



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:28 AM UTC

PDB ID : 8XZV / pdb_00008xzv
EMDB ID : EMD-38799
Title : Architecture of the spinach plastid-encoded RNA polymerase
Authors : Wang, G.-L.; Yu, L.-J.; Lu, C.
Deposited on : 2024-01-21
Resolution : 3.16 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:

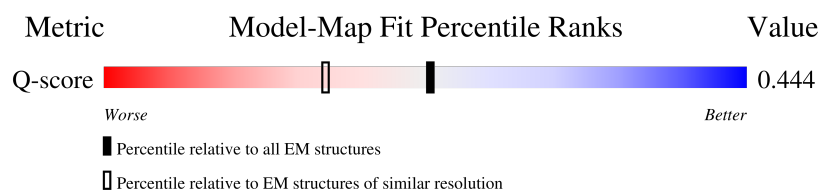
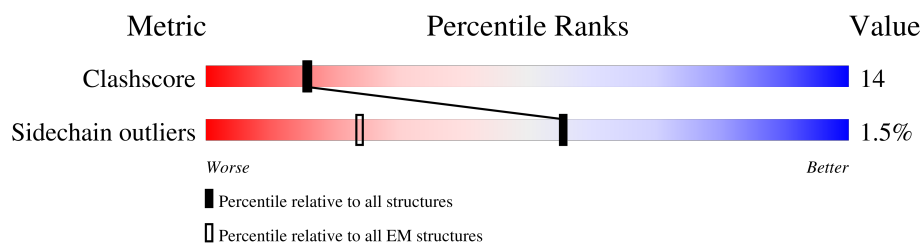
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.16 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.



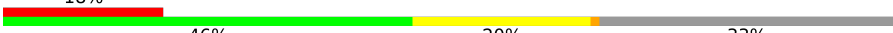
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14474 (2.66 - 3.66)

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	335	
1	O	335	
2	B	1070	
3	C	677	
4	D	1357	

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Mol	Chain	Length	Quality of chain
5	E	472	
6	F	181	
6	R	181	
7	G	518	
8	H	892	
9	I	490	
10	K	324	
11	L	284	
12	M	273	
13	N	678	
14	P	170	
15	Q	143	
16	S	583	
17	J	774	

2 Entry composition [i](#)

There are 18 unique types of molecules in this entry. The entry contains 58999 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 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	225	Total	C	N	O	S	0	0
			1775	1123	309	333	10		
1	O	223	Total	C	N	O	S	0	0
			1761	1115	307	329	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1070	Total	C	N	O	S	0	0
			8517	5403	1505	1575	34		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	677	Total	C	N	O	S	0	0
			5507	3525	969	985	28		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta''.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1216	Total	C	N	O	S	1	0
			8374	5215	1551	1582	26		

- Molecule 5 is a protein called Fructokinase-like 1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	382	Total	C	N	O	S	0	0
			3079	1957	521	584	17		

- Molecule 6 is a protein called Thioredoxin-like protein CITRX, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	116	Total	C	N	O	S	0	0
			940	596	154	181	9		
6	R	116	Total	C	N	O	S	0	0
			940	596	154	181	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	21	PHE	SER	conflict	UNP A0A9R0J865
R	21	PHE	SER	conflict	UNP A0A9R0J865

- Molecule 7 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	237	Total	C	N	O	S	0	0
			2009	1273	354	374	8		

- Molecule 8 is a protein called pTAC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	595	Total	C	N	O	S	0	0
			4653	2944	823	860	26		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	892	ALA	SER	conflict	UNP A0A9R0IP63

- Molecule 9 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 14 iso-form X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	413	Total	C	N	O	S	0	0
			3373	2162	575	615	21		

- Molecule 10 is a protein called pTAC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	214	Total	C	N	O	S	0	0
			1803	1137	320	339	7		

- Molecule 11 is a protein called superoxide dismutase.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	224	Total	C	N	O	S	0	0
			1817	1176	299	338	4		

- Molecule 12 is a protein called superoxide dismutase.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	215	Total	C	N	O	S	0	0
			1763	1145	294	318	6		

- Molecule 13 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	475	Total	C	N	O	S	0	0
			4032	2565	693	756	18		

- Molecule 14 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	105	Total	C	N	O	S	0	0
			840	525	148	162	5		

- Molecule 15 is a protein called pTAC18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	104	Total	C	N	O	S	0	0
			902	587	156	157	2		

- Molecule 16 is a protein called Fructokinase-like 2, chloroplastic isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	344	Total	C	N	O	S	0	0
			2695	1721	462	494	18		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	114	VAL	-	insertion	UNP A0A9R0K4E6
S	115	LEU	-	insertion	UNP A0A9R0K4E6
S	116	HIS	-	insertion	UNP A0A9R0K4E6
S	117	THR	-	insertion	UNP A0A9R0K4E6
S	118	GLU	-	insertion	UNP A0A9R0K4E6
S	119	MET	-	insertion	UNP A0A9R0K4E6

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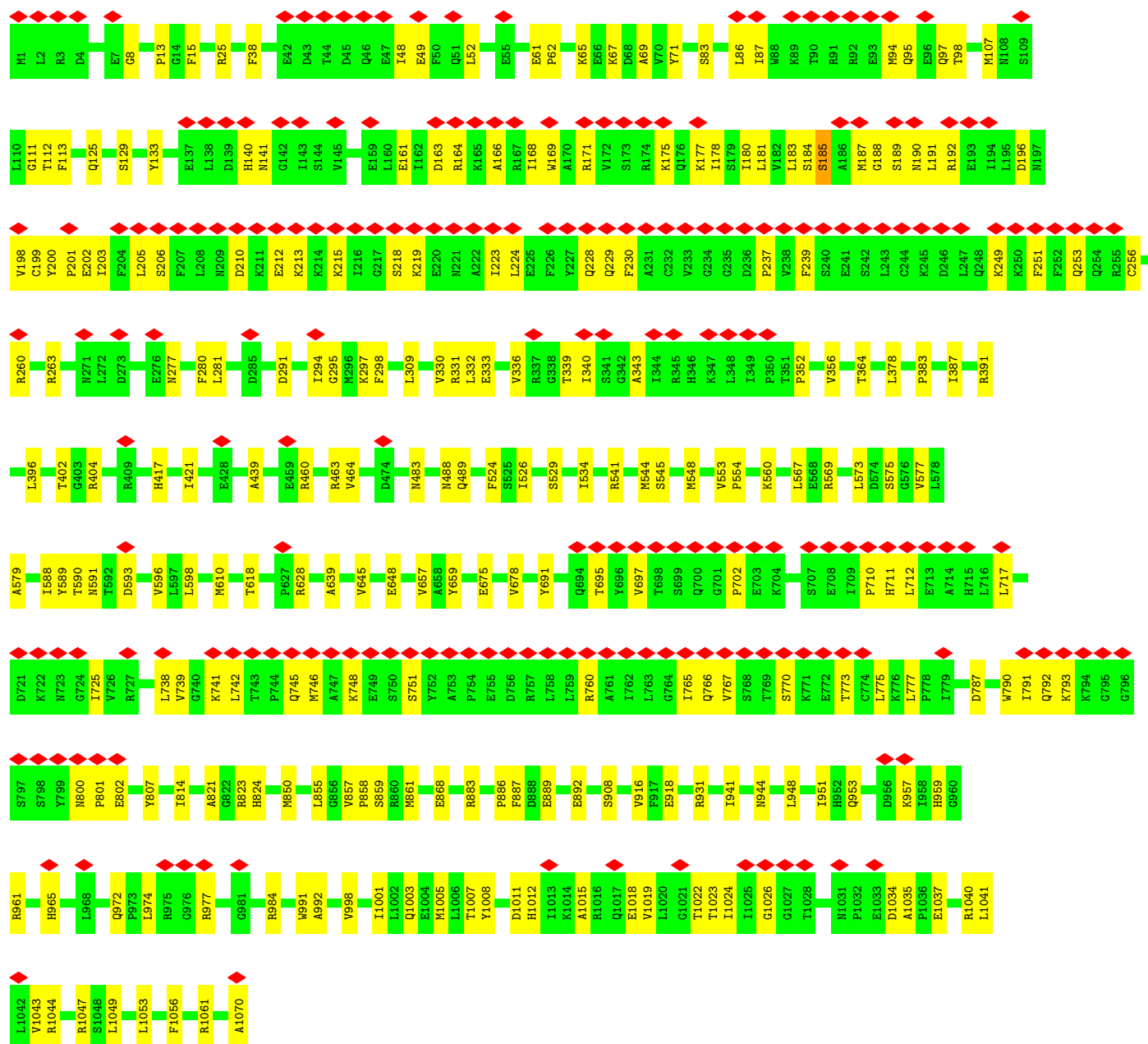
Chain	Residue	Modelled	Actual	Comment	Reference
S	120	LYS	-	insertion	UNP A0A9R0K4E6
S	121	LEU	-	insertion	UNP A0A9R0K4E6
S	122	PHE	-	insertion	UNP A0A9R0K4E6
S	123	SER	-	insertion	UNP A0A9R0K4E6

- Molecule 17 is a protein called MurE.

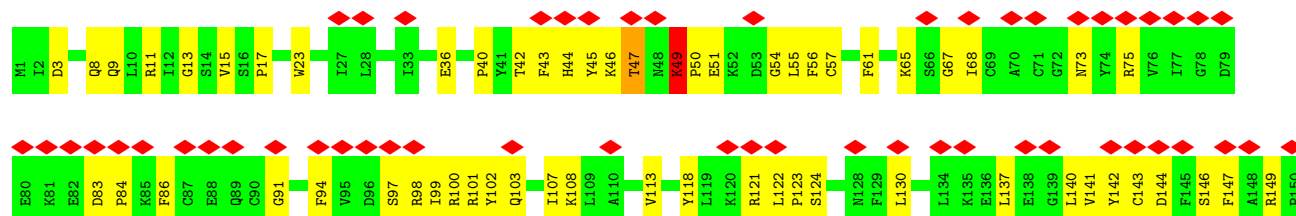
Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	546	Total	C	N	O	S	0	0
			4218	2640	726	826	26		

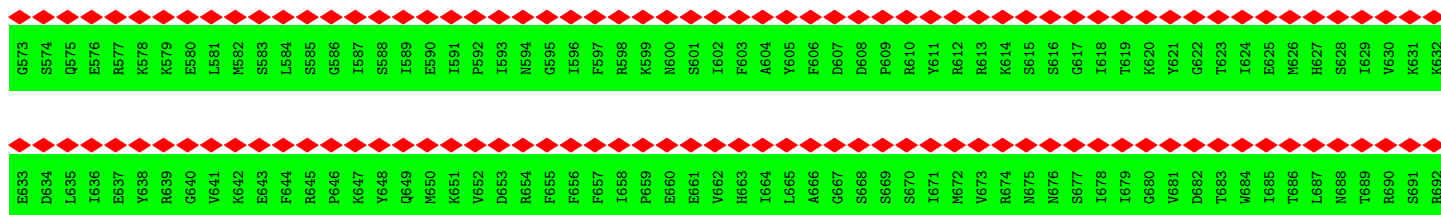
- Molecule 18 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
18	L	1	Total	Fe	0
			1	1	



• Molecule 3: DNA-directed RNA polymerase subunit beta'

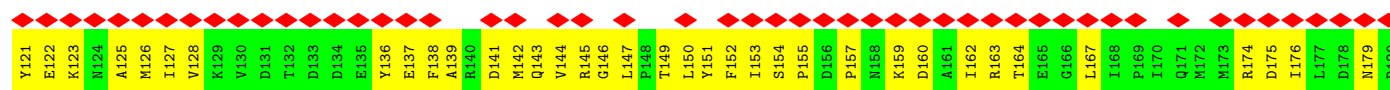
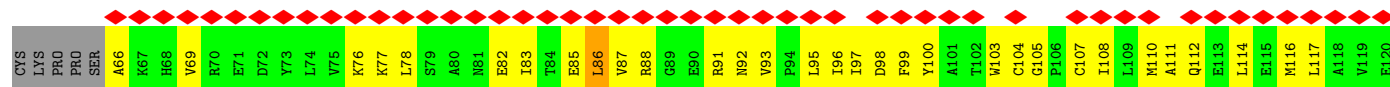
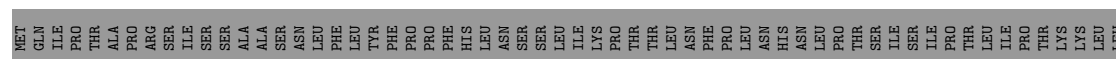
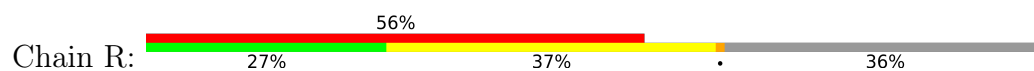




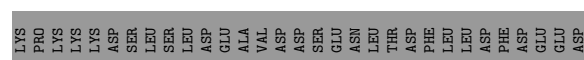
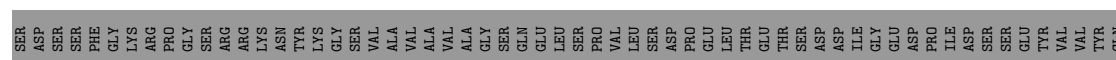
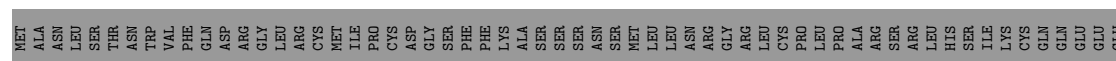
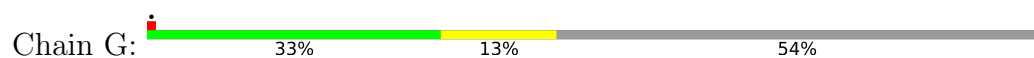




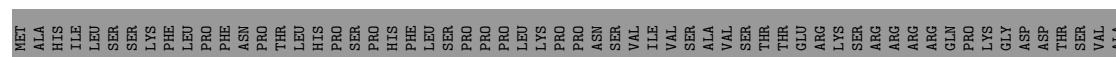
- Molecule 6: Thioredoxin-like protein CITRX, chloroplastic

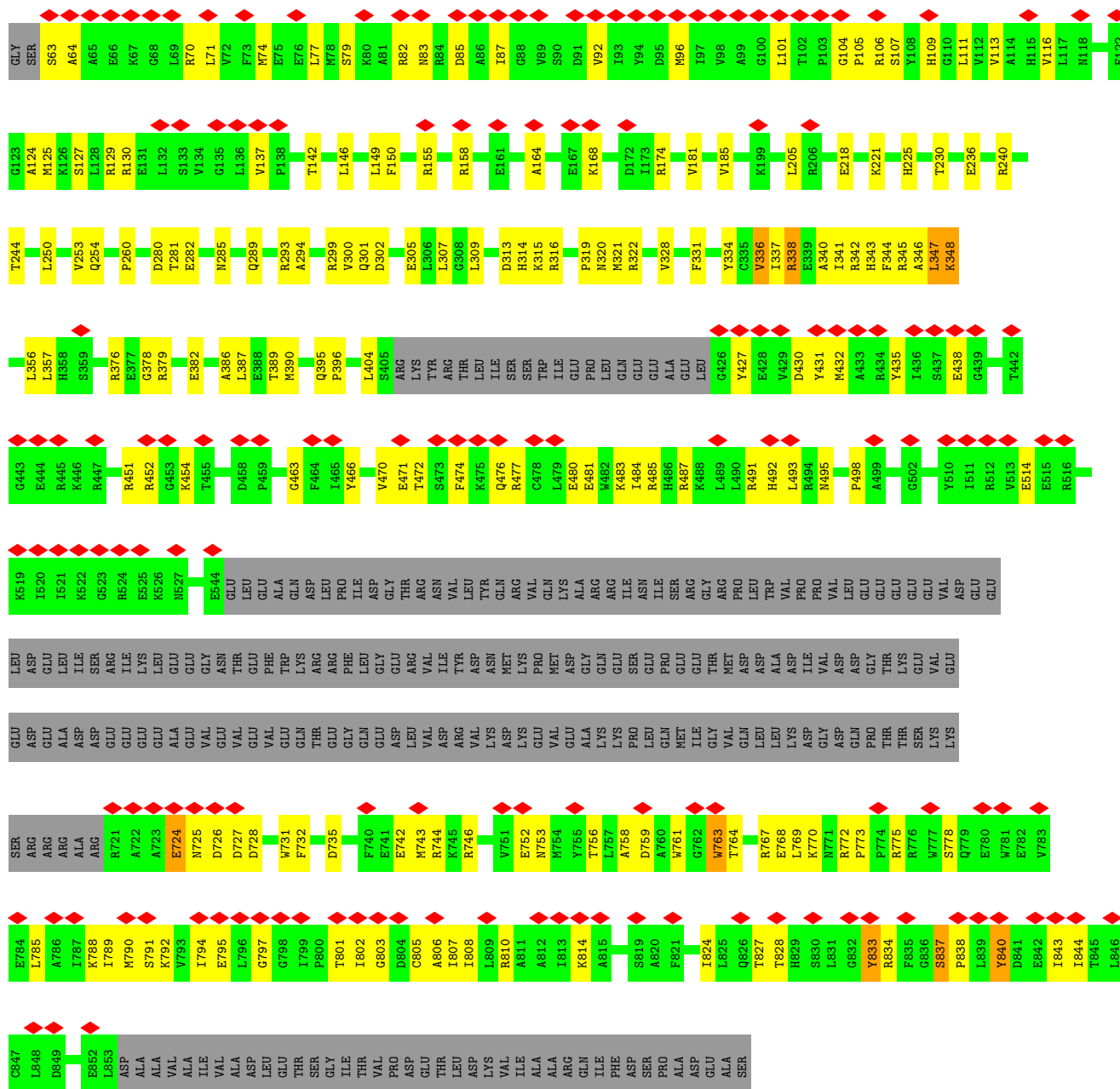


- Molecule 7: Protein PLASTID TRANSCRIPTIONALLY ACTIVE 12

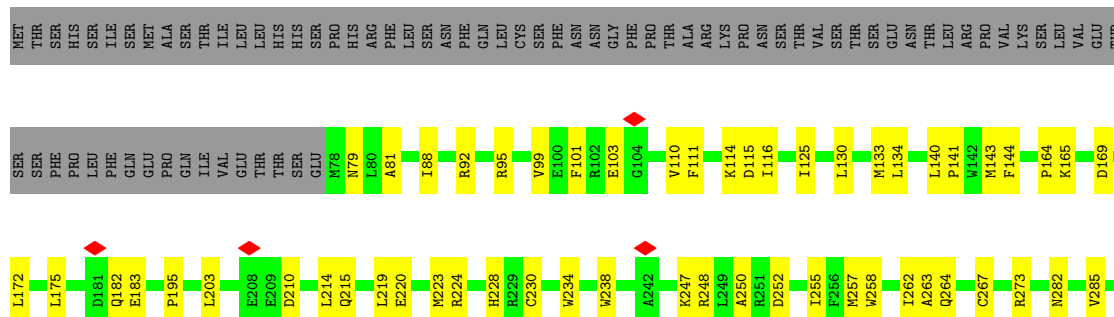


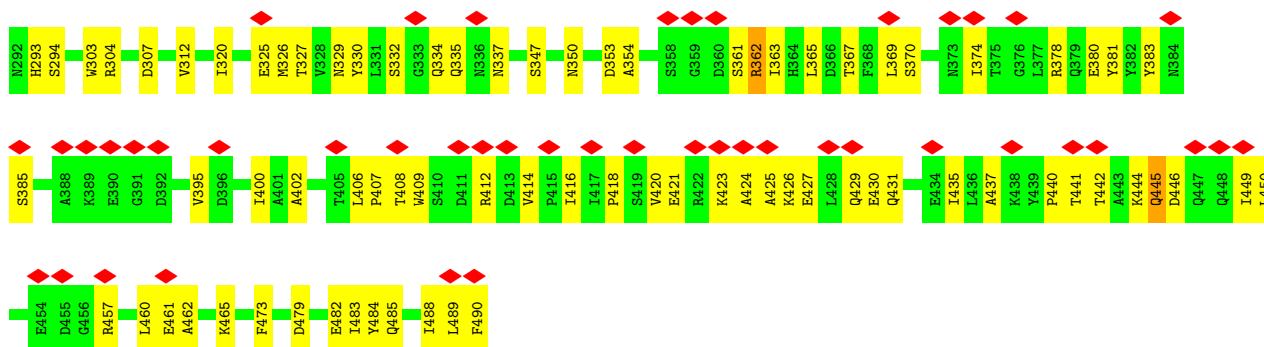
- Molecule 8: pTAC3





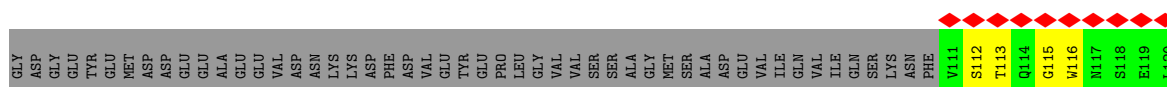
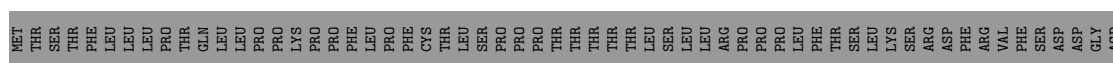
● Molecule 9: Protein PLASTID TRANSCRIPTIONALLY ACTIVE 14 isoform X2





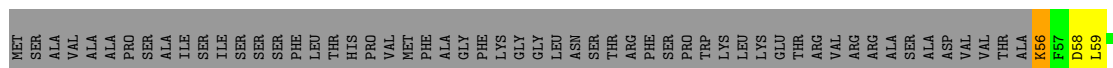
• Molecule 10: pTAC6

Chain K: 47% 19% 34%



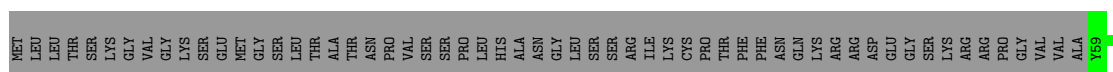
• Molecule 11: superoxide dismutase

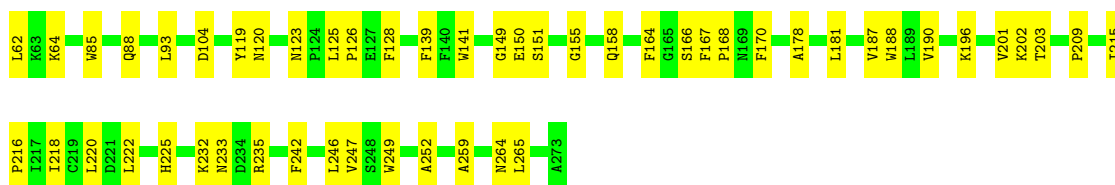
Chain L: 55% 23% 21%



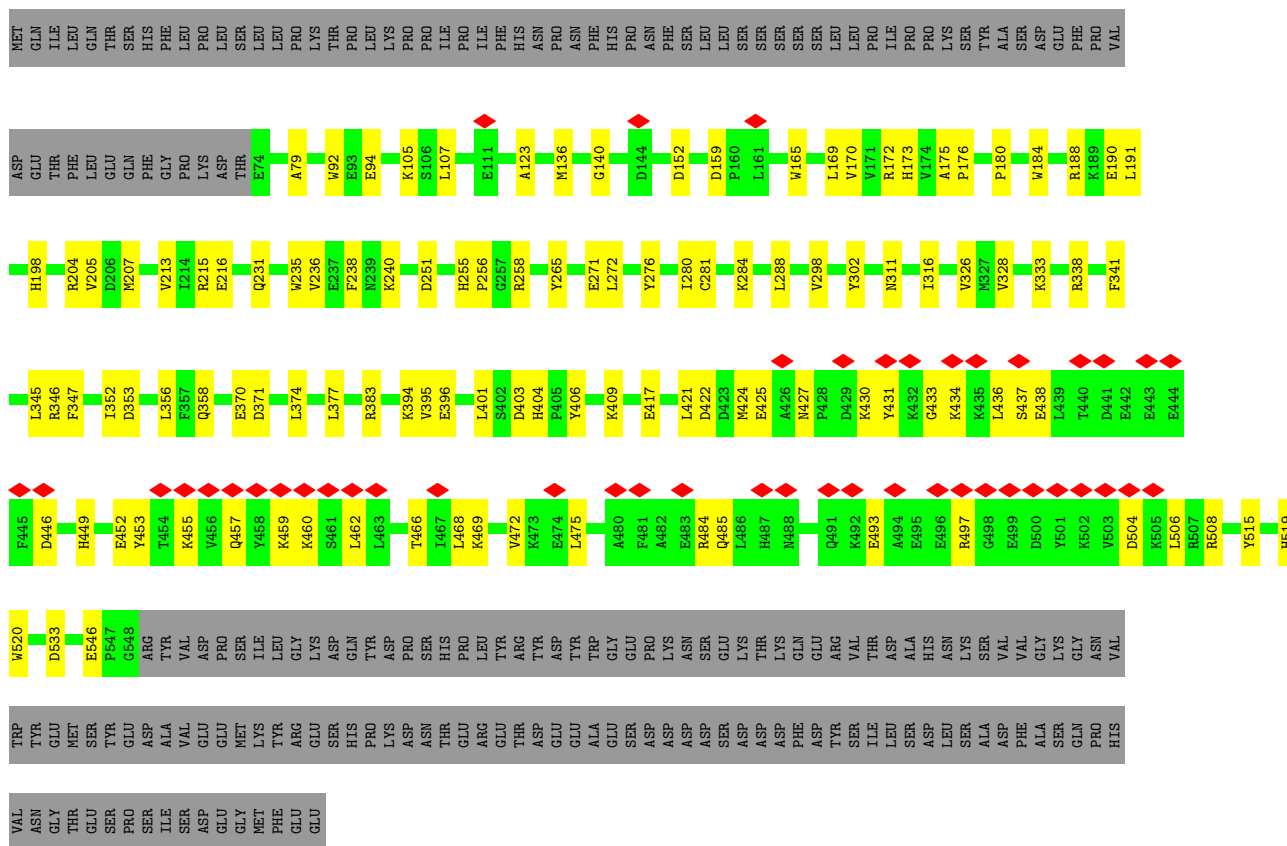
• Molecule 12: superoxide dismutase

Chain M: 60% 19% 21%

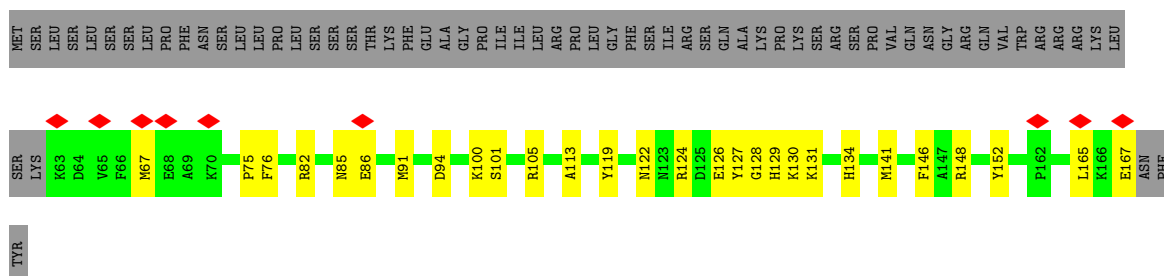




• Molecule 13: Protein PLASTID TRANSCRIPTIONALLY ACTIVE 10

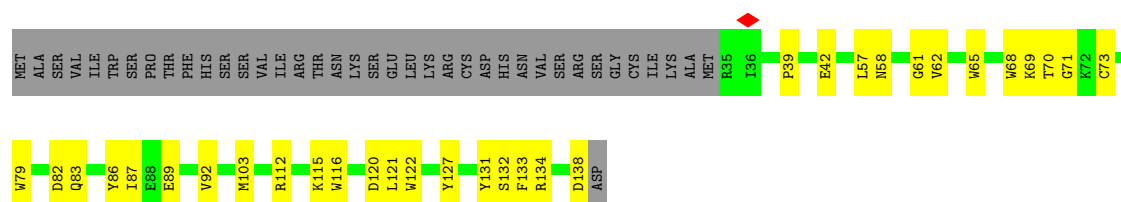


• Molecule 14: Protein PLASTID TRANSCRIPTIONALLY ACTIVE 7

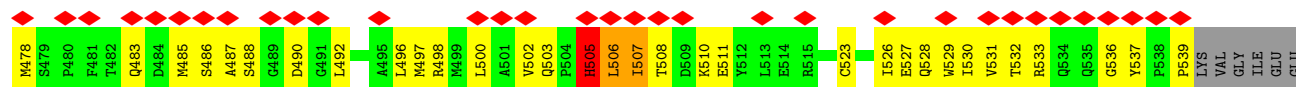
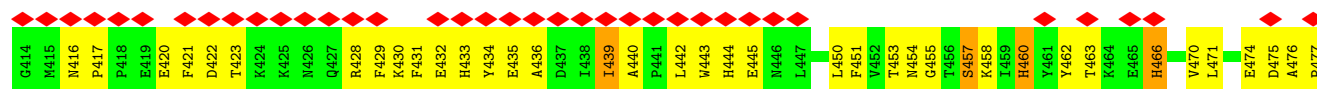
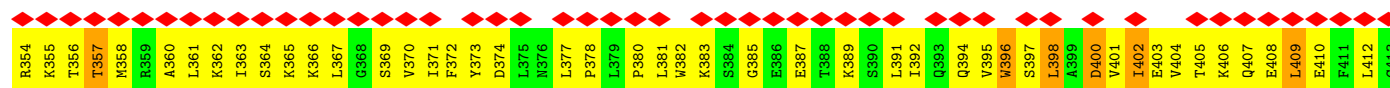
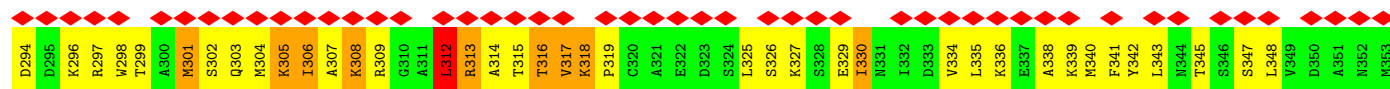
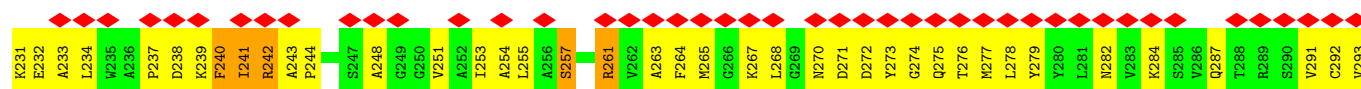
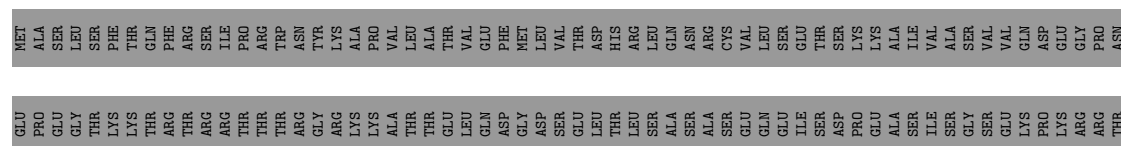
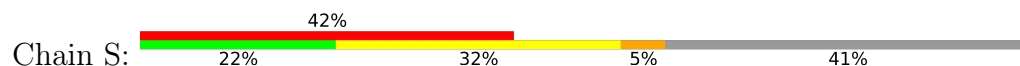


• Molecule 15: pTAC18

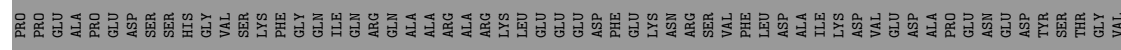
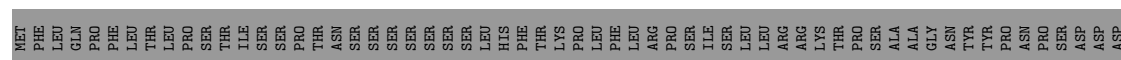




• Molecule 16: Fructokinase-like 2, chloroplastic isoform X2



• Molecule 17: MurE



SER	GLN	P241	R301	T361	V421	I481	S541	T601	L662	A723
GLY	GLY	S242	G302	A362	M422	V482	G542	P602	D663	G724
SER	LEU	F243	A303	A363	E423	M483	L543	D603	I664	K725
GLY	ARG	F244	A304	H364	A424	V484	L544	A604	L665	G726
ASP	VAL	K244	V304	L364	A424	D484	G544	L605	D666	H727
ASP	VAL	M245	A305	L365	S425	D485	G545	S606	D667	E728
LEU	ASP	T246	V306	L366	S426	D486	G546	R607	M668	A729
PHE	VAL	L247	V307	K367	M427	P487	H547	L608	L669	Y730
GLY	SER	A248	A308	T368	E428	M488	M548	L609	A670	Y731
ASP	GLU	E249	S309	K369	L429	A489	I549	D610	G671	V732
ASP	LYS	L250	K310	Y370	T430	A490	Y550	L609	G671	V732
LYS	GLU	L251	E311	E371	H431	F491	N551	D610	G671	V732
ALA	GLU	D252	T312	A372	T432	F492	I552	S611	I672	D733
ILE	PHE	E253	D313	K373	R433	I493	L553	V612	G673	G734
ALA	ASP	C254	T314	G374	C434	A494	A554	R613	W674	G735
GLN	ASP	K255	E315	L375	E435	Q495	A555	E614	T675	D735
LYS	ASP	V256	E316	R376	E436	Q496	V556	L615	M676	K736
ARG	ASP	T257	T317	T377	L437	M497	T557	Q616	Q677	K737
LYS	GLU	V258	L318	G378	D438	P498	V558	P617	D678	E738
LYS	VAL	I259	G319	K379	D439	M499	G559	R618	Y679	F739
GLY	SER	S260	C320	M380	F439	M499	G559	R619	L680	F740
LEU	GLU	V261	K321	S381	D440	V500	I560	I620	K681	D741
LEU	GLY	V262	R322	S382	I441	P501	A561	I621	H682	D742
LYS	LYS	G263	L323	V383	V443	V502	V562	T622	G683	R743
PRO	ASN	D264	V324	A384	F444	T504	A564	I624	E684	E744
ASN	GLY	D265	I325	Y385	T445	F505	P565	G625	M685	E745
PRO	SER	E266	V326	Y386	T446	A506	L566	S626	D686	C746
PRO	SER	V267	E327	V387	L447	L507	E567	G627	Y687	R747
LYS	SER	E268	D328	H388	S448	E508	D568	G628	P689	A749
GLU	LEU	T269	N330	D390	R449	M509	I569	E629	P690	L750
ARG	VAL	G271	A331	N391	M451	D511	V570	K630	L691	Q751
VAL	ALA	I272	L333	L393	S452	A512	E571	E631	P692	Y752
ASP	PHE	E273	A332	D394	H453	D513	G572	G633	M693	V753
ASP	ALA	H274	P334	F395	F454	V514	I573	K634	H695	D754
ASP	ASP	D275	A335	F396	Q455	H515	E575	R635	R696	E755
GLU	PHE	S276	L336	P396	C456	P516	V576	P636	L697	L756
LEU	ASP	R277	A337	E397	M457	L517	D577	M637	F698	H757
GLY	SER	L278	A338	A398	E458	L518	V578	A639	L699	Q758
GLU	GLU	V279	A339	N399	E459	F519	V579	K640	H700	D759
VAL	VAL	N280	F340	P400	E460	E520	P580	V641	I702	I761
ASP	ASP	S281	F341	D401	F461	L521	G581	A642	R703	D762
LEU	LEU	G282	R342	A402	V463	S522	R582	T643	R704	T763
GLU	GLU	D283	Y343	V403	V463	L523	C583	D644	V707	S764
ILE	ILE	L284	P344	L404	A464	F524	E584	K645	R708	E765
ASP	ASP	V285	T345	V405	Q465	E525	V585	S646	C709	F766
LEU	LEU	C287	K346	Q406	A466	T526	I586	D647	T767	P767
GLY	SER	C288	S347	K407	K467	T527	D587	V648	A710	W768
ASP	ASP	V289	S349	M409	L468	V528	E588	T649	V711	R769
LEU	LEU	D290	V350	A410	F469	L529	E589	M650	A712	L770
GLU	GLU	G291	I351	K411	S470	V530	Q590	L651	M713	P771
ASP	GLU	N292	G352	M412	R471	N531	A591	T652	G714	E772
LEU	LEU	L293	I353	L413	M472	T532	F592	S653	E715	S773
GLU	GLU	C294	T354	H414	V473	P533	G593	D654	G717	H774
ASP	ASP	L295	G355	N415	D474	Q534	V594	Q656	D718	
LEU	LEU	T296	T356	Q416	P475	G535	I595	S657	M719	
ASP	ASP	E297	H357	T417	D476	I536	V596	G658	V720	
GLU	GLU	A298	G358	E418	R477	L537	D597	E659	W721	
ASP	ASP	D299	K359	A419	R479	E538	H598		V722	
LEU	LEU	K300	T360	V420	K480	I539	A599			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	180924	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.697	Depositor
Minimum map value	-1.051	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.23	Depositor
Map size ($\text{\AA}$)	563.2, 563.2, 563.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.18	0/1810	0.38	0/2454
1	O	0.12	0/1796	0.33	0/2435
2	B	0.13	0/8691	0.33	1/11741 (0.0%)
3	C	0.15	0/5636	0.36	2/7617 (0.0%)
4	D	0.24	0/8497	0.48	4/11580 (0.0%)
5	E	0.12	0/3154	0.30	0/4268
6	F	0.12	0/956	0.30	0/1292
6	R	0.23	0/956	0.57	0/1292
7	G	0.14	0/2062	0.34	0/2781
8	H	0.29	0/4745	0.49	1/6417 (0.0%)
9	I	0.13	0/3456	0.39	0/4675
10	K	0.12	0/1849	0.32	0/2507
11	L	0.28	0/1877	0.47	2/2558 (0.1%)
12	M	0.11	0/1820	0.30	0/2478
13	N	0.11	0/4139	0.28	0/5582
14	P	0.14	0/857	0.41	0/1152
15	Q	0.18	0/932	0.52	0/1261
16	S	0.36	0/2756	0.86	8/3731 (0.2%)
17	J	0.14	0/4293	0.38	0/5820
All	All	0.19	0/60282	0.42	18/81641 (0.0%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	333	LEU	N-CA-C	-10.90	99.79	112.87
4	D	332	GLN	N-CA-C	-10.65	98.95	112.90
2	B	185	SER	N-CA-C	-8.75	102.74	112.72
4	D	1130	LEU	CA-C-N	-8.14	110.56	119.19
4	D	1130	LEU	C-N-CA	-8.14	110.56	119.19

There are no chirality outliers.

There are no planarity outliers.

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	1775	0	1783	61	0
1	O	1761	0	1772	44	0
2	B	8517	0	8571	177	0
3	C	5507	0	5546	164	0
4	D	8374	0	7240	200	0
5	E	3079	0	2992	46	0
6	F	940	0	934	21	0
6	R	940	0	934	95	0
7	G	2009	0	1967	58	0
8	H	4653	0	4517	160	0
9	I	3373	0	3321	98	0
10	K	1803	0	1752	53	0
11	L	1817	0	1720	54	0
12	M	1763	0	1698	34	0
13	N	4032	0	3891	88	0
14	P	840	0	804	33	0
15	Q	902	0	870	23	0
16	S	2695	0	2712	293	0
17	J	4218	0	4148	166	0
18	L	1	0	0	0	0
All	All	58999	0	57172	1653	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 14.

The worst 5 of 1653 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)
6:R:142:MET:HE1	16:S:314:ALA:HB3	1.23	1.15
8:H:96:MET:HB2	8:H:101:LEU:HB2	1.33	1.05
6:R:160:ASP:HA	16:S:305:LYS:HB3	1.42	1.00

Continued on next page...

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:S:270:ASN:O	16:S:275:GLN:HG3	1.63	0.98
16:S:304:MET:HE1	16:S:316:THR:HA	1.43	0.98

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	198/305 (65%)	194 (98%)	4 (2%)	48	68
1	O	197/305 (65%)	197 (100%)	0	100	100
2	B	929/929 (100%)	923 (99%)	6 (1%)	78	81
3	C	599/599 (100%)	595 (99%)	4 (1%)	76	80
4	D	702/1214 (58%)	686 (98%)	16 (2%)	44	66
5	E	336/418 (80%)	336 (100%)	0	100	100
6	F	104/166 (63%)	104 (100%)	0	100	100
6	R	104/166 (63%)	102 (98%)	2 (2%)	50	69
7	G	217/460 (47%)	216 (100%)	1 (0%)	81	82
8	H	470/772 (61%)	457 (97%)	13 (3%)	38	63
9	I	363/437 (83%)	360 (99%)	3 (1%)	73	78
10	K	203/305 (67%)	202 (100%)	1 (0%)	81	82
11	L	189/236 (80%)	184 (97%)	5 (3%)	40	64
12	M	186/235 (79%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	N	433/623 (70%)	431 (100%)	2 (0%)	81	82
14	P	87/147 (59%)	87 (100%)	0	100	100
15	Q	94/130 (72%)	91 (97%)	3 (3%)	34	61
16	S	290/508 (57%)	263 (91%)	27 (9%)	8	29
17	J	462/666 (69%)	458 (99%)	4 (1%)	70	77
All	All	6163/8621 (72%)	6072 (98%)	91 (2%)	55	72

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	Q	103	MET
16	S	316	THR
6	R	149	THR
16	S	305	LYS
16	S	357	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
15	Q	128	GLN
17	J	495	GLN
16	S	287	GLN
17	J	399	ASN
17	J	693	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 1 ligands modelled in this entry, 1 is 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.

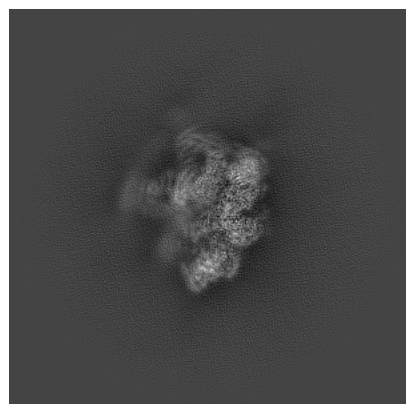
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38799. These allow visual inspection of the internal detail of the map and identification of artifacts.

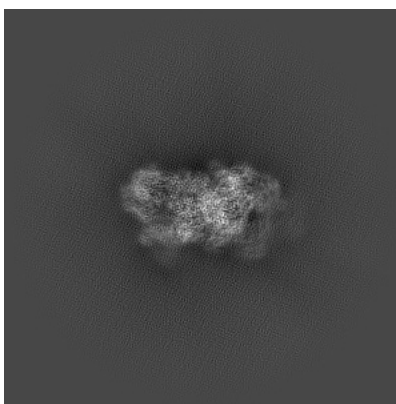
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

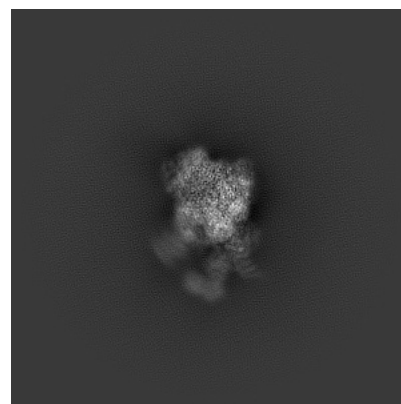
6.1.1 Primary map



X

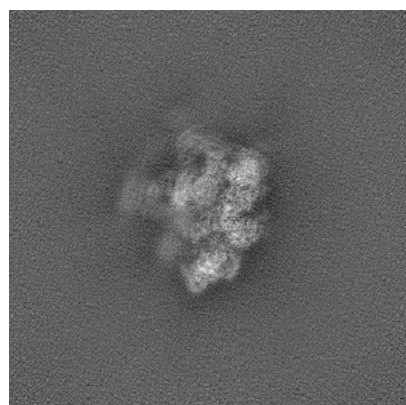


Y

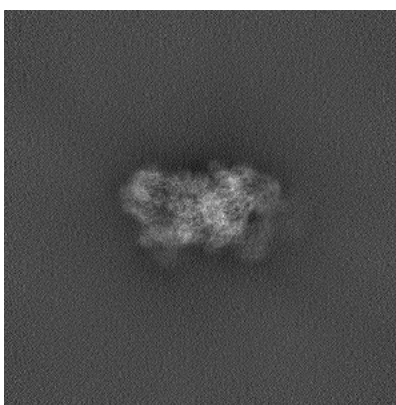


Z

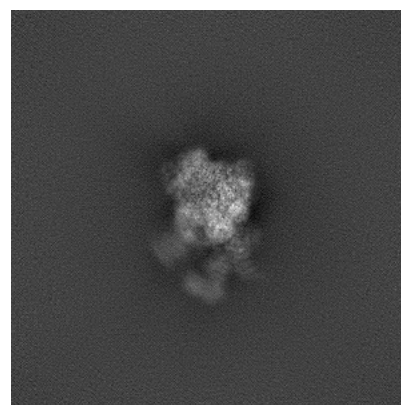
6.1.2 Raw map



X



Y

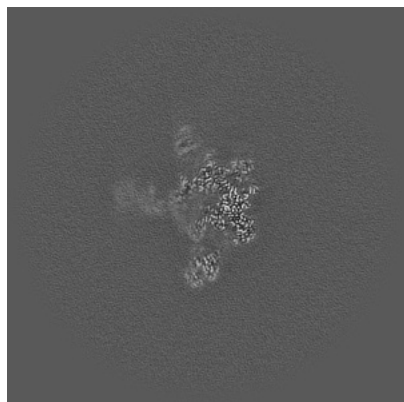


Z

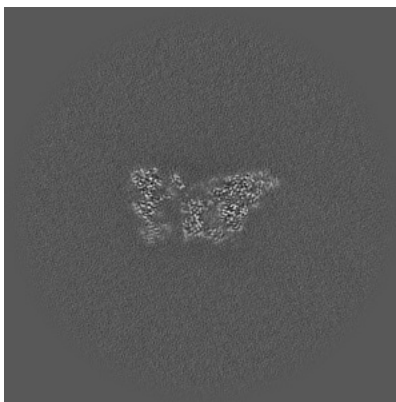
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

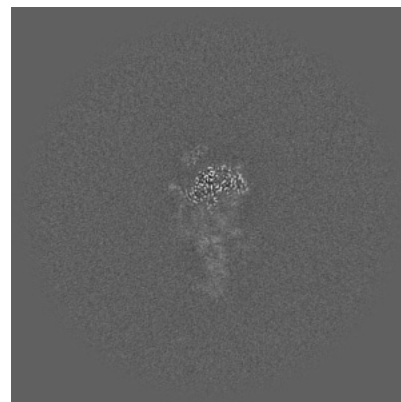
6.2.1 Primary map



X Index: 256

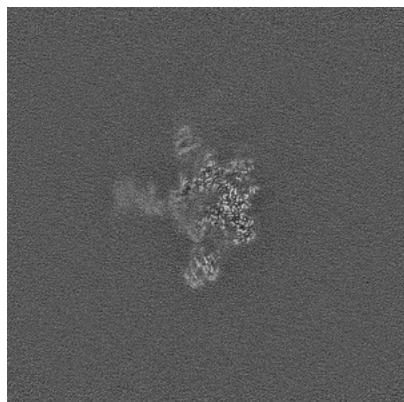


Y Index: 256

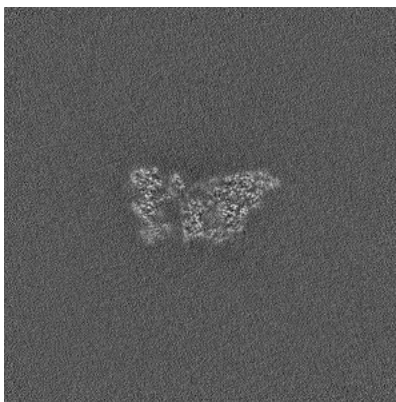


Z Index: 256

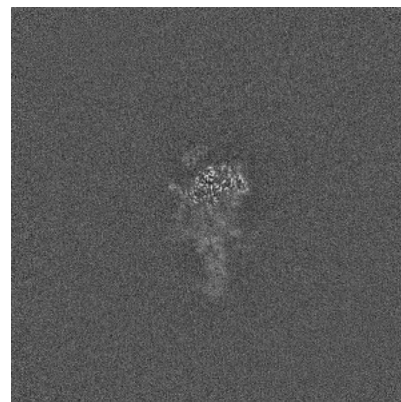
6.2.2 Raw map



X Index: 256



Y Index: 256

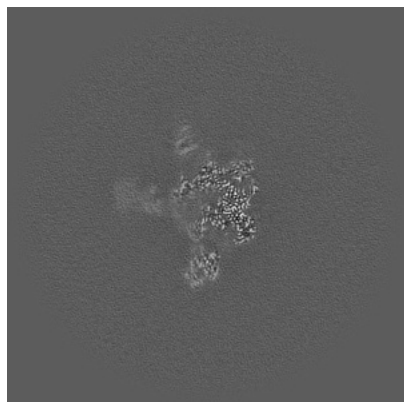


Z Index: 256

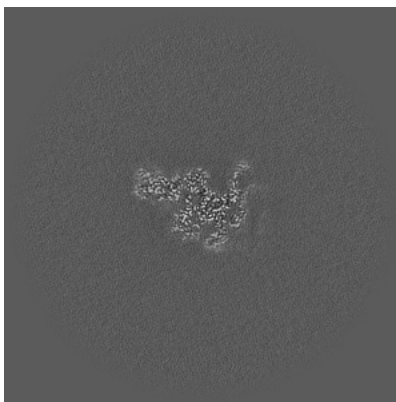
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

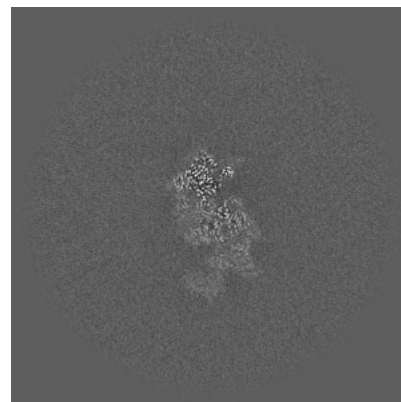
6.3.1 Primary map



X Index: 255

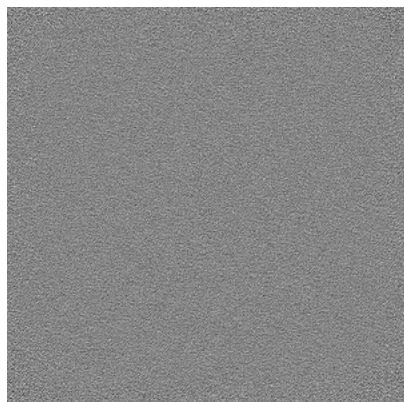


Y Index: 283

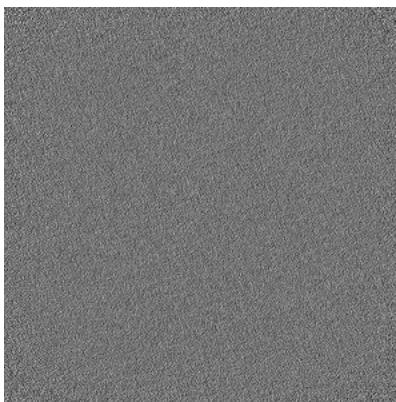


Z Index: 278

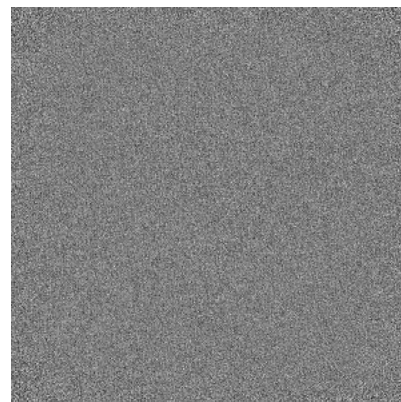
6.3.2 Raw map



X Index: 0



Y Index: 0

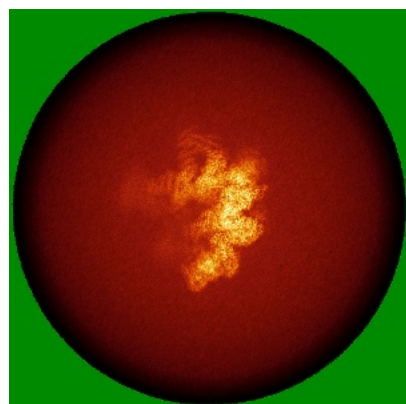


Z Index: 0

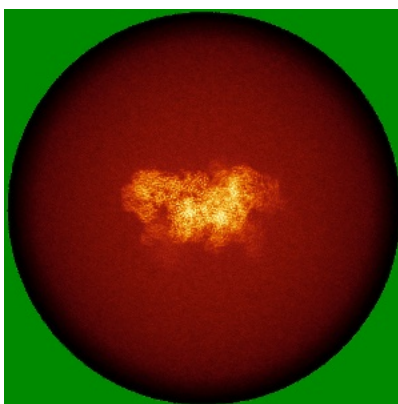
The images above show the largest variance slices of the map in three orthogonal directions.

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

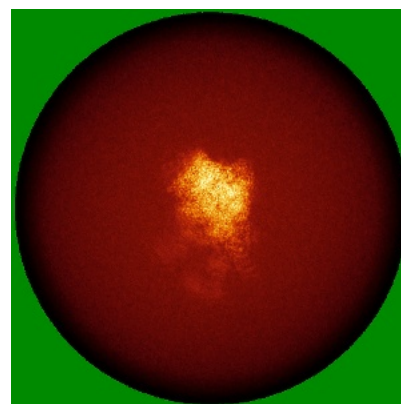
6.4.1 Primary map



X

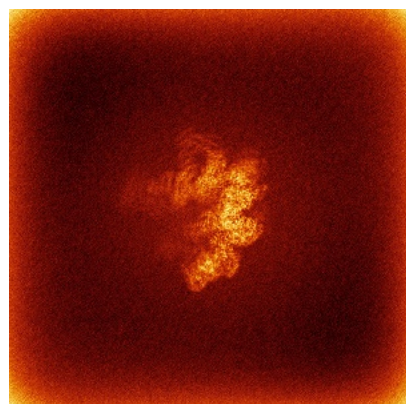


Y

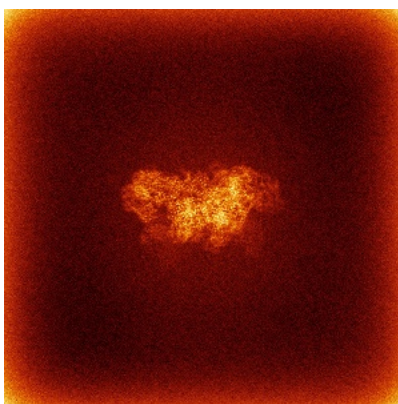


Z

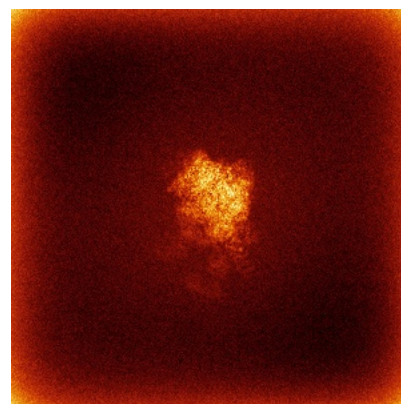
6.4.2 Raw map



X



Y

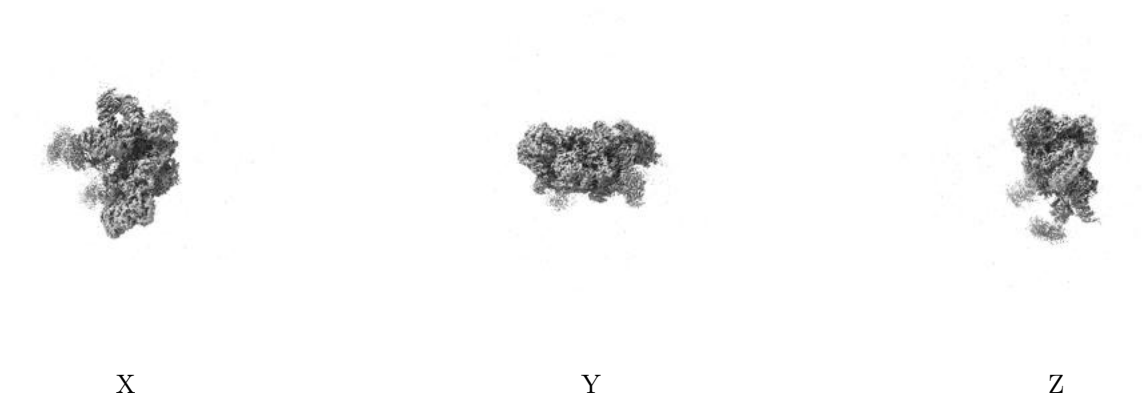


Z

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.

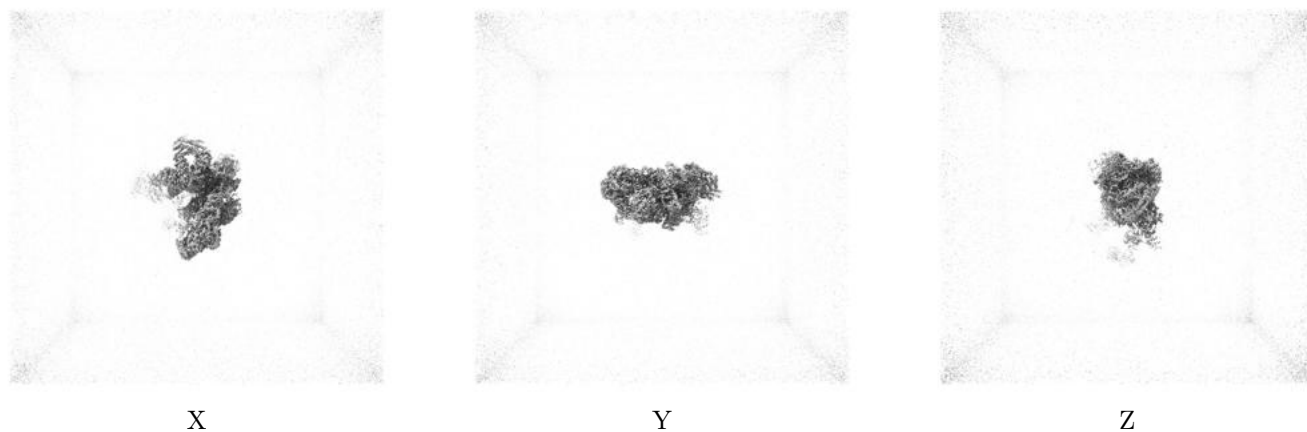
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.23. 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.

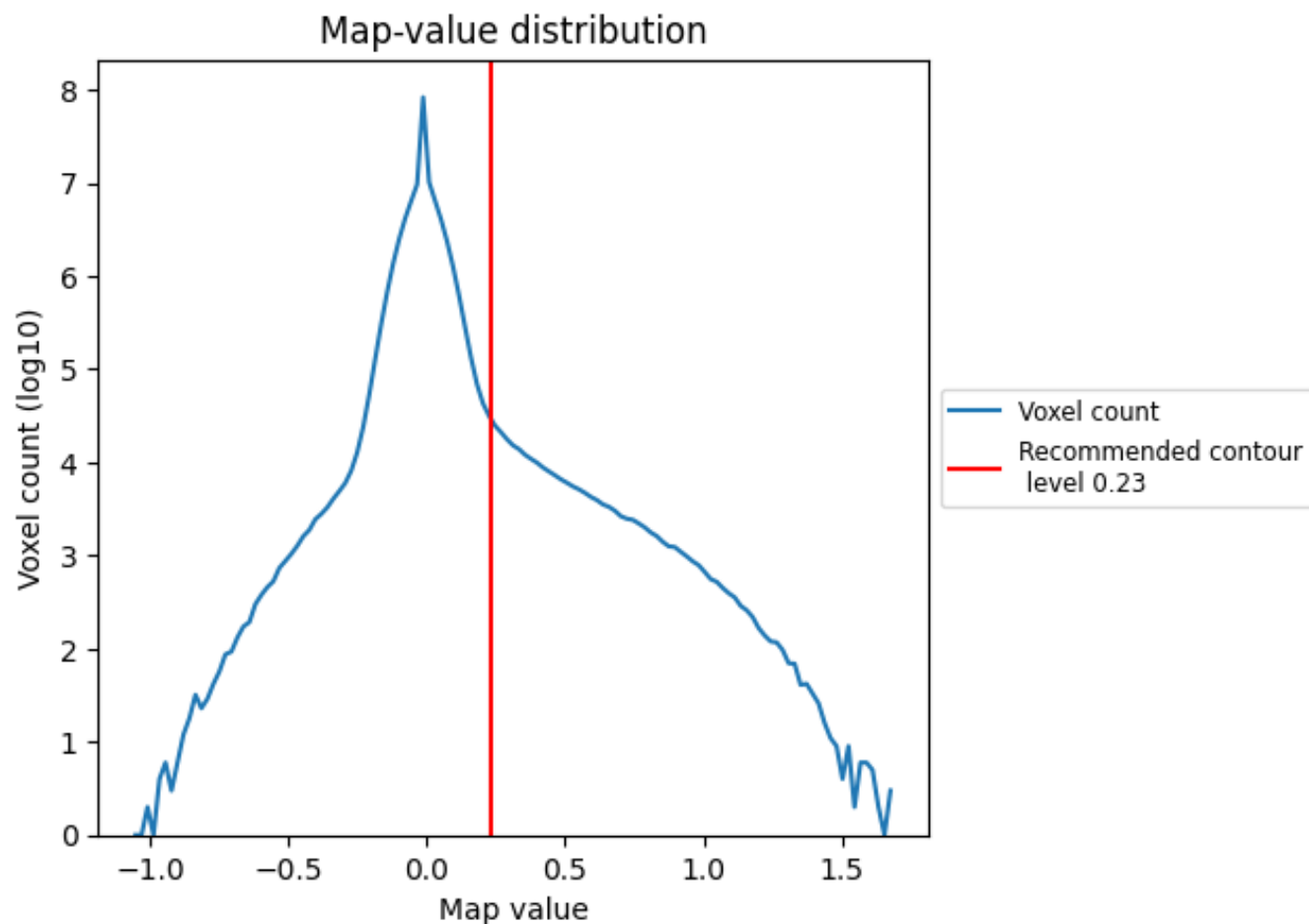
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

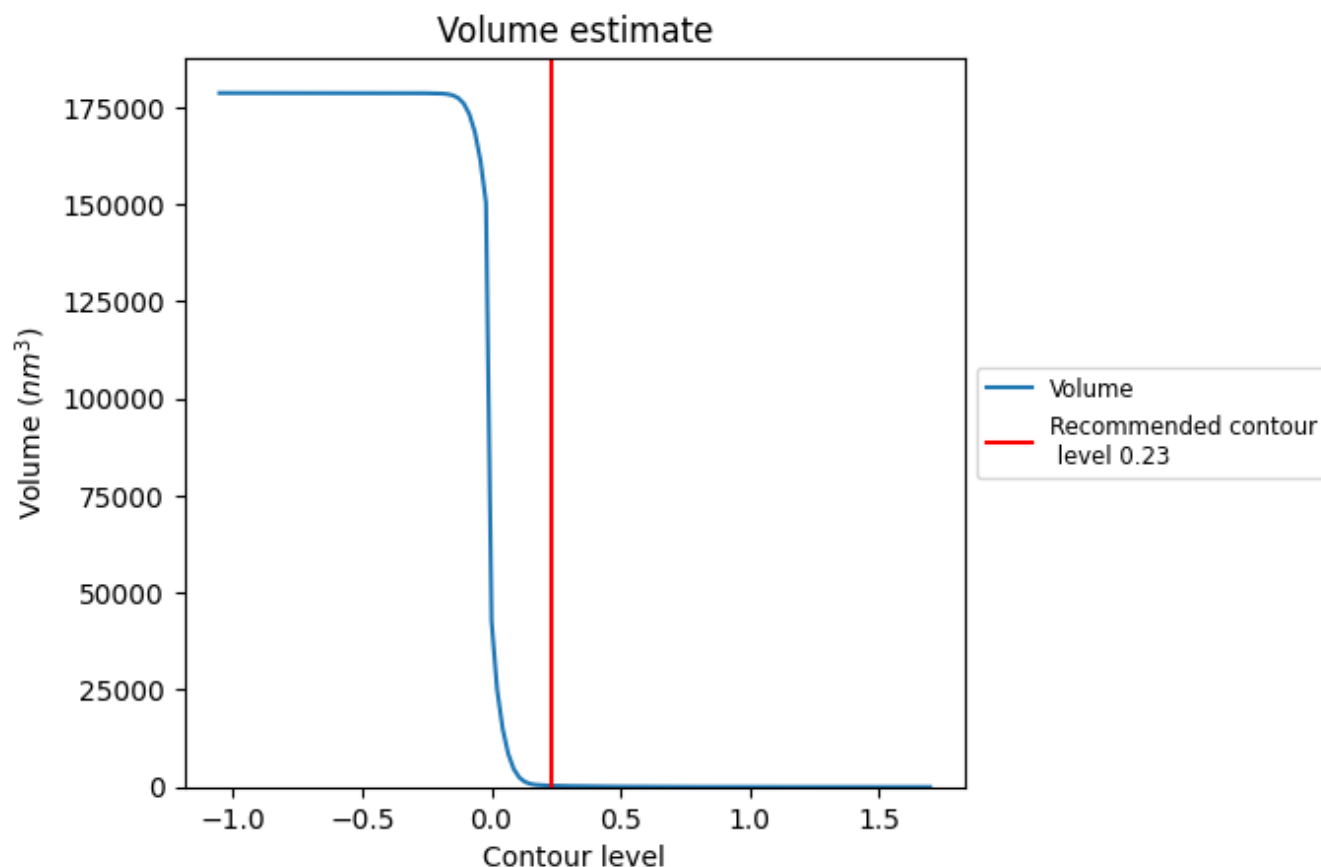
This section contains the results of statistical analysis of the map.

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.

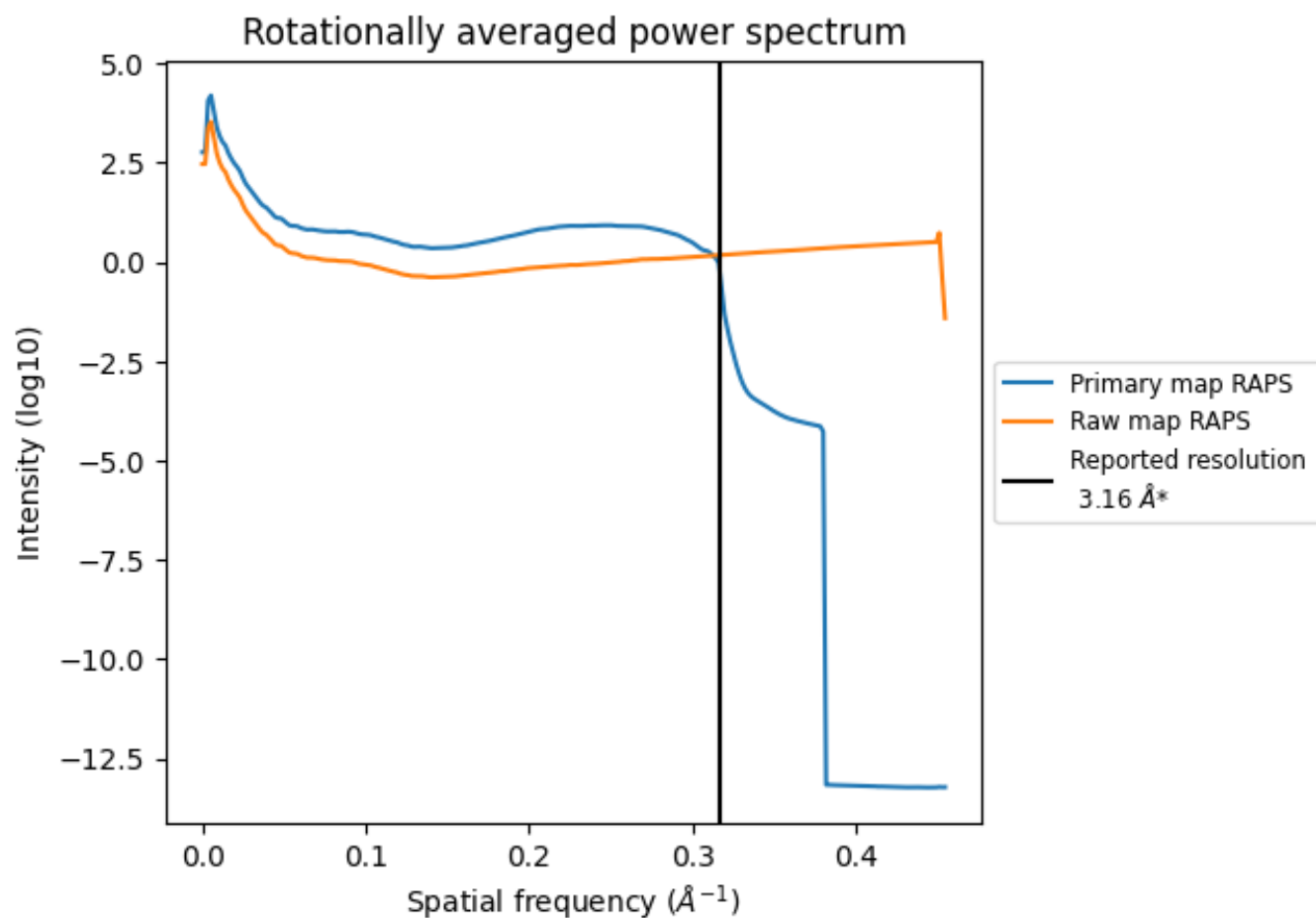
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 331 nm^3 ; this corresponds to an approximate mass of 299 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 ⓘ

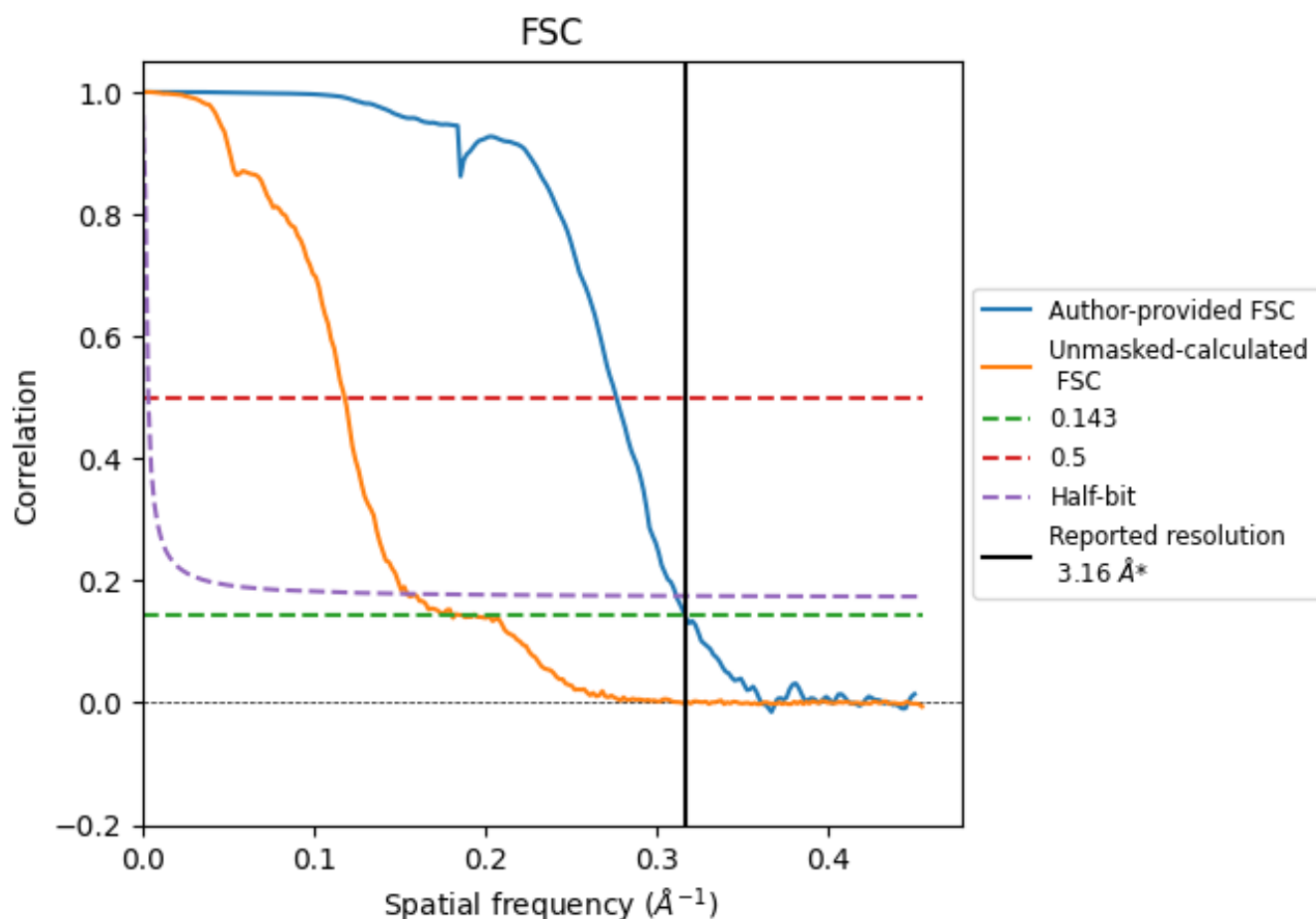


*Reported resolution corresponds to spatial frequency of 0.316 $\text{\AA}^{-1}$

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 0.316 Å⁻¹

8.2 Resolution estimates [i](#)

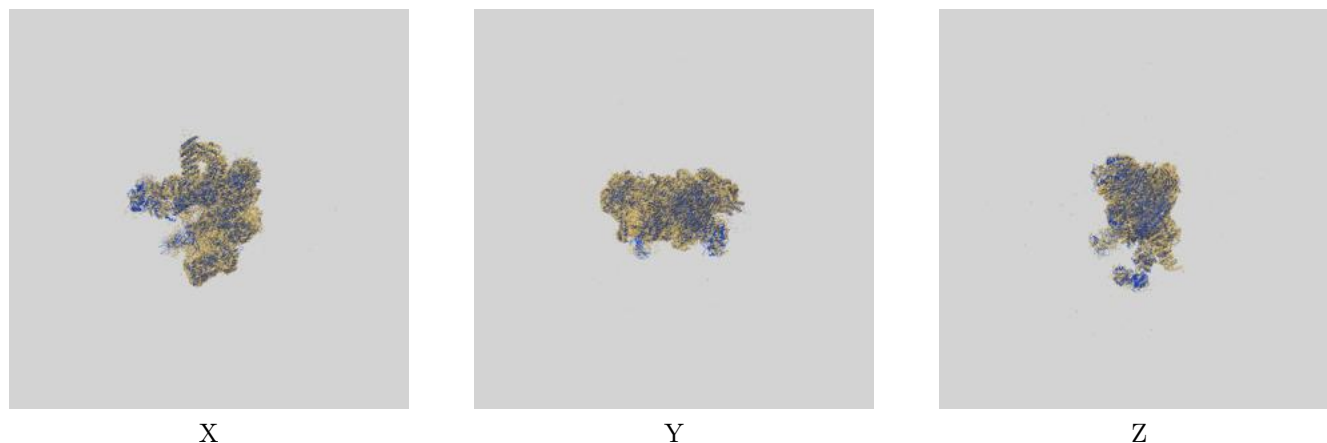
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.16	-	-
Author-provided FSC curve	3.16	3.62	3.21
Unmasked-calculated*	5.54	8.48	6.48

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.54 differs from the reported value 3.16 by more than 10 %

9 Map-model fit [i](#)

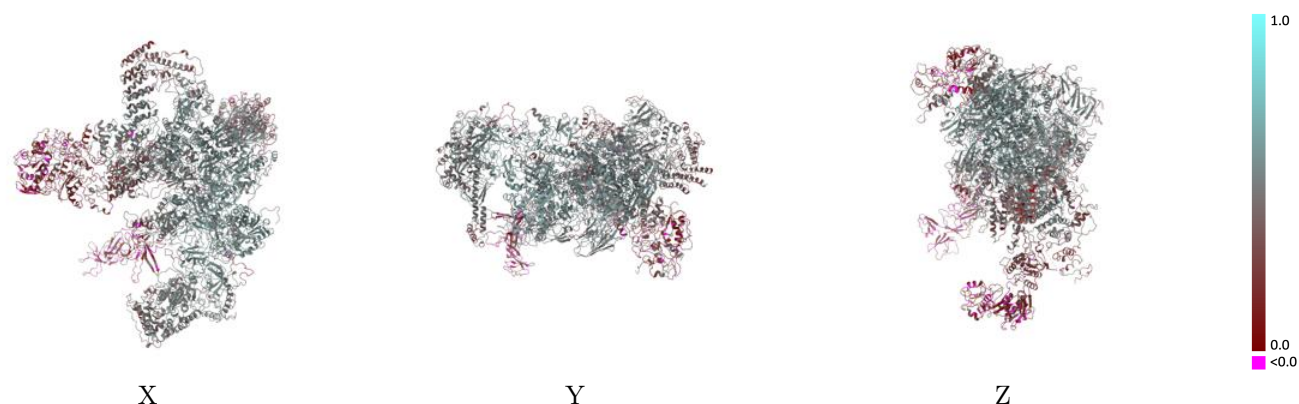
This section contains information regarding the fit between EMDB map EMD-38799 and PDB model 8XZV. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



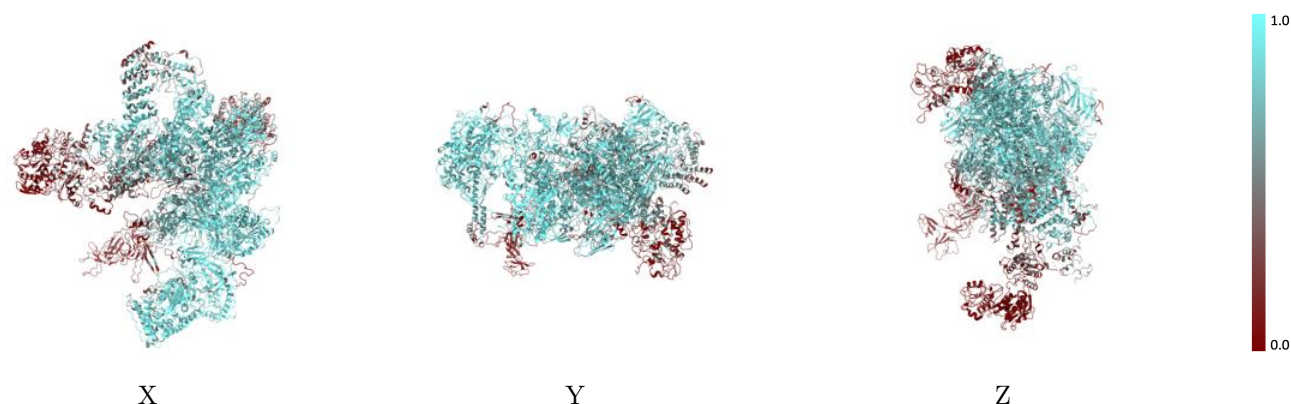
The images above show the 3D surface view of the map at the recommended contour level 0.23 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



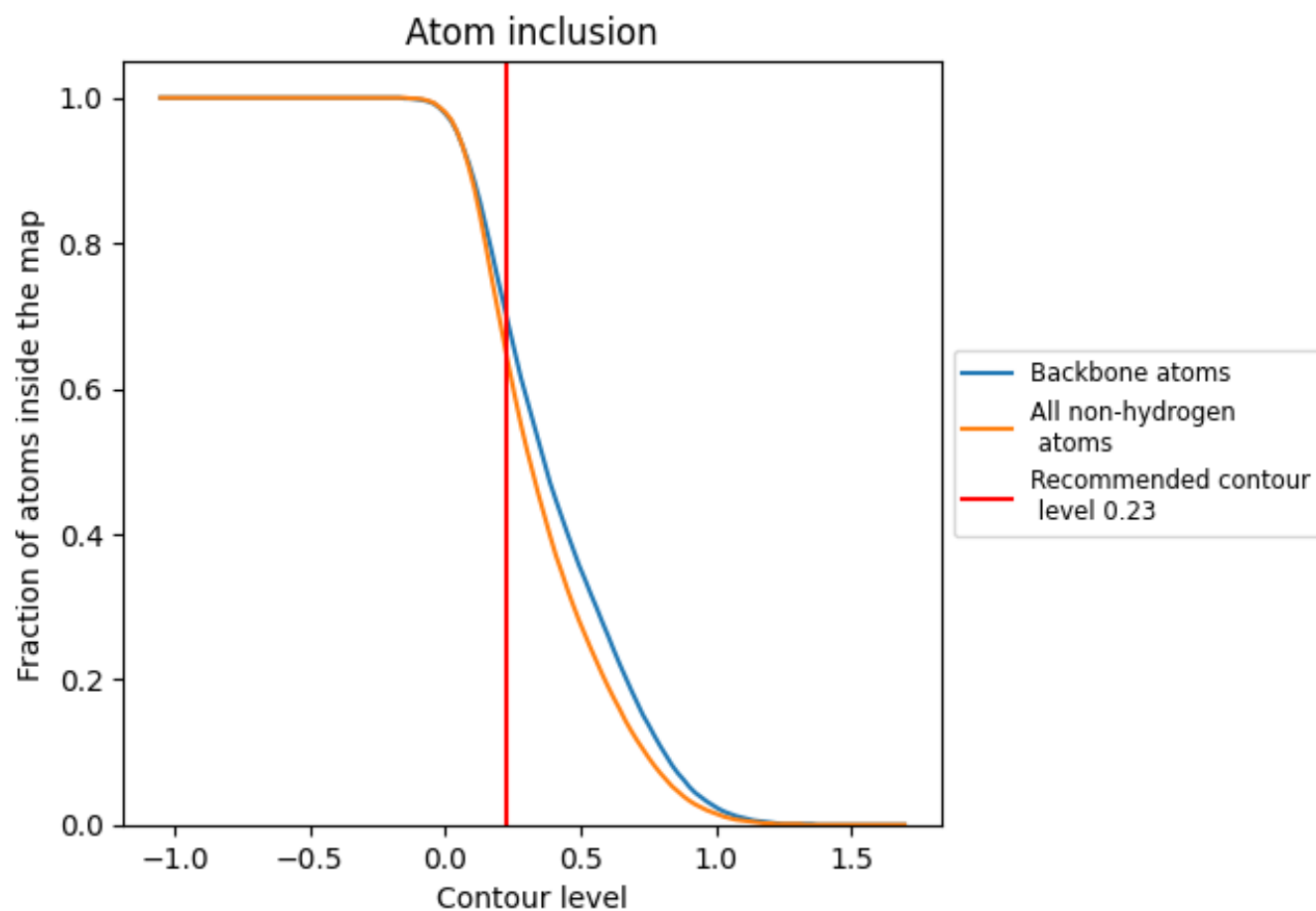
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.23).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 64% 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 (0.23) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6400	 0.4440
A	 0.7800	 0.5120
B	 0.6730	 0.4890
C	 0.5860	 0.4520
D	 0.6430	 0.4480
E	 0.8980	 0.5620
F	 0.8910	 0.5520
G	 0.8460	 0.5320
H	 0.6020	 0.3940
I	 0.7010	 0.4500
J	 0.1120	 0.2100
K	 0.7830	 0.4900
L	 0.8010	 0.4440
M	 0.8750	 0.5030
N	 0.7810	 0.4970
O	 0.7070	 0.4860
P	 0.7760	 0.5010
Q	 0.8490	 0.5150
R	 0.1770	 0.2940
S	 0.2610	 0.2770

