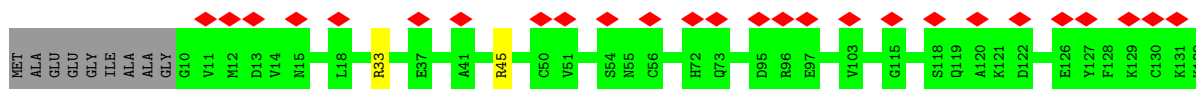
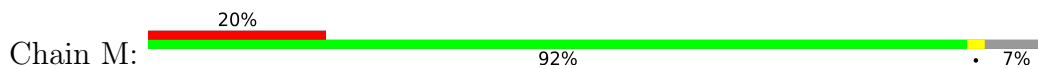


- Molecule 13: 40S ribosomal protein S11

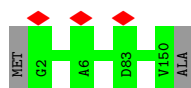
Chain L:  90% 6%



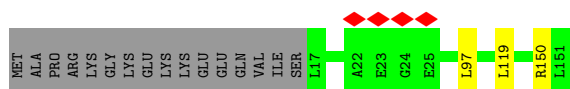
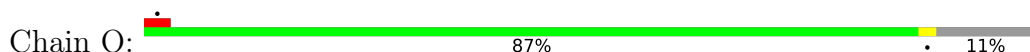
- Molecule 14: 40S ribosomal protein S12



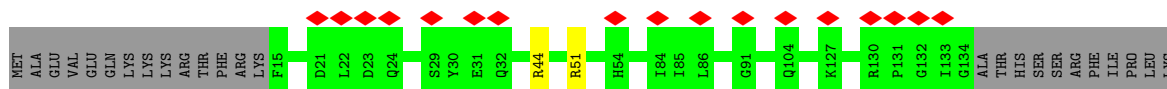
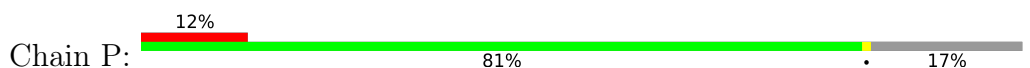
• Molecule 15: 40S ribosomal protein S13



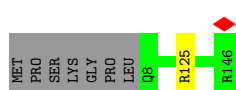
• Molecule 16: 40S ribosomal protein S14



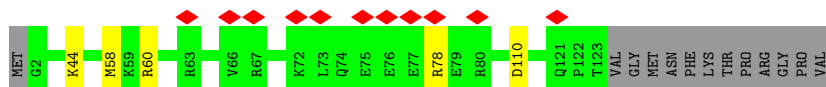
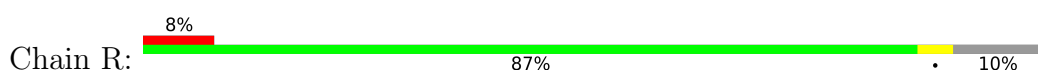
• Molecule 17: 40S ribosomal protein S15



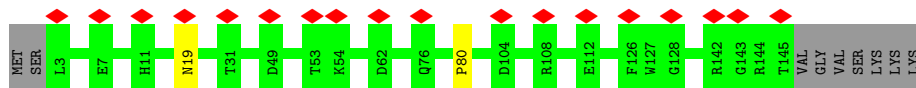
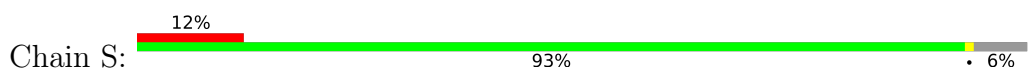
• Molecule 18: 40S ribosomal protein S16



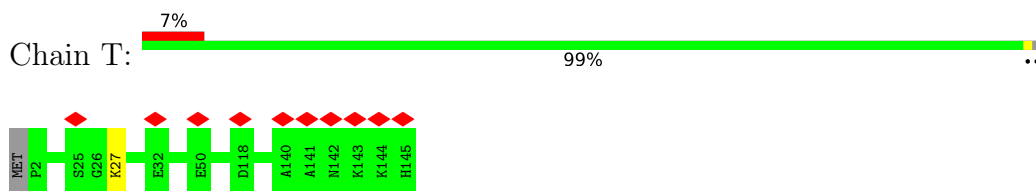
• Molecule 19: 40S ribosomal protein S17



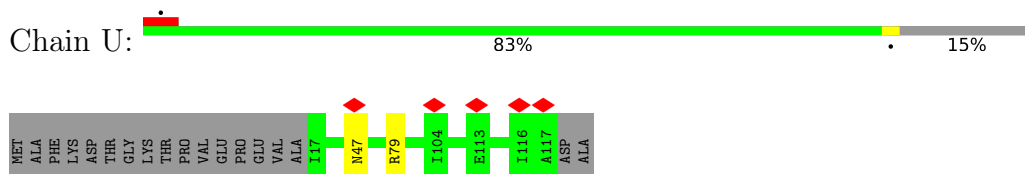
• Molecule 20: 40S ribosomal protein S18



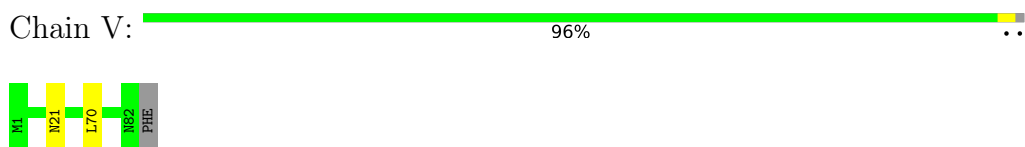
- Molecule 21: 40S ribosomal protein S19



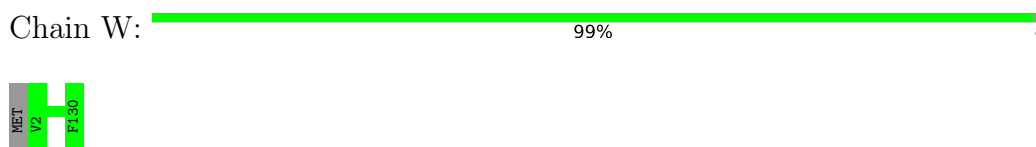
- Molecule 22: 40S ribosomal protein S20



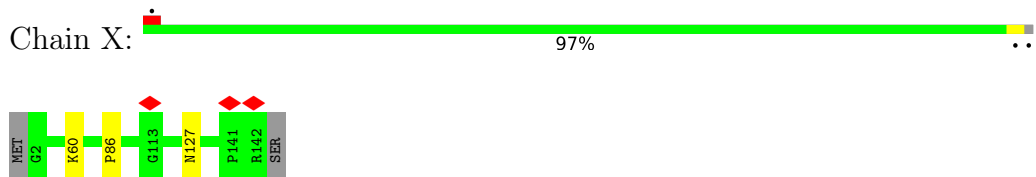
- Molecule 23: 40S ribosomal protein S21



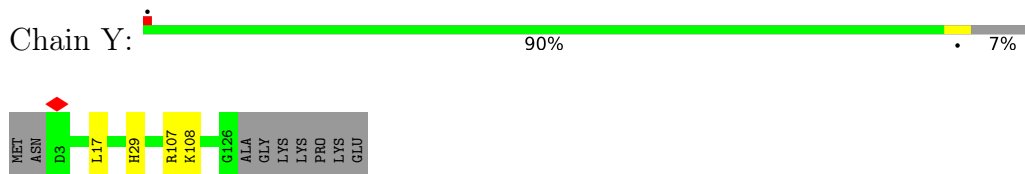
- Molecule 24: 40S ribosomal protein S15a



- Molecule 25: 40S ribosomal protein S23



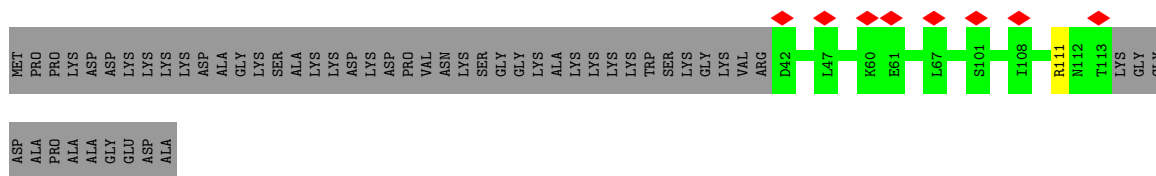
- Molecule 26: 40S ribosomal protein S24



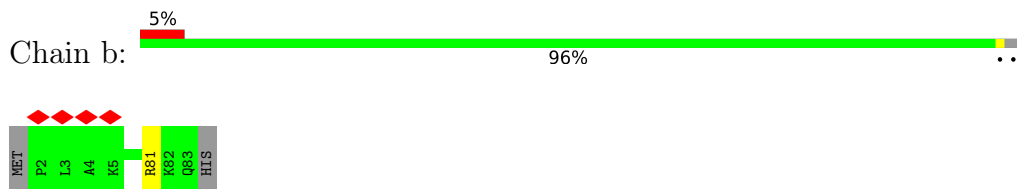
- Molecule 27: 40S ribosomal protein S25



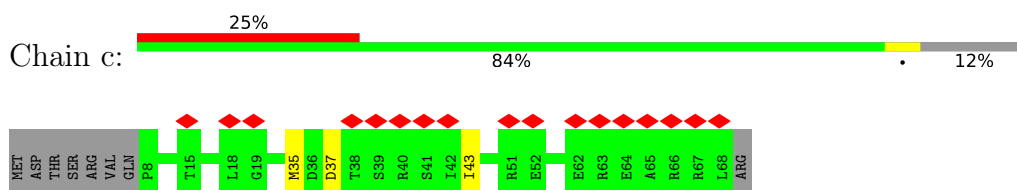




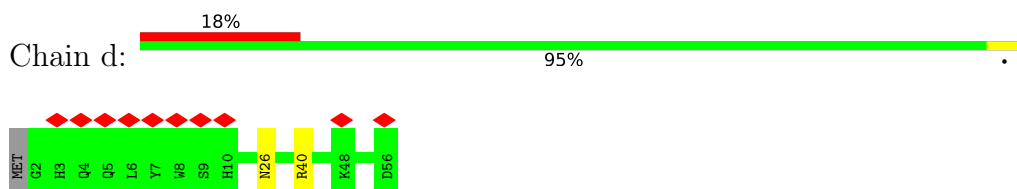
• Molecule 28: 40S ribosomal protein S27



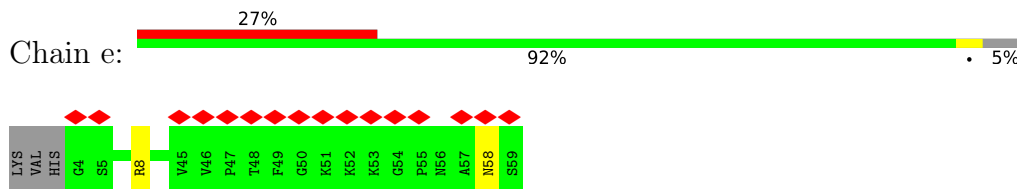
• Molecule 29: 40S ribosomal protein S28



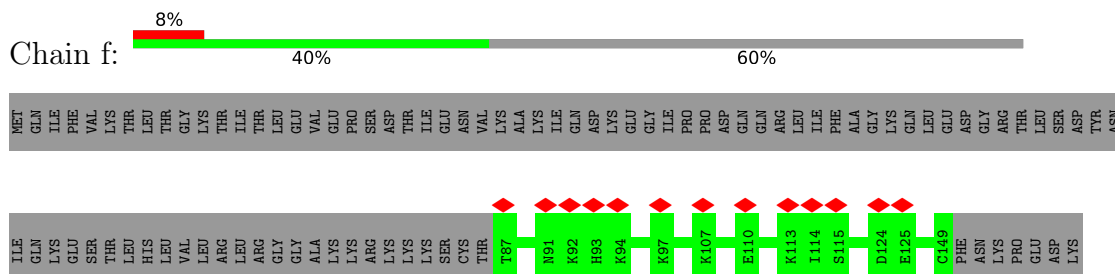
• Molecule 30: 40S ribosomal protein S29



• Molecule 31: 40S ribosomal protein S30



• Molecule 32: Ribosomal protein S27a



• Molecule 33: Receptor of activated protein C kinase 1





CYS  
ALA  
ASN  
VAL  
VAL  
ASN  
PHE  
LYS  
ASP  
PHE  
PHE  
MET  
TYR  
ILE  
ARG  
HIS  
SER  
VAL  
VAL  
ALA  
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GLU  
THR  
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LYS  
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K551  
I550  
R557  
K558  
E559  
LYS  
THR  
ALA

LYS  
THR  
LYS  
LYS  
GLY  
LYS

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83883	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 ( $e^-/\text{\AA}^2$ )	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.194	Depositor
Minimum map value	-0.068	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:  
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	2	0.92	5/39560 (0.0%)	1.36	560/61645 (0.9%)
2	A	0.54	0/1742	0.69	1/2367 (0.0%)
3	B	0.46	0/1756	0.71	1/2350 (0.0%)
4	C	0.54	0/1726	0.73	2/2332 (0.1%)
5	D	0.39	0/1780	0.69	1/2397 (0.0%)
6	E	0.54	0/2118	0.73	0/2849
7	F	0.35	0/1516	0.69	0/2037
8	G	0.40	0/1885	0.62	0/2510
9	H	0.39	0/1524	0.69	0/2042
10	I	0.44	0/1711	0.66	0/2282
11	J	0.55	0/1524	0.70	1/2035 (0.0%)
12	K	0.37	0/824	0.68	0/1112
13	L	0.58	0/1250	0.65	0/1673
14	M	0.36	0/963	0.69	0/1291
15	N	0.46	0/1226	0.68	0/1649
16	O	0.40	0/1022	0.69	1/1372 (0.1%)
17	P	0.36	0/1003	0.60	0/1341
18	Q	0.42	0/1126	0.71	0/1506
19	R	0.38	0/1002	0.70	2/1345 (0.1%)
20	S	0.32	0/1202	0.62	0/1610
21	T	0.35	0/1142	0.65	0/1530
22	U	0.38	0/813	0.70	0/1092
23	V	0.48	0/631	0.63	1/844 (0.1%)
24	W	0.60	0/1051	0.71	0/1406
25	X	0.54	0/1116	0.71	0/1490
26	Y	0.48	0/1031	0.68	0/1370
27	Z	0.33	0/580	0.70	0/780
28	b	0.41	0/653	0.69	0/876
29	c	0.36	0/481	0.80	2/643 (0.3%)
30	d	0.42	0/469	0.60	0/623
31	e	0.41	0/447	0.61	0/587
32	f	0.35	0/520	0.64	0/690

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	g	0.34	0/2497	0.66	1/3399 (0.0%)
34	x	0.41	0/1387	0.69	0/1871
35	y	0.36	0/2539	0.67	2/3430 (0.1%)
36	z	0.36	0/258	0.58	0/331
All	All	0.71	5/82075 (0.0%)	1.08	575/118707 (0.5%)

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
2	A	0	1
5	D	0	1
7	F	0	2
13	L	0	1
20	S	0	1
25	X	0	2
26	Y	0	1
29	c	0	1
33	g	0	2
34	x	0	2
35	y	0	3
All	All	0	17

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	560	A	N9-C4	-6.13	1.34	1.37
1	2	668	A	N9-C4	-5.90	1.34	1.37
1	2	46	A	N9-C4	-5.34	1.34	1.37
1	2	602	G	N9-C4	-5.22	1.33	1.38
1	2	1825	A	N9-C4	5.09	1.41	1.37

The worst 5 of 575 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	356	C	N1-C2-O2	14.05	127.33	118.90
1	2	1597	C	N1-C2-O2	12.37	126.32	118.90
1	2	1016	U	N1-C2-O2	12.37	131.46	122.80
1	2	1016	U	N3-C2-O2	-12.34	113.56	122.20
1	2	356	C	N3-C2-O2	-11.51	113.84	121.90

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	189	ILE	Peptide
5	D	194	PRO	Peptide
7	F	138	ALA	Peptide
7	F	40	ALA	Peptide
13	L	41	GLY	Peptide

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	
2	A	214/295 (72%)	196 (92%)	18 (8%)	0	100	100
3	B	211/264 (80%)	191 (90%)	20 (10%)	0	100	100
4	C	216/293 (74%)	196 (91%)	19 (9%)	1 (0%)	29	68
5	D	223/243 (92%)	202 (91%)	19 (8%)	2 (1%)	17	56
6	E	260/263 (99%)	229 (88%)	31 (12%)	0	100	100
7	F	187/204 (92%)	174 (93%)	12 (6%)	1 (0%)	29	68
8	G	228/249 (92%)	207 (91%)	21 (9%)	0	100	100
9	H	184/194 (95%)	165 (90%)	19 (10%)	0	100	100
10	I	203/208 (98%)	188 (93%)	15 (7%)	0	100	100
11	J	178/194 (92%)	165 (93%)	12 (7%)	1 (1%)	25	64
12	K	93/165 (56%)	85 (91%)	8 (9%)	0	100	100
13	L	149/158 (94%)	127 (85%)	22 (15%)	0	100	100
14	M	121/132 (92%)	107 (88%)	14 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	N	147/151 (97%)	139 (95%)	8 (5%)	0	100	100
16	O	133/151 (88%)	114 (86%)	19 (14%)	0	100	100
17	P	118/145 (81%)	109 (92%)	9 (8%)	0	100	100
18	Q	137/146 (94%)	120 (88%)	17 (12%)	0	100	100
19	R	120/135 (89%)	111 (92%)	9 (8%)	0	100	100
20	S	141/152 (93%)	127 (90%)	14 (10%)	0	100	100
21	T	142/145 (98%)	133 (94%)	9 (6%)	0	100	100
22	U	99/119 (83%)	91 (92%)	8 (8%)	0	100	100
23	V	80/83 (96%)	74 (92%)	6 (8%)	0	100	100
24	W	127/130 (98%)	113 (89%)	14 (11%)	0	100	100
25	X	139/143 (97%)	126 (91%)	12 (9%)	1 (1%)	22	61
26	Y	122/133 (92%)	104 (85%)	18 (15%)	0	100	100
27	Z	70/125 (56%)	60 (86%)	10 (14%)	0	100	100
28	b	80/84 (95%)	68 (85%)	12 (15%)	0	100	100
29	c	59/69 (86%)	53 (90%)	6 (10%)	0	100	100
30	d	53/56 (95%)	46 (87%)	7 (13%)	0	100	100
31	e	54/59 (92%)	50 (93%)	4 (7%)	0	100	100
32	f	61/156 (39%)	52 (85%)	9 (15%)	0	100	100
33	g	312/317 (98%)	268 (86%)	44 (14%)	0	100	100
34	x	173/252 (69%)	159 (92%)	14 (8%)	0	100	100
35	y	311/412 (76%)	270 (87%)	40 (13%)	1 (0%)	41	75
36	z	27/568 (5%)	23 (85%)	4 (15%)	0	100	100
All	All	5172/6593 (78%)	4642 (90%)	523 (10%)	7 (0%)	54	84

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	C	135	GLY
11	J	161	LEU
7	F	41	VAL
25	X	86	PRO
5	D	194	PRO



### 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	
2	A	180/243 (74%)	178 (99%)	2 (1%)	73	88
3	B	194/231 (84%)	193 (100%)	1 (0%)	88	94
4	C	184/225 (82%)	179 (97%)	5 (3%)	44	73
5	D	189/202 (94%)	186 (98%)	3 (2%)	62	83
6	E	224/225 (100%)	222 (99%)	2 (1%)	78	90
7	F	159/170 (94%)	156 (98%)	3 (2%)	57	80
8	G	200/218 (92%)	199 (100%)	1 (0%)	88	94
9	H	167/174 (96%)	167 (100%)	0	100	100
10	I	178/180 (99%)	175 (98%)	3 (2%)	60	82
11	J	160/168 (95%)	158 (99%)	2 (1%)	69	86
12	K	86/136 (63%)	86 (100%)	0	100	100
13	L	135/142 (95%)	127 (94%)	8 (6%)	19	53
14	M	104/108 (96%)	102 (98%)	2 (2%)	57	80
15	N	130/131 (99%)	130 (100%)	0	100	100
16	O	105/119 (88%)	103 (98%)	2 (2%)	57	80
17	P	107/130 (82%)	105 (98%)	2 (2%)	57	80
18	Q	115/121 (95%)	114 (99%)	1 (1%)	78	90
19	R	110/122 (90%)	107 (97%)	3 (3%)	44	73
20	S	124/132 (94%)	123 (99%)	1 (1%)	81	91
21	T	114/115 (99%)	113 (99%)	1 (1%)	78	90
22	U	93/107 (87%)	91 (98%)	2 (2%)	52	78
23	V	66/67 (98%)	65 (98%)	1 (2%)	65	84
24	W	112/113 (99%)	112 (100%)	0	100	100
25	X	113/115 (98%)	113 (100%)	0	100	100
26	Y	108/115 (94%)	105 (97%)	3 (3%)	43	72
27	Z	64/103 (62%)	63 (98%)	1 (2%)	62	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	b	74/76 (97%)	73 (99%)	1 (1%)	67	85
29	c	54/62 (87%)	54 (100%)	0	100	100
30	d	48/49 (98%)	46 (96%)	2 (4%)	30	63
31	e	45/48 (94%)	43 (96%)	2 (4%)	28	62
32	f	56/140 (40%)	56 (100%)	0	100	100
33	g	272/275 (99%)	270 (99%)	2 (1%)	84	93
34	x	146/208 (70%)	143 (98%)	3 (2%)	53	79
35	y	275/367 (75%)	271 (98%)	4 (2%)	65	84
36	z	28/512 (6%)	28 (100%)	0	100	100
All	All	4519/5649 (80%)	4456 (99%)	63 (1%)	68	85

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	L	132	ARG
33	g	241	PHE
17	P	51	ARG
33	g	118	ARG
35	y	71	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
17	P	79	HIS
22	U	92	HIS
18	Q	80	GLN
20	S	120	HIS
26	Y	63	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1647/1882 (87%)	534 (32%)	50 (3%)

5 of 534 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	C
1	2	4	C
1	2	5	U
1	2	14	C
1	2	17	C

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1316	C
1	2	1438	A
1	2	1868	U
1	2	1330	G
1	2	1425	G

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

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

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

There are no monosaccharides in this entry.

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

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

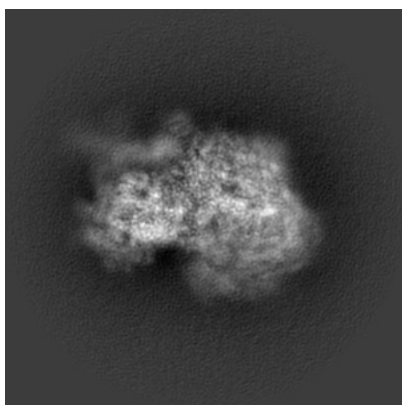
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4353. These allow visual inspection of the internal detail of the map and identification of artifacts.

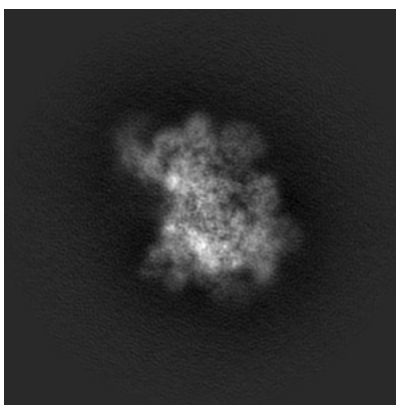
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

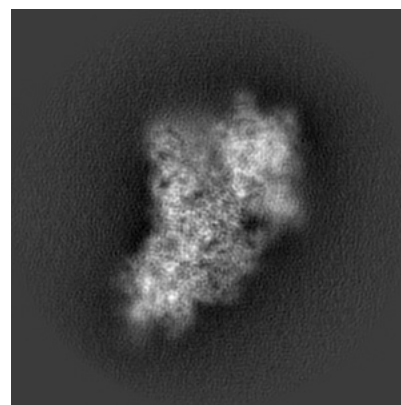
#### 6.1.1 Primary map



X



Y

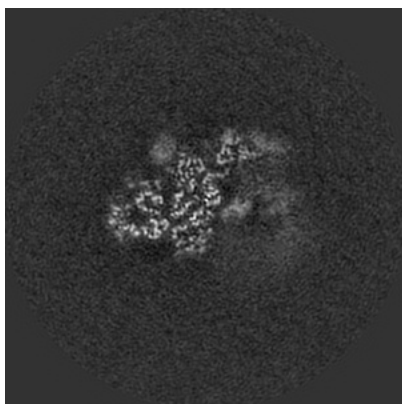


Z

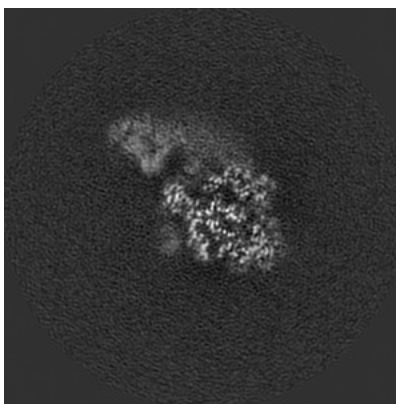
The images above show the map projected in three orthogonal directions.

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

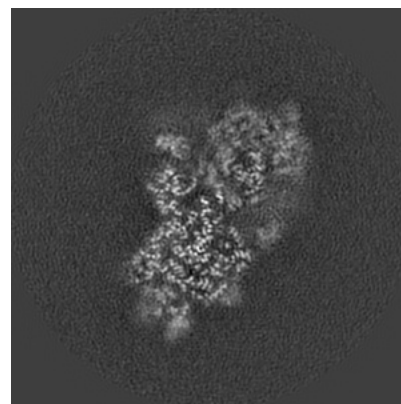
#### 6.2.1 Primary map



X Index: 180



Y Index: 180

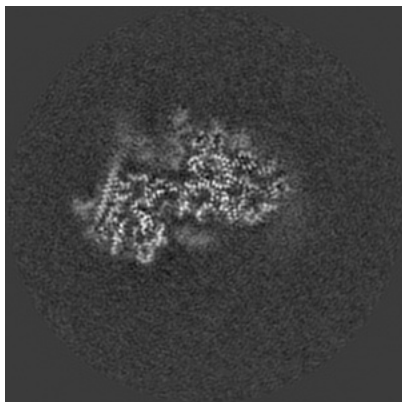


Z Index: 180

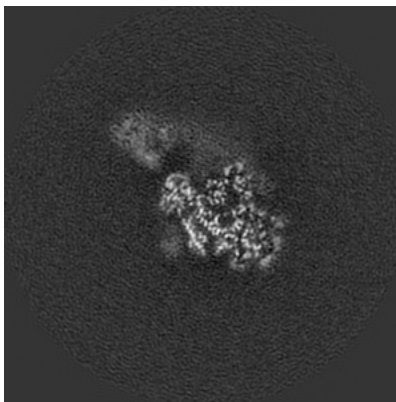
The images above show central slices of the map in three orthogonal directions.

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

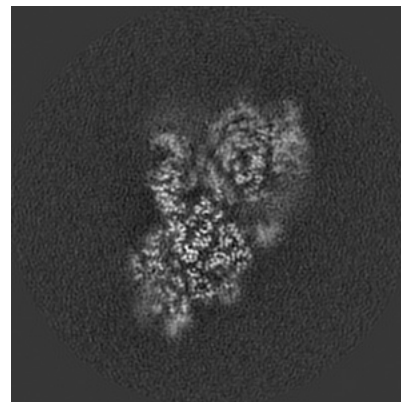
### 6.3.1 Primary map



X Index: 145



Y Index: 175



Z Index: 178

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

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

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

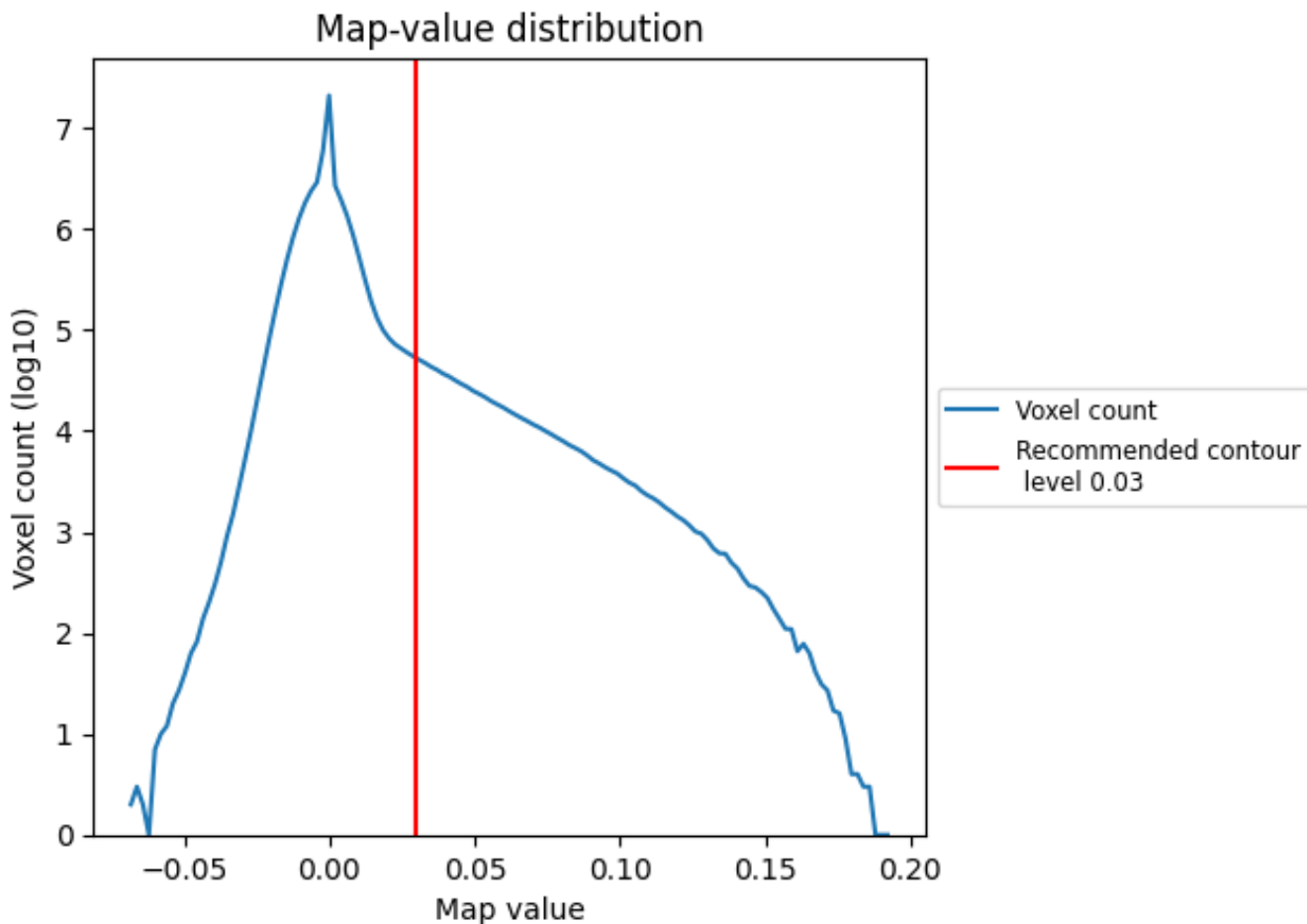
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

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

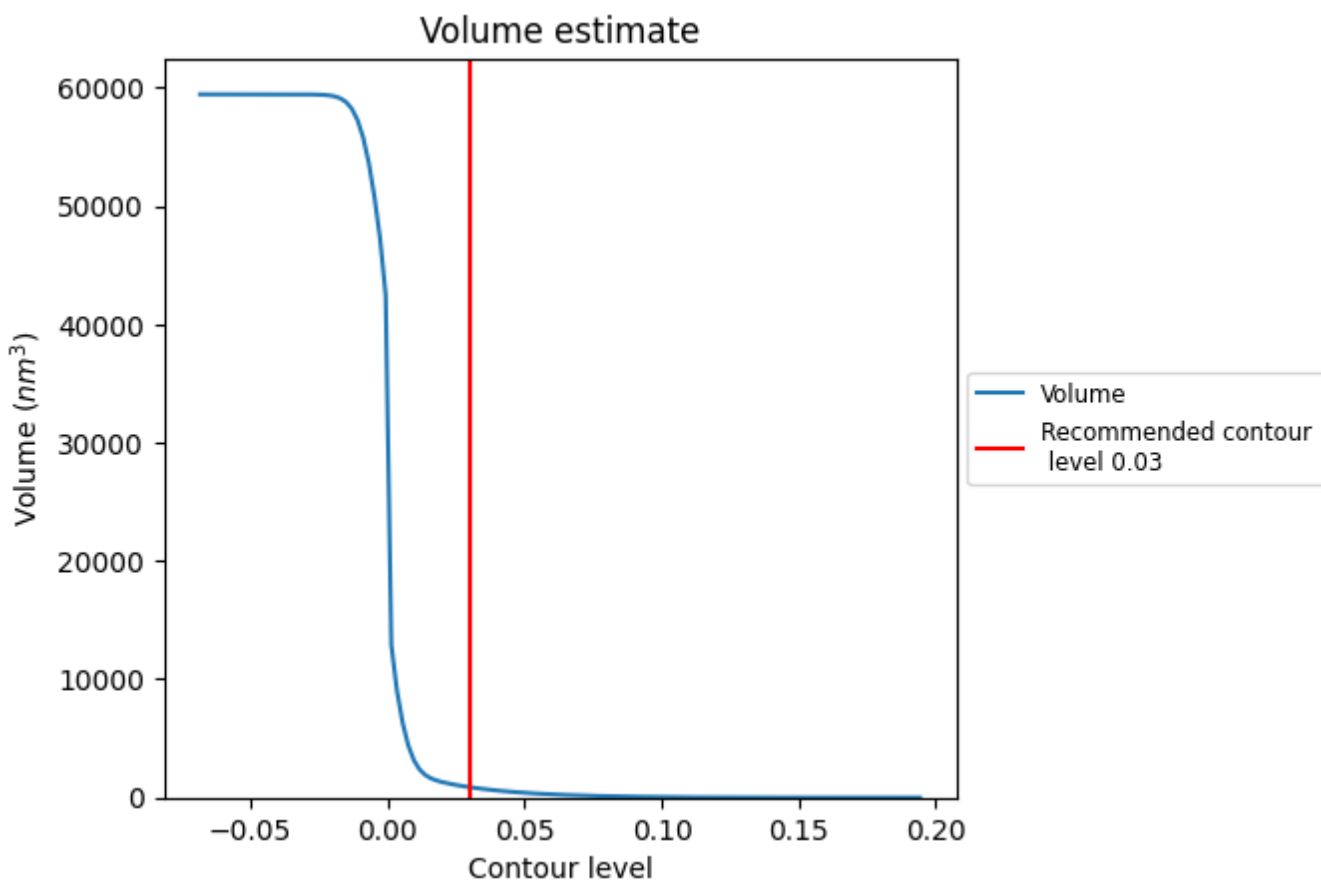
### 7.1 Map-value distribution [i](#)



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



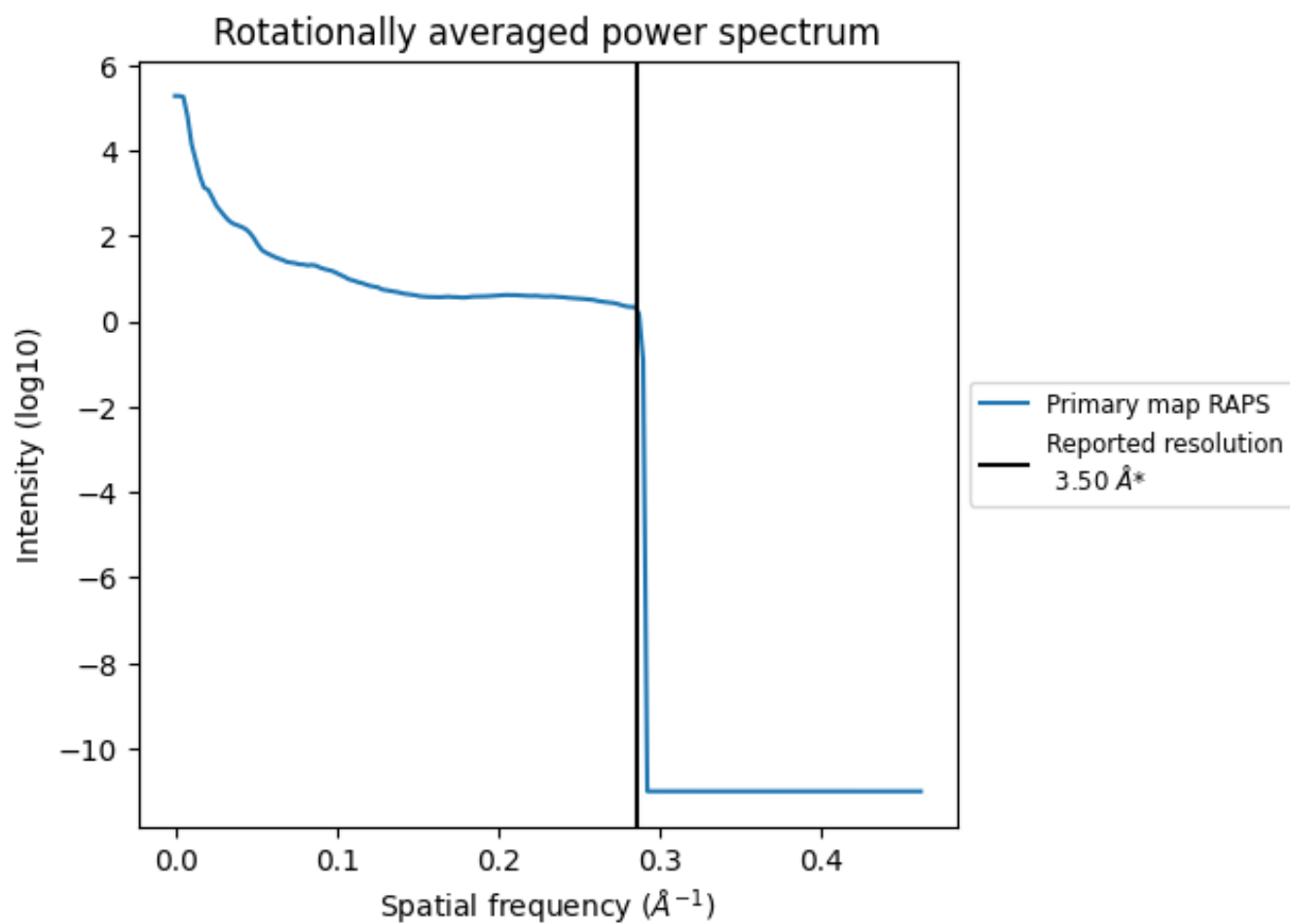
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 873 nm<sup>3</sup>; this corresponds to an approximate mass of 789 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 [\(i\)](#)

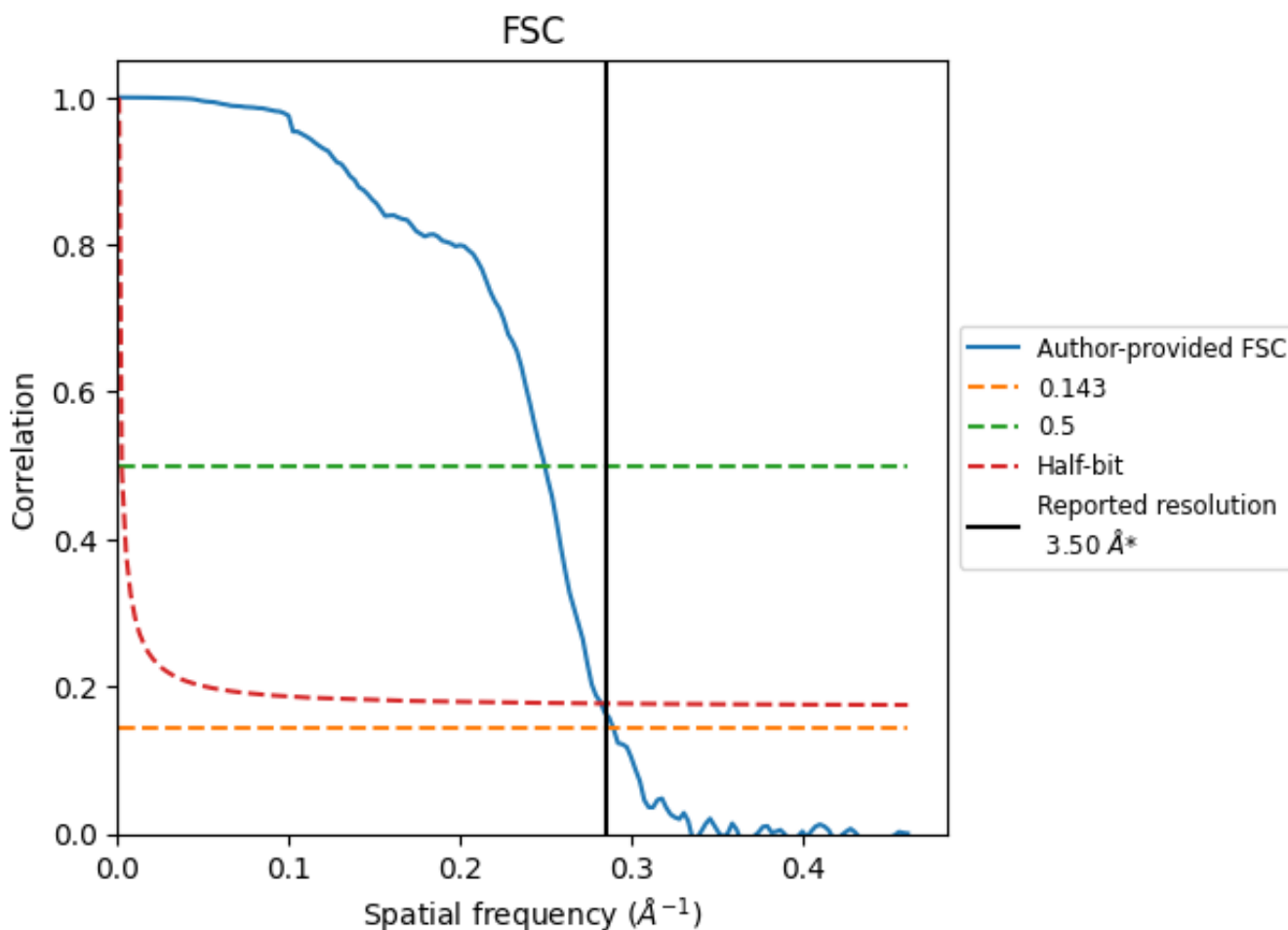


\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>

## 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 0.286 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

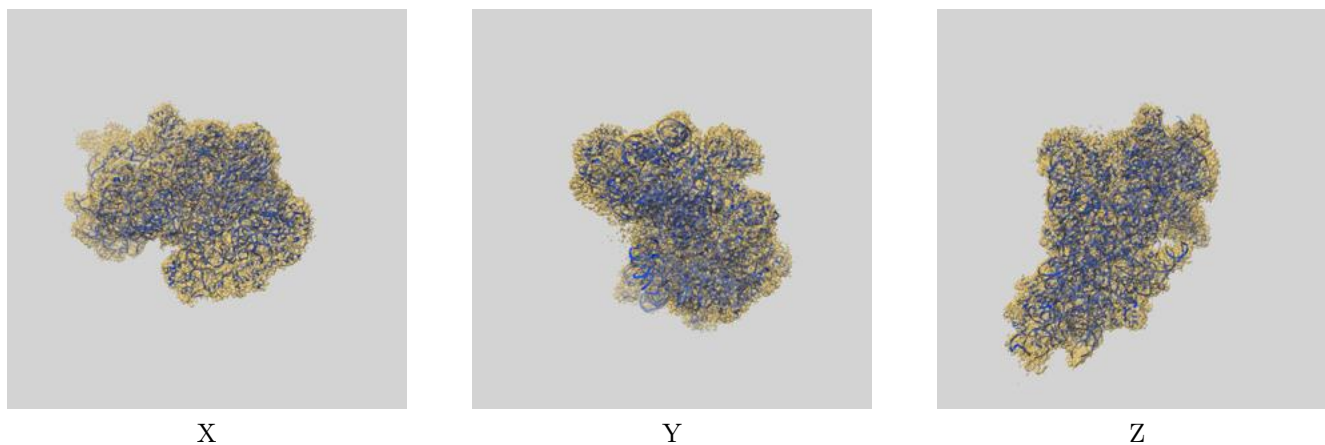
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.46	4.01	3.54
Unmasked-calculated*	-	-	-

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

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

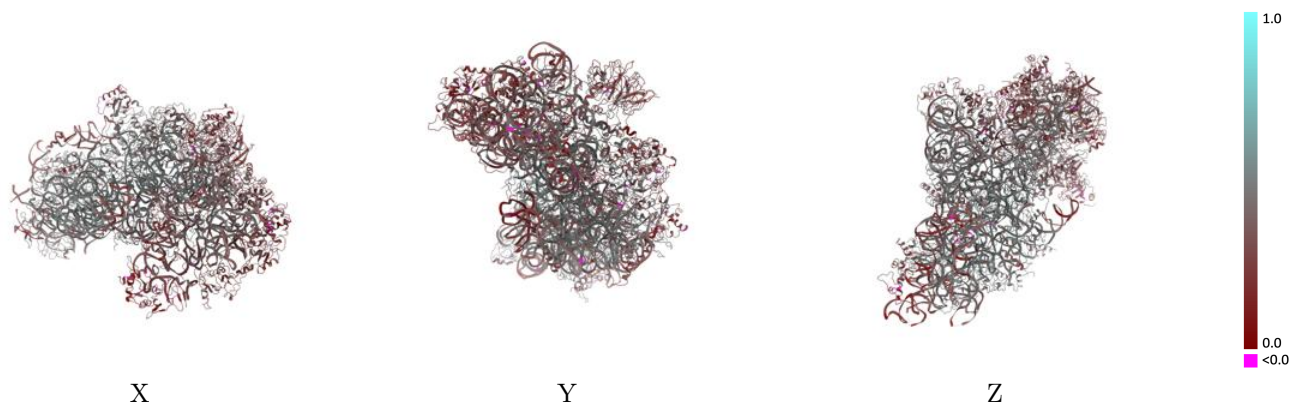
This section contains information regarding the fit between EMDB map EMD-4353 and PDB model 6G5I. Per-residue inclusion information can be found in section 3 on page 11.

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



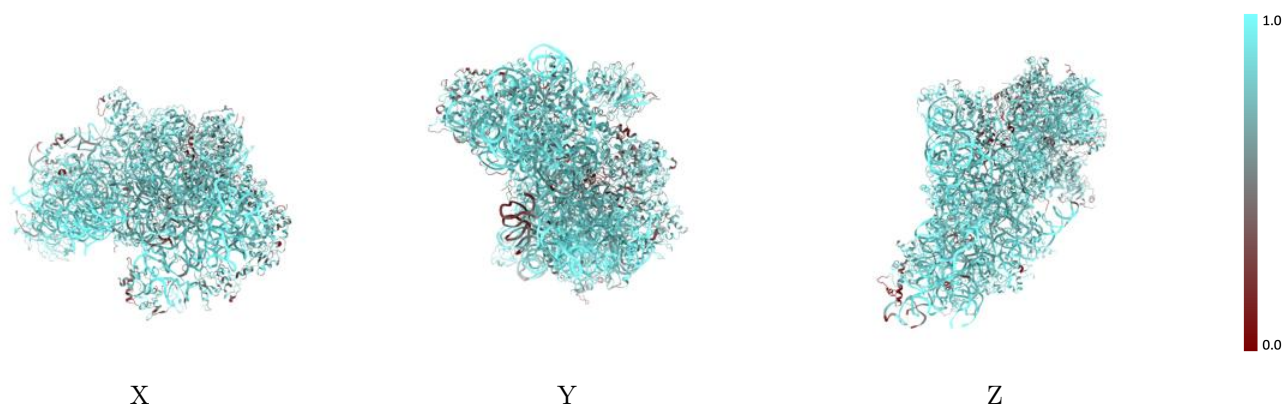
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



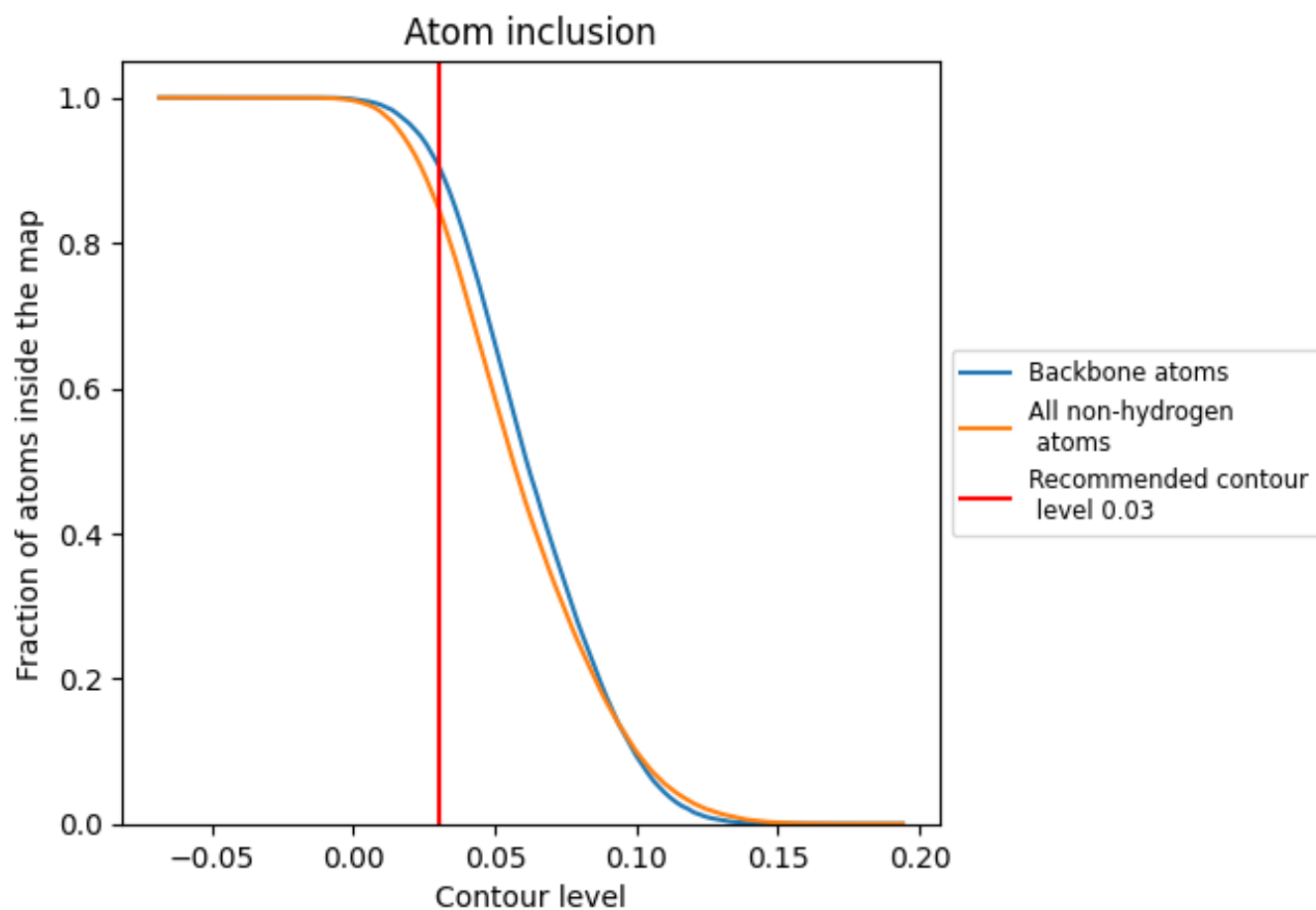
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 85% 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 (0.03) and Q-score for the entire model and for each chain.


Chain	Atom inclusion	Q-score
All	 0.8496	 0.3950
2	 0.9343	 0.4140
A	 0.8588	 0.4370
B	 0.8393	 0.4150
C	 0.8305	 0.4650
D	 0.7074	 0.3450
E	 0.8602	 0.4720
F	 0.7180	 0.2950
G	 0.8522	 0.4030
H	 0.7493	 0.3450
I	 0.7141	 0.3860
J	 0.8749	 0.4650
K	 0.8256	 0.3120
L	 0.8551	 0.4700
M	 0.6443	 0.2260
N	 0.8551	 0.4440
O	 0.8224	 0.4030
P	 0.7275	 0.3040
Q	 0.8127	 0.3760
R	 0.7277	 0.3800
S	 0.7234	 0.2690
T	 0.7784	 0.3090
U	 0.7775	 0.3640
V	 0.8298	 0.4530
W	 0.8485	 0.4890
X	 0.8422	 0.4800
Y	 0.9035	 0.4560
Z	 0.7094	 0.2580
b	 0.8089	 0.4300
c	 0.5705	 0.2700
d	 0.7302	 0.3990
e	 0.6581	 0.3720
f	 0.6398	 0.2300
g	 0.7887	 0.3220
x	 0.7485	 0.4010



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Chain	Atom inclusion	Q-score
y	 0.5770	 0.2950
z	 0.6104	 0.3640