



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 02:00 AM UTC

PDB ID : 9H74 / pdb_00009h74
EMDB ID : EMD-51911
Title : Late-stage 48S Initiation Complex with eIF3 (LS48S-eIF3 IC) guided by the trans-RNA
Authors : Nguyen, T.T.; Hashem, Y.; Rocha, R.E.O.; Boissier, F.; Qian, S.B.; Jia, L.; Uematsu, S.; Gu, Y.; Shi, S.
Deposited on : 2024-10-25
Resolution : 2.90 Å (reported)
Based on initial models : 6YAM, ., 6FYX, 8P09

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:

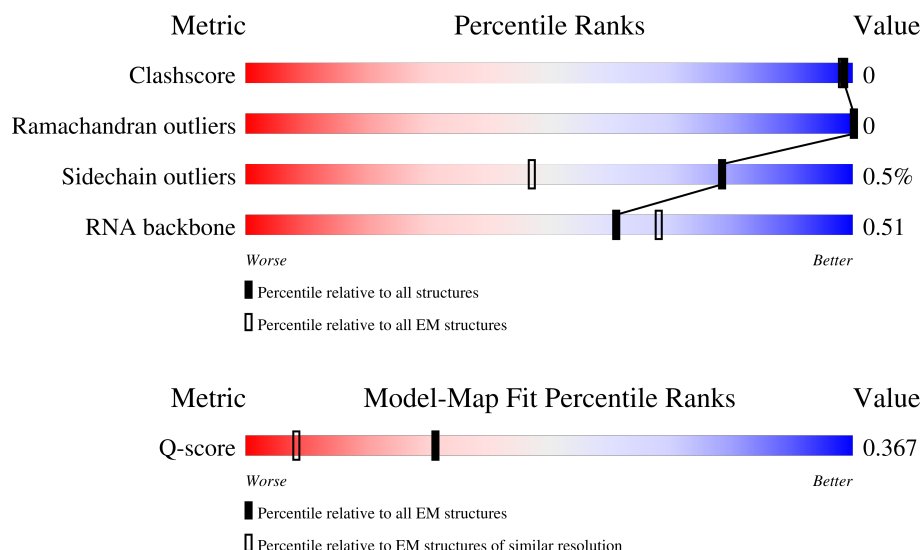
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	76	<div> <div>47%</div> <div>54%</div> <div>37%</div> <div>7%</div> <div>..</div> </div>
2	2	1863	<div> <div>10%</div> <div>64%</div> <div>23%</div> <div>6%</div> <div>7%</div> </div>

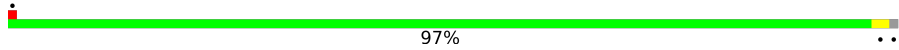
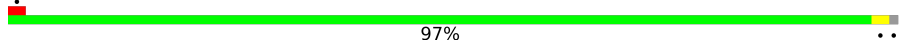
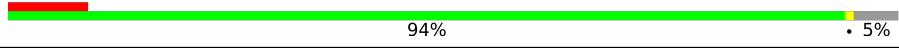

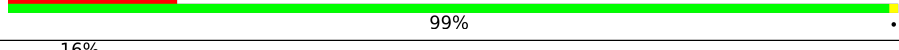
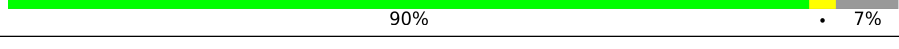
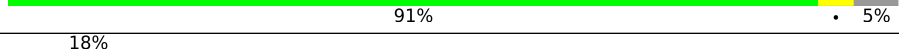
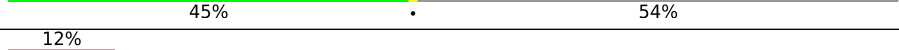
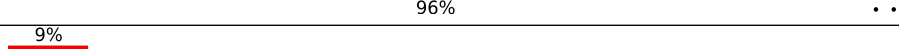
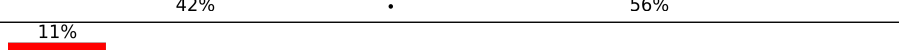

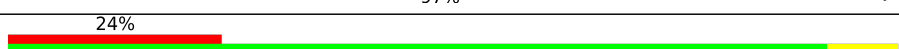





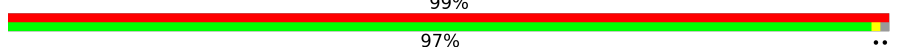

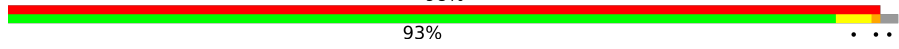
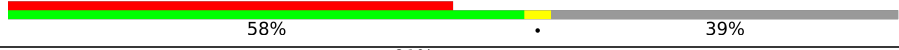



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Mol	Chain	Length	Quality of chain
3	3	160	
4	A	390	
5	B	485	
6	C	295	
7	D	264	
8	E	270	
9	F	243	
10	G	263	
11	H	204	
12	I	249	
13	J	194	
14	K	208	
15	L	194	
16	M	149	
17	N	158	
18	O	132	
19	P	151	
20	Q	151	
21	R	145	
22	S	146	
23	T	135	
24	U	152	
25	V	145	
26	W	119	
27	X	83	

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Mol	Chain	Length	Quality of chain
28	Y	130	
29	Z	143	
30	a	133	
31	b	115	
32	c	84	
33	d	69	
34	e	56	
35	f	156	
36	g	317	
37	i	133	
38	j	144	
39	k	599	
40	l	25	
41	m	557	
42	n	124	
43	o	430	
44	q	364	
45	r	352	
46	s	218	
47	t	607	
48	u	374	
49	v	913	
50	w	462	
51	y	1362	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 118867 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 RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1741	Total	C	N	O	P	0	0
			37147	16585	6650	12172	1740		

- Molecule 3 is a RNA chain called Linear mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	9	Total	C	N	O	P	0	0
			196	87	37	63	9		

- Molecule 4 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

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

- Molecule 5 is a protein called protein-synthesizing GTPase.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	422	Total	C	N	O	S	0	0
			3213	2044	561	591	17		

There are 51 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	?	-	UNK	deletion	UNP A0A5F9C3W2
B	367	VAL	UNK	conflict	UNP A0A5F9C3W2
B	368	GLY	UNK	conflict	UNP A0A5F9C3W2
B	369	GLN	UNK	conflict	UNP A0A5F9C3W2
B	370	VAL	UNK	conflict	UNP A0A5F9C3W2
B	371	LEU	UNK	conflict	UNP A0A5F9C3W2
B	372	GLY	UNK	conflict	UNP A0A5F9C3W2
B	373	ALA	UNK	conflict	UNP A0A5F9C3W2
B	374	VAL	UNK	conflict	UNP A0A5F9C3W2
B	375	GLY	UNK	conflict	UNP A0A5F9C3W2
B	376	ALA	UNK	conflict	UNP A0A5F9C3W2
B	377	LEU	UNK	conflict	UNP A0A5F9C3W2
B	378	PRO	UNK	conflict	UNP A0A5F9C3W2
B	379	GLU	UNK	conflict	UNP A0A5F9C3W2
B	380	ILE	UNK	conflict	UNP A0A5F9C3W2
B	381	PHE	UNK	conflict	UNP A0A5F9C3W2
B	382	THR	UNK	conflict	UNP A0A5F9C3W2
B	383	GLU	UNK	conflict	UNP A0A5F9C3W2
B	384	LEU	UNK	conflict	UNP A0A5F9C3W2
B	385	GLU	UNK	conflict	UNP A0A5F9C3W2
B	386	ILE	UNK	conflict	UNP A0A5F9C3W2
B	387	SER	UNK	conflict	UNP A0A5F9C3W2
B	388	TYR	UNK	conflict	UNP A0A5F9C3W2
B	389	PHE	UNK	conflict	UNP A0A5F9C3W2
B	390	LEU	UNK	conflict	UNP A0A5F9C3W2
B	391	LEU	UNK	conflict	UNP A0A5F9C3W2
B	392	ARG	UNK	conflict	UNP A0A5F9C3W2
B	393	ARG	UNK	conflict	UNP A0A5F9C3W2
B	394	LEU	UNK	conflict	UNP A0A5F9C3W2
B	395	LEU	UNK	conflict	UNP A0A5F9C3W2
B	396	GLY	UNK	conflict	UNP A0A5F9C3W2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	397	VAL	UNK	conflict	UNP A0A5F9C3W2
B	398	ARG	UNK	conflict	UNP A0A5F9C3W2
B	399	THR	UNK	conflict	UNP A0A5F9C3W2
B	400	GLU	UNK	conflict	UNP A0A5F9C3W2
B	401	GLY	UNK	conflict	UNP A0A5F9C3W2
B	402	ASP	UNK	conflict	UNP A0A5F9C3W2

- Molecule 6 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	207	Total	C	N	O	S	0	0
			1636	1042	288	298	8		

- Molecule 7 is a protein called 40S ribosomal protein S3a.

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

- Molecule 8 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	226	Total	C	N	O	S	0	0
			1754	1139	298	310	7		

- Molecule 9 is a protein called Ribosomal protein S3.

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

- Molecule 10 is a protein called 40S ribosomal protein S4.

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

- Molecule 11 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	187	Total	C	N	O	S	0	0
			1482	928	279	268	7		

- Molecule 12 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	237	Total	C	N	O	S	0	0
			1923	1199	387	330	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	130	THR	PRO	conflict	UNP G1TM55

- Molecule 13 is a protein called 40S ribosomal protein S7.

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

- Molecule 14 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	206	Total	C	N	O	S	0	0
			1679	1054	329	291	5		

- Molecule 15 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	188	Total	C	N	O	S	0	0
			1542	979	309	251	3		

- Molecule 16 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 17 is a protein called 40S ribosomal protein S11.

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

- Molecule 18 is a protein called 40S ribosomal protein S12.

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

- Molecule 19 is a protein called 40S ribosomal protein S13.

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

- Molecule 20 is a protein called 40S ribosomal protein uS11.

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

- Molecule 21 is a protein called 40S ribosomal protein uS19.

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

- Molecule 22 is a protein called Ribosomal protein S16.

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

- Molecule 23 is a protein called 40S ribosomal protein eS17.

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

- Molecule 24 is a protein called 40S ribosomal protein uS13.

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

- Molecule 25 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	141	Total	C	N	O	S	0	0
			1112	701	213	195	3		

- Molecule 26 is a protein called 40S ribosomal protein uS10.

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

- Molecule 27 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	83	Total	C	N	O	S	0	0
			637	393	117	122	5		

- Molecule 28 is a protein called Ribosomal protein S15a.

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

- Molecule 29 is a protein called 40S ribosomal protein S23.

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

- Molecule 30 is a protein called 40S ribosomal protein S24.

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

- Molecule 31 is a protein called 40S ribosomal protein S26.

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

- Molecule 32 is a protein called 40S ribosomal protein S27.

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

- Molecule 33 is a protein called 40S ribosomal protein S28.

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

- Molecule 34 is a protein called 40S ribosomal protein S29.

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

- Molecule 35 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 36 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 37 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	58	Total	C	N	O	S	0	0
			464	287	102	74	1		

- Molecule 38 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	112	Total	C	N	O	S	0	0
			903	561	173	165	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	141	THR	ILE	conflict	UNP P47813

- Molecule 39 is a protein called ATP binding cassette subfamily E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	595	Total	C	N	O	S	0	0
			4692	2995	802	864	31		

- Molecule 40 is a protein called 60S ribosomal protein L41.

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

- Molecule 41 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	365	Total	C	N	O	S	0	0
			2955	1856	517	564	18		

- Molecule 42 is a protein called 40S ribosomal protein S25.

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

- Molecule 43 is a protein called Eukaryotic translation initiation factor 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	147	Total	C	N	O	S	0	0
			1162	733	205	213	11		

- Molecule 44 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	272	Total	C	N	O	S	0	0
			2111	1330	359	410	12		

- Molecule 45 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	324	Total	C	N	O	S	0	0
			2624	1654	452	503	15		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	215	Total	C	N	O	S	0	0
			1737	1109	285	330	13		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	372	Total	C	N	O	S	0	0
			3109	2010	519	563	17		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	365	Total	C	N	O	S	0	0
			2918	1850	493	558	17		

- Molecule 49 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	554	Total	C	N	O	S	0	0
			4508	2830	800	845	33		

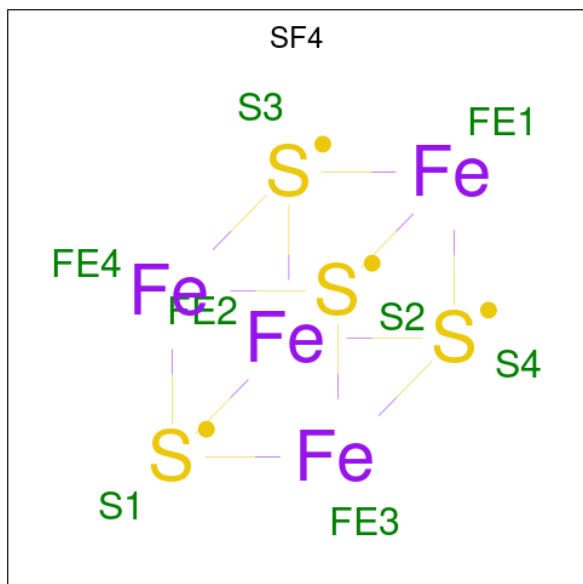
- Molecule 50 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	419	Total	C	N	O	S	0	0
			3465	2220	586	639	20		

- Molecule 51 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	y	603	Total	C	N	O	S	0	0
			4971	3133	897	920	21		

- Molecule 52 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).

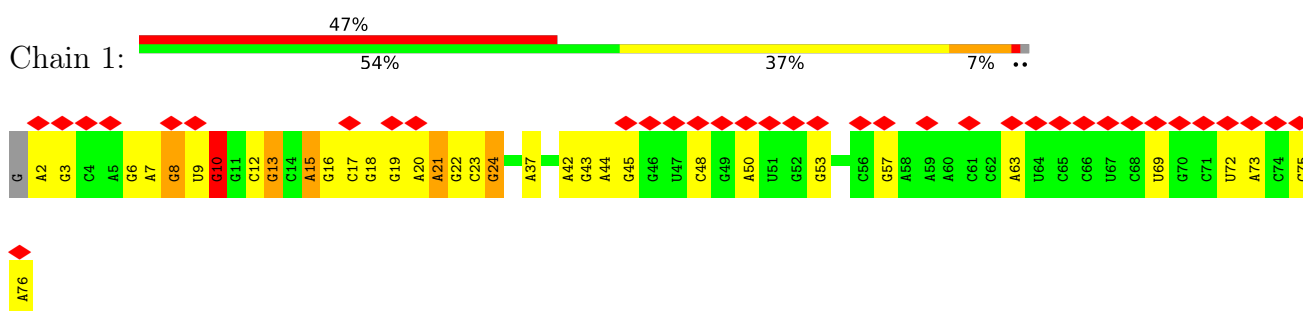


Mol	Chain	Residues	Atoms			AltConf
52	k	1	Total	Fe	S	0
			8	4	4	
52	k	1	Total	Fe	S	0
			8	4	4	

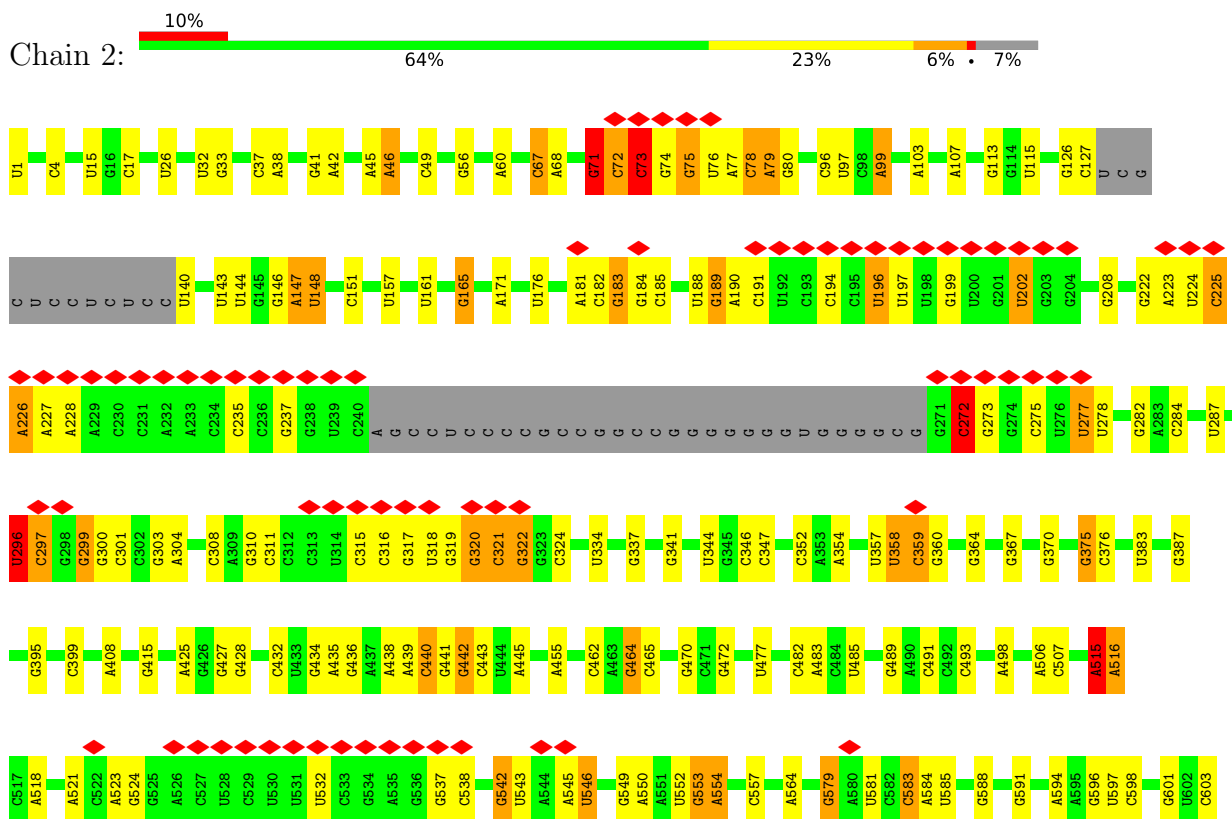
3 Residue-property plots

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: Initiator methionylated tRNA



• Molecule 2: 18S ribosomal RNA



- Molecule 3: Linear mRNA

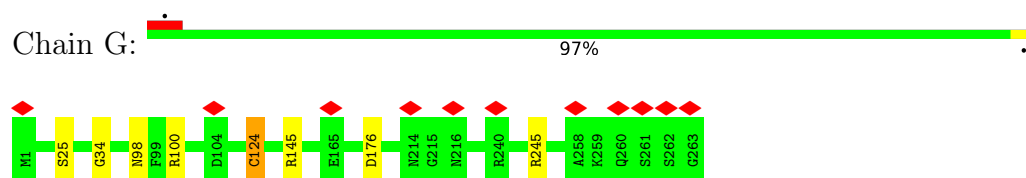
Chain 3:

94%

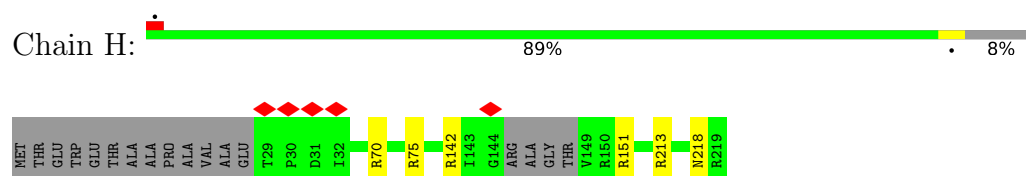
G G G A C A A U U U G C C U U C U G A C C A C A A A C C A U U G G A A A U C G G A U C C A A C U U C G G A A A A G C C U A A U A G U A A A H



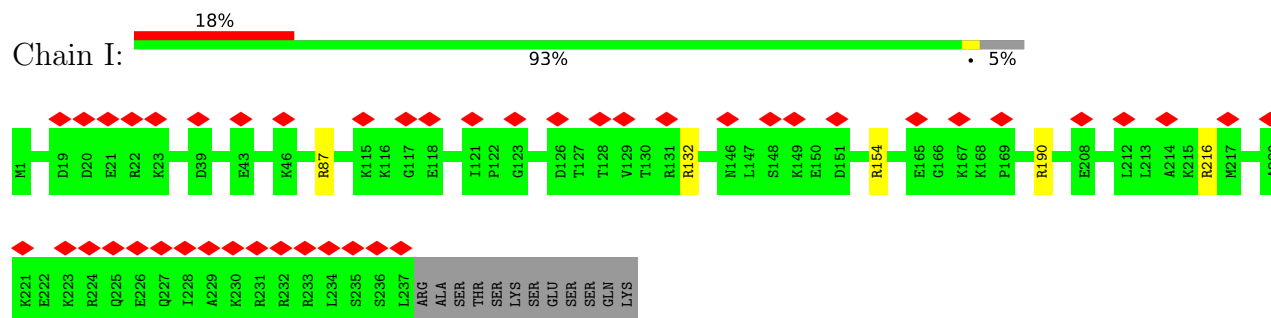
- Molecule 10: 40S ribosomal protein S4



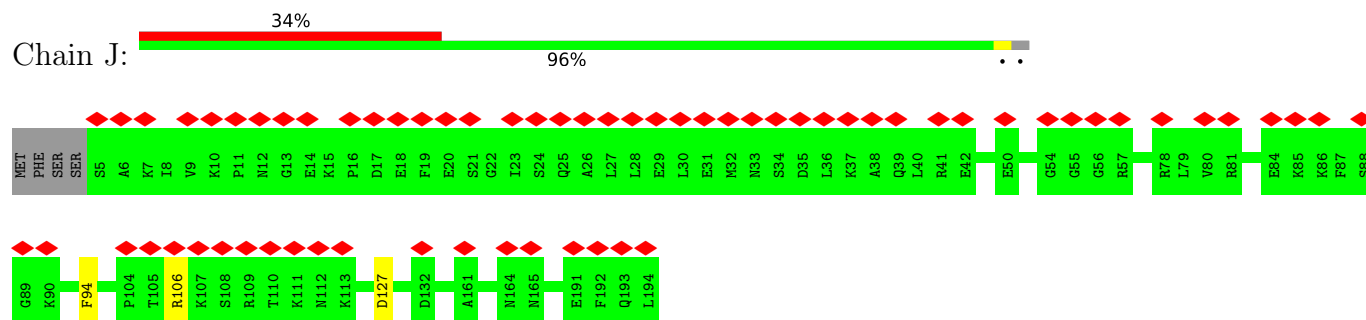
- Molecule 11: Ribosomal protein S5



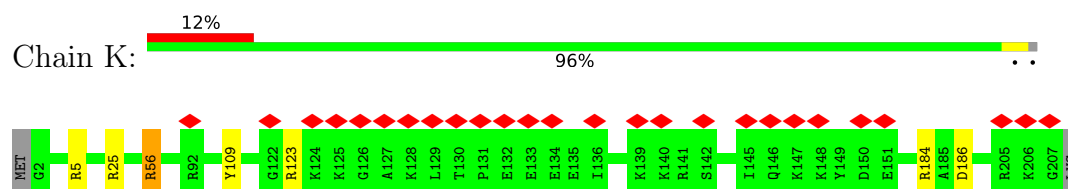
- Molecule 12: Small ribosomal subunit protein eS6



- Molecule 13: 40S ribosomal protein S7

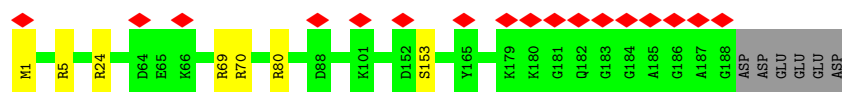


- Molecule 14: Small ribosomal subunit protein eS8

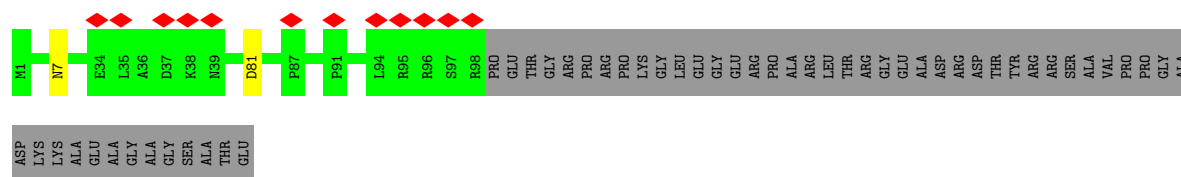


- Molecule 15: 40S ribosomal protein S9

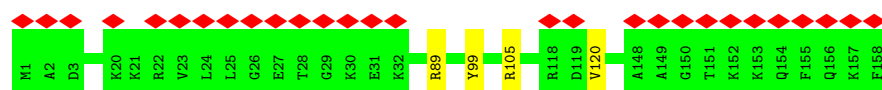




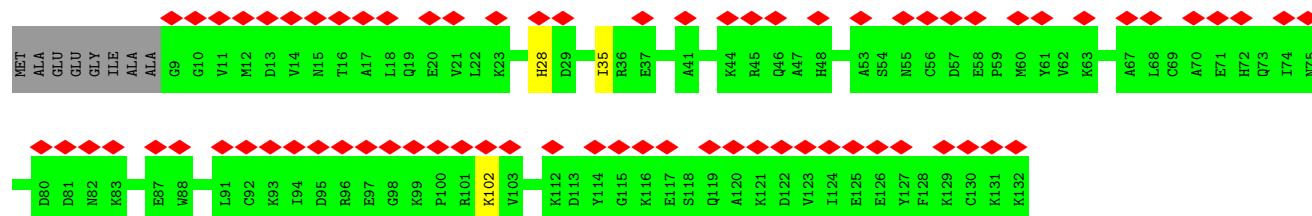
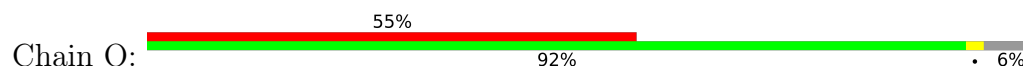
- Molecule 16: Small ribosomal subunit protein eS10



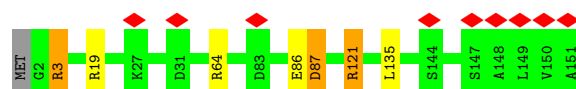
- Molecule 17: 40S ribosomal protein S11



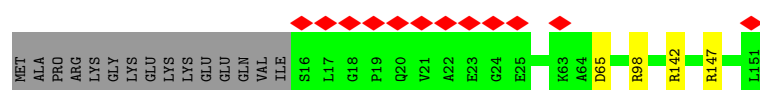
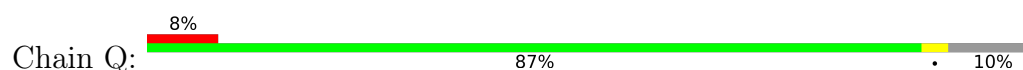
- Molecule 18: 40S ribosomal protein S12



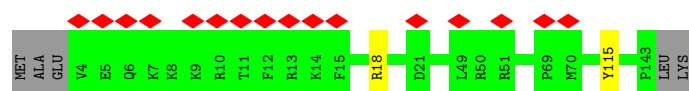
- Molecule 19: 40S ribosomal protein S13



- Molecule 20: 40S ribosomal protein uS11



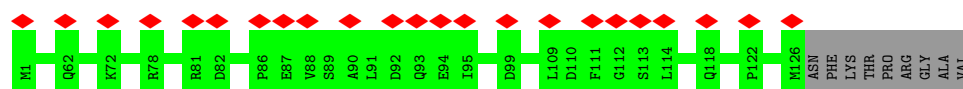
- Molecule 21: 40S ribosomal protein uS19



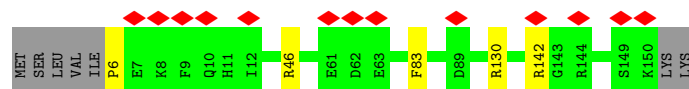
• Molecule 22: Ribosomal protein S16



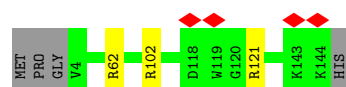
• Molecule 23: 40S ribosomal protein eS17



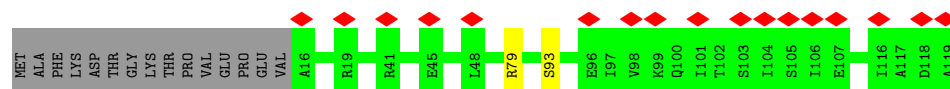
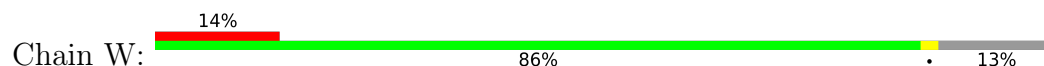
• Molecule 24: 40S ribosomal protein uS13



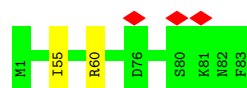
• Molecule 25: 40S ribosomal protein eS19



• Molecule 26: 40S ribosomal protein uS10

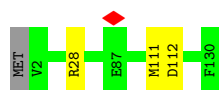


• Molecule 27: 40S ribosomal protein S21



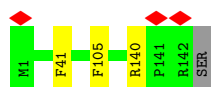
- Molecule 28: Ribosomal protein S15a

Chain Y:  97%

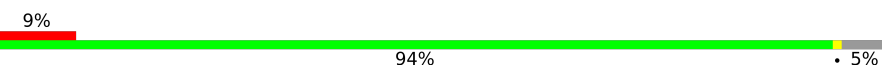


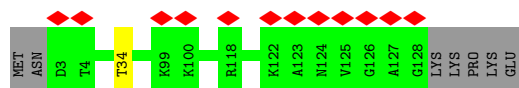
- Molecule 29: 40S ribosomal protein S23

Chain Z:  97%




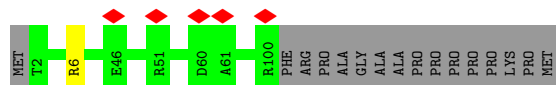
- Molecule 30: 40S ribosomal protein S24

Chain a:  9% 94% 5%



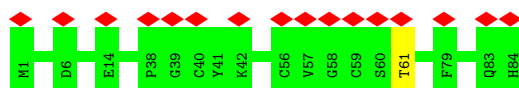
- Molecule 31: 40S ribosomal protein S26

Chain b:  85% 14%

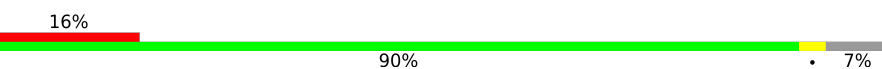


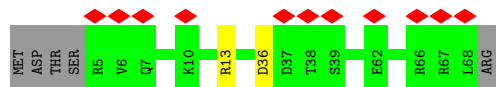
- Molecule 32: 40S ribosomal protein S27

Chain c:  19% 99%




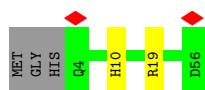
- Molecule 33: 40S ribosomal protein S28

Chain d:  16% 90% 7%

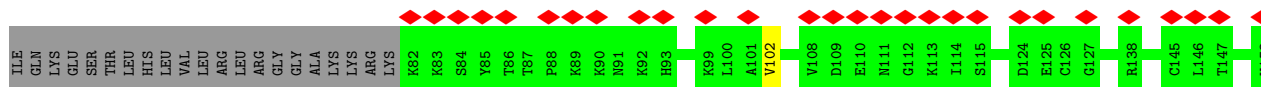
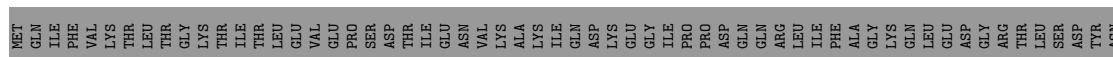
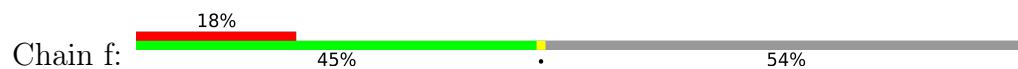


- Molecule 34: 40S ribosomal protein S29

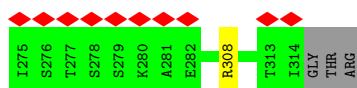
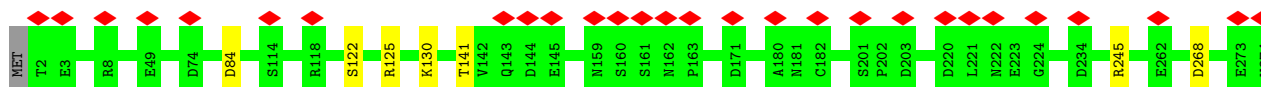
Chain e:  91% 5%



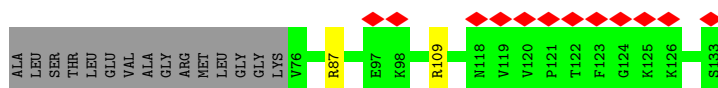
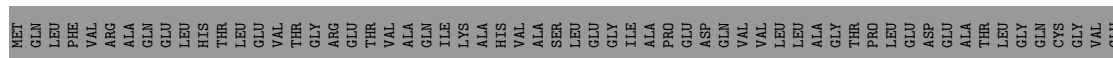
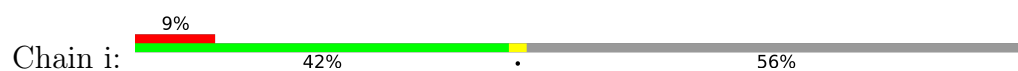
- Molecule 35: Ribosomal protein S27a



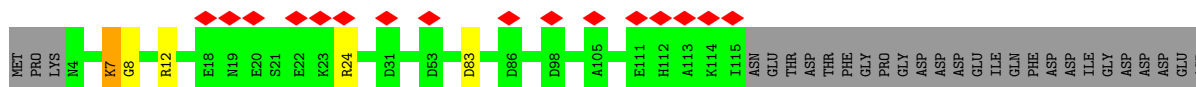
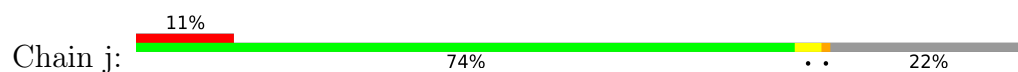
- Molecule 36: Small ribosomal subunit protein RACK1



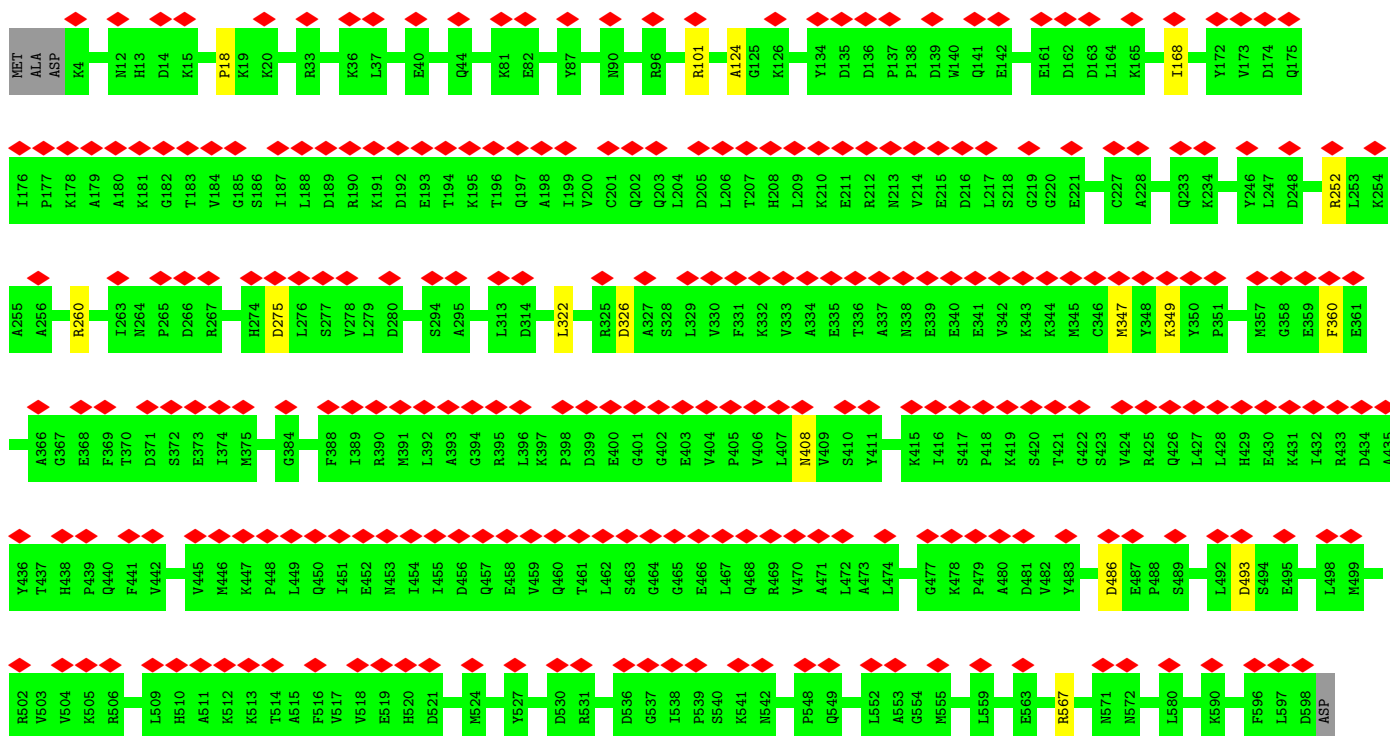
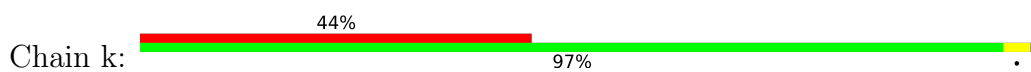
- Molecule 37: 40S ribosomal protein S30



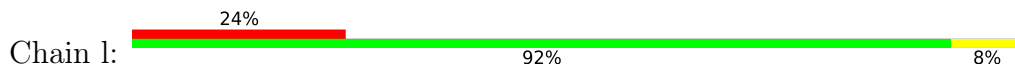
- Molecule 38: Eukaryotic translation initiation factor 1A, X-chromosomal



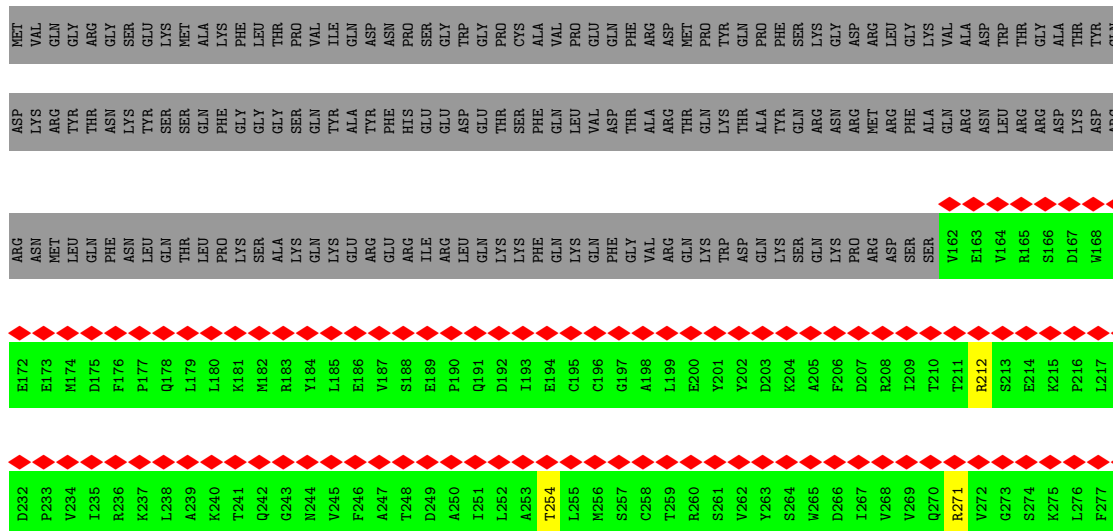
- Molecule 39: ATP binding cassette subfamily E member 1

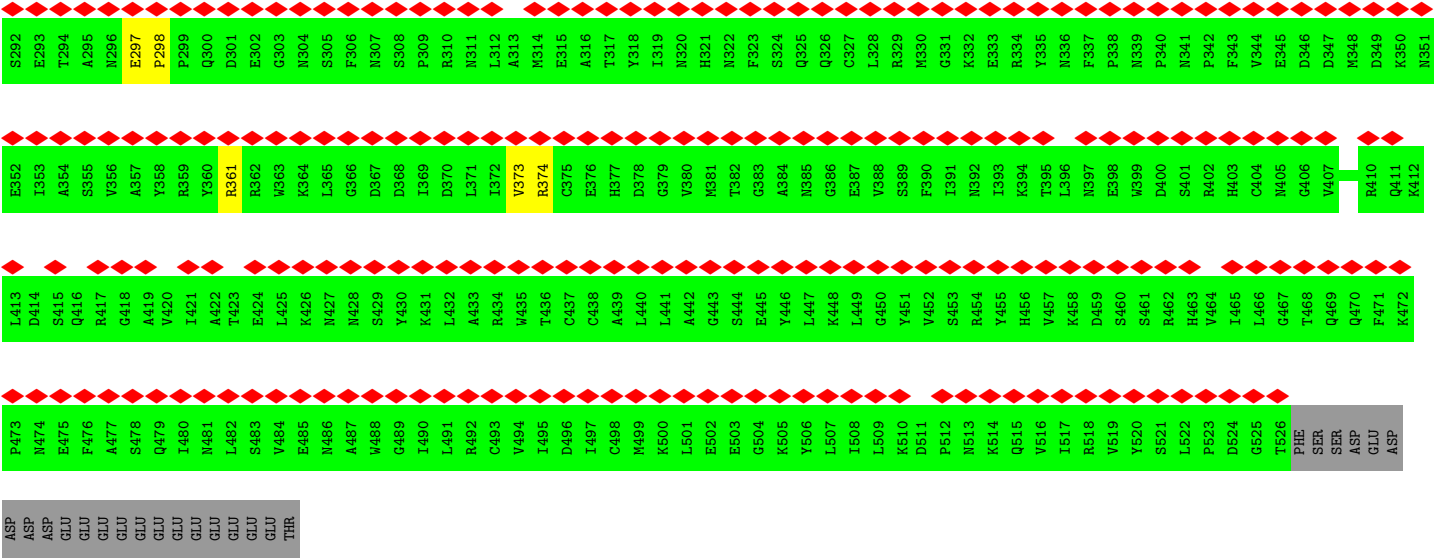


- Molecule 40: 60S ribosomal protein L41

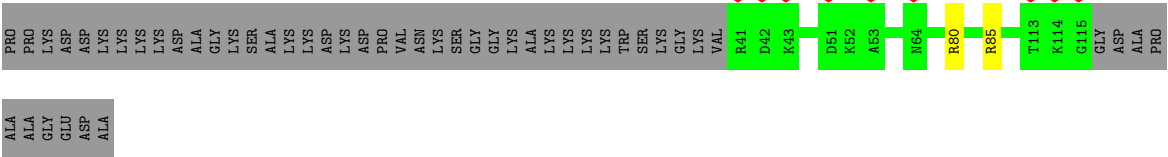


- Molecule 41: Eukaryotic translation initiation factor 3 subunit D

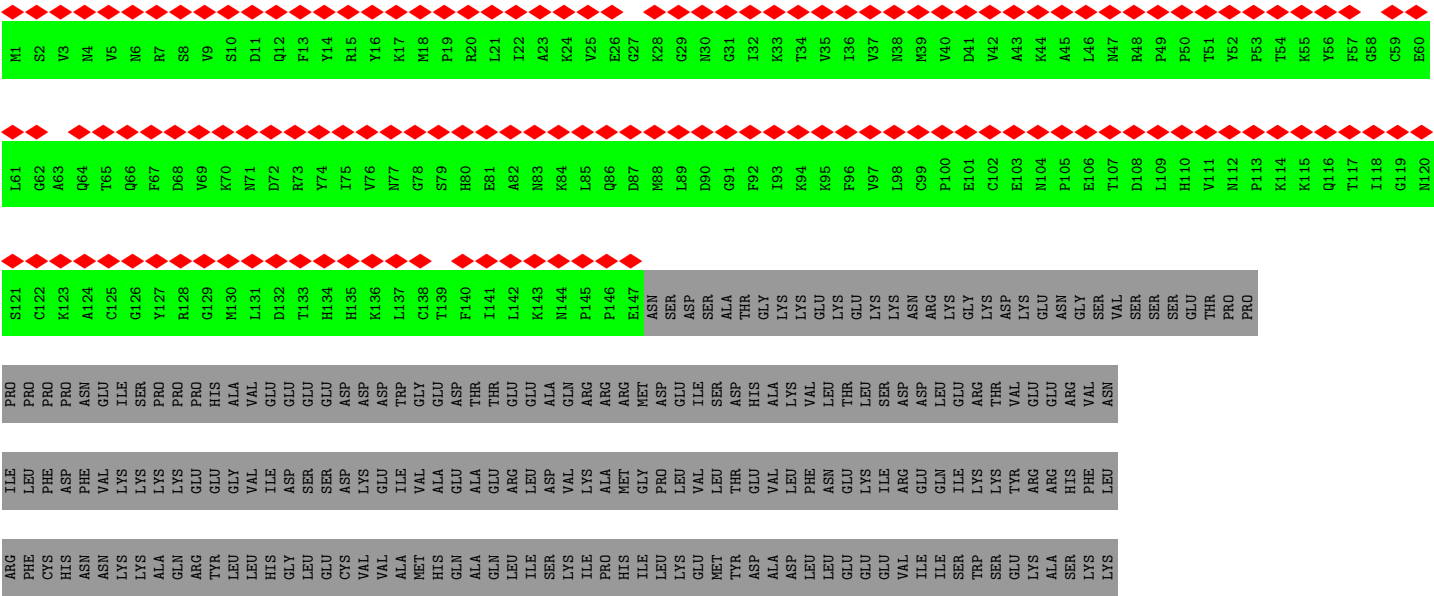




• Molecule 42: 40S ribosomal protein S25

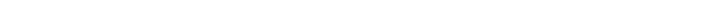


• Molecule 43: Eukaryotic translation initiation factor 5



LYS	LYS	TRP
ASP	ASP	VAL
ASP	ASP	LYS
ILE	ILE	GLU
ASP	ASP	LEU
ILE	ILE	ALA
ASP	ASP	LYS
ALA	ALA	GLU
ILE	ILE	ILE
		ARG
		VAL
		LYS
		LYS
		TRP
		LEU
		LYS
		GLU
		ALA
		GLU
		GLU
		GLU
		SER
		SER
		GLY
		GLU
		GLU
		ASP
		ASP
		ASP
		GLU
		ASN
		ILE
		GLU
		VAL
		VAL
		TRP
		LYS
		THR
		ALA
		SER
		VAL
		PRO
		LYS
		VAL
		VAL
		GLU
		THR
		VAL
		LYS
		SER
		SER
		ASP

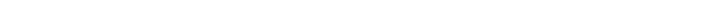
- Molecule 44: Eukaryotic translation initiation factor 3 subunit F

Chain q:  75% 71% 25%

[illegible]

L354 V355 N356 L357	L294	P234	A114
	S295	L235	R115
	G296	T236	V116
	K297	V237	H117
V298	K238	D178	G118
S299	V239	I179	T119
A300	A240	L180	L120
D301	Y241	E181	L121
N302	Y242	H182	G122
T303	D243	S183	T123
V304	T244	V184	V124
G305	E245	L185	D125
R306	R246	I186	K126
F307	G247	H187	H127
L308	G248	E188	S128
M309	V249	Y189	V129
S310	D250	Y190	E130
L311	L251	S191	V131
V312	I252	R192	T132
N313	M253	E193	M133
Q314	K254	A194	G134
V315	T255	P195	F135
F316	C256	M196	S136
K317	T257	P197	V137
I318	S258	I198	P138
V319	P259	H199	H139
P320	M260	L200	M140
D321	R261	T201	E141
D322	V262	V202	S142
F323	T263	D203	E143
E324	G264	T204	D144
T325	L265	S205	E145
M326	S266	L206	V146
L327	S267	Q207	A147
N328	D268	M208	D148
S329	L269	G209	D149
N330	Q270	R210	M150
I331	Q271	M211	E151
N332	V272	S212	F152
D333	G273	T213	A153
L334	G274	K214	K154
L335	A275	A215	M155
M336	S276	V216	M156
V337	A277	V17	V157
T338	R278	S218	E158
V339	I279	T219	L159
L340	Q280	S220	H160
A341	D281	M221	K161
N342	A282	G222	K162
L343	L283	V223	V163
T344	S284	P224	S164
Q345	T285	G225	P165
S346	V286	R226	M166
Q347	L287	T227	E167
I348	Q288	M228	L168
A349	T289	G229	I169
L350	A290	V230	L170
N351	E291	M231	G171
E352	D292	F232	W172
K353	V293	T233	Y173

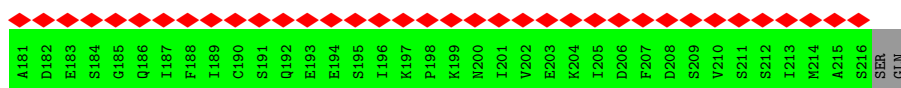
- Molecule 45: Eukaryotic translation initiation factor 3 subunit H

Chain r:  92% 89% 8%

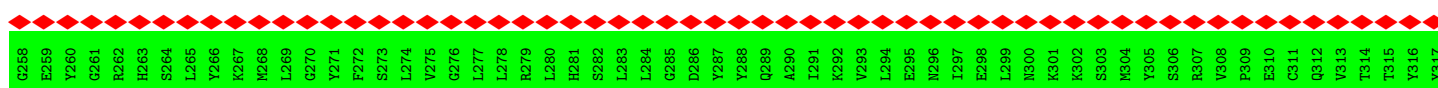
WET	ALA	SER	ARG	LYS	GLU	GLY	ALA	GLY	PRO	ASN	ALA	VAL	PRO	SER	SER	ALA	THR	GLY	ALA	ALA	LYS	GLY	GLY	LYS	GLY	GLY	LYS	G29	G30	S31	G32	D33	S34	A35	V36	K37	Q38	V39	Q40	I41	D42	G43	L44	V45	V46	L47	K48	I49	I50	K51	H52	Y53	Q54	E55	E56	G57	Q58	G59	T60
E61	V62	V63	Q64	G65	V66	L67	L68	G69	L70	L71	V72	E73	D74	R75	L76	E77	I78	T79	N80	C81	F82	P83	F84	P85	Q86	H87	T88	E89	D90	L91	D92	D93	F94	D95	E96	V97	Q98	Y99	Q100	M101	E102	M103	M104	R105	S106	L107	R108	H109	V110	N111	I112	D113	H114	L115	H116	V117	G118	E119	Y120
Q121	S122	T123	Y124	Y125	G126	S127	F128	V129	T130	R131	A132	L133	L134	D135	S136	Q137	F138	S139	Y140	Q141	H142	A143	I144	E145	E146	S147	V148	V149	L150	I151	Y152	D153	P154	I155	K156	T157	A158	Q159	G160	S161	L162	S163	L164	K165	A166	V167	R168	L169	T170	P171	K172	L173	M174	E175	V176	C177	K178	E179	K180



Chain s: 

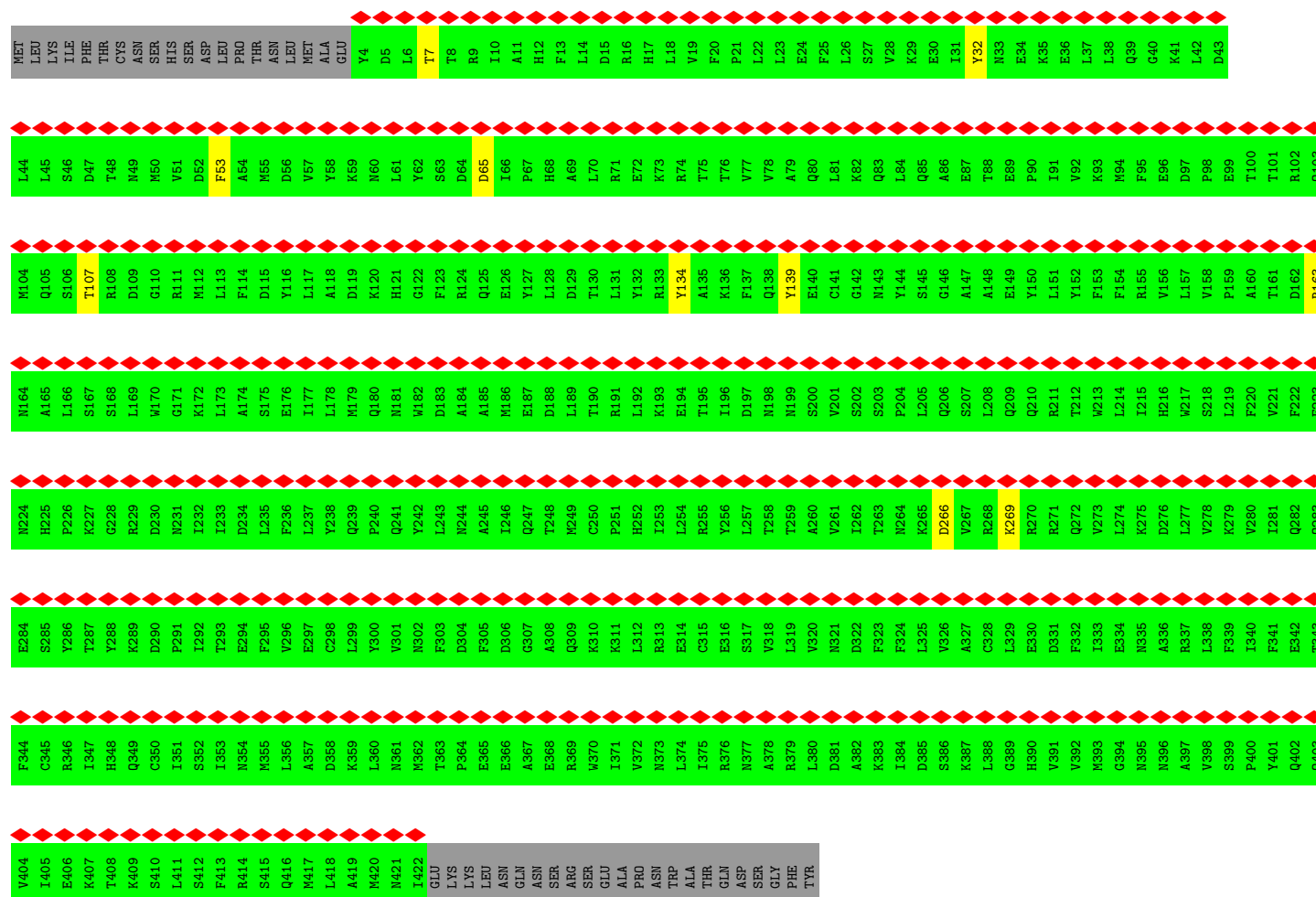
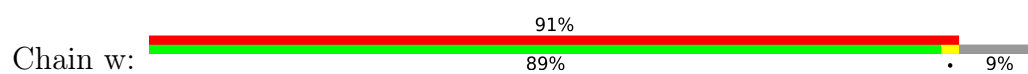


Chain t:  61% 60% 39%





- Molecule 50: Eukaryotic translation initiation factor 3 subunit E





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1000	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.157	Depositor
Minimum map value	-0.675	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.15	Depositor
Map size (\AA)	465.0, 465.0, 465.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.93, 0.93, 0.93	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: T6A, I2T, SF4

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	0.83	0/1770	1.16	2/2759 (0.1%)
2	2	0.82	0/41503	1.15	90/64683 (0.1%)
3	3	0.80	0/219	1.10	2/340 (0.6%)
4	A	0.88	0/2177	1.38	5/2935 (0.2%)
5	B	0.91	0/3266	1.40	4/4415 (0.1%)
6	C	0.85	0/1673	1.41	3/2275 (0.1%)
7	D	0.80	0/1769	1.36	2/2367 (0.1%)
8	E	0.82	0/1794	1.37	3/2430 (0.1%)
9	F	0.81	0/1792	1.34	0/2412
10	G	0.87	0/2125	1.38	7/2856 (0.2%)
11	H	0.82	0/1503	1.39	5/2020 (0.2%)
12	I	0.87	0/1945	1.40	5/2588 (0.2%)
13	J	0.85	0/1553	1.39	3/2079 (0.1%)
14	K	0.89	0/1708	1.43	4/2278 (0.2%)
15	L	0.87	0/1567	1.44	6/2092 (0.3%)
16	M	0.84	0/851	1.34	2/1147 (0.2%)
17	N	0.88	0/1319	1.38	1/1761 (0.1%)
18	O	0.85	0/968	1.37	2/1296 (0.2%)
19	P	0.85	0/1232	1.42	7/1656 (0.4%)
20	Q	0.87	0/1029	1.49	4/1380 (0.3%)
21	R	0.87	0/1177	1.39	1/1571 (0.1%)
22	S	0.87	0/1142	1.41	10/1528 (0.7%)
23	T	0.87	0/1031	1.38	0/1383
24	U	0.90	0/1212	1.44	4/1621 (0.2%)
25	V	0.84	0/1132	1.43	3/1517 (0.2%)
26	W	0.87	0/832	1.40	2/1117 (0.2%)
27	X	0.82	0/644	1.38	3/860 (0.3%)
28	Y	0.84	0/1051	1.41	3/1406 (0.2%)
29	Z	0.84	0/1124	1.45	3/1500 (0.2%)
30	a	0.86	0/1038	1.34	0/1380
31	b	0.88	0/802	1.49	1/1076 (0.1%)
32	c	0.86	0/673	1.39	0/902

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.86	0/508	1.46	2/680 (0.3%)
34	e	0.90	0/455	1.55	2/603 (0.3%)
35	f	0.91	0/593	1.30	1/786 (0.1%)
36	g	0.87	0/2493	1.36	7/3394 (0.2%)
37	i	0.88	0/469	1.49	2/617 (0.3%)
38	j	0.87	1/913 (0.1%)	1.67	7/1213 (0.6%)
39	k	0.87	0/4779	1.38	12/6452 (0.2%)
40	l	0.96	0/241	1.65	2/305 (0.7%)
41	m	0.88	1/3015 (0.0%)	1.35	5/4078 (0.1%)
42	n	0.83	0/604	1.37	2/810 (0.2%)
43	o	0.89	0/1186	1.32	0/1599
44	q	0.84	0/2149	1.39	6/2920 (0.2%)
45	r	0.86	0/2675	1.42	5/3609 (0.1%)
46	s	0.69	0/1772	1.22	1/2396 (0.0%)
47	t	0.79	1/3185 (0.0%)	1.30	5/4296 (0.1%)
48	u	0.79	0/2963	1.40	13/3998 (0.3%)
49	v	0.87	0/4587	1.39	17/6191 (0.3%)
50	w	0.79	0/3538	1.35	8/4786 (0.2%)
51	y	0.87	0/5059	1.50	11/6832 (0.2%)
All	All	0.84	3/124805 (0.0%)	1.31	295/177195 (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	0	17
2	2	0	335
4	A	0	1
6	C	0	1
7	D	0	1
9	F	0	1
10	G	0	1
11	H	0	1
14	K	0	4
15	L	0	1
17	N	0	2
19	P	0	1
20	Q	0	1
21	R	0	1
28	Y	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
38	j	0	1
41	m	0	1
44	q	0	1
45	r	0	3
48	u	0	2
49	v	0	3
50	w	0	2
51	y	0	1
All	All	0	383

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	j	8	GLY	N-CA	5.76	1.51	1.45
41	m	298	PRO	CA-C	5.68	1.55	1.51
47	t	469	THR	CB-OG1	-5.16	1.35	1.43

The worst 5 of 295 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	y	507	ILE	O-C-N	-39.51	73.19	122.57
38	j	7	LYS	O-C-N	-28.40	92.94	122.19
51	y	507	ILE	CA-C-O	-19.26	96.70	120.78
6	C	20	ALA	N-CA-C	10.26	125.18	112.87
38	j	7	LYS	CA-C-N	8.64	132.03	121.83

There are no chirality outliers.

5 of 383 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	10	G	Sidechain
1	1	2	A	Sidechain
1	1	3	G	Sidechain
1	1	6	G	Sidechain
1	1	7	A	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	1	1614	0	822	3	0
2	2	37147	0	18752	9	0
3	3	196	0	98	0	0
4	A	2146	0	2191	0	0
5	B	3213	0	3354	0	0
6	C	1636	0	1641	0	0
7	D	1741	0	1815	0	0
8	E	1754	0	1834	0	0
9	F	1764	0	1863	0	0
10	G	2083	0	2189	0	0
11	H	1482	0	1534	0	0
12	I	1923	0	2089	0	0
13	J	1530	0	1627	0	0
14	K	1679	0	1762	0	0
15	L	1542	0	1659	1	0
16	M	827	0	854	0	0
17	N	1296	0	1374	0	0
18	O	958	0	993	1	0
19	P	1208	0	1294	0	0
20	Q	1016	0	1039	0	0
21	R	1154	0	1213	0	0
22	S	1124	0	1193	0	0
23	T	1019	0	1075	0	0
24	U	1194	0	1253	0	0
25	V	1112	0	1149	0	0
26	W	822	0	887	0	0
27	X	637	0	637	0	0
28	Y	1034	0	1080	0	0
29	Z	1106	0	1179	0	0
30	a	1021	0	1085	0	0
31	b	789	0	841	0	0
32	c	659	0	683	1	0
33	d	506	0	536	0	0
34	e	445	0	442	0	0
35	f	581	0	599	0	0
36	g	2436	0	2393	1	0
37	i	464	0	511	0	0
38	j	903	0	928	0	0
39	k	4692	0	4820	2	0
40	l	240	0	289	0	0
41	m	2955	0	2897	0	0
42	n	598	0	656	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	o	1162	0	1171	0	0
44	q	2111	0	2105	7	0
45	r	2624	0	2592	1	0
46	s	1737	0	1706	1	0
47	t	3109	0	3084	1	0
48	u	2918	0	2950	1	0
49	v	4508	0	4513	3	0
50	w	3465	0	3446	0	0
51	y	4971	0	5048	8	0
52	k	16	0	0	0	0
All	All	118867	0	101745	37	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 0.

The worst 5 of 37 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)
51:y:181:ALA:HB1	51:y:196:LYS:HE2	1.44	0.99
51:y:181:ALA:HB1	51:y:196:LYS:CE	2.00	0.91
44:q:95:HIS:CE1	44:q:241:TYR:CD2	2.82	0.67
2:2:1244:I2T:OP2	2:2:1244:I2T:C6	2.48	0.62
2:2:1244:I2T:O2	2:2:1244:I2T:C32	2.47	0.59

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	
4	A	264/390 (68%)	251 (95%)	13 (5%)	0	100	100
5	B	420/485 (87%)	396 (94%)	24 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	C	205/295 (70%)	197 (96%)	8 (4%)	0	100	100
7	D	213/264 (81%)	205 (96%)	8 (4%)	0	100	100
8	E	224/270 (83%)	215 (96%)	9 (4%)	0	100	100
9	F	225/243 (93%)	217 (96%)	8 (4%)	0	100	100
10	G	261/263 (99%)	255 (98%)	6 (2%)	0	100	100
11	H	183/204 (90%)	176 (96%)	7 (4%)	0	100	100
12	I	235/249 (94%)	222 (94%)	13 (6%)	0	100	100
13	J	188/194 (97%)	181 (96%)	7 (4%)	0	100	100
14	K	204/208 (98%)	196 (96%)	8 (4%)	0	100	100
15	L	186/194 (96%)	183 (98%)	3 (2%)	0	100	100
16	M	96/149 (64%)	89 (93%)	7 (7%)	0	100	100
17	N	156/158 (99%)	146 (94%)	10 (6%)	0	100	100
18	O	122/132 (92%)	112 (92%)	10 (8%)	0	100	100
19	P	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
20	Q	134/151 (89%)	130 (97%)	4 (3%)	0	100	100
21	R	138/145 (95%)	131 (95%)	7 (5%)	0	100	100
22	S	139/146 (95%)	134 (96%)	5 (4%)	0	100	100
23	T	124/135 (92%)	120 (97%)	4 (3%)	0	100	100
24	U	143/152 (94%)	138 (96%)	5 (4%)	0	100	100
25	V	139/145 (96%)	136 (98%)	3 (2%)	0	100	100
26	W	102/119 (86%)	96 (94%)	6 (6%)	0	100	100
27	X	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
28	Y	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
29	Z	140/143 (98%)	137 (98%)	3 (2%)	0	100	100
30	a	124/133 (93%)	116 (94%)	8 (6%)	0	100	100
31	b	97/115 (84%)	94 (97%)	3 (3%)	0	100	100
32	c	82/84 (98%)	80 (98%)	2 (2%)	0	100	100
33	d	62/69 (90%)	61 (98%)	1 (2%)	0	100	100
34	e	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
35	f	69/156 (44%)	63 (91%)	6 (9%)	0	100	100
36	g	311/317 (98%)	296 (95%)	15 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	i	56/133 (42%)	54 (96%)	2 (4%)	0	100	100
38	j	110/144 (76%)	101 (92%)	9 (8%)	0	100	100
39	k	593/599 (99%)	554 (93%)	39 (7%)	0	100	100
40	l	23/25 (92%)	23 (100%)	0	0	100	100
41	m	363/557 (65%)	348 (96%)	15 (4%)	0	100	100
42	n	73/124 (59%)	71 (97%)	2 (3%)	0	100	100
43	o	145/430 (34%)	139 (96%)	6 (4%)	0	100	100
44	q	270/364 (74%)	239 (88%)	31 (12%)	0	100	100
45	r	322/352 (92%)	285 (88%)	37 (12%)	0	100	100
46	s	213/218 (98%)	208 (98%)	5 (2%)	0	100	100
47	t	370/607 (61%)	334 (90%)	36 (10%)	0	100	100
48	u	363/374 (97%)	325 (90%)	38 (10%)	0	100	100
49	v	552/913 (60%)	504 (91%)	48 (9%)	0	100	100
50	w	417/462 (90%)	376 (90%)	41 (10%)	0	100	100
51	y	601/1362 (44%)	548 (91%)	53 (9%)	0	100	100
All	All	9864/12792 (77%)	9278 (94%)	586 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	
4	A	238/347 (69%)	238 (100%)	0	100	100
5	B	354/407 (87%)	354 (100%)	0	100	100
6	C	173/244 (71%)	173 (100%)	0	100	100
7	D	196/231 (85%)	196 (100%)	0	100	100
8	E	190/214 (89%)	189 (100%)	1 (0%)	81	93
9	F	190/202 (94%)	190 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	G	225/225 (100%)	223 (99%)	2 (1%)	70	90
11	H	159/170 (94%)	159 (100%)	0	100	100
12	I	207/218 (95%)	207 (100%)	0	100	100
13	J	170/174 (98%)	170 (100%)	0	100	100
14	K	177/179 (99%)	177 (100%)	0	100	100
15	L	162/168 (96%)	162 (100%)	0	100	100
16	M	89/125 (71%)	89 (100%)	0	100	100
17	N	142/142 (100%)	141 (99%)	1 (1%)	76	92
18	O	104/108 (96%)	104 (100%)	0	100	100
19	P	130/131 (99%)	127 (98%)	3 (2%)	44	76
20	Q	106/119 (89%)	106 (100%)	0	100	100
21	R	126/130 (97%)	126 (100%)	0	100	100
22	S	117/121 (97%)	117 (100%)	0	100	100
23	T	114/121 (94%)	114 (100%)	0	100	100
24	U	125/132 (95%)	124 (99%)	1 (1%)	73	90
25	V	113/116 (97%)	113 (100%)	0	100	100
26	W	94/107 (88%)	94 (100%)	0	100	100
27	X	67/67 (100%)	67 (100%)	0	100	100
28	Y	112/113 (99%)	112 (100%)	0	100	100
29	Z	114/115 (99%)	114 (100%)	0	100	100
30	a	108/115 (94%)	107 (99%)	1 (1%)	70	90
31	b	87/99 (88%)	87 (100%)	0	100	100
32	c	76/76 (100%)	76 (100%)	0	100	100
33	d	57/62 (92%)	57 (100%)	0	100	100
34	e	47/49 (96%)	47 (100%)	0	100	100
35	f	64/140 (46%)	64 (100%)	0	100	100
36	g	272/275 (99%)	272 (100%)	0	100	100
37	i	48/106 (45%)	48 (100%)	0	100	100
38	j	94/123 (76%)	94 (100%)	0	100	100
39	k	523/526 (99%)	522 (100%)	1 (0%)	87	96
40	l	24/24 (100%)	24 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	m	329/501 (66%)	327 (99%)	2 (1%)	78	93
42	n	66/102 (65%)	66 (100%)	0	100	100
43	o	131/388 (34%)	131 (100%)	0	100	100
44	q	239/282 (85%)	237 (99%)	2 (1%)	73	90
45	r	293/309 (95%)	291 (99%)	2 (1%)	76	92
46	s	190/193 (98%)	190 (100%)	0	100	100
47	t	342/544 (63%)	341 (100%)	1 (0%)	86	96
48	u	327/335 (98%)	321 (98%)	6 (2%)	51	80
49	v	501/812 (62%)	492 (98%)	9 (2%)	51	80
50	w	384/423 (91%)	381 (99%)	3 (1%)	73	90
51	y	554/1245 (44%)	549 (99%)	5 (1%)	70	90
All	All	8750/11155 (78%)	8710 (100%)	40 (0%)	78	93

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	v	707	ARG
51	y	128	LEU
49	v	839	THR
50	w	7	THR
51	y	283	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 100 such sidechains are listed below:

Mol	Chain	Res	Type
43	o	77	ASN
47	t	366	GLN
51	y	596	GLN
44	q	95	HIS
45	r	329	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	74/76 (97%)	16 (21%)	3 (4%)
2	2	1735/1863 (93%)	246 (14%)	68 (3%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	3	8/160 (5%)	1 (12%)	0
All	All	1817/2099 (86%)	263 (14%)	71 (3%)

5 of 263 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	8	G
1	1	9	U
1	1	10	G
1	1	12	C
1	1	15	A

5 of 71 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	1489	C
2	2	1504	A
2	2	1633	G
2	2	506	A
2	2	438	A

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	1.17	3 (9%)	43,49,52	1.34	5 (11%)
2	I2T	2	1244	2	25,29,30	2.71	4 (16%)	28,42,45	1.26	4 (14%)

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
2	I2T	2	1244	2	-	3/16/34/35	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1244	I2T	CN1-N1	-9.65	1.27	1.46
2	2	1244	I2T	O2'-C2'	-7.51	1.24	1.43
1	1	37	T6A	ODA-C13	4.90	1.36	1.22
2	2	1244	I2T	C33-N34	-4.09	1.27	1.48
1	1	37	T6A	ODB-C13	-2.32	1.23	1.30

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	37	T6A	N6-C10-N11	4.68	120.20	113.77
2	2	1244	I2T	O3'-C3'-C4'	-3.64	100.64	111.08
1	1	37	T6A	O10-C10-N6	-3.46	117.49	123.64
2	2	1244	I2T	C3'-C2'-C1'	2.66	104.83	101.69
1	1	37	T6A	C14-C12-C13	2.66	114.67	110.03

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	1244	I2T	C32-C31-N3-C2
2	2	1244	I2T	C32-C31-N3-C4
1	1	37	T6A	N11-C12-C14-C15
1	1	37	T6A	N11-C12-C13-ODA
1	1	37	T6A	N11-C12-C13-ODB

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	1244	I2T	4	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

2 ligands 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	$\# Z > 2$
52	SF4	k	701	39	0,12,12	-	-	-		
52	SF4	k	702	39	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
52	SF4	k	701	39	-	-	0/6/5/5
52	SF4	k	702	39	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

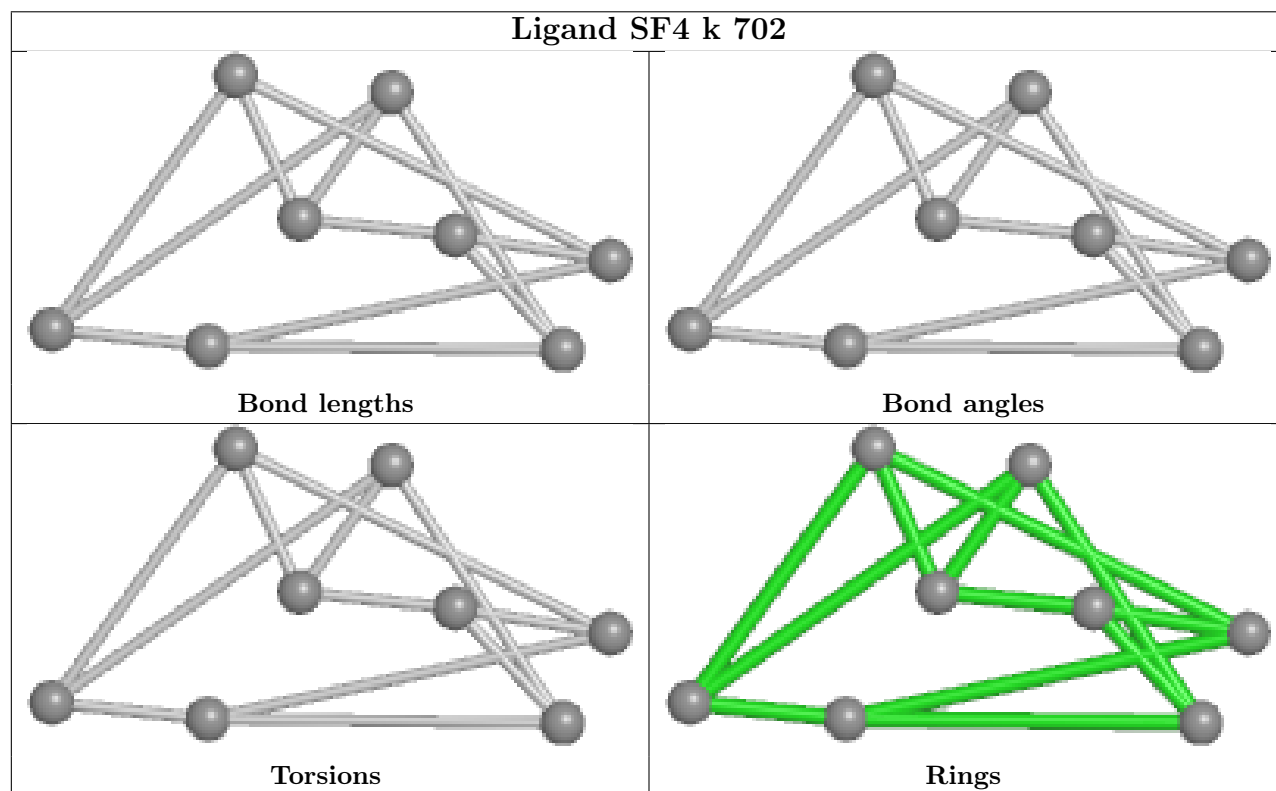
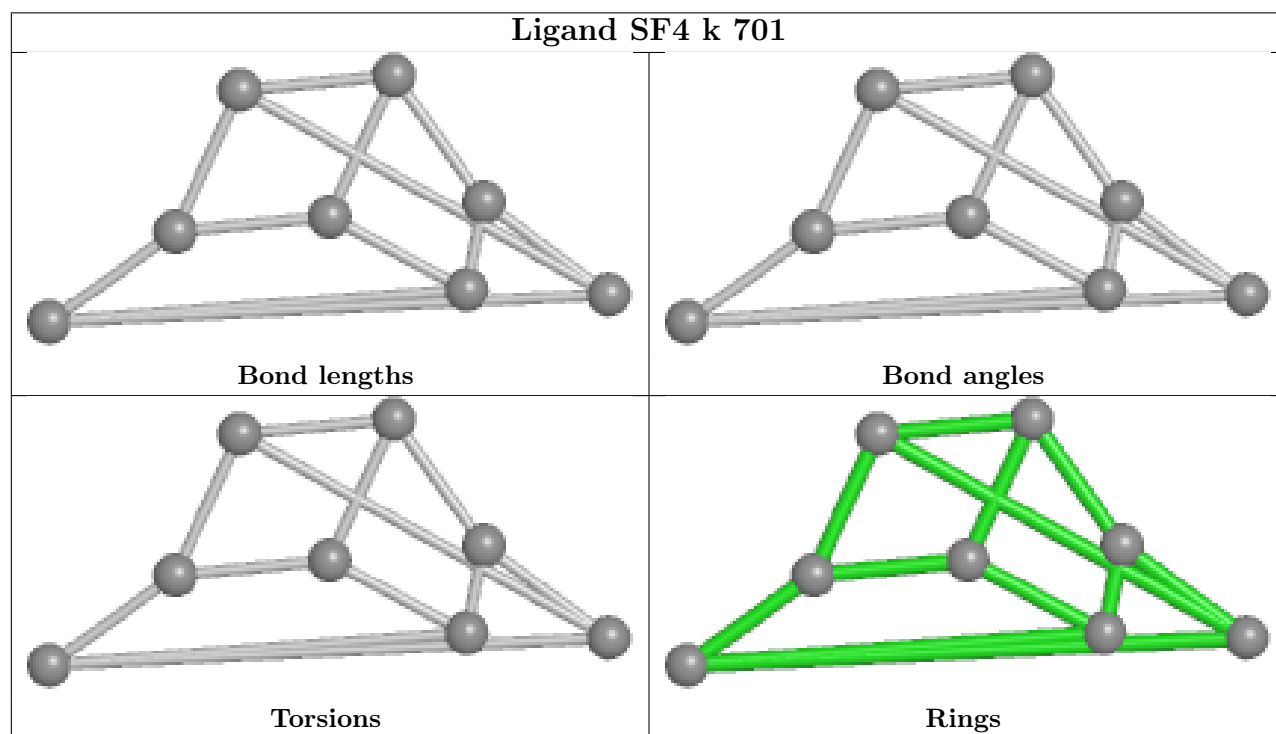
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

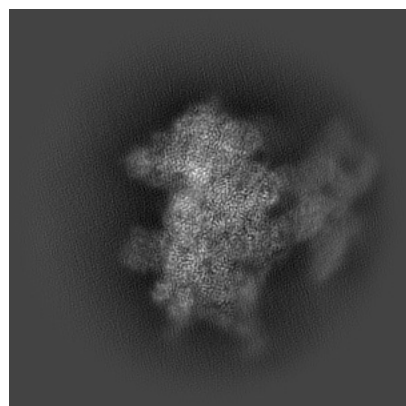
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51911. These allow visual inspection of the internal detail of the map and identification of artifacts.

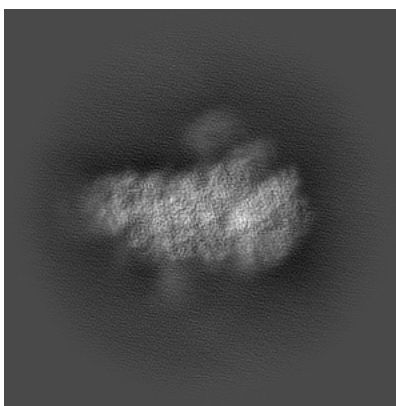
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

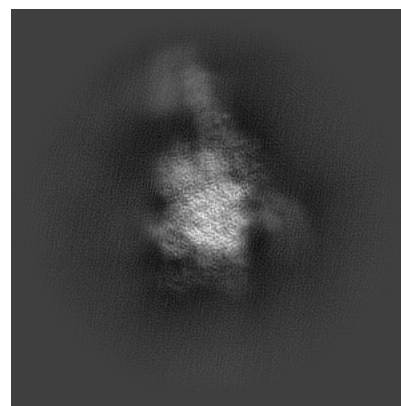
6.1.1 Primary map



X

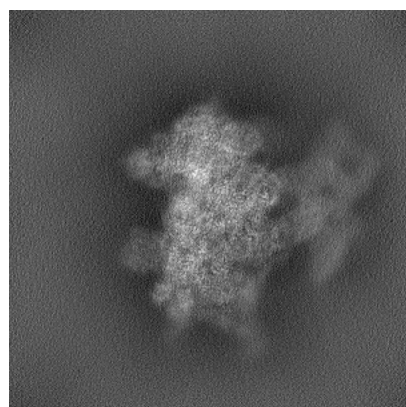


Y

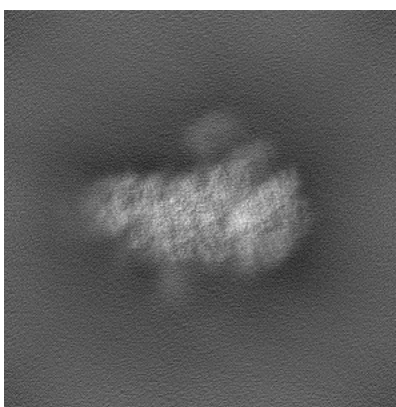


Z

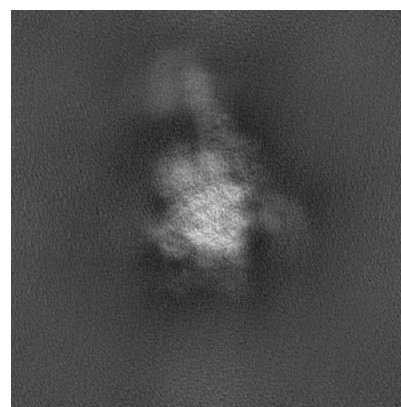
6.1.2 Raw map



X



Y

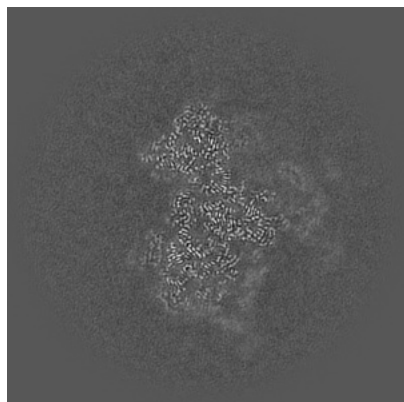


Z

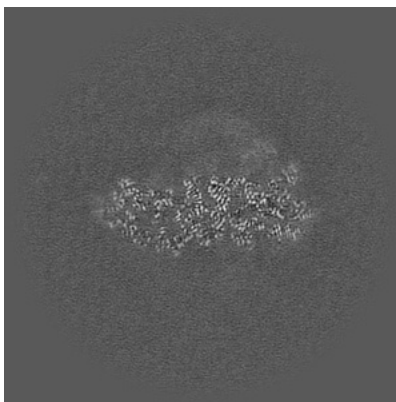
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

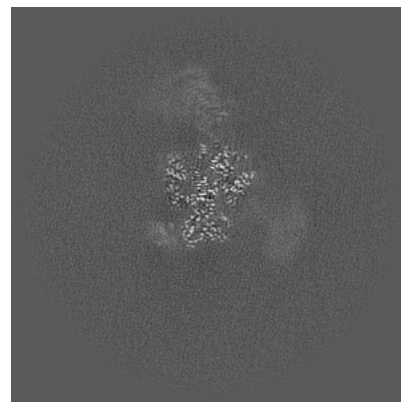
6.2.1 Primary map



X Index: 250

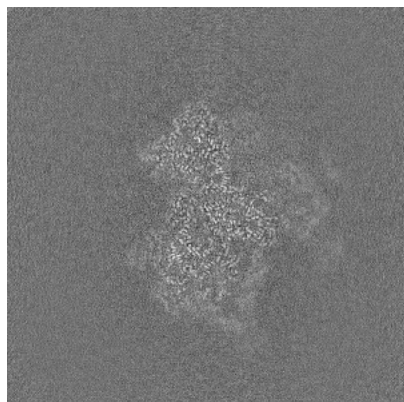


Y Index: 250

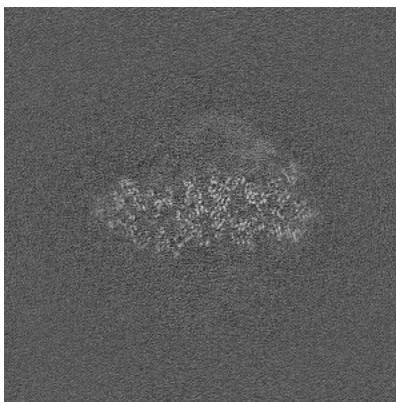


Z Index: 250

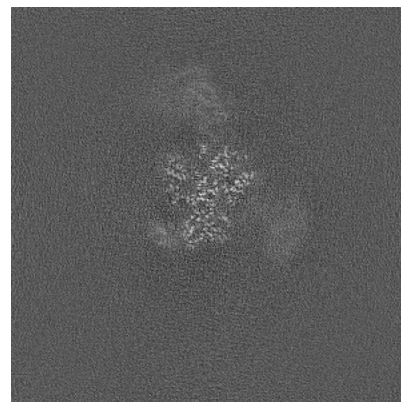
6.2.2 Raw map



X Index: 250



Y Index: 250

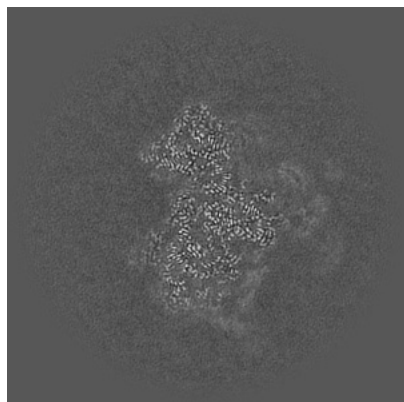


Z Index: 250

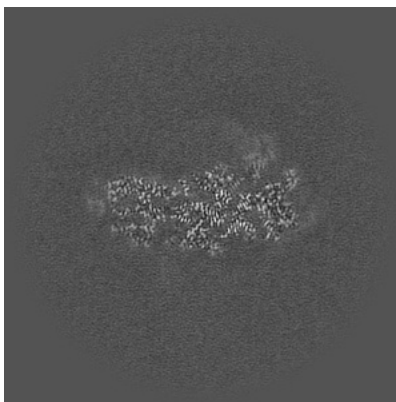
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

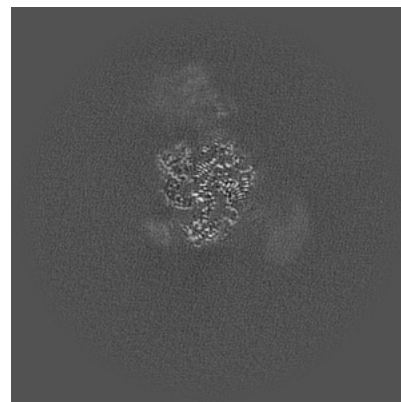
6.3.1 Primary map



X Index: 251

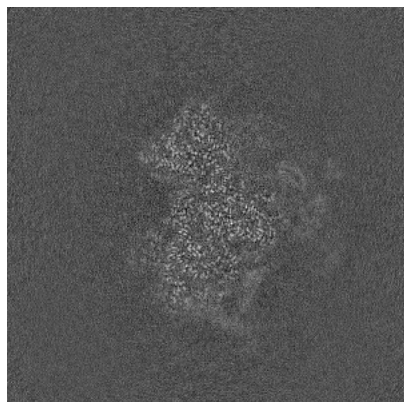


Y Index: 262

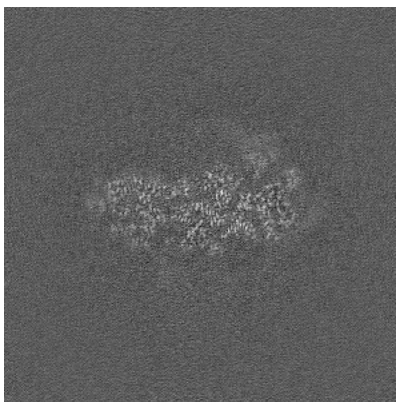


Z Index: 255

6.3.2 Raw map



X Index: 251



Y Index: 262

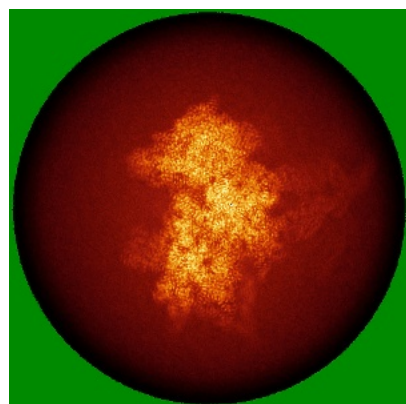


Z Index: 255

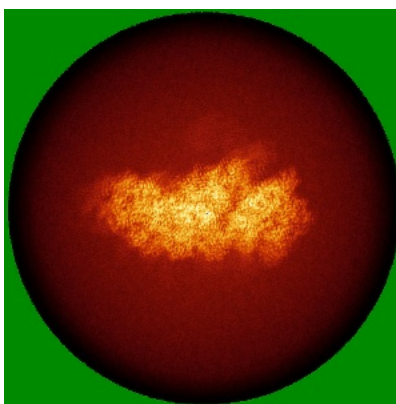
The images above show the largest variance slices of the map in three orthogonal directions.

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

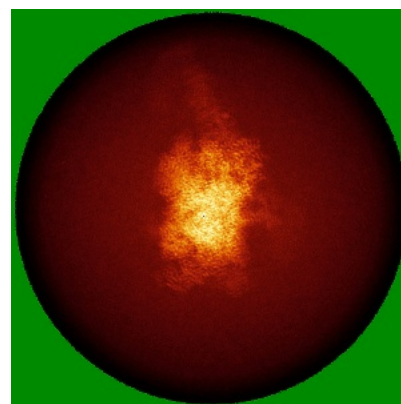
6.4.1 Primary map



X

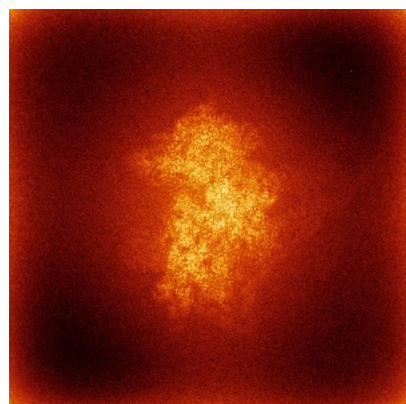


Y

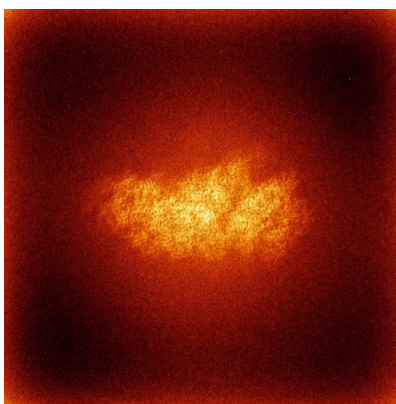


Z

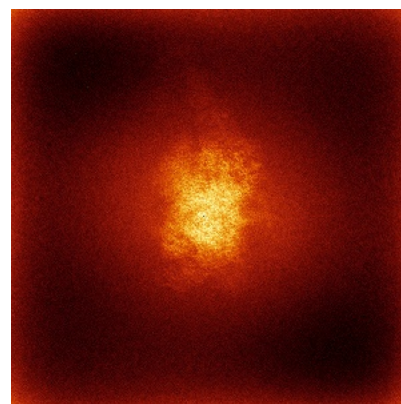
6.4.2 Raw map



X



Y



Z

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

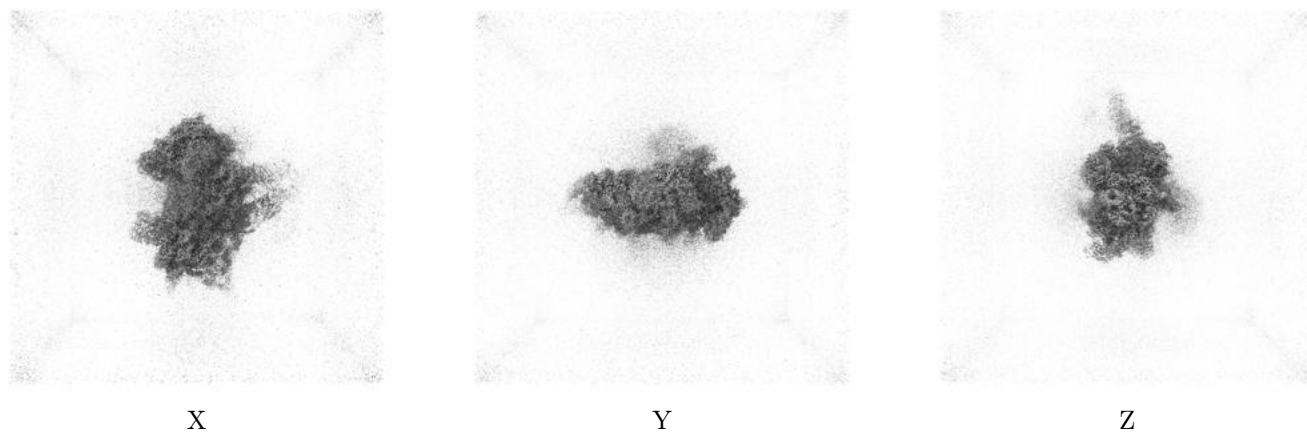
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

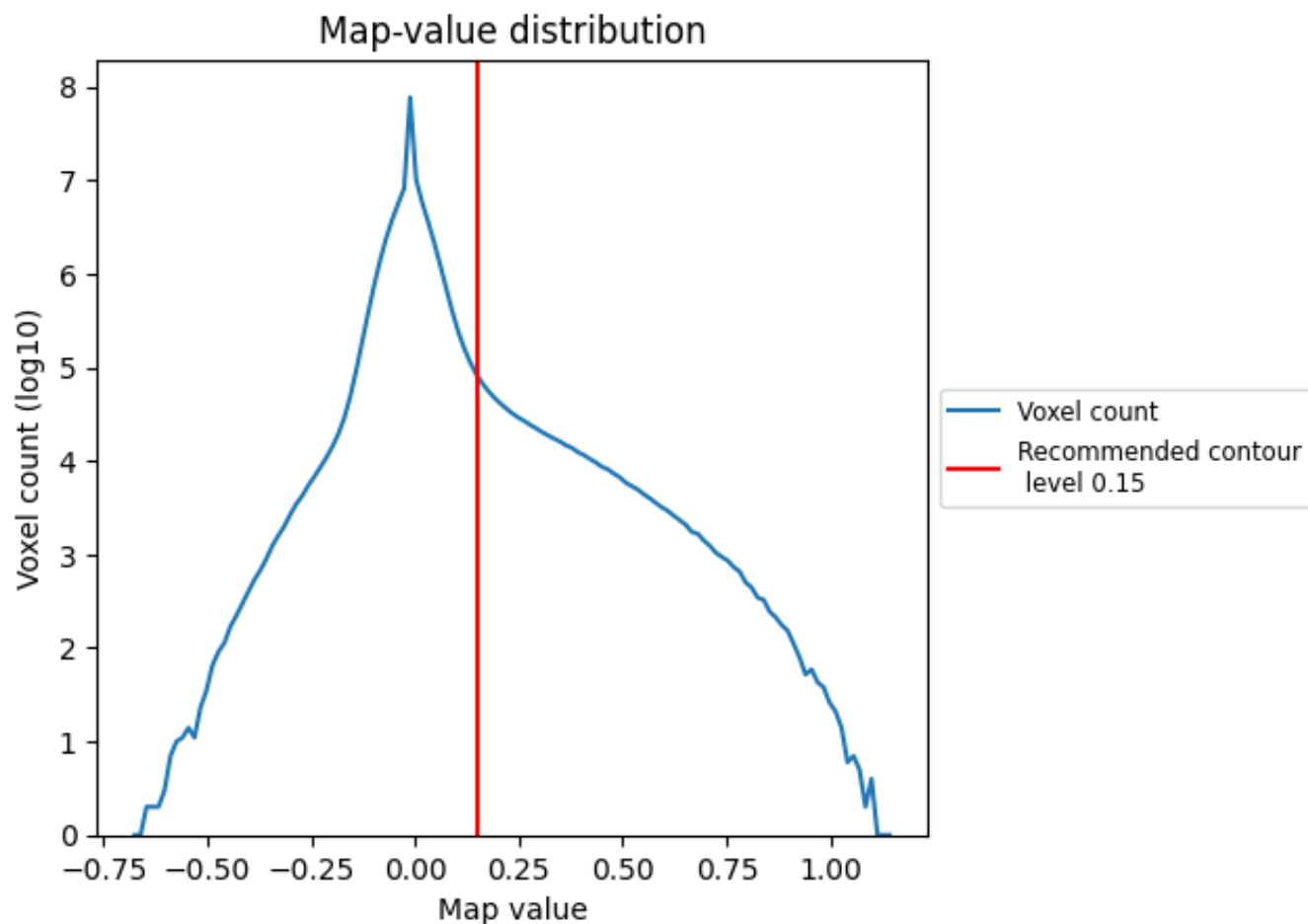
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

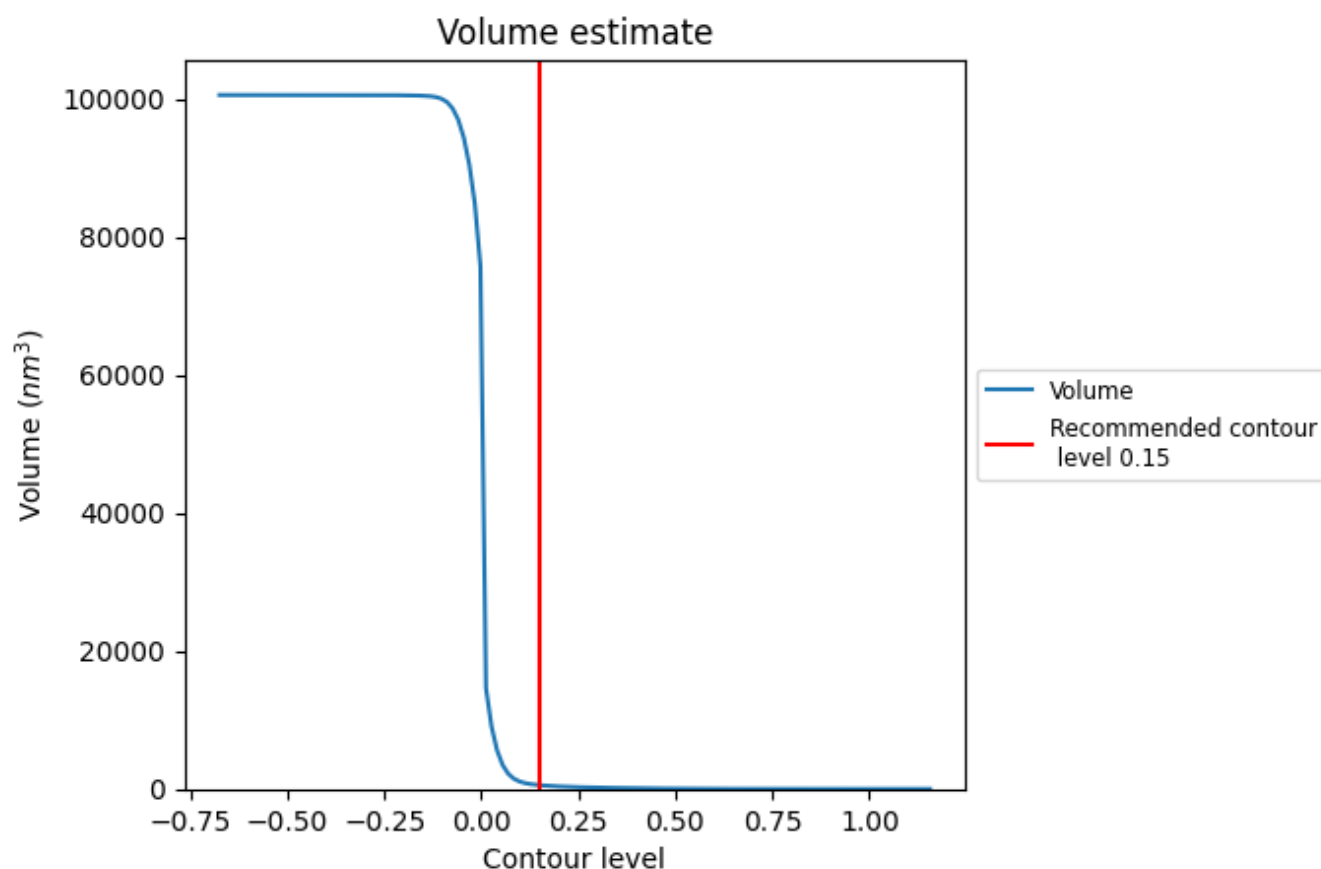
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

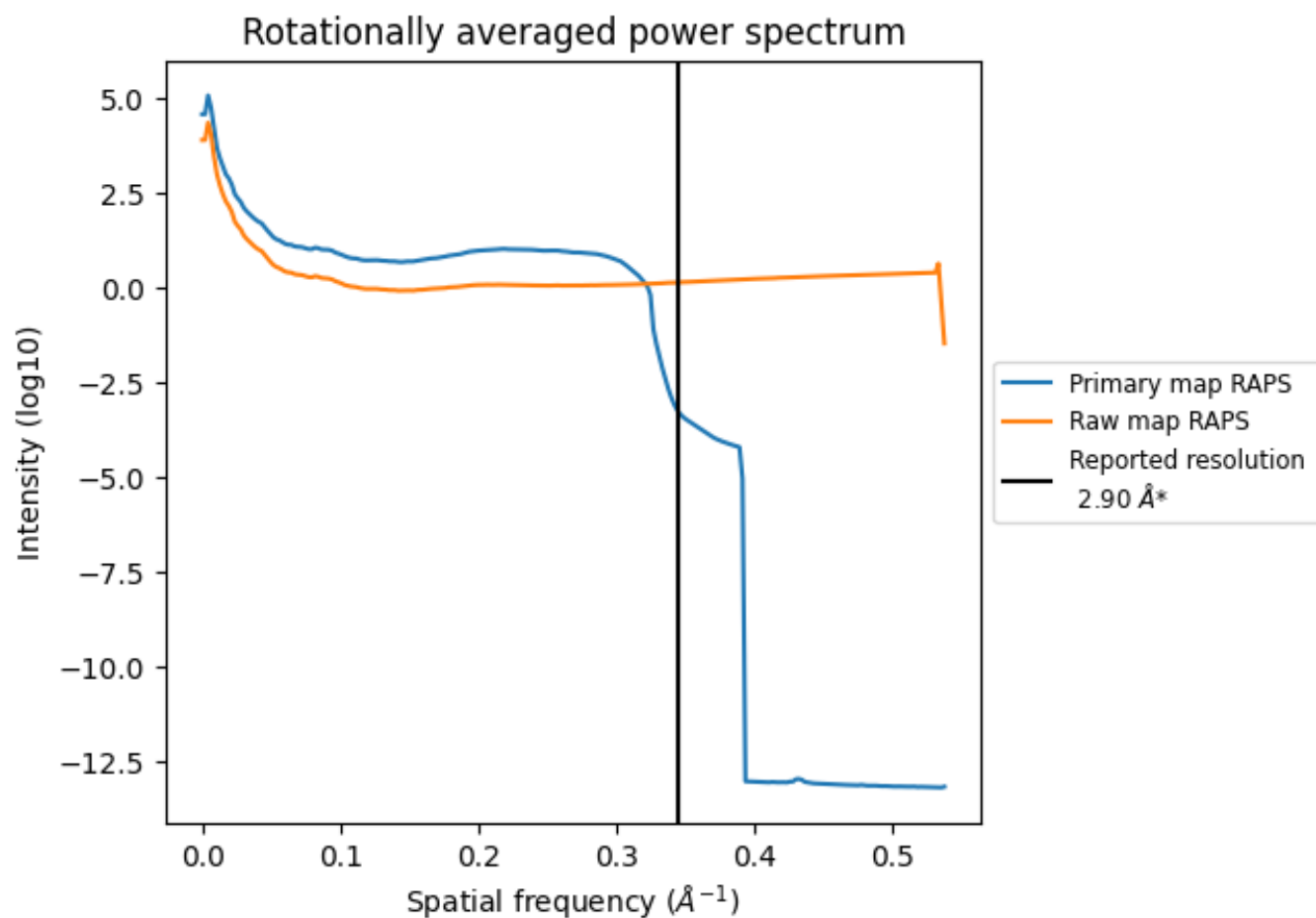
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 551 nm³; this corresponds to an approximate mass of 497 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 ⓘ

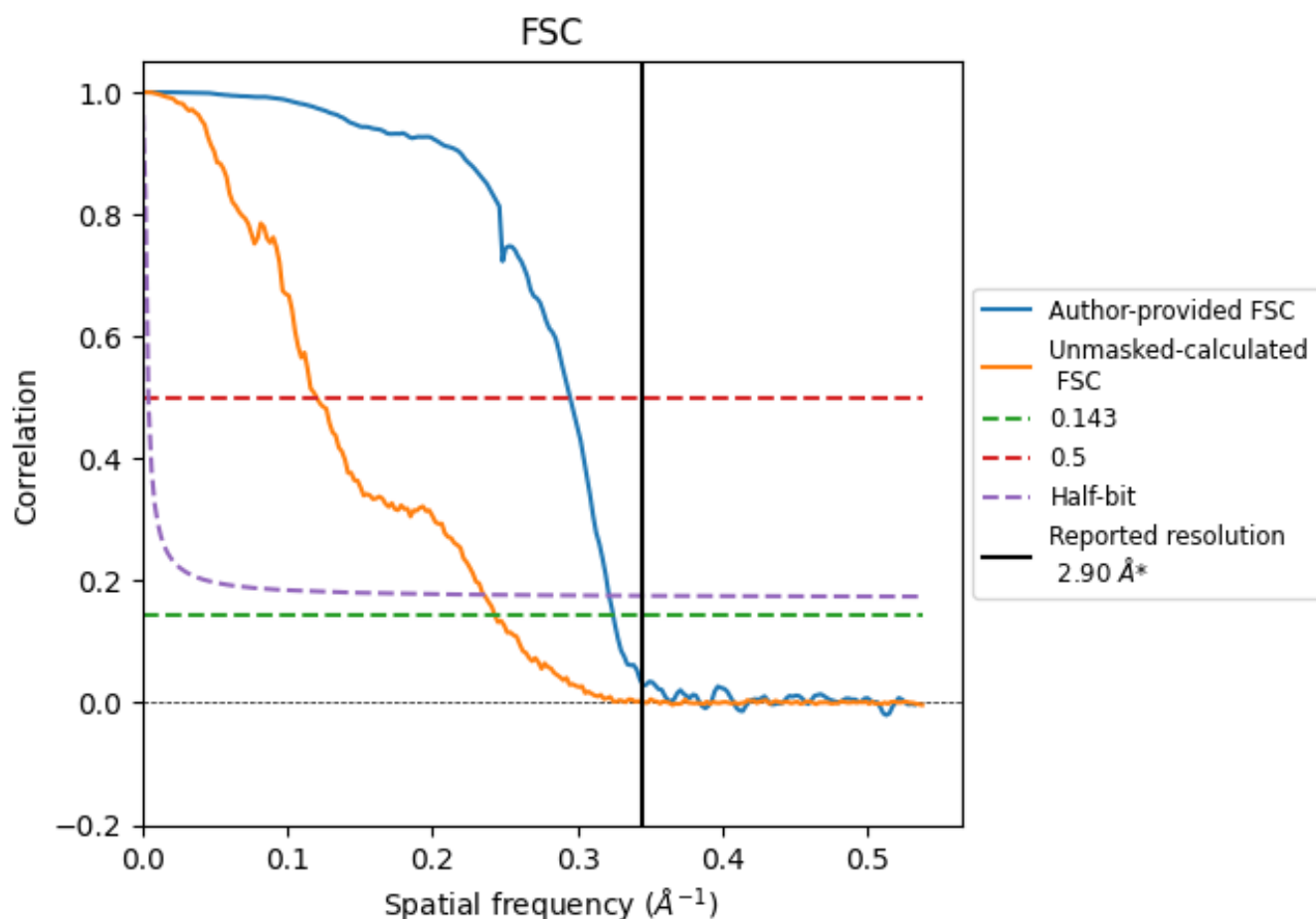


*Reported resolution corresponds to spatial frequency of 0.345 \AA^{-1}

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 0.345 \AA^{-1}

8.2 Resolution estimates [i](#)

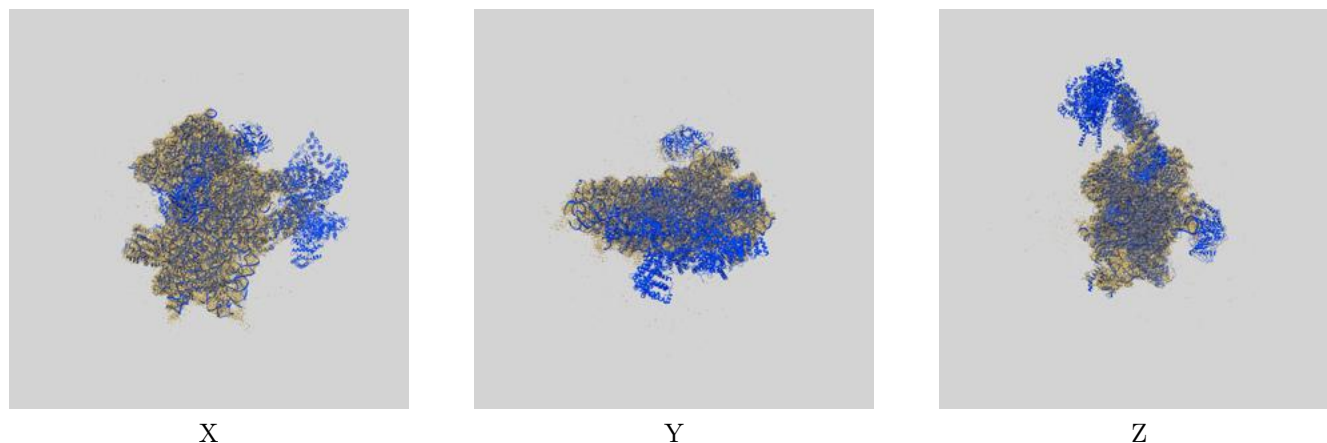
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	2.90
Author-provided FSC curve	3.08	3.39	3.11	-
Unmasked-calculated*	4.11	8.31	4.25	-

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

9 Map-model fit [i](#)

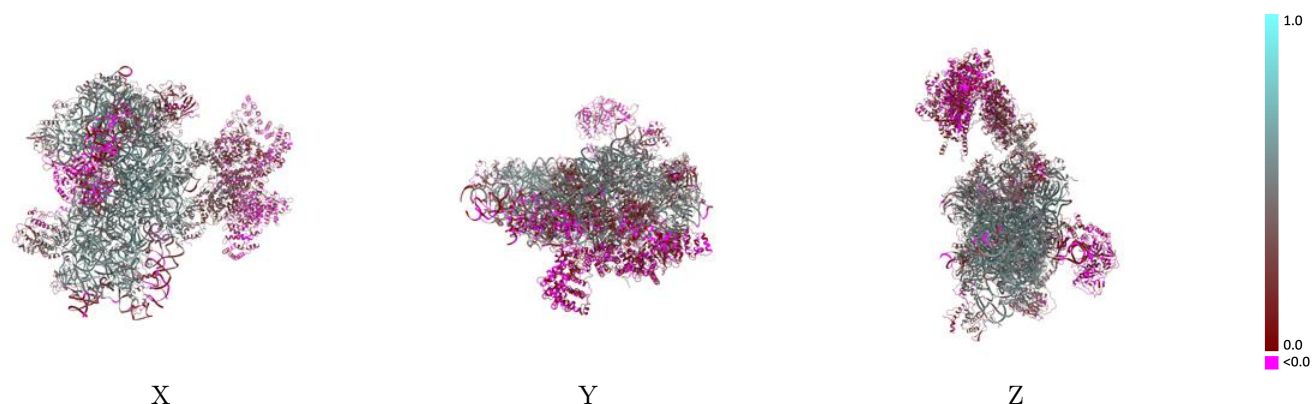
This section contains information regarding the fit between EMDB map EMD-51911 and PDB model 9H74. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



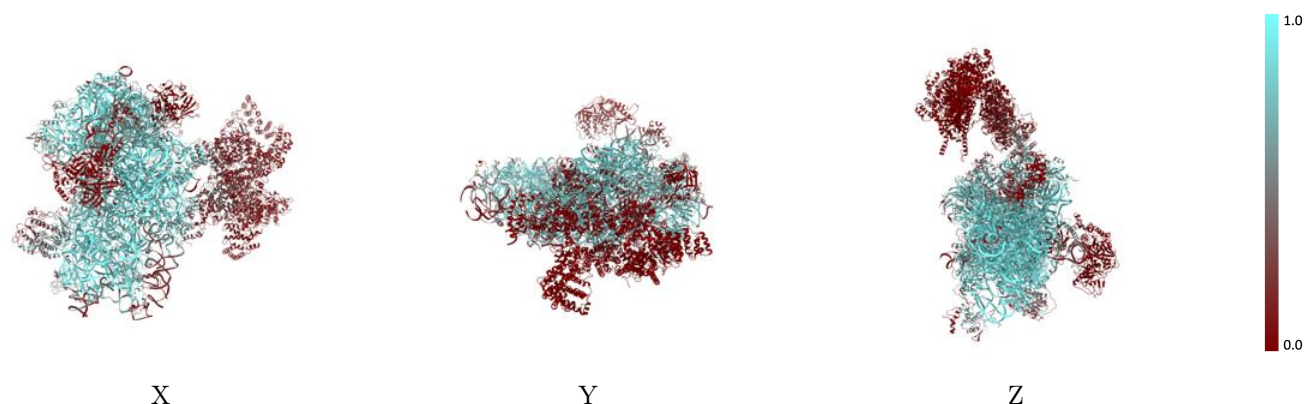
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



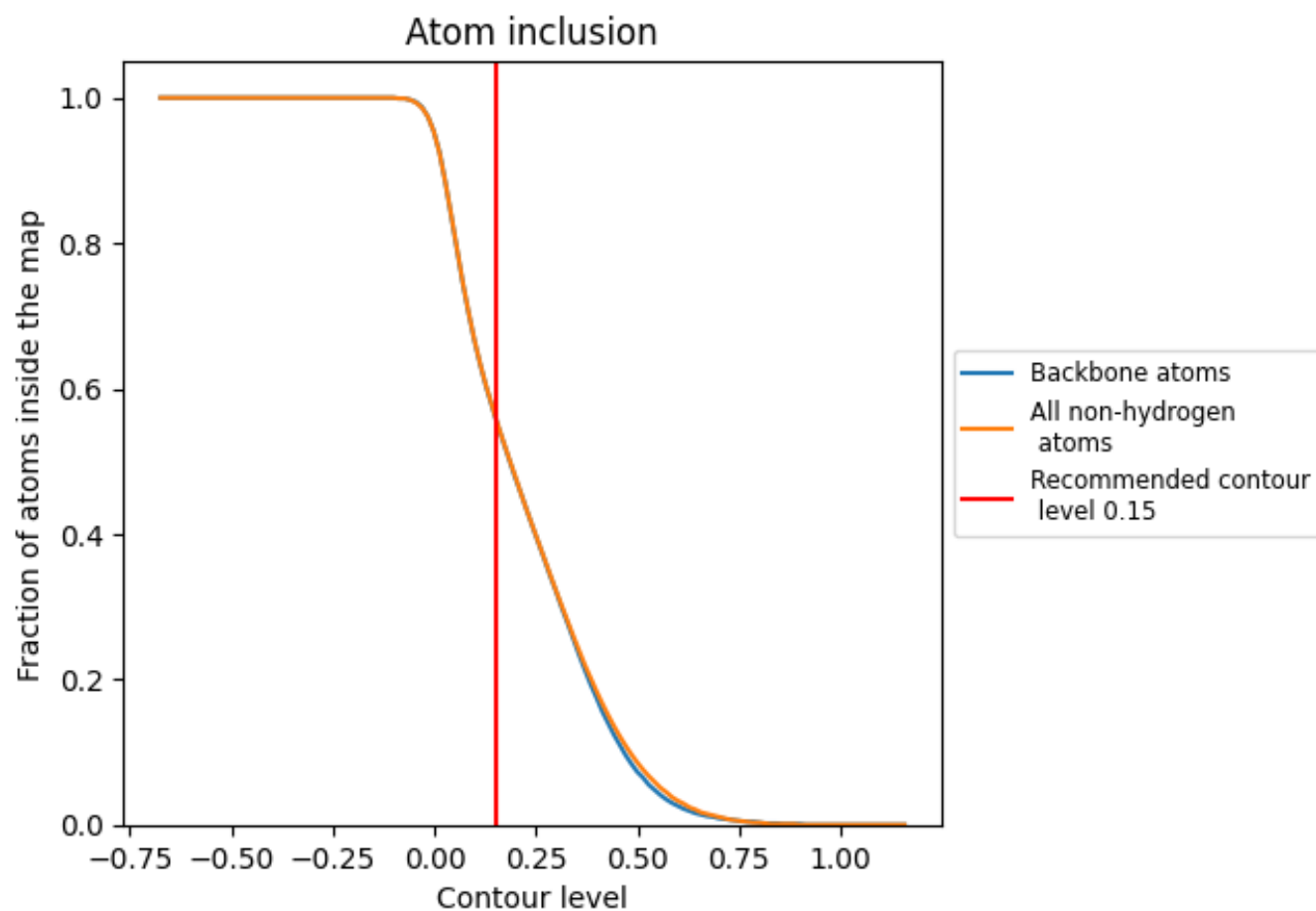
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 56% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5610	 0.3670
1	 0.4960	 0.2020
2	 0.8480	 0.4980
3	 0.9130	 0.5410
A	 0.3000	 0.1850
B	 0.0040	 0.0060
C	 0.7860	 0.4930
D	 0.7910	 0.4930
E	 0.7770	 0.5020
F	 0.7080	 0.4490
G	 0.7850	 0.4960
H	 0.8070	 0.5110
I	 0.6760	 0.4250
J	 0.5250	 0.3460
K	 0.7200	 0.4450
L	 0.7540	 0.4710
M	 0.7380	 0.4340
N	 0.7220	 0.4560
O	 0.3340	 0.2230
P	 0.7920	 0.5130
Q	 0.8030	 0.5080
R	 0.7270	 0.4470
S	 0.8470	 0.5260
T	 0.6530	 0.3960
U	 0.7650	 0.4660
V	 0.8170	 0.4950
W	 0.6620	 0.4290
X	 0.7620	 0.4710
Y	 0.8310	 0.5280
Z	 0.8410	 0.5270
a	 0.7640	 0.4680
b	 0.8260	 0.5210
c	 0.6540	 0.4210
d	 0.6730	 0.4740
e	 0.8550	 0.5200



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Chain	Atom inclusion	Q-score
f	 0.4840	 0.2900
g	 0.6920	 0.4170
i	 0.6730	 0.4140
j	 0.6450	 0.4300
k	 0.4420	 0.3270
l	 0.6800	 0.4310
m	 0.0510	 0.2610
n	 0.7030	 0.4330
o	 0.0580	 0.1640
q	 0.0010	 0.0770
r	 0.0000	 0.0880
s	 0.0000	 0.0220
t	 0.0000	 0.0450
u	 0.0010	 0.0650
v	 0.1930	 0.2730
w	 0.0030	 0.0380
y	 0.1700	 0.2600