



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 08:59 PM UTC

PDB ID : 5IY7 / pdb_00005iy7
EMDB ID : EMD-8132
Title : Human holo-PIC in the open state
Authors : He, Y.; Yan, C.; Fang, J.; Inouye, C.; Tjian, R.; Ivanov, I.; Nogales, E.
Deposited on : 2016-03-24
Resolution : 8.60 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:

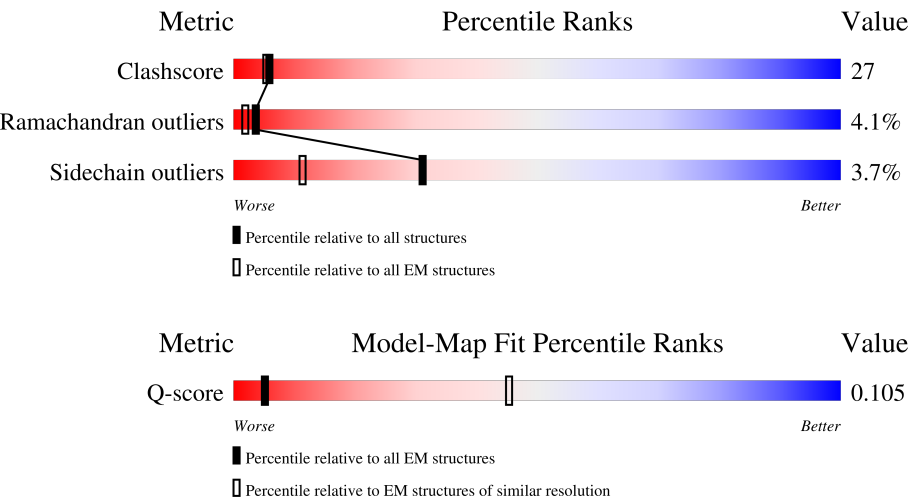
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.60 Å.

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



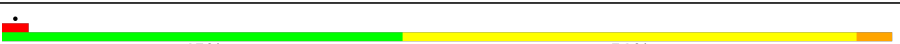
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	292 (8.10 - 9.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	1970	46% 23% • • 26%
2	B	1174	58% 35% 5% • •
3	C	275	69% 25% 6%
4	D	142	5% 82% 8% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	E	210	
6	F	127	
7	G	172	
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	M	316	
14	N	376	
15	O	109	
16	P	339	
17	Q	439	
18	R	291	
19	S	517	
20	T	249	
21	U	301	
22	V	782	
23	W	760	
24	0	395	
25	1	71	
26	2	462	
27	3	308	
28	X	77	
29	Y	77	

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 62705 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 DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1454	Total	C	N	O	S	0	0
			11515	7234	2058	2150	73		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1165	Total	C	N	O	S	0	0
			9317	5878	1637	1738	64		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2213	1386	380	440	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	129	Total	C	N	O	S	0	0
			1062	665	179	214	4		

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	210	Total	C	N	O	S	0	0
			1723	1088	301	325	9		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	86	Total	C	N	O	S	0	0
			689	437	120	127	5		

- 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
			1351	875	219	249	8		

- Molecule 8 is a protein called DNA-directed RNA polymerase II subunit RPB8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	150	Total	C	N	O	S	0	0
			1205	764	196	239	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	125	Total	C	N	O	S	0	0
			1013	626	177	198	12		

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	67	Total	C	N	O	S	0	0
			533	345	90	92	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			937	604	154	177	2		

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	46	Total	C	N	O	S	0	0
			388	241	75	66	6		

- Molecule 13 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	310	Total	C	N	O	S	0	0
			2391	1490	426	457	18		

- Molecule 14 is a protein called Transcription initiation factor IIA subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	113	Total	C	N	O	S	0	0
			930	585	152	189	4		

- Molecule 15 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	99	Total	C	N	O	S	0	0
			806	510	142	151	3		

- Molecule 16 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	185	Total	C	N	O	S	0	0
			1462	946	257	252	7		

- Molecule 17 is a protein called General transcription factor IIE subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	180	Total	C	N	O	S	0	0
			1484	938	262	273	11		

- Molecule 18 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	165	Total	C	N	O	S	0	0
			1357	865	235	253	4		

- Molecule 19 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	138	Total	C	N	O	S	0	0
			1138	719	208	208	3		

- Molecule 20 is a protein called General transcription factor IIF subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	222	Total	C	N	O	S	0	0
			1788	1127	320	338	3		

- Molecule 21 is a protein called Transcription elongation factor TFIIS.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	170	Total	C	N	O	S	0	0
			1343	818	247	263	15		

- Molecule 22 is a protein called TFIIF basal transcription factor complex helicase XPB subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	475	Total	C	N	O	S	0	0
			3855	2454	663	712	26		

- Molecule 23 is a protein called TFIIF basal transcription factor complex helicase XPD subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	665	Total	C	N	O	S	0	0
			5348	3415	932	975	26		

- Molecule 24 is a protein called General transcription factor IIF subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	0	188	Total	C	N	O	S	0	0
			1479	935	258	276	10		

- Molecule 25 is a protein called General transcription factor IIF subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1	62	Total	C	N	O	S	0	0
			491	317	77	93	4		

- Molecule 26 is a protein called General transcription factor IIF subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	2	274	Total	C	N	O	S	0	0
			2196	1417	377	392	10		

- Molecule 27 is a protein called General transcription factor IIF subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	3	193	Total	C	N	O	S	0	0
			1526	978	252	284	12		

- Molecule 28 is a DNA chain called SCP-X.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	77	Total	C	N	O	P	0	0
			1591	753	303	459	76		

- Molecule 29 is a DNA chain called SCP-Y.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	77	Total	C	N	O	P	0	0
			1561	741	279	465	76		

- Molecule 30 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
30	A	1	Total	Mg	0
			1	1	
30	B	1	Total	Mg	0
			1	1	

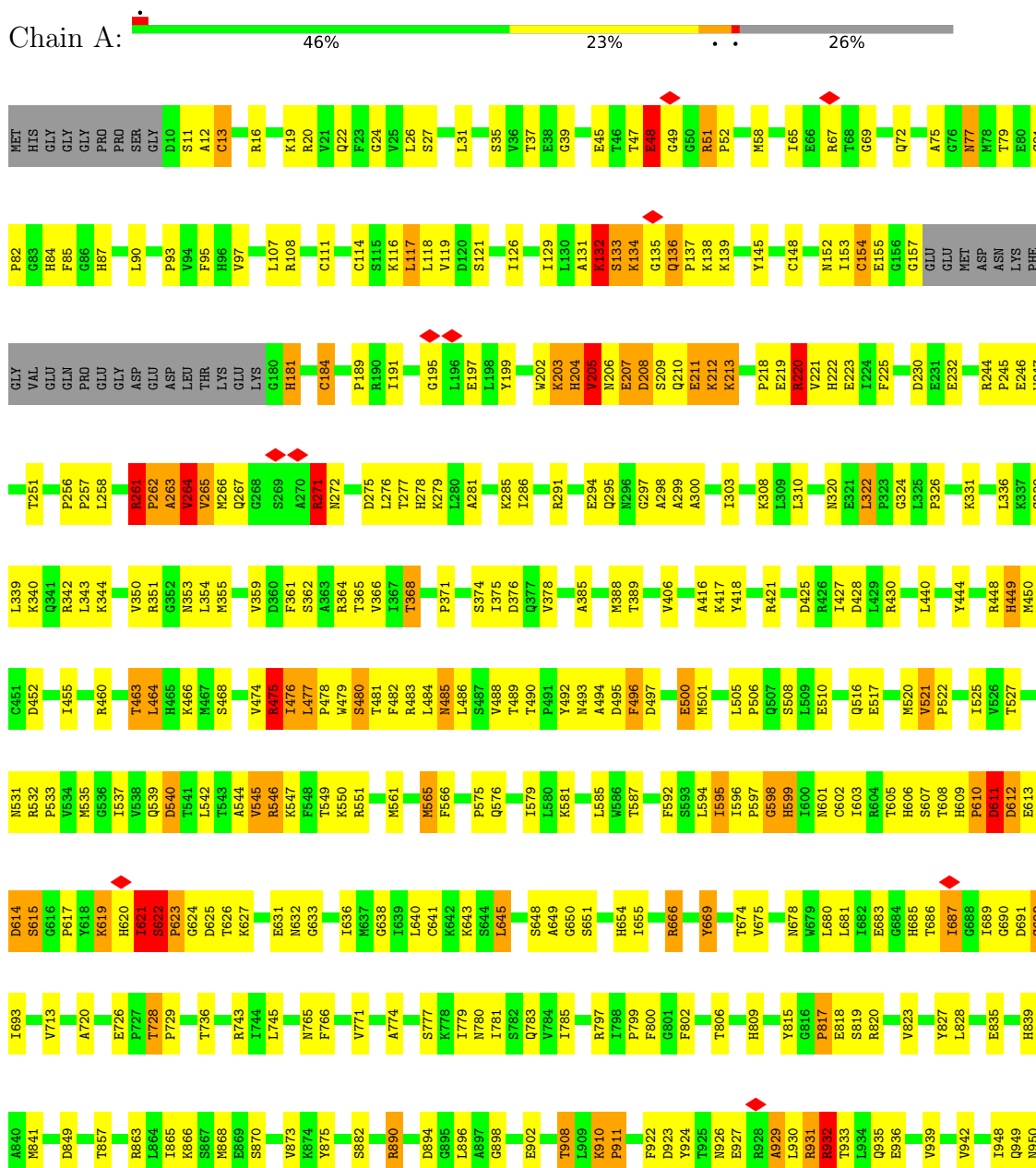
- Molecule 31 is ZINC ION (CCD ID: ZN) (formula: Zn).

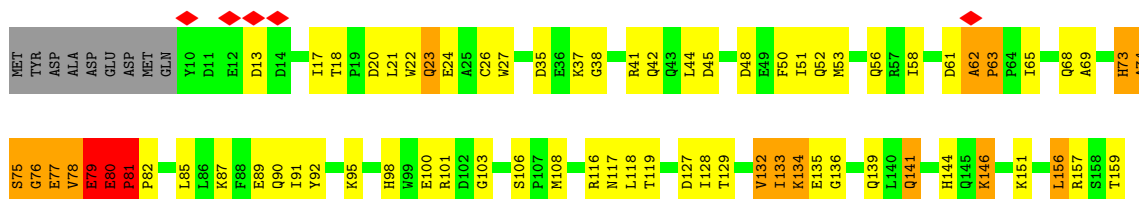
Mol	Chain	Residues	Atoms		AltConf
31	A	2	Total	Zn	0
			2	2	
31	B	2	Total	Zn	0
			2	2	
31	C	1	Total	Zn	0
			1	1	
31	I	2	Total	Zn	0
			2	2	
31	L	1	Total	Zn	0
			1	1	
31	M	1	Total	Zn	0
			1	1	
31	Q	1	Total	Zn	0
			1	1	
31	U	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

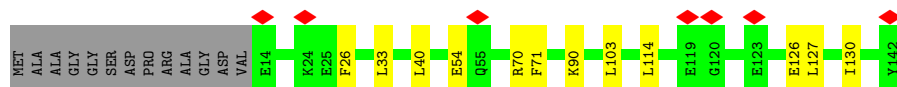
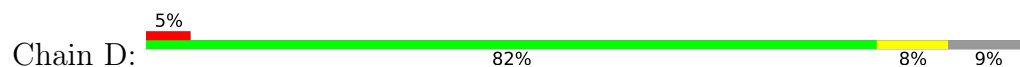
- Molecule 1: DNA-directed RNA polymerase II subunit RPB1



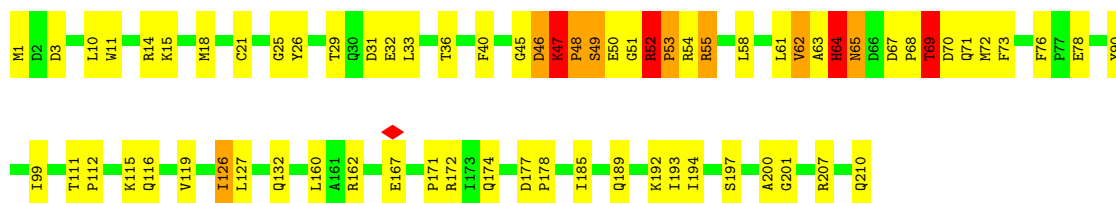




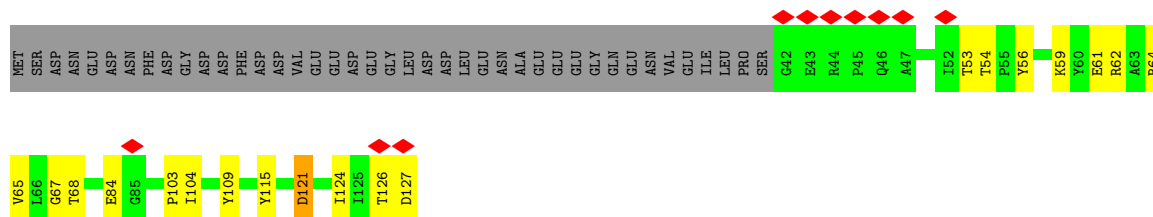
- Molecule 4: DNA-directed RNA polymerase II subunit RPB4



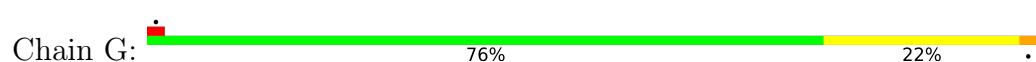
- Molecule 5: DNA-directed RNA polymerase II subunit RPB5



- Molecule 6: DNA-directed RNA polymerase II subunit RPB6



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

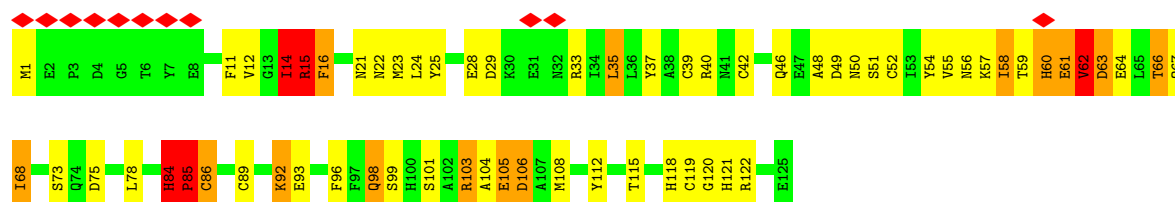


- Molecule 8: DNA-directed RNA polymerase II subunit RPB8

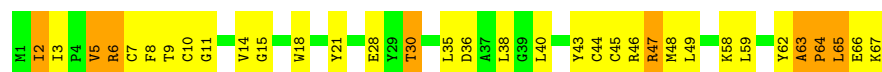




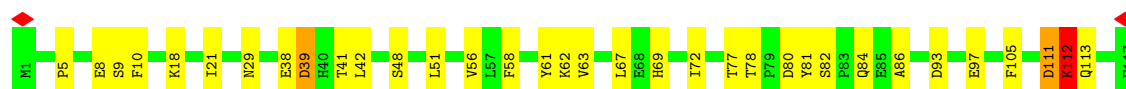
- Molecule 9: DNA-directed RNA polymerase II subunit RPB9



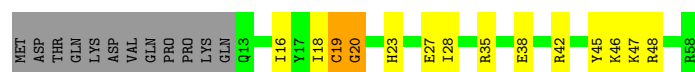
- Molecule 10: DNA-directed RNA polymerase II subunit RPB10



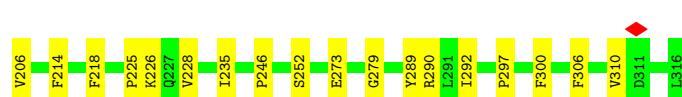
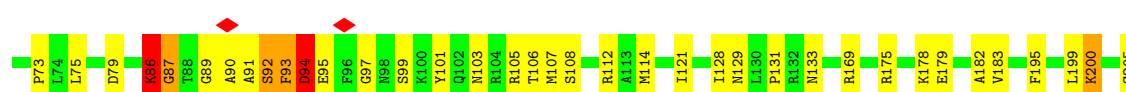
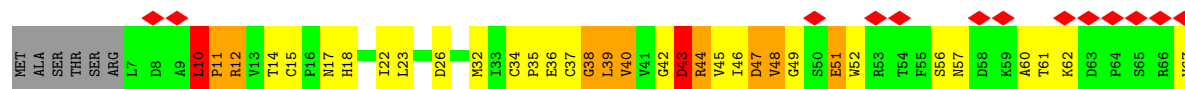
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11-a



- Molecule 12: DNA-directed RNA polymerase II subunit RPB12



- Molecule 13: Transcription initiation factor IIB



Chain N:

18% 12% 70%

Node	Parent	Label
D319	GLN	MET
V320	ALA	ALA
S321	GLN	ASN
D322	PRO	SER
E323	ALA	ALA
E324	GLN	ASN
G325	THR	THR
G326	GLN	HIS
E327	ALA	HIS
L328	PRO	HIS
F329	LEU	GLN
E332	VAL	GLN
N333	LEU	ALA
K341	GLN	ALA
L342	VAL	PRO
H343	GLY	VAL
R344	ASP	GLN
S345	THR	GLN
K346	SER	THR
W349	SER	GLN
K350	GLU	ALA
F351	GLU	GLN
H352	ASP	VAL
L353	ASP	LEU
K354	ASP	ILE
D355	GLU	VAL
G356	GLU	LEU
N359	GLU	ILE
L360	ASP	PRO
N361	ASP	ALA
G362	ASP	SER
E365	GLU	GLN
D364	GLU	GLN
K369	GLU	VAL
A370	LYS	GLY
I371	LYS	PHE
W376	GLU	HIS
G307	ASP	GLN
Q308	GLN	ALA
V309	GLN	ALA
E310	THR	THR
E311	THR	GLN
E312	THR	ASN
P313	GLY	MET
L314	GLN	GLN
N315	GLN	VAL
S316	GLN	ALA
E317	PRO	GLN

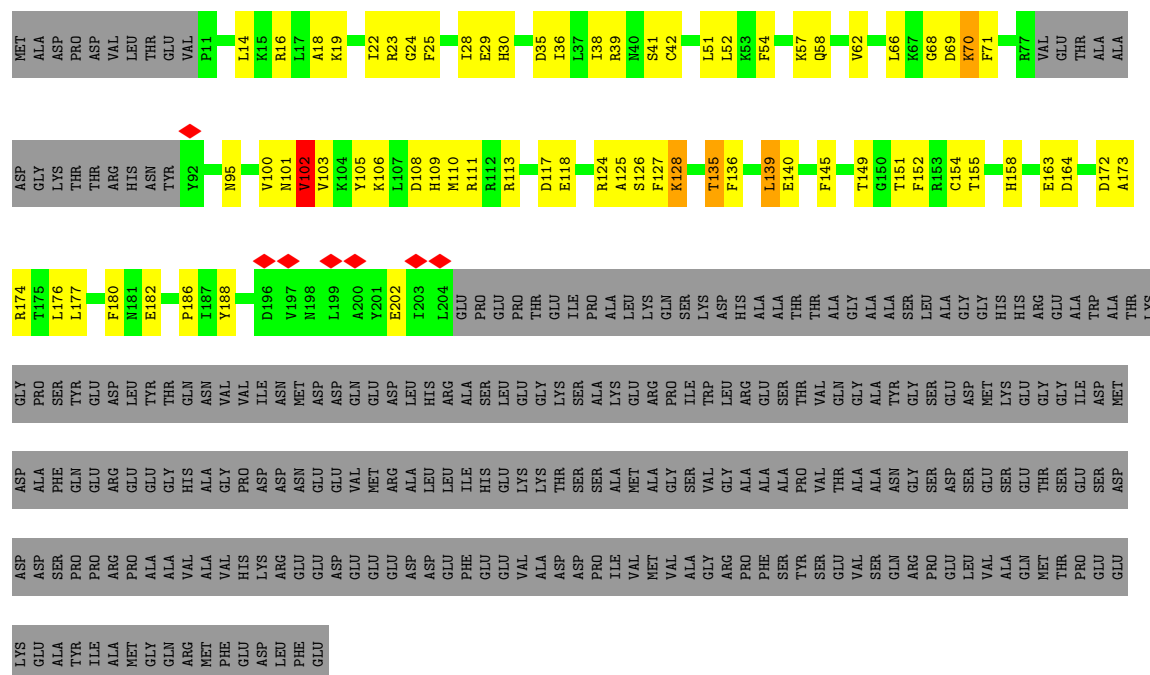
Chain O:

Residue	Category
R1	Green
A2	Green
Y3	Green
Q4	Yellow
L5	Yellow
L11	Green
L22	Yellow
I28	Yellow
L32	Green
Q35	Yellow
F40	Yellow
Q50	Red Diamond
R53	Yellow
T64	Green
Y65	Green
R66	Yellow
T73	Green
F74	Green
V75	Yellow
V79	Yellow
V84	Yellow
T85	Yellow
K92	Yellow
V93	Yellow
C98	Yellow
L99	Green
GLY	Grey
LYS	Grey
ASN	Grey
THR	Grey
THR	Grey
GLY	Grey
SER	Grey
ASN	Grey
THR	Grey
THR	Grey
GLU	Grey

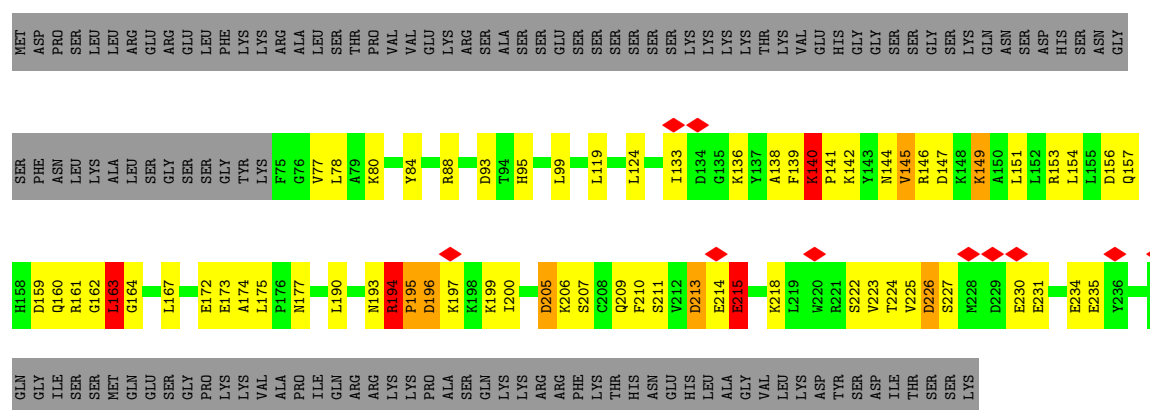
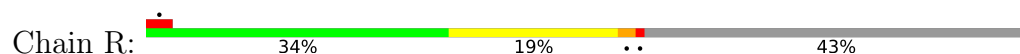
Chain P:

THR	THR	E206	P207	R208	V220	Q229	L232	R236	K236	A238	R239	V240	Q242	K243	A248	I256	Q256	R257	M258	C262	I268	R269	Q278	Y283	E284	P286	M295	K296	P298	R299	I300	V306	V311	E320	F326	I328	K333	G334	F335	R336	Y337							
GLN	GLN	LEU	PHE	HIS	SER	GLN	THR	THR	THR	ALA	PRO	LEU	PRO	GLY	THR	THR	PRO	LEU	TYR	PRO	SER	PRO	THR	ILE	THR	PRO	ALA	T153	P154	A155	S156	E157	I161	V162	P163	Q164	L165	Q166	N167	I168	T171	L180	I183	R188	R199	A190	M202	P203

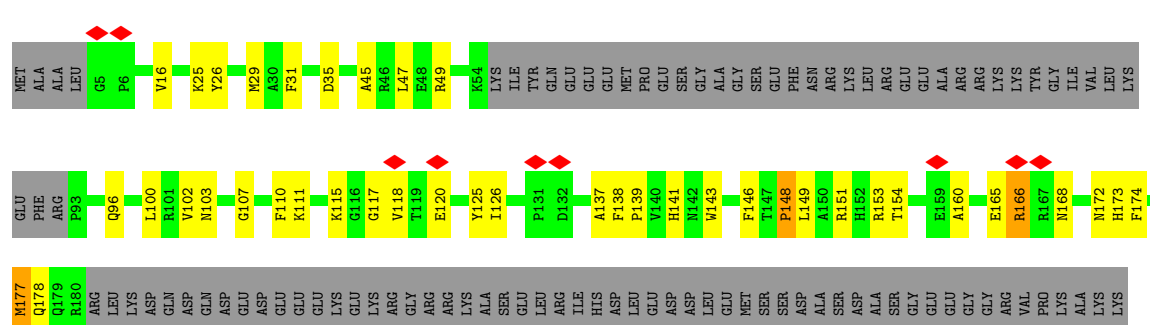
Chain Q: 25% 15% 59%



• Molecule 18: Transcription initiation factor IIE subunit beta

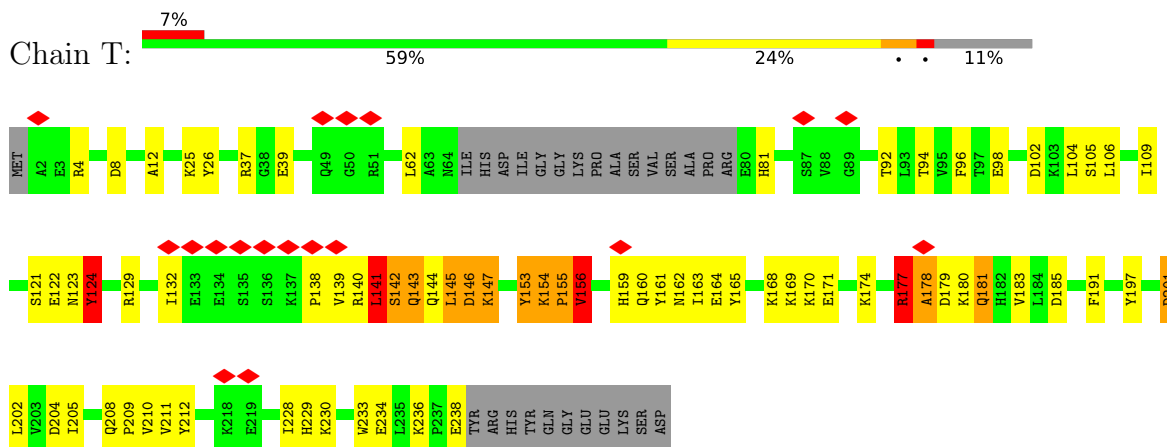


• Molecule 19: General transcription factor IIF subunit 1

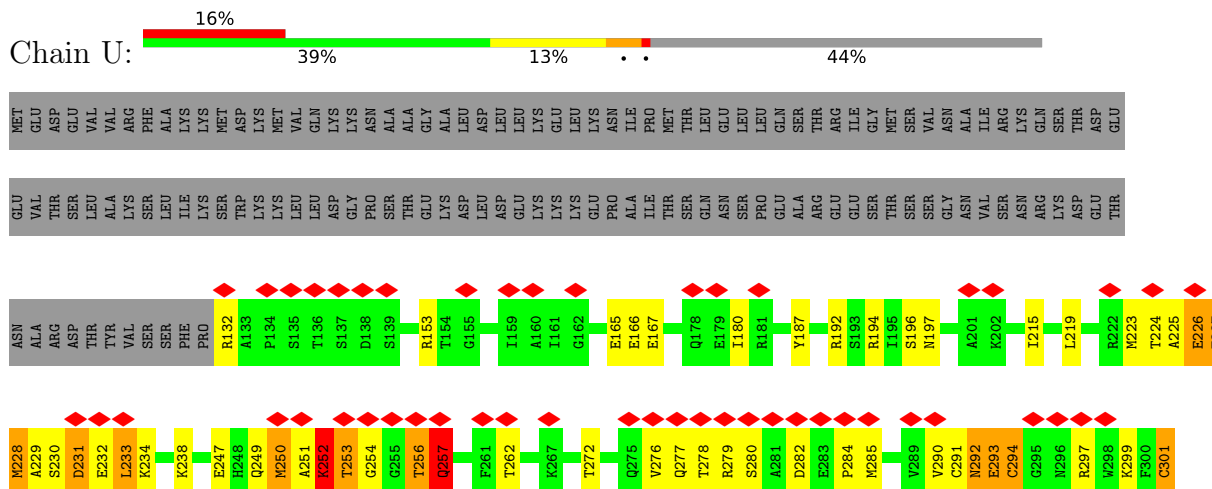




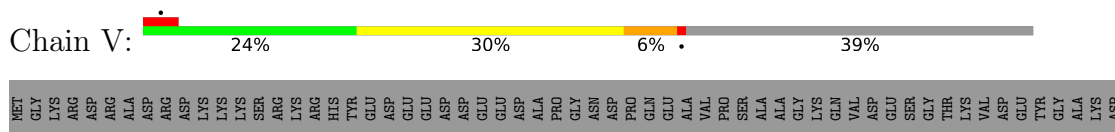
- Molecule 20: General transcription factor IIF subunit 2

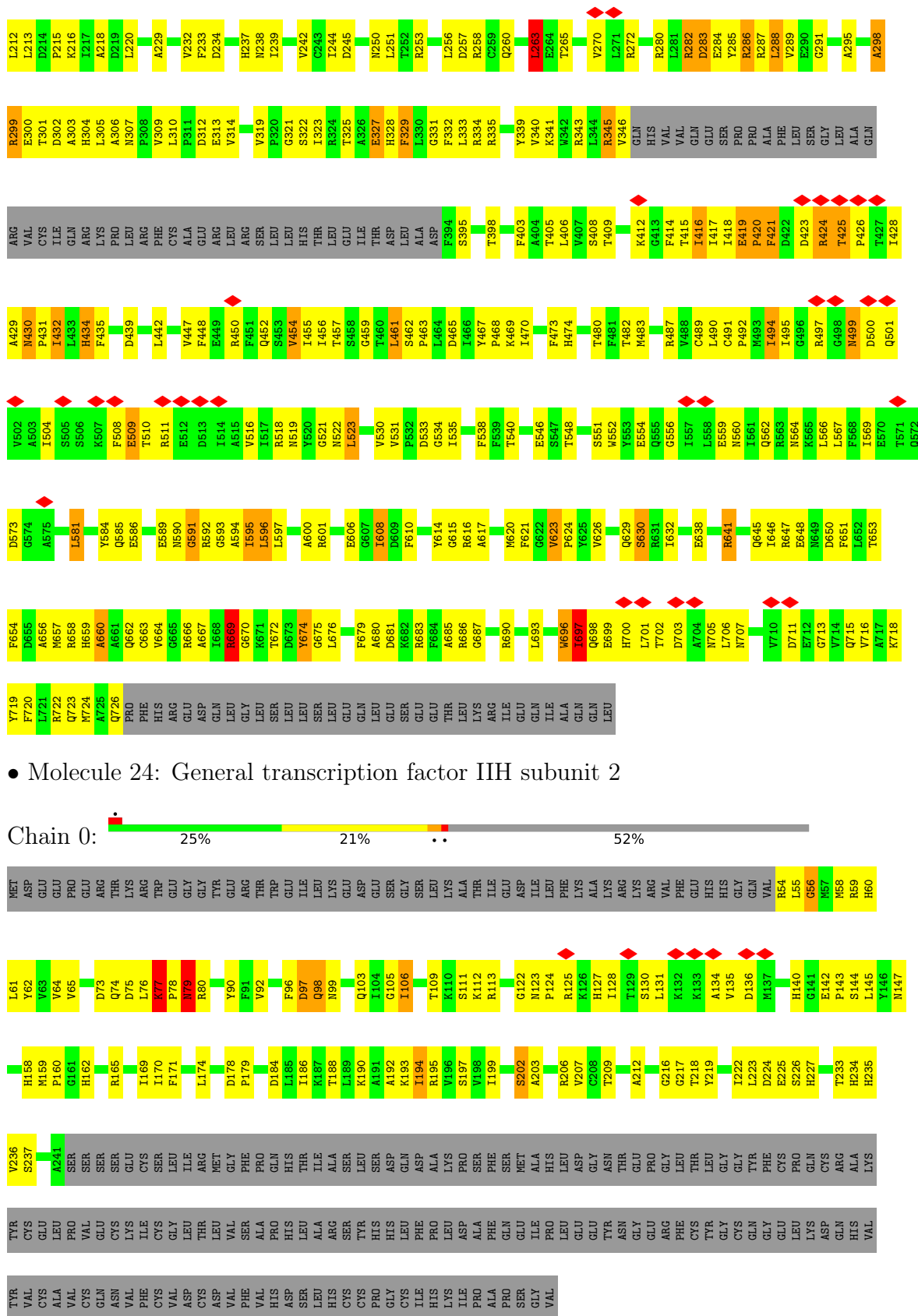


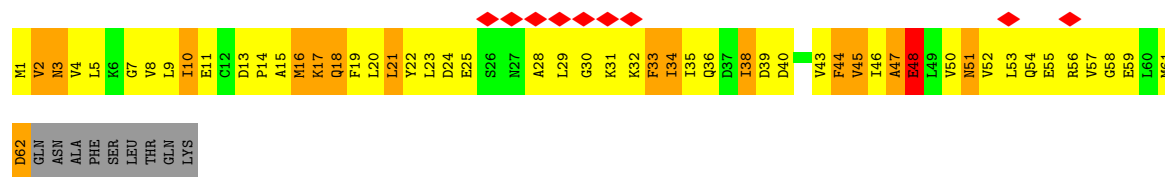
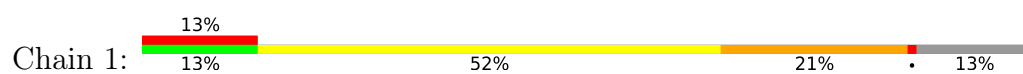
- Molecule 21: Transcription elongation factor TFIIS



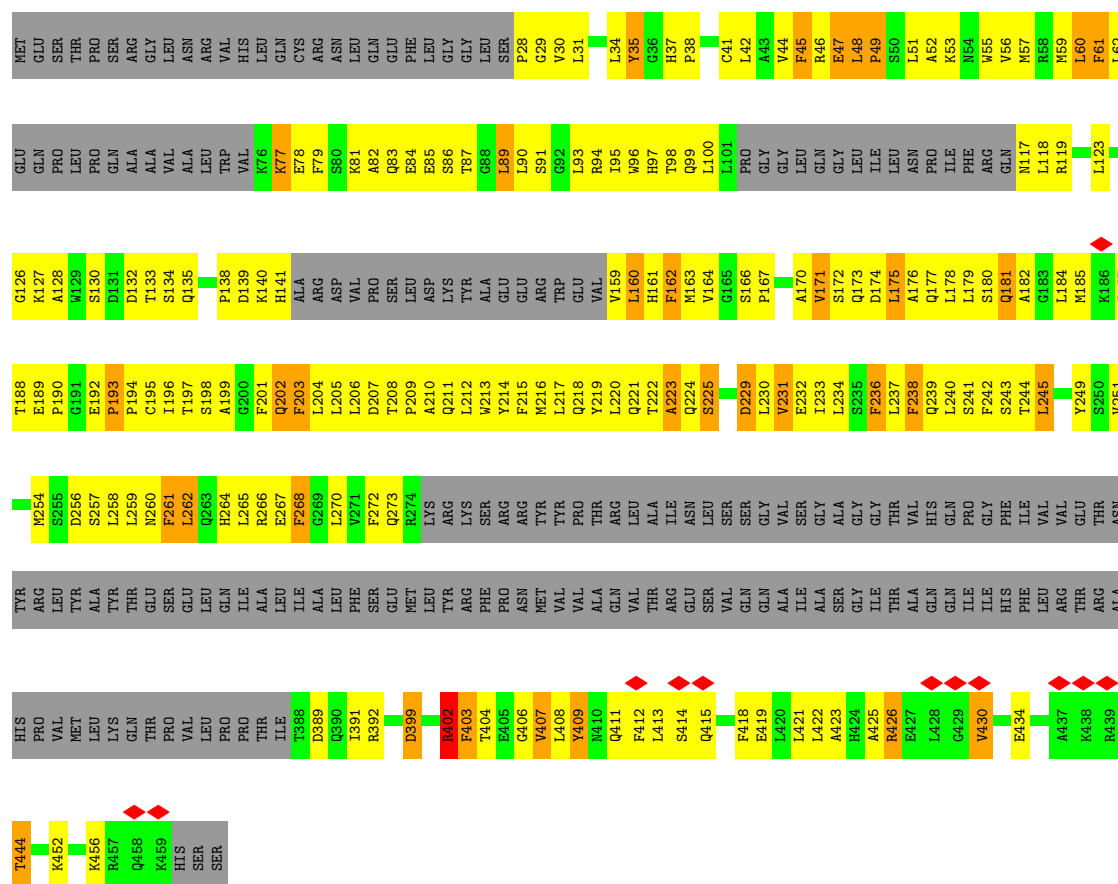
- Molecule 22: TFIIH basal transcription factor complex helicase XPB subunit



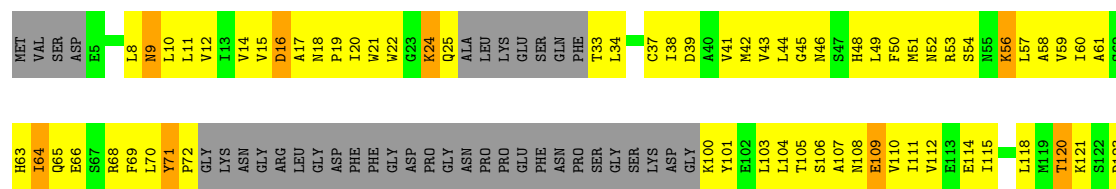


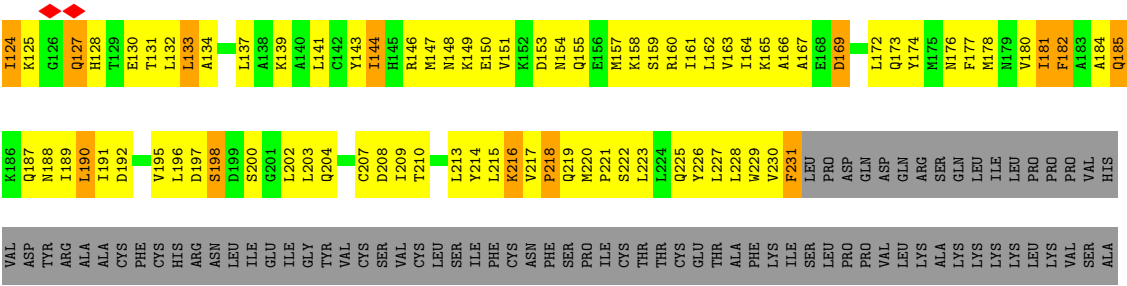


• Molecule 26: General transcription factor IIH subunit 4

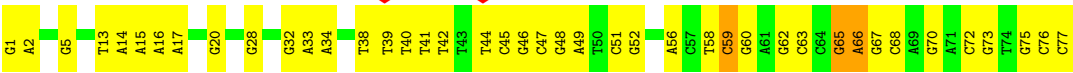


• Molecule 27: General transcription factor IIH subunit 3

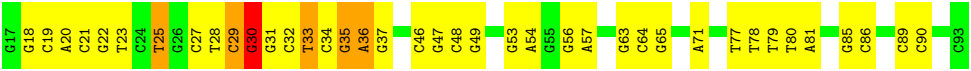




• Molecule 28: SCP-X



• Molecule 29: SCP-Y



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59271	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	27500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.150	Depositor
Minimum map value	-0.055	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	503.03998, 503.03998, 503.03998	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.62, 2.62, 2.62	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.65	2/11727 (0.0%)	1.15	67/15833 (0.4%)
2	B	0.72	5/9503 (0.1%)	1.18	76/12831 (0.6%)
3	C	0.64	0/2259	1.18	20/3073 (0.7%)
4	D	0.34	0/1077	0.88	1/1446 (0.1%)
5	E	0.52	0/1753	1.09	10/2368 (0.4%)
6	F	0.57	0/700	1.02	4/946 (0.4%)
7	G	0.35	0/1382	0.95	9/1874 (0.5%)
8	H	0.44	0/1227	0.91	1/1654 (0.1%)
9	I	0.40	0/1038	1.18	13/1407 (0.9%)
10	J	0.69	0/542	1.27	3/730 (0.4%)
11	K	0.52	0/956	1.04	7/1294 (0.5%)
12	L	0.49	0/394	0.91	0/524
13	M	0.45	0/2429	1.04	11/3281 (0.3%)
14	N	0.34	0/945	0.97	7/1274 (0.5%)
15	O	0.32	0/816	0.81	0/1105
16	P	0.37	0/1489	1.01	3/2005 (0.1%)
17	Q	0.38	0/1507	1.03	4/2023 (0.2%)
18	R	0.53	0/1380	1.17	5/1854 (0.3%)
19	S	0.33	0/1167	0.80	0/1576
20	T	0.43	0/1817	1.07	13/2445 (0.5%)
21	U	0.45	0/1358	1.05	5/1820 (0.3%)
22	V	1.87	75/3931 (1.9%)	2.32	241/5298 (4.5%)
23	W	2.03	128/5460 (2.3%)	2.41	346/7390 (4.7%)
24	0	2.09	34/1506 (2.3%)	2.31	74/2038 (3.6%)
25	1	1.29	1/496 (0.2%)	1.79	13/669 (1.9%)
26	2	1.23	0/2243	1.70	41/3024 (1.4%)
27	3	1.26	0/1548	1.55	15/2090 (0.7%)
28	X	0.64	3/1788 (0.2%)	1.01	16/2762 (0.6%)
29	Y	0.62	0/1746	1.09	25/2690 (0.9%)
All	All	1.01	248/64184 (0.4%)	1.43	1030/87324 (1.2%)

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
1	A	0	1
2	B	0	1
5	E	0	1
8	H	0	1
14	N	0	3
18	R	0	6
19	S	0	1
20	T	0	1
22	V	0	8
23	W	0	14
24	0	0	1
25	1	0	1
26	2	0	8
28	X	0	2
29	Y	0	3
All	All	0	52

The worst 5 of 248 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	0	142	GLU	N-CA	-10.09	1.37	1.45
24	0	158	HIS	CA-C	9.98	1.65	1.52
24	0	99	ASN	CA-CB	9.58	1.63	1.53
23	W	465	ASP	CA-C	9.18	1.64	1.52
22	V	590	MET	CA-C	8.93	1.64	1.52

The worst 5 of 1030 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	84	HIS	C-N-CD	-14.70	64.75	125.00
3	C	6	GLN	C-N-CD	-14.42	65.87	125.00
29	Y	35	DG	O5'-C5'-C4'	13.55	131.13	110.80
2	B	80	GLU	C-N-CD	-13.12	71.22	125.00
16	P	206	GLU	C-N-CD	-13.01	71.67	125.00

There are no chirality outliers.

5 of 52 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	475	ARG	Sidechain
2	B	234	THR	Peptide
5	E	126	ILE	Peptide
8	H	111	ARG	Peptide
14	N	324	GLU	Peptide

5.2 Too-close contacts

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	11515	0	11617	570	0
2	B	9317	0	9312	427	0
3	C	2213	0	2155	80	0
4	D	1062	0	1042	8	0
5	E	1723	0	1745	105	0
6	F	689	0	715	18	0
7	G	1351	0	1358	32	0
8	H	1205	0	1167	54	0
9	I	1013	0	936	76	0
10	J	533	0	556	49	0
11	K	937	0	959	23	0
12	L	388	0	396	14	0
13	M	2391	0	2411	150	0
14	N	930	0	888	32	0
15	O	806	0	818	23	0
16	P	1462	0	1549	68	0
17	Q	1484	0	1499	147	0
18	R	1357	0	1381	154	0
19	S	1138	0	1103	26	0
20	T	1788	0	1819	116	0
21	U	1343	0	1341	67	0
22	V	3855	0	3871	199	0
23	W	5348	0	5372	148	0
24	0	1479	0	1524	39	0
25	1	491	0	507	248	0
26	2	2196	0	2206	578	0
27	3	1526	0	1561	456	0
28	X	1591	0	865	30	0
29	Y	1561	0	865	59	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	A	1	0	0	0	0
30	B	1	0	0	0	0
31	A	2	0	0	0	0
31	B	2	0	0	0	0
31	C	1	0	0	0	0
31	I	2	0	0	0	0
31	L	1	0	0	0	0
31	M	1	0	0	0	0
31	Q	1	0	0	0	0
31	U	1	0	0	0	0
All	All	62705	0	61538	3294	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 27.

The worst 5 of 3294 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)
27:3:59:VAL:HG12	27:3:71:TYR:CD1	1.22	1.73
23:W:421:PHE:CE1	23:W:423:ASP:CB	1.83	1.62
22:V:516:PRO:CG	25:1:15:ALA:HB3	1.20	1.61
1:A:1250:ASP:CB	21:U:227:GLU:HG2	1.26	1.60
27:3:59:VAL:CG1	27:3:71:TYR:HD1	1.12	1.59

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	A	1450/1970 (74%)	1262 (87%)	123 (8%)	65 (4%)	2	17
2	B	1163/1174 (99%)	1011 (87%)	106 (9%)	46 (4%)	2	18

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	273/275 (99%)	242 (89%)	21 (8%)	10 (4%)	2	20
4	D	127/142 (89%)	118 (93%)	9 (7%)	0	100	100
5	E	208/210 (99%)	188 (90%)	13 (6%)	7 (3%)	3	21
6	F	84/127 (66%)	78 (93%)	6 (7%)	0	100	100
7	G	169/172 (98%)	164 (97%)	5 (3%)	0	100	100
8	H	148/150 (99%)	119 (80%)	19 (13%)	10 (7%)	1	11
9	I	123/125 (98%)	92 (75%)	18 (15%)	13 (11%)	0	6
10	J	65/67 (97%)	51 (78%)	8 (12%)	6 (9%)	0	8
11	K	115/117 (98%)	110 (96%)	2 (2%)	3 (3%)	4	25
12	L	44/58 (76%)	33 (75%)	9 (20%)	2 (4%)	2	17
13	M	308/316 (98%)	263 (85%)	25 (8%)	20 (6%)	1	12
14	N	109/376 (29%)	100 (92%)	7 (6%)	2 (2%)	6	34
15	O	97/109 (89%)	92 (95%)	4 (4%)	1 (1%)	12	49
16	P	183/339 (54%)	169 (92%)	9 (5%)	5 (3%)	4	25
17	Q	176/439 (40%)	154 (88%)	14 (8%)	8 (4%)	2	17
18	R	163/291 (56%)	132 (81%)	21 (13%)	10 (6%)	1	13
19	S	134/517 (26%)	123 (92%)	8 (6%)	3 (2%)	5	29
20	T	218/249 (88%)	185 (85%)	20 (9%)	13 (6%)	1	13
21	U	168/301 (56%)	149 (89%)	10 (6%)	9 (5%)	1	15
22	V	473/782 (60%)	400 (85%)	44 (9%)	29 (6%)	1	13
23	W	661/760 (87%)	570 (86%)	68 (10%)	23 (4%)	3	20
24	0	186/395 (47%)	168 (90%)	13 (7%)	5 (3%)	4	25
25	1	60/71 (84%)	53 (88%)	5 (8%)	2 (3%)	3	21
26	2	264/462 (57%)	246 (93%)	14 (5%)	4 (2%)	8	40
27	3	187/308 (61%)	176 (94%)	9 (5%)	2 (1%)	11	46
All	All	7356/10302 (71%)	6448 (88%)	610 (8%)	298 (4%)	4	18

5 of 298 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	12	ALA
1	A	48	GLU
1	A	132	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	134	LYS
1	A	154	CYS

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	1279/1748 (73%)	1230 (96%)	49 (4%)	29	50
2	B	1020/1028 (99%)	987 (97%)	33 (3%)	34	56
3	C	252/252 (100%)	250 (99%)	2 (1%)	73	80
4	D	119/126 (94%)	118 (99%)	1 (1%)	73	80
5	E	192/192 (100%)	184 (96%)	8 (4%)	26	48
6	F	74/111 (67%)	73 (99%)	1 (1%)	59	72
7	G	152/153 (99%)	150 (99%)	2 (1%)	61	74
8	H	131/131 (100%)	127 (97%)	4 (3%)	35	56
9	I	112/112 (100%)	104 (93%)	8 (7%)	13	35
10	J	56/56 (100%)	54 (96%)	2 (4%)	31	52
11	K	106/106 (100%)	100 (94%)	6 (6%)	18	40
12	L	43/55 (78%)	42 (98%)	1 (2%)	44	64
13	M	263/268 (98%)	256 (97%)	7 (3%)	39	61
14	N	105/324 (32%)	105 (100%)	0	100	100
15	O	90/98 (92%)	90 (100%)	0	100	100
16	P	159/293 (54%)	156 (98%)	3 (2%)	50	67
17	Q	164/373 (44%)	158 (96%)	6 (4%)	30	51
18	R	150/261 (58%)	146 (97%)	4 (3%)	39	61
19	S	121/448 (27%)	118 (98%)	3 (2%)	42	63
20	T	196/218 (90%)	188 (96%)	8 (4%)	27	49
21	U	148/266 (56%)	139 (94%)	9 (6%)	17	38
22	V	422/688 (61%)	405 (96%)	17 (4%)	28	49

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	577/664 (87%)	542 (94%)	35 (6%)	17	38
24	0	171/352 (49%)	163 (95%)	8 (5%)	23	45
25	1	56/64 (88%)	51 (91%)	5 (9%)	9	28
26	2	238/399 (60%)	229 (96%)	9 (4%)	29	50
27	3	171/272 (63%)	161 (94%)	10 (6%)	18	40
All	All	6567/9058 (72%)	6326 (96%)	241 (4%)	31	51

5 of 241 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	K	112	LYS
25	1	38	ILE
20	T	156	VAL
25	1	18	GLN
27	3	133	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 100 such sidechains are listed below:

Mol	Chain	Res	Type
19	S	53	ASN
22	V	599	ASN
27	3	225	GLN
19	S	173	HIS
22	V	366	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 13 ligands modelled in this entry, 13 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

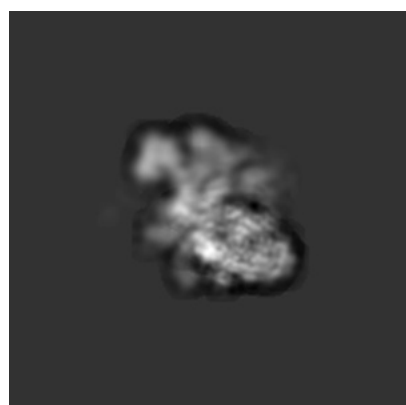
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8132. These allow visual inspection of the internal detail of the map and identification of artifacts.

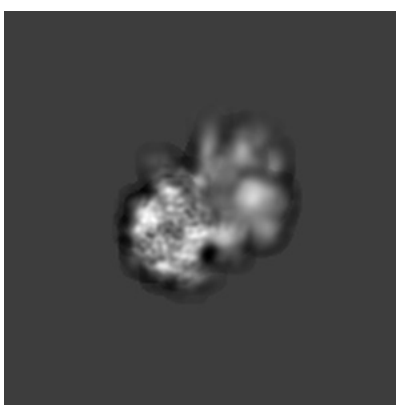
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

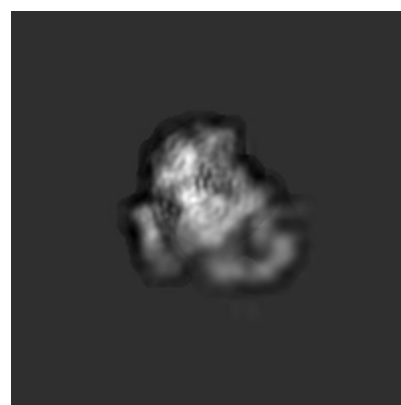
6.1.1 Primary map



X



Y

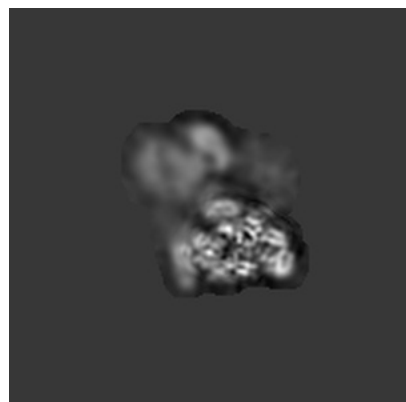


Z

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

6.2 Central slices [i](#)

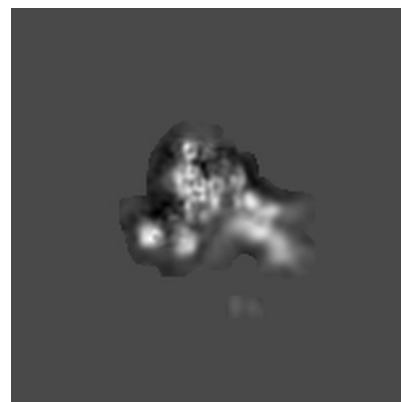
6.2.1 Primary map



X Index: 96



Y Index: 96

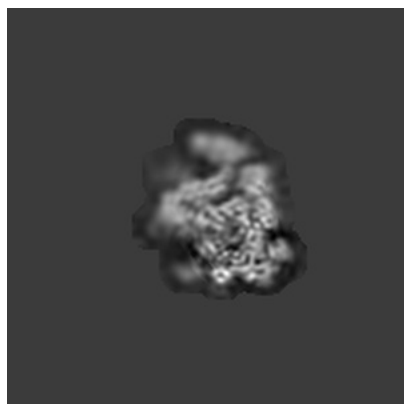


Z Index: 96

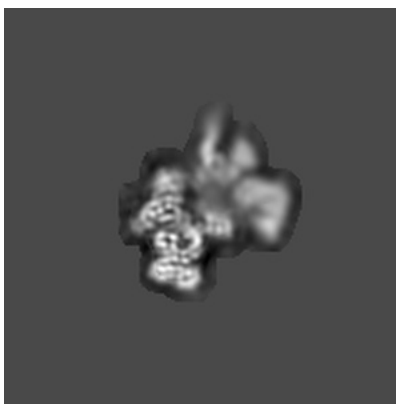
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

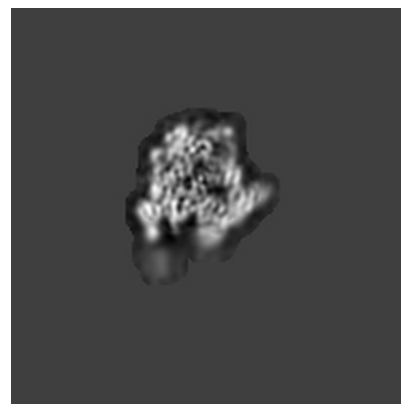
6.3.1 Primary map



X Index: 84



Y Index: 93

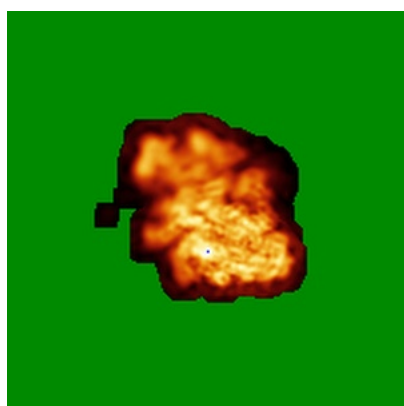


Z Index: 76

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

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

6.4.1 Primary map



X



Y

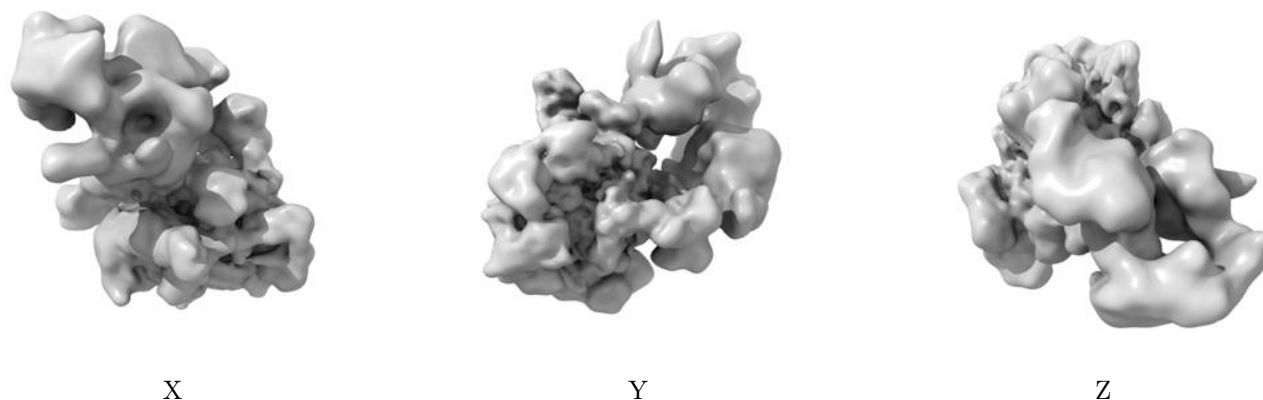


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

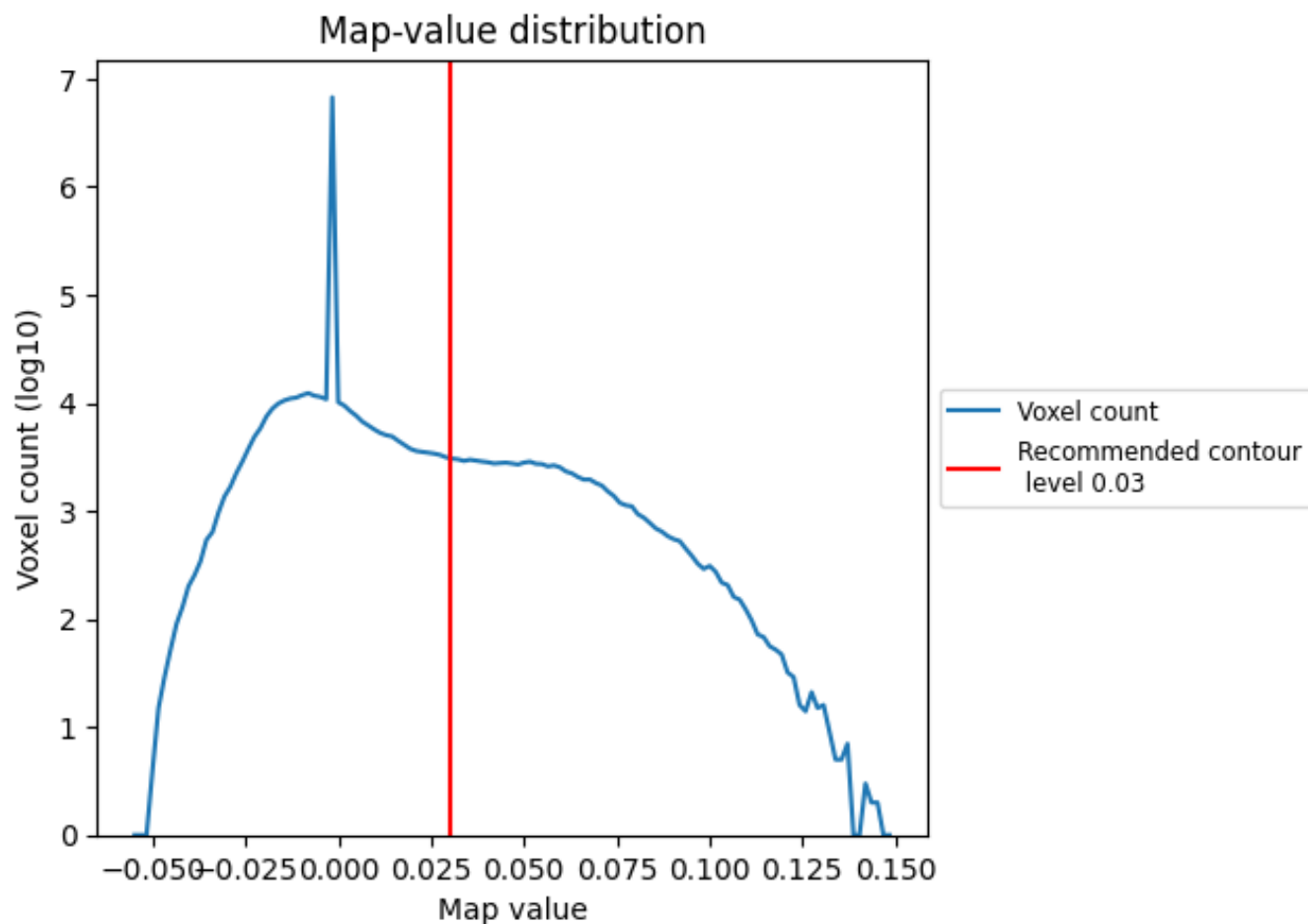
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

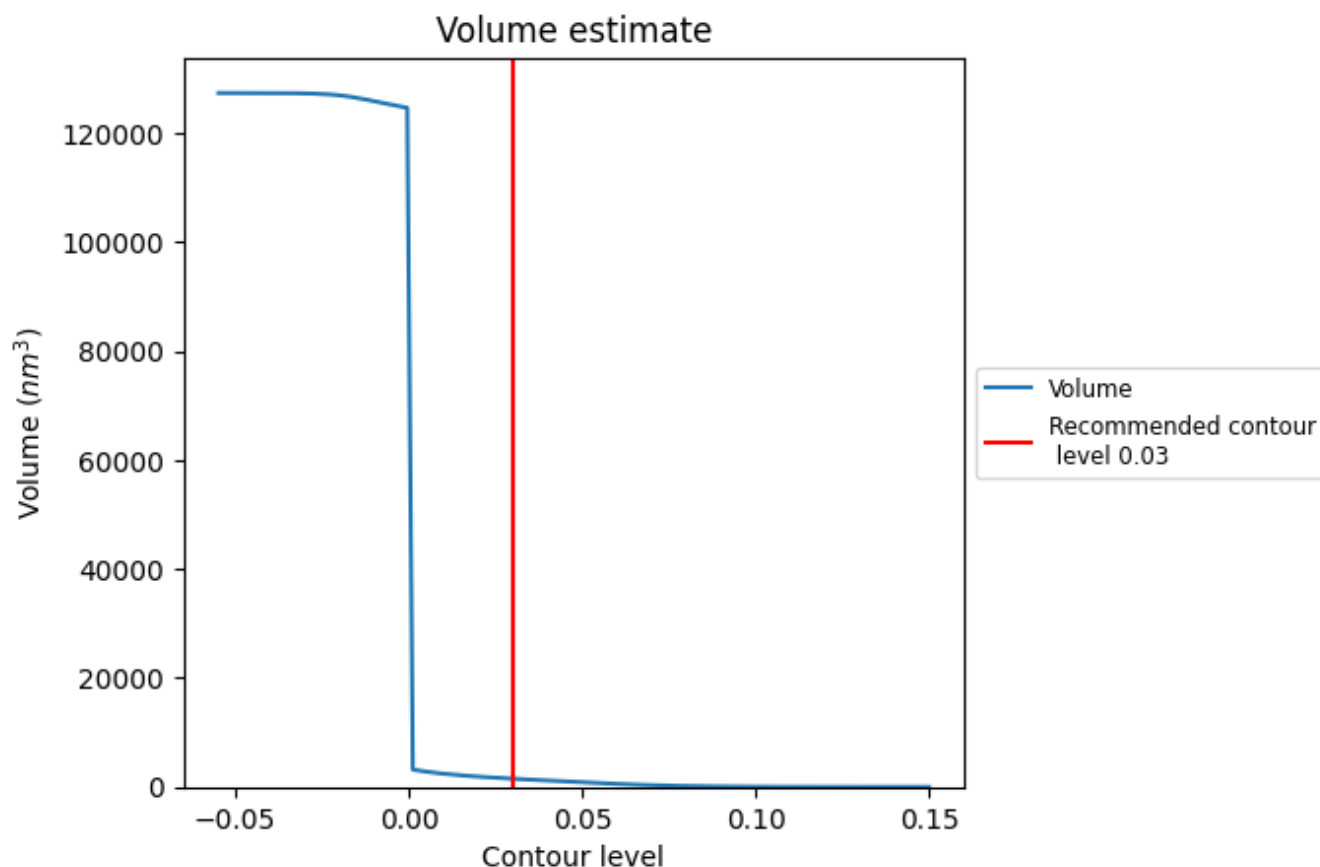
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

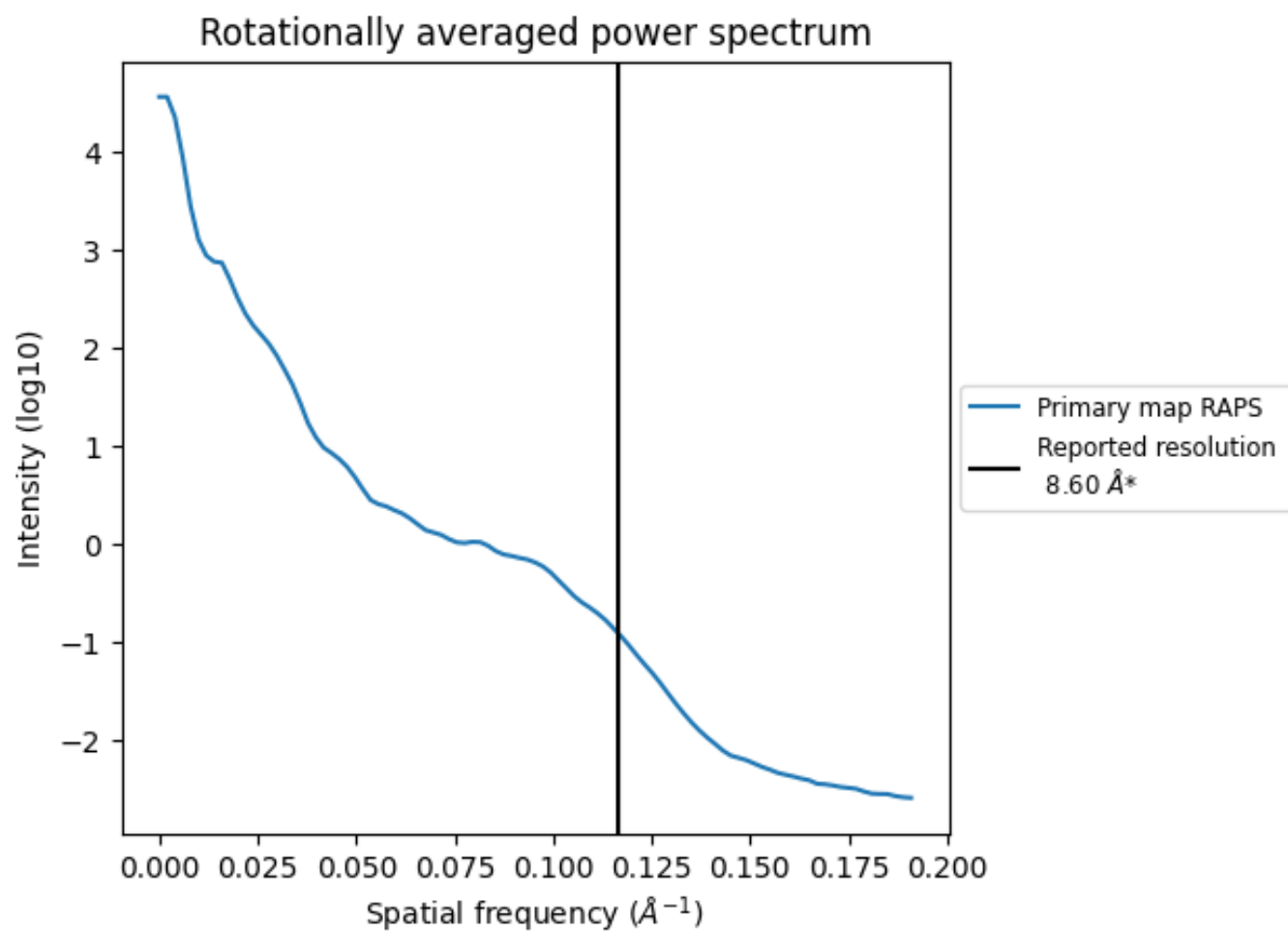
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1510 nm³; this corresponds to an approximate mass of 1364 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 ⓘ

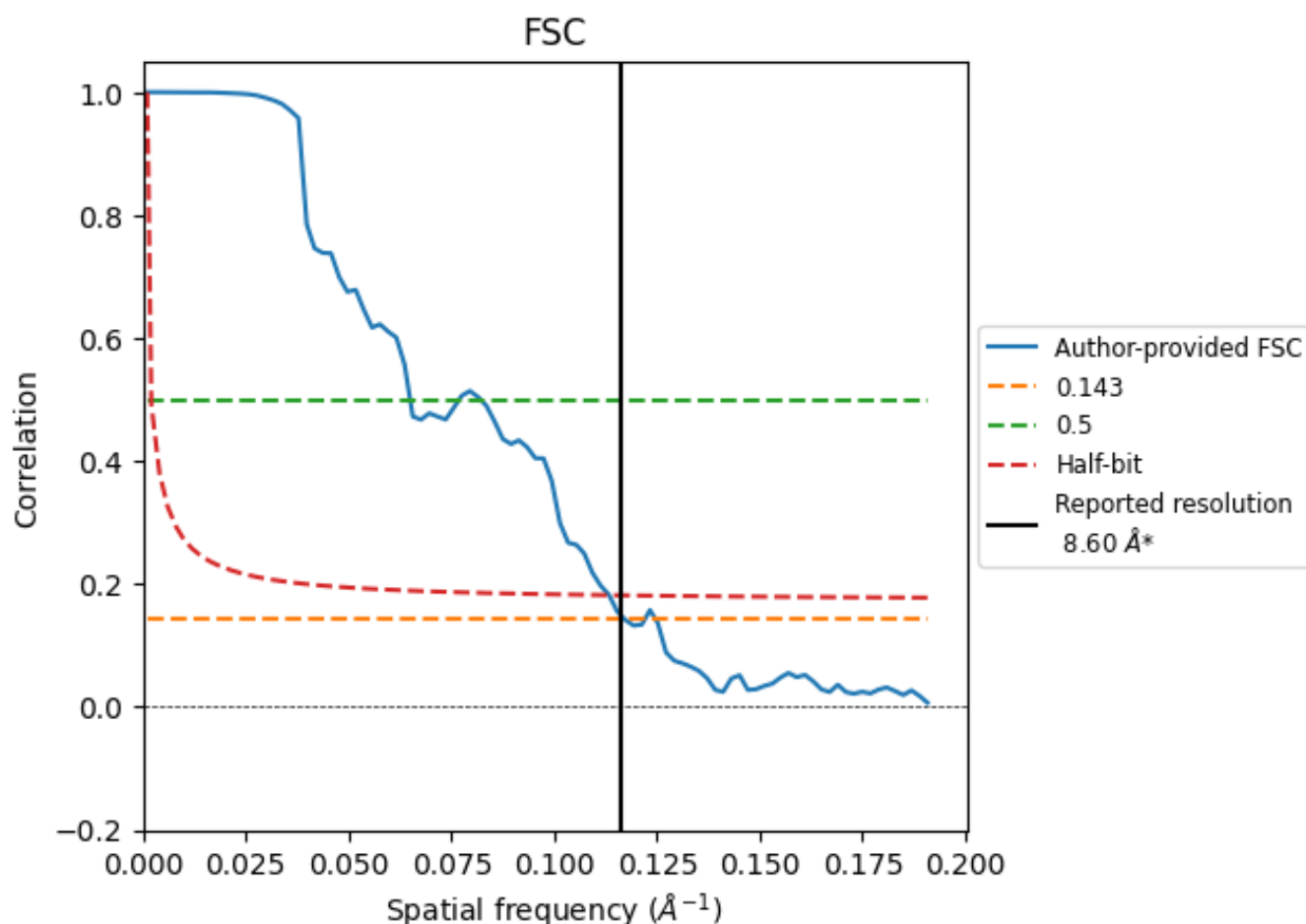


*Reported resolution corresponds to spatial frequency of 0.116 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.116 Å⁻¹

8.2 Resolution estimates [i](#)

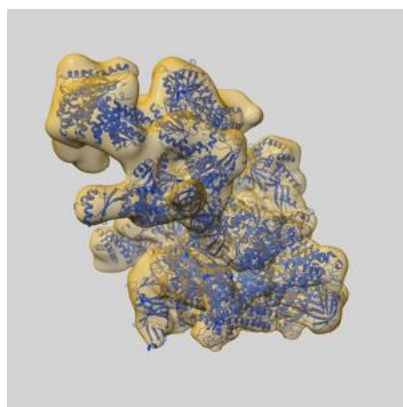
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.60	-	-
Author-provided FSC curve	8.55	15.38	8.82
Unmasked-calculated*	-	-	-

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

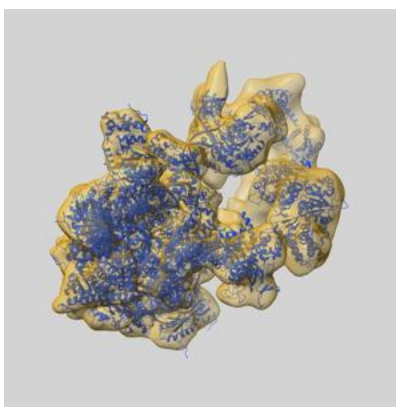
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8132 and PDB model 5IY7. Per-residue inclusion information can be found in section [3](#) on page [9](#).

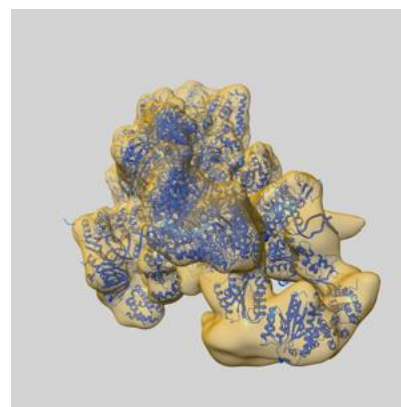
9.1 Map-model overlay [i](#)



X



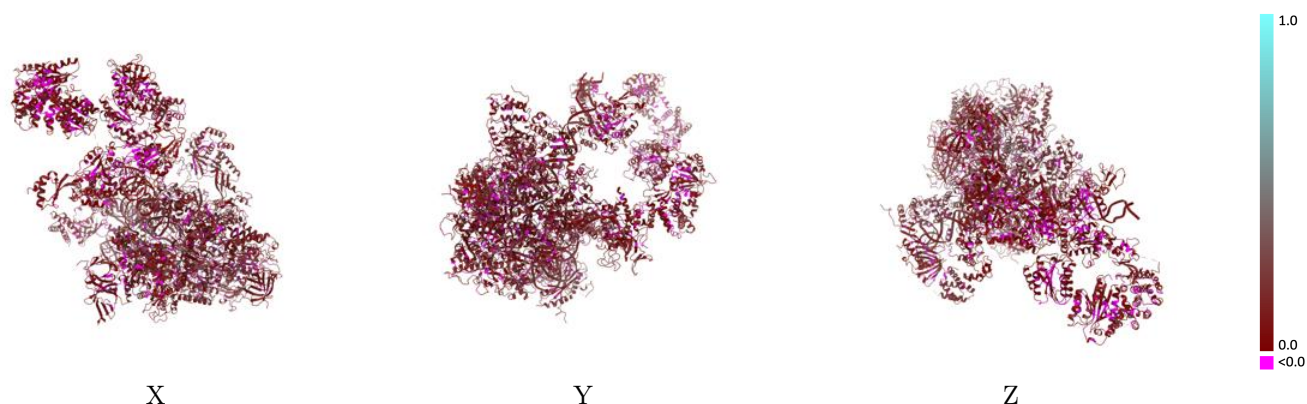
Y



Z

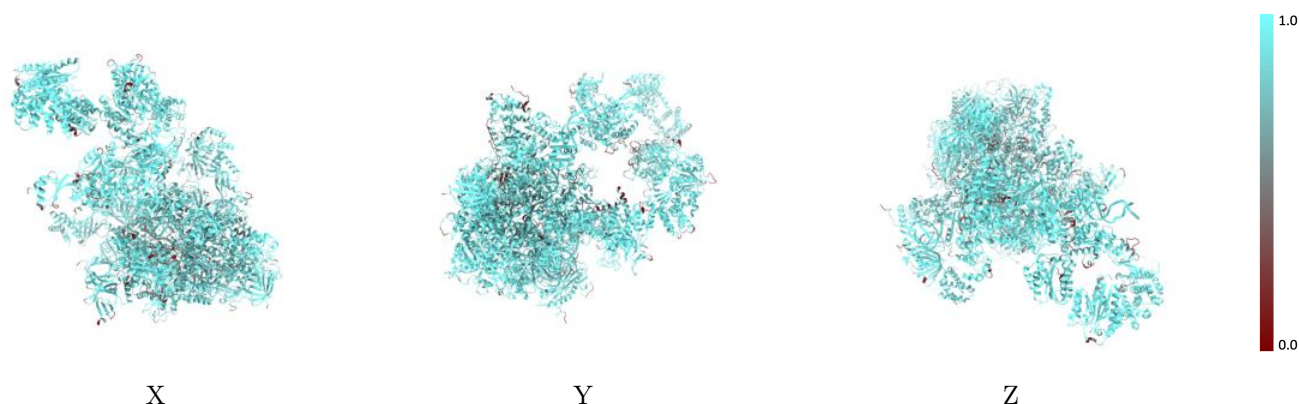
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



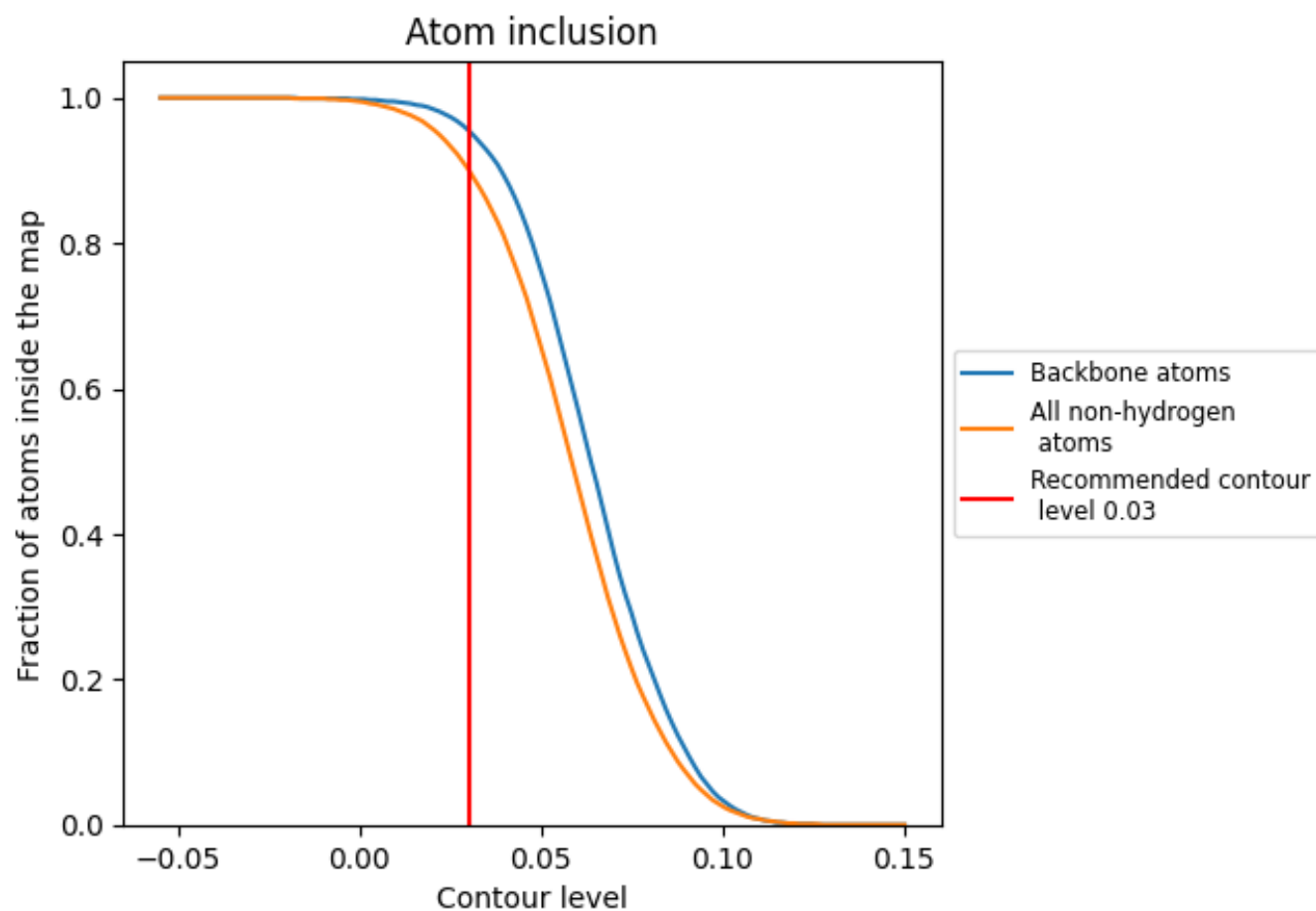
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9010	 0.1050
0	 0.9280	 0.0520
1	 0.8260	 0.0650
2	 0.9350	 0.0720
3	 0.9520	 0.0610
A	 0.8900	 0.1260
B	 0.8750	 0.1170
C	 0.9330	 0.1170
D	 0.8990	 0.1120
E	 0.9240	 0.1250
F	 0.8040	 0.1300
G	 0.9370	 0.1050
H	 0.9380	 0.1170
I	 0.8730	 0.0950
J	 0.9650	 0.1190
K	 0.9420	 0.1420
L	 0.9460	 0.1240
M	 0.8860	 0.1170
N	 0.9040	 0.0930
O	 0.9590	 0.0820
P	 0.9660	 0.1140
Q	 0.9340	 0.1030
R	 0.8850	 0.1030
S	 0.8970	 0.0720
T	 0.8800	 0.1030
U	 0.6410	 0.0780
V	 0.9220	 0.0640
W	 0.9130	 0.0670
X	 0.9430	 0.1560
Y	 0.9160	 0.1590

