



## wwPDB EM Validation Summary Report ⓘ

Sep 28, 2024 – 06:57 PM EDT

PDB ID : 7M7H  
EMDB ID : EMD-23713  
Title : 6-Deoxyerythronolide B synthase (DEBS) module 1 in complex with antibody fragment 1B2: State 1'  
Authors : Cogan, D.P.; Zhang, K.; Chiu, W.; Khosla, C.  
Deposited on : 2021-03-28  
Resolution : 4.10 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

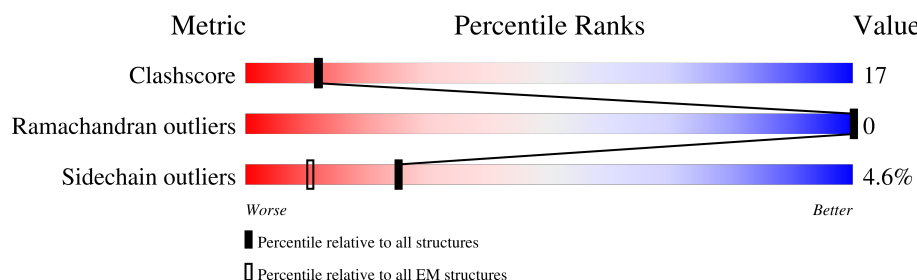
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

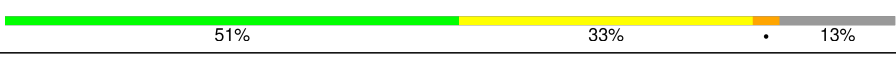
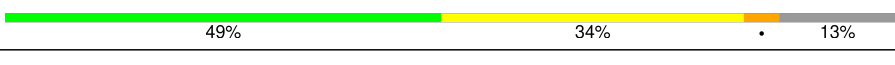
The reported resolution of this entry is 4.10 Å.

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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	1784	
1	B	1784	
2	C	249	
2	E	249	
3	D	236	
3	F	236	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 27046 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 EryAI,6-deoxyerythronolide-B synthase EryA3, modules 5 and 6 chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	1425	Total	C	N	O	S	0	0
			10513	6533	1929	2016	35		
1	A	1390	Total	C	N	O	S	0	0
			10319	6413	1899	1972	35		

There are 106 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	expression tag	UNP Q5UNP6
B	2	ALA	-	expression tag	UNP Q5UNP6
B	3	SER	-	expression tag	UNP Q5UNP6
B	4	THR	-	expression tag	UNP Q5UNP6
B	5	ASP	-	expression tag	UNP Q5UNP6
B	6	SER	-	expression tag	UNP Q5UNP6
B	7	GLU	-	expression tag	UNP Q5UNP6
B	8	LYS	-	expression tag	UNP Q5UNP6
B	9	VAL	-	expression tag	UNP Q5UNP6
B	10	ALA	-	expression tag	UNP Q5UNP6
B	11	GLU	-	expression tag	UNP Q5UNP6
B	12	TYR	-	expression tag	UNP Q5UNP6
B	13	LEU	-	expression tag	UNP Q5UNP6
B	14	ARG	-	expression tag	UNP Q5UNP6
B	15	ARG	-	expression tag	UNP Q5UNP6
B	16	ALA	-	expression tag	UNP Q5UNP6
B	17	THR	-	expression tag	UNP Q5UNP6
B	18	LEU	-	expression tag	UNP Q5UNP6
B	19	ASP	-	expression tag	UNP Q5UNP6
B	20	LEU	-	expression tag	UNP Q5UNP6
B	21	ARG	-	expression tag	UNP Q5UNP6
B	22	ALA	-	expression tag	UNP Q5UNP6
B	23	ALA	-	expression tag	UNP Q5UNP6
B	24	ARG	-	expression tag	UNP Q5UNP6
B	25	GLN	-	expression tag	UNP Q5UNP6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	26	ARG	-	expression tag	UNP Q5UNP6
B	27	ILE	-	expression tag	UNP Q5UNP6
B	28	ARG	-	expression tag	UNP Q5UNP6
B	29	GLU	-	expression tag	UNP Q5UNP6
B	30	LEU	-	expression tag	UNP Q5UNP6
B	31	GLU	-	expression tag	UNP Q5UNP6
B	1486	THR	-	linker	UNP Q5UNP6
B	1487	SER	-	linker	UNP Q5UNP6
B	1488	GLU	-	linker	UNP Q5UNP6
B	1489	LEU	-	linker	UNP Q5UNP6
B	1490	GLY	-	linker	UNP Q5UNP6
B	1768	SER	-	expression tag	UNP Q03133
B	1769	SER	-	expression tag	UNP Q03133
B	1770	VAL	-	expression tag	UNP Q03133
B	1771	ASP	-	expression tag	UNP Q03133
B	1772	LYS	-	expression tag	UNP Q03133
B	1773	LEU	-	expression tag	UNP Q03133
B	1774	ALA	-	expression tag	UNP Q03133
B	1775	ALA	-	expression tag	UNP Q03133
B	1776	ALA	-	expression tag	UNP Q03133
B	1777	LEU	-	expression tag	UNP Q03133
B	1778	GLU	-	expression tag	UNP Q03133
B	1779	HIS	-	expression tag	UNP Q03133
B	1780	HIS	-	expression tag	UNP Q03133
B	1781	HIS	-	expression tag	UNP Q03133
B	1782	HIS	-	expression tag	UNP Q03133
B	1783	HIS	-	expression tag	UNP Q03133
B	1784	HIS	-	expression tag	UNP Q03133
A	1	MET	-	expression tag	UNP Q5UNP6
A	2	ALA	-	expression tag	UNP Q5UNP6
A	3	SER	-	expression tag	UNP Q5UNP6
A	4	THR	-	expression tag	UNP Q5UNP6
A	5	ASP	-	expression tag	UNP Q5UNP6
A	6	SER	-	expression tag	UNP Q5UNP6
A	7	GLU	-	expression tag	UNP Q5UNP6
A	8	LYS	-	expression tag	UNP Q5UNP6
A	9	VAL	-	expression tag	UNP Q5UNP6
A	10	ALA	-	expression tag	UNP Q5UNP6
A	11	GLU	-	expression tag	UNP Q5UNP6
A	12	TYR	-	expression tag	UNP Q5UNP6
A	13	LEU	-	expression tag	UNP Q5UNP6
A	14	ARG	-	expression tag	UNP Q5UNP6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ARG	-	expression tag	UNP Q5UNP6
A	16	ALA	-	expression tag	UNP Q5UNP6
A	17	THR	-	expression tag	UNP Q5UNP6
A	18	LEU	-	expression tag	UNP Q5UNP6
A	19	ASP	-	expression tag	UNP Q5UNP6
A	20	LEU	-	expression tag	UNP Q5UNP6
A	21	ARG	-	expression tag	UNP Q5UNP6
A	22	ALA	-	expression tag	UNP Q5UNP6
A	23	ALA	-	expression tag	UNP Q5UNP6
A	24	ARG	-	expression tag	UNP Q5UNP6
A	25	GLN	-	expression tag	UNP Q5UNP6
A	26	ARG	-	expression tag	UNP Q5UNP6
A	27	ILE	-	expression tag	UNP Q5UNP6
A	28	ARG	-	expression tag	UNP Q5UNP6
A	29	GLU	-	expression tag	UNP Q5UNP6
A	30	LEU	-	expression tag	UNP Q5UNP6
A	31	GLU	-	expression tag	UNP Q5UNP6
A	1486	THR	-	linker	UNP Q5UNP6
A	1487	SER	-	linker	UNP Q5UNP6
A	1488	GLU	-	linker	UNP Q5UNP6
A	1489	LEU	-	linker	UNP Q5UNP6
A	1490	GLY	-	linker	UNP Q5UNP6
A	1768	SER	-	expression tag	UNP Q03133
A	1769	SER	-	expression tag	UNP Q03133
A	1770	VAL	-	expression tag	UNP Q03133
A	1771	ASP	-	expression tag	UNP Q03133
A	1772	LYS	-	expression tag	UNP Q03133
A	1773	LEU	-	expression tag	UNP Q03133
A	1774	ALA	-	expression tag	UNP Q03133
A	1775	ALA	-	expression tag	UNP Q03133
A	1776	ALA	-	expression tag	UNP Q03133
A	1777	LEU	-	expression tag	UNP Q03133
A	1778	GLU	-	expression tag	UNP Q03133
A	1779	HIS	-	expression tag	UNP Q03133
A	1780	HIS	-	expression tag	UNP Q03133
A	1781	HIS	-	expression tag	UNP Q03133
A	1782	HIS	-	expression tag	UNP Q03133
A	1783	HIS	-	expression tag	UNP Q03133
A	1784	HIS	-	expression tag	UNP Q03133

- Molecule 2 is a protein called 1B2 (heavy chain).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	205	Total	C	N	O	S	0	0
			1539	978	257	298	6		
2	E	205	Total	C	N	O	S	0	0
			1539	978	257	298	6		

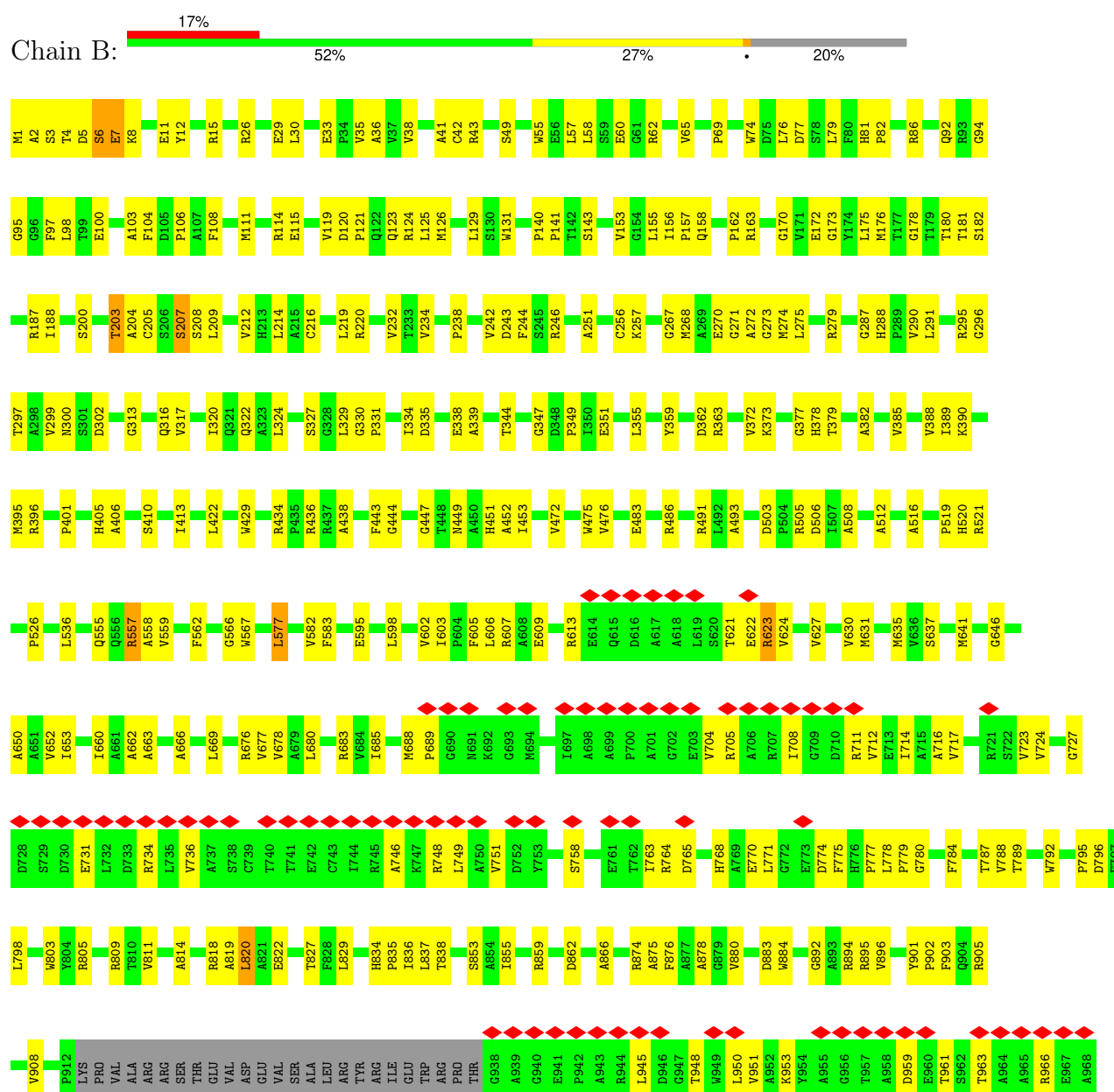
- Molecule 3 is a protein called 1B2 (light chain).

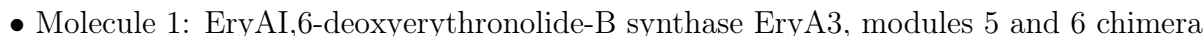
Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	206	Total	C	N	O	S	0	0
			1568	983	262	317	6		
3	F	206	Total	C	N	O	S	0	0
			1568	984	262	316	6		

### 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: EryAI,6-deoxyerythronolide-B synthase EryA3, modules 5 and 6 chimera

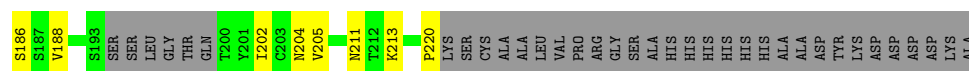




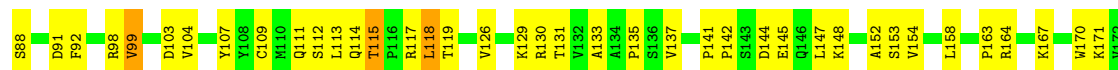


T102	V201	D302	L422	L511	E614	I697	H759	G849	T937	V997	E1057	V1120	T1195
A103	D202	D302	L423	A516	Q615	A698	V760	A850	G938	G998	R1058	R1123	A1198
F108	S208	P311	W429	A517	D616	A899	T762	D851	A939	E999	V1059	R1124	A1199
M111	L209	N312	W435	L518	A617	P700	I763	L852	G940	V1000	R1060	W1125	C1200
A118	V210	A315	R434	A822	A618	A701	R764	A854	E941	A1001	H1064	V1126	T1203
V119	H213	Q316	R436	P526	S620	G702	L767	L858	P942	V1003	G1065	R1127	D1204
D120	L214	Q317	R437	A622	T621	E703	H776	R859	A943	L1004	A1066	A1128	R1205
P121	C216	V317	R437	A632	E622	V704	L778	R860	R944	S1005	L1067	A1130	E1206
Q123	L219	A315	V440	A636	R623	A706	P777	G861	L945	L1006	W1068	P1131	S1207
R124	R220	L324	S442	L336	V624	R707	P779	L865	G947	L1007	G1069	A1132	V1208
L126	E223	S327	F443	Q655	E626	I708	G780	E870	T948	A1008	G1071	D1134	R1209
L127	S224	G330	F443	R557	V627	G709	F781	S873	W949	V1009	L1072	D1135	L1211
W131	S225	G330	H451	A558	Q628	D710	G782	S873	L950	D1010	V1073	E1136	L1212
E132	L226	D333	I454	V559	Q628	R711	D796	V880	V951	A1012	I1074	A1075	G1213
V133	A227	I334	E455	F560	Q628	V712	L798	D883	K953	E1013	A1075	L1076	G1214
F136	M228	D335	E456	P563	V630	E713	D799	R894	Y954	P1014	E1077	P1139	I1215
P141	S229	A336	E456	G564	M631	A716	G801	R895	A955	E1015	E1077	T1140	G1216
P148	G239	E338	E463	Q655	G646	V717	Y802	V896	G956	E1016	P1078	G1141	D1217
T237	M240	A339	E464	Q656	V647	N718	W803	P897	T957	A1017	A1080	T1142	D1218
Q158	L250	H340	V466	W567	E648	R721	Y804	L898	A958	P1018	V1081	V1143	V1219
P162	D243	I350	D470	W569	P649	S722	R805	P899	D959	L1019	W1082	L1144	P1220
R163	F244	A358	V471	M572	V652	V723	N806	R905	E960	A1020	L1085	G1147	S1222
E169	M247	Y359	V471	S850	I653	W725	R808	R906	E960	L1021	V1086	G1150	A1223
G170	L260	L367	V471	A584	G654	A726	F813	R907	T961	A1022	D1087	G1151	A1227
Y174	G272	L369	L477	R568	H655	G727	A814	V909	S962	L1024	V1088	V1152	T1230
L175	A273	L376	S478	E589	Q657	D728	V817	L910	T963	A1025	P1089	G1153	G1236
W176	M274	G377	A479	D592	I660	S729	R818	K313	A964	D1026	A1090	G1154	D1237
T177	L275	H378	S480	A593	A666	D730	Y825	P914	R966	T1027	G1091	W1159	D1238
G177	L276	T379	S480	L594	A674	E731	R826	V915	E967	L1028	S1092	L1160	G1239
T179	L277	Q380	L485	L594	A675	L732	L829	A916	A968	S1029	V1093	L1167	L1239
T180	E278	A381	Q488	H597	R676	D733	V830	R918	L969	V1031	A1094	L1170	G1241
T181	L280	A382	E498	L598	A679	R734	V831	R919	S971	Q1032	E1095	V1171	E1242
S182	S281	A382	H499	L598	A679	D735	S832	S919	A972	A1033	E1096	S1172	R1243
V183	D282	V385	L492	D599	S682	L736	H834	T920	G973	E1035	A1097	R1173	I1244
A184	A283	V388	A493	F600	V684	L737	P835	V922	G973	V1036	R1098	S1174	E1245
R187	E288	I389	H495	V602	I685	A738	I836	D923	R977	S1037	H1099	G1175	R1246
L194	R285	K390	E498	I603	I686	C739	T838	E924	L979	A1038	L1100	P1176	S1248
P197	G296	M395	H499	P604	T687	T740	T838	E924	V976	E1039	A1101	A1178	R1249
T297	T297	P605	Q502	F605	M688	T741	A839	V925	R977	L1039	A1102	D1179	V1252
		L606	D503	L606	P689	E742	A840	S926	E978	G1040	V1103	E1183	L1253
		R607	F504	R607	G690	C743	I841	A927	L979	P1042	V1104	L1184	R1256
		A608	R505	A608	N691	I744	E842	R929	V980	L1043	S1105	E1187	N1257
		A610	I507	A610	K692	T745	I844	Y930	V981	L1044	G1106	L1188	L1258
		A611	S510	A611	G693	R746	G845	R931	D982	T1045	G1107	A1193	F1260
		R612		R612	M694	K747	D846	I934	A983	V1046	A1108	R1194	T1261
		R613		R613	A695	R748	S848	R935	R984	T1047	G1109		T1262
					S696	L749		P936	G985	E1048	E1111		R1263
						A750			R987	S1049	Q1112		
						V751				A1050	L1113		
						D752				V1051	L1114		
						Y753				A1052	L1115		
						A754				T1053	R1116		
						S755				G1054	A1117		
						H756				P1055	D1118		
						S758				F1056	G1119		

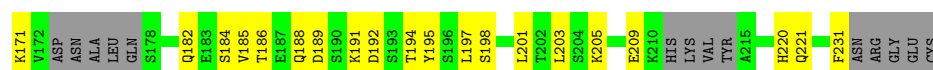




• Molecule 3: 1B2 (light chain)



• Molecule 3: 1B2 (light chain)



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	58206	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	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.525	Depositor
Minimum map value	-0.358	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.069	Depositor
Recommended contour level	0.28	Depositor
Map size (Å)	336.0, 336.0, 336.0	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	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	0.29	0/10522	0.57	0/14323
1	B	0.29	0/10715	0.57	0/14587
2	C	0.29	0/1575	0.58	0/2141
2	E	0.28	0/1575	0.58	0/2141
3	D	0.40	0/1601	0.60	1/2175 (0.0%)
3	F	0.39	0/1601	0.57	0/2174
All	All	0.30	0/27589	0.57	1/37541 (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	1
2	E	0	1
3	D	0	1
3	F	0	1
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	24	PRO	N-CA-C	-5.91	96.72	112.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	155	GLU	Peptide
3	D	115	THR	Peptide

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Mol	Chain	Res	Type	Group
2	E	155	GLU	Peptide
3	F	115	THR	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	10319	0	10164	385	0
1	B	10513	0	10362	374	0
2	C	1539	0	1511	51	0
2	E	1539	0	1511	52	0
3	D	1568	0	1528	51	0
3	F	1568	0	1533	57	0
All	All	27046	0	26609	918	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 918 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:1333:ARG:HD3	1:A:927:ALA:HB1	1.63	0.81
1:B:1144:LEU:HD13	1:B:1169:LEU:HD23	1.62	0.81
3:D:184:SER:HB3	3:D:198:SER:HB3	1.64	0.79
1:A:158:GLN:NE2	1:A:235:MET:SD	2.60	0.74
1:A:1019:LEU:HD13	1:A:1244:ILE:HG22	1.67	0.74

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	1388/1784 (78%)	1303 (94%)	85 (6%)	0	100	100
1	B	1419/1784 (80%)	1353 (95%)	66 (5%)	0	100	100
2	C	199/249 (80%)	186 (94%)	13 (6%)	0	100	100
2	E	199/249 (80%)	187 (94%)	12 (6%)	0	100	100
3	D	200/236 (85%)	182 (91%)	18 (9%)	0	100	100
3	F	200/236 (85%)	183 (92%)	17 (8%)	0	100	100
All	All	3605/4538 (79%)	3394 (94%)	211 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 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	1028/1325 (78%)	999 (97%)	29 (3%)	38	59
1	B	1047/1325 (79%)	1017 (97%)	30 (3%)	37	58
2	C	170/203 (84%)	163 (96%)	7 (4%)	26	49
2	E	170/203 (84%)	164 (96%)	6 (4%)	31	53
3	D	182/208 (88%)	153 (84%)	29 (16%)	2	13
3	F	182/208 (88%)	155 (85%)	27 (15%)	2	14
All	All	2779/3472 (80%)	2651 (95%)	128 (5%)	25	46

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	84	SER
3	F	115	THR
1	A	1070	VAL
1	A	1058	ARG
3	F	118	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	565	GLN
1	A	657	GLN
3	F	74	ASN
1	A	1112	GLN
2	C	5	GLN

### 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.



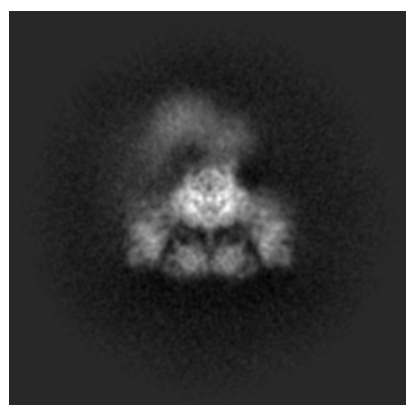
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23713. These allow visual inspection of the internal detail of the map and identification of artifacts.

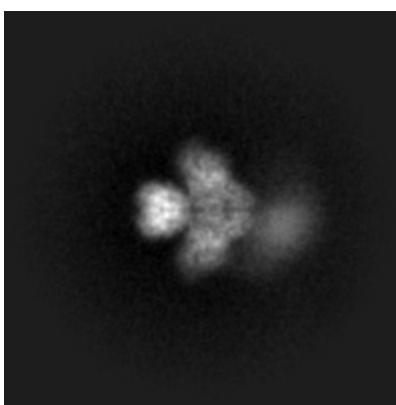
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

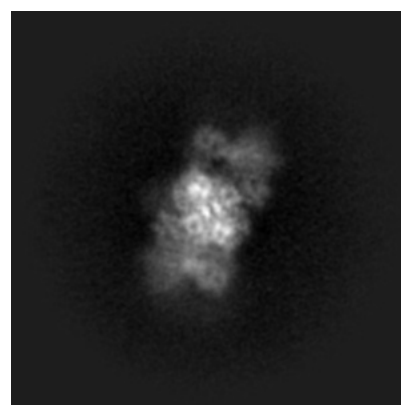
#### 6.1.1 Primary map



X



Y

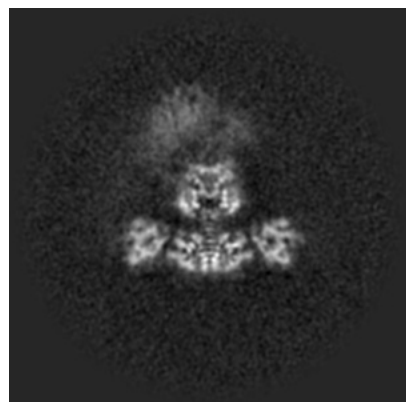


Z

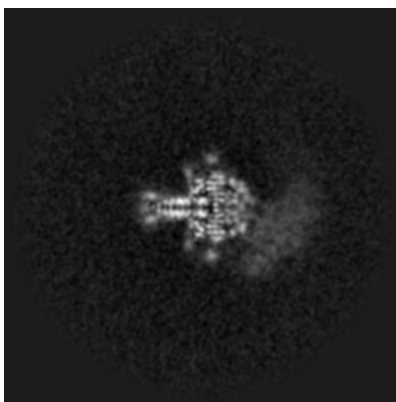
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

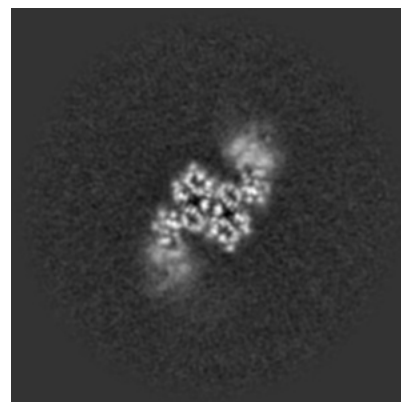
#### 6.2.1 Primary map



X Index: 168



Y Index: 168

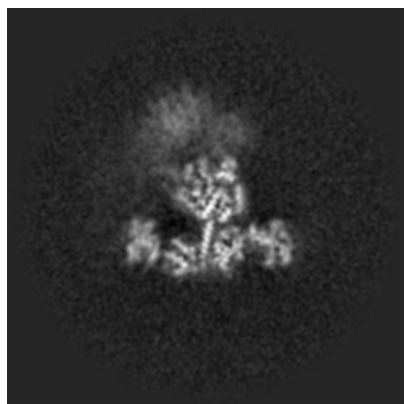


Z Index: 168

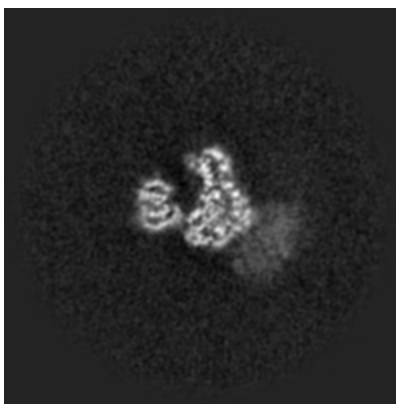
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

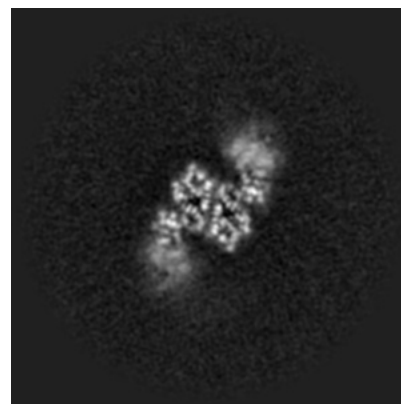
### 6.3.1 Primary map



X Index: 162



Y Index: 183

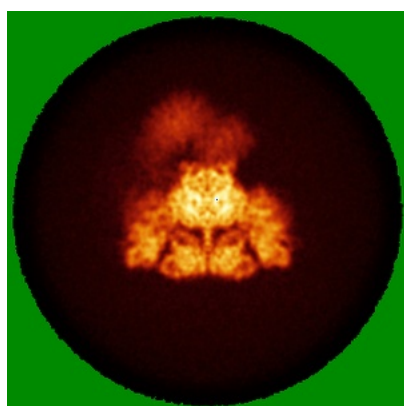


Z Index: 167

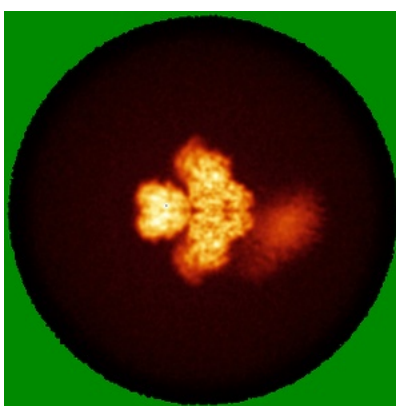
The images above show the largest variance slices of the map in three orthogonal directions.

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

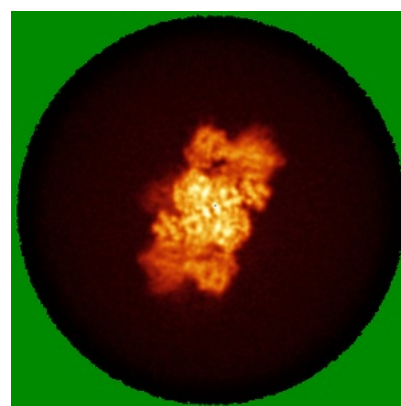
### 6.4.1 Primary map



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

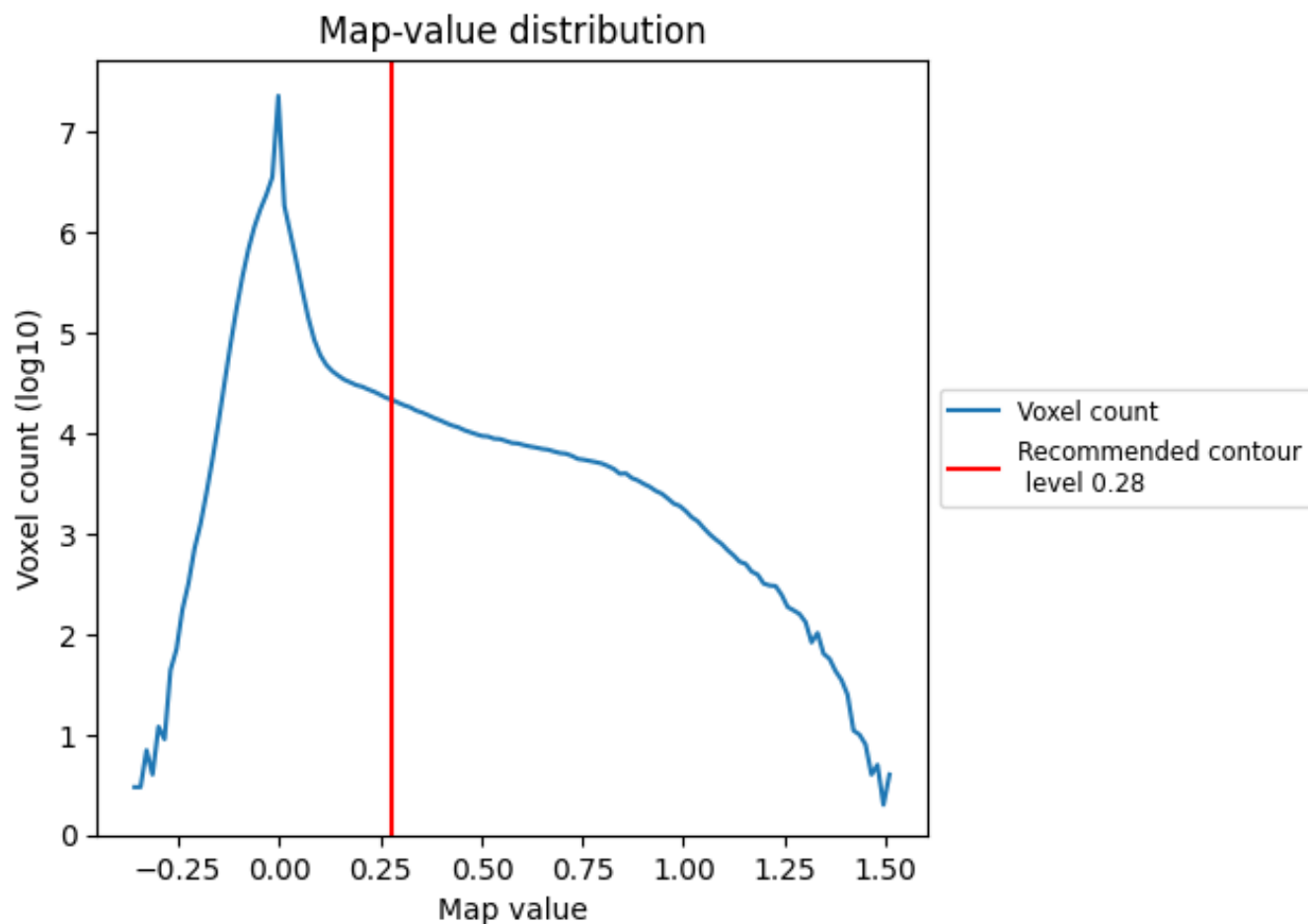
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

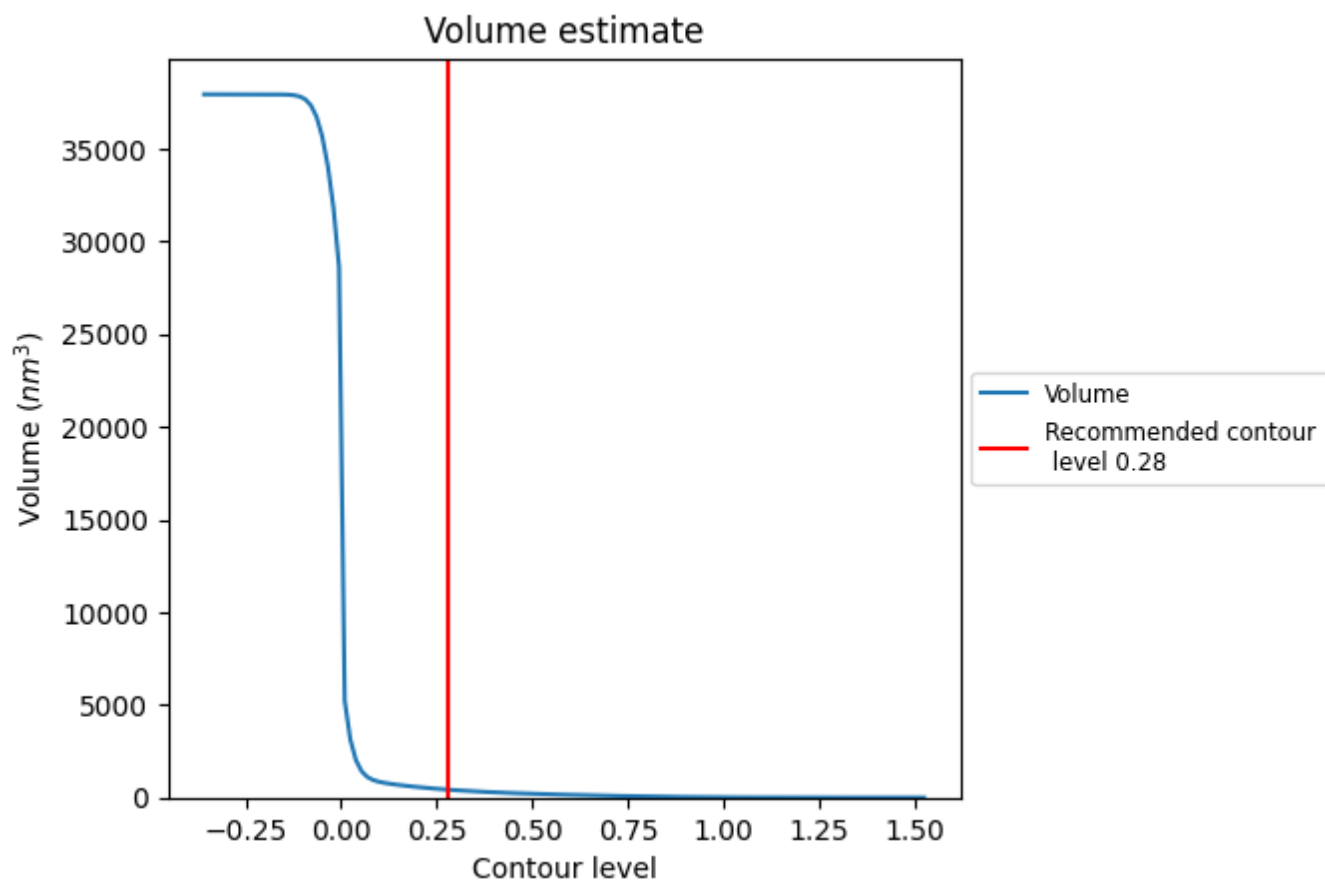
This section contains the results of statistical analysis of the map.

### 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.

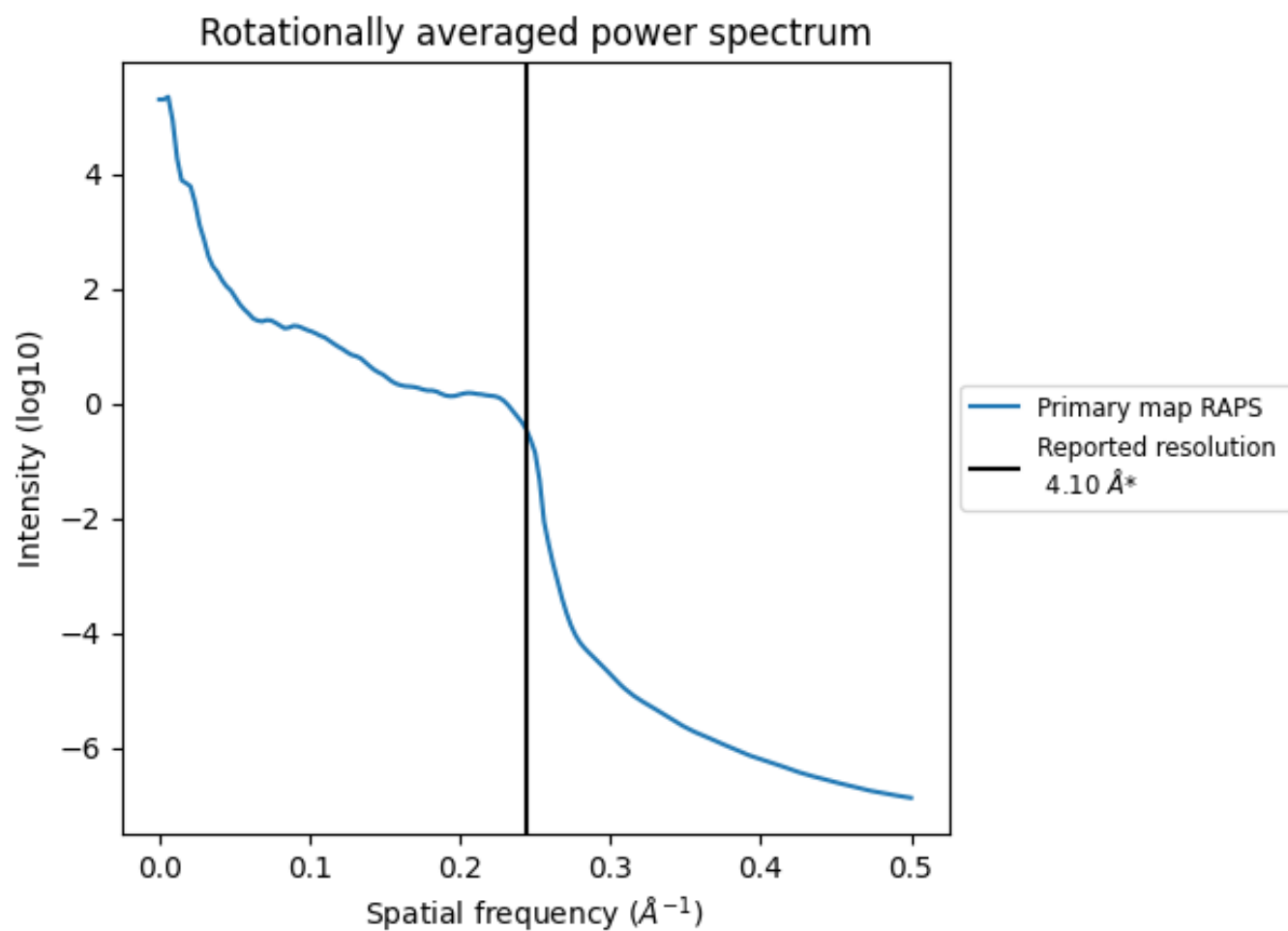
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 425 nm<sup>3</sup>; this corresponds to an approximate mass of 384 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 0.244 Å<sup>-1</sup>

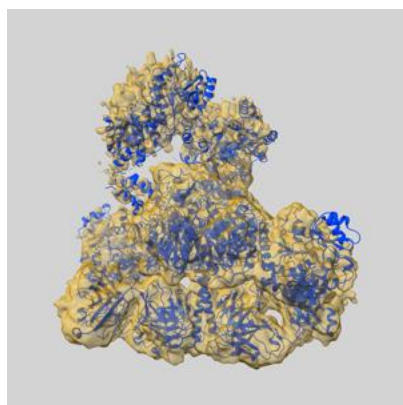
## 8 Fourier-Shell correlation

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

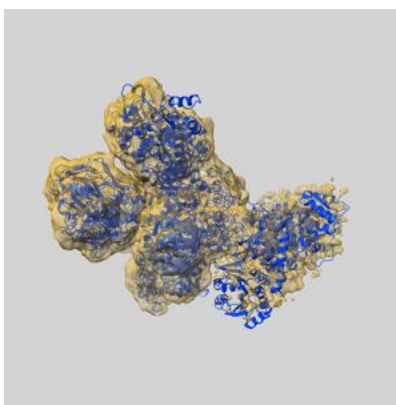
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23713 and PDB model 7M7H. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

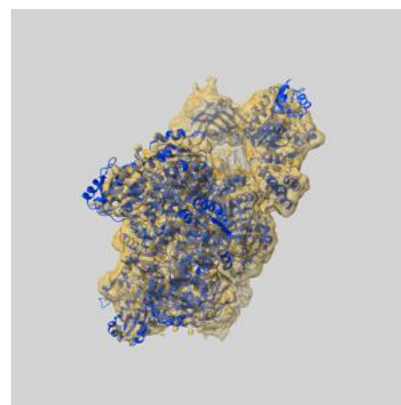
### 9.1 Map-model overlay [i](#)



X



Y

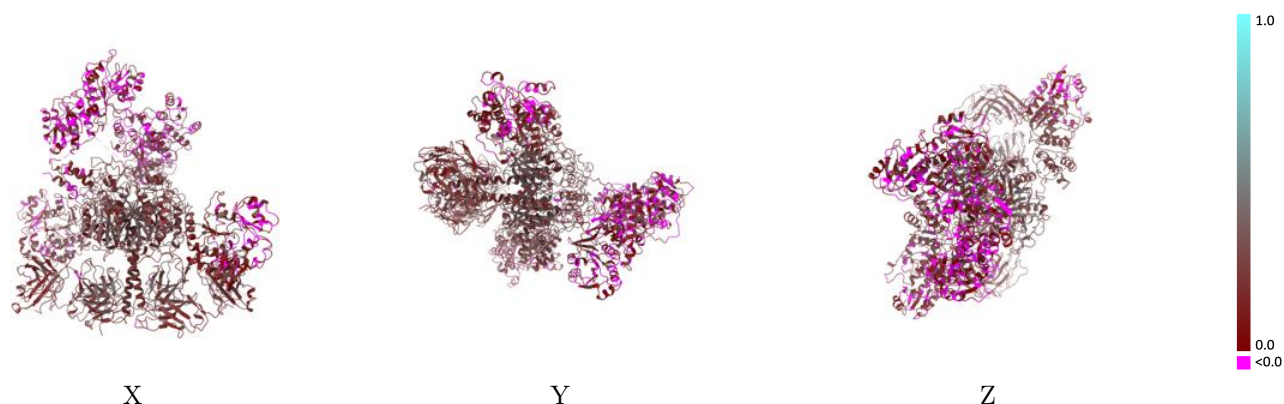


Z

The images above show the 3D surface view of the map at the recommended contour level 0.28 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.

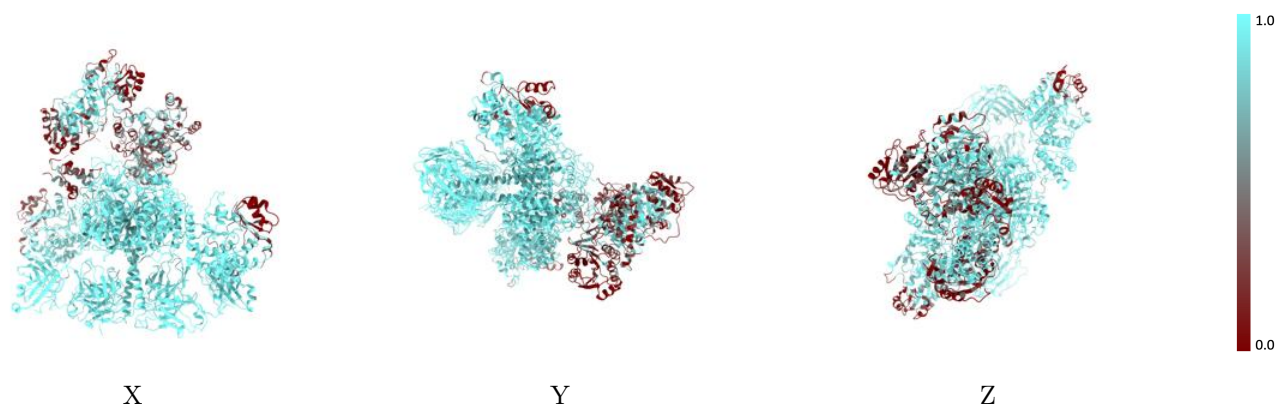


## 9.2 Q-score mapped to coordinate model [i](#)



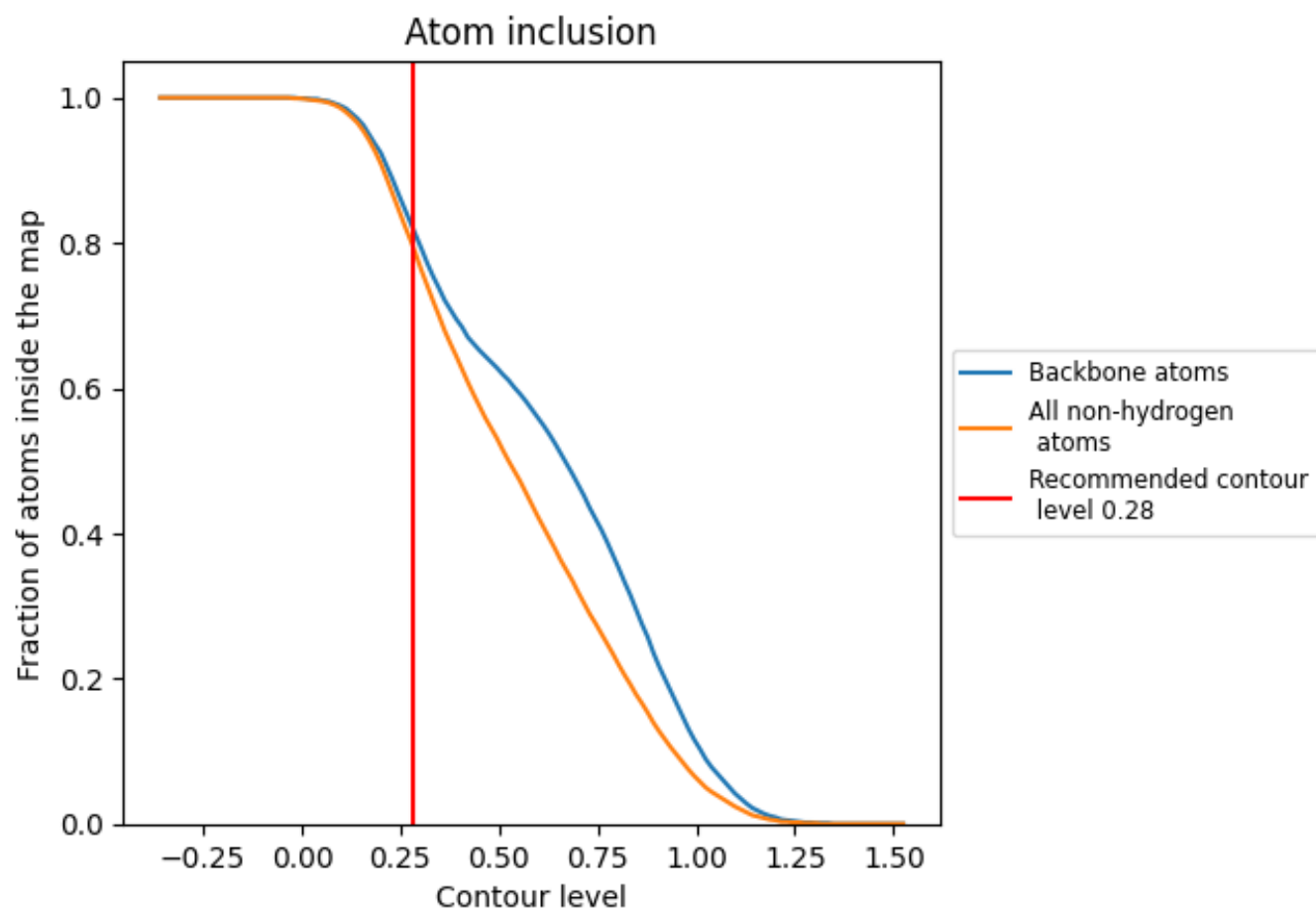
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.28).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 82% 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 (0.28) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7980	<div></div> 0.1900
A	<div></div> 0.7310	<div></div> 0.1780
B	<div></div> 0.7570	<div></div> 0.1670
C	<div></div> 0.9720	<div></div> 0.2360
D	<div></div> 0.9750	<div></div> 0.2620
E	<div></div> 0.9820	<div></div> 0.2410
F	<div></div> 0.9720	<div></div> 0.2610

