wwPDB EM Validation Summary Report (i)

Mar 8, 2026 – 04:26 PM UTC

PDB ID	:	8XXN / pdb_00008xxn
EMDB ID	:	EMD-38754
Title	:	Cryo-EM structure of the human 43S ribosome with PDCD4
Authors	:	Ye, X.; Huang, Z.; Li, Y.; Wang, M.; Cheng, J.
Deposited on	:	2024-01-18
Resolution	:	3.60 Å(reported)
Based on initial model	:	7A09

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 (i) 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 (i)) were used in the production of this report:

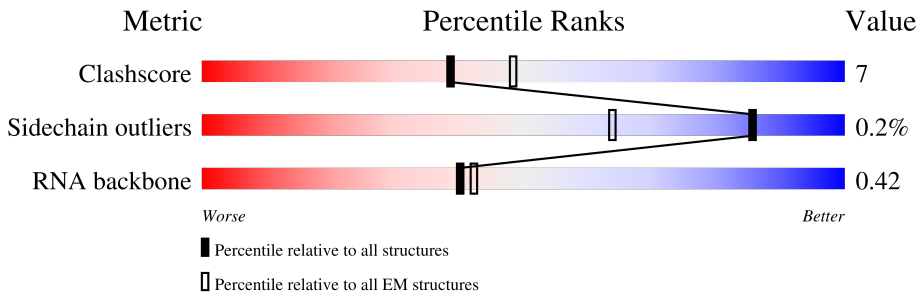
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

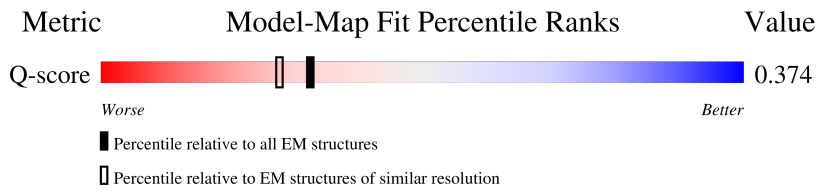
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.60 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	Ln	25	64% 32% •
2	S2	1869	54% 31% 7% 8%
3	SA	295	58% 17% 25%
4	SB	264	67% 14% • 19%

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Mol	Chain	Length	Quality of chain
5	SD	243	78% 15% 7%
6	SE	263	84% 15%
7	SF	204	70% 22% 7%
8	SH	194	78% 18%
9	SI	208	75% 23%
10	SK	165	50% 9% 41%
11	SL	158	80% 16%
12	SP	145	57% 26% 17%
13	SQ	146	74% 24%
14	SR	135	78% 20%
15	SS	152	68% 27% 5%
16	ST	145	81% 18%
17	SU	119	62% 24% 13%
18	SV	83	77% 23%
19	SX	143	80% 18%
20	Sa	115	69% 20% 11%
21	Sc	69	71% 22% 7%
22	Sd	56	71% 27%
23	Sg	317	72% 26%
24	SC	293	62% 13% 24%
25	SG	249	71% 23% 5%
26	SJ	194	70% 25% 5%
27	SM	132	64% 29% 8%
28	SN	151	89% 10%
29	SO	151	74% 19% 7%

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Mol	Chain	Length	Quality of chain
30	SW	130	82% 17%
31	SY	133	66% 32%
32	SZ	125	46% 14% 40%
33	Sb	84	77% 21%
34	Se	59	78% 20%
35	Sf	156	34% 9% 57%
36	C1	113	19% 78% 20%
37	4A	406	82% 16%
38	CD	469	73% 26%
39	3A	1382	5% 40% 10% 50%
40	3B	814	19% 62% 34%
41	3C	913	53% 16% 32%
42	3E	445	71% 23% 7%
43	3F	357	55% 20% 25%
44	3G	320	20% 7% 74%
45	3H	352	59% 25% 16%
46	3I	325	86% 92% 6%
47	3K	218	79% 20%
48	3L	564	51% 15% 34%
49	3M	374	67% 23% 10%
50	3N	548	7% 61% 20% 18%

2 Entry composition (i)

There are 52 unique types of molecules in this entry. The entry contains 114565 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 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	Ln	24	230	139	62	26	3	0	0

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	S2	1723	36535	16298	6533	11982	1722	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	SA	221	1741	1106	305	322	8	0	0

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SB	214	1738	1103	310	311	14	0	0

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SD	227	1765	1125	317	315	8	0	0

- Molecule 6 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SE	262	2076	1324	386	358	8	0	0

- Molecule 7 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	SF	189	1495	934	284	270	7	0	0

- Molecule 8 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	SH	186	1497	956	274	266	1	0	0

- Molecule 9 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	SI	206	1686	1058	332	291	5	0	0

- Molecule 10 is a protein called 40S ribosomal protein S10.

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

- Molecule 11 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	SL	153	1247	793	234	214	6	0	0

- Molecule 12 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	SP	121	985	623	185	170	7	0	0

- Molecule 13 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	SQ	144	1142	726	216	197	3	0	0

- Molecule 14 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	SR	135	1090	685	202	198	5	0	0

- Molecule 15 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	SS	145	1198	751	242	203	2	0	0

- Molecule 16 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	ST	143	1112	697	214	198	3	0	0

- Molecule 17 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	SU	103	817	511	155	147	4	0	0

- Molecule 18 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	SV	83	636	393	117	121	5	0	0

- Molecule 19 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	SX	141	1098	693	219	183	3	0	0

- Molecule 20 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	Sa	102	821	512	171	133	5	0	0

- Molecule 21 is a protein called 40S ribosomal protein S28.

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

- Molecule 22 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Sd	55	459	286	94	74	5	0	0

- Molecule 23 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 24 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	SC	222	1725	1115	298	302	10	0	0

- Molecule 25 is a protein called 40S ribosomal protein S6.

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

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	SJ	185	1525	969	306	248	2	0	0

- Molecule 27 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	SM	122	940	590	164	177	9	0	0

- Molecule 28 is a protein called 40S ribosomal protein S13.

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

- Molecule 29 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	SO	140	1049	642	204	197	6	0	0

- Molecule 30 is a protein called 40S ribosomal protein S15a.

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

- Molecule 31 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	SY	131	1065	673	209	178	5	0	0

- Molecule 32 is a protein called 40S ribosomal protein S25.

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

- Molecule 33 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Sb	83	651	408	121	115	7	0	0

- Molecule 34 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Se	58	459	284	100	74	1	0	0

- Molecule 35 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Sf	67	548	346	102	93	7	0	0

- Molecule 36 is a protein called Eukaryotic translation initiation factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
36	C1	90	443	262	90	91	0	0

- Molecule 37 is a protein called Eukaryotic initiation factor 4A-I.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	4A	342	1691	1007	342	342	0	0

- Molecule 38 is a protein called Programmed cell death protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
38	CD	347	1841	1100	368	373	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	3A	692	5379	3374	980	1003	22	0	0

- Molecule 40 is a protein called Eukaryotic translation initiation factor 3 subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	3B	536	2966	1801	580	580	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	3C	625	5070	3204	898	933	35	0	0

- Molecule 42 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	3E	416	3437	2202	585	630	20	0	0

- Molecule 43 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	3F	269	2090	1317	356	405	12	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
44	3G	84	667	418	120	129	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	3H	295	2413	1532	417	449	15	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	3I	305	1497	887	305	305	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	3K	217	1750	1116	288	334	12	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	3L	372	3111	2011	520	563	17	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	3M	338	2705	1727	457	504	17	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	3N	447	3617	2279	625	691	22	0	0

- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
51	S2	22	22	22	0
51	SG	1	1	1	0

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

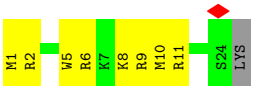
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
52	Sa	1	1	1	0
52	Sd	1	1	1	0
52	Sf	1	1	1	0

3 Residue-property plots (i)

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

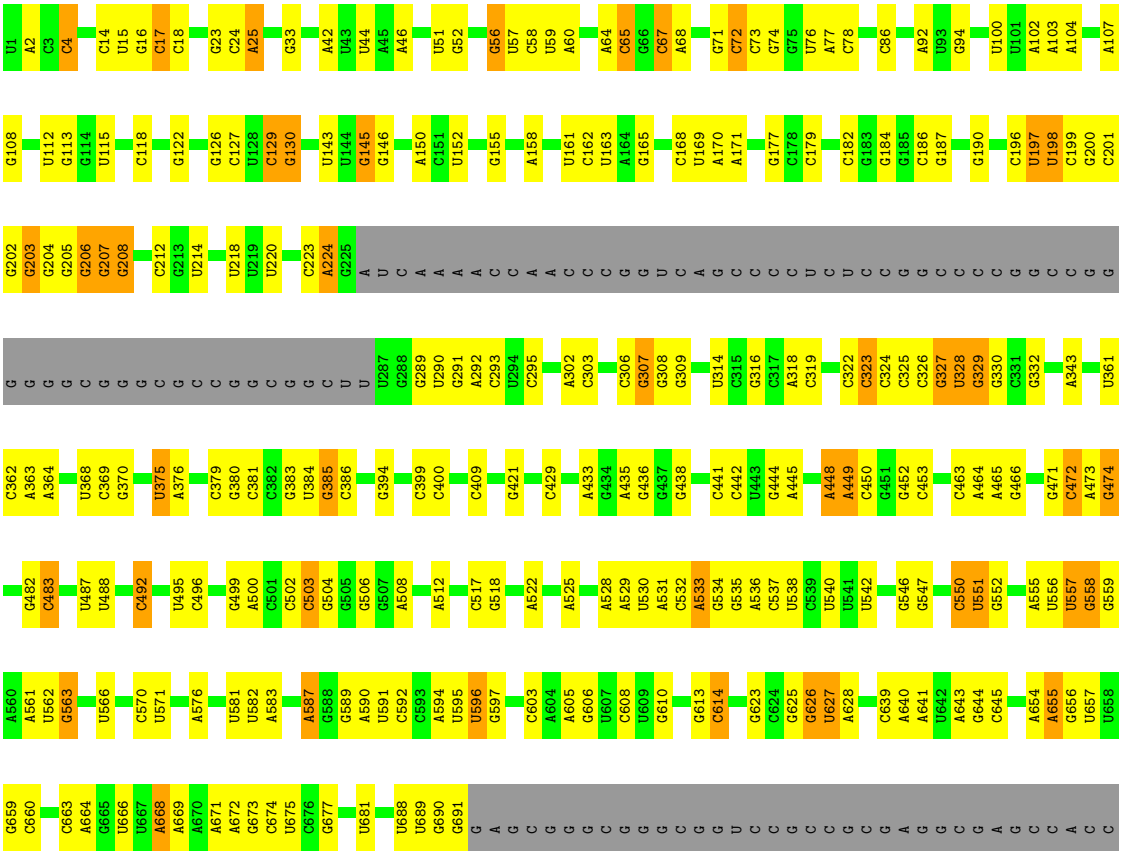
- Molecule 1: 60S ribosomal protein L41

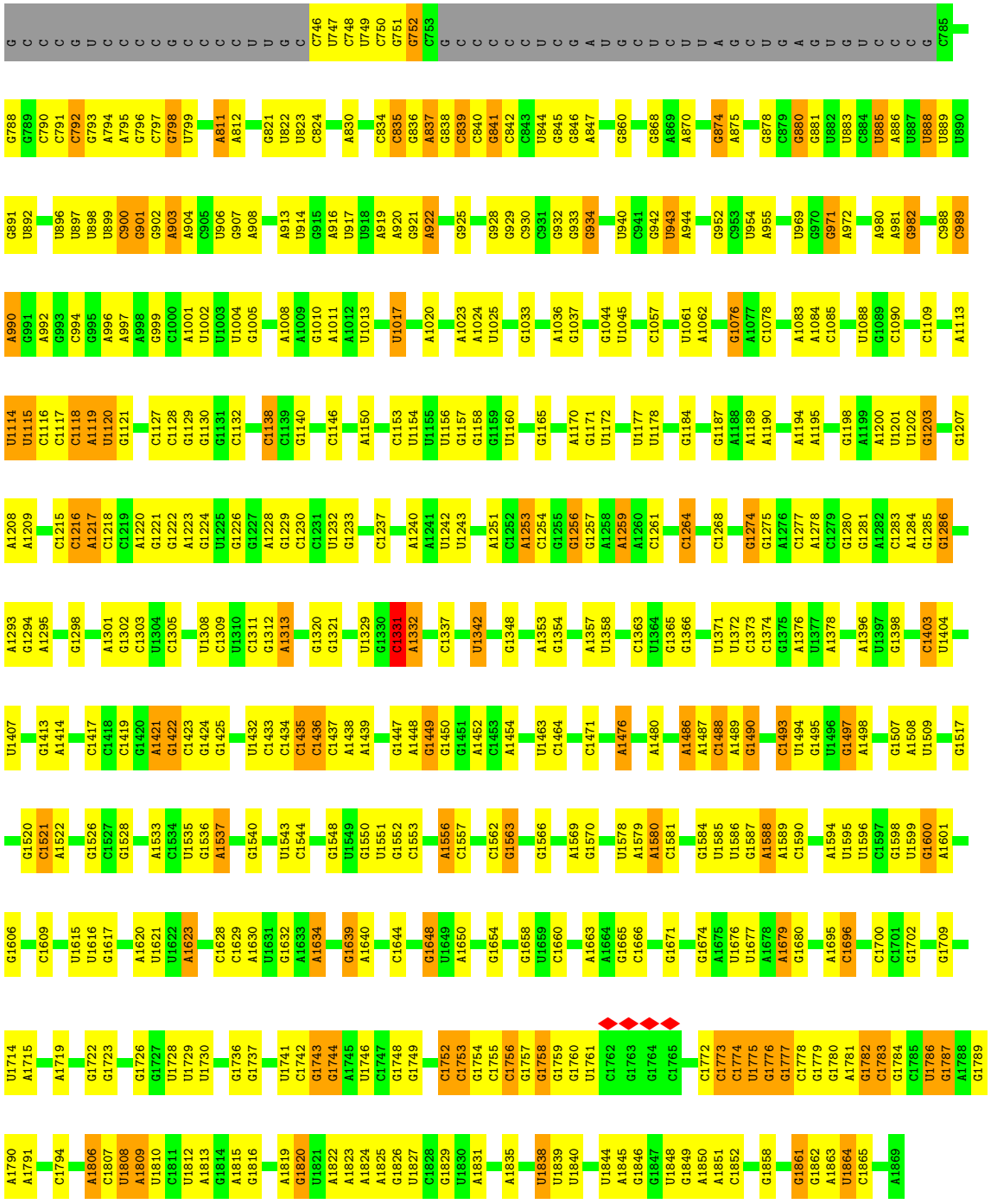
Chain Ln:



- Molecule 2: 18S rRNA

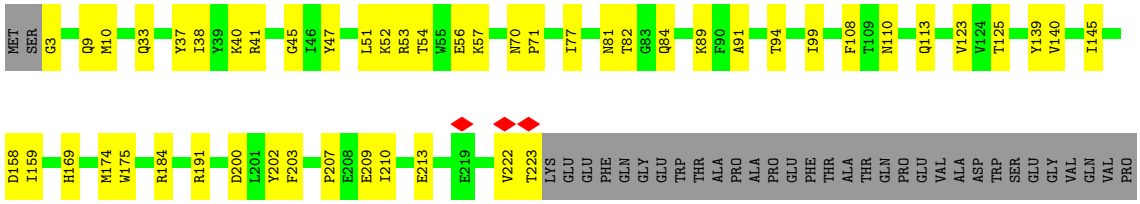
Chain S2:





• Molecule 3: 40S ribosomal protein SA

Chain SA:



SER VAL PRO ILE GLN GLN PHE PRO THR GLU ASP TRP SER ALA GLN PRO ALA THR GLU ASP TRP SER ALA ALA PRO THR ALA GLN ALA THR GLU TRP VAL GLY ALA THR THR ASP TRP SER

- Molecule 4: 40S ribosomal protein S3a

Chain SB:

MET ALA VAL GLY LYS ASN LYS ARG LEU THR LYS GLY GLY LYS LYS GLY ALA LYS LYS LYS V21 K28 V33 I41 V49 T50 L62 E68 D73 N76 R82 K83 F84 C96 L97 R107 Q118 T119 H124 L137 T143 K144 K145 I150

R151 K152 Y155 R162 E175 P190 D191 S192 I193 E198 V210 K214 K222 F223 E224 K227 H232 G233 E234 GLY SER SER SER GLY LYS ALA THR GLY ASP GLU THR GLY ALA LYS VAL GLU ARG ALA ASP GLY TYR GLU PRO PRO VAL GLN GLU SER VAL

- Molecule 5: 40S ribosomal protein S3

Chain SD:

M1 G36 T42 R45 I48 L59 R67 T70 R76 S83 L86 Y87 R94 G95 Q101 R106 C119 V122 A131 K132 V136 V137 K151 M157 T170 R173 L177 R178 Q179 V186 K187 I188 M189 L190 P191 T195

G196 K197 V211 E212 P213 K214 D215 Q226 K227 GLY GLY LYS PRO GLU PRO PRO ALA MET PRO GLN PRO VAL PRO THR ALA

- Molecule 6: 40S ribosomal protein S4, X isoform

Chain SE:

MET A2 R11 P15 M19 T24 A28 R39 I45 R51 M66 K71 V76 R77 T78 D79 I80 M87 D88 V89 I92 D93 K94 T105 R108 H112 R113 I114 T115 E118 A119 P137 T146 P150 K155 F175 G185

L189 N197 R198 V208 H209 I225 G229 P234 S237 R245 S261 S262 G263

- Molecule 7: 40S ribosomal protein S5

Chain SF:

MET THR GLU TRP GLU THR ALA ALA PRO ALA VAL ALA GLU THR PRO D16 V28 Q29 I30 L35 Q36 K44 L49 G54 A58 K59 R60 F61 R62 H79 G80 R81 K85 M88 T89 V90 R91 I92 V93 L102 L103 T104 G105 E106 L109 I117 P121

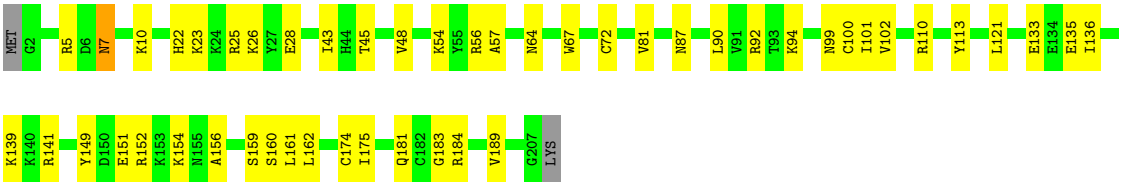
R122 E123 D124 S125 T126 R127 I128 G129 G132 T133 V134 R135 R136 D140 A150 L153 L154 R159 N165 I166 D175 I178 L196 K201 S202 N203 R204

- Molecule 8: 40S ribosomal protein S7

Chain SH:

- Molecule 9: 40S ribosomal protein S8

Chain SI:

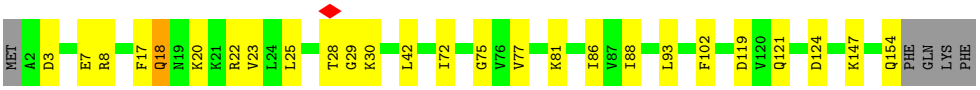


- Molecule 10: 40S ribosomal protein S10

Chain SK:

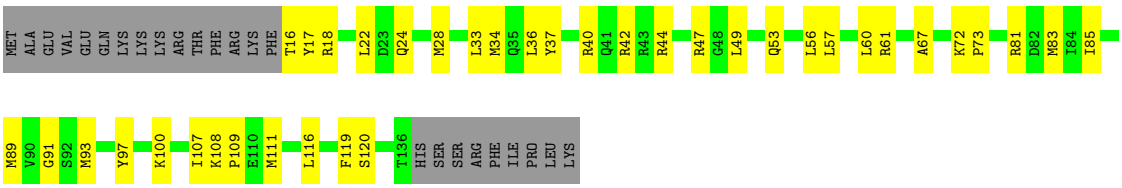
- Molecule 11: 40S ribosomal protein S11

Chain SL:



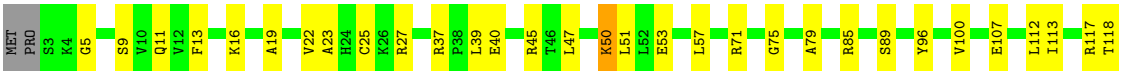
- Molecule 12: 40S ribosomal protein S15

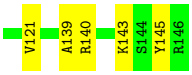
Chain SP:



- Molecule 13: 40S ribosomal protein S16

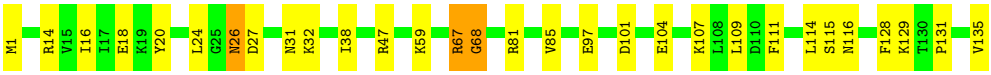
Chain SQ:





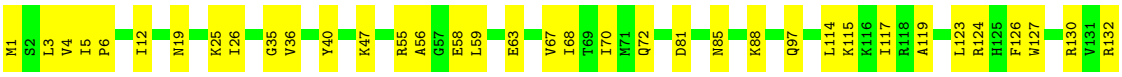
• Molecule 14: 40S ribosomal protein S17

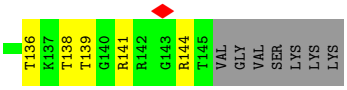
Chain SR:



• Molecule 15: 40S ribosomal protein S18

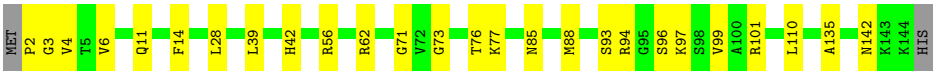
Chain SS:





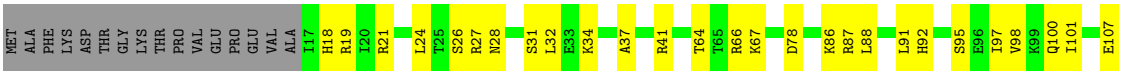
• Molecule 16: 40S ribosomal protein S19

Chain ST:



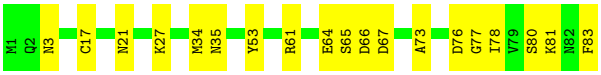
• Molecule 17: 40S ribosomal protein S20

Chain SU:



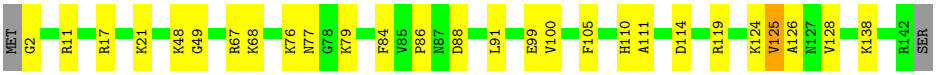
• Molecule 18: 40S ribosomal protein S21

Chain SV:



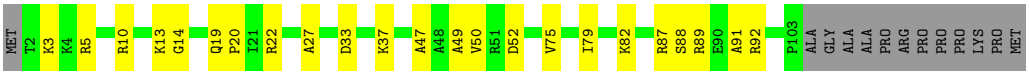
• Molecule 19: 40S ribosomal protein S23

Chain SX:



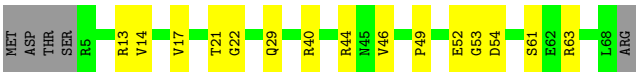
- Molecule 20: 40S ribosomal protein S26

Chain Sa:



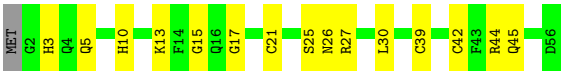
- Molecule 21: 40S ribosomal protein S28

Chain Sc:



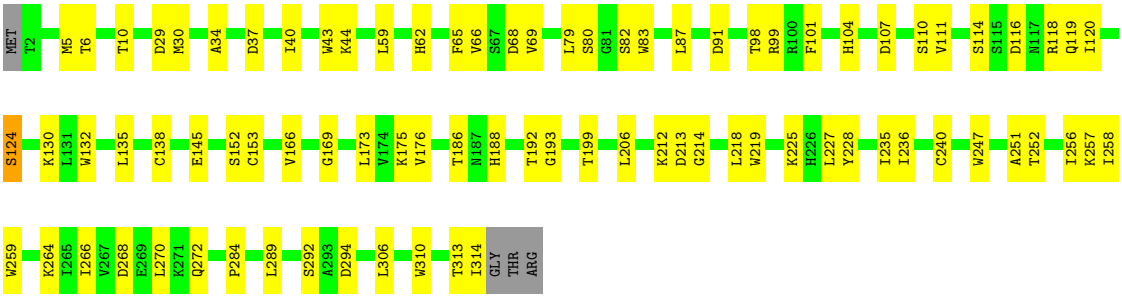
- Molecule 22: 40S ribosomal protein S29

Chain Sd:



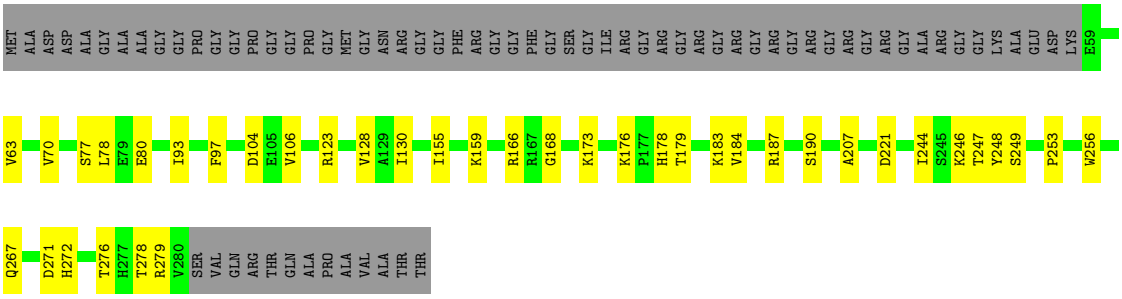
- Molecule 23: Receptor of activated protein C kinase 1

Chain Sg:



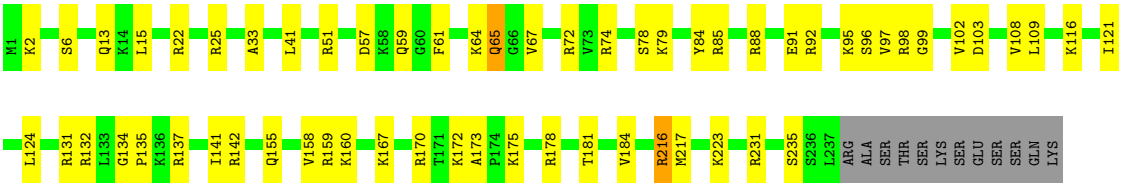
- Molecule 24: 40S ribosomal protein S2

Chain SC:



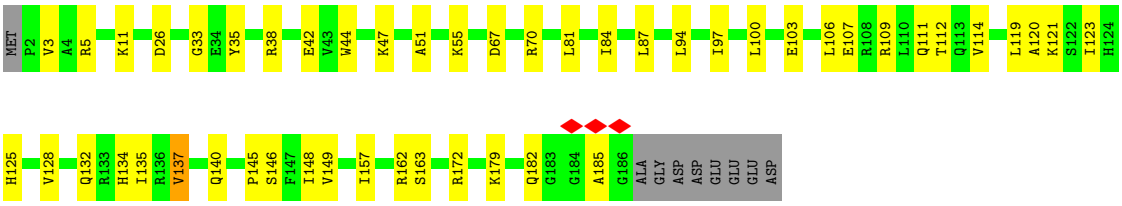
- Molecule 25: 40S ribosomal protein S6

Chain SG:



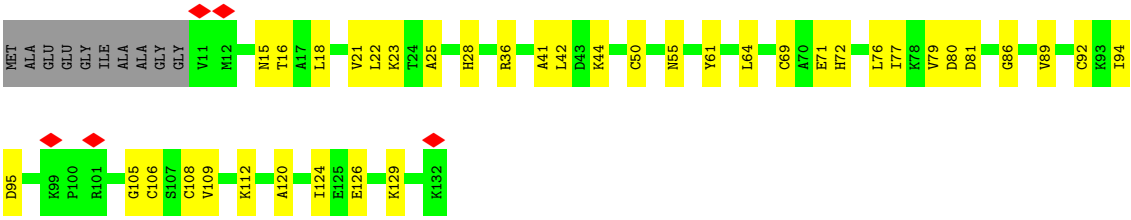
- Molecule 26: 40S ribosomal protein S9

Chain SJ:



- Molecule 27: 40S ribosomal protein S12

Chain SM:

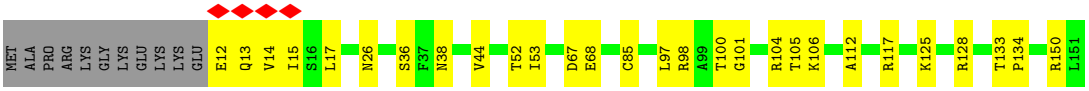


- Molecule 28: 40S ribosomal protein S13

Chain SN:

- Molecule 29: 40S ribosomal protein S14

Chain SO:

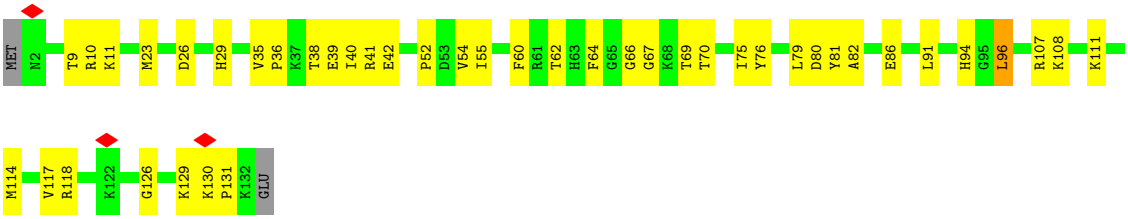


- Molecule 30: 40S ribosomal protein S15a

Chain SW:

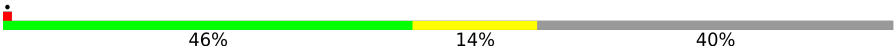
• Molecule 31: 40S ribosomal protein S24

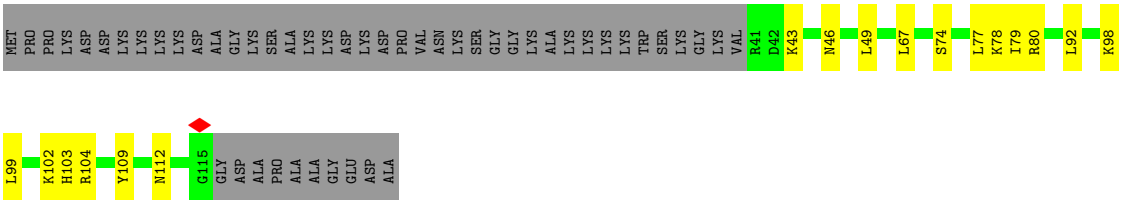
Chain SY:



• Molecule 32: 40S ribosomal protein S25

Chain SZ:



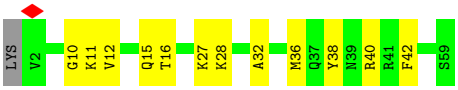


• Molecule 33: 40S ribosomal protein S27

Chain Sb:

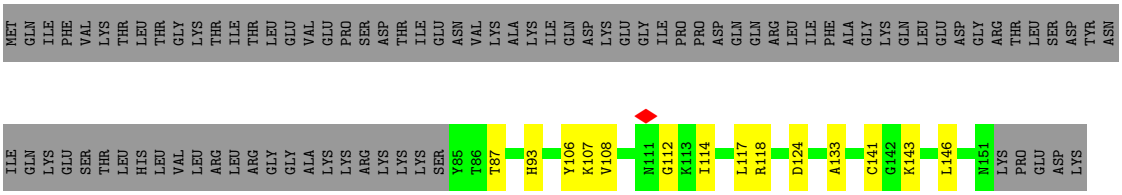
• Molecule 34: 40S ribosomal protein S30

Chain Se:



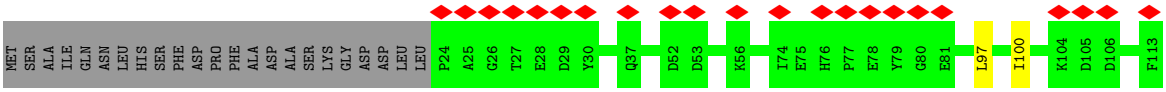
• Molecule 35: Ubiquitin-40S ribosomal protein S27a

Chain Sf:



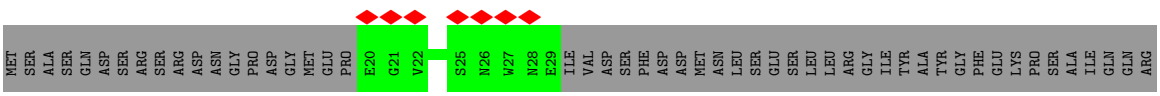
• Molecule 36: Eukaryotic translation initiation factor 1

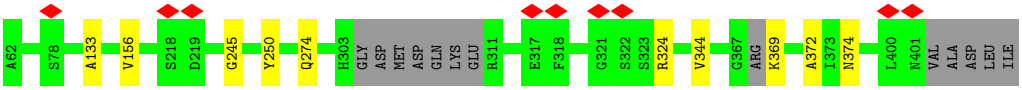
Chain C1:



- Molecule 37: Eukaryotic initiation factor 4A-I

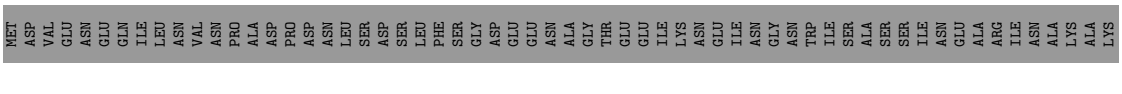
Chain 4A:

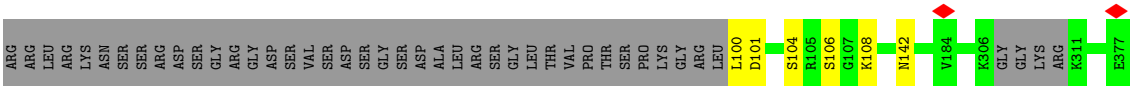


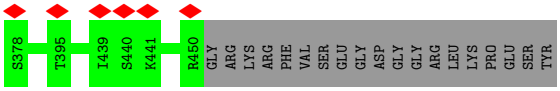


- Molecule 38: Programmed cell death protein 4

Chain CD:

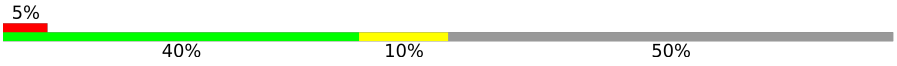


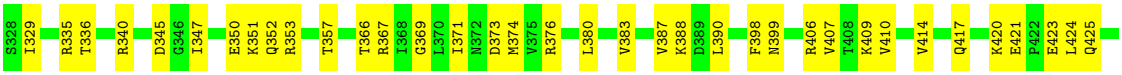


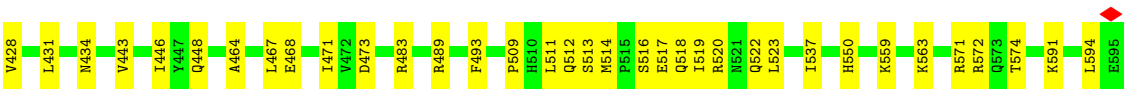


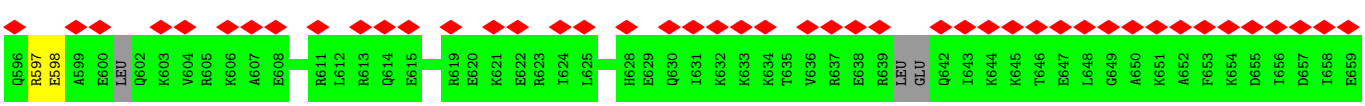
- Molecule 39: Eukaryotic translation initiation factor 3 subunit A

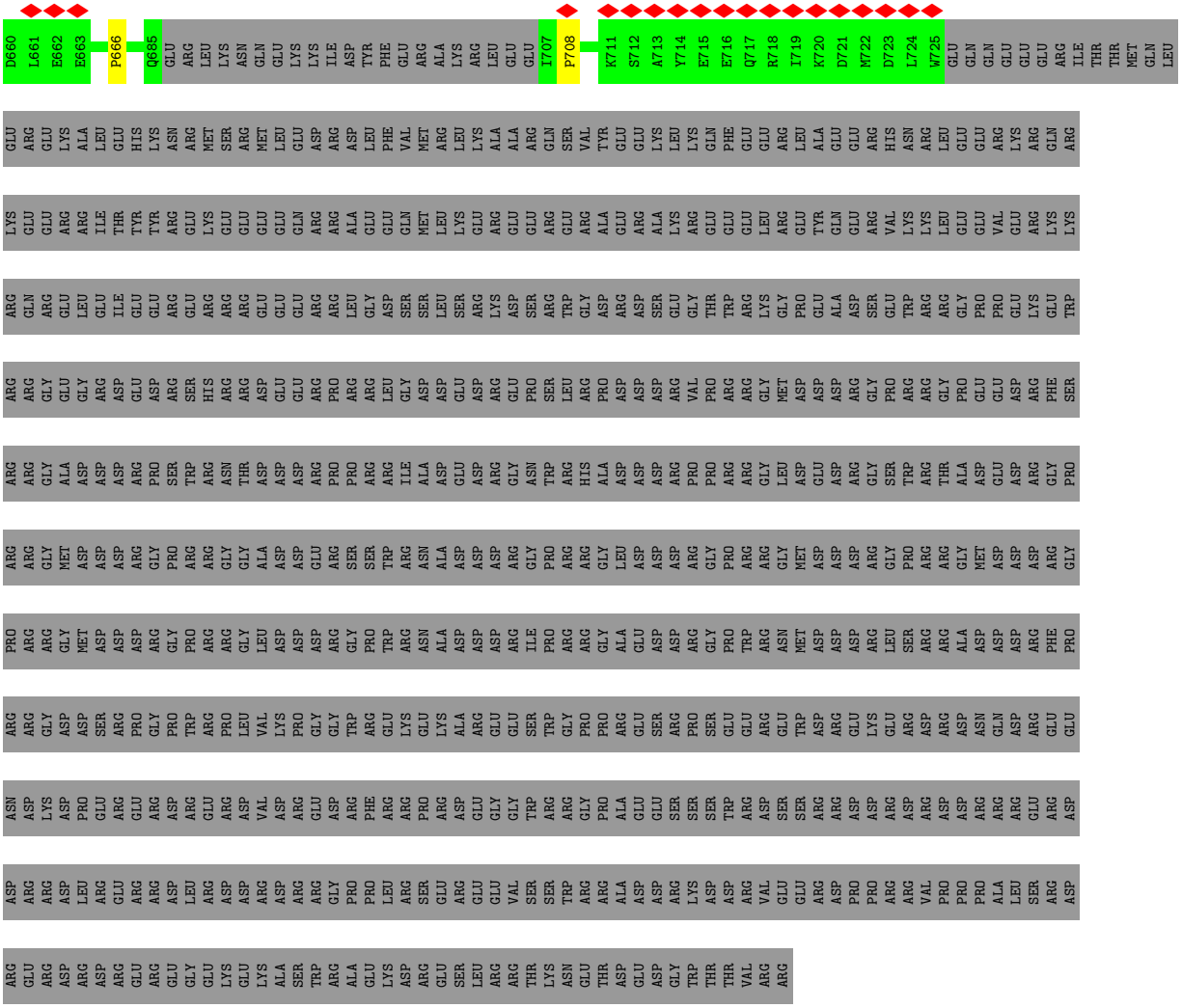
Chain 3A:

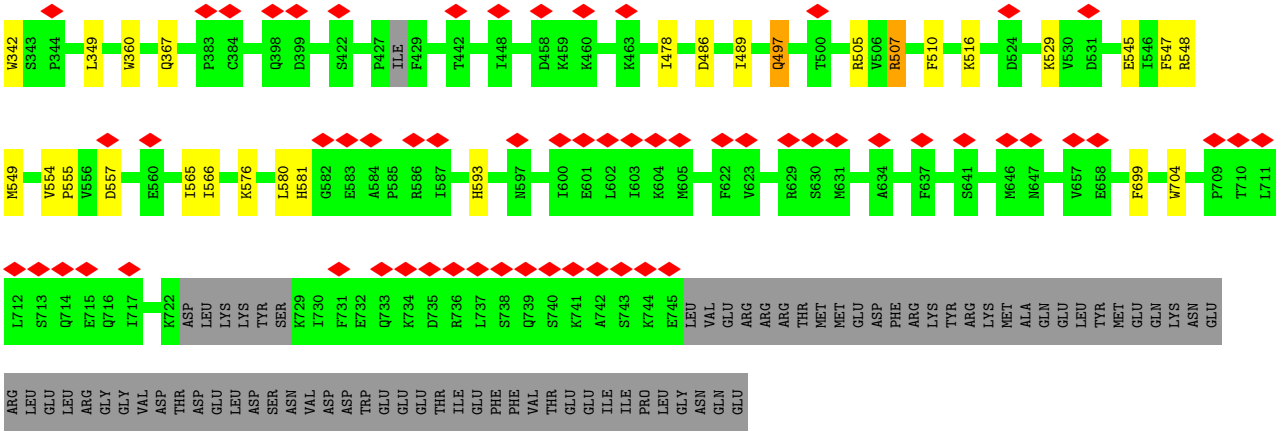






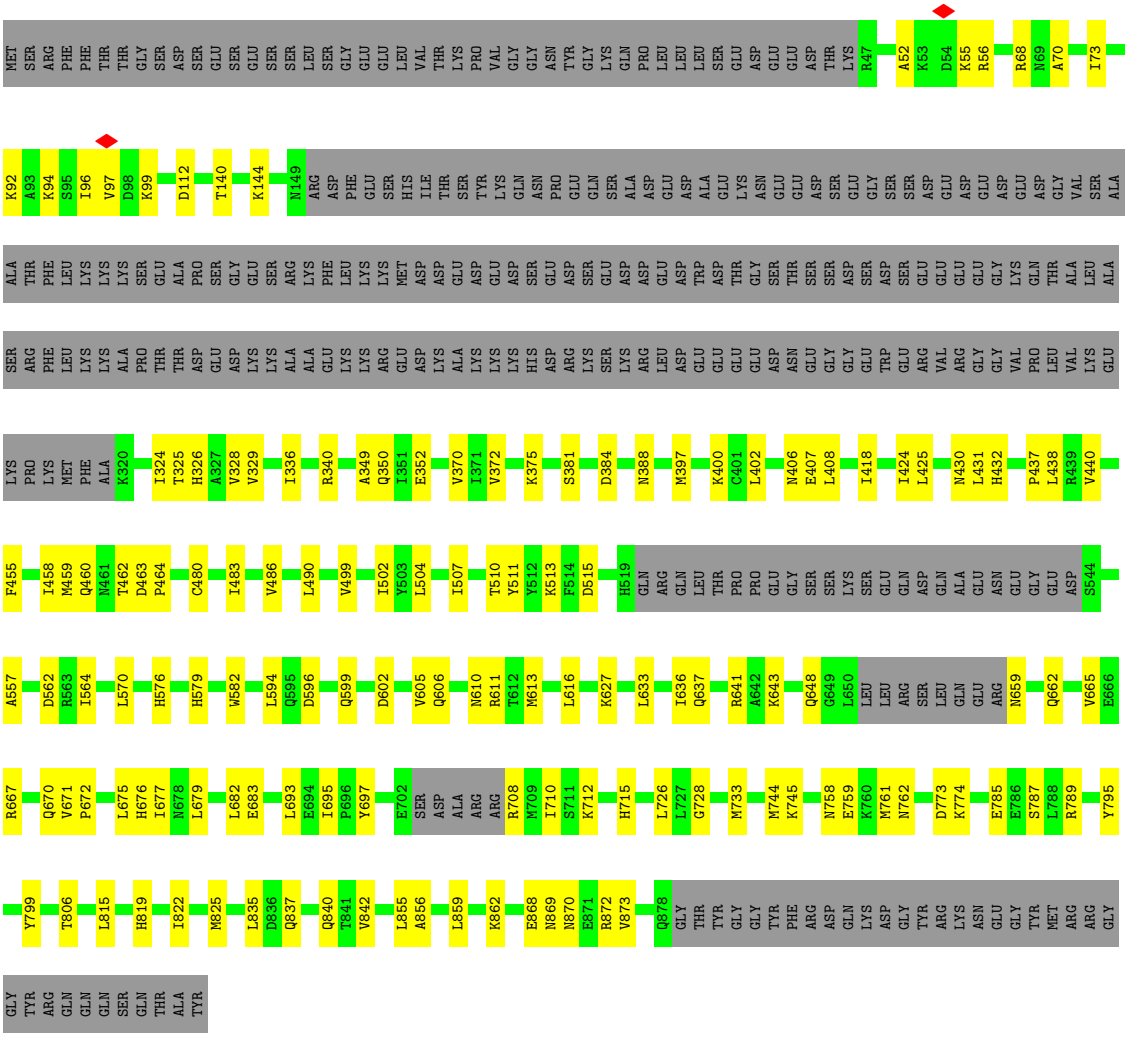



D660 L661 E662 E663 P666 Q685 GLU ARG LEU LYS ASN GLN GLU GLU LYS LYS ILE ASP TYR PHE GLU ARG ALA LYS ARG LEU GLU GLU I707 P708 K711 S712 A713 Y714 E715 E716 Q717 R718 I719 K720 D721 M722 D723 L724 W725 GLU GLN GLN GLU GLU GLU ARG ILE THR THR MET GLN LEU
GLU ARG GLU LYS ALA LEU GLU HIS LYS ASN ARG MET SER ARG MET LEU GLU ASP ARG ASP LEU PHE VAL MET ARG LEU LYS ARG LEU ALA ALA ARG GLN SER VAL TYR GLU GLU ARG LYS LEU LYS GLN PHE GLU GLU ARG LEU ALA GLU GLU ARG HIS ASN ARG LEU GLU GLU ARG GLN ARG
LYS GLU GLU ARG ARG ILE THR TYR TYR ARG GLU LYS GLU GLU GLU GLN ARG ARG ALA GLU GLU GLN MET LEU LYS LYS GLU ARG GLU GLU ARG GLU ALA ALA LYS ARG GLU GLU LEU ARG GLU TYR GLN GLU ARG VAL LYS LYS LEU GLU GLU VAL GLU ARG LYS LYS
ARG GLN ARG GLU LEU GLU ILE GLU GLU ARG ARG ARG GLU GLU GLU ARG ARG LEU GLY ASP SER SER LEU SER ARG LYS ASP SER ARG TRP GLY ASP ARG ASP SER GLU GLY THR TRP ARG LYS GLY PRO GLU ALA ASP SER GLU TRP ARG ARG GLY PRO PRO GLU LYS GLU TRP
ARG ARG GLY GLU GLY ARG ASP GLU ASP ARG SER HIS ARG ARG ASP GLU GLU GLU ARG PRO ARG ARG LEU GLY ASP ARG GLU PRO SER LEU ARG PRO ASP ASP ASP ASP ARG VAL PRO ARG ARG GLY MET ASP ASP ASP ARG GLY PRO ARG ARG GLY PRO GLU ASP ARG ARG PHE SER
ARG ARG GLY ALA ASP ASP ARG PRO SER TRP ARG ASN THR ASP ASP ASP ARG PRO PRO ARG ARG ILE ALA ASP GLU ASP ARG GLY ASN TRP ARG HIS ALA ASP ASP ASP ARG PRO PRO ARG ARG GLY GLU ASP ARG GLY GLY LEU ASP GLU GLU ARG GLY PRO
ARG ARG GLY MET ASP ASP ASP ARG GLY PRO ARG ARG GLY GLY GLY ALA ASP ASP GLU ARG SER SER SER TRP ARG ARG ASN ALA ASP ASP ASP ASP ARG GLY PRO ARG ARG ARG GLY GLY LEU ASP ASP ASP ASP ARG GLY PRO ARG ARG GLY MET ASP ASP ASP ARG GLY PRO ARG ARG GLY GLY
PRO ARG ARG GLY MET ASP ASP ASP ARG GLY PRO ARG ARG GLY GLY LEU ASP ASP ASP ARG GLY PRO TRP ARG ASN ALA ASP ASP ASP ARG ILE PRO ARG ARG ARG GLY LEU ASP ASP ASP ARG GLY PRO TRP ARG ASN MET ASP ASP ASP ARG LEU SER ARG ARG ALA ASP ASP ARG PHE PRO
ARG ARG GLY ASP ASP SER ARG PRO GLY PRO TRP ARG PRO LEU VAL LYS PRO GLY GLY TRP ARG GLU LYS GLU LYS ALA ARG GLU GLU SER TRP GLY PRO ARG GLU SER ARG PRO SER GLU GLU ARG GLU TRP ASP ARG GLU LYS GLU ARG ASP ARG ASP ASN GLN ASP ARG GLU GLU
ASN ASP LYS ASP PRO GLU ARG GLU ARG ASP ARG ASP LEU ARG ASP ARG GLU ASP ARG PHE ARG ARG PRO ARG ASP GLU GLY GLY TRP ARG ARG GLY PRO ALA GLU GLU SER SER SER SER ARG ARG ASP ASP ASP ARG ASP ASP ARG ARG ARG GLU ARG ASP
ASP ARG ARG ASP LEU ARG GLU ARG ARG ASP LEU ARG ASP ASP ARG ARG ARG GLY PRO PRO LEU ARG SER GLU ARG GLU GLU VAL SER SER TRP ARG ARG ARG LYS ASP ASP ASP ARG VAL GLU GLU ARG ARG ASP PRO PRO PRO ARG ARG VAL PRO PRO PRO ALA LEU SER ARG ASP
ARG GLU ARG ASP ARG ASP ARG GLU ARG GLU GLY GLU LYS GLU LYS ALA SER TRP ARG ALA GLU LYS ASP ARG GLU SER GLU THR LYS ASN GLU THR ASP GLU ASP GLY TRP THR THR VAL ARG ARG
• Molecule 40: Eukaryotic translation initiation factor 3 subunit B
Chain 3B:
19%
62%
34%
MET GLN ASP ALA GLU ASN VAL ALA VAL PRO GLU ALA ALA GLU GLU ARG ALA GLU PRO GLY GLN GLN GLN PRO ALA ALA GLU PRO PRO PRO ALA GLU GLY LEU LEU ARG PRO ALA GLY PRO GLY ALA PRO GLU ALA ALA GLY THR GLU ALA SER SER GLU GLU VAL GLY ILE ALA GLU ALA
GLY PRO GLU SER GLU VAL ARG THR GLU PRO ALA ALA GLU ALA GLU ALA ALA SER GLY PRO SER GLU SER PRO SER PRO PRO ALA ALA GLU GLU LEU PRO GLY SER HIS ALA GLU PRO PRO VAL PRO ALA GLN GLY GLU ALA ALA GLN GLU GLU ARG SER ASP SER ARG
ALA GLN ALA VAL SER GLU ASP ALA GLY GLY ASN GLU ARG ARG ALA ALA GLU GLY ARG ALA LEU GLU GLN ASN GLY ASP ALA ASP GLU PRO SER PHE SER ASP PRO GLU ASP PHE VAL ASP ASP VAL SER GLU GLU GLU LEU LEU GLY ASP VAL LEU LYS ASP ARG PRO GLN GLU A180
D181 G182 I183 D184 S185 V186 I187 V188 V189 D190 N191 V192 P193 Q194 V195 G196 P197 D198 R199 L200 E201 K202 L203 K204 N205 V206 I207 H208 K209 I210 F211 S212 K213 F214 G215 K216 I217 T218 N219 D220 F221 Y222 P223 E224 E225 D226 G227 K228 T229 K230 G231 Y232 I233 F234 L235 E236 Y237 A238 S239 P240
A241 H242 A243 V244 D245 A246 V247 K248 N249 A250 D251 G252 Y253 K254 L255 D256 K257 Q258 H259 T260 F261 R262 V263 N264 L265 PHE THR ASP PHE ASP LYS TYR MET THR ILE SER ASP GLU TRP ASP ILE PRO GLU LYS GLN PRO PHE LYS D289 Y306 F310 K324 D325 P326 V327 S328



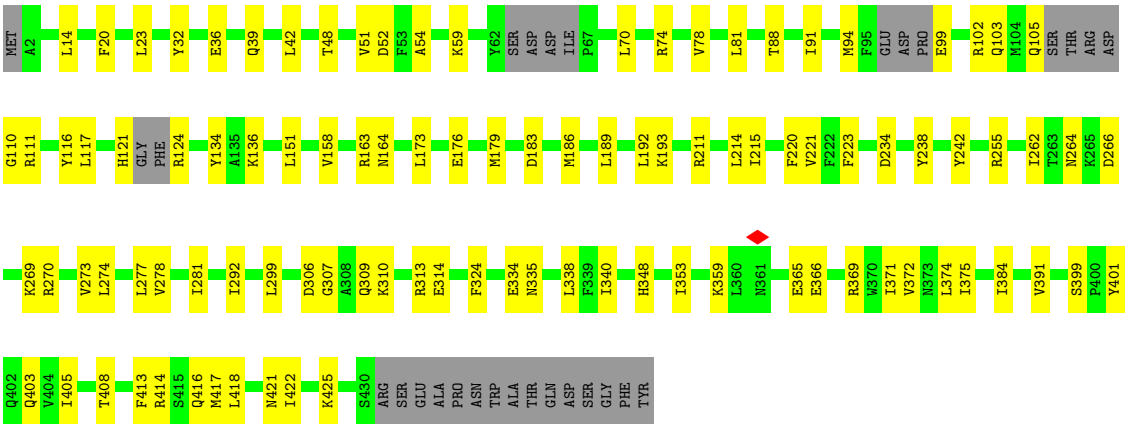
• Molecule 41: Eukaryotic translation initiation factor 3 subunit C

Chain 3C: 53% 16% 32%



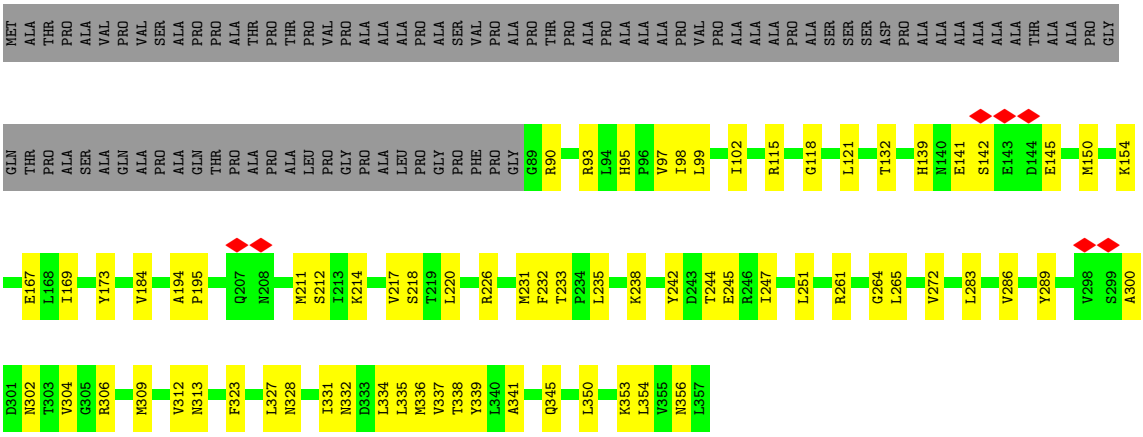
• Molecule 42: Eukaryotic translation initiation factor 3 subunit E

Chain 3E: 71% 23% 7%



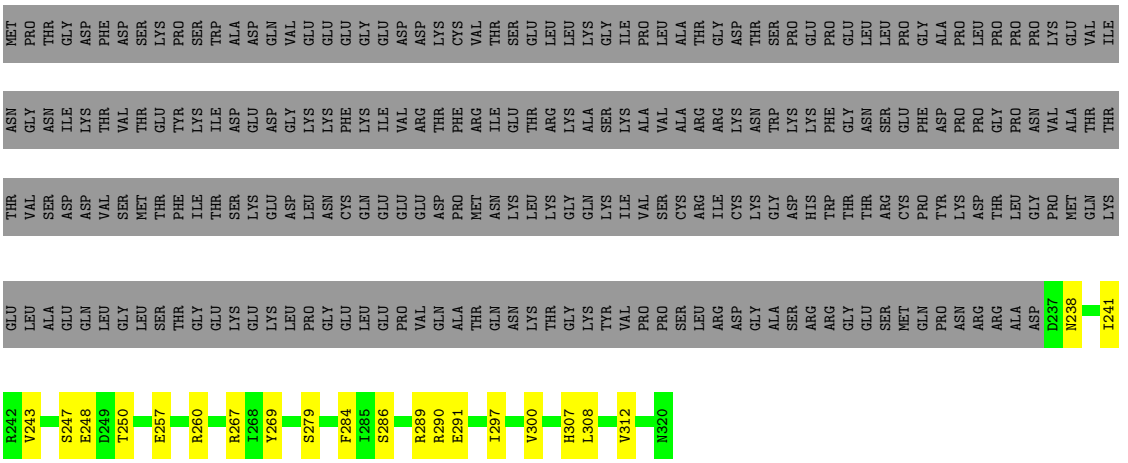
- Molecule 43: Eukaryotic translation initiation factor 3 subunit F

Chain 3F: 55% 20% 25%



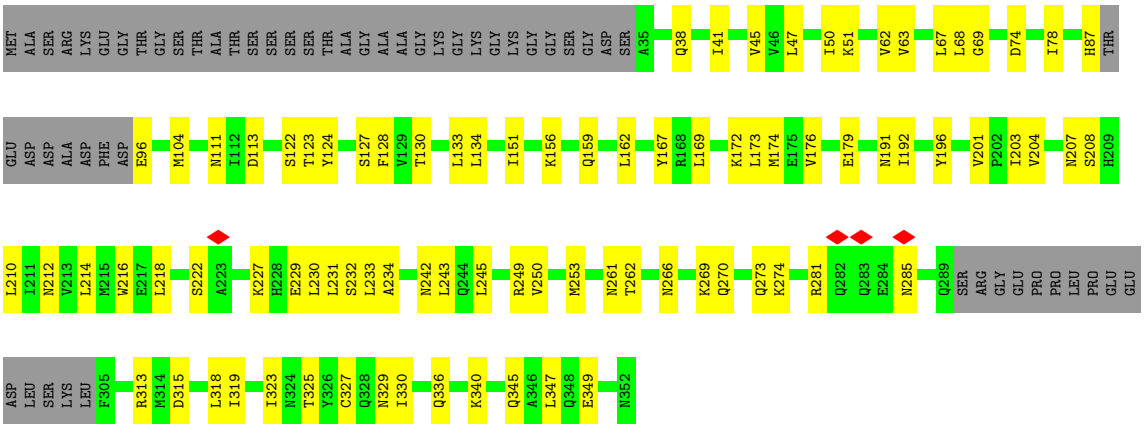
- Molecule 44: Eukaryotic translation initiation factor 3 subunit G

Chain 3G: 20% 7% 74%



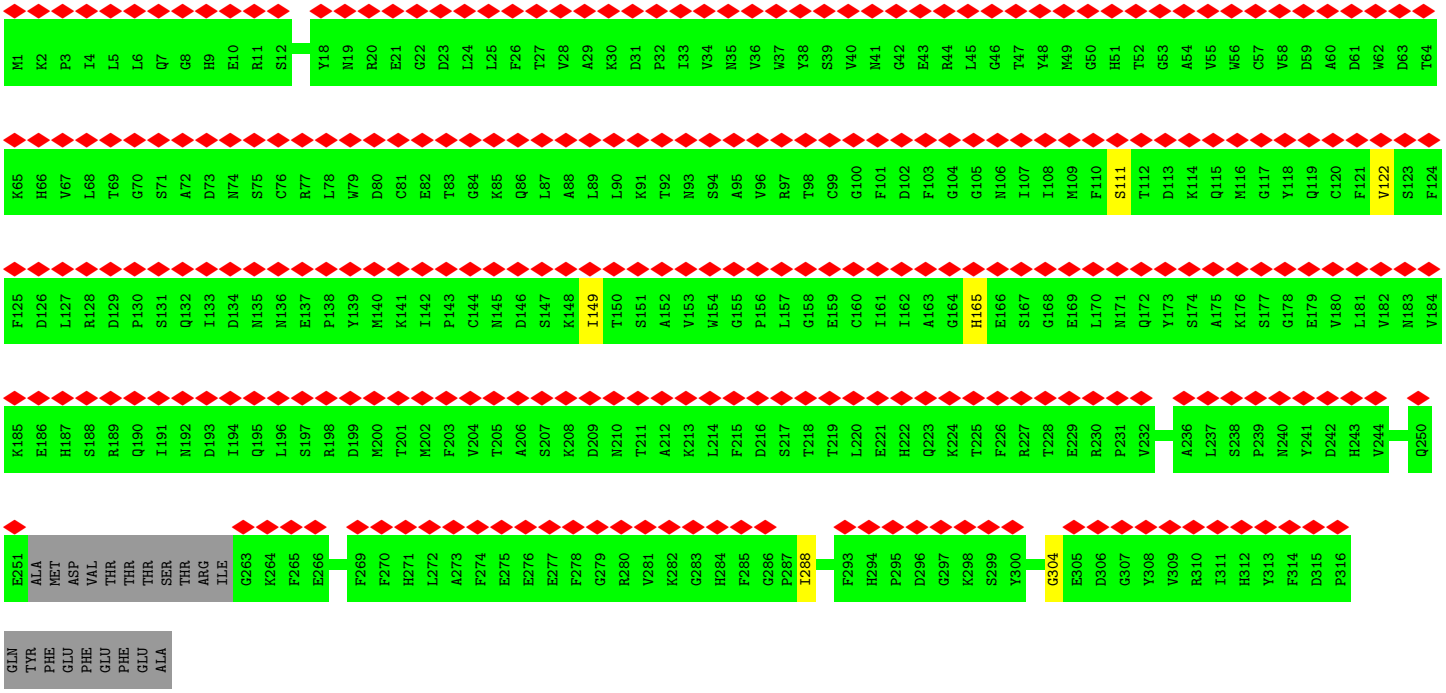
- Molecule 45: Eukaryotic translation initiation factor 3 subunit H

Chain 3H: 59% 25% 16%



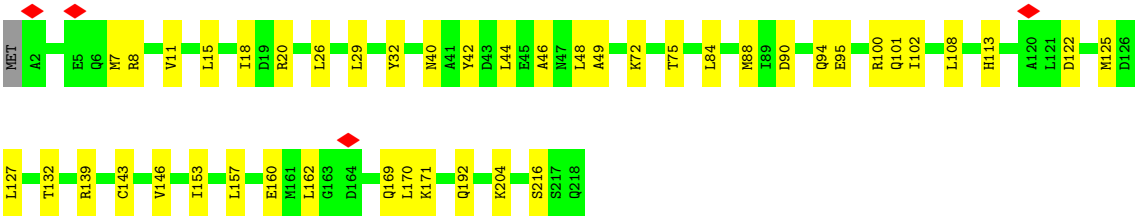
- Molecule 46: Eukaryotic translation initiation factor 3 subunit I

Chain 3I: 86% 92% 6%



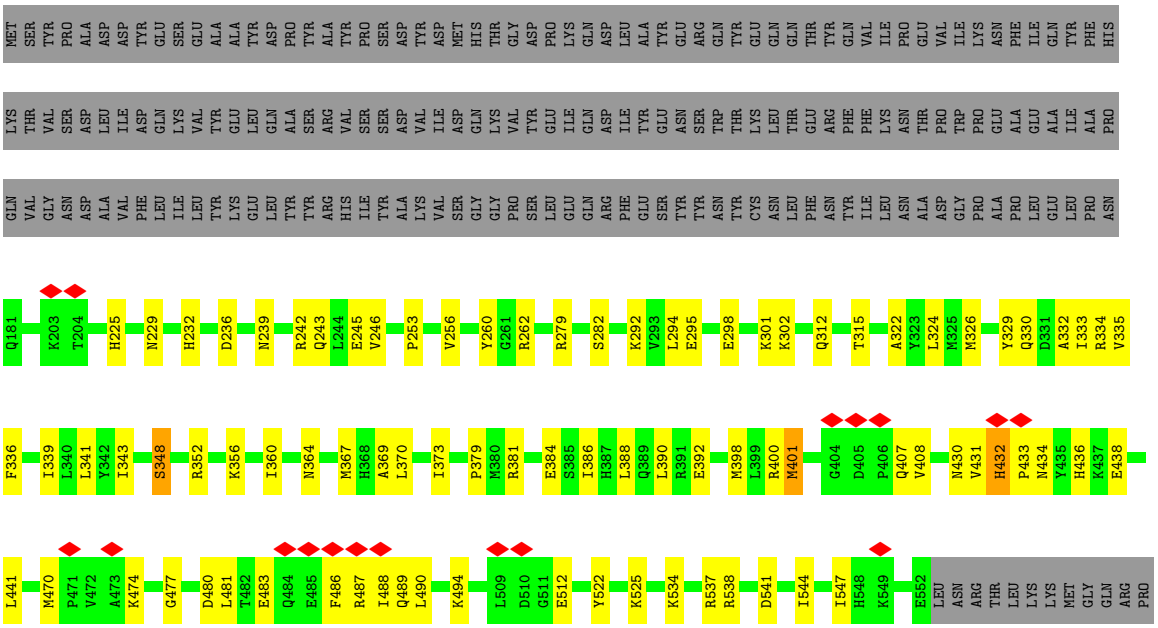
- Molecule 47: Eukaryotic translation initiation factor 3 subunit K

Chain 3K: 79% 20%



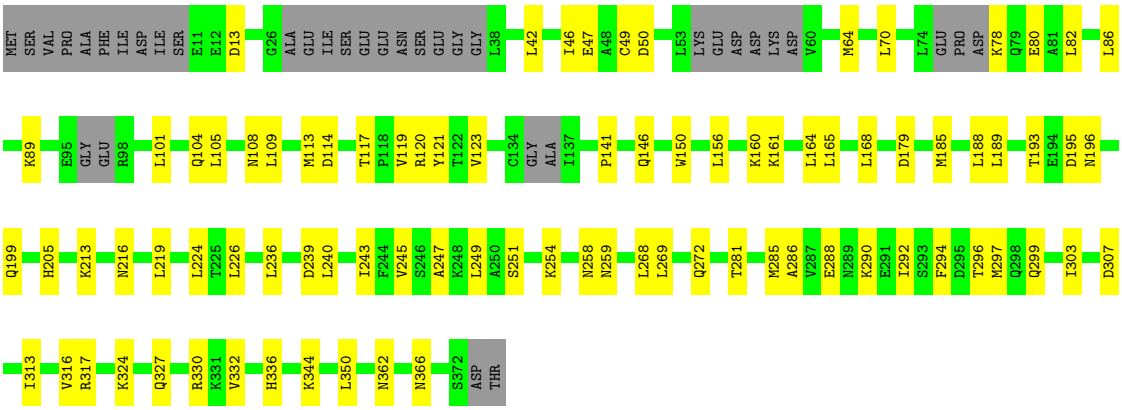
- Molecule 48: Eukaryotic translation initiation factor 3 subunit L

Chain 3L:



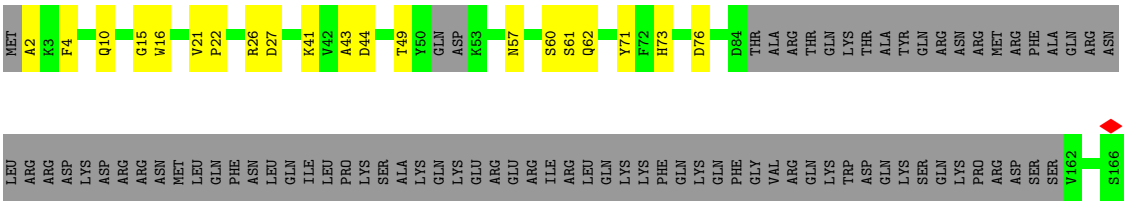
- Molecule 49: Eukaryotic translation initiation factor 3 subunit M

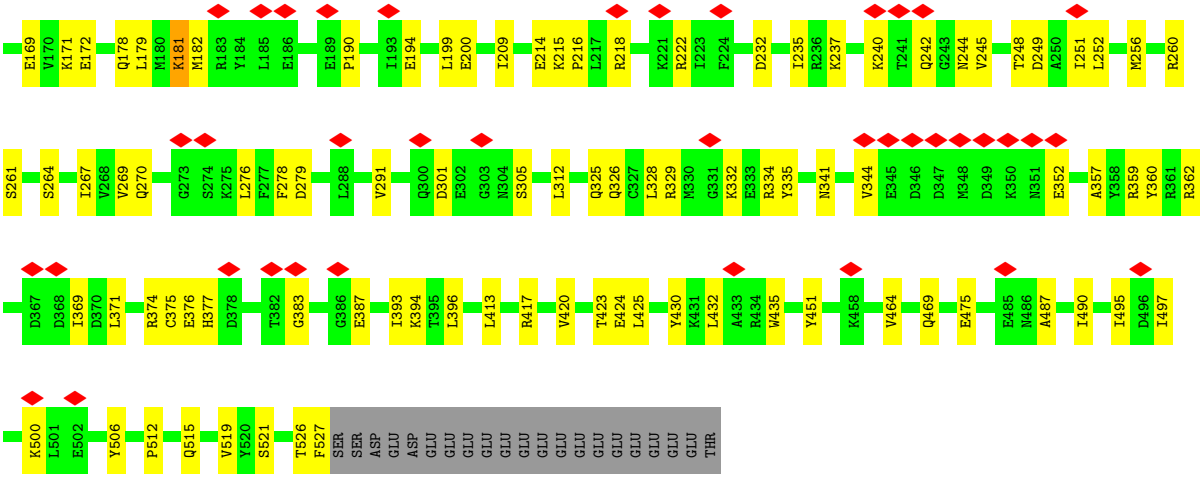
Chain 3M:



- Molecule 50: Eukaryotic translation initiation factor 3 subunit D

Chain 3N:




E169 V170 K171 E172 Q178 L179 M180 K181 M182 R183 Y184 L185 E186 E189 P190 I193 E194 L199 E200 I209 E214 K215 P216 L217 R218 K221 R222 I223 F224 D232 I235 R236 K237 K240 T241 Q242 G243 N244 V245 T248 D249 A250 I251 L252 M256 R260
S261 S264 I267 V268 V269 Q270 G273 S274 K275 L276 F277 F278 D279 L288 V291 Q300 D301 E302 G303 N304 S305 L312 Q325 Q326 C327 L328 R329 M330 G331 K332 E333 R334 Y335 N341 V344 E345 D346 D347 M348 D349 K350 N351 E352 A357 Y358 R359 Y360 R361 R362
D367 D368 I369 D370 L371 R374 C375 E376 H377 D378 T382 G383 G386 E387 I393 K394 T395 L396 L413 R417 V420 T423 E424 L425 Y430 K431 L432 A433 R434 W435 Y451 K458 V464 Q469 E475 E485 N486 A487 I490 I495 D496 I497
K500 L501 E502 Y506 P512 Q515 V519 Y520 S521 T526 F527 SER SER ASP GLU ASP GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU THR

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12788	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.375	Depositor
Minimum map value	-0.228	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	481.32, 481.32, 481.32	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.146, 1.146, 1.146	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	Ln	0.25	0/231	0.44	0/294
2	S2	0.30	0/40840	0.41	1/63635 (0.0%)
3	SA	0.35	0/1778	0.66	0/2416
4	SB	0.32	0/1765	0.75	3/2362 (0.1%)
5	SD	0.35	0/1793	0.76	1/2414 (0.0%)
6	SE	0.31	0/2118	0.67	2/2849 (0.1%)
7	SF	0.32	0/1516	0.80	2/2037 (0.1%)
8	SH	0.32	0/1519	0.78	5/2033 (0.2%)
9	SI	0.32	0/1715	0.79	0/2287
10	SK	0.29	0/851	0.67	0/1147
11	SL	0.31	0/1268	0.58	0/1696
12	SP	0.31	0/1003	0.85	0/1342
13	SQ	0.33	0/1160	0.78	2/1553 (0.1%)
14	SR	0.30	0/1105	0.79	2/1484 (0.1%)
15	SS	0.26	0/1216	0.62	0/1628
16	ST	0.31	0/1131	0.69	0/1515
17	SU	0.32	0/827	0.68	0/1110
18	SV	0.31	0/643	0.64	0/860
19	SX	0.37	0/1116	0.68	0/1490
20	Sa	0.36	0/836	0.73	0/1121
21	Sc	0.33	0/508	0.79	0/680
22	Sd	0.35	0/470	0.81	0/623
23	Sg	0.24	0/2493	0.67	2/3394 (0.1%)
24	SC	0.36	0/1762	0.71	2/2381 (0.1%)
25	SG	0.25	0/1946	0.65	2/2590 (0.1%)
26	SJ	0.34	0/1550	0.65	0/2069
27	SM	0.28	0/950	0.80	0/1275
28	SN	0.29	0/1232	0.60	0/1656
29	SO	0.40	0/1062	0.74	0/1425
30	SW	0.36	0/1051	0.58	0/1406
31	SY	0.29	0/1083	0.77	1/1438 (0.1%)
32	SZ	0.29	0/604	0.78	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Sb	0.32	0/665	0.69	0/891
34	Se	0.26	0/465	0.57	0/612
35	Sf	0.22	0/560	0.68	0/745
36	C1	0.25	0/442	0.65	0/611
37	4A	0.23	0/1687	0.69	0/2344
38	CD	0.38	0/1846	0.76	1/2550 (0.0%)
39	3A	0.22	0/5463	0.60	2/7394 (0.0%)
40	3B	0.20	0/2981	0.49	1/4115 (0.0%)
41	3C	0.25	0/5154	0.67	1/6942 (0.0%)
42	3E	0.22	0/3503	0.64	3/4728 (0.1%)
43	3F	0.22	0/2126	0.61	0/2890
44	3G	0.25	0/680	0.60	0/916
45	3H	0.21	0/2458	0.58	0/3313
46	3I	0.13	0/1495	0.38	0/2073
47	3K	0.19	0/1785	0.54	0/2414
48	3L	0.24	0/3187	0.66	6/4299 (0.1%)
49	3M	0.22	0/2743	0.60	1/3697 (0.0%)
50	3N	0.21	0/3699	0.58	2/5001 (0.0%)
All	All	0.29	0/120081	0.58	42/170555 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	SF	0	2
9	SI	0	1
14	SR	0	1
19	SX	0	5
21	Sc	0	1
26	SJ	0	1
32	SZ	0	1
33	Sb	0	2
43	3F	0	1
45	3H	0	1
48	3L	0	2
All	All	0	18

There are no bond length outliers.

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	SF	54	GLY	N-CA-C	7.70	121.44	112.50
48	3L	379	PRO	CA-C-N	7.44	135.09	121.70
48	3L	379	PRO	C-N-CA	7.44	135.09	121.70
48	3L	400	ARG	CA-C-N	-7.28	110.17	122.11
48	3L	400	ARG	C-N-CA	-7.28	110.17	122.11

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	SF	133	THR	Peptide
7	SF	79	HIS	Peptide
9	SI	159	SER	Peptide
14	SR	67	ARG	Peptide
19	SX	86	PRO	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	Ln	230	0	276	7	0
2	S2	36535	0	18416	345	0
3	SA	1741	0	1746	34	0
4	SB	1738	0	1809	25	0
5	SD	1765	0	1865	26	0
6	SE	2076	0	2177	23	0
7	SF	1495	0	1549	28	0
8	SH	1497	0	1590	18	0
9	SI	1686	0	1772	40	0
10	SK	827	0	854	10	0
11	SL	1247	0	1323	20	0
12	SP	985	0	1031	29	0
13	SQ	1142	0	1213	25	0
14	SR	1090	0	1149	23	0
15	SS	1198	0	1261	30	0
16	ST	1112	0	1146	19	0
17	SU	817	0	882	18	0
18	SV	636	0	637	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	SX	1098	0	1167	15	0
20	Sa	821	0	870	16	0
21	Sc	506	0	536	11	0
22	Sd	459	0	448	11	0
23	Sg	2436	0	2393	53	0
24	SC	1725	0	1813	27	0
25	SG	1923	0	2088	41	0
26	SJ	1525	0	1640	36	0
27	SM	940	0	965	26	0
28	SN	1208	0	1294	14	0
29	SO	1049	0	1073	18	0
30	SW	1034	0	1080	16	0
31	SY	1065	0	1142	35	0
32	SZ	598	0	656	15	0
33	Sb	651	0	672	13	0
34	Se	459	0	503	8	0
35	Sf	548	0	555	11	0
36	C1	443	0	201	2	0
37	4A	1691	0	753	5	0
38	CD	1841	0	998	5	0
39	3A	5379	0	5155	92	0
40	3B	2966	0	1764	19	0
41	3C	5070	0	5110	98	0
42	3E	3437	0	3433	70	0
43	3F	2090	0	2092	57	0
44	3G	667	0	647	14	0
45	3H	2413	0	2411	70	0
46	3I	1497	0	676	3	0
47	3K	1750	0	1717	30	0
48	3L	3111	0	3085	61	0
49	3M	2705	0	2759	55	0
50	3N	3617	0	3495	73	0
51	S2	22	0	0	0	0
51	SG	1	0	0	0	0
52	Sa	1	0	0	0	0
52	Sd	1	0	0	0	0
52	Sf	1	0	0	0	0
All	All	114565	0	93887	1511	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 7.

The worst 5 of 1511 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)
41:3C:697:TYR:HH	41:3C:708:ARG:N	1.57	1.03
2:S2:886:A:N6	2:S2:901:G:C4	2.31	0.98
2:S2:885:U:H3	2:S2:901:G:H1	1.07	0.96
20:Sa:88:SER:O	20:Sa:92:ARG:HB2	1.64	0.96
2:S2:1609:C:H42	2:S2:1630:A:H61	1.02	0.93

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Ln	23/24 (96%)	23 (100%)	0	100	100
3	SA	183/243 (75%)	183 (100%)	0	100	100
4	SB	195/231 (84%)	195 (100%)	0	100	100
5	SD	190/202 (94%)	189 (100%)	1 (0%)	81	80
6	SE	224/225 (100%)	224 (100%)	0	100	100
7	SF	159/170 (94%)	158 (99%)	1 (1%)	78	79
8	SH	166/174 (95%)	166 (100%)	0	100	100
9	SI	178/180 (99%)	177 (99%)	1 (1%)	78	79
10	SK	89/136 (65%)	89 (100%)	0	100	100
11	SL	137/142 (96%)	136 (99%)	1 (1%)	76	78
12	SP	107/130 (82%)	107 (100%)	0	100	100
13	SQ	119/121 (98%)	119 (100%)	0	100	100
14	SR	122/122 (100%)	121 (99%)	1 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	SS	126/132 (96%)	126 (100%)	0	100	100
16	ST	113/115 (98%)	112 (99%)	1 (1%)	70	76
17	SU	94/107 (88%)	94 (100%)	0	100	100
18	SV	67/67 (100%)	67 (100%)	0	100	100
19	SX	113/115 (98%)	113 (100%)	0	100	100
20	Sa	89/98 (91%)	89 (100%)	0	100	100
21	Sc	57/62 (92%)	57 (100%)	0	100	100
22	Sd	48/49 (98%)	48 (100%)	0	100	100
23	Sg	272/275 (99%)	272 (100%)	0	100	100
24	SC	188/225 (84%)	188 (100%)	0	100	100
25	SG	207/218 (95%)	206 (100%)	1 (0%)	81	80
26	SJ	161/168 (96%)	161 (100%)	0	100	100
27	SM	102/108 (94%)	102 (100%)	0	100	100
28	SN	130/131 (99%)	129 (99%)	1 (1%)	73	77
29	SO	110/119 (92%)	107 (97%)	3 (3%)	39	61
30	SW	112/113 (99%)	112 (100%)	0	100	100
31	SY	113/115 (98%)	113 (100%)	0	100	100
32	SZ	66/103 (64%)	66 (100%)	0	100	100
33	Sb	75/76 (99%)	75 (100%)	0	100	100
34	Se	47/48 (98%)	47 (100%)	0	100	100
35	Sf	60/140 (43%)	60 (100%)	0	100	100
38	CD	37/404 (9%)	37 (100%)	0	100	100
39	3A	544/1259 (43%)	544 (100%)	0	100	100
40	3B	90/702 (13%)	89 (99%)	1 (1%)	65	74
41	3C	553/811 (68%)	553 (100%)	0	100	100
42	3E	380/406 (94%)	380 (100%)	0	100	100
43	3F	237/289 (82%)	237 (100%)	0	100	100
44	3G	70/277 (25%)	70 (100%)	0	100	100
45	3H	269/310 (87%)	269 (100%)	0	100	100
47	3K	192/193 (100%)	192 (100%)	0	100	100
48	3L	342/515 (66%)	341 (100%)	1 (0%)	86	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	3M	304/335 (91%)	304 (100%)	0	100	100
50	3N	398/494 (81%)	398 (100%)	0	100	100
All	All	7658/10679 (72%)	7645 (100%)	13 (0%)	85	85

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	SN	36	GLN
29	SO	67	ASP
48	3L	407	GLN
29	SO	105	THR
40	3B	497	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
41	3C	519	HIS
45	3H	242	ASN
41	3C	637	GLN
43	3F	160	HIS
47	3K	57	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	S2	1699/1869 (90%)	431 (25%)	4 (0%)

5 of 431 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	S2	2	A
2	S2	4	C
2	S2	17	C
2	S2	23	G
2	S2	25	A

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	S2	112	U
2	S2	291	G
2	S2	688	U
2	S2	1434	C

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 26 ligands modelled in this entry, 26 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

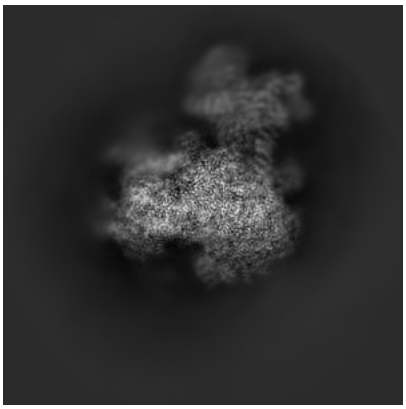
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-38754. 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



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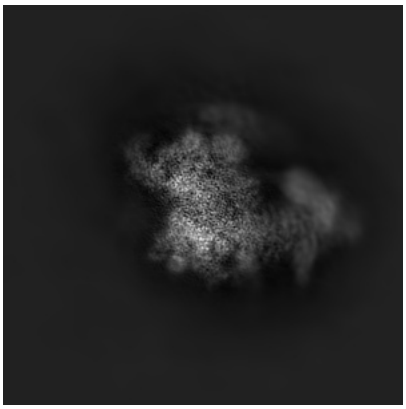
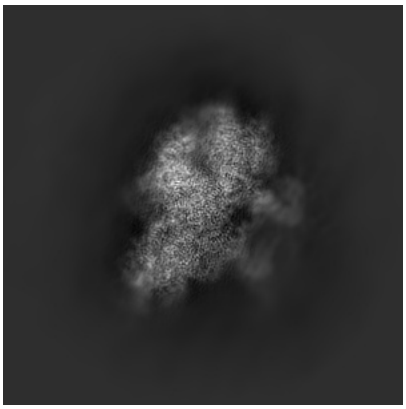
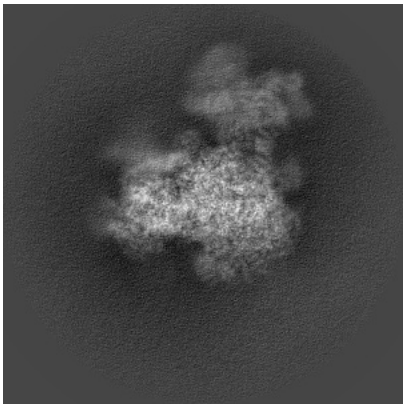


Y

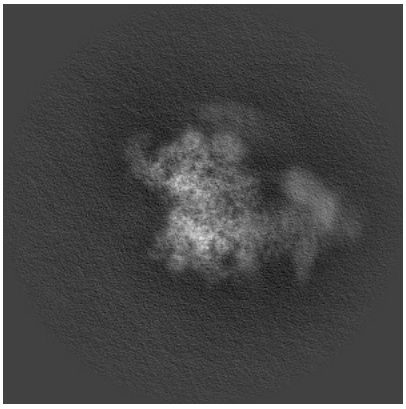


Z

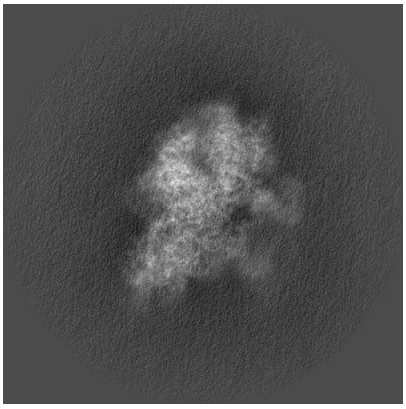
6.1.2 Raw map



X



Y



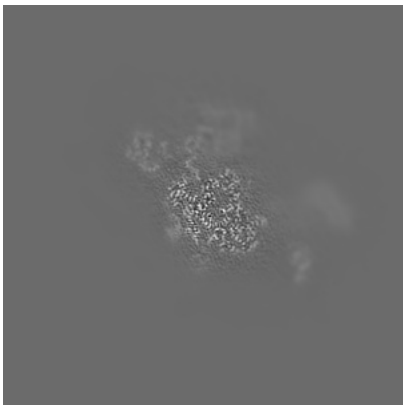
Z

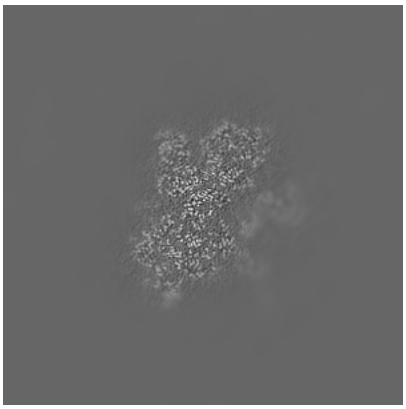
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

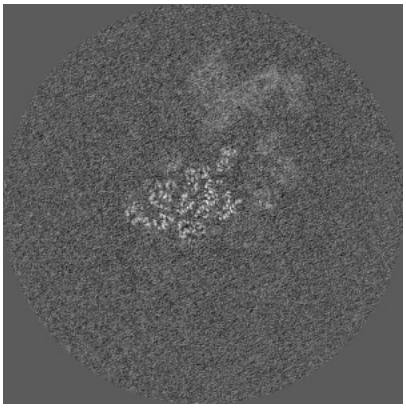
6.2.1 Primary map

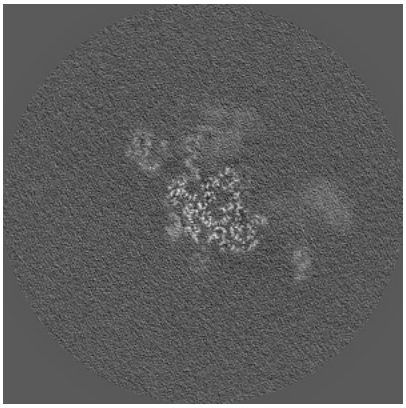
X Index: 210

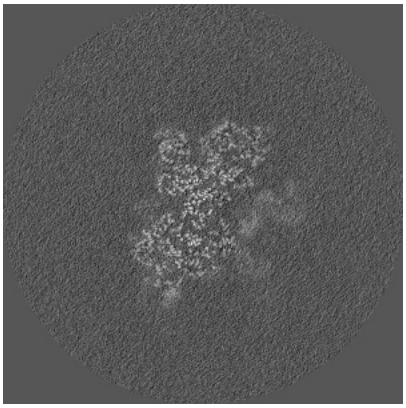

Y Index: 210


Z Index: 210

6.2.2 Raw map


X Index: 210

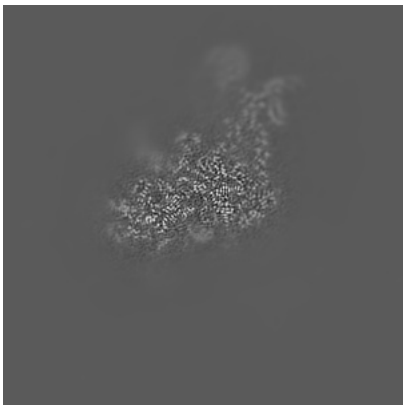

Y Index: 210


Z Index: 210

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

6.3 Largest variance slices (i)

6.3.1 Primary map



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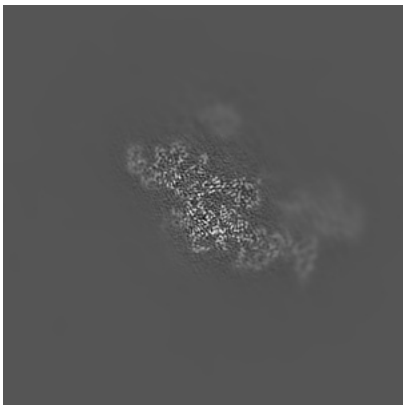
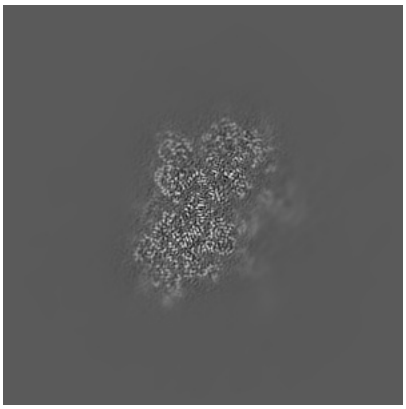


Y Index: 231



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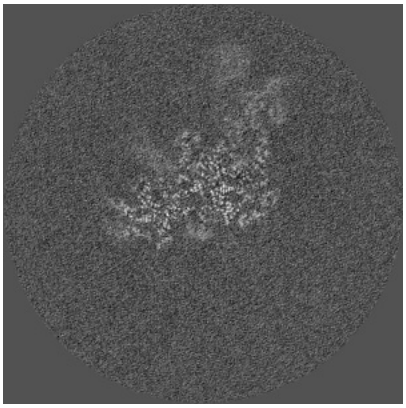
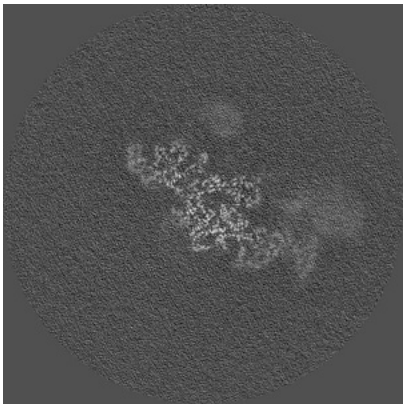
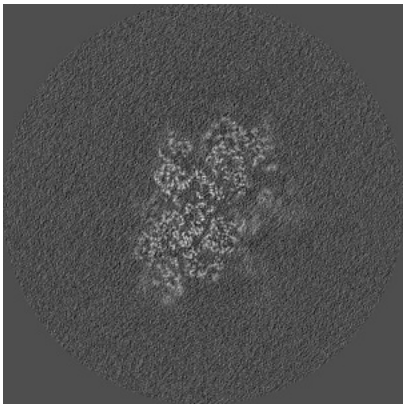
6.3.2 Raw map



X Index: 182



Y Index: 231

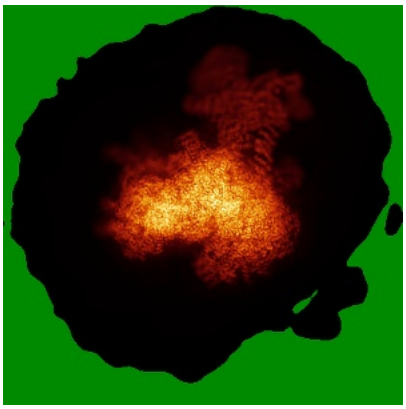


Z Index: 206

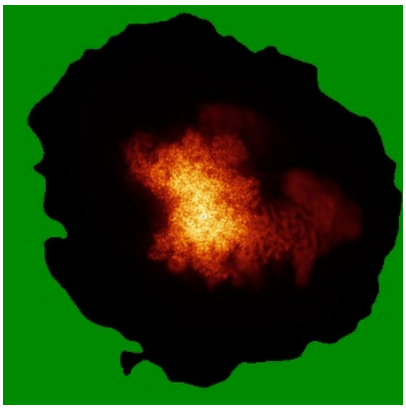
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

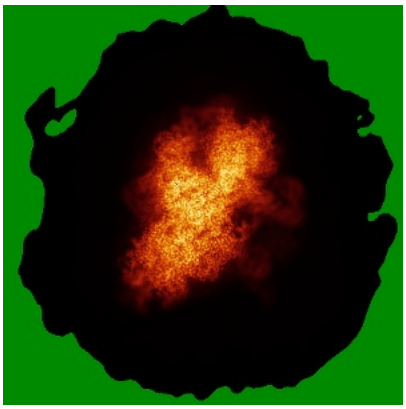
6.4.1 Primary map



X

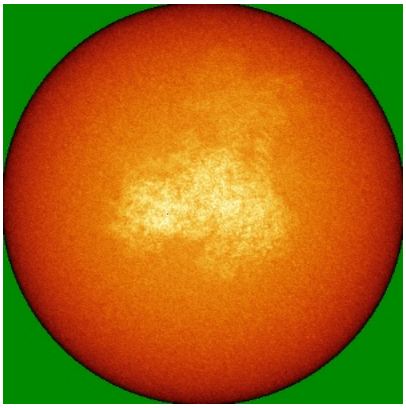


Y

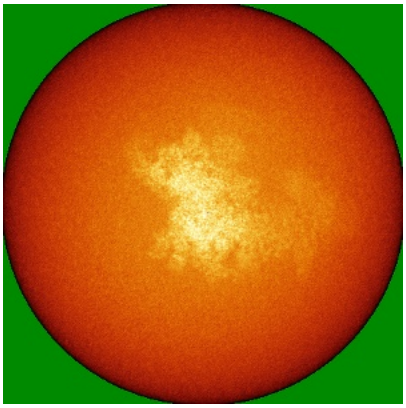


Z

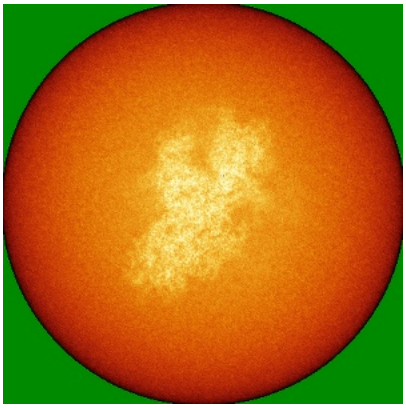
6.4.2 Raw map



X



Y

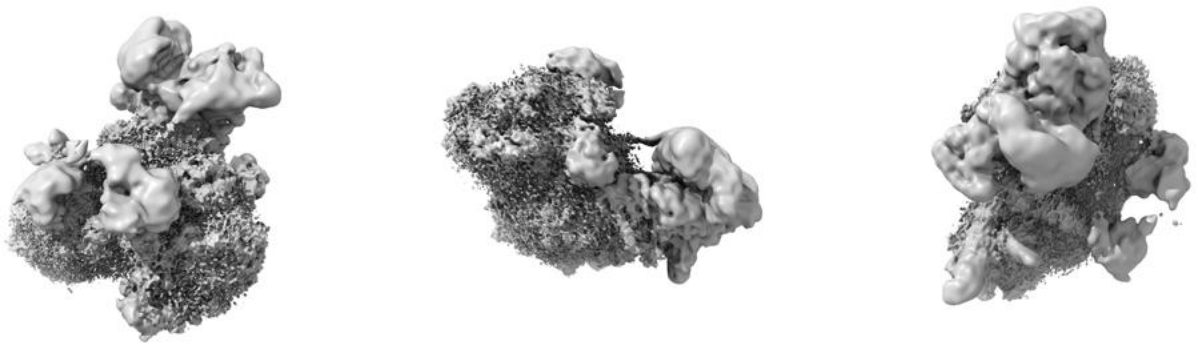


Z

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)

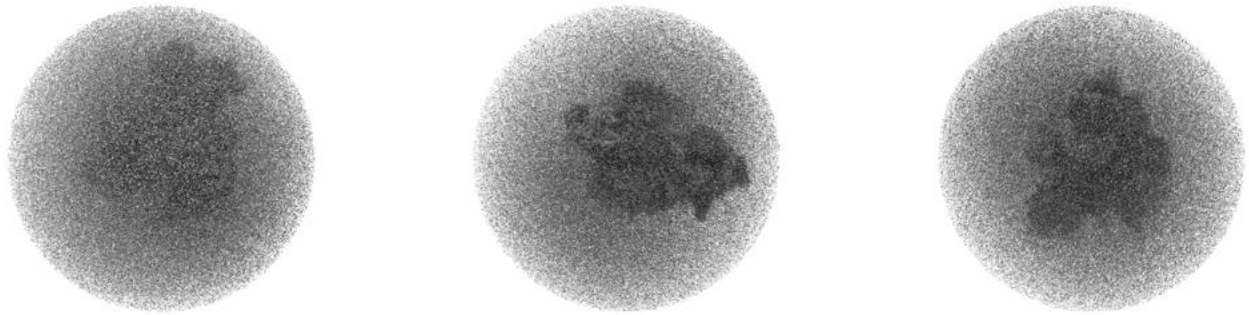
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. 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



X Y Z

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.

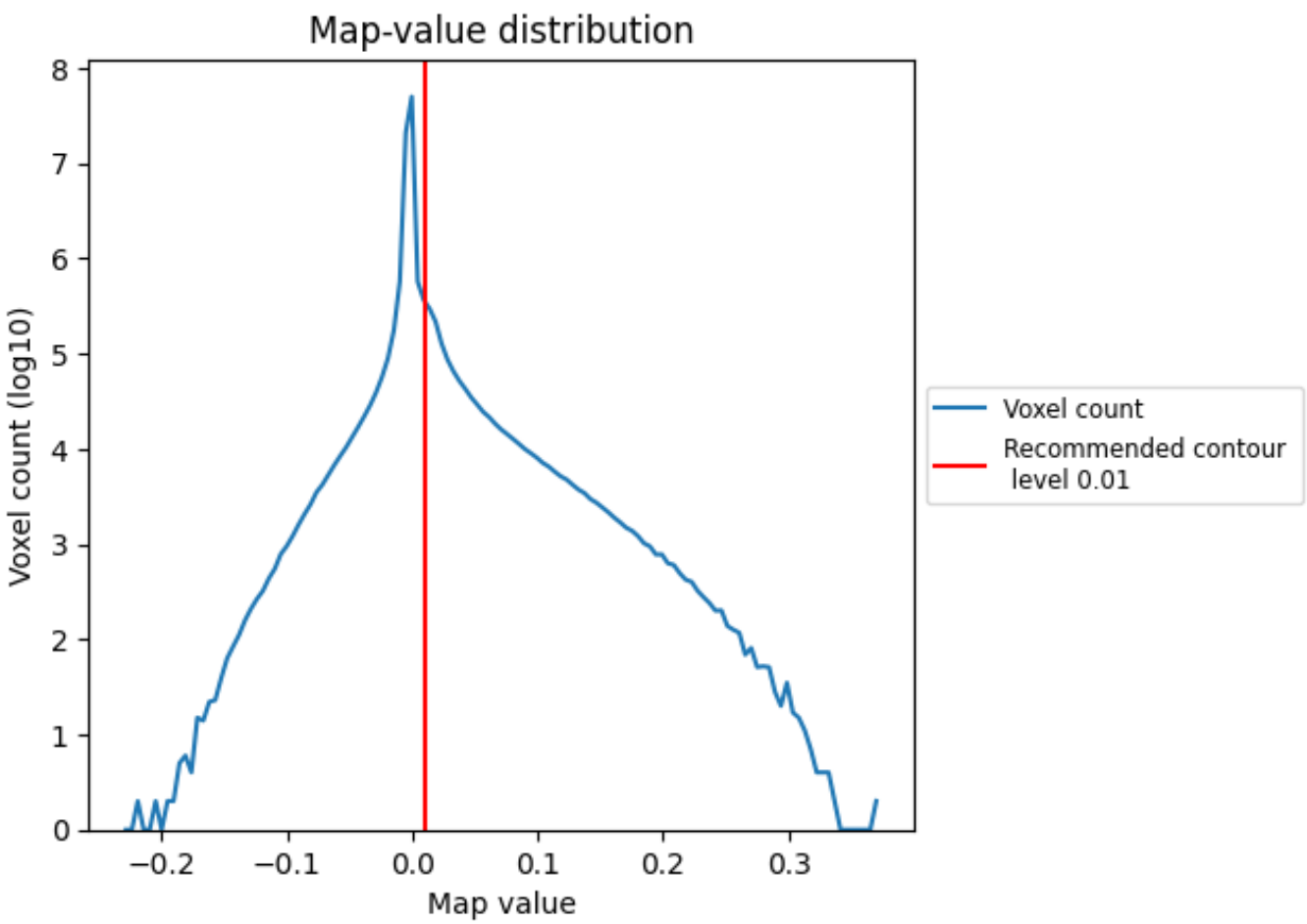
6.6 Mask visualisation (i)

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

7 Map analysis (i)

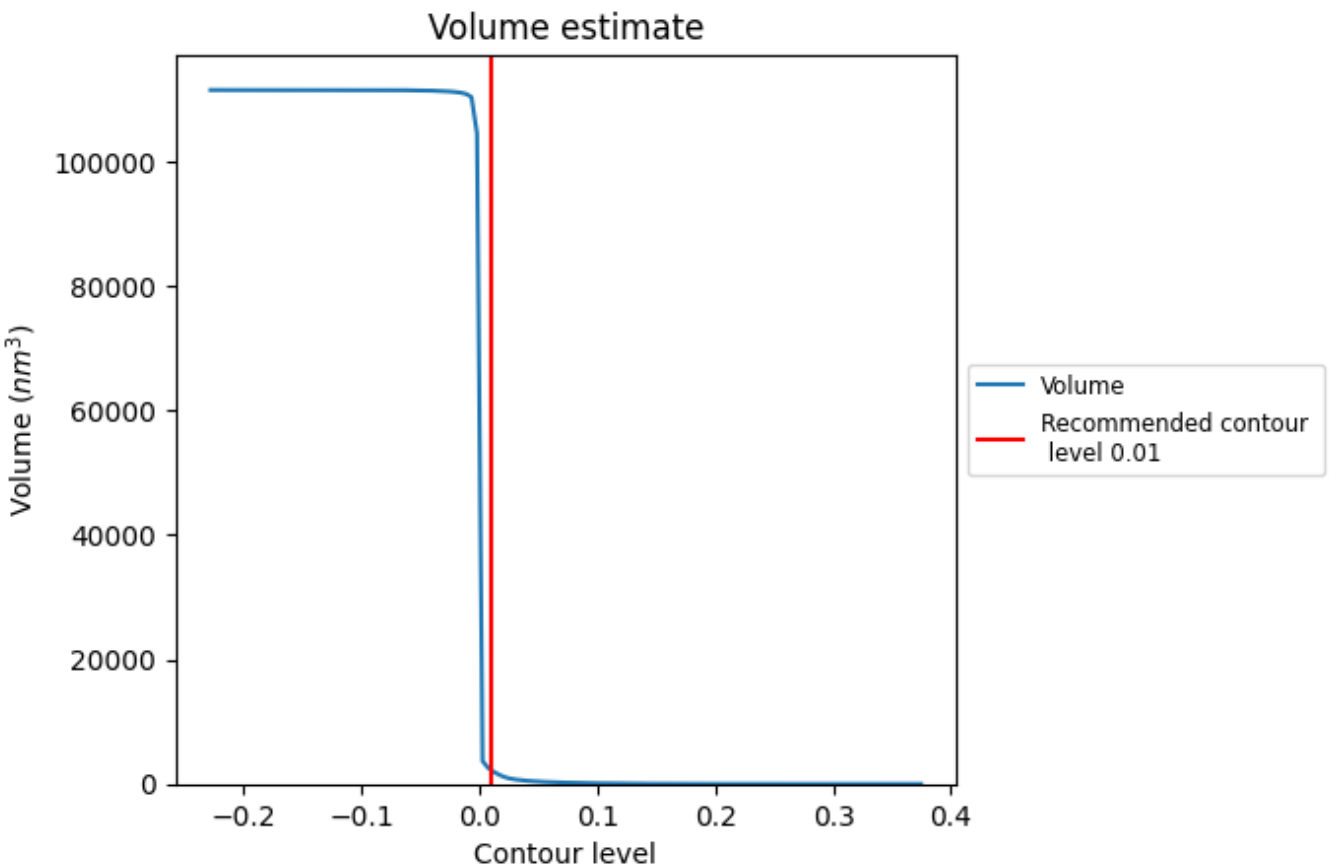
This section contains the results of statistical analysis of the map.

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.

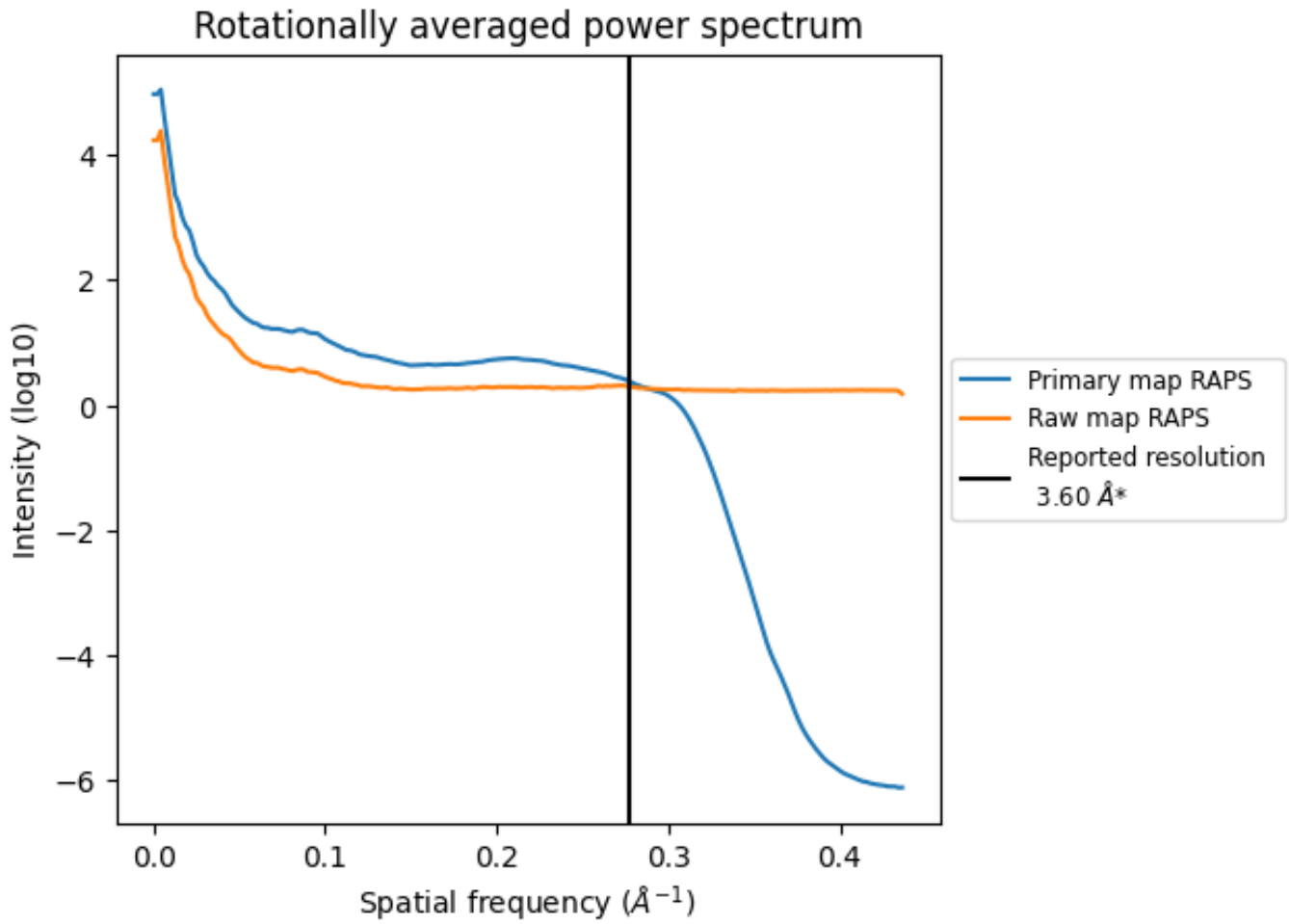
7.2 Volume estimate (i)



The volume at the recommended contour level is 2214 nm^3; this corresponds to an approximate mass of 2000 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)

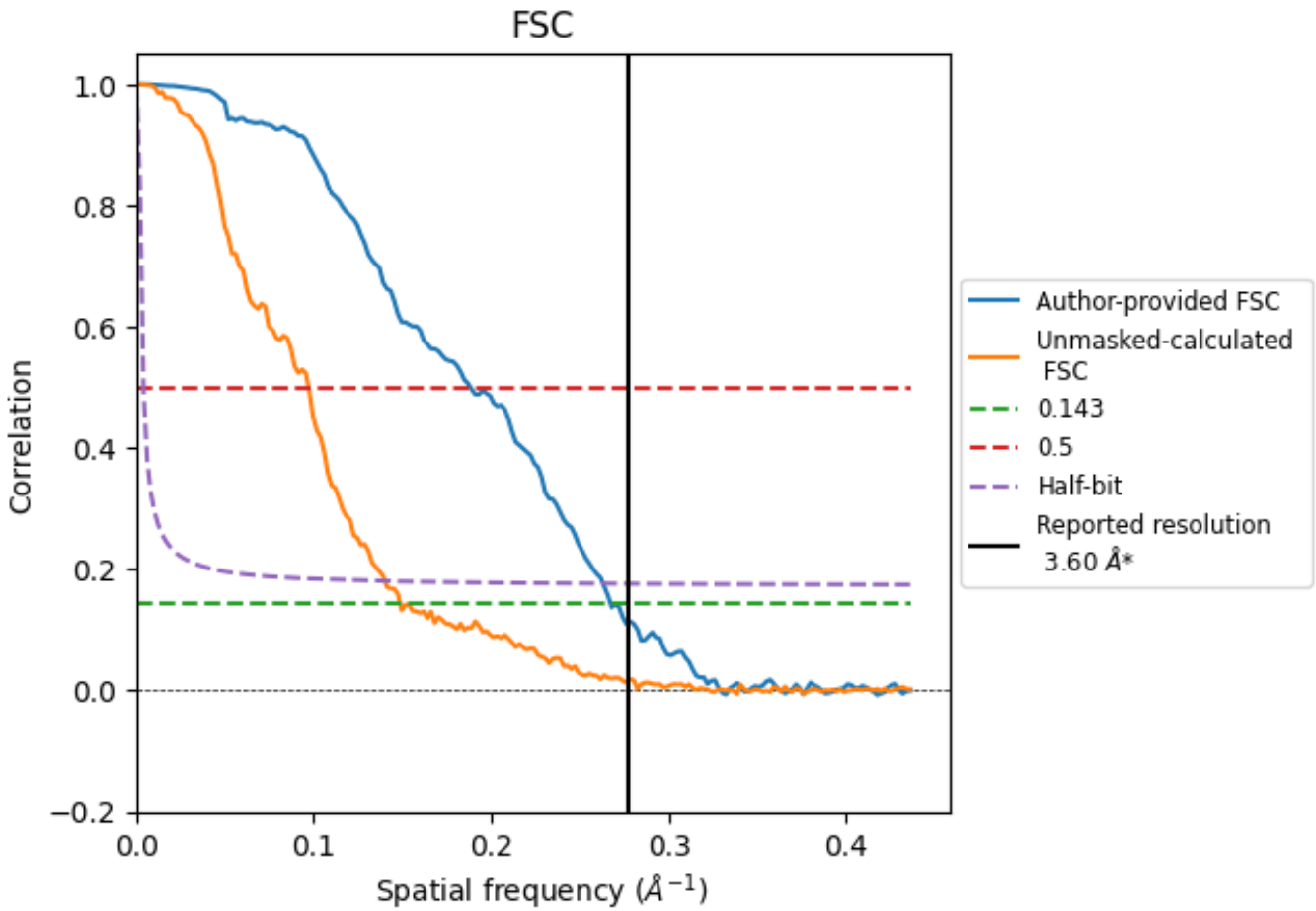


*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.74	5.31	3.80
Unmasked-calculated*	6.72	10.29	7.13

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.72 differs from the reported value 3.6 by more than 10 %

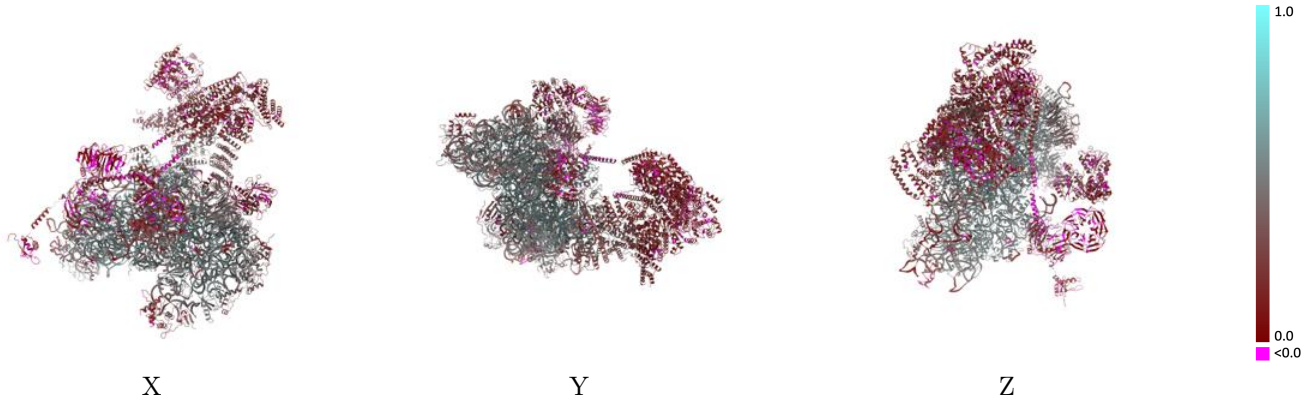
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-38754 and PDB model 8XXN. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay (i)

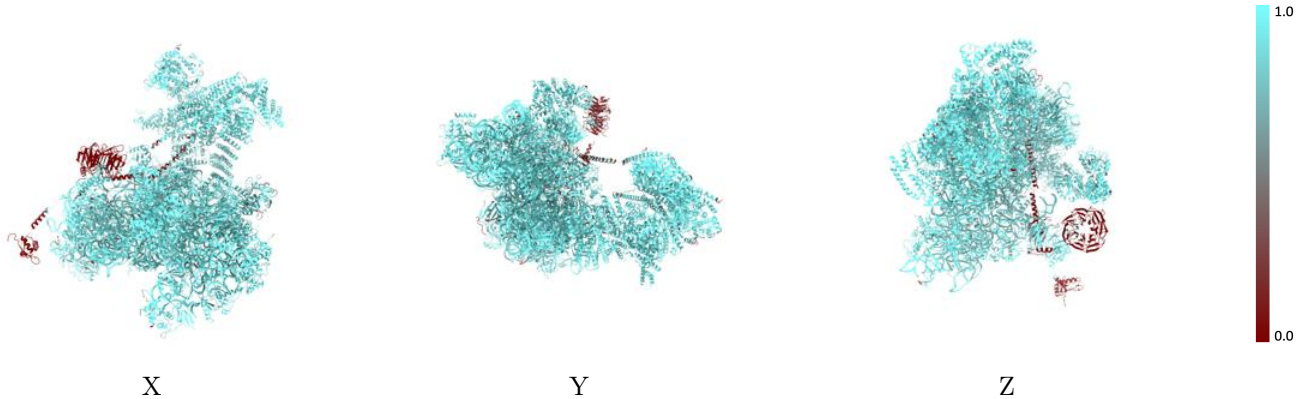
This section was not generated.

9.2 Q-score mapped to coordinate model (i)



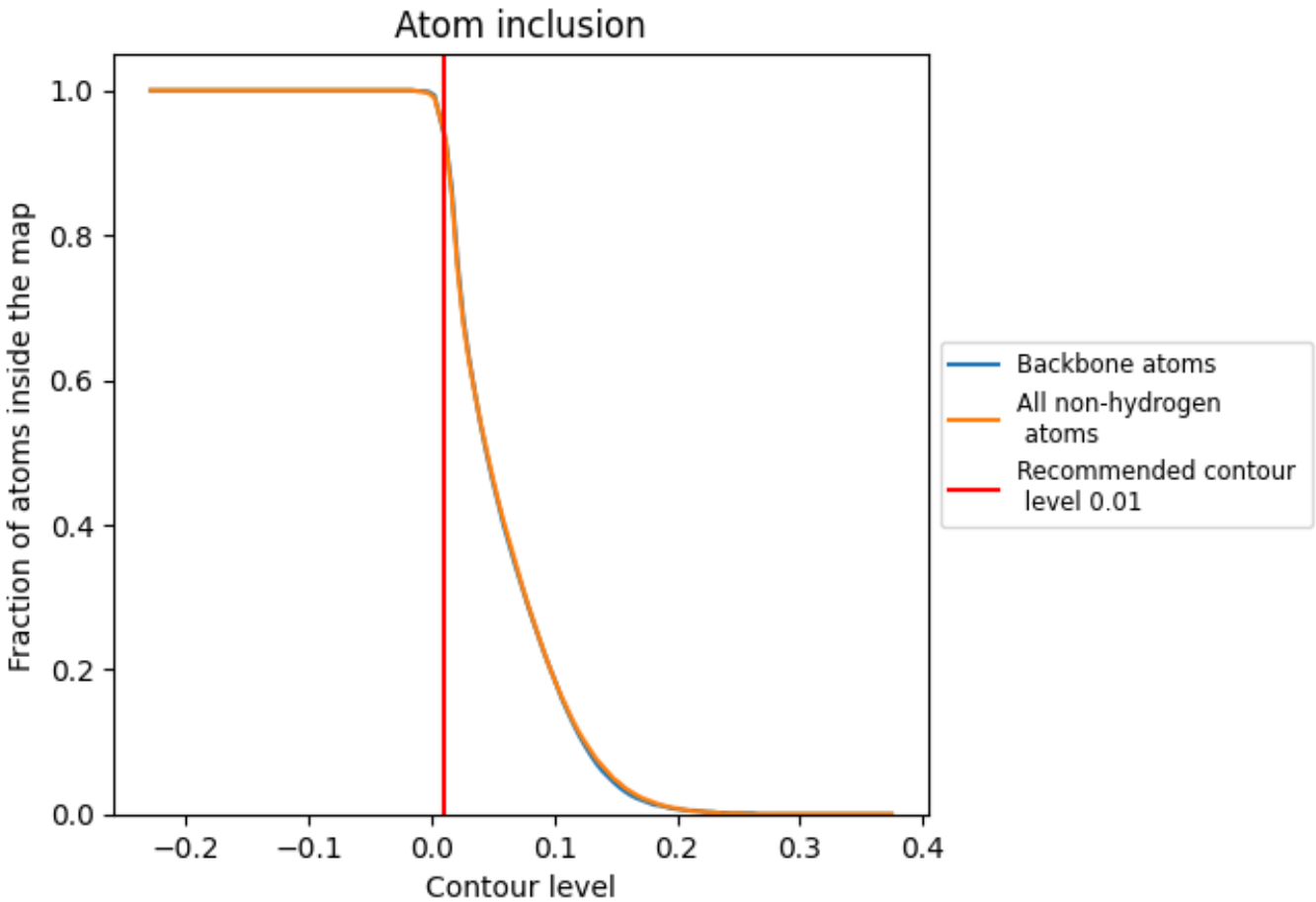
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9450	0.3740
3A	0.9040	0.2270
3B	0.7020	0.1290
3C	0.9470	0.3030
3E	0.9700	0.1700
3F	0.9620	0.1150
3G	0.9830	0.3040
3H	0.9600	0.1330
3I	0.0760	0.0340
3K	0.9530	0.1120
3L	0.9440	0.1020
3M	0.9870	0.1520
3N	0.8220	0.1860
4A	0.9480	0.1480
C1	0.6820	0.2590
CD	0.9670	0.2320
Ln	0.8520	0.3970
S2	0.9900	0.4850
SA	0.9610	0.4950
SB	0.9770	0.4800
SC	0.9740	0.5270
SD	0.9720	0.4950
SE	0.9830	0.5260
SF	0.9510	0.4530
SG	0.9840	0.4140
SH	0.9690	0.4300
SI	0.9780	0.4550
SJ	0.9730	0.5110
SK	0.9790	0.4530
SL	0.9600	0.5040
SM	0.9200	0.2250
SN	0.9800	0.5050
SO	0.9430	0.4670
SP	0.9570	0.4420
SQ	0.9600	0.4990

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Chain	Atom inclusion	Q-score
SR	0.9500	0.4640
SS	0.9470	0.4140
ST	0.9690	0.4540
SU	0.9640	0.4310
SV	0.9840	0.5070
SW	0.9810	0.5560
SX	0.9800	0.5370
SY	0.9560	0.4710
SZ	0.9190	0.3480
Sa	0.9730	0.5240
Sb	0.9560	0.4980
Sc	0.9360	0.4050
Sd	0.9820	0.5310
Se	0.9370	0.4670
Sf	0.9480	0.3020
Sg	0.9820	0.3780