



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 06:33 AM UTC

PDB ID : 6CB1 / pdb_00006cb1
EMDB ID : EMD-7445
Title : Yeast nucleolar pre-60S ribosomal subunit (state 3)
Authors : Sanghai, Z.A.; Miller, L.; Barandun, J.; Hunziker, M.; Chaker-Margot, M.;
Klinge, S.
Deposited on : 2018-02-01
Resolution : 4.60 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

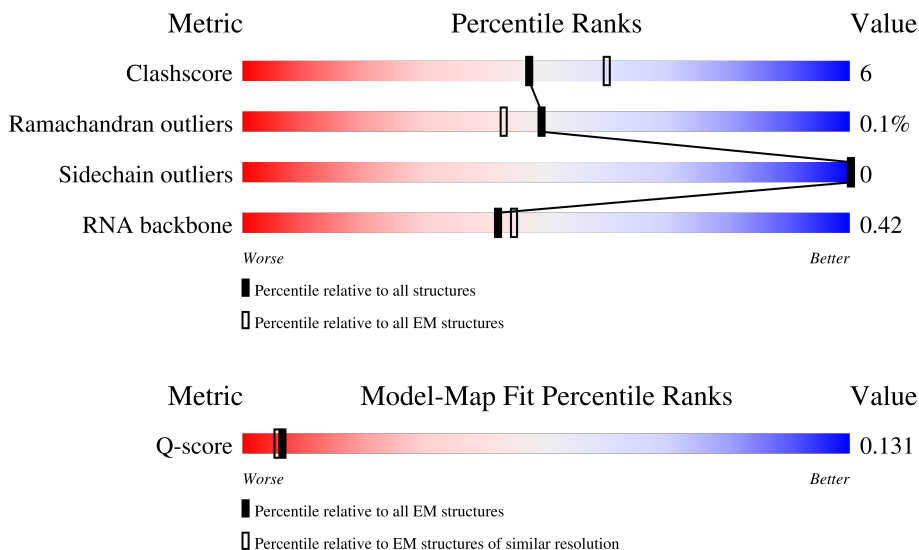
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.60 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	2407 (4.10 - 5.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3396	
2	2	158	
3	6	232	

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Mol	Chain	Length	Quality of chain
4	A	463	11% 78% 8% 15%
5	C	362	9% 84% 13%
6	D	306	60% 38%
7	E	176	15% 94% 2%
8	F	244	8% 95% 2%
9	G	256	37% 69% 27%
10	I	295	10% 92% 6%
11	K	376	32% 64% 5% 31%
12	L	199	8% 50% 47%
13	M	138	24% 91% 7%
14	N	204	25% 83% 14%
15	O	199	32% 88% 8%
16	P	184	33% 67% 33%
17	Q	186	71% 29%
18	S	172	27% 92% 7%
19	X	142	89% 89% 11%
20	Y	127	12% 94% 5%
21	Z	136	76% 95% 2%
22	7	231	23% 65% 32%
23	b	291	15% 81% 17%
24	c	105	58% 91% 8%
25	d	465	86% 99%
26	e	130	29% 87% 12%
27	f	107	25% 97% 2%
28	g	121	70% 79% 17%

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Mol	Chain	Length	Quality of chain
29	h	120	
30	i	100	
31	j	88	
32	k	78	
33	m	102	
34	n	605	
35	o	220	
36	p	505	
37	s	569	
38	t	322	
39	x	28	
40	z	278	

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 69945 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 35S pre-ribosomal RNA miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1370	29343	13096	5306	9571	1370	0	0

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	158	3353	1500	586	1109	158	0	0

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	6	87	1838	823	309	619	87	0	0

- Molecule 4 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	A	394	1946	1158	394	394	0	0

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	C	314	1553	925	314	314	0	0

- Molecule 6 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	D	190	948	564	190	190	4	0	0

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	E	170	843	503	170	170	0	0

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	F	242	1195	711	242	242	0	0

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	G	187	926	552	187	187	0	0

- Molecule 10 is a protein called Ribosome production factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	I	288	1428	852	288	288	0	0

- Molecule 11 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	K	260	1293	773	260	260	0	0

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	L	106	525	313	106	106	0	0

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	M	128	633	377	128	128	0	0

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	176	Total	C	N	O	0	0
			871	519	176	176		

- Molecule 15 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	O	184	Total	C	N	O	0	0
			908	540	184	184		

- Molecule 16 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	124	Total	C	N	O	0	0
			616	368	124	124		

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	132	Total	C	N	O	0	0
			653	389	132	132		

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	S	171	Total	C	N	O	0	0
			851	509	171	171		

- Molecule 19 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	X	141	Total	C	N	O	0	0
			700	418	141	141		

- Molecule 20 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	Y	126	Total	C	N	O	0	0
			623	371	126	126		

- Molecule 21 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Z	135	Total	C	N	O	0	0
			667	397	135	135		

- Molecule 22 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	7	156	Total	C	N	O	0	0
			773	461	156	156		

- Molecule 23 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	b	242	Total	C	N	O	0	0
			1201	717	242	242		

- Molecule 24 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	c	97	Total	C	N	O	0	0
			476	282	97	97		

- Molecule 25 is a protein called Ribosome biogenesis protein YTM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	d	465	Total	C	N	O	0	0
			2288	1358	465	465		

- Molecule 26 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	e	114	Total	C	N	O	0	0
			564	336	114	114		

- Molecule 27 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	f	106	Total	C	N	O	0	0
			522	310	106	106		

- Molecule 28 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	g	101	Total	C	N	O	0	0
			498	296	101	101		

- Molecule 29 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	h	119	Total	C	N	O	0	0
			593	355	119	119		

- Molecule 30 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	i	84	Total	C	N	O	0	0
			416	248	84	84		

- Molecule 31 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	72	Total	C	N	O	S	0	0
			357	209	72	72	4		

- Molecule 32 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	k	77	Total	C	N	O	0	0
			382	228	77	77		

- Molecule 33 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	m	74	Total	C	N	O	0	0
			370	222	74	74		

- Molecule 34 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	n	341	Total	C	N	O	0	0
			1693	1011	341	341		

- Molecule 35 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms			AltConf	Trace	
35	o	133	Total	C	N	O	0	0
			656	390	133	133		

- Molecule 36 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms			AltConf	Trace	
36	p	437	Total	C	N	O	0	0
			2158	1284	437	437		

- Molecule 37 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms			AltConf	Trace	
37	s	512	Total	C	N	O	0	0
			2537	1513	512	512		

- Molecule 38 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms			AltConf	Trace	
38	t	282	Total	C	N	O	0	0
			1397	833	282	282		

- Molecule 39 is a protein called BRX1 associated peptide.

Mol	Chain	Residues	Atoms			AltConf	Trace	
39	x	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 40 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms			AltConf	Trace	
40	z	243	Total	C	N	O	0	0
			1209	723	243	243		

- Molecule 41 is ZINC ION (CCD ID: ZN) (formula: Zn).

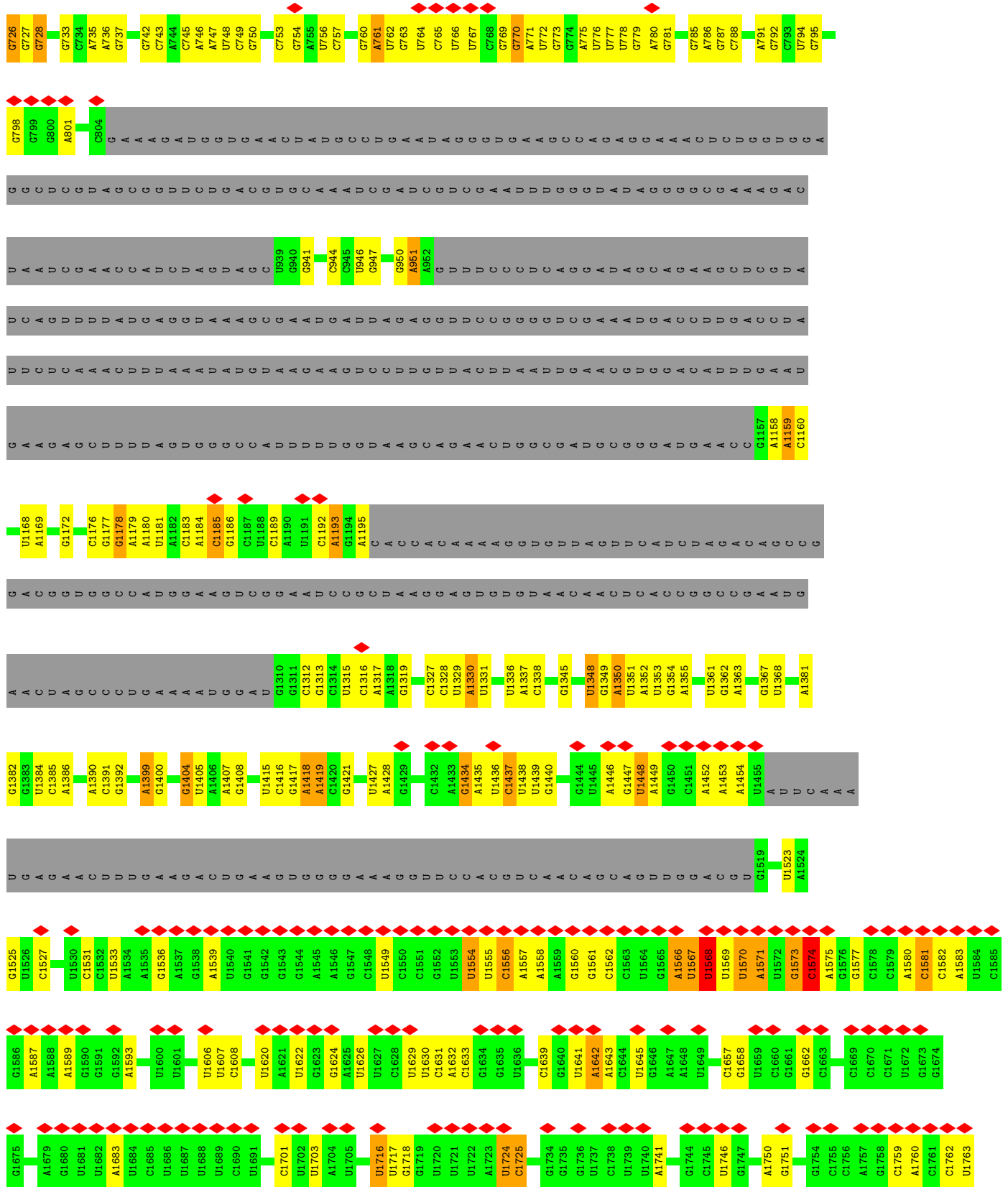
Mol	Chain	Residues	Atoms		AltConf
41	D	1	Total	Zn	0
			1	1	
41	j	1	Total	Zn	0
			1	1	

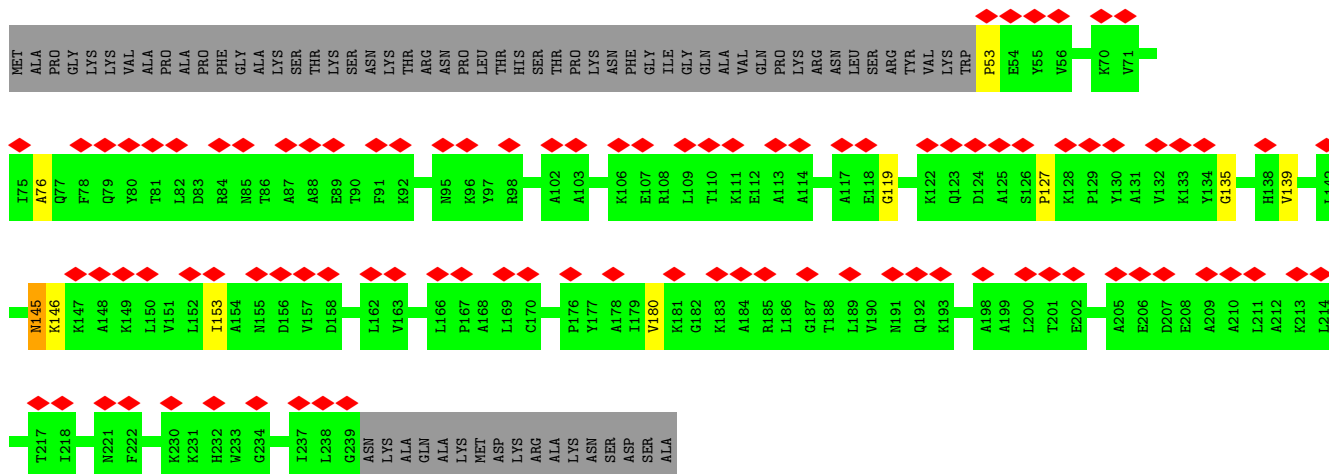
3 Residue-property plots

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

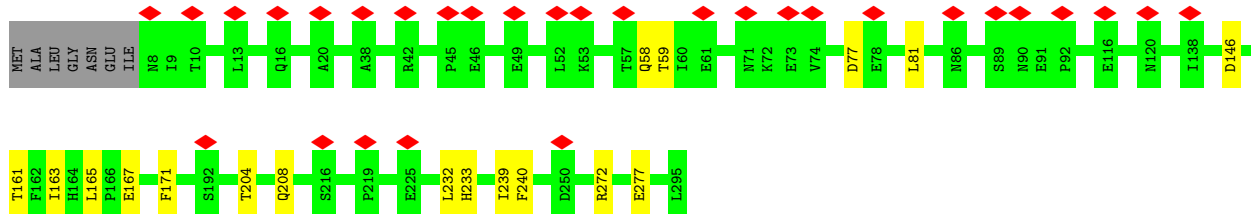
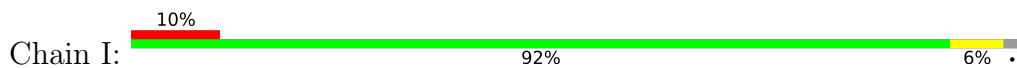
• Molecule 1: 35S pre-ribosomal RNA miscRNA



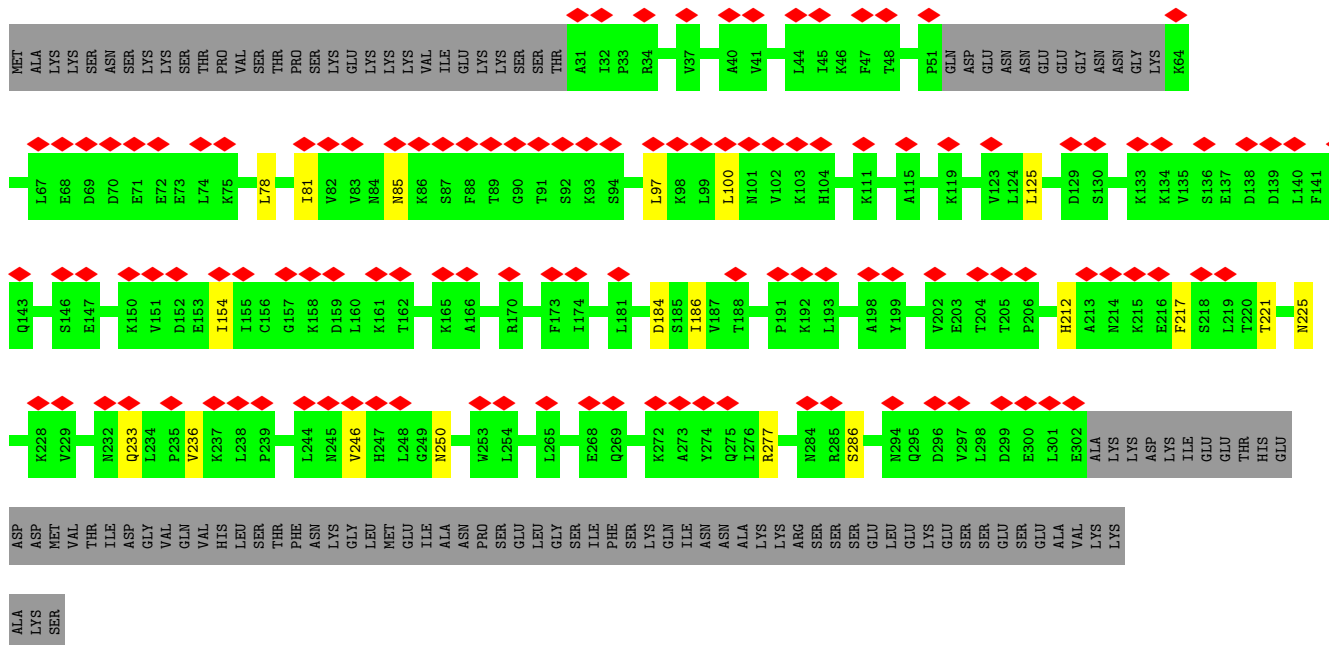




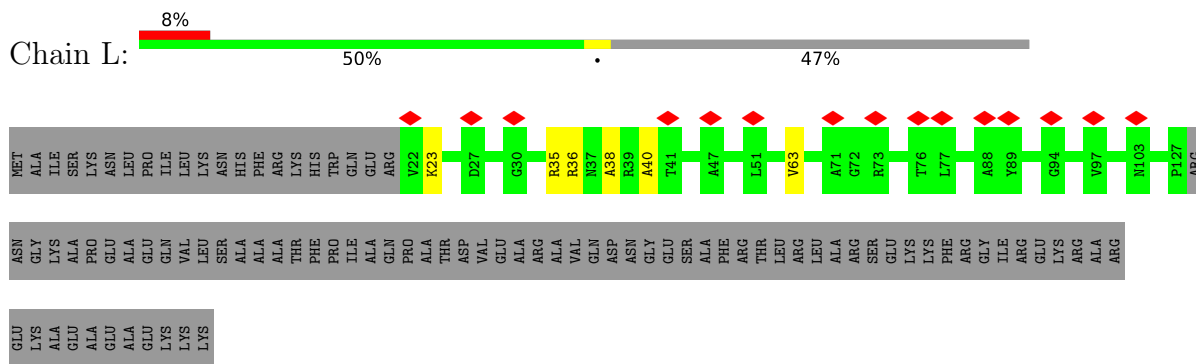
• Molecule 10: Ribosome production factor 1



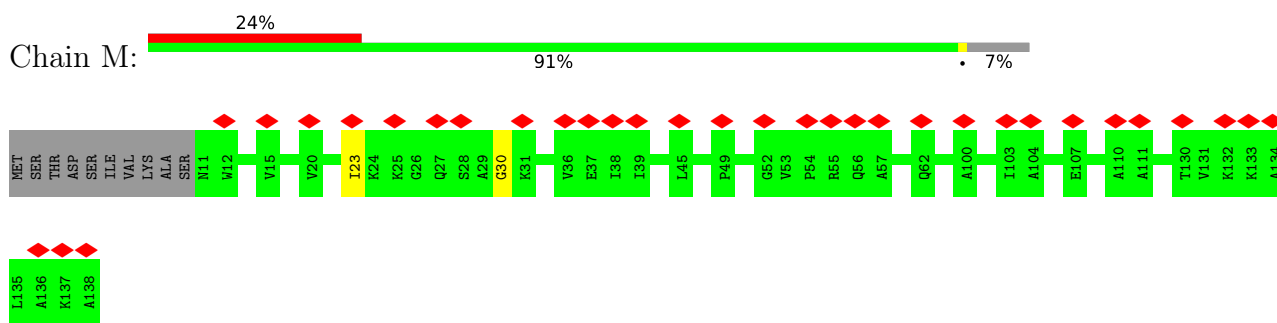
• Molecule 11: Proteasome-interacting protein CIC1



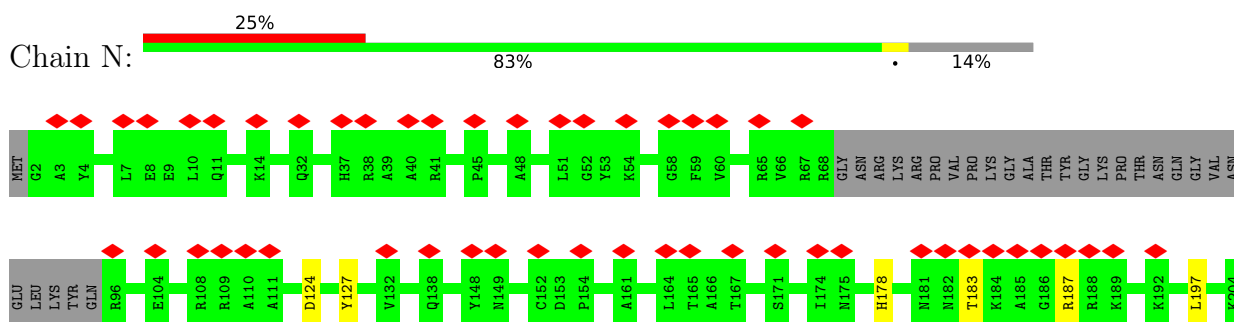
• Molecule 12: 60S ribosomal protein L13-A



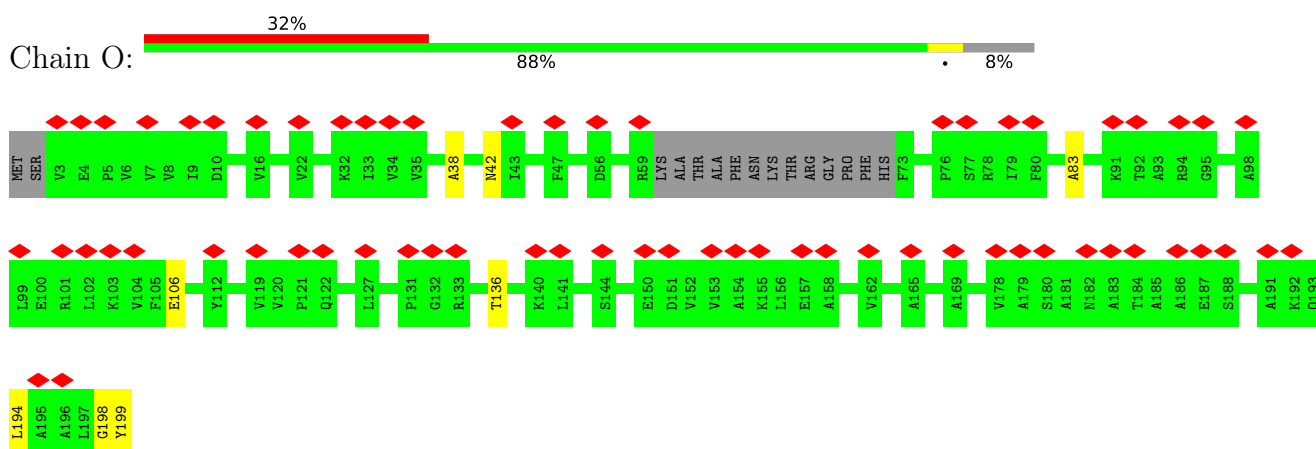
• Molecule 13: 60S ribosomal protein L14-A



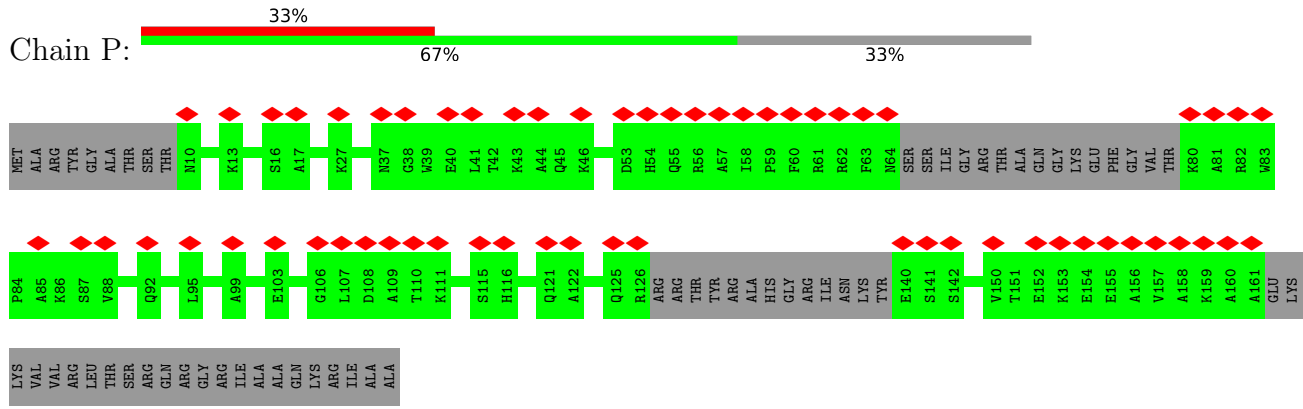
• Molecule 14: 60S ribosomal protein L15-A



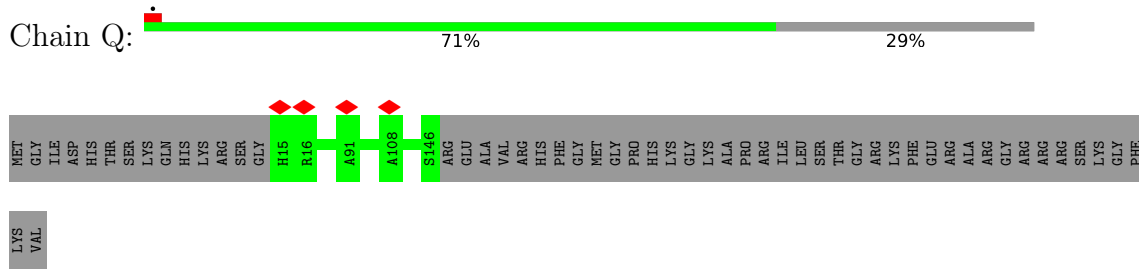
• Molecule 15: 60S ribosomal protein L16-A



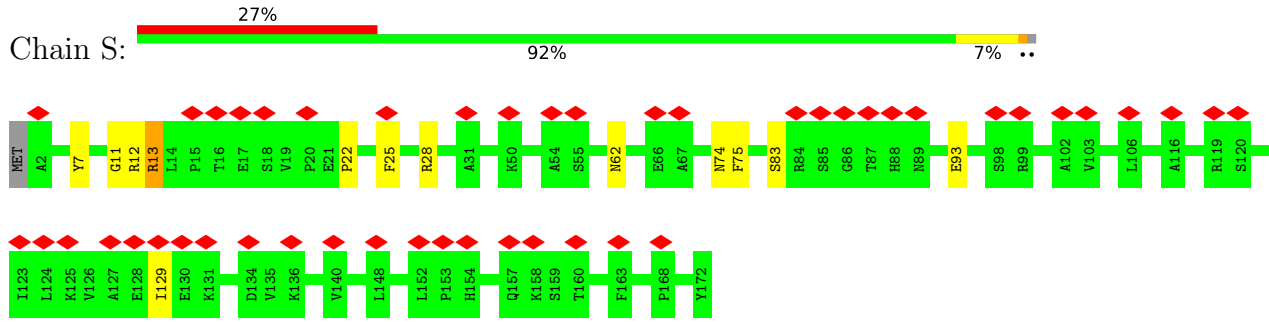
• Molecule 16: 60S ribosomal protein L17-A



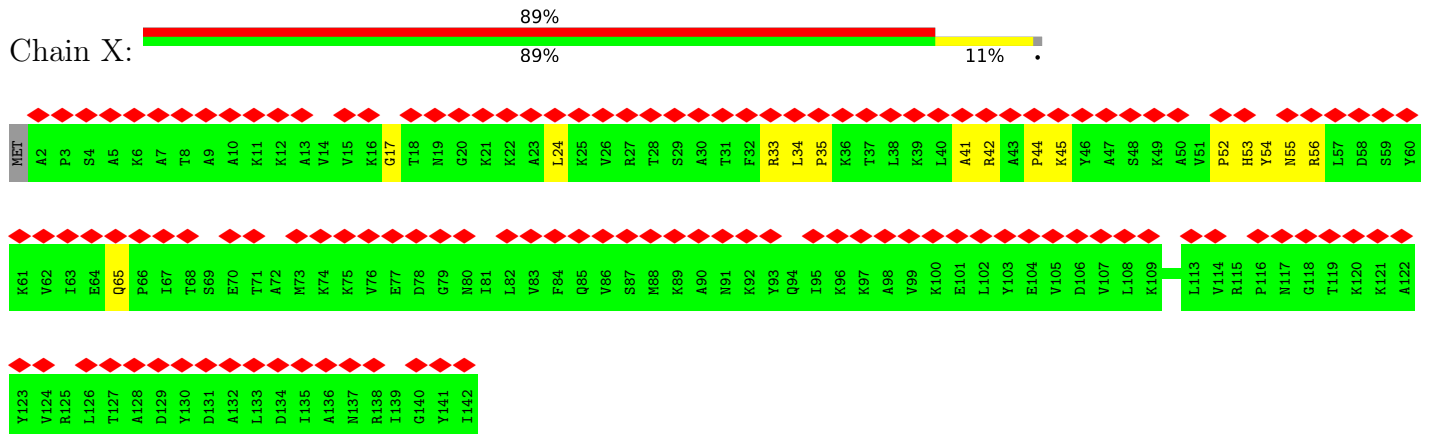
• Molecule 17: 60S ribosomal protein L18-A



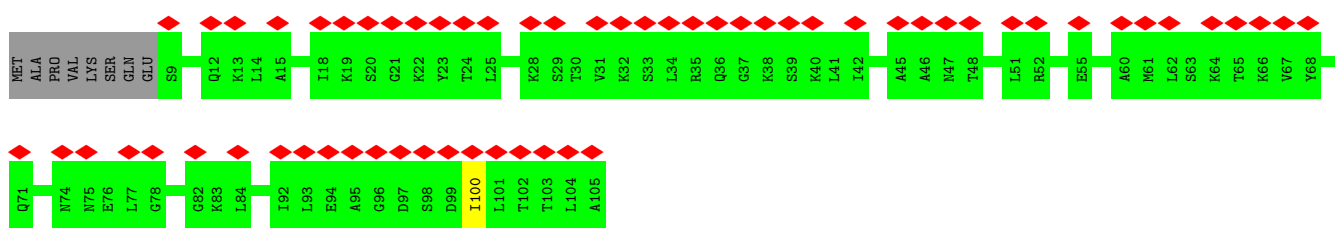
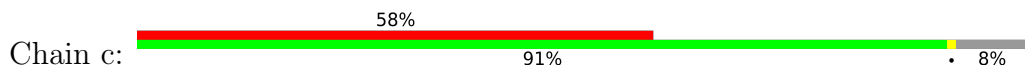
• Molecule 18: 60S ribosomal protein L20-A



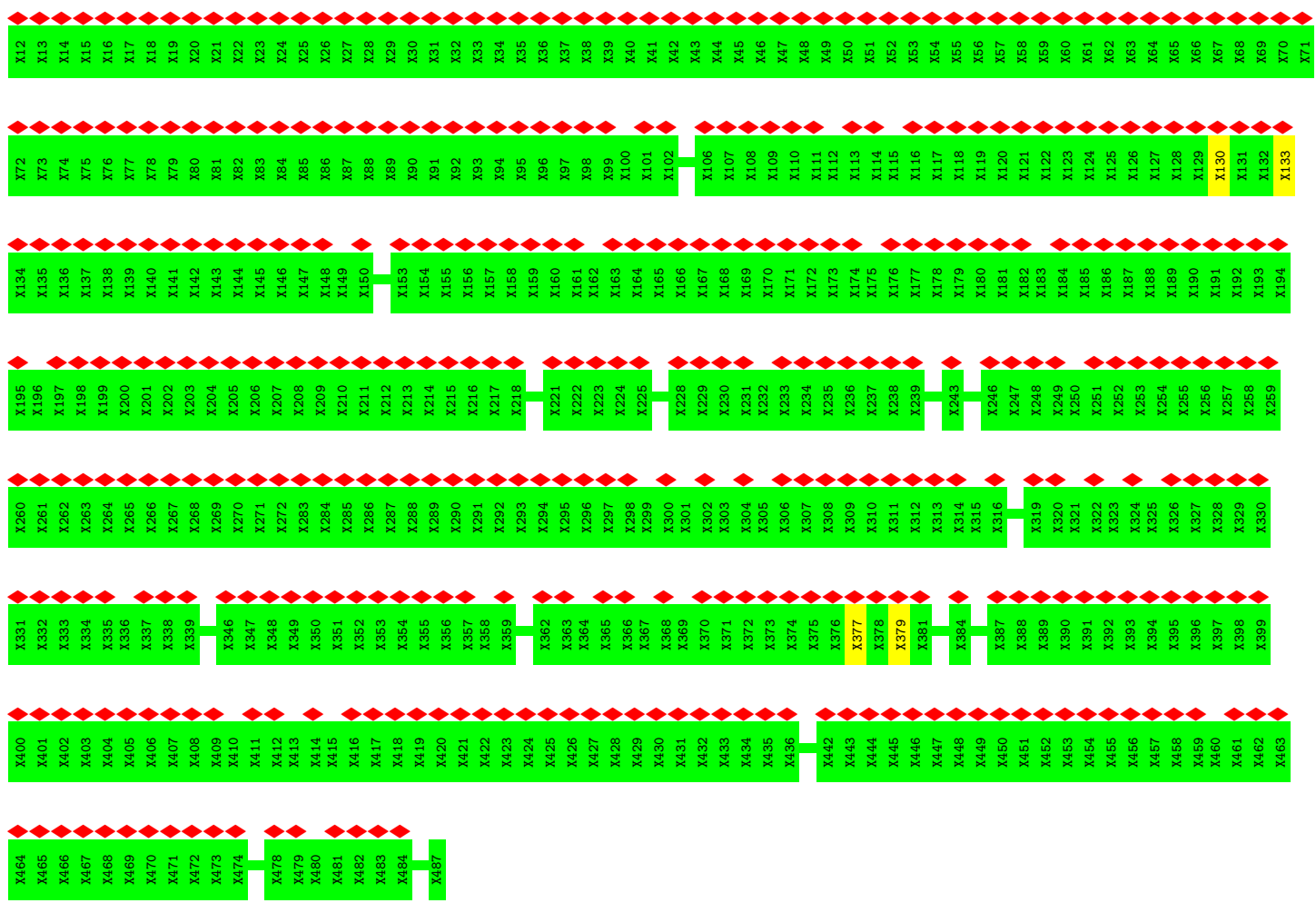
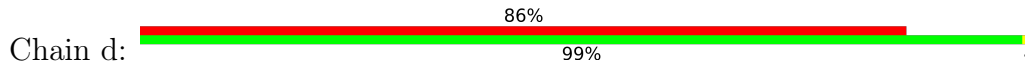
• Molecule 19: 60S ribosomal protein L25



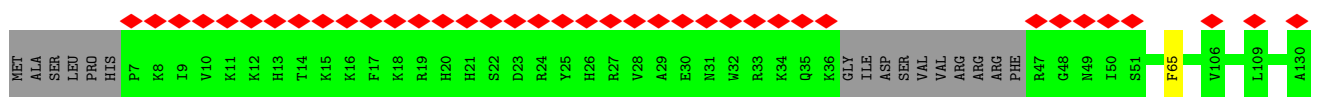
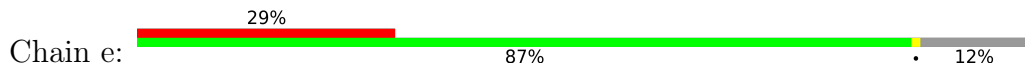
• Molecule 20: 60S ribosomal protein L26-A



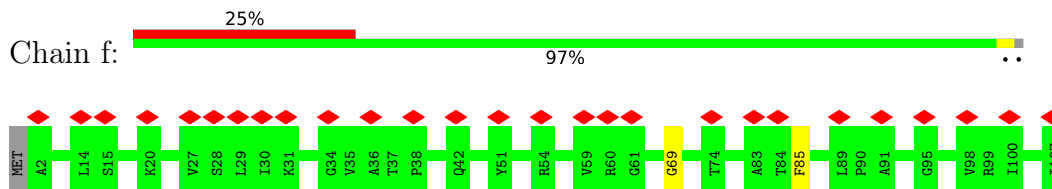
• Molecule 25: Ribosome biogenesis protein YTM1



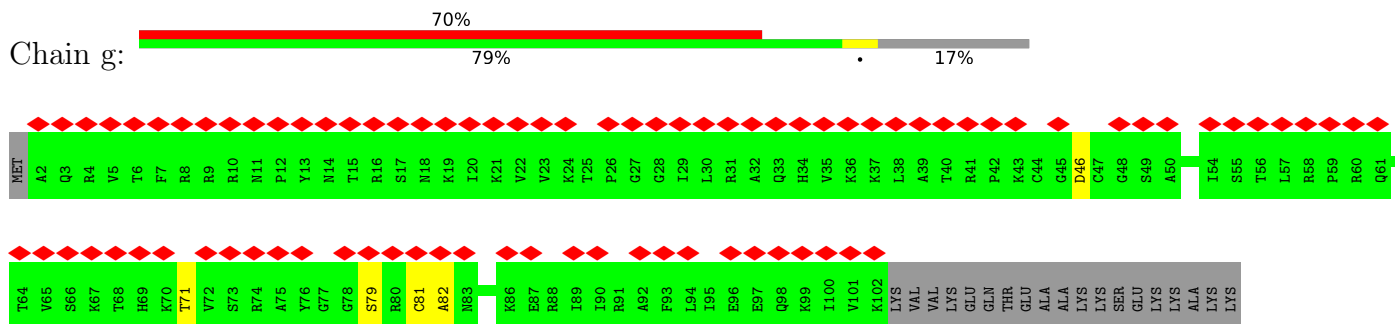
• Molecule 26: 60S ribosomal protein L32



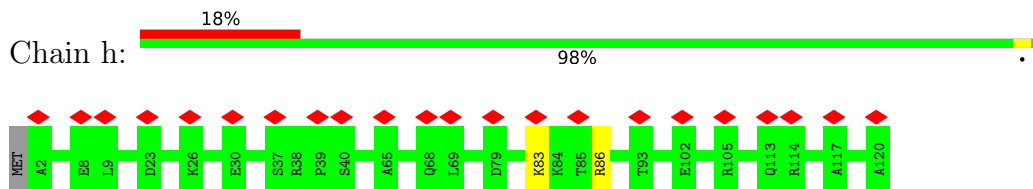
- Molecule 27: 60S ribosomal protein L33-A



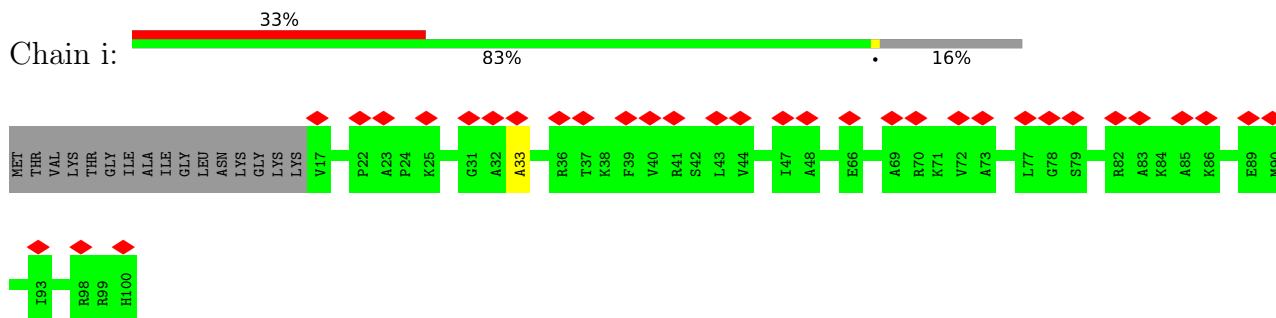
- Molecule 28: 60S ribosomal protein L34-A



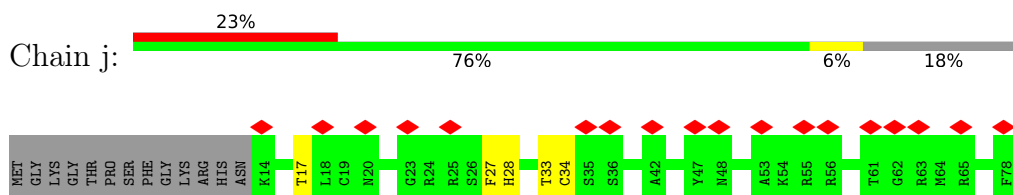
- Molecule 29: 60S ribosomal protein L35-A



- Molecule 30: 60S ribosomal protein L36-A

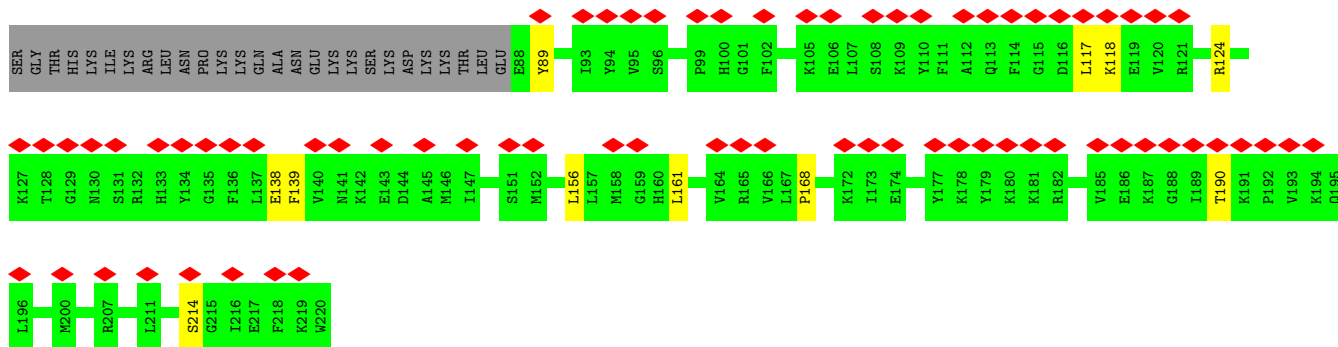


- Molecule 31: 60S ribosomal protein L37-A

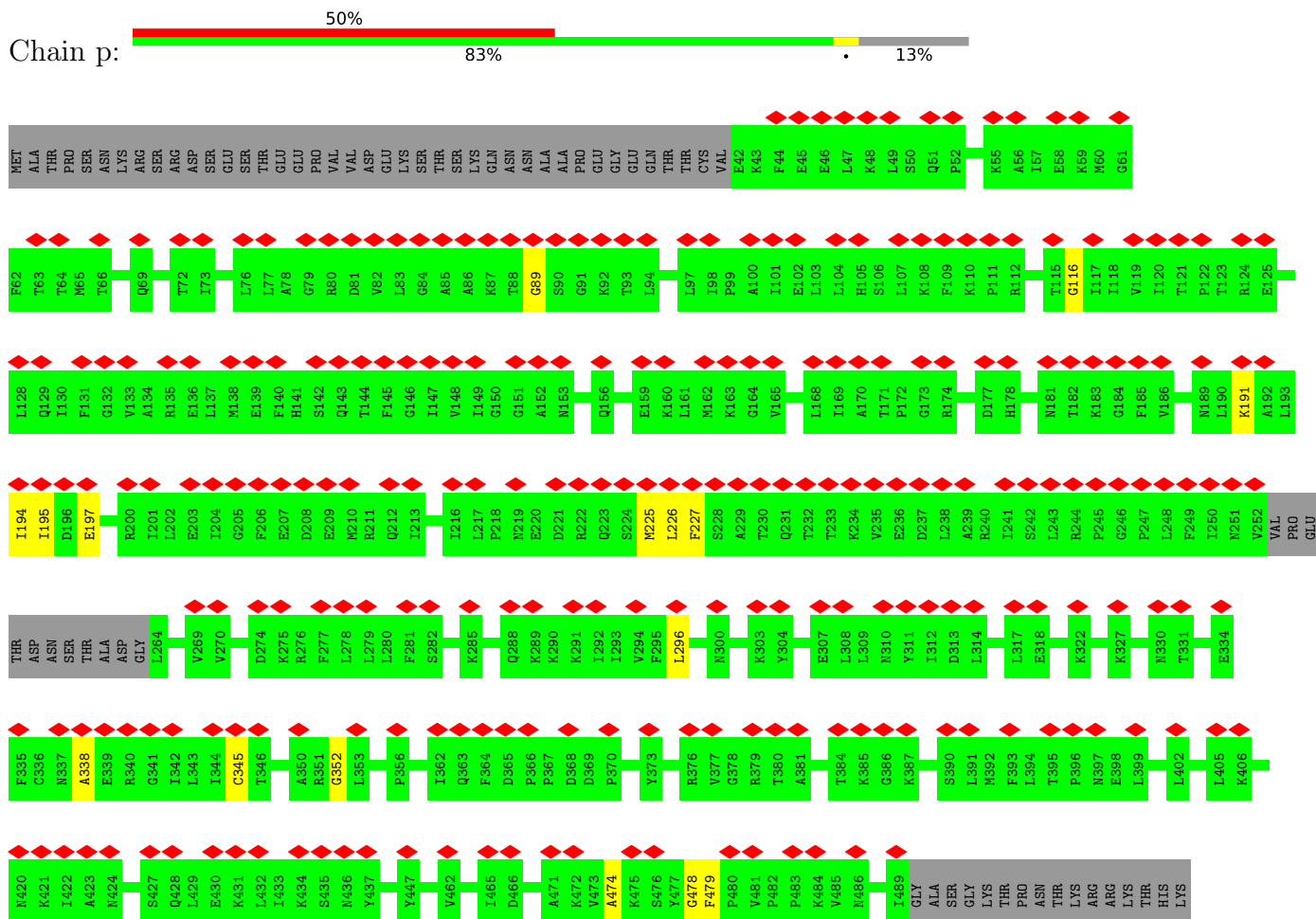


- Molecule 32: 60S ribosomal protein L38

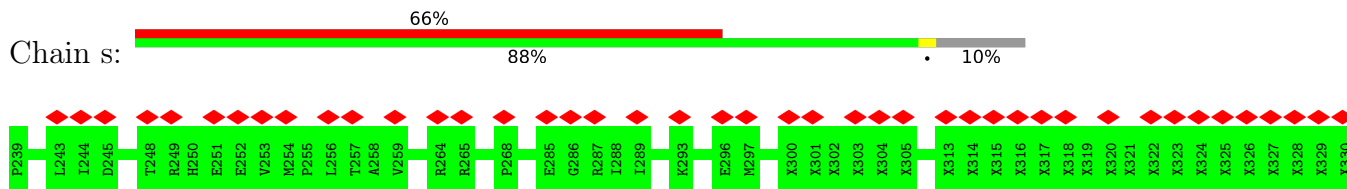


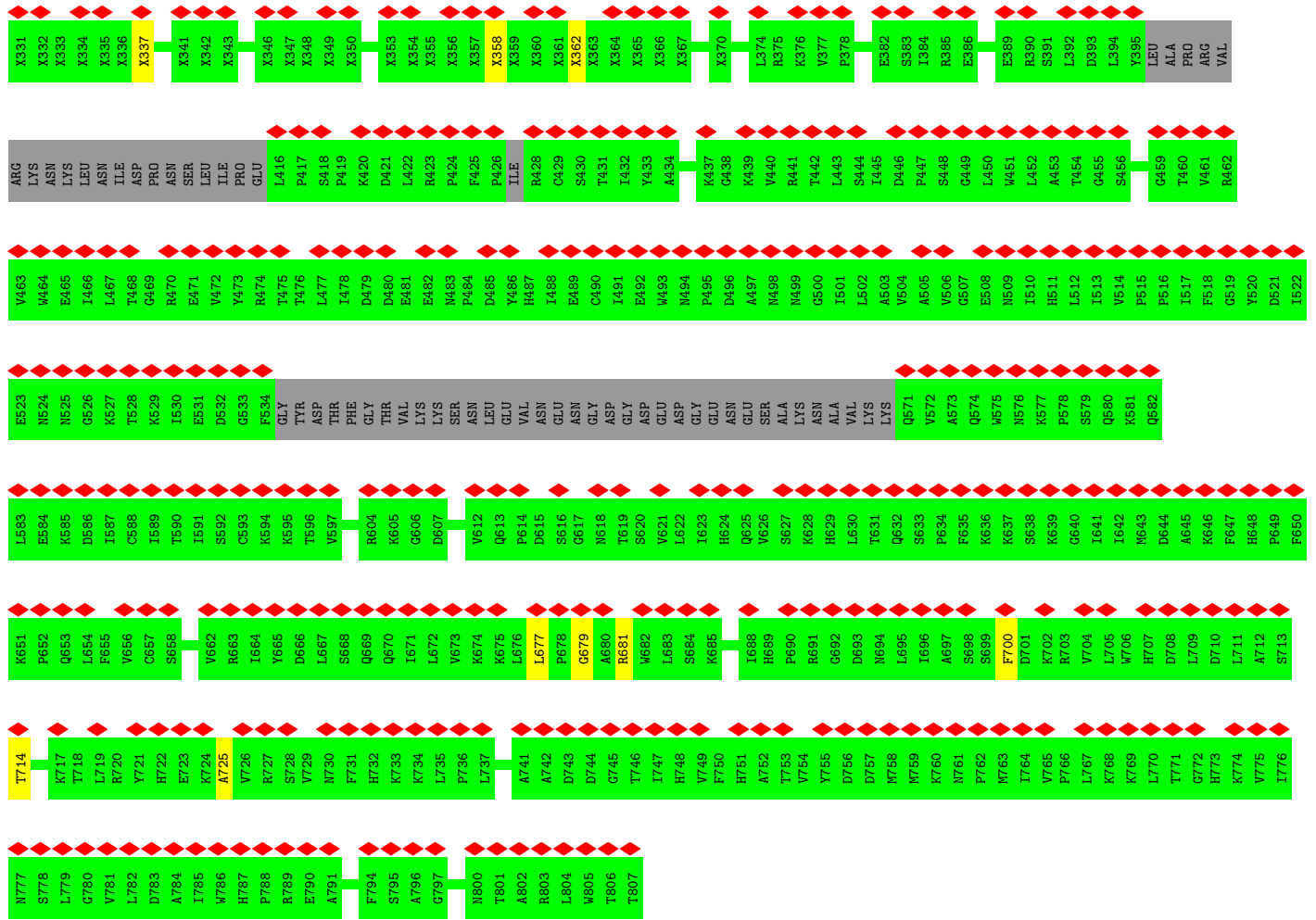


• Molecule 36: ATP-dependent RNA helicase HAS1

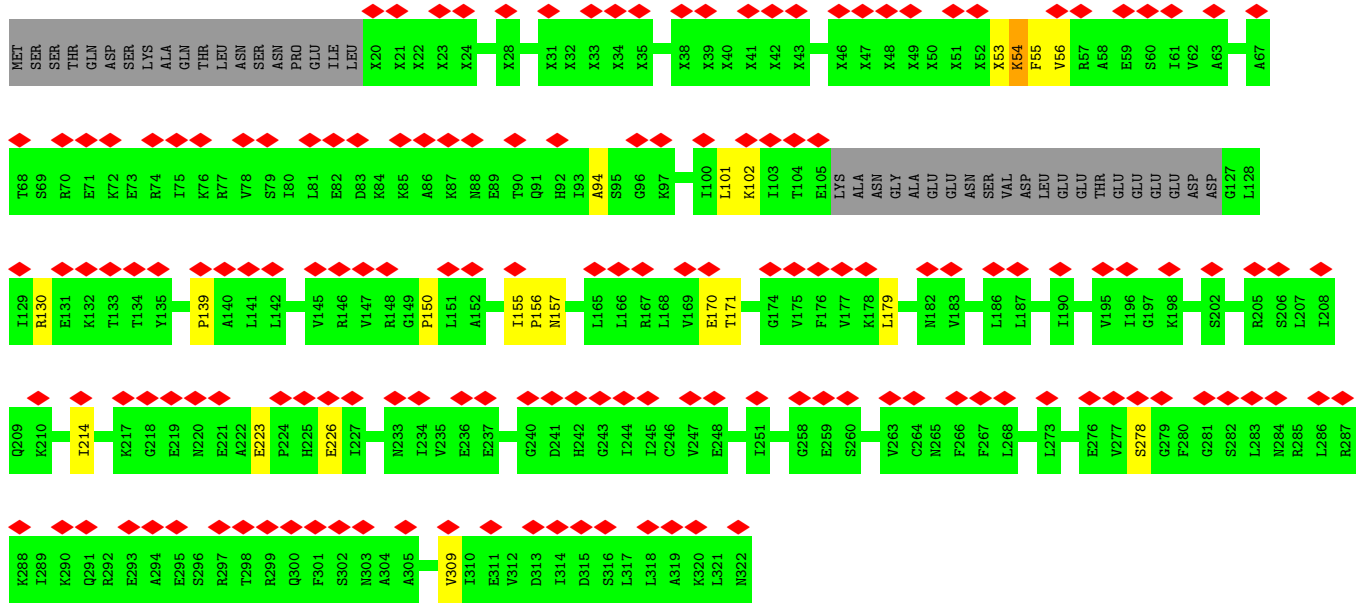
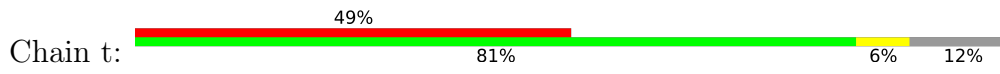


• Molecule 37: Ribosome biogenesis protein ERB1

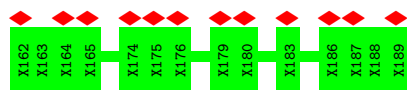
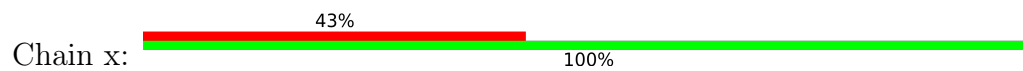




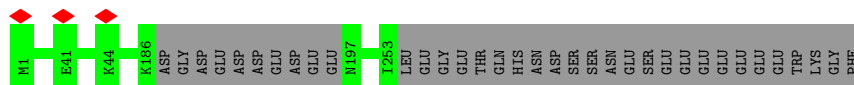
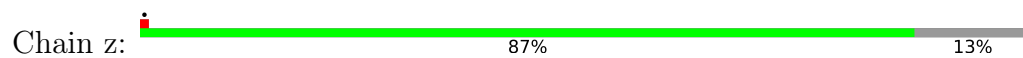
• Molecule 38: Ribosome biogenesis protein RLP7



- Molecule 39: BRX1 associated peptide



- Molecule 40: Ribosomal RNA-processing protein 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	31419	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.56	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.108	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.018	Depositor
Map size (\AA)	624.0, 624.0, 624.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.3, 1.3, 1.3	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:
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	0.38	0/32836	0.52	12/51180 (0.0%)
2	2	0.35	0/3746	0.44	0/5832
3	6	0.33	0/2050	0.57	0/3186
4	A	0.36	0/1944	0.71	4/2704 (0.1%)
5	C	0.37	0/1551	0.78	0/2158
6	D	0.39	0/947	0.67	0/1319
7	E	0.30	0/842	0.73	2/1173 (0.2%)
8	F	0.33	0/1194	0.76	2/1661 (0.1%)
9	G	0.38	0/925	0.88	4/1288 (0.3%)
10	I	0.37	0/1427	0.72	0/1989
11	K	0.29	0/1291	0.77	2/1800 (0.1%)
12	L	0.37	0/524	0.77	0/729
13	M	0.29	0/632	0.62	0/879
14	N	0.35	0/869	0.67	0/1208
15	O	0.32	0/906	0.70	0/1258
16	P	0.30	0/613	0.63	0/851
17	Q	0.34	0/652	0.64	0/907
18	S	0.31	0/850	0.77	2/1186 (0.2%)
19	X	0.60	0/699	0.87	0/974
20	Y	0.36	0/622	0.68	0/865
21	Z	0.64	0/666	0.87	0/926
22	7	0.37	0/771	0.77	2/1072 (0.2%)
23	b	0.32	0/1107	0.79	0/1538
24	c	0.63	0/475	0.88	0/658
26	e	0.35	0/562	0.67	0/780
27	f	0.38	0/521	0.68	0/723
28	g	0.64	0/497	0.99	1/690 (0.1%)
29	h	0.29	0/592	0.76	0/826
30	i	0.30	0/415	0.67	0/577
31	j	0.30	0/356	0.69	0/491
32	k	0.65	0/381	0.84	0/530
34	n	0.30	0/1689	0.68	0/2351

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	o	0.31	0/655	0.72	2/910 (0.2%)
36	p	0.31	0/2156	0.73	2/2999 (0.1%)
37	s	0.42	0/2167	0.84	0/3012
38	t	0.32	0/1225	0.84	0/1704
40	z	0.30	0/1207	0.69	0/1683
All	All	0.37	0/70562	0.63	35/104617 (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
4	A	0	2
6	D	0	1
8	F	0	1
9	G	0	1
18	S	0	4
19	X	0	2
21	Z	0	2
28	g	0	1
29	h	0	1
32	k	0	2
34	n	0	1
37	s	0	1
38	t	0	5
All	All	0	24

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	g	79	SER	N-CA-C	7.16	121.73	112.92
1	1	1716	U	C2'-C3'-O3'	6.79	119.69	109.50
1	1	1568	U	C2'-C3'-O3'	6.74	119.61	109.50
18	S	13	ARG	CA-C-N	6.71	138.17	121.80
18	S	13	ARG	C-N-CA	6.71	138.17	121.80

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	185	ALA	Peptide
4	A	53	ILE	Peptide
6	D	56	ASP	Peptide
8	F	158	LYS	Peptide
9	G	76	ALA	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	29343	0	14746	358	0
2	2	3353	0	1695	73	0
3	6	1838	0	927	31	0
4	A	1946	0	856	16	0
5	C	1553	0	748	6	0
6	D	948	0	426	2	0
7	E	843	0	380	3	0
8	F	1195	0	556	5	0
9	G	926	0	452	12	0
10	I	1428	0	590	10	0
11	K	1293	0	551	10	0
12	L	525	0	259	3	0
13	M	633	0	321	1	0
14	N	871	0	397	4	0
15	O	908	0	437	5	0
16	P	616	0	304	0	0
17	Q	653	0	314	0	0
18	S	851	0	374	5	0
19	X	700	0	336	42	0
20	Y	623	0	283	3	0
21	Z	667	0	307	18	0
22	7	773	0	339	3	0
23	b	1201	0	497	3	0
24	c	476	0	222	0	0
25	d	2288	0	471	2	0
26	e	564	0	262	1	0
27	f	522	0	239	1	0
28	g	498	0	228	1	0
29	h	593	0	274	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	i	416	0	198	1	0
31	j	357	0	172	3	0
32	k	382	0	171	0	0
33	m	370	0	76	1	0
34	n	1693	0	731	39	0
35	o	656	0	289	6	0
36	p	2158	0	965	8	0
37	s	2537	0	1013	27	0
38	t	1397	0	583	14	0
39	x	140	0	34	0	0
40	z	1209	0	522	0	0
41	D	1	0	0	0	0
41	j	1	0	0	0	0
All	All	69945	0	32545	552	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 552 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1558:A:P	9:G:53:PRO:HA	1.32	1.64
1:1:1566:A:C8	34:n:214:ASP:CB	1.83	1.58
21:Z:105:SER:C	37:s:725:ALA:HB2	1.36	1.48
1:1:1558:A:P	9:G:53:PRO:CA	2.11	1.38
1:1:1571:A:C5	34:n:150:GLN:HA	1.57	1.38

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	
4	A	390/463 (84%)	368 (94%)	22 (6%)	0	100	100
5	C	310/362 (86%)	285 (92%)	23 (7%)	2 (1%)	21	58
6	D	188/306 (61%)	177 (94%)	11 (6%)	0	100	100
7	E	168/176 (96%)	158 (94%)	10 (6%)	0	100	100
8	F	240/244 (98%)	225 (94%)	15 (6%)	0	100	100
9	G	185/256 (72%)	170 (92%)	14 (8%)	1 (0%)	24	63
10	I	286/295 (97%)	272 (95%)	14 (5%)	0	100	100
11	K	256/376 (68%)	243 (95%)	13 (5%)	0	100	100
12	L	104/199 (52%)	96 (92%)	7 (7%)	1 (1%)	12	47
13	M	126/138 (91%)	123 (98%)	3 (2%)	0	100	100
14	N	172/204 (84%)	162 (94%)	10 (6%)	0	100	100
15	O	180/199 (90%)	173 (96%)	7 (4%)	0	100	100
16	P	118/184 (64%)	113 (96%)	5 (4%)	0	100	100
17	Q	130/186 (70%)	128 (98%)	2 (2%)	0	100	100
18	S	169/172 (98%)	154 (91%)	15 (9%)	0	100	100
19	X	139/142 (98%)	130 (94%)	9 (6%)	0	100	100
20	Y	124/127 (98%)	118 (95%)	6 (5%)	0	100	100
21	Z	133/136 (98%)	124 (93%)	8 (6%)	1 (1%)	16	53
22	7	152/231 (66%)	137 (90%)	15 (10%)	0	100	100
23	b	220/291 (76%)	207 (94%)	13 (6%)	0	100	100
24	c	95/105 (90%)	93 (98%)	1 (1%)	1 (1%)	11	45
26	e	110/130 (85%)	106 (96%)	4 (4%)	0	100	100
27	f	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
28	g	99/121 (82%)	96 (97%)	2 (2%)	1 (1%)	12	47
29	h	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
30	i	82/100 (82%)	78 (95%)	4 (5%)	0	100	100
31	j	70/88 (80%)	66 (94%)	4 (6%)	0	100	100
32	k	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
34	n	333/605 (55%)	322 (97%)	11 (3%)	0	100	100
35	o	131/220 (60%)	123 (94%)	8 (6%)	0	100	100
36	p	433/505 (86%)	422 (98%)	11 (2%)	0	100	100
37	s	431/569 (76%)	416 (96%)	15 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	t	245/322 (76%)	229 (94%)	14 (6%)	2 (1%)	16	53
40	z	239/278 (86%)	228 (95%)	11 (5%)	0	100	100
All	All	6354/8035 (79%)	6024 (95%)	321 (5%)	9 (0%)	49	83

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	c	100	ILE
38	t	54	LYS
28	g	46	ASP
38	t	56	VAL
5	C	268	ALA

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	
6	D	4/274 (2%)	4 (100%)	0	100	100
31	j	4/71 (6%)	4 (100%)	0	100	100
All	All	8/345 (2%)	8 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1358/3396 (39%)	339 (24%)	42 (3%)
2	2	157/158 (99%)	35 (22%)	3 (1%)
3	6	85/232 (36%)	44 (51%)	5 (5%)
All	All	1600/3786 (42%)	418 (26%)	50 (3%)

5 of 418 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	7	C
1	1	12	A
1	1	13	A
1	1	14	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1630	U
1	1	1820	U
3	6	225	U
1	1	1641	U
1	1	1716	U

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 2 ligands modelled in this entry, 2 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
25	d	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	d	272:UNK	C	283:UNK	N	25.28
1	d	379:UNK	C	381:UNK	N	6.01

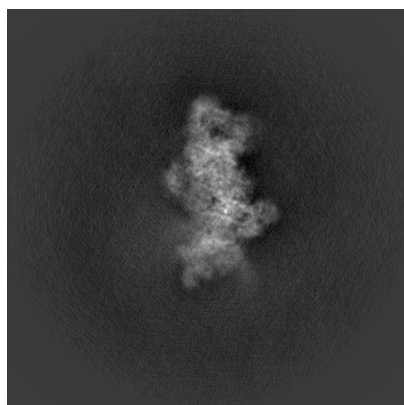
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7445. These allow visual inspection of the internal detail of the map and identification of artifacts.

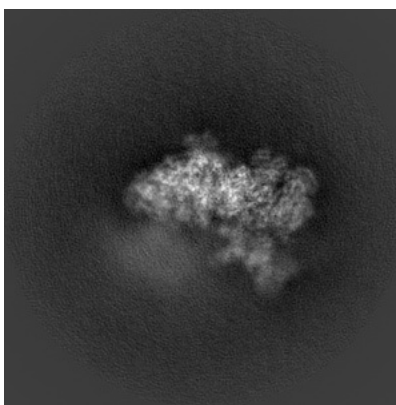
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

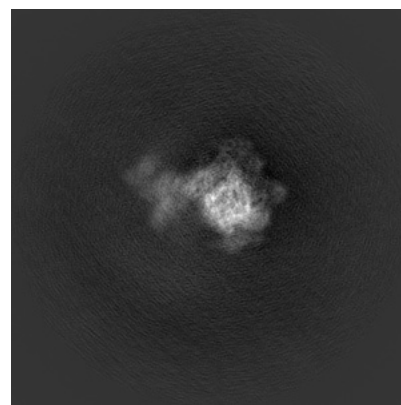
6.1.1 Primary map



X



Y

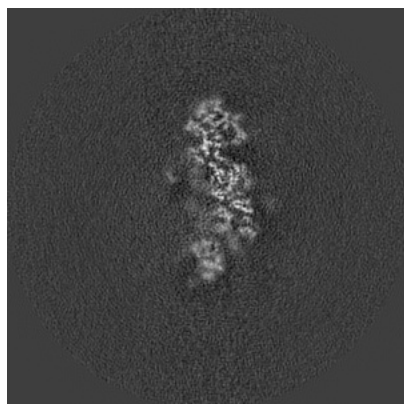


Z

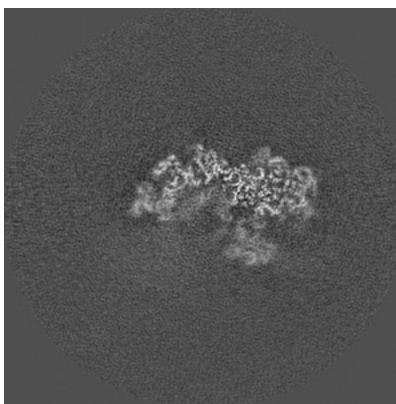
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

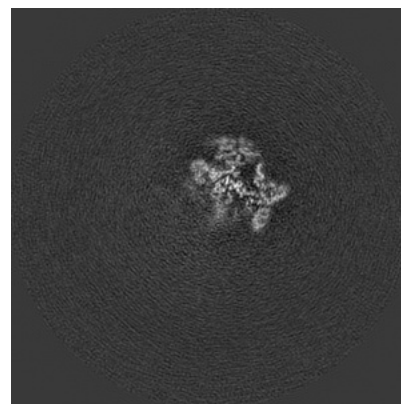
6.2.1 Primary map



X Index: 240



Y Index: 240

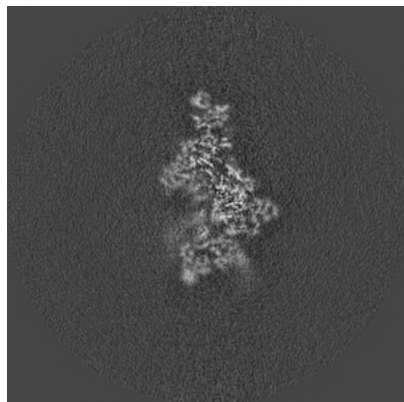


Z Index: 240

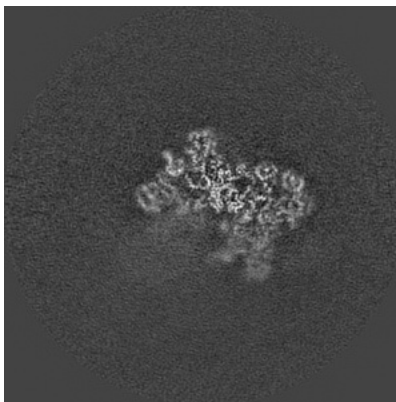
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

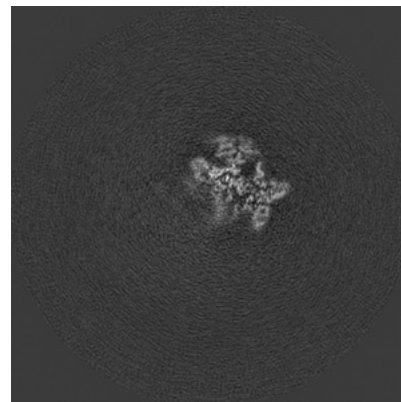
6.3.1 Primary map



X Index: 263



Y Index: 256

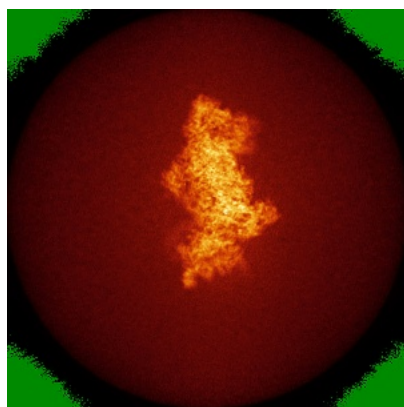


Z Index: 241

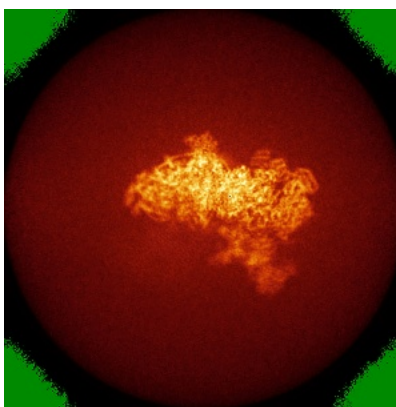
The images above show the largest variance slices of the map in three orthogonal directions.

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

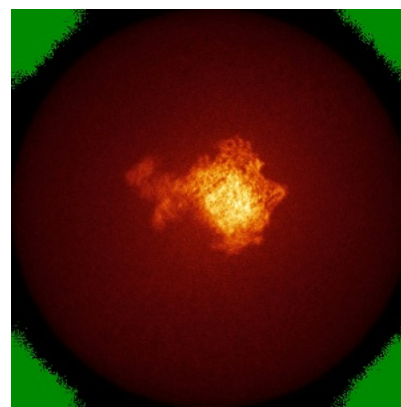
6.4.1 Primary map



X



Y

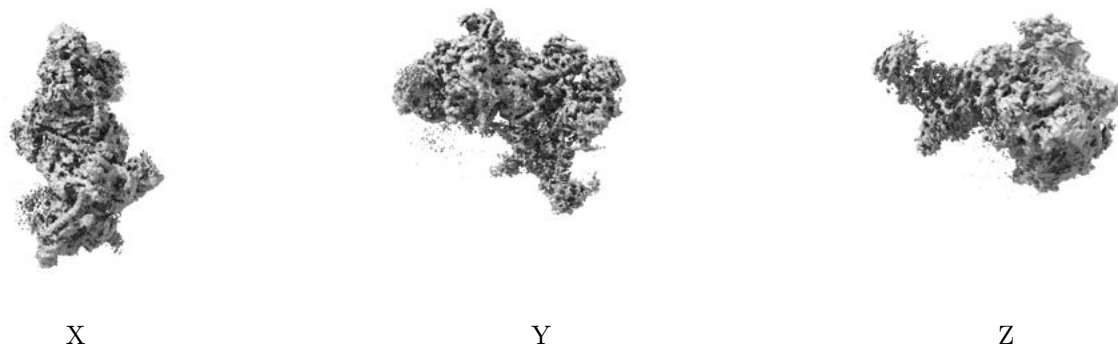


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

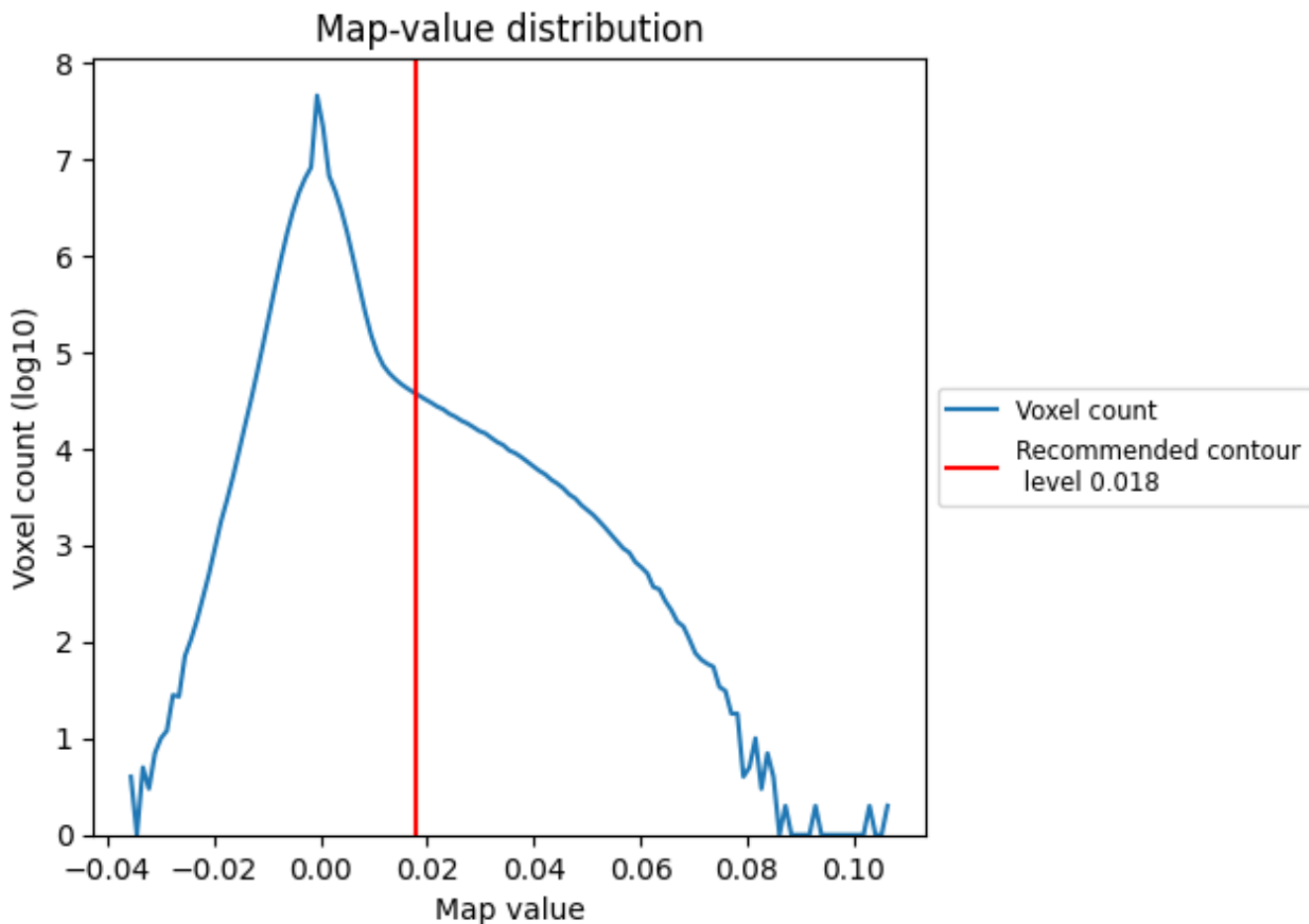
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

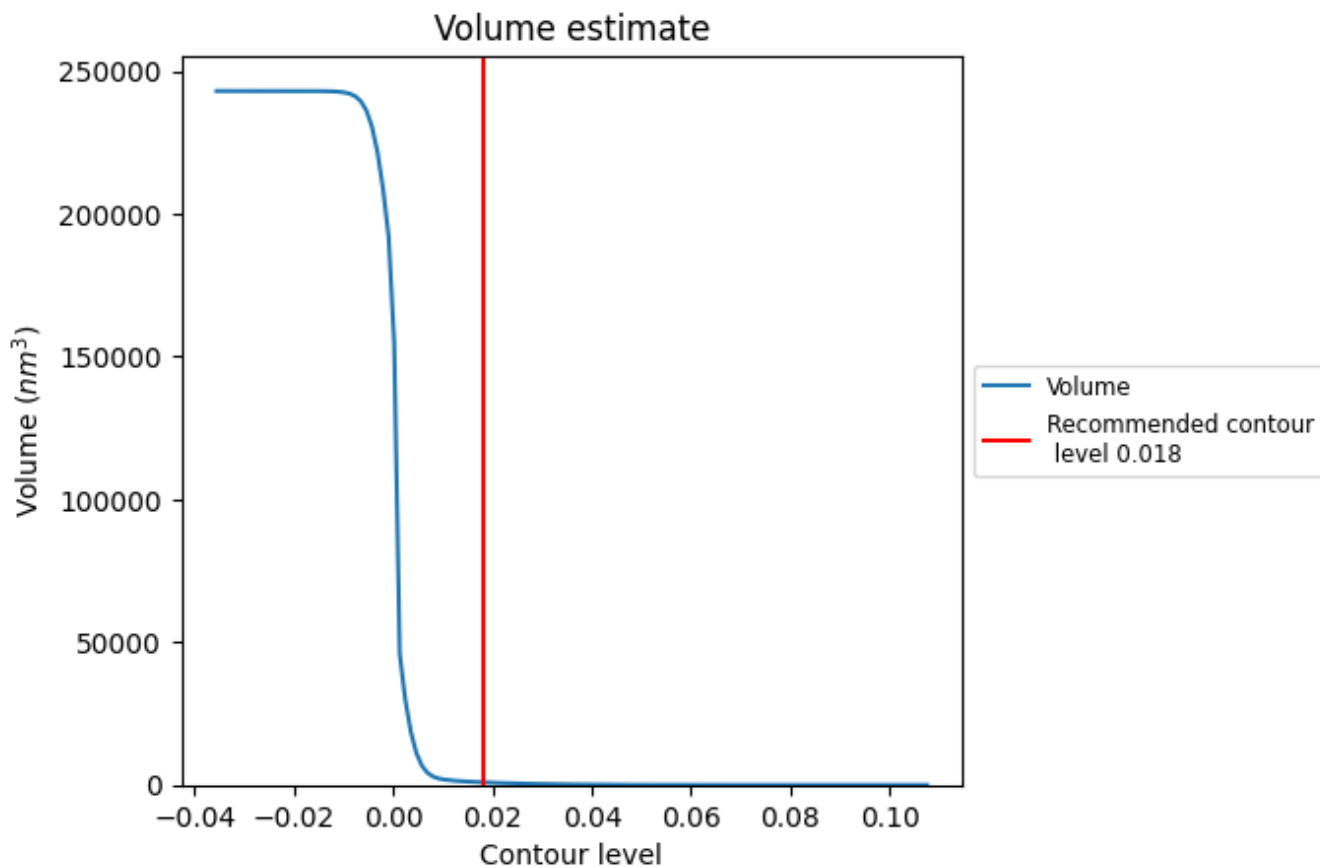
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

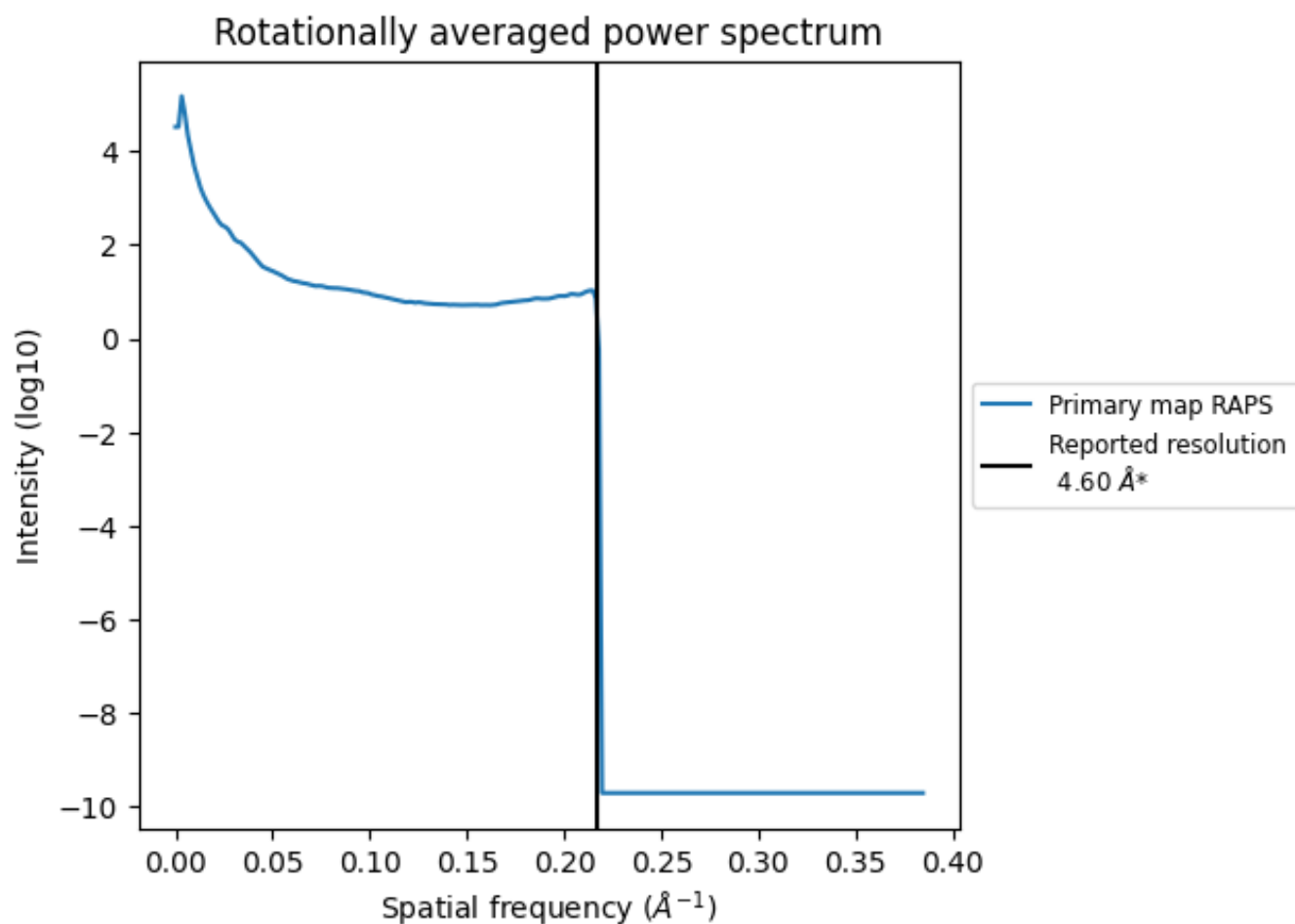
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 923 nm^3 ; this corresponds to an approximate mass of 834 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 [\(i\)](#)

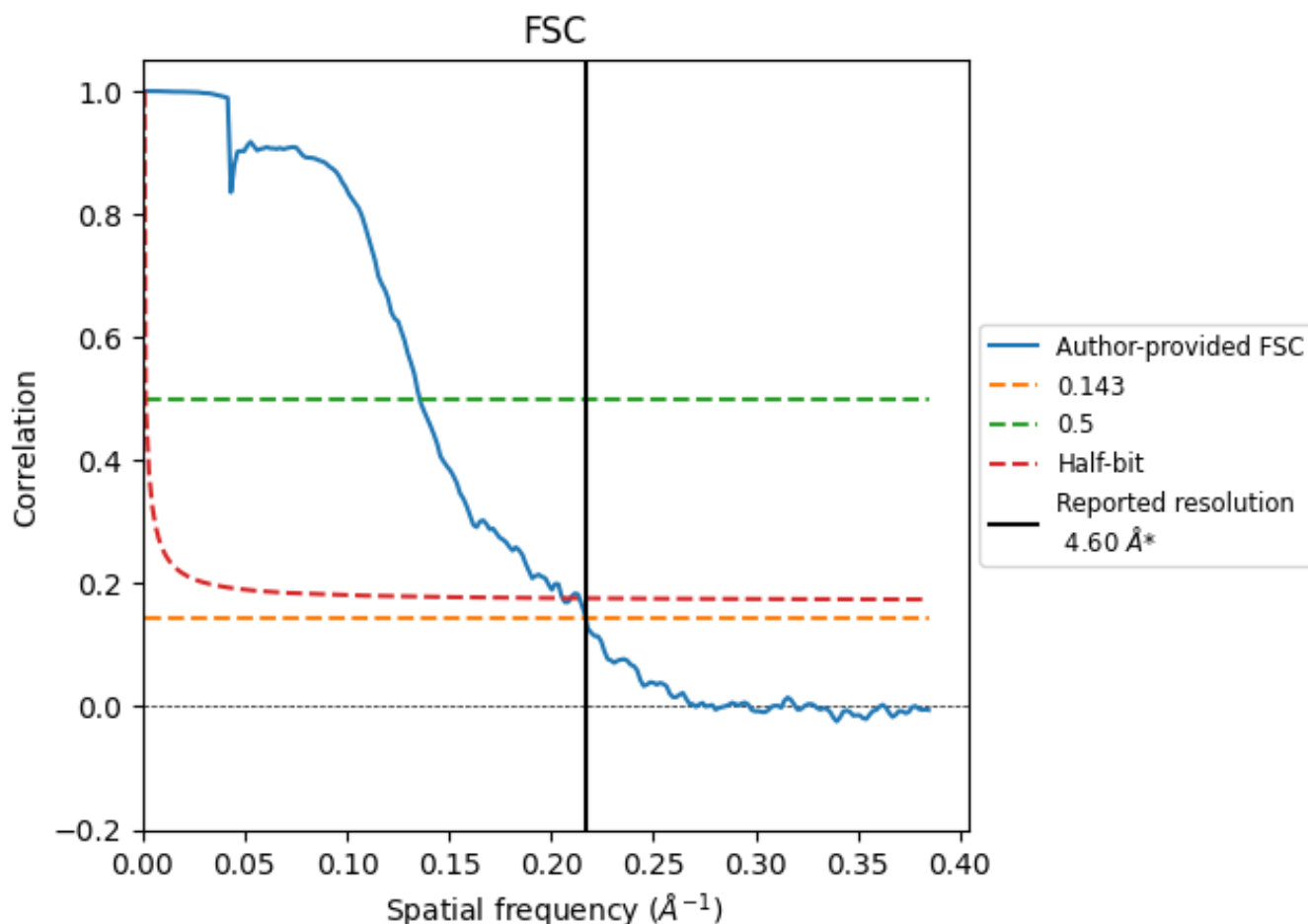


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

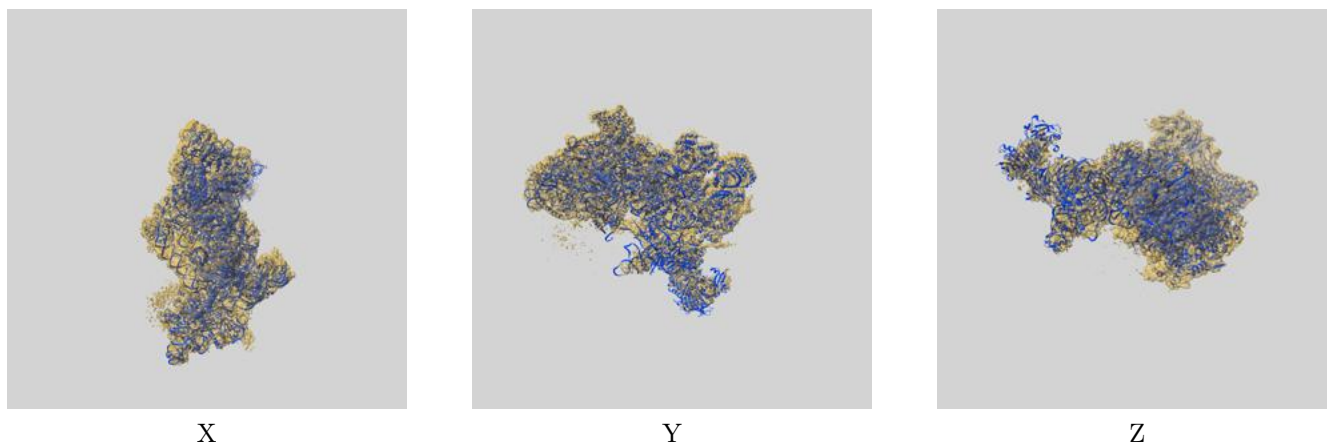
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.61	7.37	4.86
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

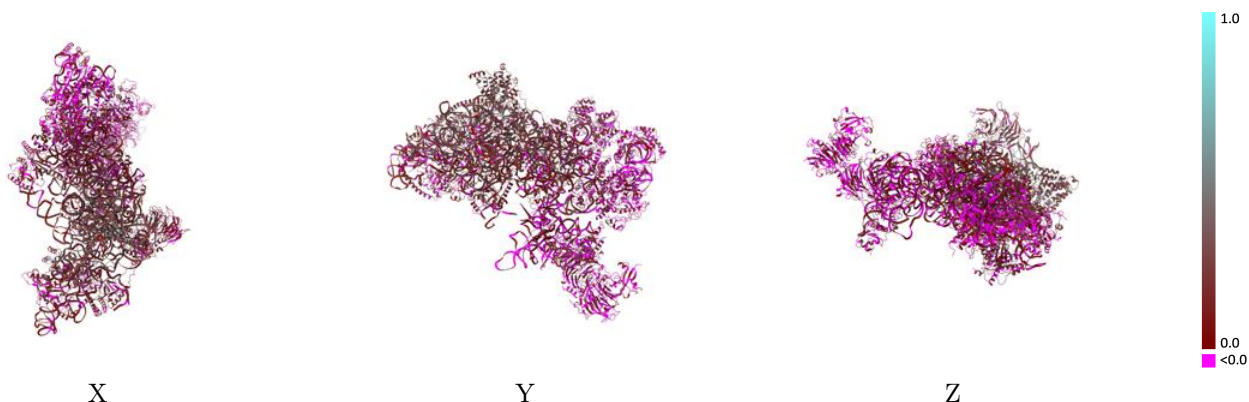
This section contains information regarding the fit between EMDB map EMD-7445 and PDB model 6CB1. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



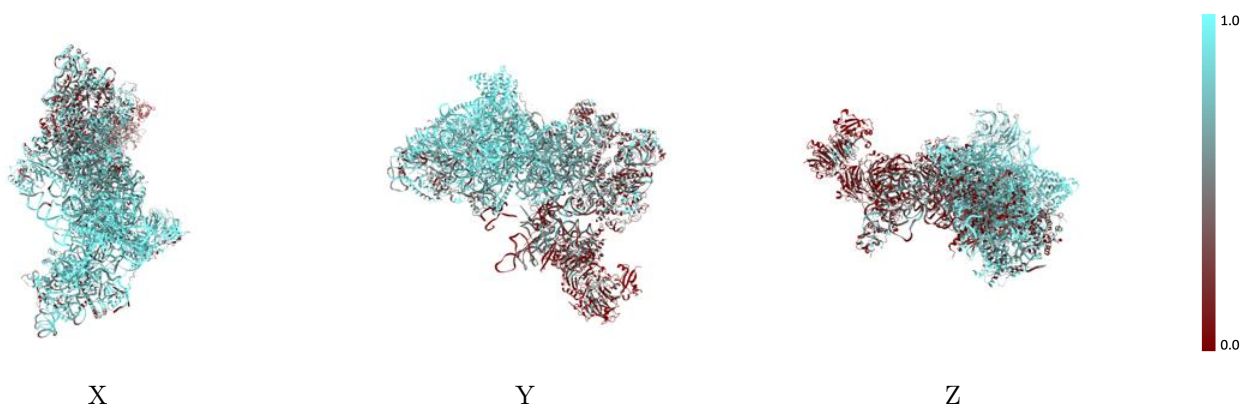
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



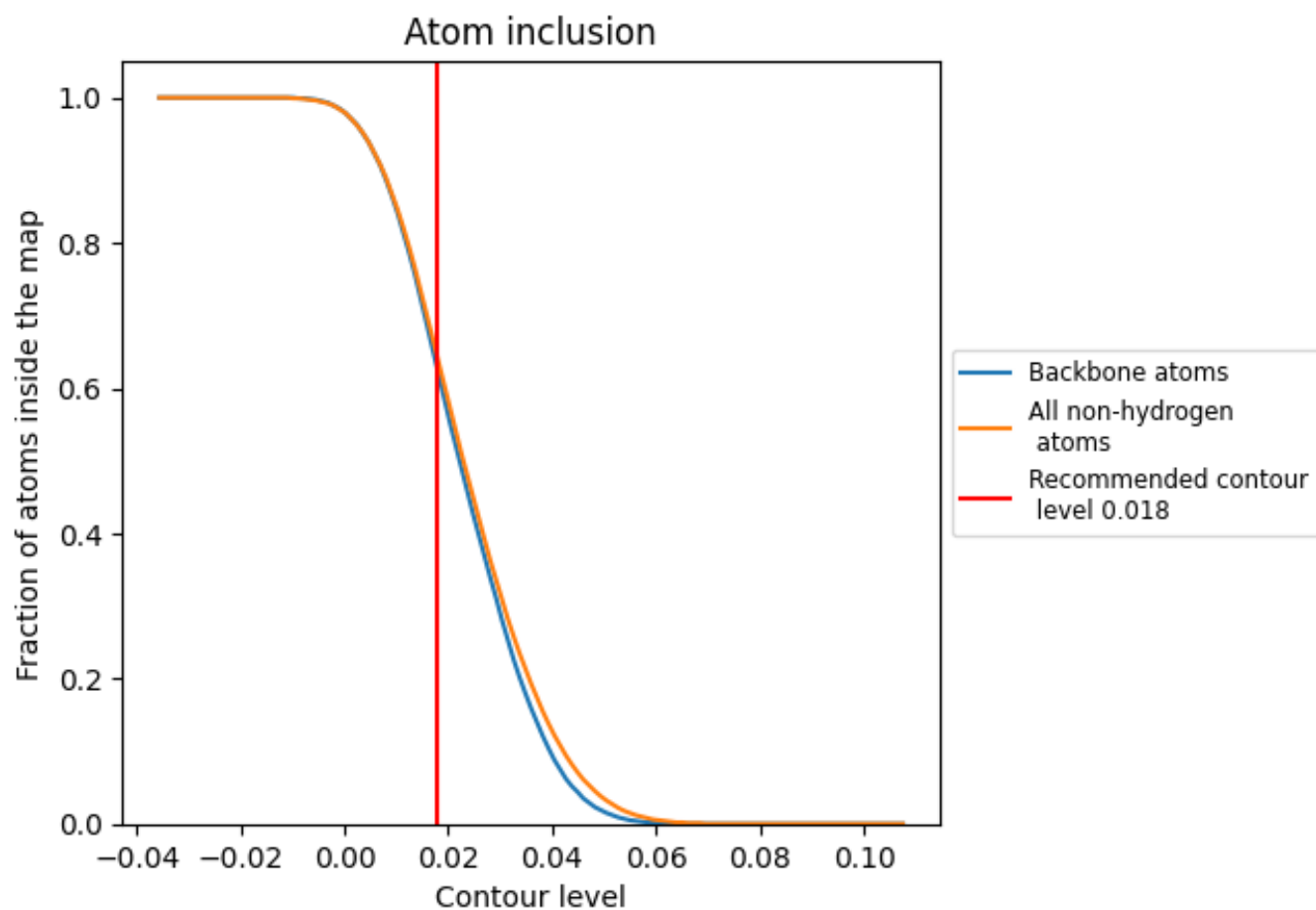
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 64% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6400	 0.1310
1	 0.6950	 0.1450
2	 0.7380	 0.1260
6	 0.5910	 0.0040
7	 0.6480	 0.1640
A	 0.8080	 0.1710
C	 0.8220	 0.2860
D	 0.8920	 0.3020
E	 0.8070	 0.2220
F	 0.8710	 0.2610
G	 0.4790	 0.0300
I	 0.8230	 0.2010
K	 0.5220	 0.0210
L	 0.7830	 0.2010
M	 0.7130	 0.1350
N	 0.6620	 0.1510
O	 0.6280	 0.0940
P	 0.4800	 0.1780
Q	 0.8960	 0.3080
S	 0.6970	 0.1130
X	 0.1170	 0.0010
Y	 0.7980	 0.1850
Z	 0.2260	 0.0240
b	 0.7880	 0.1560
c	 0.3700	 0.0280
d	 0.1690	 0.0060
e	 0.6260	 0.2380
f	 0.7180	 0.1580
g	 0.1830	 0.0370
h	 0.7390	 0.1760
i	 0.6180	 0.0960
j	 0.6960	 0.1530
k	 0.0790	 0.0250
m	 0.7840	 0.1270
n	 0.5890	 0.0790



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Chain	Atom inclusion	Q-score
o	 0.4590	 -0.0040
p	 0.4320	 0.0510
s	 0.2890	 0.0490
t	 0.4420	 0.0310
x	 0.5790	 0.1110
z	 0.9490	 0.3000