



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:56 AM UTC

PDB ID : 3IZ3 / pdb_00003iz3
EMDB ID : EMD-5233
Title : CryoEM structure of cytoplasmic polyhedrosis virus
Authors : Cheng, L.; Sun, J.; Zhang, K.; Mou, Z.; Huang, X.; Ji, G.; Sun, F.; Zhang, J.;
Zhu, P.
Deposited on : 2010-09-14
Resolution : 3.90 Å(reported)

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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

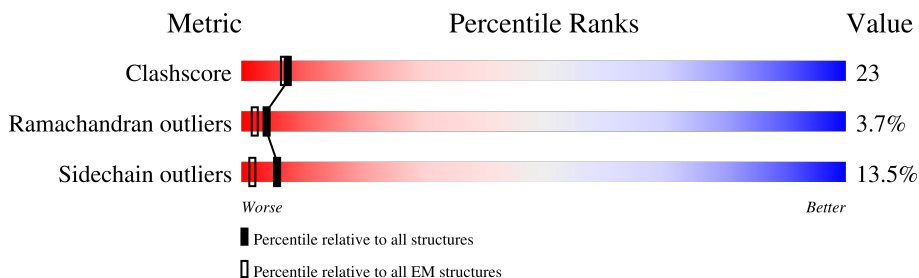
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	1058	93% 55% 34% 9% ..
2	B	1333	79% 56% 27% 5% 11%
2	C	1333	80% 60% 27% 6% 7%
3	D	291	87% 47% 40% 13% .
3	E	291	82% 41% 42% 15% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 32024 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 Structural protein VP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1047	Total	C	N	O	S	0	0
			8349	5294	1439	1572	44		

- Molecule 2 is a protein called Structural protein VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1180	Total	C	N	O	S	0	0
			9317	5889	1621	1771	36		
2	C	1244	Total	C	N	O	S	0	0
			9806	6191	1704	1873	38		

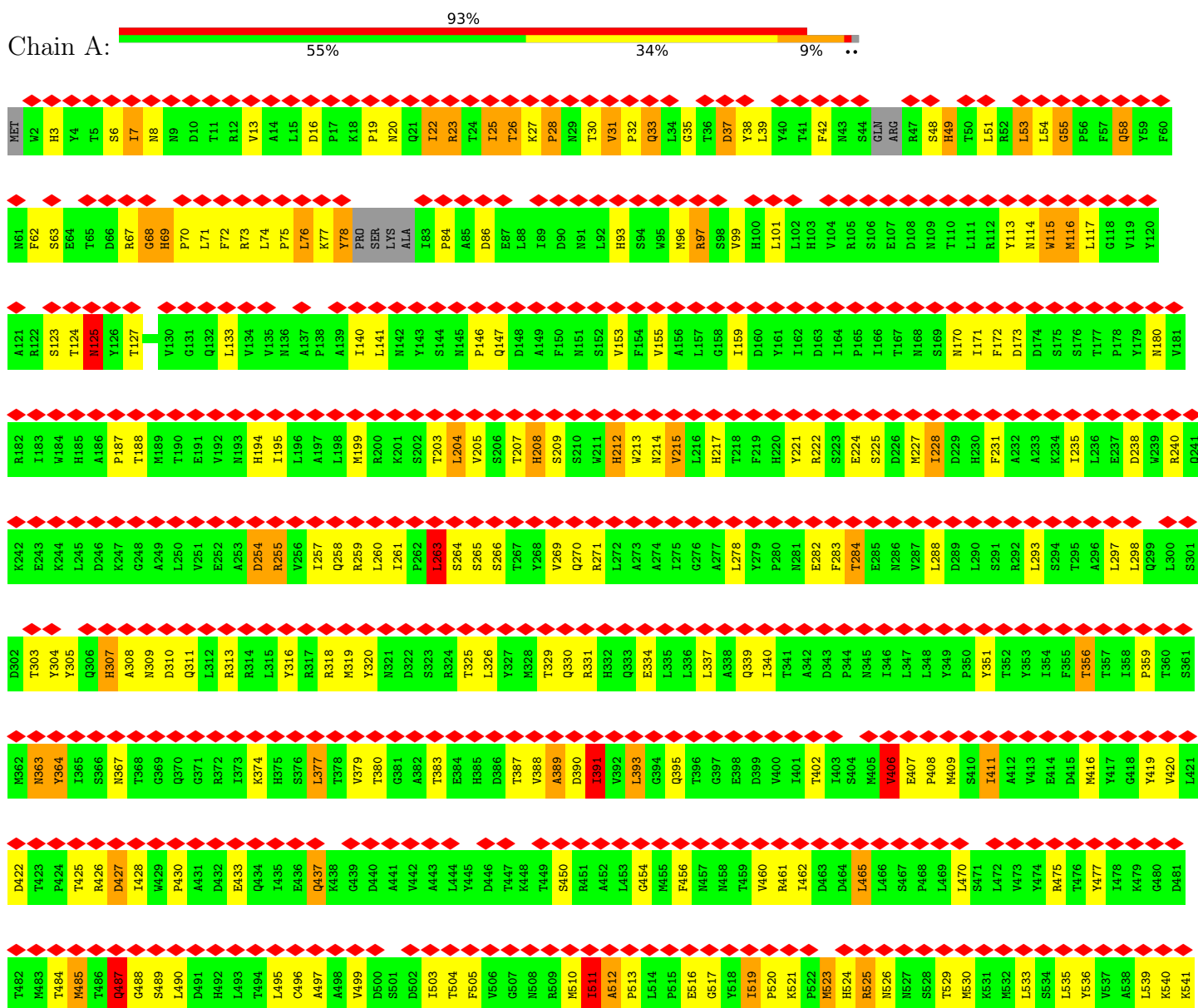
- Molecule 3 is a protein called Viral structural protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	291	Total	C	N	O	S	0	0
			2276	1446	398	424	8		
3	E	291	Total	C	N	O	S	0	0
			2276	1446	398	424	8		

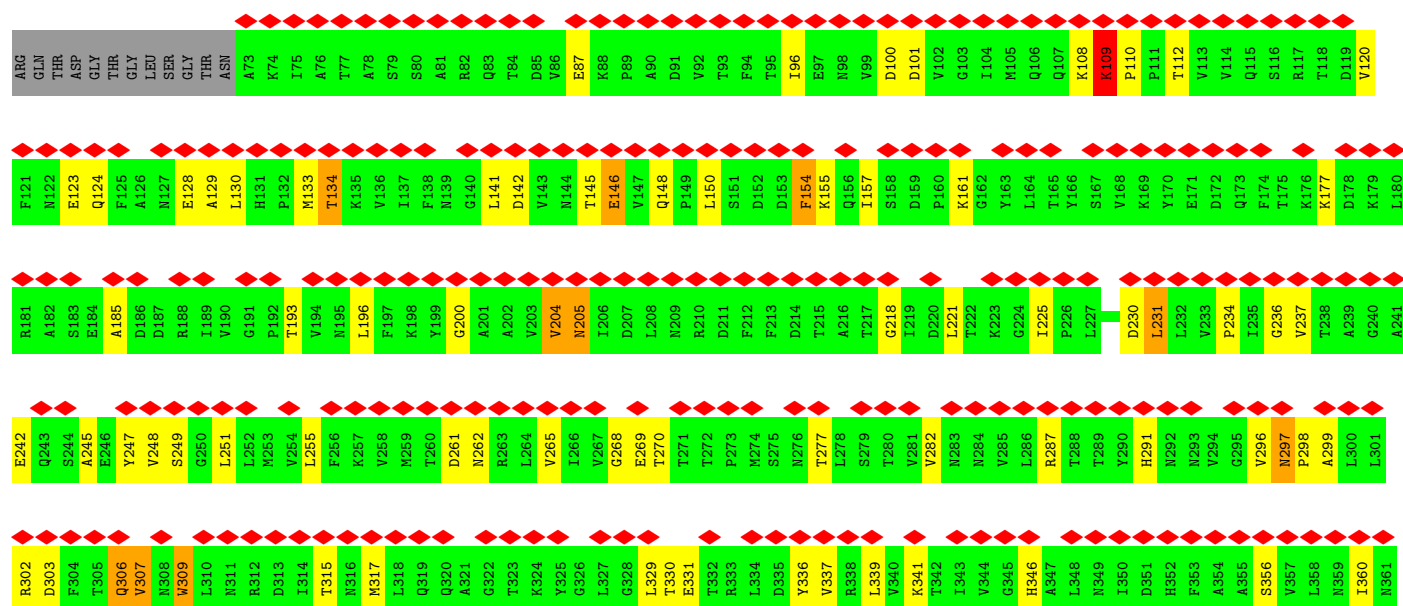
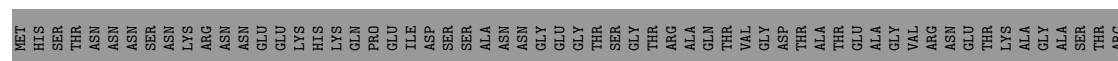
3 Residue-property plots

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.

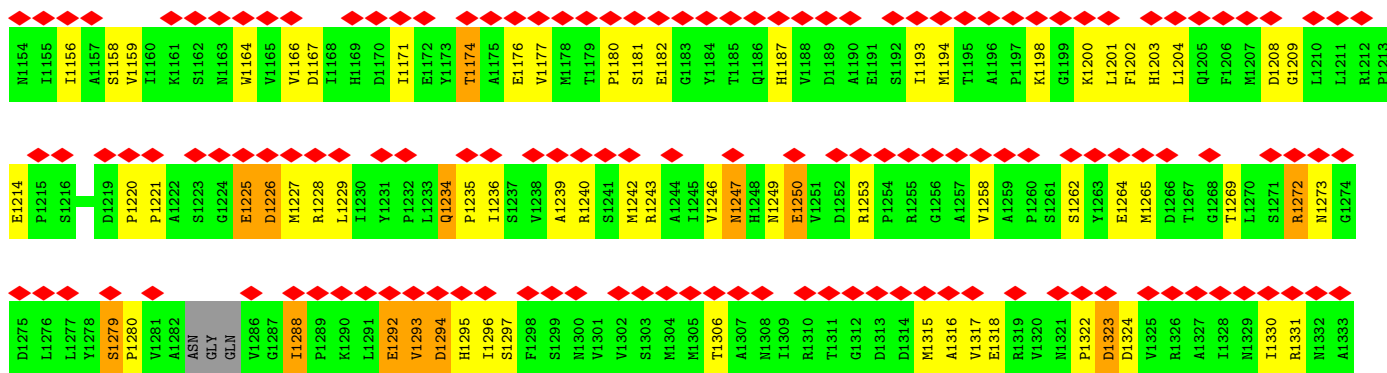
• Molecule 1: Structural protein VP3



Q966	L967	R968	A969	L970	M971	P972	T973	L974	S975	T976	S977	Q978	I979	R980	H981	I982	I983	E984	R985	I986	A987	Q988	I989	T990	ASP	VAL	ASP	SER	T995	D996	G997	G998	G999	L1000	L1001	L1002	R1003	F1004	L1005	G1006	T1007	L1008	T1009	R1010	S1011	L1012	Q1015	N1016	A1017	Q1018	I1019	R1020	R1021	Q959	I1022	T960	R1023	S961	P1024	D1025	G1026	
G846	I847	R848	H849	T850	T851	Y852	D853	Q854	Y855	L856	S857	H858	I859	R860	E861	R862	L863	H864	I865	T866	H867	V868	P869	D870	S871	H872	I873	L874	T875	H876	S877	H878	S879	H880	T881	L882	I883	S884	A885	S886	V887	Q888	H889	T890	H891	Y892	A893	Q894	A895	L896	Y897	Q898	Q899	T900	S901	I902	N903	G904	S905			
A906	S907	T908	Y909	L910	R911	E912	N913	E914	Y915	L916	V917	Y918	N919	P920	E921	Y922	Y923	D924	Y925	Y926	S927	A928	F929	A930	N931	A932	N933	L934	Q935	N936	N937	N938	N939	R940	Y941	I942	Q882	E943	F1004	L1005	S944	G1006	V945	L946	E947	I948	A949	D950	F952	D953	Q954	A955	D956	F957	I958	Q959	T960	S961	D962	A963	V964	R965
G846	I847	R848	H849	T850	T851	Y852	D853	Q854	Y855	L856	S857	H858	I859	R860	E861	R862	L863	H864	I865	T866	H867	V868	P869	D870	S871	H872	I873	L874	T875	H876	S877	H878	S879	H880	T881	L882	I883	S884	A885	S886	V887	Q888	H889	T890	H891	Y892	A893	Q894	A895	L896	Y897	Q898	Q899	T900	S901	I902	N903	G904	S905			
F727	K728	F729	D730	Q731	Y732	Y733	L734	T735	W736	F737	E738	G739	S740	Y741	K742	P743	I744	I745	E746	R747	Q748	G749	E750	T751	V752	D753	G754	L755	T756	I757	I758	D759	T760	S761	I762	V763	V764	P765	I766	L767	C768	Q769	C770	T771	Y772	P773	L774	V775	ARG	GLN	SER	GLY	LYS	GLY	VAL	ASP	ALA	VAL				
E665	R666	A667	V668	Q669	D670	D671	H672	Q673	K674	A675	T676	R677	S678	C679	T680	K681	Q682	H683	L684	R685	H686	L687	E688	T689	Q690	F691	D692	H693	I694	A695	V696	A697	H698	T699	D700	H701	L702	G703	S704	V705	Y706	A707	L708	M709	S710	M711	F712	M713	L714	M715	F716	T717	M718	M719	F720	S721	G722	N723	H724			
M604	R605	L606	F607	T608	P609	Q610	G611	F612	L613	R614	T615	D616	D617	L618	A619	I620	A621	A622	N623	F624	P625	R626	A627	S628	R629	N630	P631	Q632	T633	Y634	I635	P636	L637	T638	N639	Q640	R641	G642	T645	N646	E647	F648	A649	S650	R651	F652	R653	T654	T655	V656	A657	T658	L659	A660	N661	V662	V663	H664				
W543	Y544	P545	V546	Y548	Y549	I550	F551	I552	Q553	R554	G555	A556	T557	Y558	T559	I560	N561	A562	A563	G564	S565	F566	E567	F568	S569	G570	R571	N572	V573	K574	W575	L576	S577	L578	L579	Y580	L581	F582	F583	H584	A587	N588	R589	S590	D591	F592	D593	P593	L594	A595	G596	A597	N598	T599	I600	I601	V602	L603				
I482	A483	R484	E485	V486	S487	P488	M489	F490	N491	V492	H493	E494	L495	K496	K497	I498	A499	E500	S501	F502	E503	D504	F505	S506	S507	I508	V509	V510	V511	E512	E513	M514	L515	Q516	F517	A518	L519	F520	F521	P522	F525	N526	R527	I528	K529	G530	F531	I532	Q533	N534	V535	L536	L537	L538	F539	F540	S541	R542				
L422	E423	G424	I425	I426	V427	Q428	I429	M430	T431	G432	Y433	V434	A435	S436	A437	M438	V439	I440	R441	P442	V443	S444	E445	K446	R447	Y448	F449	P450	E451	M452	L453	Q454	Q455	M456	Q457	S458	A459	A460	R461	L462	V463	S464	A465	V466	K467	A468	R469	A470	S471	E472	A473	D474	I475	S476	S477	I478	L480	A481				
R302	D303	F304	T305	Q306	V307	N308	W309	L310	N311	R312	D313	I314	T315	N316	M317	L318	Q319	Q320	A321	G322	T323	K324	Y325	G326	L327	Q328	L329	T330	T332	R333	L334	D335	Y336	V337	R338	L339	V340	K341	T342	I343	F344	G345	H346	A347	L348	N349	I350	D351	H352	F353	A354	A355	V356	A357	L358	N359	I360	N361				
E242	Q243	S244	A245	E246	Y247	V248	S249	G250	L251	L252	M253	V254	L255	F256	K257	V258	M259	T260	D261	N262	R263	L264	V265	I266	V267	G268	E269	T270	T271	T272	P273	M274	S275	N276	T277	L278	S279	T280	V281	V282	N283	N284	V285	L286	R287	T288	T289	Y290	H291	N292	N293	V294	G295	V296	N297	P298	A299	L300	L301			



V1092	D1032	M971	R911	T851	I791	Q731	D671	T608	Y548	P488	I426	L362
P1093	D1033	P972	E912	Y852	W792	Y732	M672	P609	G549	M489	V427	R363
E1094	Q1034	T973	N913	D853	Y793	V733	Q673	Q610	I550	M489	Q428	A364
G1095	I1035	L974	E914	D854	P794	I734	K674	G611	F551	M491	I429	L365
Y1096	L1036	L916	V915	Y855	D795	T735	A675	F612	I552	M492	M430	M366
V1097	E1037	V917	L916	L856	P796	T736	T676	L613	Q553	M493	T431	E367
A1098	A1038	V918	V918	S857	T797	P737	R677	R614	R554	M494	G432	A368
I1099	A1039	M919	M919	H858	T798	E738	S678	T615	G555	M495	Y433	N369
Q1100	F1040	P920	P920	T859	T799	G739	C679	D616	A556	M496	V434	V370
Y1101	R1041	D921	D921	R860	L800	S740	T680	D617	T557	M497	A435	T371
A1102	W1042	S801	S801	E861	Q802	Y741	K681	L618	Y558	M498	A436	A372
I1103	S1043	Q802	Q802	R862	Q803	K742	Q682	A619	I498	M499	S436	A372
R1104	R1044	S803	S803	L863	L804	P743	W683	I620	T559	M500	A437	D373
R1105	Y1045	L804	L804	R864	L805	I744	L684	I620	I560	M501	M438	D374
F1106	Y1046	S805	S805	I865	S806	I745	R685	A621	A562	M502	I440	R375
L1047	L1047	Y806	Y806	T866	A807	E746	H686	A622	A563	M503	R441	K377
D1048	D1048	A807	A807	R867	Q808	R747	L687	F624	G564	M504	P442	A378
E1049	E1049	Q808	Q808	Y868	L810	Q748	E688	P625	E565	M505	V443	L379
L1050	L1050	W809	W809	T869	L811	G749	T689	R626	F566	M506	S444	Q380
R1051	R1051	R869	R869	R870	S811	T751	Q690	A627	E567	M507	E445	A381
L1052	L1052	D870	D870	P871	K812	W752	D692	S628	F568	M508	K446	H382
R1053	R1053	P872	P872	T873	L813	D753	N693	R629	V510	M509	R447	S383
L1054	L1054	R873	R873	Y874	T814	Q754	T694	M630	G570	M510	Y448	M384
S1055	L1055	Y875	Y875	I876	L815	L755	A695	P631	R571	M511	F449	I385
V1056	S1056	I876	I876	T877	P816	T756	V696	Q632	N572	M512	P450	S386
Y1057	Y1057	Q876	Q876	A877	D817	I757	A697	T633	E573	M513	E451	T387
G1058	G1058	G876	G876	R878	A818	W758	H698	Y634	K574	M514	M452	Q388
L1059	L1059	A877	A877	S878	F819	I758	T699	I635	W575	M515	L453	H390
R1060	R1060	S878	S878	T879	F820	D759	W699	P636	D576	M516	E454	Q389
L1061	L1061	P880	P880	Y881	N821	T760	D700	Y637	Q577	M517	Q455	G391
P1122	P1122	R881	R881	D882	K822	S761	H701	T638	S578	M518	M456	N392
T1124	T1124	E943	E943	R883	L824	I762	L702	N639	L579	M519	Q457	N393
G1125	G1125	S944	S944	L883	S825	W763	S703	T643	Y580	M520	F521	Q394
M1126	M1126	Y945	Y945	A884	G826	P765	V705	V644	S582	M521	P522	G395
A1127	A1127	G827	G827	A885	D828	I766	V706	E547	E583	M522	T523	A396
Y1128	Y1128	S886	S886	S887	S829	L767	A707	F648	H584	M523	E524	L397
P1129	P1129	D828	D828	T887	S830	Q769	W709	S650	F585	M524	F525	R398
S1130	S1130	R831	R831	Y887	W831	T771	T712	R651	P586	M525	N526	P399
P1131	P1131	R833	R833	D888	S832	W772	S710	R652	A587	M526	I528	E400
T1132	T1132	T890	T890	R889	W833	P773	F712	F652	L588	M527	K529	H405
G1133	G1133	H891	H891	Y892	L834	L774	M713	R653	F589	M528	G530	D406
R1134	R1134	R893	R893	D894	W835	W775	L714	I655	D591	M529	D531	H407
P1135	P1135	Y895	Y895	R896	W836	W776	L715	V656	V592	M530	I532	I408
H1136	H1136	L896	L896	T897	T837	ARG	F716	R657	P593	M531	Q533	I409
V1137	V1137	E897	E897	Y898	T838	GLN	T717	A657	P593	M532	N534	R410
M1138	M1138	Q898	Q898	Y899	E838	GLY	W718	T658	A595	M533	E472	C411
M1139	M1139	R899	R899	Y900	A839	LVS	M719	L659	V535	M534	M413	L412
T1140	T1140	D900	D900	G900	D840	GLY	F720	A660	L536	M535	A473	M414
I1141	I1141	D841	D841	G901	W841	VAL	S721	R661	I597	M536	D474	L414
M1142	M1142	D842	D842	Y901	L843	ASP	T722	V662	N598	M537	I475	A417
E1143	E1143	L844	L844	V901	W844	ALA	G722	V663	T599	M538	S476	M418
R1144	R1144	E845	E845	R902	E846	SER	W723	N664	I600	M539	S477	Y419
A1145	A1145	G846	G846	I903	T847	TLE	H724	E665	F541	M540	I478	F420
G1146	G1146	R847	R847	N903	R848	MET	W725	R666	R542	M541	H479	R421
P1086	P1086	T847	T847	G904	E849	GLU	T726	A667	W543	M542	L480	L422
D1087	D1087	R849	R849	S905	R850	E790	T727	V668	P545	M543	A481	E423
F1088	F1088	T849	T849	A906	W850	E790	P727	Q669	V546	M544	I482	G424
V1089	V1089	T850	T850	Y907	W850	E790	P728	Q669	E547	M545	A483	I425
S1148	S1148	R850	R850	T908	W850	E790	P729	Q669	E547	M546	R484	E485
K1149	K1149	W850	W850	Y909	W850	E790	P730	D570	E547	M547	R484	E485
A1152	A1152	L910	L910	L910	W850	E790	P730	D570	E547	M548	R484	E485
D1153	D1153	L910	L910	L910	W850	E790	P730	D570	E547	M549	R484	E485



K243	E183
V244	G184
T245	S185
K246	L186
T247	I187
V248	S188
D249	L189
R250	S190
V251	R191
L252	D192
E253	V193
Y254	V194
T255	N195
G256	I196
V257	K197
N258	I198
S259	L199
M260	A200
R261	F201
T262	L202
A263	T203
G264	D204
R265	L205
T266	G206
A267	S207
T268	L208
L269	E209
T270	G210
Y271	E211
D272	E212
L273	L213
S274	R214
R275	A215
H276	F216
E277	K217
F278	T218
A279	R219
A280	N220
K281	R221
F282	D222
L283	V223
Q284	L285
T286	F224
T287	R225
T288	M226
R289	M227
W290	L228
N291	F229
	T230
	M231
	S232
	T233
	A234
	V235
	A236
	A237
	N238
	V239
	V240
	N241
	R242

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	29000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	0.8	Depositor
Maximum defocus (nm)	2.8	Depositor
Magnification	75000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	18.037	Depositor
Minimum map value	-16.951	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3	Depositor
Map size ($\text{\AA}$)	761.60004, 761.60004, 595.0	wwPDB
Map dimensions	640, 640, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.19, 1.19, 1.19	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	0.50	0/8530	0.87	6/11613 (0.1%)
2	B	0.47	0/9508	0.83	10/12941 (0.1%)
2	C	0.49	0/10006	0.85	11/13622 (0.1%)
3	D	0.49	0/2322	1.00	14/3156 (0.4%)
3	E	0.51	0/2322	1.22	28/3156 (0.9%)
All	All	0.49	0/32688	0.89	69/44488 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	2

There are no bond length outliers.

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	629	ARG	N-CA-C	-12.65	100.20	114.62
3	E	235	VAL	N-CA-C	11.79	121.61	110.53
3	E	59	ALA	CB-CA-C	-11.57	92.90	110.26
3	E	253	GLU	N-CA-C	11.48	123.36	111.07
3	E	87	HIS	N-CA-C	10.67	122.91	111.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	1225	GLU	Peptide
2	C	628	SER	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	8349	0	8304	341	0
2	B	9317	0	9236	381	0
2	C	9806	0	9713	379	0
3	D	2276	0	2273	293	0
3	E	2276	0	2277	263	0
All	All	32024	0	31803	1456	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 23.

The worst 5 of 1456 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)
2:B:271:THR:CG2	2:C:237:VAL:HG23	1.18	1.64
2:B:274:MET:CG	2:C:234:PRO:HD3	1.35	1.51
3:E:46:LYS:HD3	3:E:155:HIS:CE1	1.49	1.45
2:B:1273:ASN:OD1	3:D:79:ILE:CG2	1.68	1.40
2:B:1273:ASN:ND2	3:D:191:ARG:HA	1.38	1.39

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	1039/1058 (98%)	775 (75%)	180 (17%)	84 (8%)	1 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	1172/1333 (88%)	915 (78%)	219 (19%)	38 (3%)	3	25
2	C	1238/1333 (93%)	974 (79%)	240 (19%)	24 (2%)	6	33
3	D	289/291 (99%)	253 (88%)	33 (11%)	3 (1%)	12	45
3	E	289/291 (99%)	254 (88%)	34 (12%)	1 (0%)	36	69
All	All	4027/4306 (94%)	3171 (79%)	706 (18%)	150 (4%)	4	22

5 of 150 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	ILE
1	A	25	ILE
1	A	49	HIS
1	A	55	GLY
1	A	69	HIS

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	933/943 (99%)	804 (86%)	129 (14%)	3	18
2	B	1029/1155 (89%)	907 (88%)	122 (12%)	5	21
2	C	1085/1155 (94%)	942 (87%)	143 (13%)	4	19
3	D	240/240 (100%)	201 (84%)	39 (16%)	2	14
3	E	240/240 (100%)	197 (82%)	43 (18%)	2	12
All	All	3527/3733 (94%)	3051 (86%)	476 (14%)	6	18

5 of 476 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1182	GLU
3	E	53	GLU
2	C	430	ASN
3	E	35	LEU

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Mol	Chain	Res	Type
3	E	288	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	913	ASN
2	C	1112	ASN
3	E	155	HIS
2	B	369	ASN
2	B	346	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](#)

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.

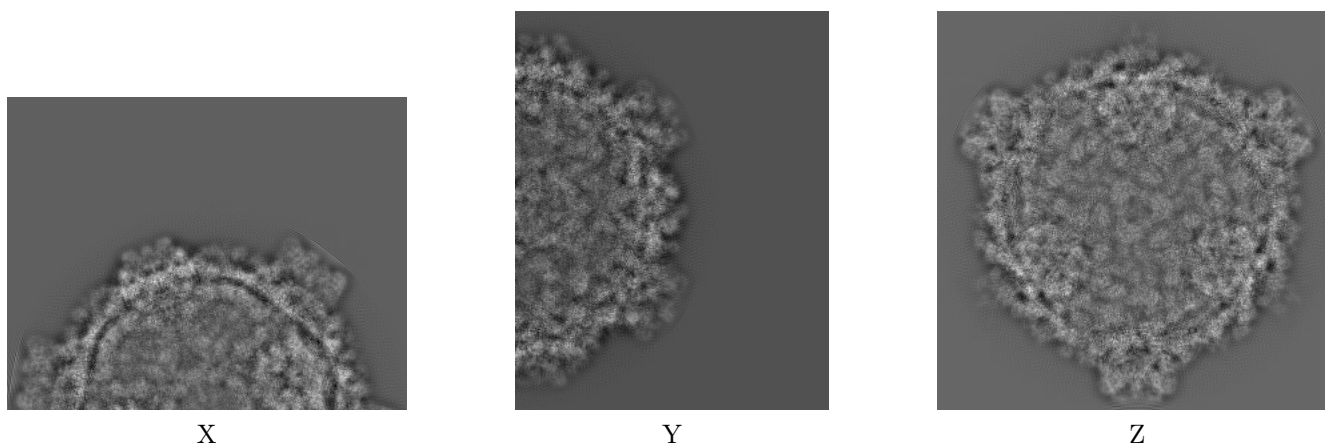
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5233. 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](#)

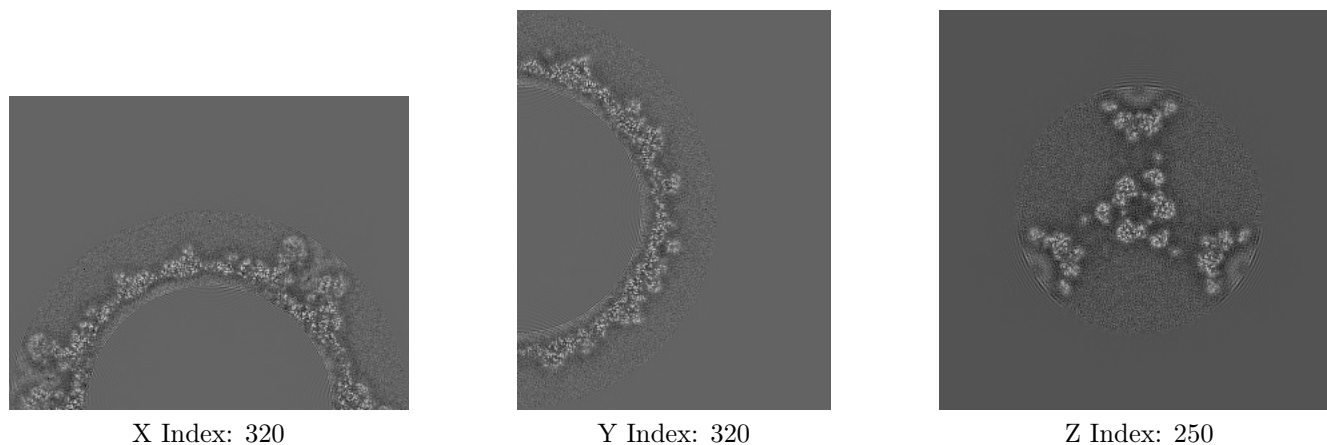
6.1.1 Primary map



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

6.2 Central slices [i](#)

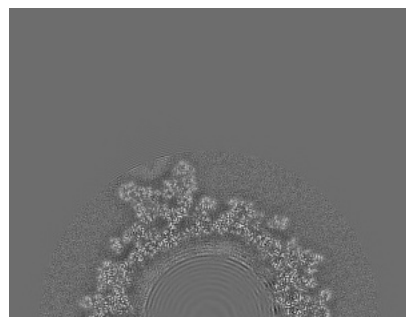
6.2.1 Primary map



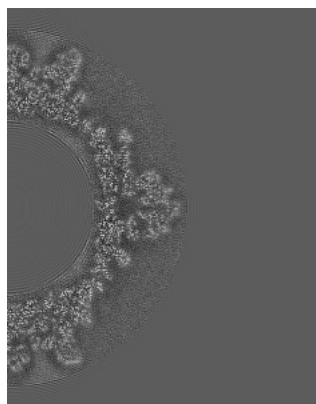
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

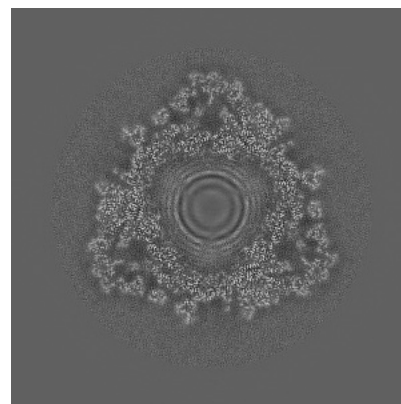
6.3.1 Primary map



X Index: 486



Y Index: 460

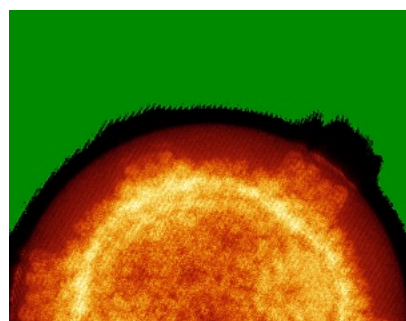


Z Index: 189

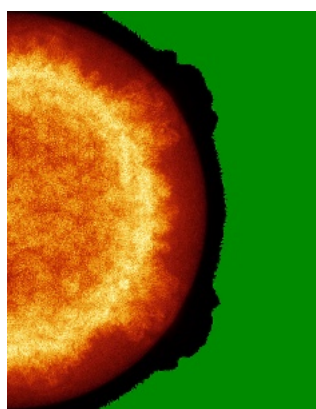
The images above show the largest variance slices of the map in three orthogonal directions.

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

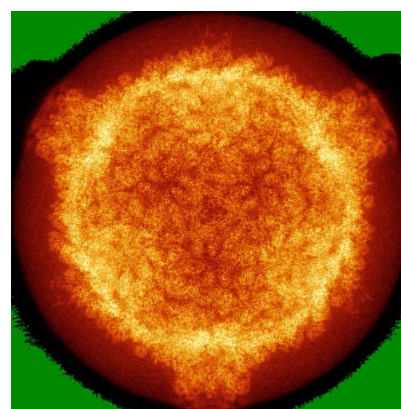
6.4.1 Primary map



X



Y

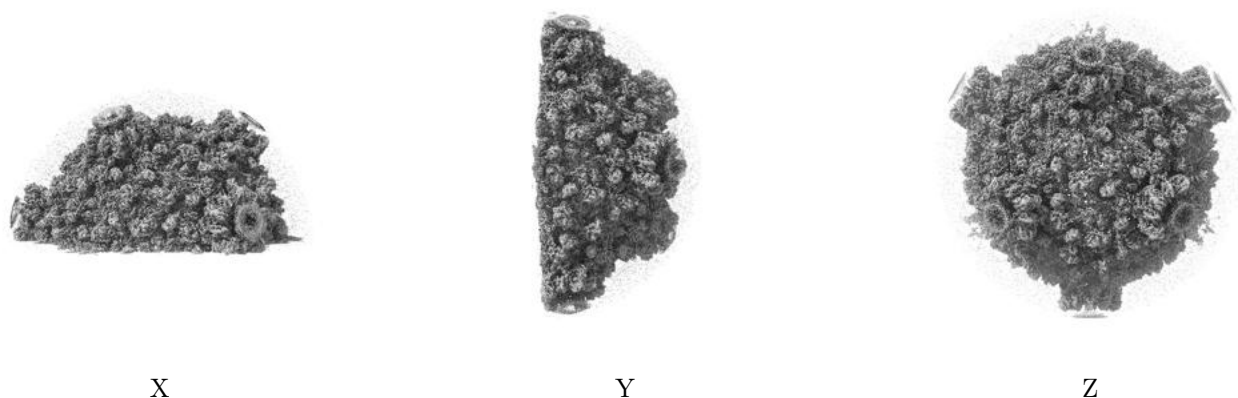


Z

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

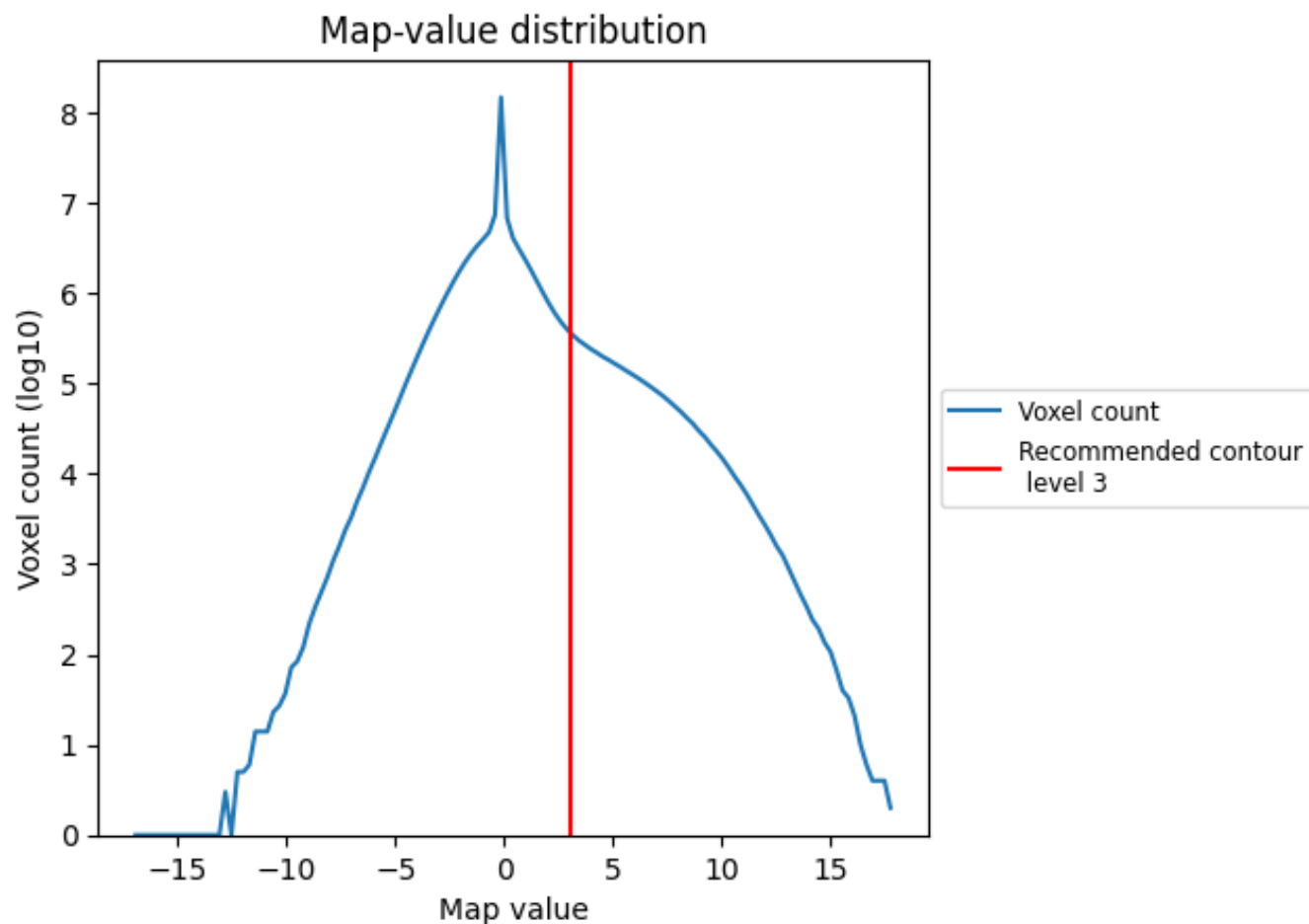
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

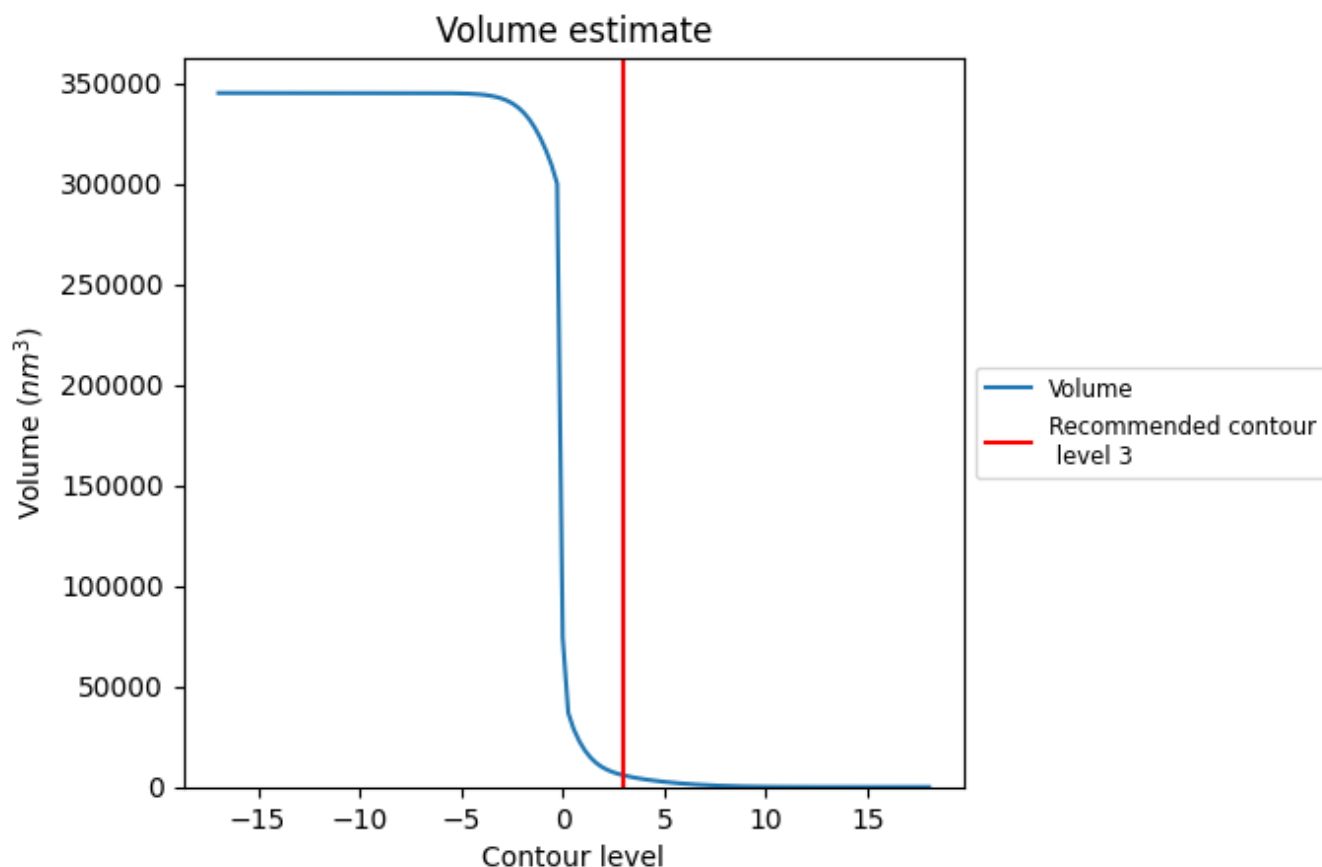
This section contains the results of statistical analysis of the map.

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 5776 nm³; this corresponds to an approximate mass of 5218 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation

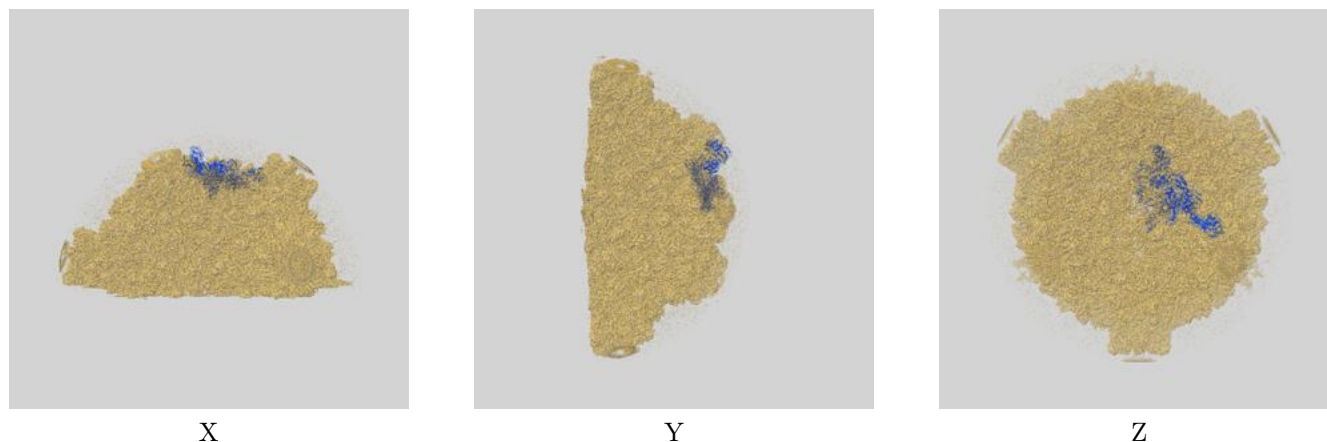
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5233 and PDB model 3IZ3. Per-residue inclusion information can be found in section [3](#) on page [4](#).

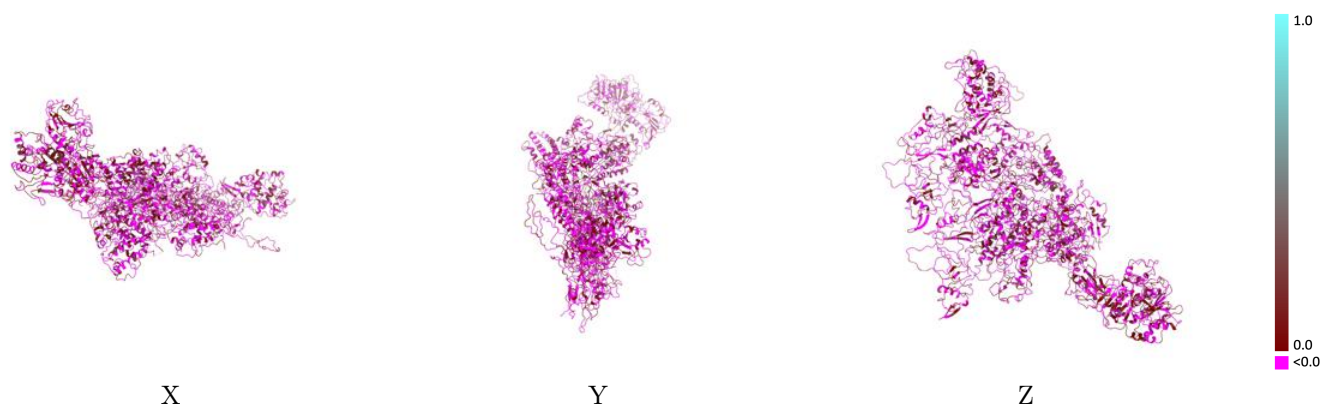
9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)



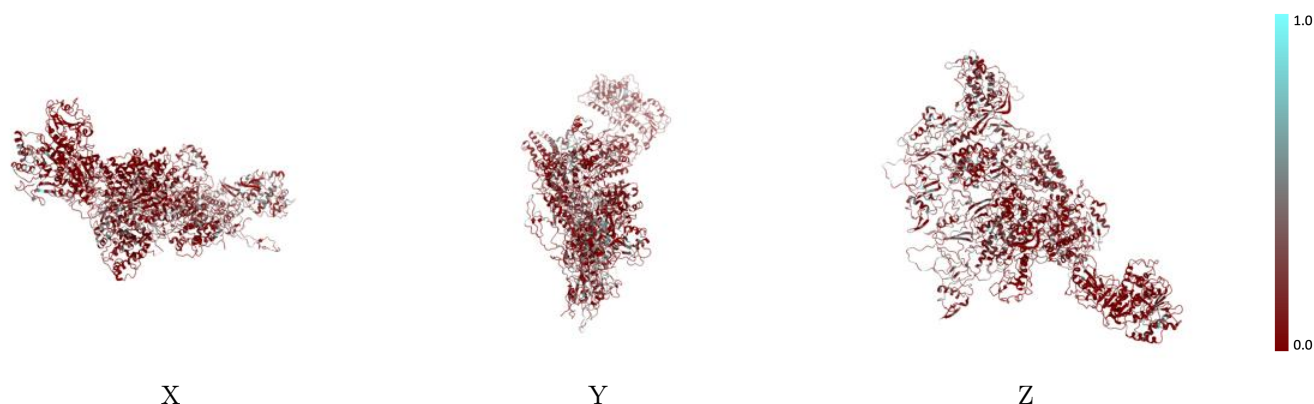
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



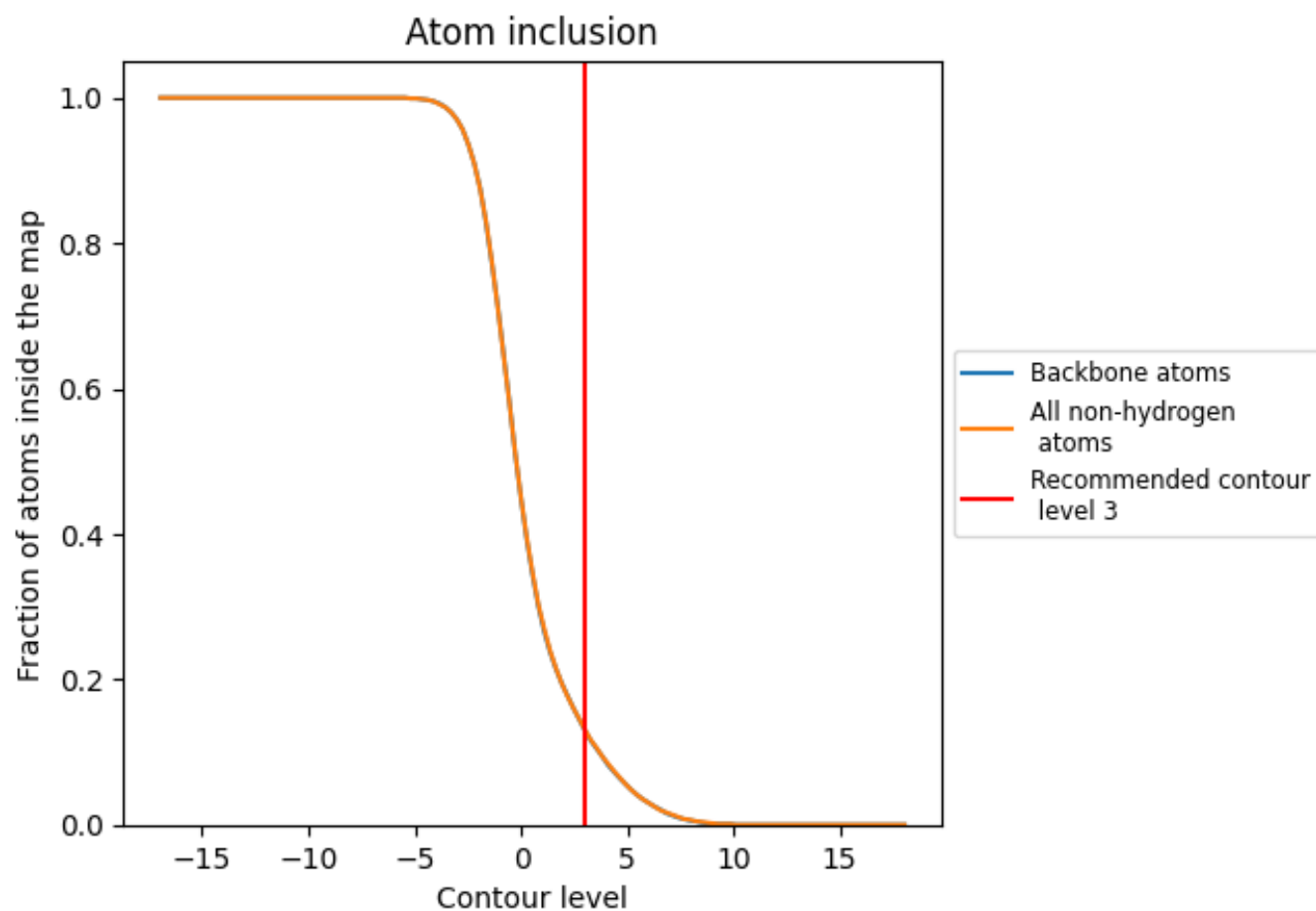
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 13% of all backbone atoms, 13% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.1310	-0.0110
A	0.0690	0.0000
B	0.1390	-0.0140
C	0.1650	-0.0200
D	0.1160	-0.0100
E	0.1940	-0.0040

