



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:50 AM UTC

PDB ID : 6R9G / pdb_00006r9g
EMDB ID : EMD-4770
Title : Structural basis of transcription inhibition by the DNA mimic Ocr protein of bacteriophage T7
Authors : Ye, F.Z.; Zhang, X.D.
Deposited on : 2019-04-03
Resolution : 3.70 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

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:

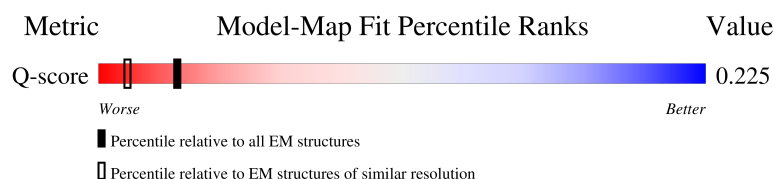
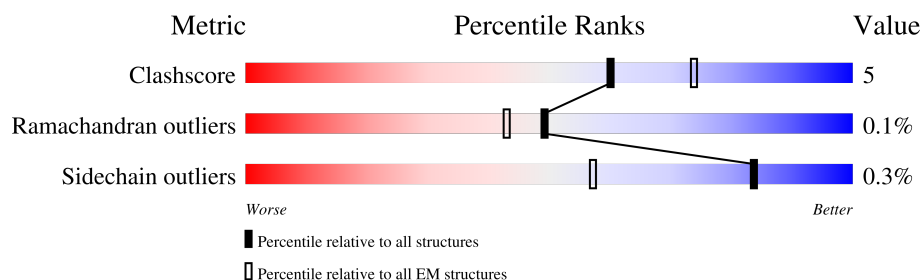
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

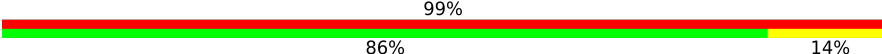
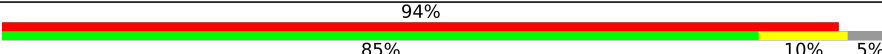
The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	329	
1	B	329	
2	C	1342	
3	D	1407	

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Mol	Chain	Length	Quality of chain
4	E	80	94% 88% 6% 6%
5	F	117	91% 79% 11% 9%
5	G	117	89% 79% 10% 11%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 25944 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	230	Total	C	N	O	S	0	0
			1765	1100	308	351	6		
1	B	231	Total	C	N	O	S	0	0
			1743	1090	301	346	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1341	Total	C	N	O	S	0	0
			10112	6334	1735	2006	37		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1334	Total	C	N	O	S	0	0
			10051	6297	1777	1934	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	75	Total	C	N	O	S	0	0
			572	351	110	109	2		

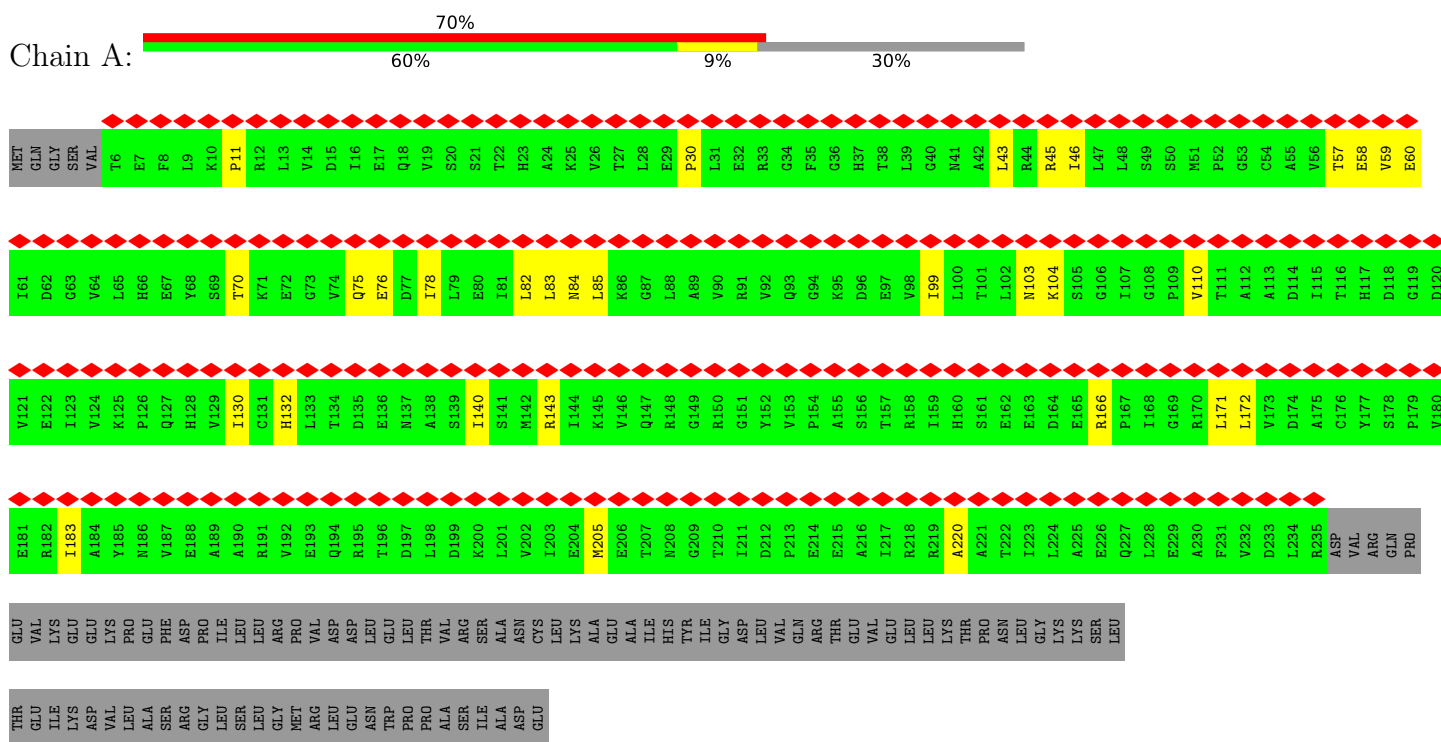
- Molecule 5 is a protein called Overcome classical restriction gp0.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	104	Total	C	N	O	S	0	0
			849	534	131	179	5		
5	F	106	Total	C	N	O	S	0	0
			852	530	136	182	4		

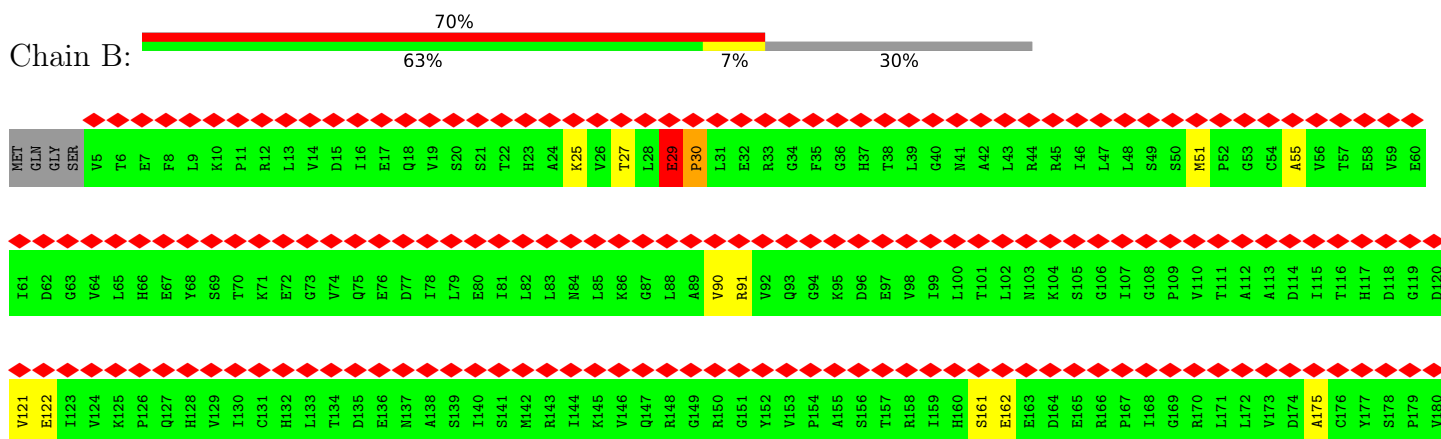
3 Residue-property plots

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

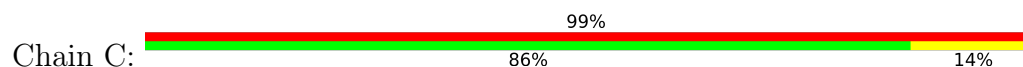


• Molecule 1: DNA-directed RNA polymerase subunit alpha



GLU	THR
VAL	GLU
ILE	ILE
LYS	LYS
GLY	ASP
GLY	VAL
LYS	LEU
PRO	ALA
GLU	SER
PHE	SER
ASP	ARG
PRO	GLY
ILE	LEU
LEU	SER
LEU	LEU
ARG	GLY
VAL	PRO
VAL	MET
ASP	ARG
Q194	LEU
R195	GLU
T196	ASP
D197	LEU
L198	PRO
VAL	THR
ARG	VAL
K200	ARG
L201	SER
V202	ALA
I203	ASN
E204	CYS
M205	LYS
E206	ALA
T207	GLU
N208	ALA
G209	ILE
T210	HIS
I211	TVR
D212	ILE
P213	GLY
E214	ASP
E215	LEU
A216	VAL
I217	GLN
R218	ARG
R219	THR
A220	LEU
A221	LYS
T222	THR
I223	PRO
L224	ASN
A225	LEU
E226	GLY
Q227	LYS
L228	SER
E229	LEU
A230	LYS
F231	LYS
V232	SER
D233	LEU
L234	LEU
R235	LEU
ASP	ASP
VAL	VAL
ARG	ARG
GLN	GLN
PRO	PRO

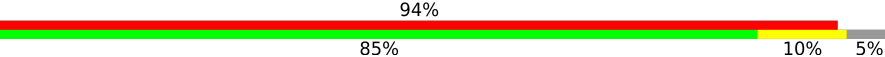
● Molecule 2: DNA-directed RNA polymerase subunit beta



E541	L481	S421	S361	Y301	L241	G181	E121	S61	V62	Y63	S63	G64	Y65	T66	E67	K68	K69	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
R542	G482	K422	A362	I302	V242	S182	V122	Y62	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
G544	L484	D424	V364	E304	E244	L184	Y123	G64	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
F545	D485	I425	E365	S305	R245	D185	G125	N65	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
E546	T486	I426	L366	T306	L246	F186	E126	S66	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
V547	L487	D427	Y367	G307	R247	E187	I127	S67	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
R548	M488	V428	R368	E308	G248	F188	P128	S68	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
D549	P489	M429	K369	L309	E249	D189	L129	Q69	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
V550	Q490	K430	M370	I310	T250	P190	M130	Y70	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
H551	D491	K431	R371	C311	A251	K191	T131	V71	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
P552	M492	L432	P372	A312	S252	D192	D132	S72	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
T553	I493	L433	G373	A313	F253	N193	N133	Y73	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
H554	N494	D434	E374	N314	D254	L194	G134	R74	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
Y555	A495	L435	P375	M315	I255	F195	T135	L75	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
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R557	P497	N437	T377	L317	A257	R197	V137	E77	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
V558	L498	G438	R378	S318	N258	I198	I138	F78	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
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P560	A500	G440	A380	D320	K260	R200	G140	F80	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
I561	E501	E441	E381	L321	V261	R201	T141	D81	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
E562	V502	V442	E382	L322	V262	R202	E142	V82	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
T563	K503	D443	S383	A323	V263	K203	R143	Q83	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
F564	E504	D444	L384	K324	E264	L204	V144	E84	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
E565	F505	I445	F385	L325	K265	P205	I145	C85	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P19	Q20	V21	L22	D23	V24	P25	Y26	L27	L28	S29	I30	Q31	L32	D33	S34	F35	Q36	K37	F38	I39	E40	Q41	D42	P43	E44	G45	Q46	Y47	G48	L49	E50	A51	A52	F53	R54	S55	V56	F57	P58	I59	Q60
G566	F506	D446	E386	S326	G266	A206	V146	Q86	Y63	S63	G64	Y65	T66	E67	L68	Q69	Y70	R10	I11	R12	K13	D14	F15	G16	K17	R18	P																																									

F1323	A1263	D1203	E1083	L1021	S961	L901	R941	D781	G721	V661	D601
N1324	Q1264	L1204	D1084	K1022	E962	L902	D842	V782	G722	S662	E602
V1325	F1265	L1205	M1085	H1023	E963	R903	T943	L783	V723	I603	I604
L1326	G1266	T1206	P1086	E1024	L964	A904	K944	A784	V724	G664	H604
L1327	G1267	S1207	Y1087	F1025	Q965	I905	L945	D785	Q725	A665	Y605
K1328	G1268	G1208	D1088	E1026	I966	F906	G946	F786	V726	S666	L606
E1329	A1269	Q1209	E1089	K1027	L967	G907	P947	P787	V727	S607	S607
I1330	F1270	I1210	M1090	K1028	E968	E908	E948	S788	D728	I608	A608
L1331	G1271	L1211	G1091	L1029	A969	K909	E949	A729	P669	I609	I609
S1332	E1272	L1212	T1092	E1030	G970	A910	I950	D790	S730	E610	E610
L1333	M1273	Y1213	P1093	A1031	L971	S911	T951	L791	R731	E611	E611
E1334	E1274	D1214	V1094	K1032	F972	D912	A952	G792	I732	G612	G612
V1335	V1275	G1215	D1095	R1033	R973	V913	D953	E793	V733	H613	H613
I1336	R1276	R1216	I1096	K1034	R974	K914	I954	L794	I734	Y614	Y614
L1337	Q1277	T1217	V1097	K1035	I975	D915	P955	A795	K735	V615	V615
E1338	K1278	G1218	L1098	I1036	R976	S916	N956	L796	V736	I616	I616
L1339	V1279	E1219	M1099	T1037	A977	S917	V957	G797	N677	A617	A617
E1340	A1280	Q1220	P1100	Q1038	V978	L918	G958	Q798	E738	R678	R678
D1341	Y1281	F1221	L1101	G1039	L979	R919	E959	N799	D739	A619	A619
G1282	G1282	E1222	G1102	D1040	V980	V920	A860	M800	E740	M620	M620
A1283	T1283	R1223	V1103	D1041	A981	P921	A861	R801	M741	S621	S621
A1284	F1284	P1224	P1104	L1042	G982	N922	L862	V902	I742	G682	G682
Y1285	Y1285	V1225	S1105	A1043	G983	G923	S963	A803	P743	A883	A883
T1286	T1286	T1226	R1106	P1044	V984	V924	K964	F904	G744	N684	N684
L1287	E1287	V1227	M1107	G1045	E985	S925	L865	M905	E745	E625	E625
Q1288	G1228	G1228	M1108	V1046	A986	G926	D966	P906	A746	Q626	Q626
E1289	Y1229	Y1229	I1109	L1047	E987	T927	E967	W807	G747	G627	G627
M1290	M1230	M1230	G1110	K1048	K988	V928	S968	N808	I748	H628	H628
L1291	R1231	R1231	Q1111	I1049	L989	I929	G969	G909	D749	F629	F629
T1292	M1232	M1232	I1112	V1050	D990	D930	I970	Y810	I750	V630	V630
V1293	L1233	K1234	L1113	K1051	K991	V931	V971	N811	Y751	E631	E631
K1294	E1174	E1174	E1114	V1052	L992	Q932	Y972	F812	N752	D632	D632
S1295	M1176	L1235	T1115	Y1053	P993	V933	G974	D814	L754	L633	L633
D1296	L1176	N1236	H1116	A1054	D995	T935	A975	S815	K755	T635	T635
H1237	R1177	H1237	L1117	A1055	R996	R936	E976	I816	Y756	C636	C636
V1298	K1178	V1238	G1118	V1056	W997	D937	V977	L817	K697	R637	R637
M1299	G1179	L1239	M1119	K1057	W997	G938	T978	V818	R758	S638	S638
G1300	M1180	D1240	A1120	R1058	E999	V939	G979	S819	S759	K639	K639
A1301	P1181	D1241	A1121	R1059	E999	V939	G979	S819	N760	G640	G640
T1302	I1182	K1242	K1122	I1060	L1000	E940	G880	R821	Q761	E641	E641
K1303	A1183	M1243	G1123	Q1061	G1001	K941	D881	R821	I761	S641	S641
M1304	T1184	H1244	I1124	P1062	L1002	D942	I882	V922	T702	S642	S642
Y1305	F1185	A1245	G1125	G1063	T1003	K943	L883	V923	G703	S643	S643
K1306	V1186	R1246	D1126	D1064	R944	R944	V884	Q924	M704	L644	L644
N1307	F1187	S1247	K1127	K1065	E1005	A945	G885	E925	I765	F645	F645
I1308	D1188	T1248	I1128	M1066	E1006	L946	K886	D926	N766	S646	S646
V1309	G1189	G1249	M1129	M1066	K1007	E947	V887	R827	Q767	R647	R647
D1310	A1190	S1250	M1130	R1069	Q1008	I948	T888	F928	A707	H647	H647
Y1251	K1191	Y1251	M1131	H1070	N1009	E949	P889	T929	V708	D648	D648
S1252	E1192	S1252	L1132	G1071	Q1010	E950	K990	T930	A709	Q649	Q649
H1313	A1193	L1253	K1133	N1072	M951	Q952	G991	I831	C770	V650	V650
Q1314	E1194	V1254	Q1134	K1073	E1012	Q952	E992	H832	D711	D651	D651
T1255	I1195	T1255	Q1135	I1076	Q1013	L953	E992	H832	S712	Y652	Y652
Q1256	K1196	Q1256	Q1136	S1077	L1014	K954	T993	I833	L773	M653	M653
E1316	E1197	Q1257	E1137	K1078	A1015	Q955	L895	E835	G774	D654	D654
P1317	L1198	P1258	V1138	L1078	E1016	A956	T996	L836	E775	V655	V655
G1318	L1199	L1259	A1139	L1079	E1017	K957	P997	A837	P776	S656	S656
M1319	K1200	G1260	A1139	N1080	Q1017	K957	P997	A837	A716	T657	T657
P1320	P1320	G1261	K1140	N1081	Y1018	K958	E998	C838	V717	Q658	Q658
E1321	E1321	K1262	L1141	I1082	D1019	D959	E999	V839	E778	Q659	Q659
S1322	S1322		R1142		E1020	L960	K900	S940	G780	R720	R720

- Molecule 3: DNA-directed RNA polymerase subunit beta'

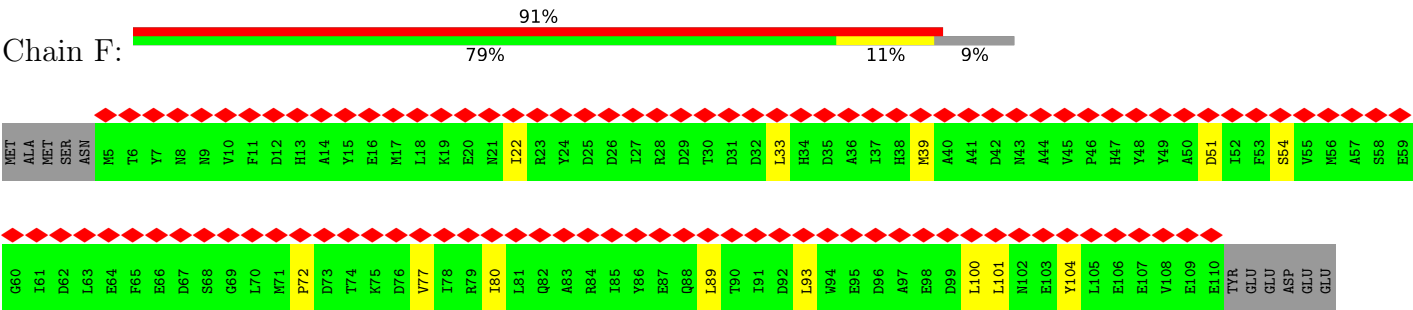
Chain D: 

I722	A662	S602	A542	A482	L422	R362	E301	V241	G181	P121	I61	ME1
Y723	E663	K603	S543	L483	L423	L363	A302	L242	A182	S122	F62	LYS
M724	I664	M604	M604	M484	N424	H364	V303	P243	E183	S122	G63	ASP
M725	Q665	L605	H545	H485	R425	Q365	D304	V244	A184	I124	P64	LEU
M726	E666	M606	A546	S486	A426	C366	A305	L245	I185	G125	V65	LYS
D727	Q667	T607	R547	T487	P427	G367	L306	P246	Q186	L126	K66	PHE
S728	F668	C608	V548	M488	T428	L368	L307	P247	A187	L127	D67	LEU
G729	Q669	Y609	K549	H489	L429	P369	D308	D248	L188	L128	Y68	ALA
A730	S670	R610	V550	L490	H430	K370	N309	L249	L189	D129	E69	GLN
R731	G671	I611	R551	L491	R431	K371	G310	R250	K190	M130	C70	THR
G732	L672	L612	I552	S492	L432	K372	R311	P251	R191	P131	L71	LYS
S733	V673	G613	T553	P493	G433	A373	R312	L252	M192	L132	C72	
A734	T674	L614	E554	A494	L434	L374	G313	V253	D193	R133	G73	E16
A735	A675	K615	Y555	M495	Q435	E375	R314	P254	L194	D134	K74	F17
Q736	G676	P616	E556	G496	A436	L376	A315	L255	E195	I135	Y75	D18
I737	E677	T617	K557	E497	F437	F377	T316	D256	Q196	E136	K76	A19
R738	R678	V618	D558	P498	E438	K378	T317	G258	E197	E137	R77	I20
Q739	Y679	I619	A559	I499	P439	P379	G318	Q259	C198	V138	L78	K21
L740	N680	F620	N560	I500	V440	F380	S319	R259	E199	L139	K79	I22
A741	G681	A621	G561	V501	L441	I381	N320	F260	Q200	Y140	H80	A23
G742	D682	E562	E562	P502	I442	Y382	K321	A261	L201	F141	R81	L24
M743	L683	Q623	L563	S503	E443	Q383	R322	T262	R202	E142	G82	A25
R744	D684	I624	V564	Q504	G444	K384	P323	D264	E204	Y144	I84	P27
G745	L685	M625	A565	D505	K445	L385	L324	L265	L205	V145	C85	D28
L746	Y626	Y626	A566	V506	A446	E386	K325	N266	N206	V146	E86	M29
M747	T627	G628	T567	V507	L447	L387	S326	D267	E207	I147	K87	I30
A748	A688	F628	S568	L508	Q448	R388	A328	L268	T208	E148	C88	R31
K749	A689	F629	L569	G509	L449	G389	D329	Y269	N209	G149	G89	S32
P750	N690	A630	K570	L510	H450	L390	M330	R270	S210	G150	V90	W33
D751	D691	Y631	D571	Y511	P451	A391	R330	Z270	E210	M150	E91	S34
G752	R692	T572	T572	Y512	L452	T392	I331	R271	E211	E111	V92	F35
S753	A693	A633	T573	M513	V453	T393	K332	V272	T212	T152	T93	G36
I754	G694	R634	V574	T514	C454	I394	G333	I273	K213	N153	Q94	E37
S694	S635	R634	Q576	R515	A455	K395	K334	N274	R214	L154	T95	V38
I755	K695	G636	Q576	D516	A456	A396	Q335	R275	K215	E155	T95	K39
E756	A696	A637	R576	C517	Y457	A397	G336	N276	K216	R156	K96	E42
T757	M697	A637	A577	Y518	M458	K398	R337	N277	L217	R157	V97	K40
F758	D698	S638	L578	V518	N458	K398	F338	R278	T218	Q158	R98	P41
I759	D699	V639	L579	N519	A459	K399	R339	L279	K219	I159	R99	E42
T760	N700	G640	W580	A520	D460	M400	Q340	K280	R220	L160	E100	T43
A761	L701	I641	M581	K521	F461	V401	N341	Z280	I221	T161	T44	N45
N762	Q702	D642	I582	G522	D462	E402	L342	R281	K222	E162	M102	Y46
F763	T703	D643	V593	E523	Q463	R403	L343	L282	K223	E163	G103	R47
R764	E704	M644	E584	G524	D464	E404	L344	D284	L224	Q164	H104	T48
E765	T705	V645	K585	M525	Q465	E405	G344	L285	E225	Y165	I105	F49
G766	V706	I646	G586	V526	M466	A406	K345	L286	A226	L166	E106	F49
L767	I707	P647	L587	L527	A467	V407	R346	A286	A226	L166	E106	F49
N768	N708	E648	P588	T528	V468	V408	V347	Z287	D107	D167	L107	K50
V769	R709	K649	Y599	G529	H469	W409	D348	P288	V228	A168	A108	P51
L770	D710	K650	S590	P530	V470	D410	Q349	D289	F227	L169	S109	E52
Q771	G711	H651	I591	K531	P471	W410	Y349	L290	Q229	E170	P110	R53
Y772	Q712	V592	V592	E532	L472	T411	R352	I291	G231	E171	T111	D54
F773	T713	I653	N593	A533	T473	L412	S353	Z291	N232	F172	A112	G55
I774	E714	I654	Q594	E534	L474	D413	V354	Y292	K233	G173	L114	E55
S775	K715	A595	L596	R535	E475	E414	L355	V292	N232	F172	L114	F57
T776	Q716	L566	A595	L536	A476	V415	T356	N294	G173	D174	E175	C58
H777	V717	A657	L597	Y537	Q477	T416	V357	E295	E235	W115	F116	A59
G778	V718	K598	G597	L538	L478	R417	G358	K296	E236	F176	F117	R60
A779	F719	A659	K599	R538	E479	E418	P359	Z297	M237	D177	L117	
R780	N720	E660	A600	G540	A480	H419	Y360	M298	I238	A178	K118	
K781	S721	V661	T601	L541	R481	P420	L361	Q300	T240	K179	S119	

● Molecule 5: Overcome classical restriction gp0.3



● Molecule 5: Overcome classical restriction gp0.3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33646	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 ($e^-/\text{\AA}^2$)	49.53	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.220	Depositor
Minimum map value	-0.151	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	270.08, 270.08, 270.08	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.055, 1.055, 1.055	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	0.19	0/1786	0.51	0/2424
1	B	0.21	0/1764	0.57	1/2398 (0.0%)
2	C	0.19	0/10263	0.52	0/13922
3	D	0.21	1/10187 (0.0%)	0.55	1/13803 (0.0%)
4	E	0.20	0/574	0.48	0/775
5	F	0.18	0/866	0.47	0/1177
5	G	0.16	0/866	0.38	0/1178
All	All	0.20	1/26306 (0.0%)	0.53	2/35677 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	925	GLU	C-N	5.02	1.40	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	885	VAL	N-CA-C	6.40	122.65	109.34
1	B	29	GLU	N-CA-C	5.49	121.95	109.81

There are no chirality outliers.

There are no planarity outliers.

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	1765	0	1775	22	0
1	B	1743	0	1741	14	0
2	C	10112	0	9785	118	0
3	D	10051	0	10034	85	0
4	E	572	0	574	3	0
5	F	852	0	772	8	0
5	G	849	0	768	7	0
All	All	25944	0	25449	229	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 5.

The worst 5 of 229 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:121:PRO:HD2	5:G:59:GLU:HG3	1.66	0.75
5:F:100:LEU:O	5:F:104:TYR:HB2	1.87	0.74
3:D:189:LEU:HD21	3:D:234:PRO:HB2	1.76	0.67
3:D:707:ILE:H	3:D:716:GLN:HG2	1.60	0.65
2:C:205:PRO:HG2	2:C:208:ILE:HG12	1.79	0.65

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	228/329 (69%)	220 (96%)	8 (4%)	0	100	100
1	B	229/329 (70%)	214 (93%)	13 (6%)	2 (1%)	14	45
2	C	1339/1342 (100%)	1226 (92%)	113 (8%)	0	100	100
3	D	1324/1407 (94%)	1198 (90%)	124 (9%)	2 (0%)	43	72
4	E	73/80 (91%)	66 (90%)	7 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	F	104/117 (89%)	100 (96%)	4 (4%)	0	100	100
5	G	102/117 (87%)	100 (98%)	2 (2%)	0	100	100
All	All	3399/3721 (91%)	3124 (92%)	271 (8%)	4 (0%)	49	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	30	PRO
3	D	886	VAL
3	D	1183	SER
1	B	29	GLU

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	194/286 (68%)	194 (100%)	0	100	100
1	B	189/286 (66%)	189 (100%)	0	100	100
2	C	1057/1157 (91%)	1052 (100%)	5 (0%)	81	80
3	D	1048/1168 (90%)	1044 (100%)	4 (0%)	84	81
4	E	58/68 (85%)	58 (100%)	0	100	100
5	F	91/105 (87%)	91 (100%)	0	100	100
5	G	91/105 (87%)	91 (100%)	0	100	100
All	All	2728/3175 (86%)	2719 (100%)	9 (0%)	84	83

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	128	LEU
3	D	324	LEU
2	C	1176	LEU
2	C	1335	ILE
3	D	119	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	495	ASN
3	D	817	HIS
3	D	504	GLN
3	D	716	GLN
3	D	1195	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.

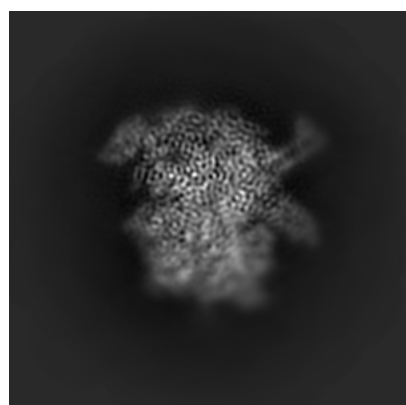
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4770. These allow visual inspection of the internal detail of the map and identification of artifacts.

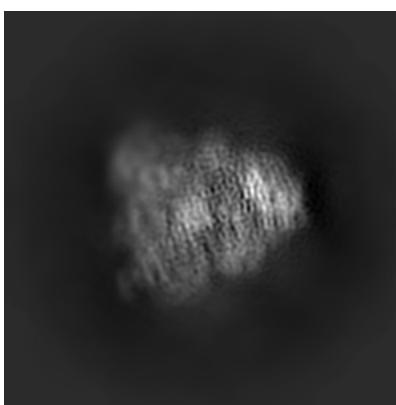
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

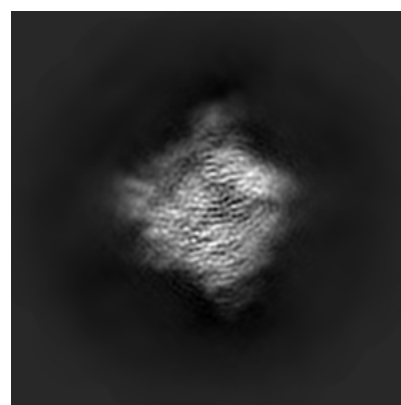
6.1.1 Primary map



X



Y

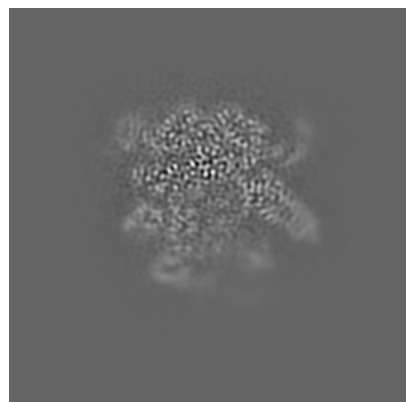


Z

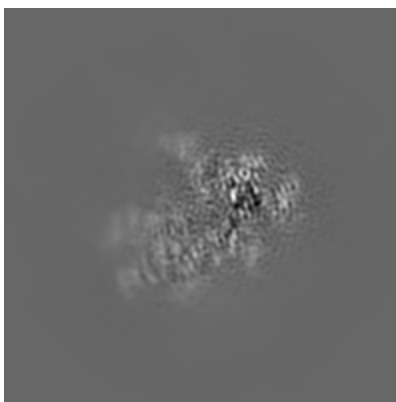
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

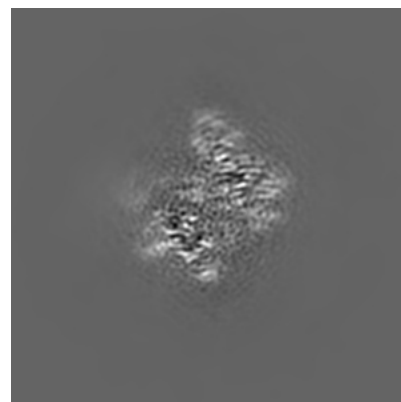
6.2.1 Primary map



X Index: 128



Y Index: 128

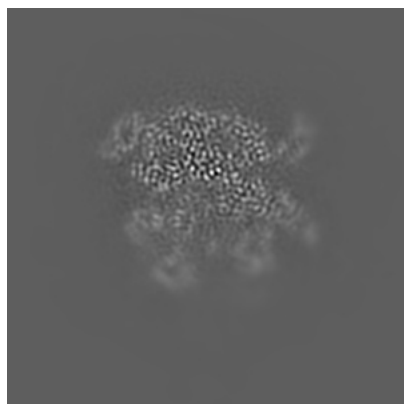


Z Index: 128

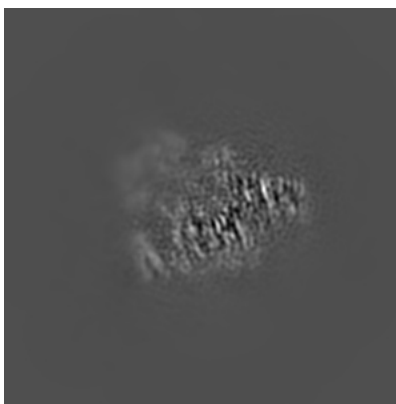
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

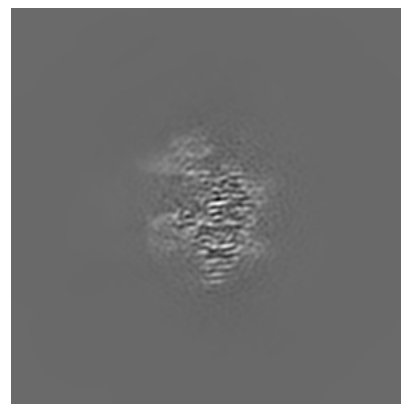
6.3.1 Primary map



X Index: 133



Y Index: 115

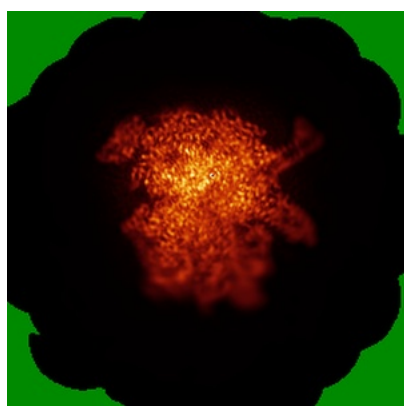


Z Index: 150

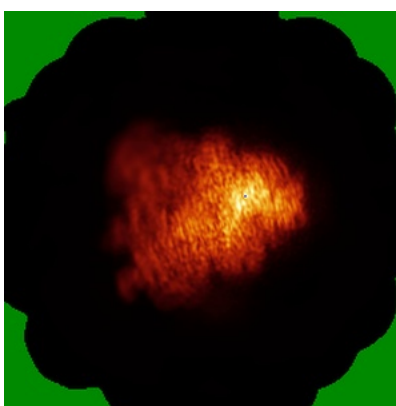
The images above show the largest variance slices of the map in three orthogonal directions.

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

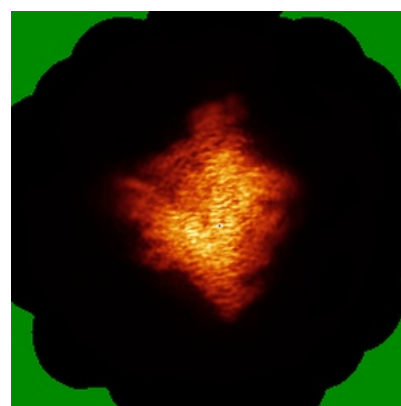
6.4.1 Primary map



X



Y

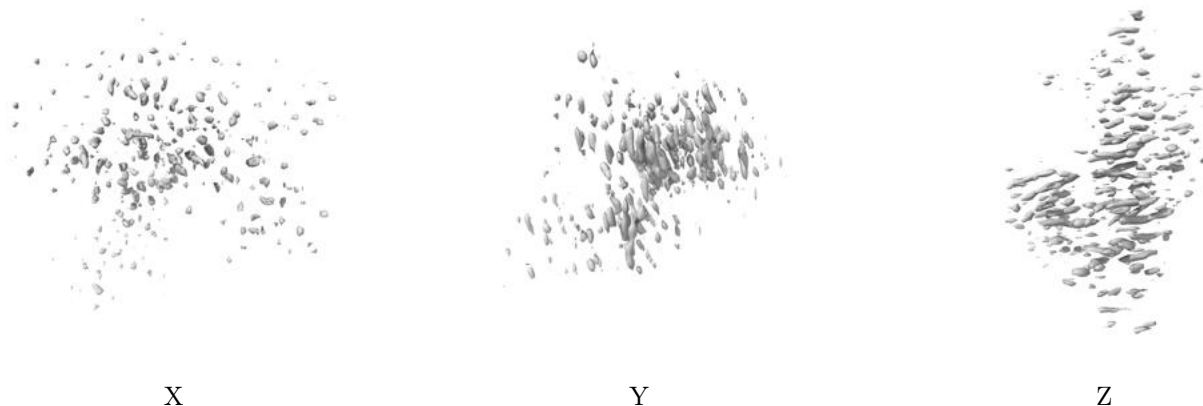


Z

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

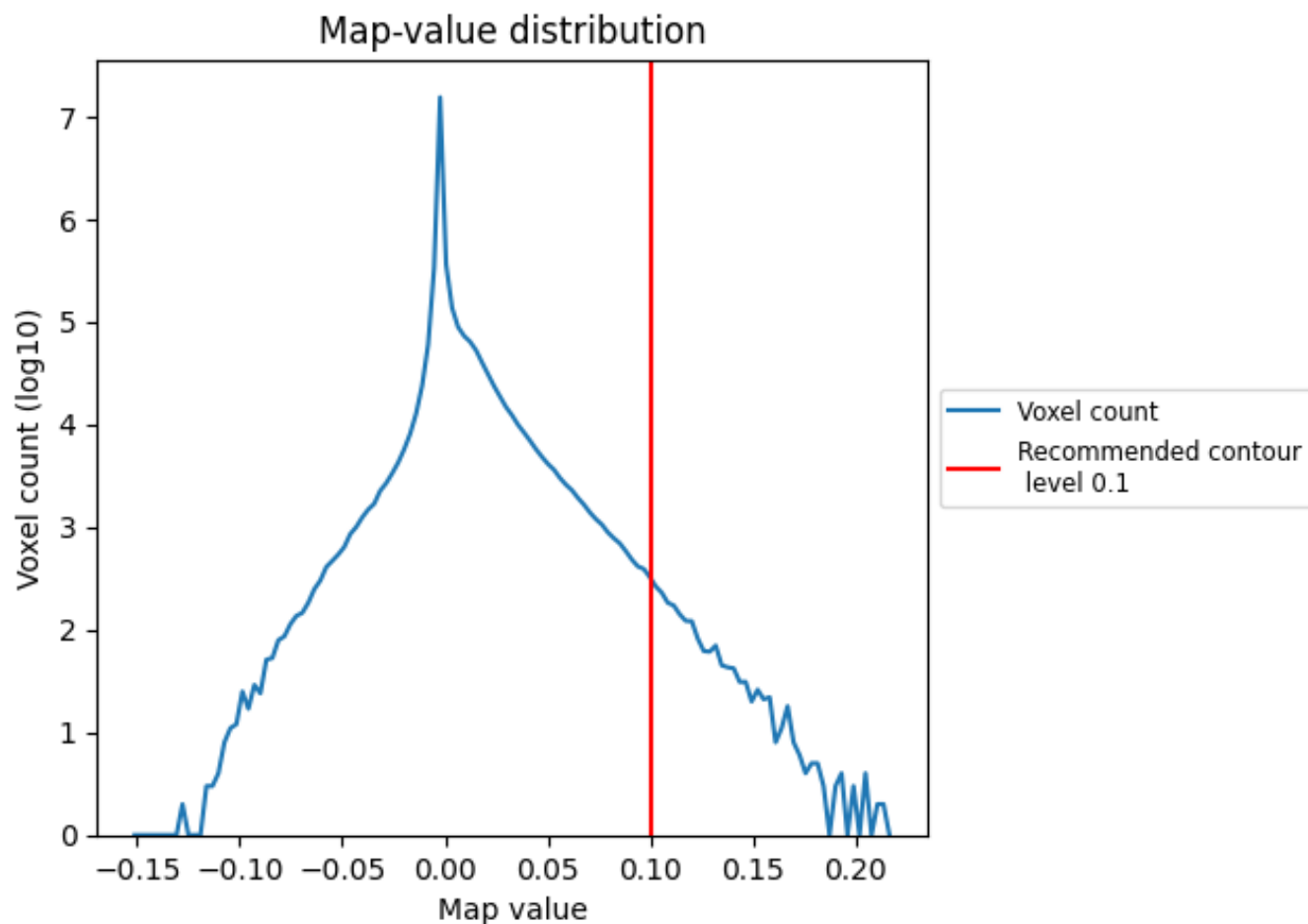
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

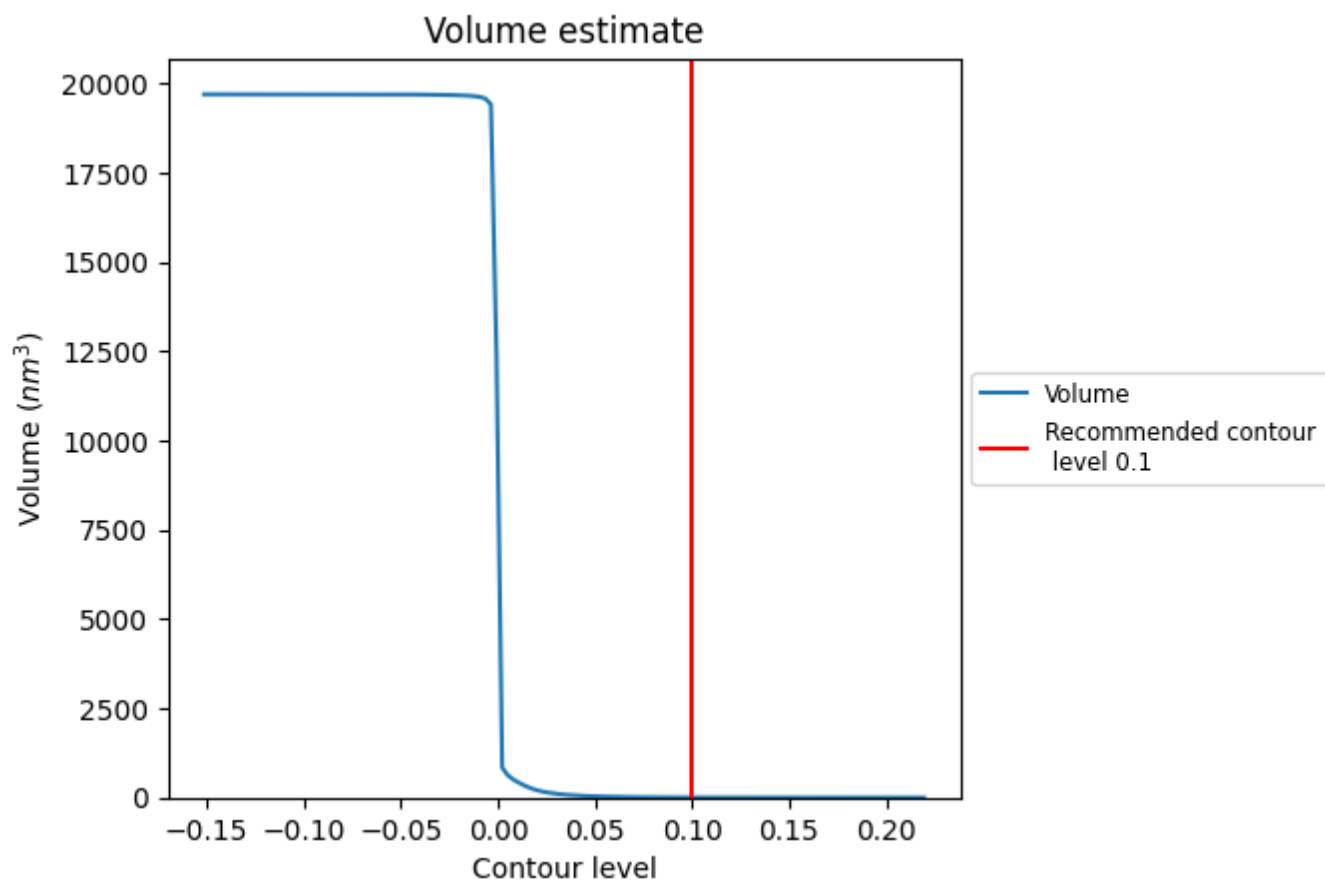
This section contains the results of statistical analysis of the map.

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.

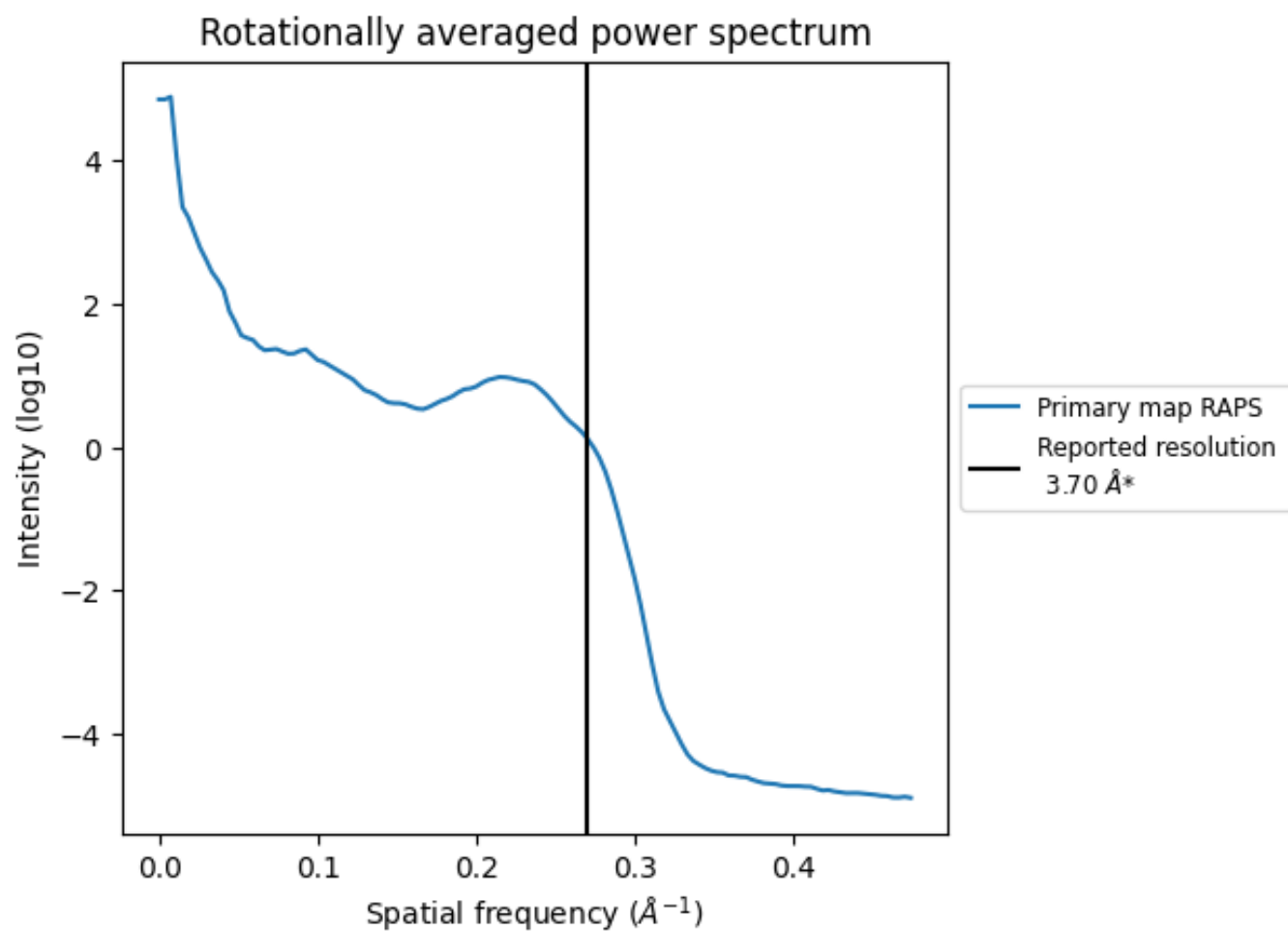
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3 nm³; this corresponds to an approximate mass of 2 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 0.270 Å⁻¹

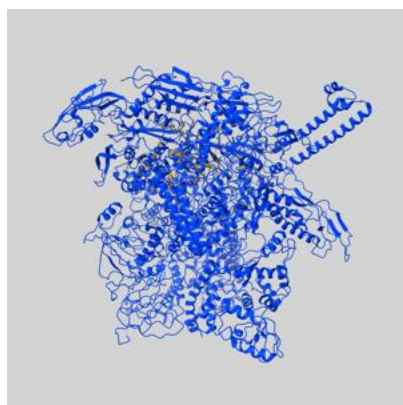
8 Fourier-Shell correlation

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

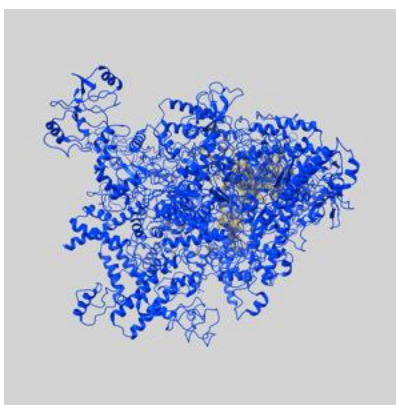
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4770 and PDB model 6R9G. Per-residue inclusion information can be found in section [3](#) on page [5](#).

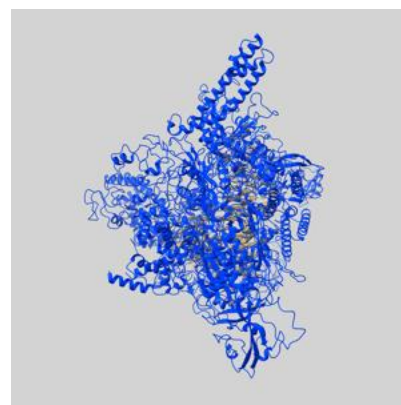
9.1 Map-model overlay [i](#)



X



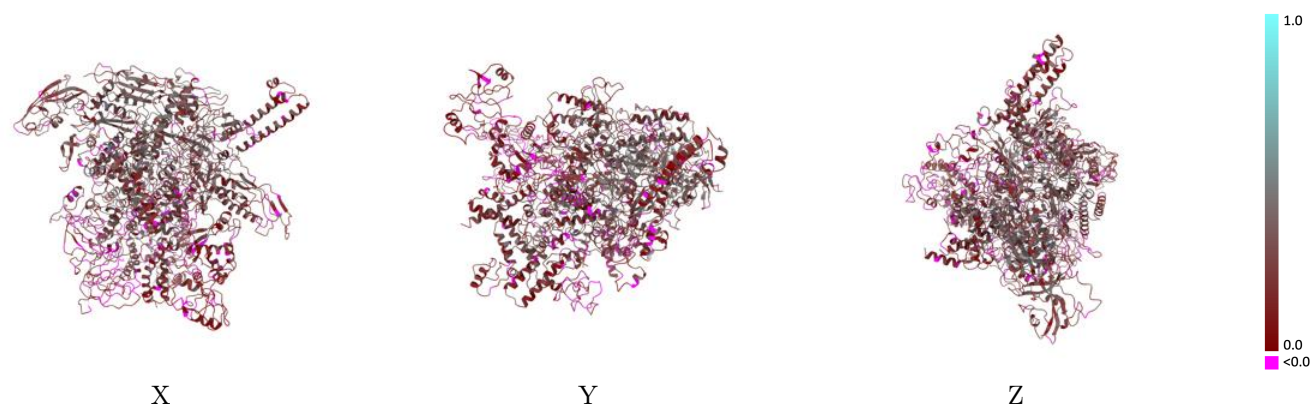
Y



Z

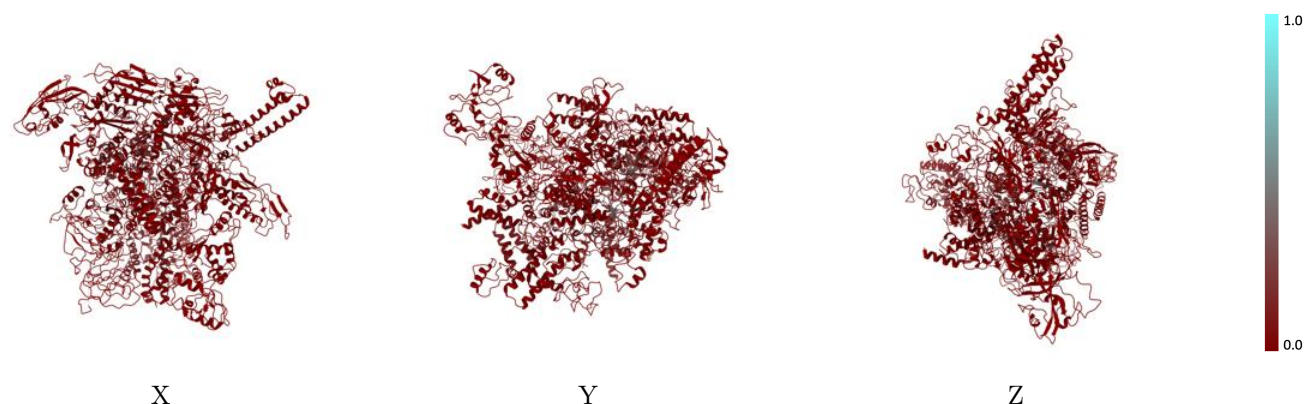
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



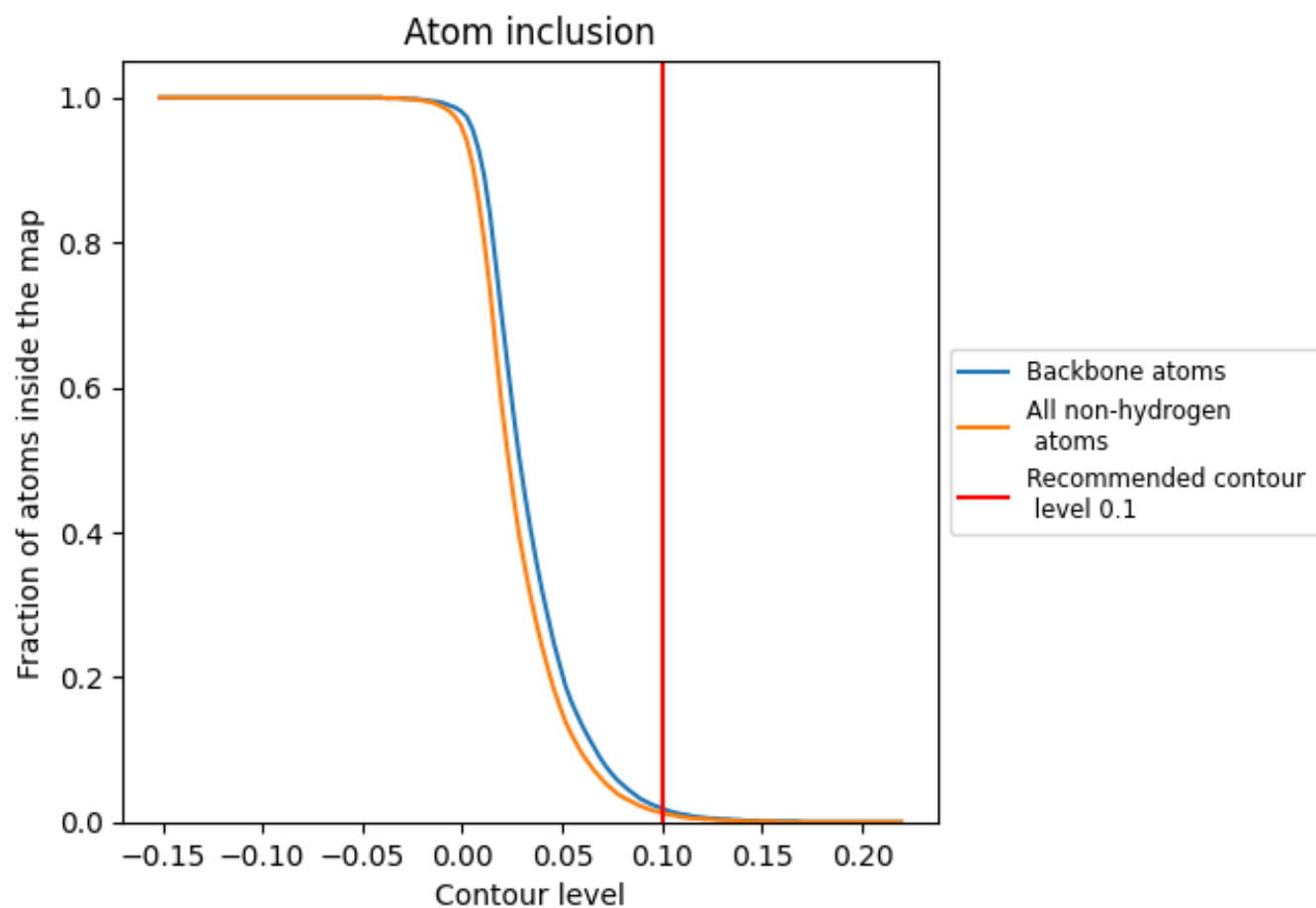
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 2% of all backbone atoms, 1% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0130	0.2250
A	0.0060	0.3070
B	0.0030	0.2760
C	0.0170	0.2340
D	0.0140	0.2030
E	0.0000	0.1290
F	0.0000	0.2230
G	0.0000	0.1720

1.0

0.0

<0.0