



Full wwPDB EM Validation Report ⓘ

Oct 13, 2024 – 08:42 AM EDT

PDB ID : 6XIR
EMDB ID : EMD-22198
Title : Cryo-EM Structure of K63 Ubiquitinated Yeast Translocating Ribosome under Oxidative Stress
Authors : Zhou, Y.; Bartesaghi, A.; Silva, G.M.
Deposited on : 2020-06-21
Resolution : 3.20 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

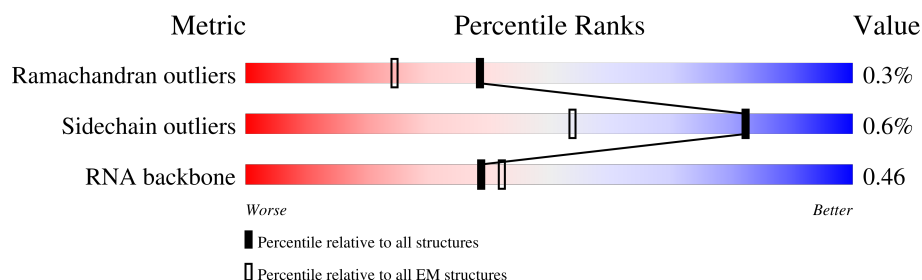
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



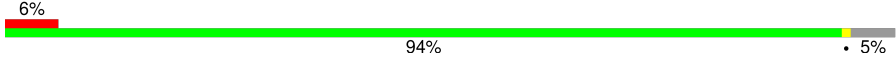
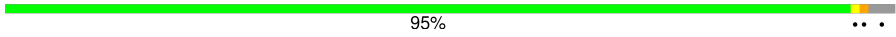
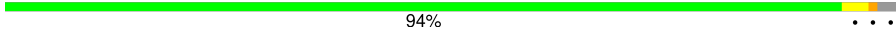
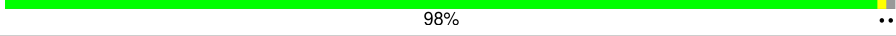
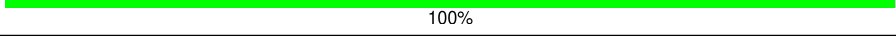
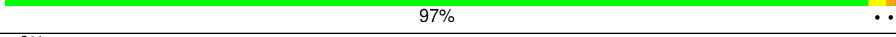
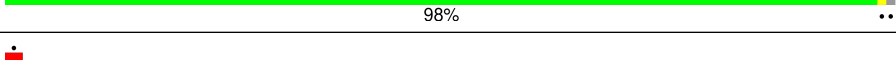
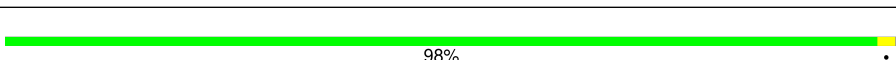
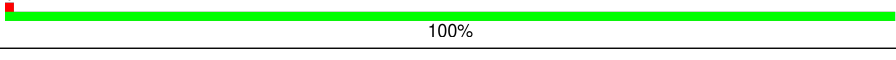
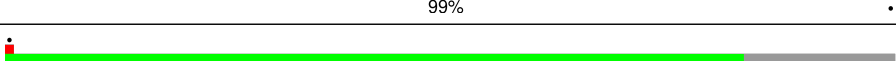
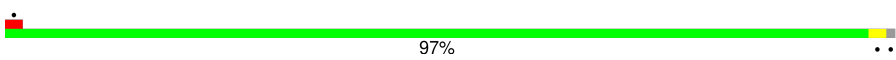

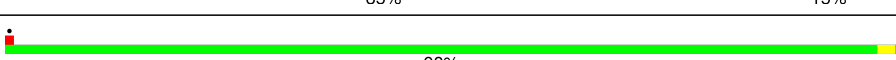
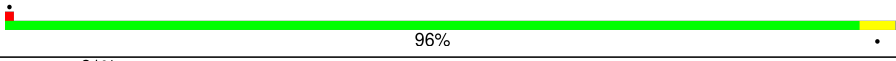
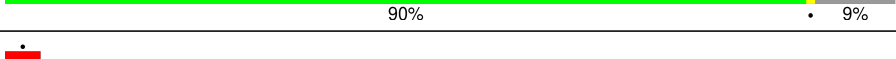



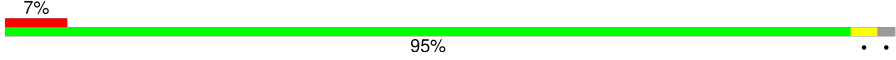
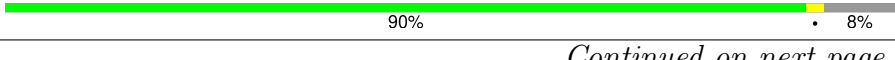


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	
2	B	387	
3	C	362	
4	D	297	
5	E	176	
6	F	244	
7	G	256	
8	H	191	

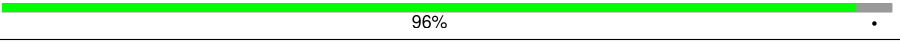
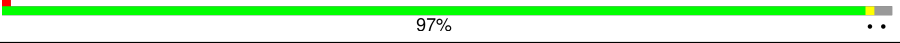
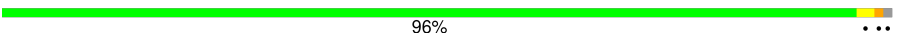

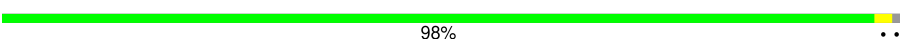
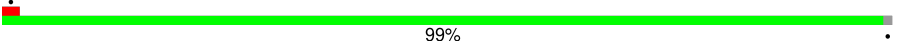

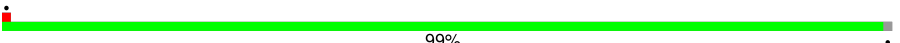
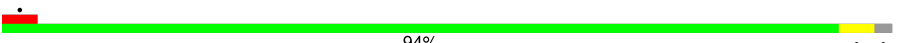

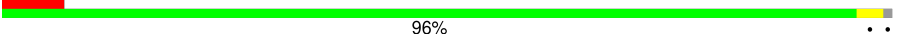
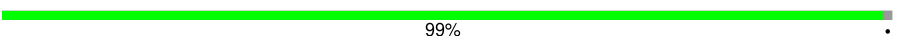





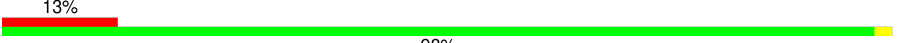





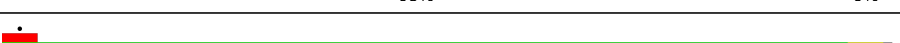
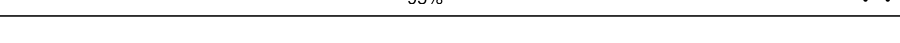
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Mol	Chain	Length	Quality of chain
9	I	221	
10	J	174	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	121	
21	V	137	
22	W	155	
23	X	142	
24	Y	127	
25	Z	136	
26	AA	105	
27	AB	156	
28	1	3395	
29	3	121	
30	4	158	
31	a	149	
32	b	59	
33	c	105	


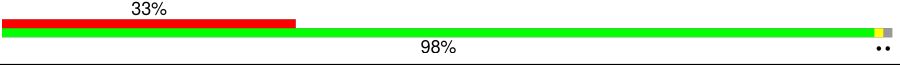

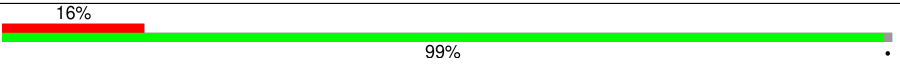
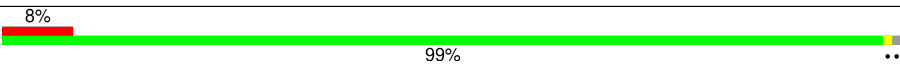

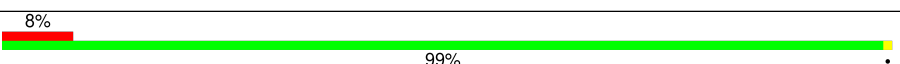
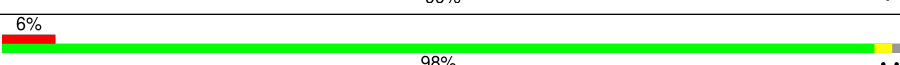
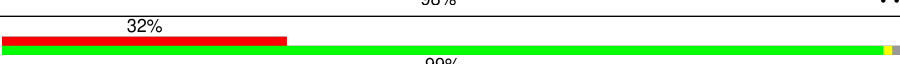
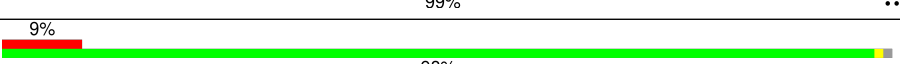
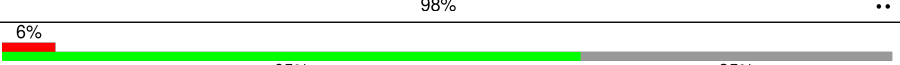
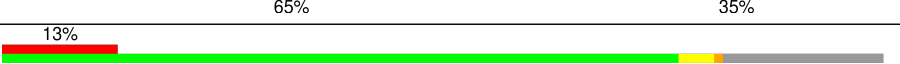
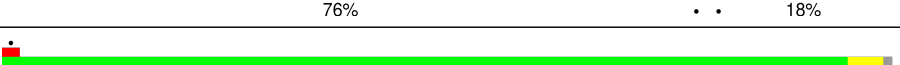
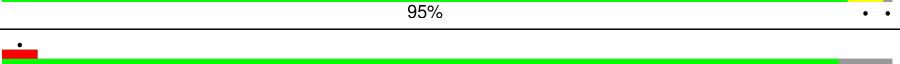
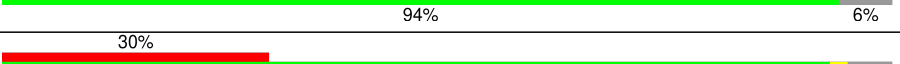
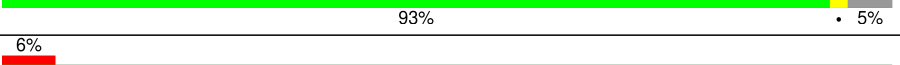

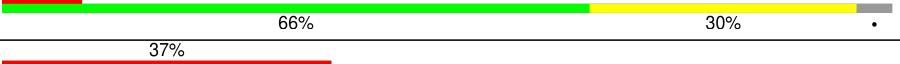
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Mol	Chain	Length	Quality of chain
34	d	113	
35	e	130	
36	f	107	
37	g	121	
38	h	120	
39	i	100	
40	j	88	
41	k	78	
42	l	51	
43	n	25	
44	o	106	
45	p	92	
46	2	1800	
47	q	252	
48	r	255	
49	s	254	
50	t	240	
51	u	261	
52	v	225	
53	w	236	
54	x	190	
55	y	200	
56	z	197	
57	AD	151	
58	AE	138	

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Mol	Chain	Length	Quality of chain
59	AF	142	
60	AG	143	
61	AH	136	
62	AI	146	
63	AJ	144	
64	AK	121	
65	AL	87	
66	AM	130	
67	AN	145	
68	AO	135	
69	AP	108	
70	AQ	119	
71	AR	82	
72	AS	67	
73	AT	56	
74	AV	319	
75	AX	76	
75	AZ	76	

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 197132 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 2 is a protein called RPL3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 3 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 4 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	296	Total	C	N	O	S	0	0
			2375	1501	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	N	O	S	0	0
			1239	800	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	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 7 is a protein called RPL8A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 8 is a protein called RPL9A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	211	Total	C	N	O	S	0	0
			1705	1083	322	294	6		

- Molecule 10 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	847	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	N	O		0	0
			1543	962	315	266			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	136	Total	C	N	O	S	0	0
			1053	675	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	N	O	S	0	0
			1720	1077	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	N	O	S	0	0
			1555	1003	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	N	O	S	0	0
			1420	882	281	257			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	185	Total	C	N	O	S	0	0
			1441	908	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	N	O	S	0	0
			1521	935	326	260			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	172	Total	C	N	O	S	0	0
			1445	930	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	N	O	S	0	0
			1276	805	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	N	O	S	0	0
			796	516	131	149			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 22 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	121	Total	C	N	O	S	0	0
			964	620	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	N	O		0	0
			993	625	192	176			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O		0	0
			1092	710	202	180			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AA	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AB	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	3113	Total	C	N	O	P	0	0
			66567	29735	11981	21738	3113		

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	N	O	P	0	0
			2579	1152	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	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 31 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 32 is a protein called RPL29 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	b	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 35 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 41 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 43 is a protein called RPL41A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	25	Total	C	N	O	S	0	0
			227	139	60	27	1		

- Molecule 44 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 45 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2	1708	Total	C	N	O	P	0	0
			36409	16277	6464	11960	1708		

- Molecule 47 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 48 is a protein called RPS1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 49 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 50 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 51 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 52 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 53 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	223	Total	C	N	O	S	0	0
			1790	1123	346	318	3		

- Molecule 54 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	x	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 55 is a protein called RPS8A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 56 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 57 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AD	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 58 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AE	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 59 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AF	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 60 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	AG	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 61 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AH	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 62 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AI	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 63 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AJ	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 64 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AK	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 65 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AL	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 66 is a protein called RPS22A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AM	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 67 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AN	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 68 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	AO	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 69 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	AP	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 70 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AQ	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 71 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AR	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 72 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AS	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 73 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AT	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 74 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AV	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

- Molecule 75 is a RNA chain called Transfer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AX	73	Total	C	N	O	P	0	0
			1564	697	282	512	73		
75	AZ	73	Total	C	N	O	P	0	0
			1564	697	282	512	73		

- Molecule 76 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of

Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
76	j	1	Total 1	Zn 1	0
76	o	1	Total 1	Zn 1	0
76	p	1	Total 1	Zn 1	0
76	AQ	1	Total 1	Zn 1	0
76	AR	1	Total 1	Zn 1	0
76	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

Chain A:  98%



- Molecule 2: RPL3 isoform 1

Chain B:  98%



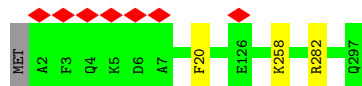
- Molecule 3: RPL4A isoform 1

Chain C:  98%



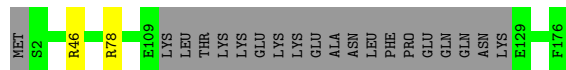
- Molecule 4: RPL5 isoform 1

Chain D:  99%




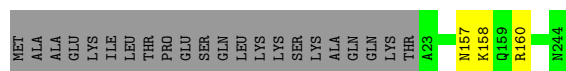
- Molecule 5: 60S ribosomal protein L6-A

Chain E:  88% 11%



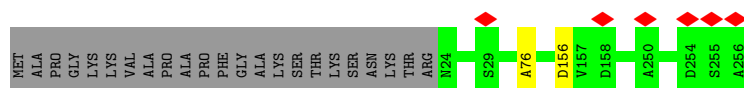
- Molecule 6: 60S ribosomal protein L7-A

Chain F:  90% 9%



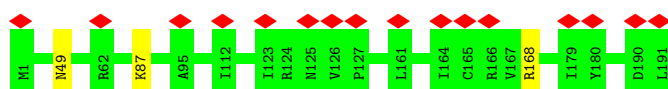
- Molecule 7: RPL8A isoform 1

Chain G:  90% 9%



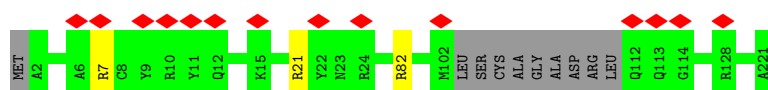
- Molecule 8: RPL9A isoform 1

Chain H:  8% 98% 5%



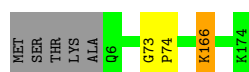
- Molecule 9: RPL10 isoform 1

Chain I:  6% 94% 5%



- Molecule 10: RPL11B isoform 1

Chain J:  95% 5%



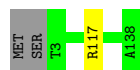
- Molecule 11: 60S ribosomal protein L13-A

Chain L:  94% 5%



- Molecule 12: 60S ribosomal protein L14-A

Chain M:  98% 2%



- Molecule 13: 60S ribosomal protein L15-A

Chain N:  100%



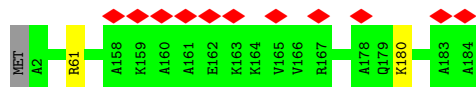
- Molecule 14: 60S ribosomal protein L16-A

Chain O:  97%



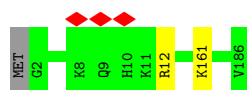
- Molecule 15: 60S ribosomal protein L17-A

Chain P:  98%



- Molecule 16: 60S ribosomal protein L18-A

Chain Q:  98%



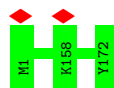
- Molecule 17: 60S ribosomal protein L19-A

Chain R:  98%



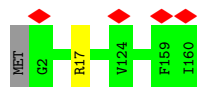
- Molecule 18: 60S ribosomal protein L20-A

Chain S:  100%




- Molecule 19: 60S ribosomal protein L21-A

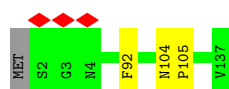
Chain T:  99%



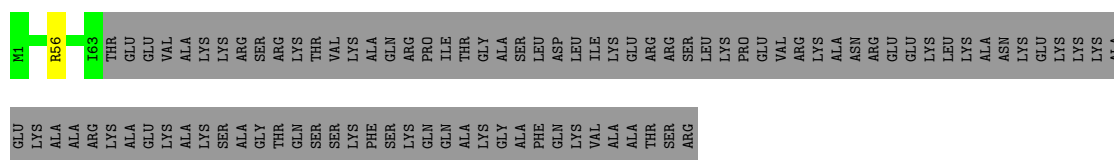
• Molecule 20: 60S ribosomal protein L22-A

Chain U:  83% 17%


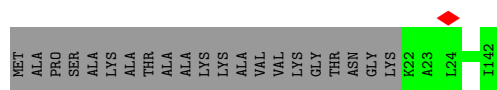
• Molecule 21: 60S ribosomal protein L23-A

Chain V:  97% ..

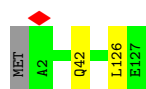
• Molecule 22: RPL24A isoform 1

Chain W:  40% 59%

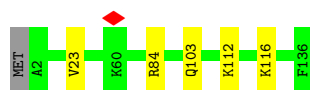
• Molecule 23: 60S ribosomal protein L25

Chain X:  85% 15%

• Molecule 24: 60S ribosomal protein L26-A

Chain Y:  98% ..


• Molecule 25: 60S ribosomal protein L27-A

Chain Z:  96% ..

• Molecule 26: 40S ribosomal protein S10-A

Chain AA:  21% 90% 9%

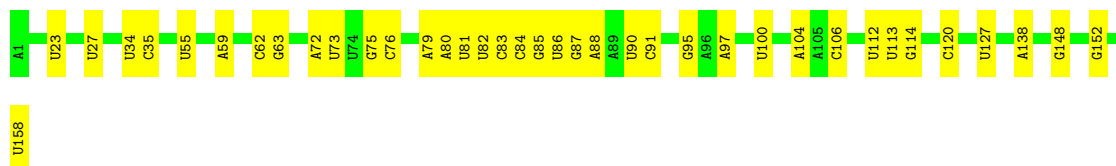
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U3319	U3196	G3030	U2860	U2565	A	G2403	U2226	U	C1761
A3320	G3197	G3031	U2861	C2566	C	A2404	C2235	G	C1762
A3033	U3198	A3032	U2862	C2567	U	C2405	U2236	U	U1763
G3036	U3207	G3033	C2867	C2568	A	U2411	A2244	A	U1764
U3068	G3208	U3068	G2871	A2569	C	G2412	C2245	G	U1765
G3069	G3216	G3069	A2872	U2570	C	U2428	G2246	A	G1770
U3078	G3217	G3078	U2873	U2571	U	U2435	C2247	A	G1773
U3079	U3218	U3079	G2874	C2572	U	G2442	A2255	C	C1774
G3080	U3219	G3080	U2875	G2573	A	A2443	U2256	C	U1775
C3092	G3220	C3092	A2887	U2574	U	C	C2257	G	G1780
G3101	G3221	G3101	U2888	A2580	A	G2444	U2258	C	A1588
U3104	U3222	U3104	G2889	U2581	G	A2445	A2259	U	A1589
U3105	A3223	U3105	U2890	U2582	U	C	U2260	C	A1593
G3109	G3224	G3109	A2900	G2585	U	A	G2261	U	G1604
G3110	G3225	G3110	U2923	G2586	C	U	A2262	U	G1798
U3111	C3226	U3111	G2924	U2587	G	G	C2263	G	U1605
C3115	A3227	C3115	U2925	A2593	A	C	U2264	C	U1606
G3116	U3228	G3116	C2926	C2594	G	U	U2266	A	A1613
G3117	A3229	G3117	U2927	G2606	U	G	U2267	U	U1620
G3118	G3230	G3118	U2782	G2607	G	G	U2269	A	U1627
U3119	U3231	U3119	U2783	U2612	U	U	G2273	A	C1628
C3120	G3232	C3120	U2795	U2613	A	C	U2274	U	U1629
U3121	C3233	U3121	G2796	G2614	G	U	U2275	C	U1630
A3122	A3234	A3122	A2799	G2615	A	G	G2276	U	C1631
A3123	G3235	A3123	A2801	G2616	A	C	U2277	C	U1636
A3129	G3236	A3129	A2802	C2627	U	A	A2279	C	A1637
A3130	G3237	A3130	A2803	A2635	G	G	A2280	C	U1821
U3131	G3238	U3131	A2804	G2644	A	U	A2281	C	C1822
A3142	A3268	A3142	A2808	G2645	A	A	G2307	C	U1840
C3143	U3269	C3143	C2809	G2646	G	C	C2308	C	A1642
U3153	G3270	U3153	C2810	U2648	U	U	U2309	C	A1643
C3154	A3271	C3154	A2817	U2652	C	G	U2310	U	C1644
U3155	U3272	U3155	G2828	U2656	U	C	U2311	G	U1645
U3156	G3273	U3156	U2834	A2656	C	C	U2312	C	G1646
U3157	U3274	U3157	U2635	G2672	G	U	G2315	U	A1647
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A3172	U3276	A3172	A2837	C2674	A	A	U2334	A	A1858
G3173	U3277	G3173	U2838	G2675	G	G	U2335	C	C1866
A3174	G3278	A3174	U2842	A2676	U	C	U2336	U	U1872
U3175	A3279	U3175	U2643	G2677	C	A	U2337	G	G1878
G3176	U3280	G3176	A2844	U2681	G	G	C2359	U	A1879
U3179	A3281	U3179	A2845	U2682	U	U	U2170	C	U1880
A3180	G3282	A3180	U2846	U2683	G	A	A2178	A	A1886
C3181	U3283	C3181	A2847	C2689	C	A	C2179	C	U1724
U3304	A3294	U3304	G2850	A2690	A	A	A2188	G	A1741
U3313	A3295	U3313	A2851	A2691	A	U	U2205	U	U1742
U3314	U3304	U3314	U3026	A2692	U	C	G2206	C	C1907
U3315	U3305	U3315	A3027	A2693	C	A	A2207	G	A1750
U3316	U3306	U3316	G3028	A2694	C	C	A2208	U	G1751
U3317	U3307	U3317	U3029	A2695	C	C	U2209	C	C1926
U3318	U3308	U3318	U3030	A2696	C	C	G2210	G	G1927
U3319	U3309	U3319	U3031	A2697	C	C			
U3320	U3310	U3320	U3032	A2698	C	C			
U3321	U3311	U3321	U3033	A2699	C	C			
U3322	U3312	U3322	U3034	A2700	C	C			
U3323	U3313	U3323	U3035	A2701	C	C			
U3324	U3314	U3324	U3036	A2702	C	C			
U3325	U3315	U3325	U3037	A2703	C	C			
U3326	U3316	U3326	U3038	A2704	C	C			
U3327	U3317	U3327	U3039	A2705	C	C			
U3328	U3318	U3328	U3040	A2706	C	C			
U3329	U3319	U3329	U3041	A2707	C	C			
U3330	U3320	U3330	U3042	A2708	C	C			
U3331	U3321	U3331	U3043	A2709	C	C			
U3332	U3322	U3332	U3044	A2710	C	C			
U3333	U3323	U3333	U3045	A2711	C	C			
U3334	U3324	U3334	U3046	A2712	C	C			
U3335	U3325	U3335	U3047	A2713	C	C			
U3336	U3326	U3336	U3048	A2714	C	C			
U3337	U3327	U3337	U3049	A2715	C	C			
U3338	U3328	U3338	U3050	A2716	C	C			
U3339	U3329	U3339	U3051	A2717	C	C			
U3340	U3330	U3340	U3052	A2718	C	C			
U3341	U3331	U3341	U3053	A2719	C	C			
U3342	U3332	U3342	U3054	A2720	C	C			
U3343	U3333	U3343	U3055	A2721	C	C			
U3344	U3334	U3344	U3056	A2722	C	C			
U3345	U3335	U3345	U3057	A2723	C	C			
U3346	U3336	U3346	U3058	A2724	C	C			
U3347	U3337	U3347	U3059	A2725	C	C			
U3348	U3338	U3348	U3060	A2726	C	C			
U3349	U3339	U3349	U3061	A2727	C	C			
U3350	U3340	U3350	U3062	A2728	C	C			
U3351	U3341	U3351	U3063	A2729	C	C			
U3352	U3342	U3352	U3064	A2730	C	C			
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U3354	U3344	U3354	U3066	A2732	C	C			
U3355	U3345	U3355	U3067	A2733	C	C			
U3356	U3346	U3356	U3068	A2734	C	C			
U3357	U3347	U3357	U3069	A2735	C	C			
U3358	U3348	U3358	U3070	A2736	C	C			
U3359	U3349	U3359	U3071	A2737	C	C			
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U3361	U3351	U3361	U3073	A2739	C	C			
U3362	U3352	U3362	U3074	A2740	C	C			
U3363	U3353	U3363	U3075	A2741	C	C			
U3364	U3354	U3364	U3076	A2742	C	C			
U3365	U3355	U3365	U3077	A2743	C	C			
U3366	U3356	U3366	U3078	A2744	C	C			
U3367	U3357	U3367	U3079	A2745	C	C			
U3368	U3358	U3368	U3080	A2746	C	C			
U3369	U3359	U3369	U3081	A2747	C	C			
U3370	U3360	U3370	U3082	A2748	C	C			
U3371	U3361	U3371	U3083	A2749	C	C			
U3372	U3362	U3372	U3084	A2750	C	C			
U3373	U3363	U3373	U3085	A2751	C	C			
U3374	U3364	U3374	U3086	A2752	C	C			
U3375	U3365	U3375	U3087	A2753	C	C			
U3376	U3366	U3376	U3088	A2754	C	C			
U3377	U3367	U3377	U3089	A2755	C	C			
U3378	U3368	U3378	U3090	A2756	C	C			
U3379	U3369	U3379	U3091	A2757	C	C			
U3380	U3370	U3380	U3092	A2758	C	C			
U3381	U3371	U3381	U3093	A2759	C	C			
U3382	U3372	U3382	U3094	A2760	C	C			
U3383	U3373	U3383	U3095	A2761	C	C			
U3384	U3374	U3384	U3096	A2762	C	C			
U3385	U3375	U3385	U3097	A2763	C	C			
U3386	U3376	U3386	U3098	A2764	C	C			
U3387	U3377	U3387	U3099	A2765	C	C			
U3388	U3378	U3388	U3100	A2766	C	C			
U3389	U3379	U3389	U3101	A2767	C	C			
U3390	U3380	U3390	U3102	A2768	C	C			
U3391	U3381	U3391	U3103	A2769	C	C			
U3392	U3382	U3392	U3104	A2770	C	C			
U3393	U3383	U3393	U3105	A2771	C	C			
U3394	U3384	U3394	U3106	A2772	C	C			
U3395	U3385	U3395	U3107	A2773	C	C			
U3396	U3386	U3396	U3108	A2774	C	C			
U3397	U3387	U3397	U3109	A2775	C	C			
U3398	U3388	U3398	U3110	A2776	C	C			
U3399	U3389	U3399	U3111	A2777	C	C			
U3400	U3390	U3400	U3112	A2778	C	C			
U3401	U3391	U3401	U3113	A2779	C	C			
U3402	U3392	U3402	U3114	A2780	C	C			
U3403	U3393	U3403	U3115	A2781	C	C			
U3404	U3394	U3404	U3116	A2782	C	C			
U3405	U3395	U3405	U3117	A2783	C	C			
U3406	U3396	U3406	U3118	A2784	C	C			
U3407	U3397	U3407	U3119	A2785	C	C			
U3408	U3398	U3408	U3120	A2786	C	C			
U3409	U3399	U3409	U3121	A2787	C	C			
U3410	U3400	U3410	U3122	A2788	C	C			
U3411	U3401	U3411	U3123	A2789	C	C			
U3412	U3402	U3412	U3124	A2790	C	C			
U3413	U3403	U3413	U3125	A2791	C	C			
U3414	U3404	U3414	U3126	A2792	C	C			
U3415	U3405	U3415	U3127	A2793	C	C			
U3416	U3406	U3416	U3128	A2794	C	C			
U3417	U3407	U3417	U3129	A2795	C	C			
U3418	U3408	U3418	U3130	A2796	C	C			
U3419	U3409	U3419	U3131	A2797	C	C			
U3420	U								

Chain 3:  83% 16%



- Molecule 30: 5.8S ribosomal RNA

Chain 4:  76% 24%



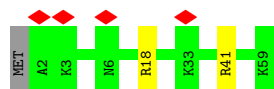
- Molecule 31: 60S ribosomal protein L28

Chain a:  97%




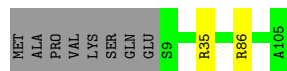
- Molecule 32: RPL29 isoform 1

Chain b:  7% 95%



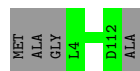
- Molecule 33: 60S ribosomal protein L30

Chain c:  90% 8%



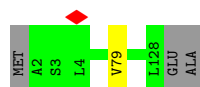
- Molecule 34: 60S ribosomal protein L31-A

Chain d:  96%



- Molecule 35: RPL32 isoform 1

Chain e:  97%




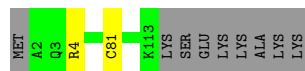
- Molecule 36: 60S ribosomal protein L33-A

Chain f:  96% ...



- Molecule 37: 60S ribosomal protein L34-A

Chain g:  91% • 7%



- Molecule 38: 60S ribosomal protein L35-A

Chain h:  98% ..



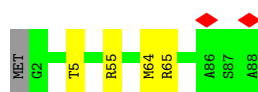
- Molecule 39: 60S ribosomal protein L36-A

Chain i:  99% •



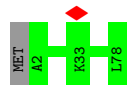
- Molecule 40: 60S ribosomal protein L37-A

Chain j:  94% 5% •



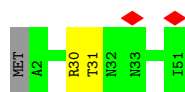
- Molecule 41: RPL38 isoform 1

Chain k:  99% •

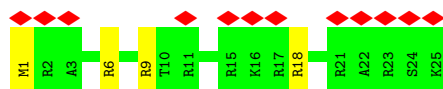
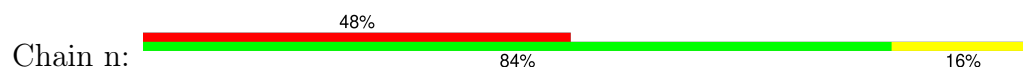


- Molecule 42: 60S ribosomal protein L39

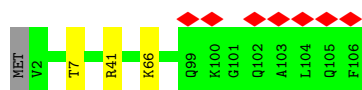
Chain l:  94% ..



- Molecule 43: RPL41A isoform 1



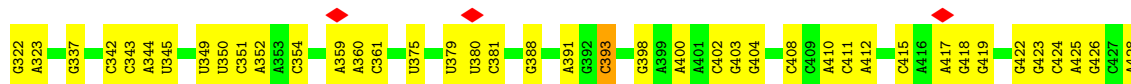
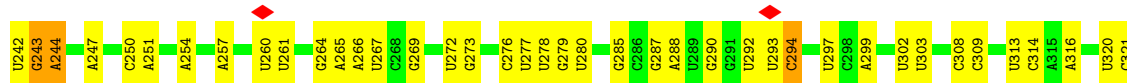
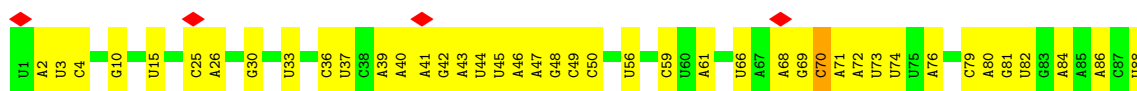
- Molecule 44: 60S ribosomal protein L42-A



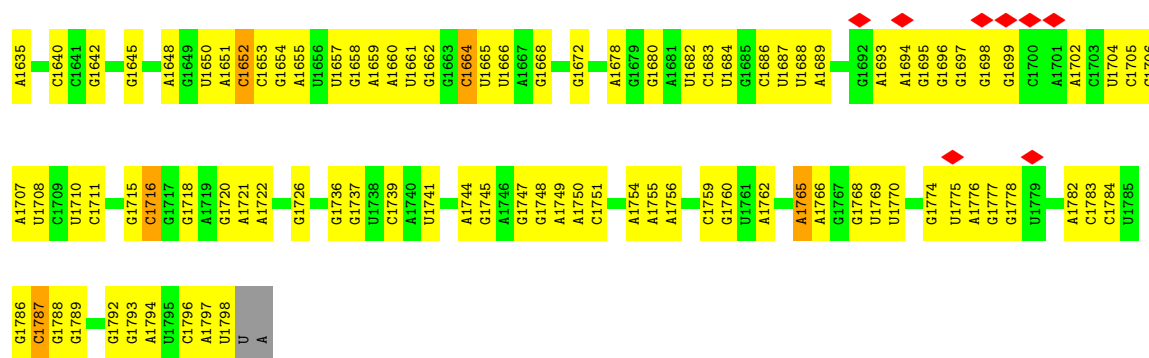
- Molecule 45: 60S ribosomal protein L43-A



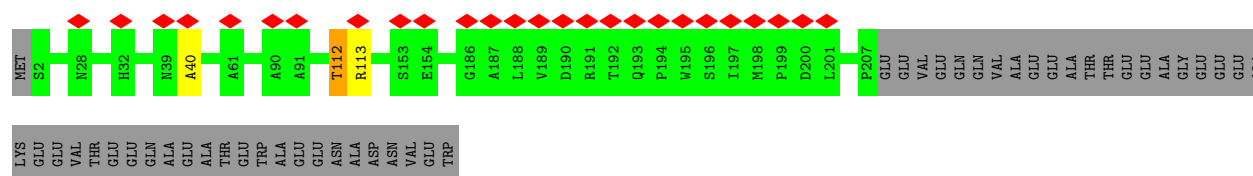
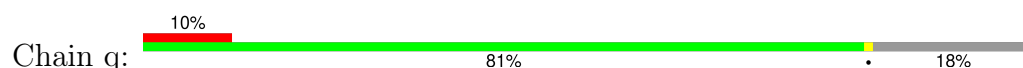
- Molecule 46: 18S ribosomal RNA



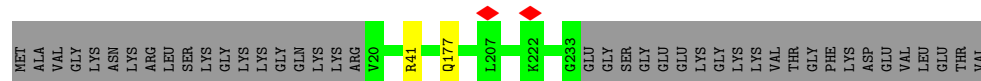
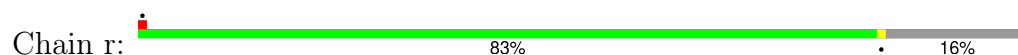




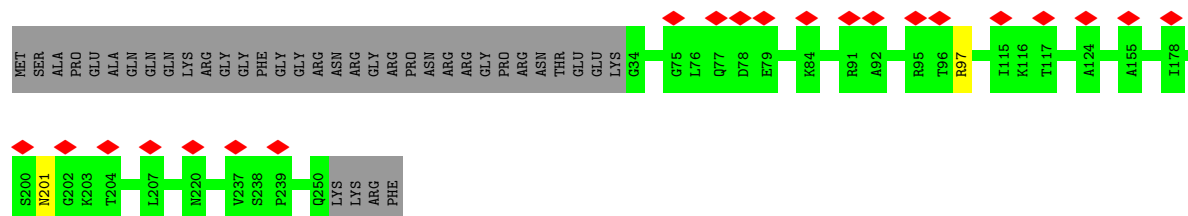
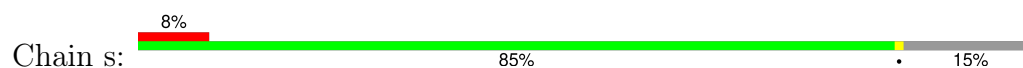
- Molecule 47: 40S ribosomal protein S0-A



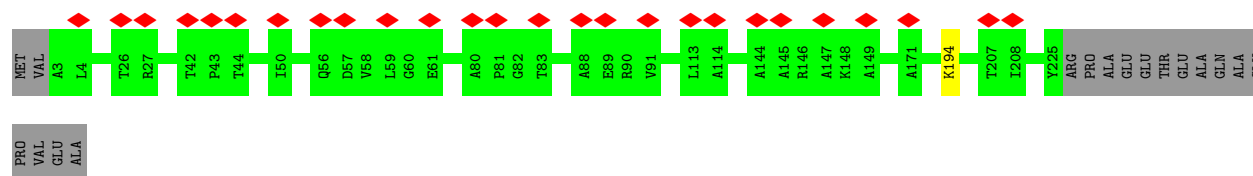
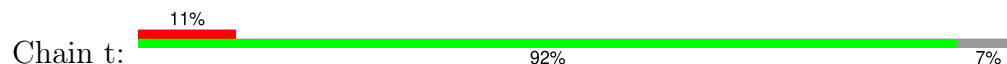
- Molecule 48: RPS1A isoform 1



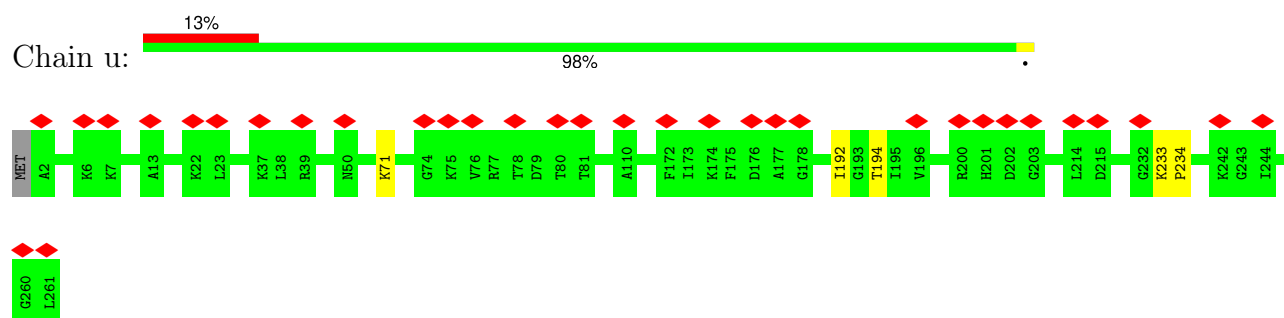
- Molecule 49: RPS2 isoform 1



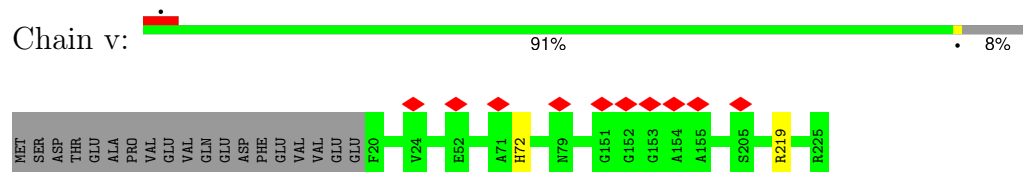
- Molecule 50: RPS3 isoform 1



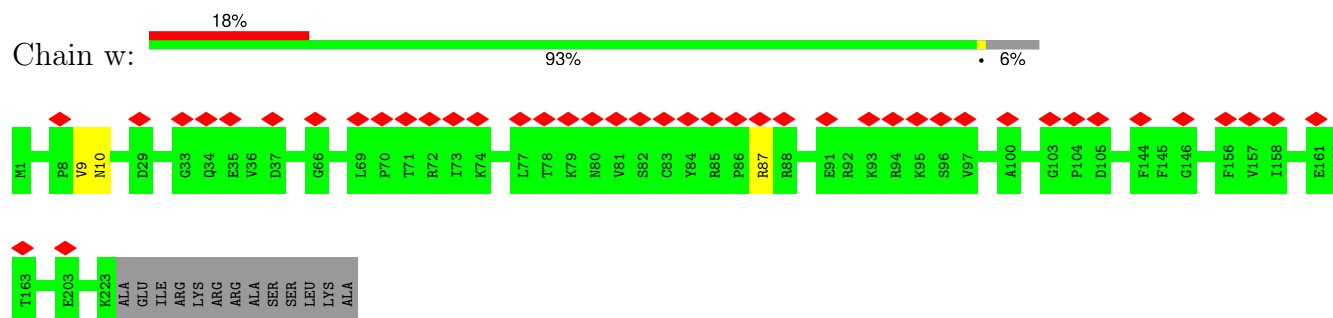
- Molecule 51: 40S ribosomal protein S4-A



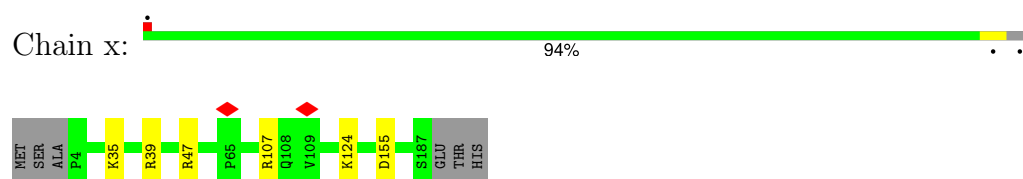
- Molecule 52: Rps5p



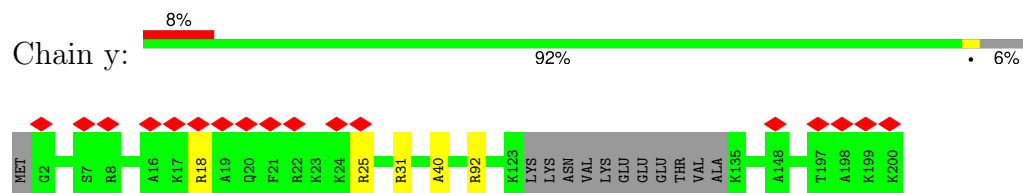
- Molecule 53: 40S ribosomal protein S6-A



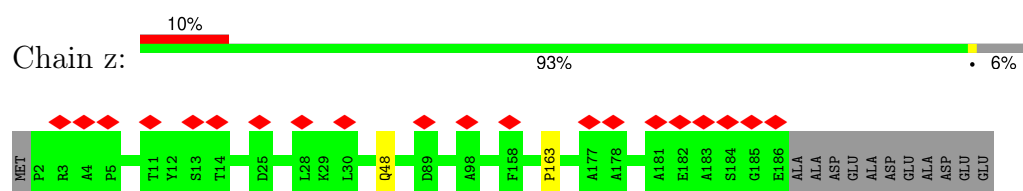
- Molecule 54: 40S ribosomal protein S7-A



- Molecule 55: RPS8A isoform 1

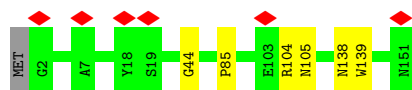


- Molecule 56: 40S ribosomal protein S9-A



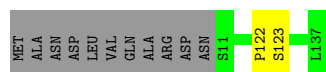
- Molecule 57: 40S ribosomal protein S13

Chain AD:  95%




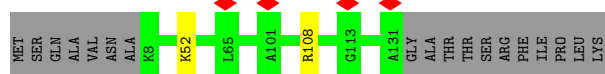
- Molecule 58: 40S ribosomal protein S14-B

Chain AE:  91% 8%



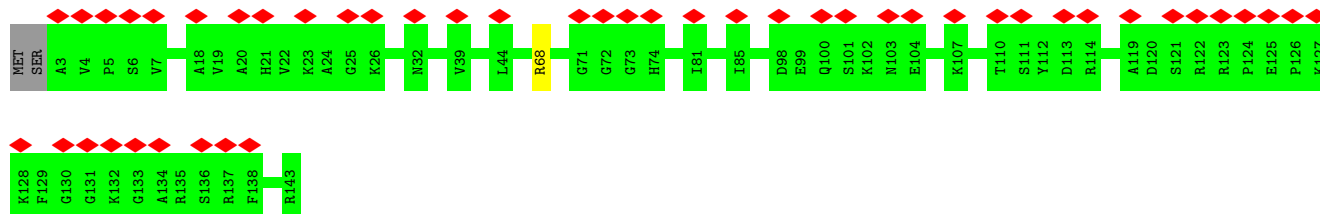
- Molecule 59: RPS15 isoform 1

Chain AF:  86% 13%




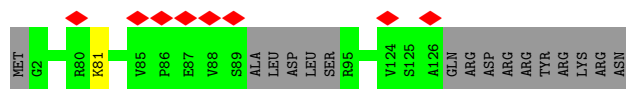
- Molecule 60: 40S ribosomal protein S16-A

Chain AG:  33% 98%



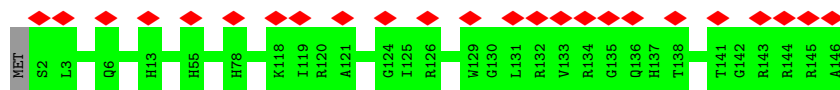
- Molecule 61: 40S ribosomal protein S17-B

Chain AH:  6% 88% 12%

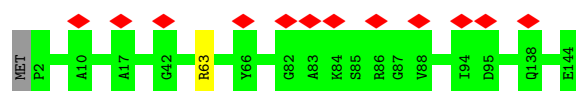


- Molecule 62: 40S ribosomal protein S18-A

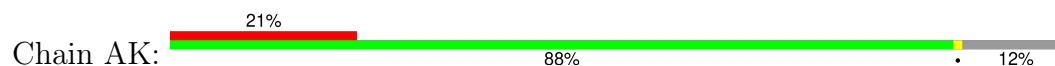
Chain AI:  16% 99%



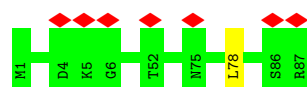
- Molecule 63: 40S ribosomal protein S19-A



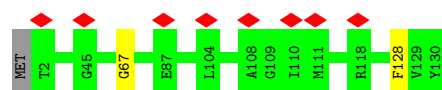
- Molecule 64: RPS20 isoform 1



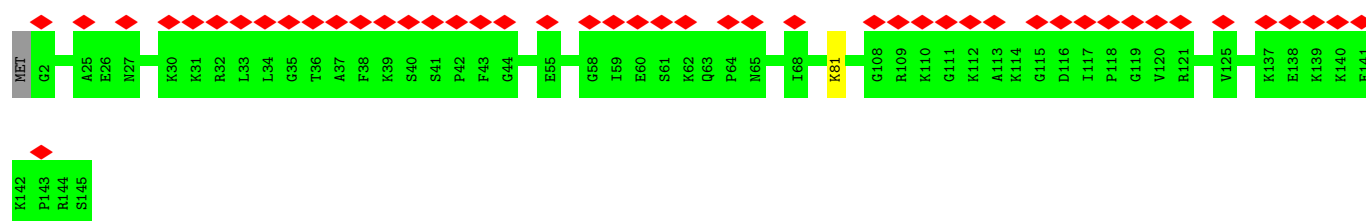
- Molecule 65: 40S ribosomal protein S21-A



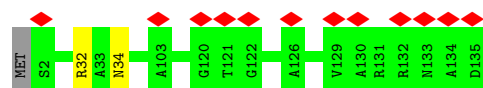
- Molecule 66: RPS22A isoform 1



- Molecule 67: 40S ribosomal protein S23-A

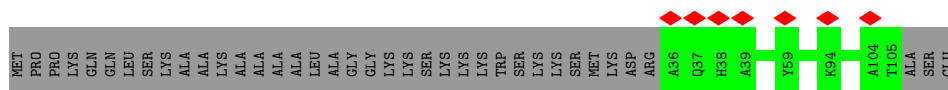


- Molecule 68: 40S ribosomal protein S24-A

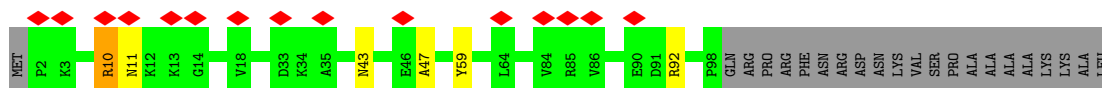
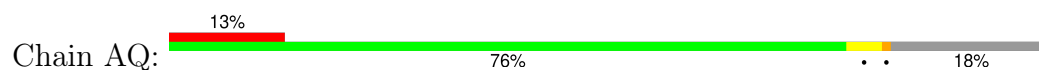


- Molecule 69: RPS25A isoform 1

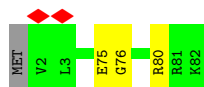




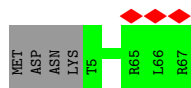
- Molecule 70: RPS26B isoform 1



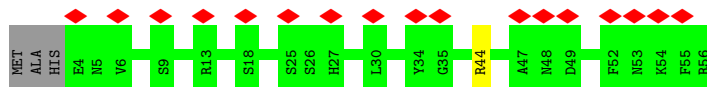
- Molecule 71: 40S ribosomal protein S27-A



- Molecule 72: RPS28A isoform 1



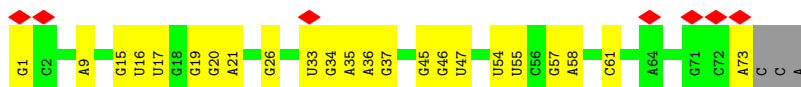
- Molecule 73: RPS29A isoform 1



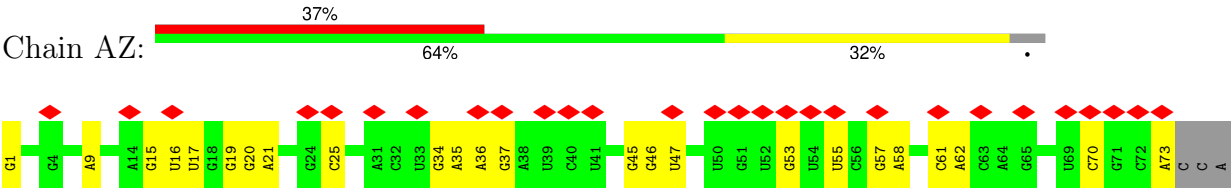
- Molecule 74: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 75: Transfer RNA



- Molecule 75: Transfer RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	87939	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	44.862	Depositor
Minimum map value	-22.382	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.6	Depositor
Map size (Å)	652.8, 652.8, 652.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	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	0.53	0/1948	0.72	1/2617 (0.0%)
2	B	0.53	0/3146	0.70	2/4228 (0.0%)
3	C	0.50	0/2800	0.71	3/3790 (0.1%)
4	D	0.40	0/2425	0.66	1/3271 (0.0%)
5	E	0.42	0/1260	0.63	1/1694 (0.1%)
6	F	0.53	0/1821	0.66	1/2451 (0.0%)
7	G	0.41	0/1836	0.60	0/2481
8	H	0.32	0/1539	0.64	0/2073
9	I	0.32	0/1741	0.66	1/2335 (0.0%)
10	J	0.33	0/1374	0.68	0/1842
11	L	0.46	0/1568	0.76	1/2106 (0.0%)
12	M	0.41	0/1068	0.65	0/1438
13	N	0.54	0/1757	0.76	0/2354
14	O	0.55	0/1585	0.67	1/2128 (0.0%)
15	P	0.50	0/1443	0.67	1/1944 (0.1%)
16	Q	0.49	0/1465	0.73	0/1965
17	R	0.44	0/1538	0.73	2/2050 (0.1%)
18	S	0.45	0/1481	0.64	0/1990
19	T	0.46	0/1300	0.66	0/1743
20	U	0.38	0/812	0.61	0/1099
21	V	0.49	0/1018	0.68	0/1369
22	W	0.49	0/533	0.68	1/707 (0.1%)
23	X	0.48	0/979	0.63	0/1321
24	Y	0.43	0/1004	0.69	1/1341 (0.1%)
25	Z	0.43	0/1118	0.61	1/1497 (0.1%)
26	AA	0.32	0/789	0.57	0/1067
27	AB	0.31	0/1185	0.67	0/1598
28	1	0.75	1/74506 (0.0%)	1.00	90/116154 (0.1%)
29	3	0.65	0/2883	0.94	1/4491 (0.0%)
30	4	0.73	0/3746	0.98	4/5832 (0.1%)
31	a	0.50	0/1204	0.69	1/1612 (0.1%)
32	b	0.37	0/473	0.66	2/629 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.44	0/751	0.64	1/1008 (0.1%)
34	d	0.49	0/897	0.68	0/1205
35	e	0.49	0/1041	0.67	0/1394
36	f	0.57	0/868	0.72	0/1168
37	g	0.47	0/890	0.75	1/1189 (0.1%)
38	h	0.41	0/978	0.71	1/1301 (0.1%)
39	i	0.40	0/778	0.70	0/1034
40	j	0.50	0/696	0.78	1/923 (0.1%)
41	k	0.38	0/618	0.63	0/826
42	l	0.44	0/443	0.79	0/588
43	n	0.40	0/228	1.10	1/293 (0.3%)
44	o	0.40	0/860	0.69	1/1136 (0.1%)
45	p	0.49	0/701	0.73	0/934
46	2	0.36	0/40725	0.94	58/63454 (0.1%)
47	q	0.31	0/1617	0.65	1/2215 (0.0%)
48	r	0.32	0/1735	0.68	0/2335
49	s	0.32	0/1665	0.62	0/2263
50	t	0.31	0/1759	0.69	0/2368
51	u	0.31	0/2109	0.66	0/2839
52	v	0.30	0/1629	0.66	1/2202 (0.0%)
53	w	0.32	0/1814	0.72	1/2425 (0.0%)
54	x	0.33	0/1506	0.69	1/2028 (0.0%)
55	y	0.31	0/1514	0.73	2/2021 (0.1%)
56	z	0.32	0/1519	0.69	0/2035
57	AD	0.34	0/1215	0.73	0/1638
58	AE	0.31	0/901	0.70	0/1217
59	AF	0.32	0/998	0.66	0/1341
60	AG	0.33	0/1125	0.64	0/1510
61	AH	0.31	0/935	0.67	0/1254
62	AI	0.31	0/1211	0.66	0/1628
63	AJ	0.33	0/1130	0.66	0/1517
64	AK	0.30	0/865	0.64	0/1169
65	AL	0.33	0/693	0.68	0/935
66	AM	0.32	0/1038	0.68	1/1395 (0.1%)
67	AN	0.31	0/1139	0.68	0/1518
68	AO	0.32	0/1087	0.69	1/1449 (0.1%)
69	AP	0.30	0/571	0.62	0/768
70	AQ	0.33	0/782	0.78	1/1047 (0.1%)
71	AR	0.30	0/620	0.67	0/838
72	AS	0.31	0/499	0.73	0/670
73	AT	0.33	0/452	0.73	1/600 (0.2%)
74	AV	0.29	0/2490	0.60	0/3389
75	AX	0.39	1/1749 (0.1%)	0.87	0/2724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	AZ	0.36	1/1749 (0.1%)	0.86	0/2724
All	All	0.55	3/211935 (0.0%)	0.88	190/311732 (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	2
4	D	0	1
6	F	0	1
7	G	0	2
10	J	0	3
11	L	0	1
14	O	0	2
16	Q	0	1
19	T	0	1
21	V	0	2
36	f	0	2
38	h	0	1
40	j	0	2
43	n	0	1
44	o	0	2
47	q	0	1
48	r	0	1
51	u	0	3
53	w	0	1
54	x	0	1
55	y	0	1
56	z	0	1
57	AD	0	2
58	AE	0	2
70	AQ	0	4
71	AR	0	1
All	All	0	43

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
75	AX	1	G	OP3-P	-10.70	1.48	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
75	AZ	1	G	OP3-P	-10.61	1.48	1.61
28	1	1561	G	O3'-P	5.90	1.68	1.61

All (190) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	2	94	U	C2-N3-C4	19.84	138.90	127.00
28	1	2545	C	C6-N1-C2	-11.16	115.84	120.30
28	1	1872	C	C6-N1-C2	-10.62	116.05	120.30
46	2	94	U	N1-C2-N3	9.80	120.78	114.90
46	2	94	U	N3-C4-C5	9.37	120.22	114.60
28	1	1872	C	N3-C2-O2	-9.32	115.37	121.90
28	1	3357	U	C5-C4-O4	9.23	131.44	125.90
28	1	2546	C	N3-C2-O2	-9.00	115.60	121.90
28	1	2546	C	N1-C2-O2	8.93	124.26	118.90
28	1	1907	C	C6-N1-C2	-8.92	116.73	120.30
28	1	1907	C	N3-C2-O2	-8.68	115.82	121.90
28	1	1907	C	N1-C2-O2	8.56	124.04	118.90
28	1	1872	C	N1-C2-O2	8.13	123.78	118.90
46	2	849	C	N3-C2-O2	-8.13	116.21	121.90
46	2	736	C	N3-C2-O2	-8.03	116.28	121.90
30	4	100	U	N3-C2-O2	-7.87	116.69	122.20
28	1	2924	U	C6-N1-C2	-7.81	116.31	121.00
37	g	81	CYS	CA-CB-SG	7.69	127.84	114.00
28	1	1496	C	C6-N1-C2	-7.56	117.28	120.30
28	1	2924	U	N3-C2-O2	-7.52	116.94	122.20
28	1	2545	C	N3-C2-O2	-7.50	116.65	121.90
3	C	182	LEU	CA-CB-CG	7.49	132.52	115.30
46	2	70	C	N1-C2-O2	7.47	123.38	118.90
46	2	1064	G	C4-N9-C1'	7.38	136.09	126.50
46	2	1028	C	C6-N1-C2	-7.23	117.41	120.30
46	2	849	C	N1-C2-O2	7.18	123.21	118.90
28	1	2644	C	C6-N1-C2	-7.08	117.47	120.30
30	4	100	U	N1-C2-O2	6.82	127.57	122.80
46	2	1064	G	C8-N9-C1'	-6.78	118.19	127.00
28	1	3181	C	N1-C2-O2	6.76	122.96	118.90
43	n	6	ARG	NE-CZ-NH2	-6.74	116.93	120.30
28	1	2836	C	N1-C2-O2	6.71	122.93	118.90
28	1	3357	U	N3-C4-O4	-6.65	114.74	119.40
46	2	736	C	C6-N1-C2	-6.61	117.66	120.30
28	1	260	C	N3-C2-O2	-6.60	117.28	121.90
28	1	1705	U	N3-C2-O2	-6.56	117.61	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	376	G	O4'-C1'-N9	6.52	113.41	108.20
46	2	736	C	N1-C2-O2	6.48	122.79	118.90
46	2	1653	C	N3-C2-O2	-6.48	117.36	121.90
46	2	1494	C	N3-C2-O2	-6.46	117.38	121.90
28	1	3181	C	C2-N1-C1'	6.43	125.88	118.80
28	1	3058	U	C2-N1-C1'	6.43	125.42	117.70
46	2	1216	C	C6-N1-C2	-6.41	117.74	120.30
46	2	1064	G	N3-C4-N9	6.41	129.84	126.00
28	1	175	C	N3-C2-O2	-6.40	117.42	121.90
46	2	543	C	N3-C2-O2	-6.40	117.42	121.90
28	1	1561	G	P-O3'-C3'	6.36	127.33	119.70
28	1	2836	C	C2-N1-C1'	6.35	125.78	118.80
46	2	647	G	C4-N9-C1'	6.35	134.75	126.50
46	2	244	A	O5'-P-OP1	-6.33	100.00	105.70
28	1	543	C	C6-N1-C2	-6.32	117.77	120.30
68	AO	32	ARG	NE-CZ-NH1	-6.29	117.16	120.30
28	1	3111	U	C5-C4-O4	-6.28	122.14	125.90
28	1	1525	G	C4-N9-C1'	6.25	134.63	126.50
46	2	768	C	C6-N1-C2	-6.24	117.80	120.30
28	1	260	C	N1-C2-O2	6.23	122.64	118.90
30	4	100	U	C6-N1-C2	-6.22	117.27	121.00
46	2	70	C	N3-C2-O2	-6.18	117.57	121.90
28	1	895	A	C4-C5-N7	6.15	113.78	110.70
28	1	2924	U	C5-C6-N1	6.15	125.77	122.70
28	1	2568	C	C6-N1-C2	-6.11	117.86	120.30
28	1	347	G	C8-N9-C4	-6.10	103.96	106.40
28	1	3233	C	C6-N1-C2	-6.08	117.87	120.30
46	2	1144	U	C2-N1-C1'	6.07	124.99	117.70
46	2	1404	C	N3-C2-O2	-6.05	117.66	121.90
28	1	1657	C	C6-N1-C2	-5.98	117.91	120.30
28	1	1705	U	N1-C2-O2	5.98	126.98	122.80
28	1	1631	C	N3-C2-O2	-5.96	117.73	121.90
46	2	294	C	N1-C2-O2	5.94	122.47	118.90
28	1	1631	C	N1-C2-O2	5.93	122.46	118.90
28	1	406	G	O4'-C1'-N9	5.88	112.91	108.20
28	1	895	A	N9-C4-C5	-5.88	103.45	105.80
28	1	3225	C	C6-N1-C2	-5.85	117.96	120.30
46	2	294	C	N3-C2-O2	-5.85	117.81	121.90
46	2	1653	C	N1-C2-O2	5.84	122.41	118.90
28	1	895	A	C6-C5-N7	-5.84	128.21	132.30
46	2	1788	G	N1-C2-N2	-5.83	110.96	116.20
28	1	2534	G	N1-C6-O6	-5.82	116.41	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	350	C	C6-N1-C2	-5.80	117.98	120.30
28	1	2225	U	C2-N1-C1'	5.80	124.66	117.70
17	R	64	ARG	NE-CZ-NH1	5.77	123.19	120.30
28	1	2114	C	C6-N1-C2	-5.77	117.99	120.30
46	2	1664	C	C6-N1-C2	-5.74	118.01	120.30
44	o	41	ARG	NE-CZ-NH1	5.73	123.17	120.30
28	1	3181	C	N3-C2-O2	-5.72	117.89	121.90
46	2	1025	A	O4'-C1'-N9	5.72	112.78	108.20
28	1	1496	C	C2-N1-C1'	5.70	125.07	118.80
28	1	2405	C	C6-N1-C2	-5.69	118.02	120.30
28	1	1496	C	N1-C2-O2	5.69	122.31	118.90
46	2	543	C	N1-C2-O2	5.68	122.31	118.90
29	3	35	C	C6-N1-C2	-5.67	118.03	120.30
46	2	1784	C	N3-C2-O2	-5.67	117.93	121.90
46	2	747	C	C6-N1-C2	-5.64	118.04	120.30
28	1	1872	C	C5-C6-N1	5.63	123.81	121.00
46	2	849	C	C6-N1-C2	-5.61	118.05	120.30
2	B	26	ARG	NE-CZ-NH1	5.61	123.11	120.30
28	1	1525	G	C8-N9-C1'	-5.59	119.73	127.00
46	2	1513	G	C8-N9-C1'	5.58	134.26	127.00
2	B	97	ARG	NE-CZ-NH1	5.57	123.09	120.30
28	1	1705	U	C2-N1-C1'	5.56	124.37	117.70
46	2	1788	G	N3-C2-N2	5.55	123.79	119.90
30	4	100	U	C5-C6-N1	5.55	125.47	122.70
53	w	87	ARG	NE-CZ-NH1	5.52	123.06	120.30
28	1	3013	U	C2-N1-C1'	5.52	124.32	117.70
3	C	197	ARG	NE-CZ-NH1	5.51	123.06	120.30
46	2	1082	C	C6-N1-C2	-5.50	118.10	120.30
28	1	2546	C	C6-N1-C2	-5.47	118.11	120.30
46	2	1652	C	C6-N1-C2	-5.47	118.11	120.30
14	O	101	ARG	NE-CZ-NH1	5.46	123.03	120.30
3	C	76	ARG	NE-CZ-NH1	5.45	123.03	120.30
28	1	2266	U	N1-C2-O2	5.45	126.61	122.80
46	2	243	G	P-O3'-C3'	5.44	126.23	119.70
28	1	2266	U	C2-N1-C1'	5.44	124.23	117.70
15	P	61	ARG	NE-CZ-NH1	5.43	123.02	120.30
28	1	175	C	C6-N1-C2	-5.43	118.13	120.30
1	A	42	ARG	NE-CZ-NH1	5.43	123.01	120.30
28	1	1907	C	C2-N1-C1'	5.42	124.76	118.80
28	1	1872	C	C2-N1-C1'	5.42	124.76	118.80
46	2	393	C	C6-N1-C2	-5.40	118.14	120.30
22	W	56	ARG	NE-CZ-NH1	5.39	123.00	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	2612	U	N3-C4-O4	5.36	123.15	119.40
46	2	1686	C	N3-C2-O2	-5.36	118.15	121.90
28	1	1566	A	N1-C2-N3	5.36	131.98	129.30
46	2	1571	C	N3-C2-O2	-5.35	118.16	121.90
46	2	647	G	C8-N9-C1'	-5.34	120.05	127.00
6	F	160	ARG	NE-CZ-NH1	5.33	122.97	120.30
46	2	1787	C	N1-C2-O2	5.33	122.09	118.90
46	2	70	C	C6-N1-C2	-5.31	118.18	120.30
52	v	219	ARG	NE-CZ-NH2	5.30	122.95	120.30
32	b	41	ARG	NE-CZ-NH1	5.30	122.95	120.30
28	1	3384	U	N3-C2-O2	-5.30	118.49	122.20
4	D	282	ARG	NE-CZ-NH1	5.28	122.94	120.30
46	2	1332	C	C6-N1-C2	-5.27	118.19	120.30
5	E	78	ARG	NE-CZ-NH1	5.27	122.94	120.30
28	1	1858	A	O4'-C1'-N9	5.27	112.41	108.20
28	1	2534	G	N3-C2-N2	5.25	123.58	119.90
46	2	1716	C	N3-C2-O2	-5.25	118.22	121.90
28	1	1604	G	C4-N9-C1'	5.24	133.31	126.50
28	1	2612	U	C5-C4-O4	-5.24	122.76	125.90
33	c	35	ARG	NE-CZ-NH1	5.24	122.92	120.30
28	1	1566	A	N7-C8-N9	5.24	116.42	113.80
9	I	7	ARG	NE-CZ-NH1	5.23	122.92	120.30
28	1	2545	C	C6-N1-C1'	5.23	127.07	120.80
46	2	94	U	N3-C2-O2	-5.23	118.54	122.20
24	Y	126	LEU	CA-CB-CG	5.20	127.26	115.30
46	2	1788	G	C6-C5-N7	-5.20	127.28	130.40
28	1	2616	C	C6-N1-C2	-5.20	118.22	120.30
38	h	86	ARG	NE-CZ-NH1	5.20	122.90	120.30
46	2	1765	A	N1-C6-N6	-5.19	115.48	118.60
73	AT	44	ARG	NE-CZ-NH1	5.19	122.89	120.30
46	2	1441	C	N3-C2-O2	-5.18	118.27	121.90
28	1	650	C	N1-C2-O2	5.17	122.00	118.90
46	2	1127	G	C4-N9-C1'	5.17	133.23	126.50
46	2	1624	C	C6-N1-C2	-5.17	118.23	120.30
28	1	2266	U	N3-C2-O2	-5.16	118.58	122.20
47	q	40	ALA	C-N-CA	5.15	134.57	121.70
54	x	47	ARG	NE-CZ-NH1	5.15	122.87	120.30
46	2	1494	C	C6-N1-C2	-5.14	118.24	120.30
28	1	3384	U	C2-N1-C1'	5.14	123.86	117.70
11	L	35	ARG	NE-CZ-NH1	5.14	122.87	120.30
32	b	18	ARG	NE-CZ-NH1	5.12	122.86	120.30
46	2	81	G	N3-C2-N2	5.12	123.48	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	1282	G	C8-N9-C4	-5.11	104.36	106.40
28	1	2644	C	N1-C2-O2	5.11	121.97	118.90
46	2	1144	U	N3-C2-O2	-5.11	118.63	122.20
28	1	3013	U	N1-C2-O2	5.10	126.37	122.80
28	1	2534	G	N1-C2-N2	-5.09	111.62	116.20
28	1	1866	C	C6-N1-C2	-5.09	118.26	120.30
66	AM	128	PHE	CB-CG-CD1	5.08	124.36	120.80
28	1	2374	C	C6-N1-C2	-5.08	118.27	120.30
28	1	347	G	N7-C8-N9	5.07	115.64	113.10
28	1	2924	U	N1-C2-O2	5.07	126.35	122.80
31	a	139	ARG	NE-CZ-NH1	5.07	122.83	120.30
28	1	2545	C	C5-C6-N1	5.06	123.53	121.00
28	1	637	C	C6-N1-C2	-5.06	118.28	120.30
28	1	3092	C	N1-C2-O2	5.06	121.94	118.90
28	1	2627	C	C6-N1-C2	-5.05	118.28	120.30
70	AQ	92	ARG	NE-CZ-NH1	5.05	122.83	120.30
46	2	761	G	C8-N9-C4	-5.05	104.38	106.40
28	1	3013	U	N3-C2-O2	-5.05	118.67	122.20
28	1	1565	G	C4-C5-N7	5.05	112.82	110.80
40	j	55	ARG	NE-CZ-NH1	5.05	122.82	120.30
28	1	3123	A	N9-C4-C5	-5.04	103.78	105.80
46	2	1158	C	C6-N1-C2	-5.04	118.28	120.30
25	Z	84	ARG	NE-CZ-NH2	5.04	122.82	120.30
55	y	92	ARG	NE-CZ-NH1	5.03	122.82	120.30
55	y	25	ARG	NE-CZ-NH1	5.03	122.81	120.30
17	R	42	ARG	NE-CZ-NH1	5.02	122.81	120.30
28	1	1496	C	C5-C6-N1	5.02	123.51	121.00
46	2	1064	G	N3-C4-C5	-5.00	126.10	128.60

There are no chirality outliers.

All (43) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	143	GLU	Peptide
57	AD	138	ASN	Peptide
57	AD	44	GLY	Peptide
58	AE	122	PRO	Peptide
58	AE	123	SER	Peptide
70	AQ	10	ARG	Peptide
70	AQ	43	ASN	Peptide
70	AQ	47	ALA	Peptide
70	AQ	59	TYR	Peptide

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Mol	Chain	Res	Type	Group
71	AR	75	GLU	Peptide
3	C	182	LEU	Peptide
3	C	318	LEU	Peptide
4	D	258	LYS	Peptide
6	F	157	ASN	Peptide
7	G	156	ASP	Peptide
7	G	76	ALA	Peptide
10	J	166	LYS	Peptide
10	J	73	GLY	Peptide
10	J	74	PRO	Peptide
11	L	47	ALA	Peptide
14	O	110	PRO	Peptide
14	O	36	VAL	Peptide
16	Q	161	LYS	Peptide
19	T	17	ARG	Peptide
21	V	104	ASN	Peptide
21	V	92	PHE	Peptide
36	f	57	LYS	Peptide
36	f	58	GLU	Peptide
38	h	90	ARG	Peptide
40	j	5	THR	Peptide
40	j	64	MET	Peptide
43	n	9	ARG	Peptide
44	o	66	LYS	Peptide
44	o	7	THR	Peptide
47	q	112	THR	Peptide
48	r	177	GLN	Peptide
51	u	192	ILE	Peptide
51	u	194	THR	Peptide
51	u	233	LYS	Peptide
53	w	9	VAL	Peptide
54	x	155	ASP	Peptide
55	y	40	ALA	Peptide
56	z	163	PRO	Peptide

5.2 Too-close contacts ⓘ

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/254 (98%)	238 (95%)	12 (5%)	0	100	100
2	B	384/387 (99%)	357 (93%)	27 (7%)	0	100	100
3	C	359/362 (99%)	320 (89%)	38 (11%)	1 (0%)	37	69
4	D	294/297 (99%)	267 (91%)	26 (9%)	1 (0%)	37	69
5	E	152/176 (86%)	142 (93%)	10 (7%)	0	100	100
6	F	220/244 (90%)	201 (91%)	18 (8%)	1 (0%)	25	60
7	G	231/256 (90%)	211 (91%)	20 (9%)	0	100	100
8	H	189/191 (99%)	164 (87%)	25 (13%)	0	100	100
9	I	207/221 (94%)	192 (93%)	15 (7%)	0	100	100
10	J	167/174 (96%)	144 (86%)	23 (14%)	0	100	100
11	L	191/199 (96%)	162 (85%)	25 (13%)	4 (2%)	5	31
12	M	134/138 (97%)	122 (91%)	12 (9%)	0	100	100
13	N	201/204 (98%)	183 (91%)	18 (9%)	0	100	100
14	O	195/199 (98%)	177 (91%)	16 (8%)	2 (1%)	13	47
15	P	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
16	Q	183/186 (98%)	173 (94%)	10 (6%)	0	100	100
17	R	186/189 (98%)	174 (94%)	12 (6%)	0	100	100
18	S	170/172 (99%)	158 (93%)	12 (7%)	0	100	100
19	T	157/160 (98%)	142 (90%)	15 (10%)	0	100	100
20	U	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
21	V	134/137 (98%)	122 (91%)	11 (8%)	1 (1%)	19	54
22	W	61/155 (39%)	58 (95%)	3 (5%)	0	100	100
23	X	119/142 (84%)	115 (97%)	4 (3%)	0	100	100
24	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
25	Z	133/136 (98%)	118 (89%)	15 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	AA	94/105 (90%)	79 (84%)	15 (16%)	0	100	100
27	AB	142/156 (91%)	123 (87%)	19 (13%)	0	100	100
31	a	146/149 (98%)	125 (86%)	20 (14%)	1 (1%)	19	54
32	b	56/59 (95%)	47 (84%)	9 (16%)	0	100	100
33	c	95/105 (90%)	86 (90%)	9 (10%)	0	100	100
34	d	107/113 (95%)	101 (94%)	6 (6%)	0	100	100
35	e	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	51
36	f	104/107 (97%)	97 (93%)	5 (5%)	2 (2%)	6	34
37	g	110/121 (91%)	101 (92%)	9 (8%)	0	100	100
38	h	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
39	i	97/100 (97%)	81 (84%)	16 (16%)	0	100	100
40	j	85/88 (97%)	73 (86%)	11 (13%)	1 (1%)	11	43
41	k	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
42	l	48/51 (94%)	40 (83%)	6 (12%)	2 (4%)	2	17
43	n	23/25 (92%)	16 (70%)	7 (30%)	0	100	100
44	o	103/106 (97%)	83 (81%)	20 (19%)	0	100	100
45	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
47	q	204/252 (81%)	166 (81%)	36 (18%)	2 (1%)	13	47
48	r	212/255 (83%)	184 (87%)	28 (13%)	0	100	100
49	s	215/254 (85%)	195 (91%)	20 (9%)	0	100	100
50	t	221/240 (92%)	198 (90%)	23 (10%)	0	100	100
51	u	258/261 (99%)	204 (79%)	53 (20%)	1 (0%)	30	64
52	v	204/225 (91%)	178 (87%)	26 (13%)	0	100	100
53	w	221/236 (94%)	173 (78%)	47 (21%)	1 (0%)	25	60
54	x	182/190 (96%)	160 (88%)	22 (12%)	0	100	100
55	y	184/200 (92%)	159 (86%)	25 (14%)	0	100	100
56	z	183/197 (93%)	166 (91%)	17 (9%)	0	100	100
57	AD	148/151 (98%)	130 (88%)	14 (10%)	4 (3%)	4	26
58	AE	125/138 (91%)	114 (91%)	11 (9%)	0	100	100
59	AF	122/142 (86%)	107 (88%)	15 (12%)	0	100	100
60	AG	139/143 (97%)	122 (88%)	17 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AH	116/136 (85%)	102 (88%)	14 (12%)	0	100	100
62	AI	143/146 (98%)	125 (87%)	18 (13%)	0	100	100
63	AJ	141/144 (98%)	131 (93%)	10 (7%)	0	100	100
64	AK	105/121 (87%)	95 (90%)	10 (10%)	0	100	100
65	AL	85/87 (98%)	71 (84%)	14 (16%)	0	100	100
66	AM	127/130 (98%)	115 (91%)	11 (9%)	1 (1%)	16	51
67	AN	142/145 (98%)	119 (84%)	23 (16%)	0	100	100
68	AO	132/135 (98%)	109 (83%)	23 (17%)	0	100	100
69	AP	68/108 (63%)	60 (88%)	8 (12%)	0	100	100
70	AQ	95/119 (80%)	62 (65%)	32 (34%)	1 (1%)	12	44
71	AR	79/82 (96%)	64 (81%)	14 (18%)	1 (1%)	10	41
72	AS	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
73	AT	51/56 (91%)	43 (84%)	8 (16%)	0	100	100
74	AV	316/319 (99%)	287 (91%)	29 (9%)	0	100	100
All	All	10615/11395 (93%)	9433 (89%)	1154 (11%)	28 (0%)	38	69

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	339	LEU
14	O	111	PRO
36	f	58	GLU
47	q	113	ARG
11	L	48	PRO
35	e	79	VAL
36	f	59	VAL
40	j	65	ARG
11	L	77	LEU
14	O	110	PRO
21	V	105	PRO
47	q	112	THR
57	AD	85	PRO
57	AD	105	ASN
71	AR	76	GLY
4	D	20	PHE
31	a	78	LEU
53	w	10	ASN

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Mol	Chain	Res	Type
57	AD	139	TRP
70	AQ	11	ASN
11	L	63	VAL
42	l	30	ARG
57	AD	104	ARG
6	F	158	LYS
42	l	31	THR
11	L	47	ALA
51	u	234	PRO
66	AM	67	GLY

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%)	192 (100%)	1 (0%)	86	93
2	B	321/323 (99%)	317 (99%)	4 (1%)	67	85
3	C	288/289 (100%)	288 (100%)	0	100	100
4	D	244/245 (100%)	244 (100%)	0	100	100
5	E	134/153 (88%)	133 (99%)	1 (1%)	81	92
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%)	168 (98%)	3 (2%)	54	77
9	I	177/187 (95%)	175 (99%)	2 (1%)	70	86
10	J	147/151 (97%)	146 (99%)	1 (1%)	81	92
11	L	154/159 (97%)	153 (99%)	1 (1%)	84	92
12	M	107/109 (98%)	106 (99%)	1 (1%)	75	89
13	N	175/176 (99%)	175 (100%)	0	100	100
14	O	160/162 (99%)	160 (100%)	0	100	100
15	P	140/146 (96%)	139 (99%)	1 (1%)	81	92
16	Q	150/151 (99%)	149 (99%)	1 (1%)	81	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	R	153/154 (99%)	152 (99%)	1 (1%)	81	92
18	S	156/156 (100%)	156 (100%)	0	100	100
19	T	136/137 (99%)	136 (100%)	0	100	100
20	U	87/107 (81%)	87 (100%)	0	100	100
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%)	104 (100%)	0	100	100
24	Y	109/110 (99%)	108 (99%)	1 (1%)	75	89
25	Z	115/116 (99%)	111 (96%)	4 (4%)	31	63
26	AA	77/98 (79%)	76 (99%)	1 (1%)	65	83
27	AB	129/137 (94%)	128 (99%)	1 (1%)	79	90
31	a	118/119 (99%)	117 (99%)	1 (1%)	79	90
32	b	46/47 (98%)	46 (100%)	0	100	100
33	c	81/88 (92%)	80 (99%)	1 (1%)	67	85
34	d	94/97 (97%)	94 (100%)	0	100	100
35	e	109/111 (98%)	109 (100%)	0	100	100
36	f	90/91 (99%)	90 (100%)	0	100	100
37	g	95/103 (92%)	94 (99%)	1 (1%)	70	86
38	h	104/105 (99%)	104 (100%)	0	100	100
39	i	81/82 (99%)	81 (100%)	0	100	100
40	j	70/71 (99%)	70 (100%)	0	100	100
41	k	68/69 (99%)	68 (100%)	0	100	100
42	l	45/46 (98%)	45 (100%)	0	100	100
43	n	22/23 (96%)	20 (91%)	2 (9%)	7	29
44	o	90/91 (99%)	90 (100%)	0	100	100
45	p	71/72 (99%)	71 (100%)	0	100	100
47	q	164/210 (78%)	164 (100%)	0	100	100
48	r	191/224 (85%)	190 (100%)	1 (0%)	86	93
49	s	176/205 (86%)	174 (99%)	2 (1%)	70	86
50	t	182/195 (93%)	181 (100%)	1 (0%)	86	93
51	u	221/222 (100%)	220 (100%)	1 (0%)	86	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	v	173/191 (91%)	172 (99%)	1 (1%)	84	92
53	w	189/201 (94%)	189 (100%)	0	100	100
54	x	165/170 (97%)	161 (98%)	4 (2%)	44	71
55	y	150/161 (93%)	148 (99%)	2 (1%)	65	83
56	z	158/166 (95%)	157 (99%)	1 (1%)	84	92
57	AD	127/128 (99%)	127 (100%)	0	100	100
58	AE	81/105 (77%)	81 (100%)	0	100	100
59	AF	101/118 (86%)	99 (98%)	2 (2%)	50	75
60	AG	117/119 (98%)	116 (99%)	1 (1%)	75	89
61	AH	94/124 (76%)	93 (99%)	1 (1%)	70	86
62	AI	128/129 (99%)	128 (100%)	0	100	100
63	AJ	115/116 (99%)	114 (99%)	1 (1%)	75	89
64	AK	100/114 (88%)	99 (99%)	1 (1%)	73	87
65	AL	74/74 (100%)	73 (99%)	1 (1%)	62	82
66	AM	110/111 (99%)	110 (100%)	0	100	100
67	AN	119/120 (99%)	118 (99%)	1 (1%)	79	90
68	AO	112/113 (99%)	111 (99%)	1 (1%)	75	89
69	AP	61/89 (68%)	61 (100%)	0	100	100
70	AQ	83/100 (83%)	82 (99%)	1 (1%)	67	85
71	AR	70/71 (99%)	69 (99%)	1 (1%)	62	82
72	AS	56/60 (93%)	56 (100%)	0	100	100
73	AT	47/49 (96%)	47 (100%)	0	100	100
74	AV	259/262 (99%)	259 (100%)	0	100	100
All	All	8966/9560 (94%)	8913 (99%)	53 (1%)	82	92

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	247	ARG
2	B	10	ARG
2	B	85	VAL
2	B	196	ARG
2	B	332	ARG
5	E	46	ARG

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Mol	Chain	Res	Type
8	H	49	ASN
8	H	87	LYS
8	H	168	ARG
9	I	21	ARG
9	I	82	ARG
10	J	166	LYS
11	L	51	LEU
12	M	117	ARG
15	P	180	LYS
16	Q	12	ARG
17	R	153	LYS
24	Y	42	GLN
25	Z	23	VAL
25	Z	103	GLN
25	Z	112	LYS
25	Z	116	LYS
26	AA	28	ASN
27	AB	141	LYS
31	a	9	ARG
33	c	86	ARG
37	g	4	ARG
43	n	1	MET
43	n	18	ARG
48	r	41	ARG
49	s	97	ARG
49	s	201	ASN
50	t	194	LYS
51	u	71	LYS
52	v	72	HIS
54	x	35	LYS
54	x	39	ARG
54	x	107	ARG
54	x	124	LYS
55	y	18	ARG
55	y	31	ARG
56	z	48	GLN
59	AF	52	LYS
59	AF	108	ARG
60	AG	68	ARG
61	AH	81	LYS
63	AJ	63	ARG
64	AK	79	TRP

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Mol	Chain	Res	Type
65	AL	78	LEU
67	AN	81	LYS
68	AO	34	ASN
70	AQ	10	ARG
71	AR	80	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
10	J	43	GLN
10	J	47	GLN
21	V	98	ASN
41	k	40	GLN
51	u	98	ASN
62	AI	12	GLN
62	AI	122	HIS
63	AJ	101	ASN
63	AJ	129	GLN
65	AL	70	ASN
68	AO	77	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	1	3109/3395 (91%)	680 (21%)	7 (0%)
29	3	120/121 (99%)	20 (16%)	0
30	4	157/158 (99%)	37 (23%)	0
46	2	1703/1800 (94%)	807 (47%)	13 (0%)
75	AX	72/76 (94%)	22 (30%)	0
75	AZ	72/76 (94%)	23 (31%)	0
All	All	5233/5626 (93%)	1589 (30%)	20 (0%)

All (1589) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	1	6	A
28	1	22	G
28	1	26	A
28	1	35	A
28	1	40	A

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Mol	Chain	Res	Type
28	1	43	A
28	1	49	A
28	1	50	U
28	1	60	A
28	1	65	A
28	1	66	A
28	1	75	G
28	1	92	G
28	1	93	C
28	1	96	G
28	1	110	G
28	1	111	C
28	1	113	C
28	1	117	U
28	1	118	U
28	1	120	G
28	1	121	A
28	1	134	U
28	1	136	G
28	1	149	U
28	1	156	G
28	1	157	A
28	1	161	G
28	1	163	C
28	1	164	A
28	1	165	A
28	1	168	U
28	1	169	U
28	1	171	G
28	1	172	G
28	1	175	C
28	1	182	U
28	1	190	U
28	1	191	U
28	1	200	C
28	1	211	A
28	1	219	A
28	1	220	G
28	1	234	G
28	1	240	U
28	1	241	G
28	1	242	C

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Mol	Chain	Res	Type
28	1	244	G
28	1	251	G
28	1	253	A
28	1	254	A
28	1	259	C
28	1	263	C
28	1	265	A
28	1	266	A
28	1	267	G
28	1	268	A
28	1	269	G
28	1	284	A
28	1	286	U
28	1	289	A
28	1	298	U
28	1	315	C
28	1	329	U
28	1	343	U
28	1	346	C
28	1	347	G
28	1	368	G
28	1	375	A
28	1	376	G
28	1	385	A
28	1	398	A
28	1	399	A
28	1	403	C
28	1	404	G
28	1	411	U
28	1	421	G
28	1	422	A
28	1	438	A
28	1	439	C
28	1	440	A
28	1	441	U
28	1	442	G
28	1	447	U
28	1	448	U
28	1	451	U
28	1	487	U
28	1	488	U
28	1	490	C

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Mol	Chain	Res	Type
28	1	492	C
28	1	494	G
28	1	495	G
28	1	498	A
28	1	512	U
28	1	520	U
28	1	521	A
28	1	523	A
28	1	533	A
28	1	534	U
28	1	535	G
28	1	540	U
28	1	541	U
28	1	542	G
28	1	543	C
28	1	544	C
28	1	552	G
28	1	553	U
28	1	554	A
28	1	555	U
28	1	557	A
28	1	558	U
28	1	559	A
28	1	560	G
28	1	582	G
28	1	597	G
28	1	604	G
28	1	607	A
28	1	611	A
28	1	619	A
28	1	620	U
28	1	621	A
28	1	645	A
28	1	649	A
28	1	662	U
28	1	677	A
28	1	678	G
28	1	681	U
28	1	691	A
28	1	705	A
28	1	712	G
28	1	715	A

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Mol	Chain	Res	Type
28	1	719	U
28	1	723	U
28	1	733	G
28	1	734	C
28	1	735	A
28	1	737	G
28	1	761	A
28	1	763	G
28	1	764	U
28	1	765	C
28	1	766	U
28	1	767	U
28	1	768	C
28	1	770	G
28	1	771	A
28	1	773	G
28	1	776	U
28	1	777	U
28	1	780	A
28	1	781	G
28	1	785	G
28	1	786	A
28	1	799	G
28	1	800	G
28	1	801	A
28	1	808	A
28	1	815	G
28	1	817	A
28	1	821	U
28	1	825	U
28	1	826	G
28	1	830	A
28	1	847	A
28	1	861	C
28	1	864	G
28	1	874	U
28	1	879	U
28	1	880	G
28	1	896	A
28	1	907	G
28	1	908	G
28	1	914	A

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Mol	Chain	Res	Type
28	1	916	G
28	1	923	C
28	1	937	G
28	1	944	C
28	1	953	G
28	1	959	C
28	1	960	U
28	1	974	G
28	1	978	G
28	1	979	U
28	1	980	A
28	1	984	G
28	1	985	U
28	1	994	G
28	1	1001	G
28	1	1002	A
28	1	1010	G
28	1	1011	A
28	1	1014	U
28	1	1015	U
28	1	1017	C
28	1	1018	G
28	1	1020	G
28	1	1024	G
28	1	1026	A
28	1	1027	A
28	1	1028	U
28	1	1029	G
28	1	1030	A
28	1	1031	C
28	1	1035	G
28	1	1036	A
28	1	1044	U
28	1	1047	A
28	1	1049	C
28	1	1063	G
28	1	1064	A
28	1	1066	G
28	1	1072	G
28	1	1075	A
28	1	1081	U
28	1	1093	A

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Mol	Chain	Res	Type
28	1	1094	U
28	1	1095	U
28	1	1097	G
28	1	1098	A
28	1	1103	A
28	1	1108	U
28	1	1116	G
28	1	1117	G
28	1	1122	U
28	1	1124	U
28	1	1131	G
28	1	1135	A
28	1	1153	A
28	1	1155	C
28	1	1157	G
28	1	1159	A
28	1	1163	A
28	1	1168	U
28	1	1177	G
28	1	1178	G
28	1	1180	A
28	1	1181	U
28	1	1190	A
28	1	1192	C
28	1	1196	C
28	1	1201	C
28	1	1203	A
28	1	1208	U
28	1	1215	U
28	1	1216	C
28	1	1217	A
28	1	1219	C
28	1	1220	U
28	1	1222	G
28	1	1223	A
28	1	1224	C
28	1	1226	G
28	1	1227	C
28	1	1228	C
28	1	1280	C
28	1	1281	G
28	1	1282	G

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Mol	Chain	Res	Type
28	1	1283	C
28	1	1285	G
28	1	1287	A
28	1	1288	U
28	1	1289	G
28	1	1294	A
28	1	1305	U
28	1	1307	G
28	1	1309	U
28	1	1313	G
28	1	1317	A
28	1	1330	A
28	1	1348	U
28	1	1350	A
28	1	1351	U
28	1	1352	A
28	1	1353	U
28	1	1356	U
28	1	1357	G
28	1	1366	A
28	1	1386	A
28	1	1399	A
28	1	1400	G
28	1	1408	G
28	1	1421	G
28	1	1434	G
28	1	1437	C
28	1	1443	G
28	1	1446	A
28	1	1458	U
28	1	1482	A
28	1	1483	G
28	1	1508	C
28	1	1511	U
28	1	1523	U
28	1	1527	C
28	1	1539	A
28	1	1555	U
28	1	1556	C
28	1	1561	G
28	1	1562	C
28	1	1563	C

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Mol	Chain	Res	Type
28	1	1566	A
28	1	1567	U
28	1	1568	U
28	1	1569	U
28	1	1570	U
28	1	1571	A
28	1	1572	U
28	1	1573	G
28	1	1575	A
28	1	1576	G
28	1	1577	G
28	1	1580	A
28	1	1581	C
28	1	1582	C
28	1	1583	A
28	1	1588	A
28	1	1589	A
28	1	1593	A
28	1	1605	A
28	1	1606	U
28	1	1613	A
28	1	1620	U
28	1	1627	U
28	1	1628	C
28	1	1629	U
28	1	1630	U
28	1	1636	U
28	1	1637	A
28	1	1642	A
28	1	1643	A
28	1	1645	U
28	1	1647	A
28	1	1657	C
28	1	1677	G
28	1	1694	U
28	1	1715	A
28	1	1717	U
28	1	1724	U
28	1	1741	A
28	1	1742	U
28	1	1750	A
28	1	1751	G

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Mol	Chain	Res	Type
28	1	1756	C
28	1	1761	C
28	1	1763	U
28	1	1764	U
28	1	1765	U
28	1	1770	G
28	1	1773	C
28	1	1775	G
28	1	1780	G
28	1	1795	U
28	1	1797	A
28	1	1808	G
28	1	1809	A
28	1	1812	G
28	1	1813	A
28	1	1814	A
28	1	1815	U
28	1	1817	G
28	1	1821	U
28	1	1822	C
28	1	1840	U
28	1	1842	A
28	1	1850	A
28	1	1855	U
28	1	1878	G
28	1	1879	A
28	1	1880	U
28	1	1886	A
28	1	1893	A
28	1	1906	G
28	1	1908	A
28	1	1926	C
28	1	1928	G
28	1	1948	G
28	1	1950	U
28	1	1952	G
28	1	1953	G
28	1	1954	G
28	1	1955	U
28	1	2094	C
28	1	2096	A
28	1	2111	G

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Mol	Chain	Res	Type
28	1	2112	U
28	1	2113	A
28	1	2122	G
28	1	2131	A
28	1	2138	A
28	1	2142	A
28	1	2158	A
28	1	2170	U
28	1	2178	A
28	1	2179	C
28	1	2188	A
28	1	2205	U
28	1	2206	G
28	1	2207	A
28	1	2208	A
28	1	2209	U
28	1	2210	G
28	1	2235	C
28	1	2244	A
28	1	2246	G
28	1	2255	A
28	1	2256	A
28	1	2258	U
28	1	2259	A
28	1	2260	U
28	1	2261	G
28	1	2262	A
28	1	2263	C
28	1	2265	C
28	1	2266	U
28	1	2269	U
28	1	2273	G
28	1	2274	U
28	1	2279	A
28	1	2281	A
28	1	2307	G
28	1	2308	C
28	1	2310	U
28	1	2313	A
28	1	2315	G
28	1	2319	U
28	1	2334	U

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Mol	Chain	Res	Type
28	1	2336	U
28	1	2359	C
28	1	2363	A
28	1	2373	A
28	1	2375	G
28	1	2388	U
28	1	2393	G
28	1	2397	A
28	1	2402	A
28	1	2403	G
28	1	2404	A
28	1	2411	U
28	1	2412	G
28	1	2428	U
28	1	2435	G
28	1	2442	G
28	1	2443	A
28	1	2507	C
28	1	2509	U
28	1	2514	U
28	1	2515	A
28	1	2522	G
28	1	2524	A
28	1	2525	G
28	1	2526	C
28	1	2529	A
28	1	2530	G
28	1	2531	C
28	1	2532	U
28	1	2533	G
28	1	2534	G
28	1	2535	A
28	1	2536	A
28	1	2537	U
28	1	2538	U
28	1	2540	A
28	1	2541	U
28	1	2542	U
28	1	2544	U
28	1	2545	C
28	1	2546	C
28	1	2549	G

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Mol	Chain	Res	Type
28	1	2552	C
28	1	2553	U
28	1	2555	G
28	1	2560	C
28	1	2561	A
28	1	2562	A
28	1	2563	G
28	1	2564	G
28	1	2566	C
28	1	2567	C
28	1	2568	C
28	1	2569	A
28	1	2570	U
28	1	2571	U
28	1	2572	C
28	1	2574	G
28	1	2579	G
28	1	2581	U
28	1	2585	G
28	1	2586	G
28	1	2587	U
28	1	2593	A
28	1	2594	C
28	1	2606	G
28	1	2607	G
28	1	2614	G
28	1	2635	A
28	1	2644	C
28	1	2645	G
28	1	2648	G
28	1	2652	U
28	1	2656	A
28	1	2672	G
28	1	2674	A
28	1	2676	A
28	1	2677	G
28	1	2681	U
28	1	2689	A
28	1	2691	A
28	1	2694	A
28	1	2695	A
28	1	2704	A

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Mol	Chain	Res	Type
28	1	2714	G
28	1	2726	C
28	1	2727	A
28	1	2728	G
28	1	2729	U
28	1	2737	C
28	1	2753	G
28	1	2760	C
28	1	2772	C
28	1	2773	C
28	1	2777	G
28	1	2778	G
28	1	2782	U
28	1	2783	U
28	1	2795	U
28	1	2796	G
28	1	2799	A
28	1	2800	G
28	1	2801	A
28	1	2802	A
28	1	2803	A
28	1	2804	A
28	1	2808	A
28	1	2810	C
28	1	2817	A
28	1	2828	G
28	1	2834	G
28	1	2836	C
28	1	2837	A
28	1	2838	A
28	1	2842	U
28	1	2844	C
28	1	2845	A
28	1	2846	U
28	1	2847	A
28	1	2850	G
28	1	2851	A
28	1	2858	U
28	1	2859	U
28	1	2861	U
28	1	2867	C
28	1	2871	G

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Mol	Chain	Res	Type
28	1	2872	A
28	1	2873	U
28	1	2875	U
28	1	2887	A
28	1	2898	G
28	1	2900	A
28	1	2923	U
28	1	2924	U
28	1	2925	C
28	1	2935	U
28	1	2936	A
28	1	2938	G
28	1	2941	A
28	1	2942	C
28	1	2945	G
28	1	2947	G
28	1	2956	A
28	1	2968	G
28	1	2971	A
28	1	2972	G
28	1	2983	C
28	1	2997	G
28	1	3011	A
28	1	3012	A
28	1	3017	A
28	1	3020	U
28	1	3021	A
28	1	3022	G
28	1	3023	U
28	1	3024	A
28	1	3026	G
28	1	3028	G
28	1	3029	A
28	1	3030	G
28	1	3031	G
28	1	3032	A
28	1	3033	A
28	1	3036	G
28	1	3059	G
28	1	3078	U
28	1	3080	G
28	1	3092	C

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Mol	Chain	Res	Type
28	1	3101	G
28	1	3104	U
28	1	3105	U
28	1	3109	G
28	1	3115	C
28	1	3116	G
28	1	3117	C
28	1	3119	U
28	1	3120	C
28	1	3121	U
28	1	3122	A
28	1	3129	A
28	1	3130	A
28	1	3131	U
28	1	3142	A
28	1	3143	C
28	1	3153	U
28	1	3154	C
28	1	3156	U
28	1	3157	U
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	3181	C
28	1	3187	A
28	1	3196	U
28	1	3198	U
28	1	3207	U
28	1	3208	G
28	1	3216	G
28	1	3217	C
28	1	3218	A
28	1	3219	G
28	1	3220	G
28	1	3222	U
28	1	3223	A
28	1	3224	G
28	1	3225	C
28	1	3226	A

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Mol	Chain	Res	Type
28	1	3227	A
28	1	3228	C
28	1	3229	G
28	1	3230	G
28	1	3231	U
28	1	3233	C
28	1	3238	G
28	1	3247	G
28	1	3253	G
28	1	3259	U
28	1	3261	C
28	1	3263	G
28	1	3268	A
28	1	3269	U
28	1	3273	A
28	1	3274	A
28	1	3276	G
28	1	3277	U
28	1	3279	A
28	1	3281	U
28	1	3294	A
28	1	3295	A
28	1	3304	U
28	1	3313	U
28	1	3316	A
28	1	3319	U
28	1	3320	A
28	1	3334	U
28	1	3335	A
28	1	3341	U
28	1	3345	G
28	1	3351	U
28	1	3352	U
28	1	3353	G
28	1	3356	G
28	1	3357	U
28	1	3368	U
28	1	3369	G
28	1	3378	C
28	1	3381	U
28	1	3382	U
28	1	3384	U

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Mol	Chain	Res	Type
28	1	3389	U
28	1	3390	G
28	1	3396	U
29	3	7	G
29	3	10	C
29	3	11	A
29	3	22	A
29	3	33	C
29	3	35	C
29	3	42	A
29	3	49	G
29	3	50	U
29	3	51	A
29	3	55	A
29	3	65	G
29	3	67	G
29	3	71	G
29	3	72	A
29	3	73	C
29	3	74	C
29	3	93	C
29	3	112	G
29	3	121	U
30	4	23	U
30	4	27	U
30	4	34	U
30	4	35	C
30	4	55	U
30	4	59	A
30	4	62	C
30	4	63	G
30	4	72	A
30	4	73	U
30	4	75	G
30	4	76	C
30	4	79	A
30	4	80	A
30	4	81	U
30	4	82	U
30	4	83	C
30	4	84	C
30	4	85	G

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Mol	Chain	Res	Type
30	4	86	U
30	4	87	G
30	4	88	A
30	4	90	U
30	4	91	C
30	4	95	G
30	4	97	A
30	4	104	A
30	4	106	C
30	4	112	U
30	4	113	U
30	4	114	G
30	4	120	C
30	4	127	U
30	4	138	A
30	4	148	G
30	4	152	G
30	4	158	U
46	2	2	A
46	2	3	U
46	2	4	C
46	2	10	G
46	2	15	U
46	2	25	C
46	2	26	A
46	2	30	G
46	2	33	U
46	2	36	C
46	2	37	U
46	2	39	A
46	2	40	A
46	2	41	A
46	2	42	G
46	2	43	A
46	2	44	U
46	2	45	U
46	2	46	A
46	2	47	A
46	2	48	G
46	2	49	C
46	2	50	C
46	2	56	U

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Mol	Chain	Res	Type
46	2	59	C
46	2	61	A
46	2	66	U
46	2	68	A
46	2	69	G
46	2	70	C
46	2	71	A
46	2	72	A
46	2	73	U
46	2	74	U
46	2	76	A
46	2	79	C
46	2	80	A
46	2	82	U
46	2	84	A
46	2	86	A
46	2	88	U
46	2	89	G
46	2	93	A
46	2	94	U
46	2	96	G
46	2	99	C
46	2	100	A
46	2	103	A
46	2	104	A
46	2	113	U
46	2	114	C
46	2	115	G
46	2	116	U
46	2	119	A
46	2	121	U
46	2	122	U
46	2	123	G
46	2	124	A
46	2	125	U
46	2	127	G
46	2	131	C
46	2	132	U
46	2	133	U
46	2	134	U
46	2	135	A
46	2	136	C

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Mol	Chain	Res	Type
46	2	141	U
46	2	142	G
46	2	143	G
46	2	144	U
46	2	147	A
46	2	148	A
46	2	149	C
46	2	150	U
46	2	152	U
46	2	153	G
46	2	154	G
46	2	156	A
46	2	157	A
46	2	158	U
46	2	159	U
46	2	160	C
46	2	161	U
46	2	162	A
46	2	164	A
46	2	167	U
46	2	170	U
46	2	171	A
46	2	174	U
46	2	175	G
46	2	177	U
46	2	178	U
46	2	180	A
46	2	181	A
46	2	182	A
46	2	187	G
46	2	189	C
46	2	191	C
46	2	193	U
46	2	194	U
46	2	195	G
46	2	196	G
46	2	197	A
46	2	199	G
46	2	200	A
46	2	202	A
46	2	204	G
46	2	208	U

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Mol	Chain	Res	Type
46	2	211	U
46	2	212	U
46	2	216	U
46	2	217	A
46	2	219	A
46	2	223	U
46	2	224	C
46	2	225	A
46	2	227	U
46	2	231	U
46	2	232	U
46	2	233	C
46	2	234	G
46	2	235	G
46	2	237	C
46	2	238	U
46	2	239	C
46	2	240	U
46	2	241	U
46	2	242	U
46	2	243	G
46	2	244	A
46	2	247	A
46	2	250	C
46	2	251	A
46	2	254	A
46	2	257	A
46	2	260	U
46	2	261	U
46	2	264	G
46	2	265	A
46	2	266	A
46	2	267	U
46	2	269	G
46	2	272	U
46	2	273	G
46	2	276	C
46	2	277	U
46	2	278	U
46	2	279	G
46	2	280	U
46	2	285	G

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Mol	Chain	Res	Type
46	2	287	G
46	2	288	A
46	2	290	G
46	2	292	U
46	2	293	U
46	2	294	C
46	2	297	U
46	2	299	A
46	2	302	U
46	2	303	U
46	2	308	C
46	2	309	C
46	2	313	U
46	2	314	C
46	2	316	A
46	2	320	U
46	2	321	C
46	2	322	G
46	2	323	A
46	2	337	G
46	2	342	C
46	2	343	C
46	2	344	A
46	2	345	U
46	2	349	U
46	2	350	U
46	2	351	C
46	2	352	A
46	2	354	C
46	2	359	A
46	2	360	A
46	2	361	C
46	2	375	U
46	2	379	U
46	2	380	U
46	2	381	C
46	2	388	G
46	2	391	A
46	2	393	C
46	2	398	G
46	2	400	A
46	2	402	C

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Mol	Chain	Res	Type
46	2	403	G
46	2	404	G
46	2	408	C
46	2	410	A
46	2	411	C
46	2	412	A
46	2	415	C
46	2	417	A
46	2	418	G
46	2	419	G
46	2	422	G
46	2	423	G
46	2	424	C
46	2	425	A
46	2	426	G
46	2	428	A
46	2	432	G
46	2	433	C
46	2	435	C
46	2	436	A
46	2	438	A
46	2	440	U
46	2	441	A
46	2	443	C
46	2	447	U
46	2	448	C
46	2	451	A
46	2	453	U
46	2	454	U
46	2	455	C
46	2	459	G
46	2	464	A
46	2	466	U
46	2	467	G
46	2	468	A
46	2	469	C
46	2	470	A
46	2	471	A
46	2	473	A
46	2	474	A
46	2	475	A
46	2	477	A

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Mol	Chain	Res	Type
46	2	478	A
46	2	485	A
46	2	487	G
46	2	489	C
46	2	491	C
46	2	492	A
46	2	495	C
46	2	497	G
46	2	498	G
46	2	502	U
46	2	503	G
46	2	504	U
46	2	505	A
46	2	507	U
46	2	508	U
46	2	509	G
46	2	511	A
46	2	513	U
46	2	514	G
46	2	515	A
46	2	518	A
46	2	519	C
46	2	525	A
46	2	526	A
46	2	533	U
46	2	534	A
46	2	538	A
46	2	539	G
46	2	540	G
46	2	541	A
46	2	542	A
46	2	543	C
46	2	544	A
46	2	545	A
46	2	546	U
46	2	551	G
46	2	553	G
46	2	557	G
46	2	558	U
46	2	561	G
46	2	563	U
46	2	564	G

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Mol	Chain	Res	Type
46	2	565	C
46	2	567	A
46	2	568	G
46	2	569	C
46	2	570	A
46	2	571	G
46	2	572	C
46	2	574	G
46	2	577	G
46	2	578	U
46	2	579	A
46	2	580	A
46	2	581	U
46	2	583	C
46	2	585	A
46	2	586	G
46	2	589	C
46	2	593	U
46	2	594	A
46	2	598	U
46	2	600	U
46	2	601	A
46	2	603	U
46	2	605	A
46	2	606	A
46	2	607	G
46	2	608	U
46	2	609	U
46	2	611	U
46	2	612	U
46	2	613	G
46	2	615	A
46	2	617	U
46	2	619	A
46	2	620	A
46	2	622	A
46	2	623	A
46	2	624	G
46	2	628	G
46	2	629	U
46	2	638	U
46	2	639	U

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Mol	Chain	Res	Type
46	2	640	U
46	2	643	G
46	2	645	C
46	2	646	C
46	2	647	G
46	2	648	G
46	2	649	U
46	2	650	U
46	2	651	G
46	2	652	G
46	2	686	C
46	2	687	G
46	2	688	G
46	2	689	G
46	2	690	G
46	2	691	C
46	2	692	C
46	2	693	U
46	2	694	U
46	2	695	U
46	2	696	C
46	2	698	U
46	2	699	U
46	2	700	C
46	2	702	G
46	2	703	G
46	2	704	C
46	2	705	U
46	2	706	A
46	2	707	A
46	2	731	C
46	2	732	G
46	2	733	A
46	2	734	A
46	2	735	C
46	2	736	C
46	2	737	A
46	2	738	G
46	2	739	G
46	2	740	A
46	2	741	C
46	2	742	U

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Mol	Chain	Res	Type
46	2	743	U
46	2	747	C
46	2	748	U
46	2	750	U
46	2	751	G
46	2	753	A
46	2	756	A
46	2	759	U
46	2	761	G
46	2	763	G
46	2	766	U
46	2	768	C
46	2	769	A
46	2	770	A
46	2	772	G
46	2	774	A
46	2	778	G
46	2	779	U
46	2	780	A
46	2	781	U
46	2	783	G
46	2	785	U
46	2	786	C
46	2	790	U
46	2	791	A
46	2	794	U
46	2	796	A
46	2	797	G
46	2	798	C
46	2	799	A
46	2	801	G
46	2	802	G
46	2	803	A
46	2	809	A
46	2	810	G
46	2	811	A
46	2	812	A
46	2	813	U
46	2	814	A
46	2	815	G
46	2	816	G
46	2	817	A

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Mol	Chain	Res	Type
46	2	819	G
46	2	820	U
46	2	821	U
46	2	824	G
46	2	825	U
46	2	827	C
46	2	828	U
46	2	830	U
46	2	831	U
46	2	833	U
46	2	834	G
46	2	835	U
46	2	837	G
46	2	841	U
46	2	842	C
46	2	848	C
46	2	849	C
46	2	850	A
46	2	853	G
46	2	855	A
46	2	856	A
46	2	857	U
46	2	858	G
46	2	859	A
46	2	863	A
46	2	864	U
46	2	865	A
46	2	869	A
46	2	873	U
46	2	888	U
46	2	894	U
46	2	897	C
46	2	898	A
46	2	902	G
46	2	905	A
46	2	906	A
46	2	907	A
46	2	913	G
46	2	920	U
46	2	932	U
46	2	933	A
46	2	934	C

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Mol	Chain	Res	Type
46	2	935	U
46	2	942	G
46	2	951	A
46	2	960	U
46	2	963	A
46	2	964	U
46	2	966	A
46	2	988	A
46	2	990	C
46	2	992	A
46	2	993	A
46	2	1004	U
46	2	1005	A
46	2	1024	U
46	2	1025	A
46	2	1026	A
46	2	1027	A
46	2	1028	C
46	2	1029	U
46	2	1030	A
46	2	1031	U
46	2	1032	G
46	2	1038	U
46	2	1039	A
46	2	1053	G
46	2	1055	U
46	2	1063	U
46	2	1064	G
46	2	1065	A
46	2	1066	C
46	2	1076	A
46	2	1081	A
46	2	1089	U
46	2	1092	A
46	2	1096	C
46	2	1097	U
46	2	1098	U
46	2	1099	U
46	2	1100	G
46	2	1113	A
46	2	1124	A
46	2	1125	A

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Mol	Chain	Res	Type
46	2	1128	C
46	2	1136	U
46	2	1137	A
46	2	1138	A
46	2	1150	G
46	2	1151	A
46	2	1156	C
46	2	1158	C
46	2	1159	C
46	2	1162	C
46	2	1163	A
46	2	1164	G
46	2	1166	A
46	2	1167	G
46	2	1168	U
46	2	1171	A
46	2	1172	G
46	2	1173	C
46	2	1175	U
46	2	1176	G
46	2	1181	U
46	2	1182	U
46	2	1185	U
46	2	1190	C
46	2	1191	U
46	2	1192	C
46	2	1194	A
46	2	1196	A
46	2	1199	G
46	2	1200	G
46	2	1201	G
46	2	1202	A
46	2	1203	A
46	2	1205	C
46	2	1207	C
46	2	1208	A
46	2	1209	C
46	2	1213	G
46	2	1214	U
46	2	1217	A
46	2	1218	G
46	2	1219	A

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Mol	Chain	Res	Type
46	2	1222	C
46	2	1224	A
46	2	1258	U
46	2	1261	G
46	2	1264	G
46	2	1265	G
46	2	1266	U
46	2	1269	U
46	2	1270	G
46	2	1273	G
46	2	1275	A
46	2	1276	U
46	2	1277	G
46	2	1280	C
46	2	1285	U
46	2	1286	U
46	2	1287	A
46	2	1295	G
46	2	1298	U
46	2	1299	G
46	2	1301	U
46	2	1307	U
46	2	1309	C
46	2	1310	U
46	2	1311	U
46	2	1312	A
46	2	1314	U
46	2	1315	U
46	2	1319	A
46	2	1320	U
46	2	1321	A
46	2	1327	C
46	2	1328	G
46	2	1329	A
46	2	1331	A
46	2	1332	C
46	2	1335	U
46	2	1336	A
46	2	1337	A
46	2	1338	C
46	2	1339	C
46	2	1340	U

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Mol	Chain	Res	Type
46	2	1341	A
46	2	1343	U
46	2	1344	A
46	2	1345	A
46	2	1347	U
46	2	1348	A
46	2	1349	G
46	2	1350	U
46	2	1353	U
46	2	1354	G
46	2	1355	C
46	2	1356	U
46	2	1357	A
46	2	1360	A
46	2	1361	U
46	2	1362	U
46	2	1363	U
46	2	1367	G
46	2	1368	G
46	2	1369	U
46	2	1370	U
46	2	1371	A
46	2	1372	U
46	2	1373	C
46	2	1374	C
46	2	1380	U
46	2	1381	U
46	2	1383	G
46	2	1386	G
46	2	1387	G
46	2	1388	A
46	2	1390	U
46	2	1392	U
46	2	1397	U
46	2	1399	C
46	2	1402	G
46	2	1403	C
46	2	1406	A
46	2	1407	U
46	2	1408	G
46	2	1409	G
46	2	1411	A

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Mol	Chain	Res	Type
46	2	1413	U
46	2	1414	U
46	2	1416	G
46	2	1418	G
46	2	1420	C
46	2	1421	A
46	2	1422	A
46	2	1424	A
46	2	1425	A
46	2	1427	A
46	2	1429	G
46	2	1431	C
46	2	1432	U
46	2	1433	G
46	2	1434	U
46	2	1435	G
46	2	1436	A
46	2	1438	G
46	2	1440	C
46	2	1441	C
46	2	1443	U
46	2	1444	A
46	2	1445	G
46	2	1446	A
46	2	1452	U
46	2	1455	G
46	2	1457	C
46	2	1458	G
46	2	1460	A
46	2	1467	C
46	2	1468	U
46	2	1469	A
46	2	1471	A
46	2	1472	C
46	2	1473	U
46	2	1474	G
46	2	1477	G
46	2	1478	G
46	2	1479	A
46	2	1480	G
46	2	1481	C
46	2	1484	G

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Mol	Chain	Res	Type
46	2	1486	G
46	2	1489	U
46	2	1490	C
46	2	1492	A
46	2	1493	A
46	2	1495	C
46	2	1496	U
46	2	1498	G
46	2	1508	U
46	2	1509	C
46	2	1511	U
46	2	1513	G
46	2	1514	U
46	2	1517	U
46	2	1518	C
46	2	1519	U
46	2	1520	U
46	2	1522	U
46	2	1523	G
46	2	1524	A
46	2	1526	A
46	2	1528	U
46	2	1530	C
46	2	1533	C
46	2	1534	G
46	2	1535	U
46	2	1536	G
46	2	1537	C
46	2	1538	U
46	2	1539	G
46	2	1540	G
46	2	1543	A
46	2	1544	U
46	2	1545	A
46	2	1554	U
46	2	1557	U
46	2	1559	A
46	2	1561	U
46	2	1562	G
46	2	1567	U
46	2	1568	C
46	2	1569	A

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Mol	Chain	Res	Type
46	2	1570	A
46	2	1573	A
46	2	1578	U
46	2	1582	U
46	2	1583	A
46	2	1584	G
46	2	1585	U
46	2	1586	A
46	2	1587	A
46	2	1596	C
46	2	1598	U
46	2	1600	A
46	2	1601	G
46	2	1603	U
46	2	1606	C
46	2	1610	G
46	2	1613	U
46	2	1614	A
46	2	1618	C
46	2	1619	C
46	2	1622	G
46	2	1624	C
46	2	1631	A
46	2	1634	C
46	2	1635	A
46	2	1640	C
46	2	1642	G
46	2	1645	G
46	2	1648	A
46	2	1650	U
46	2	1651	A
46	2	1652	C
46	2	1654	G
46	2	1655	A
46	2	1657	U
46	2	1658	G
46	2	1659	A
46	2	1660	A
46	2	1661	U
46	2	1662	G
46	2	1664	C
46	2	1665	U

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Mol	Chain	Res	Type
46	2	1666	U
46	2	1668	G
46	2	1672	G
46	2	1678	A
46	2	1680	G
46	2	1682	U
46	2	1683	C
46	2	1684	U
46	2	1687	U
46	2	1688	U
46	2	1689	A
46	2	1693	A
46	2	1694	A
46	2	1695	G
46	2	1696	G
46	2	1697	G
46	2	1698	G
46	2	1699	G
46	2	1702	A
46	2	1704	U
46	2	1705	C
46	2	1706	C
46	2	1707	A
46	2	1708	U
46	2	1710	U
46	2	1711	C
46	2	1715	G
46	2	1716	C
46	2	1718	G
46	2	1720	G
46	2	1721	A
46	2	1722	A
46	2	1726	G
46	2	1736	G
46	2	1737	G
46	2	1739	C
46	2	1741	U
46	2	1744	A
46	2	1745	G
46	2	1747	G
46	2	1749	A
46	2	1750	A

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Mol	Chain	Res	Type
46	2	1751	C
46	2	1754	A
46	2	1756	A
46	2	1759	C
46	2	1760	G
46	2	1762	A
46	2	1765	A
46	2	1766	A
46	2	1768	G
46	2	1769	U
46	2	1770	U
46	2	1774	G
46	2	1775	U
46	2	1776	A
46	2	1777	G
46	2	1778	G
46	2	1782	A
46	2	1783	C
46	2	1786	G
46	2	1787	C
46	2	1789	G
46	2	1792	G
46	2	1793	G
46	2	1794	A
46	2	1796	C
46	2	1797	A
46	2	1798	U
75	AX	9	A
75	AX	15	G
75	AX	16	U
75	AX	17	U
75	AX	19	G
75	AX	20	G
75	AX	21	A
75	AX	26	G
75	AX	33	U
75	AX	34	G
75	AX	35	A
75	AX	36	A
75	AX	37	G
75	AX	45	G
75	AX	46	G

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Mol	Chain	Res	Type
75	AX	47	U
75	AX	54	U
75	AX	55	U
75	AX	57	G
75	AX	58	A
75	AX	61	C
75	AX	73	A
75	AZ	9	A
75	AZ	15	G
75	AZ	16	U
75	AZ	17	U
75	AZ	19	G
75	AZ	20	G
75	AZ	21	A
75	AZ	25	C
75	AZ	34	G
75	AZ	35	A
75	AZ	36	A
75	AZ	37	G
75	AZ	45	G
75	AZ	46	G
75	AZ	47	U
75	AZ	53	G
75	AZ	55	U
75	AZ	57	G
75	AZ	58	A
75	AZ	61	C
75	AZ	62	A
75	AZ	70	C
75	AZ	73	A

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
28	1	619	A
28	1	734	C
28	1	1763	U
28	1	2506	U
28	1	2530	G
28	1	2543	U
28	1	2874	G
46	2	243	G

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Mol	Chain	Res	Type
46	2	518	A
46	2	537	G
46	2	621	A
46	2	687	G
46	2	904	G
46	2	1181	U
46	2	1366	U
46	2	1406	A
46	2	1585	U
46	2	1665	U
46	2	1748	G
46	2	1755	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 6 ligands modelled in this entry, 6 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

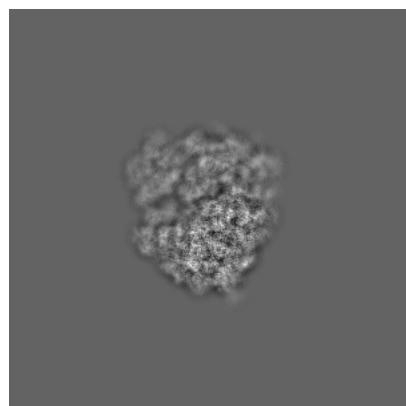
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22198. These allow visual inspection of the internal detail of the map and identification of artifacts.

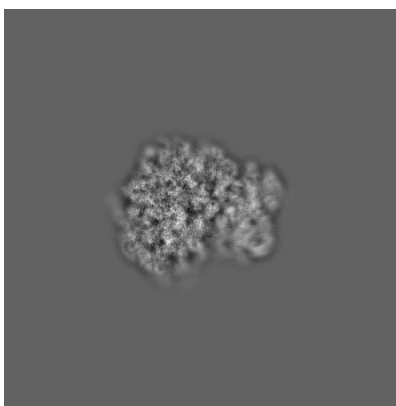
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

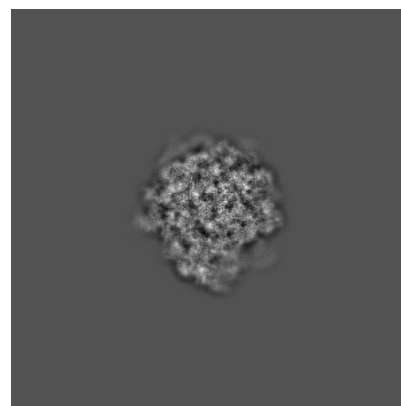
6.1.1 Primary map



X

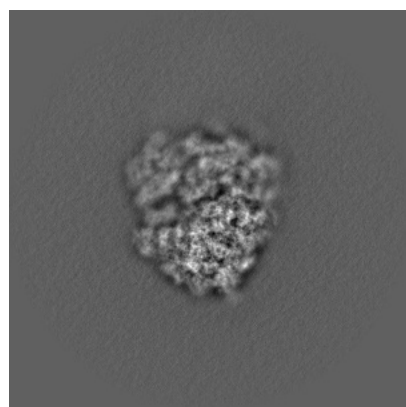


Y

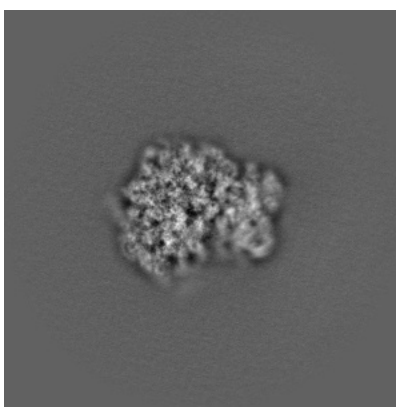


Z

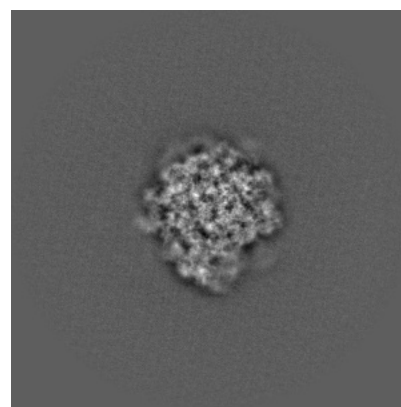
6.1.2 Raw map



X



Y

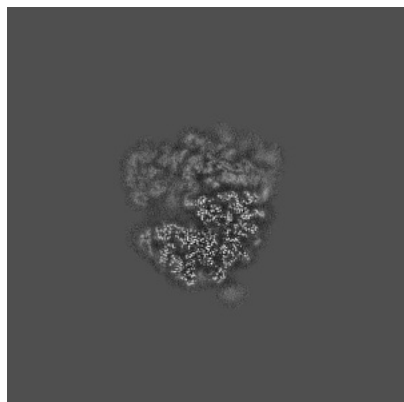


Z

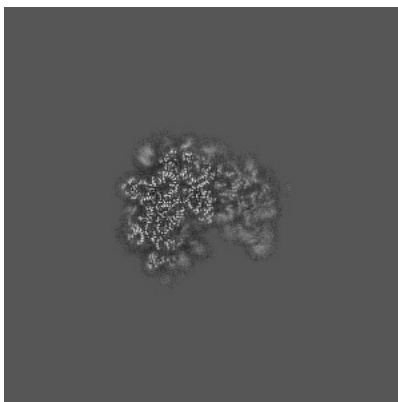
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

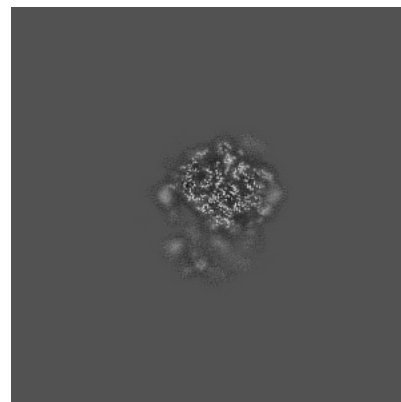
6.2.1 Primary map



X Index: 240

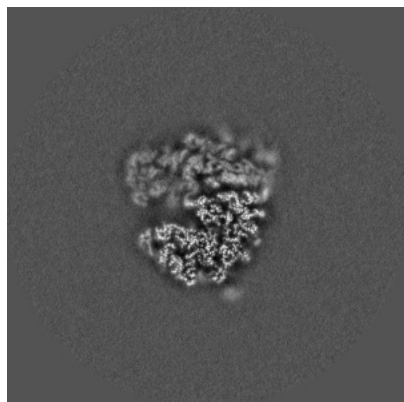


Y Index: 240

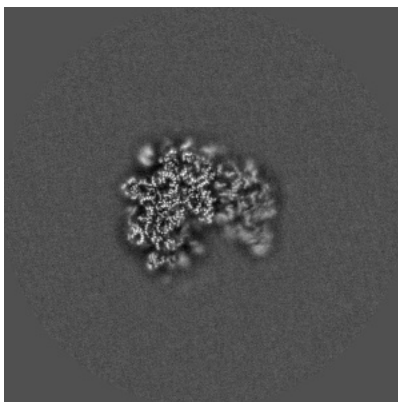


Z Index: 240

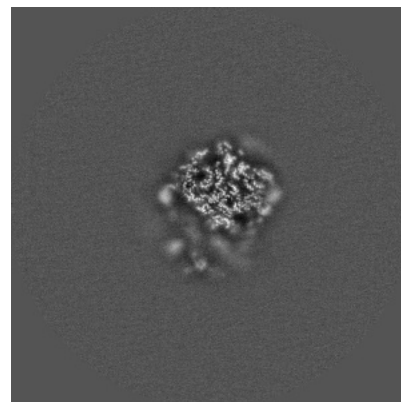
6.2.2 Raw map



X Index: 240



Y Index: 240

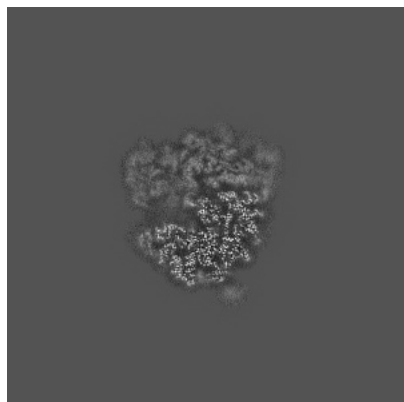


Z Index: 240

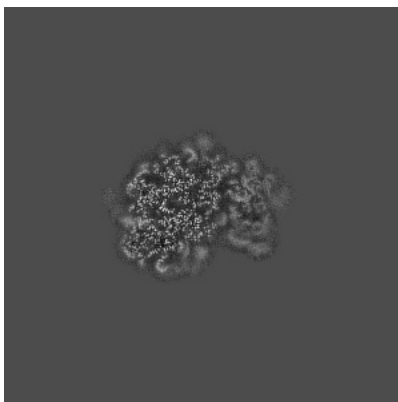
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

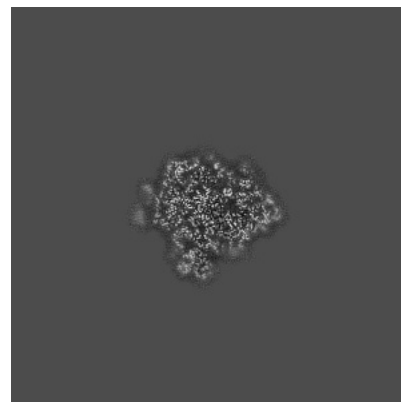
6.3.1 Primary map



X Index: 239

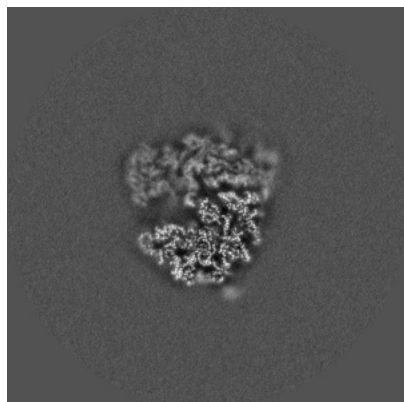


Y Index: 257

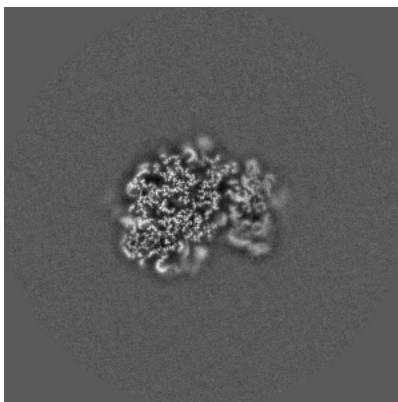


Z Index: 195

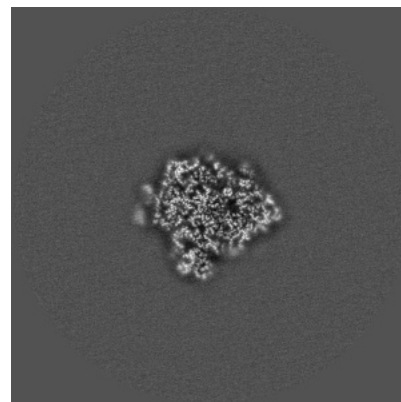
6.3.2 Raw map



X Index: 238



Y Index: 257

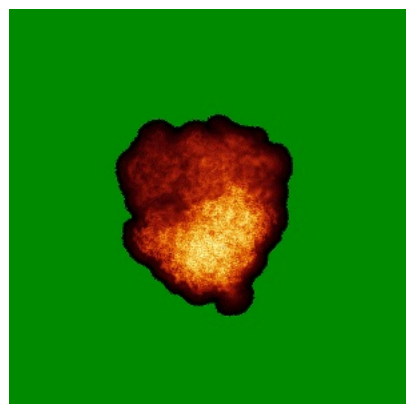


Z Index: 195

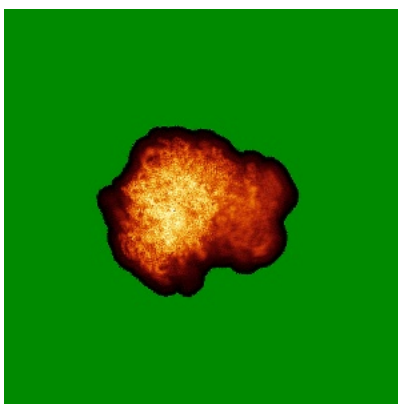
The images above show the largest variance slices of the map in three orthogonal directions.

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

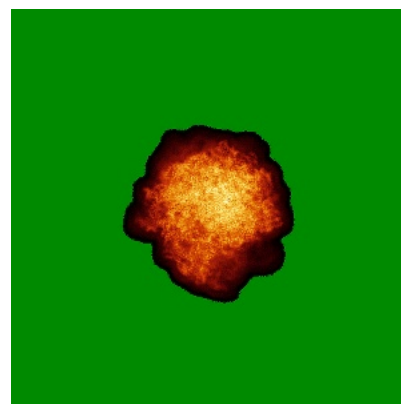
6.4.1 Primary map



X

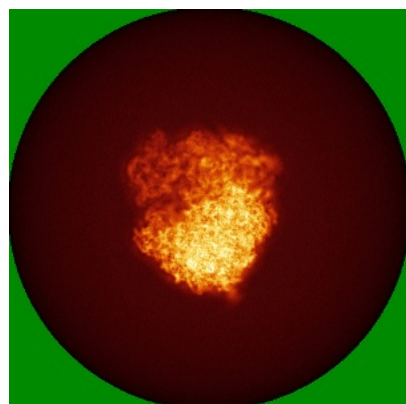


Y

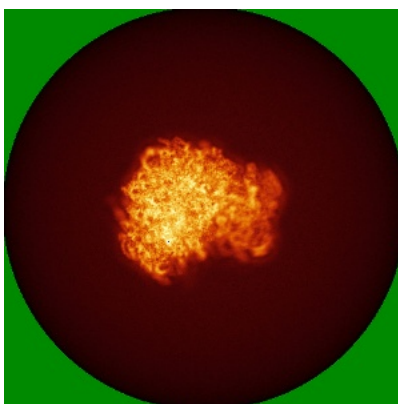


Z

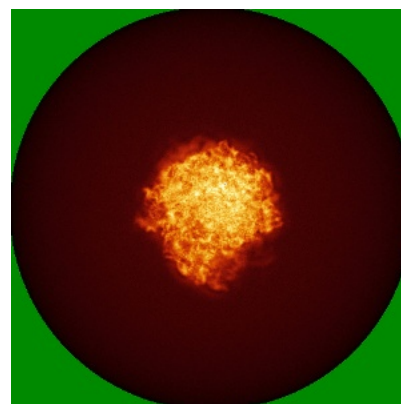
6.4.2 Raw map



X



Y

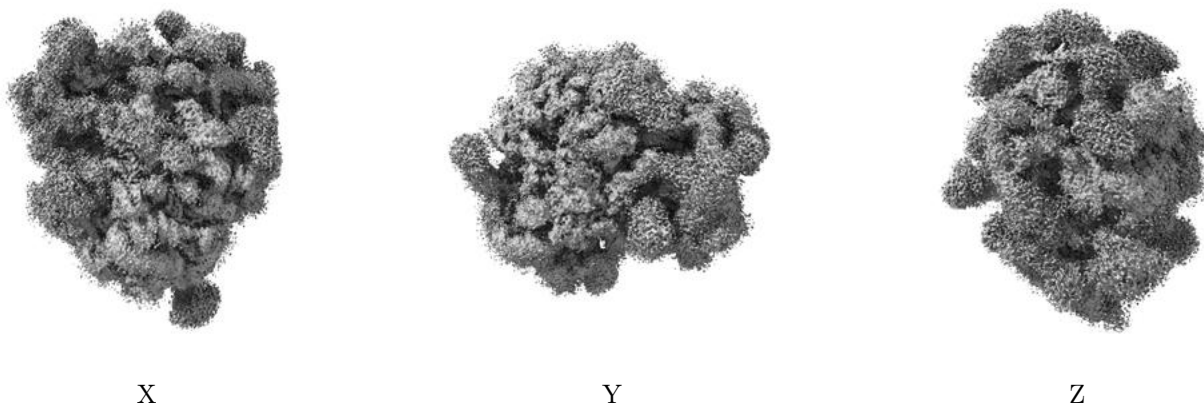


Z

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

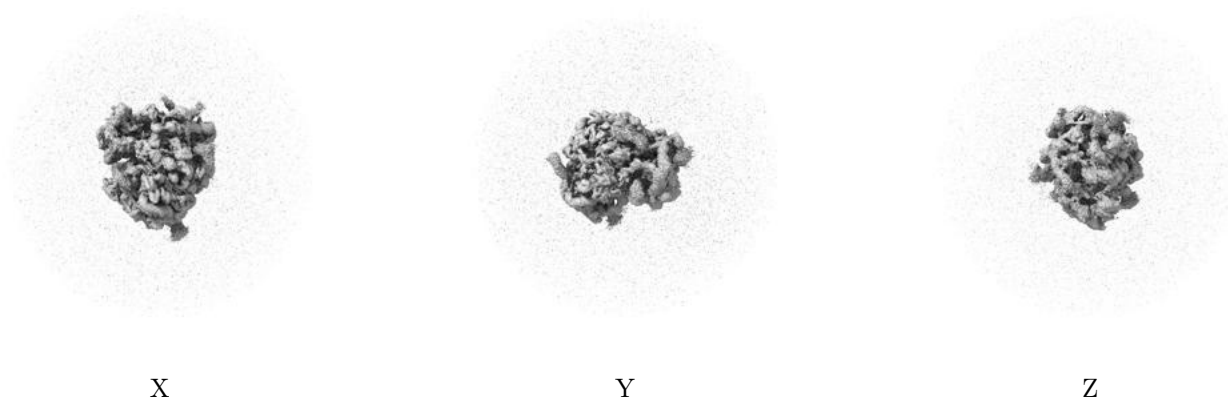
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

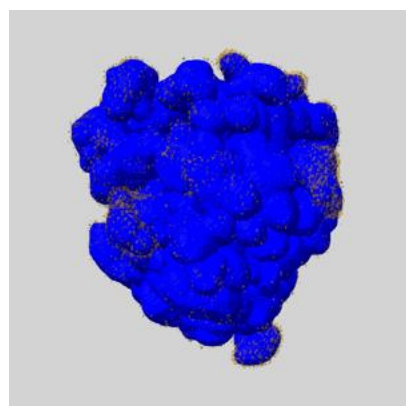
6.6 Mask visualisation [i](#)

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

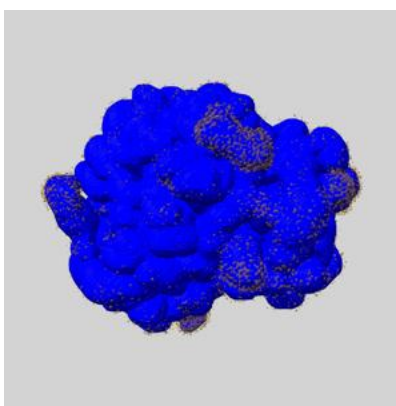
A mask typically either:

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

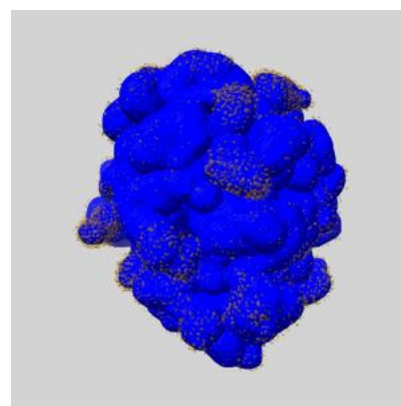
6.6.1 emd_22198_msk_1.map [i](#)



X



Y

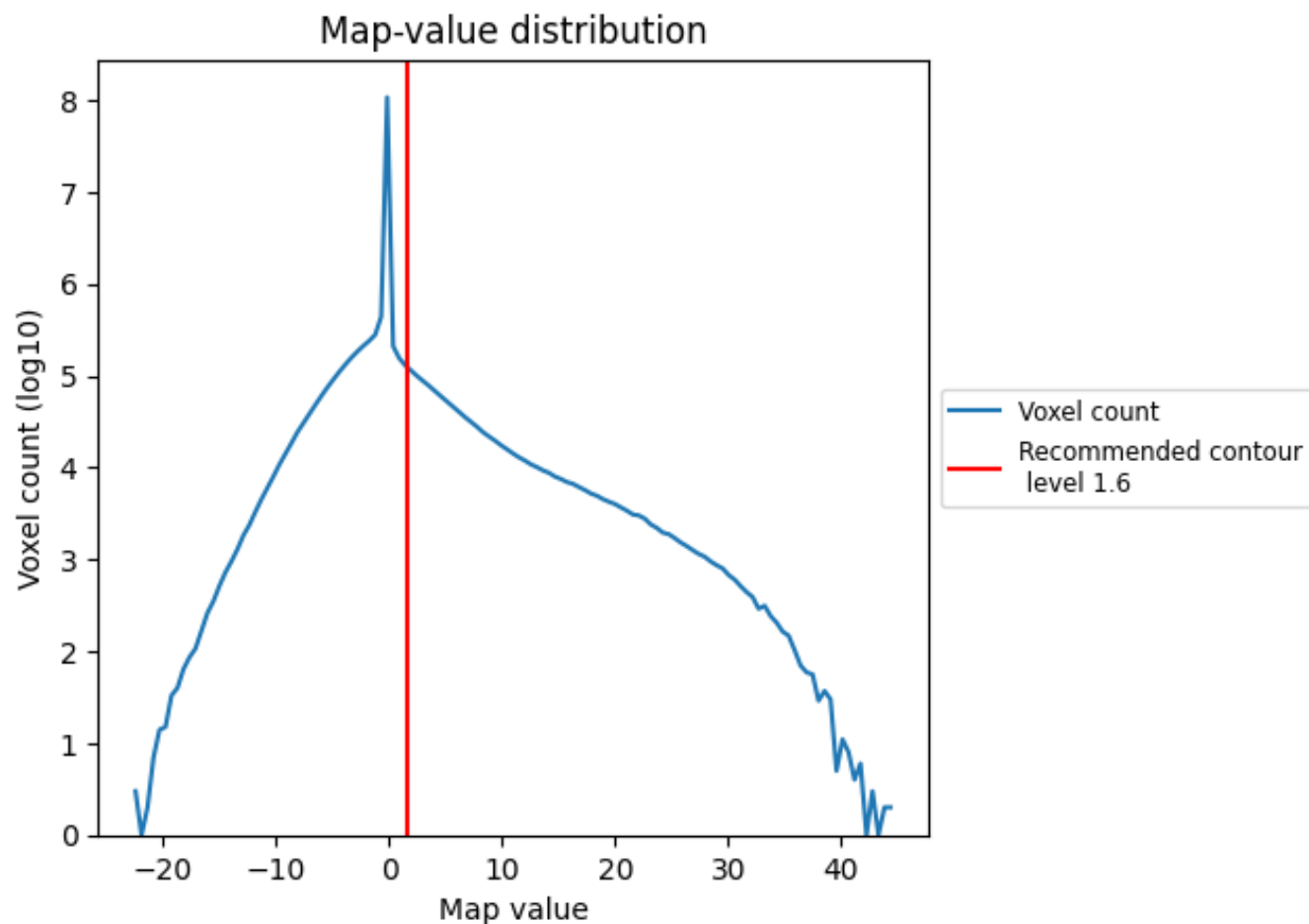


Z

7 Map analysis [i](#)

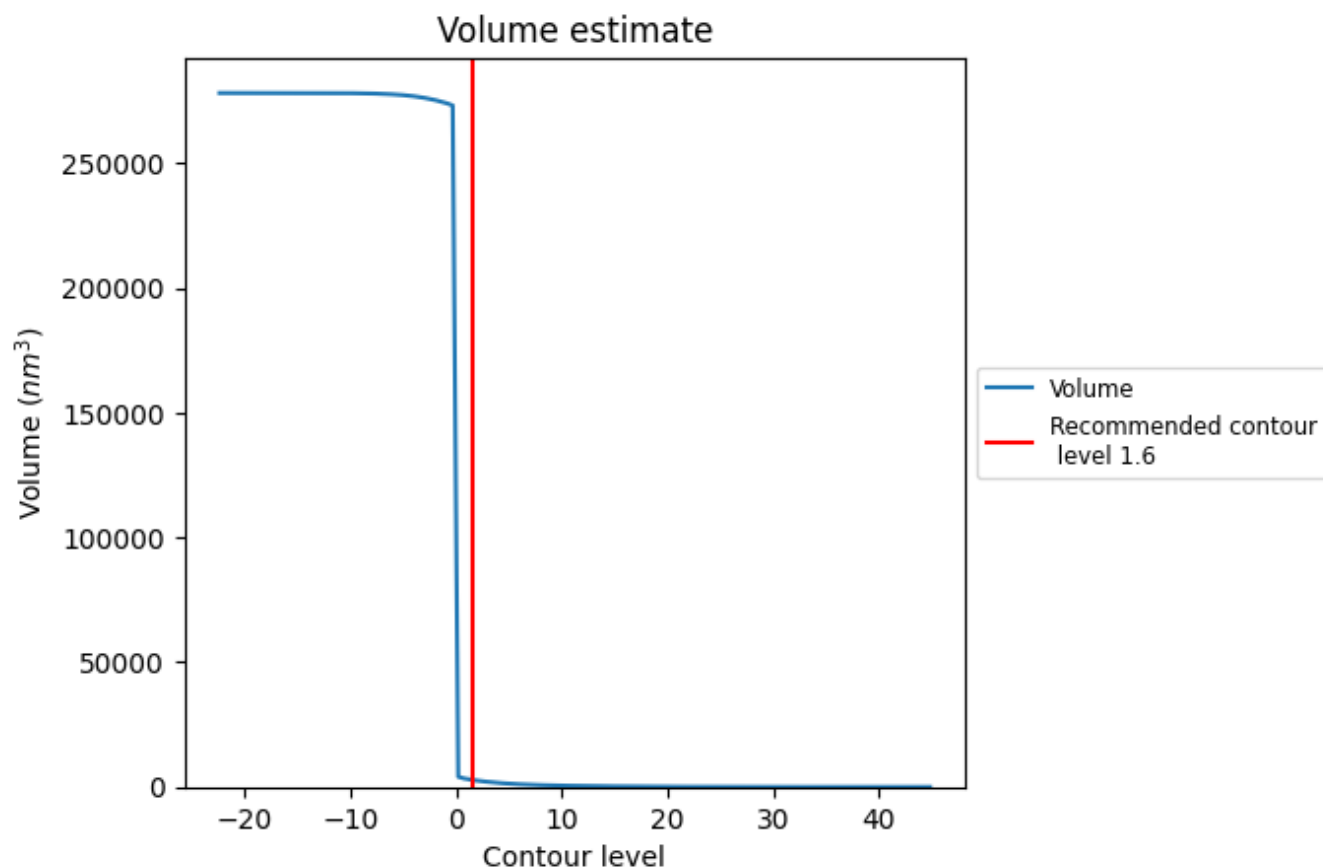
This section contains the results of statistical analysis of the map.

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.

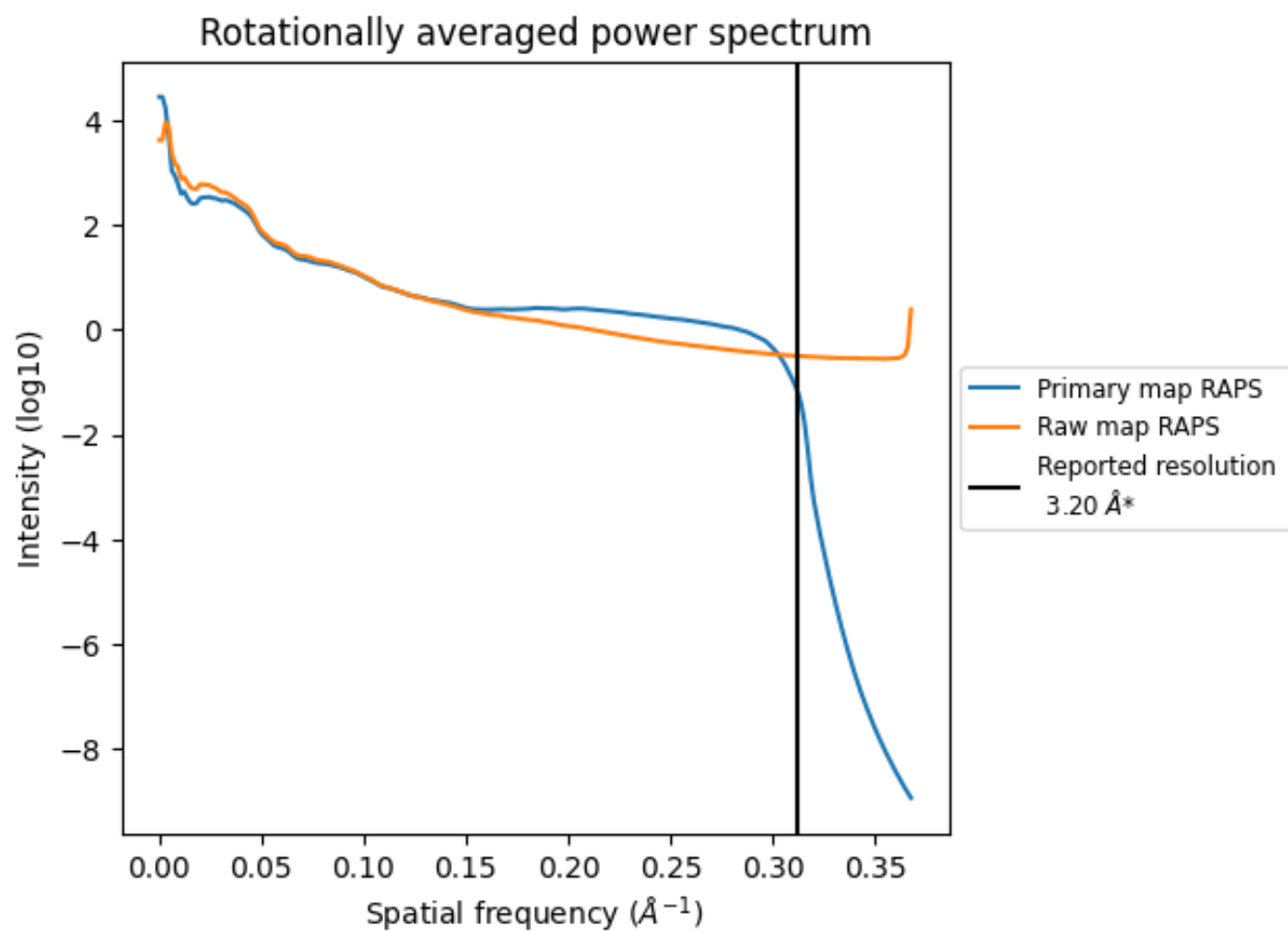
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2788 nm^3 ; this corresponds to an approximate mass of 2518 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 ⓘ

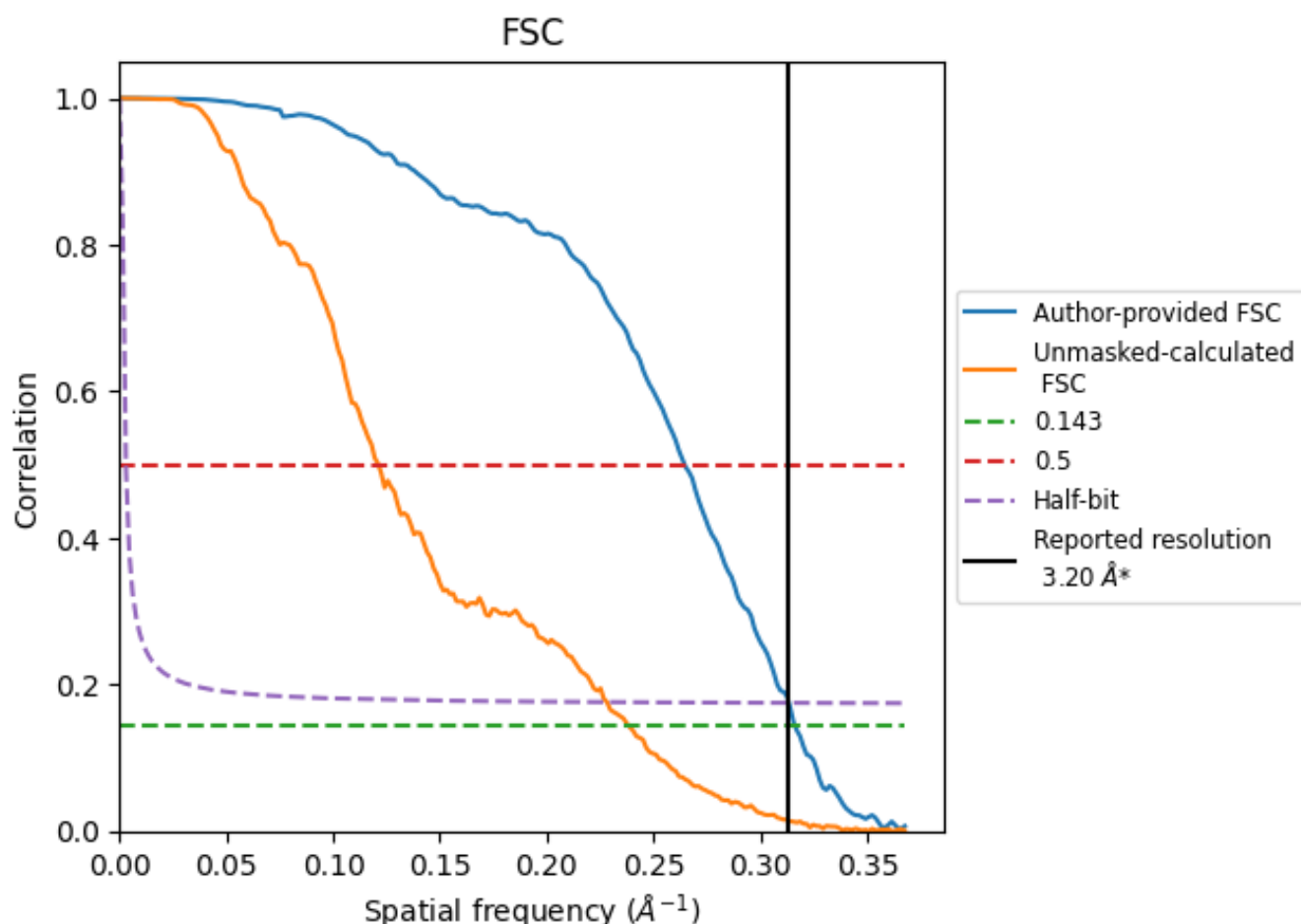


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

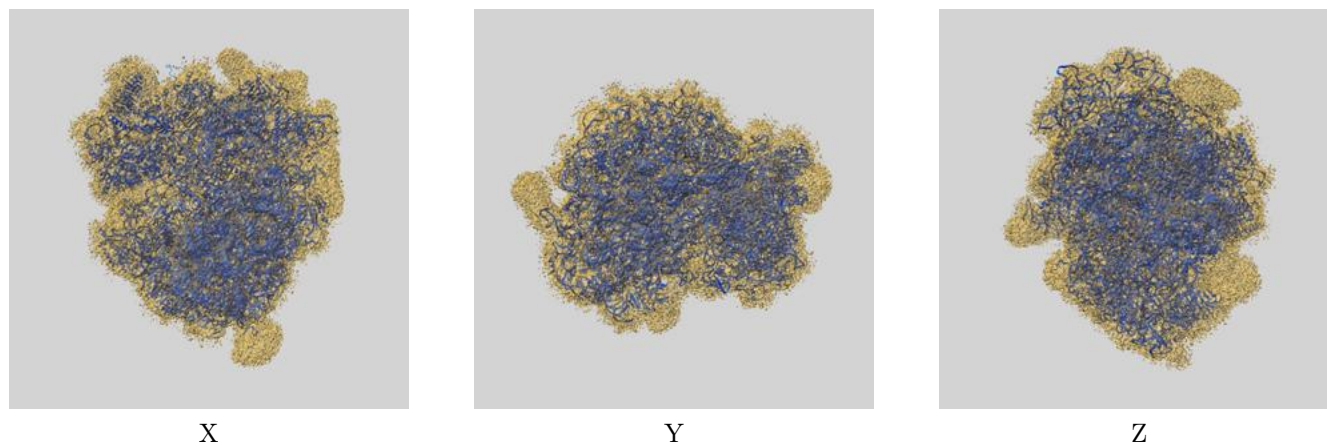
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.16	3.78	3.19
Unmasked-calculated*	4.19	8.25	4.38

*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 4.19 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

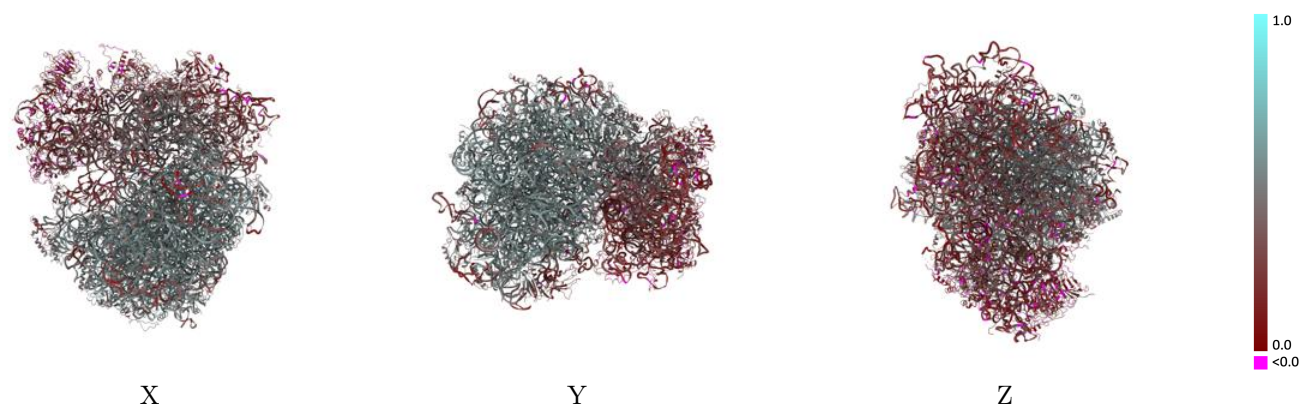
This section contains information regarding the fit between EMDB map EMD-22198 and PDB model 6XIR. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



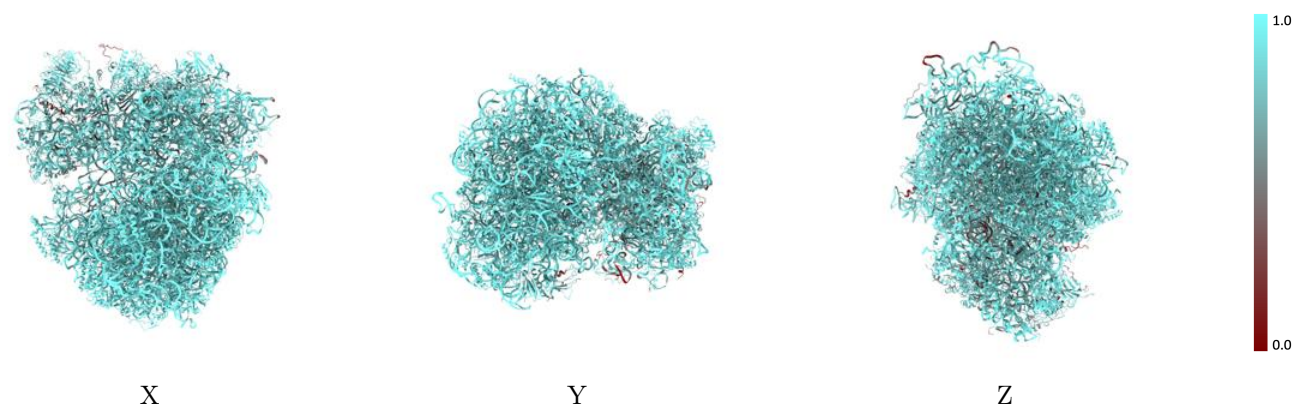
The images above show the 3D surface view of the map at the recommended contour level 1.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



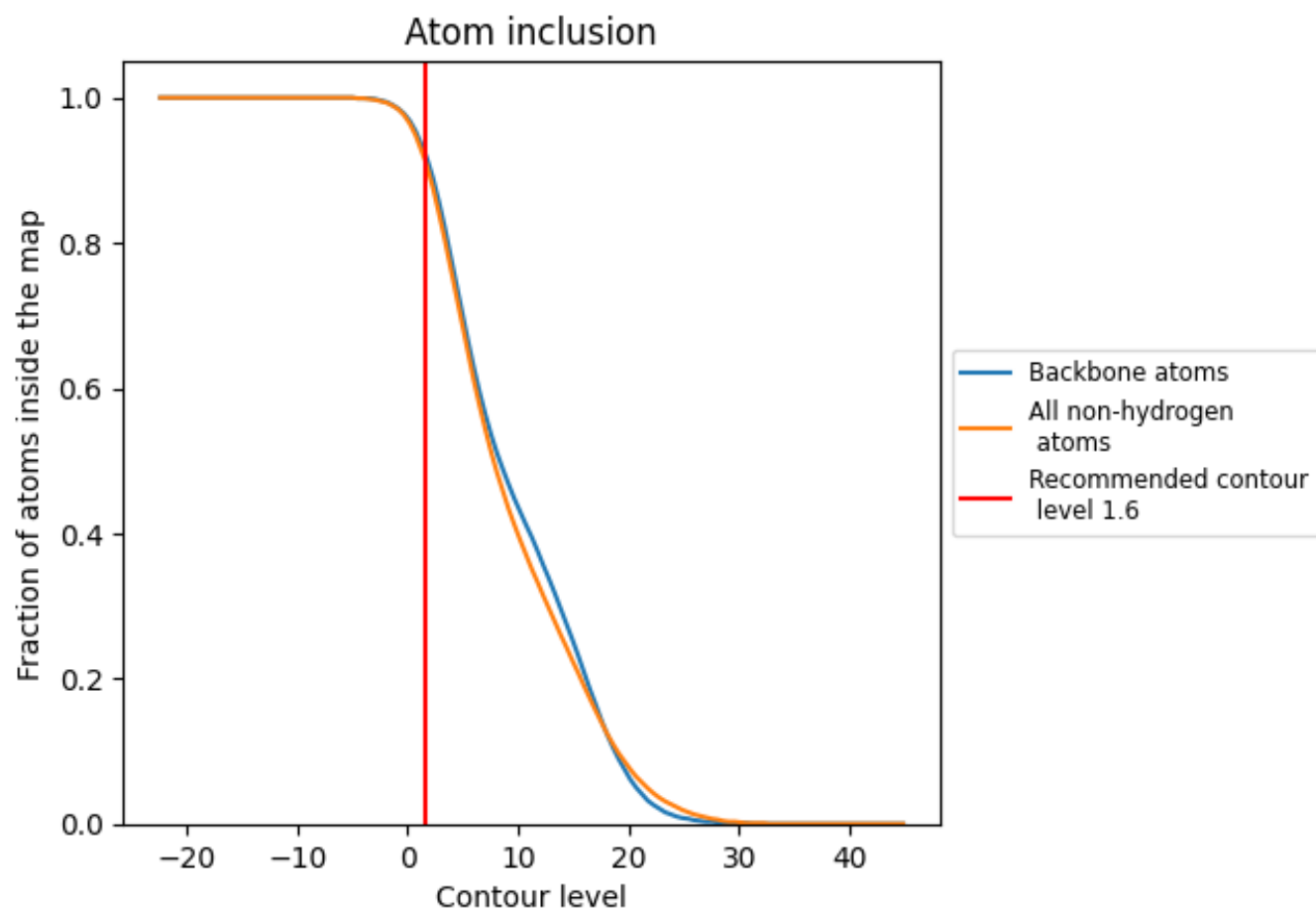
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.6).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 91% 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 (1.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9130	 0.4050
1	 0.9840	 0.4910
2	 0.8980	 0.2740
3	 0.9990	 0.5000
4	 0.9860	 0.5060
A	 0.9030	 0.5470
AA	 0.6560	 0.1760
AB	 0.8470	 0.3740
AD	 0.8620	 0.3890
AE	 0.9050	 0.4360
AF	 0.8630	 0.2210
AG	 0.5970	 0.1940
AH	 0.8430	 0.2600
AI	 0.7090	 0.1080
AJ	 0.8060	 0.2200
AK	 0.6540	 0.1760
AL	 0.8390	 0.3140
AM	 0.7980	 0.3400
AN	 0.5990	 0.2360
AO	 0.8530	 0.2020
AP	 0.8260	 0.2530
AQ	 0.6920	 0.3610
AR	 0.9190	 0.3470
AS	 0.8830	 0.3040
AT	 0.5380	 0.1300
AV	 0.8500	 0.2030
AX	 0.7230	 0.2110
AZ	 0.4880	 0.0760
B	 0.9580	 0.5460
C	 0.9580	 0.5360
D	 0.9340	 0.4330
E	 0.9600	 0.4980
F	 0.9500	 0.5220
G	 0.9290	 0.4670
H	 0.8330	 0.3160



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Chain	Atom inclusion	Q-score
I	 0.8260	 0.4120
J	 0.9490	 0.3660
L	 0.9590	 0.5110
M	 0.9510	 0.4900
N	 0.8970	 0.5520
O	 0.9480	 0.5300
P	 0.8950	 0.5140
Q	 0.9350	 0.5400
R	 0.9490	 0.4830
S	 0.9240	 0.5190
T	 0.9170	 0.5200
U	 0.9800	 0.4540
V	 0.9220	 0.5210
W	 0.9430	 0.5250
X	 0.9400	 0.5310
Y	 0.9660	 0.5190
Z	 0.9530	 0.4440
a	 0.9450	 0.5470
b	 0.8430	 0.4850
c	 0.9630	 0.4700
d	 0.9510	 0.5220
e	 0.9080	 0.5410
f	 0.9510	 0.5560
g	 0.9120	 0.5240
h	 0.9400	 0.4850
i	 0.9210	 0.4660
j	 0.9050	 0.5460
k	 0.9500	 0.4810
l	 0.8460	 0.5280
n	 0.4470	 0.0030
o	 0.8430	 0.5010
p	 0.9420	 0.5170
q	 0.8170	 0.2390
r	 0.9050	 0.3870
s	 0.7770	 0.2580
t	 0.7410	 0.2330
u	 0.7800	 0.2230
v	 0.8290	 0.3060
w	 0.6810	 0.2230
x	 0.9070	 0.2580
y	 0.8230	 0.2900
z	 0.7790	 0.2110