



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:12 PM UTC

PDB ID : 7MKQ / pdb_00007mkq
EMDB ID : EMD-23903
Title : Escherichia coli RNA polymerase and RapA binary complex
Authors : Qayyum, M.Z.; Murakami, K.S.
Deposited on : 2021-04-26
Resolution : 4.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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<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:

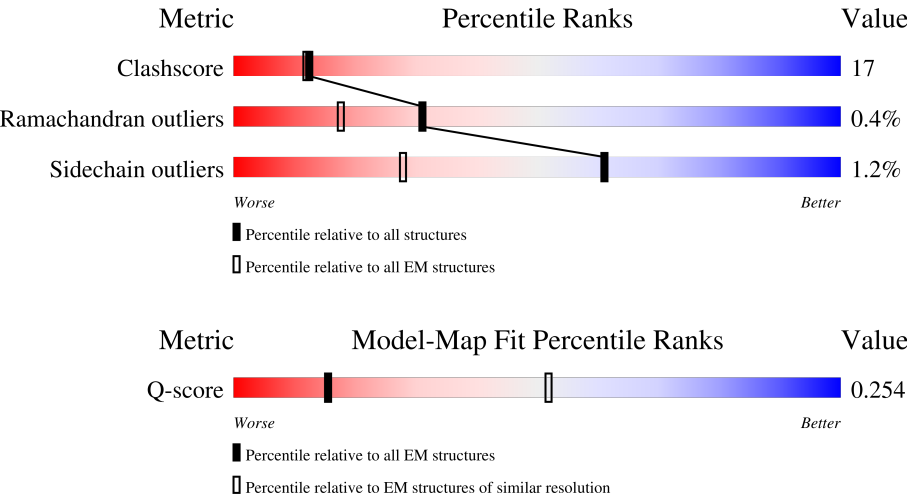
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.80 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	1575 (4.30 - 5.30)

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	237	
1	B	237	
2	C	1340	
3	D	1363	

Continued on next page...

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Mol	Chain	Length	Quality of chain
4	E	91	18% 49% 34% 16%
5	L	968	67% 33%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 32822 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	231	Total	C	N	O	S	0	0
			1794	1117	318	353	6		
1	B	230	Total	C	N	O	S	0	0
			1786	1112	317	351	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1340	Total	C	N	O	S	0	0
			10570	6631	1841	2055	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1338	Total	C	N	O	S	0	0
			10368	6514	1847	1958	49		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	76	Total	C	N	O	S	0	0
			605	368	115	121	1		

- Molecule 5 is a protein called RNA polymerase-associated protein RapA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	967	Total	C	N	O	S	0	0
			7696	4820	1378	1470	28		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	D	1	Total	Mg	0
			1	1	

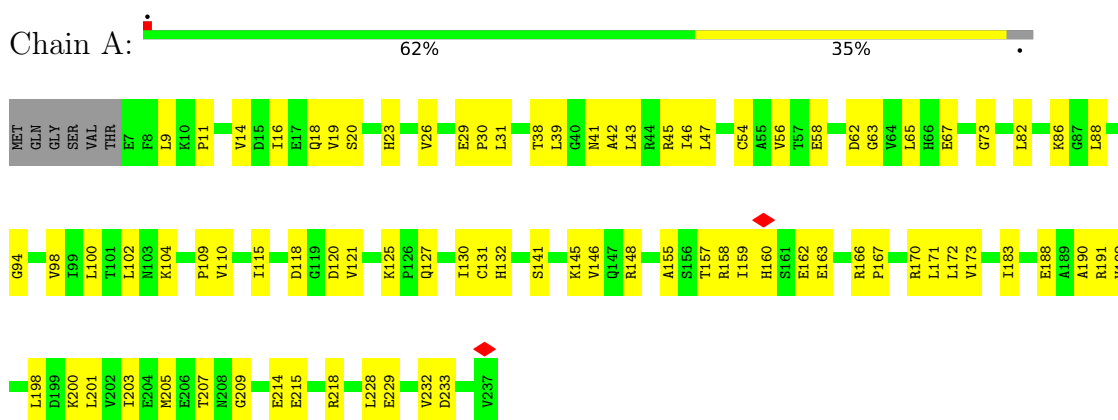
- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
7	D	2	Total	Zn	0
			2	2	

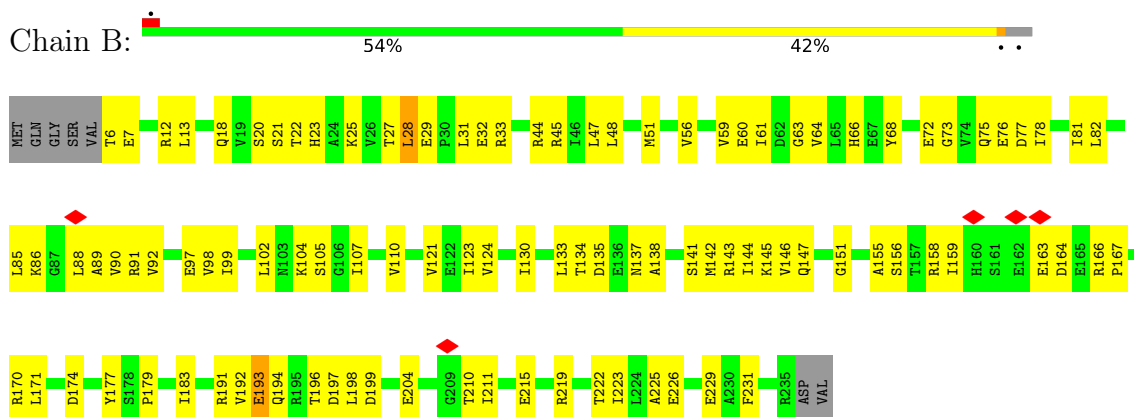
3 Residue-property plots

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

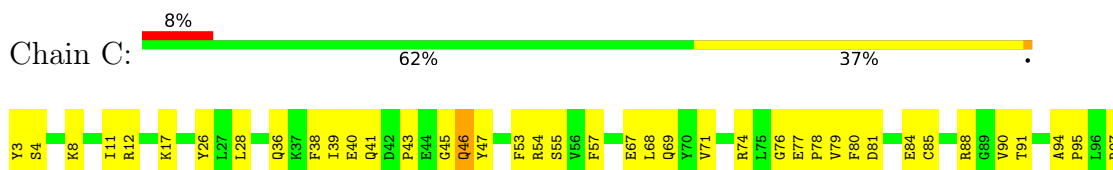
- Molecule 1: DNA-directed RNA polymerase subunit alpha



- Molecule 1: DNA-directed RNA polymerase subunit alpha



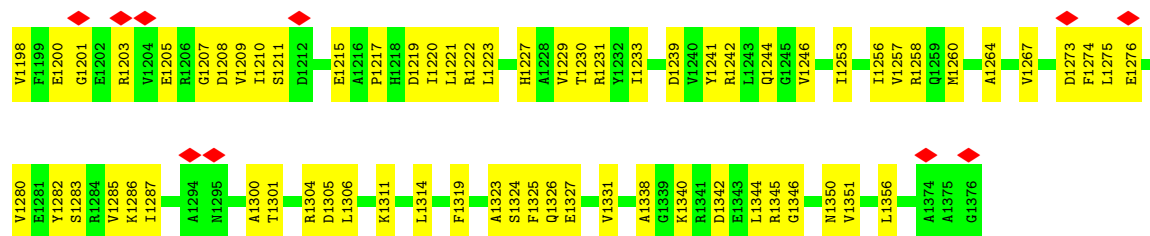
- Molecule 2: DNA-directed RNA polymerase subunit beta



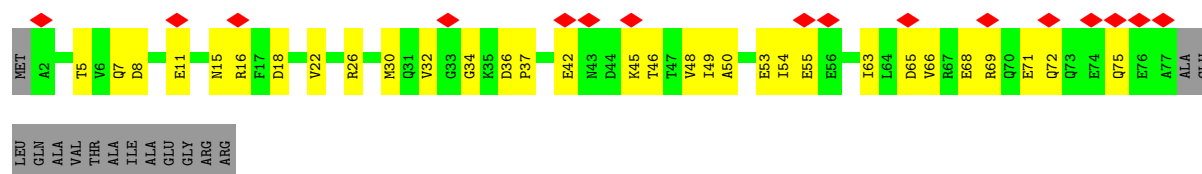
N1336	R1216	Q1111	D1004	L902	F812	D896	D801	V502	K404	L317	S252	F186	V88
E1342	R1223	E1114	E1005	I905	E813	K697	E802	K603	F405	S318	F253	E187	K99
	V1227	M1119	Q1013	E908	D814	P698	Y605	E504	L409	L319	D254	F188	R101
	G1228	A1120	E1016	A910	S819	E705	L606	M515	L410	A323	I255	E256	L102
	Y1229	A1121	Q1017	A910	D826	R706	S607	N519	E412	K324	A257	N193	E106
	M1230	K1122	Y1018	S911	R827	V714	I609	P620	E413	L325	N258	L194	R107
	M1231	G1123	L1021	D912	T829	A716	E810	L521	L414	S326	Q259	F195	E109
	L1232	I1124	K1022	V913	T829	T715	Y614	S522		Q257	K260	D199	A109
	K1234	G1125	H1023	K914	T829	A717	V615	E523	S417	K331	Y261	R200	P110
	L1235		E1024	D915	S840	V717	I616	I524		K332	V262	K203	K118
			F1025	S916	R841	K719	E624	T525	K422	R332	V263	K203	E119
	M1243		E1026	S917	R841	R720	D624	R528	D423	I333	E264	A206	Q120
	H1244		K1027	V920	T843	R726	E626	R529	D424	T335	K265		E121
	A1245		L1028	T935	G846	V727	F629	I530	I426	L336	G266	I209	V122
	L1246		L1029	R936	P847	D728	F632	I538	M429	N339	R267	I209	L129
	S1247		E1030	D937	E848	R731	D632	A543	L432	D940	R268	R211	M130
			R1033	E938	E849	V732	L633	H551	L436	L341	I269	A212	T131
	L1269		R1034	V939	T851	V733	V634	H552	R437	R272	A271	L213	D132
	F1265		K1035	E940	T854	I734	T635	T553	M437	H273	T270	N214	N133
	G1266		I1036	K941	P855	K735	C636	H554	G438	I274	R275	Y215	G134
	G1267		T1037	D942	V857	V736	S642	R557	K439	I347	Q276	T216	T135
	Q1268		D1040	K943	G864	Y742	S643	V558	G440	S348	I277	T217	I138
	R1269		L1041	E947	L865	A746	L644	C559	E441	R352	E278	E218	E142
	E1274		L1042	E950	G869	I750	R647	P560	R451	P355	K279	Q219	R143
	V1275		K1048	K957	G879	I756	V650	P564	E458	T356	D222	I220	E147
	W1276		K1059	A958	G880	K757	V655	E565		N357	L223	L221	Q148
	E1279		I1060	L960	G881	Q767	S662	N572	E461	R359	F224	F225	P153
	A1283		P1061	E963	G882	R779	V663	S574	F464	R368	E290	K227	G154
	A1284		G1062	L964	D881	L783	E672	L575	R465	R371	Y291	V228	V155
	Y1285		P1063	E964	L882	A784	H673	S576	V466	G372	F230	I229	K161
	M1290		P1064	E965	L883	V887	D674	V577	G467	G373	E231	F230	G162
	L1291		I1070	L964	G884	P787	D675	A579	V469	E374	I232	E231	K163
	L1291		G1071	E966	G885	S788	A676	N582	R470	R378	I232	I232	T164
	K1294		N1072	E967	G886	E788	M677		V471	E379	D234	D234	S167
	K1294		K1073	E968	G887	E788	R678	F586	E472	E379	N235	N235	G168
	V1298		I1076	E969	G888	P787	R678	L587	A474	E379	K236	K236	K169
	N1299		P1076	E970	G889	S788	R678	E588	V475	E379	D300	L237	V170
	G1300		P1077	E971	G890	E788	M681	T589		E382	Y301	Q238	L171
	R1301		I1078	E972	G891	L796	M684	P590	G482	N387	I302	N239	Y172
			Y1087	E973	G892	Q797	M685	Y591		L388	E297	E240	R175
				E974	G893	Q798	M686	V594		L388	A298	E240	R175
				E975	G894	Q799	M687	T595		L388	K299	E240	I176
				E976	G895	M800	Q688	D596		L388	E304	L241	I177
				E977	G896	R801	Q688	T596		L388	S305	V242	F178
				E978	G897	V802	Q689	G597		L388	E392	P243	Y179
				E979	G898	N808	T692	V599		L388	T306	E244	Y179
				E980	G899		L693	V599		L388	G307	E244	S182
				E981	G900			T600		L388	E308	R245	S182
				E982	G901					L388	L309	L246	D185
				E983	G902					L388	I310	R247	D185
				E984	G903					L388	C311	G248	D185
				E985	G904					L388	A312	E249	D185
				E986	G905					L388	A313	T250	D185
				E987	G906					L388	N314	A251	D185
				E988	G907					L388	E316		D185
				E989	G908					L388			D185
				E990	G909					L388			D185
				E991	G910					L388			D185
				E992	G911					L388			D185
				E993	G912					L388			D185
				E994	G913					L388			D185
				E995	G914					L388			D185
				E996	G915					L388			D185
				E997	G916					L388			D185
				E998	G917					L388			D185
				E999	G918					L388			D185
				E1000	G919					L388			D185
				E1001	G920					L388			D185
				E1002	G921					L388			D185
				E1003	G922					L388			D185
				E1004	G923					L388			D185
				E1005	G924					L388			D185
				E1006	G925					L388			D185
				E1007	G926					L388			D185
				E1008	G927					L388			D185
				E1009	G928					L388			D185
				E1010	G929					L388			D185
				E1011	G930					L388			D185
				E1012	G931					L388			D185
				E1013	G932					L388			D185
				E1014	G933					L388			D185
				E1015	G934					L388			D185
				E1016	G935					L388			D185
				E1017	G936					L388			D185
				E1018	G937					L388			D185
				E1019	G938					L388			D185
				E1020	G939					L388			D185
				E1021	G940					L388			D185
				E1022	G941					L388			D185
				E1023	G942					L388			D185
				E1024	G943					L388			D185
				E1025	G944					L388			D185
				E1026	G945					L388			D185
				E1027	G946					L388			D185
				E1028	G947					L388			D185
				E1029	G948					L388			D185
				E1030	G949					L388			D185
				E1031	G950					L388			D185
				E1032	G951					L388			D185
				E1033	G952					L388			D185
				E1034	G953					L388			D185
				E1035	G954					L388			D185
				E1036	G955					L388			D185
				E1037	G956					L388			D185
				E1038	G957					L388			D185
				E1039	G958					L388			D185
				E1040	G959					L388			D185
				E1041	G960					L388			D185
				E1042	G961					L388			D185
				E1043	G962					L388			D185
				E1044	G963					L388			D185
				E1045	G964					L388			D185
				E1046	G965					L388			D185
				E1047	G966					L388			D185
				E1048	G967					L388			D185
				E1049	G968					L388			D185
				E1050	G969					L388			D185
				E1051	G970					L388			D185
				E1052	G971					L388			D185
				E1053	G972					L388			D185
				E1054	G973					L388			D185
				E1055	G974					L388			D185
				E1056	G975					L388			D185
				E1057	G976					L388			D185
				E1058	G977					L388			D185
				E1059	G978					L388			D185
				E1060	G979					L388			D185
				E1061	G980					L388			D185
				E1062	G981					L388			D185
				E1063	G982					L388			D185
				E1064	G983					L388			D185
				E1065	G984					L388			D185
				E1066	G985					L388			D185
				E1067	G986					L388			D185
				E1068	G987					L388			D185
				E1069	G988					L388			D185
				E1070	G989					L388			D185
				E1071	G990					L388			D185
				E1072	G991					L388			D185
	</												

Chain D: 6% 60% 38%

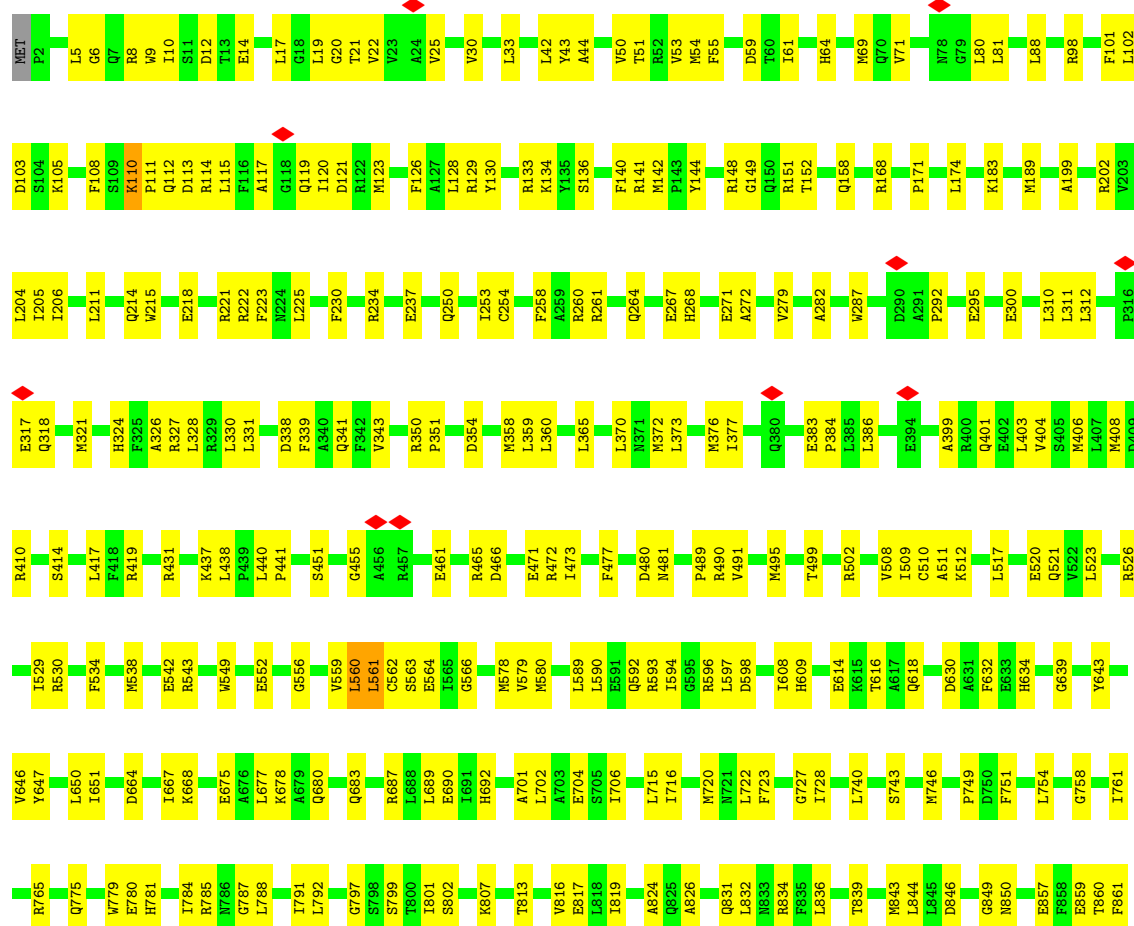


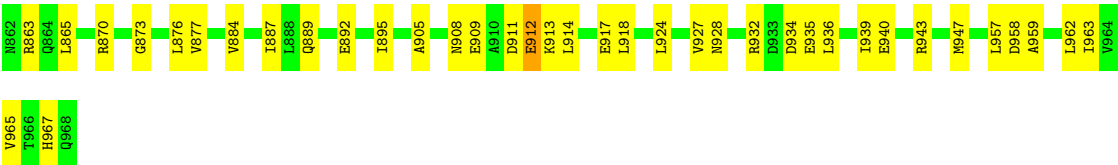


• Molecule 4: DNA-directed RNA polymerase subunit omega



• Molecule 5: RNA polymerase-associated protein RapA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	88511	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.010	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.16	0/1816	0.49	0/2461
1	B	0.25	0/1808	0.60	0/2450
2	C	0.21	0/10739	0.53	1/14489 (0.0%)
3	D	0.20	0/10525	0.55	2/14214 (0.0%)
4	E	0.13	0/607	0.40	0/817
5	L	0.16	0/7840	0.48	1/10622 (0.0%)
All	All	0.20	0/33335	0.52	4/45053 (0.0%)

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	C	0	2
3	D	0	3
5	L	0	3
All	All	0	8

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	758	PRO	CA-N-CD	-7.70	101.22	112.00
2	C	46	GLN	CA-CB-CG	5.60	125.29	114.10
5	L	912	GLU	N-CA-CB	5.58	118.07	109.98
3	D	77	ARG	CB-CG-CD	-5.42	98.84	111.30

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	236	LYS	Peptide
2	C	595	THR	Peptide
3	D	1184	ASP	Peptide
3	D	860	ARG	Peptide
3	D	901	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1794	0	1819	57	0
1	B	1786	0	1813	74	0
2	C	10570	0	10582	364	0
3	D	10368	0	10556	411	0
4	E	605	0	612	22	0
5	L	7696	0	7542	225	0
6	D	1	0	0	0	0
7	D	2	0	0	0	0
All	All	32822	0	32924	1111	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 17.

The worst 5 of 1111 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)
3:D:1061:VAL:HB	3:D:1105:ALA:HB3	1.50	0.92
5:L:414:SER:HG	5:L:692:HIS:HD1	1.18	0.88
3:D:141:PHE:HA	3:D:180:MET:HE2	1.57	0.86
3:D:1344:LEU:O	3:D:1346:GLY:N	2.08	0.85
5:L:579:VAL:HG12	5:L:609:HIS:HB2	1.57	0.84

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	229/237 (97%)	213 (93%)	16 (7%)	0	100	100
1	B	228/237 (96%)	206 (90%)	20 (9%)	2 (1%)	14	49
2	C	1338/1340 (100%)	1225 (92%)	104 (8%)	9 (1%)	18	55
3	D	1332/1363 (98%)	1216 (91%)	111 (8%)	5 (0%)	30	67
4	E	74/91 (81%)	69 (93%)	5 (7%)	0	100	100
5	L	965/968 (100%)	928 (96%)	35 (4%)	2 (0%)	43	78
All	All	4166/4236 (98%)	3857 (93%)	291 (7%)	18 (0%)	31	67

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	21	SER
2	C	199	ASP
2	C	913	VAL
2	C	938	GLY
2	C	1041	ASP

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	199/204 (98%)	199 (100%)	0	100	100
1	B	198/204 (97%)	194 (98%)	4 (2%)	48	66
2	C	1155/1155 (100%)	1123 (97%)	32 (3%)	38	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	1111/1136 (98%)	1106 (100%)	5 (0%)	81	82
4	E	65/75 (87%)	65 (100%)	0	100	100
5	L	820/829 (99%)	820 (100%)	0	100	100
All	All	3548/3603 (98%)	3507 (99%)	41 (1%)	61	73

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	940	GLU
2	C	1163	THR
2	C	941	LYS
2	C	1159	VAL
3	D	54	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	1111	GLN
5	L	626	HIS
3	D	667	GLN
5	L	297	GLN
3	D	186	GLN

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 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

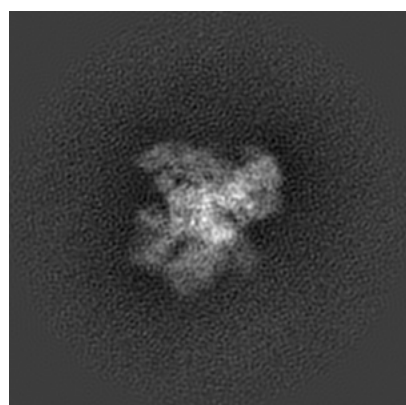
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23903. These allow visual inspection of the internal detail of the map and identification of artifacts.

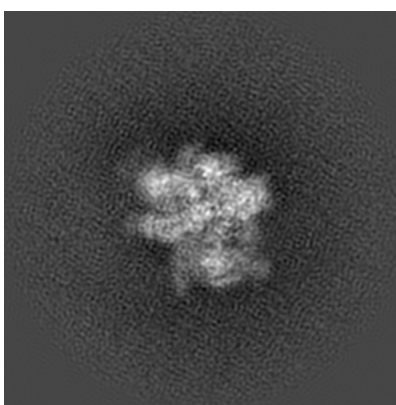
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

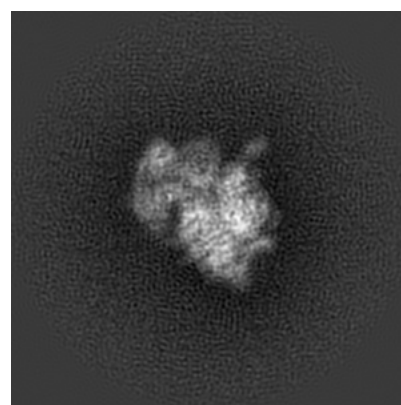
6.1.1 Primary map



X



Y

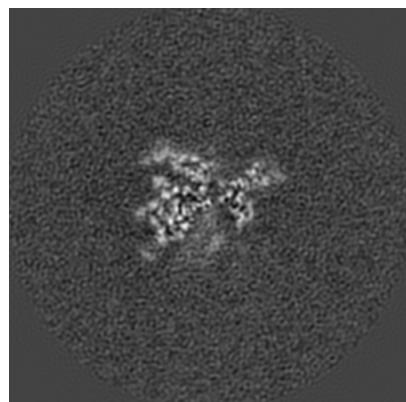


Z

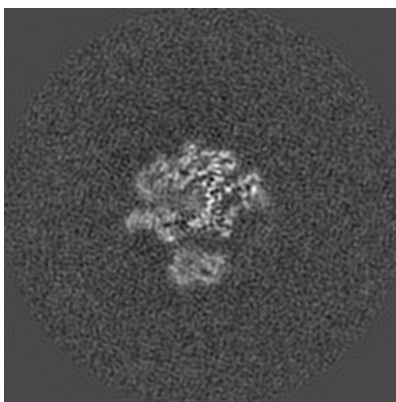
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

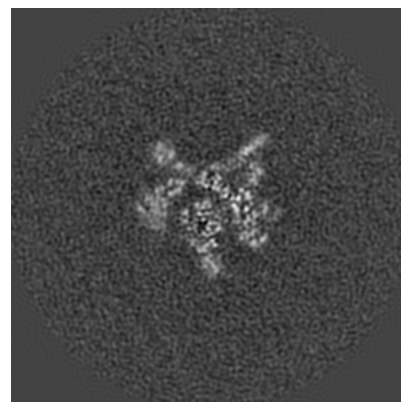
6.2.1 Primary map



X Index: 180



Y Index: 180

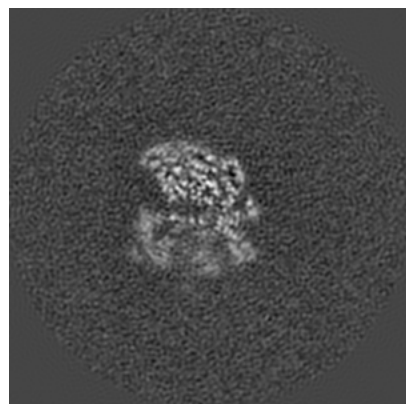


Z Index: 180

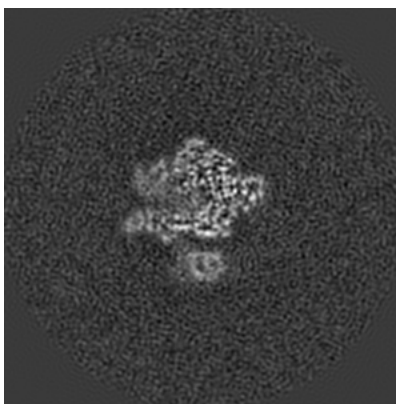
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

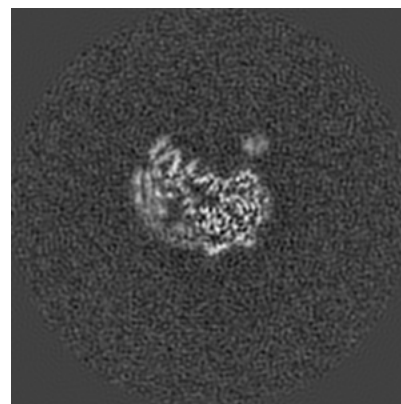
6.3.1 Primary map



X Index: 196



Y Index: 175

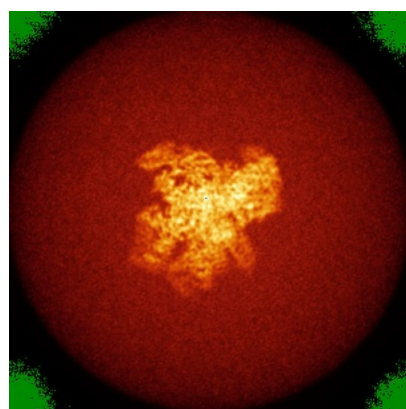


Z Index: 192

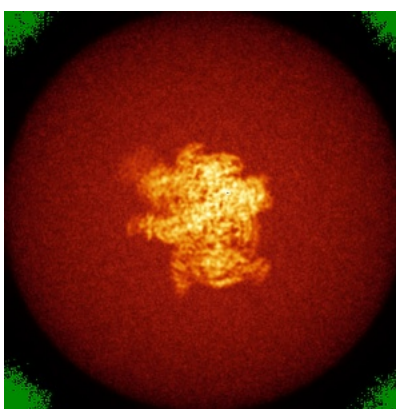
The images above show the largest variance slices of the map in three orthogonal directions.

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

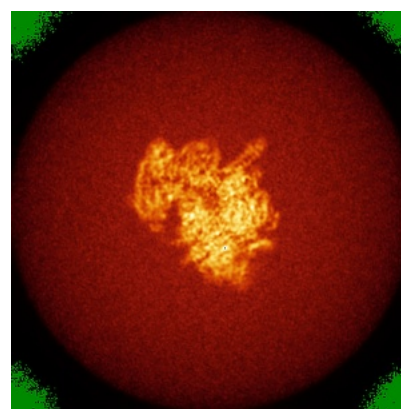
6.4.1 Primary map



X



Y

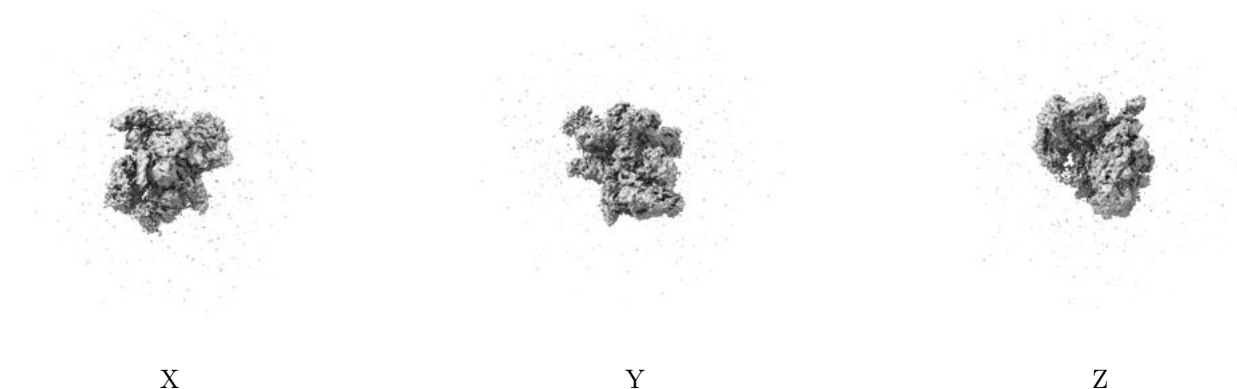


Z

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

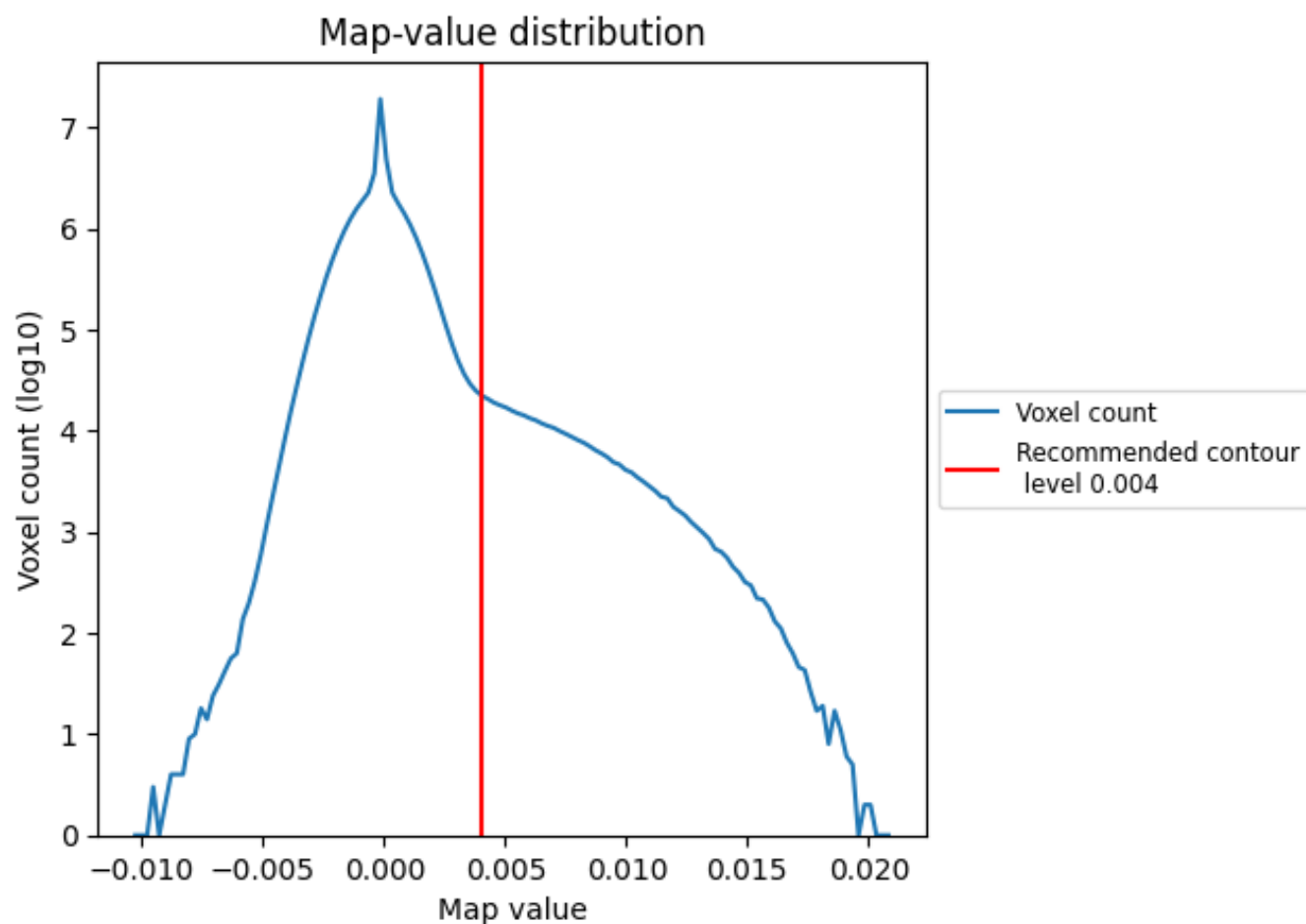
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

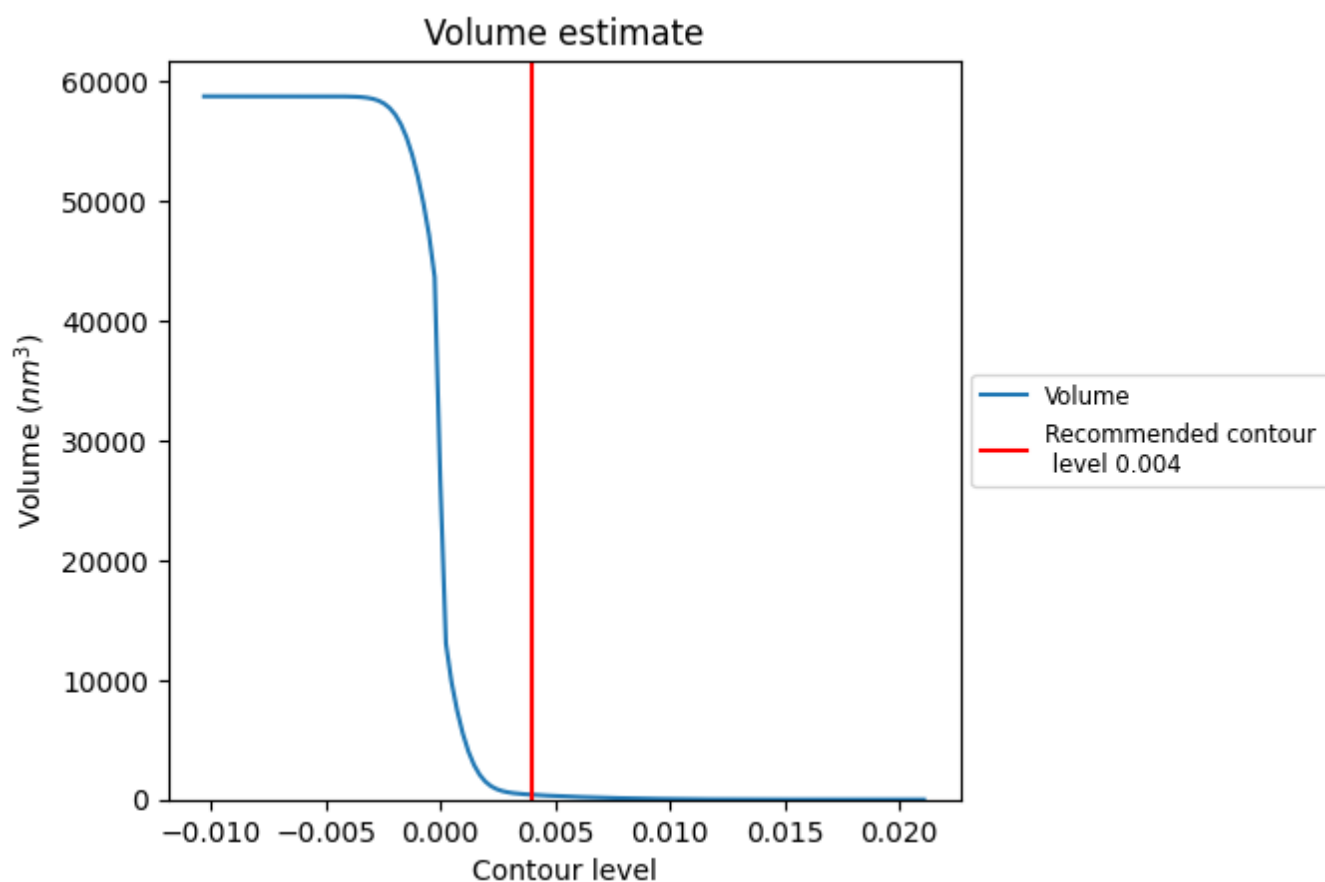
This section contains the results of statistical analysis of the map.

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.

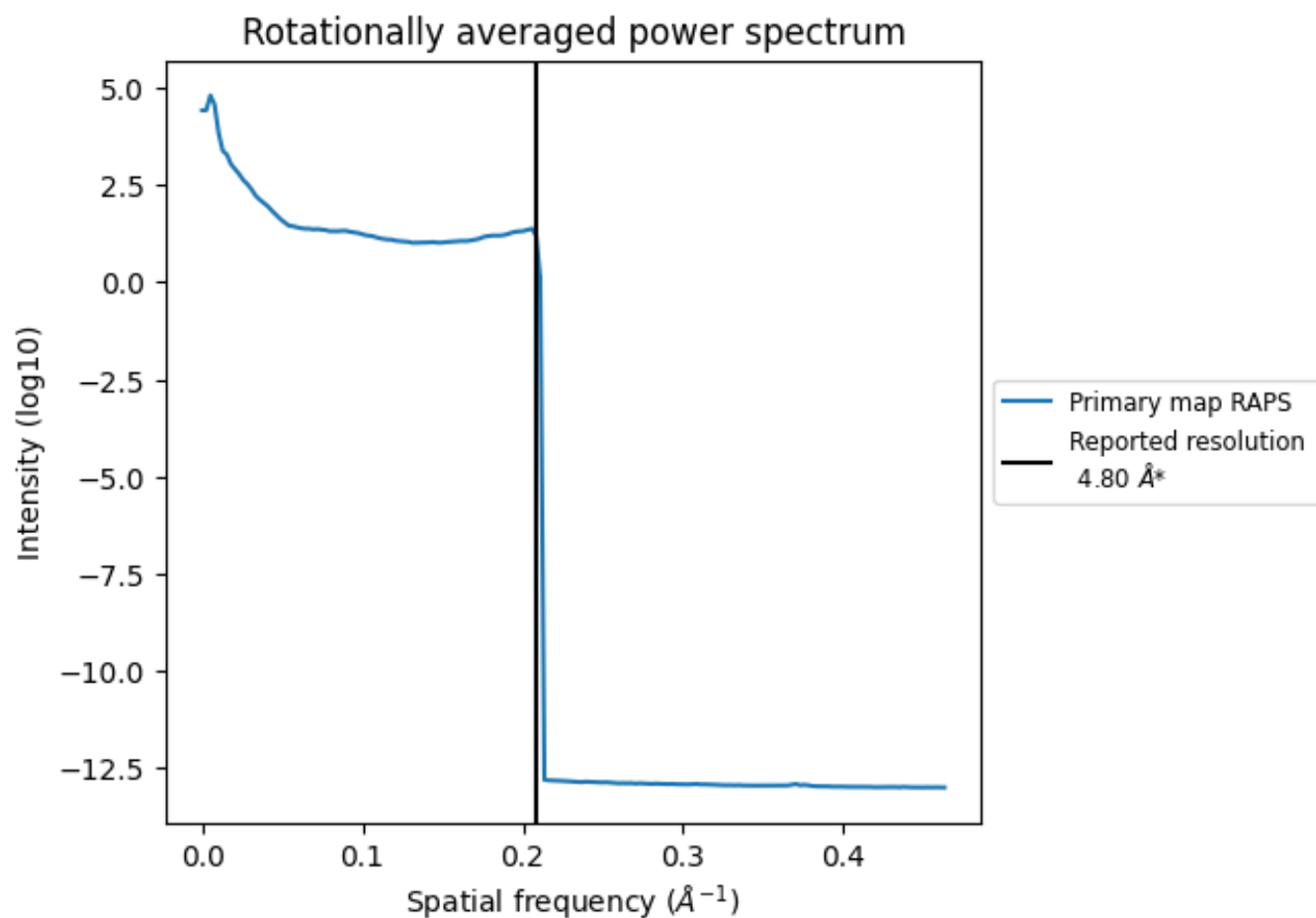
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 404 nm³; this corresponds to an approximate mass of 365 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 0.208 Å⁻¹

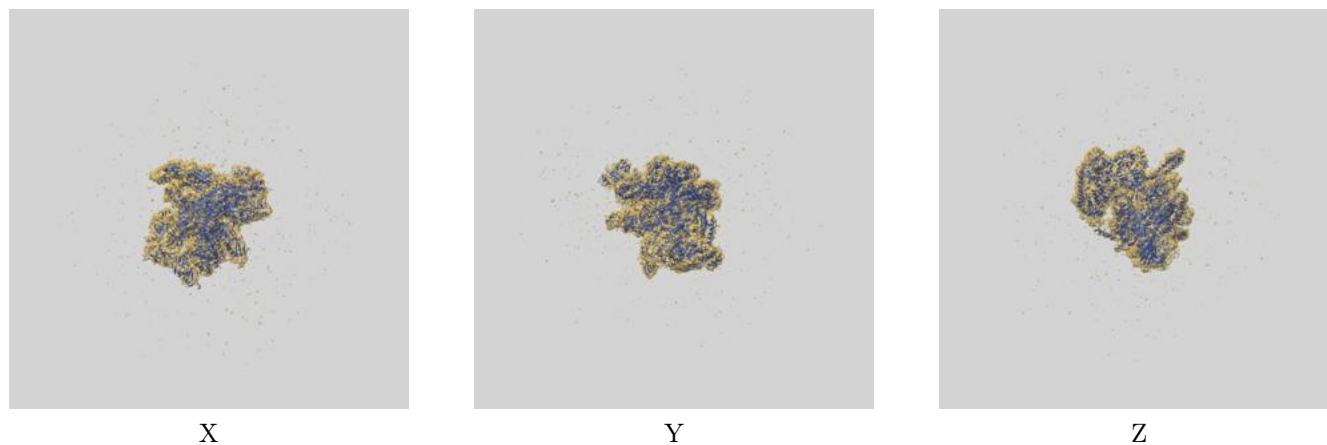
8 Fourier-Shell correlation

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-23903 and PDB model 7MKQ. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



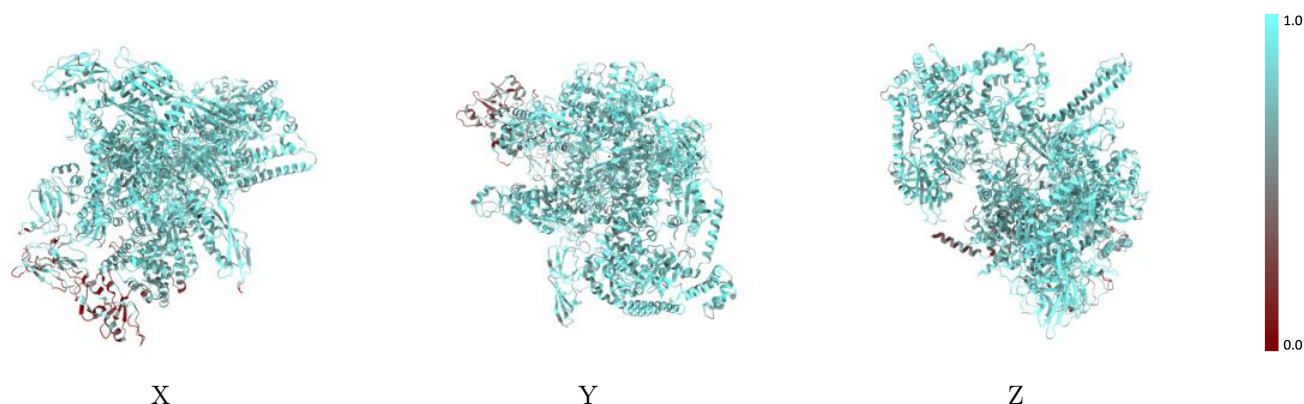
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



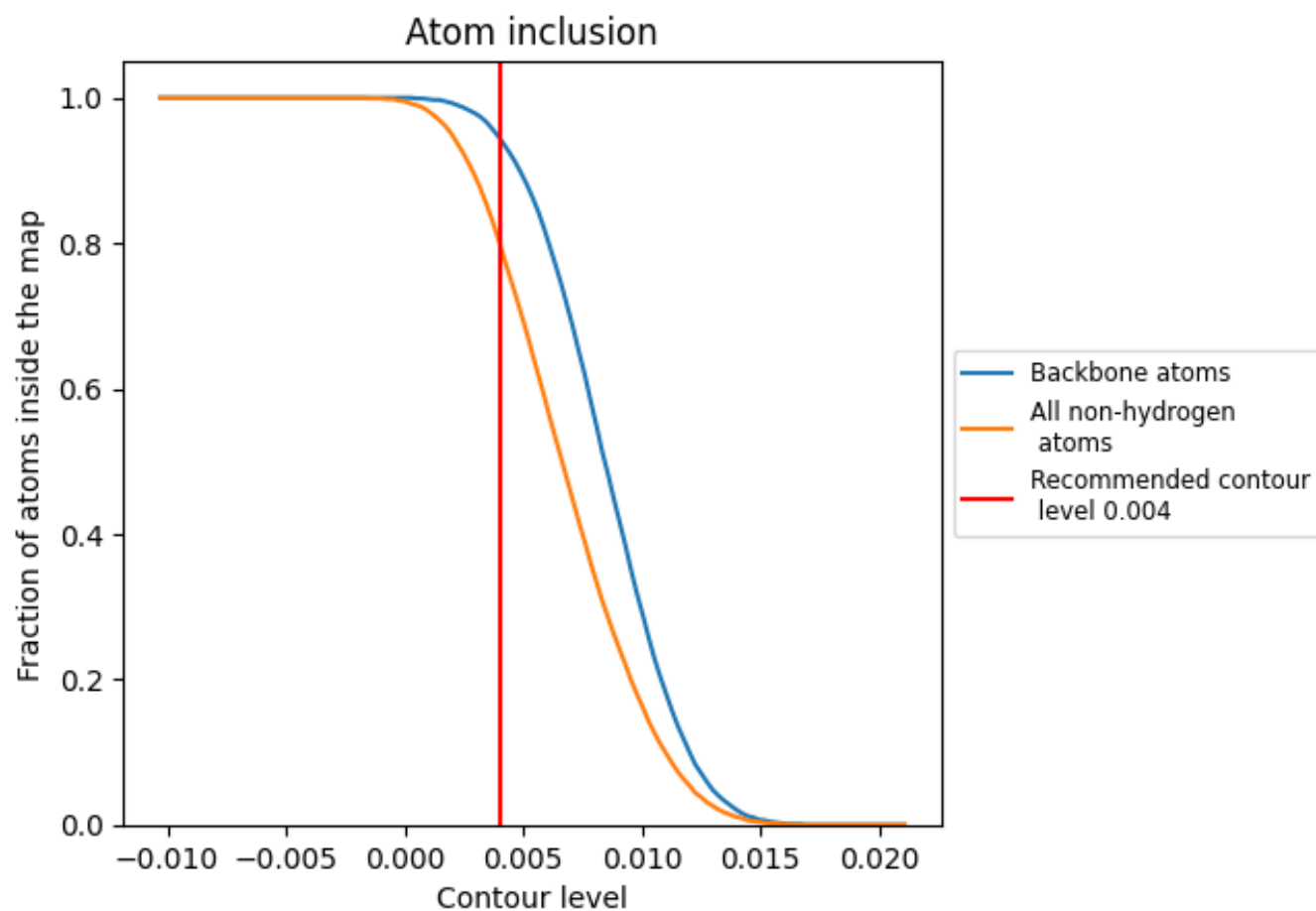
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.004).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 80% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8010	0.2540
A	0.8540	0.3050
B	0.8480	0.2620
C	0.7730	0.2610
D	0.8020	0.2520
E	0.6040	0.2230
L	0.8290	0.2350

1.0

0.0

<0.0