



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 04:04 PM EST

PDB ID : 4V6R
EMDB ID : EMD-5362
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 6 of the six classes)
Authors : Agirrezabala, X.; Liao, H.; Schreiner, E.; Fu, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-12-08
Resolution : 11.50 Å (reported)
Based on initial model : 2I2U

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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

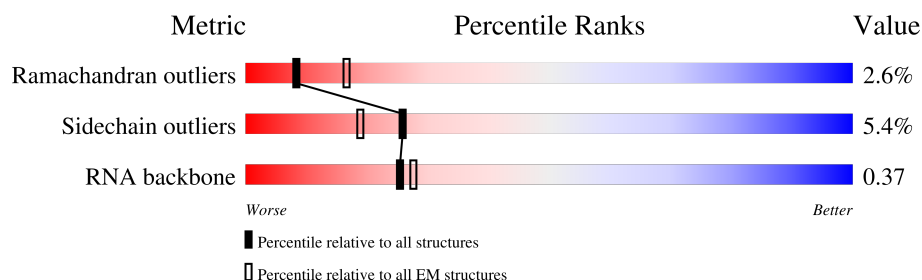
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 11.50 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.





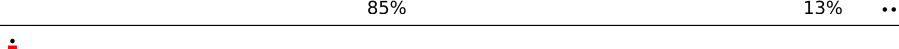
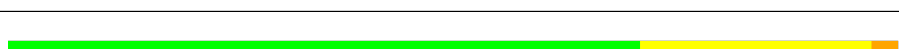



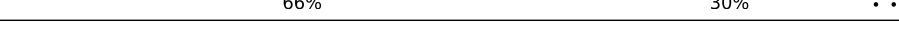



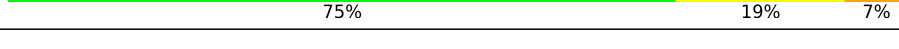

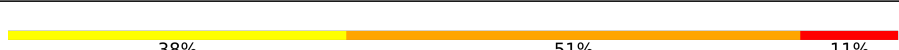


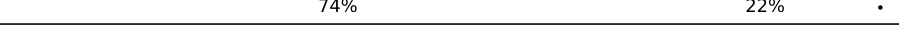







Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	AA	1542	<div> <div>32%</div> <div>53%</div> <div>14%</div> </div>
2	AB	76	<div> <div>29%</div> <div>53%</div> <div>18%</div> </div>
3	AC	47	<div> <div>9%</div> <div>17%</div> <div>45%</div> <div>38%</div> </div>
4	AD	77	<div> <div>43%</div> <div>51%</div> <div>6%</div> </div>
5	AE	240	<div> <div>76%</div> <div>21%</div> </div>
6	AF	232	<div> <div>78%</div> <div>21%</div> </div>
7	AG	205	<div> <div>77%</div> <div>20%</div> </div>
8	AH	166	<div> <div>79%</div> <div>20%</div> </div>

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Mol	Chain	Length	Quality of chain
9	AI	135	
10	AJ	178	
11	AK	129	
12	AL	129	
13	AM	103	
14	AN	128	
15	AO	123	
16	AP	117	
17	AQ	100	
18	AR	88	
19	AS	82	
20	AT	83	
21	AU	74	
22	AV	91	
23	AW	86	
24	AX	70	
25	BA	120	
26	BB	2904	
27	BC	234	
28	BD	272	
29	BE	209	
30	BF	201	
31	BG	178	
32	BH	176	
33	BI	149	

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Mol	Chain	Length	Quality of chain
34	BJ	164	
35	BK	141	
36	BL	142	
37	BM	123	
38	BN	144	
39	BO	136	
40	BP	127	
41	BQ	117	
42	BR	114	
43	BS	117	
44	BT	103	
45	BU	110	
46	BV	100	
47	BW	103	
48	BX	94	
49	BY	84	
50	BZ	77	
51	B0	63	
52	B1	58	
53	B2	70	
54	B3	56	
55	B4	54	
56	B5	46	
57	B6	64	
58	B7	38	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 152351 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1542	Total	C	N	O	P	0	0
			33089	14767	6064	10717	1541		

- Molecule 2 is a RNA chain called A site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AB	76	Total	C	N	O	P	S	0	0
			1627	731	287	532	75	2		

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	47	Total	C	N	O	P	0	0
			993	445	167	335	46		

- Molecule 4 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AD	77	Total	C	N	O	P	S	0	0
			1641	734	297	533	76	1		

- Molecule 5 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 6 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 7 is a protein called 30S ribosomal protein S4.

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

- Molecule 8 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 9 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 10 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 11 is a protein called 30S ribosomal protein S8.

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

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 15 is a protein called 30S ribosomal protein S12.

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

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 17 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 18 is a protein called 30S ribosomal protein S15.

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

- Molecule 19 is a protein called 30S ribosomal protein S16.

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

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 21 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 22 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 23 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 24 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 25 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BA	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BB	2904	Total	C	N	O	P	0	0
			62351	27824	11469	20155	2903		

- Molecule 27 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BC	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 28 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BD	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 29 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BE	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 30 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BF	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 31 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BG	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 32 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BH	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 33 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BI	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 34 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BJ	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 35 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BK	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 36 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BL	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 37 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BM	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 38 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BN	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 39 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BO	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 40 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BP	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 41 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BQ	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 42 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BR	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 43 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BS	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 44 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BT	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 45 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BU	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 46 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BV	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 47 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	103	Total	C	N	O		0	0
			789	498	148	143			

- Molecule 48 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BX	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 49 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BY	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BZ	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 51 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 52 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 53 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 54 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 55 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	B4	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 56 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	B5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

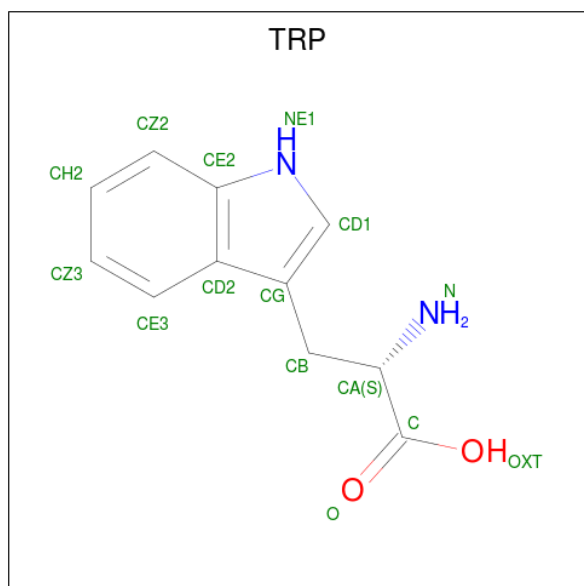
- Molecule 57 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	B6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 58 is a protein called 50S ribosomal protein L36.

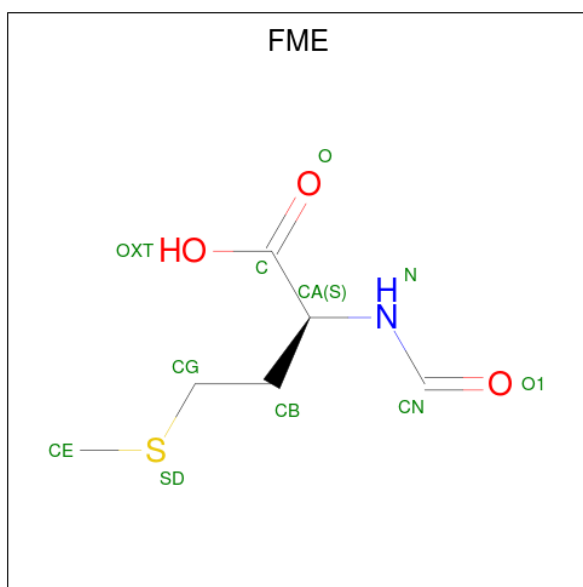
Mol	Chain	Residues	Atoms					AltConf	Trace
58	B7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 59 is TRYPTOPHAN (three-letter code: TRP) (formula: $C_{11}H_{12}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
59	AB	1	Total	C	N	O	0
			14	11	2	1	

- Molecule 60 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: $C_6H_{11}NO_3S$).

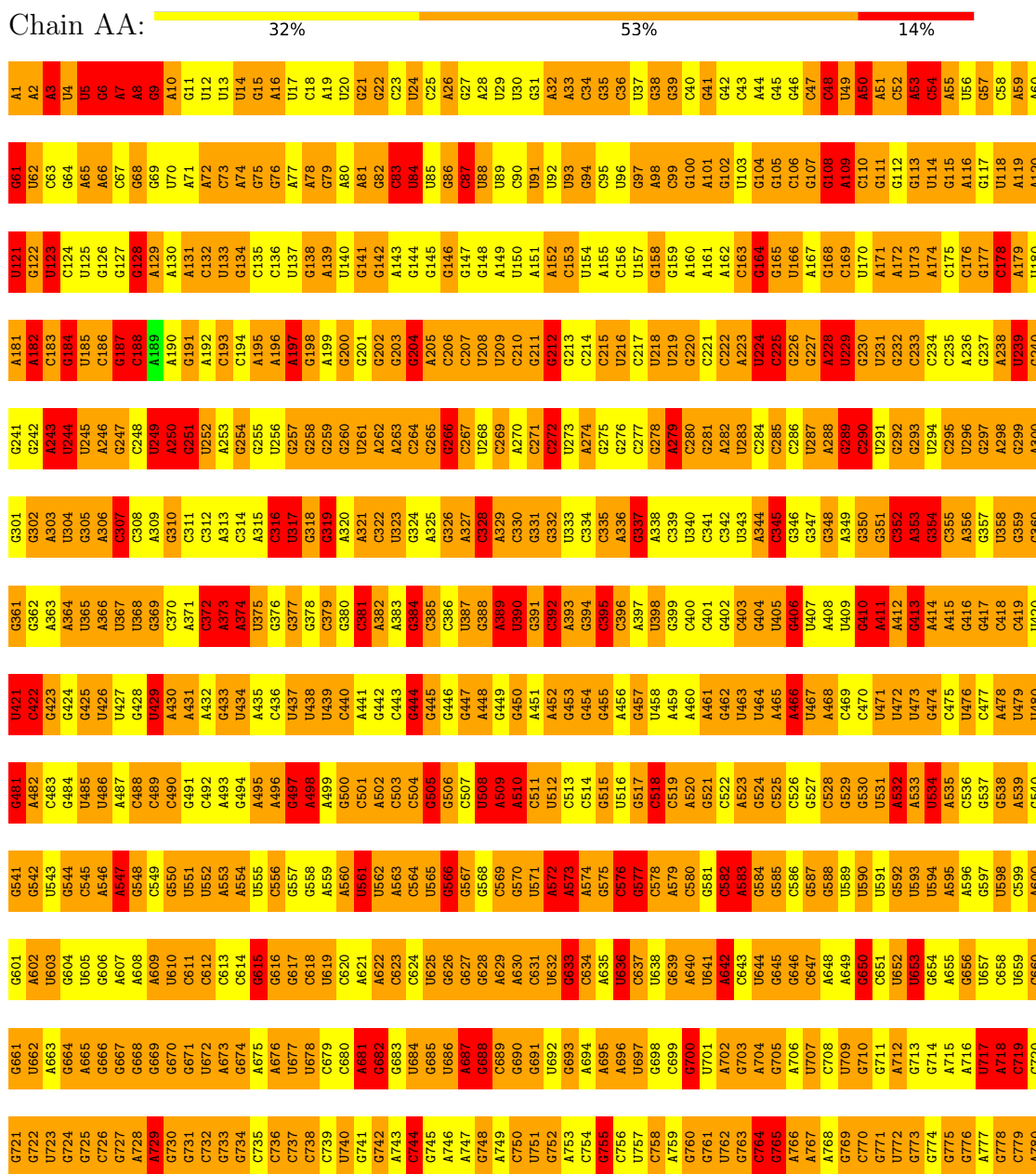


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	BB	1	10	6	1	2	1	0

3 Residue-property plots

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

• Molecule 1: 16S ribosomal RNA

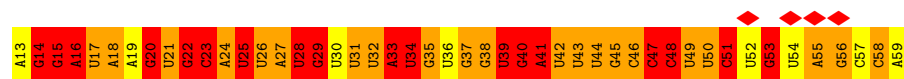


- Molecule 2: A site tRNA

Threat Level	Percentage
Not a threat	29%
Somewhat of a threat	53%
A major threat	18%

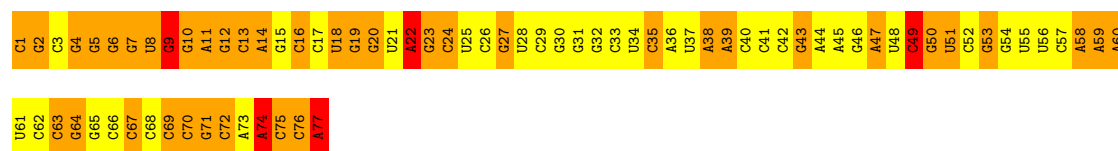
- Molecule 3: mRNA

Response	Percentage
No	9%
Yes, but not a full democracy	17%
Yes, a democracy	45%
Don't know	38%



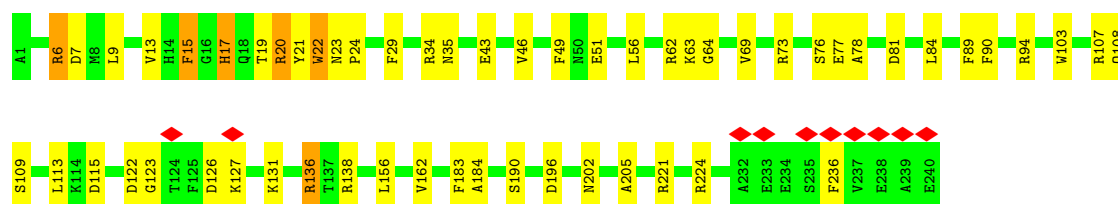
• Molecule 4: P site tRNA

Chain AD: 43% 51% 6%



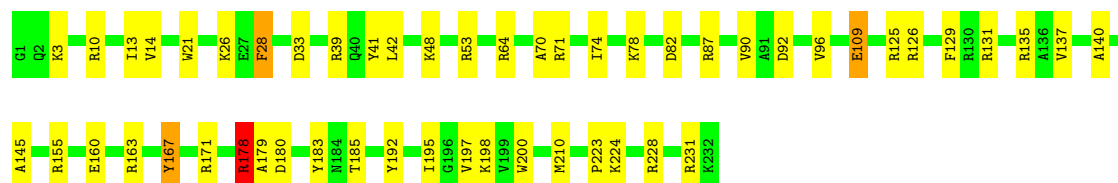
• Molecule 5: 30S ribosomal protein S2

Chain AE: 76% 21%



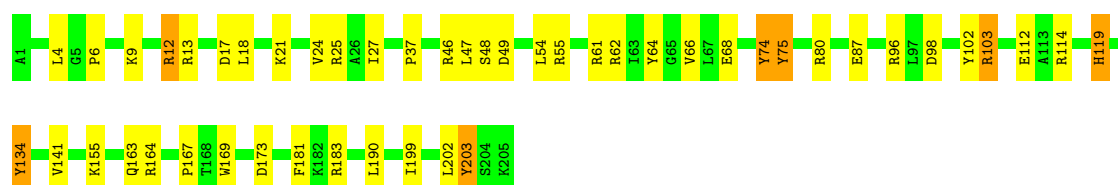
• Molecule 6: 30S ribosomal protein S3

Chain AF: 78% 21%



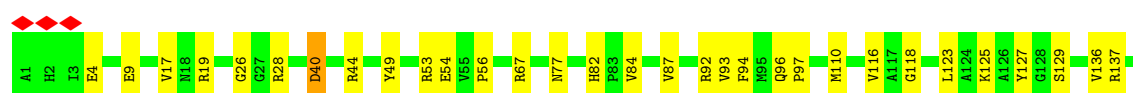
• Molecule 7: 30S ribosomal protein S4

Chain AG: 77% 20%



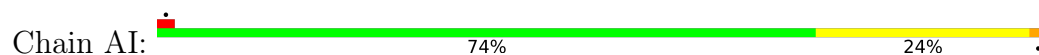
• Molecule 8: 30S ribosomal protein S5

Chain AH: 79% 20%

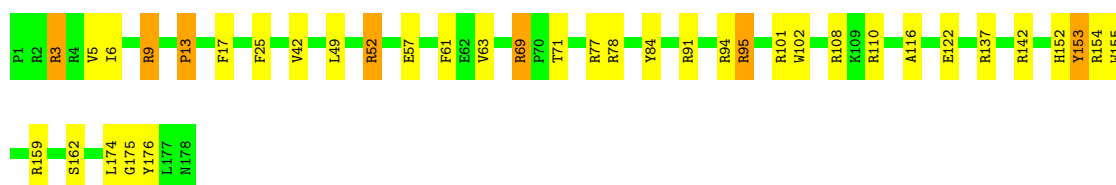
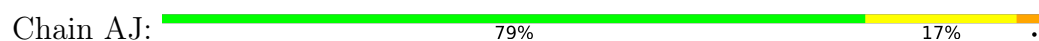




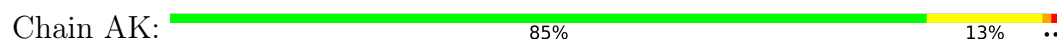
- Molecule 9: 30S ribosomal protein S6



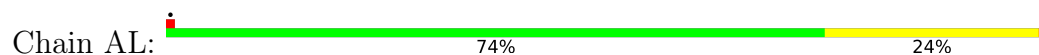
- Molecule 10: 30S ribosomal protein S7



- Molecule 11: 30S ribosomal protein S8



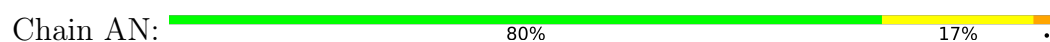
- Molecule 12: 30S ribosomal protein S9




- Molecule 13: 30S ribosomal protein S10

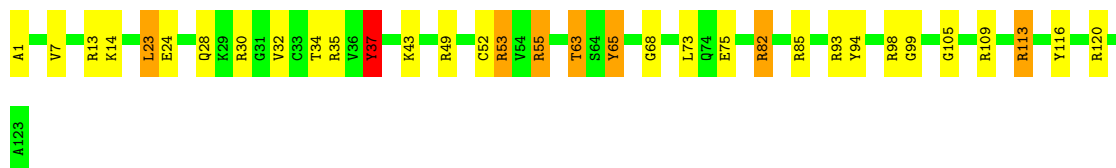


- Molecule 14: 30S ribosomal protein S11




- Molecule 15: 30S ribosomal protein S12

Chain AO:  73% 20% 6% .



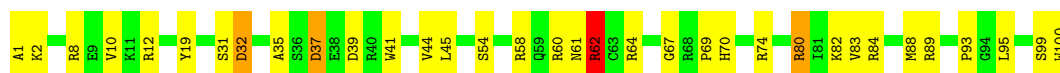
- Molecule 16: 30S ribosomal protein S13

Chain AP:  79% 18% .



- Molecule 17: 30S ribosomal protein S14

Chain AQ:  66% 30% . .




- Molecule 18: 30S ribosomal protein S15

Chain AR:  72% 25% .




- Molecule 19: 30S ribosomal protein S16

Chain AS:  79% 16% 5%



- Molecule 20: 30S ribosomal protein S17

Chain AT:  76% 17% 7%




- Molecule 21: 30S ribosomal protein S18

Chain AU:  68% 24% 7% .




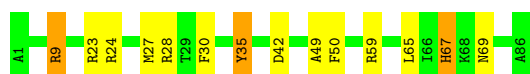
- Molecule 22: 30S ribosomal protein S19

Chain AV: 



- Molecule 23: 30S ribosomal protein S20

Chain AW: 



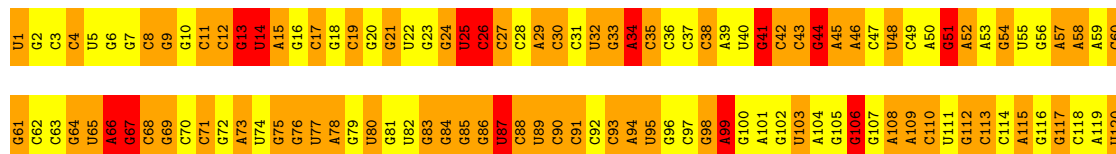
- Molecule 24: 30S ribosomal protein S21

Chain AX: 



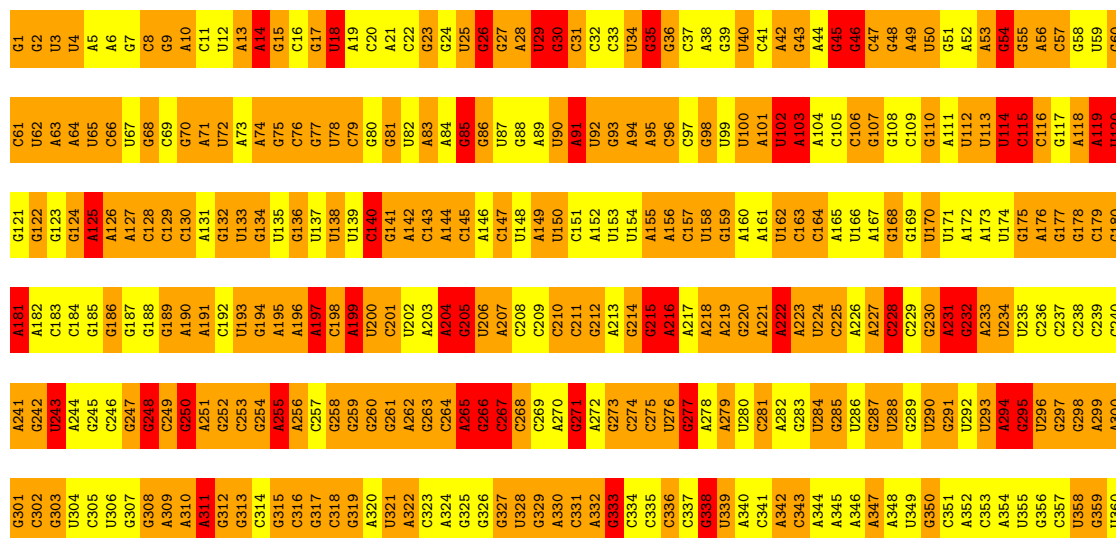
- Molecule 25: 5S ribosomal RNA

Chain BA: 



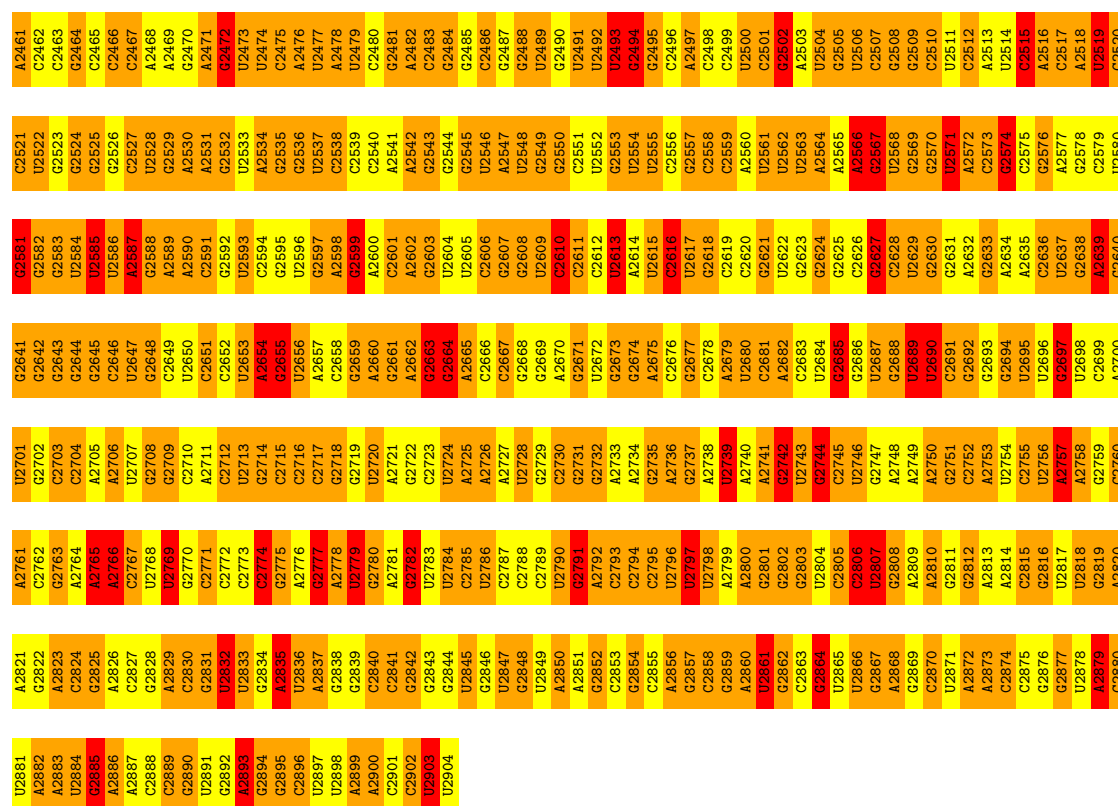
- Molecule 26: 23S ribosomal RNA

Chain BB: 

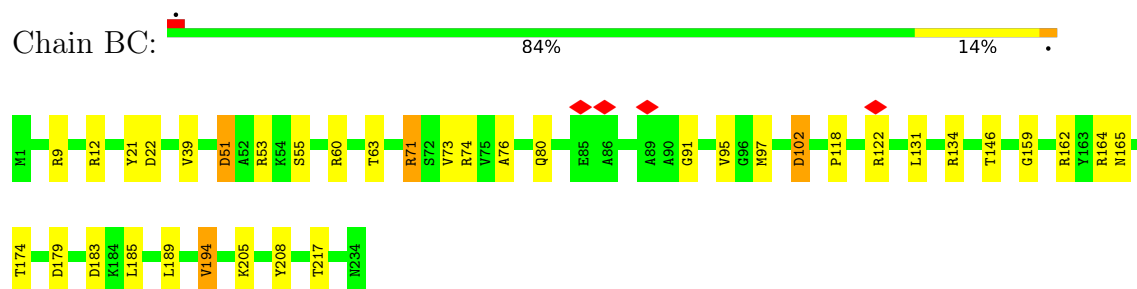


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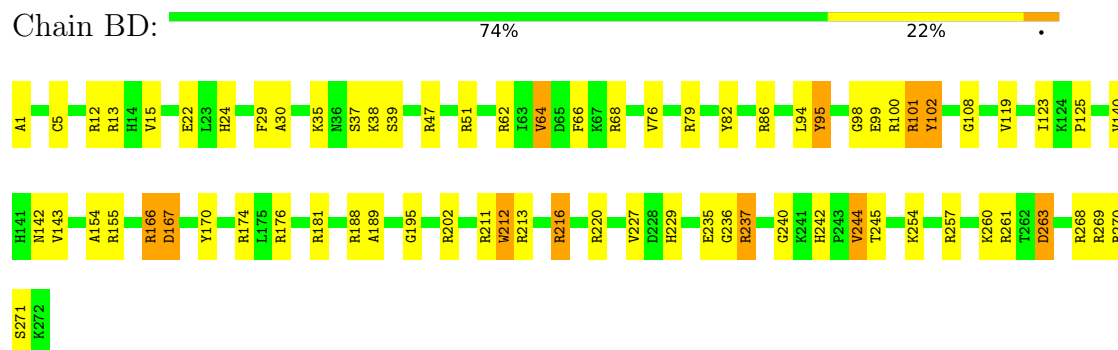
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A2435	G2375	G2315	U2255	U2195	A2135	U2075	A2015	U1955	C1895	G1835	U1775	A1595	G1535	G1475
G2436	A2376	G2316	G2256	C2196	G2136	U2076	U2016	U1956	G1896	C1836	G1776	A1596	C1536	U1476
G2437	A2377	U2317	U2257	U2197	U2137	A2077	U2017	G1957	G1897	C1837	U1777	A1597	G1537	A1477
U2438	A2378	G2318	C2258	A2198	G2138	C2078	G2018	C1958	U1898	C1838	U1778	A1598	G1538	G1478
A2439	G2379	G2319	U2259	A2199	U2139	U2079	A2019	G1959	A1899	G1839	U1779	U1599	U1539	G1479
G2440	C2380	U2320	C2260	C2200	G2140	A2080	A2020	A1960	A1900	G1840	A1780	C1600	G1540	U1480
U2441	A2381	U2321	G2261	G2201	G2141	U2081	C2021	C1961	A1901	U1841	G1781	C1601	C1541	U1481
C2442	G2382	A2322	U2262	U2202	A2142	A2082	U2022	C1962	G1902	G1842	U1782	U1602	U1542	G1482
C2443	G2383	G2323	G2263	U2203	G2143	G2083	G2023	U1963	G1903	C1843	A1783	A1603	G1543	G1483
G2444	U2384	U2324	C2264	G2204	G2144	A2084	G2024	G1964	G1904	C1844	G1784	C1604	A1544	U1484
G2445	C2385	G2325	U2265	A2205	C2145	U2085	C2025	C1965	C1905	G1845	A1785	C1605	A1545	U1485
G2446	A2386	C2326	A2266	C2206	G2146	U2086	U2026	A1966	G1906	G1846	A1786	C1606	G1546	U1486
A2448	A2388	A2328	A2268	C2207	A2148	G2088	U2028	G1967	G1907	A1848	A1787	C1607	C1547	U1487
U2449	G2389	U2329	G2269	G2209	U2149	C2089	G2029	A1969	C1909	G1849	A1789	A1609	A1549	C1489
A2450	U2390	G2330	A2270	U2210	C2150	A2090	A2030	U1970	G1910	G1850	C1790	A1610	C1550	A1490
A2451	G2391	G2331	G2271	A2211	U2151	C2091	A2031	U1971	U1911	U1851	A1791	C1611	A1551	G1491
C2452	A2392	U2332	U2272	A2212	G2152	U2092	G2032	G1972	A1912	U1852	G1792	C1612	A1552	G1492
A2453	U2393	A2333	A2273	U2213	C2153	G2093	A2033	G1973	A1913	A1853	C1793	G1613	A1553	C1493
G2454	C2394	U2334	A2274	C2214	A2154	A2094	U2034	C1974	A1914	A1854	A1794	A1614	A1554	A1494
G2455	C2395	G2335	G2275	U2215	U2155	A2095	G2035	G1975	3TD1915	U1855	C1795	G1615	G1555	A1495
A2456	G2396	A2336	G2276	G2216	G2156	C2096	C2036	U1976	A1916	U1856	U1796	A1616	G1556	A1496
U2457	G2397	G2337	G2277	G2217	G2157	A2097	A2037	A1977	U1917	G1857	G1797	C1617	C1557	U1497
G2458	U2398	C2338	A2278	G2218	A2158	U2098	U2038	A1978	U1918	A1858	G1798	A1618	C1558	C1498
A2459	G2399	C2339	G2279	U2219	U2159	U2099	G2039	A1979	A1919	U1859	G1799	G1619	C1559	C1499
U2460	G2400	A2340	G2280	U2220	G2160	G2100	G2040	G1980	C1920	G1860	C1900	G1620	G1560	G1500



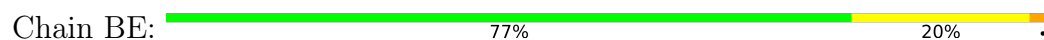
- Molecule 27: 50S ribosomal protein L1

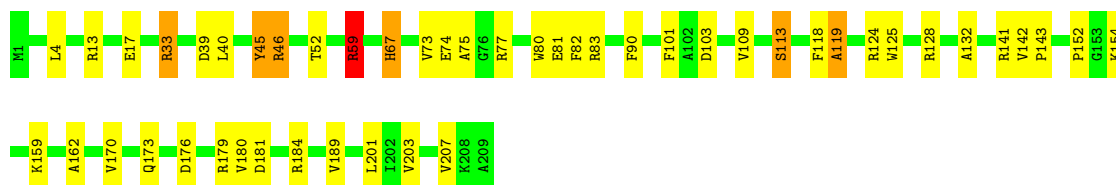


- Molecule 28: 50S ribosomal protein L2



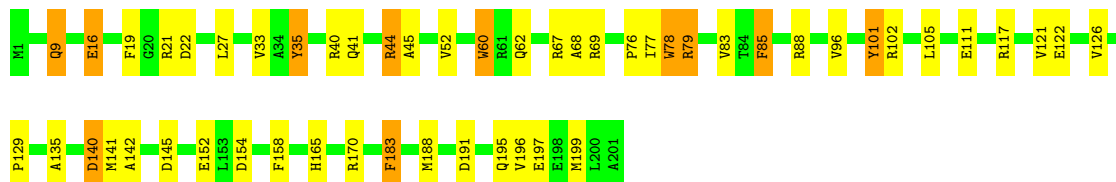
- Molecule 29: 50S ribosomal protein L3





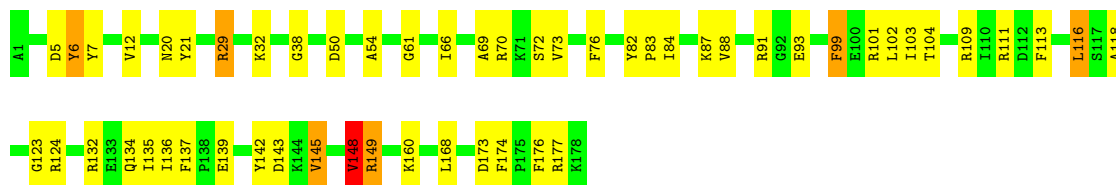
- Molecule 30: 50S ribosomal protein L4

Chain BF: 74% 20% 5%



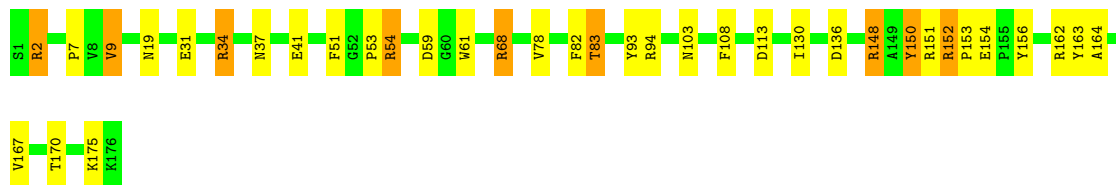
- Molecule 31: 50S ribosomal protein L5

Chain BG: 70% 26% ..



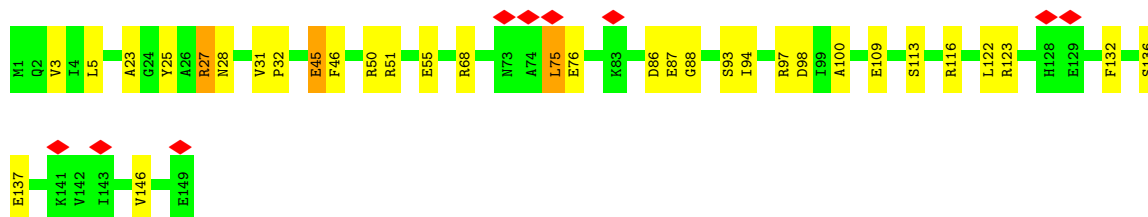
- Molecule 32: 50S ribosomal protein L6

Chain BH: 79% 16% 5%

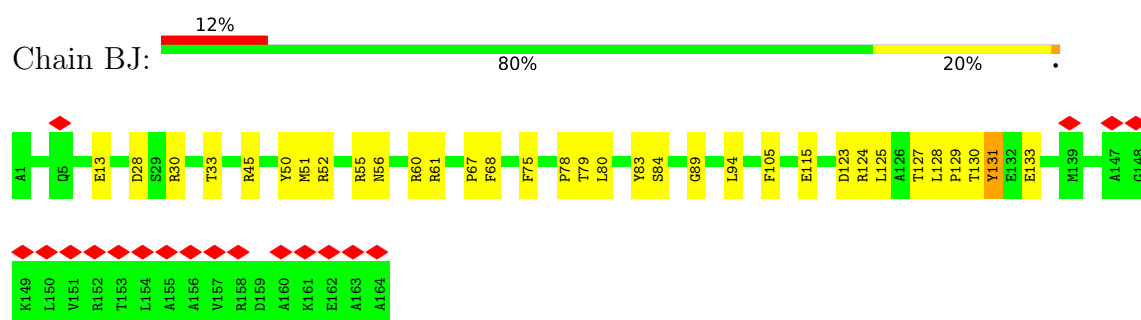


- Molecule 33: 50S ribosomal protein L9

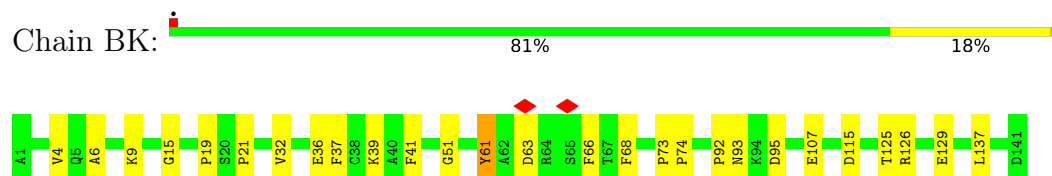
Chain BI: 6% 78% 20% .



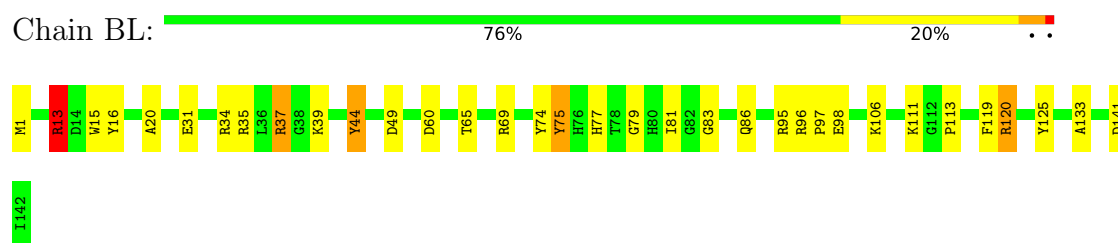
- Molecule 34: 50S ribosomal protein L10



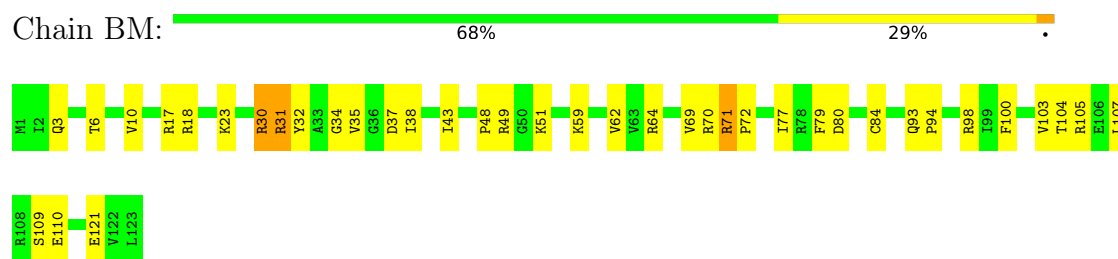
- Molecule 35: 50S ribosomal protein L11



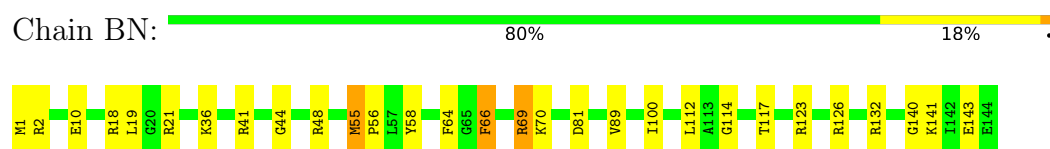
- Molecule 36: 50S ribosomal protein L13



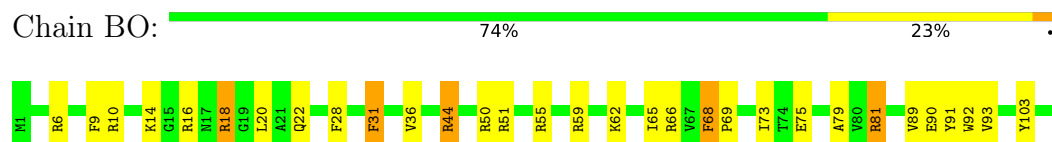
- Molecule 37: 50S ribosomal protein L14



- Molecule 38: 50S ribosomal protein L15



- Molecule 39: 50S ribosomal protein L16





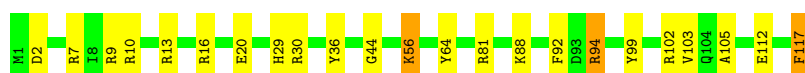
- Molecule 40: 50S ribosomal protein L17

Chain BP: 75% 22% .



- Molecule 41: 50S ribosomal protein L18

Chain BQ: 80% 17% .



- Molecule 42: 50S ribosomal protein L19

Chain BR: 76% 18% 5%



- Molecule 43: 50S ribosomal protein L20

Chain BS: 71% 26% . .



- Molecule 44: 50S ribosomal protein L21

Chain BT: 77% 19% .




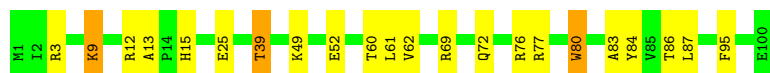
- Molecule 45: 50S ribosomal protein L22

Chain BU: 75% 24% .




- Molecule 46: 50S ribosomal protein L23

Chain BV:  78% 19% .




- Molecule 47: 50S ribosomal protein L24

Chain BW:  79% 19% .




- Molecule 48: 50S ribosomal protein L25

Chain BX:  80% 16% .




- Molecule 49: 50S ribosomal protein L27

Chain BY:  74% 20% . .




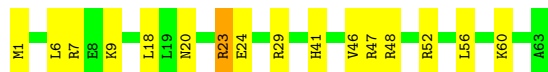
- Molecule 50: 50S ribosomal protein L28

Chain BZ:  81% 17% .




- Molecule 51: 50S ribosomal protein L29

Chain B0:  75% 24% .




- Molecule 52: 50S ribosomal protein L30

Chain B1:  76% 21% .



- Molecule 53: 50S ribosomal protein L31

Chain B2:  73% 19% 7%




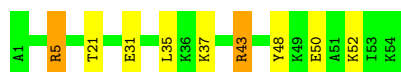
- Molecule 54: 50S ribosomal protein L32

Chain B3:  71% 21% 7%



- Molecule 55: 50S ribosomal protein L33

Chain B4:  83% 13% 0%




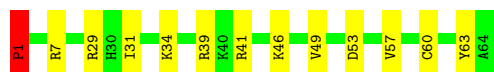
- Molecule 56: 50S ribosomal protein L34

Chain B5:  65% 30% 5%



- Molecule 57: 50S ribosomal protein L35

Chain B6:  80% 19% 1%



- Molecule 58: 50S ribosomal protein L36

Chain B7:  71% 29% 0%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Volumes were CTF-corrected in defocus groups	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	58269	Depositor
Image detector	TVIPS TEMCAM-F415 (4k x 4k)	Depositor
Maximum map value	1.575	Depositor
Minimum map value	-0.492	Depositor
Average map value	0.029	Depositor
Map value standard deviation	0.204	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	375.0, 375.0, 375.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.5, 1.5, 1.5	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 7MG, 5MC, 4SU, H2U, MIA, OMU, 2MG, CH, PSU, FME, UR3, 2MA, OMC, 3TD, 1MG, MA6, 6MZ, 5MU, 4OC, OMG

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	AA	3.08	3895/36769 (10.6%)	3.56	8470/57354 (14.8%)
2	AB	3.15	171/1600 (10.7%)	3.56	384/2492 (15.4%)
3	AC	3.09	117/1108 (10.6%)	3.61	256/1724 (14.8%)
4	AD	3.09	193/1721 (11.2%)	3.54	391/2683 (14.6%)
5	AE	1.51	6/1904 (0.3%)	1.92	45/2565 (1.8%)
6	AF	1.52	7/1852 (0.4%)	1.92	47/2490 (1.9%)
7	AG	1.49	7/1665 (0.4%)	2.08	46/2227 (2.1%)
8	AH	1.51	6/1239 (0.5%)	1.87	24/1664 (1.4%)
9	AI	1.55	6/1121 (0.5%)	1.91	29/1509 (1.9%)
10	AJ	1.47	2/1422 (0.1%)	2.07	39/1908 (2.0%)
11	AK	1.53	8/989 (0.8%)	1.89	16/1326 (1.2%)
12	AL	1.52	4/1048 (0.4%)	2.03	33/1394 (2.4%)
13	AM	1.50	5/835 (0.6%)	2.00	23/1127 (2.0%)
14	AN	1.54	6/982 (0.6%)	1.99	24/1323 (1.8%)
15	AO	1.52	4/969 (0.4%)	2.06	33/1300 (2.5%)
16	AP	1.57	5/919 (0.5%)	2.09	26/1226 (2.1%)
17	AQ	1.60	8/817 (1.0%)	1.99	27/1088 (2.5%)
18	AR	1.44	0/724	2.09	30/966 (3.1%)
19	AS	1.53	4/659 (0.6%)	1.92	13/884 (1.5%)
20	AT	1.56	2/681 (0.3%)	1.83	18/913 (2.0%)
21	AU	1.59	7/637 (1.1%)	2.19	20/851 (2.4%)
22	AV	1.48	2/744 (0.3%)	1.98	20/995 (2.0%)
23	AW	1.46	1/676 (0.1%)	1.88	14/895 (1.6%)
24	AX	1.61	4/598 (0.7%)	2.21	25/792 (3.2%)
25	BA	3.02	293/2869 (10.2%)	3.44	610/4474 (13.6%)
26	BB	3.09	7348/69257 (10.6%)	3.54	15639/108040 (14.5%)
27	BC	1.46	3/1748 (0.2%)	1.85	33/2355 (1.4%)
28	BD	1.51	10/2131 (0.5%)	2.03	68/2863 (2.4%)
29	BE	1.54	3/1586 (0.2%)	2.03	41/2134 (1.9%)
30	BF	1.53	6/1571 (0.4%)	1.97	51/2113 (2.4%)
31	BG	1.58	11/1444 (0.8%)	1.94	33/1937 (1.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	1.50	7/1343 (0.5%)	1.89	33/1816 (1.8%)
33	BI	1.50	8/1122 (0.7%)	1.93	22/1515 (1.5%)
34	BJ	1.52	4/1247 (0.3%)	1.95	29/1679 (1.7%)
35	BK	1.45	4/1046 (0.4%)	1.81	17/1410 (1.2%)
36	BL	1.53	5/1152 (0.4%)	1.98	24/1551 (1.5%)
37	BM	1.53	3/956 (0.3%)	1.99	28/1279 (2.2%)
38	BN	1.53	4/1062 (0.4%)	1.93	21/1413 (1.5%)
39	BO	1.53	6/1093 (0.5%)	1.96	31/1460 (2.1%)
40	BP	1.53	3/1021 (0.3%)	2.11	37/1364 (2.7%)
41	BQ	1.60	4/910 (0.4%)	1.96	26/1219 (2.1%)
42	BR	1.53	1/929 (0.1%)	2.18	29/1242 (2.3%)
43	BS	1.57	5/960 (0.5%)	2.38	37/1278 (2.9%)
44	BT	1.58	2/829 (0.2%)	2.03	21/1107 (1.9%)
45	BU	1.43	4/864 (0.5%)	2.00	28/1156 (2.4%)
46	BV	1.52	3/794 (0.4%)	1.92	14/1060 (1.3%)
47	BW	1.46	1/797 (0.1%)	2.06	20/1062 (1.9%)
48	BX	1.48	1/766 (0.1%)	1.93	16/1025 (1.6%)
49	BY	1.49	4/642 (0.6%)	2.00	16/848 (1.9%)
50	BZ	1.50	0/635	1.84	17/848 (2.0%)
51	B0	1.43	1/510 (0.2%)	2.02	13/677 (1.9%)
52	B1	1.54	1/453 (0.2%)	1.96	12/605 (2.0%)
53	B2	1.58	4/559 (0.7%)	1.92	13/745 (1.7%)
54	B3	1.55	2/450 (0.4%)	2.05	10/599 (1.7%)
55	B4	1.41	0/448	1.83	6/594 (1.0%)
56	B5	1.50	1/380 (0.3%)	2.36	22/498 (4.4%)
57	B6	1.43	0/513	1.79	11/676 (1.6%)
58	B7	1.44	1/303 (0.3%)	2.17	7/397 (1.8%)
All	All	2.70	12223/164069 (7.4%)	3.19	27088/244735 (11.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	910
2	AB	0	43
3	AC	0	30
4	AD	0	37
5	AE	0	1
6	AF	0	3
7	AG	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	AH	0	2
9	AI	0	5
10	AJ	0	6
11	AK	0	2
12	AL	0	3
13	AM	0	2
14	AN	0	4
15	AO	0	9
16	AP	0	4
17	AQ	0	1
18	AR	0	3
19	AS	0	3
20	AT	0	2
21	AU	0	5
22	AV	0	3
23	AW	0	2
24	AX	0	4
25	BA	0	65
26	BB	0	1685
27	BC	0	1
28	BD	0	10
29	BE	0	8
30	BF	0	6
31	BG	0	7
32	BH	0	6
33	BI	0	3
34	BJ	0	4
35	BK	0	5
36	BL	0	8
37	BM	0	4
38	BN	0	2
39	BO	0	4
40	BP	0	2
41	BQ	0	2
42	BR	0	5
43	BS	0	6
44	BT	0	3
45	BU	0	1
46	BV	0	2
47	BW	0	1
48	BX	0	5
49	BY	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
50	BZ	0	1
51	B0	0	1
53	B2	0	5
54	B3	0	4
55	B4	0	3
56	B5	0	2
57	B6	0	1
All	All	0	2959

The worst 5 of 12223 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BB	2448	A	N3-C4	21.86	1.48	1.34
1	AA	451	A	N3-C4	17.17	1.45	1.34
26	BB	492	A	N7-C5	-16.23	1.29	1.39
26	BB	2241	A	N3-C4	15.98	1.44	1.34
26	BB	833	A	N7-C5	-15.82	1.29	1.39

The worst 5 of 27088 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	AG	164	ARG	NE-CZ-NH2	-25.71	107.44	120.30
7	AG	164	ARG	NE-CZ-NH1	23.24	131.92	120.30
7	AG	114	ARG	NE-CZ-NH2	-22.43	109.08	120.30
26	BB	1929	G	C2-N3-C4	22.14	122.97	111.90
26	BB	2512	C	N3-C4-C5	-21.97	113.11	121.90

There are no chirality outliers.

5 of 2959 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	A	Sidechain
1	AA	2	A	Sidechain
1	AA	3	A	Sidechain
1	AA	5	U	Sidechain
1	AA	6	G	Sidechain

5.2 Too-close contacts [i](#)

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	AA	33089	0	16599	0	0
2	AB	1627	0	841	0	0
3	AC	993	0	498	0	0
4	AD	1641	0	839	0	0
5	AE	1872	0	1885	0	0
6	AF	1822	0	1913	0	0
7	AG	1643	0	1710	0	0
8	AH	1225	0	1273	0	0
9	AI	1101	0	1050	0	0
10	AJ	1400	0	1449	0	0
11	AK	979	0	1034	0	0
12	AL	1036	0	1084	0	0
13	AM	825	0	865	0	0
14	AN	965	0	997	0	0
15	AO	955	0	1019	0	0
16	AP	910	0	981	0	0
17	AQ	805	0	847	0	0
18	AR	716	0	742	0	0
19	AS	649	0	666	0	0
20	AT	672	0	716	0	0
21	AU	626	0	651	0	0
22	AV	727	0	769	0	0
23	AW	670	0	722	0	0
24	AX	590	0	631	0	0
25	BA	2566	0	1294	0	0
26	BB	62351	0	31277	0	0
27	BC	1733	0	1824	0	0
28	BD	2092	0	2170	0	0
29	BE	1565	0	1616	0	0
30	BF	1552	0	1619	0	0
31	BG	1420	0	1460	0	0
32	BH	1323	0	1374	0	0
33	BI	1111	0	1148	0	0
34	BJ	1233	0	1283	0	0
35	BK	1032	0	1088	0	0
36	BL	1129	0	1162	0	0
37	BM	947	0	1023	0	0
38	BN	1053	0	1129	0	0
39	BO	1074	0	1157	0	0
40	BP	1008	0	1045	0	0
41	BQ	900	0	935	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	BR	917	0	965	0	0
43	BS	947	0	1022	0	0
44	BT	816	0	839	0	0
45	BU	857	0	922	0	0
46	BV	787	0	846	0	0
47	BW	789	0	847	0	0
48	BX	753	0	780	0	0
49	BY	634	0	656	0	0
50	BZ	625	0	655	0	0
51	B0	509	0	543	0	0
52	B1	449	0	491	0	0
53	B2	549	0	552	0	0
54	B3	444	0	461	0	0
55	B4	441	0	485	0	0
56	B5	377	0	418	0	0
57	B6	504	0	574	0	0
58	B7	302	0	343	0	0
59	AB	14	0	9	0	0
60	BB	10	0	10	0	0
All	All	152351	0	103803	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	AE	238/240 (99%)	219 (92%)	10 (4%)	9 (4%)	3	24
6	AF	230/232 (99%)	215 (94%)	10 (4%)	5 (2%)	6	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	AG	203/205 (99%)	187 (92%)	13 (6%)	3 (2%)	10	46
8	AH	164/166 (99%)	151 (92%)	11 (7%)	2 (1%)	13	50
9	AI	133/135 (98%)	122 (92%)	10 (8%)	1 (1%)	19	60
10	AJ	176/178 (99%)	164 (93%)	10 (6%)	2 (1%)	14	52
11	AK	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	19	60
12	AL	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	6	33
13	AM	101/103 (98%)	92 (91%)	4 (4%)	5 (5%)	2	20
14	AN	126/128 (98%)	111 (88%)	13 (10%)	2 (2%)	9	44
15	AO	121/123 (98%)	105 (87%)	13 (11%)	3 (2%)	5	32
16	AP	115/117 (98%)	109 (95%)	4 (4%)	2 (2%)	9	42
17	AQ	98/100 (98%)	85 (87%)	6 (6%)	7 (7%)	1	14
18	AR	86/88 (98%)	80 (93%)	5 (6%)	1 (1%)	13	50
19	AS	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
20	AT	81/83 (98%)	72 (89%)	7 (9%)	2 (2%)	5	32
21	AU	72/74 (97%)	61 (85%)	7 (10%)	4 (6%)	2	19
22	AV	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	14	52
23	AW	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	13	50
24	AX	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2	22
27	BC	232/234 (99%)	215 (93%)	13 (6%)	4 (2%)	9	42
28	BD	270/272 (99%)	238 (88%)	23 (8%)	9 (3%)	4	26
29	BE	207/209 (99%)	173 (84%)	27 (13%)	7 (3%)	3	26
30	BF	199/201 (99%)	173 (87%)	17 (8%)	9 (4%)	2	22
31	BG	176/178 (99%)	152 (86%)	13 (7%)	11 (6%)	1	17
32	BH	174/176 (99%)	158 (91%)	13 (8%)	3 (2%)	9	42
33	BI	147/149 (99%)	131 (89%)	11 (8%)	5 (3%)	3	26
34	BJ	162/164 (99%)	157 (97%)	4 (2%)	1 (1%)	25	66
35	BK	139/141 (99%)	133 (96%)	5 (4%)	1 (1%)	22	63
36	BL	140/142 (99%)	119 (85%)	14 (10%)	7 (5%)	2	20
37	BM	121/123 (98%)	109 (90%)	9 (7%)	3 (2%)	5	32
38	BN	142/144 (99%)	126 (89%)	13 (9%)	3 (2%)	7	36
39	BO	134/136 (98%)	122 (91%)	10 (8%)	2 (2%)	10	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	BP	125/127 (98%)	116 (93%)	8 (6%)	1 (1%)	19	60
41	BQ	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
42	BR	112/114 (98%)	97 (87%)	12 (11%)	3 (3%)	5	31
43	BS	115/117 (98%)	107 (93%)	5 (4%)	3 (3%)	5	31
44	BT	101/103 (98%)	89 (88%)	7 (7%)	5 (5%)	2	20
45	BU	108/110 (98%)	99 (92%)	6 (6%)	3 (3%)	5	30
46	BV	98/100 (98%)	75 (76%)	19 (19%)	4 (4%)	3	23
47	BW	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	7	38
48	BX	92/94 (98%)	86 (94%)	5 (5%)	1 (1%)	14	52
49	BY	82/84 (98%)	65 (79%)	12 (15%)	5 (6%)	1	17
50	BZ	75/77 (97%)	67 (89%)	5 (7%)	3 (4%)	3	23
51	B0	61/63 (97%)	56 (92%)	3 (5%)	2 (3%)	4	26
52	B1	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
53	B2	68/70 (97%)	63 (93%)	4 (6%)	1 (2%)	10	46
54	B3	54/56 (96%)	48 (89%)	3 (6%)	3 (6%)	2	19
55	B4	52/54 (96%)	49 (94%)	1 (2%)	2 (4%)	3	24
56	B5	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	22
57	B6	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	9	44
58	B7	36/38 (95%)	29 (81%)	5 (14%)	2 (6%)	2	19
All	All	6319/6423 (98%)	5707 (90%)	447 (7%)	165 (3%)	8	31

5 of 165 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	AH	77	ASN
13	AM	57	VAL
17	AQ	2	LYS
17	AQ	61	ASN
17	AQ	70	HIS

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	AE	198/198 (100%)	186 (94%)	12 (6%)	18	44
6	AF	189/189 (100%)	180 (95%)	9 (5%)	25	51
7	AG	172/172 (100%)	166 (96%)	6 (4%)	36	59
8	AH	125/125 (100%)	116 (93%)	9 (7%)	14	39
9	AI	116/116 (100%)	109 (94%)	7 (6%)	19	44
10	AJ	146/146 (100%)	138 (94%)	8 (6%)	21	47
11	AK	104/104 (100%)	100 (96%)	4 (4%)	33	57
12	AL	106/106 (100%)	102 (96%)	4 (4%)	33	57
13	AM	90/90 (100%)	84 (93%)	6 (7%)	16	41
14	AN	98/98 (100%)	95 (97%)	3 (3%)	40	62
15	AO	103/103 (100%)	98 (95%)	5 (5%)	25	50
16	AP	95/95 (100%)	94 (99%)	1 (1%)	73	84
17	AQ	83/83 (100%)	79 (95%)	4 (5%)	25	51
18	AR	76/76 (100%)	74 (97%)	2 (3%)	46	66
19	AS	65/65 (100%)	60 (92%)	5 (8%)	13	37
20	AT	77/77 (100%)	71 (92%)	6 (8%)	12	36
21	AU	64/64 (100%)	60 (94%)	4 (6%)	18	43
22	AV	78/78 (100%)	70 (90%)	8 (10%)	7	25
23	AW	65/65 (100%)	62 (95%)	3 (5%)	27	52
24	AX	60/60 (100%)	57 (95%)	3 (5%)	24	49
27	BC	181/181 (100%)	173 (96%)	8 (4%)	28	53
28	BD	217/217 (100%)	210 (97%)	7 (3%)	39	61
29	BE	164/164 (100%)	153 (93%)	11 (7%)	16	41
30	BF	165/165 (100%)	157 (95%)	8 (5%)	25	51
31	BG	149/149 (100%)	141 (95%)	8 (5%)	22	47
32	BH	137/137 (100%)	129 (94%)	8 (6%)	20	45
33	BI	114/114 (100%)	107 (94%)	7 (6%)	18	44
34	BJ	122/122 (100%)	115 (94%)	7 (6%)	20	45
35	BK	109/109 (100%)	106 (97%)	3 (3%)	43	65
36	BL	116/116 (100%)	111 (96%)	5 (4%)	29	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BM	104/104 (100%)	96 (92%)	8 (8%)	13	37
38	BN	103/103 (100%)	96 (93%)	7 (7%)	16	41
39	BO	109/109 (100%)	102 (94%)	7 (6%)	17	42
40	BP	103/103 (100%)	98 (95%)	5 (5%)	25	50
41	BQ	87/87 (100%)	84 (97%)	3 (3%)	37	60
42	BR	99/99 (100%)	94 (95%)	5 (5%)	24	48
43	BS	89/89 (100%)	88 (99%)	1 (1%)	73	84
44	BT	84/84 (100%)	79 (94%)	5 (6%)	19	44
45	BU	93/93 (100%)	90 (97%)	3 (3%)	39	61
46	BV	84/84 (100%)	77 (92%)	7 (8%)	11	34
47	BW	84/84 (100%)	79 (94%)	5 (6%)	19	44
48	BX	78/78 (100%)	73 (94%)	5 (6%)	17	42
49	BY	62/62 (100%)	57 (92%)	5 (8%)	11	35
50	BZ	67/67 (100%)	66 (98%)	1 (2%)	65	80
51	B0	55/55 (100%)	50 (91%)	5 (9%)	9	29
52	B1	48/48 (100%)	43 (90%)	5 (10%)	7	24
53	B2	62/62 (100%)	55 (89%)	7 (11%)	6	21
54	B3	47/47 (100%)	44 (94%)	3 (6%)	17	42
55	B4	48/48 (100%)	47 (98%)	1 (2%)	53	72
56	B5	38/38 (100%)	35 (92%)	3 (8%)	12	35
57	B6	51/51 (100%)	46 (90%)	5 (10%)	8	26
58	B7	34/34 (100%)	32 (94%)	2 (6%)	19	45
All	All	5213/5213 (100%)	4934 (95%)	279 (5%)	26	47

5 of 279 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	BV	87	LEU
48	BX	10	LYS
53	B2	31	ASP
22	AV	13	HIS
21	AU	65	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1538/1542 (99%)	300 (19%)	101 (6%)
2	AB	74/76 (97%)	24 (32%)	7 (9%)
25	BA	119/120 (99%)	17 (14%)	10 (8%)
26	BB	2898/2904 (99%)	525 (18%)	177 (6%)
3	AC	46/47 (97%)	23 (50%)	12 (26%)
4	AD	76/77 (98%)	10 (13%)	5 (6%)
All	All	4751/4766 (99%)	899 (18%)	312 (6%)

5 of 899 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	3	A
1	AA	4	U
1	AA	5	U
1	AA	6	G
1	AA	7	A

5 of 312 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BB	1567	G
26	BB	2434	A
26	BB	1697	G
26	BB	2068	U
26	BB	2756	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

49 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	2MG	AA	1207	1	18,26,27	2.11	6 (33%)	16,38,41	1.71	4 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	PSU	BB	1911	26	18,21,22	1.92	4 (22%)	22,30,33	1.24	3 (13%)
26	OMG	BB	2251	26	18,26,27	1.77	5 (27%)	19,38,41	1.50	6 (31%)
26	2MG	BB	1835	26	18,26,27	1.98	7 (38%)	16,38,41	0.93	0
2	4SU	AB	8	2	18,21,22	1.67	3 (16%)	26,30,33	1.57	5 (19%)
1	7MG	AA	527	1	22,26,27	6.42	5 (22%)	29,39,42	1.86	5 (17%)
1	MA6	AA	1518	1	19,26,27	1.80	4 (21%)	18,38,41	2.43	4 (22%)
26	PSU	BB	2580	26	18,21,22	1.45	3 (16%)	22,30,33	1.40	3 (13%)
2	H2U	AB	16	2	18,21,22	1.57	5 (27%)	21,30,33	1.22	3 (14%)
26	H2U	BB	2449	26	18,21,22	1.32	1 (5%)	21,30,33	1.51	3 (14%)
2	MIA	AB	37	2	24,31,32	2.06	8 (33%)	26,44,47	2.93	7 (26%)
26	CH	BB	2575	26	16,21,22	1.54	3 (18%)	20,30,33	1.56	4 (20%)
26	5MC	BB	1962	26	18,22,23	1.57	3 (16%)	26,32,35	1.99	6 (23%)
1	2MG	AA	966	1	18,26,27	1.66	6 (33%)	16,38,41	2.07	4 (25%)
2	5MU	AB	54	2	19,22,23	1.70	5 (26%)	28,32,35	1.84	7 (25%)
4	OMC	AD	33	4	19,22,23	1.09	1 (5%)	26,31,34	1.81	9 (34%)
26	PSU	BB	955	26	18,21,22	1.36	2 (11%)	22,30,33	1.92	6 (27%)
1	4OC	AA	1402	1	20,23,24	1.58	6 (30%)	26,32,35	1.86	10 (38%)
26	PSU	BB	746	26	18,21,22	1.79	5 (27%)	22,30,33	1.57	5 (22%)
26	OMC	BB	2498	26	19,22,23	1.28	3 (15%)	26,31,34	1.09	2 (7%)
26	1MG	BB	745	26	18,26,27	1.82	5 (27%)	19,39,42	2.43	4 (21%)
26	PSU	BB	2504	26	18,21,22	2.01	6 (33%)	22,30,33	2.02	7 (31%)
26	7MG	BB	2069	26	22,26,27	4.18	3 (13%)	29,39,42	1.70	5 (17%)
1	2MG	AA	1516	1	18,26,27	1.26	1 (5%)	16,38,41	1.69	3 (18%)
26	PSU	BB	1917	26	18,21,22	2.06	8 (44%)	22,30,33	2.52	8 (36%)
1	PSU	AA	516	1	18,21,22	1.97	5 (27%)	22,30,33	1.33	3 (13%)
26	3TD	BB	1915	26	18,22,23	1.52	3 (16%)	22,32,35	1.86	5 (22%)
1	5MC	AA	1407	1	18,22,23	1.35	2 (11%)	26,32,35	2.11	9 (34%)
2	H2U	AB	17	2	18,21,22	1.36	1 (5%)	21,30,33	1.90	4 (19%)
4	H2U	AD	21	4	18,21,22	1.75	4 (22%)	21,30,33	1.90	5 (23%)
26	PSU	BB	2605	26	18,21,22	1.57	4 (22%)	22,30,33	1.30	2 (9%)
1	UR3	AA	1498	1	19,22,23	1.04	1 (5%)	26,32,35	1.39	4 (15%)
26	OMU	BB	2552	26	19,22,23	1.22	1 (5%)	26,31,34	2.06	11 (42%)
4	4SU	AD	8	4	18,21,22	1.95	3 (16%)	26,30,33	2.36	9 (34%)
26	2MA	BB	2503	26	17,25,26	1.42	5 (29%)	17,37,40	1.61	5 (29%)
26	6MZ	BB	2030	26	18,25,26	1.75	5 (27%)	16,36,39	2.35	5 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	AA	967	1	18,22,23	1.40	3 (16%)	26,32,35	1.84	9 (34%)
2	OMC	AB	32	2	19,22,23	1.32	3 (15%)	26,31,34	1.90	6 (23%)
26	2MG	BB	2445	26	18,26,27	1.23	3 (16%)	16,38,41	1.48	2 (12%)
26	5MU	BB	1939	26	19,22,23	1.72	3 (15%)	28,32,35	1.80	4 (14%)
26	6MZ	BB	1618	26	18,25,26	2.11	6 (33%)	16,36,39	1.56	3 (18%)
26	5MU	BB	747	26	19,22,23	1.93	7 (36%)	28,32,35	1.95	6 (21%)
4	PSU	AD	56	4	18,21,22	1.90	3 (16%)	22,30,33	2.16	6 (27%)
2	PSU	AB	55	2	18,21,22	1.31	1 (5%)	22,30,33	1.75	7 (31%)
26	PSU	BB	2457	26	18,21,22	1.56	4 (22%)	22,30,33	2.10	7 (31%)
4	5MU	AD	55	4	19,22,23	1.67	5 (26%)	28,32,35	1.45	4 (14%)
1	MA6	AA	1519	1	19,26,27	2.13	8 (42%)	18,38,41	1.62	3 (16%)
2	H2U	AB	20	2	18,21,22	1.27	2 (11%)	21,30,33	1.31	2 (9%)
2	7MG	AB	46	2	22,26,27	5.65	7 (31%)	29,39,42	1.80	2 (6%)

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	2MG	AA	1207	1	-	0/5/27/28	0/3/3/3
26	PSU	BB	1911	26	-	2/7/25/26	0/2/2/2
26	OMG	BB	2251	26	-	0/5/27/28	0/3/3/3
26	2MG	BB	1835	26	-	1/5/27/28	0/3/3/3
2	4SU	AB	8	2	-	6/7/25/26	0/2/2/2
1	7MG	AA	527	1	-	1/7/37/38	0/3/3/3
1	MA6	AA	1518	1	-	0/7/29/30	0/3/3/3
26	PSU	BB	2580	26	-	1/7/25/26	0/2/2/2
2	H2U	AB	16	2	-	0/7/38/39	0/2/2/2
26	H2U	BB	2449	26	-	0/7/38/39	0/2/2/2
2	MIA	AB	37	2	-	1/11/33/34	0/3/3/3
26	CH	BB	2575	26	-	0/5/25/26	0/2/2/2
26	5MC	BB	1962	26	-	2/7/25/26	0/2/2/2
1	2MG	AA	966	1	-	1/5/27/28	0/3/3/3
2	5MU	AB	54	2	-	0/7/25/26	0/2/2/2
4	OMC	AD	33	4	-	0/9/27/28	0/2/2/2
26	PSU	BB	955	26	-	0/7/25/26	0/2/2/2
1	4OC	AA	1402	1	-	0/9/29/30	0/2/2/2
26	PSU	BB	746	26	-	4/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	OMC	BB	2498	26	-	0/9/27/28	0/2/2/2
26	1MG	BB	745	26	-	0/3/25/26	0/3/3/3
26	PSU	BB	2504	26	-	0/7/25/26	0/2/2/2
26	7MG	BB	2069	26	-	0/7/37/38	0/3/3/3
1	2MG	AA	1516	1	-	0/5/27/28	0/3/3/3
26	PSU	BB	1917	26	-	2/7/25/26	0/2/2/2
1	PSU	AA	516	1	-	0/7/25/26	0/2/2/2
26	3TD	BB	1915	26	-	1/7/25/26	0/2/2/2
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
2	H2U	AB	17	2	-	0/7/38/39	0/2/2/2
4	H2U	AD	21	4	-	3/7/38/39	0/2/2/2
26	PSU	BB	2605	26	-	1/7/25/26	0/2/2/2
1	UR3	AA	1498	1	-	0/7/25/26	0/2/2/2
26	OMU	BB	2552	26	-	1/9/27/28	0/2/2/2
4	4SU	AD	8	4	-	0/7/25/26	0/2/2/2
26	2MA	BB	2503	26	-	0/3/25/26	0/3/3/3
26	6MZ	BB	2030	26	-	0/5/27/28	0/3/3/3
1	5MC	AA	967	1	-	3/7/25/26	0/2/2/2
2	OMC	AB	32	2	-	2/9/27/28	0/2/2/2
26	2MG	BB	2445	26	-	0/5/27/28	0/3/3/3
26	5MU	BB	1939	26	-	0/7/25/26	0/2/2/2
26	6MZ	BB	1618	26	-	0/5/27/28	0/3/3/3
26	5MU	BB	747	26	-	0/7/25/26	0/2/2/2
4	PSU	AD	56	4	-	1/7/25/26	0/2/2/2
2	PSU	AB	55	2	-	4/7/25/26	0/2/2/2
26	PSU	BB	2457	26	-	0/7/25/26	0/2/2/2
4	5MU	AD	55	4	-	0/7/25/26	0/2/2/2
1	MA6	AA	1519	1	-	0/7/29/30	0/3/3/3
2	H2U	AB	20	2	-	0/7/38/39	0/2/2/2
2	7MG	AB	46	2	-	2/7/37/38	0/3/3/3

The worst 5 of 197 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	527	7MG	C8-N9	-29.36	1.29	1.46
2	AB	46	7MG	C8-N9	-25.16	1.31	1.46
26	BB	2069	7MG	C8-N9	-18.65	1.35	1.46
4	AD	8	4SU	C5-C4	-6.73	1.33	1.42
2	AB	37	MIA	C2-S10	5.60	1.80	1.75

The worst 5 of 246 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	37	MIA	C11-S10-C2	11.77	111.06	102.27
26	BB	745	1MG	C2-N1-C6	8.17	127.59	120.95
1	AA	1518	MA6	N1-C6-N6	7.81	125.28	117.06
2	AB	46	7MG	N9-C8-N7	7.64	114.30	103.38
1	AA	527	7MG	N9-C8-N7	7.06	113.48	103.38

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AB	8	4SU	C2'-C1'-N1-C6
2	AB	32	OMC	O4'-C1'-N1-C2
2	AB	32	OMC	O4'-C1'-N1-C6
2	AB	37	MIA	C12-C13-C14-C16
2	AB	55	PSU	C2'-C1'-C5-C4

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands 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	$\# Z > 2$
60	FME	BB	3001	59	8,9,10	1.03	0	7,9,11	2.50	3 (42%)
59	TRP	AB	101	2,60	14,15,16	1.66	3 (21%)	13,20,22	1.34	3 (23%)

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
60	FME	BB	3001	59	-	2/7/9/11	-
59	TRP	AB	101	2,60	-	0/5/6/8	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AB	101	TRP	OXT-C	-4.73	1.22	1.42
59	AB	101	TRP	CE3-CD2	-2.20	1.37	1.42
59	AB	101	TRP	CH2-CZ2	2.20	1.41	1.36

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	BB	3001	FME	CA-N-CN	4.83	130.26	122.82
59	AB	101	TRP	CZ3-CH2-CZ2	-2.37	117.12	120.44
60	BB	3001	FME	O1-CN-N	-2.35	119.08	125.27
59	AB	101	TRP	OXT-C-CA	2.22	120.29	111.52
60	BB	3001	FME	CG-CB-CA	-2.18	106.89	112.95

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	BB	3001	FME	O1-CN-N-CA
60	BB	3001	FME	N-CA-CB-CG

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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	1457:G	O3'	1458:G	P	1.77

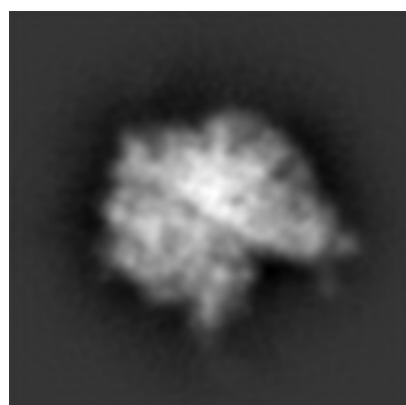
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5362. These allow visual inspection of the internal detail of the map and identification of artifacts.

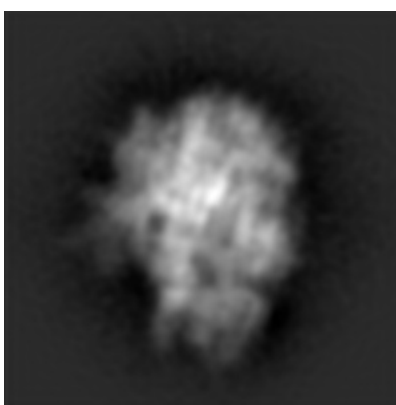
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

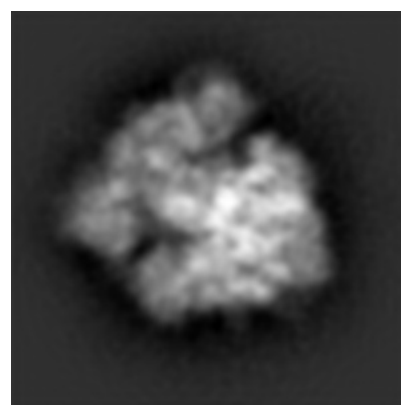
6.1.1 Primary map



X



Y

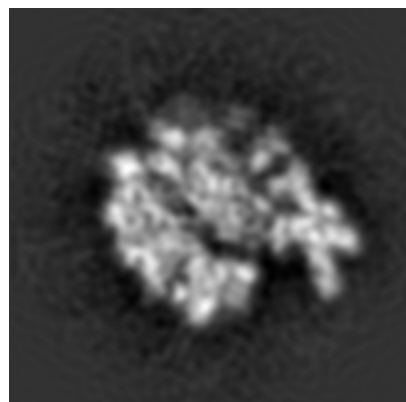


Z

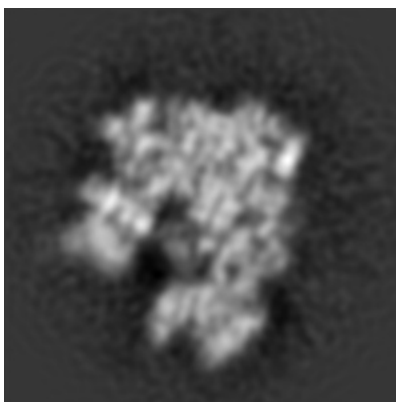
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

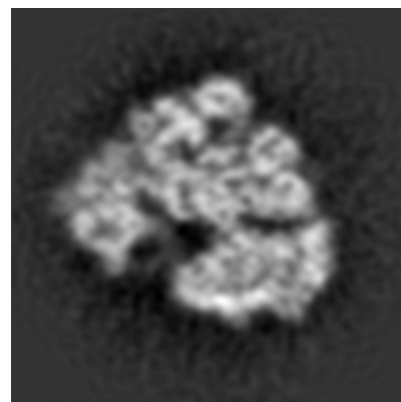
6.2.1 Primary map



X Index: 125



Y Index: 125

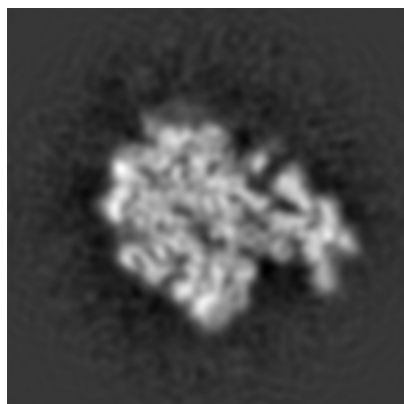


Z Index: 125

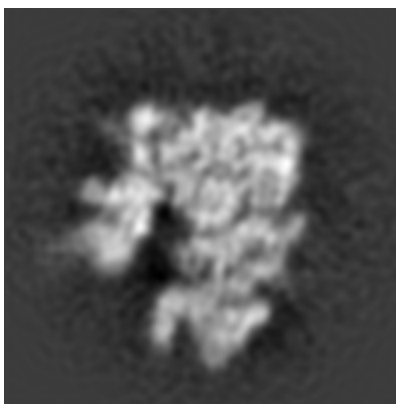
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

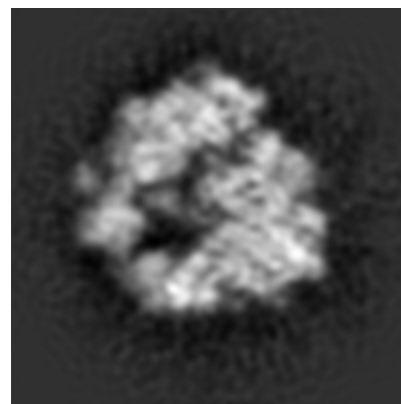
6.3.1 Primary map



X Index: 130



Y Index: 130

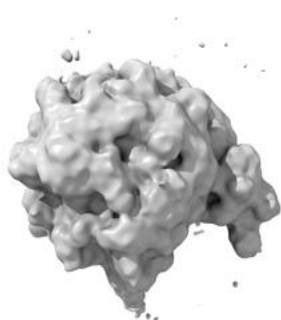


Z Index: 114

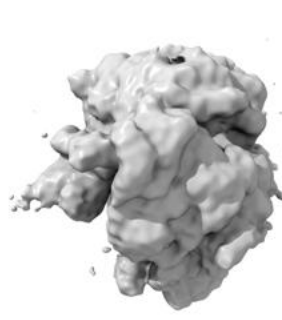
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

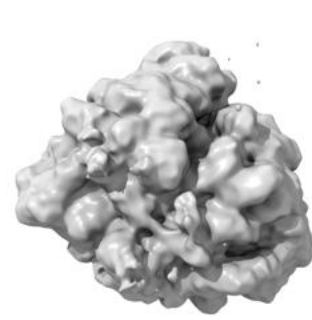
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

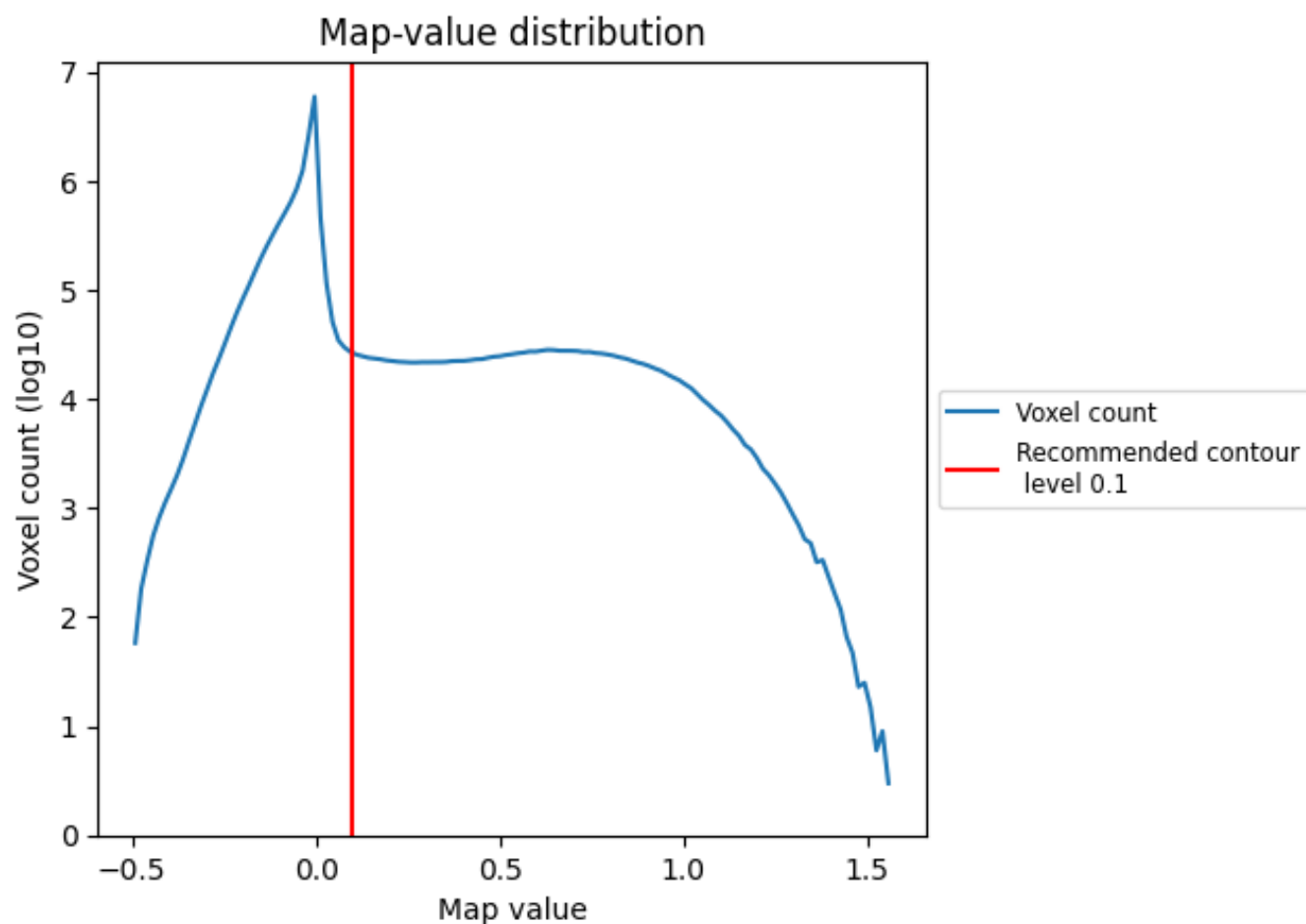
6.5 Mask visualisation

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

7 Map analysis [i](#)

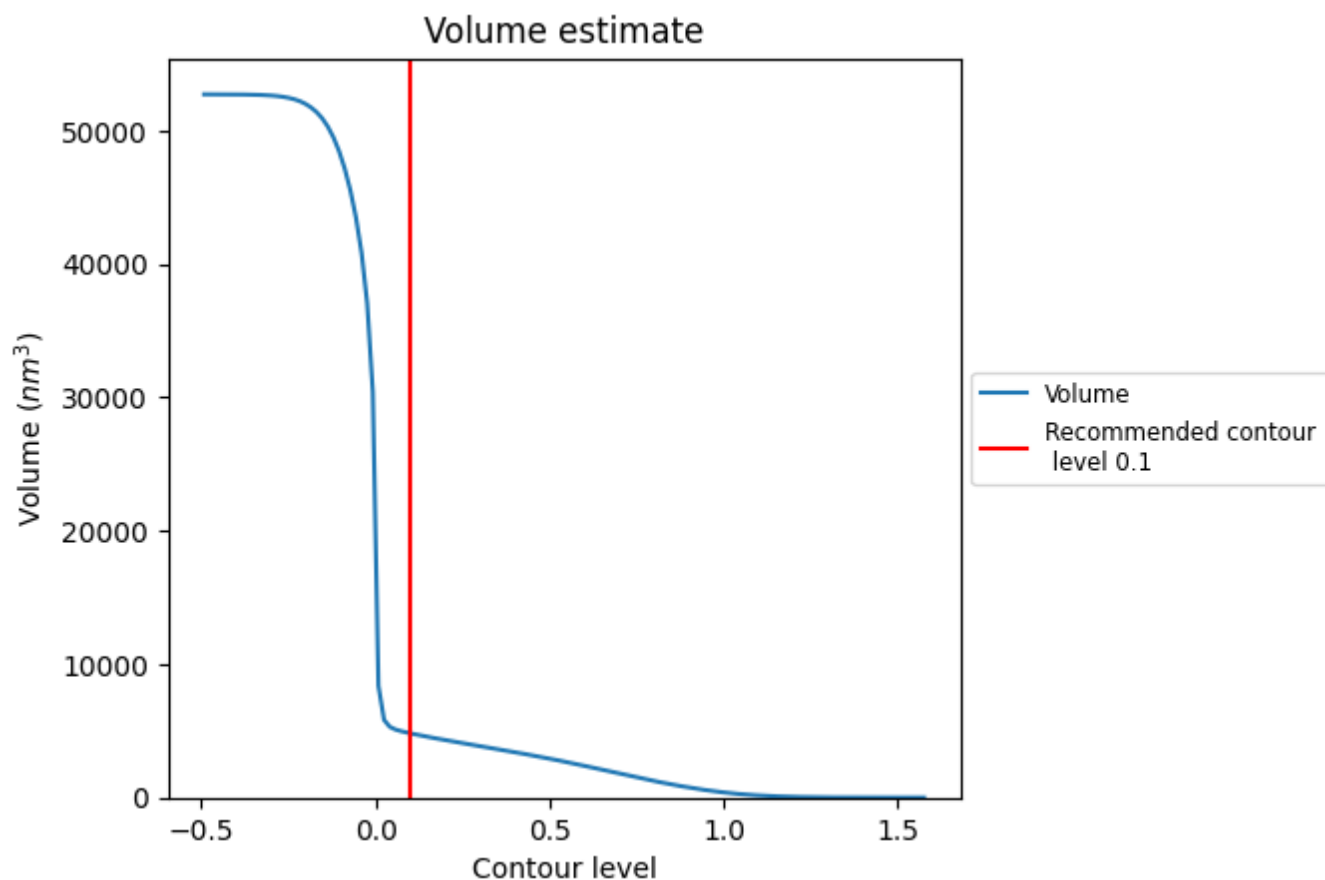
This section contains the results of statistical analysis of the map.

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.

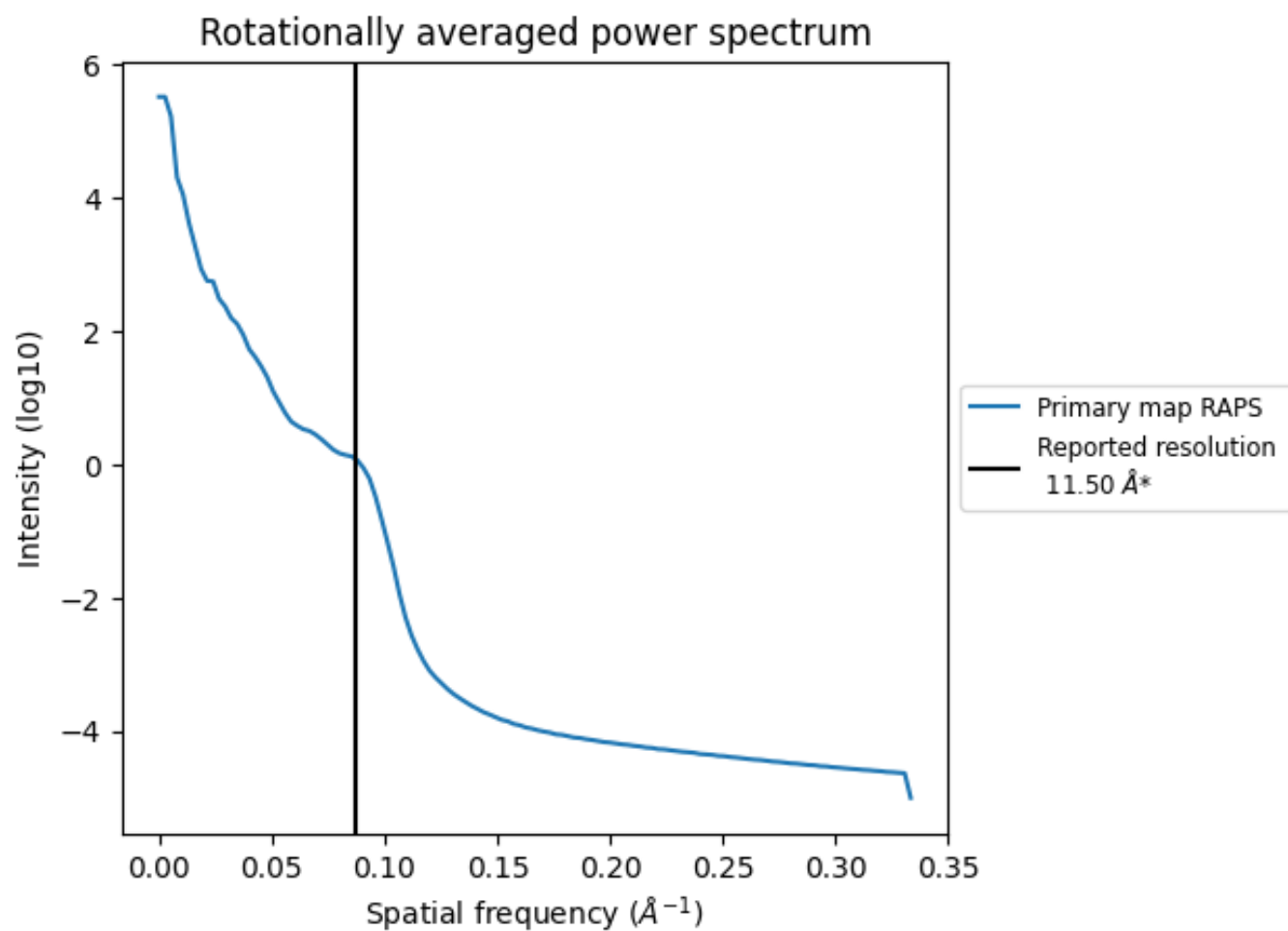
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4817 nm^3 ; this corresponds to an approximate mass of 4352 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 0.087 Å⁻¹

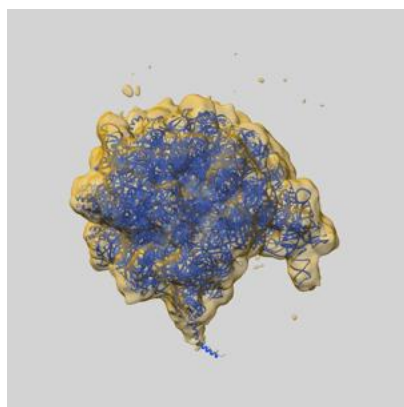
8 Fourier-Shell correlation

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

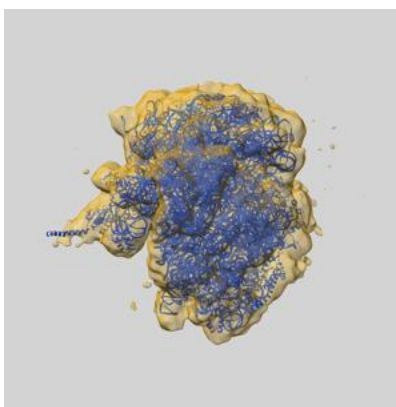
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5362 and PDB model 4V6R. Per-residue inclusion information can be found in section [3](#) on page [15](#).

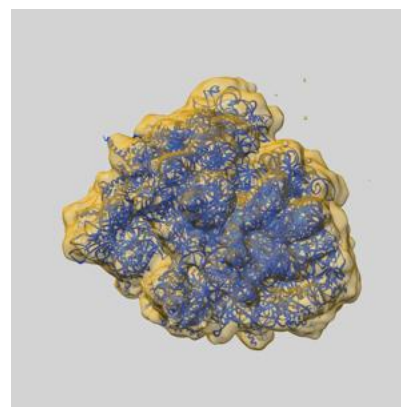
9.1 Map-model overlay [i](#)



X



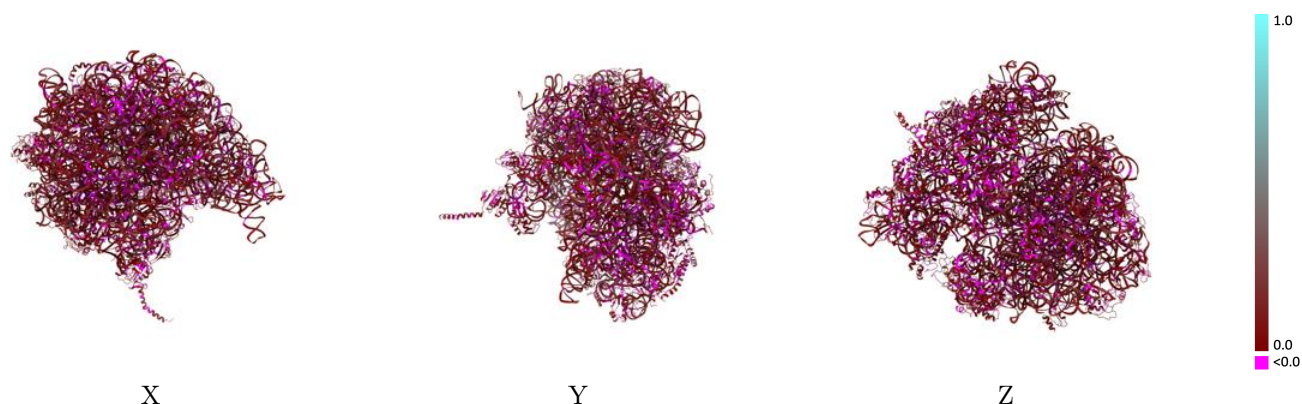
Y



Z

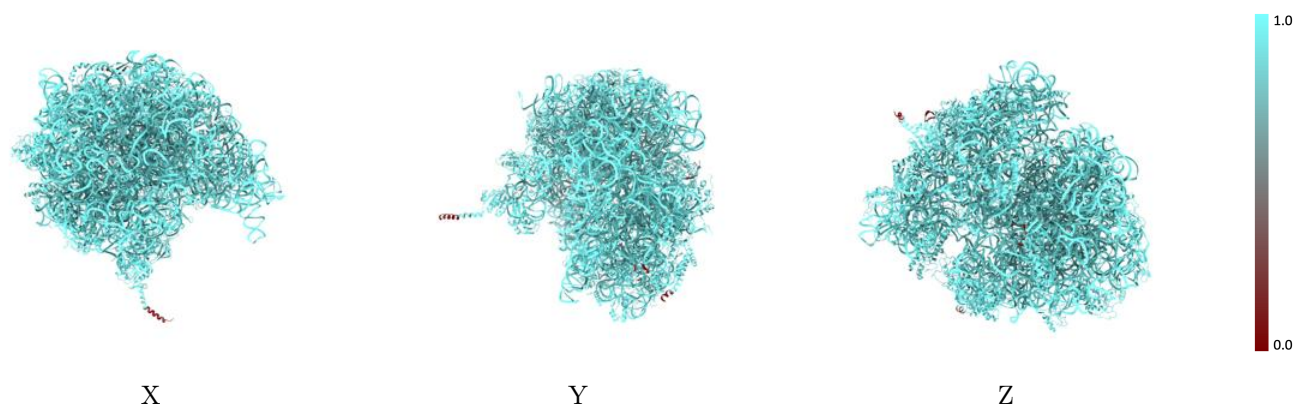
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



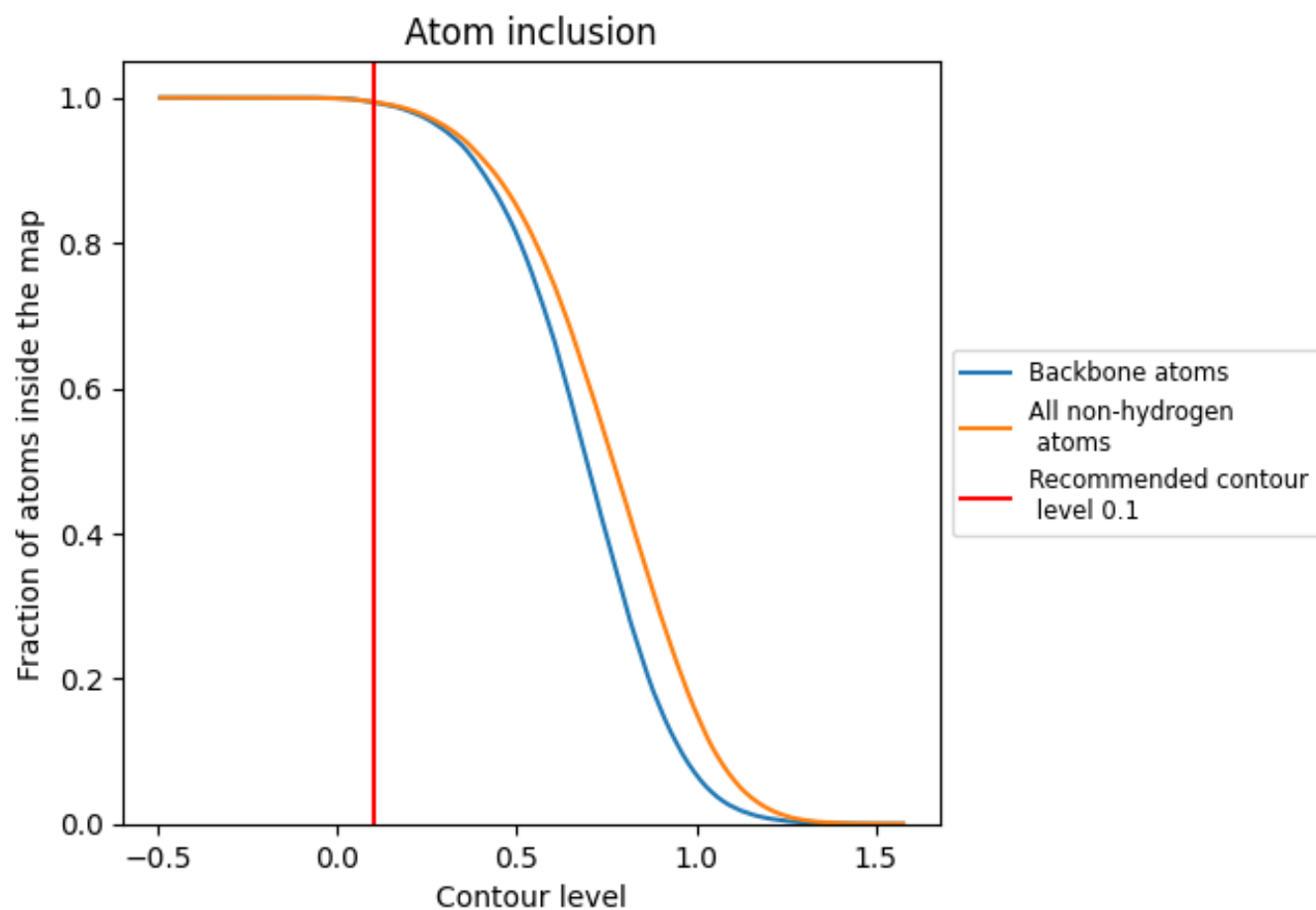
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9943	0.0730
AA	0.9994	0.0890
AB	0.9640	0.0680
AC	0.8953	0.0140
AD	0.9890	0.0900
AE	0.9457	0.0440
AF	0.9977	0.0620
AG	1.0000	0.0410
AH	0.9792	0.0420
AI	0.9767	0.0440
AJ	0.9926	0.0580
AK	0.9958	0.0360
AL	0.9839	0.0480
AM	1.0000	0.0190
AN	0.9957	0.0410
AO	0.9848	0.0310
AP	0.9852	0.0460
AQ	0.9961	0.0380
AR	1.0000	0.0560
AS	1.0000	0.0230
AT	1.0000	0.0420
AU	1.0000	0.0380
AV	0.9606	0.0280
AW	1.0000	0.0430
AX	1.0000	0.0360
B0	1.0000	0.0200
B1	0.9977	0.0540
B2	0.9665	0.0250
B3	1.0000	0.0320
B4	1.0000	0.0530
B5	1.0000	-0.0070
B6	1.0000	-0.0070
B7	1.0000	0.0400
BA	1.0000	0.0990
BB	0.9996	0.0910



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Chain	Atom inclusion	Q-score
BC	 0.9690	 0.0360
BD	 1.0000	 0.0220
BE	 0.9974	 0.0200
BF	 0.9987	 0.0620
BG	 0.9949	 0.0600
BH	 0.9946	 0.0250
BI	 0.9097	 0.0260
BJ	 0.8814	 0.0570
BK	 0.9746	 0.0420
BL	 1.0000	 0.0300
BM	 0.9913	 0.0580
BN	 1.0000	 0.0250
BO	 1.0000	 0.0420
BP	 1.0000	 0.0240
BQ	 0.9931	 0.0530
BR	 0.9899	 0.0190
BS	 0.9945	 0.0210
BT	 1.0000	 0.0630
BU	 0.9988	 0.0110
BV	 0.9961	 0.0250
BW	 0.9987	 0.0530
BX	 0.9986	 0.0620
BY	 0.9951	 0.0290
BZ	 1.0000	 0.0290