



Full wwPDB EM Validation Report ⓘ

Oct 14, 2024 – 12:38 AM EDT

PDB ID : 6XIQ
EMDB ID : EMD-22196
Title : Cryo-EM Structure of K63R Ubiquitin Mutant Ribosome under Oxidative Stress
Authors : Zhou, Y.; Bartesaghi, A.; Silva, G.M.
Deposited on : 2020-06-21
Resolution : 4.20 Å(reported)
Based on initial model : 6GQ1

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.dev113
MolProbity : 4.02b-467
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) : 2.39

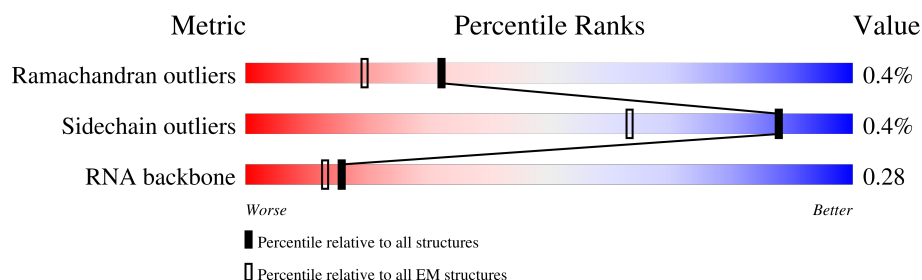
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

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




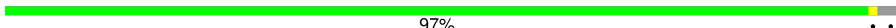
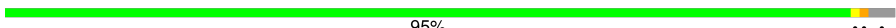
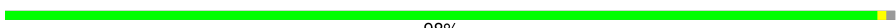
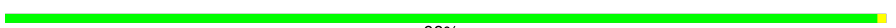








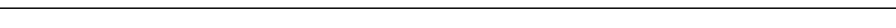


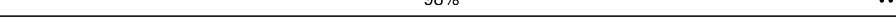
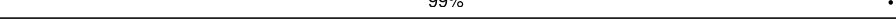

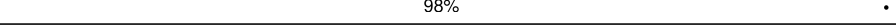





Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	254	<div> <div>5%</div> <div>97%</div> <div>..</div> </div>
2	B	387	<div> <div>99%</div> </div>
3	C	362	<div> <div>98%</div> <div>.</div> </div>
4	D	297	<div> <div>99%</div> </div>
5	E	176	<div> <div>88%</div> <div>11%</div> <div>.</div> </div>
6	F	244	<div> <div>91%</div> <div>9%</div> </div>
7	G	256	<div> <div>90%</div> <div>9%</div> </div>
8	H	191	<div> <div>99%</div> <div>.</div> </div>

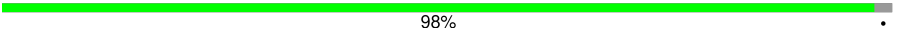

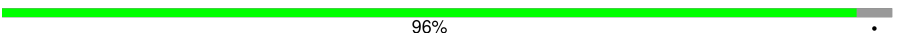
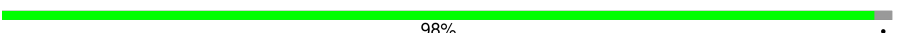











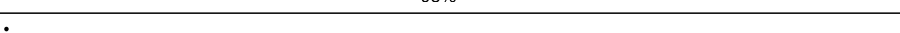





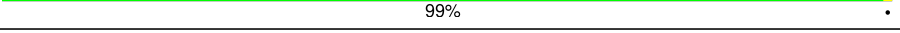


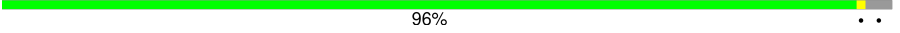
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Mol	Chain	Length	Quality of chain
9	I	221	 95% 5%
10	J	174	 97% ..
11	L	199	 95% ..
12	M	138	 98% ..
13	N	204	 98% .
14	O	199	 98% ...
15	P	184	 99% ..
16	Q	186	 99% .
17	R	189	 99% .
18	S	172	 99% .
19	T	160	 99% ..
20	U	121	 81% . 17%
21	V	137	 98% ..
22	W	155	 41% 59%
23	X	142	 85% . 15%
24	Y	127	 98% ..
25	Z	136	 99% ..
26	AA	105	 90% . 9%
27	AB	156	 98% .
28	1	3395	 38% 55% . 5%
29	3	121	 57% 41% .
30	4	158	 43% 54% .
31	P0	312	 12% 61% 39%
32	P2	165	 56% . 43%
33	a	149	 98% ..


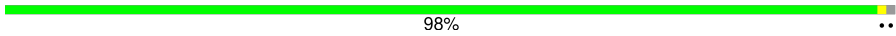


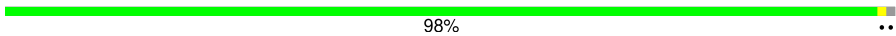

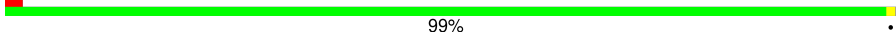
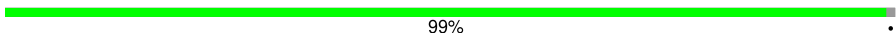

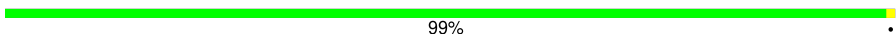
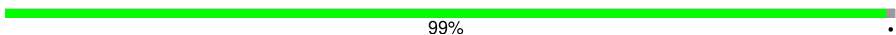
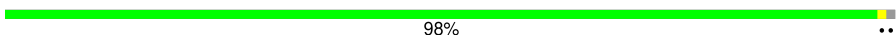



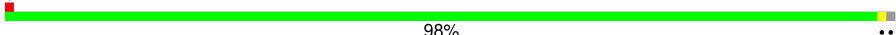
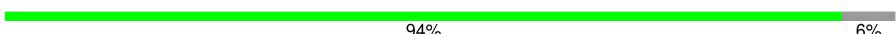


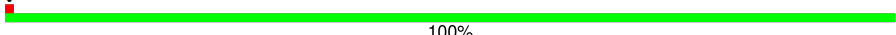




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Mol	Chain	Length	Quality of chain
34	b	59	
35	c	105	
36	d	113	
37	e	130	
38	f	107	
39	g	121	
40	h	120	
41	i	100	
42	j	88	
43	k	78	
44	l	51	
45	m	128	
46	n	25	
47	o	106	
48	p	92	
49	2	1800	
50	q	252	
51	r	255	
52	s	254	
53	t	240	
54	u	261	
55	v	225	
56	w	236	
57	x	190	
58	y	200	

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Mol	Chain	Length	Quality of chain
59	z	197	
60	AD	151	
61	AE	138	
62	AF	142	
63	AG	143	
64	AH	136	
65	AI	146	
66	AJ	144	
67	AK	121	
68	AL	87	
69	AM	130	
70	AN	145	
71	AO	135	
72	AP	108	
73	AQ	119	
74	AR	82	
75	AS	67	
76	AT	56	
77	AU	63	
78	AV	319	
79	AX	76	
79	AZ	76	
80	AY	8	
81	L1	217	

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 356903 atoms, of which 151628 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 protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	252	Total	C	H	N	O	S	0	0
			3895	1191	1981	388	334	1		

- Molecule 2 is a protein called RPL3 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	386	Total	C	H	N	O	S	0	0
			6217	1950	3142	584	533	8		

- Molecule 3 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	361	Total	C	H	N	O	S	0	0
			5607	1729	2859	522	494	3		

- Molecule 4 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	296	Total	C	H	N	O	S	0	0
			4701	1501	2326	414	458	2		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	156	Total	C	H	N	O	S	0	0
			2565	800	1326	222	216	1		

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	222	Total	C	H	N	O	S	0	0
			3646	1151	1862	324	308	1		

- Molecule 7 is a protein called RPL8A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	233	Total	C	H	N	O	S	0	0
			3681	1151	1877	323	327	3		

- Molecule 8 is a protein called RPL9A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	191	Total	C	H	N	O	S	0	0
			3105	963	1587	274	277	4		

- Molecule 9 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	211	Total	C	H	N	O	S	0	0
			3441	1083	1736	322	294	6		

- Molecule 10 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	169	Total	C	H	N	O	S	0	0
			2736	847	1383	253	249	4		

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	193	Total	C	H	N	O	0	0
			3151	962	1608	315	266		

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	M	136	Total	C	H	N	O	S	0	0
			2202	675	1149	199	177	2		

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	N	203	Total	C	H	N	O	S	0	0
			3499	1077	1779	361	281	1		

- Molecule 14 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	O	197	Total	C	H	N	O	S	0	0
			3214	1003	1659	289	262	1		

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	P	183	Total	C	H	N	O		0	0
			2857	882	1437	281	257			

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	Q	185	Total	C	H	N	O	S	0	0
			2984	908	1543	290	241	2		

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	R	188	Total	C	H	N	O		0	0
			3138	935	1617	326	260			

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	S	172	Total	C	H	N	O	S	0	0
			2932	930	1487	267	244	4		

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	T	159	Total	C	H	N	O	S	0	0
			2599	805	1323	246	221	4		

- Molecule 20 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	U	100	Total	C	H	N	O		0	0
			1608	516	812	131	149			

- Molecule 21 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	V	136	Total	C	H	N	O	S	0	0
			2051	628	1048	189	179	7		

- Molecule 22 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	W	63	Total	C	H	N	O	S	0	0
			1072	336	551	102	82	1		

- Molecule 23 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	X	121	Total	C	H	N	O	S	0	0
			1989	620	1025	169	173	2		

- Molecule 24 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Y	126	Total	C	H	N	O		0	0
			2074	625	1081	192	176			

- Molecule 25 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Z	135	Total	C	H	N	O		0	0
			2247	710	1155	202	180			

- Molecule 26 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AA	96	Total	C	H	N	O	S	0	0
			1499	499	727	126	145	2		

- Molecule 27 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	AB	153	Total	C	H	N	O	S	0	0
			2502	780	1282	231	206	3		

- Molecule 28 is a RNA chain called 35S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	1	3223	Total	C	H	N	O	P	0	0
			103566	30790	34635	12416	22502	3223		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	G	deletion	GB 380294104

- Molecule 29 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	3	121	Total	C	H	N	O	P	0	0
			3883	1152	1304	461	845	121		

- Molecule 30 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	4	158	Total	C	H	N	O	P	0	0
			5048	1500	1695	586	1109	158		

- Molecule 31 is a protein called RPP0 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	P0	189	Total	C	H	N	O	S	0	0
			2987	942	1514	257	270	4		

- Molecule 32 is a protein called RPL12A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	P2	94	Total	C	H	N	O	S	0	0
			1497	448	774	138	135	2		

- Molecule 33 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	a	148	Total	C	H	N	O	S	0	0
			2388	749	1215	231	190	3		

- Molecule 34 is a protein called RPL29 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	58	Total	C	H	N	O	0	0
			953	289	491	100	73		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
35	c	97	Total	C	H	N	O	S	0	0
			1540	479	797	124	139	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
36	d	109	Total	C	H	N	O	S	0	0
			1801	559	918	167	156	1		

- Molecule 37 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
37	e	127	Total	C	H	N	O	S	0	0
			2110	647	1090	205	167	1		

- Molecule 38 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	f	106	Total	C	H	N	O	S	0	0
			1730	540	880	165	144	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
39	g	112	Total	C	H	N	O	S	0	0
			1821	545	941	179	152	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
40	h	119	Total	C	H	N	O	S	0	0
			2047	615	1078	186	167	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
41	i	99	Total	C	H	N	O	S	0	0
			1620	481	849	156	132	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
42	j	87	Total	C	H	N	O	S	0	0
			1364	414	683	148	114	5		

- Molecule 43 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	k	77	Total	C	H	N	O	S	0	0
			1294	391	682	115	106			

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

Mol	Chain	Residues	Atoms						AltConf	Trace
44	l	50	Total	C	H	N	O	S	0	0
			911	272	475	97	65	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
45	m	52	Total	C	H	N	O	S	0	0
			873	259	456	86	67	5		

- Molecule 46 is a protein called RPL41A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	n	25	Total	C	H	N	O	S	0	0
			500	139	273	60	27	1		

- Molecule 47 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	o	105	Total	C	H	N	O	S	0	0
			1762	534	915	170	138	5		

- Molecule 48 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	p	91	Total	C	H	N	O	S	0	0
			1428	429	734	138	121	6		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	2	1743	Total	C	H	N	O	P	0	0
			55827	16603	18686	6578	12217	1743		

- Molecule 50 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	q	206	Total	C	H	N	O	S	0	0
			3144	1014	1567	278	283	2		

- Molecule 51 is a protein called RPS1A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	r	214	Total	C	H	N	O	S	0	0
			3493	1084	1784	310	311	4		

- Molecule 52 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	s	217	Total	C	H	N	O	S	0	0
			3358	1047	1723	289	297	2		

- Molecule 53 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	t	223	Total	C	H	N	O	S	0	0
			3551	1101	1817	313	314	6		

- Molecule 54 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	u	260	Total	C	H	N	O	S	0	0
			4222	1316	2154	389	360	3		

- Molecule 55 is a protein called Rps5p.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	v	206	Total	C	H	N	O	S	0	0
			3284	1007	1675	300	299	3		

- Molecule 56 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	223	Total	C	H	N	O	S	0	0
			3671	1123	1881	346	318	3		

- Molecule 57 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	x	184	Total	C	H	N	O	S	0	0
			3053	951	1572	265	265			

- Molecule 58 is a protein called RPS8A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	y	188	Total	C	H	N	O	S	0	0
			3014	925	1525	298	264	2		

- Molecule 59 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	z	185	Total	C	H	N	O	S	0	0
			3067	943	1573	289	261	1		

- Molecule 60 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	AD	150	Total	C	H	N	O	S	0	0
			2447	759	1255	224	207	2		

- Molecule 61 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	AE	127	Total	C	H	N	O	S	0	0
			1774	545	883	182	163	1		

- Molecule 62 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AF	124	Total	C	H	N	O	S	
			1979	622	1002	182	166	7	
								0	0

- Molecule 63 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AG	141	Total	C	H	N	O	S	
			2271	708	1166	203	194		
								0	0

- Molecule 64 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AH	120	Total	C	H	N	O	S	
			1856	577	930	177	170	2	
								0	0

- Molecule 65 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AI	145	Total	C	H	N	O	S	
			2414	743	1222	237	210	2	
								0	0

- Molecule 66 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AJ	143	Total	C	H	N	O	S	
			2236	694	1124	208	208	2	
								0	0

- Molecule 67 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AK	107	Total	C	H	N	O	S	
			1772	539	917	156	159	1	
								0	0

- Molecule 68 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AL	87	Total	C	H	N	O	S	
			1356	420	672	125	137	2	
								0	0

- Molecule 69 is a protein called RPS22A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	AM	129	Total	C	H	N	O	S	0	0
			2081	650	1060	188	180	3		

- Molecule 70 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	AN	144	Total	C	H	N	O	S	0	0
			2317	708	1196	220	191	2		

- Molecule 71 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	AO	134	Total	C	H	N	O		0	0
			2205	676	1132	208	189			

- Molecule 72 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	AP	70	Total	C	H	N	O		0	0
			1166	360	603	104	99			

- Molecule 73 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	AQ	97	Total	C	H	N	O	S	0	0
			1583	475	814	160	129	5		

- Molecule 74 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	AR	81	Total	C	H	N	O	S	0	0
			1242	382	632	110	113	5		

- Molecule 75 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	AS	63	Total	C	H	N	O	S	0	0
			1032	306	535	99	91	1		

- Molecule 76 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	AT	53	Total	C	H	N	O	S	0	0
			873	274	431	92	72	4		

- Molecule 77 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	AU	60	Total	C	H	N	O	S	0	0
			1000	299	525	98	77	1		

- Molecule 78 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	AV	318	Total	C	H	N	O	S	0	0
			4823	1541	2386	418	470	8		

- Molecule 79 is a RNA chain called Transfer RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	AX	76	Total	C	H	N	O	P	0	0
			2446	725	820	293	532	76		
79	AZ	76	Total	C	H	N	O	P	0	0
			2446	725	820	293	532	76		

- Molecule 80 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	AY	8	Total	C	H	N	O	P	0	0
			248	74	84	23	59	8		

- Molecule 81 is a protein called RPL1A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	L1	204	Total	C	H	N	O	S	0	0
			3310	1031	1701	279	290	9		

- Molecule 82 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
82	j	1	Total	Zn	0
			1	1	
82	m	1	Total	Zn	0
			1	1	

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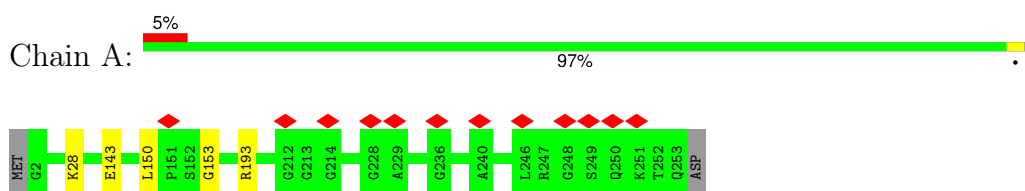
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Mol	Chain	Residues	Atoms		AltConf
82	o	1	Total 1	Zn 1	0
82	p	1	Total 1	Zn 1	0
82	AQ	1	Total 1	Zn 1	0
82	AR	1	Total 1	Zn 1	0
82	AT	1	Total 1	Zn 1	0

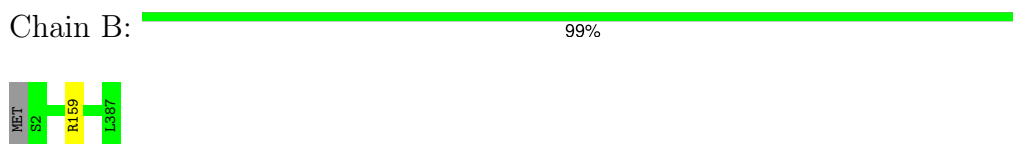
3 Residue-property plots [i](#)

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

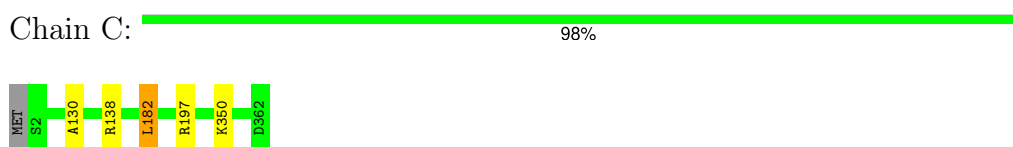
- Molecule 1: 60S ribosomal protein L2-A



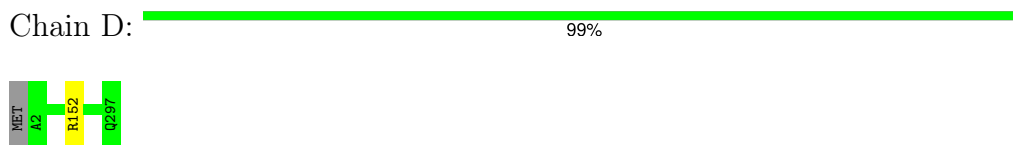
- Molecule 2: RPL3 isoform 1



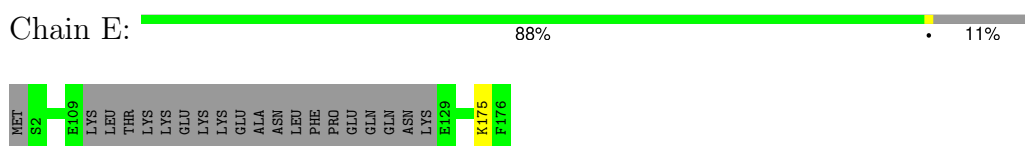
- Molecule 3: RPL4A isoform 1



- Molecule 4: RPL5 isoform 1

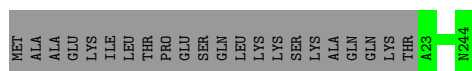


- Molecule 5: 60S ribosomal protein L6-A



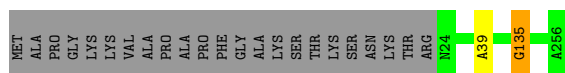
- Molecule 6: 60S ribosomal protein L7-A

Chain F:  91% 9%



- Molecule 7: RPL8A isoform 1

Chain G:  90% 9%



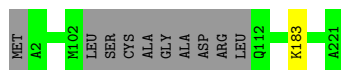
- Molecule 8: RPL9A isoform 1

Chain H:  99% .



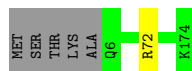
- Molecule 9: RPL10 isoform 1

Chain I:  95% 5%



- Molecule 10: RPL11B isoform 1

Chain J:  97% ..



- Molecule 11: 60S ribosomal protein L13-A

Chain L:  95% ..



- Molecule 12: 60S ribosomal protein L14-A

Chain M:  98% ..



- Molecule 13: 60S ribosomal protein L15-A

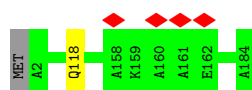
Chain N:  98% .



- Molecule 14: 60S ribosomal protein L16-A



- Molecule 15: 60S ribosomal protein L17-A



- Molecule 16: 60S ribosomal protein L18-A



- Molecule 17: 60S ribosomal protein L19-A



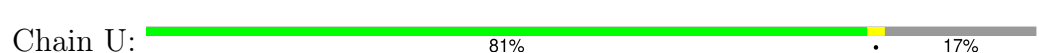
- Molecule 18: 60S ribosomal protein L20-A



- Molecule 19: 60S ribosomal protein L21-A



- Molecule 20: 60S ribosomal protein L22-A



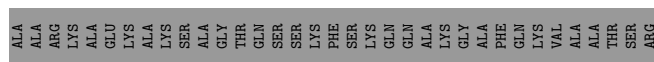
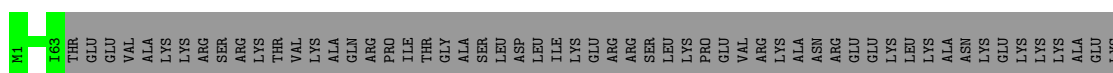
- Molecule 21: 60S ribosomal protein L23-A

Chain V:  98%

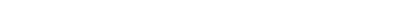


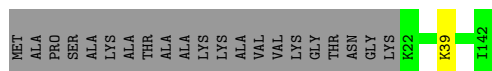
- Molecule 22: RPL24A isoform 1

Chain W:  41% 59%



- Molecule 23: 60S ribosomal protein L25

Chain X:  85% • 15%



- Molecule 24: 60S ribosomal protein L26-A

Chain Y: 98%



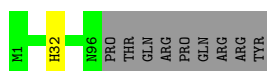
- Molecule 25: 60S ribosomal protein L27-A

Chain Z:  99%

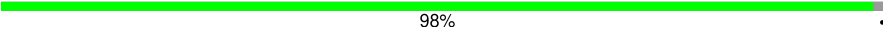


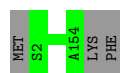
- Molecule 26: 40S ribosomal protein S10-A

Chain AA: 90% : 9%




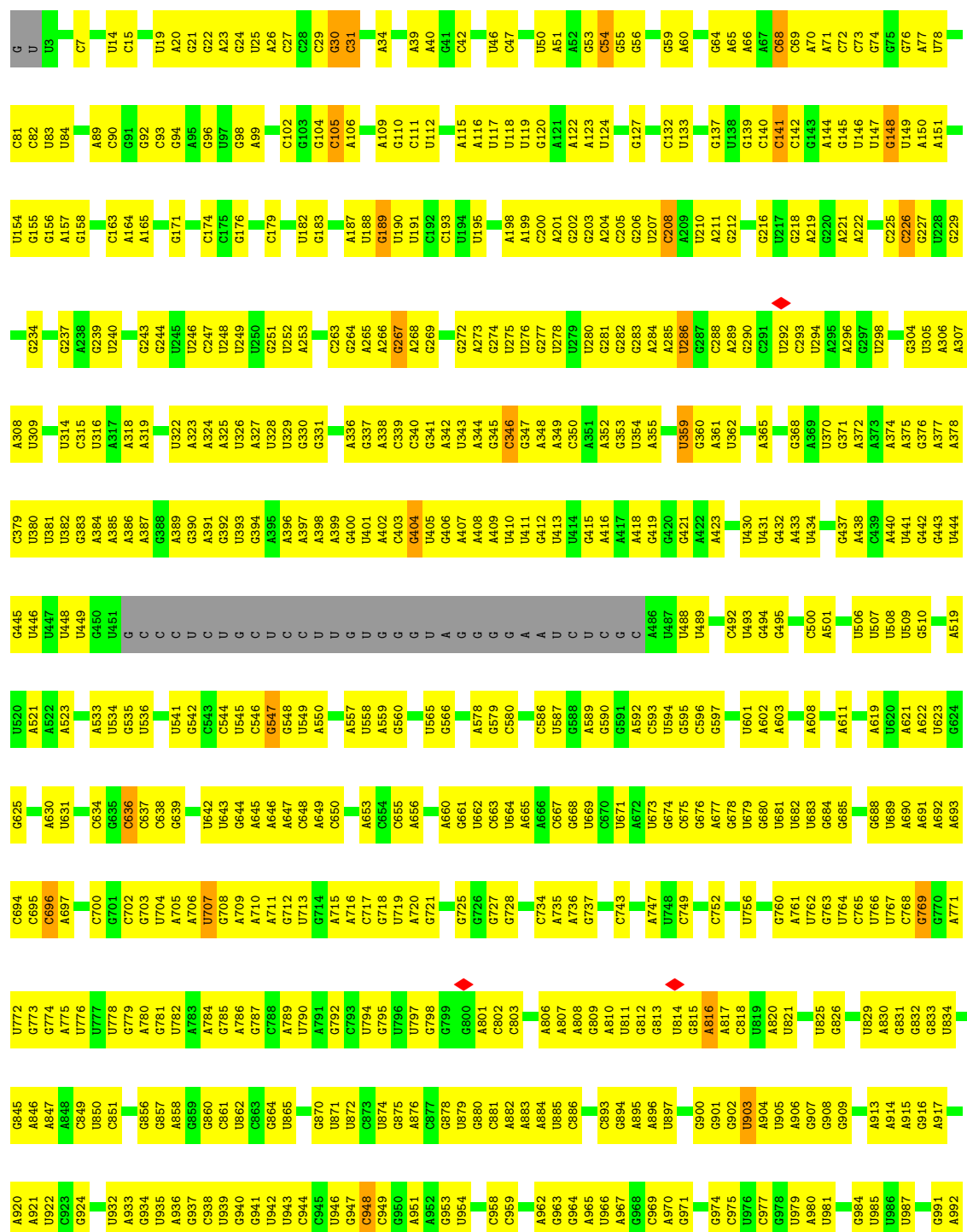
- Molecule 27: 40S ribosomal protein S11-A

Chain AB:  98%.



• Molecule 28: 35S ribosomal RNA

Chain 1:  38% 55% 5%.





U3057	U2975	G2901	G2823	C2756	A2678	A2601	U2532	A2468	G2395	C2306	U2224	A2144	C
U3058	A2976	A2902	G2824	U2757	A2679	G2602	G2533	G2469	G2396	G2307	U2225	A2145	G
G3059	G2977	A2903	C2825	C2760	C2682	G2603	G2534	G2470	A2397	G2311	U2226	C2146	C
	U2978	U2904	U2826	G2761		U2604	A2535	U2471	A2398			A2147	U
G3062	U2979	U2905	U2827	G2762	C2685	G2605	A2536	U2472	A2399		A2229	A2152	U
C3063	U2980	G2907	C2832	A2763	A2686	G2607	U2538	C2473	G2401		C2230	U2153	G
U3064	U2981	C2908	A2833	C2764	G2687	G2608	C2539	C2474	A2402		C2231	C2154	C
U3065	A2982	U2909	G2834	C2765	U2688	G2609	A2540	G2475	G2403		G2234	U2155	U
C3066	C2983	U2910	U2835	U2766	A2689	G2610	U2541	C2476	A2404		A2242	C2156	A
C3067	C2984	U2911	C2836	U2767	G2690	U2611	U2542	C2477	C2405		A2243	G2157	C
		G2912	A2837	U2768	A2691	G2612	U2543	C2478	C2406		U2244	U2158	A
A3070	G2990	G2913	A2838		C2692	G2613	U2544	C2479	C2407		G2245	U2159	U
U3071				C2772	C2693	G2614	U2545	C2480	U2408		G2246	G2160	A
C3072	G2993	U2916	C2844	C2773	C2694	G2615	C2546	U2481	G2409		G2247		
A3073			A2845	C2774	A2695	G2616	A2547	U2482	U2410		C2248	C2163	
G3074	G2997	U2919	U2846	U2775	A2696	G2617	G2548				G2249	A2164	
C3075	A2910	G2920	A2847	U2776	A2697	G2618	G2549	A2485	C2415			G2165	
C3076	A3005	U2921		C2777	G2698	G2619	U2550	A2486	C2416		U2254	A2166	
A3077	A3006	U2922	G2850	G2778	G2699	G2620	U2551	U2487	U2417		A2255	A2167	
U3078	U3007	U2923		C2779	G2700	G2621	C2552		C2418				
U3079		U2924		A2780	U2701	G2622	G2553		A2419		U2260	U2170	
G3080	U3010	C2925	U2854	U2781	A2702	G2623	A2554		C2420		U2261	U2173	
C3081	A3011	A2926	U2855	U2782	A2703	G2624	A2555				A2262	U2102	
	A3012	C2927	G2856	U2783	A2704	C2625	C2556				C2263	U2103	
A3086	C3018	C2928	U2860	G2784		U2626	A2557					A2104	
A3087	A2930	C2929		A2785	U2713	U2627	A2558					G2105	
G3088	U3019	A2931	G2863	A2786	G2714	G2628	U2559				U2269	G2110	
C3089	U3020	C2931	A2864	C2787	A2715	U2629	G2560				A2270	G2111	
U3090	A3021	U2932	U2865	U2788	U2716	G2630	A2561				A2271	C2112	
A3091	G3022	A2933	U2866	C2788	U2717	G2631	A2562					G2113	
C3092	U3023	C2934	U2867			G2632						A2188	
C3093	A3024	U2935	C2867	G2794	G2720	A2636	U2565					A2189	
	C3025	A2936	U2868	U2795	A2721	A2637						A2190	
C3099	G3026		U2869	C2796	U2722		C2568					G2192	
U3100	A3027	A2941	U2870	G2797	U2723	A2642	A2569					G2193	
G3101	G3028	C2942	C2871	C2798	U2724	A2643	A2570					G2194	
G3102	A3029	G2943	U2874	A2799	C2726	G2644	U2571					C2197	
A3103		U2944	U2875	G2800		G2645	C2572					A2198	
U3104	A3032	G2945	C2876	A2801	A2727	C2646						G2201	
C3105	C3033	U2946	C2877	A2802	G2728	A2647	A2580					G2202	
A3106	G3034	G2947	C2878	A2803	U2729	G2648	U2581					C2203	
U3107	A3035	U2948	G2879	A2804	G2730	A2649	C2582					C2204	
	G3036	G2950	U2880	G2805	U2731	G2651	C2583					U2205	
C3110		G2951	C2881	U2806		U2652	G2584					G2206	
U3111	A3040	G2952	U2882	U2807	A2734	U2653	G2585					A2207	
G3112		U2953	U2883	A2808	U2735	C2654	U2586					C2208	
A3113	C3043		U2884	C2809	A2736	U2655	G2587					U2209	
C3114	G3044	C2959	U2885	C2810	C2737	A2656	U2588					G2210	
C3115	G3045	G2960	A2887	A2811		U2657	G2589					A2213	
	A3046	C2961		C2812	C2741	A2658	A2590					A2214	
C3118	U3047	G2962	U2891	A2813	C2742	G2659	A2591					A2215	
U3119	A3048	U2965	C2892	G2814	A2747	A2660	G2592					G2218	
C3120	A3049	G2966	C2893	G2815	U2748	C2661	A2593					A2219	
U3121	U3050	A2967	C2894	G2816	A2749	C2662	A2594					A2220	
A3122	G3051	G2968	C2895	U2817	U2750	U2663						C2302	
	U3052		A2896	A2818								C2303	
U3125	G3053	A2971	C2897	U2819	G2753	U2674	U2597					A2142	
C3126	U3054	G2972	C2898	A2820	A2675	C2675	G2598					A2221	
	U3055	G2973	C2899	C2821	G2754	U2676	U2599					G2304	
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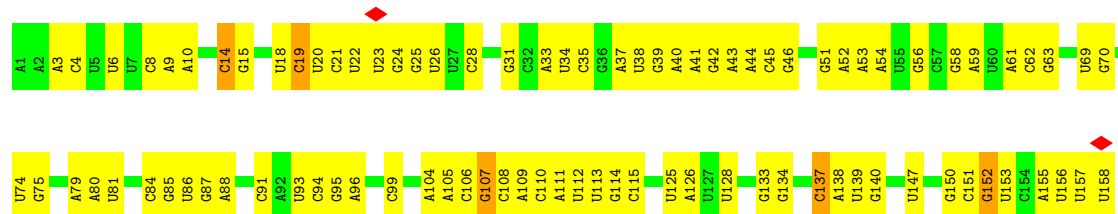
• Molecule 29: 5S ribosomal RNA

Chain 3: 57% 41%



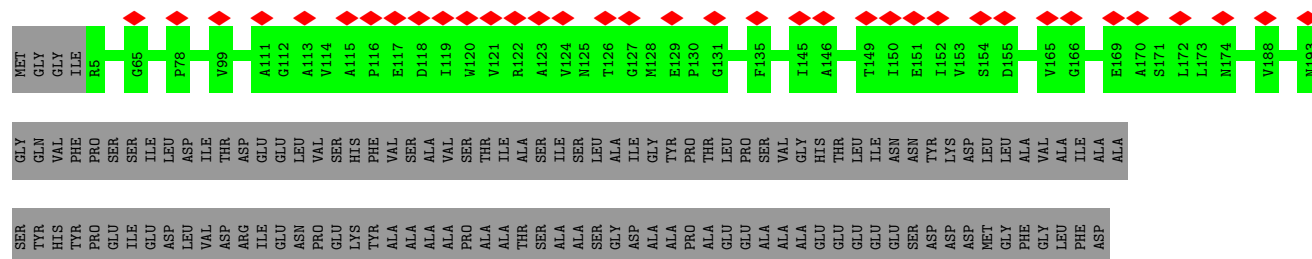
• Molecule 30: 5.8S ribosomal RNA

Chain 4: 43% 54%



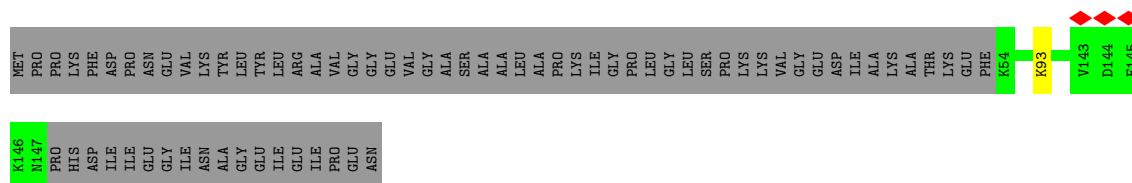
• Molecule 31: RPP0 isoform 1

Chain P0: 12% 61% 39%



• Molecule 32: RPL12A isoform 1

Chain P2: 56% 43%



- Molecule 33: 60S ribosomal protein L28

Chain a: 98%



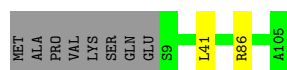
- Molecule 34: RPL29 isoform 1

Chain b: 98%



- Molecule 35: 60S ribosomal protein L30

Chain c: 90% 8%



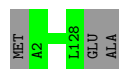
- Molecule 36: 60S ribosomal protein L31-A

Chain d: 96%



- Molecule 37: RPL32 isoform 1

Chain e: 98%




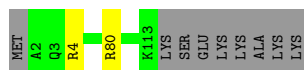
- Molecule 38: 60S ribosomal protein L33-A

Chain f: 98%



- Molecule 39: 60S ribosomal protein L34-A

Chain g:  91% • 7%



- Molecule 40: 60S ribosomal protein L35-A

Chain h:  98% ..



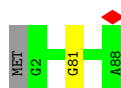
- Molecule 41: 60S ribosomal protein L36-A

Chain i:  99% .



- Molecule 42: 60S ribosomal protein L37-A

Chain j:  98% ..



- Molecule 43: RPL38 isoform 1

Chain k:  99% .



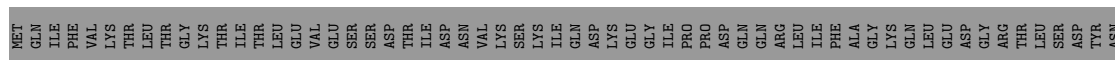
- Molecule 44: 60S ribosomal protein L39

Chain l:  98% .



- Molecule 45: 60S ribosomal protein L40

Chain m:  39% • 59%



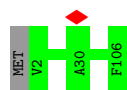
- Molecule 46: RPL41A isoform 1

Chain n:  100%

There are no outlier residues recorded for this chain.

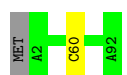
- Molecule 47: 60S ribosomal protein L42-A

Chain o:  99%



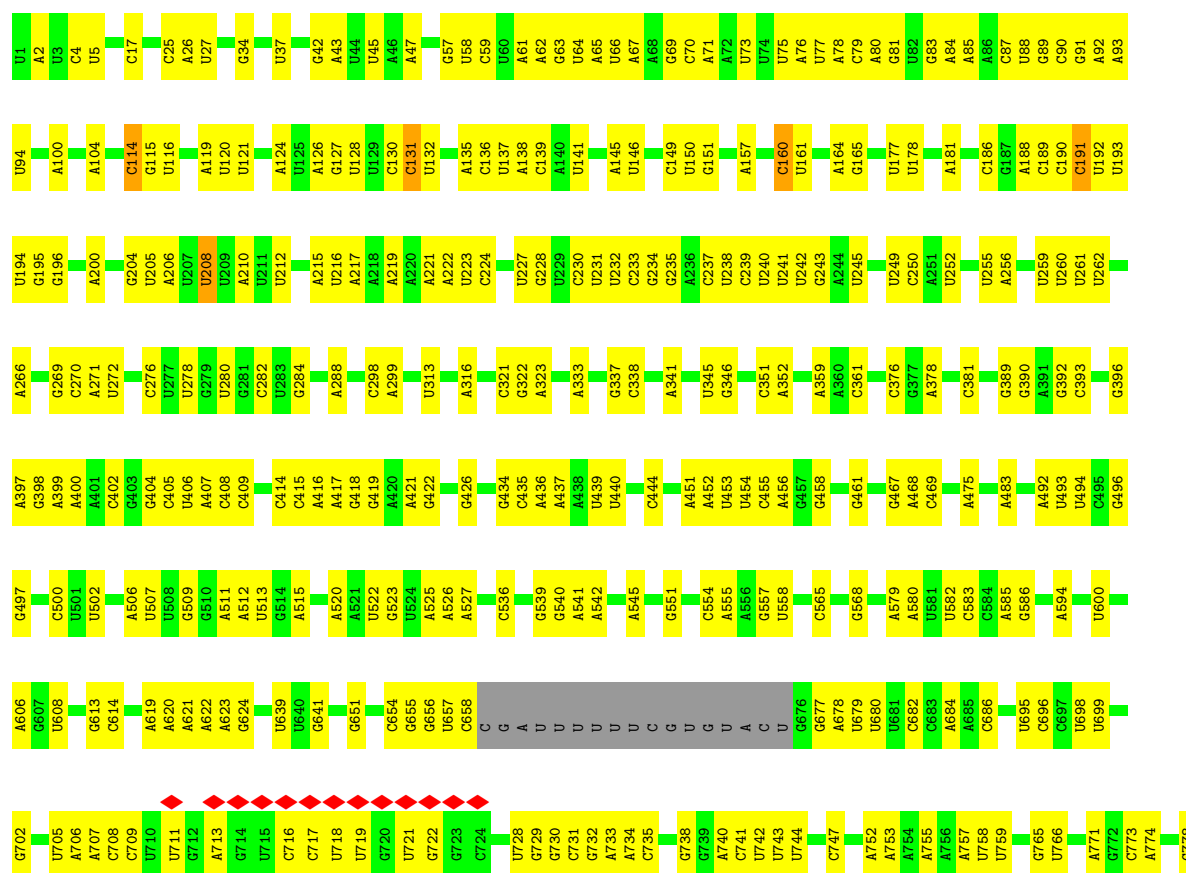
- Molecule 48: 60S ribosomal protein L43-A

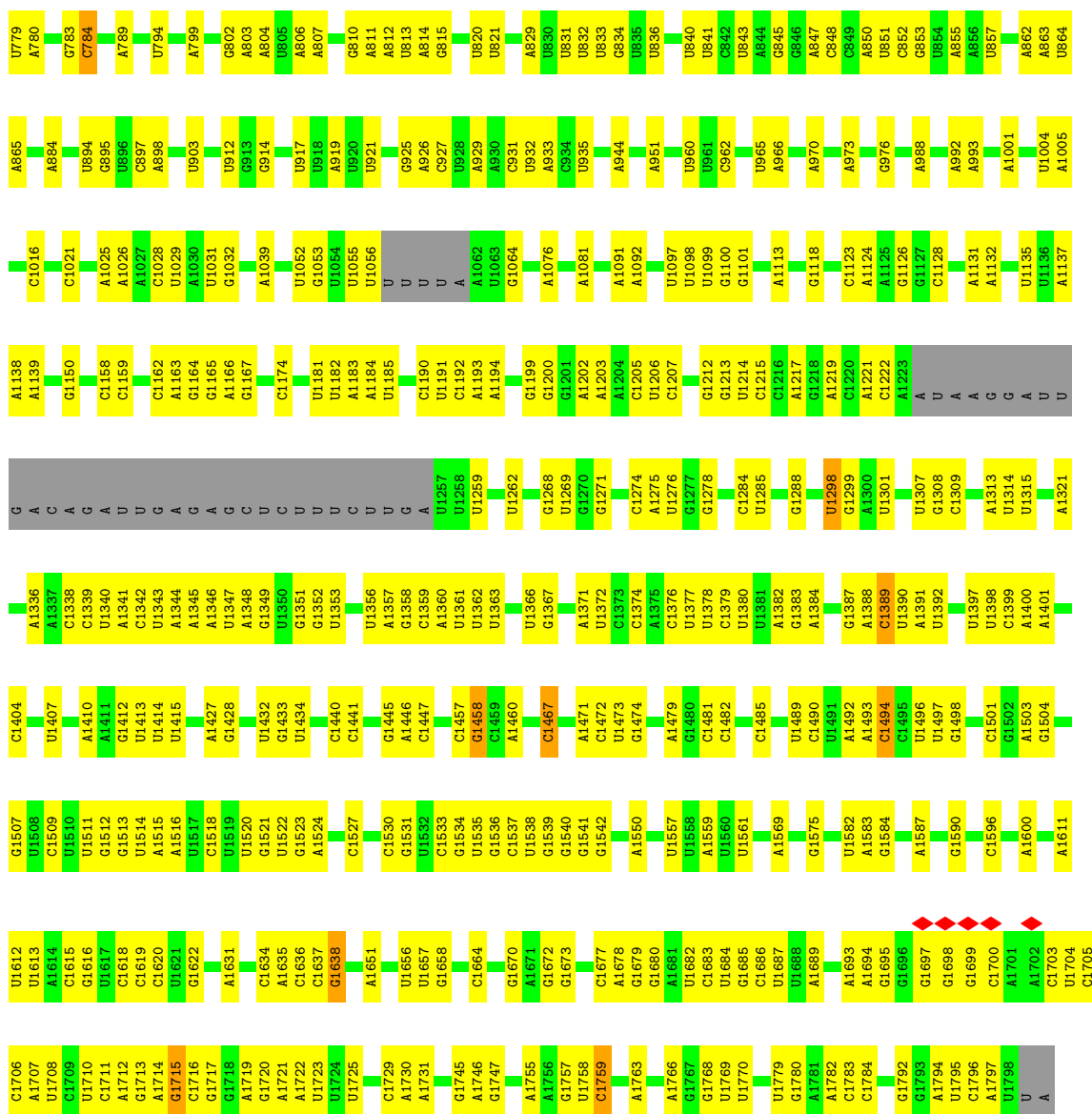
Chain p:  98%



- Molecule 49: 18S ribosomal RNA

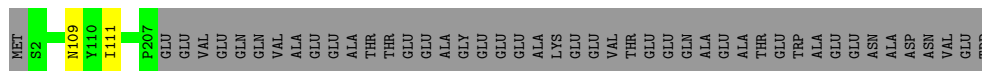
Chain 2:  58% 38%





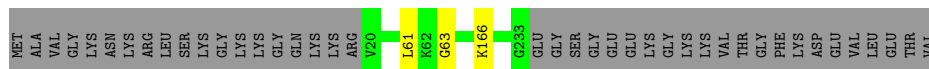
- Molecule 50: 40S ribosomal protein S0-A

Chain q: 81% 18%




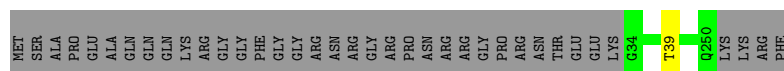
- Molecule 51: RPS1A isoform 1

Chain r: 83% 16%



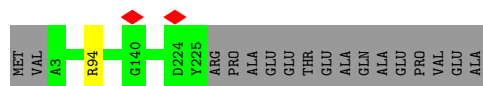
- Molecule 52: RPS2 isoform 1

Chain s:  85% 15%



- Molecule 53: RPS3 isoform 1

Chain t:  92% 7%



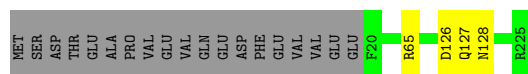
- Molecule 54: 40S ribosomal protein S4-A

Chain u:  99% .



- Molecule 55: Rps5p

Chain v:  90% . 8%



- Molecule 56: 40S ribosomal protein S6-A

Chain w:  93% . 6%



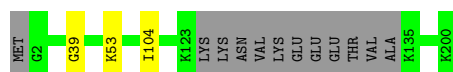
- Molecule 57: 40S ribosomal protein S7-A

Chain x:  96% . .



- Molecule 58: RPS8A isoform 1

Chain y:  92% . 6%



- Molecule 59: 40S ribosomal protein S9-A

Chain z:  92% • 6%



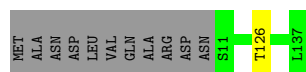
- Molecule 60: 40S ribosomal protein S13

Chain AD:  98% ..




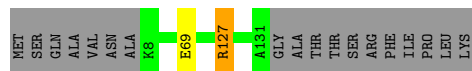
- Molecule 61: 40S ribosomal protein S14-B

Chain AE:  91% • 8%



- Molecule 62: RPS15 isoform 1

Chain AF:  86% .. 13%



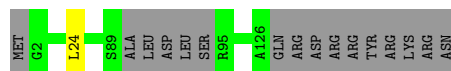
- Molecule 63: 40S ribosomal protein S16-A

Chain AG:  98% ..



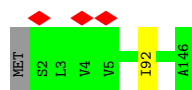
- Molecule 64: 40S ribosomal protein S17-B

Chain AH:  88% • 12%



- Molecule 65: 40S ribosomal protein S18-A

Chain AI:  99% ..




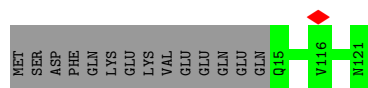
- Molecule 66: 40S ribosomal protein S19-A

Chain AJ:  99% .



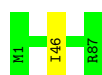
- Molecule 67: RPS20 isoform 1

Chain AK:  88% 12%



- Molecule 68: 40S ribosomal protein S21-A

Chain AL:  99% .



- Molecule 69: RPS22A isoform 1

Chain AM:  99% .



- Molecule 70: 40S ribosomal protein S23-A

Chain AN:  98% ..



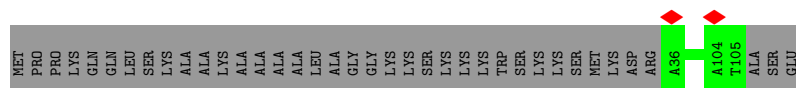
- Molecule 71: 40S ribosomal protein S24-A

Chain AO:  99% .

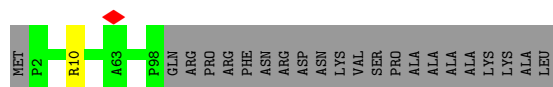
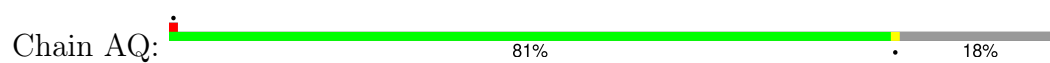


- Molecule 72: RPS25A isoform 1

Chain AP:  65% 35%



- Molecule 73: RPS26B isoform 1



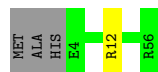
- Molecule 74: 40S ribosomal protein S27-A



- Molecule 75: RPS28A isoform 1



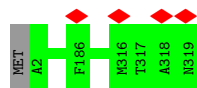
- Molecule 76: RPS29A isoform 1



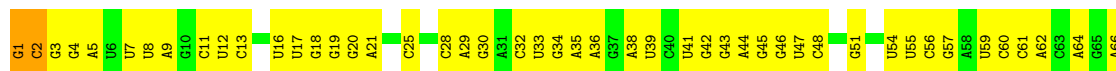
- Molecule 77: 40S ribosomal protein S30-A

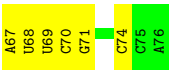


- Molecule 78: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 79: Transfer RNA





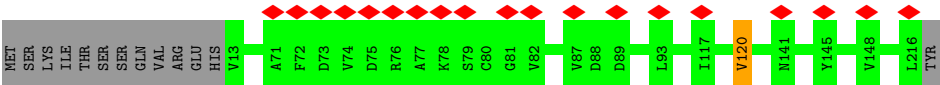
• Molecule 79: Transfer RNA



• Molecule 80: mRNA



• Molecule 81: RPL1A isoform 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9629	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	27.135	Depositor
Minimum map value	-15.154	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	545.792, 545.792, 545.792	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.066, 1.066, 1.066	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.27	0/1948	0.60	0/2617
2	B	0.27	0/3146	0.55	0/4228
3	C	0.27	0/2800	0.54	1/3790 (0.0%)
4	D	0.28	0/2425	0.53	0/3271
5	E	0.27	0/1260	0.53	0/1694
6	F	0.29	0/1821	0.52	0/2451
7	G	0.78	2/1836 (0.1%)	0.57	2/2481 (0.1%)
8	H	0.27	0/1539	0.56	0/2073
9	I	0.27	0/1741	0.55	0/2335
10	J	0.27	0/1374	0.59	0/1842
11	L	0.27	0/1568	0.57	0/2106
12	M	0.26	0/1068	0.52	0/1438
13	N	0.27	0/1757	0.58	0/2354
14	O	0.29	0/1585	0.54	0/2128
15	P	0.27	0/1443	0.53	0/1944
16	Q	0.26	0/1465	0.54	0/1965
17	R	0.27	0/1538	0.57	0/2050
18	S	0.28	0/1481	0.56	0/1990
19	T	0.28	0/1300	0.53	0/1743
20	U	0.29	0/812	0.53	1/1099 (0.1%)
21	V	0.27	0/1018	0.55	0/1369
22	W	0.28	0/533	0.56	0/707
23	X	0.27	0/979	0.50	0/1321
24	Y	0.25	0/1004	0.56	0/1341
25	Z	0.28	0/1118	0.50	0/1497
26	AA	0.31	0/789	0.53	0/1067
27	AB	0.27	0/1247	0.55	0/1681
28	1	1.52	15/77157 (0.0%)	1.05	259/120295 (0.2%)
29	3	0.36	0/2883	0.91	2/4491 (0.0%)
30	4	4.75	8/3746 (0.2%)	1.40	28/5832 (0.5%)
31	P0	0.29	0/1498	0.55	0/2025
32	P2	0.26	0/728	0.54	0/975

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	a	0.26	0/1204	0.56	0/1612
34	b	0.27	0/473	0.50	0/629
35	c	0.27	0/751	0.53	0/1008
36	d	0.26	0/897	0.55	0/1205
37	e	0.26	0/1041	0.52	0/1394
38	f	0.28	0/868	0.58	0/1168
39	g	0.29	0/890	0.61	0/1189
40	h	0.28	0/978	0.53	0/1301
41	i	0.27	0/778	0.53	0/1034
42	j	2.01	1/696 (0.1%)	0.80	3/923 (0.3%)
43	k	0.27	0/618	0.56	0/826
44	l	0.29	0/443	0.65	0/588
45	m	0.27	0/423	0.55	0/562
46	n	0.26	0/228	0.64	0/293
47	o	0.28	0/860	0.57	0/1136
48	p	0.27	0/701	0.62	0/934
49	2	0.53	6/41539 (0.0%)	1.08	65/64723 (0.1%)
50	q	0.27	0/1617	0.52	0/2215
51	r	0.26	0/1735	0.58	1/2335 (0.0%)
52	s	0.27	0/1665	0.54	0/2263
53	t	0.28	0/1759	0.55	0/2368
54	u	0.26	0/2109	0.57	0/2839
55	v	0.27	0/1629	0.56	0/2202
56	w	0.28	0/1814	0.60	0/2425
57	x	0.28	0/1506	0.54	0/2028
58	y	0.27	0/1514	0.59	0/2021
59	z	0.26	0/1519	0.55	0/2035
60	AD	0.27	0/1215	0.57	0/1638
61	AE	0.26	0/901	0.57	0/1217
62	AF	0.28	0/998	0.55	0/1341
63	AG	0.28	0/1125	0.54	0/1510
64	AH	0.27	0/935	0.58	1/1254 (0.1%)
65	AI	0.25	0/1211	0.56	0/1628
66	AJ	0.28	0/1130	0.58	0/1517
67	AK	0.26	0/865	0.53	0/1169
68	AL	0.28	0/693	0.56	0/935
69	AM	0.26	0/1038	0.55	0/1395
70	AN	0.27	0/1139	0.58	0/1518
71	AO	0.27	0/1087	0.55	0/1449
72	AP	0.27	0/571	0.53	0/768
73	AQ	0.27	0/782	0.59	0/1047
74	AR	0.25	0/620	0.50	0/838
75	AS	0.28	0/499	0.58	0/670

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AT	0.27	0/452	0.59	0/600
77	AU	0.27	0/483	0.53	0/643
78	AV	0.25	0/2490	0.52	0/3389
79	AX	0.36	1/1818 (0.1%)	0.85	1/2831 (0.0%)
79	AZ	0.35	1/1818 (0.1%)	0.86	0/2831
80	AY	0.24	0/181	0.98	0/278
81	L1	0.27	0/1634	0.53	0/2195
All	All	1.14	34/220547 (0.0%)	0.90	364/324117 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	C	0	1
7	G	0	1
11	L	0	1
14	O	0	1
39	g	0	1
45	m	0	1
54	u	0	1
55	v	0	1
81	L1	0	1
All	All	0	10

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	1	148	G	C6-N1	153.66	2.47	1.39
28	1	148	G	N3-C4	144.30	2.36	1.35
30	4	95	G	N3-C4	138.97	2.32	1.35
30	4	95	G	C6-N1	136.18	2.34	1.39
28	1	2262	A	N3-C4	134.62	2.15	1.34
28	1	148	G	N1-C2	132.42	2.43	1.37
28	1	148	G	C2-N3	130.17	2.36	1.32
30	4	95	G	C2-N3	120.09	2.28	1.32
28	1	2262	A	C6-N1	117.99	2.18	1.35
30	4	95	G	N1-C2	115.08	2.29	1.37
28	1	148	G	C5-C4	110.75	2.15	1.38
30	4	95	G	C5-C4	106.72	2.13	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	1	2262	A	C5-C4	98.47	2.07	1.38
28	1	2262	A	N1-C2	96.71	2.21	1.34
28	1	2262	A	C2-N3	94.54	2.18	1.33
28	1	148	G	C5-C6	86.69	2.29	1.42
28	1	2262	A	C5-C6	86.03	2.18	1.41
30	4	95	G	C5-C6	83.71	2.26	1.42
49	2	1759	C	C1'-N1	69.26	2.52	1.48
42	j	81	GLY	CA-C	52.34	2.35	1.51
49	2	1759	C	N1-C6	43.61	1.63	1.37
49	2	1759	C	N1-C2	31.21	1.71	1.40
7	G	135	GLY	CA-C	30.96	2.01	1.51
49	2	1759	C	C4-C5	-11.69	1.33	1.43
79	AZ	1	G	OP3-P	-10.68	1.48	1.61
79	AX	1	G	OP3-P	-10.66	1.48	1.61
49	2	1759	C	N3-C4	-8.03	1.28	1.33
28	1	148	G	C8-N7	7.78	1.35	1.30
49	2	1759	C	C2'-C1'	7.49	1.61	1.53
30	4	95	G	C8-N7	7.28	1.35	1.30
30	4	95	G	N9-C8	6.97	1.42	1.37
28	1	148	G	N9-C8	6.76	1.42	1.37
28	1	2262	A	C8-N7	5.37	1.35	1.31
7	G	135	GLY	N-CA	5.23	1.53	1.46

All (364) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	1759	C	C6-N1-C2	-126.81	69.58	120.30
49	2	1759	C	C5-C6-N1	69.15	155.57	121.00
49	2	1759	C	N3-C2-O2	-38.63	94.86	121.90
28	1	148	G	C4-C5-N7	-38.09	95.56	110.80
28	1	2262	A	N1-C2-N3	-35.62	111.49	129.30
49	2	1759	C	N1-C2-N3	34.82	143.57	119.20
49	2	1759	C	N3-C4-C5	-34.82	107.97	121.90
30	4	95	G	C4-C5-N7	-34.38	97.05	110.80
30	4	95	G	N3-C4-N9	28.80	143.28	126.00
28	1	2262	A	C2-N3-C4	27.55	124.37	110.60
28	1	148	G	N3-C4-N9	26.70	142.02	126.00
28	1	2262	A	C4-C5-N7	-26.55	97.42	110.70
28	1	148	G	C2-N3-C4	26.22	125.01	111.90
28	1	148	G	N7-C8-N9	26.02	126.11	113.10
30	4	95	G	N7-C8-N9	25.94	126.07	113.10
30	4	95	G	C2-N3-C4	24.89	124.35	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	1759	C	C2-N1-C1'	23.34	144.48	118.80
28	1	2262	A	N7-C8-N9	22.79	125.19	113.80
49	2	1759	C	C6-N1-C1'	20.94	145.93	120.80
28	1	148	G	N1-C2-N3	-20.70	111.48	123.90
30	4	95	G	N9-C4-C5	-20.06	97.38	105.40
28	1	148	G	N9-C4-C5	-19.30	97.68	105.40
30	4	95	G	N1-C2-N3	-19.19	112.38	123.90
28	1	2262	A	N9-C4-C5	-18.64	98.34	105.80
30	4	95	G	N3-C4-C5	-18.52	119.34	128.60
28	1	148	G	N3-C4-C5	-17.51	119.84	128.60
28	1	2262	A	N3-C4-N9	16.64	140.71	127.40
49	2	1759	C	O4'-C1'-N1	16.24	121.19	108.20
30	4	95	G	C6-C5-N7	15.98	139.99	130.40
28	1	148	G	C6-C5-N7	15.56	139.73	130.40
28	1	148	G	C5-N7-C8	14.76	111.68	104.30
49	2	1759	C	N3-C4-N4	14.35	128.05	118.00
28	1	2262	A	C5-N7-C8	13.29	110.55	103.90
28	1	2262	A	C6-C5-N7	12.92	141.34	132.30
42	j	81	GLY	O-C-N	-12.88	102.09	122.70
49	2	1759	C	N1-C1'-C2'	12.65	130.44	114.00
28	1	2302	G	C5-C6-O6	12.33	136.00	128.60
30	4	95	G	C5-N7-C8	12.02	110.31	104.30
28	1	2262	A	C6-N1-C2	11.61	125.56	118.60
28	1	208	C	C2-N1-C1'	11.28	131.20	118.80
28	1	2302	G	N1-C6-O6	-10.82	113.41	119.90
28	1	346	C	C2-N1-C1'	10.81	130.69	118.80
30	4	95	G	C5-C6-N1	10.66	116.83	111.50
49	2	87	C	C2-N1-C1'	10.59	130.45	118.80
28	1	2290	C	N3-C2-O2	-9.96	114.93	121.90
28	1	105	C	N1-C2-O2	9.93	124.86	118.90
49	2	1440	C	N3-C2-O2	-9.90	114.97	121.90
49	2	1759	C	C2-N3-C4	9.85	124.82	119.90
28	1	148	G	C5-C6-N1	9.80	116.40	111.50
28	1	3298	C	C2-N1-C1'	9.77	129.55	118.80
28	1	1109	U	C2-N1-C1'	9.75	129.40	117.70
28	1	346	C	N1-C2-O2	9.73	124.74	118.90
28	1	696	C	N3-C2-O2	-9.73	115.09	121.90
28	1	1608	C	C2-N1-C1'	9.66	129.42	118.80
49	2	522	U	C2-N1-C1'	9.61	129.24	117.70
28	1	105	C	N3-C2-O2	-9.47	115.27	121.90
28	1	1505	C	C6-N1-C2	-9.29	116.58	120.30
28	1	148	G	C4-C5-C6	9.16	124.30	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	208	C	N1-C2-O2	8.73	124.14	118.90
7	G	135	GLY	N-CA-C	8.68	134.81	113.10
28	1	346	C	N3-C2-O2	-8.62	115.87	121.90
28	1	1340	G	N3-C4-N9	8.60	131.16	126.00
28	1	2262	A	N3-C4-C5	-8.52	120.84	126.80
49	2	927	C	N3-C2-O2	-8.48	115.96	121.90
28	1	1340	G	C6-C5-N7	-8.44	125.34	130.40
28	1	148	G	N1-C2-N2	8.41	123.77	116.20
49	2	87	C	N1-C2-O2	8.37	123.92	118.90
28	1	208	C	C6-N1-C1'	-8.31	110.83	120.80
28	1	1255	C	N3-C2-O2	-8.27	116.11	121.90
28	1	2277	C	N1-C2-O2	8.26	123.85	118.90
28	1	3023	U	C2-N1-C1'	8.23	127.58	117.70
28	1	2290	C	C5-C4-N4	8.21	125.94	120.20
30	4	19	C	N1-C2-O2	8.18	123.81	118.90
30	4	95	G	N3-C2-N2	8.12	125.59	119.90
28	1	1280	C	N3-C2-O2	-8.04	116.27	121.90
49	2	208	U	C2-N1-C1'	8.04	127.34	117.70
28	1	2899	C	C2-N1-C1'	8.03	127.64	118.80
28	1	2627	C	N1-C2-O2	7.90	123.64	118.90
28	1	1187	C	N1-C2-O2	7.76	123.55	118.90
28	1	1381	A	O4'-C1'-N9	7.74	114.39	108.20
28	1	2290	C	C6-N1-C2	-7.73	117.21	120.30
28	1	948	C	C6-N1-C2	-7.65	117.24	120.30
28	1	696	C	N1-C2-O2	7.64	123.49	118.90
28	1	1644	C	C2-N1-C1'	7.63	127.19	118.80
28	1	1608	C	C6-N1-C1'	-7.61	111.67	120.80
49	2	414	C	N3-C2-O2	-7.60	116.58	121.90
28	1	1710	C	N1-C2-O2	7.55	123.43	118.90
28	1	346	C	C6-N1-C1'	-7.54	111.75	120.80
28	1	3265	C	N3-C2-O2	-7.54	116.62	121.90
49	2	87	C	C6-N1-C1'	-7.54	111.76	120.80
28	1	871	U	C2-N1-C1'	7.51	126.72	117.70
28	1	3020	U	C2-N1-C1'	7.47	126.66	117.70
28	1	1109	U	N3-C2-O2	-7.45	116.99	122.20
49	2	965	U	C2-N1-C1'	7.38	126.55	117.70
28	1	2666	C	C2-N1-C1'	7.37	126.91	118.80
28	1	3298	C	N1-C2-O2	7.35	123.31	118.90
28	1	2778	G	C4-N9-C1'	7.35	136.05	126.50
28	1	2098	C	N3-C2-O2	-7.34	116.76	121.90
28	1	3298	C	C6-N1-C1'	-7.32	112.02	120.80
49	2	1687	U	C5-C4-O4	7.29	130.28	125.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	1729	C	N3-C2-O2	-7.25	116.82	121.90
28	1	2302	G	N3-C4-N9	-7.21	121.67	126.00
28	1	2302	G	N9-C4-C5	7.20	108.28	105.40
49	2	522	U	N3-C2-O2	-7.20	117.16	122.20
49	2	414	C	C6-N1-C2	-7.19	117.42	120.30
42	j	81	GLY	CA-C-N	7.16	132.94	117.20
28	1	1340	G	C5-C6-O6	-7.13	124.32	128.60
28	1	2262	A	C4-C5-C6	7.05	120.53	117.00
28	1	3308	C	C6-N1-C2	-7.03	117.49	120.30
28	1	3110	C	N3-C2-O2	-7.02	116.99	121.90
28	1	359	U	C2-N1-C1'	7.01	126.11	117.70
28	1	2292	U	OP1-P-OP2	-7.01	109.09	119.60
49	2	161	U	C2-N1-C1'	6.99	126.09	117.70
28	1	346	C	C6-N1-C2	-6.98	117.51	120.30
28	1	286	U	C2-N1-C1'	6.96	126.05	117.70
28	1	2290	C	C6-N1-C1'	6.94	129.12	120.80
49	2	522	U	N1-C2-O2	6.92	127.65	122.80
28	1	148	G	N3-C2-N2	6.92	124.74	119.90
28	1	903	U	N3-C2-O2	-6.92	117.36	122.20
28	1	2307	G	N3-C2-N2	6.91	124.74	119.90
28	1	636	C	C6-N1-C2	-6.88	117.55	120.30
28	1	2290	C	N3-C4-N4	-6.88	113.19	118.00
28	1	2891	U	C5-C4-O4	6.87	130.02	125.90
30	4	95	G	C8-N9-C4	6.86	109.14	106.40
49	2	87	C	N3-C2-O2	-6.83	117.12	121.90
49	2	1687	U	N3-C4-O4	-6.82	114.63	119.40
49	2	208	U	N3-C2-O2	-6.80	117.44	122.20
49	2	114	C	O4'-C1'-N1	6.78	113.62	108.20
28	1	2302	G	N1-C2-N3	6.76	127.96	123.90
28	1	1280	C	N1-C2-O2	6.72	122.93	118.90
49	2	927	C	N1-C2-O2	6.71	122.92	118.90
28	1	1532	C	N1-C2-O2	6.69	122.91	118.90
28	1	2776	C	C6-N1-C2	-6.65	117.64	120.30
28	1	2360	C	N1-C2-O2	6.63	122.88	118.90
28	1	1340	G	N1-C6-O6	6.59	123.86	119.90
28	1	1109	U	N1-C2-O2	6.58	127.41	122.80
28	1	1737	U	C2-N1-C1'	6.58	125.60	117.70
28	1	3105	U	C2-N1-C1'	6.56	125.57	117.70
28	1	3308	C	C2-N1-C1'	6.55	126.01	118.80
28	1	2277	C	N3-C2-O2	-6.55	117.32	121.90
28	1	2983	C	C6-N1-C2	-6.54	117.69	120.30
28	1	2666	C	C6-N1-C2	-6.51	117.69	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	2778	G	C8-N9-C1'	-6.50	118.55	127.00
28	1	1188	U	C6-N1-C2	-6.46	117.12	121.00
49	2	1458	G	C4-N9-C1'	6.45	134.89	126.50
28	1	2262	A	C8-N9-C4	6.45	108.38	105.80
30	4	95	G	C4-C5-C6	6.45	122.67	118.80
49	2	87	C	C6-N1-C2	-6.44	117.72	120.30
49	2	522	U	C6-N1-C1'	-6.42	112.21	121.20
28	1	1188	U	C5-C6-N1	6.42	125.91	122.70
28	1	969	C	N1-C2-O2	6.39	122.73	118.90
28	1	2899	C	N1-C2-O2	6.38	122.73	118.90
28	1	1780	G	C4-N9-C1'	6.37	134.79	126.50
28	1	2608	G	C6-C5-N7	-6.35	126.59	130.40
28	1	1340	G	C4-N9-C1'	6.33	134.73	126.50
28	1	2786	G	C4-N9-C1'	6.33	134.73	126.50
28	1	2302	G	C4-C5-N7	-6.32	108.27	110.80
28	1	2290	C	N1-C2-N3	6.31	123.62	119.20
28	1	3308	C	N1-C2-O2	6.31	122.69	118.90
30	4	19	C	C2-N1-C1'	6.29	125.72	118.80
28	1	1725	C	N3-C2-O2	-6.29	117.50	121.90
28	1	1579	C	N3-C2-O2	-6.28	117.50	121.90
28	1	2302	G	N1-C2-N2	-6.28	110.55	116.20
28	1	3308	C	N3-C2-O2	-6.27	117.51	121.90
28	1	3110	C	N1-C2-O2	6.26	122.65	118.90
28	1	141	C	N3-C2-O2	-6.25	117.52	121.90
28	1	1857	C	C6-N1-C2	-6.23	117.81	120.30
49	2	1458	G	C8-N9-C1'	-6.23	118.91	127.00
30	4	95	G	N1-C2-N2	6.22	121.80	116.20
49	2	1715	G	C4-N9-C1'	6.21	134.57	126.50
49	2	208	U	N1-C2-O2	6.19	127.14	122.80
28	1	30	G	N3-C4-N9	6.18	129.71	126.00
7	G	135	GLY	O-C-N	-6.17	112.82	122.70
49	2	1440	C	N1-C2-O2	6.17	122.60	118.90
28	1	404	G	N3-C2-N2	6.16	124.21	119.90
28	1	3265	C	N1-C2-O2	6.15	122.59	118.90
28	1	2693	C	C6-N1-C2	-6.15	117.84	120.30
28	1	1698	C	C6-N1-C2	-6.15	117.84	120.30
28	1	2891	U	N3-C4-O4	-6.14	115.10	119.40
28	1	1029	G	C4-N9-C1'	6.14	134.48	126.50
28	1	1725	C	N1-C2-O2	6.14	122.58	118.90
28	1	3086	A	C2-N3-C4	6.13	113.67	110.60
49	2	243	G	C4-N9-C1'	6.13	134.47	126.50
28	1	404	G	N3-C4-N9	6.11	129.66	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	208	C	N3-C2-O2	-6.09	117.63	121.90
28	1	141	C	C6-N1-C2	-6.08	117.87	120.30
28	1	1939	G	C4-N9-C1'	6.06	134.38	126.50
30	4	150	G	N3-C4-N9	6.05	129.63	126.00
28	1	2307	G	N1-C2-N2	-6.05	110.76	116.20
28	1	1440	G	N9-C4-C5	-6.05	102.98	105.40
28	1	31	C	N3-C2-O2	-6.04	117.67	121.90
28	1	1710	C	N3-C2-O2	-6.04	117.67	121.90
28	1	208	C	C6-N1-C2	-6.04	117.88	120.30
28	1	30	G	C6-C5-N7	-6.03	126.78	130.40
28	1	1183	C	C6-N1-C2	-6.01	117.90	120.30
28	1	1109	U	C6-N1-C1'	-6.00	112.80	121.20
42	j	81	GLY	N-CA-C	6.00	128.11	113.10
28	1	1505	C	N3-C2-O2	-5.99	117.70	121.90
28	1	445	G	C4-N9-C1'	5.97	134.26	126.50
28	1	1340	G	N3-C4-C5	-5.95	125.63	128.60
49	2	1715	G	C8-N9-C1'	-5.95	119.27	127.00
28	1	547	G	N3-C4-N9	-5.93	122.44	126.00
28	1	2912	G	C4-N9-C1'	5.93	134.21	126.50
49	2	1458	G	N3-C4-N9	5.91	129.55	126.00
28	1	2623	G	C4-N9-C1'	5.89	134.16	126.50
49	2	1784	C	N3-C2-O2	-5.89	117.78	121.90
28	1	2302	G	C2-N3-C4	-5.89	108.96	111.90
30	4	137	C	C6-N1-C2	-5.88	117.95	120.30
28	1	3111	U	C2-N1-C1'	5.88	124.76	117.70
28	1	1505	C	N1-C2-O2	5.87	122.42	118.90
28	1	267	G	N3-C4-N9	-5.87	122.48	126.00
64	AH	24	LEU	CA-CB-CG	5.85	128.76	115.30
28	1	404	G	N9-C4-C5	-5.84	103.06	105.40
28	1	1376	C	N3-C2-O2	-5.83	117.81	121.90
28	1	2782	U	C5-C4-O4	-5.83	122.40	125.90
28	1	1644	C	N1-C2-O2	5.83	122.40	118.90
28	1	226	C	N3-C2-O2	-5.83	117.82	121.90
20	U	91	ASP	CB-CG-OD1	5.81	123.53	118.30
49	2	1440	C	C6-N1-C2	-5.80	117.98	120.30
49	2	1467	C	N1-C2-O2	5.80	122.38	118.90
28	1	148	G	C8-N9-C4	5.79	108.72	106.40
28	1	1608	C	N1-C2-O2	5.79	122.38	118.90
49	2	1729	C	N1-C2-O2	5.78	122.37	118.90
28	1	3080	G	N3-C4-C5	-5.77	125.72	128.60
28	1	668	G	C4-N9-C1'	5.75	133.98	126.50
28	1	1340	G	C8-N9-C1'	-5.75	119.52	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	1414	G	N1-C6-O6	-5.71	116.47	119.90
28	1	1255	C	N1-C2-O2	5.69	122.31	118.90
28	1	871	U	N3-C2-O2	-5.66	118.24	122.20
28	1	2899	C	N3-C2-O2	-5.66	117.94	121.90
49	2	1271	G	C5-C6-O6	5.66	131.99	128.60
28	1	1146	C	C6-N1-C2	-5.65	118.04	120.30
28	1	2786	G	N3-C4-N9	5.64	129.38	126.00
30	4	152	G	C4-N9-C1'	5.64	133.83	126.50
28	1	1639	C	N3-C2-O2	-5.64	117.95	121.90
28	1	816	A	C8-N9-C4	-5.62	103.55	105.80
49	2	191	C	C6-N1-C2	-5.62	118.05	120.30
28	1	2786	G	C8-N9-C1'	-5.61	119.70	127.00
28	1	2899	C	C6-N1-C1'	-5.59	114.09	120.80
30	4	150	G	C6-C5-N7	-5.58	127.05	130.40
28	1	1531	C	N1-C2-O2	5.56	122.24	118.90
49	2	243	G	C8-N9-C1'	-5.56	119.77	127.00
28	1	2623	G	C8-N9-C1'	-5.55	119.78	127.00
28	1	2594	C	C6-N1-C1'	5.55	127.46	120.80
79	AX	2	C	C6-N1-C2	-5.55	118.08	120.30
28	1	1790	G	C4-N9-C1'	5.54	133.70	126.50
28	1	2619	G	C4-N9-C1'	5.54	133.70	126.50
28	1	1513	G	C4-N9-C1'	5.53	133.69	126.50
49	2	1686	C	N1-C2-O2	5.53	122.22	118.90
28	1	2568	C	N1-C2-O2	5.53	122.22	118.90
28	1	2627	C	N3-C2-O2	-5.51	118.04	121.90
28	1	1513	G	N3-C4-N9	5.51	129.31	126.00
28	1	3298	C	N3-C2-O2	-5.51	118.05	121.90
28	1	31	C	O4'-C1'-N1	5.50	112.60	108.20
30	4	14	C	P-O3'-C3'	5.49	126.29	119.70
49	2	160	C	C2-N1-C1'	5.49	124.84	118.80
28	1	696	C	C6-N1-C2	-5.49	118.10	120.30
28	1	1896	A	C4-N9-C1'	5.49	136.18	126.30
28	1	404	G	C4-C5-N7	5.48	112.99	110.80
28	1	1340	G	N9-C4-C5	-5.47	103.21	105.40
49	2	500	C	N3-C2-O2	-5.47	118.07	121.90
30	4	115	C	N3-C2-O2	-5.47	118.07	121.90
28	1	2655	U	P-O3'-C3'	5.47	126.27	119.70
28	1	1440	G	C4-C5-N7	5.47	112.99	110.80
28	1	2608	G	C4-N9-C1'	5.47	133.61	126.50
28	1	2786	G	N3-C4-C5	-5.47	125.87	128.60
28	1	1392	G	C4-N9-C1'	5.45	133.59	126.50
28	1	3080	G	C2-N3-C4	5.45	114.62	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	2777	G	OP1-P-O3'	5.44	117.17	105.20
28	1	1109	U	C6-N1-C2	-5.43	117.74	121.00
28	1	707	U	P-O3'-C3'	5.43	126.22	119.70
28	1	2881	C	N1-C2-O2	5.43	122.16	118.90
28	1	871	U	N1-C2-O2	5.42	126.60	122.80
28	1	1505	C	C5-C6-N1	5.41	123.70	121.00
28	1	668	G	O4'-C1'-N9	5.41	112.53	108.20
28	1	769	G	C4-N9-C1'	5.41	133.53	126.50
28	1	141	C	N1-C2-O2	5.40	122.14	118.90
28	1	2307	G	N3-C4-N9	5.39	129.23	126.00
28	1	3080	G	C4-N9-C1'	5.38	133.50	126.50
28	1	2302	G	C6-C5-N7	5.38	133.62	130.40
28	1	54	C	N1-C2-O2	5.37	122.12	118.90
28	1	2798	C	C2-N1-C1'	5.36	124.69	118.80
49	2	784	C	N3-C2-O2	-5.36	118.15	121.90
28	1	1833	G	N3-C4-N9	5.35	129.21	126.00
28	1	2098	C	N1-C2-O2	5.34	122.11	118.90
49	2	1389	C	C2-N1-C1'	5.34	124.67	118.80
28	1	2868	U	C6-N1-C2	-5.33	117.80	121.00
28	1	1857	C	N3-C2-O2	-5.33	118.17	121.90
28	1	1644	C	C6-N1-C1'	-5.33	114.41	120.80
28	1	903	U	N1-C2-O2	5.32	126.52	122.80
49	2	1467	C	N3-C2-O2	-5.31	118.18	121.90
28	1	1698	C	C2-N1-C1'	5.30	124.63	118.80
49	2	1759	C	C5-C4-N4	5.30	123.91	120.20
28	1	189	G	C8-N9-C4	-5.29	104.28	106.40
28	1	1513	G	C8-N9-C1'	-5.29	120.13	127.00
28	1	1780	G	C8-N9-C1'	-5.28	120.14	127.00
30	4	19	C	N3-C2-O2	-5.27	118.21	121.90
28	1	3023	U	N3-C2-O2	-5.27	118.51	122.20
28	1	1939	G	C8-N9-C1'	-5.26	120.16	127.00
28	1	668	G	C8-N9-C1'	-5.26	120.16	127.00
28	1	1109	U	C5-C6-N1	5.26	125.33	122.70
28	1	1187	C	N3-C4-C5	5.25	124.00	121.90
28	1	3023	U	C6-N1-C1'	-5.25	113.85	121.20
28	1	2398	A	C2-N3-C4	5.24	113.22	110.60
49	2	965	U	C6-N1-C1'	-5.23	113.88	121.20
28	1	2360	C	N3-C2-O2	-5.22	118.24	121.90
28	1	2777	G	P-O3'-C3'	5.22	125.96	119.70
28	1	1395	G	C8-N9-C4	-5.22	104.31	106.40
28	1	816	A	N7-C8-N9	5.21	116.41	113.80
49	2	962	C	N3-C2-O2	-5.20	118.26	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	208	C	C5-C6-N1	5.19	123.59	121.00
51	r	61	LEU	CA-CB-CG	5.19	127.24	115.30
49	2	1128	C	N3-C2-O2	-5.19	118.27	121.90
28	1	547	G	C5-C6-O6	5.18	131.71	128.60
28	1	948	C	N3-C2-O2	-5.17	118.28	121.90
3	C	182	LEU	CA-CB-CG	5.16	127.18	115.30
28	1	445	G	N3-C4-C5	-5.16	126.02	128.60
30	4	150	G	C4-N9-C1'	5.16	133.21	126.50
28	1	1411	C	C6-N1-C2	-5.15	118.24	120.30
49	2	747	C	N3-C2-O2	-5.15	118.29	121.90
28	1	3212	C	C6-N1-C2	-5.15	118.24	120.30
28	1	68	C	N1-C2-O2	5.15	121.99	118.90
49	2	243	G	N3-C4-N9	5.14	129.09	126.00
49	2	1638	G	C4-N9-C1'	5.14	133.19	126.50
28	1	2290	C	P-O3'-C3'	5.14	125.87	119.70
28	1	2894	C	C2-N1-C1'	5.14	124.46	118.80
28	1	2522	G	C4-N9-C1'	5.14	133.18	126.50
28	1	1187	C	N3-C2-O2	-5.13	118.31	121.90
28	1	3020	U	C6-N1-C1'	-5.13	114.02	121.20
28	1	3023	U	N1-C2-O2	5.13	126.39	122.80
28	1	1227	C	N1-C2-O2	5.13	121.98	118.90
28	1	404	G	C6-C5-N7	-5.12	127.33	130.40
28	1	3020	U	N1-C2-O2	5.12	126.39	122.80
49	2	1298	U	O4'-C1'-N1	-5.12	104.10	108.20
29	3	49	G	N1-C6-O6	-5.12	116.83	119.90
28	1	1644	C	N3-C2-O2	-5.11	118.32	121.90
28	1	1562	C	C6-N1-C2	-5.11	118.26	120.30
28	1	1833	G	C4-N9-C1'	5.11	133.14	126.50
28	1	2594	C	C6-N1-C2	-5.11	118.26	120.30
28	1	1029	G	C8-N9-C1'	-5.11	120.36	127.00
28	1	749	C	C6-N1-C2	-5.11	118.26	120.30
28	1	2291	A	C5'-C4'-O4'	-5.10	102.98	109.10
28	1	2307	G	C6-C5-N7	-5.10	127.34	130.40
30	4	152	G	N3-C4-C5	-5.10	126.05	128.60
49	2	131	C	C6-N1-C2	-5.10	118.26	120.30
28	1	1513	G	N3-C2-N2	5.09	123.46	119.90
28	1	1340	G	C4-C5-N7	5.09	112.84	110.80
28	1	2899	C	C6-N1-C2	-5.09	118.26	120.30
30	4	107	G	C2-N3-C4	5.08	114.44	111.90
28	1	1340	G	C4-C5-C6	5.05	121.83	118.80
28	1	1392	G	N3-C4-C5	-5.05	126.08	128.60
49	2	500	C	N1-C2-O2	5.05	121.93	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	1282	G	C6-C5-N7	-5.04	127.37	130.40
28	1	707	U	OP2-P-O3'	5.04	116.30	105.20
49	2	1494	C	C6-N1-C1'	5.04	126.85	120.80
28	1	54	C	N3-C2-O2	-5.03	118.38	121.90
28	1	1780	G	N3-C4-C5	-5.03	126.09	128.60
28	1	445	G	C8-N9-C1'	-5.02	120.47	127.00
28	1	267	G	C8-N9-C1'	5.02	133.53	127.00
29	3	29	C	N3-C2-O2	-5.02	118.39	121.90
30	4	152	G	N3-C4-N9	5.02	129.01	126.00
28	1	1183	C	N3-C2-O2	-5.01	118.39	121.90
28	1	2290	C	C2-N1-C1'	-5.01	113.29	118.80
30	4	95	G	C5-C6-O6	-5.00	125.60	128.60

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	150	LEU	Peptide
3	C	182	LEU	Peptide
7	G	135	GLY	Mainchain
11	L	47	ALA	Peptide
81	L1	120	VAL	Peptide
14	O	110	PRO	Peptide
39	g	80	ARG	Peptide
45	m	126	LYS	Peptide
54	u	195	ILE	Peptide
55	v	127	GLN	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/254 (98%)	215 (86%)	33 (13%)	2 (1%)	16	54
2	B	384/387 (99%)	339 (88%)	45 (12%)	0	100	100
3	C	359/362 (99%)	314 (88%)	44 (12%)	1 (0%)	37	71
4	D	294/297 (99%)	263 (90%)	31 (10%)	0	100	100
5	E	152/176 (86%)	134 (88%)	18 (12%)	0	100	100
6	F	220/244 (90%)	198 (90%)	22 (10%)	0	100	100
7	G	231/256 (90%)	208 (90%)	22 (10%)	1 (0%)	30	67
8	H	189/191 (99%)	167 (88%)	21 (11%)	1 (0%)	25	62
9	I	207/221 (94%)	185 (89%)	22 (11%)	0	100	100
10	J	167/174 (96%)	139 (83%)	28 (17%)	0	100	100
11	L	191/199 (96%)	154 (81%)	34 (18%)	3 (2%)	8	38
12	M	134/138 (97%)	122 (91%)	11 (8%)	1 (1%)	19	56
13	N	201/204 (98%)	176 (88%)	23 (11%)	2 (1%)	13	48
14	O	195/199 (98%)	177 (91%)	17 (9%)	1 (0%)	25	62
15	P	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
16	Q	183/186 (98%)	168 (92%)	15 (8%)	0	100	100
17	R	186/189 (98%)	175 (94%)	11 (6%)	0	100	100
18	S	170/172 (99%)	148 (87%)	22 (13%)	0	100	100
19	T	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	22	59
20	U	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
21	V	134/137 (98%)	114 (85%)	18 (13%)	2 (2%)	8	40
22	W	61/155 (39%)	57 (93%)	4 (7%)	0	100	100
23	X	119/142 (84%)	107 (90%)	12 (10%)	0	100	100
24	Y	124/127 (98%)	117 (94%)	7 (6%)	0	100	100
25	Z	133/136 (98%)	117 (88%)	15 (11%)	1 (1%)	16	54
26	AA	94/105 (90%)	81 (86%)	12 (13%)	1 (1%)	12	46
27	AB	151/156 (97%)	129 (85%)	22 (15%)	0	100	100
31	P0	187/312 (60%)	143 (76%)	44 (24%)	0	100	100
32	P2	92/165 (56%)	70 (76%)	22 (24%)	0	100	100
33	a	146/149 (98%)	122 (84%)	23 (16%)	1 (1%)	19	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	b	56/59 (95%)	46 (82%)	10 (18%)	0	100	100
35	c	95/105 (90%)	87 (92%)	7 (7%)	1 (1%)	12	46
36	d	107/113 (95%)	96 (90%)	11 (10%)	0	100	100
37	e	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
38	f	104/107 (97%)	89 (86%)	14 (14%)	1 (1%)	13	48
39	g	110/121 (91%)	98 (89%)	12 (11%)	0	100	100
40	h	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
41	i	97/100 (97%)	82 (84%)	15 (16%)	0	100	100
42	j	85/88 (97%)	74 (87%)	11 (13%)	0	100	100
43	k	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
44	l	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
45	m	50/128 (39%)	37 (74%)	12 (24%)	1 (2%)	6	34
46	n	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
47	o	103/106 (97%)	84 (82%)	19 (18%)	0	100	100
48	p	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
50	q	204/252 (81%)	173 (85%)	29 (14%)	2 (1%)	13	48
51	r	212/255 (83%)	177 (84%)	34 (16%)	1 (0%)	25	62
52	s	215/254 (85%)	195 (91%)	19 (9%)	1 (0%)	25	62
53	t	221/240 (92%)	187 (85%)	34 (15%)	0	100	100
54	u	258/261 (99%)	210 (81%)	47 (18%)	1 (0%)	30	67
55	v	204/225 (91%)	172 (84%)	30 (15%)	2 (1%)	13	48
56	w	221/236 (94%)	171 (77%)	47 (21%)	3 (1%)	9	40
57	x	182/190 (96%)	156 (86%)	26 (14%)	0	100	100
58	y	184/200 (92%)	154 (84%)	28 (15%)	2 (1%)	12	46
59	z	183/197 (93%)	159 (87%)	23 (13%)	1 (0%)	25	62
60	AD	148/151 (98%)	131 (88%)	15 (10%)	2 (1%)	9	40
61	AE	125/138 (91%)	107 (86%)	17 (14%)	1 (1%)	16	54
62	AF	122/142 (86%)	98 (80%)	22 (18%)	2 (2%)	8	38
63	AG	139/143 (97%)	109 (78%)	29 (21%)	1 (1%)	19	56
64	AH	116/136 (85%)	105 (90%)	11 (10%)	0	100	100
65	AI	143/146 (98%)	125 (87%)	17 (12%)	1 (1%)	19	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	AJ	141/144 (98%)	123 (87%)	18 (13%)	0	100	100
67	AK	105/121 (87%)	84 (80%)	21 (20%)	0	100	100
68	AL	85/87 (98%)	68 (80%)	16 (19%)	1 (1%)	11	44
69	AM	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
70	AN	142/145 (98%)	113 (80%)	28 (20%)	1 (1%)	19	56
71	AO	132/135 (98%)	119 (90%)	13 (10%)	0	100	100
72	AP	68/108 (63%)	53 (78%)	15 (22%)	0	100	100
73	AQ	95/119 (80%)	69 (73%)	26 (27%)	0	100	100
74	AR	79/82 (96%)	65 (82%)	13 (16%)	1 (1%)	10	42
75	AS	61/67 (91%)	52 (85%)	9 (15%)	0	100	100
76	AT	51/56 (91%)	46 (90%)	5 (10%)	0	100	100
77	AU	58/63 (92%)	51 (88%)	7 (12%)	0	100	100
78	AV	316/319 (99%)	269 (85%)	47 (15%)	0	100	100
81	L1	202/217 (93%)	155 (77%)	46 (23%)	1 (0%)	25	62
All	All	11213/12280 (91%)	9675 (86%)	1493 (13%)	45 (0%)	32	67

All (45) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	L	47	ALA
11	L	48	PRO
11	L	62	THR
14	O	110	PRO
50	q	111	ILE
52	s	39	THR
54	u	154	ILE
56	w	10	ASN
60	AD	105	ASN
62	AF	127	ARG
3	C	130	ALA
19	T	18	ASP
21	V	105	PRO
60	AD	85	PRO
45	m	89	TYR
81	L1	120	VAL
25	Z	102	GLU
26	AA	32	HIS

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Mol	Chain	Res	Type
33	a	47	LYS
58	y	104	ILE
38	f	59	VAL
56	w	148	SER
62	AF	69	GLU
1	A	143	GLU
7	G	39	ALA
8	H	59	ASN
12	M	9	ALA
13	N	94	TYR
13	N	145	ASP
35	c	41	LEU
50	q	109	ASN
55	v	126	ASP
56	w	152	ASP
61	AE	126	THR
70	AN	112	LYS
74	AR	61	THR
55	v	128	ASN
58	y	39	GLY
65	AI	92	ILE
1	A	153	GLY
21	V	104	ASN
51	r	63	GLY
59	z	162	SER
63	AG	33	GLY
68	AL	46	ILE

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	
1	A	193/196 (98%)	191 (99%)	2 (1%)	73	81
2	B	319/323 (99%)	318 (100%)	1 (0%)	91	92
3	C	288/289 (100%)	285 (99%)	3 (1%)	73	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	244/245 (100%)	243 (100%)	1 (0%)	89	91
5	E	134/153 (88%)	133 (99%)	1 (1%)	81	86
6	F	186/205 (91%)	186 (100%)	0	100	100
7	G	187/208 (90%)	187 (100%)	0	100	100
8	H	171/171 (100%)	170 (99%)	1 (1%)	84	88
9	I	177/187 (95%)	176 (99%)	1 (1%)	84	88
10	J	147/151 (97%)	146 (99%)	1 (1%)	81	86
11	L	154/159 (97%)	154 (100%)	0	100	100
12	M	107/109 (98%)	107 (100%)	0	100	100
13	N	175/176 (99%)	174 (99%)	1 (1%)	84	88
14	O	160/162 (99%)	159 (99%)	1 (1%)	84	88
15	P	140/146 (96%)	139 (99%)	1 (1%)	81	86
16	Q	150/151 (99%)	150 (100%)	0	100	100
17	R	153/154 (99%)	153 (100%)	0	100	100
18	S	156/156 (100%)	154 (99%)	2 (1%)	65	76
19	T	136/137 (99%)	136 (100%)	0	100	100
20	U	87/107 (81%)	86 (99%)	1 (1%)	70	79
21	V	104/105 (99%)	104 (100%)	0	100	100
22	W	55/129 (43%)	55 (100%)	0	100	100
23	X	104/118 (88%)	103 (99%)	1 (1%)	73	81
24	Y	109/110 (99%)	108 (99%)	1 (1%)	75	83
25	Z	115/116 (99%)	115 (100%)	0	100	100
26	AA	77/98 (79%)	77 (100%)	0	100	100
27	AB	133/137 (97%)	133 (100%)	0	100	100
31	P0	160/254 (63%)	160 (100%)	0	100	100
32	P2	81/136 (60%)	80 (99%)	1 (1%)	67	78
33	a	118/119 (99%)	117 (99%)	1 (1%)	79	84
34	b	46/47 (98%)	46 (100%)	0	100	100
35	c	81/88 (92%)	80 (99%)	1 (1%)	67	78
36	d	94/97 (97%)	94 (100%)	0	100	100
37	e	109/111 (98%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	f	90/91 (99%)	90 (100%)	0	100	100
39	g	95/103 (92%)	94 (99%)	1 (1%)	70	79
40	h	104/105 (99%)	103 (99%)	1 (1%)	73	81
41	i	81/82 (99%)	81 (100%)	0	100	100
42	j	70/71 (99%)	70 (100%)	0	100	100
43	k	68/69 (99%)	68 (100%)	0	100	100
44	l	45/46 (98%)	45 (100%)	0	100	100
45	m	47/116 (40%)	47 (100%)	0	100	100
46	n	22/23 (96%)	22 (100%)	0	100	100
47	o	90/91 (99%)	90 (100%)	0	100	100
48	p	71/72 (99%)	70 (99%)	1 (1%)	62	75
50	q	164/210 (78%)	164 (100%)	0	100	100
51	r	191/224 (85%)	190 (100%)	1 (0%)	86	90
52	s	176/205 (86%)	176 (100%)	0	100	100
53	t	182/195 (93%)	181 (100%)	1 (0%)	86	90
54	u	221/222 (100%)	221 (100%)	0	100	100
55	v	173/191 (91%)	172 (99%)	1 (1%)	84	88
56	w	189/201 (94%)	188 (100%)	1 (0%)	86	90
57	x	165/170 (97%)	164 (99%)	1 (1%)	84	88
58	y	150/161 (93%)	149 (99%)	1 (1%)	81	86
59	z	158/166 (95%)	156 (99%)	2 (1%)	65	76
60	AD	127/128 (99%)	127 (100%)	0	100	100
61	AE	81/105 (77%)	81 (100%)	0	100	100
62	AF	101/118 (86%)	100 (99%)	1 (1%)	73	81
63	AG	117/119 (98%)	117 (100%)	0	100	100
64	AH	94/124 (76%)	94 (100%)	0	100	100
65	AI	128/129 (99%)	128 (100%)	0	100	100
66	AJ	115/116 (99%)	115 (100%)	0	100	100
67	AK	100/114 (88%)	100 (100%)	0	100	100
68	AL	74/74 (100%)	74 (100%)	0	100	100
69	AM	110/111 (99%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	AN	119/120 (99%)	118 (99%)	1 (1%)	79	84
71	AO	112/113 (99%)	112 (100%)	0	100	100
72	AP	61/89 (68%)	61 (100%)	0	100	100
73	AQ	83/100 (83%)	82 (99%)	1 (1%)	67	78
74	AR	70/71 (99%)	70 (100%)	0	100	100
75	AS	56/60 (93%)	56 (100%)	0	100	100
76	AT	47/49 (96%)	46 (98%)	1 (2%)	48	66
77	AU	51/54 (94%)	50 (98%)	1 (2%)	50	68
78	AV	259/262 (99%)	259 (100%)	0	100	100
81	L1	185/198 (93%)	185 (100%)	0	100	100
All	All	9492/10318 (92%)	9454 (100%)	38 (0%)	88	91

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LYS
1	A	193	ARG
2	B	159	ARG
3	C	138	ARG
3	C	197	ARG
3	C	350	LYS
4	D	152	ARG
5	E	175	LYS
8	H	106	LYS
9	I	183	LYS
10	J	72	ARG
13	N	109	ARG
14	O	82	LYS
15	P	118	GLN
18	S	13	ARG
18	S	117	ARG
20	U	70	LYS
23	X	39	LYS
24	Y	42	GLN
32	P2	93	LYS
33	a	59	ARG
35	c	86	ARG
39	g	4	ARG

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Mol	Chain	Res	Type
40	h	26	LYS
48	p	60	CYS
51	r	166	LYS
53	t	94	ARG
55	v	65	ARG
56	w	94	ARG
57	x	107	ARG
58	y	53	LYS
59	z	29	LYS
59	z	138	LYS
62	AF	127	ARG
70	AN	123	LYS
73	AQ	10	ARG
76	AT	12	ARG
77	AU	10	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
8	H	9	GLN
12	M	126	GLN
15	P	118	GLN
24	Y	81	GLN
34	b	19	ASN
45	m	120	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	1	3220/3395 (94%)	1863 (57%)	158 (4%)
29	3	120/121 (99%)	49 (40%)	5 (4%)
30	4	157/158 (99%)	86 (54%)	9 (5%)
49	2	1739/1800 (96%)	675 (38%)	20 (1%)
79	AX	76/76 (100%)	51 (67%)	3 (3%)
79	AZ	75/76 (98%)	40 (53%)	1 (1%)
80	AY	7/8 (87%)	6 (85%)	0
All	All	5394/5634 (95%)	2770 (51%)	196 (3%)

All (2770) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	1	7	C
28	1	14	U
28	1	15	C
28	1	19	U
28	1	20	A
28	1	21	G
28	1	22	G
28	1	23	A
28	1	24	G
28	1	25	U
28	1	26	A
28	1	27	C
28	1	29	C
28	1	30	G
28	1	31	C
28	1	34	A
28	1	39	A
28	1	40	A
28	1	42	C
28	1	47	C
28	1	50	U
28	1	51	A
28	1	53	G
28	1	54	C
28	1	55	G
28	1	56	G
28	1	60	A
28	1	64	G
28	1	65	A
28	1	66	A
28	1	68	C
28	1	69	C
28	1	70	A
28	1	71	A
28	1	72	C
28	1	73	C
28	1	74	G
28	1	76	G
28	1	77	A
28	1	78	U
28	1	81	C
28	1	82	C
28	1	83	U

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Mol	Chain	Res	Type
28	1	84	U
28	1	89	A
28	1	90	C
28	1	92	G
28	1	93	C
28	1	94	G
28	1	96	G
28	1	98	G
28	1	99	A
28	1	102	C
28	1	104	G
28	1	105	C
28	1	106	A
28	1	109	A
28	1	110	G
28	1	111	C
28	1	112	U
28	1	115	A
28	1	116	A
28	1	117	U
28	1	118	U
28	1	119	U
28	1	120	G
28	1	122	A
28	1	123	A
28	1	124	U
28	1	127	G
28	1	132	C
28	1	133	U
28	1	137	G
28	1	139	G
28	1	140	C
28	1	141	C
28	1	142	C
28	1	144	A
28	1	145	G
28	1	146	U
28	1	147	U
28	1	148	G
28	1	149	U
28	1	150	A
28	1	151	A

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Mol	Chain	Res	Type
28	1	154	U
28	1	155	G
28	1	156	G
28	1	157	A
28	1	158	G
28	1	163	C
28	1	164	A
28	1	165	A
28	1	171	G
28	1	174	C
28	1	176	G
28	1	179	C
28	1	182	U
28	1	183	G
28	1	187	A
28	1	188	U
28	1	189	G
28	1	190	U
28	1	191	U
28	1	193	C
28	1	195	U
28	1	198	A
28	1	199	A
28	1	200	C
28	1	201	A
28	1	202	G
28	1	203	G
28	1	204	A
28	1	205	C
28	1	206	G
28	1	208	C
28	1	210	U
28	1	211	A
28	1	212	G
28	1	216	G
28	1	218	G
28	1	219	A
28	1	221	A
28	1	222	A
28	1	225	C
28	1	226	C
28	1	227	G

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Mol	Chain	Res	Type
28	1	229	G
28	1	234	G
28	1	237	G
28	1	239	G
28	1	240	U
28	1	243	G
28	1	244	G
28	1	246	U
28	1	247	C
28	1	248	U
28	1	249	U
28	1	251	G
28	1	252	U
28	1	253	A
28	1	263	C
28	1	264	G
28	1	265	A
28	1	266	A
28	1	267	G
28	1	268	A
28	1	269	G
28	1	272	G
28	1	273	A
28	1	274	G
28	1	275	U
28	1	276	U
28	1	277	G
28	1	278	U
28	1	280	U
28	1	281	G
28	1	282	G
28	1	283	G
28	1	284	A
28	1	285	A
28	1	286	U
28	1	288	C
28	1	289	A
28	1	290	G
28	1	292	U
28	1	293	C
28	1	294	U
28	1	296	A

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Mol	Chain	Res	Type
28	1	298	U
28	1	304	G
28	1	305	U
28	1	306	A
28	1	308	A
28	1	309	U
28	1	314	U
28	1	315	C
28	1	316	U
28	1	318	A
28	1	319	A
28	1	323	A
28	1	324	A
28	1	325	A
28	1	326	U
28	1	327	A
28	1	328	U
28	1	329	U
28	1	330	G
28	1	331	G
28	1	337	G
28	1	338	A
28	1	339	C
28	1	340	C
28	1	341	G
28	1	342	A
28	1	343	U
28	1	344	A
28	1	345	G
28	1	346	C
28	1	347	G
28	1	348	A
28	1	349	A
28	1	350	C
28	1	352	A
28	1	353	G
28	1	354	U
28	1	355	A
28	1	359	U
28	1	360	G
28	1	361	A
28	1	362	U

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Mol	Chain	Res	Type
28	1	365	A
28	1	368	G
28	1	370	U
28	1	371	G
28	1	372	A
28	1	374	A
28	1	375	A
28	1	376	G
28	1	377	A
28	1	378	A
28	1	379	C
28	1	380	U
28	1	381	U
28	1	382	U
28	1	383	G
28	1	384	A
28	1	385	A
28	1	386	A
28	1	387	A
28	1	389	A
28	1	390	G
28	1	391	A
28	1	392	G
28	1	393	U
28	1	394	G
28	1	396	A
28	1	397	A
28	1	398	A
28	1	399	A
28	1	400	G
28	1	401	U
28	1	402	A
28	1	403	C
28	1	404	G
28	1	405	U
28	1	406	G
28	1	407	A
28	1	408	A
28	1	409	A
28	1	410	U
28	1	411	U
28	1	412	G

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Mol	Chain	Res	Type
28	1	413	U
28	1	415	G
28	1	416	A
28	1	419	G
28	1	421	G
28	1	423	A
28	1	430	U
28	1	431	U
28	1	432	G
28	1	433	A
28	1	434	U
28	1	437	G
28	1	438	A
28	1	440	A
28	1	441	U
28	1	442	G
28	1	443	G
28	1	444	U
28	1	446	U
28	1	448	U
28	1	449	U
28	1	488	U
28	1	489	U
28	1	492	C
28	1	493	U
28	1	494	G
28	1	495	G
28	1	500	C
28	1	501	A
28	1	506	U
28	1	507	U
28	1	508	U
28	1	509	U
28	1	510	G
28	1	519	A
28	1	521	A
28	1	523	A
28	1	533	A
28	1	534	U
28	1	535	G
28	1	536	U
28	1	541	U

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Mol	Chain	Res	Type
28	1	542	G
28	1	544	C
28	1	545	U
28	1	546	C
28	1	547	G
28	1	548	G
28	1	549	U
28	1	550	A
28	1	557	A
28	1	558	U
28	1	559	A
28	1	560	G
28	1	565	U
28	1	566	G
28	1	578	A
28	1	579	G
28	1	580	C
28	1	586	C
28	1	587	U
28	1	589	A
28	1	590	G
28	1	592	A
28	1	593	C
28	1	594	U
28	1	595	G
28	1	596	C
28	1	597	G
28	1	601	U
28	1	602	A
28	1	603	A
28	1	608	A
28	1	611	A
28	1	619	A
28	1	621	A
28	1	622	A
28	1	623	U
28	1	625	G
28	1	631	U
28	1	634	C
28	1	636	C
28	1	637	C
28	1	638	C

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Mol	Chain	Res	Type
28	1	639	G
28	1	642	U
28	1	643	U
28	1	644	G
28	1	645	A
28	1	646	A
28	1	647	A
28	1	648	C
28	1	649	A
28	1	650	C
28	1	653	A
28	1	655	C
28	1	656	A
28	1	660	A
28	1	661	G
28	1	662	U
28	1	663	C
28	1	664	U
28	1	665	A
28	1	667	C
28	1	669	U
28	1	671	U
28	1	673	U
28	1	674	G
28	1	675	C
28	1	676	G
28	1	677	A
28	1	678	G
28	1	679	U
28	1	680	G
28	1	681	U
28	1	682	U
28	1	683	U
28	1	684	G
28	1	685	G
28	1	688	G
28	1	689	U
28	1	690	A
28	1	691	A
28	1	692	A
28	1	694	C
28	1	695	C

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Mol	Chain	Res	Type
28	1	696	C
28	1	697	A
28	1	700	C
28	1	702	C
28	1	703	G
28	1	704	U
28	1	705	A
28	1	706	A
28	1	707	U
28	1	708	G
28	1	709	A
28	1	710	A
28	1	711	A
28	1	712	G
28	1	713	U
28	1	715	A
28	1	716	A
28	1	717	C
28	1	718	G
28	1	719	U
28	1	720	A
28	1	721	G
28	1	725	G
28	1	727	G
28	1	728	G
28	1	734	C
28	1	735	A
28	1	736	A
28	1	737	G
28	1	743	C
28	1	747	A
28	1	752	C
28	1	756	U
28	1	760	G
28	1	761	A
28	1	762	U
28	1	763	G
28	1	764	U
28	1	765	C
28	1	766	U
28	1	767	U
28	1	768	C

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Mol	Chain	Res	Type
28	1	769	G
28	1	771	A
28	1	772	U
28	1	773	G
28	1	774	G
28	1	775	A
28	1	776	U
28	1	779	G
28	1	780	A
28	1	781	G
28	1	782	U
28	1	784	A
28	1	785	G
28	1	786	A
28	1	787	G
28	1	789	A
28	1	790	U
28	1	792	G
28	1	794	U
28	1	795	G
28	1	797	U
28	1	798	G
28	1	801	A
28	1	802	C
28	1	803	C
28	1	806	A
28	1	807	A
28	1	808	A
28	1	809	G
28	1	810	A
28	1	811	U
28	1	812	G
28	1	813	G
28	1	814	U
28	1	815	G
28	1	816	A
28	1	817	A
28	1	818	C
28	1	820	A
28	1	821	U
28	1	825	U
28	1	826	G

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Mol	Chain	Res	Type
28	1	829	U
28	1	830	A
28	1	831	G
28	1	832	G
28	1	833	G
28	1	834	U
28	1	845	G
28	1	846	A
28	1	847	A
28	1	849	C
28	1	850	U
28	1	851	C
28	1	857	G
28	1	858	A
28	1	860	G
28	1	861	C
28	1	862	U
28	1	864	G
28	1	865	U
28	1	870	G
28	1	872	U
28	1	874	U
28	1	875	G
28	1	876	A
28	1	878	G
28	1	879	U
28	1	880	G
28	1	881	C
28	1	882	A
28	1	883	A
28	1	884	A
28	1	885	U
28	1	886	C
28	1	893	C
28	1	894	G
28	1	895	A
28	1	896	A
28	1	897	U
28	1	901	G
28	1	902	G
28	1	903	U
28	1	904	A

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Mol	Chain	Res	Type
28	1	905	U
28	1	906	A
28	1	907	G
28	1	908	G
28	1	909	G
28	1	913	A
28	1	914	A
28	1	915	A
28	1	916	G
28	1	917	A
28	1	920	A
28	1	921	A
28	1	922	U
28	1	924	G
28	1	933	A
28	1	934	G
28	1	935	U
28	1	936	A
28	1	937	G
28	1	938	C
28	1	939	U
28	1	940	G
28	1	941	G
28	1	942	U
28	1	943	U
28	1	944	C
28	1	946	U
28	1	947	G
28	1	948	C
28	1	949	C
28	1	951	A
28	1	953	G
28	1	954	U
28	1	958	C
28	1	959	C
28	1	962	A
28	1	963	G
28	1	965	A
28	1	966	U
28	1	967	A
28	1	970	A
28	1	971	G

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Mol	Chain	Res	Type
28	1	974	G
28	1	975	C
28	1	977	C
28	1	979	U
28	1	980	A
28	1	981	U
28	1	984	G
28	1	985	U
28	1	987	U
28	1	991	G
28	1	992	A
28	1	993	G
28	1	994	G
28	1	995	U
28	1	997	A
28	1	999	G
28	1	1000	C
28	1	1001	G
28	1	1002	A
28	1	1003	A
28	1	1006	A
28	1	1007	U
28	1	1008	U
28	1	1010	G
28	1	1014	U
28	1	1016	C
28	1	1018	G
28	1	1020	G
28	1	1023	C
28	1	1024	G
28	1	1025	A
28	1	1029	G
28	1	1031	C
28	1	1034	U
28	1	1035	G
28	1	1038	C
28	1	1043	C
28	1	1047	A
28	1	1049	C
28	1	1057	A
28	1	1058	U
28	1	1063	G

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Mol	Chain	Res	Type
28	1	1064	A
28	1	1066	G
28	1	1067	U
28	1	1069	C
28	1	1071	U
28	1	1072	G
28	1	1073	U
28	1	1075	A
28	1	1076	C
28	1	1081	U
28	1	1082	U
28	1	1085	A
28	1	1087	G
28	1	1089	G
28	1	1090	G
28	1	1093	A
28	1	1094	U
28	1	1096	U
28	1	1097	G
28	1	1098	A
28	1	1099	A
28	1	1100	U
28	1	1101	G
28	1	1104	G
28	1	1105	A
28	1	1110	U
28	1	1111	U
28	1	1112	A
28	1	1113	G
28	1	1114	U
28	1	1115	G
28	1	1117	G
28	1	1118	C
28	1	1119	C
28	1	1120	A
28	1	1124	U
28	1	1127	G
28	1	1128	U
28	1	1129	A
28	1	1131	G
28	1	1133	A
28	1	1134	G

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Mol	Chain	Res	Type
28	1	1138	U
28	1	1140	G
28	1	1141	C
28	1	1142	G
28	1	1143	A
28	1	1144	U
28	1	1145	G
28	1	1146	C
28	1	1147	G
28	1	1148	G
28	1	1150	A
28	1	1151	U
28	1	1152	G
28	1	1153	A
28	1	1154	A
28	1	1155	C
28	1	1156	C
28	1	1157	G
28	1	1161	G
28	1	1162	U
28	1	1163	A
28	1	1164	G
28	1	1165	A
28	1	1166	G
28	1	1167	U
28	1	1168	U
28	1	1170	A
28	1	1171	G
28	1	1173	U
28	1	1174	G
28	1	1175	C
28	1	1176	C
28	1	1177	G
28	1	1178	G
28	1	1180	A
28	1	1181	U
28	1	1182	A
28	1	1183	C
28	1	1184	A
28	1	1188	U
28	1	1189	C
28	1	1190	A

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Mol	Chain	Res	Type
28	1	1192	C
28	1	1196	C
28	1	1197	A
28	1	1199	C
28	1	1200	A
28	1	1203	A
28	1	1204	A
28	1	1205	A
28	1	1206	G
28	1	1207	G
28	1	1208	U
28	1	1211	U
28	1	1217	A
28	1	1219	C
28	1	1220	U
28	1	1221	A
28	1	1225	A
28	1	1226	G
28	1	1227	C
28	1	1228	C
28	1	1229	G
28	1	1231	A
28	1	1232	C
28	1	1233	G
28	1	1234	G
28	1	1236	G
28	1	1238	C
28	1	1240	A
28	1	1241	U
28	1	1242	G
28	1	1243	G
28	1	1244	A
28	1	1245	A
28	1	1247	U
28	1	1248	C
28	1	1249	G
28	1	1250	G
28	1	1253	U
28	1	1254	C
28	1	1257	C
28	1	1258	U
28	1	1259	A

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Mol	Chain	Res	Type
28	1	1260	A
28	1	1261	G
28	1	1262	G
28	1	1263	A
28	1	1264	G
28	1	1265	U
28	1	1266	G
28	1	1268	G
28	1	1269	U
28	1	1271	A
28	1	1272	C
28	1	1274	A
28	1	1277	C
28	1	1279	C
28	1	1280	C
28	1	1282	G
28	1	1283	C
28	1	1284	C
28	1	1295	G
28	1	1300	G
28	1	1301	A
28	1	1304	A
28	1	1305	U
28	1	1306	G
28	1	1307	G
28	1	1308	A
28	1	1309	U
28	1	1310	G
28	1	1311	G
28	1	1312	C
28	1	1313	G
28	1	1315	U
28	1	1316	C
28	1	1317	A
28	1	1318	A
28	1	1319	G
28	1	1323	G
28	1	1324	U
28	1	1325	U
28	1	1326	A
28	1	1327	C
28	1	1328	C

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Mol	Chain	Res	Type
28	1	1330	A
28	1	1331	U
28	1	1332	A
28	1	1334	U
28	1	1335	C
28	1	1336	U
28	1	1339	C
28	1	1341	U
28	1	1342	C
28	1	1343	A
28	1	1348	U
28	1	1349	G
28	1	1350	A
28	1	1351	U
28	1	1352	A
28	1	1353	U
28	1	1354	G
28	1	1355	A
28	1	1357	G
28	1	1364	C
28	1	1366	A
28	1	1367	G
28	1	1368	U
28	1	1369	A
28	1	1370	G
28	1	1371	G
28	1	1372	C
28	1	1373	A
28	1	1374	G
28	1	1375	G
28	1	1376	C
28	1	1377	G
28	1	1378	U
28	1	1379	G
28	1	1380	G
28	1	1381	A
28	1	1386	A
28	1	1387	G
28	1	1389	G
28	1	1390	A
28	1	1391	C
28	1	1392	G

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Mol	Chain	Res	Type
28	1	1393	A
28	1	1394	A
28	1	1395	G
28	1	1396	C
28	1	1399	A
28	1	1400	G
28	1	1401	A
28	1	1402	C
28	1	1405	U
28	1	1406	A
28	1	1407	A
28	1	1408	G
28	1	1409	G
28	1	1410	U
28	1	1411	C
28	1	1412	G
28	1	1413	G
28	1	1414	G
28	1	1416	C
28	1	1418	A
28	1	1419	A
28	1	1420	C
28	1	1423	C
28	1	1426	C
28	1	1427	U
28	1	1428	A
28	1	1429	G
28	1	1430	U
28	1	1431	G
28	1	1432	C
28	1	1433	A
28	1	1435	A
28	1	1436	U
28	1	1437	C
28	1	1440	G
28	1	1441	G
28	1	1442	U
28	1	1444	G
28	1	1445	U
28	1	1446	A
28	1	1447	G
28	1	1448	U

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Mol	Chain	Res	Type
28	1	1449	A
28	1	1450	G
28	1	1453	A
28	1	1454	A
28	1	1455	U
28	1	1456	A
28	1	1457	U
28	1	1458	U
28	1	1464	G
28	1	1465	A
28	1	1466	G
28	1	1467	A
28	1	1468	A
28	1	1469	C
28	1	1470	U
28	1	1476	G
28	1	1480	G
28	1	1481	A
28	1	1482	A
28	1	1483	G
28	1	1484	U
28	1	1485	G
28	1	1486	G
28	1	1494	U
28	1	1497	C
28	1	1498	A
28	1	1499	C
28	1	1500	G
28	1	1502	C
28	1	1504	A
28	1	1506	A
28	1	1507	G
28	1	1508	C
28	1	1509	A
28	1	1510	G
28	1	1511	U
28	1	1512	U
28	1	1514	G
28	1	1516	C
28	1	1517	G
28	1	1520	G
28	1	1521	G

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Mol	Chain	Res	Type
28	1	1522	U
28	1	1523	U
28	1	1524	A
28	1	1525	G
28	1	1526	U
28	1	1528	G
28	1	1529	A
28	1	1530	U
28	1	1531	C
28	1	1532	C
28	1	1533	U
28	1	1534	A
28	1	1535	A
28	1	1536	G
28	1	1541	G
28	1	1542	G
28	1	1543	G
28	1	1544	G
28	1	1546	A
28	1	1547	G
28	1	1548	C
28	1	1551	C
28	1	1553	U
28	1	1554	U
28	1	1556	C
28	1	1557	A
28	1	1558	A
28	1	1559	A
28	1	1560	G
28	1	1562	C
28	1	1563	C
28	1	1564	U
28	1	1565	G
28	1	1566	A
28	1	1569	U
28	1	1570	U
28	1	1571	A
28	1	1574	C
28	1	1575	A
28	1	1577	G
28	1	1578	C
28	1	1580	A

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Mol	Chain	Res	Type
28	1	1581	C
28	1	1582	C
28	1	1584	U
28	1	1585	C
28	1	1586	G
28	1	1587	A
28	1	1588	A
28	1	1589	A
28	1	1590	G
28	1	1591	G
28	1	1592	G
28	1	1593	A
28	1	1595	U
28	1	1596	C
28	1	1597	C
28	1	1598	G
28	1	1600	U
28	1	1601	U
28	1	1603	A
28	1	1604	G
28	1	1605	A
28	1	1607	U
28	1	1608	C
28	1	1609	C
28	1	1610	G
28	1	1611	G
28	1	1619	A
28	1	1620	U
28	1	1627	U
28	1	1628	C
28	1	1629	U
28	1	1631	C
28	1	1632	A
28	1	1635	G
28	1	1640	G
28	1	1641	U
28	1	1642	A
28	1	1643	A
28	1	1644	C
28	1	1645	U
28	1	1646	G
28	1	1651	U

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Mol	Chain	Res	Type
28	1	1655	G
28	1	1656	A
28	1	1657	C
28	1	1659	U
28	1	1660	C
28	1	1661	G
28	1	1663	C
28	1	1664	G
28	1	1665	C
28	1	1666	G
28	1	1667	A
28	1	1669	C
28	1	1670	C
28	1	1672	U
28	1	1675	G
28	1	1676	A
28	1	1679	A
28	1	1680	G
28	1	1681	U
28	1	1682	U
28	1	1683	A
28	1	1688	U
28	1	1689	U
28	1	1693	C
28	1	1694	U
28	1	1696	A
28	1	1698	C
28	1	1699	A
28	1	1702	U
28	1	1703	U
28	1	1709	C
28	1	1713	G
28	1	1714	A
28	1	1715	A
28	1	1716	U
28	1	1719	G
28	1	1720	U
28	1	1721	U
28	1	1722	U
28	1	1724	U
28	1	1725	C
28	1	1726	C

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Mol	Chain	Res	Type
28	1	1727	G
28	1	1728	G
28	1	1729	A
28	1	1730	G
28	1	1731	A
28	1	1733	G
28	1	1734	G
28	1	1737	U
28	1	1738	C
28	1	1740	U
28	1	1746	U
28	1	1748	G
28	1	1749	A
28	1	1750	A
28	1	1751	G
28	1	1752	A
28	1	1753	G
28	1	1754	G
28	1	1757	A
28	1	1760	A
28	1	1761	C
28	1	1762	C
28	1	1764	U
28	1	1765	U
28	1	1772	U
28	1	1773	C
28	1	1777	U
28	1	1778	G
28	1	1780	G
28	1	1781	C
28	1	1785	U
28	1	1786	G
28	1	1787	A
28	1	1788	C
28	1	1790	G
28	1	1793	C
28	1	1794	G
28	1	1795	U
28	1	1797	A
28	1	1798	A
28	1	1799	A
28	1	1801	U

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Mol	Chain	Res	Type
28	1	1807	G
28	1	1808	G
28	1	1809	A
28	1	1813	A
28	1	1814	A
28	1	1819	U
28	1	1821	U
28	1	1822	C
28	1	1830	G
28	1	1832	C
28	1	1833	G
28	1	1835	A
28	1	1836	C
28	1	1838	G
28	1	1839	A
28	1	1840	U
28	1	1842	A
28	1	1843	C
28	1	1844	C
28	1	1846	C
28	1	1848	G
28	1	1849	C
28	1	1850	A
28	1	1851	G
28	1	1852	G
28	1	1853	U
28	1	1856	C
28	1	1857	C
28	1	1858	A
28	1	1859	A
28	1	1863	G
28	1	1864	A
28	1	1866	C
28	1	1867	A
28	1	1869	C
28	1	1871	U
28	1	1872	C
28	1	1873	U
28	1	1874	A
28	1	1875	G
28	1	1876	U
28	1	1877	U

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Mol	Chain	Res	Type
28	1	1879	A
28	1	1880	U
28	1	1882	G
28	1	1883	A
28	1	1884	A
28	1	1886	A
28	1	1887	A
28	1	1888	U
28	1	1894	U
28	1	1897	G
28	1	1900	A
28	1	1901	A
28	1	1902	G
28	1	1903	U
28	1	1905	G
28	1	1906	G
28	1	1908	A
28	1	1909	A
28	1	1910	A
28	1	1911	A
28	1	1912	U
28	1	1913	A
28	1	1914	G
28	1	1915	A
28	1	1920	U
28	1	1922	A
28	1	1924	U
28	1	1927	G
28	1	1932	A
28	1	1938	U
28	1	1939	G
28	1	1940	G
28	1	1941	C
28	1	1942	U
28	1	1946	A
28	1	1947	G
28	1	1948	G
28	1	1950	U
28	1	1951	C
28	1	1952	G
28	1	1953	G
28	1	1954	G

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Mol	Chain	Res	Type
28	1	1955	U
28	1	2095	G
28	1	2098	C
28	1	2100	A
28	1	2101	C
28	1	2103	U
28	1	2104	A
28	1	2105	G
28	1	2110	G
28	1	2111	G
28	1	2112	U
28	1	2114	C
28	1	2115	G
28	1	2116	G
28	1	2117	A
28	1	2118	C
28	1	2119	A
28	1	2120	A
28	1	2121	G
28	1	2122	G
28	1	2126	A
28	1	2127	U
28	1	2129	U
28	1	2131	A
28	1	2132	C
28	1	2133	U
28	1	2134	G
28	1	2136	C
28	1	2137	U
28	1	2138	A
28	1	2139	A
28	1	2140	U
28	1	2141	U
28	1	2142	A
28	1	2143	A
28	1	2144	A
28	1	2145	A
28	1	2146	C
28	1	2147	A
28	1	2152	A
28	1	2154	U
28	1	2155	G

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Mol	Chain	Res	Type
28	1	2156	C
28	1	2157	G
28	1	2159	U
28	1	2160	G
28	1	2163	C
28	1	2165	G
28	1	2167	A
28	1	2170	U
28	1	2173	U
28	1	2174	G
28	1	2175	U
28	1	2176	U
28	1	2177	G
28	1	2178	A
28	1	2179	C
28	1	2188	A
28	1	2192	C
28	1	2194	G
28	1	2197	C
28	1	2198	A
28	1	2201	G
28	1	2202	C
28	1	2203	U
28	1	2204	C
28	1	2205	U
28	1	2206	G
28	1	2208	A
28	1	2209	U
28	1	2210	G
28	1	2213	A
28	1	2214	A
28	1	2215	A
28	1	2218	G
28	1	2220	A
28	1	2224	A
28	1	2225	U
28	1	2226	U
28	1	2229	A
28	1	2230	C
28	1	2231	C
28	1	2234	G
28	1	2242	A

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Mol	Chain	Res	Type
28	1	2243	A
28	1	2244	A
28	1	2246	G
28	1	2248	C
28	1	2249	G
28	1	2254	U
28	1	2255	A
28	1	2261	G
28	1	2262	A
28	1	2263	C
28	1	2269	U
28	1	2270	A
28	1	2271	A
28	1	2273	G
28	1	2274	U
28	1	2276	G
28	1	2278	C
28	1	2280	A
28	1	2282	U
28	1	2283	G
28	1	2288	G
28	1	2289	U
28	1	2290	C
28	1	2291	A
28	1	2292	U
28	1	2293	C
28	1	2294	U
28	1	2296	A
28	1	2297	U
28	1	2299	A
28	1	2302	G
28	1	2303	A
28	1	2304	C
28	1	2305	G
28	1	2306	C
28	1	2307	G
28	1	2311	G
28	1	2314	U
28	1	2315	G
28	1	2324	A
28	1	2325	G
28	1	2326	A

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Mol	Chain	Res	Type
28	1	2328	U
28	1	2336	U
28	1	2340	U
28	1	2342	U
28	1	2348	A
28	1	2349	U
28	1	2352	A
28	1	2354	C
28	1	2355	G
28	1	2356	A
28	1	2357	A
28	1	2358	A
28	1	2359	C
28	1	2360	C
28	1	2361	A
28	1	2362	C
28	1	2363	A
28	1	2364	G
28	1	2365	C
28	1	2370	G
28	1	2371	G
28	1	2372	A
28	1	2373	A
28	1	2374	C
28	1	2375	G
28	1	2378	C
28	1	2379	U
28	1	2383	C
28	1	2385	G
28	1	2386	A
28	1	2387	A
28	1	2389	C
28	1	2390	A
28	1	2391	G
28	1	2392	C
28	1	2394	G
28	1	2396	G
28	1	2397	A
28	1	2398	A
28	1	2399	A
28	1	2400	G
28	1	2401	A

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Mol	Chain	Res	Type
28	1	2402	A
28	1	2403	G
28	1	2404	A
28	1	2406	C
28	1	2409	G
28	1	2410	U
28	1	2415	C
28	1	2416	U
28	1	2417	U
28	1	2419	A
28	1	2420	C
28	1	2423	U
28	1	2425	G
28	1	2427	U
28	1	2429	G
28	1	2432	A
28	1	2433	U
28	1	2434	U
28	1	2435	G
28	1	2436	U
28	1	2440	G
28	1	2441	A
28	1	2442	G
28	1	2446	U
28	1	2447	A
28	1	2450	G
28	1	2452	G
28	1	2455	U
28	1	2458	A
28	1	2459	A
28	1	2460	U
28	1	2462	A
28	1	2463	G
28	1	2464	U
28	1	2468	A
28	1	2469	G
28	1	2470	C
28	1	2471	U
28	1	2473	C
28	1	2477	G
28	1	2479	C
28	1	2480	A

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Mol	Chain	Res	Type
28	1	2481	G
28	1	2482	U
28	1	2485	A
28	1	2487	U
28	1	2490	C
28	1	2491	A
28	1	2492	C
28	1	2493	U
28	1	2494	A
28	1	2496	C
28	1	2498	U
28	1	2499	U
28	1	2500	A
28	1	2501	U
28	1	2503	G
28	1	2504	U
28	1	2505	U
28	1	2506	U
28	1	2508	U
28	1	2509	U
28	1	2511	A
28	1	2513	U
28	1	2514	U
28	1	2515	A
28	1	2516	U
28	1	2517	U
28	1	2518	C
28	1	2521	U
28	1	2523	A
28	1	2525	G
28	1	2526	C
28	1	2530	G
28	1	2531	C
28	1	2532	U
28	1	2534	G
28	1	2536	A
28	1	2537	U
28	1	2539	C
28	1	2540	A
28	1	2542	U
28	1	2543	U
28	1	2544	U

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Mol	Chain	Res	Type
28	1	2545	C
28	1	2546	C
28	1	2547	A
28	1	2549	G
28	1	2550	U
28	1	2551	U
28	1	2553	U
28	1	2554	A
28	1	2555	G
28	1	2557	A
28	1	2558	U
28	1	2560	C
28	1	2562	A
28	1	2565	U
28	1	2569	A
28	1	2570	U
28	1	2571	U
28	1	2572	C
28	1	2580	A
28	1	2581	U
28	1	2582	C
28	1	2583	C
28	1	2585	G
28	1	2586	G
28	1	2587	U
28	1	2588	U
28	1	2589	G
28	1	2591	A
28	1	2592	G
28	1	2593	A
28	1	2594	C
28	1	2597	U
28	1	2598	G
28	1	2599	U
28	1	2600	C
28	1	2601	A
28	1	2603	G
28	1	2604	U
28	1	2605	G
28	1	2606	G
28	1	2607	G
28	1	2608	G

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Mol	Chain	Res	Type
28	1	2610	G
28	1	2611	U
28	1	2614	G
28	1	2615	G
28	1	2617	U
28	1	2618	G
28	1	2619	G
28	1	2620	G
28	1	2622	C
28	1	2627	C
28	1	2628	A
28	1	2629	U
28	1	2632	G
28	1	2634	U
28	1	2635	A
28	1	2636	A
28	1	2637	A
28	1	2642	A
28	1	2644	C
28	1	2645	G
28	1	2647	A
28	1	2648	G
28	1	2649	A
28	1	2650	U
28	1	2651	G
28	1	2652	U
28	1	2653	C
28	1	2655	U
28	1	2656	A
28	1	2658	G
28	1	2667	A
28	1	2668	U
28	1	2674	A
28	1	2675	C
28	1	2676	A
28	1	2677	G
28	1	2678	A
28	1	2679	A
28	1	2682	C
28	1	2686	A
28	1	2688	U
28	1	2689	A

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Mol	Chain	Res	Type
28	1	2690	G
28	1	2692	A
28	1	2694	A
28	1	2696	A
28	1	2697	A
28	1	2698	G
28	1	2699	G
28	1	2700	G
28	1	2702	A
28	1	2703	A
28	1	2704	A
28	1	2713	U
28	1	2715	A
28	1	2716	U
28	1	2717	U
28	1	2720	G
28	1	2722	U
28	1	2723	U
28	1	2726	C
28	1	2728	G
28	1	2729	U
28	1	2731	U
28	1	2735	U
28	1	2736	A
28	1	2737	C
28	1	2741	C
28	1	2742	C
28	1	2747	A
28	1	2748	A
28	1	2749	G
28	1	2750	U
28	1	2753	G
28	1	2755	C
28	1	2756	C
28	1	2757	U
28	1	2760	C
28	1	2762	A
28	1	2763	U
28	1	2764	C
28	1	2765	C
28	1	2766	U
28	1	2767	U

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Mol	Chain	Res	Type
28	1	2768	U
28	1	2772	C
28	1	2773	C
28	1	2774	C
28	1	2775	U
28	1	2776	C
28	1	2778	G
28	1	2779	A
28	1	2781	U
28	1	2783	U
28	1	2784	G
28	1	2785	A
28	1	2786	G
28	1	2787	G
28	1	2788	C
28	1	2794	G
28	1	2795	U
28	1	2796	G
28	1	2798	C
28	1	2799	A
28	1	2800	G
28	1	2801	A
28	1	2802	A
28	1	2803	A
28	1	2805	G
28	1	2806	U
28	1	2807	U
28	1	2808	A
28	1	2809	C
28	1	2810	C
28	1	2811	A
28	1	2813	A
28	1	2814	G
28	1	2815	G
28	1	2816	G
28	1	2817	A
28	1	2819	A
28	1	2820	A
28	1	2821	C
28	1	2823	G
28	1	2824	G
28	1	2826	U

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Mol	Chain	Res	Type
28	1	2827	U
28	1	2833	A
28	1	2835	U
28	1	2837	A
28	1	2838	A
28	1	2844	C
28	1	2845	A
28	1	2846	U
28	1	2847	A
28	1	2850	G
28	1	2855	U
28	1	2856	G
28	1	2860	U
28	1	2863	G
28	1	2865	U
28	1	2866	U
28	1	2867	C
28	1	2868	U
28	1	2869	U
28	1	2870	C
28	1	2871	G
28	1	2874	G
28	1	2875	U
28	1	2877	G
28	1	2878	G
28	1	2879	C
28	1	2880	U
28	1	2881	C
28	1	2882	U
28	1	2883	U
28	1	2887	A
28	1	2893	C
28	1	2894	C
28	1	2895	G
28	1	2896	A
28	1	2898	G
28	1	2899	C
28	1	2900	A
28	1	2901	G
28	1	2902	A
28	1	2903	A
28	1	2905	U

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Mol	Chain	Res	Type
28	1	2906	C
28	1	2908	G
28	1	2909	U
28	1	2910	A
28	1	2911	A
28	1	2913	C
28	1	2916	U
28	1	2919	A
28	1	2920	U
28	1	2923	U
28	1	2924	U
28	1	2926	A
28	1	2928	C
28	1	2929	C
28	1	2930	A
28	1	2931	C
28	1	2932	U
28	1	2933	A
28	1	2935	U
28	1	2936	A
28	1	2941	A
28	1	2942	C
28	1	2943	G
28	1	2944	U
28	1	2945	G
28	1	2946	A
28	1	2947	G
28	1	2950	G
28	1	2951	G
28	1	2952	G
28	1	2953	U
28	1	2959	C
28	1	2960	C
28	1	2964	G
28	1	2965	U
28	1	2966	G
28	1	2968	G
28	1	2971	A
28	1	2972	G
28	1	2973	G
28	1	2974	U
28	1	2975	U

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Mol	Chain	Res	Type
28	1	2976	A
28	1	2977	G
28	1	2978	U
28	1	2979	U
28	1	2982	A
28	1	2983	C
28	1	2984	C
28	1	2990	G
28	1	2993	G
28	1	2997	G
28	1	3005	A
28	1	3006	A
28	1	3007	U
28	1	3010	U
28	1	3011	A
28	1	3012	A
28	1	3018	C
28	1	3019	U
28	1	3021	A
28	1	3022	G
28	1	3023	U
28	1	3024	A
28	1	3025	C
28	1	3026	G
28	1	3027	A
28	1	3028	G
28	1	3029	A
28	1	3032	A
28	1	3034	C
28	1	3035	A
28	1	3036	G
28	1	3040	A
28	1	3043	C
28	1	3044	G
28	1	3045	G
28	1	3047	U
28	1	3049	A
28	1	3051	U
28	1	3052	G
28	1	3053	G
28	1	3055	U
28	1	3056	U

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Mol	Chain	Res	Type
28	1	3057	U
28	1	3058	U
28	1	3059	G
28	1	3062	G
28	1	3064	U
28	1	3065	G
28	1	3067	C
28	1	3070	A
28	1	3071	U
28	1	3073	A
28	1	3074	G
28	1	3075	G
28	1	3076	C
28	1	3077	A
28	1	3078	U
28	1	3080	G
28	1	3081	C
28	1	3087	A
28	1	3088	G
28	1	3090	U
28	1	3092	C
28	1	3093	C
28	1	3099	C
28	1	3100	U
28	1	3101	G
28	1	3102	G
28	1	3103	A
28	1	3105	U
28	1	3106	A
28	1	3107	U
28	1	3112	G
28	1	3114	A
28	1	3115	C
28	1	3118	C
28	1	3120	C
28	1	3122	A
28	1	3125	U
28	1	3126	C
28	1	3130	A
28	1	3131	U
28	1	3132	C
28	1	3133	C

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Mol	Chain	Res	Type
28	1	3137	C
28	1	3138	U
28	1	3139	A
28	1	3142	A
28	1	3143	C
28	1	3144	G
28	1	3151	U
28	1	3152	U
28	1	3153	U
28	1	3154	C
28	1	3155	U
28	1	3156	U
28	1	3157	U
28	1	3169	U
28	1	3170	A
28	1	3171	U
28	1	3172	A
28	1	3173	G
28	1	3174	A
28	1	3176	G
28	1	3179	U
28	1	3180	A
28	1	3181	C
28	1	3182	G
28	1	3185	U
28	1	3186	A
28	1	3187	A
28	1	3196	U
28	1	3198	U
28	1	3199	G
28	1	3206	C
28	1	3207	U
28	1	3209	A
28	1	3211	C
28	1	3212	C
28	1	3213	A
28	1	3216	G
28	1	3217	C
28	1	3218	A
28	1	3219	G
28	1	3220	G
28	1	3224	G

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Mol	Chain	Res	Type
28	1	3226	A
28	1	3228	C
28	1	3229	G
28	1	3230	G
28	1	3234	A
28	1	3235	C
28	1	3236	U
28	1	3237	U
28	1	3238	G
28	1	3242	G
28	1	3251	U
28	1	3252	G
28	1	3255	U
28	1	3256	G
28	1	3258	U
28	1	3259	U
28	1	3260	G
28	1	3261	C
28	1	3262	U
28	1	3265	C
28	1	3267	A
28	1	3270	U
28	1	3271	G
28	1	3273	A
28	1	3275	U
28	1	3277	U
28	1	3278	C
28	1	3279	A
28	1	3281	U
28	1	3289	G
28	1	3290	G
28	1	3292	A
28	1	3293	U
28	1	3294	A
28	1	3298	C
28	1	3299	A
28	1	3301	U
28	1	3303	G
28	1	3304	U
28	1	3305	A
28	1	3306	U
28	1	3307	A

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Mol	Chain	Res	Type
28	1	3308	C
28	1	3309	G
28	1	3310	A
28	1	3311	C
28	1	3312	U
28	1	3313	U
28	1	3316	A
28	1	3317	U
28	1	3318	G
28	1	3319	U
28	1	3320	A
28	1	3326	G
28	1	3331	U
28	1	3332	U
28	1	3333	G
28	1	3335	A
28	1	3336	A
28	1	3337	G
28	1	3339	A
28	1	3341	U
28	1	3342	A
28	1	3343	G
28	1	3345	G
28	1	3346	U
28	1	3348	G
28	1	3350	C
28	1	3351	U
28	1	3352	U
28	1	3353	G
28	1	3354	U
28	1	3355	U
28	1	3358	U
28	1	3359	A
28	1	3360	C
28	1	3361	G
28	1	3362	A
28	1	3368	U
28	1	3369	G
28	1	3370	A
28	1	3371	G
28	1	3372	A
28	1	3374	U

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Mol	Chain	Res	Type
28	1	3375	A
28	1	3376	A
28	1	3377	G
28	1	3379	C
28	1	3380	U
28	1	3381	U
28	1	3382	U
28	1	3385	U
28	1	3389	U
28	1	3390	G
28	1	3391	A
28	1	3393	U
28	1	3394	U
28	1	3396	U
29	3	6	C
29	3	7	G
29	3	10	C
29	3	11	A
29	3	12	U
29	3	15	C
29	3	20	A
29	3	22	A
29	3	23	A
29	3	24	A
29	3	25	G
29	3	26	C
29	3	28	C
29	3	29	C
29	3	31	U
29	3	33	C
29	3	36	C
29	3	37	G
29	3	42	A
29	3	44	C
29	3	45	A
29	3	47	C
29	3	48	U
29	3	49	G
29	3	52	G
29	3	53	U
29	3	54	U
29	3	62	U

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Mol	Chain	Res	Type
29	3	64	A
29	3	65	G
29	3	68	C
29	3	73	C
29	3	74	C
29	3	75	G
29	3	77	G
29	3	78	U
29	3	80	G
29	3	83	U
29	3	85	G
29	3	86	U
29	3	87	G
29	3	91	G
29	3	93	C
29	3	97	A
29	3	98	C
29	3	104	A
29	3	105	C
29	3	112	G
29	3	121	U
30	4	3	A
30	4	4	C
30	4	6	U
30	4	8	C
30	4	9	A
30	4	10	A
30	4	14	C
30	4	15	G
30	4	18	U
30	4	19	C
30	4	20	U
30	4	21	C
30	4	22	U
30	4	23	U
30	4	24	G
30	4	25	G
30	4	26	U
30	4	28	C
30	4	31	G
30	4	33	A
30	4	34	U

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Mol	Chain	Res	Type
30	4	35	C
30	4	37	A
30	4	38	U
30	4	39	G
30	4	40	A
30	4	41	A
30	4	42	G
30	4	43	A
30	4	44	A
30	4	45	C
30	4	46	G
30	4	51	G
30	4	52	A
30	4	53	A
30	4	54	A
30	4	56	G
30	4	58	G
30	4	59	A
30	4	61	A
30	4	62	C
30	4	63	G
30	4	70	G
30	4	74	U
30	4	75	G
30	4	79	A
30	4	80	A
30	4	81	U
30	4	84	C
30	4	85	G
30	4	86	U
30	4	87	G
30	4	88	A
30	4	91	C
30	4	93	U
30	4	94	C
30	4	96	A
30	4	99	C
30	4	104	A
30	4	105	A
30	4	106	C
30	4	107	G
30	4	108	C

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Mol	Chain	Res	Type
30	4	109	A
30	4	110	C
30	4	111	A
30	4	112	U
30	4	113	U
30	4	114	G
30	4	125	U
30	4	126	A
30	4	128	U
30	4	133	G
30	4	134	G
30	4	137	C
30	4	138	A
30	4	139	U
30	4	140	G
30	4	147	U
30	4	151	C
30	4	152	G
30	4	153	U
30	4	155	A
30	4	156	U
30	4	157	U
30	4	158	U
49	2	2	A
49	2	4	C
49	2	5	U
49	2	17	C
49	2	25	C
49	2	26	A
49	2	27	U
49	2	34	G
49	2	37	U
49	2	42	G
49	2	43	A
49	2	45	U
49	2	47	A
49	2	57	G
49	2	58	U
49	2	59	C
49	2	61	A
49	2	62	A
49	2	63	G

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Mol	Chain	Res	Type
49	2	64	U
49	2	65	A
49	2	66	U
49	2	67	A
49	2	69	G
49	2	70	C
49	2	71	A
49	2	73	U
49	2	75	U
49	2	76	A
49	2	77	U
49	2	78	A
49	2	79	C
49	2	80	A
49	2	81	G
49	2	83	G
49	2	84	A
49	2	85	A
49	2	88	U
49	2	89	G
49	2	90	C
49	2	91	G
49	2	92	A
49	2	93	A
49	2	94	U
49	2	100	A
49	2	104	A
49	2	114	C
49	2	115	G
49	2	116	U
49	2	119	A
49	2	120	U
49	2	121	U
49	2	124	A
49	2	126	A
49	2	127	G
49	2	128	U
49	2	130	C
49	2	131	C
49	2	132	U
49	2	135	A
49	2	136	C

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Mol	Chain	Res	Type
49	2	137	U
49	2	138	A
49	2	139	C
49	2	141	U
49	2	145	A
49	2	146	U
49	2	149	C
49	2	150	U
49	2	151	G
49	2	157	A
49	2	160	C
49	2	164	A
49	2	165	G
49	2	177	U
49	2	178	U
49	2	181	A
49	2	186	C
49	2	188	A
49	2	189	C
49	2	190	C
49	2	191	C
49	2	192	U
49	2	193	U
49	2	194	U
49	2	195	G
49	2	196	G
49	2	200	A
49	2	204	G
49	2	205	U
49	2	206	A
49	2	208	U
49	2	210	A
49	2	212	U
49	2	215	A
49	2	216	U
49	2	217	A
49	2	219	A
49	2	221	A
49	2	222	A
49	2	223	U
49	2	224	C
49	2	227	U

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Mol	Chain	Res	Type
49	2	228	G
49	2	230	C
49	2	231	U
49	2	232	U
49	2	233	C
49	2	234	G
49	2	235	G
49	2	237	C
49	2	238	U
49	2	239	C
49	2	240	U
49	2	241	U
49	2	242	U
49	2	245	U
49	2	249	U
49	2	250	C
49	2	252	U
49	2	255	U
49	2	256	A
49	2	259	U
49	2	260	U
49	2	261	U
49	2	262	U
49	2	266	A
49	2	269	G
49	2	270	C
49	2	271	A
49	2	272	U
49	2	276	C
49	2	278	U
49	2	280	U
49	2	282	C
49	2	284	G
49	2	288	A
49	2	298	C
49	2	299	A
49	2	313	U
49	2	316	A
49	2	321	C
49	2	322	G
49	2	323	A
49	2	333	A

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Mol	Chain	Res	Type
49	2	337	G
49	2	338	C
49	2	341	A
49	2	345	U
49	2	346	G
49	2	351	C
49	2	352	A
49	2	359	A
49	2	361	C
49	2	376	C
49	2	378	A
49	2	381	C
49	2	389	G
49	2	390	G
49	2	392	G
49	2	393	C
49	2	396	G
49	2	397	A
49	2	398	G
49	2	399	A
49	2	400	A
49	2	402	C
49	2	404	G
49	2	405	C
49	2	406	U
49	2	407	A
49	2	408	C
49	2	409	C
49	2	415	C
49	2	416	A
49	2	417	A
49	2	418	G
49	2	419	G
49	2	421	A
49	2	422	G
49	2	426	G
49	2	434	G
49	2	435	C
49	2	436	A
49	2	437	A
49	2	439	U
49	2	440	U

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Mol	Chain	Res	Type
49	2	444	C
49	2	451	A
49	2	452	A
49	2	453	U
49	2	454	U
49	2	455	C
49	2	456	A
49	2	458	G
49	2	461	G
49	2	467	G
49	2	468	A
49	2	469	C
49	2	475	A
49	2	483	A
49	2	492	A
49	2	493	U
49	2	494	U
49	2	496	G
49	2	497	G
49	2	502	U
49	2	506	A
49	2	507	U
49	2	509	G
49	2	511	A
49	2	512	A
49	2	513	U
49	2	515	A
49	2	520	A
49	2	523	G
49	2	525	A
49	2	526	A
49	2	527	A
49	2	536	C
49	2	539	G
49	2	540	G
49	2	541	A
49	2	542	A
49	2	545	A
49	2	551	G
49	2	554	C
49	2	555	A
49	2	557	G

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Mol	Chain	Res	Type
49	2	558	U
49	2	565	C
49	2	568	G
49	2	579	A
49	2	580	A
49	2	582	U
49	2	583	C
49	2	585	A
49	2	586	G
49	2	594	A
49	2	600	U
49	2	606	A
49	2	608	U
49	2	613	G
49	2	614	C
49	2	619	A
49	2	620	A
49	2	621	A
49	2	622	A
49	2	623	A
49	2	624	G
49	2	639	U
49	2	641	G
49	2	651	G
49	2	654	C
49	2	655	G
49	2	656	G
49	2	657	U
49	2	658	C
49	2	677	G
49	2	678	A
49	2	679	U
49	2	680	U
49	2	682	C
49	2	684	A
49	2	686	C
49	2	695	U
49	2	696	C
49	2	698	U
49	2	699	U
49	2	702	G
49	2	705	U

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Mol	Chain	Res	Type
49	2	706	A
49	2	707	A
49	2	708	C
49	2	709	C
49	2	711	U
49	2	713	A
49	2	716	C
49	2	717	C
49	2	718	U
49	2	719	U
49	2	721	U
49	2	722	G
49	2	728	U
49	2	729	G
49	2	730	G
49	2	731	C
49	2	732	G
49	2	733	A
49	2	734	A
49	2	735	C
49	2	738	G
49	2	740	A
49	2	741	C
49	2	742	U
49	2	743	U
49	2	744	U
49	2	752	A
49	2	753	A
49	2	755	A
49	2	757	A
49	2	758	U
49	2	759	U
49	2	765	G
49	2	766	U
49	2	771	A
49	2	773	C
49	2	774	A
49	2	778	G
49	2	779	U
49	2	780	A
49	2	783	G
49	2	784	C

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Mol	Chain	Res	Type
49	2	789	A
49	2	794	U
49	2	799	A
49	2	802	G
49	2	803	A
49	2	804	A
49	2	806	A
49	2	807	A
49	2	810	G
49	2	811	A
49	2	812	A
49	2	813	U
49	2	814	A
49	2	815	G
49	2	820	U
49	2	821	U
49	2	829	A
49	2	831	U
49	2	832	U
49	2	833	U
49	2	834	G
49	2	836	U
49	2	840	U
49	2	841	U
49	2	843	U
49	2	845	G
49	2	847	A
49	2	848	C
49	2	850	A
49	2	851	U
49	2	852	C
49	2	853	G
49	2	855	A
49	2	857	U
49	2	862	A
49	2	863	A
49	2	864	U
49	2	865	A
49	2	884	A
49	2	894	U
49	2	895	G
49	2	897	C

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Mol	Chain	Res	Type
49	2	898	A
49	2	903	U
49	2	912	U
49	2	914	G
49	2	917	U
49	2	919	A
49	2	921	U
49	2	925	G
49	2	926	A
49	2	929	A
49	2	931	C
49	2	932	U
49	2	933	A
49	2	935	U
49	2	944	A
49	2	951	A
49	2	960	U
49	2	966	A
49	2	970	A
49	2	973	A
49	2	976	G
49	2	988	A
49	2	992	A
49	2	993	A
49	2	1001	A
49	2	1004	U
49	2	1005	A
49	2	1016	C
49	2	1021	C
49	2	1025	A
49	2	1026	A
49	2	1028	C
49	2	1029	U
49	2	1031	U
49	2	1032	G
49	2	1039	A
49	2	1052	U
49	2	1053	G
49	2	1055	U
49	2	1056	U
49	2	1064	G
49	2	1076	A

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Mol	Chain	Res	Type
49	2	1081	A
49	2	1091	A
49	2	1092	A
49	2	1097	U
49	2	1098	U
49	2	1099	U
49	2	1100	G
49	2	1101	G
49	2	1113	A
49	2	1118	G
49	2	1124	A
49	2	1126	G
49	2	1131	A
49	2	1132	A
49	2	1135	U
49	2	1137	A
49	2	1138	A
49	2	1139	A
49	2	1150	G
49	2	1158	C
49	2	1159	C
49	2	1162	C
49	2	1163	A
49	2	1164	G
49	2	1165	G
49	2	1166	A
49	2	1167	G
49	2	1174	C
49	2	1182	U
49	2	1183	A
49	2	1184	A
49	2	1185	U
49	2	1190	C
49	2	1191	U
49	2	1192	C
49	2	1193	A
49	2	1194	A
49	2	1199	G
49	2	1200	G
49	2	1202	A
49	2	1203	A
49	2	1205	C

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Mol	Chain	Res	Type
49	2	1206	U
49	2	1207	C
49	2	1212	G
49	2	1213	G
49	2	1214	U
49	2	1215	C
49	2	1217	A
49	2	1219	A
49	2	1221	A
49	2	1222	C
49	2	1259	U
49	2	1262	U
49	2	1268	G
49	2	1269	U
49	2	1274	C
49	2	1275	A
49	2	1276	U
49	2	1278	G
49	2	1284	C
49	2	1285	U
49	2	1288	G
49	2	1298	U
49	2	1299	G
49	2	1301	U
49	2	1307	U
49	2	1308	G
49	2	1309	C
49	2	1313	A
49	2	1314	U
49	2	1315	U
49	2	1321	A
49	2	1336	A
49	2	1338	C
49	2	1339	C
49	2	1340	U
49	2	1341	A
49	2	1342	C
49	2	1343	U
49	2	1344	A
49	2	1345	A
49	2	1346	A
49	2	1347	U

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Mol	Chain	Res	Type
49	2	1348	A
49	2	1349	G
49	2	1351	G
49	2	1352	G
49	2	1353	U
49	2	1356	U
49	2	1357	A
49	2	1358	G
49	2	1359	C
49	2	1360	A
49	2	1361	U
49	2	1362	U
49	2	1363	U
49	2	1366	U
49	2	1367	G
49	2	1371	A
49	2	1372	U
49	2	1374	C
49	2	1376	C
49	2	1377	U
49	2	1378	U
49	2	1380	U
49	2	1382	A
49	2	1383	G
49	2	1384	A
49	2	1387	G
49	2	1388	A
49	2	1389	C
49	2	1390	U
49	2	1391	A
49	2	1392	U
49	2	1397	U
49	2	1398	U
49	2	1399	C
49	2	1400	A
49	2	1401	A
49	2	1404	C
49	2	1407	U
49	2	1410	A
49	2	1412	G
49	2	1413	U
49	2	1414	U

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Mol	Chain	Res	Type
49	2	1415	U
49	2	1427	A
49	2	1428	G
49	2	1432	U
49	2	1433	G
49	2	1434	U
49	2	1441	C
49	2	1445	G
49	2	1446	A
49	2	1447	C
49	2	1457	C
49	2	1458	G
49	2	1460	A
49	2	1467	C
49	2	1471	A
49	2	1472	C
49	2	1473	U
49	2	1474	G
49	2	1479	A
49	2	1481	C
49	2	1482	C
49	2	1485	C
49	2	1489	U
49	2	1490	C
49	2	1492	A
49	2	1493	A
49	2	1494	C
49	2	1496	U
49	2	1498	G
49	2	1501	C
49	2	1503	A
49	2	1504	G
49	2	1507	G
49	2	1509	C
49	2	1511	U
49	2	1512	G
49	2	1514	U
49	2	1515	A
49	2	1516	A
49	2	1518	C
49	2	1520	U
49	2	1521	G

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Mol	Chain	Res	Type
49	2	1522	U
49	2	1523	G
49	2	1524	A
49	2	1527	C
49	2	1530	C
49	2	1531	G
49	2	1533	C
49	2	1534	G
49	2	1535	U
49	2	1536	G
49	2	1537	C
49	2	1538	U
49	2	1539	G
49	2	1540	G
49	2	1541	G
49	2	1542	G
49	2	1550	A
49	2	1557	U
49	2	1559	A
49	2	1561	U
49	2	1569	A
49	2	1575	G
49	2	1582	U
49	2	1583	A
49	2	1584	G
49	2	1587	A
49	2	1590	G
49	2	1596	C
49	2	1600	A
49	2	1611	A
49	2	1612	U
49	2	1613	U
49	2	1615	C
49	2	1616	G
49	2	1618	C
49	2	1619	C
49	2	1620	C
49	2	1622	G
49	2	1631	A
49	2	1634	C
49	2	1635	A
49	2	1636	C

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Mol	Chain	Res	Type
49	2	1637	C
49	2	1638	G
49	2	1651	A
49	2	1656	U
49	2	1657	U
49	2	1658	G
49	2	1664	C
49	2	1670	G
49	2	1672	G
49	2	1673	G
49	2	1677	C
49	2	1678	A
49	2	1679	G
49	2	1680	G
49	2	1682	U
49	2	1683	C
49	2	1685	G
49	2	1689	A
49	2	1693	A
49	2	1694	A
49	2	1695	G
49	2	1697	G
49	2	1698	G
49	2	1699	G
49	2	1700	C
49	2	1703	C
49	2	1704	U
49	2	1705	C
49	2	1706	C
49	2	1707	A
49	2	1708	U
49	2	1710	U
49	2	1711	C
49	2	1712	A
49	2	1713	G
49	2	1714	A
49	2	1715	G
49	2	1716	C
49	2	1717	G
49	2	1719	A
49	2	1720	G
49	2	1721	A

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Mol	Chain	Res	Type
49	2	1722	A
49	2	1723	U
49	2	1725	U
49	2	1730	A
49	2	1731	A
49	2	1745	G
49	2	1746	A
49	2	1747	G
49	2	1755	A
49	2	1757	G
49	2	1758	U
49	2	1759	C
49	2	1763	A
49	2	1766	A
49	2	1768	G
49	2	1769	U
49	2	1770	U
49	2	1779	U
49	2	1780	G
49	2	1782	A
49	2	1783	C
49	2	1792	G
49	2	1794	A
49	2	1795	U
49	2	1796	C
49	2	1797	A
79	AX	2	C
79	AX	3	G
79	AX	4	G
79	AX	5	A
79	AX	7	U
79	AX	8	U
79	AX	9	A
79	AX	11	C
79	AX	12	U
79	AX	13	C
79	AX	16	U
79	AX	17	U
79	AX	18	G
79	AX	19	G
79	AX	20	G
79	AX	21	A

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Mol	Chain	Res	Type
79	AX	25	C
79	AX	28	C
79	AX	29	A
79	AX	30	G
79	AX	32	C
79	AX	33	U
79	AX	34	G
79	AX	35	A
79	AX	36	A
79	AX	38	A
79	AX	39	U
79	AX	41	U
79	AX	42	G
79	AX	43	G
79	AX	44	A
79	AX	45	G
79	AX	46	G
79	AX	47	U
79	AX	48	C
79	AX	51	G
79	AX	54	U
79	AX	55	U
79	AX	56	C
79	AX	57	G
79	AX	59	U
79	AX	60	C
79	AX	61	C
79	AX	62	A
79	AX	64	A
79	AX	66	A
79	AX	68	U
79	AX	69	U
79	AX	70	C
79	AX	71	G
79	AX	74	C
80	AY	44	A
80	AY	45	A
80	AY	46	U
80	AY	48	U
80	AY	49	U
80	AY	50	U
79	AZ	2	C

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Mol	Chain	Res	Type
79	AZ	4	G
79	AZ	5	A
79	AZ	7	U
79	AZ	8	U
79	AZ	9	A
79	AZ	12	U
79	AZ	13	C
79	AZ	16	U
79	AZ	17	U
79	AZ	18	G
79	AZ	19	G
79	AZ	20	G
79	AZ	21	A
79	AZ	25	C
79	AZ	27	C
79	AZ	28	C
79	AZ	32	C
79	AZ	34	G
79	AZ	35	A
79	AZ	36	A
79	AZ	38	A
79	AZ	39	U
79	AZ	41	U
79	AZ	44	A
79	AZ	45	G
79	AZ	46	G
79	AZ	47	U
79	AZ	48	C
79	AZ	54	U
79	AZ	55	U
79	AZ	56	C
79	AZ	59	U
79	AZ	62	A
79	AZ	68	U
79	AZ	69	U
79	AZ	70	C
79	AZ	71	G
79	AZ	73	A
79	AZ	74	C

All (196) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
28	1	19	U
28	1	46	U
28	1	50	U
28	1	53	G
28	1	55	G
28	1	59	G
28	1	141	C
28	1	149	U
28	1	187	A
28	1	198	A
28	1	201	A
28	1	202	G
28	1	207	U
28	1	251	G
28	1	265	A
28	1	267	G
28	1	283	G
28	1	289	A
28	1	307	A
28	1	318	A
28	1	322	U
28	1	323	A
28	1	336	A
28	1	345	G
28	1	391	A
28	1	418	A
28	1	431	U
28	1	443	G
28	1	500	C
28	1	509	U
28	1	547	G
28	1	578	A
28	1	595	G
28	1	630	A
28	1	646	A
28	1	693	A
28	1	696	C
28	1	707	U
28	1	778	U
28	1	831	G
28	1	846	A
28	1	856	G
28	1	885	U

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Mol	Chain	Res	Type
28	1	900	G
28	1	902	G
28	1	932	U
28	1	935	U
28	1	940	G
28	1	964	G
28	1	998	A
28	1	999	G
28	1	1002	A
28	1	1042	U
28	1	1066	G
28	1	1084	A
28	1	1110	U
28	1	1112	A
28	1	1113	G
28	1	1128	U
28	1	1147	G
28	1	1165	A
28	1	1166	G
28	1	1300	G
28	1	1325	U
28	1	1375	G
28	1	1389	G
28	1	1390	A
28	1	1410	U
28	1	1435	A
28	1	1448	U
28	1	1501	U
28	1	1525	G
28	1	1529	A
28	1	1535	A
28	1	1565	G
28	1	1574	C
28	1	1597	C
28	1	1639	C
28	1	1640	G
28	1	1650	G
28	1	1664	G
28	1	1665	C
28	1	1668	G
28	1	1678	G
28	1	1829	G

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Mol	Chain	Res	Type
28	1	1837	U
28	1	1852	G
28	1	1855	U
28	1	1868	G
28	1	1875	G
28	1	1902	G
28	1	1926	C
28	1	1949	G
28	1	2103	U
28	1	2140	U
28	1	2155	G
28	1	2177	G
28	1	2223	A
28	1	2247	G
28	1	2260	U
28	1	2270	A
28	1	2290	C
28	1	2303	A
28	1	2325	G
28	1	2353	G
28	1	2360	C
28	1	2361	A
28	1	2378	C
28	1	2391	G
28	1	2467	G
28	1	2469	G
28	1	2480	A
28	1	2491	A
28	1	2498	U
28	1	2517	U
28	1	2520	A
28	1	2541	U
28	1	2545	C
28	1	2609	A
28	1	2633	U
28	1	2635	A
28	1	2655	U
28	1	2685	C
28	1	2696	A
28	1	2699	G
28	1	2734	A
28	1	2749	G

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Mol	Chain	Res	Type
28	1	2765	C
28	1	2777	G
28	1	2801	A
28	1	2816	G
28	1	2823	G
28	1	2832	C
28	1	2836	C
28	1	2837	A
28	1	2844	C
28	1	2854	U
28	1	2855	U
28	1	2894	C
28	1	2904	U
28	1	2928	C
28	1	2930	A
28	1	2959	C
28	1	2981	U
28	1	3006	A
28	1	3021	A
28	1	3046	A
28	1	3050	U
28	1	3052	G
28	1	3101	G
28	1	3113	A
28	1	3136	G
28	1	3138	U
28	1	3143	C
28	1	3210	A
28	1	3229	G
28	1	3305	A
28	1	3315	G
29	3	25	G
29	3	47	C
29	3	61	G
29	3	67	G
29	3	84	A
30	4	3	A
30	4	14	C
30	4	20	U
30	4	43	A
30	4	44	A
30	4	53	A

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Mol	Chain	Res	Type
30	4	69	U
30	4	86	U
30	4	133	G
49	2	88	U
49	2	240	U
49	2	706	A
49	2	757	A
49	2	1123	C
49	2	1138	A
49	2	1164	G
49	2	1181	U
49	2	1190	C
49	2	1205	C
49	2	1298	U
49	2	1358	G
49	2	1379	C
49	2	1497	U
49	2	1513	G
49	2	1541	G
49	2	1684	U
49	2	1715	G
49	2	1746	A
49	2	1758	U
79	AX	1	G
79	AX	42	G
79	AX	67	A
79	AZ	67	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

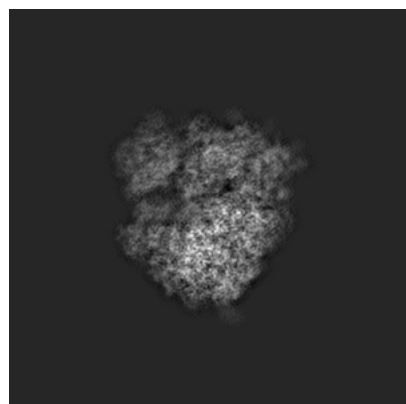
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22196. These allow visual inspection of the internal detail of the map and identification of artifacts.

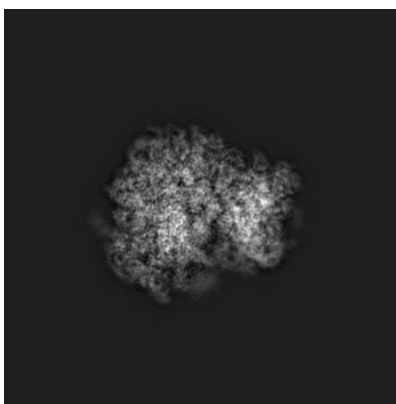
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

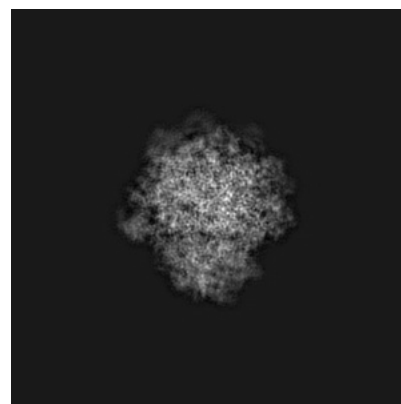
6.1.1 Primary map



X

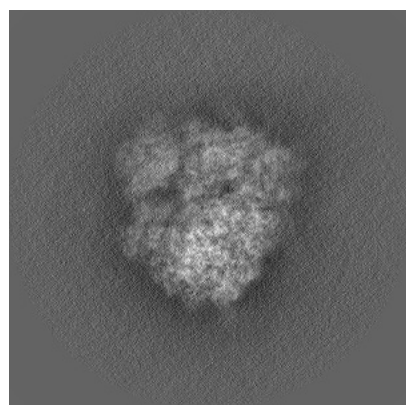


Y

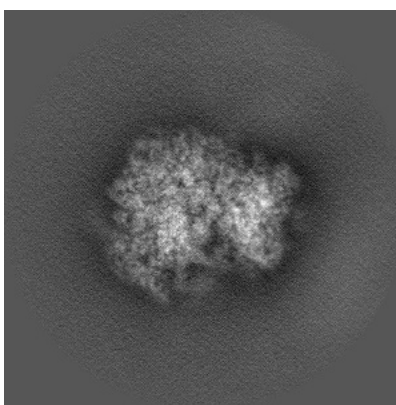


Z

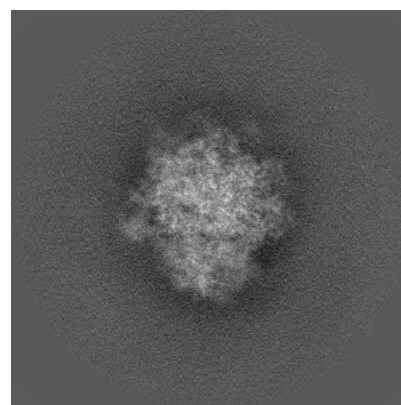
6.1.2 Raw map



X



Y

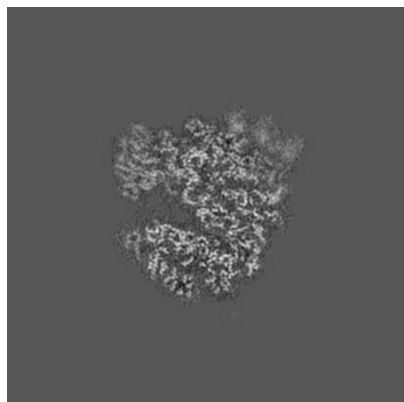


Z

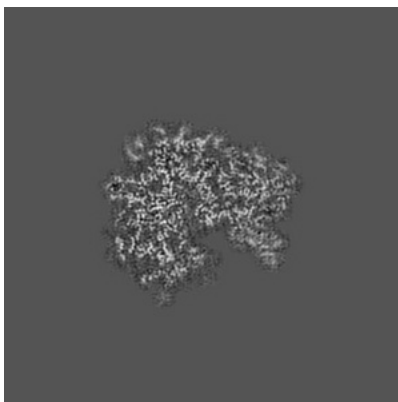
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

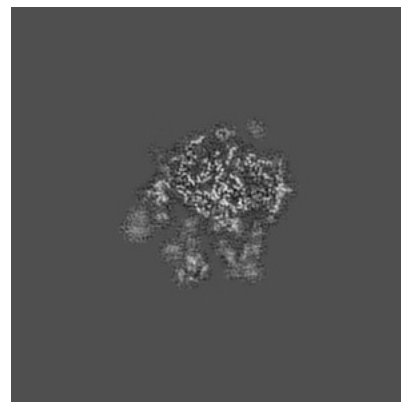
6.2.1 Primary map



X Index: 256

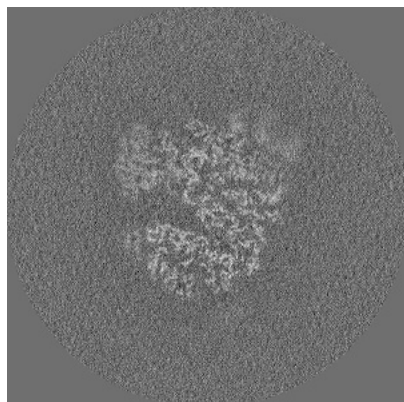


Y Index: 256

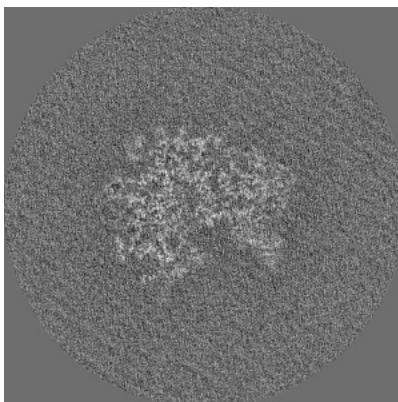


Z Index: 256

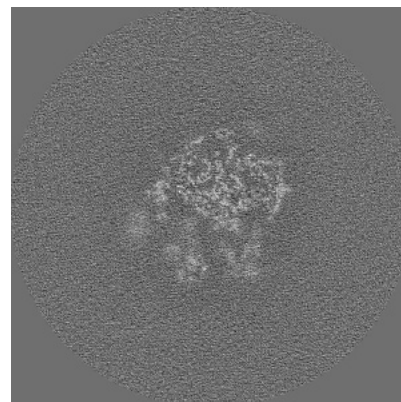
6.2.2 Raw map



X Index: 256



Y Index: 256

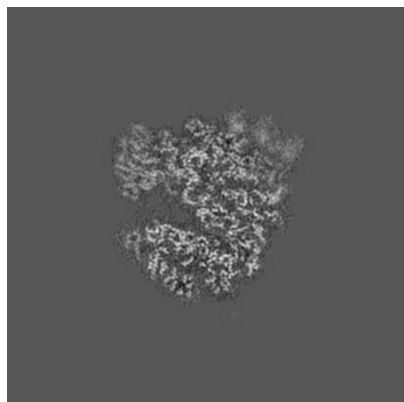


Z Index: 256

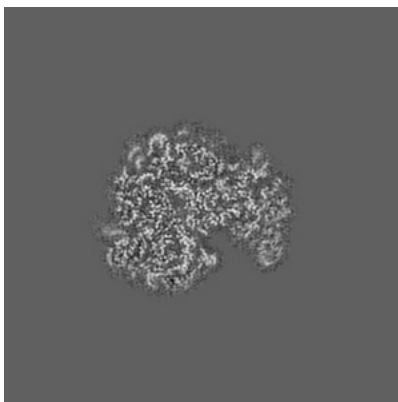
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

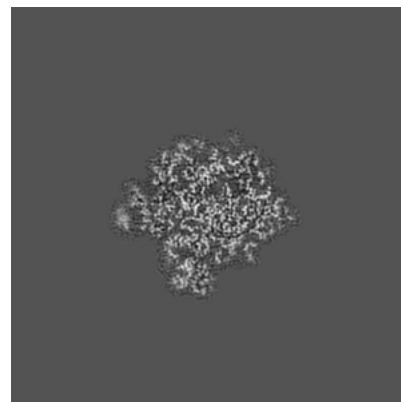
6.3.1 Primary map



X Index: 256

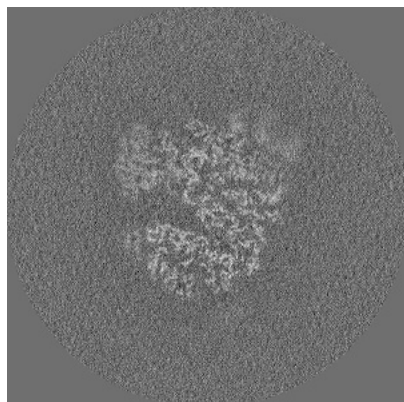


Y Index: 266

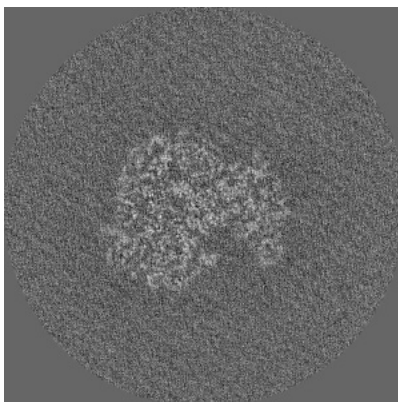


Z Index: 206

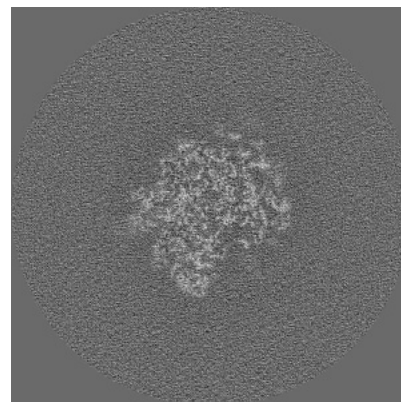
6.3.2 Raw map



X Index: 256



Y Index: 267

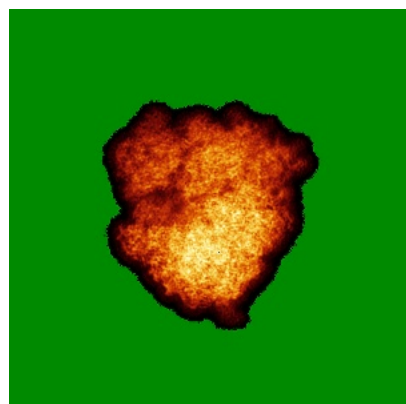


Z Index: 227

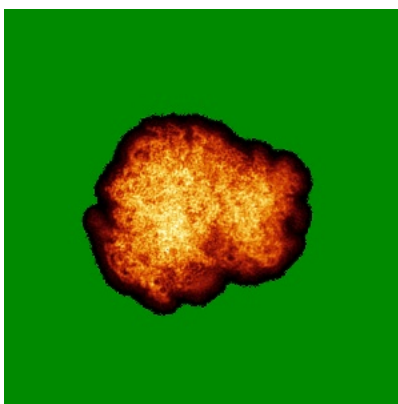
The images above show the largest variance slices of the map in three orthogonal directions.

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

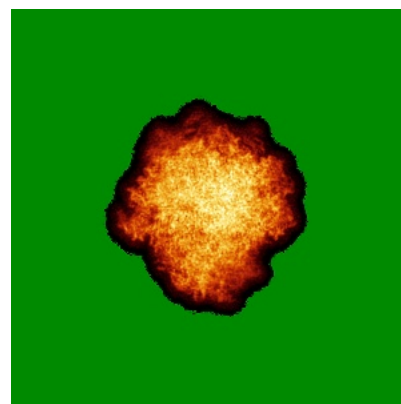
6.4.1 Primary map



X

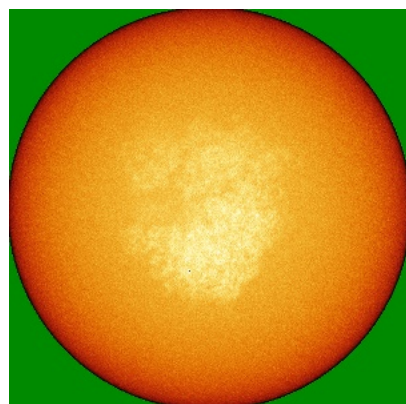


Y

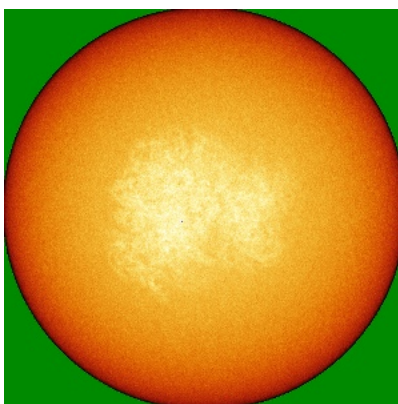


Z

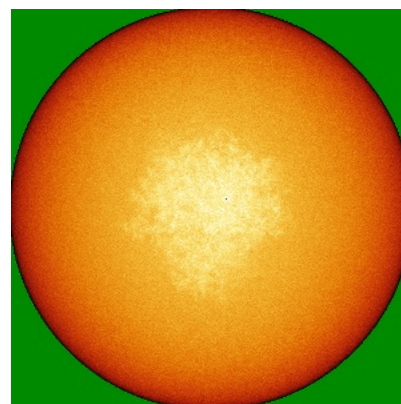
6.4.2 Raw map



X



Y

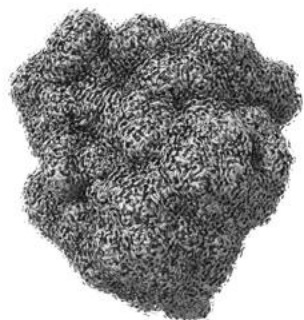


Z

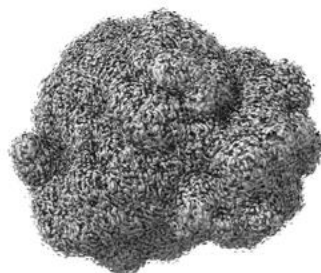
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



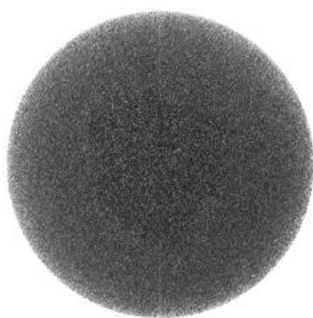
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

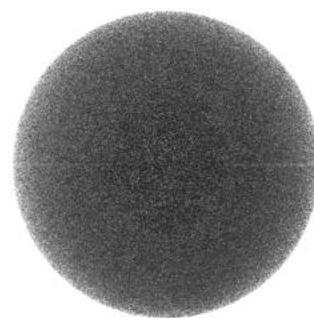
6.5.2 Raw map



X



Y



Z

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

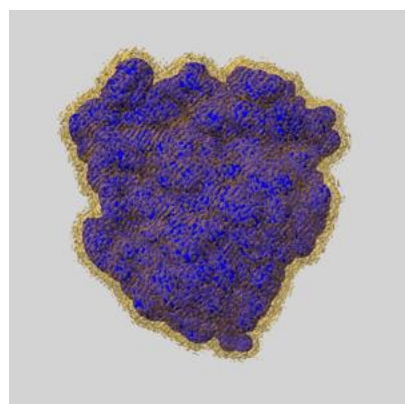
6.6 Mask visualisation [i](#)

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

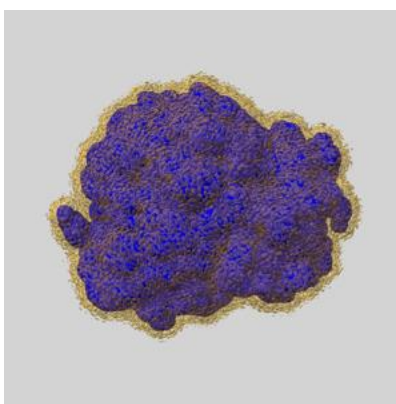
A mask typically either:

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

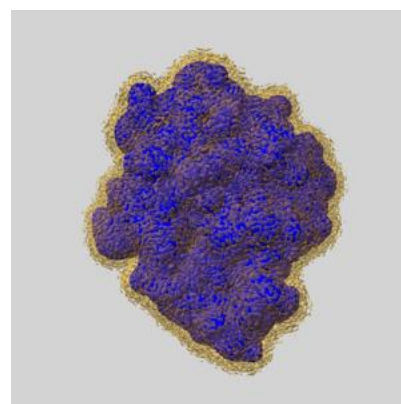
6.6.1 emd_22196_msk_1.map [i](#)



X



Y

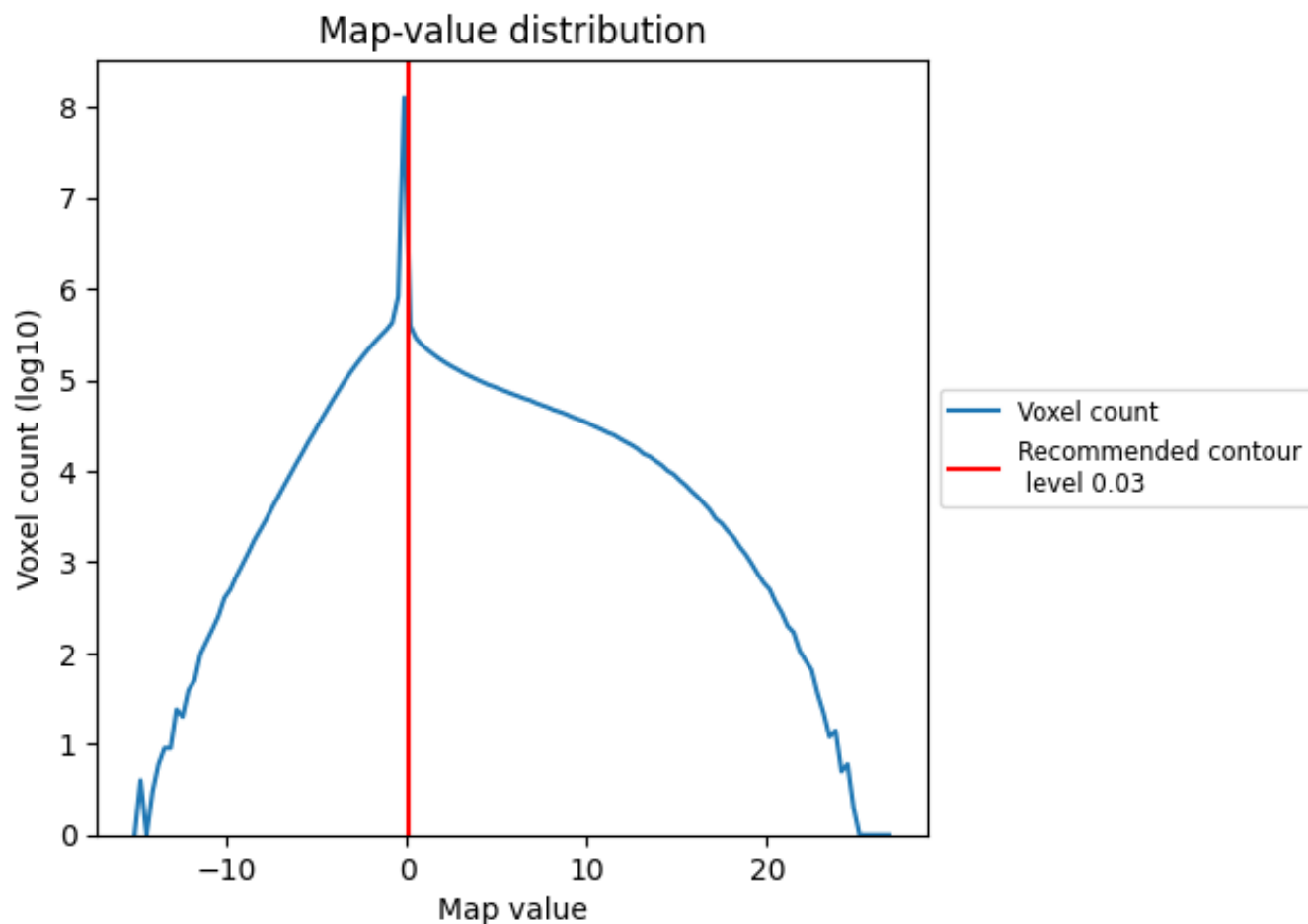


Z

7 Map analysis [i](#)

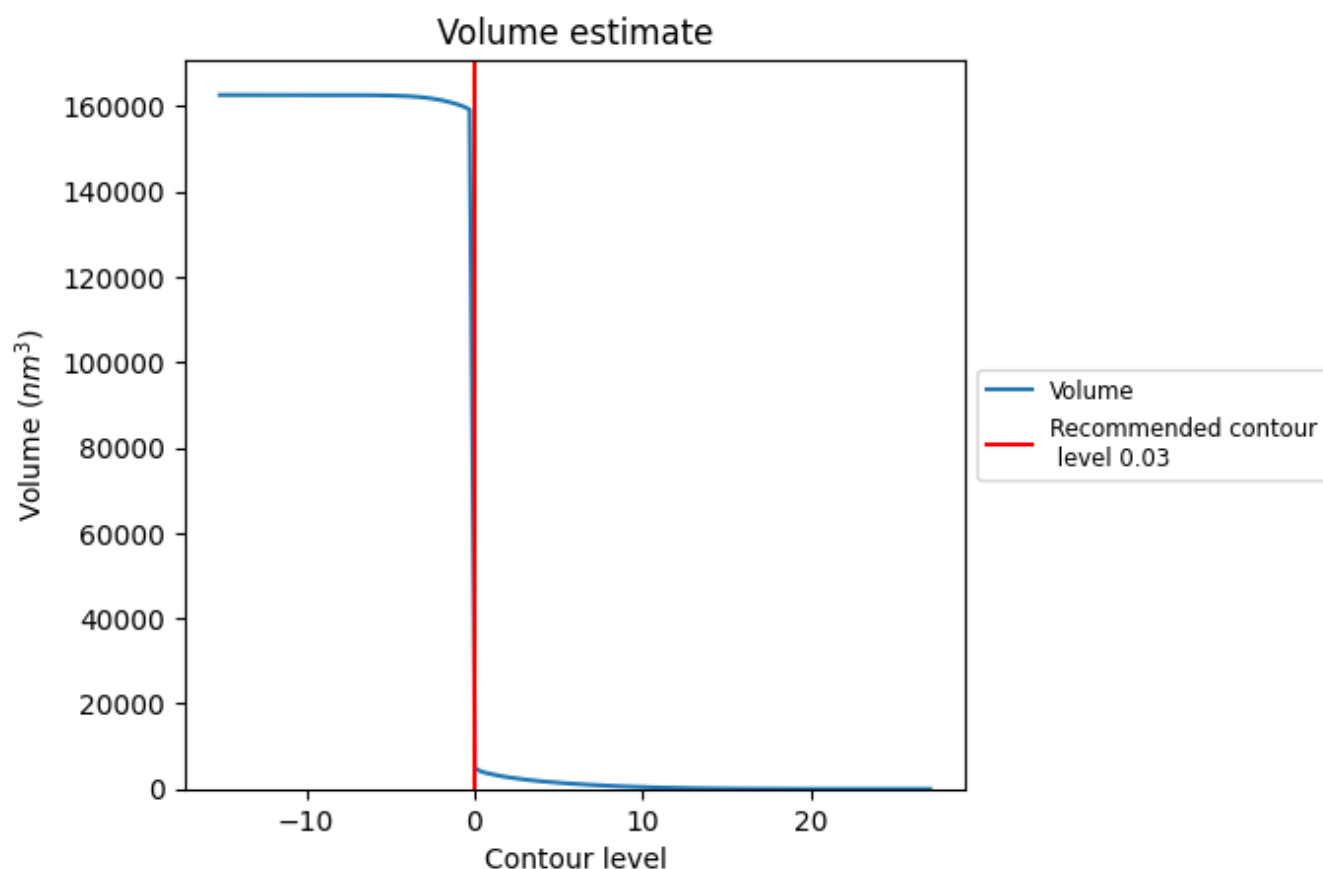
This section contains the results of statistical analysis of the map.

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.

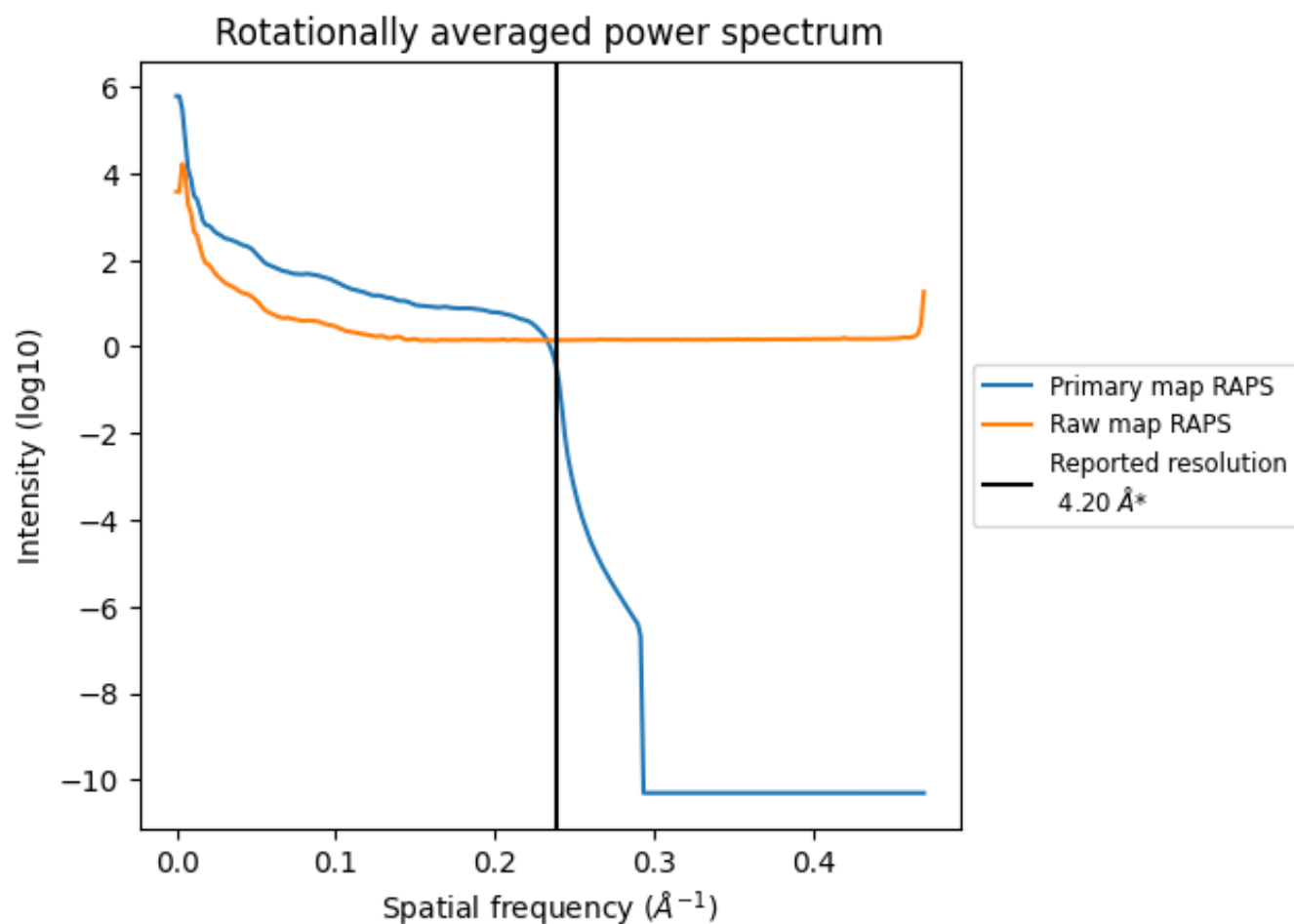
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 11315 nm³; this corresponds to an approximate mass of 10221 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

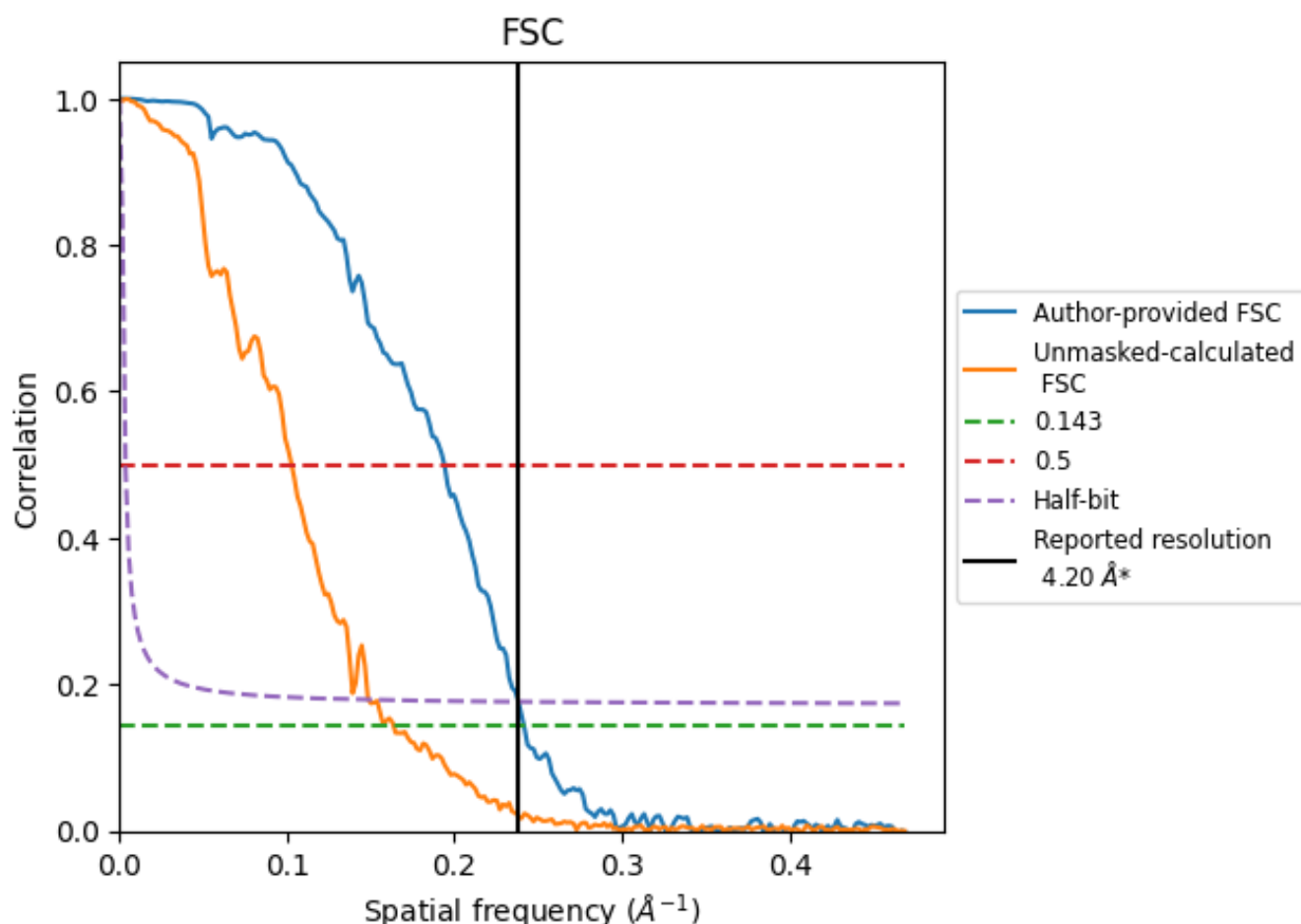


*Reported resolution corresponds to spatial frequency of 0.238 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8.2 Resolution estimates [i](#)

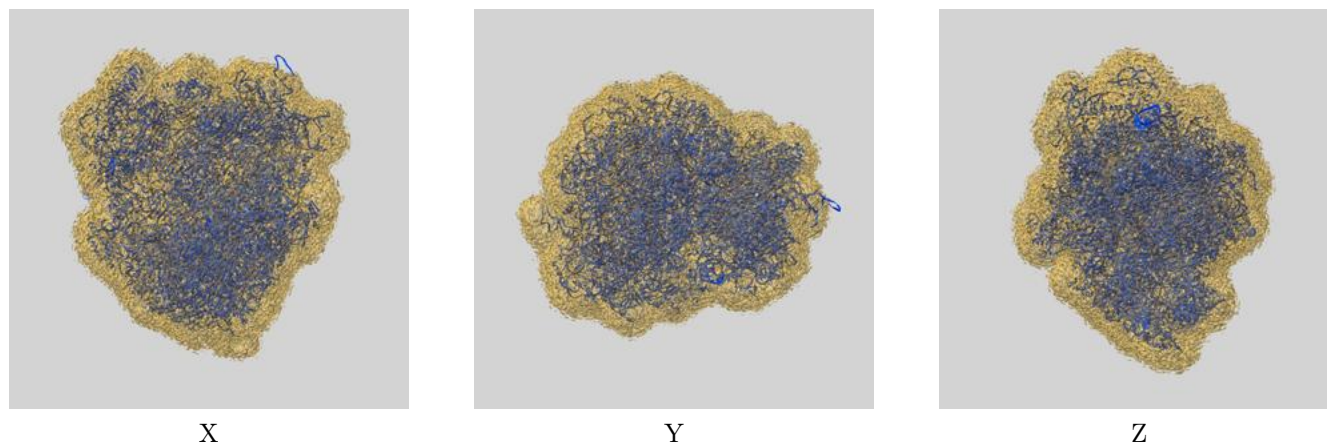
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.14	5.15	4.20
Unmasked-calculated*	6.11	9.73	6.72

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.11 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

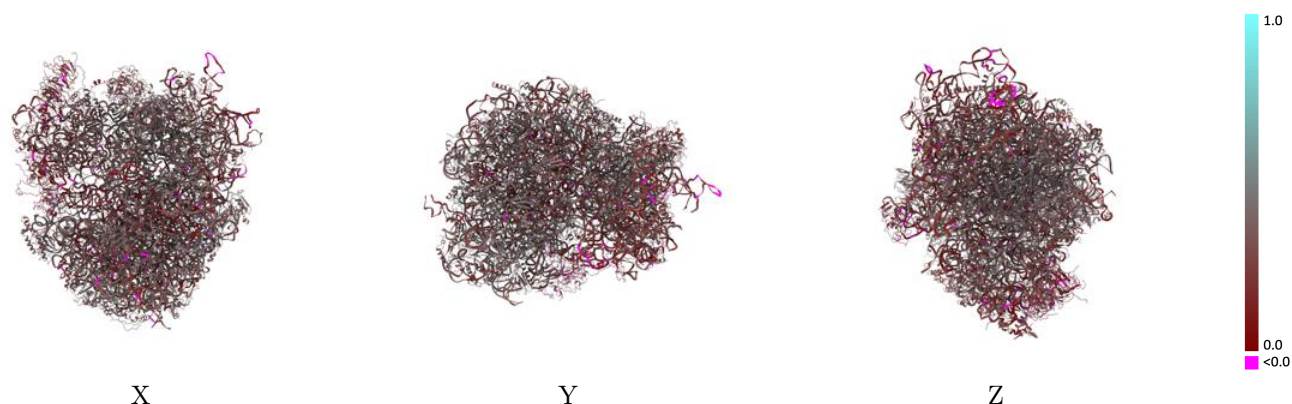
This section contains information regarding the fit between EMDB map EMD-22196 and PDB model 6XIQ. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



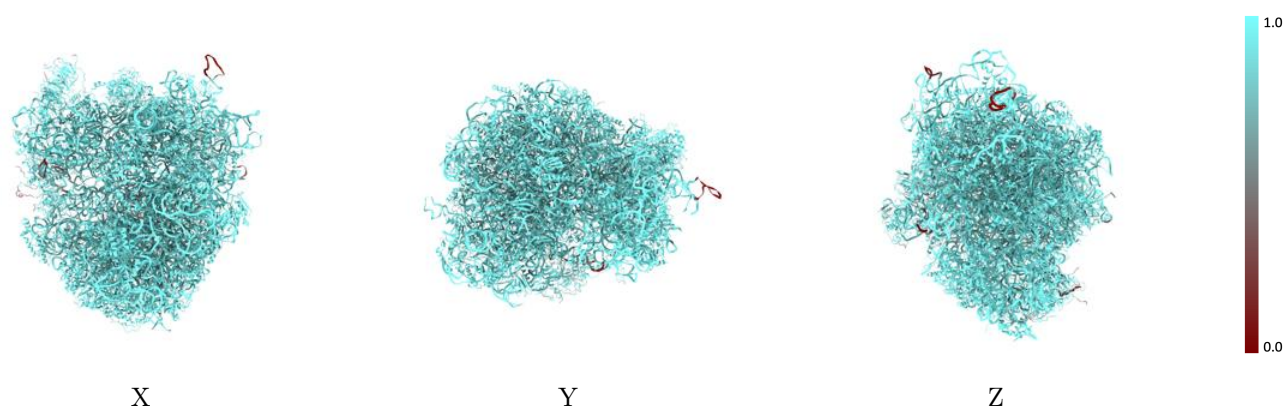
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



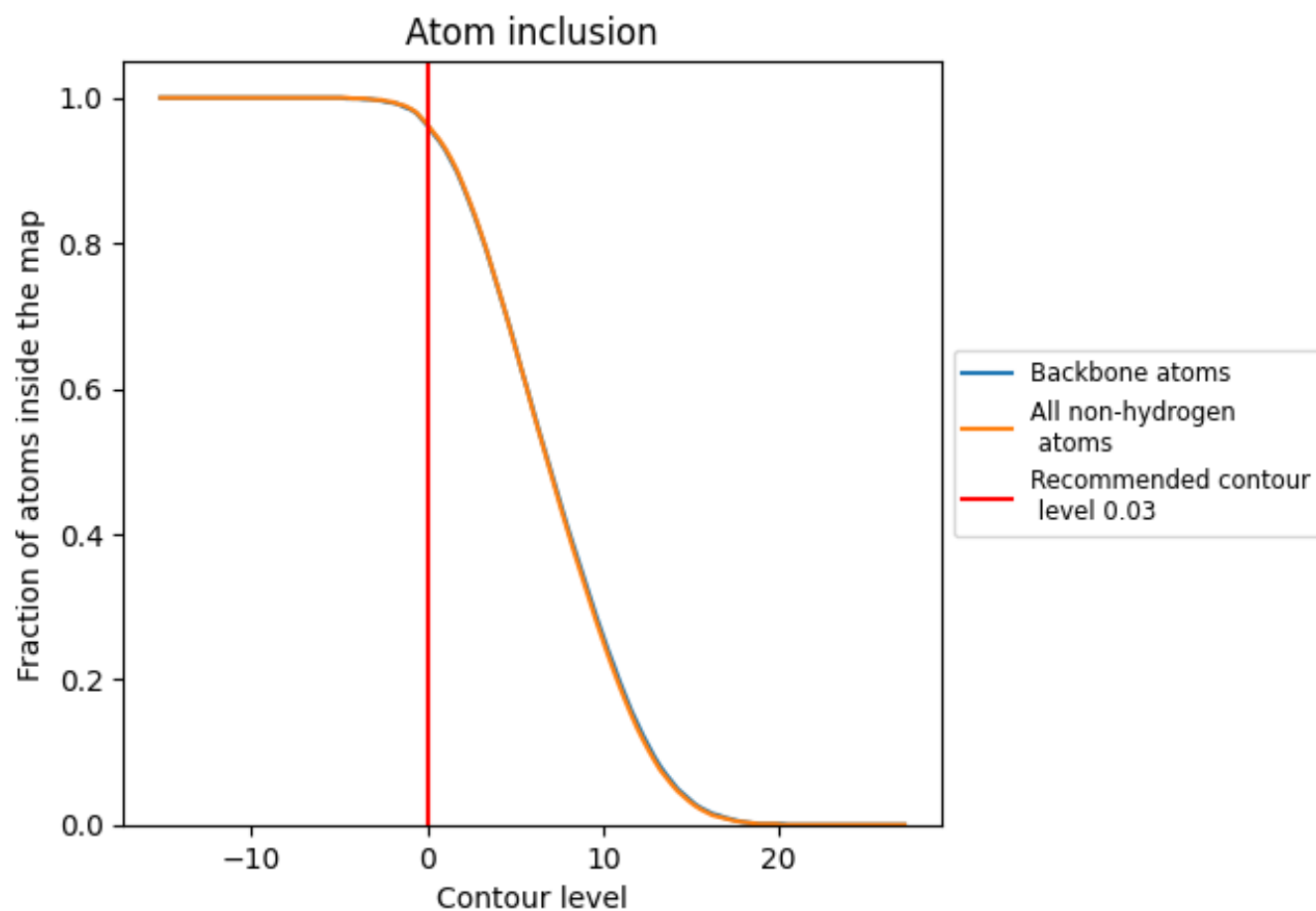
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9630	 0.3300
1	 0.9460	 0.3020
2	 0.9800	 0.3130
3	 0.9850	 0.3560
4	 0.9370	 0.3160
A	 0.9130	 0.3910
AA	 0.9880	 0.2740
AB	 0.9730	 0.3670
AD	 0.9730	 0.3810
AE	 0.9760	 0.3990
AF	 0.9810	 0.3200
AG	 0.9620	 0.2480
AH	 0.9760	 0.3200
AI	 0.9730	 0.3100
AJ	 0.9880	 0.2840
AK	 0.9320	 0.2860
AL	 0.9850	 0.3640
AM	 0.9800	 0.4010
AN	 0.9830	 0.3760
AO	 0.9910	 0.2670
AP	 0.9450	 0.2230
AQ	 0.9550	 0.3660
AR	 0.9750	 0.3550
AS	 0.9870	 0.3590
AT	 0.9510	 0.3260
AU	 0.9800	 0.3360
AV	 0.9560	 0.2660
AX	 0.9320	 0.2360
AY	 0.9080	 0.2590
AZ	 0.9100	 0.1690
B	 0.9850	 0.4250
C	 0.9860	 0.4240
D	 0.9860	 0.3640
E	 0.9880	 0.4020
F	 0.9850	 0.4110















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Chain	Atom inclusion	Q-score
G	 0.9780	 0.3790
H	 0.9790	 0.3860
I	 0.9820	 0.4020
J	 0.9850	 0.3620
L	 0.9830	 0.4090
L1	 0.8370	 0.1930
M	 0.9890	 0.3960
N	 0.9790	 0.4210
O	 0.9790	 0.4110
P	 0.9690	 0.4140
P0	 0.7510	 0.2000
P2	 0.8960	 0.2190
Q	 0.9850	 0.4280
R	 0.9820	 0.3940
S	 0.9880	 0.4210
T	 0.9850	 0.4200
U	 0.9940	 0.3910
V	 0.9650	 0.4290
W	 0.9940	 0.4230
X	 0.9930	 0.4360
Y	 0.9930	 0.4230
Z	 0.9850	 0.4050
a	 0.9720	 0.4170
b	 0.9800	 0.3850
c	 0.9810	 0.3940
d	 0.9880	 0.4270
e	 0.9860	 0.4440
f	 0.9830	 0.4430
g	 0.9810	 0.4180
h	 0.9820	 0.3880
i	 0.9790	 0.3870
j	 0.9850	 0.4250
k	 0.9920	 0.3930
l	 0.9610	 0.3970
m	 0.7720	 0.1770
n	 0.9860	 0.4250
o	 0.9720	 0.4050
p	 0.9700	 0.4120
q	 0.9740	 0.3570
r	 0.9760	 0.3740
s	 0.9800	 0.3910
t	 0.9670	 0.3370

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Chain	Atom inclusion	Q-score
u	 0.9800	 0.3090
v	 0.9800	 0.3140
w	 0.9590	 0.2640
x	 0.9810	 0.3390
y	 0.9830	 0.3340
z	 0.9750	 0.2930