



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 04:46 PM UTC

PDB ID : 5SVA / pdb_00005sva
EMDB ID : EMD-8305
Title : Mediator-RNA Polymerase II Pre-Initiation Complex
Authors : Robinson, P.J.; Bushnell, D.A.; Kornberg, R.D.
Deposited on : 2016-08-05
Resolution : 15.30 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

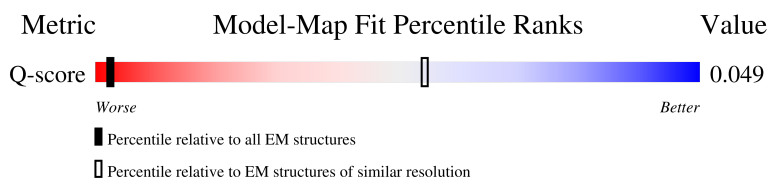
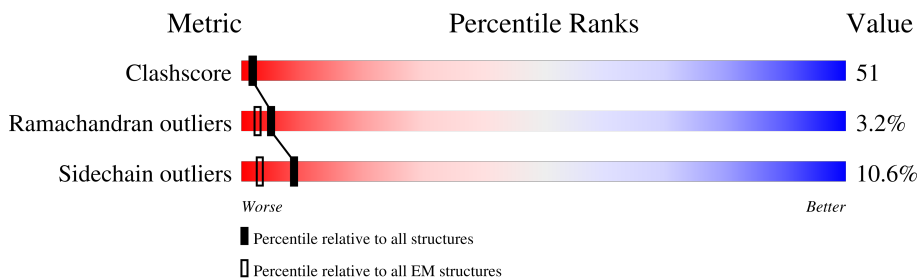
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 15.30 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.



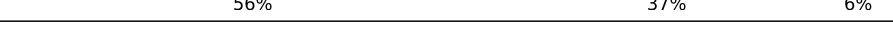
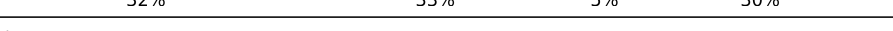
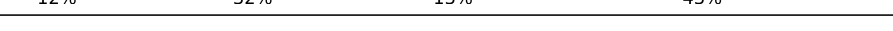
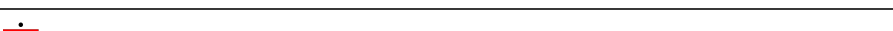
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	35 (14.90 - 15.60)

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	A	1733	
2	B	1224	
3	C	318	
4	D	221	

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Mol	Chain	Length	Quality of chain
5	E	215	
6	F	155	
7	G	171	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	70	
13	M	295	
14	N	223	
15	O	115	
16	P	687	
17	Q	307	
18	R	210	
19	S	121	
20	T	284	
21	U	222	
22	V	149	
23	W	140	
24	X	127	
25	Y	778	
26	Z	843	
27	a	513	
28	b	72	
29	c	345	

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Mol	Chain	Length	Quality of chain
30	d	286	
31	e	122	
32	f	735	
33	g	400	
34	h	482	
35	i	328	
36	j	240	
37	k	25	
38	l	108	
39	m	108	
40	n	244	

2 Entry composition

There are 42 unique types of molecules in this entry. The entry contains 66759 atoms, of which 626 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 DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1422	Total	C	N	O	S	0	0
			11174	7036	1954	2122	62		

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1156	Total	C	N	O	S	0	0
			9140	5781	1606	1697	56		

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	266	Total	C	N	O	S	0	0
			2095	1317	348	417	13		

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	178	Total	C	N	O	S	0	0
			1434	887	257	288	2		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	214	Total	C	N	O	S	0	0
			1752	1111	309	321	11		

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	84	Total	C	N	O	S	0	0
			679	434	115	127	3		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1340	861	222	249	8		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	133	Total	C	N	O	S	0	0
			1068	673	180	211	4		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	119	Total	C	N	O	S	0	0
			971	596	179	186	10		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	65	Total	C	N	O	S	0	0
			532	339	93	94	6		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	115	Total	C	N	O	S	0	1
			920	590	157	171	2		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	46	Total	C	N	O	S	0	0
			363	224	72	63	4		

- Molecule 13 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	156	Total	C	N	O	S	0	0
			777	464	156	156	1		

- Molecule 14 is a protein called Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	168	Total	C	N	O	0	0
			891	542	172	177		

- Molecule 15 is a protein called Mediator of RNA polymerase II transcription subunit 11.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	O	103	Total	C	N	O	0	0
			511	305	103	103		

- Molecule 16 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	487	Total	C	N	O	0	0
			2421	1447	487	487		

- Molecule 17 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	253	Total	C	N	O	S	0	0
			1979	1255	330	384	10		

- Molecule 18 is a protein called Mediator of RNA polymerase II transcription subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	209	Total	C	N	O	S	0	0
			1600	1011	269	315	5		

- Molecule 19 is a protein called Mediator of RNA polymerase II transcription subunit 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	109	Total	C	N	O	0	0
			544	326	109	109		

- Molecule 20 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	91	Total	C	N	O	S	0	0
			756	475	125	154	2		

- Molecule 21 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	156	Total	C	N	O	S	0	0
			1310	847	220	238	5		

- Molecule 22 is a protein called Mediator of RNA polymerase II transcription subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	85	Total	C	N	O	S	0	0
			720	451	133	135	1		

- Molecule 23 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	119	Total	C	N	O	S	0	0
			965	608	160	193	4		

- Molecule 24 is a protein called Mediator of RNA polymerase II transcription subunit 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	92	Total	C	N	O	S	0	0
			767	506	116	141	4		

- Molecule 25 is a protein called DNA repair helicase RAD3.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Y	562	Total	C	H	N	O	S	0	0
			5175	2901	626	777	838	33		

- Molecule 26 is a protein called DNA repair helicase RAD25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	469	Total	C	N	O	S	0	0
			3769	2370	660	716	23		

- Molecule 27 is a protein called RNA polymerase II transcription factor B subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	a	62	Total	C	N	O	0	0
			518	334	83	101		

- Molecule 28 is a protein called RNA polymerase II transcription factor B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	63	Total	C	N	O	S	0	0
			499	316	88	93	2		

- Molecule 29 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	189	Total	C	N	O	S	0	0
			1357	838	240	267	12		

- Molecule 30 is a protein called Transcription initiation factor IIA large subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	116	Total	C	N	O	S	0	0
			956	599	159	195	3		

- Molecule 31 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	101	Total	C	N	O	S	0	0
			792	500	132	156	4		

- Molecule 32 is a protein called Transcription initiation factor IIF subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	149	Total	C	N	O	S	0	0
			1243	788	222	229	4		

- Molecule 33 is a protein called Transcription initiation factor IIF subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	172	Total	C	N	O	S	0	0
			1443	922	248	267	6		

- Molecule 34 is a protein called Transcription initiation factor IIE subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	118	Total	C	N	O	S	0	0
			960	625	158	172	5		

- Molecule 35 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	120	Total	C	N	O	S	0	0
			987	636	161	187	3		

- Molecule 36 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	180	Total	C	N	O	S	0	0
			1416	921	242	247	6		

- Molecule 37 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	k	25	Total	C	N	O	0	0
			184	116	25	43		

- Molecule 38 is a DNA chain called 108bp HIS4 Promoter Non-template Strand (-92/+16).

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	62	Total	C	N	O	P	0	0
			1271	609	222	378	62		

- Molecule 39 is a DNA chain called 108bp HIS4 Promoter Template Strand (+16/-92).

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	62	Total	C	N	O	P	0	0
			1271	607	236	366	62		

- Molecule 40 is a protein called Transcription initiation factor TFIID subunit 14.

Mol	Chain	Residues	Atoms		AltConf	Trace
40	n	200	Total	C	0	200
			200	200		

- Molecule 41 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
41	A	2	Total	Zn	0
			2	2	
41	B	1	Total	Zn	0
			1	1	
41	C	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
41	I	2	Total 2	Zn 2	0
41	J	1	Total 1	Zn 1	0
41	L	1	Total 1	Zn 1	0

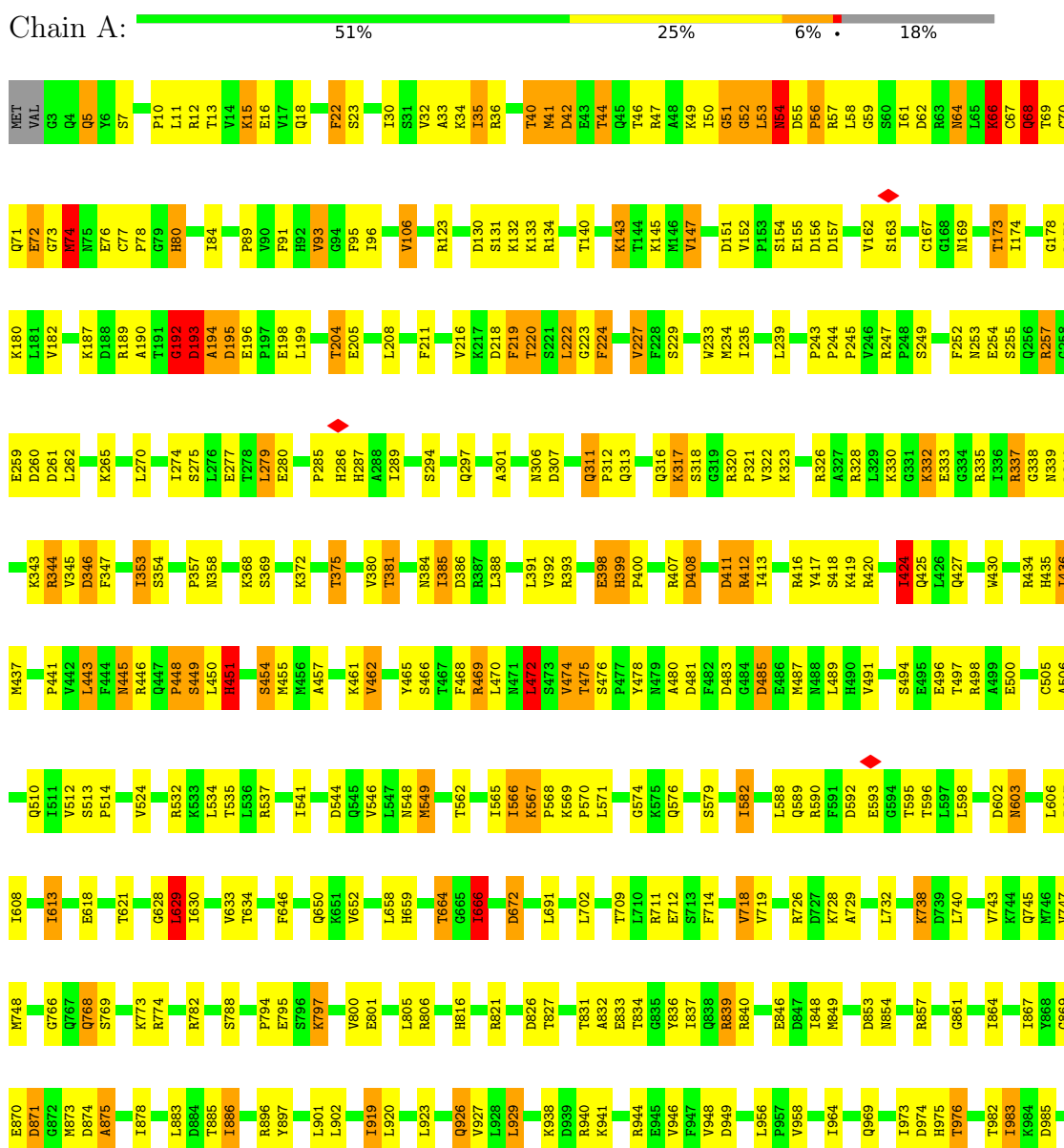
- Molecule 42 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
42	A	1	Total 1	Mg 1	0

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: DNA-directed RNA polymerase II subunit RPB1

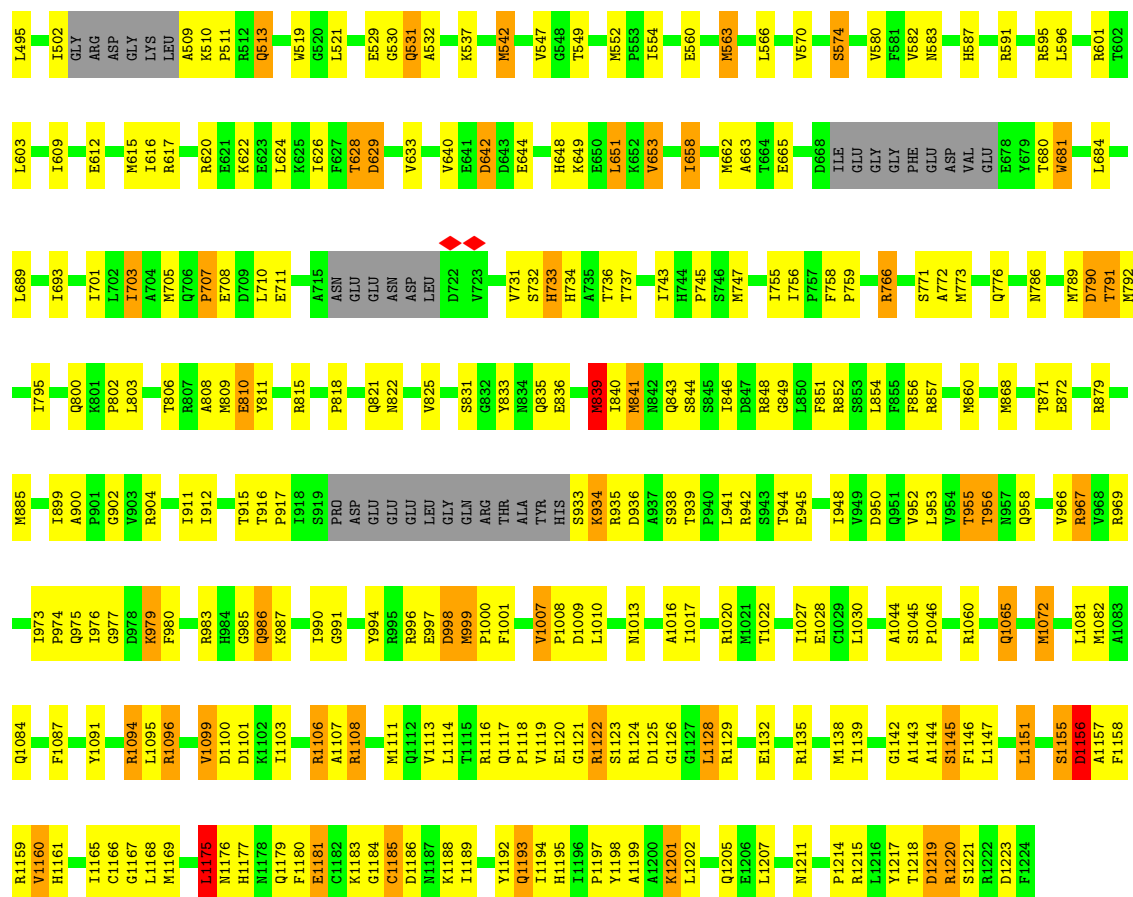


L993	K1092	L1197	M1312	T1405	GLU	PRO	PRO	ALA
Q994	K1093	K1205	E1315	V1406	SER	THR	THR	TTR
L998	M1094	K1205	E1315	E1407	GLY	SER	SER	SER
Y999	T1095	K1205	E1315	E1407	LEU	TYR	TYR	PRO
L1000	M1111	T1208	M1317	L1409	VAL	PRO	PRO	LYS
R1001	K1112	Q1218	D1323	A1414	ASN	THR	THR	GLN
N1004	T1113	D1223	F1324	S1415	ASP	SER	SER	ASP
N1009	P1114	D1223	T1326	L1418	LEU	PRO	PRO	GLU
V1015	S1115	V1226	R1326	L1418	ASP	TYR	TYR	GLN
T1016	L1116	V1226	I1327	V1424	VAL	SER	PRO	LYS
L1017	T1117	D1231	T1329	S1425	ASP	THR	THR	ASN
F1018	V1118	D1231	M1336	E1426	GLU	SER	THR	GLU
C1019	Y1119	L1236	M1336	N1427	LEU	PRO	PRO	ASN
G1020	E1121	I1237	M1336	N1427	PRO	PRO	PRO	GLU
L1021	E1121	I1238	I1341	T1429	PHE	TYR	TYR	ASN
L1022	H1124	V1242	I1341	T1430	SER	SER	PRO	SER
R1023	Q1130	V1243	G1344	G1431	PRO	PRO	PRO	ARG
S1024	L1133	ARG	R1345	G1432	VAL	THR	THR	
R1025	L1133	LYS	R1345	M1433	ASP	SER	SER	
R1029	I1134	PRO	L1348	T1436	SER	PRO	PRO	
R1030	R1135	SER	Y1349	T1437	GLY	TYR	TYR	
Y1035	I1138	ASP	V1352	T1438	ASN	PRO	PRO	
R1036	T1142	ALA	V1355	F1441	ASP	THR	THR	
L1046	T1148	THR	I1356	D1442	ALA	SER	SER	
S1047	I1149	GLU	V1363	M1443	MET	PRO	PRO	
V1057	S1150	E1255	V1363	I1445	ALA	THR	THR	
V1058	E1151	E1256	R1366	D1446	GLY	SER	SER	
E1062	Y1154	D1257	V1372	L1450	PHE	PRO	PRO	
M1063	T1161	M1259	D1373	V1451	THR	THR	THR	
L1067	Q1171	K1261	T1376	Y1453	ALA	PRO	PRO	
I1072	L1172	K1262	T1377	M1454	GLY	ASN	ASN	
G1073	H1173	K1262	T1382	P1455	TYR	TYR	TYR	
E1074	F1174	T1266	R1386	GLN	GLY	SER	SER	
T1077	S1175	E1269	G1388	LYS	ALA	PRO	PRO	
M1079	L1176	L1273	F1389	ILE	THR	THR	THR	
LEU	LEU	I1279	N1390	THR	PRO	PRO	PRO	
ASN	GLU	E1280	R1391	GLU	PHE	PRO	PRO	
THR	ALA	R1281	S1392	ASP	GLY	TYR	TYR	
PHE	GLN	V1291	M1393	GLY	GLN	PRO	PRO	
HIS	ASP	T1295	T1394	ASP	GLY	TYR	TYR	
ALA	PHE	G1296	L1397	GLY	GLY	PRO	PRO	
GLY	ASP	E1297	M1398	VAL	VAL	THR	THR	
VAL	Q1187	T1308	R1399	THR	THR	SER	SER	
SER	L1193	D1309	C1400	PRO	PRO	PRO	PRO	
	L1194		S1401	TYR	TYR	GLY	GLY	
	L1195		F1403	SER	THR	TYR	TYR	
	E1196		E1404	ASN	PHE	PRO	PRO	

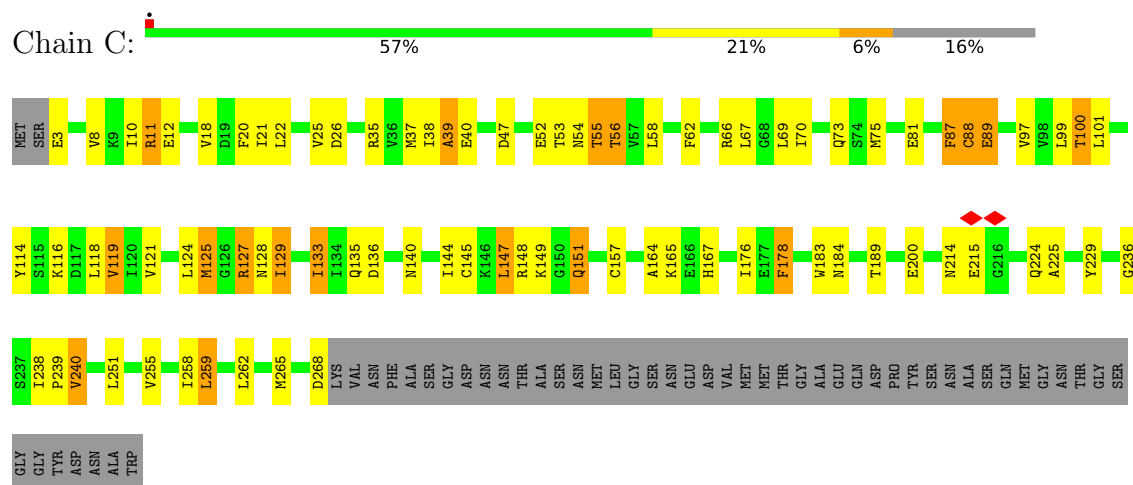
• Molecule 2: DNA-directed RNA polymerase II subunit RPB2

Chain B: 58% 29% 6% • 6%

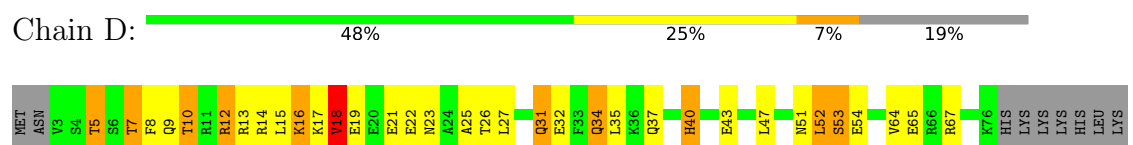
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SER	I95	M199	D295	Q394
ASP	I95	E296	E296	Q395
LEU	V102	I204	I297	K404
ALA	N103	I205	E299	R405
ASN	E104	G207	H300	L406
SER	H110	V211	D307	D407
GLU	A111	E216	L311	L408
LYS	L112	R217	F312	L416
TYR	N121	S218	M313	F417
THR	L122	A219	L314	K418
ASP	S125	I222	K315	T419
GLY	L128	F226	P316	T425
PHE	K134	A238	I324	F429
GLU	R135	E239	Q325	R430
D290	E138	I240	D326	T431
I25	D141	G247	I334	M432
I25	VAL	S248	R337	Q433
D29	PRO	L43	G338	E438
S35	GLY	Q46	T339	A439
R39	ARG	F54	D441	H440
E40	E146	T58	L341	A441
K41	L151	L39	G42	F442
G42	ILE	Q60	R249	M449
L43	ALA	D61	I251	A450
Q46	GLU	I62	V256	K451
F54	GLU	I63	K347	T454
T58	SER	C64	R349	L457
L39	ASP	E65	L258	Q350
Q60	GLU	D66	K257	Y351
D61	ASP	R261	R261	I355
I62	SER	E262	E262	L356
I63	GLU	R267	T268	Q357
C64	SER	I269	K164	F360
E65	GLU	T272	R169	H363
D66	ASP	L273	L170	I364
S67	GLU	P171	P171	K365
T68	GLU	L174	L276	Q366
L69	GLU	Q277	K277	F370
I70	GLU	N178	I280	R476
L71	GLU	E183	P281	V482
E72	GLU	Y190	I282	N383
Q73	GLU	K193	R287	R384
S81	GLU	E89	I291	L385
R86	GLU	I90		T487

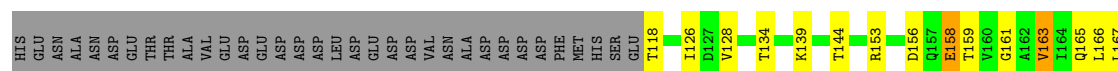


• Molecule 3: DNA-directed RNA polymerase II subunit RPB3

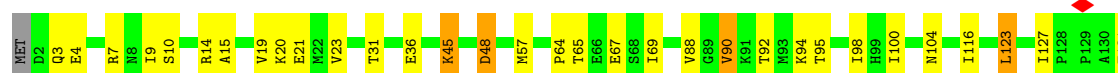


• Molecule 4: DNA-directed RNA polymerase II subunit RPB4

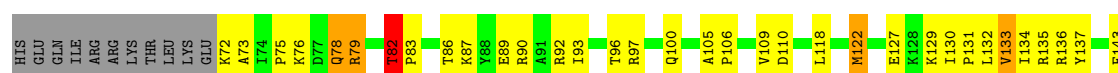
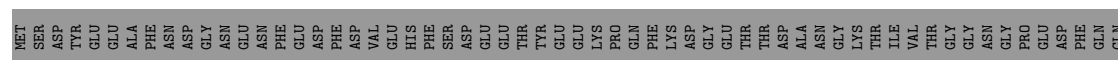
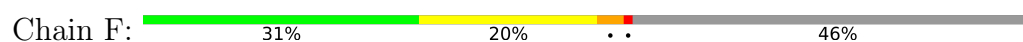




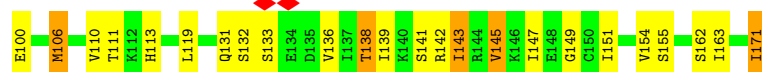
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2



- Molecule 7: DNA-directed RNA polymerase II subunit RPB7

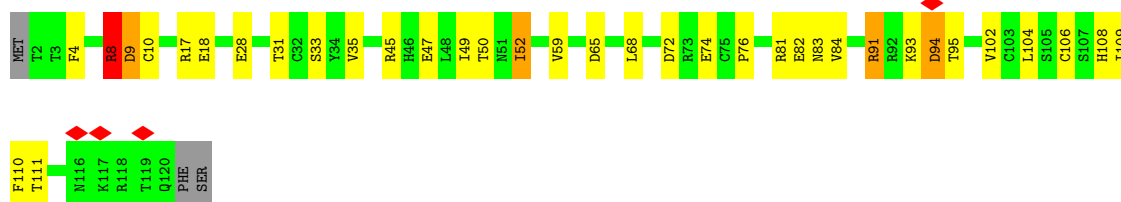


- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

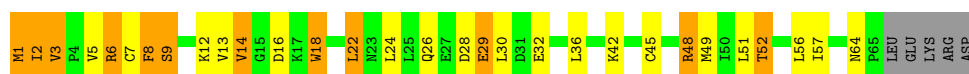




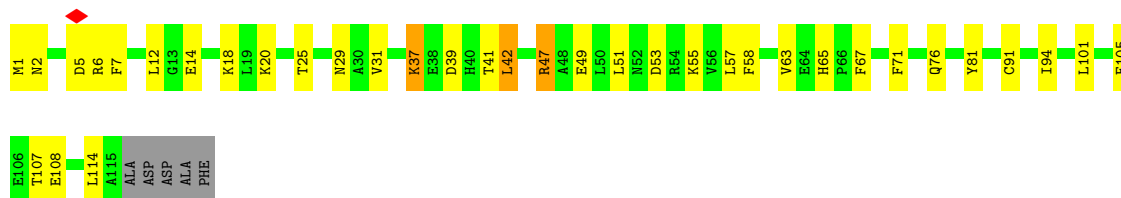
- Molecule 9: DNA-directed RNA polymerase II subunit RPB9



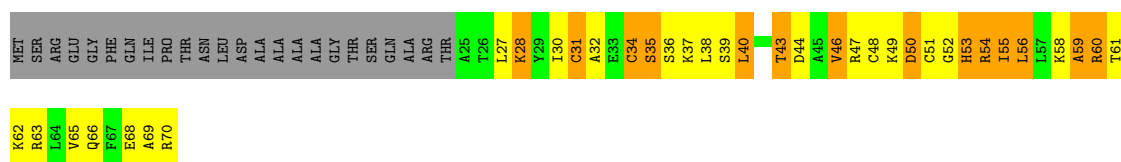
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



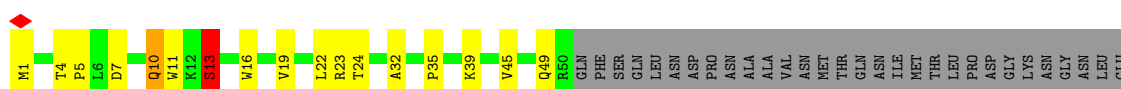
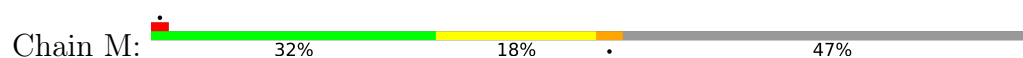
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11

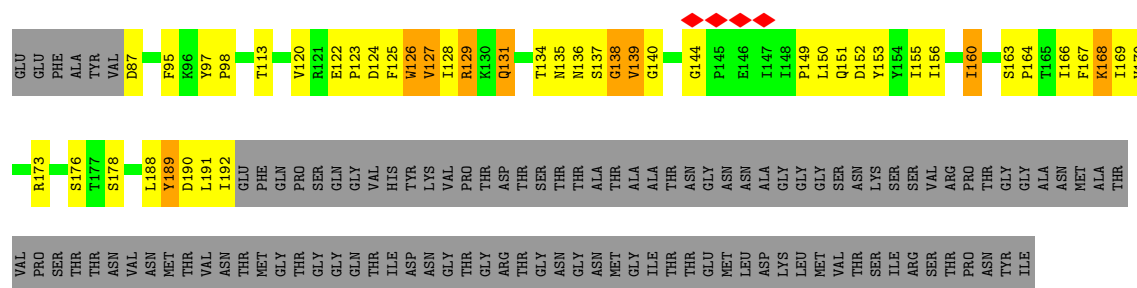


- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



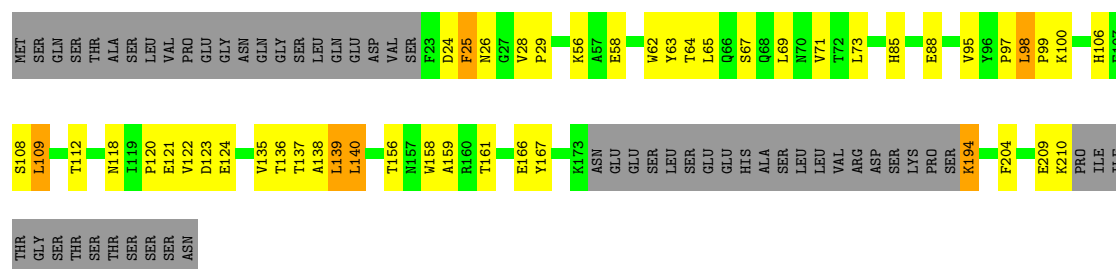
- Molecule 13: Mediator of RNA polymerase II transcription subunit 6





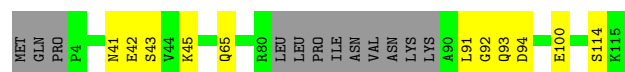
• Molecule 14: Mediator of RNA polymerase II transcription subunit 8

Chain N: 54% 19% 25%



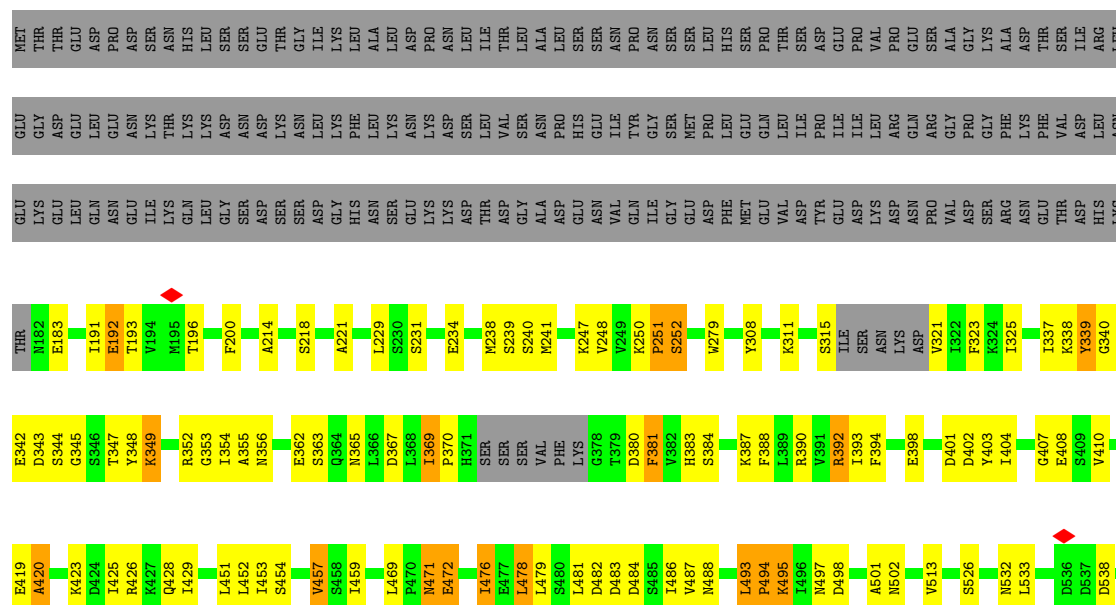
• Molecule 15: Mediator of RNA polymerase II transcription subunit 11

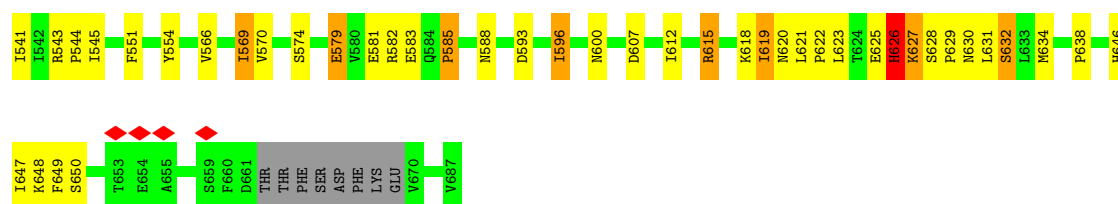
Chain O: 80% 10% 10%



• Molecule 16: Mediator of RNA polymerase II transcription subunit 17

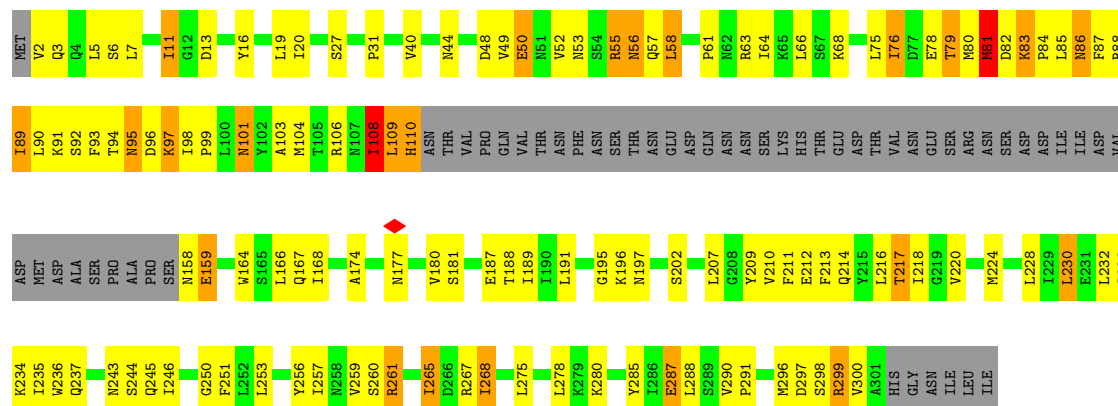
Chain P: 49% 18% 29%





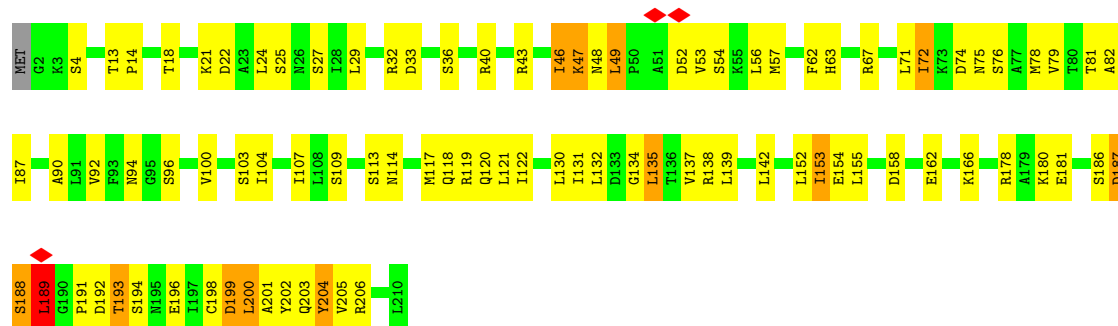
• Molecule 17: Mediator of RNA polymerase II transcription subunit 18

Chain Q: 42% 33% 7% 18%



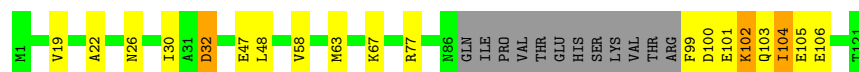
• Molecule 18: Mediator of RNA polymerase II transcription subunit 20

Chain R: 56% 37% 6%



• Molecule 19: Mediator of RNA polymerase II transcription subunit 22

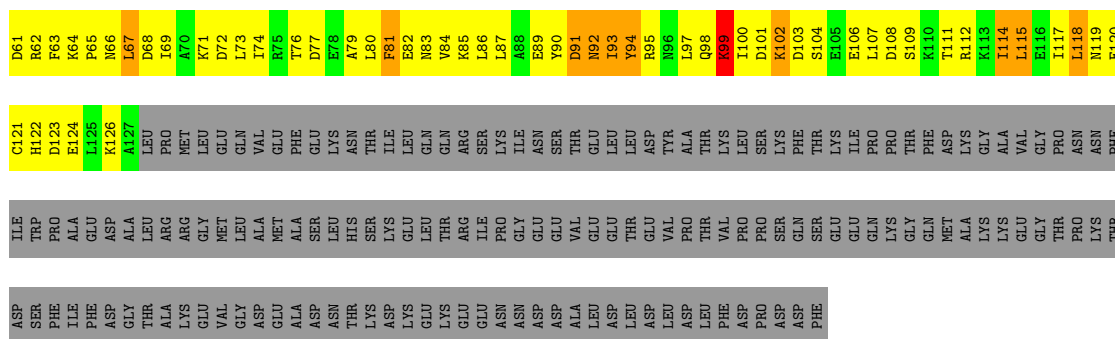
Chain S: 74% 13% 10%



• Molecule 20: Mediator of RNA polymerase II transcription subunit 4

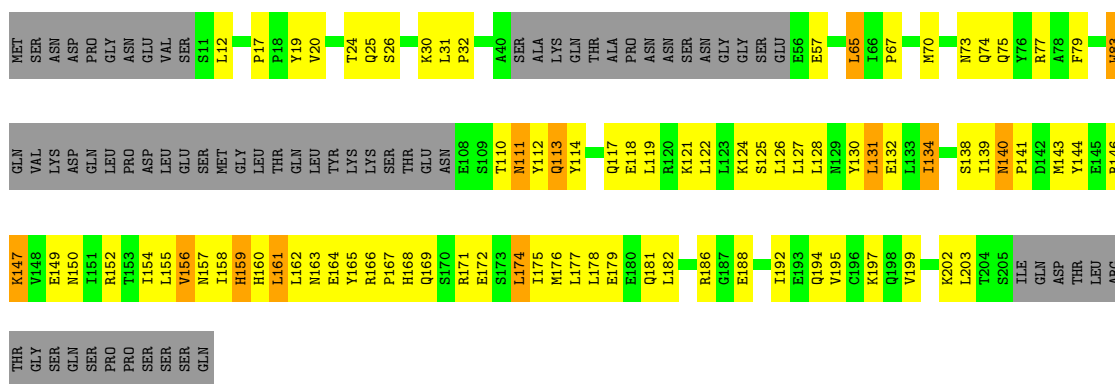
Chain T: 5% 23% 68%





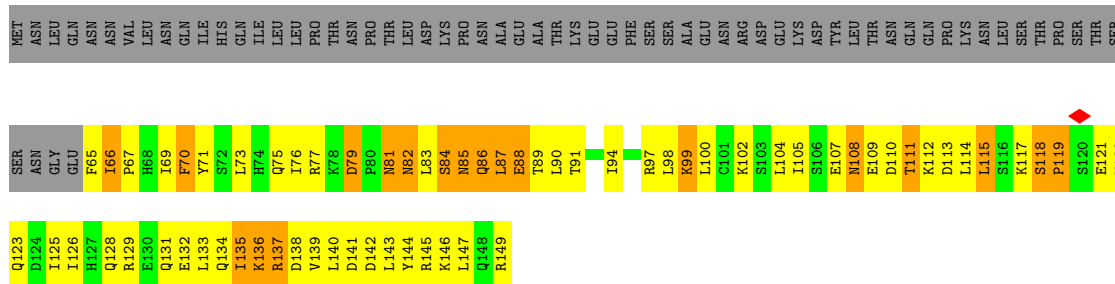
• Molecule 21: Mediator of RNA polymerase II transcription subunit 7

Chain U: 32% 33% 5% 30%



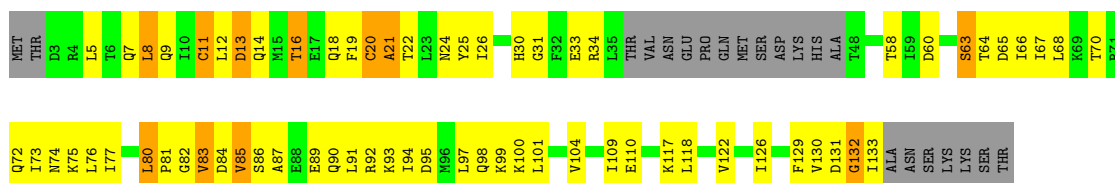
• Molecule 22: Mediator of RNA polymerase II transcription subunit 9

Chain V: 12% 32% 13% 43%

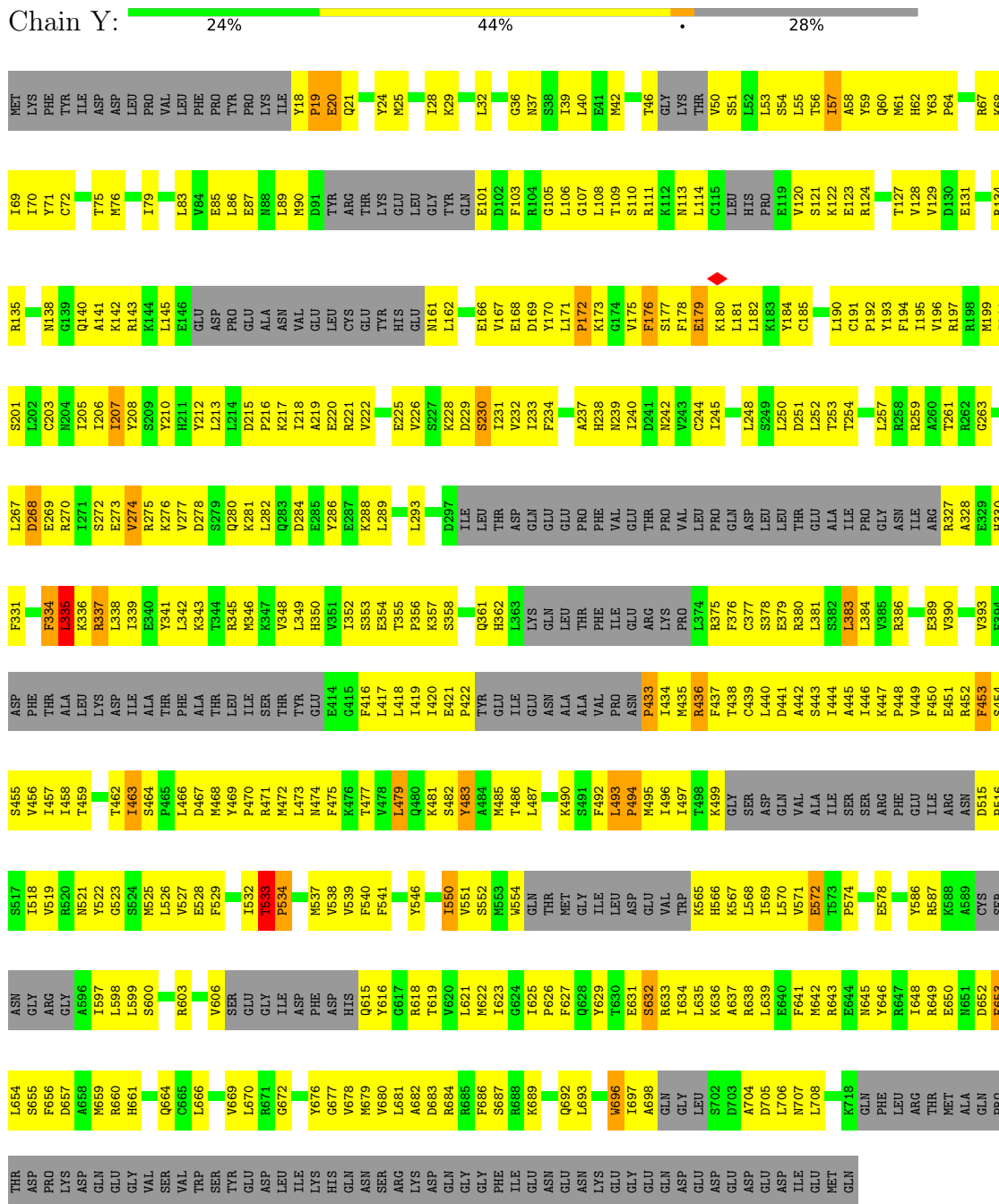


• Molecule 23: Mediator of RNA polymerase II transcription subunit 21

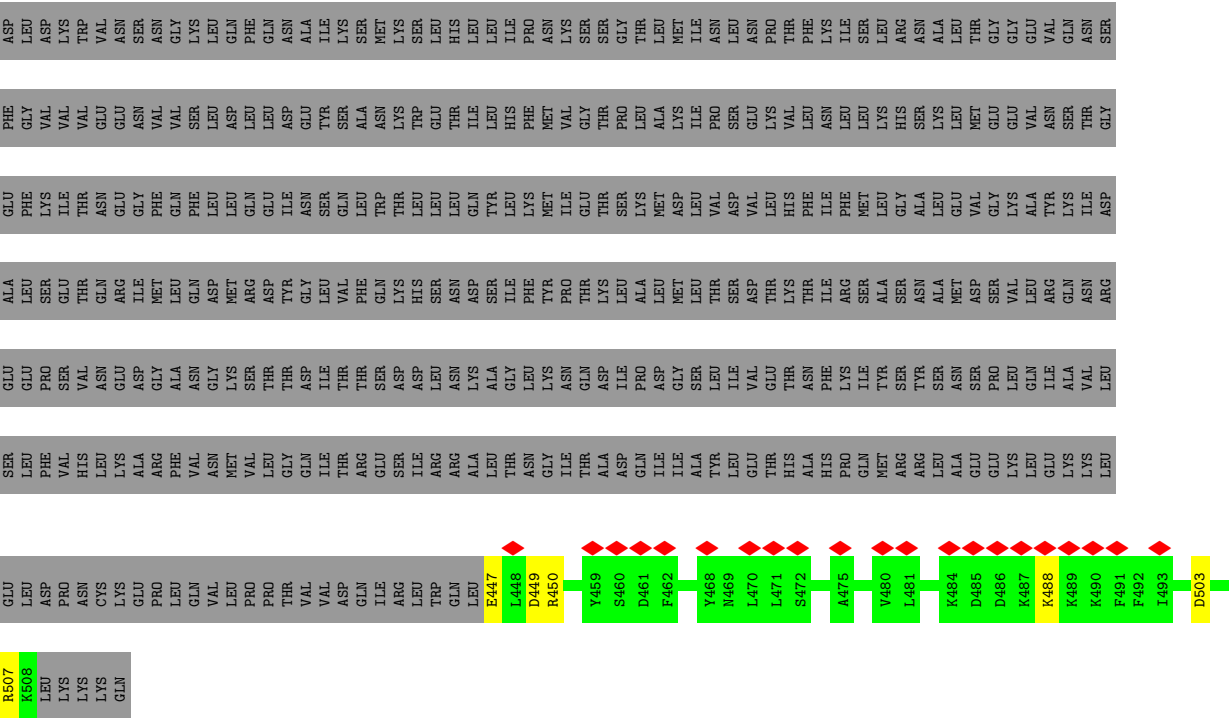
Chain W: 36% 41% 8% 15%



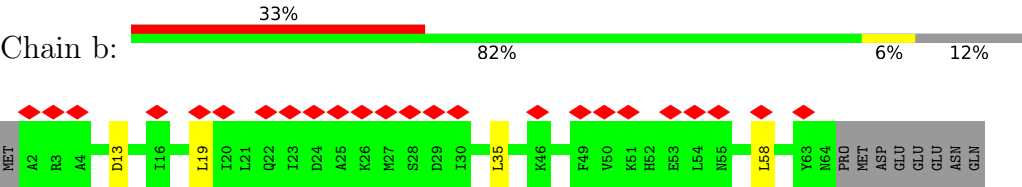
• Molecule 24: Mediator of RNA polymerase II transcription subunit 31



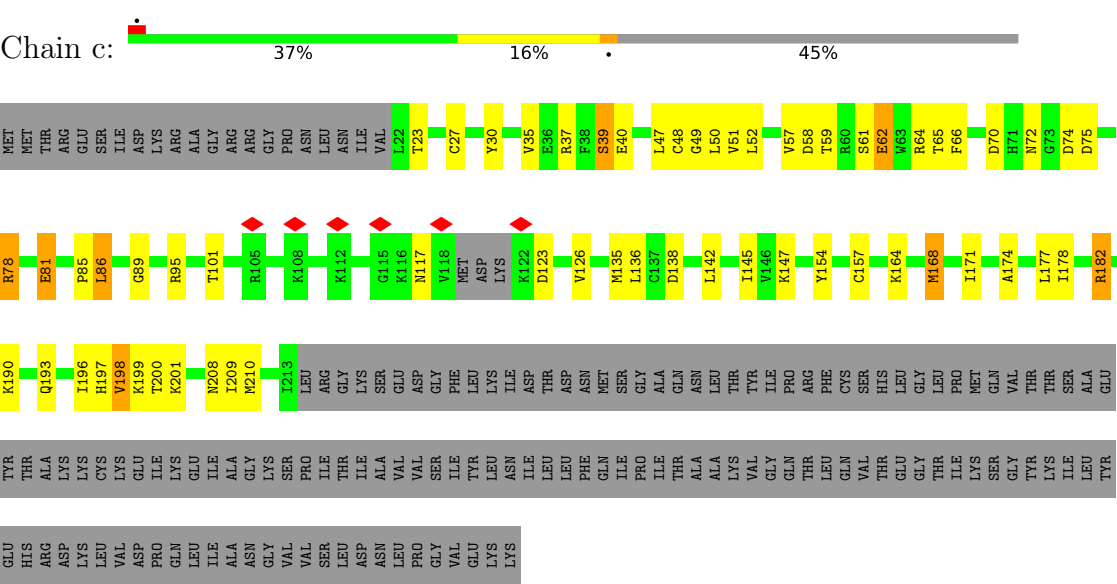




• Molecule 28: RNA polymerase II transcription factor B subunit 5

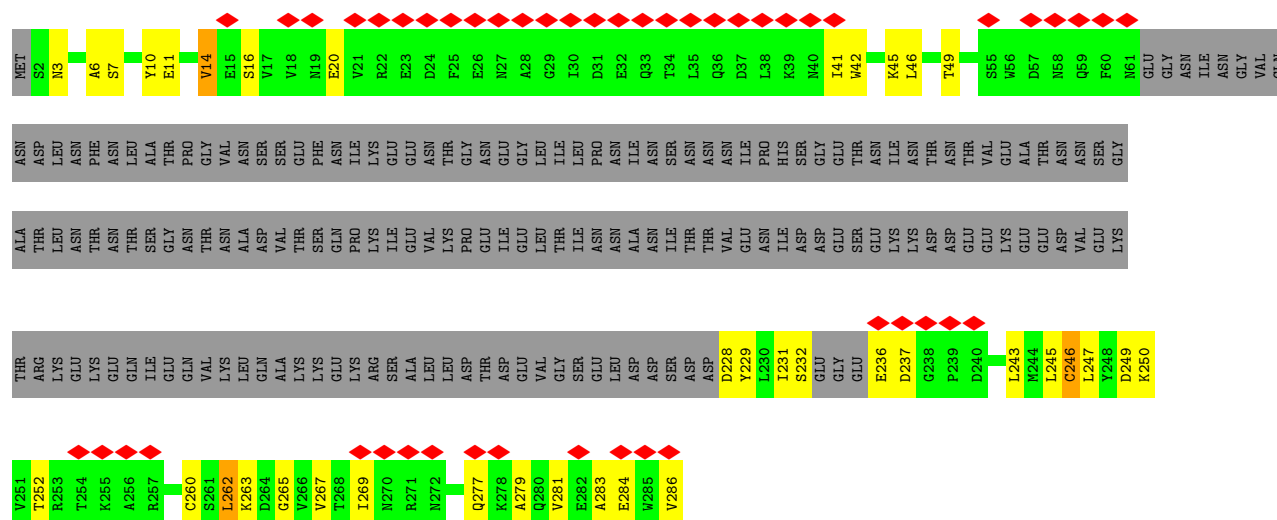


• Molecule 29: Transcription initiation factor IIB

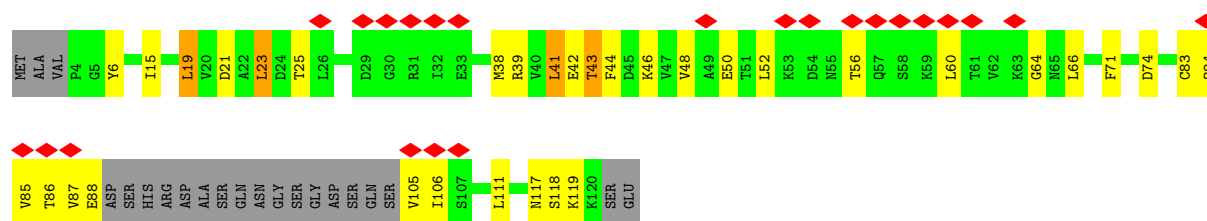


• Molecule 30: Transcription initiation factor IIA large subunit

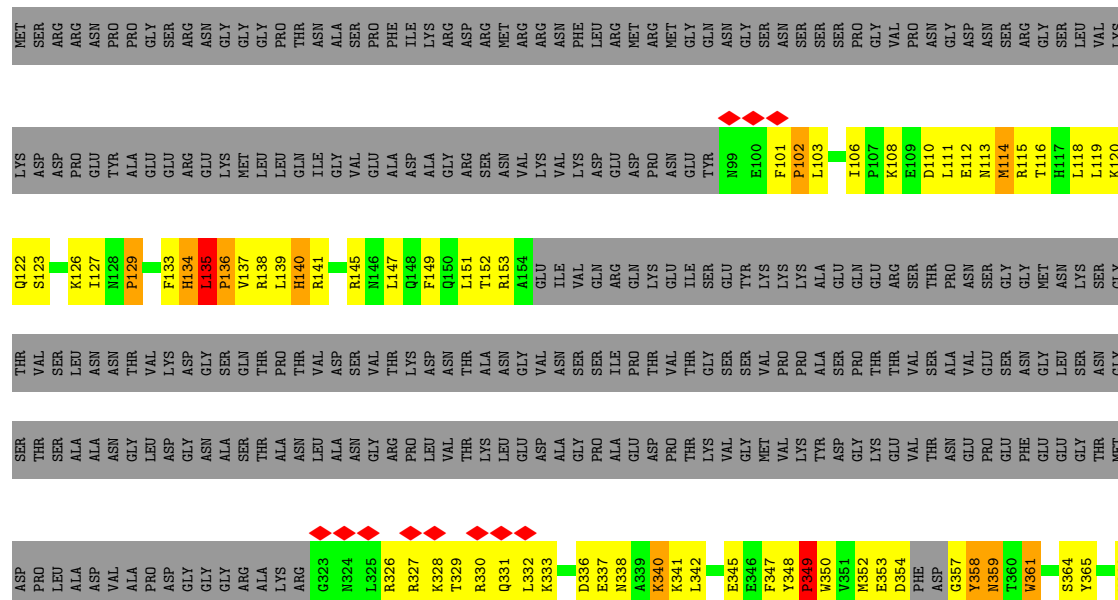


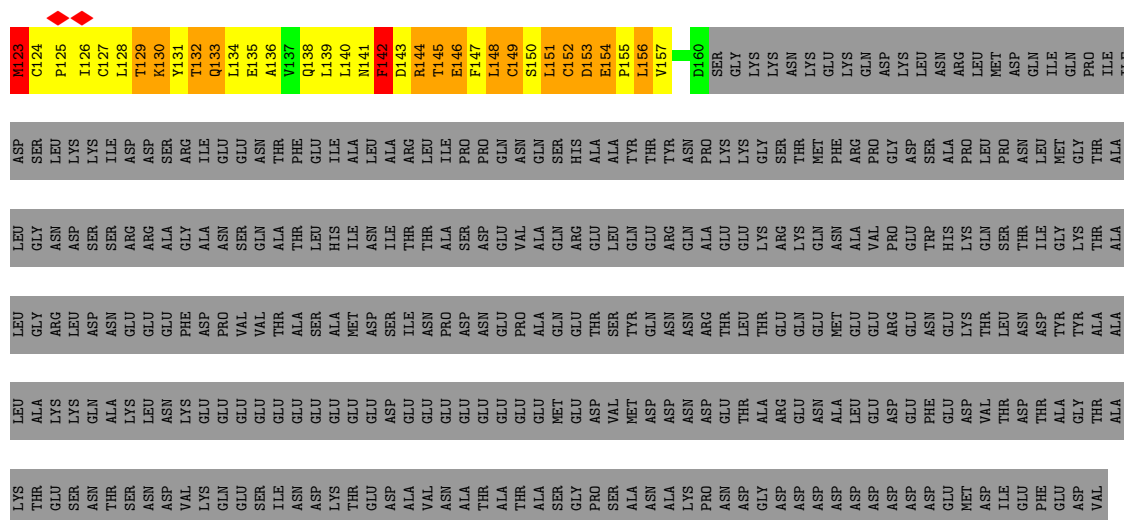


• Molecule 31: Transcription initiation factor IIA subunit 2

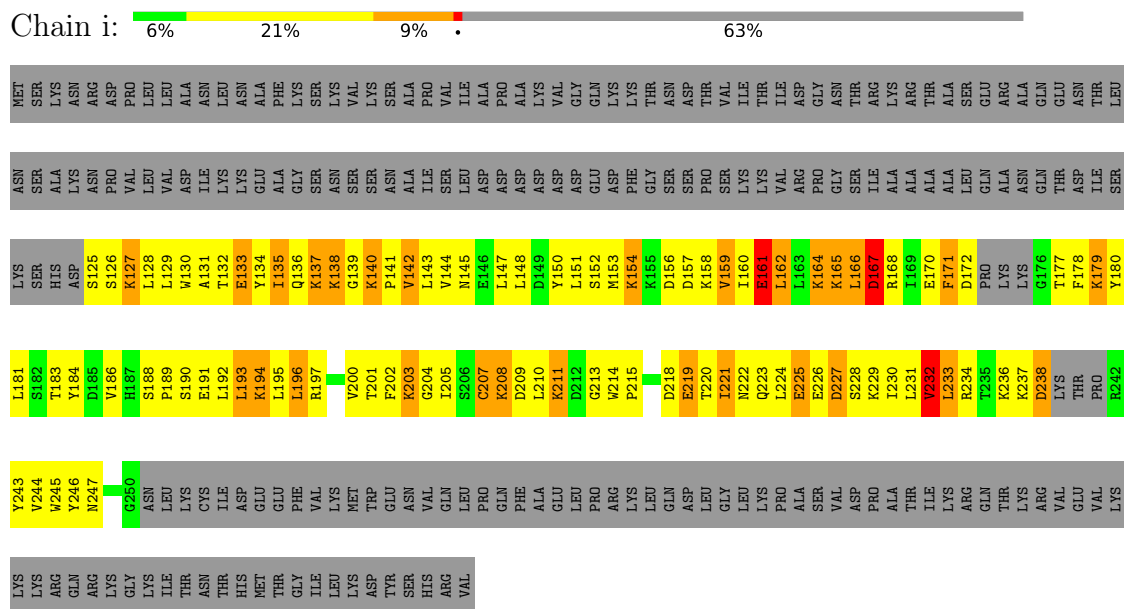


• Molecule 32: Transcription initiation factor IIF subunit alpha





• Molecule 35: Transcription initiation factor IIE subunit beta



• Molecule 36: TATA-box-binding protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	170600	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI 20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	0.153	Depositor
Minimum map value	-0.044	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	503.8, 503.8, 503.8	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.29, 2.29, 2.29	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A	0.85	7/11374 (0.1%)	1.45	101/15384 (0.7%)
2	B	0.80	6/9317 (0.1%)	1.32	69/12567 (0.5%)
3	C	0.84	0/2133	1.42	15/2891 (0.5%)
4	D	0.87	2/1444 (0.1%)	1.61	20/1935 (1.0%)
5	E	0.82	0/1788	1.42	13/2406 (0.5%)
6	F	0.97	1/691 (0.1%)	1.39	5/933 (0.5%)
7	G	0.86	1/1368 (0.1%)	1.39	10/1844 (0.5%)
8	H	0.86	0/1086	1.43	15/1470 (1.0%)
9	I	0.83	0/989	1.36	7/1331 (0.5%)
10	J	0.91	0/541	1.60	8/727 (1.1%)
11	K	0.77	0/938	1.35	1/1267 (0.1%)
12	L	0.68	0/365	1.07	2/485 (0.4%)
13	M	1.05	2/775 (0.3%)	1.71	18/1077 (1.7%)
14	N	0.83	0/893	1.48	5/1237 (0.4%)
15	O	0.85	0/509	1.44	5/707 (0.7%)
16	P	1.02	3/2417 (0.1%)	1.57	40/3369 (1.2%)
17	Q	0.71	0/2014	1.06	6/2728 (0.2%)
18	R	0.68	0/1626	1.00	3/2205 (0.1%)
19	S	0.91	0/542	1.41	0/755
20	T	0.86	0/763	1.52	11/1025 (1.1%)
21	U	0.58	0/1339	0.97	9/1808 (0.5%)
22	V	0.95	1/732 (0.1%)	1.51	13/984 (1.3%)
23	W	0.61	0/973	1.06	6/1308 (0.5%)
24	X	0.47	0/789	0.90	2/1077 (0.2%)
25	Y	0.81	3/4616 (0.1%)	1.07	26/6196 (0.4%)
26	Z	1.09	2/3837 (0.1%)	1.44	46/5177 (0.9%)
27	a	0.73	0/527	0.78	0/704
28	b	0.70	0/504	0.79	0/679
29	c	0.43	0/1373	0.80	2/1863 (0.1%)
30	d	0.48	0/970	0.88	1/1310 (0.1%)
31	e	0.51	0/800	0.86	1/1080 (0.1%)
32	f	0.49	2/1267 (0.2%)	1.01	9/1700 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.98	3/1469 (0.2%)	1.02	9/1972 (0.5%)
34	h	1.34	0/978	1.57	9/1321 (0.7%)
35	i	0.45	0/1003	0.99	5/1345 (0.4%)
36	j	0.48	0/1443	0.89	1/1942 (0.1%)
37	k	0.98	0/194	1.06	0/270
38	l	0.24	0/1423	0.62	3/2195 (0.1%)
39	m	0.24	0/1427	0.66	4/2199 (0.2%)
All	All	0.81	33/67237 (0.0%)	1.28	500/91473 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
13	M	0	2
16	P	0	3
17	Q	0	1
25	Y	0	1
26	Z	0	1
All	All	0	9

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	P	342	GLU	CA-C	10.55	1.61	1.52
1	A	1394	THR	C-N	-9.83	1.21	1.33
4	D	25	ALA	CA-C	8.40	1.62	1.53
25	Y	20	GLU	CA-C	8.23	1.63	1.52
33	g	88	HIS	CD2-NE2	8.19	1.46	1.37

The worst 5 of 500 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	369	ILE	CA-C-N	18.34	142.76	119.84
16	P	369	ILE	C-N-CA	18.34	142.76	119.84
14	N	98	LEU	CA-C-N	15.70	139.46	119.84
14	N	98	LEU	C-N-CA	15.70	139.46	119.84
26	Z	505	ILE	CB-CA-C	-15.55	91.62	110.91

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	43	LEU	Mainchain
13	M	10	GLN	Peptide
13	M	138	GLY	Peptide
16	P	471	ASN	Peptide
16	P	532	ASN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11174	0	11227	558	0
2	B	9140	0	9111	389	0
3	C	2095	0	2051	56	0
4	D	1434	0	1460	88	0
5	E	1752	0	1776	27	0
6	F	679	0	698	109	0
7	G	1340	0	1355	227	0
8	H	1068	0	1040	25	0
9	I	971	0	927	24	0
10	J	532	0	542	17	0
11	K	920	0	929	21	0
12	L	363	0	386	56	0
13	M	777	0	329	39	0
14	N	891	0	455	26	0
15	O	511	0	215	4	0
16	P	2421	0	1017	117	0
17	Q	1979	0	1977	250	0
18	R	1600	0	1614	105	0
19	S	544	0	241	12	0
20	T	756	0	761	272	0
21	U	1310	0	1339	153	0
22	V	720	0	725	288	0
23	W	965	0	987	140	0
24	X	767	0	752	47	0
25	Y	4549	626	4642	1311	0
26	Z	3769	0	3697	920	0
27	a	518	0	514	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	b	499	0	525	3	0
29	c	1357	0	1266	98	0
30	d	956	0	916	33	0
31	e	792	0	806	37	0
32	f	1243	0	1239	447	0
33	g	1443	0	1461	443	0
34	h	960	0	973	415	0
35	i	987	0	999	516	0
36	j	1416	0	1491	158	0
37	k	184	0	163	114	0
38	l	1271	0	705	183	0
39	m	1271	0	699	127	0
40	n	200	0	0	16	0
41	A	2	0	0	0	0
41	B	1	0	0	0	0
41	C	1	0	0	0	0
41	I	2	0	0	0	0
41	J	1	0	0	0	0
41	L	1	0	0	0	0
42	A	1	0	0	0	0
All	All	66133	626	62010	6543	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 51.

The worst 5 of 6543 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)
25:Y:254:THR:HG23	25:Y:286:TYR:CE1	1.20	1.71
36:j:190:PHE:CE1	38:l:18:DA:C5	1.74	1.67
25:Y:352:ILE:HB	25:Y:380:ARG:CZ	1.23	1.66
26:Z:757:ARG:HH12	26:Z:760:LEU:CG	1.04	1.66
32:f:139:LEU:HD22	32:f:350:TRP:CH2	1.18	1.65

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	A	1414/1733 (82%)	1254 (89%)	112 (8%)	48 (3%)	3	21
2	B	1142/1224 (93%)	1022 (90%)	84 (7%)	36 (3%)	3	21
3	C	264/318 (83%)	242 (92%)	20 (8%)	2 (1%)	16	54
4	D	174/221 (79%)	149 (86%)	17 (10%)	8 (5%)	2	17
5	E	212/215 (99%)	195 (92%)	13 (6%)	4 (2%)	6	32
6	F	82/155 (53%)	75 (92%)	7 (8%)	0	100	100
7	G	169/171 (99%)	157 (93%)	9 (5%)	3 (2%)	6	34
8	H	129/146 (88%)	106 (82%)	14 (11%)	9 (7%)	1	11
9	I	117/122 (96%)	98 (84%)	16 (14%)	3 (3%)	4	25
10	J	63/70 (90%)	51 (81%)	9 (14%)	3 (5%)	2	16
11	K	113/120 (94%)	109 (96%)	4 (4%)	0	100	100
12	L	44/70 (63%)	19 (43%)	14 (32%)	11 (25%)	0	1
13	M	152/295 (52%)	115 (76%)	20 (13%)	17 (11%)	0	5
14	N	164/223 (74%)	133 (81%)	16 (10%)	15 (9%)	0	8
15	O	99/115 (86%)	92 (93%)	4 (4%)	3 (3%)	3	23
16	P	479/687 (70%)	385 (80%)	61 (13%)	33 (7%)	1	11
17	Q	249/307 (81%)	217 (87%)	25 (10%)	7 (3%)	4	24
18	R	207/210 (99%)	190 (92%)	12 (6%)	5 (2%)	4	27
19	S	105/121 (87%)	91 (87%)	7 (7%)	7 (7%)	1	12
20	T	89/284 (31%)	69 (78%)	20 (22%)	0	100	100
21	U	150/222 (68%)	127 (85%)	22 (15%)	1 (1%)	18	56
22	V	83/149 (56%)	73 (88%)	5 (6%)	5 (6%)	1	13
23	W	115/140 (82%)	95 (83%)	18 (16%)	2 (2%)	7	36
24	X	90/127 (71%)	86 (96%)	4 (4%)	0	100	100
25	Y	534/778 (69%)	503 (94%)	23 (4%)	8 (2%)	8	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Z	461/843 (55%)	430 (93%)	26 (6%)	5 (1%)	11	46
27	a	60/513 (12%)	60 (100%)	0	0	100	100
28	b	61/72 (85%)	58 (95%)	3 (5%)	0	100	100
29	c	185/345 (54%)	164 (89%)	19 (10%)	2 (1%)	11	46
30	d	110/286 (38%)	103 (94%)	7 (6%)	0	100	100
31	e	97/122 (80%)	93 (96%)	4 (4%)	0	100	100
32	f	143/735 (20%)	130 (91%)	9 (6%)	4 (3%)	4	24
33	g	164/400 (41%)	148 (90%)	12 (7%)	4 (2%)	4	27
34	h	112/482 (23%)	100 (89%)	10 (9%)	2 (2%)	6	34
35	i	114/328 (35%)	102 (90%)	9 (8%)	3 (3%)	4	25
36	j	178/240 (74%)	170 (96%)	5 (3%)	3 (2%)	7	36
37	k	23/25 (92%)	9 (39%)	6 (26%)	8 (35%)	0	0
All	All	8147/12614 (65%)	7220 (89%)	666 (8%)	261 (3%)	5	21

5 of 261 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	MET
1	A	189	ARG
1	A	195	ASP
1	A	286	HIS
1	A	317	LYS

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	A	1240/1520 (82%)	1052 (85%)	188 (15%)	3	12
2	B	985/1061 (93%)	854 (87%)	131 (13%)	4	14
3	C	234/274 (85%)	204 (87%)	30 (13%)	4	15
4	D	160/200 (80%)	123 (77%)	37 (23%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	196/197 (100%)	173 (88%)	23 (12%)	5	18
6	F	74/137 (54%)	65 (88%)	9 (12%)	5	17
7	G	152/152 (100%)	136 (90%)	16 (10%)	6	21
8	H	117/128 (91%)	101 (86%)	16 (14%)	3	14
9	I	113/116 (97%)	105 (93%)	8 (7%)	13	35
10	J	60/65 (92%)	48 (80%)	12 (20%)	1	7
11	K	99/102 (97%)	86 (87%)	13 (13%)	4	15
12	L	40/57 (70%)	38 (95%)	2 (5%)	22	43
13	M	1/259 (0%)	1 (100%)	0	100	100
14	N	16/207 (8%)	14 (88%)	2 (12%)	4	16
17	Q	226/280 (81%)	202 (89%)	24 (11%)	6	21
18	R	177/178 (99%)	163 (92%)	14 (8%)	11	32
20	T	87/258 (34%)	81 (93%)	6 (7%)	14	36
21	U	149/208 (72%)	141 (95%)	8 (5%)	20	41
22	V	84/144 (58%)	78 (93%)	6 (7%)	13	35
23	W	113/132 (86%)	108 (96%)	5 (4%)	25	47
24	X	87/117 (74%)	82 (94%)	5 (6%)	18	40
25	Y	512/707 (72%)	503 (98%)	9 (2%)	51	68
26	Z	412/737 (56%)	376 (91%)	36 (9%)	9	29
27	a	57/468 (12%)	57 (100%)	0	100	100
28	b	57/66 (86%)	57 (100%)	0	100	100
29	c	136/299 (46%)	118 (87%)	18 (13%)	4	15
30	d	107/260 (41%)	104 (97%)	3 (3%)	38	60
31	e	91/108 (84%)	86 (94%)	5 (6%)	19	41
32	f	136/641 (21%)	135 (99%)	1 (1%)	76	81
33	g	162/363 (45%)	159 (98%)	3 (2%)	50	67
34	h	108/429 (25%)	90 (83%)	18 (17%)	2	10
35	i	113/295 (38%)	83 (74%)	30 (26%)	0	3
36	j	152/205 (74%)	143 (94%)	9 (6%)	18	39
37	k	25/25 (100%)	25 (100%)	0	100	100
All	All	6478/10395 (62%)	5791 (89%)	687 (11%)	9	21

5 of 687 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	J	13	VAL
26	Z	487	LEU
11	K	37	LYS
10	J	12	LYS
18	R	189	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 163 such sidechains are listed below:

Mol	Chain	Res	Type
26	Z	366	GLN
31	e	57	GLN
26	Z	447	GLN
26	Z	761	GLN
33	g	131	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8305. 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

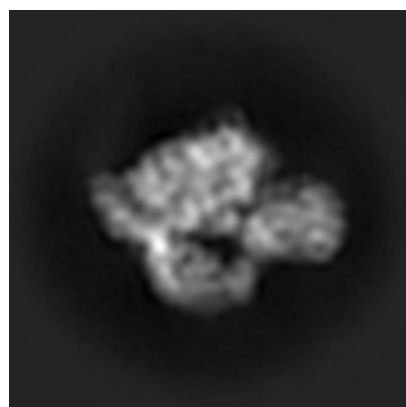


Y

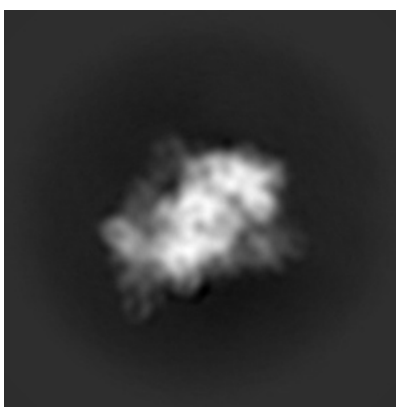


Z

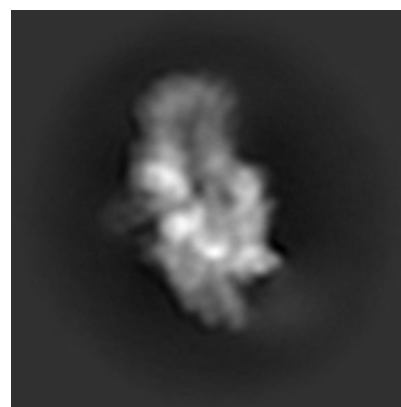
6.1.2 Raw map



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: 110

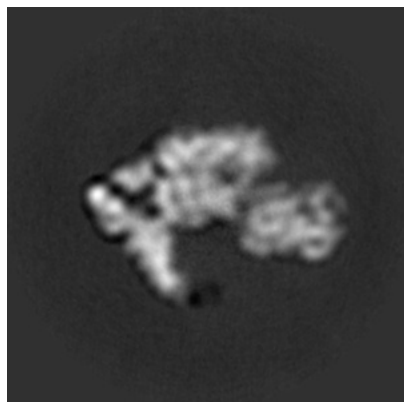


Y Index: 110

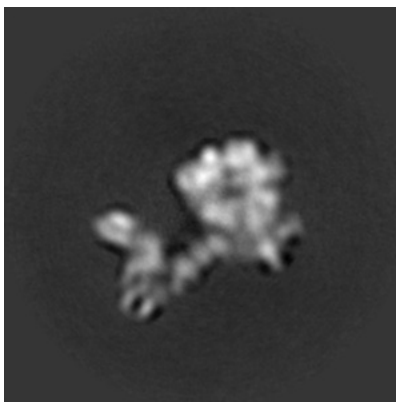


Z Index: 110

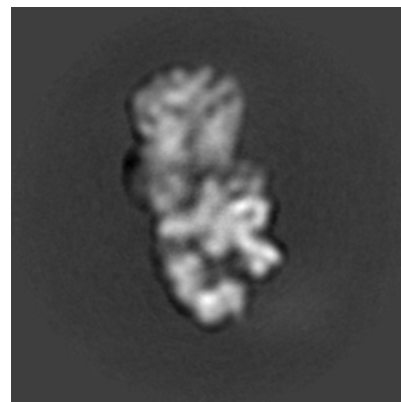
6.2.2 Raw map



X Index: 110



Y Index: 110



Z Index: 110

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: 90

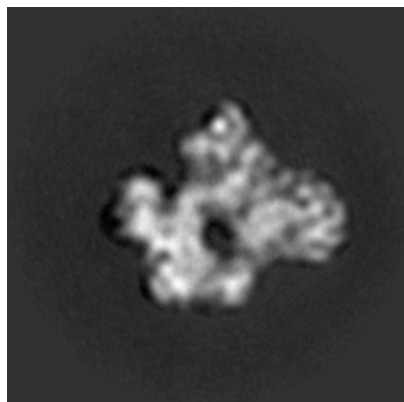


Y Index: 86

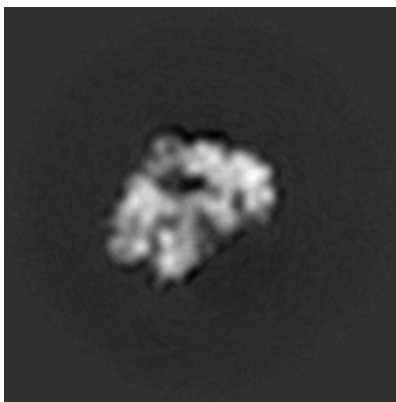


Z Index: 103

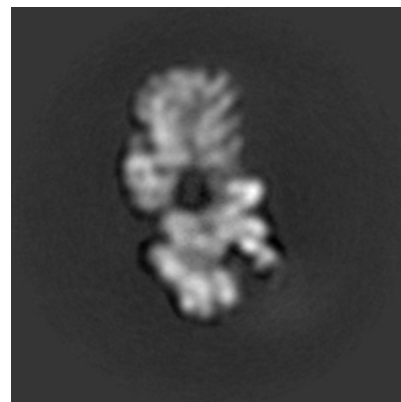
6.3.2 Raw map



X Index: 90



Y Index: 86



Z Index: 103

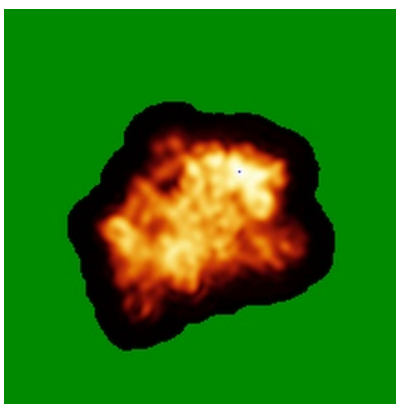
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

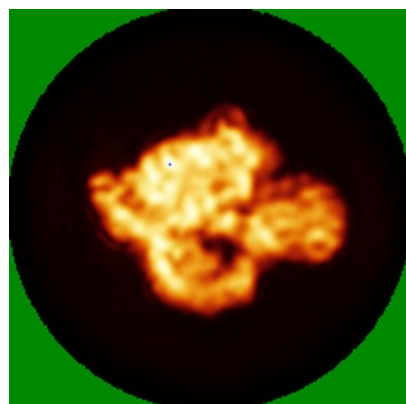


Y

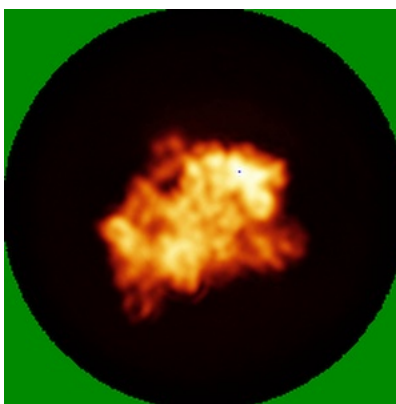


Z

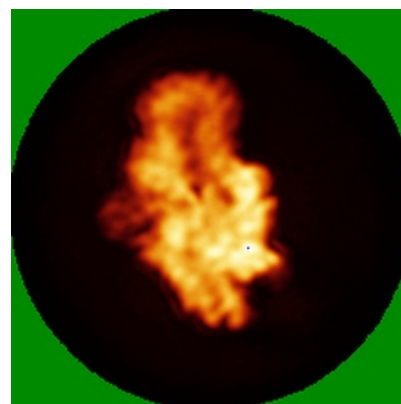
6.4.2 Raw map



X



Y

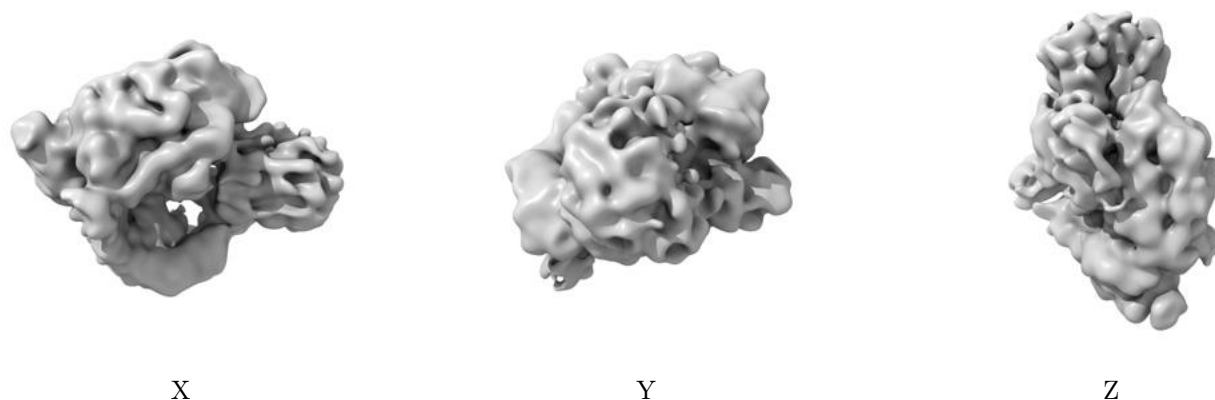


Z

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.

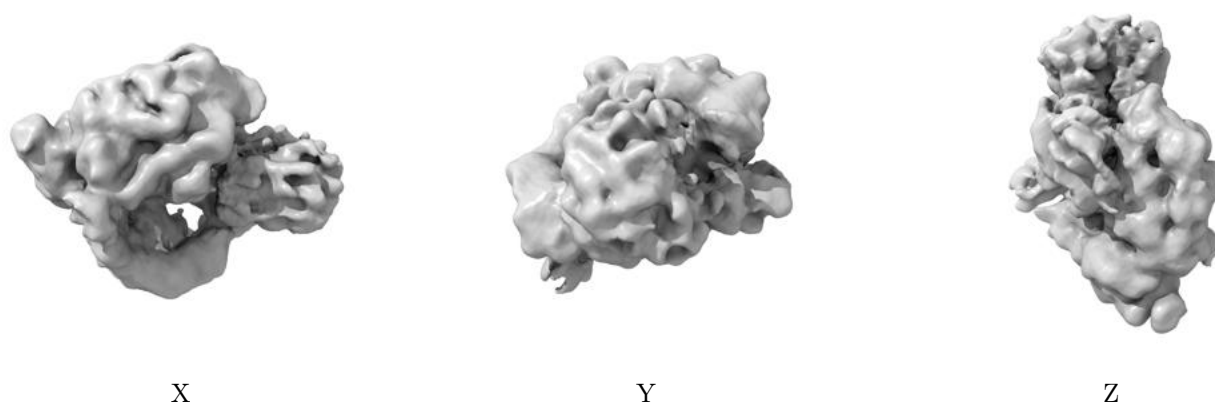
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. 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.

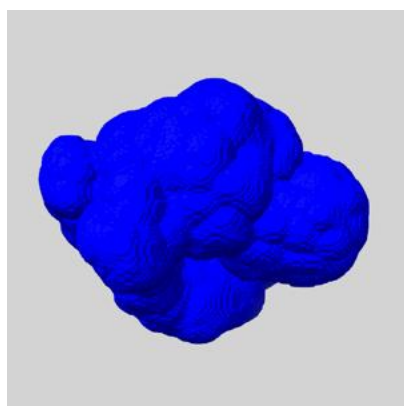
6.6 Mask visualisation [i](#)

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

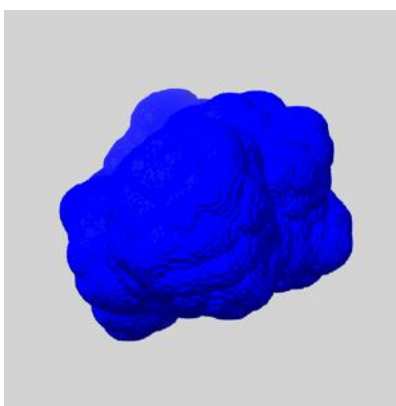
A mask typically either:

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

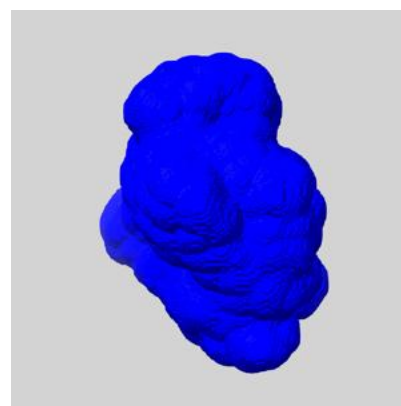
6.6.1 emd_8305_msk_1.map [i](#)



X



Y

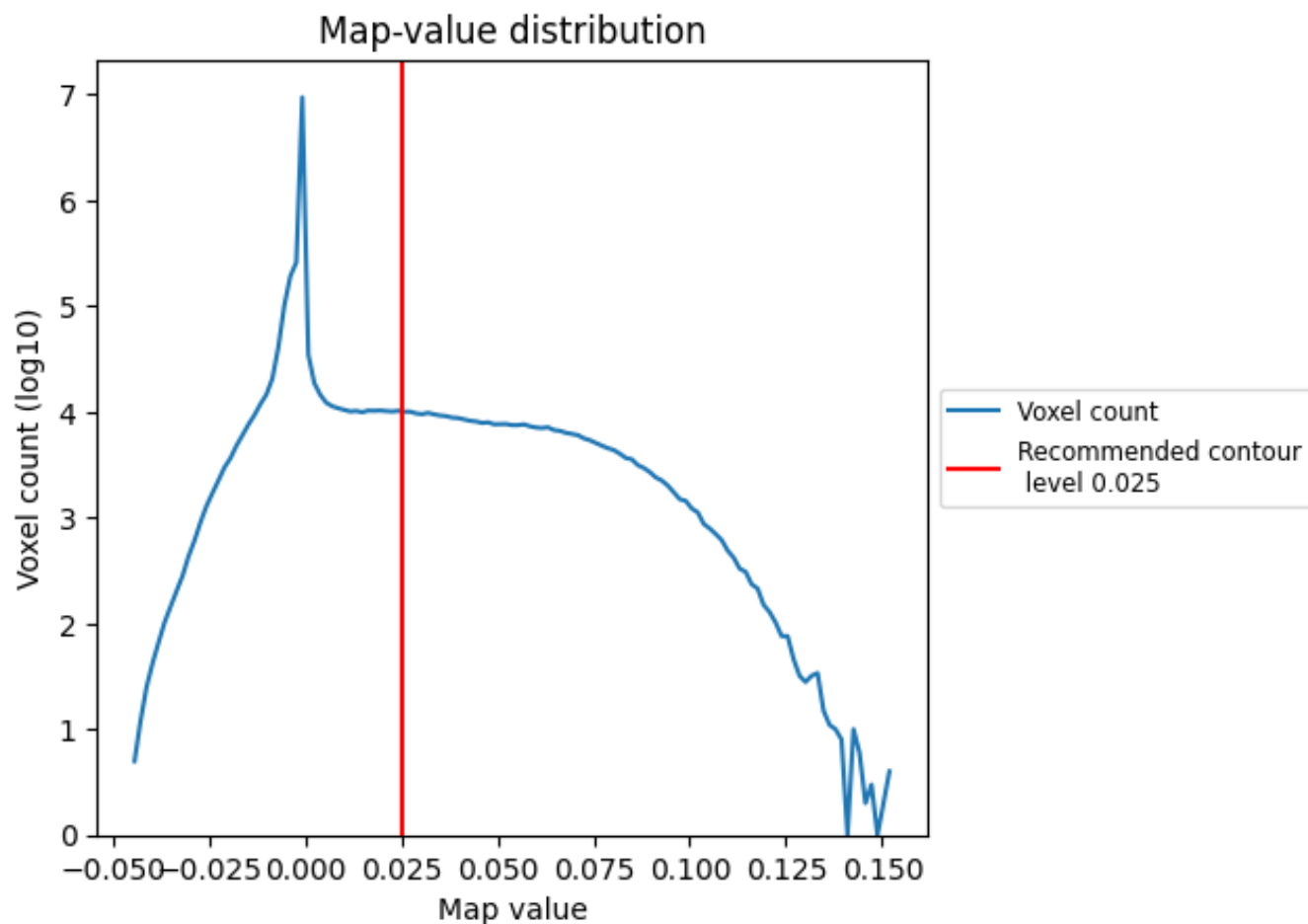


Z

7 Map analysis [i](#)

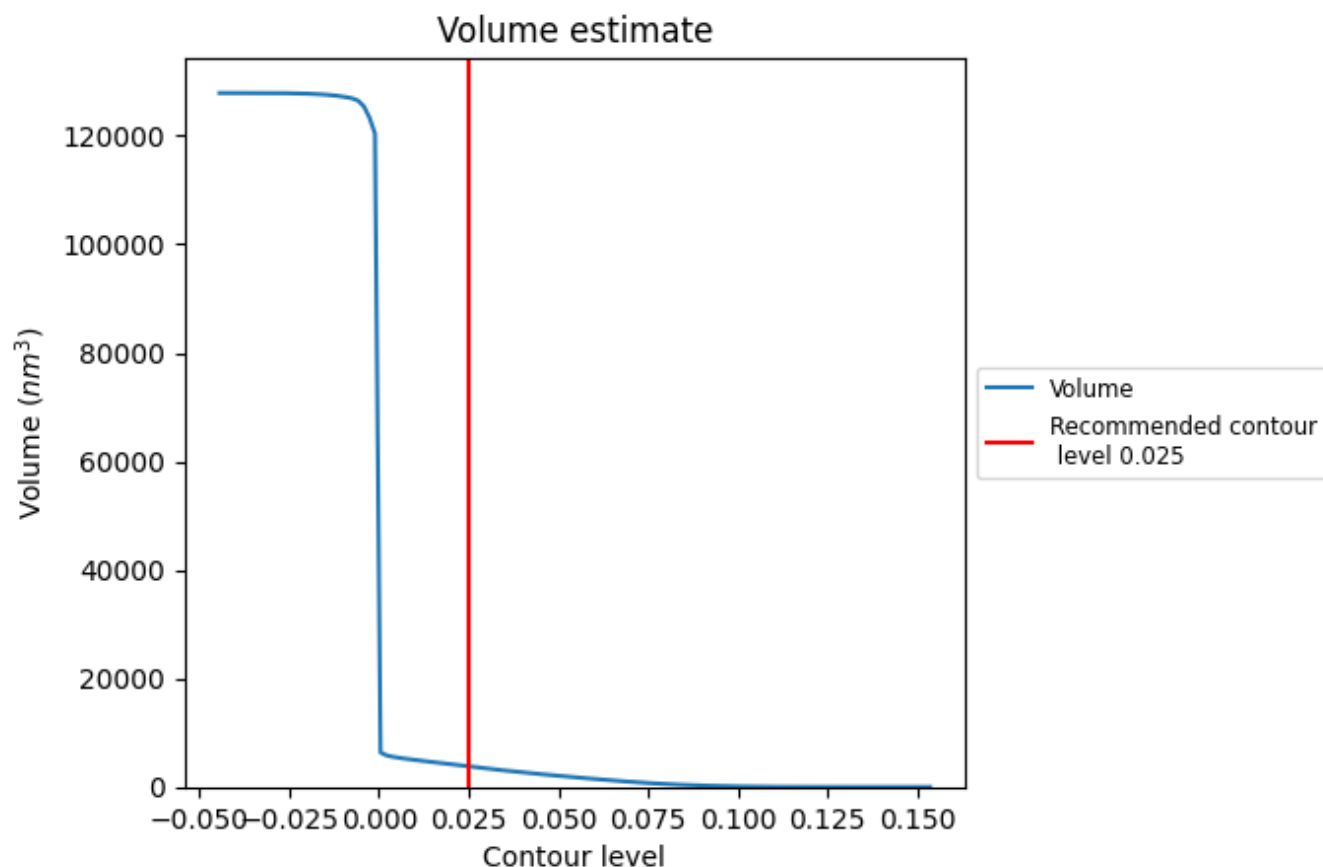
This section contains the results of statistical analysis of the map.

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.

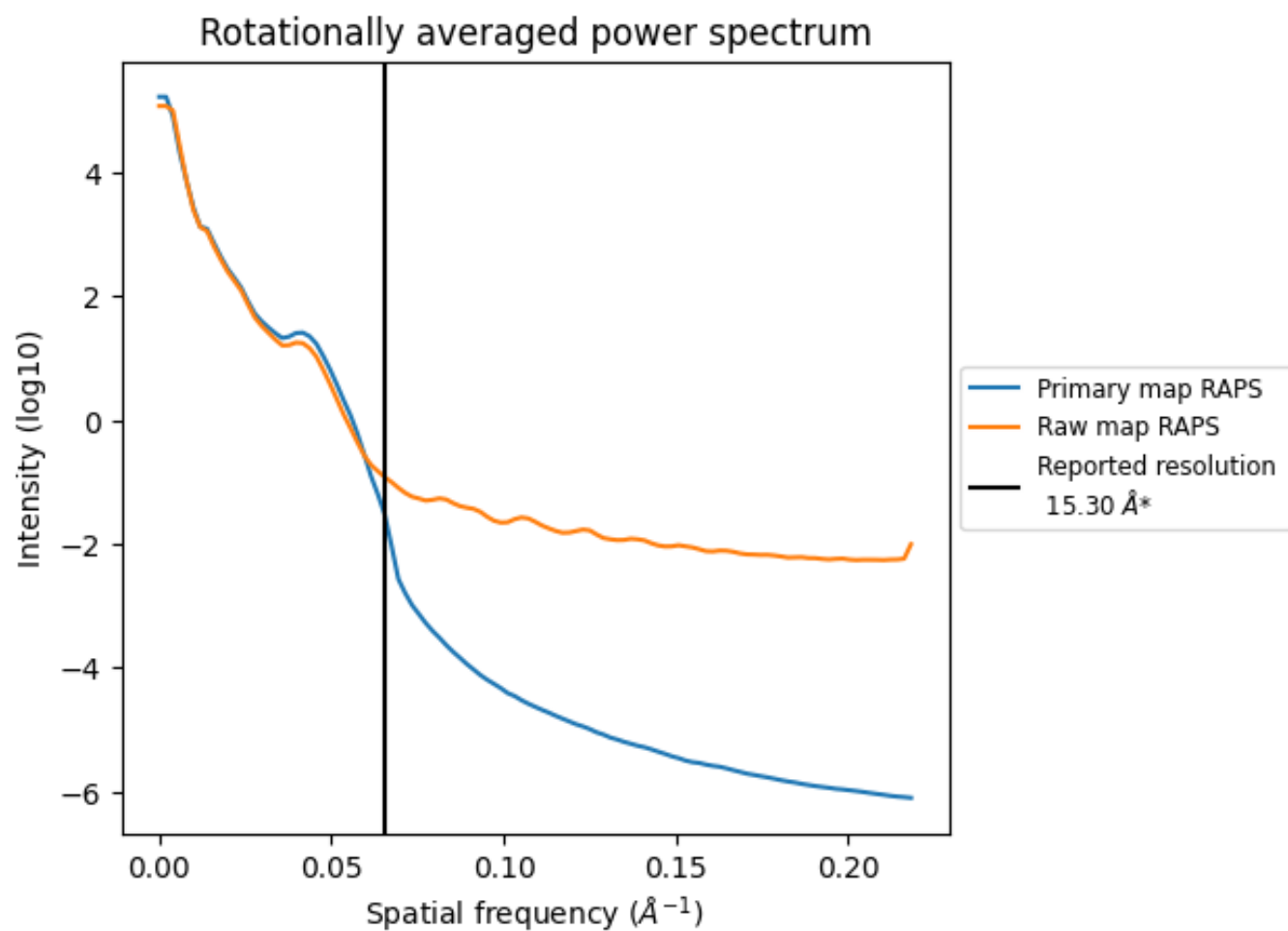
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3796 nm³; this corresponds to an approximate mass of 3429 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 ⓘ

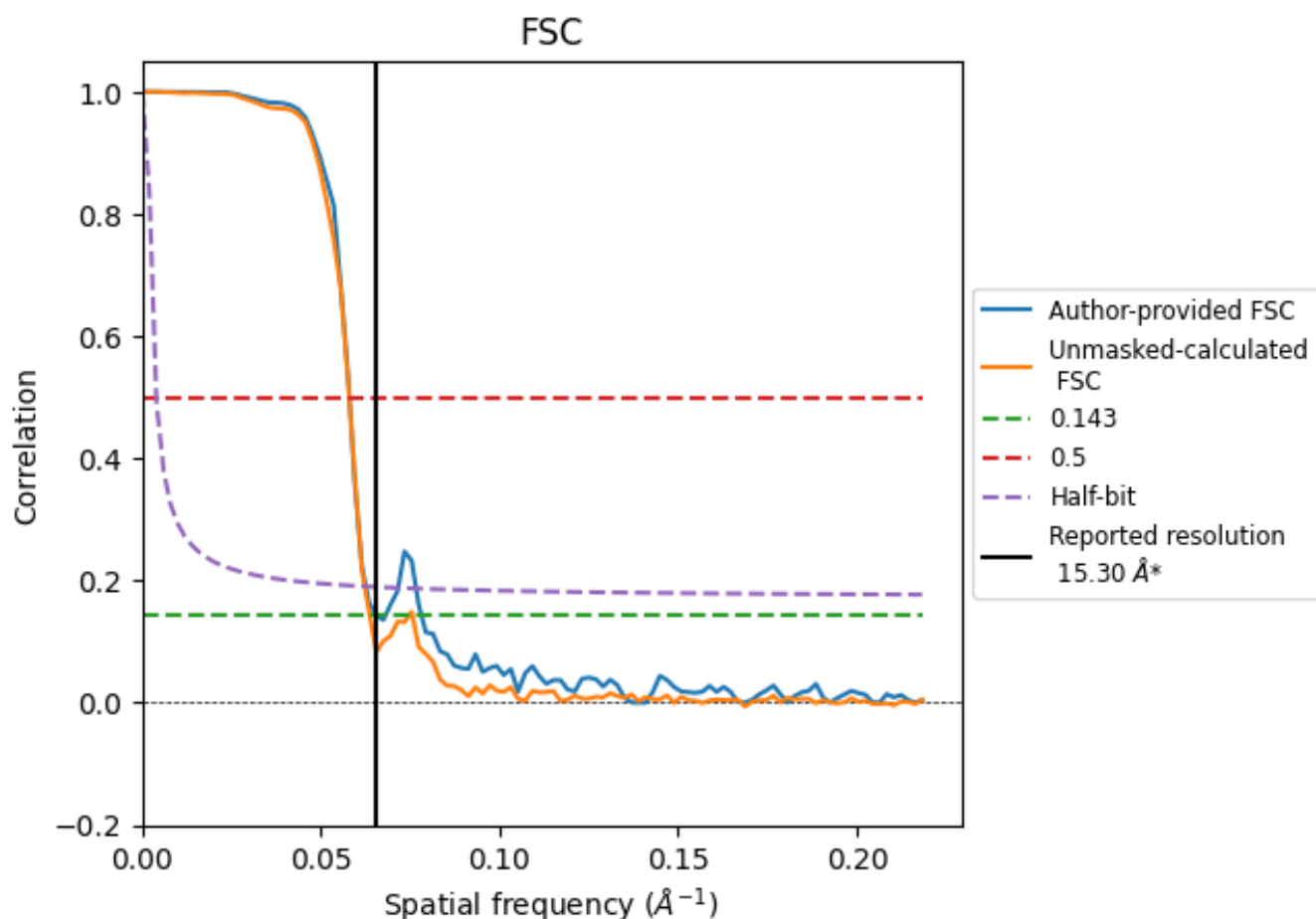


*Reported resolution corresponds to spatial frequency of 0.065 $\text{\AA}^{-1}$

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 0.065 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

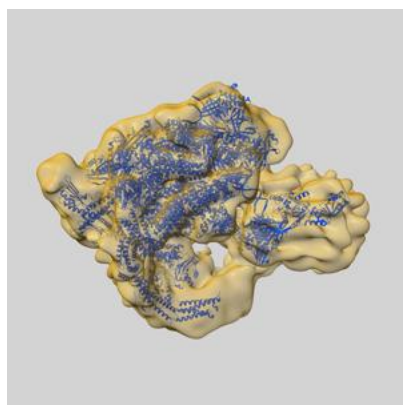
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	15.30	-	-
Author-provided FSC curve	15.27	17.24	15.97
Unmasked-calculated*	15.70	17.27	16.05

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

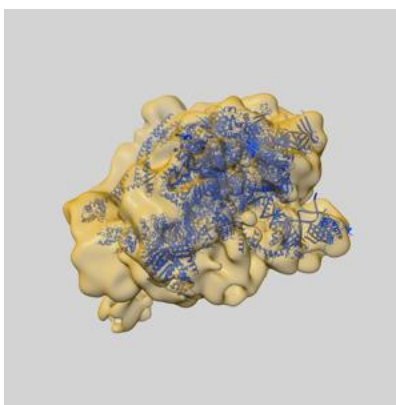
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8305 and PDB model 5SVA. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

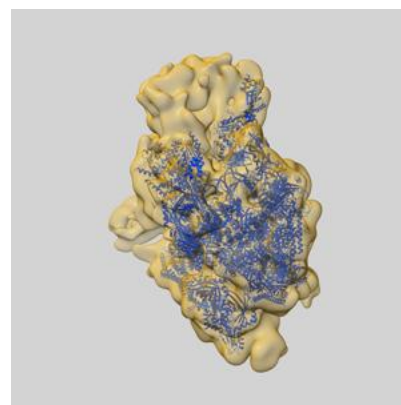
9.1 Map-model overlay [i](#)



X



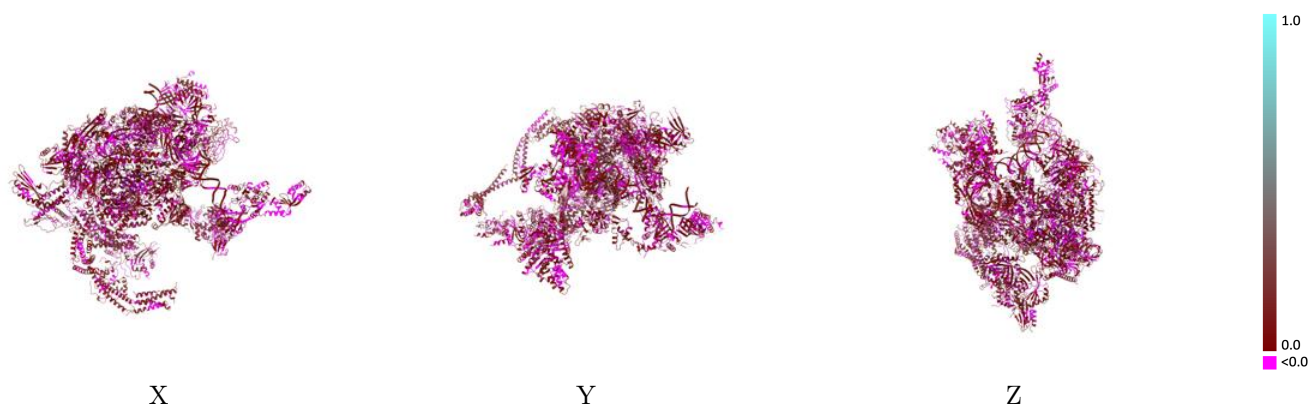
Y



Z

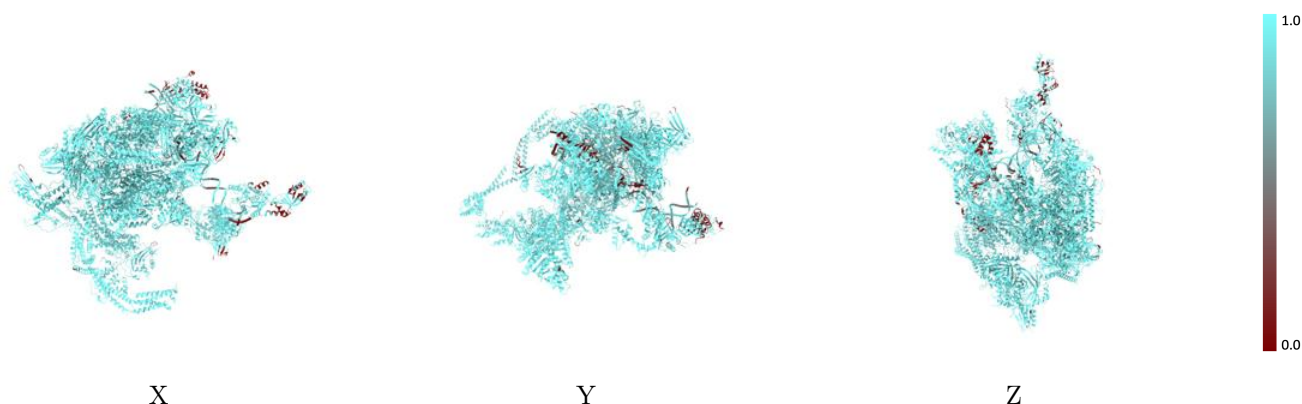
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



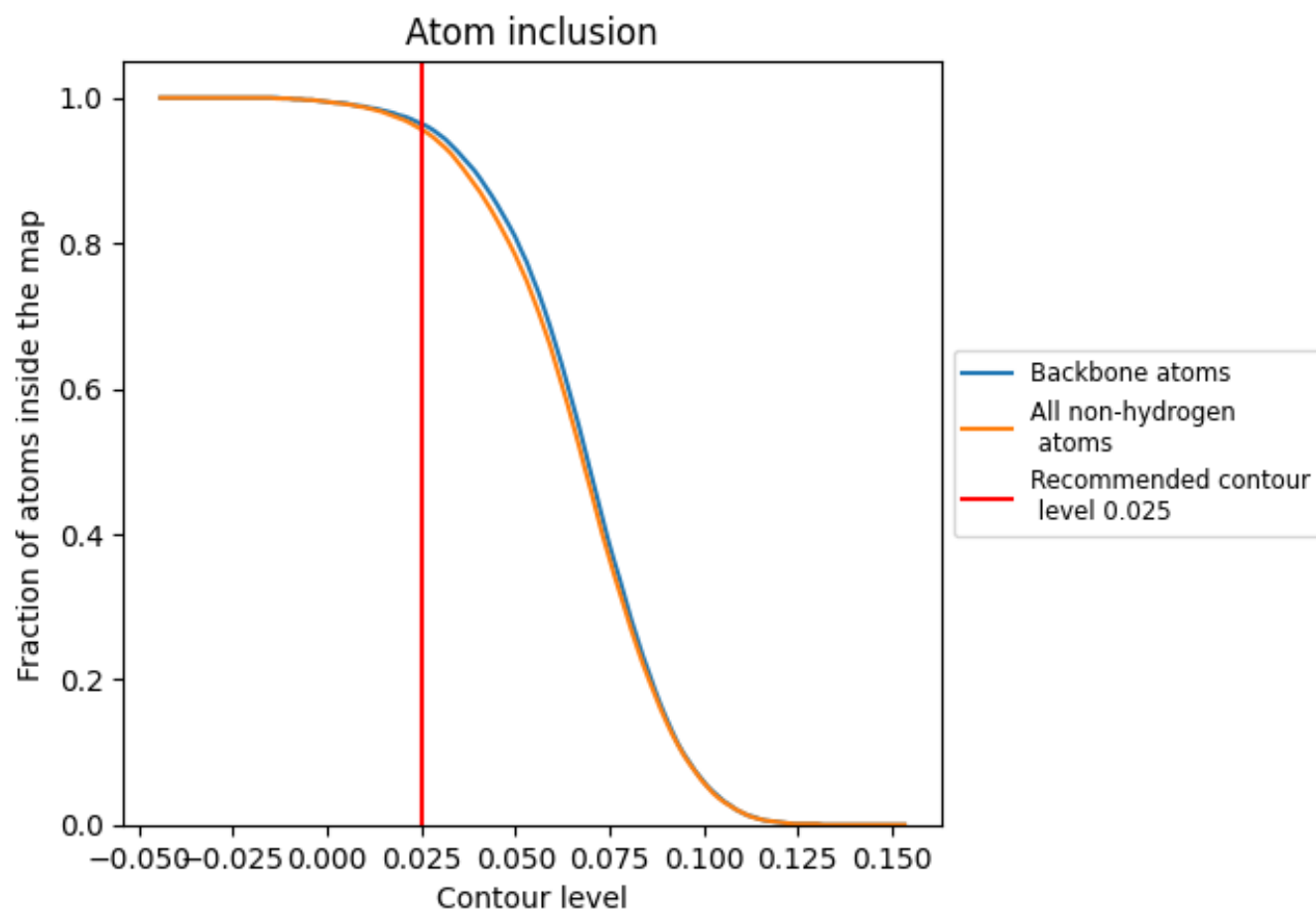
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9570	 0.0490
A	 0.9930	 0.0610
B	 0.9960	 0.0400
C	 0.9900	 0.0500
D	 0.9780	 0.0630
E	 0.9930	 0.0720
F	 0.9970	 0.0640
G	 0.9760	 0.0570
H	 0.9510	 0.0380
I	 0.9440	 0.0490
J	 1.0000	 0.0810
K	 0.9750	 0.0720
L	 1.0000	 0.0570
M	 0.9670	 0.0290
N	 0.9990	 0.0450
O	 1.0000	 0.0700
P	 0.9850	 0.0610
Q	 0.9920	 0.0460
R	 0.9810	 0.0630
S	 1.0000	 0.0330
T	 0.9800	 0.0460
U	 0.9960	 0.0700
V	 0.9770	 0.1040
W	 0.9960	 0.0940
X	 0.9850	 0.0080
Y	 0.9920	 0.0450
Z	 0.9340	 0.0360
a	 0.6090	 -0.0120
b	 0.6040	 0.0000
c	 0.9680	 0.0260
d	 0.5480	 0.0070
e	 0.7380	 0.0220
f	 0.9130	 0.0170
g	 0.9820	 0.0240
h	 0.9610	 0.0620



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Chain	Atom inclusion	Q-score
i	 1.0000	 0.0750
j	 0.8260	 0.0390
k	 1.0000	 -0.0140
l	 0.7680	 0.0630
m	 0.8250	 0.0540
n	 0.8600	 0.0390