Full wwPDB EM Validation Report

Aug 30, 2023 – 05:11 am BST

PDB ID	:	8P60
EMDB ID	:	EMD-17457
Title	:	Spraguea lophii ribosome dimer
Authors	:	Gil Diez, P.; McLaren, M.; Isupov, M.N.; Daum, B.; Conners, R.; Williams, B.
Deposited on	:	2023-05-24
Resolution	:	14.30 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

EMDB validation analysis	:	0.0.1.dev50
MolProbity	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 14.30 Å.

There are no overall percentile quality scores available for this entry.

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

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 343629 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 RNA 28S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L50	2499	Total 53655	C 23950	N 9876	O 17330	P 2499	0	0
1	K50	2499	Total 53655	C 23950	N 9876	O 17330	P 2499	0	0

- Molecule 2 is a RNA chain called RNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L70	119	Total 2542	C 1136	N 459	O 828	P 119	0	0
2	K70	119	Total 2542	C 1136	N 459	O 828	P 119	0	0

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LA0	245	Total 1889	C 1189	N 361	O 334	S 5	0	0
3	KA0	245	Total 1889	C 1189	N 361	O 334	S 5	0	0

- Molecule 4 is a protein called Ribosomal protein L18e/L15P.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LAA	147	Total 1167	C 738	N 229	O 194	S 6	0	0
4	KAA	147	Total 1167	C 738	N 229	O 194	S 6	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		
5	KB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		
6	KC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		
7	KCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		
8	KD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		

- Molecule 9 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		
9	KDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	KE0	165	Total 1371	C 879	N 227	O 262	S 3	0	0

- Molecule 11 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LEE	135	Total 1090	C 697	N 205	O 182	S 6	0	0
11	KEE	135	Total 1090	C 697	N 205	O 182	S 6	0	0

- Molecule 12 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LF0	231	Total 1933	C 1234	N 342	O 350	S 7	0	0
12	KF0	231	Total 1933	C 1234	N 342	O 350	S 7	0	0

- Molecule 13 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LFF	111	Total 893	C 567	N 159	O 162	S 5	0	0
13	KFF	111	Total 893	C 567	N 159	O 162	S 5	0	0

- Molecule 14 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG0	199	Total 1590	C 1015	N 275	O 290	S 10	0	0
14	KG0	199	Total 1590	C 1015	N 275	O 290	S 10	0	0

- Molecule 15 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LGG	104	Total 819	C 504	N 169	O 139	S 7	0	0
15	KGG	104	Total 819	C 504	N 169	O 139	S 7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		
16	KH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		

- Molecule 17 is a protein called Ribosomal L29 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		
17	KHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		

- Molecule 18 is a protein called S60 ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		
18	KI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		

- Molecule 19 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		
19	KII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		

- Molecule 20 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		
20	KJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		

- Molecule 21 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		
21	KJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		

- Molecule 22 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		
22	KL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		

- Molecule 23 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		
23	KLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		

- Molecule 24 is a protein called Transposase.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		
24	KM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		

- Molecule 25 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		
25	KMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		

- Molecule 26 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	KN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

- Molecule 27 is a protein called Ribosomal protein L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		
27	KO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		

- Molecule 28 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		
28	KOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		

- Molecule 29 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		
29	KP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		

- Molecule 30 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		
30	KPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		

- Molecule 31 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		
31	KQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		

- Molecule 32 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		
32	KR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		

- Molecule 33 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		
33	KS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		

- Molecule 34 is a protein called 60s ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		
34	KT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		

- Molecule 35 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		
35	KU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		

- Molecule 36 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		
36	KV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		

- Molecule 37 is a protein called Ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		
37	KW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		

- Molecule 38 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		
38	KX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		

- Molecule 39 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		
39	KY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		

- Molecule 40 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		
40	KZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		

- Molecule 41 is a protein called DNL-type domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	MD1	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		
41	MD2	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		

- Molecule 42 is a RNA chain called RNA 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S60	1354	Total	C	N	O	P	0	0
			29181	13024	5463	9340	1354		

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Mol	Chain	Residues	Atoms					AltConf	Trace
42	R60	1354	Total 29181	C 13024	N 5463	O 9340	P 1354	0	0

- Molecule 43 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SA0	220	Total 1725	C 1091	N 292	O 328	S 14	0	0
43	RA0	220	Total 1725	C 1091	N 292	O 328	S 14	0	0

- Molecule 44 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SAA	101	Total 827	C 513	N 163	O 145	S 6	0	0
44	RAA	101	Total 827	C 513	N 163	O 145	S 6	0	0

- Molecule 45 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SB0	204	Total 1609	C 1018	N 286	O 298	S 7	0	0
45	RB0	204	Total 1609	C 1018	N 286	O 298	S 7	0	0

- Molecule 46 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SBB	81	Total 627	C 394	N 108	O 116	S 9	0	0
46	RBB	81	Total 627	C 394	N 108	O 116	S 9	0	0

- Molecule 47 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC0	226	Total 1727	C 1099	N 300	O 321	S 7	0	0
47	RC0	226	Total 1727	C 1099	N 300	O 321	S 7	0	0

- Molecule 48 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		
48	RCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		
49	RD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		

- Molecule 50 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		
50	RDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		
51	RE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		

- Molecule 52 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	SEE	56	Total	C	N	O	0	0
			447	284	89	74		
52	REE	56	Total	C	N	O	0	0
			447	284	89	74		

- Molecule 53 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		
53	RF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		

- Molecule 54 is a protein called Ubiquitin/40s ribosomal protein S27a fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SFF	58	Total	C	N	O	S	0	0
			422	261	77	79	5		
54	RFF	58	Total	C	N	O	S	0	0
			417	259	74	79	5		

- Molecule 55 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SG0	229	Total	C	N	O	S	0	0
			1836	1179	325	328	4		
55	RG0	229	Total	C	N	O	S	0	0
			1836	1179	325	328	4		

- Molecule 56 is a protein called Guanine nucleotide binding protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		
56	RGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		
57	RH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	RI0	167	Total 1347	C 834	N 266	O 240	S 7	0	0

- Molecule 59 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ0	168	Total 1379	C 880	N 252	O 243	S 4	0	0
59	RJ0	168	Total 1379	C 880	N 252	O 243	S 4	0	0

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK0	88	Total 737	C 472	N 127	O 135	S 3	0	0
60	RK0	88	Total 737	C 472	N 127	O 135	S 3	0	0

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL0	150	Total 1229	C 790	N 217	O 216	S 6	0	0
61	RL0	150	Total 1229	C 790	N 217	O 216	S 6	0	0

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SM0	113	Total 876	C 553	N 156	O 162	S 5	0	0
62	RM0	113	Total 876	C 553	N 156	O 162	S 5	0	0

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SN0	142	Total 1130	C 728	N 196	O 202	S 4	0	0
63	RN0	142	Total 1130	C 728	N 196	O 202	S 4	0	0

- Molecule 64 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		
64	RO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		

- Molecule 65 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		
65	RQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		

- Molecule 66 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		
66	RR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		

- Molecule 67 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		
67	RS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		

- Molecule 68 is a protein called 40S Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		
68	RT0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		

- Molecule 69 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		
69	RU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		

- Molecule 70 is a protein called Ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		
70	RV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		

- Molecule 71 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		
71	RW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		

- Molecule 72 is a protein called Ribosomal protein S12/S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		
72	RX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		

- Molecule 73 is a protein called 40s ribosomal protein s24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		
73	RY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		

- Molecule 74 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
74	RZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

- Molecule 75 is a protein called Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		
75	RP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		

- Molecule 76 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
76	LGG	1	Total	Zn	0
			1	1	
76	LJJ	1	Total	Zn	0
			1	1	
76	LMM	1	Total	Zn	0
			1	1	
76	LOO	1	Total	Zn	0
			1	1	
76	LPP	1	Total	Zn	0
			1	1	
76	SAA	1	Total	Zn	0
			1	1	
76	SBB	1	Total	Zn	0
			1	1	
76	SDD	1	Total	Zn	0
			1	1	
76	SFF	1	Total	Zn	0
			1	1	
76	KGG	1	Total	Zn	0
			1	1	
76	KJJ	1	Total	Zn	0
			1	1	
76	KMM	1	Total	Zn	0
			1	1	
76	KOO	1	Total	Zn	0
			1	1	
76	KPP	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
76	RAA	1	Total Zn 1 1	0
76	RBB	1	Total Zn 1 1	0
76	RDD	1	Total Zn 1 1	0
76	RFF	1	Total Zn 1 1	0

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

3 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of subtomograms used	1344	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 ($e^-/Å^2$)	120, 120	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.850	Depositor
Minimum map value	-1.211	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.118	Depositor
Recommended contour level	0.58	Depositor
Map size (Å)	772.8, 772.8, 772.8	wwPDB
Map dimensions	168, 168, 168	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	4.6, 4.6, 4.6	Depositor

4 Model quality

4.1 Standard geometry

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

4.2 Too-close contacts

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

4.3 Torsion angles

4.3.1 Protein backbone

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

4.3.2 Protein sidechains

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

4.3.3 RNA

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

4.4 Non-standard residues in protein, DNA, RNA chains

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

4.5 Carbohydrates

There are no monosaccharides in this entry.

4.6 Ligand geometry

Of 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

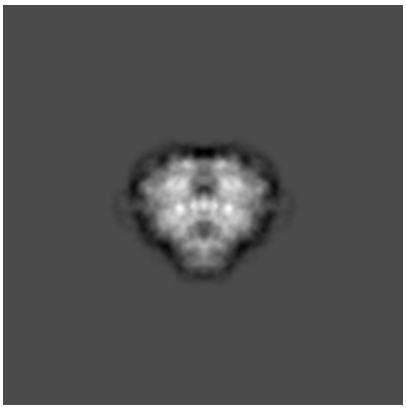
5 Map visualisation

This section contains visualisations of the EMDB entry EMD-17457. These allow visual inspection of the internal detail of the map and identification of artifacts.

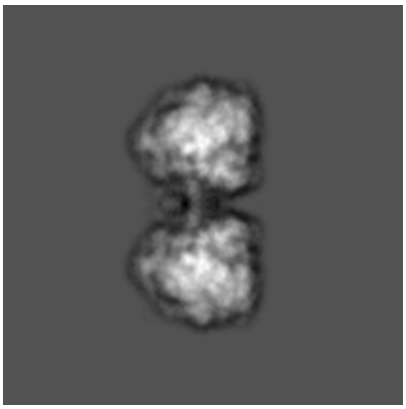
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections

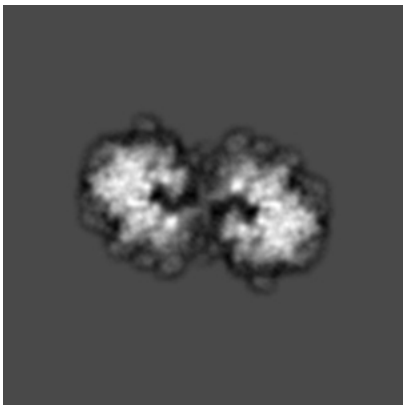
5.1.1 Primary map



X

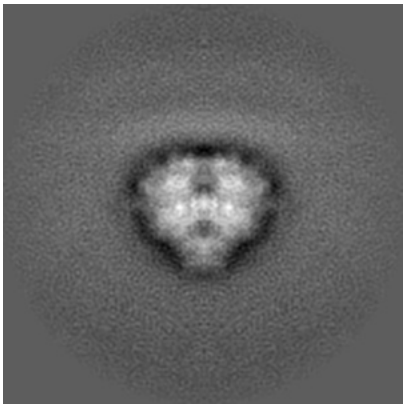


Y

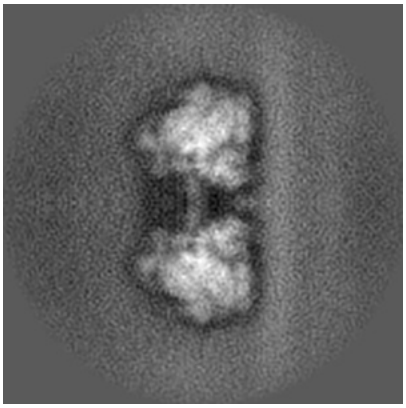


Z

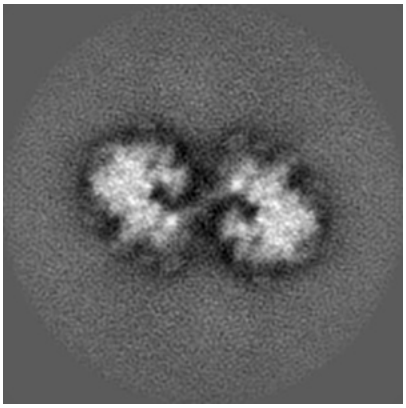
5.1.2 Raw map



X



Y



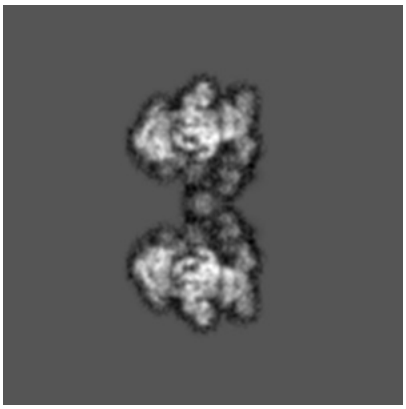
Z

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

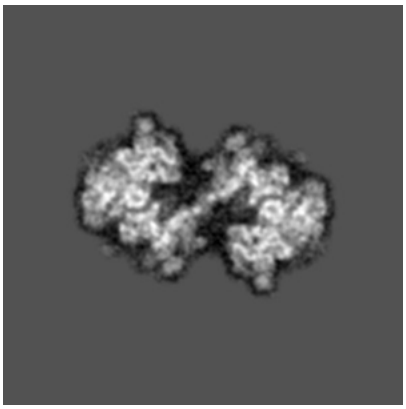
5.2 Central slices (i)

5.2.1 Primary map

X Index: 84

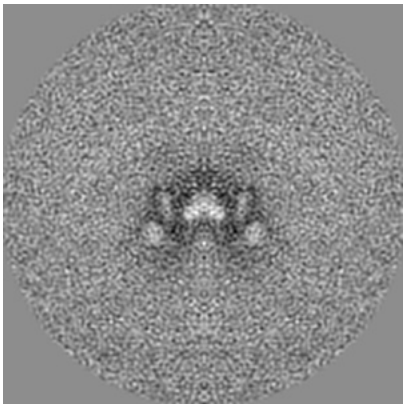


Y Index: 84

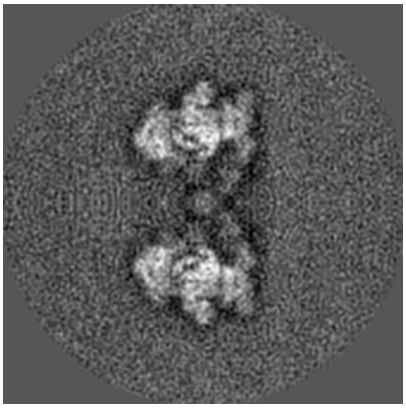


Z Index: 84

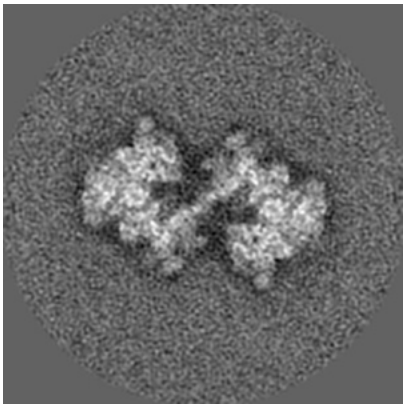
5.2.2 Raw map



X Index: 84



Y Index: 84

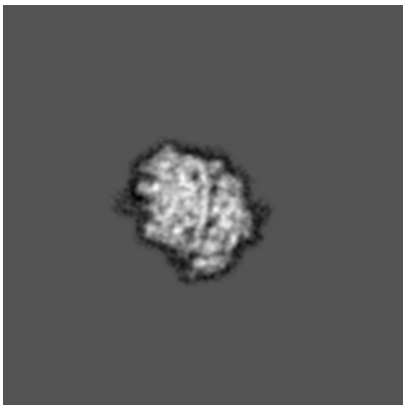


Z Index: 84

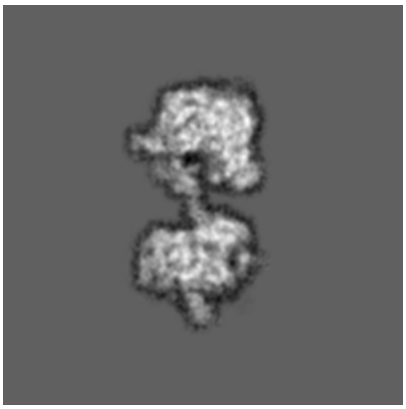
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices (i)

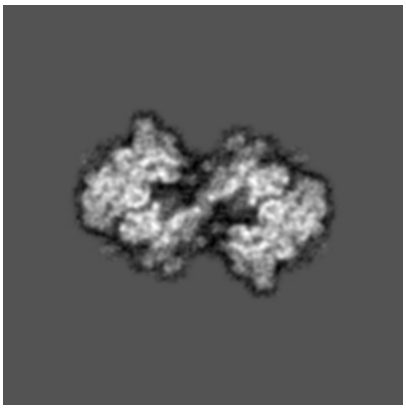
5.3.1 Primary map



X Index: 114

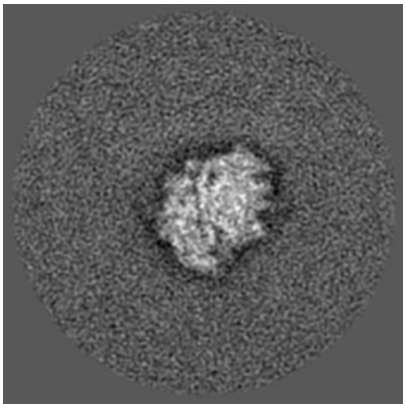


Y Index: 76

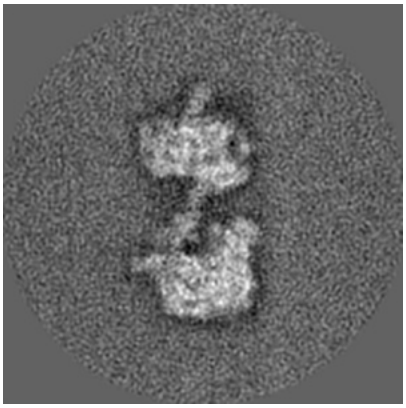


Z Index: 83

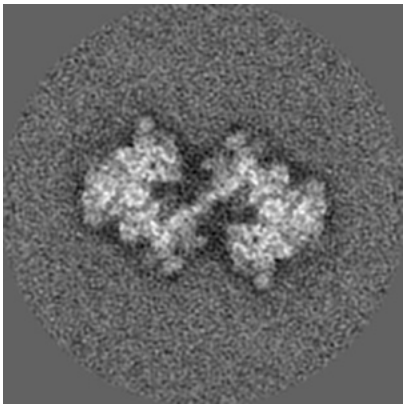
5.3.2 Raw map



X Index: 55



Y Index: 92

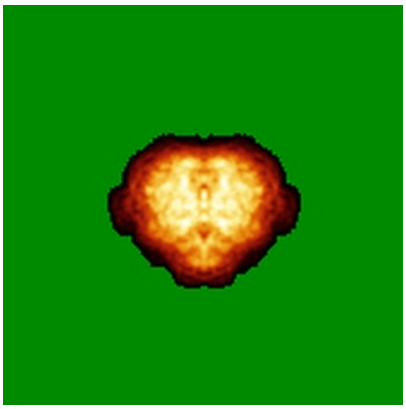


Z Index: 84

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

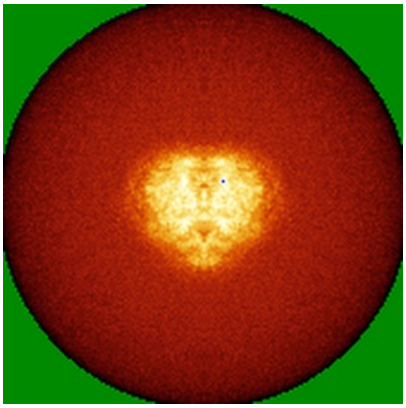


X

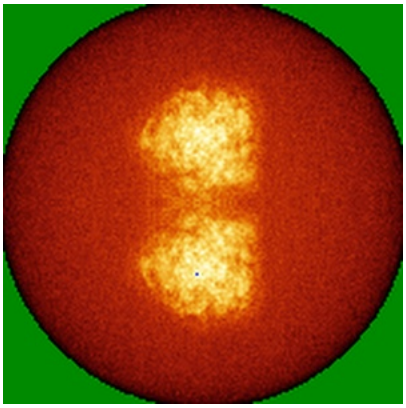
Y

Z

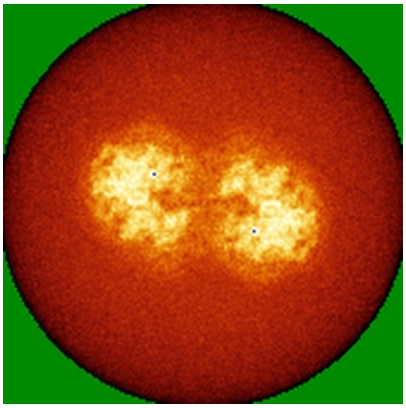
5.4.2 Raw map



X



Y

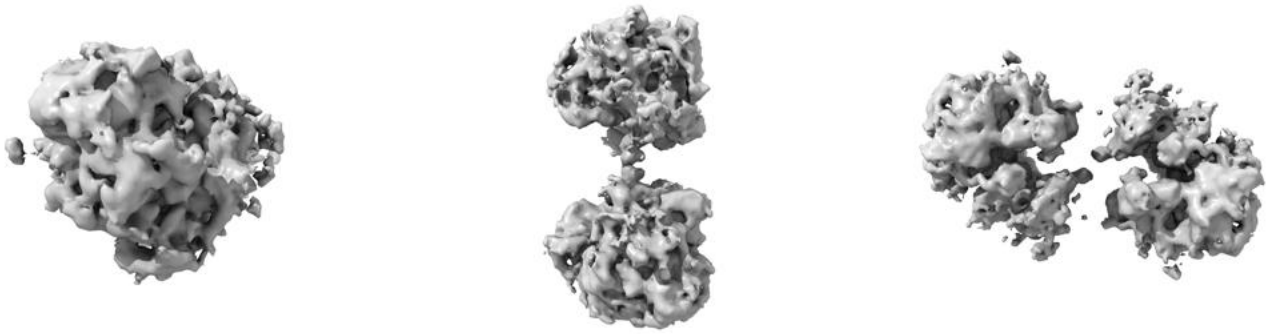


Z

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.

5.5 Orthogonal surface views (i)

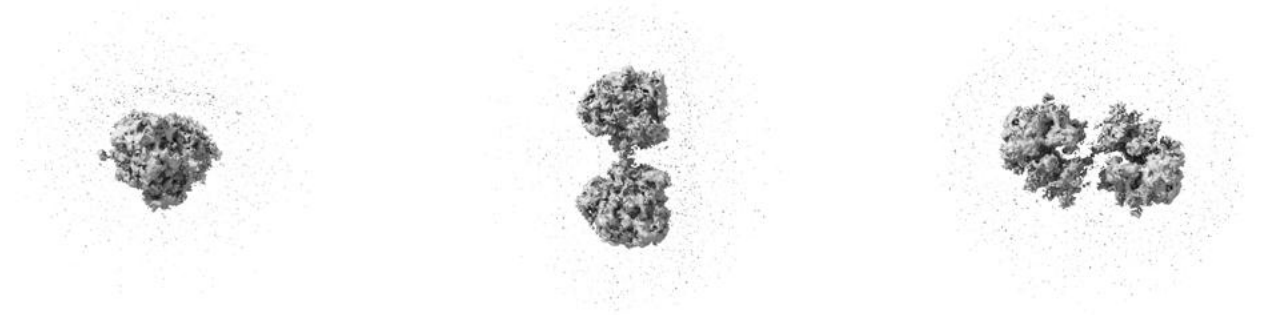
5.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.58. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

5.5.2 Raw map



X Y Z

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.

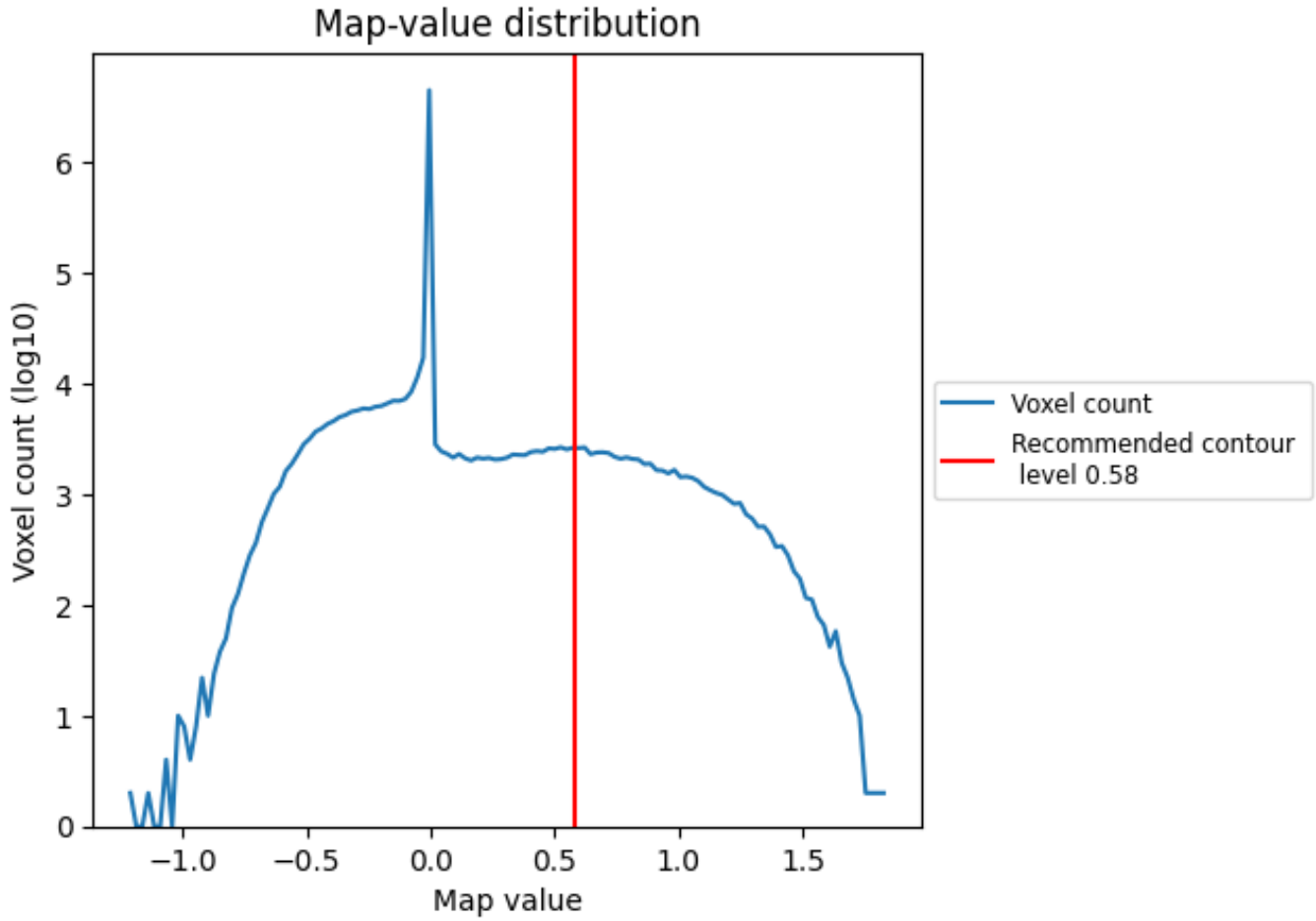
5.6 Mask visualisation (i)

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

6 Map analysis

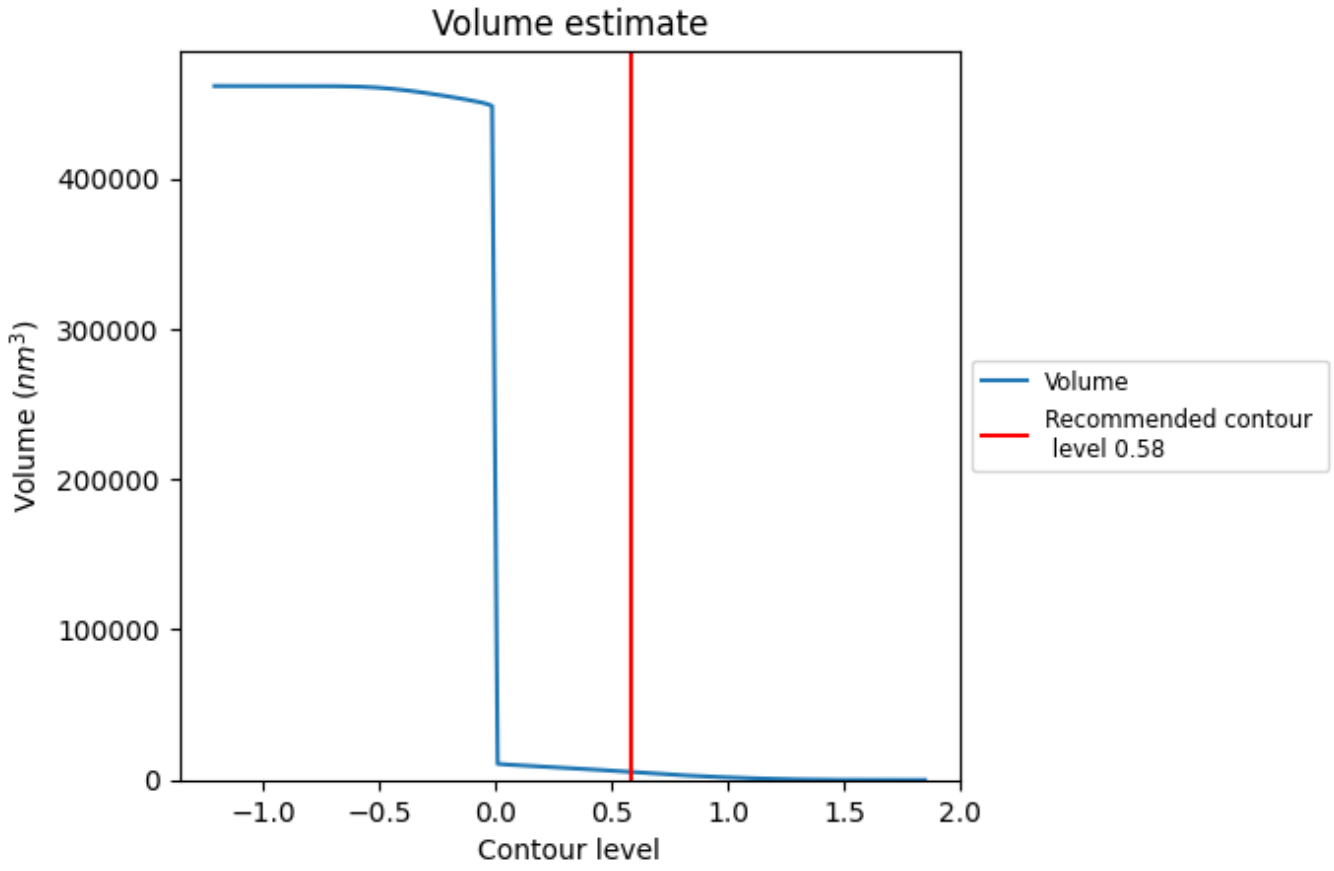
This section contains the results of statistical analysis of the map.

6.1 Map-value distribution



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.

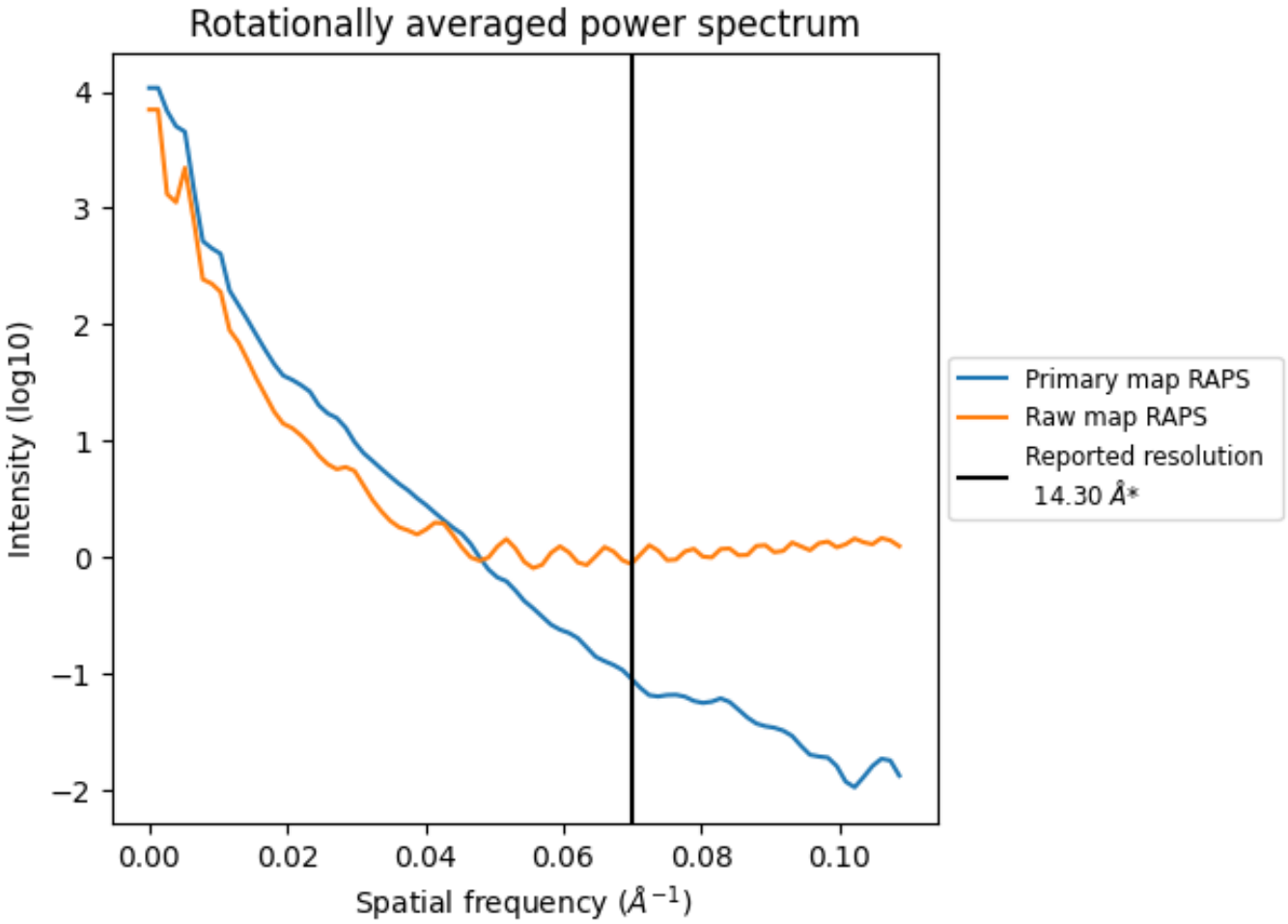
6.2 Volume estimate



The volume at the recommended contour level is 5294 nm^3; this corresponds to an approximate mass of 4782 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 (i)

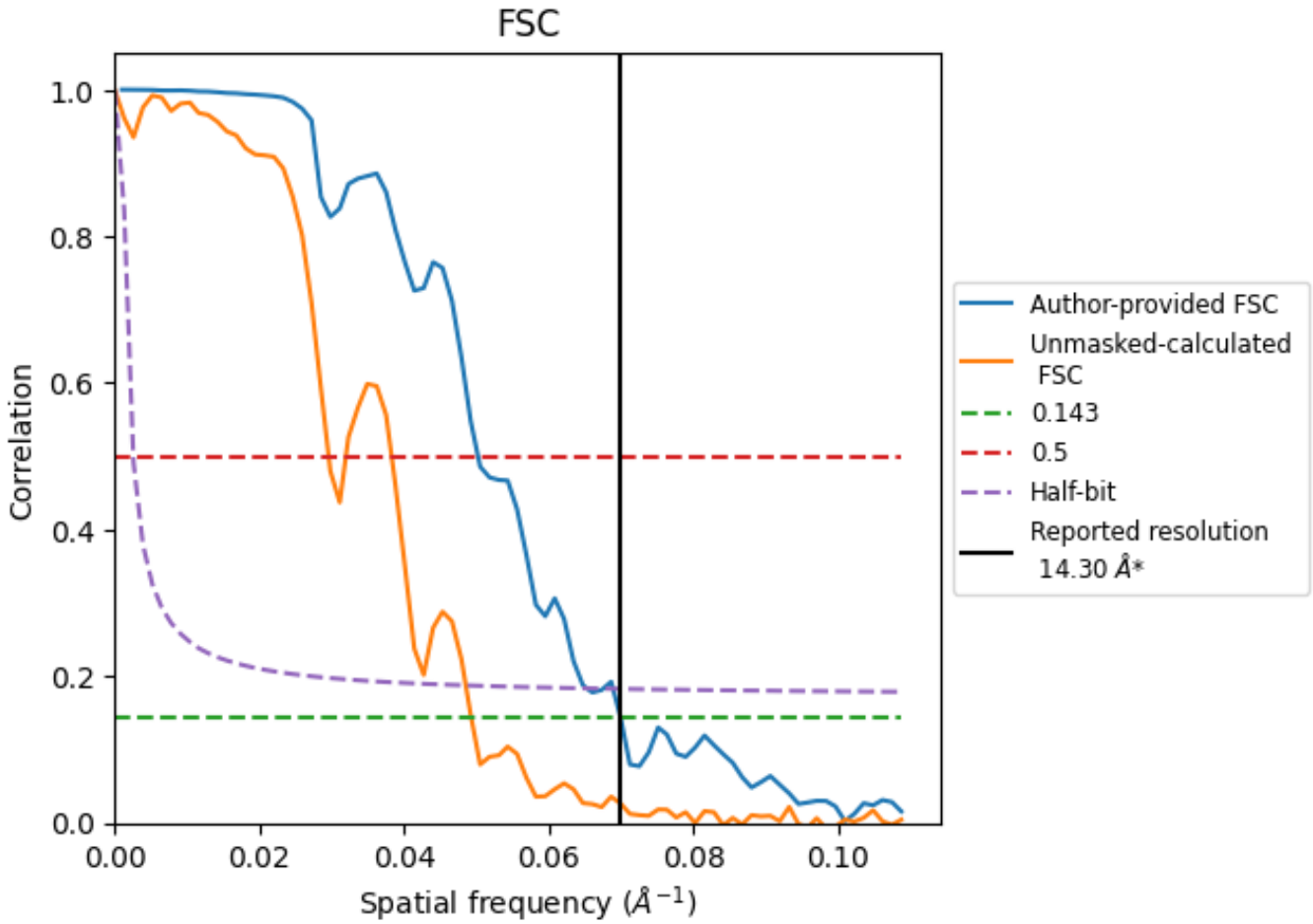


*Reported resolution corresponds to spatial frequency of 0.070 Å^{-1}

7 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.070 Å^{-1}

7.2 Resolution estimates (i)

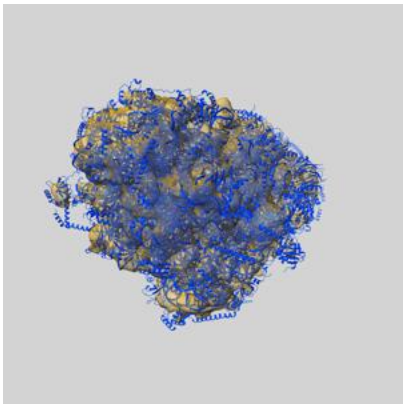
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	14.30	-	-
Author-provided FSC curve	14.31	19.92	15.31
Unmasked-calculated*	20.33	33.90	20.62

*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 20.33 differs from the reported value 14.3 by more than 10 %

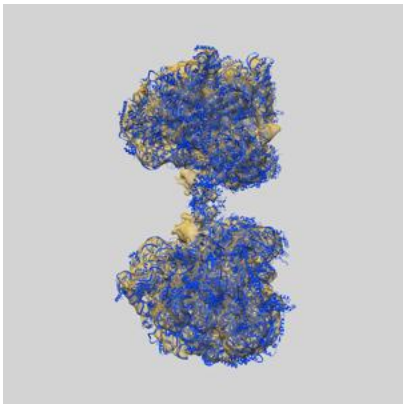
8 Map-model fit

This section contains information regarding the fit between EMDB map EMD-17457 and PDB model 8P60. Per-residue inclusion information can be found in section **??** on page **??**.

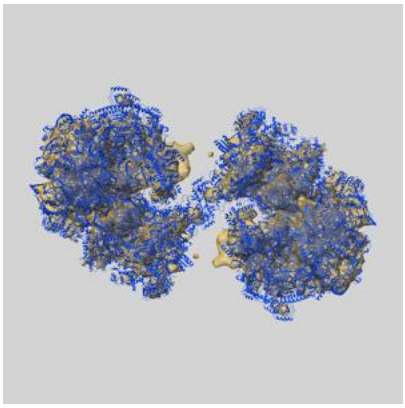
8.1 Map-model overlay



X



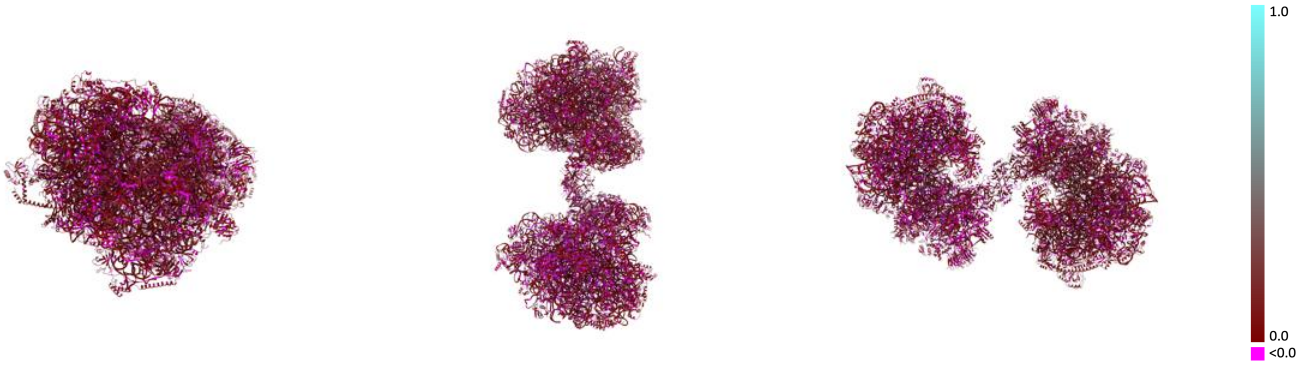
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.58 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.

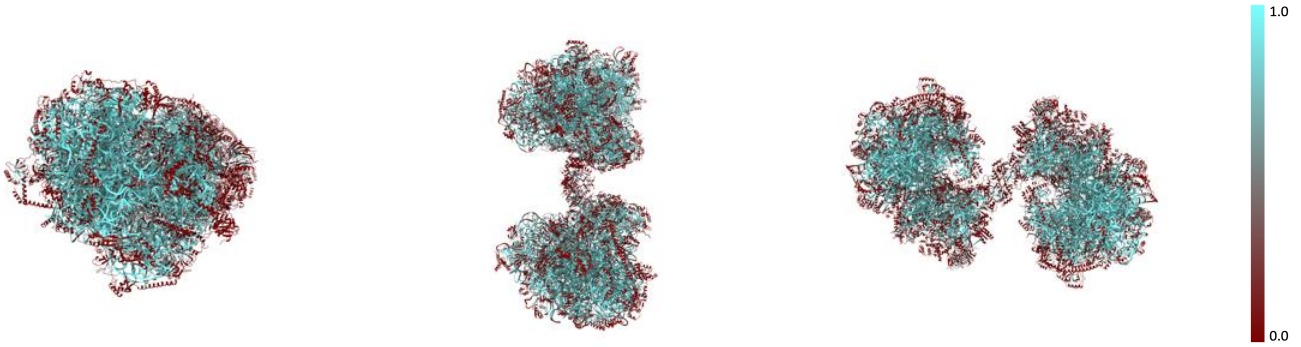
8.2 Q-score mapped to coordinate model (i)



X Y Z

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.

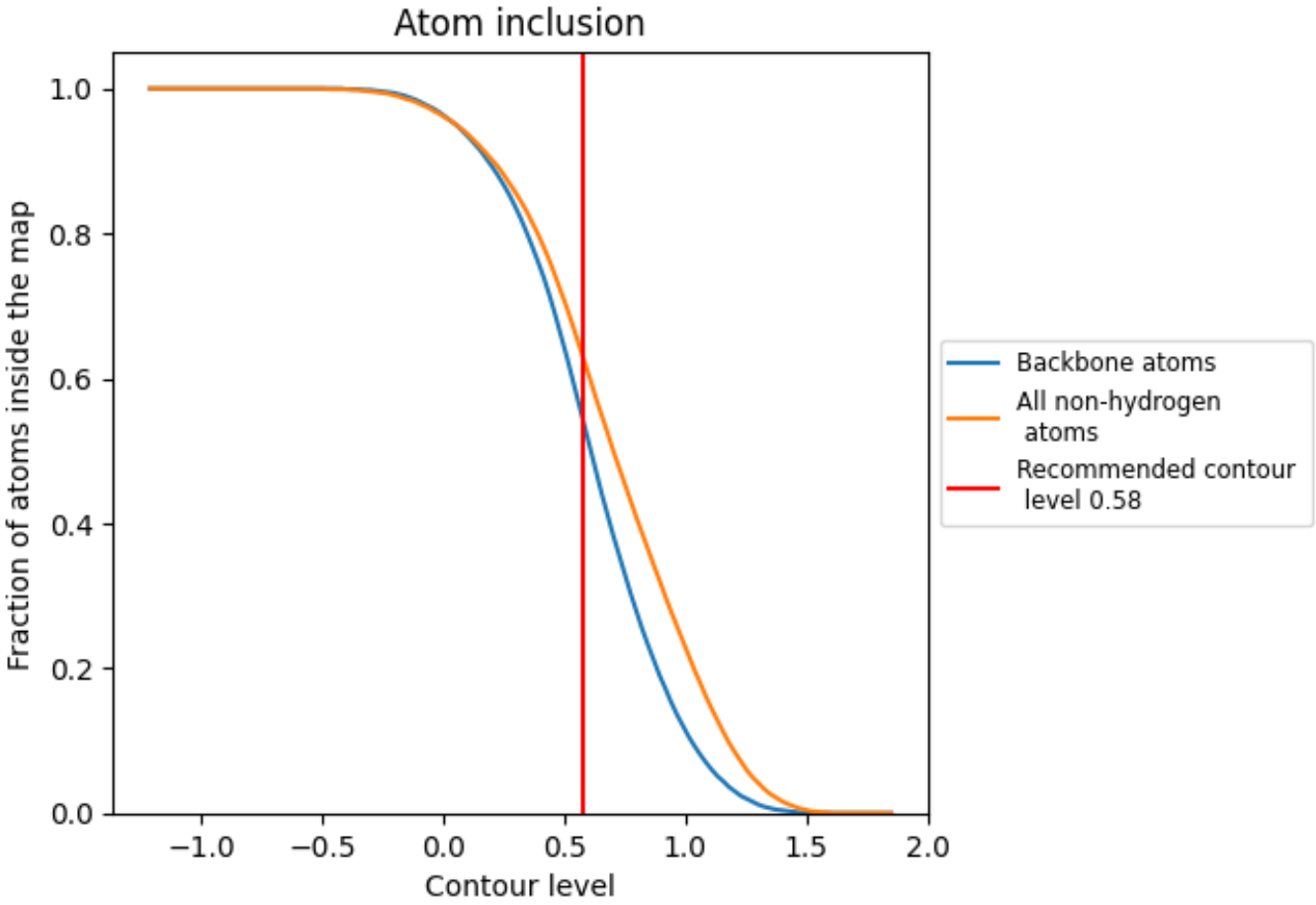
8.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.58).

8.4 Atom inclusion (i)



At the recommended contour level, 54% of all backbone atoms, 63% 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 (0.58) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6260	0.0540
K50	0.8580	0.0630
K70	0.7670	0.0610
KA0	0.5520	0.0200
KAA	0.6240	0.0140
KB0	0.5200	0.0110
KC0	0.4360	0.0230
KCC	0.2870	0.0540
KD0	0.3260	0.0420
KDD	0.4740	0.0260
KE0	0.1230	0.0420
KEE	0.4530	0.0270
KF0	0.3250	0.0420
KFF	0.2800	0.0500
KG0	0.2560	0.0580
KGG	0.5730	-0.0070
KH0	0.3900	0.0390
KHH	0.2960	0.0600
KI0	0.5110	-0.0030
KII	0.4200	0.0400
KJ0	0.3960	0.0380
KJJ	0.6830	-0.0100
KL0	0.4180	0.0410
KLL	0.6380	0.0030
KM0	0.0800	0.0500
KMM	0.6050	0.0210
KN0	0.9390	-0.0100
KO0	0.4170	0.0420
KOO	0.8010	0.0230
KP0	0.4330	0.0310
KPP	0.6120	0.0370
KQ0	0.3460	0.0270
KR0	0.4390	0.0290
KS0	0.2010	0.0370
KT0	0.3500	0.0200

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
KU0	0.2750	0.0620
KV0	0.6120	0.0110
KW0	0.4180	0.0120
KX0	0.4740	0.0360
KY0	0.3800	0.0290
KZ0	0.2300	0.0570
L50	0.9000	0.0850
L70	0.8660	0.0940
LA0	0.5590	0.0370
LAA	0.6880	0.0230
LB0	0.4720	0.0150
LC0	0.5420	0.0370
LCC	0.2740	0.0730
LD0	0.4090	0.0460
LDD	0.5280	0.0200
LE0	0.1580	0.0650
LEE	0.5620	0.0310
LF0	0.3910	0.0650
LFF	0.3930	0.0430
LG0	0.2280	0.0480
LGG	0.5520	-0.0050
LH0	0.3950	0.0480
LHH	0.3930	0.0350
LI0	0.4970	0.0350
LII	0.4230	0.0440
LJ0	0.3090	0.0450
LJJ	0.7950	0.0110
LL0	0.5090	0.0270
LLL	0.7060	-0.0100
LM0	0.0820	0.0860
LMM	0.4270	0.0060
LN0	0.9350	-0.0060
LO0	0.4440	0.0560
LOO	0.5440	0.0230
LP0	0.5800	0.0310
LPP	0.4830	0.0260
LQ0	0.4650	0.0530
LR0	0.4090	0.0300
LS0	0.3030	0.0660
LT0	0.4470	0.0340
LU0	0.2700	0.0550
LV0	0.4030	0.0280

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Chain	Atom inclusion	Q-score
LW0	0.2350	0.0290
LX0	0.4970	0.0050
LY0	0.3750	0.0250
LZ0	0.2290	0.0520
MD1	0.3180	0.0670
MD2	0.2550	0.0530
R60	0.8020	0.0570
RA0	0.1510	0.0330
RAA	0.5920	0.0270
RB0	0.3410	0.0420
RBB	0.3870	0.0380
RC0	0.3840	0.0320
RCC	0.4480	0.0420
RD0	0.2490	0.0300
RDD	0.5530	0.0150
RE0	0.4410	0.0280
REE	0.3780	0.0110
RF0	0.5270	0.0390
RFF	0.0000	0.0240
RG0	0.1790	0.0430
RGG	0.2130	0.0330
RH0	0.1090	0.0540
RI0	0.3660	0.0280
RJ0	0.5560	0.0190
RK0	0.1440	0.0310
RL0	0.3810	0.0260
RM0	0.1100	0.0270
RN0	0.4650	0.0160
RO0	0.5900	0.0200
RP0	0.1940	0.0270
RQ0	0.4880	0.0270
RR0	0.3250	0.0450
RS0	0.2330	0.0480
RT0	0.3610	0.0260
RU0	0.2610	0.0370
RV0	0.2720	0.0440
RW0	0.5430	-0.0050
RX0	0.1600	-0.0150
RY0	0.3650	0.0420
RZ0	0.2810	0.0740
S60	0.8830	0.0860
SA0	0.1240	0.0520

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Chain	Atom inclusion	Q-score
SAA	0.5660	0.0280
SB0	0.3380	0.0610
SBB	0.2980	0.0560
SC0	0.3530	0.0580
SCC	0.3280	0.0550
SD0	0.1760	0.0560
SDD	0.4240	0.0470
SE0	0.3410	0.0350
SEE	0.2550	0.0470
SF0	0.4790	0.0480
SFF	0.0260	0.0360
SG0	0.2580	0.0480
SGG	0.2120	0.0490
SH0	0.0650	0.0690
SI0	0.4710	0.0310
SJ0	0.3660	0.0420
SK0	0.1040	0.0580
SL0	0.3580	0.0360
SM0	0.0600	0.0490
SN0	0.4900	0.0320
SO0	0.5760	0.0340
SP0	0.3560	0.0630
SQ0	0.4150	0.0420
SR0	0.2010	0.0360
SS0	0.4100	0.0640
ST0	0.3710	0.0440
SU0	0.2500	0.0420
SV0	0.2680	0.0660
SW0	0.4280	0.0370
SX0	0.2780	0.0240
SY0	0.2830	0.0750
SZ0	0.2860	0.0740