



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:57 AM UTC

PDB ID : 8PV7 / pdb_00008pv7
EMDB ID : EMD-17956
Title : Chaetomium thermophilum pre-60S State 1 - pre-5S rotation (Arx1/Nog2 state) - Composite structure
Authors : Thoms, M.; Cheng, J.; Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2023-07-17
Resolution : 2.12 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

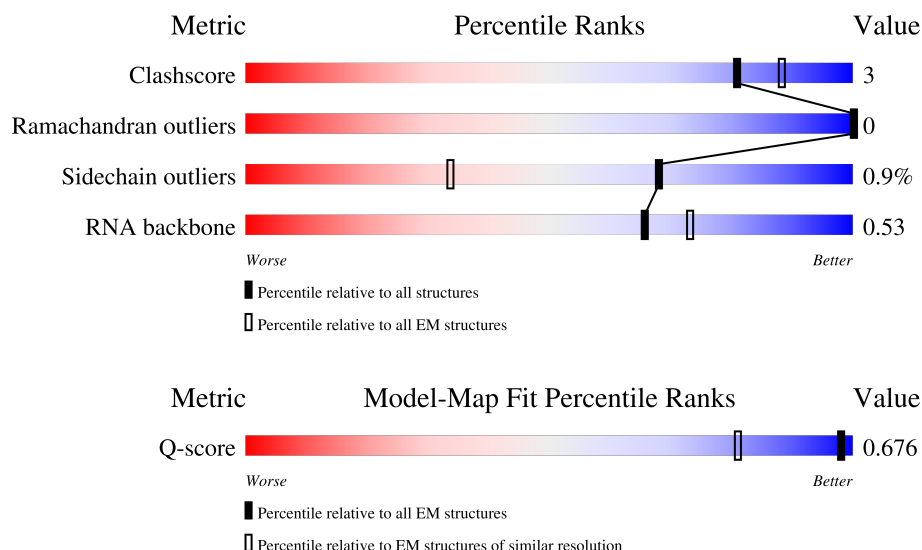
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.12 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2398 (1.64 - 2.62)

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	C1	3342	
2	C2	156	
3	C3	162	

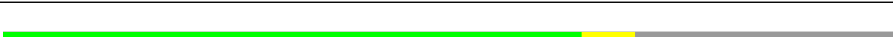
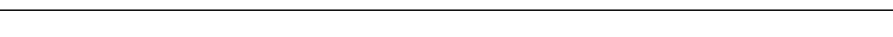
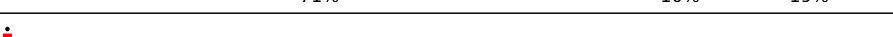
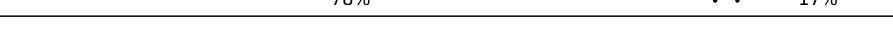
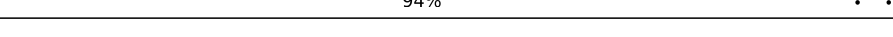
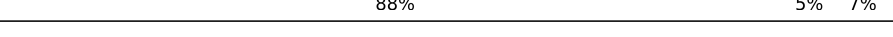
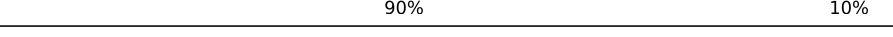
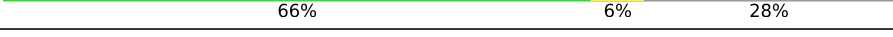
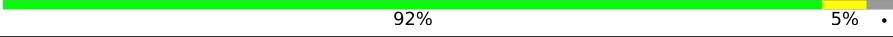
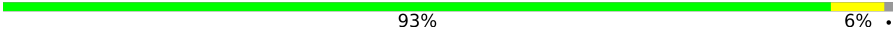
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Mol	Chain	Length	Quality of chain
4	C4	119	
5	CB	391	
6	CF	270	
7	CH	661	
8	CI	414	
9	CJ	679	
10	CK	261	
11	CL	558	
12	CM	249	
12	LF	249	
13	CN	246	
14	CO	120	
15	CQ	225	
16	Lq	147	
17	Cb	117	
18	Cd	627	
19	Ce	443	
20	Cf	350	
21	Cg	202	
22	Ch	517	
23	Cz	123	
24	LA	254	
25	LB	392	
26	LC	365	
27	LD	304	

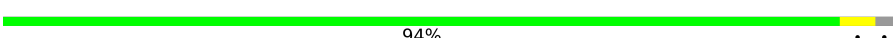
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Mol	Chain	Length	Quality of chain
28	LE	200	
29	LG	262	
30	LH	229	
31	LJ	173	
32	LK	165	
33	LL	213	
34	LM	142	
35	LN	203	
36	LO	204	
37	LP	187	
38	LQ	213	
39	LR	2898	
40	LS	174	
41	LT	160	
42	LU	127	
43	LV	139	
44	LX	156	
45	LY	138	
46	LZ	135	
47	La	149	
48	Lc	108	
49	Ld	120	
50	Le	131	
51	Lf	109	
52	Lg	119	

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Mol	Chain	Length	Quality of chain
53	Lh	935	
54	Li	110	
55	Lj	95	
56	Lk	94	
57	Ll	51	
58	Lp	92	

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 157262 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 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	3078	Total	C	N	O	P	0	0
			65888	29429	11926	21455	3078		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	156	Total	C	N	O	P	0	0
			3319	1484	589	1090	156		

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	82	Total	C	N	O	P	0	0
			1754	780	316	576	82		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C4	119	Total	C	N	O	P	0	0
			2536	1131	453	833	119		

- Molecule 5 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CB	267	Total	C	N	O	S	0	0
			2119	1359	373	384	3		

- Molecule 6 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CF	245	Total	C	N	O	S	0	0
			1934	1215	350	360	9		

- Molecule 7 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CH	627	Total	C	N	O	S	0	0
			5063	3181	924	939	19		

- Molecule 8 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CI	152	Total	C	N	O	S	0	0
			1234	791	230	208	5		

- Molecule 9 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CJ	382	Total	C	N	O	S	0	0
			3116	2008	548	550	10		

- Molecule 10 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CK	237	Total	C	N	O	S	0	0
			1903	1198	368	333	4		

- Molecule 11 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CL	79	Total	C	N	O	S	0	0
			622	389	125	108			

- Molecule 12 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CM	217	Total	C	N	O	S	0	0
			1773	1144	329	297	3		
12	LF	248	Total	C	N	O	S	0	0
			2023	1297	377	346	3		

- Molecule 13 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CN	246	Total	C	N	O	S	0	0
			1853	1156	322	368	7		

- Molecule 14 is a protein called DUF2423 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CO	62	Total	C	N	O	S	0	0
			468	290	94	82	2		

- Molecule 15 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CQ	183	Total	C	N	O	S	0	0
			1480	925	304	241	10		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	Lq	139	Total	C	N	O	0	0
			1073	672	213	188		

- Molecule 17 is a protein called Zinc finger domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Cb	101	Total	C	N	O	S	0	0
			830	517	161	148	4		

- Molecule 18 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Cd	462	Total	C	N	O	S	0	0
			3691	2350	671	659	11		

- Molecule 19 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Ce	262	Total	C	N	O	S	0	0
			2148	1337	413	394	4		

- Molecule 20 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Cf	285	Total	C	N	O	S	0	0
			2282	1443	417	401	21		

- Molecule 21 is a protein called Ribosome biogenesis regulatory protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Cg	188	Total	C	N	O	S	0	0
			1478	924	283	270	1		

- Molecule 22 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ch	485	Total	C	N	O	S	1	0
			3812	2396	696	710	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ch	117	ASP	GLU	engineered mutation	UNP G0SC29

- Molecule 23 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Cz	101	Total	C	N	O	S	0	0
			869	541	180	144	4		

- Molecule 24 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LA	191	Total	C	N	O	S	0	0
			1454	917	278	256	3		

- Molecule 25 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LB	389	Total	C	N	O	S	0	0
			3104	1973	579	539	13		

- Molecule 26 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LC	363	Total	C	N	O	S	0	0
			2751	1737	527	478	9		

- Molecule 27 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LD	286	Total	C	N	O	S	0	0
			2266	1434	407	422	3		

- Molecule 28 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LE	191	Total	C	N	O	S	0	0
			1477	944	267	263	3		

- Molecule 29 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LG	235	Total	C	N	O	S	0	0
			1889	1210	350	324	5		

- Molecule 30 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LH	190	Total	C	N	O	S	0	0
			1495	949	268	272	6		

- Molecule 31 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LJ	169	Total	C	N	O	S	0	0
			1357	850	266	235	6		

- Molecule 32 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LK	158	Total	C	N	O	S	0	0
			1184	743	215	224	2		

- Molecule 33 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LL	203	Total	C	N	O	S	0	0
			1587	989	325	271	2		

- Molecule 34 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LM	141	Total	C	N	O	S	0	0
			1126	714	216	195	1		

- Molecule 35 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LN	202	Total	C	N	O	S	0	0
			1704	1062	360	278	4		

- Molecule 36 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LO	203	Total	C	N	O	S	0	0
			1611	1034	305	267	5		

- Molecule 37 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LP	171	Total	C	N	O	S	0	0
			1343	834	274	232	3		

- Molecule 38 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LQ	150	Total	C	N	O	S	0	0
			1200	759	239	200	2		

- Molecule 39 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LR	155	Total	C	N	O	S	0	0
			1241	772	262	203	4		

- Molecule 40 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LS	174	Total	C	N	O	S	0	0
			1426	917	266	238	5		

- Molecule 41 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LT	129	Total	C	N	O	S	0	0
			1027	651	195	179	2		

- Molecule 42 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LU	105	Total	C	N	O	S	0	0
			846	548	146	151	1		

- Molecule 43 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LV	135	Total	C	N	O	S	0	0
			991	630	184	170	7		

- Molecule 44 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LX	145	Total	C	N	O		0	0
			1133	723	211	199			

- Molecule 45 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LY	133	Total	C	N	O	S	0	0
			1056	658	213	183	2		

- Molecule 46 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LZ	135	Total	C	N	O	S	0	0
			1112	713	207	188	4		

- Molecule 47 is a protein called 60S ribosomal protein L28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	La	108	Total	C	N	O	S	0	0
			872	556	168	147	1		

- Molecule 48 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lc	95	Total	C	N	O	S	0	0
			705	449	122	129	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ld	110	Total	C	N	O	S	0	0
			875	555	171	148	1		

- Molecule 50 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Le	126	Total	C	N	O	S	0	0
			1017	640	208	163	6		

- Molecule 51 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lf	108	Total	C	N	O	S	0	0
			862	546	171	144	1		

- Molecule 52 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Lg	118	Total	C	N	O	S	0	0
			914	567	186	157	4		

- Molecule 53 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	Lh	122	Total	C	N	O	0	0
			1003	637	198	168		

- Molecule 54 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Li	101	Total	C	N	O	S	0	0
			827	509	181	136	1		

- Molecule 55 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Lj	88	Total	C	N	O	S	0	0
			698	427	154	112	5		

- Molecule 56 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lk	76	Total	C	N	O	S	0	0
			632	400	121	109	2		

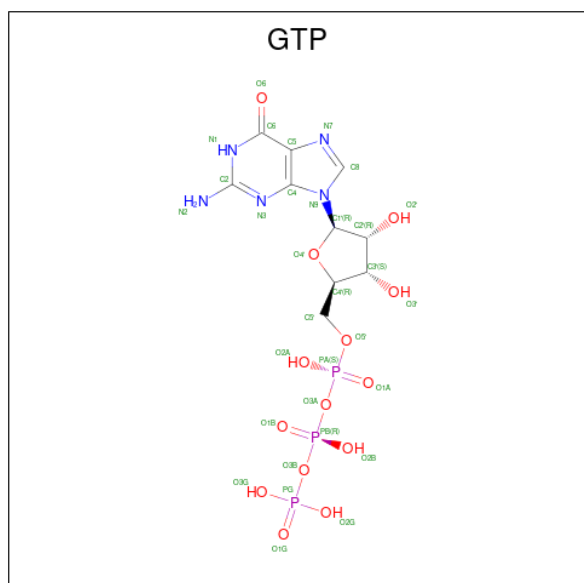
- Molecule 57 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	Ll	50	Total	C	N	O	0	0
			436	275	97	64		

- Molecule 58 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Lp	91	Total	C	N	O	S	0	0
			698	430	138	124	6		

- Molecule 59 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
59	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
59	Cd	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	CH	1	Total	Mg	0
			1	1	
60	Cd	2	Total	Mg	0
			2	2	

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	CQ	1	Total	Zn	0
			1	1	
61	Cb	1	Total	Zn	0
			1	1	
61	Lg	1	Total	Zn	0
			1	1	
61	Lj	1	Total	Zn	0
			1	1	
61	Lp	1	Total	Zn	0
			1	1	

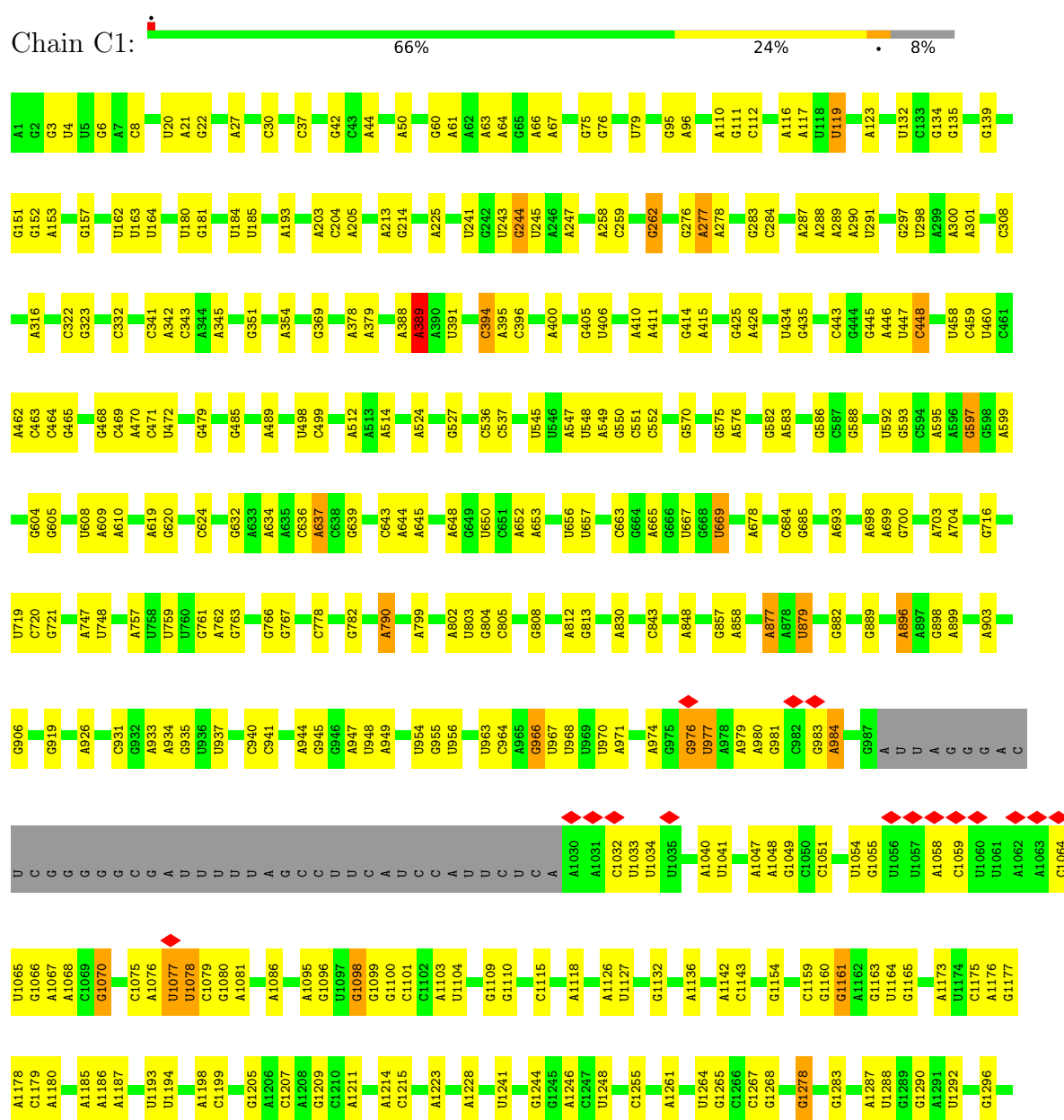
- Molecule 62 is water.

Mol	Chain	Residues	Atoms		AltConf
62	CH	1	Total	O	0
			1	1	
62	Cd	2	Total	O	0
			2	2	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 26S rRNA



C2803	G2889	G2582	U2397	G	A2205	G2074	U1799	U1505	U1305
A2804	U2690	G2583	G2398	A	A2206	U2075	C1800	U1536	C1306
U2805	C2584	C2585	U2399	U2277	G2212	A2076	U1801	U1537	A1313
A2806	A2692	A2585	G2400	U2278	G2216	G2084	G1809	U1538	C1323
C2807	A2693	U2592	A2403	G2279	U2217	G2085	C1812	C1539	U1324
G2808	A2706	U	A2406	A2280	A2218	A2089	U1813	A1541	A1331
G2809	A2707	A	C	U2281	A2219	A2090	U1814	A1542	G1332
A2810	G2713	A	U	C2220	C2221	A2091	A1815	G1543	A1333
G2812	A2717	A	A	U2221	U2222	G2092	C1816	U1549	A1334
C2816	A2718	C	G	A2223	A2224	G2093	A1822	U1550	A1335
U2817	C2723	A	A	U2225	U2226	A2094	C1826	C1551	C1336
U	C2724	U	A	C2227	U2228	A2101	C1829	U1552	G1337
U2820	U2730	A	U	U2229	U2230	U2102	U1702	G1553	U1350
U2821	C2731	A	U	U2231	U2232	U2103	U1704	U1554	U1351
G2822	C2732	C	U	A	U2233	A2121	C1842	C1555	G1370
C2826	G2736	G2604	U	A	A2243	U2122	U1843	U1560	G1372
U2827	A2737	C2605	A	G	A	G2123	A1844	G1561	U1371
U2828	U2744	U2609	U	U2307	U2308	G2124	A1845	U1562	G1372
G2836	U2754	U2614	A	A2315	A2316	C2125	C1846	G1563	G1382
G2837	C2755	A2615	A	A2320	A2321	C2126	A1847	A1567	A1383
C2838	G2756	A2632	U	A2326	A2327	A2130	U1856	A1568	G1395
A2846	C2757	A2633	G	G2327	U2327	A2131	U1857	A1569	C1403
G2857	C2757	C2634	U	A2330	A2331	G2132	A1859	A1573	
C2858	A2758	A2635	U	A2331	A2332	A2151	U1860	G1576	U1413
A2859	A2761	G2636	G	A2332	A2333	U2156	A1866	C1577	G1417
G2860	A2762	U2642	A	G2340	A2341	G2157	A1867	A1583	A1418
U2863	A2763	U2647	G	A2348	A2349	C2158	U1868	U1584	U1419
U2882	C2769	A2650	U	U2351	U2352	C2160	G1877	A1585	C1420
U2883	C2770	A2651	U	C2355	C2356	A2161	G1878	U1586	U1421
C2884	A2771	A2656	G	G2356	G2357	G2164	G1879	C1595	A1429
C2886	A2772	G2657	C	U2359	U2360	C2167	G1758	U1596	G1430
C2887	A2776	G2658	C	G2359	G2360	G2168	G1759	U1599	U1431
A2889	U	A2663	C	A2362	A2363	G2169	G1760	U1609	G1433
C2890	A	A2664	A	G2363	G2364	A2170	U1762	G1610	U1438
U2891	C	G2665	U	A2364	A2365	U2171	C1763	C1611	G1449
A2892	U2781	U2666	G	U2373	U2374	U2172	G1766	G1614	G1458
U2893	G2782	C2667	U	U2374	U2375	A2176	A1767	C1619	A1464
A2894	C2783	U2672	A	A2376	A2377	A2186	G1776	A1622	G1485
A2895	U2785	G2673	A	G2377	G2378	U2188	A1777	A1623	C1624
A2899	G2789	A2674	U	U2380	U2381	A2192	A1778	A1624	G1491
U2903	U2790	U2675	A	G2382	G2383	C2197	A1779	A1638	G1492
G2904	C2791	U2571	A	U2383	U2384	G2203	A1780	A1639	G1493
A2905	A2796	U2572	U	C2384	C2385	U2204	G1792	G1640	G1503
G2906	U2801	G2577	C	U2396	U2397	U2205	A1793	U1795	G1504
U2914	U2802	U2578	C				A1794	G1938	

53% . 44%



85% 5% 9%



Response	Percentage
Yes, it is a crisis	86%
No, it is not a crisis	13%



ALA
GLY
LEU
TRP
GLY
ASP
GLU
GLN
THR
GLU
GLY
ASP
LYS
MET
GLU
ALA

- Molecule 12: 60S ribosomal protein l7-like protein

Chain CM:  78% 8% 13%

MET SER SER THR THR VAL PRO THR GLN ASN ASP ILE L113 R22 K23 K27 A35 LEU GLU LYS ARG LYS LYS ALA ASN LYS GLU LYS ARG GLN V49 G79 SER PHE HIS ILE PRO ALA ALA A87 V90 R94 I95 Q110 L114 R115 V121 F122 V123 T126

T129 M132 V162 A173 E177 N178 Y182 H192 Q203 E238 E239 N249

- Molecule 12: 60S ribosomal protein l7-like protein

Chain LF:  94% 6%

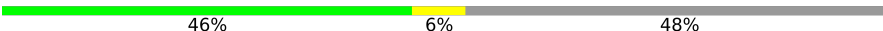
MET S2 D11 K56 Y61 E65 V90 F91 V92 K104 L114 G120 V121 I174 M178 Y182 Q203 R223 N249

- Molecule 13: Eukaryotic translation initiation factor 6

Chain CN:  89% 10%

M1 G14 N21 E32 R50 R61 R67 T74 D91 L101 G105 N106 Y107 I108 V109 D112 H118 L121 G149 M152 A153 L154 V161 Q168 S175 V186 T210 E214 I218 Y246

- Molecule 14: DUF2423 domain-containing protein

Chain CO:  46% 6% 48%

MET A2 N13 R16 T40 A43 PRO LYS LYS PRO ASP ASP ILE GLU MET LYS GLU SER GLU GLU ALA ALA GLU GLN PRO LYS THR SER THR LYS ASP ASP THR MET ASP VAL ASP GLY ALA LYS PRO THR LEU S83 K89 R93 K94 D95 SER ARG LYS ARG

ARG GLY LYS LYS S104 S105 I106 V107 M110 LYS LYS PRO LYS ARG ASN ASN LEU LYS LYS

- Molecule 15: Ribosome biogenesis protein RLP24

Chain CQ:  73% 8% 19%

M1 S16 K17 G18 F31 R74 T59 N93 L137 R138 E141 K142 R143 L145 A150 E151 V154 D155 L159 E163 S173 K174 E179 V180 R181 R182 V183 ARG VAL ARG THR ASP GLY VAL GLU GLU ILE THR GLU SER PHE GLY LYS ASN

VAL ASP GLU MET ASP ASP HIS ASP SER ASP ARG ASP ASP ASP MET ASP THR ASP

- Molecule 16: Putative 60S ribosomal protein

Category	Count
MET	1
S2	2
I9	9
W10	10
E11	11
R14	14
L20	20
D31	31
N34	34
V47	47
R88	88
K92	92
K131	131
R140	140
ALA	1
ALA	1
ALA	1
ALA	1
GLY	1
LYS	1
GLN	1

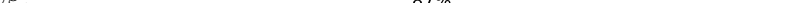
- [illegible]

- [illegible]

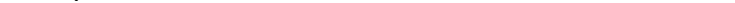
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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|
| ASP | SER | ALA | TRP | GLU | PHE | GLY | GLU | ASP | GLY | GLU | GLY | ALA | LYS | K295 | K316 | K317 | K318 | R319 | E320 | E331 | E353 | MET | SER | ASP | ASP | SER | E360 | D363 | E378 | D391 | L396 | K397 | R413 | E417 | A418 | R419 | R425 | A428 | E434 | R435 | | | | | | | | | | |
| GLU | LEU | ILE | ARG | ILE | LYS | LYS | VAL | ALA | GLY | GLU | HIS | GLU | THR | THR | VAL | ASP | ILE | ILE | ASP | ALA | T156 | A161 | GLN | ASP | PRO | ILE | GLU | PRO | VAL | ARG | PRO | VAL | LEU | PRO | LYS | P180 | E237 | R240 | A258 | A259 | E260 | E269 | MET | SER | GLU | TRP | GLU | | | |
| ALA | VAL | LEU | PHE | THR | ILE | ASP | VAL | GLY | ASP | ALA | SER | LEU | LYS | ARG | GLY | GLY | GLN | LYS | ASP | PRO | ILE | GLU | LYS | LYS | GLN | ASP | PRO | VAL | ARG | PRO | VAL | LEU | PRO | ILE | LEU | VAL | ILE | ARG | GLN | ARG | GLY | THR | ASN | TYR | ALA | GLU | THR | LYS | PRO | LYS |

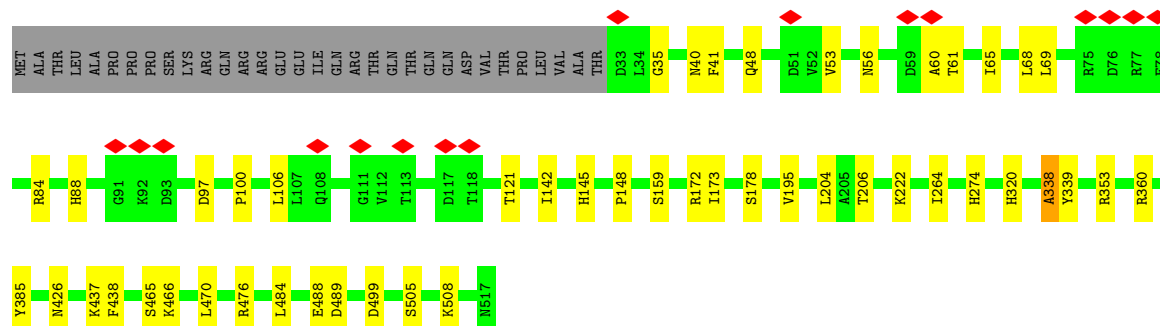
- 
- WORLD WIDE
PDB
PROTEIN DATA BANK

VAL	ASN	MET
GLU	ASN	LEU
ALA	ASP	ARG
GLY	GLY	ILE
SER	GLU	GLN
GLY	ASN	LYS
GLU	PRO	P7
LYS	ALA	123
LYS	PRO	
LYS	LEU	
LYS	PRO	C30
LYS	GLY	L31
VAL	MET	F32
VAL	THR	
LYS	ASP	T36
GLY	PRO	
	ARG	M47
	SER	D48
	ILE	
	PRO	R59
	SER	
	SER	K62
	SER	K63
	Q221	
	L227	L86
	M253	R96
	D254	P97
	F255	H98
	R261	R104
	T277	D112
	P278	M113
	Q279	
	D290	F116
	D294	P120
		Y123
	R298	A145
	M301	M159
	R319	D166
GLY	ARG	R169
ASP	GLU	
ASP	ASP	P172
GLU	GLU	
GLY	GLY	T188
GLU	GLU	P192
ASP	THR	THR
ARG	SER	SER
THR	THR	THR
ASP	ASP	SER
VAL	VAL	THR

Chain Cg:  87% 5% 7%



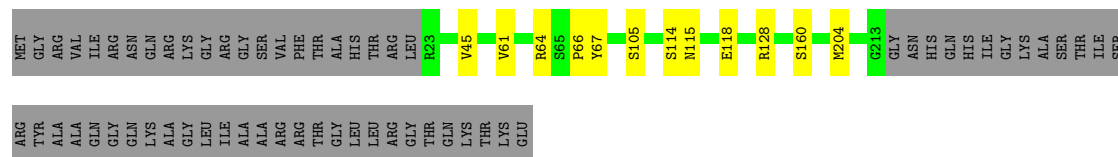
Chain Ch:  84% 9% 6%

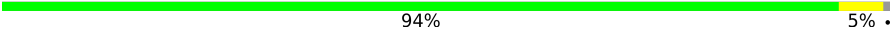


Chain Cz: 75% 7% 18%



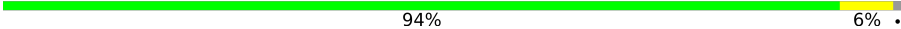
Chain LA: 70% 5% 25%

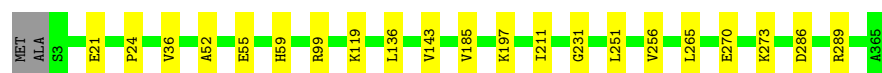


Chain LB:  94% 5%



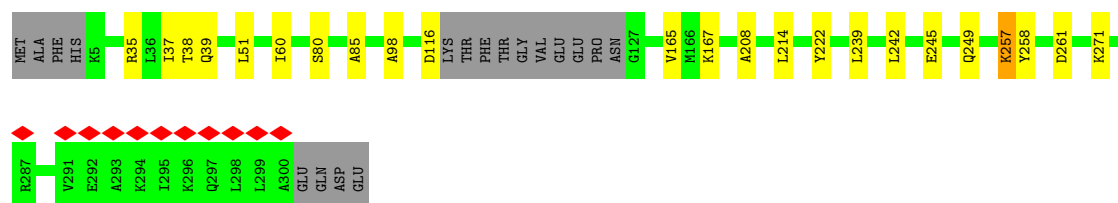
- Molecule 26: 60S ribosomal protein L4-like protein

Chain LC:  94% 6%



- Molecule 27: 60S ribosomal protein l5-like protein

Chain LD:  87% 7% 6%



- Molecule 28: 60S ribosomal protein L6

Chain LE:  86% 10%



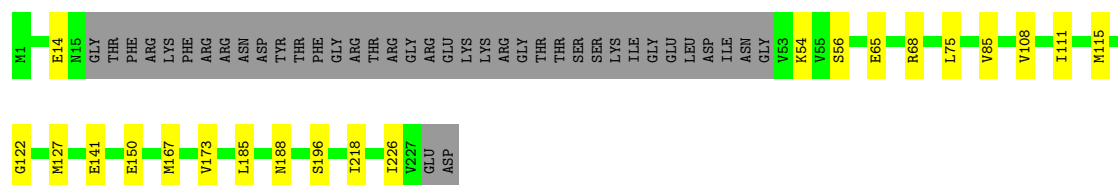
- Molecule 29: 60S ribosomal protein L8

Chain LG:  84% 5% 10%



- Molecule 30: 60S ribosomal protein l9-like protein

Chain LH:  74% 9% 17%



- Molecule 31: Putative ribosomal protein

Chain LJ:  84% 12% ..



- Molecule 32: 60S ribosomal protein L12-like protein

Chain LK:  88% 8% .



- Molecule 33: 60S ribosomal protein L13

Chain LL:  92% . 5%



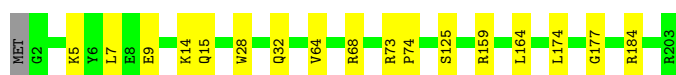
- Molecule 34: 60S ribosomal protein L14-like protein

Chain LM:  84% 15% .

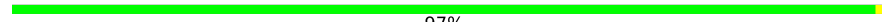


- Molecule 35: Ribosomal protein L15

Chain LN:  91% 8%



- Molecule 36: 60S ribosomal protein L16-like protein

Chain LO:  97% .



- Molecule 37: 60S ribosomal protein l17-like protein

Chain LP:  86% 5% 9%



- Molecule 38: Ribosomal protein L18-like protein

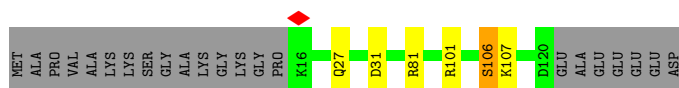
Digital Tool	Percentage
Video Conferencing Tool	65%
Virtual Reality Tool	6%
Social Media Tool	30%



Frequency	Percentage
Daily	5%
Not daily	95%







- Molecule 43: 60S ribosomal protein l23-like protein

Chain LV: 94%



- Molecule 44: 60S ribosomal protein L25-like protein

Chain LX: 88% 5% 7%



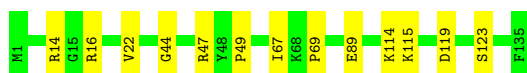
- Molecule 45: 60S ribosomal protein L26-like protein

Chain LY: 85% 12%



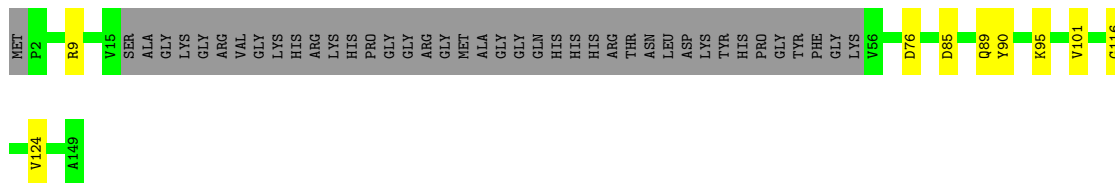
- Molecule 46: 60S ribosomal protein L27

Chain LZ: 90% 10%



- Molecule 47: 60S ribosomal protein L28-like protein

Chain La: 66% 6% 28%



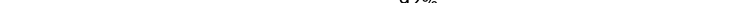
- Molecule 48: 60S ribosomal protein l30-like protein

Chain Lc: 80% 8% 12%

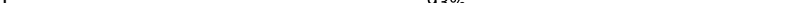


- Molecule 49: Putative 60S ribosomal protein

MET	SER	SER	SER	THR	GLN	LYS	LYS	GLN	ARG	SER	A11	L28	T32	A40	K66	R96	E119	E120
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- Chain Le:  92% 5% .

MET	V2	I39	I56	I97	S102	R106	A125	K126	V127	THR	THR	GLU	VAL
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- Chain Lf:  93% 6%

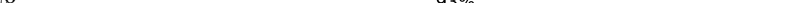
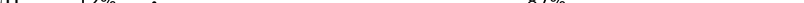
- Chain Lg: 

Figure 1: Schematic representation of the 19 amino acid residues of the C-terminal domain of the human p150Gluc. The residues are shown as colored blocks: MET (grey), A2 (green), R22 (yellow), L34 (yellow), R75 (green), A76 (green), Y77 (yellow), R81 (yellow), N84 (yellow), K103 (yellow), K114 (green), K115 (green), A116 (green), S117 (green), K118 (green), and K119 (green). Red diamonds above K114-K119 indicate the binding site for the p150Gluc C-terminal domain.

- Chain Lh:  12% 87%

NET	SER	SER	N4	Q11	K15	L34	S41	S42	K45	L46	I49	K66	D84	E107	A126	ALA	THR	TYR	SER	SER	GLU	GLY	PRO	ALA	LEU	SER	SER	ILE	TYR	HIS	SER	HIS	GLN	ARG	GLU	GLU	ALA	ALA	CYS	CYS	SER	LEU	VAL	PHE	GLU	PRO	PRO	GLU	LEU
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GLU	LEU	LEU	LEU	LEU	PRO	VAL	ALA	ALA	ALA	SER	LEU	LYS	GLY	PRO	ASN	PHE	THR	ARG	ARG	ASN	PRO	PRO	SER	GLU	GLU	ALA	ALA	THR	MET	SER	ALA	ALA	GLU	GLU	PRO	PRO	LEU	LEU	LEU	ALA	SER	ALA	ALA	GLY	LYS	GLY	LYS	SER	THR	ARG	SER	VAL	ARG	LEU	VAL	ALA	ALA	TLE	LEU	VAL
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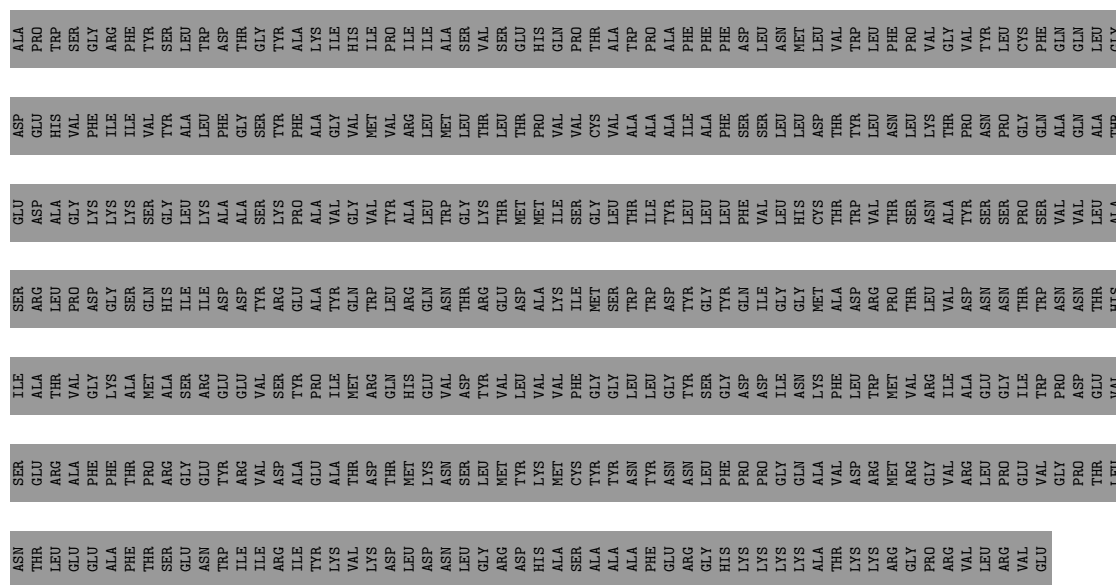
LEU	ILE	ALA	ALA	ALA	VAL	ALA	SER	ARG	ARG	LEU	PHE	SER	VAL	ILE	ILE	HIS	GLU	GLU	SER	ILE	ILE	HIS	PHE	ASP	PRO	TRP	PHE	PHE	ASN	ASN	ALA	THR	LYS	TYR	TYR	LYS	PHE	TRP	TRP	ASP	ASP	ARG	THR	THR	PRO	HIS	LEU	LEU	GLY	ARG	VAL	THR
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GLY	GLY	THR	LEU	TYR	PRO	GLY	LEU	MET	VAL	THR	SER	GLY	VAL	ILE	TYR	HIS	LEU	LEU	ARG	PHE	LEU	THR	VAL	PRO	VAL	ASP	ILE	ILE	ARG	ASN	CYS	VAL	LEU	LEU	ALA	ALA	PRO	GLY	PHE	SER	GLY	LEU	LEU	THR	THR	THR	SER	PRO	ALA
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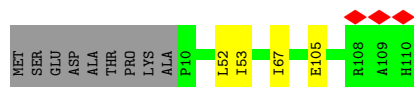
GLY LEU LEU LEU ALA ALA ALA PHE MET MET GLY ILE ILE ALA ALA PRO GLY TYR ILE ILE ILE ARG ARG SER SER VAL ASN ASN GLU GLU ALA ILE ILE ILE ILE PHE LEU LEU LEU VAL PHE PHE PHE PHE LEU LEU TRP TRP ILE ILE LYS LYS LEU LEU LYS GLN GLY GLY SER SER MET MET TRP TRP GLY ALA GLY LEU LEU CYS CYS ALA ALA LEU LEU PHE PHE TYR TYR

TYR	NET	VAL	ALA	SER	TRP	GLY	TYR	ALA	ALA	PHE	ILE	THR	CYS	LEU	PRO	LEU	LEU	HIS	SER	PHE	VAL	LEU	ILE	CYS	NET	GLY	ARG	TYR	SER	THR	ARG	TYR	VAL	ALA	ALA	THR	THR	TRP	TYR	ALA	LEU	GLY	THR	LEU	ALA	SER	SER	GLN	ILE	PHE	PRO	VAL	LYS
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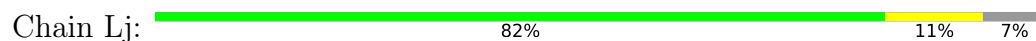
THR	SER	GLU	HIS	MET	PRO	ALA	LEU	GLY	ILE	PHE	GLY	PHE	LEU	GLN	LEU	LEU	ALA	PHE	LEU	ASP	TYR	VAL	ARG	SER	THR	ILE	SER	SER	ARG	GLN	PHE	GLN	THR	THR	LEU	TRP	LEU	PHE	PHE	ALA	GLY	ILE	GLY	PHE	GLY	LEU	LEU	LEU	GLY	LEU	VAL	ILE	THR	THR	SER	ALA	GLY	ILE	LEU
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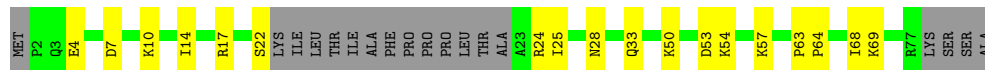
- Molecule 54: 60S ribosomal protein L36



- Molecule 55: Ribosomal protein L37



- Molecule 56: 60S ribosomal protein L38-like protein



- Molecule 57: Ribosomal protein eL39



- Molecule 58: 60S ribosomal protein L43-like protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	745895	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 ($e^-/\text{\AA}^2$)	45.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	10.768	Depositor
Minimum map value	0.000	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.175	Depositor
Recommended contour level	0.55	Depositor
Map size ($\text{\AA}$)	522.5, 522.5, 522.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMU, A2M, ZN, GTP, OMG, OMC, 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	C1	0.27	1/72882 (0.0%)	0.37	0/113631
2	C2	0.27	0/3710	0.35	0/5778
3	C3	0.22	0/1958	0.35	0/3050
4	C4	0.23	0/2833	0.34	0/4414
5	CB	0.21	0/2166	0.44	0/2945
6	CF	0.23	0/1972	0.42	1/2660 (0.0%)
7	CH	0.22	0/5147	0.43	0/6926
8	CI	0.26	0/1265	0.63	0/1702
9	CJ	0.23	0/3196	0.40	0/4319
10	CK	0.23	0/1939	0.43	0/2608
11	CL	0.20	0/631	0.42	0/843
12	CM	0.24	0/1805	0.48	0/2417
12	LF	0.26	0/2061	0.46	0/2765
13	CN	0.20	0/1878	0.48	0/2555
14	CO	0.22	0/470	0.42	0/619
15	CQ	0.23	0/1504	0.44	0/2000
16	Lq	0.20	0/1091	0.42	0/1468
17	Cb	0.19	0/845	0.41	0/1128
18	Cd	0.22	0/3770	0.42	1/5082 (0.0%)
19	Ce	0.21	0/2173	0.40	0/2890
20	Cf	0.20	0/2326	0.41	0/3113
21	Cg	0.23	0/1508	0.41	0/2051
22	Ch	0.24	0/3914	0.51	1/5319 (0.0%)
23	Cz	0.25	0/877	0.53	0/1148
24	LA	0.23	0/1488	0.47	0/2009
25	LB	0.23	0/3172	0.45	0/4260
26	LC	0.21	0/2808	0.40	0/3785
27	LD	0.21	0/2308	0.41	1/3105 (0.0%)
28	LE	0.20	0/1504	0.43	0/2027
29	LG	0.26	0/1918	0.46	0/2565
30	LH	0.25	0/1515	0.49	0/2037
31	LJ	0.20	0/1379	0.47	0/1844

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LK	0.22	0/1198	0.50	0/1611
33	LL	0.19	0/1614	0.38	0/2168
34	LM	0.23	0/1145	0.45	0/1539
35	LN	0.24	0/1741	0.41	0/2332
36	LO	0.24	0/1645	0.41	0/2205
37	LP	0.21	0/1364	0.42	0/1835
38	LQ	0.24	0/1218	0.43	0/1639
39	LR	0.21	0/1260	0.38	0/1683
40	LS	0.23	0/1461	0.45	0/1966
41	LT	0.24	0/1046	0.51	0/1409
42	LU	0.21	0/859	0.46	0/1151
43	LV	0.20	0/1009	0.40	0/1357
44	LX	0.25	0/1151	0.49	0/1547
45	LY	0.21	0/1070	0.47	0/1432
46	LZ	0.21	0/1135	0.41	0/1519
47	La	0.21	0/892	0.37	0/1200
48	Lc	0.19	0/714	0.39	0/960
49	Ld	0.21	0/889	0.38	0/1192
50	Le	0.22	0/1035	0.44	0/1379
51	Lf	0.22	0/883	0.35	0/1187
52	Lg	0.22	0/927	0.42	0/1244
53	Lh	0.22	0/1014	0.42	0/1349
54	Li	0.21	0/834	0.44	0/1099
55	Lj	0.23	0/712	0.50	2/944 (0.2%)
56	Lk	0.19	0/640	0.36	0/850
57	Ll	0.21	0/446	0.35	0/593
58	Lp	0.23	0/706	0.53	0/940
All	All	0.25	1/166621 (0.0%)	0.41	6/241393 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	848	A2M	O3'-P	5.19	1.61	1.56

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	Cd	95	MET	CB-CG-SD	5.77	130.02	112.70
55	Lj	69	THR	CA-C-N	5.52	123.72	120.24
55	Lj	69	THR	C-N-CA	5.52	123.72	120.24
27	LD	257	LYS	CB-CG-CD	5.41	123.74	111.30
6	CF	176	LYS	CB-CG-CD	5.32	123.54	111.30

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	C1	65888	0	33239	280	0
2	C2	3319	0	1678	12	0
3	C3	1754	0	890	17	0
4	C4	2536	0	1286	17	0
5	CB	2119	0	2170	25	0
6	CF	1934	0	1945	8	0
7	CH	5063	0	5157	35	0
8	CI	1234	0	1245	19	0
9	CJ	3116	0	3122	14	0
10	CK	1903	0	1990	9	0
11	CL	622	0	641	8	0
12	CM	1773	0	1879	14	0
12	LF	2023	0	2132	9	0
13	CN	1853	0	1852	17	0
14	CO	468	0	503	5	0
15	CQ	1480	0	1523	11	0
16	Lq	1073	0	1130	7	0
17	Cb	830	0	838	5	0
18	Cd	3691	0	3817	21	0
19	Ce	2148	0	2250	19	0
20	Cf	2282	0	2347	21	0
21	Cg	1478	0	1517	7	0
22	Ch	3812	0	3715	25	0
23	Cz	869	0	956	5	0
24	LA	1454	0	1490	6	0
25	LB	3104	0	3221	16	0
26	LC	2751	0	2875	12	0
27	LD	2266	0	2219	13	0
28	LE	1477	0	1567	13	0
29	LG	1889	0	2043	9	0
30	LH	1495	0	1573	10	0
31	LJ	1357	0	1385	15	0
32	LK	1184	0	1249	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	LL	1587	0	1655	6	0
34	LM	1126	0	1198	14	0
35	LN	1704	0	1767	12	0
36	LO	1611	0	1702	5	0
37	LP	1343	0	1369	8	0
38	LQ	1200	0	1296	7	0
39	LR	1241	0	1298	11	0
40	LS	1426	0	1481	15	0
41	LT	1027	0	1076	11	0
42	LU	846	0	883	5	0
43	LV	991	0	1044	4	0
44	LX	1133	0	1234	5	0
45	LY	1056	0	1143	9	0
46	LZ	1112	0	1181	9	0
47	La	872	0	903	7	0
48	Lc	705	0	751	5	0
49	Ld	875	0	918	4	0
50	Le	1017	0	1092	5	0
51	Lf	862	0	891	3	0
52	Lg	914	0	960	6	0
53	Lh	1003	0	1116	7	0
54	Li	827	0	906	2	0
55	Lj	698	0	726	7	0
56	Lk	632	0	693	10	0
57	Ll	436	0	473	2	0
58	Lp	698	0	737	6	0
59	CH	32	0	12	0	0
59	Cd	32	0	12	0	0
60	CH	1	0	0	0	0
60	Cd	2	0	0	0	0
61	CQ	1	0	0	0	0
61	Cb	1	0	0	0	0
61	Lg	1	0	0	0	0
61	Lj	1	0	0	0	0
61	Lp	1	0	0	0	0
62	CH	1	0	0	0	0
62	Cd	2	0	0	0	0
All	All	157262	0	123961	728	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 3.

The worst 5 of 728 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:C1:3289:G:H1	1:C1:3298:U:H3	1.19	0.90
3:C3:40:G:H1	3:C3:45:U:H3	1.22	0.88
1:C1:2400:G:H1	1:C1:2473:U:H3	1.13	0.87
41:LT:79:ARG:NH1	41:LT:81:LYS:O	2.18	0.77
45:LY:30:MET:HB3	45:LY:100:PRO:HG2	1.65	0.77

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CB	261/391 (67%)	256 (98%)	5 (2%)	0	100	100
6	CF	243/270 (90%)	238 (98%)	5 (2%)	0	100	100
7	CH	621/661 (94%)	614 (99%)	7 (1%)	0	100	100
8	CI	150/414 (36%)	149 (99%)	1 (1%)	0	100	100
9	CJ	376/679 (55%)	374 (100%)	2 (0%)	0	100	100
10	CK	231/261 (88%)	226 (98%)	5 (2%)	0	100	100
11	CL	77/558 (14%)	77 (100%)	0	0	100	100
12	CM	211/249 (85%)	207 (98%)	4 (2%)	0	100	100
12	LF	246/249 (99%)	240 (98%)	6 (2%)	0	100	100
13	CN	244/246 (99%)	238 (98%)	6 (2%)	0	100	100
14	CO	56/120 (47%)	56 (100%)	0	0	100	100
15	CQ	181/225 (80%)	179 (99%)	2 (1%)	0	100	100
16	Lq	137/147 (93%)	132 (96%)	5 (4%)	0	100	100
17	Cb	99/117 (85%)	98 (99%)	1 (1%)	0	100	100
18	Cd	458/627 (73%)	454 (99%)	4 (1%)	0	100	100
19	Ce	252/443 (57%)	251 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	Cf	281/350 (80%)	279 (99%)	2 (1%)	0	100	100
21	Cg	186/202 (92%)	186 (100%)	0	0	100	100
22	Ch	484/517 (94%)	471 (97%)	13 (3%)	0	100	100
23	Cz	99/123 (80%)	98 (99%)	1 (1%)	0	100	100
24	LA	189/254 (74%)	187 (99%)	2 (1%)	0	100	100
25	LB	387/392 (99%)	381 (98%)	6 (2%)	0	100	100
26	LC	361/365 (99%)	355 (98%)	6 (2%)	0	100	100
27	LD	282/304 (93%)	278 (99%)	4 (1%)	0	100	100
28	LE	187/200 (94%)	184 (98%)	3 (2%)	0	100	100
29	LG	233/262 (89%)	228 (98%)	5 (2%)	0	100	100
30	LH	188/229 (82%)	186 (99%)	2 (1%)	0	100	100
31	LJ	167/173 (96%)	166 (99%)	1 (1%)	0	100	100
32	LK	156/165 (94%)	155 (99%)	1 (1%)	0	100	100
33	LL	201/213 (94%)	200 (100%)	1 (0%)	0	100	100
34	LM	139/142 (98%)	135 (97%)	4 (3%)	0	100	100
35	LN	200/203 (98%)	196 (98%)	4 (2%)	0	100	100
36	LO	201/204 (98%)	199 (99%)	2 (1%)	0	100	100
37	LP	167/187 (89%)	164 (98%)	3 (2%)	0	100	100
38	LQ	148/213 (70%)	147 (99%)	1 (1%)	0	100	100
39	LR	153/2898 (5%)	152 (99%)	1 (1%)	0	100	100
40	LS	172/174 (99%)	170 (99%)	2 (1%)	0	100	100
41	LT	127/160 (79%)	126 (99%)	1 (1%)	0	100	100
42	LU	103/127 (81%)	101 (98%)	2 (2%)	0	100	100
43	LV	133/139 (96%)	132 (99%)	1 (1%)	0	100	100
44	LX	143/156 (92%)	142 (99%)	1 (1%)	0	100	100
45	LY	131/138 (95%)	128 (98%)	3 (2%)	0	100	100
46	LZ	133/135 (98%)	132 (99%)	1 (1%)	0	100	100
47	La	104/149 (70%)	104 (100%)	0	0	100	100
48	Lc	93/108 (86%)	93 (100%)	0	0	100	100
49	Ld	108/120 (90%)	108 (100%)	0	0	100	100
50	Le	124/131 (95%)	123 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	Lf	106/109 (97%)	106 (100%)	0	0	100	100
52	Lg	116/119 (98%)	115 (99%)	1 (1%)	0	100	100
53	Lh	120/935 (13%)	117 (98%)	3 (2%)	0	100	100
54	Li	99/110 (90%)	99 (100%)	0	0	100	100
55	Lj	86/95 (90%)	85 (99%)	1 (1%)	0	100	100
56	Lk	74/94 (79%)	74 (100%)	0	0	100	100
57	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
58	Lp	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
All	All	10361/16395 (63%)	10225 (99%)	136 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	CB	228/329 (69%)	227 (100%)	1 (0%)	84	89
6	CF	212/236 (90%)	211 (100%)	1 (0%)	81	87
7	CH	549/575 (96%)	544 (99%)	5 (1%)	70	78
8	CI	124/336 (37%)	121 (98%)	3 (2%)	43	48
9	CJ	331/579 (57%)	330 (100%)	1 (0%)	86	91
10	CK	206/225 (92%)	203 (98%)	3 (2%)	57	65
11	CL	61/458 (13%)	60 (98%)	1 (2%)	55	63
12	CM	185/215 (86%)	181 (98%)	4 (2%)	45	52
12	LF	213/215 (99%)	212 (100%)	1 (0%)	81	87
13	CN	205/206 (100%)	203 (99%)	2 (1%)	68	76
14	CO	48/99 (48%)	48 (100%)	0	100	100
15	CQ	144/192 (75%)	143 (99%)	1 (1%)	76	83
16	Lq	109/112 (97%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	Cb	85/101 (84%)	83 (98%)	2 (2%)	43	48
18	Cd	403/541 (74%)	403 (100%)	0	100	100
19	Ce	223/383 (58%)	221 (99%)	2 (1%)	70	78
20	Cf	250/310 (81%)	249 (100%)	1 (0%)	84	89
21	Cg	158/176 (90%)	155 (98%)	3 (2%)	50	57
22	Ch	408/436 (94%)	404 (99%)	4 (1%)	68	76
23	Cz	89/107 (83%)	86 (97%)	3 (3%)	32	35
24	LA	150/198 (76%)	148 (99%)	2 (1%)	61	69
25	LB	329/331 (99%)	329 (100%)	0	100	100
26	LC	282/285 (99%)	280 (99%)	2 (1%)	76	83
27	LD	221/253 (87%)	219 (99%)	2 (1%)	70	78
28	LE	157/166 (95%)	156 (99%)	1 (1%)	78	85
29	LG	200/222 (90%)	199 (100%)	1 (0%)	81	87
30	LH	167/200 (84%)	165 (99%)	2 (1%)	63	71
31	LJ	140/150 (93%)	137 (98%)	3 (2%)	47	54
32	LK	127/136 (93%)	127 (100%)	0	100	100
33	LL	158/176 (90%)	157 (99%)	1 (1%)	78	85
34	LM	116/117 (99%)	114 (98%)	2 (2%)	53	61
35	LN	179/180 (99%)	178 (99%)	1 (1%)	78	85
36	LO	162/163 (99%)	162 (100%)	0	100	100
37	LP	133/152 (88%)	133 (100%)	0	100	100
38	LQ	128/178 (72%)	127 (99%)	1 (1%)	73	80
39	LR	125/2396 (5%)	123 (98%)	2 (2%)	55	63
40	LS	152/154 (99%)	152 (100%)	0	100	100
41	LT	110/135 (82%)	107 (97%)	3 (3%)	39	44
42	LU	92/108 (85%)	91 (99%)	1 (1%)	65	74
43	LV	98/102 (96%)	98 (100%)	0	100	100
44	LX	122/129 (95%)	120 (98%)	2 (2%)	55	63
45	LY	116/119 (98%)	113 (97%)	3 (3%)	40	45
46	LZ	121/121 (100%)	121 (100%)	0	100	100
47	La	93/122 (76%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	Lc	76/88 (86%)	75 (99%)	1 (1%)	61	69
49	Ld	90/105 (86%)	90 (100%)	0	100	100
50	Le	109/114 (96%)	109 (100%)	0	100	100
51	Lf	89/90 (99%)	87 (98%)	2 (2%)	45	52
52	Lg	95/102 (93%)	95 (100%)	0	100	100
53	Lh	109/781 (14%)	109 (100%)	0	100	100
54	Li	85/93 (91%)	83 (98%)	2 (2%)	43	48
55	Lj	72/78 (92%)	70 (97%)	2 (3%)	38	42
56	Lk	73/88 (83%)	72 (99%)	1 (1%)	59	67
57	Ll	45/46 (98%)	45 (100%)	0	100	100
58	Lp	73/74 (99%)	71 (97%)	2 (3%)	39	44
All	All	8825/13783 (64%)	8748 (99%)	77 (1%)	68	78

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	LR	68	LEU
54	Li	105	GLU
41	LT	115	LEU
45	LY	78	VAL
58	Lp	11	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
41	LT	127	GLN
47	La	62	HIS
51	Lf	7	HIS
19	Ce	223	GLN
18	Cd	409	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3069/3342 (91%)	550 (17%)	23 (0%)
2	C2	155/156 (99%)	21 (13%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C3	80/162 (49%)	21 (26%)	0
4	C4	118/119 (99%)	23 (19%)	0
All	All	3422/3779 (90%)	615 (17%)	23 (0%)

5 of 615 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	4	U
1	C1	6	G
1	C1	27	A
1	C1	44	A
1	C1	50	A

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3079	U
1	C1	3210	U
1	C1	3205	G
1	C1	3230	G
1	C1	1267	C

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

34 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	A2M	C1	2289	1	22,25,26	4.01	11 (50%)	30,36,39	3.31	13 (43%)
1	A2M	C1	637	1	22,25,26	3.97	11 (50%)	30,36,39	3.35	13 (43%)
1	OMG	C1	646	1	23,26,27	0.55	0	32,38,41	0.59	0
1	A2M	C1	858	1	22,25,26	4.03	12 (54%)	30,36,39	3.36	14 (46%)
1	OMG	C1	385	1	23,26,27	0.53	0	32,38,41	0.51	0
1	A2M	C1	1223	1	22,25,26	3.98	11 (50%)	30,36,39	3.28	15 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMU	C1	1868	1	19,22,23	3.02	7 (36%)	25,31,34	2.00	5 (20%)
1	OMU	C1	2690	1	19,22,23	3.02	7 (36%)	25,31,34	1.84	4 (16%)
1	OMC	C1	1420	1	19,22,23	0.70	0	25,31,34	1.27	4 (16%)
1	A2M	C1	1847	1	22,25,26	3.97	12 (54%)	30,36,39	3.48	14 (46%)
1	OMG	C1	787	1	23,26,27	0.53	0	32,38,41	0.61	0
1	OMU	C1	2380	1	19,22,23	3.01	7 (36%)	25,31,34	1.79	5 (20%)
1	A2M	C1	389	1	22,25,26	3.99	11 (50%)	30,36,39	3.35	12 (40%)
1	OMG	C1	2881	1	23,26,27	0.50	0	32,38,41	0.49	0
1	OMU	C1	2683	1	19,22,23	3.01	7 (36%)	25,31,34	1.84	5 (20%)
1	OMU	C1	2384	1	19,22,23	3.07	7 (36%)	25,31,34	1.81	5 (20%)
1	OMC	C1	2918	1	19,22,23	0.62	0	25,31,34	0.79	0
1	OMU	C1	1917	1	19,22,23	3.06	6 (31%)	25,31,34	1.85	6 (24%)
1	OMG	C1	2578	1	23,26,27	0.53	0	32,38,41	0.65	0
1	OMG	C1	2876	1	23,26,27	0.50	0	32,38,41	0.51	0
1	OMU	C1	2277	1	19,22,23	3.04	6 (31%)	25,31,34	1.79	5 (20%)
1	OMC	C1	778	1	19,22,23	0.58	0	25,31,34	0.86	1 (4%)
1	OMC	C1	2300	1	19,22,23	0.60	0	25,31,34	0.67	0
1	OMG	C1	2774	1	23,26,27	0.56	0	32,38,41	0.55	0
1	OMG	C1	627	1	23,26,27	0.55	0	32,38,41	0.63	0
1	OMG	C1	1433	1	23,26,27	0.58	0	32,38,41	0.51	0
1	OMG	C1	2358	1	23,26,27	0.54	0	32,38,41	0.56	0
1	OMC	C1	2838	1	19,22,23	0.76	1 (5%)	25,31,34	1.59	4 (16%)
1	OMC	C1	1836	1	19,22,23	0.61	0	25,31,34	0.72	0
1	OMC	C1	1491	1	19,22,23	0.60	0	25,31,34	0.69	0
1	A2M	C1	848	1	22,25,26	3.98	11 (50%)	30,36,39	3.44	15 (50%)
1	A2M	C1	1432	1	22,25,26	3.97	11 (50%)	30,36,39	3.38	13 (43%)
1	OMU	C1	2688	1	19,22,23	3.04	6 (31%)	25,31,34	1.77	5 (20%)
1	OMC	C1	1812	1	19,22,23	0.63	0	25,31,34	1.44	2 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	C1	2289	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	637	1	-	1/9/27/28	0/3/3/3
1	OMG	C1	646	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	858	1	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	C1	385	1	-	2/9/27/28	0/3/3/3
1	A2M	C1	1223	1	-	1/9/27/28	0/3/3/3
1	OMU	C1	1868	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2690	1	-	2/9/27/28	0/2/2/2
1	OMC	C1	1420	1	-	2/9/27/28	0/2/2/2
1	A2M	C1	1847	1	-	3/9/27/28	0/3/3/3
1	OMG	C1	787	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	2380	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	389	1	-	3/9/27/28	0/3/3/3
1	OMG	C1	2881	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	2683	1	-	1/9/27/28	0/2/2/2
1	OMU	C1	2384	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	2918	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	1917	1	-	2/9/27/28	0/2/2/2
1	OMG	C1	2578	1	-	3/9/27/28	0/3/3/3
1	OMG	C1	2876	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	2277	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	778	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	2300	1	-	1/9/27/28	0/2/2/2
1	OMG	C1	2774	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	627	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	1433	1	-	3/9/27/28	0/3/3/3
1	OMG	C1	2358	1	-	0/9/27/28	0/3/3/3
1	OMC	C1	2838	1	-	2/9/27/28	0/2/2/2
1	OMC	C1	1836	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	1491	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	848	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	1432	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	2688	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	1812	1	-	2/9/27/28	0/2/2/2

The worst 5 of 144 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	2289	A2M	C3'-C2'	-13.20	1.24	1.53
1	C1	858	A2M	C3'-C2'	-13.11	1.24	1.53
1	C1	637	A2M	C3'-C2'	-12.99	1.24	1.53
1	C1	1223	A2M	C3'-C2'	-12.98	1.24	1.53
1	C1	1432	A2M	C3'-C2'	-12.93	1.24	1.53

The worst 5 of 160 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1847	A2M	C1'-N9-C8	-9.40	106.23	127.09
1	C1	389	A2M	C1'-N9-C8	-9.03	107.05	127.09
1	C1	637	A2M	C1'-N9-C8	-8.95	107.23	127.09
1	C1	848	A2M	C1'-N9-C8	-8.87	107.42	127.09
1	C1	1432	A2M	C1'-N9-C8	-8.82	107.52	127.09

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C1	389	A2M	C1'-C2'-O2'-CM'
1	C1	637	A2M	C1'-C2'-O2'-CM'
1	C1	1433	OMG	O4'-C4'-C5'-O5'
1	C1	1812	OMC	C1'-C2'-O2'-CM2
1	C1	1917	OMU	O4'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C1	637	A2M	1	0
1	C1	1420	OMC	1	0
1	C1	389	A2M	1	0
1	C1	2277	OMU	1	0
1	C1	2838	OMC	1	0
1	C1	1432	A2M	1	0
1	C1	1812	OMC	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	GTP	Cd	1000	60	33,34,34	0.86	0	50,54,54	1.56	9 (18%)
59	GTP	CH	701	60	33,34,34	0.91	0	50,54,54	1.58	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	GTP	Cd	1000	60	-	3/22/38/38	0/3/3/3
59	GTP	CH	701	60	-	7/22/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	CH	701	GTP	C5-C4-N3	-4.84	120.69	128.39
59	Cd	1000	GTP	C5-C4-N3	-4.65	121.00	128.39
59	Cd	1000	GTP	C2-N3-C4	4.50	120.06	112.30
59	CH	701	GTP	C2-N3-C4	4.36	119.81	112.30
59	CH	701	GTP	N9-C4-N3	3.15	132.25	125.95

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

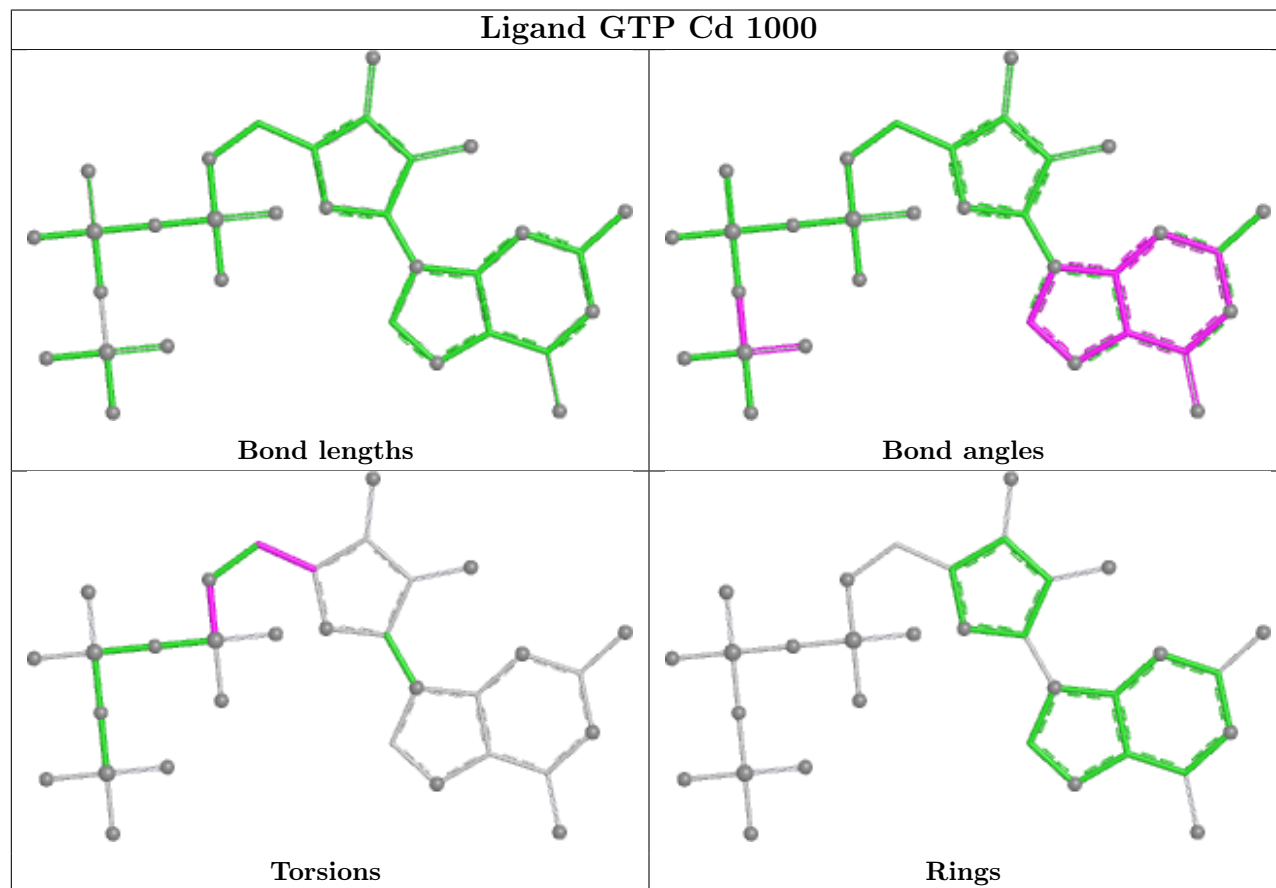
Mol	Chain	Res	Type	Atoms
59	CH	701	GTP	O4'-C4'-C5'-O5'
59	CH	701	GTP	C3'-C4'-C5'-O5'
59	Cd	1000	GTP	C3'-C4'-C5'-O5'
59	CH	701	GTP	C5'-O5'-PA-O3A
59	CH	701	GTP	C5'-O5'-PA-O1A

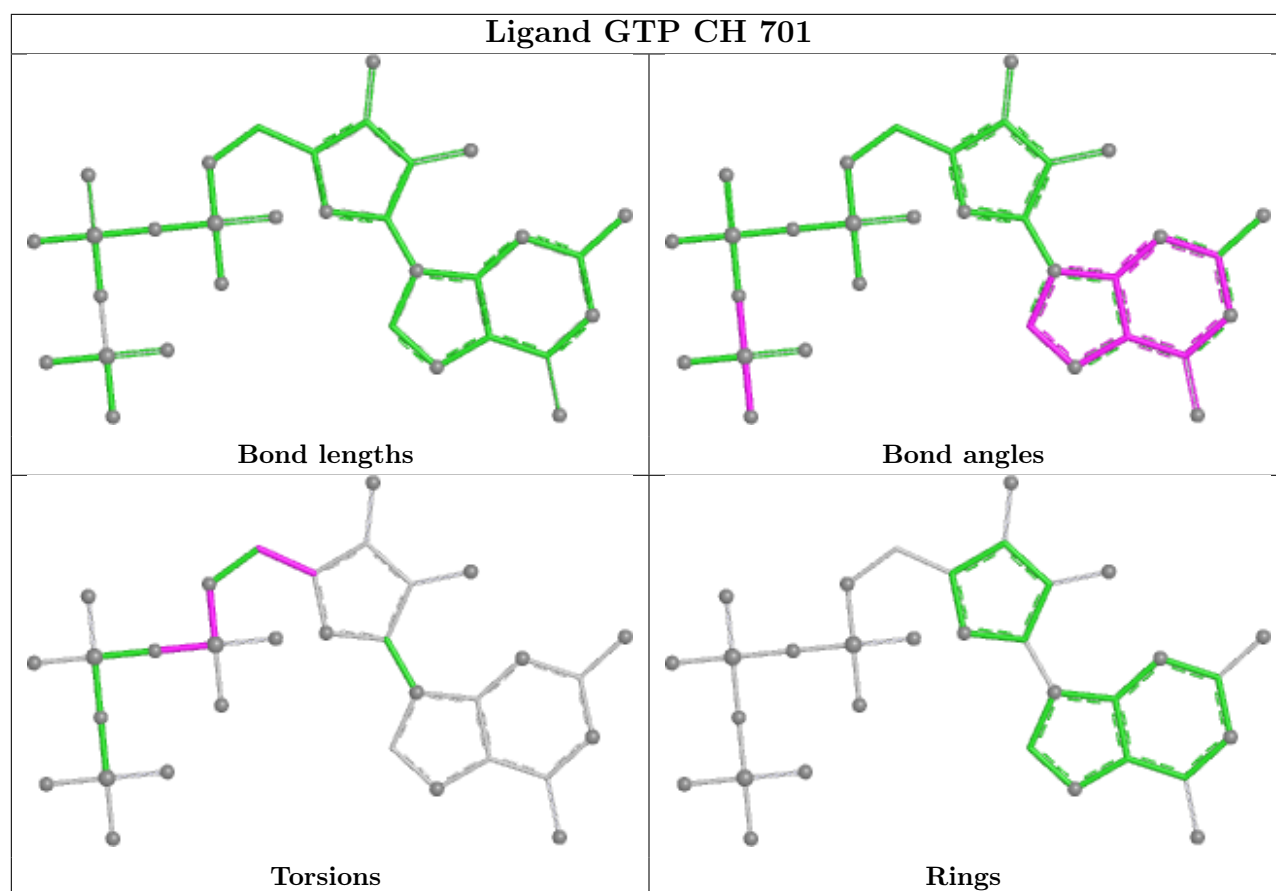
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

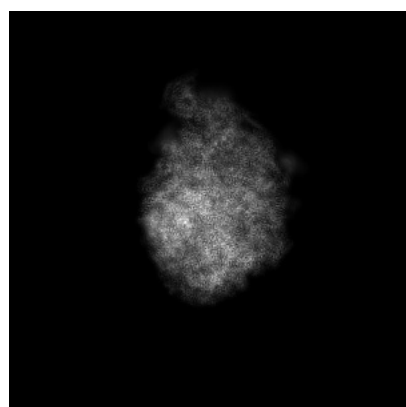
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17956. These allow visual inspection of the internal detail of the map and identification of artifacts.

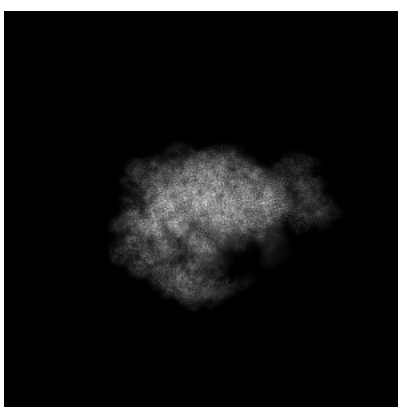
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

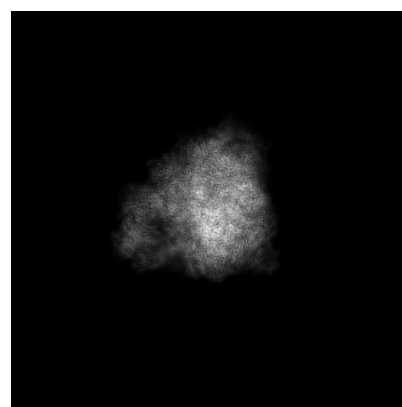
6.1.1 Primary map



X



Y

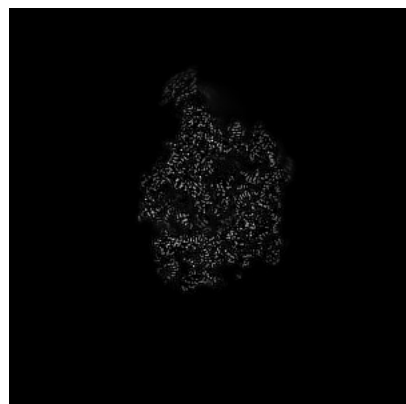


Z

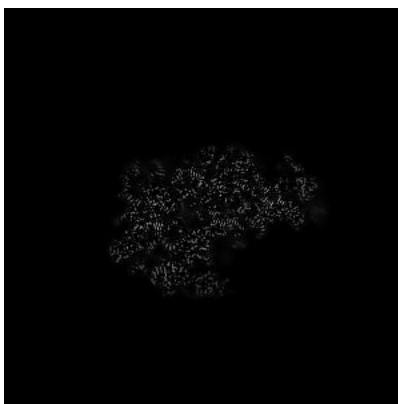
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

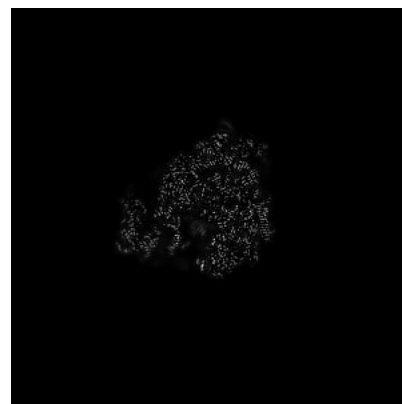
6.2.1 Primary map



X Index: 250



Y Index: 250

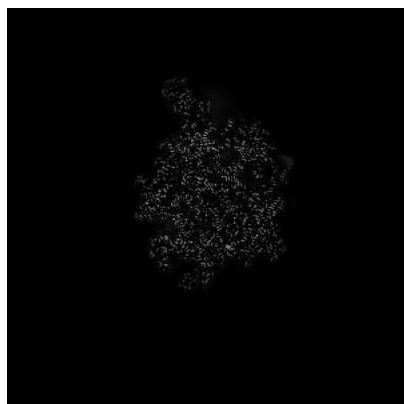


Z Index: 250

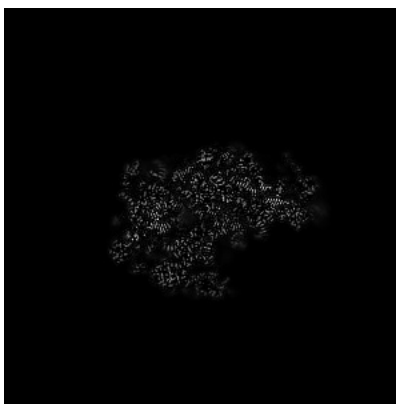
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

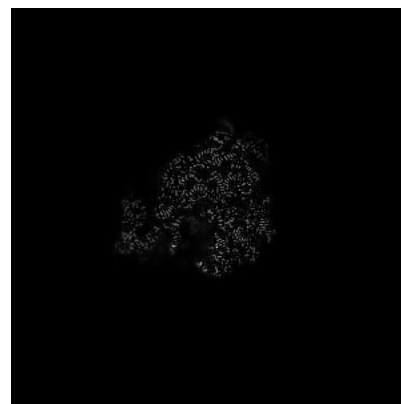
6.3.1 Primary map



X Index: 259



Y Index: 248

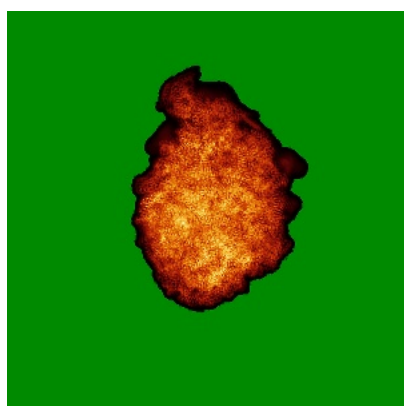


Z Index: 252

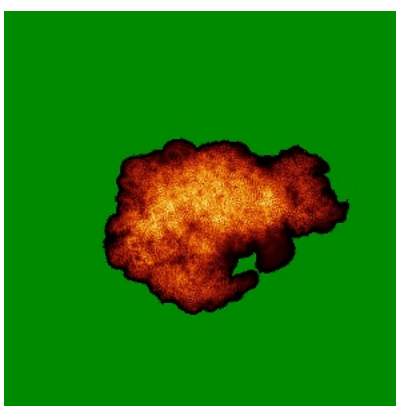
The images above show the largest variance slices of the map in three orthogonal directions.

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

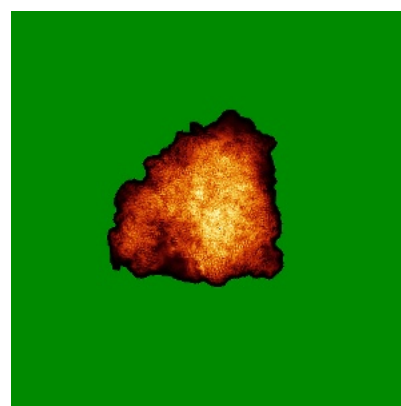
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

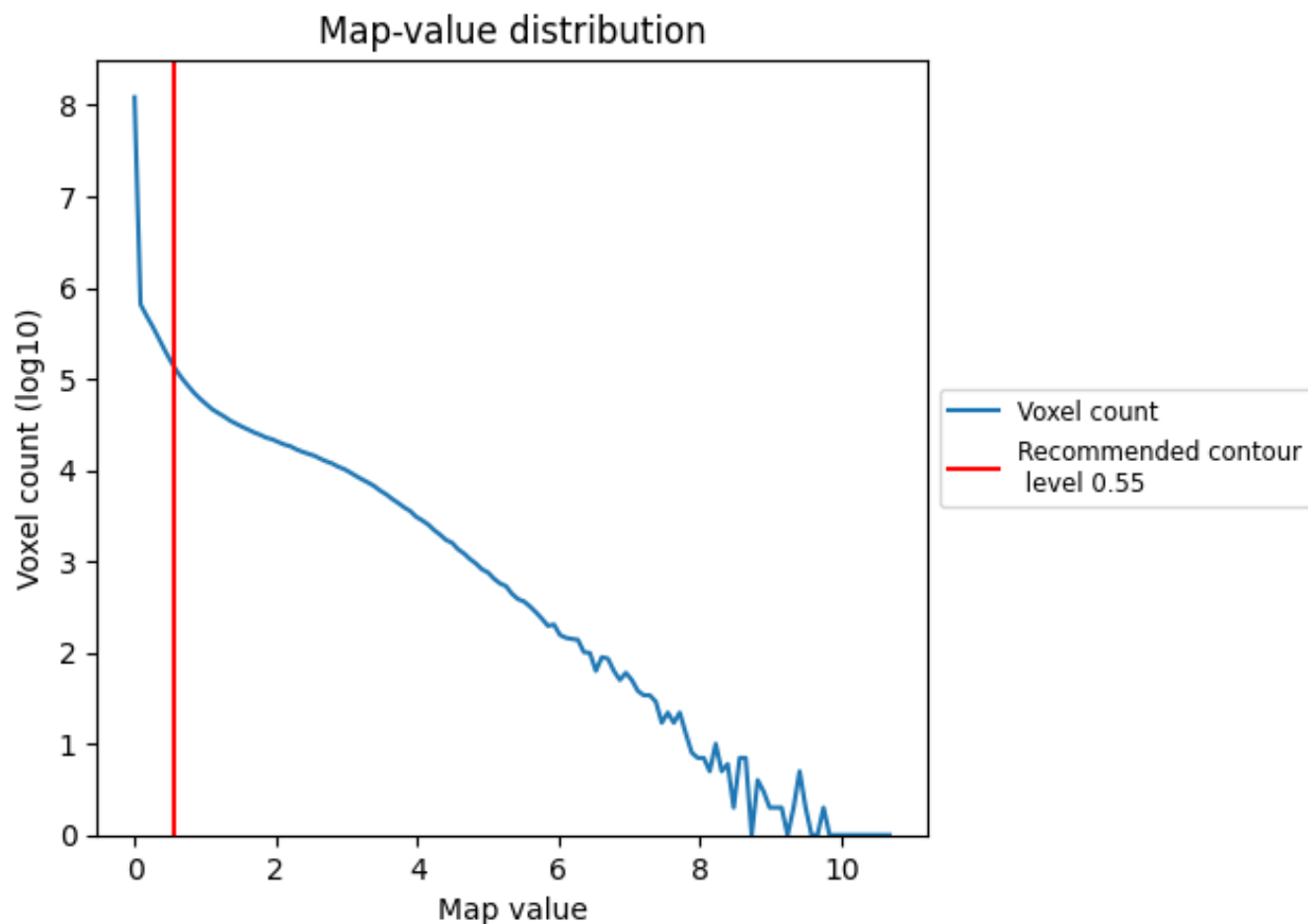
6.6 Mask visualisation

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

7 Map analysis [i](#)

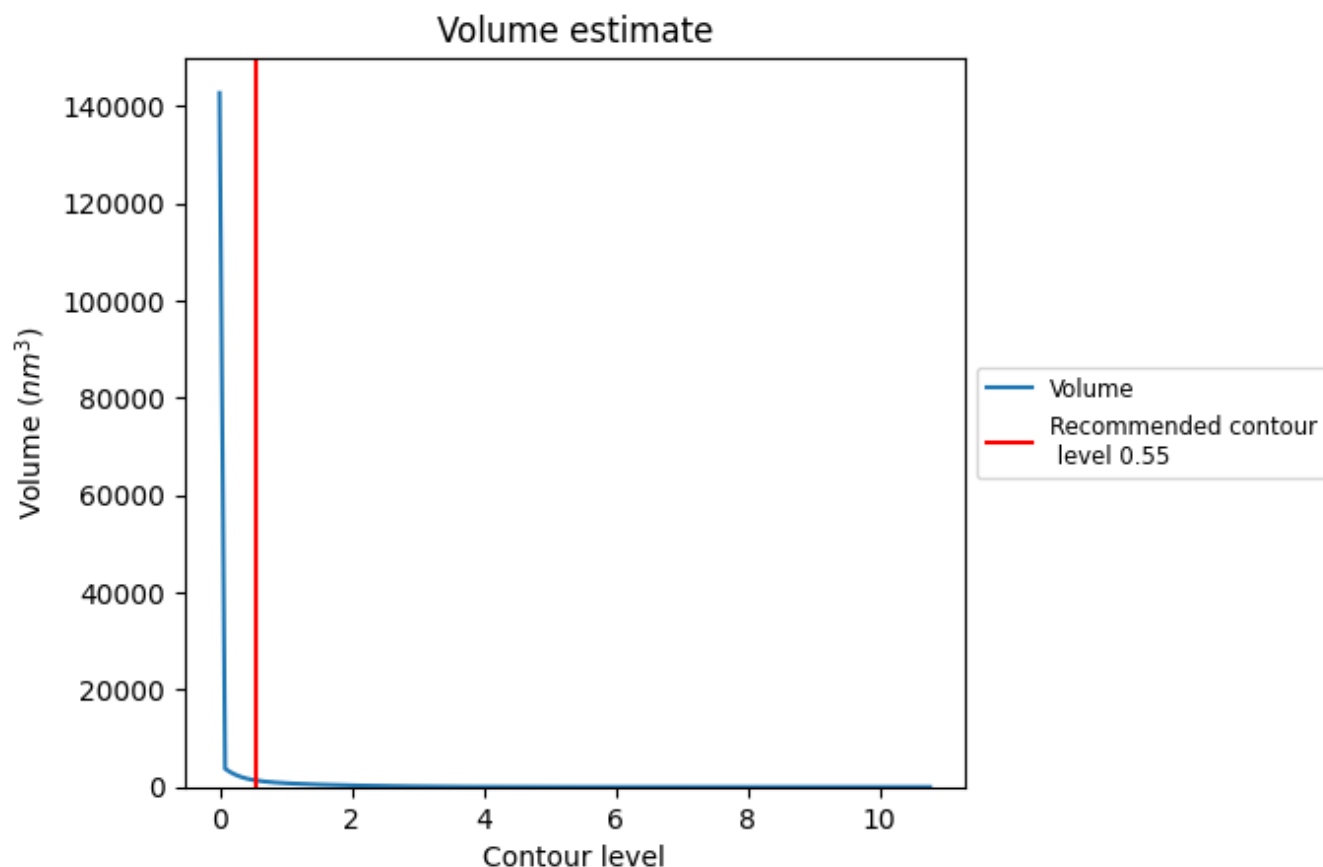
This section contains the results of statistical analysis of the map.

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.

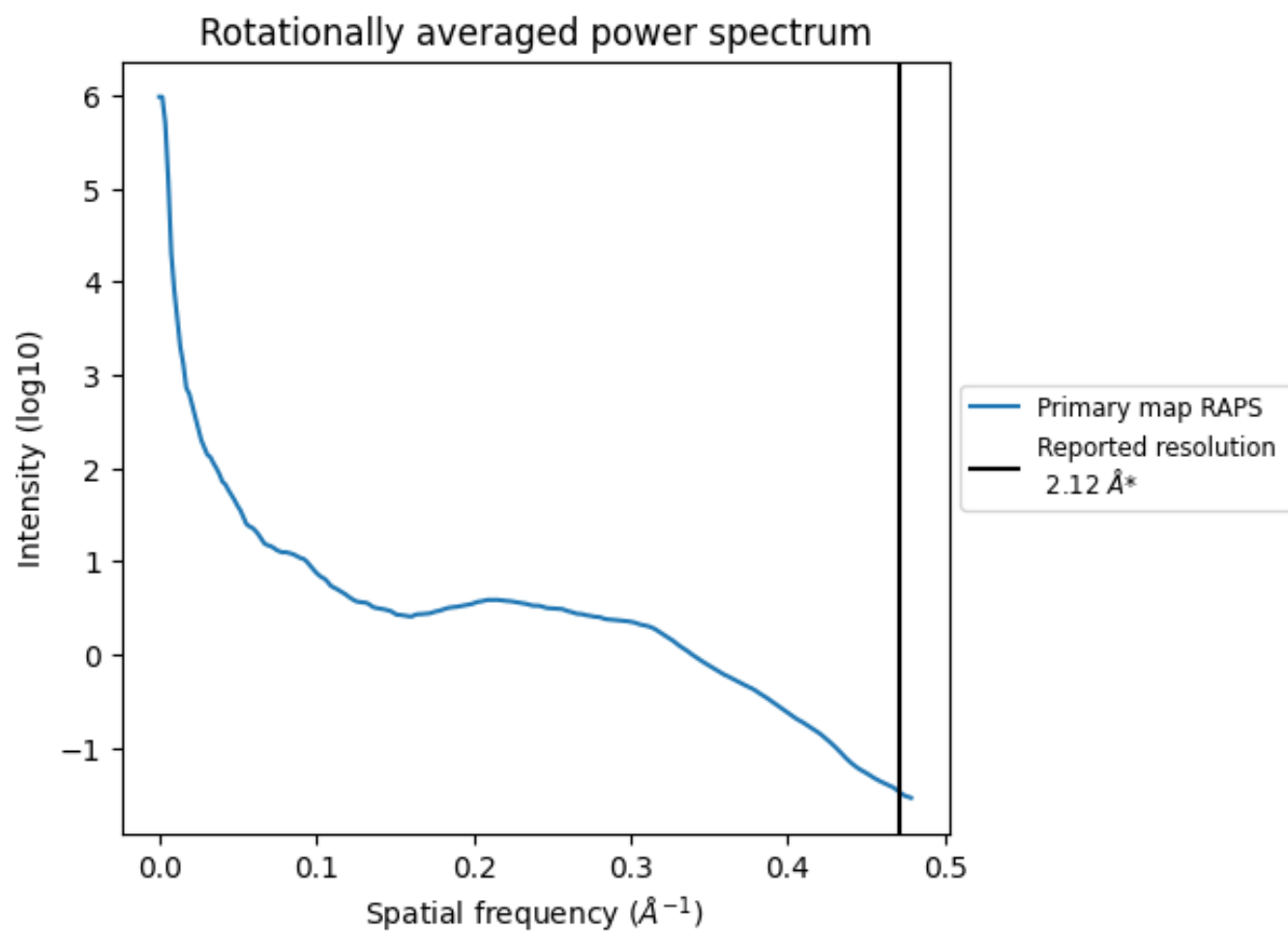
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1355 nm^3 ; this corresponds to an approximate mass of 1224 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 0.472 Å⁻¹

8 Fourier-Shell correlation

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

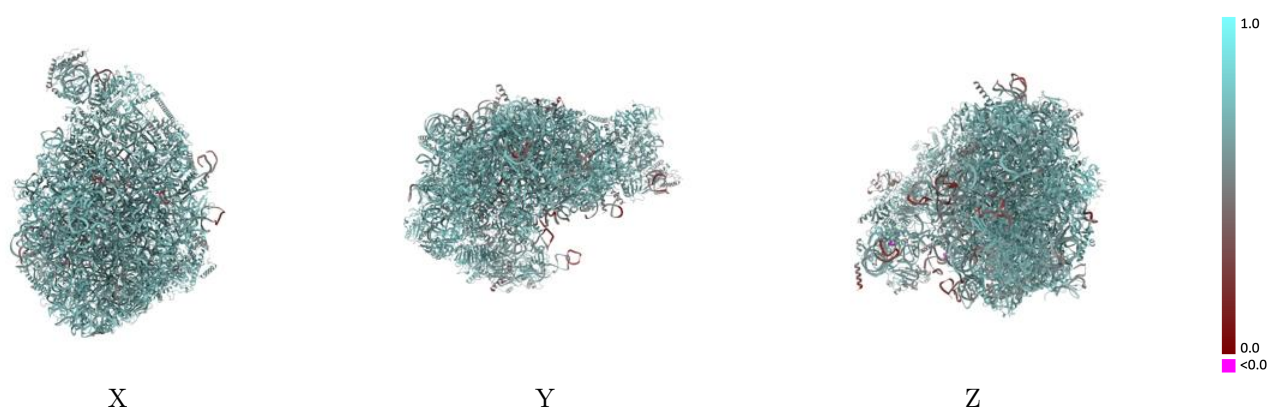
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17956 and PDB model 8PV7. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

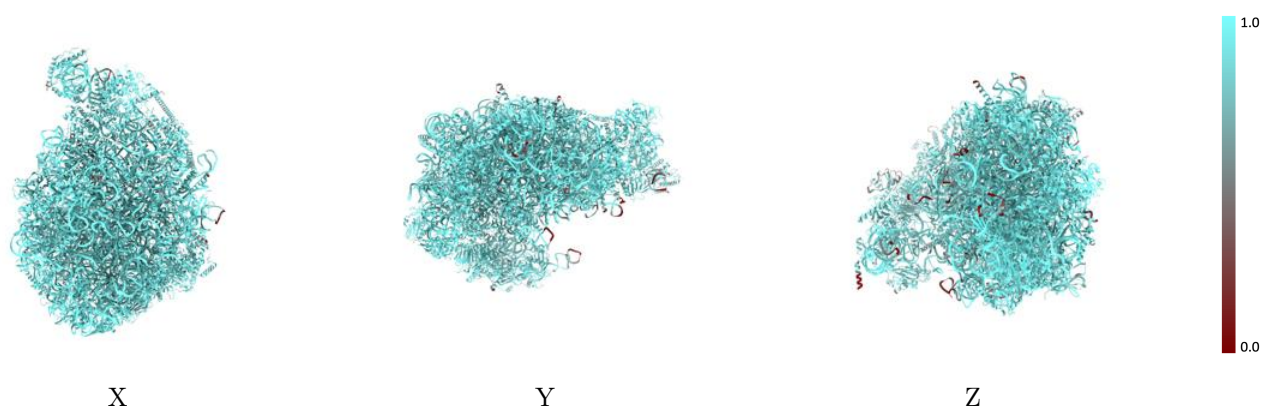
This section was not generated.

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



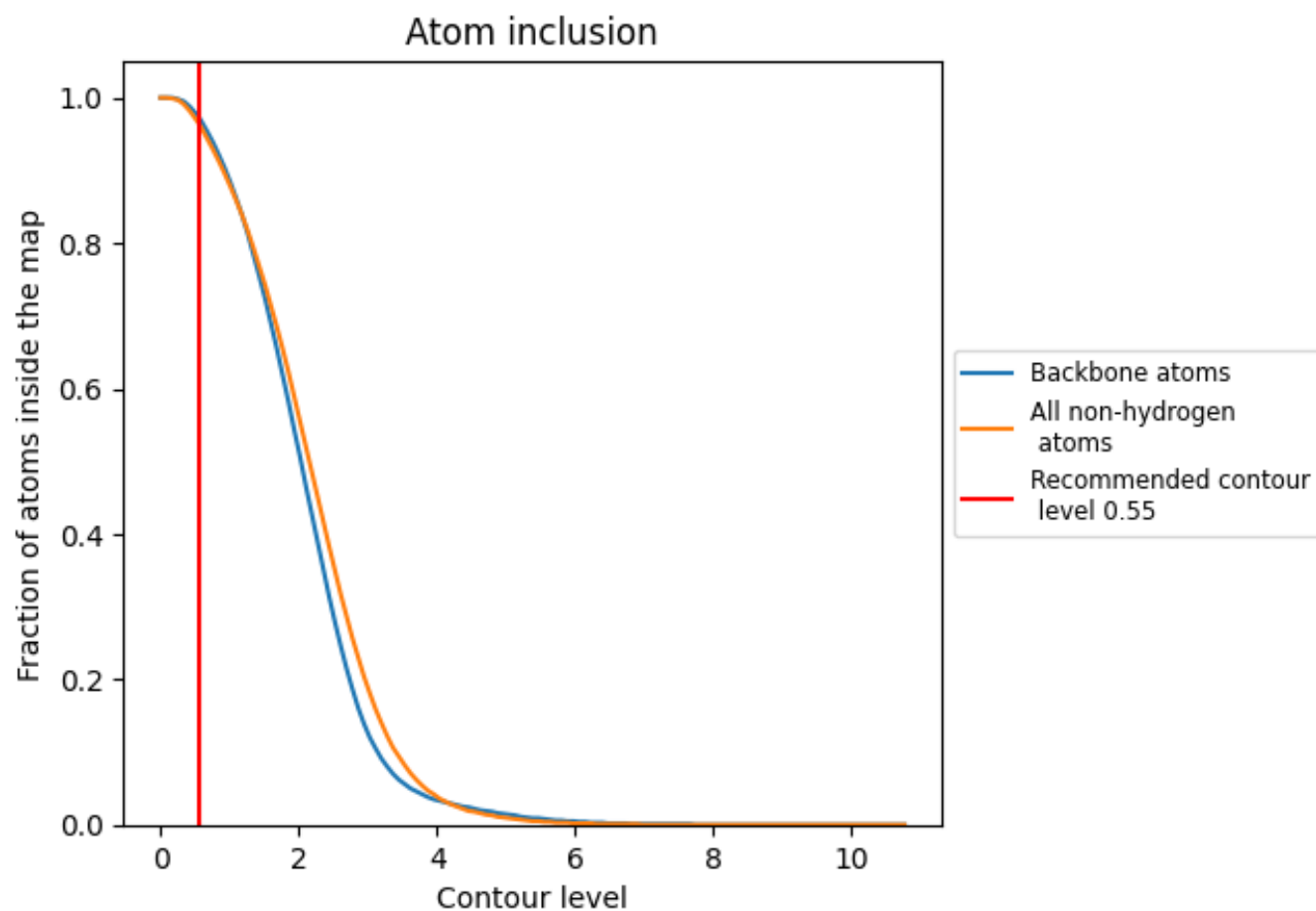
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.55).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9650	 0.6760
C1	 0.9770	 0.6650
C2	 0.9770	 0.6890
C3	 0.8300	 0.5370
C4	 0.9280	 0.5990
CB	 0.9290	 0.6250
CF	 0.9670	 0.6860
CH	 0.9490	 0.6920
CI	 0.9200	 0.6380
CJ	 0.9840	 0.6940
CK	 0.9860	 0.7230
CL	 0.9440	 0.6420
CM	 0.9520	 0.6590
CN	 0.9730	 0.7110
CO	 0.9520	 0.7060
CQ	 0.9210	 0.6770
Cb	 0.9750	 0.7070
Cd	 0.9690	 0.7000
Ce	 0.8940	 0.6380
Cf	 0.9640	 0.6740
Cg	 0.9650	 0.6590
Ch	 0.9210	 0.6570
Cz	 0.8810	 0.5970
LA	 0.9870	 0.7100
LB	 0.9850	 0.7300
LC	 0.9810	 0.7230
LD	 0.9300	 0.6620
LE	 0.9440	 0.6810
LF	 0.9770	 0.7050
LG	 0.9720	 0.6990
LH	 0.9730	 0.7150
LJ	 0.9290	 0.5920
LK	 0.9410	 0.6470
LL	 0.9610	 0.7030
LM	 0.9730	 0.7060



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Chain	Atom inclusion	Q-score
LN	 0.9960	 0.7310
LO	 0.9890	 0.7290
LP	 0.9870	 0.7210
LQ	 0.9860	 0.7000
LR	 0.9620	 0.7080
LS	 0.9880	 0.7080
LT	 0.9490	 0.6280
LU	 0.9410	 0.6620
LV	 0.9910	 0.7310
LX	 0.9730	 0.6940
LY	 0.9770	 0.7080
LZ	 0.9670	 0.7020
La	 0.9730	 0.7060
Lc	 0.9600	 0.6890
Ld	 0.9660	 0.7160
Le	 0.9880	 0.7310
Lf	 0.9960	 0.7380
Lg	 0.9340	 0.6940
Lh	 0.9460	 0.6620
Li	 0.9500	 0.6780
Lj	 0.9930	 0.7390
Lk	 0.9170	 0.6740
Ll	 0.9980	 0.7390
Lp	 0.9480	 0.6910
Lq	 0.9690	 0.6970