



Full wwPDB EM Validation Report ⓘ

Mar 19, 2024 – 03:38 PM JST

PDB ID : 5ZRV
EMDB ID : EMD-6944
Title : Structure of human mitochondrial trifunctional protein, octamer
Authors : Liang, K.; Li, N.; Dai, J.; Wang, X.; Liu, P.; Chen, X.; Wang, C.; Gao, N.;
Xiao, J.
Deposited on : 2018-04-25
Resolution : 7.70 Å(reported)

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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.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

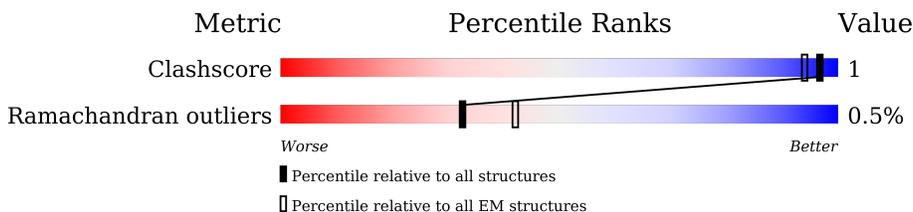
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.70 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023

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	763	 93% 91% • 7%
1	C	763	 93% 92% • 7%
1	E	763	 87% 92% • 7%
1	G	763	 93% 92% • 7%
2	B	474	 89% 87% • 11%
2	D	474	 89% 87% • 11%
2	F	474	 72% 87% • 11%
2	H	474	 84% 87% • 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18096 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 Trifunctional enzyme subunit alpha, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	711	2844	1422	711	711	0	0
1	C	711	2844	1422	711	711	0	0
1	E	711	2844	1422	711	711	0	0
1	G	711	2844	1422	711	711	0	0

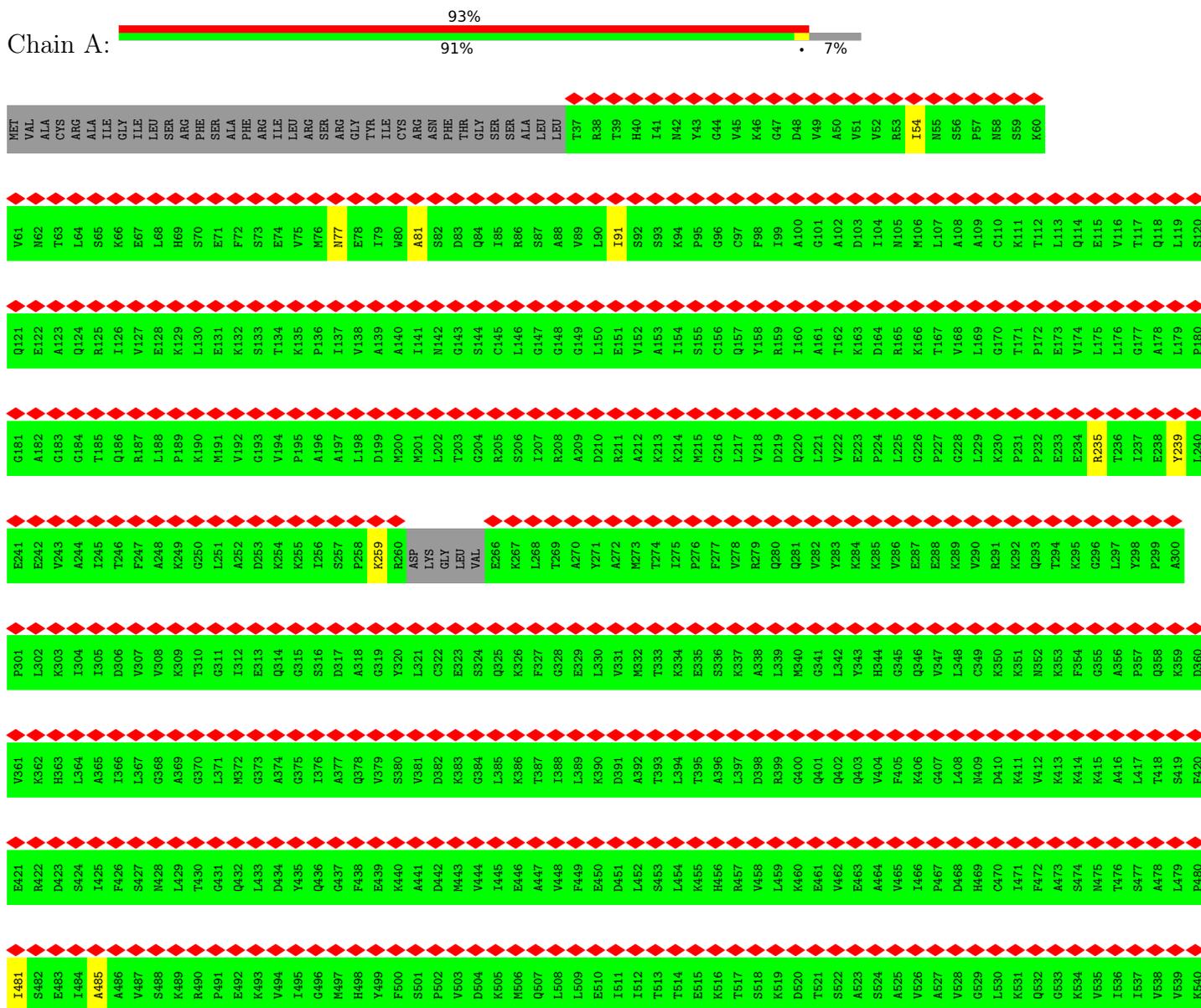
- Molecule 2 is a protein called Trifunctional enzyme subunit beta, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	420	1680	840	420	420	0	0
2	D	420	1680	840	420	420	0	0
2	F	420	1680	840	420	420	0	0
2	H	420	1680	840	420	420	0	0

3 Residue-property plots

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

- Molecule 1: Trifunctional enzyme subunit alpha, mitochondrial



V558	I659	L618	L619	T679	T678	V678	V679	A738	A739
R560	I661	T620	Q621	R680	F681	R680	R681	Y740	Y740
L562	Q663	M622	M623	F681	F681	F681	F681	G741	G741
E564	Q665	V623	V624	M683	M683	M683	M683	K742	K742
G665	V666	S624	S624	E684	E684	E684	E684	F744	F744
V667	V667	K625	K625	A685	A685	A685	A685	T745	T745
P668	P668	G626	G626	R686	R686	R686	R686	P746	P746
K569	K570	F627	F627	M687	M687	M687	M687	C747	C747
L571	D572	L628	L628	C688	C688	C688	C688	Q748	Q748
S573	S573	G629	G629	L689	L689	L689	L689	L749	L749
L574	L574	R630	R630	Q690	Q690	Q690	Q690	L750	L750
T576	T576	K631	K631	E691	E691	E691	E691	A751	A751
S577	S577	S632	S632	G692	G692	G692	G692	D752	D752
F578	F578	G633	G633	I693	I693	I693	I693	H753	H753
G579	G579	K634	K634	L694	L694	L694	L694	A754	A754
F580	F580	G635	G635	A695	A695	A695	A695	N755	N755
P581	P581	F636	F636	T696	T696	T696	T696	S756	S756
V582	V582	TYR	TYR	P697	P697	P697	P697	P757	P757
G583	G583	ILE	ILE	A698	A698	A698	A698	N758	N758
A584	A584	TYR	TYR	E699	E699	E699	E699	K759	K759
A585	A585	GLN	GLN	G700	G700	G700	G700	K760	K760
T586	T586	GLU	GLU	D701	D701	D701	D701	F761	F761
L587	L587	VAL	VAL	I702	I702	I702	I702	Y762	Y762
V588	V588	LYS	LYS	G703	G703	G703	G703	Q763	Q763
D589	D589	ASP	ASP	A704	A704	A704	A704		
E590	E590	L648	L648	V705	V705	V705	V705		
V591	V591	N649	N649	F706	F706	F706	F706		
G592	G592	S650	S650	G707	G707	G707	G707		
V593	V593	D651	D651	L708	L708	L708	L708		
D594	D594	M652	M652	G709	G709	G709	G709		
V595	V595	D653	D653	F710	F710	F710	F710		
A596	A596	S654	S654	P711	P711	P711	P711		
K597	K597	L655	L655	P712	P712	P712	P712		
H598	H598	L656	L656	C713	C713	C713	C713		
V599	V599	A657	A657	L714	L714	L714	L714		
A600	A600	S658	S658	G715	G715	G715	G715		
E601	E601	L659	L659	G716	G716	G716	G716		
D602	D602	K660	K660	P717	P717	P717	P717		
L603	L603	L661	L661	F718	F718	F718	F718		
G604	G604	P662	P662	R719	R719	R719	R719		
K605	K605	P663	P663	F720	F720	F720	F720		
V606	V606	K664	K664	V721	V721	V721	V721		
F607	F607	D665	D665	D722	D722	D722	D722		
G608	G608	S665	S665	L723	L723	L723	L723		
E609	E609	V666	V666	Y724	Y724	Y724	Y724		
R610	R610	S668	S668	G725	G725	G725	G725		
F611	F611	S669	S669	A726	A726	A726	A726		
G612	G612	D670	D670	Q727	Q727	Q727	Q727		
G613	G613	E671	E671	K728	K728	K728	K728		
N615	N615	D672	D672	I729	I729	I729	I729		
P616	P616	I673	I673	D730	D730	D730	D730		
E617	E617	Q674	Q674	R731	R731	R731	R731		
		F675	F675	R732	R732	R732	R732		
		R676	R676	L733	L733	L733	L733		
		L677	L677	K734	K734	K734	K734		
				Y735	Y735	Y735	Y735		
				E736	E736	E736	E736		

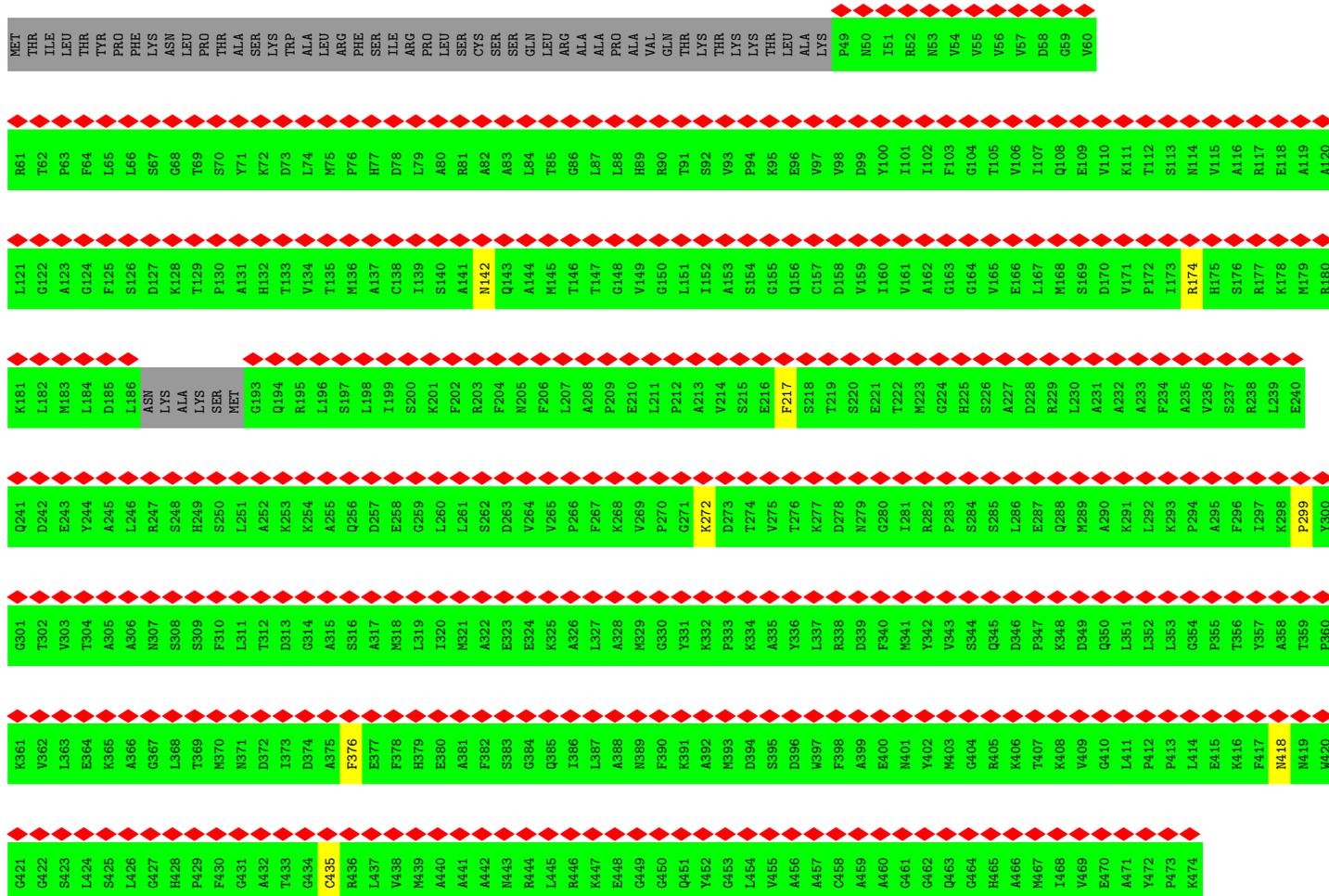
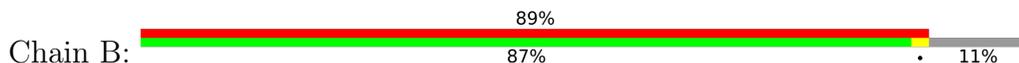
• Molecule 1: Trifunctional enzyme subunit alpha, mitochondrial



MET	VAL	ALA	CYS	ALA	ILE	GLY	LEU	SER	ARG	PHE	SER	ALA	ARG	LEU	GLY	THR	THR	GLY	SER	SER	ALA	LEU	LEU	T37	R38	T39	H40	I41	N42	Y43	G44	V45	R46	G47	D48	V49	A50	V51	V52	R53	R54	M55	S56	F57	N58	S59	R60												
N61	N62	T63	L64	S65	E66	L68	H69	S70	E71	F72	S73	E74	W75	M76	N77	E78	I79	M80	A81	S82	D83	Q84	I85	R86	S87	A88	W89	L90	I91	S92	S93	K94	P95	G96	C97	F98	I99	A100	G101	A102	D103	I104	M105	M106	L107	A108	A109	C110	K111	T112	L113	Q114	E115	V116	T117	Q118	L119	S120	
Q121	E122	A123	Q124	R125	I126	V127	E128	K129	L130	E131	K132	S133	T134	K135	P136	I137	V138	A139	A140	I141	N142	G143	S144	C145	L146	G147	G148	G149	L150	E151	V152	A153	I154	S155	C156	Q157	V158	R159	I160	A161	T162	K163	D164	R165	K166	T167	V168	L169	G170	T171	P172	E173	V174	L175	L176	G177	A178	L179	P180
G181	A182	G183	G184	T185	Q186	R187	L188	P189	K190	M191	V192	G193	V194	P195	A196	A197	L198	D199	M200	M201	L202	T203	G204	R205	S206	I207	R208	A209	D210	R211	A212	K213	K214	M215	G216	L217	V218	D219	Q220	L221	V222	E223	P224	L225	G226	P227	G228	L229	K230	P231	P232	E233	E234	R235	T236	I237	E238	Y239	L240
E241	E242	V243	A244	T245	T246	F247	A248	K249	G250	L251	A252	D253	Q254	K255	T256	S257	P258	K259	R260	ASP	LYS	GLY	LEU	VAL	E266	K267	L268	T269	A270	Y271	A272	M273	T274	L275	P276	F277	V278	R279	Q280	Q281	V282	K284	K285	V286	E287	E288	K289	V290	R291	K292	Q293	K295	T294	G296	L297	Y298	P299	A300	
P301	L302	K303	I304	I305	D306	V307	V308	K309	T310	G311	K312	G313	Q314	G315	S316	D317	A318	G319	Y320	L321	C322	E323	S324	Q325	K326	F327	G328	L329	E330	V331	K332	T333	E335	S336	K337	A338	L339	H340	G341	Q342	Q343	H344	G345	G346	V347	L348	C349	D350	K351	N352	K353	F354	G355	A356	P357	K358	D360		
V361	K362	H363	L364	A365	I366	L367	G368	A369	G370	L371	K372	G373	A374	G375	I376	A377	Q378	V379	S380	V381	D382	K383	G384	L385	K386	T387	I388	L389	K390	D391	A392	T393	L394	T395	A396	L397	D398	R399	G400	Q401	Q402	Q403	V404	F405	K406	G407	L408	M409	D410	K411	V412	K413	K414	K415	A416	L417	T418	S419	F420
E421	R422	D423	S424	I425	F426	S427	N428	L429	T430	G431	Q432	L433	D434	Y435	Q436	G437	F438	E439	K440	A441	D442	M443	V444	I445	E446	A447	V448	F449	E450	D451	L452	S453	T454	E455	K456	H457	R458	L459	K460	E461	V462	E463	A464	V465	I466	P467	D468	H469	C470	I471	F472	S474	M475	T476	S477	A478	L479	P480	
I481	S482	E483	I484	A485	A486	V487	S488	K489	R490	P491	E492	K493	V494	I495	Q496	M497	H498	Y499	F500	S501	D502	V503	D504	K505	M506	Q507	V508	L509	E510	I511	I512	T513	T514	E515	K516	T517	S518	K519	D520	T521	S522	A523	S524	A525	V526	A527	V528	G529	L530	K531	Q532	G533	K534	V535	I536	I537	V538	V539	K540



• Molecule 2: Trifunctional enzyme subunit beta, mitochondrial

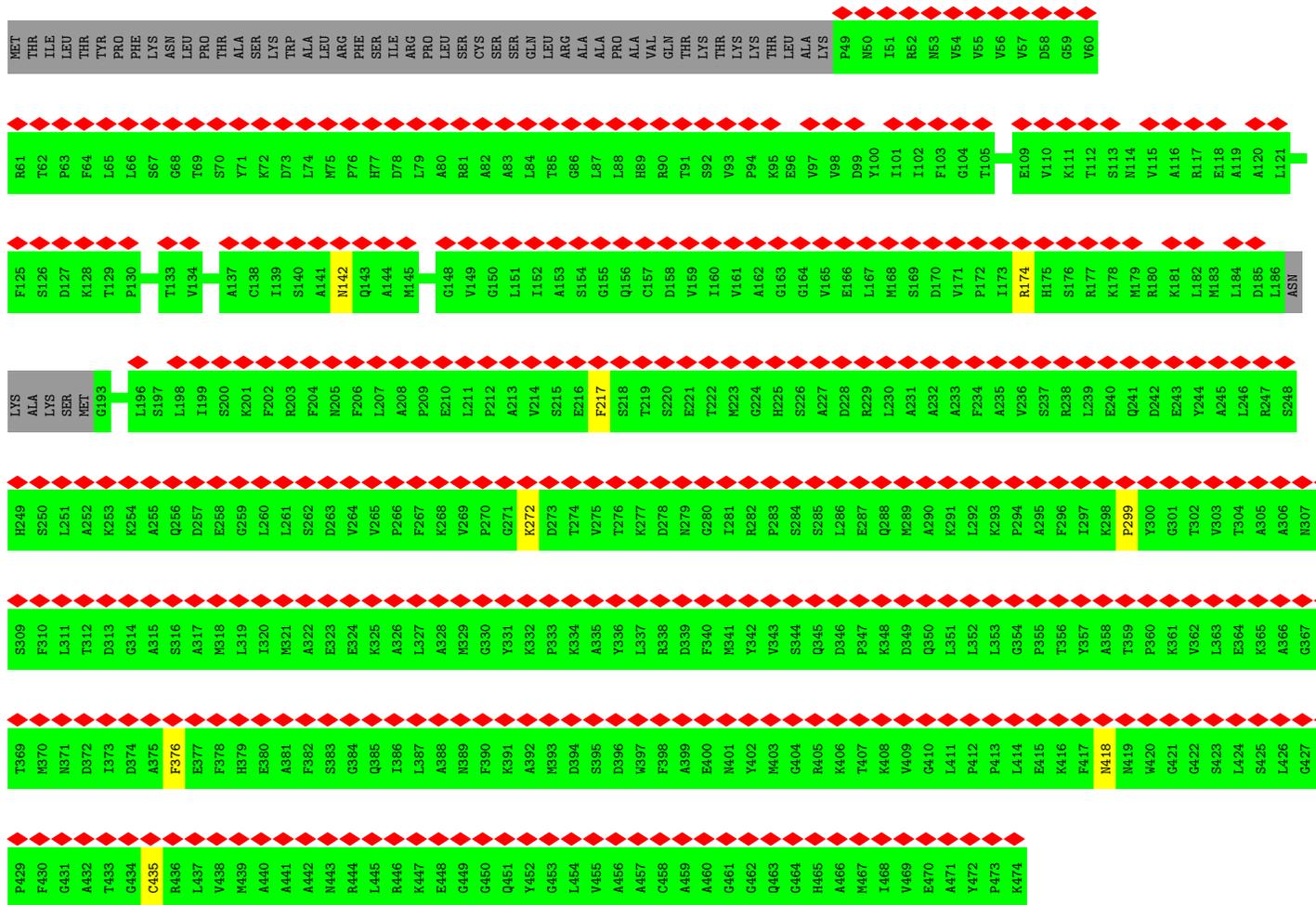
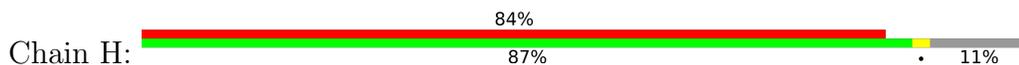


• Molecule 2: Trifunctional enzyme subunit beta, mitochondrial





• Molecule 2: Trifunctional enzyme subunit beta, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48564	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 ($e^-/\text{\AA}^2$)	50	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	0.793	Depositor
Minimum map value	-0.659	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.029	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	337.92, 337.92, 337.92	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.64, 2.64, 2.64	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.33	0/2841	0.61	0/3546
1	C	0.33	0/2841	0.61	0/3546
1	E	0.33	0/2841	0.61	0/3546
1	G	0.33	0/2841	0.61	0/3546
2	B	0.36	0/1678	0.67	0/2094
2	D	0.36	0/1678	0.68	0/2094
2	F	0.36	0/1678	0.68	0/2094
2	H	0.36	0/1678	0.68	0/2094
All	All	0.34	0/18076	0.64	0/22560

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	5
2	D	0	5
2	F	0	5
2	H	0	5
All	All	0	20

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	142	ASN	Peptide
2	B	174	ARG	Peptide
2	B	272	LYS	Peptide

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Mol	Chain	Res	Type	Group
2	B	376	PHE	Peptide
2	B	435	CYS	Peptide
2	D	142	ASN	Peptide
2	D	174	ARG	Peptide
2	D	272	LYS	Peptide
2	D	376	PHE	Peptide
2	D	435	CYS	Peptide
2	F	142	ASN	Peptide
2	F	174	ARG	Peptide
2	F	272	LYS	Peptide
2	F	376	PHE	Peptide
2	F	435	CYS	Peptide
2	H	142	ASN	Peptide
2	H	174	ARG	Peptide
2	H	272	LYS	Peptide
2	H	376	PHE	Peptide
2	H	435	CYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2844	0	801	5	0
1	C	2844	0	801	4	0
1	E	2844	0	801	3	0
1	G	2844	0	801	5	0
2	B	1680	0	468	0	0
2	D	1680	0	468	0	0
2	F	1680	0	468	0	0
2	H	1680	0	468	0	0
All	All	18096	0	5076	17	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 1.

All (17) 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)
1:A:235:ARG:O	1:A:239:TYR:N	2.49	0.46
1:C:235:ARG:O	1:C:239:TYR:N	2.49	0.46
1:G:235:ARG:O	1:G:239:TYR:N	2.49	0.45
1:E:235:ARG:O	1:E:239:TYR:N	2.49	0.45
1:C:77:ASN:O	1:C:81:ALA:N	2.50	0.45
1:A:77:ASN:O	1:A:81:ALA:N	2.50	0.45
1:E:77:ASN:O	1:E:81:ALA:N	2.50	0.45
1:G:77:ASN:O	1:G:81:ALA:N	2.50	0.44
1:A:603:LEU:O	1:A:608:GLY:N	2.47	0.44
1:G:603:LEU:O	1:G:608:GLY:N	2.47	0.44
1:A:54:ILE:N	1:A:91:ILE:O	2.53	0.42
1:G:54:ILE:N	1:G:91:ILE:O	2.53	0.42
1:E:481:ILE:O	1:E:485:ALA:N	2.54	0.41
1:C:603:LEU:O	1:C:608:GLY:N	2.47	0.41
1:G:481:ILE:O	1:G:485:ALA:N	2.54	0.41
1:C:481:ILE:O	1:C:485:ALA:N	2.53	0.41
1:A:481:ILE:O	1:A:485:ALA:N	2.54	0.41

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	705/763 (92%)	626 (89%)	76 (11%)	3 (0%)	34	72
1	C	705/763 (92%)	626 (89%)	77 (11%)	2 (0%)	41	77
1	E	705/763 (92%)	626 (89%)	76 (11%)	3 (0%)	34	72
1	G	705/763 (92%)	626 (89%)	77 (11%)	2 (0%)	41	77
2	B	416/474 (88%)	354 (85%)	59 (14%)	3 (1%)	22	63
2	D	416/474 (88%)	352 (85%)	61 (15%)	3 (1%)	22	63
2	F	416/474 (88%)	353 (85%)	60 (14%)	3 (1%)	22	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	416/474 (88%)	352 (85%)	61 (15%)	3 (1%)	22	63
All	All	4484/4948 (91%)	3915 (87%)	547 (12%)	22 (0%)	32	69

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	758	ASN
1	C	758	ASN
1	E	758	ASN
1	G	758	ASN
1	A	259	LYS
1	E	259	LYS
1	A	662	PRO
2	B	217	PHE
2	B	299	PRO
2	B	418	ASN
1	C	662	PRO
2	D	217	PHE
2	D	299	PRO
2	D	418	ASN
1	E	662	PRO
2	F	217	PHE
2	F	299	PRO
2	F	418	ASN
1	G	662	PRO
2	H	217	PHE
2	H	299	PRO
2	H	418	ASN

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

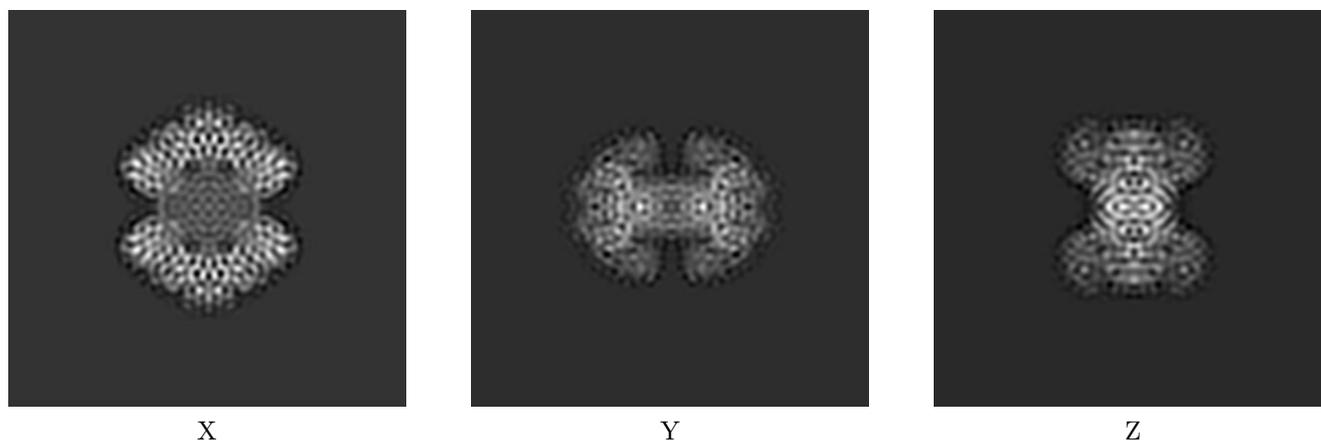
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6944. 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](#)

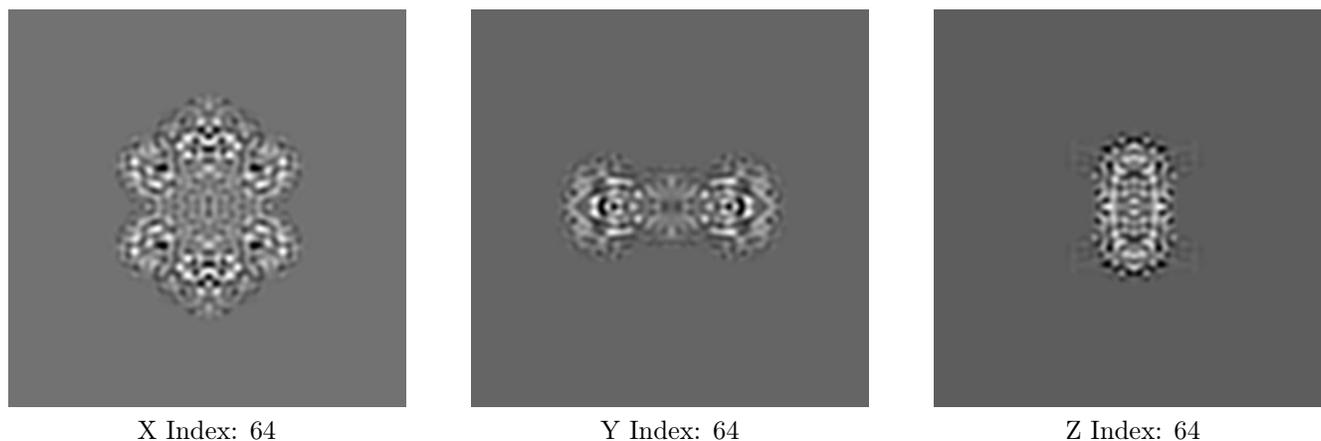
6.1.1 Primary map



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

6.2 Central slices [i](#)

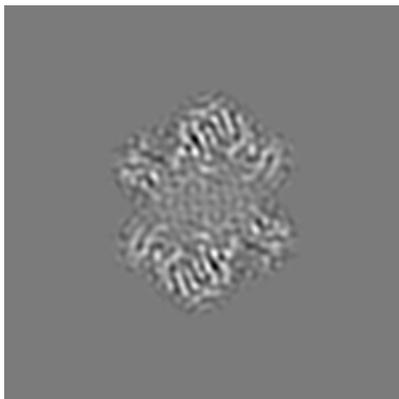
6.2.1 Primary map



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: 68



Y Index: 68

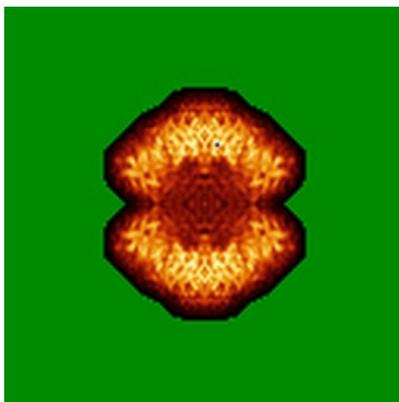


Z Index: 47

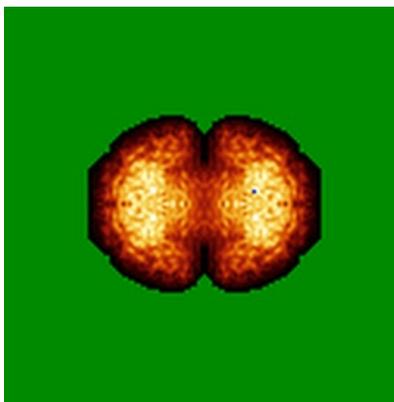
The images above show the largest variance slices of the map in three orthogonal directions.

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

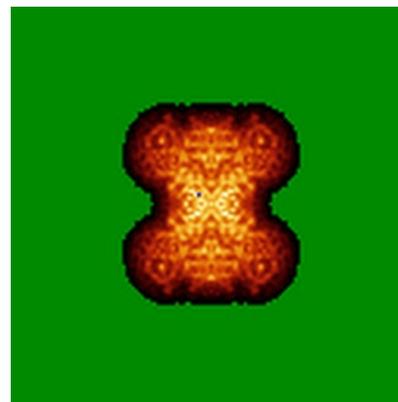
6.4.1 Primary map



X



Y

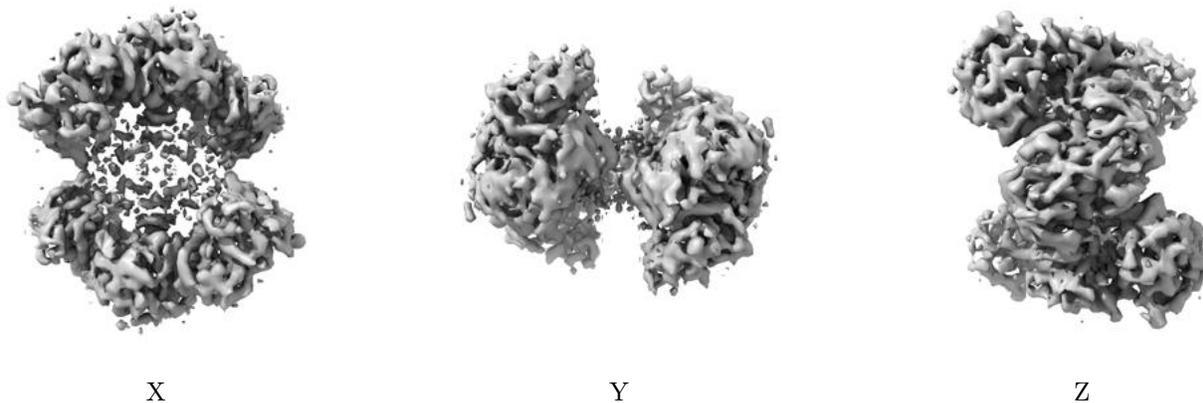


Z

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 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

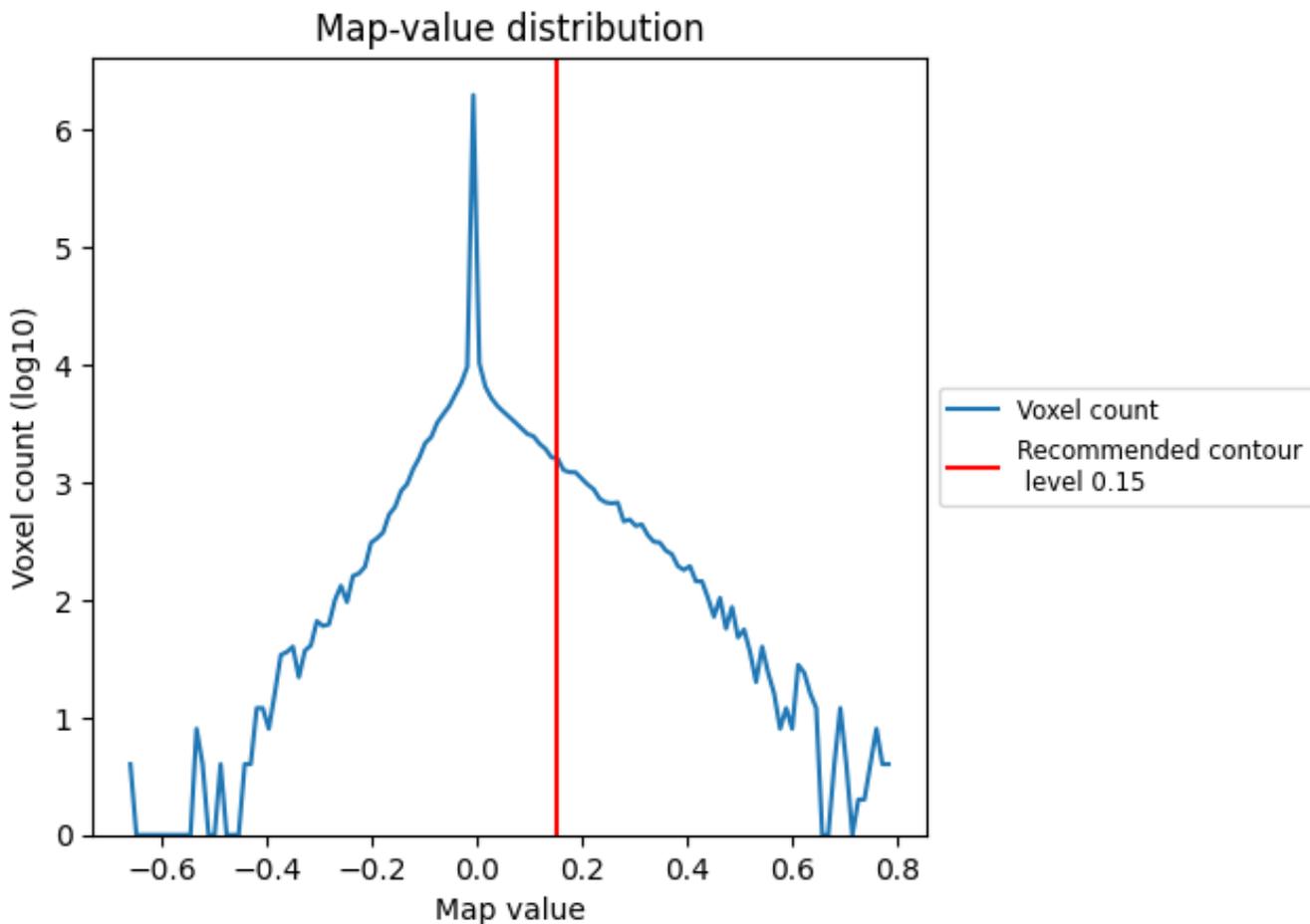
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

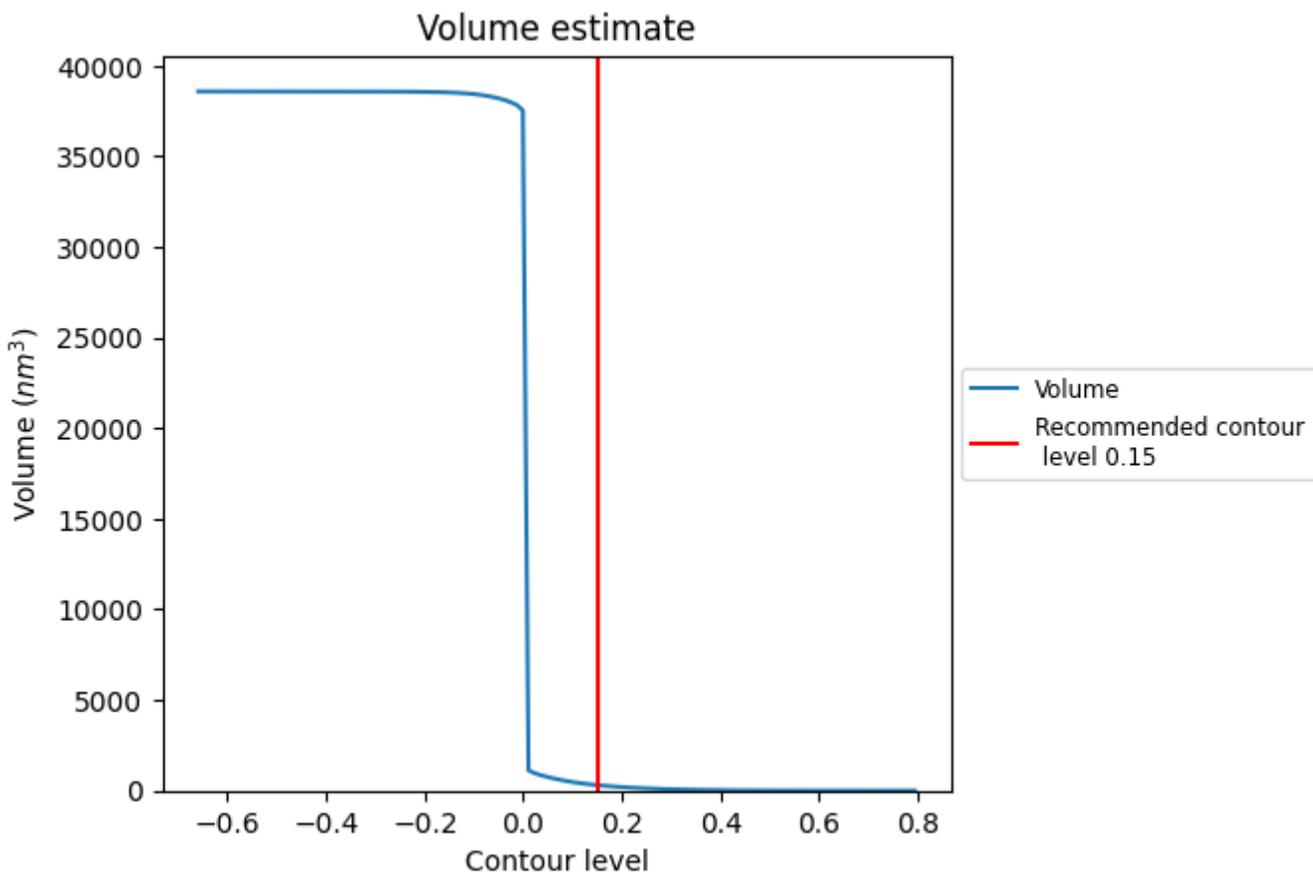
This section contains the results of statistical analysis of the map.

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.

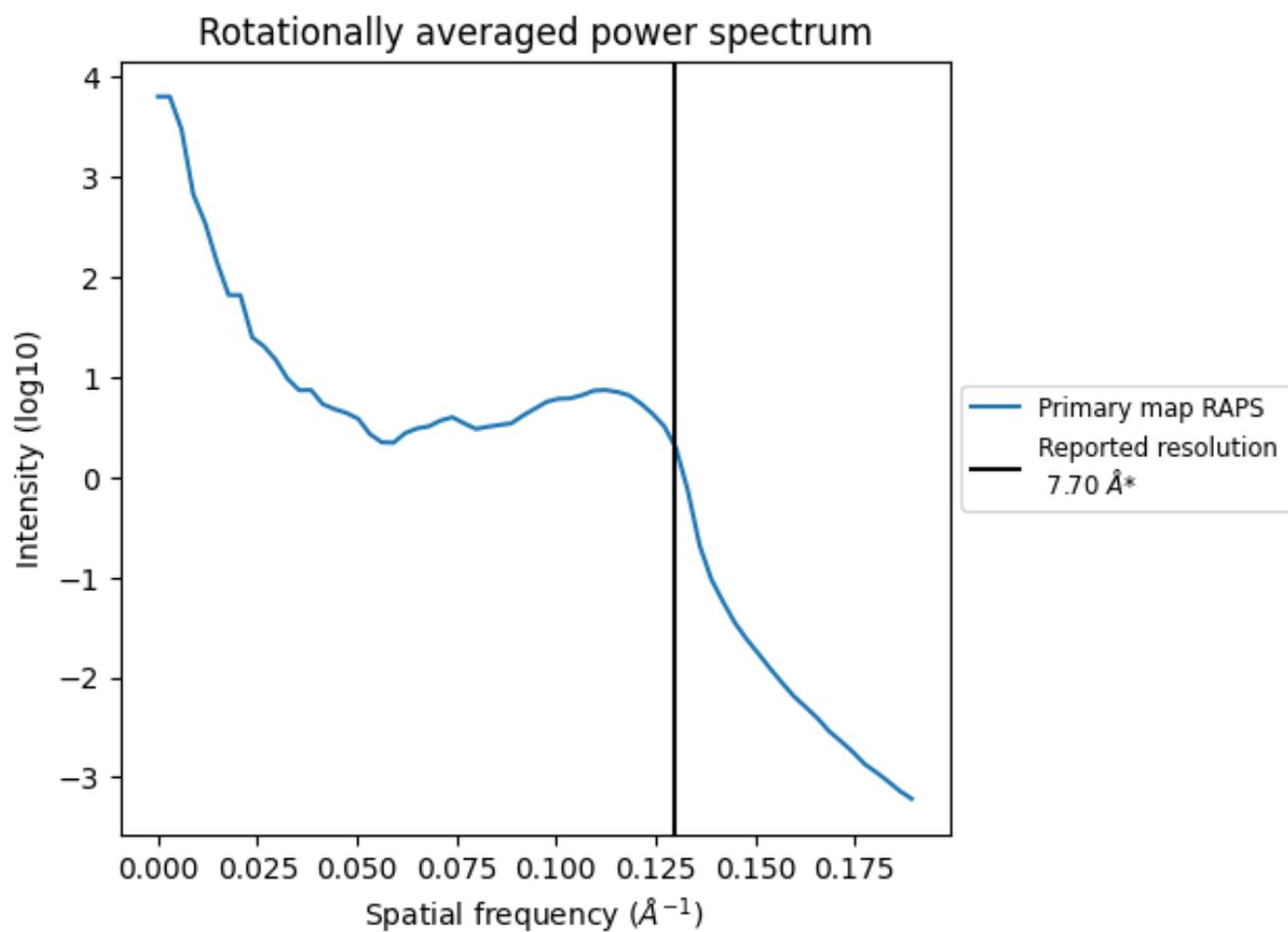
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 301 nm³; this corresponds to an approximate mass of 272 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 0.130\AA^{-1}

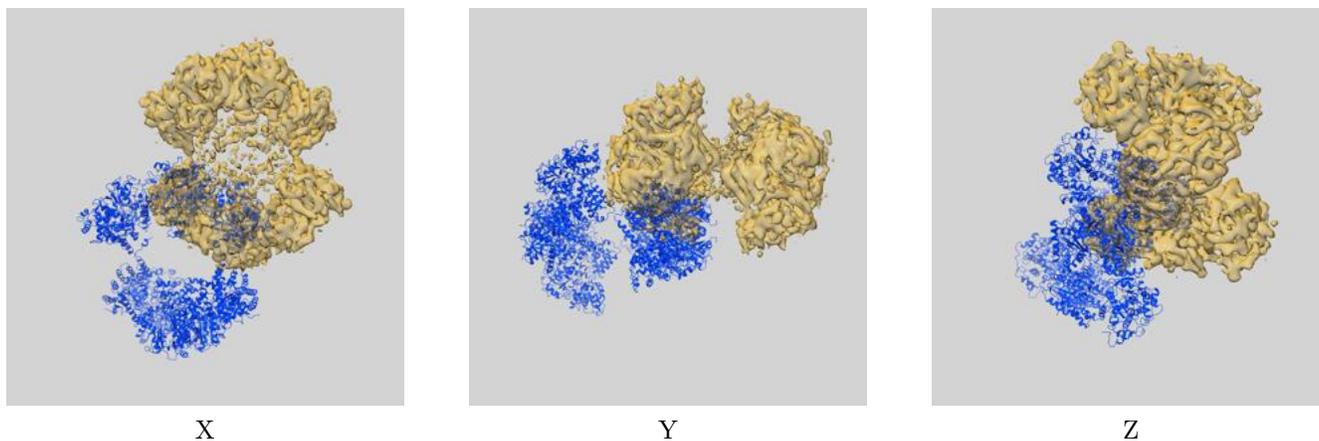
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

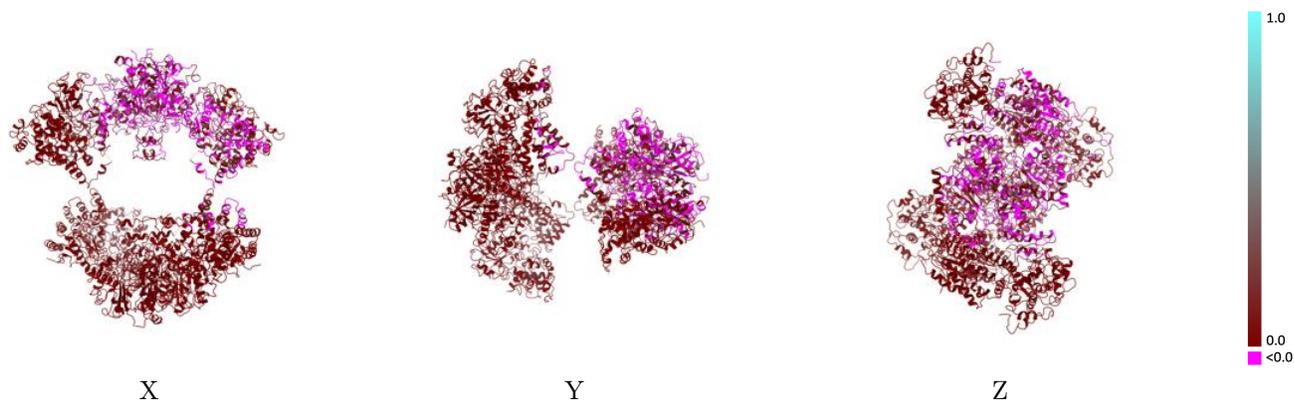
This section contains information regarding the fit between EMDB map EMD-6944 and PDB model 5ZRV. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



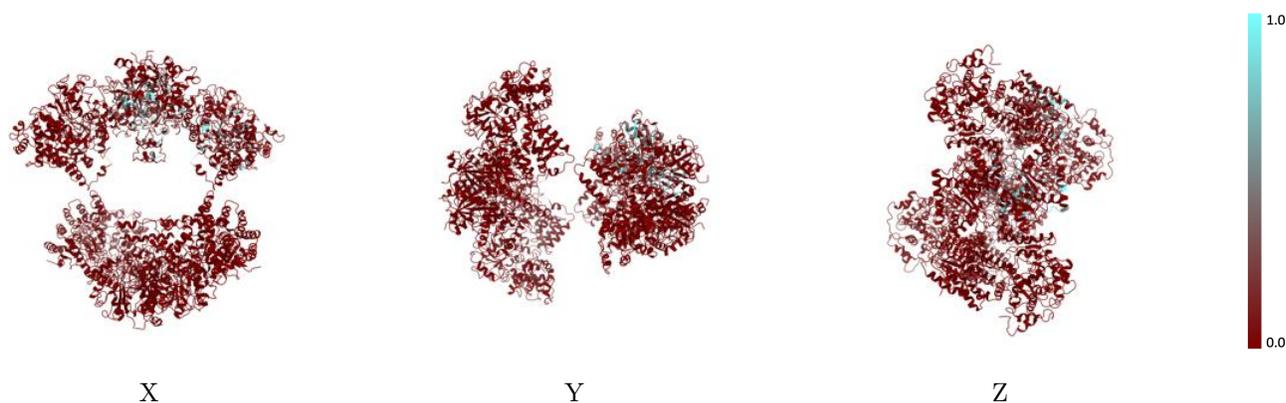
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



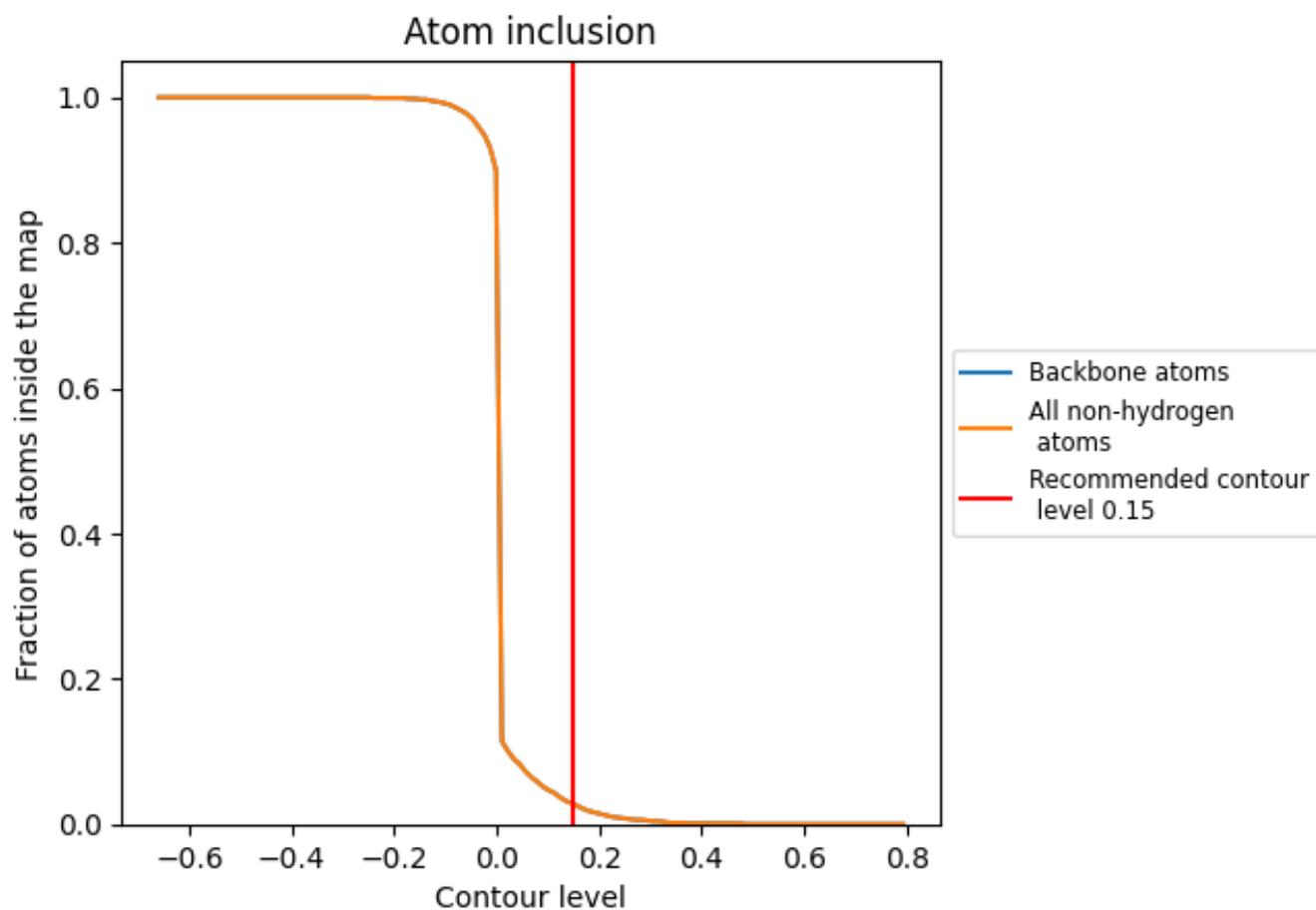
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 3% of all backbone atoms, 3% 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	 0.0280	 0.0020
A	 0.0000	 0.0050
B	 0.0000	 0.0000
C	 0.0000	 0.0000
D	 0.0000	 0.0000
E	 0.0550	 0.0040
F	 0.1590	 -0.0000
G	 0.0010	 0.0050
H	 0.0430	 0.0010

