



wwPDB EM Validation Summary Report ⓘ

Aug 25, 2026 – 04:53 am BST

PDB ID : 6YAL / pdb_00006yal
EMDB ID : EMD-10760
Title : Mammalian 48S late-stage initiation complex with beta-globin mRNA
Authors : Bochler, A.; Simonetti, A.; Guca, E.; Hashem, Y.
Deposited on : 2020-03-12
Resolution : 3.00 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:

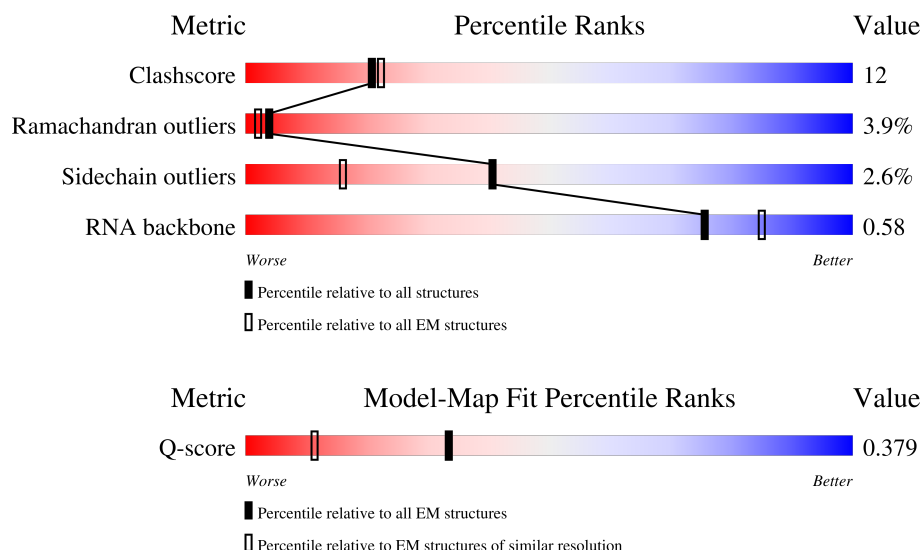
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	1	75	<div> <div>79%</div> <div> <div>61%</div> <div>28%</div> <div>7%</div> <div>.</div> </div> </div>
2	1	25	<div> <div>28%</div> <div>100%</div> </div>
3	C	209	<div> <div>12%</div> <div>93%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
4	D	264	
5	E	226	
6	F	243	
7	G	263	
8	H	191	
9	I	237	
10	J	192	
11	K	206	
12	L	182	
13	M	98	
14	N	158	
15	O	132	
16	P	150	
17	Q	151	
18	S	141	
19	T	135	
20	V	141	
21	W	119	
22	X	82	
23	Y	130	
24	Z	143	
25	a	133	
26	b	115	
27	c	84	
28	d	69	

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Mol	Chain	Length	Quality of chain
29	e	56	
30	f	71	
31	g	313	
32	n	124	
33	i	133	
34	2	1863	
35	A	284	
36	B	422	
37	j	111	
38	k	595	
39	U	152	
40	R	145	
41	3	42	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
34	C4J	2	1244	X	-	-	-
42	SF4	k	701	-	-	X	-
42	SF4	k	702	-	-	X	-
44	GNP	k	704	-	-	X	-
44	GNP	k	705	-	-	X	-

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 90085 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 initiator methionylated tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	75	Total	C	N	O	P	0	0
			1614	722	299	519	74		

- Molecule 2 is a protein called 60s ribosomal protein ul41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 3 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	208	Total	C	N	O	S	0	0
			1643	1045	289	301	8		

- Molecule 4 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	215	Total	C	N	O	S	0	0
			1741	1107	309	310	15		

- Molecule 5 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	226	Total	C	N	O	S	0	0
			1743	1127	300	307	9		

- Molecule 6 is a protein called 40S Ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	227	Total	C	N	O	S	0	0
			1764	1124	317	315	8		

- Molecule 7 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	263	Total	C	N	O	S	0	0
			2083	1329	385	359	10		

- Molecule 8 is a protein called 40S Ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 9 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	237	Total	C	N	O	S	0	0
			1924	1200	387	330	7		

- Molecule 10 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	190	Total	C	N	O	S	0	0
			1530	975	281	273	1		

- Molecule 11 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	206	Total	C	N	O	S	0	0
			1680	1054	329	292	5		

- Molecule 12 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	182	Total	C	N	O	S	0	0
			1499	952	300	245	2		

- Molecule 13 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	98	Total	C	N	O	S	0	0
			828	539	148	135	6		

- Molecule 14 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 15 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 16 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 17 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 18 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 19 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 20 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	141	Total	C	N	O	S	0	0
			1113	701	213	196	3		

- Molecule 21 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 22 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	82	Total	C	N	O	S	0	0
			620	378	117	120	5		

- Molecule 23 is a protein called 40S ribosomal protein uS8.

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

- Molecule 24 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	142	Total	C	N	O	S	0	0
			1106	698	220	184	4		

- Molecule 25 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	126	Total	C	N	O	S	0	0
			1021	645	198	173	5		

- Molecule 26 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	99	Total	C	N	O	S	0	0
			789	491	162	130	6		

- Molecule 27 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	84	Total	C	N	O	S	0	0
			659	413	122	116	8		

- Molecule 28 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 29 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 30 is a protein called 40S ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	71	Total	C	N	O	S	0	0
			582	367	109	99	7		

- Molecule 31 is a protein called ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	313	Total	C	N	O	S	0	0
			2437	1535	424	466	12		

- Molecule 32 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	n	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 33 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	59	Total	C	N	O	S	0	0
			473	293	104	75	1		

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2	1744	Total	C	N	O	P	0	0
			37204	16614	6663	12187	1740		

- Molecule 35 is a protein called Eukaryotic translation initiation factor 2 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A	266	Total	C	N	O	S	0	0
			2146	1354	376	405	11		

- Molecule 36 is a protein called Eukaryotic translation initiation factor 2 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B	422	Total	C	N	O	S	0	0
			3214	2044	561	592	17		

- Molecule 37 is a protein called eukaryotic translation initiation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	109	Total	C	N	O	S	0	0
			883	549	168	162	4		

- Molecule 38 is a protein called ATP-binding cassette sub-family E member 1 (ABCE1).

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	595	Total	C	N	O	S	0	0
			4693	2995	802	865	31		

- Molecule 39 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	U	145	Total	C	N	O	S	0	0
			1194	747	243	203	1		

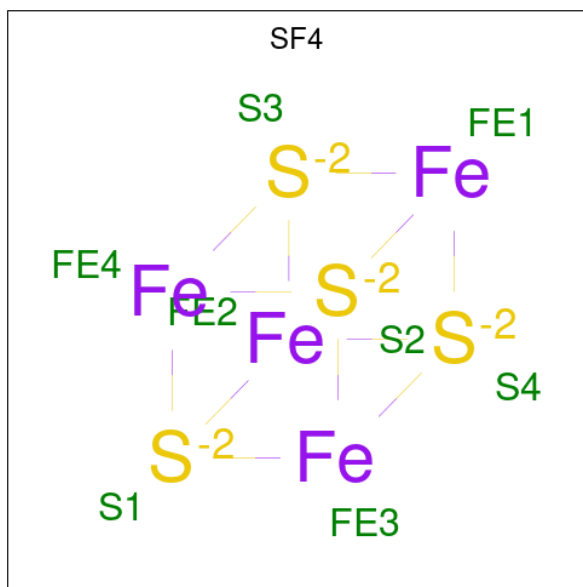
- Molecule 40 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	140	Total	C	N	O	S	0	0
			1154	733	219	195	7		

- Molecule 41 is a RNA chain called beta-globin mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	3	42	Total	C	N	O	P	0	0
			892	401	166	284	41		

- Molecule 42 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).

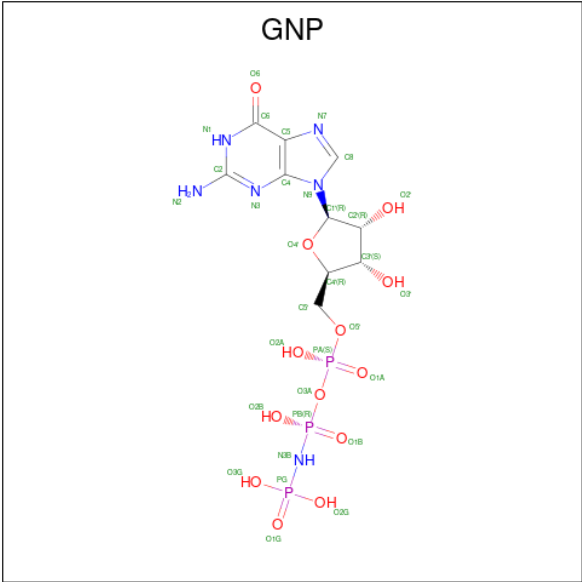


Mol	Chain	Residues	Atoms			AltConf
42	k	1	Total	Fe	S	0
			8	4	4	
42	k	1	Total	Fe	S	0
			8	4	4	

- Molecule 43 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
43	k	1	Total	Mg	0
			1	1	

- Molecule 44 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).

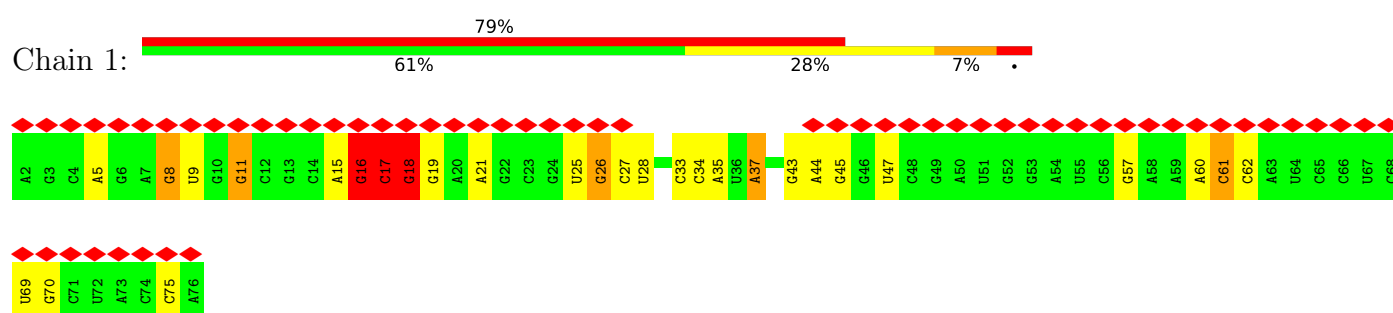


Mol	Chain	Residues	Atoms					AltConf
44	k	1	Total	C	N	O	P	0
			32	10	6	13	3	
44	k	1	Total	C	N	O	P	0
			32	10	6	13	3	

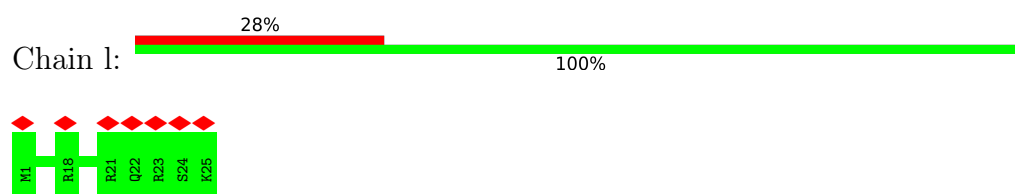
3 Residue-property plots [i](#)

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.

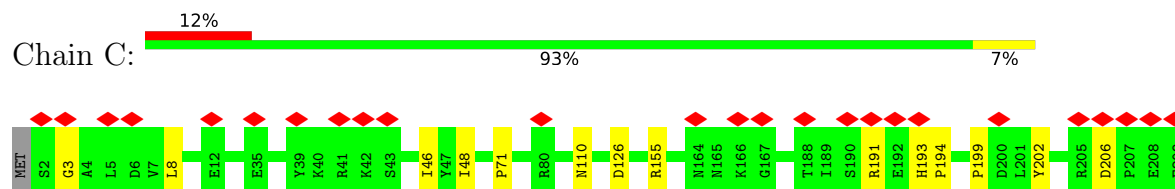
- Molecule 1: initiator methionylated tRNA



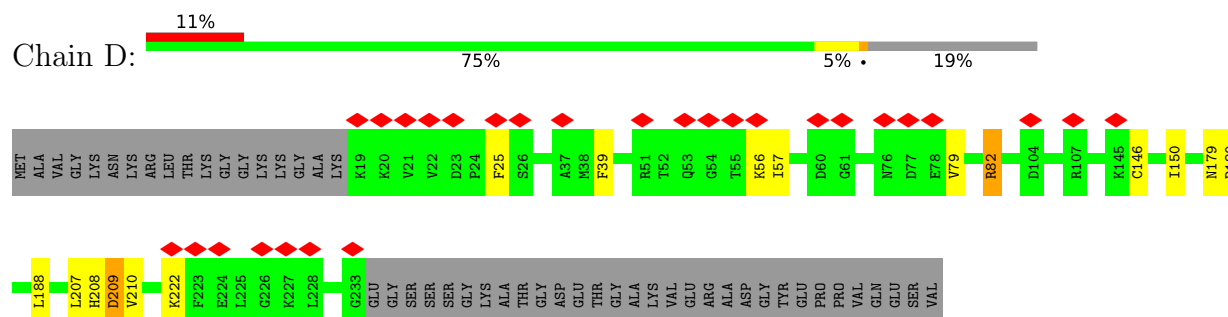
- Molecule 2: 60s ribosomal protein ul41



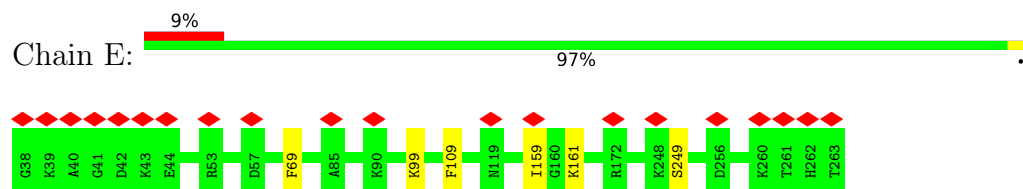
- Molecule 3: 40S ribosomal protein uS2



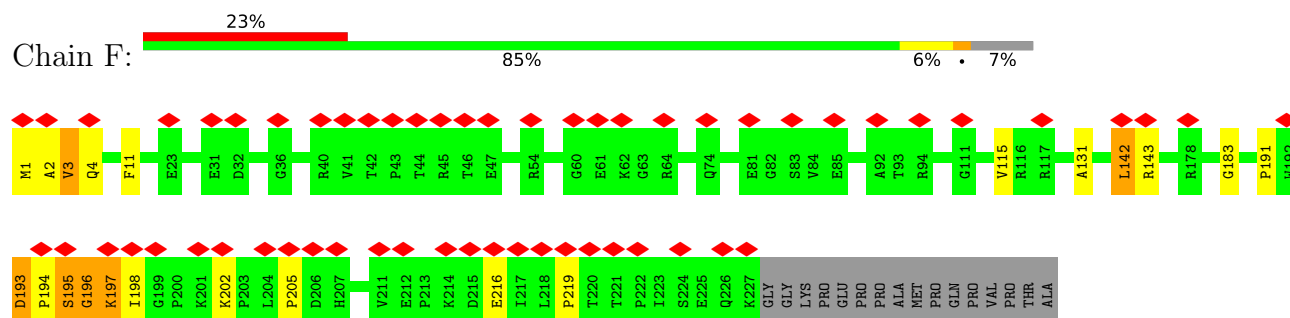
- Molecule 4: 40S ribosomal protein eS1



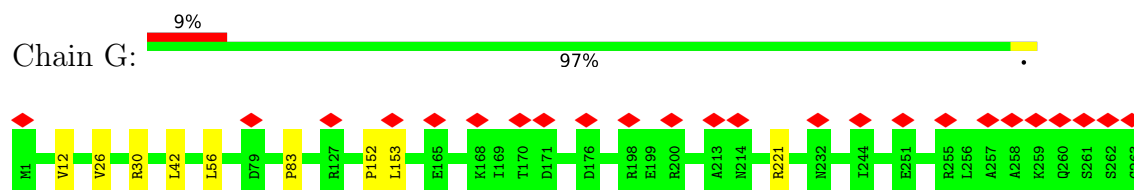
- Molecule 5: 40S ribosomal protein uS5



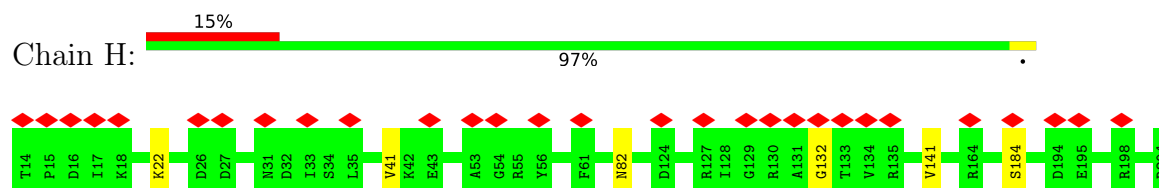
- Molecule 6: 40S Ribosomal protein uS3



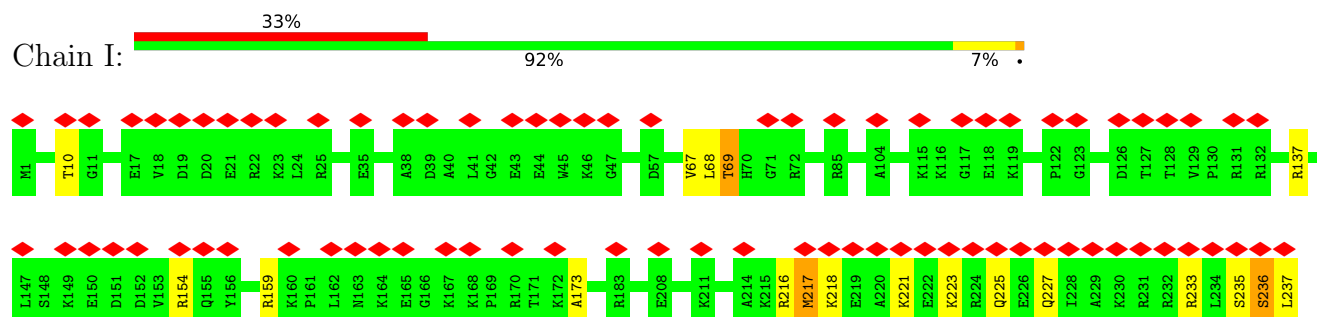
- Molecule 7: 40S ribosomal protein eS4



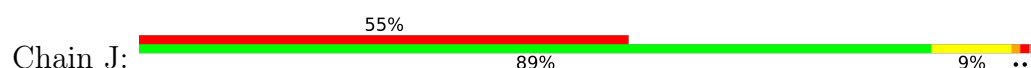
- Molecule 8: 40S Ribosomal protein uS7

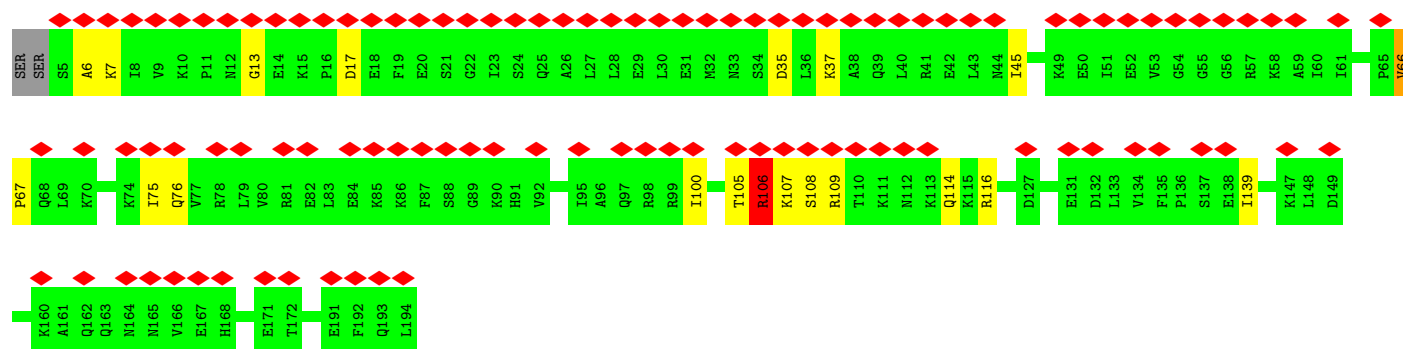


- Molecule 9: 40S ribosomal protein eS6

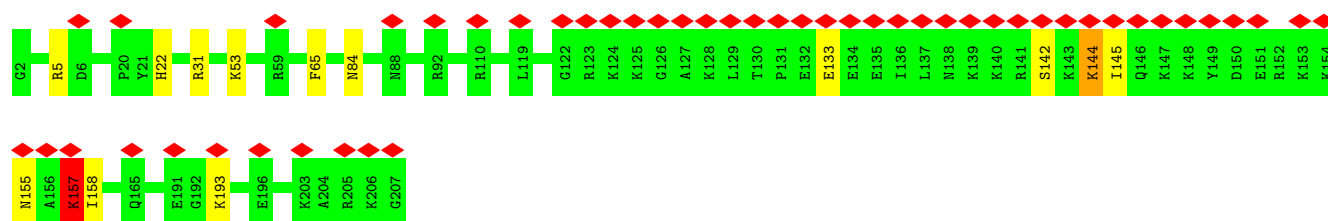


- Molecule 10: 40S ribosomal protein eS7

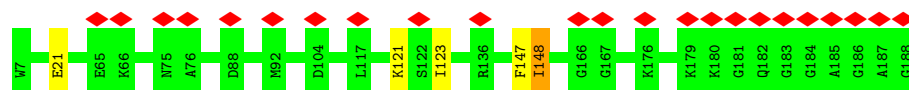




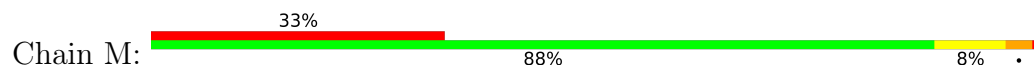
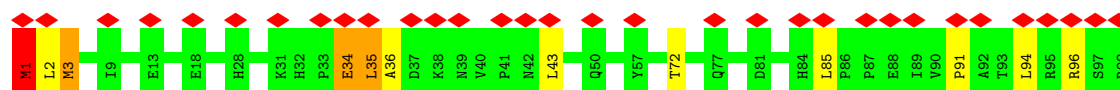
- Molecule 11: 40S ribosomal protein eS8



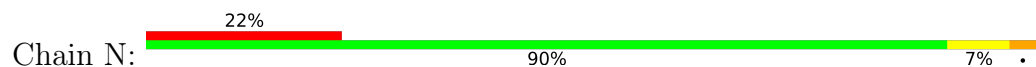
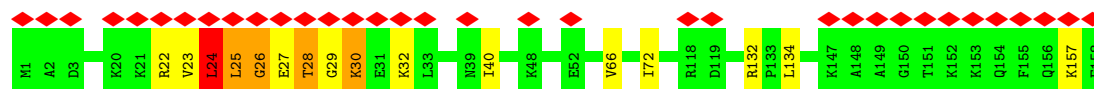
- Molecule 12: 40S ribosomal protein uS4



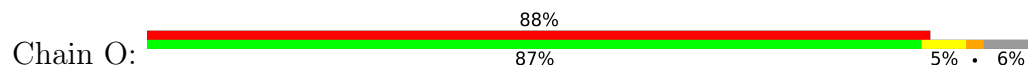
- Molecule 13: 40S ribosomal protein eS10

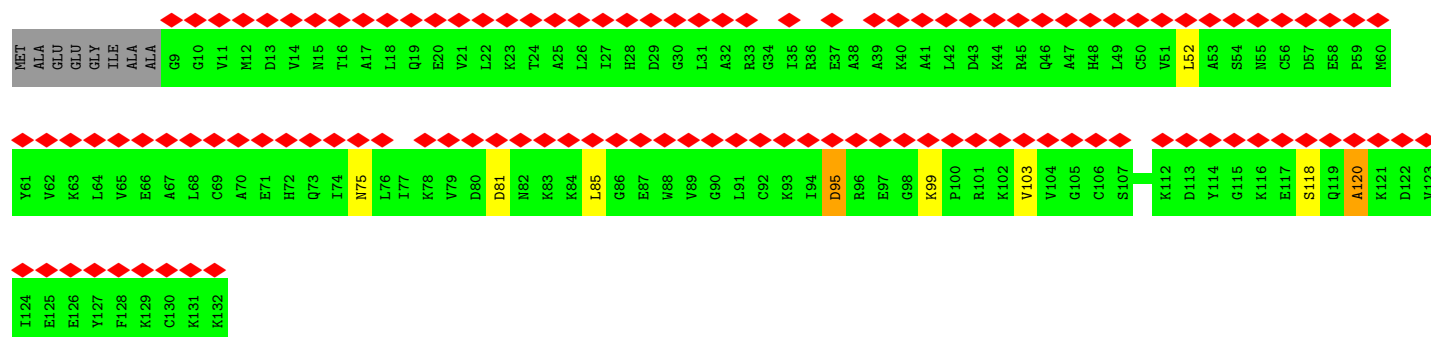


- Molecule 14: 40S ribosomal protein uS17

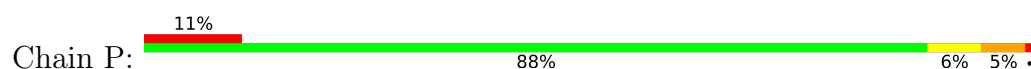
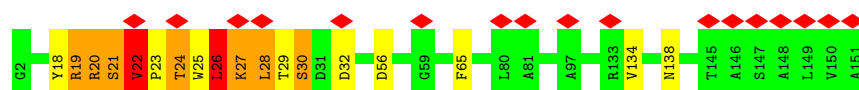


- Molecule 15: 40S ribosomal protein eS12

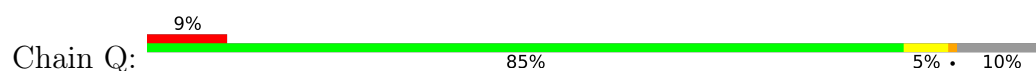
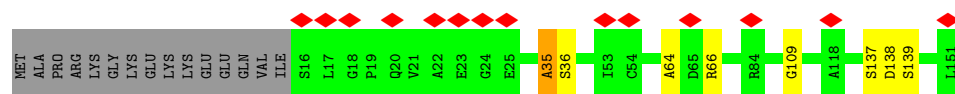




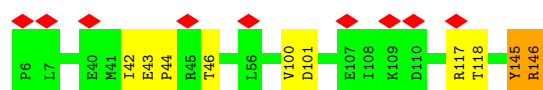
• Molecule 16: 40S ribosomal protein uS15



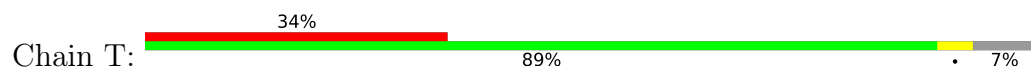
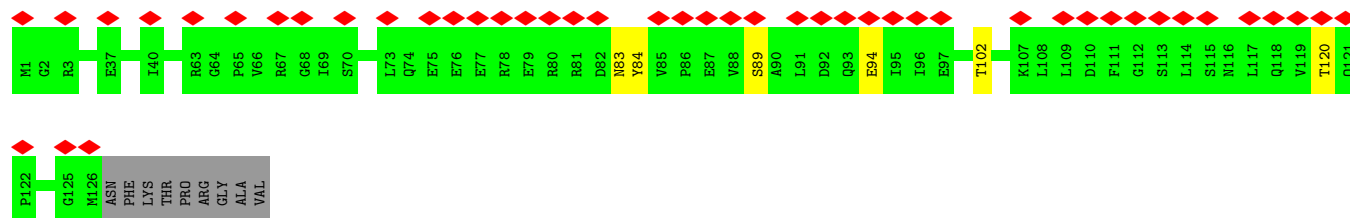
• Molecule 17: 40S ribosomal protein uS11



• Molecule 18: 40S ribosomal protein uS9

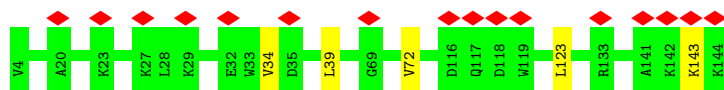


• Molecule 19: 40S ribosomal protein eS17

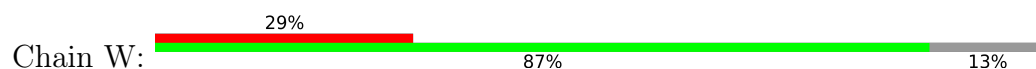
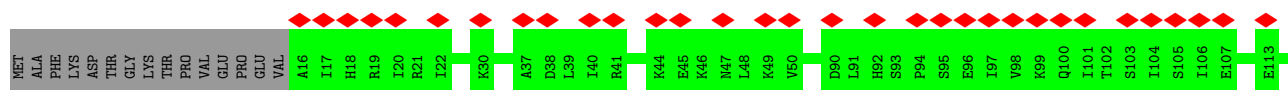


• Molecule 20: 40S ribosomal protein eS19

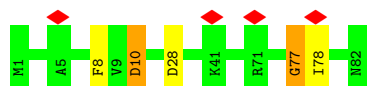




- Molecule 21: 40S ribosomal protein uS10



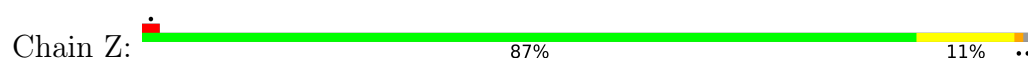
- Molecule 22: 40S ribosomal protein eS21



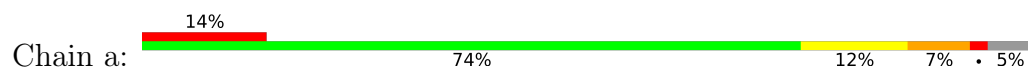
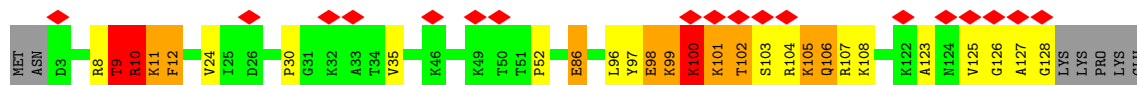
- Molecule 23: 40S ribosomal protein uS8



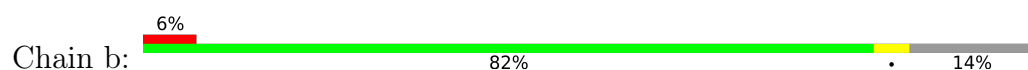
- Molecule 24: 40S ribosomal protein uS12

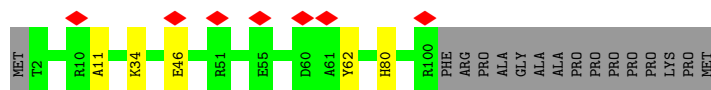


- Molecule 25: 40S ribosomal protein eS24

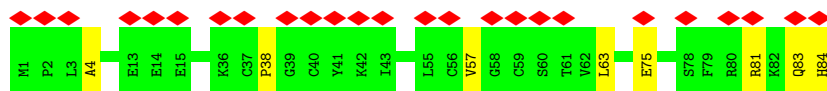


- Molecule 26: 40S ribosomal protein eS26

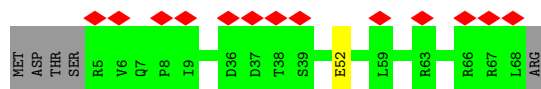




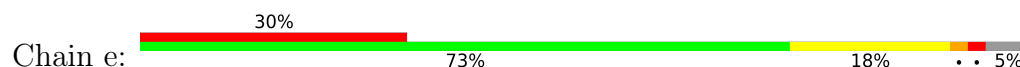
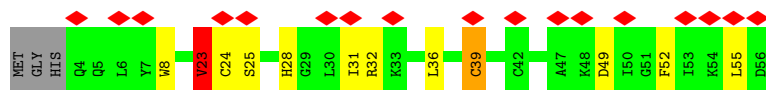
- Molecule 27: 40S ribosomal protein eS27



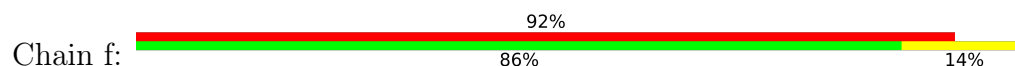
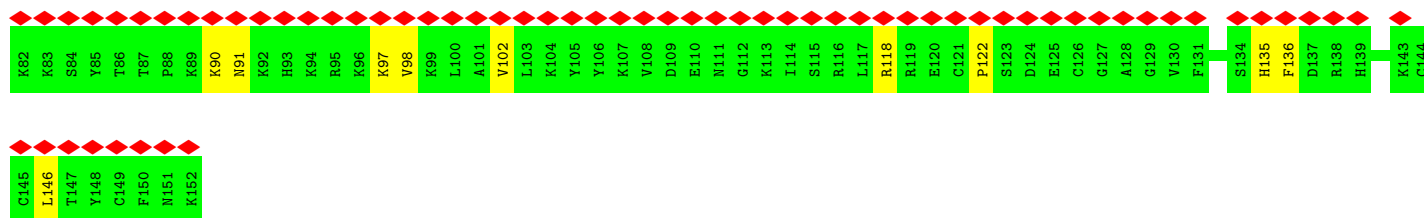
- Molecule 28: 40S ribosomal protein eS28



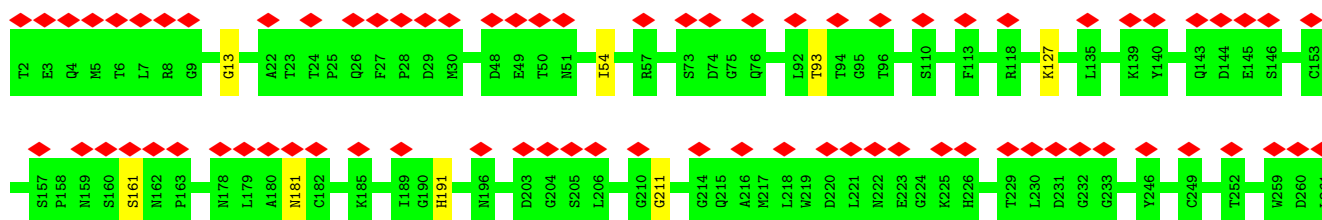
- Molecule 29: 40S ribosomal protein uS14

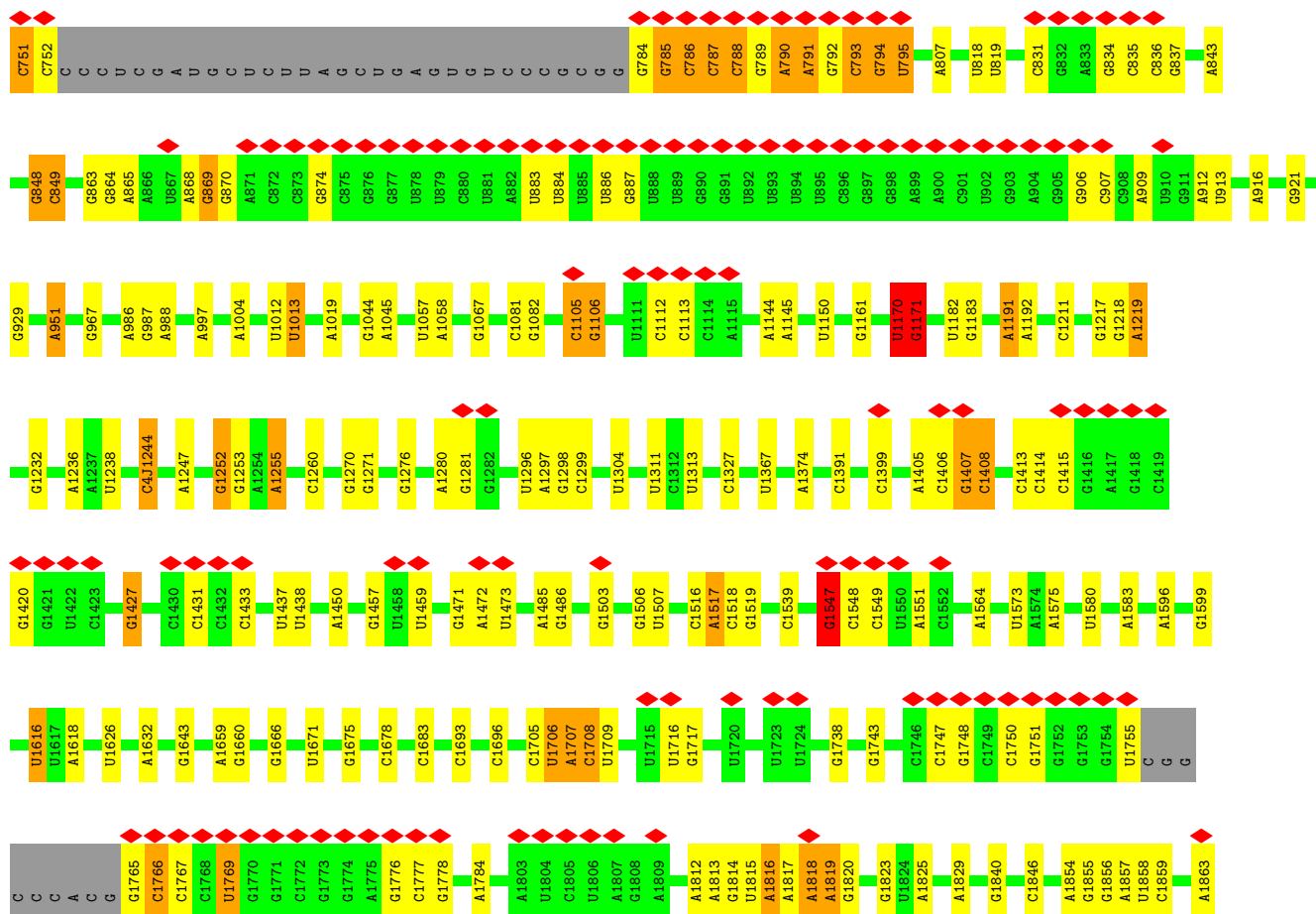


- Molecule 30: 40S ribosomal protein eS31



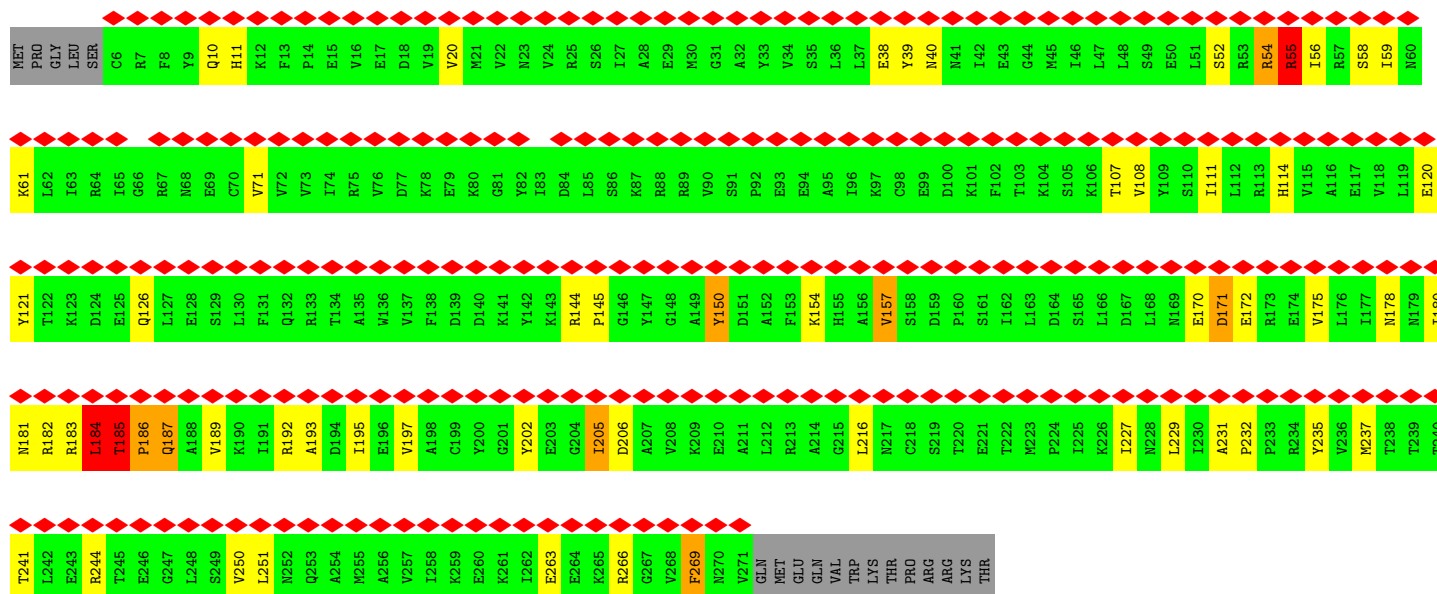
- Molecule 31: ribosomal protein RACK1



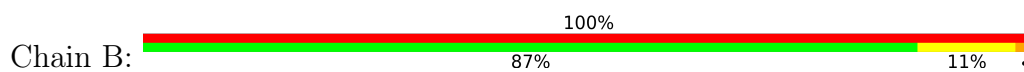
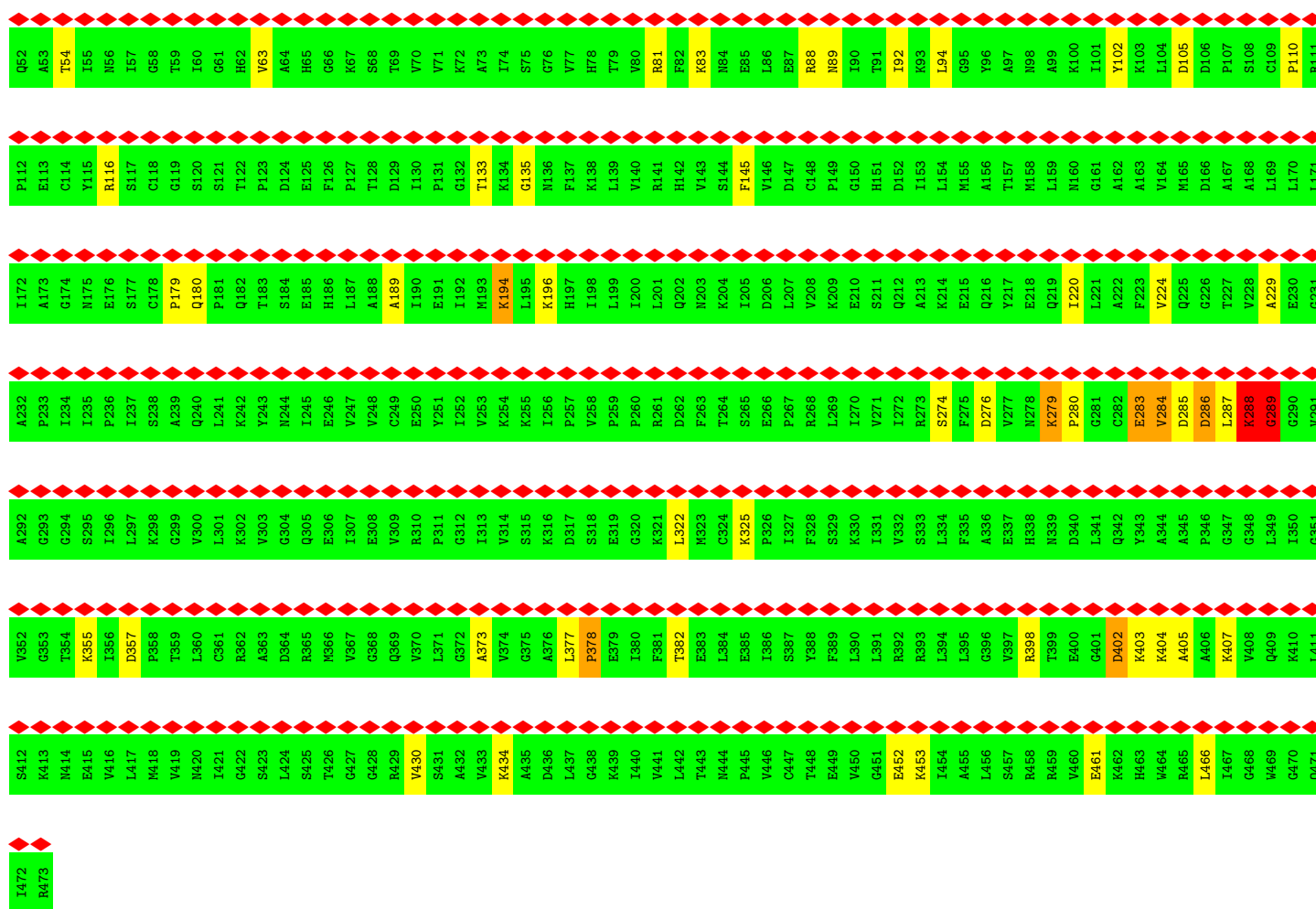


• Molecule 35: Eukaryotic translation initiation factor 2 subunit alpha

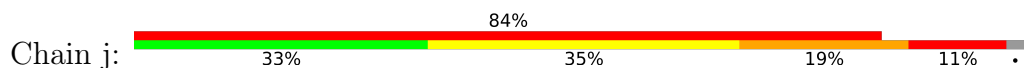
Chain A: 93% 72% 18% 6%



• Molecule 36: Eukaryotic translation initiation factor 2 subunit gamma

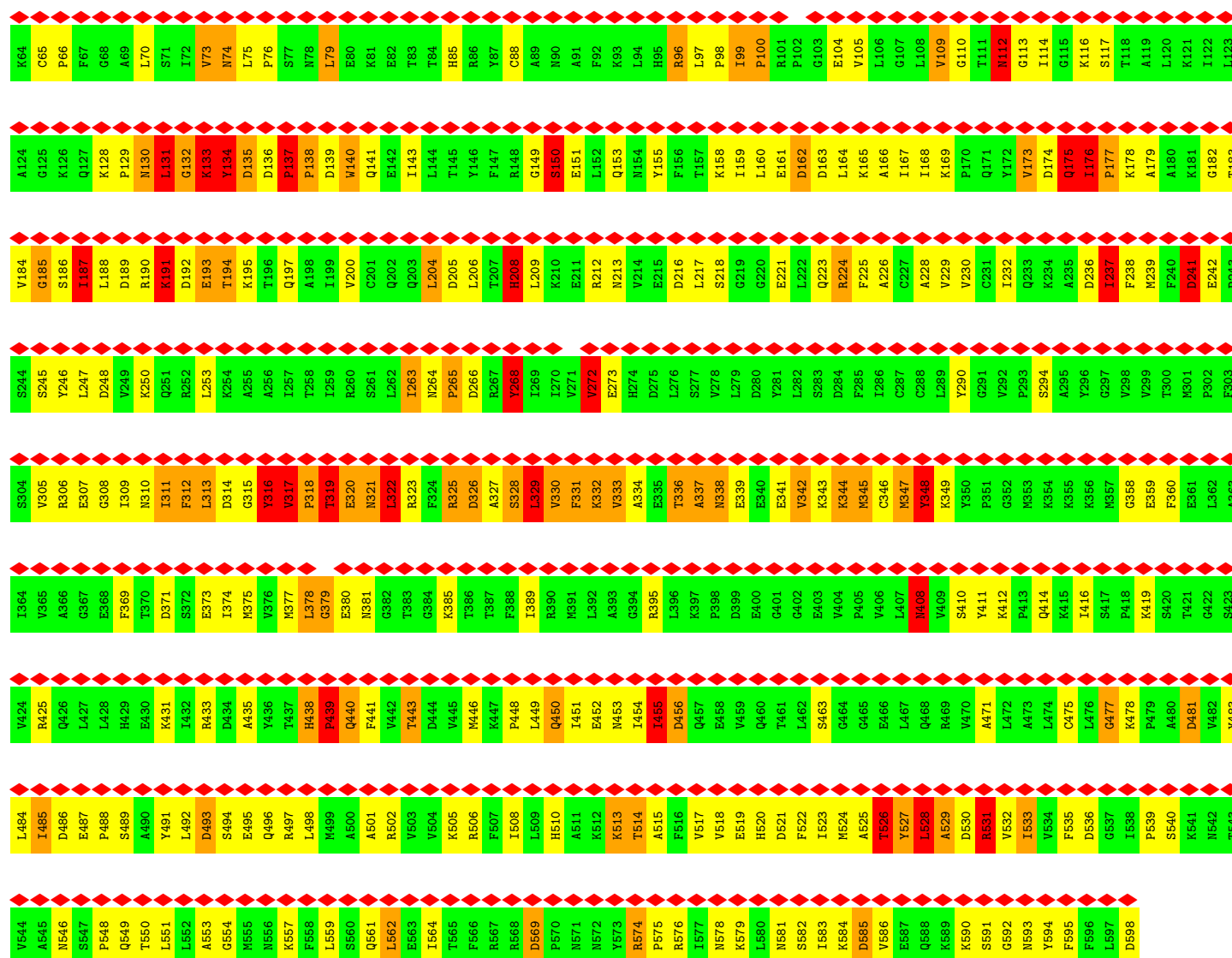


• Molecule 37: eukaryotic translation initiation factor 1A

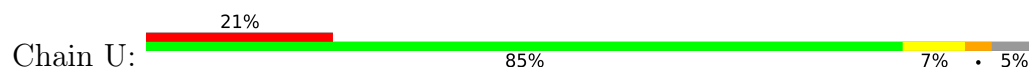
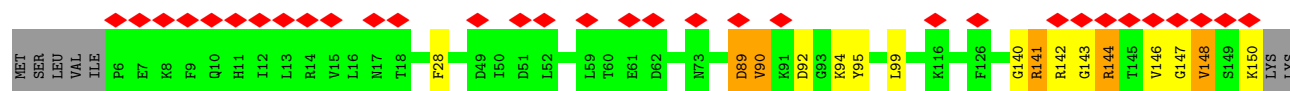


• Molecule 38: ATP-binding cassette sub-family E member 1 (ABCE1)

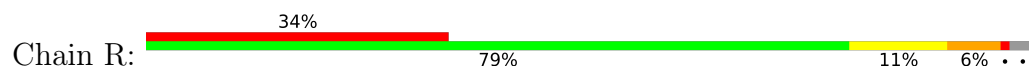
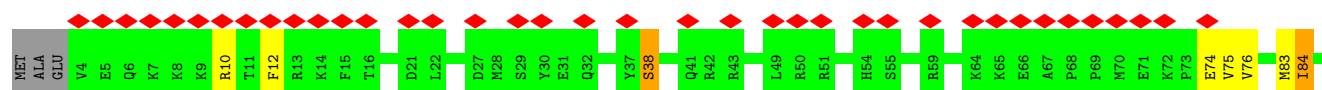




• Molecule 39: 40S ribosomal protein uS13

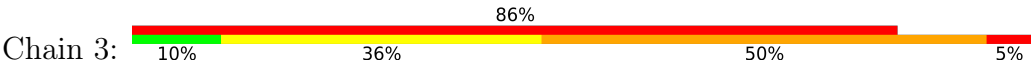


• Molecule 40: 40S ribosomal protein uS19





• Molecule 41: beta-globin mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	252000	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 ($e^-/\text{\AA}^2$)	26	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.147	Depositor
Minimum map value	-0.078	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, GNP, C4J, MG, T6A

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	1.44	8/1770 (0.5%)	1.29	11/2759 (0.4%)
2	l	1.60	0/241	1.35	0/305
3	C	1.24	0/1680	1.43	4/2283 (0.2%)
4	D	1.19	0/1769	1.44	16/2367 (0.7%)
5	E	1.18	0/1779	1.34	4/2399 (0.2%)
6	F	1.24	1/1792 (0.1%)	1.36	5/2412 (0.2%)
7	G	1.26	0/2125	1.36	7/2856 (0.2%)
8	H	1.26	0/1531	1.40	1/2059 (0.0%)
9	I	1.28	1/1947 (0.1%)	1.33	3/2590 (0.1%)
10	J	1.22	0/1553	1.43	6/2079 (0.3%)
11	K	1.29	0/1709	1.42	6/2278 (0.3%)
12	L	1.33	1/1523 (0.1%)	1.40	0/2031
13	M	1.25	0/852	1.49	7/1147 (0.6%)
14	N	1.22	0/1319	1.30	5/1761 (0.3%)
15	O	1.20	0/968	1.50	5/1296 (0.4%)
16	P	1.19	0/1232	1.43	3/1656 (0.2%)
17	Q	1.31	0/1029	1.45	4/1380 (0.3%)
18	S	1.31	0/1142	1.45	6/1528 (0.4%)
19	T	1.25	0/1031	1.39	2/1383 (0.1%)
20	V	1.25	0/1133	1.45	4/1517 (0.3%)
21	W	1.29	0/832	1.37	0/1117
22	X	1.42	1/627 (0.2%)	1.44	4/839 (0.5%)
23	Y	1.28	0/1051	1.39	2/1406 (0.1%)
24	Z	1.27	0/1124	1.35	0/1500
25	a	1.37	1/1038 (0.1%)	1.47	7/1380 (0.5%)
26	b	1.32	0/802	1.37	1/1076 (0.1%)
27	c	1.24	0/673	1.38	2/902 (0.2%)
28	d	1.39	0/508	1.17	0/680
29	e	1.35	0/455	1.46	2/603 (0.3%)
30	f	1.24	0/594	1.47	3/786 (0.4%)
31	g	1.23	0/2494	1.33	6/3394 (0.2%)
32	n	1.25	0/604	1.34	2/810 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	1.35	0/478	1.40	2/628 (0.3%)
34	2	0.89	8/41567 (0.0%)	0.99	23/64783 (0.0%)
35	A	0.97	3/2177 (0.1%)	1.50	11/2935 (0.4%)
36	B	1.19	2/3267 (0.1%)	1.46	24/4415 (0.5%)
37	j	0.96	2/893 (0.2%)	1.54	10/1186 (0.8%)
38	k	2.27	16/4772 (0.3%)	2.46	72/6428 (1.1%)
39	U	1.31	0/1211	1.45	3/1618 (0.2%)
40	R	1.24	0/1177	1.40	8/1571 (0.5%)
41	3	0.67	1/998 (0.1%)	0.80	3/1553 (0.2%)
All	All	1.18	45/95467 (0.0%)	1.30	284/137696 (0.2%)

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	1	3	2
3	C	0	1
4	D	0	1
9	I	0	3
10	J	0	2
11	K	0	2
12	L	0	2
13	M	0	5
17	Q	0	2
18	S	0	2
22	X	0	1
25	a	0	1
26	b	0	1
27	c	0	1
29	e	0	4
30	f	0	1
33	i	0	3
34	2	1	47
35	A	0	7
36	B	0	8
37	j	0	12
38	k	0	33
39	U	0	3
All	All	4	144

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	k	455	ILE	C-N	-63.41	0.45	1.33
38	k	562	LEU	C-N	-59.66	0.52	1.33
38	k	408	ASN	C-N	-48.21	0.68	1.33
38	k	481	ASP	C-N	-43.98	0.79	1.33
38	k	378	LEU	C-N	42.00	1.94	1.33

The worst 5 of 284 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	k	531	ARG	CA-C-N	-67.13	35.77	122.37
38	k	531	ARG	C-N-CA	-67.13	35.77	122.37
38	k	160	LEU	O-C-N	53.40	178.73	122.12
38	k	160	LEU	CA-C-N	-38.23	59.19	122.65
38	k	160	LEU	C-N-CA	-38.23	59.19	122.65

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	17	C	C2',C3'
1	1	18	G	C3'
34	2	1244	C4J	C4'

5 of 144 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	18	G	Sidechain
1	1	26	G	Sidechain
3	C	193	HIS	Peptide
4	D	208	HIS	Peptide
9	I	68	LEU	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1614	0	822	49	0
2	1	240	0	289	0	0
3	C	1643	0	1646	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1741	0	1815	0	0
5	E	1743	0	1836	1	0
6	F	1764	0	1863	23	0
7	G	2083	0	2189	0	0
8	H	1509	0	1563	1	0
9	I	1924	0	2089	16	0
10	J	1530	0	1627	22	0
11	K	1680	0	1762	12	0
12	L	1499	0	1608	0	0
13	M	828	0	854	1	0
14	N	1296	0	1374	29	0
15	O	958	0	993	1	0
16	P	1208	0	1294	62	0
17	Q	1016	0	1039	1	0
18	S	1124	0	1193	7	0
19	T	1019	0	1075	0	0
20	V	1113	0	1149	0	0
21	W	822	0	887	0	0
22	X	620	0	622	0	0
23	Y	1034	0	1080	1	0
24	Z	1106	0	1179	48	0
25	a	1021	0	1085	77	0
26	b	789	0	839	1	0
27	c	659	0	683	2	0
28	d	506	0	536	0	0
29	e	445	0	442	1	0
30	f	582	0	599	1	0
31	g	2437	0	2393	0	0
32	n	598	0	656	0	0
33	i	473	0	524	34	0
34	2	37204	0	18784	424	0
35	A	2146	0	2191	130	0
36	B	3214	0	3353	49	0
37	j	883	0	903	254	0
38	k	4693	0	4798	728	0
39	U	1194	0	1252	60	0
40	R	1154	0	1213	93	0
41	3	892	0	458	129	0
42	k	16	0	0	14	0
43	k	1	0	0	0	0
44	k	64	0	26	30	0
All	All	90085	0	72583	1862	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 12.

The worst 5 of 1862 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)
10:J:109:ARG:CB	34:2:740:G:H1'	1.18	1.62
35:A:235:TYR:CD1	36:B:285:ASP:CG	1.76	1.60
35:A:229:LEU:HD22	36:B:284:VAL:CG2	1.14	1.60
38:k:332:LYS:HG2	38:k:527:TYR:CD2	1.25	1.60
38:k:73:VAL:HB	38:k:322:LEU:CD2	1.30	1.59

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	I	23/25 (92%)	23 (100%)	0	0	100	100
3	C	206/209 (99%)	177 (86%)	21 (10%)	8 (4%)	2	14
4	D	213/264 (81%)	191 (90%)	16 (8%)	6 (3%)	4	21
5	E	224/226 (99%)	208 (93%)	14 (6%)	2 (1%)	14	48
6	F	225/243 (93%)	202 (90%)	14 (6%)	9 (4%)	2	14
7	G	261/263 (99%)	233 (89%)	24 (9%)	4 (2%)	8	35
8	H	189/191 (99%)	169 (89%)	17 (9%)	3 (2%)	7	34
9	I	235/237 (99%)	209 (89%)	22 (9%)	4 (2%)	7	32
10	J	188/192 (98%)	161 (86%)	18 (10%)	9 (5%)	2	11
11	K	204/206 (99%)	178 (87%)	20 (10%)	6 (3%)	3	20
12	L	180/182 (99%)	167 (93%)	11 (6%)	2 (1%)	11	43
13	M	96/98 (98%)	74 (77%)	16 (17%)	6 (6%)	1	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	N	156/158 (99%)	130 (83%)	22 (14%)	4 (3%)	4	23
15	O	122/132 (92%)	105 (86%)	13 (11%)	4 (3%)	3	17
16	P	148/150 (99%)	130 (88%)	11 (7%)	7 (5%)	2	11
17	Q	134/151 (89%)	118 (88%)	13 (10%)	3 (2%)	5	26
18	S	139/141 (99%)	126 (91%)	11 (8%)	2 (1%)	9	36
19	T	124/135 (92%)	112 (90%)	8 (6%)	4 (3%)	3	18
20	V	139/141 (99%)	128 (92%)	8 (6%)	3 (2%)	5	26
21	W	102/119 (86%)	93 (91%)	9 (9%)	0	100	100
22	X	80/82 (98%)	71 (89%)	7 (9%)	2 (2%)	4	23
23	Y	127/130 (98%)	117 (92%)	6 (5%)	4 (3%)	3	19
24	Z	140/143 (98%)	128 (91%)	8 (6%)	4 (3%)	3	20
25	a	124/133 (93%)	104 (84%)	10 (8%)	10 (8%)	1	3
26	b	97/115 (84%)	90 (93%)	5 (5%)	2 (2%)	5	27
27	c	82/84 (98%)	69 (84%)	9 (11%)	4 (5%)	1	10
28	d	62/69 (90%)	57 (92%)	4 (6%)	1 (2%)	7	34
29	e	51/56 (91%)	40 (78%)	7 (14%)	4 (8%)	1	4
30	f	69/71 (97%)	51 (74%)	12 (17%)	6 (9%)	0	3
31	g	311/313 (99%)	273 (88%)	33 (11%)	5 (2%)	7	34
32	n	73/124 (59%)	69 (94%)	3 (4%)	1 (1%)	9	36
33	i	57/133 (43%)	49 (86%)	7 (12%)	1 (2%)	6	31
35	A	264/284 (93%)	233 (88%)	25 (10%)	6 (2%)	5	25
36	B	420/422 (100%)	352 (84%)	48 (11%)	20 (5%)	2	11
37	j	107/111 (96%)	64 (60%)	27 (25%)	16 (15%)	0	0
38	k	577/595 (97%)	431 (75%)	95 (16%)	51 (9%)	0	3
39	U	141/152 (93%)	123 (87%)	12 (8%)	6 (4%)	2	12
40	R	138/145 (95%)	107 (78%)	18 (13%)	13 (9%)	0	2
All	All	6228/6625 (94%)	5362 (86%)	624 (10%)	242 (4%)	4	14

5 of 242 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	191	ARG
4	D	209	ASP

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Mol	Chain	Res	Type
6	F	3	VAL
6	F	193	ASP
6	F	219	PRO

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	I	24/24 (100%)	24 (100%)	0	100	100
3	C	174/175 (99%)	172 (99%)	2 (1%)	65	83
4	D	196/231 (85%)	196 (100%)	0	100	100
5	E	187/187 (100%)	187 (100%)	0	100	100
6	F	190/202 (94%)	189 (100%)	1 (0%)	81	89
7	G	225/225 (100%)	225 (100%)	0	100	100
8	H	161/161 (100%)	160 (99%)	1 (1%)	78	88
9	I	207/207 (100%)	207 (100%)	0	100	100
10	J	170/172 (99%)	169 (99%)	1 (1%)	78	88
11	K	177/177 (100%)	175 (99%)	2 (1%)	65	83
12	L	157/157 (100%)	156 (99%)	1 (1%)	78	88
13	M	89/89 (100%)	89 (100%)	0	100	100
14	N	142/142 (100%)	138 (97%)	4 (3%)	38	70
15	O	104/108 (96%)	101 (97%)	3 (3%)	37	70
16	P	130/130 (100%)	125 (96%)	5 (4%)	29	63
17	Q	106/119 (89%)	106 (100%)	0	100	100
18	S	117/117 (100%)	116 (99%)	1 (1%)	70	85
19	T	114/121 (94%)	114 (100%)	0	100	100
20	V	113/113 (100%)	113 (100%)	0	100	100
21	W	94/107 (88%)	94 (100%)	0	100	100
22	X	67/67 (100%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	Y	112/113 (99%)	112 (100%)	0	100	100
24	Z	114/115 (99%)	114 (100%)	0	100	100
25	a	108/115 (94%)	102 (94%)	6 (6%)	19	52
26	b	87/99 (88%)	87 (100%)	0	100	100
27	c	76/76 (100%)	76 (100%)	0	100	100
28	d	57/62 (92%)	57 (100%)	0	100	100
29	e	47/49 (96%)	44 (94%)	3 (6%)	16	48
30	f	64/64 (100%)	64 (100%)	0	100	100
31	g	272/272 (100%)	272 (100%)	0	100	100
32	n	66/102 (65%)	66 (100%)	0	100	100
33	i	49/106 (46%)	47 (96%)	2 (4%)	27	61
35	A	238/255 (93%)	232 (98%)	6 (2%)	42	72
36	B	354/354 (100%)	337 (95%)	17 (5%)	23	57
37	j	92/93 (99%)	67 (73%)	25 (27%)	0	2
38	k	523/523 (100%)	466 (89%)	57 (11%)	6	26
39	U	125/132 (95%)	124 (99%)	1 (1%)	73	86
40	R	126/130 (97%)	121 (96%)	5 (4%)	28	62
All	All	5454/5691 (96%)	5311 (97%)	143 (3%)	41	72

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	k	325	ARG
38	k	332	LYS
38	k	526	THR
36	B	378	PRO
36	B	284	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 88 such sidechains are listed below:

Mol	Chain	Res	Type
30	f	135	HIS
35	A	181	ASN
31	g	14	HIS
31	g	191	HIS

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Mol	Chain	Res	Type
37	j	112	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	74/75 (98%)	13 (17%)	3 (4%)
34	2	1737/1863 (93%)	242 (13%)	7 (0%)
41	3	41/42 (97%)	26 (63%)	1 (2%)
All	All	1852/1980 (93%)	281 (15%)	11 (0%)

5 of 281 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	9	U
1	1	11	G
1	1	15	A
1	1	16	G
1	1	17	C

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	2	1270	G
34	2	1716	U
41	3	39	U
34	2	1857	A
34	2	739	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	T6A	1	37	1	31,34,35	1.39	4 (12%)	44,49,52	2.51	18 (40%)
34	C4J	2	1244	34	24,29,30	0.79	1 (4%)	29,42,45	1.03	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	T6A	1	37	1	-	6/23/41/42	0/3/3/3
34	C4J	2	1244	34	1/1/7/7	9/16/34/35	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	37	T6A	C5-C4	4.59	1.47	1.39
1	1	37	T6A	C5-C6	2.61	1.48	1.41
1	1	37	T6A	C8-N7	2.30	1.36	1.31
1	1	37	T6A	C5-N7	-2.19	1.34	1.39
34	2	1244	C4J	C1'-C5	-2.11	1.45	1.50

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	37	T6A	C12-N11-C10	8.51	136.12	121.94
1	1	37	T6A	C5-C4-N3	-5.87	119.09	126.75
1	1	37	T6A	N3-C4-N9	4.64	134.73	127.08
1	1	37	T6A	C2-N3-C4	3.85	120.85	111.75
1	1	37	T6A	C14-C12-C13	3.70	116.49	110.19

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
34	2	1244	C4J	C4'

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	37	T6A	C14-C12-N11-C10
34	2	1244	C4J	C31-C3-N3-C2
34	2	1244	C4J	C31-C3-N3-C4

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Mol	Chain	Res	Type	Atoms
34	2	1244	C4J	N3-C3-C31-C32
34	2	1244	C4J	C3-C31-C32-C34

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	37	T6A	1	0
34	2	1244	C4J	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
42	SF4	k	701	38	0,12,12	-	-	-		
44	GNP	k	705	-	33,34,34	1.30	2 (6%)	46,54,54	0.89	2 (4%)
44	GNP	k	704	43	33,34,34	1.28	2 (6%)	46,54,54	0.87	2 (4%)
42	SF4	k	702	38	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
42	SF4	k	701	38	-	-	0/6/5/5
44	GNP	k	705	-	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
44	GNP	k	704	43	-	6/18/38/38	0/3/3/3
42	SF4	k	702	38	-	-	0/6/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	k	705	GNP	PG-O2G	-4.54	1.44	1.56
44	k	704	GNP	PG-O2G	-4.53	1.44	1.56
44	k	705	GNP	PB-O2B	-4.02	1.45	1.56
44	k	704	GNP	PB-O2B	-3.74	1.46	1.56

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	k	704	GNP	O2G-PG-O3G	-2.56	100.82	107.64
44	k	705	GNP	O2G-PG-O3G	-2.51	100.96	107.64
44	k	704	GNP	O3G-PG-O1G	-2.16	108.02	113.45
44	k	705	GNP	O3G-PG-O1G	-2.11	108.14	113.45

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
44	k	704	GNP	PG-N3B-PB-O1B
44	k	704	GNP	PG-N3B-PB-O3A
44	k	704	GNP	PA-O3A-PB-O1B
44	k	704	GNP	PA-O3A-PB-O2B
44	k	705	GNP	PG-N3B-PB-O1B

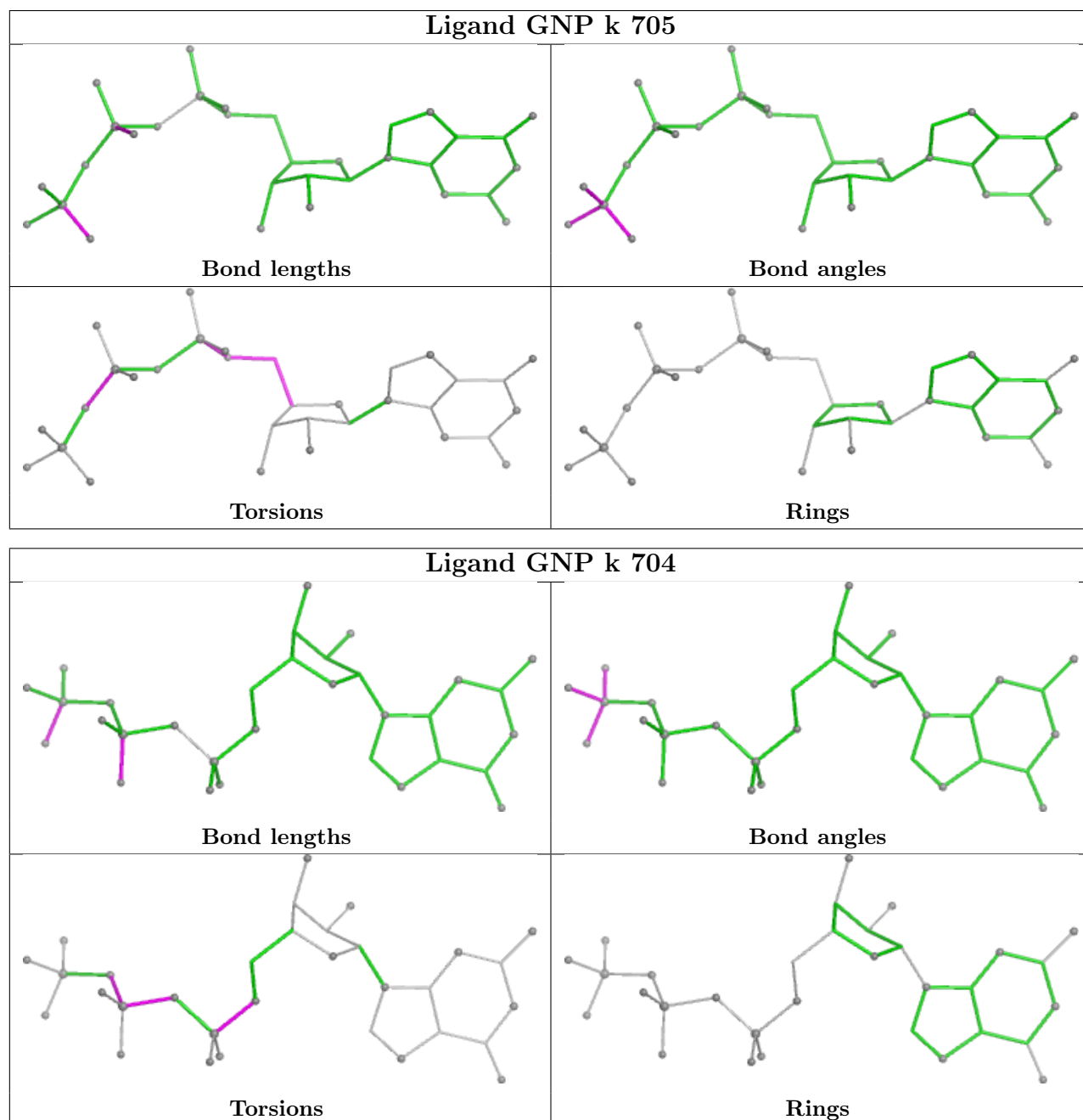
There are no ring outliers.

4 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
42	k	701	SF4	7	0
44	k	705	GNP	18	0
44	k	704	GNP	12	0
42	k	702	SF4	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
38	k	23
34	2	4
1	1	2
39	U	1
25	a	1
41	3	1
37	j	1

The worst 5 of 33 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	730:C	O3'	731:C	P	8.58
1	k	521:ASP	C	522:PHE	N	2.98
1	U	142:ARG	C	143:GLY	N	2.92
1	k	451:ILE	C	452:GLU	N	2.79
1	k	373:GLU	C	374:ILE	N	2.70

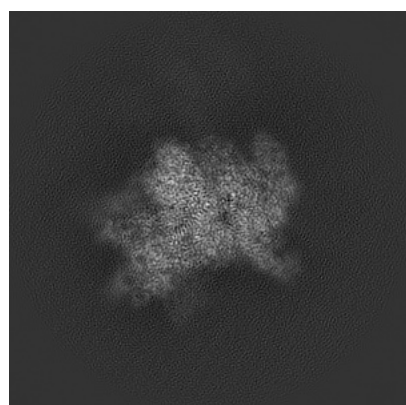
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10760. These allow visual inspection of the internal detail of the map and identification of artifacts.

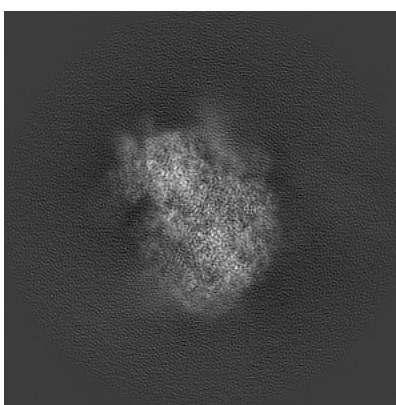
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

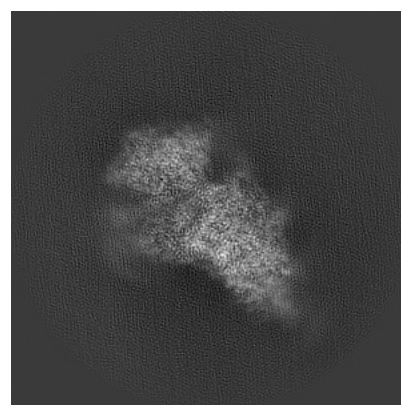
6.1.1 Primary map



X



Y

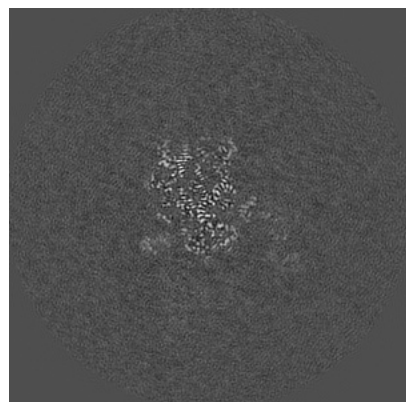


Z

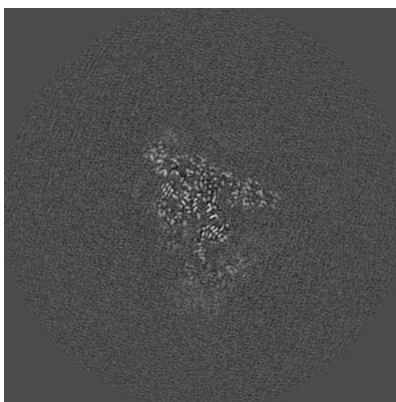
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

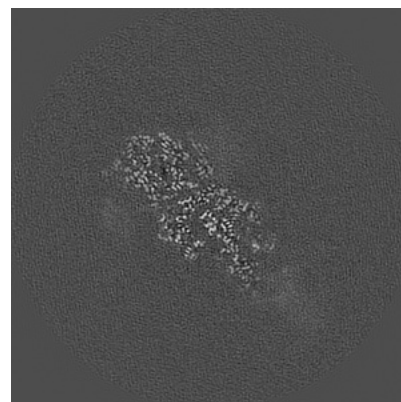
6.2.1 Primary map



X Index: 192



Y Index: 192

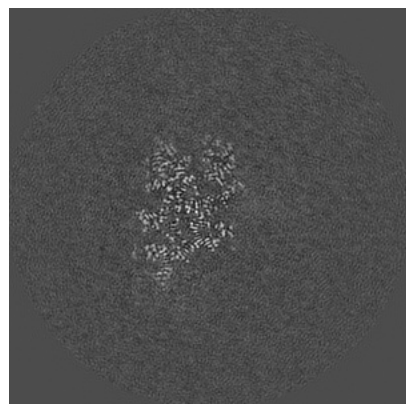


Z Index: 192

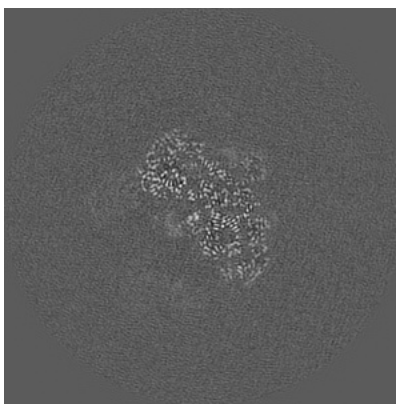
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

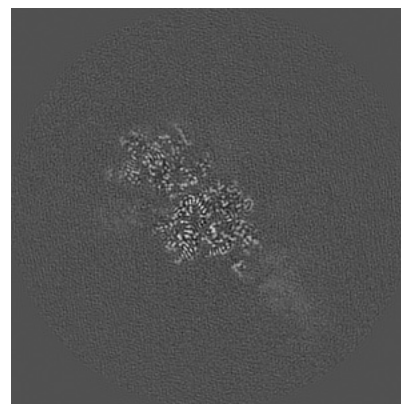
6.3.1 Primary map



X Index: 205



Y Index: 161

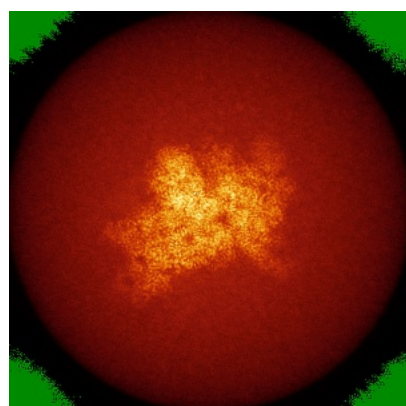


Z Index: 199

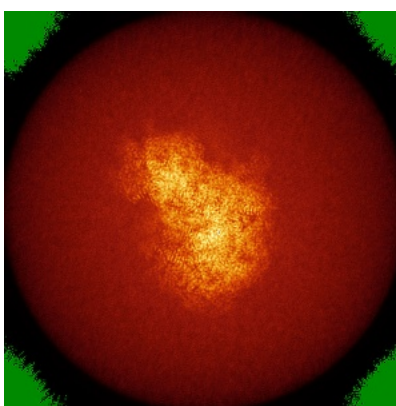
The images above show the largest variance slices of the map in three orthogonal directions.

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

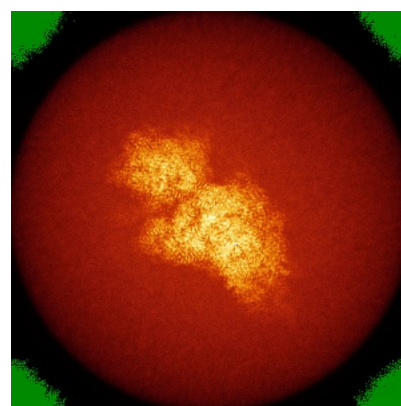
6.4.1 Primary map



X



Y

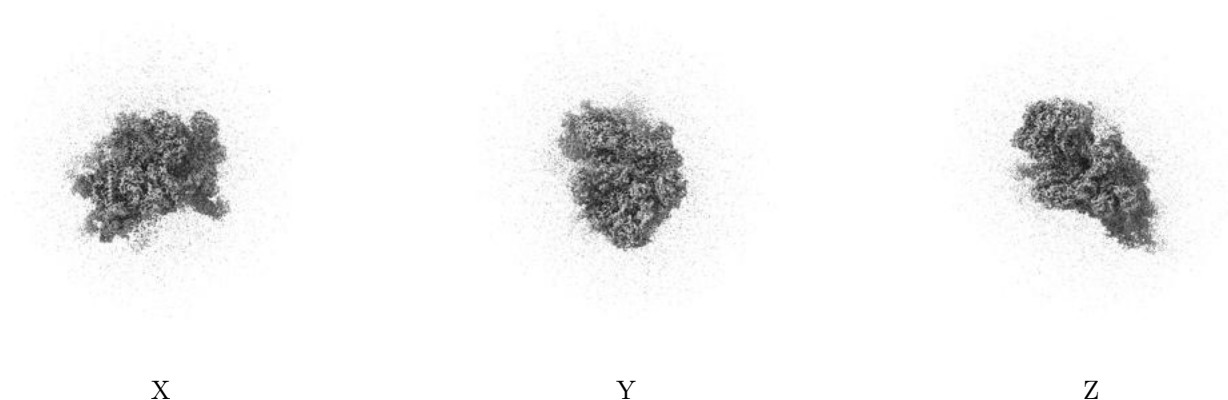


Z

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

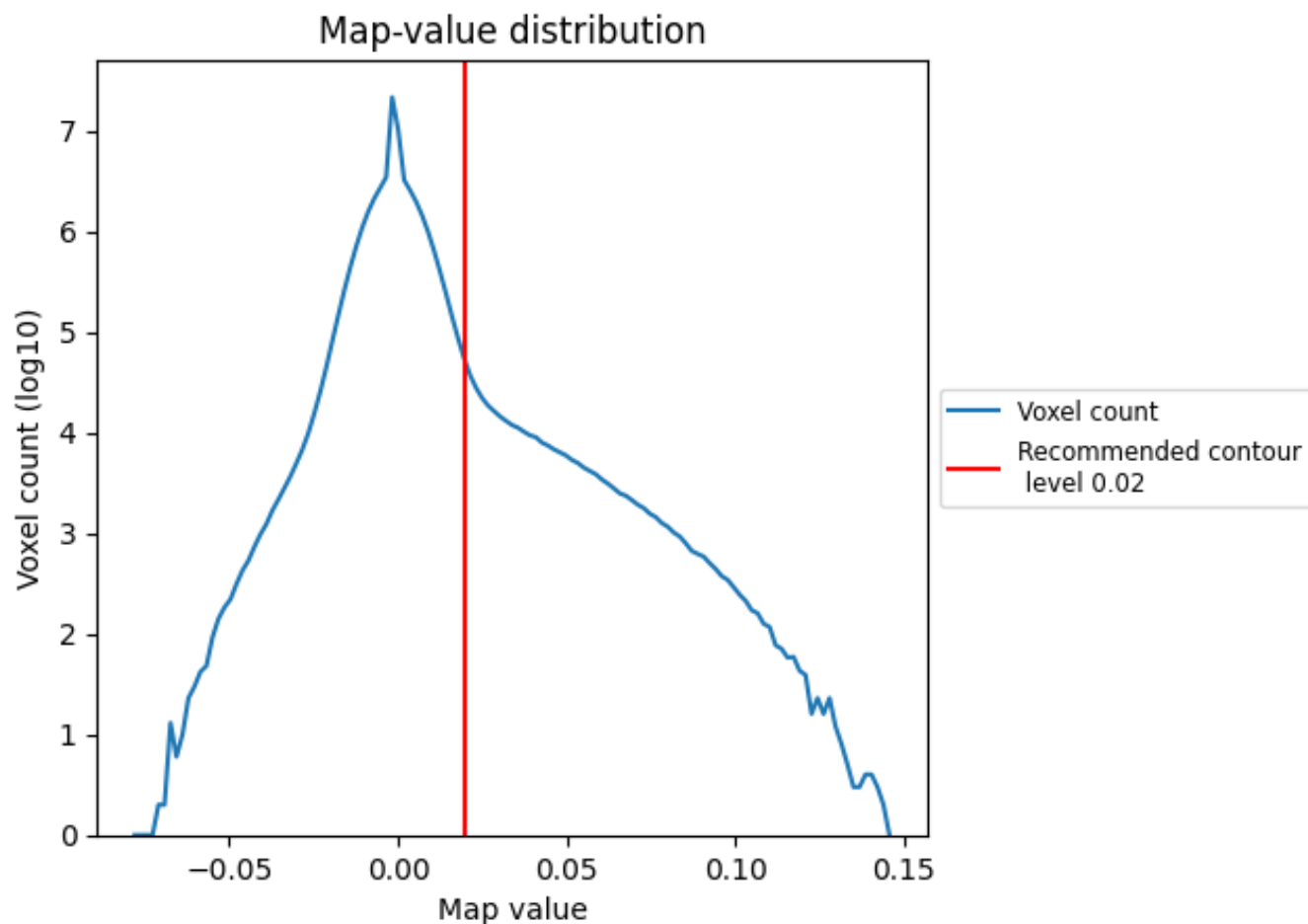
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

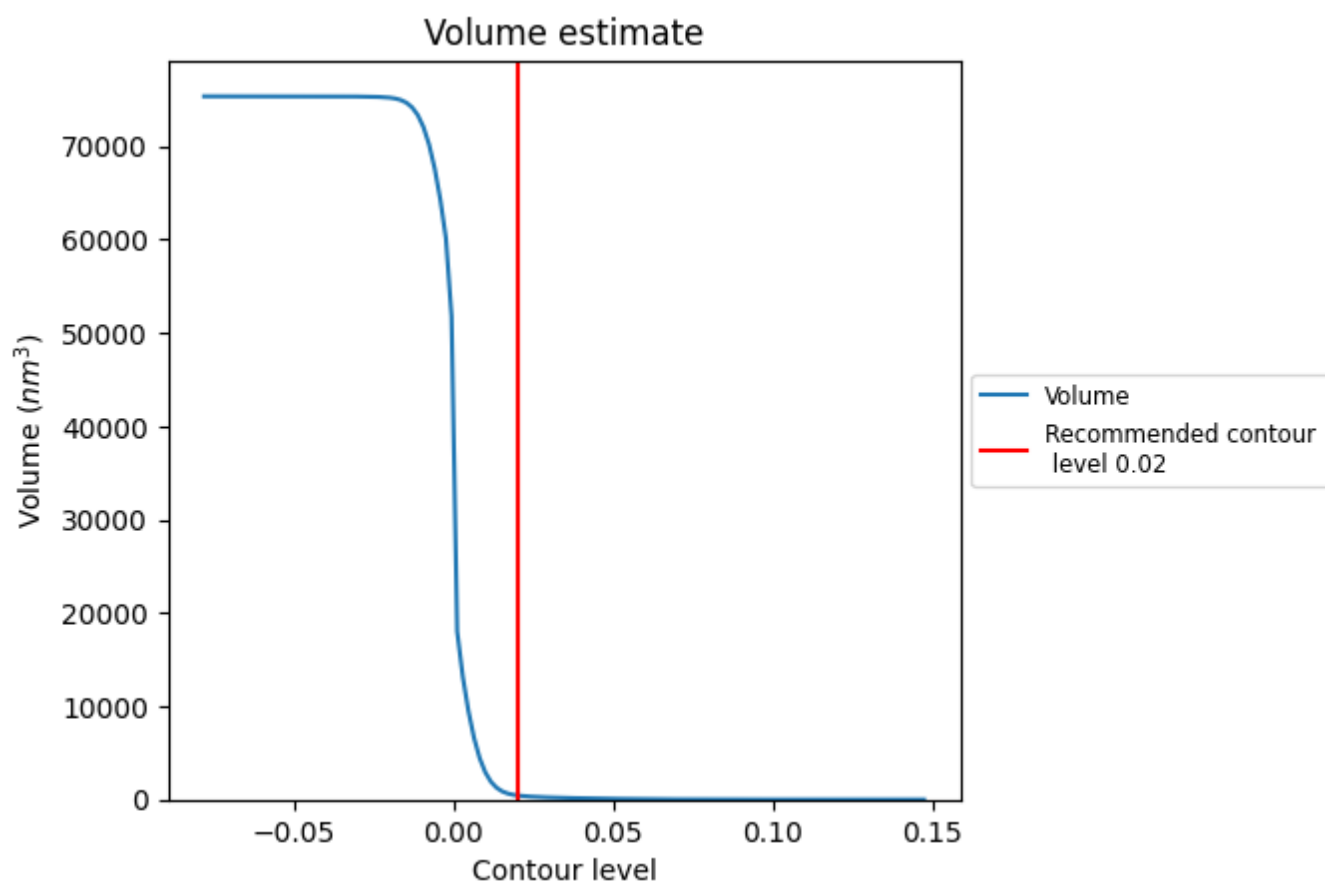
This section contains the results of statistical analysis of the map.

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.

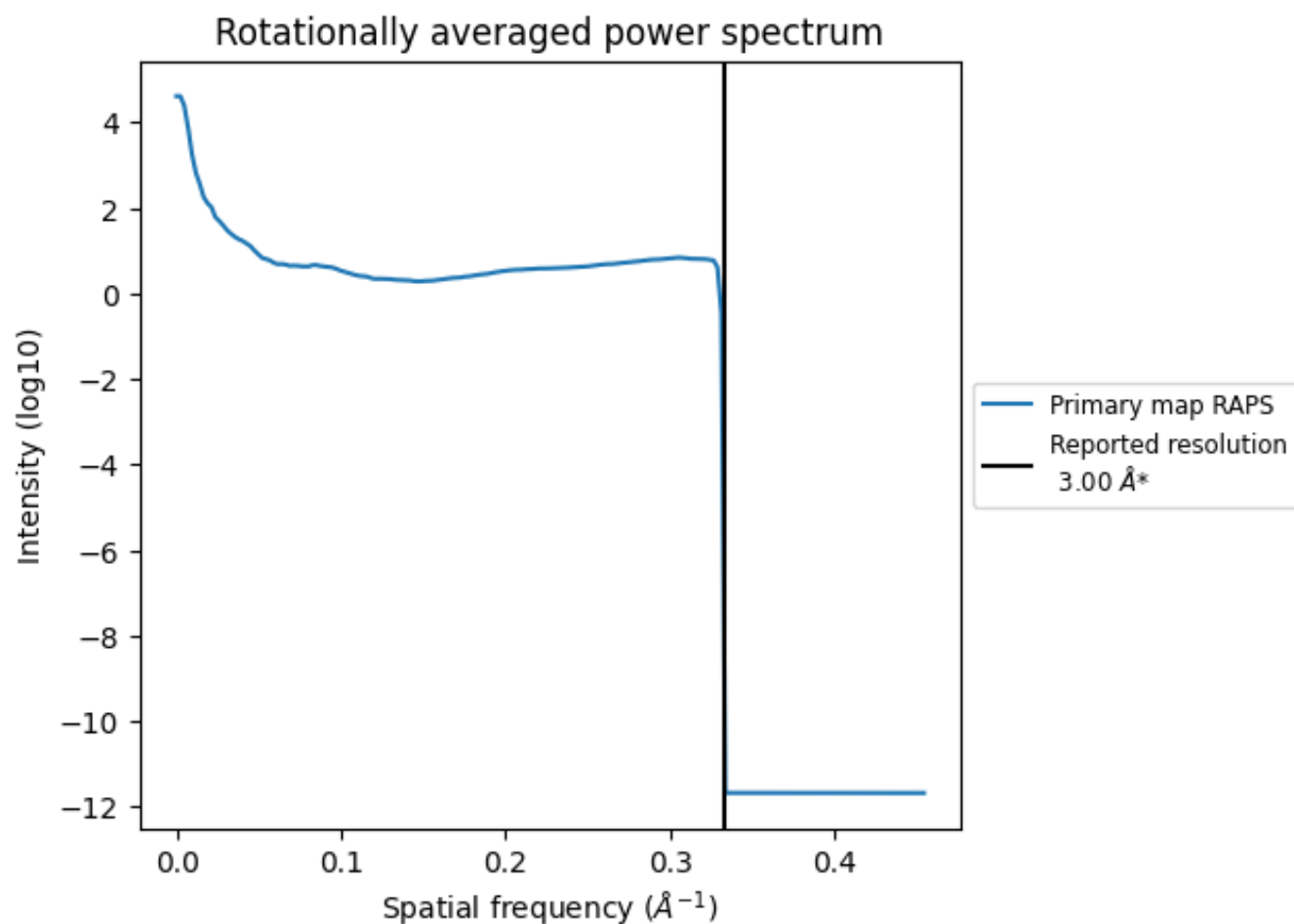
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 449 nm³; this corresponds to an approximate mass of 406 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 0.333 $\text{\AA}^{-1}$

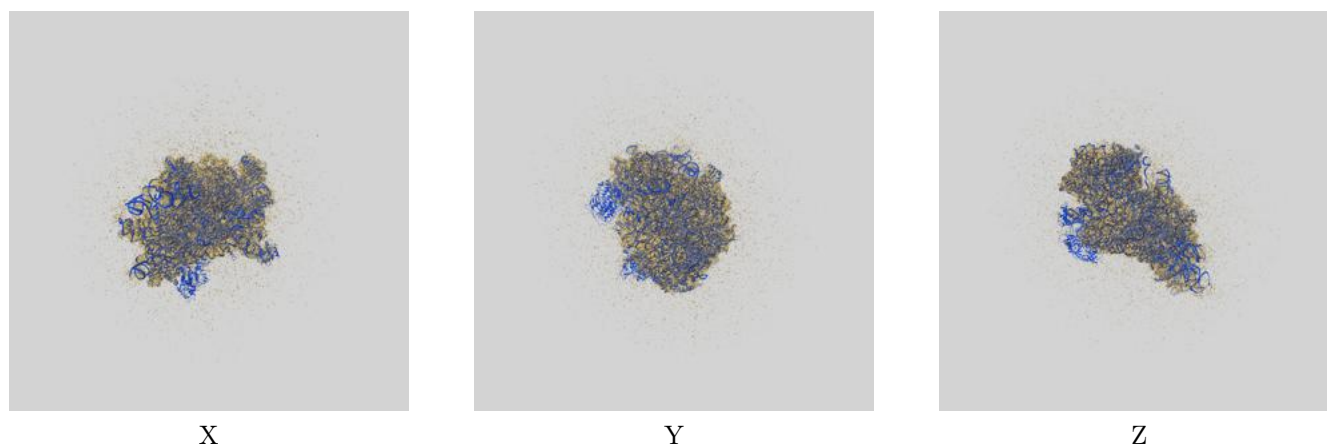
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

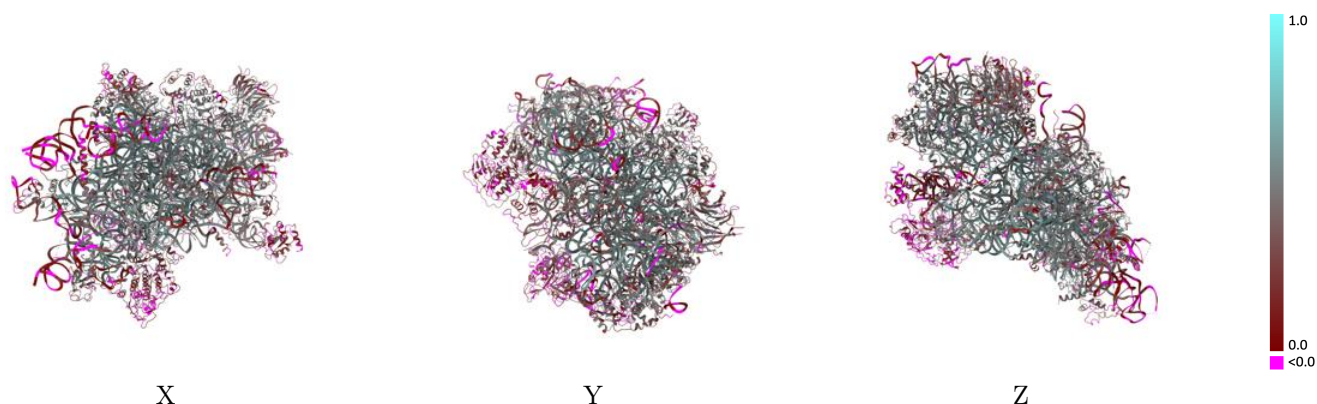
This section contains information regarding the fit between EMDB map EMD-10760 and PDB model 6YAL. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



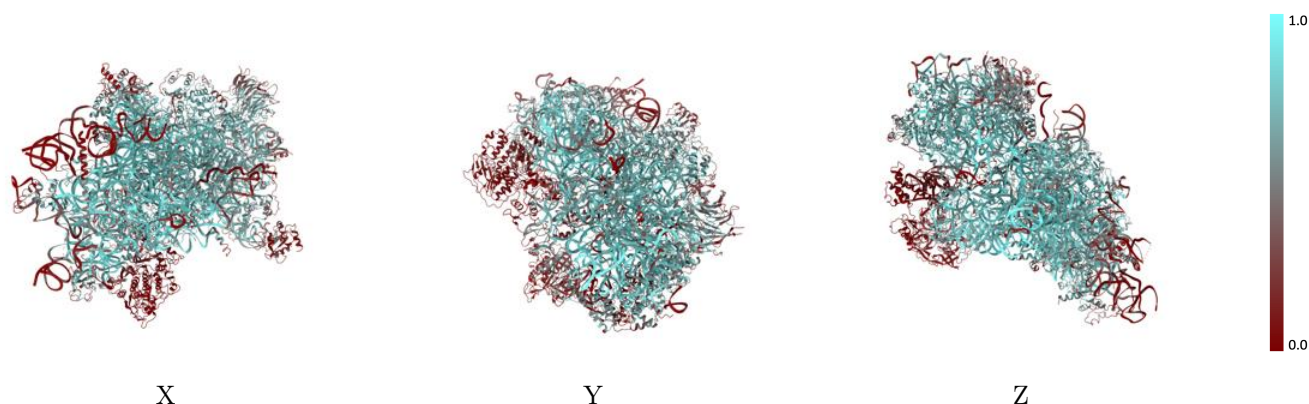
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



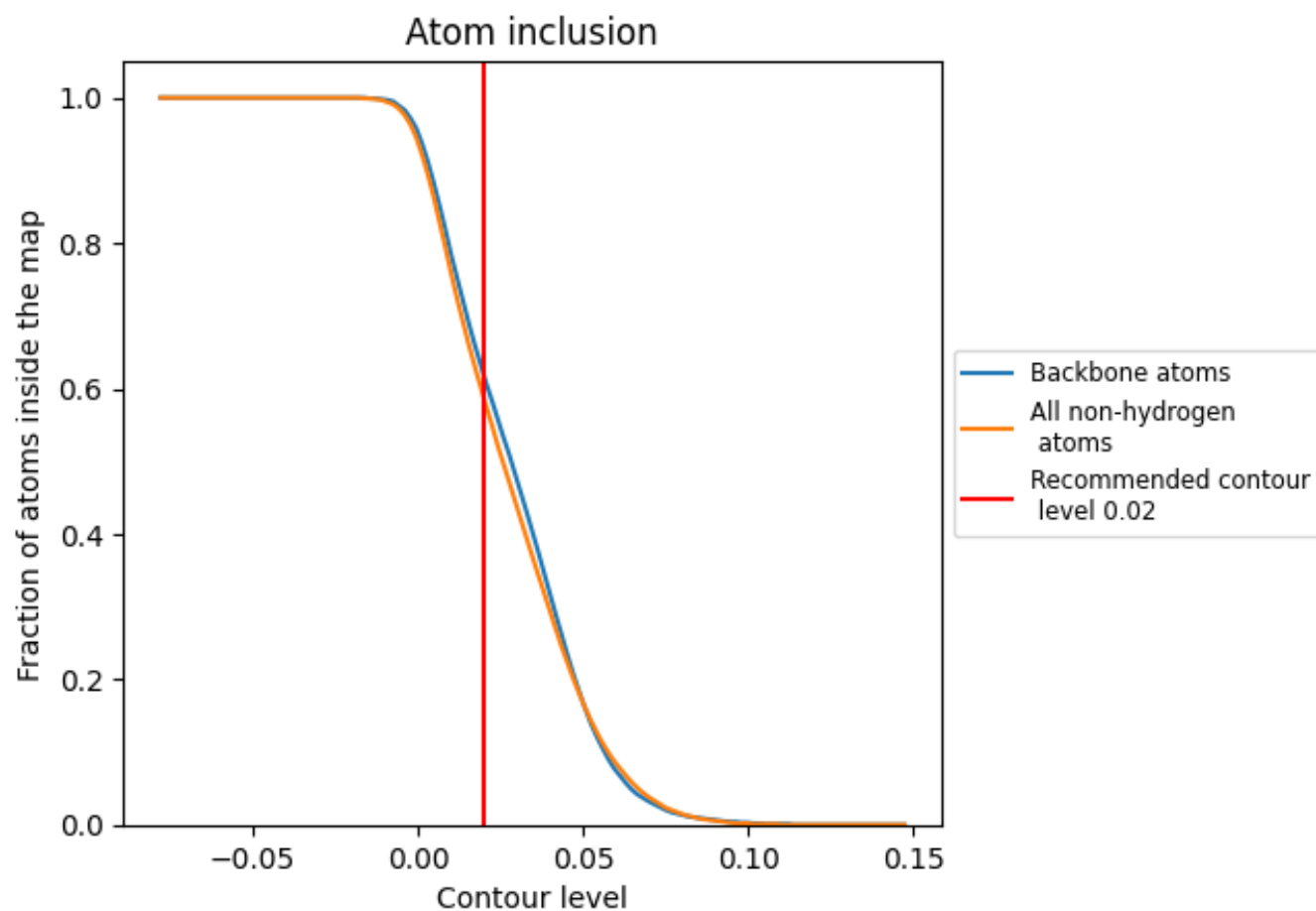
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 59% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5860	 0.3790
1	 0.2280	 0.1570
2	 0.7700	 0.4650
3	 0.1330	 0.1270
A	 0.0440	 0.0980
B	 0.0020	 0.0100
C	 0.6800	 0.4320
D	 0.6480	 0.4170
E	 0.7120	 0.4660
F	 0.5430	 0.3560
G	 0.6900	 0.4550
H	 0.6310	 0.4090
I	 0.5000	 0.3310
J	 0.3730	 0.2690
K	 0.5910	 0.3850
L	 0.6780	 0.4330
M	 0.5200	 0.3330
N	 0.6270	 0.4100
O	 0.1320	 0.1360
P	 0.6790	 0.4410
Q	 0.6600	 0.4160
R	 0.4990	 0.3280
S	 0.6850	 0.4480
T	 0.5250	 0.3300
U	 0.5770	 0.3850
V	 0.6740	 0.4310
W	 0.5440	 0.3660
X	 0.6580	 0.4160
Y	 0.7660	 0.4940
Z	 0.7490	 0.4730
a	 0.6380	 0.4020
b	 0.7120	 0.4570
c	 0.5580	 0.3600
d	 0.5450	 0.3650
e	 0.5480	 0.2680



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Chain	Atom inclusion	Q-score
f	 0.1480	 0.1270
g	 0.4910	 0.3590
i	 0.4630	 0.3140
j	 0.2020	 0.2240
k	 0.0400	 0.1780
l	 0.5750	 0.3940
n	 0.4600	 0.3510