Full wwPDB EM Validation Report ⓘ

Jul 9, 2023 – 11:48 am BST

PDB ID	:	8BPO
EMDB ID	:	EMD-16155
Title	:	Structure of rabbit 80S ribosome translating beta-tubulin in complex with tetratricopeptide protein 5 (TTC5) and S-phase Cyclin A Associated Protein residing in the ER (SCAPER)
Authors	:	Hopfler, M.; Absmeier, E.; Passmore, L.A.; Hegde, R.S.
Deposited on	:	2022-11-17
Resolution	:	2.80 Å(reported)

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

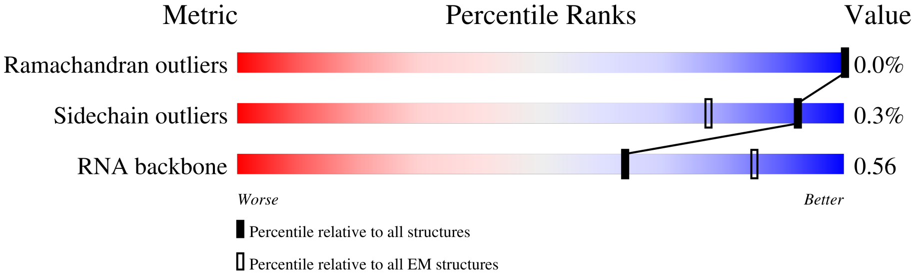
EMDB validation analysis	:	0.0.1.dev50
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

1 Overall quality at a glance ⓘ

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

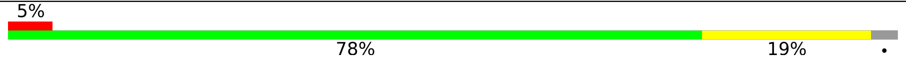
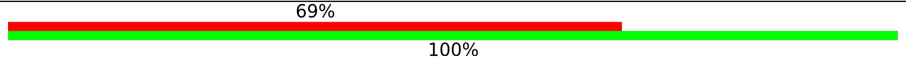
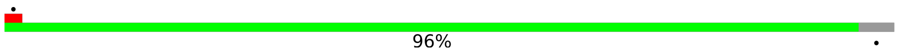
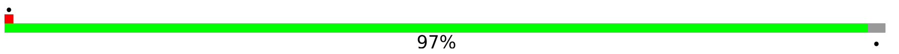
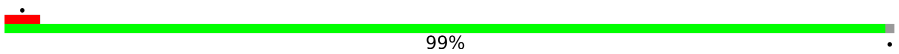
The reported resolution of this entry is 2.80 Å.

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 <=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	A1	4380	
2	B1	120	
3	C1	156	
4	D1	29	
5	A2	257	
6	B2	403	
7	C2	425	
8	D2	297	

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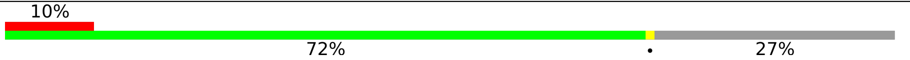
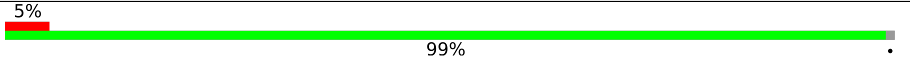
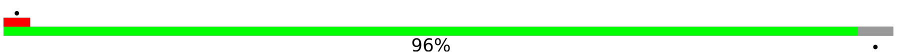
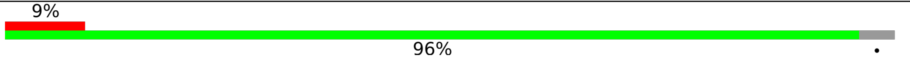
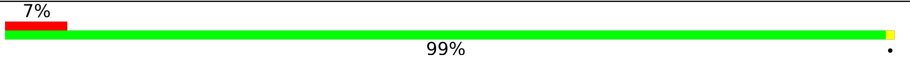
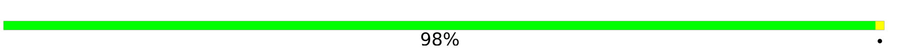
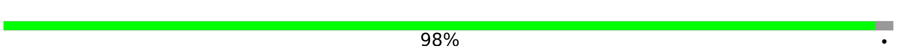
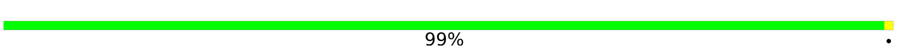
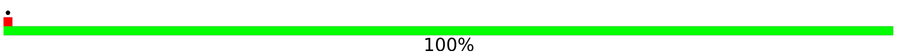
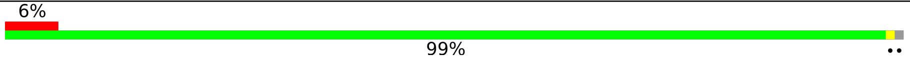
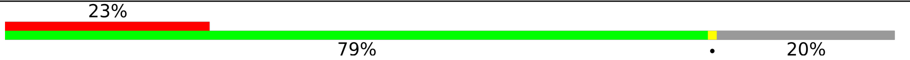
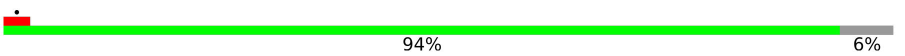
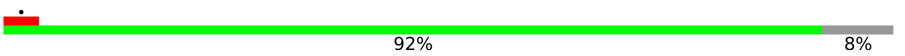
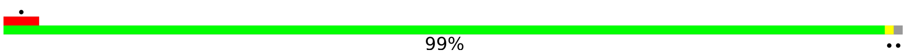
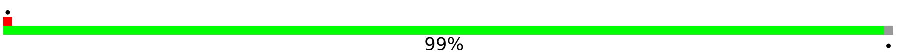
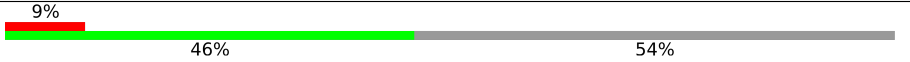
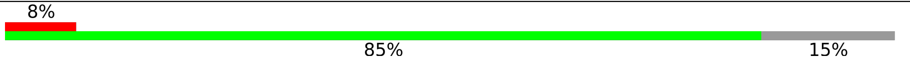
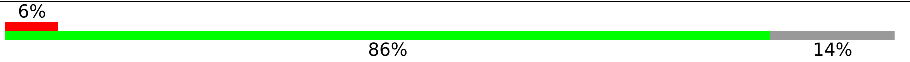
Mol	Chain	Length	Quality of chain
9	E2	291	
10	F2	247	
11	G2	319	
12	H2	192	
13	I2	214	
14	J2	178	
15	K2	211	
16	L2	218	
17	M2	204	
18	N2	203	
19	O2	184	
20	P2	187	
21	Q2	196	
22	R2	176	
23	S2	160	
24	T2	128	
25	U2	140	
26	V2	157	
27	W2	156	
28	X2	145	
29	Y2	136	
30	Z2	148	
31	a2	226	
32	b2	115	
33	c2	125	

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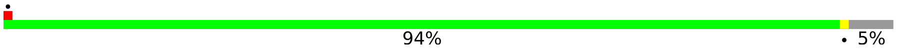
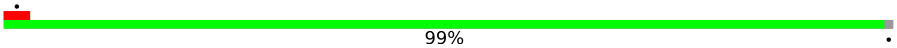
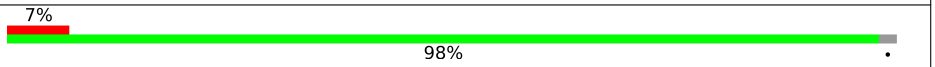
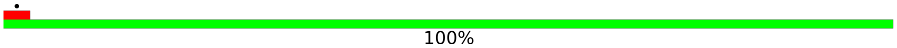
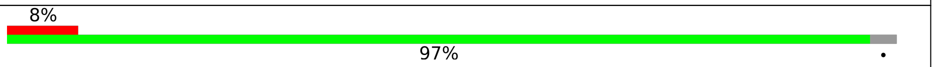
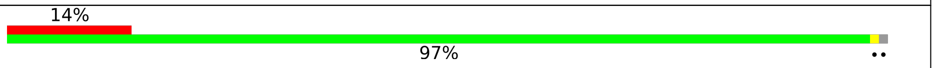
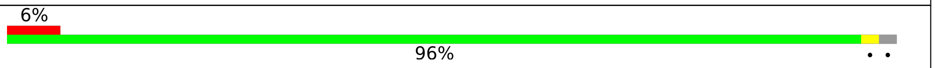
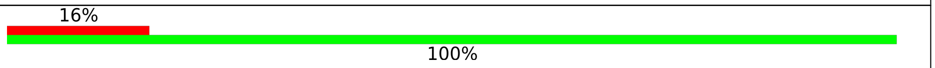
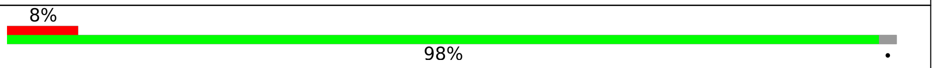
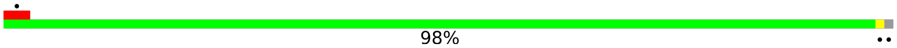
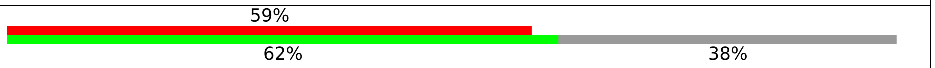
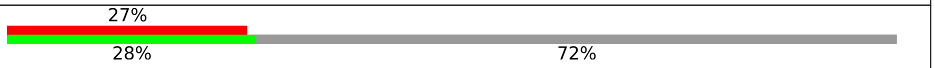
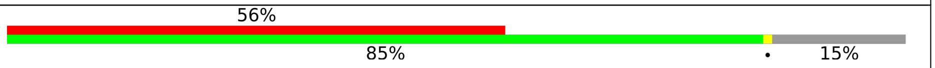
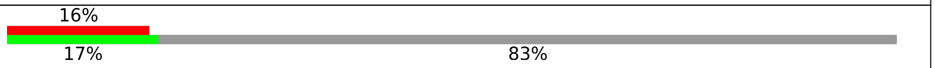
Mol	Chain	Length	Quality of chain
34	d2	135	
35	e2	110	
36	f2	116	
37	g2	122	
38	h2	105	
39	i2	97	
40	j2	70	
41	k2	51	
42	l2	102	
43	m2	25	
44	n2	106	
45	o2	92	
46	p2	137	
47	q2	318	
48	r2	165	
49	s2	1411	
50	t2	489	
51	u2	64	

2 Entry composition ⓘ

There are 53 unique types of molecules in this entry. The entry contains 143326 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A1	3543	75972	33833	13910	24686	3543	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B1	120	2558	1141	456	842	119	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C1	151	3208	1432	564	1062	150	0	0

- Molecule 4 is a protein called Nascent polypeptide-associated complex subunit alpha N-terminal region.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D1	29	150	92	29	29	0	0

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A2	248	1898	1189	389	314	6	0	0

- Molecule 6 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	B2	394	3172	2020	597	542	13	0	0

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C2	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 8 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D2	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E2	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F2	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 11 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G2	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G2	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H2	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 13 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I2	205	Total 1664	C 1056	N 321	O 274	S 13	0	0

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J2	170	Total 1362	C 861	N 254	O 241	S 6	0	0

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K2	210	Total 1702	C 1065	N 354	O 279	S 4	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K2	74	ARG	HIS	conflict	UNP G1TKB3
K2	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L2	138	Total 1137	C 727	N 221	O 182	S 7	0	0

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M2	203	Total 1701	C 1072	N 359	O 266	S 4	0	0

- Molecule 18 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N2	199	Total 1630	C 1051	N 319	O 255	S 5	0	0

- Molecule 19 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	O2	153	1242	777	241	215	9	0	0

- Molecule 20 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	P2	187	1514	946	315	249	4	0	0

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	Q2	155	1294	808	278	199	9	0	0

- Molecule 22 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	R2	176	1462	930	285	236	11	0	0

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	S2	159	1298	823	252	217	6	0	0

- Molecule 24 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	T2	102	834	534	146	152	2	0	0

- Molecule 25 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	U2	131	979	618	184	172	5	0	0

- Molecule 26 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	V2	63	528	337	103	85	3	0	0

- Molecule 27 is a protein called Ribosomal_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	W2	118	967	618	181	167	1	0	0

- Molecule 28 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	X2	134	1115	700	226	186	3	0	0

- Molecule 29 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	Y2	135	1107	714	208	182	3	0	0

- Molecule 30 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Z2	147	1162	734	239	185	4	0	0

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	a2	104	848	527	189	129	3	0	0

- Molecule 32 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	b2	98	761	481	134	140	6	0	0

- Molecule 33 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c2	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 34 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d2	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 35 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e2	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 36 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f2	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 37 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g2	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h2	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 39 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i2	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 40 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	j2	69	569	366	103	99	1	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j2	24	LYS	ASN	conflict	UNP G1U001

- Molecule 41 is a protein called 60S ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	k2	50	447	286	96	64	1	0	0

- Molecule 42 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	l2	52	429	266	90	67	6	0	0

- Molecule 43 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	m2	25	239	145	64	27	3	0	0

- Molecule 44 is a protein called 60S ribosomal protein L36a-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	n2	104	851	533	174	138	6	0	0

- Molecule 45 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	o2	91	708	445	136	120	7	0	0

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	p2	124	994	616	205	167	6	0	0

- Molecule 47 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	q2	196	1507	959	263	276	9	0	0

- Molecule 48 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	r2	153	1160	722	218	217	3	0	0

- Molecule 49 is a protein called S phase cyclin A-associated protein in the endoplasmic reticulum.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	s2	395	3050	1943	525	557	25	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s2	-10	MET	-	initiating methionine	UNP Q9BY12
s2	-9	ASP	-	expression tag	UNP Q9BY12
s2	-8	TYR	-	expression tag	UNP Q9BY12
s2	-7	LYS	-	expression tag	UNP Q9BY12
s2	-6	ASP	-	expression tag	UNP Q9BY12
s2	-5	ASP	-	expression tag	UNP Q9BY12
s2	-4	ASP	-	expression tag	UNP Q9BY12
s2	-3	ASP	-	expression tag	UNP Q9BY12
s2	-2	LYS	-	expression tag	UNP Q9BY12
s2	-1	GLY	-	expression tag	UNP Q9BY12
s2	0	SER	-	expression tag	UNP Q9BY12

- Molecule 50 is a protein called Tetratricopeptide repeat protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	t2	418	3262	2050	573	626	13	0	0

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t2	-48	MET	-	initiating methionine	UNP Q8N0Z6
t2	-47	GLY	-	expression tag	UNP Q8N0Z6
t2	-46	HIS	-	expression tag	UNP Q8N0Z6
t2	-45	HIS	-	expression tag	UNP Q8N0Z6
t2	-44	HIS	-	expression tag	UNP Q8N0Z6
t2	-43	HIS	-	expression tag	UNP Q8N0Z6
t2	-42	HIS	-	expression tag	UNP Q8N0Z6
t2	-41	HIS	-	expression tag	UNP Q8N0Z6
t2	-40	GLU	-	expression tag	UNP Q8N0Z6
t2	-39	ASN	-	expression tag	UNP Q8N0Z6
t2	-38	LEU	-	expression tag	UNP Q8N0Z6
t2	-37	TYR	-	expression tag	UNP Q8N0Z6
t2	-36	PHE	-	expression tag	UNP Q8N0Z6
t2	-35	GLN	-	expression tag	UNP Q8N0Z6
t2	-34	GLY	-	expression tag	UNP Q8N0Z6
t2	-33	SER	-	expression tag	UNP Q8N0Z6
t2	-32	ALA	-	expression tag	UNP Q8N0Z6
t2	-31	TRP	-	expression tag	UNP Q8N0Z6
t2	-30	SER	-	expression tag	UNP Q8N0Z6
t2	-29	HIS	-	expression tag	UNP Q8N0Z6
t2	-28	PRO	-	expression tag	UNP Q8N0Z6
t2	-27	GLN	-	expression tag	UNP Q8N0Z6
t2	-26	PHE	-	expression tag	UNP Q8N0Z6
t2	-25	GLU	-	expression tag	UNP Q8N0Z6
t2	-24	LYS	-	expression tag	UNP Q8N0Z6
t2	-23	GLY	-	expression tag	UNP Q8N0Z6
t2	-22	GLY	-	expression tag	UNP Q8N0Z6
t2	-21	GLY	-	expression tag	UNP Q8N0Z6
t2	-20	SER	-	expression tag	UNP Q8N0Z6
t2	-19	GLY	-	expression tag	UNP Q8N0Z6
t2	-18	GLY	-	expression tag	UNP Q8N0Z6
t2	-17	GLY	-	expression tag	UNP Q8N0Z6
t2	-16	SER	-	expression tag	UNP Q8N0Z6
t2	-15	GLY	-	expression tag	UNP Q8N0Z6
t2	-14	GLY	-	expression tag	UNP Q8N0Z6
t2	-13	SER	-	expression tag	UNP Q8N0Z6
t2	-12	ALA	-	expression tag	UNP Q8N0Z6
t2	-11	TRP	-	expression tag	UNP Q8N0Z6
t2	-10	SER	-	expression tag	UNP Q8N0Z6
t2	-9	HIS	-	expression tag	UNP Q8N0Z6
t2	-8	PRO	-	expression tag	UNP Q8N0Z6
t2	-7	GLN	-	expression tag	UNP Q8N0Z6

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Chain	Residue	Modelled	Actual	Comment	Reference
t2	-6	PHE	-	expression tag	UNP Q8N0Z6
t2	-5	GLU	-	expression tag	UNP Q8N0Z6
t2	-4	LYS	-	expression tag	UNP Q8N0Z6
t2	-3	GLY	-	expression tag	UNP Q8N0Z6
t2	-2	SER	-	expression tag	UNP Q8N0Z6
t2	-1	SER	-	expression tag	UNP Q8N0Z6
t2	0	GLY	-	expression tag	UNP Q8N0Z6

- Molecule 51 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u2	11	Total 82	C 50	N 18	O 13	S 1	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u2	61	MET	-	expression tag	UNP P07437
u2	62	LYS	-	expression tag	UNP P07437
u2	63	LEU	-	expression tag	UNP P07437
u2	64	VAL	-	expression tag	UNP P07437

- Molecule 52 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	A1	194	Total 194	Mg 194	0
52	B1	7	Total 7	Mg 7	0
52	C1	6	Total 6	Mg 6	0
52	B2	1	Total 1	Mg 1	0
52	I2	1	Total 1	Mg 1	0
52	O2	2	Total 2	Mg 2	0
52	U2	1	Total 1	Mg 1	0
52	Z2	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms	AltConf
52	f2	1	Total Mg 1 1	0

- Molecule 53 is ZINC ION (three-letter code: ZN) (formula: Zn).

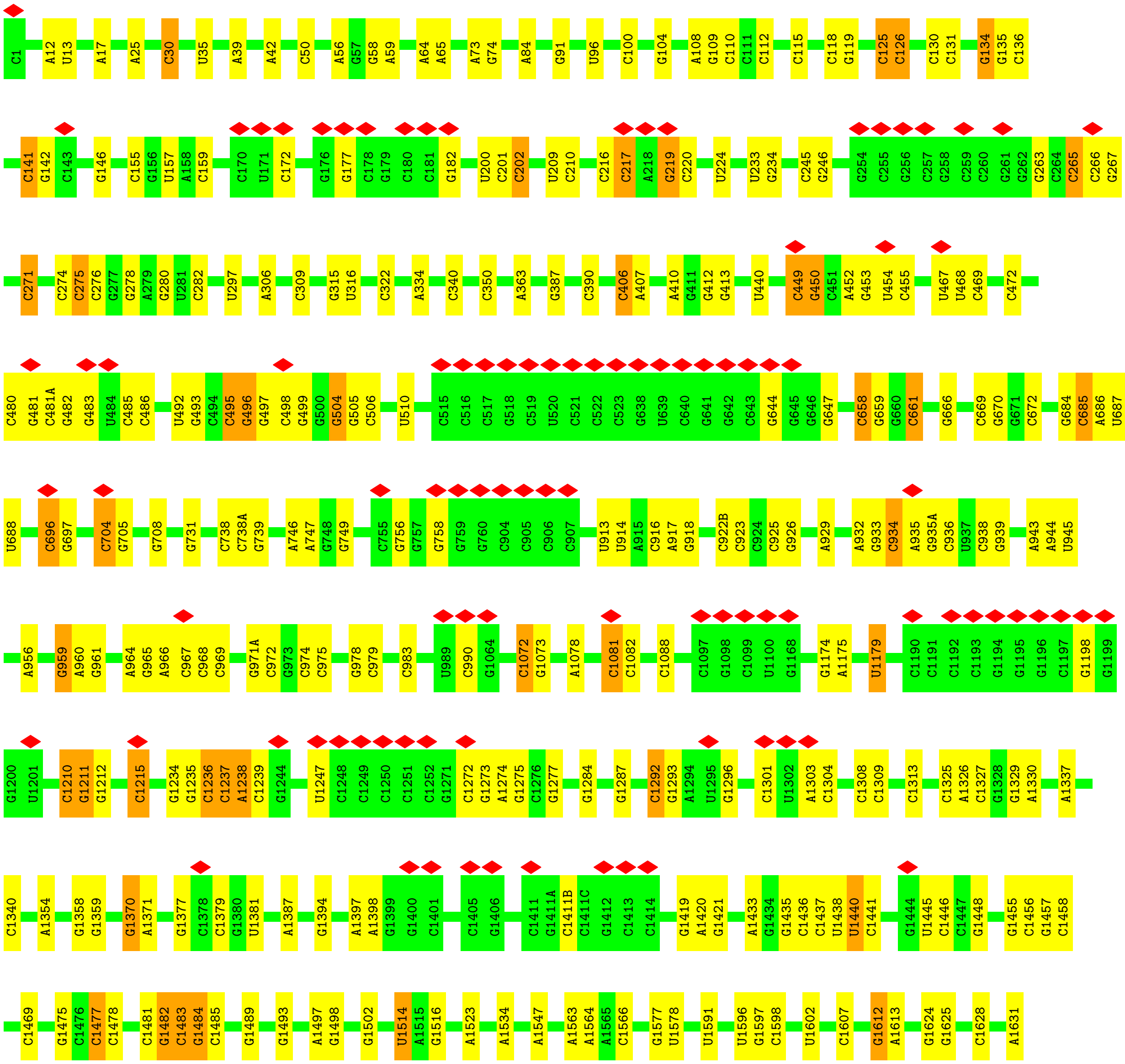
Mol	Chain	Residues	Atoms	AltConf
53	f2	1	Total Zn 1 1	0
53	i2	1	Total Zn 1 1	0
53	l2	1	Total Zn 1 1	0
53	n2	1	Total Zn 1 1	0
53	o2	1	Total Zn 1 1	0

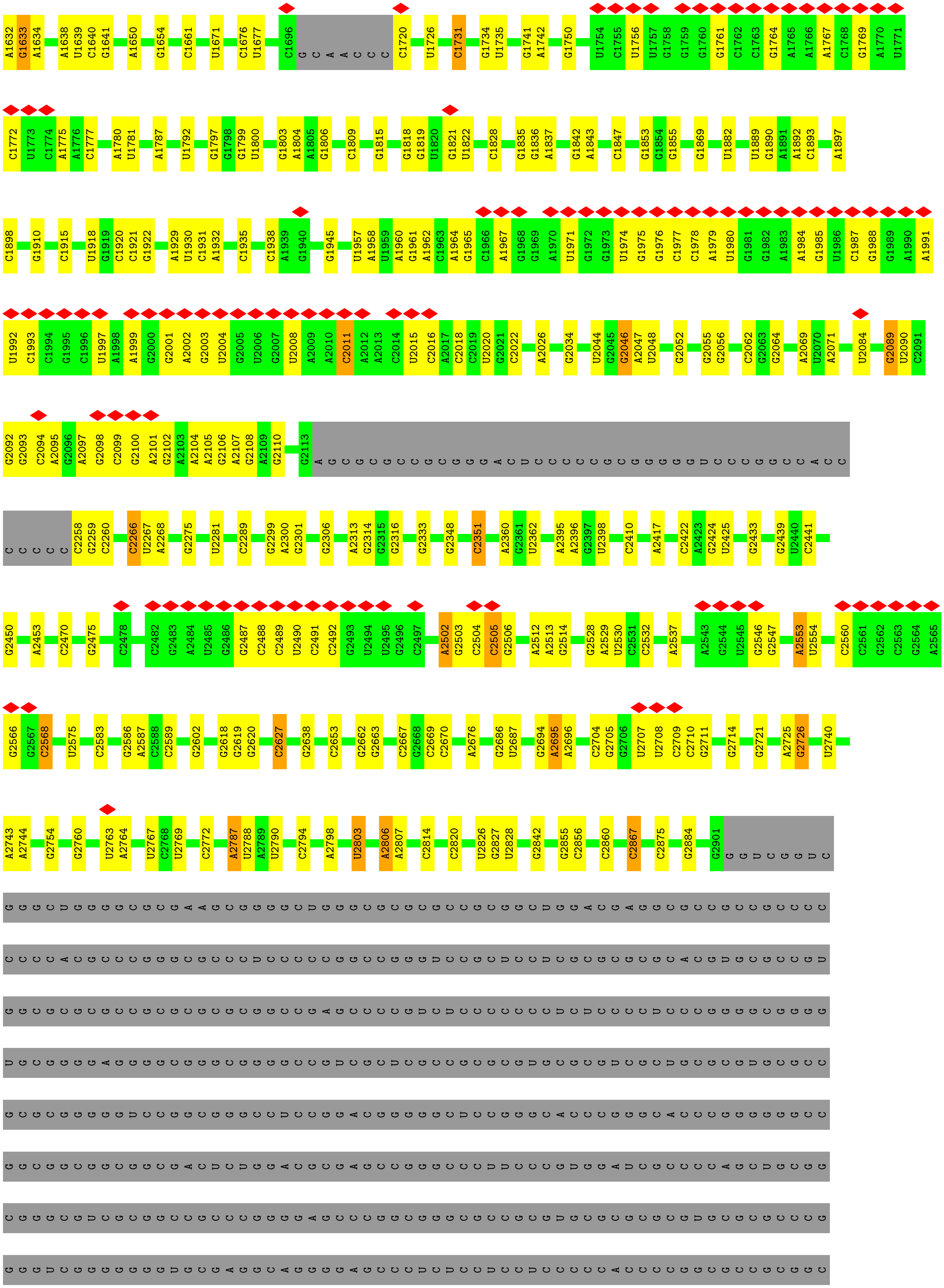
3 Residue-property plots ⓘ

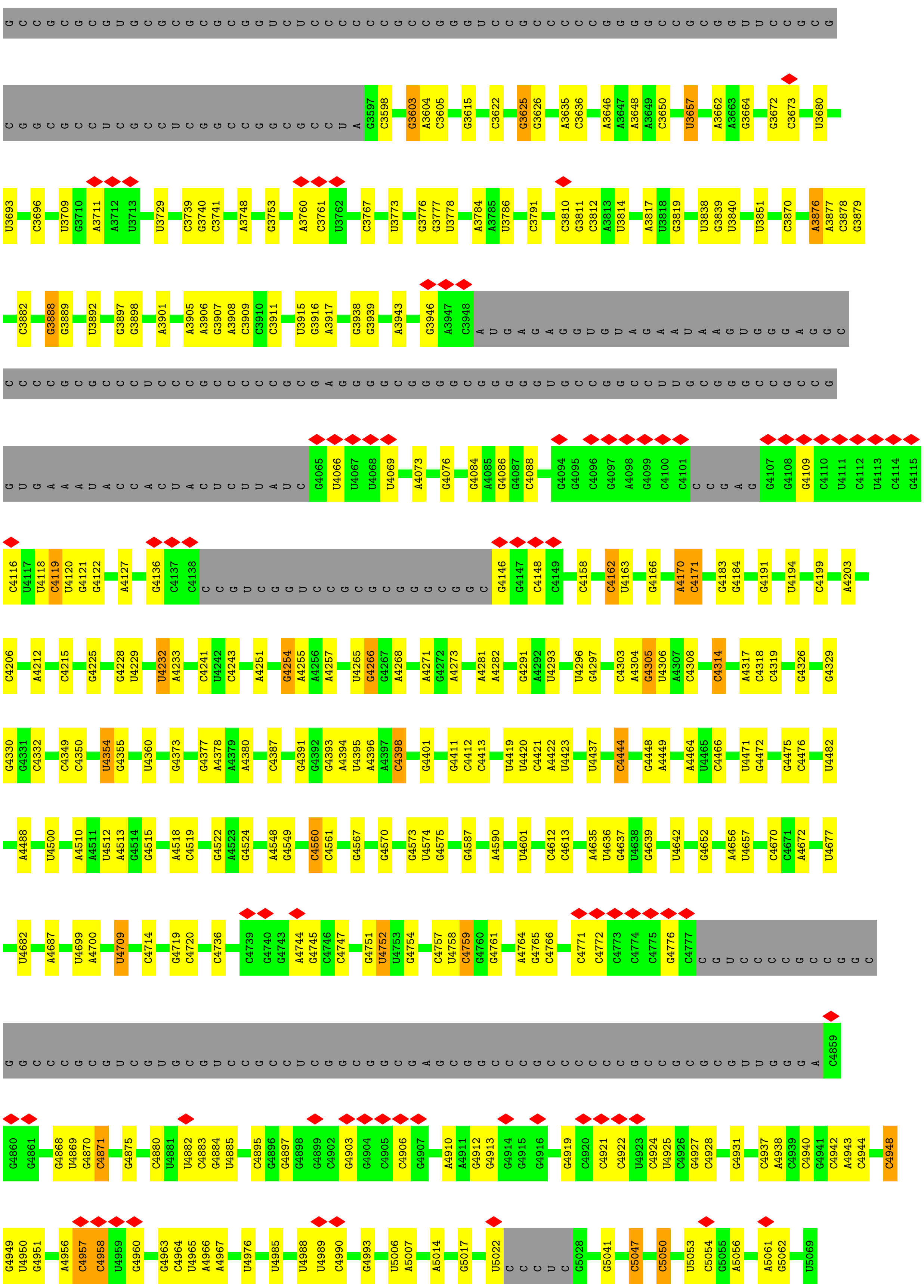
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 28S ribosomal RNA

Chain A1:

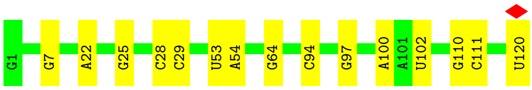



A1632 G1633 A1634 A1638 U1639 C1640 G1641 A1650 G1654 C1661 U1671 C1676 U1677 C1696 G C A A C C C C1720 U1726 C1731 G1734 U1735 G1741 A1742 G1750 U1754 C1755 U1756 U1757 G1758 G1759 G1760 G1761 C1762 C1763 G1764 A1765 A1766 A1767 C1768 G1769 A1770 U1771
C1772 U1773 C1774 A1775 A1776 C1777 A1780 U1781 A1787 U1792 G1797 G1798 G1799 U1800 G1803 A1804 A1805 G1806 C1809 G1815 G1818 G1819 U1820 G1821 U1822 C1828 G1835 G1836 A1837 G1842 A1843 C1847 G1853 G1854 G1855 G1869 U1882 U1889 G1890 A1891 A1892 C1893 A1897
C1898 G1910 C1915 U1918 G1919 C1920 C1921 G1922 A1929 U1930 C1931 A1932 C1935 C1938 A1939 G1940 G1945 U1957 A1958 U1959 A1960 G1961 A1962 C1963 A1964 G1965 C1966 A1967 G1968 G1969 A1970 U1971 G1972 G1973 U1974 G1975 G1976 C1977 C1978 A1979 U1980 G1981 G1982 A1983 A1984 G1985 U1986 C1987 G1988 G1989 A1990 A1991
U1992 C1993 C1994 G1995 C1996 U1997 A1998 A1999 G2000 G2001 A2002 G2003 U2004 G2005 U2006 G2007 U2008 A2009 A2010 C2011 A2012 A2013 C2014 U2015 C2016 A2017 C2018 C2019 U2020 G2021 C2022 A2026 G2034 U2044 G2045 G2046 A2047 U2048 G2052 G2055 G2056 C2062 G2063 G2064 A2069 U2070 A2071 U2084 G2089 U2090 C2091
G2092 G2093 C2094 A2095 G2096 A2097 G2098 C2099 G2100 A2101 G2102 A2103 A2104 A2105 G2106 A2107 G2108 A2109 G2110 G2113 A G C G C G C C G C G G G A C U C C C C C G C G G G G G U C C C G G C C A C C
C C C C C C2258 G2259 C2260 C2266 U2267 A2268 G2275 U2281 C2289 G2299 A2300 G2301 G2306 A2313 G2314 G2315 G2316 C2333 G2348 C2351 A2360 G2361 U2362 A2395 A2396 G2397 U2398 C2410 A2417 C2422 A2423 G2424 U2425 G2433 G2439 U2440 C2441
G2450 A2453 C2470 G2475 C2478 C2482 G2483 A2484 U2485 G2486 G2487 C2488 C2489 U2490 C2491 C2492 G2493 U2494 U2495 G2496 C2497 A2502 G2503 C2504 C2505 G2506 A2512 A2513 G2514 G2528 A2529 U2530 C2531 C2532 A2537 A2543 G2544 U2545 G2546 G2547 A2553 U2554 C2560 C2561 G2562 C2563 G2564 A2565
G2566 G2567 C2568 U2575 C2583 G2586 A2587 C2588 C2589 G2602 G2618 G2619 G2620 C2627 G2638 C2653 G2662 G2663 C2667 G2668 C2669 C2670 A2676 G2686 U2687 G2694 A2695 A2696 C2704 G2705 G2706 U2707 U2708 C2709 C2710 G2711 G2714 G2721 A2725 G2726 U2740
A2743 A2744 G2754 G2760 U2763 A2764 U2767 C2768 U2769 C2772 A2787 U2788 A2789 U2790 C2794 A2798 U2803 A2806 A2807 C2814 C2820 U2826 G2827 U2828 G2842 G2855 C2856 C2860 C2867 C2875 G2884 G2901 G G U C G G U C
G G G C U G G G G C G C G A A G C G G G G C U G G G C G C G C G C C G C G G C U G G A C G A G G C G C C G C C G C C C C
C C C C A C G C C C G G G C G C C C U C C C C C G G C C G G G U C C G C U C C U C G C G C G C G C A C G U G C G C C G U
G G C G C G C G C C G C G C G C G C G G C C G A G C C C C G U C U C C C C C C C U C U C C C C U C C C G G G G C G G G G
U G C G G G G A G G G G C G G G C G G G G C C G U C G C U C G C C G C G C G U G C G C G U C G C U G C G C G U G C G C C
G C G C G G G G G U C C G G C G G G C C U C C G G A C G G G G G C U C C G G G C A C C C G G G C A C C C G G G G G G C C
G G C G G C G G C G G C G A C U C U G G A C G C G A G C C G G G C C C U U C C C G U G G A U C G C C C C A G C U G C G G
C G G G C G U C G C G G C C G C C C G G G G A G C C C G G C G G G C G C C G C G U G C G C G C G C G U G C G C G C C C G
G G G U C G G G G G G G U G C G A G G C A G G G G A G C C C U C U C C U C C U C C C C C A C C C C G G C G C C G C G G C



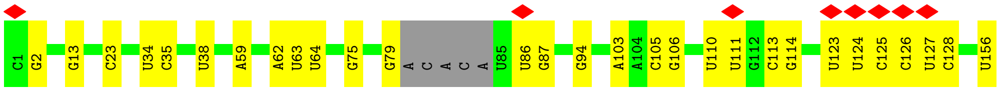
- Molecule 2: 5S ribosomal RNA

Chain B1:



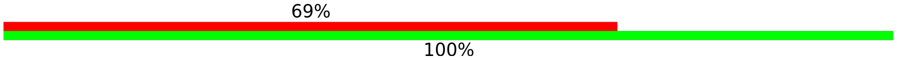
- Molecule 3: 5.8S ribosomal RNA

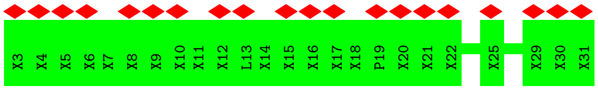
Chain C1:



- Molecule 4: Nascent polypeptide-associated complex subunit alpha N-terminal region

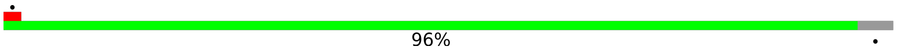
Chain D1:

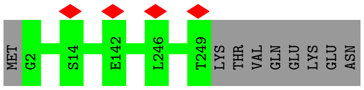




- Molecule 5: 60S ribosomal protein L8

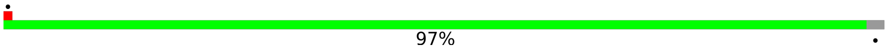
Chain A2:

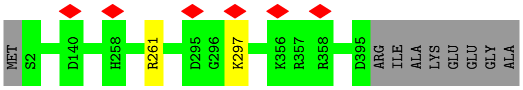




- Molecule 6: Ribosomal protein L3

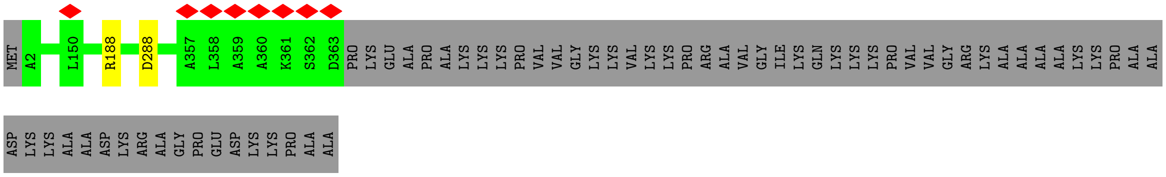
Chain B2:





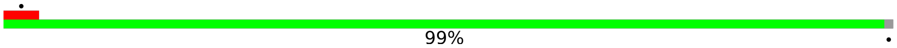
- Molecule 7: 60S ribosomal protein L4

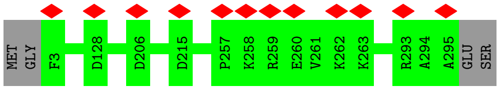
Chain C2:



- Molecule 8: Ribosomal_L18_c domain-containing protein

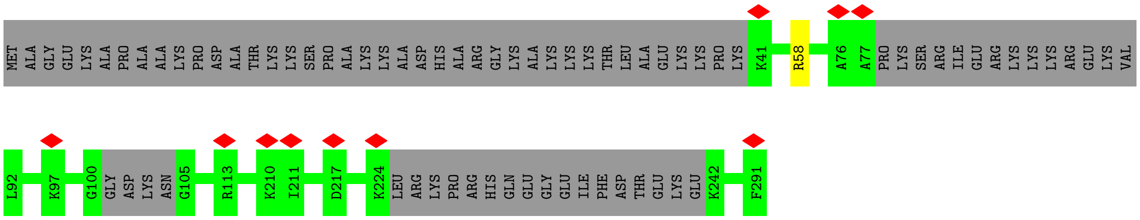
Chain D2:





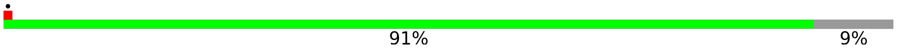
- Molecule 9: 60S ribosomal protein L6

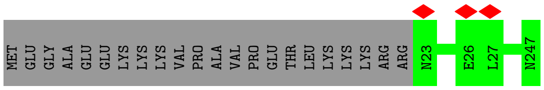
Chain E2:



- Molecule 10: 60S ribosomal protein L7

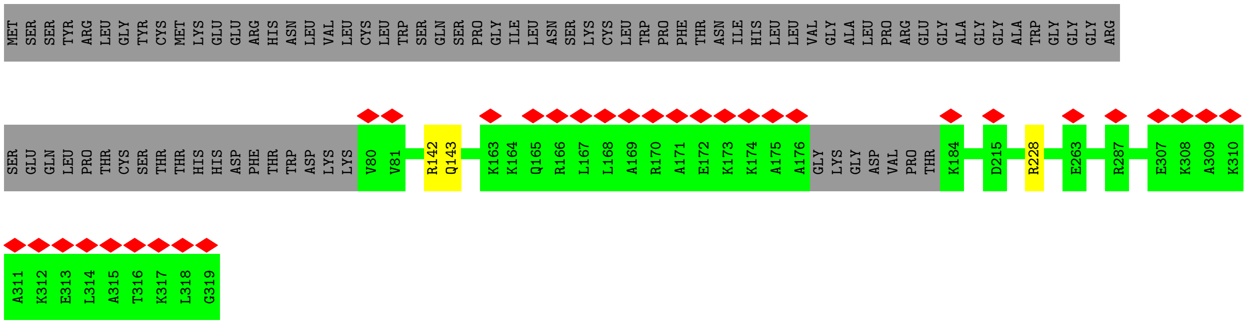
Chain F2:





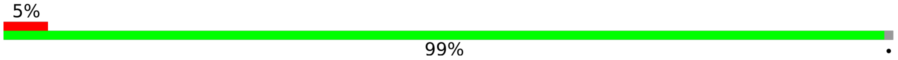
- Molecule 11: 60S ribosomal protein L7a

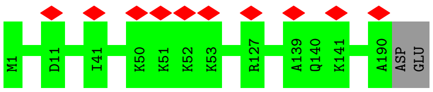
Chain G2:



- Molecule 12: 60S ribosomal protein L9

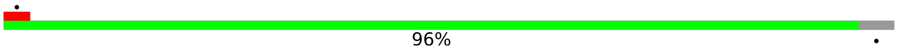
Chain H2:

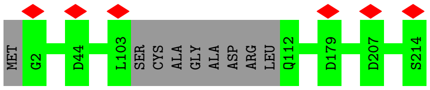




- Molecule 13: Ribosomal protein L10

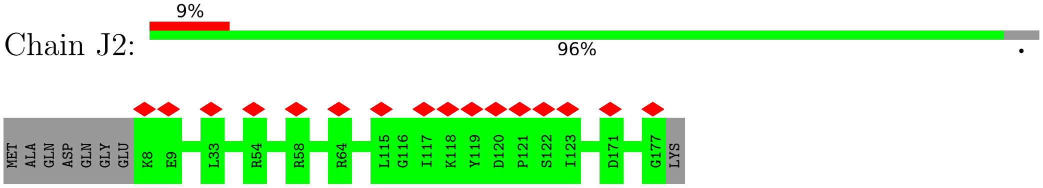
Chain I2:





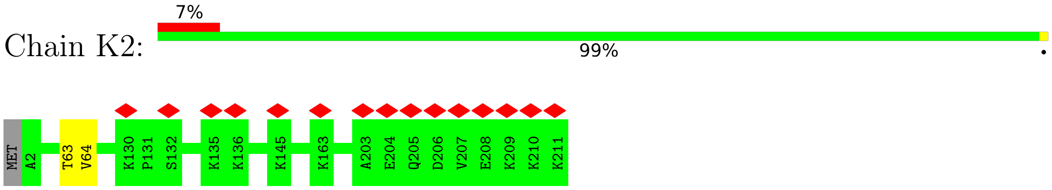
- Molecule 14: 60S ribosomal protein L11

Chain J2:



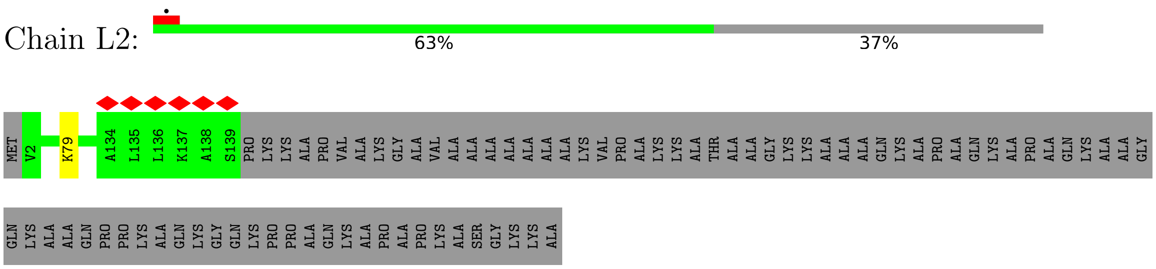
- Molecule 15: 60S ribosomal protein L13

Chain K2:



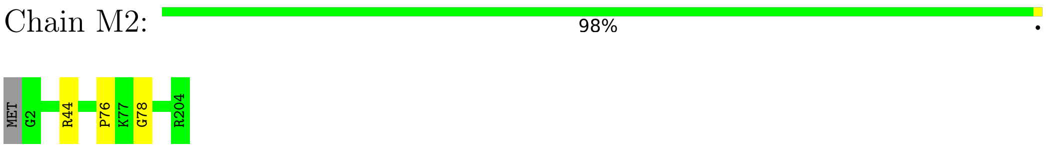
- Molecule 16: 60S ribosomal protein L14

Chain L2:



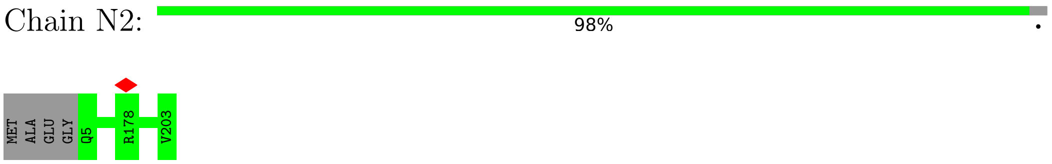
- Molecule 17: Ribosomal protein L15

Chain M2:



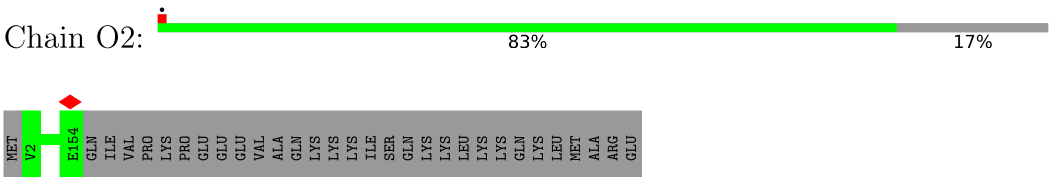
- Molecule 18: 60S ribosomal protein L13a

Chain N2:



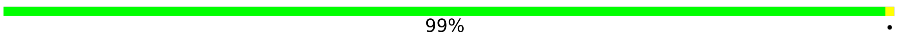
- Molecule 19: 60S ribosomal protein L17

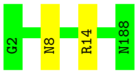
Chain O2:



- Molecule 20: Ribosomal protein L18

Chain P2:



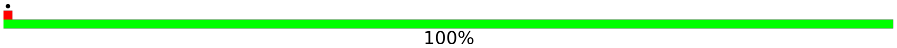


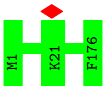
- Molecule 21: 60S ribosomal protein L19

Chain Q2:

- Molecule 22: 60S ribosomal protein L18a

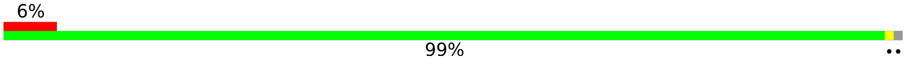
Chain R2:

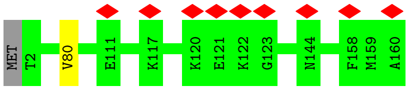




- Molecule 23: 60S ribosomal protein L21

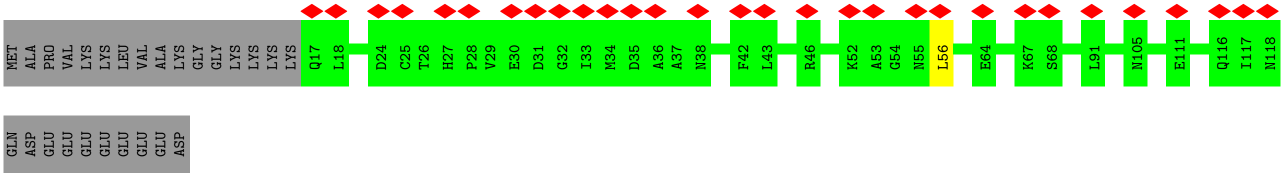
Chain S2:





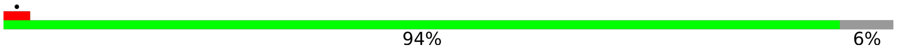
- Molecule 24: 60S ribosomal protein L22

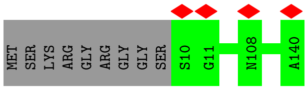
Chain T2:



- Molecule 25: 60S ribosomal protein L23

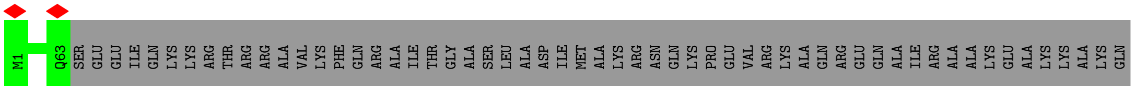
Chain U2:





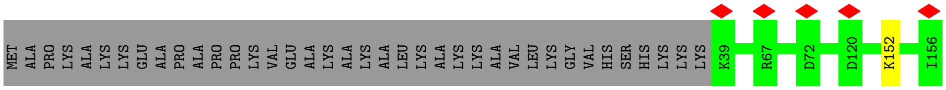
- Molecule 26: Ribosomal protein L24

Chain V2:

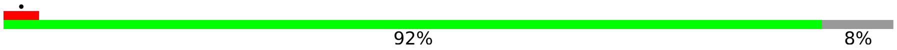


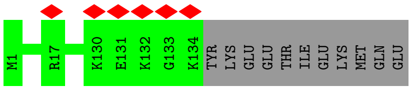
- Molecule 27: Ribosomal_L23eN domain-containing protein

Chain W2:

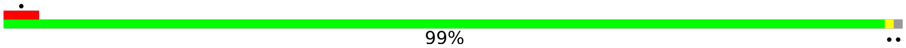



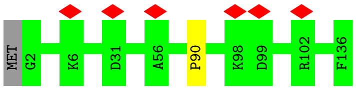
- Molecule 28: Ribosomal protein L26

Chain X2:


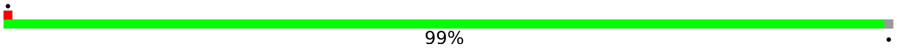


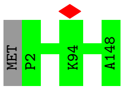
- Molecule 29: 60S ribosomal protein L27

Chain Y2:




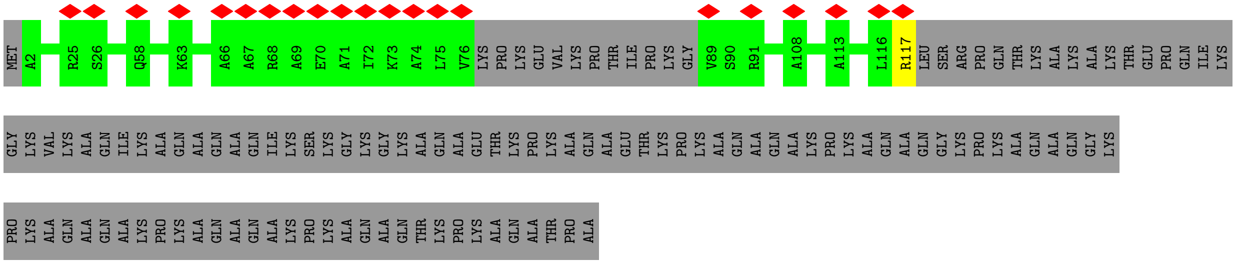
- Molecule 30: 60S ribosomal protein L27a

Chain Z2:




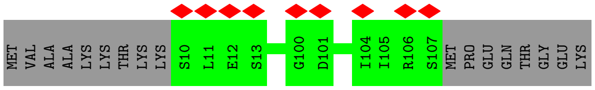
- Molecule 31: 60S ribosomal protein L29

Chain a2:

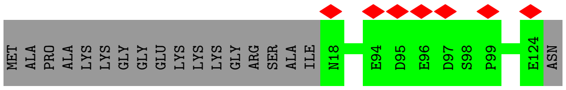
- Molecule 32: 60S ribosomal protein L30

Chain b2:

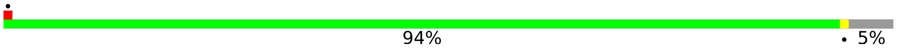
- Molecule 33: 60S ribosomal protein L31

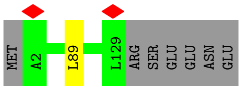
Chain c2:



- Molecule 34: Ribosomal protein L32

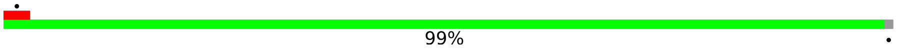
Chain d2:

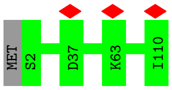




- Molecule 35: 60S ribosomal protein L35a

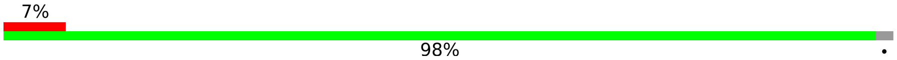
Chain e2:

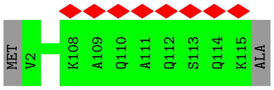




- Molecule 36: 60S ribosomal protein L34

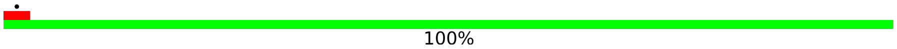
Chain f2:

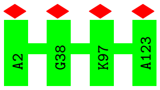




- Molecule 37: 60S ribosomal protein L35

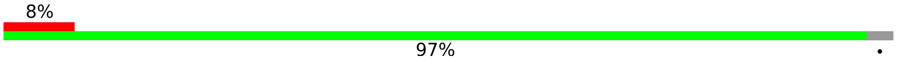
Chain g2:

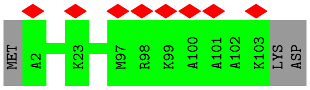




- Molecule 38: 60S ribosomal protein L36

Chain h2:



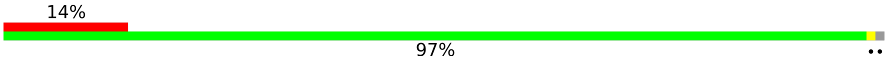


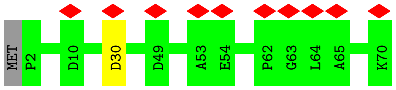
- Molecule 39: Ribosomal protein L37

Chain i2:

- Molecule 40: 60S ribosomal protein L38

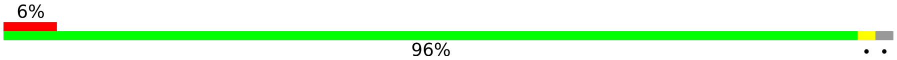
Chain j2:

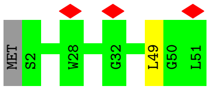




- Molecule 41: 60S ribosomal protein L39-like

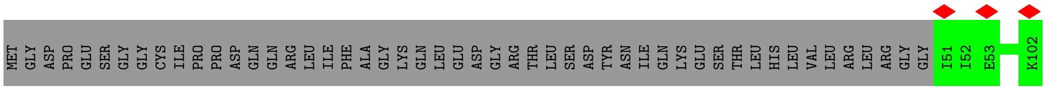
Chain k2:





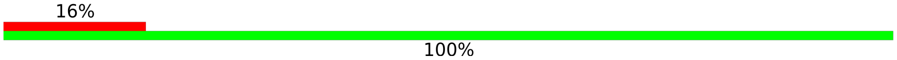
- Molecule 42: Ubiquitin-60S ribosomal protein L40

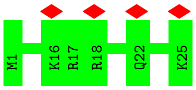
Chain l2:



- Molecule 43: 60S ribosomal protein L41

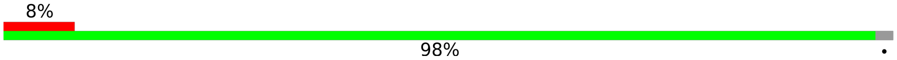
Chain m2:

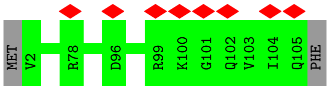




- Molecule 44: 60S ribosomal protein L36a-like

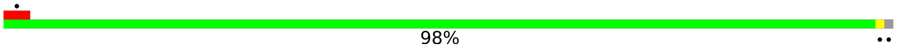
Chain n2:

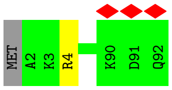




- Molecule 45: 60S ribosomal protein L37a

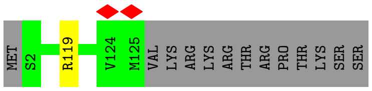
Chain o2:





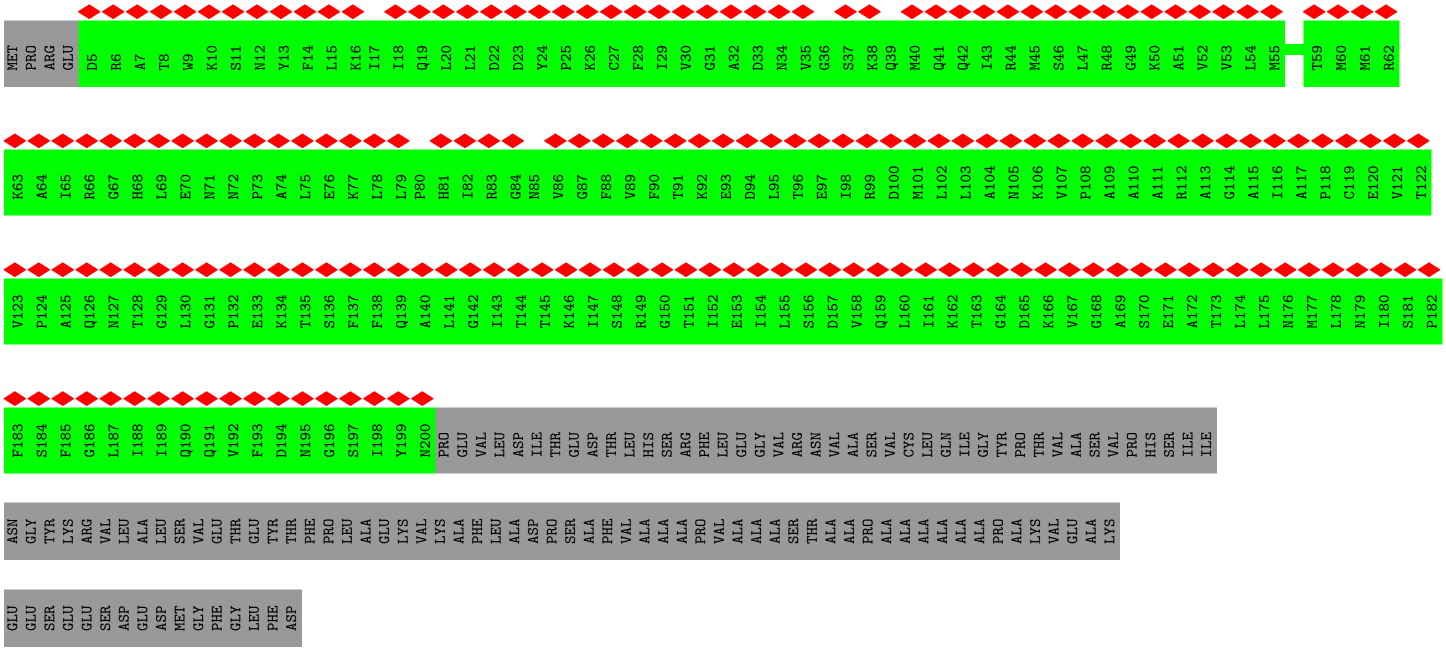
- Molecule 46: 60S ribosomal protein L28

Chain p2:



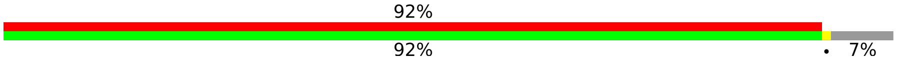
- Molecule 47: 60S acidic ribosomal protein P0

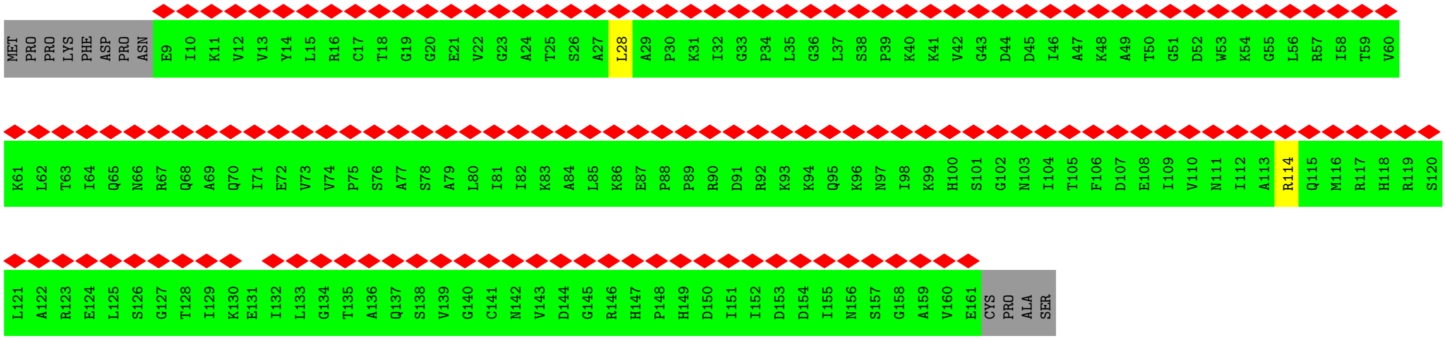
Chain q2:



- Molecule 48: 60S ribosomal protein L12

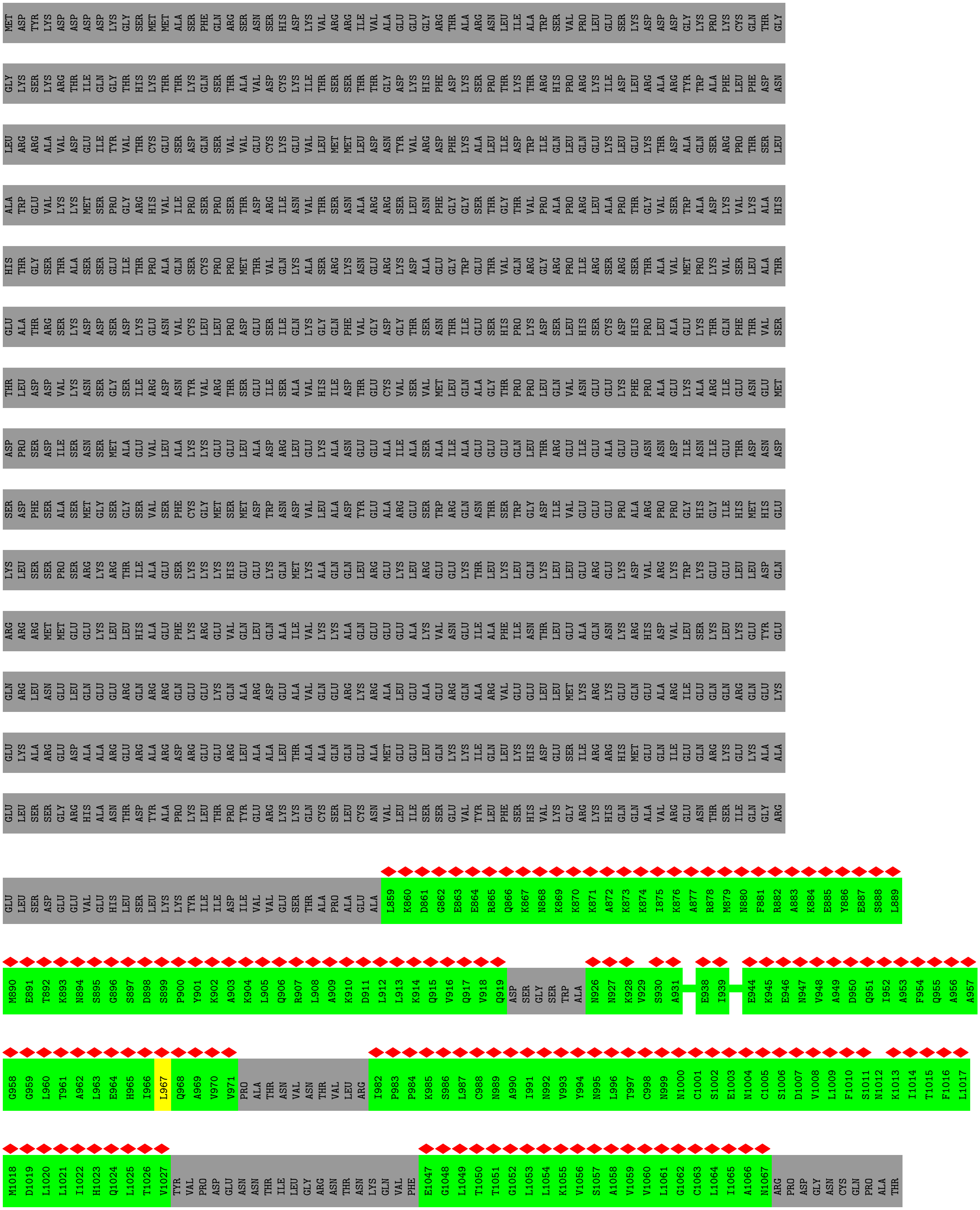
Chain r2:





- Molecule 49: S phase cyclin A-associated protein in the endoplasmic reticulum

Chain s2:



MET ASP TYR LYS ASP ASP ASP ASP LYS GLY SER MET MET ALA SER PHE GLN ARG SER ASN SER HIS ASP LYS VAL ARG ARG ILE VAL ALA GLU GLU GLY ARG THR ALA ARG ASN LEU ILE ALA TRP SER VAL PRO LEU GLU SER LYS ASP ASP ASP GLY LYS PRO LYS CYS GLN THR GLY

GLY LYS SER LYS ARG THR ILE GLN GLY THR HIS LYS THR THR LYS GLN SER THR ALA VAL ASP CYS LYS ILE THR SER SER THR THR GLY ASP LYS HIS PHE ASP LYS SER PRO THR LYS THR ARG HIS PRO ARG LYS ILE ASP LEU ARG ALA ARG TYR TRP ALA PHE LEU PHE ASP ASN

LEU ARG ARG ALA VAL ASP GLU ILE TYR VAL THR CYS GLU SER ASP GLN SER VAL VAL GLU CYS LYS GLU VAL LEU MET MET LEU ASP ASN TYR VAL ARG ASP PHE LYS ALA LEU ILE ASP TRP ILE GLN LEU GLN GLU LYS LEU GLU LYS THR ASP ALA GLN SER ARG PRO THR SER LEU

ALA TRP GLU VAL LYS LYS MET SER PRO GLY ARG HIS VAL ILE PRO SER PRO SER THR ASP ARG ILE ASN VAL THR SER ASN ALA ARG ARG SER LEU ASN PHE GLY GLY SER THR GLY THR VAL PRO ALA PRO ARG LEU ALA PRO THR GLY VAL SER TRP ALA ASP LYS VAL LYS ALA HIS

HIS THR GLY SER THR ALA SER SER GLU ILE THR PRO ALA GLN SER CYS PRO PRO MET THR VAL GLN LYS ALA SER ARG LYS ASN GLU ARG LYS ASP ALA GLU GLY TRP GLU THR VAL GLN ARG GLY ARG PRO ILE ARG SER ARG SER THR ALA VAL MET PRO LYS VAL SER LEU ALA THR

GLU ALA THR ARG SER LYS ASP ASP SER ASP LYS GLU ASN VAL CYS LEU LEU PRO ASP GLU SER ILE GLN LYS GLY GLN PHE VAL GLY ASP GLY THR SER ASN THR ILE GLU SER HIS PRO LYS ASP SER LEU HIS SER CYS ASP HIS PRO LEU ALA GLU LYS THR GLN PHE THR VAL SER

THR LEU ASP ASP VAL LYS ASN SER GLY SER ILE ARG ASP ASN TYR VAL ARG THR SER GLU ILE SER ALA VAL HIS ILE ASP THR GLU CYS VAL SER VAL MET LEU GLN ALA GLY THR PRO PRO LEU GLN VAL ASN GLU GLU LYS PHE PRO ALA GLU LYS ALA ARG ILE GLU ASN GLU MET

ASP PRO SER ASP ILE SER ASN SER MET ALA GLU VAL LEU ALA LYS LYS GLU GLU LEU ALA ASP ARG LEU GLU LYS ALA ASN GLU GLU ALA ILE ALA SER ALA ILE ALA GLU GLU GLU GLN LEU THR ARG GLU ILE GLU ALA GLU GLU ASN ASN ASP ILE ASN ILE GLU THR ASP ASN ASP

SER ASP PHE SER ALA SER MET GLY SER GLY SER VAL SER PHE CYS GLY MET SER MET ASP TRP ASN ASP VAL LEU ALA ASP TYR GLU ALA ARG GLU SER TRP ARG GLN ASN THR SER TRP GLY ASP ILE VAL GLU GLU GLU PRO ALA ARG PRO PRO GLY HIS GLY ILE HIS MET HIS GLU

LYS LEU SER SER PRO SER ARG LYS ARG THR ILE ALA GLU SER LYS LYS LYS HIS GLU GLU LYS GLN MET LYS ALA GLN GLN LEU ARG GLU LYS LEU ARG GLU GLU LYS THR LEU LYS LEU GLN LYS LEU LEU GLU ARG GLU LYS ASP VAL ARG LYS TRP LYS GLU GLU LEU LEU ASP GLN

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GLN ARG LEU ASN GLU LEU GLN GLU GLU ARG GLN ARG ARG GLN GLU GLU LYS GLN ALA ARG ASP GLU ALA VAL GLN GLU ARG LYS ARG ALA LEU GLU ALA GLU ARG GLN ALA ARG VAL GLU GLU LEU LEU MET LYS ARG LYS GLU GLN GLU ALA ARG ILE GLU GLN GLN ARG GLN GLU LYS

GLU LYS ALA ARG GLU ASP ALA ALA ARG GLU ARG ALA ARG ASP ARG GLU GLU ARG LEU ALA ALA LEU THR ALA ALA GLN GLN GLU ALA MET GLU GLU LEU GLN LYS LYS ILE GLN LEU LYS HIS ASP GLU SER ILE ARG ARG HIS MET GLU GLN ILE GLU GLN ARG LYS GLU LYS ALA ALA

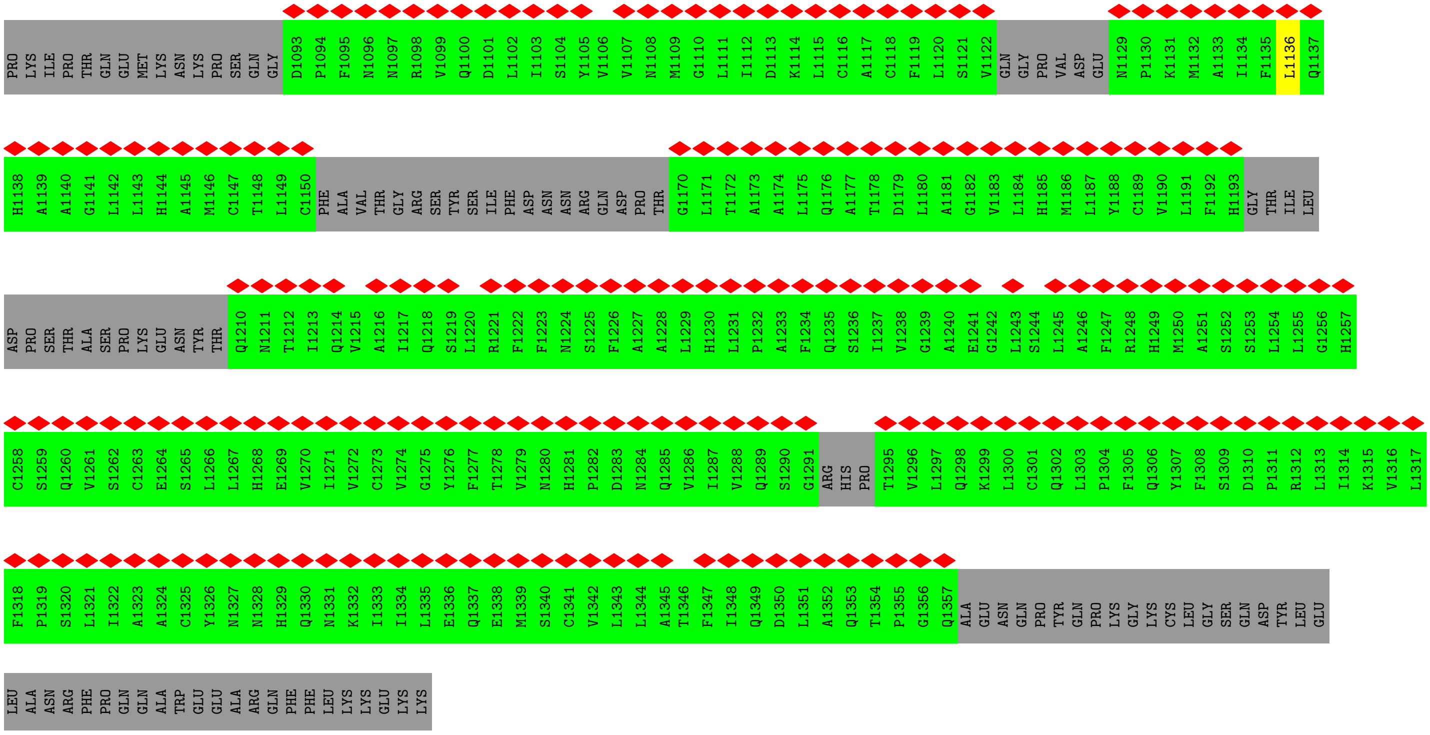
GLU LEU SER SER GLY ARG HIS ALA ASN THR ASP TYR ALA PRO LYS LEU THR PRO TYR GLU ARG LYS LYS GLN CYS SER LEU CYS ASN VAL LEU ILE SER SER GLU VAL TYR LEU PHE SER HIS VAL LYS GLY ARG LYS HIS GLN GLN ALA VAL ARG GLU ASN THR SER ILE GLN GLY ARG

GLU LEU SER ASP GLU GLU VAL GLU HIS LEU SER LEU LYS LYS TYR ILE ILE ASP ILE VAL VAL GLU SER THR ALA PRO ALA GLU ALA L859 K860 D861 G862 E863 E864 R865 Q866 K867 N868 K869 K870 K871 A872 K873 K874 I875 K876 A877 R878 M879 N880 F881 R882 A883 K884 E885 Y886 E887 S888 L889

M890 E891 T892 K893 N894 S895 G896 S897 D898 S899 P900 Y901 K902 A903 K904 L905 Q906 R907 L908 A909 K910 D911 L912 L913 K914 Q915 V916 Q917 V918 Q919 ASP SER GLY SER TRP ALA N926 N927 K928 V929 S930 A931 E938 I939 E944 K945 E946 N947 V948 A949 D950 Q951 I952 A953 F954 Q955 A956 A957

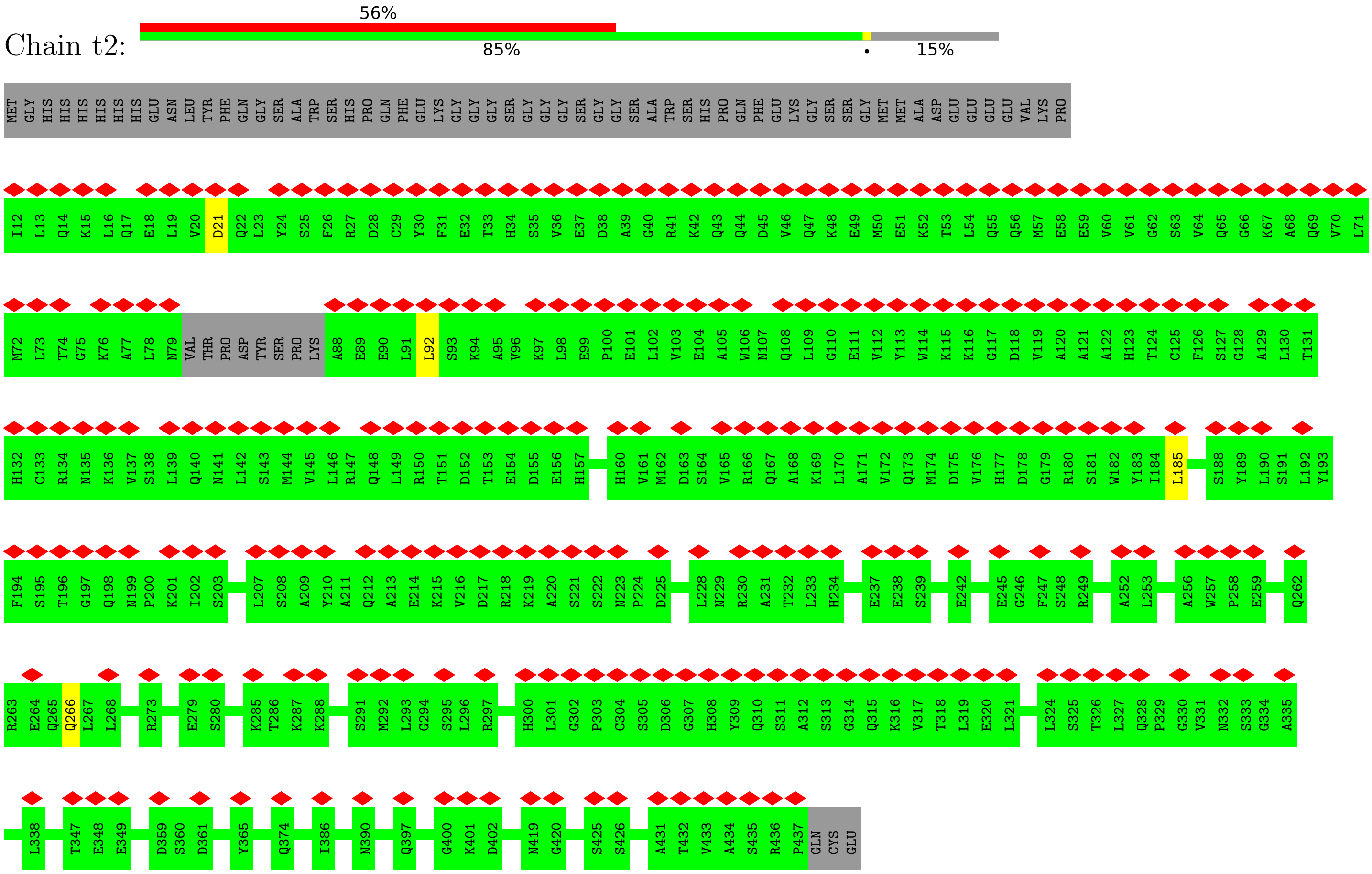
G958 G959 L960 T961 A962 L963 E964 H965 I966 L967 Q968 A969 V970 V971 PRO ALA THR ASN VAL ASN THR VAL LEU ARG I982 P983 P984 K985 S986 L987 C988 N989 A990 I991 N992 V993 Y994 N995 L996 T997 C998 N999 N1000 C1001 S1002 E1003 N1004 C1005 S1006 D1007 V1008 L1009 F1010 S1011 N1012 K1013 I1014 T1015 F1016 L1017

M1018 D1019 L1020 L1021 I1022 H1023 Q1024 L1025 T1026 V1027 TYR VAL PRO ASP GLU ASN ASN THR ILE LEU GLY ARG ASN THR ASN LYS GLN VAL PHE E1047 G1048 L1049 T1050 T1051 G1052 L1053 L1054 K1055 V1056 S1057 A1058 V1059 V1060 L1061 G1062 C1063 L1064 I1065 A1066 N1067 ARG PRO ASP GLY ASN CYS GLN PRO ALA THR

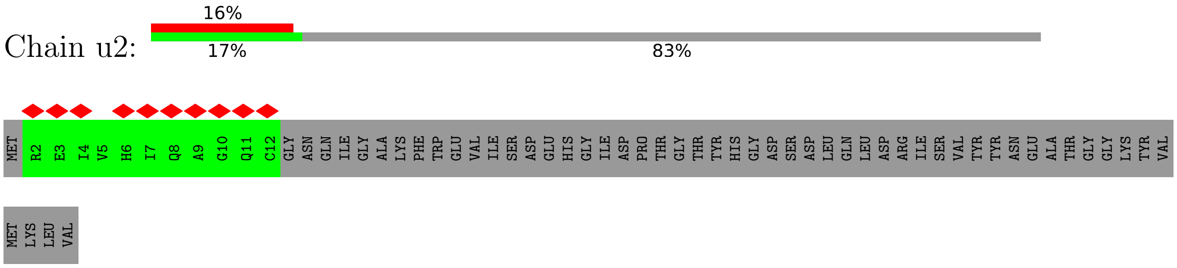


- Molecule 50: Tetratricopeptide repeat protein 5

Chain t2:



- Molecule 51: Tubulin beta chain



4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18949	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 $(e^-/\text{Å}^2)$	44.7	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	431.08, 431.08, 431.08	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.829, 0.829, 0.829	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A1	0.32	0/84976	1.06	399/132520 (0.3%)
2	B1	0.29	0/2858	1.01	11/4455 (0.2%)
3	C1	0.30	0/3581	1.00	2/5577 (0.0%)
4	D1	0.31	0/14	0.52	0/16
5	A2	0.29	0/1936	0.63	0/2596
6	B2	0.28	0/3240	0.60	0/4339
7	C2	0.28	0/2937	0.65	1/3946 (0.0%)
8	D2	0.28	0/2437	0.56	0/3264
9	E2	0.27	0/1762	0.62	0/2362
10	F2	0.28	0/1911	0.59	0/2549
11	G2	0.28	0/1910	0.59	0/2569
12	H2	0.29	0/1535	0.64	0/2063
13	I2	0.27	0/1702	0.58	0/2272
14	J2	0.30	0/1385	0.68	0/1852
15	K2	0.28	0/1733	0.64	0/2316
16	L2	0.28	0/1158	0.62	0/1547
17	M2	0.28	0/1746	0.66	1/2338 (0.0%)
18	N2	0.30	0/1662	0.64	0/2222
19	O2	0.29	0/1268	0.59	0/1700
20	P2	0.27	0/1538	0.66	0/2054
21	Q2	0.32	0/1310	0.70	0/1734
22	R2	0.29	0/1501	0.65	0/2012
23	S2	0.27	0/1326	0.58	0/1770
24	T2	0.32	0/848	0.72	1/1138 (0.1%)
25	U2	0.29	0/993	0.61	0/1332
26	V2	0.29	0/541	0.60	0/720
27	W2	0.27	0/984	0.62	0/1323
28	X2	0.27	0/1132	0.63	0/1504
29	Y2	0.29	0/1130	0.63	0/1507
30	Z2	0.28	0/1191	0.60	0/1590
31	a2	0.24	0/861	0.59	0/1138
32	b2	0.32	0/771	0.63	0/1034

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	c2	0.28	0/903	0.63	0/1216
34	d2	0.27	0/1071	0.62	1/1429 (0.1%)
35	e2	0.29	0/895	0.63	0/1198
36	f2	0.27	0/916	0.64	0/1220
37	g2	0.27	0/1021	0.64	0/1348
38	h2	0.29	0/841	0.67	0/1112
39	i2	0.26	0/720	0.64	0/952
40	j2	0.30	0/575	0.71	1/761 (0.1%)
41	k2	0.26	0/459	0.68	1/608 (0.2%)
42	l2	0.26	0/435	0.61	0/575
43	m2	0.31	0/240	0.82	0/305
44	n2	0.27	0/864	0.57	0/1140
45	o2	0.26	0/718	0.59	0/953
46	p2	0.27	0/1010	0.69	0/1354
47	q2	0.27	0/1530	0.61	0/2064
48	r2	0.28	0/1174	0.70	1/1582 (0.1%)
49	s2	0.34	0/3090	0.69	2/4169 (0.0%)
50	t2	0.30	0/3323	0.65	3/4494 (0.1%)
51	u2	0.22	0/82	0.62	0/109
All	All	0.31	0/153744	0.92	424/225948 (0.2%)

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
15	K2	0	1
17	M2	0	2
23	S2	0	1
All	All	0	4

There are no bond length outliers.

All (424) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	2258	C	N1-C2-O2	13.81	127.18	118.90
1	A1	2258	C	C2-N1-C1’	13.16	133.28	118.80
1	A1	2258	C	N3-C2-O2	-11.55	113.82	121.90
1	A1	2505	C	C6-N1-C2	-10.26	116.20	120.30
1	A1	2258	C	C6-N1-C2	-9.90	116.34	120.30
1	A1	100	C	C2-N1-C1’	9.62	129.38	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A1	4948	C	N1-C2-O2	9.54	124.63	118.90
1	A1	2627	C	N1-C2-O2	9.44	124.56	118.90
1	A1	2505	C	N1-C2-O2	9.33	124.50	118.90
2	B1	29	C	N1-C2-O2	9.04	124.32	118.90
1	A1	2505	C	N3-C2-O2	-8.96	115.63	121.90
1	A1	4759	C	N1-C2-O2	8.92	124.25	118.90
1	A1	4948	C	C2-N1-C1’	8.90	128.59	118.80
1	A1	2867	C	N3-C2-O2	-8.80	115.74	121.90
1	A1	2258	C	C6-N1-C1’	-8.76	110.29	120.80
1	A1	100	C	N1-C2-O2	8.62	124.07	118.90
1	A1	4413	C	C2-N1-C1’	8.60	128.25	118.80
1	A1	4948	C	N3-C2-O2	-8.41	116.01	121.90
1	A1	2627	C	C2-N1-C1’	8.33	127.96	118.80
1	A1	1639	U	C2-N1-C1’	8.24	127.59	117.70
1	A1	4759	C	C2-N1-C1’	8.05	127.66	118.80
1	A1	3739	C	C2-N1-C1’	8.04	127.65	118.80
1	A1	4880	C	C2-N1-C1’	7.99	127.59	118.80
1	A1	4354	U	C2-N1-C1’	7.99	127.28	117.70
1	A1	1612	G	N3-C4-N9	7.97	130.78	126.00
2	B1	29	C	C2-N1-C1’	7.97	127.57	118.80
1	A1	4413	C	N1-C2-O2	7.97	123.68	118.90
1	A1	3909	C	N1-C2-O2	7.91	123.65	118.90
1	A1	271	C	N1-C2-O2	7.90	123.64	118.90
1	A1	4758	U	C2-N1-C1’	7.89	127.17	117.70
1	A1	4423	U	C2-N1-C1’	7.85	127.12	117.70
1	A1	2627	C	N3-C2-O2	-7.82	116.42	121.90
1	A1	4148	C	N1-C2-O2	7.81	123.59	118.90
1	A1	2410	C	C2-N1-C1’	7.81	127.39	118.80
1	A1	1639	U	N1-C2-O2	7.75	128.22	122.80
1	A1	1081	C	N3-C2-O2	-7.75	116.48	121.90
1	A1	4303	C	C2-N1-C1’	7.73	127.30	118.80
2	B1	29	C	N3-C2-O2	-7.70	116.51	121.90
1	A1	1993	C	N1-C2-O2	7.63	123.48	118.90
1	A1	1381	U	C2-N1-C1’	7.57	126.78	117.70
1	A1	4413	C	N3-C2-O2	-7.56	116.61	121.90
1	A1	1484	G	N3-C4-C5	-7.55	124.82	128.60
1	A1	219	G	C4-N9-C1’	7.54	136.30	126.50
1	A1	2820	C	N1-C2-O2	7.52	123.41	118.90
1	A1	100	C	N3-C2-O2	-7.51	116.64	121.90
1	A1	219	G	N3-C4-C5	-7.51	124.85	128.60
1	A1	141	C	C2-N1-C1’	7.47	127.01	118.80
50	t2	21	ASP	CB-CG-OD1	7.46	125.01	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	2258	C	C5-C6-N1	7.42	124.71	121.00
1	A1	1484	G	N3-C4-N9	7.42	130.45	126.00
1	A1	1484	G	C4-N9-C1'	7.39	136.11	126.50
1	A1	4758	U	N1-C2-O2	7.39	127.97	122.80
1	A1	4444	C	N1-C2-O2	7.33	123.30	118.90
1	A1	4241	C	N1-C2-O2	7.32	123.29	118.90
1	A1	1481	C	C2-N1-C1'	7.31	126.84	118.80
1	A1	4420	U	C2-N1-C1'	7.30	126.46	117.70
1	A1	4759	C	N3-C2-O2	-7.24	116.83	121.90
1	A1	4354	U	N1-C2-O2	7.24	127.86	122.80
1	A1	1612	G	C4-N9-C1'	7.22	135.88	126.50
1	A1	4880	C	N1-C2-O2	7.20	123.22	118.90
1	A1	2016	C	N1-C2-O2	7.17	123.20	118.90
1	A1	1381	U	N3-C2-O2	-7.16	117.19	122.20
1	A1	3909	C	C2-N1-C1'	7.14	126.65	118.80
1	A1	4305	G	C4-N9-C1'	7.12	135.75	126.50
1	A1	4420	U	N1-C2-O2	7.08	127.76	122.80
1	A1	2528	G	C4-N9-C1'	7.07	135.69	126.50
1	A1	3741	C	N3-C2-O2	-7.06	116.96	121.90
1	A1	3909	C	N3-C2-O2	-7.04	116.97	121.90
1	A1	4709	U	N1-C2-O2	7.04	127.73	122.80
1	A1	2803	U	N3-C2-O2	-7.00	117.30	122.20
1	A1	4423	U	N1-C2-O2	7.00	127.70	122.80
1	A1	2046	G	P-O3'-C3'	7.00	128.10	119.70
1	A1	2695	A	P-O3'-C3'	6.98	128.08	119.70
1	A1	1598	C	N1-C2-O2	6.97	123.08	118.90
1	A1	112	C	C2-N1-C1'	6.96	126.46	118.80
1	A1	1639	U	N3-C2-O2	-6.95	117.34	122.20
1	A1	4423	U	N3-C2-O2	-6.94	117.34	122.20
49	s2	1136	LEU	CA-CB-CG	6.94	131.26	115.30
2	B1	29	C	C6-N1-C2	-6.92	117.53	120.30
1	A1	4612	C	N1-C2-O2	6.91	123.05	118.90
1	A1	2627	C	C6-N1-C2	-6.89	117.55	120.30
1	A1	1381	U	N1-C2-O2	6.88	127.62	122.80
1	A1	3909	C	C6-N1-C2	-6.87	117.55	120.30
1	A1	685	C	P-O3'-C3'	6.86	127.93	119.70
1	A1	472	C	N1-C2-O2	6.82	122.99	118.90
1	A1	4758	U	N3-C2-O2	-6.80	117.44	122.20
1	A1	2505	C	C5-C6-N1	6.79	124.39	121.00
1	A1	4420	U	N3-C2-O2	-6.76	117.47	122.20
1	A1	220	C	C2-N1-C1'	6.75	126.23	118.80
1	A1	130	C	N3-C2-O2	-6.74	117.18	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	3636	C	C6-N1-C2	-6.74	117.60	120.30
1	A1	4709	U	N3-C2-O2	-6.71	117.50	122.20
1	A1	2528	G	N3-C4-C5	-6.70	125.25	128.60
1	A1	219	G	N3-C4-N9	6.70	130.02	126.00
1	A1	100	C	C6-N1-C1'	-6.70	112.76	120.80
1	A1	2568	C	N1-C2-O2	6.68	122.91	118.90
1	A1	4303	C	N1-C2-O2	6.66	122.89	118.90
1	A1	4354	U	N3-C2-O2	-6.65	117.54	122.20
1	A1	282	C	N1-C2-O2	6.65	122.89	118.90
1	A1	1777	C	N1-C2-O2	6.63	122.88	118.90
1	A1	4958	C	N1-C2-O2	6.61	122.87	118.90
1	A1	1072	C	P-O3'-C3'	6.60	127.62	119.70
1	A1	1612	G	C8-N9-C1'	-6.56	118.47	127.00
1	A1	4880	C	N3-C2-O2	-6.55	117.31	121.90
1	A1	2351	C	C2-N1-C1'	6.55	126.00	118.80
1	A1	1612	G	N3-C4-C5	-6.53	125.33	128.60
1	A1	4303	C	C6-N1-C2	-6.53	117.69	120.30
3	C1	64	U	N3-C2-O2	-6.52	117.64	122.20
1	A1	1735	U	N1-C2-O2	6.51	127.36	122.80
1	A1	4444	C	N3-C2-O2	-6.51	117.34	121.90
1	A1	2803	U	N1-C2-O2	6.51	127.36	122.80
1	A1	4413	C	C6-N1-C2	-6.50	117.70	120.30
1	A1	2704	C	C2-N1-C1'	6.48	125.93	118.80
7	C2	288	ASP	CB-CG-OD1	6.47	124.13	118.30
1	A1	1671	U	N3-C2-O2	-6.47	117.67	122.20
1	A1	4314	C	N1-C2-O2	6.46	122.78	118.90
1	A1	2089	G	P-O3'-C3'	6.46	127.45	119.70
40	j2	30	ASP	CB-CG-OD1	6.45	124.11	118.30
1	A1	74	G	C4-N9-C1'	6.43	134.86	126.50
1	A1	74	G	C8-N9-C1'	-6.42	118.66	127.00
1	A1	271	C	N3-C2-O2	-6.40	117.42	121.90
1	A1	1247	U	N1-C2-O2	6.38	127.26	122.80
1	A1	2806	A	O4'-C1'-N9	6.38	113.30	108.20
1	A1	3657	U	N3-C2-O2	-6.32	117.78	122.20
1	A1	2528	G	N3-C4-N9	6.28	129.77	126.00
1	A1	2008	U	C2-N1-C1'	6.27	125.22	117.70
1	A1	2410	C	C5-C6-N1	6.26	124.13	121.00
1	A1	4303	C	N3-C2-O2	-6.26	117.52	121.90
1	A1	1210	C	C2-N1-C1'	6.25	125.67	118.80
1	A1	4266	G	N3-C4-C5	-6.24	125.48	128.60
1	A1	1993	C	N3-C2-O2	-6.24	117.53	121.90
1	A1	3876	A	P-O3'-C3'	6.21	127.16	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A1	1484	G	C8-N9-C1’	-6.20	118.95	127.00
1	A1	4682	U	N3-C2-O2	-6.18	117.88	122.20
1	A1	50	C	N1-C2-O2	6.18	122.61	118.90
1	A1	1081	C	N1-C2-O2	6.17	122.60	118.90
1	A1	271	C	C2-N1-C1’	6.17	125.59	118.80
1	A1	4869	U	C2-N1-C1’	6.17	125.10	117.70
1	A1	4171	C	N1-C2-O2	6.17	122.60	118.90
1	A1	1777	C	C2-N1-C1’	6.16	125.58	118.80
1	A1	4948	C	C6-N1-C1’	-6.16	113.41	120.80
1	A1	1210	C	N1-C2-O2	6.14	122.58	118.90
1	A1	2860	C	N1-C2-O2	6.14	122.58	118.90
1	A1	100	C	C6-N1-C2	-6.13	117.85	120.30
1	A1	115	C	C2-N1-C1’	6.12	125.54	118.80
1	A1	219	G	C8-N9-C1’	-6.12	119.04	127.00
1	A1	4241	C	C2-N1-C1’	6.12	125.53	118.80
1	A1	2410	C	C6-N1-C2	-6.12	117.85	120.30
1	A1	219	G	C2-N3-C4	6.11	114.96	111.90
1	A1	3657	U	N1-C2-O2	6.11	127.08	122.80
1	A1	978	G	N3-C4-N9	-6.10	122.34	126.00
1	A1	2016	C	N3-C2-O2	-6.09	117.64	121.90
1	A1	2820	C	N3-C2-O2	-6.08	117.64	121.90
1	A1	4148	C	N3-C2-O2	-6.08	117.65	121.90
41	k2	49	LEU	CA-CB-CG	6.07	129.27	115.30
1	A1	1993	C	C2-N1-C1’	6.07	125.48	118.80
1	A1	661	C	C2-N1-C1’	6.06	125.47	118.80
1	A1	1792	U	C2-N1-C1’	6.06	124.97	117.70
1	A1	3741	C	N1-C2-O2	6.06	122.53	118.90
1	A1	4871	C	N1-C2-O2	6.05	122.53	118.90
1	A1	1800	U	N3-C2-O2	-6.03	117.98	122.20
1	A1	4444	C	C6-N1-C2	-6.03	117.89	120.30
1	A1	4232	U	P-O3’-C3’	6.03	126.93	119.70
1	A1	4747	C	C2-N1-C1’	6.02	125.42	118.80
1	A1	2867	C	C6-N1-C2	-6.01	117.90	120.30
1	A1	1632	A	C2-N3-C4	6.00	113.60	110.60
1	A1	1735	U	N3-C2-O2	-6.00	118.00	122.20
1	A1	2008	U	N1-C2-O2	6.00	127.00	122.80
2	B1	102	U	N1-C2-O2	5.99	126.99	122.80
1	A1	1340	C	C5-C6-N1	5.97	123.98	121.00
1	A1	1458	C	N1-C2-O2	5.97	122.48	118.90
1	A1	4241	C	N3-C2-O2	-5.96	117.73	121.90
1	A1	4682	U	N1-C2-O2	5.95	126.96	122.80
1	A1	3739	C	C6-N1-C2	-5.94	117.92	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	1440	U	P-O3'-C3'	5.93	126.82	119.70
1	A1	4476	C	C2-N1-C1'	5.93	125.33	118.80
1	A1	4148	C	C2-N1-C1'	5.93	125.32	118.80
1	A1	4759	C	C6-N1-C2	-5.92	117.93	120.30
1	A1	1514	U	N1-C2-O2	5.92	126.94	122.80
1	A1	2011	C	N1-C2-O2	5.91	122.45	118.90
1	A1	4199	C	N1-C2-O2	5.91	122.45	118.90
1	A1	1370	G	P-O3'-C3'	5.91	126.79	119.70
1	A1	2266	C	P-O3'-C3'	5.91	126.79	119.70
1	A1	4266	G	C4-N9-C1'	5.90	134.17	126.50
1	A1	4714	C	N1-C2-O2	5.90	122.44	118.90
1	A1	1671	U	N1-C2-O2	5.89	126.92	122.80
1	A1	658	C	N1-C2-O2	5.89	122.43	118.90
1	A1	3888	G	P-O3'-C3'	5.89	126.77	119.70
1	A1	4266	G	N3-C4-N9	5.88	129.53	126.00
1	A1	4880	C	C6-N1-C2	-5.88	117.95	120.30
2	B1	28	C	N1-C2-O2	5.88	122.42	118.90
1	A1	406	C	P-O3'-C3'	5.87	126.75	119.70
1	A1	2560	C	C2-N1-C1'	5.87	125.25	118.80
1	A1	696	C	P-O3'-C3'	5.86	126.74	119.70
1	A1	2008	U	N3-C2-O2	-5.84	118.11	122.20
17	M2	44	ARG	CG-CD-NE	5.83	124.04	111.80
1	A1	2528	G	C8-N9-C1'	-5.82	119.44	127.00
1	A1	1847	C	C2-N1-C1'	5.81	125.19	118.80
1	A1	134	G	P-O3'-C3'	5.81	126.67	119.70
1	A1	265	C	P-O3'-C3'	5.80	126.66	119.70
1	A1	2502	A	OP1-P-O3'	5.80	117.95	105.20
1	A1	2281	U	N1-C2-O2	5.79	126.86	122.80
1	A1	1247	U	N3-C2-O2	-5.79	118.14	122.20
1	A1	3693	U	N1-C2-O2	5.79	126.85	122.80
1	A1	155	C	N3-C2-O2	-5.79	117.85	121.90
1	A1	1215	C	N1-C2-O2	5.78	122.37	118.90
34	d2	89	LEU	CA-CB-CG	5.78	128.60	115.30
1	A1	112	C	C6-N1-C2	-5.78	117.99	120.30
1	A1	4354	U	C5-C6-N1	5.78	125.59	122.70
1	A1	4948	C	C6-N1-C2	-5.78	117.99	120.30
1	A1	2505	C	C2-N1-C1'	5.76	125.14	118.80
1	A1	2410	C	N1-C2-O2	5.76	122.35	118.90
1	A1	4413	C	O4'-C1'-N1	5.76	112.81	108.20
1	A1	449	C	P-O3'-C3'	5.75	126.60	119.70
1	A1	220	C	C6-N1-C2	-5.74	118.00	120.30
50	t2	92	LEU	CB-CG-CD2	5.73	120.74	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A1	4413	C	C6-N1-C1'	-5.72	113.93	120.80
1	A1	3870	C	C2-N1-C1'	5.72	125.09	118.80
1	A1	1237	C	N1-C2-O2	5.71	122.33	118.90
24	T2	56	LEU	CA-CB-CG	5.71	128.44	115.30
1	A1	1731	C	C2-N1-C1'	5.71	125.08	118.80
1	A1	4170	A	P-O3'-C3'	5.70	126.55	119.70
1	A1	4766	C	C2-N1-C1'	5.70	125.07	118.80
1	A1	4146	G	N3-C4-N9	5.70	129.42	126.00
1	A1	263	G	C4-N9-C1'	5.68	133.88	126.50
1	A1	4612	C	N3-C2-O2	-5.68	117.93	121.90
1	A1	1577	G	N3-C2-N2	-5.67	115.93	119.90
1	A1	4243	C	C6-N1-C2	-5.67	118.03	120.30
1	A1	4752	U	N1-C2-O2	5.66	126.76	122.80
1	A1	4709	U	C2-N1-C1'	5.66	124.49	117.70
1	A1	2803	U	C2-N1-C1'	5.65	124.48	117.70
1	A1	4613	C	N1-C2-O2	5.64	122.29	118.90
1	A1	115	C	N1-C2-O2	5.64	122.28	118.90
1	A1	1485	C	N1-C2-O2	5.64	122.28	118.90
1	A1	2568	C	N3-C2-O2	-5.63	117.96	121.90
1	A1	1483	C	N1-C2-O2	5.63	122.28	118.90
1	A1	2016	C	C6-N1-C2	-5.62	118.05	120.30
1	A1	3693	U	N3-C2-O2	-5.61	118.27	122.20
1	A1	1481	C	N1-C2-O2	5.60	122.26	118.90
1	A1	1477	C	P-O3'-C3'	5.59	126.41	119.70
1	A1	4194	U	N3-C2-O2	-5.59	118.28	122.20
1	A1	2532	C	C2-N1-C1'	5.59	124.95	118.80
1	A1	3622	C	N1-C2-O2	5.59	122.25	118.90
1	A1	282	C	N3-C2-O2	-5.59	117.99	121.90
1	A1	1598	C	N3-C2-O2	-5.59	117.99	121.90
1	A1	202	C	C2-N1-C1'	5.58	124.94	118.80
1	A1	3876	A	OP2-P-O3'	5.57	117.46	105.20
1	A1	4215	C	N1-C2-O2	5.57	122.24	118.90
1	A1	4206	C	C2-N1-C1'	5.56	124.92	118.80
1	A1	217	C	C2-N1-C1'	5.56	124.91	118.80
1	A1	3778	U	N1-C2-O2	5.56	126.69	122.80
1	A1	1514	U	N3-C2-O2	-5.55	118.31	122.20
1	A1	974	C	N1-C2-O2	5.55	122.23	118.90
1	A1	1325	C	N1-C2-O2	5.54	122.23	118.90
1	A1	2856	C	N1-C2-O2	5.54	122.23	118.90
1	A1	2667	C	N1-C2-O2	5.54	122.22	118.90
1	A1	131	C	N1-C2-O2	5.53	122.22	118.90
1	A1	472	C	N3-C2-O2	-5.53	118.03	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	4146	G	C4-N9-C1’	5.53	133.68	126.50
1	A1	1485	C	C2-N1-C1’	5.52	124.88	118.80
1	A1	1929	A	C4-N9-C1’	5.51	136.22	126.30
1	A1	1309	C	C5-C6-N1	5.51	123.75	121.00
1	A1	1639	U	C6-N1-C1’	-5.50	113.49	121.20
2	B1	102	U	N3-C2-O2	-5.50	118.35	122.20
1	A1	1633	G	P-O3’-C3’	5.50	126.30	119.70
1	A1	4958	C	N3-C2-O2	-5.50	118.05	121.90
48	r2	28	LEU	CA-CB-CG	5.50	127.95	115.30
1	A1	3709	U	C2-N1-C1’	5.47	124.27	117.70
1	A1	496	G	N3-C4-N9	5.47	129.28	126.00
1	A1	126	C	C2-N1-C1’	5.47	124.81	118.80
1	A1	704	C	C2-N1-C1’	5.46	124.81	118.80
1	A1	4305	G	C8-N9-C1’	-5.46	119.89	127.00
1	A1	118	C	N1-C2-O2	5.46	122.18	118.90
1	A1	2351	C	C6-N1-C2	-5.46	118.12	120.30
1	A1	978	G	C4-N9-C1’	-5.46	119.41	126.50
1	A1	141	C	C6-N1-C1’	-5.45	114.26	120.80
1	A1	934	C	N1-C2-O2	5.45	122.17	118.90
1	A1	975	C	C6-N1-C2	-5.44	118.12	120.30
1	A1	4869	U	N3-C2-O2	-5.43	118.40	122.20
49	s2	967	LEU	CA-CB-CG	5.43	127.79	115.30
1	A1	1993	C	C6-N1-C2	-5.43	118.13	120.30
1	A1	2705	G	N3-C4-N9	5.42	129.25	126.00
1	A1	3657	U	C2-N1-C1’	5.42	124.21	117.70
1	A1	1514	U	C2-N1-C1’	5.42	124.21	117.70
1	A1	4482	U	N3-C2-O2	-5.42	118.41	122.20
1	A1	1853	G	C4-N9-C1’	5.41	133.53	126.50
1	A1	3739	C	C5-C6-N1	5.41	123.70	121.00
1	A1	4243	C	C2-N1-C1’	5.41	124.75	118.80
1	A1	2470	C	N1-C2-O2	5.40	122.14	118.90
1	A1	1929	A	C2-N3-C4	5.39	113.30	110.60
1	A1	3739	C	C6-N1-C1’	-5.38	114.34	120.80
1	A1	469	C	N1-C2-O2	5.37	122.12	118.90
1	A1	4759	C	C6-N1-C1’	-5.37	114.36	120.80
1	A1	1477	C	C6-N1-C2	-5.37	118.15	120.30
1	A1	4254	G	N3-C4-C5	-5.36	125.92	128.60
2	B1	28	C	C6-N1-C2	-5.33	118.17	120.30
1	A1	4360	U	N3-C2-O2	-5.33	118.47	122.20
1	A1	271	C	C6-N1-C2	-5.33	118.17	120.30
1	A1	4561	C	N1-C2-O2	5.33	122.10	118.90
1	A1	922(B)	C	P-O3’-C3’	5.33	126.09	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	1482	G	O4'-C1'-N9	5.32	112.46	108.20
1	A1	1308	C	C6-N1-C2	-5.32	118.17	120.30
1	A1	1292	C	C2-N1-C1'	5.32	124.65	118.80
1	A1	1726	U	N3-C2-O2	-5.31	118.48	122.20
1	A1	1236	C	C6-N1-C2	-5.31	118.17	120.30
1	A1	3761	C	N1-C2-O2	5.31	122.09	118.90
1	A1	4880	C	C6-N1-C1'	-5.31	114.43	120.80
1	A1	472	C	C2-N1-C1'	5.31	124.64	118.80
1	A1	495	C	C2-N1-C1'	5.31	124.64	118.80
1	A1	1238	A	P-O3'-C3'	5.31	126.07	119.70
1	A1	2627	C	C6-N1-C1'	-5.30	114.44	120.80
50	t2	185	LEU	CA-CB-CG	5.30	127.49	115.30
1	A1	4560	C	N1-C2-O2	5.29	122.08	118.90
1	A1	4752	U	N3-C2-O2	-5.29	118.50	122.20
1	A1	390	C	C6-N1-C2	-5.29	118.19	120.30
1	A1	450	G	O5'-P-OP2	-5.29	100.94	105.70
1	A1	1327	C	C5-C6-N1	5.28	123.64	121.00
1	A1	2704	C	N1-C2-O2	5.28	122.07	118.90
1	A1	5050	C	C2-N1-C1'	5.28	124.60	118.80
1	A1	50	C	N3-C2-O2	-5.27	118.21	121.90
1	A1	1577	G	C2-N3-C4	5.27	114.54	111.90
1	A1	4119	C	P-O3'-C3'	5.27	126.02	119.70
1	A1	3911	C	C5-C6-N1	5.26	123.63	121.00
1	A1	1720	C	N1-C2-O2	5.26	122.06	118.90
1	A1	2860	C	N3-C2-O2	-5.26	118.22	121.90
1	A1	4305	G	N3-C4-C5	-5.26	125.97	128.60
1	A1	30	C	C2-N1-C1'	5.26	124.58	118.80
1	A1	1482	G	C4-N9-C1'	5.25	133.33	126.50
1	A1	4194	U	C2-N1-C1'	5.25	124.00	117.70
2	B1	94	C	N1-C2-O2	5.25	122.05	118.90
1	A1	1628	C	C5-C6-N1	5.25	123.62	121.00
1	A1	4314	C	N3-C2-O2	-5.24	118.23	121.90
3	C1	64	U	N1-C2-O2	5.24	126.47	122.80
1	A1	4601	U	N1-C2-O2	5.23	126.46	122.80
1	A1	275	C	P-O3'-C3'	5.23	125.98	119.70
1	A1	1800	U	N1-C2-O2	5.23	126.46	122.80
1	A1	1792	U	N1-C2-O2	5.23	126.46	122.80
1	A1	2787	A	C2-N3-C4	5.22	113.21	110.60
1	A1	4254	G	C4-N9-C1'	5.22	133.29	126.50
1	A1	1915	C	N1-C2-O2	5.21	122.03	118.90
1	A1	1211	G	P-O3'-C3'	5.21	125.95	119.70
1	A1	4869	U	N1-C2-O2	5.21	126.45	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A1	263	G	N3-C4-N9	5.21	129.12	126.00
1	A1	220	C	C5-C6-N1	5.21	123.60	121.00
2	B1	28	C	N3-C2-O2	-5.21	118.25	121.90
1	A1	4293	U	N3-C2-O2	-5.20	118.56	122.20
1	A1	922(B)	C	OP1-P-O3’	5.19	116.62	105.20
1	A1	2362	U	N3-C2-O2	-5.19	118.57	122.20
1	A1	661	C	C6-N1-C2	-5.18	118.23	120.30
1	A1	4308	C	N1-C2-O2	5.18	122.01	118.90
1	A1	100	C	O4’-C1’-N1	5.18	112.34	108.20
1	A1	112	C	N1-C2-O2	5.18	122.01	118.90
1	A1	2281	U	N3-C2-O2	-5.18	118.58	122.20
1	A1	2705	G	C4-N9-C1’	5.18	133.23	126.50
1	A1	1309	C	C6-N1-C2	-5.17	118.23	120.30
1	A1	1247	U	C2-N1-C1’	5.17	123.90	117.70
1	A1	472	C	C6-N1-C2	-5.17	118.23	120.30
1	A1	2787	A	C4-N9-C1’	5.17	135.60	126.30
1	A1	3739	C	N1-C2-O2	5.17	122.00	118.90
1	A1	126	C	C6-N1-C2	-5.16	118.23	120.30
1	A1	1325	C	N3-C2-O2	-5.16	118.29	121.90
1	A1	3625	G	P-O3’-C3’	5.16	125.89	119.70
1	A1	2627	C	C5-C6-N1	5.15	123.58	121.00
1	A1	4758	U	C6-N1-C1’	-5.15	113.99	121.20
1	A1	504	G	P-O3’-C3’	5.15	125.88	119.70
1	A1	4305	G	C8-N9-C4	-5.15	104.34	106.40
1	A1	112	C	C5-C6-N1	5.14	123.57	121.00
1	A1	3882	C	C2-N1-C1’	5.14	124.46	118.80
1	A1	4303	C	O4’-C1’-N1	5.14	112.31	108.20
1	A1	4171	C	N3-C2-O2	-5.14	118.30	121.90
2	B1	29	C	C5-C6-N1	5.13	123.57	121.00
1	A1	685	C	O5’-P-OP2	-5.13	101.08	105.70
1	A1	2860	C	C6-N1-C2	-5.13	118.25	120.30
1	A1	217	C	N1-C2-O2	5.13	121.98	118.90
1	A1	118	C	C2-N1-C1’	5.12	124.44	118.80
1	A1	263	G	C8-N9-C1’	-5.12	120.34	127.00
1	A1	4162	C	N1-C2-O2	5.12	121.97	118.90
1	A1	4482	U	N1-C2-O2	5.12	126.38	122.80
1	A1	96	U	N3-C2-O2	-5.11	118.62	122.20
1	A1	2410	C	C6-N1-C1’	-5.10	114.67	120.80
1	A1	495	C	C6-N1-C2	-5.10	118.26	120.30
1	A1	916	C	N1-C2-O2	5.10	121.96	118.90
1	A1	4254	G	N3-C4-N9	5.10	129.06	126.00
1	A1	1179	U	C2-N1-C1’	5.10	123.81	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	496	G	N3-C4-C5	-5.09	126.05	128.60
1	A1	4444	C	C2-N1-C1’	5.09	124.40	118.80
1	A1	1792	U	N3-C2-O2	-5.09	118.64	122.20
1	A1	155	C	N1-C2-O2	5.09	121.95	118.90
1	A1	2553	A	O4’-C1’-N9	5.08	112.26	108.20
1	A1	4642	U	N3-C2-O2	-5.08	118.65	122.20
1	A1	1210	C	N3-C2-O2	-5.08	118.35	121.90
1	A1	118	C	C6-N1-C2	-5.07	118.27	120.30
1	A1	4906	C	C2-N1-C1’	5.07	124.38	118.80
1	A1	1088	C	C6-N1-C2	-5.07	118.27	120.30
1	A1	3650	C	C6-N1-C2	-5.06	118.28	120.30
1	A1	125	C	P-O3’-C3’	5.06	125.77	119.70
1	A1	3603	G	P-O3’-C3’	5.05	125.77	119.70
1	A1	4412	C	C2-N1-C1’	5.05	124.36	118.80
1	A1	2502	A	P-O3’-C3’	5.05	125.76	119.70
1	A1	959	G	P-O3’-C3’	5.05	125.76	119.70
1	A1	1484	G	C2-N3-C4	5.04	114.42	111.90
1	A1	2767	U	N3-C2-O2	-5.04	118.67	122.20
1	A1	4243	C	N1-C2-O2	5.04	121.92	118.90
1	A1	4423	U	C6-N1-C1’	-5.04	114.15	121.20
1	A1	5047	C	N1-C2-O2	5.04	121.92	118.90
1	A1	4942	C	C2-N1-C1’	5.03	124.34	118.80
1	A1	4957	C	N1-C2-O2	5.03	121.92	118.90
1	A1	1481	C	C6-N1-C1’	-5.03	114.76	120.80
1	A1	141	C	N1-C2-O2	5.03	121.92	118.90
1	A1	1607	C	N3-C2-O2	-5.03	118.38	121.90
1	A1	4398	C	C6-N1-C2	-5.03	118.29	120.30
1	A1	4560	C	C2-N1-C1’	5.03	124.33	118.80
1	A1	1469	C	C6-N1-C2	-5.03	118.29	120.30
1	A1	390	C	C5-C6-N1	5.03	123.51	121.00
1	A1	4601	U	N3-C2-O2	-5.03	118.68	122.20
1	A1	274	C	C2-N1-C1’	5.03	124.33	118.80
1	A1	2439	G	C4-N9-C1’	5.03	133.03	126.50
1	A1	2362	U	N1-C2-O2	5.02	126.31	122.80
1	A1	4199	C	N3-C2-O2	-5.01	118.39	121.90
1	A1	4206	C	C6-N1-C2	-5.01	118.30	120.30
1	A1	1411(B)	C	N1-C2-O2	5.01	121.91	118.90
1	A1	2726	G	C4-N9-C1’	5.01	133.01	126.50
1	A1	658	C	N3-C2-O2	-5.01	118.39	121.90
1	A1	1777	C	N3-C2-O2	-5.00	118.40	121.90

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	K2	63	THR	Peptide
17	M2	76	PRO	Peptide
17	M2	78	GLY	Peptide
23	S2	80	VAL	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
4	D1	2/29 (7%)	1 (50%)	1 (50%)	0	100	100
5	A2	246/257 (96%)	234 (95%)	12 (5%)	0	100	100
6	B2	392/403 (97%)	384 (98%)	8 (2%)	0	100	100
7	C2	360/425 (85%)	343 (95%)	17 (5%)	0	100	100
8	D2	291/297 (98%)	283 (97%)	8 (3%)	0	100	100
9	E2	208/291 (72%)	201 (97%)	7 (3%)	0	100	100
10	F2	223/247 (90%)	215 (96%)	8 (4%)	0	100	100
11	G2	229/319 (72%)	223 (97%)	6 (3%)	0	100	100
12	H2	188/192 (98%)	181 (96%)	7 (4%)	0	100	100
13	I2	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
14	J2	168/178 (94%)	166 (99%)	2 (1%)	0	100	100
15	K2	208/211 (99%)	197 (95%)	10 (5%)	1 (0%)	29	61
16	L2	136/218 (62%)	131 (96%)	5 (4%)	0	100	100
17	M2	201/204 (98%)	194 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	N2	197/203 (97%)	192 (98%)	5 (2%)	0	100	100
19	O2	151/184 (82%)	149 (99%)	2 (1%)	0	100	100
20	P2	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
21	Q2	153/196 (78%)	148 (97%)	5 (3%)	0	100	100
22	R2	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
23	S2	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
24	T2	100/128 (78%)	96 (96%)	4 (4%)	0	100	100
25	U2	129/140 (92%)	125 (97%)	4 (3%)	0	100	100
26	V2	61/157 (39%)	57 (93%)	4 (7%)	0	100	100
27	W2	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
28	X2	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
29	Y2	133/136 (98%)	125 (94%)	7 (5%)	1 (1%)	19	49
30	Z2	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
31	a2	100/226 (44%)	99 (99%)	1 (1%)	0	100	100
32	b2	96/115 (84%)	96 (100%)	0	0	100	100
33	c2	105/125 (84%)	100 (95%)	5 (5%)	0	100	100
34	d2	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
35	e2	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
36	f2	112/116 (97%)	110 (98%)	2 (2%)	0	100	100
37	g2	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
38	h2	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
39	i2	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
40	j2	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
41	k2	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
42	l2	50/102 (49%)	49 (98%)	1 (2%)	0	100	100
43	m2	23/25 (92%)	23 (100%)	0	0	100	100
44	n2	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
45	o2	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
46	p2	122/137 (89%)	117 (96%)	5 (4%)	0	100	100
47	q2	194/318 (61%)	185 (95%)	9 (5%)	0	100	100
48	r2	151/165 (92%)	133 (88%)	18 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	s2	377/1411 (27%)	368 (98%)	9 (2%)	0	100	100
50	t2	414/489 (85%)	402 (97%)	12 (3%)	0	100	100
51	u2	9/64 (14%)	9 (100%)	0	0	100	100
All	All	7482/9782 (76%)	7227 (97%)	253 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	K2	64	VAL
29	Y2	90	PRO

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	
4	D1	2/2 (100%)	2 (100%)	0	100	100
5	A2	190/199 (96%)	190 (100%)	0	100	100
6	B2	342/348 (98%)	340 (99%)	2 (1%)	86	96
7	C2	302/347 (87%)	301 (100%)	1 (0%)	92	98
8	D2	247/250 (99%)	247 (100%)	0	100	100
9	E2	190/251 (76%)	189 (100%)	1 (0%)	88	96
10	F2	196/215 (91%)	196 (100%)	0	100	100
11	G2	200/272 (74%)	197 (98%)	3 (2%)	65	89
12	H2	169/171 (99%)	169 (100%)	0	100	100
13	I2	175/181 (97%)	175 (100%)	0	100	100
14	J2	143/149 (96%)	143 (100%)	0	100	100
15	K2	175/176 (99%)	175 (100%)	0	100	100
16	L2	117/161 (73%)	116 (99%)	1 (1%)	78	94
17	M2	171/172 (99%)	171 (100%)	0	100	100
18	N2	171/173 (99%)	171 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	O2	134/163 (82%)	134 (100%)	0	100	100
20	P2	164/164 (100%)	162 (99%)	2 (1%)	71	92
21	Q2	138/175 (79%)	138 (100%)	0	100	100
22	R2	157/157 (100%)	157 (100%)	0	100	100
23	S2	139/140 (99%)	139 (100%)	0	100	100
24	T2	92/114 (81%)	92 (100%)	0	100	100
25	U2	101/107 (94%)	101 (100%)	0	100	100
26	V2	55/126 (44%)	55 (100%)	0	100	100
27	W2	106/134 (79%)	105 (99%)	1 (1%)	78	94
28	X2	124/135 (92%)	124 (100%)	0	100	100
29	Y2	117/118 (99%)	117 (100%)	0	100	100
30	Z2	119/120 (99%)	119 (100%)	0	100	100
31	a2	84/172 (49%)	83 (99%)	1 (1%)	71	92
32	b2	84/98 (86%)	84 (100%)	0	100	100
33	c2	98/110 (89%)	98 (100%)	0	100	100
34	d2	114/121 (94%)	114 (100%)	0	100	100
35	e2	88/89 (99%)	88 (100%)	0	100	100
36	f2	98/99 (99%)	98 (100%)	0	100	100
37	g2	109/109 (100%)	109 (100%)	0	100	100
38	h2	86/89 (97%)	86 (100%)	0	100	100
39	i2	73/80 (91%)	72 (99%)	1 (1%)	67	90
40	j2	64/65 (98%)	64 (100%)	0	100	100
41	k2	47/48 (98%)	47 (100%)	0	100	100
42	l2	48/90 (53%)	48 (100%)	0	100	100
43	m2	24/24 (100%)	24 (100%)	0	100	100
44	n2	92/94 (98%)	92 (100%)	0	100	100
45	o2	74/75 (99%)	73 (99%)	1 (1%)	67	90
46	p2	108/121 (89%)	107 (99%)	1 (1%)	78	94
47	q2	164/258 (64%)	164 (100%)	0	100	100
48	r2	126/137 (92%)	125 (99%)	1 (1%)	81	94
49	s2	342/1239 (28%)	342 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	t2	360/416 (86%)	359 (100%)	1 (0%)	92	98
51	u2	8/53 (15%)	8 (100%)	0	100	100
All	All	6527/8307 (79%)	6510 (100%)	17 (0%)	92	98

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	B2	261	ARG
6	B2	297	LYS
7	C2	188	ARG
9	E2	58	ARG
11	G2	142	ARG
11	G2	143	GLN
11	G2	228	ARG
16	L2	79	LYS
20	P2	8	ASN
20	P2	14	ARG
27	W2	152	LYS
31	a2	117	ARG
39	i2	20	ARG
45	o2	4	ARG
46	p2	119	ARG
48	r2	114	ARG
50	t2	266	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
20	P2	8	ASN
22	R2	125	GLN
23	S2	69	GLN
33	c2	28	ASN
49	s2	1218	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A1	3516/4380 (80%)	723 (20%)	45 (1%)
2	B1	119/120 (99%)	11 (9%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C1	149/156 (95%)	28 (18%)	1 (0%)
All	All	3784/4656 (81%)	762 (20%)	46 (1%)

All (762) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A1	12	A
1	A1	13	U
1	A1	17	A
1	A1	25	A
1	A1	30	C
1	A1	35	U
1	A1	39	A
1	A1	42	A
1	A1	56	A
1	A1	58	G
1	A1	59	A
1	A1	64	A
1	A1	65	A
1	A1	73	A
1	A1	84	A
1	A1	91	G
1	A1	104	G
1	A1	108	A
1	A1	109	G
1	A1	110	C
1	A1	119	G
1	A1	126	C
1	A1	134	G
1	A1	135	G
1	A1	136	C
1	A1	141	C
1	A1	142	G
1	A1	146	G
1	A1	157	U
1	A1	159	C
1	A1	172	C
1	A1	177	G
1	A1	182	G
1	A1	200	U
1	A1	201	C
1	A1	202	C

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Mol	Chain	Res	Type
1	A1	209	U
1	A1	210	C
1	A1	216	C
1	A1	217	C
1	A1	219	G
1	A1	224	U
1	A1	233	U
1	A1	234	G
1	A1	246	G
1	A1	265	C
1	A1	266	C
1	A1	267	G
1	A1	271	C
1	A1	276	C
1	A1	278	G
1	A1	280	G
1	A1	297	U
1	A1	306	A
1	A1	309	C
1	A1	315	G
1	A1	316	U
1	A1	322	C
1	A1	334	A
1	A1	340	C
1	A1	350	C
1	A1	363	A
1	A1	387	G
1	A1	407	A
1	A1	410	A
1	A1	412	G
1	A1	413	G
1	A1	440	U
1	A1	449	C
1	A1	450	G
1	A1	452	A
1	A1	453	G
1	A1	454	U
1	A1	455	C
1	A1	467	U
1	A1	468	U
1	A1	481	G
1	A1	481(A)	C

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Mol	Chain	Res	Type
1	A1	482	G
1	A1	483	G
1	A1	486	C
1	A1	492	U
1	A1	493	G
1	A1	495	C
1	A1	496	G
1	A1	497	G
1	A1	498	C
1	A1	499	G
1	A1	505	G
1	A1	506	C
1	A1	510	U
1	A1	644	G
1	A1	647	G
1	A1	658	C
1	A1	659	G
1	A1	661	C
1	A1	666	G
1	A1	669	C
1	A1	670	G
1	A1	672	C
1	A1	685	C
1	A1	686	A
1	A1	687	U
1	A1	688	U
1	A1	696	C
1	A1	697	G
1	A1	704	C
1	A1	705	G
1	A1	708	G
1	A1	731	G
1	A1	738	C
1	A1	738(A)	C
1	A1	739	G
1	A1	746	A
1	A1	747	A
1	A1	749	G
1	A1	756	G
1	A1	758	G
1	A1	913	U
1	A1	914	U

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Mol	Chain	Res	Type
1	A1	917	A
1	A1	918	G
1	A1	923	C
1	A1	925	C
1	A1	926	G
1	A1	929	A
1	A1	932	A
1	A1	933	G
1	A1	934	C
1	A1	935	A
1	A1	935(A)	G
1	A1	936	C
1	A1	938	C
1	A1	939	G
1	A1	943	A
1	A1	944	A
1	A1	945	U
1	A1	956	A
1	A1	959	G
1	A1	960	A
1	A1	961	G
1	A1	964	A
1	A1	965	G
1	A1	966	A
1	A1	967	C
1	A1	968	C
1	A1	969	C
1	A1	972	C
1	A1	979	C
1	A1	983	C
1	A1	990	C
1	A1	1072	C
1	A1	1073	G
1	A1	1078	A
1	A1	1081	C
1	A1	1082	C
1	A1	1175	A
1	A1	1179	U
1	A1	1198	G
1	A1	1210	C
1	A1	1211	G
1	A1	1212	G

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Mol	Chain	Res	Type
1	A1	1215	C
1	A1	1234	G
1	A1	1235	G
1	A1	1236	C
1	A1	1237	C
1	A1	1238	A
1	A1	1239	C
1	A1	1272	C
1	A1	1273	G
1	A1	1274	A
1	A1	1275	G
1	A1	1277	G
1	A1	1284	G
1	A1	1287	G
1	A1	1292	C
1	A1	1293	G
1	A1	1296	G
1	A1	1301	C
1	A1	1303	A
1	A1	1304	C
1	A1	1313	C
1	A1	1326	A
1	A1	1330	A
1	A1	1337	A
1	A1	1354	A
1	A1	1358	G
1	A1	1359	G
1	A1	1371	A
1	A1	1377	G
1	A1	1379	C
1	A1	1387	A
1	A1	1394	G
1	A1	1397	A
1	A1	1398	A
1	A1	1419	G
1	A1	1420	A
1	A1	1421	G
1	A1	1433	A
1	A1	1435	G
1	A1	1436	C
1	A1	1437	C
1	A1	1438	U

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Mol	Chain	Res	Type
1	A1	1440	U
1	A1	1441	C
1	A1	1445	U
1	A1	1446	C
1	A1	1448	G
1	A1	1456	C
1	A1	1457	G
1	A1	1475	G
1	A1	1478	C
1	A1	1482	G
1	A1	1483	C
1	A1	1484	G
1	A1	1489	G
1	A1	1493	G
1	A1	1497	A
1	A1	1498	G
1	A1	1502	G
1	A1	1514	U
1	A1	1516	G
1	A1	1523	A
1	A1	1534	A
1	A1	1547	A
1	A1	1563	A
1	A1	1564	A
1	A1	1566	C
1	A1	1578	U
1	A1	1591	U
1	A1	1596	U
1	A1	1597	G
1	A1	1602	U
1	A1	1612	G
1	A1	1613	A
1	A1	1624	G
1	A1	1625	G
1	A1	1631	A
1	A1	1633	G
1	A1	1634	A
1	A1	1638	A
1	A1	1640	C
1	A1	1641	G
1	A1	1650	A
1	A1	1654	G

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Mol	Chain	Res	Type
1	A1	1661	C
1	A1	1676	C
1	A1	1677	U
1	A1	1731	C
1	A1	1734	G
1	A1	1741	G
1	A1	1742	A
1	A1	1750	G
1	A1	1756	U
1	A1	1761	G
1	A1	1764	G
1	A1	1767	A
1	A1	1769	G
1	A1	1772	C
1	A1	1775	A
1	A1	1780	A
1	A1	1781	U
1	A1	1787	A
1	A1	1797	G
1	A1	1799	G
1	A1	1803	G
1	A1	1804	A
1	A1	1806	G
1	A1	1809	C
1	A1	1815	G
1	A1	1818	G
1	A1	1819	G
1	A1	1821	G
1	A1	1822	U
1	A1	1828	C
1	A1	1835	G
1	A1	1836	G
1	A1	1837	A
1	A1	1842	G
1	A1	1843	A
1	A1	1855	G
1	A1	1869	G
1	A1	1882	U
1	A1	1889	U
1	A1	1890	G
1	A1	1892	A
1	A1	1893	C

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Mol	Chain	Res	Type
1	A1	1897	A
1	A1	1898	C
1	A1	1910	G
1	A1	1918	U
1	A1	1920	C
1	A1	1921	C
1	A1	1922	G
1	A1	1930	U
1	A1	1931	C
1	A1	1932	A
1	A1	1935	C
1	A1	1938	C
1	A1	1945	G
1	A1	1957	U
1	A1	1958	A
1	A1	1960	A
1	A1	1961	G
1	A1	1962	A
1	A1	1964	A
1	A1	1965	G
1	A1	1967	A
1	A1	1971	U
1	A1	1974	U
1	A1	1975	G
1	A1	1976	G
1	A1	1977	C
1	A1	1978	C
1	A1	1979	A
1	A1	1980	U
1	A1	1984	A
1	A1	1985	G
1	A1	1987	C
1	A1	1988	G
1	A1	1991	A
1	A1	1992	U
1	A1	1997	U
1	A1	1999	A
1	A1	2001	G
1	A1	2002	A
1	A1	2003	G
1	A1	2004	U
1	A1	2011	C

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Mol	Chain	Res	Type
1	A1	2015	U
1	A1	2018	C
1	A1	2020	U
1	A1	2022	C
1	A1	2026	A
1	A1	2034	G
1	A1	2044	U
1	A1	2046	G
1	A1	2047	A
1	A1	2048	U
1	A1	2052	G
1	A1	2055	G
1	A1	2056	G
1	A1	2062	C
1	A1	2064	G
1	A1	2069	A
1	A1	2071	A
1	A1	2084	U
1	A1	2090	U
1	A1	2092	G
1	A1	2093	G
1	A1	2094	C
1	A1	2095	A
1	A1	2097	A
1	A1	2098	G
1	A1	2099	C
1	A1	2100	G
1	A1	2101	A
1	A1	2102	G
1	A1	2104	A
1	A1	2105	A
1	A1	2106	G
1	A1	2107	A
1	A1	2108	G
1	A1	2110	G
1	A1	2259	G
1	A1	2260	C
1	A1	2267	U
1	A1	2268	A
1	A1	2275	G
1	A1	2289	C
1	A1	2299	G

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Mol	Chain	Res	Type
1	A1	2300	A
1	A1	2301	G
1	A1	2306	G
1	A1	2313	A
1	A1	2314	G
1	A1	2316	G
1	A1	2333	G
1	A1	2348	G
1	A1	2351	C
1	A1	2360	A
1	A1	2395	A
1	A1	2396	A
1	A1	2398	U
1	A1	2417	A
1	A1	2422	C
1	A1	2424	G
1	A1	2425	U
1	A1	2433	G
1	A1	2441	C
1	A1	2450	G
1	A1	2453	A
1	A1	2475	G
1	A1	2487	G
1	A1	2488	C
1	A1	2489	C
1	A1	2490	U
1	A1	2491	C
1	A1	2492	C
1	A1	2503	G
1	A1	2504	C
1	A1	2505	C
1	A1	2506	G
1	A1	2512	A
1	A1	2513	A
1	A1	2514	G
1	A1	2529	A
1	A1	2530	U
1	A1	2537	A
1	A1	2546	G
1	A1	2547	G
1	A1	2553	A
1	A1	2554	U

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Mol	Chain	Res	Type
1	A1	2566	G
1	A1	2568	C
1	A1	2575	U
1	A1	2583	C
1	A1	2586	G
1	A1	2587	A
1	A1	2589	C
1	A1	2602	G
1	A1	2618	G
1	A1	2619	G
1	A1	2620	G
1	A1	2627	C
1	A1	2638	G
1	A1	2653	C
1	A1	2662	G
1	A1	2663	G
1	A1	2669	C
1	A1	2670	C
1	A1	2676	A
1	A1	2686	G
1	A1	2687	U
1	A1	2694	G
1	A1	2695	A
1	A1	2696	A
1	A1	2707	U
1	A1	2708	U
1	A1	2709	C
1	A1	2710	C
1	A1	2711	G
1	A1	2714	G
1	A1	2721	G
1	A1	2725	A
1	A1	2726	G
1	A1	2740	U
1	A1	2743	A
1	A1	2744	A
1	A1	2754	G
1	A1	2760	G
1	A1	2763	U
1	A1	2764	A
1	A1	2769	U
1	A1	2772	C

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Mol	Chain	Res	Type
1	A1	2787	A
1	A1	2788	U
1	A1	2790	U
1	A1	2794	C
1	A1	2798	A
1	A1	2803	U
1	A1	2806	A
1	A1	2807	A
1	A1	2814	C
1	A1	2826	U
1	A1	2827	G
1	A1	2828	U
1	A1	2842	G
1	A1	2855	G
1	A1	2867	C
1	A1	2875	C
1	A1	2884	G
1	A1	3598	C
1	A1	3604	A
1	A1	3605	C
1	A1	3615	G
1	A1	3625	G
1	A1	3626	G
1	A1	3635	A
1	A1	3646	A
1	A1	3648	A
1	A1	3657	U
1	A1	3662	A
1	A1	3664	G
1	A1	3672	G
1	A1	3673	C
1	A1	3680	U
1	A1	3696	C
1	A1	3711	A
1	A1	3729	U
1	A1	3740	G
1	A1	3748	A
1	A1	3753	G
1	A1	3760	A
1	A1	3767	C
1	A1	3773	U
1	A1	3776	G

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Mol	Chain	Res	Type
1	A1	3777	G
1	A1	3784	A
1	A1	3786	U
1	A1	3791	C
1	A1	3810	C
1	A1	3811	G
1	A1	3812	C
1	A1	3814	U
1	A1	3817	A
1	A1	3819	G
1	A1	3838	U
1	A1	3839	G
1	A1	3840	U
1	A1	3851	U
1	A1	3876	A
1	A1	3877	A
1	A1	3878	C
1	A1	3879	G
1	A1	3889	G
1	A1	3892	U
1	A1	3897	G
1	A1	3898	G
1	A1	3901	A
1	A1	3905	A
1	A1	3906	A
1	A1	3907	G
1	A1	3908	A
1	A1	3915	U
1	A1	3916	G
1	A1	3917	A
1	A1	3938	G
1	A1	3939	G
1	A1	3943	A
1	A1	3946	G
1	A1	4066	U
1	A1	4069	U
1	A1	4073	A
1	A1	4076	G
1	A1	4084	G
1	A1	4086	G
1	A1	4088	C
1	A1	4109	G

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Mol	Chain	Res	Type
1	A1	4116	C
1	A1	4118	U
1	A1	4119	C
1	A1	4120	U
1	A1	4121	G
1	A1	4122	G
1	A1	4127	A
1	A1	4136	G
1	A1	4158	C
1	A1	4162	C
1	A1	4163	U
1	A1	4166	G
1	A1	4170	A
1	A1	4171	C
1	A1	4183	G
1	A1	4184	G
1	A1	4191	G
1	A1	4203	A
1	A1	4212	A
1	A1	4225	G
1	A1	4228	G
1	A1	4229	U
1	A1	4233	A
1	A1	4251	A
1	A1	4254	G
1	A1	4255	A
1	A1	4257	A
1	A1	4265	U
1	A1	4266	G
1	A1	4268	A
1	A1	4271	A
1	A1	4273	A
1	A1	4281	A
1	A1	4282	A
1	A1	4291	G
1	A1	4296	U
1	A1	4297	G
1	A1	4304	A
1	A1	4305	G
1	A1	4306	U
1	A1	4314	C
1	A1	4317	A

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Mol	Chain	Res	Type
1	A1	4318	C
1	A1	4319	C
1	A1	4326	G
1	A1	4329	G
1	A1	4330	G
1	A1	4332	C
1	A1	4349	C
1	A1	4350	C
1	A1	4354	U
1	A1	4355	G
1	A1	4373	G
1	A1	4377	G
1	A1	4378	A
1	A1	4380	A
1	A1	4387	C
1	A1	4391	G
1	A1	4393	G
1	A1	4394	A
1	A1	4395	U
1	A1	4396	A
1	A1	4398	C
1	A1	4401	G
1	A1	4411	G
1	A1	4419	U
1	A1	4421	C
1	A1	4422	A
1	A1	4437	U
1	A1	4444	C
1	A1	4448	G
1	A1	4449	A
1	A1	4464	A
1	A1	4466	C
1	A1	4471	U
1	A1	4472	G
1	A1	4475	G
1	A1	4488	A
1	A1	4500	U
1	A1	4510	A
1	A1	4512	U
1	A1	4513	A
1	A1	4515	G
1	A1	4518	A

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Mol	Chain	Res	Type
1	A1	4519	C
1	A1	4522	G
1	A1	4524	G
1	A1	4548	A
1	A1	4549	G
1	A1	4560	C
1	A1	4567	G
1	A1	4570	G
1	A1	4573	G
1	A1	4574	U
1	A1	4575	G
1	A1	4587	G
1	A1	4590	A
1	A1	4635	A
1	A1	4636	U
1	A1	4637	G
1	A1	4639	G
1	A1	4652	G
1	A1	4656	A
1	A1	4657	U
1	A1	4670	C
1	A1	4672	A
1	A1	4677	U
1	A1	4687	A
1	A1	4700	A
1	A1	4709	U
1	A1	4720	C
1	A1	4736	C
1	A1	4744	A
1	A1	4745	G
1	A1	4751	G
1	A1	4752	U
1	A1	4754	G
1	A1	4757	C
1	A1	4759	C
1	A1	4761	G
1	A1	4764	A
1	A1	4765	G
1	A1	4771	C
1	A1	4772	C
1	A1	4776	G
1	A1	4868	G

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Mol	Chain	Res	Type
1	A1	4870	G
1	A1	4871	C
1	A1	4875	G
1	A1	4882	U
1	A1	4883	C
1	A1	4885	U
1	A1	4895	C
1	A1	4897	G
1	A1	4903	G
1	A1	4910	A
1	A1	4912	G
1	A1	4913	G
1	A1	4919	G
1	A1	4921	C
1	A1	4922	C
1	A1	4924	C
1	A1	4925	U
1	A1	4927	G
1	A1	4928	C
1	A1	4931	G
1	A1	4937	C
1	A1	4938	A
1	A1	4940	C
1	A1	4943	A
1	A1	4944	C
1	A1	4948	C
1	A1	4949	G
1	A1	4950	U
1	A1	4951	G
1	A1	4956	A
1	A1	4957	C
1	A1	4958	C
1	A1	4960	G
1	A1	4963	G
1	A1	4964	C
1	A1	4965	U
1	A1	4966	A
1	A1	4967	A
1	A1	4976	U
1	A1	4985	U
1	A1	4988	U
1	A1	4989	U

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Mol	Chain	Res	Type
1	A1	4990	C
1	A1	4993	G
1	A1	5006	U
1	A1	5007	A
1	A1	5014	A
1	A1	5017	G
1	A1	5022	U
1	A1	5041	G
1	A1	5047	C
1	A1	5050	C
1	A1	5053	U
1	A1	5054	C
1	A1	5056	A
1	A1	5061	A
1	A1	5062	G
2	B1	7	G
2	B1	22	A
2	B1	25	G
2	B1	53	U
2	B1	54	A
2	B1	64	G
2	B1	97	G
2	B1	100	A
2	B1	110	G
2	B1	111	C
2	B1	120	U
3	C1	2	G
3	C1	13	G
3	C1	23	C
3	C1	34	U
3	C1	35	C
3	C1	38	U
3	C1	59	A
3	C1	62	A
3	C1	63	U
3	C1	75	G
3	C1	79	G
3	C1	86	U
3	C1	87	G
3	C1	94	G
3	C1	103	A
3	C1	105	C

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Mol	Chain	Res	Type
3	C1	106	G
3	C1	110	U
3	C1	111	U
3	C1	113	C
3	C1	114	G
3	C1	123	U
3	C1	124	U
3	C1	125	C
3	C1	126	C
3	C1	127	U
3	C1	128	C
3	C1	156	U

All (46) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A1	125	C
1	A1	134	G
1	A1	245	C
1	A1	265	C
1	A1	275	C
1	A1	406	C
1	A1	449	C
1	A1	480	C
1	A1	485	C
1	A1	504	G
1	A1	684	G
1	A1	685	C
1	A1	696	C
1	A1	959	G
1	A1	971(A)	G
1	A1	1072	C
1	A1	1174	G
1	A1	1211	G
1	A1	1236	C
1	A1	1238	A
1	A1	1329	G
1	A1	1370	G
1	A1	1440	U
1	A1	1445	U
1	A1	1455	G
1	A1	1477	C

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Mol	Chain	Res	Type
1	A1	1633	G
1	A1	2046	G
1	A1	2089	G
1	A1	2266	C
1	A1	2502	A
1	A1	2546	G
1	A1	2695	A
1	A1	3603	G
1	A1	3625	G
1	A1	3876	A
1	A1	3888	G
1	A1	4119	C
1	A1	4170	A
1	A1	4232	U
1	A1	4448	G
1	A1	4699	U
1	A1	4719	G
1	A1	4884	G
1	A1	4989	U
3	C1	124	U

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 219 ligands modelled in this entry, 219 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A1	19

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	1252:C	O3'	1271:G	P	37.11
1	A1	1219:G	O3'	1233:G	P	19.96
1	A1	990:C	O3'	1064:G	P	18.26
1	A1	523:C	O3'	638:G	P	16.85
1	A1	1406(C):G	O3'	1411:C	P	16.23
1	A1	760:G	O3'	904:C	P	14.91
1	A1	1364:U	O3'	1368:A	P	14.23
1	A1	182:G	O3'	189:G	P	12.21
1	A1	1180:C	O3'	1183:C	P	9.84
1	A1	4729:A	O3'	4735:G	P	8.98
1	A1	1100:U	O3'	1168:G	P	7.94
1	A1	512:U	O3'	515:C	P	6.73
1	A1	500:G	O3'	504:G	P	6.06
1	A1	170:C	O3'	171:U	P	5.80
1	A1	1239:C	O3'	1244:G	P	5.07
1	A1	4740:G	O3'	4743:G	P	4.74
1	A1	751:G	O3'	752:G	P	3.37
1	A1	4899:G	O3'	4902:C	P	3.32
1	A1	5020:G	O3'	5021:C	P	3.29

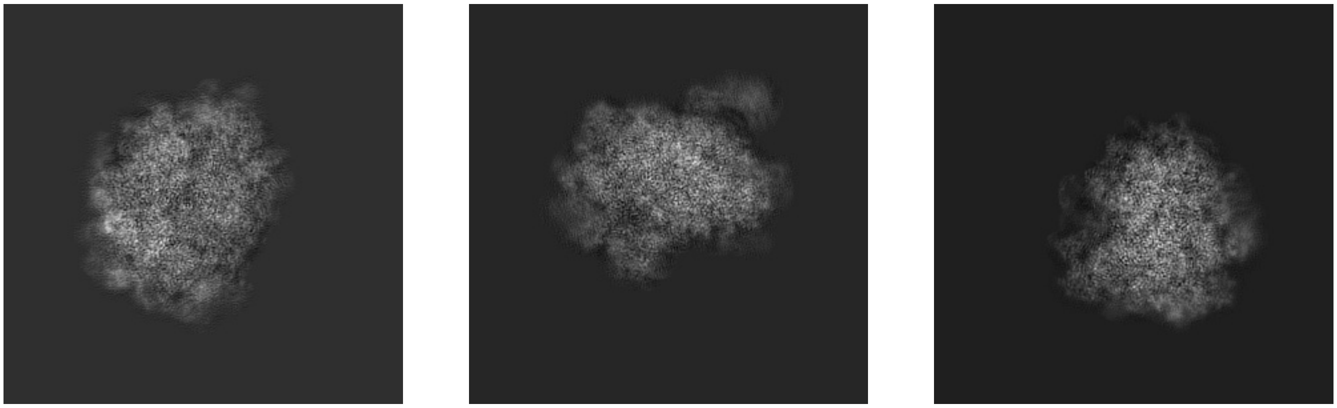
6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-16155. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

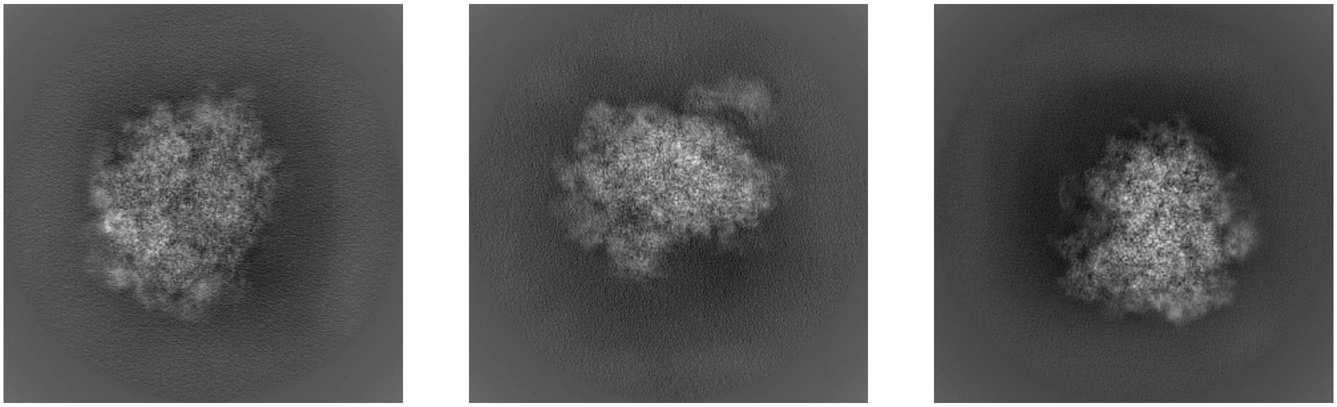
6.1 Orthogonal projections ⓘ

6.1.1 Primary map



X Y Z

6.1.2 Raw map



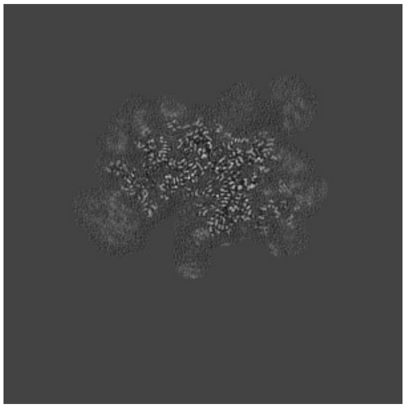
X Y Z

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

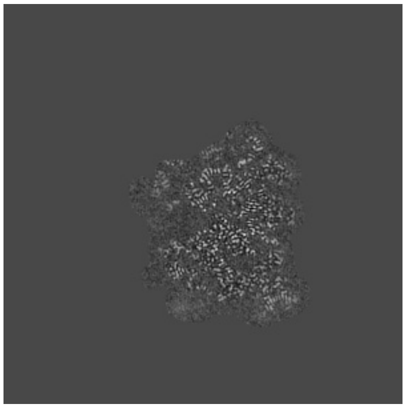
6.2 Central slices

6.2.1 Primary map

X Index: 260

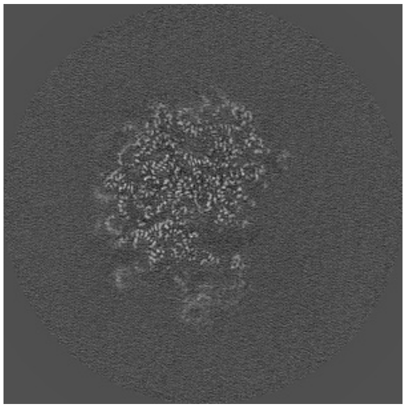


Y Index: 260

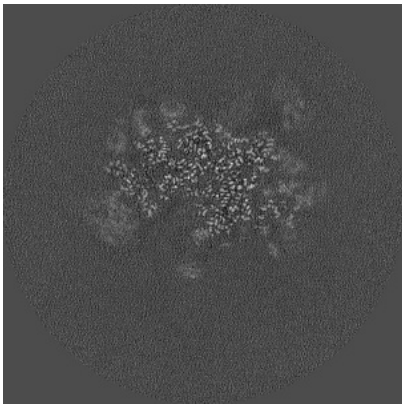


Z Index: 260

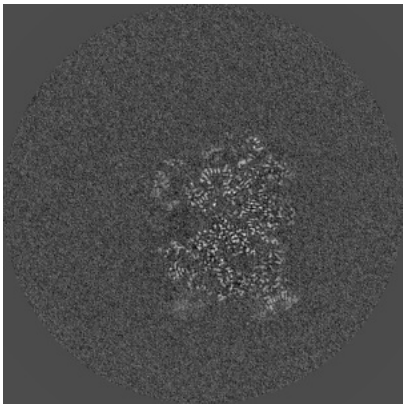
6.2.2 Raw map



X Index: 260



Y Index: 260

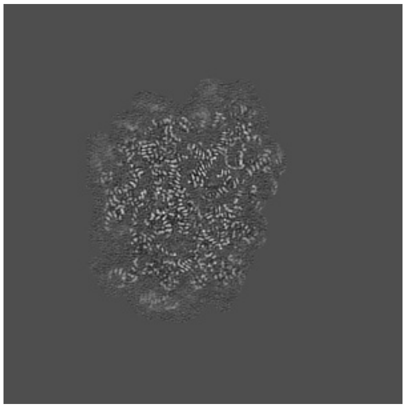


Z Index: 260

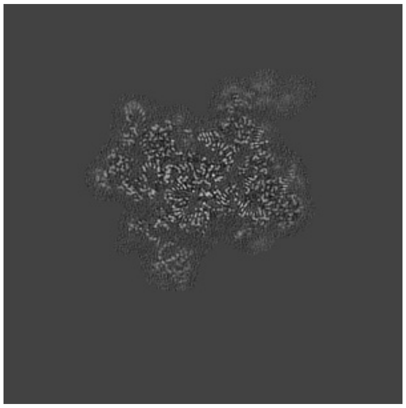
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

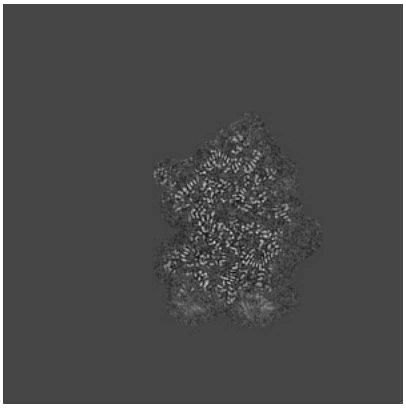
6.3.1 Primary map



X Index: 282

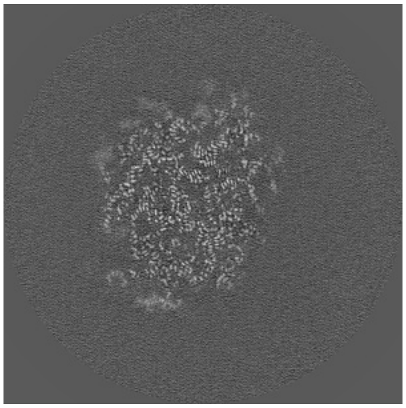


Y Index: 210

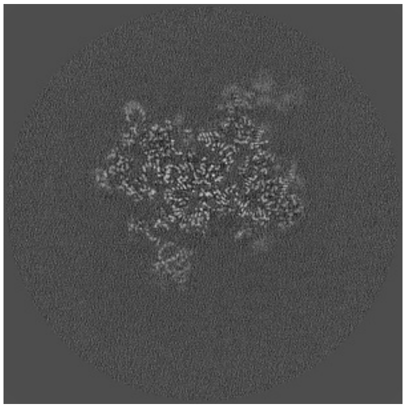


Z Index: 275

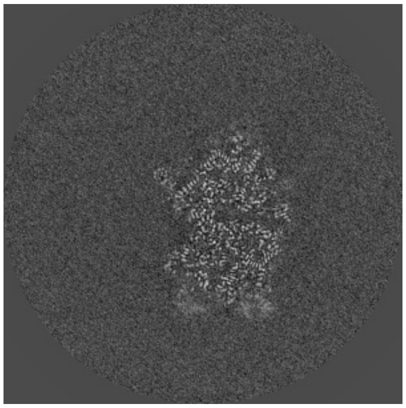
6.3.2 Raw map



X Index: 285



Y Index: 210

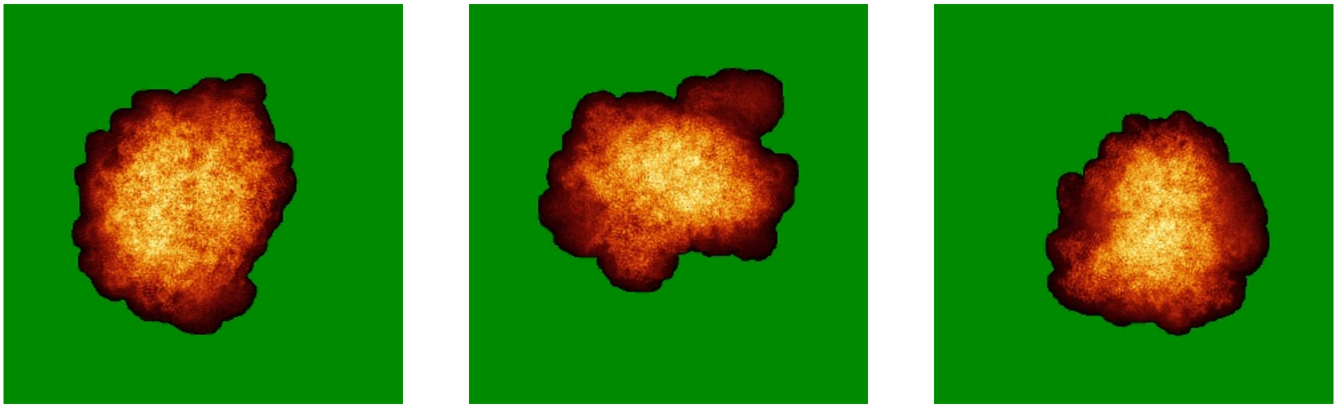


Z Index: 275

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

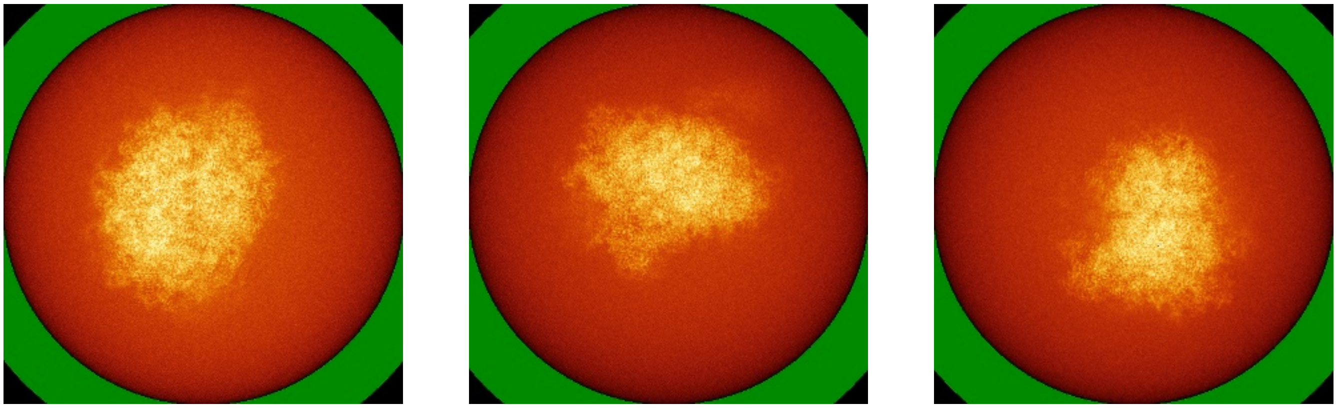
6.4 Orthogonal standard-deviation projections (False-color)

6.4.1 Primary map



X Y Z

6.4.2 Raw map



X Y Z

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

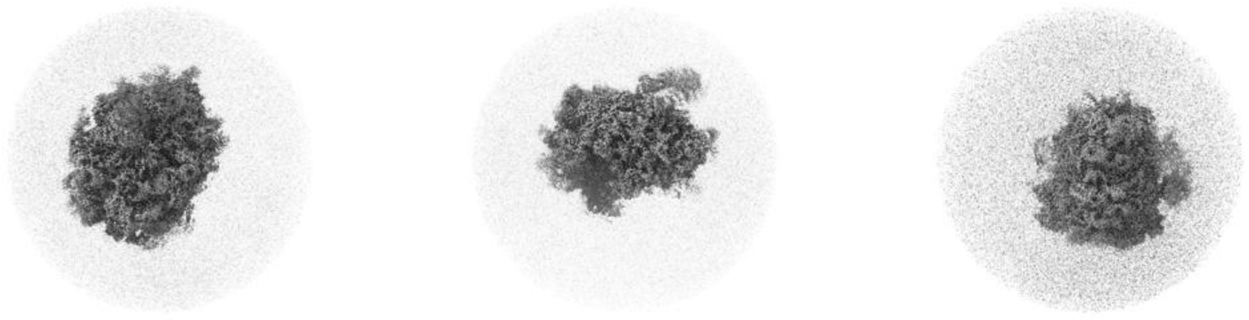
6.5 Orthogonal surface views ⓘ

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

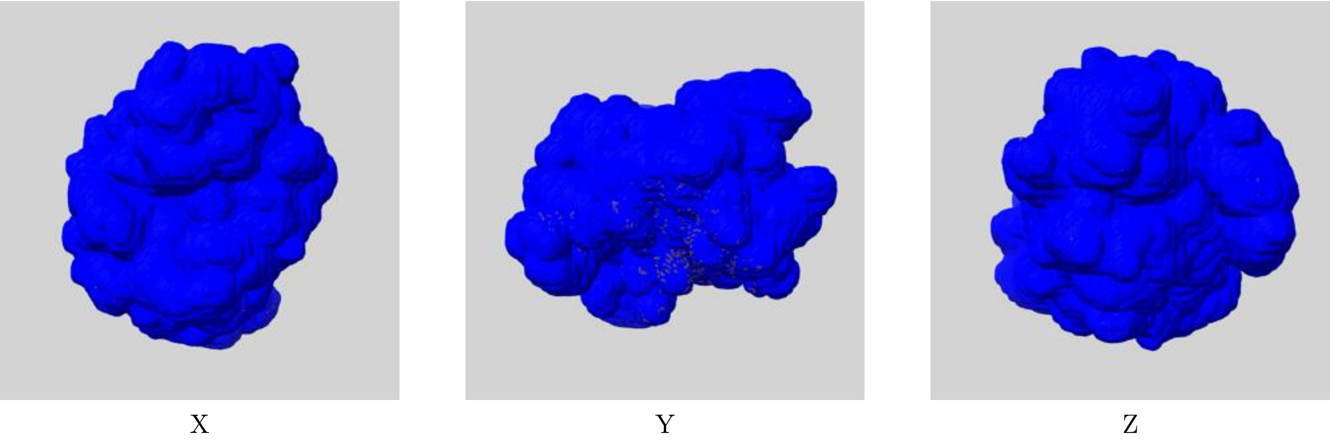
6.6 Mask visualisation ⓘ

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

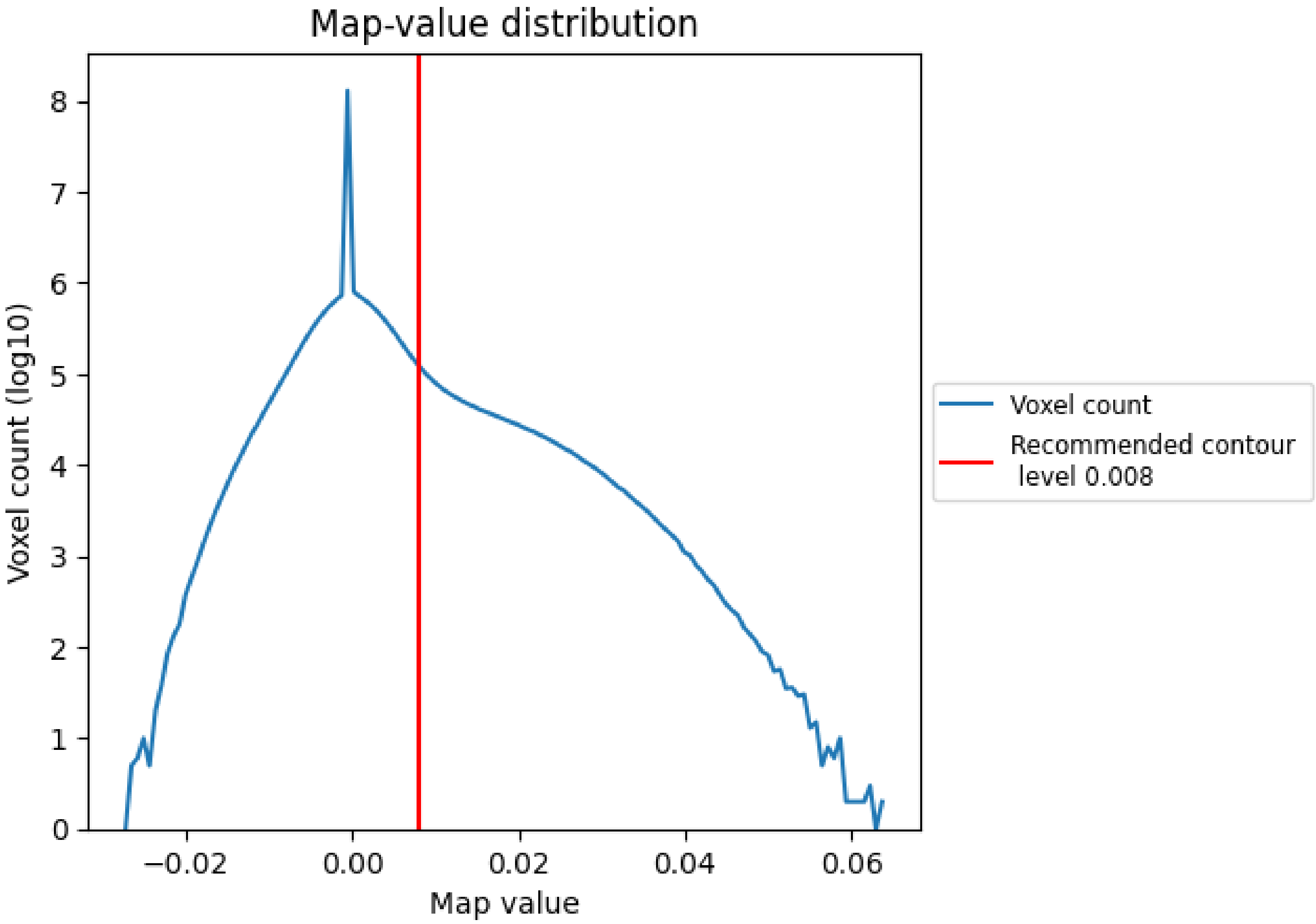
6.6.1 emd_16155_msk_1.map ⓘ



7 Map analysis ⓘ

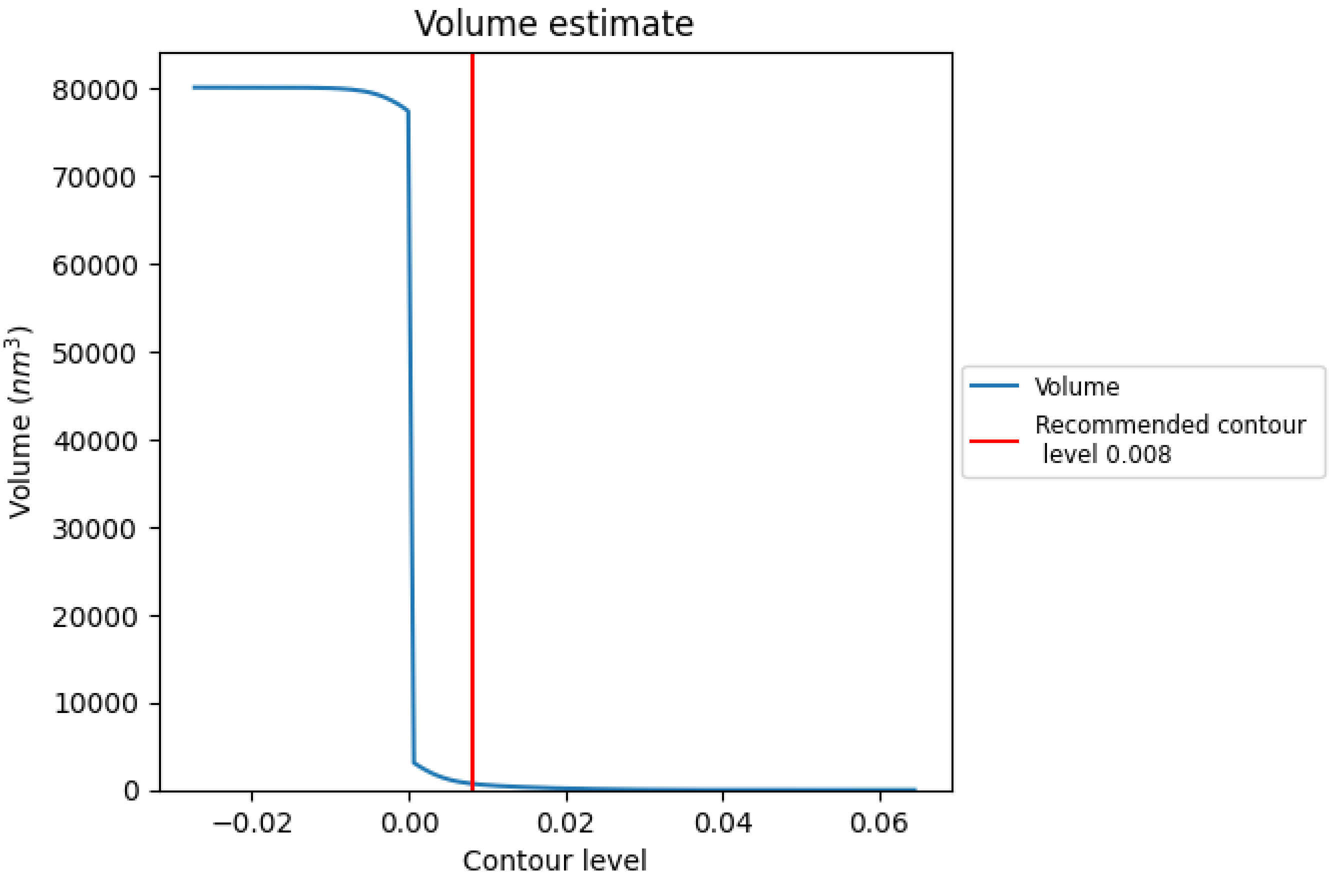
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

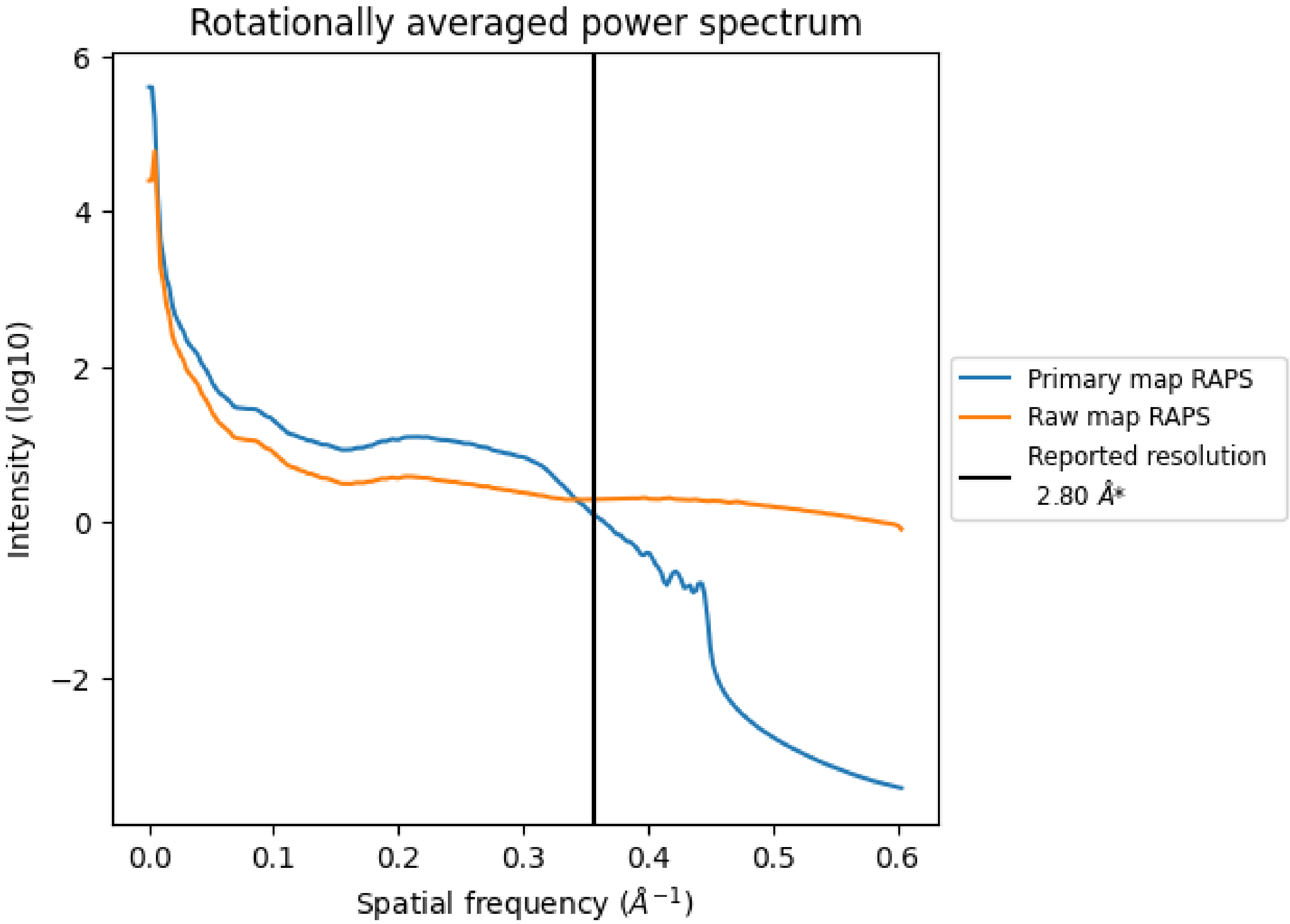
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 717 nm^3; this corresponds to an approximate mass of 648 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 ⓘ

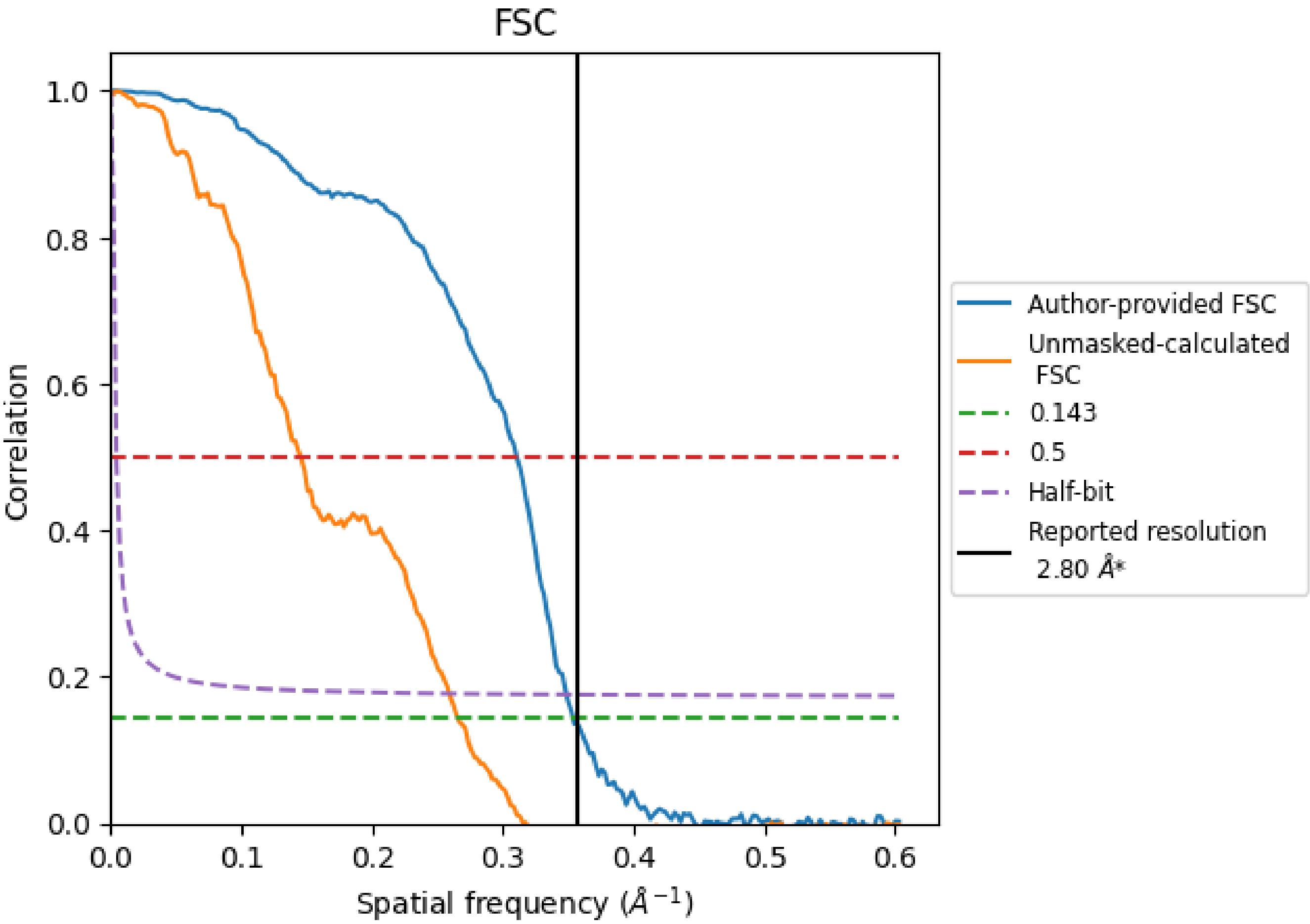


*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

8 Fourier-Shell correlation ⓘ

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC ⓘ



*Reported resolution corresponds to spatial frequency of 0.357 $Å^{-1}$

8.2 Resolution estimates ⓘ

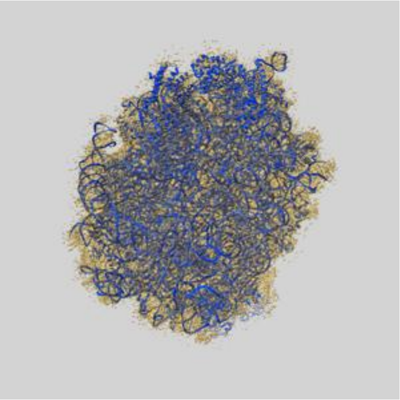
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.83	3.22	2.87
Unmasked-calculated*	3.76	6.87	3.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.76 differs from the reported value 2.8 by more than 10 %

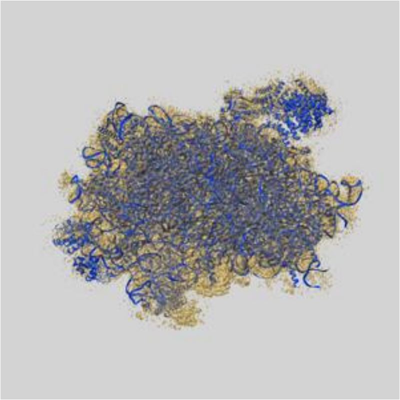
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-16155 and PDB model 8BPO. Per-residue inclusion information can be found in section 3 on page 16.

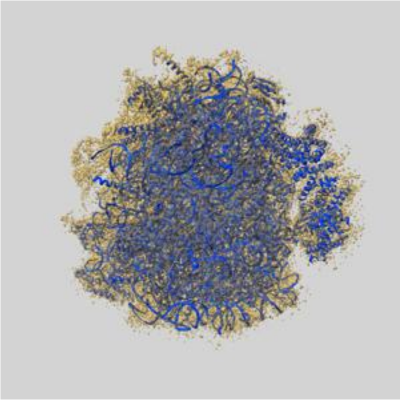
9.1 Map-model overlay ⓘ



X



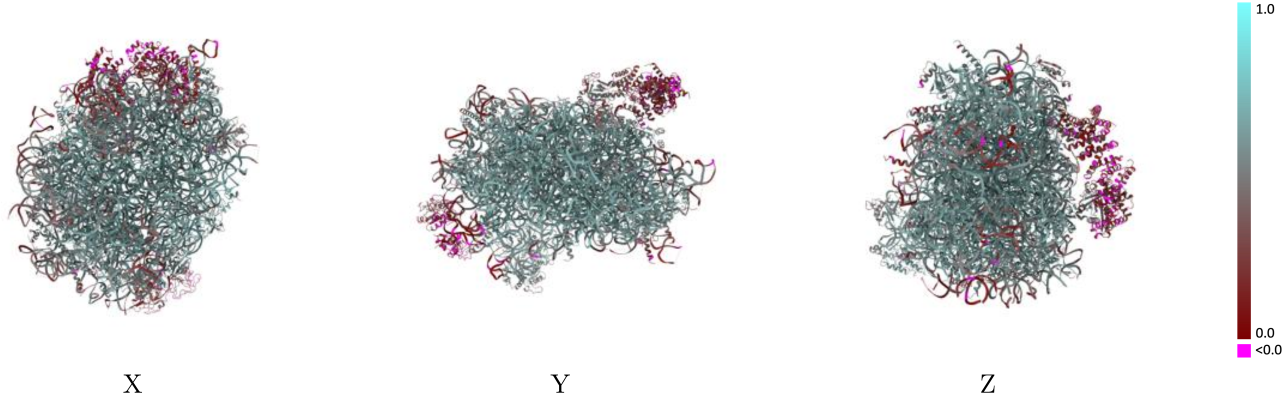
Y



Z

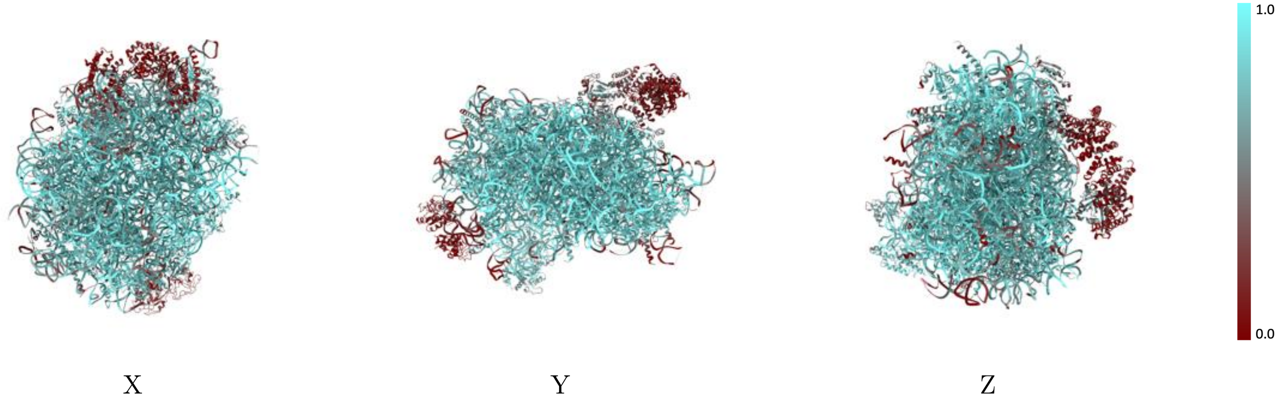
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model ⓘ



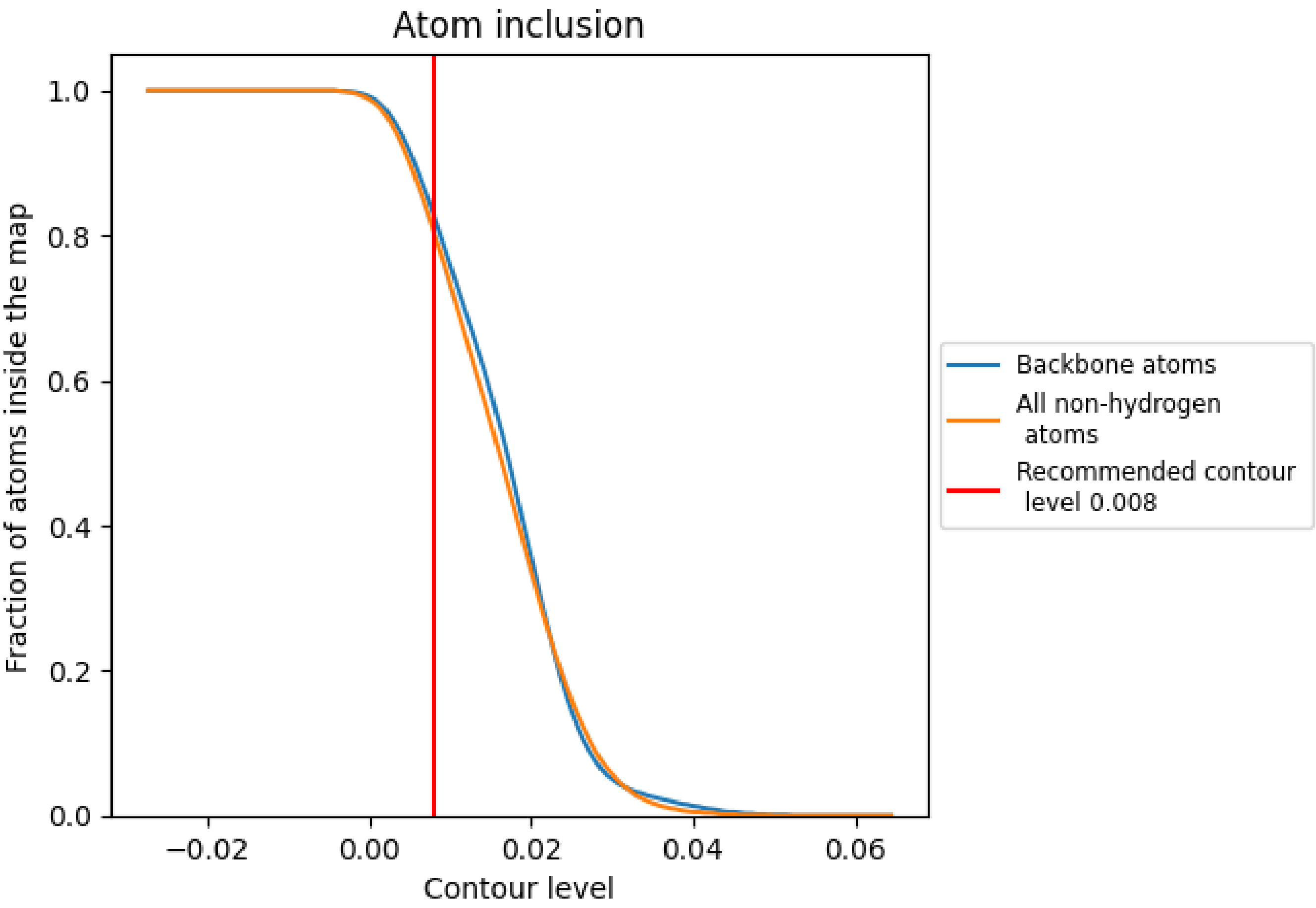
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model ⓘ



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 (0.008).

9.4 Atom inclusion ⓘ



At the recommended contour level, 83% of all backbone atoms, 80% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8040	0.5490
A1	0.8560	0.5610
A2	0.8830	0.6230
B1	0.9580	0.6180
B2	0.8650	0.6080
C1	0.8970	0.5890
C2	0.8700	0.6000
D1	0.3130	0.3710
D2	0.8190	0.5710
E2	0.7860	0.5580
F2	0.8760	0.6160
G2	0.7120	0.5270
H2	0.7650	0.5660
I2	0.8470	0.6040
J2	0.6960	0.5040
K2	0.8050	0.5680
L2	0.8270	0.5780
M2	0.9070	0.6300
N2	0.8680	0.6050
O2	0.8660	0.6140
P2	0.8900	0.6180
Q2	0.8310	0.5890
R2	0.8740	0.6070
S2	0.8140	0.5760
T2	0.5580	0.4390
U2	0.8390	0.6030
V2	0.8070	0.6030
W2	0.7950	0.5720
X2	0.8150	0.5800
Y2	0.8100	0.5680
Z2	0.9110	0.6270
a2	0.6750	0.5250
b2	0.7660	0.5320
c2	0.8060	0.5720
d2	0.8850	0.6240

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Chain	Atom inclusion	Q-score
e2	0.8970	0.6220
f2	0.8260	0.5860
g2	0.7890	0.5720
h2	0.7650	0.5490
i2	0.9140	0.6270
j2	0.6500	0.5190
k2	0.8150	0.5820
l2	0.8150	0.5860
m2	0.6240	0.4990
n2	0.8150	0.5990
o2	0.8100	0.5920
p2	0.8740	0.5970
q2	0.1120	0.1880
r2	0.0370	0.1160
s2	0.1280	0.1880
t2	0.3250	0.2750
u2	0.2370	0.2500