



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 08:01 PM UTC

PDB ID : 7OE0 / pdb_00007oe0
EMDB ID : EMD-12856
Title : E. coli pre-30S delta rbfA ribosomal subunit class F
Authors : Maksimova, E.; Korepanov, A.; Baymukhametov, T.; Kravchenko, O.; Stoboushkina, E.
Deposited on : 2021-04-30
Resolution : 2.69 Å(reported)
Based on initial model : 4V4Q

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

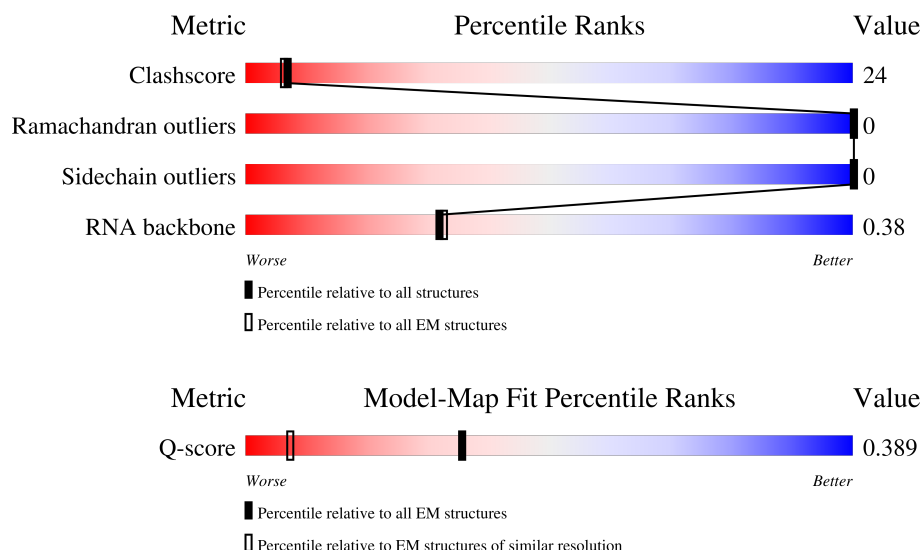
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.69 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	9309 (2.19 - 3.19)

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	B	240	
2	D	205	
3	E	166	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	F	135	
5	H	129	
6	K	128	
7	L	123	
8	O	89	
9	P	82	
10	Q	83	
11	R	74	
12	T	86	
13	A	1542	
14	C	232	
15	G	178	
16	I	129	
17	J	103	
18	M	117	
19	N	100	
20	S	91	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 50296 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 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 2 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 3 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 4 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 5 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 6 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	95	Total	C	N	O	S	0	0
			702	433	137	130	2		

- Molecule 7 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 8 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 9 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 10 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 11 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	50	Total	C	N	O	0	0
			407	259	76	72		

- Molecule 12 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 13 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A	1510	Total	C	N	O	P	0	0
			32408	14454	5952	10493	1509		

- Molecule 14 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 15 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	83	Total	C	N	O	S	0	0
			642	406	119	114	3		

- Molecule 16 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 17 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 18 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 19 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 20 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

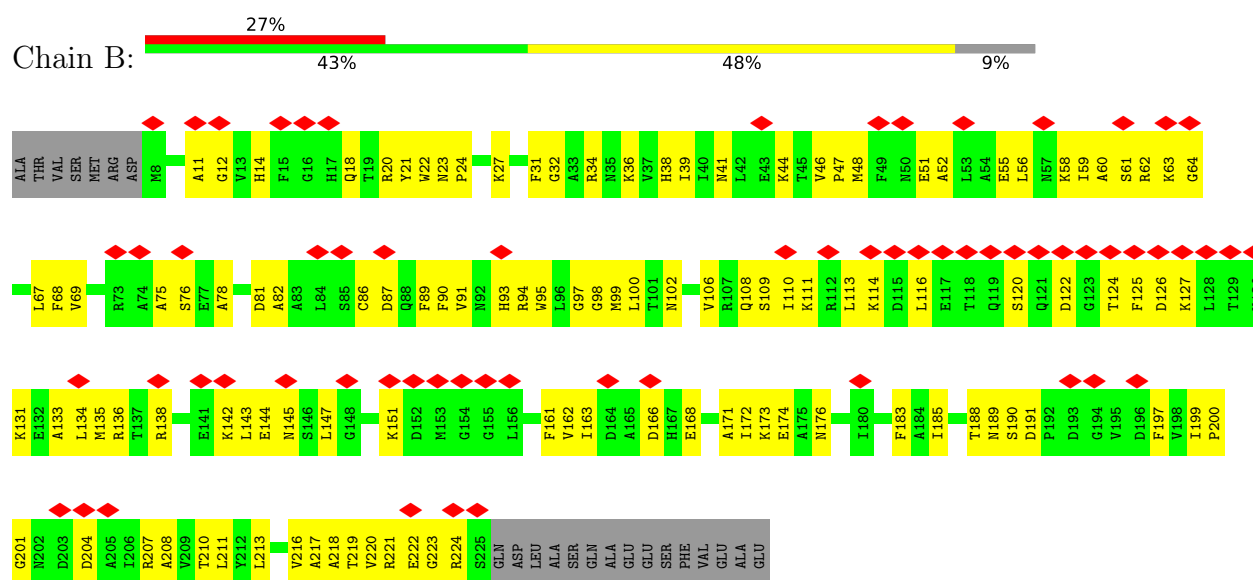
- Molecule 21 is water.

Mol	Chain	Residues	Atoms		AltConf
21	D	7	Total 7	O 7	0
21	H	9	Total 9	O 9	0
21	L	6	Total 6	O 6	0
21	O	1	Total 1	O 1	0
21	P	9	Total 9	O 9	0
21	Q	3	Total 3	O 3	0
21	R	1	Total 1	O 1	0
21	T	10	Total 10	O 10	0
21	A	484	Total 484	O 484	0

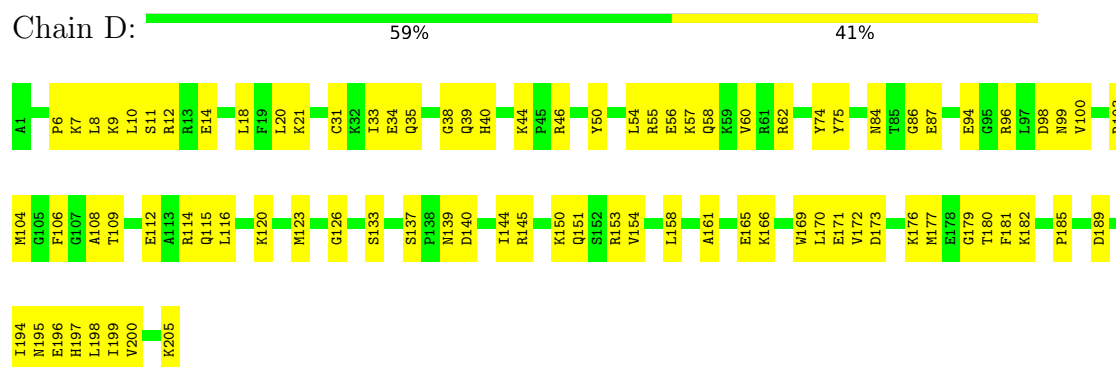
3 Residue-property plots

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: 30S ribosomal protein S2

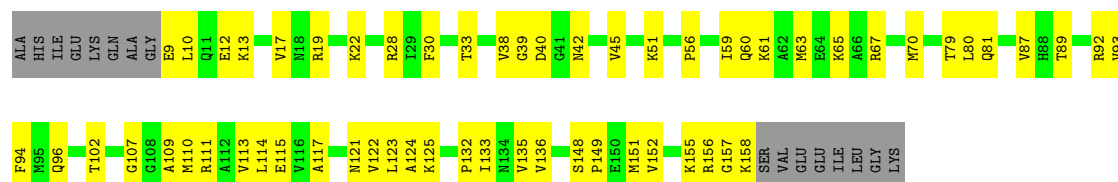


• Molecule 2: 30S ribosomal protein S4

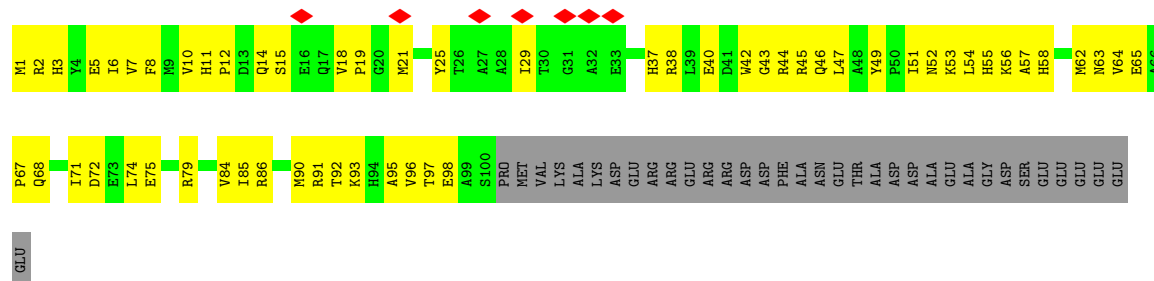


• Molecule 3: 30S ribosomal protein S5

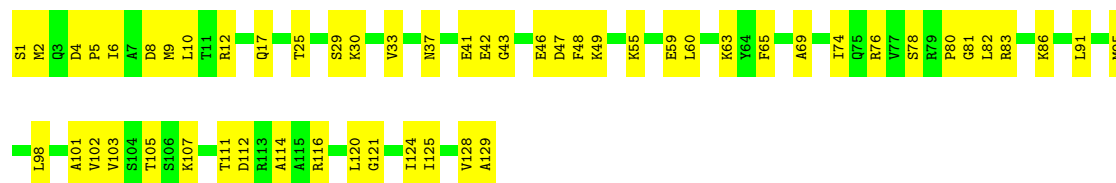




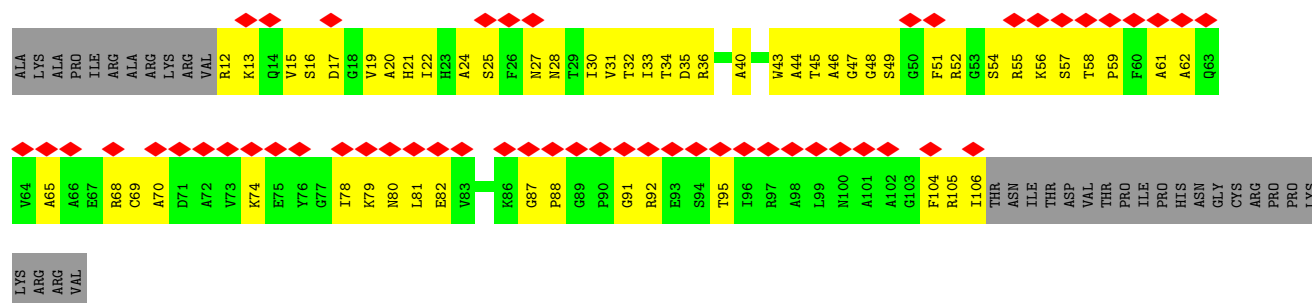
- Molecule 4: 30S ribosomal protein S6, fully modified isoform



- Molecule 5: 30S ribosomal protein S8

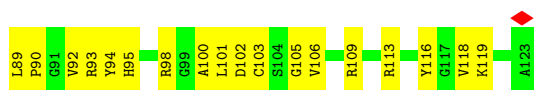


- Molecule 6: 30S ribosomal protein S11

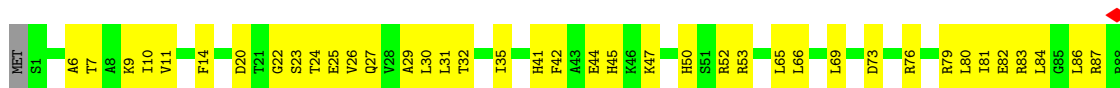


- Molecule 7: 30S ribosomal protein S12

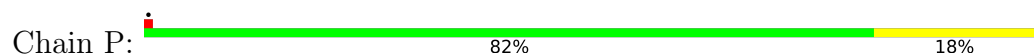




- Molecule 8: 30S ribosomal protein S15



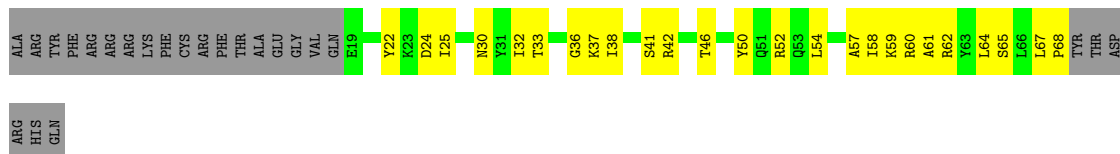
- Molecule 9: 30S ribosomal protein S16



- Molecule 10: 30S ribosomal protein S17



- Molecule 11: 30S ribosomal protein S18



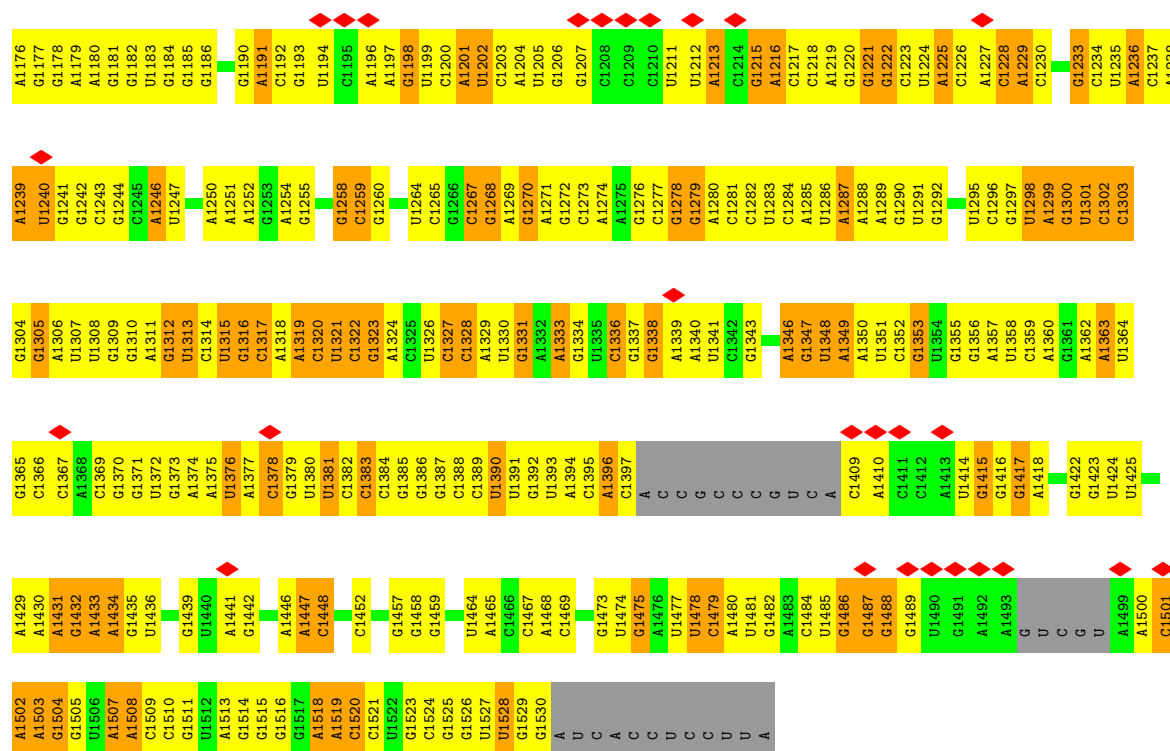
- Molecule 12: 30S ribosomal protein S20



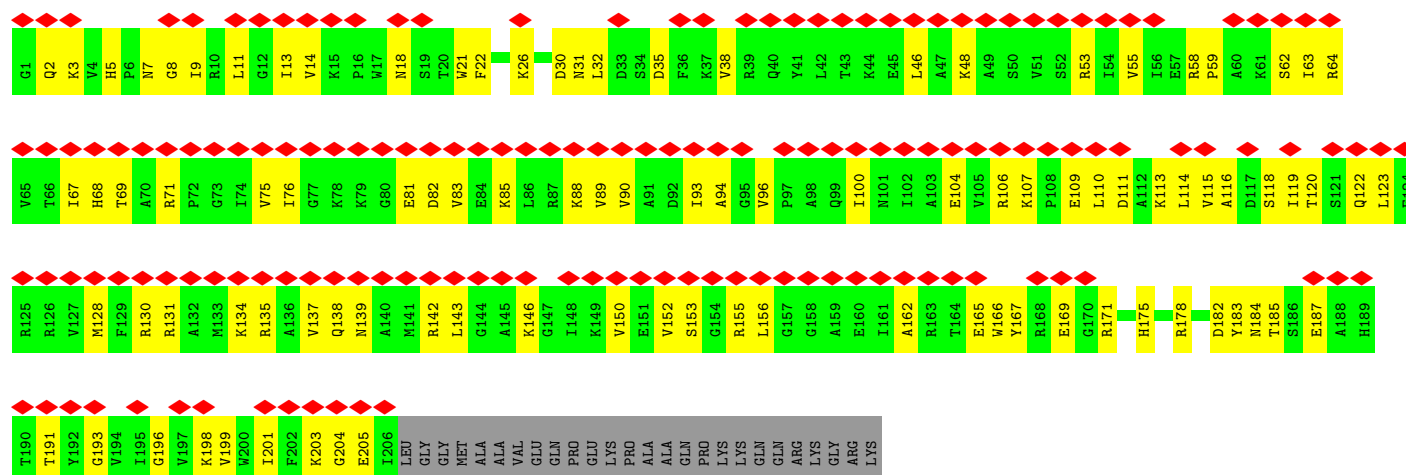
- Molecule 13: 16S rRNA



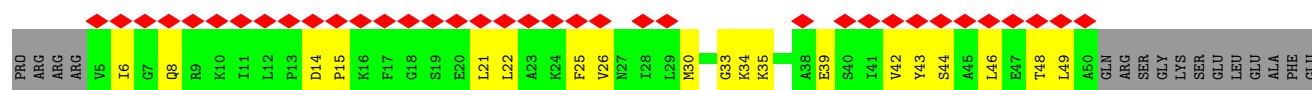
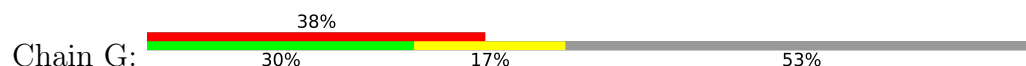
A1111	C1112	U1115	U1116	A1117	U1118	U1119	U1120	U1121	U1122	U1123	G1124	U1125	U1126	U1127	A1130	G1131	C1132	G1133	U1134	U1135	C1136	C1137	U1138	G1139	C1140	G1143	A1144	A1145	A1146	U1085	U1086	G1087	U1088	G1089	U1090	U1091	A1092	A1093	G1094	U1095	U1096	C1097	U1098	C1099	G1100	A1101	A1102	C1103	G1104	A1105	A1106	G1107	U1108	C1109	U1110	A1110	G1175
C984	C985	U986	G987	G988	U989	C990	U991	U992	G993	U994	C995	A996	U997	C998	C999	A1000	C1001	G1002	G1003	A1004	A1005	U1009	U1010	C1011	A1012	G1013	A1014	G1015	A1016	U1019	G1020	U1021	A1022	U1023	G1024	U1025	G1026	A1027	C1028	U1029	U1030	C1031	A1163	G1164	U1103	A1104	C1105	A1106	G1107	U1108	C1109	U1110	G1041				
G1047	U1048	U1049	G1050	C1051	U1052	G1053	U1054	A1055	U1056	G1057	G1058	C1059	U1060	G1061	U1062	C1063	U1065	C1066	C1069	U1070	U1071	G1072	U1073	G1074	U1075	U1076	G1077	A1080	A1081	U1085	U1086	G1087	U1088	G1089	U1090	U1091	A1092	A1093	G1094	U1095	U1096	C1097	U1098	C1099	G1100	A1101	A1102	C1103	G1104	A1105	A1106	G1107	U1108	C1109	U1110	G1041	
G922	A923	C924	G925	G926	G927	G928	U929	C930	C931	C932	G933	C934	A935	A938	G939	C940	G941	G942	U943	G944	G945	A946	G947	C948	U949	U950	G951	U952	G953	G954	U955	U956	U957	A958	A959	U960	U961	C962	G963	A964	U965	G966	C967	A968	A969	C970	G971	A974	A975	G976	A977	A978	C979	C980	U981	U982	
C984	C985	U986	U987	U988	U989	C990	U991	U992	G993	U994	C995	A996	U997	C998	C999	A1000	C1001	G1002	G1003	A1004	A1005	U1009	U1010	C1011	A1012	G1013	A1014	G1015	A1016	U1019	G1020	U1021	A1022	U1023	G1024	U1025	G1026	A1027	C1028	U1029	U1030	C1031	A1163	G1164	U1103	A1104	C1105	A1106	G1107	U1108	C1109	U1110	G1041				
A80	A81	G82	C83	U84	U85	G86	C87	U88	U89	C90	U91	U92	U93	G94	C95	U96	G97	A98	C99	G107	G108	A109	G113	U114	G115	A119	A120	U121	G122	U123	C124	U125	G126	G127	G128	A129	A130	A131	U132	U133	G134	C135	A139	U140	G146	G147	G148	A149	U150	A151	A152	U157	G158				
G159	A160	A161	A162	C163	G164	G165	C169	U170	U171	A172	U173	A174	G177	U178	A179	U180	A181	A182	C183	G184	G187	C188	A189	A190	C194	A195	A196	U191	A197	G201	G202	G203	G204	A205	C206	U208	U209	C210	G211	G212	A213	C214	C215	U216	U217	U218	U219	G226	C235	A236	G237	A238					
U239	A243	U244	U245	U246	G247	G251	U252	A253	G254	G255	U256	G257	G258	C264	G265	G266	C267	U268	C269	A270	C271	G279	C280	G289	G292	U296	G297	A298	G299	A300	G301	C302	U304	G305	A306	A307	C308	A309	C311	C312	A313	C314	A320	A321	A325	G326	A327	C328									
A329	C330	G331	G332	U333	C334	C335	G336	G337	A338	U340	U343	A344	C345	G346	G350	C351	C352	A353	G354	C355	A356	G360	G361	G362	A363	U367	U368	G369	C370	A371	C372	A373	A374	U375	C381	U382	A383	G384	U387	U390	G391	C392	G399	G406	U407	A408	U409	G410									
A411	A412	G413	A414	A415	U421	C422	G423	G424	U427	G428	U429	A430	A431	A432	G433	U434	A435	C436	U437	U438	U439	C440	A441	G442	C443	G444	A448	G449	U450	A451	G452	G453	G457	U458	A459	A460	U461	U462	U464	A465	A466	U467	A468	C469	U472	U473	G474	C475	U476	U480	G481	A482					
C483	G484	U485	U486	A487	C490	C491	G492	A493	G494	A495	A496	G497	A498	U499	G500	C501	A502	C503	G504	G505	G506	C511	C514	G515	U516	G517	C518	C519	A520	G521	A522	A523	G524	C525	G526	G527	C528	G529	U531	A532	A533	C536	G537	G538	A539	G540	G541	G542	U543	G544	G545	A546	A547	C631			
A554	U555	C556	A559	A560	U561	U562	A563	C564	U565	G566	C569	U570	U571	A572	A573	A574	G575	C576	G577	C578	A579	C580	G581	C586	G587	G592	U593	U594	A595	G601	A602	U603	G604	U605	G606	A607	A608	A609	U610	C613	C614	G615	C618	U619	G625	G626	G627	G628	A629	A630	C631						
U632	G633	U636	C637	U641	A642	C643	A649	G650	C651	U652	U653	C654	A655	U656	U657	C658	U659	C660	G664	A665	G666	G667	C668	G669	G670	G671	U672	A673	A675	A676	U677	U678	C679	C680	A681	G682	G683	U684	G685	U686	A687	G688	C689	G690	G691	U692	G693	A694	A695	A696	U697	G698	C699	G700			
U701	A702	G703	A704	G705	A706	U707	G710	G711	A712	G713	G714	A715	A716	U717	A718	C719	C720	G721	G722	U723	G724	G725	C726	G731	C732	G733	G734	C735	C736	C737	G741	A742	A743	G744	G745	A746	A747	G748	A749	C750	U751	G752	G755	C756	U757	G758	A759	A767	A768	G769	C770	G771	G774				
G775	G776	A777	G778	C779	A780	U781	A782	C783	A784	G785	G786	A787	U788	U789	A790	G791	A792	U793	A794	C795	C796	C797	U798	G799	G800	U801	A802	C803	U804	C810	C811	G812	U813	A814	A815	A816	C817	G818	A819	U820	G821	U827	U828	G829	C830	A831	U835	G836	U837	G838	C839	A840	C841	U842	U843	G844	
A845	G846	G847	C848	U849	U850	G851	U854	C857	G858	G859	A860	G861	A864	A865	C866	G867	C868	G869	U870	U871	A872	A873	A874	U875	A878	G881	C882	U884	G890	G896	C899	A900	A901	G902	G903	U904	U905	A906	A907	A908	A909	C910	U911	C912	A913	A914	A918	A919	U920	U921							
G922	A923	C924	G925	G926	G927	G928	U929	C930	C931	C932	G933	C934	A935	A938	G939	C940	G941	G942	U943	G944	G945	A946	G947	C948	U949	U950	G951	U952	G953	G954	U955	U956	U957	A958	A959	U960	U961	C962	G963	A964	U965	G966	C967	A968	A969	C970	G971	A974	A975	G976	A977	A978	C979	C980	U981	U982	
C984	C985	U986	U987	U988	U989	C990	U991	U992	G993	U994	C995	A996	U997	C998	C999	A1000	C1001	G1002	G1003	A1004	A1005	U1009	U1010	C1011	A1012	G1013	A1014	G1015	A1016	U1019	G1020	U1021	A1022	U1023	G1024	U1025	G1026	A1027	C1028	U1029	U1030	C1031	A1163	G1164	U1103	A1104	C1105	A1106	G1107	U1108	C1109	U1110	G1041				
A80	A81	G82	C83	U84	U85	G86	C87	U88	U89	C90	U91	U92	U93	G94	C95	U96	G97	A98	C99	G107	G108	A109	G113	U114	G115	A119	A120	U121	G122	U123	C124	U125	G126	G127	G128	A129	A130	A131	U132	U133	G134	C135	A139	U140	G146	G147	G148	A149	U150	A151	A152	U157	G158				
G159	A160	A161	A162	C163	G164	G165	C169	U170	U171	A172	U173	A174	G177	U178	A179	U180	A181	A182	C183	G184	G187	C188	A189	A190	C194	A195	A196	U191	A197	G201	G202	G203	G204	A205	C206	U208	U209	C210	G211	G212	A213	C214	C215	U216	U217	U218	U219	G226	C235	A236	G237	A238					
U239	A243	U244	U245	U246	G247	G251	U252	A253	G254	G255	U256	G257	G258	C264	G265	G266	C267	U268	C269	A270	C271	G279	C280	G289	G292	U296	G297	A298	G299	A300	G301	C302	U304	G305	A306	A307	C308	A309	C311	C312	A313	C314	A320	A321	A325	G326	A327	C328									
A329	C330	G331	G332	U333	C334	C335	G336	G337	A338	U340	U343	A344	C345	G346	G350	C351	C352	A353	G354	C355	A356	G360	G361	G362	A363	U367	U368	G369	C370	A371	C372	A373	A374	U375	C381	U382	A383	G384	U387	U390	G391	C392	G399	G406	U407	A408	U409	G410									
A411	A412	G413	A414	A415	U421	C422	G423	G424	U427	G428	U429	A430	A431	A432	G433	U434	A435	C436	U437	U438	U439	C440	A441	G442	C443	G444	A448	G449	U450	A451	G452	G453	G457	U458	A459	A460	U461	U462	U464	A465	A466	U467	A468	C469	U472	U473	G474	C475	U476	U480	G481	A482					
C483	G484	U485	U486	A487	C490	C491	G492	A493	G494	A495	A496	G497	A498	U499	G500	C501	A502	C503	G504	G505	G506	C511	C514	G515	U516	G517	C518	C519	A520	G521	A522	A523	G524	C525	G526	G527	C528	G529	U531	A532	A533	C536	G537	G538	A539	G540	G541	G542	U543	G544	G545	A546	A547	C631			
A554	U555	C556	A559	A560	U561	U562	A563	C564	U565	G566	C569	U570	U571	A572	A573	A574	G575	C576	G577	C578	A579	C580	G581	C586	G587	G592	U593	U594	A595	G601	A602	U603	G604	U605	G606	A607	A608	A609	U610	C613	C614	G615	C618	U619	G625	G626	G627	G628	A629	A630	C631						
U632	G633	U636	C637	U641	A642	C643	A649	G650	C651	U652	U653	C654	A655	U656	U657	C658	U659	C660	G664	A665	G666	G667	C668	G669	G670	G671	U672	A673	A675	A676	U677	U678	C679	C680	A681	G682	G683	U684	G685	U686	A687	G688	C689	G690	G691	U692	G693	A694	A695	A696	U697	G698	C699	G700			
U701	A702	G703	A704	G705	A706	U707	G710	G711	A712	G713	G714	A715	A716	U717	A718	C719	C720	G721	G722	U723	G724	G725	C726	G731	C732	G733	G734	C735	C736	C737	G741	A742	A743	G744	G745	A746	A747	G748	A749	C750	U751	G752	G755	C756	U757	G758	A759	A767	A768	G769	C770	G771	G774				
G775	G776	A777	G778	C779	A780	U781	A782	C783	A784	G785	G786	A787	U788	U789	A790	G791	A7																																								

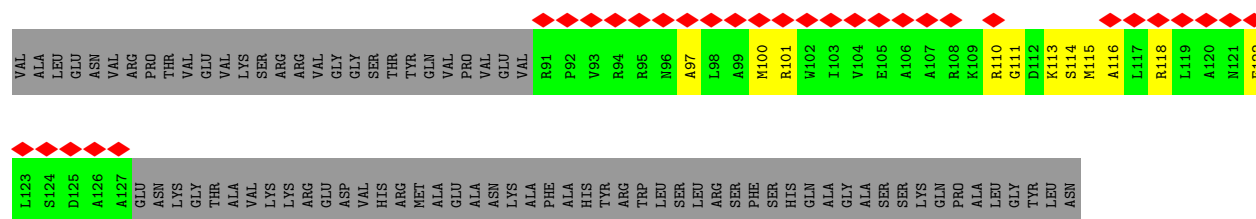


• Molecule 14: 30S ribosomal protein S3

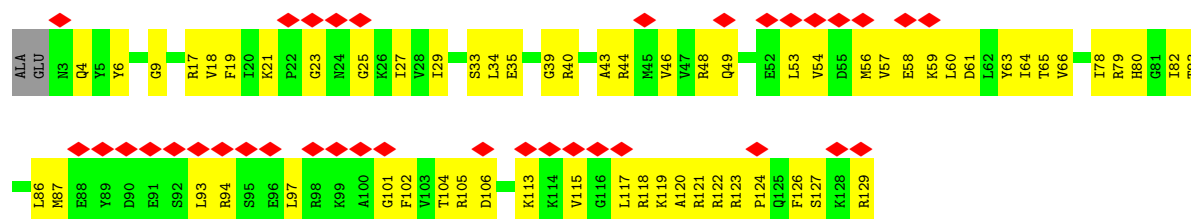


• Molecule 15: 30S ribosomal protein S7

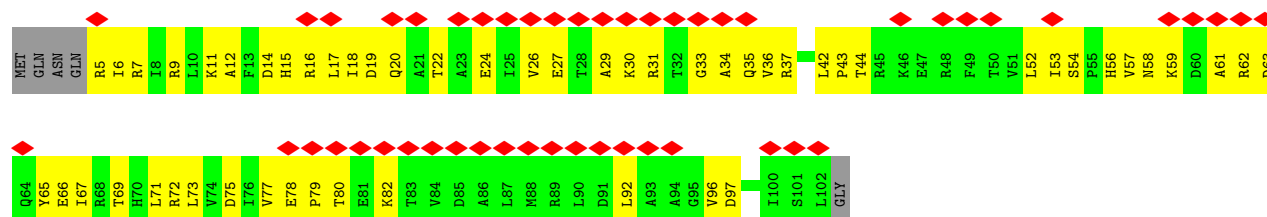




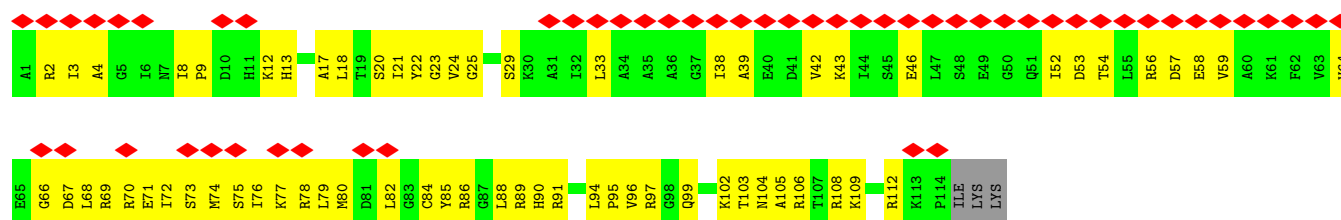
• Molecule 16: 30S ribosomal protein S9



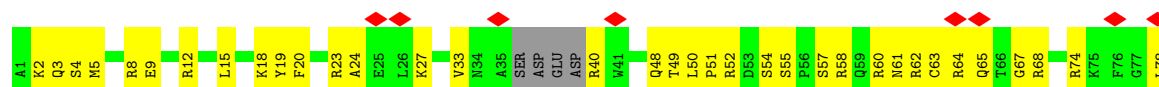
• Molecule 17: 30S ribosomal protein S10

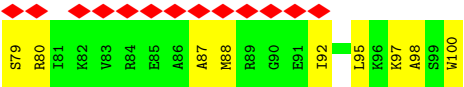


• Molecule 18: 30S ribosomal protein S13

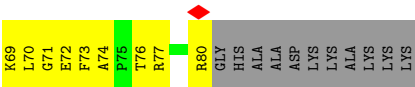
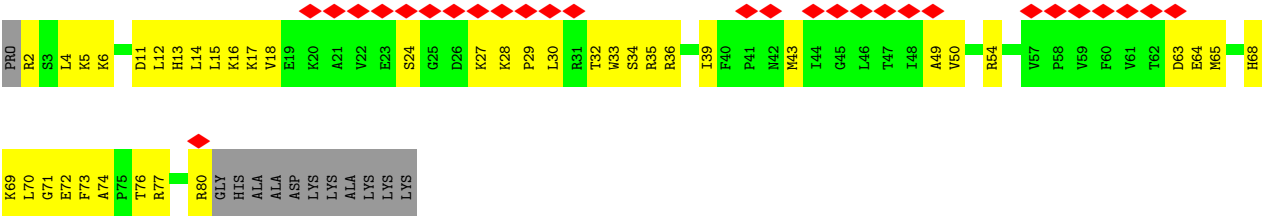


• Molecule 19: 30S ribosomal protein S14





• Molecule 20: 30S ribosomal protein S19



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	138247	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	6.844	Depositor
Minimum map value	-2.889	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.29	Depositor
Map size ($\text{\AA}$)	378.4, 378.4, 378.4	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.86, 0.86, 0.86	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	B	0.24	0/1735	0.52	0/2338
2	D	0.68	0/1665	0.78	0/2227
3	E	0.61	0/1118	0.68	0/1504
4	F	0.22	0/835	0.47	0/1128
5	H	0.78	0/989	0.77	0/1326
6	K	0.19	0/713	0.42	0/960
7	L	0.84	0/969	0.92	0/1300
8	O	0.52	0/724	0.69	0/966
9	P	0.96	0/659	0.89	0/884
10	Q	0.75	0/657	0.69	0/881
11	R	0.32	0/412	0.58	0/553
12	T	0.84	0/671	0.90	0/888
13	A	0.78	0/36289	0.51	2/56610 (0.0%)
14	C	0.14	0/1651	0.42	0/2225
15	G	0.15	0/648	0.45	0/868
16	I	0.30	0/1034	0.56	0/1375
17	J	0.15	0/796	0.47	0/1077
18	M	0.15	0/892	0.49	0/1193
19	N	0.14	0/785	0.40	0/1043
20	S	0.19	0/652	0.51	0/877
All	All	0.70	0/53894	0.55	2/80223 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A	1396	A	N9-C1'-C2'	5.17	119.76	112.00
13	A	328	C	P-O3'-C3'	5.02	127.72	120.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1704	0	1732	101	0
2	D	1643	0	1710	92	0
3	E	1105	0	1148	53	0
4	F	817	0	808	65	0
5	H	979	0	1034	54	0
6	K	702	0	702	55	0
7	L	955	0	1019	71	0
8	O	716	0	742	57	0
9	P	649	0	666	15	0
10	Q	648	0	691	23	0
11	R	407	0	438	28	0
12	T	665	0	714	20	0
13	A	32408	0	16290	1118	0
14	C	1624	0	1699	82	0
15	G	642	0	685	31	0
16	I	1022	0	1070	71	0
17	J	786	0	828	42	0
18	M	883	0	944	79	0
19	N	774	0	827	55	0
20	S	637	0	665	50	0
21	A	484	0	0	24	0
21	D	7	0	0	0	0
21	H	9	0	0	0	0
21	L	6	0	0	2	0
21	O	1	0	0	0	0
21	P	9	0	0	1	0
21	Q	3	0	0	0	0
21	R	1	0	0	0	0
21	T	10	0	0	1	0
All	All	50296	0	34412	1935	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 24.

The worst 5 of 1935 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)
4:F:51:ILE:CD1	4:F:86:ARG:HH22	1.24	1.46
9:P:8:ARG:NH1	13:A:391:G:H4'	1.59	1.18
13:A:771:G:H4'	21:A:1894:HOH:O	1.44	1.18
4:F:51:ILE:CD1	4:F:86:ARG:NH2	2.05	1.16
4:F:51:ILE:HD13	4:F:86:ARG:HH22	1.15	1.09

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	B	216/240 (90%)	188 (87%)	28 (13%)	0	100	100
2	D	203/205 (99%)	181 (89%)	22 (11%)	0	100	100
3	E	148/166 (89%)	131 (88%)	17 (12%)	0	100	100
4	F	98/135 (73%)	89 (91%)	9 (9%)	0	100	100
5	H	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
6	K	93/128 (73%)	87 (94%)	6 (6%)	0	100	100
7	L	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
8	O	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
9	P	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
10	Q	78/83 (94%)	68 (87%)	10 (13%)	0	100	100
11	R	48/74 (65%)	41 (85%)	7 (15%)	0	100	100
12	T	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
14	C	204/232 (88%)	185 (91%)	19 (9%)	0	100	100
15	G	79/178 (44%)	72 (91%)	7 (9%)	0	100	100
16	I	125/129 (97%)	111 (89%)	14 (11%)	0	100	100
17	J	96/103 (93%)	77 (80%)	19 (20%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	M	112/117 (96%)	100 (89%)	12 (11%)	0	100	100
19	N	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
20	S	77/91 (85%)	66 (86%)	11 (14%)	0	100	100
All	All	2166/2490 (87%)	1947 (90%)	219 (10%)	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	B	180/198 (91%)	180 (100%)	0	100	100
2	D	172/172 (100%)	172 (100%)	0	100	100
3	E	113/125 (90%)	113 (100%)	0	100	100
4	F	87/116 (75%)	87 (100%)	0	100	100
5	H	104/104 (100%)	104 (100%)	0	100	100
6	K	69/98 (70%)	69 (100%)	0	100	100
7	L	103/103 (100%)	103 (100%)	0	100	100
8	O	76/77 (99%)	76 (100%)	0	100	100
9	P	65/65 (100%)	65 (100%)	0	100	100
10	Q	74/77 (96%)	74 (100%)	0	100	100
11	R	43/64 (67%)	43 (100%)	0	100	100
12	T	65/65 (100%)	65 (100%)	0	100	100
14	C	170/189 (90%)	170 (100%)	0	100	100
15	G	67/146 (46%)	67 (100%)	0	100	100
16	I	105/106 (99%)	105 (100%)	0	100	100
17	J	86/90 (96%)	86 (100%)	0	100	100
18	M	92/95 (97%)	92 (100%)	0	100	100
19	N	79/83 (95%)	79 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	S	70/78 (90%)	70 (100%)	0	100	100
All	All	1820/2051 (89%)	1820 (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. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
15	G	96	ASN
18	M	99	GLN
19	N	61	ASN
16	I	125	GLN
4	F	46	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	A	1507/1542 (97%)	403 (26%)	21 (1%)

5 of 403 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
13	A	6	G
13	A	7	A
13	A	9	G
13	A	15	G
13	A	20	U

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
13	A	1201	A
13	A	1300	G
13	A	1528	U
13	A	1507	A
13	A	1278	G

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.

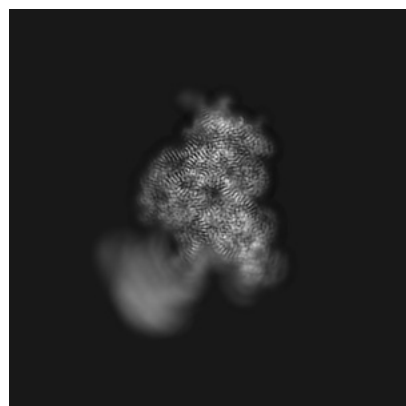
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12856. These allow visual inspection of the internal detail of the map and identification of artifacts.

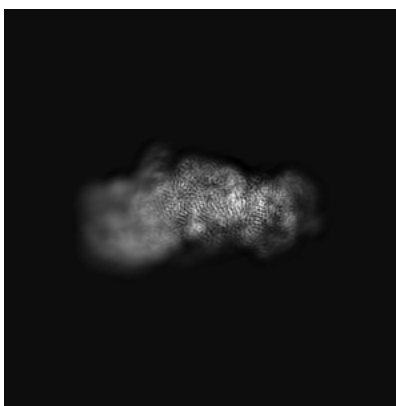
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

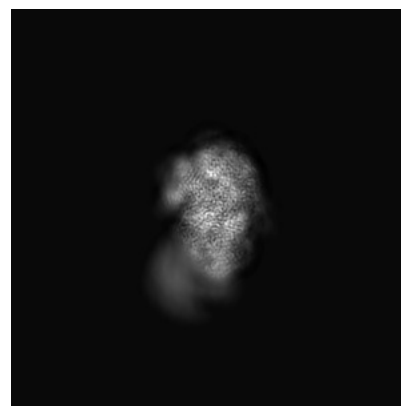
6.1.1 Primary map



X

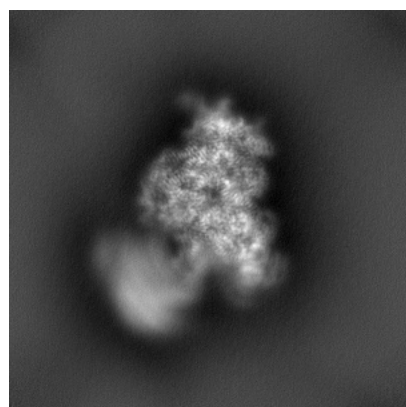


Y

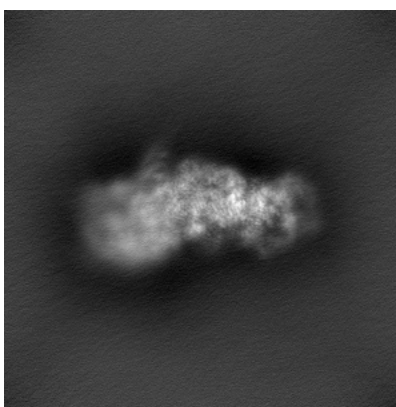


Z

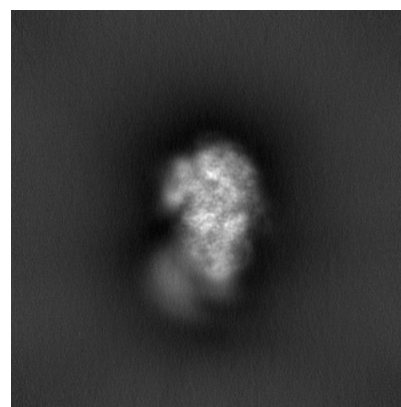
6.1.2 Raw map



X



Y

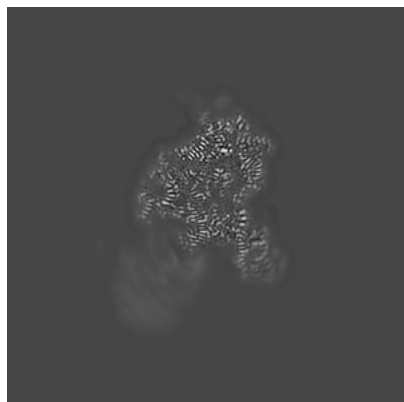


Z

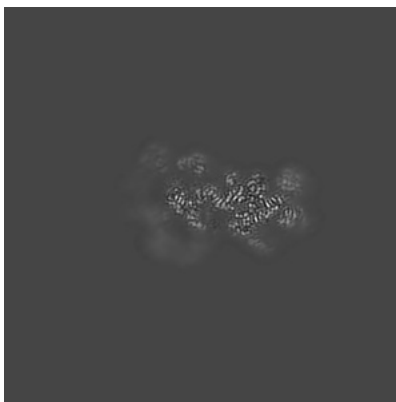
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

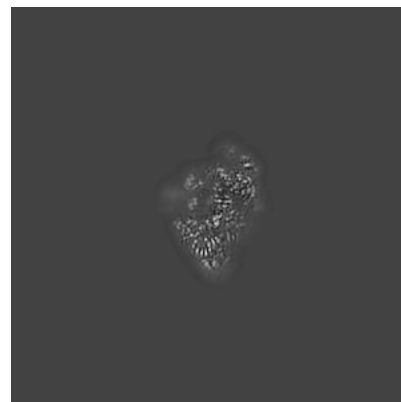
6.2.1 Primary map



X Index: 220

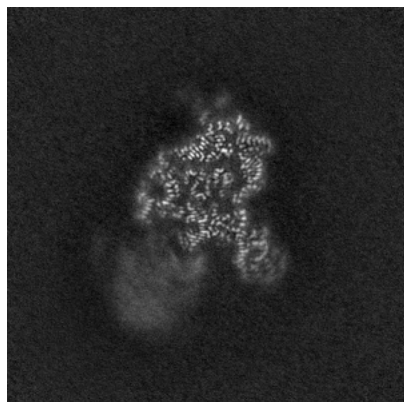


Y Index: 220

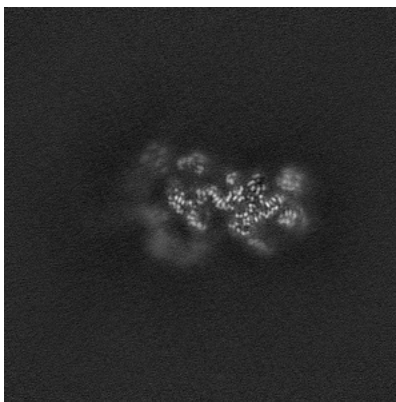


Z Index: 220

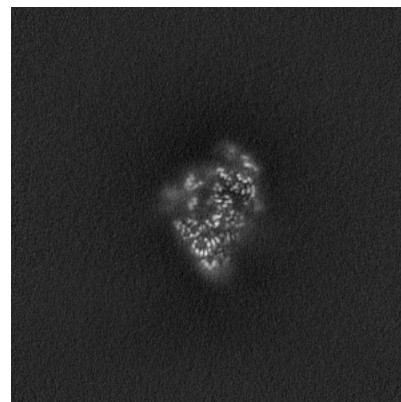
6.2.2 Raw map



X Index: 220



Y Index: 220

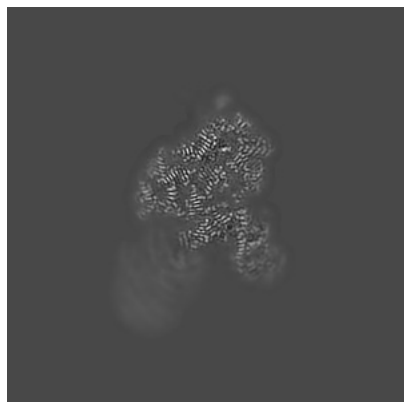


Z Index: 220

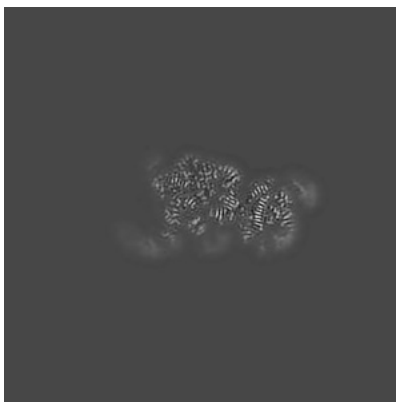
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

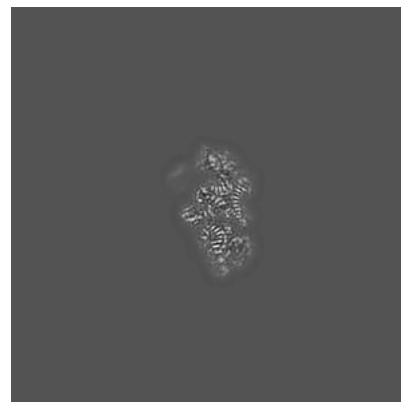
6.3.1 Primary map



X Index: 224

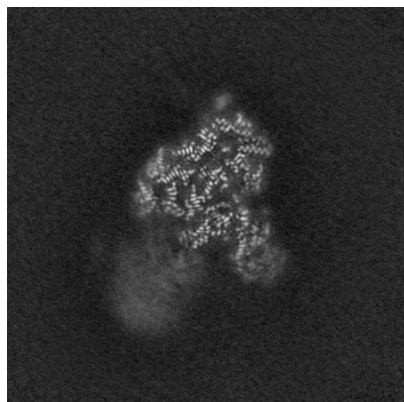


Y Index: 239

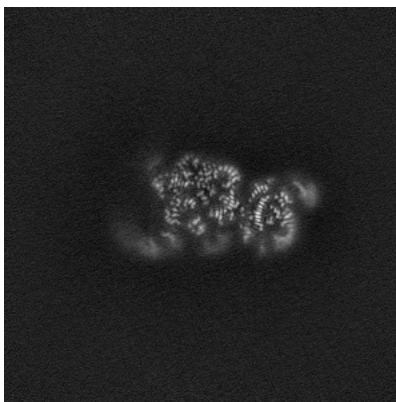


Z Index: 251

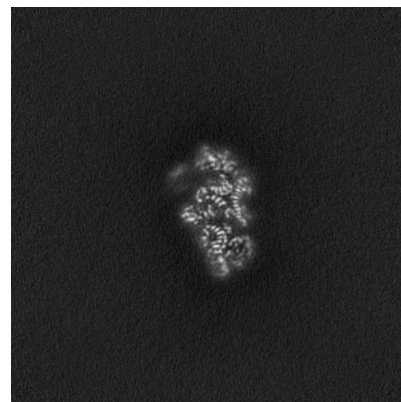
6.3.2 Raw map



X Index: 225



Y Index: 239

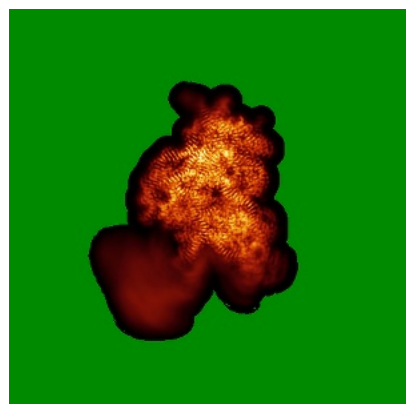


Z Index: 251

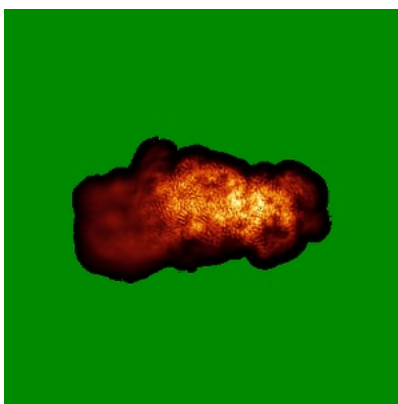
The images above show the largest variance slices of the map in three orthogonal directions.

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

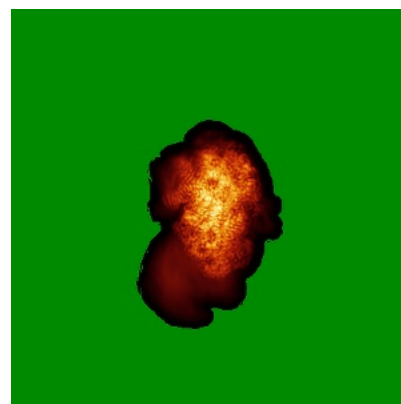
6.4.1 Primary map



X

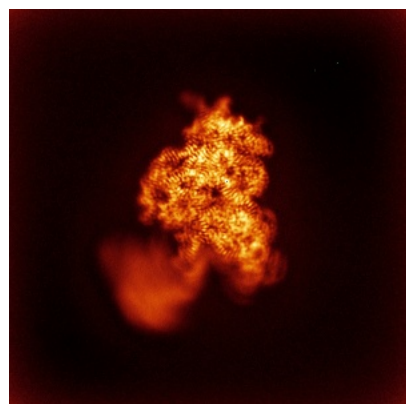


Y

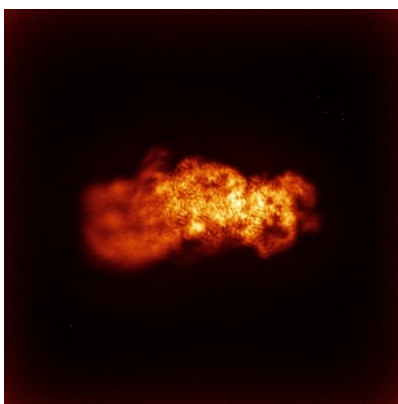


Z

6.4.2 Raw map



X



Y

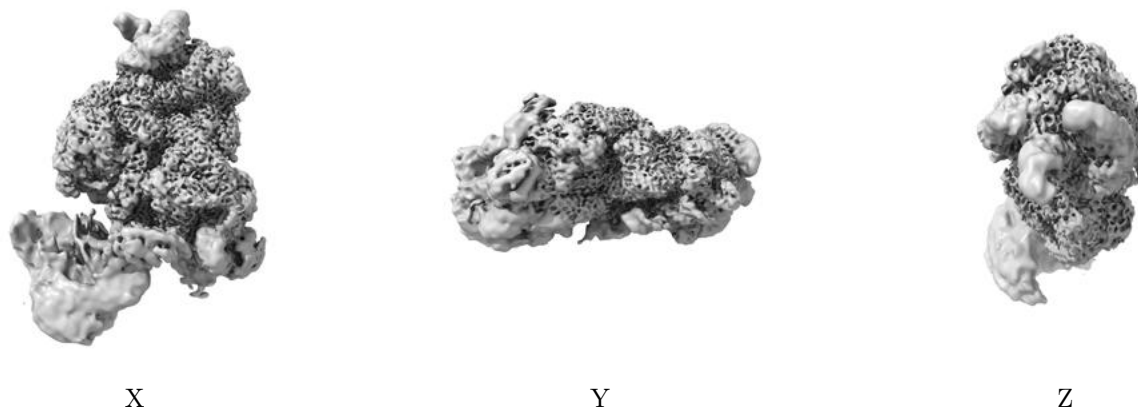


Z

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.

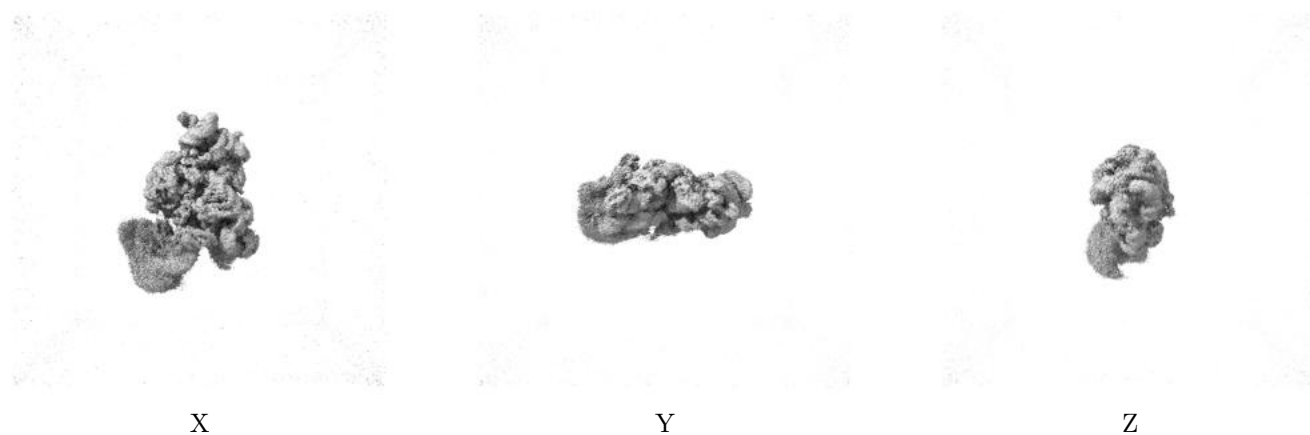
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.29. 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.

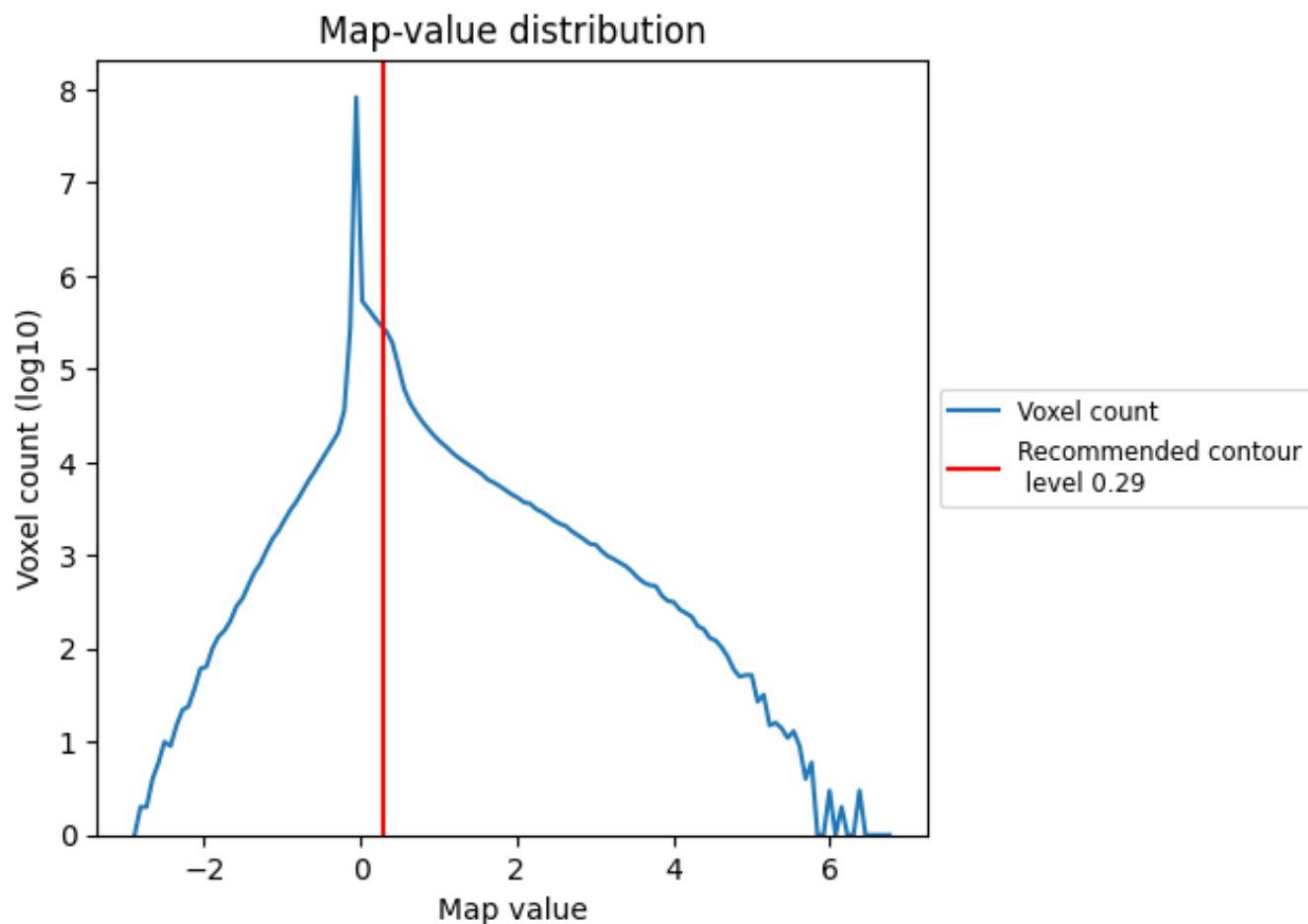
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

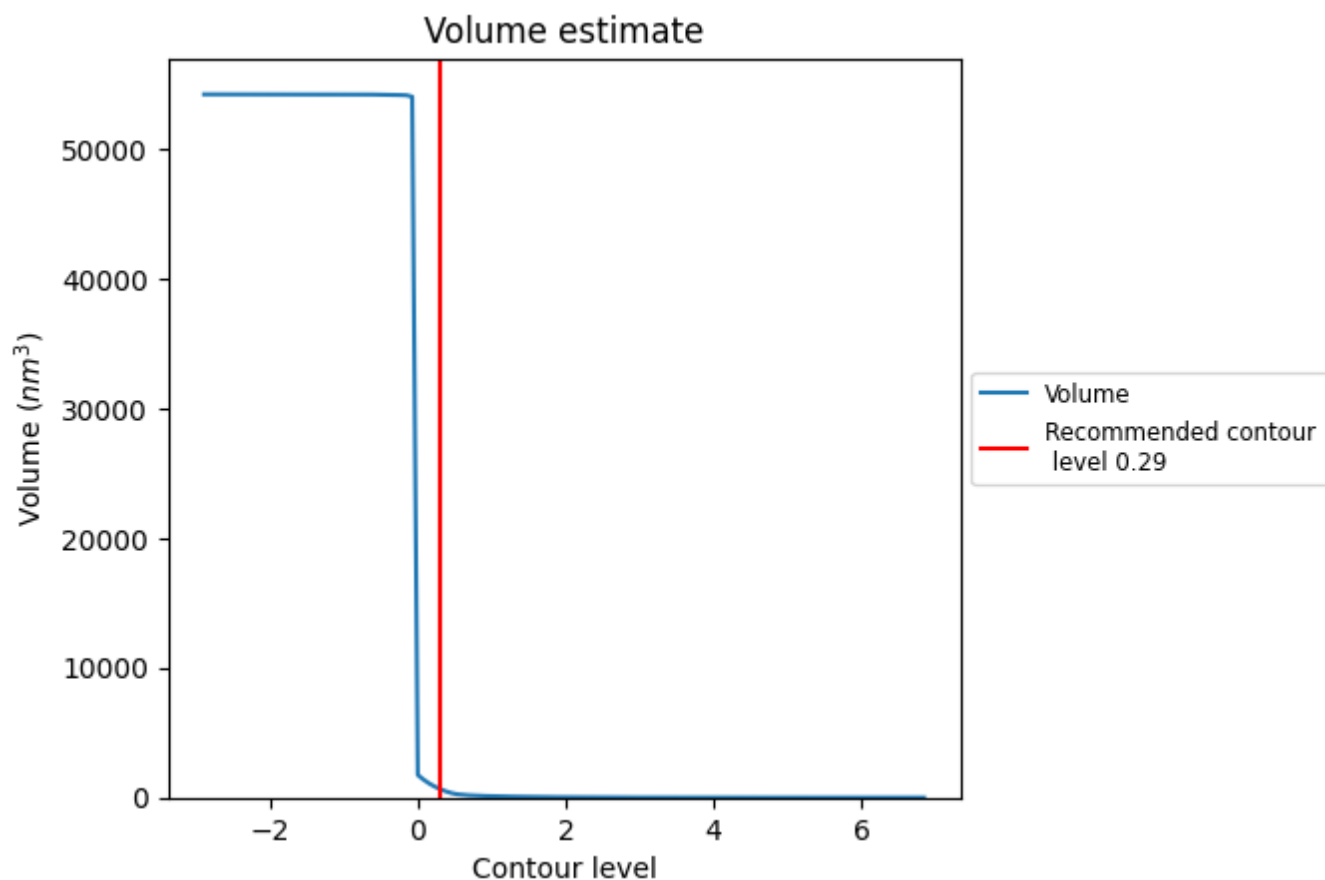
This section contains the results of statistical analysis of the map.

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.

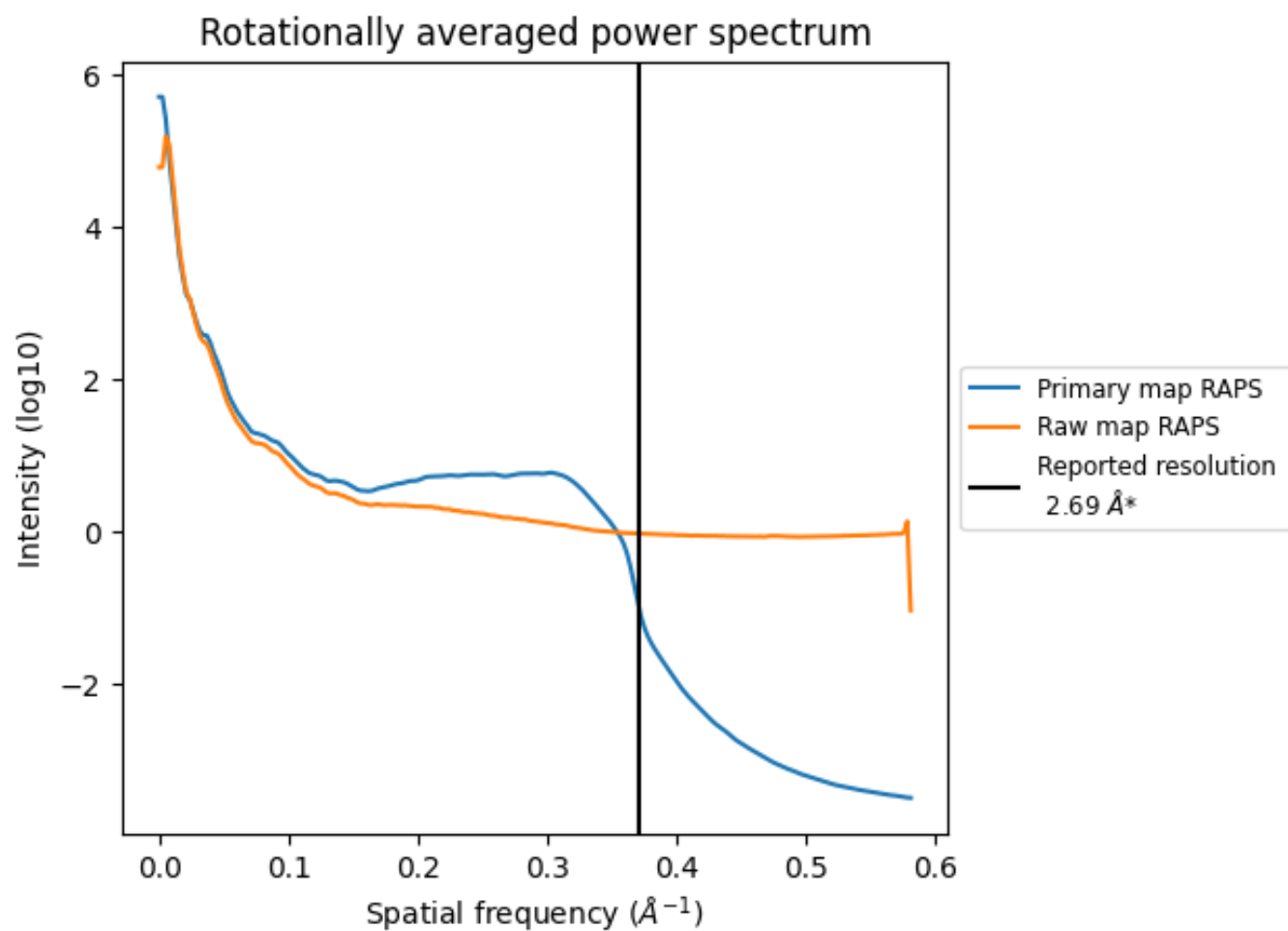
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 688 nm³; this corresponds to an approximate mass of 622 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 ⓘ

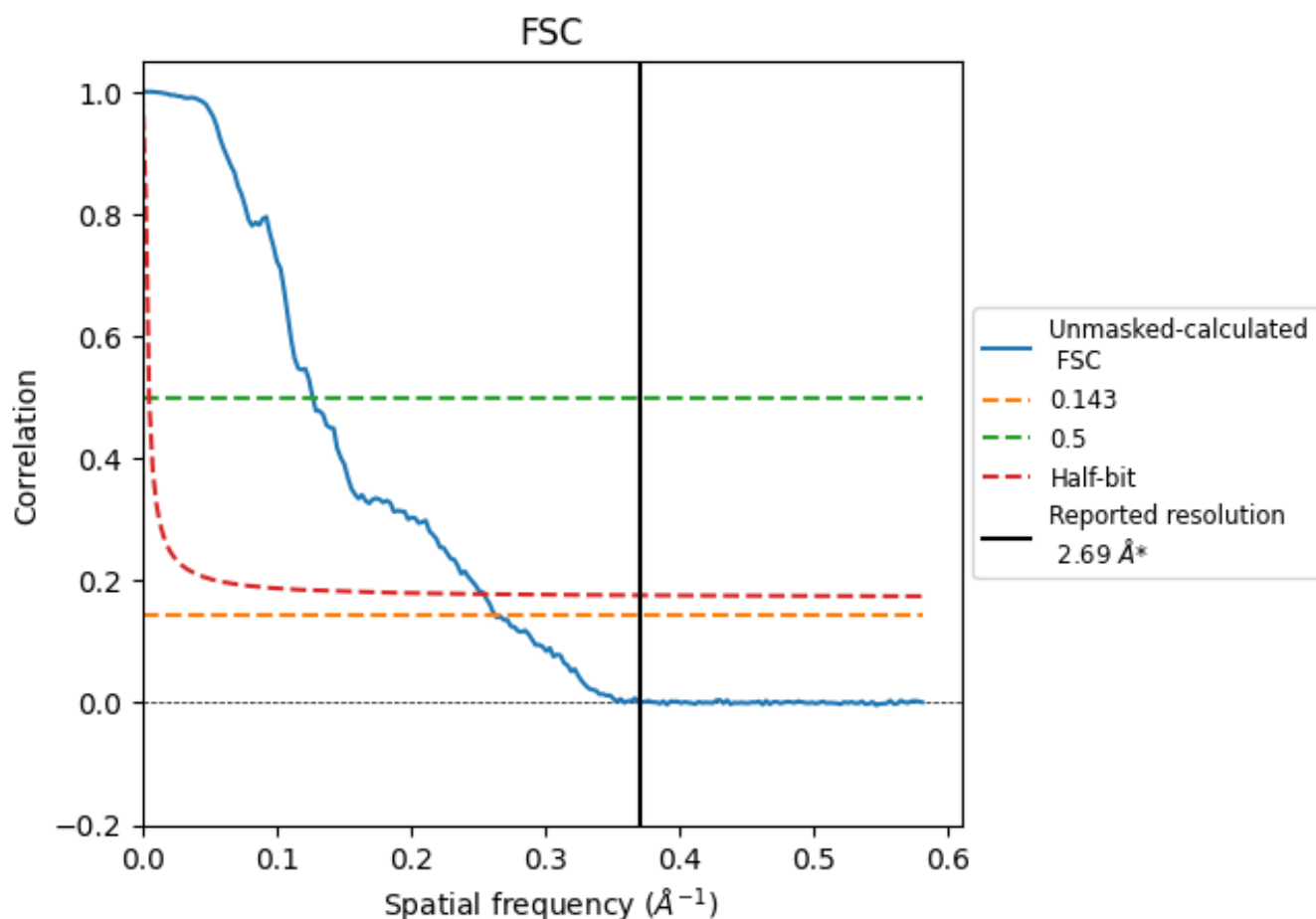


*Reported resolution corresponds to spatial frequency of 0.372 $\text{\AA}^{-1}$

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 0.372 Å⁻¹

8.2 Resolution estimates [i](#)

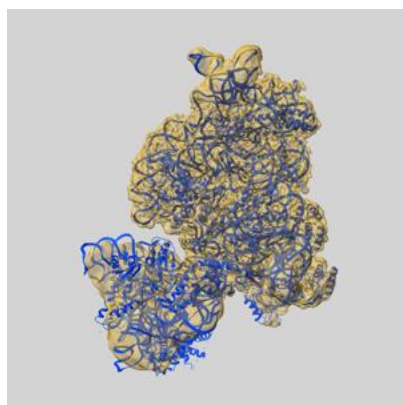
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.69	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.80	7.87	3.93

*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 3.80 differs from the reported value 2.69 by more than 10 %

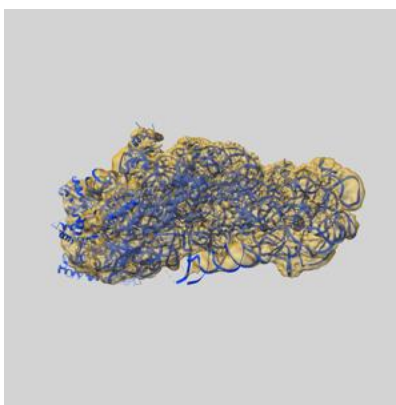
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12856 and PDB model 7OE0. Per-residue inclusion information can be found in section [3](#) on page [8](#).

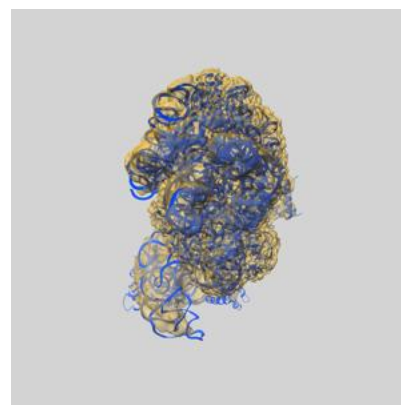
9.1 Map-model overlay [i](#)



X



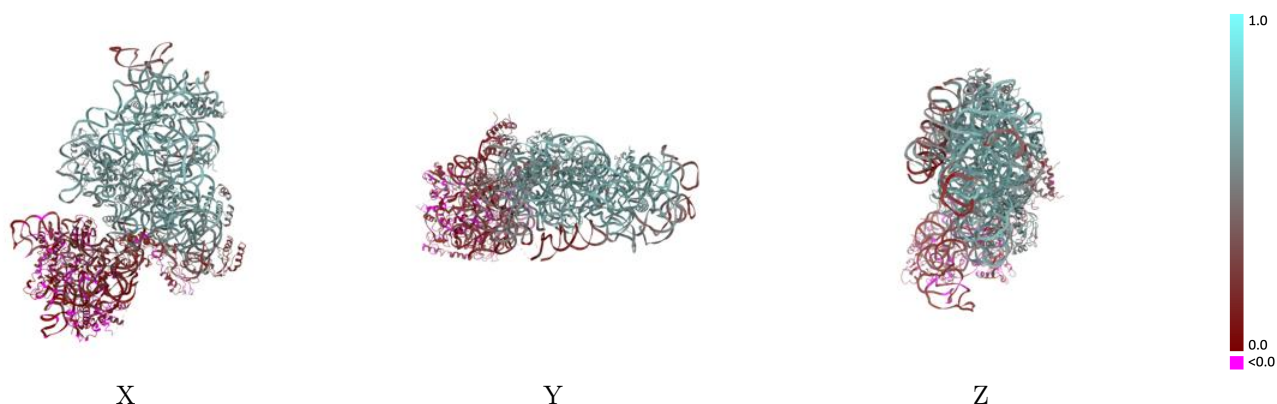
Y



Z

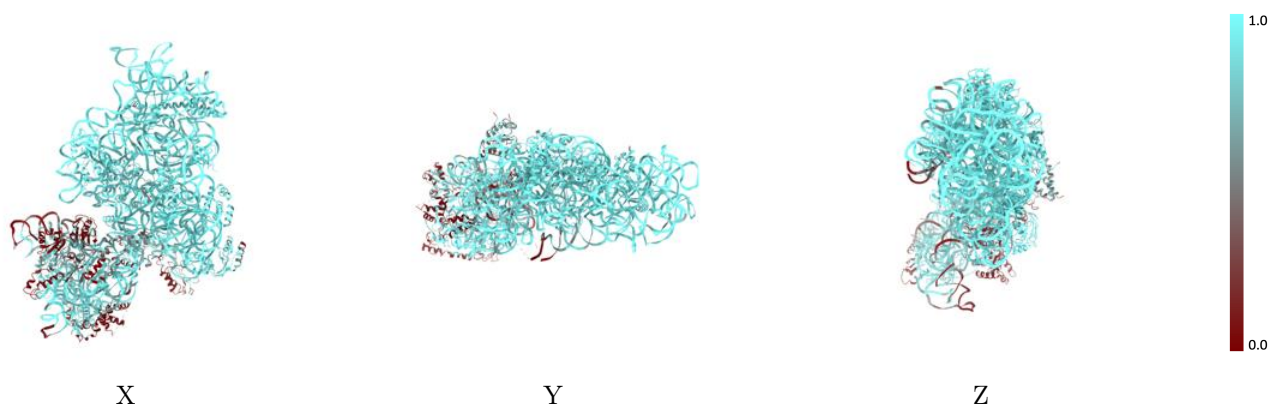
The images above show the 3D surface view of the map at the recommended contour level 0.29 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



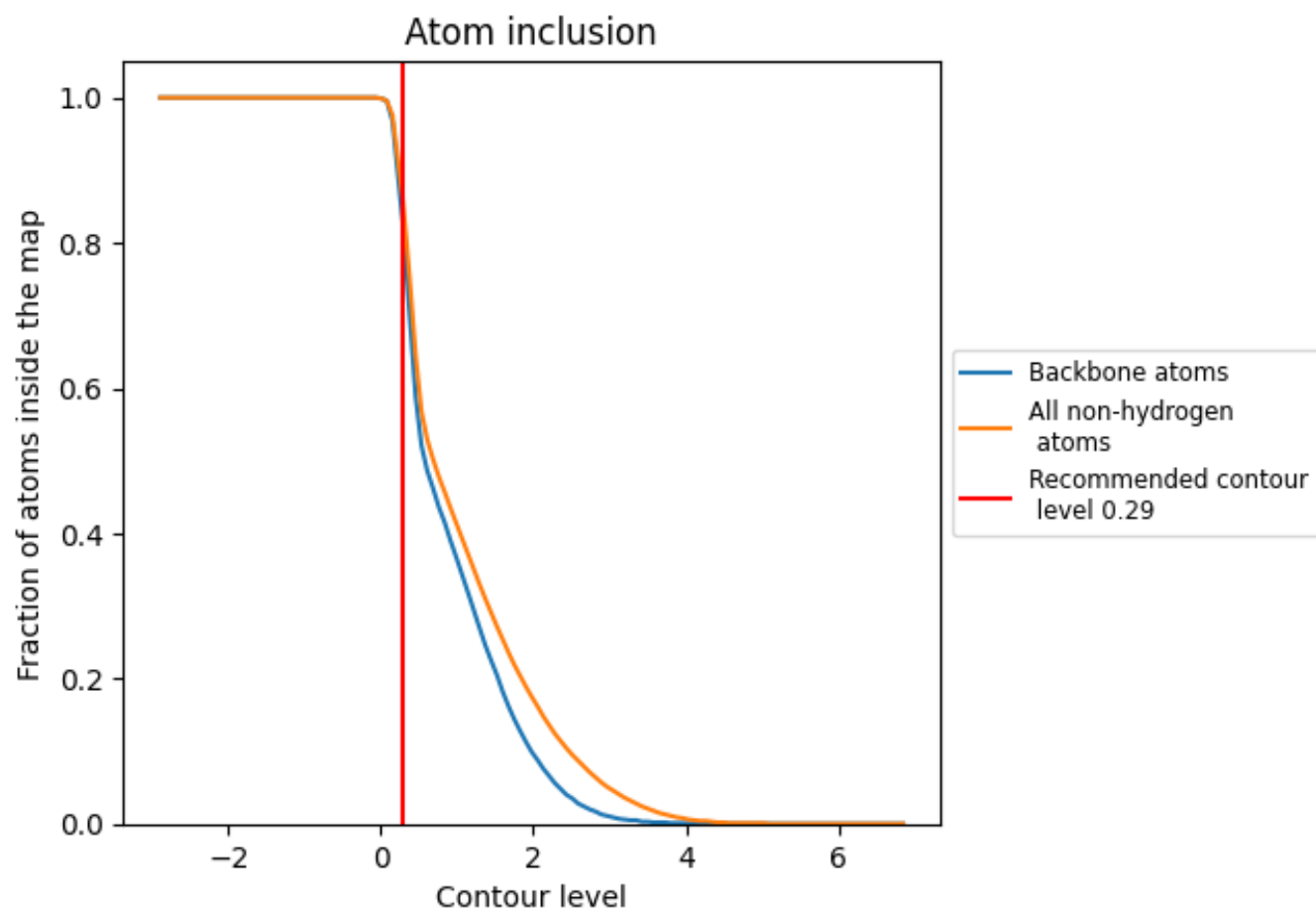
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.29).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 86% 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 (0.29) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8590	 0.3890
A	 0.9340	 0.4270
B	 0.5730	 0.2560
C	 0.2430	 0.0910
D	 0.9670	 0.5470
E	 0.9760	 0.5780
F	 0.8220	 0.2890
G	 0.1910	 0.0230
H	 0.9720	 0.5960
I	 0.6570	 0.0520
J	 0.4870	 0.0560
K	 0.3900	 0.1240
L	 0.9650	 0.5870
M	 0.5050	 0.0370
N	 0.7480	 0.0230
O	 0.9520	 0.5060
P	 0.9650	 0.6260
Q	 0.9860	 0.5940
R	 0.9260	 0.4250
S	 0.6230	 0.0670
T	 0.9940	 0.5990

