



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 11:19 PM UTC

PDB ID : 7QVP / pdb_00007qvp
EMDB ID : EMD-14181
Title : Human collided disome (di-ribosome) stalled on XBP1 mRNA
Authors : Denk, T.G.; Tesina, P.; Beckmann, R.
Deposited on : 2022-01-22
Resolution : 3.00 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	:	FAILED
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

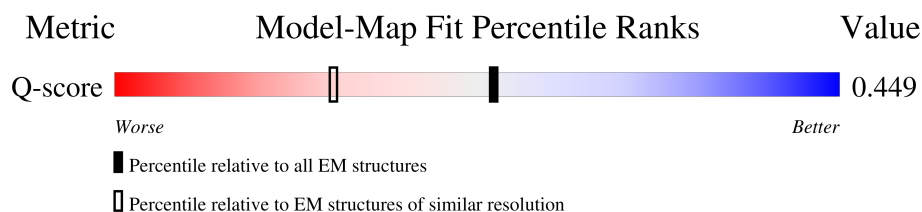
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	14081 (2.50 - 3.50)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 417512 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 RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A4	14	Total	C	N	O	P	0	0
			280	126	28	112	14		

- Molecule 2 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A5	11	Total	C	N	O	P	0	0
			220	99	22	88	11		

- Molecule 3 is a RNA chain called tRNA P/P.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B4	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		
3	D5	73	Total	C	N	O	P	0	0
			1559	696	283	508	72		

- Molecule 4 is a RNA chain called tRNA P/E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B5	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 5 is a RNA chain called tRNA E/E.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CC	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	11	C	U	conflict	GB 176418

- Molecule 6 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L1	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		
6	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 7 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L5	3611	Total	C	N	O	P	0	0
			77405	34468	14160	25167	3610		
7	L6	3572	Total	C	N	O	P	0	0
			76565	34095	14005	24894	3571		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		
8	L9	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 9 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		
9	MA	248	Total	C	N	O	S	0	0
			1886	1183	386	311	6		

- Molecule 10 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LB	395	Total	C	N	O	S	0	0
			3183	2027	597	545	14		
10	MB	393	Total	C	N	O	S	0	0
			3101	1979	583	525	14		

- Molecule 11 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	364	Total	C	N	O	S	0	0
			2884	1814	576	479	15		
11	MC	365	Total	C	N	O	S	0	0
			2894	1819	578	482	15		

- Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	293	Total	C	N	O	S	0	0
			2361	1496	430	421	14		
12	MD	293	Total	C	N	O	S	0	0
			2287	1455	426	392	14		

- Molecule 13 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	219	Total	C	N	O	S	0	0
			1754	1129	334	287	4		
13	ME	220	Total	C	N	O	S	0	0
			1713	1104	326	279	4		

- Molecule 14 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		
14	MF	225	Total	C	N	O	S	0	0
			1844	1189	355	291	9		

- Molecule 15 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	229	Total	C	N	O	S	0	0
			1818	1157	351	306	4		
15	MG	229	Total	C	N	O	S	0	0
			1733	1106	335	288	4		

- Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
16	MH	189	Total	C	N	O	S	0	0
			1439	910	273	250	6		

- Molecule 17 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	206	Total	C	N	O	S	0	0
			1651	1051	318	268	14		
17	MI	203	Total	C	N	O	S	0	0
			1581	1007	306	254	14		

- Molecule 18 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	169	Total	C	N	O	S	0	0
			1329	841	250	232	6		
18	MJ	167	Total	C	N	O	S	0	0
			1226	780	228	212	6		

- Molecule 19 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LL	205	Total	C	N	O	S	0	0
			1630	1020	340	266	4		
19	ML	204	Total	C	N	O	S	0	0
			1580	992	335	249	4		

- Molecule 20 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LM	139	Total	C	N	O	S	0	0
			1122	720	216	179	7		
20	MM	136	Total	C	N	O	S	0	0
			1097	705	211	174	7		

- Molecule 21 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		
21	MN	203	Total	C	N	O	S	0	0
			1693	1068	359	262	4		

- Molecule 22 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LO	200	Total	C	N	O	S	0	0
			1633	1053	318	257	5		
22	MO	201	Total	C	N	O	S	0	0
			1613	1042	318	248	5		

- Molecule 23 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LP	153	Total	C	N	O	S	0	0
			1234	771	240	214	9		

- Molecule 24 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LQ	187	Total	C	N	O	S	0	0
			1502	939	313	245	5		
24	MQ	187	Total	C	N	O	S	0	0
			1493	931	311	246	5		

- Molecule 25 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	176	Total	C	N	O	S	0	0
			1452	898	318	227	9		
25	MR	175	Total	C	N	O	S	0	0
			1412	874	312	218	8		

- Molecule 26 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	175	Total	C	N	O	S	0	0
			1452	925	283	234	10		
26	MS	175	Total	C	N	O	S	0	0
			1436	915	281	230	10		

- Molecule 27 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	159	Total	C	N	O	S	0	0
			1282	813	250	213	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
27	MT	159	Total	C	N	O	S	0	0
			1268	805	249	209	5		

- Molecule 28 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	101	Total	C	N	O	S	0	0
			799	515	140	142	2		
28	MU	101	Total	C	N	O	S	0	0
			768	497	136	133	2		

- Molecule 29 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LV	131	Total	C	N	O	S	0	0
			971	613	183	170	5		
29	MV	131	Total	C	N	O	S	0	0
			954	604	180	165	5		

- Molecule 30 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LW	115	Total	C	N	O	S	0	0
			808	506	160	139	3		
30	MW	115	Total	C	N	O	S	0	0
			784	493	154	135	2		

- Molecule 31 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LX	120	Total	C	N	O	S	0	0
			981	627	184	169	1		
31	MX	120	Total	C	N	O	S	0	0
			950	611	182	156	1		

- Molecule 32 is a protein called KOW domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LY	134	Total	C	N	O	S	0	0
			1111	697	225	186	3		
32	MY	134	Total	C	N	O	S	0	0
			1084	681	220	180	3		

- Molecule 33 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		
33	MZ	135	Total	C	N	O	S	0	0
			1082	703	207	169	3		

- Molecule 34 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	La	147	Total	C	N	O	S	0	0
			1154	731	236	184	3		
34	Ma	146	Total	C	N	O	S	0	0
			1145	726	233	183	3		

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lb	75	Total	C	N	O	S	0	0
			590	367	123	97	3		
35	Mb	63	Total	C	N	O	S	0	0
			499	310	107	80	2		

- Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lc	97	Total	C	N	O	S	0	0
			742	473	130	133	6		
36	Mc	93	Total	C	N	O	S	0	0
			716	456	125	129	6		

- Molecule 37 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ld	107	Total	C	N	O	S	0	0
			874	554	171	147	2		
37	Md	107	Total	C	N	O	S	0	0
			856	546	168	140	2		

- Molecule 38 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Le	128	Total	C	N	O	S	0	0
			1049	664	215	165	5		
38	Me	127	Total	C	N	O	S	0	0
			1045	661	215	164	5		

- Molecule 39 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		
39	Mf	109	Total	C	N	O	S	0	0
			864	547	173	141	3		

- Molecule 40 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lg	114	Total	C	N	O	S	0	0
			889	557	184	142	6		
40	Mg	110	Total	C	N	O	S	0	0
			851	531	175	139	6		

- Molecule 41 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lh	121	Total	C	N	O	S	0	0
			1006	635	203	167	1		
41	Mh	121	Total	C	N	O	S	0	0
			975	617	200	157	1		

- Molecule 42 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Li	102	Total	C	N	O	S	0	0
			813	510	176	123	4		
42	Mi	101	Total	C	N	O	S	0	0
			797	500	170	122	5		

- Molecule 43 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
43	Mj	86	Total	C	N	O	S	0	0
			701	431	154	111	5		

- Molecule 44 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lk	69	Total	C	N	O	S	0	0
			542	350	100	91	1		
44	Mk	69	Total	C	N	O	S	0	0
			528	339	99	89	1		

- Molecule 45 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		
45	Ml	50	Total	C	N	O	S	0	0
			440	278	97	64	1		

- Molecule 46 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lm	52	Total	C	N	O	S	0	0
			425	264	90	65	6		
46	Mm	50	Total	C	N	O	S	0	0
			393	244	82	61	6		

- Molecule 47 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		
47	Mn	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 48 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lo	105	Total	C	N	O	S	0	0
			848	532	173	137	6		
48	Mo	98	Total	C	N	O	S	0	0
			774	488	159	121	6		

- Molecule 49 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lp	91	Total	C	N	O	S	0	0
			696	440	135	114	7		
49	Mp	91	Total	C	N	O	S	0	0
			689	436	132	114	7		

- Molecule 50 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lr	125	Total	C	N	O	S	0	0
			997	618	207	168	4		
50	Mr	125	Total	C	N	O	S	0	0
			982	609	205	164	4		

- Molecule 51 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	MP	153	Total	C	N	O	S	0	0
			1203	754	238	202	9		

- Molecule 52 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RA	212	Total	C	N	O	S	0	0
			1575	1016	285	266	8		
52	SA	216	Total	C	N	O	S	0	0
			1671	1068	297	298	8		

- Molecule 53 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RB	214	Total	C	N	O	S	0	0
			1627	1041	296	277	13		
53	SB	213	Total	C	N	O	S	0	0
			1718	1092	308	304	14		

- Molecule 54 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RC	217	Total	C	N	O	S	0	0
			1590	1039	276	266	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
54	SC	219	Total	C	N	O	S	0	0
			1661	1076	284	291	10		

- Molecule 55 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RD	215	Total	C	N	O	S	0	0
			1475	950	267	251	7		
55	SD	223	Total	C	N	O	S	0	0
			1580	1016	286	271	7		

- Molecule 56 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RE	257	Total	C	N	O	S	0	0
			1891	1218	358	307	8		
56	SE	262	Total	C	N	O	S	0	0
			1972	1270	370	324	8		

- Molecule 57 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RF	180	Total	C	N	O	S	0	0
			1365	861	261	237	6		
57	SF	187	Total	C	N	O	S	0	0
			1416	886	269	254	7		

- Molecule 58 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	RG	213	Total	C	N	O	S	0	0
			1551	972	313	260	6		
58	SG	231	Total	C	N	O	S	0	0
			1634	1026	332	269	7		

- Molecule 59 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RH	176	Total	C	N	O	S	0	0
			1342	871	249	221	1		
59	SH	183	Total	C	N	O		0	0
			1274	819	242	213			

- Molecule 60 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RI	187	Total	C	N	O	S	0	0
			1450	910	286	249	5		
60	SI	206	Total	C	N	O	S	0	0
			1574	989	308	272	5		

- Molecule 61 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	RJ	176	Total	C	N	O	S	0	0
			1407	899	280	226	2		
61	SJ	179	Total	C	N	O	S	0	0
			1431	915	290	224	2		

- Molecule 62 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RK	95	Total	C	N	O	S	0	0
			736	482	131	119	4		
62	SK	96	Total	C	N	O	S	0	0
			726	479	127	115	5		

- Molecule 63 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RL	140	Total	C	N	O	S	0	0
			1139	725	214	194	6		
63	SL	144	Total	C	N	O	S	0	0
			1143	730	213	194	6		

- Molecule 64 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	RN	150	Total	C	N	O	S	0	0
			1199	766	229	203	1		
64	SN	150	Total	C	N	O	S	0	0
			1182	758	226	197	1		

- Molecule 65 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	RO	135	Total	C	N	O	S	0	0
			1003	615	198	184	6		
65	SO	134	Total	C	N	O	S	0	0
			969	596	194	173	6		

- Molecule 66 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RP	127	Total	C	N	O	S	0	0
			1001	636	188	170	7		
66	SP	128	Total	C	N	O	S	0	0
			975	617	185	167	6		

- Molecule 67 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	RQ	141	Total	C	N	O	S	0	0
			1078	690	207	178	3		
67	SQ	142	Total	C	N	O	S	0	0
			1071	687	204	177	3		

- Molecule 68 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	RR	125	Total	C	N	O	S	0	0
			879	551	166	159	3		
68	SR	131	Total	C	N	O	S	0	0
			942	600	179	159	4		

- Molecule 69 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	RS	138	Total	C	N	O	S	0	0
			1080	684	220	175	1		
69	SS	141	Total	C	N	O	S	0	0
			1118	706	226	185	1		

- Molecule 70 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	RT	141	Total	C	N	O	S	0	0
			993	624	195	172	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
70	ST	143	Total	C	N	O	S	0	0
			1081	679	210	189	3		

- Molecule 71 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	RU	100	Total	C	N	O	S	0	0
			749	470	143	134	2		
71	SU	101	Total	C	N	O	S	0	0
			713	447	137	125	4		

- Molecule 72 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	RV	83	Total	C	N	O	S	0	0
			589	369	111	104	5		
72	SV	83	Total	C	N	O	S	0	0
			618	385	115	113	5		

- Molecule 73 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	RW	129	Total	C	N	O	S	0	0
			1027	655	192	174	6		
73	SW	129	Total	C	N	O	S	0	0
			1026	655	193	172	6		

- Molecule 74 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	RX	141	Total	C	N	O	S	0	0
			1048	663	206	176	3		
74	SX	141	Total	C	N	O	S	0	0
			1078	682	212	181	3		

- Molecule 75 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	RY	113	Total	C	N	O	S	0	0
			855	544	164	143	4		
75	SY	123	Total	C	N	O	S	0	0
			927	588	183	152	4		

- Molecule 76 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	RZ	70	Total	C	N	O	S	0	0
			487	311	90	85	1		
76	SZ	75	Total	C	N	O	S	0	0
			559	361	105	92	1		

- Molecule 77 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ra	99	Total	C	N	O	S	0	0
			762	478	157	122	5		
77	Sa	99	Total	C	N	O	S	0	0
			781	487	165	124	5		

- Molecule 78 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Rb	83	Total	C	N	O	S	0	0
			617	390	114	109	4		
78	Sb	83	Total	C	N	O	S	0	0
			618	386	118	107	7		

- Molecule 79 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Rc	61	Total	C	N	O	S	0	0
			430	267	83	78	2		
79	Sc	63	Total	C	N	O	S	0	0
			472	289	92	89	2		

- Molecule 80 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Rd	52	Total	C	N	O	S	0	0
			420	264	83	69	4		
80	Sd	53	Total	C	N	O	S	0	0
			433	271	87	70	5		

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Re	51	Total	C	N	O	S	0	0
			386	240	83	62	1		
81	Se	57	Total	C	N	O	S	0	0
			426	259	96	70	1		

- Molecule 82 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Rf	78	Total	C	N	O	S	0	0
			483	307	90	82	4		

- Molecule 83 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Rg	283	Total	C	N	O	S	0	0
			1952	1243	341	359	9		
83	Sg	308	Total	C	N	O	S	0	0
			2172	1388	379	394	11		

- Molecule 84 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Rh	41	Total	C	N	O	S	0	0
			269	168	54	44	3		

- Molecule 85 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	S2	1714	Total	C	N	O	P	0	0
			36582	16329	6568	11972	1713		
85	S3	1705	Total	C	N	O	P	0	0
			36401	16247	6542	11908	1704		

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53848	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 ($e^-/\text{\AA}^2$)	43.6	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.570	Depositor
Minimum map value	-0.176	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	668.8, 668.8, 668.8	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

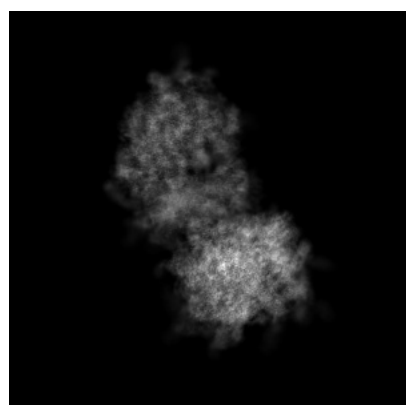
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14181. These allow visual inspection of the internal detail of the map and identification of artifacts.

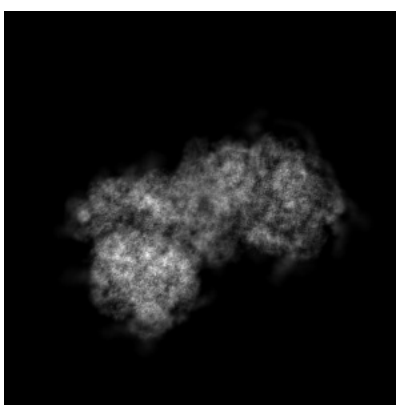
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

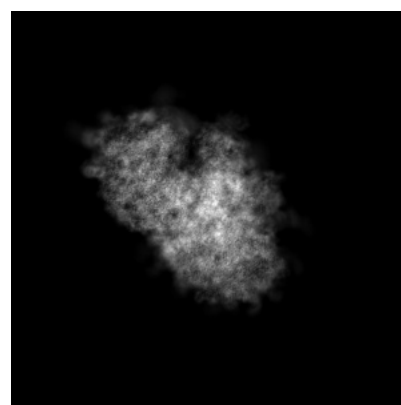
5.1.1 Primary map



X



Y

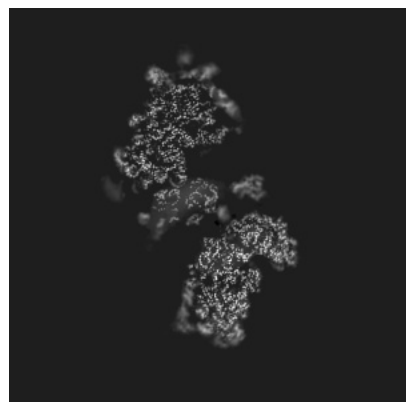


Z

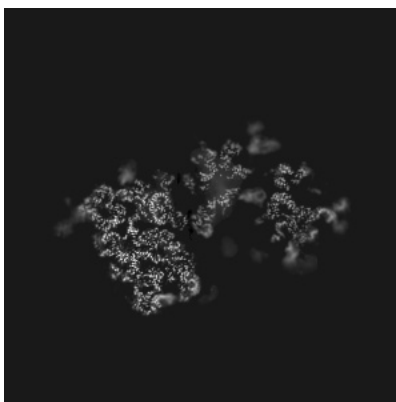
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

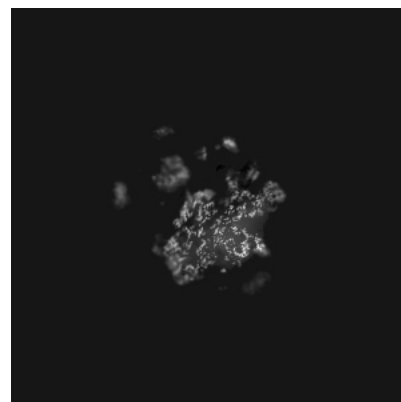
5.2.1 Primary map



X Index: 320



Y Index: 320

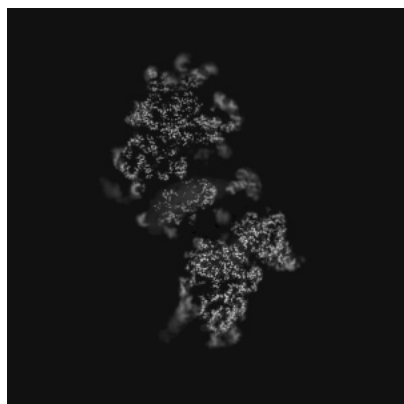


Z Index: 320

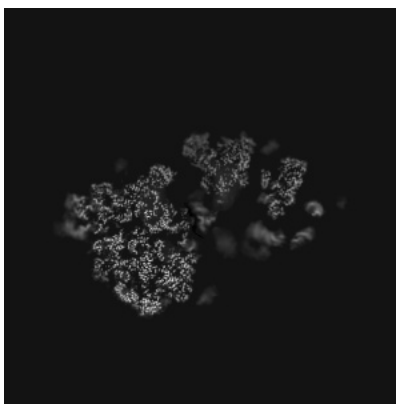
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

5.3.1 Primary map



X Index: 327



Y Index: 336

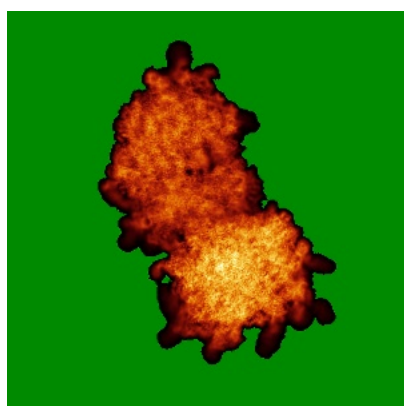


Z Index: 231

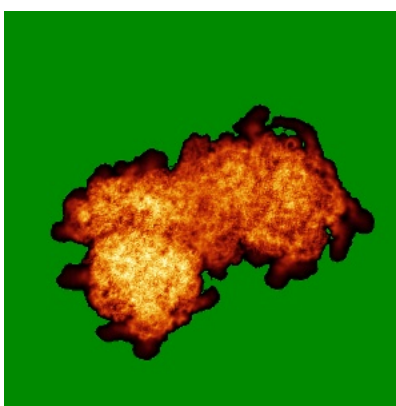
The images above show the largest variance slices of the map in three orthogonal directions.

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

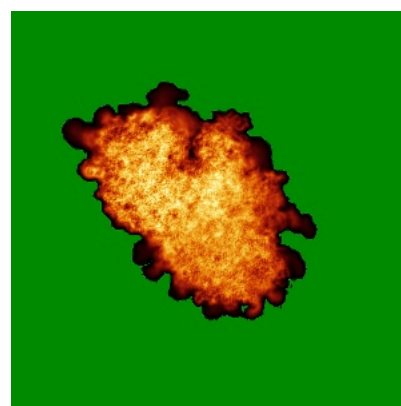
5.4.1 Primary map



X



Y

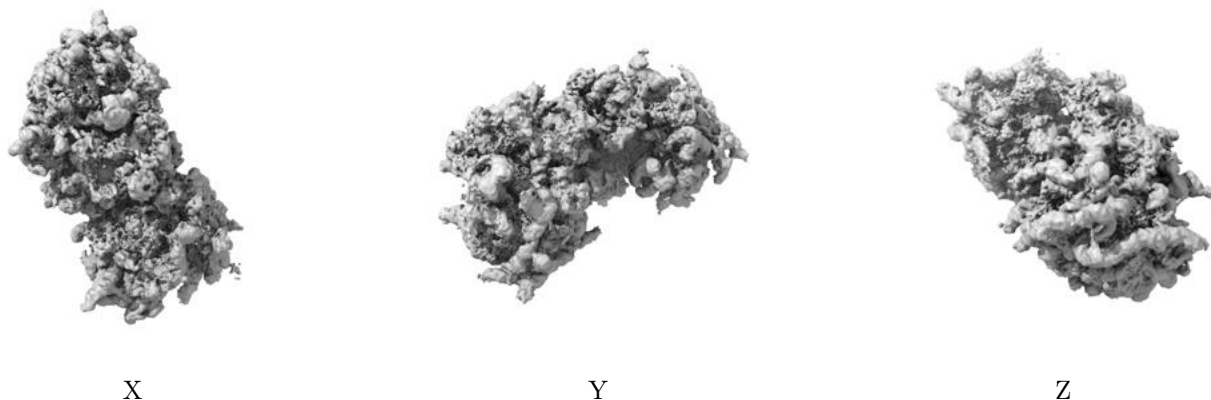


Z

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.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

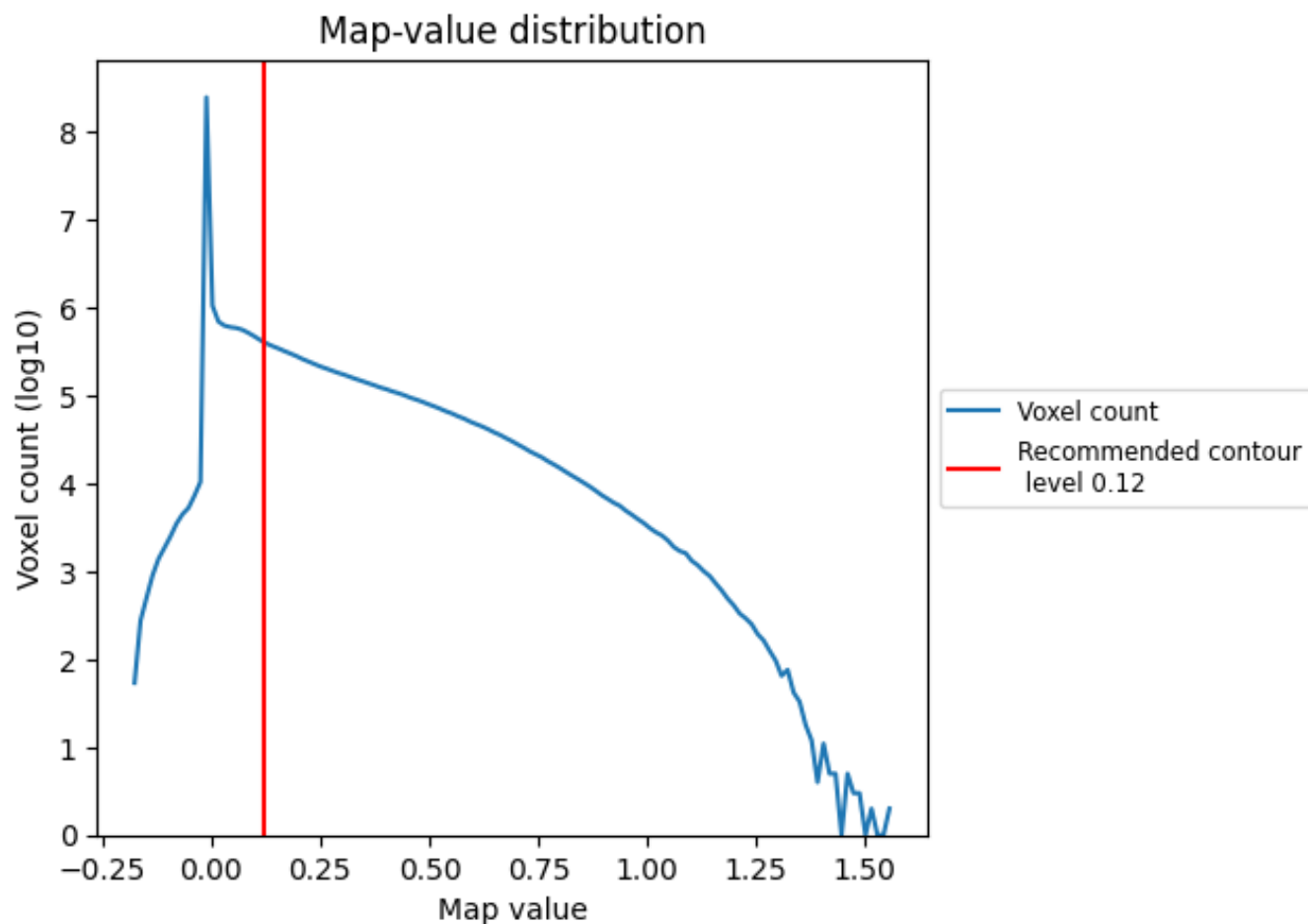
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

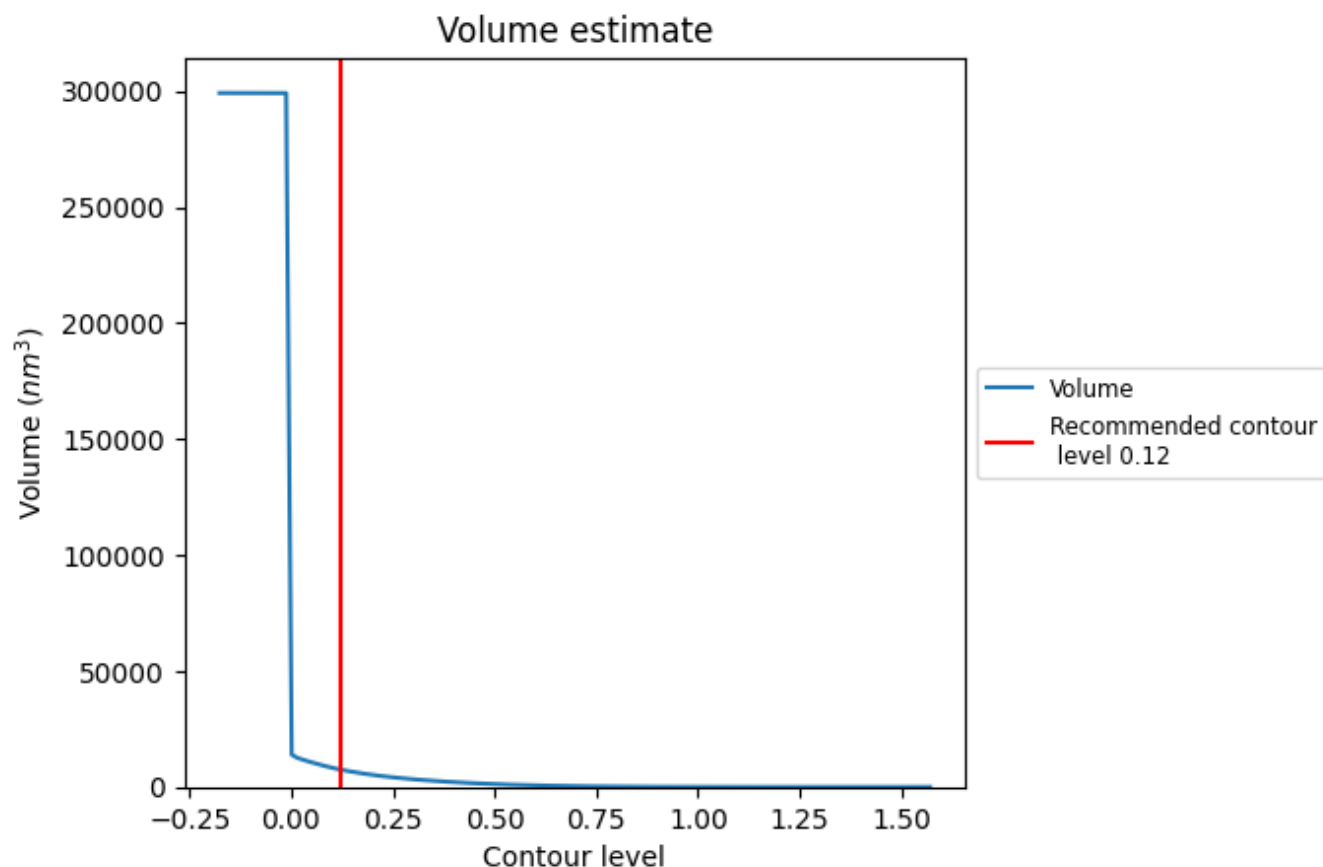
This section contains the results of statistical analysis of the map.

6.1 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.

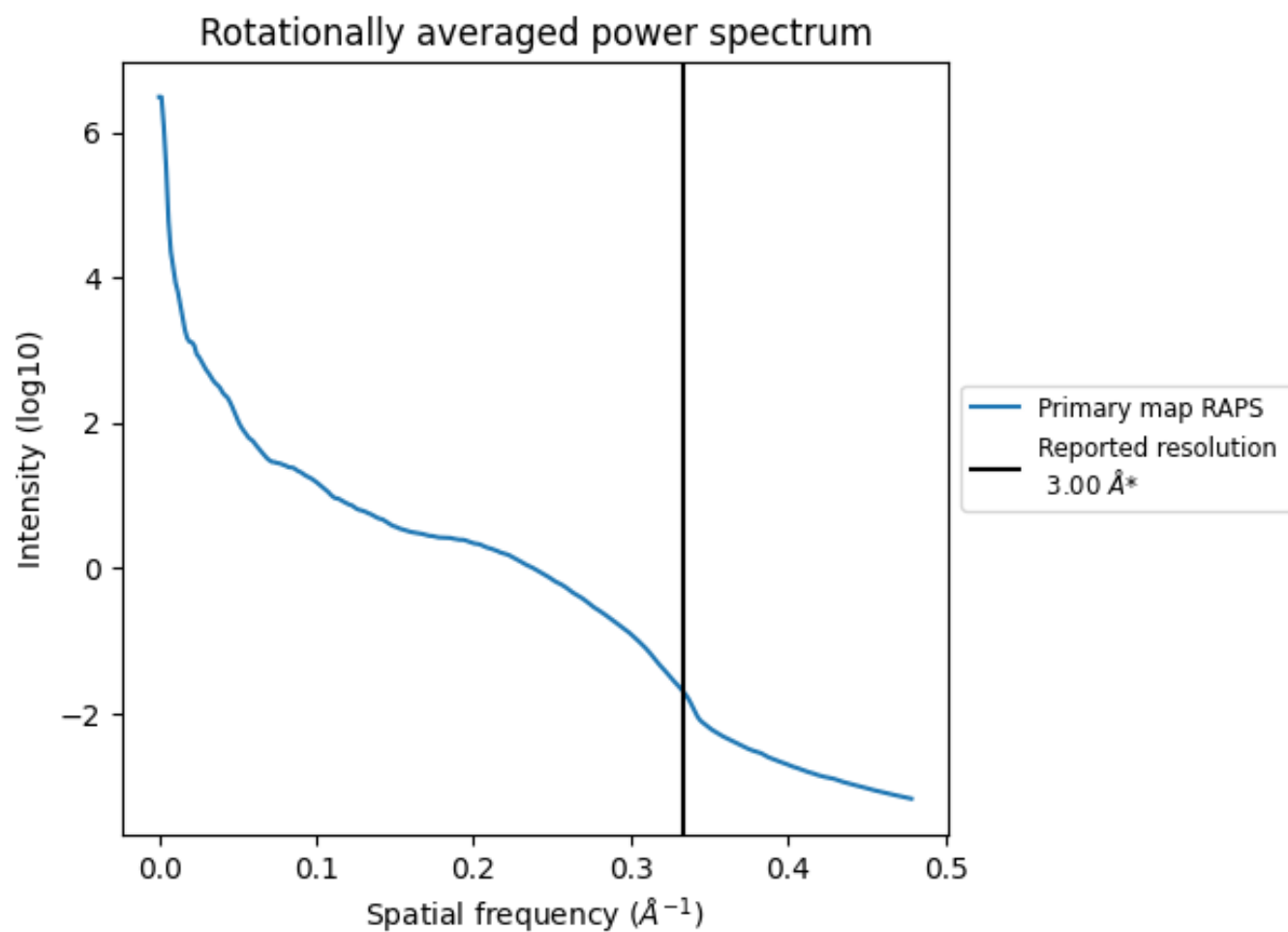
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 7521 nm³; this corresponds to an approximate mass of 6794 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.

6.3 Rotationally averaged power spectrum ⓘ

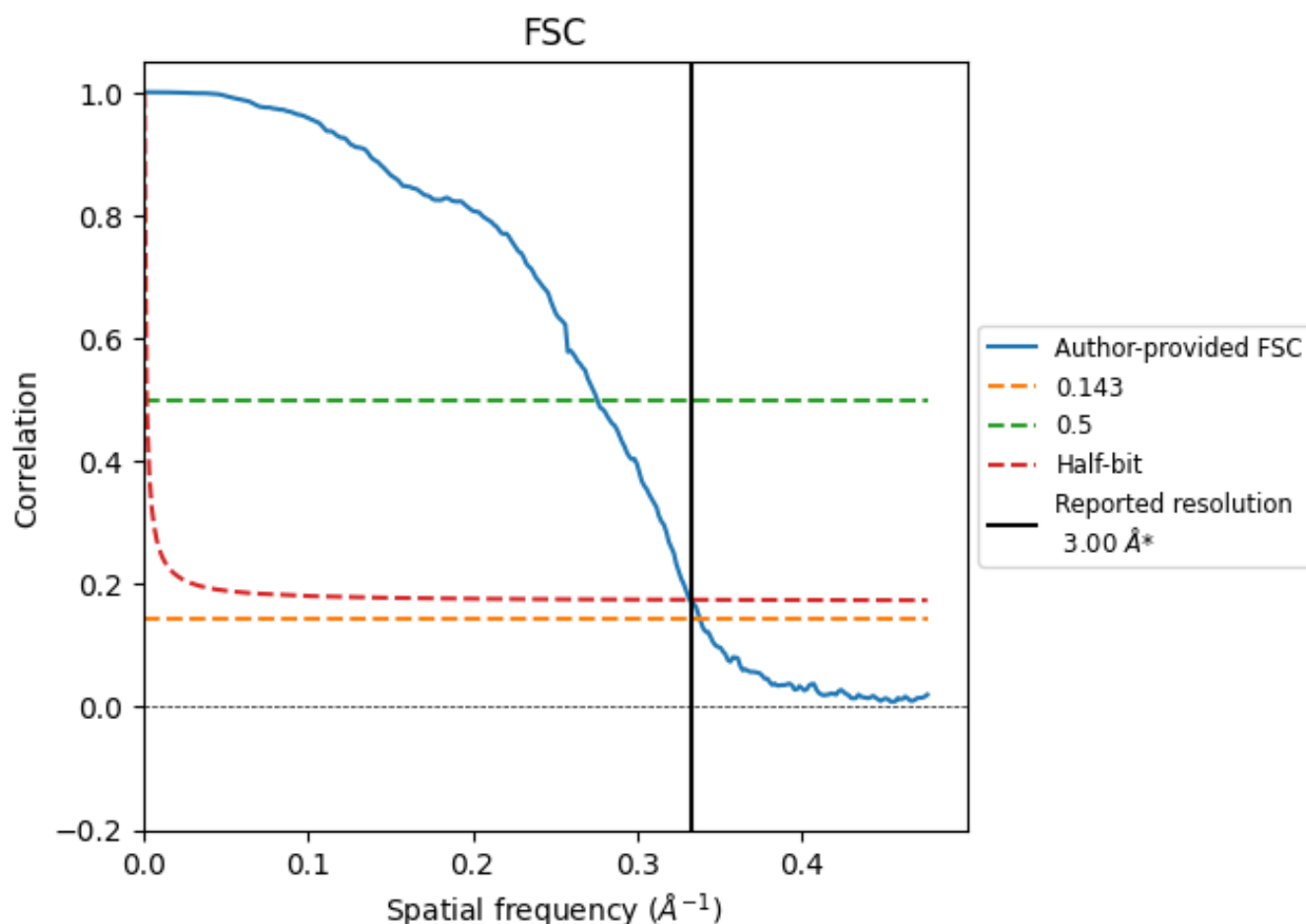


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

7 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.

7.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

7.2 Resolution estimates [i](#)

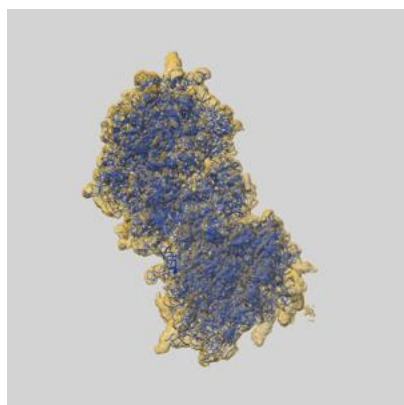
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.96	3.63	3.01
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

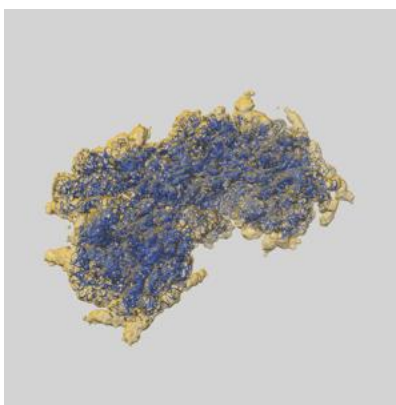
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14181 and PDB model 7QVP. Per-residue inclusion information can be found in section ?? on page ??.

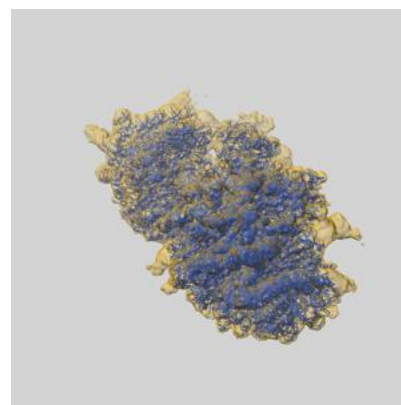
8.1 Map-model overlay [i](#)



X



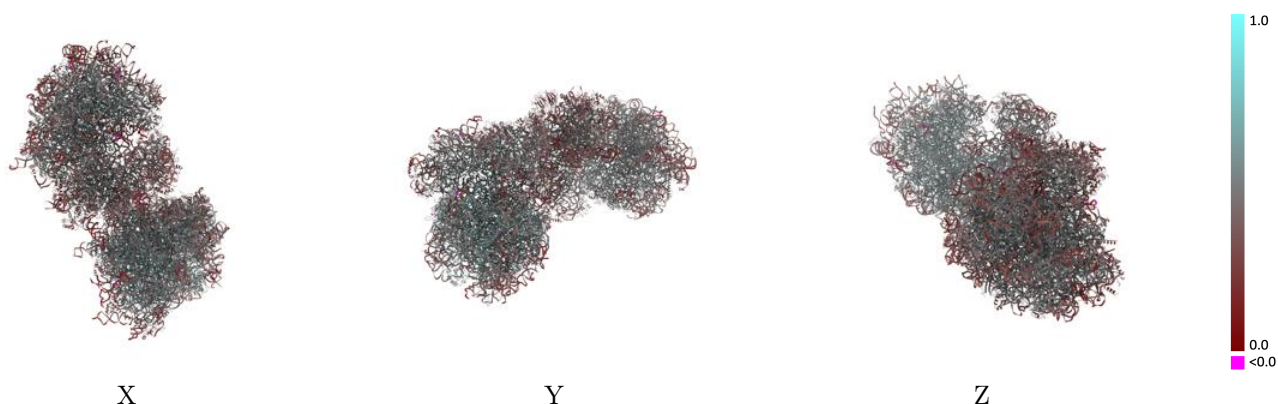
Y



Z

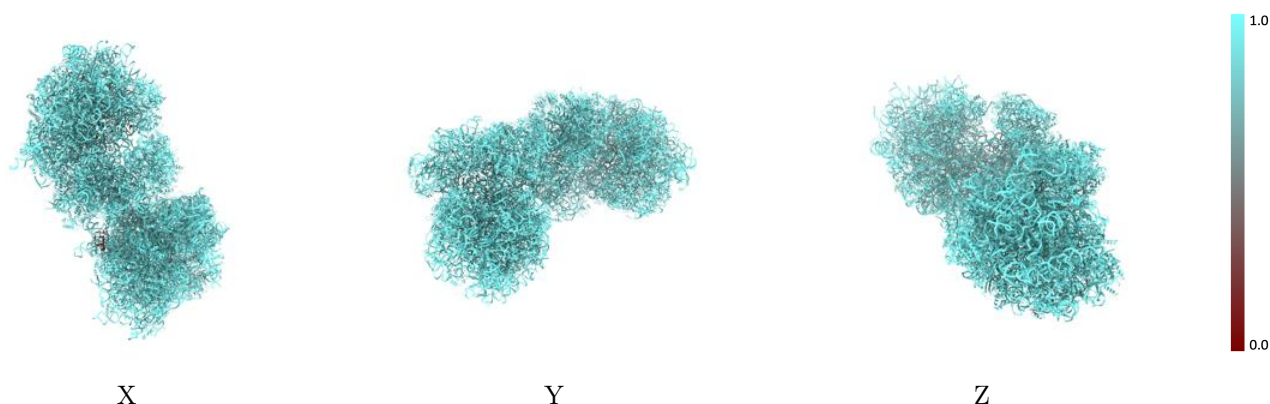
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



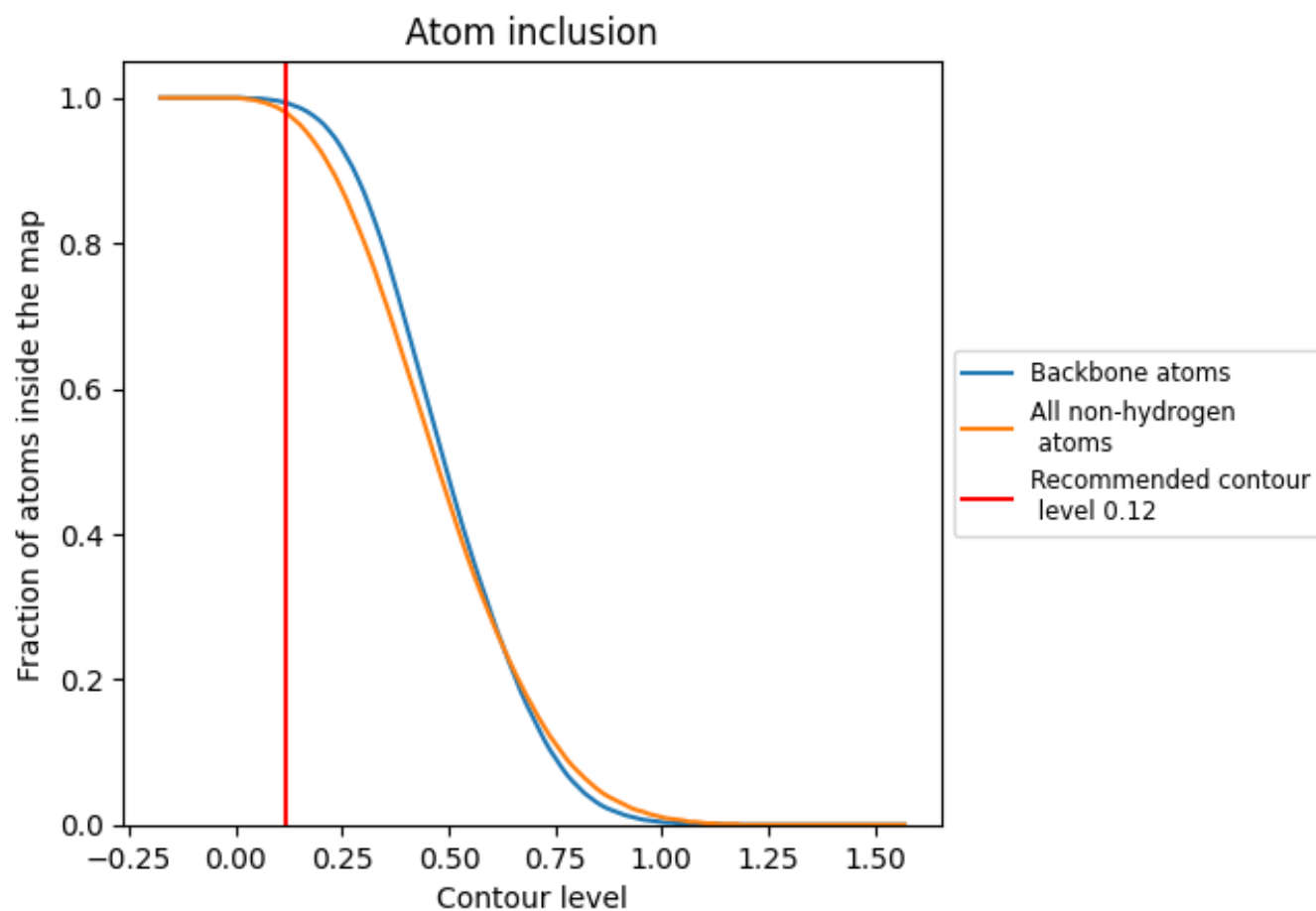
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 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 (0.12).

8.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9790	 0.4490
A4	 0.8540	 0.3350
A5	 0.9860	 0.3950
B4	 0.9830	 0.4260
B5	 0.9860	 0.3010
CC	 0.8660	 0.2510
D5	 0.7960	 0.1770
L1	 0.9870	 0.4450
L5	 0.9970	 0.4900
L6	 0.9910	 0.4420
L7	 1.0000	 0.5190
L8	 0.9930	 0.4970
L9	 0.9990	 0.4420
LA	 0.9840	 0.5510
LB	 0.9830	 0.5220
LC	 0.9850	 0.5210
LD	 0.9960	 0.4660
LE	 0.9880	 0.4810
LF	 0.9830	 0.5130
LG	 0.9540	 0.4520
LH	 0.9860	 0.4930
LI	 0.9760	 0.5120
LJ	 0.9770	 0.4570
LL	 0.9740	 0.5010
LM	 0.9910	 0.4810
LN	 0.9850	 0.5500
LO	 0.9890	 0.5220
LP	 0.9840	 0.5360
LQ	 0.9830	 0.5380
LR	 0.9830	 0.4920
LS	 0.9930	 0.5330
LT	 0.9720	 0.5030
LU	 0.9860	 0.4480
LV	 0.9780	 0.5380
LW	 0.9730	 0.4080



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Chain	Atom inclusion	Q-score
LX	 0.9800	 0.5070
LY	 0.9900	 0.4970
LZ	 0.9920	 0.4820
La	 0.9900	 0.5360
Lb	 0.9480	 0.4570
Lc	 0.9660	 0.4990
Ld	 0.9780	 0.5040
Le	 0.9800	 0.5450
Lf	 0.9830	 0.5460
Lg	 0.9670	 0.5120
Lh	 0.9750	 0.4760
Li	 0.9680	 0.4760
Lj	 0.9930	 0.5360
Lk	 0.9660	 0.4500
Ll	 0.9670	 0.5220
Lm	 0.9760	 0.5050
Ln	 0.9670	 0.5420
Lo	 0.9560	 0.5180
Lp	 0.9620	 0.5210
Lr	 0.9880	 0.5200
MA	 0.8940	 0.4880
MB	 0.9550	 0.4770
MC	 0.9370	 0.4690
MD	 0.9830	 0.4140
ME	 0.9810	 0.4330
MF	 0.9230	 0.4560
MG	 0.9480	 0.3970
MH	 0.9470	 0.4350
MI	 0.9410	 0.4500
MJ	 0.9730	 0.4280
ML	 0.9410	 0.4440
MM	 0.9670	 0.4310
MN	 0.9210	 0.4970
MO	 0.9220	 0.4660
MP	 0.9550	 0.4920
MQ	 0.9150	 0.4880
MR	 0.9430	 0.4210
MS	 0.9540	 0.4810
MT	 0.9260	 0.4530
MU	 0.9810	 0.3800
MV	 0.9150	 0.4870
MW	 0.8780	 0.3850

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Chain	Atom inclusion	Q-score
MX	 0.9270	 0.4360
MY	 0.9690	 0.4400
MZ	 0.9690	 0.4350
Ma	 0.9470	 0.4820
Mb	 0.9360	 0.4500
Mc	 0.9460	 0.4250
Md	 0.9390	 0.4540
Me	 0.9070	 0.4890
Mf	 0.9520	 0.4910
Mg	 0.9000	 0.4680
Mh	 0.9500	 0.4280
Mi	 0.9520	 0.4110
Mj	 0.9430	 0.5000
Mk	 0.9480	 0.3940
Ml	 0.8500	 0.4650
Mm	 0.9420	 0.4720
Mn	 0.8520	 0.3940
Mo	 0.9360	 0.4780
Mp	 0.8930	 0.4930
Mr	 0.9630	 0.4740
RA	 0.9860	 0.3930
RB	 0.9540	 0.4130
RC	 0.9490	 0.4300
RD	 0.9230	 0.3520
RE	 0.9270	 0.3620
RF	 0.9210	 0.3530
RG	 0.9540	 0.3130
RH	 0.9710	 0.3220
RI	 0.9500	 0.3380
RJ	 0.9160	 0.3250
RK	 0.9220	 0.2950
RL	 0.9320	 0.3920
RN	 0.9150	 0.3670
RO	 0.9210	 0.3980
RP	 0.9670	 0.3710
RQ	 0.9260	 0.3500
RR	 0.9580	 0.3350
RS	 0.9620	 0.3640
RT	 0.9680	 0.3550
RU	 0.9160	 0.3300
RV	 0.9600	 0.4210
RW	 0.9710	 0.3980

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Chain	Atom inclusion	Q-score
RX	 0.9850	 0.4020
RY	 0.9360	 0.3000
RZ	 0.9600	 0.2930
Ra	 0.9730	 0.4230
Rb	 0.9840	 0.3760
Rc	 0.9190	 0.3660
Rd	 0.9280	 0.3820
Re	 0.8960	 0.3560
Rf	 0.9790	 0.2200
Rg	 0.9800	 0.2750
Rh	 0.9850	 0.2510
S2	 0.9970	 0.4600
S3	 0.9810	 0.3930
SA	 0.9840	 0.4550
SB	 0.9230	 0.4720
SC	 0.9860	 0.4890
SD	 0.9760	 0.4260
SE	 0.9900	 0.4710
SF	 0.9590	 0.4180
SG	 0.9950	 0.3960
SH	 0.9920	 0.4360
SI	 0.9880	 0.4840
SJ	 0.9850	 0.4520
SK	 0.9850	 0.3710
SL	 0.9720	 0.5210
SN	 0.9630	 0.4870
SO	 0.9600	 0.5020
SP	 0.9880	 0.4060
SQ	 0.9780	 0.4370
SR	 0.9730	 0.4260
SS	 0.9850	 0.4190
ST	 0.9880	 0.4130
SU	 0.9970	 0.4220
SV	 0.9900	 0.4700
SW	 0.9850	 0.5060
SX	 0.9780	 0.5110
SY	 0.9880	 0.4140
SZ	 0.9710	 0.3980
Sa	 0.9770	 0.5030
Sb	 0.9640	 0.4480
Sc	 0.9430	 0.4460
Sd	 0.9810	 0.4560

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Chain	Atom inclusion	Q-score
Se	 0.9470	 0.4330
Sg	 0.9740	 0.3650