



Full wwPDB EM Validation Report ⓘ

Apr 1, 2025 – 09:23 pm BST

PDB ID : 7O9M / pdb_00007o9m
EMDB ID : EMD-12764
Title : Human mitochondrial ribosome large subunit assembly intermediate with MTERF4-NSUN4, MRM2, MTG1 and the MALSU module
Authors : Valentin Gese, G.; Hallberg, B.M.
Deposited on : 2021-04-16
Resolution : 2.60 Å(reported)
Based on initial model : 5OOL

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

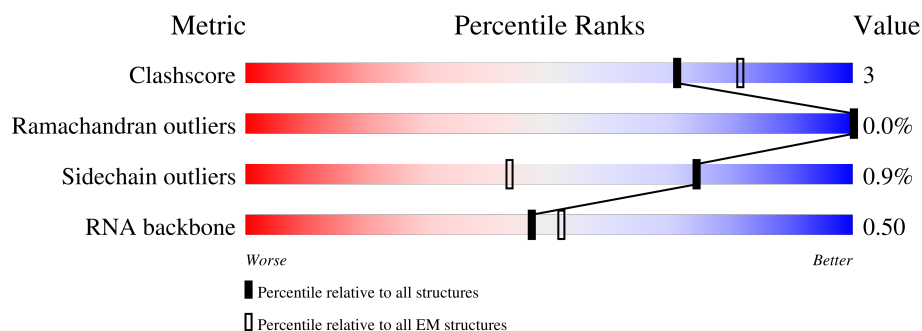
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1559	
2	B	69	
3	C	333	
4	D	305	
5	E	348	
6	F	311	
7	H	267	

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Mol	Chain	Length	Quality of chain
8	I	261	
9	J	192	
10	K	178	
11	L	145	
12	M	296	
13	N	251	
14	O	175	
15	P	179	
16	Q	292	
17	R	149	
18	S	205	
19	T	212	
20	U	153	
21	V	216	
22	W	148	
23	X	256	
24	Y	250	
25	Z	161	
26	a	142	
27	0	188	
28	1	65	
29	2	92	
30	3	188	
31	4	103	
32	5	423	

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Mol	Chain	Length	Quality of chain
33	6	380	
34	7	338	
35	8	206	
36	9	137	
37	b	215	
38	c	332	
39	d	302	
40	e	279	
41	f	212	
42	g	166	
43	h	158	
44	i	128	
45	j	123	
46	k	112	
47	l	138	
48	m	128	
49	o	102	
50	p	205	
51	q	222	
52	r	196	
53	s	439	
54	n	246	
55	A1	384	
56	A2	381	
57	v	70	

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Mol	Chain	Length	Quality of chain
58	u	234	
59	t1	198	
59	t2	198	
59	t3	198	
59	t4	198	
59	t5	198	
59	t6	198	
60	w	156	
61	UNK	26	

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 110342 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1454	Total	C	N	O	P	0	0
			30864	13851	5568	9991	1454		

- Molecule 2 is a RNA chain called MT-TRNAVAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	60	Total	C	N	O	P	0	0
			1275	572	230	413	60		

- Molecule 3 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	240	Total	C	N	O	S	0	0
			1878	1195	330	342	11		

- Molecule 4 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	238	Total	C	N	O	S	0	0
			1859	1157	376	317	9		

- Molecule 5 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	304	Total	C	N	O	S	0	0
			2396	1539	416	430	11		

- Molecule 6 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 7 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	90	Total	C	N	O	0	0
			749	477	146	126		

- Molecule 8 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	205	Total	C	N	O	S	0	0
			1646	1059	293	283	11		

- Molecule 9 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	140	Total	C	N	O	S	0	0
			1061	680	192	187	2		

- Molecule 10 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 11 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 12 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 13 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	206	Total	C	N	O	S	0	0
			1676	1076	302	289	9		

- Molecule 14 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 15 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	141	Total	C	N	O	S	0	0
			1148	719	221	203	5		

- Molecule 16 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	217	Total	C	N	O	S	0	0
			1805	1159	317	320	9		

- Molecule 17 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	140	Total	C	N	O	S	0	0
			1153	732	231	186	4		

- Molecule 18 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 19 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 20 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	139	Total	C	N	O	S	0	0
			1154	734	220	197	3		

- Molecule 21 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	202	Total	C	N	O	S	0	0
			1652	1053	294	297	8		

- Molecule 22 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	101	Total	C	N	O	S	0	0
			805	520	151	131	3		

- Molecule 23 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 24 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 25 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	120	Total	C	N	O	S	0	0
			978	626	183	166	3		

- Molecule 26 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	82	Total	C	N	O	S	0	0
			686	434	124	123	5		

- Molecule 27 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 28 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 29 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	45	Total	C	N	O	S	0	0
			367	227	81	58	1		

- Molecule 30 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 31 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 32 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	392	Total	C	N	O	S	0	0
			3199	2067	558	563	11		

- Molecule 33 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	324	Total	C	N	O	S	0	0
			2723	1743	488	484	8		

- Molecule 34 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	7	287	Total	C	N	O	S	0	0
			2334	1495	397	425	17		

- Molecule 35 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	8	85	Total	C	N	O	S	0	0
			719	454	129	134	2		

- Molecule 36 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	9	123	Total	C	N	O	S	0	0
			992	642	169	179	2		

- Molecule 37 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 38 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	c	286	Total	C	N	O	S	0	0
			2300	1469	396	426	9		

- Molecule 39 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	d	220	Total	C	N	O	S	0	0
			1819	1170	310	327	12		

- Molecule 40 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	e	217	Total	C	N	O	S	0	0
			1762	1124	310	323	5		

- Molecule 41 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	f	130	Total	C	N	O	S	0	0
			1044	669	172	200	3		

- Molecule 42 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	g	131	Total	C	N	O	S	0	0
			1085	701	190	192	2		

- Molecule 43 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	h	105	Total	C	N	O	S	0	0
			862	548	151	160	3		

- Molecule 44 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 45 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	j	85	Total	C	N	O	S	0	0
			684	423	133	126	2		

- Molecule 46 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	k	95	Total	C	N	O	S	0	0
			732	456	139	132	5		

- Molecule 47 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	l	44	Total	C	N	O	S	0	0
			395	251	76	67	1		

- Molecule 48 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	m	42	Total	C	N	O	S	0	0
			345	216	70	57	2		

- Molecule 49 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	o	80	Total	C	N	O	S	0	0
			670	423	131	113	3		

- Molecule 50 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	127	Total	C	N	O	S	0	0
			1058	661	201	192	4		

- Molecule 51 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	135	Total	C	N	O	S	0	0
			1134	705	222	202	5		

- Molecule 52 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	157	Total	C	N	O	S	0	0
			1283	817	245	213	8		

- Molecule 53 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	372	Total	C	N	O	S	0	0
			3052	1956	544	538	14		

- Molecule 54 is a protein called rRNA methyltransferase 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	n	215	Total	C	N	O	S	0	0
			1667	1055	303	303	6		

- Molecule 55 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A1	335	Total	C	N	O	S	0	0
			2652	1690	463	482	17		

- Molecule 56 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	A2	238	Total	C	N	O	S	0	0
			1942	1244	336	350	12		

- Molecule 57 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	v	69	Total	C	N	O		0	0
			589	372	116	101			

- Molecule 58 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	u	129	Total	C	N	O	S	0	0
			1064	685	175	194	10		

- Molecule 59 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	t1	46	Total	C	N	O		0	0
			354	228	56	70			
59	t2	30	Total	C	N	O		0	0
			238	154	38	46			
59	t3	30	Total	C	N	O		0	0
			238	154	38	46			
59	t4	29	Total	C	N	O		0	0
			229	148	36	45			
59	t6	27	Total	C	N	O		0	0
			214	137	34	43			
59	t5	29	Total	C	N	O		0	0
			229	148	36	45			

- Molecule 60 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	w	87	Total	C	N	O	S	0	0
			705	452	103	144	6		

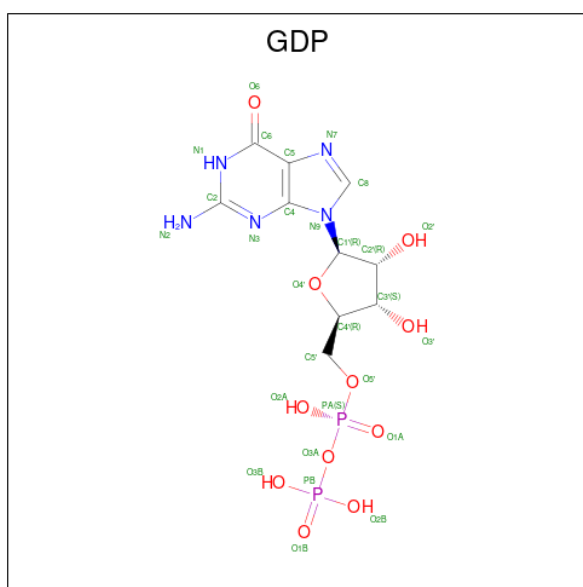
- Molecule 61 is a protein called Unknown residues.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	UNK	26	Total	C	N	O		0	0
			130	78	26	26			

- Molecule 62 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
62	A	101	Total	Mg	0
			101	101	
62	D	1	Total	Mg	0
			1	1	
62	F	1	Total	Mg	0
			1	1	
62	n	1	Total	Mg	0
			1	1	

- Molecule 63 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

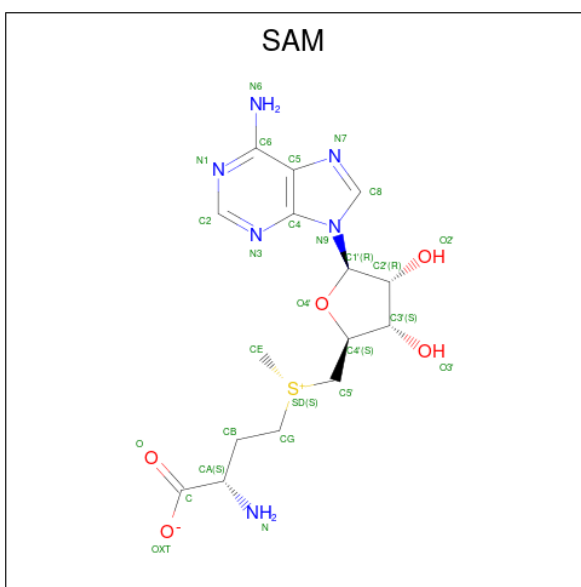


Mol	Chain	Residues	Atoms					AltConf
63	C	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 64 is ZINC ION (CCD ID: ZN) (formula: Zn).

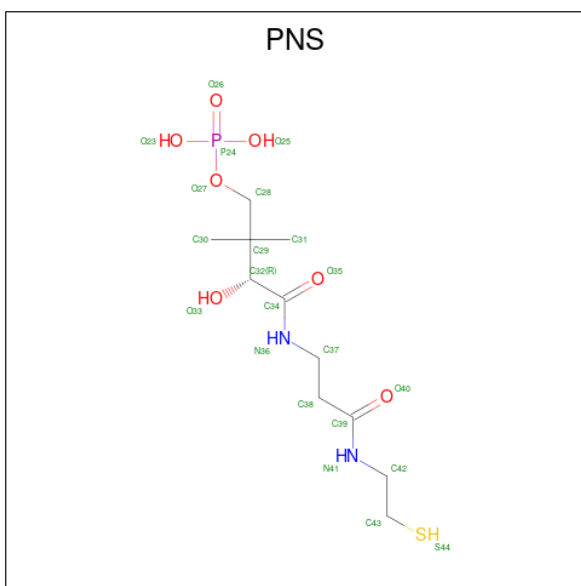
Mol	Chain	Residues	Atoms		AltConf
64	0	1	Total	Zn	0
			1	1	
64	4	1	Total	Zn	0
			1	1	

- Molecule 65 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: C₁₅H₂₂N₆O₅S).



Mol	Chain	Residues	Atoms					AltConf
65	A1	1	Total	C	N	O	S	0
			27	15	6	5	1	

- Molecule 66 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: $C_{11}H_{23}N_2O_7PS$).

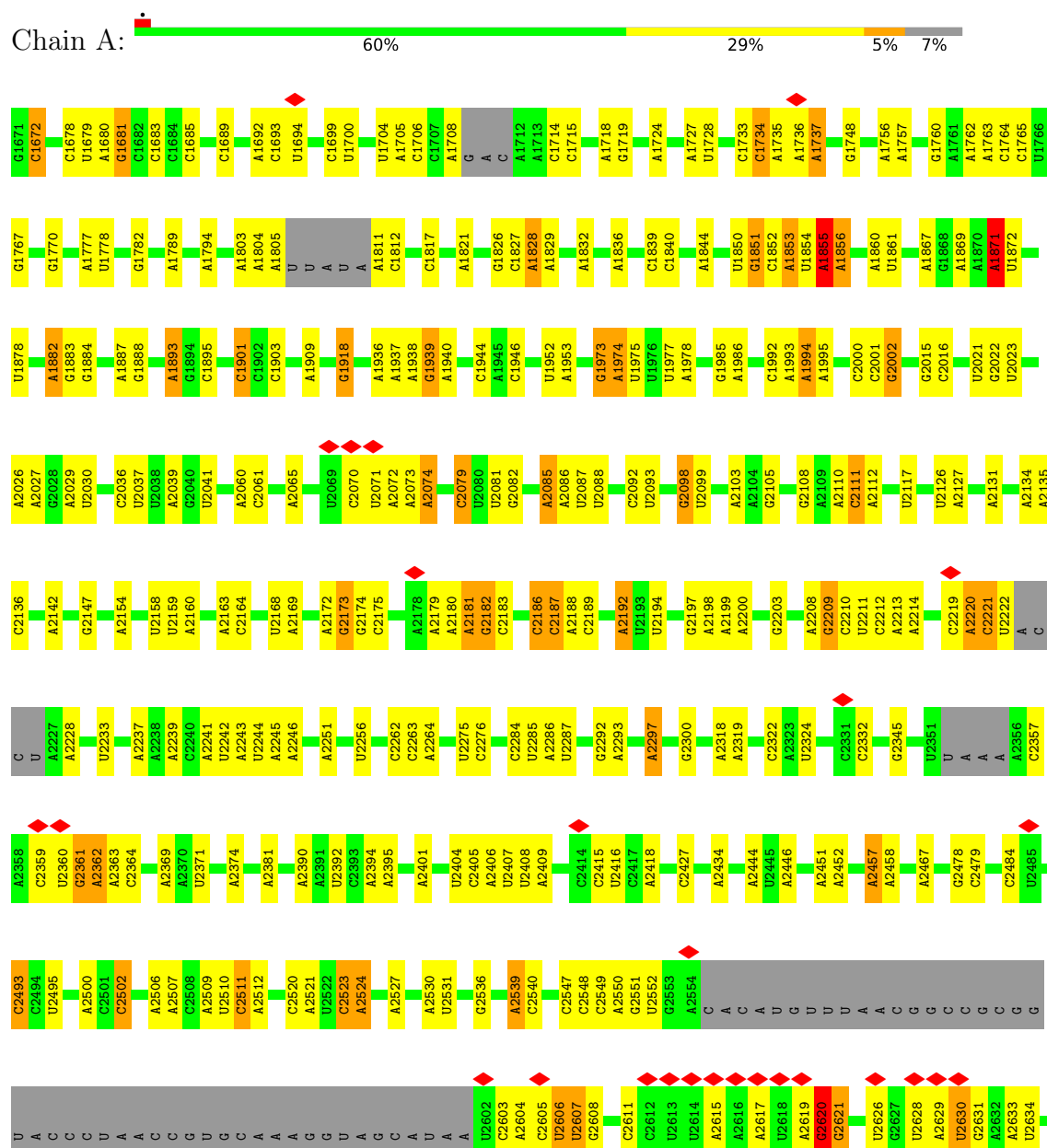


Mol	Chain	Residues	Atoms						AltConf
66	w	1	Total	C	N	O	P	S	0
			21	11	2	6	1	1	

3 Residue-property plots

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

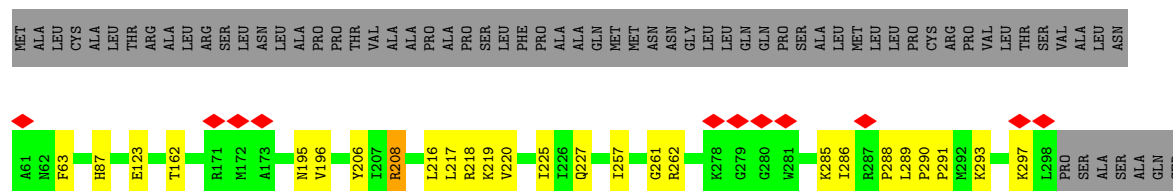
• Molecule 1: 16S rRNA





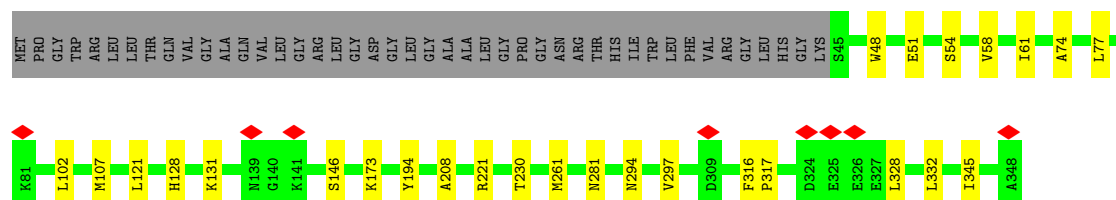
- Molecule 4: 39S ribosomal protein L2, mitochondrial

Chain D: 70% 8% 22%



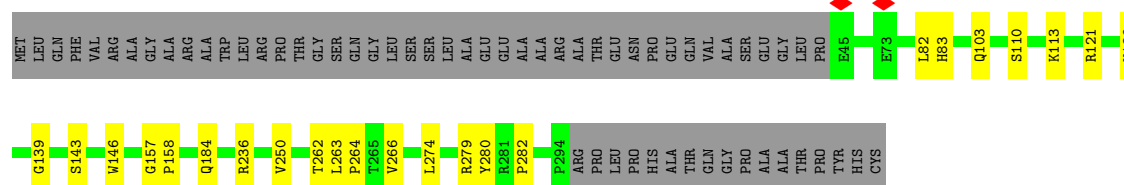
- Molecule 5: 39S ribosomal protein L3, mitochondrial

Chain E: 80% 8% 13%



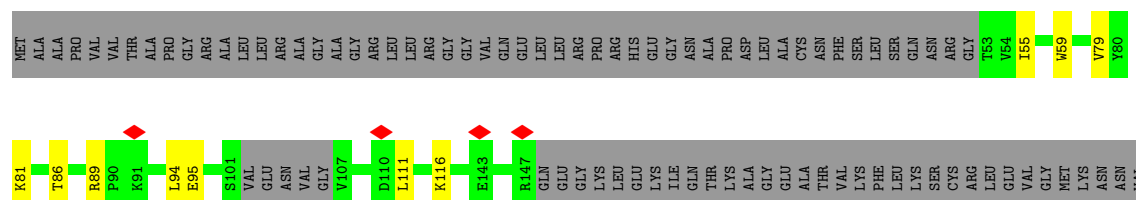
- Molecule 6: 39S ribosomal protein L4, mitochondrial

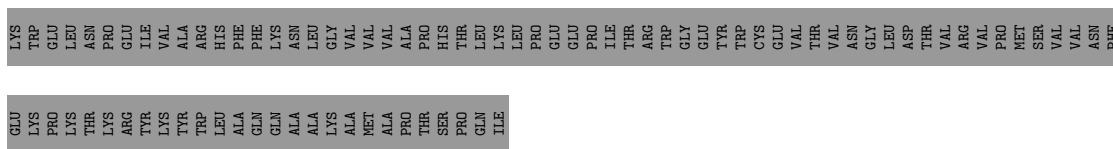
Chain F: 73% 7% 20%



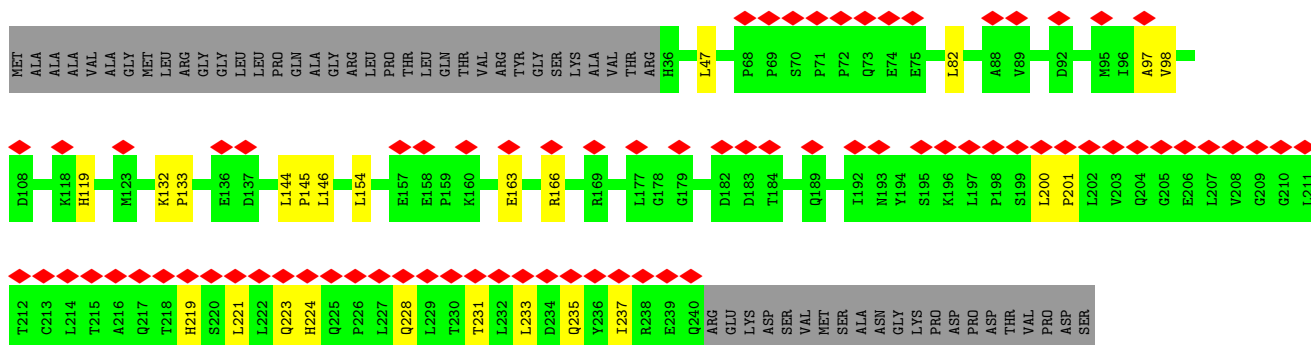
- Molecule 7: 39S ribosomal protein L9, mitochondrial

Chain H: 30% 66%

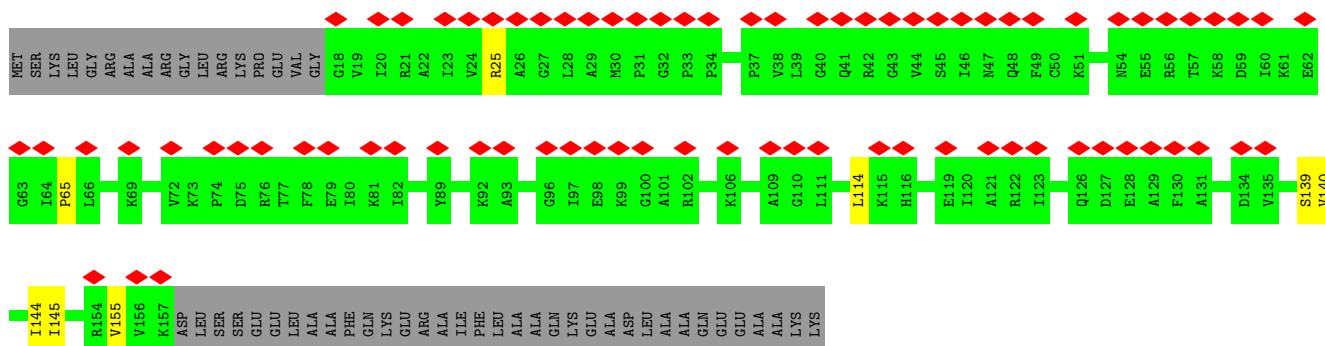
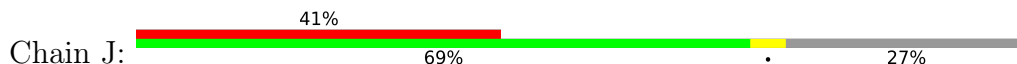




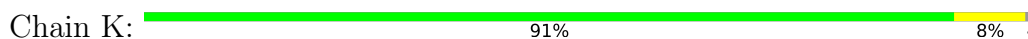
- Molecule 8: 39S ribosomal protein L10, mitochondrial



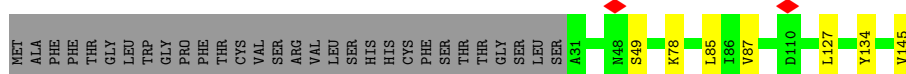
- Molecule 9: 39S ribosomal protein L11, mitochondrial




- Molecule 10: 39S ribosomal protein L13, mitochondrial



- Molecule 11: 39S ribosomal protein L14, mitochondrial




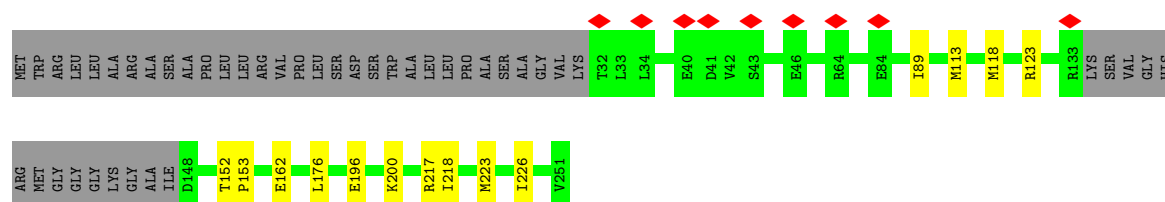
- Molecule 12: 39S ribosomal protein L15, mitochondrial

Chain M:  87% 10%




- Molecule 13: 39S ribosomal protein L16, mitochondrial

Chain N:  76% 6% 18%



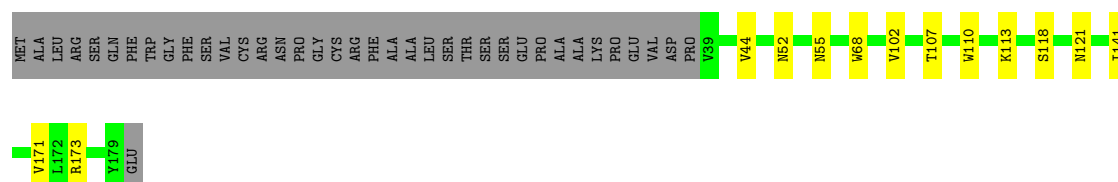
- Molecule 14: 39S ribosomal protein L17, mitochondrial

Chain O:  79% 7% 13%



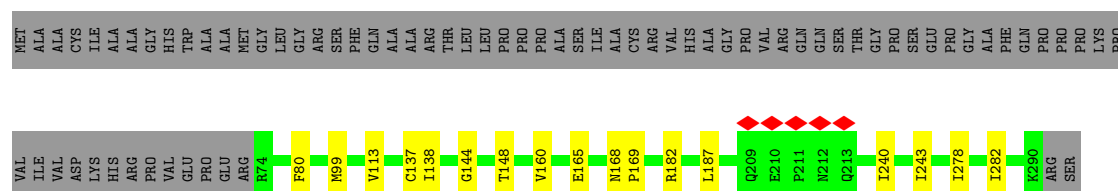
- Molecule 15: Mitochondrial ribosomal protein L18, isoform CRA_b

Chain P:  72% 7% 21%




- Molecule 16: 39S ribosomal protein L19, mitochondrial

Chain Q:  68% 6% 26%



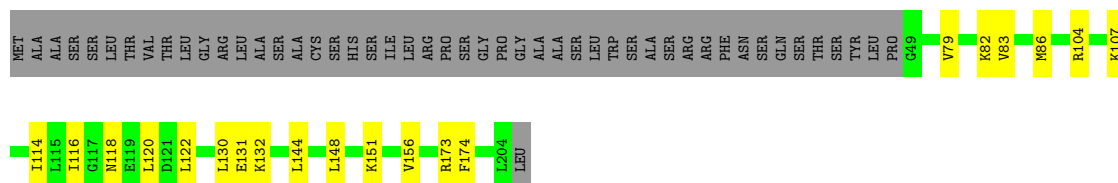
- Molecule 17: 39S ribosomal protein L20, mitochondrial

Chain R:  87% 7% • 6%



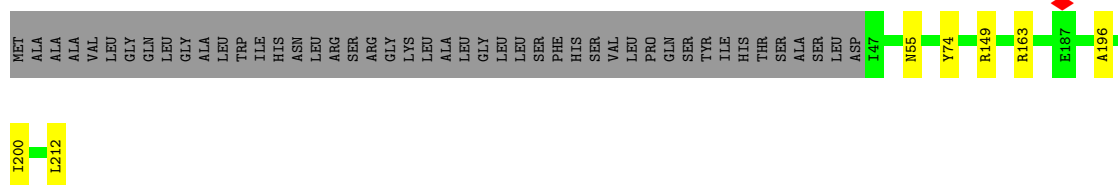
- Molecule 18: 39S ribosomal protein L21, mitochondrial

Chain S:  66% 10% 24%




- Molecule 19: 39S ribosomal protein L22, mitochondrial

Chain T:  75% • 22%




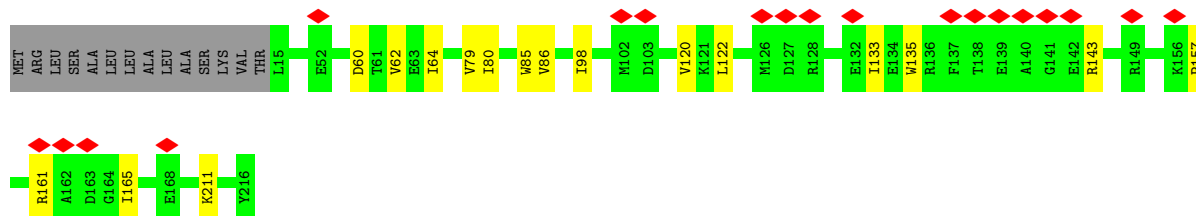
- Molecule 20: 39S ribosomal protein L23, mitochondrial

Chain U:  82% 8% • 9%



- Molecule 21: 39S ribosomal protein L24, mitochondrial

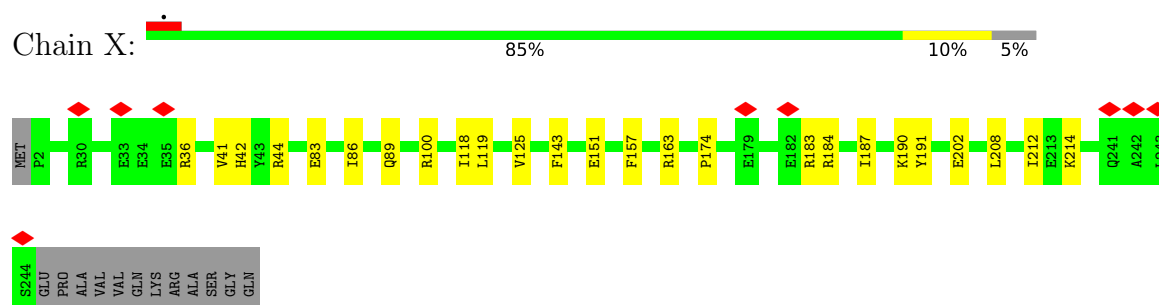
Chain V:  9% 86% 8% 6%



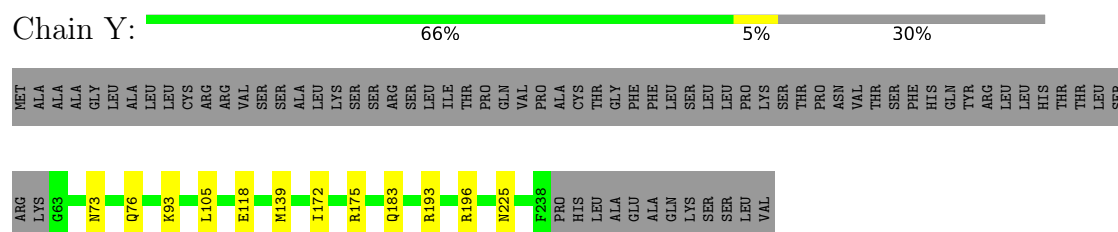
- Molecule 22: 39S ribosomal protein L27, mitochondrial

Chain W:  59% 8% 32%

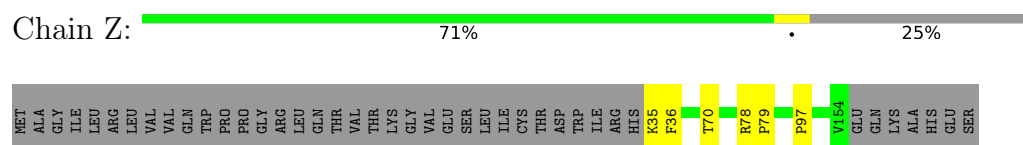
- Molecule 23: 39S ribosomal protein L28, mitochondrial



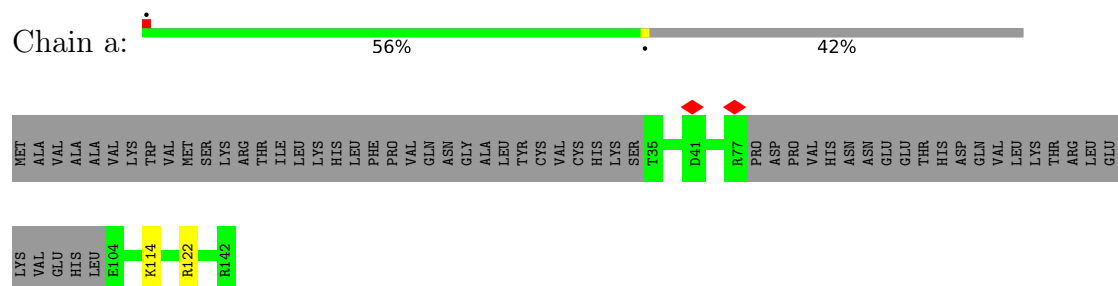
- Molecule 24: 39S ribosomal protein L47, mitochondrial



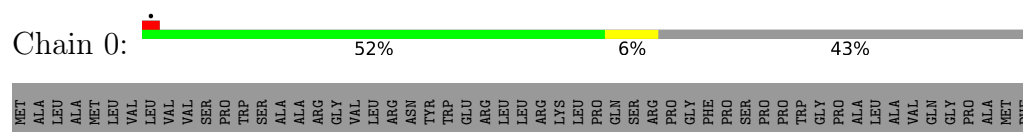
- Molecule 25: 39S ribosomal protein L30, mitochondrial



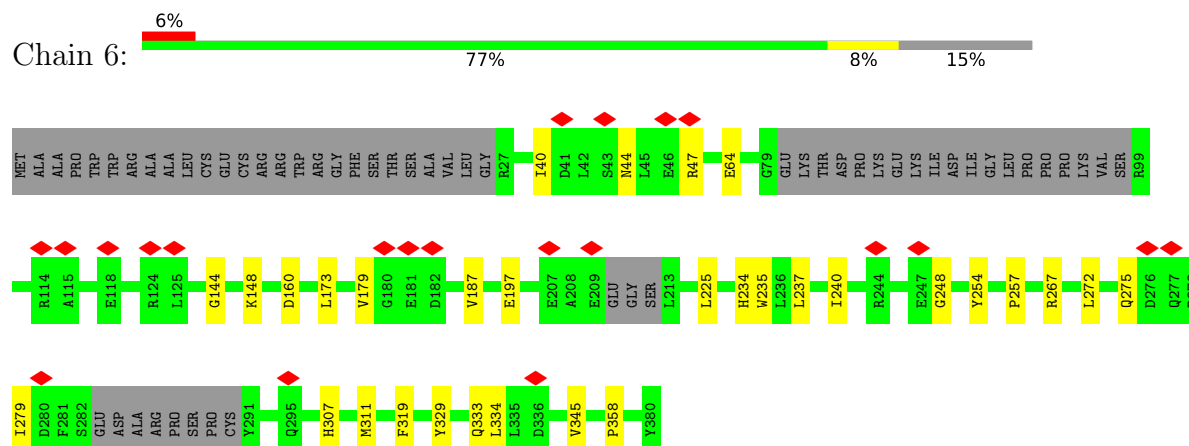
- Molecule 26: 39S ribosomal protein L42, mitochondrial



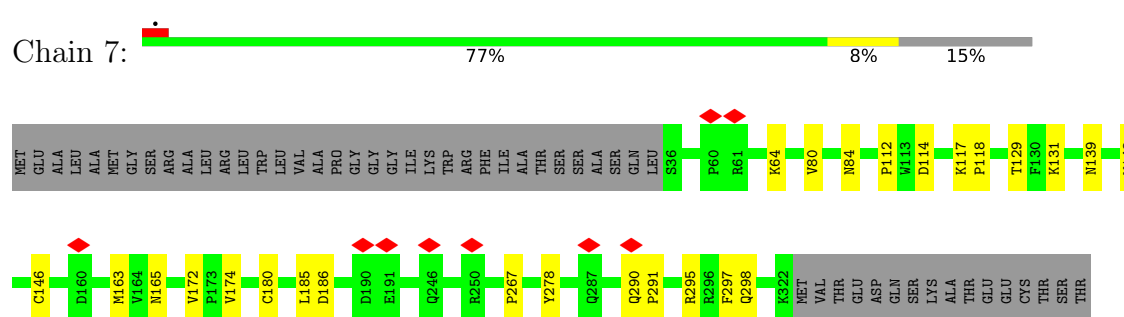
- Molecule 27: 39S ribosomal protein L32, mitochondrial



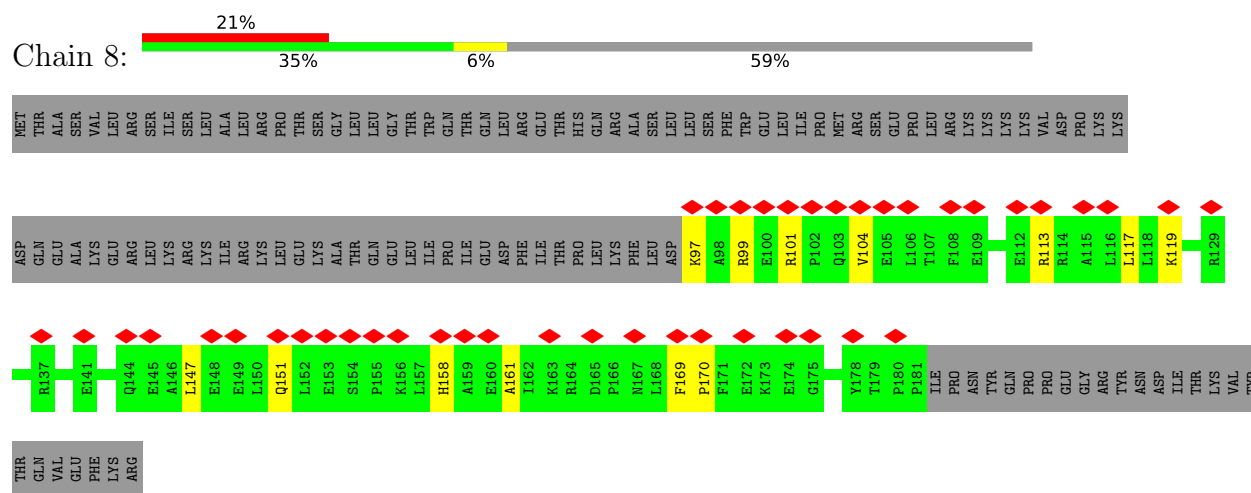
- Molecule 33: 39S ribosomal protein L38, mitochondrial



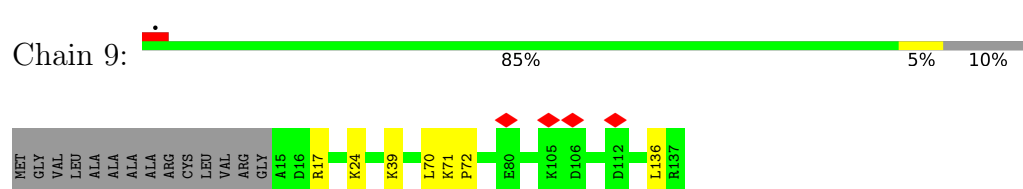
- Molecule 34: 39S ribosomal protein L39, mitochondrial



- Molecule 35: 39S ribosomal protein L40, mitochondrial

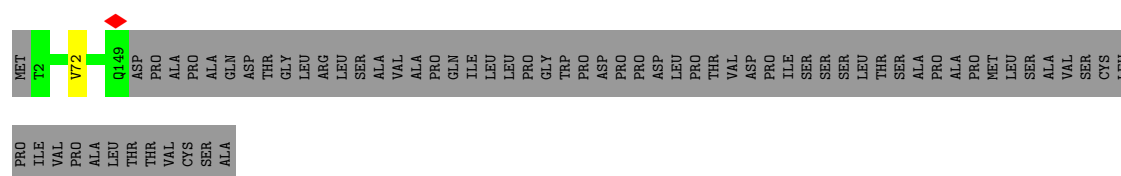


- Molecule 36: 39S ribosomal protein L41, mitochondrial




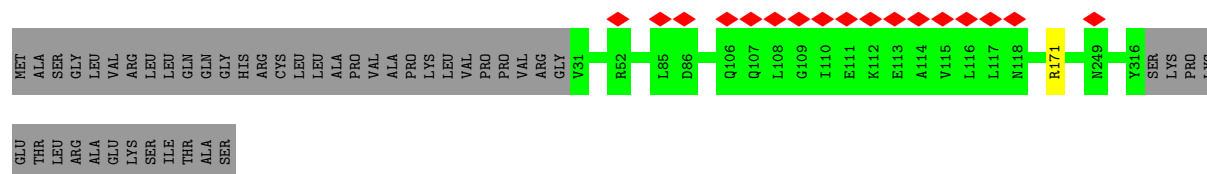
- Molecule 37: 39S ribosomal protein L43, mitochondrial

Chain b:  68% 31%




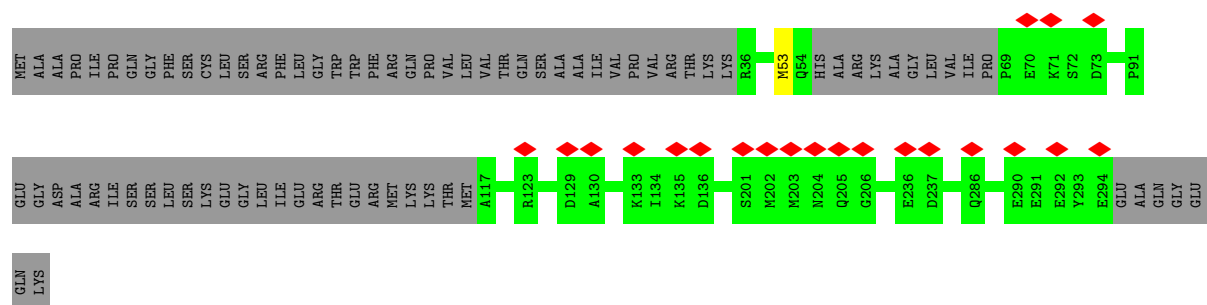
- Molecule 38: 39S ribosomal protein L44, mitochondrial

Chain c:  5% 86% 14%



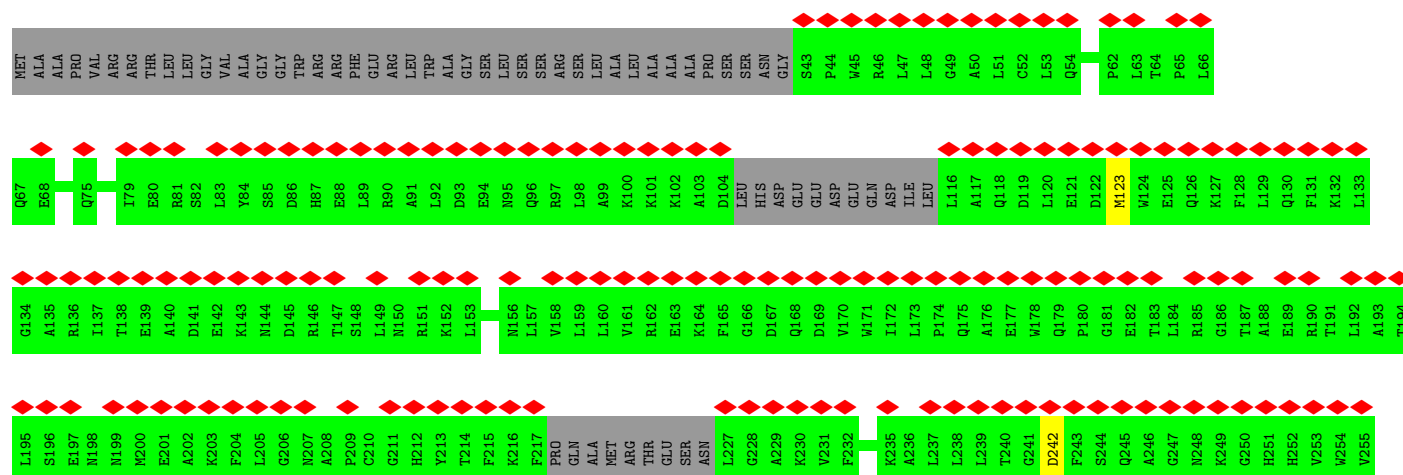
- Molecule 39: 39S ribosomal protein L45, mitochondrial

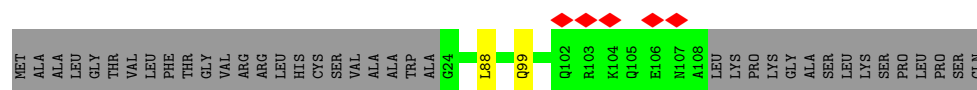
Chain d:  7% 73% 27%



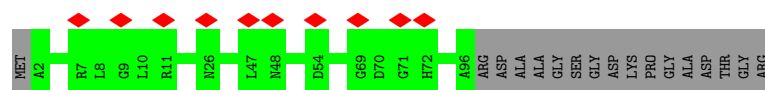
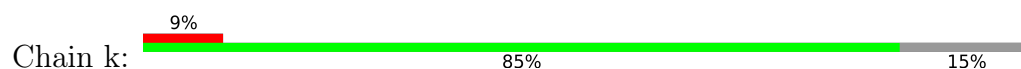
- Molecule 40: 39S ribosomal protein L46, mitochondrial

Chain e:  64% 77% 22%

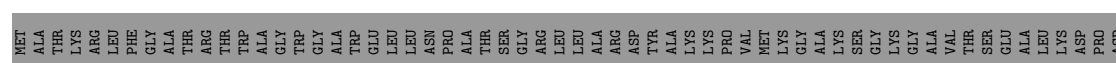




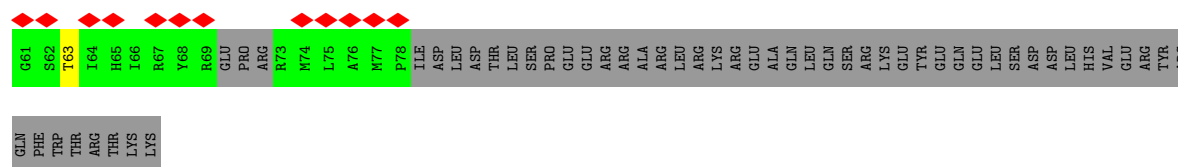
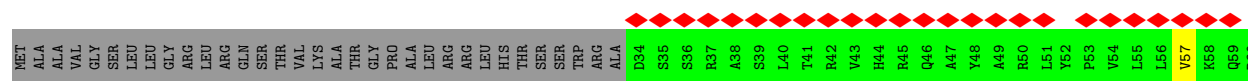
- Molecule 46: 39S ribosomal protein L53, mitochondrial



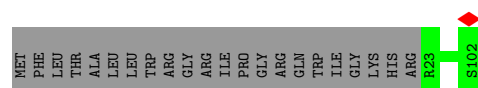
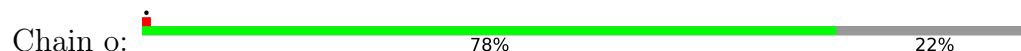
- Molecule 47: 39S ribosomal protein L54, mitochondrial



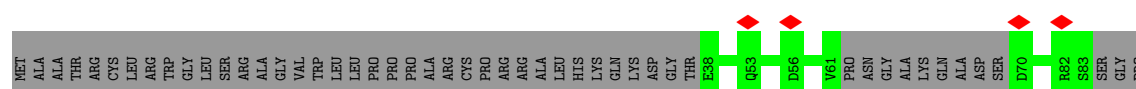
- Molecule 48: 39S ribosomal protein L55, mitochondrial

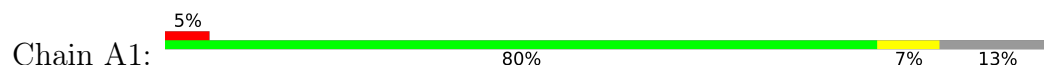


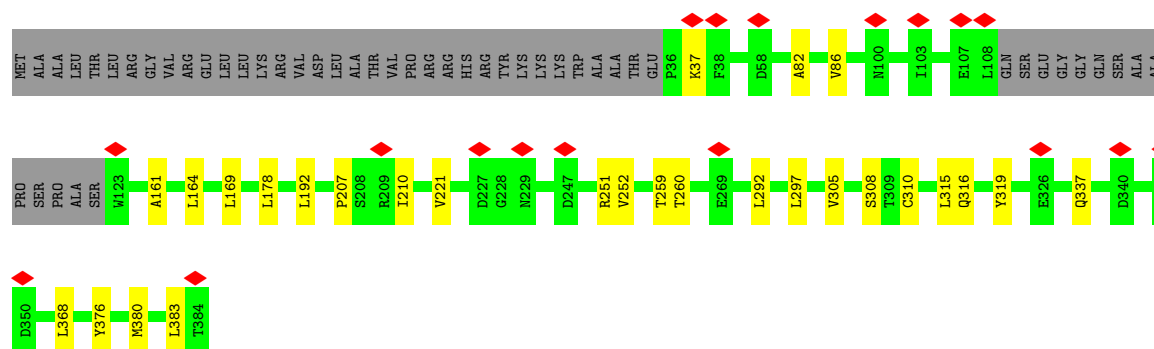
- Molecule 49: Ribosomal protein 63, mitochondrial



- Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial

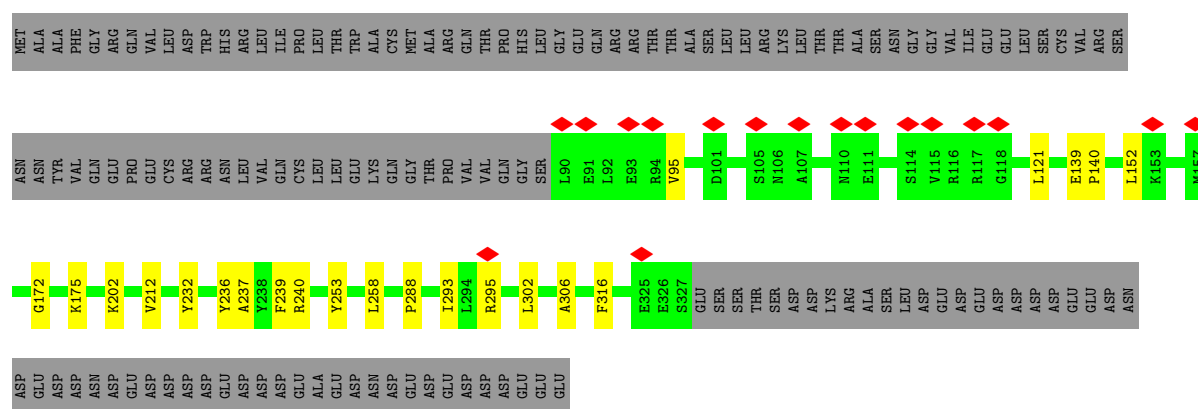






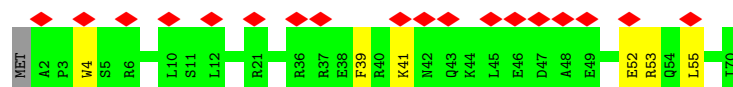
- Molecule 56: Transcription termination factor 4, mitochondrial

Chain A2: 57% 6% 38%



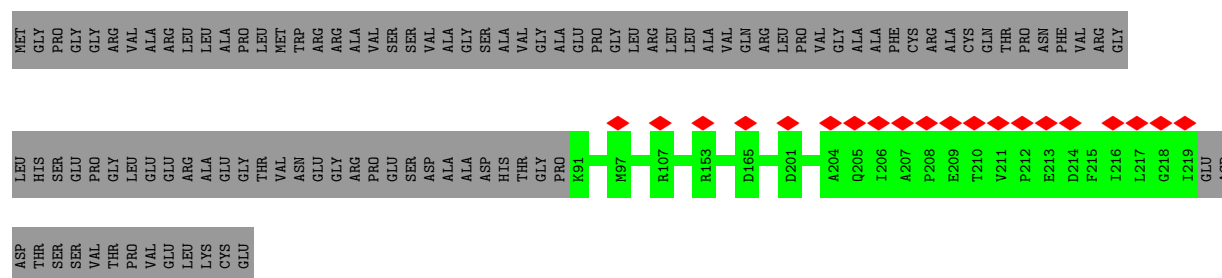
- Molecule 57: MIEF1 upstream open reading frame protein

Chain v: 26% 90% 9%



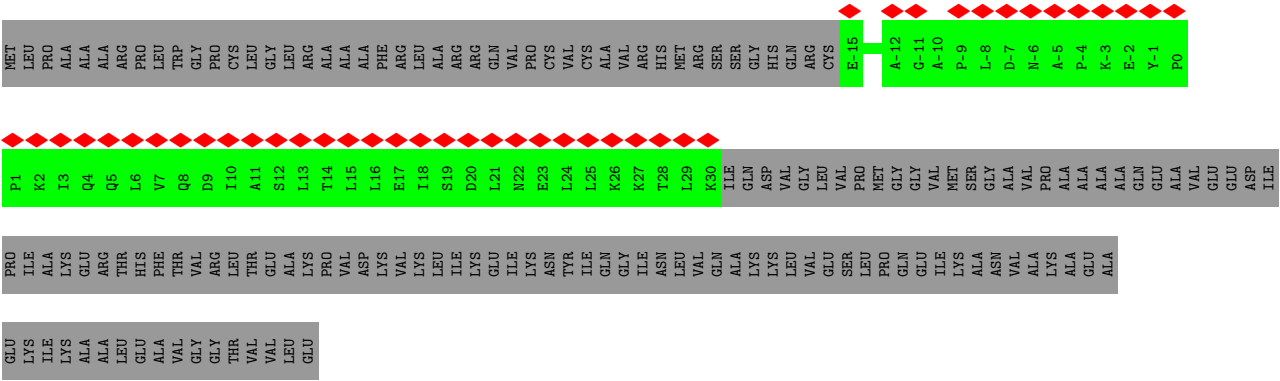
- Molecule 58: Mitochondrial assembly of ribosomal large subunit protein 1

Chain u: 9% 55% 45%

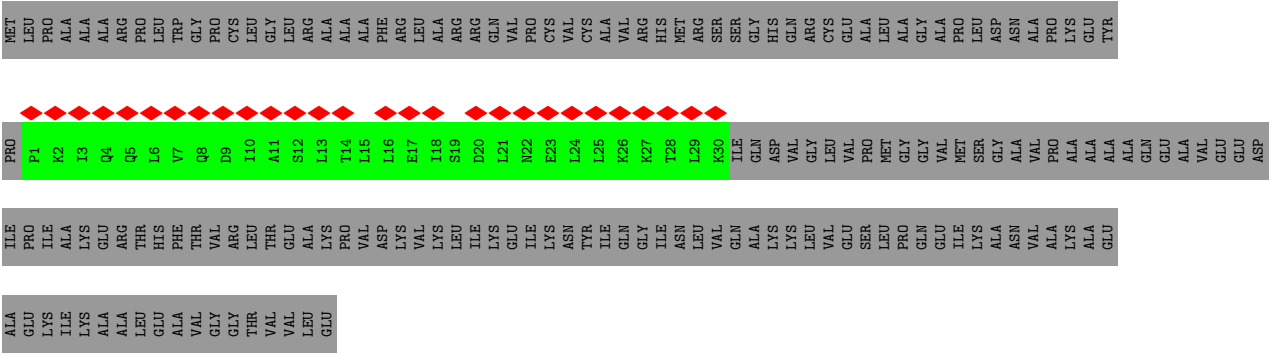


- Molecule 59: 39S ribosomal protein L12, mitochondrial

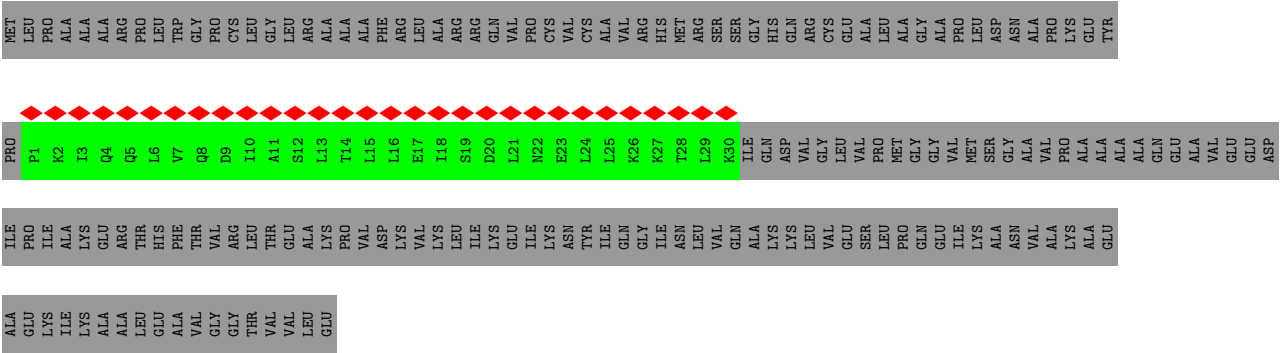
Chain t1: 22% 23% 77%



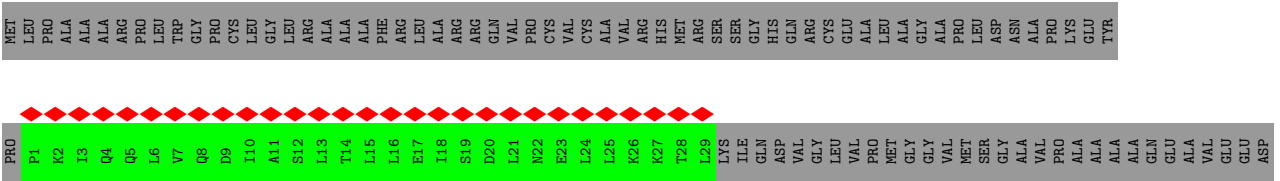
• Molecule 59: 39S ribosomal protein L12, mitochondrial



• Molecule 59: 39S ribosomal protein L12, mitochondrial



• Molecule 59: 39S ribosomal protein L12, mitochondrial



- Molecule 59: 39S ribosomal protein L12, mitochondrial

Chain t6:  14% 14% 86%

[illegible]

- Molecule 59: 39S ribosomal protein L12, mitochondrial

Chain t5:  15% 14% 85%

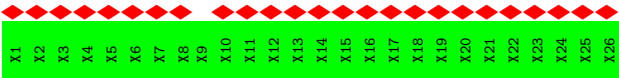
[illegible]

- Molecule 60: Acyl carrier protein, mitochondrial

Chain w: 

D124	E125	F126	G127	F128	E129	P131	D132	I133	D134	A135	E136	K137	L138	M139	Q142	E143	I144	V145	D146	I147	I148	A149	D150	K151	K152	D153	V154	Y155	E156																										
VAL	THR	GLN	LEU	CYS	ARG	GLN	TYR	SER	D70	M71	P72	P73	L74	A135	T75	L76	E77	G78	L79	Q80	D81	R82	V83	L84	V85	R86	L87	X88	L89	Y90	D91	K92	I93	D94	P95	E96	K97	L98	S99	V100	M101	S102	H103	F104	M105	K106	D107	L108							
MET	ALA	SER	VAL	LEU	SER	ALA	TYR	VAL	SER	ARG	LEU	PRO	ALA	PHE	ALA	PRO	LEU	PRO	ARG	VAL	ARG	MET	LEU	ALA	VAL	ALA	ARG	PRO	SER	THR	ALA	CYS	SER	ALA	GLY	THR	GLN	THR	ARG	LEU	GLY	THR	LEU	GLN	PRO	ALA	LEU	VAL	LEU	ALA	GLN	VAL	PRO	GLY	ARG

- Molecule 61: Unknown residues



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48646	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.254	Depositor
Minimum map value	-0.513	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.081	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	215.22, 279.47998, 250.92	wwPDB
Map dimensions	246, 274, 211	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.02, 1.02, 1.02	Depositor

5 Model quality

5.1 Standard geometry

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

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	A	0.43	0/34501	0.73	8/53693 (0.0%)
2	B	0.45	0/1423	0.72	1/2206 (0.0%)
3	C	0.28	0/1905	0.56	3/2573 (0.1%)
4	D	0.27	0/1896	0.63	0/2549
5	E	0.27	0/2465	0.58	0/3344
6	F	0.26	0/2071	0.59	0/2817
7	H	0.27	0/762	0.66	0/1022
8	I	0.28	0/1682	0.59	0/2280
9	J	0.28	0/1077	0.65	0/1452
10	K	0.26	0/1495	0.57	0/2029
11	L	0.26	0/904	0.62	0/1218
12	M	0.27	0/2359	0.62	0/3185
13	N	0.27	0/1721	0.60	0/2322
14	O	0.26	0/1269	0.59	0/1708
15	P	0.26	0/1173	0.61	0/1588
16	Q	0.25	0/1846	0.61	0/2487
17	R	0.25	0/1174	0.60	0/1572
18	S	0.26	0/1276	0.62	0/1729
19	T	0.26	0/1402	0.61	0/1886
20	U	0.27	0/1183	0.63	0/1600
21	V	0.26	0/1697	0.62	0/2302
22	W	0.27	0/827	0.60	0/1118
23	X	0.25	0/2090	0.59	0/2825
24	Y	0.25	0/1552	0.58	0/2079
25	Z	0.26	0/1003	0.62	0/1354
26	a	0.29	0/709	0.60	0/963
27	0	0.32	0/895	0.62	0/1201
28	1	0.25	0/438	0.63	0/583
29	2	0.28	0/373	0.60	0/496
30	3	0.25	0/852	0.60	0/1136
31	4	0.35	0/350	0.63	0/461
32	5	0.26	0/3294	0.59	0/4488

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	6	0.27	0/2809	0.60	0/3818
34	7	0.26	0/2391	0.59	0/3234
35	8	0.27	0/734	0.62	0/986
36	9	0.28	0/1020	0.61	0/1374
37	b	0.28	0/1202	0.61	0/1626
38	c	0.26	0/2348	0.59	0/3174
39	d	0.26	0/1872	0.61	0/2536
40	e	0.27	0/1797	0.62	0/2422
41	f	0.27	0/1063	0.63	0/1430
42	g	0.26	0/1121	0.60	0/1528
43	h	0.28	0/884	0.60	0/1203
44	i	0.26	0/849	0.58	0/1135
45	j	0.29	0/698	0.58	0/940
46	k	0.27	0/743	0.62	0/1003
47	l	0.26	0/407	0.59	0/547
48	m	0.29	0/350	0.66	0/469
49	o	0.26	0/687	0.57	0/924
50	p	0.27	0/1071	0.61	0/1433
51	q	0.27	0/1165	0.58	0/1575
52	r	0.27	0/1322	0.61	0/1793
53	s	0.26	0/3130	0.59	0/4247
54	n	0.27	0/1703	0.60	0/2314
55	A1	0.26	0/2713	0.58	0/3681
56	A2	0.25	0/1973	0.58	0/2651
57	v	0.26	0/598	0.63	0/796
58	u	0.25	0/1089	0.60	0/1474
59	t1	0.24	0/358	0.37	0/486
59	t2	0.22	0/238	0.36	0/319
59	t3	0.22	0/238	0.37	0/319
59	t4	0.22	0/229	0.32	0/308
59	t5	0.22	0/229	0.45	0/308
59	t6	0.22	0/213	0.33	0/286
60	w	0.26	0/717	0.61	0/967
All	All	0.33	0/115625	0.64	12/163572 (0.0%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1855	A	C2'-C3'-O3'	7.38	125.74	109.50
1	A	2457	A	C2'-C3'-O3'	6.78	124.55	113.70
1	A	1973	G	C2'-C3'-O3'	6.71	124.44	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	209	PRO	C-N-CA	-6.51	105.42	121.70
1	A	2209	G	C2'-C3'-O3'	6.25	123.70	113.70
1	A	2905	A	C2'-C3'-O3'	6.22	123.65	113.70
2	B	1607	U	C2'-C3'-O3'	5.95	123.21	113.70
1	A	1871	A	C2'-C3'-O3'	5.88	123.11	113.70
1	A	2182	G	C2'-C3'-O3'	5.49	122.48	113.70
1	A	2620	G	C2'-C3'-O3'	5.32	122.22	113.70
3	C	209	PRO	O-C-N	5.28	131.15	122.70
3	C	209	PRO	CA-C-N	-5.01	106.17	117.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	30864	0	15681	157	0
2	B	1275	0	650	8	0
3	C	1878	0	1949	18	0
4	D	1859	0	1920	18	0
5	E	2396	0	2402	15	0
6	F	2013	0	2043	15	0
7	H	749	0	798	6	0
8	I	1646	0	1731	14	0
9	J	1061	0	1141	4	0
10	K	1451	0	1448	8	0
11	L	889	0	941	4	0
12	M	2305	0	2378	16	0
13	N	1676	0	1694	8	0
14	O	1245	0	1283	8	0
15	P	1148	0	1148	8	0
16	Q	1805	0	1841	11	0
17	R	1153	0	1214	8	0
18	S	1251	0	1322	11	0
19	T	1368	0	1410	4	0
20	U	1154	0	1154	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	V	1652	0	1658	11	0
22	W	805	0	829	10	0
23	X	2035	0	2054	15	0
24	Y	1517	0	1561	10	0
25	Z	978	0	1030	4	0
26	a	686	0	658	0	0
27	0	880	0	902	7	0
28	1	433	0	475	3	0
29	2	367	0	393	3	0
30	3	831	0	883	5	0
31	4	342	0	361	5	0
32	5	3199	0	3196	34	0
33	6	2723	0	2615	19	0
34	7	2334	0	2343	13	0
35	8	719	0	723	6	0
36	9	992	0	984	6	0
37	b	1178	0	1180	0	0
38	c	2300	0	2313	0	0
39	d	1819	0	1793	0	0
40	e	1762	0	1767	0	0
41	f	1044	0	1046	0	0
42	g	1085	0	1077	0	0
43	h	862	0	845	0	0
44	i	827	0	857	0	0
45	j	684	0	673	0	0
46	k	732	0	745	0	0
47	l	395	0	391	0	0
48	m	345	0	360	0	0
49	o	670	0	665	0	0
50	p	1058	0	1083	0	0
51	q	1134	0	1110	0	0
52	r	1283	0	1310	0	0
53	s	3052	0	3037	0	0
54	n	1667	0	1673	0	0
55	A1	2652	0	2632	14	0
56	A2	1942	0	2035	11	0
57	v	589	0	604	0	0
58	u	1064	0	1060	0	0
59	t1	354	0	380	0	0
59	t2	238	0	270	0	0
59	t3	238	0	270	0	0
59	t4	229	0	257	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	t5	229	0	257	0	0
59	t6	214	0	236	0	0
60	w	705	0	691	0	0
61	UNK	130	0	28	0	0
62	A	101	0	0	0	0
62	D	1	0	0	0	0
62	F	1	0	0	0	0
62	n	1	0	0	0	0
63	C	28	0	12	0	0
64	0	1	0	0	0	0
64	4	1	0	0	0	0
65	A1	27	0	22	0	0
66	w	21	0	21	0	0
All	All	110342	0	95513	463	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (463) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5:126:THR:HG22	32:5:372:ASN:HB2	1.46	0.95
20:U:24:PHE:HB2	20:U:45:PRO:HG3	1.60	0.84
24:Y:93:LYS:HD2	36:9:70:LEU:HD21	1.65	0.79
27:0:179:ARG:HH12	27:0:182:PRO:HG3	1.48	0.79
8:I:221:LEU:HA	8:I:224:HIS:HD2	1.52	0.75
6:F:262:THR:HG22	6:F:264:PRO:HD2	1.68	0.74
33:6:237:LEU:HB3	33:6:240:ILE:HD11	1.69	0.74
4:D:285:LYS:HD2	4:D:293:LYS:HE3	1.71	0.72
34:7:114:ASP:HB2	34:7:117:LYS:HB2	1.73	0.69
32:5:181:VAL:HG21	32:5:347:THR:HG21	1.75	0.69
1:A:3013:G:HO2'	31:4:66:PHE:N	1.90	0.68
1:A:1826:G:H4'	1:A:1828:A:C2	2.29	0.68
27:0:90:ASN:O	27:0:94:ARG:HG2	1.93	0.67
4:D:217:LEU:HD13	4:D:227:GLN:HB2	1.76	0.67
1:A:1826:G:H4'	1:A:1828:A:H2	1.60	0.67
1:A:2607:U:H2'	1:A:2608:G:H8	1.61	0.66
55:A1:207:PRO:HA	55:A1:210:ILE:HG22	1.77	0.66
3:C:65:ARG:HH12	3:C:105:LEU:HD13	1.61	0.66
1:A:2830:A:H2'	1:A:2836:C:H42	1.61	0.65
32:5:122:TRP:HA	32:5:253:LEU:HD23	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2086:A:H2'	1:A:2087:U:C6	2.32	0.65
1:A:1994:A:H61	1:A:2736:C:H4'	1.61	0.65
1:A:2187:C:H2'	1:A:2188:A:C8	2.31	0.64
3:C:60:ILE:HB	3:C:63:SER:HB2	1.79	0.64
18:S:131:GLU:HG2	18:S:151:LYS:HE3	1.78	0.64
1:A:1706:C:OP1	24:Y:193:ARG:NH2	2.32	0.63
1:A:2103:A:HO2'	25:Z:35:LYS:N	1.97	0.63
6:F:184:GLN:HE22	12:M:22:VAL:H	1.47	0.62
1:A:2186:C:H2'	1:A:2187:C:C6	2.35	0.62
7:H:86:THR:HG23	7:H:89:ARG:HE	1.64	0.62
22:W:67:ILE:HG21	22:W:131:VAL:HG11	1.82	0.61
30:3:149:PHE:HB2	33:6:358:PRO:O	1.99	0.61
4:D:217:LEU:CD1	4:D:227:GLN:HB2	2.31	0.61
1:A:3123:G:HO2'	1:A:3124:U:H6	1.47	0.61
34:7:143:TRP:HE1	34:7:172:VAL:HG13	1.66	0.61
12:M:142:GLU:HB2	12:M:162:LEU:HD23	1.83	0.61
12:M:222:TYR:HE2	12:M:262:PRO:HB3	1.65	0.60
1:A:1977:U:H2'	1:A:1978:A:H8	1.66	0.60
34:7:112:PRO:HB2	34:7:267:PRO:HG2	1.83	0.60
4:D:290:PRO:HA	4:D:293:LYS:HE2	1.83	0.60
1:A:2292:G:C8	17:R:11:ARG:HB3	2.35	0.60
1:A:2816:G:H2'	1:A:2817:G:H8	1.65	0.60
1:A:1871:A:N3	30:3:104:ARG:NH2	2.50	0.60
4:D:286:ILE:O	4:D:290:PRO:HD3	2.02	0.60
1:A:1855:A:H5''	1:A:2695:G:H22	1.66	0.60
16:Q:278:ILE:O	16:Q:282:ILE:HG12	2.02	0.60
1:A:1839:C:H2'	1:A:1840:C:C6	2.37	0.59
32:5:115:GLU:HB2	32:5:119:GLN:HB2	1.84	0.59
15:P:102:VAL:HG11	15:P:141:ILE:HD11	1.83	0.59
1:A:2523:C:H4'	1:A:2524:A:OP1	2.03	0.59
5:E:107:MET:HG2	5:E:121:LEU:HD11	1.85	0.59
13:N:196:GLU:HG3	13:N:200:LYS:HE2	1.85	0.59
33:6:187:VAL:HG13	33:6:319:PHE:HB3	1.84	0.59
1:A:2016:C:OP2	12:M:59:ARG:NH1	2.36	0.58
1:A:2105:G:O2'	1:A:2837:A:N6	2.36	0.58
1:A:2953:U:H5''	31:4:71:VAL:HG22	1.84	0.58
4:D:286:ILE:HG23	4:D:288:PRO:HD2	1.85	0.58
1:A:2117:U:H1'	1:A:2837:A:C8	2.38	0.58
32:5:215:ARG:O	32:5:218:LEU:HB2	2.02	0.58
9:J:145:ILE:HD11	9:J:155:VAL:HG21	1.86	0.58
13:N:218:ILE:HG23	13:N:223:MET:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1778:U:C5	6:F:121:ARG:HD2	2.39	0.57
1:A:2275:U:H1'	17:R:12:ASN:OD1	2.05	0.57
1:A:2816:G:H2'	1:A:2817:G:C8	2.39	0.57
32:5:392:ILE:HG12	32:5:397:VAL:HG22	1.86	0.57
1:A:2467:A:O2'	1:A:3154:U:H4'	2.05	0.57
21:V:135:TRP:HB3	21:V:143:ARG:HH21	1.69	0.57
3:C:49:VAL:HG11	3:C:147:MET:HG2	1.86	0.57
13:N:217:ARG:HG2	13:N:223:MET:HE1	1.87	0.56
1:A:2192:A:H4'	9:J:139:SER:HB3	1.86	0.56
33:6:307:HIS:O	33:6:311:MET:HB3	2.06	0.56
56:A2:202:LYS:HG3	56:A2:212:VAL:HG21	1.88	0.56
5:E:208:ALA:HB2	5:E:297:VAL:HG12	1.87	0.56
20:U:110:LEU:HD12	24:Y:118:GLU:HG2	1.86	0.56
1:A:3189:C:H5''	31:4:86:GLY:H	1.70	0.56
18:S:107:LYS:HD3	19:T:212:LEU:HD22	1.87	0.55
22:W:51:GLN:HE22	22:W:71:ARG:HB2	1.70	0.55
33:6:240:ILE:HD13	33:6:248:GLY:HA3	1.88	0.55
6:F:113:LYS:HG3	6:F:157:GLY:H	1.70	0.55
25:Z:36:PHE:HE2	25:Z:79:PRO:HG3	1.71	0.55
1:A:2187:C:H2'	1:A:2188:A:H8	1.72	0.55
1:A:2523:C:C2'	1:A:2523:C:O2	2.54	0.55
2:B:1628:C:H2'	2:B:1629:A:H8	1.72	0.55
1:A:1939:G:H1'	1:A:1974:A:OP1	2.06	0.54
12:M:202:LYS:HD2	12:M:263:ARG:HD3	1.88	0.54
21:V:60:ASP:HB2	21:V:157:PRO:HG3	1.88	0.54
8:I:97:ALA:HB3	8:I:154:LEU:HB2	1.89	0.54
23:X:202:GLU:HB3	23:X:214:LYS:NZ	2.22	0.54
1:A:2606:U:O2'	1:A:2607:U:O2	2.26	0.54
3:C:148:VAL:HG21	3:C:160:ILE:HD11	1.90	0.54
23:X:118:ILE:HD11	23:X:191:TYR:CD2	2.43	0.53
5:E:128:HIS:HB2	5:E:173:LYS:HE3	1.91	0.53
12:M:177:ALA:HA	12:M:222:TYR:CD1	2.43	0.53
3:C:278:LYS:HE2	3:C:278:LYS:HA	1.90	0.53
22:W:49:ARG:HD3	22:W:49:ARG:H	1.73	0.53
18:S:132:LYS:HA	18:S:148:LEU:HD22	1.91	0.53
17:R:10:LEU:HB3	17:R:13:ARG:HD2	1.91	0.53
1:A:2511:C:H3'	1:A:2512:A:H8	1.73	0.53
16:Q:182:ARG:HG3	16:Q:187:LEU:HD11	1.91	0.53
21:V:161:ARG:HD2	21:V:165:ILE:HG12	1.91	0.53
35:8:147:LEU:O	35:8:151:GLN:HG2	2.08	0.53
1:A:3134:C:O4'	1:A:3134:C:O2	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2685:U:O2'	1:A:3104:U:H5'	2.09	0.52
13:N:113:MET:HG3	13:N:118:MET:HG3	1.92	0.52
1:A:3067:U:H2'	1:A:3068:G:H5''	1.91	0.52
1:A:2220:A:H4'	1:A:2221:C:OP1	2.09	0.52
20:U:8:PRO:HA	24:Y:183:GLN:HE22	1.75	0.52
1:A:1782:G:O6	6:F:121:ARG:HD3	2.09	0.52
1:A:2275:U:H2'	1:A:2276:C:C6	2.45	0.52
1:A:3212:C:O2	1:A:3212:C:O4'	2.28	0.52
1:A:2361:G:H4'	1:A:2362:A:OP1	2.10	0.52
1:A:1737:A:H61	1:A:1760:G:H1'	1.74	0.52
3:C:112:ASN:HB3	3:C:115:LYS:HB3	1.91	0.52
15:P:118:SER:OG	15:P:121:ASN:ND2	2.43	0.52
21:V:79:VAL:HG22	21:V:86:VAL:HG12	1.92	0.52
1:A:2523:C:O2	1:A:2523:C:H2'	2.10	0.52
3:C:119:VAL:HA	3:C:122:ILE:HD12	1.92	0.52
4:D:293:LYS:HD2	56:A2:239:PHE:CD1	2.44	0.51
13:N:123:ARG:NH1	13:N:162:GLU:OE2	2.43	0.51
23:X:125:VAL:HG11	23:X:157:PHE:HE2	1.76	0.51
32:5:126:THR:HG21	32:5:357:PHE:HE1	1.75	0.51
1:A:2079:C:O4'	1:A:2079:C:O2	2.28	0.51
1:A:3054:G:H2'	1:A:3055:U:C6	2.46	0.51
1:A:3123:G:O2'	1:A:3124:U:H6	1.93	0.51
20:U:88:LYS:NZ	20:U:91:ASP:OD1	2.42	0.51
3:C:100:LEU:HD12	3:C:105:LEU:HD22	1.92	0.51
4:D:257:ILE:HG23	4:D:262:ARG:HB2	1.91	0.51
32:5:310:ARG:HA	32:5:313:MET:HE2	1.92	0.51
32:5:391:VAL:HB	32:5:399:GLU:HB2	1.91	0.51
4:D:289:LEU:N	4:D:290:PRO:CD	2.73	0.51
19:T:55:ASN:ND2	19:T:74:TYR:O	2.39	0.51
33:6:235:TRP:HB3	33:6:254:TYR:HA	1.93	0.51
1:A:2502:C:H1'	1:A:3096:U:H5'	1.91	0.51
1:A:2961:C:H2'	1:A:2961:C:O2	2.09	0.51
32:5:313:MET:HE1	32:5:353:HIS:HB2	1.92	0.51
34:7:185:LEU:HD13	34:7:295:ARG:HD3	1.93	0.51
3:C:285:LEU:HD23	3:C:290:ASN:HB3	1.93	0.51
12:M:229:PHE:N	12:M:230:PRO:HD2	2.27	0.51
15:P:44:VAL:HG12	33:6:225:LEU:HB3	1.93	0.51
1:A:2213:A:H2'	1:A:2214:A:H5'	1.93	0.50
3:C:73:LEU:HD21	3:C:105:LEU:HD12	1.94	0.50
55:A1:260:THR:HA	55:A1:310:CYS:SG	2.51	0.50
56:A2:302:LEU:HA	56:A2:306:ALA:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2740:A:H2'	1:A:2741:A:C8	2.46	0.50
34:7:290:GLN:HB2	34:7:291:PRO:HD3	1.92	0.50
32:5:113:LEU:HD12	32:5:311:ALA:HB1	1.93	0.50
1:A:2085:A:H2'	1:A:2086:A:C8	2.47	0.50
10:K:80:HIS:CD2	10:K:81:THR:O	2.65	0.50
24:Y:73:ASN:HA	24:Y:76:GLN:HG3	1.93	0.50
19:T:196:ALA:O	19:T:200:ILE:HG12	2.12	0.50
1:A:1952:U:H2'	1:A:1953:A:C8	2.46	0.49
5:E:74:ALA:HA	5:E:77:LEU:HD23	1.94	0.49
5:E:221:ARG:HG3	5:E:261:MET:HB3	1.94	0.49
10:K:7:ALA:HB3	10:K:8:PRO:HD3	1.94	0.49
23:X:36:ARG:NH2	23:X:151:GLU:HB2	2.27	0.49
30:3:172:TYR:HB2	30:3:175:ASP:HB2	1.94	0.49
1:A:1672:C:O2'	19:T:149:ARG:O	2.25	0.49
1:A:2169:A:H1'	1:A:2192:A:C2	2.47	0.49
1:A:2740:A:N3	1:A:2921:A:O2'	2.38	0.49
27:0:119:LYS:O	27:0:120:HIS:ND1	2.45	0.49
32:5:260:SER:OG	32:5:262:ILE:HG12	2.12	0.49
1:A:2256:U:O2'	18:S:118:ASN:ND2	2.45	0.49
24:Y:172:ILE:CD1	29:2:70:LEU:HD13	2.42	0.49
4:D:257:ILE:O	4:D:262:ARG:HG3	2.12	0.49
8:I:47:LEU:HD22	13:N:226:ILE:HG12	1.95	0.49
11:L:145:VAL:HG11	16:Q:160:VAL:HG11	1.94	0.49
1:A:3078:C:H2'	1:A:3079:G:C8	2.47	0.49
7:H:94:LEU:HD22	7:H:116:LYS:HA	1.95	0.49
1:A:3039:U:H2'	1:A:3040:OMG:C8	2.48	0.49
9:J:25:ARG:HA	9:J:65:PRO:HA	1.95	0.49
12:M:247:ILE:HG22	12:M:253:PHE:HD1	1.78	0.49
55:A1:161:ALA:HA	55:A1:164:LEU:HD23	1.94	0.49
8:I:98:VAL:HG11	8:I:146:LEU:HB3	1.94	0.49
23:X:41:VAL:HG11	23:X:83:GLU:HB3	1.95	0.49
1:A:3158:A:H2'	1:A:3159:A:C8	2.48	0.48
23:X:208:LEU:O	23:X:212:ILE:HG12	2.13	0.48
55:A1:169:LEU:HG	55:A1:251:ARG:HD3	1.96	0.48
9:J:140:VAL:O	9:J:144:ILE:HG12	2.13	0.48
1:A:2127:A:H4'	1:A:2251:A:C5	2.49	0.48
3:C:92:GLU:HB3	3:C:318:MET:SD	2.53	0.48
18:S:79:VAL:HA	18:S:82:LYS:HE3	1.95	0.48
23:X:119:LEU:HD22	32:5:53:PRO:HD2	1.95	0.48
18:S:120:LEU:HB3	18:S:122:LEU:HD12	1.96	0.48
20:U:11:ARG:HG3	21:V:211:LYS:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:A2:95:VAL:HG21	56:A2:121:LEU:HB3	1.95	0.48
1:A:2702:G:H5'	10:K:114:LYS:HE2	1.96	0.48
32:5:126:THR:HG21	32:5:357:PHE:CE1	2.48	0.48
33:6:160:ASP:OD2	33:6:267:ARG:NH2	2.47	0.48
14:O:130:LEU:HD22	27:O:134:THR:HG23	1.96	0.48
20:U:64:PRO:HB2	20:U:100:ALA:HB3	1.96	0.48
8:I:144:LEU:N	8:I:145:PRO:HD2	2.29	0.48
24:Y:175:ARG:NH2	29:2:83:MET:SD	2.84	0.48
1:A:1683:C:N4	24:Y:225:ASN:HD21	2.12	0.47
2:B:1620:A:H2'	2:B:1621:A:H4'	1.96	0.47
8:I:233:LEU:O	8:I:237:ILE:HG13	2.13	0.47
1:A:2686:G:H5'	1:A:3104:U:H4'	1.96	0.47
32:5:123:LEU:HD22	32:5:220:LEU:HD21	1.95	0.47
7:H:59:TRP:NE1	7:H:81:LYS:HG2	2.28	0.47
32:5:176:TYR:HA	32:5:179:VAL:HG12	1.96	0.47
1:A:1852:C:H2'	1:A:1853:A:C4	2.49	0.47
33:6:44:ASN:HD22	33:6:47:ARG:HB2	1.79	0.47
55:A1:178:LEU:HB3	55:A1:252:VAL:HG22	1.96	0.47
1:A:3201:A:H2'	1:A:3202:U:C6	2.50	0.47
24:Y:193:ARG:HA	24:Y:196:ARG:HE	1.80	0.47
1:A:2275:U:H2'	1:A:2276:C:H6	1.80	0.47
16:Q:99:MET:HE1	16:Q:144:GLY:HA2	1.97	0.47
1:A:2620:G:H2'	1:A:2621:G:C8	2.49	0.47
1:A:3011:A:O2'	1:A:3173:G:N2	2.47	0.47
2:B:1642:G:H4'	35:8:119:LYS:HG3	1.96	0.47
16:Q:148:THR:HG22	16:Q:165:GLU:HG2	1.97	0.47
22:W:123:GLY:HA3	33:6:40:ILE:HG21	1.96	0.47
23:X:42:HIS:CG	23:X:86:ILE:HD11	2.50	0.47
33:6:173:LEU:HD13	33:6:272:LEU:HD22	1.97	0.47
1:A:1705:A:C8	36:9:39:LYS:HD3	2.50	0.47
22:W:125:VAL:HG21	33:6:64:GLU:HG3	1.96	0.47
28:1:22:SER:HB3	28:1:56:PHE:CZ	2.49	0.47
32:5:181:VAL:CG2	32:5:347:THR:HG21	2.44	0.47
6:F:279:ARG:HH12	6:F:282:PRO:HD3	1.80	0.46
1:A:1680:A:H5'	1:A:1681:G:OP2	2.15	0.46
1:A:2840:C:O2	1:A:2840:C:O4'	2.28	0.46
14:O:141:HIS:O	14:O:147:GLN:NE2	2.48	0.46
16:Q:113:VAL:O	16:Q:137:CYS:O	2.33	0.46
3:C:256:TYR:HA	3:C:275:LYS:HD3	1.96	0.46
5:E:131:LYS:HB3	5:E:146:SER:HB2	1.98	0.46
18:S:130:LEU:HB2	18:S:156:VAL:HG23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:252:VAL:HB	55:A1:305:VAL:HG12	1.97	0.46
1:A:2607:U:H2'	1:A:2608:G:C8	2.47	0.46
1:A:2898:U:H2'	1:A:2899:C:O4'	2.15	0.46
1:A:3151:A:N1	1:A:3163:G:O2'	2.41	0.46
1:A:2081:U:H2'	1:A:2082:G:C8	2.50	0.46
1:A:2873:A:H4'	22:W:90:TYR:CZ	2.50	0.46
4:D:196:VAL:HG22	4:D:206:TYR:HB2	1.97	0.46
18:S:130:LEU:HB2	18:S:156:VAL:CG2	2.46	0.46
56:A2:172:GLY:H	56:A2:175:LYS:HB2	1.81	0.46
6:F:280:TYR:CD1	12:M:125:ARG:HD2	2.51	0.46
1:A:1839:C:H2'	1:A:1840:C:H6	1.79	0.46
32:5:300:ARG:N	32:5:301:PRO:HD2	2.30	0.46
55:A1:315:LEU:HA	55:A1:319:TYR:HD2	1.81	0.46
1:A:2297:A:H5'	17:R:40:ARG:HH22	1.80	0.46
1:A:2484:C:O2	1:A:2484:C:O4'	2.33	0.46
1:A:3078:C:H2'	1:A:3079:G:H8	1.81	0.46
14:O:30:ARG:HD2	14:O:78:PHE:O	2.16	0.46
1:A:3027:U:H4'	1:A:3173:G:H5'	1.98	0.45
6:F:110:SER:O	6:F:158:PRO:HA	2.16	0.45
8:I:231:THR:O	8:I:235:GLN:HG2	2.16	0.45
1:A:2827:A:H2'	1:A:2828:G:C8	2.51	0.45
1:A:3026:U:H5'	31:4:68:ASN:OD1	2.16	0.45
28:1:16:ILE:HD11	28:1:34:ARG:NH2	2.32	0.45
32:5:73:PRO:HG2	32:5:75:PHE:CZ	2.51	0.45
55:A1:192:LEU:HD13	55:A1:221:VAL:HG21	1.98	0.45
1:A:1733:C:O2'	1:A:1734:C:H5'	2.17	0.45
2:B:1660:G:H2'	2:B:1661:A:C8	2.51	0.45
8:I:119:HIS:HB3	8:I:163:GLU:HG3	1.98	0.45
15:P:52:ASN:HB3	15:P:55:ASN:HB2	1.99	0.45
1:A:1993:A:N3	1:A:1993:A:H2'	2.31	0.45
32:5:305:GLN:HB2	32:5:308:GLN:HG3	1.97	0.45
35:8:97:LYS:HB3	35:8:99:ARG:HH11	1.82	0.45
18:S:114:ILE:HD12	18:S:116:ILE:HD11	1.99	0.45
20:U:19:VAL:HB	36:9:136:LEU:HD23	1.98	0.45
35:8:169:PHE:HB2	35:8:170:PRO:HD3	1.99	0.45
1:A:2073:A:C5	1:A:2074:A:H1'	2.51	0.45
1:A:2180:A:H4'	1:A:2181:A:H8	1.81	0.45
1:A:3111:A:O2'	1:A:3112:A:H5''	2.16	0.45
5:E:328:LEU:HD13	5:E:332:LEU:HD11	1.99	0.45
1:A:1952:U:H2'	1:A:1953:A:H8	1.82	0.45
22:W:102:GLU:HB2	22:W:130:PHE:CD1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3173:G:H2'	1:A:3174:U:O4'	2.17	0.45
3:C:60:ILE:HD12	3:C:220:LEU:HD23	1.98	0.45
1:A:2854:U:H4'	30:3:138:PRO:HG2	1.98	0.45
2:B:1622:A:H2'	2:B:1623:G:C8	2.52	0.45
22:W:70:GLN:O	22:W:71:ARG:HB3	2.17	0.45
56:A2:139:GLU:HB2	56:A2:140:PRO:HD3	1.99	0.45
1:A:1871:A:N7	1:A:1901:C:N4	2.65	0.44
1:A:2408:U:H2'	1:A:2409:A:C8	2.52	0.44
20:U:11:ARG:HH21	32:5:82:TYR:HE1	1.64	0.44
23:X:183:ARG:O	23:X:187:ILE:HG12	2.17	0.44
25:Z:70:THR:HG22	25:Z:97:PRO:HA	1.99	0.44
2:B:1607:U:H2'	2:B:1608:G:C8	2.52	0.44
2:B:1626:C:H2'	2:B:1627:C:C6	2.52	0.44
3:C:60:ILE:O	3:C:60:ILE:HG13	2.18	0.44
12:M:73:PRO:O	12:M:77:ARG:HG3	2.18	0.44
55:A1:259:THR:HG23	55:A1:316:GLN:HE22	1.82	0.44
1:A:1860:A:H2'	1:A:1861:U:C6	2.53	0.44
1:A:1918:G:O5'	29:2:63:LYS:NZ	2.49	0.44
1:A:2087:U:H2'	1:A:2088:U:C6	2.52	0.44
1:A:2802:A:H2'	1:A:2803:A:C8	2.53	0.44
1:A:3088:C:H4'	1:A:3089:A:C5	2.52	0.44
5:E:316:PHE:HB3	5:E:317:PRO:HD3	2.00	0.44
15:P:110:TRP:HA	15:P:113:LYS:HB2	1.99	0.44
1:A:1756:A:H2'	1:A:1757:A:H8	1.83	0.44
6:F:103:GLN:HE22	6:F:250:VAL:H	1.65	0.44
8:I:219:HIS:O	8:I:223:GLN:HG2	2.17	0.44
1:A:2286:A:H2'	1:A:2287:U:C6	2.53	0.44
3:C:83:ASN:ND2	3:C:154:VAL:O	2.43	0.44
21:V:62:VAL:HG12	21:V:122:LEU:HD23	1.98	0.44
1:A:2989:G:H5''	1:A:2990:A:C2	2.52	0.44
28:1:16:ILE:HD12	28:1:61:LYS:HG3	1.99	0.44
55:A1:82:ALA:O	55:A1:86:VAL:HG23	2.17	0.44
1:A:1884:G:H1'	1:A:1895:C:H1'	1.99	0.44
1:A:2668:A:H2'	1:A:2669:A:C8	2.53	0.44
1:A:2684:C:N3	17:R:32:ARG:HD3	2.33	0.44
4:D:63:PHE:HB3	4:D:87:HIS:HA	1.99	0.44
5:E:194:TYR:HD1	5:E:281:ASN:HD21	1.63	0.44
13:N:89:ILE:HD11	13:N:176:LEU:HB3	2.00	0.44
1:A:1718:A:H2'	1:A:1719:G:O4'	2.18	0.44
56:A2:237:ALA:HB2	56:A2:253:TYR:CZ	2.53	0.44
1:A:1994:A:H2'	1:A:2002:G:N7	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2173:G:H2'	1:A:2174:G:H8	1.83	0.43
1:A:2805:A:H2'	1:A:2806:U:C6	2.53	0.43
1:A:2970:C:H2'	1:A:2971:A:O4'	2.18	0.43
3:C:111:THR:HA	3:C:122:ILE:HD11	2.00	0.43
33:6:144:GLY:O	33:6:148:LYS:HG2	2.17	0.43
1:A:2041:U:H5'	12:M:56:GLU:HB3	1.98	0.43
3:C:207:LEU:H	3:C:207:LEU:HD23	1.83	0.43
23:X:89:GLN:HE21	23:X:100:ARG:HG2	1.83	0.43
33:6:333:GLN:HG2	33:6:334:LEU:HD12	2.00	0.43
1:A:2750:U:H2'	1:A:2751:G:C8	2.53	0.43
1:A:2898:U:O2	1:A:2898:U:O4'	2.34	0.43
3:C:118:ASN:O	3:C:122:ILE:HG13	2.18	0.43
33:6:234:HIS:HE1	33:6:257:PRO:HA	1.83	0.43
36:9:71:LYS:HB3	36:9:72:PRO:HD2	2.00	0.43
1:A:2679:U:O2'	27:0:81:PRO:O	2.35	0.43
1:A:2847:C:H2'	1:A:2848:A:O4'	2.18	0.43
1:A:2395:A:H1'	32:5:385:HIS:HB2	2.00	0.43
6:F:113:LYS:HD2	6:F:157:GLY:HA2	1.99	0.43
22:W:143:LYS:HE2	33:6:345:VAL:HG11	2.00	0.43
31:4:69:LYS:HB2	31:4:72:LEU:HD23	1.99	0.43
34:7:64:LYS:HD2	34:7:80:VAL:HG12	2.01	0.43
1:A:1789:A:H5''	36:9:17:ARG:HH21	1.82	0.43
1:A:2677:A:H2'	1:A:2678:A:C8	2.53	0.43
21:V:80:ILE:HB	21:V:85:TRP:HB2	2.00	0.43
1:A:2392:U:H2'	1:A:2394:A:H62	1.84	0.43
1:A:1882:A:N6	1:A:1893:A:O4'	2.51	0.43
1:A:2098:G:H2'	1:A:2099:U:C6	2.54	0.43
1:A:2801:A:H2'	1:A:2802:A:C8	2.54	0.43
4:D:123:GLU:HG2	4:D:162:THR:HG22	2.01	0.43
5:E:54:SER:O	5:E:58:VAL:HG23	2.19	0.43
8:I:163:GLU:O	8:I:166:ARG:HG2	2.18	0.43
12:M:211:VAL:N	12:M:212:PRO:HD2	2.34	0.43
21:V:122:LEU:HD12	21:V:133:ILE:HG13	1.99	0.43
11:L:49:SER:OG	11:L:78:LYS:HD2	2.19	0.43
23:X:163:ARG:HE	32:5:55:LEU:HD13	1.83	0.43
32:5:310:ARG:HD3	32:5:378:SER:HB3	2.00	0.43
33:6:329:TYR:HB3	33:6:333:GLN:HE22	1.84	0.43
55:A1:292:LEU:HD21	55:A1:380:MET:HE1	2.01	0.43
1:A:1851:G:C2	1:A:2099:U:H4'	2.54	0.43
1:A:2111:C:C4	1:A:2945:A:H5'	2.54	0.43
1:A:2607:U:C2	1:A:2608:G:N7	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:86:VAL:HG21	21:V:120:VAL:HG21	2.01	0.43
1:A:2493:C:O4'	1:A:2493:C:O2	2.37	0.42
1:A:2510:U:C5	1:A:2539:A:C6	3.07	0.42
6:F:263:LEU:HA	6:F:266:VAL:HG12	2.01	0.42
12:M:217:ALA:O	12:M:220:ARG:HD2	2.19	0.42
20:U:74:HIS:HB2	36:9:24:LYS:HE3	2.00	0.42
34:7:180:CYS:HA	34:7:297:PHE:O	2.20	0.42
1:A:1839:C:H5'	10:K:115:ASN:HB2	2.00	0.42
1:A:2212:C:H2'	1:A:2213:A:H8	1.84	0.42
1:A:2700:G:H2'	1:A:2701:G:C8	2.54	0.42
1:A:2479:C:O2	5:E:230:THR:HB	2.19	0.42
1:A:1977:U:H2'	1:A:1978:A:C8	2.52	0.42
1:A:2495:U:O4	1:A:2509:A:H2	2.02	0.42
33:6:275:GLN:HE21	33:6:279:ILE:HG22	1.85	0.42
34:7:146:CYS:O	34:7:278:TYR:OH	2.36	0.42
1:A:2186:C:H2'	1:A:2187:C:H6	1.81	0.42
32:5:123:LEU:HD22	32:5:220:LEU:CD2	2.50	0.42
35:8:113:ARG:O	35:8:117:LEU:HG	2.20	0.42
55:A1:308:SER:HA	55:A1:376:TYR:O	2.20	0.42
1:A:2293:A:H5'	17:R:12:ASN:HB2	2.01	0.42
1:A:2814:G:H1	1:A:2988:C:H42	1.67	0.42
5:E:102:LEU:HD21	5:E:294:ASN:HA	2.02	0.42
6:F:83:HIS:CG	6:F:274:LEU:HD11	2.54	0.42
7:H:55:ILE:HG21	23:X:44:ARG:HG2	2.01	0.42
32:5:351:VAL:HG22	32:5:381:LEU:HB3	2.02	0.42
32:5:208:THR:HA	32:5:224:GLY:O	2.20	0.42
1:A:1851:G:H21	1:A:2134:A:N6	2.17	0.42
7:H:95:GLU:HB3	7:H:111:LEU:HD11	2.01	0.42
11:L:87:VAL:HG12	11:L:127:LEU:HD11	2.02	0.42
13:N:152:THR:HA	13:N:153:PRO:HD3	1.90	0.42
55:A1:368:LEU:HD21	56:A2:316:PHE:HB2	2.02	0.42
10:K:27:PRO:HG2	10:K:30:LYS:HB2	2.02	0.42
12:M:153:ASN:HB2	12:M:256:LEU:HD23	2.02	0.41
16:Q:165:GLU:HB2	16:Q:168:ASN:HB2	2.00	0.41
25:Z:36:PHE:CE2	25:Z:79:PRO:HG3	2.53	0.41
30:3:175:ASP:HB3	30:3:178:GLN:HB2	2.01	0.41
8:I:132:LYS:HB3	8:I:133:PRO:HD3	2.01	0.41
10:K:60:MET:HB3	10:K:133:ILE:HD11	2.02	0.41
12:M:176:THR:HG21	12:M:213:TYR:HE1	1.84	0.41
32:5:313:MET:CE	32:5:353:HIS:HB2	2.49	0.41
1:A:2026:A:H2'	1:A:2027:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L:85:LEU:HD11	11:L:134:TYR:HE1	1.84	0.41
14:O:62:TYR:CD2	14:O:75:MET:HG2	2.55	0.41
1:A:2072:A:H2'	1:A:2073:A:C8	2.55	0.41
1:A:2173:G:H2'	1:A:2174:G:C8	2.55	0.41
4:D:216:LEU:HD21	4:D:219:LYS:HD2	2.02	0.41
5:E:61:ILE:HD11	14:O:149:LEU:HD22	2.02	0.41
14:O:134:PRO:HD3	27:O:130:VAL:HG21	2.01	0.41
55:A1:337:GLN:HB2	55:A1:383:LEU:HD11	2.02	0.41
56:A2:288:PRO:HG2	56:A2:293:ILE:HD11	2.03	0.41
5:E:48:TRP:CZ2	5:E:51:GLU:HG3	2.56	0.41
8:I:221:LEU:HA	8:I:224:HIS:CD2	2.43	0.41
14:O:106:ARG:HD3	14:O:135:LEU:HD21	2.03	0.41
15:P:68:TRP:CH2	22:W:132:HIS:HE1	2.39	0.41
16:Q:240:ILE:HG21	16:Q:243:ILE:HD12	2.03	0.41
32:5:228:ALA:HB1	32:5:292:TYR:HB2	2.02	0.41
12:M:177:ALA:HB1	12:M:203:ARG:HH22	1.85	0.41
16:Q:80:PHE:HB3	16:Q:282:ILE:HG21	2.03	0.41
34:7:139:ASN:HB3	34:7:174:VAL:HG21	2.02	0.41
1:A:1756:A:H2'	1:A:1757:A:C8	2.56	0.41
5:E:345:ILE:HG12	16:Q:169:PRO:HB2	2.03	0.41
34:7:84:ASN:O	34:7:118:PRO:HB3	2.21	0.41
1:A:2318:A:H2'	1:A:2319:A:C8	2.56	0.41
1:A:2748:A:H2'	1:A:2749:A:C8	2.56	0.41
1:A:3117:C:H2'	1:A:3118:U:C6	2.56	0.41
14:O:18:MET:HG3	14:O:25:ARG:HG3	2.02	0.41
15:P:107:THR:O	15:P:113:LYS:HG3	2.21	0.41
34:7:163:MET:HB3	34:7:186:ASP:HB3	2.02	0.41
1:A:1851:G:H2'	1:A:1852:C:C6	2.55	0.41
1:A:1974:A:H5'	4:D:261:GLY:HA2	2.02	0.41
1:A:2630:U:H2'	1:A:2631:G:C4	2.56	0.41
1:A:2726:C:H2'	1:A:2727:C:C6	2.56	0.41
1:A:2734:A:H2'	1:A:2735:G:H8	1.86	0.41
4:D:218:ARG:HG2	4:D:225:ILE:HB	2.02	0.41
6:F:143:SER:HG	6:F:146:TRP:HD1	1.69	0.41
10:K:138:LEU:HD23	10:K:138:LEU:HA	1.97	0.41
15:P:171:VAL:HG12	15:P:173:ARG:H	1.86	0.41
21:V:64:ILE:HG13	21:V:120:VAL:HG12	2.02	0.41
24:Y:105:LEU:HD13	24:Y:139:MET:HG2	2.03	0.41
27:O:166:SER:H	27:O:169:ASP:HB2	1.85	0.41
33:6:179:VAL:HG11	33:6:197:GLU:HG2	2.02	0.41
34:7:129:THR:HG23	34:7:131:LYS:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:A2:236:TYR:CE2	56:A2:240:ARG:HD3	2.56	0.41
1:A:2203:G:H21	1:A:2208:A:H62	1.69	0.41
1:A:2726:C:H2'	1:A:2727:C:H6	1.86	0.41
17:R:17:ARG:O	17:R:21:ILE:HG12	2.21	0.41
18:S:83:VAL:HA	18:S:86:MET:HE3	2.03	0.41
32:5:177:CYS:O	32:5:180:ILE:HG22	2.20	0.41
32:5:257:TYR:CD1	32:5:258:PRO:HA	2.56	0.41
1:A:2072:A:N6	1:A:2831:G:H5'	2.36	0.40
1:A:2948:C:H2'	1:A:2949:C:C6	2.56	0.40
1:A:3155:C:H2'	1:A:3156:A:C8	2.56	0.40
4:D:195:ASN:ND2	4:D:208:ARG:HB3	2.36	0.40
4:D:290:PRO:N	4:D:291:PRO:HD2	2.37	0.40
6:F:82:LEU:HD22	6:F:266:VAL:HG21	2.04	0.40
10:K:25:MET:HB2	10:K:151:ILE:HG12	2.03	0.40
20:U:130:LEU:HD11	21:V:98:ILE:HD11	2.02	0.40
1:A:1855:A:H2'	1:A:1856:A:C8	2.56	0.40
1:A:3117:C:H2'	1:A:3118:U:H6	1.87	0.40
2:B:1659:U:H2'	2:B:1660:G:C8	2.56	0.40
8:I:200:LEU:N	8:I:201:PRO:HD2	2.36	0.40
32:5:52:ILE:HA	32:5:53:PRO:HD3	1.86	0.40
32:5:115:GLU:HB3	32:5:118:LYS:HB2	2.03	0.40
56:A2:232:TYR:HD2	56:A2:258:LEU:HD11	1.86	0.40
1:A:3163:G:H2'	1:A:3164:C:C6	2.56	0.40
7:H:79:VAL:HG22	23:X:89:GLN:HB2	2.04	0.40
17:R:51:VAL:HG21	18:S:174:PHE:HB3	2.03	0.40
23:X:143:PHE:HE2	23:X:190:LYS:HE2	1.87	0.40
34:7:180:CYS:HB3	34:7:298:GLN:HG2	2.03	0.40
35:8:158:HIS:HA	35:8:161:ALA:HB3	2.04	0.40
6:F:126:LYS:HG3	6:F:139:GLY:HA2	2.04	0.40
8:I:224:HIS:O	8:I:228:GLN:N	2.51	0.40
16:Q:138:ILE:HA	16:Q:187:LEU:HB2	2.04	0.40
23:X:174:PRO:HA	23:X:184:ARG:NE	2.36	0.40
32:5:211:ALA:HB1	32:5:322:LEU:HD23	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
3	C	234/333 (70%)	231 (99%)	3 (1%)	0	100	100
4	D	236/305 (77%)	229 (97%)	6 (2%)	1 (0%)	30	52
5	E	302/348 (87%)	290 (96%)	12 (4%)	0	100	100
6	F	248/311 (80%)	243 (98%)	5 (2%)	0	100	100
7	H	86/267 (32%)	85 (99%)	1 (1%)	0	100	100
8	I	203/261 (78%)	196 (97%)	7 (3%)	0	100	100
9	J	138/192 (72%)	134 (97%)	4 (3%)	0	100	100
10	K	175/178 (98%)	172 (98%)	3 (2%)	0	100	100
11	L	113/145 (78%)	109 (96%)	4 (4%)	0	100	100
12	M	285/296 (96%)	280 (98%)	5 (2%)	0	100	100
13	N	202/251 (80%)	201 (100%)	1 (0%)	0	100	100
14	O	150/175 (86%)	150 (100%)	0	0	100	100
15	P	139/179 (78%)	135 (97%)	4 (3%)	0	100	100
16	Q	215/292 (74%)	210 (98%)	5 (2%)	0	100	100
17	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
18	S	154/205 (75%)	151 (98%)	3 (2%)	0	100	100
19	T	164/212 (77%)	160 (98%)	4 (2%)	0	100	100
20	U	135/153 (88%)	132 (98%)	3 (2%)	0	100	100
21	V	200/216 (93%)	196 (98%)	4 (2%)	0	100	100
22	W	99/148 (67%)	94 (95%)	5 (5%)	0	100	100
23	X	241/256 (94%)	235 (98%)	6 (2%)	0	100	100
24	Y	174/250 (70%)	171 (98%)	3 (2%)	0	100	100
25	Z	118/161 (73%)	114 (97%)	4 (3%)	0	100	100
26	a	78/142 (55%)	76 (97%)	2 (3%)	0	100	100
27	0	106/188 (56%)	102 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	1	50/65 (77%)	50 (100%)	0	0	100	100
29	2	43/92 (47%)	42 (98%)	1 (2%)	0	100	100
30	3	93/188 (50%)	91 (98%)	2 (2%)	0	100	100
31	4	36/103 (35%)	36 (100%)	0	0	100	100
32	5	390/423 (92%)	381 (98%)	9 (2%)	0	100	100
33	6	316/380 (83%)	310 (98%)	6 (2%)	0	100	100
34	7	285/338 (84%)	268 (94%)	17 (6%)	0	100	100
35	8	83/206 (40%)	80 (96%)	3 (4%)	0	100	100
36	9	121/137 (88%)	120 (99%)	1 (1%)	0	100	100
37	b	146/215 (68%)	139 (95%)	7 (5%)	0	100	100
38	c	284/332 (86%)	279 (98%)	5 (2%)	0	100	100
39	d	214/302 (71%)	208 (97%)	6 (3%)	0	100	100
40	e	211/279 (76%)	200 (95%)	11 (5%)	0	100	100
41	f	124/212 (58%)	121 (98%)	2 (2%)	1 (1%)	16	34
42	g	129/166 (78%)	125 (97%)	4 (3%)	0	100	100
43	h	101/158 (64%)	100 (99%)	1 (1%)	0	100	100
44	i	95/128 (74%)	91 (96%)	4 (4%)	0	100	100
45	j	83/123 (68%)	83 (100%)	0	0	100	100
46	k	93/112 (83%)	90 (97%)	3 (3%)	0	100	100
47	l	42/138 (30%)	41 (98%)	0	1 (2%)	5	9
48	m	38/128 (30%)	35 (92%)	3 (8%)	0	100	100
49	o	78/102 (76%)	78 (100%)	0	0	100	100
50	p	119/205 (58%)	115 (97%)	4 (3%)	0	100	100
51	q	133/222 (60%)	132 (99%)	1 (1%)	0	100	100
52	r	153/196 (78%)	152 (99%)	1 (1%)	0	100	100
53	s	368/439 (84%)	359 (98%)	8 (2%)	1 (0%)	37	59
54	n	213/246 (87%)	211 (99%)	2 (1%)	0	100	100
55	A1	331/384 (86%)	328 (99%)	3 (1%)	0	100	100
56	A2	236/381 (62%)	233 (99%)	3 (1%)	0	100	100
57	v	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
58	u	127/234 (54%)	125 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	t1	44/198 (22%)	43 (98%)	1 (2%)	0	100	100
59	t2	28/198 (14%)	28 (100%)	0	0	100	100
59	t3	28/198 (14%)	28 (100%)	0	0	100	100
59	t4	27/198 (14%)	27 (100%)	0	0	100	100
59	t5	27/198 (14%)	27 (100%)	0	0	100	100
59	t6	25/198 (13%)	25 (100%)	0	0	100	100
60	w	85/156 (54%)	82 (96%)	3 (4%)	0	100	100
All	All	9399/13661 (69%)	9179 (98%)	216 (2%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
47	l	102	GLY
53	s	272	PRO
4	D	220	VAL
41	f	179	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	
3	C	211/286 (74%)	208 (99%)	3 (1%)	62	82
4	D	192/245 (78%)	190 (99%)	2 (1%)	73	88
5	E	259/290 (89%)	259 (100%)	0	100	100
6	F	217/262 (83%)	216 (100%)	1 (0%)	86	95
7	H	82/228 (36%)	82 (100%)	0	100	100
8	I	189/232 (82%)	188 (100%)	1 (0%)	86	95
9	J	113/150 (75%)	112 (99%)	1 (1%)	75	90
10	K	155/156 (99%)	153 (99%)	2 (1%)	65	84
11	L	98/124 (79%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	M	245/249 (98%)	242 (99%)	3 (1%)	67	85
13	N	179/211 (85%)	179 (100%)	0	100	100
14	O	133/150 (89%)	133 (100%)	0	100	100
15	P	123/154 (80%)	123 (100%)	0	100	100
16	Q	199/256 (78%)	199 (100%)	0	100	100
17	R	118/126 (94%)	115 (98%)	3 (2%)	42	68
18	S	141/180 (78%)	138 (98%)	3 (2%)	48	73
19	T	146/182 (80%)	145 (99%)	1 (1%)	81	93
20	U	124/135 (92%)	122 (98%)	2 (2%)	58	79
21	V	180/191 (94%)	180 (100%)	0	100	100
22	W	83/119 (70%)	82 (99%)	1 (1%)	67	85
23	X	219/229 (96%)	219 (100%)	0	100	100
24	Y	159/223 (71%)	159 (100%)	0	100	100
25	Z	111/147 (76%)	110 (99%)	1 (1%)	75	90
26	a	78/133 (59%)	76 (97%)	2 (3%)	41	67
27	0	97/164 (59%)	97 (100%)	0	100	100
28	1	49/60 (82%)	49 (100%)	0	100	100
29	2	39/72 (54%)	39 (100%)	0	100	100
30	3	88/166 (53%)	88 (100%)	0	100	100
31	4	37/89 (42%)	37 (100%)	0	100	100
32	5	353/368 (96%)	351 (99%)	2 (1%)	84	94
33	6	286/332 (86%)	286 (100%)	0	100	100
34	7	263/303 (87%)	262 (100%)	1 (0%)	89	96
35	8	77/190 (40%)	75 (97%)	2 (3%)	41	67
36	9	104/112 (93%)	104 (100%)	0	100	100
37	b	130/186 (70%)	129 (99%)	1 (1%)	79	91
38	c	250/288 (87%)	249 (100%)	1 (0%)	89	96
39	d	204/271 (75%)	203 (100%)	1 (0%)	86	95
40	e	188/236 (80%)	186 (99%)	2 (1%)	70	86
41	f	114/188 (61%)	112 (98%)	2 (2%)	54	77
42	g	121/148 (82%)	119 (98%)	2 (2%)	56	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	h	100/148 (68%)	99 (99%)	1 (1%)	73	88
44	i	86/110 (78%)	84 (98%)	2 (2%)	45	71
45	j	68/97 (70%)	66 (97%)	2 (3%)	37	64
46	k	80/90 (89%)	80 (100%)	0	100	100
47	l	43/116 (37%)	40 (93%)	3 (7%)	12	27
48	m	37/113 (33%)	35 (95%)	2 (5%)	18	39
49	o	68/87 (78%)	68 (100%)	0	100	100
50	p	117/180 (65%)	116 (99%)	1 (1%)	75	90
51	q	115/178 (65%)	115 (100%)	0	100	100
52	r	143/169 (85%)	137 (96%)	6 (4%)	25	50
53	s	328/381 (86%)	324 (99%)	4 (1%)	67	85
54	n	179/209 (86%)	178 (99%)	1 (1%)	84	94
55	A1	290/328 (88%)	288 (99%)	2 (1%)	81	93
56	A2	221/350 (63%)	219 (99%)	2 (1%)	75	90
57	v	59/60 (98%)	53 (90%)	6 (10%)	6	12
58	u	120/200 (60%)	120 (100%)	0	100	100
59	t1	40/158 (25%)	40 (100%)	0	100	100
59	t2	29/158 (18%)	29 (100%)	0	100	100
59	t3	29/158 (18%)	29 (100%)	0	100	100
59	t4	28/158 (18%)	28 (100%)	0	100	100
59	t5	28/158 (18%)	27 (96%)	1 (4%)	30	56
59	t6	26/158 (16%)	26 (100%)	0	100	100
60	w	81/136 (60%)	78 (96%)	3 (4%)	29	55
All	All	8469/11731 (72%)	8393 (99%)	76 (1%)	74	90

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	278	LYS
3	C	288	THR
3	C	290	ASN
4	D	208	ARG
4	D	297	LYS
6	F	236	ARG

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Mol	Chain	Res	Type
8	I	82	LEU
9	J	114	LEU
10	K	2	SER
10	K	124	ARG
12	M	44	ARG
12	M	65	LEU
12	M	132	LEU
17	R	13	ARG
17	R	29	ARG
17	R	37	ARG
18	S	104	ARG
18	S	144	LEU
18	S	173	ARG
19	T	163	ARG
20	U	24	PHE
20	U	79	ARG
22	W	49	ARG
25	Z	78	ARG
26	a	114	LYS
26	a	122	ARG
32	5	55	LEU
32	5	67	VAL
34	7	165	ASN
35	8	101	ARG
35	8	104	VAL
37	b	72	VAL
38	c	171	ARG
39	d	53	MET
40	e	123	MET
40	e	242	ASP
41	f	171	LEU
41	f	207	LEU
42	g	43	ASP
42	g	137	VAL
43	h	58	ARG
44	i	34	ILE
44	i	84	LYS
45	j	88	LEU
45	j	99	GLN
47	l	106	THR
47	l	110	LEU
47	l	114	SER

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Mol	Chain	Res	Type
48	m	57	VAL
48	m	63	THR
50	p	116	ARG
52	r	39	VAL
52	r	56	THR
52	r	58	LYS
52	r	70	CYS
52	r	135	LEU
52	r	159	VAL
53	s	66	TRP
53	s	81	ARG
53	s	165	ARG
53	s	271	LEU
54	n	113	LEU
55	A1	37	LYS
55	A1	297	LEU
56	A2	152	LEU
56	A2	295	ARG
57	v	4	TRP
57	v	39	PHE
57	v	41	LYS
57	v	52	GLU
57	v	53	ARG
57	v	55	LEU
59	t5	27	LYS
60	w	88	LYS
60	w	132	ASP
60	w	137	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	195	ASN
5	E	125	GLN
5	E	277	ASN
5	E	280	HIS
5	E	286	ASN
6	F	103	GLN
6	F	184	GLN
6	F	249	ASN
7	H	136	ASN
10	K	70	ASN

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Mol	Chain	Res	Type
10	K	80	HIS
12	M	53	HIS
14	O	100	GLN
15	P	147	GLN
18	S	118	ASN
20	U	74	HIS
22	W	51	GLN
23	X	236	GLN
24	Y	92	ASN
24	Y	183	GLN
24	Y	225	ASN
32	5	183	ASN
32	5	343	GLN
33	6	354	GLN
35	8	143	GLN
36	9	129	GLN
36	9	134	ASN
37	b	90	HIS
37	b	129	GLN
38	c	65	ASN
38	c	172	ASN
40	e	67	GLN
43	h	67	GLN
45	j	31	GLN
46	k	15	GLN
51	q	120	HIS
52	r	184	ASN
53	s	420	GLN
55	A1	85	HIS
55	A1	230	GLN
55	A1	290	GLN
55	A1	316	GLN
56	A2	217	HIS
59	t5	5	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1447/1559 (92%)	363 (25%)	48 (3%)
2	B	56/69 (81%)	13 (23%)	2 (3%)
All	All	1503/1628 (92%)	376 (25%)	50 (3%)

All (376) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1672	C
1	A	1678	C
1	A	1679	U
1	A	1681	G
1	A	1685	C
1	A	1689	C
1	A	1692	A
1	A	1693	C
1	A	1694	U
1	A	1699	C
1	A	1700	U
1	A	1704	U
1	A	1708	A
1	A	1714	C
1	A	1715	C
1	A	1724	A
1	A	1727	A
1	A	1728	U
1	A	1734	C
1	A	1735	A
1	A	1736	A
1	A	1737	A
1	A	1748	G
1	A	1762	A
1	A	1763	A
1	A	1764	C
1	A	1765	C
1	A	1767	G
1	A	1770	G
1	A	1777	A
1	A	1794	A
1	A	1803	A
1	A	1804	A
1	A	1805	A
1	A	1812	C
1	A	1817	C
1	A	1821	A
1	A	1827	C
1	A	1828	A
1	A	1829	A
1	A	1832	A
1	A	1836	A

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Mol	Chain	Res	Type
1	A	1844	A
1	A	1850	U
1	A	1851	G
1	A	1853	A
1	A	1854	U
1	A	1855	A
1	A	1856	A
1	A	1867	A
1	A	1869	A
1	A	1871	A
1	A	1872	U
1	A	1878	U
1	A	1882	A
1	A	1883	G
1	A	1887	A
1	A	1888	G
1	A	1893	A
1	A	1901	C
1	A	1903	C
1	A	1909	A
1	A	1918	G
1	A	1936	A
1	A	1937	A
1	A	1938	A
1	A	1939	G
1	A	1940	A
1	A	1944	C
1	A	1946	C
1	A	1974	A
1	A	1975	U
1	A	1985	G
1	A	1986	A
1	A	1992	C
1	A	1994	A
1	A	1995	A
1	A	2000	C
1	A	2001	C
1	A	2002	G
1	A	2015	G
1	A	2021	U
1	A	2022	G
1	A	2023	U

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Mol	Chain	Res	Type
1	A	2029	A
1	A	2030	U
1	A	2036	C
1	A	2037	U
1	A	2039	A
1	A	2060	A
1	A	2061	C
1	A	2065	A
1	A	2070	C
1	A	2071	U
1	A	2074	A
1	A	2079	C
1	A	2085	A
1	A	2092	C
1	A	2093	U
1	A	2098	G
1	A	2108	G
1	A	2110	A
1	A	2111	C
1	A	2112	A
1	A	2126	U
1	A	2131	A
1	A	2136	C
1	A	2142	A
1	A	2147	G
1	A	2154	A
1	A	2158	U
1	A	2159	U
1	A	2163	A
1	A	2164	C
1	A	2168	U
1	A	2172	A
1	A	2173	G
1	A	2175	C
1	A	2179	A
1	A	2181	A
1	A	2182	G
1	A	2183	C
1	A	2187	C
1	A	2189	C
1	A	2192	A
1	A	2194	U

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Mol	Chain	Res	Type
1	A	2197	G
1	A	2198	A
1	A	2199	A
1	A	2200	A
1	A	2210	C
1	A	2211	U
1	A	2220	A
1	A	2221	C
1	A	2222	U
1	A	2228	A
1	A	2233	U
1	A	2237	A
1	A	2239	A
1	A	2241	A
1	A	2242	U
1	A	2243	A
1	A	2244	U
1	A	2245	A
1	A	2246	A
1	A	2262	C
1	A	2263	C
1	A	2264	A
1	A	2284	C
1	A	2285	U
1	A	2297	A
1	A	2300	G
1	A	2322	C
1	A	2324	U
1	A	2332	C
1	A	2345	G
1	A	2357	C
1	A	2359	C
1	A	2360	U
1	A	2361	G
1	A	2362	A
1	A	2363	A
1	A	2364	C
1	A	2369	A
1	A	2371	U
1	A	2374	A
1	A	2381	A
1	A	2390	A

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Mol	Chain	Res	Type
1	A	2401	A
1	A	2404	U
1	A	2405	C
1	A	2406	A
1	A	2407	U
1	A	2415	C
1	A	2416	U
1	A	2418	A
1	A	2427	C
1	A	2434	A
1	A	2444	A
1	A	2446	A
1	A	2451	A
1	A	2452	A
1	A	2458	A
1	A	2478	G
1	A	2493	C
1	A	2500	A
1	A	2502	C
1	A	2507	A
1	A	2511	C
1	A	2520	C
1	A	2521	A
1	A	2523	C
1	A	2524	A
1	A	2527	A
1	A	2530	A
1	A	2531	U
1	A	2536	G
1	A	2539	A
1	A	2540	C
1	A	2547	C
1	A	2548	C
1	A	2549	C
1	A	2550	A
1	A	2551	G
1	A	2552	U
1	A	2603	C
1	A	2604	A
1	A	2605	C
1	A	2606	U
1	A	2607	U

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Mol	Chain	Res	Type
1	A	2611	C
1	A	2615	A
1	A	2617	A
1	A	2619	A
1	A	2621	G
1	A	2626	U
1	A	2628	U
1	A	2629	A
1	A	2630	U
1	A	2633	A
1	A	2634	U
1	A	2638	U
1	A	2644	A
1	A	2645	G
1	A	2654	U
1	A	2655	G
1	A	2656	U
1	A	2660	U
1	A	2683	C
1	A	2684	C
1	A	2686	G
1	A	2693	A
1	A	2694	A
1	A	2696	A
1	A	2698	G
1	A	2699	C
1	A	2706	A
1	A	2709	A
1	A	2718	C
1	A	2719	G
1	A	2722	A
1	A	2724	G
1	A	2732	G
1	A	2733	G
1	A	2739	U
1	A	2740	A
1	A	2744	U
1	A	2745	A
1	A	2756	C
1	A	2803	A
1	A	2804	A
1	A	2810	G

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Mol	Chain	Res	Type
1	A	2814	G
1	A	2815	G
1	A	2816	G
1	A	2829	C
1	A	2831	G
1	A	2832	A
1	A	2833	A
1	A	2841	U
1	A	2843	C
1	A	2844	G
1	A	2847	C
1	A	2854	U
1	A	2861	A
1	A	2864	U
1	A	2865	C
1	A	2889	C
1	A	2893	A
1	A	2895	U
1	A	2906	C
1	A	2913	A
1	A	2915	C
1	A	2916	G
1	A	2917	G
1	A	2918	A
1	A	2922	A
1	A	2926	A
1	A	2928	C
1	A	2935	A
1	A	2936	U
1	A	2937	A
1	A	2938	A
1	A	2939	C
1	A	2941	G
1	A	2942	C
1	A	2943	G
1	A	2944	C
1	A	2945	A
1	A	2956	A
1	A	2962	C
1	A	2963	A
1	A	2965	A
1	A	2982	C

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Mol	Chain	Res	Type
1	A	2989	G
1	A	2990	A
1	A	2991	U
1	A	2992	G
1	A	2993	U
1	A	2995	G
1	A	3000	A
1	A	3005	A
1	A	3016	G
1	A	3018	A
1	A	3022	G
1	A	3038	U
1	A	3042	U
1	A	3043	C
1	A	3044	A
1	A	3049	U
1	A	3051	A
1	A	3053	A
1	A	3054	G
1	A	3056	C
1	A	3059	A
1	A	3060	C
1	A	3061	G
1	A	3063	G
1	A	3068	G
1	A	3069	A
1	A	3086	U
1	A	3089	A
1	A	3090	G
1	A	3097	U
1	A	3100	U
1	A	3102	U
1	A	3108	U
1	A	3109	U
1	A	3110	C
1	A	3111	A
1	A	3112	A
1	A	3113	A
1	A	3114	U
1	A	3122	U
1	A	3123	G
1	A	3124	U

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Mol	Chain	Res	Type
1	A	3140	A
1	A	3141	A
1	A	3150	U
1	A	3151	A
1	A	3157	C
1	A	3158	A
1	A	3162	C
1	A	3168	C
1	A	3169	C
1	A	3172	C
1	A	3173	G
1	A	3180	A
1	A	3184	C
1	A	3189	C
1	A	3190	A
1	A	3199	U
1	A	3200	U
1	A	3201	A
1	A	3207	A
1	A	3208	C
1	A	3209	A
1	A	3211	C
1	A	3212	C
1	A	3217	A
1	A	3218	A
1	A	3220	A
1	A	3228	U
2	B	1608	G
2	B	1609	U
2	B	1610	A
2	B	1611	G
2	B	1615	A
2	B	1617	C
2	B	1620	A
2	B	1621	A
2	B	1634	A
2	B	1644	G
2	B	1645	A
2	B	1651	A
2	B	1669	G

All (50) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1736	A
1	A	1811	A
1	A	1853	A
1	A	1855	A
1	A	1871	A
1	A	1888	G
1	A	1936	A
1	A	1973	G
1	A	1974	A
1	A	1994	A
1	A	2021	U
1	A	2029	A
1	A	2065	A
1	A	2135	A
1	A	2160	A
1	A	2182	G
1	A	2186	C
1	A	2209	G
1	A	2219	C
1	A	2220	A
1	A	2245	A
1	A	2359	C
1	A	2361	G
1	A	2363	A
1	A	2457	A
1	A	2506	A
1	A	2530	A
1	A	2548	C
1	A	2605	C
1	A	2620	G
1	A	2628	U
1	A	2643	G
1	A	2653	C
1	A	2660	U
1	A	2698	G
1	A	2744	U
1	A	2815	G
1	A	2846	G
1	A	2905	A
1	A	2938	A
1	A	2943	G
1	A	2988	C
1	A	2989	G

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Mol	Chain	Res	Type
1	A	2991	U
1	A	2992	G
1	A	3041	U
1	A	3059	A
1	A	3123	G
2	B	1607	U
2	B	1620	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OMG	A	3040	1	18,26,27	1.02	1 (5%)	19,38,41	1.21	3 (15%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	A	3040	1	-	1/5/27/28	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3040	OMG	C6-N1	-2.04	1.34	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3040	OMG	C5-C6-N1	2.47	118.31	113.95
1	A	3040	OMG	C8-N7-C5	2.24	107.26	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3040	OMG	O2'-C2'-C1'	2.12	113.30	109.09

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	3040	OMG	C1'-C2'-O2'-CM2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	3040	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 109 ligands modelled in this entry, 106 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
65	SAM	A1	401	-	24,29,29	0.70	1 (4%)	23,42,42	1.11	3 (13%)
66	PNS	w	201	60	13,20,21	0.30	0	18,26,29	0.78	0
63	GDP	C	401	-	24,30,30	0.93	1 (4%)	30,47,47	1.26	4 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
65	SAM	A1	401	-	-	1/12/33/33	0/3/3/3
66	PNS	w	201	60	-	11/24/26/27	-
63	GDP	C	401	-	-	3/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	C	401	GDP	C6-N1	-2.35	1.34	1.37
65	A1	401	SAM	OXT-C	-2.09	1.23	1.30

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	A1	401	SAM	OXT-C-O	-2.88	117.55	124.09
63	C	401	GDP	C3'-C2'-C1'	2.73	105.09	100.98
63	C	401	GDP	PA-O3A-PB	-2.59	123.94	132.83
63	C	401	GDP	C8-N7-C5	2.53	107.81	102.99
65	A1	401	SAM	OXT-C-CA	2.35	121.40	113.38
63	C	401	GDP	C5-C6-N1	2.19	117.83	113.95
65	A1	401	SAM	C5-C6-N6	2.09	123.53	120.35

There are no chirality outliers.

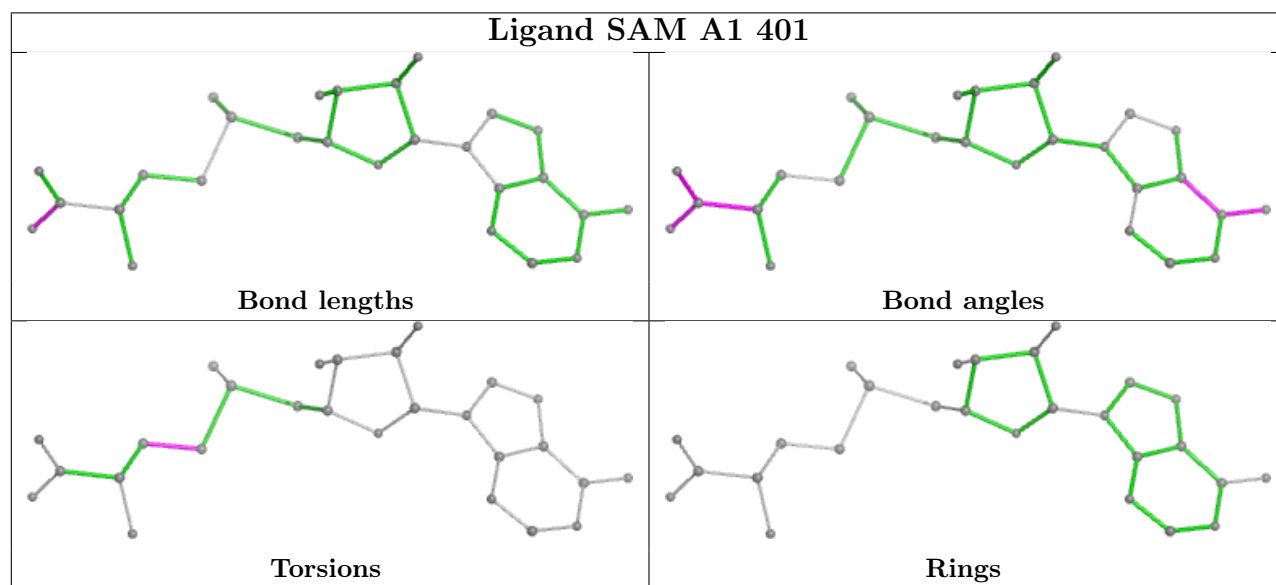
All (15) torsion outliers are listed below:

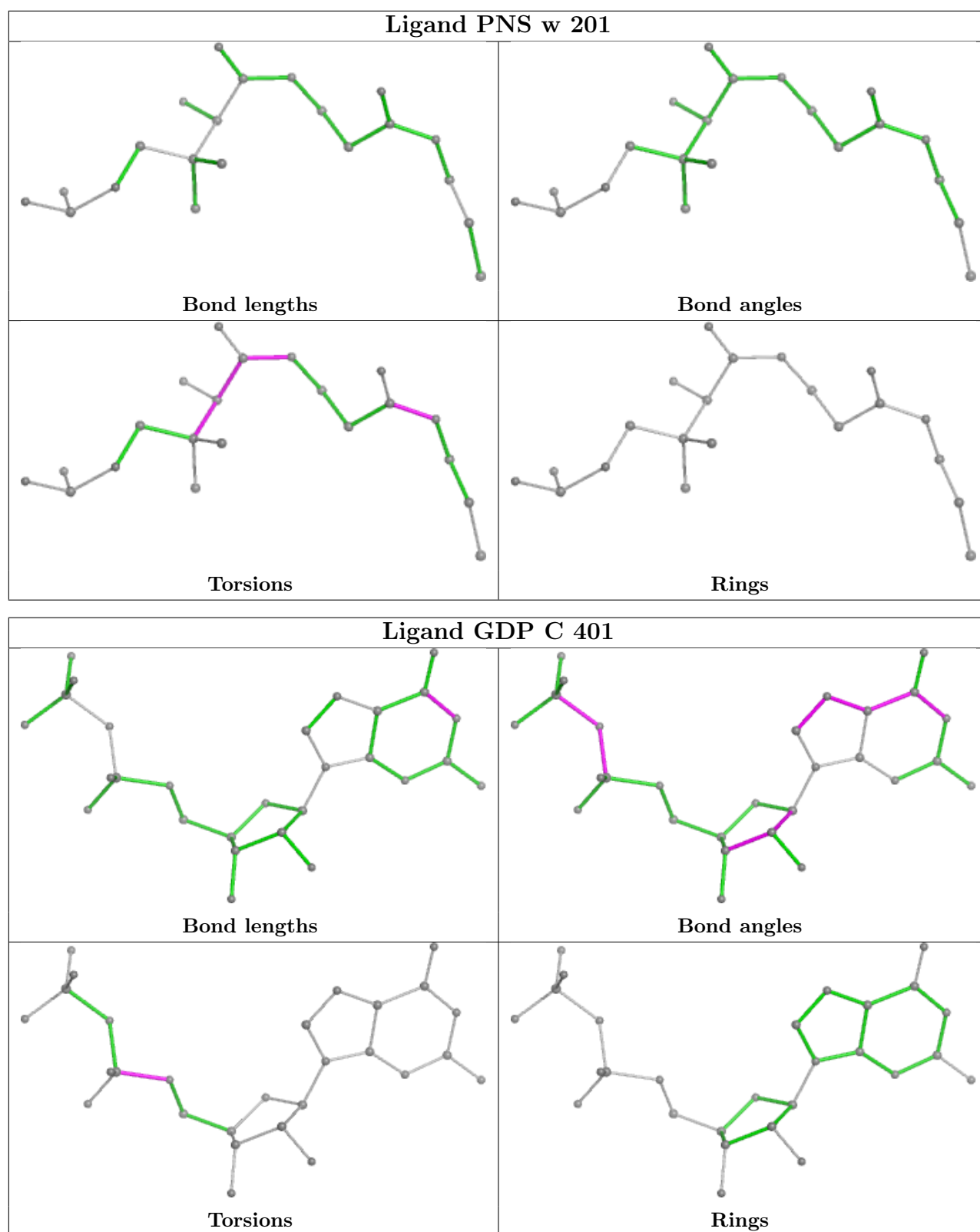
Mol	Chain	Res	Type	Atoms
63	C	401	GDP	C5'-O5'-PA-O1A
63	C	401	GDP	C5'-O5'-PA-O2A
66	w	201	PNS	C28-C29-C32-O33
66	w	201	PNS	C28-C29-C32-C34
66	w	201	PNS	C30-C29-C32-C34
66	w	201	PNS	C31-C29-C32-O33
66	w	201	PNS	C31-C29-C32-C34
66	w	201	PNS	O33-C32-C34-O35
66	w	201	PNS	C32-C34-N36-C37
66	w	201	PNS	C38-C39-N41-C42
66	w	201	PNS	O35-C34-N36-C37
66	w	201	PNS	O40-C39-N41-C42
65	A1	401	SAM	CA-CB-CG-SD
63	C	401	GDP	C5'-O5'-PA-O3A
66	w	201	PNS	C30-C29-C32-O33

There are no ring outliers.

No monomer is involved in short contacts.

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





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

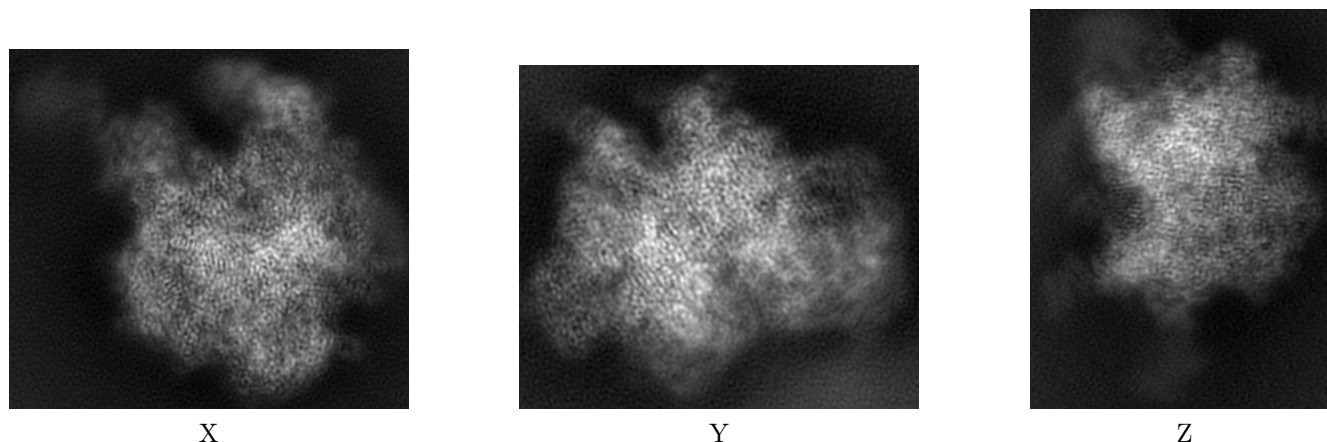
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12764. These allow visual inspection of the internal detail of the map and identification of artifacts.

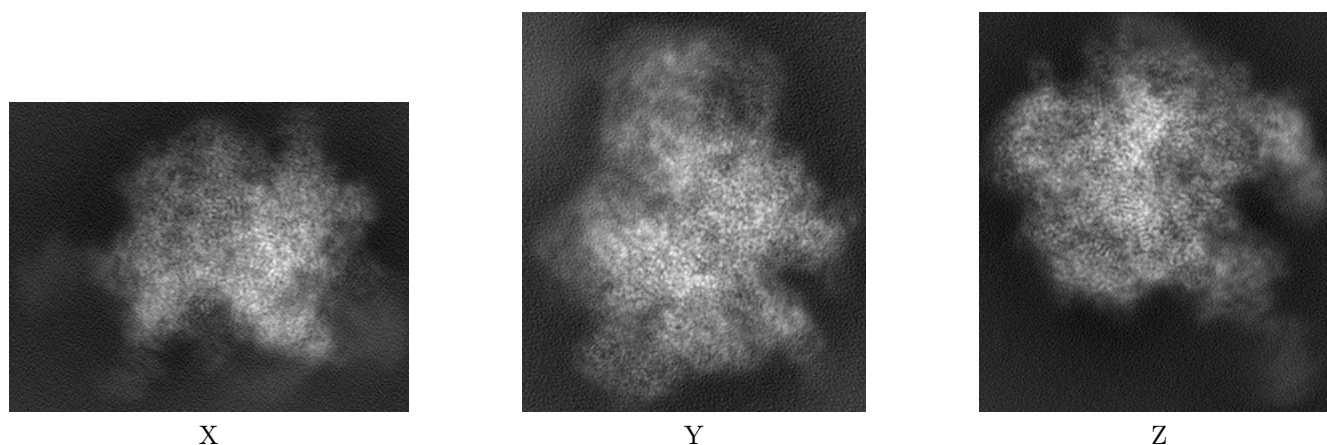
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



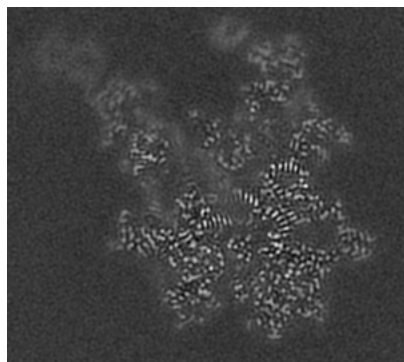
6.1.2 Raw map



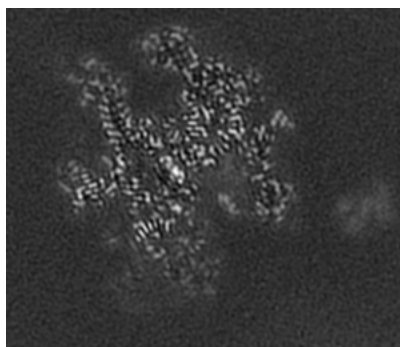
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

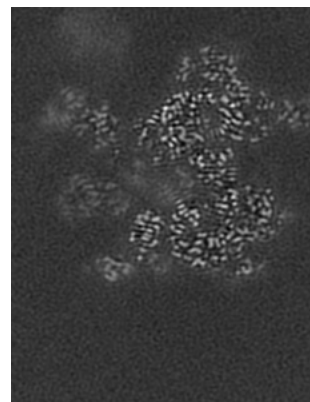
6.2.1 Primary map



X Index: 105

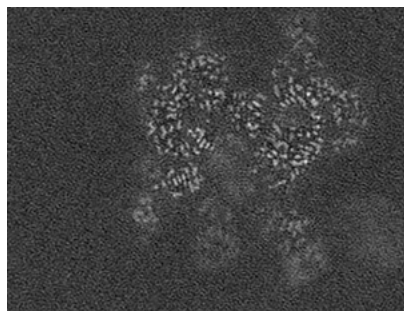


Y Index: 137

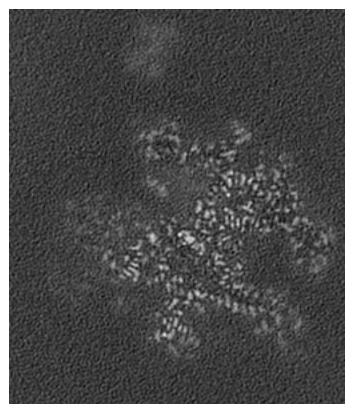


Z Index: 123

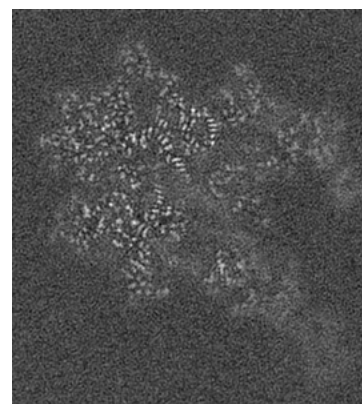
6.2.2 Raw map



X Index: 123



Y Index: 137

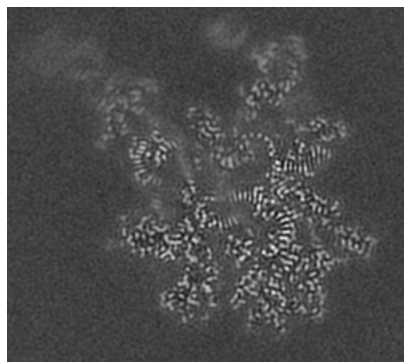


Z Index: 105

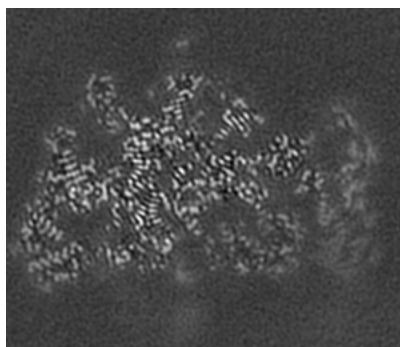
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

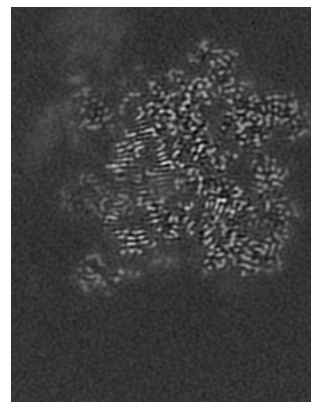
6.3.1 Primary map



X Index: 102

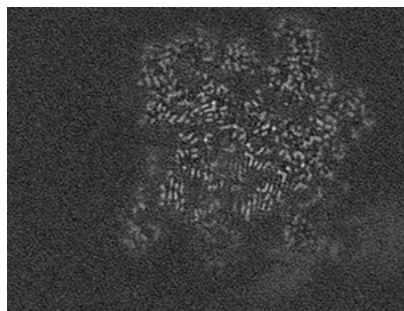


Y Index: 181

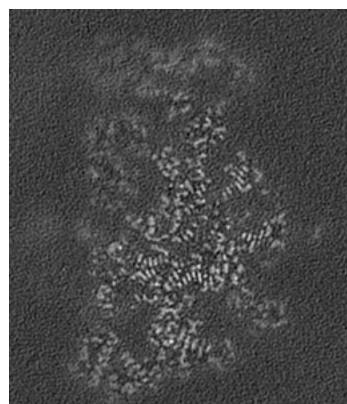


Z Index: 114

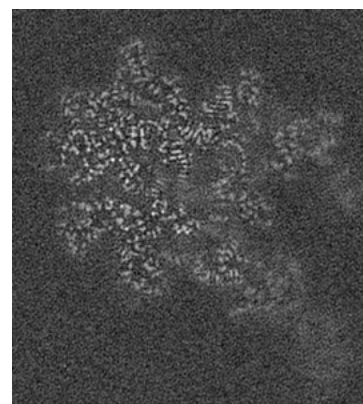
6.3.2 Raw map



X Index: 114



Y Index: 181

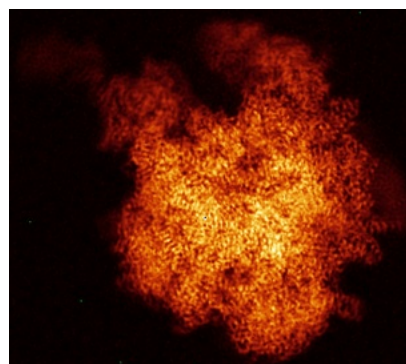


Z Index: 101

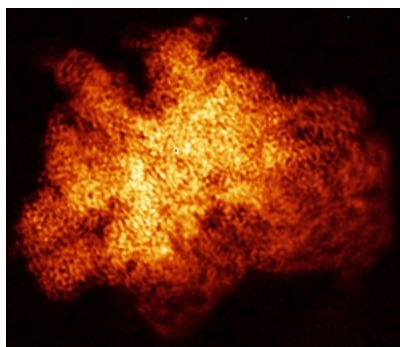
The images above show the largest variance slices of the map in three orthogonal directions.

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

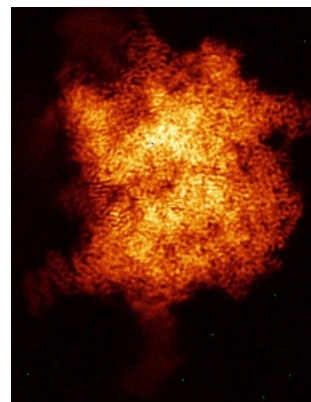
6.4.1 Primary map



X

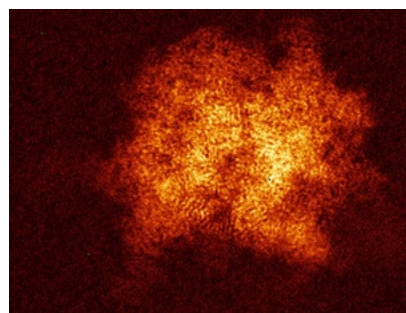


Y

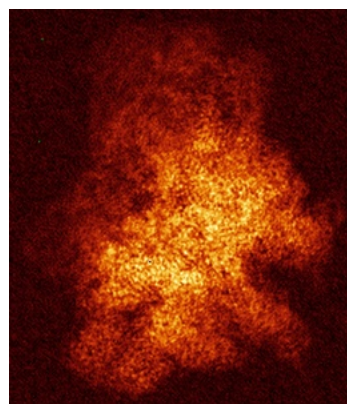


Z

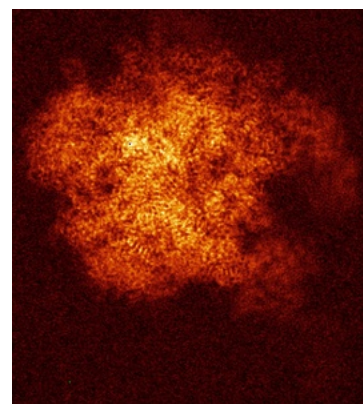
6.4.2 Raw map



X



Y

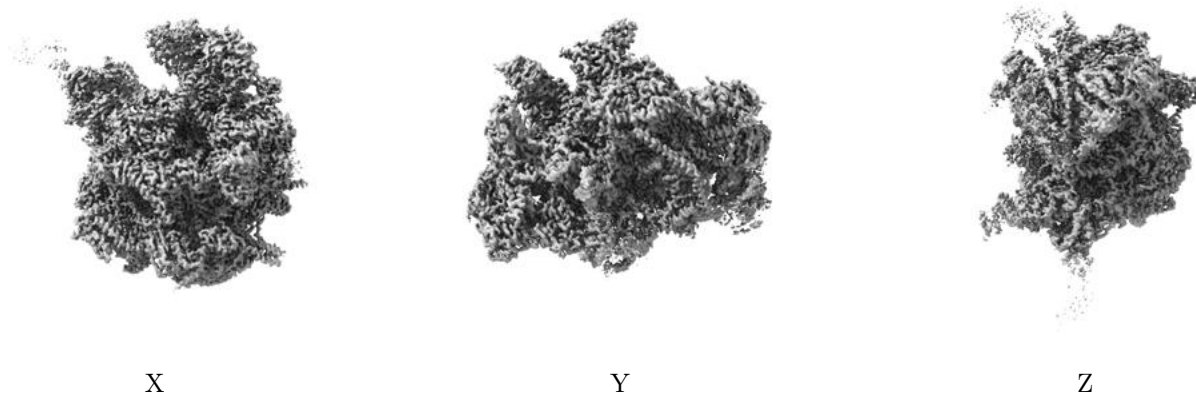


Z

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

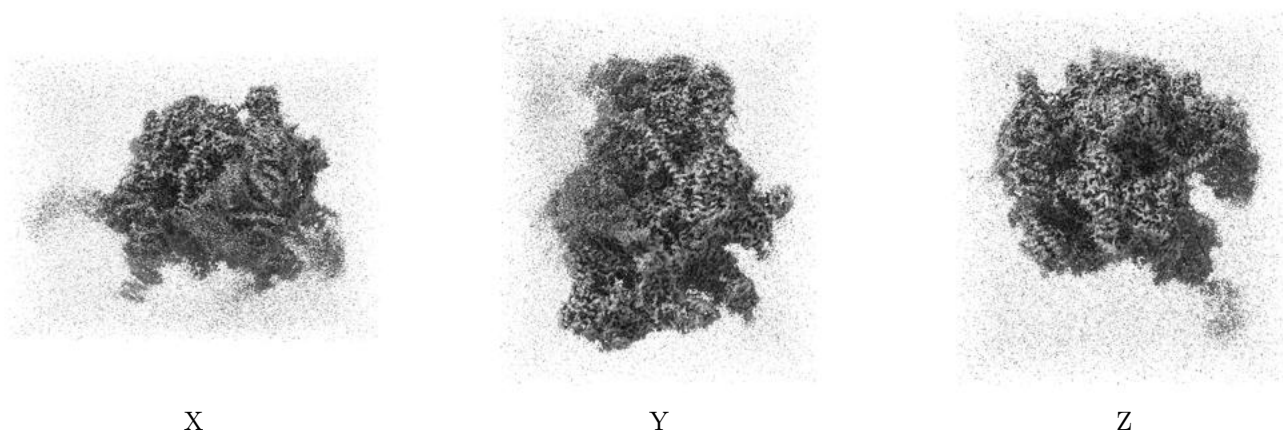
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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



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

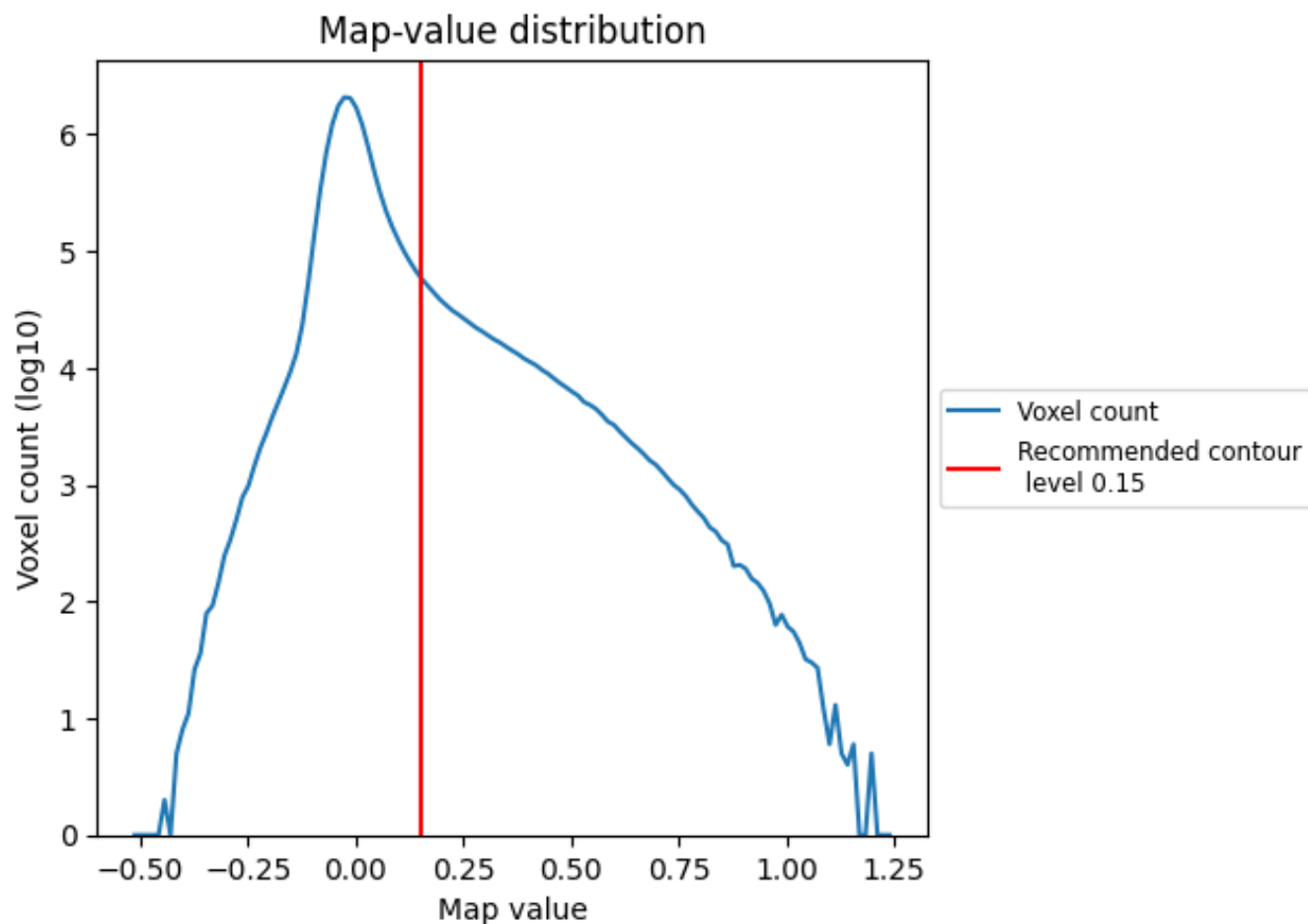
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

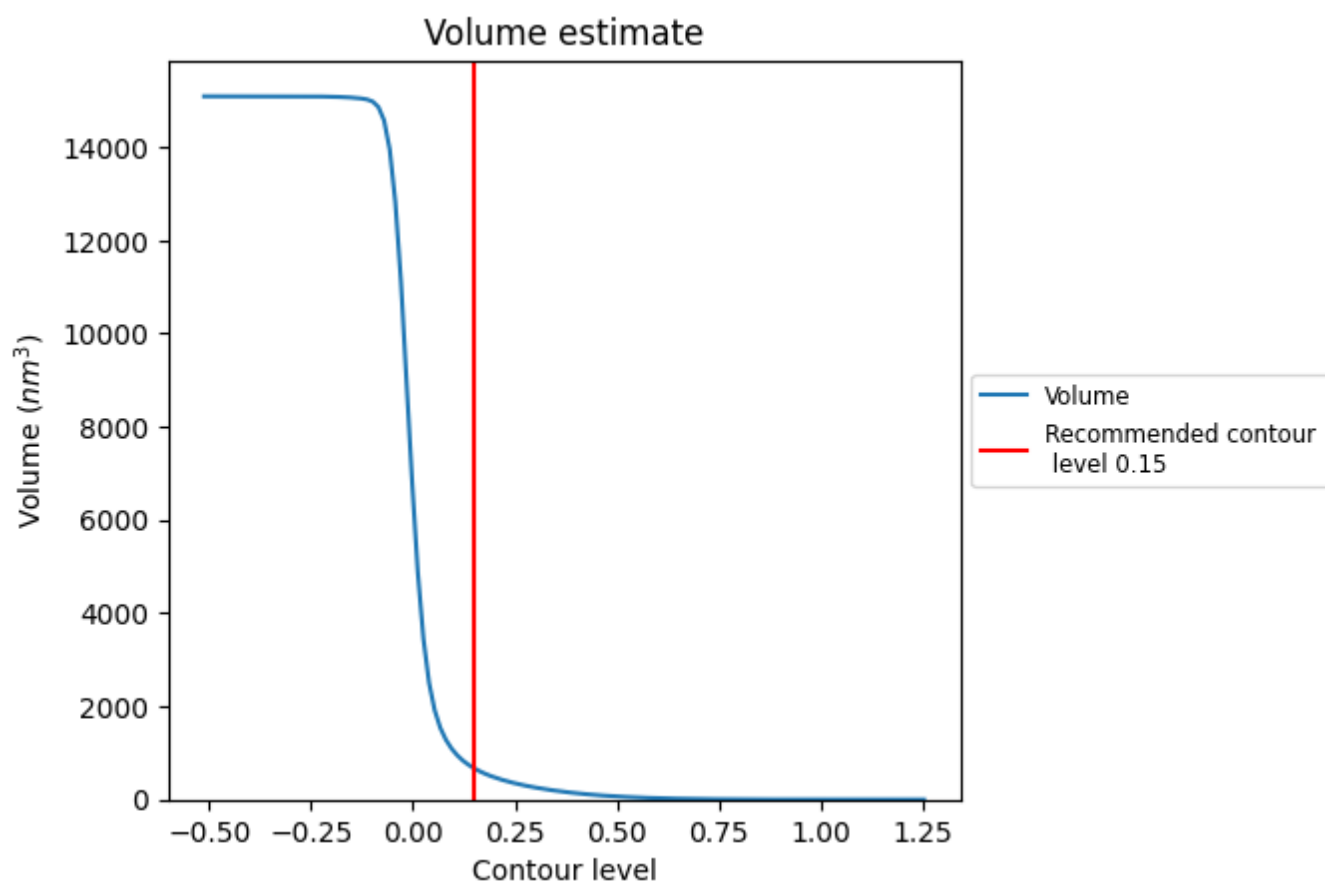
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 671 nm³; this corresponds to an approximate mass of 606 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

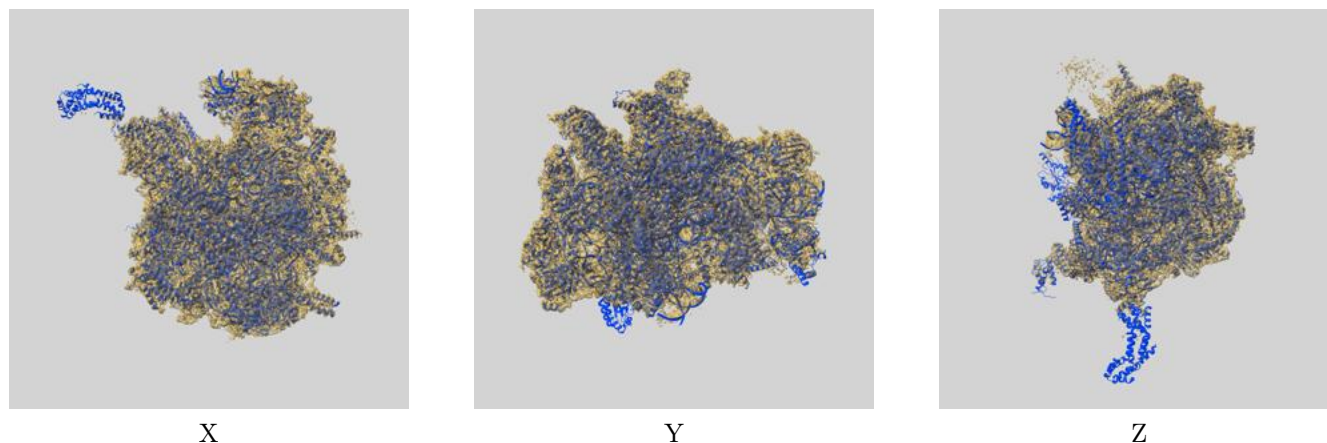
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

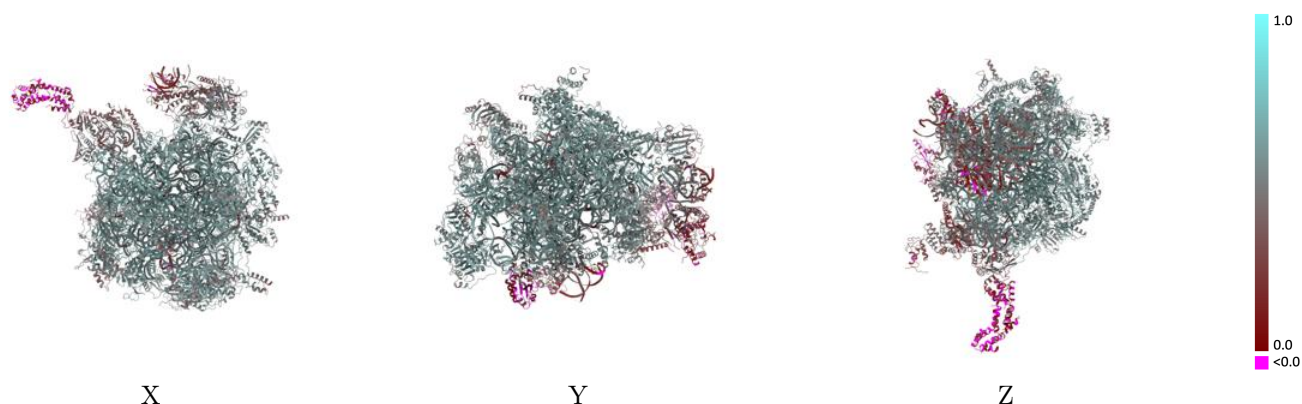
This section contains information regarding the fit between EMDB map EMD-12764 and PDB model 7O9M. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



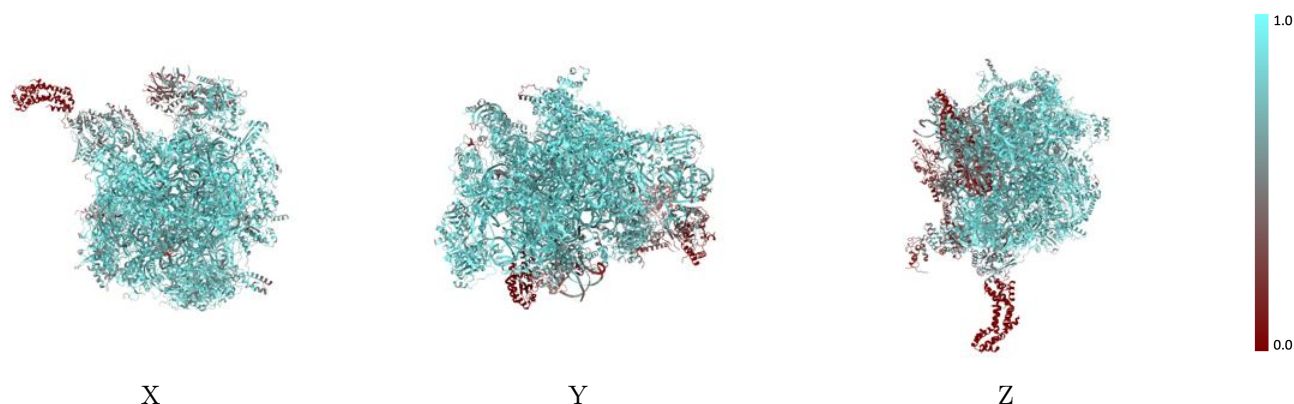
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



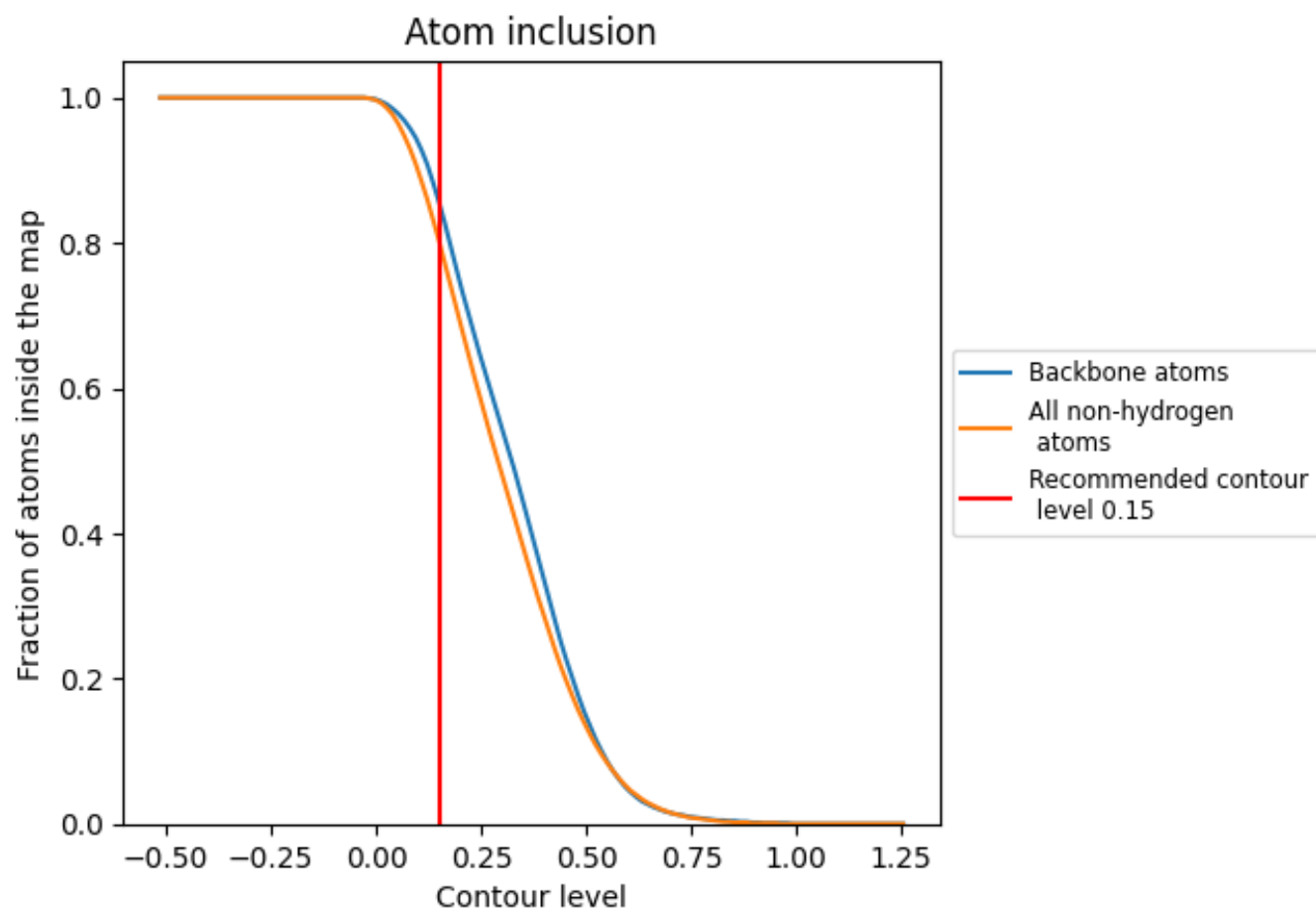
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8030	 0.5200
0	 0.8640	 0.5660
1	 0.8210	 0.5560
2	 0.9740	 0.6290
3	 0.9540	 0.6120
4	 0.9170	 0.6030
5	 0.8650	 0.5590
6	 0.7810	 0.4920
7	 0.7830	 0.5180
8	 0.3910	 0.2560
9	 0.8300	 0.5560
A	 0.9370	 0.5640
A1	 0.7350	 0.5280
A2	 0.7040	 0.4950
B	 0.7660	 0.3510
C	 0.0400	 0.1520
D	 0.8710	 0.5690
E	 0.8980	 0.5820
F	 0.9070	 0.5880
H	 0.7750	 0.5140
I	 0.4740	 0.3300
J	 0.3600	 0.2510
K	 0.9290	 0.5980
L	 0.8710	 0.5710
M	 0.9090	 0.5830
N	 0.8090	 0.5500
O	 0.8990	 0.5900
P	 0.8350	 0.5340
Q	 0.8560	 0.5670
R	 0.9190	 0.5940
S	 0.9010	 0.5880
T	 0.9180	 0.5960
U	 0.8880	 0.5780
UNK	 0.2850	 0.2430
V	 0.7450	 0.5060



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Chain	Atom inclusion	Q-score
W	 0.9250	 0.5930
X	 0.8400	 0.5550
Y	 0.8720	 0.5770
Z	 0.9010	 0.5930
a	 0.8860	 0.5800
b	 0.9200	 0.5940
c	 0.8110	 0.5460
d	 0.7490	 0.5080
e	 0.1970	 0.1870
f	 0.5390	 0.3900
g	 0.8990	 0.5760
h	 0.7840	 0.5250
i	 0.9360	 0.6050
j	 0.8290	 0.5630
k	 0.6640	 0.4360
l	 0.6410	 0.4200
m	 0.1800	 0.2060
n	 0.4930	 0.4950
o	 0.9010	 0.5850
p	 0.7490	 0.5070
q	 0.7550	 0.5150
r	 0.8740	 0.5600
s	 0.8910	 0.5790
t1	 0.0680	 0.0990
t2	 0.0500	 0.1070
t3	 0.0000	 0.0380
t4	 0.0000	 0.0660
t5	 0.0000	 0.0150
t6	 0.0000	 0.0170
u	 0.6970	 0.5090
v	 0.5950	 0.4160
w	 0.1510	 0.2180