



wwPDB EM Validation Summary Report ⓘ

Apr 20, 2024 – 07:12 pm BST

PDB ID : 7QP7
EMDB ID : EMD-14114
Title : Structure of the human 48S initiation complex in closed state (h48S AUG closed)
Authors : Yi, S.-H.; Petrychenko, V.; Schliep, J.E.; Goyal, A.; Linden, A.; Chari, A.; Urlaub, H.; Stark, H.; Rodnina, M.V.; Adio, S.; Fischer, N.
Deposited on : 2022-01-03
Resolution : 3.70 Å (reported)
Based on initial model : 6ZMW

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:

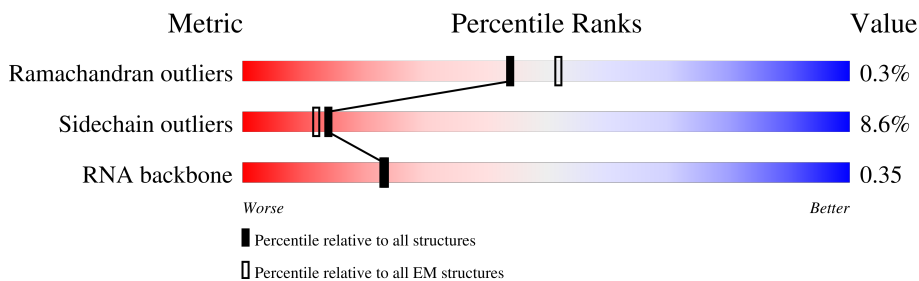
EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

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 3.70 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.











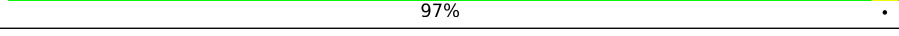
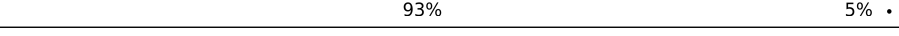
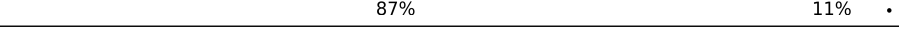
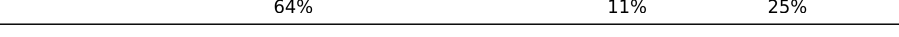

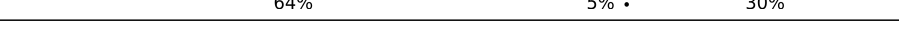


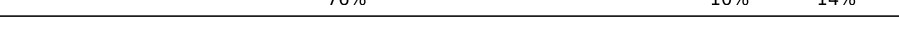

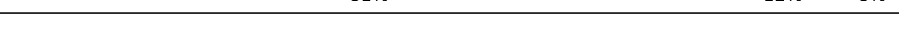






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	1	813	19% (Upper red bar) 55% (Green) 45% (Grey)
2	3	218	64% (Red) 97% (Green) . (Grey)
3	4	357	15% (Upper red bar) 71% (Green) . (Yellow) 28% (Grey)
4	5	564	17% (Upper red bar) 57% (Green) 43% (Grey)
5	6	374	32% (Upper red bar) 93% (Green) 6% (Grey)
6	7	255	. . . (Yellow, Orange, Red) 92% (Green)
7	8	352	21% (Upper red bar) 89% (Green) . (Yellow) 10% (Grey)
8	9	25	92% (Green) . . (Yellow, Grey)



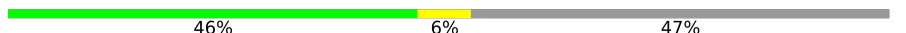











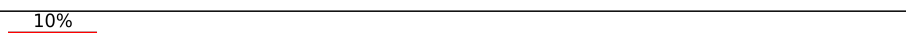
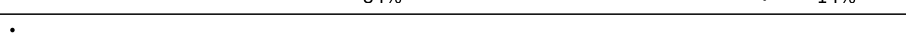


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	A	1869	 63% 28% 8%
10	B	158	 81% 9% 10%
11	C	263	 90% 8%
12	D	194	 87% 9%
13	E	143	 88% 10%
14	F	59	 75% 5% 20%
15	G	194	 81% 10% 9%
16	H	84	 83% 13%
17	I	151	 97%
18	J	130	 93% 5%
19	K	83	 87% 11%
20	L	293	 64% 11% 25%
21	M	135	 82% 10% 7%
22	N	295	 64% 5% 30%
23	O	264	 80% 20%
24	P	151	 74% 14% 12%
25	Q	115	 76% 10% 14%
26	R	208	 88% 8% 5%
27	S	249	 81% 12% 8%
28	T	133	 85% 9% 6%
29	V	204	 83% 7% 10%
30	Y	146	 90% 6%
31	Z	243	 79% 14% 7%
32	a	165	 56% 40%
33	b	145	 67% 9% 24%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	c	317	 85% 13%
35	d	145	 90% 8%
36	e	125	 46% 6% 47%
37	f	152	 85% 9% 7%
38	h	119	 75% 12% 13%
39	i	56	 79% 11% 11%
40	k	156	 26% 8% 66%
41	m	132	 5% 85% 8% 8%
42	n	69	 78% 12% 9%
43	o	320	 23% 76%
44	q	144	 53% 17% 30%
45	r	315	 73% 14% 13%
46	t	472	 75% 25%
47	u	1382	 10% 50% 49%
48	v	445	 10% 84% 14%
49	w	75	 44% 56%
50	x	548	 13% 74% 23%
51	y	913	 69% 30%

2 Entry composition [i](#)

There are 52 unique types of molecules in this entry. The entry contains 108194 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 Eukaryotic translation initiation factor 3 subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	1	447	2560	1570	492	493	5	0	0

- Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	3	213	1057	631	213	213	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	4	257	1272	757	257	258	0	0

- Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	5	319	1581	943	319	319	0	0

- Molecule 5 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	6	350	1917	1159	376	380	2	0	0

- Molecule 6 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	7	21	441	199	78	144	20	0	0

- Molecule 7 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	8	317	1571	936	317	318	0	0

- Molecule 8 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	9	24	230	139	62	26	3	0	0

- Molecule 9 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	A	1719	36668	16378	6574	11998	1718	0	0

- Molecule 10 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	B	142	1166	743	218	199	6	0	0

- Molecule 11 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	C	256	2035	1302	378	347	8	0	0

- Molecule 12 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	D	177	1477	941	295	239	2	0	0

- Molecule 13 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	E	140	1087	687	215	182	3	0	0

- Molecule 14 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	47	Total	C	N	O	S	0	0
			378	231	85	61	1		

- Molecule 15 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	177	Total	C	N	O	S	0	0
			1430	917	260	252	1		

- Molecule 16 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	81	Total	C	N	O	S	0	0
			631	397	116	111	7		

- Molecule 17 is a protein called 40S ribosomal protein S13.

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

- Molecule 18 is a protein called 40S ribosomal protein S15a.

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

- Molecule 19 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	81	Total	C	N	O	S	0	0
			617	380	114	118	5		

- Molecule 20 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	220	Total	C	N	O	S	0	0
			1707	1104	292	301	10		

- Molecule 21 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	125	Total	C	N	O	S	0	0
			1015	639	185	187	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	207	Total	C	N	O	S	0	0
			1633	1040	288	297	8		

- Molecule 23 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	211	Total	C	N	O	S	0	0
			1715	1088	307	306	14		

- Molecule 24 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	133	Total	C	N	O	S	0	0
			997	610	196	185	6		

- Molecule 25 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 26 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	198	Total	C	N	O	S	0	0
			1627	1021	322	279	5		

- Molecule 27 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 28 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 29 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 30 is a protein called 40S ribosomal protein S16.

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

- Molecule 31 is a protein called 40S ribosomal protein S3.

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

- Molecule 32 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	99	Total	C	N	O	S	0	0
			834	544	149	135	6		

- Molecule 33 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	110	Total	C	N	O	S	0	0
			913	580	168	158	7		

- Molecule 34 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 35 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	142	Total	C	N	O	S	0	0
			1105	692	213	197	3		

- Molecule 36 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	66	Total	C	N	O	S	0	0
			523	338	93	91	1		

- Molecule 37 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	142	Total	C	N	O	S	0	0
			1176	737	239	199	1		

- Molecule 38 is a protein called 40S ribosomal protein S20.

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

- Molecule 39 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	50	Total	C	N	O	S	0	0
			419	262	85	67	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	53	Total	C	N	O	S	0	0
			435	276	82	70	7		

- Molecule 41 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	122	Total	C	N	O	S	0	0
			950	596	168	177	9		

- Molecule 42 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	63	Total	C	N	O	S	0	0
			498	302	101	93	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
43	o	77	Total	C	N	O	0	0
			616	389	111	116		

- Molecule 44 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	101	Total	C	N	O	S	0	0
			782	494	141	143	4		

- Molecule 45 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	275	Total	C	N	O	S	0	0
			2215	1398	387	418	12		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	t	356	Total	C	N	O	0	0
			1750	1038	356	356		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	u	706	Total	C	N	O	S	1	0
			5383	3379	982	999	23		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	384	Total	C	N	O	S	0	0
			2635	1657	477	489	12		

- Molecule 49 is a RNA chain called Initiator Met-tRNA-i.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	w	75	1604	717	298	515	74	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	x	421	2831	1746	521	555	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	y	642	5197	3274	925	963	35	0	0

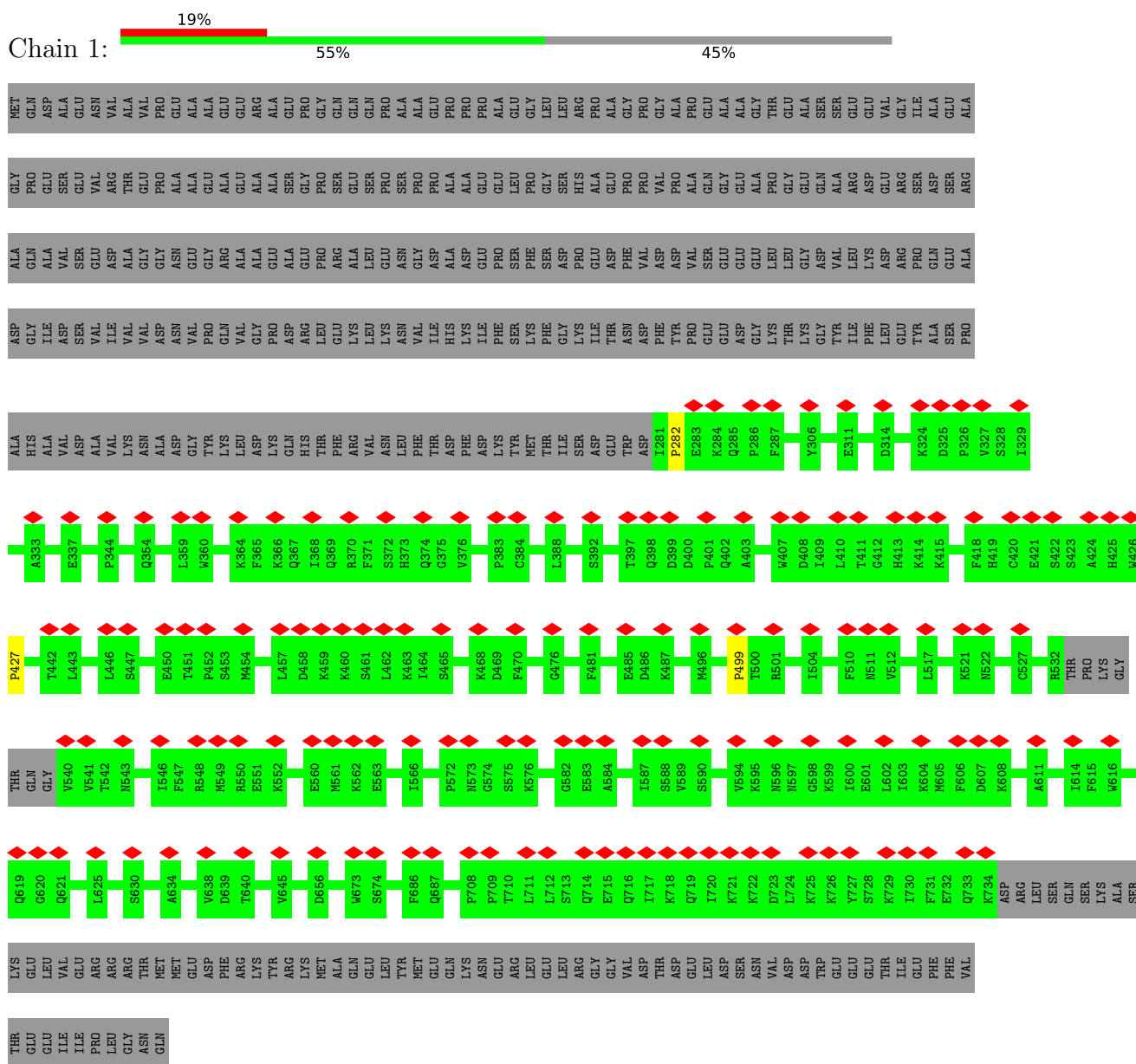
- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	Q	1	Total	Zn	0
			1	1	
52	k	1	Total	Zn	0
			1	1	

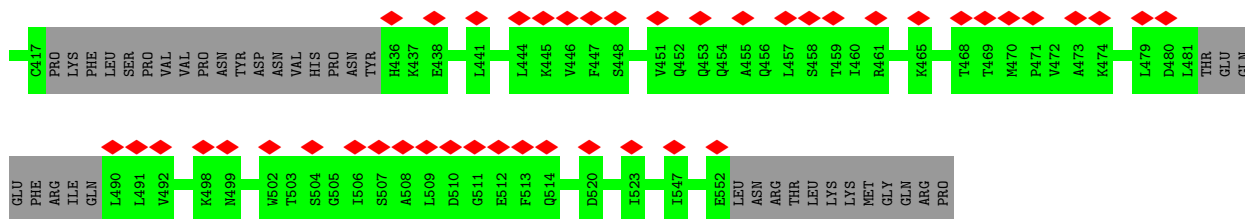
3 Residue-property plots

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.

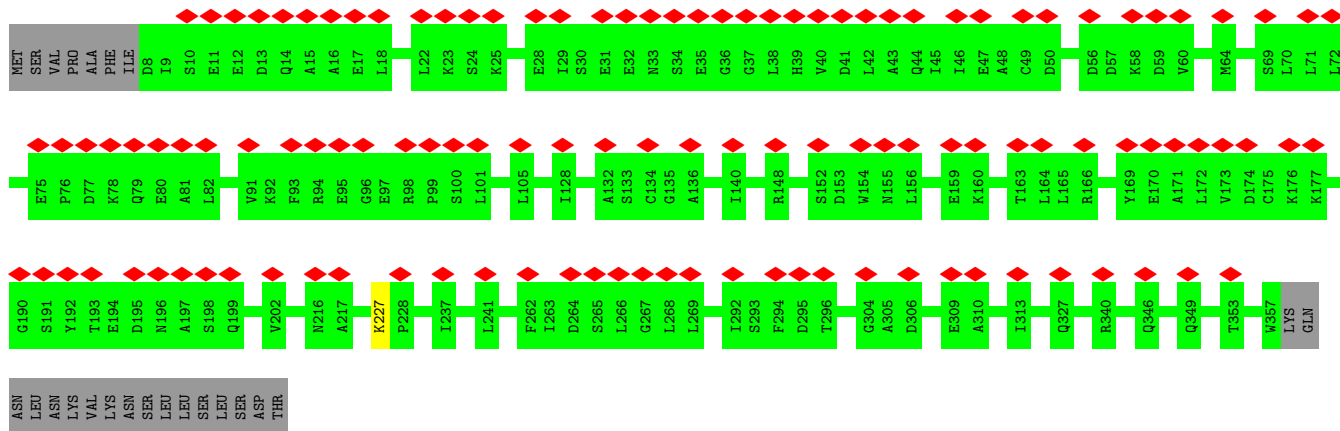
- Molecule 1: Eukaryotic translation initiation factor 3 subunit B



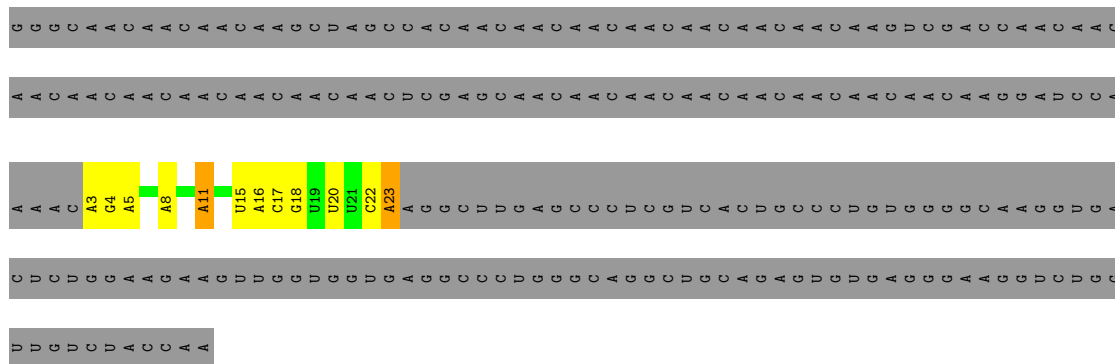
- Molecule 2: Eukaryotic translation initiation factor 3 subunit K



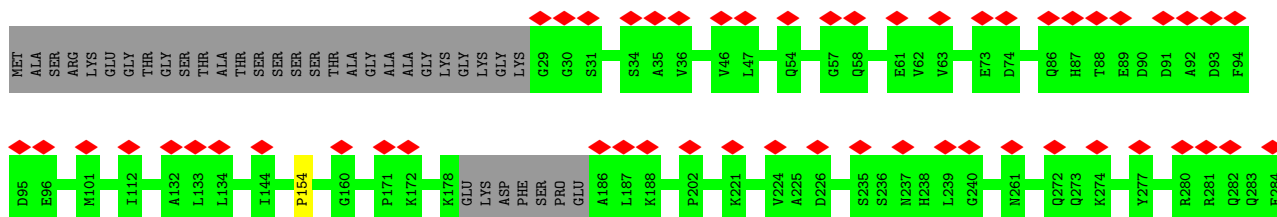
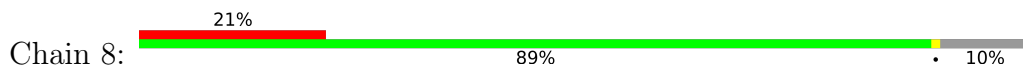
● Molecule 5: Eukaryotic translation initiation factor 3 subunit M

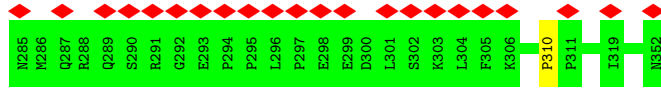


● Molecule 6: mRNA



● Molecule 7: Eukaryotic translation initiation factor 3 subunit H

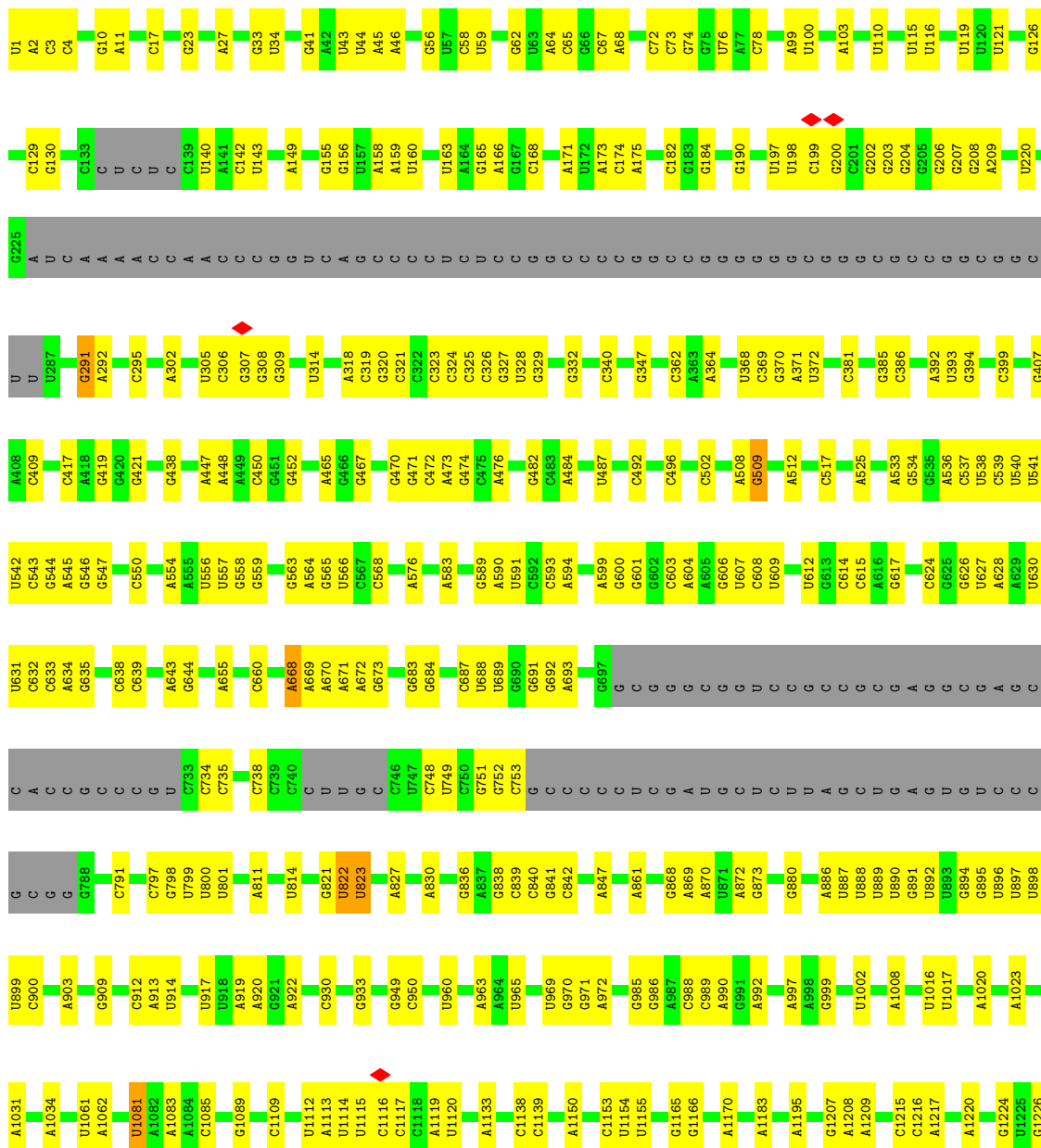


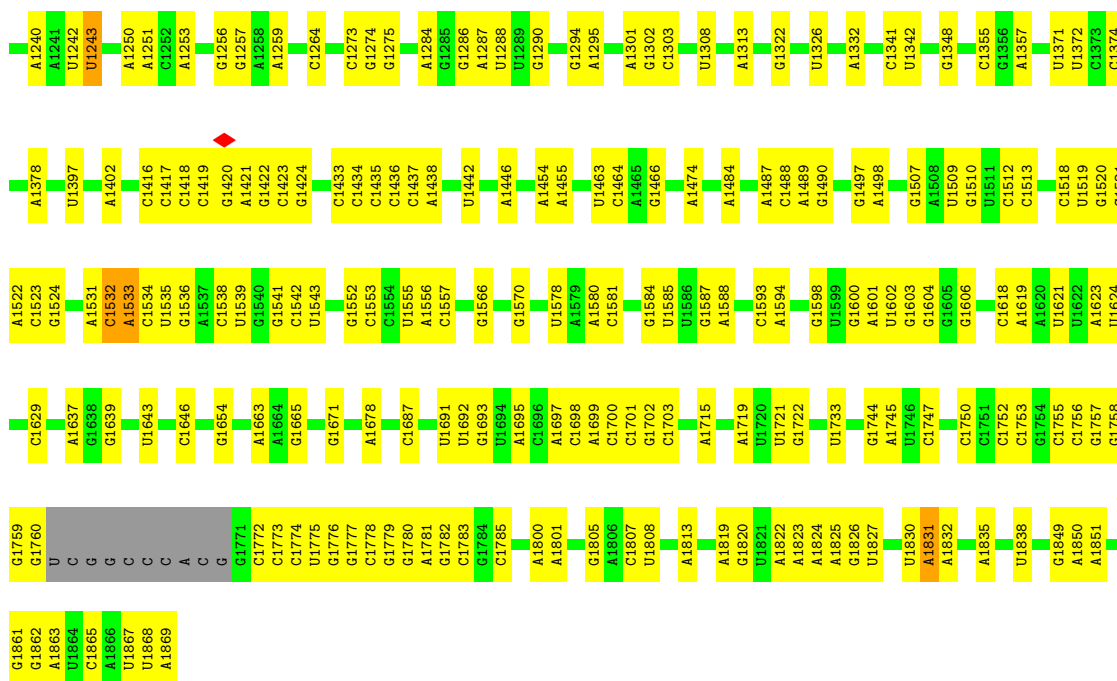


• Molecule 8: 60S ribosomal protein L41

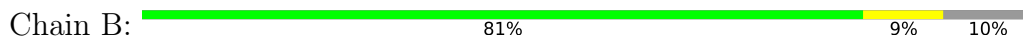


• Molecule 9: 18S rRNA

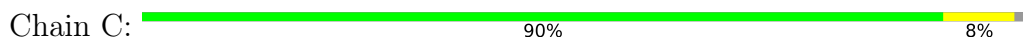




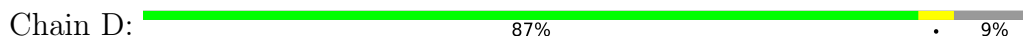
- Molecule 10: 40S ribosomal protein S11



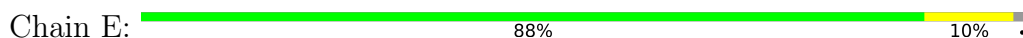
- Molecule 11: 40S ribosomal protein S4, X isoform



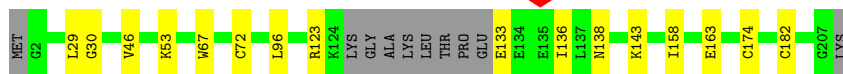
- Molecule 12: 40S ribosomal protein S9



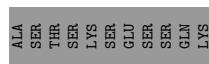
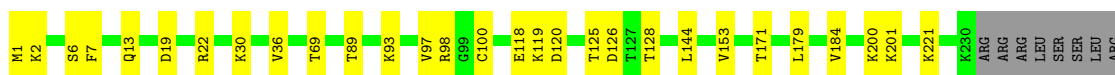
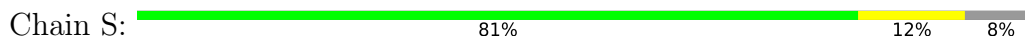
- Molecule 13: 40S ribosomal protein S23



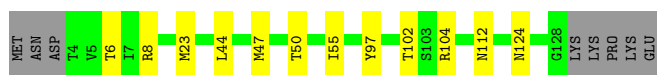
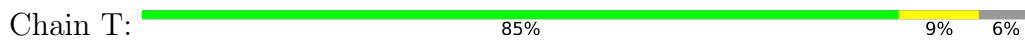
- Molecule 14: 40S ribosomal protein S30



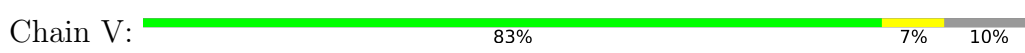
• Molecule 27: 40S ribosomal protein S6



• Molecule 28: 40S ribosomal protein S24



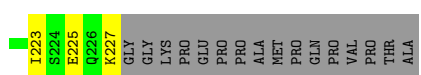
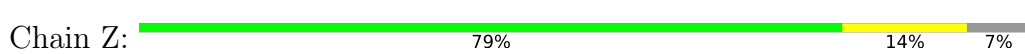
• Molecule 29: 40S ribosomal protein S5



• Molecule 30: 40S ribosomal protein S16

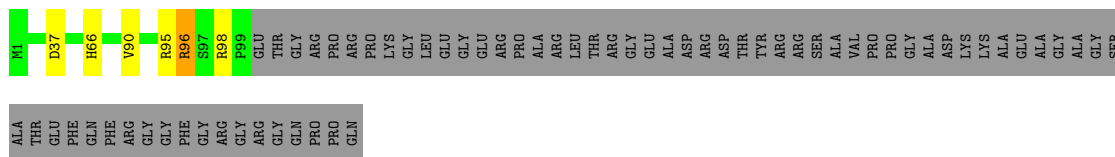


• Molecule 31: 40S ribosomal protein S3



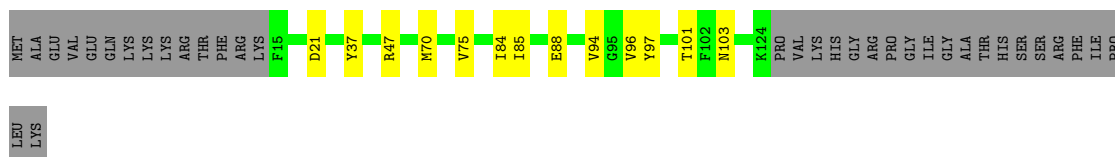
• Molecule 32: 40S ribosomal protein S10





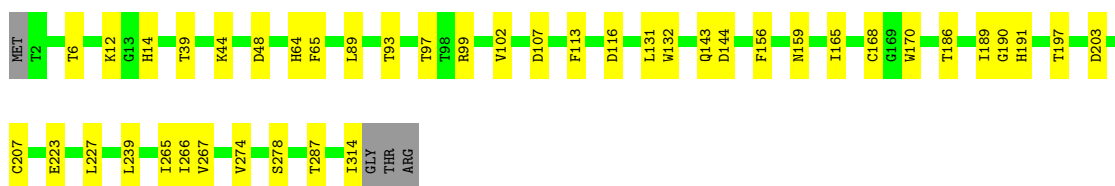
- Molecule 33: 40S ribosomal protein S15

Chain b: 67% 9% 24%



- Molecule 34: Receptor of activated protein C kinase 1

Chain c: 85% 13%



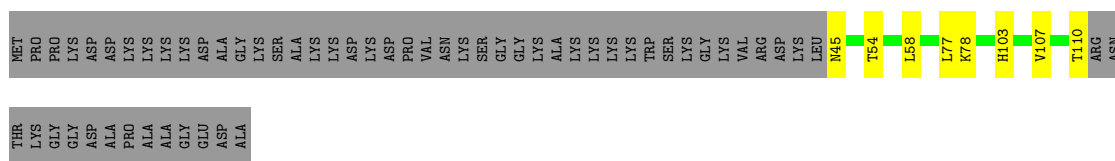
- Molecule 35: 40S ribosomal protein S19

Chain d: 90% 8%



- Molecule 36: 40S ribosomal protein S25

Chain e: 46% 6% 47%



- Molecule 37: 40S ribosomal protein S18

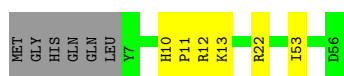
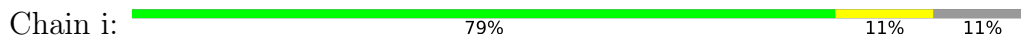
Chain f: 85% 9% 7%



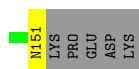
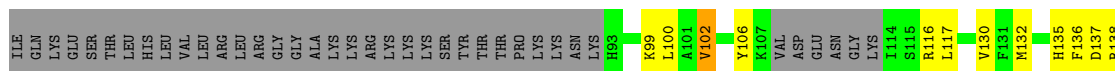
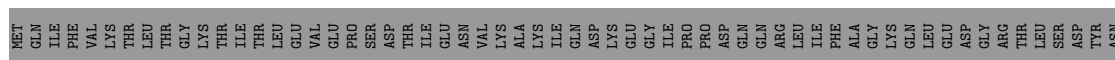
- Molecule 38: 40S ribosomal protein S20



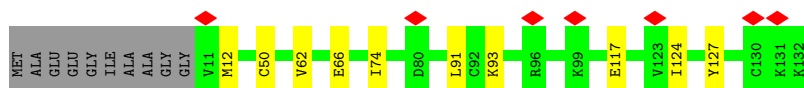
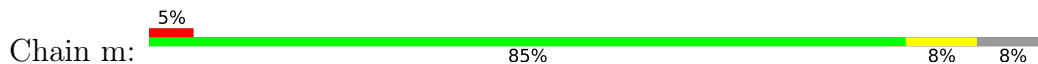
- Molecule 39: 40S ribosomal protein S29



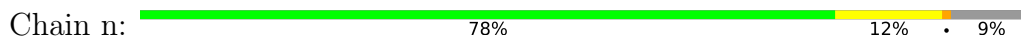
- Molecule 40: Ubiquitin-40S ribosomal protein S27a



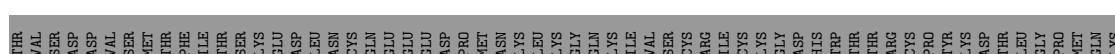
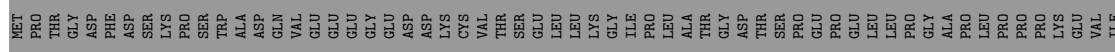
- Molecule 41: 40S ribosomal protein S12

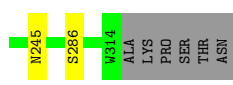
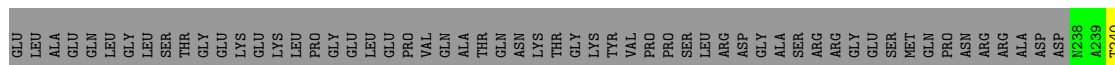


- Molecule 42: 40S ribosomal protein S28

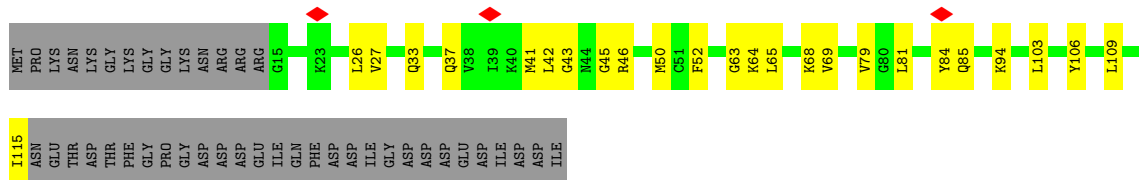


- Molecule 43: Eukaryotic translation initiation factor 3 subunit G

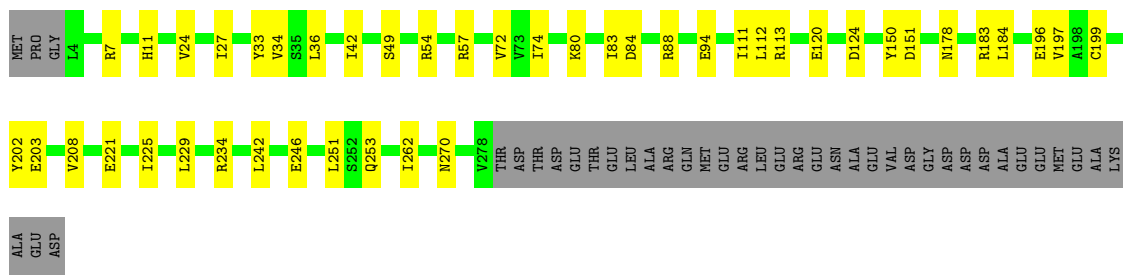




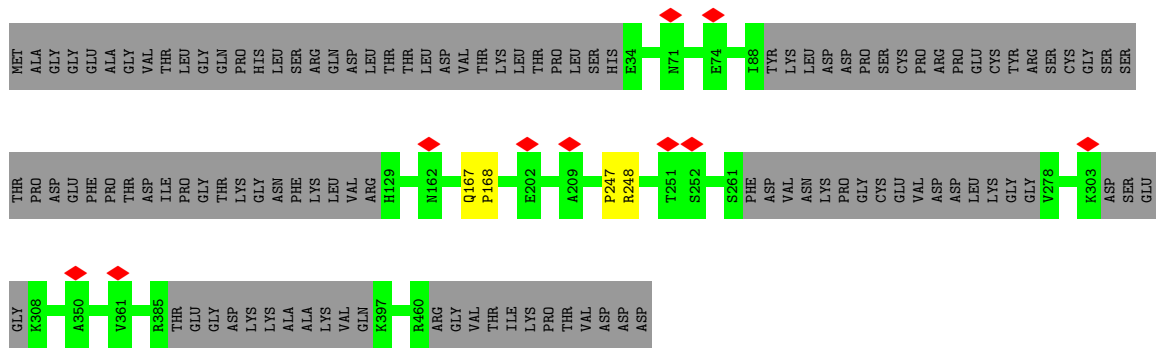
• Molecule 44: Eukaryotic translation initiation factor 1A, X-chromosomal



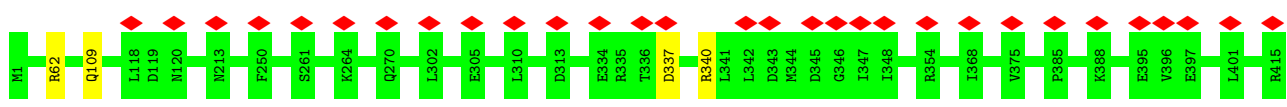
• Molecule 45: Eukaryotic translation initiation factor 2 subunit 1



• Molecule 46: Eukaryotic translation initiation factor 2 subunit 3



• Molecule 47: Eukaryotic translation initiation factor 3 subunit A



T841	GLY
P849	SER
L863	LEU
	VAL
	GLU
	ASN
	ASN
	GLU
	ARG
	VAL
	PHE
	ASP
	HIS
	LYS
	GLN
	GLY
	THR
	TYR
	GLY
	GLY
	TYR
	PHE
	ARG
	ARG
	ASP
	ASP
	GLN
	LYS
	ASP
	GLY
	TYR
	TYR
	ARG
	LYS
	ASN
	GLU
	GLY
	TYR
	MET
	ARG
	ARG
	GLY
	GLY
	TYR
	ARG
	GLN
	GLN
	GLN
	SER
	GLN
	THR
	ALA
	TYR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	364950	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 ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	24.271	Depositor
Minimum map value	-11.101	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.15	Depositor
Map size (Å)	417.59998, 417.59998, 417.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	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: OMC, ZN, OMG, A2M, UR3, OMU, 5MU, MA6, PSU, 5MC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.45	0/2581	0.71	0/3561
2	3	0.35	0/1055	0.54	0/1469
3	4	0.47	0/1269	0.68	0/1762
4	5	0.36	0/1575	0.52	0/2187
5	6	0.42	0/1926	0.64	1/2669 (0.0%)
6	7	0.87	2/492 (0.4%)	1.23	3/764 (0.4%)
7	8	0.44	0/1569	0.66	0/2183
8	9	0.96	0/231	0.74	0/294
9	A	0.41	0/40362	0.69	4/62905 (0.0%)
10	B	0.84	0/1186	0.86	2/1585 (0.1%)
11	C	0.83	0/2077	0.81	1/2796 (0.0%)
12	D	0.84	0/1502	0.79	0/2008
13	E	0.96	0/1105	0.95	2/1476 (0.1%)
14	F	0.83	0/380	0.88	0/496
15	G	0.74	0/1451	0.84	0/1942
16	H	0.82	0/644	0.82	0/864
17	I	0.84	0/1232	0.82	0/1656
18	J	1.03	0/1051	0.98	5/1406 (0.4%)
19	K	0.93	0/623	0.93	1/833 (0.1%)
20	L	1.01	0/1743	0.93	2/2354 (0.1%)
21	M	0.81	0/1029	0.85	0/1383
22	N	0.94	0/1670	0.94	3/2271 (0.1%)
23	O	0.40	0/1742	0.62	0/2330
24	P	0.98	0/1010	0.99	1/1353 (0.1%)
25	Q	0.87	0/805	0.91	1/1079 (0.1%)
26	R	0.70	0/1654	0.79	2/2203 (0.1%)
27	S	0.62	0/1885	0.77	0/2510
28	T	0.80	0/1032	0.75	0/1371
29	V	0.94	0/1481	0.86	2/1988 (0.1%)
30	Y	0.93	0/1142	0.89	2/1528 (0.1%)
31	Z	0.87	0/1793	0.92	3/2414 (0.1%)
32	a	0.82	0/859	0.79	1/1159 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.73	0/929	0.78	1/1241 (0.1%)
34	c	0.73	0/2493	0.85	3/3394 (0.1%)
35	d	0.87	0/1123	0.81	1/1504 (0.1%)
36	e	0.79	0/529	0.85	2/712 (0.3%)
37	f	0.79	0/1194	0.84	1/1599 (0.1%)
38	h	0.85	0/827	0.91	1/1110 (0.1%)
39	i	0.90	0/429	0.86	0/568
40	k	0.58	0/444	0.86	2/588 (0.3%)
41	m	0.42	0/960	0.67	0/1286
42	n	0.86	0/500	0.89	0/669
43	o	0.45	0/628	0.77	0/846
44	q	0.62	0/792	0.98	4/1062 (0.4%)
45	r	0.58	0/2247	0.81	2/3029 (0.1%)
46	t	0.39	0/1745	0.61	0/2417
47	u	0.42	0/5475	0.66	1/7432 (0.0%)
48	v	0.44	0/2672	0.70	2/3647 (0.1%)
49	w	0.33	0/1795	0.66	0/2798
50	x	0.42	0/2874	0.69	1/3925 (0.0%)
51	y	0.40	0/5284	0.67	3/7123 (0.0%)
All	All	0.59	2/113096 (0.0%)	0.75	60/161749 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	7	23	A	C1 ¹ -N9	-5.25	1.39	1.46
6	7	11	A	C5-C4	-5.14	1.35	1.38

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	y	146	ARG	NE-CZ-NH2	-13.68	113.46	120.30
22	N	7	VAL	N-CA-C	-12.54	77.15	111.00
51	y	146	ARG	NE-CZ-NH1	9.22	124.91	120.30
44	q	42	LEU	N-CA-C	-9.21	86.14	111.00
10	B	53	GLY	N-CA-C	9.19	136.07	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1	443/813 (54%)	414 (94%)	26 (6%)	3 (1%)	22	59
2	3	209/218 (96%)	205 (98%)	3 (1%)	1 (0%)	29	66
3	4	251/357 (70%)	229 (91%)	19 (8%)	3 (1%)	13	48
4	5	307/564 (54%)	301 (98%)	6 (2%)	0	100	100
5	6	348/374 (93%)	318 (91%)	30 (9%)	0	100	100
7	8	313/352 (89%)	276 (88%)	35 (11%)	2 (1%)	25	62
8	9	22/25 (88%)	22 (100%)	0	0	100	100
10	B	138/158 (87%)	136 (99%)	2 (1%)	0	100	100
11	C	254/263 (97%)	249 (98%)	5 (2%)	0	100	100
12	D	175/194 (90%)	174 (99%)	1 (1%)	0	100	100
13	E	138/143 (96%)	134 (97%)	3 (2%)	1 (1%)	22	59
14	F	43/59 (73%)	43 (100%)	0	0	100	100
15	G	171/194 (88%)	163 (95%)	7 (4%)	1 (1%)	25	62
16	H	79/84 (94%)	76 (96%)	2 (2%)	1 (1%)	12	47
17	I	148/151 (98%)	147 (99%)	1 (1%)	0	100	100
18	J	127/130 (98%)	124 (98%)	2 (2%)	1 (1%)	19	56
19	K	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
20	L	218/293 (74%)	215 (99%)	2 (1%)	1 (0%)	29	66
21	M	123/135 (91%)	121 (98%)	2 (2%)	0	100	100
22	N	205/295 (70%)	201 (98%)	3 (2%)	1 (0%)	29	66
23	O	209/264 (79%)	193 (92%)	16 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	P	131/151 (87%)	123 (94%)	7 (5%)	1 (1%)	19	56
25	Q	97/115 (84%)	93 (96%)	4 (4%)	0	100	100
26	R	194/208 (93%)	194 (100%)	0	0	100	100
27	S	228/249 (92%)	223 (98%)	5 (2%)	0	100	100
28	T	123/133 (92%)	122 (99%)	1 (1%)	0	100	100
29	V	180/204 (88%)	175 (97%)	5 (3%)	0	100	100
30	Y	139/146 (95%)	136 (98%)	3 (2%)	0	100	100
31	Z	225/243 (93%)	223 (99%)	2 (1%)	0	100	100
32	a	97/165 (59%)	97 (100%)	0	0	100	100
33	b	108/145 (74%)	107 (99%)	1 (1%)	0	100	100
34	c	311/317 (98%)	301 (97%)	10 (3%)	0	100	100
35	d	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
36	e	64/125 (51%)	64 (100%)	0	0	100	100
37	f	140/152 (92%)	134 (96%)	6 (4%)	0	100	100
38	h	101/119 (85%)	97 (96%)	4 (4%)	0	100	100
39	i	48/56 (86%)	47 (98%)	0	1 (2%)	7	38
40	k	49/156 (31%)	44 (90%)	4 (8%)	1 (2%)	7	39
41	m	120/132 (91%)	118 (98%)	2 (2%)	0	100	100
42	n	61/69 (88%)	59 (97%)	1 (2%)	1 (2%)	9	43
43	o	75/320 (23%)	73 (97%)	2 (3%)	0	100	100
44	q	99/144 (69%)	83 (84%)	12 (12%)	4 (4%)	3	26
45	r	273/315 (87%)	255 (93%)	17 (6%)	1 (0%)	34	69
46	t	346/472 (73%)	337 (97%)	5 (1%)	4 (1%)	13	48
47	u	705/1382 (51%)	672 (95%)	32 (4%)	1 (0%)	51	83
48	v	380/445 (85%)	350 (92%)	30 (8%)	0	100	100
50	x	415/548 (76%)	386 (93%)	29 (7%)	0	100	100
51	y	636/913 (70%)	610 (96%)	25 (4%)	1 (0%)	47	78
All	All	9485/12718 (75%)	9077 (96%)	378 (4%)	30 (0%)	44	74

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	282	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	427	PRO
3	4	264	GLY
16	H	56	CYS
24	P	136	PRO

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	1	97/701 (14%)	97 (100%)	0	100	100
5	6	49/335 (15%)	49 (100%)	0	100	100
8	9	23/24 (96%)	22 (96%)	1 (4%)	29	58
10	B	129/142 (91%)	117 (91%)	12 (9%)	9	35
11	C	220/225 (98%)	201 (91%)	19 (9%)	10	39
12	D	158/168 (94%)	150 (95%)	8 (5%)	24	55
13	E	112/115 (97%)	101 (90%)	11 (10%)	8	33
14	F	38/48 (79%)	35 (92%)	3 (8%)	12	42
15	G	159/174 (91%)	141 (89%)	18 (11%)	6	28
16	H	73/76 (96%)	63 (86%)	10 (14%)	3	21
17	I	130/131 (99%)	126 (97%)	4 (3%)	40	65
18	J	112/113 (99%)	108 (96%)	4 (4%)	35	63
19	K	65/67 (97%)	57 (88%)	8 (12%)	4	24
20	L	186/225 (83%)	156 (84%)	30 (16%)	2	15
21	M	114/122 (93%)	100 (88%)	14 (12%)	4	24
22	N	173/243 (71%)	158 (91%)	15 (9%)	10	38
23	O	192/231 (83%)	191 (100%)	1 (0%)	88	94
24	P	104/119 (87%)	85 (82%)	19 (18%)	1	10
25	Q	86/98 (88%)	75 (87%)	11 (13%)	4	23
26	R	172/180 (96%)	158 (92%)	14 (8%)	11	41

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	S	200/218 (92%)	171 (86%)	29 (14%)	3	18
28	T	107/115 (93%)	95 (89%)	12 (11%)	6	28
29	V	156/170 (92%)	143 (92%)	13 (8%)	11	40
30	Y	117/121 (97%)	110 (94%)	7 (6%)	19	50
31	Z	190/202 (94%)	158 (83%)	32 (17%)	2	14
32	a	90/136 (66%)	84 (93%)	6 (7%)	16	47
33	b	100/130 (77%)	88 (88%)	12 (12%)	5	25
34	c	272/275 (99%)	233 (86%)	39 (14%)	3	19
35	d	112/115 (97%)	101 (90%)	11 (10%)	8	33
36	e	58/103 (56%)	52 (90%)	6 (10%)	7	31
37	f	123/132 (93%)	111 (90%)	12 (10%)	8	33
38	h	94/107 (88%)	81 (86%)	13 (14%)	3	21
39	i	44/49 (90%)	39 (89%)	5 (11%)	5	27
40	k	47/140 (34%)	36 (77%)	11 (23%)	1	5
41	m	104/108 (96%)	94 (90%)	10 (10%)	8	34
42	n	56/62 (90%)	47 (84%)	9 (16%)	2	15
43	o	64/277 (23%)	61 (95%)	3 (5%)	26	56
44	q	77/123 (63%)	60 (78%)	17 (22%)	1	6
45	r	247/280 (88%)	206 (83%)	41 (17%)	2	14
47	u	528/1259 (42%)	520 (98%)	8 (2%)	65	81
48	v	206/406 (51%)	198 (96%)	8 (4%)	32	60
50	x	206/494 (42%)	194 (94%)	12 (6%)	20	52
51	y	563/811 (69%)	555 (99%)	8 (1%)	67	82
All	All	6153/9370 (66%)	5627 (92%)	526 (8%)	14	40

5 of 526 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	r	88	ARG
45	r	197	VAL
45	r	83	ILE
51	y	116	TYR
26	R	133	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
50	x	68	GLN
50	x	296	ASN
28	T	124	ASN
28	T	112	ASN
50	x	416	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	w	74/75 (98%)	42 (56%)	0
6	7	21/255 (8%)	11 (52%)	3 (14%)
9	A	1708/1869 (91%)	506 (29%)	69 (4%)
All	All	1803/2199 (81%)	559 (31%)	72 (3%)

5 of 559 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	7	4	G
6	7	5	A
6	7	8	A
6	7	11	A
6	7	15	U

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	1600	G
9	A	1831	A
9	A	1637	A
9	A	1757	G
9	A	839	C

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

26 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
9	PSU	A	612	9	18,21,22	1.50	5 (27%)	22,30,33	2.04	4 (18%)
9	PSU	A	119	9	18,21,22	1.46	4 (22%)	22,30,33	2.17	5 (22%)
9	A2M	A	668	9	18,25,26	0.98	0	18,36,39	1.54	2 (11%)
9	5MU	A	814	9	19,22,23	1.56	4 (21%)	28,32,35	2.34	9 (32%)
9	PSU	A	822	9	18,21,22	1.53	4 (22%)	22,30,33	2.22	5 (22%)
9	OMG	A	683	9	18,26,27	1.06	1 (5%)	19,38,41	1.24	2 (10%)
9	MA6	A	1851	9	18,26,27	1.23	2 (11%)	19,38,41	1.88	6 (31%)
9	OMC	A	174	9	19,22,23	0.93	0	26,31,34	1.12	2 (7%)
9	A2M	A	27	9	18,25,26	0.99	1 (5%)	18,36,39	1.30	2 (11%)
9	A2M	A	159	9	18,25,26	0.95	1 (5%)	18,36,39	1.23	2 (11%)
9	A2M	A	1031	9	18,25,26	0.98	1 (5%)	18,36,39	1.31	2 (11%)
9	PSU	A	823	9	18,21,22	1.59	5 (27%)	22,30,33	2.03	4 (18%)
9	OMU	A	116	9	19,22,23	1.33	3 (15%)	26,31,34	1.83	5 (19%)
9	OMG	A	644	9	18,26,27	1.10	1 (5%)	19,38,41	1.26	4 (21%)
9	5MC	A	1374	9	18,22,23	1.08	2 (11%)	26,32,35	1.51	5 (19%)
9	OMC	A	1703	9	19,22,23	1.05	1 (5%)	26,31,34	1.15	1 (3%)
9	A2M	A	166	9	18,25,26	1.05	1 (5%)	18,36,39	1.26	2 (11%)
9	PSU	A	1243	9	18,21,22	1.54	5 (27%)	22,30,33	2.05	4 (18%)
9	OMU	A	121	9	19,22,23	1.43	4 (21%)	26,31,34	1.85	6 (23%)
9	OMG	A	509	9	18,26,27	1.15	1 (5%)	19,38,41	1.19	2 (10%)
9	MA6	A	1850	9	18,26,27	1.26	1 (5%)	19,38,41	1.97	5 (26%)
9	A2M	A	1678	9	18,25,26	1.04	0	18,36,39	1.48	3 (16%)
9	UR3	A	1830	9	19,22,23	1.04	1 (5%)	26,32,35	2.02	7 (26%)
9	A2M	A	484	9	18,25,26	1.00	1 (5%)	18,36,39	1.20	2 (11%)
9	PSU	A	1081	9	18,21,22	1.72	5 (27%)	22,30,33	2.35	6 (27%)
9	OMC	A	517	9	19,22,23	0.98	1 (5%)	26,31,34	1.17	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
9	PSU	A	612	9	-	1/7/25/26	0/2/2/2
9	PSU	A	119	9	-	1/7/25/26	0/2/2/2
9	A2M	A	668	9	-	2/5/27/28	0/3/3/3
9	5MU	A	814	9	-	0/7/25/26	0/2/2/2
9	PSU	A	822	9	-	0/7/25/26	0/2/2/2
9	OMG	A	683	9	-	1/5/27/28	0/3/3/3
9	MA6	A	1851	9	-	4/7/29/30	0/3/3/3
9	OMC	A	174	9	-	0/9/27/28	0/2/2/2
9	A2M	A	27	9	-	1/5/27/28	0/3/3/3
9	A2M	A	159	9	-	1/5/27/28	0/3/3/3
9	A2M	A	1031	9	-	1/5/27/28	0/3/3/3
9	PSU	A	823	9	-	1/7/25/26	0/2/2/2
9	OMU	A	116	9	-	1/9/27/28	0/2/2/2
9	OMG	A	644	9	-	2/5/27/28	0/3/3/3
9	5MC	A	1374	9	-	0/7/25/26	0/2/2/2
9	OMC	A	1703	9	-	2/9/27/28	0/2/2/2
9	A2M	A	166	9	-	0/5/27/28	0/3/3/3
9	PSU	A	1243	9	-	0/7/25/26	0/2/2/2
9	OMU	A	121	9	-	0/9/27/28	0/2/2/2
9	OMG	A	509	9	-	2/5/27/28	0/3/3/3
9	MA6	A	1850	9	-	1/7/29/30	0/3/3/3
9	A2M	A	1678	9	-	0/5/27/28	0/3/3/3
9	UR3	A	1830	9	-	2/7/25/26	0/2/2/2
9	A2M	A	484	9	-	1/5/27/28	0/3/3/3
9	PSU	A	1081	9	-	2/7/25/26	0/2/2/2
9	OMC	A	517	9	-	1/9/27/28	0/2/2/2

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1081	PSU	C4-N3	-3.67	1.32	1.38
9	A	823	PSU	C4-N3	-3.44	1.32	1.38
9	A	814	5MU	C4-N3	-3.44	1.32	1.38
9	A	509	OMG	C6-N1	-3.35	1.32	1.37
9	A	121	OMU	C4-N3	-3.27	1.32	1.38

The worst 5 of 99 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	822	PSU	N1-C2-N3	6.57	122.58	115.13
9	A	1081	PSU	N1-C2-N3	6.48	122.47	115.13

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	119	PSU	N1-C2-N3	6.13	122.07	115.13
9	A	823	PSU	N1-C2-N3	6.09	122.03	115.13
9	A	1243	PSU	N1-C2-N3	6.03	121.96	115.13

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	27	A2M	C1'-C2'-O2'-CM'
9	A	116	OMU	C1'-C2'-O2'-CM2
9	A	159	A2M	C1'-C2'-O2'-CM'
9	A	484	A2M	C1'-C2'-O2'-CM'
9	A	517	OMC	C1'-C2'-O2'-CM2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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

There are no chain breaks in this entry.

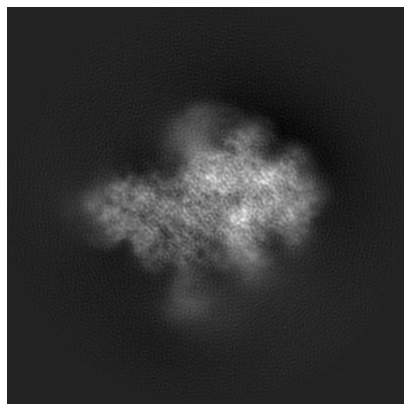
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14114. These allow visual inspection of the internal detail of the map and identification of artifacts.

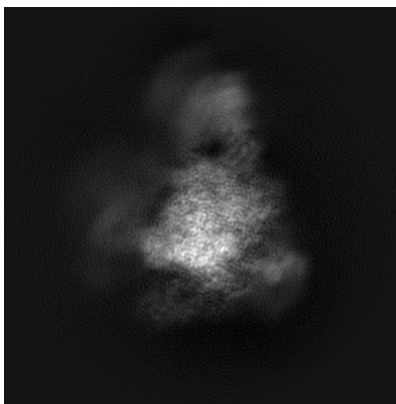
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

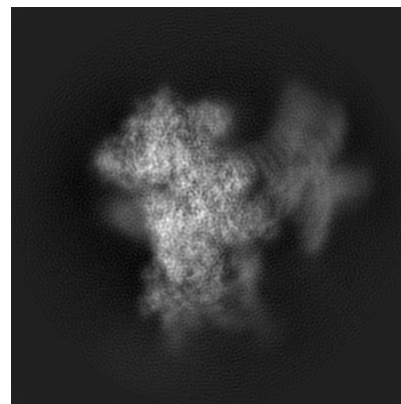
6.1.1 Primary map



X

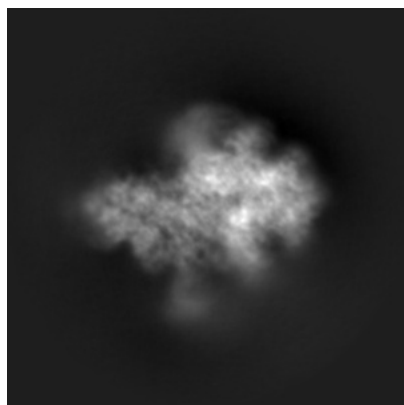


Y

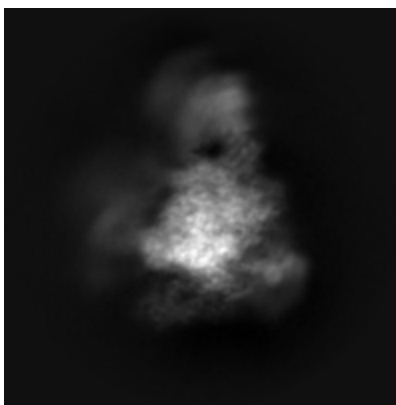


Z

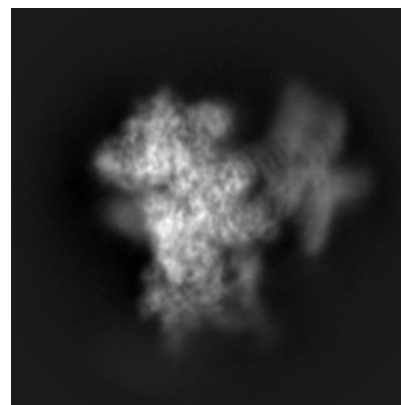
6.1.2 Raw map



X



Y

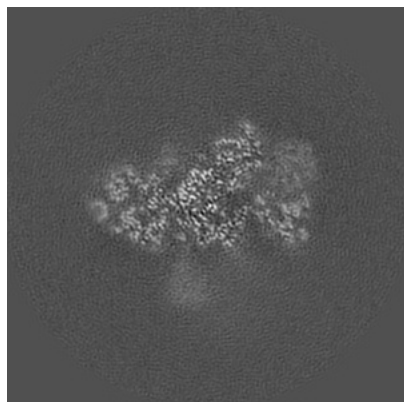


Z

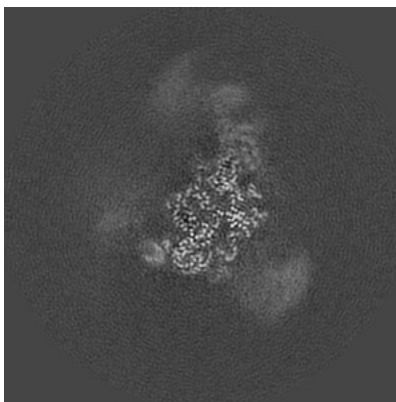
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

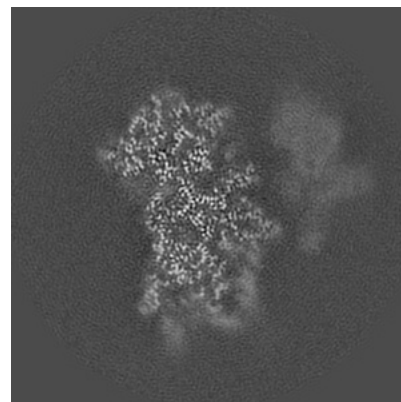
6.2.1 Primary map



X Index: 180

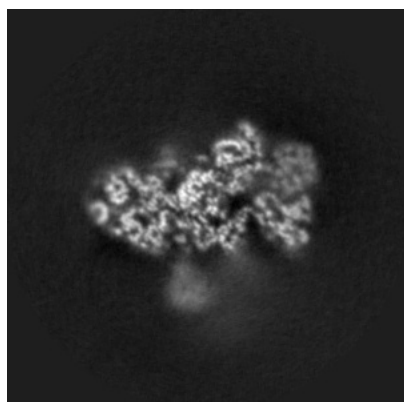


Y Index: 180

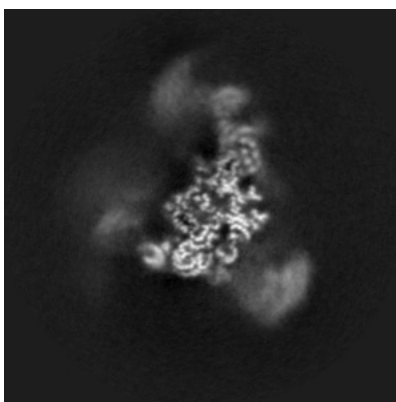


Z Index: 180

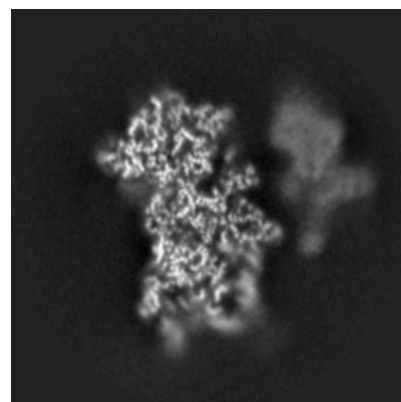
6.2.2 Raw map



X Index: 180



Y Index: 180

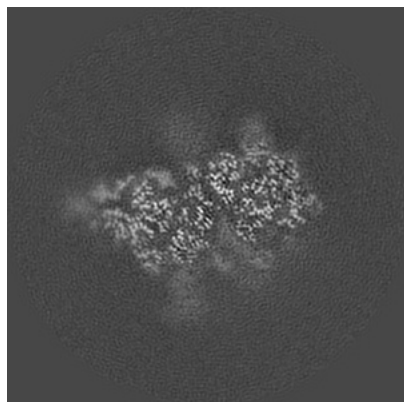


Z Index: 180

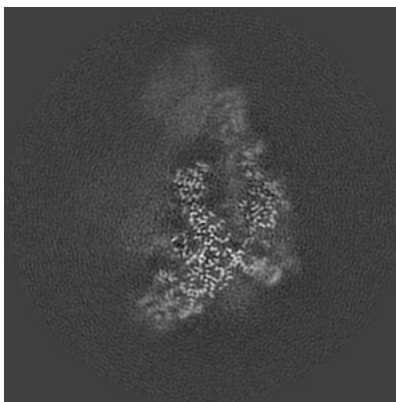
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

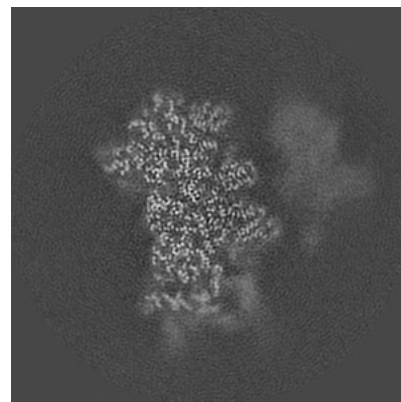
6.3.1 Primary map



X Index: 149

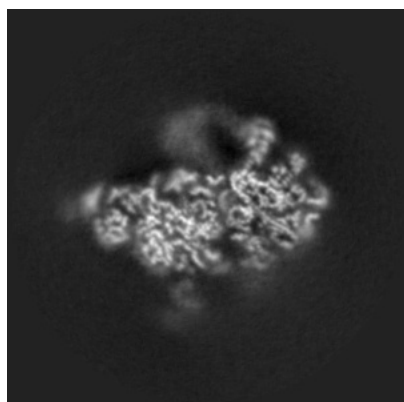


Y Index: 213

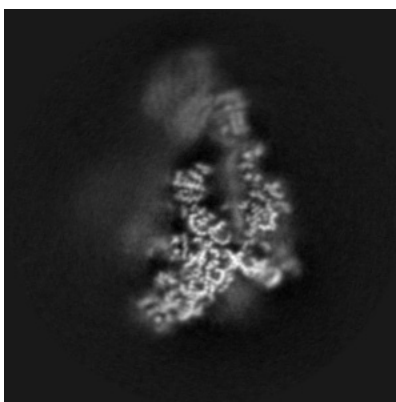


Z Index: 176

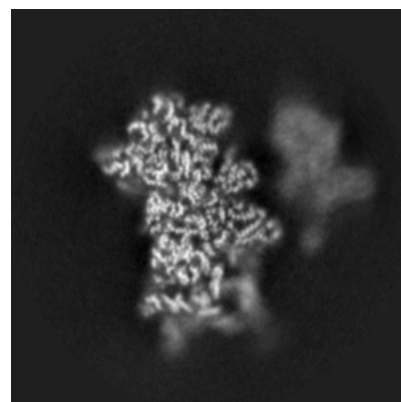
6.3.2 Raw map



X Index: 139



Y Index: 213

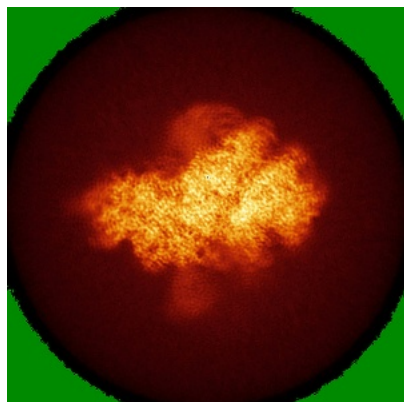


Z Index: 176

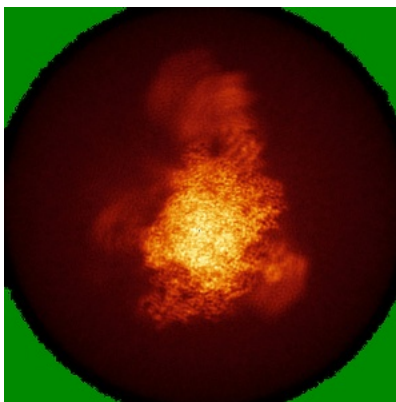
The images above show the largest variance slices of the map in three orthogonal directions.

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

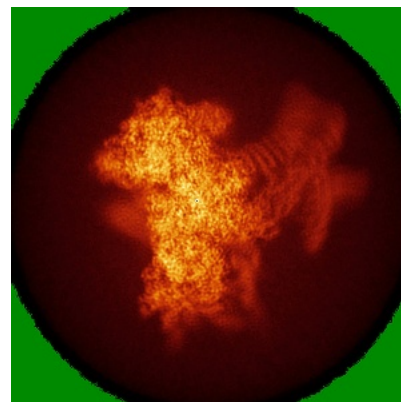
6.4.1 Primary map



X

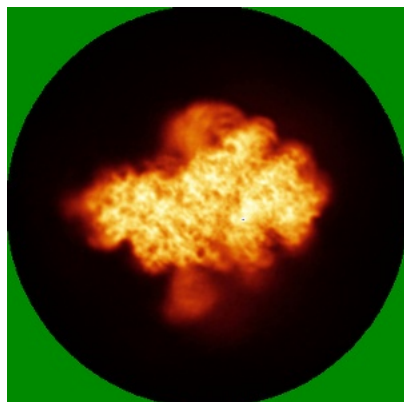


Y

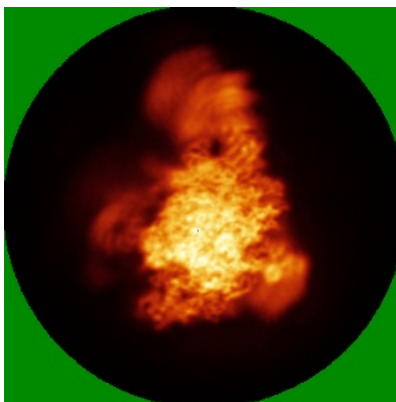


Z

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](#)

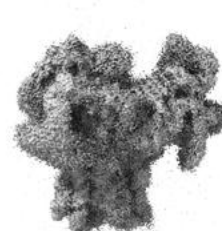
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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 shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

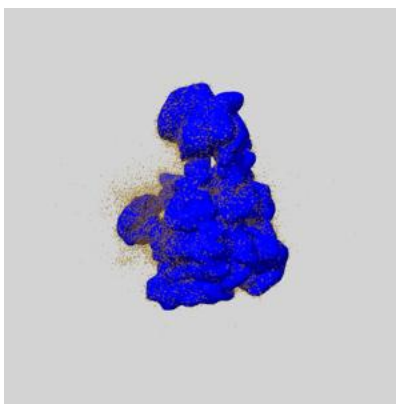
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

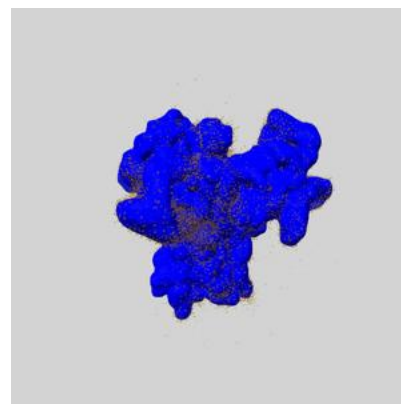
6.6.1 emd_14114_msk_1.map [i](#)



X



Y

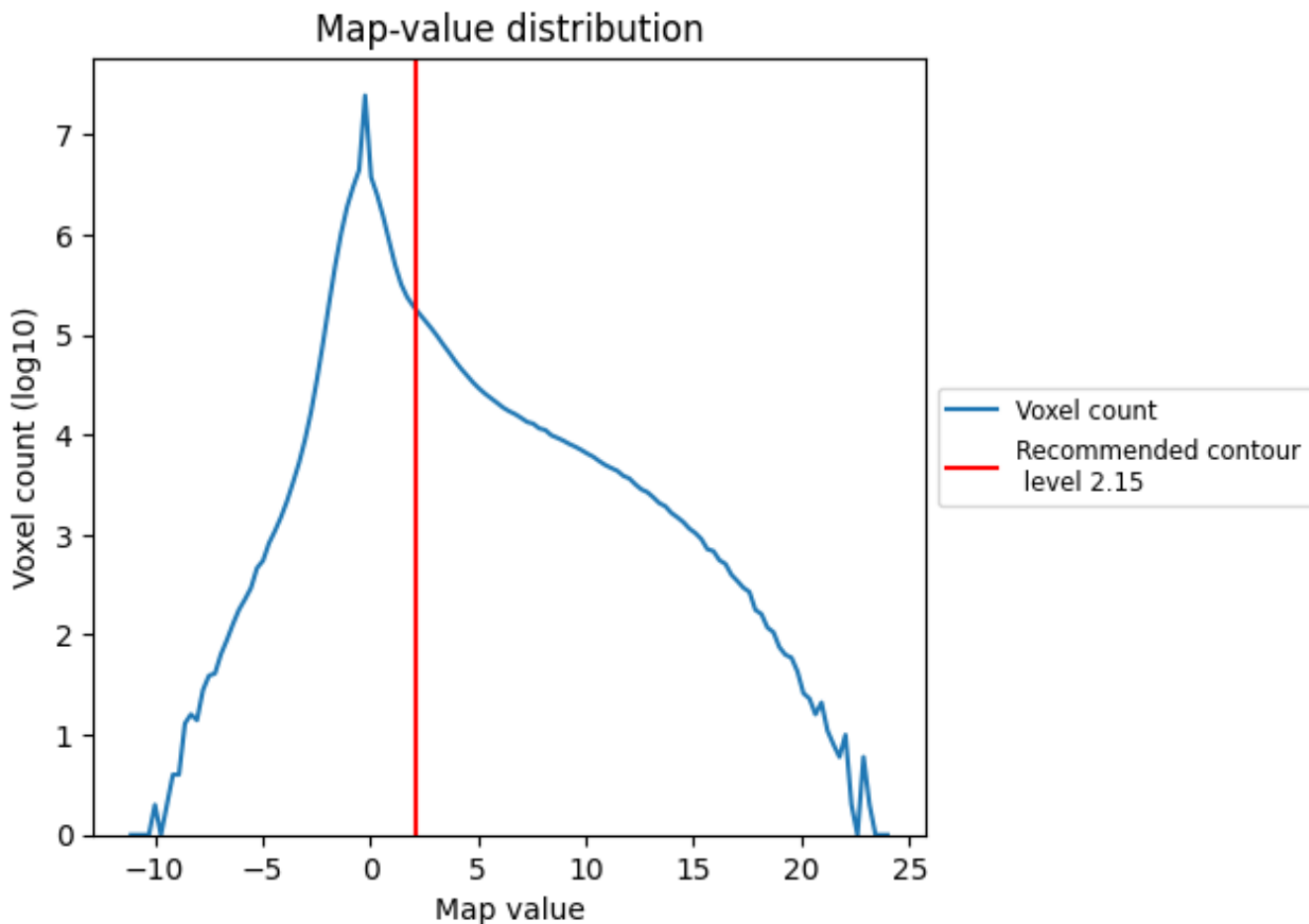


Z

7 Map analysis [i](#)

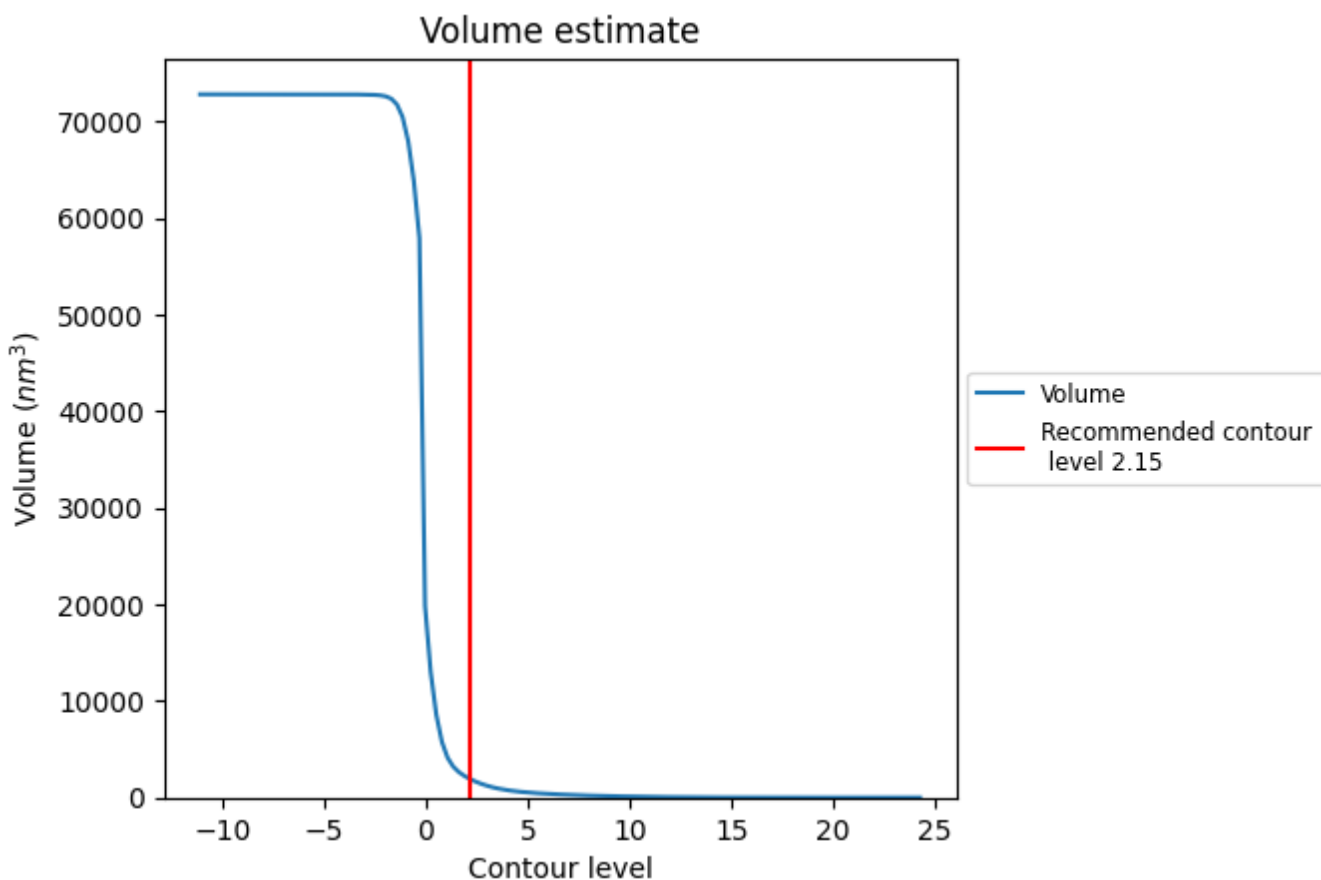
This section contains the results of statistical analysis of the map.

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.

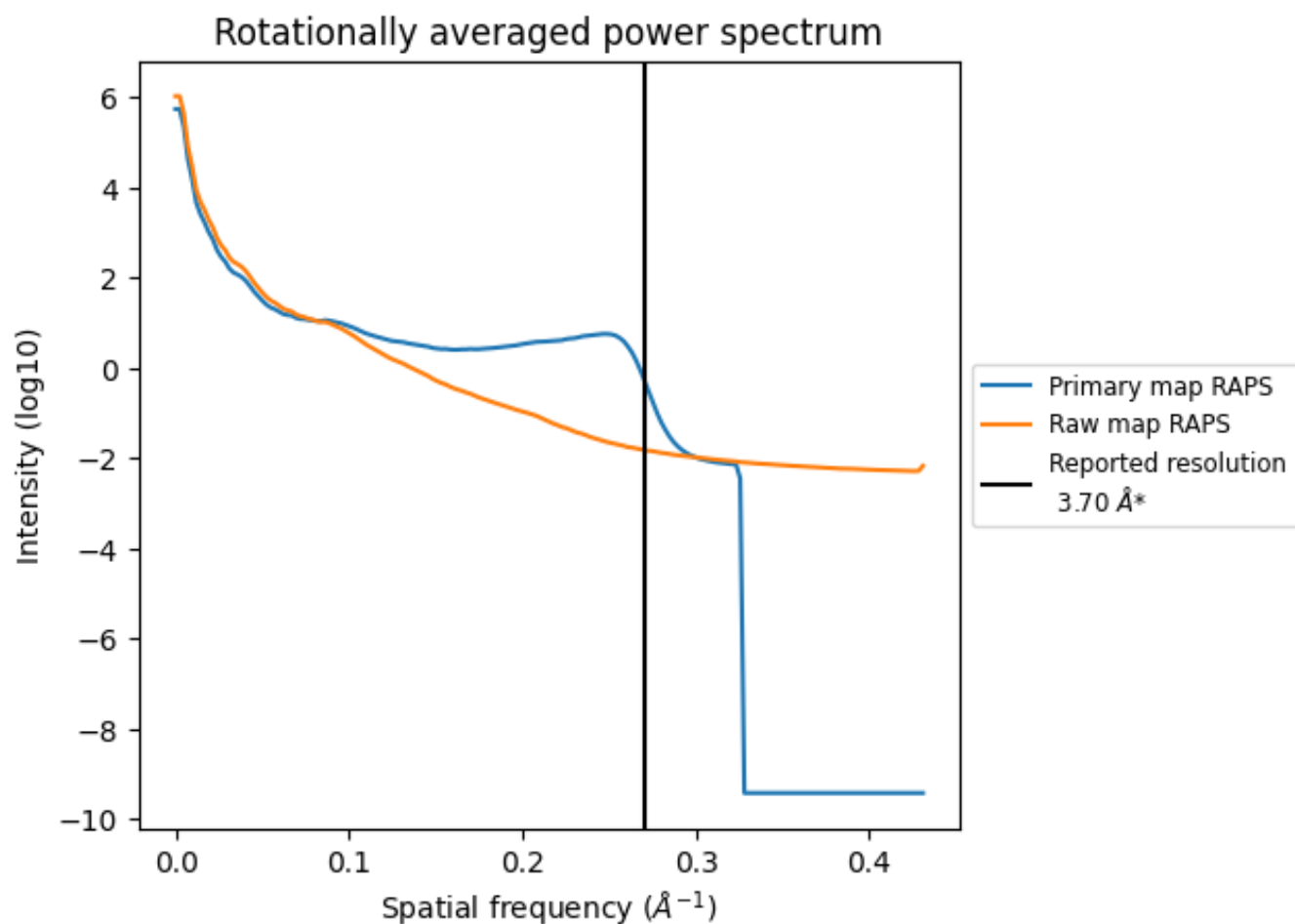
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1935 nm³; this corresponds to an approximate mass of 1748 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](#)

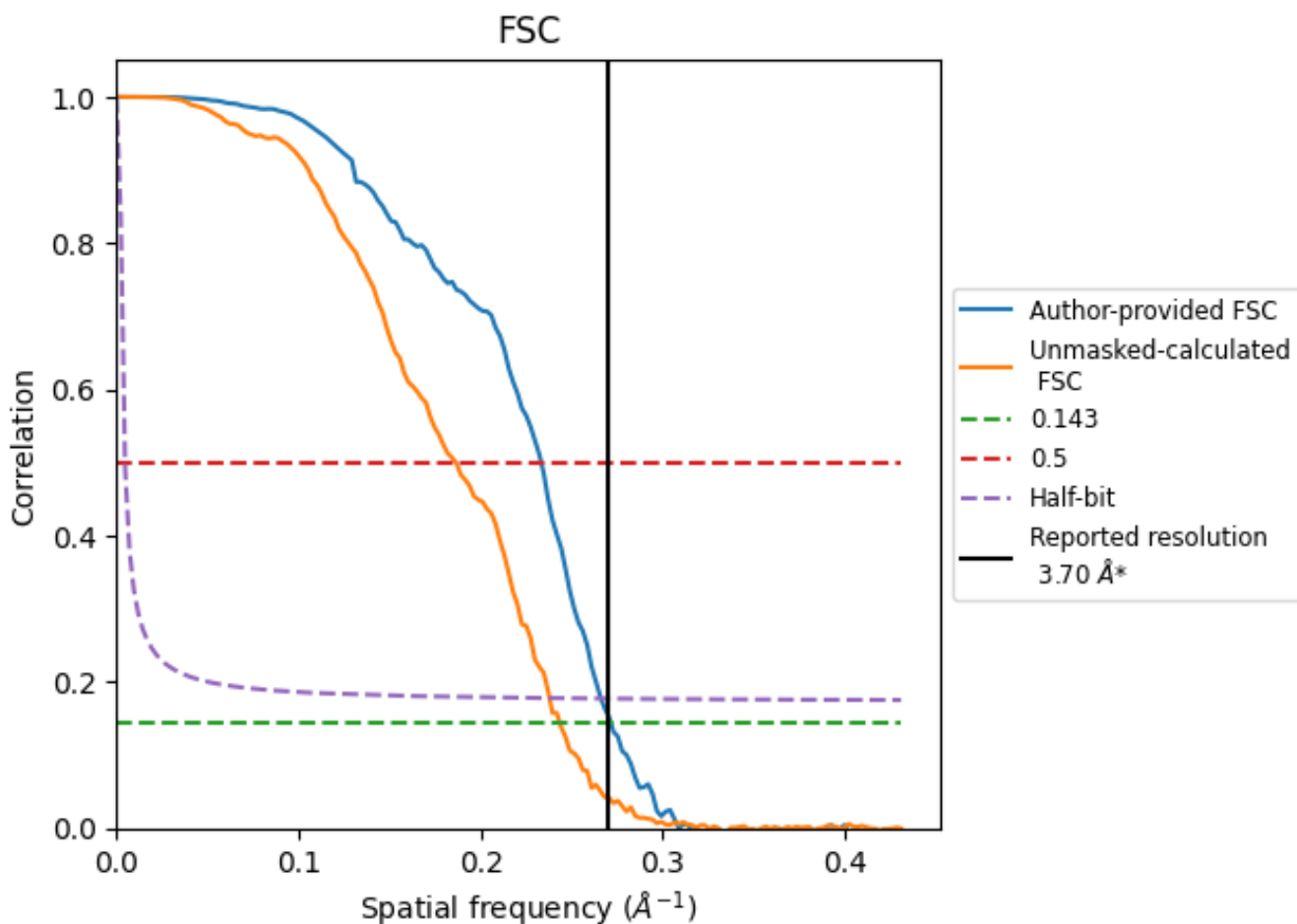


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270\AA^{-1}

8.2 Resolution estimates [i](#)

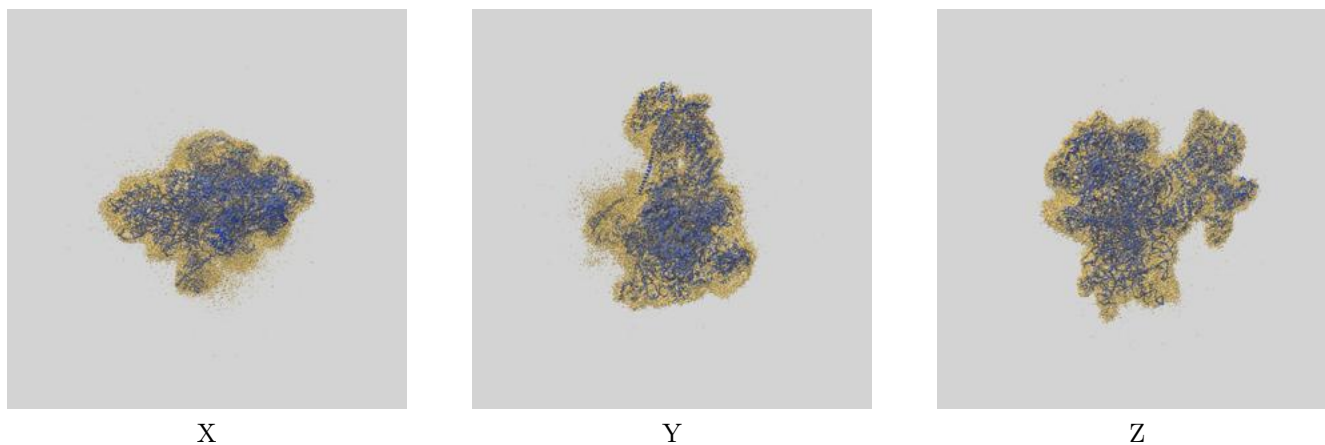
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.68	4.29	3.76
Unmasked-calculated*	4.11	5.36	4.20

*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 4.11 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

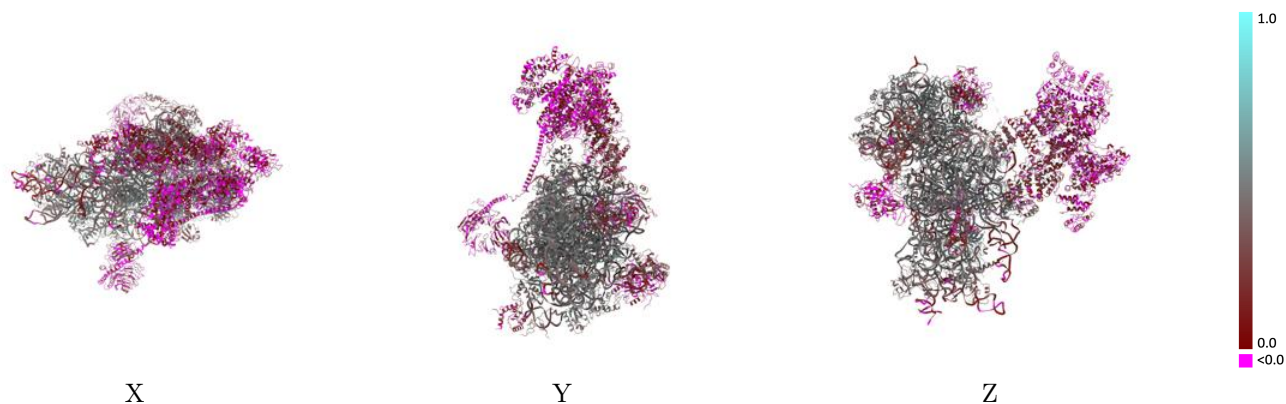
This section contains information regarding the fit between EMDB map EMD-14114 and PDB model 7QP7. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



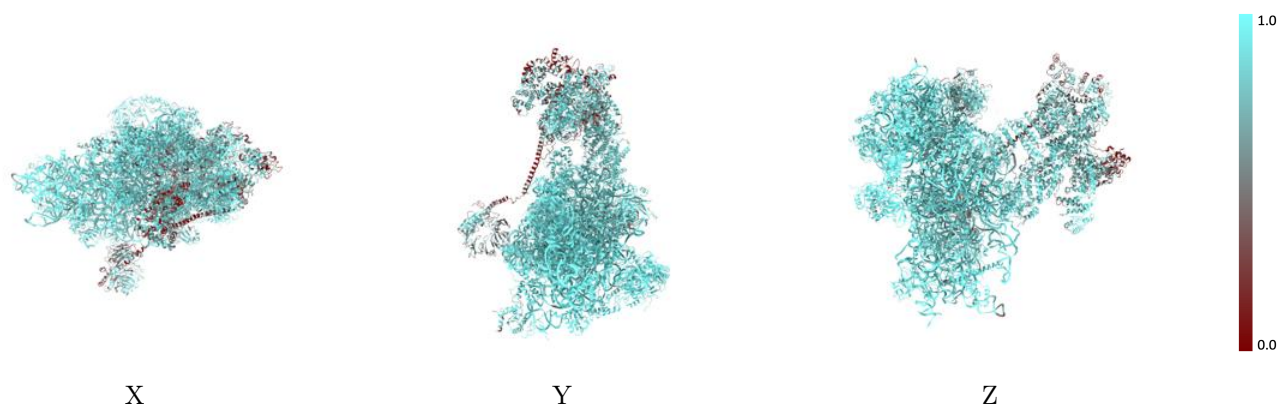
The images above show the 3D surface view of the map at the recommended contour level 2.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



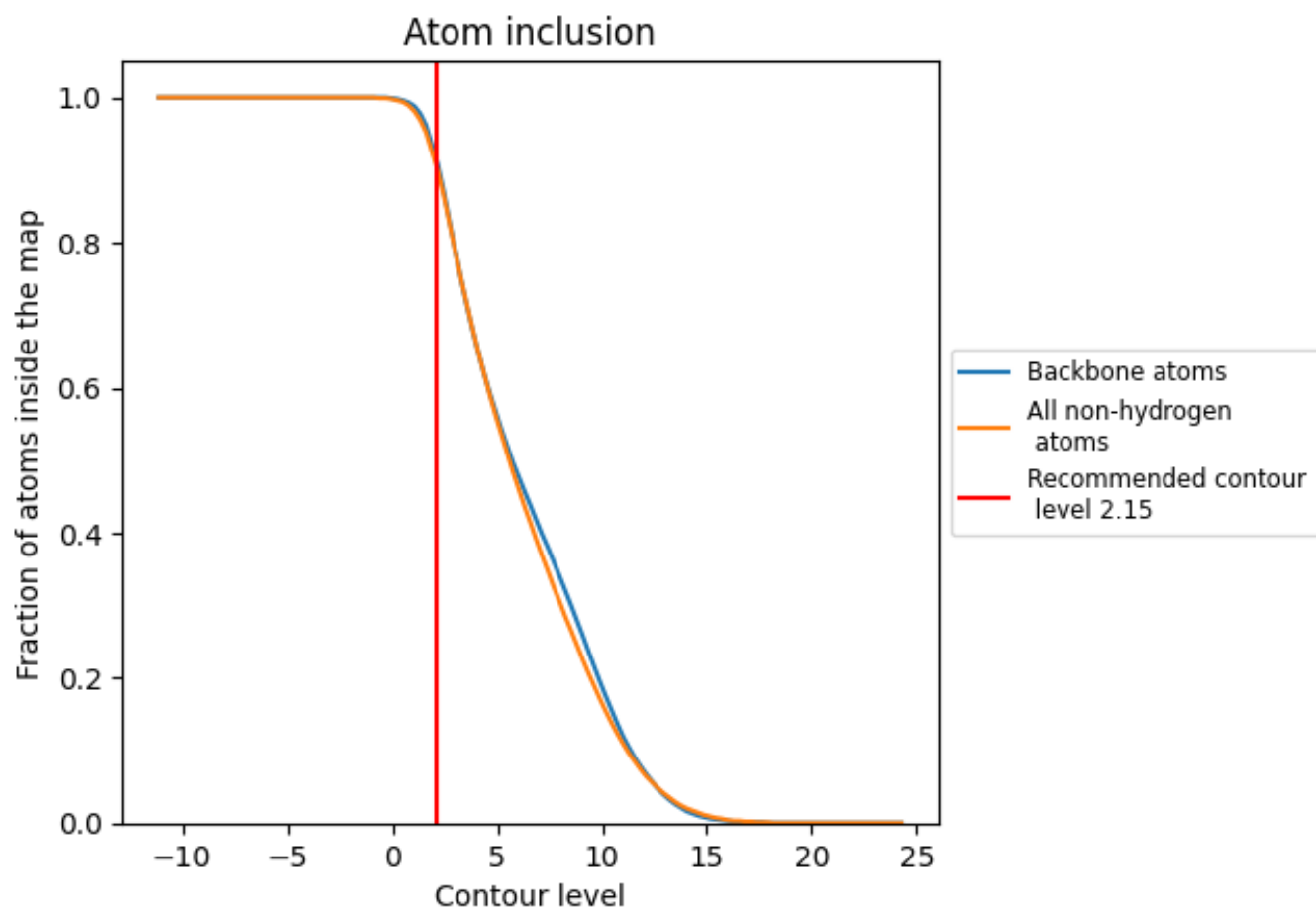
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% 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 (2.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9010	 0.3370
1	 0.5900	 0.0480
3	 0.4050	 0.0230
4	 0.7400	 0.0390
5	 0.6400	 0.0290
6	 0.6270	 0.0200
7	 0.8870	 0.2360
8	 0.6980	 0.0350
9	 0.9710	 0.4920
A	 0.9850	 0.4050
B	 0.9680	 0.4940
C	 0.9720	 0.4950
D	 0.9680	 0.4890
E	 0.9700	 0.5100
F	 0.9730	 0.4820
G	 0.9300	 0.4390
H	 0.9440	 0.4800
I	 0.9800	 0.4910
J	 0.9610	 0.5170
K	 0.9720	 0.5040
L	 0.9490	 0.5010
M	 0.9250	 0.4600
N	 0.9540	 0.4940
O	 0.9210	 0.3930
P	 0.9660	 0.4860
Q	 0.9590	 0.5090
R	 0.9640	 0.4350
S	 0.9660	 0.4150
T	 0.9850	 0.4700
V	 0.9650	 0.4930
Y	 0.9650	 0.4950
Z	 0.9400	 0.4750
a	 0.9580	 0.4660
b	 0.9610	 0.4650
c	 0.9590	 0.4390



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
d	 0.9780	 0.4840
e	 0.9590	 0.4570
f	 0.9580	 0.4520
h	 0.9670	 0.4650
i	 0.9530	 0.4940
k	 0.9430	 0.3350
m	 0.8100	 0.1540
n	 0.9370	 0.4830
o	 0.8600	 0.2190
q	 0.8380	 0.3450
r	 0.9560	 0.3330
t	 0.9320	 0.0370
u	 0.7040	 0.1200
v	 0.7640	 0.0480
w	 0.9740	 0.2120
x	 0.7010	 0.1440
y	 0.7970	 0.1610