



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 09:12 PM UTC

PDB ID : 6EML / pdb_00006eml
EMDB ID : EMD-3886
Title : Cryo-EM structure of a late pre-40S ribosomal subunit from *Saccharomyces cerevisiae*
Authors : Heuer, A.; Thomson, E.; Schmidt, C.; Berninghausen, O.; Becker, T.; Hurt, E.; Beckmann, R.
Deposited on : 2017-10-02
Resolution : 3.60 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:

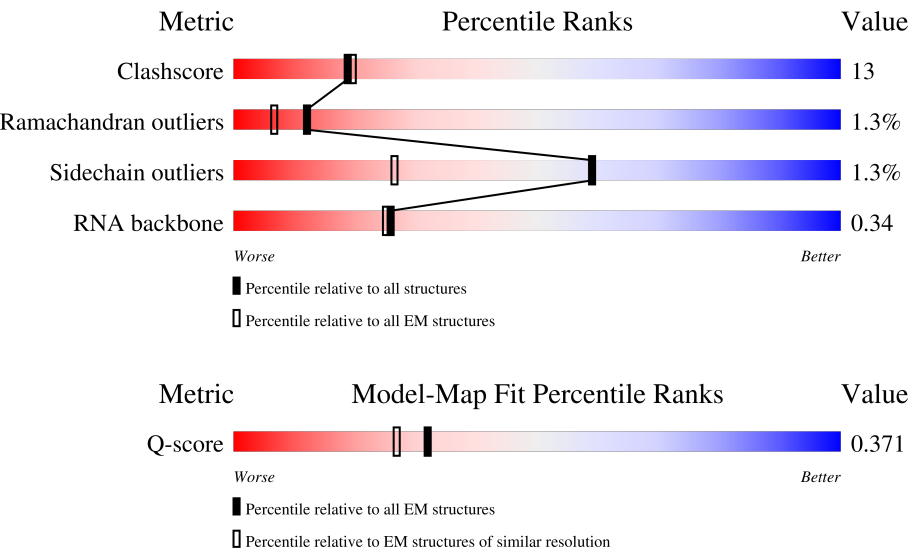
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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	2	1800	
2	D	143	
3	B	225	

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Mol	Chain	Length	Quality of chain
4	C	136	
5	E	142	
6	F	143	
7	H	146	
8	I	144	
9	K	108	
10	L	67	
11	N	152	
12	P	252	
13	Q	255	
14	R	254	
15	S	261	
16	T	236	
17	U	190	
18	V	200	
19	W	197	
20	X	156	
21	Y	151	
22	Z	137	
23	a	87	
24	b	130	
25	c	145	
26	d	135	
27	f	82	
28	t	788	

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Mol	Chain	Length	Quality of chain
29	g	63	51%67%22%6%5%
30	p	274	27%44%22%32%
31	r	425	58%21%39%38%
32	e	483	44%49%46%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 75886 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 pre-18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1675	Total	C	N	O	P	0	0
			35695	15958	6312	11750	1675		

- Molecule 2 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	124	Total	C	N	O	S	0	0
			892	561	156	173	2		

- Molecule 3 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	202	Total	C	N	O	S	0	0
			1592	998	296	295	3		

- Molecule 4 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	114	Total	C	N	O	S	0	0
			871	541	169	159	2		

- Molecule 5 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	117	Total	C	N	O	S	0	0
			928	590	172	159	7		

- Molecule 6 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 7 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	122	Total	C	N	O	S	0	0
			1009	636	193	178	2		

- Molecule 8 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 9 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	K	64	Total	C	N	O	0	0
			519	332	95	92		

- Molecule 10 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	62	Total	C	N	O	S	0	0
			486	300	95	90	1		

- Molecule 11 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 12 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 13 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 14 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	220	Total	C	N	O	S	0	0
			1662	1065	295	300	2		

- Molecule 15 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 16 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 17 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	184	Total	C	N	O	S	0	0
			1481	951	265	265			

- Molecule 18 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 19 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 20 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 21 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 22 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Z	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	c	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
26	d	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 27 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 28 is a protein called Ribosome biogenesis protein TSR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	t	633	Total	C	N	O	S	0	0
			5037	3220	875	929	13		

- Molecule 29 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 30 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	p	185	Total	C	N	O	S	0	0
			1473	942	267	260	4		

- Molecule 31 is a protein called Serine/threonine-protein kinase RIO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	r	264	Total	C	N	O	S	0	0
			2166	1379	384	387	16		

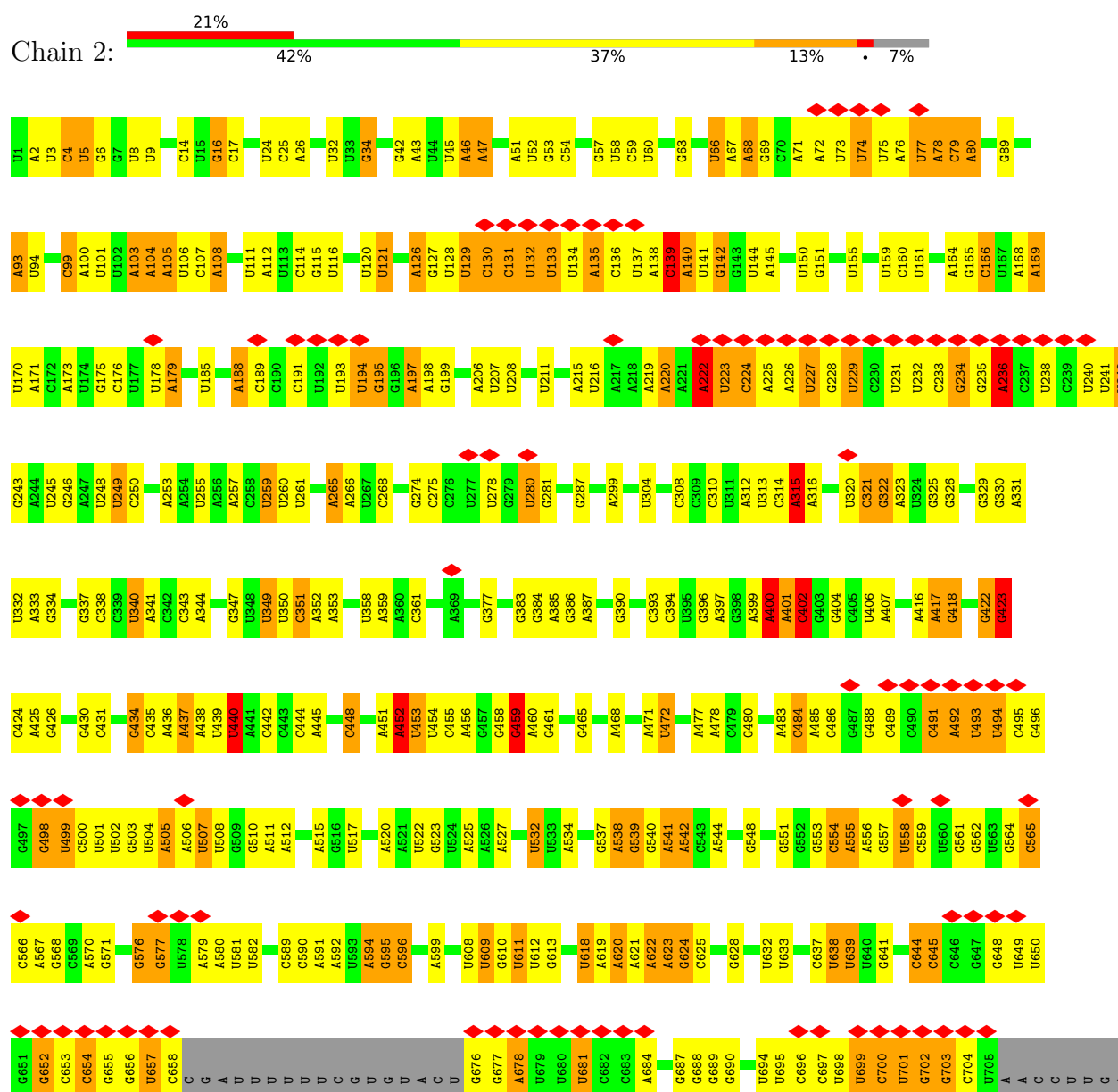
- Molecule 32 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	261	Total	C	N	O		0	0
			1045	523	261	261			

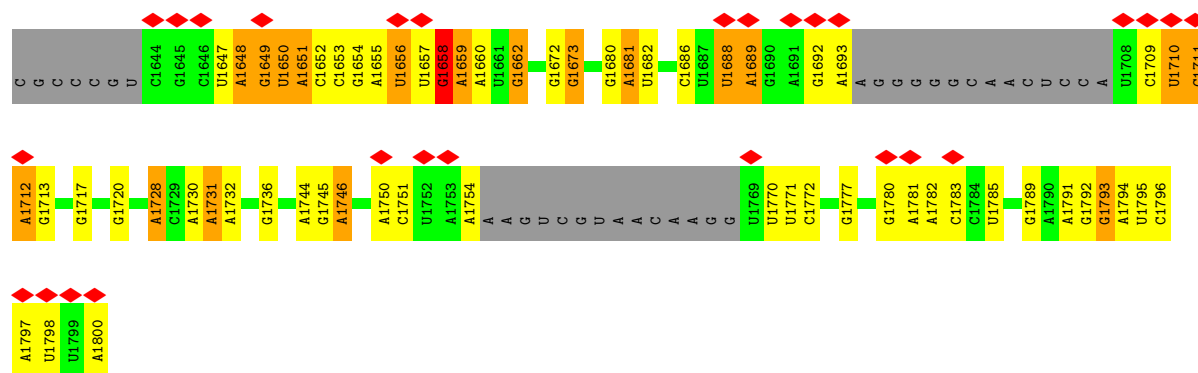
3 Residue-property plots

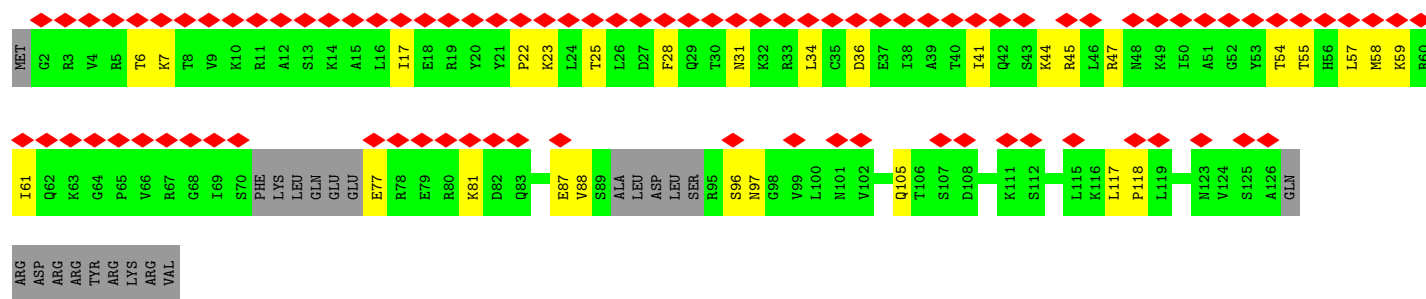
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: pre-18S ribosomal RNA

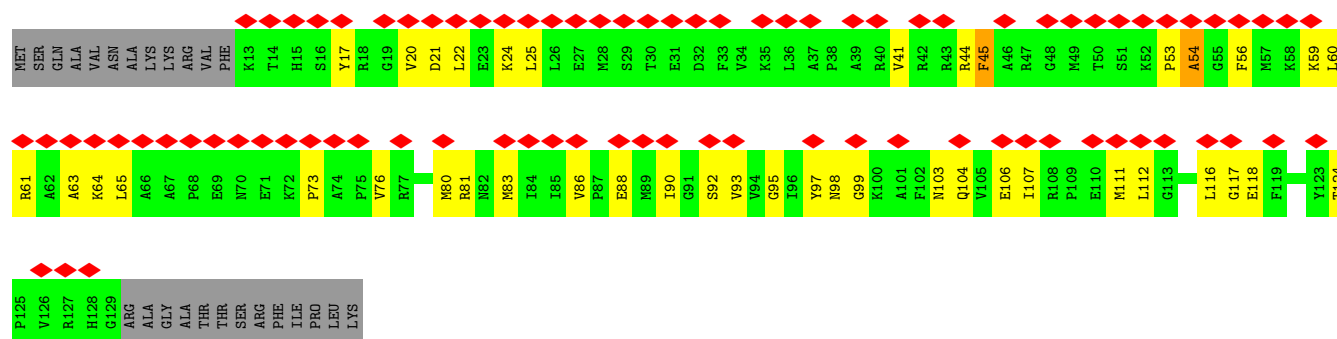




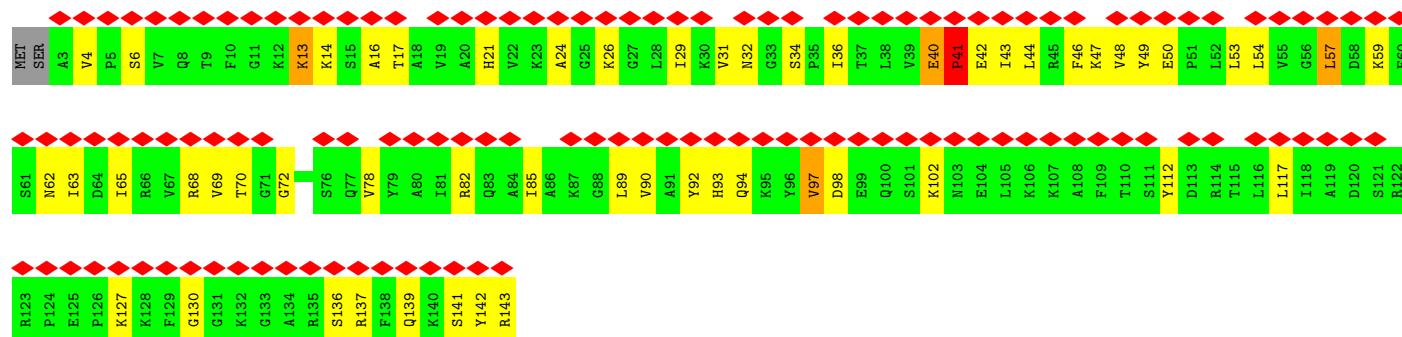
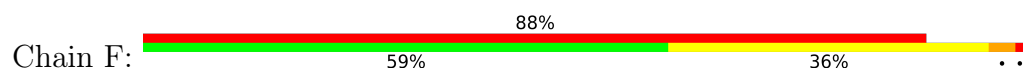




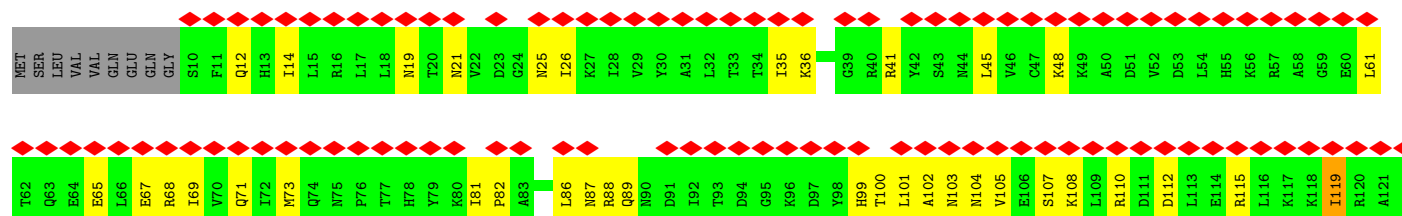
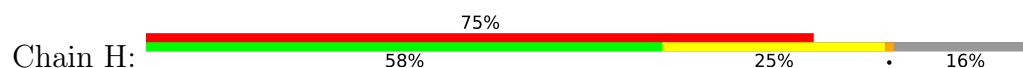
• Molecule 5: 40S ribosomal protein S15

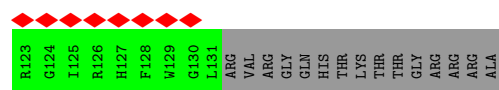


• Molecule 6: 40S ribosomal protein S16-A

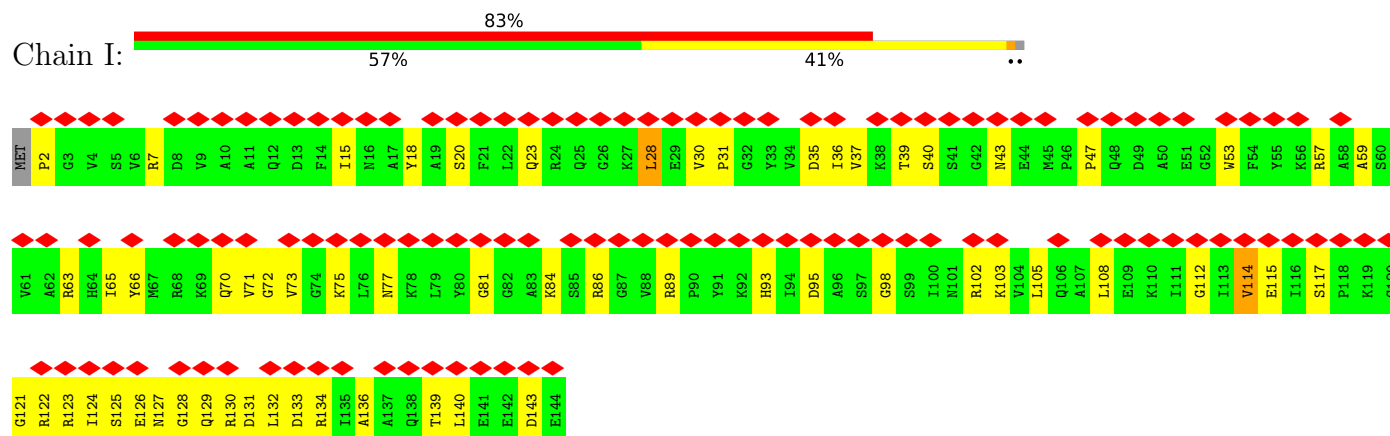


• Molecule 7: 40S ribosomal protein S18-A

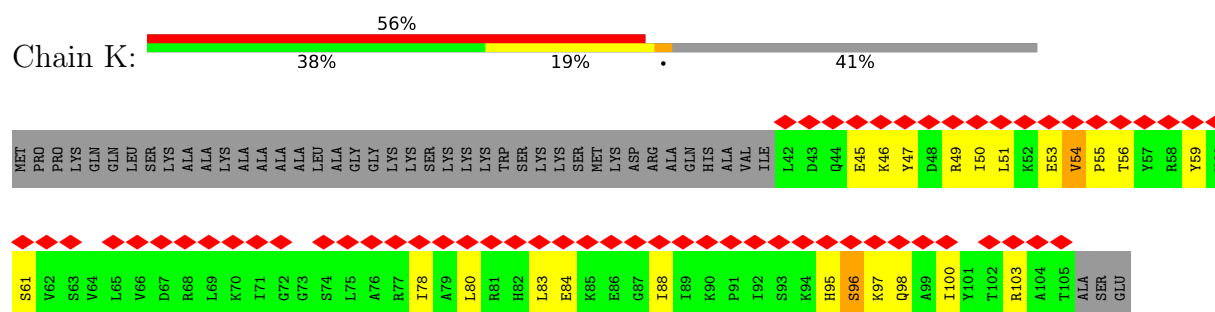




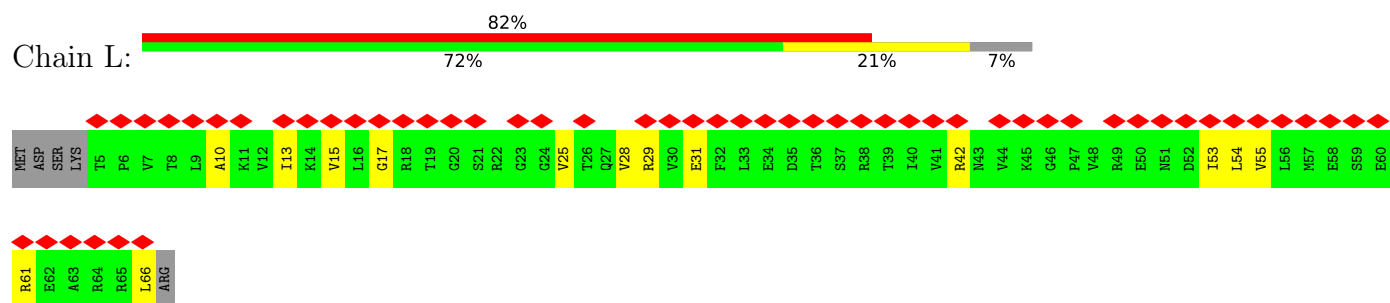
• Molecule 8: 40S ribosomal protein S19-A



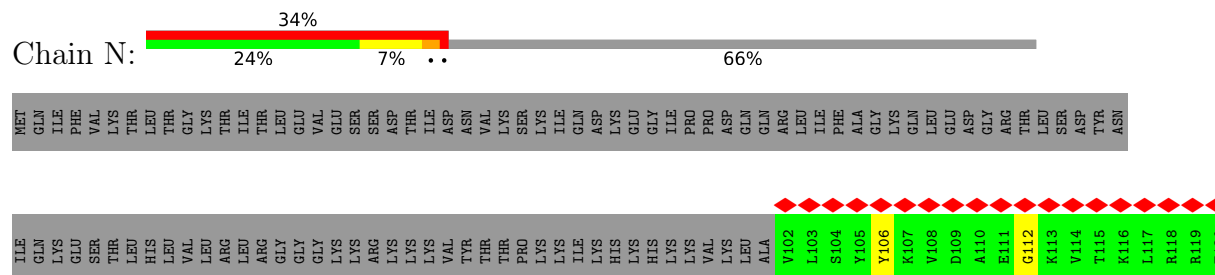
• Molecule 9: 40S ribosomal protein S25-A



• Molecule 10: 40S ribosomal protein S28-B

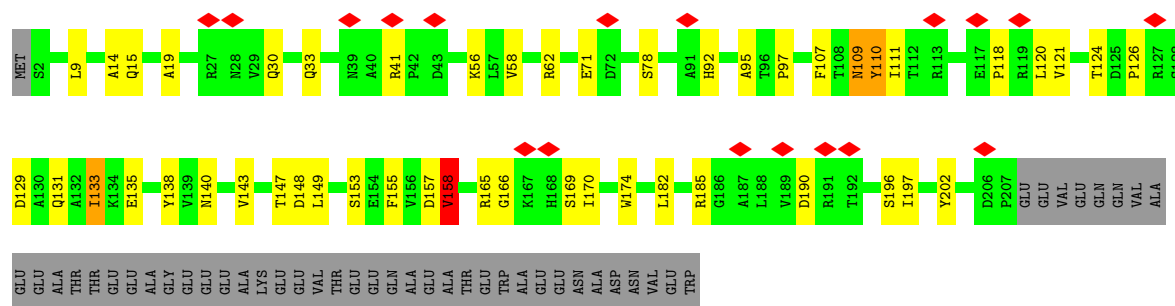


• Molecule 11: Ubiquitin-40S ribosomal protein S31

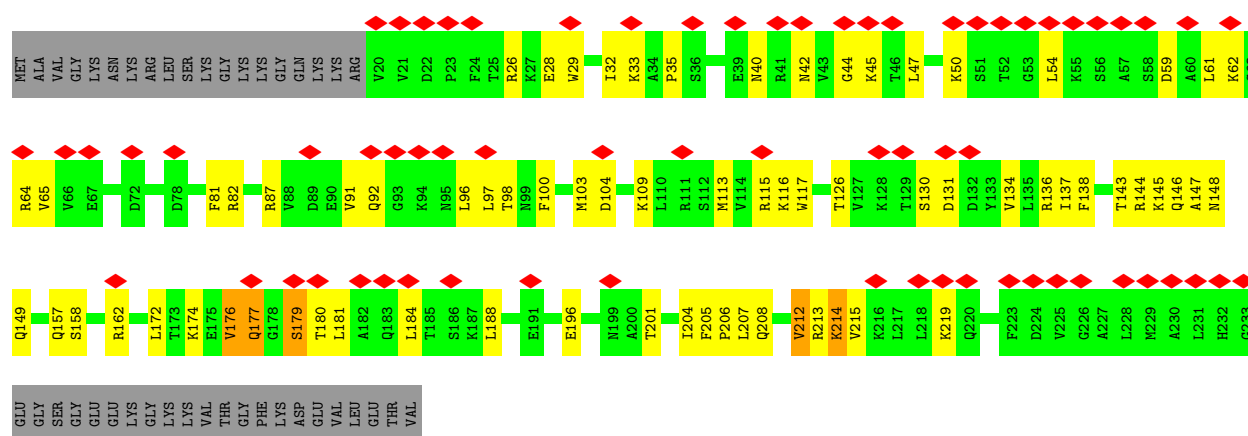




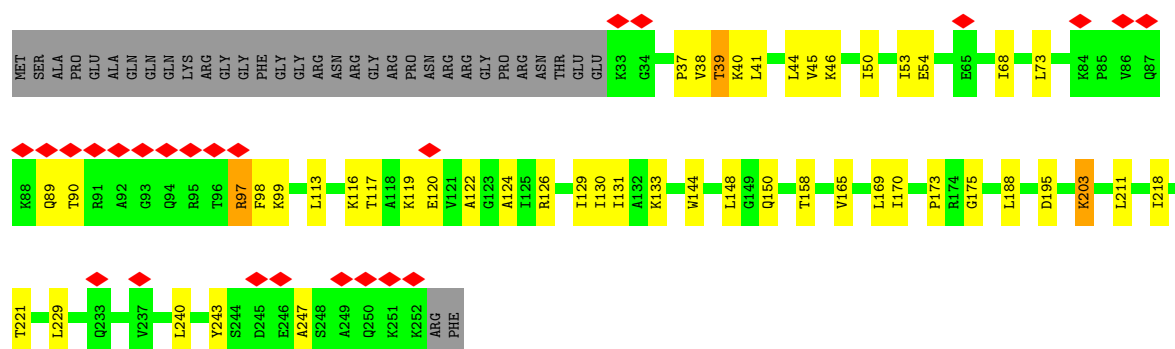
- Molecule 12: 40S ribosomal protein S0-A



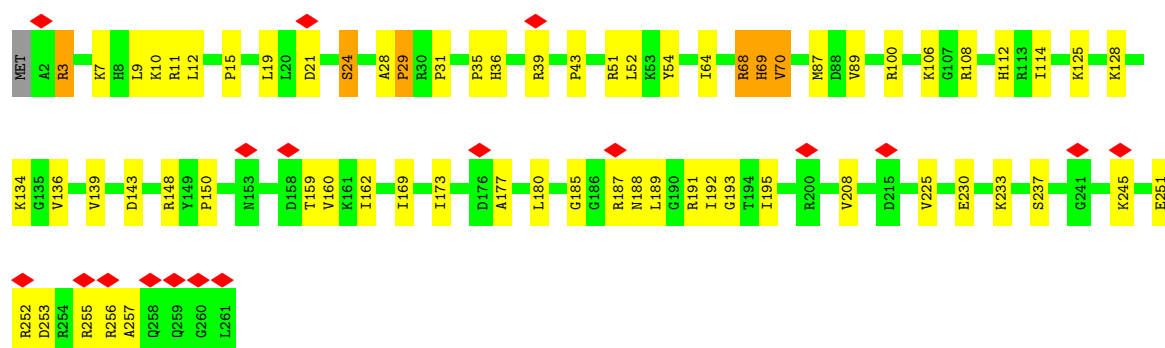
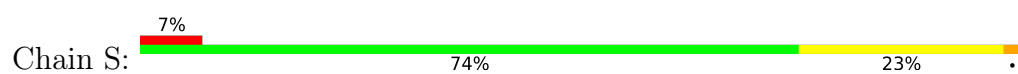
- Molecule 13: 40S ribosomal protein S1-A



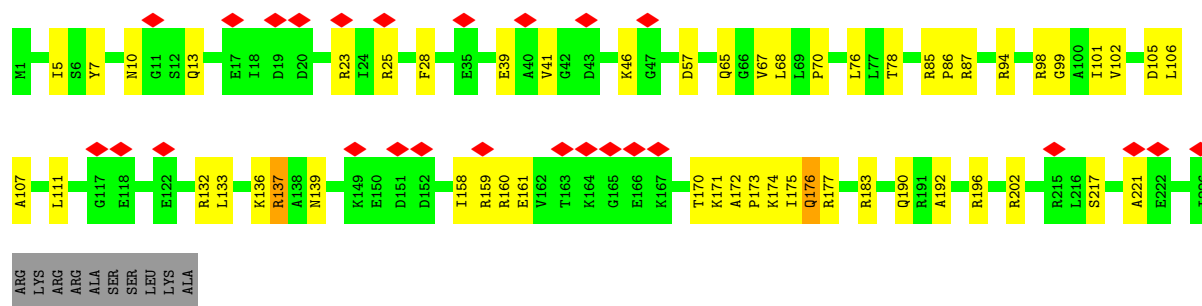
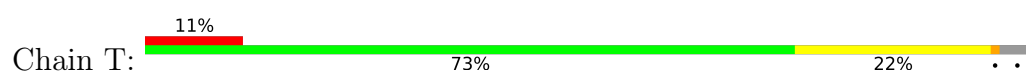
- Molecule 14: 40S ribosomal protein S2



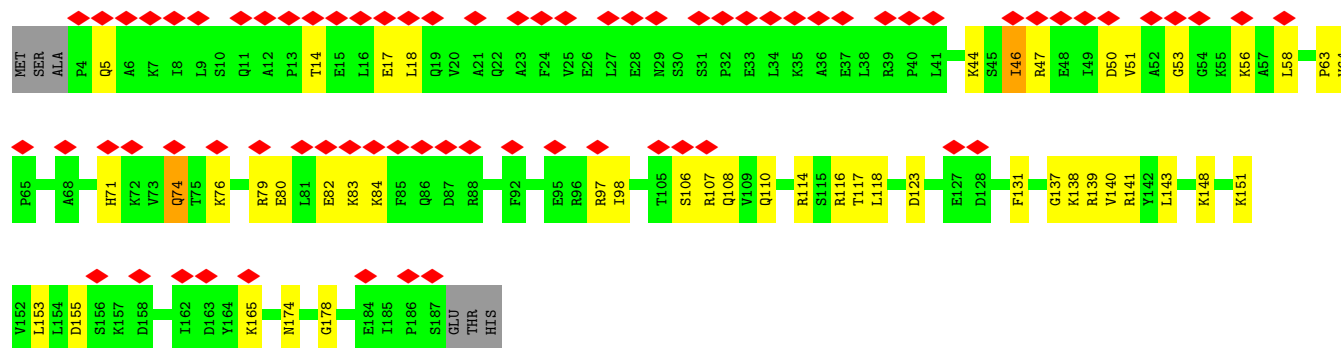
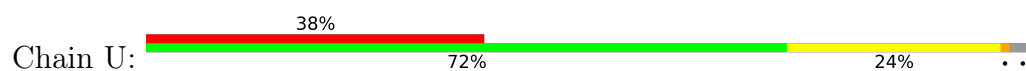
- Molecule 15: 40S ribosomal protein S4-A



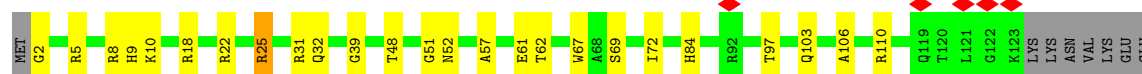
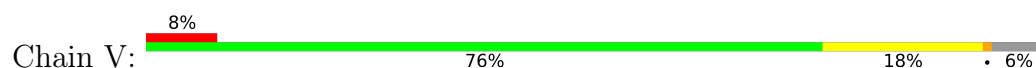
- Molecule 16: 40S ribosomal protein S6-A



- Molecule 17: 40S ribosomal protein S7-A

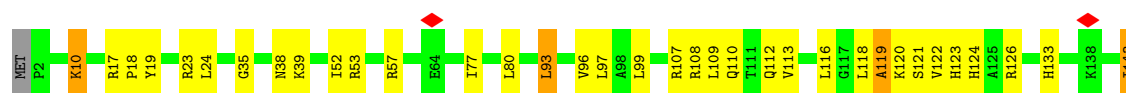


- Molecule 18: 40S ribosomal protein S8-A

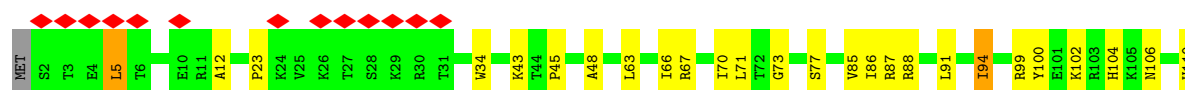
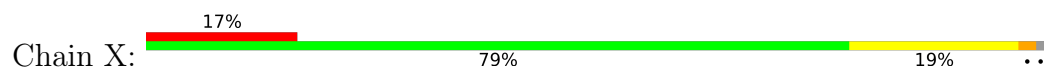




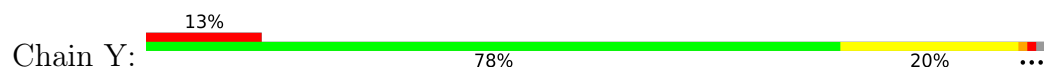
- Molecule 19: 40S ribosomal protein S9-A



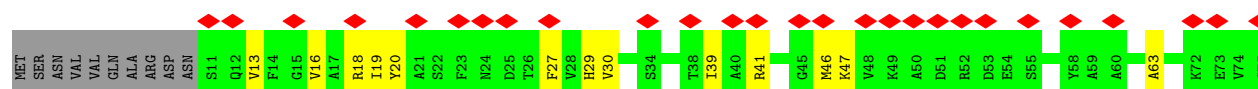
- Molecule 20: 40S ribosomal protein S11-A



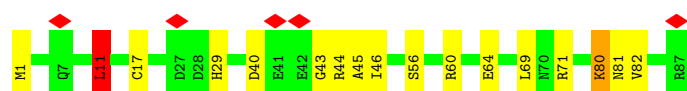
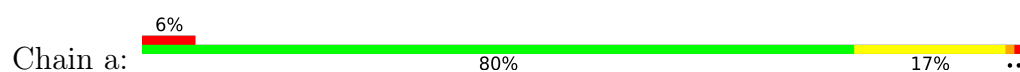
- Molecule 21: 40S ribosomal protein S13



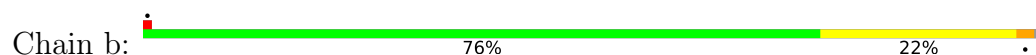
- Molecule 22: 40S ribosomal protein S14-A



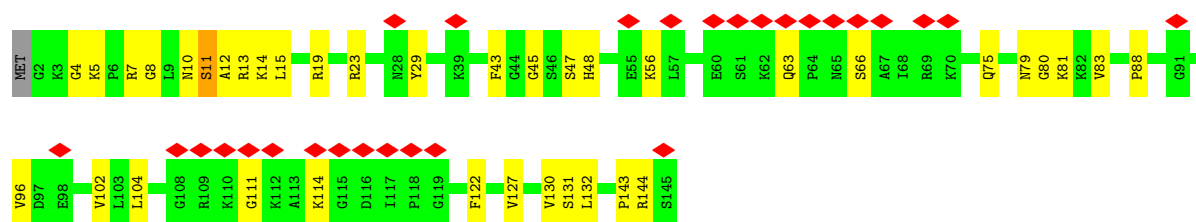
- Molecule 23: 40S ribosomal protein S21-A



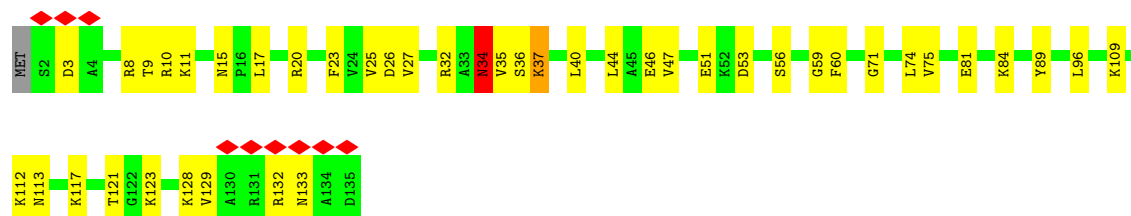
- Molecule 24: 40S ribosomal protein S22-A



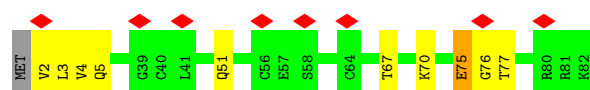
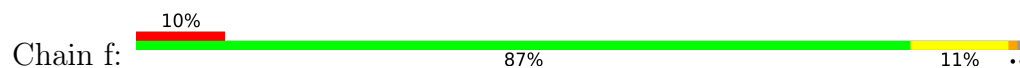
- Molecule 25: 40S ribosomal protein S23-A



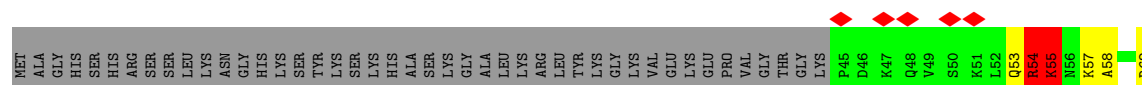
- Molecule 26: 40S ribosomal protein S24-A

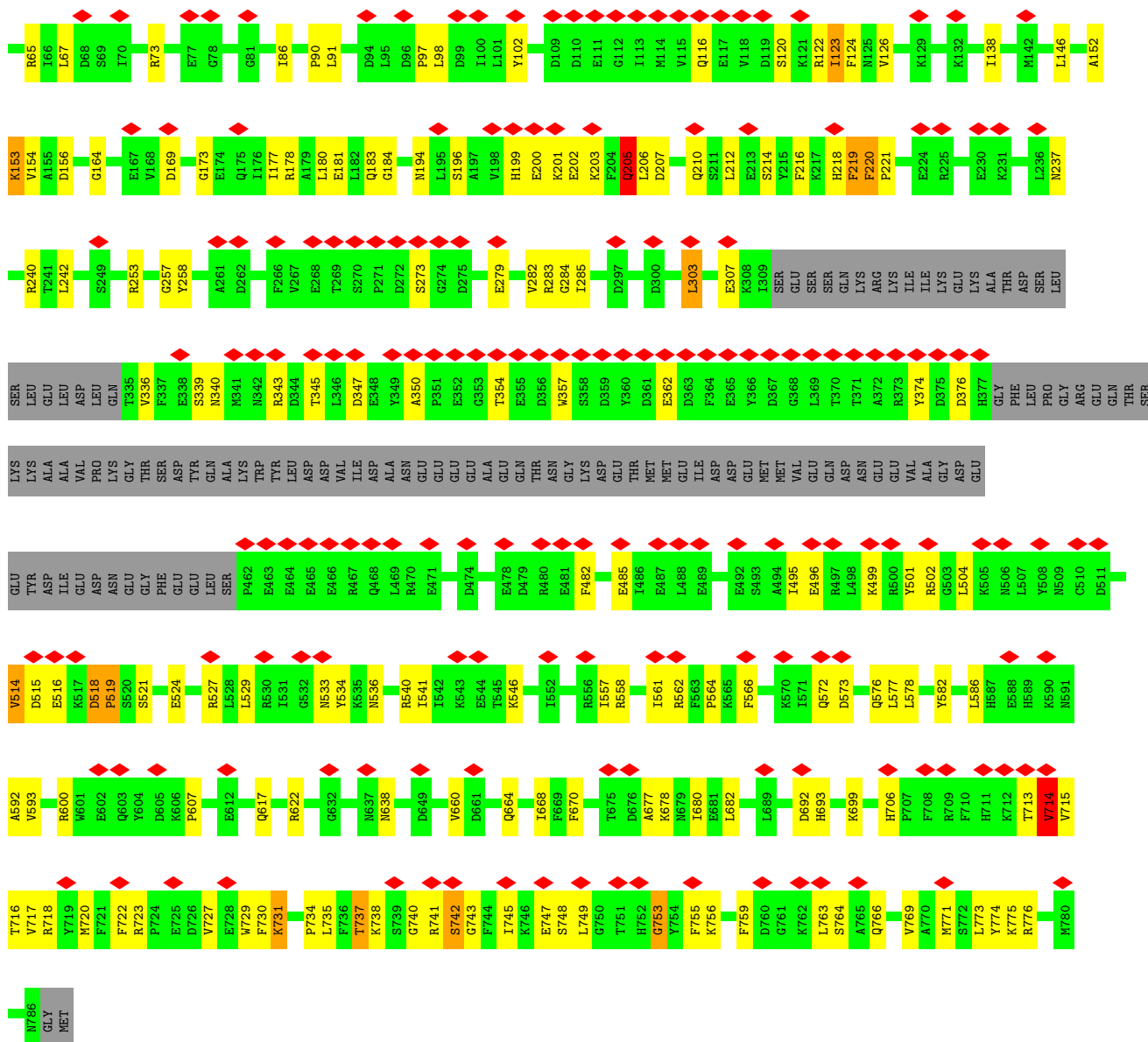


- Molecule 27: 40S ribosomal protein S27-A

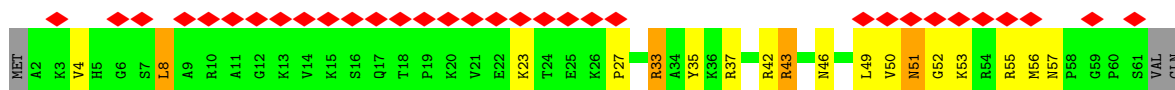


- Molecule 28: Ribosome biogenesis protein TSR1





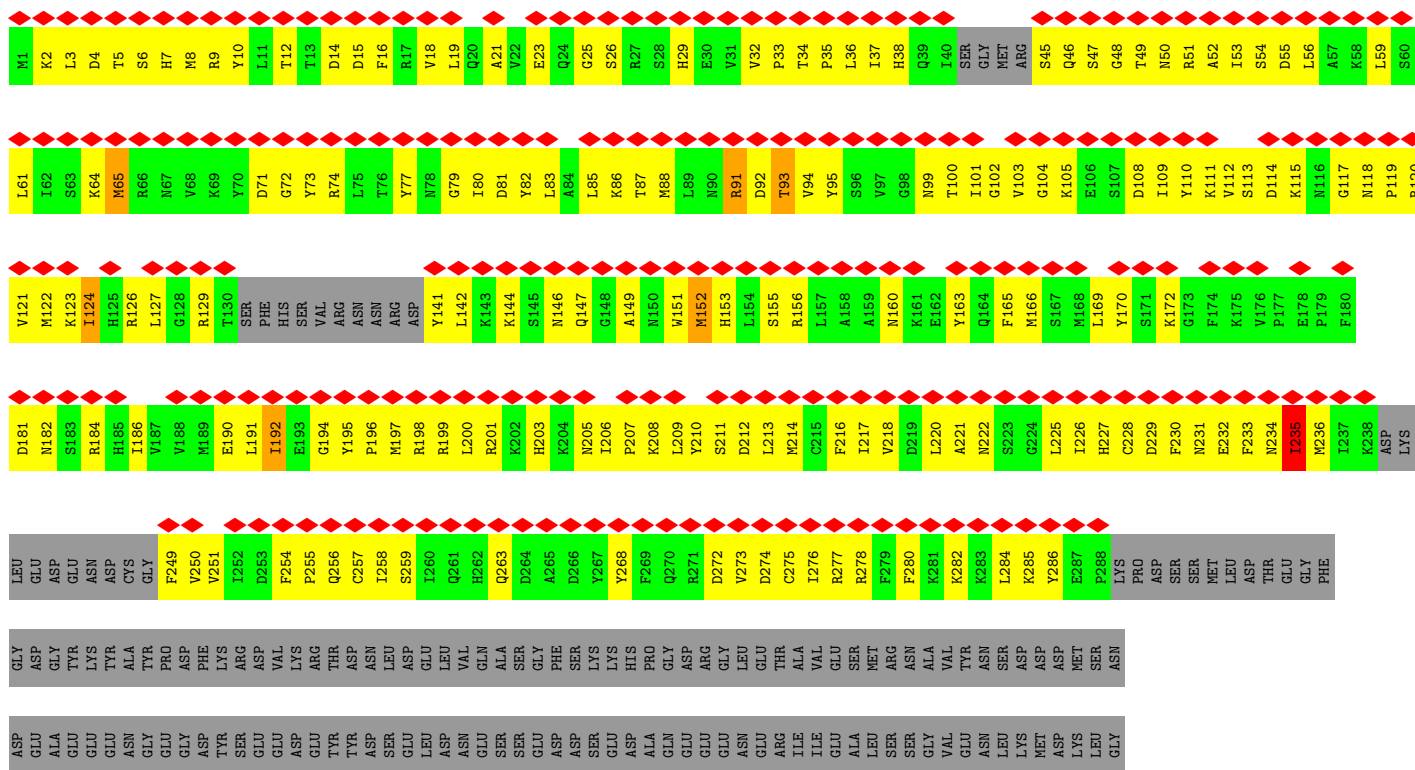
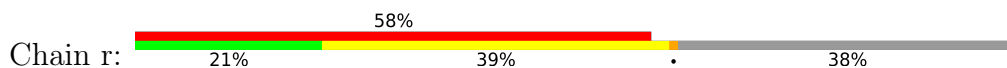
- Molecule 29: 40S ribosomal protein S30-A



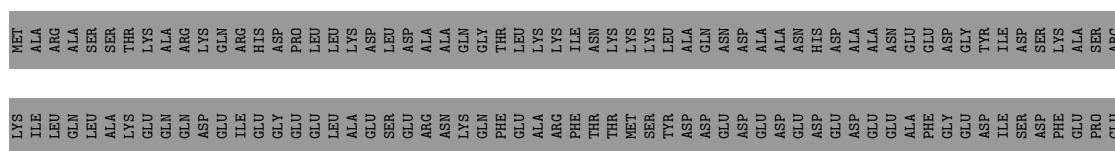
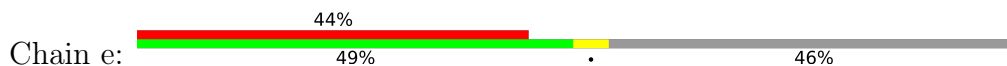
- Molecule 30: Pre-rRNA-processing protein PNO1



- Molecule 31: Serine/threonine-protein kinase RIO2



- Molecule 32: Essential nuclear protein 1



GLY	ASP	TYR	LYS	GLU	GLU	GLU	ILE	VAL	GLU	ILE	ASP	GLU	GLU	ASP	GLU	ASP	GLN	ASP	ASP
GLU	PRO	LEU	ALA	ASN	GLU	GLN	ASN	THR	SER	ARG	GLY	ASN	ILE	SER	GLY	GLN	VAL	GLU	ASP
W242	Q243	D244	V245	T246	Y247	V248	T249	N250	P251	E252	E253	W254	S255	P256	H257	V258	W259	Y260	E261
A262	T263	K264	L265	F266	V267	S268	N269	L270	T271	A272	K273	E274	S275	Q276	K277	F278	I279	N280	L281
L282	L283	L284	E285	R286	F287	R288	N290	I291	E292	T293	S294	E295	D296	H297	S298	L299	N300	Y301	
H302	I303	Y304	R305	A306	Y307	K308	R309	S310	L311	Y312	S315	A316	F317	F318	K319	G320	F321	L322	F323
P324	L325	V326	E327	T328	G329	C330	N331	V332	R333	E334	A335	T336	I337	A338	G339	S340	V341	L342	A343
K344	V345	S346	V347	F348	A349	L350	H351	S352	S353	A354	A355	L356	S357	Y358	L359	R360	R361	L362	
P363	F364	S365	P366	P367	T368	T369	V370	F371	I372	K373	I374	L375	L376	D377	K378	K379	Y380	A381	L382
P383	Y384	Q385	T386	V387	D388	D389	C390	V391	Y392	M395	R396	F397	R398	I399	L400	D401	D402	Q403	S404
N405	Q406	E407	D408	A409	T410	R411	V412	L413	P414	V415	H418	K419	A420	F421	L422	T423	F424		
A425	Q426	R427	Y428	K429	N430	D431	I432	T433	Q434	D435	Q436	R437	D438	L441	V444	R445	Q446	R447	G448
H449	K450	D451	I452	G453	P454	E455	I456	R457	L460	L461	A462	Q463	A464	S465	ARG	GLU	PHE	VAL	ASP
PRO	GLN	GLU	ALA	ASN	ASP	LEU	MET	ILE	ASP	VAL	ASN								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84100	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 ($e^-/\text{\AA}^2$)	2.4	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	0.523	Depositor
Minimum map value	-0.262	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.0722	Depositor
Map size ($\text{\AA}$)	416.25598, 416.25598, 416.25598	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2	0.79	38/39917 (0.1%)	0.84	74/62179 (0.1%)
2	D	0.62	0/900	0.98	1/1223 (0.1%)
3	B	0.54	0/1611	0.81	1/2177 (0.0%)
4	C	0.61	0/878	0.92	1/1177 (0.1%)
5	E	0.57	0/948	0.88	0/1273
6	F	0.56	0/1125	0.78	0/1510
7	H	0.52	0/1027	0.80	1/1383 (0.1%)
8	I	0.56	0/1130	0.85	0/1517
9	K	0.53	0/526	0.89	0/706
10	L	0.51	0/488	0.74	0/656
11	N	0.54	0/404	0.93	0/542
12	P	1.18	3/1617 (0.2%)	1.05	4/2215 (0.2%)
13	Q	0.84	1/1735 (0.1%)	0.96	0/2335
14	R	1.25	5/1692 (0.3%)	1.03	0/2296
15	S	1.36	6/2109 (0.3%)	1.13	4/2839 (0.1%)
16	T	0.98	1/1823 (0.1%)	0.94	1/2439 (0.0%)
17	U	0.85	0/1506	0.99	1/2028 (0.0%)
18	V	1.22	2/1514 (0.1%)	1.09	1/2021 (0.0%)
19	W	1.32	7/1519 (0.5%)	1.15	2/2035 (0.1%)
20	X	1.49	11/1239 (0.9%)	1.18	1/1673 (0.1%)
21	Y	1.18	2/1215 (0.2%)	1.08	4/1638 (0.2%)
22	Z	0.78	0/901	0.90	1/1217 (0.1%)
23	a	1.19	0/693	1.13	0/935
24	b	1.65	8/1038 (0.8%)	1.24	1/1395 (0.1%)
25	c	1.42	8/1139 (0.7%)	1.28	2/1518 (0.1%)
26	d	1.14	2/1087 (0.2%)	1.04	1/1449 (0.1%)
27	f	1.02	0/620	1.00	0/838
28	t	0.85	3/5150 (0.1%)	0.91	5/6972 (0.1%)
29	g	1.07	2/483 (0.4%)	1.17	2/643 (0.3%)
30	p	0.81	1/1500 (0.1%)	0.86	0/2020
31	r	0.25	0/2209	0.66	1/2965 (0.0%)
32	e	0.29	0/1044	0.82	3/1304 (0.2%)
All	All	0.89	100/80787 (0.1%)	0.91	112/117118 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	2	0	11
2	D	0	1
3	B	0	1
4	C	0	2
5	E	0	2
6	F	0	2
9	K	0	3
12	P	0	3
13	Q	0	5
14	R	0	1
15	S	0	1
17	U	0	3
18	V	0	1
19	W	0	2
20	X	0	1
21	Y	0	1
22	Z	0	1
23	a	0	3
24	b	0	1
25	c	0	1
28	t	0	8
29	g	0	1
31	r	0	2
All	All	0	57

The worst 5 of 100 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	220	A	C6-N1	-16.34	1.02	1.35
1	2	222	A	C6-N1	-15.35	1.04	1.35
1	2	1235	C	C1'-N1	13.44	1.68	1.48
1	2	831	U	C2-N3	11.90	1.61	1.37
1	2	833	U	C2-N3	11.42	1.60	1.37

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1023	A	C4'-C3'-O3'	9.21	123.21	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	452	A	C1'-C2'-O2'	-8.97	98.34	111.80
1	2	400	A	C4'-C3'-O3'	8.80	122.60	109.40
1	2	322	G	C2'-C3'-O3'	8.24	121.85	109.50
21	Y	10	GLY	CA-C-O	-7.90	114.47	121.58

There are no chirality outliers.

5 of 57 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2	222	A	Sidechain
1	2	236	A	Sidechain
1	2	440	U	Sidechain
1	2	507	U	Sidechain
1	2	618	U	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	35695	0	17919	699	0
2	D	892	0	892	16	0
3	B	1592	0	1660	45	0
4	C	871	0	876	18	0
5	E	928	0	960	33	0
6	F	1105	0	1164	57	0
7	H	1009	0	1029	24	0
8	I	1112	0	1124	48	0
9	K	519	0	558	15	0
10	L	486	0	522	9	0
11	N	397	0	398	45	0
12	P	1577	0	1567	33	0
13	Q	1709	0	1784	53	0
14	R	1662	0	1762	30	0
15	S	2068	0	2154	56	0
16	T	1799	0	1879	50	0
17	U	1481	0	1572	40	0
18	V	1489	0	1525	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	W	1494	0	1573	38	0
20	X	1213	0	1257	16	0
21	Y	1192	0	1255	24	0
22	Z	891	0	883	26	0
23	a	684	0	672	10	0
24	b	1021	0	1060	15	0
25	c	1121	0	1196	28	0
26	d	1073	0	1132	32	0
27	f	610	0	633	9	0
28	t	5037	0	4895	134	0
29	g	475	0	525	23	0
30	p	1473	0	1554	42	0
31	r	2166	0	2176	377	0
32	e	1045	0	266	39	0
All	All	75886	0	58422	1672	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 13.

The worst 5 of 1672 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)
1:2:565:C:H5''	31:r:47:SER:CB	1.18	1.62
31:r:198:ARG:HG3	31:r:233:PHE:CD2	1.17	1.60
1:2:1235:C:N1	1:2:1235:C:C1'	1.68	1.56
1:2:1269:U:H3	32:e:296:ASP:C	1.08	1.56
11:N:121:CYS:SG	11:N:145:HIS:CD2	2.02	1.53

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	
2	D	122/143 (85%)	89 (73%)	30 (25%)	3 (2%)	4	28
3	B	198/225 (88%)	168 (85%)	28 (14%)	2 (1%)	12	45
4	C	108/136 (79%)	92 (85%)	14 (13%)	2 (2%)	6	33
5	E	115/142 (81%)	93 (81%)	21 (18%)	1 (1%)	14	46
6	F	139/143 (97%)	121 (87%)	14 (10%)	4 (3%)	3	26
7	H	120/146 (82%)	107 (89%)	13 (11%)	0	100	100
8	I	141/144 (98%)	129 (92%)	11 (8%)	1 (1%)	18	51
9	K	62/108 (57%)	49 (79%)	10 (16%)	3 (5%)	2	16
10	L	60/67 (90%)	54 (90%)	6 (10%)	0	100	100
11	N	49/152 (32%)	32 (65%)	12 (24%)	5 (10%)	0	5
12	P	204/252 (81%)	168 (82%)	32 (16%)	4 (2%)	6	32
13	Q	212/255 (83%)	172 (81%)	38 (18%)	2 (1%)	14	46
14	R	218/254 (86%)	186 (85%)	29 (13%)	3 (1%)	9	38
15	S	258/261 (99%)	226 (88%)	31 (12%)	1 (0%)	30	61
16	T	224/236 (95%)	206 (92%)	17 (8%)	1 (0%)	30	61
17	U	182/190 (96%)	158 (87%)	22 (12%)	2 (1%)	11	43
18	V	184/200 (92%)	160 (87%)	21 (11%)	3 (2%)	7	36
19	W	183/197 (93%)	156 (85%)	24 (13%)	3 (2%)	7	36
20	X	153/156 (98%)	133 (87%)	19 (12%)	1 (1%)	18	51
21	Y	148/151 (98%)	130 (88%)	17 (12%)	1 (1%)	18	51
22	Z	125/137 (91%)	110 (88%)	15 (12%)	0	100	100
23	a	85/87 (98%)	66 (78%)	16 (19%)	3 (4%)	3	23
24	b	127/130 (98%)	118 (93%)	8 (6%)	1 (1%)	16	49
25	c	142/145 (98%)	116 (82%)	23 (16%)	3 (2%)	5	31
26	d	132/135 (98%)	121 (92%)	9 (7%)	2 (2%)	8	37
27	f	79/82 (96%)	60 (76%)	17 (22%)	2 (2%)	4	28
28	t	627/788 (80%)	542 (86%)	78 (12%)	7 (1%)	11	43
29	g	58/63 (92%)	42 (72%)	14 (24%)	2 (3%)	3	23
30	p	183/274 (67%)	168 (92%)	15 (8%)	0	100	100
31	r	256/425 (60%)	227 (89%)	26 (10%)	3 (1%)	10	41
32	e	259/483 (54%)	242 (93%)	14 (5%)	3 (1%)	10	41
All	All	5153/6307 (82%)	4441 (86%)	644 (12%)	68 (1%)	12	39

5 of 68 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	K	97	LYS
11	N	148	TYR
12	P	110	TYR
12	P	111	ILE
15	S	69	HIS

5.3.2 Protein sidechains ⓘ

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	D	89/119 (75%)	89 (100%)	0	100	100
3	B	173/191 (91%)	173 (100%)	0	100	100
4	C	88/124 (71%)	88 (100%)	0	100	100
5	E	98/118 (83%)	98 (100%)	0	100	100
6	F	117/119 (98%)	115 (98%)	2 (2%)	53	69
7	H	109/129 (84%)	107 (98%)	2 (2%)	51	68
8	I	115/116 (99%)	113 (98%)	2 (2%)	53	69
9	K	57/89 (64%)	56 (98%)	1 (2%)	51	68
10	L	55/60 (92%)	55 (100%)	0	100	100
11	N	43/135 (32%)	40 (93%)	3 (7%)	14	41
12	P	164/210 (78%)	161 (98%)	3 (2%)	51	68
13	Q	191/224 (85%)	190 (100%)	1 (0%)	81	80
14	R	179/205 (87%)	176 (98%)	3 (2%)	53	69
15	S	221/222 (100%)	220 (100%)	1 (0%)	81	80
16	T	188/201 (94%)	187 (100%)	1 (0%)	81	80
17	U	165/170 (97%)	163 (99%)	2 (1%)	63	73
18	V	150/161 (93%)	149 (99%)	1 (1%)	76	78
19	W	158/166 (95%)	157 (99%)	1 (1%)	78	79
20	X	129/137 (94%)	127 (98%)	2 (2%)	55	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	Y	127/128 (99%)	125 (98%)	2 (2%)	55	69
22	Z	81/105 (77%)	80 (99%)	1 (1%)	63	73
23	a	74/74 (100%)	72 (97%)	2 (3%)	39	61
24	b	110/111 (99%)	108 (98%)	2 (2%)	51	68
25	c	119/120 (99%)	119 (100%)	0	100	100
26	d	112/113 (99%)	111 (99%)	1 (1%)	70	76
27	f	70/71 (99%)	70 (100%)	0	100	100
28	t	533/703 (76%)	525 (98%)	8 (2%)	57	70
29	g	51/54 (94%)	50 (98%)	1 (2%)	48	66
30	p	162/238 (68%)	154 (95%)	8 (5%)	22	49
31	r	242/384 (63%)	239 (99%)	3 (1%)	63	73
All	All	4170/4997 (84%)	4117 (99%)	53 (1%)	59	72

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	a	11	LEU
28	t	123	ILE
30	p	262	ASN
23	a	69	LEU
26	d	121	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
26	d	133	ASN
31	r	146	ASN
28	t	116	GLN
28	t	706	HIS
11	N	145	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1664/1800 (92%)	592 (35%)	68 (4%)

5 of 592 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	U
1	2	4	C
1	2	5	U
1	2	8	U
1	2	9	U

5 of 68 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1441	C
1	2	1481	C
1	2	1680	G
1	2	401	A
1	2	400	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	401:A	O3'	402:C	P	1.78

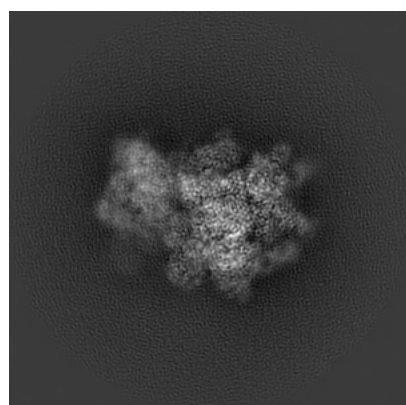
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3886. These allow visual inspection of the internal detail of the map and identification of artifacts.

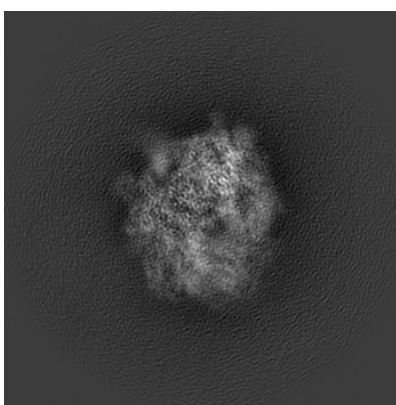
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

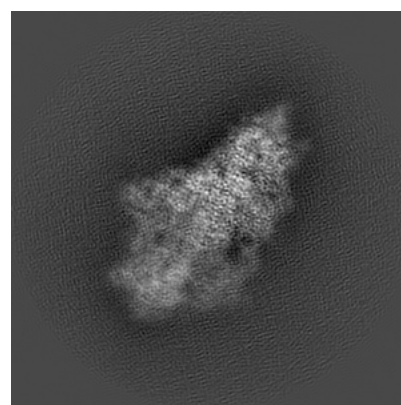
6.1.1 Primary map



X



Y

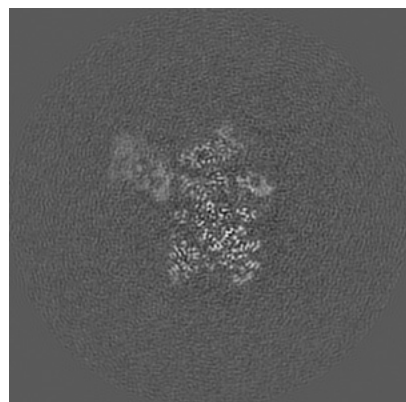


Z

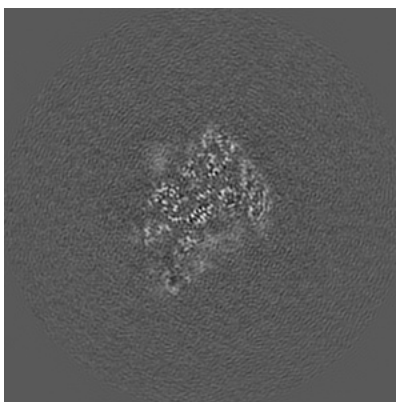
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

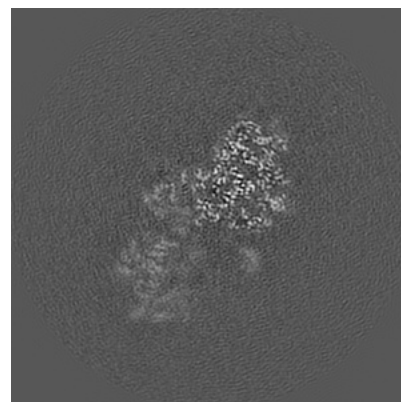
6.2.1 Primary map



X Index: 192



Y Index: 192

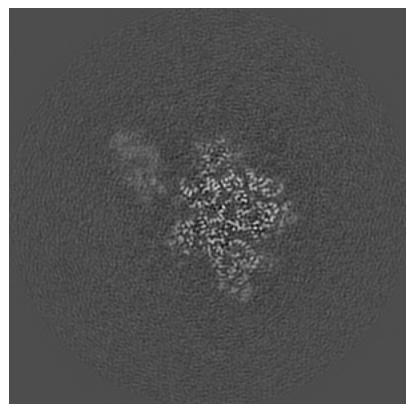


Z Index: 192

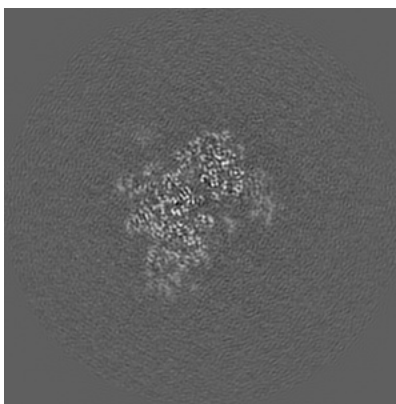
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

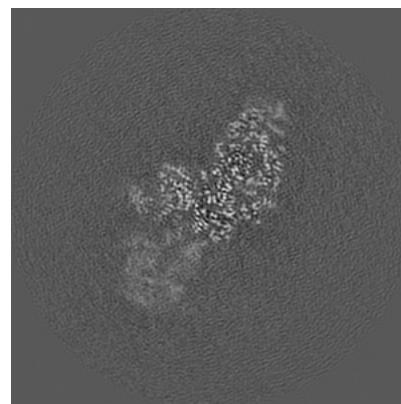
6.3.1 Primary map



X Index: 209



Y Index: 214

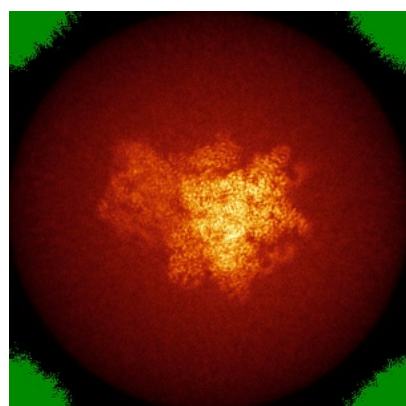


Z Index: 178

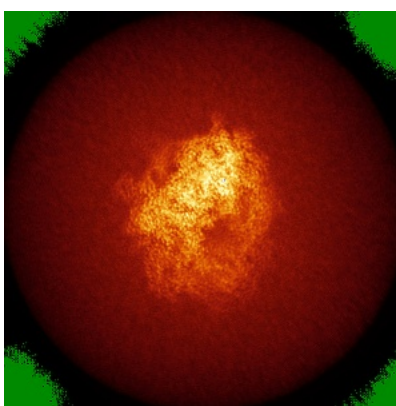
The images above show the largest variance slices of the map in three orthogonal directions.

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

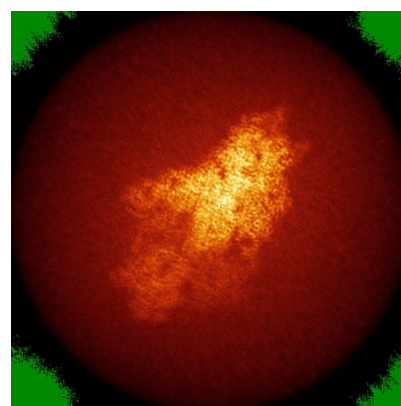
6.4.1 Primary map



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 0.0722. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

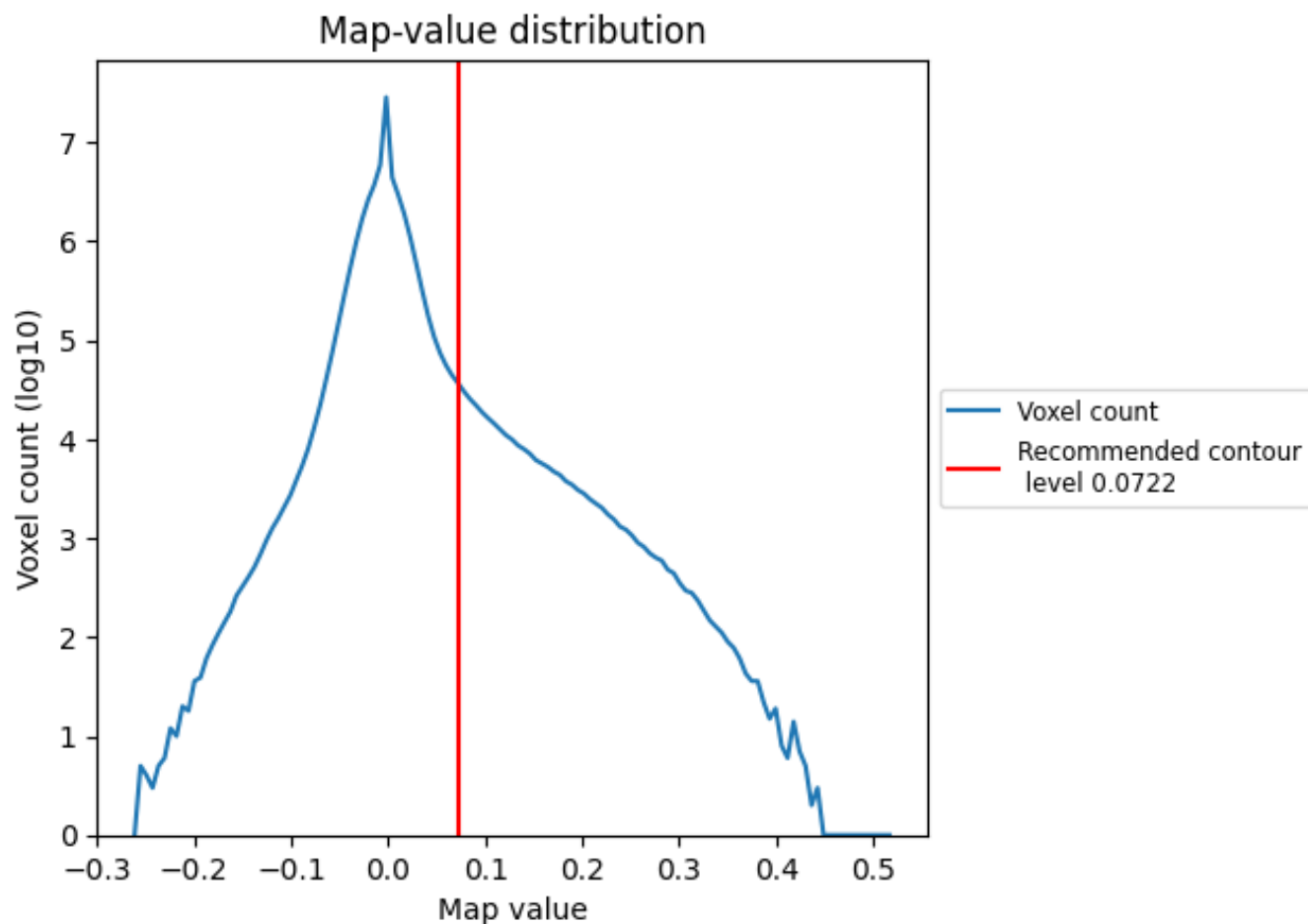
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

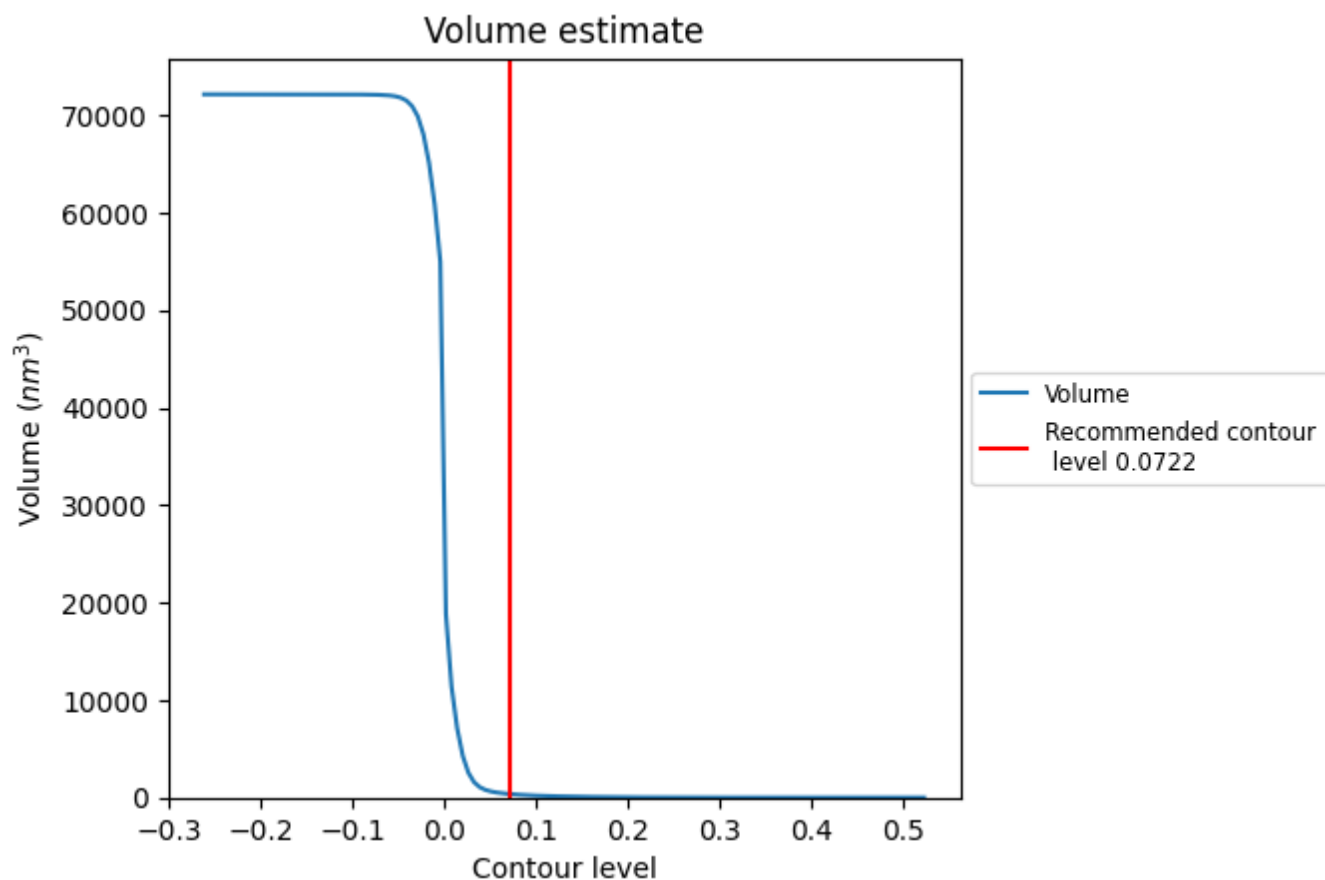
This section contains the results of statistical analysis of the map.

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.

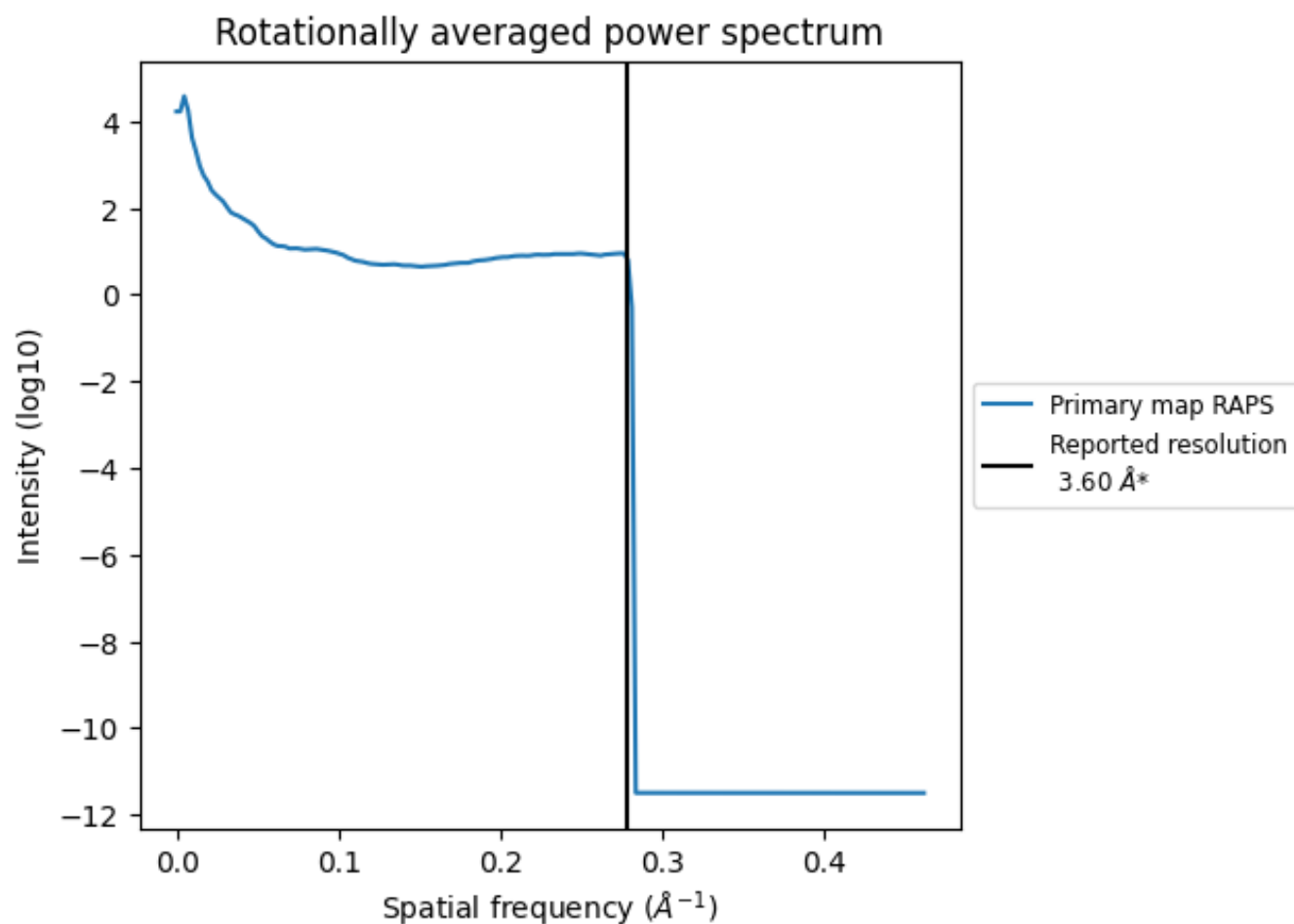
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 359 nm³; this corresponds to an approximate mass of 324 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

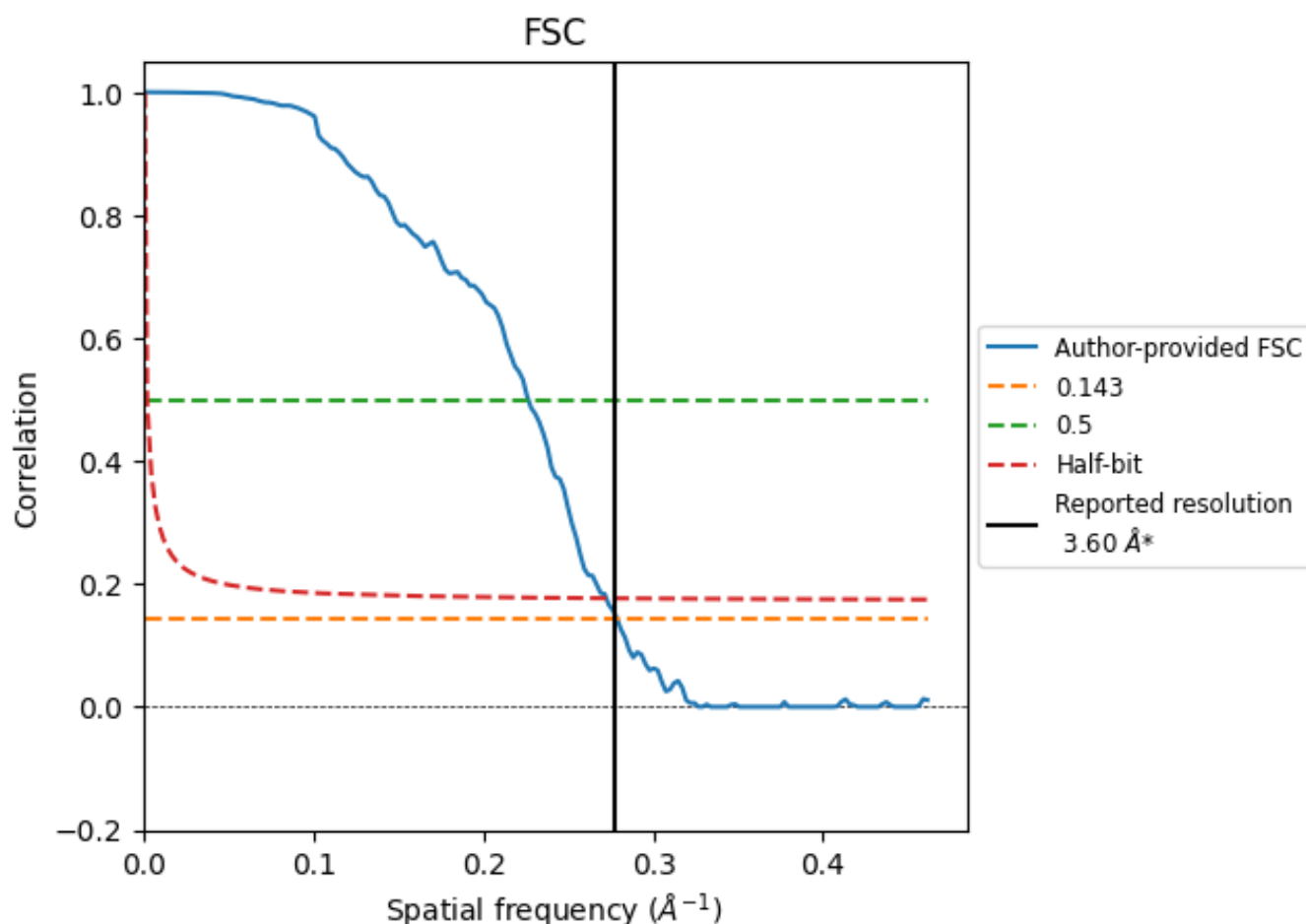


*Reported resolution corresponds to spatial frequency of 0.278 $\text{\AA}^{-1}$

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

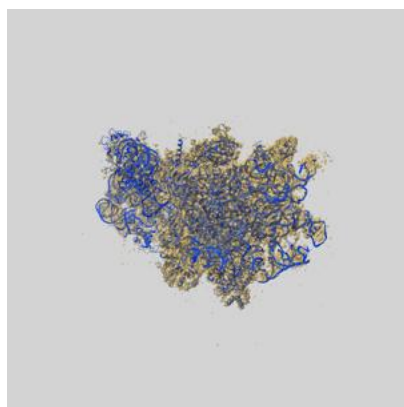
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	4.41	3.67
Unmasked-calculated*	-	-	-

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

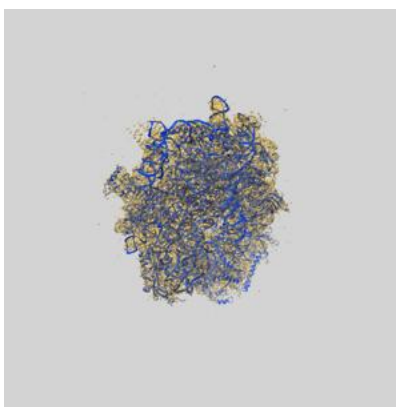
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3886 and PDB model 6EML. Per-residue inclusion information can be found in section [3](#) on page [10](#).

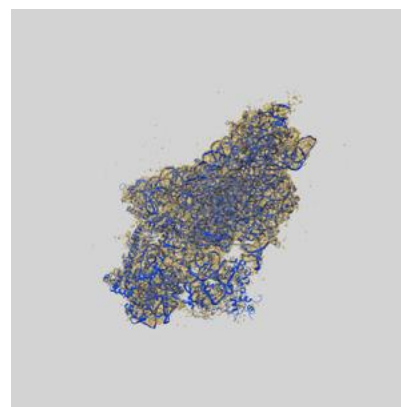
9.1 Map-model overlay [i](#)



X



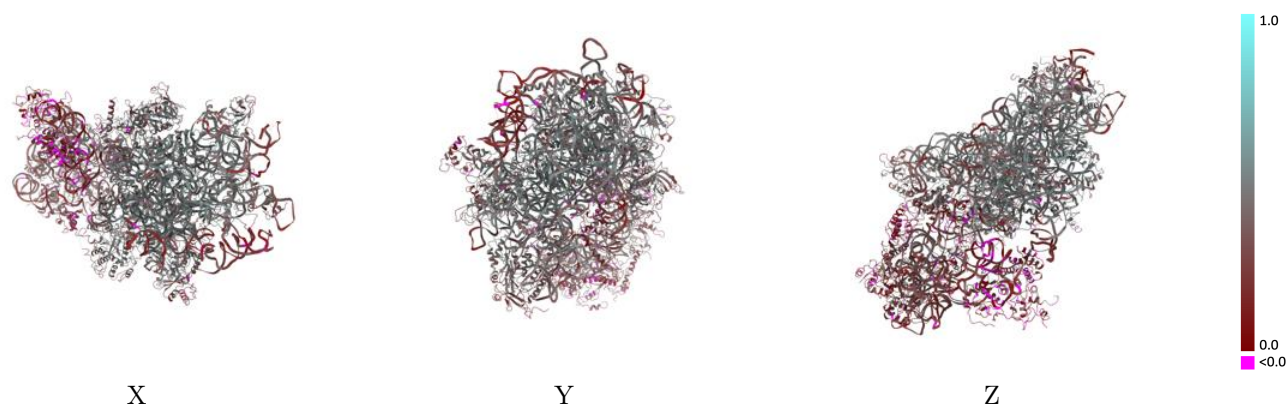
Y



Z

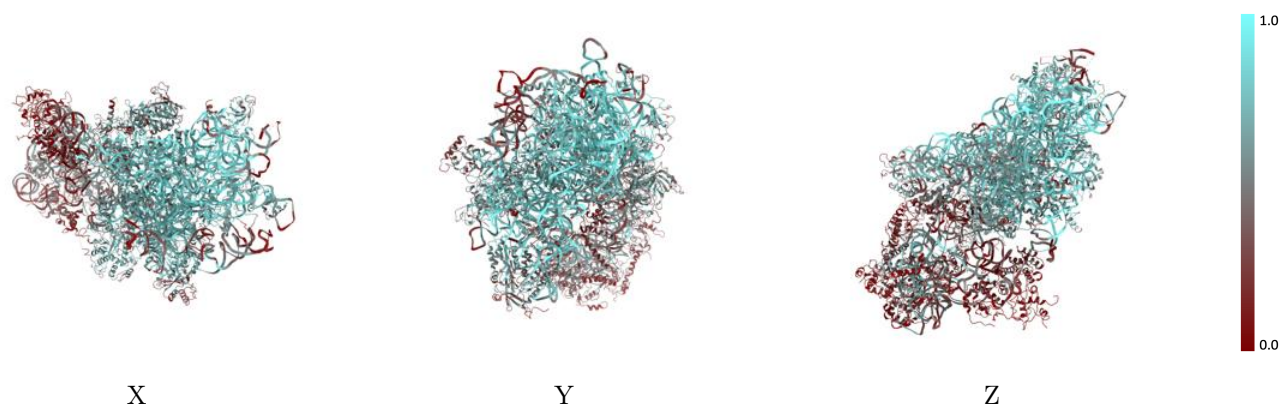
The images above show the 3D surface view of the map at the recommended contour level 0.0722 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



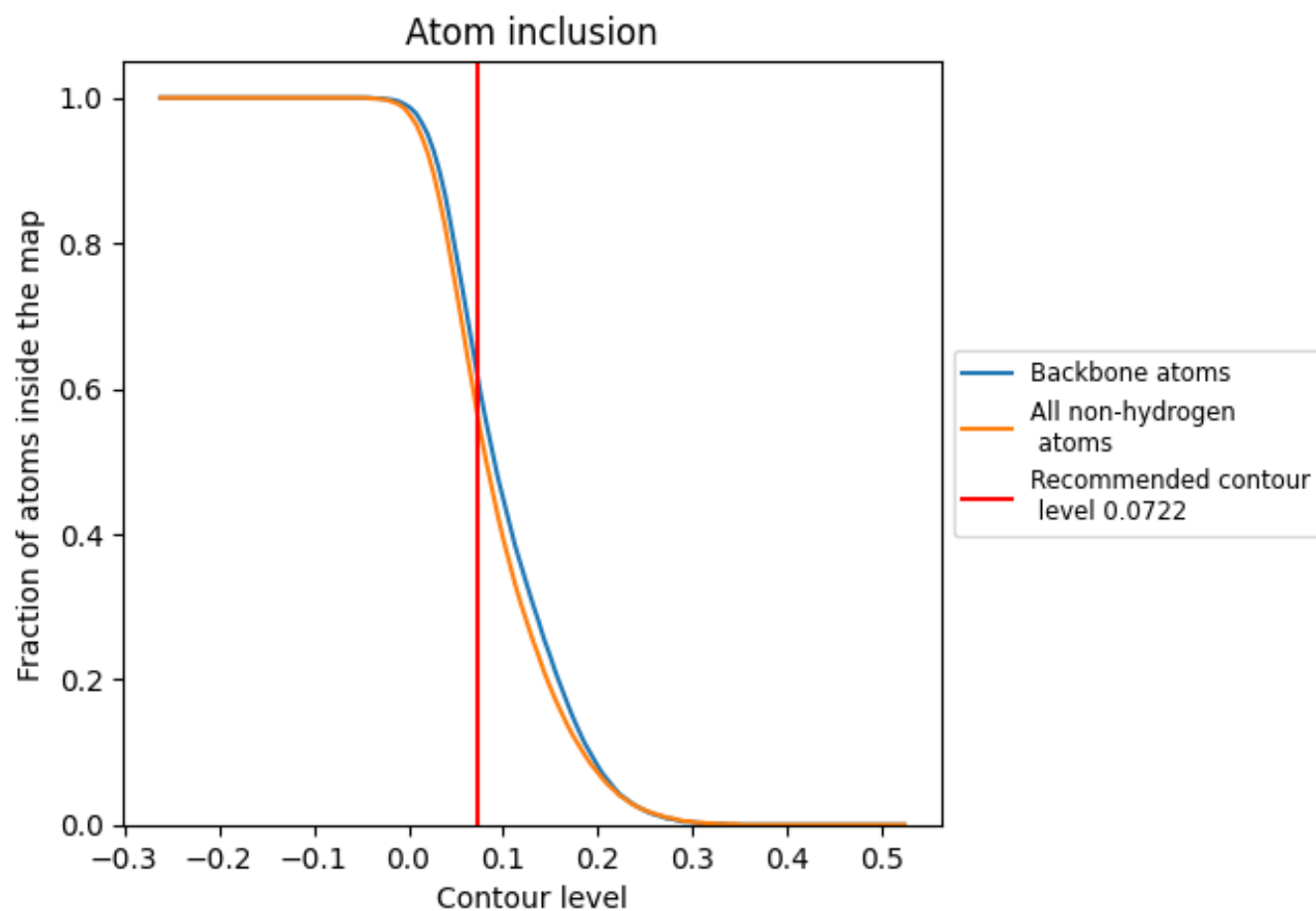
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0722).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 57% 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 (0.0722) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5680	 0.3710
2	 0.6670	 0.3790
B	 0.2300	 0.2400
C	 0.1810	 0.2180
D	 0.0450	 0.1680
E	 0.2590	 0.2530
F	 0.1600	 0.2270
H	 0.1810	 0.2510
I	 0.2110	 0.2440
K	 0.1050	 0.2120
L	 0.1750	 0.2370
N	 0.0310	 0.1090
P	 0.6650	 0.4400
Q	 0.5110	 0.3880
R	 0.6510	 0.4630
S	 0.7200	 0.4930
T	 0.6590	 0.4410
U	 0.4790	 0.3780
V	 0.7080	 0.4540
W	 0.7100	 0.4740
X	 0.6810	 0.4750
Y	 0.7000	 0.4510
Z	 0.4870	 0.3840
a	 0.6760	 0.4490
b	 0.7710	 0.5160
c	 0.6170	 0.4600
d	 0.6960	 0.4720
e	 0.1670	 0.1520
f	 0.6750	 0.4590
g	 0.3860	 0.3360
p	 0.4150	 0.3700
r	 0.1450	 0.1400
t	 0.5280	 0.4020

