



Full wwPDB EM Validation Report ⓘ

Sep 22, 2025 – 10:58 AM EDT

PDB ID : 9000 / pdb_00009000
EMDB ID : EMD-70667
Title : Human delta 2 receptor with R710W Cerebellar Ataxia mutation in the apo closed state
Authors : Wang, H.; Ahmed, F.; Khau, J.; Mondal, A.K.; Twomey, E.C.
Deposited on : 2025-05-16
Resolution : 3.68 Å(reported)

This is a Full wwPDB EM Validation 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:

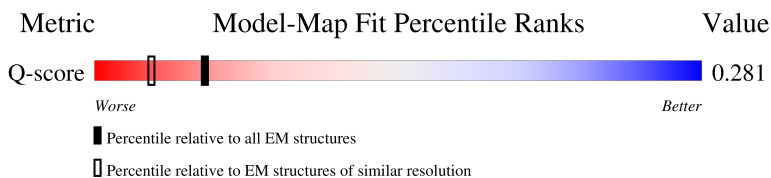
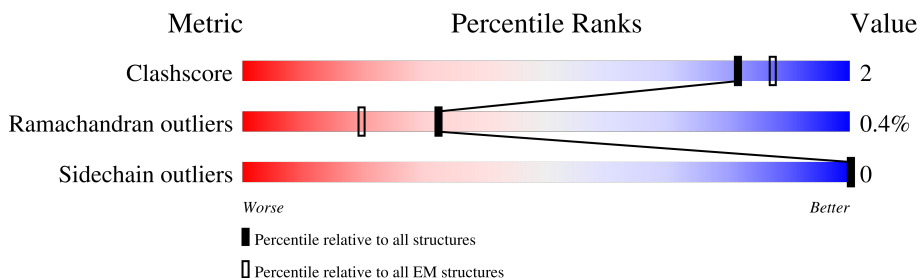
EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

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 3.68 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	11376 (3.18 - 4.18)

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	836	<div> <div>14%</div> <div>95%</div> <div>.</div> </div>
1	B	836	<div> <div>23%</div> <div>94%</div> <div>6%</div> </div>
1	C	836	<div> <div>60%</div> <div>91%</div> <div>8%</div> </div>
1	D	836	<div> <div>88%</div> <div>92%</div> <div>8%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 26512 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 Glutamate receptor ionotropic, delta-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	836	Total	C	N	O	S	0	0
			6628	4217	1130	1242	39		
1	B	836	Total	C	N	O	S	0	0
			6628	4217	1130	1242	39		
1	C	836	Total	C	N	O	S	0	0
			6628	4217	1130	1242	39		
1	D	836	Total	C	N	O	S	0	0
			6628	4217	1130	1242	39		

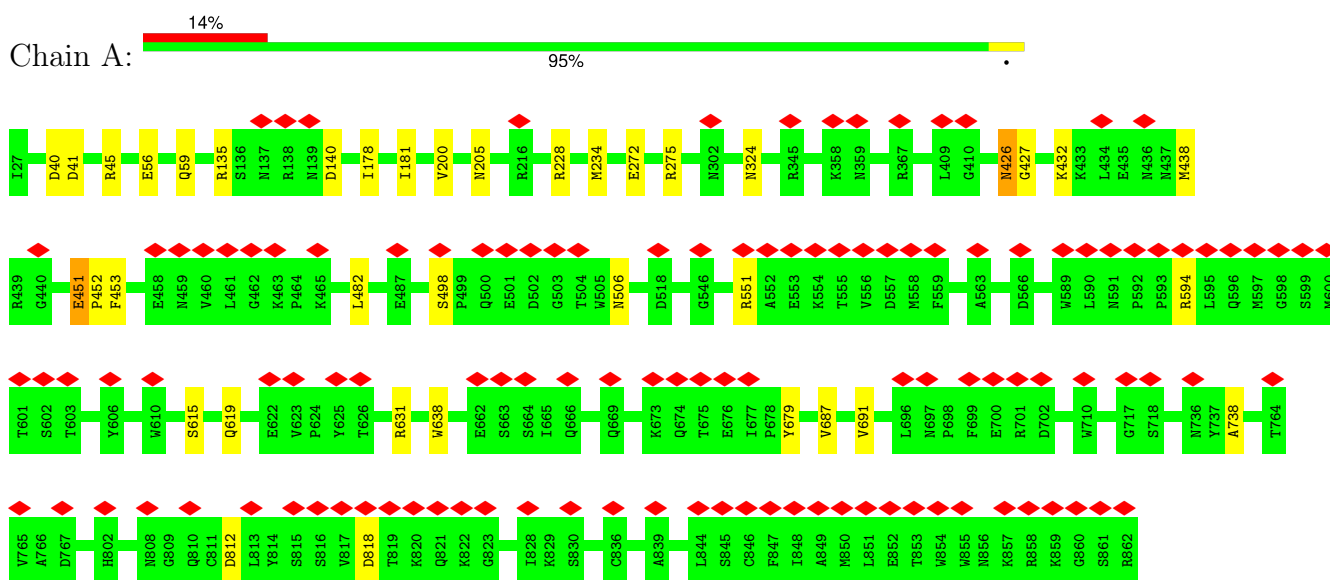
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	710	TRP	ARG	engineered mutation	UNP O43424
B	710	TRP	ARG	engineered mutation	UNP O43424
C	710	TRP	ARG	engineered mutation	UNP O43424
D	710	TRP	ARG	engineered mutation	UNP O43424

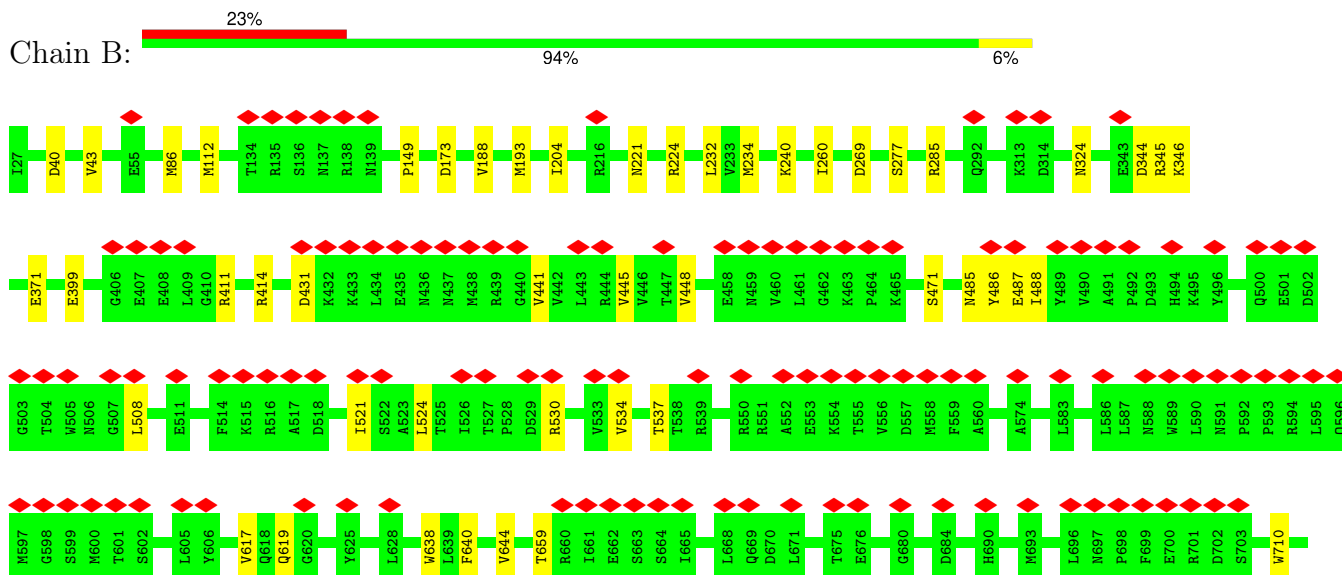
3 Residue-property plots

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.

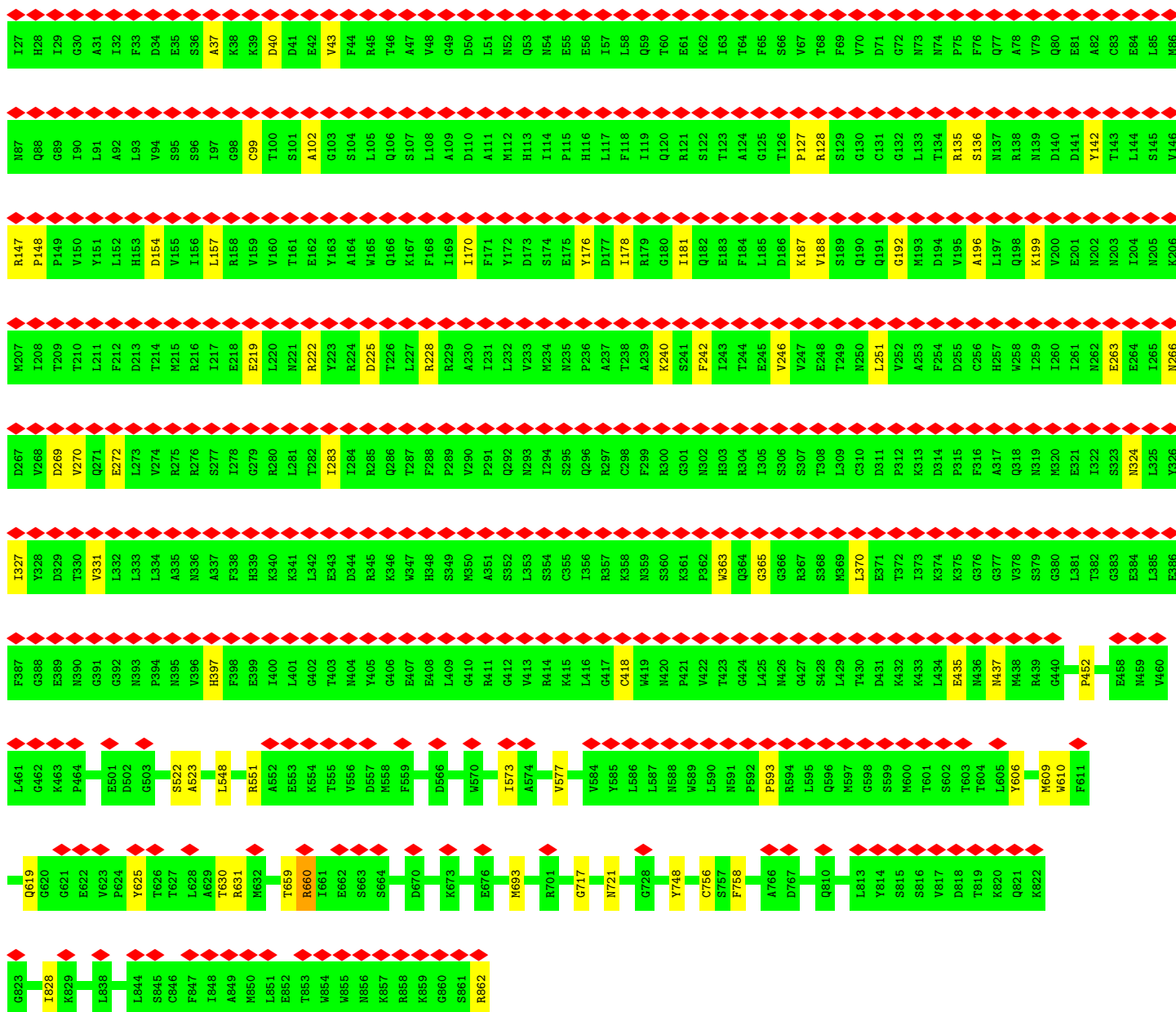
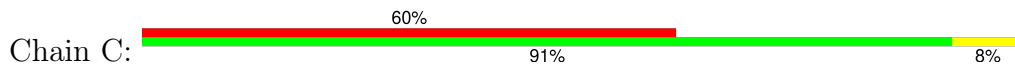
- Molecule 1: Glutamate receptor ionotropic, delta-2



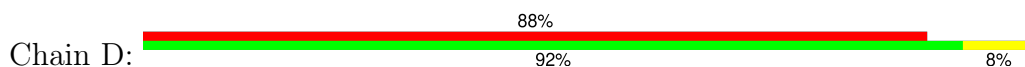
- Molecule 1: Glutamate receptor ionotropic, delta-2



- Molecule 1: Glutamate receptor ionotropic, delta-2



- Molecule 1: Glutamate receptor ionotropic, delta-2



H802	K803	W804	W805	P806	K807	N808	G809	Q810	C811	D812	L813	Y814	S815	S816	V817	D818	T819	K820	Q821	K822	D827	I828	K829	S830	G833	C836	I837	L838	A839	A840	S845	C846	F847	I848	A849	M850	L851	E852	T853	W854	W855	N856	K857	R858	K859	G860	S861	R862													
D742	A743	A744	A745	L746	E747	Y748	V749	A750	I751	D752	D753	P754	D755	C756	S757	F758	Y759	T760	I761	G762	N763	T764	V765	A766	D767	G768	G769	Y770	I771	I772	A773	L774	Q775	H776	G777	S778	P779	W780	R781	D782	V783	F784	S785	Q786	R787	I788	L789	E790	L791	Q792	Q793	N794	G795	D796	Y797	D798	I799	L800	K801		
T681	V682	L683	D684	S685	A686	V687	Y688	A689	H690	V691	R692	M693	K694	G695	L696	N697	P698	F699	E700	R701	D702	S703	M704	Y705	S706	W707	W708	W709	W710	I711	I712	N713	N714	S715	N716	G717	S718	E719	N720	N721	V722	L723	E724	S725	Q726	I729	Q730	K731	K732	K733	Y734	G735	N736	Y737	A738	F739	V740	W741			
L586	L587	N588	W589	L590	P593	R594	L595	Q596	M597	G598	S599	M600	T601	S602	T603	T604	L605	Y606	W610	V617	Q618	Q619	G620	G621	E622	P624	Y625	A629	M633	T659	R660	I661	E662	S663	S664	I665	V666	V667	L668	Q669	D670	L671	S672	K673	Q674	T675	E676	I677	P678	Y679	G680										
G507	L508	V509	G510	E511	L512	V513	F514	K515	R516	A517	D518	I519	G520	I521	S522	A523	L524	T525	I526	T527	P528	D529	R530	E531	N532	V533	V534	D535	F536	T537	T538	R539	Y540	M541	D542	Y543	S544	V545	G546	V547	L548	L549	R550	R551	A552	E553	K554	T555	V556	D557	M558	F559	A560	D566	L569	I573					
T447	V448	L449	E450	E451	F452	F453	V454	M455	V456	S457	E458	M459	V460	L461	Q462	K463	P464	K465	K466	Y467	Q468	G469	F470	S471	I472	D473	V474	L475	D476	A477	L478	S479	M480	Y481	L482	G483	F484	M485	Y486	E487	L488	Y489	V490	A491	D492	D493	H494	E495	K496	G497	S498	P499	Q500	E501	D502	G503	T504	W505	N506		
F387	G388	E389	N390	G391	G392	N393	P394	N395	V396	H397	F398	E399	I400	L401	Q402	T403	N404	Y405	G406	E407	F408	L409	G410	R411	G412	V413	R414	K415	L416	G417	C418	W419	N420	P421	V422	T423	G424	L425	N426	G427	S428	L429	T430	D431	K432	K433	L434	K375	N436	N437	M438	R439	G440	V441	V442	L443	R444	V445	V446		
I327	Y328	D329	T330	V331	L332	L333	L334	A335	N336	A337	F338	H339	K340	K341	L342	E343	D344	R345	K346	W347	H348	S349	M350	A351	S352	L353	S354	C355	L356	R357	K358	N359	S360	K361	P362	W363	Q364	G365	G366	R367	S368	L369	L370	E371	T372	L373	K374	K375	G376	G377	V378	S379	Q380	L381	T382	G383	E384	L385	E386		
D267	V268	D269	V270	Q271	E272	L273	Y274	R275	R276	S277	T278	G279	R280	L281	T282	I283	L284	R285	Q286	T287	F288	P289	V290	P291	Q292	N293	L294	S295	Q296	R297	C298	F299	R300	G301	N302	R303	L243	T244	E245	V246	S307	T308	L309	C310	D311	K312	K313	D314	D255	P315	G316	A317	Q318	R319	M320	E321	I322	S323	N324	L325	Y326
M207	T208	T209	T210	L211	F212	D213	T214	R215	R216	I217	E218	E219	R220	N221	R222	Y223	R224	D225	T226	L227	R228	R229	A230	I231	L232	V233	M234	N235	P236	A237	T238	A239	R240	S241	N302	R303	L243	T244	E245	V246	S307	T247	E248	T249	N250	L251	V252	A253	D254	D255	C256	H257	W258	I259	I260	I261	N262	E263	E264	I265	N266
R147	P148	P149	V150	Y151	L152	H153	D154	V155	I156	L157	R158	V159	W160	T161	E162	Y163	A164	W165	Q166	L167	F168	I169	I170	A171	M172	D173	S174	E175	Y176	D177	I178	R179	G180	I181	Q182	E183	F184	L185	D186	K187	V188	S189	Q190	Q191	G192	M193	D194	V195	D255	L197	Q198	R199	N199	D140	E201	N202	T204	N205	K206		
N87	Q88	G89	T90	L91	A92	L93	V94	S95	S96	I97	G98	C99	T100	S101	A102	G103	S104	L105	Q106	S107	L108	A109	D110	A111	M112	H113	I114	P115	H116	L117	F118	I119	Q120	R121	S122	T123	A124	G125	T126	P127	R128	S129	Q130	C131	G132	L133	T134	R135	S136	N137	R138	N139	D140	E81	A82	C83	E84	L85	N86		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	153060	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.0	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.449	Depositor
Minimum map value	-1.581	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.25	Depositor
Map size (\AA)	407.04, 407.04, 407.04	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.59, 1.59, 1.59	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	0.13	0/6770	0.43	1/9180 (0.0%)
1	B	0.14	0/6770	0.43	0/9180
1	C	0.13	0/6770	0.41	1/9180 (0.0%)
1	D	0.13	0/6770	0.40	0/9180
All	All	0.13	0/27080	0.42	2/36720 (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
1	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	451	GLU	C-N-CD	-6.93	96.58	125.00
1	C	660	ARG	N-CA-C	5.18	121.84	110.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	228	ARG	Sidechain

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	6628	0	6549	23	0
1	B	6628	0	6549	33	0
1	C	6628	0	6549	42	0
1	D	6628	0	6549	37	0
All	All	26512	0	26196	126	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 2.

All (126) 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:B:188:VAL:HG13	1:B:193:MET:HE2	1.59	0.84
1:A:56:GLU:O	1:A:59:GLN:NE2	2.16	0.78
1:C:246:VAL:HG13	1:C:251:LEU:HB2	1.68	0.76
1:C:147:ARG:NH2	1:C:263:GLU:OE1	2.23	0.71
1:C:37:ALA:HB1	1:C:40:ASP:HB2	1.73	0.71
1:B:40:ASP:OD1	1:B:324:ASN:ND2	2.26	0.69
1:D:155:VAL:HG11	1:D:284:ILE:HG21	1.77	0.67
1:B:537:THR:OG1	1:B:772:ILE:N	2.27	0.65
1:A:40:ASP:OD1	1:A:324:ASN:ND2	2.31	0.63
1:A:615:SER:HB2	1:A:638:TRP:HE1	1.63	0.62
1:C:178:ILE:O	1:C:181:ILE:HG12	2.02	0.60
1:C:43:VAL:HG21	1:C:324:ASN:HB3	1.82	0.60
1:C:225:ASP:OD1	1:C:228:ARG:NH1	2.35	0.59
1:D:128:ARG:NH2	1:D:148:PRO:O	2.29	0.59
1:D:225:ASP:OD1	1:D:228:ARG:NH1	2.32	0.59
1:C:266:ASN:ND2	1:C:269:ASP:OD2	2.36	0.58
1:A:812:ASP:HB2	1:B:710:TRP:CZ2	2.39	0.58
1:D:717:GLY:O	1:D:721:ASN:ND2	2.35	0.58
1:A:631:ARG:HH21	1:C:610:TRP:CD1	2.22	0.57
1:D:267:ASP:OD1	1:D:285:ARG:NH1	2.23	0.57
1:D:274:VAL:O	1:D:411:ARG:NH1	2.38	0.57
1:B:285:ARG:NE	1:B:399:GLU:OE2	2.38	0.56
1:A:272:GLU:OE2	1:A:275:ARG:NH1	2.38	0.56
1:B:521:ILE:HA	1:B:772:ILE:HG23	1.87	0.55
1:B:344:ASP:OD2	1:B:346:LYS:NZ	2.34	0.55
1:C:659:THR:O	1:C:660:ARG:HG2	2.07	0.55
1:C:128:ARG:NH2	1:C:148:PRO:O	2.33	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:VAL:HG21	1:A:234:MET:HE1	1.88	0.55
1:C:270:VAL:HG13	1:C:283:ILE:HD12	1.89	0.54
1:C:625:TYR:HE2	1:C:630:THR:HB	1.72	0.54
1:B:43:VAL:HG21	1:B:324:ASN:HB3	1.89	0.53
1:D:173:ASP:OD1	1:D:176:TYR:N	2.42	0.53
1:D:162:GLU:HG2	1:D:429:LEU:HB2	1.90	0.52
1:B:537:THR:N	1:B:772:ILE:O	2.38	0.52
1:B:780:TYR:HB3	1:B:784:PHE:CE2	2.45	0.52
1:B:221:ASN:OD1	1:B:224:ARG:NH1	2.42	0.52
1:A:205:ASN:ND2	1:C:693:MET:SD	2.81	0.52
1:B:277:SER:O	1:B:411:ARG:NH2	2.43	0.52
1:A:451:GLU:C	1:A:453:PHE:H	2.19	0.51
1:B:232:LEU:HB2	1:B:260:ILE:HG13	1.93	0.50
1:B:445:VAL:N	1:B:487:GLU:O	2.45	0.50
1:B:173:ASP:N	1:B:173:ASP:OD1	2.43	0.49
1:B:471:SER:HB3	1:B:772:ILE:HD11	1.95	0.49
1:C:240:LYS:NZ	1:C:272:GLU:OE1	2.44	0.49
1:C:625:TYR:CE2	1:C:630:THR:HB	2.48	0.49
1:D:216:ARG:NH1	1:D:219:GLU:OE2	2.39	0.48
1:B:524:LEU:HD23	1:B:530:ARG:HD3	1.95	0.48
1:B:232:LEU:HD22	1:B:234:MET:HE3	1.95	0.48
1:D:153:HIS:HB2	1:D:184:PHE:HB2	1.95	0.48
1:D:549:LEU:HD22	1:D:759:TYR:OH	2.14	0.48
1:A:438:MET:HE1	1:A:482:LEU:HD13	1.96	0.48
1:B:640:PHE:O	1:B:644:VAL:HG23	2.14	0.48
1:A:551:ARG:NH1	1:A:818:ASP:OD1	2.47	0.47
1:B:617:VAL:HG23	1:B:619:GLN:HG2	1.96	0.47
1:D:121:ARG:NH1	1:D:323:SER:OG	2.47	0.47
1:B:445:VAL:HB	1:B:488:ILE:HG12	1.95	0.47
1:C:154:ASP:OD1	1:C:187:LYS:NZ	2.34	0.47
1:B:371:GLU:O	1:B:371:GLU:HG2	2.15	0.47
1:A:426:ASN:CG	1:A:427:GLY:H	2.23	0.47
1:A:451:GLU:O	1:A:453:PHE:N	2.47	0.47
1:B:414:ARG:NH2	1:B:431:ASP:OD2	2.43	0.47
1:D:154:ASP:OD1	1:D:187:LYS:NZ	2.40	0.46
1:C:142:TYR:CD2	1:C:370:LEU:HD22	2.51	0.46
1:A:679:TYR:HB3	1:A:738:ALA:HB3	1.98	0.45
1:B:445:VAL:HB	1:B:488:ILE:HA	1.99	0.45
1:B:204:ILE:H	1:B:204:ILE:HD12	1.80	0.45
1:B:534:VAL:HA	1:B:776:HIS:HB2	1.96	0.45
1:C:573:ILE:O	1:C:577:VAL:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:LYS:NZ	1:B:269:ASP:OD1	2.37	0.45
1:D:522:SER:OG	1:D:523:ALA:N	2.50	0.45
1:D:659:THR:HG22	1:D:660:ARG:N	2.32	0.45
1:D:493:ASP:O	1:D:495:LYS:N	2.48	0.45
1:C:99:CYS:HA	1:C:102:ALA:HB3	1.99	0.45
1:C:219:GLU:OE2	1:C:222:ARG:NH2	2.50	0.45
1:C:435:GLU:OE1	1:C:437:ASN:ND2	2.49	0.45
1:C:828:ILE:HD12	1:C:828:ILE:H	1.81	0.45
1:D:741:TRP:HB3	1:D:746:LEU:HD21	1.99	0.44
1:D:146:VAL:HG12	1:D:326:TYR:HD1	1.83	0.44
1:B:448:VAL:HG23	1:B:508:LEU:HD13	2.00	0.44
1:C:551:ARG:NH2	1:C:756:CYS:SG	2.91	0.44
1:B:445:VAL:HG21	1:B:486:TYR:HB2	1.99	0.44
1:D:522:SER:C	1:D:524:LEU:H	2.26	0.43
1:B:441:VAL:O	1:B:485:ASN:N	2.48	0.43
1:A:619:GLN:HG3	1:B:638:TRP:CG	2.54	0.43
1:C:606:TYR:HA	1:C:609:MET:HG3	2.01	0.43
1:A:432:LYS:HB3	1:A:432:LYS:HE3	1.80	0.43
1:D:548:LEU:HB2	1:D:746:LEU:HD13	2.01	0.43
1:D:739:PHE:CE2	1:D:741:TRP:HB2	2.52	0.43
1:D:72:GLY:HA2	1:D:97:ILE:HD11	2.00	0.43
1:D:544:SER:OG	1:D:763:ASN:O	2.35	0.43
1:A:498:SER:N	1:A:506:ASN:OD1	2.51	0.43
1:A:41:ASP:CG	1:A:45:ARG:HE	2.27	0.43
1:C:631:ARG:HB3	1:D:610:TRP:CH2	2.54	0.42
1:D:144:LEU:HB3	1:D:387:PHE:CE1	2.54	0.42
1:D:558:MET:HE3	1:D:833:GLY:HA2	2.00	0.42
1:D:142:TYR:CD2	1:D:370:LEU:HD22	2.53	0.42
1:D:617:VAL:C	1:D:619:GLN:H	2.27	0.42
1:C:717:GLY:O	1:C:721:ASN:ND2	2.40	0.42
1:D:183:GLU:HG2	1:D:187:LYS:HE3	2.02	0.42
1:A:638:TRP:CD2	1:C:619:GLN:HG3	2.55	0.42
1:C:170:ILE:N	1:C:196:ALA:O	2.45	0.42
1:D:548:LEU:C	1:D:549:LEU:HD12	2.44	0.42
1:C:327:ILE:O	1:C:331:VAL:HG23	2.20	0.42
1:C:157:LEU:HD22	1:C:187:LYS:HD3	2.02	0.42
1:C:452:PRO:HB3	1:C:748:TYR:CZ	2.55	0.42
1:D:493:ASP:C	1:D:495:LYS:H	2.27	0.42
1:A:135:ARG:NH2	1:A:140:ASP:O	2.53	0.41
1:C:397:HIS:HE1	1:C:418:CYS:HB3	1.85	0.41
1:A:594:ARG:NH2	1:C:862:ARG:O	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:631:ARG:HH21	1:C:610:TRP:CG	2.38	0.41
1:C:363:TRP:CH2	1:C:365:GLY:HA3	2.55	0.41
1:A:687:VAL:O	1:A:691:VAL:HG23	2.21	0.41
1:D:43:VAL:HG21	1:D:324:ASN:CG	2.46	0.41
1:B:86:MET:HE1	1:B:112:MET:HG3	2.03	0.41
1:D:246:VAL:HG22	1:D:251:LEU:HD12	2.03	0.41
1:C:127:PRO:HB2	1:C:176:TYR:CE1	2.56	0.41
1:C:135:ARG:NH1	1:C:136:SER:O	2.51	0.41
1:C:199:LYS:N	1:D:186:ASP:OD1	2.54	0.41
1:C:548:LEU:HD11	1:C:758:PHE:HB3	2.03	0.41
1:D:733:LYS:HB2	1:D:758:PHE:CZ	2.55	0.41
1:C:188:VAL:O	1:C:192:GLY:N	2.52	0.40
1:B:445:VAL:CG2	1:B:486:TYR:HB2	2.51	0.40
1:C:242:PHE:O	1:C:246:VAL:HG23	2.22	0.40
1:C:522:SER:OG	1:C:523:ALA:N	2.54	0.40
1:D:307:SER:HA	1:D:310:CYS:SG	2.61	0.40
1:D:414:ARG:NH2	1:D:431:ASP:OD1	2.47	0.40

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	834/836 (100%)	782 (94%)	48 (6%)	4 (0%)	25	57
1	B	834/836 (100%)	762 (91%)	68 (8%)	4 (0%)	25	57
1	C	834/836 (100%)	791 (95%)	42 (5%)	1 (0%)	48	78
1	D	834/836 (100%)	791 (95%)	38 (5%)	5 (1%)	22	54
All	All	3336/3344 (100%)	3126 (94%)	196 (6%)	14 (0%)	32	61

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	452	PRO
1	A	178	ILE
1	A	181	ILE
1	D	551	ARG
1	D	494	HIS
1	D	715	SER
1	B	149	PRO
1	B	659	THR
1	D	523	ALA
1	A	426	ASN
1	B	345	ARG
1	B	767	ASP
1	C	593	PRO
1	D	594	ARG

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	726/726 (100%)	726 (100%)	0	100	100
1	B	726/726 (100%)	726 (100%)	0	100	100
1	C	726/726 (100%)	726 (100%)	0	100	100
1	D	726/726 (100%)	726 (100%)	0	100	100
All	All	2904/2904 (100%)	2904 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	293	ASN
1	A	296	GLN
1	A	324	ASN
1	A	336	ASN
1	A	348	HIS

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Mol	Chain	Res	Type
1	A	437	ASN
1	B	205	ASN
1	B	404	ASN
1	B	436	ASN
1	B	459	ASN
1	B	588	ASN
1	B	713	ASN
1	B	776	HIS
1	C	73	ASN
1	C	74	ASN
1	C	77	GLN
1	C	182	GLN
1	C	293	ASN
1	C	296	GLN
1	C	690	HIS
1	D	303	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 ⓘ

There are no chain breaks in this entry.

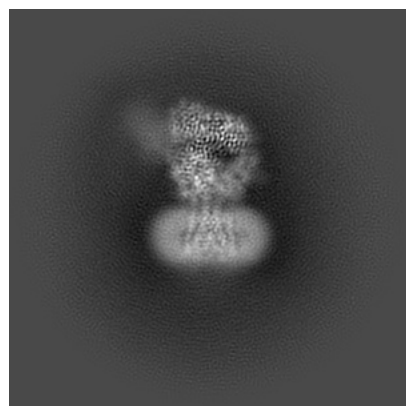
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70667. These allow visual inspection of the internal detail of the map and identification of artifacts.

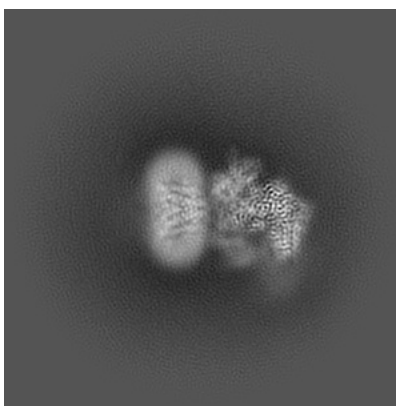
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

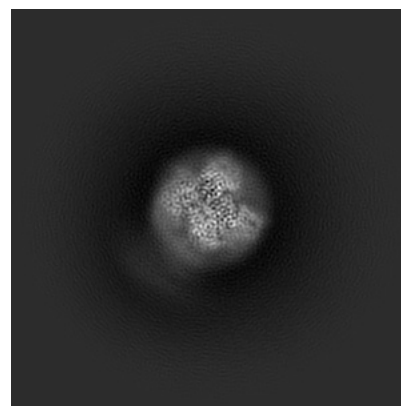
6.1.1 Primary map



X

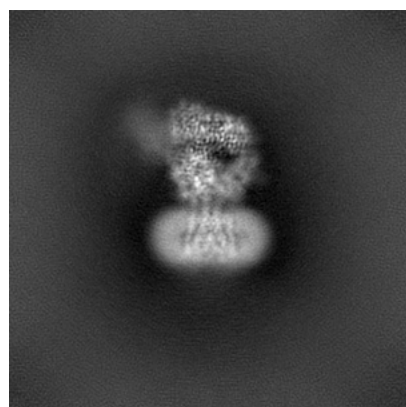


Y

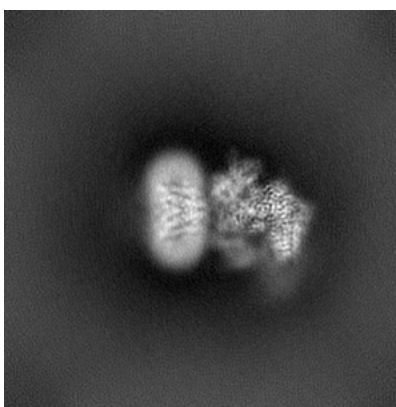


Z

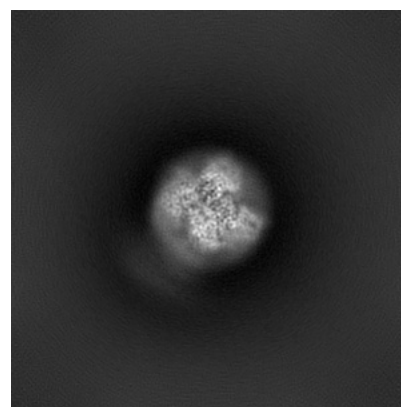
6.1.2 Raw map



X



Y

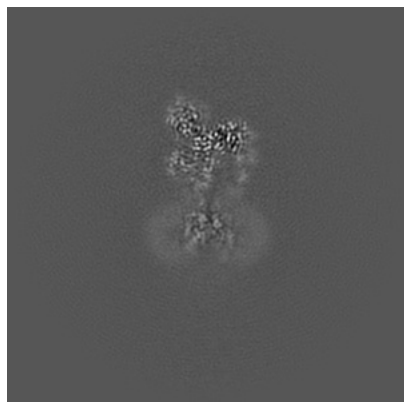


Z

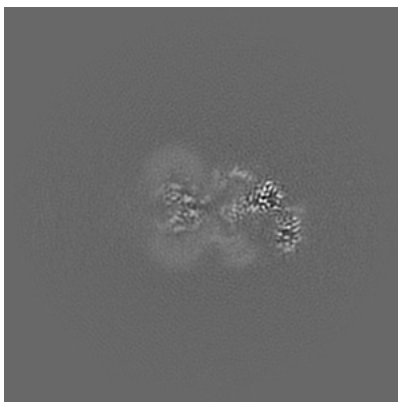
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

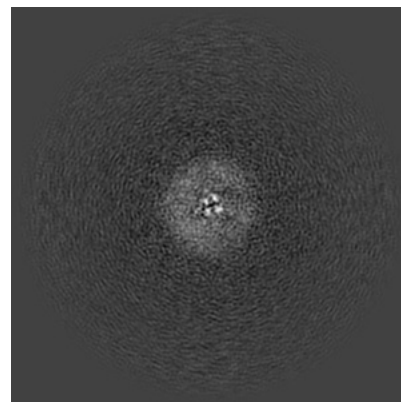
6.2.1 Primary map



X Index: 128

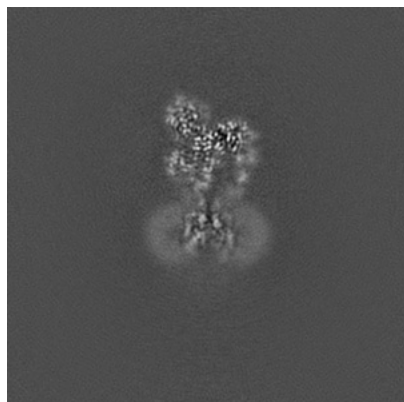


Y Index: 128

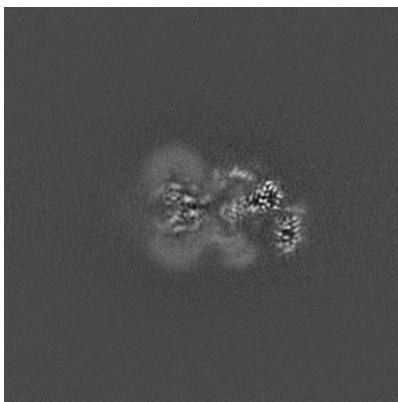


Z Index: 128

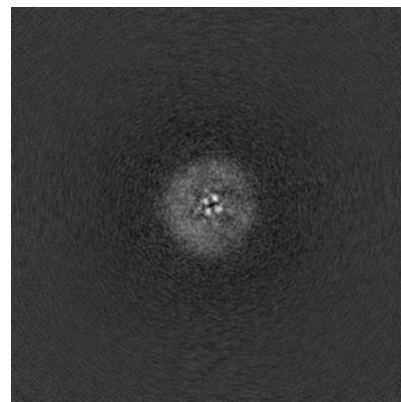
6.2.2 Raw map



X Index: 128



Y Index: 128

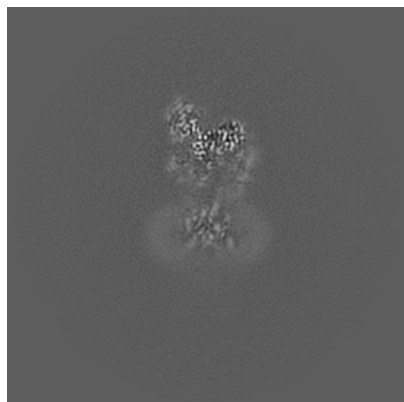


Z Index: 128

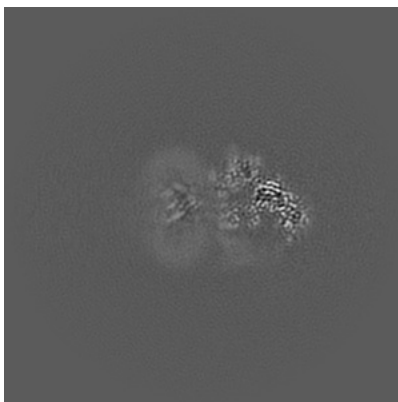
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

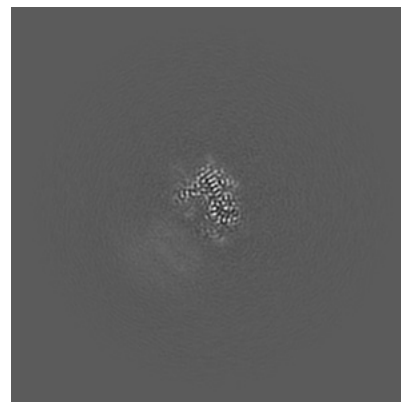
6.3.1 Primary map



X Index: 130

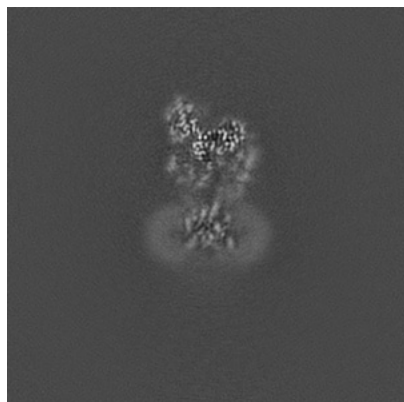


Y Index: 120

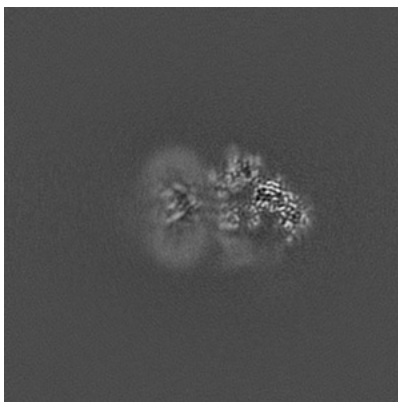


Z Index: 172

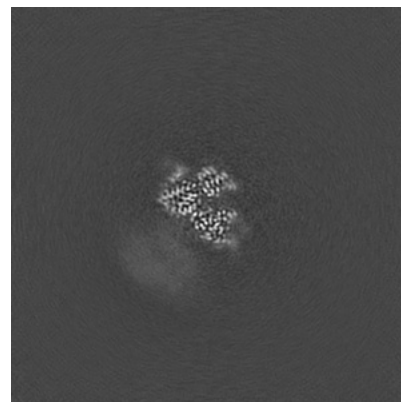
6.3.2 Raw map



X Index: 130



Y Index: 120

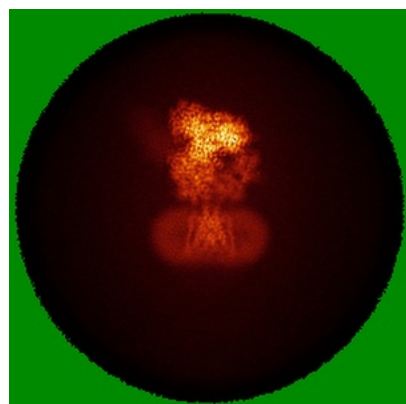


Z Index: 179

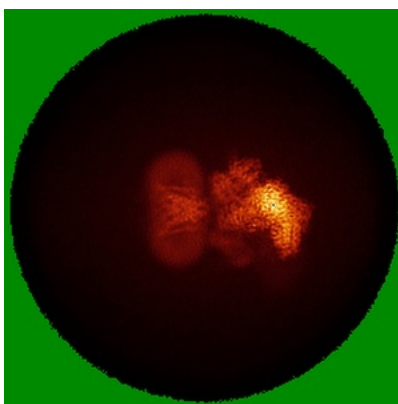
The images above show the largest variance slices of the map in three orthogonal directions.

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

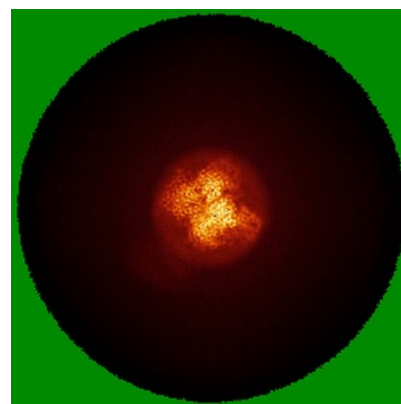
6.4.1 Primary map



X

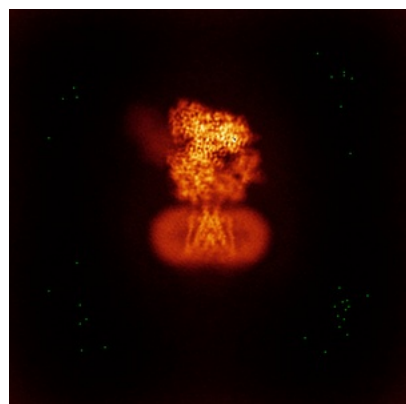


Y

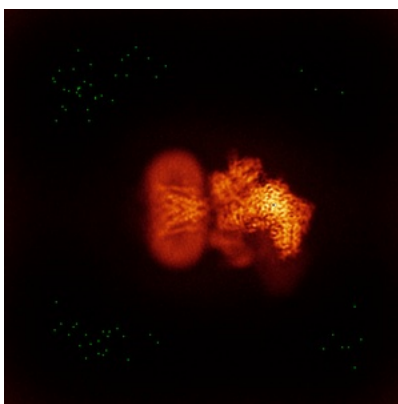


Z

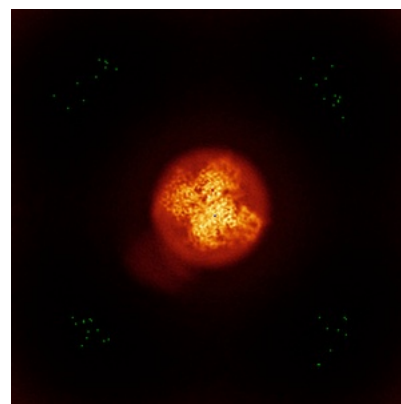
6.4.2 Raw map



X



Y

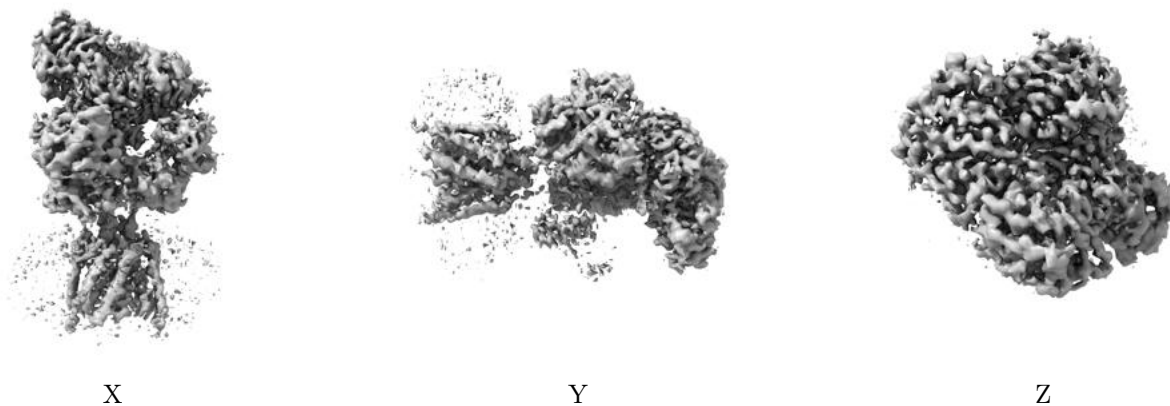


Z

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.

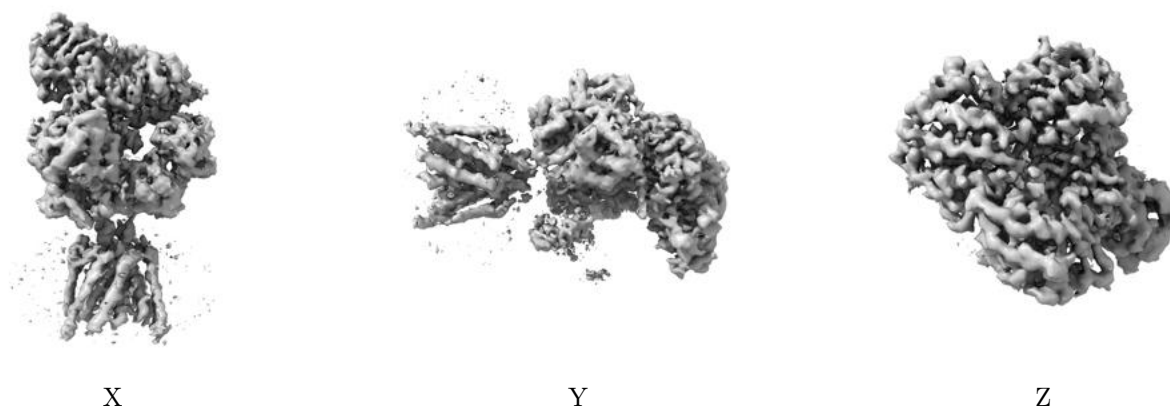
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

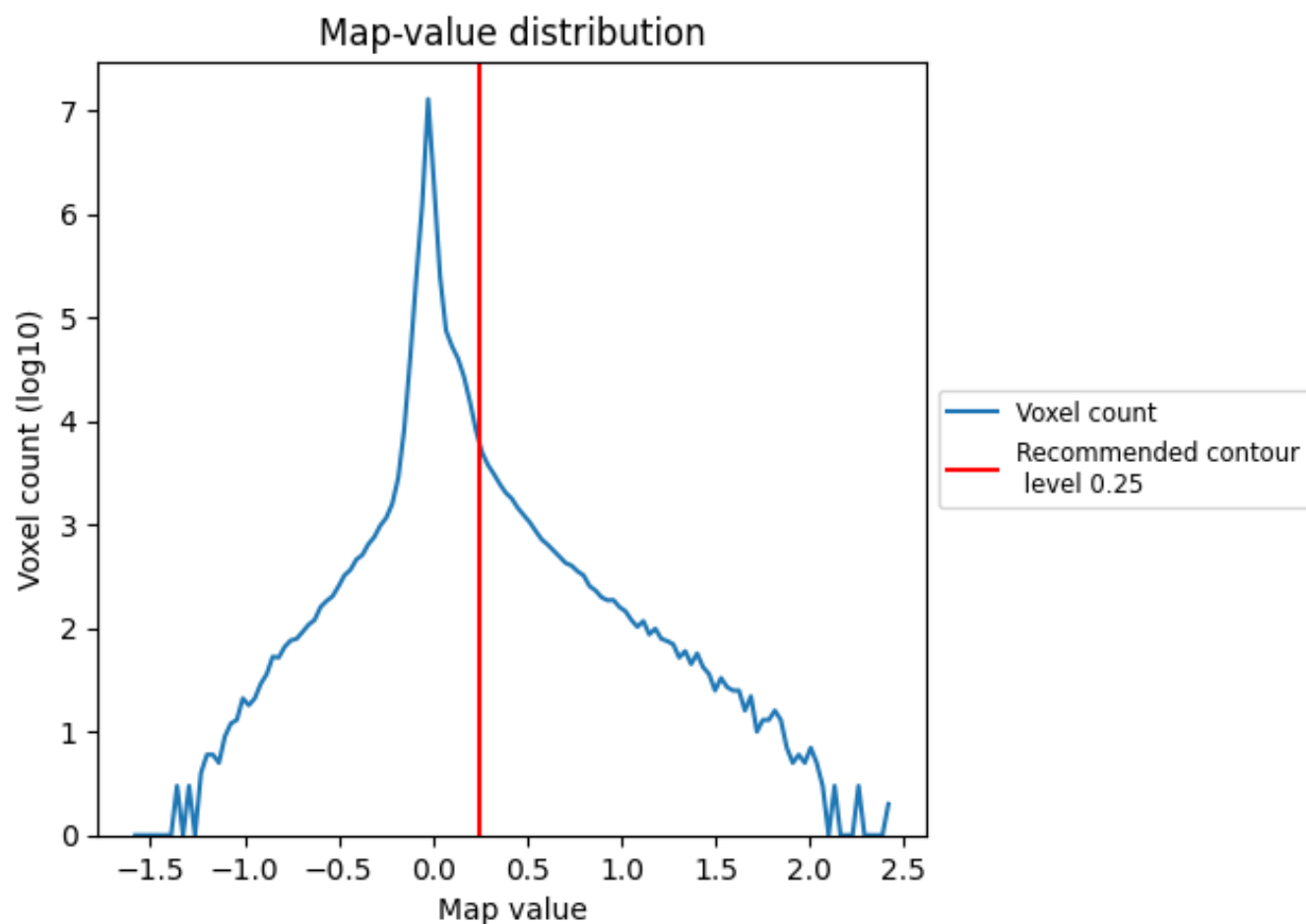
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

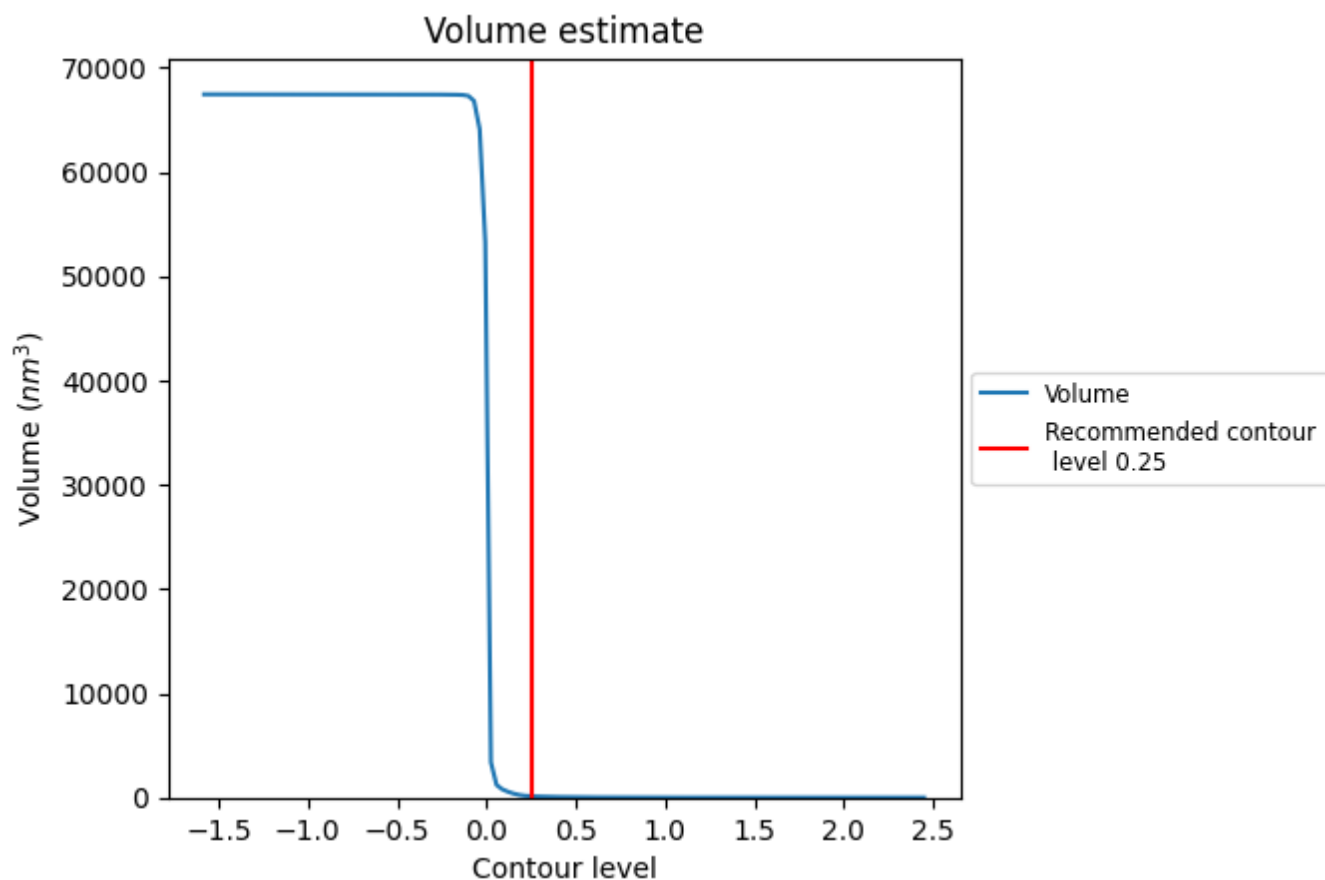
This section contains the results of statistical analysis of the map.

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.

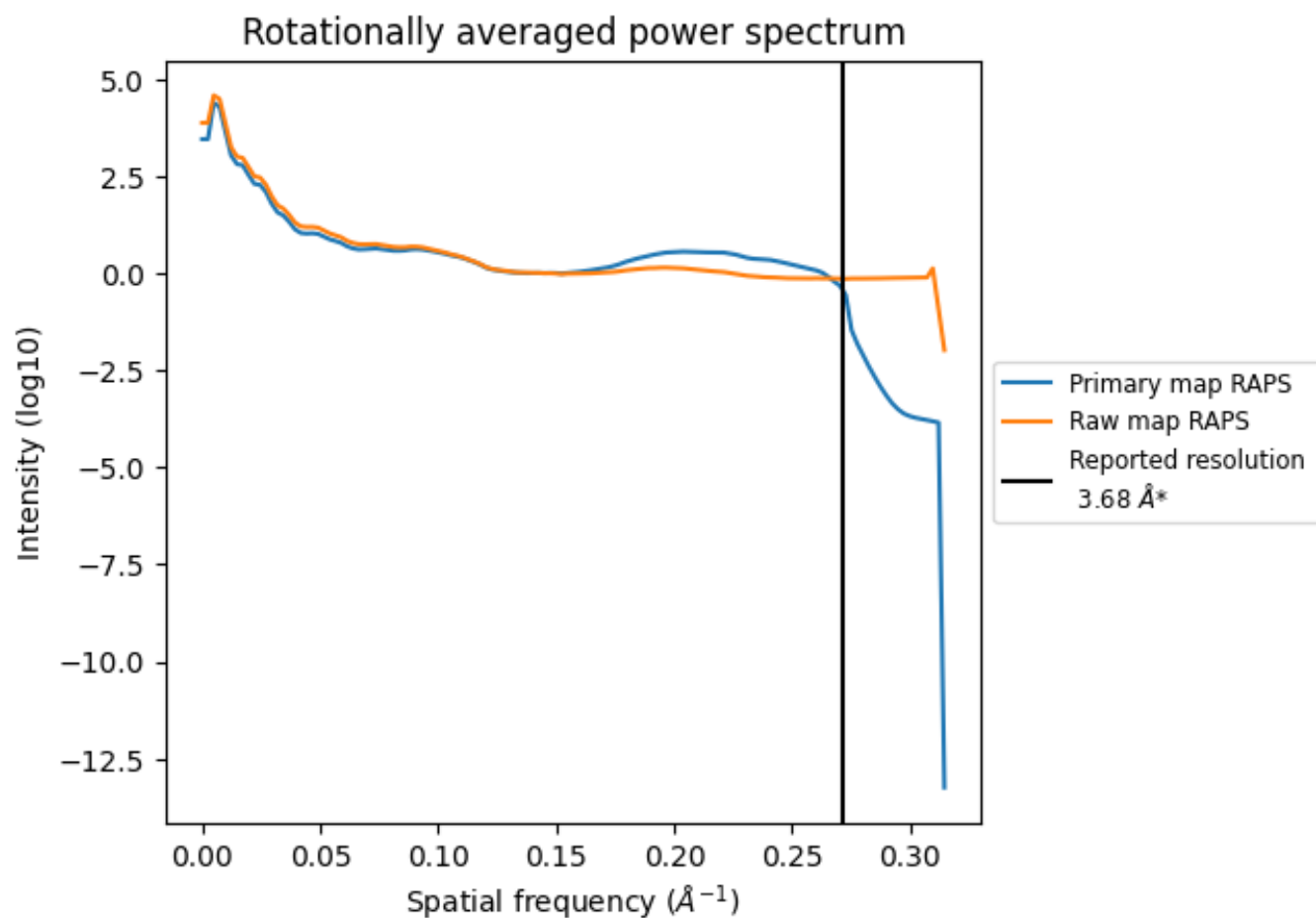
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 127 nm³; this corresponds to an approximate mass of 115 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 ⓘ

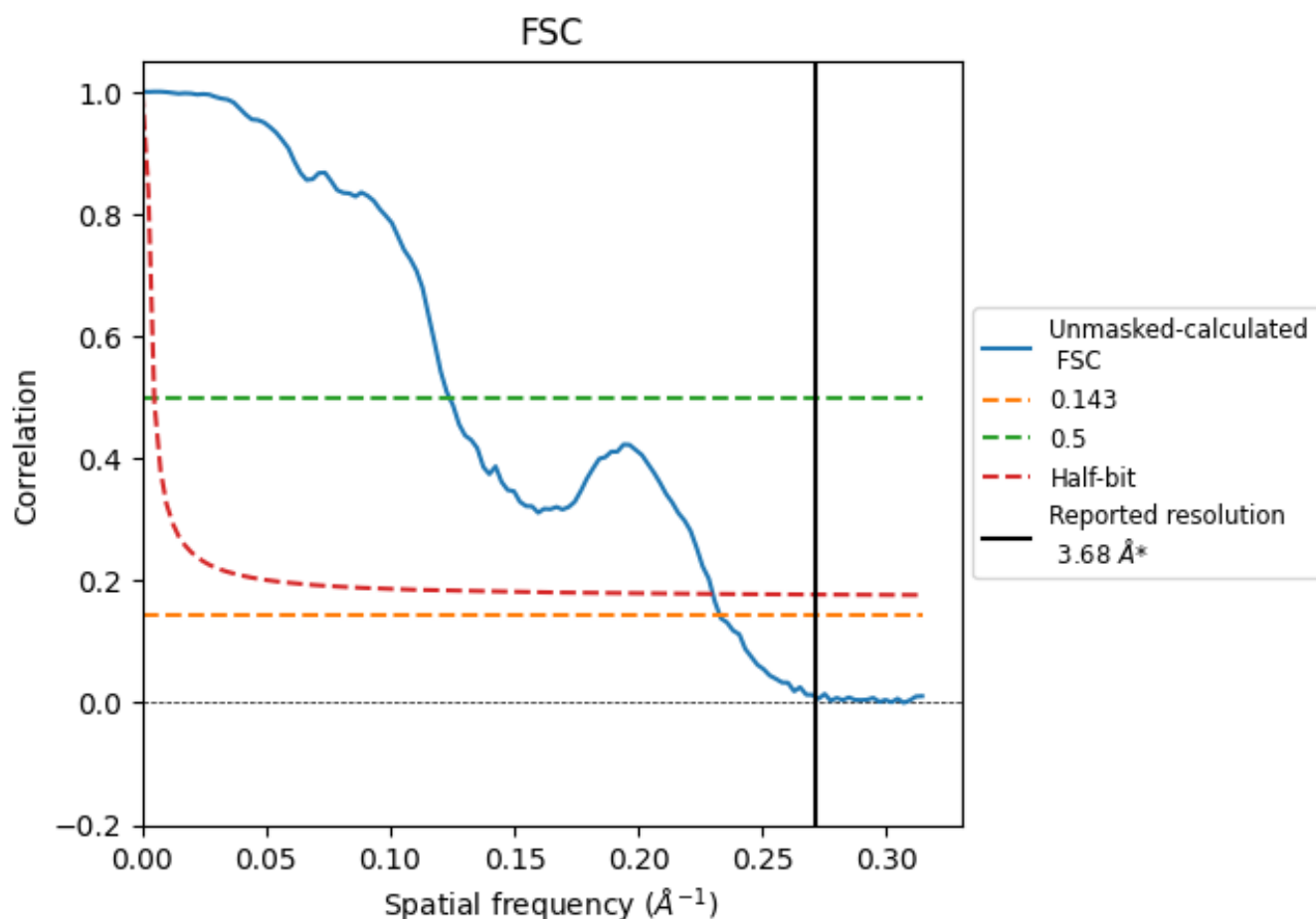


*Reported resolution corresponds to spatial frequency of 0.272 Å⁻¹

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 0.272 Å⁻¹

8.2 Resolution estimates [i](#)

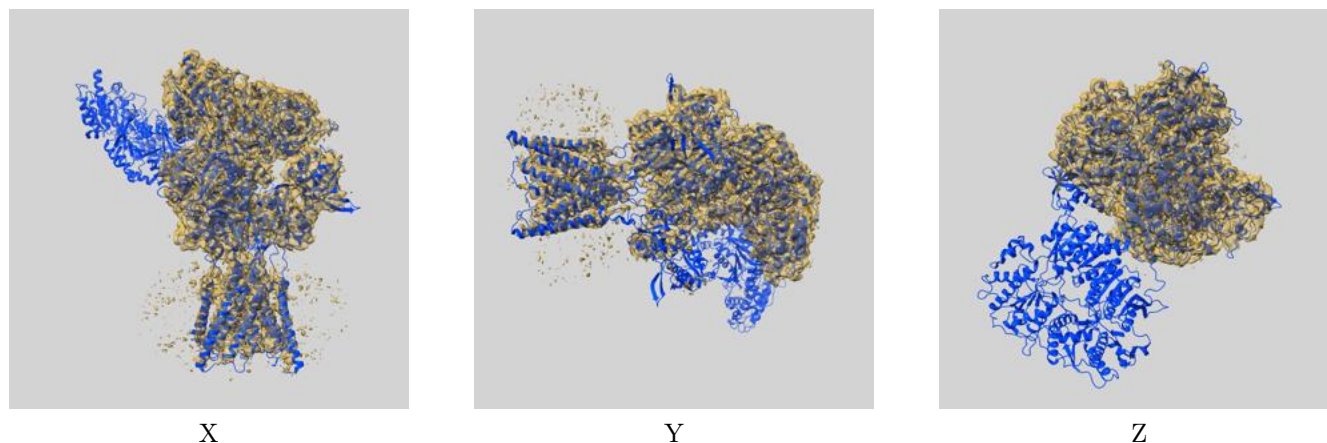
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.68	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.29	8.08	4.35

*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 4.29 differs from the reported value 3.68 by more than 10 %

9 Map-model fit [i](#)

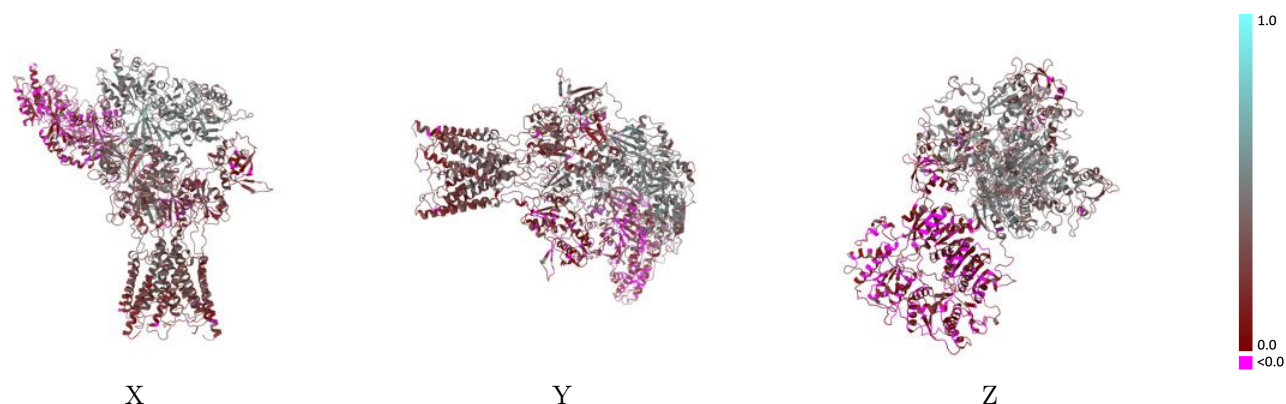
This section contains information regarding the fit between EMDB map EMD-70667 and PDB model 9000. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



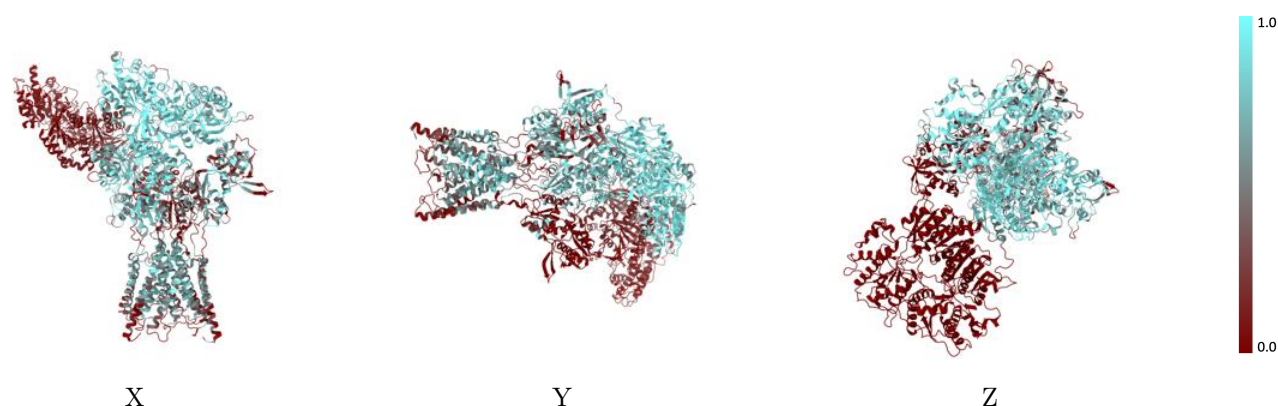
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



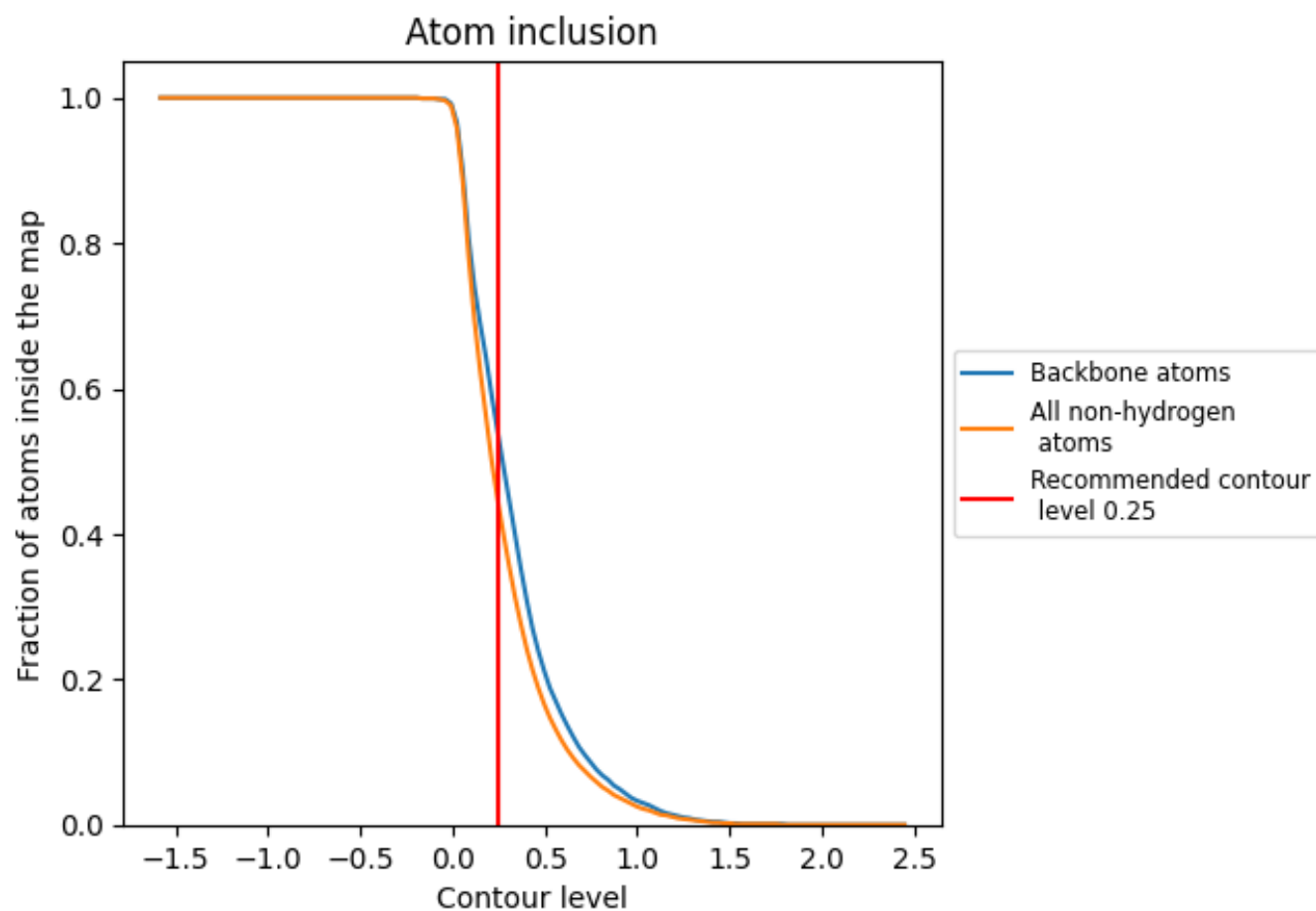
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 53% of all backbone atoms, 44% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4400	<div></div> 0.2810
A	<div></div> 0.7020	<div></div> 0.3930
B	<div></div> 0.6420	<div></div> 0.3550
C	<div></div> 0.3130	<div></div> 0.2270
D	<div></div> 0.1010	<div></div> 0.1470

