



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 06:32 AM UTC

PDB ID : 9G8O / pdb_00009g8o
EMDB ID : EMD-51134
Title : human 40S ribosome bound by a SKI238-exosome complex
Authors : Koegel, A.; Keidel, A.; Loukeri, M.J.; Kuhn, C.C.; Langer, L.M.; Schaefer, I.B.; Conti, E.
Deposited on : 2024-07-23
Resolution : 3.40 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
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

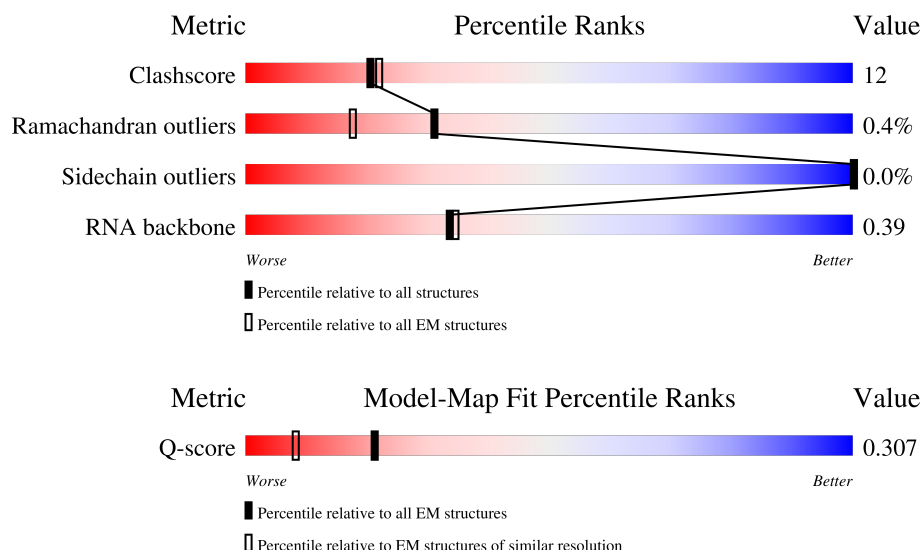
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	B	1568	59% 41% 19% 40%
2	C	305	100% 67% 33%
2	D	305	100% 60% 40%

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Mol	Chain	Length	Quality of chain
3	F	295	
4	J	199	
5	K	443	
6	L	280	
7	N	245	
8	O	239	
9	A	1246	
10	E	274	
11	G	272	
12	H	279	
13	I	297	
14	X	250	
15	Ln	25	
16	M	1096	
17	S2	1869	
18	SA	295	
19	SB	264	
20	SC	293	
21	SD	243	
22	SE	263	
23	SF	204	
24	SG	249	
25	SH	194	
26	SI	208	
27	SJ	194	

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Mol	Chain	Length	Quality of chain
28	SK	165	
29	SL	158	
30	SM	132	
31	SN	151	
32	SO	151	
33	SP	145	
34	SQ	146	
35	SR	135	
36	SS	152	
37	ST	145	
38	SU	119	
39	SV	83	
40	SW	130	
41	SX	143	
42	SY	133	
43	SZ	125	
44	Sa	115	
45	Sb	84	
46	Sc	69	
47	Sd	56	
48	Se	59	
49	Sf	156	
50	Sg	317	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 125225 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 Superkiller complex protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	934	Total	C	N	O	S	0	0
			7299	4637	1259	1359	44		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP Q6PGP7
B	-2	PRO	-	expression tag	UNP Q6PGP7
B	-1	ASP	-	expression tag	UNP Q6PGP7
B	0	SER	-	expression tag	UNP Q6PGP7

- Molecule 2 is a protein called WD repeat-containing protein 61.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	305	Total	C	N	O	S	0	0
			2373	1507	399	462	5		
2	D	305	Total	C	N	O	S	0	0
			2373	1507	399	462	5		

- Molecule 3 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	286	Total	C	N	O	S	0	0
			2194	1373	374	432	15		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-3	GLY	-	expression tag	UNP Q15024
F	-2	PRO	-	expression tag	UNP Q15024
F	-1	ASP	-	expression tag	UNP Q15024
F	0	SER	-	expression tag	UNP Q15024

- Molecule 4 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	184	Total	C	N	O	S	0	0
			1414	889	248	267	10		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-3	GLY	-	expression tag	UNP Q9Y3B2
J	-2	PRO	-	expression tag	UNP Q9Y3B2
J	-1	ASP	-	expression tag	UNP Q9Y3B2
J	0	SER	-	expression tag	UNP Q9Y3B2

- Molecule 5 is a protein called Exosome complex component RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	353	Total	C	N	O	S	0	0
			2764	1734	482	529	19		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-3	GLY	-	expression tag	UNP Q06265
K	-2	PRO	-	expression tag	UNP Q06265
K	-1	ASP	-	expression tag	UNP Q06265
K	0	SER	-	expression tag	UNP Q06265

- Molecule 6 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	265	Total	C	N	O	S	0	0
			2020	1272	337	397	14		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-3	GLY	-	expression tag	UNP Q96B26
L	-2	PRO	-	expression tag	UNP Q96B26
L	-1	ASP	-	expression tag	UNP Q96B26
L	0	SER	-	expression tag	UNP Q96B26

- Molecule 7 is a protein called Exosome complex component RRP41.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	N	241	Total	C	N	O	S	0	0
			1819	1123	343	344	9		

- Molecule 8 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	208	Total	C	N	O	S	0	0
			1566	979	278	297	12		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	-3	GLY	-	expression tag	UNP Q9NQT4
O	-2	PRO	-	expression tag	UNP Q9NQT4
O	-1	ASP	-	expression tag	UNP Q9NQT4
O	0	SER	-	expression tag	UNP Q9NQT4

- Molecule 9 is a protein called Helicase SKI2W.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	1112	Total	C	N	O	S	0	0
			8706	5519	1526	1613	48		

- Molecule 10 is a protein called Isoform 2 of HBS1-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	66	Total	C	N	O	S	0	0
			525	340	89	95	1		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	365	GLY	-	expression tag	UNP Q9Y450
E	366	PRO	-	expression tag	UNP Q9Y450
E	367	ASP	-	expression tag	UNP Q9Y450
E	368	SER	-	expression tag	UNP Q9Y450
E	633	LEU	-	expression tag	UNP Q9Y450
E	634	GLU	-	expression tag	UNP Q9Y450
E	635	VAL	-	expression tag	UNP Q9Y450
E	636	LEU	-	expression tag	UNP Q9Y450
E	637	PHE	-	expression tag	UNP Q9Y450
E	638	GLN	-	expression tag	UNP Q9Y450

- Molecule 11 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	251	Total	C	N	O	S	0	0
			1852	1149	352	344	7		

- Molecule 12 is a protein called Exosome complex component RRP40.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	237	Total	C	N	O	S	0	0
			1806	1136	329	329	12		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-3	GLY	-	expression tag	UNP Q9NQT5
H	-2	PRO	-	expression tag	UNP Q9NQT5
H	-1	ASP	-	expression tag	UNP Q9NQT5
H	0	SER	-	expression tag	UNP Q9NQT5
H	225	HIS	TYR	variant	UNP Q9NQT5

- Molecule 13 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	289	Total	C	N	O	S	0	0
			2263	1424	405	419	15		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	-3	GLY	-	expression tag	UNP Q13868
I	-2	PRO	-	expression tag	UNP Q13868
I	-1	ASP	-	expression tag	UNP Q13868
I	0	SER	-	expression tag	UNP Q13868

- Molecule 14 is a RNA chain called CrPV-IRES RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	X	123	Total	C	N	O	P	0	0
			2514	1126	375	890	123		

- Molecule 15 is a protein called 60S ribosomal protein L41.

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

- Molecule 16 is a protein called DIS3-like exonuclease 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	975	Total	C	N	O	S	0	0
			7903	4986	1405	1471	41		

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-41	MET	-	initiating methionine	UNP Q8TF46
M	-40	SER	-	expression tag	UNP Q8TF46
M	-39	ALA	-	expression tag	UNP Q8TF46
M	-38	TRP	-	expression tag	UNP Q8TF46
M	-37	SER	-	expression tag	UNP Q8TF46
M	-36	HIS	-	expression tag	UNP Q8TF46
M	-35	PRO	-	expression tag	UNP Q8TF46
M	-34	GLN	-	expression tag	UNP Q8TF46
M	-33	PHE	-	expression tag	UNP Q8TF46
M	-32	GLU	-	expression tag	UNP Q8TF46
M	-31	LYS	-	expression tag	UNP Q8TF46
M	-30	GLY	-	expression tag	UNP Q8TF46
M	-29	GLY	-	expression tag	UNP Q8TF46
M	-28	GLY	-	expression tag	UNP Q8TF46
M	-27	SER	-	expression tag	UNP Q8TF46
M	-26	GLY	-	expression tag	UNP Q8TF46
M	-25	GLY	-	expression tag	UNP Q8TF46
M	-24	GLY	-	expression tag	UNP Q8TF46
M	-23	SER	-	expression tag	UNP Q8TF46
M	-22	GLY	-	expression tag	UNP Q8TF46
M	-21	GLY	-	expression tag	UNP Q8TF46
M	-20	SER	-	expression tag	UNP Q8TF46
M	-19	ALA	-	expression tag	UNP Q8TF46
M	-18	TRP	-	expression tag	UNP Q8TF46
M	-17	SER	-	expression tag	UNP Q8TF46
M	-16	HIS	-	expression tag	UNP Q8TF46
M	-15	PRO	-	expression tag	UNP Q8TF46
M	-14	GLN	-	expression tag	UNP Q8TF46
M	-13	PHE	-	expression tag	UNP Q8TF46
M	-12	GLU	-	expression tag	UNP Q8TF46
M	-11	LYS	-	expression tag	UNP Q8TF46

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Chain	Residue	Modelled	Actual	Comment	Reference
M	-10	THR	-	expression tag	UNP Q8TF46
M	-9	ALA	-	expression tag	UNP Q8TF46
M	-8	GLY	-	expression tag	UNP Q8TF46
M	-7	LEU	-	expression tag	UNP Q8TF46
M	-6	GLU	-	expression tag	UNP Q8TF46
M	-5	VAL	-	expression tag	UNP Q8TF46
M	-4	LEU	-	expression tag	UNP Q8TF46
M	-3	PHE	-	expression tag	UNP Q8TF46
M	-2	GLN	-	expression tag	UNP Q8TF46
M	-1	GLY	-	expression tag	UNP Q8TF46
M	0	PRO	-	expression tag	UNP Q8TF46
M	486	ASN	ASP	conflict	UNP Q8TF46

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S2	1739	Total	C	N	O	P	0	0
			36835	16429	6582	12086	1738		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SA	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 19 is a protein called 40S ribosomal protein S3a.

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

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

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

- Molecule 21 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SD	224	Total	C	N	O	S	0	0
			1745	1112	314	312	7		

- Molecule 22 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 23 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SF	182	Total	C	N	O	S	0	0
			1445	906	271	261	7		

- Molecule 24 is a protein called 40S ribosomal protein S6.

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

- Molecule 25 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

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

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

- Molecule 27 is a protein called 40S ribosomal protein S9.

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

- Molecule 28 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SK	97	Total	C	N	O	S	0	0
			816	533	144	133	6		

- Molecule 29 is a protein called 40S ribosomal protein S11.

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

- Molecule 30 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SM	104	Total	C	N	O	S	0	0
			793	496	139	152	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

- Molecule 31 is a protein called 40S ribosomal protein S13.

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

- Molecule 32 is a protein called 40S ribosomal protein S14.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SP	123	Total	C	N	O	S	0	0
			1005	638	188	172	7		

- Molecule 34 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	SQ	139	Total	C	N	O	S	0	0
			1105	704	207	191	3		

- Molecule 35 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	SR	131	Total	C	N	O	S	0	0
			1064	668	198	194	4		

- Molecule 36 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	SS	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 37 is a protein called 40S ribosomal protein S19.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 39 is a protein called 40S ribosomal protein S21.

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

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

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

- Molecule 41 is a protein called 40S ribosomal protein S23.

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

- Molecule 42 is a protein called 40S ribosomal protein S24.

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

- Molecule 43 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SZ	72	Total	C	N	O	S	0	0
			570	366	104	99	1		

- Molecule 44 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Sa	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 45 is a protein called 40S ribosomal protein S27.

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

- Molecule 46 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Sc	59	Total	C	N	O	S	0	0
			464	281	93	88	2		

- Molecule 47 is a protein called 40S ribosomal protein S29.

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

- Molecule 48 is a protein called 40S ribosomal protein S30.

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

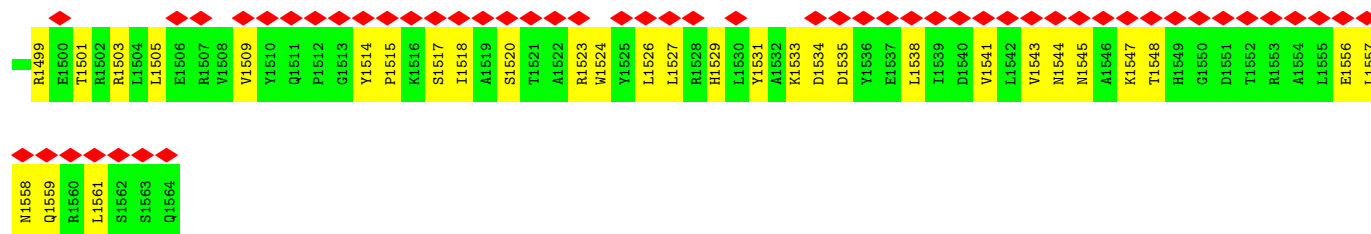
- Molecule 49 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Sf	64	Total	C	N	O	S	0	0
			522	329	99	87	7		

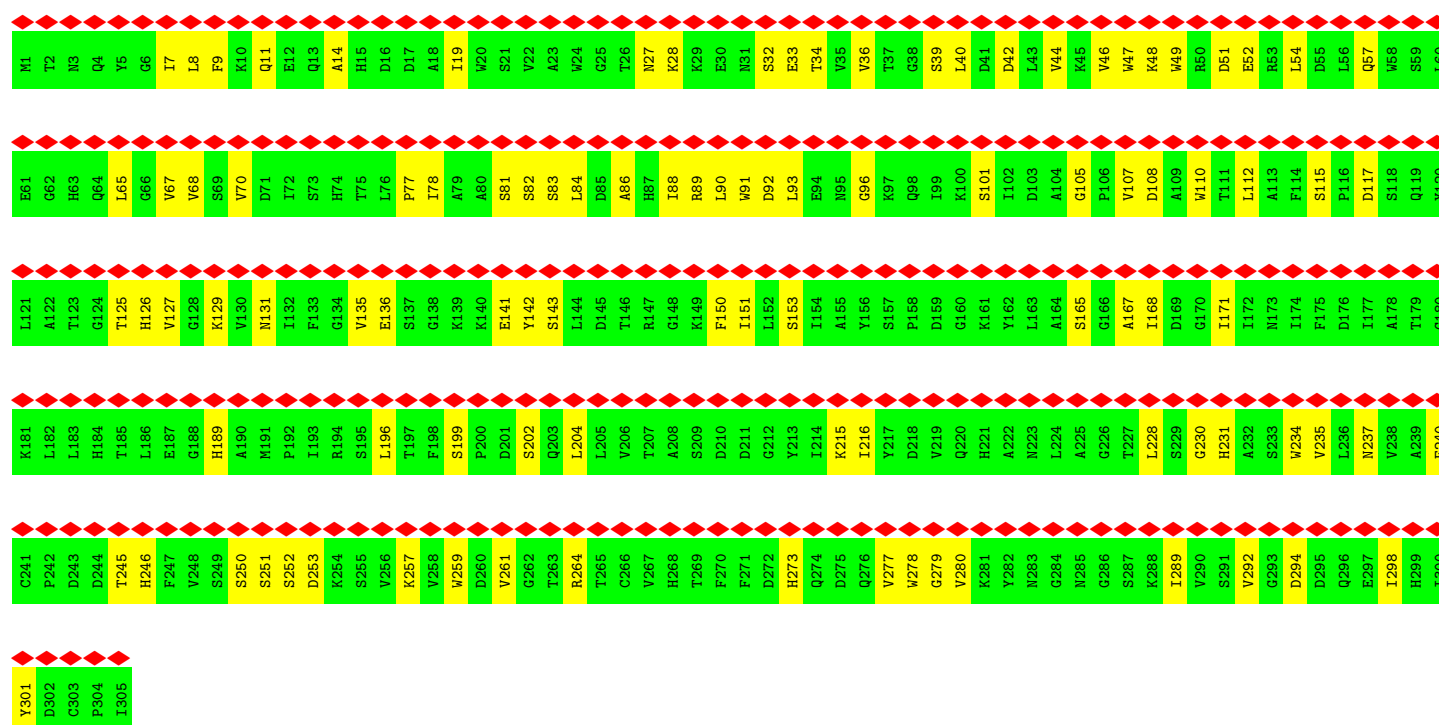
- Molecule 50 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Sg	312	Total	C	N	O	S	0	0
			2429	1531	423	463	12		

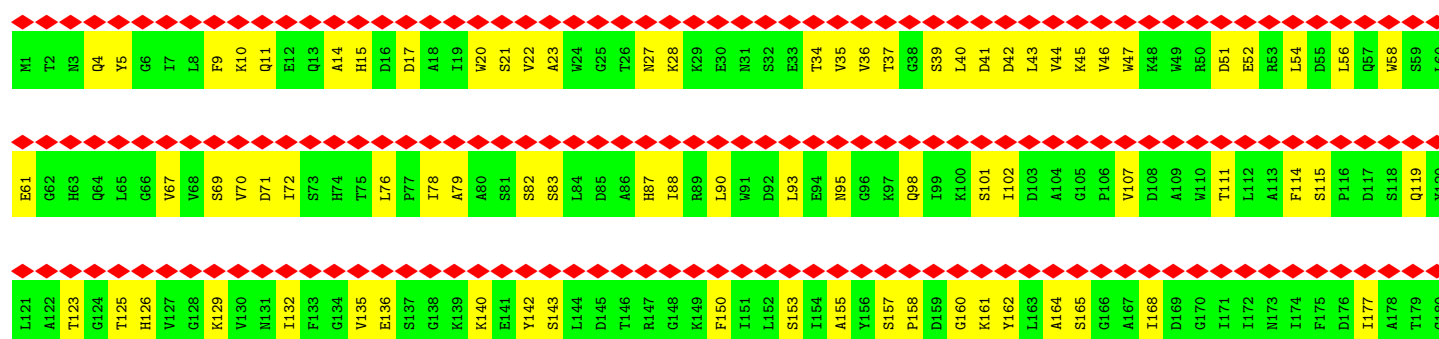
S1437	G1438	K1439	L1440	S1441	S1442	L1443	L1444	R1445	L1446	A1447	L1448	L1449	A1450	L1451	L1452	V1453	C1454	M1455	A1456	M1457	L1458	S1459	N1460	D1461	H1462	W1463	P1464	S1465	L1466	V1467	Q1468	A1469	E1470	T1471	T1472	E1473	A1474	L1475	K1476	L1477	C1478	F1479	C1480	P1481	P1482	A1483	V1484	L1485	L1486	Q1487	L1488	L1489	L1490	Q1491	F1492	K1493	R1494	K1495	M1496
F1317	E1318	N1319	Y1320	N1321	K1322	S1323	L1324	E1325	K1326	W1327	S1328	L1329	S1330	Q1331	A1332	V1333	T1334	G1335	L1336	T1337	D1338	T1339	G1340	R1341	I1342	S1343	E1344	A1345	E1346	T1347	L1348	C1349	T1350	K1351	N1352	L1353	K1354	S1355	N1356	P1357	D1358	Q1359	P1360	A1361	V1362	I1363	L1364	L1365	L1366	R1367	Q1368	V1369	Q1370	C1371	K1372	P1373	L1374	L1375	E1376
S1377	Q1378	K1379	P1380	L1381	P1382	D1383	A1384	V1385	L1386	E1387	E1388	L1389	Q1390	K1391	T1392	V1393	M1394	S1395	M1396	S1397	L1398	S1399	V1400	P1401	A1402	W1403	Q1404	L1405	L1406	A1407	H1408	V1409	Y1410	Q1411	S1412	Q1413	G1414	M1415	M1416	R1417	L1418	A1419	E1420	M1421	C1422	Y1423	R1424	K1425	S1426	L1427	Q1428	L1429	A1430	S1431	Q1432	R1433	K1434	S1435	W1436
N777	T778	W779	C780	D781	L782	G783	I784	N785	Y786	Y787	R788	Q789	A790	Q791	H792	L793	A794	E795	T796	G797	S798	N799	M800	N801	D802	L803	K804	E805	L806	L807	G808	K809	S810	L811	H812	C813	L814	K815	K816	A817	V818	R819	L820	D821	S822	N823	N824	H825	L826	Y827	W828	N829	A830	L831	G832	V833	Y834	A835	C836



• Molecule 2: WD repeat-containing protein 61

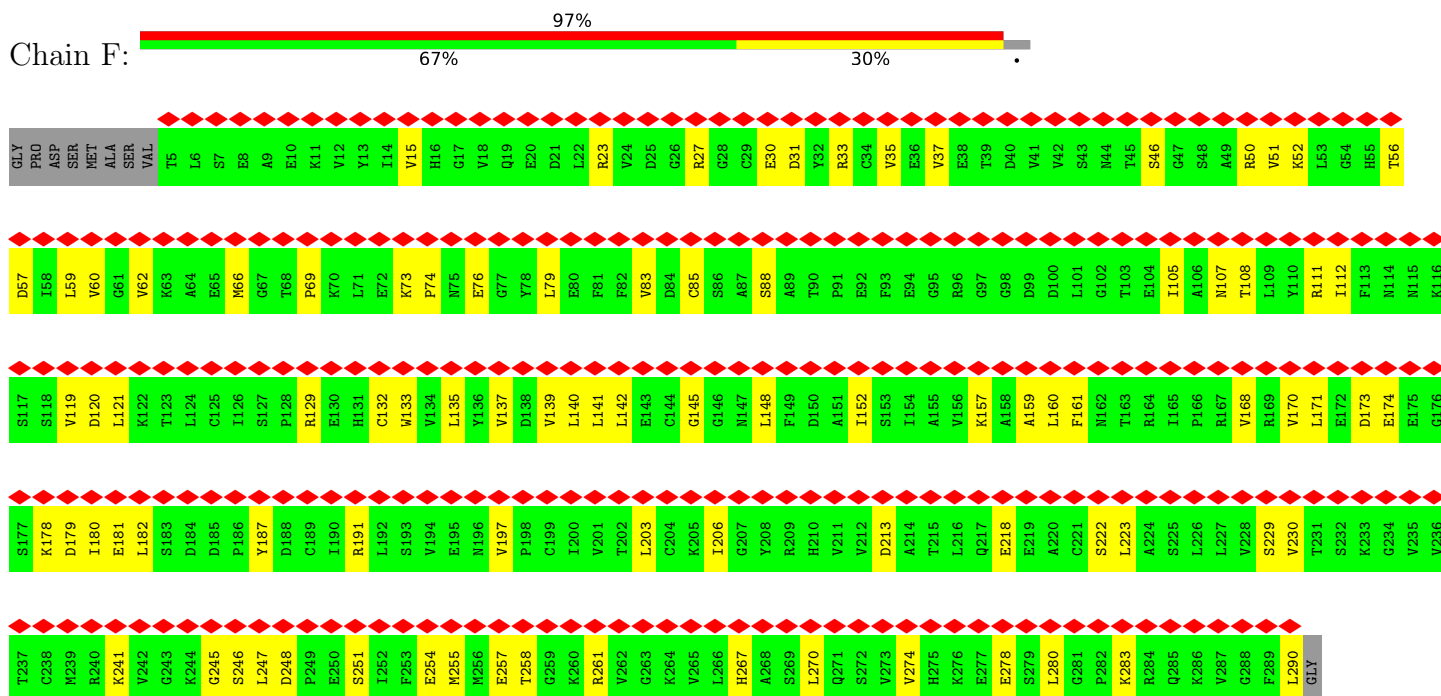


• Molecule 2: WD repeat-containing protein 61

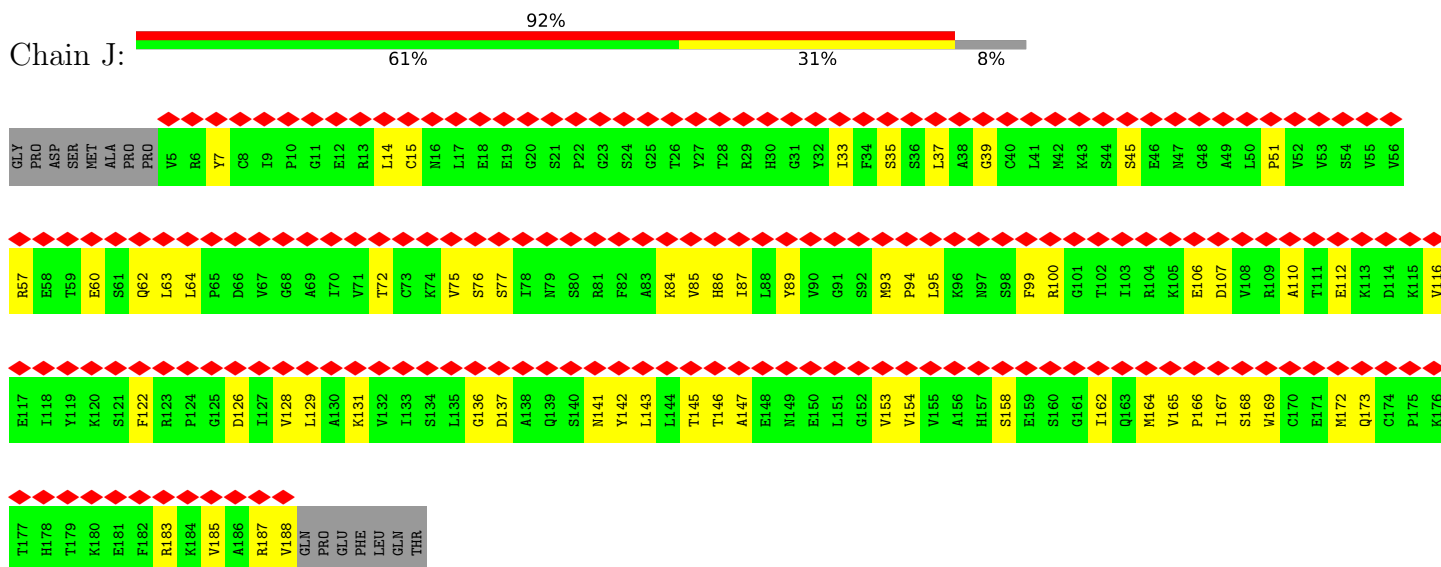




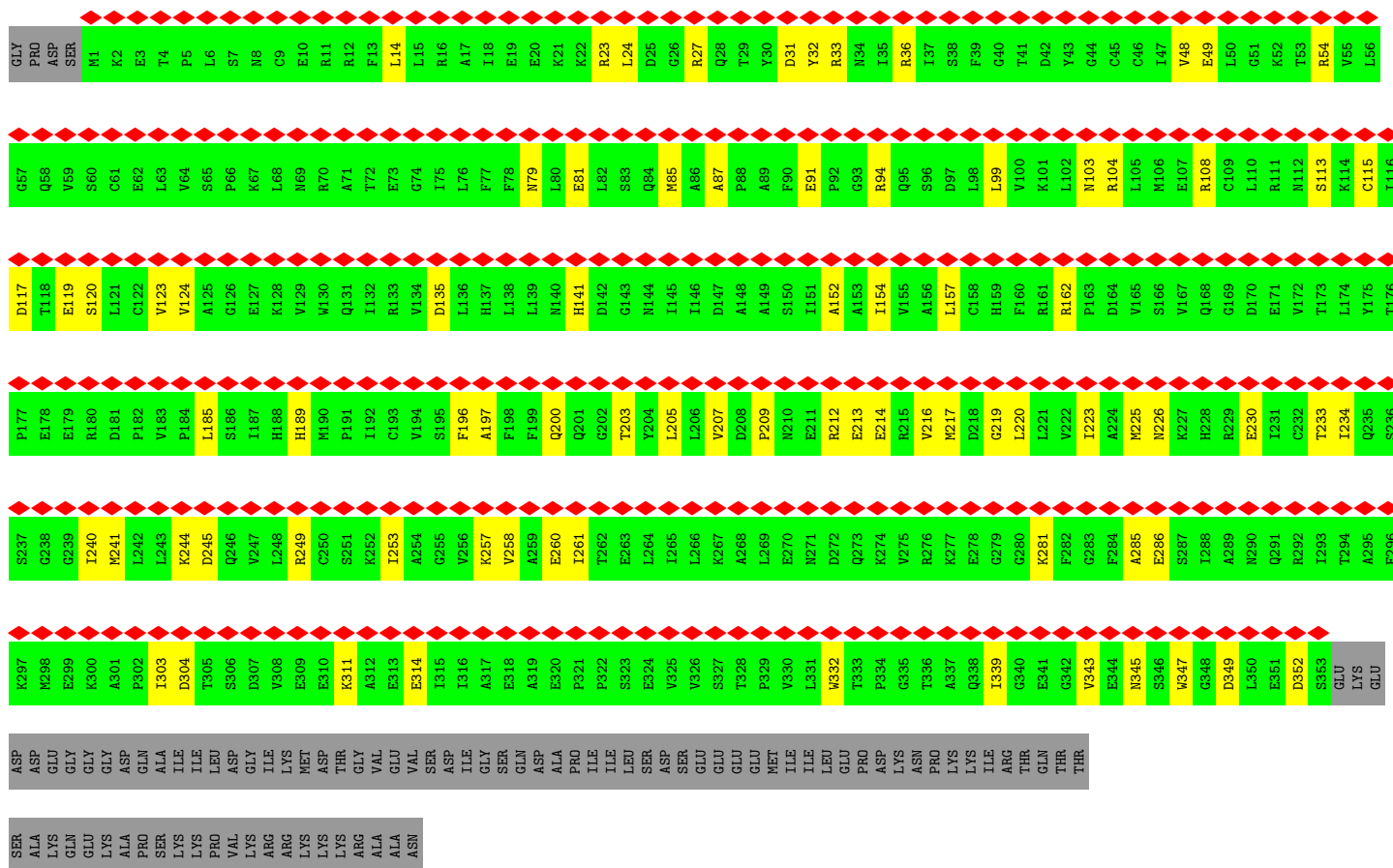
- Molecule 3: Exosome complex component RRP42



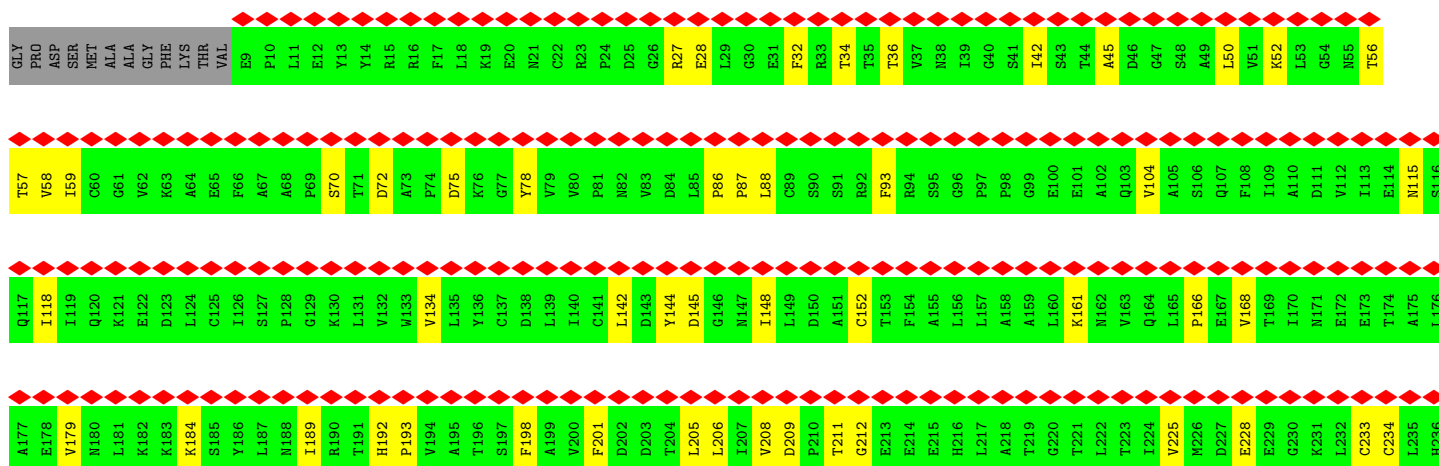
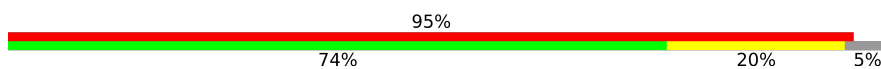
- Molecule 4: Exosome complex component CSL4

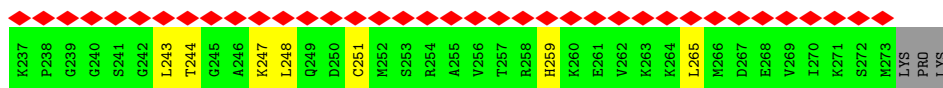


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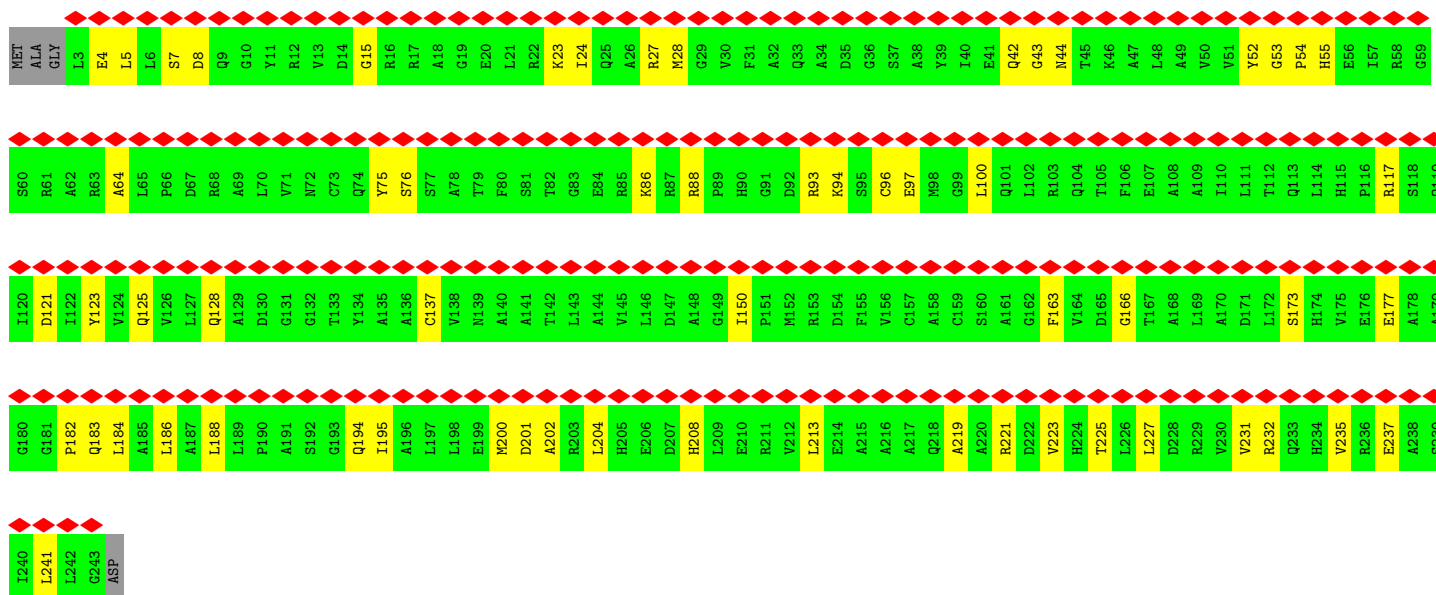
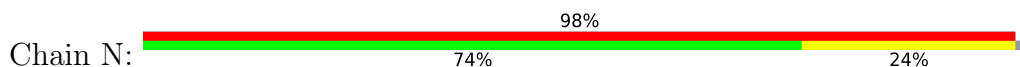


Chain L:

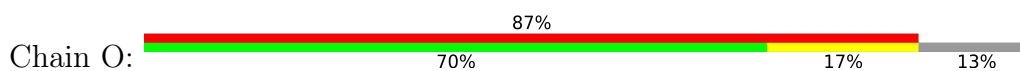




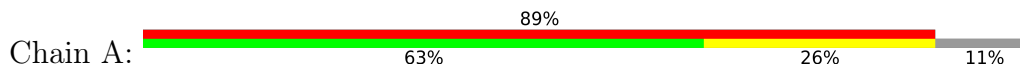
• Molecule 7: Exosome complex component RRP41



• Molecule 8: Exosome complex component RRP46

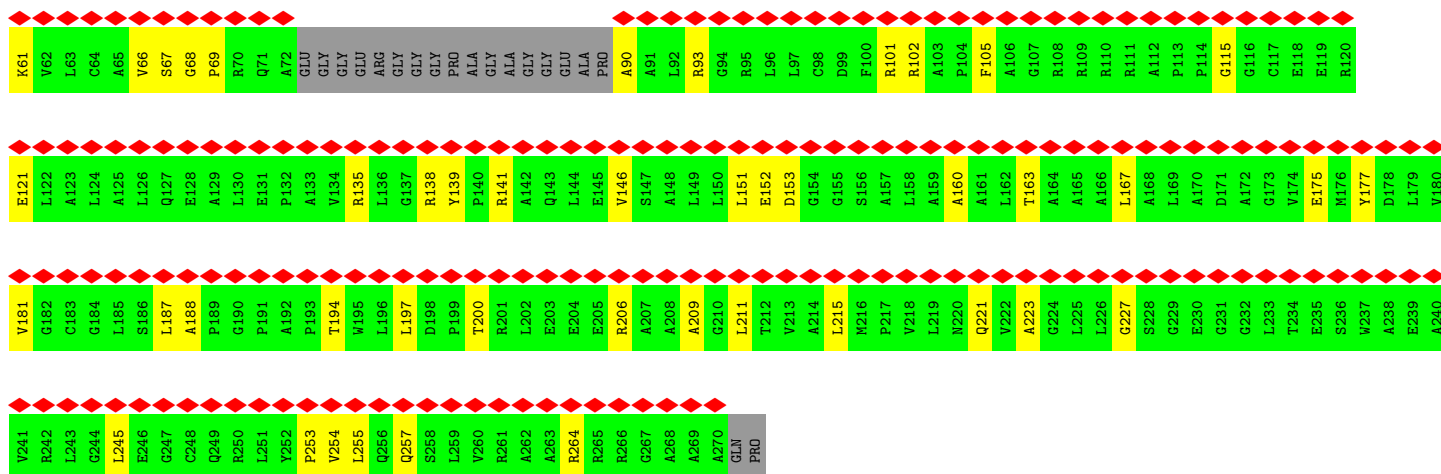


• Molecule 9: Helicase SKI2W

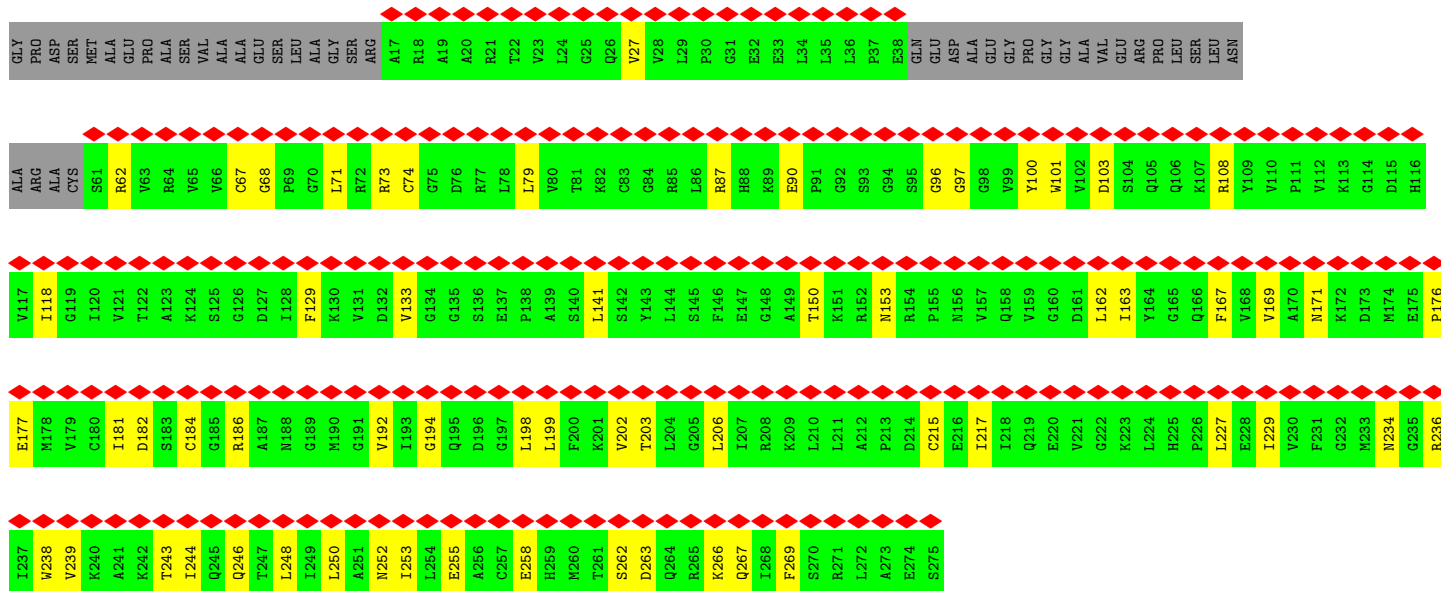
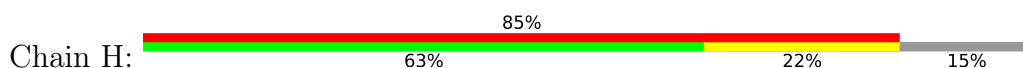






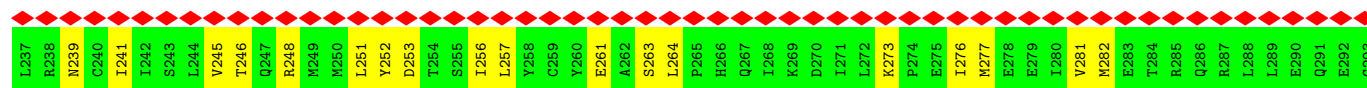


• Molecule 12: Exosome complex component RRP40

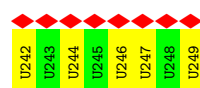
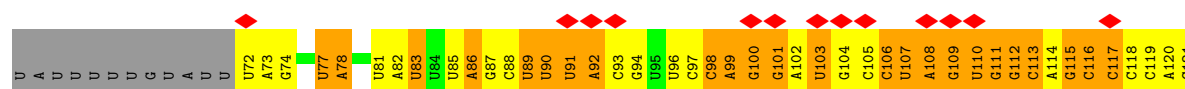
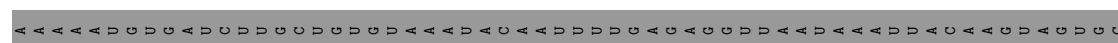
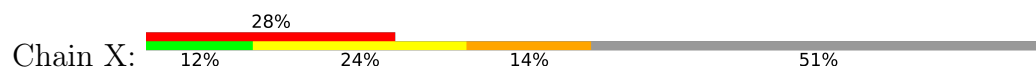


• Molecule 13: Exosome complex component RRP4

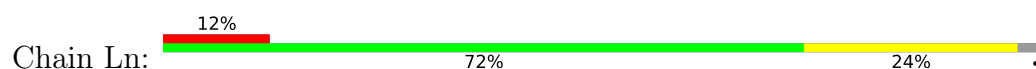




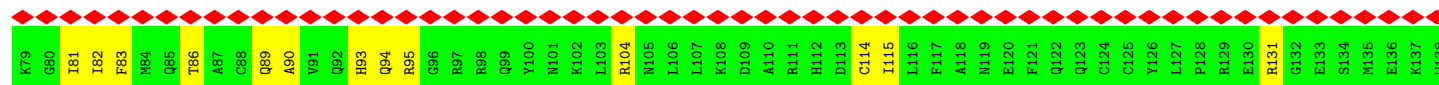
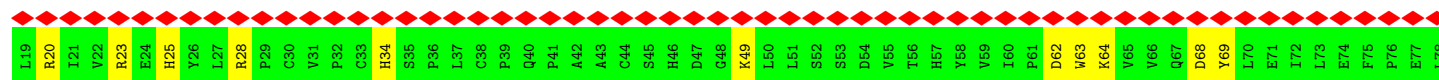
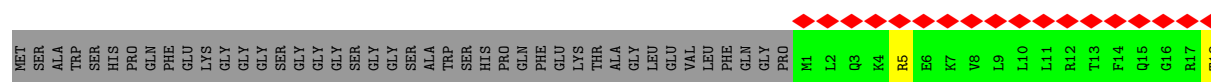
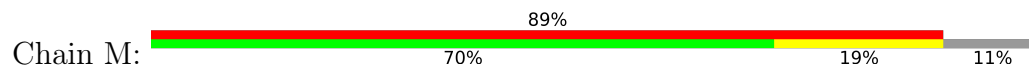
• Molecule 14: CrPV-IRES RNA



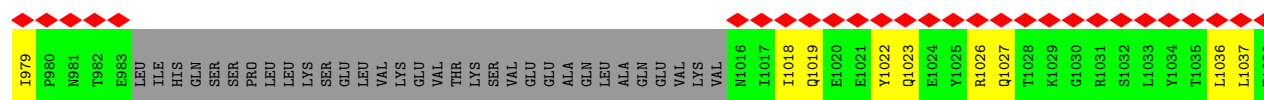
• Molecule 15: 60S ribosomal protein L41



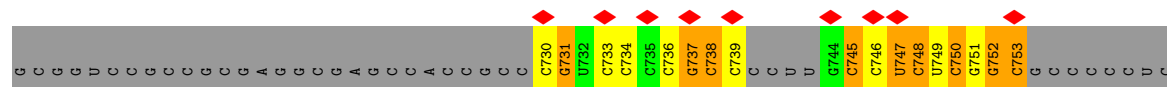
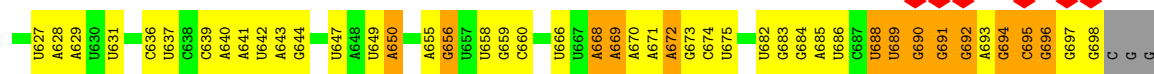
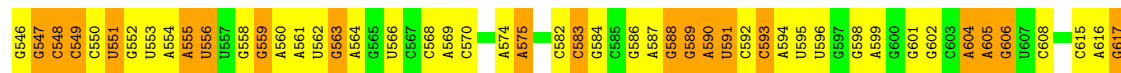
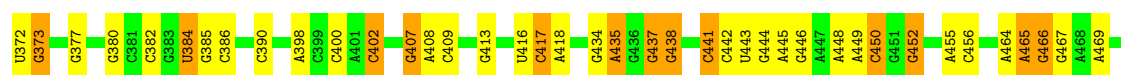
• Molecule 16: DIS3-like exonuclease 1



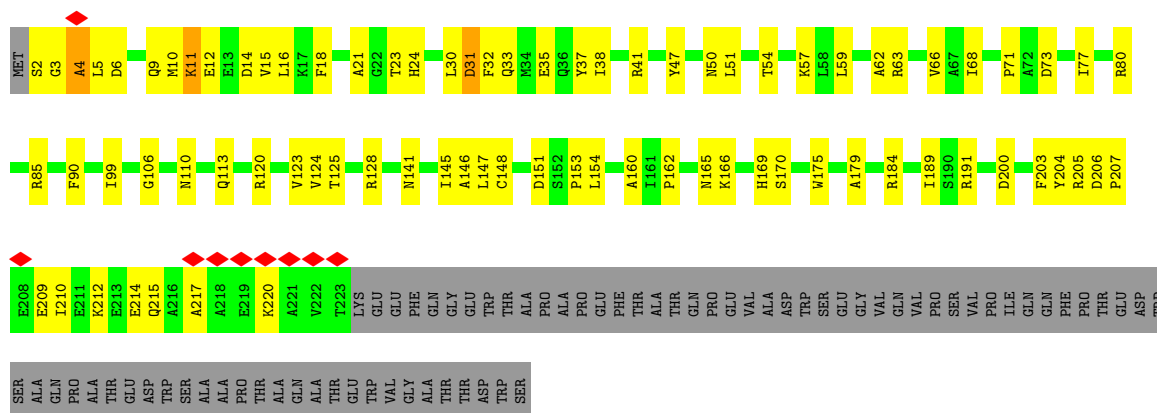
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T140	H200	F260	ALA	E440	E500	S560	A620	T680	A740	R800	C860	E920
R141	E201	V261	GLY	A441	L501	I561	K621	V681	D741	R801	M861	W921
S142	L202	R262	GLU	Q442	G502	M562	L622	A682	S742	Y802	Y862	K922
I143	C203	L263	SER	M443	H503	M563	E623	E683	L743	S803	F863	P923
Y144	D204	G264	PRO	C444	H504	E564	E624	C684	D744	D804	K864	G924
N145	S205	GLN	SER	E445	I505	L565	L625	M685	N745	I805	D865	S925
A146	I206	ALA	E327	M446	A506	D566	V626	T686	A746	W806	K866	L926
A147	L207	ALA	P328	P447	D507	K567	W627	L687	N747	Y807	D867	Q927
V148	Q208	LYS	M329	V448	V508	A568	A628	A688	D748	H808	P868	R928
W149	S209	ASP	F330	M449	T509	S569	L629	N689	P749	R809	A869	F929
Y150	R210	ASP	G332	T450	H510	Y570	G630	H690	H750	L810	T870	Q930
Y151	R211	LEU	R333	P451	F511	E571	K631	W691	D751	L811	E871	N931
H152	E212	VAL	V334	E452	V512	I572	L632	W692	P752	M812	E872	K932
H153	R213	D276	V335	S453	A513	K573	T633	A693	T753	A813	R873	I933
C154	E214	I277	G336	P454	P514	K574	D634	K694	V754	A814	C874	T934
Q155	N215	L278	I337	W455	M515	V575	L635	K695	N755	I815	T875	S935
D156	E216	I279	L338	K456	S516	W576	A636	T696	R756	S816	S876	T936
R157	S217	I279	L338	V457	Y517	Y577	R637	W697	L757	R817	D877	T937
M158	Q218	H280	Q339	S458	I518	G578	H638	E698	L758	D818	G878	T938
P159	Q218	G281	K340	P459	D519	R579	V639	S699	R759	R819	W879	D939
I160	S220	M282	N341	P459	D519	T580	R640	F700	S760	K820	I880	G940
V161	H221	A284	W342	E460	I520	I581	A641	P701	M761	M821	Y881	E941
M162	G222	R285	R343	E462	A522	I582	K642	H702	A762	E822	S882	S942
V163	K223	N286	D344	Q463	R523	S883	R643	Q703	T763	I823	I883	Y943
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E165	Y225	R288	V346	Y405	R525	A585	G645	L705	A765	G825	T885	F945
D166	P226	S288	V347	P406	A526	Y586	C646	L706	M766	M826	N886	H946
E167	E227	I289	T348	M407	T527	K587	G647	R707	S767	L827	G887	L947
E168	H228	H290	F349	G408	T528	L588	A648	Q708	N768	F828	W888	F948
A169	L229	G291	P350	H409	Y529	F589	L649	H709	A769	S829	L889	D949
I170	P230	D292	S351	R469	Y530	Y590	E650	P710	L770	M830	L890	H950
Q171	L231	V293	K352	F410	L531	E591	L651	P711	Y771	K831	F891	Y951
Y172	E232	V294	E353	V411	A532	A592	E652	P712	F772	D832	I892	T952
Y173	V233	V296	E354	V413	D533	A593	G653	H713	S773	L833	P893	V953
G174	L234	E297	V355	L414	R534	Q594	V654	Q714	T774	E834	R894	R954
S175	E235	L298	Q356	G415	R535	E595	E655	F715	G775	E835	F895	I955
E176	A236	L299	S357	R416	Y536	L596	V656	E716	S776	L836	C896	S956
T177	G237	P300	Q358	I417	D537	L597	C657	F717	C777	C837	I897	I957
E178	I238	K301	K360	G418	M538	D598	V658	S718	A778	R838	K898	Q958
G179	K239	N302	N361	D419	L539	G599	Q659	E719	E779	H839	G899	A959
V180	S240	E303	A362	L420	P540	N600	L660	L720	E780	T840	A900	S960
F181	G241	W304	Q363	E421	S541	L601	D661	R721	E781	M841	A901	R961
I182	R242	K305	K364	G422	V542	SER	D662	E722	F782	N842	Q902	C962
I183	Y243	G306	I365	E423	L543	VAL	K663	C723	H783	R843	L903	H963
T184	I244	R307	L366	E424	S544	VAL	K664	A724	H784	N844	K904	S964
F185	Q245	THR	V367	A425	A545	ASP	N665	K725	T785	Q845	N905	D965
K186	G246	VAL	T368	T426	D546	ILE	T666	A726	G786	A846	K906	T966
N187	I247	LEU	P369	D427	L547	PRO	H667	K727	L787	A847	D907	I967
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L189	N249	GLY	W370	V429	S549	LYS	L669	F729	L789	H849	L909	L969
D190	V250	ASP	D371	E430	L550	ASP	T670	F730	D790	S850	V910	E970
N191	N251	ASP	R373	M431	L551	LEU	P671	I731	K791	Q851	I911	I971
F192	K252	CYS	I374	S432	G552	D514	K672	D732	Y792	R852	I912	I972
W193	H253	ASP	P375	I433	G553	E615	Q673	T733	T793	Q853	C913	S973
P194	R254	ASP	K376	S434	V554	K616	P674	R734	H794	S854	Q914	N974
D195	A255	ASP	I377	W435	D555	S617	L675	S735	F795	T855	P915	K975
L196	Q256	ASP	R378	I436	R556	R618	E676	N736	T796	E856	D916	P976
K197	I257	ASP	R378	F437	Y557		V677	K737	S797	L857	S917	Y977
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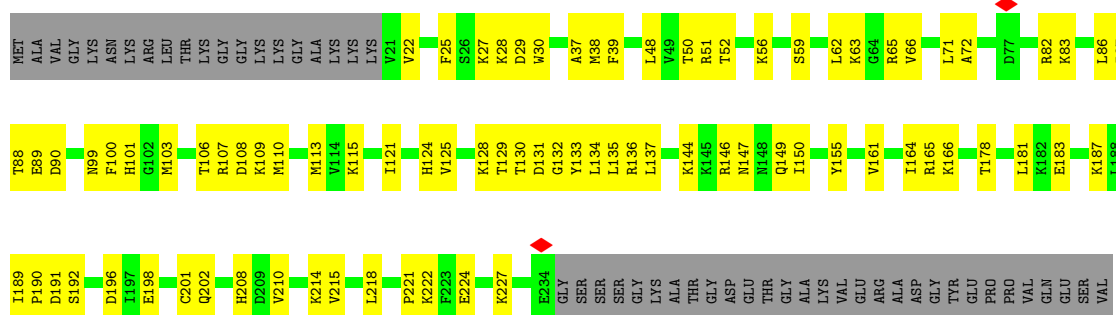
• Molecule 17: 18S ribosomal RNA



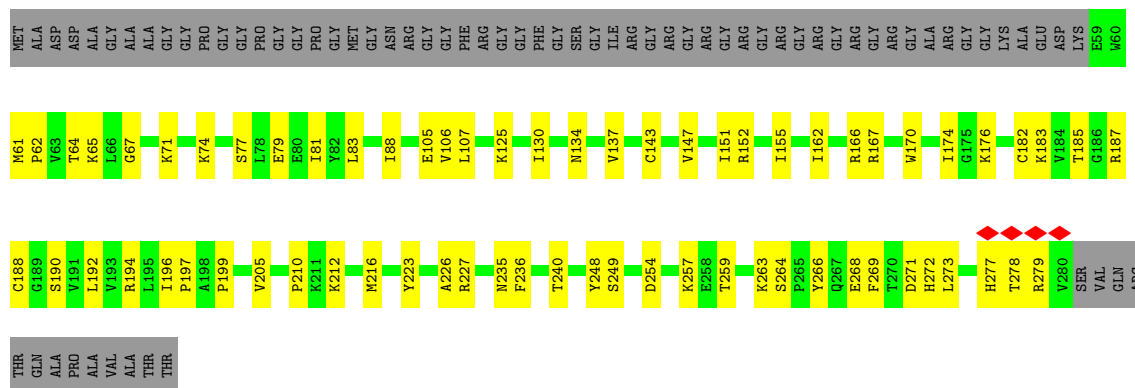




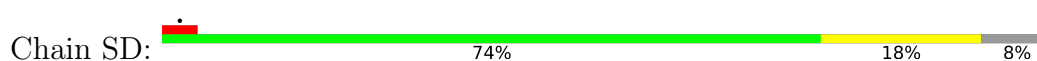
• Molecule 19: 40S ribosomal protein S3a

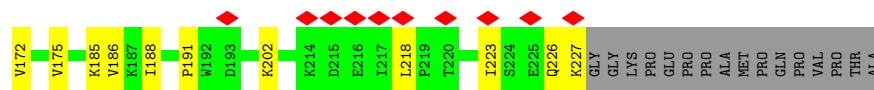


• Molecule 20: 40S ribosomal protein S2

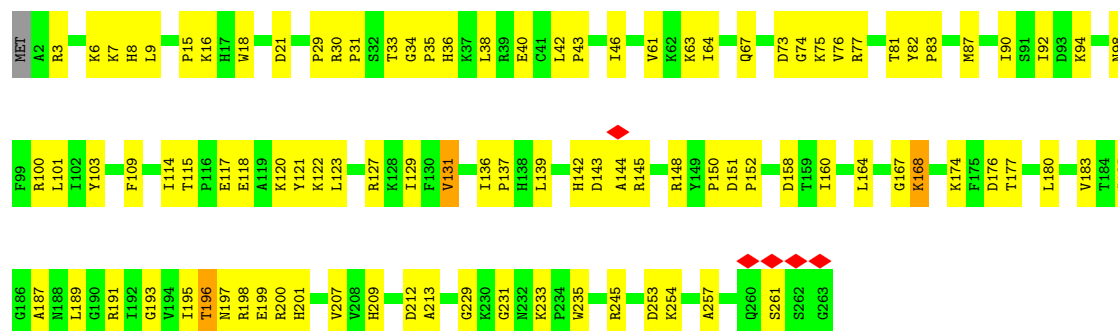


• Molecule 21: 40S ribosomal protein S3

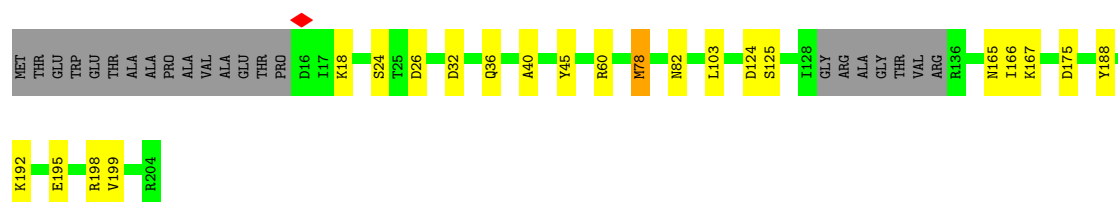
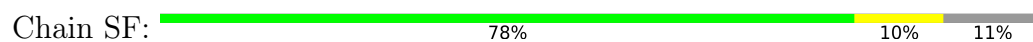




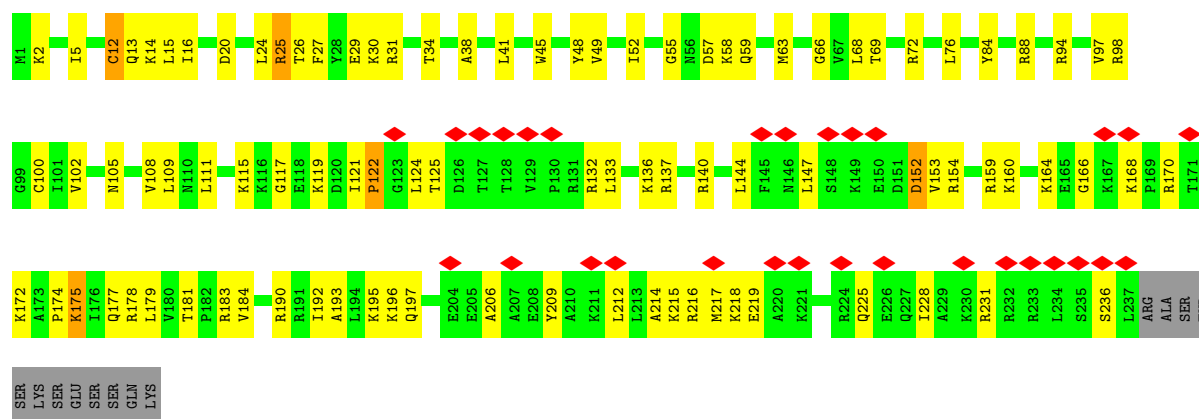
- Molecule 22: 40S ribosomal protein S4, X isoform



- Molecule 23: 40S ribosomal protein S5



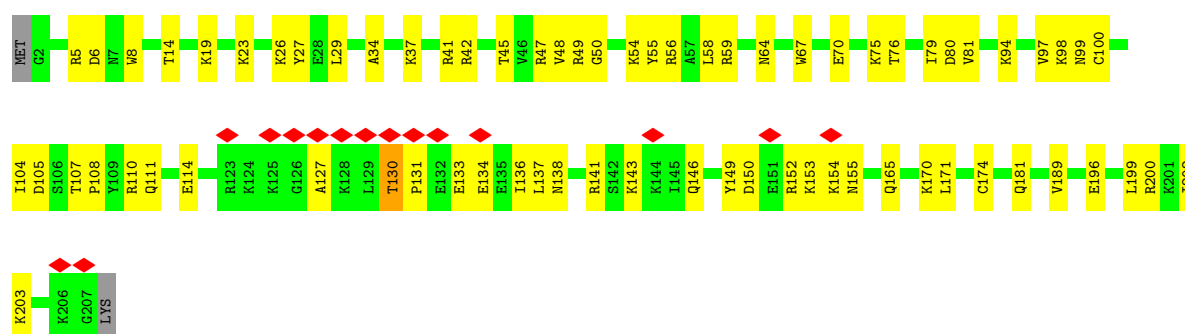
- Molecule 24: 40S ribosomal protein S6



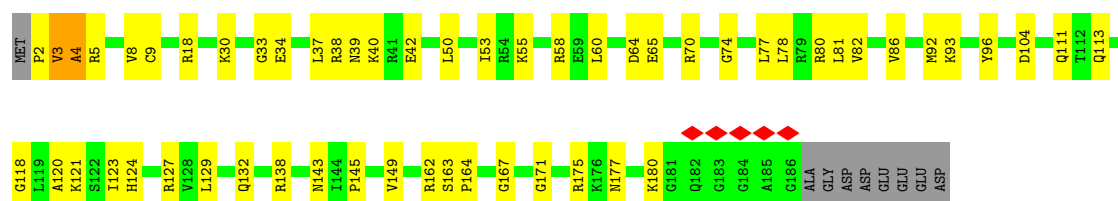
- Molecule 25: 40S ribosomal protein S7



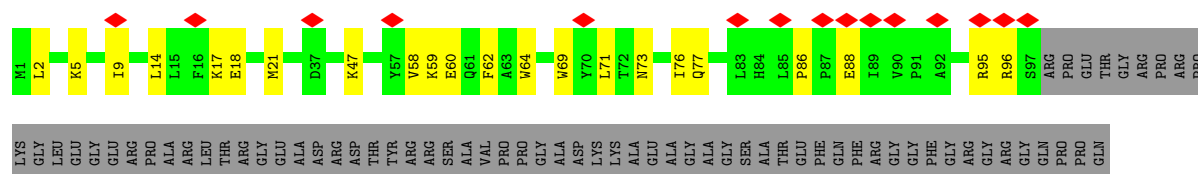
- Molecule 26: 40S ribosomal protein S8



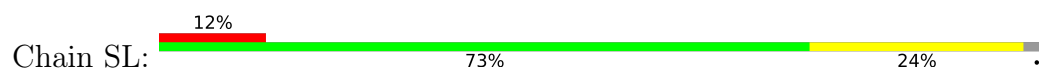
- Molecule 27: 40S ribosomal protein S9

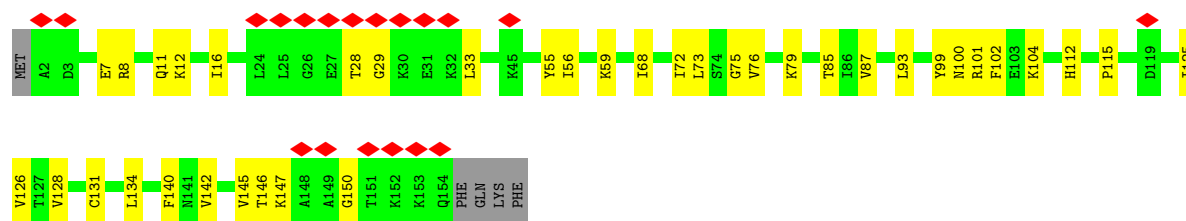


- Molecule 28: 40S ribosomal protein S10

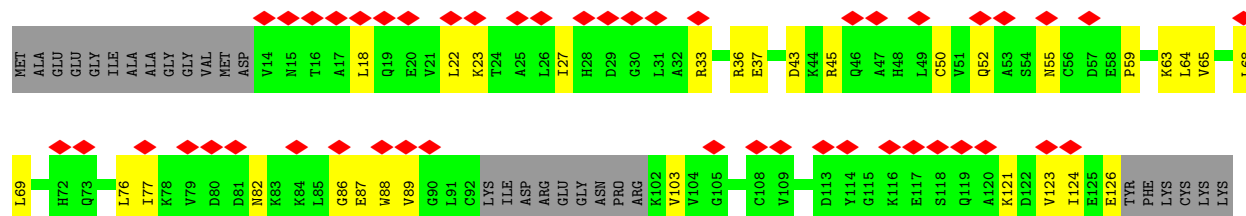


- Molecule 29: 40S ribosomal protein S11

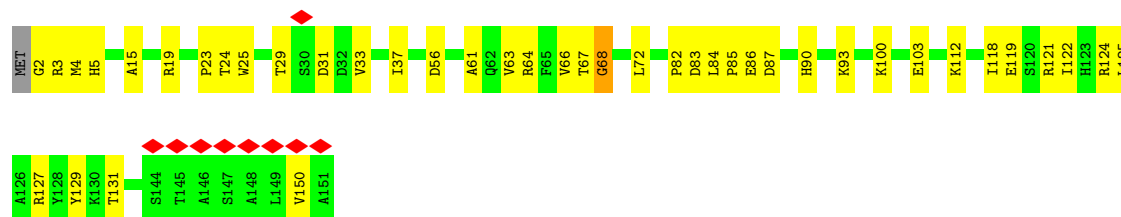
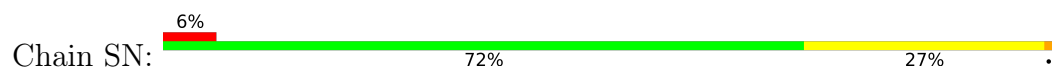




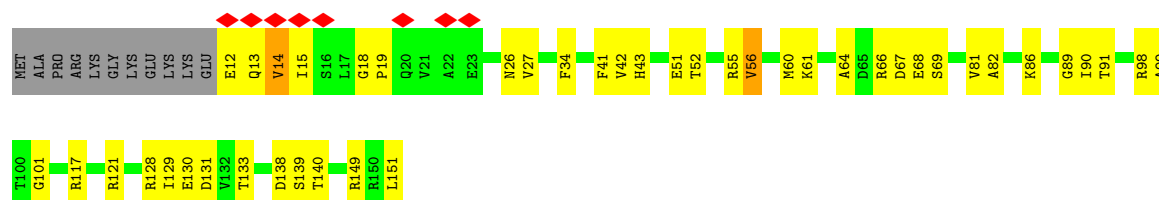
- Molecule 30: 40S ribosomal protein S12



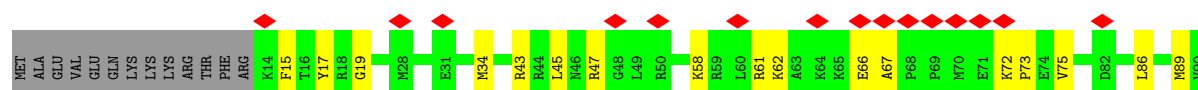
- Molecule 31: 40S ribosomal protein S13

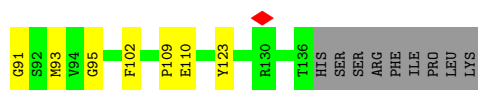


- Molecule 32: 40S ribosomal protein S14

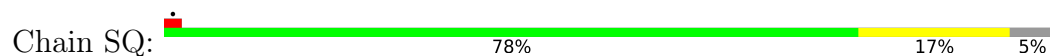


- Molecule 33: 40S ribosomal protein S15

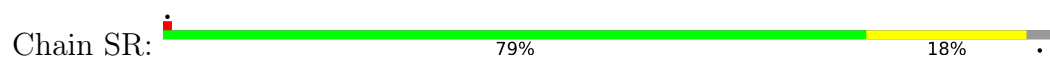




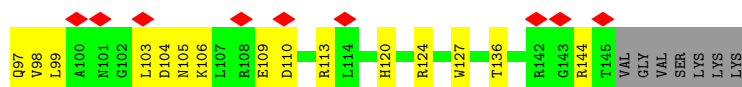
- Molecule 34: 40S ribosomal protein S16



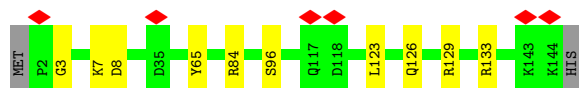
- Molecule 35: 40S ribosomal protein S17



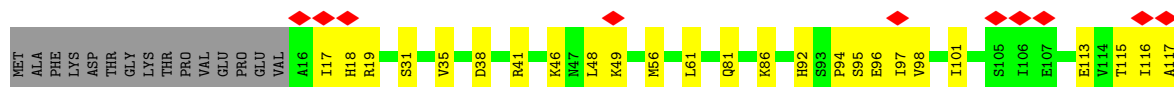
- Molecule 36: 40S ribosomal protein S18



- Molecule 37: 40S ribosomal protein S19

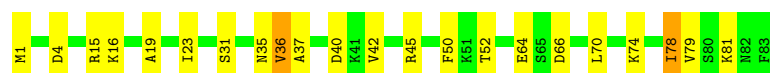


- Molecule 38: 40S ribosomal protein S20



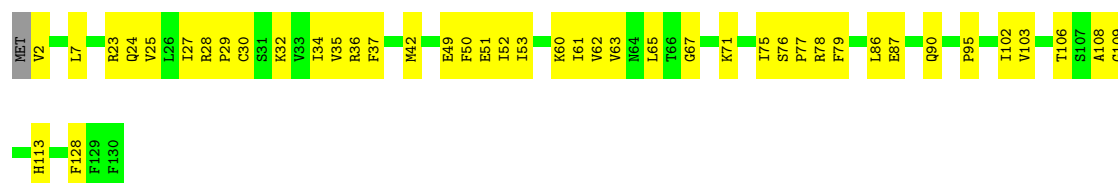
- Molecule 39: 40S ribosomal protein S21

Chain SV:  73% 24% .



- Molecule 40: 40S ribosomal protein S15a

Chain SW:  66% 33% .



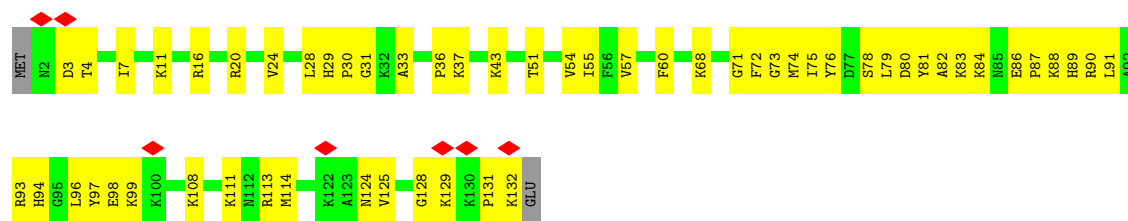
- Molecule 41: 40S ribosomal protein S23

Chain SX:  67% 31% ..



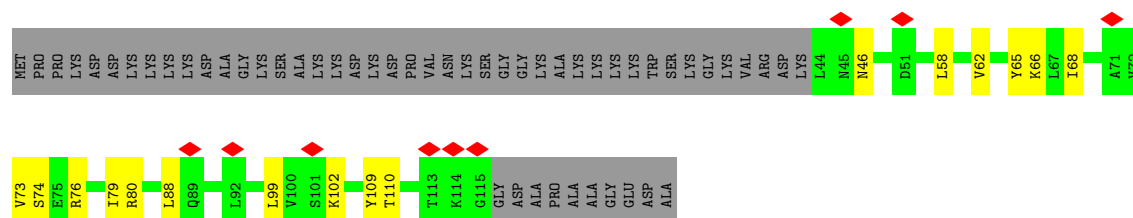
- Molecule 42: 40S ribosomal protein S24

Chain SY:  5% 56% 42% .



- Molecule 43: 40S ribosomal protein S25

Chain SZ:  7% 45% 13% 42%



- Molecule 44: 40S ribosomal protein S26



- Molecule 45: 40S ribosomal protein S27



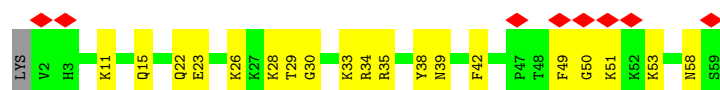
- Molecule 46: 40S ribosomal protein S28



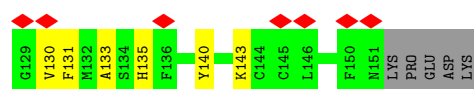
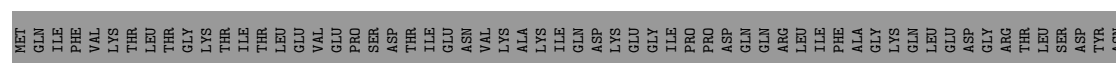
- Molecule 47: 40S ribosomal protein S29



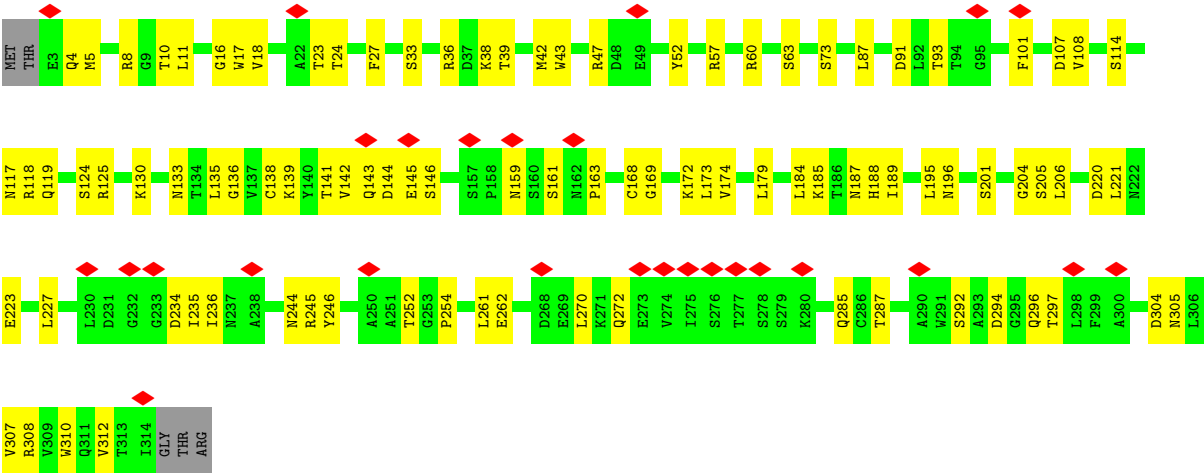
- Molecule 48: 40S ribosomal protein S30



- Molecule 49: Ubiquitin



- Molecule 50: Receptor of activated protein C kinase 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53460	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 ($e^-/\text{\AA}^2$)	64.2	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.053	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	708.19836, 708.19836, 708.19836	wwPDB
Map dimensions	832, 832, 832	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8512, 0.8512, 0.8512	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	B	0.15	0/7429	0.35	0/10058
2	C	0.14	0/2432	0.40	0/3311
2	D	0.15	0/2432	0.42	0/3311
3	F	0.13	0/2225	0.33	0/3007
4	J	0.14	0/1438	0.35	0/1942
5	K	0.13	0/2807	0.32	0/3792
6	L	0.14	0/2053	0.36	0/2786
7	N	0.13	0/1843	0.32	0/2492
8	O	0.14	0/1586	0.34	0/2145
9	A	0.15	0/8881	0.37	0/12039
10	E	0.14	0/535	0.36	0/722
11	G	0.13	0/1881	0.33	0/2551
12	H	0.12	0/1832	0.33	0/2467
13	I	0.13	0/2296	0.37	0/3092
14	X	0.23	0/2792	0.42	0/4331
15	Ln	0.30	0/231	0.62	0/294
16	M	0.11	0/8072	0.30	0/10916
17	S2	0.29	0/41169	0.36	2/64139 (0.0%)
18	SA	0.32	0/1784	0.62	2/2424 (0.1%)
19	SB	0.29	0/1765	0.52	0/2362
20	SC	0.32	0/1762	0.54	0/2381
21	SD	0.24	0/1773	0.42	0/2387
22	SE	0.29	0/2118	0.57	0/2849
23	SF	0.26	0/1465	0.45	2/1969 (0.1%)
24	SG	0.25	0/1946	0.53	0/2590
25	SH	0.24	0/1544	0.49	0/2068
26	SI	0.28	0/1715	0.50	0/2287
27	SJ	0.33	0/1550	0.66	2/2069 (0.1%)
28	SK	0.23	0/840	0.47	0/1133
29	SL	0.30	0/1268	0.45	0/1696
30	SM	0.18	0/799	0.44	0/1076
31	SN	0.28	0/1232	0.47	0/1656
32	SO	0.27	0/1062	0.59	2/1425 (0.1%)
33	SP	0.22	0/1024	0.37	0/1369

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	SQ	0.25	0/1122	0.46	0/1503
35	SR	0.25	0/1078	0.46	0/1447
36	SS	0.20	0/1202	0.38	0/1610
37	ST	0.24	0/1131	0.36	0/1515
38	SU	0.25	0/831	0.42	0/1115
39	SV	0.30	0/643	0.50	0/860
40	SW	0.33	0/1051	0.52	0/1406
41	SX	0.30	0/1116	0.47	0/1490
42	SY	0.29	0/1083	0.53	0/1438
43	SZ	0.20	0/576	0.41	0/774
44	Sa	0.30	0/863	0.56	0/1159
45	Sb	0.25	0/665	0.51	0/891
46	Sc	0.23	0/465	0.40	0/621
47	Sd	0.26	0/470	0.40	0/623
48	Se	0.26	0/465	0.49	0/612
49	Sf	0.15	0/533	0.36	0/706
50	Sg	0.22	0/2486	0.45	0/3384
All	All	0.24	0/131361	0.40	10/186290 (0.0%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	SJ	4	ALA	CA-C-N	10.76	141.07	121.70
27	SJ	4	ALA	C-N-CA	10.76	141.07	121.70
18	SA	4	ALA	CA-C-N	9.35	138.53	121.70
18	SA	4	ALA	C-N-CA	9.35	138.53	121.70
17	S2	1442	U	OP1-P-O3'	-9.18	80.45	108.00

There are no chirality outliers.

There are no planarity outliers.

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	B	7299	0	7423	247	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	2373	0	2290	68	0
2	D	2373	0	2290	77	0
3	F	2194	0	2205	56	0
4	J	1414	0	1441	44	0
5	K	2764	0	2790	63	0
6	L	2020	0	2035	38	0
7	N	1819	0	1818	44	0
8	O	1566	0	1605	29	0
9	A	8706	0	8814	251	0
10	E	525	0	536	16	0
11	G	1852	0	1881	39	0
12	H	1806	0	1865	44	0
13	I	2263	0	2337	56	0
14	X	2514	0	1273	74	0
15	Ln	230	0	276	8	0
16	M	7903	0	7833	141	0
17	S2	36835	0	18567	761	0
18	SA	1747	0	1751	61	0
19	SB	1738	0	1809	78	0
20	SC	1725	0	1813	50	0
21	SD	1745	0	1839	32	0
22	SE	2076	0	2177	74	0
23	SF	1445	0	1495	15	0
24	SG	1923	0	2089	81	0
25	SH	1521	0	1616	55	0
26	SI	1686	0	1772	61	0
27	SJ	1525	0	1640	51	0
28	SK	816	0	841	16	0
29	SL	1247	0	1323	25	0
30	SM	793	0	811	34	0
31	SN	1208	0	1294	30	0
32	SO	1049	0	1073	36	0
33	SP	1005	0	1053	16	0
34	SQ	1105	0	1172	16	0
35	SR	1064	0	1118	16	0
36	SS	1184	0	1244	24	0
37	ST	1112	0	1146	13	0
38	SU	821	0	883	20	0
39	SV	636	0	637	21	0
40	SW	1034	0	1080	35	0
41	SX	1098	0	1167	34	0
42	SY	1065	0	1142	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	SZ	570	0	626	18	0
44	Sa	847	0	899	32	0
45	Sb	651	0	672	17	0
46	Sc	464	0	488	7	0
47	Sd	459	0	452	3	0
48	Se	459	0	503	22	0
49	Sf	522	0	533	17	0
50	Sg	2429	0	2386	68	0
All	All	125225	0	107823	2808	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 2808 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)
30:SM:52:GLN:CD	30:SM:76:LEU:HD11	1.40	1.44
30:SM:69:LEU:CD1	30:SM:76:LEU:HD12	1.68	1.22
30:SM:50:CYS:SG	30:SM:69:LEU:HD11	1.93	1.08
30:SM:52:GLN:NE2	30:SM:76:LEU:HD11	1.77	0.98
17:S2:70:G:N2	17:S2:79:A:H62	1.60	0.98

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	932/1568 (59%)	874 (94%)	58 (6%)	0	100	100
2	C	303/305 (99%)	272 (90%)	31 (10%)	0	100	100
2	D	303/305 (99%)	259 (86%)	44 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	284/295 (96%)	267 (94%)	16 (6%)	1 (0%)	30	59
4	J	182/199 (92%)	158 (87%)	23 (13%)	1 (0%)	24	54
5	K	351/443 (79%)	331 (94%)	20 (6%)	0	100	100
6	L	263/280 (94%)	247 (94%)	16 (6%)	0	100	100
7	N	239/245 (98%)	225 (94%)	14 (6%)	0	100	100
8	O	206/239 (86%)	199 (97%)	7 (3%)	0	100	100
9	A	1104/1246 (89%)	1023 (93%)	80 (7%)	1 (0%)	48	78
10	E	60/274 (22%)	51 (85%)	9 (15%)	0	100	100
11	G	247/272 (91%)	239 (97%)	8 (3%)	0	100	100
12	H	233/279 (84%)	213 (91%)	20 (9%)	0	100	100
13	I	285/297 (96%)	261 (92%)	24 (8%)	0	100	100
15	Ln	22/25 (88%)	19 (86%)	3 (14%)	0	100	100
16	M	965/1096 (88%)	921 (95%)	44 (5%)	0	100	100
18	SA	220/295 (75%)	191 (87%)	26 (12%)	3 (1%)	9	31
19	SB	212/264 (80%)	181 (85%)	29 (14%)	2 (1%)	14	42
20	SC	220/293 (75%)	186 (84%)	32 (14%)	2 (1%)	14	42
21	SD	222/243 (91%)	216 (97%)	6 (3%)	0	100	100
22	SE	260/263 (99%)	219 (84%)	36 (14%)	5 (2%)	6	26
23	SF	178/204 (87%)	167 (94%)	11 (6%)	0	100	100
24	SG	235/249 (94%)	197 (84%)	31 (13%)	7 (3%)	3	18
25	SH	187/194 (96%)	154 (82%)	31 (17%)	2 (1%)	11	38
26	SI	204/208 (98%)	177 (87%)	25 (12%)	2 (1%)	12	40
27	SJ	183/194 (94%)	160 (87%)	20 (11%)	3 (2%)	7	29
28	SK	95/165 (58%)	87 (92%)	8 (8%)	0	100	100
29	SL	151/158 (96%)	127 (84%)	24 (16%)	0	100	100
30	SM	100/132 (76%)	90 (90%)	10 (10%)	0	100	100
31	SN	148/151 (98%)	142 (96%)	3 (2%)	3 (2%)	6	25
32	SO	138/151 (91%)	107 (78%)	27 (20%)	4 (3%)	3	19
33	SP	121/145 (83%)	115 (95%)	6 (5%)	0	100	100
34	SQ	137/146 (94%)	130 (95%)	7 (5%)	0	100	100
35	SR	129/135 (96%)	125 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	SS	141/152 (93%)	137 (97%)	4 (3%)	0	100	100
37	ST	141/145 (97%)	140 (99%)	1 (1%)	0	100	100
38	SU	102/119 (86%)	96 (94%)	6 (6%)	0	100	100
39	SV	81/83 (98%)	65 (80%)	14 (17%)	2 (2%)	4	21
40	SW	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
41	SX	139/143 (97%)	126 (91%)	12 (9%)	1 (1%)	18	47
42	SY	129/133 (97%)	115 (89%)	12 (9%)	2 (2%)	7	29
43	SZ	70/125 (56%)	65 (93%)	5 (7%)	0	100	100
44	Sa	105/115 (91%)	81 (77%)	23 (22%)	1 (1%)	12	40
45	Sb	81/84 (96%)	66 (82%)	15 (18%)	0	100	100
46	Sc	57/69 (83%)	53 (93%)	4 (7%)	0	100	100
47	Sd	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
48	Se	56/59 (95%)	43 (77%)	13 (23%)	0	100	100
49	Sf	62/156 (40%)	57 (92%)	5 (8%)	0	100	100
50	Sg	310/317 (98%)	288 (93%)	22 (7%)	0	100	100
All	All	10773/12844 (84%)	9829 (91%)	902 (8%)	42 (0%)	31	59

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	SA	32	PHE
19	SB	147	ASN
22	SE	76	VAL
24	SG	25	ARG
24	SG	122	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	780/1316 (59%)	780 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	260/260 (100%)	260 (100%)	0	100	100
2	D	260/260 (100%)	260 (100%)	0	100	100
3	F	249/255 (98%)	249 (100%)	0	100	100
4	J	160/173 (92%)	160 (100%)	0	100	100
5	K	307/384 (80%)	307 (100%)	0	100	100
6	L	227/238 (95%)	227 (100%)	0	100	100
7	N	183/186 (98%)	183 (100%)	0	100	100
8	O	172/196 (88%)	172 (100%)	0	100	100
9	A	953/1062 (90%)	953 (100%)	0	100	100
10	E	57/251 (23%)	57 (100%)	0	100	100
11	G	178/188 (95%)	178 (100%)	0	100	100
12	H	196/224 (88%)	196 (100%)	0	100	100
13	I	251/257 (98%)	251 (100%)	0	100	100
15	Ln	23/24 (96%)	23 (100%)	0	100	100
16	M	873/973 (90%)	873 (100%)	0	100	100
18	SA	184/243 (76%)	183 (100%)	1 (0%)	81	81
19	SB	195/231 (84%)	195 (100%)	0	100	100
20	SC	188/225 (84%)	188 (100%)	0	100	100
21	SD	188/202 (93%)	188 (100%)	0	100	100
22	SE	224/225 (100%)	224 (100%)	0	100	100
23	SF	155/170 (91%)	155 (100%)	0	100	100
24	SG	207/218 (95%)	207 (100%)	0	100	100
25	SH	169/174 (97%)	169 (100%)	0	100	100
26	SI	178/180 (99%)	178 (100%)	0	100	100
27	SJ	161/168 (96%)	161 (100%)	0	100	100
28	SK	88/136 (65%)	88 (100%)	0	100	100
29	SL	137/142 (96%)	137 (100%)	0	100	100
30	SM	86/108 (80%)	86 (100%)	0	100	100
31	SN	130/131 (99%)	130 (100%)	0	100	100
32	SO	110/119 (92%)	110 (100%)	0	100	100
33	SP	109/130 (84%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	SQ	115/121 (95%)	115 (100%)	0	100	100
35	SR	119/122 (98%)	119 (100%)	0	100	100
36	SS	124/132 (94%)	124 (100%)	0	100	100
37	ST	113/115 (98%)	113 (100%)	0	100	100
38	SU	94/107 (88%)	94 (100%)	0	100	100
39	SV	67/67 (100%)	67 (100%)	0	100	100
40	SW	112/113 (99%)	112 (100%)	0	100	100
41	SX	113/115 (98%)	113 (100%)	0	100	100
42	SY	113/115 (98%)	113 (100%)	0	100	100
43	SZ	63/103 (61%)	63 (100%)	0	100	100
44	Sa	90/98 (92%)	90 (100%)	0	100	100
45	Sb	75/76 (99%)	75 (100%)	0	100	100
46	Sc	52/62 (84%)	52 (100%)	0	100	100
47	Sd	48/49 (98%)	48 (100%)	0	100	100
48	Se	47/48 (98%)	47 (100%)	0	100	100
49	Sf	57/140 (41%)	57 (100%)	0	100	100
50	Sg	271/275 (98%)	271 (100%)	0	100	100
All	All	9311/10907 (85%)	9310 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	SA	31	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
27	SJ	111	GLN
36	SS	73	ASN
30	SM	52	GLN
34	SQ	8	GLN
39	SV	29	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	X	121/250 (48%)	72 (59%)	3 (2%)
17	S2	1710/1869 (91%)	462 (27%)	19 (1%)
All	All	1831/2119 (86%)	534 (29%)	22 (1%)

5 of 534 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	X	77	U
14	X	78	A
14	X	81	U
14	X	82	A
14	X	83	U

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	S2	980	A
17	S2	1137	U
17	S2	1061	U
17	S2	1325	G
17	S2	339	A

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

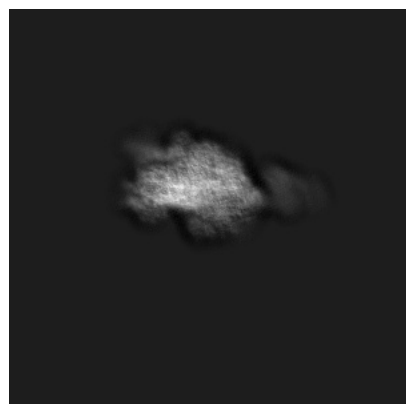
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51134. These allow visual inspection of the internal detail of the map and identification of artifacts.

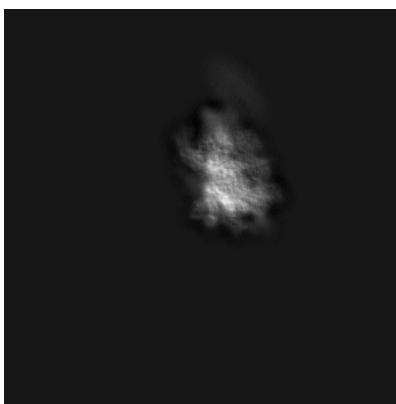
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

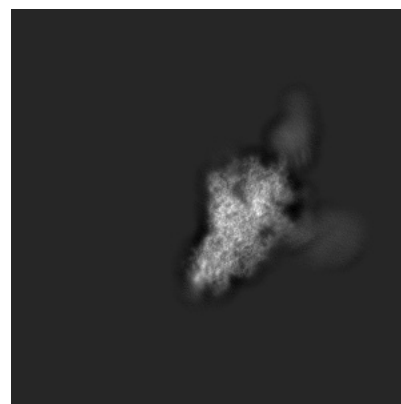
6.1.1 Primary map



X

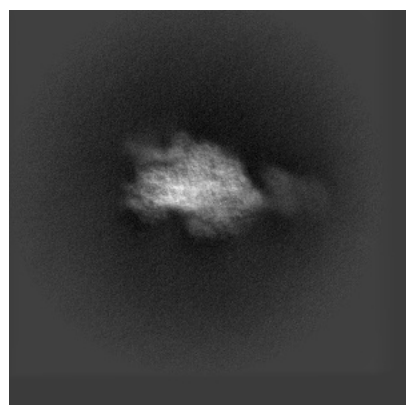


Y

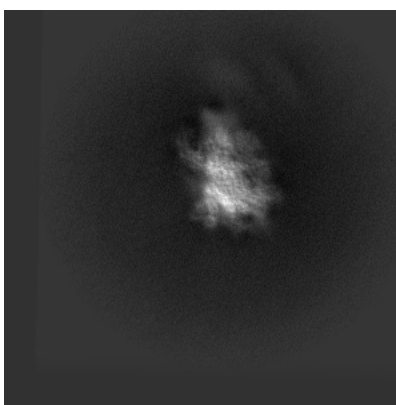


Z

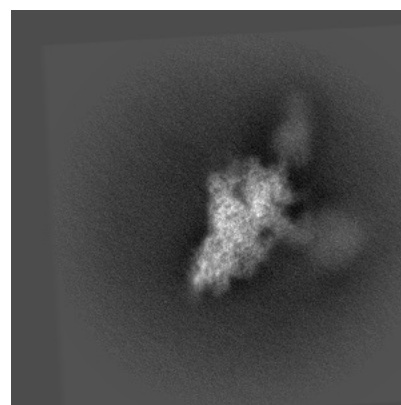
6.1.2 Raw map



X



Y

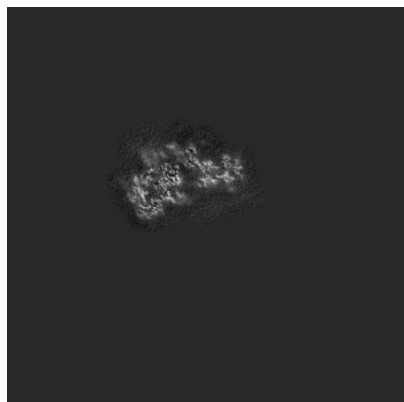


Z

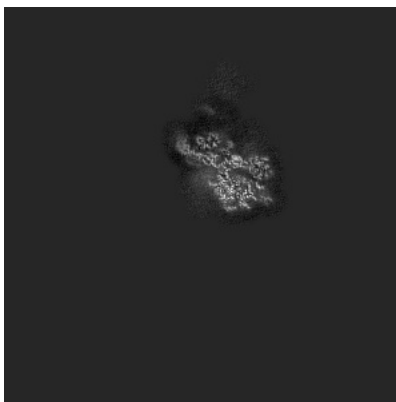
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

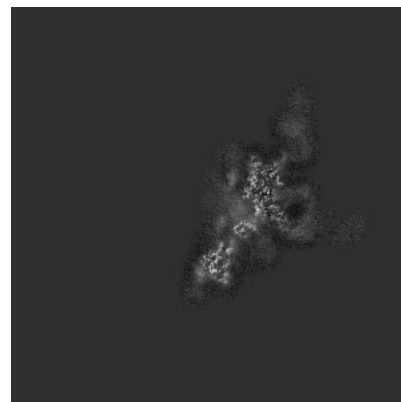
6.2.1 Primary map



X Index: 416

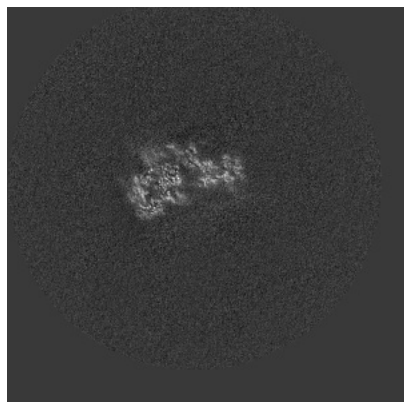


Y Index: 416

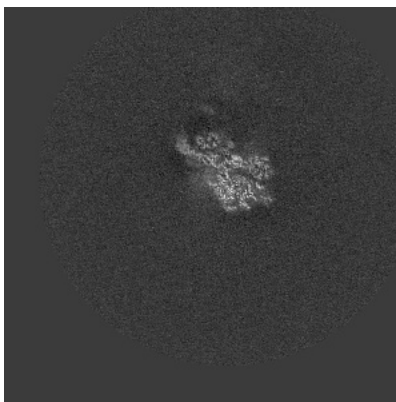


Z Index: 416

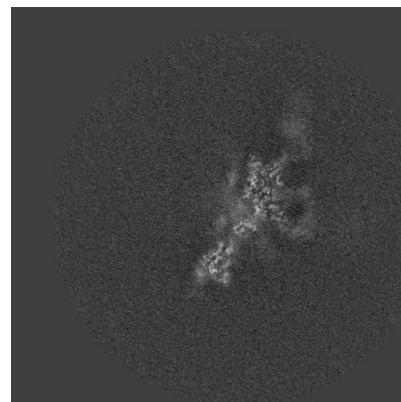
6.2.2 Raw map



X Index: 416



Y Index: 416

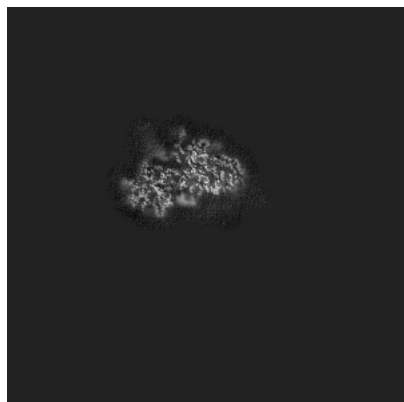


Z Index: 416

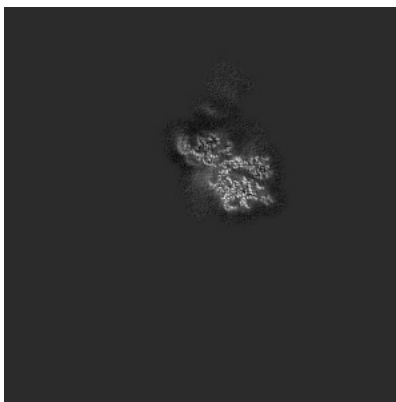
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

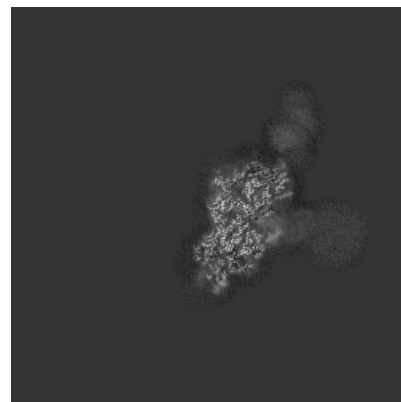
6.3.1 Primary map



X Index: 433

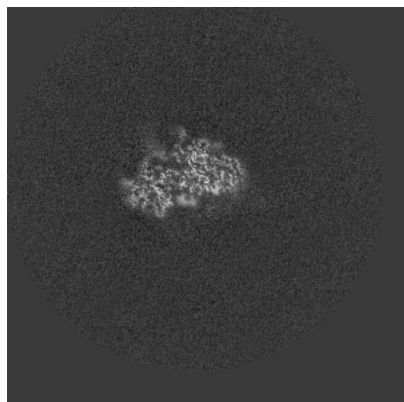


Y Index: 414

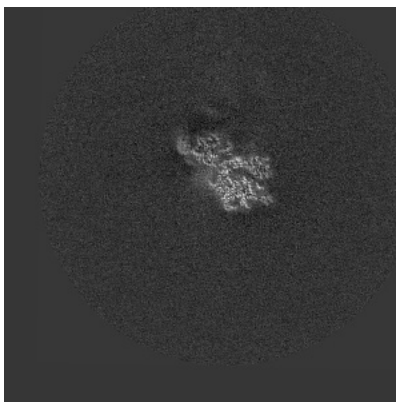


Z Index: 462

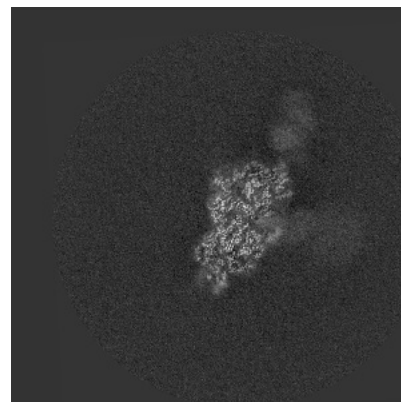
6.3.2 Raw map



X Index: 433



Y Index: 414

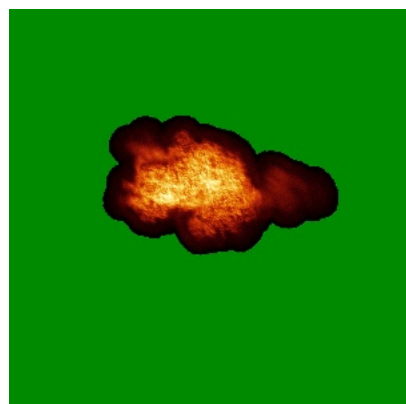


Z Index: 462

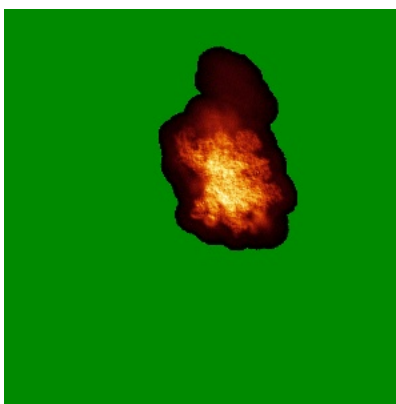
The images above show the largest variance slices of the map in three orthogonal directions.

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

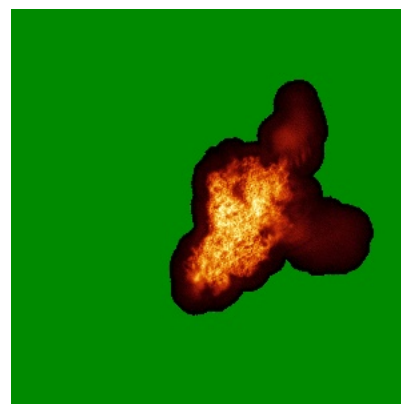
6.4.1 Primary map



X

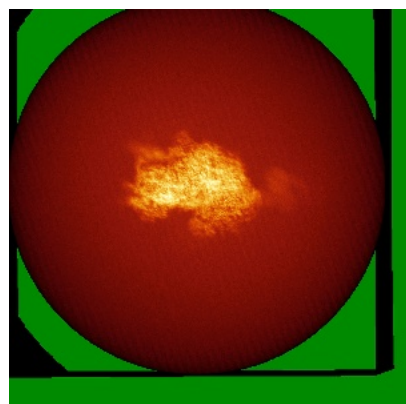


Y

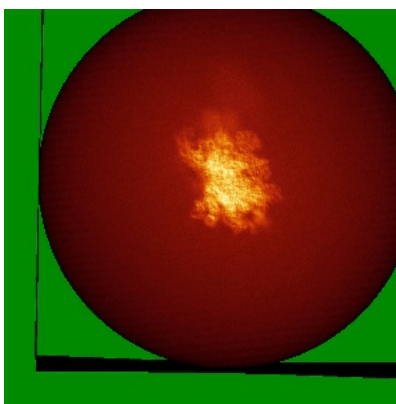


Z

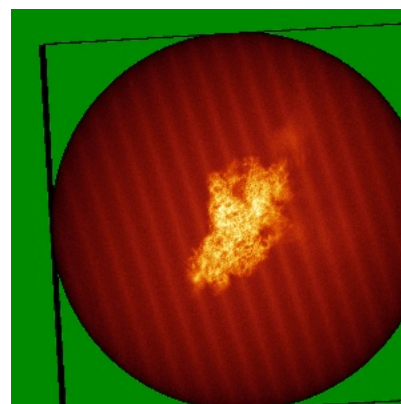
6.4.2 Raw map



X



Y

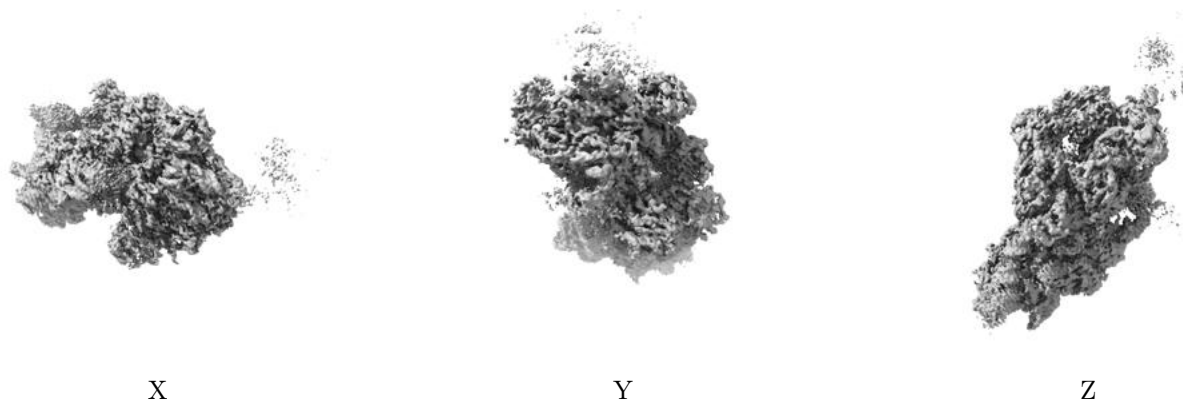


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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



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.

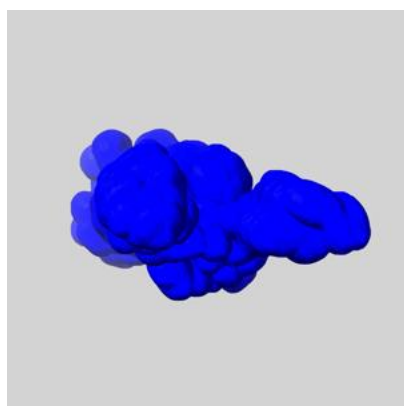
6.6 Mask visualisation [i](#)

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

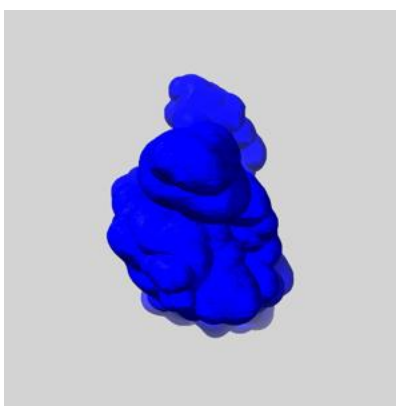
A mask typically either:

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

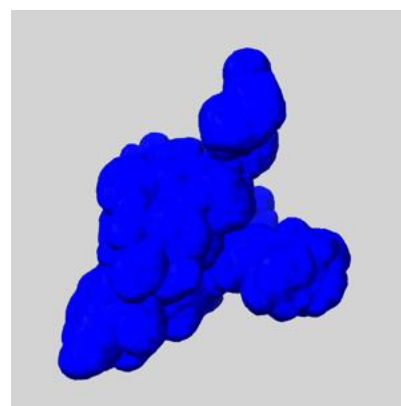
6.6.1 emd_51134_msk_1.map [i](#)



X



Y

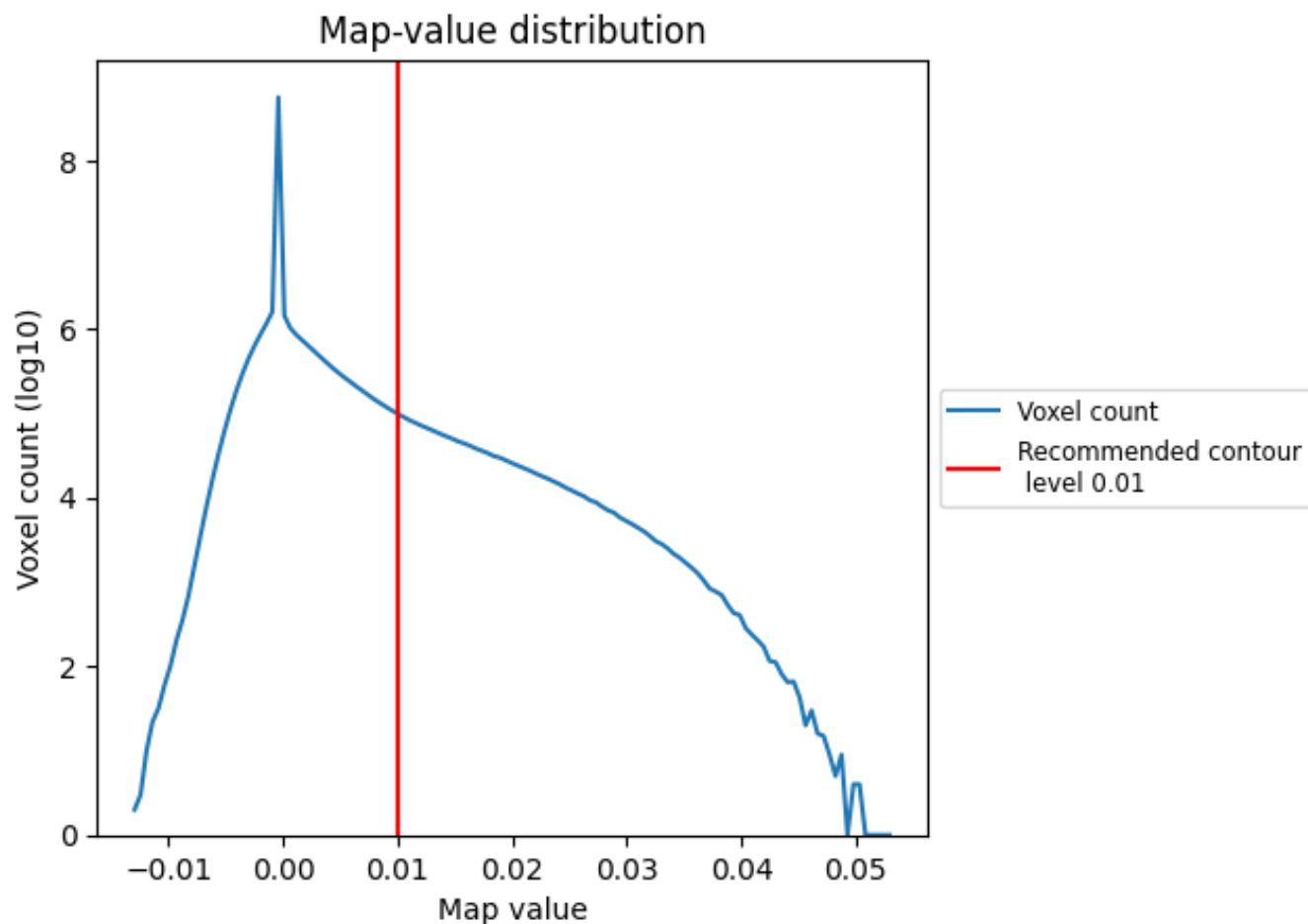


Z

7 Map analysis [i](#)

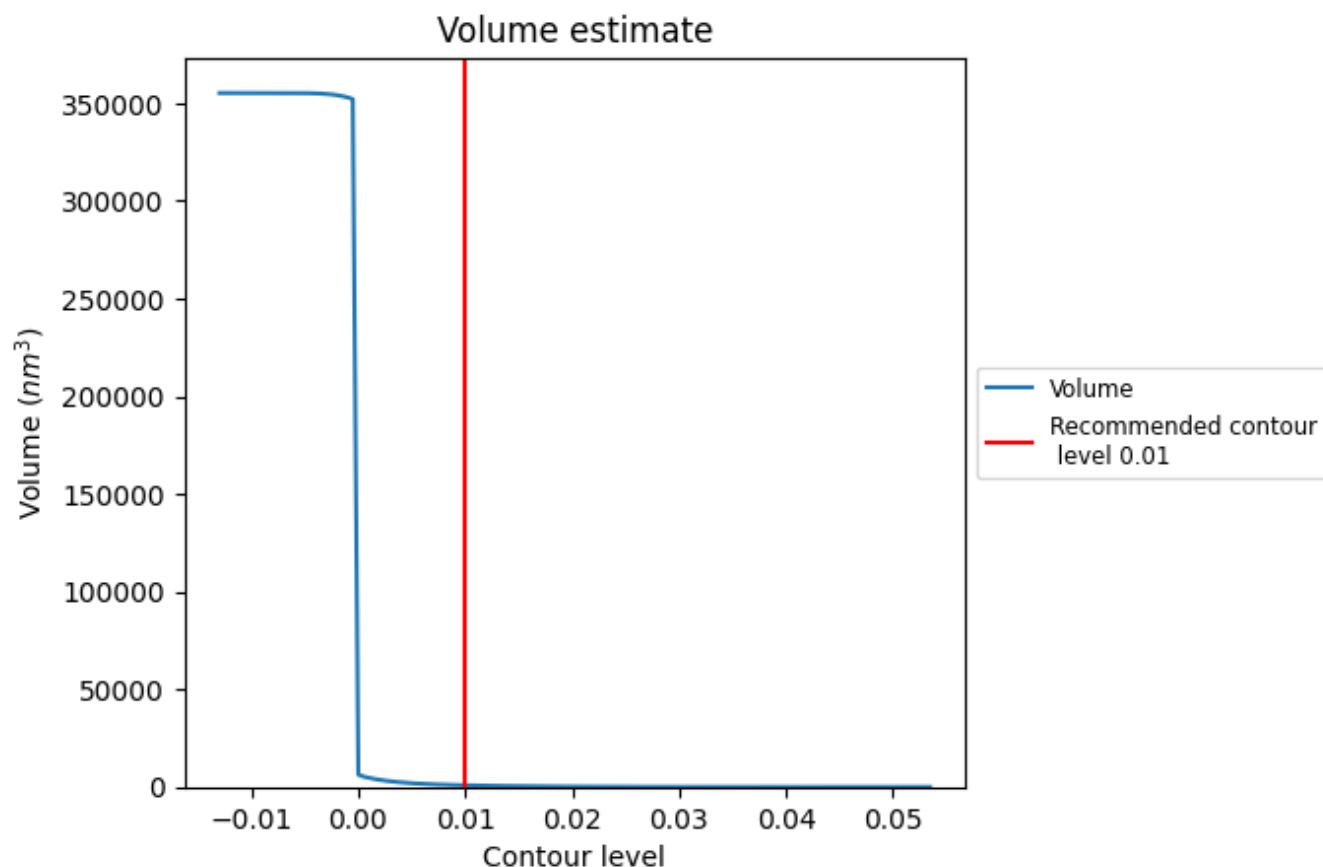
This section contains the results of statistical analysis of the map.

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.

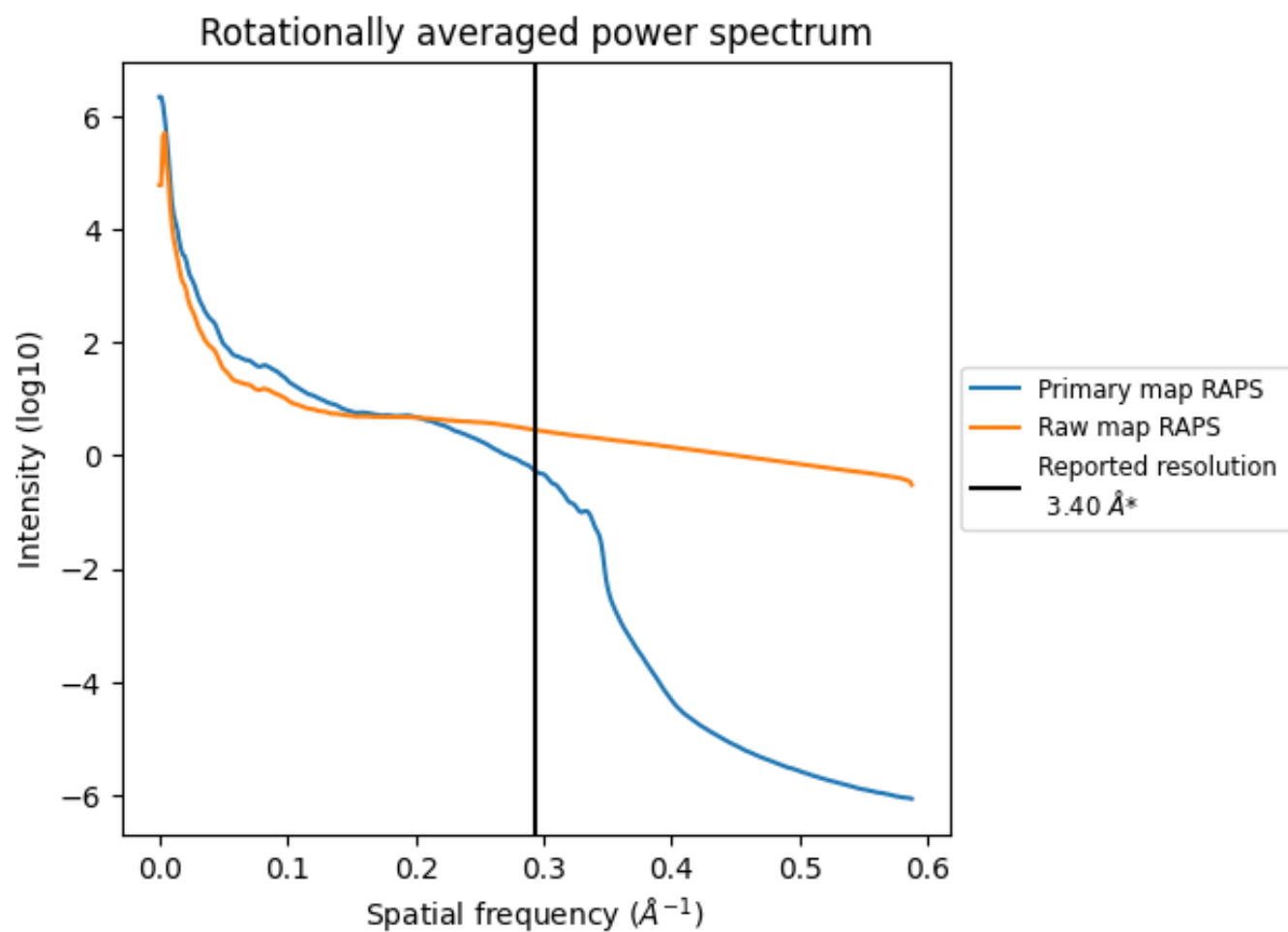
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 840 nm^3 ; this corresponds to an approximate mass of 759 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

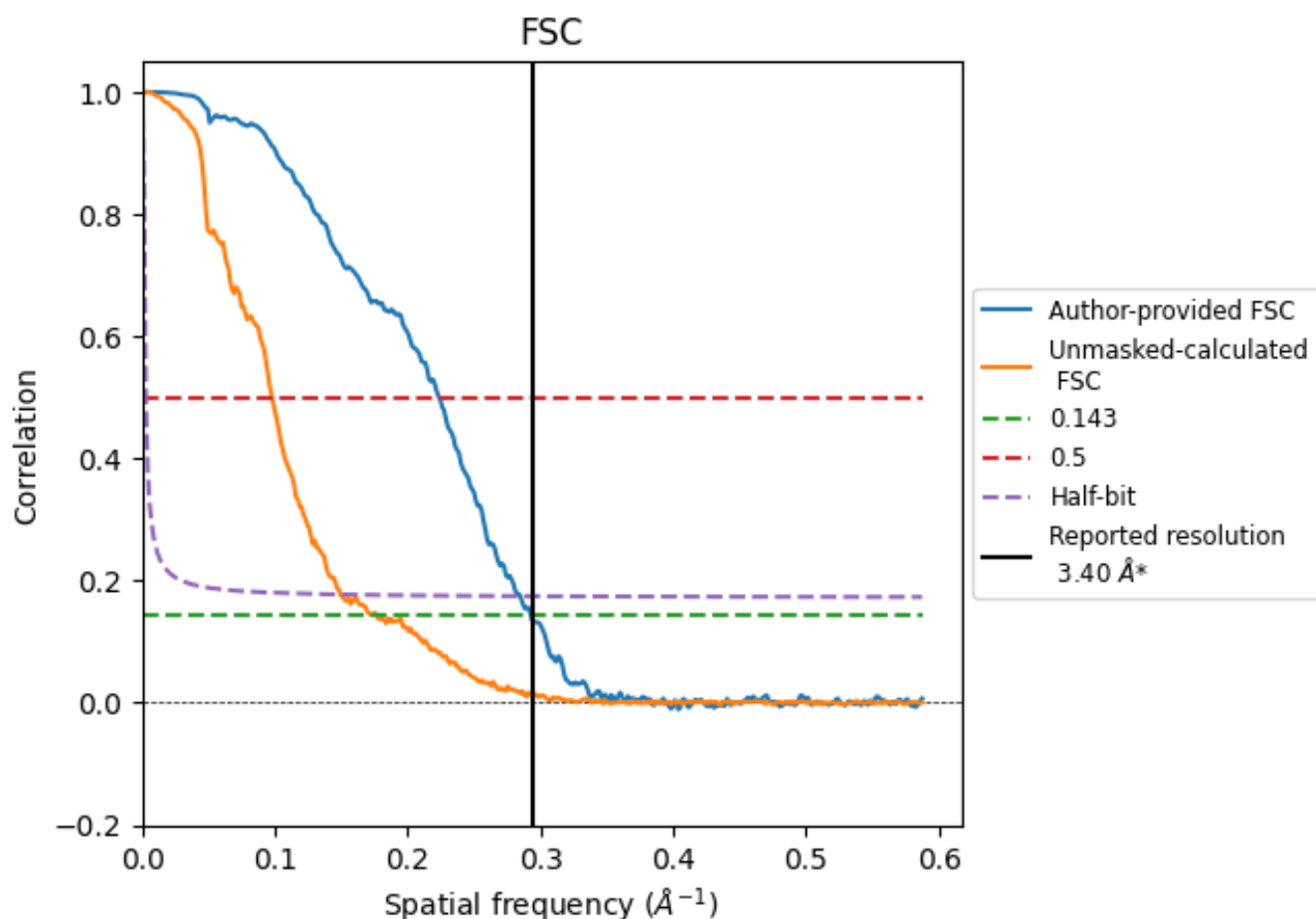


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

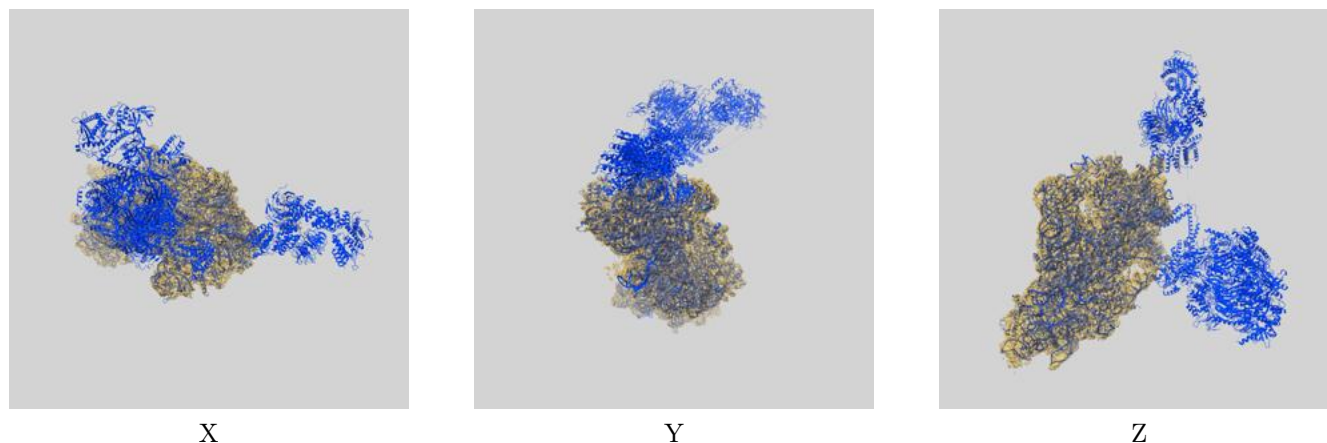
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.42	4.47	3.51
Unmasked-calculated*	5.67	10.22	6.69

*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 5.67 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

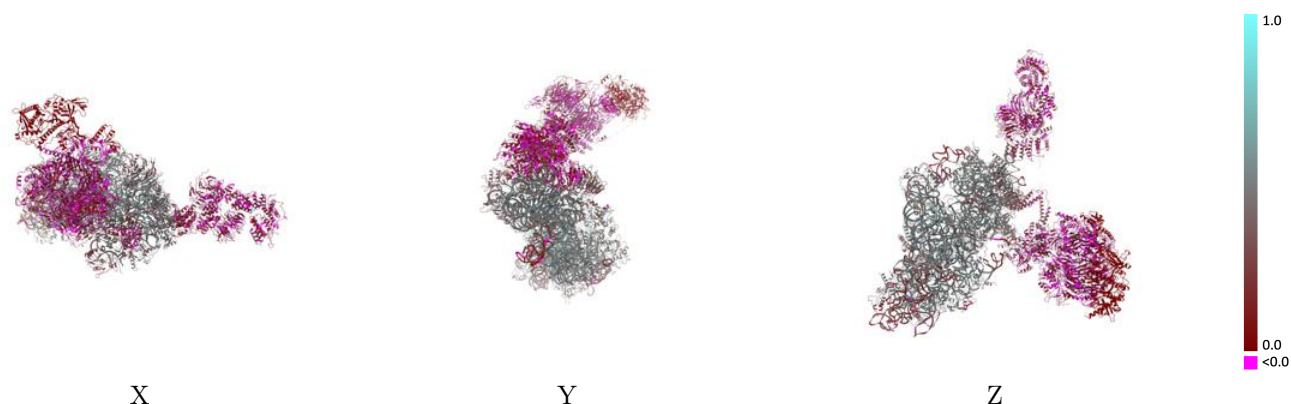
This section contains information regarding the fit between EMDB map EMD-51134 and PDB model 9G8O. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



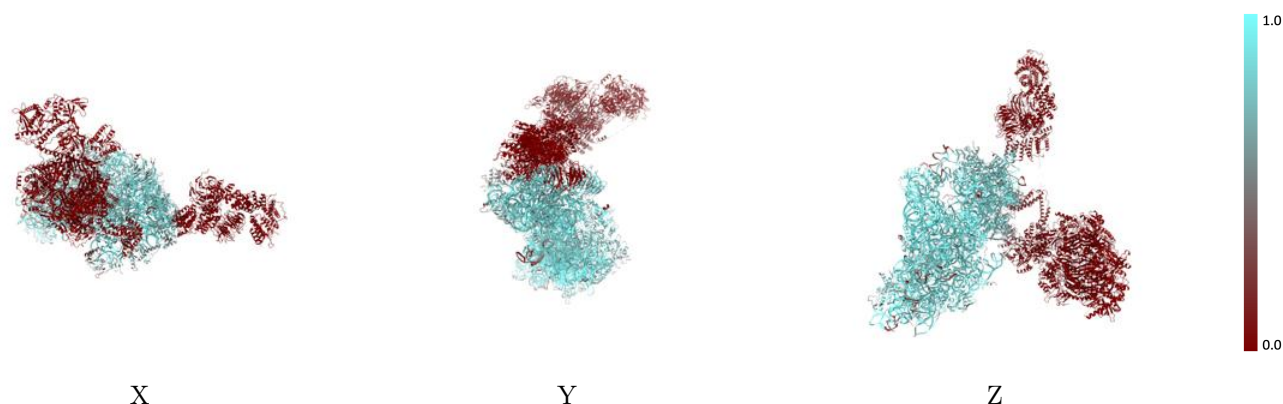
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



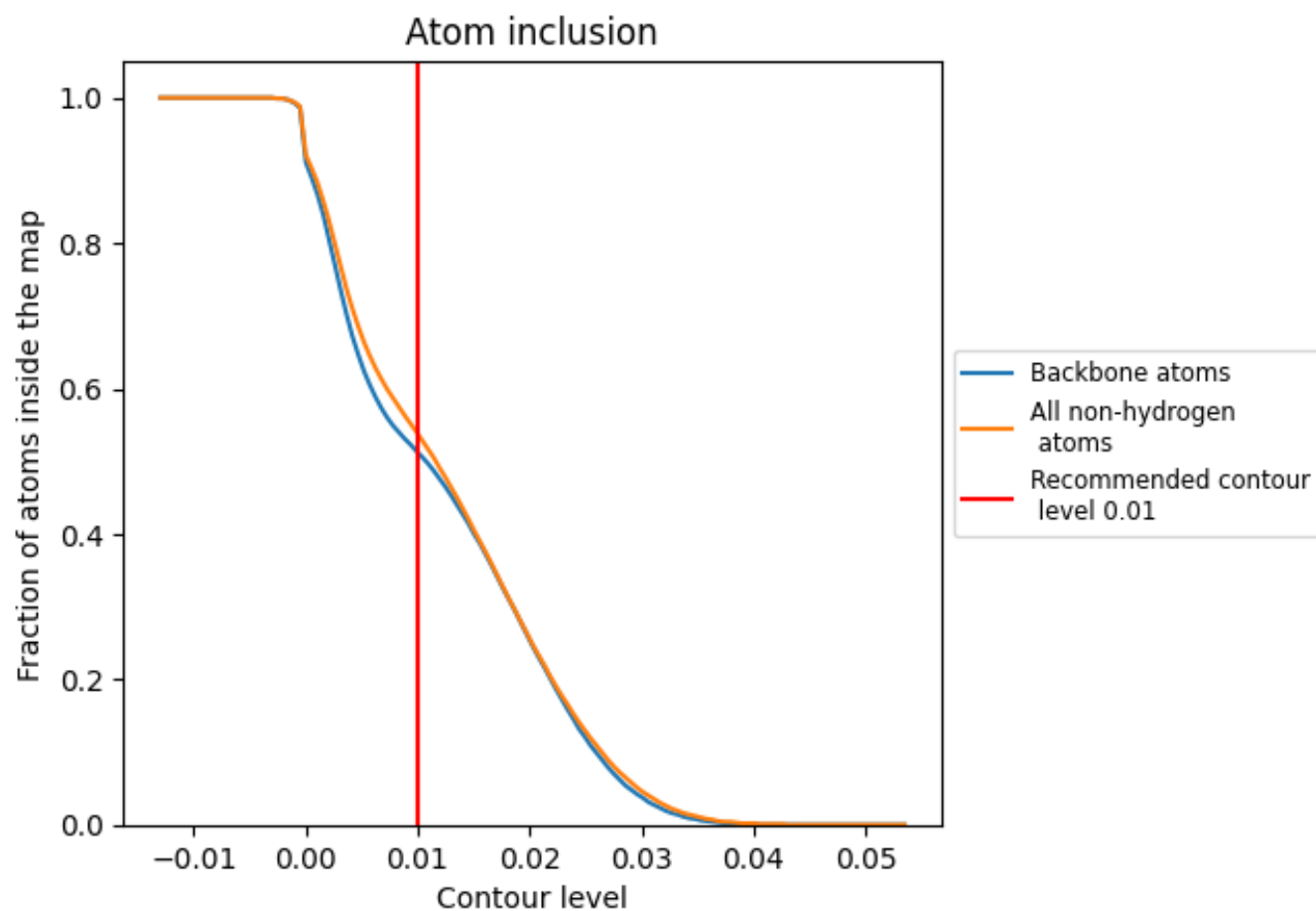
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 51% of all backbone atoms, 54% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.5380	 0.3070
A	 0.0070	 0.1160
B	 0.0180	 0.1110
C	 0.0010	 0.0890
D	 0.0080	 0.1020
E	 0.0000	 0.0830
F	 0.0000	 0.0810
G	 0.0000	 0.0790
H	 0.0000	 0.0750
I	 0.0000	 0.0670
J	 0.0000	 0.0770
K	 0.0000	 0.0750
L	 0.0000	 0.0950
Ln	 0.8130	 0.4340
M	 0.0000	 0.0030
N	 0.0000	 0.0570
O	 0.0000	 0.0840
S2	 0.9450	 0.4670
SA	 0.8690	 0.4550
SB	 0.8860	 0.4580
SC	 0.9220	 0.4970
SD	 0.8130	 0.4480
SE	 0.8440	 0.4780
SF	 0.8180	 0.4700
SG	 0.7160	 0.3400
SH	 0.6920	 0.3960
SI	 0.8340	 0.4340
SJ	 0.9020	 0.4780
SK	 0.6710	 0.4530
SL	 0.7950	 0.4740
SM	 0.4430	 0.2760
SN	 0.8380	 0.4840
SO	 0.8680	 0.4560
SP	 0.6950	 0.4450
SQ	 0.8250	 0.4960



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Chain	Atom inclusion	Q-score
SR	 0.8330	 0.4370
SS	 0.6580	 0.4200
ST	 0.7530	 0.4680
SU	 0.7250	 0.4440
SV	 0.8760	 0.4750
SW	 0.9190	 0.5020
SX	 0.9520	 0.5080
SY	 0.8310	 0.4380
SZ	 0.6390	 0.4010
Sa	 0.8830	 0.4700
Sb	 0.8450	 0.4400
Sc	 0.8660	 0.4890
Sd	 0.9160	 0.5360
Se	 0.7610	 0.3800
Sf	 0.4040	 0.2960
Sg	 0.7540	 0.3860
X	 0.3770	 0.1040