



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 08:32 AM UTC

PDB ID : 7EDX / pdb_00007edx
EMDB ID : EMD-31075
Title : p53-bound TFIIID-based core PIC on HDM2 promoter
Authors : Chen, X.; Qi, Y.; Hou, H.; Wang, X.; Wu, Z.; Li, J.; Xu, Y.
Deposited on : 2021-03-17
Resolution : 4.50 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:

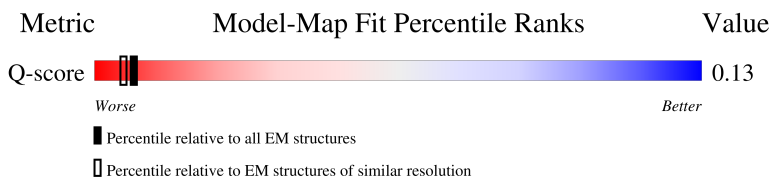
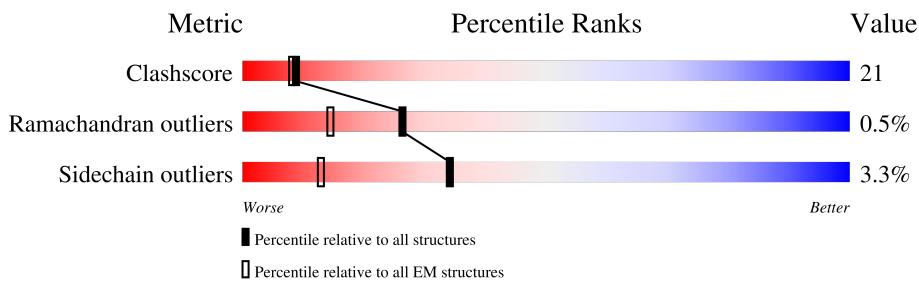
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.50 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	2937 (4.00 - 5.00)

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	1872	<p>8% (upper red bar), 21% (red), 9% (orange), 68% (grey)</p>
2	B	1199	<p>68% (green), 12% (yellow), 20% (grey)</p>
3	D	1085	<p>9% (green), 5% (yellow), 85% (grey)</p>
3	d	1085	<p>10% (red), 12% (orange), 85% (grey)</p>

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Mol	Chain	Length	Quality of chain
4	E	800	53% 15% 32%
4	e	800	46% 59% 8% 33%
5	F	677	9% 35% 20% 40%
5	f	677	19% 46% 12% 40%
6	G	349	8% 28% 12% 58%
7	H	310	6% 42% 24% 33%
8	I	264	30% 16% 55%
8	i	264	36% 40% 6% 54%
9	J	218	28% 13% 59%
9	j	218	28% 39% 5% 56%
10	L	161	27% 20% 53%
10	l	161	57% 50% 16% 34%
11	O	109	28% 47% 10% 11%
12	P	339	36% 13% 48%
13	Q	376	14% 16% 68%
14	R	316	50% 26% 22%
15	S	517	15% 10% 74%
16	T	249	29% 16% 55%
17	X	84	10% 54% 37% 8%
18	Y	84	14% 64% 27% 8%
19	c	929	8% 12% 86%
20	k	211	40% 43% 54%
21	m	124	70% 60% 9% 30%
22	o	1970	49% 23% 28%
23	p	1174	72% 24% 4% 2%

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Mol	Chain	Length	Quality of chain
24	q	275	
25	r	142	
26	s	210	
27	t	127	
28	v	150	
29	w	125	
30	x	67	
31	y	117	
32	z	58	
33	u	172	

2 Entry composition [i](#)

There are 35 unique types of molecules in this entry. The entry contains 81790 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 Transcription initiation factor TFIID subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	602	Total	C	N	O	S	0	0
			4927	3142	858	899	28		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	963	Total	C	N	O	S	0	0
			7796	5011	1315	1412	58		

- Molecule 3 is a protein called Transcription initiation factor TFIID subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	165	Total	C	N	O	S	0	0
			1377	858	257	258	4		
3	d	158	Total	C	N	O	S	0	0
			1307	814	238	252	3		

- Molecule 4 is a protein called Transcription initiation factor TFIID subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	546	Total	C	N	O	S	0	0
			4364	2766	757	820	21		
4	e	539	Total	C	N	O	S	0	0
			4327	2746	748	814	19		

- Molecule 5 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	404	Total	C	N	O	S	0	0
			3081	1954	537	572	18		
5	f	403	Total	C	N	O	S	0	0
			3081	1954	533	576	18		

- Molecule 6 is a protein called Transcription initiation factor TFIID subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	145	1180	748	217	211	4	0	0

- Molecule 7 is a protein called Transcription initiation factor TFIID subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	H	209	1633	1034	283	311	5	0	0

- Molecule 8 is a protein called Transcription initiation factor TFIID subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	I	120	959	610	166	177	6	0	0
8	i	121	967	615	167	178	7	0	0

- Molecule 9 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	89	709	457	114	134	4	0	0
9	j	95	759	488	124	143	4	0	0

- Molecule 10 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	L	76	622	388	109	122	3	0	0
10	l	107	876	547	158	166	5	0	0

- Molecule 11 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	O	97	771	491	133	145	2	0	0

- Molecule 12 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	P	177	1412	918	249	238	7	0	0

- Molecule 13 is a protein called Transcription initiation factor IIA subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	Q	122	996	623	162	207	4	0	0

- Molecule 14 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	R	248	1913	1200	338	358	17	0	0

- Molecule 15 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	S	134	1101	698	199	202	2	0	0

- Molecule 16 is a protein called General transcription factor IIF subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	T	113	876	545	160	169	2	0	0

- Molecule 17 is a DNA chain called DNA (84-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
17	X	77	1582	752	283	470	77	0	0

- Molecule 18 is a DNA chain called DNA (84-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
18	Y	77	1575	747	297	454	77	0	0

- Molecule 19 is a protein called Transcription initiation factor TFIID subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	c	127	1011	638	174	193	6	0	0

- Molecule 20 is a protein called Transcription initiation factor TFIID subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	k	98	785	499	142	139	5	0	0

- Molecule 21 is a protein called Transcription initiation factor TFIID subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	m	87	724	456	131	131	6	0	0

- Molecule 22 is a protein called RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	o	1427	11308	7114	2023	2099	72	0	0

- Molecule 23 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	p	1134	9062	5732	1595	1671	64	0	0

- Molecule 24 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	q	257	2059	1294	351	408	6	0	0

- Molecule 25 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	r	128	1005	632	172	197	4	0	0

- Molecule 26 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	s	209	1720	1089	300	323	8	0	0

- Molecule 27 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	t	79	635	406	108	116	5	0	0

- Molecule 28 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	v	148	1186	750	194	237	5	0	0

- Molecule 29 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	w	114	927	571	166	179	11	0	0

- Molecule 30 is a protein called RPB10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	x	64	507	328	86	87	6	0	0

- Molecule 31 is a protein called RNA_pol_L_2 domain-containing protein.

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

- Molecule 32 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	z	44	372	231	72	63	6	0	0

- Molecule 33 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	u	171	Total	C	N	O	S	0	0
			1351	875	219	249	8		

- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
34	R	1	Total	Zn	0
			1	1	
34	o	2	Total	Zn	0
			2	2	
34	p	1	Total	Zn	0
			1	1	
34	q	1	Total	Zn	0
			1	1	
34	w	2	Total	Zn	0
			2	2	
34	x	1	Total	Zn	0
			1	1	
34	z	1	Total	Zn	0
			1	1	

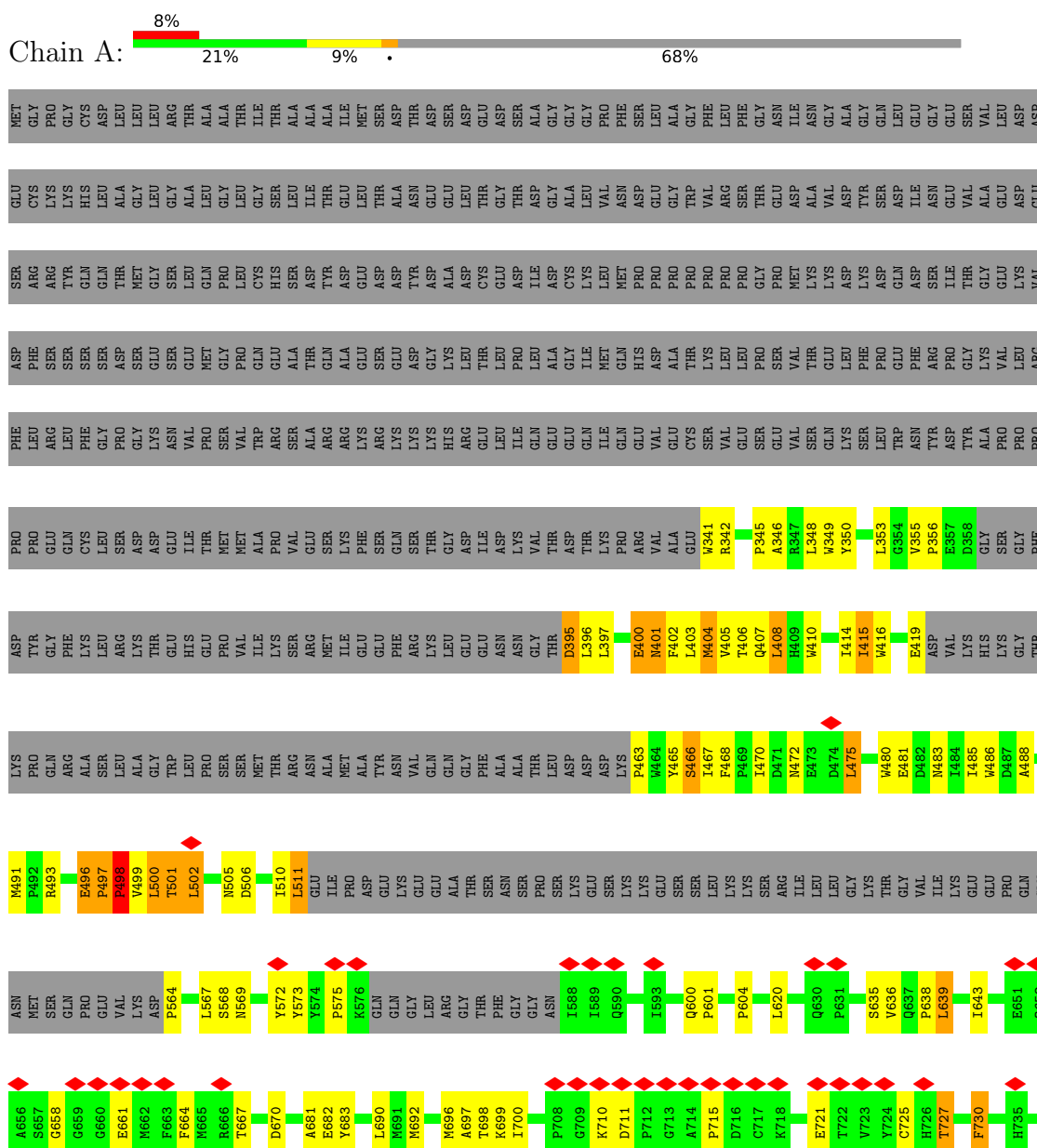
- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

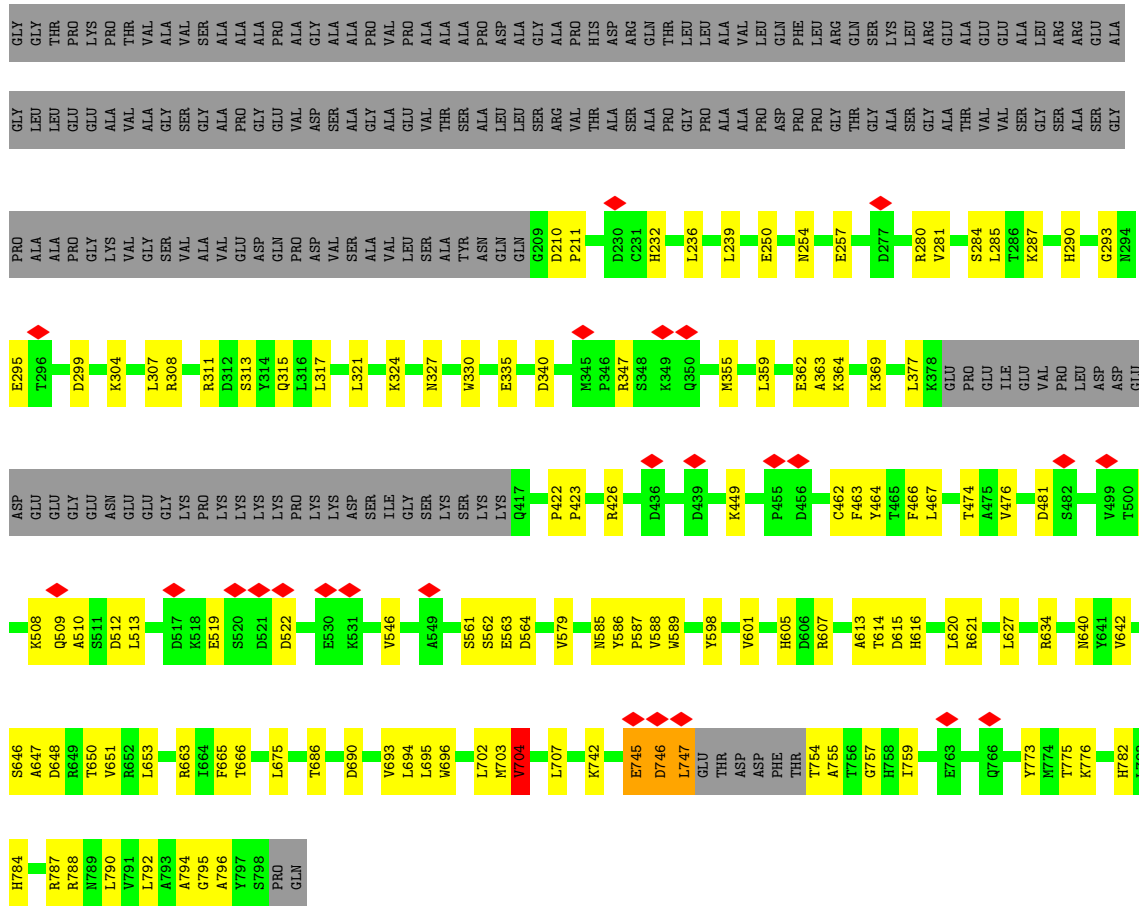
Mol	Chain	Residues	Atoms		AltConf
35	o	1	Total	Mg	0
			1	1	

3 Residue-property plots

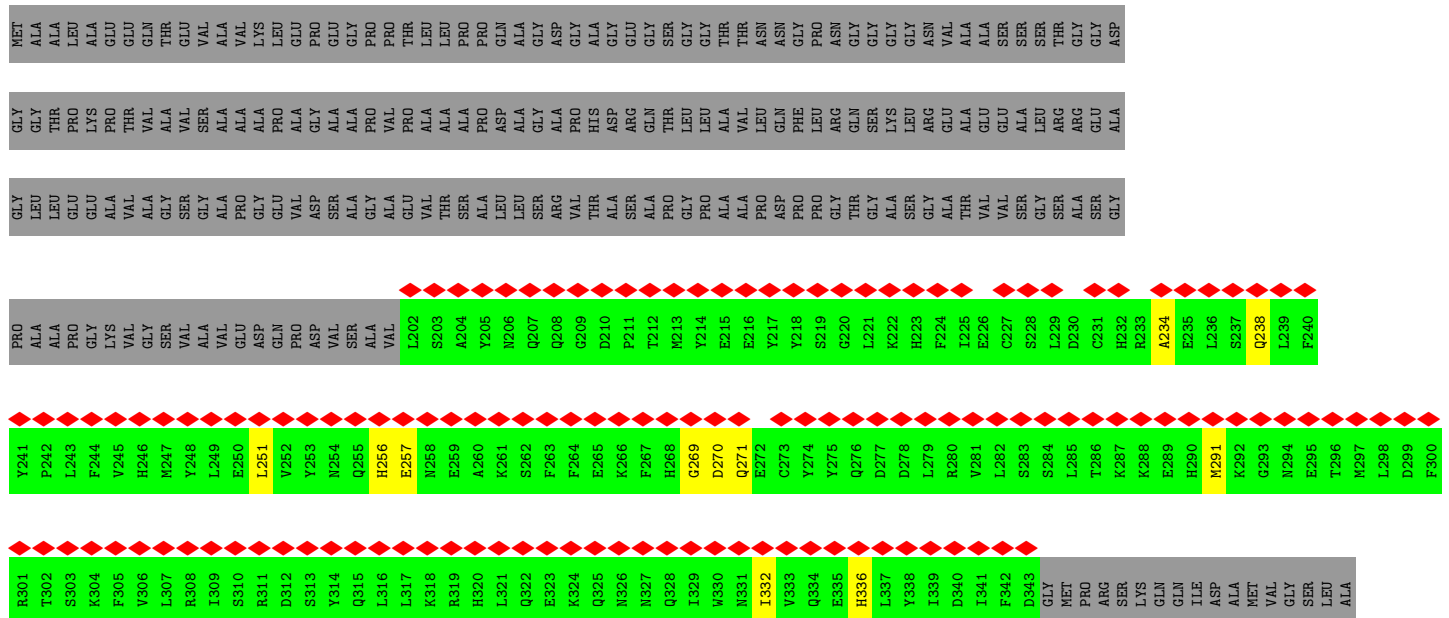
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

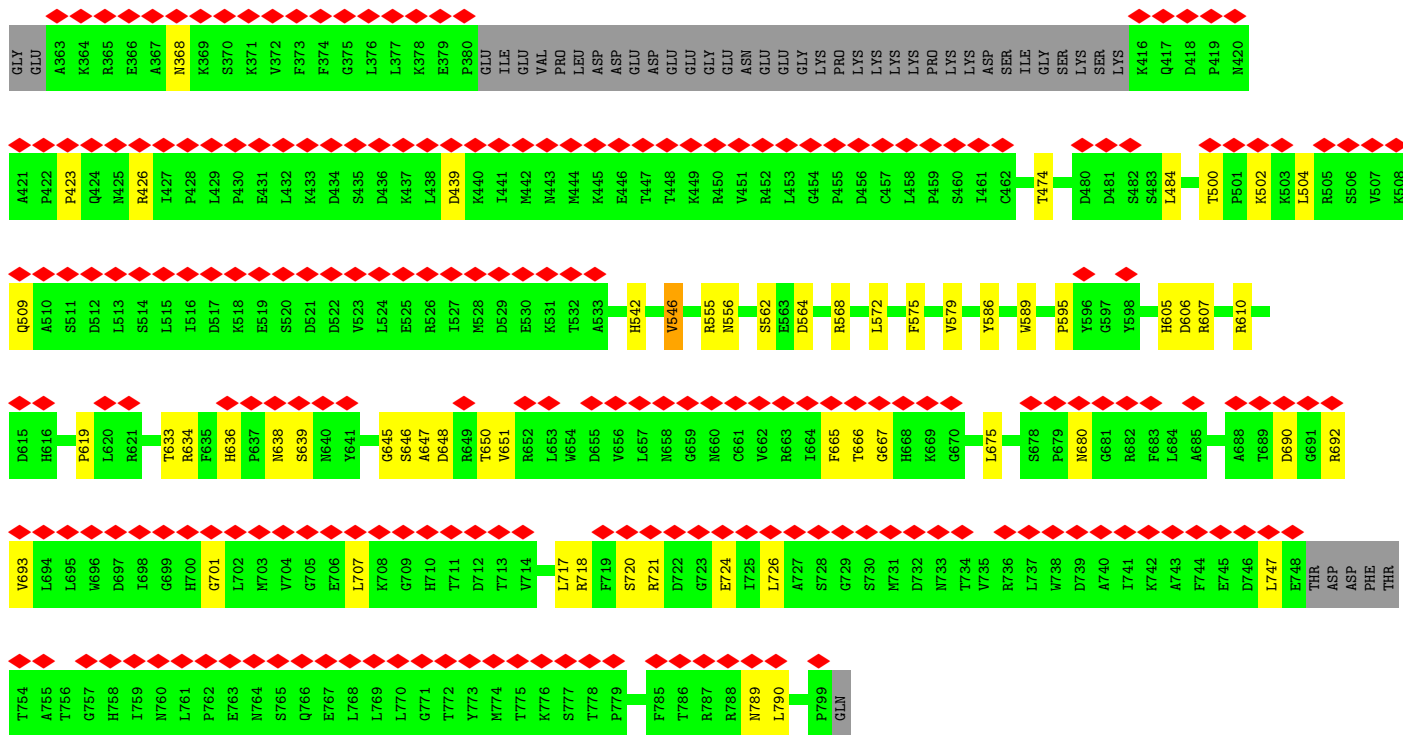
- Molecule 1: Transcription initiation factor TFIID subunit 1



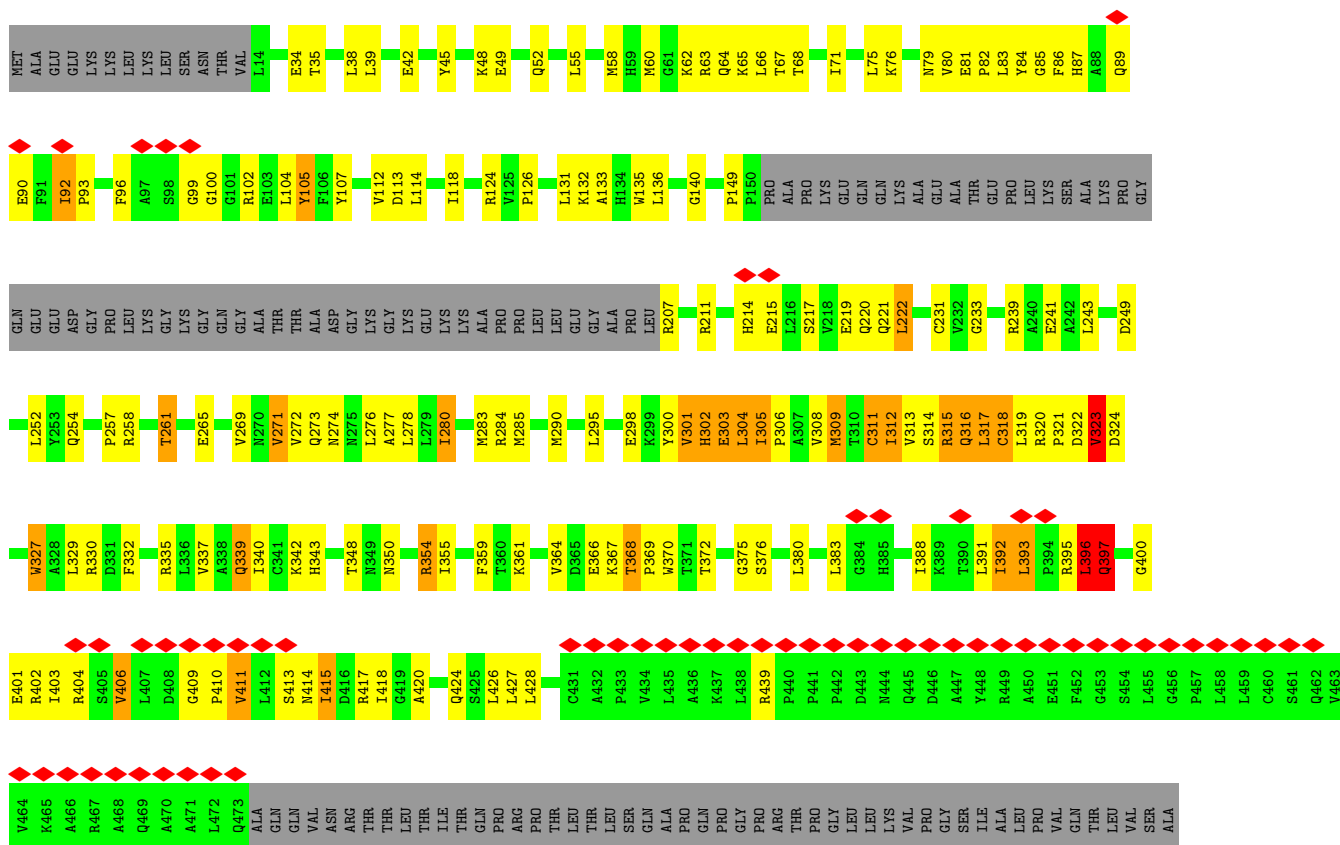
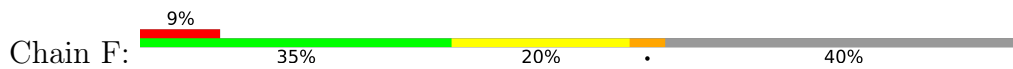


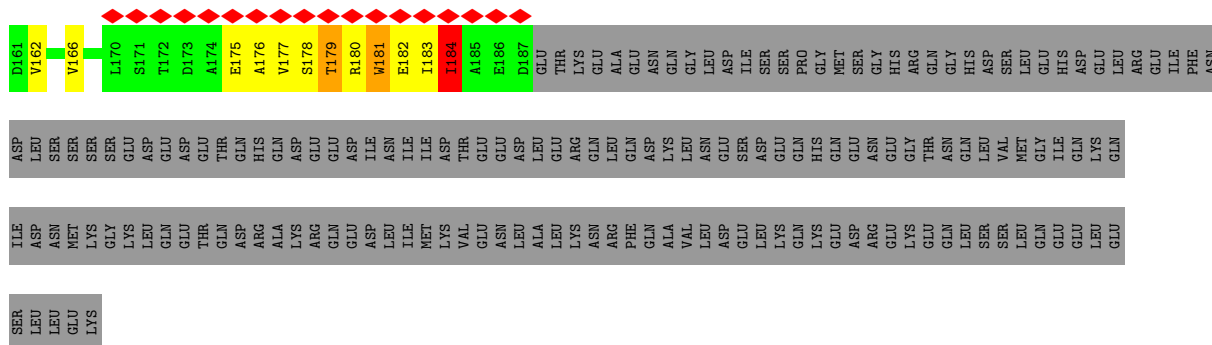
• Molecule 4: Transcription initiation factor TFIID subunit 5



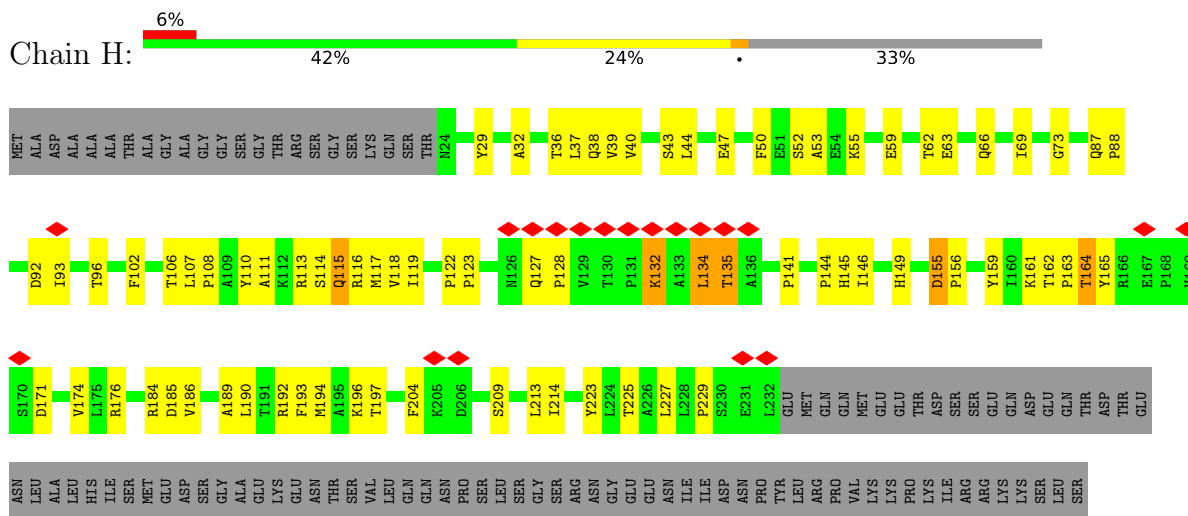


● Molecule 5: Transcription initiation factor TFIID subunit 6

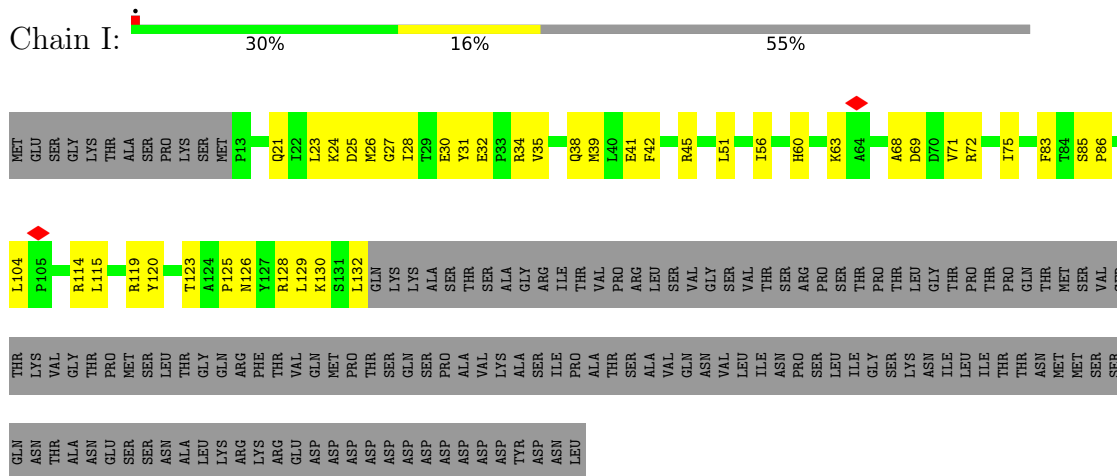




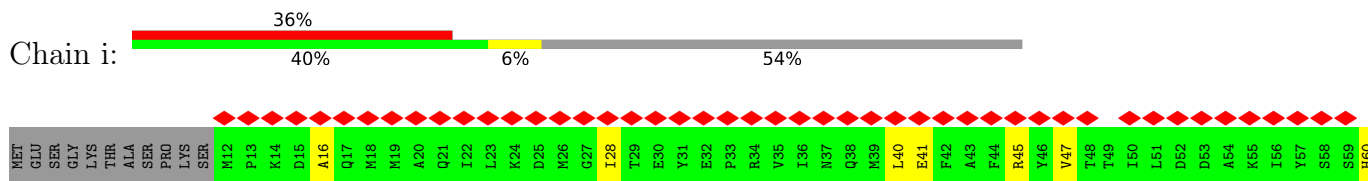
• Molecule 7: Transcription initiation factor TFIID subunit 8

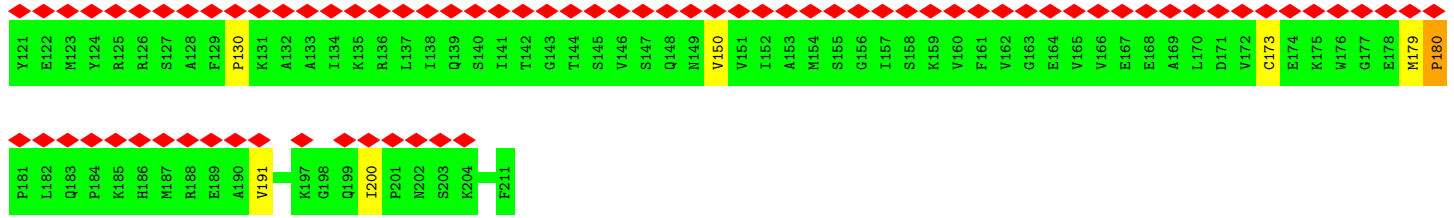


• Molecule 8: Transcription initiation factor TFIID subunit 9



• Molecule 8: Transcription initiation factor TFIID subunit 9

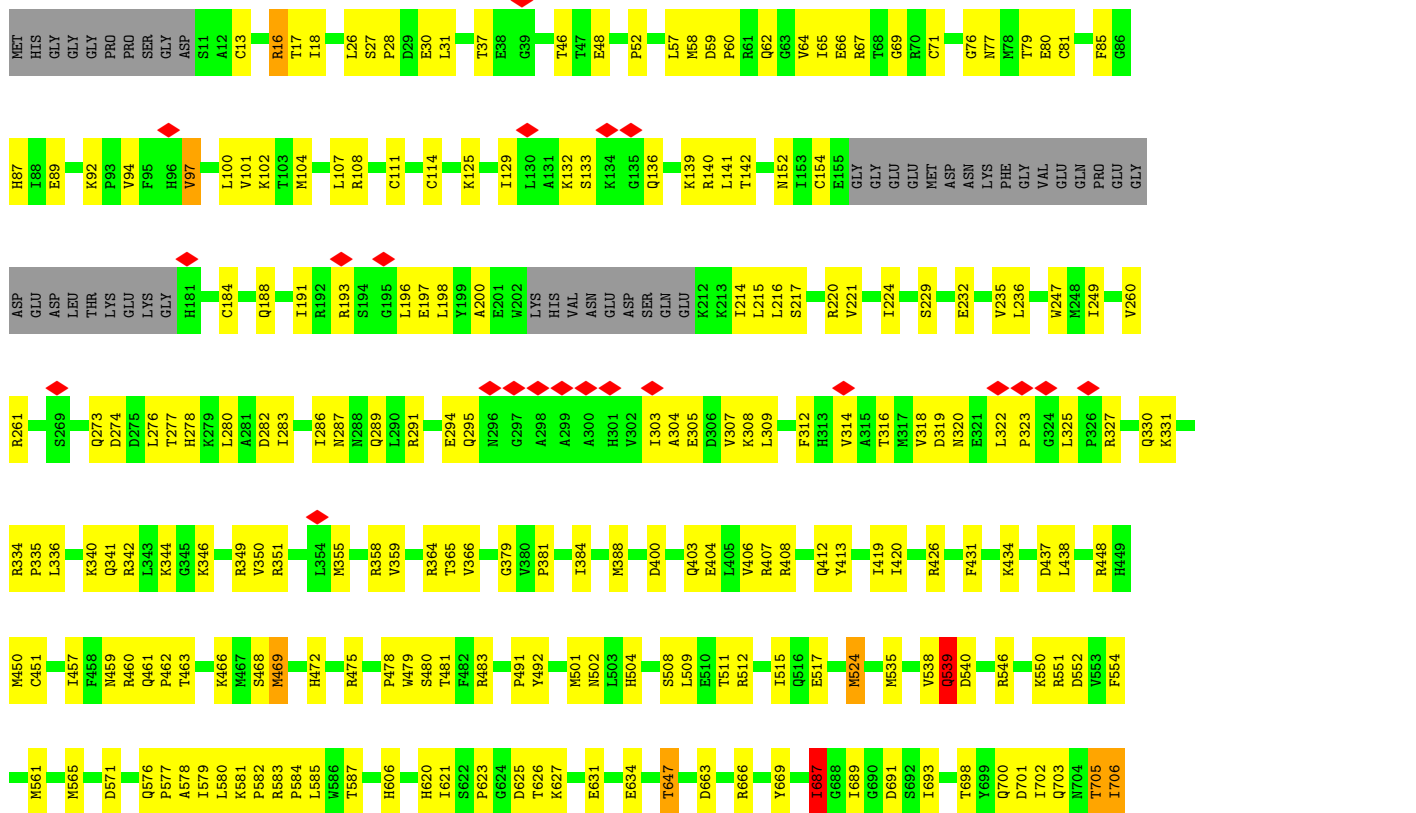


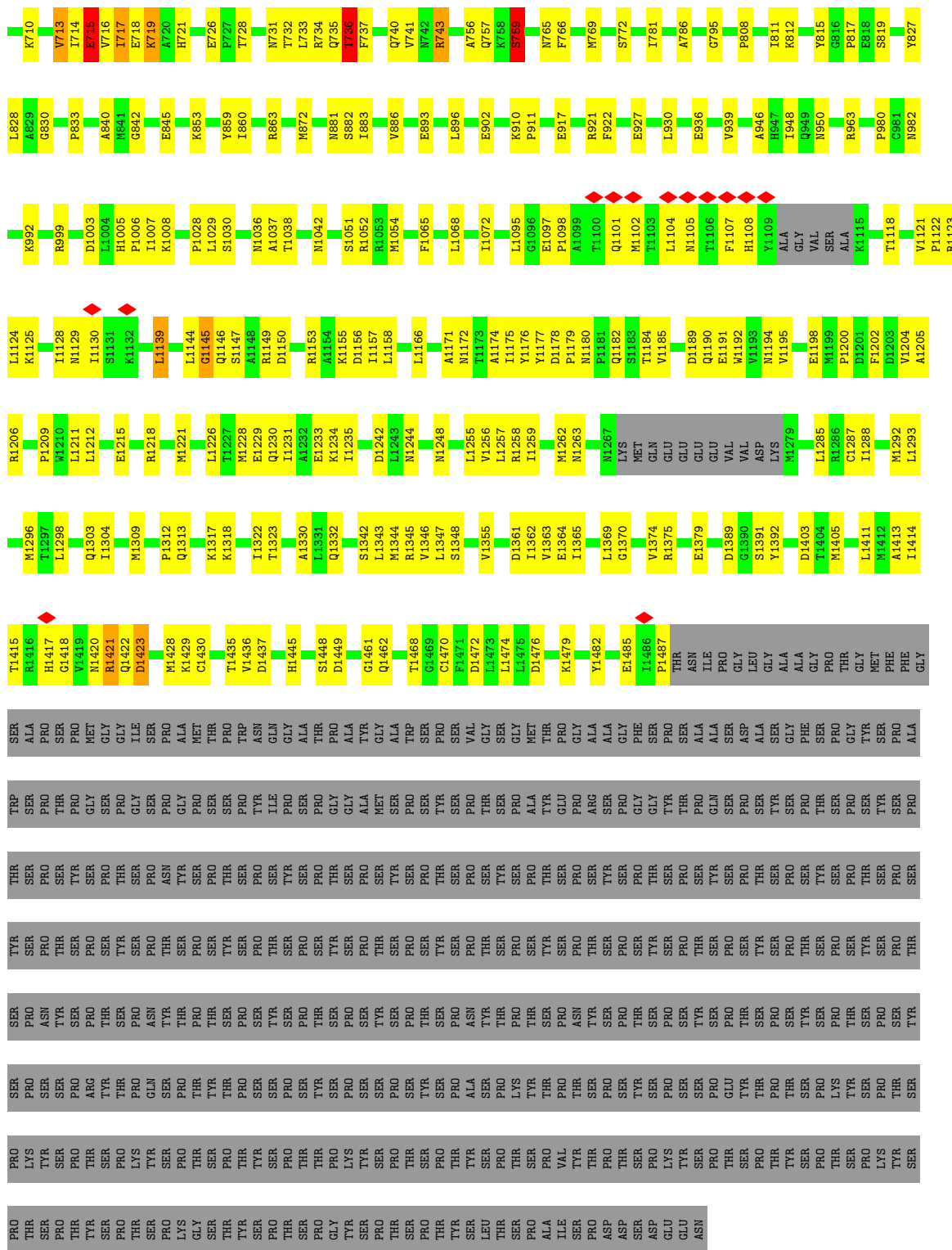


• Molecule 21: Transcription initiation factor TFIID subunit 13



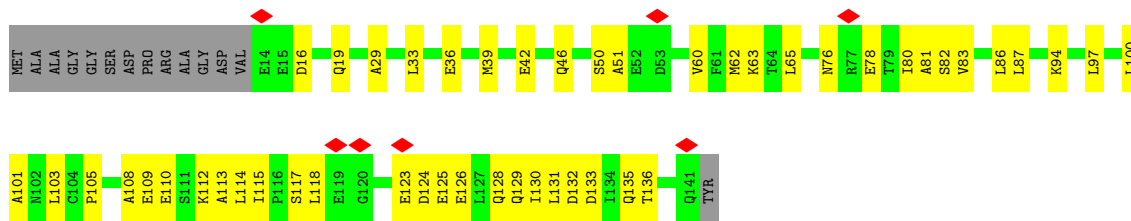
• Molecule 22: RPB1



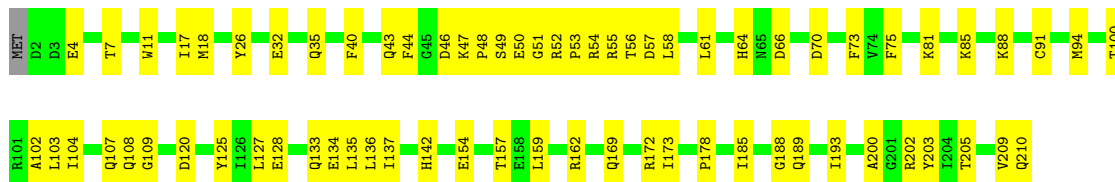


• Molecule 23: DNA-directed RNA polymerase subunit beta

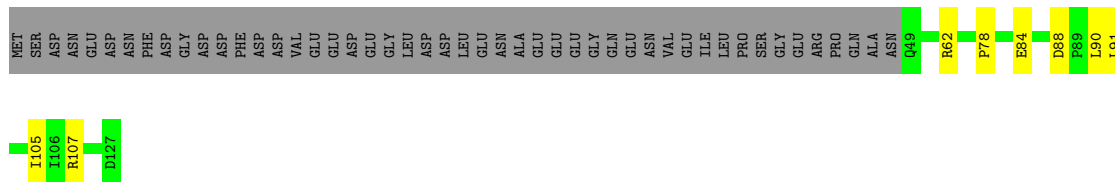




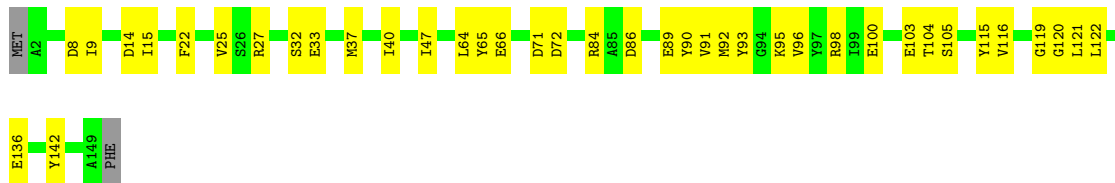
• Molecule 26: DNA-directed RNA polymerase II subunit E



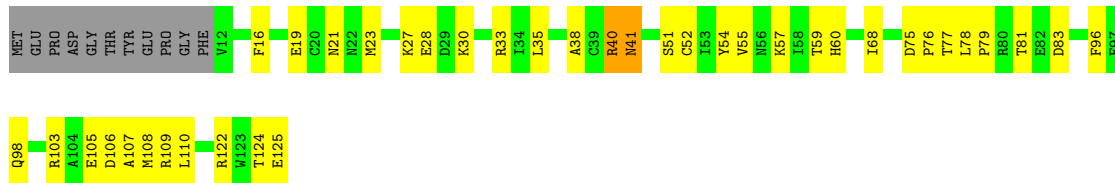
• Molecule 27: DNA-directed RNA polymerase II subunit F



• Molecule 28: DNA-directed RNA polymerases I, II, and III subunit RPABC3

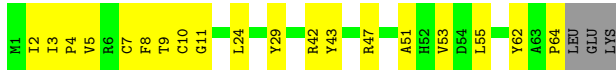


• Molecule 29: DNA-directed RNA polymerase II subunit RPB9




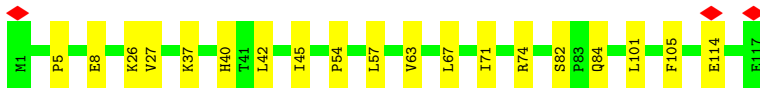
• Molecule 30: RPB10

Chain x:  67% 28%



- Molecule 31: RNA_pol_L_2 domain-containing protein

Chain y:  84% 16%



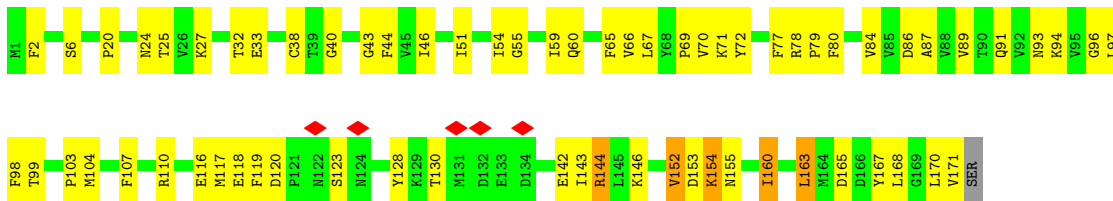
- Molecule 32: RPB12

Chain z:  47% 29% 24%



- Molecule 33: DNA-directed RNA polymerase II subunit RPB7

Chain u:  60% 36%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	99580	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.612	Depositor
Minimum map value	-0.877	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.15	Depositor
Map size (\AA)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.66	0/5046	0.96	10/6810 (0.1%)
2	B	0.47	1/7993 (0.0%)	0.68	5/10836 (0.0%)
3	D	0.72	1/1391 (0.1%)	0.96	2/1859 (0.1%)
3	d	0.26	0/1321	0.48	0/1772
4	E	0.33	0/4469	0.58	3/6050 (0.0%)
4	e	0.28	0/4433	0.53	0/6004
5	F	0.71	0/3139	1.11	9/4264 (0.2%)
5	f	0.46	0/3140	0.80	6/4268 (0.1%)
6	G	0.72	0/1199	1.05	3/1612 (0.2%)
7	H	0.50	0/1673	0.76	3/2285 (0.1%)
8	I	0.21	0/981	0.41	0/1332
8	i	0.21	0/989	0.40	0/1343
9	J	0.28	0/724	0.50	0/982
9	j	0.22	0/775	0.44	0/1049
10	L	0.41	0/630	0.72	0/852
10	l	0.32	0/888	0.61	0/1194
11	O	0.79	1/781 (0.1%)	1.19	10/1061 (0.9%)
12	P	0.94	0/1438	1.30	6/1935 (0.3%)
13	Q	0.60	0/1013	1.12	9/1366 (0.7%)
14	R	0.44	0/1941	1.01	5/2622 (0.2%)
15	S	0.46	0/1130	0.86	1/1528 (0.1%)
16	T	0.36	0/887	0.89	2/1193 (0.2%)
17	X	0.38	0/1772	0.88	2/2735 (0.1%)
18	Y	0.37	0/1768	0.85	0/2724
19	c	0.48	0/1035	0.67	0/1406
20	k	0.29	0/799	0.53	1/1070 (0.1%)
21	m	0.31	0/733	0.55	0/977
22	o	0.46	4/11516 (0.0%)	0.66	10/15548 (0.1%)
23	p	0.39	0/9243	0.59	1/12475 (0.0%)
24	q	0.32	0/2102	0.44	0/2857
25	r	0.17	0/1019	0.45	0/1374
26	s	0.22	0/1751	0.47	0/2366

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	t	0.29	0/645	0.47	0/871
28	v	0.28	0/1207	0.47	0/1628
29	w	0.27	0/948	0.50	1/1284 (0.1%)
30	x	0.36	0/516	0.44	0/696
31	y	0.31	0/956	0.47	0/1294
32	z	0.27	0/377	0.43	0/500
33	u	0.43	0/1382	0.82	3/1874 (0.2%)
All	All	0.46	7/83750 (0.0%)	0.74	92/113896 (0.1%)

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
23	p	0	1
All	All	0	2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	o	715	GLU	CA-C	-6.82	1.44	1.52
3	D	1001	GLN	C-O	6.57	1.32	1.24
22	o	702	ILE	CA-CB	-6.34	1.46	1.54
2	B	61	ASN	C-O	-6.19	1.18	1.24
22	o	706	ILE	CA-CB	-5.56	1.47	1.54

The worst 5 of 92 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	P	203	ARG	CB-CA-C	9.62	130.65	111.22
14	R	112	ARG	N-CA-C	-9.21	101.24	111.28
5	f	149	PRO	O-C-N	9.21	125.55	121.31
12	P	202	MET	CA-C-N	-8.50	107.34	123.32
12	P	202	MET	C-N-CA	-8.50	107.34	123.32

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	821	ARG	Peptide
23	p	1000	THR	Mainchain

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	4927	0	4871	304	0
2	B	7796	0	7751	190	0
3	D	1377	0	1399	293	0
3	d	1307	0	1318	38	0
4	E	4364	0	4244	218	0
4	e	4327	0	4197	45	0
5	F	3081	0	3016	333	0
5	f	3081	0	3012	165	0
6	G	1180	0	1235	103	0
7	H	1633	0	1621	258	0
8	I	959	0	969	122	0
8	i	967	0	977	46	0
9	J	709	0	710	120	0
9	j	759	0	759	17	0
10	L	622	0	620	154	0
10	l	876	0	891	96	0
11	O	771	0	764	221	0
12	P	1412	0	1506	58	0
13	Q	996	0	924	182	0
14	R	1913	0	1956	111	0
15	S	1101	0	1065	90	0
16	T	876	0	884	48	0
17	X	1582	0	870	75	0
18	Y	1575	0	862	59	0
19	c	1011	0	975	25	0
20	k	785	0	818	7	0
21	m	724	0	744	11	0
22	o	11308	0	11427	558	0
23	p	9062	0	9107	450	0
24	q	2059	0	2008	117	0
25	r	1005	0	962	55	0
26	s	1720	0	1737	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	t	635	0	665	12	0
28	v	1186	0	1147	73	0
29	w	927	0	859	74	0
30	x	507	0	523	54	0
31	y	937	0	959	23	0
32	z	372	0	379	45	0
33	u	1351	0	1358	93	0
34	R	1	0	0	0	0
34	o	2	0	0	0	0
34	p	1	0	0	0	0
34	q	1	0	0	0	0
34	w	2	0	0	0	0
34	x	1	0	0	0	0
34	z	1	0	0	0	0
35	o	1	0	0	0	0
All	All	81790	0	80089	3399	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 21.

The worst 5 of 3399 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)
4:E:694:LEU:CD1	4:E:703:MET:HE1	1.30	1.61
8:I:60:HIS:CE1	10:L:118:LEU:HD22	1.36	1.61
8:I:60:HIS:CE1	10:L:118:LEU:CD2	1.83	1.60
23:p:1040:GLN:HG2	24:q:203:TRP:CZ2	1.18	1.60
5:F:320:ARG:HD3	5:F:415:ILE:CB	1.21	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	584/1872 (31%)	543 (93%)	32 (6%)	9 (2%)	8	38
2	B	959/1199 (80%)	911 (95%)	48 (5%)	0	100	100
3	D	159/1085 (15%)	147 (92%)	9 (6%)	3 (2%)	6	32
3	d	154/1085 (14%)	150 (97%)	4 (3%)	0	100	100
4	E	540/800 (68%)	505 (94%)	33 (6%)	2 (0%)	30	67
4	e	531/800 (66%)	484 (91%)	47 (9%)	0	100	100
5	F	400/677 (59%)	374 (94%)	18 (4%)	8 (2%)	6	31
5	f	399/677 (59%)	378 (95%)	21 (5%)	0	100	100
6	G	139/349 (40%)	132 (95%)	5 (4%)	2 (1%)	9	39
7	H	207/310 (67%)	189 (91%)	15 (7%)	3 (1%)	9	39
8	I	118/264 (45%)	115 (98%)	3 (2%)	0	100	100
8	i	119/264 (45%)	115 (97%)	4 (3%)	0	100	100
9	J	85/218 (39%)	82 (96%)	3 (4%)	0	100	100
9	j	91/218 (42%)	89 (98%)	2 (2%)	0	100	100
10	L	74/161 (46%)	69 (93%)	5 (7%)	0	100	100
10	l	105/161 (65%)	101 (96%)	4 (4%)	0	100	100
11	O	95/109 (87%)	81 (85%)	10 (10%)	4 (4%)	2	17
12	P	175/339 (52%)	169 (97%)	4 (2%)	2 (1%)	11	45
13	Q	118/376 (31%)	108 (92%)	9 (8%)	1 (1%)	16	53
14	R	244/316 (77%)	235 (96%)	8 (3%)	1 (0%)	30	67
15	S	130/517 (25%)	124 (95%)	4 (3%)	2 (2%)	8	38
16	T	109/249 (44%)	102 (94%)	4 (4%)	3 (3%)	4	24
19	c	125/929 (14%)	116 (93%)	9 (7%)	0	100	100
20	k	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
21	m	85/124 (68%)	79 (93%)	6 (7%)	0	100	100
22	o	1417/1970 (72%)	1305 (92%)	110 (8%)	2 (0%)	48	83
23	p	1128/1174 (96%)	1051 (93%)	75 (7%)	2 (0%)	43	77
24	q	253/275 (92%)	226 (89%)	27 (11%)	0	100	100
25	r	126/142 (89%)	119 (94%)	7 (6%)	0	100	100
26	s	207/210 (99%)	196 (95%)	11 (5%)	0	100	100
27	t	77/127 (61%)	74 (96%)	3 (4%)	0	100	100
28	v	146/150 (97%)	132 (90%)	14 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	w	112/125 (90%)	102 (91%)	9 (8%)	1 (1%)	14	49
30	x	62/67 (92%)	59 (95%)	3 (5%)	0	100	100
31	y	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
32	z	42/58 (72%)	38 (90%)	4 (10%)	0	100	100
33	u	169/172 (98%)	157 (93%)	11 (6%)	1 (1%)	21	58
All	All	9695/17897 (54%)	9057 (93%)	592 (6%)	46 (0%)	26	63

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1000	LEU
1	A	1158	SER
3	D	958	LYS
5	F	323	VAL
5	F	396	LEU

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	536/1665 (32%)	473 (88%)	63 (12%)	5	19
2	B	876/1083 (81%)	861 (98%)	15 (2%)	53	67
3	D	149/815 (18%)	133 (89%)	16 (11%)	6	22
3	d	146/815 (18%)	144 (99%)	2 (1%)	59	71
4	E	478/657 (73%)	475 (99%)	3 (1%)	78	80
4	e	475/657 (72%)	473 (100%)	2 (0%)	84	82
5	F	320/574 (56%)	289 (90%)	31 (10%)	8	25
5	f	322/574 (56%)	310 (96%)	12 (4%)	30	51
6	G	133/322 (41%)	118 (89%)	15 (11%)	5	20
7	H	181/270 (67%)	175 (97%)	6 (3%)	33	55
8	I	106/235 (45%)	106 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	i	107/235 (46%)	107 (100%)	0	100	100
9	J	78/154 (51%)	78 (100%)	0	100	100
9	j	83/154 (54%)	83 (100%)	0	100	100
10	L	71/141 (50%)	71 (100%)	0	100	100
10	l	98/141 (70%)	97 (99%)	1 (1%)	68	76
11	O	84/98 (86%)	72 (86%)	12 (14%)	3	15
12	P	153/293 (52%)	138 (90%)	15 (10%)	7	24
13	Q	111/324 (34%)	100 (90%)	11 (10%)	7	24
14	R	211/268 (79%)	197 (93%)	14 (7%)	15	37
15	S	117/448 (26%)	110 (94%)	7 (6%)	17	39
16	T	94/218 (43%)	93 (99%)	1 (1%)	65	74
19	c	113/833 (14%)	111 (98%)	2 (2%)	51	67
20	k	87/182 (48%)	87 (100%)	0	100	100
21	m	80/106 (76%)	79 (99%)	1 (1%)	61	72
22	o	1257/1748 (72%)	1226 (98%)	31 (2%)	42	62
23	p	993/1027 (97%)	970 (98%)	23 (2%)	44	63
24	q	234/252 (93%)	234 (100%)	0	100	100
25	r	106/126 (84%)	106 (100%)	0	100	100
26	s	191/192 (100%)	191 (100%)	0	100	100
27	t	69/111 (62%)	69 (100%)	0	100	100
28	v	129/131 (98%)	129 (100%)	0	100	100
29	w	103/112 (92%)	102 (99%)	1 (1%)	68	76
30	x	53/56 (95%)	53 (100%)	0	100	100
31	y	106/106 (100%)	106 (100%)	0	100	100
32	z	41/55 (74%)	41 (100%)	0	100	100
33	u	152/153 (99%)	150 (99%)	2 (1%)	61	72
All	All	8643/15331 (56%)	8357 (97%)	286 (3%)	34	55

5 of 286 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	o	67	ARG
22	o	539	GLN

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Mol	Chain	Res	Type
23	p	248	LYS
5	F	63	ARG
4	E	745	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 167 such sidechains are listed below:

Mol	Chain	Res	Type
22	o	289	GLN
23	p	755	GLN
22	o	590	GLN
22	o	1248	ASN
23	p	1117	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 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.

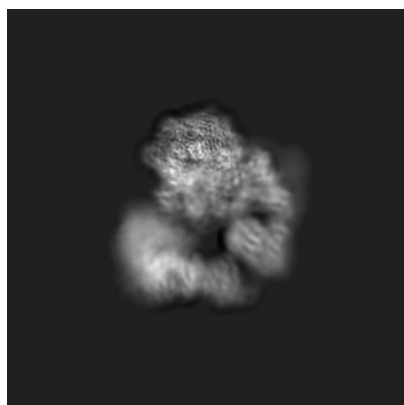
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31075. These allow visual inspection of the internal detail of the map and identification of artifacts.

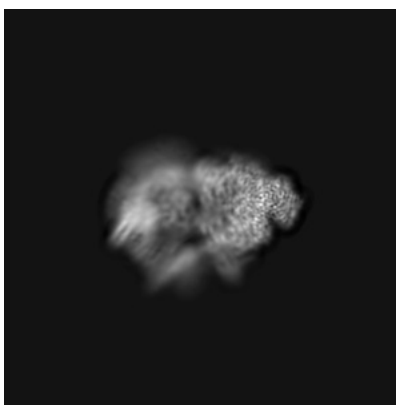
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

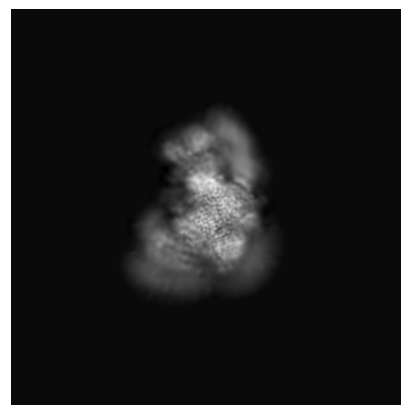
6.1.1 Primary map



X



Y

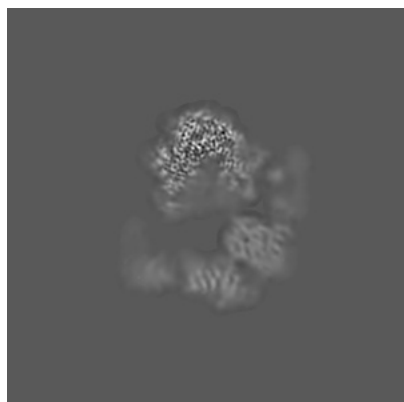


Z

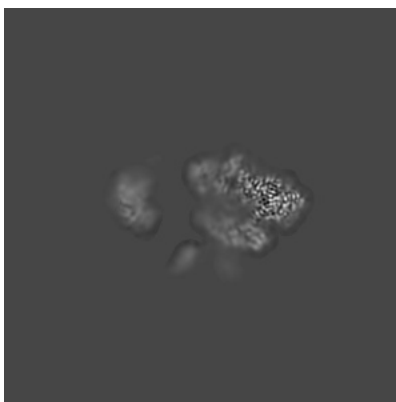
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 240



Y Index: 240

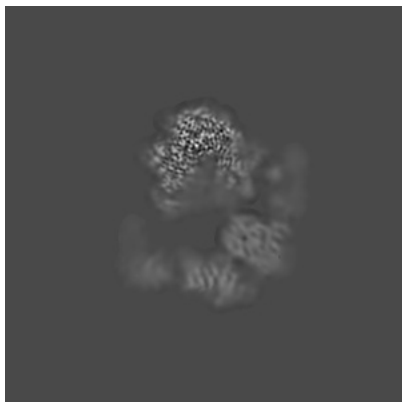


Z Index: 240

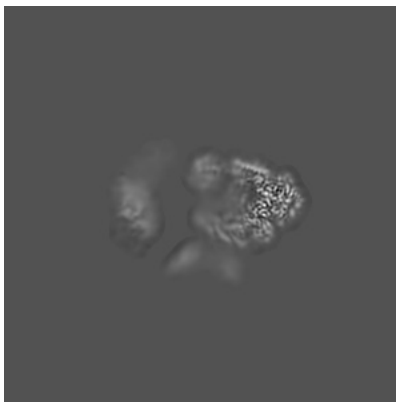
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

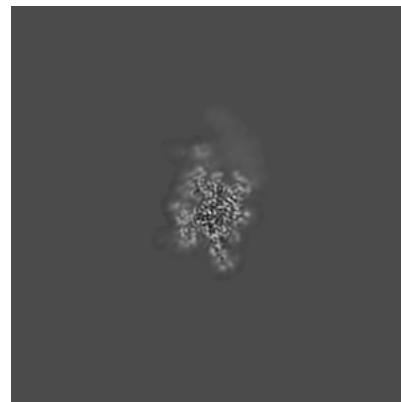
6.3.1 Primary map



X Index: 241



Y Index: 230

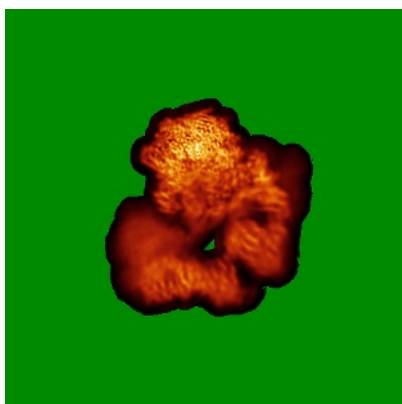


Z Index: 307

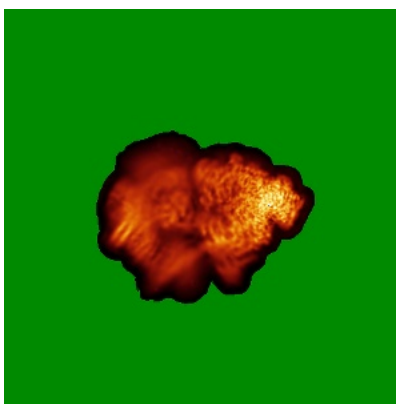
The images above show the largest variance slices of the map in three orthogonal directions.

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

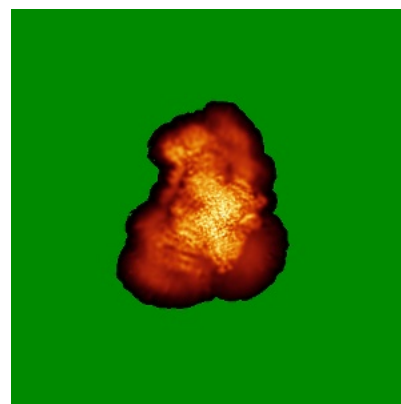
6.4.1 Primary map



X



Y

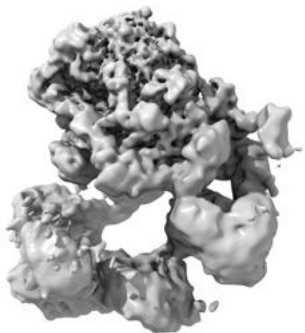


Z

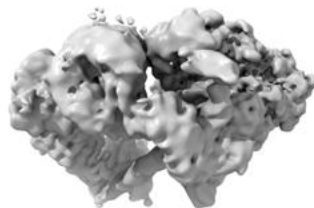
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

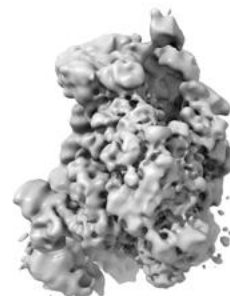
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

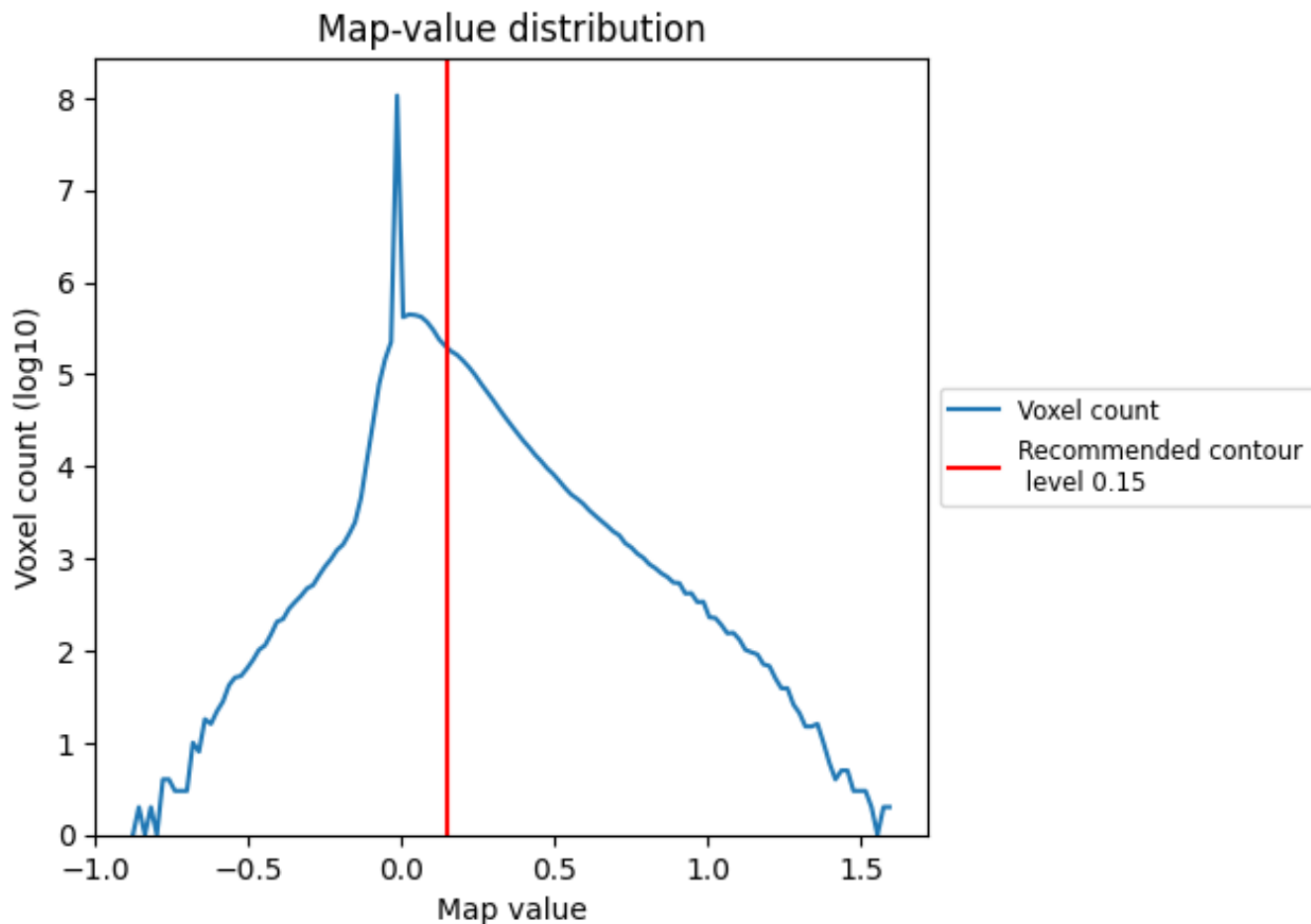
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

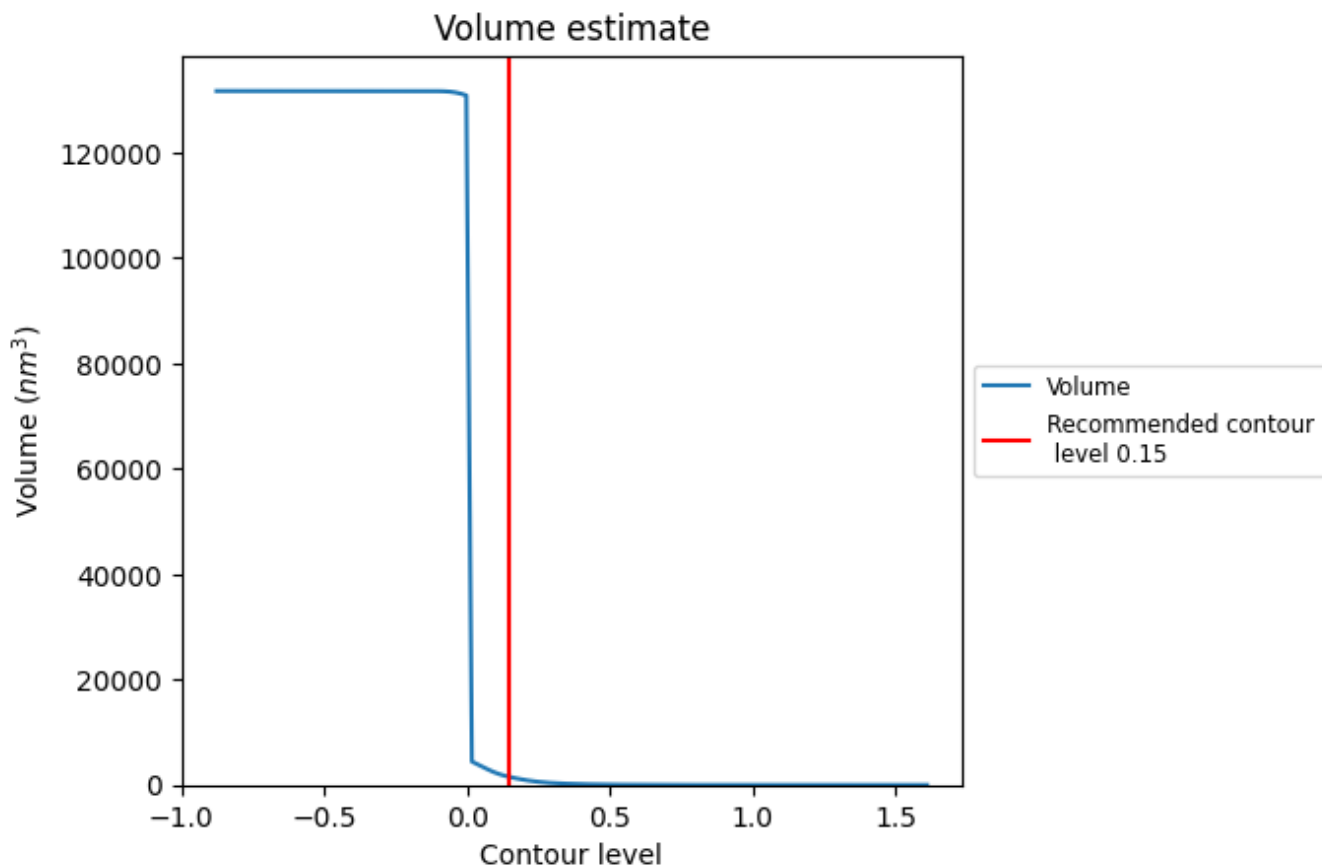
This section contains the results of statistical analysis of the map.

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.

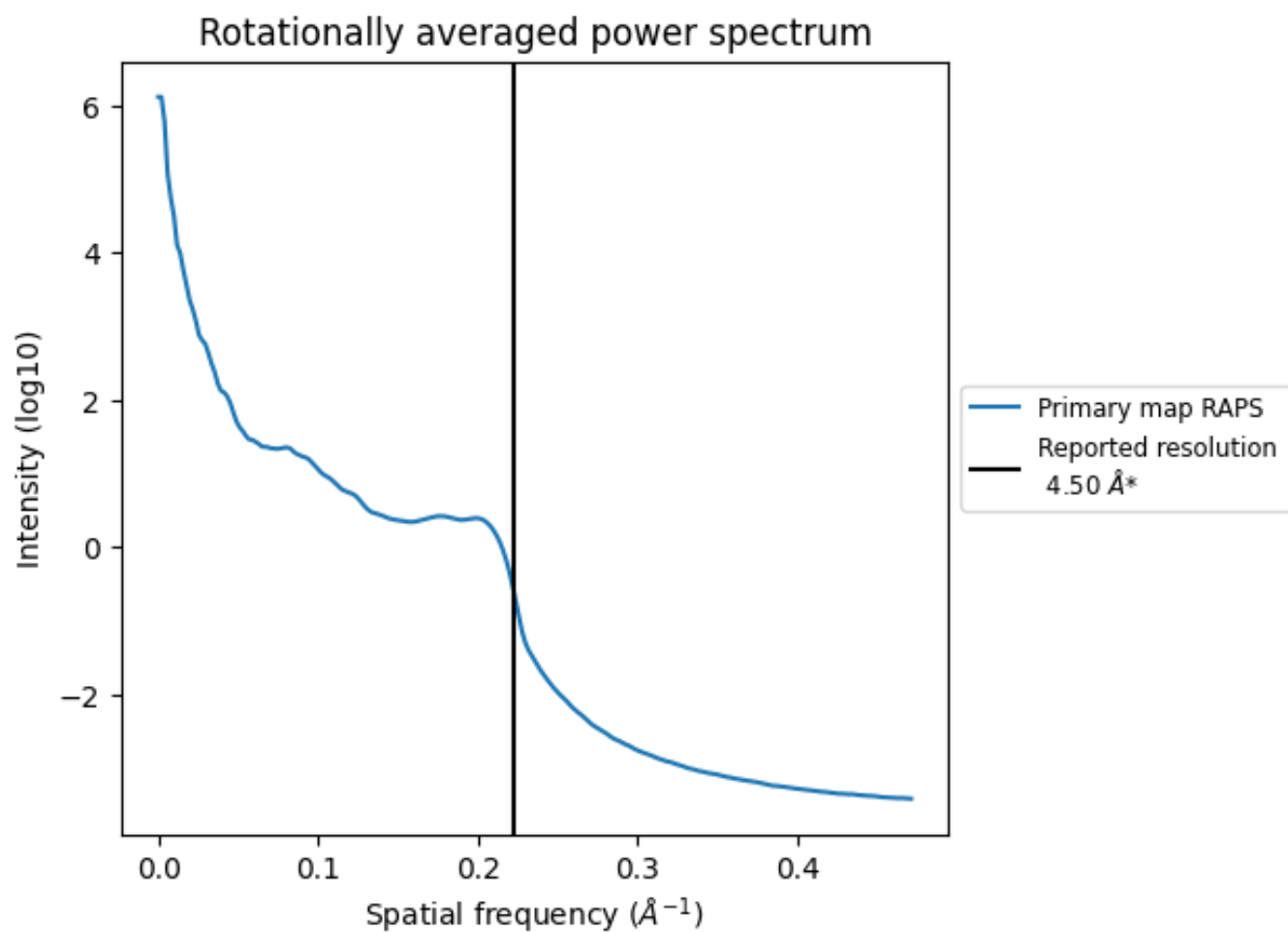
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1509 nm^3 ; this corresponds to an approximate mass of 1363 kDa.

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

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

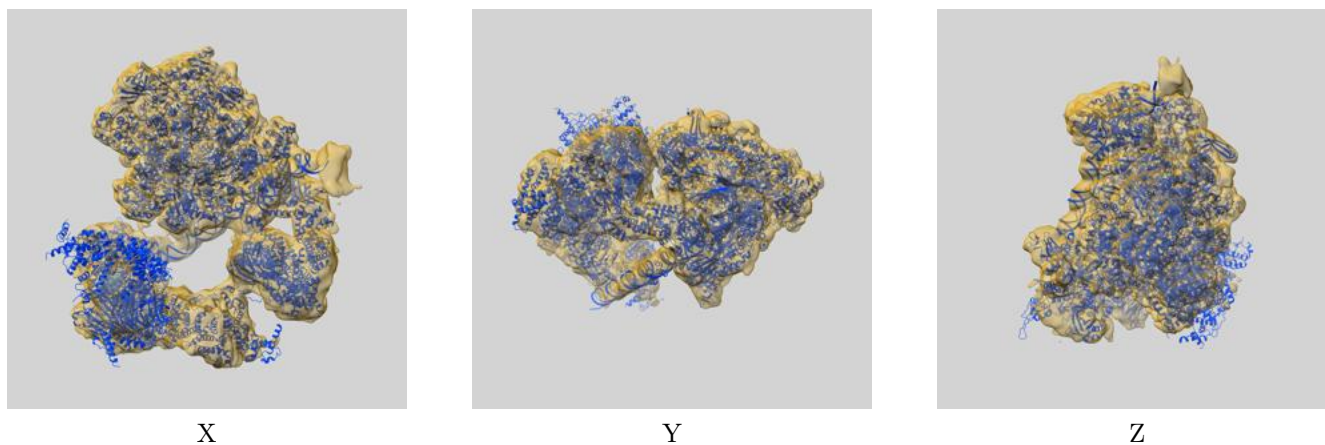
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

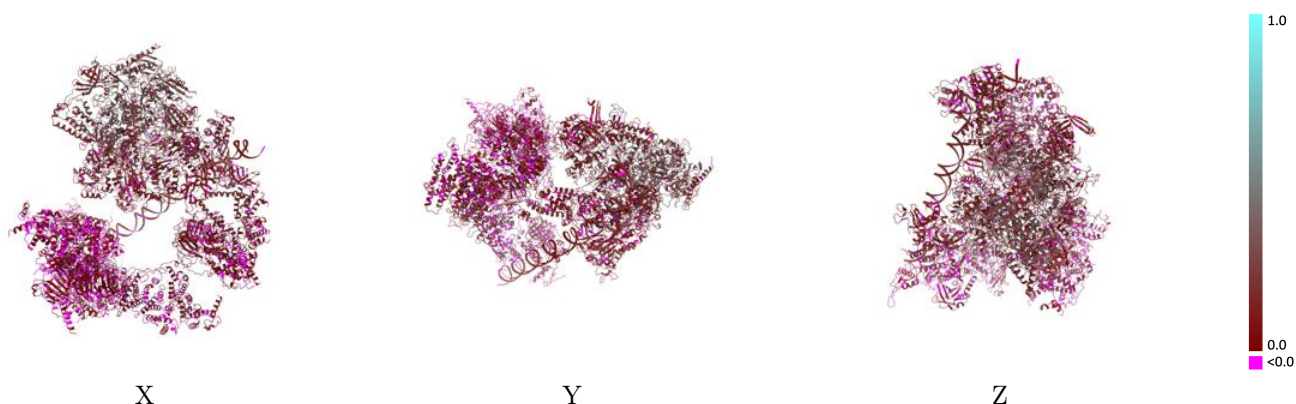
This section contains information regarding the fit between EMDB map EMD-31075 and PDB model 7EDX. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



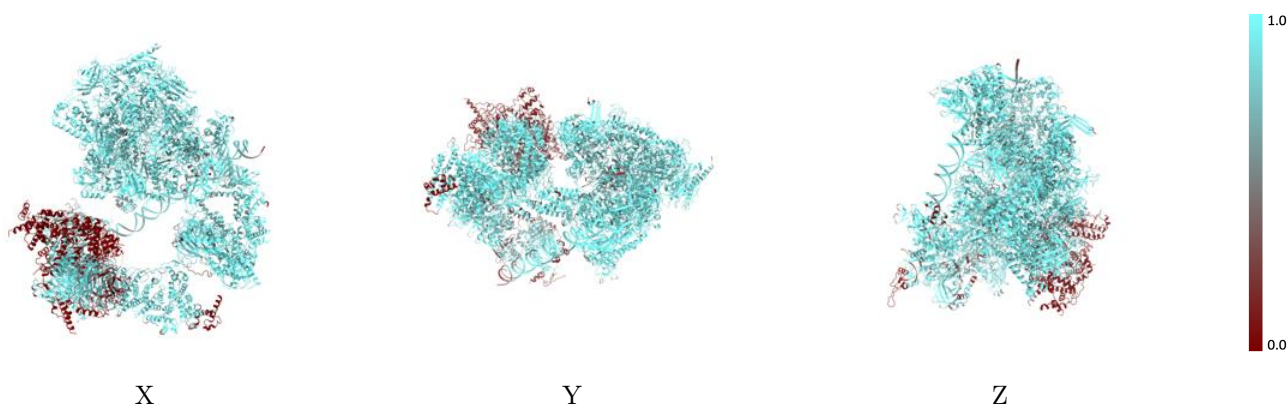
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



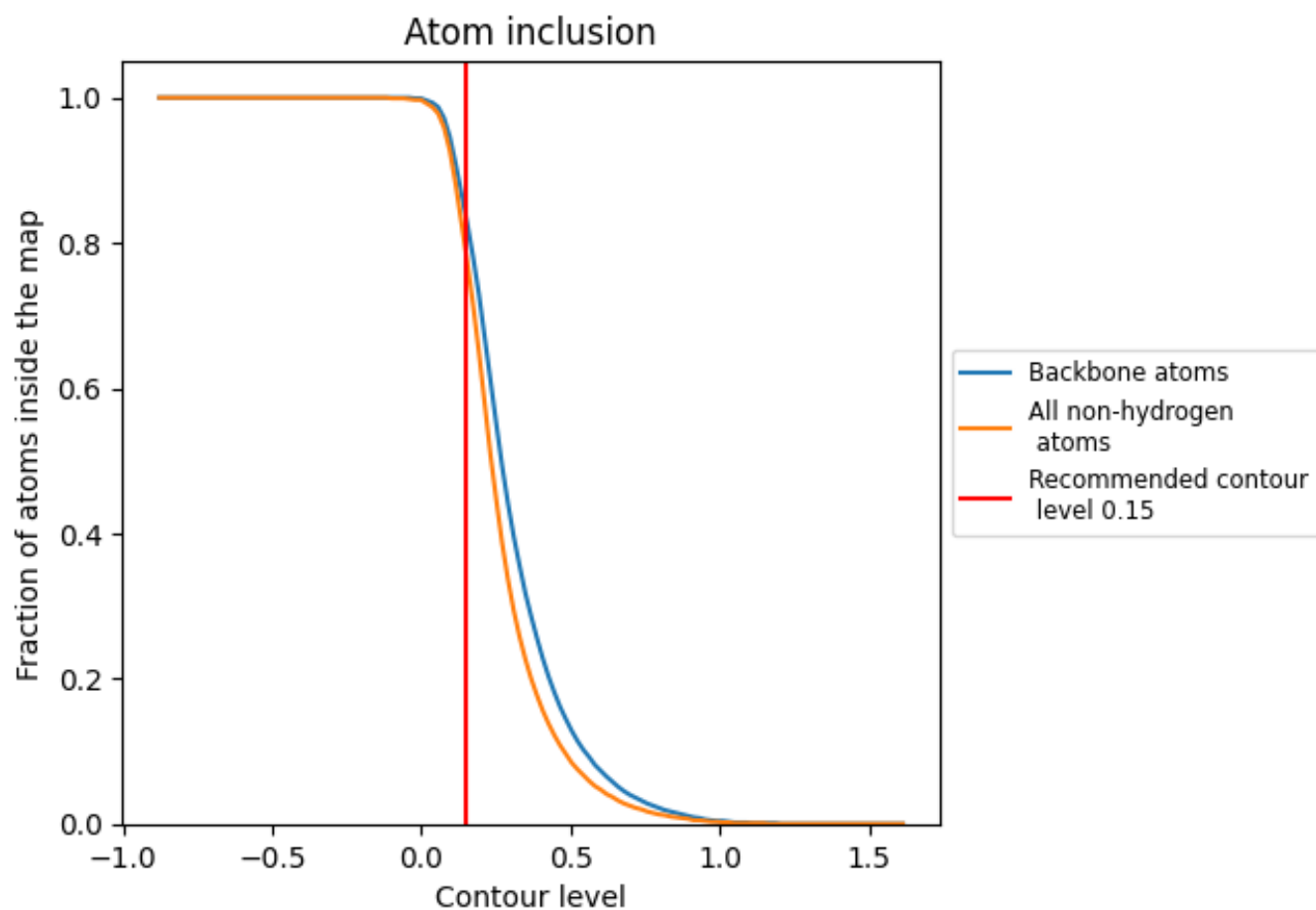
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 78% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7850	 0.1300
A	 0.7320	 0.0490
B	 0.8960	 0.0780
D	 0.8660	 0.1150
E	 0.9060	 0.0940
F	 0.8200	 0.0910
G	 0.7500	 0.0360
H	 0.8650	 0.0890
I	 0.9400	 0.0780
J	 0.9680	 0.0620
L	 0.9200	 0.1140
O	 0.9290	 0.1400
P	 0.9700	 0.1270
Q	 0.9280	 0.0970
R	 0.9030	 0.1670
S	 0.8560	 0.0980
T	 0.8910	 0.1130
X	 0.7990	 0.1150
Y	 0.7750	 0.1120
c	 0.4460	 0.0240
d	 0.2820	 0.0290
e	 0.3020	 0.0310
f	 0.6410	 0.0430
i	 0.2250	 0.0250
j	 0.3380	 0.0260
k	 0.1280	 0.0230
l	 0.1280	 0.0200
m	 0.0060	 0.0120
o	 0.8920	 0.2240
p	 0.8560	 0.2220
q	 0.9420	 0.2680
r	 0.8690	 0.1400
s	 0.9300	 0.2020
t	 0.9290	 0.2630
u	 0.9350	 0.1370



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Chain	Atom inclusion	Q-score
v	 0.9080	 0.2410
w	 0.9410	 0.1850
x	 0.9460	 0.3130
y	 0.8930	 0.2800
z	 0.9550	 0.2230