



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 12:36 AM UTC

PDB ID : 8OJ5 / pdb_00008oj5
EMDB ID : EMD-16905
Title : 60S ribosomal subunit bound to the E3-UFM1 complex - state 3 (in-vitro reconstitution)
Authors : Penchev, I.; DaRosa, P.A.; Peter, J.J.; Kulathu, Y.; Becker, T.; Beckmann, R.; Kopito, R.
Deposited on : 2023-03-23
Resolution : 2.90 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:

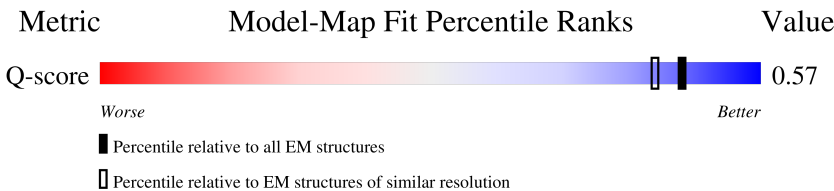
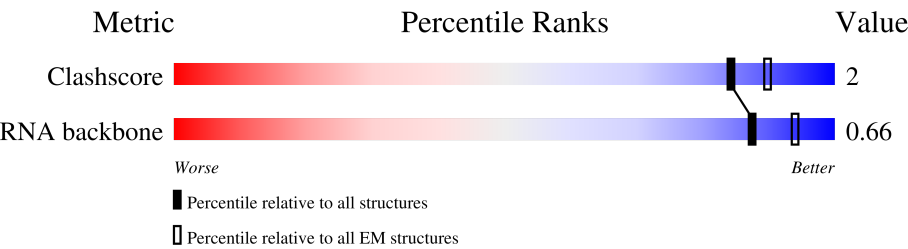
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	5	5070	56% 12% • 31%
2	7	121	85% 12% ••
3	8	157	78% 16% 6%
4	A	794	12% 77% 10% 13%
5	B	506	23% 74% 6% 20%

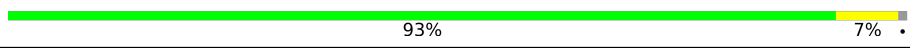
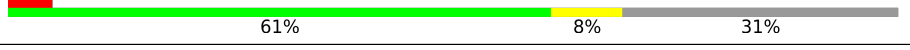
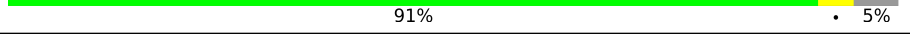
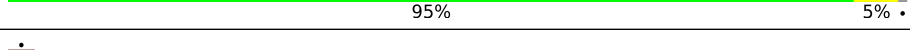
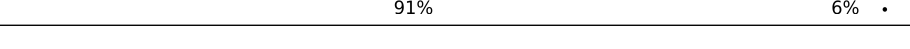
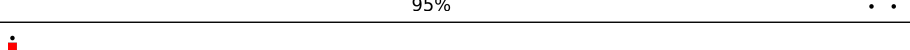
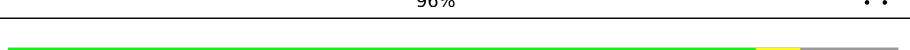
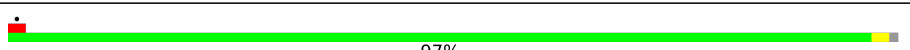
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Mol	Chain	Length	Quality of chain
6	C	314	
7	D	85	
8	LA	257	
9	LB	403	
10	LC	427	
11	LD	297	
12	LE	288	
13	LF	248	
14	LG	266	
15	LH	192	
16	LI	214	
17	LJ	178	
18	LL	211	
19	LM	215	
20	LN	204	
21	LO	203	
22	LP	184	
23	LQ	188	
24	LR	196	
25	LS	176	
26	LT	160	
27	LU	128	
28	LV	140	
29	LW	157	
30	LX	156	

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Mol	Chain	Length	Quality of chain
31	LY	145	
32	LZ	136	
33	La	148	
34	Lb	159	
35	Lc	115	
36	Ld	125	
37	Le	135	
38	Lf	110	
39	Lg	117	
40	Lh	123	
41	Li	105	
42	Lj	97	
43	Lk	70	
44	Ll	51	
45	Lm	128	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	Lz	217	

2 Entry composition [i](#)

There are 51 unique types of molecules in this entry. The entry contains 145041 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 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3474	Total	C	N	O	P	0	0
			74502	33181	13653	24195	3473		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	148	Total	C	N	O	P	0	0
			3152	1407	563	1035	147		

- Molecule 4 is a protein called E3 UFM1-protein ligase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	692	Total	C	N	O	S	0	0
			5479	3453	957	1050	19		

- Molecule 5 is a protein called CDK5 regulatory subunit-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	403	Total	C	N	O	S	0	0
			3234	2049	545	624	16		

- Molecule 6 is a protein called DDRGK domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	188	Total	C	N	O	S	0	0
			1547	954	279	313	1		

- Molecule 7 is a protein called Ubiquitin-fold modifier 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	78	Total	C	N	O	S	0	0
			588	382	96	109	1		

- Molecule 8 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LB	402	Total	C	N	O	S	0	0
			3239	2060	608	557	14		

- Molecule 10 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 12 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LE	220	Total	C	N	O	S	0	0
			1765	1136	334	291	4		

- Molecule 13 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 14 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 15 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 16 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LI	202	Total	C	N	O	S	0	0
			1634	1038	314	269	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	87	ILE	MET	conflict	UNP Q96L21

- Molecule 17 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LJ	175	Total	C	N	O	S	0	0
			1401	882	261	252	6		

- Molecule 18 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LL	194	Total	C	N	O	S	0	0
			1573	987	327	255	4		

- Molecule 19 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LM	136	Total	C	N	O	S	0	0
			1120	719	215	179	7		

- Molecule 20 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 21 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 22 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 23 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 24 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LR	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

- Molecule 25 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 26 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 27 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 28 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 29 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 30 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LX	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 31 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 32 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 33 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 34 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 35 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 36 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 37 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 38 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 39 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 40 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 41 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 42 is a protein called 60S ribosomal protein L37.

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

- Molecule 43 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 44 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 45 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 46 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lo	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 47 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 49 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lz	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 50 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
50	5	207	Total	Mg	0
			207	207	
50	7	2	Total	Mg	0
			2	2	
50	8	5	Total	Mg	0
			5	5	
50	LP	1	Total	Mg	0
			1	1	
50	LV	1	Total	Mg	0
			1	1	
50	Le	2	Total	Mg	0
			2	2	
50	Lf	1	Total	Mg	0
			1	1	
50	Lj	1	Total	Mg	0
			1	1	

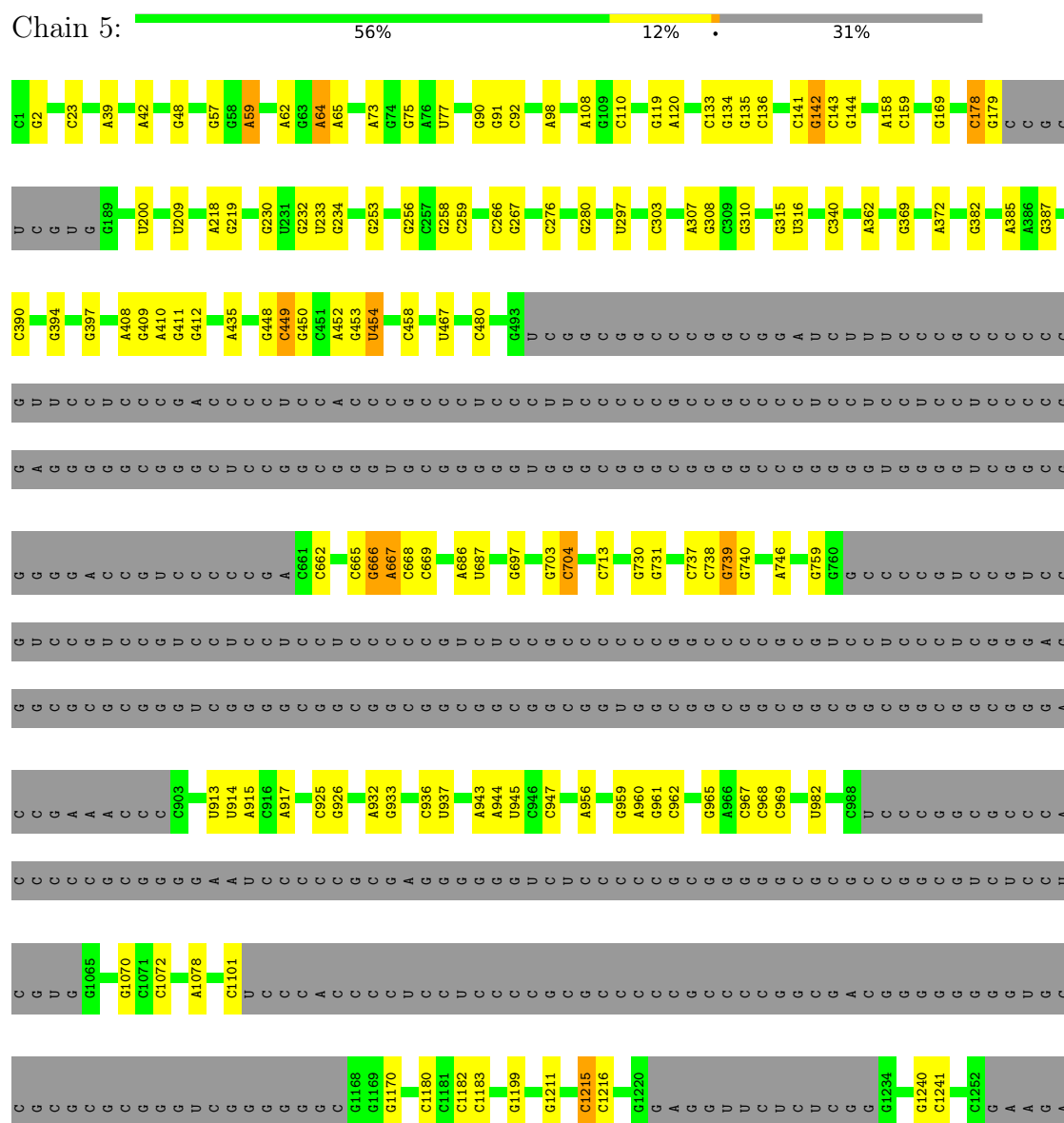
- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
51	Lg	1	Total	Zn	0
			1	1	
51	Lj	1	Total	Zn	0
			1	1	
51	Lm	1	Total	Zn	0
			1	1	
51	Lo	1	Total	Zn	0
			1	1	
51	Lp	1	Total	Zn	0
			1	1	

3 Residue-property plots [i](#)

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.

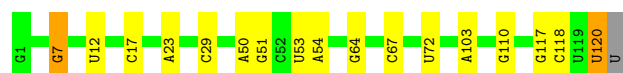
• Molecule 1: 28S rRNA



G1258	A1443	A1646	G1818	G	G2045	C	C2257	C2470	C2563	C2768	A	C	C
G1266	A1444	A1654	G1819	G	G2046	C	C2258	G2471	A2563	U2769	G	A	G
G1269	G1451	G1654	G1820	C	A2047	C	C2259	G2474	A2573	G2778	C	C	C
A1270	G1461	G1661	G1821	G	U2048	C	C2260	G2475	G2579	G2779	C	C	C
G1271	C1467	C1669	G1830	G	G2055	C	C2266	C2478	G2582	U2788	C	C	C
G1272	G1476	A1676	G1833	U	G2056	C	U2267	G2479	A2583	A2789	U	U	U
G1273	C	C1677	U1834	G	C2062	C	G2296	C2482	A2587	U2790	C	C	C
A1279	C	U1677	G1835	C	A2069	C	A2300	G	C2588	U2803	C	C	C
G1280	C	C1682	G1836	A	G	G	G2301	A	C2589	G2809	C	C	C
G1281	C	C1692	A1837	U	C2084	A	A2313	U	A2601	G2810	C	C	C
G1284	C	G1697	G1842	G	G2089	C	G2318	G	C2607	C2814	C	C	C
G1287	C	C1698	G1843	A	U2090	C	U2319	C	C2627	U2826	C	C	C
G1287	C	A1699	G1844	A	C2091	C	G2340	C	U2637	G2827	C	C	C
G1287	C	G1700	G1844	G	G2092	C	G2348	U	G2640	U2828	C	C	C
G1283	C	A1701	U1852	U	A2093	C	G2351	C	C2653	U2829	C	C	C
A1326	G1488	C1704	G1855	C	G2094	C	C2360	G2496	A2660	G2838	C	C	C
A1354	A1497	G1705	G1869	G	A2095	C	G2378	C2499	C2667	U2843	C	C	C
G1355	G1498	A1706	G1872	A	G2096	C	A2379	C2504	G2668	A2844	C	C	C
G1359	G1502	C	G1877	U	U2097	C	G2380	C2506	C2669	A2845	C	C	C
U1364	A1503	C	G1890	C	G2099	C	A2381	A2513	G2681	G2855	C	C	C
G1366	A1534	C	A1897	A	G2103	C	G2396	G2515	U2687	C2856	C	C	C
G1366	A1547	C	U1918	G	G2106	C	A2396	G2517	G2694	U2869	C	C	C
G1377	A1554	C	G1919	G	C2107	C	G2398	A2518	A2696	A2881	C	C	C
G1380	G1562	C	G1920	A	G	C	U2406	U2519	G	G2902	C	C	C
A1387	A1565	C	C1921	G	G	C	G2407	C2520	U2708	G	C	C	C
G1390	G1573	C	G1922	U	G	C	C2411	U2524	G2711	C	C	C	C
G1393	G1578	C	G1925	U	G	C	G2416	U2525	G2716	C	C	C	C
G1394	U1578	C	C1926	G	G	C	A2417	C2526	G2717	C	C	C	C
A1397	U1590	C	U1930	A	G	C	G2421	A2527	U2718	C	C	C	C
C1405	U1591	C	A1932	C	C	C	G2427	G2528	G2725	C	C	C	C
G	U1596	C	G1940	A	G	C	U2434	A2529	A2743	C	C	C	C
C	C1614	C	A1941	C	C	C	A2438	U2530	A2744	C	C	C	C
C	G1624	C	G1948	C	C	C	U2440	G2537	G2758	C	C	C	C
U	G1625	C	U1949	C	C	C	U2447	U2538	U2761	C	C	C	C
C	A1631	C	G1952	C	C	C	A2460	C2539	G2762	C	C	C	C
G1412	A1632	C	C1958	U	G2021	C	U2460	A2543	U2763	C	C	C	C
G1415	A1633	C	A1958	C	G2024	C	U2460	G	A2764	C	C	C	C
A1433	A1634	C	A1780	C	A2025	C	U2460	U2547	A2765	C	C	C	C
A1437	A1638	C	A1787	C	A2026	C	U2460	G2547	C	C	C	C	C
U1438	A1639	C	A1804	C	G	C	U2460	A2553	C	C	C	C	C
C1439	C1640	C	C1966	A	A2042	C	C2256	U2554	C	C	C	C	C

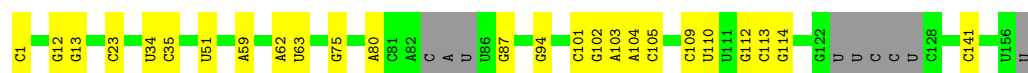
- Molecule 2: 5S rRNA

Chain 7: 



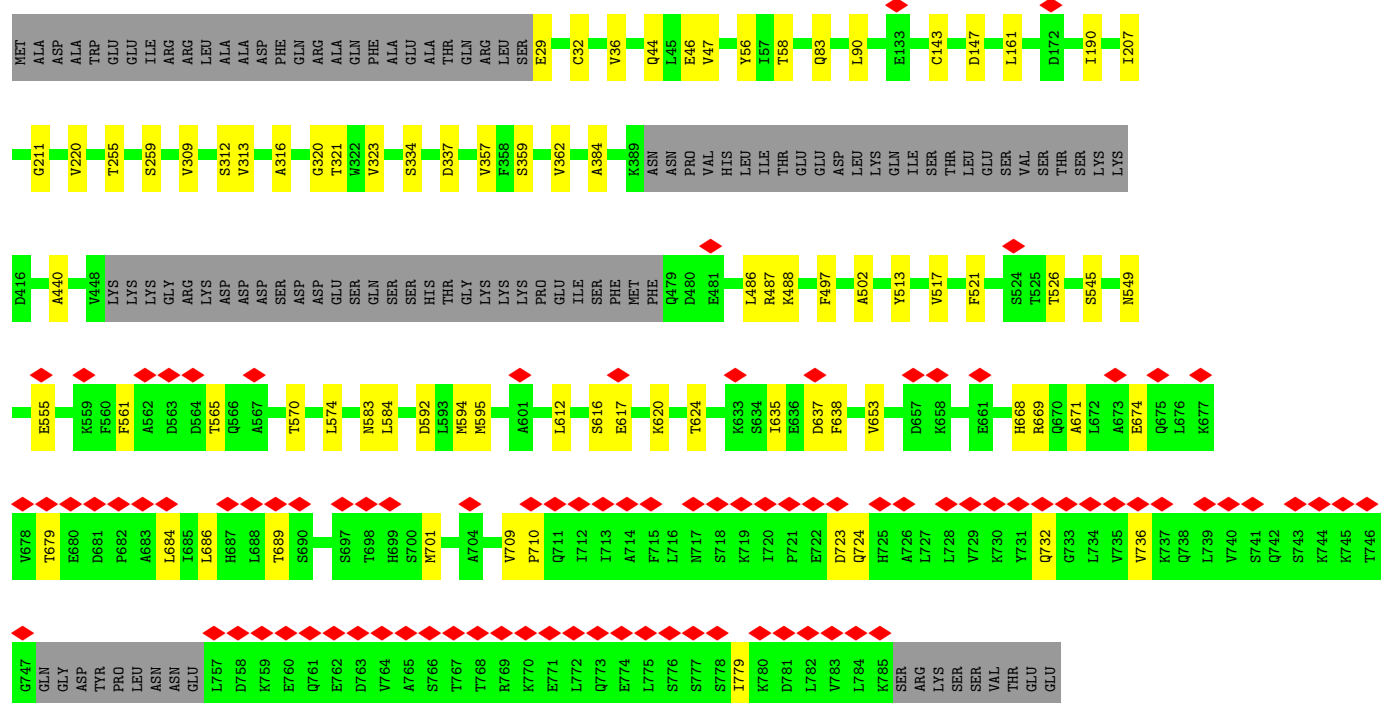
• Molecule 3: 5.8S rRNA

Chain 8: 



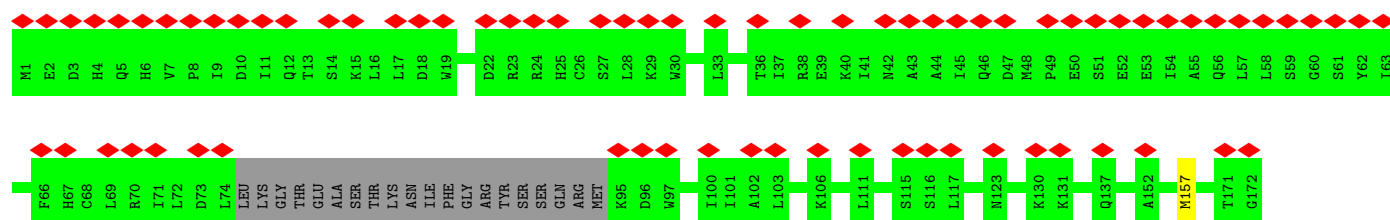
• Molecule 4: E3 UFM1-protein ligase 1

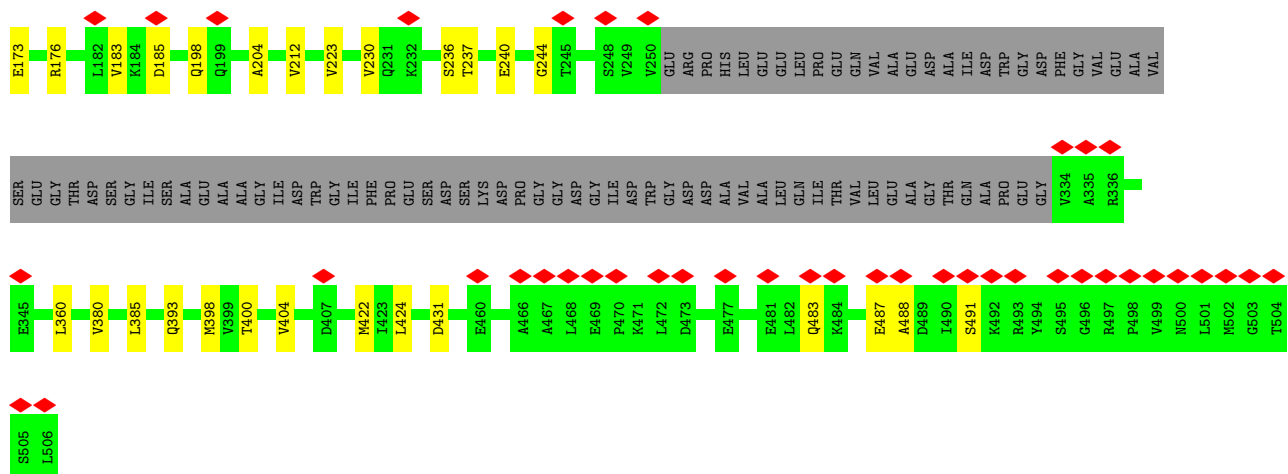
Chain A: 



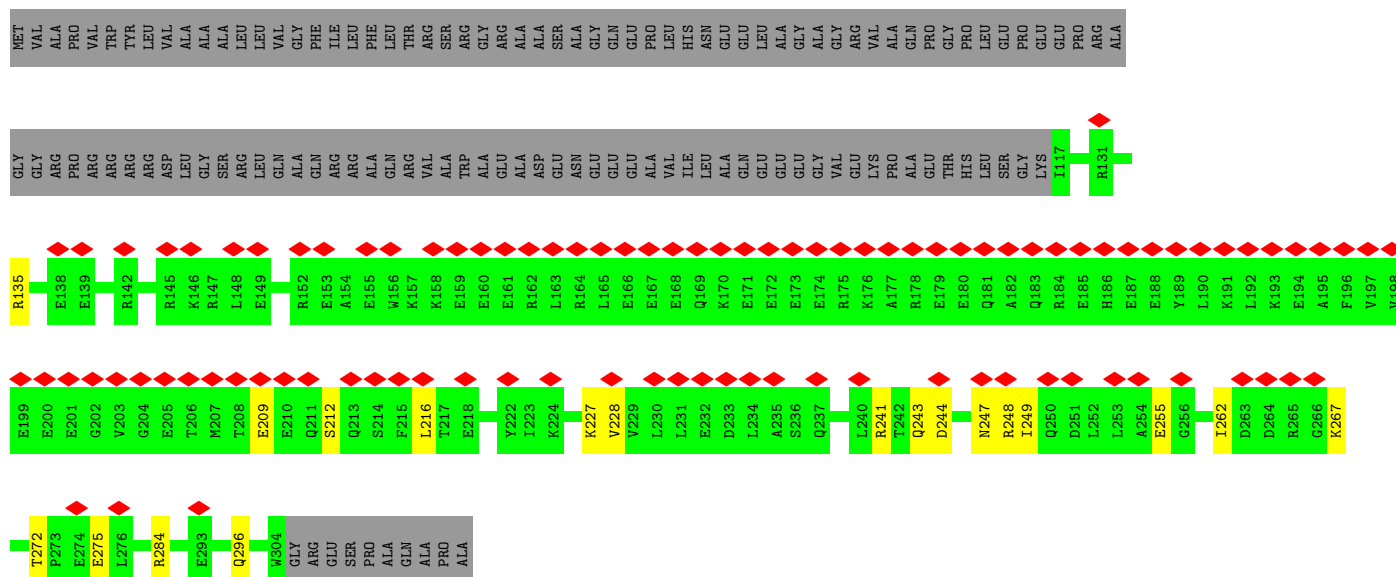
• Molecule 5: CDK5 regulatory subunit-associated protein 3

Chain B: 

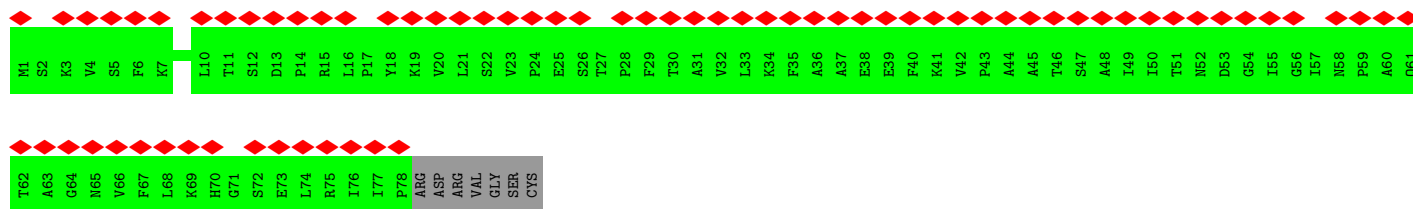
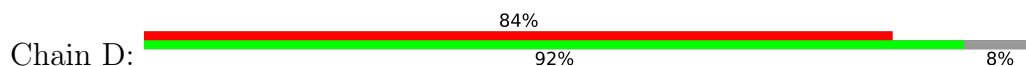




• Molecule 6: DDRGK domain-containing protein 1

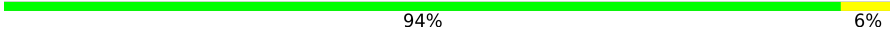


• Molecule 7: Ubiquitin-fold modifier 1



• Molecule 8: 60S ribosomal protein L8



Chain LN:  94% 6%



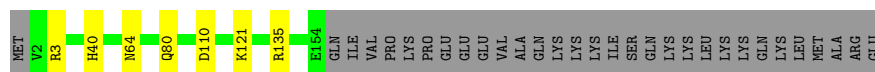
- Molecule 21: 60S ribosomal protein L13a

Chain LO:  90% 9%

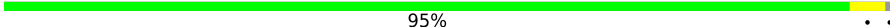


- Molecule 22: 60S ribosomal protein L17

Chain LP:  79% 17%



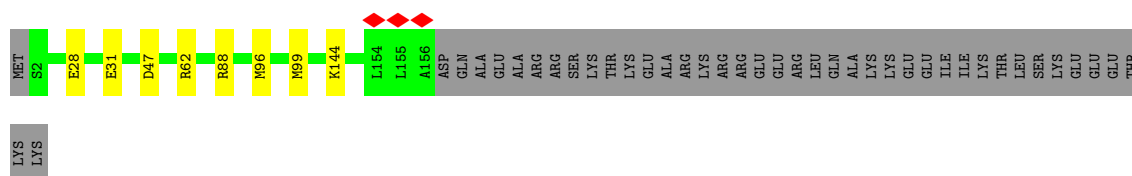
- Molecule 23: 60S ribosomal protein L18

Chain LQ:  95%

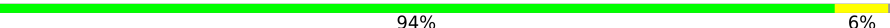


- Molecule 24: 60S ribosomal protein L19

Chain LR:  75% 21%

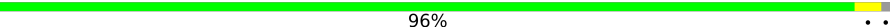


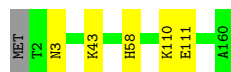
- Molecule 25: 60S ribosomal protein L18a

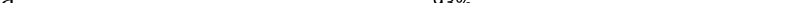
Chain LS:  94% 6%

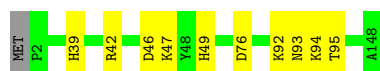


- Molecule 26: 60S ribosomal protein L21

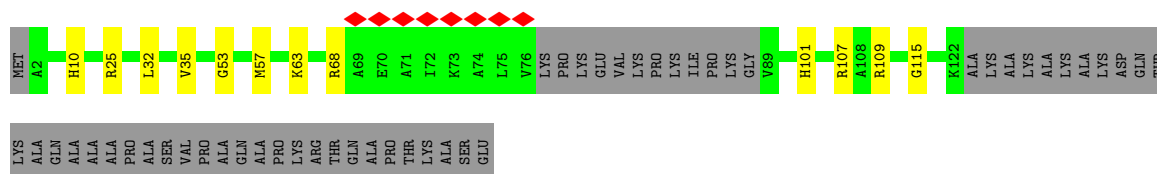
Chain LT:  96%



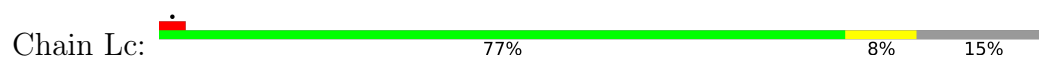
- Chain La:  93% 7%



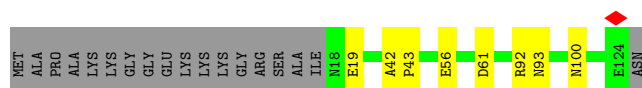
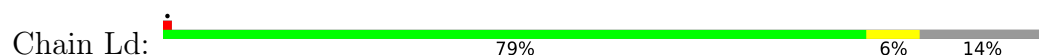
- Molecule 34: 60S ribosomal protein L29



- Molecule 35: 60S ribosomal protein L30



- Molecule 36: 60S ribosomal protein L31



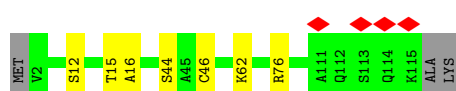
- Molecule 37: 60S ribosomal protein L32



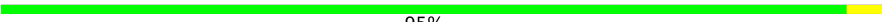
- Molecule 38: 60S ribosomal protein L35a

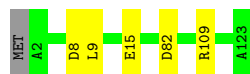


- Molecule 39: 60S ribosomal protein L34



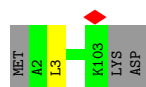
- Molecule 40: 60S ribosomal protein L35

Chain Lh:  95% ..



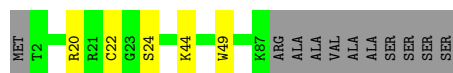
- Molecule 41: 60S ribosomal protein L36

Chain Li:  96% ..



- Molecule 42: 60S ribosomal protein L37

Chain Lj:  84% 5% 11%



- Molecule 43: 60S ribosomal protein L38

Chain Lk:  93% 6% .



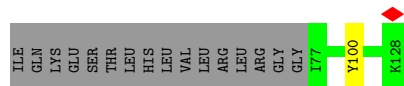
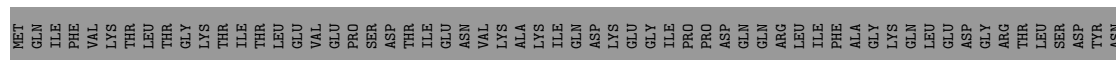
- Molecule 44: 60S ribosomal protein L39

Chain Ll:  82% 16% .

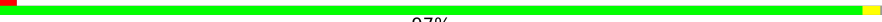


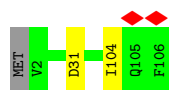
- Molecule 45: Ubiquitin-60S ribosomal protein L40

Chain Lm:  40% . 59%

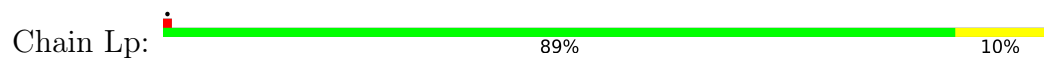


- Molecule 46: 60S ribosomal protein L36a

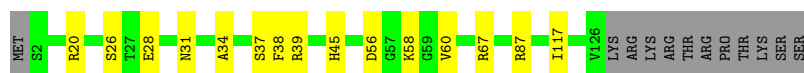
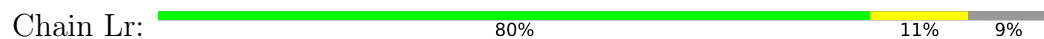
Chain Lo:  97% ..



- Molecule 47: 60S ribosomal protein L37a



- Molecule 48: 60S ribosomal protein L28



- Molecule 49: 60S ribosomal protein L10a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35935	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.100	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	377.1, 377.1, 377.1	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.838, 0.838, 0.838	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	5	0.07	0/83342	0.15	0/129985
2	7	0.06	0/2861	0.14	0/4459
3	8	0.06	0/3520	0.15	0/5481
4	A	0.14	0/5549	0.25	0/7469
5	B	0.08	0/3280	0.19	0/4426
6	C	0.07	0/1560	0.16	0/2085
7	D	0.10	0/601	0.21	0/818
8	LA	0.09	0/1936	0.20	0/2596
9	LB	0.08	0/3307	0.20	0/4424
10	LC	0.08	0/2981	0.20	0/4002
11	LD	0.09	0/2428	0.20	0/3252
12	LE	0.08	0/1799	0.23	0/2414
13	LF	0.07	0/1905	0.19	0/2539
14	LG	0.09	0/1960	0.21	0/2637
15	LH	0.09	0/1537	0.22	0/2066
16	LI	0.10	0/1673	0.22	0/2234
17	LJ	0.08	0/1424	0.19	0/1904
18	LL	0.08	0/1604	0.20	0/2149
19	LM	0.08	0/1142	0.19	0/1527
20	LN	0.09	0/1746	0.19	0/2338
21	LO	0.08	0/1682	0.21	0/2250
22	LP	0.08	0/1268	0.20	0/1701
23	LQ	0.10	0/1537	0.21	0/2052
24	LR	0.10	0/1310	0.23	0/1734
25	LS	0.09	0/1493	0.22	0/2003
26	LT	0.09	0/1326	0.22	0/1770
27	LU	0.09	0/839	0.21	0/1126
28	LV	0.09	0/993	0.22	0/1332
29	LW	0.09	0/532	0.16	0/708
30	LX	0.07	0/984	0.20	0/1323
31	LY	0.09	0/1132	0.21	0/1504
32	LZ	0.10	0/1130	0.19	0/1507

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	La	0.07	0/1191	0.20	0/1591
34	Lb	0.10	0/889	0.23	0/1175
35	Lc	0.10	0/774	0.19	0/1038
36	Ld	0.11	0/903	0.25	0/1216
37	Le	0.09	0/1071	0.20	0/1429
38	Lf	0.10	0/895	0.23	0/1198
39	Lg	0.09	0/916	0.22	0/1220
40	Lh	0.08	0/1023	0.18	0/1351
41	Li	0.09	0/843	0.18	0/1115
42	Lj	0.09	0/720	0.20	0/952
43	Lk	0.08	0/575	0.20	0/761
44	Ll	0.11	0/454	0.20	0/599
45	Lm	0.10	0/435	0.21	0/575
46	Lo	0.09	0/877	0.21	0/1156
47	Lp	0.10	0/718	0.20	0/953
48	Lr	0.09	0/1017	0.21	0/1364
49	Lz	0.09	0/1772	0.23	0/2375
All	All	0.08	0/155454	0.18	0/227883

There are no bond length outliers.

There are no bond angle outliers.

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	5	74502	0	37637	233	0
2	7	2561	0	1295	12	0
3	8	3152	0	1601	9	0
4	A	5479	0	5608	57	0
5	B	3234	0	3287	20	0
6	C	1547	0	1543	12	0
7	D	588	0	616	0	0
8	LA	1898	0	1993	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	LB	3239	0	3376	31	0
10	LC	2927	0	3104	13	0
11	LD	2382	0	2410	17	0
12	LE	1765	0	1917	14	0
13	LF	1870	0	1996	8	0
14	LG	1927	0	2074	6	0
15	LH	1518	0	1601	13	0
16	LI	1634	0	1673	12	0
17	LJ	1401	0	1428	10	0
18	LL	1573	0	1681	7	0
19	LM	1120	0	1187	8	0
20	LN	1701	0	1749	8	0
21	LO	1650	0	1794	15	0
22	LP	1242	0	1269	5	0
23	LQ	1513	0	1628	6	0
24	LR	1294	0	1434	9	0
25	LS	1453	0	1490	7	0
26	LT	1298	0	1366	4	0
27	LU	825	0	850	8	0
28	LV	979	0	1039	10	0
29	LW	519	0	533	1	0
30	LX	967	0	1040	7	0
31	LY	1115	0	1205	5	0
32	LZ	1107	0	1182	9	0
33	La	1162	0	1213	8	0
34	Lb	876	0	948	10	0
35	Lc	764	0	804	5	0
36	Ld	888	0	930	5	0
37	Le	1053	0	1147	4	0
38	Lf	876	0	912	4	0
39	Lg	906	0	998	7	0
40	Lh	1015	0	1148	4	0
41	Li	832	0	917	1	0
42	Lj	705	0	737	4	0
43	Lk	569	0	637	3	0
44	Ll	444	0	483	5	0
45	Lm	429	0	465	1	0
46	Lo	863	0	929	3	0
47	Lp	708	0	756	7	0
48	Lr	1002	0	1068	10	0
49	Lz	1744	0	1859	21	0
50	5	207	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	7	2	0	0	0	0
50	8	5	0	0	0	0
50	LP	1	0	0	0	0
50	LV	1	0	0	0	0
50	Le	2	0	0	0	0
50	Lf	1	0	0	0	0
50	Lj	1	0	0	0	0
51	Lg	1	0	0	0	0
51	Lj	1	0	0	0	0
51	Lm	1	0	0	0	0
51	Lo	1	0	0	0	0
51	Lp	1	0	0	0	0
All	All	145041	0	108557	564	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 2.

All (564) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:3641:U:OP2	1:5:3646:A:N6	2.07	0.88
1:5:4620:U:OP2	1:5:4670:C:N4	2.07	0.86
1:5:1591:U:OP2	1:5:2856:C:O2'	1.94	0.85
47:Lp:32:SER:OG	47:Lp:69:TRP:O	1.97	0.83
1:5:4522:G:O2'	1:5:4525:C:OP2	1.97	0.81
40:Lh:15:GLU:N	40:Lh:15:GLU:OE1	2.14	0.81
4:A:29:GLU:N	4:A:32:CYS:HG	1.79	0.80
21:LO:190:ASP:OD1	21:LO:191:LYS:N	2.15	0.79
19:LM:105:THR:OG1	19:LM:108:ASP:OD1	2.01	0.79
33:La:46:ASP:OD1	33:La:47:LYS:N	2.16	0.78
4:A:594:MET:HA	4:A:594:MET:HE3	1.66	0.77
1:5:2257:C:O2'	1:5:2259:G:OP2	2.01	0.77
1:5:4546:A:N7	8:LA:215:ASN:ND2	2.33	0.77
1:5:1397:A:O2'	1:5:1467:C:O2'	2.01	0.77
1:5:2588:C:OP1	1:5:2768:C:O2'	2.02	0.77
4:A:190:ILE:HG21	4:A:220:VAL:HG11	1.67	0.76
1:5:1293:G:N2	1:5:1293:G:OP2	2.17	0.76
2:7:7:G:OP1	11:LD:33:ARG:NH1	2.19	0.76
16:LI:210:ARG:O	16:LI:214:SER:OG	2.04	0.76
14:LG:46:GLN:OE1	14:LG:49:ARG:NH2	2.20	0.75
1:5:4472:G:O2'	45:Lm:100:TYR:O	2.04	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2758:G:O2'	1:5:2765:A:N3	2.19	0.75
3:8:12:G:OP1	22:LP:3:ARG:NH1	2.20	0.75
1:5:2716:C:O3'	27:LU:107:LYS:NZ	2.20	0.74
49:Lz:144:MET:HE3	49:Lz:144:MET:H	1.52	0.74
1:5:308:G:N2	1:5:308:G:OP2	2.20	0.74
12:LE:202:ASP:O	12:LE:260:LYS:NZ	2.20	0.74
1:5:1705:G:N2	1:5:1705:G:OP1	2.21	0.74
48:Lr:26:SER:OG	48:Lr:28:GLU:OE1	2.04	0.74
12:LE:161:ARG:NH1	12:LE:273:SER:OG	2.21	0.73
46:Lo:104:ILE:HD12	46:Lo:104:ILE:O	1.89	0.73
1:5:3654:G:O2'	1:5:3693:U:OP1	2.07	0.73
4:A:334:SER:OG	4:A:337:ASP:OD2	2.06	0.72
1:5:3823:G:OP2	1:5:3823:G:N2	2.22	0.72
1:5:3653:A:O2'	8:LA:179:ILE:O	2.04	0.72
42:Lj:22:CYS:SG	42:Lj:24:SER:OG	2.48	0.71
1:5:1269:G:OP2	34:Lb:107:ARG:NH2	2.23	0.71
1:5:4289:U:HO2'	1:5:4320:G:HO2'	1.36	0.71
1:5:1698:C:O2'	1:5:1699:A:OP2	2.07	0.71
1:5:4039:G:O2'	1:5:4040:C:OP2	2.09	0.71
1:5:4670:C:O2'	1:5:4672:A:OP2	2.09	0.71
1:5:1326:A:OP2	1:5:4445:U:O2'	2.09	0.70
1:5:2267:U:OP1	48:Lr:37:SER:OG	2.06	0.70
1:5:2573:A:O2'	32:LZ:112:ARG:NH2	2.24	0.70
6:C:243:GLN:O	6:C:247:ASN:ND2	2.25	0.69
28:LV:83:ARG:NH2	28:LV:118:THR:O	2.25	0.69
1:5:1890:G:N2	1:5:1890:G:OP2	2.23	0.69
36:Ld:19:GLU:OE1	36:Ld:92:ARG:NH1	2.25	0.69
2:7:117:G:OP1	11:LD:253:TYR:OH	2.11	0.69
1:5:2520:C:O2	1:5:2640:G:N2	2.26	0.69
4:A:612:LEU:O	4:A:620:LYS:NZ	2.25	0.69
1:5:4623:G:OP1	9:LB:19:ARG:NH2	2.26	0.69
5:B:385:LEU:HD13	5:B:385:LEU:O	1.93	0.69
1:5:408:A:O2'	1:5:411:G:OP2	2.07	0.68
1:5:1958:A:O2'	1:5:2025:A:N1	2.26	0.68
1:5:2089:G:O2'	10:LC:307:LYS:NZ	2.26	0.68
33:La:39:HIS:O	33:La:42:ARG:N	2.25	0.68
12:LE:72:LYS:NZ	34:Lb:115:GLY:O	2.28	0.67
24:LR:31:GLU:N	24:LR:31:GLU:OE2	2.27	0.67
1:5:1669:A:N3	1:5:1852:U:O2'	2.27	0.66
1:5:4927:G:OP2	1:5:4927:G:N2	2.27	0.66
1:5:2447:U:O2'	1:5:2744:A:N3	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:7:23:A:N3	2:7:118:C:O2'	2.26	0.66
6:C:227:LYS:NZ	6:C:275:GLU:OE2	2.27	0.66
14:LG:164:ILE:O	14:LG:168:VAL:HG13	1.95	0.65
1:5:1397:A:HO2'	1:5:1467:C:HO2'	1.43	0.65
32:LZ:30:ASP:O	32:LZ:39:SER:OG	2.15	0.65
6:C:255:GLU:N	6:C:255:GLU:OE2	2.30	0.65
26:LT:43:LYS:O	26:LT:58:HIS:ND1	2.30	0.65
1:5:5040:U:OP2	9:LB:396:ARG:NH1	2.29	0.65
1:5:2779:C:O2'	3:8:112:G:OP1	2.09	0.65
14:LG:90:GLN:N	14:LG:90:GLN:OE1	2.30	0.65
21:LO:186:GLU:N	21:LO:186:GLU:OE2	2.30	0.65
49:Lz:41:TYR:OH	49:Lz:47:LYS:O	2.12	0.65
1:5:1439:C:OP2	13:LF:31:LYS:NZ	2.28	0.64
1:5:4580:U:O2'	9:LB:182:GLU:OE2	2.11	0.64
17:LJ:110:GLN:N	17:LJ:110:GLN:OE1	2.29	0.64
1:5:1704:C:O3'	13:LF:46:ARG:NH1	2.31	0.64
1:5:2553:A:N6	1:5:2765:A:N7	2.46	0.64
1:5:4617:G:OP2	9:LB:358:ARG:NH2	2.30	0.64
1:5:2583:C:OP2	39:Lg:76:ARG:NH1	2.30	0.64
20:LN:119:TYR:OH	20:LN:131:GLU:OE1	2.10	0.64
39:Lg:44:SER:OG	39:Lg:46:CYS:SG	2.54	0.64
11:LD:232:THR:OG1	11:LD:234:ASP:OD1	2.13	0.64
1:5:1833:G:N2	1:5:1835:G:O4'	2.30	0.63
1:5:4343:U:O2'	46:Lo:31:ASP:OD1	2.16	0.63
12:LE:133:PHE:O	12:LE:138:ARG:NH2	2.31	0.63
49:Lz:12:GLU:N	49:Lz:12:GLU:OE1	2.32	0.63
1:5:62:A:N3	1:5:77:U:O2'	2.31	0.63
1:5:2318:G:N2	1:5:2321:G:OP2	2.27	0.63
1:5:4420:U:O4	1:5:4475:G:N2	2.32	0.63
5:B:483:GLN:NE2	5:B:487:GLU:OE2	2.31	0.62
4:A:617:GLU:OE1	4:A:617:GLU:N	2.31	0.62
6:C:272:THR:OG1	6:C:275:GLU:OE1	2.14	0.62
1:5:2296:G:O2'	10:LC:242:PRO:O	2.13	0.62
4:A:545:SER:O	4:A:549:ASN:ND2	2.31	0.62
8:LA:112:ILE:HD13	47:Lp:79:VAL:HG22	1.82	0.62
3:8:102:G:OP2	3:8:104:A:O2'	2.16	0.62
1:5:2809:G:O2'	1:5:4644:G:OP1	2.17	0.61
4:A:359:SER:HB3	4:A:362:VAL:HG22	1.83	0.61
9:LB:317:LEU:HD21	9:LB:382:MET:HG2	1.82	0.61
1:5:1807:C:O3'	26:LT:110:LYS:NZ	2.33	0.61
1:5:2416:G:N2	1:5:2427:G:O6	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:689:THR:HG21	4:A:779:ILE:CG2	2.31	0.61
1:5:2524:U:O2	1:5:2529:A:N6	2.33	0.61
1:5:746:A:N6	1:5:913:U:O2	2.33	0.61
5:B:240:GLU:O	5:B:244:GLY:N	2.34	0.60
1:5:3611:A:O2'	1:5:5016:A:O2'	2.17	0.60
1:5:4694:G:N2	1:5:4694:G:OP1	2.33	0.60
1:5:4748:U:OP1	38:Lf:54:LYS:NZ	2.26	0.60
5:B:198:GLN:NE2	5:B:230:VAL:O	2.33	0.60
1:5:1818:G:OP2	1:5:1818:G:N2	2.30	0.60
4:A:723:ASP:OD1	4:A:724:GLN:N	2.34	0.60
5:B:204:ALA:HB1	5:B:360:LEU:HD21	1.82	0.60
18:LL:126:LEU:N	18:LL:138:ASP:OD2	2.34	0.60
27:LU:63:ILE:HD12	27:LU:71:THR:O	2.02	0.60
1:5:4322:G:N2	1:5:4325:A:OP2	2.32	0.60
11:LD:260:GLU:OE1	11:LD:260:GLU:N	2.35	0.60
49:Lz:82:ILE:HD12	49:Lz:82:ILE:O	2.01	0.60
1:5:2378:G:N2	1:5:2381:A:OP2	2.35	0.60
15:LH:37:ASP:OD1	15:LH:39:ASN:ND2	2.34	0.60
27:LU:108:GLU:N	27:LU:108:GLU:OE1	2.34	0.60
10:LC:205:ARG:NH2	10:LC:228:THR:OG1	2.35	0.59
31:LY:37:GLU:N	31:LY:37:GLU:OE1	2.34	0.59
1:5:1437:C:O2'	1:5:2099:G:OP2	2.17	0.59
1:5:2091:C:O2	1:5:2094:G:O2'	2.13	0.59
1:5:2579:G:N2	1:5:2582:A:OP2	2.29	0.59
1:5:4541:G:N2	1:5:4544:A:OP2	2.29	0.59
2:7:51:G:H21	17:LJ:12:MET:HE1	1.64	0.59
49:Lz:54:ARG:NH1	49:Lz:150:GLU:OE2	2.35	0.59
1:5:4731:G:N2	1:5:4731:G:OP2	2.35	0.59
5:B:398:MET:HE3	5:B:398:MET:HA	1.84	0.59
4:A:46:GLU:N	4:A:46:GLU:OE1	2.36	0.59
1:5:369:G:N2	1:5:372:A:OP2	2.34	0.59
1:5:4115:G:OP2	1:5:4115:G:N2	2.31	0.59
48:Lr:56:ASP:OD2	48:Lr:58:LYS:NZ	2.35	0.59
1:5:454:U:O2'	37:Le:5:ARG:NH1	2.35	0.58
1:5:1502:G:OP2	23:LQ:65:ARG:NH1	2.36	0.58
1:5:1757:U:O2'	1:5:1758:G:O5'	2.16	0.58
1:5:4163:U:OP2	14:LG:53:ARG:NH1	2.36	0.58
8:LA:117:GLU:O	8:LA:162:ASN:ND2	2.35	0.58
1:5:2844:A:N6	1:5:3839:G:O2'	2.36	0.58
19:LM:119:ARG:NH2	21:LO:182:GLU:OE2	2.36	0.58
10:LC:1:MET:SD	10:LC:2:ALA:N	2.76	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LX:72:ASP:OD1	30:LX:74:TYR:N	2.37	0.58
1:5:4206:C:O2'	1:5:4335:C:O2'	2.20	0.57
29:LW:45:ASN:OD1	29:LW:47:ARG:NH1	2.36	0.57
49:Lz:114:GLU:N	49:Lz:114:GLU:OE1	2.37	0.57
4:A:488:LYS:O	4:A:488:LYS:NZ	2.22	0.57
1:5:1562:G:N2	1:5:1565:A:OP2	2.35	0.57
15:LH:14:GLU:C	15:LH:14:GLU:OE1	2.47	0.57
4:A:161:LEU:HD12	4:A:161:LEU:O	2.04	0.57
1:5:2407:G:N2	1:5:2407:G:OP2	2.37	0.57
4:A:486:LEU:HD12	4:A:487:ARG:N	2.20	0.57
16:LI:61:SER:HA	16:LI:126:VAL:HG12	1.87	0.57
1:5:3690:U:O2'	1:5:3817:A:N3	2.33	0.57
21:LO:185:VAL:HG12	21:LO:185:VAL:O	2.05	0.57
27:LU:63:ILE:HD11	27:LU:70:ILE:HG23	1.86	0.56
1:5:1240:G:HO2'	12:LE:63:TYR:HH	1.53	0.56
1:5:937:U:OP1	19:LM:46:ARG:NH1	2.39	0.56
1:5:2092:G:O2'	1:5:2093:A:OP2	2.21	0.56
32:LZ:33:THR:OG1	32:LZ:35:ASP:OD1	2.16	0.56
1:5:4272:G:OP2	1:5:4272:G:N2	2.29	0.56
27:LU:98:ASP:OD2	27:LU:98:ASP:N	2.38	0.56
49:Lz:31:THR:N	49:Lz:209:THR:OG1	2.37	0.56
5:B:236:SER:OG	5:B:237:THR:N	2.38	0.56
36:Ld:93:ASN:ND2	36:Ld:100:ASN:O	2.38	0.56
6:C:296:GLN:O	6:C:296:GLN:NE2	2.39	0.55
49:Lz:142:GLU:OE2	49:Lz:147:LYS:NZ	2.36	0.55
1:5:5005:G:N2	1:5:5041:G:O2'	2.39	0.55
4:A:47:VAL:HG12	4:A:58:THR:HG22	1.87	0.55
1:5:1787:A:N3	1:5:4210:U:O2'	2.39	0.55
4:A:689:THR:HG21	4:A:779:ILE:HG21	1.89	0.55
1:5:1646:A:O2'	42:Lj:49:TRP:O	2.23	0.55
10:LC:209:ILE:HD11	10:LC:227:ILE:HD12	1.87	0.55
1:5:3663:A:N6	1:5:4168:G:O2'	2.39	0.55
16:LI:193:ASP:O	16:LI:193:ASP:OD2	2.23	0.55
1:5:4582:C:O2'	9:LB:99:LEU:O	2.20	0.55
4:A:570:THR:O	4:A:574:LEU:HD13	2.07	0.55
8:LA:36:GLU:OE2	8:LA:163:ARG:NH1	2.40	0.54
36:Ld:61:ASP:O	36:Ld:61:ASP:OD2	2.25	0.54
36:Ld:56:GLU:C	36:Ld:56:GLU:OE1	2.49	0.54
1:5:713:C:O2	12:LE:130:LYS:NZ	2.35	0.54
27:LU:63:ILE:HD11	27:LU:70:ILE:CG2	2.38	0.54
1:5:382:G:N1	1:5:385:A:OP2	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:3809:G:OP2	1:5:3809:G:N2	2.33	0.54
1:5:2516:G:O2'	39:Lg:62:LYS:NZ	2.40	0.53
1:5:4127:A:N6	1:5:4157:A:N7	2.54	0.53
6:C:241:ARG:N	6:C:244:ASP:OD2	2.40	0.53
4:A:561:PHE:CE2	4:A:565:THR:HG23	2.44	0.53
4:A:679:THR:OG1	4:A:684:LEU:HD23	2.07	0.53
11:LD:231:VAL:HA	11:LD:235:MET:HE2	1.89	0.53
33:La:93:ASN:OD1	33:La:94:LYS:N	2.41	0.53
1:5:1180:C:OP2	11:LD:289:ARG:NH1	2.39	0.53
49:Lz:42:ASP:N	49:Lz:46:ASP:OD2	2.39	0.53
11:LD:136:ASP:OD1	11:LD:136:ASP:N	2.38	0.53
1:5:458:C:HO2'	12:LE:110:ARG:HH22	1.57	0.53
2:7:120:U:OP2	11:LD:262:LYS:NZ	2.41	0.53
17:LJ:120:ASP:OD2	17:LJ:122:SER:OG	2.26	0.53
47:Lp:8:VAL:O	47:Lp:11:VAL:HG22	2.08	0.53
1:5:1830:G:O2'	34:Lb:68:ARG:NH2	2.41	0.53
5:B:393:GLN:O	49:Lz:1:MET:N	2.42	0.53
20:LN:104:GLU:OE2	20:LN:108:ARG:NH2	2.42	0.53
1:5:390:C:OP1	6:C:135:ARG:NE	2.42	0.53
1:5:1390:G:N2	1:5:1393:G:OP2	2.39	0.53
1:5:1596:U:O2'	22:LP:135:ARG:NH2	2.41	0.53
1:5:4771:C:N4	1:5:4863:G:O6	2.42	0.53
9:LB:56:ILE:HD13	9:LB:365:LEU:HD22	1.91	0.53
2:7:72:U:O2	2:7:103:A:N6	2.42	0.53
1:5:2045:G:O6	1:5:3870:C:O2'	2.27	0.53
39:Lg:15:THR:HG22	39:Lg:16:ALA:N	2.24	0.53
1:5:75:G:O6	18:LL:103:ARG:NH1	2.39	0.52
4:A:320:GLY:O	4:A:321:THR:OG1	2.19	0.52
1:5:4760:G:OP1	21:LO:117:ARG:NH2	2.42	0.52
13:LF:27:GLU:OE1	13:LF:27:GLU:N	2.39	0.52
1:5:1355:G:OP1	23:LQ:108:ARG:NH2	2.39	0.52
1:5:1692:C:O2'	23:LQ:143:ARG:NH2	2.43	0.52
1:5:4206:C:HO2'	1:5:4335:C:HO2'	1.56	0.52
4:A:521:PHE:CE1	4:A:526:THR:HG21	2.45	0.52
19:LM:43:THR:HG22	19:LM:43:THR:O	2.09	0.52
1:5:3689:G:O2'	1:5:3818:U:OP2	2.25	0.52
27:LU:63:ILE:HD13	27:LU:72:VAL:HG22	1.92	0.52
15:LH:43:VAL:HG21	15:LH:73:ILE:HD13	1.92	0.52
1:5:315:G:OP2	1:5:4354:U:O2'	2.17	0.52
1:5:2042:A:O4'	1:5:4462:C:O2'	2.28	0.52
1:5:4626:A:OP2	9:LB:224:LYS:NZ	2.32	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LI:181:PHE:CZ	16:LI:197:VAL:HG11	2.45	0.52
1:5:57:G:N2	1:5:59:A:N3	2.59	0.51
1:5:1930:U:OP2	21:LO:49:ARG:NH1	2.39	0.51
4:A:362:VAL:HG21	4:A:497:PHE:CD1	2.45	0.51
46:Lo:104:ILE:HD12	46:Lo:104:ILE:C	2.34	0.51
2:7:29:C:O2	2:7:50:A:N6	2.42	0.51
4:A:359:SER:CB	4:A:362:VAL:HG22	2.39	0.51
1:5:1780:A:N3	16:LI:198:LYS:NZ	2.58	0.51
8:LA:112:ILE:CD1	47:Lp:79:VAL:HG22	2.40	0.51
49:Lz:197:ASN:OD1	49:Lz:198:TRP:N	2.41	0.51
1:5:1927:U:OP1	1:5:1949:U:O2'	2.21	0.51
1:5:2411:C:O2'	1:5:2526:C:O2	2.28	0.51
1:5:3938:G:O6	1:5:4172:A:N6	2.41	0.51
32:LZ:76:ASN:OD1	32:LZ:77:TYR:N	2.43	0.51
35:Lc:24:SER:OG	35:Lc:101:ASP:OD2	2.17	0.51
1:5:2062:C:OP1	25:LS:2:LYS:N	2.44	0.51
40:Lh:8:ASP:OD2	40:Lh:9:LEU:N	2.44	0.51
34:Lb:101:HIS:O	34:Lb:109:ARG:NH1	2.44	0.51
1:5:4924:C:O2	1:5:4926:C:N4	2.44	0.51
9:LB:57:VAL:HG22	9:LB:73:VAL:HG22	1.93	0.50
1:5:730:G:OP2	13:LF:76:ARG:NH2	2.43	0.50
8:LA:147:ARG:HG2	8:LA:157:VAL:HG22	1.93	0.50
28:LV:57:VAL:HG13	28:LV:84:GLN:OE1	2.10	0.50
1:5:2725:A:N6	24:LR:88:ARG:O	2.45	0.50
4:A:732:GLN:O	4:A:736:VAL:HG23	2.11	0.50
9:LB:358:ARG:HG2	9:LB:358:ARG:HH11	1.76	0.50
35:Lc:14:ILE:HD12	35:Lc:17:ARG:HD2	1.94	0.50
1:5:2266:C:O2'	48:Lr:39:ARG:NH1	2.44	0.50
1:5:3777:G:O2'	1:5:3815:G:O6	2.28	0.50
18:LL:16:LYS:O	18:LL:21:ARG:NH2	2.45	0.50
49:Lz:31:THR:N	49:Lz:209:THR:HG1	2.10	0.50
1:5:1872:G:O2'	1:5:4219:A:N3	2.37	0.50
1:5:4467:A:O2'	1:5:4510:A:N3	2.37	0.50
10:LC:214:ASP:OD2	10:LC:218:ILE:HD12	2.12	0.50
1:5:1757:U:O2'	1:5:1758:G:P	2.70	0.50
1:5:4582:C:OP2	9:LB:28:LYS:NZ	2.43	0.50
5:B:236:SER:OG	5:B:240:GLU:OE1	2.19	0.50
28:LV:111:GLU:N	28:LV:111:GLU:OE1	2.45	0.50
1:5:1433:A:N6	1:5:1451:G:O2'	2.45	0.50
49:Lz:8:ASP:OD1	49:Lz:9:THR:N	2.45	0.50
1:5:947:C:OP1	10:LC:336:ARG:NH1	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:316:ALA:O	4:A:320:GLY:N	2.45	0.49
11:LD:186:GLU:OE2	11:LD:186:GLU:N	2.38	0.49
1:5:2479:G:N2	1:5:2499:C:O2	2.42	0.49
1:5:4083:U:OP1	8:LA:123:ARG:NH1	2.44	0.49
5:B:380:VAL:HG12	49:Lz:1:MET:SD	2.52	0.49
9:LB:188:GLY:O	9:LB:193:LYS:NZ	2.45	0.49
1:5:307:A:N3	1:5:310:G:O2'	2.41	0.49
16:LI:54:SER:HB2	16:LI:135:ILE:HD11	1.94	0.49
25:LS:71:SER:O	25:LS:76:LYS:NZ	2.45	0.49
1:5:3896:C:O2'	9:LB:268:ARG:NH1	2.44	0.49
15:LH:128:MET:HE2	15:LH:128:MET:HA	1.95	0.49
2:7:12:U:OP2	2:7:67:C:O2'	2.29	0.49
5:B:173:GLU:N	5:B:173:GLU:OE1	2.45	0.49
9:LB:370:THR:O	9:LB:370:THR:HG22	2.12	0.49
13:LF:122:PHE:O	13:LF:205:ASN:ND2	2.44	0.49
17:LJ:26:VAL:HG23	17:LJ:28:GLU:H	1.77	0.49
1:5:4195:G:O2'	1:5:4442:U:OP1	2.19	0.49
5:B:212:VAL:HG21	5:B:223:VAL:HG11	1.94	0.49
9:LB:153:MET:HE2	9:LB:194:LEU:HD21	1.94	0.49
37:Le:78:LEU:O	48:Lr:20:ARG:NH1	2.45	0.49
1:5:666:G:O2'	1:5:668:C:OP1	2.30	0.49
1:5:1279:A:O2'	1:5:1281:G:N7	2.44	0.49
4:A:486:LEU:HD13	4:A:502:ALA:HB1	1.95	0.49
1:5:267:G:OP1	40:Lh:109:ARG:NH2	2.45	0.49
1:5:4763:U:HO2'	25:LS:174:THR:HG1	1.57	0.49
1:5:90:G:OP2	1:5:92:C:N4	2.44	0.49
1:5:1741:G:O6	2:7:103:A:O2'	2.18	0.49
49:Lz:144:MET:H	49:Lz:144:MET:CE	2.23	0.49
1:5:458:C:O2'	12:LE:110:ARG:NH2	2.41	0.48
1:5:2838:G:OP1	9:LB:248:LEU:N	2.46	0.48
4:A:513:TYR:O	4:A:517:VAL:HG23	2.13	0.48
11:LD:152:ARG:O	11:LD:157:ASN:ND2	2.46	0.48
15:LH:21:LYS:O	15:LH:24:THR:HG22	2.13	0.48
1:5:1961:G:N2	1:5:2024:G:O2'	2.43	0.48
1:5:3696:C:O2'	1:5:3816:A:N1	2.39	0.48
4:A:44:GLN:O	6:C:284:ARG:NH2	2.46	0.48
4:A:357:VAL:HG12	4:A:359:SER:O	2.13	0.48
12:LE:112:MET:O	48:Lr:87:ARG:NH1	2.44	0.48
4:A:312:SER:OG	4:A:323:VAL:HG21	2.13	0.48
43:Lk:23:VAL:HG22	43:Lk:36:VAL:HG22	1.94	0.48
35:Lc:103:ASP:O	35:Lc:103:ASP:OD2	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:3893:C:O2'	1:5:4979:A:N1	2.46	0.48
8:LA:20:VAL:HG12	8:LA:23:ARG:HD2	1.95	0.48
30:LX:145:ASP:OD1	30:LX:147:LEU:N	2.47	0.48
33:La:76:ASP:N	33:La:76:ASP:OD1	2.47	0.48
34:Lb:63:LYS:HE2	34:Lb:63:LYS:HA	1.95	0.48
35:Lc:21:VAL:O	35:Lc:25:GLY:N	2.43	0.48
30:LX:72:ASP:OD1	30:LX:72:ASP:C	2.57	0.48
4:A:32:CYS:O	4:A:36:VAL:HG23	2.13	0.48
2:7:51:G:H21	17:LJ:12:MET:CE	2.27	0.47
1:5:1877:G:O6	34:Lb:10:HIS:NE2	2.47	0.47
48:Lr:31:ASN:OD1	48:Lr:34:ALA:N	2.47	0.47
1:5:362:A:N6	44:Li:37:TYR:O	2.44	0.47
1:5:1844:G:O3'	34:Lb:25:ARG:NH2	2.46	0.47
1:5:2843:U:O2'	1:5:4632:U:OP1	2.26	0.47
16:LI:181:PHE:CE1	16:LI:197:VAL:HG11	2.50	0.47
4:A:83:GLN:OE1	4:A:90:LEU:N	2.48	0.47
4:A:555:GLU:HG2	4:A:635:ILE:HG21	1.97	0.47
21:LO:27:VAL:O	21:LO:101:ARG:NH1	2.48	0.47
25:LS:3:ALA:O	25:LS:111:ARG:NH2	2.48	0.47
1:5:4196:G:OP1	16:LI:116:ARG:NH2	2.48	0.47
13:LF:83:VAL:HG23	13:LF:83:VAL:O	2.15	0.47
18:LL:172:GLU:OE2	41:Li:3:LEU:N	2.48	0.47
20:LN:124:ASP:OD1	20:LN:126:THR:N	2.42	0.47
1:5:2846:G:O2'	28:LV:19:GLY:O	2.27	0.47
1:5:3896:C:O2'	9:LB:268:ARG:NH2	2.47	0.47
5:B:204:ALA:CB	5:B:360:LEU:HD21	2.45	0.47
21:LO:158:GLU:C	21:LO:158:GLU:OE1	2.58	0.47
37:Le:84:GLU:O	37:Le:87:VAL:HG22	2.15	0.47
1:5:4266:G:N3	1:5:4266:G:H2'	2.30	0.47
28:LV:92:ASP:C	28:LV:92:ASP:OD1	2.57	0.47
1:5:2582:A:N1	1:5:2681:G:O2'	2.44	0.47
19:LM:108:ASP:OD1	19:LM:108:ASP:N	2.48	0.47
24:LR:28:GLU:N	24:LR:28:GLU:OE1	2.48	0.47
1:5:158:A:N1	1:5:276:C:O2'	2.39	0.47
1:5:4475:G:OP2	15:LH:173:ARG:NH2	2.48	0.47
1:5:4699:U:H4'	1:5:4700:A:OP1	2.15	0.47
1:5:4075:U:OP1	14:LG:249:ARG:NH1	2.48	0.46
5:B:176:ARG:NH2	5:B:431:ASP:OD1	2.47	0.46
1:5:1700:G:OP2	1:5:1704:C:N4	2.48	0.46
4:A:686:LEU:C	4:A:686:LEU:HD23	2.39	0.46
17:LJ:56:THR:OG1	17:LJ:64:ARG:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Ld:42:ALA:HB3	36:Ld:43:PRO:HD3	1.97	0.46
13:LF:219:GLY:O	13:LF:246:ARG:NH2	2.49	0.46
17:LJ:42:GLN:OE1	17:LJ:117:ILE:HD12	2.15	0.46
44:Ll:20:ASN:ND2	44:Ll:42:ARG:O	2.45	0.46
1:5:3813:A:N3	1:5:4538:G:O2'	2.43	0.46
1:5:3877:A:N3	1:5:4401:G:O2'	2.42	0.46
4:A:709:VAL:N	4:A:710:PRO:HD2	2.30	0.46
15:LH:43:VAL:HG21	15:LH:73:ILE:CD1	2.46	0.46
15:LH:80:MET:O	15:LH:84:VAL:HG22	2.15	0.46
16:LI:193:ASP:OD2	16:LI:193:ASP:C	2.59	0.46
1:5:1952:G:OP1	25:LS:139:ARG:NE	2.47	0.46
3:8:75:G:OP2	31:LY:74:TYR:OH	2.26	0.46
32:LZ:47:ASP:N	32:LZ:69:LYS:O	2.44	0.46
1:5:2845:A:H61	1:5:3843:C:H42	1.64	0.46
6:C:216:LEU:HD21	6:C:248:ARG:NH1	2.30	0.46
22:LP:40:HIS:NE2	22:LP:110:ASP:O	2.47	0.46
1:5:2434:G:O2'	1:5:2527:A:N1	2.40	0.46
1:5:4478:G:N2	1:5:4608:G:O2'	2.48	0.46
9:LB:289:GLN:O	9:LB:289:GLN:NE2	2.48	0.46
14:LG:117:ARG:NH2	14:LG:128:VAL:O	2.48	0.46
1:5:4208:U:OP1	1:5:4334:U:O2'	2.32	0.46
4:A:669:ARG:C	4:A:669:ARG:HE	2.23	0.46
5:B:422:MET:SD	5:B:422:MET:N	2.77	0.46
19:LM:43:THR:O	19:LM:43:THR:CG2	2.64	0.46
13:LF:171:ASP:OD1	13:LF:172:ASN:N	2.49	0.46
15:LH:41:ILE:HG22	15:LH:43:VAL:HG13	1.98	0.45
32:LZ:54:THR:HG22	32:LZ:55:ALA:N	2.31	0.45
5:B:488:ALA:O	5:B:491:SER:OG	2.32	0.45
1:5:3717:A:OP2	1:5:3735:G:N2	2.47	0.45
33:La:46:ASP:OD1	33:La:46:ASP:C	2.59	0.45
1:5:1554:A:N7	1:5:1573:G:N2	2.60	0.45
1:5:5001:U:H5''	9:LB:317:LEU:HD22	1.97	0.45
3:8:101:C:O3'	42:Lj:20:ARG:NH1	2.49	0.45
4:A:668:HIS:HD2	4:A:701:MET:SD	2.38	0.45
1:5:1280:C:O2'	10:LC:321:ASN:OD1	2.21	0.45
1:5:2778:G:N2	3:8:113:C:OP2	2.50	0.45
4:A:207:ILE:O	4:A:211:GLY:N	2.49	0.45
4:A:701:MET:HE3	4:A:701:MET:HA	1.99	0.45
9:LB:292:LEU:C	9:LB:292:LEU:HD12	2.42	0.45
49:Lz:88:GLU:OE2	49:Lz:88:GLU:N	2.31	0.45
1:5:1961:G:N2	1:5:2025:A:N7	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:5001:U:C5'	9:LB:317:LEU:HD22	2.46	0.45
4:A:595:MET:SD	4:A:595:MET:C	3.00	0.45
5:B:400:THR:O	5:B:404:VAL:HG23	2.17	0.45
23:LQ:154:LYS:O	23:LQ:163:THR:OG1	2.22	0.45
49:Lz:65:VAL:HG11	49:Lz:148:VAL:HG13	1.99	0.45
1:5:3909:C:O2'	4:A:440:ALA:O	2.29	0.45
15:LH:34:LEU:HD12	15:LH:84:VAL:HG13	1.98	0.45
15:LH:73:ILE:O	15:LH:77:VAL:HG23	2.17	0.45
40:Lh:82:ASP:OD1	40:Lh:82:ASP:N	2.48	0.45
1:5:2811:G:N2	1:5:2814:C:OP2	2.48	0.45
4:A:36:VAL:HG11	4:A:56:TYR:CE2	2.51	0.45
31:LY:37:GLU:N	31:LY:37:GLU:CD	2.75	0.45
1:5:230:G:OP1	31:LY:15:ARG:NH1	2.49	0.44
1:5:2601:A:O2'	1:5:2743:A:OP2	2.29	0.44
1:5:5063:G:O6	9:LB:124:LYS:NZ	2.45	0.44
3:8:1:C:O2	3:8:1:C:O4'	2.35	0.44
3:8:141:C:OP1	20:LN:38:ARG:NH1	2.50	0.44
11:LD:186:GLU:H	11:LD:186:GLU:CD	2.24	0.44
1:5:64:A:N1	1:5:108:A:O2'	2.48	0.44
1:5:2514:G:OP1	39:Lg:15:THR:HG21	2.17	0.44
1:5:4250:G:OP1	17:LJ:97:ASN:ND2	2.50	0.44
1:5:178:C:H41	1:5:258:G:H21	1.65	0.44
28:LV:30:ASP:OD1	28:LV:32:THR:HG22	2.17	0.44
1:5:1819:G:H1'	11:LD:115:MET:HE1	1.99	0.44
47:Lp:88:GLU:O	47:Lp:92:GLN:NE2	2.51	0.44
1:5:1364:U:OP2	18:LL:36:ARG:NH2	2.42	0.44
23:LQ:122:THR:OG1	23:LQ:124:ASP:OD1	2.31	0.44
32:LZ:5:MET:HE2	32:LZ:5:MET:HA	1.99	0.44
4:A:620:LYS:O	4:A:624:THR:OG1	2.28	0.44
10:LC:211:TYR:OH	10:LC:218:ILE:HD11	2.17	0.44
12:LE:49:VAL:O	12:LE:49:VAL:HG13	2.16	0.44
48:Lr:60:VAL:HG12	48:Lr:117:ILE:HG21	2.00	0.44
6:C:209:GLU:O	6:C:212:SER:OG	2.22	0.44
12:LE:281:ILE:HD13	12:LE:286:LEU:HD11	2.00	0.43
22:LP:64:ASN:ND2	22:LP:80:GLN:OE1	2.47	0.43
32:LZ:99:ASP:OD2	32:LZ:102:ARG:NH1	2.51	0.43
1:5:1697:G:N2	1:5:2084:C:OP1	2.47	0.43
1:5:2537:A:OP1	43:Lk:2:PRO:N	2.50	0.43
1:5:4589:A:N1	1:5:4621:C:O2'	2.47	0.43
12:LE:68:MET:HE3	12:LE:68:MET:HA	2.01	0.43
25:LS:164:LYS:CB	25:LS:165:PRO:CD	2.96	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:665:C:O4'	1:5:667:A:N6	2.50	0.43
4:A:671:ALA:O	4:A:674:GLU:N	2.51	0.43
11:LD:217:ASP:OD1	11:LD:217:ASP:N	2.51	0.43
1:5:2340:C:H4'	10:LC:42:THR:HG23	2.00	0.43
15:LH:105:ILE:CD1	15:LH:112:VAL:HG22	2.49	0.43
35:Lc:34:THR:HG23	35:Lc:95:ALA:HB2	2.00	0.43
1:5:2360:A:N6	1:5:3861:A:N7	2.61	0.43
1:5:4648:A:OP1	24:LR:62:ARG:NH1	2.51	0.43
47:Lp:52:VAL:O	47:Lp:52:VAL:HG13	2.19	0.43
1:5:394:G:N2	1:5:397:G:OP2	2.36	0.43
1:5:2438:A:O2'	1:5:2440:U:OP2	2.36	0.43
4:A:686:LEU:HD23	4:A:686:LEU:O	2.19	0.43
32:LZ:54:THR:HB	32:LZ:57:MET:HE3	2.00	0.43
34:Lb:63:LYS:O	34:Lb:63:LYS:HD3	2.18	0.43
1:5:3620:G:OP1	1:5:3622:C:N4	2.52	0.43
4:A:583:ASN:OD1	4:A:584:LEU:N	2.52	0.43
5:B:183:VAL:HG13	5:B:424:LEU:HD21	2.01	0.43
8:LA:171:GLY:O	47:Lp:68:ALA:HB2	2.18	0.43
20:LN:155:VAL:O	20:LN:162:ARG:NH2	2.52	0.43
38:Lf:103:VAL:HG13	38:Lf:103:VAL:O	2.18	0.43
1:5:435:A:O2'	37:Le:26:ASP:OD2	2.32	0.43
30:LX:92:ASP:OD1	30:LX:92:ASP:N	2.52	0.43
3:8:13:G:O2'	22:LP:121:LYS:O	2.36	0.43
10:LC:209:ILE:CD1	10:LC:227:ILE:HG23	2.49	0.43
24:LR:47:ASP:OD2	24:LR:47:ASP:N	2.52	0.43
24:LR:99:MET:CA	24:LR:99:MET:HE2	2.49	0.43
21:LO:110:PRO:N	21:LO:111:PRO:CD	2.82	0.43
4:A:637:ASP:OD1	4:A:638:PHE:N	2.52	0.42
49:Lz:129:ASN:OD1	49:Lz:130:LYS:N	2.52	0.42
1:5:2667:C:C1'	24:LR:96:MET:HE2	2.49	0.42
1:5:3786:U:OP1	1:5:4550:G:O2'	2.26	0.42
1:5:4587:G:OP1	21:LO:61:ARG:NH1	2.53	0.42
1:5:4874:A:O2'	25:LS:170:LYS:NZ	2.51	0.42
2:7:17:C:OP1	17:LJ:156:ARG:NH2	2.52	0.42
9:LB:153:MET:CE	9:LB:194:LEU:HD21	2.49	0.42
24:LR:144:LYS:HD2	24:LR:144:LYS:C	2.44	0.42
1:5:4759:C:OP2	21:LO:171:LYS:NZ	2.41	0.42
4:A:594:MET:HA	4:A:594:MET:CE	2.43	0.42
18:LL:142:GLU:HA	18:LL:142:GLU:OE1	2.19	0.42
1:5:2517:A:N3	1:5:2539:C:O2'	2.51	0.42
1:5:4212:A:N1	26:LT:3:ASN:ND2	2.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:228:VAL:HG12	6:C:267:LYS:HD3	2.01	0.42
48:Lr:38:PHE:O	48:Lr:45:HIS:NE2	2.42	0.42
1:5:1215:C:O2'	1:5:1216:C:OP1	2.30	0.42
1:5:1279:A:OP1	12:LE:131:LYS:NZ	2.41	0.42
1:5:2378:G:O2'	1:5:2380:G:N7	2.51	0.42
5:B:157:MET:SD	5:B:157:MET:C	3.02	0.42
11:LD:293:ARG:HA	11:LD:293:ARG:NH1	2.35	0.42
1:5:480:C:OP1	48:Lr:67:ARG:NH1	2.53	0.42
34:Lb:32:LEU:O	34:Lb:35:VAL:HG22	2.20	0.42
1:5:2637:U:HO2'	1:5:2718:U:HO2'	1.67	0.42
9:LB:224:LYS:HG2	9:LB:340:THR:HG22	2.01	0.42
21:LO:186:GLU:OE2	21:LO:187:LYS:N	2.52	0.42
30:LX:118:ASP:OD1	30:LX:118:ASP:N	2.52	0.42
39:Lg:15:THR:HG22	39:Lg:16:ALA:H	1.83	0.42
1:5:4451:G:N2	1:5:4452:U:O4	2.51	0.42
1:5:4635:A:H3'	1:5:4636:U:H4'	2.02	0.42
9:LB:56:ILE:HD12	9:LB:56:ILE:C	2.45	0.42
18:LL:7:GLY:O	33:La:49:HIS:NE2	2.52	0.42
27:LU:76:VAL:O	27:LU:78:PHE:N	2.53	0.42
1:5:4943:A:OP1	12:LE:158:ARG:NH1	2.52	0.42
9:LB:53:MET:HE2	9:LB:53:MET:HB3	1.97	0.42
9:LB:128:LYS:O	9:LB:131:THR:OG1	2.20	0.42
26:LT:111:GLU:CD	26:LT:111:GLU:C	2.87	0.42
49:Lz:67:VAL:O	49:Lz:67:VAL:HG23	2.20	0.42
1:5:23:C:OP1	42:Lj:44:LYS:NZ	2.35	0.42
1:5:4676:G:OP1	9:LB:281:ASN:ND2	2.49	0.42
28:LV:43:LYS:HG3	28:LV:60:MET:HE2	2.01	0.42
28:LV:106:VAL:HG12	28:LV:112:MET:HA	2.02	0.42
1:5:2869:U:O2'	1:5:2881:A:N7	2.40	0.41
38:Lf:47:CYS:SG	38:Lf:74:VAL:HG23	2.60	0.41
44:Ll:12:PHE:CE2	44:Ll:51:LEU:HD13	2.54	0.41
1:5:142:G:O2'	1:5:144:G:O5'	2.38	0.41
1:5:3974:G:OP2	1:5:4040:C:N4	2.53	0.41
1:5:1377:G:H21	1:5:1380:G:H5'	1.86	0.41
1:5:2406:G:N7	44:Ll:2:SER:N	2.68	0.41
1:5:3969:G:N1	1:5:4053:A:N1	2.64	0.41
1:5:4095:G:HO2'	1:5:4096:C:H6	1.67	0.41
4:A:309:VAL:O	4:A:313:VAL:HG23	2.19	0.41
4:A:384:ALA:CB	4:A:517:VAL:HG22	2.50	0.41
4:A:616:SER:O	4:A:620:LYS:N	2.48	0.41
16:LI:44:ASP:OD1	16:LI:44:ASP:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LV:32:THR:HG23	28:LV:34:ALA:H	1.85	0.41
1:5:1920:C:H3'	1:5:1921:C:H5''	2.03	0.41
1:5:2519:U:O2'	1:5:2530:U:O2	2.37	0.41
9:LB:288:GLY:N	9:LB:330:PHE:O	2.47	0.41
38:Lf:83:MET:HE3	38:Lf:83:MET:HB3	1.98	0.41
49:Lz:141:ASN:OD1	49:Lz:141:ASN:N	2.53	0.41
49:Lz:205:TYR:OH	49:Lz:215:ARG:NH2	2.53	0.41
4:A:143:CYS:O	4:A:147:ASP:N	2.53	0.41
5:B:185:ASP:N	5:B:185:ASP:OD1	2.52	0.41
1:5:303:C:OP2	20:LN:68:ARG:NH2	2.52	0.41
1:5:2607:C:C5'	24:LR:96:MET:HE1	2.50	0.41
1:5:4978:G:O2'	1:5:4980:C:OP2	2.25	0.41
16:LI:80:CYS:SG	16:LI:147:HIS:ND1	2.93	0.41
43:Lk:70:LYS:N	43:Lk:70:LYS:HD2	2.36	0.41
1:5:448:G:H5''	1:5:449:C:OP2	2.20	0.41
2:7:120:U:O4'	11:LD:262:LYS:NZ	2.37	0.41
4:A:592:ASP:OD2	17:LJ:58:ARG:NH2	2.53	0.41
1:5:739:G:OP2	19:LM:71:LYS:NZ	2.54	0.41
1:5:1354:A:N6	1:5:1503:A:O4'	2.54	0.41
1:5:1497:A:N6	23:LQ:175:GLU:O	2.53	0.41
1:5:2460:A:O2'	20:LN:96:ARG:NH2	2.53	0.41
1:5:2803:U:O2'	39:Lg:12:SER:O	2.24	0.41
1:5:4565:C:OP1	21:LO:65:ASN:ND2	2.44	0.41
4:A:653:VAL:O	4:A:653:VAL:HG23	2.19	0.41
9:LB:119:TYR:OH	9:LB:129:ALA:N	2.54	0.41
10:LC:150:LEU:HD12	10:LC:150:LEU:O	2.21	0.41
10:LC:162:LYS:N	10:LC:166:GLU:OE2	2.49	0.41
16:LI:36:LEU:N	16:LI:36:LEU:HD23	2.35	0.41
20:LN:43:THR:OG1	20:LN:131:GLU:OE2	2.34	0.41
33:La:93:ASN:OD1	33:La:95:THR:HG22	2.21	0.41
4:A:384:ALA:HB1	4:A:517:VAL:HG22	2.03	0.41
21:LO:26:GLN:OE1	21:LO:31:ARG:NH2	2.53	0.41
30:LX:148:ASP:OD1	30:LX:148:ASP:C	2.64	0.41
33:La:92:LYS:O	33:La:92:LYS:HG2	2.20	0.41
1:5:737:C:OP2	19:LM:71:LYS:NZ	2.49	0.40
1:5:1705:G:H21	1:5:1705:G:P	2.43	0.40
6:C:249:ILE:HG21	6:C:262:ILE:HD11	2.03	0.40
11:LD:184:ASP:N	11:LD:189:GLU:O	2.44	0.40
28:LV:107:ASN:OD1	28:LV:111:GLU:N	2.54	0.40
34:Lb:53:GLY:O	34:Lb:57:MET:HG3	2.20	0.40
1:5:703:G:H2'	1:5:704:C:H4'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4579:U:OP1	9:LB:120:LYS:NZ	2.32	0.40
21:LO:190:ASP:OD1	21:LO:190:ASP:C	2.62	0.40
4:A:255:THR:O	4:A:259:SER:OG	2.35	0.40
15:LH:105:ILE:HD12	15:LH:112:VAL:HG22	2.02	0.40
30:LX:143:ASP:OD2	30:LX:143:ASP:C	2.64	0.40
44:Ll:28:ARG:NH2	44:Ll:36:ARG:O	2.50	0.40
1:5:232:G:O6	31:LY:61:HIS:N	2.45	0.40
1:5:4772:C:N4	1:5:4862:G:O6	2.47	0.40
4:A:190:ILE:CG2	4:A:220:VAL:HG11	2.44	0.40
11:LD:184:ASP:OD1	11:LD:187:SER:OG	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3451/5070 (68%)	365 (10%)	5 (0%)
2	7	119/121 (98%)	6 (5%)	0
3	8	145/157 (92%)	15 (10%)	0
All	All	3715/5348 (69%)	386 (10%)	5 (0%)

All (386) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	39	A
1	5	42	A
1	5	48	G
1	5	59	A

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Mol	Chain	Res	Type
1	5	64	A
1	5	65	A
1	5	73	A
1	5	91	G
1	5	98	A
1	5	110	C
1	5	119	G
1	5	120	A
1	5	133	C
1	5	134	G
1	5	135	G
1	5	136	C
1	5	141	C
1	5	142	G
1	5	143	C
1	5	159	C
1	5	169	G
1	5	178	C
1	5	179	G
1	5	200	U
1	5	209	U
1	5	218	A
1	5	219	G
1	5	233	U
1	5	234	G
1	5	253	G
1	5	256	G
1	5	259	C
1	5	266	C
1	5	280	G
1	5	297	U
1	5	316	U
1	5	340	C
1	5	387	G
1	5	409	G
1	5	410	A
1	5	412	G
1	5	449	C
1	5	450	G
1	5	452	A
1	5	453	G
1	5	454	U

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Mol	Chain	Res	Type
1	5	467	U
1	5	662	C
1	5	666	G
1	5	667	A
1	5	669	C
1	5	686	A
1	5	687	U
1	5	697	G
1	5	704	C
1	5	731	G
1	5	738	C
1	5	739	G
1	5	740	G
1	5	759	G
1	5	914	U
1	5	915	A
1	5	917	A
1	5	925	C
1	5	926	G
1	5	932	A
1	5	933	G
1	5	936	C
1	5	943	A
1	5	944	A
1	5	945	U
1	5	956	A
1	5	959	G
1	5	960	A
1	5	961	G
1	5	962	C
1	5	965	G
1	5	967	C
1	5	968	C
1	5	969	C
1	5	982	U
1	5	1070	G
1	5	1072	C
1	5	1078	A
1	5	1101	C
1	5	1170	G
1	5	1182	C
1	5	1183	C

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Mol	Chain	Res	Type
1	5	1199	G
1	5	1211	G
1	5	1215	C
1	5	1241	C
1	5	1266	G
1	5	1269	G
1	5	1270	A
1	5	1272	C
1	5	1273	G
1	5	1284	G
1	5	1287	G
1	5	1326	A
1	5	1354	A
1	5	1359	G
1	5	1366	G
1	5	1387	A
1	5	1394	G
1	5	1397	A
1	5	1415	G
1	5	1438	U
1	5	1439	C
1	5	1443	A
1	5	1444	G
1	5	1498	G
1	5	1502	G
1	5	1534	A
1	5	1547	A
1	5	1578	U
1	5	1591	U
1	5	1596	U
1	5	1614	C
1	5	1624	G
1	5	1625	G
1	5	1631	A
1	5	1633	G
1	5	1634	A
1	5	1638	A
1	5	1640	C
1	5	1654	G
1	5	1661	C
1	5	1676	C
1	5	1677	U

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Mol	Chain	Res	Type
1	5	1697	G
1	5	1699	A
1	5	1701	A
1	5	1734	G
1	5	1742	A
1	5	1755	C
1	5	1758	G
1	5	1765	A
1	5	1766	A
1	5	1767	A
1	5	1768	C
1	5	1787	A
1	5	1804	A
1	5	1821	G
1	5	1836	G
1	5	1837	A
1	5	1842	G
1	5	1855	G
1	5	1869	G
1	5	1897	A
1	5	1918	U
1	5	1921	C
1	5	1922	G
1	5	1925	G
1	5	1931	C
1	5	1932	A
1	5	1940	G
1	5	1941	A
1	5	1948	G
1	5	1961	G
1	5	2026	A
1	5	2046	G
1	5	2048	U
1	5	2055	G
1	5	2056	G
1	5	2069	A
1	5	2084	C
1	5	2092	G
1	5	2093	A
1	5	2096	G
1	5	2098	G
1	5	2103	G

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Mol	Chain	Res	Type
1	5	2106	G
1	5	2107	C
1	5	2261	G
1	5	2300	A
1	5	2301	G
1	5	2313	A
1	5	2348	G
1	5	2351	C
1	5	2360	A
1	5	2395	A
1	5	2397	G
1	5	2398	U
1	5	2417	A
1	5	2421	G
1	5	2470	C
1	5	2471	G
1	5	2474	G
1	5	2475	G
1	5	2478	C
1	5	2504	C
1	5	2505	C
1	5	2506	G
1	5	2513	A
1	5	2554	U
1	5	2583	C
1	5	2587	A
1	5	2589	C
1	5	2601	A
1	5	2627	C
1	5	2653	C
1	5	2660	A
1	5	2669	C
1	5	2687	U
1	5	2694	G
1	5	2695	A
1	5	2696	A
1	5	2708	U
1	5	2711	G
1	5	2743	A
1	5	2761	U
1	5	2764	A
1	5	2769	U

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Mol	Chain	Res	Type
1	5	2788	U
1	5	2790	U
1	5	2814	C
1	5	2826	U
1	5	2827	G
1	5	2829	U
1	5	2855	G
1	5	3597	G
1	5	3605	C
1	5	3615	G
1	5	3618	C
1	5	3626	G
1	5	3635	A
1	5	3653	A
1	5	3662	A
1	5	3673	C
1	5	3709	U
1	5	3710	G
1	5	3753	G
1	5	3774	A
1	5	3776	G
1	5	3777	G
1	5	3783	A
1	5	3784	A
1	5	3811	G
1	5	3814	U
1	5	3817	A
1	5	3819	G
1	5	3838	U
1	5	3840	U
1	5	3877	A
1	5	3878	C
1	5	3879	G
1	5	3897	G
1	5	3901	A
1	5	3906	A
1	5	3907	G
1	5	3908	A
1	5	3915	U
1	5	3939	G
1	5	3951	G
1	5	3956	G

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Mol	Chain	Res	Type
1	5	3957	U
1	5	3958	G
1	5	3961	G
1	5	3965	A
1	5	3966	A
1	5	3967	G
1	5	3968	U
1	5	3973	G
1	5	3974	G
1	5	3975	C
1	5	4040	C
1	5	4045	G
1	5	4046	A
1	5	4047	A
1	5	4048	A
1	5	4049	U
1	5	4050	A
1	5	4051	C
1	5	4061	G
1	5	4076	G
1	5	4084	G
1	5	4096	C
1	5	4098	A
1	5	4119	C
1	5	4122	G
1	5	4163	U
1	5	4170	A
1	5	4183	G
1	5	4184	G
1	5	4191	G
1	5	4203	A
1	5	4229	U
1	5	4233	A
1	5	4251	A
1	5	4254	G
1	5	4266	G
1	5	4268	A
1	5	4273	A
1	5	4281	A
1	5	4291	G
1	5	4305	G
1	5	4330	G

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Mol	Chain	Res	Type
1	5	4339	A
1	5	4373	G
1	5	4377	G
1	5	4378	A
1	5	4387	C
1	5	4394	A
1	5	4422	A
1	5	4448	G
1	5	4452	U
1	5	4464	A
1	5	4465	U
1	5	4512	U
1	5	4513	A
1	5	4524	G
1	5	4548	A
1	5	4549	G
1	5	4560	C
1	5	4567	G
1	5	4584	A
1	5	4590	A
1	5	4636	U
1	5	4637	G
1	5	4670	C
1	5	4672	A
1	5	4700	A
1	5	4708	A
1	5	4709	U
1	5	4730	C
1	5	4732	G
1	5	4734	A
1	5	4741	C
1	5	4742	G
1	5	4743	G
1	5	4745	G
1	5	4750	G
1	5	4754	G
1	5	4757	C
1	5	4759	C
1	5	4761	G
1	5	4765	G
1	5	4771	C
1	5	4772	C

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Mol	Chain	Res	Type
1	5	4870	G
1	5	4871	C
1	5	4882	U
1	5	4883	C
1	5	4895	C
1	5	4900	C
1	5	4901	G
1	5	4910	A
1	5	4912	G
1	5	4913	G
1	5	4914	C
1	5	4938	A
1	5	4943	A
1	5	4976	U
1	5	4988	U
1	5	4990	C
1	5	4991	U
1	5	4994	G
1	5	5017	G
1	5	5034	A
1	5	5041	G
1	5	5050	C
1	5	5062	G
1	5	5069	U
2	7	7	G
2	7	53	U
2	7	54	A
2	7	64	G
2	7	110	G
2	7	120	U
3	8	23	C
3	8	34	U
3	8	35	C
3	8	51	U
3	8	59	A
3	8	62	A
3	8	63	U
3	8	80	A
3	8	87	G
3	8	94	G
3	8	103	A
3	8	105	C

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Mol	Chain	Res	Type
3	8	109	C
3	8	110	U
3	8	114	G

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	1590	C
1	5	1633	G
1	5	1757	U
1	5	4095	G
1	5	4699	U

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](#)

Of 225 ligands modelled in this entry, 225 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.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

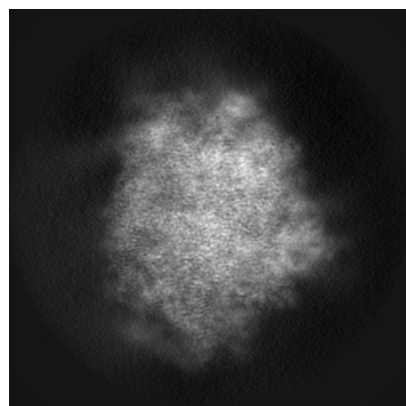
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16905. These allow visual inspection of the internal detail of the map and identification of artifacts.

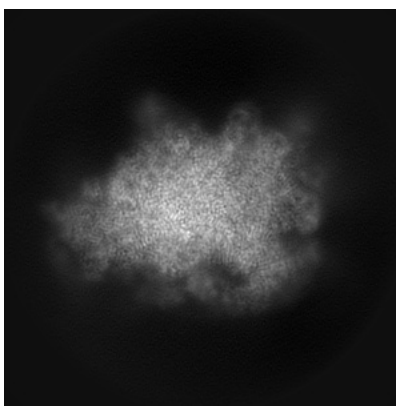
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

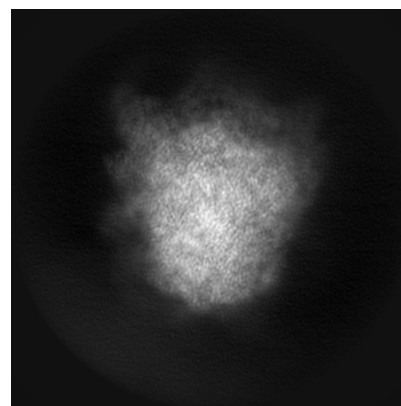
6.1.1 Primary map



X

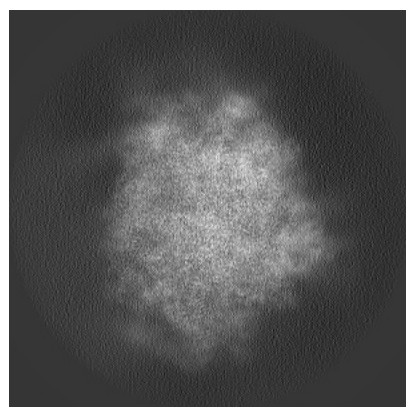


Y

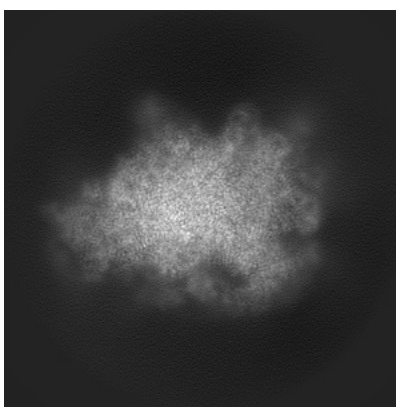


Z

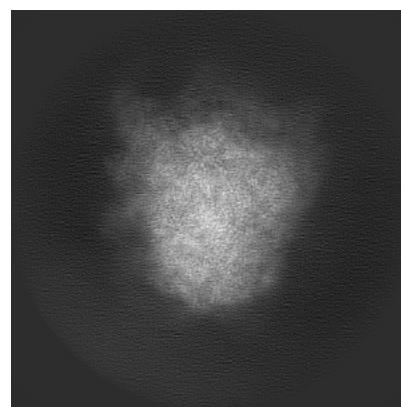
6.1.2 Raw map



X



Y

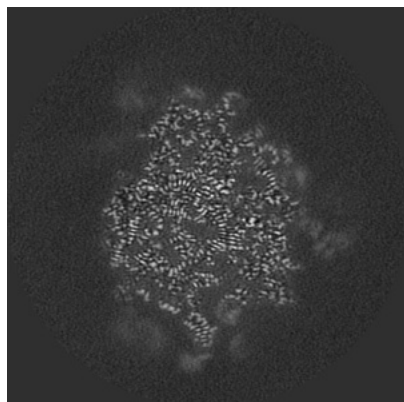


Z

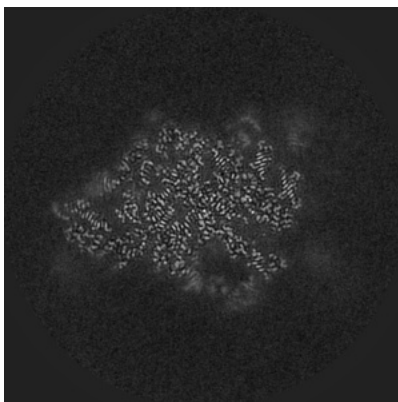
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

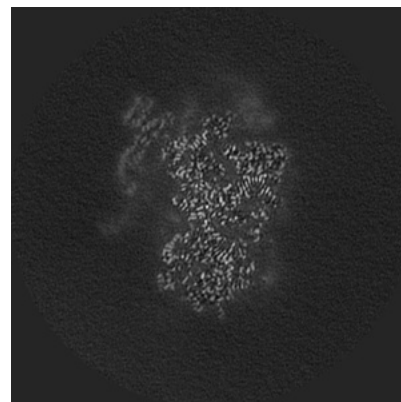
6.2.1 Primary map



X Index: 225

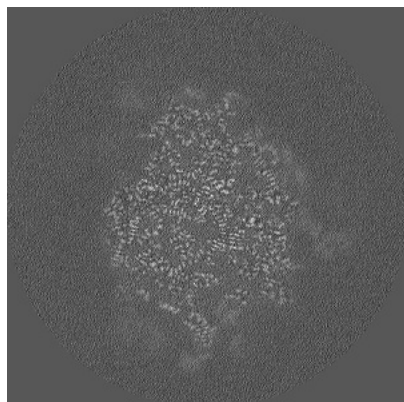


Y Index: 225

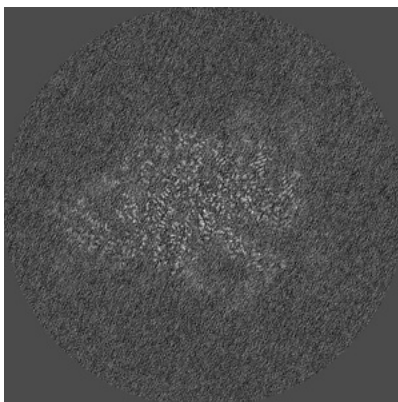


Z Index: 225

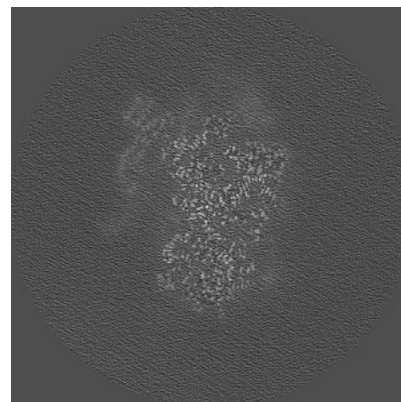
6.2.2 Raw map



X Index: 225



Y Index: 225

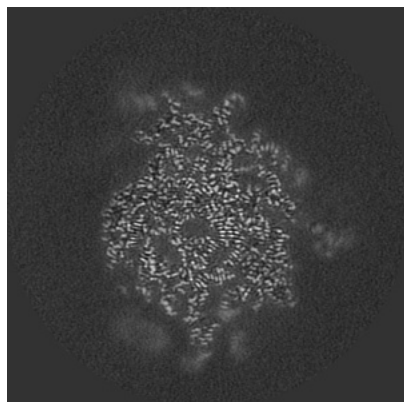


Z Index: 225

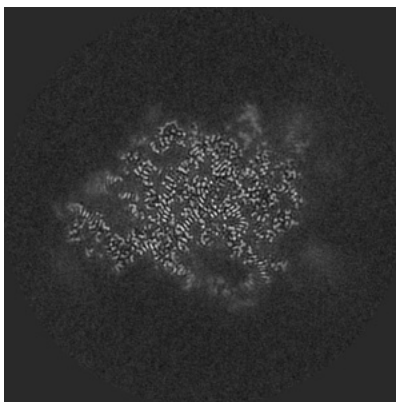
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

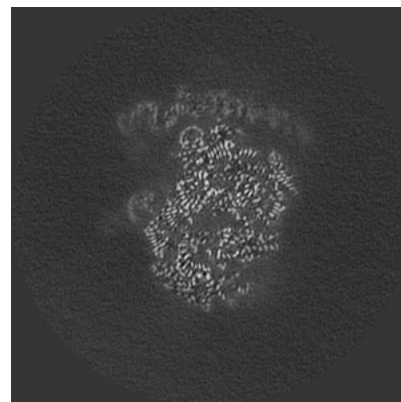
6.3.1 Primary map



X Index: 221

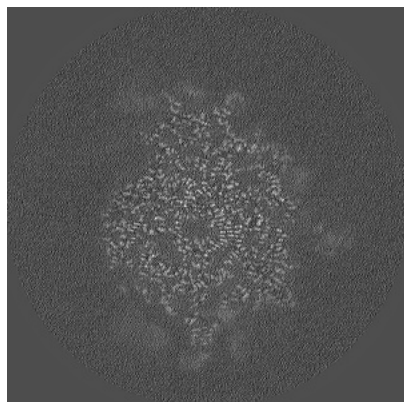


Y Index: 230

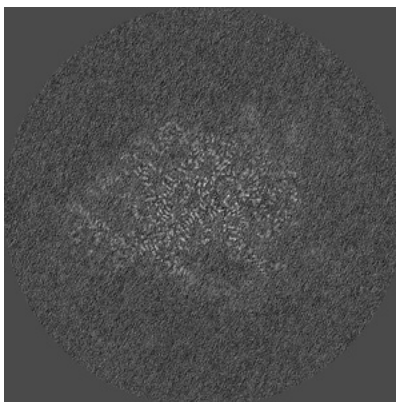


Z Index: 205

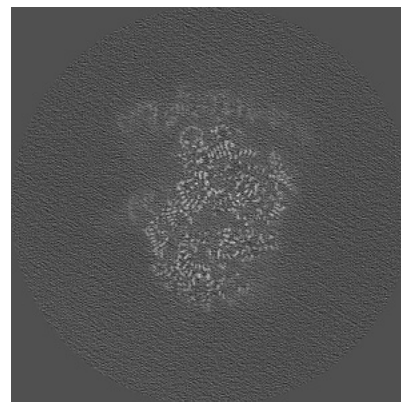
6.3.2 Raw map



X Index: 222



Y Index: 229

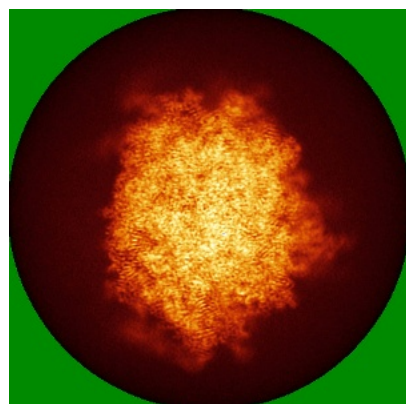


Z Index: 205

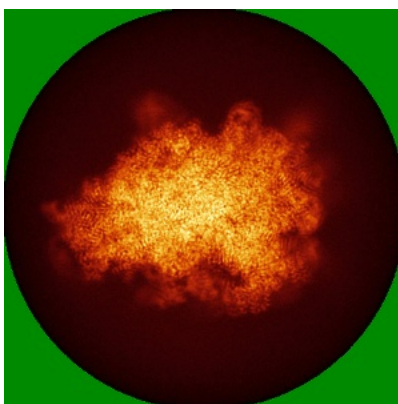
The images above show the largest variance slices of the map in three orthogonal directions.

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

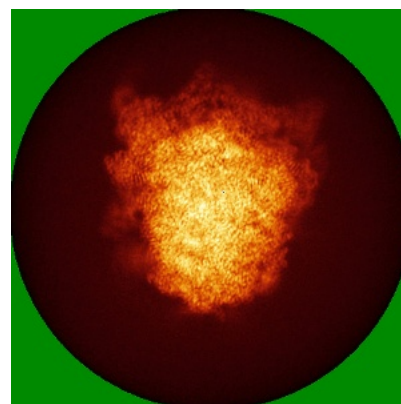
6.4.1 Primary map



X

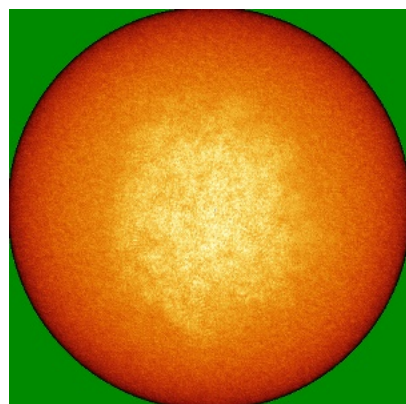


Y

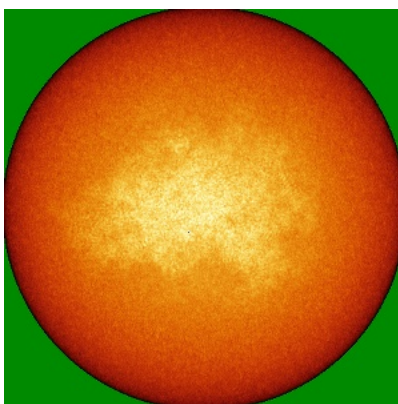


Z

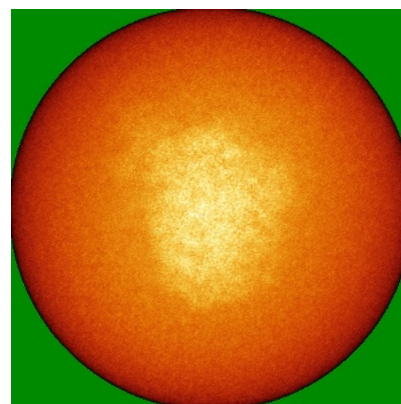
6.4.2 Raw map



X



Y

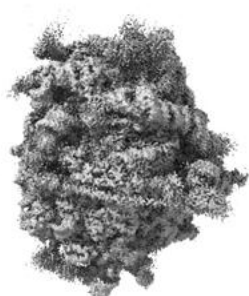


Z

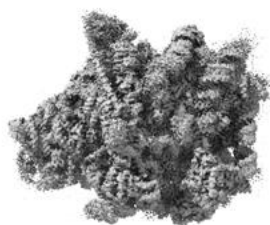
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



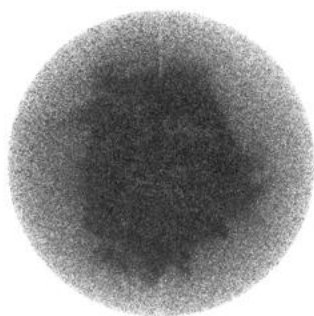
Y



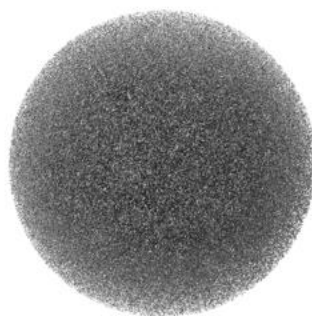
Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

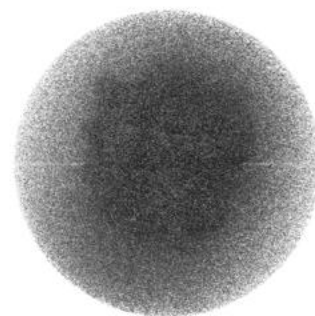
6.5.2 Raw map



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.

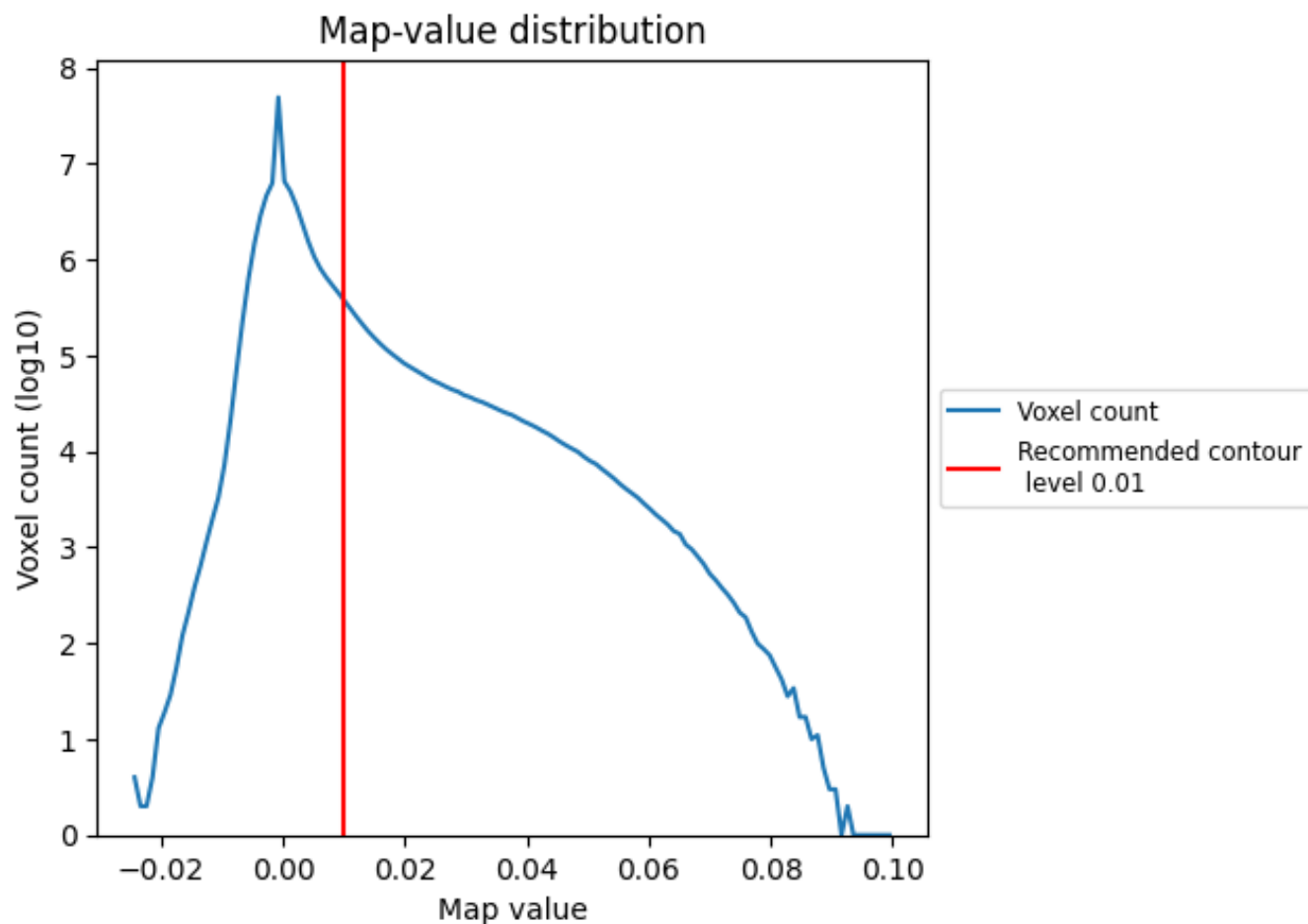
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

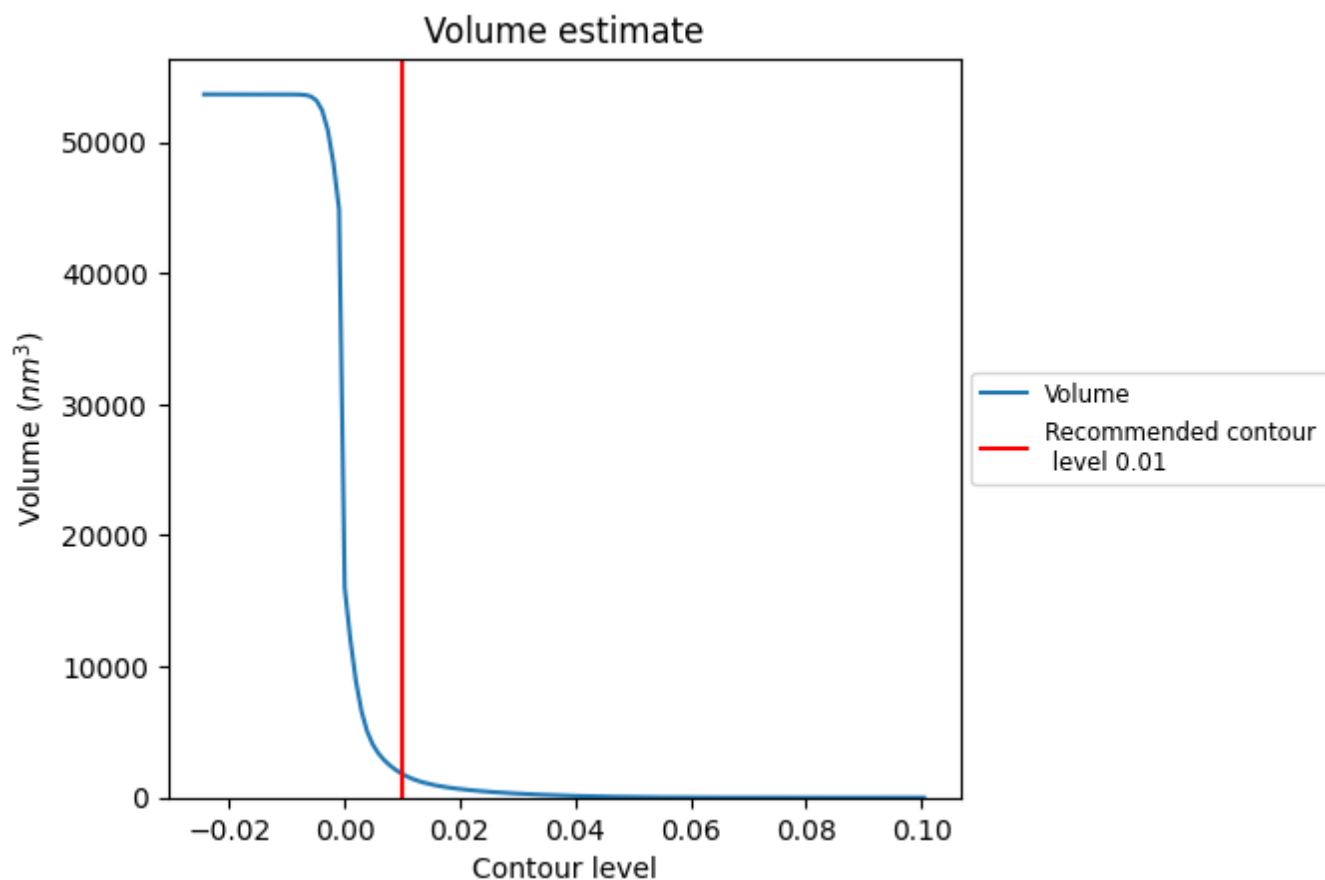
This section contains the results of statistical analysis of the map.

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.

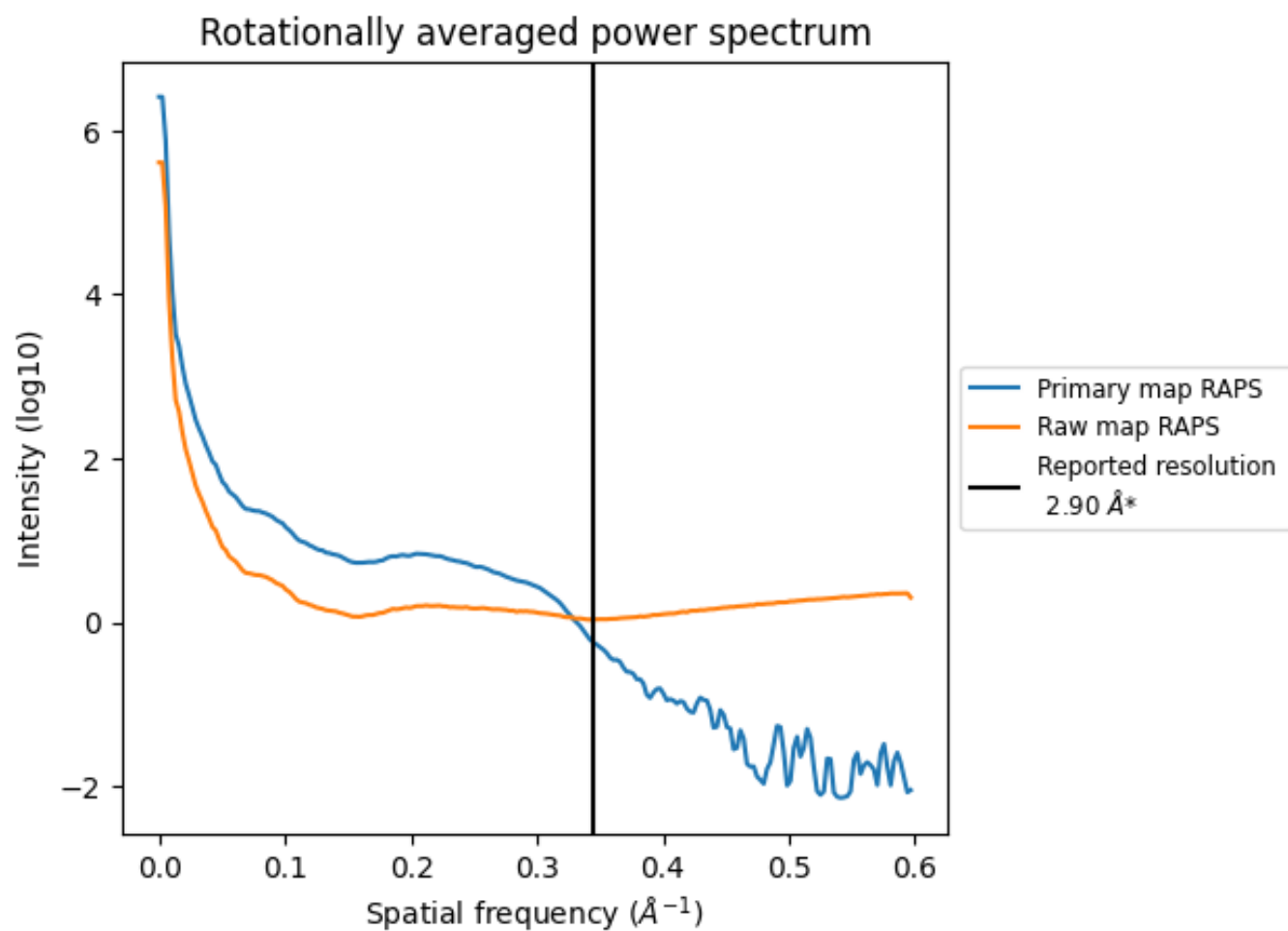
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1811 nm^3 ; this corresponds to an approximate mass of 1636 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 ⓘ

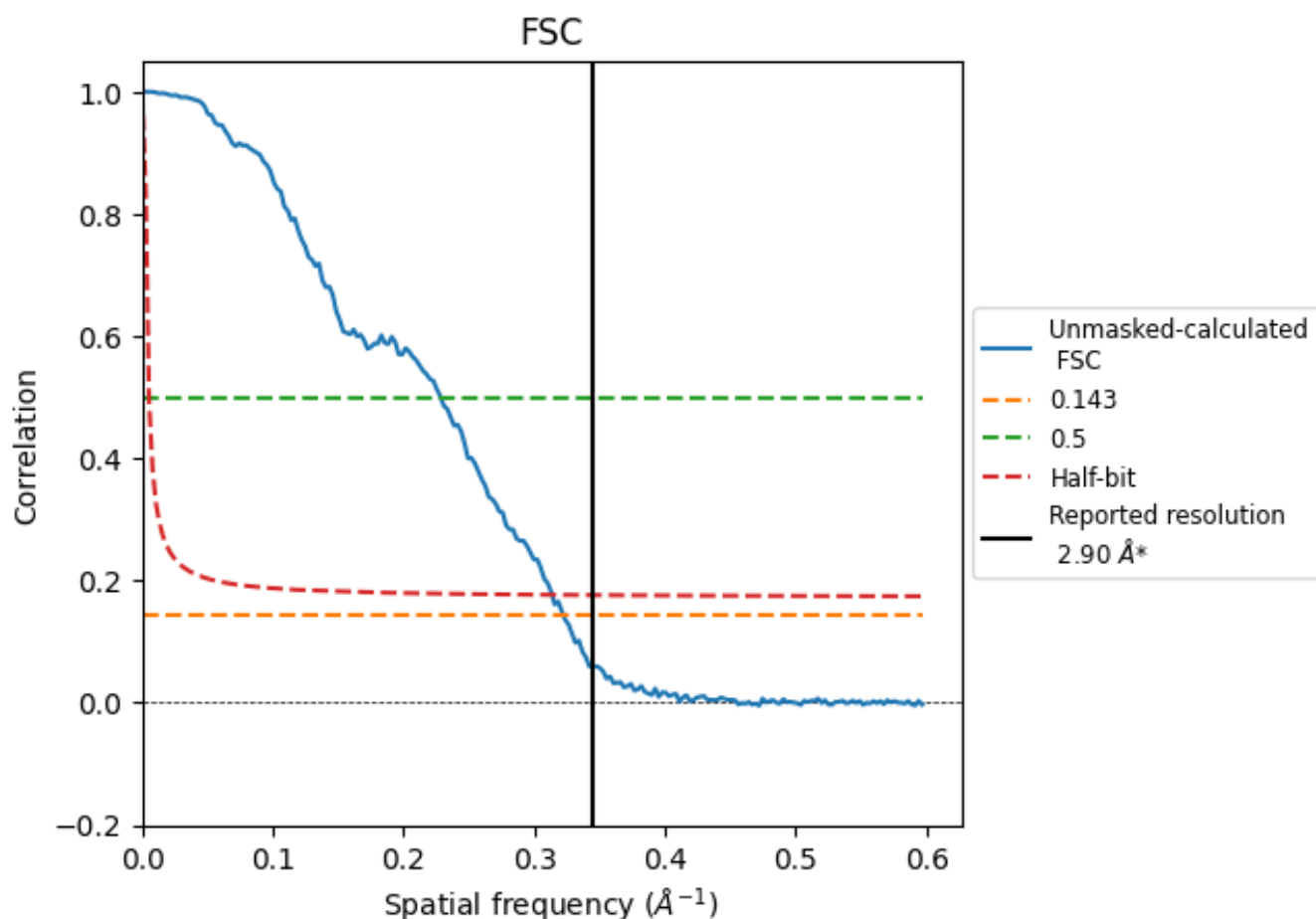


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

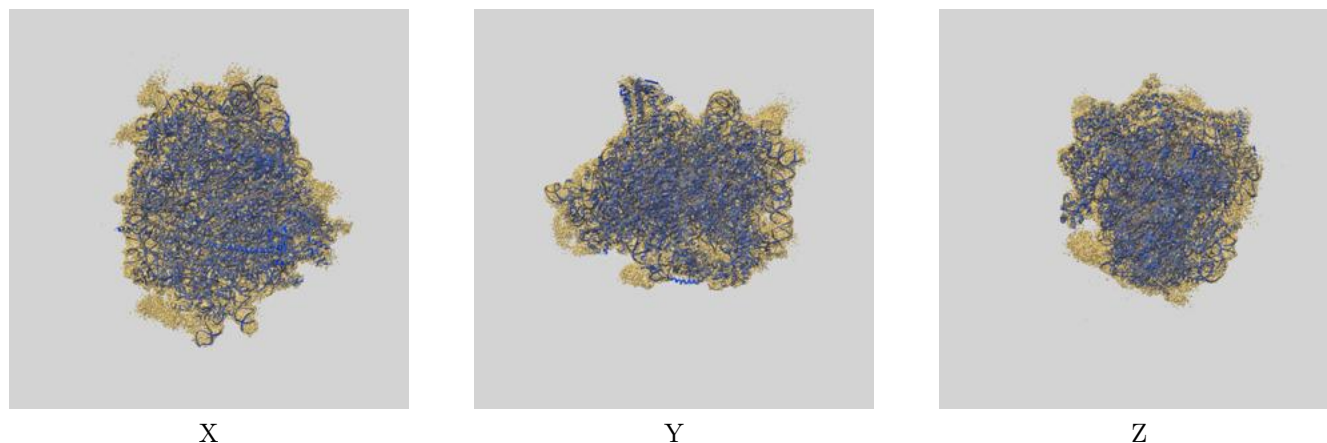
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.10	4.38	3.19

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

9 Map-model fit [i](#)

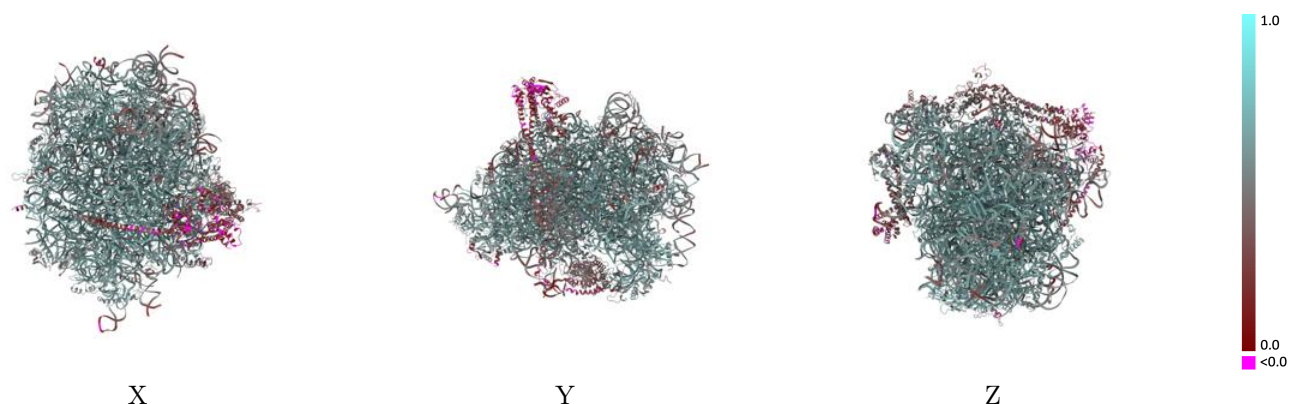
This section contains information regarding the fit between EMDB map EMD-16905 and PDB model 8OJ5. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



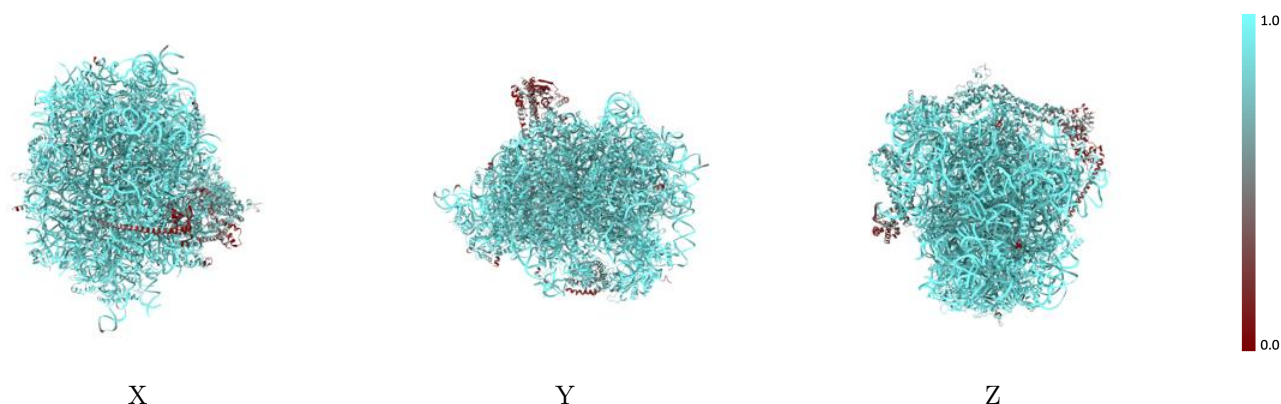
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



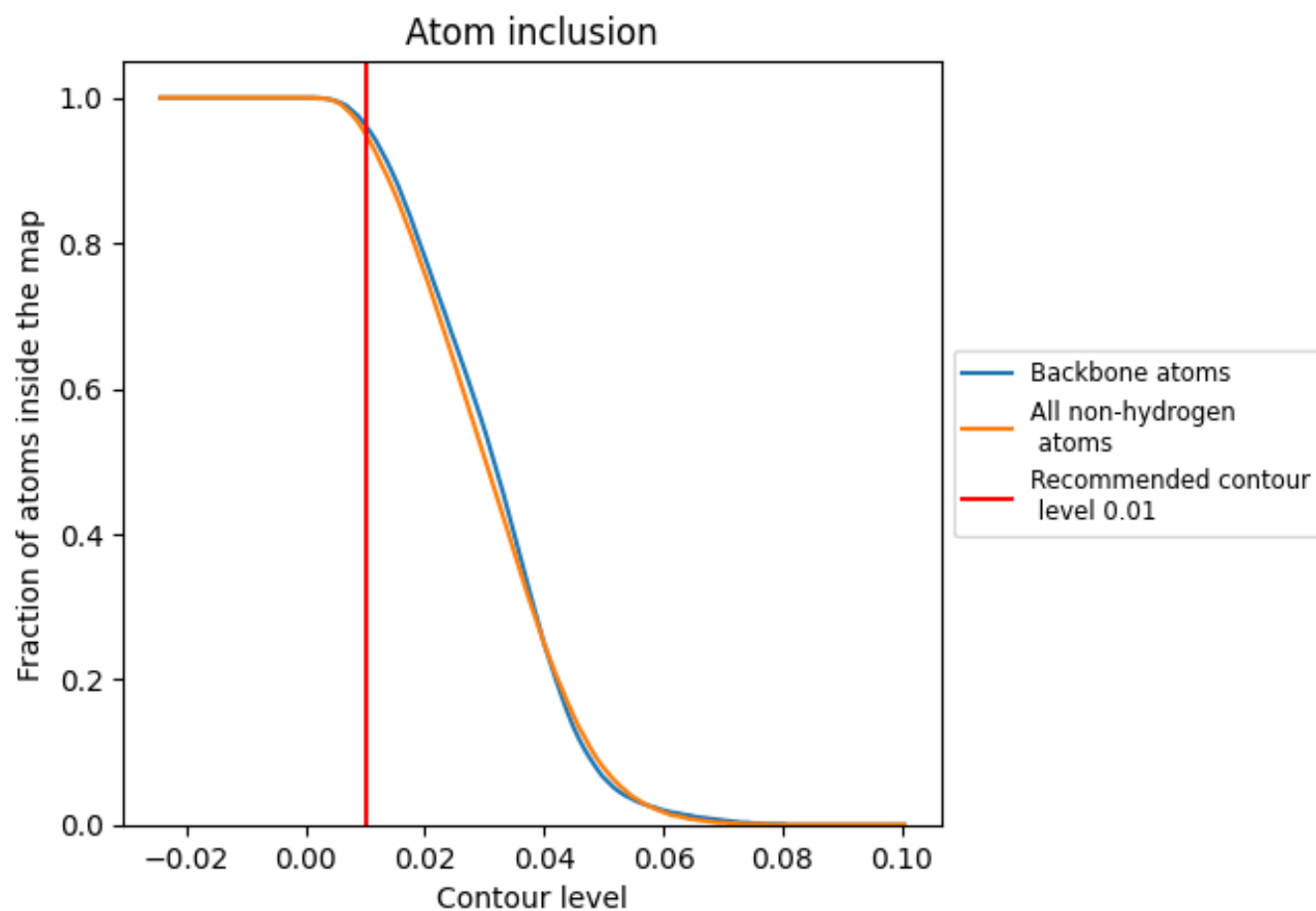
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9510	 0.5700
5	 0.9870	 0.5890
7	 0.9950	 0.6310
8	 0.9970	 0.6240
A	 0.7360	 0.3690
B	 0.5800	 0.2310
C	 0.4020	 0.2010
D	 0.1360	 0.0880
LA	 0.9910	 0.6390
LB	 0.9580	 0.6120
LC	 0.9690	 0.6030
LD	 0.9620	 0.5810
LE	 0.9730	 0.5660
LF	 0.9910	 0.6230
LG	 0.8990	 0.5490
LH	 0.9680	 0.6000
LI	 0.9870	 0.6210
LJ	 0.9050	 0.5320
LL	 0.9660	 0.5840
LM	 0.9830	 0.6100
LN	 0.9980	 0.6460
LO	 0.9810	 0.6220
LP	 0.9900	 0.6290
LQ	 0.9930	 0.6280
LR	 0.9560	 0.5870
LS	 0.9910	 0.6320
LT	 0.9910	 0.6100
LU	 0.8870	 0.5050
LV	 0.9770	 0.6040
LW	 0.9800	 0.6040
LX	 0.9810	 0.6130
LY	 0.9640	 0.6030
LZ	 0.9640	 0.5830
La	 0.9900	 0.6300
Lb	 0.9090	 0.5250



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Chain	Atom inclusion	Q-score
Lc	 0.9290	 0.5590
Ld	 0.9700	 0.5880
Le	 0.9940	 0.6350
Lf	 0.9950	 0.6440
Lg	 0.9430	 0.5890
Lh	 0.9690	 0.5970
Li	 0.9640	 0.5790
Lj	 0.9970	 0.6500
Lk	 0.8830	 0.5560
Ll	 0.9950	 0.6000
Lm	 0.9660	 0.6070
Lo	 0.9760	 0.6120
Lp	 0.9740	 0.6070
Lr	 0.9830	 0.6070
Lz	 0.8450	 0.4080