



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 11:53 AM UTC

PDB ID : 9CPA / pdb_00009cpa
EMDB ID : EMD-3057
Title : Structure of a Mammalian DHX29-bound 43S Pre-initiation Complex
Authors : Cui, D.; des Georges, A.
Deposited on : 2024-07-18
Resolution : 6.00 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:

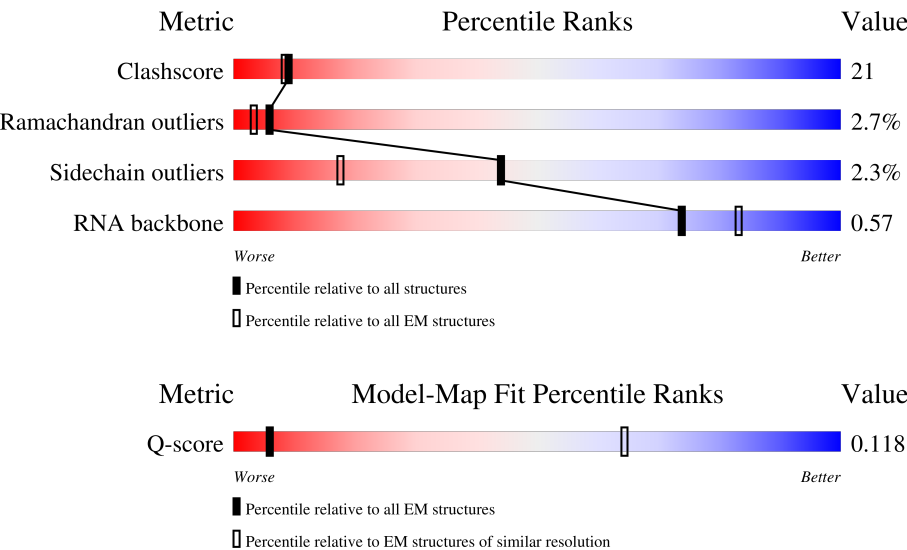
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13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

1 Overall quality at a glance i

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

The reported resolution of this entry is 6.00 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.



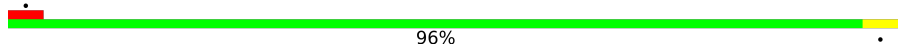
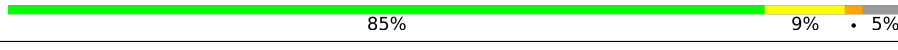
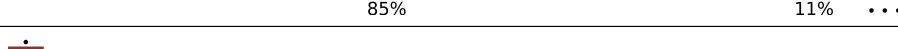
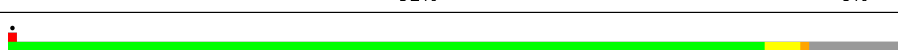
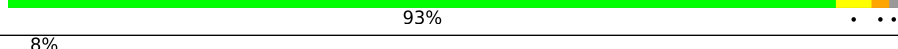
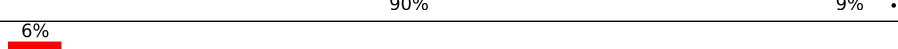
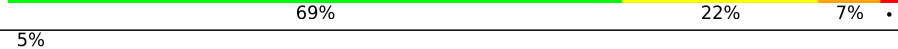
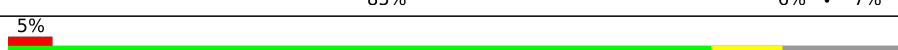
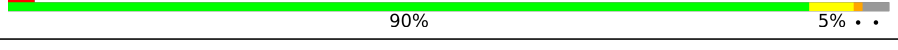
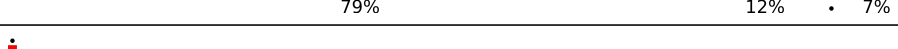
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	257 (8.50 - 9.50)

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	l	25	16% 100%
2	C	295	7% 64% 12% 24%
3	E	226	9% 94% 6%

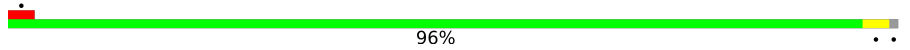
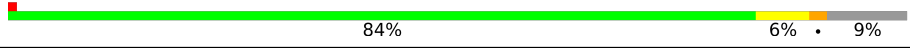
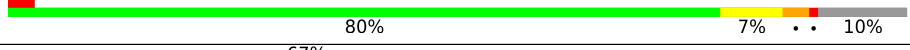
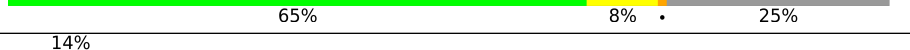
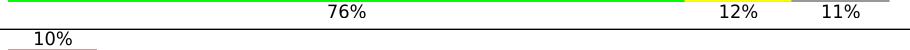
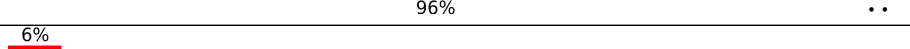
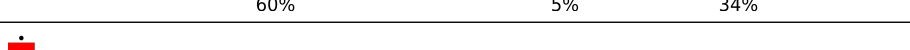
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Mol	Chain	Length	Quality of chain
4	G	263	
5	I	249	
6	J	194	
7	K	208	
8	L	194	
9	N	158	
10	P	151	
11	X	83	
12	Y	130	
13	Z	143	
14	a	133	
15	c	84	
16	i	133	
17	2	1863	
18	F	243	
19	H	219	
20	M	165	
21	O	132	
22	S	146	
23	T	135	
24	V	145	
25	W	119	
26	d	69	
27	e	56	
28	f	156	

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Mol	Chain	Length	Quality of chain
29	g	317	
30	n	124	
31	U	152	
32	R	145	
33	D	557	
34	y	1350	
35	q	364	
36	r	366	
37	s	218	
38	t	564	
39	u	374	
40	l	75	
41	A	284	
42	B	422	
43	p	814	
44	z	342	
45	x	264	
46	o	151	
47	Q	462	
48	j	320	
49	b	115	
50	k	913	
51	h	1369	

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
17	I2T	2	1244	-	-	X	-

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 129228 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 protein called eL41.

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

- Molecule 2 is a protein called uS2 (SA).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	225	Total	C	N	O	S	0	0
			1774	1125	310	331	8		

- Molecule 3 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 4 is a protein called 40S ribosomal protein S4.

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

- Molecule 5 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 6 is a protein called 40S ribosomal protein S7.

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

- Molecule 7 is a protein called Small ribosomal subunit protein eS8.

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

- Molecule 8 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	173	Total	C	N	O	S	0	0
			1450	925	289	234	2		

- Molecule 9 is a protein called Ribosomal protein S11.

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

- Molecule 10 is a protein called Ribosomal protein S13.

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

- Molecule 11 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	X	82	Total	C	N	O	S	0	0
			619	378	117	119	5		

- Molecule 12 is a protein called Ribosomal protein S15a.

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

- Molecule 13 is a protein called uS12.

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

- Molecule 14 is a protein called 40S ribosomal protein S24.

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

- Molecule 15 is a protein called 40S ribosomal protein S27.

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

- Molecule 16 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	i	54	Total	C	N	O	S	0	0
			437	271	96	69	1		

- Molecule 17 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	2	1863	Total	C	N	O	P	0	0
			39726	17732	7093	13039	1862		

- Molecule 18 is a protein called Ribosomal protein S3.

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

- Molecule 19 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 20 is a protein called S10_ plectin domain-containing protein.

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

- Molecule 21 is a protein called 40S ribosomal protein S12.

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

- Molecule 22 is a protein called uS9.

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 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 eS19.

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

- Molecule 25 is a protein called uS10.

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

- Molecule 26 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	68	Total	C	N	O	S	0	0
			520	317	103	98	2		

- Molecule 27 is a protein called eS29.

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

- Molecule 28 is a protein called Ribosomal protein S27a.

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

- Molecule 29 is a protein called RACK1.

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

- Molecule 30 is a protein called eS25.

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

- Molecule 31 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	139	Total	C	N	O	S	0	0
			1154	722	236	195	1		

- Molecule 32 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R	131	Total	C	N	O	S	0	0
			1083	688	205	183	7		

- Molecule 33 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	D	456	Total	C	N	O	S	0	0
			3666	2307	635	704	20		

- Molecule 34 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	y	656	Total	C	N	O	S	0	0
			5441	3429	979	1011	22		

- Molecule 35 is a protein called Eukaryotic translation initiation factor 3 subunit F.

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

- Molecule 36 is a protein called Eukaryotic translation initiation factor 3 subunit H.

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

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	29	GLY	LYS	conflict	UNP A0A5F9CZR4
r	30	GLY	PRO	conflict	UNP A0A5F9CZR4
r	31	SER	PHE	conflict	UNP A0A5F9CZR4
r	32	GLY	LEU	conflict	UNP A0A5F9CZR4
r	33	ASP	VAL	conflict	UNP A0A5F9CZR4
r	34	SER	ALA	conflict	UNP A0A5F9CZR4
r	35	ALA	TYR	conflict	UNP A0A5F9CZR4
r	38	GLN	PRO	conflict	UNP A0A5F9CZR4
r	39	VAL	CYS	conflict	UNP A0A5F9CZR4
r	40	GLN	PHE	conflict	UNP A0A5F9CZR4
r	41	ILE	SER	conflict	UNP A0A5F9CZR4
r	42	ASP	ARG	conflict	UNP A0A5F9CZR4
r	43	GLY	THR	conflict	UNP A0A5F9CZR4
r	44	LEU	ARG	conflict	UNP A0A5F9CZR4

- Molecule 37 is a protein called Eukaryotic translation initiation factor 3 subunit K.

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

- Molecule 38 is a protein called Eukaryotic translation initiation factor 3 subunit L.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	13	ALA	VAL	conflict	UNP G1SED9
t	53	LYS	ARG	conflict	UNP G1SED9
t	117	ALA	THR	conflict	UNP G1SED9
t	151	GLU	ALA	conflict	UNP G1SED9

- Molecule 39 is a protein called Eukaryotic translation initiation factor 3 subunit M.

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

- Molecule 40 is a RNA chain called initiator methionylated tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	1	75	Total	C	N	O	P	0	0
			1614	722	299	519	74		

- Molecule 41 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

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

- Molecule 42 is a protein called protein-synthesizing GTPase.

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

- Molecule 43 is a protein called eukaryotic translation initiation factor 3 subunit b.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	613	Total	C	N	O	S	0	0
			5034	3228	871	915	20		

- Molecule 44 is a protein called eukaryotic translation initiation factor 3 subunit i.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	342	Total	C	N	O	S	0	0
			2693	1711	443	530	9		

- Molecule 45 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	220	Total	C	N	O	S	0	0
			1757	1115	312	315	15		

- Molecule 46 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	0	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	447	Total	C	N	O	S	0	0
			3692	2358	626	687	21		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
48	j	77	Total	C	N	O	0	0
			379	225	77	77		

- Molecule 49 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	b	108	Total	C	N	O	S	0	0
			828	514	168	139	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	k	584	Total	C	N	O	S	0	0
			4699	2947	837	882	33		

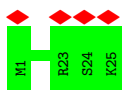
- Molecule 51 is a protein called ATP-dependent RNA helicase DHX29.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	h	1024	Total	C	N	O	0	0
			5070	3022	1024	1024		

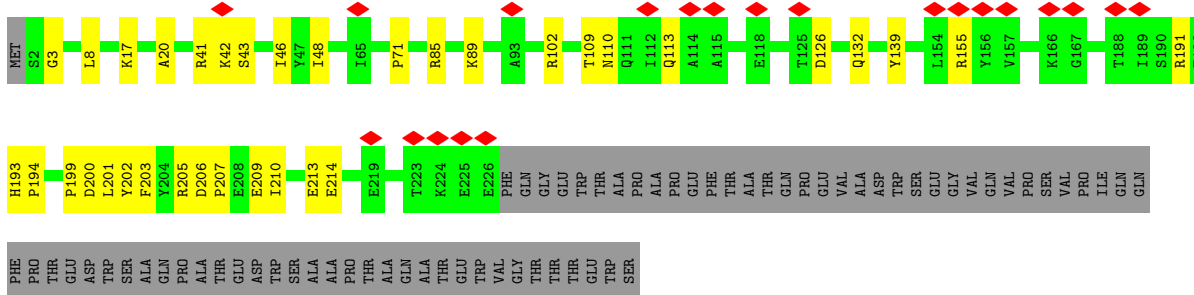
3 Residue-property plots

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: eL41



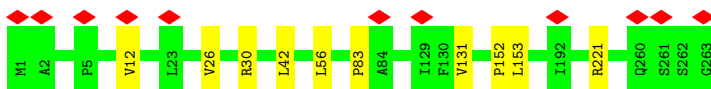
- Molecule 2: uS2 (SA)



- Molecule 3: Small ribosomal subunit protein uS5



- Molecule 4: 40S ribosomal protein S4



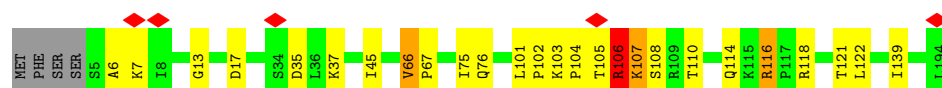
- Molecule 5: 40S ribosomal protein S6

Chain I:  85% 9% 5%

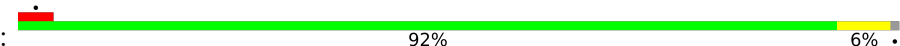


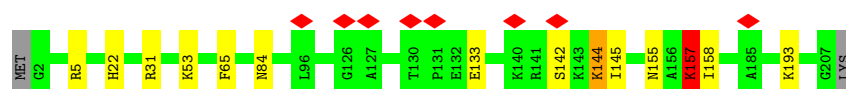
- Molecule 6: 40S ribosomal protein S7

Chain J:  85% 11% ...



- Molecule 7: Small ribosomal subunit protein eS8

Chain K:  92% 6% .

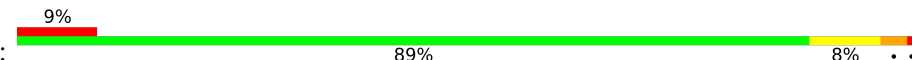


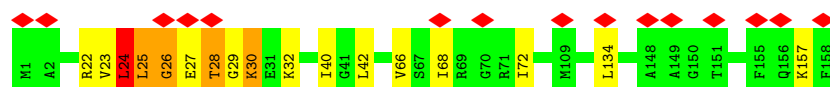
- Molecule 8: Ribosomal protein S9 (Predicted)

Chain L:  85% . . 11%



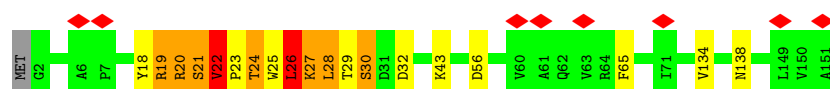
- Molecule 9: Ribosomal protein S11

Chain N:  9% 89% 8% . .



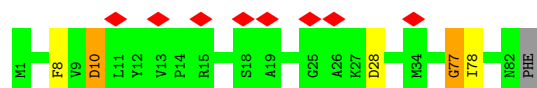
- Molecule 10: Ribosomal protein S13

Chain P:  5% 87% 7% 5% ..

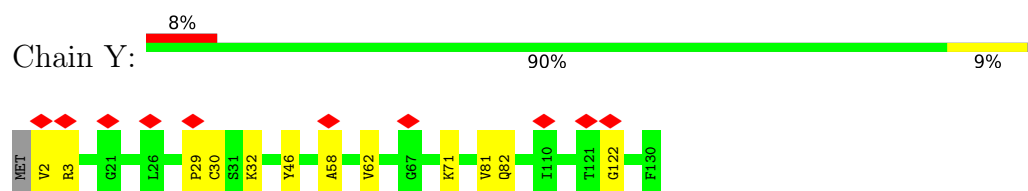


- Molecule 11: 40S ribosomal protein S21

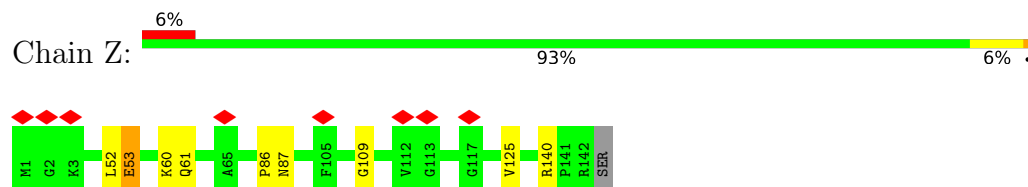
Chain X:  10% 93% . . .



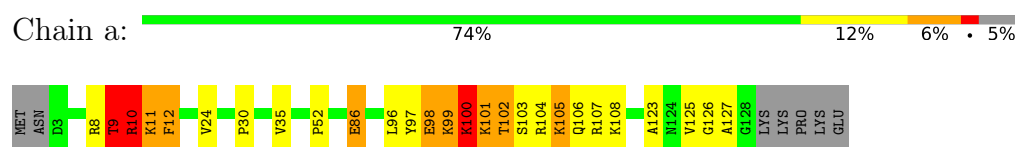
- Molecule 12: Ribosomal protein S15a



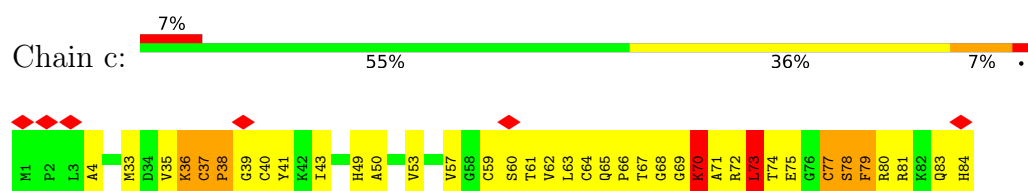
- Molecule 13: uS12



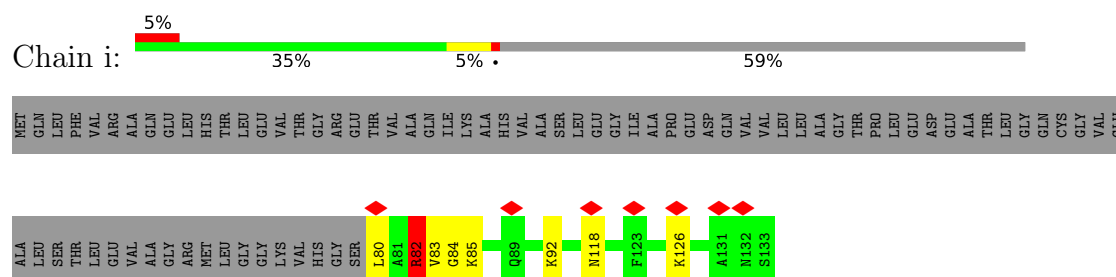
- Molecule 14: 40S ribosomal protein S24



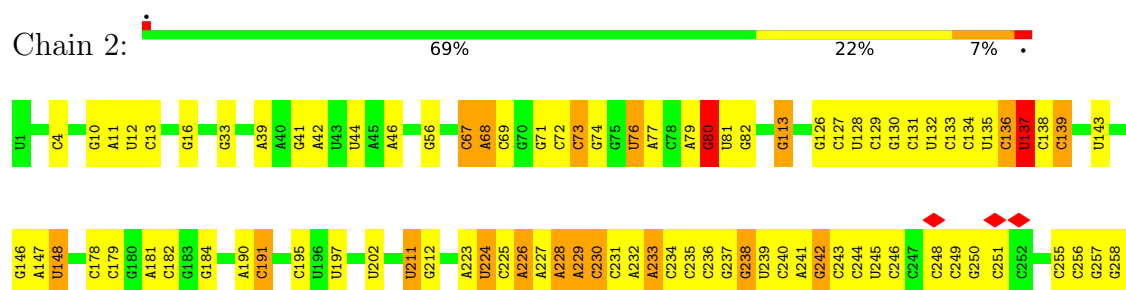
- Molecule 15: 40S ribosomal protein S27

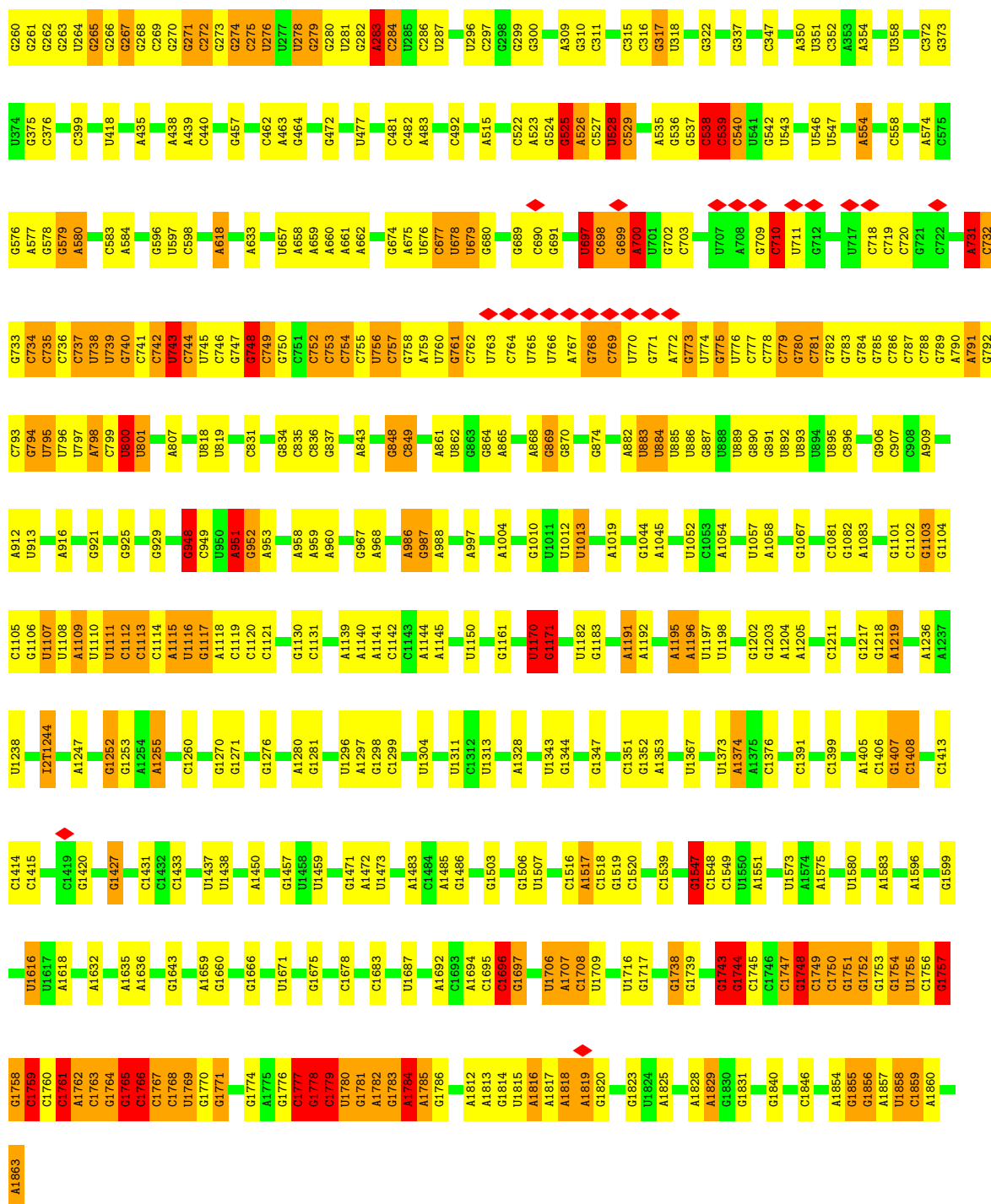


- Molecule 16: 40S ribosomal protein S30

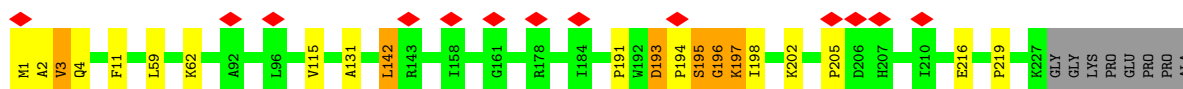
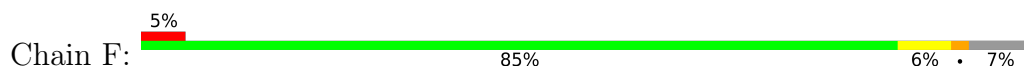


- Molecule 17: 18S ribosomal RNA





• Molecule 18: Ribosomal protein S3



MET
PRO
GLN
PRO
VAL
PRO
THR
ALA

- Molecule 19: Small ribosomal subunit protein uS7

Chain H: 

MET
ALA
THR
ALA
PRO
GLY
VAL
SER
ALA
VAL
GLN
ASP
ARG
LEU
THR
GLY
MET
THR
GLU
TRP
GLU
THR
ALA
ALA
PRO
ALA
VAL
ALA
GLU
T14
P15
D16
K22
D27
V28
Q29
I33
D37
Y38
I39
A40
V41
F61
N62
N63
Q64
E123
G129
R130
A131
G132
T133
V134
R135
V141
S184
L35
D194
R198
K201
R204

- Molecule 20: S10_pectin domain-containing protein

Chain M: 

M1
L2
M3
E34
L35
A36
P41
M42
L43
T72
L85
E88
P91
L94
R95
R96
S97
PRO
GLU
THR
GLY
ARG
PRO
ARG
PRO
LYS
GLY
LEU
GLU
GLY
ARG
PRO
ALA
ARG
LEU
THR
ARG
GLY
ALA
ASP
ARG
ASP
THR
TYR
ARG
ARG
SER
ALA
VAL
PRO
PRO
GLY
ALA
ASP
LYS
LYS
ALA
GLU
ALA
GLY
GLY
SER
THR
ALA
GLN
PHE
PHE
ARG
GLY
PHE
PHE
GLY
ARG
GLY
GLY
GLY
GLN
PRO
PRO
GLN

- Molecule 21: 40S ribosomal protein S12

Chain O: 

MET
ALA
GLU
SER
GLY
ILE
ALA
G9
L42
L52
N75
D81
L85
L91
C92
K93
I94
R96
E97
G98
K99
V103
S118
Q119
A120
K131
K132

- Molecule 22: uS9

Chain S: 

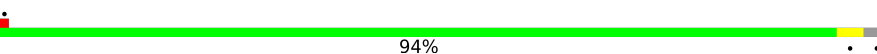
MET
PRO
SER
LYS
GLY
P6
I42
E43
P44
E45
T46
I88
V100
D101
R117
T118
P135
Y145
R146

- Molecule 23: eS17

Chain T: 

M1
G2
R3
R81
D82
N83
Y84
V85
P86
E87
V88
S89
A90
L91
D92
Q93
E94
I95
I96
T102
L117
Q118
V119
T120
Q121
P122
T123
V124
G125
M126
ASN
PHE
LYS
THR
PRO
ARG
GLY
ALA
VAL

- Molecule 24: eS19

Chain V: 

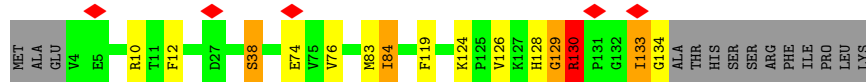
- Molecule 31: uS13

Chain U:  84% 6% 9%



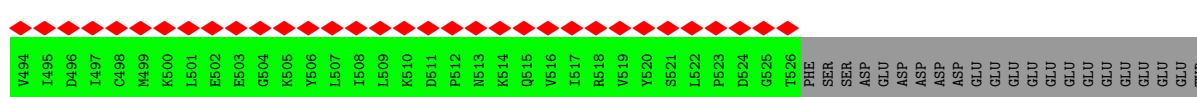
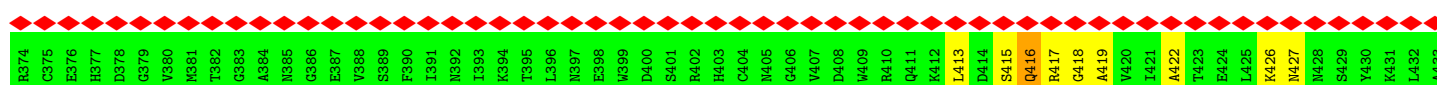
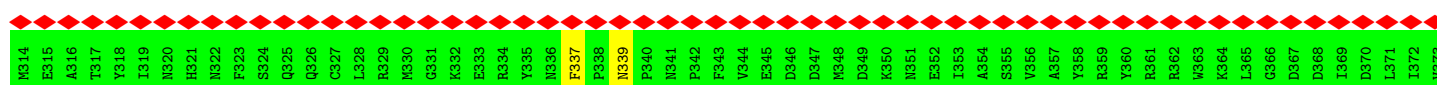
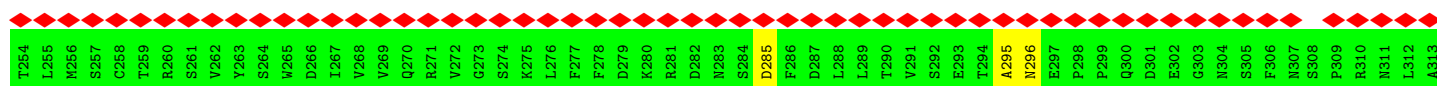
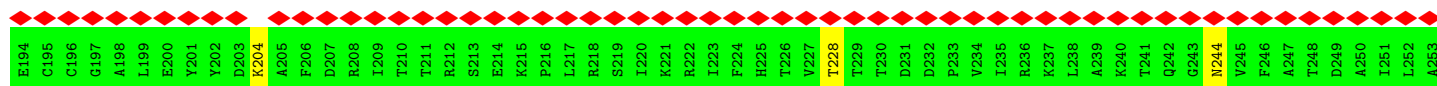
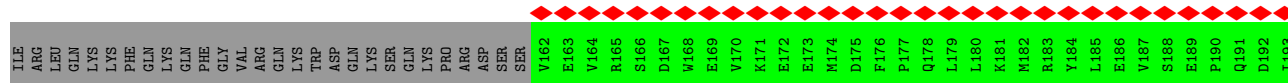
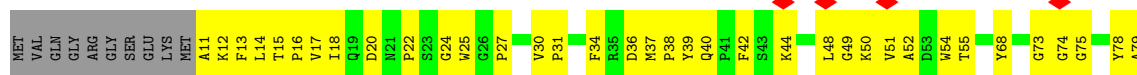
- Molecule 32: uS19

Chain R:  80% 7% 10%



- Molecule 33: Eukaryotic translation initiation factor 3 subunit D

Chain D:  67% 69% 12% 18%

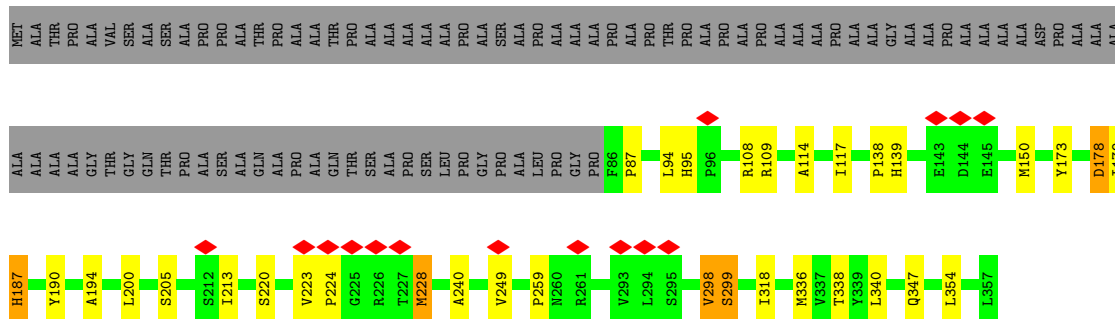


Chain y:

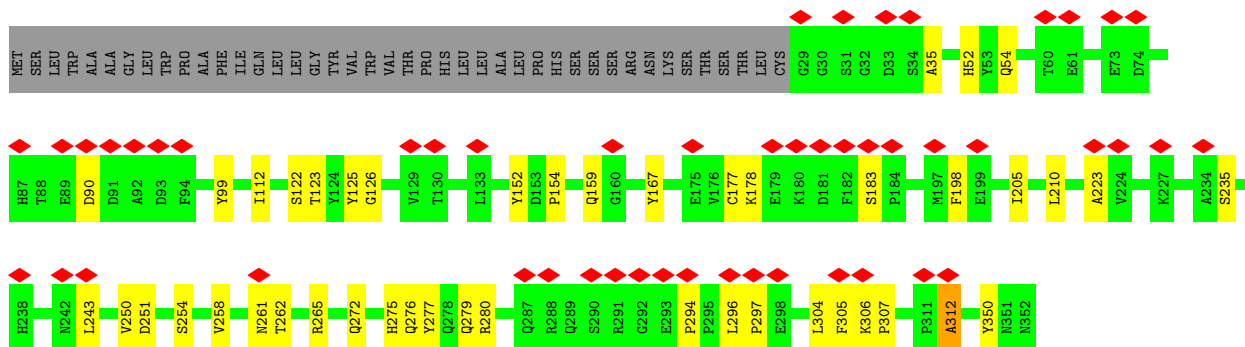
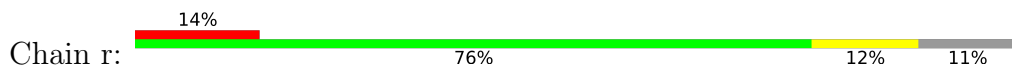




- Molecule 35: Eukaryotic translation initiation factor 3 subunit F



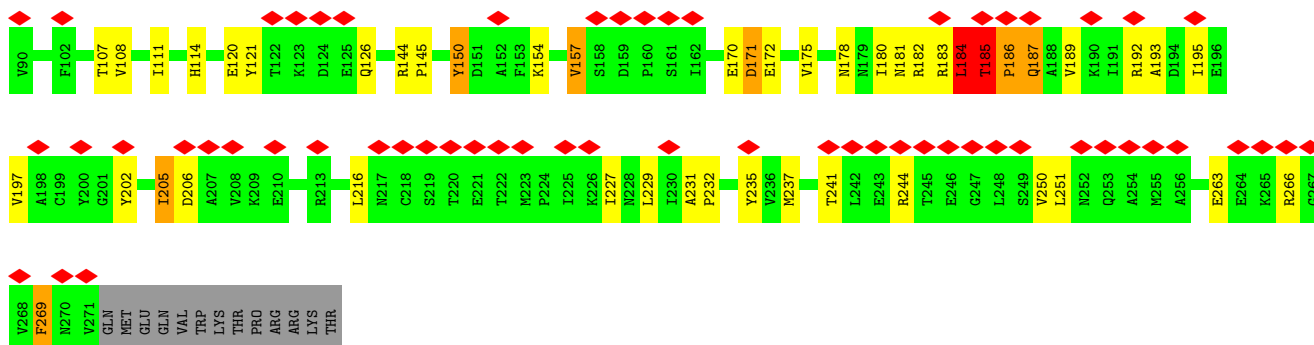
- Molecule 36: Eukaryotic translation initiation factor 3 subunit H



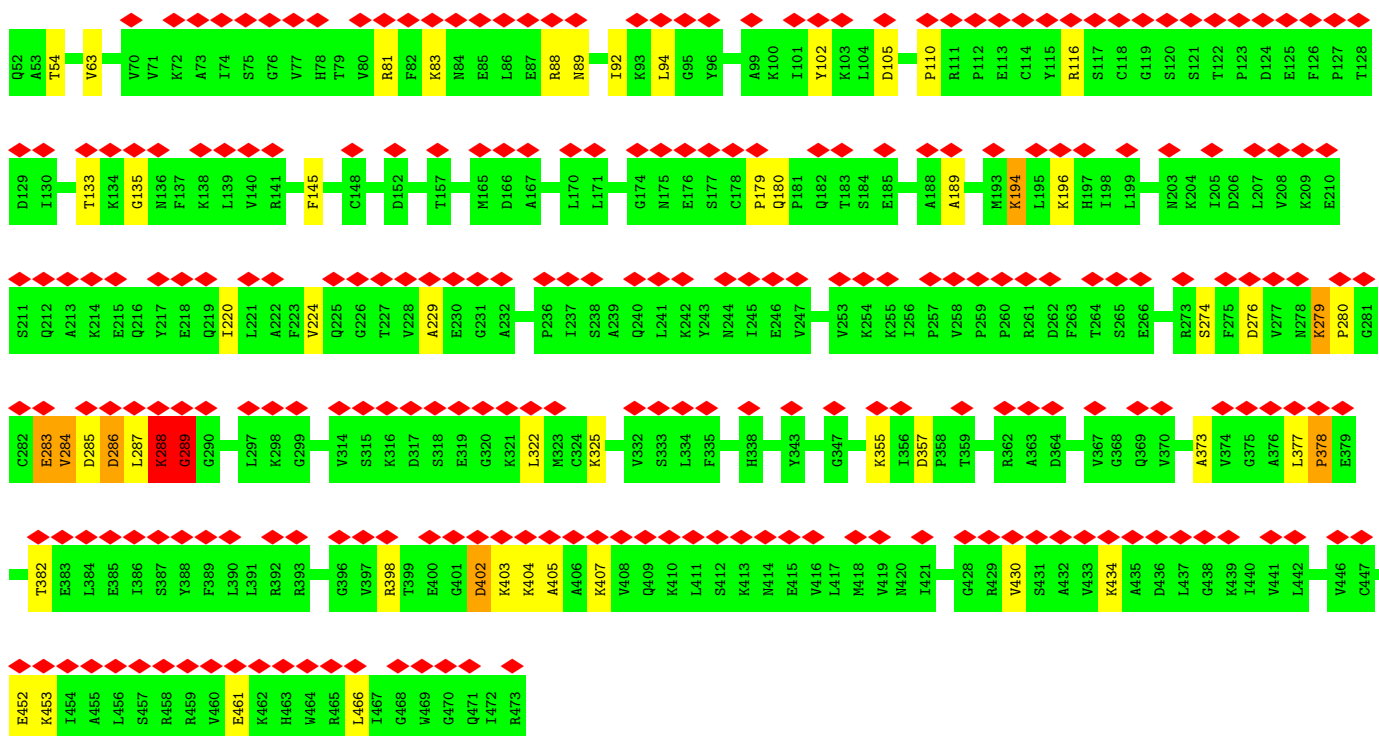
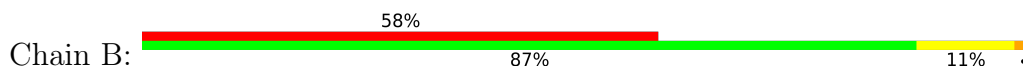
- Molecule 37: Eukaryotic translation initiation factor 3 subunit K



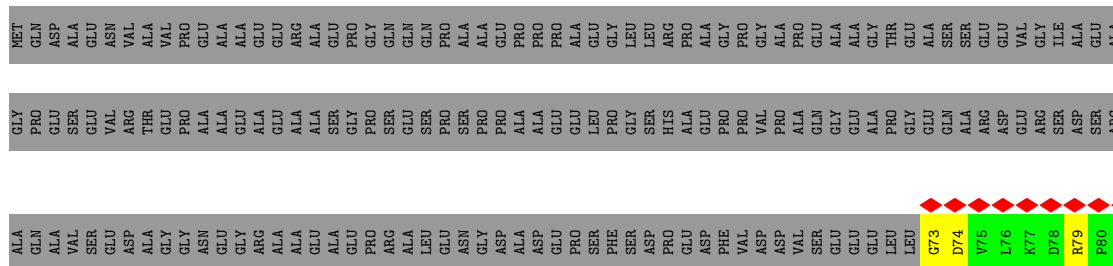


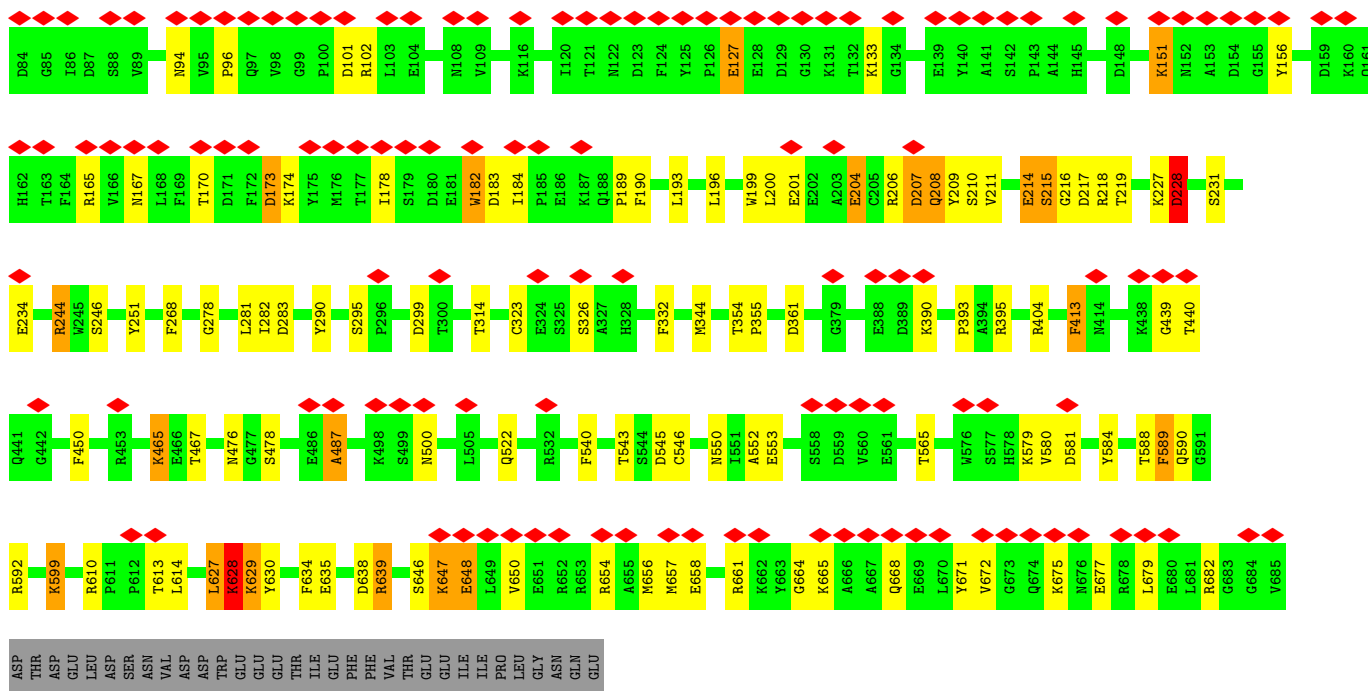


• Molecule 42: protein-synthesizing GTPase

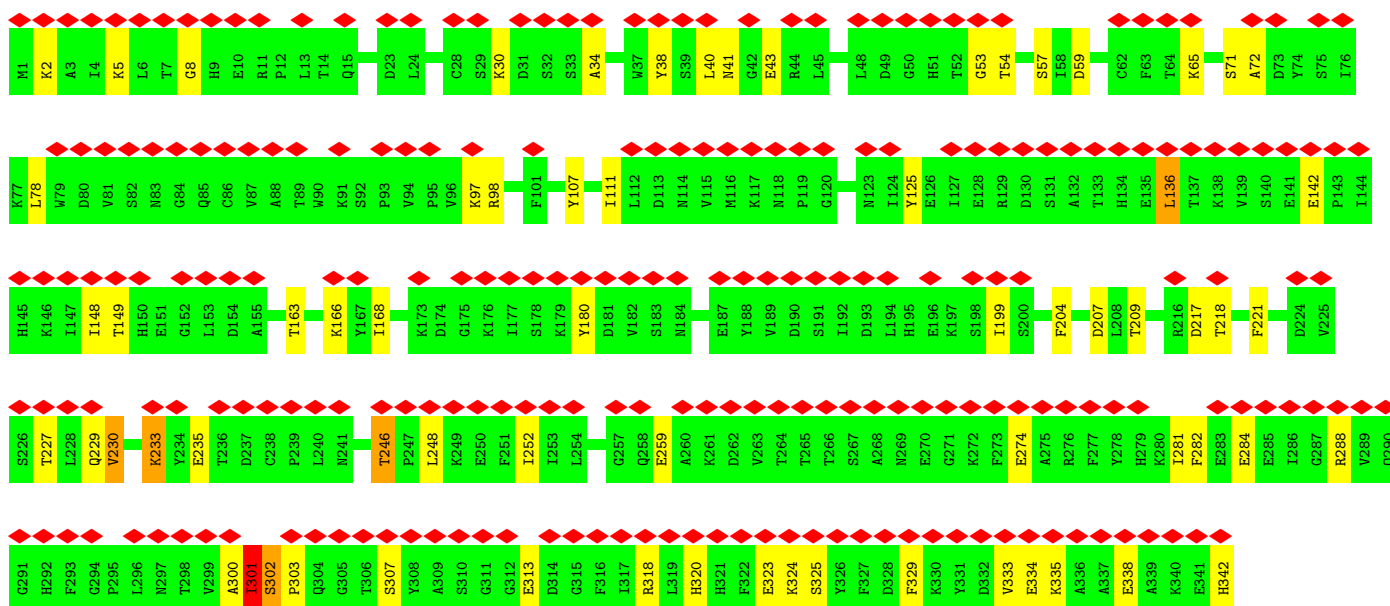
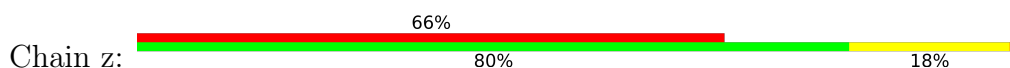


• Molecule 43: eukaryotic translation initiation factor 3 subunit b





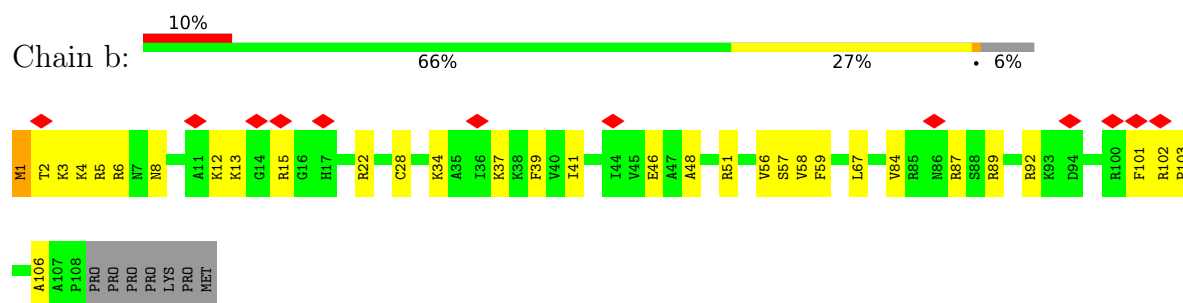
- Molecule 44: eukaryotic translation initiation factor 3 subunit i



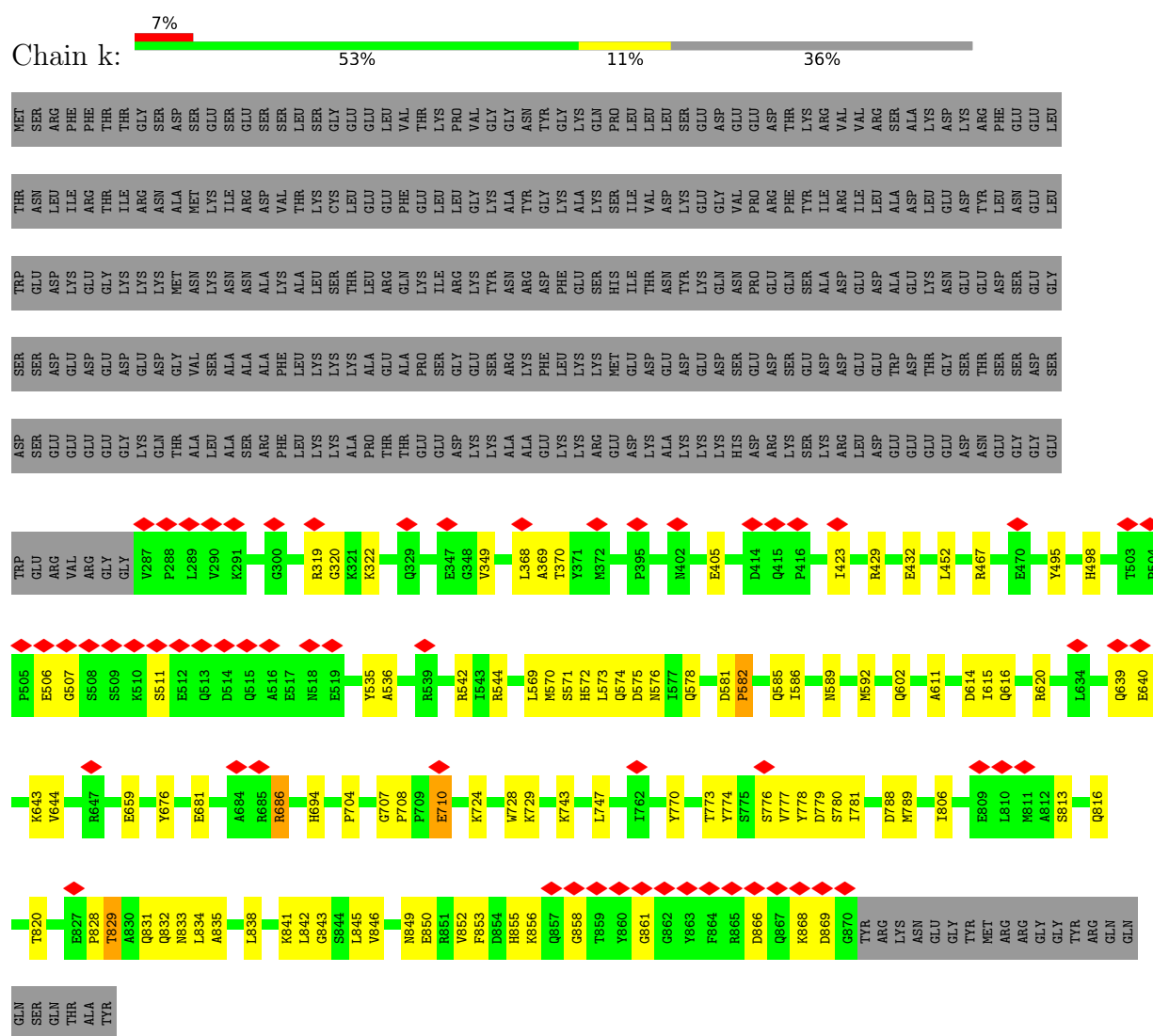
- Molecule 45: Small ribosomal subunit protein eS1



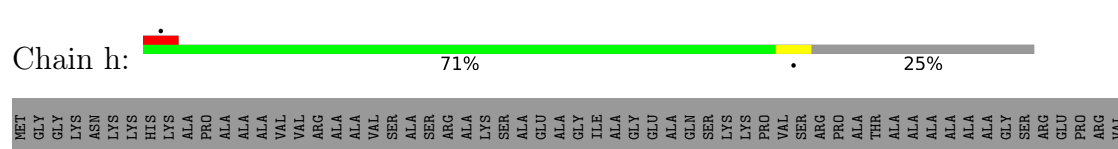
- Molecule 49: 40S ribosomal protein S26

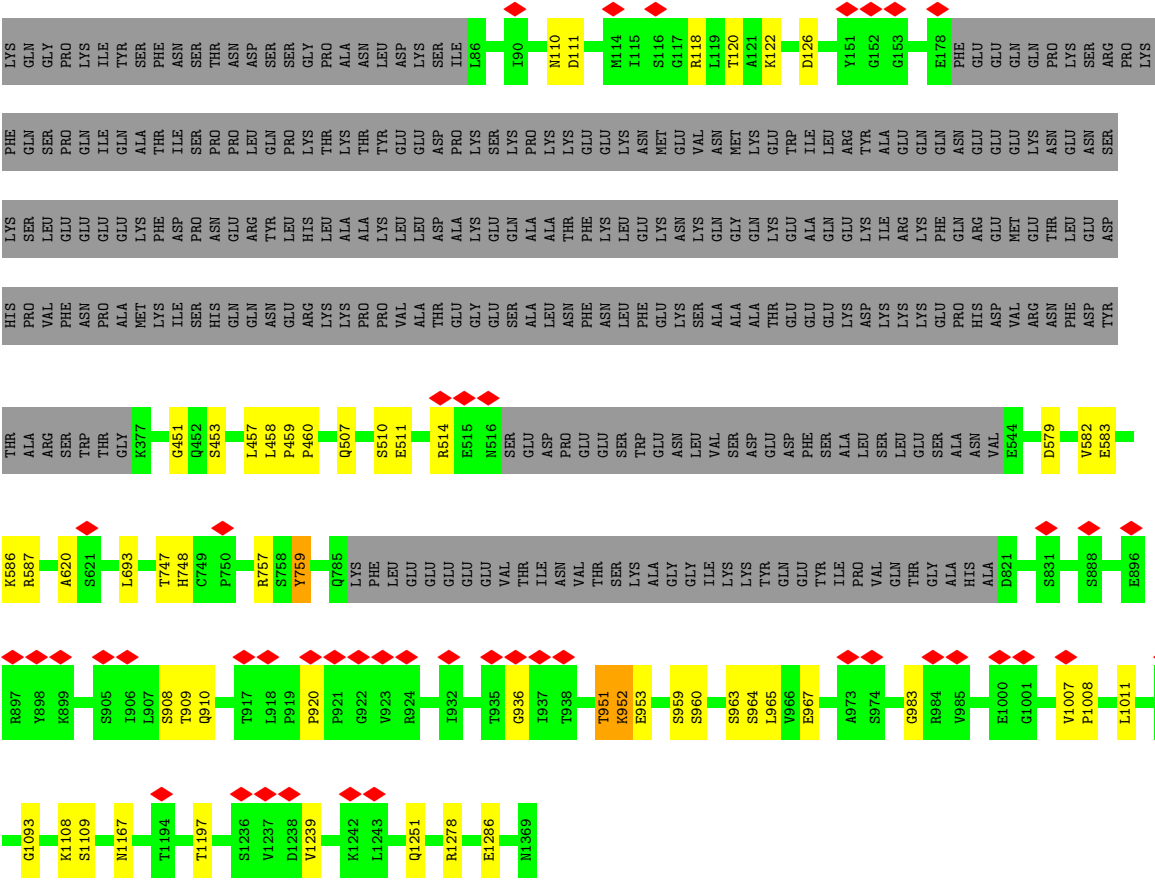


- Molecule 50: Eukaryotic translation initiation factor 3 subunit C



- Molecule 51: ATP-dependent RNA helicase DHX29





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84850	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	10000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	0.404	Depositor
Minimum map value	-0.263	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	498.0, 498.0, 498.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.66, 1.66, 1.66	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: T6A, I2T

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	I	1.60	0/241	1.35	0/305
2	C	1.20	0/1810	1.42	4/2455 (0.2%)
3	E	1.18	0/1779	1.34	4/2399 (0.2%)
4	G	1.26	0/2125	1.36	7/2856 (0.2%)
5	I	1.27	1/1946 (0.1%)	1.33	4/2590 (0.2%)
6	J	1.22	0/1553	1.43	6/2079 (0.3%)
7	K	1.29	0/1708	1.42	6/2278 (0.3%)
8	L	1.34	1/1474 (0.1%)	1.41	0/1969
9	N	1.23	0/1319	1.30	3/1761 (0.2%)
10	P	1.19	0/1232	1.43	3/1656 (0.2%)
11	X	1.42	1/626 (0.2%)	1.44	4/839 (0.5%)
12	Y	1.28	0/1051	1.40	2/1406 (0.1%)
13	Z	1.28	0/1124	1.35	0/1500
14	a	1.37	1/1038 (0.1%)	1.47	7/1380 (0.5%)
15	c	1.10	0/673	1.33	1/902 (0.1%)
16	i	1.36	0/441	1.36	2/579 (0.3%)
17	2	1.05	51/44370 (0.1%)	1.10	118/69138 (0.2%)
18	F	1.24	0/1792	1.36	5/2412 (0.2%)
19	H	1.25	0/1531	1.41	1/2059 (0.0%)
20	M	1.25	0/851	1.49	7/1147 (0.6%)
21	O	1.20	0/968	1.50	5/1296 (0.4%)
22	S	1.31	0/1142	1.45	6/1528 (0.4%)
23	T	1.25	0/1031	1.39	2/1383 (0.1%)
24	V	1.25	0/1132	1.45	4/1517 (0.3%)
25	W	1.29	0/832	1.37	0/1117
26	d	1.25	0/522	1.17	1/701 (0.1%)
27	e	1.35	0/455	1.46	3/603 (0.5%)
28	f	1.24	0/593	1.47	3/786 (0.4%)
29	g	1.23	0/2493	1.33	6/3394 (0.2%)
30	n	1.25	0/604	1.34	2/810 (0.2%)
31	U	1.33	0/1171	1.47	3/1564 (0.2%)
32	R	1.28	0/1103	1.44	8/1470 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	D	1.18	1/3748 (0.0%)	1.32	14/5074 (0.3%)
34	y	0.88	2/5534 (0.0%)	1.22	22/7461 (0.3%)
35	q	1.18	0/2149	1.46	15/2920 (0.5%)
36	r	1.19	0/2675	1.51	20/3609 (0.6%)
37	s	1.12	0/1772	1.41	3/2396 (0.1%)
38	t	1.18	0/3185	1.47	15/4296 (0.3%)
39	u	1.14	0/2963	1.52	20/3998 (0.5%)
40	l	1.43	8/1770 (0.5%)	1.29	11/2759 (0.4%)
41	A	0.98	3/2177 (0.1%)	1.50	11/2935 (0.4%)
42	B	1.19	2/3267 (0.1%)	1.46	24/4415 (0.5%)
43	p	0.87	2/5168 (0.0%)	1.59	56/6985 (0.8%)
44	z	1.30	10/2757 (0.4%)	1.19	8/3733 (0.2%)
45	x	1.14	0/1785	1.40	15/2392 (0.6%)
46	o	1.31	0/1029	1.45	4/1380 (0.3%)
47	Q	0.72	0/3770	1.13	2/5098 (0.0%)
48	j	1.47	2/378 (0.5%)	0.86	3/524 (0.6%)
49	b	0.78	0/840	1.19	1/1128 (0.1%)
50	k	0.84	1/4780 (0.0%)	1.35	4/6450 (0.1%)
51	h	0.88	3/5065 (0.1%)	1.30	12/7053 (0.2%)
All	All	1.11	89/135542 (0.1%)	1.29	487/192485 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	1
5	I	0	1
6	J	0	2
7	K	0	2
8	L	0	2
11	X	0	1
14	a	0	1
15	c	0	1
16	i	0	2
17	2	1	60
20	M	0	5
22	S	0	2
27	e	0	4
28	f	0	1
31	U	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
33	D	0	1
34	y	0	8
35	q	0	6
36	r	0	10
37	s	0	1
38	t	0	5
39	u	0	9
40	1	3	2
41	A	0	7
42	B	0	8
43	p	3	22
45	x	0	1
46	0	0	2
48	j	0	1
49	b	0	1
50	k	0	5
51	h	0	2
All	All	7	179

The worst 5 of 89 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	2	1195	A	O3'-P	-88.38	0.28	1.61
17	2	1696	C	O3'-P	-45.93	0.92	1.61
17	2	948	G	O3'-P	-42.09	0.98	1.61
51	h	951	THR	C-N	-39.71	0.78	1.33
48	j	271	ALA	C-N	-26.29	0.98	1.33

The worst 5 of 487 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	2	1195	A	P-O3'-C3'	-60.35	29.68	120.20
17	2	743	U	P-O3'-C3'	-40.58	59.33	120.20
17	2	800	U	P-O3'-C3'	-39.48	60.97	120.20
17	2	283	A	O3'-P-O5'	-38.98	45.53	104.00
17	2	731	A	OP1-P-O3'	-32.15	11.54	108.00

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
17	2	1784	A	C3'
40	1	17	C	C3',C2'

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Mol	Chain	Res	Type	Atom
40	1	18	G	C3'
43	p	211	VAL	CA
43	p	213	PHE	CA

5 of 179 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	193	HIS	Peptide
5	I	217	MET	Mainchain
6	J	105	THR	Peptide
6	J	66	VAL	Peptide
7	K	144	LYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	l	240	0	289	0	0
2	C	1774	0	1771	172	0
3	E	1743	0	1836	20	0
4	G	2083	0	2189	1	0
5	I	1923	0	2088	63	0
6	J	1530	0	1622	78	0
7	K	1679	0	1762	12	0
8	L	1450	0	1562	22	0
9	N	1296	0	1374	42	0
10	P	1208	0	1294	63	0
11	X	619	0	622	0	0
12	Y	1034	0	1080	25	0
13	Z	1106	0	1179	5	0
14	a	1021	0	1085	65	0
15	c	659	0	678	151	0
16	i	437	0	487	19	0
17	2	39726	0	20030	1607	0
18	F	1764	0	1863	25	0
19	H	1509	0	1563	61	0
20	M	827	0	852	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	O	958	0	993	1	0
22	S	1124	0	1193	24	0
23	T	1019	0	1074	155	0
24	V	1112	0	1149	0	0
25	W	822	0	887	0	0
26	d	520	0	536	84	0
27	e	445	0	442	1	0
28	f	581	0	599	1	0
29	g	2436	0	2393	0	0
30	n	598	0	656	0	0
31	U	1154	0	1206	48	0
32	R	1083	0	1144	12	0
33	D	3666	0	3528	387	0
34	y	5441	0	5501	1280	0
35	q	2111	0	2105	35	0
36	r	2624	0	2592	114	0
37	s	1737	0	1706	1	0
38	t	3109	0	3084	92	0
39	u	2918	0	2950	5	0
40	l	1614	0	822	94	0
41	A	2146	0	2188	219	0
42	B	3214	0	3353	48	0
43	p	5034	0	4948	345	0
44	z	2693	0	2608	123	0
45	x	1757	0	1806	87	0
46	o	1016	0	1038	90	0
47	Q	3692	0	3649	363	0
48	j	379	0	176	40	0
49	b	828	0	851	108	0
50	k	4699	0	4637	516	0
51	h	5070	0	2223	77	0
All	All	129228	0	107263	4713	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 21.

The worst 5 of 4713 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)
17:2:127:C:H2'	17:2:129:C:C6	1.20	1.68
35:q:336:MET:CE	47:Q:418:TYR:HE1	1.04	1.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:A:235:TYR:CD1	42:B:285:ASP:CG	1.77	1.64
34:y:246:TRP:CD1	50:k:707:GLY:HA3	1.20	1.63
34:y:710:ILE:CD1	43:p:613:THR:HG21	1.20	1.63

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	
1	l	23/25 (92%)	23 (100%)	0	0	100	100
2	C	221/295 (75%)	193 (87%)	21 (10%)	7 (3%)	3	21
3	E	224/226 (99%)	208 (93%)	14 (6%)	2 (1%)	14	50
4	G	261/263 (99%)	233 (89%)	24 (9%)	4 (2%)	8	39
5	I	235/249 (94%)	209 (89%)	23 (10%)	3 (1%)	9	42
6	J	188/194 (97%)	161 (86%)	18 (10%)	9 (5%)	2	16
7	K	204/208 (98%)	178 (87%)	20 (10%)	6 (3%)	3	23
8	L	171/194 (88%)	160 (94%)	9 (5%)	2 (1%)	10	44
9	N	156/158 (99%)	130 (83%)	22 (14%)	4 (3%)	4	25
10	P	148/151 (98%)	130 (88%)	11 (7%)	7 (5%)	2	16
11	X	80/83 (96%)	71 (89%)	7 (9%)	2 (2%)	4	26
12	Y	127/130 (98%)	117 (92%)	6 (5%)	4 (3%)	3	22
13	Z	140/143 (98%)	129 (92%)	7 (5%)	4 (3%)	3	23
14	a	124/133 (93%)	104 (84%)	10 (8%)	10 (8%)	1	9
15	c	82/84 (98%)	56 (68%)	16 (20%)	10 (12%)	0	4
16	i	52/133 (39%)	46 (88%)	6 (12%)	0	100	100
18	F	225/243 (93%)	202 (90%)	14 (6%)	9 (4%)	2	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	H	189/219 (86%)	169 (89%)	17 (9%)	3 (2%)	7	37
20	M	96/165 (58%)	74 (77%)	16 (17%)	6 (6%)	1	12
21	O	122/132 (92%)	105 (86%)	13 (11%)	4 (3%)	3	21
22	S	139/146 (95%)	126 (91%)	11 (8%)	2 (1%)	9	40
23	T	124/135 (92%)	112 (90%)	8 (6%)	4 (3%)	3	21
24	V	139/145 (96%)	128 (92%)	8 (6%)	3 (2%)	5	29
25	W	102/119 (86%)	93 (91%)	9 (9%)	0	100	100
26	d	66/69 (96%)	59 (89%)	6 (9%)	1 (2%)	8	39
27	e	51/56 (91%)	40 (78%)	7 (14%)	4 (8%)	1	9
28	f	69/156 (44%)	51 (74%)	12 (17%)	6 (9%)	0	8
29	g	311/317 (98%)	273 (88%)	33 (11%)	5 (2%)	7	37
30	n	73/124 (59%)	69 (94%)	3 (4%)	1 (1%)	9	40
31	U	135/152 (89%)	119 (88%)	12 (9%)	4 (3%)	3	22
32	R	129/145 (89%)	107 (83%)	13 (10%)	9 (7%)	1	11
33	D	452/557 (81%)	422 (93%)	26 (6%)	4 (1%)	14	50
34	y	652/1350 (48%)	508 (78%)	85 (13%)	59 (9%)	0	8
35	q	270/364 (74%)	226 (84%)	32 (12%)	12 (4%)	2	17
36	r	322/366 (88%)	267 (83%)	42 (13%)	13 (4%)	2	18
37	s	213/218 (98%)	201 (94%)	10 (5%)	2 (1%)	14	50
38	t	370/564 (66%)	329 (89%)	37 (10%)	4 (1%)	11	46
39	u	363/374 (97%)	308 (85%)	47 (13%)	8 (2%)	5	29
41	A	264/284 (93%)	233 (88%)	25 (10%)	6 (2%)	5	28
42	B	420/422 (100%)	352 (84%)	48 (11%)	20 (5%)	2	16
43	p	611/814 (75%)	534 (87%)	56 (9%)	21 (3%)	3	21
44	z	340/342 (99%)	323 (95%)	16 (5%)	1 (0%)	36	72
45	x	218/264 (83%)	186 (85%)	24 (11%)	8 (4%)	2	19
46	0	134/151 (89%)	119 (89%)	12 (9%)	3 (2%)	5	29
47	Q	445/462 (96%)	440 (99%)	5 (1%)	0	100	100
48	j	75/320 (23%)	68 (91%)	7 (9%)	0	100	100
49	b	106/115 (92%)	99 (93%)	5 (5%)	2 (2%)	6	32
50	k	580/913 (64%)	560 (97%)	17 (3%)	3 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	h	1014/1369 (74%)	982 (97%)	26 (3%)	6 (1%)	21	59
All	All	11255/14241 (79%)	10032 (89%)	916 (8%)	307 (3%)	6	25

5 of 307 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	191	ARG
6	J	106	ARG
7	K	158	ILE
8	L	148	ILE
9	N	66	VAL

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	
1	l	24/24 (100%)	24 (100%)	0	100	100
2	C	187/244 (77%)	185 (99%)	2 (1%)	65	76
3	E	187/187 (100%)	187 (100%)	0	100	100
4	G	225/225 (100%)	225 (100%)	0	100	100
5	I	207/218 (95%)	207 (100%)	0	100	100
6	J	170/174 (98%)	169 (99%)	1 (1%)	78	82
7	K	177/179 (99%)	175 (99%)	2 (1%)	65	76
8	L	155/168 (92%)	154 (99%)	1 (1%)	78	82
9	N	142/142 (100%)	138 (97%)	4 (3%)	38	60
10	P	130/131 (99%)	125 (96%)	5 (4%)	29	50
11	X	67/68 (98%)	67 (100%)	0	100	100
12	Y	112/113 (99%)	112 (100%)	0	100	100
13	Z	114/115 (99%)	114 (100%)	0	100	100
14	a	108/115 (94%)	102 (94%)	6 (6%)	19	40
15	c	76/76 (100%)	72 (95%)	4 (5%)	20	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	i	45/106 (42%)	43 (96%)	2 (4%)	25	47
18	F	190/202 (94%)	189 (100%)	1 (0%)	81	83
19	H	161/181 (89%)	160 (99%)	1 (1%)	78	82
20	M	89/136 (65%)	89 (100%)	0	100	100
21	O	104/108 (96%)	101 (97%)	3 (3%)	37	58
22	S	117/121 (97%)	116 (99%)	1 (1%)	70	78
23	T	114/121 (94%)	114 (100%)	0	100	100
24	V	113/116 (97%)	113 (100%)	0	100	100
25	W	94/107 (88%)	94 (100%)	0	100	100
26	d	56/62 (90%)	54 (96%)	2 (4%)	31	52
27	e	47/49 (96%)	44 (94%)	3 (6%)	16	37
28	f	64/140 (46%)	64 (100%)	0	100	100
29	g	272/275 (99%)	272 (100%)	0	100	100
30	n	66/102 (65%)	66 (100%)	0	100	100
31	U	120/132 (91%)	120 (100%)	0	100	100
32	R	118/130 (91%)	116 (98%)	2 (2%)	53	69
33	D	400/501 (80%)	397 (99%)	3 (1%)	73	80
34	y	605/1233 (49%)	518 (86%)	87 (14%)	3	13
35	q	239/282 (85%)	237 (99%)	2 (1%)	73	80
36	r	293/329 (89%)	293 (100%)	0	100	100
37	s	190/193 (98%)	190 (100%)	0	100	100
38	t	342/515 (66%)	341 (100%)	1 (0%)	86	85
39	u	327/335 (98%)	323 (99%)	4 (1%)	63	75
41	A	238/255 (93%)	232 (98%)	6 (2%)	42	62
42	B	354/354 (100%)	337 (95%)	17 (5%)	23	44
43	p	547/698 (78%)	528 (96%)	19 (4%)	32	53
44	z	297/297 (100%)	284 (96%)	13 (4%)	25	47
45	x	194/231 (84%)	188 (97%)	6 (3%)	35	56
46	0	106/119 (89%)	106 (100%)	0	100	100
47	Q	408/423 (96%)	401 (98%)	7 (2%)	53	69
49	b	86/99 (87%)	85 (99%)	1 (1%)	63	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	k	511/812 (63%)	506 (99%)	5 (1%)	68	78
All	All	8988/10943 (82%)	8777 (98%)	211 (2%)	44	64

5 of 211 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	y	341	LEU
42	B	81	ARG
47	Q	54	LEU
34	y	350	GLU
35	q	187	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 183 such sidechains are listed below:

Mol	Chain	Res	Type
36	r	212	ASN
41	A	114	HIS
36	r	279	GLN
38	t	366	GLN
43	p	597	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
17	2	1857/1863 (99%)	294 (15%)	20 (1%)
40	1	74/75 (98%)	13 (17%)	3 (4%)
All	All	1931/1938 (99%)	307 (15%)	23 (1%)

5 of 307 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
17	2	4	C
17	2	33	G
17	2	41	G
17	2	42	A
17	2	44	U

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	2	1696	C
17	2	1767	C
17	2	1765	G
17	2	1784	A
17	2	699	G

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	$\# Z > 2$
40	T6A	1	37	40	31,34,35	1.42	4 (12%)	43,49,52	2.52	18 (41%)
17	I2T	2	1244	17	25,29,30	1.06	2 (8%)	28,42,45	2.92	2 (7%)

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
40	T6A	1	37	40	-	6/23/41/42	0/3/3/3
17	I2T	2	1244	17	-	9/16/34/35	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	1	37	T6A	C5-C4	4.75	1.47	1.39
17	2	1244	I2T	C4-C5	-3.55	1.39	1.47
40	1	37	T6A	C5-C6	2.82	1.48	1.41
40	1	37	T6A	C5-N7	-2.32	1.34	1.39
40	1	37	T6A	C8-N7	2.23	1.36	1.31

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	2	1244	I2T	C1'-C5-C4	14.48	139.59	117.61
40	1	37	T6A	C12-N11-C10	8.53	136.19	121.99
40	1	37	T6A	C5-C4-N3	-5.54	119.09	126.72
40	1	37	T6A	N3-C4-N9	4.47	134.76	127.17
40	1	37	T6A	C14-C12-C13	3.74	116.55	110.03

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	2	1244	I2T	C32-C31-N3-C2
17	2	1244	I2T	C32-C31-N3-C4
17	2	1244	I2T	C31-C32-C33-C34
17	2	1244	I2T	C31-C32-C33-N34
40	1	37	T6A	C14-C12-N11-C10

There are no ring outliers.

2 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
40	1	37	T6A	1	0
17	2	1244	I2T	22	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
17	2	19
51	h	2
40	1	2
48	j	2
50	k	1
2	C	1
31	U	1
14	a	1

The worst 5 of 29 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	716:G	O3'	717:U	P	4.79
1	2	776:U	O3'	777:C	P	4.39
1	h	458:LEU	C	459:PRO	N	4.33
1	2	698:C	O3'	699:G	P	4.26
1	k	859:THR	C	860:TYR	N	4.22

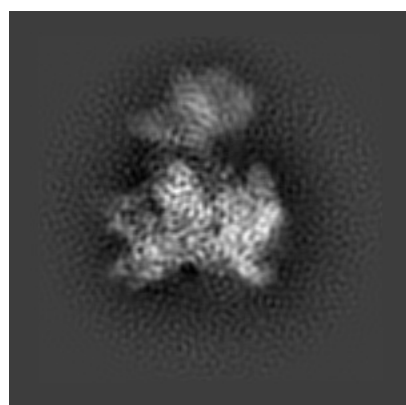
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3057. These allow visual inspection of the internal detail of the map and identification of artifacts.

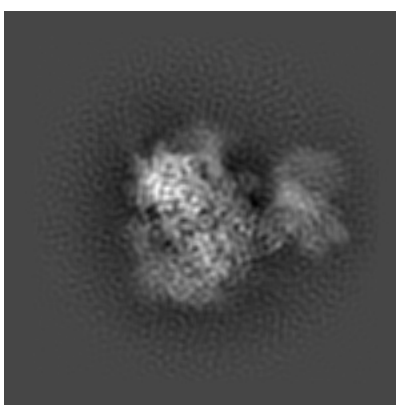
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

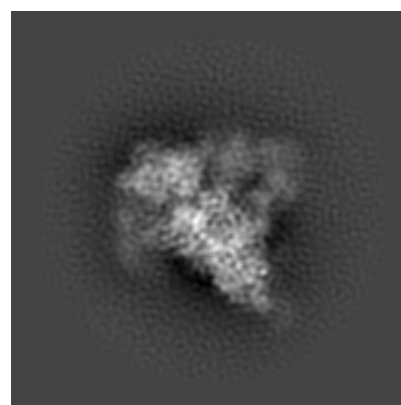
6.1.1 Primary map



X



Y

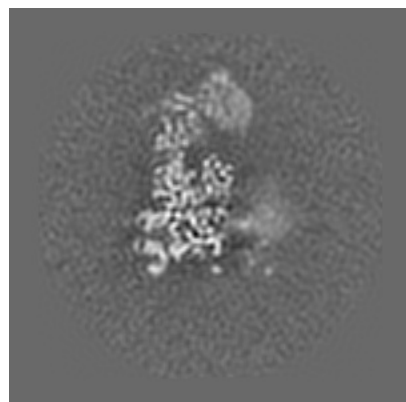


Z

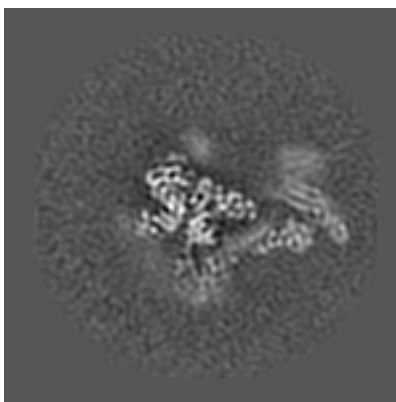
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

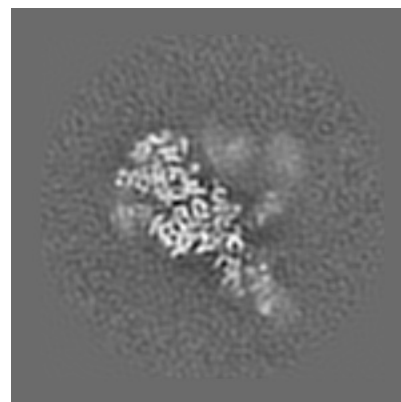
6.2.1 Primary map



X Index: 150



Y Index: 150

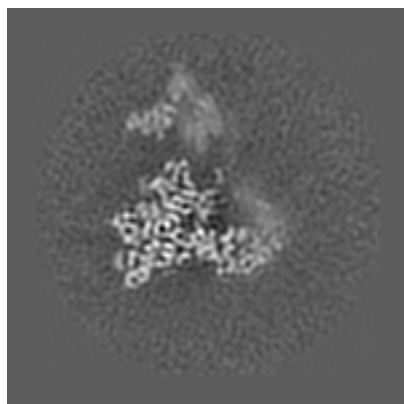


Z Index: 150

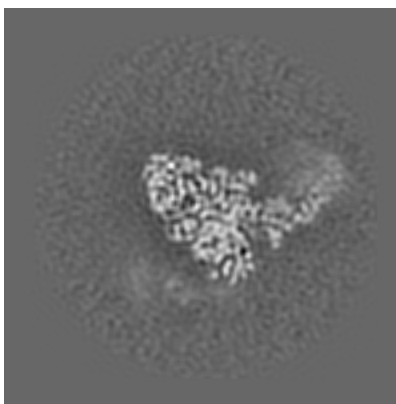
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

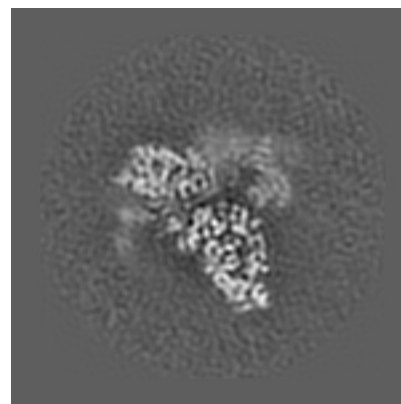
6.3.1 Primary map



X Index: 164



Y Index: 127

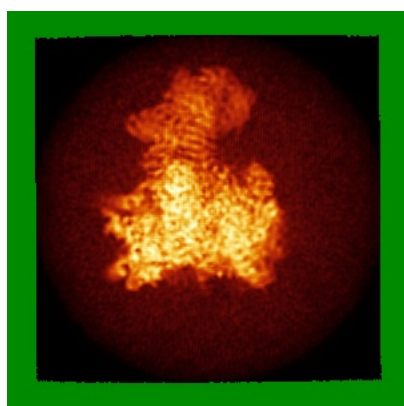


Z Index: 136

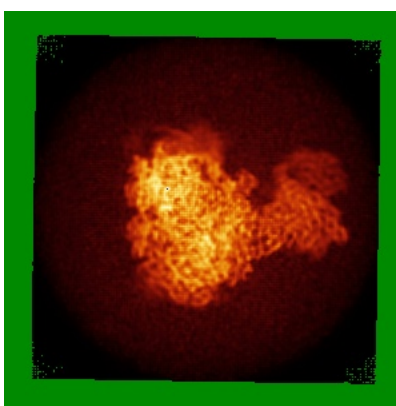
The images above show the largest variance slices of the map in three orthogonal directions.

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

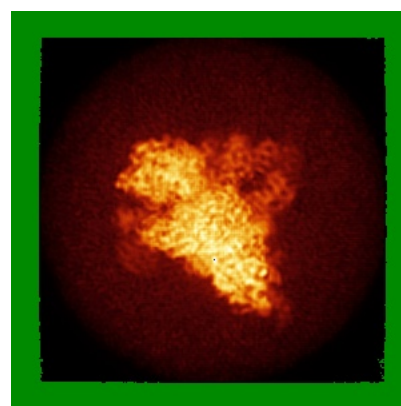
6.4.1 Primary map



X



Y

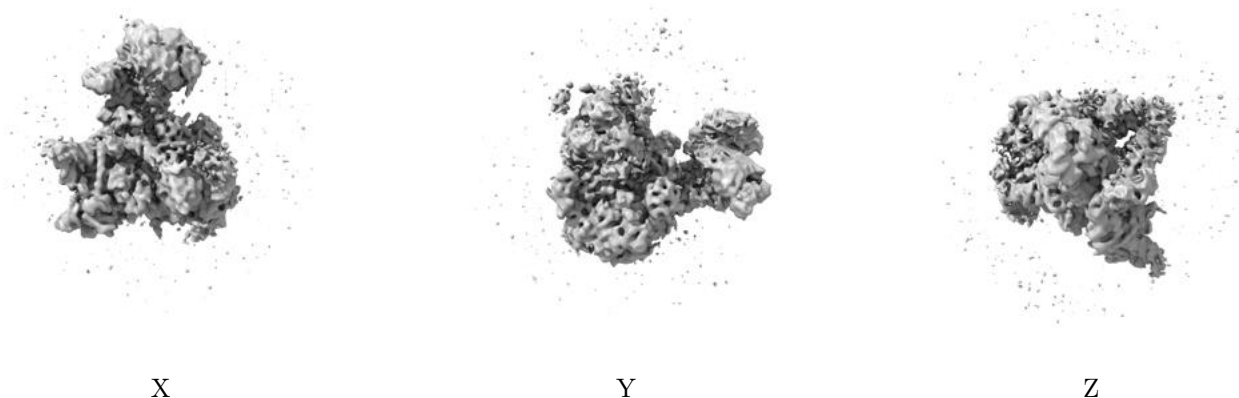


Z

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

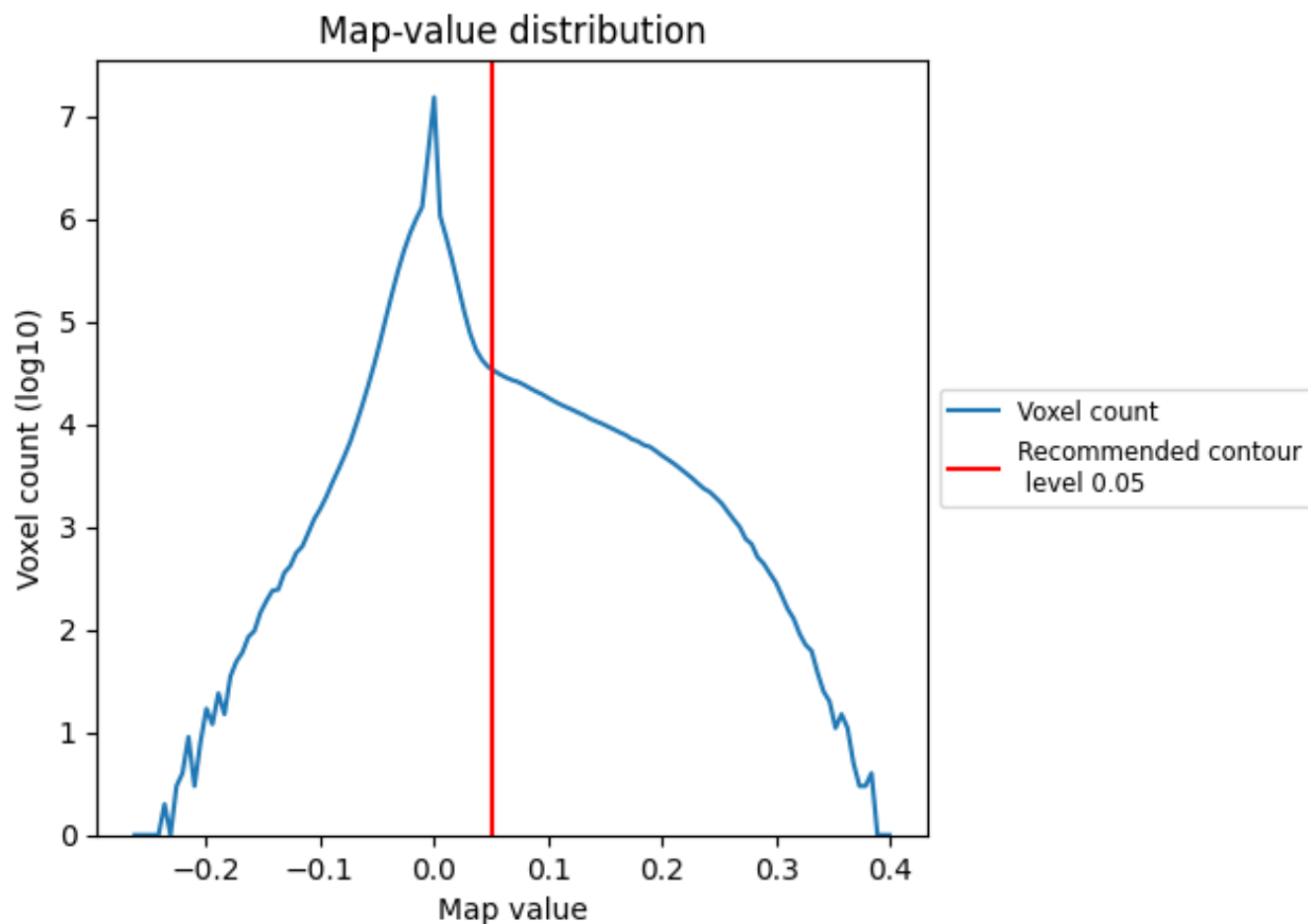
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

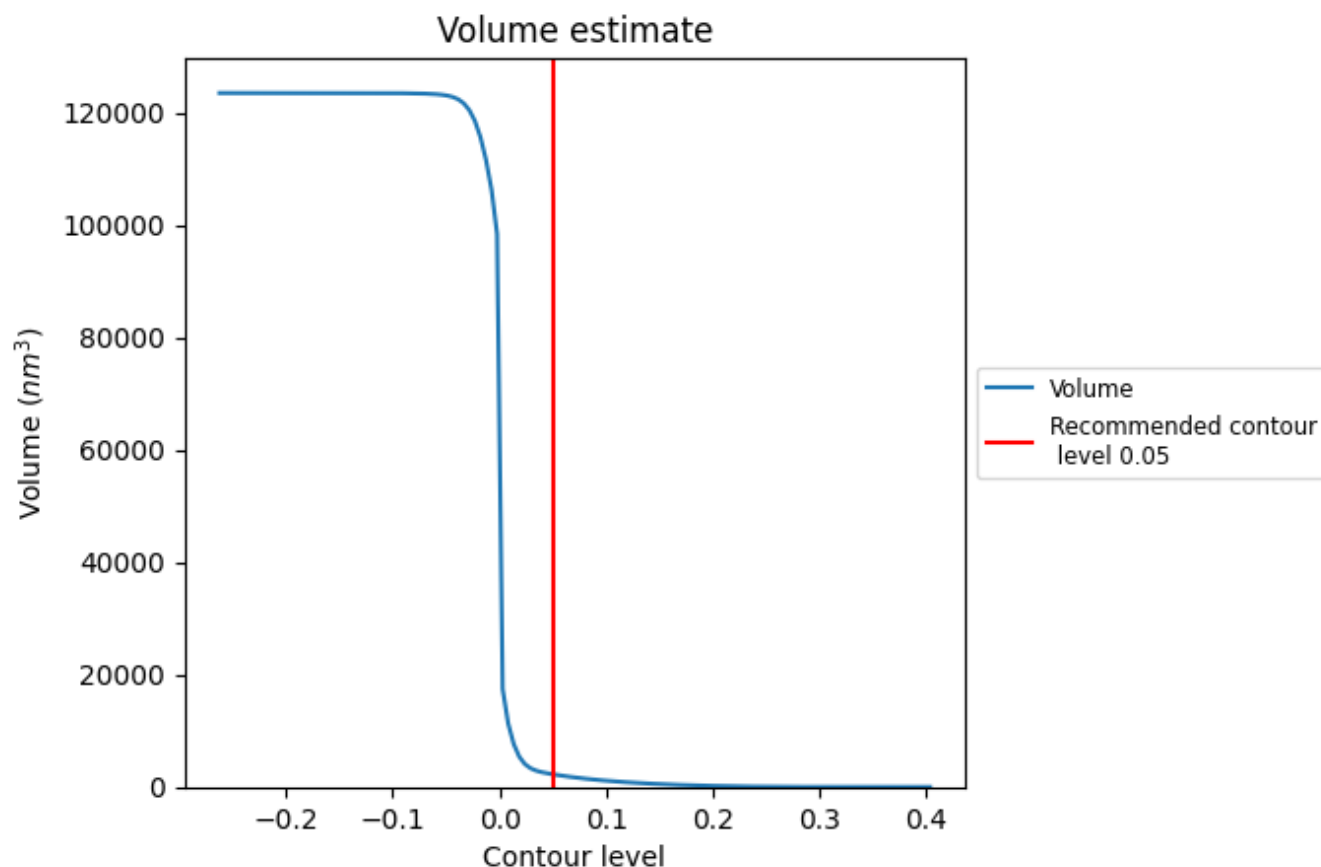
This section contains the results of statistical analysis of the map.

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.

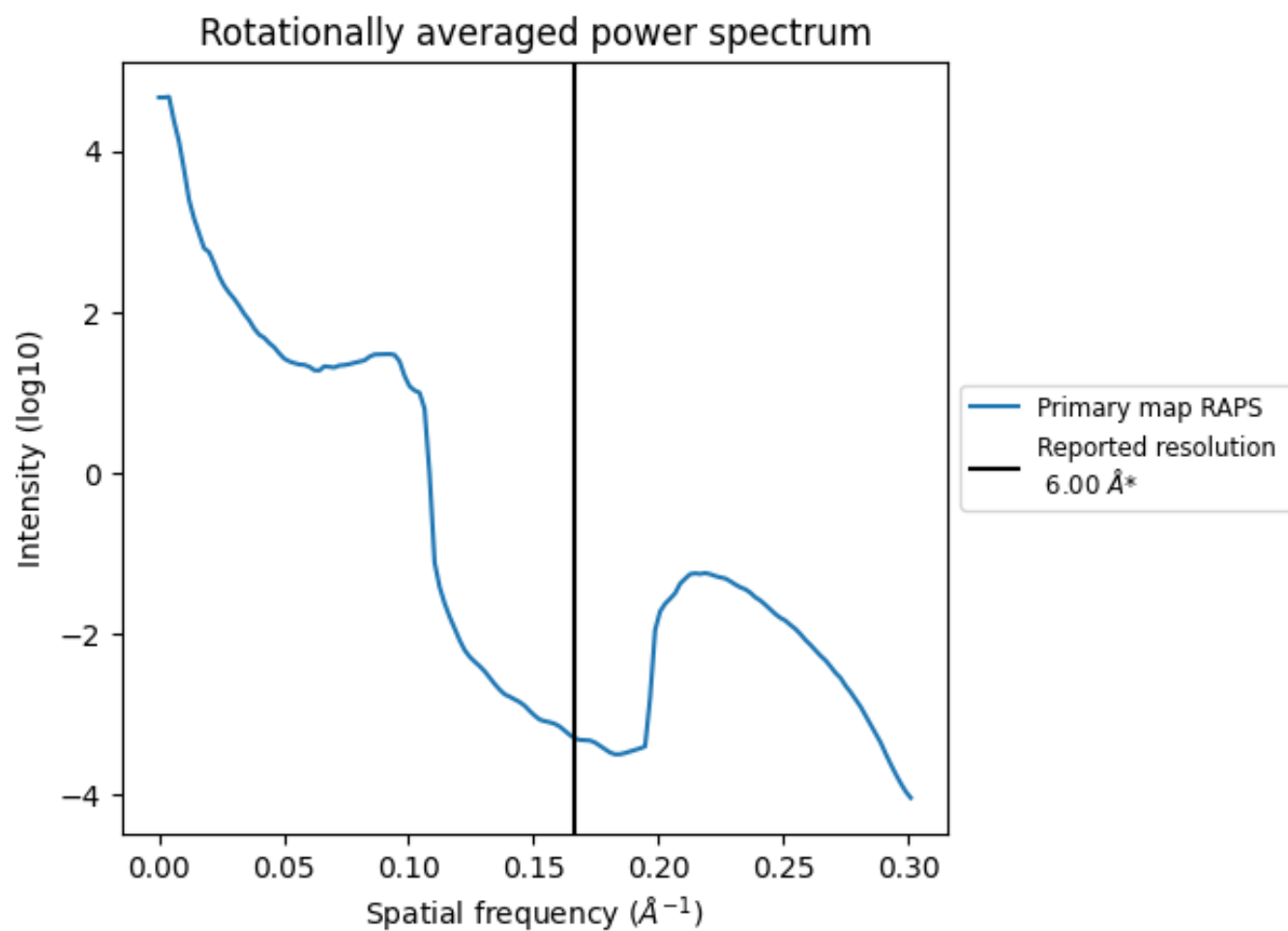
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2255 nm³; this corresponds to an approximate mass of 2037 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.167 Å⁻¹

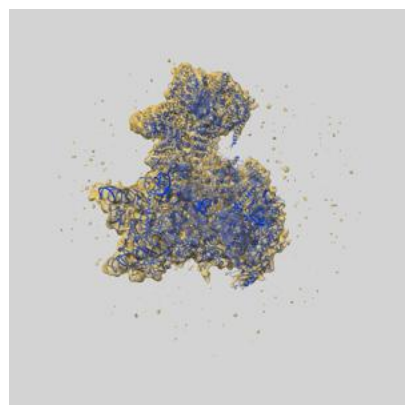
8 Fourier-Shell correlation

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

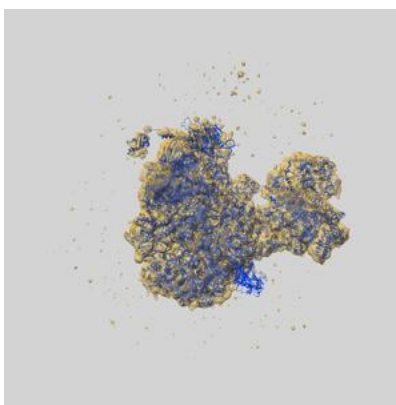
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3057 and PDB model 9CPA. Per-residue inclusion information can be found in section 3 on page 14.

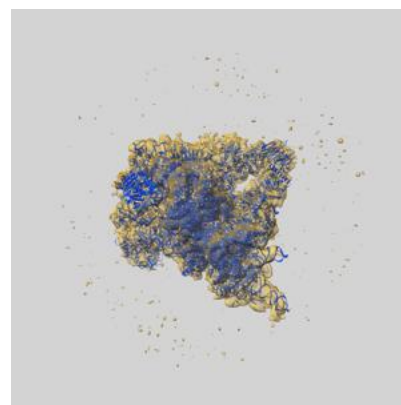
9.1 Map-model overlay [i](#)



X



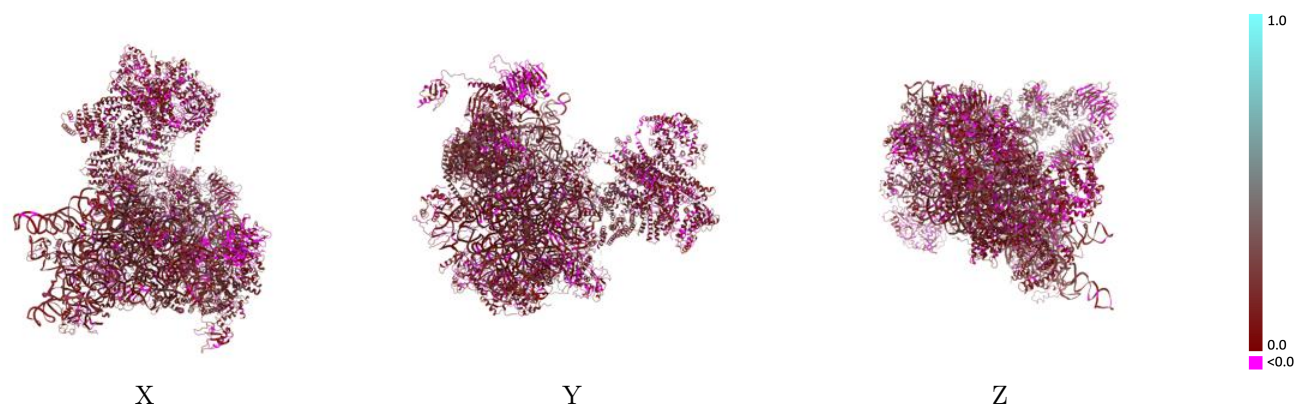
Y



Z

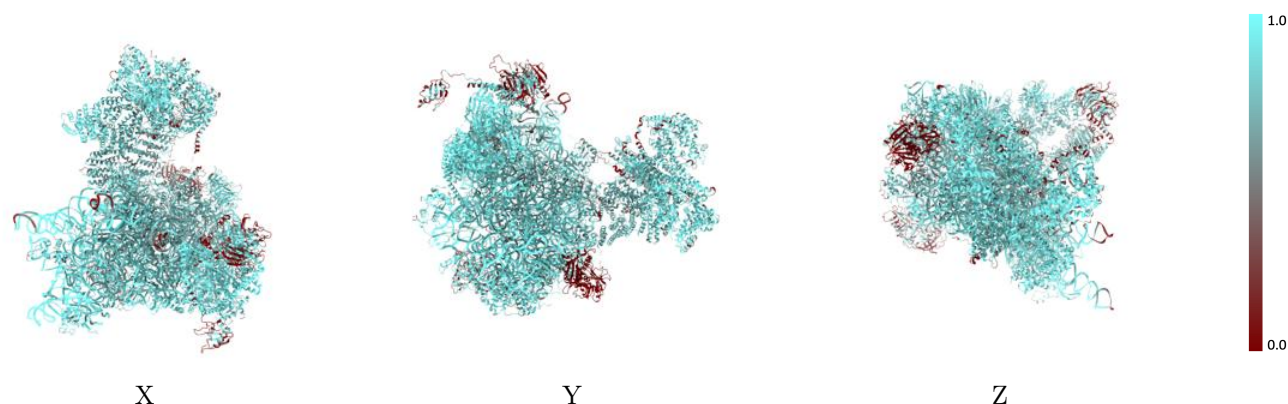
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



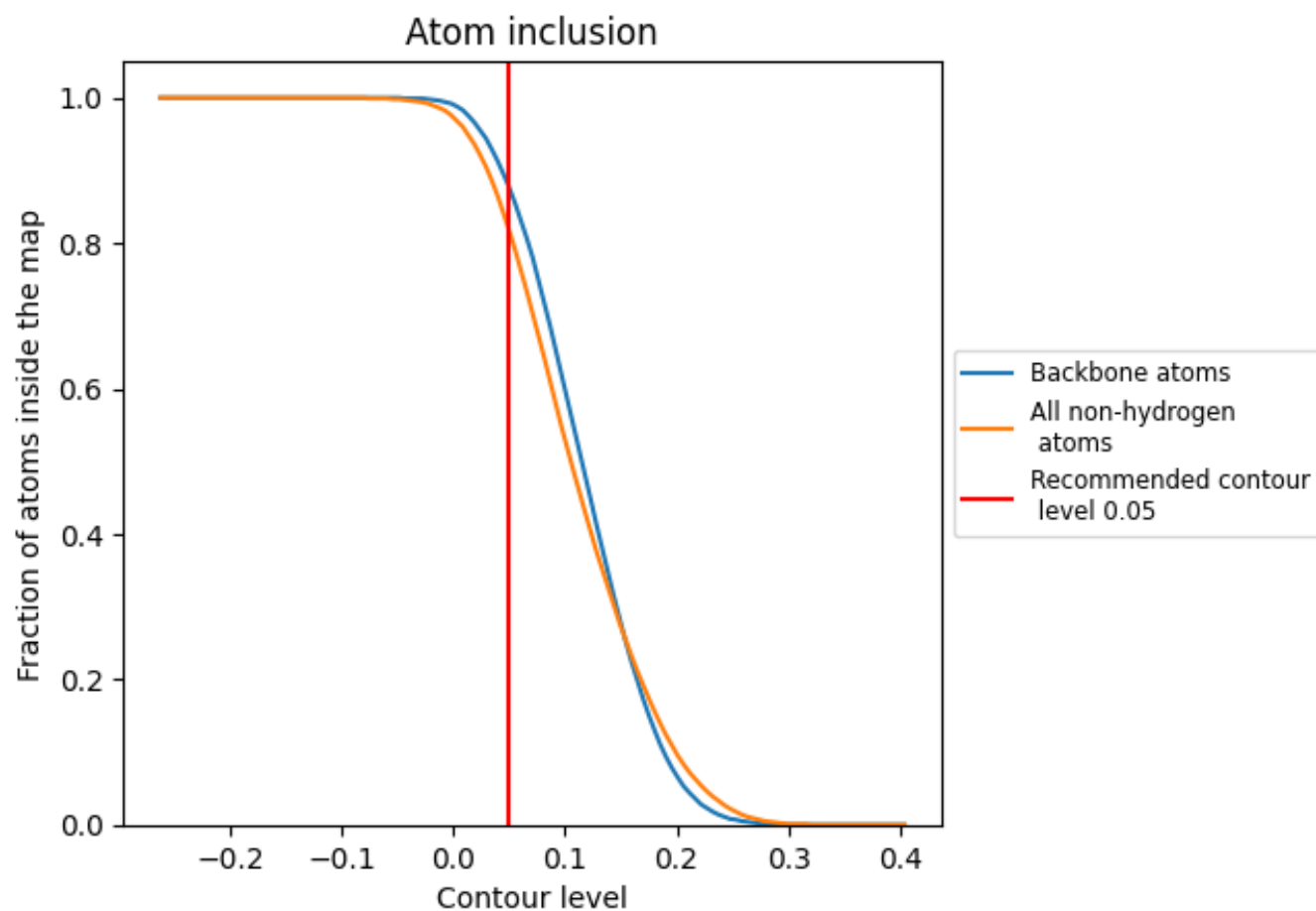
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 82% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8170	 0.1180
0	 0.7620	 0.0720
1	 0.7230	 0.1380
2	 0.9560	 0.1590
A	 0.5760	 0.0830
B	 0.3710	 0.0370
C	 0.7730	 0.1130
D	 0.1740	 0.0740
E	 0.7290	 0.0960
F	 0.7660	 0.0960
G	 0.8260	 0.0970
H	 0.7940	 0.0940
I	 0.8920	 0.1120
J	 0.7920	 0.1100
K	 0.8660	 0.1010
L	 0.7700	 0.1100
M	 0.8400	 0.1190
N	 0.7990	 0.0980
O	 0.8150	 0.0960
P	 0.7990	 0.1250
Q	 0.8550	 0.1150
R	 0.8710	 0.0970
S	 0.8610	 0.0870
T	 0.7850	 0.1230
U	 0.8960	 0.1120
V	 0.8780	 0.1050
W	 0.8060	 0.1040
X	 0.7880	 0.1120
Y	 0.7630	 0.0930
Z	 0.7780	 0.0890
a	 0.8690	 0.1100
b	 0.7420	 0.1040
c	 0.7700	 0.0880
d	 0.7610	 0.1340
e	 0.7540	 0.0420



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Chain	Atom inclusion	Q-score
f	 0.8600	 0.0820
g	 0.8730	 0.1130
h	 0.9430	 0.1700
i	 0.6790	 0.0780
j	 0.9080	 0.1040
k	 0.7850	 0.1140
l	 0.6210	 0.0730
n	 0.8800	 0.1350
p	 0.6920	 0.0970
q	 0.8710	 0.0850
r	 0.7740	 0.0740
s	 0.8300	 0.0670
t	 0.8360	 0.0720
u	 0.8960	 0.1030
x	 0.8330	 0.1240
y	 0.8220	 0.1310
z	 0.3160	 0.0080